



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 20, 2017 – 01:05 AM EST

PDB ID : 5DGE
Title : Coping with proline stalling: structural basis of hypusine-induced protein synthesis by the eukaryotic ribosome
Authors : Melnikov, S.; Mailliot, J.; Shin, B.-S.; Rigger, L.; Yusupova, G.; Micura, R.; Dever, T.E.; Yusupov, M.
Deposited on : 2015-08-27
Resolution : 3.45 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028442

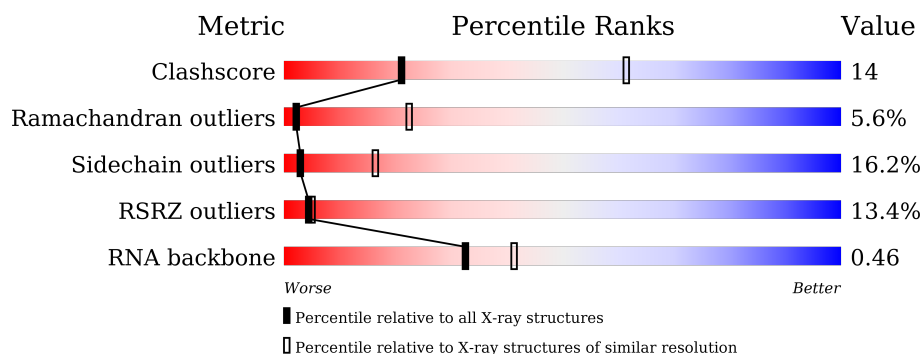
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.45 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1090 (3.56-3.36)
Ramachandran outliers	100387	1057 (3.56-3.36)
Sidechain outliers	100360	1058 (3.56-3.36)
RSRZ outliers	91569	1005 (3.56-3.36)
RNA backbone	2183	1045 (4.10-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	2	1800	<div> <div>6%</div> <div>38%</div> <div>46%</div> <div>14%</div> <div>..</div> </div>
1	6	1800	<div> <div>3%</div> <div>39%</div> <div>45%</div> <div>15%</div> <div>.</div> </div>
2	S0	251	<div> <div>25%</div> <div>26%</div> <div>45%</div> <div>10%</div> <div>18%</div> </div>
2	s0	251	<div> <div>8%</div> <div>63%</div> <div>18%</div> <div>.</div> <div>18%</div> </div>
3	S1	254	<div> <div>31%</div> <div>24%</div> <div>46%</div> <div>13%</div> <div>.</div> <div>16%</div> </div>
3	s1	254	<div> <div>14%</div> <div>67%</div> <div>19%</div> <div>15%</div> </div>

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Mol	Chain	Length	Quality of chain
4	S2	253	
4	s2	253	
5	S3	239	
5	s3	239	
6	S4	260	
6	s4	260	
7	S5	224	
7	s5	224	
8	S6	236	
8	s6	236	
9	S7	189	
9	s7	189	
10	S8	200	
10	s8	200	
11	S9	196	
11	s9	196	
12	C0	105	
12	c0	105	
13	C1	155	
13	c1	155	
14	C2	142	
14	c2	142	
15	C3	150	
15	c3	150	
16	C4	136	

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Mol	Chain	Length	Quality of chain
16	c4	136	
17	C5	141	
17	c5	141	
18	C6	142	
18	c6	142	
19	C7	136	
19	c7	136	
20	C8	145	
20	c8	145	
21	C9	143	
21	c9	143	
22	D0	120	
22	d0	120	
23	D1	87	
23	d1	87	
24	D2	129	
24	d2	129	
25	D3	144	
25	d3	144	
26	D4	134	
26	d4	134	
27	D5	107	
27	d5	107	
28	D6	97	
28	d6	97	

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Mol	Chain	Length	Quality of chain
29	D7	81	
29	d7	81	
30	D8	66	
30	d8	66	
31	D9	55	
31	d9	55	
32	E0	60	
33	E1	76	
33	e1	76	
34	SR	318	
34	sR	318	
35	SM	273	
35	sM	273	
36	1	3396	
36	5	3396	
37	3	121	
37	7	121	
38	4	158	
38	8	158	
39	L2	253	
39	l2	253	
40	L3	386	
40	l3	386	
41	L4	361	
41	l4	361	

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Mol	Chain	Length	Quality of chain
42	L5	296	
42	l5	296	
43	L6	175	
43	l6	175	
44	L7	243	
44	l7	243	
45	L8	255	
45	l8	255	
46	L9	191	
46	l9	191	
47	M0	220	
47	m0	220	
48	M1	173	
48	m1	173	
49	M3	198	
49	m3	198	
50	M4	137	
50	m4	137	
51	M5	203	
51	m5	203	
52	M6	198	
52	m6	198	
53	M7	183	
53	m7	183	
54	M8	185	

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Mol	Chain	Length	Quality of chain
54	m8	185	
55	M9	188	
55	m9	188	
56	N0	172	
56	n0	172	
57	N1	159	
57	n1	159	
58	N2	120	
58	n2	120	
59	N3	136	
59	n3	136	
60	N4	155	
60	n4	155	
61	N5	141	
61	n5	141	
62	N6	126	
62	n6	126	
63	N7	135	
63	n7	135	
64	N8	148	
64	n8	148	
65	N9	58	
65	n9	58	
66	O0	104	
66	o0	104	

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Mol	Chain	Length	Quality of chain
67	O1	112	
67	o1	112	
68	O2	129	
68	o2	129	
69	O3	106	
69	o3	106	
70	O4	119	
70	o4	119	
71	O5	119	
71	o5	119	
72	O6	99	
72	o6	99	
73	O7	87	
73	o7	87	
74	O8	77	
74	o8	77	
75	O9	50	
75	o9	50	
76	Q0	52	
76	q0	52	
77	Q1	25	
77	q1	25	
78	Q2	105	
78	q2	105	
79	Q3	91	

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Mol	Chain	Length	Quality of chain
79	q3	91	
80	e0	62	
81	m2	165	
82	p0	311	
83	p1	106	
83	p2	106	
84	f	157	
85	B	4	
85	C	4	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
84	5CT	f	51	X	-	-	-
86	MG	1	3401	-	-	-	X
86	MG	1	3403	-	-	-	X
86	MG	1	3406	-	-	-	X
86	MG	1	3407	-	-	-	X
86	MG	1	3413	-	-	-	X
86	MG	1	3414	-	-	-	X
86	MG	1	3415	-	-	-	X
86	MG	1	3419	-	-	-	X
86	MG	1	3422	-	-	-	X
86	MG	1	3426	-	-	-	X
86	MG	1	3429	-	-	-	X
86	MG	1	3433	-	-	-	X
86	MG	1	3437	-	-	-	X
86	MG	1	3440	-	-	-	X
86	MG	1	3441	-	-	-	X
86	MG	1	3448	-	-	-	X
86	MG	1	3454	-	-	-	X
86	MG	1	3464	-	-	-	X
86	MG	1	3465	-	-	-	X
86	MG	1	3466	-	-	-	X
86	MG	1	3467	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
86	MG	1	3469	-	-	-	X
86	MG	1	3472	-	-	-	X
86	MG	1	3476	-	-	-	X
86	MG	1	3477	-	-	-	X
86	MG	1	3479	-	-	-	X
86	MG	1	3481	-	-	-	X
86	MG	1	3482	-	-	-	X
86	MG	1	3488	-	-	-	X
86	MG	1	3490	-	-	-	X
86	MG	1	3495	-	-	-	X
86	MG	1	3496	-	-	-	X
86	MG	1	3497	-	-	-	X
86	MG	1	3498	-	-	-	X
86	MG	1	3501	-	-	-	X
86	MG	1	3506	-	-	-	X
86	MG	1	3507	-	-	-	X
86	MG	1	3509	-	-	-	X
86	MG	1	3511	-	-	-	X
86	MG	1	3516	-	-	-	X
86	MG	1	3517	-	-	-	X
86	MG	1	3523	-	-	-	X
86	MG	1	3524	-	-	-	X
86	MG	1	3527	-	-	-	X
86	MG	1	3530	-	-	-	X
86	MG	1	3531	-	-	-	X
86	MG	1	3538	-	-	-	X
86	MG	1	3539	-	-	-	X
86	MG	1	3540	-	-	-	X
86	MG	1	3545	-	-	-	X
86	MG	1	3546	-	-	-	X
86	MG	1	3554	-	-	-	X
86	MG	1	3555	-	-	-	X
86	MG	1	3556	-	-	-	X
86	MG	1	3557	-	-	-	X
86	MG	1	3559	-	-	-	X
86	MG	1	3560	-	-	-	X
86	MG	1	3561	-	-	-	X
86	MG	1	3562	-	-	-	X
86	MG	1	3563	-	-	-	X
86	MG	1	3567	-	-	-	X
86	MG	1	3570	-	-	-	X
86	MG	1	3572	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
86	MG	1	3573	-	-	-	X
86	MG	1	3575	-	-	-	X
86	MG	1	3576	-	-	-	X
86	MG	1	3578	-	-	-	X
86	MG	1	3580	-	-	-	X
86	MG	1	3582	-	-	-	X
86	MG	1	3583	-	-	-	X
86	MG	1	3585	-	-	-	X
86	MG	1	3586	-	-	-	X
86	MG	1	3587	-	-	-	X
86	MG	1	3588	-	-	-	X
86	MG	1	3589	-	-	-	X
86	MG	1	3609	-	-	-	X
86	MG	1	3618	-	-	-	X
86	MG	1	3627	-	-	-	X
86	MG	1	3642	-	-	-	X
86	MG	1	3653	-	-	-	X
86	MG	1	3661	-	-	-	X
86	MG	1	3664	-	-	-	X
86	MG	1	3668	-	-	-	X
86	MG	1	3670	-	-	-	X
86	MG	1	3681	-	-	-	X
86	MG	1	3687	-	-	-	X
86	MG	1	3696	-	-	-	X
86	MG	1	3705	-	-	-	X
86	MG	1	3715	-	-	-	X
86	MG	1	3719	-	-	-	X
86	MG	1	3732	-	-	-	X
86	MG	1	3735	-	-	-	X
86	MG	1	3737	-	-	-	X
86	MG	1	3738	-	-	-	X
86	MG	1	3739	-	-	-	X
86	MG	1	3742	-	-	-	X
86	MG	1	3743	-	-	-	X
86	MG	1	3756	-	-	-	X
86	MG	1	3757	-	-	-	X
86	MG	1	4112	-	-	-	X
86	MG	1	4115	-	-	-	X
86	MG	1	4116	-	-	-	X
86	MG	2	1909	-	-	-	X
86	MG	2	1910	-	-	-	X
86	MG	2	1911	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
86	MG	2	1912	-	-	-	X
86	MG	2	1920	-	-	-	X
86	MG	2	1922	-	-	-	X
86	MG	2	1926	-	-	-	X
86	MG	2	1931	-	-	-	X
86	MG	2	1932	-	-	-	X
86	MG	2	1937	-	-	-	X
86	MG	2	1938	-	-	-	X
86	MG	2	1950	-	-	-	X
86	MG	2	1962	-	-	-	X
86	MG	2	1975	-	-	-	X
86	MG	2	1981	-	-	-	X
86	MG	2	1989	-	-	-	X
86	MG	3	204	-	-	-	X
86	MG	4	207	-	-	-	X
86	MG	4	233	-	-	-	X
86	MG	5	3403	-	-	-	X
86	MG	5	3405	-	-	-	X
86	MG	5	3407	-	-	-	X
86	MG	5	3409	-	-	-	X
86	MG	5	3412	-	-	-	X
86	MG	5	3413	-	-	-	X
86	MG	5	3416	-	-	-	X
86	MG	5	3419	-	-	-	X
86	MG	5	3420	-	-	-	X
86	MG	5	3421	-	-	-	X
86	MG	5	3426	-	-	-	X
86	MG	5	3428	-	-	-	X
86	MG	5	3436	-	-	-	X
86	MG	5	3440	-	-	-	X
86	MG	5	3451	-	-	-	X
86	MG	5	3455	-	-	-	X
86	MG	5	3456	-	-	-	X
86	MG	5	3457	-	-	-	X
86	MG	5	3462	-	-	-	X
86	MG	5	3465	-	-	-	X
86	MG	5	3471	-	-	-	X
86	MG	5	3472	-	-	-	X
86	MG	5	3491	-	-	-	X
86	MG	5	3493	-	-	-	X
86	MG	5	3495	-	-	-	X
86	MG	5	3497	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
86	MG	5	3501	-	-	-	X
86	MG	5	3505	-	-	-	X
86	MG	5	3506	-	-	-	X
86	MG	5	3507	-	-	-	X
86	MG	5	3508	-	-	-	X
86	MG	5	3512	-	-	-	X
86	MG	5	3513	-	-	-	X
86	MG	5	3517	-	-	-	X
86	MG	5	3519	-	-	-	X
86	MG	5	3521	-	-	-	X
86	MG	5	3522	-	-	-	X
86	MG	5	3527	-	-	-	X
86	MG	5	3530	-	-	-	X
86	MG	5	3537	-	-	-	X
86	MG	5	3541	-	-	-	X
86	MG	5	3543	-	-	-	X
86	MG	5	3544	-	-	-	X
86	MG	5	3545	-	-	-	X
86	MG	5	3546	-	-	-	X
86	MG	5	3550	-	-	-	X
86	MG	5	3553	-	-	-	X
86	MG	5	3555	-	-	-	X
86	MG	5	3556	-	-	-	X
86	MG	5	3560	-	-	-	X
86	MG	5	3561	-	-	-	X
86	MG	5	3563	-	-	-	X
86	MG	5	3564	-	-	-	X
86	MG	5	3565	-	-	-	X
86	MG	5	3566	-	-	-	X
86	MG	5	3569	-	-	-	X
86	MG	5	3570	-	-	-	X
86	MG	5	3577	-	-	-	X
86	MG	5	3581	-	-	-	X
86	MG	5	3582	-	-	-	X
86	MG	5	3584	-	-	-	X
86	MG	5	3585	-	-	-	X
86	MG	5	3586	-	-	-	X
86	MG	5	3588	-	-	-	X
86	MG	5	3589	-	-	-	X
86	MG	5	3590	-	-	-	X
86	MG	5	3591	-	-	-	X
86	MG	5	3592	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
86	MG	5	3593	-	-	-	X
86	MG	5	3594	-	-	-	X
86	MG	5	3596	-	-	-	X
86	MG	5	3597	-	-	-	X
86	MG	5	3599	-	-	-	X
86	MG	5	3601	-	-	-	X
86	MG	5	3606	-	-	-	X
86	MG	5	3617	-	-	-	X
86	MG	5	3638	-	-	-	X
86	MG	5	3643	-	-	-	X
86	MG	5	3644	-	-	-	X
86	MG	5	3651	-	-	-	X
86	MG	5	3654	-	-	-	X
86	MG	5	3656	-	-	-	X
86	MG	5	3672	-	-	-	X
86	MG	5	3674	-	-	-	X
86	MG	5	3677	-	-	-	X
86	MG	5	3678	-	-	-	X
86	MG	5	3680	-	-	-	X
86	MG	5	3682	-	-	-	X
86	MG	5	3686	-	-	-	X
86	MG	5	3705	-	-	-	X
86	MG	5	3717	-	-	-	X
86	MG	5	3719	-	-	-	X
86	MG	5	3720	-	-	-	X
86	MG	5	3729	-	-	-	X
86	MG	5	3735	-	-	-	X
86	MG	5	3737	-	-	-	X
86	MG	5	3741	-	-	-	X
86	MG	5	3744	-	-	-	X
86	MG	5	3767	-	-	-	X
86	MG	5	3769	-	-	-	X
86	MG	5	3774	-	-	-	X
86	MG	5	3779	-	-	-	X
86	MG	5	3783	-	-	-	X
86	MG	5	3785	-	-	-	X
86	MG	5	3794	-	-	-	X
86	MG	5	3796	-	-	-	X
86	MG	5	3800	-	-	-	X
86	MG	5	4172	-	-	-	X
86	MG	5	4174	-	-	-	X
86	MG	5	4175	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
86	MG	5	4176	-	-	-	X
86	MG	6	1901	-	-	-	X
86	MG	6	1904	-	-	-	X
86	MG	6	1906	-	-	-	X
86	MG	6	1910	-	-	-	X
86	MG	6	1915	-	-	-	X
86	MG	6	1918	-	-	-	X
86	MG	6	1923	-	-	-	X
86	MG	6	1925	-	-	-	X
86	MG	6	1929	-	-	-	X
86	MG	6	1933	-	-	-	X
86	MG	6	1938	-	-	-	X
86	MG	6	1943	-	-	-	X
86	MG	6	1944	-	-	-	X
86	MG	6	1951	-	-	-	X
86	MG	6	1952	-	-	-	X
86	MG	6	1966	-	-	-	X
86	MG	6	1968	-	-	-	X
86	MG	6	1974	-	-	-	X
86	MG	6	1975	-	-	-	X
86	MG	6	1978	-	-	-	X
86	MG	6	1981	-	-	-	X
86	MG	6	1990	-	-	-	X
86	MG	6	2005	-	-	-	X
86	MG	6	2006	-	-	-	X
86	MG	6	2010	-	-	-	X
86	MG	7	203	-	-	-	X
86	MG	8	203	-	-	-	X
86	MG	8	206	-	-	-	X
86	MG	B	103	-	-	-	X
86	MG	C	102	-	-	-	X
86	MG	L2	302	-	-	-	X
86	MG	L7	302	-	-	-	X
86	MG	M7	202	-	-	-	X
86	MG	N3	201	-	-	-	X
86	MG	O7	102	-	-	-	X
86	MG	d2	201	-	-	-	X
86	MG	d6	102	-	-	-	X
86	MG	l2	301	-	-	-	X
86	MG	l2	302	-	-	-	X
86	MG	l3	402	-	-	-	X
86	MG	m5	301	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
86	MG	m7	201	-	-	-	X
86	MG	n3	201	-	-	-	X
86	MG	n6	201	-	-	-	X
86	MG	n8	201	-	-	-	X
86	MG	s8	302	-	-	-	X
87	OHX	1	3778	-	-	-	X
87	OHX	1	3782	-	-	-	X
87	OHX	1	3784	-	-	-	X
87	OHX	1	3786	-	-	-	X
87	OHX	1	3791	-	-	-	X
87	OHX	1	3793	-	-	-	X
87	OHX	1	3794	-	-	-	X
87	OHX	1	3798	-	-	-	X
87	OHX	1	3800	-	-	-	X
87	OHX	1	3807	-	-	-	X
87	OHX	1	3808	-	-	-	X
87	OHX	1	3815	-	-	-	X
87	OHX	1	3820	-	-	-	X
87	OHX	1	3822	-	-	-	X
87	OHX	1	3825	-	-	-	X
87	OHX	1	3830	-	-	-	X
87	OHX	1	3834	-	-	-	X
87	OHX	1	3835	-	-	-	X
87	OHX	1	3838	-	-	-	X
87	OHX	1	3841	-	-	-	X
87	OHX	1	3843	-	-	-	X
87	OHX	1	3846	-	-	-	X
87	OHX	1	3849	-	-	-	X
87	OHX	1	3853	-	-	-	X
87	OHX	1	3854	-	-	X	-
87	OHX	1	3856	-	-	-	X
87	OHX	1	3859	-	-	-	X
87	OHX	1	3871	-	-	-	X
87	OHX	1	3874	-	-	-	X
87	OHX	1	3875	-	-	-	X
87	OHX	1	3876	-	-	-	X
87	OHX	1	3879	-	-	-	X
87	OHX	1	3883	-	-	-	X
87	OHX	1	3884	-	-	-	X
87	OHX	1	3885	-	-	-	X
87	OHX	1	3886	-	-	-	X
87	OHX	1	3887	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
87	OHX	1	3888	-	-	-	X
87	OHX	1	3889	-	-	X	-
87	OHX	1	3890	-	-	-	X
87	OHX	1	3896	-	-	-	X
87	OHX	1	3897	-	-	-	X
87	OHX	1	3898	-	-	-	X
87	OHX	1	3899	-	-	-	X
87	OHX	1	3903	-	-	-	X
87	OHX	1	3906	-	-	-	X
87	OHX	1	3911	-	-	-	X
87	OHX	1	3915	-	-	-	X
87	OHX	1	3920	-	-	-	X
87	OHX	1	3923	-	-	-	X
87	OHX	1	3936	-	-	-	X
87	OHX	1	3938	-	-	-	X
87	OHX	1	3939	-	-	-	X
87	OHX	1	3940	-	-	X	-
87	OHX	1	3947	-	-	-	X
87	OHX	1	3955	-	-	-	X
87	OHX	1	3962	-	-	-	X
87	OHX	1	3963	-	-	-	X
87	OHX	1	3966	-	-	-	X
87	OHX	1	3968	-	-	-	X
87	OHX	1	3971	-	-	-	X
87	OHX	1	3976	-	-	-	X
87	OHX	1	3983	-	-	-	X
87	OHX	1	3985	-	-	-	X
87	OHX	1	3992	-	-	-	X
87	OHX	1	3993	-	-	-	X
87	OHX	1	4000	-	-	-	X
87	OHX	1	4003	-	-	-	X
87	OHX	1	4004	-	-	-	X
87	OHX	1	4005	-	-	-	X
87	OHX	1	4006	-	-	-	X
87	OHX	1	4008	-	-	-	X
87	OHX	1	4010	-	-	-	X
87	OHX	1	4015	-	-	-	X
87	OHX	1	4016	-	-	-	X
87	OHX	1	4024	-	-	-	X
87	OHX	1	4027	-	-	-	X
87	OHX	1	4030	-	-	-	X
87	OHX	1	4032	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
87	OHX	1	4038	-	-	-	X
87	OHX	1	4043	-	-	-	X
87	OHX	1	4048	-	-	-	X
87	OHX	1	4058	-	-	-	X
87	OHX	1	4062	-	-	-	X
87	OHX	1	4064	-	-	-	X
87	OHX	1	4066	-	-	-	X
87	OHX	1	4071	-	-	X	X
87	OHX	1	4072	-	-	-	X
87	OHX	1	4074	-	-	-	X
87	OHX	1	4082	-	-	X	-
87	OHX	1	4083	-	-	-	X
87	OHX	1	4084	-	-	-	X
87	OHX	1	4085	-	-	X	-
87	OHX	1	4095	-	-	-	X
87	OHX	1	4105	-	-	-	X
87	OHX	1	4107	-	-	-	X
87	OHX	2	1995	-	-	-	X
87	OHX	2	1998	-	-	-	X
87	OHX	2	2008	-	-	-	X
87	OHX	2	2010	-	-	-	X
87	OHX	2	2011	-	-	-	X
87	OHX	2	2022	-	-	-	X
87	OHX	2	2027	-	-	-	X
87	OHX	2	2032	-	-	-	X
87	OHX	2	2037	-	-	-	X
87	OHX	2	2047	-	-	-	X
87	OHX	2	2051	-	-	-	X
87	OHX	2	2056	-	-	-	X
87	OHX	2	2057	-	-	-	X
87	OHX	2	2058	-	-	X	-
87	OHX	2	2091	-	-	-	X
87	OHX	2	2095	-	-	-	X
87	OHX	2	2097	-	-	-	X
87	OHX	2	2099	-	-	X	-
87	OHX	2	2106	-	-	-	X
87	OHX	2	2108	-	-	-	X
87	OHX	2	2117	-	-	-	X
87	OHX	2	2119	-	-	-	X
87	OHX	2	2120	-	-	-	X
87	OHX	2	2121	-	-	-	X
87	OHX	2	2125	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
87	OHX	2	2129	-	-	-	X
87	OHX	2	2131	-	-	X	-
87	OHX	2	2132	-	-	-	X
87	OHX	2	2134	-	-	-	X
87	OHX	2	2136	-	-	-	X
87	OHX	2	2141	-	-	-	X
87	OHX	2	2144	-	-	-	X
87	OHX	2	2148	-	-	-	X
87	OHX	2	2151	-	-	-	X
87	OHX	3	210	-	-	-	X
87	OHX	3	211	-	-	-	X
87	OHX	3	212	-	-	-	X
87	OHX	3	214	-	-	-	X
87	OHX	3	219	-	-	-	X
87	OHX	4	216	-	-	-	X
87	OHX	4	224	-	-	-	X
87	OHX	4	231	-	-	-	X
87	OHX	5	3818	-	-	-	X
87	OHX	5	3822	-	-	-	X
87	OHX	5	3833	-	-	-	X
87	OHX	5	3839	-	-	-	X
87	OHX	5	3843	-	-	-	X
87	OHX	5	3844	-	-	-	X
87	OHX	5	3845	-	-	-	X
87	OHX	5	3851	-	-	-	X
87	OHX	5	3854	-	-	-	X
87	OHX	5	3855	-	-	-	X
87	OHX	5	3862	-	-	-	X
87	OHX	5	3865	-	-	-	X
87	OHX	5	3868	-	-	-	X
87	OHX	5	3873	-	-	-	X
87	OHX	5	3875	-	-	-	X
87	OHX	5	3877	-	-	-	X
87	OHX	5	3881	-	-	-	X
87	OHX	5	3888	-	-	-	X
87	OHX	5	3893	-	-	-	X
87	OHX	5	3894	-	-	-	X
87	OHX	5	3899	-	-	-	X
87	OHX	5	3900	-	-	-	X
87	OHX	5	3903	-	-	-	X
87	OHX	5	3904	-	-	-	X
87	OHX	5	3909	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
87	OHX	5	3910	-	-	-	X
87	OHX	5	3911	-	-	-	X
87	OHX	5	3912	-	-	-	X
87	OHX	5	3914	-	-	X	X
87	OHX	5	3915	-	-	-	X
87	OHX	5	3916	-	-	-	X
87	OHX	5	3917	-	-	X	-
87	OHX	5	3922	-	-	-	X
87	OHX	5	3923	-	-	-	X
87	OHX	5	3928	-	-	-	X
87	OHX	5	3931	-	-	-	X
87	OHX	5	3935	-	-	-	X
87	OHX	5	3937	-	-	-	X
87	OHX	5	3939	-	-	-	X
87	OHX	5	3940	-	-	-	X
87	OHX	5	3941	-	-	-	X
87	OHX	5	3942	-	-	-	X
87	OHX	5	3943	-	-	-	X
87	OHX	5	3947	-	-	-	X
87	OHX	5	3948	-	-	-	X
87	OHX	5	3949	-	-	-	X
87	OHX	5	3954	-	-	X	-
87	OHX	5	3956	-	-	-	X
87	OHX	5	3962	-	-	-	X
87	OHX	5	3964	-	-	-	X
87	OHX	5	3965	-	-	-	X
87	OHX	5	3966	-	-	-	X
87	OHX	5	3974	-	-	-	X
87	OHX	5	3976	-	-	-	X
87	OHX	5	3984	-	-	-	X
87	OHX	5	3986	-	-	-	X
87	OHX	5	3989	-	-	-	X
87	OHX	5	3995	-	-	-	X
87	OHX	5	3998	-	-	-	X
87	OHX	5	4000	-	-	X	-
87	OHX	5	4001	-	-	X	-
87	OHX	5	4007	-	-	-	X
87	OHX	5	4008	-	-	-	X
87	OHX	5	4010	-	-	-	X
87	OHX	5	4011	-	-	-	X
87	OHX	5	4012	-	-	-	X
87	OHX	5	4019	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
87	OHX	5	4024	-	-	-	X
87	OHX	5	4025	-	-	-	X
87	OHX	5	4027	-	-	-	X
87	OHX	5	4033	-	-	-	X
87	OHX	5	4038	-	-	-	X
87	OHX	5	4042	-	-	-	X
87	OHX	5	4046	-	-	-	X
87	OHX	5	4048	-	-	-	X
87	OHX	5	4049	-	-	-	X
87	OHX	5	4052	-	-	-	X
87	OHX	5	4053	-	-	-	X
87	OHX	5	4054	-	-	-	X
87	OHX	5	4072	-	-	-	X
87	OHX	5	4076	-	-	-	X
87	OHX	5	4077	-	-	-	X
87	OHX	5	4082	-	-	-	X
87	OHX	5	4083	-	-	X	X
87	OHX	5	4086	-	-	-	X
87	OHX	5	4088	-	-	-	X
87	OHX	5	4093	-	-	-	X
87	OHX	5	4099	-	-	-	X
87	OHX	5	4101	-	-	-	X
87	OHX	5	4103	-	-	-	X
87	OHX	5	4106	-	-	-	X
87	OHX	5	4115	-	-	-	X
87	OHX	5	4117	-	-	-	X
87	OHX	5	4120	-	-	-	X
87	OHX	5	4123	-	-	-	X
87	OHX	5	4124	-	-	-	X
87	OHX	5	4126	-	-	-	X
87	OHX	5	4132	-	-	-	X
87	OHX	5	4134	-	-	-	X
87	OHX	5	4142	-	-	-	X
87	OHX	5	4158	-	-	-	X
87	OHX	5	4159	-	-	-	X
87	OHX	5	4162	-	-	-	X
87	OHX	5	4164	-	-	-	X
87	OHX	5	4169	-	-	-	X
87	OHX	6	2020	-	-	-	X
87	OHX	6	2025	-	-	-	X
87	OHX	6	2029	-	-	-	X
87	OHX	6	2032	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
87	OHX	6	2041	-	-	-	X
87	OHX	6	2043	-	-	-	X
87	OHX	6	2044	-	-	-	X
87	OHX	6	2045	-	-	-	X
87	OHX	6	2051	-	-	-	X
87	OHX	6	2058	-	-	-	X
87	OHX	6	2065	-	-	-	X
87	OHX	6	2067	-	-	X	-
87	OHX	6	2072	-	-	-	X
87	OHX	6	2073	-	-	-	X
87	OHX	6	2088	-	-	-	X
87	OHX	6	2089	-	-	-	X
87	OHX	6	2092	-	-	-	X
87	OHX	6	2097	-	-	-	X
87	OHX	6	2102	-	-	-	X
87	OHX	6	2106	-	-	-	X
87	OHX	6	2107	-	-	-	X
87	OHX	6	2110	-	-	-	X
87	OHX	6	2122	-	-	-	X
87	OHX	6	2124	-	-	X	-
87	OHX	6	2126	-	-	-	X
87	OHX	6	2127	-	-	-	X
87	OHX	6	2128	-	-	-	X
87	OHX	6	2131	-	-	-	X
87	OHX	6	2137	-	-	-	X
87	OHX	6	2146	-	-	-	X
87	OHX	6	2150	-	-	-	X
87	OHX	6	2153	-	-	-	X
87	OHX	6	2155	-	-	-	X
87	OHX	6	2158	-	-	-	X
87	OHX	6	2161	-	-	-	X
87	OHX	6	2162	-	-	-	X
87	OHX	6	2164	-	-	-	X
87	OHX	6	2178	-	-	-	X
87	OHX	7	216	-	-	-	X
87	OHX	7	218	-	-	-	X
87	OHX	7	219	-	-	-	X
87	OHX	7	220	-	-	-	X
87	OHX	7	221	-	-	-	X
87	OHX	7	222	-	-	-	X
87	OHX	7	224	-	-	-	X
87	OHX	8	214	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
87	OHX	8	218	-	-	-	X
87	OHX	8	220	-	-	-	X
87	OHX	8	222	-	-	-	X
87	OHX	8	224	-	-	-	X
87	OHX	8	225	-	-	-	X
87	OHX	C5	201	-	-	X	-
87	OHX	M0	302	-	-	-	X
87	OHX	M0	303	-	-	X	-
87	OHX	N9	101	-	-	-	X
87	OHX	O7	103	-	-	X	-
87	OHX	O9	101	-	-	-	X
87	OHX	S9	201	-	-	X	-
87	OHX	SR	401	-	-	X	-
87	OHX	c5	202	-	-	-	X
87	OHX	l9	201	-	-	-	X
87	OHX	o7	503	-	-	-	X
88	ZN	d7	101	-	-	-	X
89	SPS	5	3402	-	-	-	X

2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 413121 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	2	1781	Total	C	N	O	P	0	1	0
			37970	16975	6720	12493	1782			
1	6	1795	Total	C	N	O	P	0	1	0
			38260	17105	6763	12596	1796			

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	S0	206	Total	C	N	O	S	0	0	0
			1577	1014	278	283	2			
2	s0	206	Total	C	N	O	S	0	0	0
			1583	1017	281	283	2			

- Molecule 3 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	S1	214	Total	C	N	O	S	0	0	0
			1709	1084	310	311	4			
3	s1	216	Total	C	N	O	S	0	0	0
			1722	1091	312	315	4			

- Molecule 4 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	S2	217	Total	C	N	O	S	0	0	0
			1635	1047	289	297	2			
4	s2	217	Total	C	N	O	S	0	0	0
			1635	1047	289	297	2			

- Molecule 5 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	S3	223	Total	C	N	O	S	0	0	0
			1734	1101	313	314	6			
5	s3	223	Total	C	N	O	S	0	0	0
			1734	1101	313	314	6			

- Molecule 6 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	S4	260	Total	C	N	O	S	0	0	0
			2068	1316	389	360	3			
6	s4	260	Total	C	N	O	S	0	0	0
			2068	1316	389	360	3			

- Molecule 7 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	S5	206	Total	C	N	O	S	0	0	0
			1609	1007	300	299	3			
7	s5	206	Total	C	N	O	S	0	0	0
			1609	1007	300	299	3			

- Molecule 8 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	S6	226	Total	C	N	O	S	0	0	0
			1799	1129	346	321	3			
8	s6	218	Total	C	N	O	S	0	0	0
			1755	1102	337	313	3			

- Molecule 9 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	S7	184	Total	C	N	O	0	0	0
			1481	951	265	265			
9	s7	186	Total	C	N	O	0	0	0
			1491	957	267	267			

- Molecule 10 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	S8	188	Total	C	N	O	S	0	0	0
			1489	925	298	264	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	s8	188	Total	C	N	O	S	0	0	0
			1489	925	298	264	2			

- Molecule 11 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	S9	185	Total	C	N	O	S	0	0	0
			1494	943	289	261	1			
11	s9	185	Total	C	N	O	S	0	0	0
			1494	943	289	261	1			

- Molecule 12 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	C0	96	Total	C	N	O	S	0	0	0
			773	500	126	145	2			
12	c0	96	Total	C	N	O	S	0	0	0
			762	491	125	144	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C0	89	ALA	GLY	conflict	UNP Q08745
c0	89	ALA	GLY	conflict	UNP Q08745

- Molecule 13 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	C1	155	Total	C	N	O	S	0	0	0
			1214	775	230	206	3			
13	c1	146	Total	C	N	O	S	0	0	0
			1168	747	221	197	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C1	147	ALA	GLY	conflict	UNP P0CX47
c1	147	ALA	GLY	conflict	UNP P0CX47

- Molecule 14 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	C2	124	Total	C	N	O	S	0	0	0
			892	562	156	172	2			
14	c2	124	Total	C	N	O	S	0	0	0
			892	562	156	172	2			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C2	104	ALA	GLY	conflict	UNP P48589
C2	110	ALA	GLY	conflict	UNP P48589
c2	104	ALA	GLY	conflict	UNP P48589
c2	110	ALA	GLY	conflict	UNP P48589

- Molecule 15 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	C3	150	Total	C	N	O	S	0	0	0
			1192	759	224	207	2			
15	c3	150	Total	C	N	O	S	0	0	0
			1192	759	224	207	2			

- Molecule 16 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	C4	127	Total	C	N	O	S	0	0	0
			891	545	182	163	1			
16	c4	128	Total	C	N	O	S	0	0	0
			949	582	188	176	3			

- Molecule 17 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	C5	124	Total	C	N	O	S	0	0	0
			977	622	182	166	7			
17	c5	135	Total	C	N	O	S	0	0	0
			1039	658	196	178	7			

- Molecule 18 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	C6	141	Total	C	N	O		0	0	0
			1105	708	203	194				

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	c6	142	Total	C	N	O			
			1111	711	204	196	0	0	0

- Molecule 19 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
19	C7	120	Total	C	N	O	S		
			926	577	177	170	2	0	0
19	c7	117	Total	C	N	O	S		
			906	563	174	167	2	0	0

- Molecule 20 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
20	C8	145	Total	C	N	O	S		
			1192	743	237	210	2	0	0
20	c8	145	Total	C	N	O	S		
			1192	743	237	210	2	0	0

- Molecule 21 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	C9	143	Total	C	N	O	S		
			1112	694	208	208	2	0	0
21	c9	143	Total	C	N	O	S		
			1112	694	208	208	2	0	0

- Molecule 22 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
22	D0	107	Total	C	N	O	S		
			855	539	156	159	1	0	0
22	d0	110	Total	C	N	O	S		
			882	554	161	166	1	0	0

- Molecule 23 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
23	D1	87	Total	C	N	O	S		
			684	420	125	137	2	0	0
23	d1	87	Total	C	N	O	S		
			684	420	125	137	2	0	0

- Molecule 24 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	D2	129	Total	C	N	O	S	0	0	0
			1021	650	188	180	3			
24	d2	129	Total	C	N	O	S	0	0	0
			1021	650	188	180	3			

- Molecule 25 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	D3	144	Total	C	N	O	S	0	0	0
			1121	708	220	191	2			
25	d3	144	Total	C	N	O	S	0	0	0
			1121	708	220	191	2			

- Molecule 26 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
26	D4	134	Total	C	N	O	0	0	0
			1073	676	208	189			
26	d4	134	Total	C	N	O	0	0	0
			1073	676	208	189			

- Molecule 27 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
27	D5	70	Total	C	N	O	0	0	0
			563	360	104	99			
27	d5	69	Total	C	N	O	0	0	0
			558	357	103	98			

- Molecule 28 is a protein called 40S ribosomal protein S26-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	D6	97	Total	C	N	O	S	0	0	0
			769	475	160	129	5			
28	d6	97	Total	C	N	O	S	0	0	0
			769	475	160	129	5			

- Molecule 29 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	D7	81	Total	C	N	O	S	0	0	0
			610	382	110	113	5			
29	d7	81	Total	C	N	O	S	0	0	0
			610	382	110	113	5			

- Molecule 30 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	D8	63	Total	C	N	O	S	0	0	0
			497	306	99	91	1			
30	d8	63	Total	C	N	O	S	0	0	0
			497	306	99	91	1			

- Molecule 31 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	D9	53	Total	C	N	O	S	0	0	0
			442	274	92	72	4			
31	d9	53	Total	C	N	O	S	0	0	0
			442	274	92	72	4			

- Molecule 32 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	E0	60	Total	C	N	O	S	0	0	0
			475	299	98	77	1			

- Molecule 33 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	E1	71	Total	C	N	O	S	0	0	0
			566	362	106	94	4			
33	e1	76	Total	C	N	O	S	0	0	0
			608	388	117	99	4			

- Molecule 34 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	SR	318	Total	C	N	O	S	0	0	0
			2436	1541	418	469	8			
34	sR	318	Total	C	N	O	S	0	0	0
			2441	1544	418	471	8			

- Molecule 35 is a protein called Suppressor protein STM1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
35	SM	159	Total	C	N	O	0	0	0
			1104	652	221	231			
35	sM	104	Total	C	N	O	0	0	0
			680	403	140	137			

- Molecule 36 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	1	3149	Total	C	N	O	P	0	0	0
			67355	30086	12142	21978	3149			
36	5	3150	Total	C	N	O	P	0	0	0
			67376	30095	12145	21987	3149			

- Molecule 37 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	3	121	Total	C	N	O	P	0	0	0
			2579	1152	461	845	121			
37	7	121	Total	C	N	O	P	0	0	0
			2579	1152	461	845	121			

- Molecule 38 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	4	158	Total	C	N	O	P	0	0	0
			3353	1500	586	1109	158			
38	8	158	Total	C	N	O	P	0	0	0
			3353	1500	586	1109	158			

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	L2	252	Total	C	N	O	S	0	0	0
			1914	1191	388	334	1			
39	12	252	Total	C	N	O	S	0	0	0
			1912	1190	388	333	1			

- Molecule 40 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	L3	386	Total	C	N	O	S	0	0	0
			3075	1950	584	533	8			
40	l3	386	Total	C	N	O	S	0	0	0
			3075	1950	584	533	8			

- Molecule 41 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	L4	361	Total	C	N	O	S	0	0	0
			2748	1729	522	494	3			
41	l4	361	Total	C	N	O	S	0	0	0
			2748	1729	522	494	3			

- Molecule 42 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	L5	296	Total	C	N	O	S	0	0	0
			2375	1501	414	458	2			
42	l5	294	Total	C	N	O	S	0	0	0
			2359	1489	412	456	2			

- Molecule 43 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	L6	156	Total	C	N	O	S	0	0	0
			1239	800	222	216	1			
43	l6	157	Total	C	N	O	S	0	0	0
			1248	806	224	217	1			

- Molecule 44 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	L7	222	Total	C	N	O	S	0	0	0
			1784	1151	324	308	1			
44	l7	223	Total	C	N	O	S	0	0	0
			1791	1155	325	310	1			

- Molecule 45 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	L8	233	Total	C	N	O	S	0	0	0
			1804	1151	323	327	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	l8	231	Total	C	N	O	S	0	0	0
			1764	1131	316	314	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L8	119	ALA	GLY	conflict	UNP P17076
l8	119	ALA	GLY	conflict	UNP P17076

- Molecule 46 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	L9	191	Total	C	N	O	S	0	0	0
			1518	963	274	277	4			
46	l9	191	Total	C	N	O	S	0	0	0
			1518	963	274	277	4			

- Molecule 47 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	M0	211	Total	C	N	O	S	0	0	0
			1705	1083	322	294	6			
47	m0	213	Total	C	N	O	S	0	0	0
			1722	1094	325	297	6			

- Molecule 48 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	M1	169	Total	C	N	O	S	0	0	0
			1353	847	253	249	4			
48	m1	169	Total	C	N	O	S	0	0	0
			1353	847	253	249	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M1	3	THR	ALA	conflict	UNP P0C0W9
m1	3	THR	ALA	conflict	UNP P0C0W9

- Molecule 49 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	M3	193	Total	C	N	O	0	0	0
			1543	962	315	266			
49	m3	194	Total	C	N	O	0	0	0
			1548	965	316	267			

- Molecule 50 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	M4	136	Total	C	N	O	S	0	0	0
			1053	675	199	177	2			
50	m4	137	Total	C	N	O	S	0	0	0
			1059	678	200	179	2			

- Molecule 51 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	M5	203	Total	C	N	O	S	0	0	0
			1720	1077	361	281	1			
51	m5	203	Total	C	N	O	S	0	0	0
			1720	1077	361	281	1			

- Molecule 52 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	M6	197	Total	C	N	O	S	0	0	0
			1555	1003	289	262	1			
52	m6	197	Total	C	N	O	S	0	0	0
			1555	1003	289	262	1			

- Molecule 53 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
53	M7	183	Total	C	N	O	0	0	0
			1420	882	281	257			
53	m7	155	Total	C	N	O	0	0	0
			1227	764	238	225			

- Molecule 54 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	M8	185	Total	C	N	O	S	0	0	0
			1441	908	290	241	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	m8	185	Total	C	N	O	S	0	0	0
			1441	908	290	241	2			

- Molecule 55 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	M9	188	Total	C	N	O		0	0	0
			1521	935	326	260				
55	m9	188	Total	C	N	O		0	0	0
			1521	935	326	260				

- Molecule 56 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	N0	172	Total	C	N	O	S	0	0	0
			1445	930	267	244	4			
56	n0	172	Total	C	N	O	S	0	0	0
			1445	930	267	244	4			

- Molecule 57 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	N1	159	Total	C	N	O	S	0	0	0
			1276	805	246	221	4			
57	n1	159	Total	C	N	O	S	0	0	0
			1276	805	246	221	4			

- Molecule 58 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	N2	100	Total	C	N	O		0	0	0
			796	516	131	149				
58	n2	98	Total	C	N	O		0	0	0
			778	505	127	146				

- Molecule 59 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
59	N3	136	Total	C	N	O	S	0	0	0
			1003	628	189	179	7			
59	n3	136	Total	C	N	O	S	0	0	0
			1003	628	189	179	7			

- Molecule 60 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
60	N4	98	Total	C	N	O	S	0	0	0
			699	443	137	118	1			
60	n4	135	Total	C	N	O	S	0	0	0
			1038	651	206	180	1			

- Molecule 61 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
61	N5	121	Total	C	N	O	S	0	0	0
			964	620	169	173	2			
61	n5	120	Total	C	N	O	S	0	0	0
			959	617	168	172	2			

- Molecule 62 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
62	N6	126	Total	C	N	O	0	0	0
			993	625	192	176			
62	n6	126	Total	C	N	O	0	0	0
			993	625	192	176			

- Molecule 63 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
63	N7	135	Total	C	N	O	0	0	0
			1092	710	202	180			
63	n7	135	Total	C	N	O	0	0	0
			1092	710	202	180			

- Molecule 64 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
64	N8	148	Total	C	N	O	S	0	0	0
			1173	749	231	190	3			
64	n8	148	Total	C	N	O	S	0	0	0
			1173	749	231	190	3			

- Molecule 65 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
65	N9	58	Total	C	N	O	0	0	0
			462	289	100	73			
65	n9	58	Total	C	N	O	0	0	0
			462	289	100	73			

- Molecule 66 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
66	O0	97	Total	C	N	O	S	0	0	0
			742	479	124	138	1			
66	o0	100	Total	C	N	O	S	0	0	0
			766	492	128	145	1			

- Molecule 67 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
67	O1	109	Total	C	N	O	S	0	0	0
			876	556	167	152	1			
67	o1	109	Total	C	N	O	S	0	0	0
			883	559	167	156	1			

- Molecule 68 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
68	O2	127	Total	C	N	O	S	0	0	0
			1020	647	205	167	1			
68	o2	127	Total	C	N	O	S	0	0	0
			1020	647	205	167	1			

- Molecule 69 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
69	O3	106	Total	C	N	O	S	0	0	0
			850	540	165	144	1			
69	o3	106	Total	C	N	O	S	0	0	0
			850	540	165	144	1			

- Molecule 70 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
70	O4	112	Total	C	N	O	S	0	0	0
			880	545	179	152	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
70	o4	112	Total	C	N	O	S	0	0	0
			880	545	179	152	4			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O4	110	GLU	-	expression tag	UNP P87262
O4	111	ALA	-	expression tag	UNP P87262
O4	112	ALA	-	expression tag	UNP P87262
O4	113	LYS	-	expression tag	UNP P87262
O4	114	SER	-	expression tag	UNP P87262
O4	115	GLU	-	expression tag	UNP P87262
O4	116	LYS	-	expression tag	UNP P87262
O4	117	LYS	-	expression tag	UNP P87262
O4	118	ALA	-	expression tag	UNP P87262
O4	119	LYS	-	expression tag	UNP P87262
O4	120	LYS	-	expression tag	UNP P87262
o4	110	GLU	-	expression tag	UNP P87262
o4	111	ALA	-	expression tag	UNP P87262
o4	112	ALA	-	expression tag	UNP P87262
o4	113	LYS	-	expression tag	UNP P87262
o4	114	SER	-	expression tag	UNP P87262
o4	115	GLU	-	expression tag	UNP P87262
o4	116	LYS	-	expression tag	UNP P87262
o4	117	LYS	-	expression tag	UNP P87262
o4	118	ALA	-	expression tag	UNP P87262
o4	119	LYS	-	expression tag	UNP P87262
o4	120	LYS	-	expression tag	UNP P87262

- Molecule 71 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
71	O5	119	Total	C	N	O	S	0	0	0
			969	615	186	167	1			
71	o5	119	Total	C	N	O	S	0	0	0
			965	612	185	167	1			

- Molecule 72 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
72	O6	99	Total	C	N	O	S	0	0	0
			771	481	156	132	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
72	o6	99	Total	C	N	O	S	0	0	0
			770	481	156	131	2			

- Molecule 73 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
73	O7	87	Total	C	N	O	S	0	0	0
			681	414	148	114	5			
73	o7	87	Total	C	N	O	S	0	0	0
			681	414	148	114	5			

- Molecule 74 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
74	O8	77	Total	C	N	O	S	0	0	0
			612	391	115	106				
74	o8	77	Total	C	N	O	S	0	0	0
			608	388	114	106				

- Molecule 75 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
75	O9	50	Total	C	N	O	S	0	0	0
			436	272	97	65	2			
75	o9	50	Total	C	N	O	S	0	0	0
			436	272	97	65	2			

- Molecule 76 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
76	Q0	52	Total	C	N	O	S	0	0	0
			417	259	86	67	5			
76	q0	52	Total	C	N	O	S	0	0	0
			417	259	86	67	5			

- Molecule 77 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
77	Q1	25	Total	C	N	O	S	0	0	0
			233	142	63	27	1			
77	q1	25	Total	C	N	O	S	0	0	0
			233	142	63	27	1			

- Molecule 78 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
78	Q2	105	Total	C	N	O	S	0	0	0
			847	534	170	138	5			
78	q2	105	Total	C	N	O	S	0	0	0
			847	534	170	138	5			

- Molecule 79 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
79	Q3	91	Total	C	N	O	S	0	0	0
			694	429	138	121	6			
79	q3	91	Total	C	N	O	S	0	0	0
			694	429	138	121	6			

- Molecule 80 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
80	e0	62	Total	C	N	O	S	0	0	0
			491	309	101	80	1			

- Molecule 81 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
81	m2	150	Total	C	N	O	0	0	0
			739	439	150	150			

- Molecule 82 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
82	p0	143	Total	C	N	O	S	0	0	0
			1077	687	192	195	3			

- Molecule 83 is a protein called 60S acidic ribosomal protein P1-alpha.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
83	p1	47	Total	C	N	O	0	0	0
			235	141	47	47			
83	p2	46	Total	C	N	O	0	0	0
			230	138	46	46			

- Molecule 84 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
84	f	148	Total	C	N	O	S	0	0	0
			1122	696	189	228	9			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
f	51	5CT	LYS	conflict	UNP P23301

- Molecule 85 is a RNA chain called DNA (5'-R(*CP*CP*(NA))-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
85	B	4	Total	C	N	O	P	0	0	0
			66	33	13	18	2			
85	C	4	Total	C	N	O	P	0	0	0
			69	33	13	20	3			

- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
86	L7	3	Total	Mg	0	0
			3	3		
86	n8	2	Total	Mg	0	0
			2	2		
86	B	1	Total	Mg	0	0
			1	1		
86	6	113	Total	Mg	0	0
			113	113		
86	sM	1	Total	Mg	0	0
			1	1		
86	O4	1	Total	Mg	0	0
			1	1		
86	m5	2	Total	Mg	0	0
			2	2		
86	l3	2	Total	Mg	0	0
			2	2		
86	n0	1	Total	Mg	0	0
			1	1		
86	d6	1	Total	Mg	0	0
			1	1		
86	2	90	Total	Mg	0	0
			90	90		
86	O3	1	Total	Mg	0	0
			1	1		

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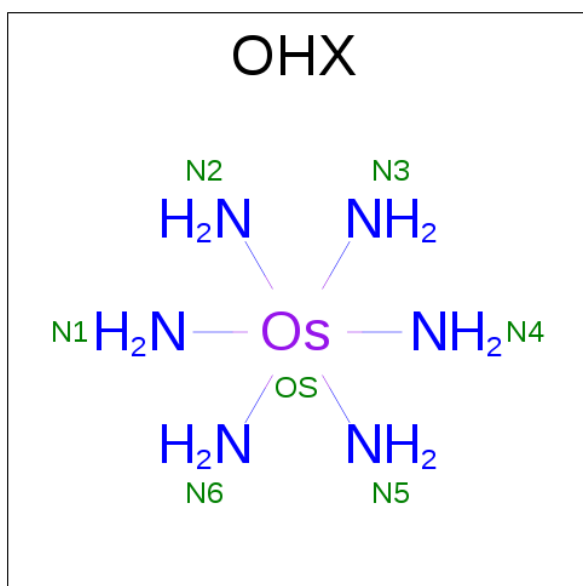
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
86	f	1	Total 1	Mg 1	0	0
86	l7	2	Total 2	Mg 2	0	0
86	M5	1	Total 1	Mg 1	0	0
86	m3	1	Total 1	Mg 1	0	0
86	S2	1	Total 1	Mg 1	0	0
86	N6	1	Total 1	Mg 1	0	0
86	D3	1	Total 1	Mg 1	0	0
86	M9	1	Total 1	Mg 1	0	0
86	SM	1	Total 1	Mg 1	0	0
86	o4	1	Total 1	Mg 1	0	0
86	M0	1	Total 1	Mg 1	0	0
86	5	419	Total 419	Mg 419	0	0
86	c8	1	Total 1	Mg 1	0	0
86	O7	1	Total 1	Mg 1	0	0
86	l4	1	Total 1	Mg 1	0	0
86	1	366	Total 366	Mg 366	0	0
86	d2	1	Total 1	Mg 1	0	0
86	n6	1	Total 1	Mg 1	0	0
86	Q2	1	Total 1	Mg 1	0	0
86	d3	1	Total 1	Mg 1	0	0
86	q3	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
86	o3	1	Total 1	Mg 1	0	0
86	N3	1	Total 1	Mg 1	0	0
86	N8	1	Total 1	Mg 1	0	0
86	4	15	Total 15	Mg 15	0	0
86	L2	2	Total 2	Mg 2	0	0
86	l5	1	Total 1	Mg 1	0	0
86	M7	4	Total 4	Mg 4	0	0
86	L6	1	Total 1	Mg 1	0	0
86	s8	2	Total 2	Mg 2	0	0
86	o2	1	Total 1	Mg 1	0	0
86	C	1	Total 1	Mg 1	0	0
86	m7	2	Total 2	Mg 2	0	0
86	7	13	Total 13	Mg 13	0	0
86	n3	1	Total 1	Mg 1	0	0
86	q1	1	Total 1	Mg 1	0	0
86	L3	1	Total 1	Mg 1	0	0
86	s4	1	Total 1	Mg 1	0	0
86	l2	2	Total 2	Mg 2	0	0
86	8	9	Total 9	Mg 9	0	0
86	M6	2	Total 2	Mg 2	0	0
86	3	8	Total 8	Mg 8	0	0

- Molecule 87 is osmium (III) hexammine (three-letter code: OHX) (formula: $\text{H}_{12}\text{N}_6\text{Os}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	1	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	1	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	1	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	1	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	1	0
			7	6	1		
87	2	1	Total	N	Os	0	0
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87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
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			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
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			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
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87	2	1	Total	N	Os	0	0
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87	2	1	Total	N	Os	0	0
			7	6	1		
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			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
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			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
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87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
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			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
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87	2	1	Total	N	Os	0	0
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87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
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87	2	1	Total	N	Os	0	0
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87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
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87	2	1	Total	N	Os	0	0
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87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
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			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	1	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
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87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	2	1	Total	N	Os	0	0
			7	6	1		
87	2	1	Total	N	Os	0	0
			7	6	1		
87	S1	1	Total	N	Os	0	0
			7	6	1		
87	S6	1	Total	N	Os	0	0
			7	6	1		
87	S8	1	Total	N	Os	0	0
			7	6	1		
87	S9	1	Total	N	Os	0	0
			7	6	1		
87	C3	1	Total	N	Os	0	0
			7	6	1		
87	C5	1	Total	N	Os	0	0
			7	6	1		
87	C8	1	Total	N	Os	0	0
			7	6	1		
87	D9	1	Total	N	Os	0	0
			7	6	1		
87	SR	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	1	0
			7	6	1		
87	1	1	Total	N	Os	1	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	1	0
			7	6	1		
87	1	1	Total	N	Os	1	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	1	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	2	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	1	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	1	1	Total	N	Os	0	0
			7	6	1		
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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			7	6	1		
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	2	0
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87	1	1	Total	N	Os	1	0
			7	6	1		
87	1	1	Total	N	Os	0	0
			7	6	1		
87	1	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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87	1	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	3	1	Total	N	Os	0	0
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87	4	1	Total	N	Os	0	0
			7	6	1		
87	4	1	Total	N	Os	0	0
			7	6	1		
87	4	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	4	1	Total 7	N 6	Os 1	1	0
87	4	1	Total 7	N 6	Os 1	0	0
87	4	1	Total 7	N 6	Os 1	0	0
87	4	1	Total 7	N 6	Os 1	0	0
87	4	1	Total 7	N 6	Os 1	0	0
87	4	1	Total 7	N 6	Os 1	0	0
87	4	1	Total 7	N 6	Os 1	0	0
87	4	1	Total 7	N 6	Os 1	1	0
87	4	1	Total 7	N 6	Os 1	0	0
87	4	1	Total 7	N 6	Os 1	0	0
87	4	1	Total 7	N 6	Os 1	0	0
87	4	1	Total 7	N 6	Os 1	0	0
87	L3	1	Total 7	N 6	Os 1	0	0
87	L3	1	Total 7	N 6	Os 1	0	0
87	L3	1	Total 7	N 6	Os 1	0	0
87	L4	1	Total 7	N 6	Os 1	0	0
87	L5	1	Total 7	N 6	Os 1	0	0
87	M0	1	Total 7	N 6	Os 1	0	0
87	M0	1	Total 7	N 6	Os 1	0	0
87	M5	1	Total 7	N 6	Os 1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	M6	1	Total	N	Os	0	0
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87	M7	1	Total	N	Os	0	0
			7	6	1		
87	M8	1	Total	N	Os	0	0
			7	6	1		
87	M9	1	Total	N	Os	0	0
			7	6	1		
87	N8	1	Total	N	Os	0	0
			7	6	1		
87	N9	1	Total	N	Os	0	0
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87	O4	1	Total	N	Os	0	0
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87	O7	1	Total	N	Os	0	0
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87	O9	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	6	1	Total	N	Os	0	0
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87	6	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	6	1	Total	N	Os	0	0
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87	6	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	6	1	Total	N	Os	0	0
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87	6	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	6	1	Total	N	Os	0	0
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87	6	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	6	1	Total	N	Os	0	0
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87	6	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	6	1	Total	N	Os	0	0
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87	6	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	6	1	Total	N	Os	0	0
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87	6	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	s1	1	Total	N	Os	0	0
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87	s1	1	Total	N	Os	0	0
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87	s4	1	Total	N	Os	0	0
			7	6	1		
87	s8	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	c3	1	Total	N	Os	0	0
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87	c5	1	Total	N	Os	0	0
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87	c5	1	Total	N	Os	0	0
			7	6	1		
87	c8	1	Total	N	Os	0	0
			7	6	1		
87	d4	1	Total	N	Os	0	0
			7	6	1		
87	d9	1	Total	N	Os	0	0
			7	6	1		
87	sR	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	5	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	5	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
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			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
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			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
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			7	6	1		
87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	1	0
			7	6	1		
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87	5	1	Total	N	Os	0	0
			7	6	1		
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			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
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			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	1	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	1	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
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87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	1	0
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87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
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			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	1	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
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			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	1	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
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87	5	1	Total	N	Os	0	0
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			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	1	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	1	0
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87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
			7	6	1		
87	5	1	Total	N	Os	0	0
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87	7	1	Total	N	Os	0	0
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87	7	1	Total	N	Os	0	0
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			7	6	1		
87	7	1	Total	N	Os	0	0
			7	6	1		
87	7	1	Total	N	Os	0	0
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87	7	1	Total	N	Os	1	0
			7	6	1		
87	7	1	Total	N	Os	1	0
			7	6	1		
87	7	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	8	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	1	0
			7	6	1		
87	8	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	1	0
			7	6	1		
87	8	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	0	0
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87	8	1	Total	N	Os	1	0
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87	8	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	0	0
			7	6	1		
87	8	1	Total	N	Os	0	0
			7	6	1		
87	13	1	Total	N	Os	0	0
			7	6	1		
87	13	1	Total	N	Os	0	0
			7	6	1		
87	14	1	Total	N	Os	0	0
			7	6	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	l4	1	Total 7	N 6	Os 1	0	0
87	l5	1	Total 7	N 6	Os 1	0	0
87	l5	1	Total 7	N 6	Os 1	1	0
87	l9	1	Total 7	N 6	Os 1	0	0
87	m0	1	Total 7	N 6	Os 1	0	0
87	m0	1	Total 7	N 6	Os 1	0	0
87	m1	1	Total 7	N 6	Os 1	0	0
87	m4	1	Total 7	N 6	Os 1	0	0
87	m5	1	Total 7	N 6	Os 1	0	0
87	m5	1	Total 7	N 6	Os 1	0	0
87	m5	1	Total 7	N 6	Os 1	0	0
87	m5	1	Total 7	N 6	Os 1	0	0
87	m6	1	Total 7	N 6	Os 1	0	0
87	m7	1	Total 7	N 6	Os 1	0	0
87	m8	1	Total 7	N 6	Os 1	0	0
87	m9	1	Total 7	N 6	Os 1	0	0
87	n3	1	Total 7	N 6	Os 1	0	0
87	n9	1	Total 7	N 6	Os 1	0	0
87	o3	1	Total 7	N 6	Os 1	0	0
87	o6	1	Total 7	N 6	Os 1	0	0
87	o7	1	Total 7	N 6	Os 1	0	0
87	o7	1	Total 7	N 6	Os 1	0	0

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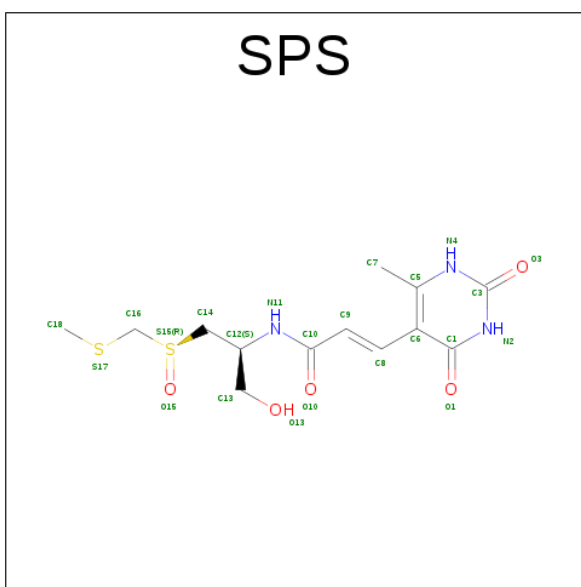
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
87	q2	1	Total	N	Os	0	0
			7	6	1		

- Molecule 88 is ZINC ION (three-letter code: ZN) (formula: Zn).

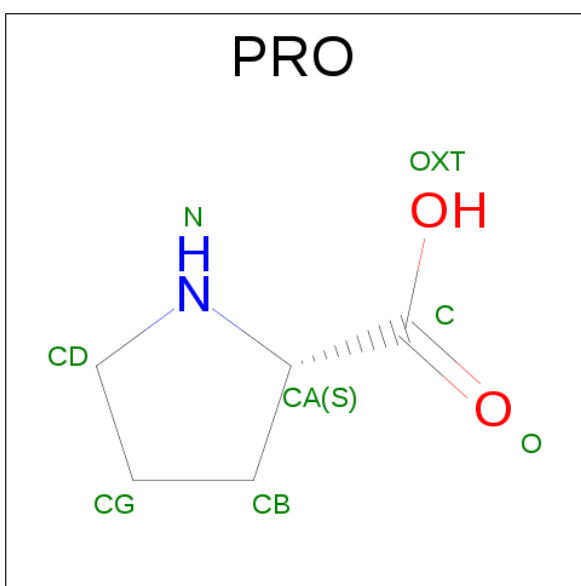
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
88	q0	1	Total	Zn	0	0
			1	1		
88	D6	1	Total	Zn	0	0
			1	1		
88	Q2	1	Total	Zn	0	0
			1	1		
88	e1	1	Total	Zn	0	0
			1	1		
88	Q3	1	Total	Zn	0	0
			1	1		
88	D9	1	Total	Zn	0	0
			1	1		
88	E1	1	Total	Zn	0	0
			1	1		
88	Q0	1	Total	Zn	0	0
			1	1		
88	d7	1	Total	Zn	0	0
			1	1		
88	q3	1	Total	Zn	0	0
			1	1		
88	d9	1	Total	Zn	0	0
			1	1		
88	D7	1	Total	Zn	0	0
			1	1		
88	d6	1	Total	Zn	0	0
			1	1		
88	o7	1	Total	Zn	0	0
			1	1		
88	O7	1	Total	Zn	0	0
			1	1		
88	q2	1	Total	Zn	0	0
			1	1		

- Molecule 89 is SPARSOMYCIN (three-letter code: SPS) (formula: C₁₃H₁₉N₃O₅S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
89	5	1	Total	C	N	O	S	0	0
			23	13	3	5	2		
89	B	1	Total	C	N	O	S	0	0
			23	13	3	5	2		

- Molecule 90 is PROLINE (three-letter code: PRO) (formula: $C_5H_9NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
90	B	1	Total	C	N	O	0	0
			7	5	1	1		
90	C	1	Total	C	N	O	0	0
			7	5	1	1		

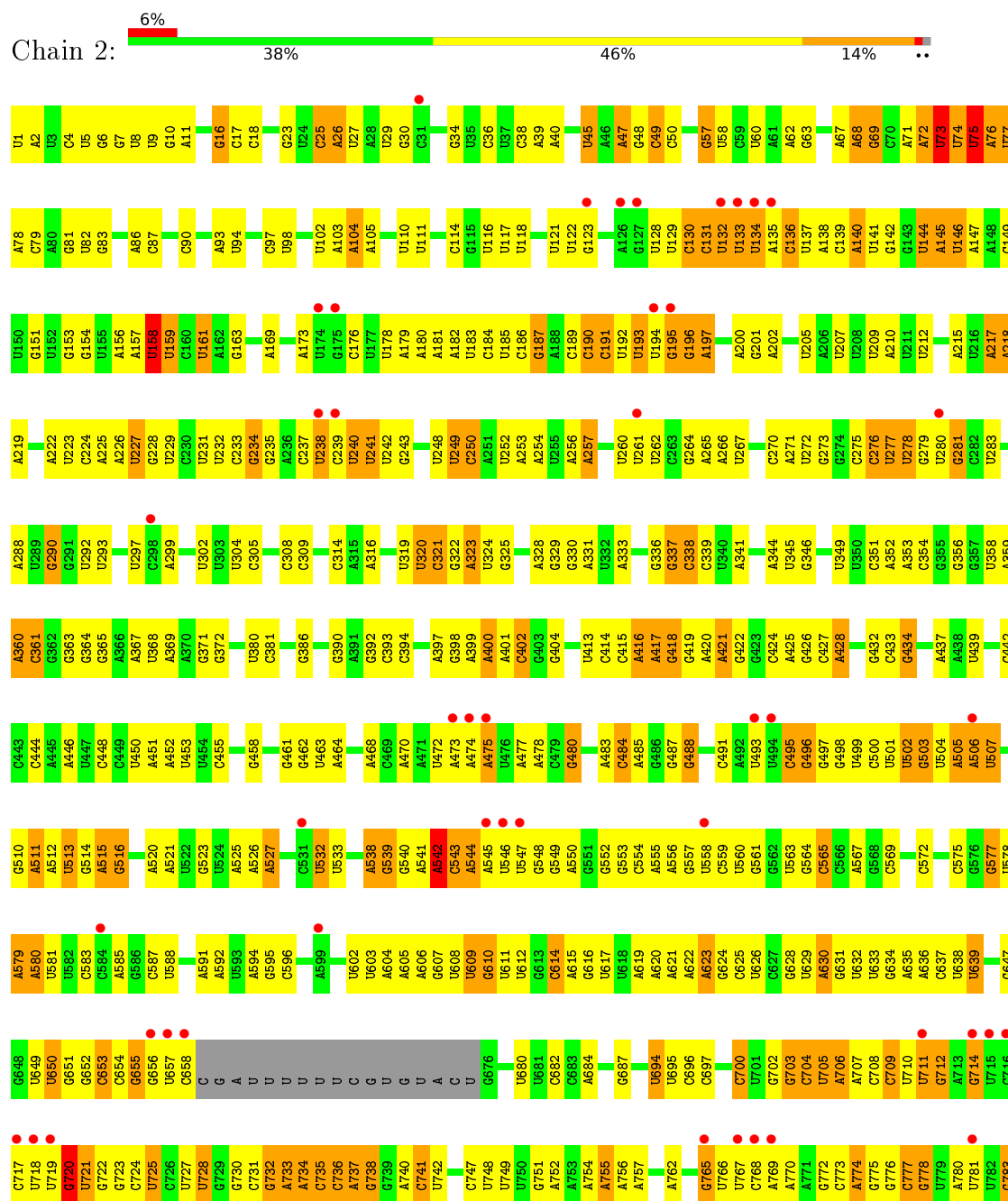
- Molecule 91 is water.

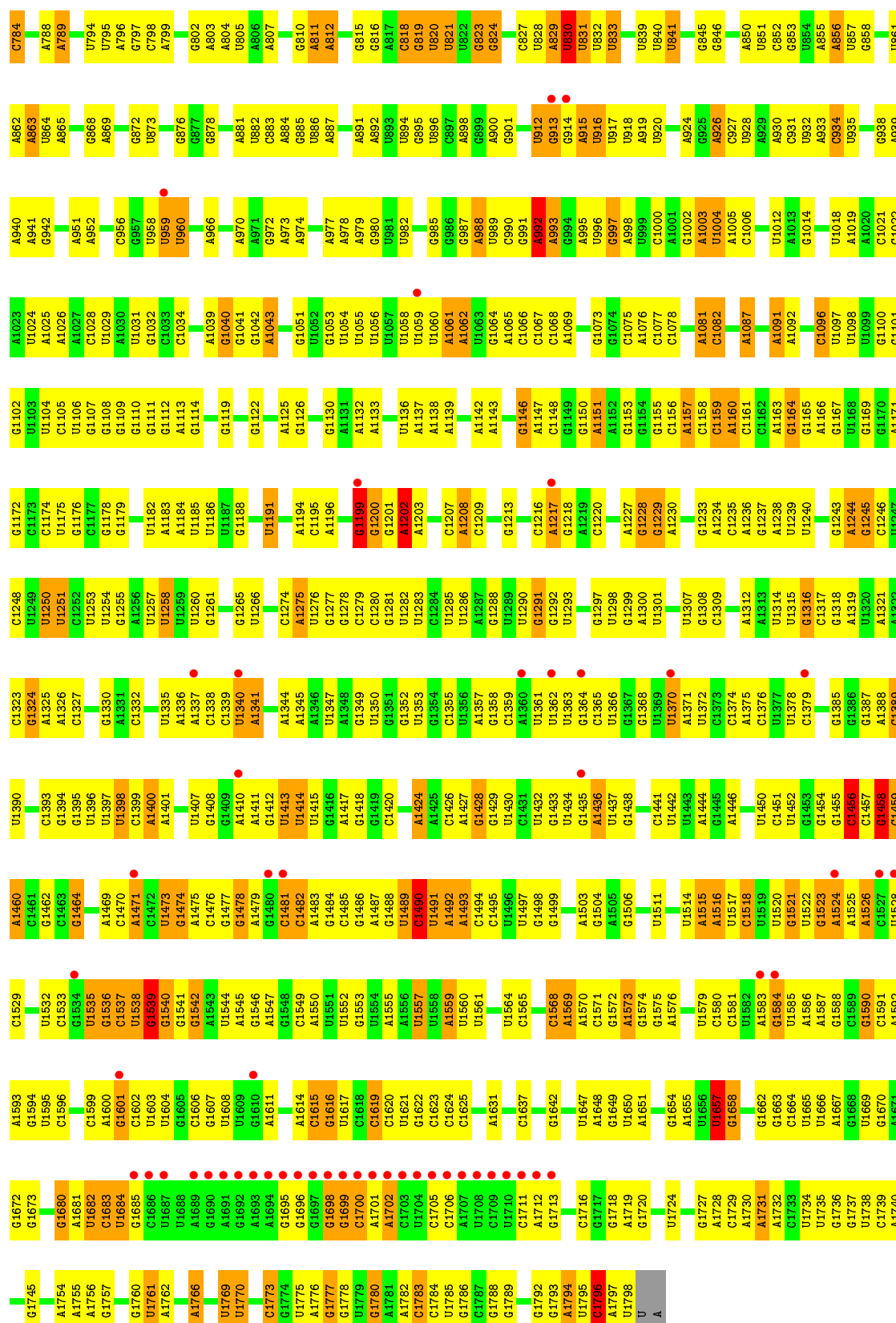
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
91	5	6	Total 6	O 6	0	0
91	f	6	Total 6	O 6	0	0

3 Residue-property plots

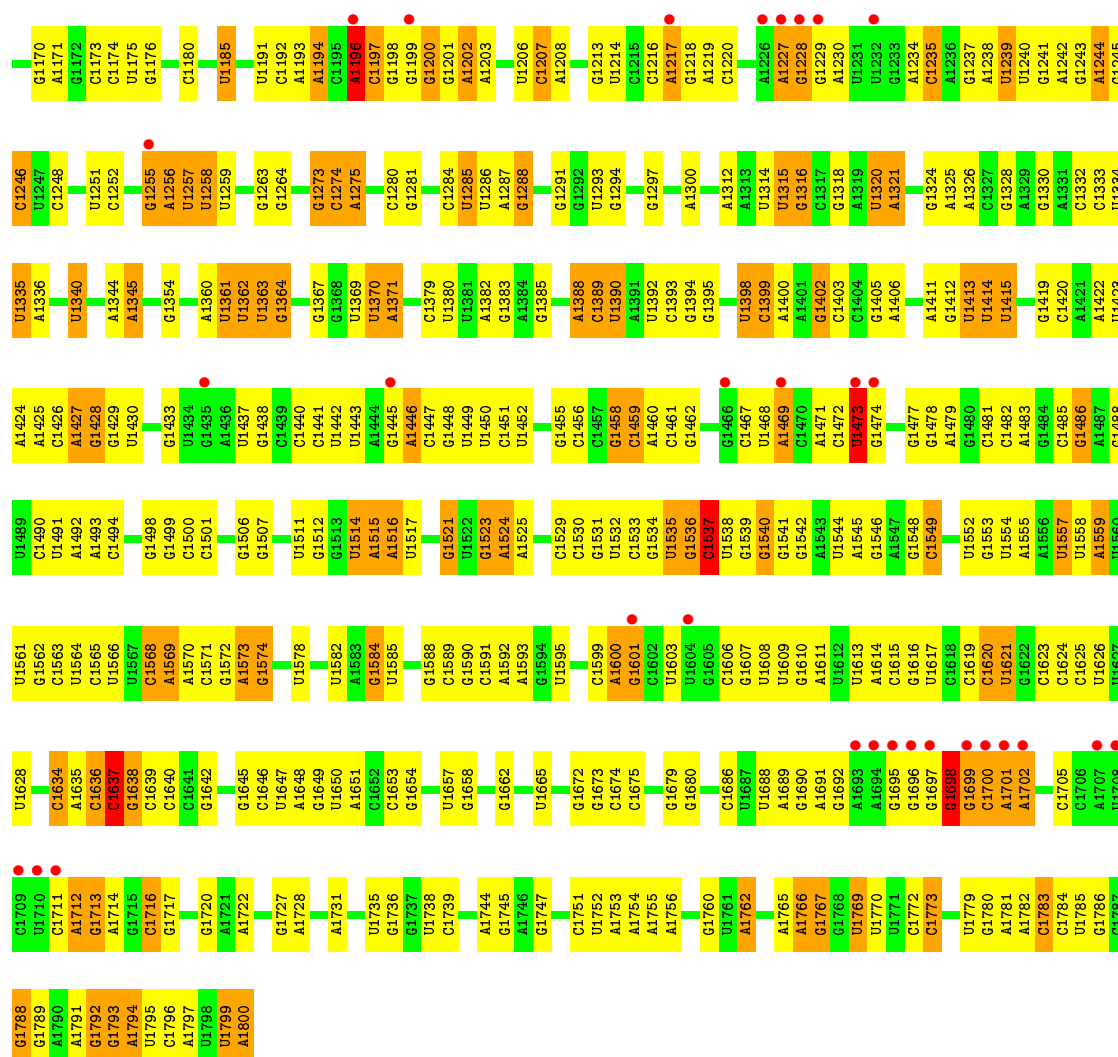
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 18S ribosomal RNA

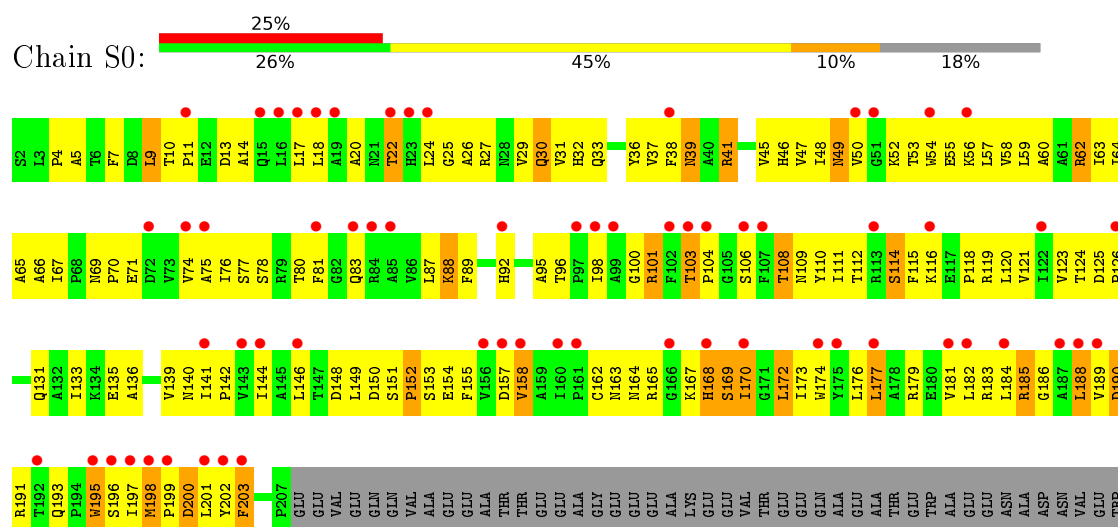




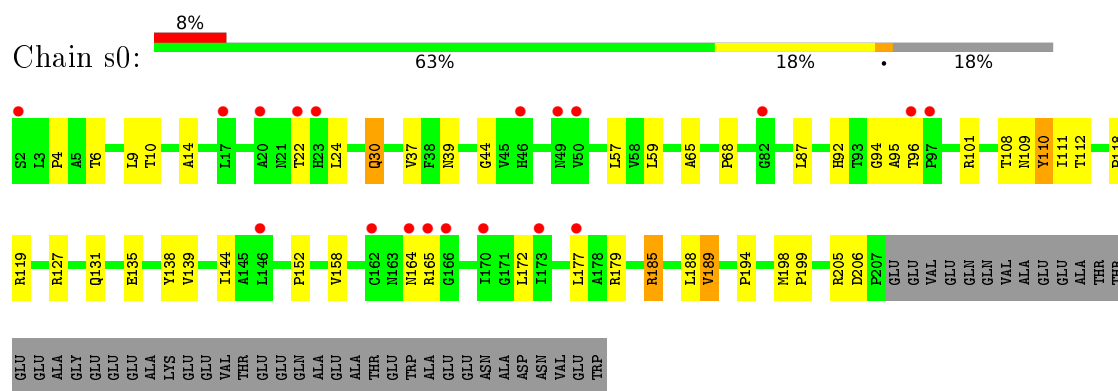




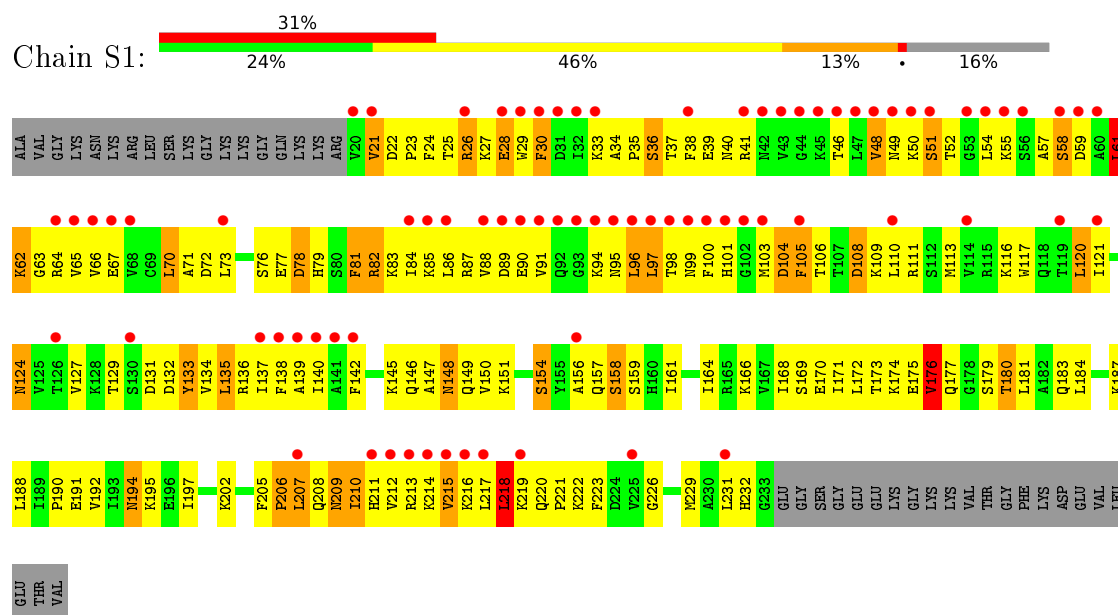
- Molecule 2: 40S ribosomal protein S0-A



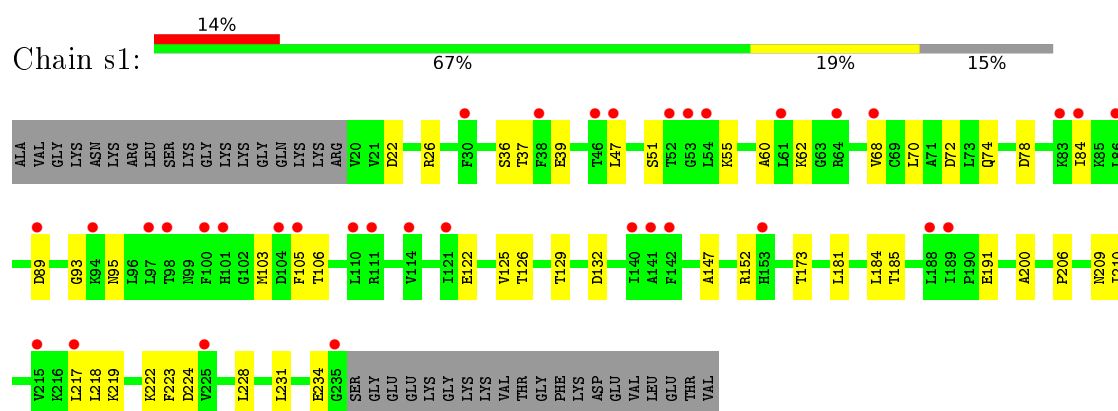
- Molecule 2: 40S ribosomal protein S0-A



• Molecule 3: 40S ribosomal protein S1-A

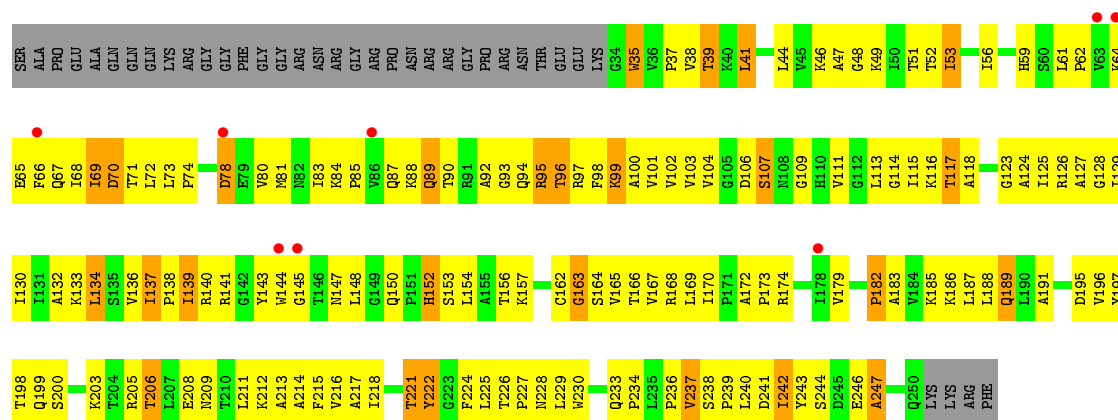


• Molecule 3: 40S ribosomal protein S1-A

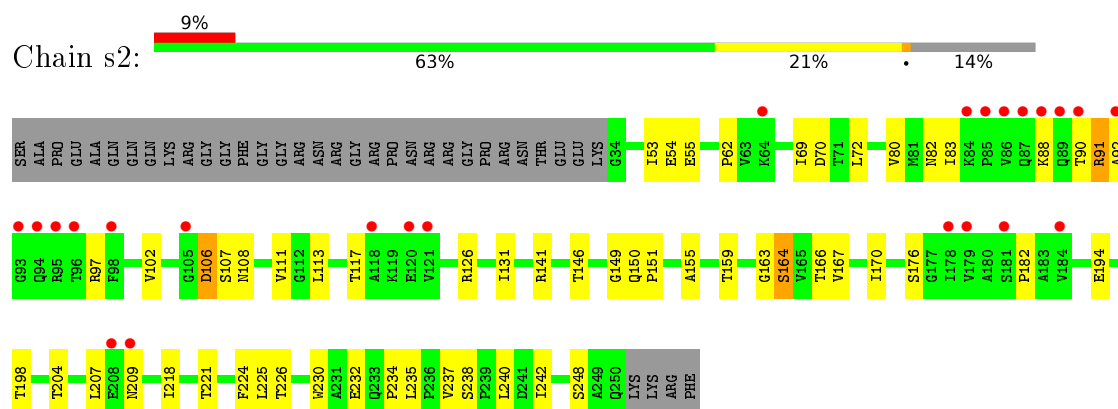


• Molecule 4: 40S ribosomal protein S2

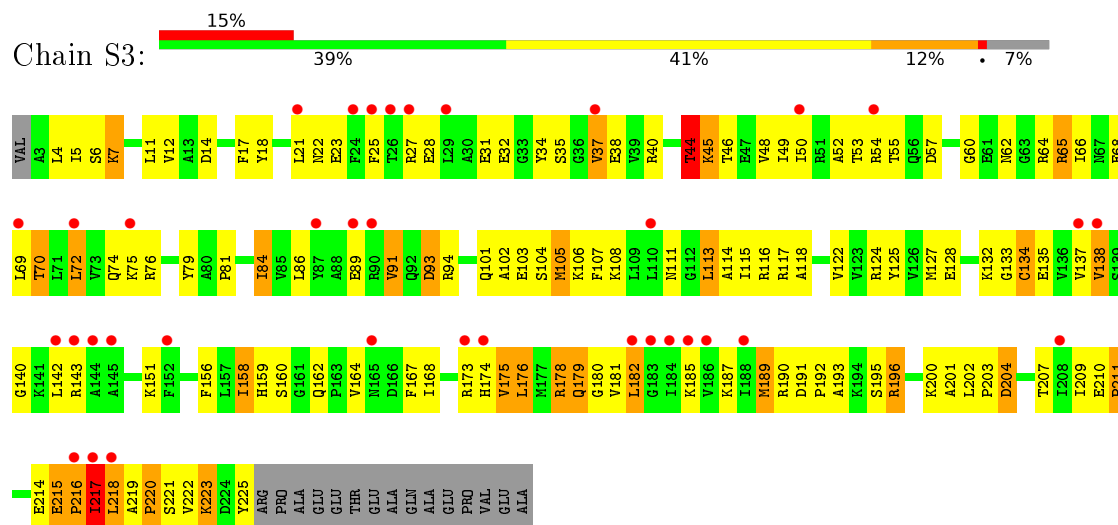




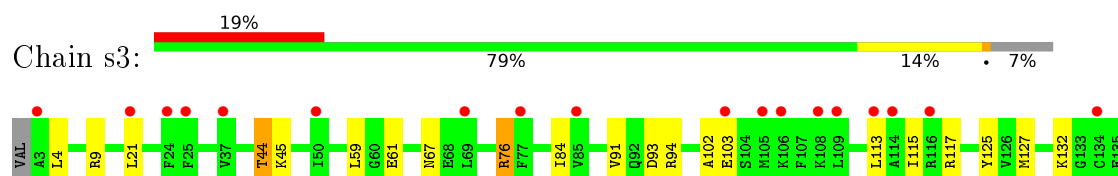
- Molecule 4: 40S ribosomal protein S2

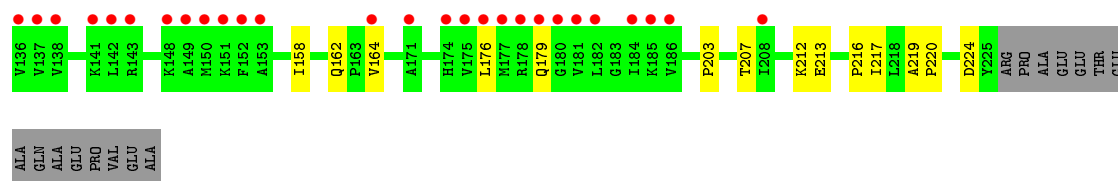


- Molecule 5: 40S ribosomal protein S3

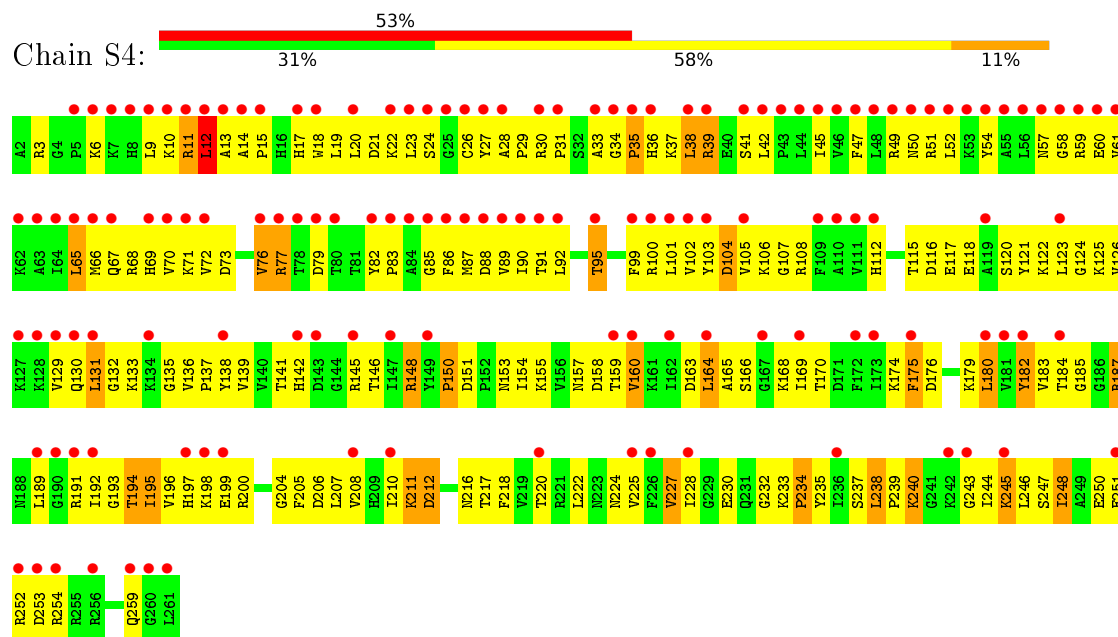


- Molecule 5: 40S ribosomal protein S3

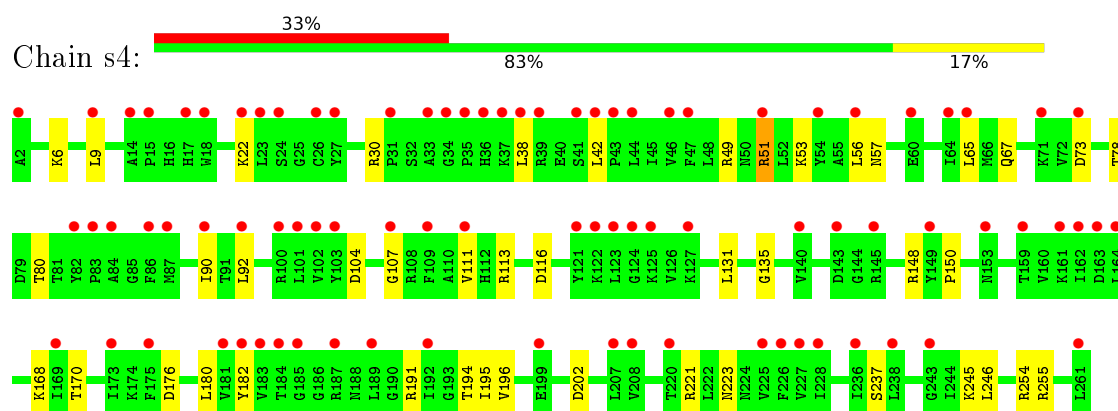




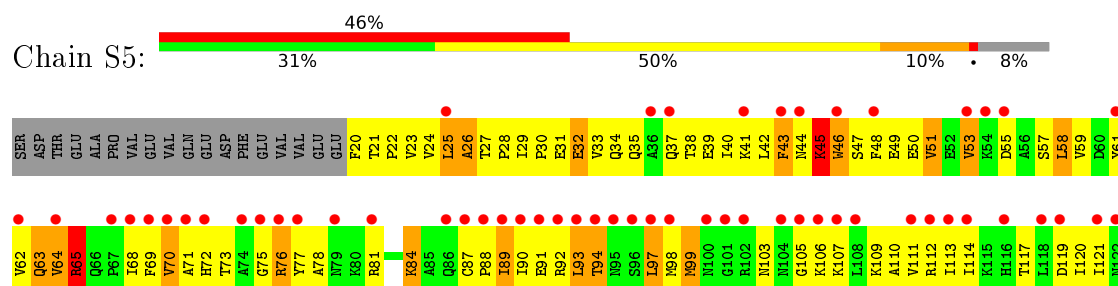
• Molecule 6: 40S ribosomal protein S4-A

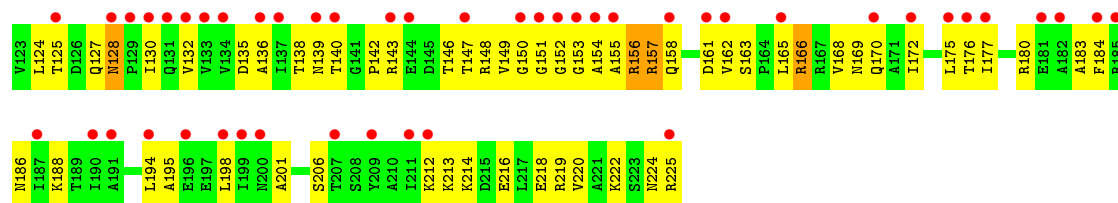


• Molecule 6: 40S ribosomal protein S4-A

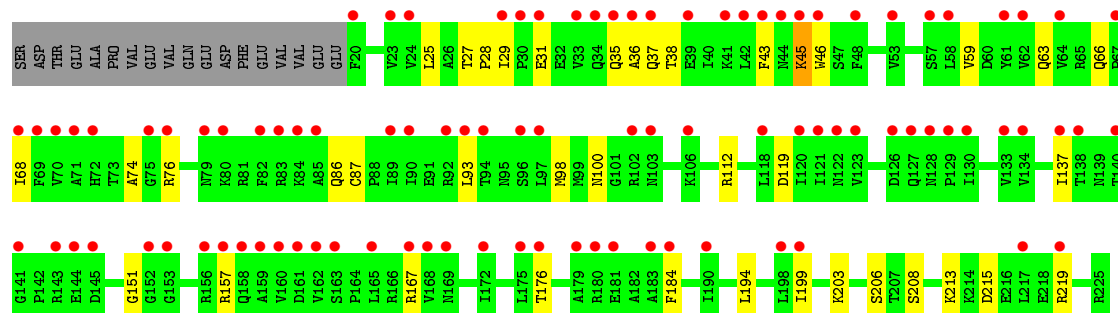
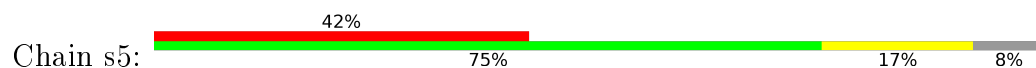


• Molecule 7: 40S ribosomal protein S5

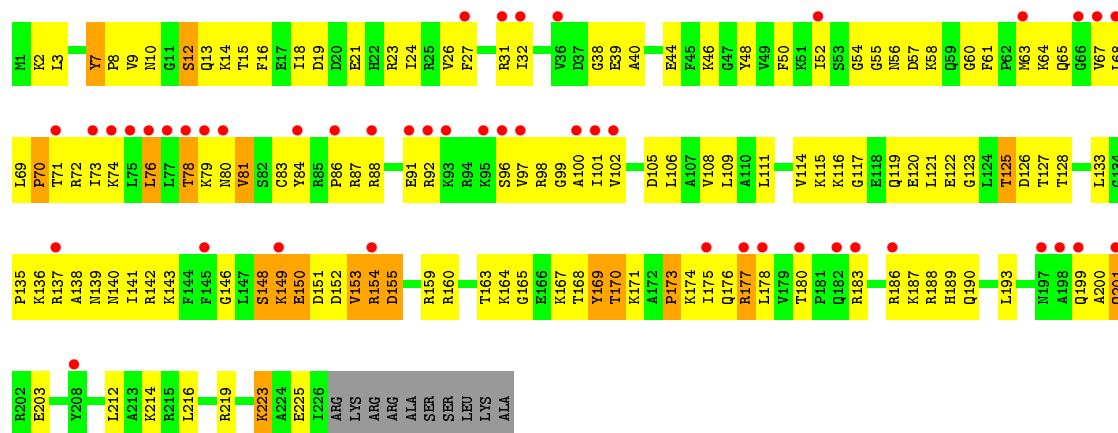




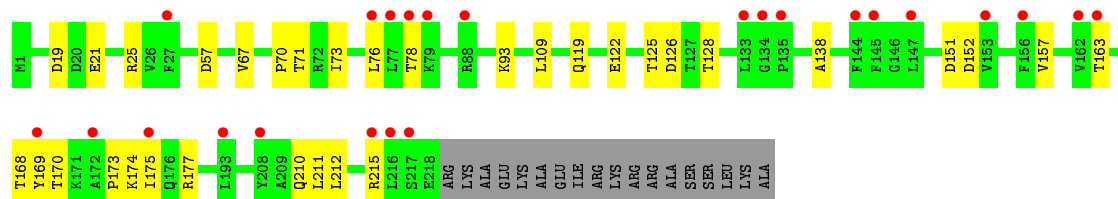
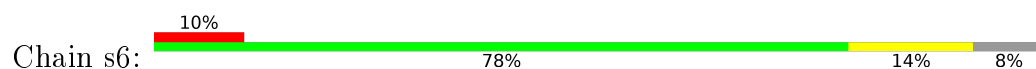
• Molecule 7: 40S ribosomal protein S5



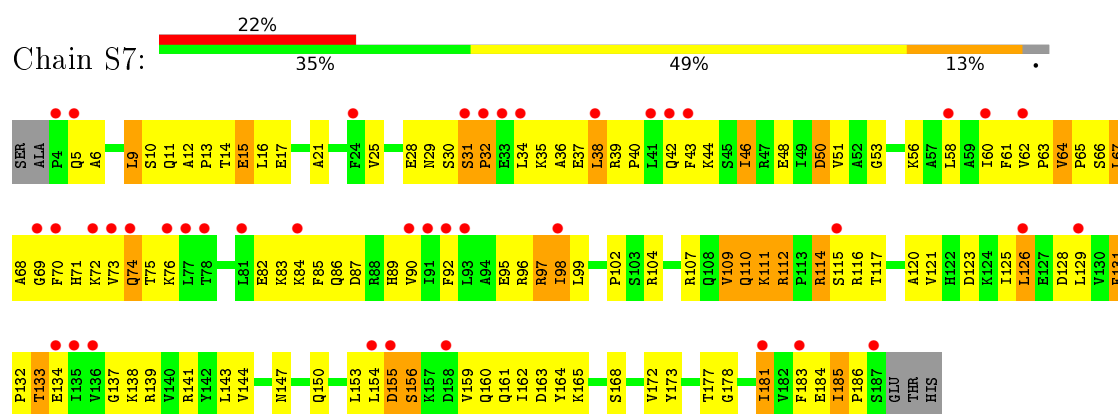
• Molecule 8: 40S ribosomal protein S6-A



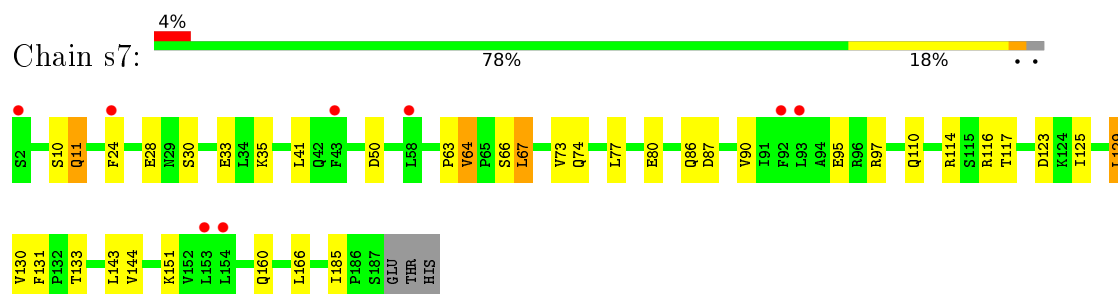
• Molecule 8: 40S ribosomal protein S6-A



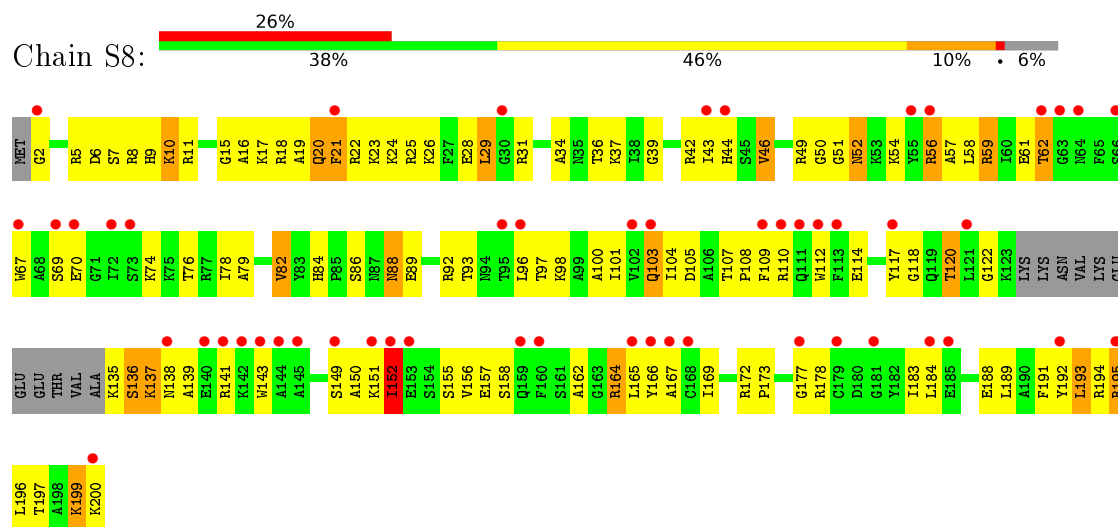
• Molecule 9: 40S ribosomal protein S7-A



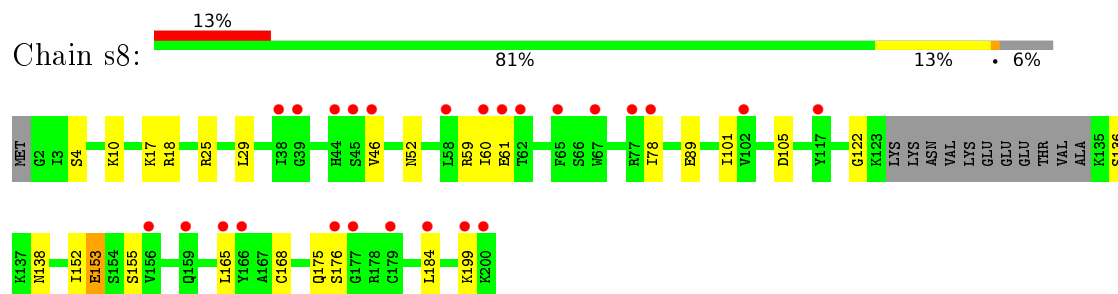
• Molecule 9: 40S ribosomal protein S7-A



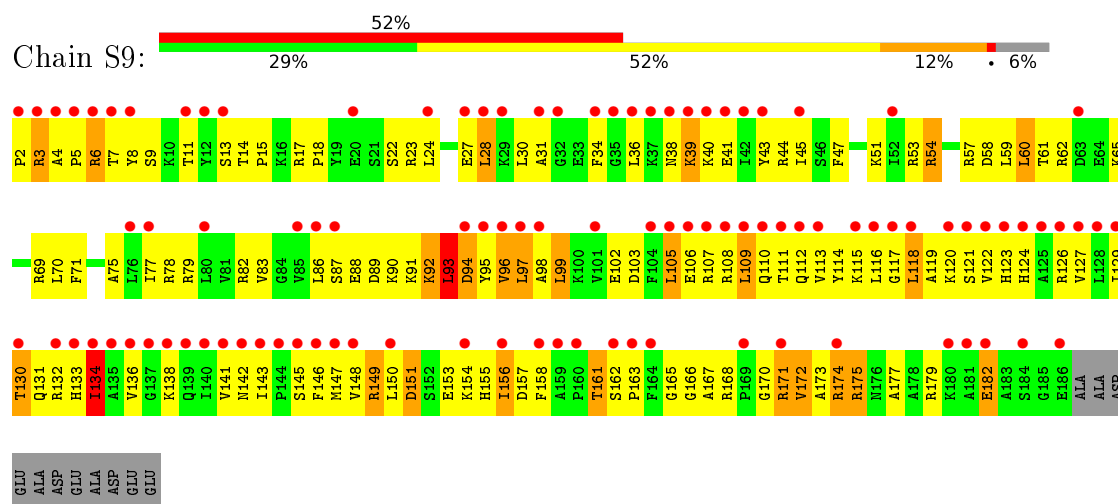
• Molecule 10: 40S ribosomal protein S8-A



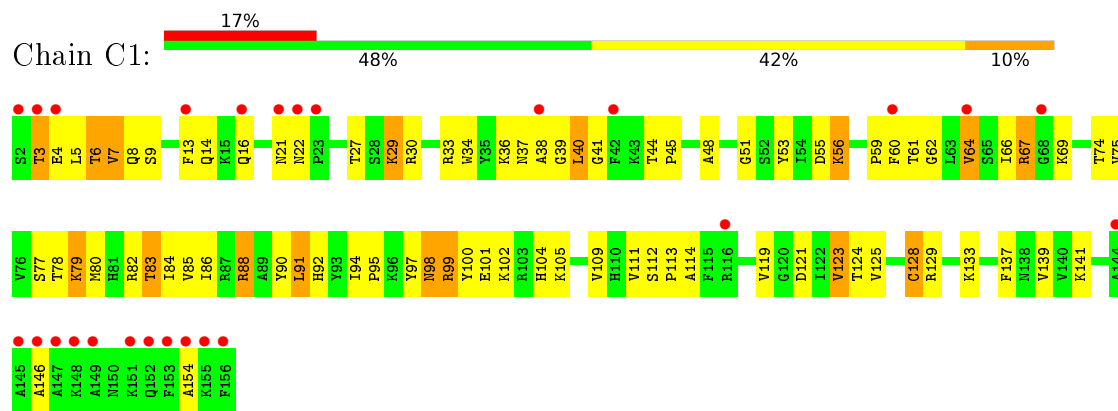
• Molecule 10: 40S ribosomal protein S8-A



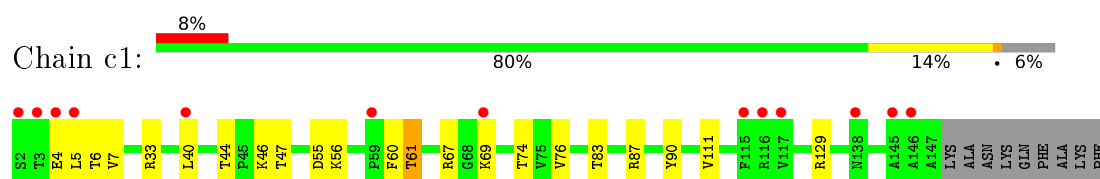
- Molecule 11: 40S ribosomal protein S9-A



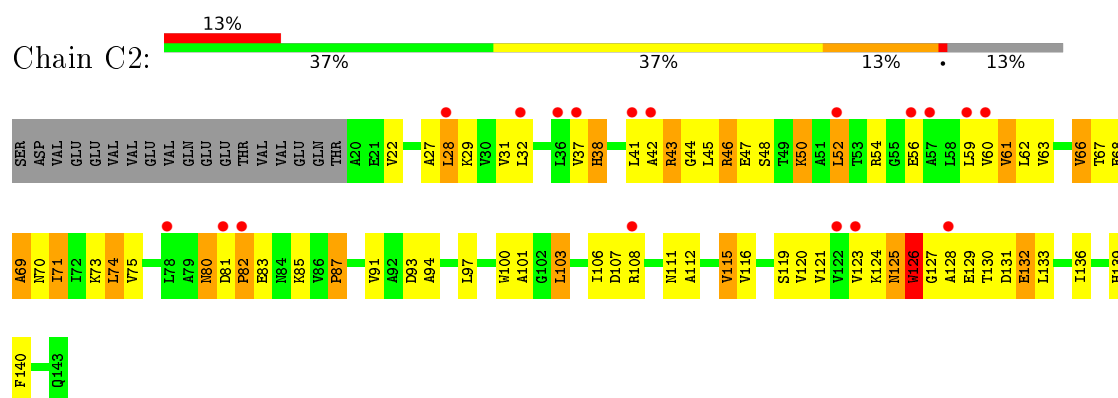
- Molecule 13: 40S ribosomal protein S11-A



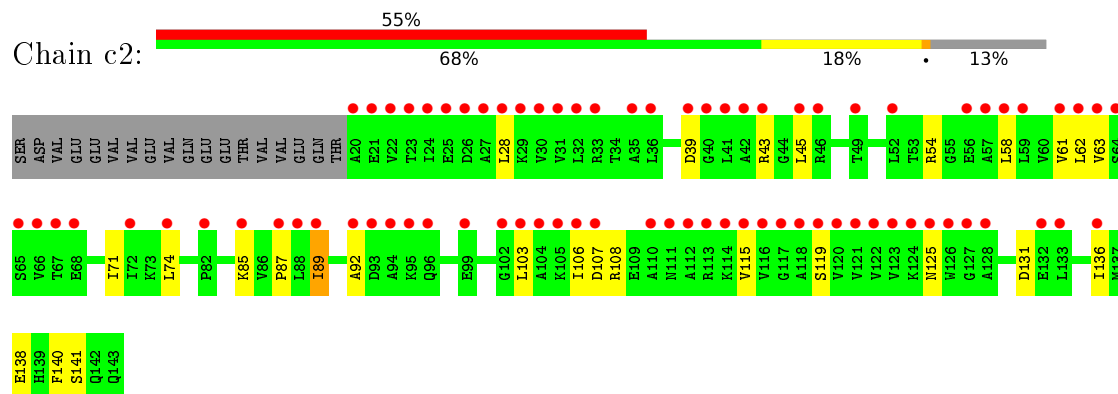
- Molecule 13: 40S ribosomal protein S11-A



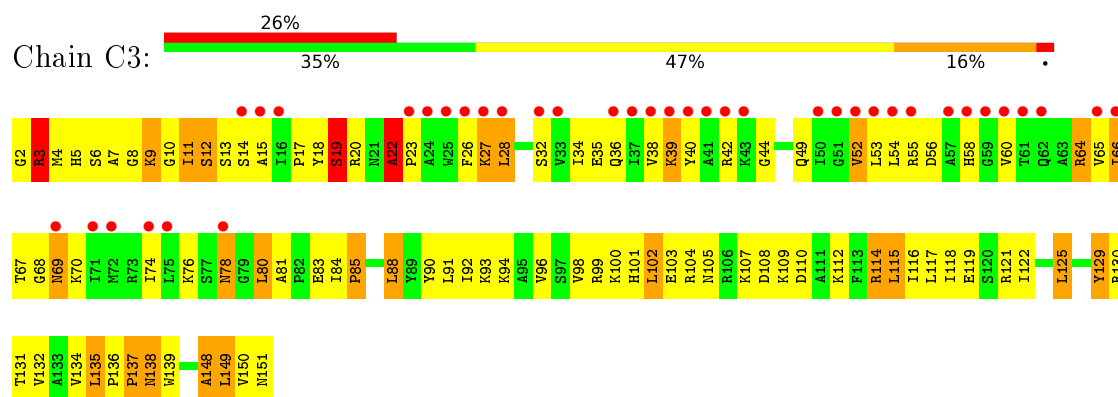
- Molecule 14: 40S ribosomal protein S12



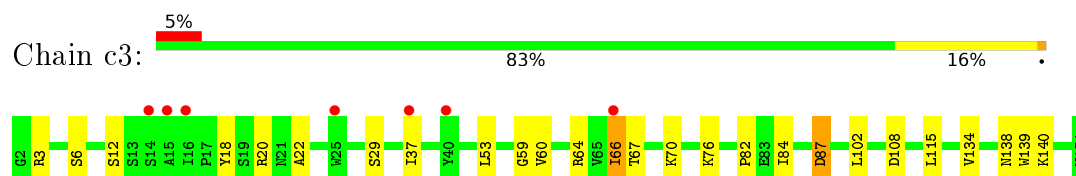
- Molecule 14: 40S ribosomal protein S12



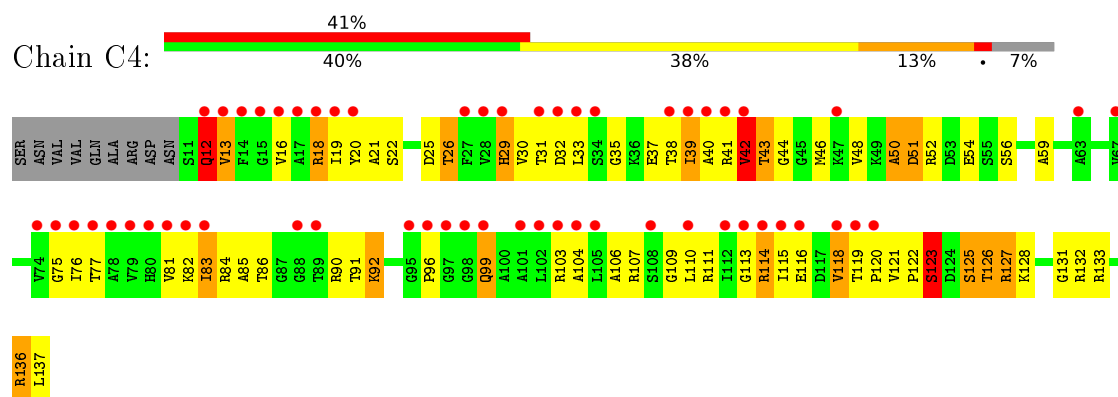
- Molecule 15: 40S ribosomal protein S13



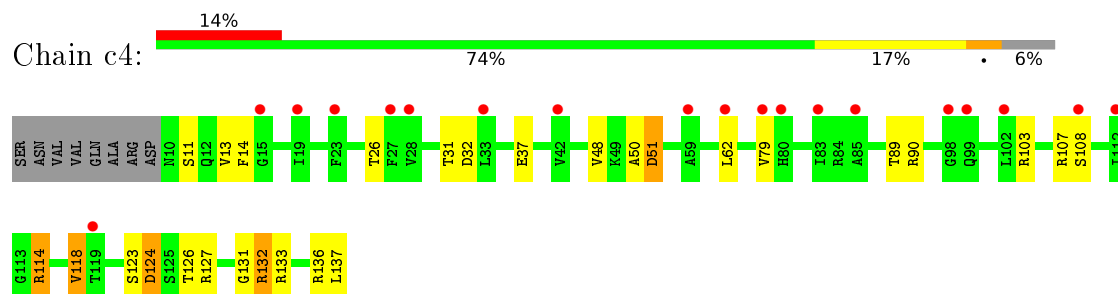
• Molecule 15: 40S ribosomal protein S13



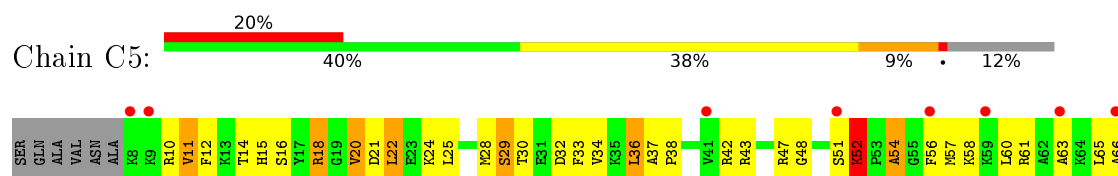
• Molecule 16: 40S ribosomal protein S14-A

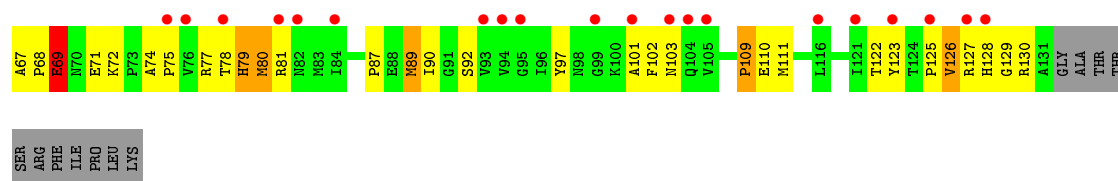


• Molecule 16: 40S ribosomal protein S14-A

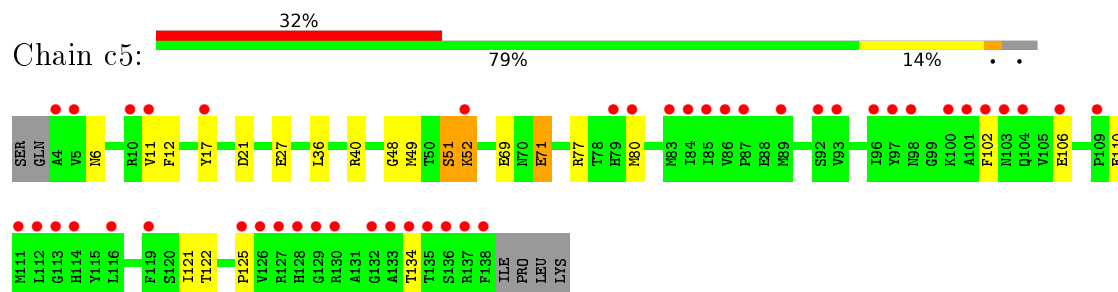


• Molecule 17: 40S ribosomal protein S15

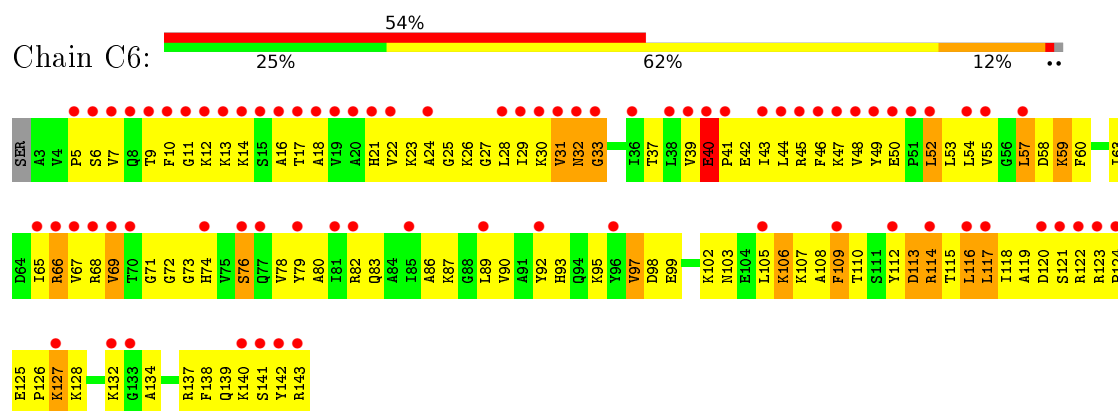




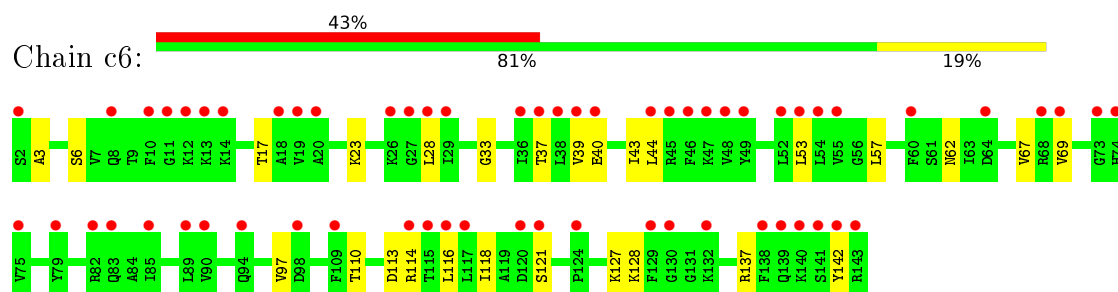
- Molecule 17: 40S ribosomal protein S15



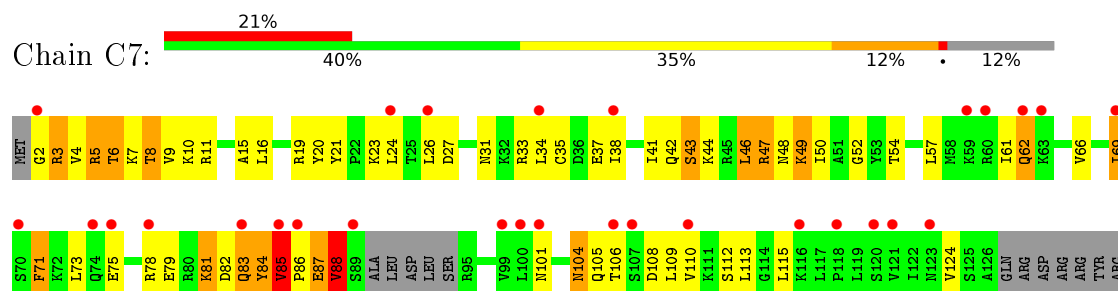
- Molecule 18: 40S ribosomal protein S16-A



- Molecule 18: 40S ribosomal protein S16-A




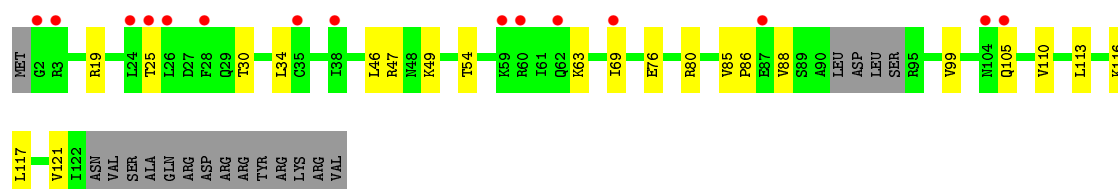
- Molecule 19: 40S ribosomal protein S17-A



LYS
ARG
VAL

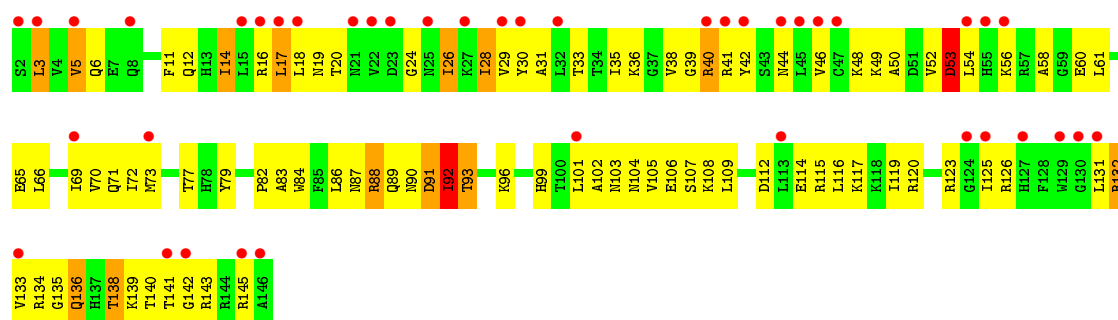
• Molecule 19: 40S ribosomal protein S17-A

Chain c7: 




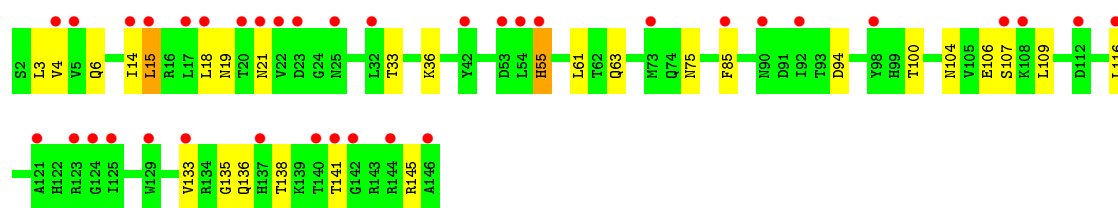
• Molecule 20: 40S ribosomal protein S18-A

Chain C8: 



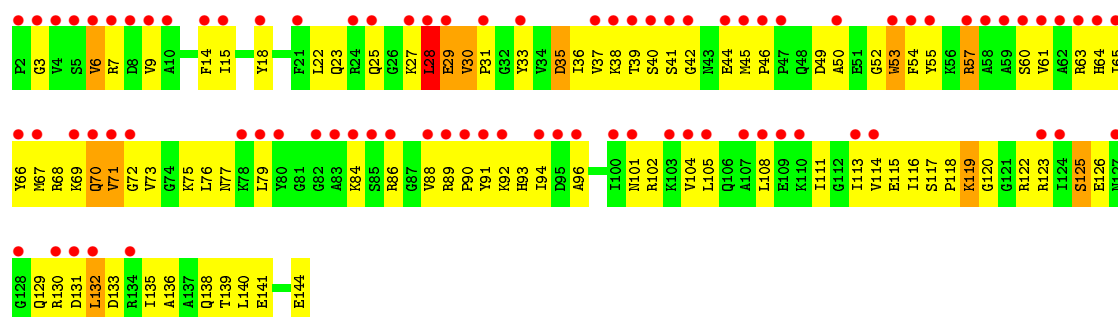
• Molecule 20: 40S ribosomal protein S18-A

Chain c8: 

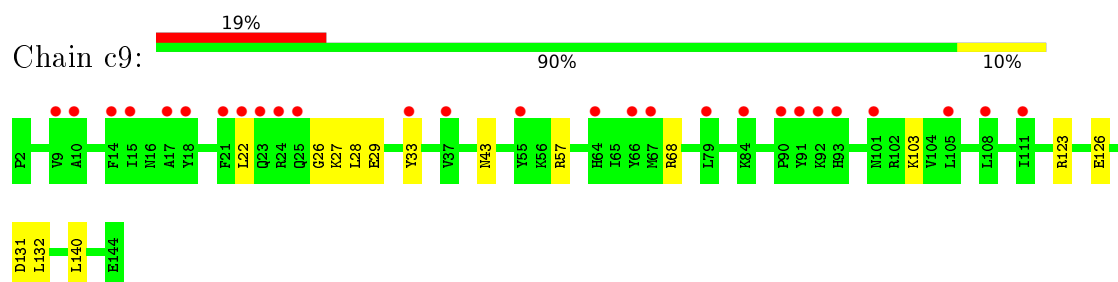


• Molecule 21: 40S ribosomal protein S19-A

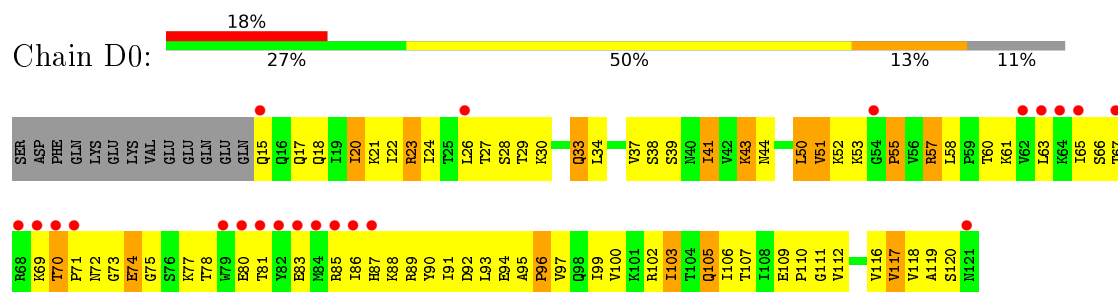
Chain C9: 



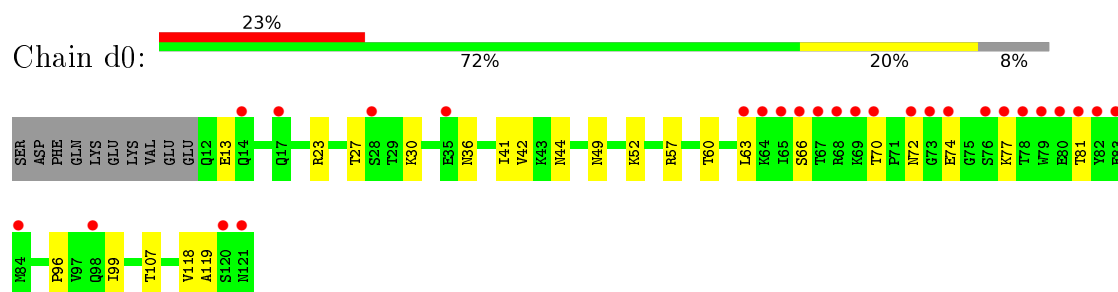
- Molecule 21: 40S ribosomal protein S19-A



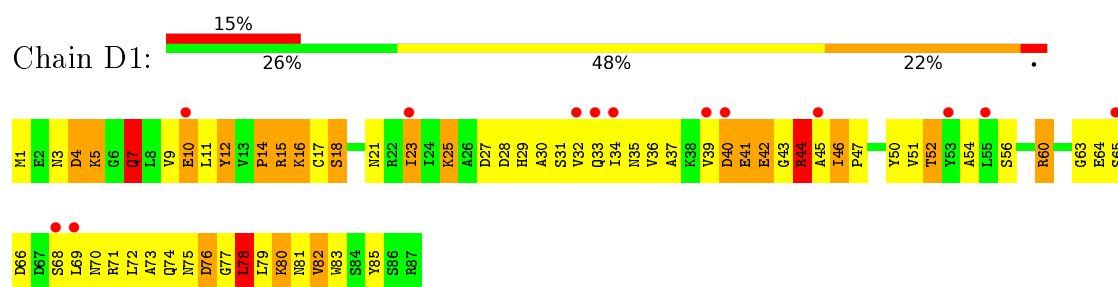
- Molecule 22: 40S ribosomal protein S20



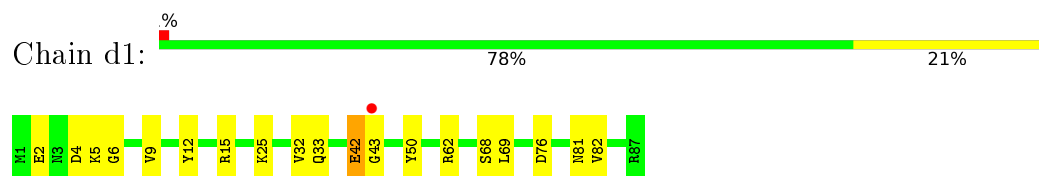
- Molecule 22: 40S ribosomal protein S20



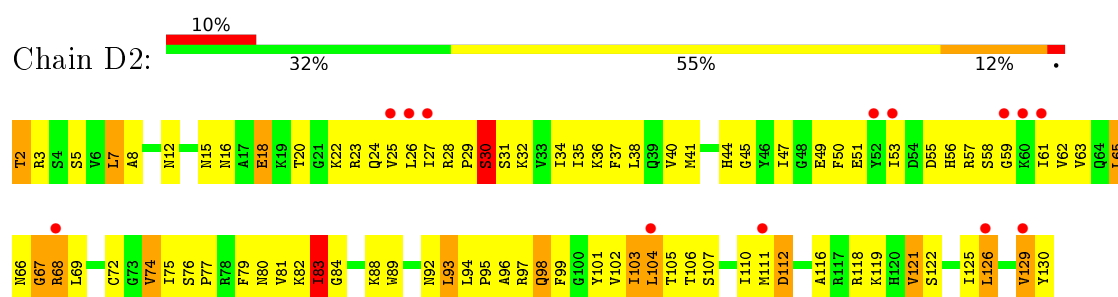
- Molecule 23: 40S ribosomal protein S21-A



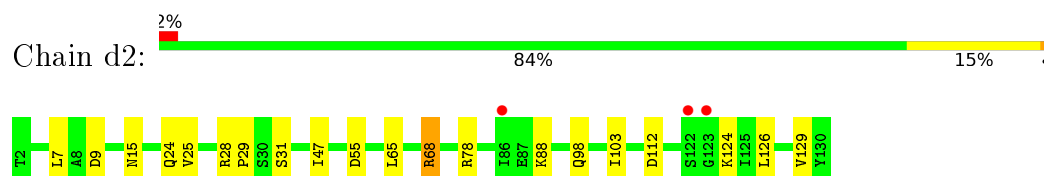
- Molecule 23: 40S ribosomal protein S21-A



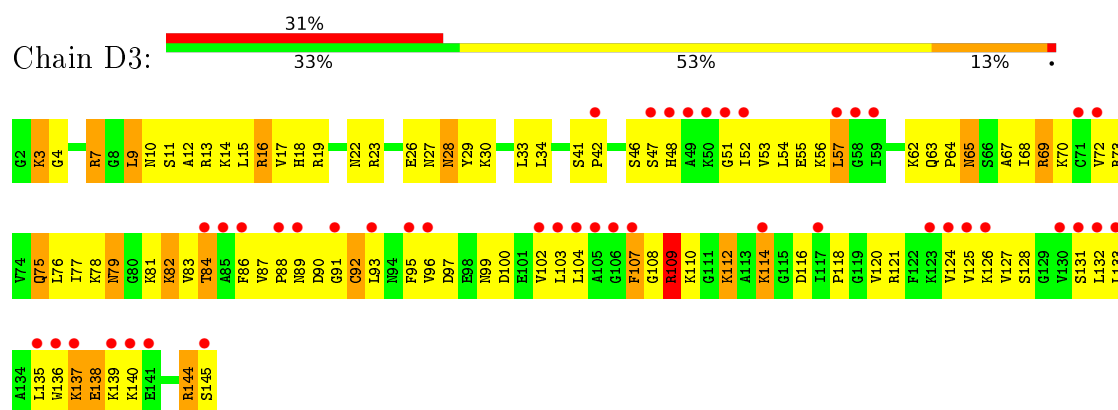
- Molecule 24: 40S ribosomal protein S22-A



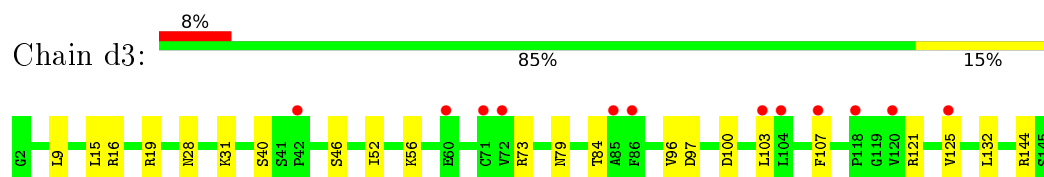
- Molecule 24: 40S ribosomal protein S22-A



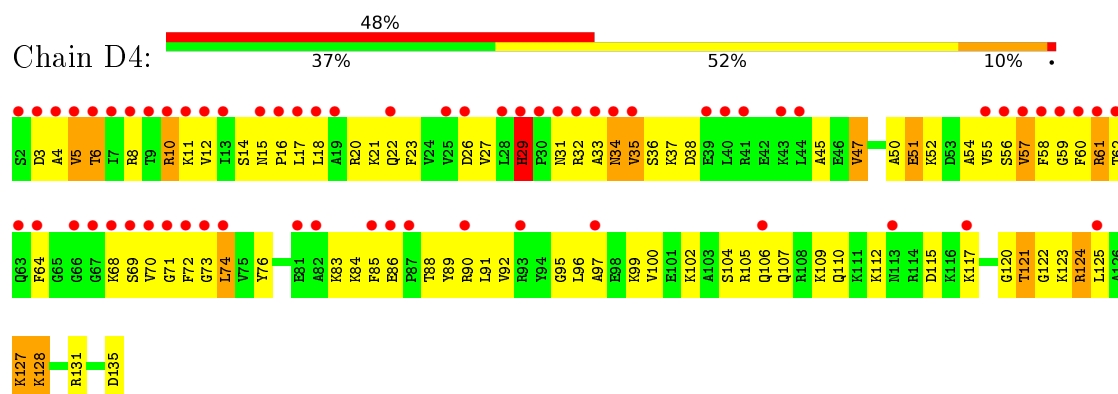
- Molecule 25: 40S ribosomal protein S23-A



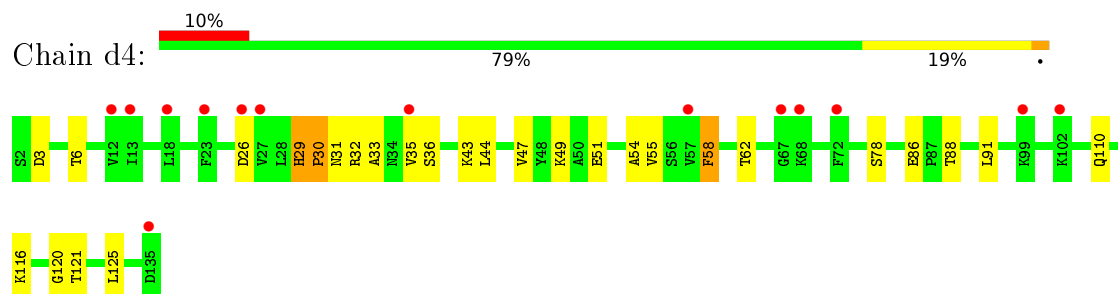
- Molecule 25: 40S ribosomal protein S23-A



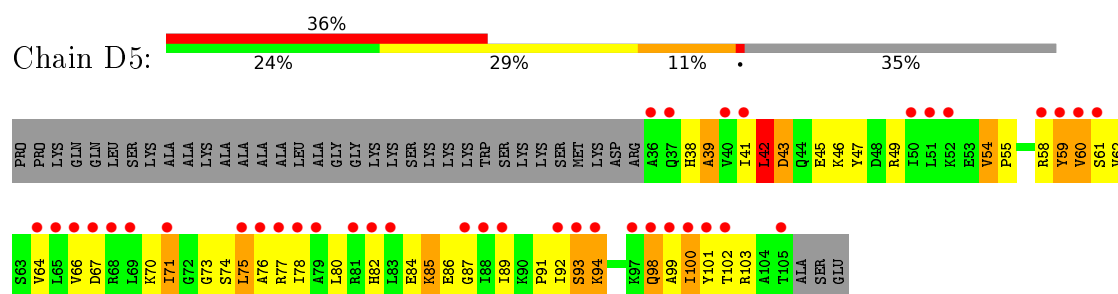
- Molecule 26: 40S ribosomal protein S24-A



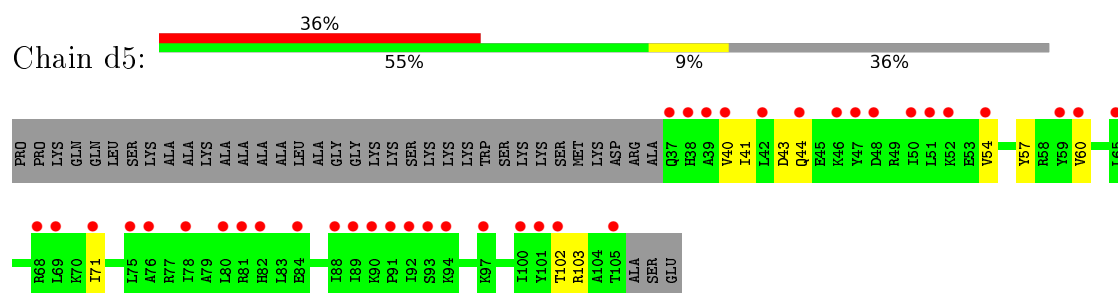
- Molecule 26: 40S ribosomal protein S24-A



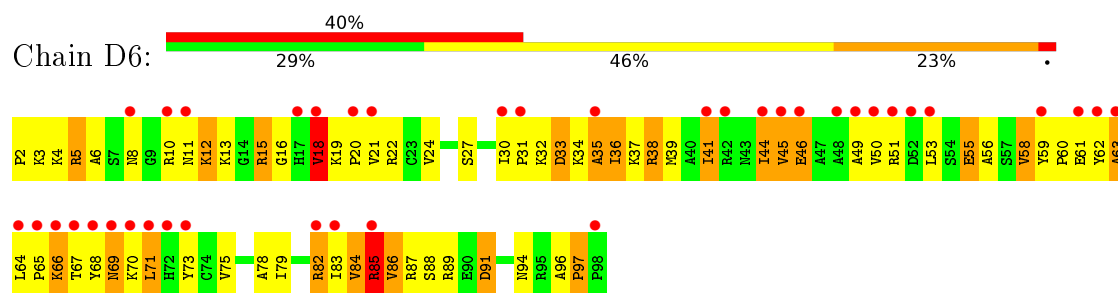
- Molecule 27: 40S ribosomal protein S25-A



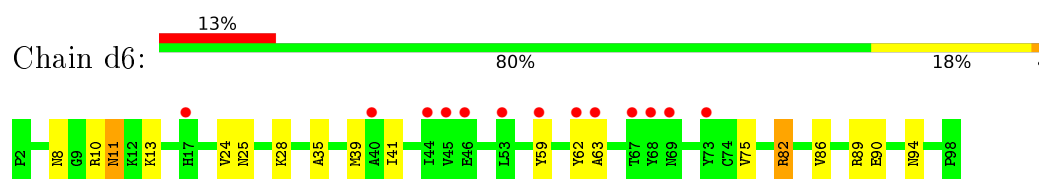
- Molecule 27: 40S ribosomal protein S25-A



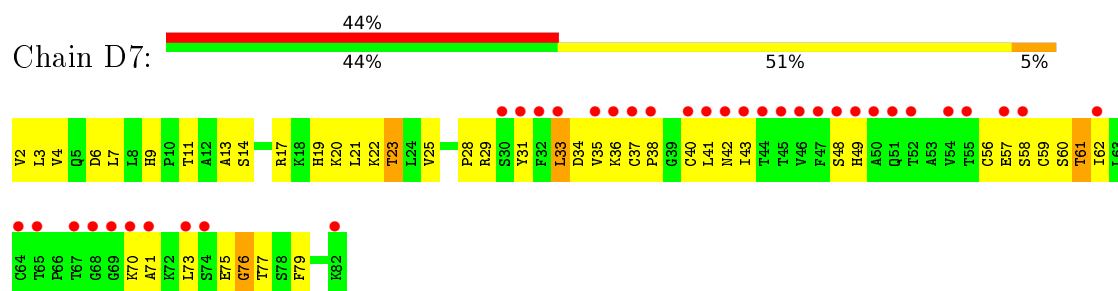
- Molecule 28: 40S ribosomal protein S26-A



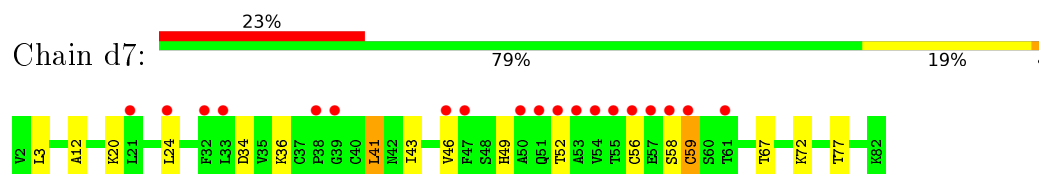
- Molecule 28: 40S ribosomal protein S26-A



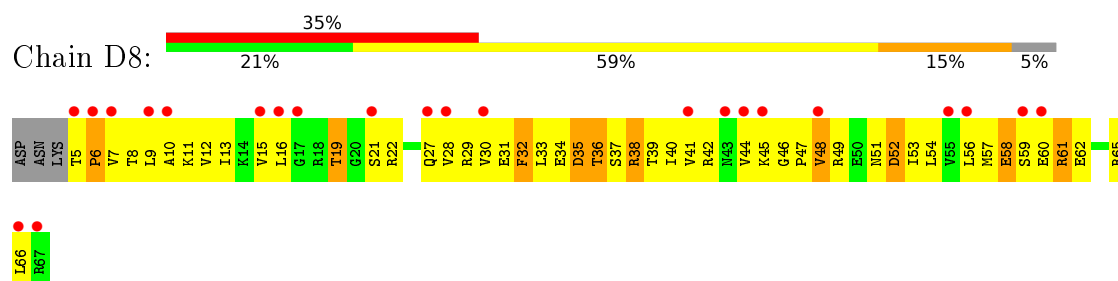
- Molecule 29: 40S ribosomal protein S27-A



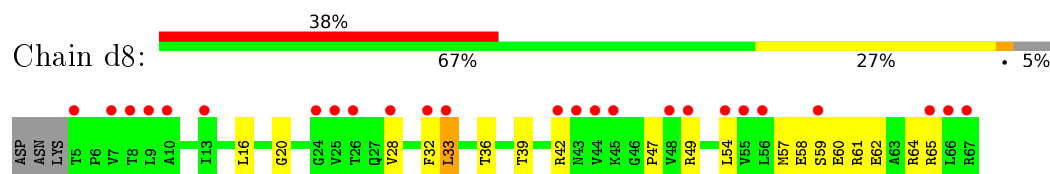
- Molecule 29: 40S ribosomal protein S27-A



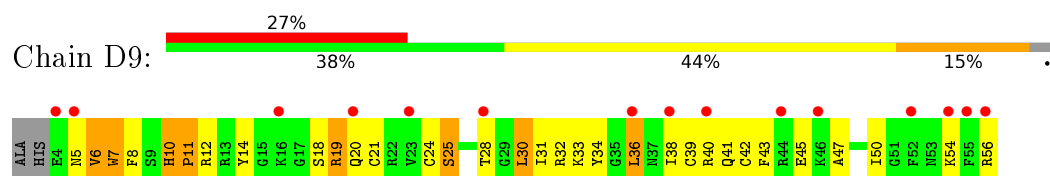
- Molecule 30: 40S ribosomal protein S28-A



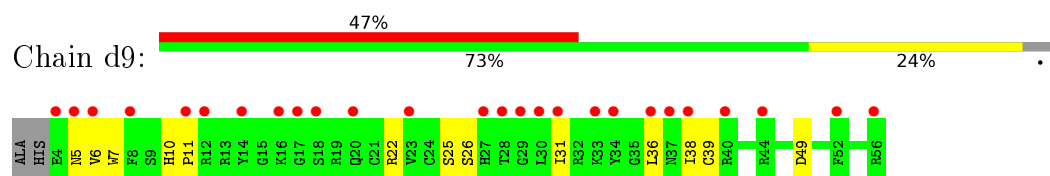
- Molecule 30: 40S ribosomal protein S28-A



- Molecule 31: 40S ribosomal protein S29-A

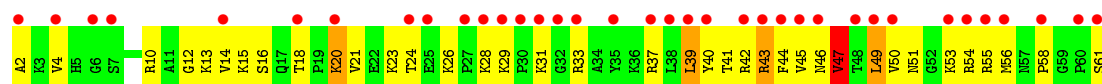


- Molecule 31: 40S ribosomal protein S29-A

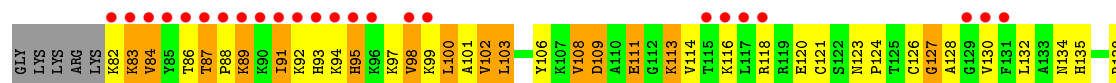


- Molecule 32: 40S ribosomal protein S30-A

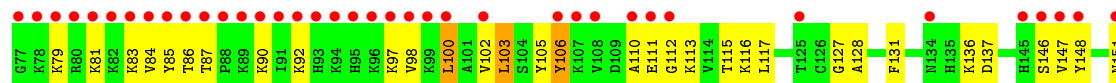




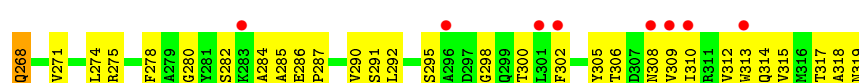
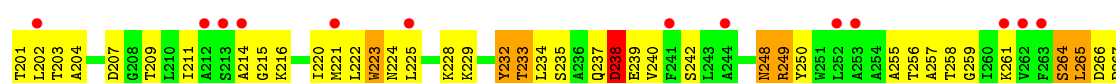
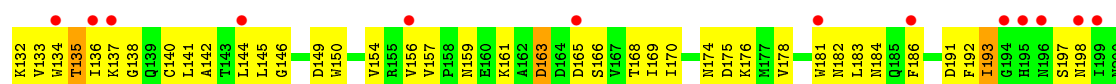
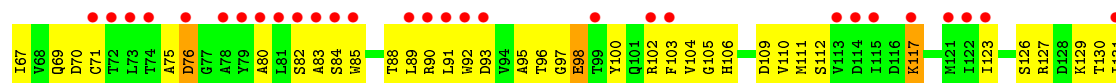
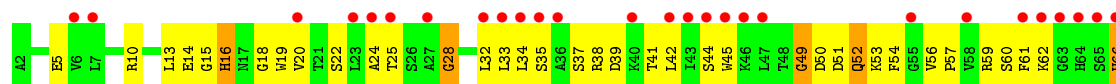
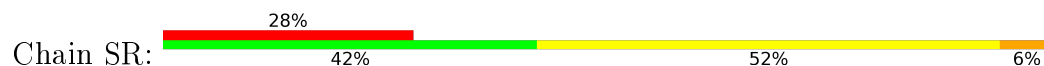
• Molecule 33: Ubiquitin-40S ribosomal protein S31



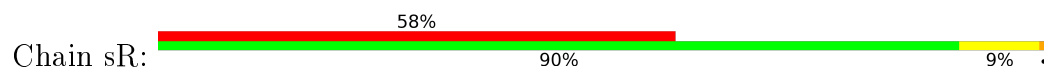
• Molecule 33: Ubiquitin-40S ribosomal protein S31

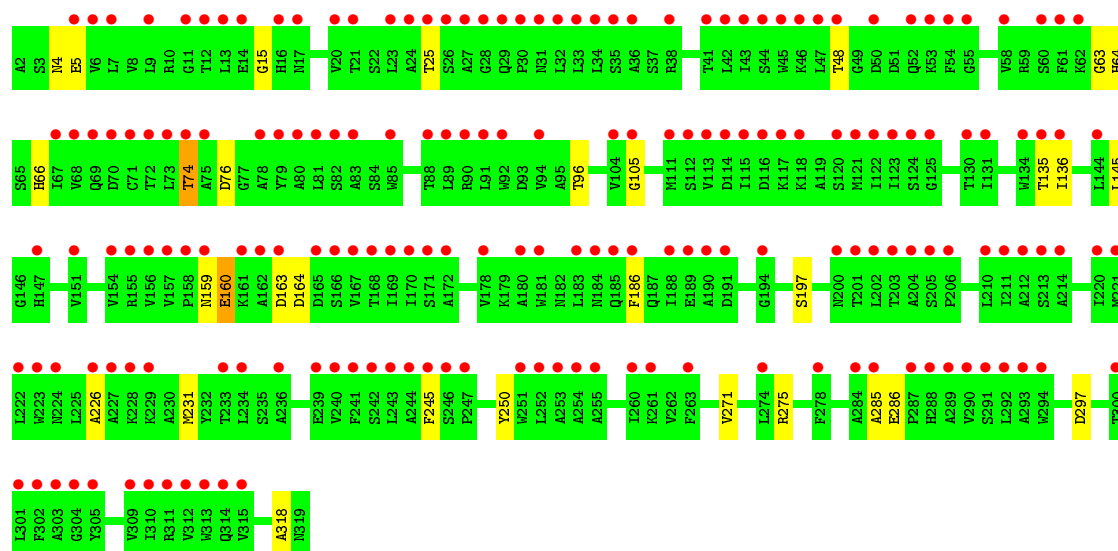


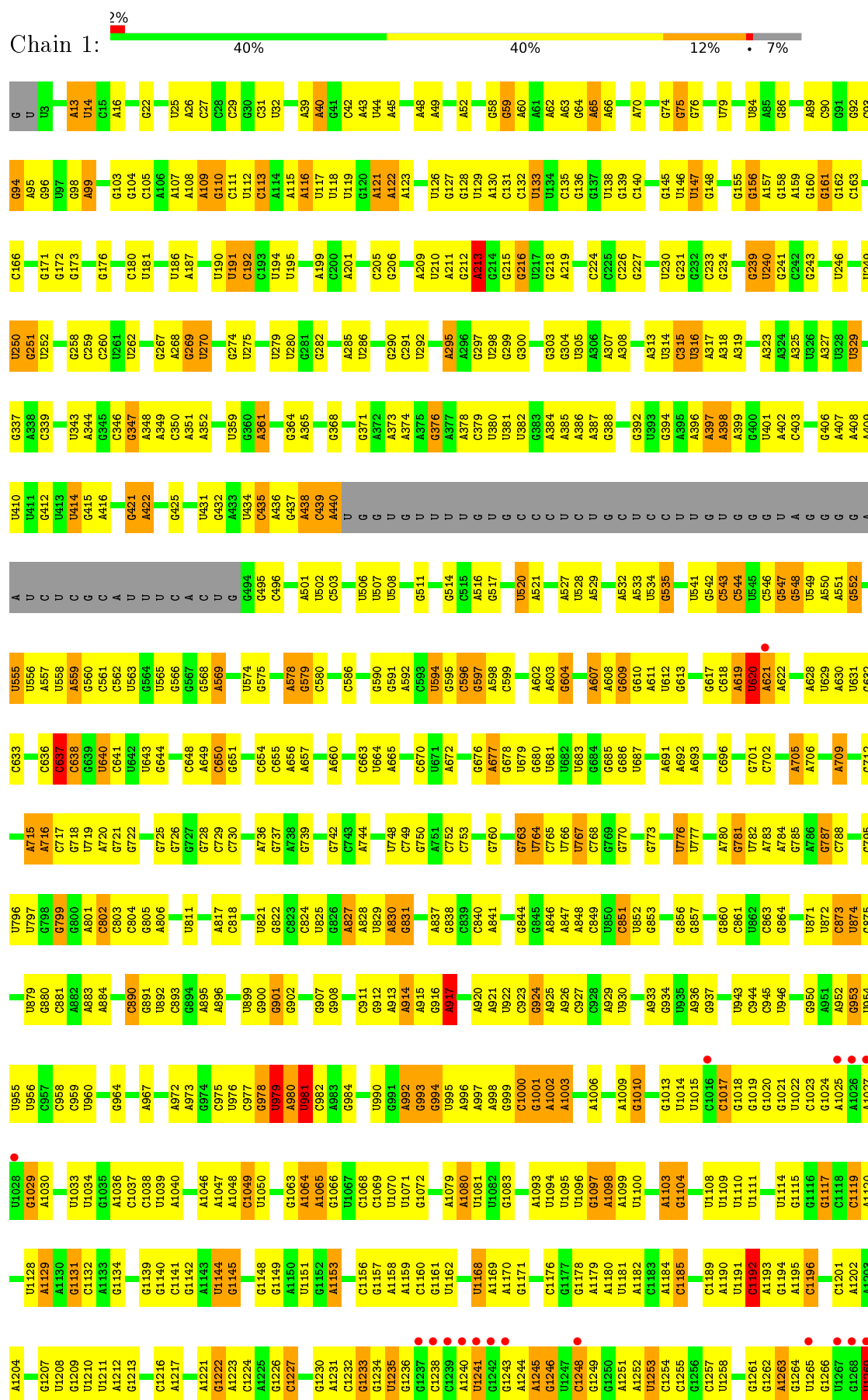
• Molecule 34: Guanine nucleotide-binding protein subunit beta-like protein



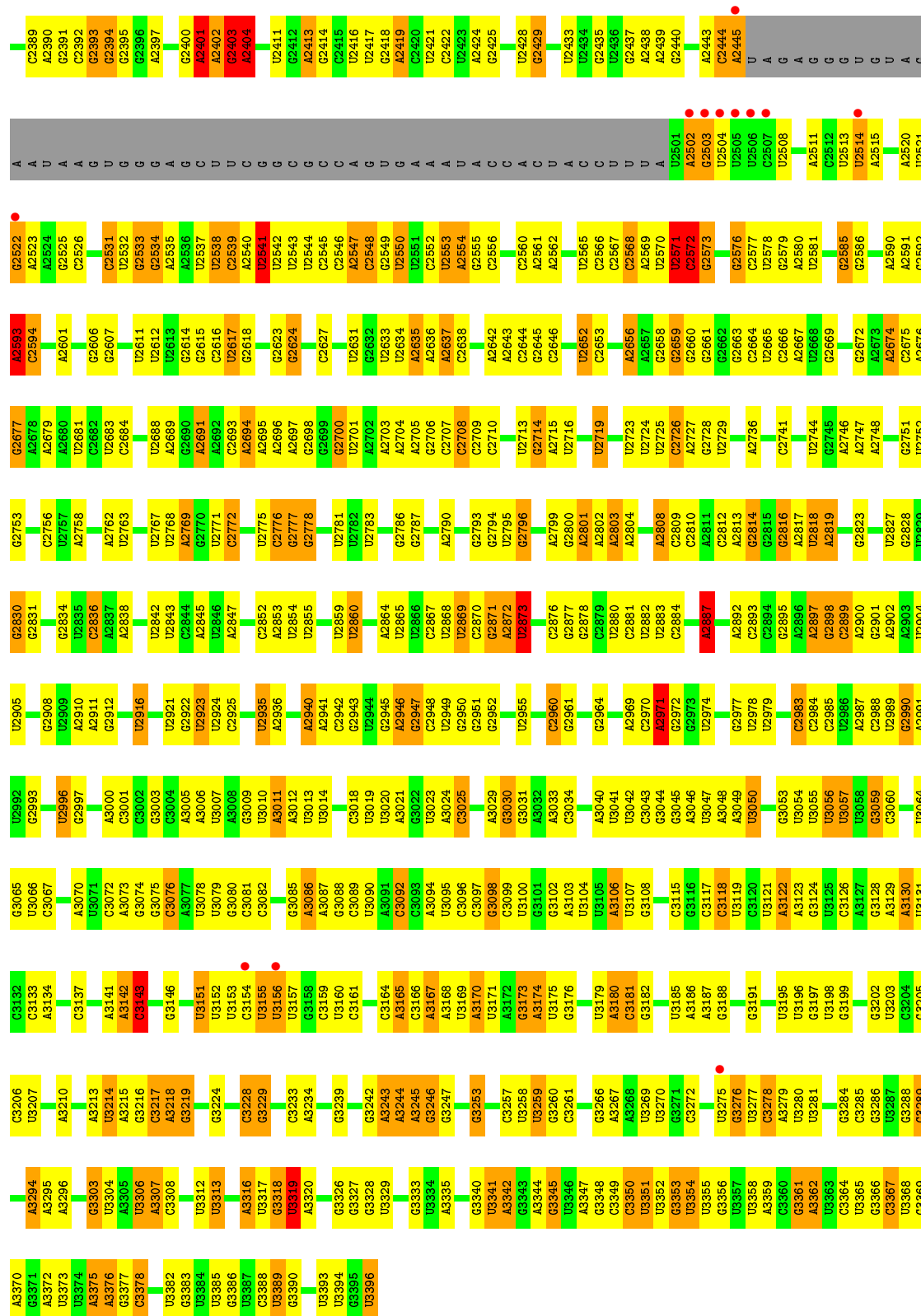
• Molecule 34: Guanine nucleotide-binding protein subunit beta-like protein







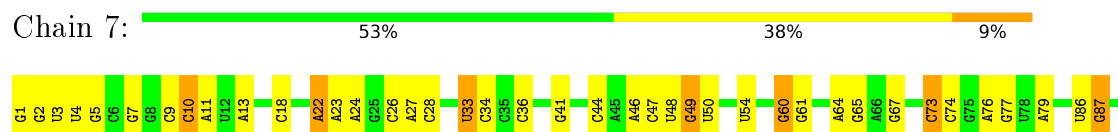
U2310	C2335	A2158	U	A1813	U1759	G1653	C1595	G1507	G1346	A1270
G2311	G2236	U2162	A	A1814	U1740	A1654	G1586	C1508	U1347	A1271
A2312	U2162	C2163	C	A1815	A1741	C1657	A1587	G1514	U1348	C1272
A2313	C2163	A2164	U	A1816	U1742	C1657	A1588	G1514	A1349	A1273
G2314	C2163	A2164	A	A1817	G1743	C1657	A1589	G1520	U1350	C1274
G2315	G2165	A2165	U	A1818	G1744	U1659	A1592	G1520	U1351	G1275
G2316	A2166	A2166	U	A1819	G1748	C1660	A1593	G1521	U1352	U1276
A2317	G2169	G2169	A	A1820	A1749	C1661	A1594	U1522	A1353	C1277
U2318	U2170	G2171	G	A1821	A1750	C1665	U1595	G1525	U1354	C1278
A2321	C2244	G2171	C	A1822	A1751	G1666	C1596	G1526	A1355	C1279
C2322	C2244	G2171	C	A1823	A1752	A1667	G1597	C1527	A1356	C1280
G2323	C2244	G2171	C	U1824	G1753	G1668	G1598	G1528	G1357	
A2324	U2175	U2175	U	G1829	G1758	C1669	G1599			
C2325	U2176	U2176	C	A1830	G1761	U1672	A1602	U1533	C1360	G1285
A2326	A2177	A2177	C	U1831	C1762	G1673	A1603	A1534	U1361	A1286
C2327	G2185	G2185	U	G1832	C1761	G1674	A1604	A1534	G1362	A1287
U2328	U2186	U2186	U	G1833	U1763	G1675	G1605	G1535	U1363	
C2329	G2187	G2187	U	U1834	U1764	A1677	U1606	A1537	C1364	U1293
A2330	A2188	A2188	G	A1835	G1765	G1677	U1607	G1541	A1365	U1294
C2331	U2189	U2189	U	U1836	G1766	C1677	C1608	G1542	A1366	G1295
U2332	C2261	C2261	C	G1837	C1767	U1682	U1608	G1543	U1367	C1296
C2333	G2192	G2192	A	U1838	U1768	A1683			U1368	C1297
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C2335	C2194	C2194	U	U1840	G1770	U1688	A1612	U1550	A1301	
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A2343	U2205	U2205	G	A1849	G1786	G1712	G1622	A1558	G1313	
U2344	G2206	G2206	U	A1850	A1787	G1713	G1624	G1560	C1314	
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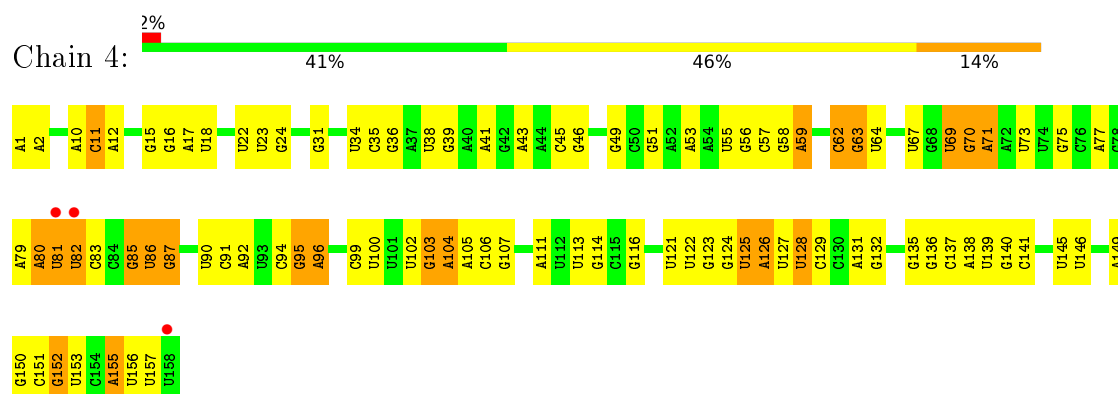
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G1238	U1074	U1074	U990	U828	U642	U642			A422	U253	C174		G24
A1239	A1075	A1075	G993	A829	U643	U643	C573	U492	U431	A254	U178		U25
U1241	U1076	U1076	G994	G830	G644	G644	U574	G495	G436	A255	C179		A26
G1242	U1077	U1077	G995	G831	A646	A646	C575	U496	A437	G256	U180		C29
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G1249	G1161	A1085	A1002	C840	A744	A744	A592	G514	G443	A269	U190		A43
	U1162	C1086	C927	A847			C593	C515	U	U270	U191		A44
				A848	C655	C655	U594		U	C192	U192		U44
A1252	A1170	C1087	G934	A849	A656	A656	U595	U520	U	G193	C193		A45
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G1255	U1094	U1094	A936	U850	G658	G658	G590	A522	C	G196	G197		A49
G1256	U1095	U1095	G937	C851	A660	A660	A591	U524	C	U126	G127		U50
G1257	U1096	U1096	C938	U852			A592	C525	U	U127	G128		A51
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A1259	A1098	U1015	U942	U854	A665	A665	U594	U520	U	G282	C200		G56
A1260	U1099	C1016	U943	U855			A598	A523	C	G283	A201		G57
G1261	A1178	A1098	C944	G856	G674	G674	C598	U524	U	G284	G202		G58
G1262	G1101	G1018	C945	G857	G675	G675	G600	U528	C	A285	C208		G59
A1263	A1102	G1019	C945	G860	G676	G676	U601	C525	U	U286	A209		A60
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G1266	A1105		A952	G863	U681	U681	G604	A529	U	A289	A211		G63
			G953	G864	U682	U682		G530	C	G290	G212		G64
A1270	U1108	A1025	U954	G869	U683	U683	A607	G531	C	C291	A213		G65
A1271	U1109	A1026	U955		G684	G684	A608	A532	C	A295	G218		A66
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G1277	G1113	C873	C957	C873	U777	U777	A610	U536	U		G220		A71
A1278	U1114	U1074	C958	U874	A691	A691	A611		U	U309	A221		C72
C1279	C1196	C959	G875	G875	G781	G781	U612	U541	U		A222		C73
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G1281	C1118	U1034	C961		A699	A699	C614	G542	G	U314	G148		G75
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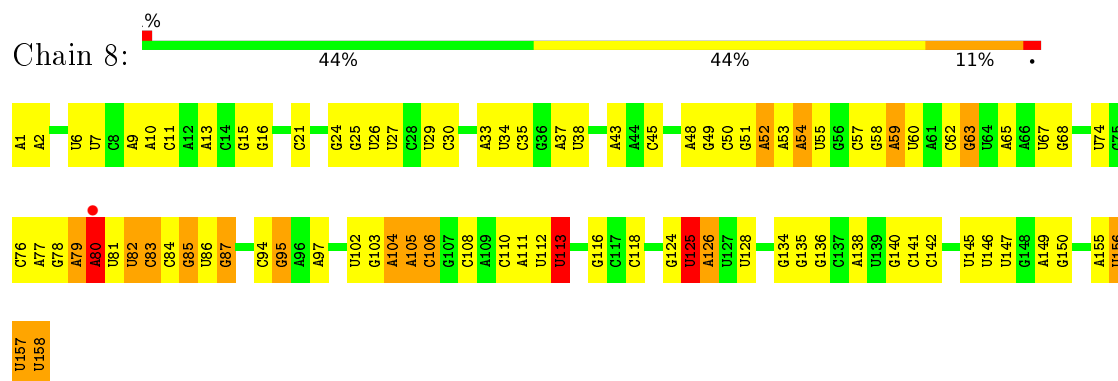




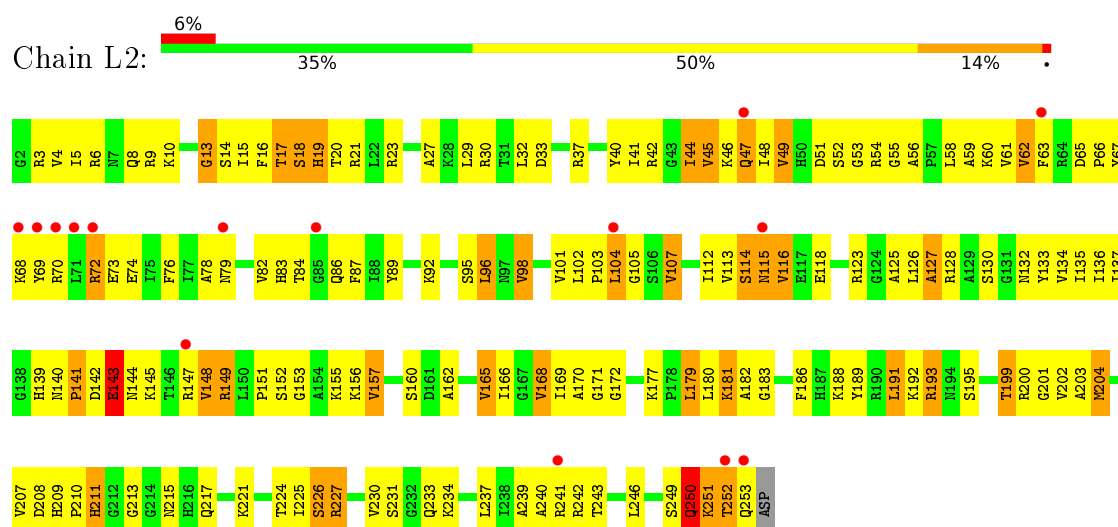
• Molecule 38: 5.8S ribosomal RNA



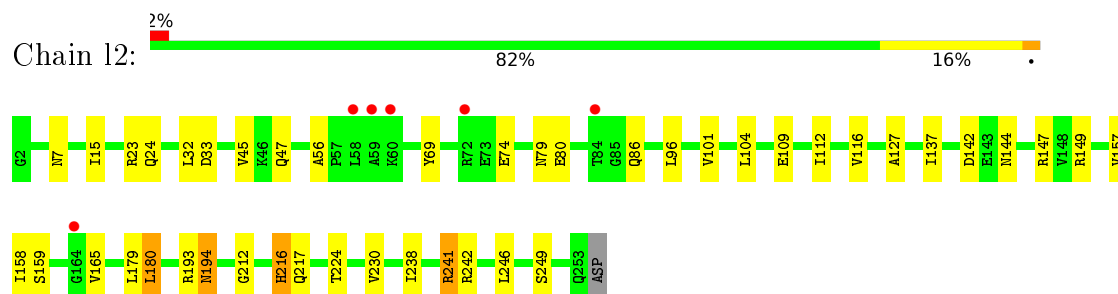
• Molecule 38: 5.8S ribosomal RNA



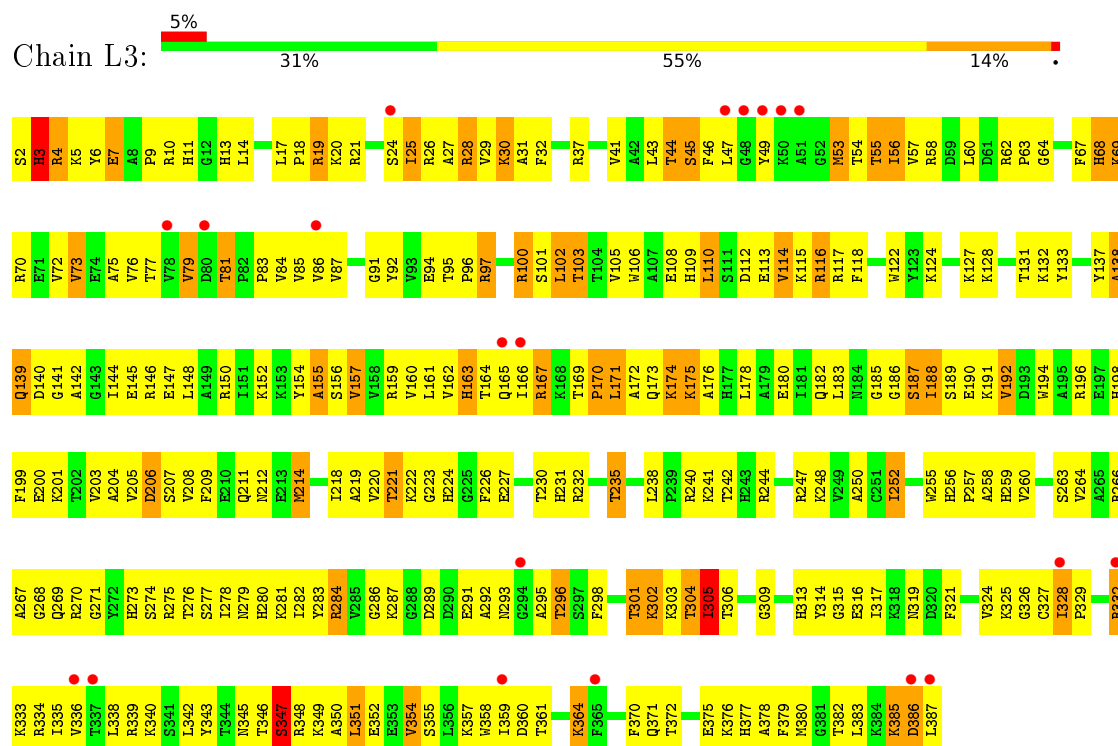
• Molecule 39: 60S ribosomal protein L2-A



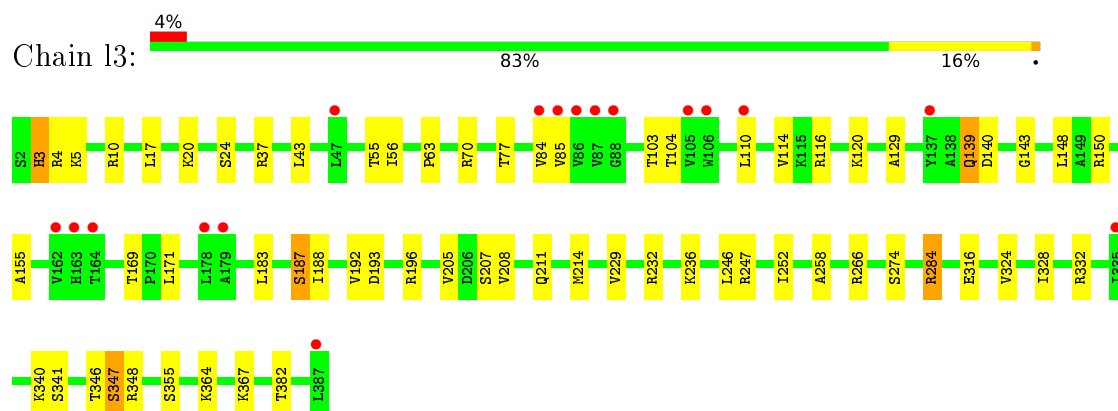
- Molecule 39: 60S ribosomal protein L2-A



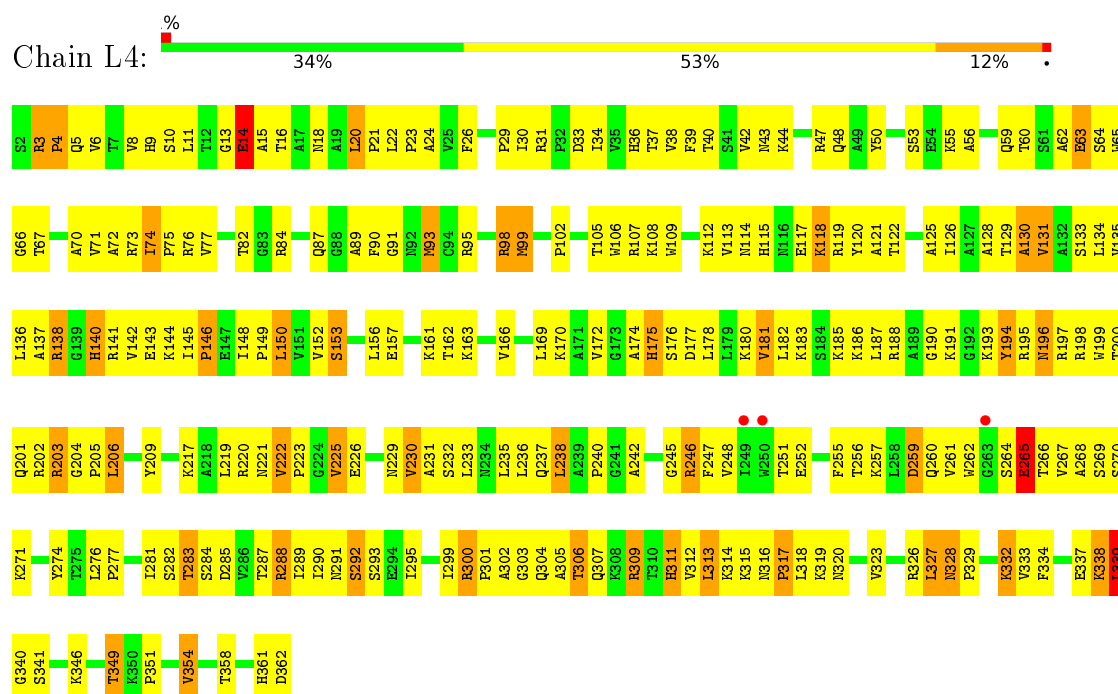
- Molecule 40: 60S ribosomal protein L3



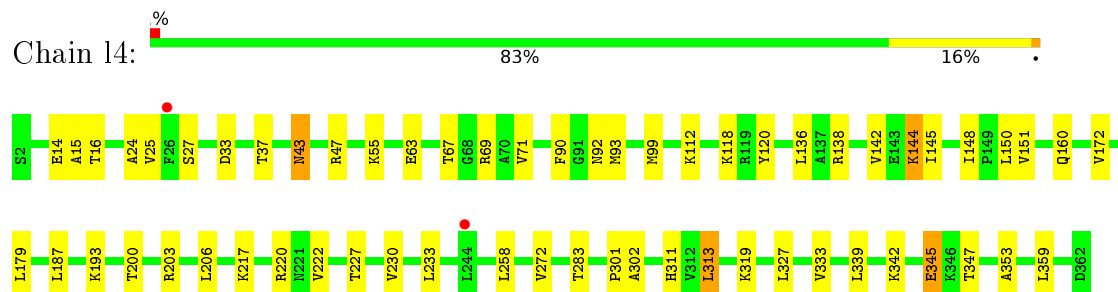
- Molecule 40: 60S ribosomal protein L3



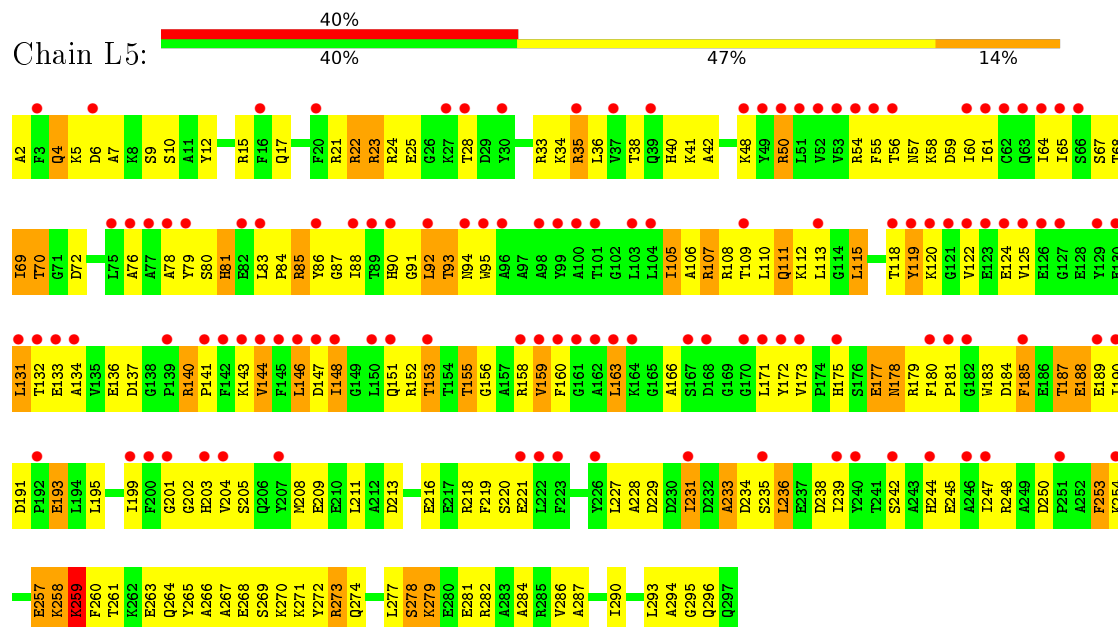
- Molecule 41: 60S ribosomal protein L4-A



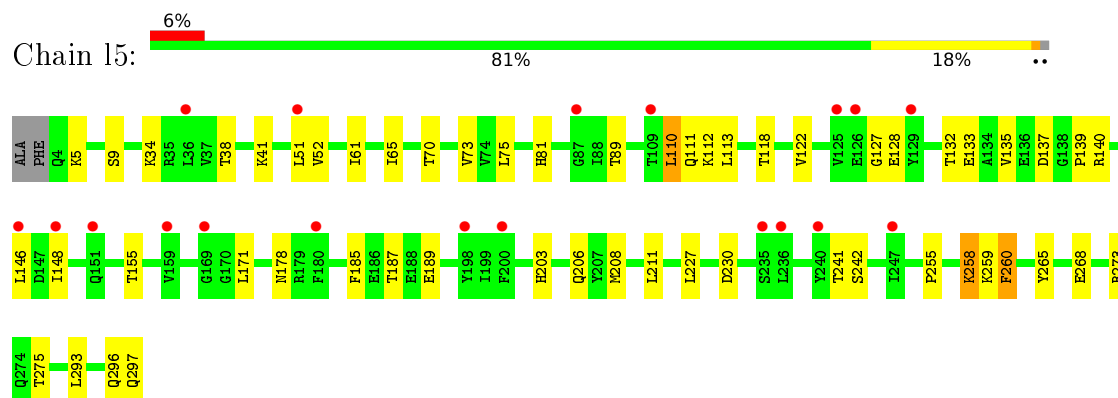
- Molecule 41: 60S ribosomal protein L4-A



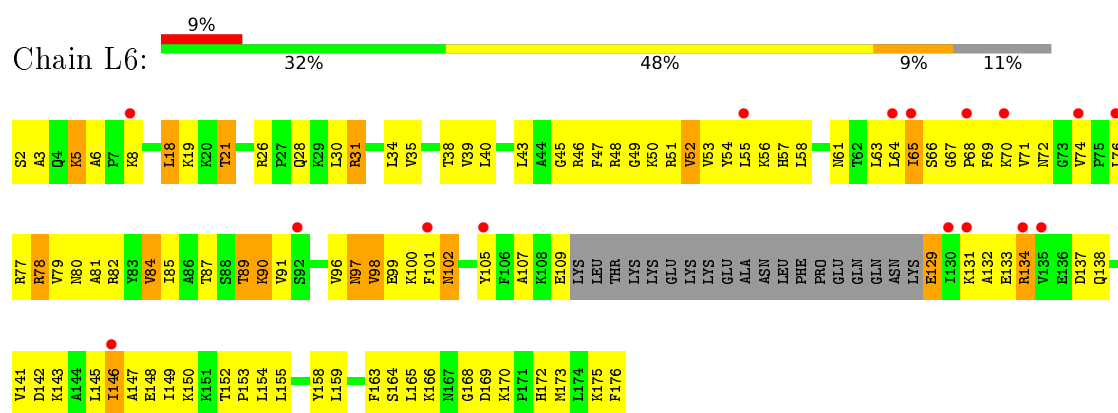
- Molecule 42: 60S ribosomal protein L5



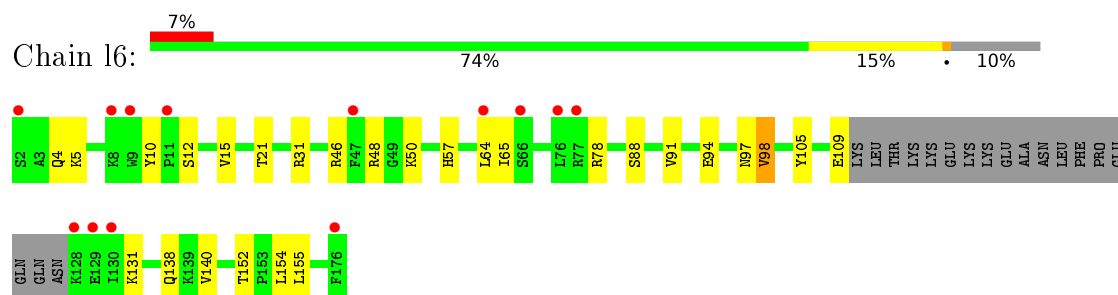
- Molecule 42: 60S ribosomal protein L5



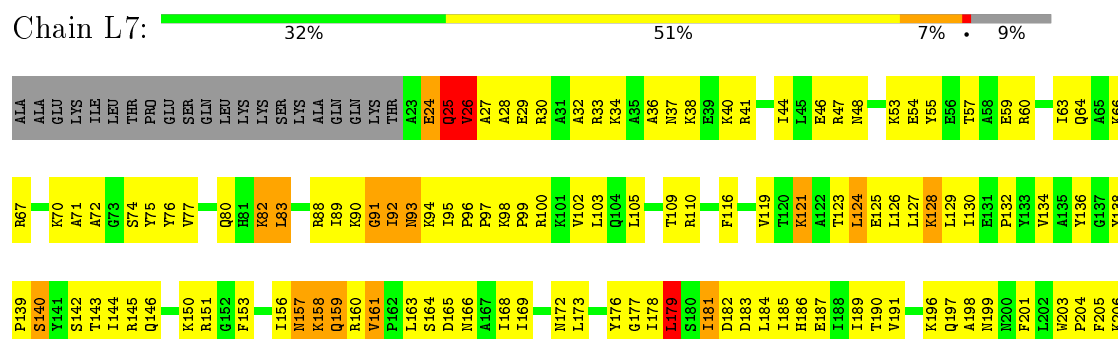
- Molecule 43: 60S ribosomal protein L6-A

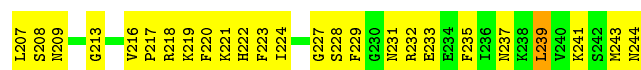


- Molecule 43: 60S ribosomal protein L6-A



- Molecule 44: 60S ribosomal protein L7-A





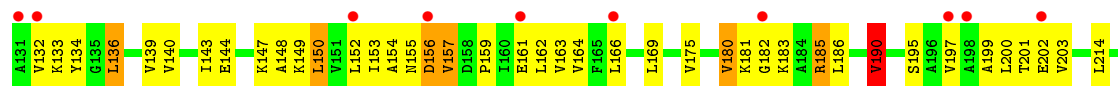
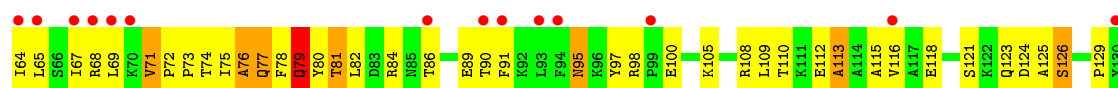
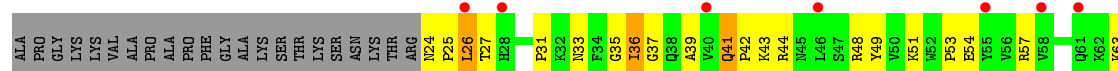
• Molecule 44: 60S ribosomal protein L7-A

Chain L7: 80% 10% 8%



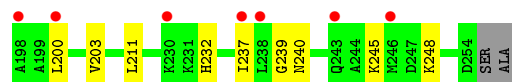
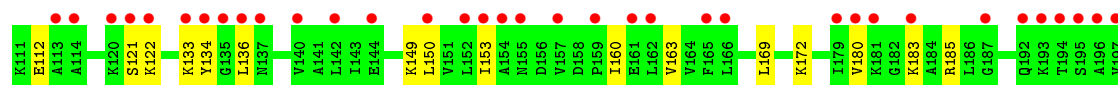
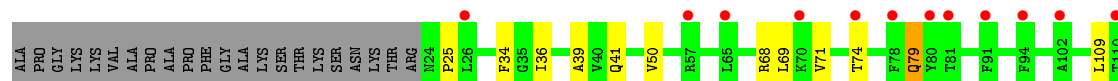
• Molecule 45: 60S ribosomal protein L8-A

Chain L8: 15% 44% 40% 7% 9%



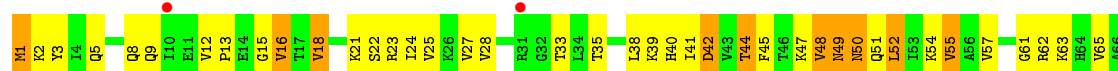
• Molecule 45: 60S ribosomal protein L8-A

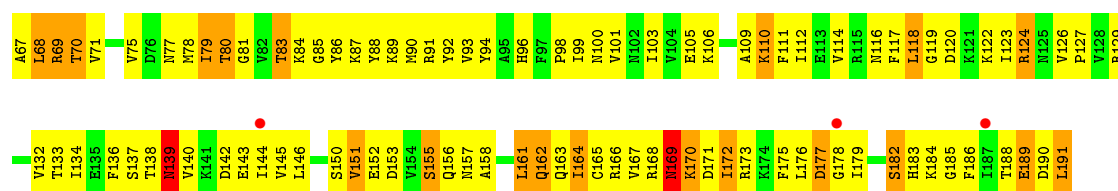
Chain l8: 21% 76% 14% 9%



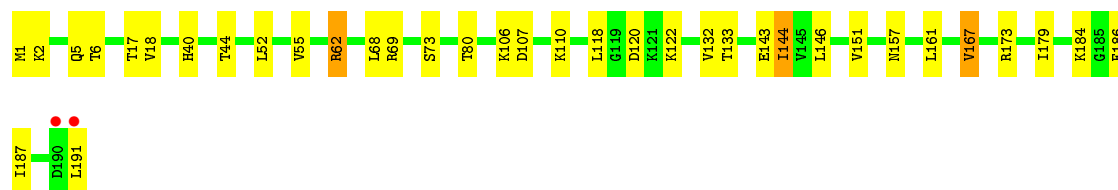
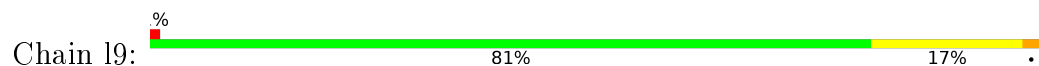
• Molecule 46: 60S ribosomal protein L9-A

Chain L9: 3% 29% 54% 16%

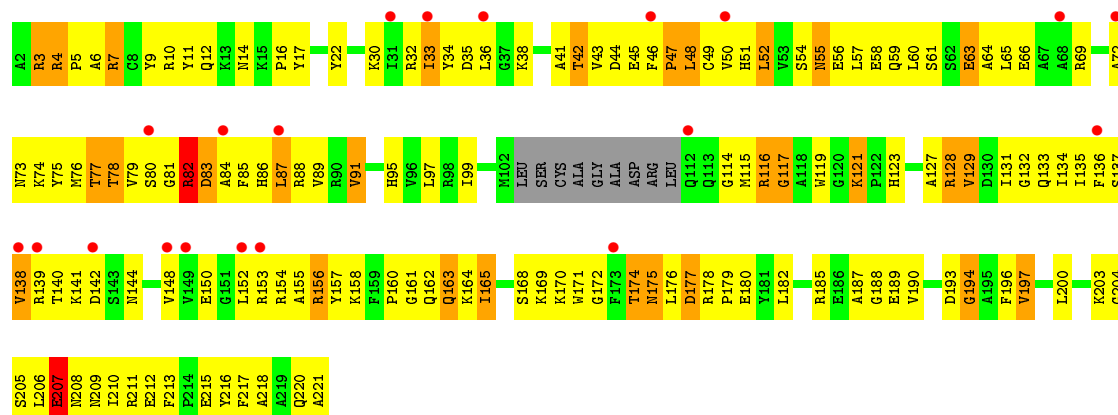




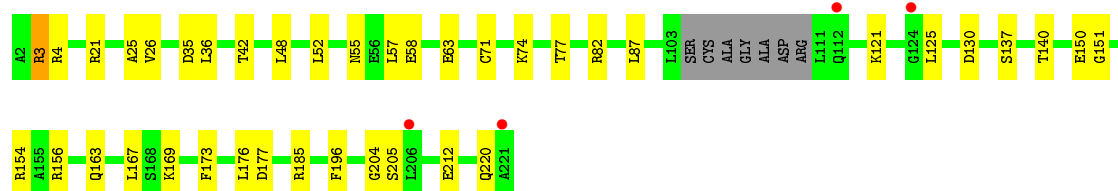
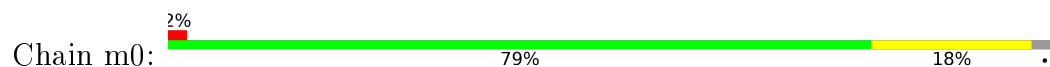
• Molecule 46: 60S ribosomal protein L9-A



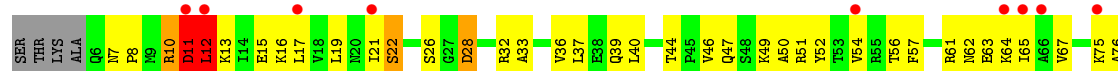
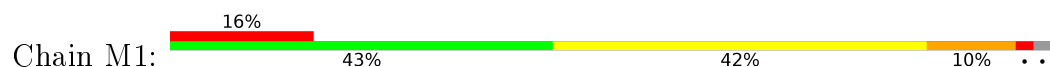
• Molecule 47: 60S ribosomal protein L10

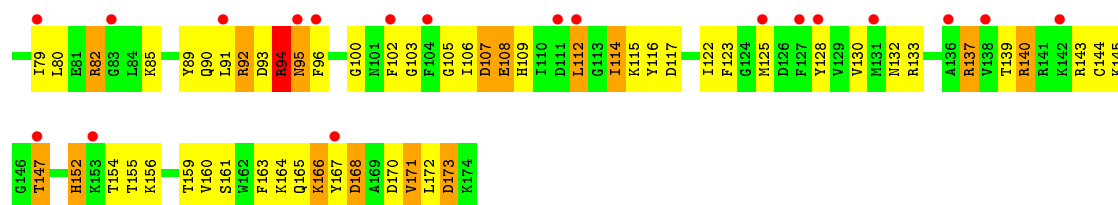


• Molecule 47: 60S ribosomal protein L10

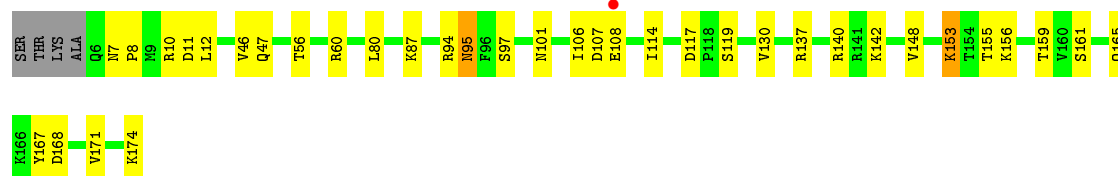
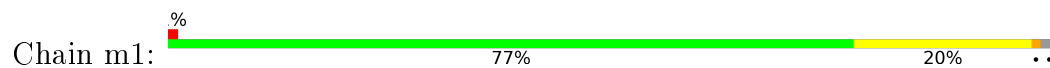


• Molecule 48: 60S ribosomal protein L11-A

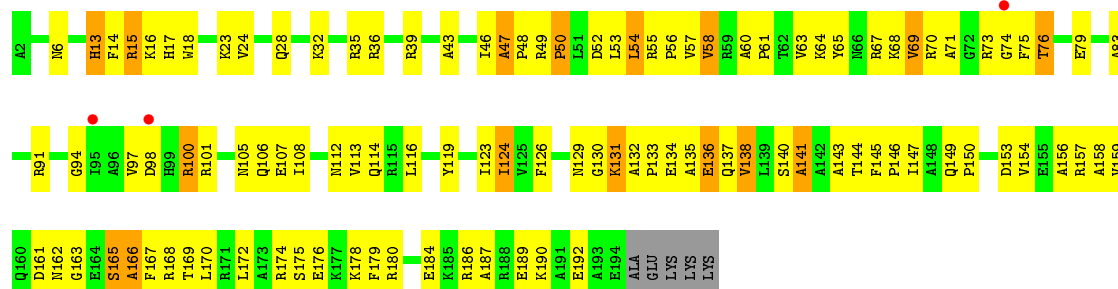
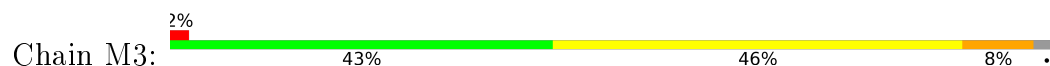




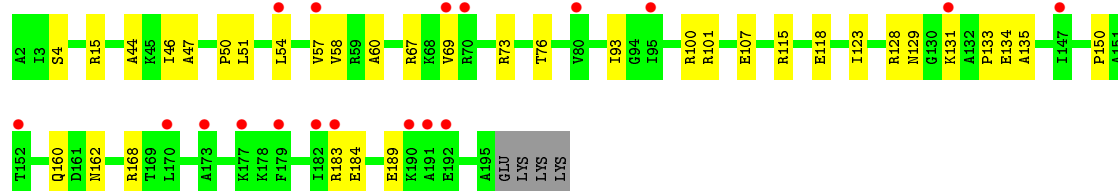
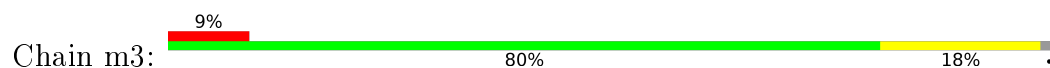
• Molecule 48: 60S ribosomal protein L11-A



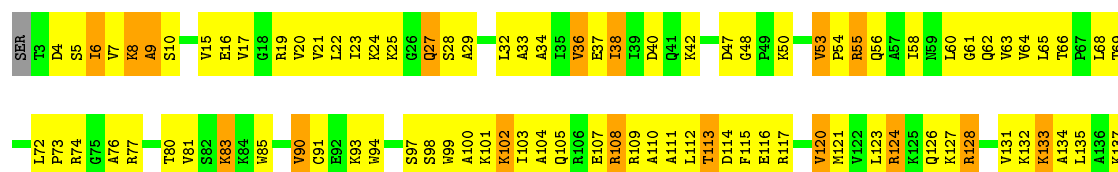
• Molecule 49: 60S ribosomal protein L13-A



• Molecule 49: 60S ribosomal protein L13-A




• Molecule 50: 60S ribosomal protein L14-A

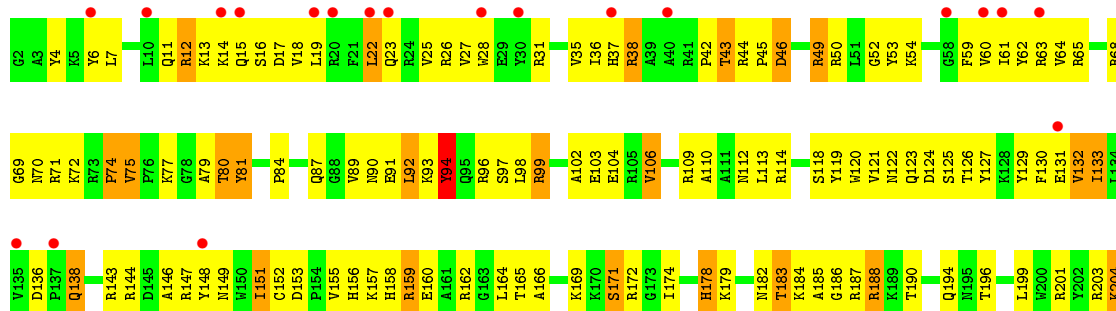


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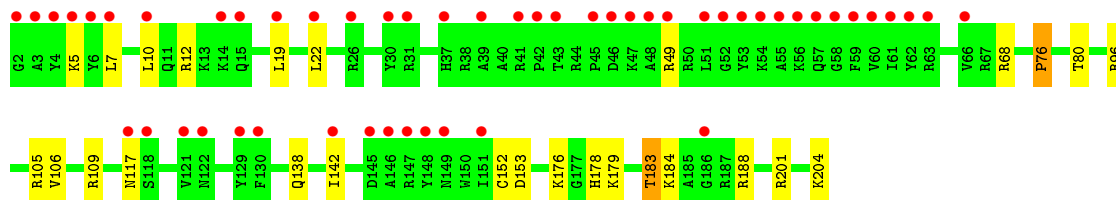
- Molecule 50: 60S ribosomal protein L14-A

Chain m4:  83% 16% .

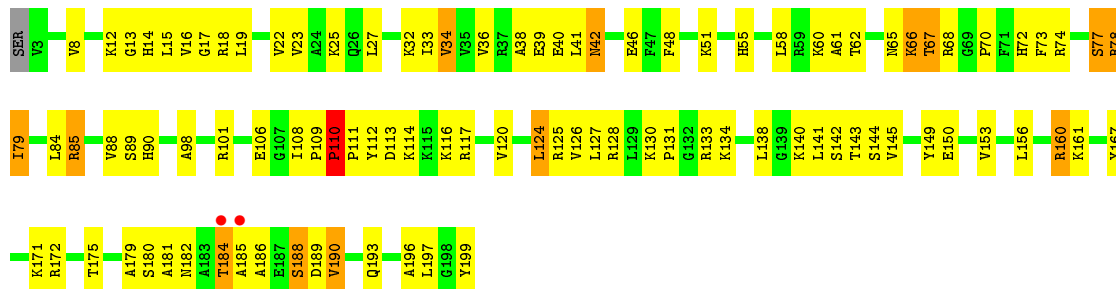
- Molecule 51: 60S ribosomal protein L15-A

Chain M5:  10% 37% 51% 11%

- Molecule 51: 60S ribosomal protein L15-A

Chain m5:  26% 87% 12% .

- Molecule 52: 60S ribosomal protein L16-A

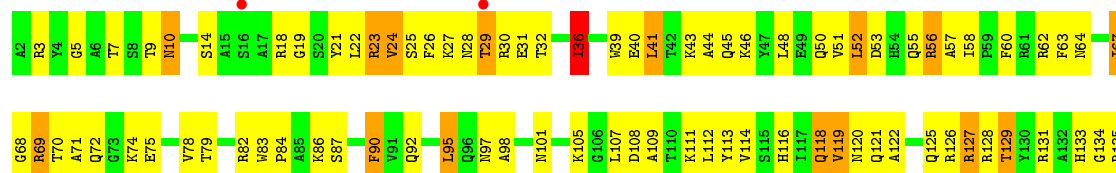
Chain M6:  49% 43% 7% .

- Molecule 52: 60S ribosomal protein L16-A

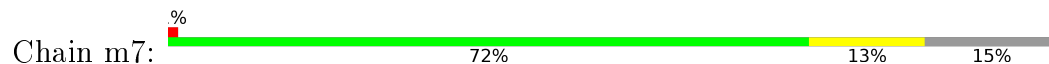
Chain m6:  90% 10% .



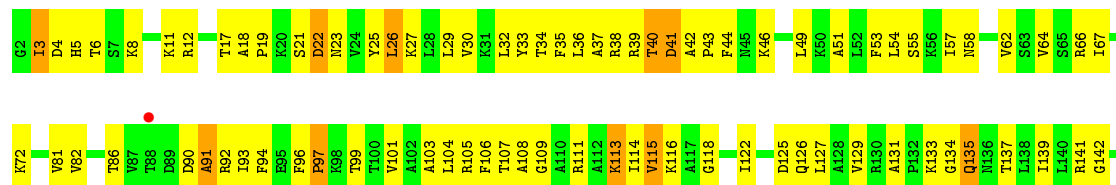
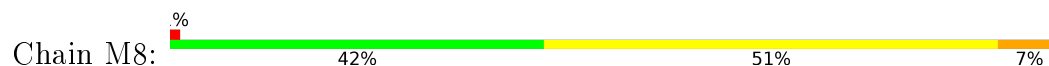
- Molecule 53: 60S ribosomal protein L17-A



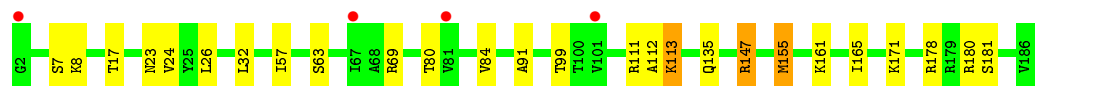
- Molecule 53: 60S ribosomal protein L17-A



- Molecule 54: 60S ribosomal protein L18-A

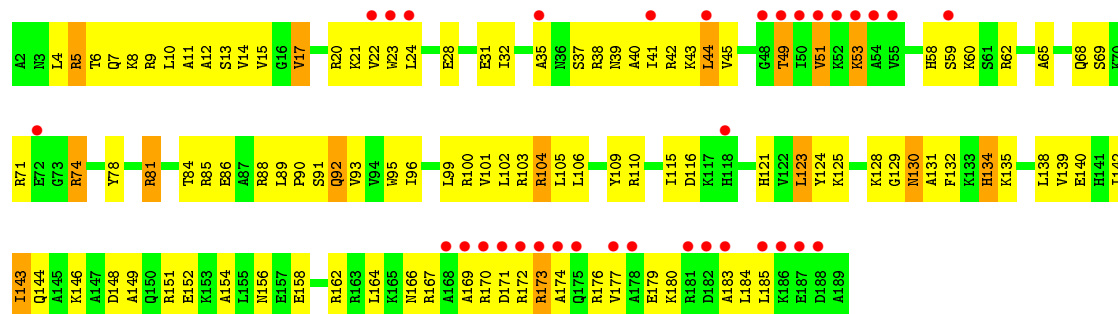


- Molecule 54: 60S ribosomal protein L18-A

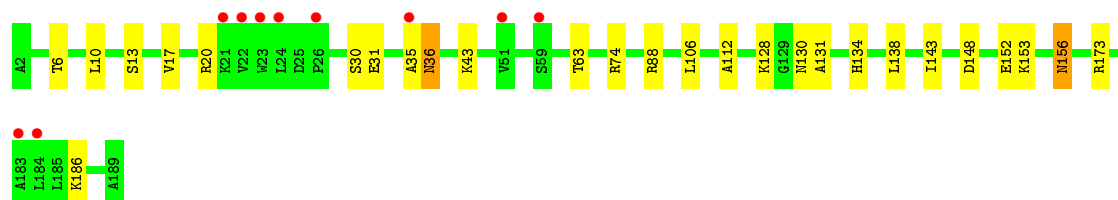
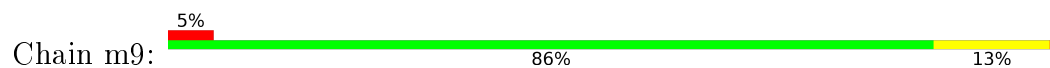


- Molecule 55: 60S ribosomal protein L19-A

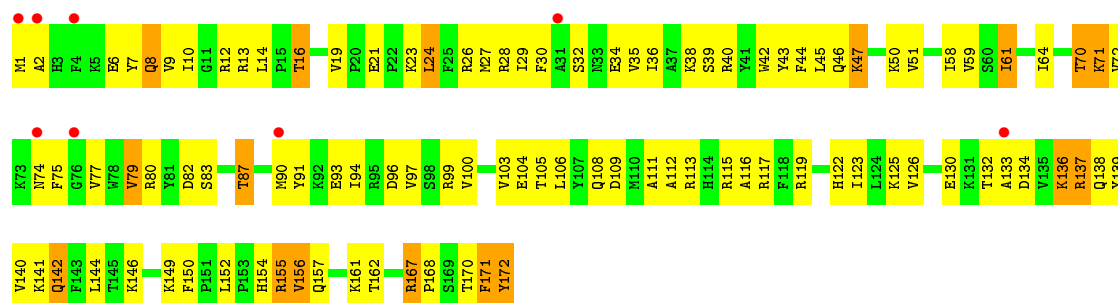
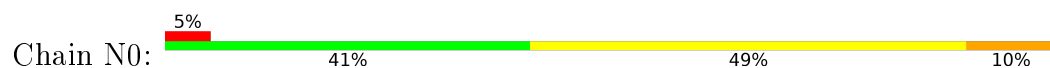




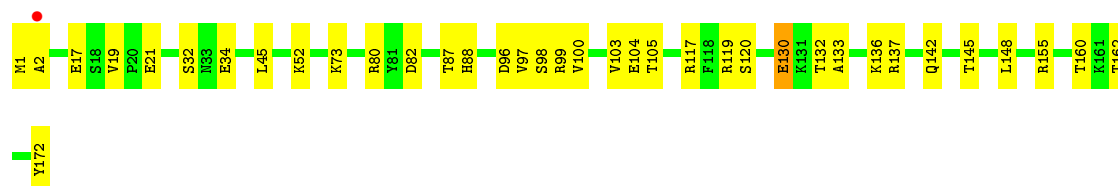
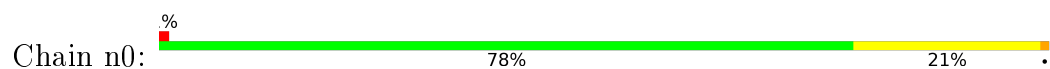
• Molecule 55: 60S ribosomal protein L19-A



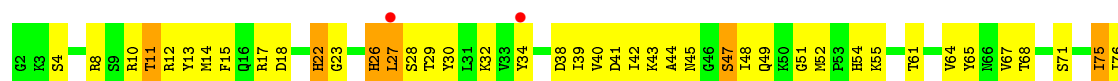
• Molecule 56: 60S ribosomal protein L20-A

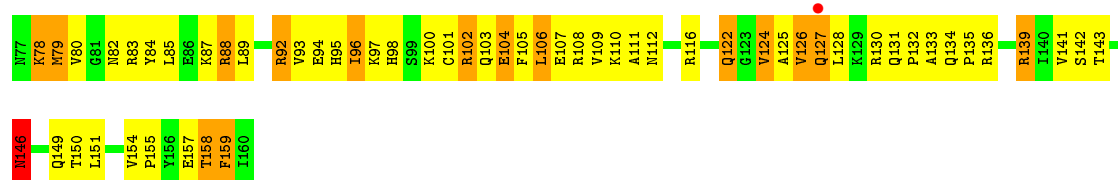


• Molecule 56: 60S ribosomal protein L20-A

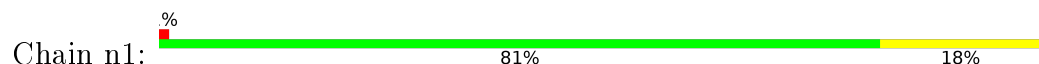


• Molecule 57: 60S ribosomal protein L21-A

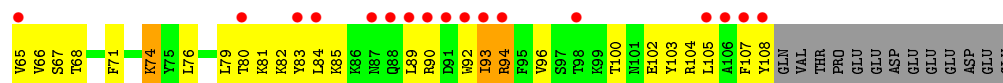
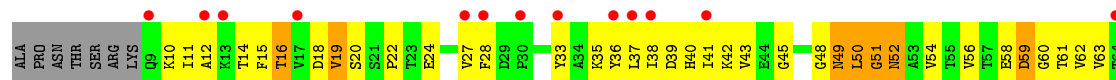




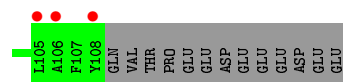
- Molecule 57: 60S ribosomal protein L21-A



- Molecule 58: 60S ribosomal protein L22-A



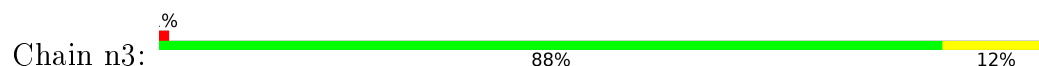
- Molecule 58: 60S ribosomal protein L22-A

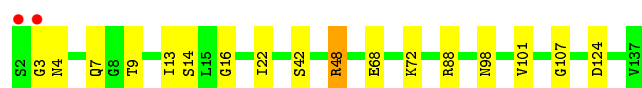


- Molecule 59: 60S ribosomal protein L23-A

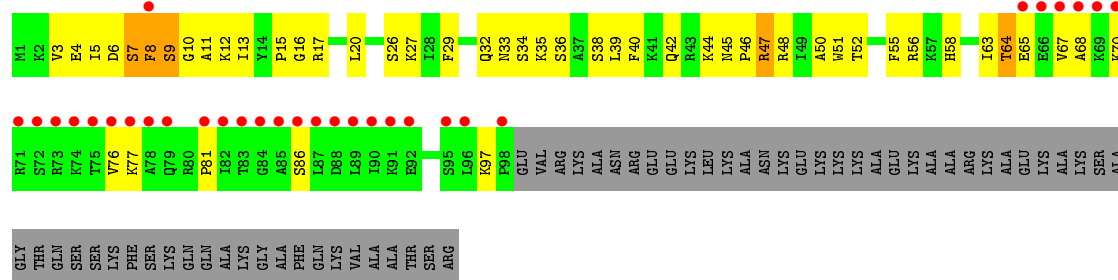


- Molecule 59: 60S ribosomal protein L23-A

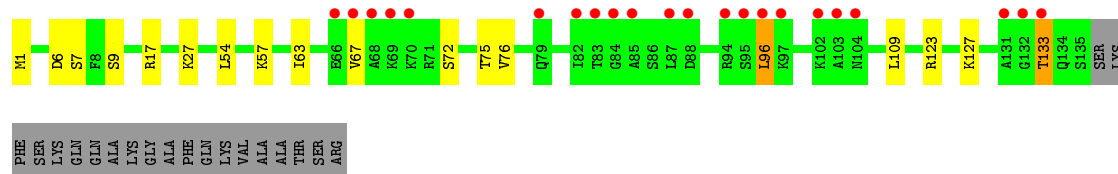
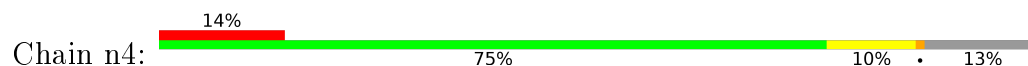




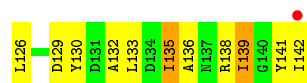
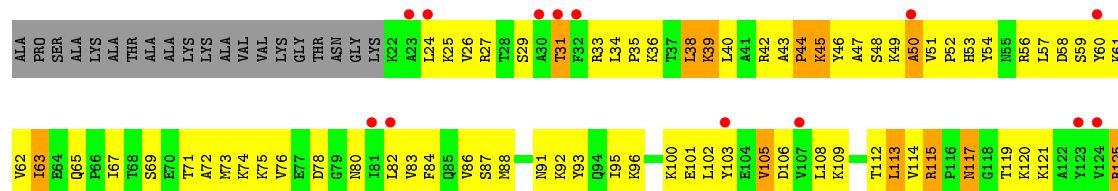
- Molecule 60: 60S ribosomal protein L24-A



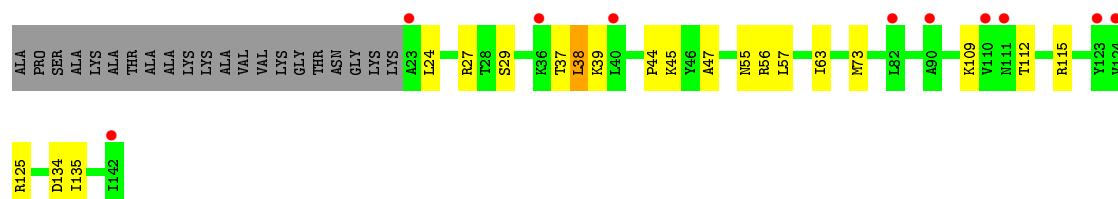
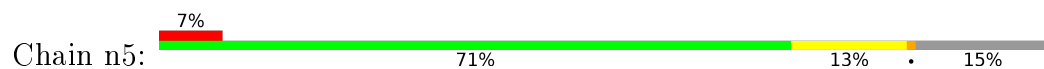
- Molecule 60: 60S ribosomal protein L24-A



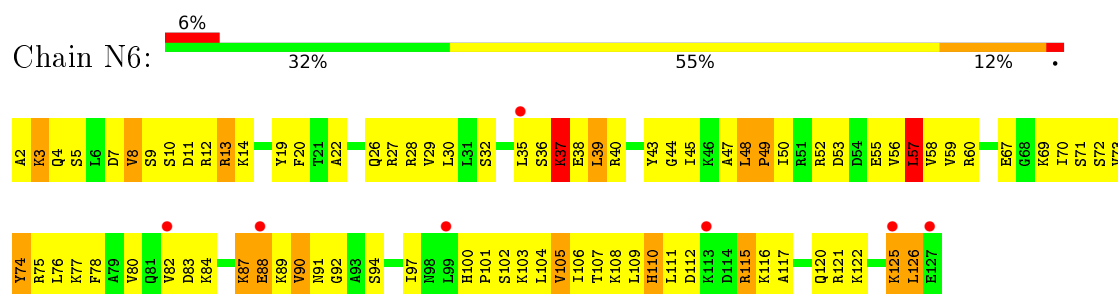
- Molecule 61: 60S ribosomal protein L25



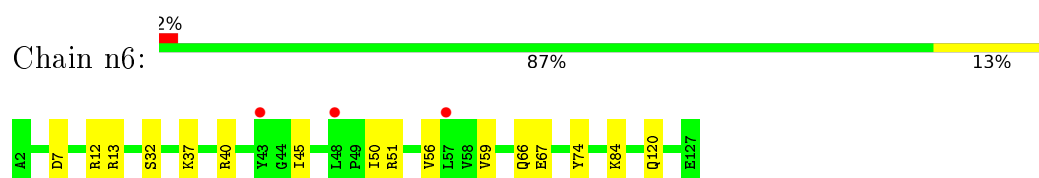
- Molecule 61: 60S ribosomal protein L25



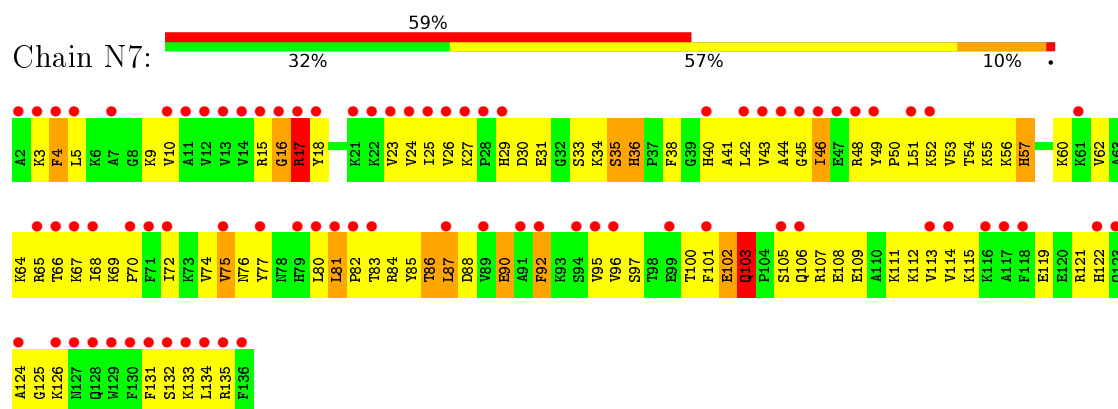
- Molecule 62: 60S ribosomal protein L26-A



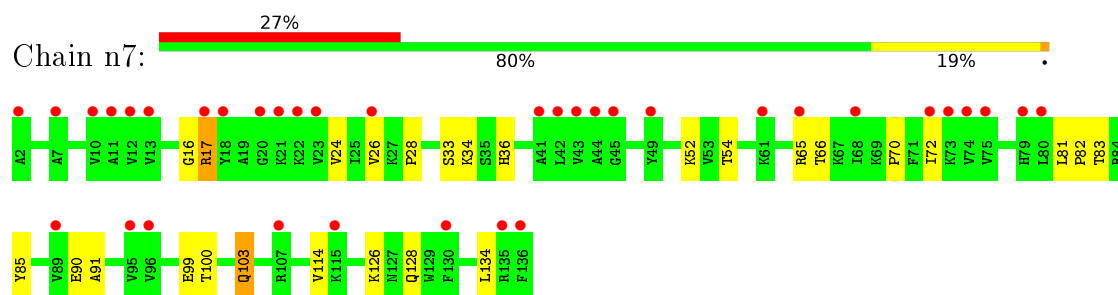
- Molecule 62: 60S ribosomal protein L26-A



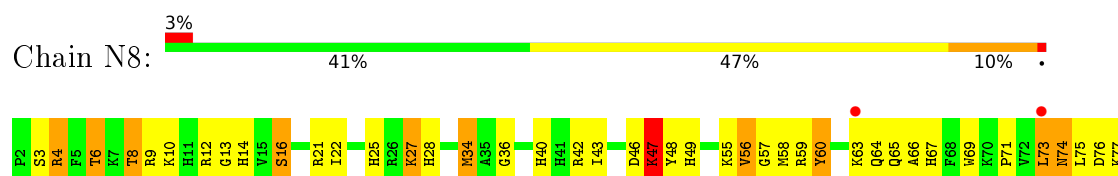
- Molecule 63: 60S ribosomal protein L27-A

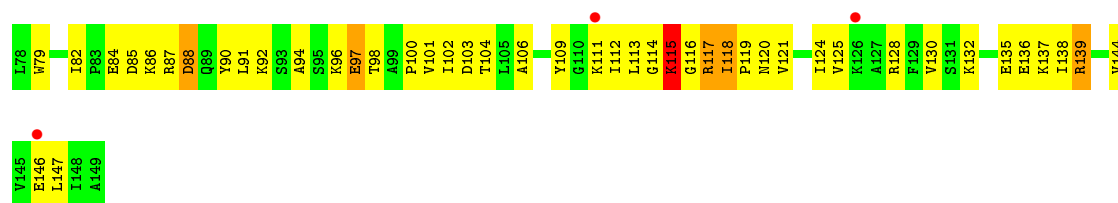


- Molecule 63: 60S ribosomal protein L27-A

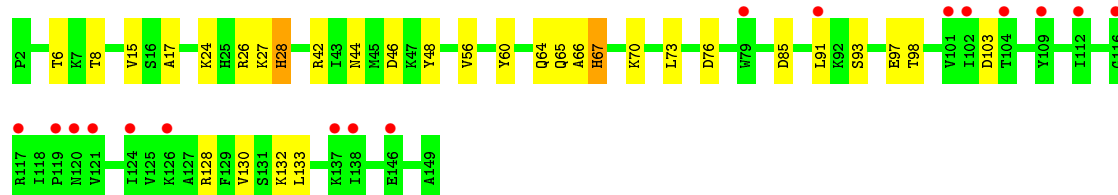
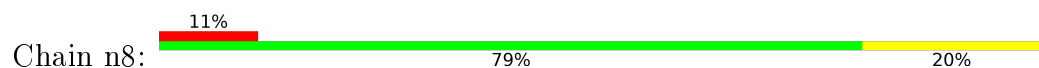


- Molecule 64: 60S ribosomal protein L28

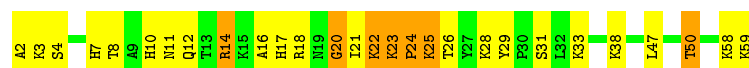




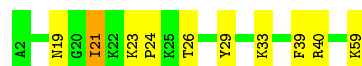
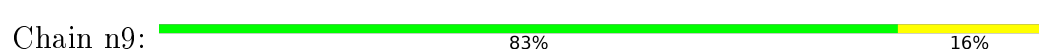
- Molecule 64: 60S ribosomal protein L28



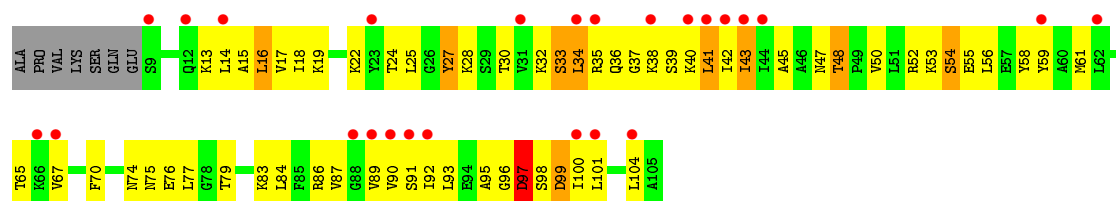
- Molecule 65: 60S ribosomal protein L29



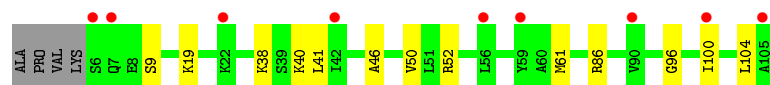
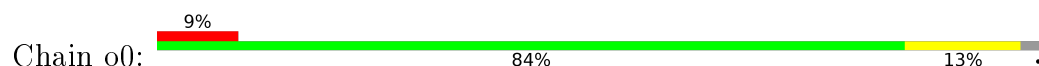
- Molecule 65: 60S ribosomal protein L29



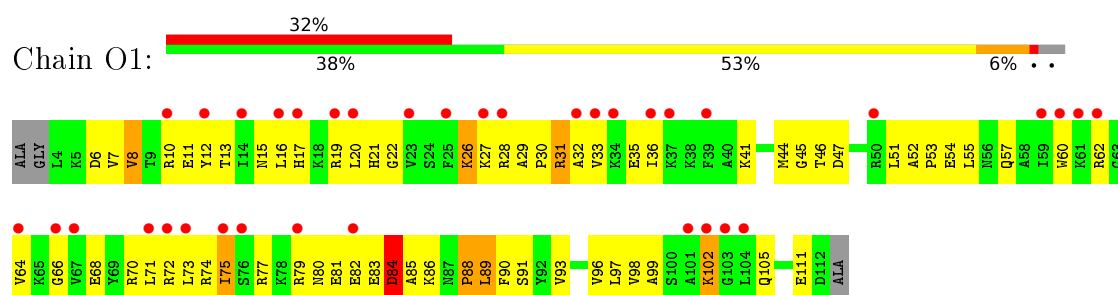
- Molecule 66: 60S ribosomal protein L30



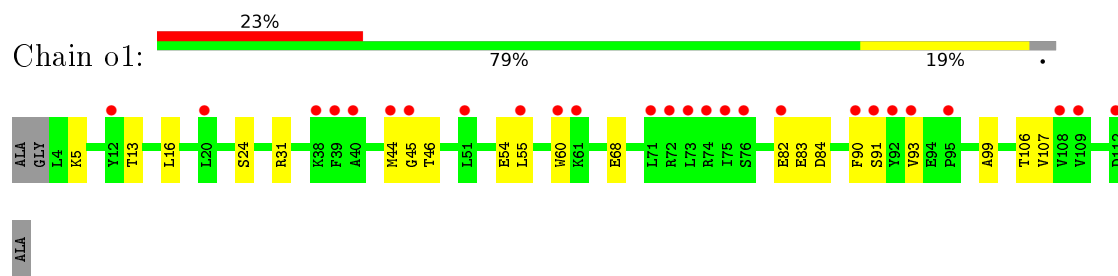
- Molecule 66: 60S ribosomal protein L30



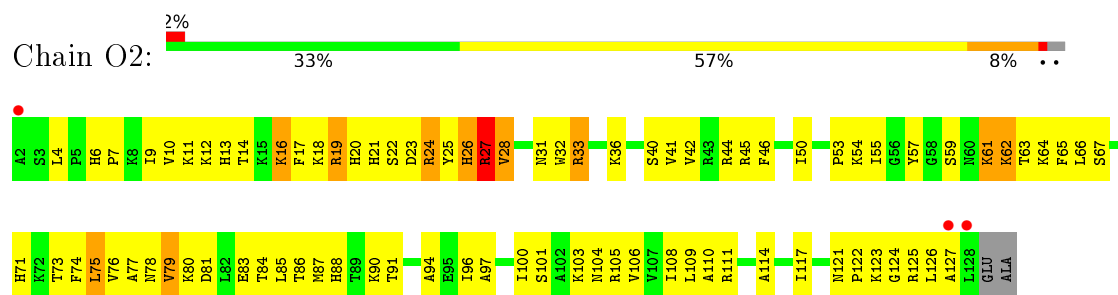
- Molecule 67: 60S ribosomal protein L31-A



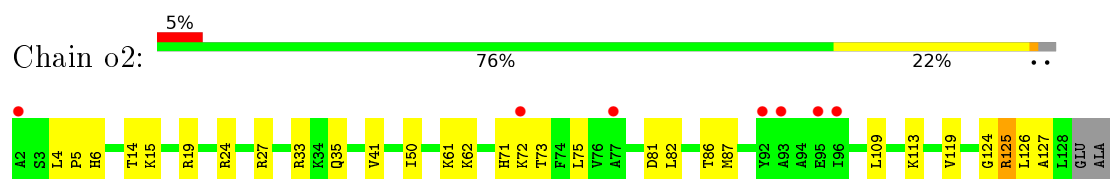
- Molecule 67: 60S ribosomal protein L31-A



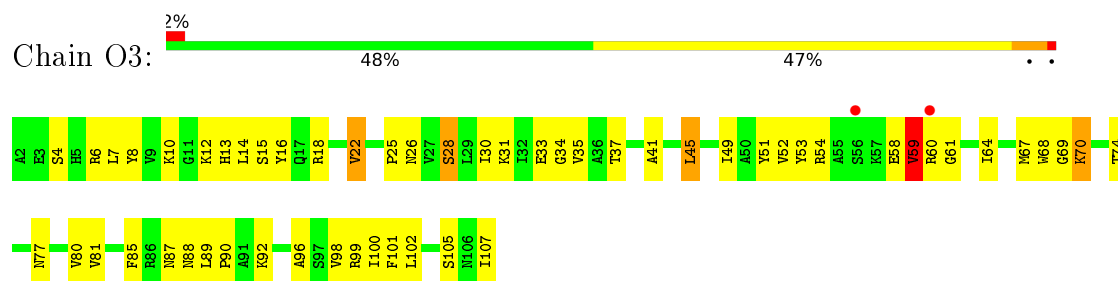
- Molecule 68: 60S ribosomal protein L32



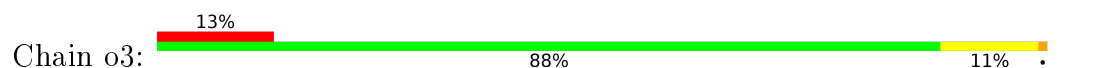
- Molecule 68: 60S ribosomal protein L32

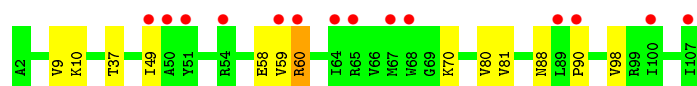


- Molecule 69: 60S ribosomal protein L33-A

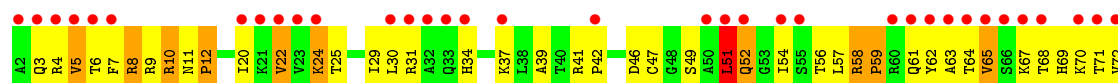


- Molecule 69: 60S ribosomal protein L33-A

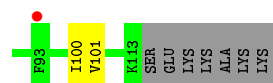
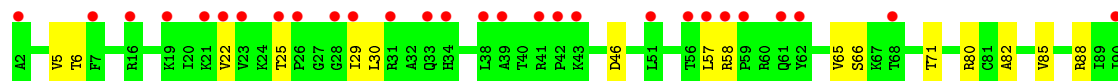
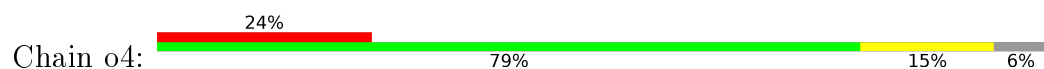




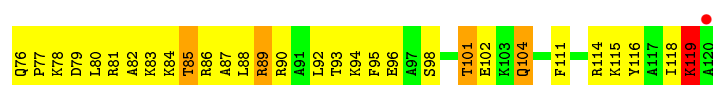
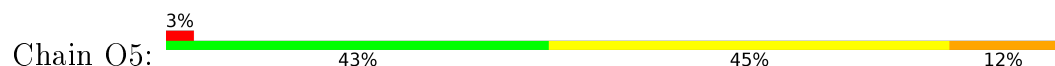
- Molecule 70: 60S ribosomal protein L34-A



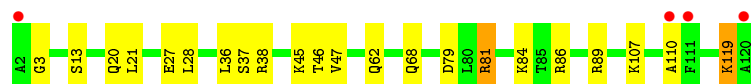
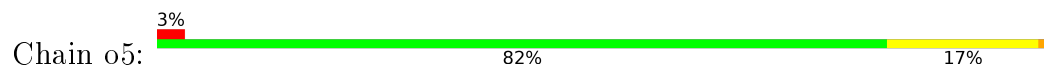
- Molecule 70: 60S ribosomal protein L34-A



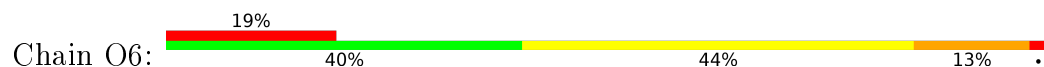
- Molecule 71: 60S ribosomal protein L35-A

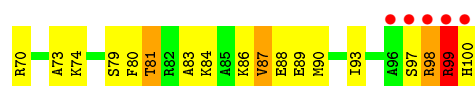


- Molecule 71: 60S ribosomal protein L35-A

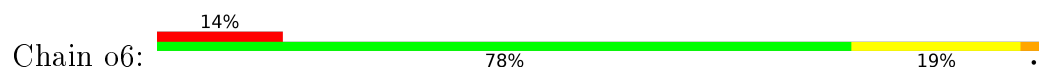


- Molecule 72: 60S ribosomal protein L36-A





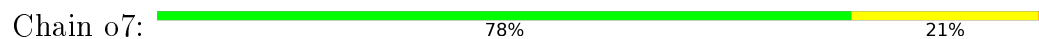
- Molecule 72: 60S ribosomal protein L36-A



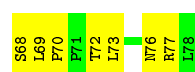
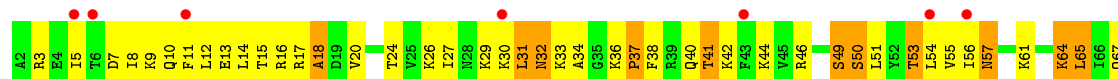
- Molecule 73: 60S ribosomal protein L37-A



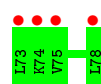
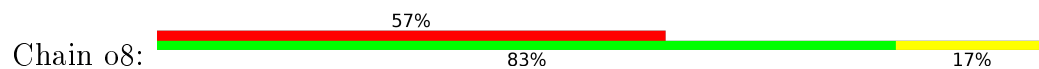
- Molecule 73: 60S ribosomal protein L37-A



- Molecule 74: 60S ribosomal protein L38



- Molecule 74: 60S ribosomal protein L38

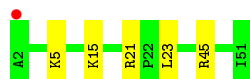
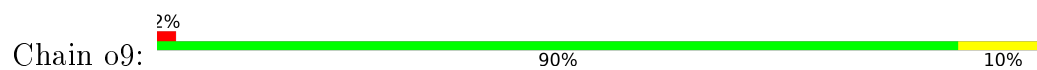


- Molecule 75: 60S ribosomal protein L39

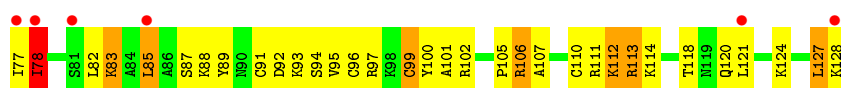




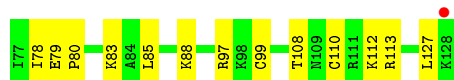
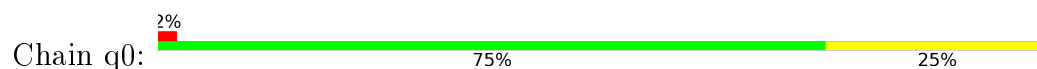
- Molecule 75: 60S ribosomal protein L39



- Molecule 76: Ubiquitin-60S ribosomal protein L40



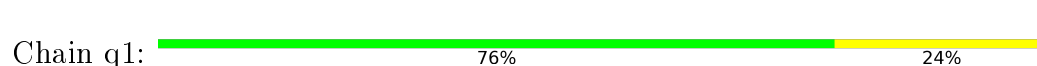
- Molecule 76: Ubiquitin-60S ribosomal protein L40



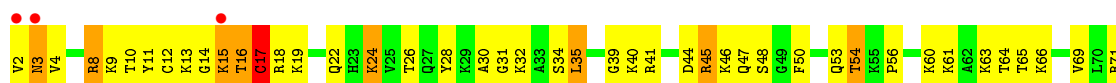
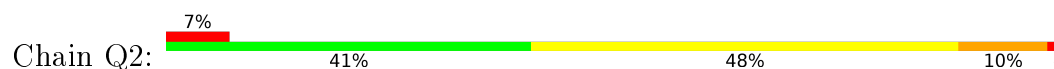
- Molecule 77: 60S ribosomal protein L41-A



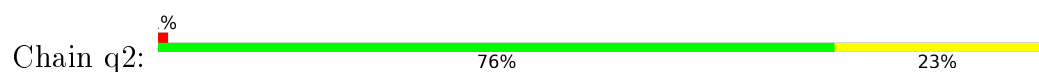
- Molecule 77: 60S ribosomal protein L41-A



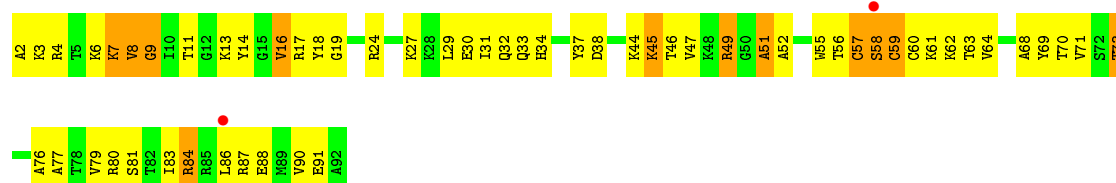
- Molecule 78: 60S ribosomal protein L42-A



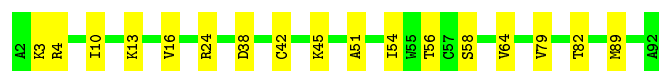
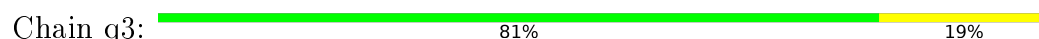
- Molecule 78: 60S ribosomal protein L42-A



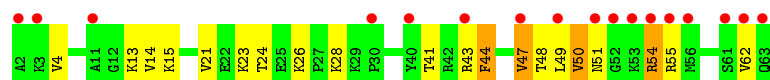
- Molecule 79: 60S ribosomal protein L43-A



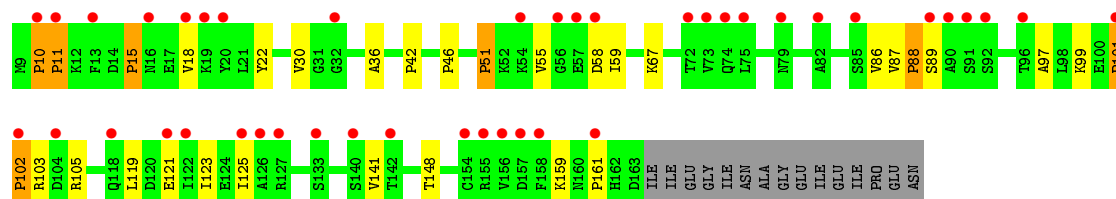
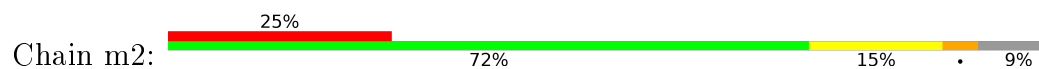
- Molecule 79: 60S ribosomal protein L43-A



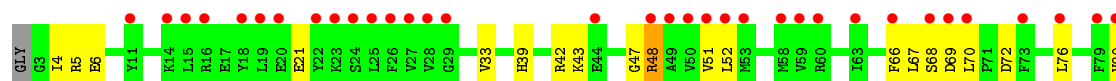
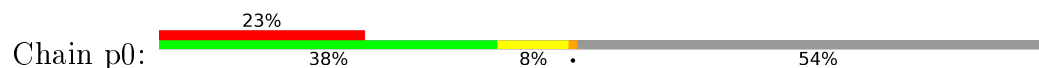
- Molecule 80: 40S ribosomal protein S30-A

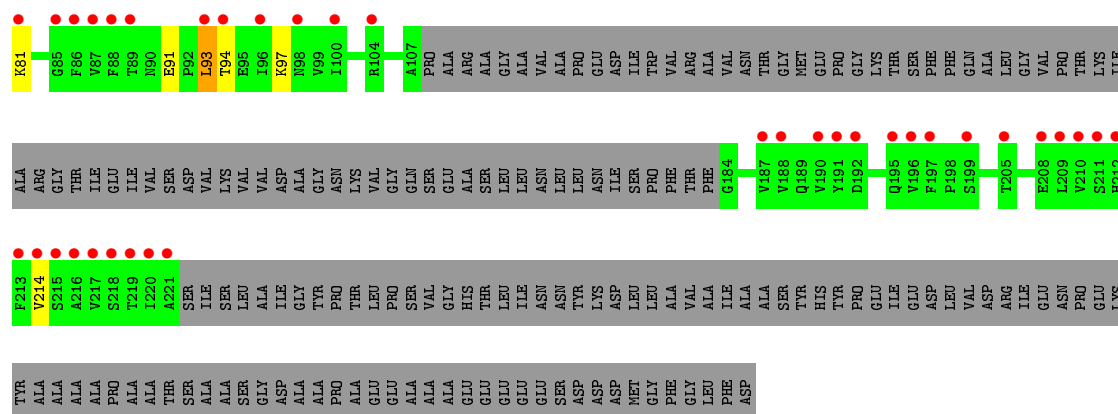


- Molecule 81: 60S ribosomal protein L12-A

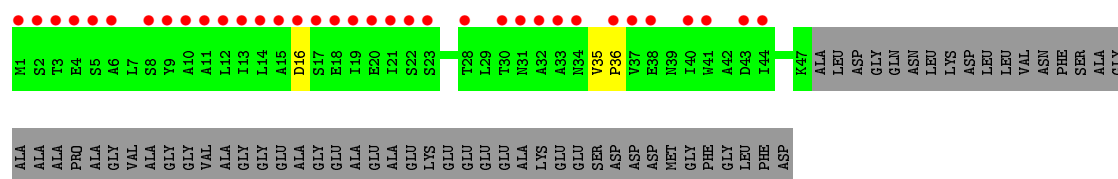
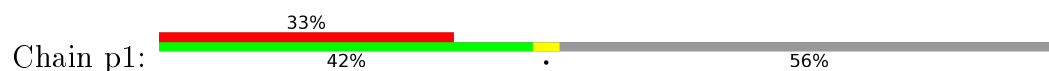


- Molecule 82: 60S acidic ribosomal protein P0

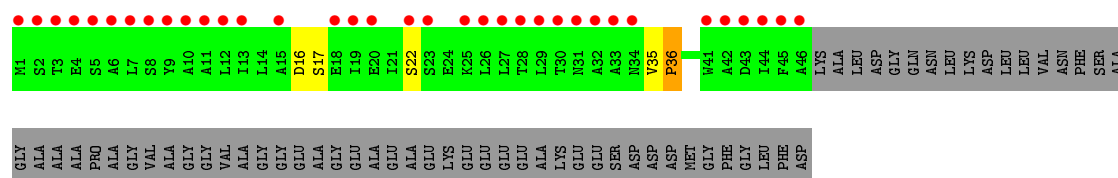
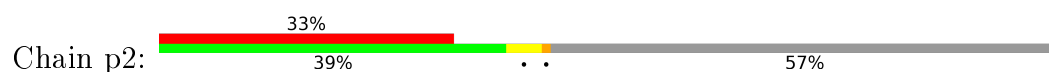




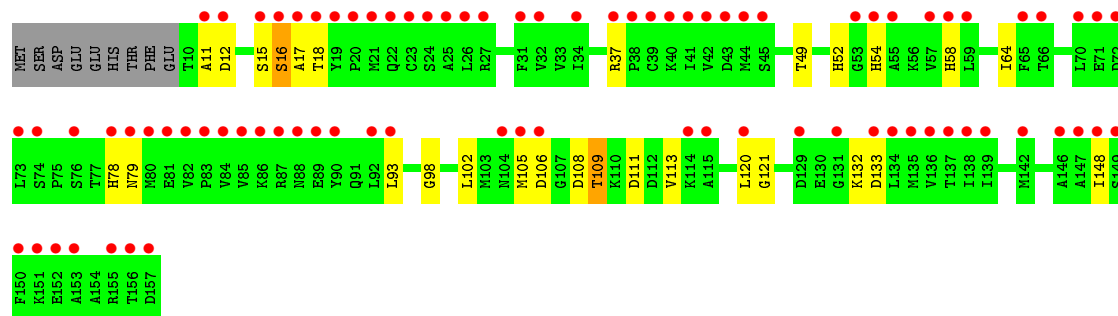
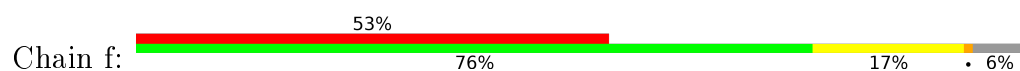
• Molecule 83: 60S acidic ribosomal protein P1-alpha



• Molecule 83: 60S acidic ribosomal protein P1-alpha



• Molecule 84: Eukaryotic translation initiation factor 5A-1




• Molecule 85: DNA (5'-R(*CP*CP*(NA))-3')





- Molecule 85: DNA (5'-R(*CP*CP*(NA))-3')

Chain C:  75% 25%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	438.00 Å 289.05 Å 305.26 Å 90.00° 98.95° 90.00°	Depositor
Resolution (Å)	122.88 – 3.45 123.03 – 3.45	Depositor EDS
% Data completeness (in resolution range)	99.9 (122.88-3.45) 99.9 (123.03-3.45)	Depositor EDS
R_{merge}	0.38	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 3.49 Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.207 , 0.263 0.195 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	90.1	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 92.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	413121	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 5CT, SPS, MG, OHX, 8AN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	2	0.44	0/42467	0.98	58/66169 (0.1%)
1	6	0.53	0/42790	1.04	77/66673 (0.1%)
2	S0	0.33	0/1617	0.55	0/2215
2	s0	0.36	0/1623	0.58	0/2222
3	S1	0.30	0/1735	0.53	1/2335 (0.0%)
3	s1	0.34	0/1748	0.56	0/2352
4	S2	0.34	0/1665	0.56	0/2263
4	s2	0.41	0/1665	0.63	0/2263
5	S3	0.33	0/1759	0.53	0/2368
5	s3	0.33	0/1759	0.50	0/2368
6	S4	0.34	0/2109	0.57	0/2839
6	s4	0.39	0/2109	0.62	0/2839
7	S5	0.31	0/1629	0.52	0/2202
7	s5	0.30	0/1629	0.51	0/2202
8	S6	0.34	0/1823	0.52	0/2439
8	s6	0.39	0/1779	0.61	0/2379
9	S7	0.32	0/1506	0.54	0/2028
9	s7	0.34	0/1516	0.57	0/2043
10	S8	0.36	0/1514	0.53	0/2021
10	s8	0.41	0/1514	0.58	0/2021
11	S9	0.33	0/1519	0.49	0/2035
11	s9	0.38	0/1519	0.57	0/2035
12	C0	0.31	0/790	0.54	1/1069 (0.1%)
12	c0	0.30	0/777	0.59	3/1049 (0.3%)
13	C1	0.38	0/1240	0.56	0/1675
13	c1	0.44	0/1194	0.61	0/1610
14	C2	0.29	0/900	0.51	0/1224
14	c2	0.25	0/900	0.48	0/1224
15	C3	0.35	0/1215	0.56	1/1638 (0.1%)
15	c3	0.37	0/1215	0.58	0/1638
16	C4	0.30	0/901	0.56	0/1217
16	c4	0.35	0/960	0.56	0/1290

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	C5	0.34	0/998	0.56	0/1341
17	c5	0.36	0/1060	0.57	0/1426
18	C6	0.32	0/1125	0.57	2/1510 (0.1%)
18	c6	0.34	0/1131	0.54	0/1518
19	C7	0.36	0/935	0.59	0/1254
19	c7	0.32	0/914	0.54	0/1224
20	C8	0.35	0/1211	0.54	1/1628 (0.1%)
20	c8	0.34	0/1211	0.57	1/1628 (0.1%)
21	C9	0.32	0/1130	0.52	0/1517
21	c9	0.33	0/1130	0.51	0/1517
22	D0	0.32	0/865	0.55	0/1169
22	d0	0.35	0/892	0.54	0/1205
23	D1	0.34	0/693	0.53	0/935
23	d1	0.37	0/693	0.61	0/935
24	D2	0.34	0/1038	0.61	1/1395 (0.1%)
24	d2	0.41	0/1038	0.62	0/1395
25	D3	0.39	0/1139	0.59	0/1518
25	d3	0.45	0/1139	0.62	0/1518
26	D4	0.34	0/1087	0.50	0/1449
26	d4	0.39	0/1087	0.62	0/1449
27	D5	0.32	0/571	0.57	0/768
27	d5	0.33	0/566	0.53	0/761
28	D6	0.33	0/782	0.54	0/1047
28	d6	0.38	0/782	0.58	0/1047
29	D7	0.32	0/620	0.52	0/838
29	d7	0.36	0/620	0.57	0/838
30	D8	0.29	0/499	0.51	0/670
30	d8	0.32	0/499	0.57	0/670
31	D9	0.40	0/452	0.57	0/600
31	d9	0.35	0/452	0.52	0/600
32	E0	0.32	0/483	0.49	0/643
33	E1	0.35	0/577	0.61	0/770
33	e1	0.34	0/619	0.61	0/822
34	SR	0.29	0/2489	0.51	0/3389
34	sR	0.28	0/2494	0.49	0/3395
35	SM	0.38	0/1113	0.57	2/1502 (0.1%)
35	sM	0.34	0/683	0.55	1/923 (0.1%)
36	1	0.66	6/75394 (0.0%)	1.15	212/117545 (0.2%)
36	5	0.71	8/75414 (0.0%)	1.18	277/117575 (0.2%)
37	3	0.57	0/2883	1.03	1/4491 (0.0%)
37	7	0.69	0/2883	1.15	7/4491 (0.2%)
38	4	0.60	0/3746	1.07	5/5832 (0.1%)
38	8	0.60	0/3746	1.08	7/5832 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	L2	0.43	0/1948	0.62	0/2617
39	l2	0.45	0/1946	0.65	0/2614
40	L3	0.46	0/3146	0.63	0/4228
40	l3	0.53	0/3146	0.63	0/4228
41	L4	0.49	0/2800	0.67	0/3790
41	l4	0.47	0/2800	0.66	0/3790
42	L5	0.41	0/2425	0.57	0/3271
42	l5	0.51	0/2408	0.64	1/3248 (0.0%)
43	L6	0.45	0/1260	0.61	0/1694
43	l6	0.47	0/1269	0.61	0/1705
44	L7	0.49	0/1821	0.64	1/2451 (0.0%)
44	l7	0.52	0/1828	0.65	1/2461 (0.0%)
45	L8	0.36	0/1836	0.54	0/2481
45	l8	0.38	0/1796	0.57	0/2431
46	L9	0.43	0/1539	0.60	0/2073
46	l9	0.51	0/1539	0.64	0/2073
47	M0	0.45	0/1741	0.58	0/2335
47	m0	0.51	0/1758	0.65	0/2358
48	M1	0.37	0/1374	0.57	0/1842
48	m1	0.45	0/1374	0.60	0/1842
49	M3	0.44	0/1568	0.65	0/2106
49	m3	0.46	0/1573	0.61	0/2113
50	M4	0.44	0/1068	0.59	0/1438
50	m4	0.49	0/1074	0.64	0/1446
51	M5	0.46	0/1757	0.59	0/2354
51	m5	0.44	0/1757	0.58	0/2354
52	M6	0.53	0/1585	0.54	0/2128
52	m6	0.62	0/1585	0.57	0/2128
53	M7	0.48	0/1443	0.62	0/1944
53	m7	0.54	0/1250	0.63	0/1683
54	M8	0.48	0/1465	0.65	0/1965
54	m8	0.47	0/1465	0.67	0/1965
55	M9	0.37	0/1538	0.54	0/2050
55	m9	0.40	0/1538	0.55	0/2050
56	N0	0.46	0/1481	0.61	1/1990 (0.1%)
56	n0	0.54	0/1481	0.65	0/1990
57	N1	0.45	0/1300	0.60	0/1743
57	n1	0.53	0/1300	0.59	0/1743
58	N2	0.35	0/812	0.55	0/1099
58	n2	0.39	0/794	0.58	0/1076
59	N3	0.46	0/1018	0.59	0/1369
59	n3	0.54	0/1018	0.69	1/1369 (0.1%)
60	N4	0.37	0/712	0.55	0/958

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
60	n4	0.44	0/1052	0.60	0/1398
61	N5	0.40	0/979	0.59	0/1321
61	n5	0.41	0/974	0.62	0/1314
62	N6	0.43	0/1004	0.63	1/1341 (0.1%)
62	n6	0.42	0/1004	0.60	0/1341
63	N7	0.36	0/1118	0.56	0/1497
63	n7	0.38	0/1118	0.52	0/1497
64	N8	0.47	0/1204	0.68	0/1612
64	n8	0.49	0/1204	0.66	1/1612 (0.1%)
65	N9	0.45	0/473	0.67	0/629
65	n9	0.53	0/473	0.74	0/629
66	O0	0.33	0/750	0.54	0/1008
66	o0	0.38	0/774	0.59	0/1040
67	O1	0.41	0/890	0.57	0/1196
67	o1	0.49	0/897	0.67	0/1205
68	O2	0.51	0/1041	0.62	0/1394
68	o2	0.52	0/1041	0.66	0/1394
69	O3	0.55	0/868	0.63	0/1168
69	o3	0.54	0/868	0.63	0/1168
70	O4	0.39	0/890	0.60	1/1189 (0.1%)
70	o4	0.44	0/890	0.59	0/1189
71	O5	0.43	0/978	0.61	0/1301
71	o5	0.41	0/974	0.59	0/1297
72	O6	0.40	0/778	0.59	0/1034
72	o6	0.42	0/777	0.61	0/1033
73	O7	0.48	0/696	0.70	0/923
73	o7	0.46	0/696	0.65	1/923 (0.1%)
74	O8	0.34	0/618	0.52	0/826
74	o8	0.38	0/614	0.60	0/822
75	O9	0.48	0/443	0.64	0/588
75	o9	0.45	0/443	0.63	0/588
76	Q0	0.48	0/423	0.72	0/562
76	q0	0.55	0/423	0.65	0/562
77	Q1	0.43	0/234	0.55	0/300
77	q1	0.50	0/234	0.65	0/300
78	Q2	0.61	1/860 (0.1%)	0.72	1/1136 (0.1%)
78	q2	0.58	1/860 (0.1%)	0.67	1/1136 (0.1%)
79	Q3	0.46	0/701	0.65	0/934
79	q3	0.50	0/701	0.61	0/934
80	e0	0.38	0/499	0.62	0/665
81	m2	0.34	0/736	0.76	10/1019 (1.0%)
82	p0	0.30	0/1092	0.52	0/1474
83	p1	0.29	0/234	0.49	1/326 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
83	p2	0.31	0/229	0.46	1/319 (0.3%)
84	f	0.40	0/1121	0.61	0/1508
85	B	0.66	0/47	1.57	0/68
85	C	0.58	0/50	1.12	0/72
All	All	0.54	16/433278 (0.0%)	0.94	681/635910 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
9	s7	0	1
16	C4	0	1
17	c5	0	1
18	c6	0	1
19	C7	0	1
39	L2	0	2
40	l3	0	1
52	M6	0	1
53	m7	0	1
56	n0	0	1
65	N9	0	1
84	f	1	0
All	All	1	12

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
78	Q2	17	CYS	CB-SG	9.97	1.99	1.82
78	q2	17	CYS	CB-SG	8.34	1.96	1.82
36	5	1152	G	N9-C4	-6.27	1.32	1.38
36	5	2401	A	N9-C4	6.26	1.41	1.37
36	5	2860	U	N1-C2	5.96	1.44	1.38
36	5	2401	A	N3-C4	5.91	1.38	1.34
36	1	2401	A	N3-C4	5.75	1.38	1.34
36	1	2401	A	C5-C4	5.70	1.42	1.38
36	1	48	A	N9-C4	-5.56	1.34	1.37
36	5	2401	A	C5-C4	5.55	1.42	1.38
36	5	2326	A	N9-C4	-5.39	1.34	1.37
36	5	1915	A	N9-C4	-5.39	1.34	1.37
36	1	2401	A	N9-C4	5.34	1.41	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	1	1369	A	N9-C4	-5.17	1.34	1.37
36	1	1192	C	N3-C4	5.14	1.37	1.33
36	5	1303	A	N9-C4	-5.04	1.34	1.37

All (681) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	1152	G	N3-C4-N9	-11.84	118.90	126.00
36	5	2355	G	N1-C6-O6	11.18	126.61	119.90
1	6	321	C	N1-C2-O2	11.14	125.58	118.90
36	5	1152	G	N3-C4-C5	11.03	134.11	128.60
36	5	1897	G	N1-C6-O6	10.10	125.96	119.90
36	5	1152	G	C2-N3-C4	-10.07	106.87	111.90
36	1	3278	C	N1-C2-O2	9.98	124.89	118.90
36	5	1307	G	P-O3'-C3'	9.97	131.66	119.70
1	6	321	C	C2-N1-C1'	9.85	129.64	118.80
36	1	3217	C	C2-N1-C1'	9.42	129.16	118.80
38	8	80	A	C8-N9-C4	-9.32	102.07	105.80
36	1	2572	C	N1-C2-O2	8.85	124.21	118.90
36	5	3207	U	C2-N1-C1'	-8.83	107.11	117.70
1	2	75	U	C2-N1-C1'	8.70	128.14	117.70
1	6	321	C	N3-C2-O2	-8.69	115.82	121.90
36	1	2617	U	C5-C4-O4	8.54	131.03	125.90
36	5	2943	G	C6-C5-N7	-8.52	125.29	130.40
36	5	2572	C	N1-C2-O2	8.49	123.99	118.90
36	5	2572	C	C2-N1-C1'	8.34	127.97	118.80
1	2	75	U	N1-C2-O2	8.33	128.63	122.80
36	5	2403	G	N1-C6-O6	8.32	124.89	119.90
36	5	2964	G	N1-C6-O6	-8.28	114.93	119.90
38	8	80	A	N7-C8-N9	8.16	117.88	113.80
36	5	3154	C	C2-N1-C1'	8.06	127.66	118.80
36	5	3154	C	N1-C2-O2	8.06	123.73	118.90
36	1	1604	G	C4-N9-C1'	8.02	136.93	126.50
1	2	1096	C	N1-C2-O2	8.00	123.70	118.90
36	1	2572	C	C2-N1-C1'	7.97	127.56	118.80
36	5	2355	G	C6-C5-N7	-7.93	125.64	130.40
36	5	3245	A	C2-N3-C4	-7.93	106.64	110.60
36	5	2403	G	C5-C6-N1	-7.88	107.56	111.50
1	6	1637	C	N1-C2-O2	7.86	123.61	118.90
1	6	453	U	C2-N1-C1'	7.73	126.97	117.70
36	5	2403	G	C4-C5-C6	7.67	123.41	118.80
36	1	3278	C	N3-C2-O2	-7.65	116.54	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	2943	G	N1-C6-O6	7.64	124.48	119.90
36	5	1028	U	C2-N1-C1'	7.64	126.86	117.70
36	1	3278	C	C2-N1-C1'	7.62	127.18	118.80
36	1	672	A	C8-N9-C4	7.61	108.84	105.80
36	5	1152	G	C8-N9-C1'	7.55	136.81	127.00
36	5	609	G	C5-C6-O6	-7.54	124.07	128.60
36	5	1200	A	N1-C6-N6	7.54	123.12	118.60
36	1	2572	C	N3-C2-O2	-7.53	116.63	121.90
36	5	2943	G	C4-C5-N7	7.53	113.81	110.80
36	1	780	A	N1-C6-N6	-7.53	114.08	118.60
36	5	1152	G	N3-C2-N2	-7.48	114.66	119.90
1	2	1096	C	C2-N1-C1'	7.47	127.02	118.80
1	6	194	U	C2-N1-C1'	7.47	126.66	117.70
36	1	2838	A	C8-N9-C4	7.45	108.78	105.80
36	5	1152	G	C5-N7-C8	-7.43	100.58	104.30
36	5	3197	G	N3-C4-C5	7.43	132.31	128.60
36	5	2355	G	C5-C6-N1	-7.40	107.80	111.50
36	5	3245	A	N1-C6-N6	7.38	123.03	118.60
36	5	2943	G	C5-C6-O6	-7.38	124.17	128.60
36	5	2964	G	C5-C6-O6	7.37	133.02	128.60
1	6	14	C	C6-N1-C2	-7.37	117.35	120.30
36	1	2314	U	C5-C6-N1	7.37	126.39	122.70
36	1	3217	C	C6-N1-C1'	-7.36	111.97	120.80
36	1	637	C	P-O3'-C3'	7.34	128.51	119.70
36	1	2617	U	N1-C2-N3	7.34	119.31	114.90
1	6	1637	C	C2-N1-C1'	7.30	126.83	118.80
1	6	321	C	C6-N1-C1'	-7.26	112.09	120.80
36	1	2617	U	C4-C5-C6	7.22	124.03	119.70
36	1	2197	C	C6-N1-C2	7.21	123.19	120.30
36	1	1308	A	C8-N9-C4	-7.19	102.92	105.80
36	1	2726	C	N3-C4-N4	-7.16	112.99	118.00
36	5	3207	U	C6-N1-C1'	7.16	131.22	121.20
36	5	648	C	O5'-P-OP1	-7.15	99.27	105.70
1	6	453	U	N1-C2-O2	7.14	127.80	122.80
36	5	2842	U	N3-C2-O2	-7.13	117.20	122.20
1	6	1473	U	N1-C2-O2	7.10	127.77	122.80
36	1	2403	G	N1-C6-O6	7.10	124.16	119.90
36	1	1269	U	C2-N1-C1'	7.06	126.17	117.70
36	1	2617	U	N3-C2-O2	-7.06	117.26	122.20
36	5	2726	C	C5-C4-N4	7.05	125.14	120.20
1	6	453	U	N3-C2-O2	-7.05	117.26	122.20
1	2	507	U	C2-N1-C1'	7.03	126.13	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	6	1000	C	C2-N1-C1'	7.03	126.53	118.80
62	N6	57	LEU	CA-CB-CG	7.02	131.44	115.30
36	1	1484	U	P-O3'-C3'	7.02	128.12	119.70
36	5	2964	G	C4-C5-N7	-6.95	108.02	110.80
36	1	1604	G	N3-C4-C5	-6.94	125.13	128.60
36	1	2726	C	N3-C2-O2	-6.93	117.05	121.90
36	5	1481	A	C8-N9-C4	-6.92	103.03	105.80
18	C6	40	GLU	C-N-CD	-6.91	105.40	120.60
1	2	831	U	C2-N1-C1'	6.91	125.99	117.70
1	2	75	U	N3-C2-O2	-6.89	117.38	122.20
36	5	1152	G	N1-C6-O6	6.88	124.03	119.90
36	1	1131	G	N1-C6-O6	6.84	124.01	119.90
36	5	658	G	C8-N9-C4	-6.84	103.66	106.40
1	6	101	U	N3-C2-O2	-6.82	117.42	122.20
36	5	339	C	C6-N1-C2	-6.80	117.58	120.30
1	2	1657	U	N1-C2-O2	6.80	127.56	122.80
36	1	2403	G	C6-C5-N7	-6.79	126.33	130.40
1	2	507	U	N1-C2-O2	6.78	127.55	122.80
36	1	2816	G	N1-C6-O6	6.76	123.96	119.90
36	5	2726	C	C6-N1-C2	-6.74	117.61	120.30
36	5	2199	G	N1-C6-O6	6.73	123.94	119.90
1	2	1096	C	C6-N1-C1'	-6.72	112.73	120.80
36	1	3143	C	N1-C2-O2	-6.72	114.87	118.90
36	5	1897	G	C5-C6-O6	-6.71	124.57	128.60
36	5	2404	A	N1-C6-N6	6.71	122.63	118.60
36	5	2964	G	N9-C4-C5	6.69	108.08	105.40
36	5	942	U	N3-C4-C5	-6.69	110.59	114.60
36	5	3245	A	C5-N7-C8	-6.67	100.57	103.90
37	7	49	G	N1-C6-O6	6.66	123.90	119.90
36	5	1367	G	N1-C6-O6	6.64	123.89	119.90
38	4	137	C	C6-N1-C2	6.64	122.95	120.30
38	8	125	U	N1-C2-O2	6.64	127.45	122.80
36	5	3362	A	N1-C6-N6	6.63	122.58	118.60
1	2	1039	A	O4'-C1'-N9	6.63	113.50	108.20
36	1	3277	U	N3-C2-O2	-6.62	117.56	122.20
36	5	2629	U	N3-C2-O2	6.61	126.83	122.20
36	1	1604	G	N3-C4-N9	6.60	129.96	126.00
36	1	1594	A	N1-C6-N6	-6.59	114.64	118.60
36	1	1604	G	C8-N9-C1'	-6.58	118.44	127.00
36	1	648	C	C6-N1-C2	-6.58	117.67	120.30
36	1	2627	C	N1-C2-O2	-6.57	114.96	118.90
36	5	1177	G	C6-C5-N7	-6.56	126.46	130.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	1	2193	U	N1-C2-O2	6.55	127.39	122.80
36	5	3208	G	N1-C6-O6	6.54	123.83	119.90
36	1	1119	C	C6-N1-C2	6.54	122.92	120.30
36	5	645	A	N1-C6-N6	-6.54	114.68	118.60
37	7	73	C	N1-C2-O2	6.51	122.81	118.90
73	o7	65	ARG	NE-CZ-NH1	6.51	123.56	120.30
36	5	1556	C	N1-C2-O2	6.49	122.79	118.90
1	2	1773	C	C6-N1-C2	-6.47	117.71	120.30
37	7	87	G	C5-C6-O6	-6.47	124.72	128.60
36	5	2199	G	C6-C5-N7	-6.46	126.52	130.40
36	1	1296	C	C6-N1-C2	-6.44	117.72	120.30
36	1	2193	U	N3-C2-O2	-6.43	117.70	122.20
1	6	101	U	N1-C2-O2	6.43	127.30	122.80
36	5	1897	G	C6-C5-N7	-6.43	126.54	130.40
36	5	641	C	N1-C2-N3	-6.43	114.70	119.20
36	5	1487	G	C8-N9-C4	-6.43	103.83	106.40
12	c0	97	PRO	N-CA-CB	6.42	111.01	103.30
36	1	3217	C	N1-C2-O2	6.42	122.75	118.90
1	6	1473	U	N3-C2-O2	-6.41	117.71	122.20
36	1	1495	U	C5-C6-N1	-6.41	119.50	122.70
36	5	639	G	N1-C6-O6	6.41	123.74	119.90
36	5	3207	U	C5-C4-O4	6.40	129.74	125.90
12	C0	88	PRO	N-CA-CB	6.39	110.97	103.30
1	6	194	U	N1-C2-O2	6.39	127.27	122.80
36	1	676	G	C6-C5-N7	-6.38	126.57	130.40
36	5	2684	C	C6-N1-C2	-6.38	117.75	120.30
36	5	3245	A	N7-C8-N9	6.37	116.98	113.80
36	5	2572	C	N3-C2-O2	-6.37	117.44	121.90
36	5	1481	A	N7-C8-N9	6.36	116.98	113.80
36	5	2197	C	C6-N1-C2	6.34	122.83	120.30
36	5	2777	G	C4-N9-C1'	-6.33	118.27	126.50
36	1	2996	U	N1-C2-O2	6.33	127.23	122.80
36	5	2800	G	C8-N9-C4	-6.33	103.87	106.40
36	5	3362	A	C6-C5-N7	-6.33	127.87	132.30
36	1	406	G	O4'-C1'-N9	6.32	113.26	108.20
1	6	1473	U	C2-N1-C1'	6.32	125.28	117.70
1	6	1698	G	P-O3'-C3'	6.32	127.28	119.70
1	6	1637	C	N3-C2-O2	-6.31	117.48	121.90
36	5	2552	C	C2-N1-C1'	6.31	125.74	118.80
36	5	3245	A	C6-C5-N7	-6.31	127.89	132.30
36	5	3197	G	N3-C4-N9	-6.31	122.22	126.00
1	6	687	G	N3-C2-N2	-6.30	115.49	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	963	G	N1-C6-O6	-6.29	116.12	119.90
1	2	507	U	N3-C2-O2	-6.29	117.79	122.20
36	5	3351	U	C2-N1-C1'	6.29	125.25	117.70
1	2	1389	C	C6-N1-C2	-6.28	117.79	120.30
78	Q2	93	LEU	CA-CB-CG	6.28	129.75	115.30
36	1	2617	U	N3-C4-C5	-6.28	110.83	114.60
1	2	75	U	C6-N1-C1'	-6.28	112.41	121.20
36	1	672	A	N1-C6-N6	6.28	122.37	118.60
36	5	939	U	O5'-P-OP1	6.28	118.23	110.70
36	5	3093	C	C6-N1-C2	6.28	122.81	120.30
36	1	2819	A	O5'-P-OP2	-6.27	100.06	105.70
35	sM	167	PRO	N-CA-CB	6.27	110.83	103.30
81	m2	42	PRO	N-CA-CB	6.27	110.83	103.30
36	1	1604	G	C6-C5-N7	-6.27	126.64	130.40
36	5	2978	U	O4'-C1'-N1	6.27	113.21	108.20
36	5	942	U	N3-C4-O4	6.26	123.78	119.40
36	1	676	G	C8-N9-C4	-6.26	103.89	106.40
36	1	2803	A	O5'-P-OP1	-6.26	100.06	105.70
36	1	2726	C	C5-C4-N4	6.26	124.58	120.20
1	2	1389	C	N1-C2-O2	6.25	122.65	118.90
36	5	1481	A	P-O3'-C3'	6.24	127.19	119.70
36	5	1399	A	N1-C6-N6	6.24	122.34	118.60
36	5	2842	U	N1-C2-O2	6.23	127.16	122.80
36	1	2946	A	N1-C6-N6	6.23	122.34	118.60
36	5	2376	G	C4-C5-N7	6.23	113.29	110.80
36	1	59	G	N1-C6-O6	6.22	123.63	119.90
81	m2	46	PRO	N-CA-CB	6.22	110.77	103.30
36	5	1190	A	C4-N9-C1'	6.22	137.49	126.30
36	5	2827	U	C2-N1-C1'	6.22	125.16	117.70
1	6	194	U	N3-C2-O2	-6.21	117.85	122.20
36	5	283	G	C4-C5-N7	6.21	113.28	110.80
36	5	2376	G	C5-C6-O6	-6.21	124.88	128.60
36	1	2978	U	O4'-C1'-N1	6.20	113.16	108.20
36	5	2403	G	C6-C5-N7	-6.19	126.69	130.40
1	2	831	U	C5-C6-N1	6.19	125.79	122.70
36	5	2355	G	C4-C5-C6	6.19	122.51	118.80
36	1	1269	U	N1-C2-O2	6.18	127.13	122.80
36	5	2572	C	C6-N1-C1'	-6.18	113.38	120.80
36	5	2272	G	O4'-C1'-N9	6.18	113.14	108.20
36	5	1190	A	C4-C5-C6	6.17	120.08	117.00
1	2	1698	G	P-O3'-C3'	6.17	127.10	119.70
1	6	1097	U	P-O3'-C3'	6.17	127.10	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	c0	83	PRO	N-CA-CB	6.17	110.70	103.30
36	1	3180	A	C2-N3-C4	-6.16	107.52	110.60
36	5	1170	A	C8-N9-C4	6.15	108.26	105.80
81	m2	101	PRO	N-CA-CB	6.15	110.67	103.30
36	1	1820	U	P-O3'-C3'	6.14	127.07	119.70
36	5	922	U	C5-C6-N1	-6.14	119.63	122.70
36	1	3362	A	O4'-C1'-N9	6.12	113.10	108.20
36	1	3118	C	C6-N1-C2	-6.11	117.86	120.30
36	1	2571	U	C2-N1-C1'	6.11	125.03	117.70
36	5	2288	G	C4-N9-C1'	6.10	134.43	126.50
83	p1	36	PRO	N-CA-CB	6.10	110.62	103.30
36	5	2156	C	C6-N1-C2	6.10	122.74	120.30
35	SM	167	PRO	N-CA-CB	6.10	110.62	103.30
36	5	410	U	N1-C2-O2	-6.09	118.53	122.80
36	1	2355	G	N1-C6-O6	6.09	123.55	119.90
1	6	858	G	O4'-C1'-N9	6.08	113.07	108.20
36	5	2777	G	C6-C5-N7	6.08	134.04	130.40
1	6	75	U	P-O3'-C3'	6.07	126.99	119.70
36	1	65	A	P-O3'-C3'	6.06	126.97	119.70
36	5	3154	C	N3-C2-O2	-6.06	117.66	121.90
1	6	804	A	C8-N9-C4	-6.05	103.38	105.80
36	5	2199	G	N7-C8-N9	6.04	116.12	113.10
36	5	3040	A	C8-N9-C4	6.04	108.22	105.80
36	1	3277	U	C2-N1-C1'	6.04	124.94	117.70
36	5	1556	C	C2-N1-C1'	6.03	125.43	118.80
36	5	523	A	N1-C6-N6	-6.02	114.99	118.60
81	m2	88	PRO	N-CA-CB	6.02	110.53	103.30
36	5	934	G	C4-N9-C1'	6.01	134.32	126.50
1	2	934	C	C2-N1-C1'	6.01	125.41	118.80
36	1	2571	U	N1-C2-O2	6.00	127.00	122.80
36	5	3245	A	N1-C2-N3	6.00	132.30	129.30
36	1	1369	A	C2-N3-C4	-6.00	107.60	110.60
36	1	2350	C	N3-C2-O2	-6.00	117.70	121.90
36	5	1156	C	C6-N1-C2	-6.00	117.90	120.30
36	1	2404	A	N1-C6-N6	5.99	122.19	118.60
36	5	1143	A	C2-N3-C4	-5.99	107.61	110.60
36	5	1028	U	N1-C2-O2	5.98	126.98	122.80
1	2	1389	C	C2-N1-C1'	5.98	125.37	118.80
36	5	876	A	C8-N9-C4	5.96	108.19	105.80
36	5	1152	G	C4-N9-C1'	-5.96	118.76	126.50
36	1	1306	G	N1-C6-O6	5.95	123.47	119.90
36	5	2288	G	C8-N9-C1'	-5.95	119.27	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	m2	51	PRO	N-CA-CB	5.94	110.43	103.30
36	1	2700	G	C6-C5-N7	-5.94	126.84	130.40
36	5	2130	G	C4-N9-C1'	-5.94	118.78	126.50
36	5	2619	G	N3-C4-N9	5.93	129.56	126.00
1	2	1796	C	C6-N1-C2	-5.93	117.93	120.30
36	5	3195	U	C2-N1-C1'	5.92	124.80	117.70
36	5	641	C	C2-N3-C4	5.92	122.86	119.90
81	m2	161	PRO	N-CA-CB	5.91	110.40	103.30
36	1	435	C	C6-N1-C2	5.91	122.66	120.30
36	1	917	A	N1-C6-N6	-5.91	115.06	118.60
1	2	581	U	C2-N1-C1'	5.90	124.78	117.70
36	5	1437	C	C2-N1-C1'	5.90	125.29	118.80
1	2	1539	G	N7-C8-N9	5.90	116.05	113.10
1	2	720	G	OP1-P-O3'	5.89	118.16	105.20
1	6	163	G	N3-C4-N9	-5.89	122.47	126.00
36	5	1878	G	C4-N9-C1'	5.89	134.16	126.50
1	2	992	A	O4'-C1'-N9	5.89	112.91	108.20
36	1	2827	U	N3-C4-O4	-5.89	115.28	119.40
1	2	16	G	N3-C4-C5	-5.88	125.66	128.60
36	1	2664	C	C6-N1-C2	-5.88	117.95	120.30
83	p2	36	PRO	N-CA-CB	5.88	110.36	103.30
38	4	94	C	C6-N1-C2	5.88	122.65	120.30
1	6	151	G	N3-C2-N2	-5.87	115.79	119.90
36	5	776	U	N1-C2-N3	5.87	118.42	114.90
36	1	1001	G	N1-C6-O6	5.87	123.42	119.90
12	c0	88	PRO	N-CA-CB	5.87	110.34	103.30
36	5	2727	A	N1-C6-N6	-5.87	115.08	118.60
36	5	1490	A	C8-N9-C4	-5.86	103.46	105.80
36	5	2621	G	N1-C6-O6	5.85	123.41	119.90
1	2	1291	G	N3-C4-N9	-5.85	122.49	126.00
36	5	2199	G	C8-N9-C4	-5.85	104.06	106.40
1	6	524	U	N3-C2-O2	-5.85	118.11	122.20
81	m2	10	PRO	N-CA-CB	5.85	110.32	103.30
36	5	1765	U	O5'-P-OP1	5.85	117.72	110.70
36	1	1858	A	C2-N3-C4	5.84	113.52	110.60
36	5	2944	U	N1-C2-O2	5.84	126.89	122.80
36	5	2620	G	C4-N9-C1'	-5.84	118.91	126.50
38	8	125	U	N3-C2-O2	-5.84	118.11	122.20
36	1	2553	U	C2-N1-C1'	5.83	124.70	117.70
36	1	1489	A	N1-C6-N6	5.83	122.10	118.60
36	1	2887	A	C2-N3-C4	5.82	113.51	110.60
1	6	104	A	O4'-C1'-N9	5.82	112.85	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	1480	G	C8-N9-C4	5.81	108.72	106.40
36	5	2283	G	N1-C6-O6	5.80	123.38	119.90
36	1	1305	U	N1-C2-O2	5.80	126.86	122.80
36	1	981	U	C5-C6-N1	5.79	125.60	122.70
36	5	2777	G	N3-C4-N9	-5.79	122.52	126.00
1	2	1389	C	N3-C2-O2	-5.79	117.85	121.90
1	6	781	U	N1-C2-O2	5.77	126.84	122.80
36	5	776	U	C4-C5-C6	5.77	123.16	119.70
36	5	1161	G	C2-N3-C4	5.77	114.78	111.90
36	5	2584	G	C4-N9-C1'	5.76	134.00	126.50
36	5	383	G	C8-N9-C4	5.76	108.70	106.40
36	1	1307	G	O4'-C1'-N9	5.76	112.81	108.20
1	6	548	G	N1-C6-O6	5.75	123.35	119.90
44	L7	179	LEU	CA-CB-CG	5.75	128.52	115.30
36	1	361	A	N1-C6-N6	-5.74	115.16	118.60
36	1	637	C	C2-N1-C1'	5.74	125.12	118.80
36	1	3367	C	C6-N1-C2	5.74	122.60	120.30
36	5	793	C	C6-N1-C2	-5.74	118.00	120.30
36	5	3078	U	N3-C2-O2	-5.74	118.18	122.20
36	5	1177	G	N1-C6-O6	5.73	123.34	119.90
1	6	542	A	P-O3'-C3'	5.73	126.58	119.70
1	2	1456	C	C2-N1-C1'	5.73	125.10	118.80
36	5	2176	U	N3-C2-O2	-5.72	118.19	122.20
36	5	3154	C	C6-N1-C1'	-5.72	113.94	120.80
36	1	3303	G	C8-N9-C4	5.72	108.69	106.40
36	5	719	U	C5-C6-N1	5.72	125.56	122.70
36	1	780	A	N9-C4-C5	5.71	108.09	105.80
36	5	2392	C	N3-C4-C5	5.71	124.18	121.90
81	m2	15	PRO	N-CA-CB	5.71	110.15	103.30
36	5	2821	C	N1-C2-O2	-5.71	115.48	118.90
38	4	39	G	N1-C6-O6	-5.70	116.48	119.90
36	1	3319	U	P-O3'-C3'	5.70	126.53	119.70
81	m2	102	PRO	N-CA-CB	5.70	110.13	103.30
36	1	922	U	C2-N1-C1'	5.69	124.53	117.70
36	5	2788	C	C6-N1-C2	5.69	122.58	120.30
36	1	1000	C	C6-N1-C2	5.69	122.58	120.30
36	1	2309	A	N1-C6-N6	5.69	122.02	118.60
70	O4	51	LEU	CA-CB-CG	5.69	128.39	115.30
36	1	1160	C	N1-C2-O2	-5.69	115.49	118.90
36	5	2860	U	N3-C2-O2	-5.69	118.22	122.20
36	5	3197	G	C4-N9-C1'	-5.69	119.11	126.50
36	1	2298	U	O4'-C1'-N1	5.68	112.75	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	1	901	G	N1-C6-O6	5.68	123.31	119.90
36	5	1434	G	C5-C6-O6	-5.68	125.19	128.60
36	5	1495	U	C2-N1-C1'	5.68	124.51	117.70
36	5	2205	U	O4'-C1'-N1	5.67	112.74	108.20
36	1	640	U	N3-C4-O4	5.67	123.37	119.40
78	q2	17	CYS	CA-CB-SG	5.67	124.20	114.00
36	5	2278	C	N1-C2-O2	5.66	122.30	118.90
36	5	2945	G	C5-C6-O6	-5.66	125.20	128.60
36	5	3328	G	N1-C6-O6	-5.66	116.50	119.90
1	6	18	C	C6-N1-C2	-5.66	118.03	120.30
36	1	3106	A	N1-C6-N6	-5.66	115.20	118.60
36	1	1269	U	N3-C2-O2	-5.65	118.24	122.20
36	5	2860	U	O4'-C1'-N1	5.65	112.72	108.20
36	5	2885	C	C6-N1-C2	5.65	122.56	120.30
1	6	1098	U	C2-N1-C1'	5.64	124.47	117.70
36	1	2601	A	C8-N9-C4	5.64	108.06	105.80
36	5	1303	A	C8-N9-C4	5.64	108.06	105.80
36	5	1556	C	N3-C2-O2	-5.64	117.95	121.90
36	5	3078	U	N1-C2-O2	5.64	126.75	122.80
36	1	2827	U	C5-C4-O4	5.63	129.28	125.90
36	5	1495	U	C5-C6-N1	5.63	125.52	122.70
1	6	1000	C	C6-N1-C2	-5.63	118.05	120.30
36	5	3362	A	C5-N7-C8	-5.63	101.09	103.90
36	5	410	U	N3-C4-C5	-5.62	111.23	114.60
3	S1	218	LEU	CA-CB-CG	5.62	128.23	115.30
36	1	2572	C	C6-N1-C1'	-5.62	114.05	120.80
36	5	2625	C	C6-N1-C2	5.62	122.55	120.30
36	1	1716	U	P-O3'-C3'	5.61	126.44	119.70
36	5	934	G	N3-C4-C5	-5.61	125.80	128.60
36	1	2808	A	O5'-P-OP1	-5.60	100.66	105.70
36	5	3057	U	C2-N1-C1'	5.60	124.42	117.70
37	7	73	C	N3-C2-O2	-5.60	117.98	121.90
1	2	1456	C	N1-C2-O2	5.59	122.26	118.90
1	6	1274	C	C2-N1-C1'	5.59	124.95	118.80
36	5	3026	G	N1-C6-O6	5.59	123.25	119.90
37	7	73	C	C6-N1-C2	-5.58	118.07	120.30
36	5	2205	U	C5-C6-N1	5.58	125.49	122.70
18	C6	40	GLU	C-N-CA	5.57	145.41	122.00
36	5	406	G	N3-C4-N9	-5.57	122.66	126.00
36	5	2303	A	C8-N9-C4	5.57	108.03	105.80
36	5	1447	G	O4'-C1'-N9	5.57	112.65	108.20
36	5	2622	C	C6-N1-C2	-5.56	118.07	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	577	G	C4-C5-N7	5.56	113.03	110.80
36	1	3277	U	N1-C2-O2	5.56	126.69	122.80
36	5	1192	C	N1-C2-O2	5.56	122.24	118.90
1	2	1324	G	N3-C4-N9	-5.56	122.67	126.00
1	6	1058	U	OP1-P-O3'	5.56	117.42	105.20
36	5	2978	U	C5-C6-N1	-5.55	119.92	122.70
1	6	1773	C	N3-C4-C5	-5.55	119.68	121.90
37	7	10	C	C2-N1-C1'	5.55	124.90	118.80
36	1	676	G	N7-C8-N9	5.55	115.87	113.10
1	6	151	G	N3-C4-N9	-5.54	122.67	126.00
36	5	2943	G	C5-N7-C8	-5.54	101.53	104.30
36	5	1311	G	O5'-P-OP2	-5.54	100.72	105.70
38	8	125	U	C2-N1-C1'	5.53	124.34	117.70
36	1	2617	U	C6-N1-C2	-5.53	117.68	121.00
36	5	1403	C	C6-N1-C2	5.53	122.51	120.30
36	5	1177	G	C4-N9-C1'	5.53	133.69	126.50
36	5	2943	G	N3-C4-N9	5.53	129.32	126.00
36	5	3351	U	N1-C2-O2	5.52	126.67	122.80
1	6	163	G	C2-N3-C4	-5.52	109.14	111.90
1	6	163	G	C8-N9-C4	-5.52	104.19	106.40
36	5	1132	C	C6-N1-C2	5.52	122.51	120.30
36	5	2288	G	N3-C4-N9	5.52	129.31	126.00
36	1	2314	U	C2-N1-C1'	5.51	124.31	117.70
1	2	959	U	N1-C2-O2	5.51	126.65	122.80
36	1	2719	U	N1-C2-O2	-5.50	118.95	122.80
36	1	3306	U	C5-C4-O4	5.50	129.20	125.90
36	5	546	C	N1-C2-O2	5.50	122.20	118.90
1	6	558	U	P-O3'-C3'	5.50	126.30	119.70
1	2	542	A	O4'-C1'-N9	5.50	112.60	108.20
24	D2	93	LEU	CA-CB-CG	5.49	127.92	115.30
36	5	915	A	C2-N3-C4	5.49	113.34	110.60
1	6	139	C	P-O3'-C3'	5.48	126.28	119.70
36	5	2330	C	N1-C2-O2	-5.48	115.61	118.90
36	1	2185	G	C8-N9-C4	-5.48	104.21	106.40
1	2	728	U	C2-N1-C1'	5.47	124.27	117.70
36	1	496	C	C5-C6-N1	5.47	123.74	121.00
36	5	1307	G	OP2-P-O3'	5.47	117.24	105.20
36	5	2777	G	C8-N9-C1'	5.47	134.11	127.00
36	1	1367	G	N1-C6-O6	5.47	123.18	119.90
36	5	2704	A	O5'-P-OP1	-5.47	100.78	105.70
36	5	2867	C	C6-N1-C2	5.47	122.49	120.30
36	1	1296	C	C5-C6-N1	5.46	123.73	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1657	U	N3-C2-O2	-5.46	118.38	122.20
36	1	3076	C	C6-N1-C2	-5.45	118.12	120.30
1	6	1	U	N3-C2-O2	-5.45	118.39	122.20
36	1	934	G	C4-C5-N7	5.44	112.98	110.80
36	1	3216	G	N1-C6-O6	5.44	123.16	119.90
1	6	965	U	N3-C2-O2	-5.43	118.40	122.20
36	1	637	C	N1-C2-O2	5.43	122.16	118.90
36	1	89	A	N1-C6-N6	-5.43	115.34	118.60
36	5	639	G	C6-C5-N7	-5.43	127.14	130.40
36	5	1152	G	N7-C8-N9	5.43	115.81	113.10
36	5	353	G	C4-N9-C1'	-5.43	119.44	126.50
1	2	959	U	N3-C2-O2	-5.42	118.40	122.20
36	5	609	G	N1-C6-O6	5.42	123.15	119.90
36	1	2275	A	C8-N9-C4	-5.42	103.63	105.80
36	5	1028	U	N3-C2-O2	-5.42	118.41	122.20
42	l5	110	LEU	CA-CB-CG	5.42	127.76	115.30
36	1	851	C	C2-N1-C1'	5.42	124.76	118.80
81	m2	11	PRO	N-CA-CB	5.42	109.80	103.30
36	5	2758	A	O4'-C1'-N9	5.41	112.53	108.20
36	1	2693	C	C6-N1-C2	5.40	122.46	120.30
36	1	216	G	O5'-P-OP1	-5.39	100.84	105.70
36	5	2842	U	C2-N1-C1'	5.39	124.17	117.70
36	5	2376	G	C6-C5-N7	-5.39	127.17	130.40
36	5	1000	C	C6-N1-C2	5.39	122.45	120.30
1	2	830	U	N3-C2-O2	-5.38	118.43	122.20
36	1	1733	G	N3-C4-C5	-5.38	125.91	128.60
36	5	24	G	N1-C6-O6	5.38	123.13	119.90
36	1	1822	C	C6-N1-C2	-5.38	118.15	120.30
36	1	2624	G	C8-N9-C4	-5.38	104.25	106.40
36	5	2288	G	C6-C5-N7	-5.38	127.17	130.40
1	2	1199	G	C4-N9-C1'	5.38	133.49	126.50
36	1	2550	U	N3-C2-O2	-5.38	118.43	122.20
38	4	11	C	N1-C2-O2	-5.38	115.67	118.90
36	5	1604	G	C4-N9-C1'	5.38	133.49	126.50
36	1	213	A	C8-N9-C4	5.38	107.95	105.80
36	1	2112	U	P-O3'-C3'	5.38	126.15	119.70
36	5	1192	C	C2-N1-C1'	5.38	124.72	118.80
36	1	2776	C	C6-N1-C2	5.38	122.45	120.30
20	c8	15	LEU	CA-CB-CG	5.37	127.66	115.30
36	1	2314	U	C5-C4-O4	-5.37	122.68	125.90
1	6	813	U	C2-N1-C1'	5.37	124.14	117.70
36	1	1481	A	P-O3'-C3'	5.37	126.14	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	1	344	A	N1-C6-N6	-5.36	115.38	118.60
36	5	1897	G	C4-C5-N7	5.36	112.94	110.80
36	1	851	C	C5-C6-N1	5.36	123.68	121.00
36	1	1368	U	C2-N1-C1'	5.36	124.13	117.70
36	1	2991	A	N1-C6-N6	5.36	121.81	118.60
1	2	1458	G	C4-N9-C1'	5.35	133.46	126.50
36	1	1820	U	OP2-P-O3'	5.35	116.97	105.20
36	1	2137	U	C2-N1-C1'	5.35	124.12	117.70
36	1	2719	U	C2-N1-C1'	-5.35	111.28	117.70
36	1	1495	U	C4-C5-C6	5.35	122.91	119.70
36	5	591	G	N1-C6-O6	5.35	123.11	119.90
1	2	36	C	C5-C4-N4	-5.35	116.46	120.20
36	1	1351	U	N1-C2-O2	5.35	126.54	122.80
36	5	1152	G	C8-N9-C4	-5.35	104.26	106.40
36	5	1858	A	C8-N9-C4	-5.34	103.66	105.80
36	1	2700	G	C5-C6-O6	-5.34	125.39	128.60
36	1	648	C	O5'-P-OP1	-5.34	100.89	105.70
36	1	1355	A	P-O3'-C3'	5.34	126.11	119.70
36	1	984	G	N3-C4-C5	-5.34	125.93	128.60
36	1	2309	A	C4-C5-N7	5.34	113.37	110.70
36	5	1222	G	P-O3'-C3'	5.34	126.11	119.70
1	6	1642	G	N1-C6-O6	5.33	123.10	119.90
36	1	2643	A	C8-N9-C4	5.33	107.93	105.80
36	1	2868	U	N3-C2-O2	-5.33	118.47	122.20
1	6	695	U	N3-C2-O2	-5.33	118.47	122.20
36	5	1180	A	O4'-C1'-N9	-5.33	103.94	108.20
1	6	1747	G	C8-N9-C4	5.32	108.53	106.40
36	5	3377	G	C5-C6-O6	-5.32	125.41	128.60
36	1	1306	G	C5-C6-O6	-5.32	125.41	128.60
36	1	1847	A	N1-C6-N6	-5.32	115.41	118.60
1	2	158	U	P-O3'-C3'	5.32	126.08	119.70
36	1	2935	U	C2-N1-C1'	5.32	124.08	117.70
36	5	718	G	C4-N9-C1'	5.31	133.41	126.50
36	1	1930	A	C8-N9-C4	5.31	107.92	105.80
1	6	639	U	C2-N1-C1'	5.30	124.07	117.70
36	5	3195	U	O4'-C1'-N1	5.30	112.44	108.20
44	17	83	LEU	CA-CB-CG	5.30	127.50	115.30
36	1	913	A	C8-N9-C4	-5.30	103.68	105.80
36	1	2869	U	O5'-P-OP1	-5.30	100.93	105.70
36	1	1160	C	N3-C2-O2	5.30	125.61	121.90
38	4	103	G	N3-C4-C5	-5.30	125.95	128.60
36	5	2171	G	N1-C6-O6	-5.29	116.72	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	2249	G	C8-N9-C4	-5.29	104.28	106.40
36	1	831	G	C8-N9-C4	5.29	108.52	106.40
1	2	1560	U	N3-C2-O2	-5.29	118.50	122.20
36	1	2303	A	N1-C6-N6	5.29	121.77	118.60
36	1	979	U	P-O3'-C3'	5.29	126.04	119.70
36	5	1190	A	C8-N9-C1'	-5.28	118.19	127.70
64	n8	28	HIS	N-CA-C	5.28	125.27	111.00
36	1	2572	C	C6-N1-C2	-5.28	118.19	120.30
36	1	2873	U	C5-C4-O4	5.28	129.07	125.90
36	1	2971	A	O4'-C1'-N9	5.28	112.42	108.20
1	6	1389	C	C2-N1-C1'	5.28	124.61	118.80
36	1	3306	U	N3-C2-O2	-5.28	118.51	122.20
36	1	880	G	O4'-C1'-N9	5.27	112.42	108.20
1	6	1340	U	N1-C2-O2	5.27	126.49	122.80
36	1	2541	U	P-O3'-C3'	5.27	126.02	119.70
36	1	992	A	C8-N9-C4	-5.27	103.69	105.80
1	2	1291	G	N3-C4-C5	5.26	131.23	128.60
36	5	1582	C	C6-N1-C2	-5.26	118.19	120.30
36	1	641	C	C6-N1-C2	5.26	122.41	120.30
36	5	2868	U	N1-C2-O2	5.26	126.48	122.80
36	1	672	A	N9-C4-C5	-5.26	103.70	105.80
36	1	799	G	C8-N9-C4	5.26	108.50	106.40
36	1	1352	A	P-O3'-C3'	5.26	126.01	119.70
36	5	641	C	C5-C6-N1	5.26	123.63	121.00
1	6	359	A	C8-N9-C4	5.25	107.90	105.80
36	5	3362	A	N7-C8-N9	5.25	116.43	113.80
1	6	523	G	N3-C4-N9	5.25	129.15	126.00
36	5	2620	G	C6-C5-N7	5.25	133.55	130.40
36	1	3244	A	O5'-P-OP2	-5.25	100.98	105.70
36	5	2983	C	O5'-P-OP1	-5.25	100.98	105.70
36	1	3361	G	N3-C4-N9	5.25	129.15	126.00
36	5	1149	G	N3-C4-C5	-5.25	125.98	128.60
1	2	728	U	N1-C2-O2	5.25	126.47	122.80
36	1	3278	C	C6-N1-C1'	-5.24	114.51	120.80
36	5	718	G	O4'-C1'-N9	5.24	112.39	108.20
36	5	3143	C	N3-C4-C5	-5.24	119.80	121.90
36	1	1508	C	C6-N1-C2	-5.24	118.20	120.30
36	1	2413	A	C4-C5-C6	-5.24	114.38	117.00
36	5	2403	G	C8-N9-C1'	-5.24	120.19	127.00
38	8	113	U	C2-N1-C1'	5.24	123.98	117.70
36	5	3049	A	N1-C6-N6	5.23	121.74	118.60
1	6	1097	U	N3-C2-O2	-5.23	118.54	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	1239	C	C5-C6-N1	5.23	123.62	121.00
36	5	1434	G	N1-C6-O6	5.23	123.04	119.90
1	2	720	G	P-O3'-C3'	5.23	125.98	119.70
1	2	1761	U	P-O3'-C3'	5.23	125.98	119.70
36	5	404	G	O5'-P-OP2	-5.23	100.99	105.70
15	C3	22	ALA	C-N-CD	-5.23	109.10	120.60
1	2	1539	G	C8-N9-C4	-5.22	104.31	106.40
36	1	2836	C	N3-C2-O2	-5.22	118.25	121.90
36	5	406	G	C4-N9-C1'	-5.22	119.72	126.50
1	2	1490	C	C6-N1-C2	-5.22	118.21	120.30
36	5	3362	A	O4'-C1'-N9	5.21	112.37	108.20
36	1	3216	G	C5-C6-O6	-5.21	125.47	128.60
36	5	1156	C	C2-N1-C1'	5.21	124.53	118.80
36	1	1422	G	N1-C6-O6	5.21	123.02	119.90
36	5	2976	A	N1-C2-N3	5.21	131.90	129.30
35	SM	134	ASP	CB-CG-OD2	5.20	122.98	118.30
36	1	1296	C	C2-N1-C1'	5.19	124.51	118.80
1	6	639	U	N1-C2-O2	5.19	126.43	122.80
36	5	2231	C	C2-N1-C1'	5.19	124.51	118.80
36	5	2945	G	O5'-P-OP1	-5.19	101.03	105.70
37	3	58	C	C6-N1-C2	-5.19	118.22	120.30
36	1	1469	C	N1-C2-O2	5.19	122.01	118.90
36	5	942	U	C6-N1-C2	-5.18	117.89	121.00
36	5	2182	A	N1-C6-N6	5.18	121.71	118.60
36	5	1449	A	C8-N9-C4	5.18	107.87	105.80
36	5	3362	A	C4-C5-N7	5.18	113.29	110.70
36	1	59	G	C5-C6-O6	-5.17	125.50	128.60
36	5	641	C	C4-C5-C6	-5.17	114.81	117.40
36	5	2772	C	P-O3'-C3'	5.17	125.91	119.70
36	1	1000	C	N1-C2-N3	-5.17	115.58	119.20
1	2	1332	C	C6-N1-C2	-5.17	118.23	120.30
36	1	650	C	N1-C2-O2	-5.17	115.80	118.90
1	2	1573	A	P-O3'-C3'	5.17	125.90	119.70
36	1	1556	C	C2-N1-C1'	5.17	124.48	118.80
1	6	1196	A	P-O3'-C3'	5.17	125.90	119.70
36	5	3161	C	C6-N1-C2	-5.16	118.23	120.30
36	5	3214	U	N3-C2-O2	-5.16	118.58	122.20
36	1	1149	G	N3-C4-N9	-5.16	122.90	126.00
1	6	194	U	C5-C6-N1	5.16	125.28	122.70
1	6	781	U	N3-C2-O2	-5.16	118.59	122.20
1	6	1274	C	N1-C2-O2	5.16	122.00	118.90
36	5	1323	G	N3-C4-C5	-5.16	126.02	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	1657	C	N1-C2-O2	5.15	121.99	118.90
36	1	3217	C	N3-C2-O2	-5.14	118.30	121.90
36	5	2385	G	N3-C4-C5	5.14	131.17	128.60
1	6	321	C	C6-N1-C2	-5.14	118.24	120.30
1	2	829	A	P-O3'-C3'	5.14	125.86	119.70
1	2	73	U	O4'-C1'-N1	5.13	112.31	108.20
1	2	278	U	P-O3'-C3'	5.13	125.86	119.70
36	5	2630	C	C2-N1-C1'	5.13	124.45	118.80
1	2	1081	A	O4'-C1'-N9	5.13	112.31	108.20
36	5	2726	C	N3-C4-N4	-5.13	114.41	118.00
36	1	620	U	C2-N1-C1'	-5.13	111.55	117.70
1	6	1537	C	C5-C6-N1	5.13	123.56	121.00
1	6	158	U	P-O3'-C3'	5.12	125.85	119.70
37	7	92	A	N1-C6-N6	5.12	121.67	118.60
1	2	728	U	N3-C2-O2	-5.12	118.61	122.20
36	5	966	U	N3-C2-O2	-5.12	118.62	122.20
36	5	1352	A	P-O3'-C3'	5.12	125.84	119.70
36	1	2193	U	C2-N1-C1'	5.11	123.83	117.70
36	5	2399	A	C8-N9-C4	5.11	107.84	105.80
36	5	2948	C	N1-C2-O2	5.10	121.96	118.90
36	1	890	C	N1-C2-O2	5.10	121.96	118.90
1	6	687	G	N1-C2-N2	5.10	120.79	116.20
1	6	858	G	C4-N9-C1'	5.10	133.13	126.50
36	5	2531	C	N1-C2-O2	5.10	121.96	118.90
36	5	1355	A	P-O3'-C3'	5.10	125.82	119.70
38	8	54	A	C8-N9-C4	-5.10	103.76	105.80
36	1	2403	G	C4-C5-C6	5.10	121.86	118.80
36	1	2847	A	C8-N9-C4	5.10	107.84	105.80
36	1	1362	G	C8-N9-C4	5.09	108.44	106.40
1	6	1098	U	N1-C2-O2	5.09	126.37	122.80
1	6	1751	C	O5'-P-OP2	-5.09	101.11	105.70
36	1	881	C	N1-C2-O2	5.09	121.96	118.90
36	5	2156	C	C5-C6-N1	-5.09	118.45	121.00
36	5	3347	A	C8-N9-C4	5.09	107.84	105.80
36	1	347	G	C4-C5-N7	5.09	112.84	110.80
36	5	960	U	N1-C2-O2	5.09	126.36	122.80
36	5	2403	G	C4-N9-C1'	5.09	133.12	126.50
36	1	1429	G	O4'-C1'-N9	-5.09	104.13	108.20
36	1	2230	C	C6-N1-C2	-5.09	118.27	120.30
36	5	2526	C	N1-C2-O2	5.09	121.95	118.90
1	2	1324	G	N3-C2-N2	-5.08	116.34	119.90
36	5	180	C	N3-C2-O2	-5.08	118.34	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	2643	A	C8-N9-C4	5.08	107.83	105.80
1	6	1031	U	OP2-P-O3'	5.08	116.37	105.20
36	1	2808	A	N1-C6-N6	5.08	121.64	118.60
36	5	2288	G	N1-C2-N3	5.08	126.94	123.90
36	5	406	G	C6-C5-N7	5.07	133.44	130.40
59	n3	48	ARG	NE-CZ-NH1	5.07	122.83	120.30
36	5	406	G	N1-C6-O6	-5.07	116.86	119.90
36	5	546	C	C2-N1-C1'	5.07	124.38	118.80
36	1	1716	U	OP1-P-O3'	5.07	116.35	105.20
36	1	1589	A	N1-C6-N6	-5.07	115.56	118.60
56	N0	24	LEU	CA-CB-CG	5.06	126.95	115.30
36	1	2593	A	P-O3'-C3'	5.06	125.77	119.70
1	2	1202	A	C8-N9-C4	-5.06	103.78	105.80
36	5	2376	G	N1-C6-O6	5.06	122.94	119.90
36	5	2644	C	C6-N1-C2	5.06	122.32	120.30
36	5	30	G	C8-N9-C4	5.06	108.42	106.40
36	1	3214	U	O4'-C1'-N1	5.06	112.25	108.20
1	6	1637	C	C6-N1-C1'	-5.05	114.74	120.80
36	5	2375	G	O4'-C1'-N9	5.05	112.24	108.20
36	1	94	G	C8-N9-C4	5.05	108.42	106.40
36	1	2872	A	C2-N3-C4	5.05	113.13	110.60
36	5	674	G	N3-C4-C5	5.05	131.12	128.60
36	1	2624	G	N7-C8-N9	5.05	115.62	113.10
36	1	14	U	O5'-P-OP2	-5.04	101.16	105.70
36	1	2093	A	C2-N3-C4	5.04	113.12	110.60
1	6	14	C	C5-C6-N1	5.04	123.52	121.00
36	5	767	U	O4'-C1'-N1	5.04	112.23	108.20
36	1	979	U	C6-N1-C2	-5.04	117.98	121.00
36	5	2943	G	N7-C8-N9	5.04	115.62	113.10
36	1	1437	C	C2-N1-C1'	5.04	124.34	118.80
1	6	187	G	OP1-P-O3'	5.04	116.28	105.20
36	1	2372	A	N3-C4-C5	-5.04	123.27	126.80
36	5	2827	U	N1-C2-O2	5.04	126.33	122.80
36	5	3189	G	C5-C6-N1	-5.04	108.98	111.50
36	1	2413	A	C8-N9-C4	5.03	107.81	105.80
36	1	3057	U	N1-C2-N3	5.03	117.92	114.90
36	5	3245	A	C4-C5-N7	5.03	113.21	110.70
1	6	3	U	C6-N1-C2	5.02	124.01	121.00
1	6	1549	C	C6-N1-C2	-5.02	118.29	120.30
36	5	1779	C	C6-N1-C2	5.02	122.31	120.30
36	5	3002	C	C6-N1-C2	5.02	122.31	120.30
36	5	3195	U	C6-N1-C1'	-5.02	114.17	121.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	1	1129	A	N1-C6-N6	5.02	121.61	118.60
36	1	3278	C	C6-N1-C2	-5.02	118.29	120.30
1	6	151	G	N9-C4-C5	5.02	107.41	105.40
1	6	151	G	N1-C2-N2	5.02	120.72	116.20
1	6	1185	U	N1-C2-O2	5.02	126.31	122.80
36	5	805	G	C8-N9-C4	5.02	108.41	106.40
36	1	1417	G	C8-N9-C4	5.02	108.41	106.40
36	5	1177	G	C8-N9-C1'	-5.02	120.48	127.00
36	5	1592	G	N1-C6-O6	5.01	122.91	119.90
36	5	406	G	C8-N9-C1'	5.01	133.52	127.00
36	5	2355	G	C5-C6-O6	-5.01	125.59	128.60
36	5	942	U	C5-C6-N1	5.01	125.20	122.70
36	5	3357	U	P-O3'-C3'	5.01	125.71	119.70
36	1	1151	U	N3-C4-C5	-5.00	111.60	114.60
36	5	2830	G	N1-C2-N3	5.00	126.90	123.90
20	C8	3	LEU	CA-CB-CG	5.00	126.80	115.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
84	f	51	5CT	C2

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
16	C4	123	SER	Peptide
19	C7	85	VAL	Peptide
39	L2	142	ASP	Peptide
39	L2	19	HIS	Peptide
52	M6	110	PRO	Peptide
65	N9	20	GLY	Peptide
17	c5	52	LYS	Peptide
18	c6	40	GLU	Peptide
40	l3	346	THR	Peptide
53	m7	66	SER	Peptide
56	n0	133	ALA	Peptide
9	s7	130	VAL	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	37970	0	19106	870	0
1	6	38260	0	19250	845	0
2	S0	1577	0	1567	157	0
2	s0	1583	0	1578	0	0
3	S1	1709	0	1784	145	0
3	s1	1722	0	1793	0	0
4	S2	1635	0	1723	145	0
4	s2	1635	0	1723	0	0
5	S3	1734	0	1817	131	0
5	s3	1734	0	1817	0	0
6	S4	2068	0	2154	177	0
6	s4	2068	0	2154	0	0
7	S5	1609	0	1675	129	0
7	s5	1609	0	1675	0	0
8	S6	1799	0	1879	114	0
8	s6	1755	0	1846	0	0
9	S7	1481	0	1572	107	0
9	s7	1491	0	1578	0	0
10	S8	1489	0	1525	107	0
10	s8	1489	0	1525	0	0
11	S9	1494	0	1573	143	0
11	s9	1494	0	1573	0	0
12	C0	773	0	729	62	0
12	c0	762	0	699	0	0
13	C1	1214	0	1259	67	0
13	c1	1168	0	1231	0	0
14	C2	892	0	891	59	0
14	c2	892	0	891	0	0
15	C3	1192	0	1255	94	0
15	c3	1192	0	1255	0	0
16	C4	891	0	883	84	0
16	c4	949	0	985	0	0
17	C5	977	0	1002	74	0
17	c5	1039	0	1050	0	0
18	C6	1105	0	1166	106	0
18	c6	1111	0	1171	0	0
19	C7	926	0	930	70	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	c7	906	0	909	0	0
20	C8	1192	0	1222	94	0
20	c8	1192	0	1222	0	0
21	C9	1112	0	1124	82	0
21	c9	1112	0	1124	0	0
22	D0	855	0	917	75	0
22	d0	882	0	939	0	0
23	D1	684	0	672	85	0
23	d1	684	0	672	0	0
24	D2	1021	0	1060	87	0
24	d2	1021	0	1060	0	0
25	D3	1121	0	1196	88	0
25	d3	1121	0	1196	0	0
26	D4	1073	0	1132	78	0
26	d4	1073	0	1132	0	0
27	D5	563	0	603	45	0
27	d5	558	0	598	0	0
28	D6	769	0	814	80	0
28	d6	769	0	814	0	0
29	D7	610	0	630	41	0
29	d7	610	0	631	0	0
30	D8	497	0	535	50	0
30	d8	497	0	535	0	0
31	D9	442	0	428	28	0
31	d9	442	0	428	0	0
32	E0	475	0	525	38	0
33	E1	566	0	601	53	0
33	e1	608	0	656	0	0
34	SR	2436	0	2386	145	0
34	sR	2441	0	2392	0	0
35	SM	1104	0	996	53	0
35	sM	680	0	607	0	0
36	1	67355	0	33846	1383	0
36	5	67376	0	33856	1308	0
37	3	2579	0	1304	58	0
37	7	2579	0	1304	52	0
38	4	3353	0	1695	81	0
38	8	3353	0	1695	77	0
39	L2	1914	0	1981	167	0
39	l2	1912	0	1976	0	0
40	L3	3075	0	3142	262	0
40	l3	3075	0	3142	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
41	L4	2748	0	2859	227	0
41	l4	2748	0	2859	0	0
42	L5	2375	0	2325	201	0
42	l5	2359	0	2311	0	0
43	L6	1239	0	1326	95	0
43	l6	1248	0	1339	0	0
44	L7	1784	0	1862	139	0
44	l7	1791	0	1869	0	0
45	L8	1804	0	1875	110	0
45	l8	1764	0	1821	0	0
46	L9	1518	0	1587	113	0
46	l9	1518	0	1587	0	0
47	M0	1705	0	1736	176	0
47	m0	1722	0	1755	0	0
48	M1	1353	0	1383	85	0
48	m1	1353	0	1383	0	0
49	M3	1543	0	1608	107	0
49	m3	1548	0	1613	0	0
50	M4	1053	0	1149	104	0
50	m4	1059	0	1154	0	0
51	M5	1720	0	1779	143	0
51	m5	1720	0	1779	0	0
52	M6	1555	0	1659	90	0
52	m6	1555	0	1659	0	0
53	M7	1420	0	1437	113	0
53	m7	1227	0	1236	0	0
54	M8	1441	0	1543	90	0
54	m8	1441	0	1543	0	0
55	M9	1521	0	1616	121	0
55	m9	1521	0	1617	0	0
56	N0	1445	0	1487	104	0
56	n0	1445	0	1487	0	0
57	N1	1276	0	1323	93	0
57	n1	1276	0	1323	0	0
58	N2	796	0	812	50	0
58	n2	778	0	791	0	0
59	N3	1003	0	1048	81	0
59	n3	1003	0	1047	0	0
60	N4	699	0	640	31	0
60	n4	1038	0	1071	0	0
61	N5	964	0	1025	75	0
61	n5	959	0	1023	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	N6	993	0	1081	93	0
62	n6	993	0	1081	0	0
63	N7	1092	0	1155	96	0
63	n7	1092	0	1155	0	0
64	N8	1173	0	1215	96	0
64	n8	1173	0	1215	0	0
65	N9	462	0	491	29	0
65	n9	462	0	491	0	0
66	O0	742	0	797	50	0
66	o0	766	0	816	0	0
67	O1	876	0	912	49	0
67	o1	883	0	918	0	0
68	O2	1020	0	1090	70	0
68	o2	1020	0	1090	0	0
69	O3	850	0	880	48	0
69	o3	850	0	880	0	0
70	O4	880	0	945	78	0
70	o4	880	0	945	0	0
71	O5	969	0	1078	80	0
71	o5	965	0	1067	0	0
72	O6	771	0	849	55	0
72	o6	770	0	846	0	0
73	O7	681	0	683	53	0
73	o7	681	0	683	0	0
74	O8	612	0	682	43	0
74	o8	608	0	671	0	0
75	O9	436	0	475	49	0
75	o9	436	0	475	0	0
76	Q0	417	0	455	28	0
76	q0	417	0	456	0	0
77	Q1	233	0	284	23	0
77	q1	233	0	284	0	0
78	Q2	847	0	914	54	0
78	q2	847	0	914	0	0
79	Q3	694	0	734	69	0
79	q3	694	0	734	0	0
80	e0	491	0	542	0	0
81	m2	739	0	343	0	0
82	p0	1077	0	1041	0	0
83	p1	235	0	119	0	0
83	p2	230	0	117	0	0
84	f	1122	0	1115	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	B	66	0	41	0	0
85	C	69	0	40	1	0
86	1	366	0	0	0	0
86	2	90	0	0	0	0
86	3	8	0	0	0	0
86	4	15	0	0	0	0
86	5	419	0	0	0	0
86	6	113	0	0	0	0
86	7	13	0	0	0	0
86	8	9	0	0	0	0
86	B	1	0	0	0	0
86	C	1	0	0	0	0
86	D3	1	0	0	0	0
86	L2	2	0	0	0	0
86	L3	1	0	0	0	0
86	L6	1	0	0	0	0
86	L7	3	0	0	0	0
86	M0	1	0	0	0	0
86	M5	1	0	0	0	0
86	M6	2	0	0	0	0
86	M7	4	0	0	0	0
86	M9	1	0	0	0	0
86	N3	1	0	0	0	0
86	N6	1	0	0	0	0
86	N8	1	0	0	0	0
86	O3	1	0	0	0	0
86	O4	1	0	0	0	0
86	O7	1	0	0	0	0
86	Q2	1	0	0	0	0
86	S2	1	0	0	0	0
86	SM	1	0	0	0	0
86	c8	1	0	0	0	0
86	d2	1	0	0	0	0
86	d3	1	0	0	0	0
86	d6	1	0	0	0	0
86	f	1	0	0	0	0
86	l2	2	0	0	0	0
86	l3	2	0	0	0	0
86	l4	1	0	0	0	0
86	l5	1	0	0	0	0
86	l7	2	0	0	0	0
86	m3	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	m5	2	0	0	0	0
86	m7	2	0	0	0	0
86	n0	1	0	0	0	0
86	n3	1	0	0	0	0
86	n6	1	0	0	0	0
86	n8	2	0	0	0	0
86	o2	1	0	0	0	0
86	o3	1	0	0	0	0
86	o4	1	0	0	0	0
86	q1	1	0	0	0	0
86	q3	1	0	0	0	0
86	s4	1	0	0	0	0
86	s8	2	0	0	0	0
86	sM	1	0	0	0	0
87	1	2457	0	0	236	0
87	2	1134	0	0	124	0
87	3	77	0	0	3	0
87	4	126	0	0	14	0
87	5	2492	0	0	243	0
87	6	1204	0	0	118	0
87	7	77	0	0	4	0
87	8	147	0	0	11	0
87	C3	7	0	0	3	0
87	C5	7	0	0	5	0
87	C8	7	0	0	0	0
87	D9	7	0	0	0	0
87	L3	21	0	0	3	0
87	L4	7	0	0	3	0
87	L5	7	0	0	1	0
87	M0	14	0	0	7	0
87	M5	14	0	0	2	0
87	M6	7	0	0	0	0
87	M7	7	0	0	1	0
87	M8	7	0	0	0	0
87	M9	7	0	0	1	0
87	N8	7	0	0	0	0
87	N9	7	0	0	2	0
87	O1	7	0	0	2	0
87	O3	7	0	0	1	0
87	O4	7	0	0	2	0
87	O7	7	0	0	6	0
87	O9	7	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	Q2	7	0	0	2	0
87	S1	7	0	0	3	0
87	S6	7	0	0	3	0
87	S8	7	0	0	1	0
87	S9	7	0	0	4	0
87	SR	7	0	0	5	0
87	c3	7	0	0	0	0
87	c5	14	0	0	0	0
87	c8	7	0	0	0	0
87	d4	7	0	0	0	0
87	d9	7	0	0	0	0
87	l3	14	0	0	0	0
87	l4	14	0	0	0	0
87	l5	14	0	0	0	0
87	l9	7	0	0	0	0
87	m0	14	0	0	0	0
87	m1	7	0	0	0	0
87	m4	7	0	0	0	0
87	m5	21	0	0	0	0
87	m6	7	0	0	0	0
87	m7	7	0	0	0	0
87	m8	7	0	0	0	0
87	m9	7	0	0	0	0
87	n3	7	0	0	0	0
87	n9	7	0	0	0	0
87	o3	7	0	0	0	0
87	o6	7	0	0	0	0
87	o7	14	0	0	0	0
87	q2	7	0	0	0	0
87	s1	14	0	0	0	0
87	s4	7	0	0	0	0
87	s8	7	0	0	0	0
87	s9	7	0	0	0	0
87	sR	7	0	0	0	0
88	D6	1	0	0	0	0
88	D7	1	0	0	0	0
88	D9	1	0	0	0	0
88	E1	1	0	0	0	0
88	O7	1	0	0	0	0
88	Q0	1	0	0	1	0
88	Q2	1	0	0	0	0
88	Q3	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
88	d6	1	0	0	0	0
88	d7	1	0	0	0	0
88	d9	1	0	0	0	0
88	e1	1	0	0	0	0
88	o7	1	0	0	0	0
88	q0	1	0	0	0	0
88	q2	1	0	0	0	0
88	q3	1	0	0	0	0
89	5	23	0	18	6	0
89	B	23	0	18	2	0
90	B	7	0	7	0	0
90	C	7	0	7	0	0
91	5	6	0	0	0	0
91	f	6	0	0	0	0
All	All	413121	0	299176	9882	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

All (9882) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2208:A:N1	87:1:3940:OHX:N6	2.03	1.05
36:1:2403:G:OP2	87:1:4071:OHX:N5	1.95	0.99
73:O7:87:SER:O	87:O7:103:OHX:N3	1.96	0.98
36:1:860:G:OP1	79:Q3:17:ARG:NH1	1.98	0.96
36:1:2392:C:O2'	40:L3:266:ARG:NH2	1.98	0.96
40:L3:41:VAL:HA	40:L3:185:GLY:HA3	1.52	0.95
47:M0:49:CYS:HB3	47:M0:168:SER:HB3	2.12	0.94
36:1:25:U:O4	87:1:3766:OHX:N3	2.00	0.94
1:2:992:A:H2	1:2:1012:U:H3	1.15	0.93
1:6:1665:U:O4	87:6:2089:OHX:N6	2.01	0.93
36:1:768:C:OP1	49:M3:186:ARG:NH2	2.02	0.92
36:5:437:G:N7	87:5:4170:OHX:N3	2.18	0.91
73:O7:65:ARG:HG3	73:O7:65:ARG:HH11	1.53	0.90
56:N0:90:MET:HG3	36:5:1213:G:H4'	317.90	0.90
36:5:3128:G:OP2	87:5:4071:OHX:N3	2.05	0.89
42:L5:134:ALA:HB2	42:L5:141:PRO:HD3	4.07	0.89
36:1:640:U:OP1	64:N8:21:ARG:NH2	2.06	0.89
36:5:274:G:O6	87:5:3976:OHX:N1	2.04	0.88
36:1:3202:G:O6	87:1:4085:OHX:N1	2.07	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:437:G:N7	87:5:4170:OHX:N5	2.22	0.88
1:6:1537:C:N3	87:6:2124:OHX:N6	2.22	0.88
36:1:3272:C:OP2	43:L6:78:ARG:NH1	2.05	0.88
78:Q2:12:CYS:SG	78:Q2:17:CYS:HB3	2.60	0.87
31:D9:24:CYS:HB3	31:D9:42:CYS:SG	3.47	0.87
36:1:3182:G:OP1	52:M6:160:ARG:NH2	2.06	0.87
70:O4:74:ARG:NH2	36:5:1639:C:OP2	200.76	0.87
64:N8:21:ARG:NH2	36:5:640:U:OP1	182.81	0.87
54:M8:122:ILE:HG23	54:M8:126:GLN:HB2	1.57	0.86
1:2:1203:A:OP2	87:2:2080:OHX:N5	2.07	0.86
28:D6:87:ARG:HB3	28:D6:91:ASP:HB3	1.57	0.86
36:5:2533:G:O6	87:5:3954:OHX:N1	2.08	0.86
5:S3:94:ARG:NH2	35:SM:134:ASP:OD1	2.08	0.86
48:M1:137:ARG:NH1	37:7:28:C:OP1	303.17	0.86
33:E1:91:ILE:HG12	33:E1:92:LYS:HG2	6.38	0.86
36:1:1565:G:N2	36:1:1574:C:N3	2.22	0.86
34:SR:89:LEU:HB2	34:SR:103:PHE:HB2	1.89	0.86
36:1:1233:G:H1	36:1:1255:C:H42	1.22	0.85
51:M5:38:ARG:NH1	38:8:142:C:OP1	113.34	0.85
5:S3:70:THR:HG22	5:S3:86:LEU:HB2	3.82	0.85
36:5:437:G:H1	36:5:622:A:H61	1.22	0.85
2:S0:9:LEU:HD11	2:S0:14:ALA:HB2	2.26	0.85
1:6:454:U:H5"	1:6:455:C:H5	1.40	0.85
16:C4:38:THR:HG21	1:6:895:G:H21	265.20	0.85
31:D9:21:CYS:HB2	31:D9:39:CYS:HB3	2.94	0.85
2:S0:124:THR:HG22	2:S0:174:TRP:HE1	1.74	0.85
10:S8:34:ALA:HB2	10:S8:56:ARG:HD3	2.21	0.85
76:Q0:99:CYS:SG	88:Q0:500:ZN:ZN	1.64	0.85
17:C5:123:TYR:OH	20:C8:126:ARG:NH1	2.10	0.84
36:1:1170:A:OP2	87:1:3854:OHX:N6	2.10	0.84
1:2:320:U:H3'	1:2:321:C:H5"	1.58	0.84
1:2:218:A:N6	1:2:830:U:O4	2.10	0.84
47:M0:174:THR:HG23	47:M0:176:LEU:H	1.42	0.84
50:M4:55:ARG:NH2	50:M4:76:ALA:O	2.34	0.84
53:M7:25:SER:HB3	53:M7:28:ASN:HB2	2.32	0.84
6:S4:52:LEU:O	6:S4:54:TYR:N	2.61	0.84
36:1:2123:G:N7	87:1:4000:OHX:N2	2.26	0.84
73:O7:87:SER:O	87:O7:103:OHX:N5	2.11	0.84
19:C7:82:ASP:O	19:C7:83:GLN:NE2	2.11	0.84
36:5:1409:G:O6	87:5:4075:OHX:N6	2.11	0.84
36:5:652:G:OP2	87:5:4083:OHX:N5	2.10	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:3:17:A:OP1	42:L5:2:ALA:N	2.10	0.83
43:L6:43:LEU:HD11	43:L6:85:ILE:HG13	1.60	0.83
36:1:2129:U:O4	87:1:4040:OHX:N3	2.10	0.83
36:5:2770:G:N7	87:5:4068:OHX:N5	2.26	0.83
36:1:1639:C:OP2	70:O4:74:ARG:NH2	2.11	0.83
1:2:732:G:N7	87:2:2099:OHX:N3	2.25	0.83
24:D2:83:ILE:HD13	24:D2:122:SER:HB2	1.59	0.83
1:2:702:G:O6	1:2:737:A:N6	2.11	0.83
63:N7:67:LYS:NZ	36:5:1630:U:OP1	197.62	0.83
36:1:329:U:OP2	87:1:3939:OHX:N6	2.12	0.83
79:Q3:4:ARG:NH1	36:5:837:A:OP2	239.15	0.83
5:S3:125:TYR:OH	35:SM:134:ASP:OD2	1.97	0.83
36:1:687:U:OP2	49:M3:36:ARG:NH2	2.11	0.83
36:5:1878:G:OP1	87:5:3872:OHX:N5	2.12	0.82
51:M5:188:ARG:NH2	36:5:31:C:OP2	121.72	0.82
19:C7:41:ILE:HD12	19:C7:47:ARG:HG2	2.46	0.82
71:O5:101:THR:HG23	71:O5:104:GLN:HB2	1.61	0.82
63:N7:83:THR:HG23	63:N7:85:TYR:H	1.83	0.82
36:1:2895:G:O2'	76:Q0:100:TYR:O	1.97	0.82
36:1:1222:G:O2'	36:1:1285:G:N1	2.12	0.82
43:L6:31:ARG:NH1	69:O3:107:ILE:O	2.82	0.82
8:S6:98:ARG:NH2	8:S6:101:ILE:O	2.17	0.82
1:2:1559:A:H5''	20:C8:135:GLY:HA3	1.60	0.82
26:D4:29:HIS:HB3	26:D4:32:ARG:HB2	6.07	0.82
36:1:2120:A:OP2	87:1:3904:OHX:N2	2.12	0.82
25:D3:90:ASP:O	25:D3:136:TRP:NE1	2.13	0.82
41:L4:206:LEU:HB2	41:L4:246:ARG:HD3	3.02	0.82
9:S7:89:HIS:HD1	9:S7:168:SER:HG	1.27	0.82
36:5:2273:G:O6	87:5:4117:OHX:N5	2.12	0.82
59:N3:48:ARG:HH11	59:N3:48:ARG:HG3	2.35	0.82
6:S4:187:ARG:NH2	1:6:753:A:N7	375.40	0.82
1:2:732:G:O6	87:2:2099:OHX:N4	2.13	0.82
41:L4:300:ARG:O	54:M8:39:ARG:NH1	2.13	0.82
44:L7:217:PRO:O	87:5:3917:OHX:N6	261.07	0.82
44:L7:150:LYS:HG2	44:L7:151:ARG:HG2	1.60	0.82
15:C3:55:ARG:NH1	15:C3:56:ASP:OD2	2.12	0.81
44:L7:121:LYS:HB2	57:N1:133:ALA:HB3	1.62	0.81
36:1:1481:A:O2'	36:1:1858:A:N3	2.13	0.81
11:S9:126:ARG:NH1	1:6:475:A:OP2	425.65	0.81
41:L4:269:SER:O	41:L4:271:LYS:N	2.13	0.81
47:M0:150:GLU:HG2	47:M0:153:ARG:HH21	5.32	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:N8:65:GLN:O	64:N8:67:HIS:N	4.01	0.81
36:1:1887:A:OP1	87:1:3981:OHX:N3	2.13	0.81
1:6:565:C:N3	87:6:2123:OHX:N4	2.29	0.81
36:1:3188:G:O6	87:1:4085:OHX:N3	2.14	0.81
56:N0:155:ARG:NH2	56:N0:171:PHE:O	2.14	0.81
36:1:3050:U:OP2	87:1:4082:OHX:N6	2.14	0.81
36:5:155:G:H5''	36:5:156:G:C8	2.15	0.81
36:1:2656:A:H4'	78:Q2:98:LYS:HD2	1.63	0.81
10:S8:98:LYS:HB3	1:6:329:G:H5''	275.74	0.81
36:5:2812:C:H2'	36:5:2813:A:H8	1.42	0.81
36:5:3274:A:H3'	36:5:3275:U:H5''	1.62	0.81
7:S5:94:THR:HG22	7:S5:114:ILE:HG13	2.00	0.81
27:D5:71:ILE:HG21	27:D5:76:ALA:HB2	2.59	0.81
54:M8:176:ARG:NH1	64:N8:46:ASP:OD2	2.52	0.81
1:2:732:G:O6	87:2:2099:OHX:N6	2.14	0.81
36:1:2234:G:O6	87:1:3940:OHX:N1	2.15	0.80
40:L3:232:ARG:NH1	40:L3:269:GLN:O	2.15	0.80
40:L3:171:LEU:O	87:L3:403:OHX:N6	2.13	0.80
54:M8:158:HIS:H	54:M8:186:VAL:HG12	1.45	0.80
4:S2:179:VAL:O	4:S2:198:THR:OG1	2.21	0.80
79:Q3:4:ARG:NH2	36:5:838:G:O6	238.32	0.80
40:L3:152:LYS:HG2	40:L3:192:VAL:HG11	1.88	0.80
1:6:470:A:OP2	87:6:2069:OHX:N1	2.14	0.80
10:S8:36:THR:HG21	10:S8:173:PRO:HB2	1.90	0.80
36:1:3049:A:H5''	40:L3:53:MET:HG3	1.62	0.80
1:2:1029:U:O4	87:2:2120:OHX:N3	2.15	0.80
36:1:1634:G:N7	63:N7:17:ARG:NH2	2.29	0.80
69:O3:14:LEU:HD11	69:O3:31:LYS:HB2	2.09	0.80
36:1:1752:A:OP2	87:1:3942:OHX:N5	2.15	0.80
36:1:409:A:OP2	87:1:3950:OHX:N6	2.15	0.80
1:6:33:U:O4	87:6:2054:OHX:N2	2.15	0.80
41:L4:20:LEU:HD23	41:L4:21:PRO:HD2	4.54	0.80
87:1:3978:OHX:N4	55:M9:14:VAL:O	2.15	0.80
8:S6:13:GLN:OE1	1:6:151:G:N2	312.70	0.80
1:2:349:U:O4	87:2:2097:OHX:N3	2.15	0.80
44:L7:151:ARG:NH1	44:L7:244:ASN:O	2.63	0.80
68:O2:101:SER:OG	68:O2:104:ASN:OD1	4.13	0.80
1:2:1067:C:H5''	3:S1:150:VAL:HG23	1.60	0.80
36:1:2970:C:O2'	87:1:4060:OHX:N1	2.15	0.80
1:6:1280:C:H2'	1:6:1281:G:C8	2.17	0.80
1:6:1542:G:N2	1:6:1569:A:OP2	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:M7:18:ARG:NH2	53:M7:147:GLU:OE1	2.13	0.80
1:2:878:G:N7	87:2:2049:OHX:N2	2.30	0.80
4:S2:78:ASP:HB3	4:S2:104:VAL:HG12	1.64	0.80
4:S2:56:ILE:HG23	4:S2:61:LEU:HB2	1.99	0.80
36:5:2169:G:O6	87:5:3869:OHX:N5	2.15	0.79
18:C6:82:ARG:HH22	18:C6:114:ARG:HG3	3.91	0.79
47:M0:43:VAL:HG21	47:M0:197:VAL:HB	1.63	0.79
62:N6:47:ALA:O	62:N6:122:LYS:NZ	4.17	0.79
30:D8:8:THR:HG1	30:D8:59:SER:HG	2.24	0.79
70:O4:41:ARG:HG2	70:O4:56:THR:HG21	1.87	0.79
43:L6:175:LYS:O	50:M4:117:ARG:NH2	2.15	0.79
36:5:1555:U:O4	36:5:1557:A:N6	2.16	0.79
55:M9:74:ARG:NH1	36:5:1942:U:OP2	210.18	0.79
1:6:74:U:H3'	1:6:75:U:H3'	1.64	0.79
43:L6:51:ARG:NH1	50:M4:114:ASP:OD2	2.15	0.79
1:2:1246:C:OP2	87:2:2127:OHX:N4	2.16	0.79
36:5:2704:A:OP2	87:5:3816:OHX:N5	2.14	0.79
1:2:1542:G:N2	1:2:1569:A:OP2	2.15	0.79
58:N2:42:LYS:NZ	36:5:1686:U:OP1	178.13	0.79
39:L2:30:ARG:NH2	39:L2:33:ASP:OD2	2.24	0.79
62:N6:56:VAL:HG11	62:N6:104:LEU:HD13	1.65	0.79
28:D6:15:ARG:NH1	1:6:936:G:N7	320.37	0.79
7:S5:81:ARG:HH21	30:D8:47:PRO:HB3	2.91	0.79
46:L9:47:LYS:HB2	50:M4:7:VAL:HB	1.63	0.79
36:5:2123:G:O6	87:5:4008:OHX:N1	2.16	0.79
36:5:2404:A:N7	36:5:2872:A:N6	2.31	0.79
36:5:2945:G:N7	87:5:4057:OHX:N2	2.30	0.79
9:S7:107:ARG:NH2	1:6:741:C:O2	349.84	0.79
1:6:833:U:O4	87:6:2067:OHX:N5	2.16	0.78
64:N8:6:THR:HG23	64:N8:8:THR:HG23	1.64	0.78
11:S9:109:LEU:HB2	11:S9:146:PHE:HB3	1.65	0.78
36:5:3153:U:H4'	36:5:3154:C:H5'	1.65	0.78
57:N1:101:CYS:HB3	36:5:990:U:H1'	253.28	0.78
13:C1:60:PHE:O	13:C1:62:GLY:N	3.98	0.78
87:1:3854:OHX:N6	44:L7:217:PRO:O	2.15	0.78
1:2:579:A:OP2	5:S3:179:GLN:NE2	2.17	0.78
10:S8:61:GLU:HG2	10:S8:62:THR:HG23	3.29	0.78
19:C7:27:ASP:O	19:C7:31:ASN:ND2	2.12	0.78
36:1:1808:G:O6	87:1:3877:OHX:N3	2.16	0.78
58:N2:74:LYS:NZ	36:5:1677:G:N7	149.96	0.78
40:L3:19:ARG:NH2	36:5:3045:G:OP1	233.26	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:O9:24:PRO:HB2	75:O9:27:ILE:HD12	5.45	0.78
1:6:877:G:H5'	1:6:937:C:H1'	1.65	0.78
51:M5:49:ARG:NH1	36:5:149:U:OP2	101.55	0.78
72:O6:58:ILE:HG22	72:O6:90:MET:HG3	2.70	0.78
1:6:1280:C:H2'	1:6:1281:G:H8	1.48	0.78
21:C9:119:LYS:NZ	1:6:1369:U:OP1	444.03	0.78
1:6:1720:G:O6	87:6:2060:OHX:N6	2.16	0.78
13:C1:125:VAL:HG12	13:C1:139:VAL:HA	2.55	0.78
15:C3:65:VAL:HG23	15:C3:66:ILE:HG23	5.69	0.78
43:L6:40:LEU:HD13	43:L6:84:VAL:HG11	2.00	0.78
78:Q2:73:GLU:OE1	78:Q2:80:ARG:NH1	3.30	0.78
36:1:2371:G:O6	87:1:3768:OHX:N5	2.16	0.78
42:L5:91:GLY:O	42:L5:94:ASN:ND2	2.16	0.78
63:N7:25:ILE:HA	63:N7:43:VAL:HG12	1.82	0.78
40:L3:291:GLU:OE1	40:L3:302:LYS:NZ	4.88	0.78
43:L6:175:LYS:HD3	50:M4:111:ALA:HA	1.64	0.78
58:N2:43:VAL:O	58:N2:45:GLY:N	3.07	0.78
53:M7:169:THR:H	69:O3:60:ARG:HH11	1.31	0.78
36:5:2569:A:H4'	36:5:2570:U:H5'	1.66	0.77
26:D4:29:HIS:O	26:D4:31:ASN:N	3.67	0.77
40:L3:346:THR:O	40:L3:348:ARG:N	2.24	0.77
55:M9:176:ARG:HA	55:M9:179:GLU:HB2	1.65	0.77
36:1:1942:U:OP2	55:M9:74:ARG:NH1	2.16	0.77
36:5:1752:A:OP2	87:5:3991:OHX:N6	2.16	0.77
2:S0:101:ARG:NH2	1:6:1321:A:OP2	402.94	0.77
13:C1:99:ARG:NH1	25:D3:7:ARG:O	2.31	0.77
27:D5:71:ILE:HG23	27:D5:73:GLY:H	6.43	0.77
57:N1:92:ARG:NH1	36:5:2736:A:OP1	236.92	0.77
40:L3:76:VAL:HG12	40:L3:325:LYS:HA	1.66	0.77
1:6:1060:U:H4'	1:6:1061:A:H5''	1.66	0.77
1:6:58:U:O2'	1:6:451:A:N3	2.15	0.77
26:D4:38:ASP:OD1	26:D4:52:LYS:NZ	5.44	0.77
48:M1:10:ARG:HH12	48:M1:133:ARG:HH21	2.85	0.77
48:M1:28:ASP:OD2	48:M1:32:ARG:NH2	6.31	0.77
49:M3:157:ARG:HH11	64:N8:124:ILE:HG21	4.14	0.77
1:6:357:G:OP2	87:6:2041:OHX:N4	2.18	0.77
23:D1:42:GLU:O	23:D1:44:ARG:NH1	2.17	0.77
36:1:883:A:H5'	53:M7:133:HIS:HA	1.66	0.77
73:O7:48:ASN:OD1	73:O7:54:LYS:NZ	3.28	0.77
36:1:2531:C:N4	36:1:2548:C:O2	2.17	0.77
1:6:1588:G:H1	1:6:1608:U:H3	1.33	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:S9:133:HIS:NE2	1:6:513:U:OP1	449.31	0.77
73:O7:72:ARG:NH1	38:8:95:G:OP2	52.32	0.77
44:L7:27:ALA:HA	44:L7:30:ARG:HB3	1.65	0.77
36:5:1759:C:N4	36:5:1766:G:O6	2.16	0.77
36:5:3194:C:O2	36:5:3197:G:N2	2.18	0.77
36:5:2233:A:OP2	87:5:3877:OHX:N5	2.18	0.77
1:6:197:A:H2'	1:6:198:A:H8	1.49	0.77
25:D3:92:CYS:HA	25:D3:95:PHE:HD2	1.48	0.77
63:N7:46:ILE:HD13	63:N7:68:ILE:HG23	1.67	0.77
16:C4:127:ARG:HG3	28:D6:22:ARG:HH12	1.50	0.77
25:D3:70:LYS:HB3	25:D3:93:LEU:HD22	1.94	0.77
3:S1:229:MET:SD	3:S1:232:HIS:ND1	2.55	0.77
36:1:1038:C:H4'	42:L5:5:LYS:HZ1	1.50	0.77
36:1:3275:U:H5'	69:O3:68:TRP:HZ2	1.50	0.77
1:2:1529:C:OP1	7:S5:112:ARG:NH1	2.18	0.77
1:6:1385:G:N7	87:6:2087:OHX:N6	2.32	0.77
2:S0:88:LYS:NZ	19:C7:82:ASP:OD1	3.36	0.77
42:L5:177:GLU:O	42:L5:179:ARG:N	2.16	0.77
56:N0:77:VAL:HG13	56:N0:126:VAL:HG22	1.66	0.77
73:O7:2:GLY:N	36:5:2138:A:HO2'	173.63	0.77
46:L9:18:VAL:HB	46:L9:27:VAL:HG22	1.65	0.76
34:SR:258:THR:O	34:SR:275:ARG:NH1	2.17	0.76
36:1:2178:A:H3'	39:L2:132:ASN:HD21	1.51	0.76
44:L7:88:ARG:NH1	44:L7:91:GLY:O	2.28	0.76
36:1:722:G:OP1	87:1:4098:OHX:N6	2.18	0.76
41:L4:144:LYS:HG2	41:L4:145:ILE:H	4.76	0.76
47:M0:221:ALA:O	87:M0:303:OHX:N4	2.19	0.76
36:1:2823:G:O6	87:1:3800:OHX:N1	2.18	0.76
36:1:13:A:OP2	87:1:4102:OHX:N5	2.19	0.76
36:1:3049:A:OP2	87:1:4082:OHX:N4	2.19	0.76
36:1:3087:A:OP1	87:1:4082:OHX:N2	2.19	0.76
36:5:2836:C:H5	36:5:2852:C:H42	1.34	0.76
1:6:647:G:N2	1:6:687:G:H22	1.82	0.76
45:L8:116:VAL:HG22	45:L8:125:ALA:HB3	1.68	0.76
6:S4:9:LEU:HB2	6:S4:30:ARG:HB2	2.78	0.76
10:S8:76:THR:HG22	10:S8:108:PRO:HG2	1.66	0.76
41:L4:204:GLY:O	41:L4:246:ARG:NH1	2.28	0.76
47:M0:3:ARG:NH2	36:5:2854:U:OP2	291.45	0.76
36:5:2533:G:O6	87:5:3954:OHX:N5	2.19	0.76
64:N8:13:GLY:HA2	36:5:943:U:H3'	164.45	0.76
78:Q2:63:LYS:NZ	36:5:2761:G:N7	211.95	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:837:A:OP2	79:Q3:4:ARG:NH1	2.19	0.76
1:2:1202:A:OP1	87:2:2080:OHX:N5	2.19	0.76
49:M3:15:ARG:NH2	36:5:96:G:OP1	154.31	0.76
16:C4:29:HIS:HB3	16:C4:41:ARG:HG3	1.67	0.76
41:L4:203:ARG:NH1	41:L4:226:GLU:OE2	3.04	0.76
55:M9:105:LEU:HD12	55:M9:135:LYS:HD2	1.66	0.76
36:1:1304:A:N6	36:1:2860:U:OP1	2.20	0.75
36:5:2537:U:O2'	36:5:2538:U:O4'	2.04	0.75
49:M3:63:VAL:HG22	36:5:72:C:H5'	114.33	0.75
1:6:1735:U:O4	87:6:2089:OHX:N5	2.19	0.75
52:M6:98:ALA:HA	52:M6:101:ARG:HD2	1.68	0.75
63:N7:101:PHE:HA	63:N7:107:ARG:HE	2.41	0.75
66:O0:40:LYS:HB3	66:O0:101:LEU:HD21	1.66	0.75
36:1:3020:U:O4	87:1:3884:OHX:N4	2.19	0.75
36:1:2296:A:OP1	87:1:4046:OHX:N2	2.18	0.75
1:2:1018:U:H2'	1:2:1019:A:H8	1.52	0.75
36:5:2534:G:H1	36:5:2545:C:H42	1.33	0.75
36:5:2841:G:OP2	87:5:4045:OHX:N1	2.19	0.75
42:L5:265:TYR:OH	37:7:121:U:OP2	313.47	0.75
51:M5:110:ALA:HB1	51:M5:113:LEU:HD23	1.68	0.75
68:O2:100:ILE:O	68:O2:105:ARG:NH1	2.41	0.75
78:Q2:8:ARG:HH21	78:Q2:83:LEU:HD13	2.94	0.75
6:S4:192:ILE:HG13	6:S4:243:GLY:HA3	1.69	0.75
1:2:788:A:OP2	6:S4:108:ARG:NH1	2.19	0.75
1:6:1413:U:O2	87:6:2053:OHX:N5	2.19	0.75
40:L3:25:ILE:H	40:L3:25:ILE:HD13	1.50	0.75
1:2:79:C:H1'	8:S6:174:LYS:HD3	1.68	0.75
36:5:1194:G:OP1	87:5:3928:OHX:N6	2.20	0.75
25:D3:69:ARG:NH2	1:6:568:G:N7	366.33	0.75
20:C8:120:ARG:NH2	35:SM:58:GLU:OE2	2.19	0.75
51:M5:178:HIS:HD2	51:M5:179:LYS:HG2	6.20	0.75
36:1:3095:U:H2'	36:1:3096:C:H6	1.52	0.75
1:2:1670:G:N7	87:2:2092:OHX:N3	2.35	0.75
17:C5:69:GLU:OE1	87:C5:201:OHX:N4	2.20	0.75
20:C8:30:TYR:HE2	20:C8:40:ARG:HH11	1.33	0.75
56:N0:155:ARG:NH1	36:5:3206:C:O2	311.27	0.75
62:N6:60:ARG:HB2	62:N6:103:LYS:HB3	1.69	0.75
70:O4:3:GLN:HB3	70:O4:30:LEU:HD12	1.68	0.75
1:2:40:A:OP1	11:S9:3:ARG:NH1	2.19	0.75
1:2:1473:U:O2'	7:S5:103:ASN:ND2	2.20	0.75
1:2:982:U:OP1	87:2:2106:OHX:N1	2.19	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:3374:U:O4	87:5:3948:OHX:N3	2.19	0.75
24:D2:2:THR:N	1:6:1034:C:HO2'	339.64	0.75
33:E1:82:LYS:O	33:E1:84:VAL:N	4.92	0.75
41:L4:338:LYS:O	41:L4:340:GLY:N	2.19	0.75
6:S4:3:ARG:HB3	1:6:93:A:H1'	327.66	0.75
6:S4:79:ASP:HB3	6:S4:82:TYR:HB2	1.67	0.75
1:2:478:A:HO2'	11:S9:124:HIS:HD1	1.33	0.75
36:1:1420:C:OP2	41:L4:193:LYS:NZ	2.15	0.75
36:1:2748:A:H1'	42:L5:36:LEU:HD23	1.69	0.75
1:2:1522:U:OP2	87:2:2026:OHX:N3	2.20	0.75
1:2:1537:C:N3	87:2:2131:OHX:N5	2.34	0.75
1:6:761:G:O6	87:6:2050:OHX:N1	2.20	0.75
26:D4:37:LYS:NZ	1:6:523:G:OP2	415.46	0.75
46:L9:48:VAL:HG13	46:L9:52:LEU:HB3	1.68	0.75
72:O6:74:LYS:HD2	72:O6:80:PHE:HD2	1.51	0.75
36:1:1019:G:O6	87:1:3952:OHX:N1	2.19	0.75
36:5:2442:G:N2	36:5:2506:U:O4	2.20	0.75
47:M0:156:ARG:NH1	47:M0:163:GLN:O	2.66	0.75
11:S9:3:ARG:NH1	1:6:40:A:OP1	374.65	0.75
1:6:918:U:H2'	1:6:919:A:H8	1.52	0.74
1:6:628:G:N1	1:6:970:A:OP2	2.19	0.74
25:D3:68:ILE:O	25:D3:70:LYS:NZ	2.19	0.74
67:O1:44:MET:O	67:O1:46:THR:N	2.70	0.74
73:O7:88:ALA:HB3	38:8:68:G:P	22.35	0.74
6:S4:13:ALA:O	6:S4:39:ARG:NH2	2.19	0.74
11:S9:117:GLY:O	11:S9:119:ALA:N	2.60	0.74
36:5:1239:C:H42	36:5:1249:G:H1	1.33	0.74
63:N7:95:VAL:HG21	63:N7:113:VAL:HG11	1.67	0.74
67:O1:88:PRO:HG2	67:O1:89:LEU:HD22	1.68	0.74
1:2:651:G:O6	87:2:2072:OHX:N4	2.21	0.74
1:6:1571:C:OP2	87:6:2124:OHX:N2	2.20	0.74
3:S1:48:VAL:HG21	3:S1:61:LEU:HD22	5.65	0.74
8:S6:57:ASP:HA	8:S6:106:LEU:HA	1.69	0.74
36:1:2112:U:O2	87:1:3855:OHX:N1	2.21	0.74
36:1:979:U:H1'	36:1:980:A:C8	2.23	0.74
45:L8:185:ARG:HD2	38:8:155:A:H5'	143.41	0.74
18:C6:21:HIS:HB2	18:C6:66:ARG:HB3	4.07	0.74
66:O0:75:ASN:HA	66:O0:86:ARG:HB2	3.17	0.74
5:S3:222:VAL:HG11	34:SR:229:LYS:HA	2.70	0.74
36:1:148:G:OP2	51:M5:4:TYR:OH	2.04	0.74
36:1:3041:U:OP1	59:N3:12:ARG:NH1	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:1:3785:OHX:N5	57:N1:13:TYR:O	2.20	0.74
1:6:1097:U:H4'	1:6:1098:U:H5'	1.69	0.74
1:6:1318:G:N7	87:6:2131:OHX:N5	2.36	0.74
21:C9:9:VAL:HG21	21:C9:136:ALA:HB1	2.24	0.74
54:M8:66:ARG:NH2	36:5:744:A:OP1	166.97	0.74
36:1:1841:A:H2	75:O9:45:ARG:HH22	1.35	0.74
5:S3:102:ALA:HB1	5:S3:173:ARG:HG3	2.57	0.74
8:S6:153:VAL:O	8:S6:155:ASP:N	2.20	0.74
11:S9:107:ARG:NH2	11:S9:148:VAL:O	2.20	0.74
1:2:1280:C:H2'	1:2:1281:G:C8	2.23	0.74
52:M6:36:VAL:HB	52:M6:108:ILE:HG22	4.91	0.74
36:1:1672:U:OP1	55:M9:60:LYS:NZ	2.21	0.74
1:2:346:G:O6	87:2:2095:OHX:N5	2.21	0.74
36:5:285:A:OP2	87:5:3894:OHX:N5	2.20	0.74
58:N2:28:PHE:HE1	58:N2:83:TYR:HE2	2.15	0.74
36:5:2251:G:N2	36:5:2265:C:O2	2.18	0.74
17:C5:69:GLU:OE1	87:C5:201:OHX:N6	2.19	0.74
43:L6:55:LEU:HB2	43:L6:64:LEU:HB3	3.08	0.74
47:M0:72:ALA:HB2	47:M0:155:ALA:HB2	1.81	0.74
36:1:1723:A:OP1	55:M9:128:LYS:NZ	2.20	0.74
36:1:3376:A:OP2	87:1:3803:OHX:N5	2.20	0.74
36:1:2859:U:O2'	87:1:3763:OHX:N4	2.21	0.74
1:2:1280:C:H2'	1:2:1281:G:H8	1.51	0.74
1:6:40:A:O2'	87:6:2074:OHX:N1	2.21	0.74
15:C3:17:PRO:HG3	29:D7:28:PRO:HG3	1.70	0.74
39:L2:83:HIS:HB3	79:Q3:64:VAL:HG13	3.14	0.74
46:L9:105:GLU:HG3	46:L9:109:ALA:H	1.51	0.74
47:M0:87:LEU:HD23	47:M0:138:VAL:HG22	2.80	0.74
71:O5:78:LYS:HA	71:O5:81:ARG:HD3	2.61	0.74
36:1:1807:G:H5''	63:N7:135:ARG:HH22	1.53	0.73
36:1:3375:A:O2'	36:1:3378:C:OP2	2.06	0.73
37:3:112:G:OP2	87:3:214:OHX:N3	2.20	0.73
1:6:1486:G:OP2	87:6:2083:OHX:N3	2.20	0.73
36:1:2403:G:OP2	87:1:4071:OHX:N1	2.20	0.73
36:1:2403:G:OP2	87:1:4071:OHX:N3	2.21	0.73
36:5:3126:C:OP1	87:5:4116:OHX:N5	2.21	0.73
1:6:1237:G:H1	1:6:1248:C:H42	1.35	0.73
21:C9:84:LYS:HD3	21:C9:94:ILE:HG13	6.54	0.73
14:C2:54:ARG:HH21	33:E1:127:GLY:HA3	1.54	0.73
2:S0:55:GLU:HG2	23:D1:79:LEU:HD22	2.72	0.73
1:2:87:C:O2'	1:2:169:A:N1	2.21	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2371:G:O6	87:5:3825:OHX:N4	2.21	0.73
22:D0:20:ILE:HD12	22:D0:100:VAL:HG21	4.07	0.73
64:N8:96:LYS:O	64:N8:98:THR:N	2.21	0.73
6:S4:199:GLU:HB2	6:S4:207:LEU:HB2	1.70	0.73
1:2:1745:G:O6	87:2:2055:OHX:N6	2.22	0.73
1:2:583:C:OP1	87:2:1994:OHX:N3	2.22	0.73
40:L3:218:ILE:HG12	40:L3:276:THR:HG23	3.65	0.73
42:L5:50:ARG:HG2	42:L5:147:ASP:HB2	3.94	0.73
53:M7:32:THR:HG22	53:M7:58:ILE:HG13	1.69	0.73
36:1:562:C:OP2	50:M4:77:ARG:NH1	2.19	0.73
72:O6:84:LYS:NZ	36:5:309:U:OP1	145.80	0.73
13:C1:59:PRO:HB3	13:C1:66:ILE:HD11	2.95	0.73
36:5:1615:C:H2'	36:5:1616:U:H6	1.54	0.73
36:1:2318:U:O4	87:1:3936:OHX:N2	2.21	0.73
36:1:2960:C:OP1	87:1:3897:OHX:N4	2.21	0.73
1:2:381:C:O2'	1:2:755:A:N1	2.22	0.73
36:5:3074:G:O6	87:5:4013:OHX:N4	2.22	0.73
1:6:1637:C:OP2	87:6:2081:OHX:N4	2.20	0.73
1:6:1395:G:O6	87:6:2055:OHX:N1	2.20	0.73
15:C3:2:GLY:N	1:6:1035:G:OP1	336.58	0.73
13:C1:101:GLU:OE2	25:D3:16:ARG:NH2	3.26	0.73
36:1:824:C:H5"	39:L2:21:ARG:HD3	1.70	0.73
41:L4:3:ARG:O	41:L4:5:GLN:N	2.22	0.73
43:L6:52:VAL:HG11	43:L6:65:ILE:HG23	4.36	0.73
49:M3:180:ARG:HD3	72:O6:11:LEU:HD21	1.71	0.73
11:S9:23:ARG:NH1	11:S9:27:GLU:OE2	2.80	0.73
1:2:738:G:O6	87:2:2066:OHX:N1	2.22	0.73
36:5:964:G:OP1	87:5:3922:OHX:N1	2.20	0.73
38:8:55:U:O2	87:8:217:OHX:N5	2.22	0.73
59:N3:2:SER:N	59:N3:56:ASP:OD1	6.62	0.73
78:Q2:15:LYS:HA	78:Q2:18:ARG:HH11	3.94	0.73
10:S8:39:GLY:HA2	10:S8:61:GLU:HB3	1.70	0.73
36:1:1477:A:OP1	36:1:3075:G:O2'	2.07	0.73
36:1:410:U:O4	87:1:3950:OHX:N6	2.21	0.73
1:2:700:C:H42	1:2:738:G:H1	1.34	0.73
36:5:1778:G:O2'	36:5:1780:G:OP2	2.06	0.73
47:M0:221:ALA:O	87:M0:303:OHX:N2	2.21	0.73
1:2:1424:A:H1'	4:S2:92:ALA:HB1	1.71	0.73
8:S6:120:GLU:HG3	8:S6:125:THR:HB	1.71	0.73
36:1:2974:U:O4	87:1:3991:OHX:N2	2.21	0.73
1:2:1230:A:H2'	1:2:1258:U:H5	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1413:U:O2	87:2:2039:OHX:N3	2.21	0.73
50:M4:128:ARG:NH2	36:5:3214:U:OP2	281.72	0.73
36:5:899:U:O4	87:5:3878:OHX:N5	2.22	0.73
36:5:900:G:H1'	36:5:1589:A:N6	2.04	0.73
18:C6:95:LYS:O	34:SR:59:ARG:NH2	2.21	0.73
62:N6:2:ALA:N	36:5:213:A:OP1	82.00	0.73
31:D9:19:ARG:HD2	31:D9:32:ARG:HD2	1.70	0.72
2:S0:112:THR:HG23	2:S0:114:SER:H	4.03	0.72
8:S6:137:ARG:HH21	8:S6:177:ARG:HE	1.36	0.72
36:5:2169:G:O6	87:5:3869:OHX:N1	2.22	0.72
1:6:1745:G:O6	87:6:2044:OHX:N4	2.21	0.72
12:C0:54:TYR:HD2	12:C0:72:GLY:HA2	4.41	0.72
28:D6:38:ARG:HH21	28:D6:83:ILE:HG21	1.52	0.72
45:L8:54:GLU:HG2	45:L8:57:ARG:HH12	3.21	0.72
52:M6:12:LYS:O	56:N0:167:ARG:NH2	2.22	0.72
5:S3:178:ARG:H	5:S3:178:ARG:HE	1.34	0.72
1:2:1537:C:O2'	1:2:1540:G:O6	2.07	0.72
36:1:439:C:H3'	36:1:440:A:H8	1.54	0.72
87:5:3914:OHX:N4	37:7:86:U:O2	2.22	0.72
1:6:1158:C:H42	1:6:1163:A:H61	1.36	0.72
1:6:67:A:O2'	1:6:69:G:OP1	2.03	0.72
3:S1:51:SER:HB3	3:S1:57:ALA:H	2.70	0.72
36:1:3060:C:OP1	87:1:3935:OHX:N4	2.23	0.72
36:5:2533:G:N2	36:5:2546:C:N3	2.36	0.72
40:L3:128:LYS:NZ	36:5:3294:A:OP1	199.39	0.72
36:5:128:G:O6	87:5:3848:OHX:N4	2.23	0.72
42:L5:270:LYS:HB3	37:7:1:G:O2'	323.25	0.72
39:L2:193:ARG:NH2	36:5:2181:C:OP1	198.38	0.72
41:L4:193:LYS:HA	41:L4:198:ARG:HA	1.72	0.72
42:L5:227:LEU:O	42:L5:229:ASP:N	2.22	0.72
63:N7:52:LYS:O	63:N7:65:ARG:NH1	2.22	0.72
17:C5:129:GLY:HA3	35:SM:74:LYS:HG2	3.24	0.72
49:M3:79:GLU:OE1	49:M3:112:ASN:ND2	2.21	0.72
57:N1:130:ARG:NH1	36:5:1098:A:OP2	254.86	0.72
9:S7:66:SER:O	9:S7:68:ALA:N	2.69	0.72
36:1:2535:A:H61	36:1:2544:U:H3	1.36	0.72
36:1:368:G:OP1	87:1:3779:OHX:N5	2.23	0.72
36:1:517:G:O6	87:1:4003:OHX:N5	2.22	0.72
1:2:1533:C:OP2	27:D5:77:ARG:NH2	2.23	0.72
1:6:709:C:O2	1:6:730:G:N2	2.23	0.72
39:L2:133:TYR:HB3	39:L2:168:VAL:HB	3.26	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:L2:52:SER:HB3	39:L2:191:LEU:HD22	1.72	0.72
43:L6:146:ILE:HG22	43:L6:150:LYS:HE3	4.39	0.72
22:D0:89:ARG:NH2	1:6:1383:G:OP1	448.97	0.72
1:6:591:A:H2'	1:6:592:A:C8	2.24	0.72
17:C5:60:LEU:HD21	17:C5:92:SER:HB3	1.71	0.72
49:M3:74:GLY:O	49:M3:101:ARG:NH1	2.62	0.72
60:N4:13:ILE:HG12	60:N4:32:GLN:HB2	3.18	0.72
62:N6:112:ASP:HB3	62:N6:115:ARG:HB2	3.76	0.72
74:O8:9:LYS:NZ	74:O8:13:GLU:OE2	2.23	0.72
79:Q3:59:CYS:O	79:Q3:61:LYS:N	2.19	0.72
6:S4:191:ARG:HD3	6:S4:245:LYS:HB2	1.70	0.72
36:1:2225:U:H2'	36:1:2226:U:H6	1.55	0.72
36:5:2996:U:OP1	36:5:2996:U:H4'	1.90	0.72
36:5:770:G:N7	87:5:4004:OHX:N6	2.38	0.72
36:5:2151:C:OP1	87:5:4171:OHX:N4	2.22	0.72
73:O7:21:ARG:NH2	73:O7:41:ALA:O	2.47	0.72
74:O8:69:LEU:HD12	74:O8:73:LEU:HD23	1.71	0.72
3:S1:36:SER:OG	3:S1:231:LEU:O	4.65	0.72
1:2:1669:U:OP2	87:2:2092:OHX:N6	2.22	0.71
2:S0:182:LEU:HB3	2:S0:188:LEU:HD23	1.71	0.71
34:SR:282:SER:H	34:SR:285:ALA:HB3	1.54	0.71
36:5:1534:A:OP1	87:5:3838:OHX:N1	2.23	0.71
1:6:1727:G:H2'	1:6:1728:A:C8	2.25	0.71
71:O5:63:ARG:NH2	38:8:97:A:OP1	57.59	0.71
1:2:329:G:H5''	10:S8:98:LYS:HB3	1.72	0.71
42:L5:68:THR:HG22	42:L5:70:THR:H	1.55	0.71
1:2:25:C:O2	87:2:2052:OHX:N1	2.23	0.71
40:L3:2:SER:N	36:5:2940:A:N7	239.12	0.71
25:D3:91:GLY:O	25:D3:93:LEU:N	2.22	0.71
28:D6:37:LYS:O	28:D6:38:ARG:NH1	2.23	0.71
48:M1:49:LYS:HB3	48:M1:62:ASN:HA	1.71	0.71
64:N8:3:SER:OG	36:5:1430:U:O4	140.86	0.71
36:1:1592:G:OP2	70:O4:37:LYS:NZ	2.21	0.71
1:2:1665:U:O4	87:2:2108:OHX:N3	2.23	0.71
20:C8:28:ILE:HD11	20:C8:56:LYS:HB2	7.22	0.71
36:1:560:G:OP1	50:M4:83:LYS:NZ	2.23	0.71
36:1:3155:U:H3'	36:1:3156:U:H4'	1.71	0.71
1:2:151:G:O6	26:D4:124:ARG:NH2	2.23	0.71
37:3:60:G:H2'	37:3:61:G:H8	1.56	0.71
27:D5:66:VAL:HA	27:D5:71:ILE:HG22	5.23	0.71
27:D5:93:SER:OG	27:D5:94:LYS:N	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:L2:152:SER:OG	36:5:2157:G:N7	217.58	0.71
39:L2:204:MET:HG2	36:5:914:A:C2	196.23	0.71
1:6:454:U:H5''	1:6:455:C:C5	2.26	0.71
1:6:75:U:O2'	1:6:76:A:O5'	2.05	0.71
16:C4:85:ALA:H	16:C4:119:THR:HG22	1.55	0.71
49:M3:168:ARG:HH21	49:M3:172:LEU:HD21	1.56	0.71
56:N0:74:ASN:HD21	56:N0:144:LEU:HD21	1.55	0.71
3:S1:190:PRO:HG2	3:S1:192:VAL:HG23	2.90	0.71
1:2:222:A:H61	1:2:839:U:H3	1.37	0.71
33:E1:139:LEU:HB2	33:E1:151:ASN:HB3	5.09	0.71
48:M1:107:ASP:N	48:M1:107:ASP:OD1	2.21	0.71
36:1:2964:G:N7	87:1:3958:OHX:N1	2.39	0.71
1:2:513:U:OP1	11:S9:133:HIS:NE2	2.24	0.71
1:2:703:G:H1	1:2:735:C:H42	1.37	0.71
36:5:3290:G:N7	87:5:4010:OHX:N5	2.39	0.71
1:6:205:U:O4	87:6:2095:OHX:N6	2.23	0.71
22:D0:69:LYS:HE2	22:D0:80:GLU:HB2	1.73	0.71
40:L3:4:ARG:HD3	40:L3:7:GLU:HA	1.71	0.71
63:N7:23:VAL:HG12	63:N7:45:GLY:HA3	1.97	0.71
69:O3:59:VAL:O	69:O3:61:GLY:N	2.62	0.71
4:S2:153:SER:OG	4:S2:154:LEU:N	2.83	0.71
34:SR:93:ASP:OD2	34:SR:100:TYR:OH	3.14	0.71
1:2:1571:C:OP2	87:2:2131:OHX:N2	2.24	0.71
36:5:652:G:OP2	87:5:4083:OHX:N3	2.23	0.71
1:6:1722:A:OP2	87:6:2058:OHX:N1	2.24	0.71
13:C1:77:SER:HB3	13:C1:85:VAL:HB	1.73	0.71
41:L4:283:THR:HG22	41:L4:285:ASP:H	1.54	0.71
60:N4:6:ASP:HB3	60:N4:11:ALA:H	3.15	0.71
66:O0:22:LYS:HB2	66:O0:93:LEU:HB2	1.72	0.71
5:S3:44:THR:HB	5:S3:45:LYS:HG3	1.73	0.71
36:1:1134:G:O2'	36:1:2642:A:N3	2.19	0.70
36:1:1938:U:O4	87:1:3811:OHX:N5	2.24	0.70
1:2:1588:G:H1	1:2:1608:U:H3	1.38	0.70
36:5:618:C:O2'	36:5:621:A:N3	2.20	0.70
1:6:652:G:N2	1:6:683:C:N3	2.39	0.70
19:C7:20:TYR:CG	19:C7:38:ILE:HD11	2.26	0.70
49:M3:166:ALA:HB1	64:N8:147:LEU:HD21	1.73	0.70
78:Q2:17:CYS:HB2	78:Q2:77:CYS:SG	2.96	0.70
2:S0:22:THR:HG21	2:S0:173:ILE:HD11	2.85	0.70
10:S8:57:ALA:HB2	10:S8:177:GLY:HA2	2.21	0.70
1:2:1235:C:H5'	33:E1:146:SER:HB2	1.70	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D3:63:GLN:HA	25:D3:65:ASN:H	1.57	0.70
47:M0:72:ALA:O	47:M0:76:MET:HG3	2.45	0.70
51:M5:94:TYR:CE1	51:M5:96:ARG:HB2	2.27	0.70
78:Q2:50:PHE:O	87:Q2:503:OHX:N2	2.24	0.70
6:S4:31:PRO:HB2	6:S4:38:LEU:HD22	1.73	0.70
38:8:141:C:OP2	87:8:230:OHX:N6	2.25	0.70
18:C6:37:THR:O	18:C6:45:ARG:NH1	2.46	0.70
36:1:3085:G:OP1	60:N4:34:SER:OG	2.08	0.70
60:N4:9:SER:HB2	60:N4:51:TRP:CZ3	2.92	0.70
63:N7:27:LYS:HG3	63:N7:29:HIS:HE1	1.55	0.70
1:6:1380:U:O2'	1:6:1516:A:N1	2.24	0.70
1:6:1765:A:OP1	87:6:2092:OHX:N2	2.23	0.70
1:6:699:U:O4	87:6:2040:OHX:N1	2.24	0.70
38:8:80:A:H2	38:8:83:C:H41	1.37	0.70
14:C2:48:SER:OG	14:C2:120:VAL:O	3.03	0.70
25:D3:28:ASN:N	25:D3:28:ASN:OD1	2.25	0.70
63:N7:16:GLY:O	63:N7:18:TYR:N	2.29	0.70
8:S6:177:ARG:NH2	1:6:143:G:N7	313.32	0.70
36:1:551:A:O2'	36:1:552:G:O5'	2.10	0.70
38:4:150:G:N7	87:4:220:OHX:N4	2.39	0.70
21:C9:37:VAL:HG12	21:C9:39:THR:H	6.04	0.70
33:E1:144:CYS:HB3	33:E1:147:VAL:HG13	1.72	0.70
40:L3:167:ARG:O	87:L3:403:OHX:N5	5.84	0.70
50:M4:25:LYS:HE3	50:M4:62:GLN:HA	1.74	0.70
36:1:900:G:H1'	36:1:1589:A:N6	2.05	0.70
1:2:364:G:OP1	87:2:2074:OHX:N2	2.24	0.70
1:6:1449:U:O4	87:6:2039:OHX:N2	2.25	0.70
44:L7:224:ILE:HG23	56:N0:36:ILE:HG12	2.39	0.70
47:M0:42:THR:HG23	47:M0:45:GLU:HB2	1.74	0.70
51:M5:91:GLU:OE1	87:M5:302:OHX:N5	2.25	0.70
53:M7:25:SER:O	53:M7:29:THR:HG23	1.90	0.70
1:2:993:A:OP1	1:2:1777:G:N2	2.22	0.70
21:C9:52:GLY:O	21:C9:54:PHE:N	2.22	0.70
42:L5:294:ALA:HB1	47:M0:217:PHE:HB3	1.74	0.70
47:M0:55:ASN:HA	47:M0:131:ILE:HG23	2.47	0.70
36:1:361:A:OP1	73:O7:24:ARG:NH1	2.23	0.70
7:S5:206:SER:O	7:S5:212:LYS:NZ	2.24	0.70
1:6:1087:A:H2'	1:6:1088:A:C8	2.27	0.70
18:C6:106:LYS:O	18:C6:110:THR:OG1	3.58	0.70
18:C6:16:ALA:HB2	18:C6:72:GLY:HA3	1.74	0.70
68:O2:41:VAL:HG12	68:O2:46:PHE:HB2	3.75	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:O7:88:ALA:O	87:O7:103:OHX:N1	2.24	0.70
3:S1:28:GLU:OE2	3:S1:94:LYS:NZ	2.25	0.70
11:S9:113:VAL:HG12	11:S9:119:ALA:HB2	2.73	0.70
36:1:2269:U:O2'	36:1:2271:A:N7	2.24	0.70
36:1:299:G:N7	87:1:3974:OHX:N2	2.39	0.70
36:5:1765:U:H4'	36:5:1765:U:OP1	1.91	0.70
40:L3:376:LYS:NZ	36:5:3329:U:OP1	220.60	0.70
1:6:822:U:H2'	1:6:823:G:H5''	1.73	0.70
12:C0:44:LYS:HD3	12:C0:47:GLN:HG2	4.67	0.70
70:O4:64:THR:OG1	87:O4:202:OHX:N3	2.24	0.70
4:S2:56:ILE:HA	4:S2:61:LEU:HD12	1.77	0.70
1:2:1488:G:H3'	1:2:1515:A:H61	1.56	0.70
1:2:987:G:C2	39:L2:249:SER:HB2	2.26	0.70
44:L7:217:PRO:O	87:5:3917:OHX:N3	261.82	0.70
71:O5:118:ILE:HG22	71:O5:119:LYS:H	2.94	0.70
36:1:3066:U:O4	87:1:4033:OHX:N5	2.25	0.69
36:5:172:G:O6	87:5:3988:OHX:N4	2.25	0.69
36:5:3352:U:O2	87:5:4153:OHX:N5	2.25	0.69
36:5:920:A:OP1	36:5:922:U:H5	1.75	0.69
1:6:1202:A:OP1	87:6:2096:OHX:N2	2.25	0.69
36:1:686:G:OP2	49:M3:39:ARG:NH2	2.25	0.69
52:M6:130:LYS:HD3	52:M6:131:PRO:HD2	5.06	0.69
53:M7:56:ARG:NH1	53:M7:75:GLU:OE2	2.21	0.69
56:N0:134:ASP:O	56:N0:136:LYS:NZ	3.98	0.69
62:N6:39:LEU:HD22	62:N6:43:TYR:HE2	2.91	0.69
64:N8:103:ASP:HB3	64:N8:106:ALA:HB3	2.86	0.69
36:5:2287:C:O2	87:5:3861:OHX:N5	2.25	0.69
78:Q2:12:CYS:SG	78:Q2:17:CYS:CB	3.03	0.69
79:Q3:84:ARG:HG3	79:Q3:87:ARG:HH22	4.82	0.69
3:S1:24:PHE:HA	3:S1:27:LYS:HG2	3.04	0.69
36:1:678:G:O6	87:1:3868:OHX:N4	2.25	0.69
1:2:1478:G:OP1	21:C9:39:THR:OG1	2.07	0.69
36:5:863:C:OP1	87:5:3833:OHX:N3	2.24	0.69
21:C9:28:LEU:HA	21:C9:111:ILE:HD11	5.25	0.69
49:M3:123:ILE:HG22	71:O5:118:ILE:HG23	3.66	0.69
7:S5:43:PHE:N	7:S5:46:TRP:O	3.38	0.69
36:5:1565:G:N1	36:5:1574:C:N3	2.40	0.69
36:5:162:G:N2	36:5:259:C:O2	2.20	0.69
1:6:74:U:C4	1:6:76:A:H5''	2.28	0.69
14:C2:87:PRO:HA	14:C2:140:PHE:HE1	1.59	0.69
39:L2:118:GLU:HG3	39:L2:126:LEU:HD21	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:L8:109:LEU:O	45:L8:113:ALA:N	2.25	0.69
52:M6:140:LYS:NZ	52:M6:150:GLU:OE1	2.22	0.69
36:1:116:A:OP1	72:O6:36:ARG:NH1	2.25	0.69
1:2:1662:G:O6	87:2:2008:OHX:N3	2.25	0.69
49:M3:14:PHE:HE1	36:5:665:A:H1'	135.18	0.69
19:C7:2:GLY:N	1:6:1312:A:N7	396.50	0.69
16:C4:50:ALA:O	16:C4:52:ARG:N	2.31	0.69
20:C8:30:TYR:O	20:C8:33:THR:OG1	2.11	0.69
25:D3:144:ARG:HD2	25:D3:145:SER:H	1.57	0.69
44:L7:168:ILE:O	44:L7:172:ASN:ND2	5.04	0.69
47:M0:190:VAL:HG13	47:M0:197:VAL:HG21	2.77	0.69
66:O0:16:LEU:HD13	66:O0:97:ASP:HB3	1.74	0.69
68:O2:123:LYS:HA	68:O2:126:LEU:HD12	2.28	0.69
24:D2:18:GLU:HG3	24:D2:69:LEU:HD23	2.62	0.69
47:M0:220:GLN:O	87:M0:303:OHX:N1	2.25	0.69
63:N7:102:GLU:H	63:N7:107:ARG:HH21	1.74	0.69
3:S1:150:VAL:HG23	1:6:1067:C:H5''	355.01	0.69
36:1:2250:G:O6	87:1:3826:OHX:N6	2.25	0.69
36:1:2836:C:H5	36:1:2852:C:H42	1.39	0.69
36:1:1208:U:O4	87:1:3921:OHX:N5	2.26	0.69
1:2:1358:G:H2'	1:2:1359:C:C6	2.27	0.69
36:5:368:G:OP1	87:5:3840:OHX:N4	2.26	0.69
17:C5:22:LEU:HA	17:C5:25:LEU:HB2	3.15	0.69
24:D2:5:SER:O	24:D2:7:LEU:N	3.72	0.69
41:L4:327:LEU:HA	44:L7:166:ASN:HD21	1.58	0.69
63:N7:17:ARG:NH2	36:5:1634:G:N7	198.69	0.69
36:1:1238:C:N4	36:1:1245:A:OP2	2.25	0.69
36:1:1724:U:H1'	36:1:1725:C:C6	2.28	0.69
35:SM:31:SER:OG	36:5:2667:A:OP1	289.95	0.69
36:5:283:G:OP2	36:5:285:A:O2'	2.08	0.69
1:6:800:U:H2'	1:6:801:G:C8	2.27	0.69
55:M9:62:ARG:NH2	36:5:3068:U:OP2	172.93	0.69
62:N6:36:SER:HB3	62:N6:105:VAL:HG13	1.73	0.69
62:N6:32:SER:HA	62:N6:49:PRO:HA	2.48	0.69
34:SR:156:VAL:HA	34:SR:169:ILE:HG22	1.94	0.69
36:1:1758:G:H1	36:1:1767:C:H42	1.39	0.69
36:1:2315:G:OP2	87:1:3897:OHX:N3	2.26	0.69
1:2:169:A:H5''	8:S6:176:GLN:HG2	1.74	0.69
36:5:1231:A:H5''	36:5:1232:C:H5'	1.74	0.69
1:6:58:U:O4	87:6:2056:OHX:N2	2.26	0.69
26:D4:3:ASP:O	26:D4:5:VAL:N	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:D8:36:THR:OG1	30:D8:37:SER:N	2.26	0.69
63:N7:115:LYS:NZ	63:N7:119:GLU:OE2	2.25	0.69
6:S4:146:THR:HG21	1:6:123:G:H21	343.39	0.69
36:1:2404:A:H8	36:1:2404:A:H5'	1.56	0.69
36:1:343:U:OP2	87:1:3779:OHX:N6	2.26	0.69
13:C1:111:VAL:HG23	13:C1:139:VAL:HG21	2.80	0.69
2:S0:119:ARG:HH11	2:S0:119:ARG:HB3	1.59	0.69
1:2:1595:U:H3	1:2:1600:A:H2	1.39	0.69
1:2:1642:G:O6	87:2:1991:OHX:N6	2.26	0.69
78:Q2:41:ARG:NH1	36:5:284:A:OP2	158.12	0.69
15:C3:76:LYS:HA	15:C3:81:ALA:HB2	1.80	0.69
16:C4:115:ILE:HG21	28:D6:44:ILE:HG21	6.08	0.69
28:D6:12:LYS:HE2	28:D6:16:GLY:H	1.59	0.69
44:L7:140:SER:HB3	44:L7:237:ASN:HD21	1.57	0.69
63:N7:135:ARG:NH2	36:5:2556:C:O2'	200.27	0.69
74:O8:24:THR:HG22	74:O8:76:ASN:HB3	1.75	0.69
36:1:194:U:H2'	36:1:195:U:H6	1.58	0.68
36:1:3284:G:OP1	87:1:4048:OHX:N3	2.26	0.68
1:2:621:A:N3	1:2:1107:G:H1'	2.08	0.68
36:5:2568:C:N4	36:5:2574:G:O6	2.26	0.68
1:6:1336:A:OP1	87:6:2149:OHX:N1	2.26	0.68
1:6:318:U:O4	87:6:2127:OHX:N4	2.27	0.68
1:6:482:U:H3	1:6:505:A:H61	1.37	0.68
13:C1:90:TYR:OH	13:C1:105:LYS:NZ	2.26	0.68
51:M5:93:LYS:HG3	36:5:289:A:C2	146.18	0.68
44:L7:80:GLN:HB2	57:N1:135:PRO:HB2	1.76	0.68
34:SR:280:GLY:O	87:SR:401:OHX:N4	4.34	0.68
36:1:1245:A:H3'	36:1:1246:G:H5''	1.73	0.68
36:1:2208:A:N1	87:1:3940:OHX:N4	2.40	0.68
36:1:3350:C:H2'	36:1:3351:U:H3'	1.75	0.68
36:1:3377:G:O6	87:1:3932:OHX:N2	2.26	0.68
36:5:1552:G:OP2	87:5:4169:OHX:N3	2.25	0.68
17:C5:68:PRO:HG2	17:C5:71:GLU:HB3	1.73	0.68
41:L4:203:ARG:HH21	41:L4:240:PRO:HB3	2.45	0.68
50:M4:24:LYS:NZ	50:M4:61:GLY:O	2.20	0.68
2:S0:31:VAL:HG12	2:S0:33:GLN:H	1.58	0.68
3:S1:157:GLN:O	3:S1:159:SER:N	2.26	0.68
6:S4:240:LYS:HE2	6:S4:240:LYS:H	1.59	0.68
36:1:1464:G:N7	87:O1:201:OHX:N6	2.41	0.68
15:C3:67:THR:O	15:C3:67:THR:OG1	2.42	0.68
2:S0:52:LYS:HD2	23:D1:82:VAL:HA	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:3:HIS:O	40:L3:5:LYS:N	2.27	0.68
47:M0:215:GLU:O	87:M0:303:OHX:N6	2.25	0.68
36:1:618:C:H5'	53:M7:169:THR:HG22	1.75	0.68
55:M9:148:ASP:OD1	55:M9:151:ARG:NH2	2.25	0.68
6:S4:90:ILE:HB	6:S4:99:PHE:HB2	1.74	0.68
1:2:1160:A:H2'	1:2:1161:C:C6	2.29	0.68
1:2:1456:C:H5''	1:2:1457:C:H5''	1.75	0.68
36:5:1019:G:O6	87:5:4148:OHX:N2	2.27	0.68
44:L7:206:LYS:HB3	36:5:1334:U:H5''	237.41	0.68
36:5:2823:G:N7	87:5:3868:OHX:N2	2.40	0.68
1:6:1050:G:O6	87:6:2180:OHX:N4	2.27	0.68
39:L2:242:ARG:HD3	39:L2:246:LEU:HD12	6.00	0.68
49:M3:83:ALA:HB2	49:M3:113:VAL:HG13	1.75	0.68
36:1:2916:U:H1'	59:N3:44:SER:HB3	1.74	0.68
57:N1:18:ASP:OD2	57:N1:18:ASP:N	4.78	0.68
2:S0:121:VAL:HG23	2:S0:141:ILE:HG21	1.75	0.68
7:S5:117:THR:HG21	7:S5:194:LEU:HD12	1.74	0.68
11:S9:168:ARG:HG2	11:S9:170:GLY:H	1.58	0.68
36:1:2255:A:OP1	87:1:3830:OHX:N3	2.26	0.68
36:1:385:A:H2'	36:1:386:A:C8	2.29	0.68
1:2:1518:C:OP2	87:2:2089:OHX:N2	2.26	0.68
38:4:136:G:OP1	61:N5:48:SER:OG	2.12	0.68
36:5:201:A:OP2	87:5:3901:OHX:N3	2.27	0.68
1:6:800:U:H2'	1:6:801:G:H8	1.59	0.68
23:D1:74:GLN:NE2	23:D1:83:TRP:O	4.10	0.68
42:L5:205:SER:HB2	42:L5:233:ALA:HB1	1.74	0.68
55:M9:171:ASP:HA	55:M9:174:ALA:HB3	1.76	0.68
36:1:2984:C:H2'	36:1:2985:C:H6	1.58	0.68
36:1:1234:G:O6	87:1:3999:OHX:N5	2.26	0.68
1:6:1206:U:OP1	87:6:2094:OHX:N6	2.26	0.68
1:6:1370:U:O4	87:6:2110:OHX:N4	2.27	0.68
40:L3:139:GLN:O	40:L3:141:GLY:N	3.75	0.68
40:L3:21:ARG:NH2	36:5:3309:G:O6	200.09	0.68
54:M8:157:PRO:HD3	64:N8:47:LYS:HB2	1.74	0.68
3:S1:157:GLN:OE1	87:S1:301:OHX:N3	6.92	0.68
36:1:1230:G:H1	36:1:1279:C:H42	1.41	0.68
36:1:1587:A:OP1	87:1:3839:OHX:N6	2.26	0.68
36:1:2403:G:O6	87:1:4076:OHX:N3	2.27	0.68
36:1:437:G:H22	36:1:622:A:H61	1.42	0.68
1:2:290:G:O6	87:2:2128:OHX:N5	2.26	0.68
36:5:552:G:O6	87:5:3911:OHX:N5	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:O4:64:THR:OG1	87:5:4103:OHX:N3	154.84	0.68
36:5:604:G:N7	87:5:4081:OHX:N2	2.42	0.68
1:6:1060:U:O2'	87:6:2156:OHX:N5	2.27	0.68
1:6:738:G:O6	87:6:2040:OHX:N1	2.27	0.68
14:C2:59:LEU:HA	14:C2:87:PRO:HB2	1.75	0.68
61:N5:39:LYS:HG3	36:5:13:A:H4'	119.91	0.68
36:1:718:G:OP1	64:N8:117:ARG:NH2	2.27	0.68
1:2:1773:C:OP2	77:Q1:2:ARG:NH1	2.26	0.68
36:5:23:A:H2'	36:5:24:G:C8	2.29	0.68
36:5:3242:G:H5''	36:5:3245:A:H8	1.58	0.68
17:C5:67:ALA:O	87:C5:201:OHX:N2	2.55	0.68
18:C6:40:GLU:HA	18:C6:42:GLU:N	2.09	0.68
48:M1:109:HIS:CD2	48:M1:123:PHE:H	2.11	0.68
67:O1:54:GLU:OE2	67:O1:54:GLU:N	2.27	0.68
2:S0:110:TYR:O	2:S0:112:THR:N	4.68	0.68
36:1:2217:U:H2'	36:1:2218:G:H8	1.59	0.68
38:4:103:G:O6	87:4:216:OHX:N6	2.27	0.68
10:S8:138:ASN:HD22	1:6:197:A:H61	279.95	0.68
25:D3:75:GLN:HG3	25:D3:82:LYS:HG3	1.74	0.68
42:L5:85:ARG:NH1	42:L5:86:TYR:OH	2.27	0.68
46:L9:172:ILE:H	46:L9:172:ILE:HD13	1.58	0.68
49:M3:47:ALA:HB1	49:M3:48:PRO:HD2	1.84	0.68
63:N7:54:THR:OG1	63:N7:55:LYS:N	2.26	0.68
2:S0:56:LYS:HZ1	2:S0:158:VAL:HA	3.29	0.68
3:S1:183:GLN:HG2	3:S1:187:LYS:HE3	1.75	0.68
9:S7:28:GLU:HG2	9:S7:35:LYS:HA	4.34	0.68
36:1:2193:U:H5'	36:1:2194:G:H5'	1.76	0.67
1:2:207:U:O2	10:S8:178:ARG:NH1	2.27	0.67
36:5:651:G:O2'	36:5:1435:A:OP1	2.12	0.67
36:5:1170:A:OP2	87:5:3917:OHX:N4	2.27	0.67
47:M0:174:THR:OG1	47:M0:175:ASN:O	5.94	0.67
48:M1:143:ARG:NH2	37:7:5:G:OP1	293.07	0.67
62:N6:3:LYS:HG3	62:N6:8:VAL:HG13	1.76	0.67
2:S0:26:ALA:H	2:S0:149:LEU:HD12	1.59	0.67
8:S6:155:ASP:OD1	87:S6:301:OHX:N6	2.27	0.67
11:S9:92:LYS:O	11:S9:94:ASP:N	2.22	0.67
36:1:3253:G:O6	87:1:3949:OHX:N5	2.27	0.67
66:O0:50:VAL:HG11	36:5:2552:C:H2'	235.14	0.67
36:5:2762:A:OP2	87:5:3903:OHX:N2	2.27	0.67
1:6:1058:U:H4'	1:6:1059:U:OP1	1.93	0.67
37:7:2:G:O2'	37:7:23:A:N1	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1550:A:OP2	17:C5:42:ARG:NH2	2.27	0.67
21:C9:86:ARG:HD2	21:C9:92:LYS:HG2	6.64	0.67
36:1:2522:G:O6	39:L2:70:ARG:NH2	2.27	0.67
42:L5:270:LYS:HE3	42:L5:273:ARG:HA	8.90	0.67
36:1:58:G:OP1	51:M5:157:LYS:NZ	2.24	0.67
36:5:209:A:H4'	36:5:211:A:C8	2.29	0.67
36:5:2510:U:O2'	36:5:2511:A:O5'	2.10	0.67
36:5:2983:C:OP1	87:5:4152:OHX:N6	2.28	0.67
36:5:3312:U:OP1	87:5:3934:OHX:N1	2.28	0.67
36:1:2395:G:H5''	40:L3:255:TRP:CD1	2.28	0.67
62:N6:36:SER:O	62:N6:39:LEU:N	2.25	0.67
36:1:2213:A:H2'	36:1:2214:A:C8	2.29	0.67
36:5:172:G:O6	87:5:3988:OHX:N2	2.27	0.67
36:5:1806:A:OP2	87:5:3938:OHX:N5	2.28	0.67
1:6:915:A:OP1	87:6:2037:OHX:N4	2.28	0.67
22:D0:51:VAL:HG13	22:D0:94:GLU:HB2	1.75	0.67
24:D2:27:ILE:HG12	24:D2:61:ILE:HB	1.77	0.67
66:O0:16:LEU:HB2	66:O0:98:SER:HB2	2.91	0.67
69:O3:13:HIS:NE2	69:O3:28:SER:OG	2.27	0.67
6:S4:131:LEU:HD12	1:6:252:U:H4'	326.67	0.67
7:S5:23:VAL:O	7:S5:34:GLN:NE2	2.98	0.67
11:S9:108:ARG:HB2	11:S9:111:THR:HG23	2.54	0.67
36:1:2946:A:H5''	36:1:2947:G:H5'	1.76	0.67
1:2:972:G:O2'	36:1:847:A:N1	2.27	0.67
1:2:1186:U:OP1	1:2:1456:C:O2'	2.12	0.67
1:2:1339:C:O2'	1:2:1341:A:N7	2.27	0.67
1:2:1564:U:H2'	1:2:1565:C:C6	2.30	0.67
1:2:565:C:O2	87:2:2006:OHX:N5	2.27	0.67
1:6:1690:G:H1	1:6:1711:C:H42	1.42	0.67
42:L5:152:ARG:HG3	37:7:44:C:H4'	283.68	0.67
44:L7:88:ARG:HA	44:L7:134:VAL:HG12	2.77	0.67
48:M1:52:TYR:HA	48:M1:61:ARG:HG3	3.28	0.67
60:N4:45:ASN:HB3	60:N4:48:ARG:HG3	1.77	0.67
41:L4:64:SER:HA	41:L4:75:PRO:HA	1.77	0.67
34:SR:207:ASP:OD1	34:SR:209:THR:OG1	2.27	0.67
36:5:1769:G:O6	87:5:4139:OHX:N2	2.28	0.67
40:L3:266:ARG:NH2	36:5:2392:C:O2'	210.03	0.67
36:5:1734:G:N7	87:5:3884:OHX:N5	2.42	0.67
1:6:454:U:H3'	1:6:455:C:H6	1.60	0.67
16:C4:126:THR:HG21	1:6:888:U:H1'	275.70	0.67
38:8:102:U:H2'	38:8:103:G:C8	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:D8:12:VAL:HA	30:D8:30:VAL:HG12	1.76	0.67
39:L2:3:ARG:HG2	39:L2:4:VAL:H	1.80	0.67
36:1:3108:G:H21	46:L9:163:GLN:HE22	1.41	0.67
49:M3:56:PRO:HG3	49:M3:74:GLY:O	2.01	0.67
51:M5:96:ARG:NH2	51:M5:104:GLU:OE1	3.52	0.67
58:N2:12:ALA:HB2	58:N2:68:THR:HG23	4.89	0.67
59:N3:71:LYS:NZ	36:5:2294:U:OP2	278.53	0.67
64:N8:128:ARG:HB2	72:O6:8:ALA:HB2	3.80	0.67
75:O9:23:LEU:HD11	75:O9:35:ILE:HG22	2.11	0.67
3:S1:70:LEU:HB3	3:S1:79:HIS:HB3	4.98	0.67
4:S2:98:PHE:CZ	35:SM:116:GLU:HG3	2.30	0.67
36:1:385:A:H2'	36:1:386:A:H8	1.58	0.67
1:2:477:A:H61	1:2:511:A:H61	1.43	0.67
36:5:173:G:H1'	36:5:174:C:H5'	1.77	0.67
1:6:1156:C:OP1	87:6:2132:OHX:N1	2.28	0.67
1:6:422:G:OP1	87:6:2022:OHX:N3	2.28	0.67
1:2:777:C:H5	26:D4:10:ARG:HH12	1.42	0.67
1:2:1797:A:N7	28:D6:87:ARG:NH1	2.43	0.67
30:D8:10:ALA:HA	30:D8:32:PHE:HA	1.76	0.67
41:L4:26:PHE:HD1	41:L4:130:ALA:HB2	2.17	0.67
43:L6:3:ALA:HB1	68:O2:75:LEU:HD13	2.64	0.67
49:M3:126:PHE:O	71:O5:114:ARG:NH2	2.25	0.67
56:N0:133:ALA:HA	56:N0:141:LYS:HZ3	1.59	0.67
7:S5:40:ILE:HG23	7:S5:42:LEU:HD22	1.75	0.67
10:S8:52:ASN:OD1	87:6:2103:OHX:N3	312.43	0.67
36:1:1765:U:H5''	55:M9:43:LYS:HE2	1.77	0.67
36:1:162:G:N2	36:1:259:C:O2	2.25	0.67
1:2:324:U:OP1	13:C1:133:LYS:NZ	2.26	0.67
36:5:409:A:OP2	87:5:4011:OHX:N3	2.28	0.67
1:6:1239:U:O4	87:6:2063:OHX:N5	2.26	0.67
29:D7:36:LYS:HE2	29:D7:43:ILE:HG22	4.71	0.67
42:L5:211:LEU:HB3	42:L5:219:PHE:HB2	1.85	0.67
49:M3:140:SER:OG	49:M3:141:ALA:N	2.28	0.67
36:1:2356:A:H5'	53:M7:138:LYS:HE2	1.76	0.67
53:M7:62:ARG:NH1	36:5:412:G:OP1	160.49	0.67
58:N2:50:LEU:O	58:N2:52:ASN:N	2.80	0.67
73:O7:17:THR:HG22	73:O7:18:LEU:H	1.58	0.67
9:S7:138:LYS:O	9:S7:139:ARG:NE	2.28	0.67
36:1:3224:G:O6	87:1:3789:OHX:N4	2.28	0.67
36:5:2369:G:OP2	87:5:3825:OHX:N5	2.28	0.67
52:M6:160:ARG:NH2	36:5:3182:G:OP1	281.45	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L4:16:THR:HG22	41:L4:18:ASN:H	1.60	0.67
41:L4:337:GLU:HB2	41:L4:339:LEU:HD23	1.75	0.67
45:L8:133:LYS:HB2	45:L8:199:ALA:O	3.52	0.67
59:N3:32:ARG:O	59:N3:32:ARG:NH1	7.66	0.67
36:1:2108:C:O2'	36:1:3362:A:N6	2.27	0.66
36:1:3191:G:O6	87:1:4027:OHX:N3	2.27	0.66
42:L5:38:THR:HG23	57:N1:30:TYR:HB3	3.28	0.66
43:L6:50:LYS:HE3	43:L6:72:ASN:HB2	1.76	0.66
36:1:1369:A:OP1	64:N8:21:ARG:NH1	2.28	0.66
36:1:1953:G:O6	36:1:2094:C:N4	2.25	0.66
36:1:1502:C:OP1	87:1:3774:OHX:N3	2.29	0.66
1:2:738:G:O6	87:2:2066:OHX:N4	2.29	0.66
1:2:819:G:O2'	1:2:821:U:OP2	2.13	0.66
1:6:65:A:O2'	1:6:67:A:OP2	2.11	0.66
42:L5:33:ARG:NH1	37:7:7:G:OP1	271.86	0.66
17:C5:81:ARG:NH1	17:C5:97:TYR:O	2.28	0.66
23:D1:3:ASN:ND2	23:D1:7:GLN:O	3.72	0.66
27:D5:42:LEU:HD22	27:D5:47:TYR:HB2	6.82	0.66
42:L5:284:ALA:HA	42:L5:287:ALA:HB3	1.76	0.66
55:M9:13:SER:OG	55:M9:38:ARG:NH1	4.24	0.66
78:Q2:45:ARG:O	78:Q2:48:SER:OG	2.48	0.66
36:1:2746:A:H2	42:L5:146:LEU:HB3	1.60	0.66
38:4:95:G:OP2	73:O7:72:ARG:NH1	2.27	0.66
38:8:79:A:H3'	38:8:80:A:C8	2.31	0.66
40:L3:186:GLY:O	40:L3:190:GLU:HB2	2.40	0.66
41:L4:122:THR:HG22	41:L4:235:LEU:HB2	2.12	0.66
41:L4:197:ARG:NH1	36:5:1381:A:OP1	109.86	0.66
48:M1:15:GLU:HB3	48:M1:130:VAL:HG22	3.31	0.66
63:N7:26:VAL:HG21	63:N7:96:VAL:HB	1.78	0.66
70:O4:100:ILE:HA	70:O4:103:LYS:HG2	1.78	0.66
75:O9:23:LEU:HD23	75:O9:24:PRO:HD2	1.77	0.66
36:1:3050:U:O2'	60:N4:16:GLY:O	2.13	0.66
36:5:2546:C:H2'	36:5:2547:A:H8	1.60	0.66
36:5:2818:U:H6	36:5:2818:U:H5'	1.61	0.66
15:C3:4:MET:HE1	15:C3:121:ARG:HG3	1.77	0.66
62:N6:87:LYS:HB2	62:N6:97:ILE:HD11	4.39	0.66
36:1:1769:G:O6	87:1:4067:OHX:N4	2.28	0.66
36:1:64:G:OP2	51:M5:169:LYS:NZ	2.28	0.66
1:2:1535:U:O2'	1:2:1536:G:N3	2.29	0.66
36:5:1912:U:N3	36:5:2122:G:OP2	2.26	0.66
36:5:652:G:OP2	87:5:4083:OHX:N6	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:S9:17:ARG:NH1	1:6:4:C:O2'	391.19	0.66
8:S6:159:ARG:NH2	1:6:79:C:OP1	351.48	0.66
17:C5:14:THR:HB	17:C5:22:LEU:HB2	1.77	0.66
40:L3:204:ALA:O	40:L3:207:SER:OG	2.13	0.66
37:3:121:U:H3	42:L5:268:GLU:HB3	1.59	0.66
45:L8:33:ASN:O	45:L8:35:GLY:N	2.86	0.66
45:L8:91:PHE:O	45:L8:95:ASN:ND2	3.53	0.66
53:M7:120:ASN:N	53:M7:120:ASN:OD1	3.03	0.66
63:N7:46:ILE:HA	63:N7:70:PRO:HA	2.30	0.66
1:2:1274:C:H41	35:SM:95:SER:HA	1.59	0.66
34:SR:38:ARG:HA	34:SR:67:ILE:HG23	1.78	0.66
36:1:2669:G:N7	87:1:3964:OHX:N4	2.44	0.66
36:1:729:C:H2'	36:1:730:C:H6	1.60	0.66
43:L6:78:ARG:NH1	36:5:3272:C:OP2	248.21	0.66
20:C8:138:THR:HB	1:6:1459:C:H2'	347.93	0.66
1:6:197:A:H2'	1:6:198:A:C8	2.29	0.66
18:C6:79:TYR:HA	18:C6:82:ARG:HG2	2.16	0.66
25:D3:54:LEU:HD21	25:D3:75:GLN:HB2	3.52	0.66
41:L4:143:GLU:O	87:L4:401:OHX:N2	2.29	0.66
74:O8:24:THR:HG23	74:O8:44:LYS:HB2	4.71	0.66
5:S3:72:LEU:HD22	12:C0:65:TYR:HD1	2.33	0.66
8:S6:148:SER:O	8:S6:150:GLU:N	2.28	0.66
9:S7:144:VAL:HG22	24:D2:49:GLU:HB3	3.51	0.66
10:S8:20:GLN:NE2	10:S8:22:ARG:O	5.04	0.66
1:2:878:G:O2'	15:C3:108:ASP:OD2	2.13	0.66
89:5:3402:SPS:H81	85:C:76:8AN:H8	1.78	0.66
36:5:1587:A:OP1	87:5:3905:OHX:N5	2.28	0.66
1:6:1738:U:O4	87:6:2028:OHX:N5	2.28	0.66
41:L4:326:ARG:O	44:L7:41:ARG:NH2	4.05	0.66
36:1:2663:G:H5'	42:L5:152:ARG:HD3	1.78	0.66
45:L8:153:ILE:HG22	45:L8:197:VAL:HG12	4.81	0.66
63:N7:77:TYR:HA	63:N7:80:LEU:HD12	2.20	0.66
4:S2:227:PRO:HA	4:S2:230:TRP:CE2	2.31	0.66
36:5:1615:C:H2'	36:5:1616:U:C6	2.30	0.66
36:5:3053:G:O6	87:5:4086:OHX:N3	2.29	0.66
18:C6:46:PHE:HA	18:C6:49:TYR:HB2	1.78	0.66
41:L4:205:PRO:HG2	41:L4:225:VAL:HG13	1.76	0.66
48:M1:108:GLU:HG2	48:M1:122:ILE:HG21	2.11	0.66
59:N3:66:LYS:HE3	59:N3:68:GLU:HB2	8.01	0.66
63:N7:62:VAL:O	63:N7:66:THR:OG1	3.22	0.66
8:S6:180:THR:HG23	8:S6:183:ARG:H	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2871:G:OP2	87:1:4071:OHX:N1	2.29	0.66
87:1:3813:OHX:N5	51:M5:204:LYS:O	2.28	0.66
1:2:1064:G:O6	87:2:2150:OHX:N5	2.28	0.66
1:6:1679:G:O6	87:6:2170:OHX:N4	2.29	0.66
44:L7:145:ARG:HA	44:L7:185:ILE:HD13	1.78	0.66
47:M0:208:ASN:HB3	47:M0:211:ARG:HH11	3.08	0.66
51:M5:96:ARG:HG2	51:M5:96:ARG:HH11	1.60	0.66
54:M8:91:ALA:HB3	64:N8:77:LYS:HE3	5.03	0.66
62:N6:3:LYS:HD2	62:N6:8:VAL:HG23	5.26	0.66
74:O8:46:ARG:NH2	74:O8:50:SER:O	3.31	0.66
35:SM:46:LYS:HA	36:5:1018:G:H4'	326.09	0.66
36:1:1409:G:O6	87:1:3960:OHX:N3	2.29	0.66
1:2:1695:G:H21	1:2:1706:C:H41	1.44	0.66
1:2:354:C:H5''	10:S8:16:ALA:HB2	1.78	0.66
1:6:489:C:O2'	1:6:490:C:O4'	2.13	0.66
23:D1:81:ASN:O	23:D1:83:TRP:N	2.29	0.66
8:S6:116:LYS:HD2	8:S6:125:THR:HG21	1.78	0.66
10:S8:76:THR:HB	10:S8:105:ASP:HB2	1.86	0.66
36:1:1010:G:N2	47:M0:193:ASP:OD2	2.29	0.65
36:1:3029:A:OP2	87:1:3967:OHX:N5	2.29	0.65
36:1:829:U:H3	36:1:895:A:N6	1.94	0.65
1:2:1183:A:N6	17:C5:122:THR:O	2.28	0.65
1:2:475:A:OP2	11:S9:126:ARG:NH1	2.29	0.65
16:C4:81:VAL:HG13	16:C4:115:ILE:HG23	3.32	0.65
26:D4:83:LYS:HE2	26:D4:96:LEU:HB3	1.76	0.65
42:L5:54:ARG:NH1	42:L5:148:ILE:O	2.28	0.65
36:1:1719:G:OP1	55:M9:110:ARG:NH2	2.29	0.65
75:O9:27:ILE:HD13	38:8:52:A:H62	75.95	0.65
36:1:2636:A:H5''	36:1:2637:A:H5'	1.78	0.65
36:1:2818:U:H6	36:1:2818:U:H5'	1.61	0.65
36:1:1661:G:O6	87:1:3781:OHX:N6	2.28	0.65
36:1:508:U:O4	87:1:3899:OHX:N6	2.29	0.65
1:2:1041:G:OP1	87:2:2123:OHX:N3	2.28	0.65
1:2:83:G:OP2	87:2:2034:OHX:N5	2.29	0.65
36:5:3112:G:N7	87:5:3834:OHX:N6	2.43	0.65
1:6:1680:G:O6	87:6:2170:OHX:N1	2.29	0.65
40:L3:147:GLU:OE2	40:L3:150:ARG:NH1	2.93	0.65
44:L7:33:ARG:NH2	36:5:595:G:OP1	231.66	0.65
9:S7:96:ARG:NH2	9:S7:128:ASP:OD2	2.28	0.65
36:1:2871:G:OP2	87:1:4071:OHX:N4	2.29	0.65
36:1:2902:A:OP1	46:L9:170:LYS:NZ	2.28	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:3308:C:N3	53:M7:69:ARG:NH1	2.44	0.65
37:7:91:G:H2'	37:7:92:A:C8	2.32	0.65
16:C4:99:GLN:NE2	28:D6:44:ILE:O	4.21	0.65
40:L3:30:LYS:O	87:5:4014:OHX:N1	249.33	0.65
42:L5:290:ILE:HG12	47:M0:206:LEU:HD21	5.51	0.65
53:M7:78:VAL:HG22	53:M7:79:THR:H	2.07	0.65
56:N0:8:GLN:HB2	56:N0:64:ILE:HD11	1.78	0.65
59:N3:132:ASN:N	59:N3:132:ASN:OD1	2.28	0.65
11:S9:27:GLU:HB3	11:S9:39:LYS:HD2	1.78	0.65
36:1:1806:A:OP2	87:1:3877:OHX:N4	2.29	0.65
36:1:2538:U:O2'	36:1:2541:U:O4	2.10	0.65
1:2:372:G:H5'	24:D2:88:LYS:HZ1	1.62	0.65
55:M9:60:LYS:NZ	36:5:1672:U:OP2	173.67	0.65
56:N0:161:LYS:NZ	36:5:3208:G:O3'	278.88	0.65
36:5:2311:G:OP2	87:5:3893:OHX:N2	2.29	0.65
51:M5:172:ARG:NH2	36:5:63:A:OP1	104.40	0.65
49:M3:58:VAL:HG13	36:5:75:G:H5''	88.87	0.65
1:6:1139:A:OP2	87:6:2038:OHX:N4	2.30	0.65
30:D8:52:ASP:OD1	30:D8:52:ASP:N	2.25	0.65
45:L8:78:PHE:C	45:L8:80:TYR:H	1.99	0.65
63:N7:88:ASP:HB3	63:N7:121:ARG:HH22	1.61	0.65
5:S3:66:ILE:O	5:S3:70:THR:OG1	2.13	0.65
7:S5:166:ARG:HD3	30:D8:45:LYS:HG3	1.78	0.65
7:S5:51:VAL:O	7:S5:65:ARG:NH2	2.28	0.65
1:2:1542:G:H22	1:2:1568:C:H1'	1.62	0.65
1:2:1051:G:N7	87:2:2142:OHX:N5	2.45	0.65
36:5:1717:U:H2'	36:5:1718:G:C8	2.32	0.65
2:S0:200:ASP:HB2	19:C7:85:VAL:HG22	1.79	0.65
36:1:2146:C:OP1	39:L2:200:ARG:NH1	2.30	0.65
47:M0:10:ARG:HG2	47:M0:11:TYR:CD1	2.62	0.65
50:M4:19:ARG:HA	50:M4:69:THR:HG22	3.32	0.65
51:M5:159:ARG:HB2	51:M5:164:LEU:HB2	2.62	0.65
4:S2:168:ARG:HD3	4:S2:170:ILE:HD11	1.78	0.65
5:S3:175:VAL:HG13	5:S3:182:LEU:HB2	1.76	0.65
6:S4:73:ASP:OD2	6:S4:122:LYS:NZ	2.28	0.65
36:5:2579:G:O6	87:5:3945:OHX:N3	2.30	0.65
42:L5:22:ARG:HA	42:L5:25:GLU:HG3	3.63	0.65
48:M1:94:ARG:O	48:M1:96:PHE:N	2.29	0.65
71:O5:10:ARG:NH1	71:O5:60:GLU:OE1	3.49	0.65
19:C7:33:ARG:NH2	34:SR:109:ASP:OD2	2.86	0.65
1:2:1623:C:H2'	1:2:1624:C:C6	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:828:A:OP2	87:5:4165:OHX:N6	2.30	0.65
1:6:1203:A:OP2	87:6:2096:OHX:N4	2.30	0.65
28:D6:30:ILE:HD11	28:D6:34:LYS:HD2	6.35	0.65
41:L4:328:ASN:OD1	44:L7:48:ASN:ND2	2.30	0.65
47:M0:99:ILE:HG12	47:M0:123:HIS:HB2	4.98	0.65
62:N6:57:LEU:HD22	62:N6:58:VAL:H	2.68	0.65
66:O0:58:TYR:OH	70:O4:97:GLU:OE2	2.09	0.65
5:S3:34:TYR:HE2	5:S3:37:VAL:HG13	2.08	0.65
10:S8:79:ALA:HB3	10:S8:103:GLN:HB3	1.77	0.65
1:2:1034:C:HO2'	24:D2:2:THR:N	1.95	0.65
1:2:912:U:H4'	1:2:913:G:H3'	1.78	0.65
40:L3:28:ARG:NH2	36:5:3140:G:N7	233.24	0.65
40:L3:385:LYS:NZ	36:5:3328:G:OP1	209.28	0.65
6:S4:66:MET:HB3	1:6:454:U:C4	377.16	0.65
38:8:77:A:OP2	87:8:216:OHX:N1	2.30	0.65
24:D2:29:PRO:HB2	24:D2:58:SER:HB2	1.79	0.65
40:L3:303:LYS:HD2	40:L3:361:THR:HG21	1.92	0.65
47:M0:142:ASP:OD1	47:M0:178:ARG:NH2	2.74	0.65
41:L4:281:ILE:HD12	54:M8:29:LEU:HG	1.79	0.65
62:N6:11:ASP:HB3	62:N6:14:LYS:HG3	2.30	0.65
78:Q2:72:LEU:HD11	78:Q2:83:LEU:HB2	2.77	0.65
5:S3:69:LEU:HA	5:S3:72:LEU:HD12	1.79	0.65
6:S4:90:ILE:HD11	6:S4:101:LEU:HD11	2.39	0.65
36:1:964:G:OP1	87:1:3860:OHX:N2	2.29	0.65
36:5:3280:U:O2'	36:5:3281:U:H5''	1.96	0.65
38:4:155:A:H5'	45:L8:185:ARG:CZ	2.27	0.65
46:L9:8:GLN:NE2	46:L9:69:ARG:HG2	3.34	0.65
62:N6:53:ASP:HB2	62:N6:110:HIS:HD2	1.62	0.65
66:O0:37:GLY:O	66:O0:39:SER:N	2.82	0.65
73:O7:52:LYS:HA	73:O7:55:ARG:HD2	3.41	0.65
73:O7:88:ALA:O	87:O7:103:OHX:N3	2.30	0.65
4:S2:225:LEU:HD12	24:D2:68:ARG:HA	3.19	0.65
1:2:330:G:OP2	10:S8:172:ARG:NH1	2.30	0.65
34:SR:132:LYS:HB2	34:SR:134:TRP:HE1	1.61	0.65
34:SR:302:PHE:HA	34:SR:312:VAL:HG12	1.78	0.65
36:1:1015:U:O2'	36:1:1017:C:OP2	2.15	0.65
36:1:2572:C:O2'	36:1:2573:G:O4'	2.15	0.65
75:O9:2:ALA:N	36:5:1493:G:O6	123.48	0.65
36:5:2960:C:OP1	87:5:3887:OHX:N6	2.29	0.65
53:M7:101:ASN:OD1	36:5:388:G:N2	115.17	0.65
1:6:679:U:O4	87:6:2141:OHX:N2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:C4:81:VAL:H	16:C4:115:ILE:HG22	1.62	0.65
30:D8:58:GLU:O	30:D8:60:GLU:N	3.88	0.65
36:1:3115:C:OP1	46:L9:62:ARG:NH2	2.29	0.65
52:M6:27:LEU:HD22	52:M6:101:ARG:HB2	1.78	0.65
78:Q2:28:TYR:HB3	78:Q2:69:VAL:HB	1.78	0.65
8:S6:163:THR:HA	8:S6:168:THR:HA	1.77	0.65
36:1:3115:C:O2'	36:1:3117:C:N4	2.30	0.64
36:1:3199:G:H5''	50:M4:6:ILE:HG21	1.78	0.64
36:5:1819:U:O4	87:5:3963:OHX:N5	2.31	0.64
10:S8:141:ARG:NH2	1:6:196:G:N7	280.24	0.64
32:E0:43:ARG:HH12	1:6:590:C:H5''	420.55	0.64
1:6:828:U:H2'	1:6:829:A:H5''	1.79	0.64
1:6:833:U:O4	87:6:2067:OHX:N1	2.29	0.64
1:2:1459:C:OP1	20:C8:126:ARG:NH2	2.30	0.64
27:D5:60:VAL:HG13	27:D5:101:TYR:HB2	2.58	0.64
46:L9:24:ILE:HD11	46:L9:39:LYS:HD2	3.85	0.64
54:M8:86:THR:HG22	54:M8:105:ARG:HB2	1.78	0.64
63:N7:38:PHE:O	63:N7:40:HIS:ND1	2.28	0.64
36:1:361:A:O3'	73:O7:45:ARG:NH2	2.30	0.64
36:1:2307:G:O2'	36:1:2310:U:OP2	2.14	0.64
36:1:3276:G:H1	69:O3:60:ARG:HH22	1.43	0.64
1:2:1335:U:H2'	1:2:1336:A:C8	2.32	0.64
36:5:1691:U:OP1	87:5:4163:OHX:N2	2.30	0.64
36:5:2546:C:H2'	36:5:2547:A:C8	2.33	0.64
8:S6:176:GLN:HG2	1:6:169:A:H5''	329.65	0.64
1:6:1060:U:O2'	87:6:2156:OHX:N3	2.30	0.64
8:S6:176:GLN:NE2	1:6:268:C:OP1	336.01	0.64
13:C1:5:LEU:O	13:C1:7:VAL:N	2.27	0.64
36:1:3024:A:H5''	46:L9:96:HIS:CD2	2.32	0.64
61:N5:69:SER:OG	61:N5:72:ALA:N	2.30	0.64
64:N8:125:VAL:HG21	64:N8:138:ILE:HD13	1.79	0.64
11:S9:106:GLU:O	11:S9:111:THR:OG1	3.24	0.64
34:SR:133:VAL:O	34:SR:141:LEU:N	2.26	0.64
36:5:1104:G:H2'	36:5:1105:A:H8	1.62	0.64
36:5:1506:A:H1'	36:5:1848:G:O6	1.98	0.64
36:5:2429:G:OP2	87:5:3958:OHX:N5	2.30	0.64
21:C9:15:ILE:HD11	21:C9:63:ARG:HD3	3.25	0.64
26:D4:20:ARG:HA	26:D4:76:TYR:HA	2.56	0.64
28:D6:3:LYS:HD3	28:D6:6:ALA:HA	3.71	0.64
39:L2:211:HIS:O	39:L2:213:GLY:N	3.80	0.64
46:L9:79:ILE:O	46:L9:81:GLY:N	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:M0:161:GLY:O	47:M0:163:GLN:NE2	2.93	0.64
36:1:670:C:OP1	54:M8:147:ARG:NH2	2.30	0.64
55:M9:109:TYR:HB3	55:M9:115:ILE:HG12	3.98	0.64
2:S0:164:ASN:HA	2:S0:170:ILE:HG12	3.07	0.64
5:S3:40:ARG:HG2	22:D0:110:PRO:HB3	1.78	0.64
36:1:2623:G:H2'	36:1:2624:G:H8	1.62	0.64
1:2:118:U:O4	87:2:2130:OHX:N5	2.30	0.64
1:2:820:U:H2'	1:2:821:U:H4'	1.79	0.64
37:3:7:G:H5''	42:L5:22:ARG:HD3	1.79	0.64
36:5:1530:U:OP1	87:5:3905:OHX:N1	2.29	0.64
55:M9:39:ASN:ND2	36:5:1765:U:OP2	95.12	0.64
1:6:1711:C:H2'	1:6:1712:A:H5''	1.79	0.64
24:D2:37:PHE:CZ	24:D2:103:ILE:HD11	5.09	0.64
29:D7:19:HIS:HE1	29:D7:21:LEU:HD12	3.73	0.64
41:L4:229:ASN:OD1	41:L4:231:ALA:N	2.97	0.64
49:M3:70:ARG:HD2	49:M3:71:ALA:O	1.98	0.64
5:S3:94:ARG:HH21	35:SM:134:ASP:CG	1.99	0.64
36:1:2157:G:N7	39:L2:152:SER:OG	2.28	0.64
36:1:2983:C:OP1	87:1:4097:OHX:N1	2.30	0.64
36:1:2783:U:OP2	87:1:4110:OHX:N5	2.31	0.64
1:2:780:A:H8	26:D4:8:ARG:HB3	1.63	0.64
8:S6:87:ARG:NH2	1:6:161:U:OP2	316.49	0.64
74:O8:32:ASN:O	74:O8:34:ALA:N	2.30	0.64
6:S4:121:TYR:OH	6:S4:235:TYR:O	3.69	0.64
36:1:1624:G:O6	87:1:3937:OHX:N2	2.30	0.64
36:1:2878:G:O6	87:1:4072:OHX:N2	2.29	0.64
36:1:3119:U:OP2	87:1:3787:OHX:N4	2.30	0.64
36:1:542:G:O6	87:1:3951:OHX:N2	2.31	0.64
36:5:1538:G:OP2	87:5:4169:OHX:N2	2.30	0.64
1:6:158:U:O2'	1:6:160:C:OP2	2.16	0.64
45:L8:78:PHE:O	45:L8:79:GLN:HB3	2.71	0.64
47:M0:175:ASN:OD1	47:M0:176:LEU:N	4.89	0.64
54:M8:23:ASN:HB3	54:M8:26:LEU:HB2	1.78	0.64
56:N0:8:GLN:HG3	56:N0:26:ARG:HE	1.63	0.64
56:N0:75:PHE:CE1	56:N0:99:ARG:HG3	3.09	0.64
9:S7:117:THR:HG22	9:S7:120:ALA:H	2.66	0.64
9:S7:73:VAL:O	9:S7:75:THR:N	2.29	0.64
36:1:2287:C:O2	87:1:3810:OHX:N1	2.30	0.64
36:1:2814:G:N7	87:1:4071:OHX:N2	2.45	0.64
36:1:3042:U:OP2	36:1:3092:C:N4	2.31	0.64
1:2:1680:G:O6	87:2:2078:OHX:N5	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:473:A:H5'	1:2:769:A:H1'	1.79	0.64
12:C0:62:GLN:NE2	31:D9:25:SER:OG	3.02	0.64
41:L4:181:VAL:O	41:L4:183:LYS:N	2.31	0.64
53:M7:178:ALA:HA	53:M7:181:ARG:HB3	1.80	0.64
75:O9:27:ILE:HG23	75:O9:30:ARG:HE	1.62	0.64
7:S5:163:SER:HB2	30:D8:48:VAL:HG13	1.79	0.64
36:1:3103:A:OP2	87:1:4065:OHX:N5	2.31	0.64
1:2:1542:G:N2	1:2:1568:C:H1'	2.13	0.64
1:6:1561:U:H4'	1:6:1599:C:H4'	1.80	0.64
22:D0:106:ILE:HG13	22:D0:107:THR:H	1.63	0.64
39:L2:227:ARG:HB2	39:L2:239:ALA:HB2	3.65	0.64
41:L4:114:ASN:HB2	41:L4:117:GLU:HB2	2.13	0.64
61:N5:33:ARG:HE	36:5:1580:A:N6	154.12	0.64
69:O3:10:LYS:HB2	69:O3:33:GLU:HG3	1.80	0.64
4:S2:81:MET:HB2	4:S2:101:VAL:HB	2.51	0.64
87:S9:201:OHX:N2	1:6:759:U:OP1	382.41	0.64
56:N0:96:ASP:OD1	56:N0:97:VAL:N	2.31	0.64
43:L6:3:ALA:HB2	68:O2:77:ALA:HB2	1.80	0.64
6:S4:124:GLY:HA2	6:S4:142:HIS:CE1	2.33	0.64
34:SR:248:ASN:HD21	34:SR:298:GLY:HA3	1.62	0.64
55:M9:85:ARG:NH2	36:5:1916:U:O3'	231.85	0.64
15:C3:114:ARG:HH11	15:C3:114:ARG:HG2	1.63	0.64
15:C3:22:ALA:HB1	15:C3:23:PRO:HA	1.81	0.64
15:C3:27:LYS:H	15:C3:27:LYS:HE2	1.62	0.64
39:L2:116:VAL:HG13	39:L2:126:LEU:HB2	1.95	0.64
45:L8:48:ARG:HH21	45:L8:49:TYR:HE2	1.99	0.64
67:O1:72:ARG:NH1	67:O1:105:GLN:O	2.19	0.64
9:S7:35:LYS:O	9:S7:37:GLU:N	2.31	0.64
36:5:1049:C:H2'	36:5:1050:U:C6	2.33	0.63
53:M7:69:ARG:HD3	36:5:3308:C:O2	186.82	0.63
36:5:90:C:H2'	36:5:91:G:H5'	1.79	0.63
1:6:413:U:H2'	1:6:414:C:H6	1.63	0.63
21:C9:49:ASP:OD1	21:C9:53:TRP:N	2.30	0.63
40:L3:81:THR:HG23	40:L3:205:VAL:HG21	4.31	0.63
42:L5:110:LEU:HA	42:L5:113:LEU:HB2	2.76	0.63
51:M5:43:THR:OG1	51:M5:131:GLU:OE2	2.14	0.63
56:N0:23:LYS:O	57:N1:146:ASN:ND2	2.29	0.63
50:M4:55:ARG:HD3	56:N0:70:THR:HB	3.55	0.63
36:1:2701:U:OP2	57:N1:22:HIS:ND1	2.30	0.63
36:1:180:C:H2'	36:1:181:U:H6	1.64	0.63
36:1:2401:A:H5'	41:L4:70:ALA:HB2	1.78	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2960:C:H2'	36:1:2961:G:C8	2.33	0.63
38:4:122:U:H2'	38:4:123:G:H8	1.63	0.63
42:L5:140:ARG:HD3	36:5:1080:A:OP1	228.69	0.63
36:5:1196:C:O2	87:5:3914:OHX:N1	2.31	0.63
16:C4:123:SER:HB2	1:6:885:G:H21	287.73	0.63
14:C2:129:GLU:HA	14:C2:133:LEU:HD22	1.81	0.63
20:C8:131:LEU:HA	20:C8:145:ARG:HH12	1.63	0.63
28:D6:79:ILE:HA	28:D6:84:VAL:HG11	1.81	0.63
51:M5:178:HIS:CD2	51:M5:179:LYS:HG2	5.29	0.63
54:M8:36:LEU:O	54:M8:40:THR:OG1	2.15	0.63
2:S0:163:ASN:O	2:S0:165:ARG:N	2.67	0.63
36:1:1194:G:OP1	87:1:3859:OHX:N3	2.32	0.63
36:1:155:G:H5''	36:1:156:G:C8	2.32	0.63
36:1:2343:C:H2'	36:1:2344:U:H6	1.64	0.63
36:1:847:A:H2'	36:1:848:A:C8	2.33	0.63
28:D6:3:LYS:HA	1:6:1792:G:H5''	340.47	0.63
1:6:1140:G:OP2	87:6:2038:OHX:N1	2.31	0.63
1:6:235:G:H2'	1:6:236:A:C8	2.32	0.63
47:M0:66:GLU:OE1	47:M0:69:ARG:NH2	2.32	0.63
48:M1:166:LYS:HD3	48:M1:167:TYR:CE1	2.34	0.63
51:M5:27:VAL:HB	51:M5:122:ASN:ND2	2.13	0.63
73:O7:28:HIS:CD2	73:O7:31:LYS:HE2	2.48	0.63
6:S4:17:HIS:HB2	6:S4:108:ARG:HA	1.81	0.63
34:SR:286:GLU:OE2	87:SR:401:OHX:N6	4.75	0.63
36:1:1231:A:O2'	36:1:1261:G:O2'	2.17	0.63
36:1:2579:G:O6	87:1:3823:OHX:N2	2.31	0.63
1:2:1720:G:O6	87:2:2050:OHX:N5	2.32	0.63
65:N9:50:THR:HB	36:5:1073:U:H1'	207.58	0.63
36:5:1148:G:N7	87:5:4128:OHX:N5	2.45	0.63
7:S5:25:LEU:HB2	18:C6:27:GLY:HA3	2.56	0.63
41:L4:3:ARG:HH11	41:L4:22:LEU:HD12	1.63	0.63
59:N3:135:VAL:HG11	60:N4:26:SER:HB3	1.80	0.63
36:1:1632:A:OP1	63:N7:69:LYS:NZ	2.31	0.63
68:O2:9:ILE:HG23	68:O2:63:THR:HB	3.03	0.63
4:S2:163:GLY:O	4:S2:165:VAL:N	4.52	0.63
6:S4:130:GLN:HB3	6:S4:138:TYR:CZ	4.33	0.63
36:1:1508:C:OP1	53:M7:127:ARG:NH2	2.32	0.63
36:1:1553:U:H4'	36:1:1554:U:H5'	1.79	0.63
36:1:412:G:OP1	53:M7:62:ARG:NH1	2.31	0.63
1:2:1349:G:H1'	1:2:1379:C:H42	1.63	0.63
1:6:696:C:H4'	1:6:697:C:H6	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:C3:151:ASN:O	87:C3:201:OHX:N3	2.69	0.63
27:D5:60:VAL:HG22	27:D5:101:TYR:HB2	1.79	0.63
30:D8:15:VAL:HA	30:D8:28:VAL:HG22	1.80	0.63
33:E1:121:CYS:HB3	33:E1:130:VAL:HG11	5.77	0.63
39:L2:52:SER:HB3	39:L2:191:LEU:HD12	5.21	0.63
40:L3:56:ILE:HD13	40:L3:76:VAL:HG21	1.81	0.63
42:L5:148:ILE:HG23	42:L5:151:GLN:HB3	2.43	0.63
44:L7:25:GLN:HA	44:L7:28:ALA:HB3	1.80	0.63
51:M5:15:GLN:OE1	87:5:4143:OHX:N6	151.03	0.63
54:M8:170:ARG:O	54:M8:171:LYS:HB2	2.56	0.63
66:O0:45:ALA:HB2	66:O0:77:LEU:HD22	3.36	0.63
1:2:580:A:H5''	5:S3:143:ARG:HH12	1.63	0.63
1:6:1006:C:O2	87:6:2111:OHX:N1	2.31	0.63
39:L2:114:SER:OG	39:L2:115:ASN:N	2.31	0.63
40:L3:227:GLU:HB3	40:L3:232:ARG:HB2	2.05	0.63
41:L4:22:LEU:HD22	41:L4:23:PRO:HD2	1.80	0.63
42:L5:76:ALA:HB3	42:L5:109:THR:HG22	1.79	0.63
36:1:2853:A:O3'	47:M0:64:ALA:HB2	1.99	0.63
62:N6:36:SER:OG	62:N6:106:ILE:O	2.13	0.63
5:S3:160:SER:O	1:6:1420:C:O2'	416.47	0.63
34:SR:42:LEU:HD21	34:SR:82:SER:HB3	1.80	0.63
36:1:1580:A:H5'	36:1:2522:G:C5	2.33	0.63
36:1:3289:G:O6	87:1:4030:OHX:N4	2.32	0.63
1:2:1469:A:H4'	1:2:1541:G:H4'	1.80	0.63
1:2:58:U:OP2	87:2:2145:OHX:N3	2.32	0.63
1:2:623:A:OP1	87:2:2136:OHX:N1	2.32	0.63
36:5:1541:G:OP2	87:5:4001:OHX:N1	2.31	0.63
36:5:3227:A:H2'	36:5:3228:C:H5'	1.81	0.63
36:5:1861:G:O6	87:5:3966:OHX:N2	2.32	0.63
1:6:1595:U:H3	1:6:1600:A:H2	1.45	0.63
17:C5:15:HIS:H	17:C5:22:LEU:HD22	4.01	0.63
47:M0:54:SER:HB3	47:M0:135:ILE:HD11	1.80	0.63
63:N7:10:VAL:HB	63:N7:83:THR:HG21	1.81	0.63
4:S2:67:GLN:HA	4:S2:70:ASP:HB3	1.79	0.63
34:SR:237:GLN:HG2	34:SR:261:LYS:HE2	1.80	0.63
36:1:3214:U:OP2	50:M4:128:ARG:NH2	2.31	0.63
36:1:1878:G:OP1	87:1:3824:OHX:N4	2.31	0.63
36:1:715:A:H5''	64:N8:114:GLY:O	1.99	0.63
1:6:138:A:H62	1:6:266:A:H61	1.47	0.63
16:C4:35:GLY:HA3	1:6:919:A:H5'	270.65	0.63
15:C3:115:LEU:HD22	15:C3:119:GLU:HG3	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:C9:65:ILE:HG12	21:C9:71:VAL:HG23	1.80	0.63
41:L4:145:ILE:O	87:L4:401:OHX:N5	2.32	0.63
46:L9:49:ASN:O	46:L9:51:GLN:N	2.32	0.63
48:M1:109:HIS:HD2	48:M1:123:PHE:H	1.47	0.63
56:N0:42:TRP:HE1	56:N0:58:ILE:HD11	3.08	0.63
71:O5:85:THR:HG22	71:O5:88:LEU:H	3.81	0.63
78:Q2:46:LYS:O	87:Q2:503:OHX:N6	2.32	0.63
4:S2:170:ILE:HB	4:S2:197:TYR:HB2	2.50	0.63
5:S3:168:ILE:HG22	5:S3:189:MET:HB2	2.00	0.63
1:2:1316:G:O2'	1:2:1401:A:O2'	2.17	0.63
1:2:1492:A:HO2'	1:2:1493:A:H8	1.47	0.63
1:2:1525:A:H2'	1:2:1526:A:C8	2.34	0.63
36:5:2255:A:H5'	36:5:2261:G:H22	1.64	0.63
36:5:2514:U:OP1	36:5:2514:U:H6	1.82	0.63
36:5:3242:G:H5''	36:5:3245:A:C8	2.33	0.63
13:C1:6:THR:O	13:C1:8:GLN:N	2.25	0.63
28:D6:10:ARG:HB2	28:D6:34:LYS:HA	1.81	0.63
52:M6:22:VAL:HG11	52:M6:120:VAL:HG11	2.79	0.63
52:M6:15:LEU:HD21	52:M6:125:ARG:HG3	1.81	0.63
57:N1:8:ARG:O	57:N1:11:THR:OG1	2.16	0.63
9:S7:132:PRO:O	9:S7:133:THR:OG1	4.60	0.63
9:S7:126:LEU:HB2	9:S7:173:TYR:HE2	4.61	0.63
9:S7:32:PRO:HD2	9:S7:34:LEU:HB2	1.80	0.63
36:1:1611:G:H2'	36:1:1612:A:H8	1.63	0.62
36:1:1895:A:O2'	36:1:3053:G:H4'	1.99	0.62
1:2:1547:A:OP1	20:C8:115:ARG:NH2	2.28	0.62
1:2:973:A:H2'	1:2:974:A:H8	1.62	0.62
51:M5:49:ARG:NH2	36:5:115:A:OP1	101.77	0.62
71:O5:81:ARG:NH2	36:5:18:G:OP1	76.52	0.62
36:5:3065:G:O6	87:5:4013:OHX:N3	2.32	0.62
36:5:3366:G:H2'	36:5:3367:C:C6	2.34	0.62
39:L2:21:ARG:HD3	36:5:824:C:H5''	171.21	0.62
1:6:453:U:O4	87:6:2027:OHX:N4	2.32	0.62
17:C5:126:VAL:HG13	17:C5:127:ARG:H	1.64	0.62
39:L2:46:LYS:HD2	39:L2:62:VAL:HG11	1.79	0.62
45:L8:116:VAL:HG11	45:L8:123:GLN:HA	1.81	0.62
47:M0:77:THR:O	47:M0:81:GLY:N	2.40	0.62
48:M1:16:LYS:HG2	48:M1:130:VAL:HG13	2.80	0.62
53:M7:138:LYS:HG3	53:M7:140:GLU:HG3	1.80	0.62
53:M7:23:ARG:HE	53:M7:125:GLN:HG3	1.64	0.62
36:1:2736:A:OP1	57:N1:92:ARG:NH1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:N6:60:ARG:NH2	36:5:190:U:H2'	84.92	0.62
65:N9:20:GLY:O	65:N9:21:ILE:HB	2.47	0.62
7:S5:37:GLN:HB3	18:C6:53:LEU:HD22	1.81	0.62
36:1:3054:U:OP2	87:1:3782:OHX:N3	2.32	0.62
1:2:515:A:OP2	87:2:2038:OHX:N3	2.32	0.62
36:5:508:U:O4	87:5:3935:OHX:N1	2.32	0.62
24:D2:105:THR:HG22	1:6:804:A:N3	367.84	0.62
15:C3:64:ARG:NH2	1:6:861:U:OP1	347.67	0.62
20:C8:83:ALA:O	20:C8:89:GLN:NE2	3.31	0.62
47:M0:84:ALA:O	47:M0:140:THR:HB	2.26	0.62
36:1:2635:A:H2	57:N1:10:ARG:HH12	1.45	0.62
62:N6:111:LEU:HD23	62:N6:116:LYS:HE3	1.80	0.62
66:O0:99:ASP:N	66:O0:99:ASP:OD2	2.32	0.62
74:O8:11:PHE:HD1	74:O8:12:LEU:HD22	1.79	0.62
7:S5:99:MET:HB2	7:S5:180:ARG:NH2	5.03	0.62
34:SR:135:THR:HG22	34:SR:141:LEU:HD11	2.11	0.62
36:1:992:A:H5''	57:N1:43:LYS:HD3	1.80	0.62
1:2:320:U:H3'	1:2:321:C:C5'	2.26	0.62
36:5:2254:U:H2'	36:5:2261:G:N2	2.13	0.62
36:5:2904:U:OP1	87:5:3955:OHX:N3	2.32	0.62
36:5:415:G:OP2	87:5:4140:OHX:N4	2.32	0.62
5:S3:27:ARG:HD2	12:C0:60:SER:HB2	1.81	0.62
27:D5:61:SER:H	27:D5:64:VAL:HB	1.65	0.62
39:L2:224:THR:HG21	36:5:2201:G:H21	223.46	0.62
41:L4:38:VAL:HG13	41:L4:113:VAL:HG11	2.35	0.62
43:L6:131:LYS:HG2	43:L6:133:GLU:HB3	1.79	0.62
46:L9:126:VAL:HG21	46:L9:161:LEU:HA	1.81	0.62
58:N2:37:LEU:HD23	58:N2:41:ILE:HD11	1.81	0.62
59:N3:54:LEU:HD21	59:N3:119:GLY:HA3	2.93	0.62
61:N5:105:VAL:HG12	61:N5:130:TYR:CD2	2.35	0.62
66:O0:24:THR:HG22	66:O0:91:SER:HB3	1.81	0.62
2:S0:41:ARG:HE	2:S0:45:VAL:HB	1.62	0.62
36:1:2534:G:H2'	36:1:2535:A:H8	1.65	0.62
1:2:1056:U:O4	87:2:2150:OHX:N6	2.32	0.62
36:5:2812:C:H2'	36:5:2813:A:C8	2.30	0.62
14:C2:66:VAL:HG11	14:C2:71:ILE:HD12	1.82	0.62
16:C4:19:ILE:HB	16:C4:83:ILE:HD12	1.80	0.62
17:C5:18:ARG:NH1	20:C8:90:ASN:OD1	4.47	0.62
23:D1:3:ASN:HD21	23:D1:7:GLN:HB2	2.42	0.62
25:D3:125:VAL:HG12	25:D3:126:LYS:HG3	1.80	0.62
33:E1:135:HIS:HB2	33:E1:138:ARG:HB3	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L4:299:ILE:HG23	54:M8:39:ARG:HB3	1.86	0.62
55:M9:106:LEU:HD21	55:M9:123:LEU:HB3	1.82	0.62
78:Q2:66:LYS:HG2	36:5:2793:G:H5'	211.07	0.62
78:Q2:17:CYS:CB	78:Q2:77:CYS:SG	3.22	0.62
2:S0:11:PRO:HA	2:S0:14:ALA:HB3	2.77	0.62
5:S3:176:LEU:HA	5:S3:181:VAL:HG12	2.20	0.62
9:S7:164:TYR:CE1	9:S7:165:LYS:HG3	2.76	0.62
11:S9:96:VAL:HA	11:S9:99:LEU:HD22	1.81	0.62
35:SM:140:ASP:OD1	35:SM:140:ASP:N	2.32	0.62
34:SR:45:TRP:HA	34:SR:57:PRO:HA	1.81	0.62
36:1:2534:G:O6	87:1:3893:OHX:N6	2.33	0.62
1:2:1157:A:OP1	87:2:2101:OHX:N2	2.33	0.62
36:5:1635:G:N2	36:5:1638:A:OP2	2.25	0.62
36:5:1119:C:OP2	87:5:3900:OHX:N2	2.32	0.62
1:6:1238:A:OP2	87:6:2063:OHX:N1	2.32	0.62
55:M9:172:ARG:NH1	1:6:852:C:OP2	322.10	0.62
28:D6:87:ARG:NH2	28:D6:91:ASP:O	3.03	0.62
58:N2:59:ASP:OD1	58:N2:60:GLY:N	3.70	0.62
59:N3:83:LYS:NZ	59:N3:84:SER:O	3.03	0.62
65:N9:14:ARG:HH12	65:N9:18:ARG:HH11	2.43	0.62
4:S2:241:ASP:HA	4:S2:244:SER:HB3	4.35	0.62
36:1:1038:C:H4'	42:L5:5:LYS:NZ	2.14	0.62
36:5:839:C:O2'	36:5:1724:U:OP1	2.11	0.62
36:5:1724:U:H1'	36:5:1725:C:C6	2.34	0.62
29:D7:20:LYS:NZ	1:6:959:U:OP2	349.48	0.62
39:L2:21:ARG:NH1	36:5:825:U:OP1	172.76	0.62
41:L4:24:ALA:HB2	41:L4:264:SER:HB2	1.81	0.62
44:L7:138:TYR:HE2	44:L7:233:GLU:HG2	1.64	0.62
48:M1:47:GLN:HG3	48:M1:67:VAL:HG12	1.82	0.62
54:M8:64:VAL:HG12	54:M8:93:ILE:HD11	4.61	0.62
63:N7:36:HIS:CD2	63:N7:74:VAL:HG11	4.13	0.62
79:Q3:84:ARG:HG3	79:Q3:87:ARG:NH2	5.47	0.62
5:S3:137:VAL:HB	5:S3:185:LYS:HB2	1.81	0.62
11:S9:54:ARG:NH2	1:6:761:G:OP1	396.08	0.62
36:1:1651:U:H2'	36:1:1652:G:H8	1.65	0.62
36:1:1798:A:H2'	36:1:1799:A:C8	2.34	0.62
36:1:980:A:H2'	36:1:981:U:N1	2.14	0.62
36:5:900:G:H1'	36:5:1589:A:H61	1.62	0.62
36:5:3089:C:H2'	36:5:3090:U:O4'	2.00	0.62
1:6:1161:C:H1'	1:6:1619:C:H42	1.63	0.62
15:C3:101:HIS:HA	15:C3:104:ARG:HE	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:4:140:G:O3'	51:M5:109:ARG:NH1	2.31	0.62
59:N3:39:VAL:O	59:N3:42:SER:OG	3.20	0.62
38:4:70:G:O6	87:O7:103:OHX:N1	2.32	0.62
4:S2:227:PRO:HA	4:S2:230:TRP:CD1	2.92	0.62
36:1:3197:G:H2'	36:1:3198:U:H5''	1.82	0.62
36:1:3316:A:OP1	36:1:3318:G:N2	2.31	0.62
36:1:3064:U:O4	87:1:4033:OHX:N6	2.33	0.62
1:2:520:A:H2'	1:2:521:A:C8	2.35	0.62
1:2:569:C:H41	25:D3:69:ARG:HH12	1.47	0.62
38:4:135:G:OP2	61:N5:56:ARG:NH2	2.33	0.62
36:5:901:G:H2'	36:5:902:G:H8	1.64	0.62
18:C6:40:GLU:OE2	18:C6:45:ARG:NH2	3.71	0.62
22:D0:58:LEU:HD12	22:D0:88:LYS:HB3	2.80	0.62
40:L3:81:THR:HG22	40:L3:321:PHE:HA	5.28	0.62
41:L4:10:SER:OG	41:L4:13:GLY:O	2.15	0.62
52:M6:73:PHE:CD2	52:M6:78:ARG:HG2	3.03	0.62
56:N0:155:ARG:HD3	56:N0:172:TYR:CG	2.52	0.62
75:O9:37:TYR:HD2	75:O9:37:TYR:H	1.47	0.62
87:1:3889:OHX:N5	37:3:86:U:O2	2.33	0.62
1:2:1592:A:H2'	1:2:1593:A:H8	1.64	0.62
1:2:1738:U:H2'	1:2:1739:C:C6	2.35	0.62
13:C1:39:GLY:HA3	1:6:246:G:H21	326.50	0.62
18:C6:7:VAL:HG21	18:C6:92:TYR:HA	2.29	0.62
33:E1:108:VAL:HB	33:E1:114:VAL:HG22	1.81	0.62
46:L9:167:VAL:HB	46:L9:172:ILE:HG22	1.81	0.62
56:N0:133:ALA:HA	56:N0:141:LYS:NZ	2.14	0.62
63:N7:4:PHE:CE2	66:O0:35:ARG:HA	2.35	0.62
64:N8:47:LYS:O	64:N8:49:HIS:N	2.70	0.62
36:1:1926:C:H5''	79:Q3:7:LYS:HD2	1.82	0.62
10:S8:122:GLY:O	87:S8:301:OHX:N6	2.32	0.62
36:1:1110:U:H2'	36:1:1111:U:C6	2.35	0.62
36:1:3174:A:H2'	36:1:3175:U:H5'	1.82	0.62
36:1:533:A:O2'	36:1:535:G:OP2	2.18	0.62
1:2:1520:U:OP2	21:C9:75:LYS:NZ	2.26	0.62
55:M9:8:LYS:NZ	36:5:1473:G:OP2	126.42	0.62
1:6:1767:G:OP1	1:6:1770:U:H4'	2.00	0.62
12:C0:32:HIS:CD2	12:C0:33:GLU:H	2.55	0.62
16:C4:131:GLY:O	16:C4:133:ARG:N	3.05	0.62
45:L8:81:THR:OG1	45:L8:82:LEU:N	2.33	0.62
71:O5:78:LYS:HA	71:O5:81:ARG:HD2	1.82	0.62
78:Q2:35:LEU:HD23	78:Q2:35:LEU:H	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:643:U:O2'	36:1:1153:A:N1	2.32	0.61
36:1:2094:C:H2'	36:1:2095:G:H8	1.65	0.61
36:1:2225:U:H2'	36:1:2226:U:C6	2.35	0.61
36:1:3118:C:H4'	76:Q0:106:ARG:HH22	1.65	0.61
36:1:2677:G:OP2	87:1:3943:OHX:N4	2.33	0.61
36:1:439:C:H3'	36:1:440:A:C8	2.35	0.61
36:5:1307:G:H1'	36:5:1308:A:C8	2.35	0.61
1:6:1315:U:OP1	1:6:1328:G:N2	2.32	0.61
1:6:1485:C:OP1	87:6:2083:OHX:N5	2.33	0.61
32:E0:31:LYS:NZ	1:6:544:A:O3'	420.02	0.61
14:C2:38:HIS:O	14:C2:125:ASN:ND2	2.33	0.61
18:C6:63:ILE:HD12	18:C6:65:ILE:HD11	4.00	0.61
29:D7:23:THR:HG21	29:D7:29:ARG:HH22	4.35	0.61
43:L6:131:LYS:HD3	43:L6:132:ALA:H	5.61	0.61
9:S7:83:LYS:HE3	9:S7:84:LYS:HE2	1.82	0.61
35:SM:41:SER:O	35:SM:43:ASP:N	2.32	0.61
36:1:1307:G:H1'	36:1:1308:A:C8	2.35	0.61
36:1:2700:G:H5''	57:N1:17:ARG:HB2	1.80	0.61
36:1:3259:U:H5''	36:1:3261:C:H5	1.64	0.61
36:1:3018:C:OP2	87:1:3884:OHX:N2	2.33	0.61
36:1:978:G:O2'	36:1:979:U:O2	2.17	0.61
1:2:1102:G:OP2	25:D3:7:ARG:NH1	2.33	0.61
1:2:1657:U:N3	87:2:2058:OHX:N2	2.48	0.61
36:5:3026:G:N7	87:5:3855:OHX:N3	2.48	0.61
36:5:582:G:O6	87:5:3935:OHX:N5	2.33	0.61
1:6:1521:G:O2'	1:6:1523:G:OP2	2.08	0.61
38:8:82:U:O5'	87:8:228:OHX:N2	2.33	0.61
23:D1:74:GLN:HG2	23:D1:79:LEU:HB2	5.57	0.61
32:E0:18:THR:HG21	1:6:584:C:H1'	391.39	0.61
44:L7:90:LYS:NZ	36:5:1158:A:OP2	242.14	0.61
51:M5:14:LYS:HE2	51:M5:120:TRP:HZ3	1.64	0.61
52:M6:182:ASN:O	52:M6:186:ALA:N	3.51	0.61
1:2:1738:U:O4	87:2:2008:OHX:N4	2.33	0.61
1:2:636:A:H5''	24:D2:31:SER:HB3	1.81	0.61
36:5:1878:G:H2'	36:5:1879:A:O4'	2.00	0.61
36:5:1222:G:O6	87:5:4036:OHX:N1	2.33	0.61
1:6:1062:A:OP1	87:6:2181:OHX:N5	2.33	0.61
14:C2:61:VAL:HG13	14:C2:121:VAL:HG23	1.82	0.61
18:C6:32:ASN:N	18:C6:67:VAL:O	2.29	0.61
26:D4:117:LYS:HG2	1:6:159:U:H5'	332.24	0.61
39:L2:234:LYS:NZ	36:5:2162:U:OP1	198.02	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:17:LEU:HD12	40:L3:18:PRO:HA	3.70	0.61
46:L9:161:LEU:HD22	46:L9:179:ILE:HD12	1.82	0.61
56:N0:16:THR:HG1	56:N0:19:VAL:H	2.52	0.61
36:1:1522:U:OP2	61:N5:121:LYS:NZ	2.32	0.61
11:S9:143:ILE:HD12	1:6:768:C:C2	421.92	0.61
11:S9:133:HIS:HD2	11:S9:162:SER:HB2	3.18	0.61
36:1:1819:U:O4	87:1:3937:OHX:N4	2.34	0.61
36:1:422:A:C2	36:1:2363:A:H4'	2.35	0.61
1:2:730:G:O6	87:2:2133:OHX:N4	2.33	0.61
1:6:413:U:H2'	1:6:414:C:C6	2.36	0.61
1:6:621:A:N3	1:6:1107:G:H1'	2.15	0.61
13:C1:109:VAL:HG12	13:C1:137:PHE:HB2	5.10	0.61
13:C1:33:ARG:NH1	13:C1:53:TYR:O	3.22	0.61
13:C1:99:ARG:HB3	25:D3:9:LEU:HD22	1.83	0.61
46:L9:47:LYS:HZ2	50:M4:5:SER:HB2	1.84	0.61
48:M1:50:ALA:HB2	48:M1:65:ILE:HD11	1.83	0.61
1:2:1065:A:OP1	87:S1:301:OHX:N3	2.32	0.61
53:M7:67:ILE:HD11	36:5:1447:G:H3'	166.03	0.61
1:6:209:U:H2'	1:6:210:A:C8	2.35	0.61
1:6:742:U:OP2	87:6:2157:OHX:N5	2.34	0.61
16:C4:86:THR:HG21	16:C4:90:ARG:HD2	1.82	0.61
26:D4:120:GLY:O	26:D4:122:GLY:N	3.54	0.61
42:L5:155:THR:HA	42:L5:179:ARG:HA	1.87	0.61
44:L7:157:ASN:O	44:L7:159:GLN:HG2	2.00	0.61
45:L8:241:LYS:HD3	36:5:2586:G:C8	186.04	0.61
64:N8:60:TYR:CD2	64:N8:63:LYS:HD2	4.89	0.61
3:S1:30:PHE:HB3	3:S1:96:LEU:HD22	3.87	0.61
36:1:1343:A:H2'	36:1:1344:G:C8	2.36	0.61
36:1:722:G:O6	87:1:3911:OHX:N6	2.34	0.61
36:5:1656:A:O2'	87:5:4092:OHX:N6	2.34	0.61
36:5:507:U:H2'	36:5:508:U:C6	2.34	0.61
1:6:235:G:H2'	1:6:236:A:H8	1.66	0.61
16:C4:103:ARG:HD2	16:C4:107:ARG:HH22	1.65	0.61
40:L3:128:LYS:HG3	36:5:3294:A:H5''	199.50	0.61
41:L4:264:SER:O	41:L4:266:THR:N	2.33	0.61
43:L6:58:LEU:HD12	43:L6:78:ARG:HD3	1.82	0.61
48:M1:100:GLY:HA3	48:M1:154:THR:HB	3.20	0.61
36:1:2433:U:H1'	51:M5:125:SER:HB2	1.83	0.61
3:S1:85:LYS:HB3	3:S1:101:HIS:HB3	3.41	0.61
7:S5:62:VAL:HG13	7:S5:89:ILE:HG12	1.83	0.61
36:1:2623:G:H2'	36:1:2624:G:C8	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:414:U:H2'	36:1:415:G:H8	1.66	0.61
1:2:1413:U:O2	87:2:2039:OHX:N4	2.33	0.61
1:2:720:G:H1'	1:2:721:U:H5''	1.82	0.61
36:5:999:G:C6	36:5:1000:C:N4	2.68	0.61
1:6:340:U:H2'	1:6:341:A:C8	2.36	0.61
8:S6:142:ARG:NH2	8:S6:149:LYS:O	6.87	0.61
36:1:1635:G:N2	36:1:1638:A:OP2	2.29	0.61
36:1:1721:U:O4	55:M9:128:LYS:NZ	2.29	0.61
1:2:1735:U:O4	87:2:2108:OHX:N4	2.34	0.61
38:4:55:U:O2	87:4:222:OHX:N6	2.34	0.61
36:5:2299:A:OP2	87:5:3875:OHX:N1	2.34	0.61
36:5:2549:G:C8	36:5:2549:G:H5'	2.35	0.61
36:5:2897:A:H2'	36:5:2899:C:H5''	1.83	0.61
20:C8:145:ARG:NH2	1:6:1460:A:OP2	339.71	0.61
1:6:1600:A:H4'	1:6:1601:G:OP1	2.00	0.61
1:6:845:G:H2'	1:6:846:G:H8	1.66	0.61
21:C9:25:GLN:O	21:C9:27:LYS:N	3.30	0.61
33:E1:109:ASP:O	33:E1:111:GLU:N	2.75	0.61
41:L4:354:VAL:HG11	57:N1:143:THR:HG21	4.15	0.61
42:L5:106:ALA:HA	42:L5:171:LEU:HD11	2.39	0.61
47:M0:4:ARG:NH2	47:M0:99:ILE:HG22	5.69	0.61
58:N2:50:LEU:HB3	58:N2:54:VAL:HG23	1.82	0.61
64:N8:76:ASP:HB2	64:N8:115:LYS:HB2	1.82	0.61
3:S1:35:PRO:HB3	3:S1:231:LEU:HD21	6.02	0.61
5:S3:22:ASN:OD1	5:S3:34:TYR:OH	2.36	0.61
36:1:2248:C:OP2	87:1:3777:OHX:N6	2.33	0.61
36:1:2667:A:O2'	36:1:2691:A:OP1	2.18	0.61
36:1:568:G:N7	87:1:3840:OHX:N4	2.49	0.61
37:3:92:A:C5	37:3:93:C:H1'	2.36	0.61
36:5:437:G:H1	36:5:622:A:N6	1.95	0.61
1:2:632:U:OP1	13:C1:102:LYS:HG3	2.01	0.61
19:C7:26:LEU:HD21	19:C7:62:GLN:HG3	4.47	0.61
20:C8:116:LEU:HA	20:C8:119:ILE:HG22	4.44	0.61
41:L4:304:GLN:O	41:L4:306:THR:N	2.98	0.61
48:M1:132:ASN:HA	48:M1:154:THR:HG21	1.82	0.61
57:N1:108:ARG:HA	57:N1:111:ALA:HB3	1.83	0.61
64:N8:16:SER:HA	36:5:942:U:N3	170.62	0.61
3:S1:137:ILE:HG13	3:S1:172:LEU:HD13	1.83	0.61
4:S2:44:LEU:HG	4:S2:247:ALA:HB2	1.83	0.61
10:S8:84:HIS:NE2	10:S8:97:THR:OG1	2.28	0.61
1:2:209:U:H2'	1:2:210:A:C8	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1304:A:OP1	87:5:4046:OHX:N3	2.34	0.61
74:O8:44:LYS:NZ	36:5:1748:G:OP1	137.69	0.61
36:5:3377:G:O6	87:5:3997:OHX:N2	2.34	0.61
71:O5:49:LYS:NZ	38:8:63:G:O2'	50.75	0.61
20:C8:140:THR:O	20:C8:143:ARG:NH1	2.34	0.61
23:D1:71:ARG:O	23:D1:75:ASN:ND2	2.34	0.61
31:D9:6:VAL:O	31:D9:8:PHE:N	4.85	0.61
41:L4:157:GLU:HG3	41:L4:251:THR:HG21	2.65	0.61
42:L5:61:ILE:HG23	42:L5:79:TYR:CE1	2.67	0.61
44:L7:173:LEU:HB3	44:L7:178:ILE:HB	1.82	0.61
47:M0:177:ASP:OD2	47:M0:177:ASP:N	3.65	0.61
49:M3:161:ASP:O	49:M3:163:GLY:N	3.38	0.61
51:M5:106:VAL:HG11	51:M5:132:VAL:HG21	1.82	0.61
36:1:269:G:H5'	51:M5:120:TRP:CE3	2.36	0.61
59:N3:93:LEU:HB2	60:N4:20:LEU:HD22	1.82	0.61
1:2:1239:U:OP1	87:2:2116:OHX:N5	2.33	0.60
1:2:804:A:N3	24:D2:105:THR:HG22	2.15	0.60
38:4:43:A:OP1	87:4:227:OHX:N5	2.34	0.60
36:5:2786:G:O6	87:5:4060:OHX:N2	2.32	0.60
36:5:2310:U:OP1	87:5:4117:OHX:N2	2.34	0.60
36:5:618:C:H2'	36:5:619:A:C8	2.36	0.60
19:C7:7:LYS:N	1:6:1316:G:OP1	412.24	0.60
1:6:1370:U:O4	87:6:2110:OHX:N6	2.34	0.60
1:6:1636:C:H4'	1:6:1637:C:H5'	1.83	0.60
39:L2:204:MET:HG3	39:L2:208:ASP:HB2	1.82	0.60
47:M0:59:GLN:HG2	47:M0:128:ARG:HG3	1.83	0.60
59:N3:28:ASN:HD21	59:N3:112:SER:HB2	1.65	0.60
60:N4:9:SER:HB2	60:N4:51:TRP:HZ3	2.44	0.60
63:N7:135:ARG:O	36:5:2555:G:N2	211.24	0.60
64:N8:116:GLY:O	64:N8:137:LYS:NZ	5.90	0.60
5:S3:79:TYR:CE2	5:S3:84:ILE:HG13	2.36	0.60
6:S4:68:ARG:HH12	6:S4:76:VAL:HG21	1.65	0.60
36:1:3143:C:O2'	87:1:3796:OHX:N2	2.34	0.60
1:2:1018:U:H2'	1:2:1019:A:C8	2.35	0.60
1:2:1153:G:H1	1:2:1625:C:H42	1.49	0.60
36:5:3057:U:H5'	36:5:3086:A:H61	1.66	0.60
1:6:1713:G:O6	1:6:1714:A:N6	2.34	0.60
11:S9:79:ARG:NH2	1:6:762:A:OP1	409.20	0.60
1:6:891:A:H2'	1:6:892:A:C8	2.36	0.60
17:C5:43:ARG:NH2	1:6:1552:U:OP2	404.90	0.60
20:C8:17:LEU:HD21	20:C8:66:LEU:HD13	6.04	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:D0:96:PRO:HG2	22:D0:99:ILE:HD11	5.65	0.60
29:D7:36:LYS:HG2	29:D7:43:ILE:HA	5.35	0.60
40:L3:108:GLU:HG2	40:L3:109:HIS:CD2	4.29	0.60
40:L3:114:VAL:HG22	40:L3:163:HIS:CE1	2.37	0.60
40:L3:81:THR:HB	40:L3:205:VAL:HG21	1.83	0.60
52:M6:65:ASN:O	52:M6:67:THR:N	2.34	0.60
59:N3:120:LYS:HB2	59:N3:137:VAL:CG2	3.00	0.60
61:N5:38:LEU:O	61:N5:39:LYS:HB2	4.44	0.60
63:N7:33:SER:OG	63:N7:35:SER:O	5.02	0.60
37:3:60:G:H2'	37:3:61:G:C8	2.36	0.60
36:5:2578:U:OP1	87:5:4037:OHX:N4	2.34	0.60
18:C6:55:VAL:HG21	18:C6:105:LEU:HG	2.07	0.60
2:S0:50:VAL:HG23	19:C7:109:LEU:HD21	3.37	0.60
21:C9:68:ARG:NH1	1:6:1523:G:N7	414.49	0.60
2:S0:63:ILE:HG12	23:D1:36:VAL:HG22	2.35	0.60
2:S0:185:ARG:HB2	23:D1:45:ALA:H	1.66	0.60
42:L5:259:LYS:HE2	42:L5:259:LYS:H	5.84	0.60
44:L7:178:ILE:HA	44:L7:183:ASP:HB3	2.54	0.60
46:L9:47:LYS:HZ2	50:M4:6:ILE:H	1.50	0.60
53:M7:26:PHE:HE1	53:M7:120:ASN:HA	1.83	0.60
3:S1:134:VAL:HB	3:S1:219:LYS:HB2	1.83	0.60
4:S2:137:ILE:HG12	4:S2:138:PRO:HD2	2.60	0.60
8:S6:10:ASN:HB3	8:S6:128:THR:HA	4.36	0.60
1:2:694:U:H3	9:S7:98:ILE:HD12	1.66	0.60
11:S9:58:ASP:O	11:S9:61:THR:OG1	2.56	0.60
34:SR:159:ASN:O	34:SR:161:LYS:N	4.44	0.60
36:1:239:G:O2'	36:1:240:U:OP1	2.15	0.60
36:1:3095:U:H2'	36:1:3096:C:C6	2.36	0.60
1:2:358:U:O4	87:2:2027:OHX:N1	2.34	0.60
38:4:11:C:H2'	38:4:12:A:H8	1.66	0.60
70:O4:37:LYS:NZ	36:5:1656:A:OP2	163.85	0.60
36:5:1790:G:O6	87:5:4113:OHX:N4	2.35	0.60
36:5:498:A:H2'	36:5:499:G:C8	2.36	0.60
12:C0:21:VAL:HB	12:C0:66:TYR:HB2	2.53	0.60
13:C1:123:VAL:HG12	13:C1:125:VAL:HG13	3.37	0.60
13:C1:16:GLN:HE22	13:C1:33:ARG:HA	6.68	0.60
14:C2:68:GLU:O	14:C2:70:ASN:N	2.27	0.60
39:L2:144:ASN:O	39:L2:160:SER:N	2.77	0.60
39:L2:8:GLN:HA	36:5:2163:C:H4'	185.13	0.60
42:L5:178:ASN:HA	42:L5:183:TRP:CG	2.48	0.60
57:N1:45:ASN:OD1	57:N1:47:SER:OG	3.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:M3:64:LYS:HG3	64:N8:69:TRP:CG	2.36	0.60
67:O1:11:GLU:OE2	67:O1:74:ARG:NH2	2.34	0.60
6:S4:107:GLY:HA2	6:S4:189:LEU:HG	1.88	0.60
8:S6:186:ARG:O	8:S6:190:GLN:HG2	2.01	0.60
9:S7:153:LEU:HD22	9:S7:184:GLU:HB2	1.82	0.60
36:1:2218:G:H2'	36:1:2219:A:H8	1.67	0.60
87:1:3854:OHX:N4	44:L7:217:PRO:O	2.35	0.60
1:6:187:G:H4'	1:6:188:A:OP1	2.02	0.60
1:6:1010:C:OP2	87:6:2086:OHX:N4	2.34	0.60
15:C3:64:ARG:HG3	15:C3:70:LYS:HG2	1.84	0.60
22:D0:95:ALA:HB1	22:D0:99:ILE:HG13	5.35	0.60
40:L3:92:TYR:HB2	40:L3:157:VAL:HG22	1.82	0.60
36:1:3098:G:H4'	40:L3:278:ILE:HD11	1.84	0.60
49:M3:28:GLN:HB3	51:M5:201:ARG:HD3	1.82	0.60
57:N1:104:GLU:O	57:N1:107:GLU:N	3.46	0.60
62:N6:36:SER:HB2	62:N6:37:LYS:HE2	2.29	0.60
63:N7:97:SER:O	63:N7:100:THR:OG1	3.43	0.60
10:S8:10:LYS:HG2	13:C1:133:LYS:HE2	6.61	0.60
35:SM:119:ALA:O	35:SM:121:LYS:N	3.18	0.60
1:2:1785:U:H2'	1:2:1786:G:H8	1.66	0.60
1:2:336:G:OP2	87:2:2075:OHX:N3	2.34	0.60
37:3:71:G:H2'	37:3:72:A:C8	2.36	0.60
36:5:1066:G:OP1	87:5:4151:OHX:N2	2.35	0.60
1:6:500:C:O2'	1:6:501:U:O4'	2.19	0.60
15:C3:65:VAL:O	15:C3:67:THR:N	3.59	0.60
20:C8:52:VAL:HG21	20:C8:69:ILE:HD11	1.92	0.60
26:D4:105:ARG:NH2	1:6:459:G:OP2	365.92	0.60
42:L5:12:TYR:OH	36:5:2688:U:OP1	300.87	0.60
45:L8:41:GLN:HG3	45:L8:44:ARG:HH12	1.66	0.60
36:1:3124:G:OP1	52:M6:134:LYS:NZ	2.35	0.60
52:M6:73:PHE:CG	52:M6:78:ARG:HG2	2.37	0.60
54:M8:64:VAL:HG11	54:M8:113:LYS:HD2	3.17	0.60
1:2:1724:U:H4'	60:N4:47:ARG:NH2	2.16	0.60
61:N5:132:ALA:O	61:N5:135:ILE:HG22	2.29	0.60
63:N7:88:ASP:HB3	63:N7:121:ARG:HH12	2.15	0.60
66:O0:34:LEU:HD23	66:O0:59:TYR:HB3	4.04	0.60
3:S1:147:ALA:O	3:S1:148:ASN:ND2	2.34	0.60
36:1:1742:U:H2'	36:1:1743:G:C8	2.37	0.60
36:1:2786:G:N7	87:1:3938:OHX:N1	2.49	0.60
36:1:2828:G:OP2	47:M0:7:ARG:NH2	2.33	0.60
36:1:829:U:H3	36:1:895:A:H62	1.48	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2507:C:O2'	36:5:2508:U:OP1	2.18	0.60
14:C2:103:LEU:HD23	14:C2:115:VAL:HA	2.07	0.60
28:D6:51:ARG:HH11	30:D8:60:GLU:HG2	1.67	0.60
41:L4:317:PRO:O	41:L4:319:LYS:N	2.35	0.60
60:N4:6:ASP:HB3	60:N4:10:GLY:H	1.66	0.60
70:O4:29:ILE:HD11	70:O4:31:ARG:HH21	1.67	0.60
36:1:1493:G:O6	75:O9:2:ALA:HB2	2.01	0.60
4:S2:128:GLY:O	4:S2:132:ALA:N	2.90	0.60
6:S4:159:THR:OG1	6:S4:160:VAL:N	4.34	0.60
9:S7:14:THR:OG1	9:S7:15:GLU:N	2.32	0.60
11:S9:143:ILE:O	11:S9:145:SER:N	2.79	0.60
34:SR:16:HIS:CE1	34:SR:37:SER:HB2	2.36	0.60
36:1:2169:G:O6	87:1:3809:OHX:N2	2.35	0.60
1:2:930:A:OP1	28:D6:32:LYS:NZ	2.34	0.60
23:D1:3:ASN:HD21	23:D1:5:LYS:HE3	1.66	0.60
5:S3:202:LEU:O	5:S3:204:ASP:N	2.80	0.60
6:S4:139:VAL:HG13	6:S4:150:PRO:HG3	1.83	0.60
1:2:399:A:H4'	6:S4:3:ARG:HG2	1.83	0.60
7:S5:55:ASP:HB3	7:S5:58:LEU:HD12	1.84	0.60
36:1:147:U:OP2	45:L8:136:LEU:N	2.35	0.60
36:1:1733:G:OP2	87:1:3812:OHX:N2	2.35	0.60
1:2:386:G:H5''	10:S8:23:LYS:HE2	1.82	0.60
1:6:454:U:H3'	1:6:455:C:C6	2.36	0.60
1:6:591:A:H2'	1:6:592:A:H8	1.66	0.60
33:E1:113:LYS:HD2	33:E1:113:LYS:H	1.67	0.60
40:L3:224:HIS:HB2	40:L3:270:ARG:HG2	3.13	0.60
41:L4:181:VAL:HG12	41:L4:182:LEU:H	1.67	0.60
45:L8:65:LEU:O	45:L8:69:LEU:HD13	2.40	0.60
45:L8:75:ILE:HG22	45:L8:76:ALA:H	1.66	0.60
46:L9:28:VAL:HG13	46:L9:33:THR:HB	1.81	0.60
52:M6:39:GLU:HG2	52:M6:40:GLU:HG2	2.14	0.60
62:N6:37:LYS:HG2	62:N6:38:GLU:H	1.67	0.60
8:S6:10:ASN:ND2	8:S6:127:THR:O	2.35	0.60
36:1:2314:U:O2'	36:1:2315:G:OP1	2.19	0.60
36:1:3094:A:H2'	36:1:3095:U:C6	2.37	0.60
1:2:86:A:O2'	1:2:147:A:N3	2.32	0.60
16:C4:20:TYR:HD1	16:C4:84:ARG:HG3	5.41	0.60
17:C5:37:ALA:O	17:C5:42:ARG:NH1	3.46	0.60
23:D1:60:ARG:HA	23:D1:65:SER:HB2	2.90	0.60
25:D3:96:VAL:HG12	25:D3:127:VAL:HG11	1.82	0.60
42:L5:28:THR:O	36:5:2703:A:N6	281.63	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:O3:18:ARG:HD3	36:5:1178:G:H5'	239.62	0.60
78:Q2:17:CYS:SG	78:Q2:77:CYS:CB	2.70	0.60
36:1:138:U:H2'	36:1:139:G:C8	2.37	0.59
36:1:1556:C:H2'	36:1:2169:G:N1	2.16	0.59
36:1:86:G:O2'	36:1:98:G:O6	2.18	0.59
1:2:1114:G:O6	87:2:2042:OHX:N6	2.35	0.59
37:3:11:A:O2'	37:3:13:A:OP2	2.19	0.59
65:N9:38:LYS:NZ	36:5:1076:C:O3'	218.07	0.59
36:5:1661:G:O6	87:5:3836:OHX:N1	2.34	0.59
1:6:1039:A:O2'	1:6:1040:G:O5'	2.18	0.59
5:S3:179:GLN:NE2	1:6:1438:G:O2'	398.47	0.59
14:C2:62:LEU:HD22	14:C2:75:VAL:HG11	1.84	0.59
29:D7:11:THR:O	29:D7:13:ALA:N	2.78	0.59
36:1:943:U:H3'	64:N8:13:GLY:HA2	1.83	0.59
71:O5:68:GLN:HA	71:O5:71:LYS:HB2	1.84	0.59
74:O8:31:LEU:HA	74:O8:37:PRO:HA	1.83	0.59
5:S3:64:ARG:NH1	5:S3:68:GLU:OE1	2.48	0.59
9:S7:123:ASP:OD1	9:S7:138:LYS:NZ	2.34	0.59
36:1:1278:A:O2'	36:1:1279:C:O5'	2.20	0.59
36:1:2526:C:O2'	45:L8:241:LYS:NZ	2.30	0.59
36:5:2102:U:H2'	36:5:2103:U:H6	1.67	0.59
17:C5:65:LEU:O	87:C5:201:OHX:N1	2.35	0.59
31:D9:47:ALA:HA	31:D9:50:ILE:HD12	3.18	0.59
39:L2:104:LEU:HD22	39:L2:162:ALA:HB3	2.94	0.59
48:M1:91:LEU:HD22	48:M1:95:ASN:HD22	1.66	0.59
52:M6:58:LEU:HA	52:M6:72:HIS:CD2	2.84	0.59
53:M7:116:HIS:HB3	53:M7:149:VAL:HB	1.85	0.59
55:M9:78:TYR:HA	55:M9:81:ARG:HD3	1.84	0.59
63:N7:84:ARG:NH1	63:N7:85:TYR:OH	2.35	0.59
36:1:1211:U:H2'	36:1:1212:A:C8	2.37	0.59
36:1:1740:U:H1'	36:1:1741:A:H2	1.67	0.59
36:1:3313:U:H4'	40:L3:173:GLN:OE1	2.03	0.59
36:1:799:G:HO2'	49:M3:18:TRP:HE1	1.50	0.59
1:2:732:G:O2'	1:2:733:A:O4'	2.20	0.59
36:5:2102:U:H2'	36:5:2103:U:C6	2.38	0.59
36:5:3199:G:O6	87:5:4052:OHX:N5	2.36	0.59
1:6:1213:G:O6	87:6:2039:OHX:N6	2.35	0.59
1:2:159:U:H5'	26:D4:117:LYS:HD3	1.83	0.59
26:D4:12:VAL:HG22	26:D4:23:PHE:HB3	2.13	0.59
30:D8:9:LEU:HB3	30:D8:33:LEU:HD12	8.21	0.59
47:M0:200:LEU:HD12	47:M0:213:PHE:HB2	4.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:N2:18:ASP:N	58:N2:103:TYR:O	2.85	0.59
63:N7:57:HIS:HB3	63:N7:62:VAL:HG22	1.83	0.59
64:N8:59:ARG:NH1	36:5:90:C:OP1	153.20	0.59
4:S2:89:GLN:HA	4:S2:94:GLN:HA	2.85	0.59
10:S8:22:ARG:HE	10:S8:25:ARG:HD2	6.74	0.59
34:SR:66:HIS:HB3	34:SR:85:TRP:HB2	1.84	0.59
36:1:1902:G:C6	36:1:1903:U:C2	2.91	0.59
1:2:1298:U:O3'	4:S2:212:LYS:NZ	2.36	0.59
1:6:1263:G:C2	1:6:1264:G:H1'	2.37	0.59
4:S2:200:SER:OG	1:6:4:C:OP1	385.15	0.59
24:D2:31:SER:HB2	1:6:636:A:H5''	361.83	0.59
1:6:819:G:O2'	1:6:821:U:OP2	2.20	0.59
42:L5:155:THR:HG23	37:7:36:C:H4'	271.86	0.59
13:C1:33:ARG:NH2	13:C1:51:GLY:O	3.33	0.59
19:C7:6:THR:OG1	19:C7:7:LYS:N	2.33	0.59
21:C9:125:SER:O	21:C9:129:GLN:N	2.29	0.59
30:D8:13:ILE:HD11	30:D8:31:GLU:HB2	1.84	0.59
33:E1:120:GLU:HB2	33:E1:130:VAL:HB	6.28	0.59
40:L3:275:ARG:NH1	36:5:3045:G:O3'	235.22	0.59
43:L6:105:TYR:HE1	43:L6:134:ARG:HD3	1.97	0.59
46:L9:89:LYS:HG2	46:L9:145:VAL:HG22	2.06	0.59
47:M0:3:ARG:CZ	47:M0:63:GLU:HG3	2.33	0.59
49:M3:16:LYS:NZ	36:5:98:G:OP1	134.24	0.59
53:M7:31:GLU:CG	53:M7:60:PHE:HA	3.38	0.59
56:N0:141:LYS:HA	56:N0:144:LEU:HD12	2.01	0.59
74:O8:26:LYS:HE3	36:5:1751:G:C8	128.79	0.59
79:Q3:46:THR:HB	79:Q3:58:SER:HB3	3.59	0.59
4:S2:227:PRO:HA	4:S2:230:TRP:CG	2.88	0.59
10:S8:117:TYR:CD1	10:S8:150:ALA:HB2	2.37	0.59
36:1:2128:C:OP1	87:1:3853:OHX:N2	2.35	0.59
36:1:3122:A:N1	46:L9:70:THR:HG21	2.17	0.59
36:1:2137:U:OP1	87:1:3838:OHX:N6	2.35	0.59
37:3:36:C:H4'	42:L5:155:THR:HG23	1.85	0.59
39:L2:243:THR:HG23	36:5:2242:A:H5'	234.21	0.59
36:5:2373:A:N7	36:5:2867:C:H1'	2.17	0.59
36:5:421:G:O6	36:5:2383:C:O2'	2.17	0.59
73:O7:43:LYS:NZ	36:5:55:G:OP1	114.44	0.59
1:6:1500:C:H2'	1:6:1501:C:H6	1.67	0.59
1:6:680:U:OP1	87:6:2138:OHX:N4	2.35	0.59
1:6:884:A:H2'	1:6:885:G:C8	2.38	0.59
2:S0:55:GLU:OE2	23:D1:80:LYS:N	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:D8:31:GLU:OE2	30:D8:36:THR:OG1	2.16	0.59
39:L2:13:GLY:HA2	39:L2:16:PHE:HB2	1.85	0.59
44:L7:89:ILE:HG22	44:L7:220:PHE:HE1	1.67	0.59
47:M0:99:ILE:HG22	47:M0:123:HIS:HB2	1.83	0.59
53:M7:50:GLN:OE1	53:M7:56:ARG:HD3	2.02	0.59
57:N1:13:TYR:O	87:5:3827:OHX:N4	262.15	0.59
64:N8:58:MET:SD	36:5:2786:G:N2	156.68	0.59
71:O5:85:THR:HB	71:O5:88:LEU:HB2	2.41	0.59
2:S0:189:VAL:HG22	2:S0:190:ASP:H	1.67	0.59
3:S1:34:ALA:HB3	3:S1:41:ARG:HA	1.84	0.59
3:S1:36:SER:OG	3:S1:41:ARG:NH2	6.56	0.59
34:SR:300:THR:HG23	34:SR:314:GLN:HG2	1.83	0.59
36:1:211:A:OP1	41:L4:220:ARG:HD2	2.02	0.59
36:1:3151:U:OP1	40:L3:128:LYS:NZ	2.34	0.59
36:1:2236:G:OP1	87:1:4014:OHX:N6	2.36	0.59
36:1:599:C:OP1	41:L4:332:LYS:NZ	2.36	0.59
79:Q3:17:ARG:NH1	36:5:860:G:OP1	220.14	0.59
1:6:1584:G:N2	1:6:1611:A:OP2	2.27	0.59
37:7:27:A:H2'	37:7:28:C:C6	2.38	0.59
40:L3:370:PHE:HB3	40:L3:375:GLU:HG2	1.85	0.59
2:S0:71:GLU:O	2:S0:96:THR:HG22	2.19	0.59
4:S2:99:LYS:HG3	4:S2:117:THR:HB	4.03	0.59
7:S5:128:ASN:N	7:S5:128:ASN:OD1	2.35	0.59
35:SM:153:ASP:O	35:SM:155:LEU:N	2.32	0.59
35:SM:54:PRO:HB2	35:SM:59:GLY:HA2	1.83	0.59
34:SR:13:LEU:HB2	34:SR:310:ILE:HB	1.85	0.59
1:2:145:A:O2'	1:2:146:U:O5'	2.19	0.59
1:2:1533:C:H4'	1:2:1539:G:N1	2.17	0.59
1:2:1233:G:OP2	87:2:2127:OHX:N5	2.35	0.59
1:2:591:A:H2'	1:2:592:A:C8	2.38	0.59
36:5:1049:C:H2'	36:5:1050:U:H6	1.66	0.59
36:5:1743:G:O6	87:5:4009:OHX:N1	2.35	0.59
36:5:92:G:H5'	36:5:93:C:H5''	1.84	0.59
27:D5:77:ARG:NH1	1:6:1533:C:OP2	355.30	0.59
1:6:249:U:H3'	1:6:250:C:H5'	1.84	0.59
1:6:532:U:H2'	1:6:533:U:O4'	2.03	0.59
16:C4:16:VAL:O	16:C4:30:VAL:HA	2.02	0.59
26:D4:20:ARG:NH1	26:D4:22:GLN:OE1	2.31	0.59
32:E0:42:ARG:O	32:E0:44:PHE:N	3.51	0.59
42:L5:34:LYS:O	42:L5:38:THR:OG1	3.04	0.59
46:L9:124:ARG:HG2	46:L9:164:ILE:HD12	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:M4:23:ILE:HA	50:M4:63:VAL:HG23	1.84	0.59
54:M8:116:LYS:NZ	64:N8:88:ASP:OD2	2.36	0.59
55:M9:28:GLU:OE2	87:M9:202:OHX:N6	2.35	0.59
64:N8:85:ASP:OD1	64:N8:86:LYS:N	2.35	0.59
36:1:3159:C:H2'	36:1:3160:U:H6	1.68	0.59
36:1:541:U:O4	87:1:3951:OHX:N6	2.36	0.59
1:2:1429:G:H1'	22:D0:74:GLU:HG2	1.83	0.59
1:2:358:U:OP2	87:2:2057:OHX:N4	2.36	0.59
1:6:1324:G:OP2	87:6:2070:OHX:N2	2.36	0.59
40:L3:58:ARG:NH1	40:L3:352:GLU:OE1	2.26	0.59
43:L6:35:VAL:O	43:L6:38:THR:OG1	2.15	0.59
45:L8:82:LEU:HD13	45:L8:222:PHE:HE2	1.68	0.59
75:O9:50:ASN:OD1	87:O9:101:OHX:N5	2.36	0.59
4:S2:90:THR:HG21	1:6:1424:A:H4'	389.25	0.59
34:SR:69:GLN:HG2	34:SR:111:MET:HA	1.85	0.59
36:1:532:A:H2	36:1:560:G:H22	1.50	0.59
1:2:1434:U:O2'	1:2:1436:A:OP1	2.19	0.59
1:2:1370:U:O4	87:2:2089:OHX:N6	2.36	0.59
36:5:3035:A:OP2	87:5:3964:OHX:N5	2.35	0.59
36:5:549:U:H2'	36:5:550:A:C8	2.38	0.59
44:L7:241:LYS:NZ	36:5:576:C:OP1	275.88	0.59
20:C8:135:GLY:HA3	1:6:1559:A:H5''	368.02	0.59
1:6:207:U:H3	1:6:258:C:H42	1.49	0.59
8:S6:160:ARG:HH12	1:6:68:A:H5'	347.66	0.59
14:C2:28:LEU:HD22	14:C2:32:LEU:HG	2.57	0.59
7:S5:73:THR:HG23	18:C6:114:ARG:HD3	1.82	0.59
19:C7:75:GLU:O	19:C7:79:GLU:HG2	2.03	0.59
20:C8:92:ILE:HG23	20:C8:93:THR:HG23	2.83	0.59
21:C9:61:VAL:HG11	21:C9:105:LEU:HD21	3.07	0.59
22:D0:28:SER:HB2	22:D0:112:VAL:HA	1.84	0.59
39:L2:143:GLU:O	39:L2:145:LYS:N	2.75	0.59
36:1:1334:U:O2'	44:L7:151:ARG:NH2	2.35	0.59
62:N6:69:LYS:O	62:N6:83:ASP:N	3.28	0.59
8:S6:56:ASN:ND2	8:S6:60:GLY:O	2.35	0.59
8:S6:87:ARG:NH1	1:6:159:U:O2'	322.83	0.59
36:1:1887:A:OP2	87:1:3788:OHX:N4	2.36	0.59
36:1:3358:U:H2'	36:1:3359:A:O4'	2.01	0.59
1:2:1347:U:O2	1:2:1516:A:H5''	2.03	0.59
1:2:1794:A:H1'	28:D6:79:ILE:HD12	1.83	0.59
1:2:9:U:O4	87:2:2132:OHX:N6	2.36	0.59
1:2:918:U:H2'	1:2:919:A:C8	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1108:U:H2'	36:5:1109:U:H6	1.68	0.59
36:5:3005:A:OP2	87:5:4014:OHX:N2	2.35	0.59
36:5:439:C:H4'	36:5:440:A:H5'	1.85	0.59
24:D2:101:TYR:O	24:D2:129:VAL:N	3.05	0.59
28:D6:24:VAL:HG11	28:D6:71:LEU:HD13	1.84	0.59
40:L3:293:ASN:HB2	40:L3:304:THR:HA	1.84	0.59
36:1:337:G:OP2	41:L4:196:ASN:ND2	2.35	0.59
41:L4:233:LEU:HD22	41:L4:238:LEU:HD11	2.38	0.59
63:N7:33:SER:HB2	63:N7:40:HIS:CE1	2.38	0.59
72:O6:33:ALA:O	72:O6:34:SER:HB3	2.03	0.59
87:4:218:OHX:N6	73:O7:60:GLY:O	2.35	0.59
3:S1:134:VAL:HB	3:S1:219:LYS:H	2.80	0.59
3:S1:87:ARG:NH2	3:S1:220:GLN:OE1	3.54	0.59
5:S3:21:LEU:HD22	5:S3:25:PHE:HE2	1.67	0.59
6:S4:112:HIS:NE2	6:S4:237:SER:HB2	2.84	0.59
9:S7:99:LEU:HG	9:S7:116:ARG:HG2	2.31	0.59
36:1:314:U:H2'	36:1:315:C:C6	2.37	0.58
36:1:2704:A:OP2	87:1:3765:OHX:N4	2.34	0.58
36:1:980:A:H2'	36:1:981:U:C2	2.38	0.58
36:5:1239:C:N4	36:5:1249:G:H1	2.01	0.58
36:5:1667:A:H2'	36:5:1668:G:C8	2.38	0.58
36:5:529:A:H2'	36:5:530:G:O4'	2.03	0.58
1:6:985:G:O6	87:6:2014:OHX:N6	2.37	0.58
12:C0:58:GLN:HB3	12:C0:65:TYR:HB2	3.49	0.58
17:C5:18:ARG:NH1	20:C8:90:ASN:O	3.54	0.58
22:D0:24:ILE:HG12	22:D0:116:VAL:HG22	1.85	0.58
22:D0:65:ILE:HD12	31:D9:43:PHE:CE2	2.38	0.58
31:D9:12:ARG:HG3	31:D9:18:SER:HA	1.85	0.58
1:2:588:U:OP2	32:E0:26:LYS:NZ	2.34	0.58
39:L2:201:GLY:O	39:L2:204:MET:HG2	2.03	0.58
39:L2:27:ALA:HB3	39:L2:128:ARG:NH2	2.46	0.58
41:L4:38:VAL:O	41:L4:42:VAL:HG23	2.02	0.58
71:O5:85:THR:HB	71:O5:88:LEU:H	1.68	0.58
49:M3:106:GLN:HB2	72:O6:20:MET:HG3	2.15	0.58
7:S5:77:TYR:CZ	7:S5:87:CYS:HB2	2.71	0.58
34:SR:286:GLU:OE2	87:SR:401:OHX:N5	2.36	0.58
36:1:764:U:O4	87:1:3858:OHX:N2	2.36	0.58
36:5:419:G:N7	87:8:210:OHX:N3	2.49	0.58
15:C3:13:SER:OG	15:C3:14:SER:N	2.36	0.58
15:C3:20:ARG:HD3	24:D2:56:HIS:CD2	4.18	0.58
22:D0:118:VAL:HG13	22:D0:119:ALA:H	3.58	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1335:U:H5'	22:D0:85:ARG:HH22	1.68	0.58
33:E1:116:LYS:NZ	33:E1:120:GLU:OE2	2.35	0.58
41:L4:283:THR:OG1	41:L4:284:SER:N	4.52	0.58
43:L6:55:LEU:HD11	43:L6:66:SER:HB2	4.41	0.58
47:M0:205:SER:OG	47:M0:205:SER:O	3.21	0.58
47:M0:208:ASN:HA	47:M0:211:ARG:HG2	3.82	0.58
49:M3:69:VAL:O	49:M3:149:GLN:NE2	2.30	0.58
56:N0:26:ARG:HH11	57:N1:150:THR:HG21	2.69	0.58
69:O3:41:ALA:HB3	69:O3:74:THR:HG22	2.18	0.58
10:S8:9:HIS:ND1	10:S8:10:LYS:HG3	2.17	0.58
1:2:1274:C:N4	35:SM:95:SER:HA	2.17	0.58
36:1:1246:G:OP2	87:1:3999:OHX:N4	2.36	0.58
1:2:1349:G:H1	1:2:1376:C:H42	1.49	0.58
1:2:855:A:C2	1:2:857:U:H1'	2.38	0.58
1:6:921:U:O4	87:6:2150:OHX:N3	2.36	0.58
5:S3:211:PRO:HG3	19:C7:20:TYR:CZ	2.39	0.58
22:D0:34:LEU:HD21	22:D0:89:ARG:HD2	4.07	0.58
44:L7:96:PRO:O	44:L7:99:PRO:HD2	2.27	0.58
45:L8:71:VAL:HG22	45:L8:76:ALA:HB2	1.85	0.58
46:L9:87:LYS:HE2	46:L9:89:LYS:HE3	1.86	0.58
36:1:268:A:C4	51:M5:12:ARG:HG2	2.39	0.58
53:M7:172:GLN:OE1	69:O3:60:ARG:NH1	2.36	0.58
76:Q0:96:CYS:HA	76:Q0:121:LEU:HD22	2.23	0.58
10:S8:136:SER:OG	10:S8:137:LYS:N	2.36	0.58
34:SR:109:ASP:HB2	34:SR:127:ARG:HG3	1.85	0.58
36:1:787:G:H2'	36:1:788:C:C6	2.37	0.58
36:1:830:A:OP1	87:1:3906:OHX:N3	2.35	0.58
1:2:422:G:N7	87:2:2076:OHX:N3	2.50	0.58
38:4:53:A:OP1	75:O9:19:GLN:NE2	2.36	0.58
36:5:90:C:C2'	36:5:91:G:H5'	2.34	0.58
1:6:87:C:O2'	1:6:169:A:N1	2.34	0.58
1:6:1699:G:H22	1:6:1702:A:H5''	1.69	0.58
1:2:337:G:H3'	13:C1:133:LYS:HB2	1.83	0.58
15:C3:148:ALA:O	87:C3:201:OHX:N4	8.15	0.58
1:2:1479:A:OP1	21:C9:57:ARG:NH1	2.35	0.58
27:D5:38:HIS:CE1	27:D5:70:LYS:HD3	2.39	0.58
40:L3:7:GLU:HG2	36:5:2915:U:C5	258.33	0.58
43:L6:91:VAL:HG23	43:L6:148:GLU:HG3	4.95	0.58
47:M0:114:GLY:HA2	36:5:2864:A:H5''	243.48	0.58
47:M0:12:GLN:HG2	47:M0:59:GLN:HG2	4.74	0.58
68:O2:33:ARG:HH11	36:5:944:C:H4'	162.63	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S0:65:ALA:O	2:S0:67:ILE:N	3.61	0.58
3:S1:70:LEU:HD21	3:S1:79:HIS:CD2	2.38	0.58
4:S2:81:MET:N	4:S2:101:VAL:O	2.36	0.58
5:S3:38:GLU:OE2	5:S3:40:ARG:NH2	2.37	0.58
34:SR:239:GLU:O	34:SR:257:ALA:N	2.82	0.58
38:4:127:U:H2'	38:4:128:U:H5'	1.85	0.58
36:5:1481:A:H2'	36:5:1858:A:H1'	1.86	0.58
21:C9:72:GLY:HA3	1:6:1498:G:H5''	423.02	0.58
41:L4:194:TYR:H	41:L4:194:TYR:HD1	1.50	0.58
47:M0:216:TYR:O	87:M0:302:OHX:N4	67.25	0.58
58:N2:22:PRO:HB2	58:N2:28:PHE:HB2	1.85	0.58
49:M3:157:ARG:NH1	64:N8:146:GLU:OE1	3.03	0.58
6:S4:175:PHE:HE2	6:S4:198:LYS:HD3	4.79	0.58
6:S4:88:ASP:OD1	6:S4:122:LYS:NZ	2.36	0.58
7:S5:35:GLN:O	7:S5:37:GLN:N	3.65	0.58
7:S5:57:SER:O	7:S5:59:VAL:N	2.30	0.58
1:2:159:U:O2'	8:S6:87:ARG:NH1	2.36	0.58
34:SR:264:SER:HB2	34:SR:271:VAL:HG23	1.84	0.58
36:1:2736:A:O2'	57:N1:68:THR:HG21	2.03	0.58
36:1:1790:G:O6	87:1:4066:OHX:N4	2.37	0.58
1:2:654:C:H3'	1:2:655:G:H5''	1.86	0.58
36:5:2696:A:H2'	36:5:2697:A:C8	2.38	0.58
39:L2:181:LYS:HB3	36:5:860:G:C5	214.52	0.58
12:C0:15:LEU:HD13	12:C0:21:VAL:HG23	1.85	0.58
12:C0:14:TYR:OH	12:C0:34:GLU:OE1	2.38	0.58
1:2:1544:U:H4'	20:C8:132:ARG:NH2	2.18	0.58
40:L3:170:PRO:HG2	40:L3:314:TYR:CZ	2.39	0.58
46:L9:101:VAL:HG22	46:L9:114:VAL:HG22	1.85	0.58
52:M6:172:ARG:HA	52:M6:175:THR:HG22	1.84	0.58
53:M7:28:ASN:O	53:M7:32:THR:HG23	2.66	0.58
65:N9:23:LYS:HG3	65:N9:24:PRO:HD3	1.85	0.58
2:S0:169:SER:O	2:S0:173:ILE:HG12	2.02	0.58
3:S1:131:ASP:O	3:S1:133:TYR:N	2.35	0.58
10:S8:25:ARG:O	10:S8:28:GLU:HG2	2.14	0.58
36:1:3169:U:H2'	36:1:3170:A:O4'	2.03	0.58
36:1:1753:G:O6	87:1:3942:OHX:N6	2.36	0.58
1:2:1592:A:H2'	1:2:1593:A:C8	2.38	0.58
37:3:27:A:O5'	42:L5:57:ASN:ND2	2.36	0.58
62:N6:60:ARG:HH22	36:5:190:U:H2'	85.00	0.58
36:5:339:C:OP1	36:5:1380:G:O2'	2.18	0.58
1:6:899:G:H2'	1:6:900:A:H8	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:8:106:C:H5''	38:8:108:C:OP2	2.03	0.58
14:C2:124:LYS:O	14:C2:126:TRP:N	2.35	0.58
1:2:587:C:OP2	32:E0:23:LYS:NZ	2.35	0.58
41:L4:287:THR:O	41:L4:291:ASN:ND2	4.85	0.58
42:L5:38:THR:HG22	57:N1:30:TYR:HB3	1.84	0.58
47:M0:86:HIS:HB3	47:M0:139:ARG:HG2	2.21	0.58
48:M1:7:ASN:HA	48:M1:10:ARG:HD2	2.02	0.58
56:N0:9:VAL:HG22	56:N0:61:ILE:HD13	1.86	0.58
67:O1:27:LYS:O	67:O1:31:ARG:HB2	2.03	0.58
68:O2:21:HIS:ND1	68:O2:24:ARG:HD2	2.18	0.58
2:S0:14:ALA:HA	2:S0:17:LEU:HD12	3.54	0.58
3:S1:137:ILE:HD11	3:S1:172:LEU:HB3	1.85	0.58
3:S1:59:ASP:HA	3:S1:62:LYS:HD3	1.86	0.58
4:S2:183:ALA:HB1	4:S2:211:LEU:HD21	2.37	0.58
5:S3:21:LEU:HD22	5:S3:25:PHE:CE2	2.39	0.58
7:S5:117:THR:HA	7:S5:120:ILE:HD12	2.45	0.58
9:S7:9:LEU:HD21	9:S7:17:GLU:HB3	1.86	0.58
34:SR:126:SER:OG	34:SR:127:ARG:N	2.36	0.58
36:1:1240:A:H2	36:1:1248:C:H41	1.52	0.58
36:1:1683:A:OP2	58:N2:85:LYS:HE3	2.04	0.58
36:1:2169:G:O6	87:1:3809:OHX:N4	2.37	0.58
40:L3:278:ILE:HD11	36:5:3098:G:H5'	260.47	0.58
47:M0:76:MET:HE1	47:M0:148:VAL:HG13	1.93	0.58
53:M7:27:LYS:HD3	53:M7:63:PHE:HB3	1.84	0.58
54:M8:170:ARG:NH1	64:N8:56:VAL:O	2.36	0.58
62:N6:37:LYS:HA	62:N6:40:ARG:HG2	5.32	0.58
68:O2:81:ASP:O	68:O2:84:THR:HG23	2.03	0.58
6:S4:170:THR:OG1	6:S4:170:THR:O	4.22	0.58
6:S4:248:ILE:HB	11:S9:71:PHE:HE2	5.23	0.58
36:1:2688:U:OP1	42:L5:12:TYR:OH	2.18	0.58
36:1:3029:A:C5	36:1:3030:G:H1'	2.38	0.58
36:1:421:G:OP1	87:1:3920:OHX:N4	2.37	0.58
36:1:872:U:H2'	36:1:873:C:C6	2.39	0.58
1:2:1516:A:OP1	22:D0:88:LYS:NZ	2.28	0.58
1:2:1696:G:H21	1:2:1705:C:H5	1.51	0.58
1:2:812:A:OP1	1:2:858:G:N2	2.37	0.58
62:N6:9:SER:OG	36:5:336:A:OP2	79.79	0.58
1:6:820:U:O2'	1:6:821:U:H5''	2.04	0.58
17:C5:122:THR:HG21	1:6:1455:G:OP1	372.03	0.58
19:C7:47:ARG:NH1	19:C7:48:ASN:OD1	2.44	0.58
30:D8:32:PHE:O	30:D8:34:GLU:N	3.16	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:E1:86:THR:O	33:E1:87:THR:OG1	2.58	0.58
39:L2:135:ILE:HB	39:L2:149:ARG:HB3	3.04	0.58
39:L2:149:ARG:HE	39:L2:252:THR:HG21	1.69	0.58
40:L3:68:HIS:O	40:L3:70:ARG:N	2.37	0.58
46:L9:22:SER:OG	46:L9:23:ARG:N	2.36	0.58
61:N5:80:ASN:ND2	61:N5:126:LEU:O	2.52	0.58
38:4:131:A:H5''	61:N5:93:TYR:CE2	2.39	0.58
3:S1:27:LYS:NZ	3:S1:49:ASN:OD1	2.33	0.58
6:S4:105:VAL:HG11	6:S4:245:LYS:H	2.02	0.58
6:S4:166:SER:O	6:S4:168:LYS:HG2	4.28	0.58
11:S9:78:ARG:HH22	11:S9:82:ARG:HH21	1.51	0.58
36:1:2881:C:H2'	36:1:2882:U:H6	1.69	0.58
36:1:852:U:H2'	36:1:853:G:C8	2.39	0.58
36:5:1073:U:H2'	36:5:1074:U:C6	2.38	0.58
36:5:717:C:OP1	36:5:718:G:N2	2.37	0.58
1:6:1037:C:H2'	1:6:1038:U:C6	2.39	0.58
19:C7:21:TYR:OH	19:C7:62:GLN:OE1	2.45	0.58
40:L3:169:THR:CG2	40:L3:171:LEU:HB2	4.16	0.58
40:L3:206:ASP:OD1	40:L3:206:ASP:N	2.31	0.58
51:M5:42:PRO:HG3	51:M5:61:ILE:HG13	2.47	0.58
55:M9:101:VAL:HA	55:M9:104:ARG:CZ	2.34	0.58
55:M9:11:ALA:O	55:M9:15:VAL:HG23	2.04	0.58
3:S1:226:GLY:HA2	36:5:2536:A:H4'	258.12	0.58
3:S1:62:LYS:O	3:S1:64:ARG:N	2.35	0.58
36:1:3215:A:O5'	50:M4:121:MET:HE1	2.04	0.57
36:1:796:U:H2'	36:1:797:U:H6	1.69	0.57
1:2:1396:U:H2'	1:2:1397:U:H6	1.69	0.57
1:2:647:G:H22	1:2:687:G:H1	1.52	0.57
36:5:1696:A:OP2	87:5:4100:OHX:N6	2.37	0.57
57:N1:54:HIS:CD2	36:5:2724:U:H4'	230.35	0.57
36:5:83:U:OP2	87:5:4124:OHX:N4	2.37	0.57
1:6:1297:G:N2	1:6:1300:A:OP2	2.37	0.57
1:6:333:A:C6	1:6:334:G:C6	2.92	0.57
13:C1:133:LYS:HB2	1:6:337:G:H3'	291.43	0.57
15:C3:112:LYS:O	15:C3:116:ILE:HD13	4.86	0.57
40:L3:185:GLY:O	40:L3:191:LYS:NZ	2.27	0.57
40:L3:20:LYS:HG2	40:L3:21:ARG:N	4.06	0.57
47:M0:95:HIS:HB2	47:M0:128:ARG:HD2	2.75	0.57
49:M3:50:PRO:O	49:M3:52:ASP:N	2.97	0.57
41:L4:282:SER:HB3	54:M8:126:GLN:HE21	4.65	0.57
54:M8:3:ILE:HB	54:M8:5:HIS:CE1	3.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:M9:68:GLN:O	55:M9:71:ARG:N	2.35	0.57
56:N0:93:GLU:HG3	56:N0:137:ARG:HD2	3.53	0.57
3:S1:41:ARG:HH22	3:S1:232:HIS:HA	3.03	0.57
9:S7:28:GLU:HG2	9:S7:38:LEU:HD13	1.85	0.57
36:1:2726:C:O2'	36:1:2727:A:H2'	2.04	0.57
36:1:2908:G:O6	87:1:3770:OHX:N4	2.37	0.57
1:2:297:U:H5''	6:S4:37:LYS:HG2	1.84	0.57
1:2:472:U:O2'	1:2:769:A:N3	2.28	0.57
54:M8:38:ARG:NH2	36:5:1348:U:OP2	188.54	0.57
1:6:1699:G:C2	1:6:1701:A:H5''	2.39	0.57
1:6:118:U:O4	87:6:2173:OHX:N4	2.37	0.57
1:6:263:C:H4'	1:6:292:U:H5'	1.85	0.57
14:C2:128:ALA:HB3	14:C2:133:LEU:HD22	3.95	0.57
22:D0:52:LYS:HB3	22:D0:93:LEU:HD23	1.86	0.57
40:L3:100:ARG:NH2	36:5:3244:A:OP2	249.69	0.57
71:O5:89:ARG:HD2	38:8:38:U:C4	69.69	0.57
36:1:1492:G:O2'	75:O9:48:LYS:NZ	2.37	0.57
77:Q1:13:LEU:HD13	77:Q1:17:ARG:NH2	2.19	0.57
2:S0:38:PHE:O	2:S0:39:ASN:ND2	4.86	0.57
4:S2:53:ILE:HG12	4:S2:73:LEU:HD22	4.55	0.57
1:2:788:A:N1	6:S4:51:ARG:NH2	2.52	0.57
35:SM:61:ILE:HD12	35:SM:62:ARG:HG2	1.85	0.57
34:SR:169:ILE:HG13	34:SR:181:TRP:HB2	1.86	0.57
36:1:1611:G:H2'	36:1:1612:A:C8	2.38	0.57
36:1:1730:G:N7	66:O0:28:LYS:HB2	2.20	0.57
36:1:1804:A:H5''	70:O4:67:LYS:HE3	1.84	0.57
36:1:191:U:H2'	36:1:192:C:C6	2.39	0.57
36:1:750:G:H1	36:1:783:A:H2	1.52	0.57
1:2:1524:A:H2'	1:2:1525:A:C8	2.39	0.57
1:2:649:U:O2'	1:2:650:U:O4'	2.21	0.57
38:4:62:C:O2	87:4:222:OHX:N6	2.37	0.57
36:5:2660:G:OP1	36:5:2750:U:O2'	2.22	0.57
37:7:91:G:H2'	37:7:92:A:H8	1.68	0.57
22:D0:106:ILE:HG23	22:D0:107:THR:HG23	1.87	0.57
39:L2:53:GLY:O	39:L2:192:LYS:NZ	3.17	0.57
36:1:2402:A:H5''	41:L4:67:THR:OG1	2.04	0.57
43:L6:142:ASP:O	43:L6:146:ILE:HG13	4.42	0.57
45:L8:91:PHE:CE1	45:L8:185:ARG:HD2	2.39	0.57
47:M0:218:ALA:O	87:M0:302:OHX:N3	74.05	0.57
59:N3:89:ASP:OD1	59:N3:90:GLY:N	3.56	0.57
62:N6:83:ASP:O	62:N6:84:LYS:HB2	2.27	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:Q3:38:ASP:HA	79:Q3:45:LYS:HA	2.03	0.57
3:S1:209:ASN:O	3:S1:210:ILE:HG13	3.42	0.57
11:S9:143:ILE:HG13	1:6:767:U:H5	424.50	0.57
11:S9:93:LEU:HA	11:S9:96:VAL:HG13	1.90	0.57
36:1:1440:G:H2'	36:1:1441:G:H8	1.69	0.57
36:1:2787:G:O6	87:1:3938:OHX:N3	2.37	0.57
36:1:528:U:H2'	36:1:529:A:C8	2.40	0.57
1:2:1006:C:OP1	87:2:2002:OHX:N1	2.38	0.57
1:2:1169:G:N1	1:2:1575:G:OP2	2.34	0.57
1:2:1236:A:C1'	33:E1:138:ARG:HH22	2.17	0.57
1:2:1570:A:OP1	87:2:2131:OHX:N6	2.37	0.57
36:5:1701:C:H2'	36:5:1702:U:O4'	2.04	0.57
36:5:3311:C:OP1	87:5:4156:OHX:N1	2.36	0.57
1:6:1160:A:H2'	1:6:1161:C:C6	2.39	0.57
1:6:992:A:O2'	1:6:1785:U:O2	2.22	0.57
8:S6:136:LYS:NZ	1:6:65:A:O5'	337.66	0.57
20:C8:53:ASP:HB3	20:C8:56:LYS:HG3	1.85	0.57
27:D5:93:SER:HB3	27:D5:100:ILE:HB	3.38	0.57
41:L4:42:VAL:C	41:L4:44:LYS:H	2.70	0.57
46:L9:70:THR:HG21	36:5:3122:A:N1	325.66	0.57
48:M1:166:LYS:C	48:M1:168:ASP:H	2.20	0.57
50:M4:134:ALA:HA	50:M4:137:LYS:HG3	3.48	0.57
51:M5:93:LYS:HG3	36:5:289:A:H2	146.92	0.57
63:N7:46:ILE:HD11	63:N7:49:TYR:CD2	4.36	0.57
63:N7:83:THR:HG23	63:N7:85:TYR:N	2.19	0.57
51:M5:143:ARG:HH21	71:O5:92:LEU:HD23	1.70	0.57
72:O6:58:ILE:HG12	72:O6:59:ASP:N	2.46	0.57
11:S9:161:THR:HG22	11:S9:162:SER:H	2.02	0.57
36:1:1851:G:OP2	87:1:3873:OHX:N4	2.38	0.57
36:1:172:G:N7	87:1:3887:OHX:N5	2.52	0.57
36:1:621:A:O2'	87:1:4061:OHX:N5	2.37	0.57
1:2:885:G:H21	16:C4:123:SER:HB2	1.68	0.57
36:5:1238:C:H2'	36:5:1239:C:C6	2.38	0.57
36:5:956:U:OP1	87:5:4065:OHX:N2	2.38	0.57
10:S8:141:ARG:NH2	1:6:195:G:O6	278.09	0.57
32:E0:14:VAL:HG21	1:6:567:A:N3	380.18	0.57
20:C8:49:LYS:NZ	20:C8:79:TYR:O	2.37	0.57
30:D8:13:ILE:HB	30:D8:29:ARG:HG3	5.00	0.57
44:L7:64:GLN:HA	44:L7:67:ARG:HB2	2.59	0.57
36:1:1048:A:H2'	47:M0:22:TYR:CZ	2.40	0.57
48:M1:93:ASP:OD2	48:M1:156:LYS:NZ	4.08	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:M8:169:GLY:O	54:M8:174:ARG:HD2	3.91	0.57
36:1:2635:A:H2	57:N1:10:ARG:NH1	2.01	0.57
57:N1:127:GLN:O	57:N1:127:GLN:NE2	3.34	0.57
59:N3:17:LEU:O	59:N3:52:ALA:N	2.80	0.57
38:4:99:C:OP1	61:N5:53:HIS:NE2	2.37	0.57
79:Q3:62:LYS:HZ2	36:5:2554:A:H62	218.29	0.57
4:S2:69:ILE:HG12	4:S2:133:LYS:HB3	2.81	0.57
4:S2:89:GLN:HG3	4:S2:93:GLY:O	3.45	0.57
7:S5:97:LEU:O	7:S5:180:ARG:NH2	4.11	0.57
7:S5:20:PHE:CZ	7:S5:22:PRO:HB3	3.22	0.57
8:S6:167:LYS:HE2	8:S6:169:TYR:HE2	1.69	0.57
11:S9:3:ARG:H	11:S9:3:ARG:HD3	2.12	0.57
36:1:1721:U:OP2	55:M9:124:TYR:OH	2.08	0.57
36:1:781:G:O6	87:1:3837:OHX:N3	2.38	0.57
36:5:1025:A:H3'	36:5:1026:A:H4'	1.86	0.57
36:5:1478:C:H2'	36:5:1479:U:C6	2.40	0.57
36:5:2213:A:H2'	36:5:2214:A:C8	2.40	0.57
36:5:328:U:O4	87:8:214:OHX:N1	2.38	0.57
38:8:10:A:H2'	38:8:11:C:C6	2.38	0.57
15:C3:84:ILE:H	15:C3:84:ILE:HD13	4.37	0.57
40:L3:188:ILE:HD12	40:L3:189:SER:H	1.70	0.57
44:L7:123:THR:HA	44:L7:126:LEU:HD12	1.87	0.57
52:M6:74:ARG:O	52:M6:142:SER:OG	3.06	0.57
61:N5:67:ILE:HB	61:N5:83:VAL:HG12	2.51	0.57
63:N7:88:ASP:HB3	63:N7:121:ARG:NH1	2.79	0.57
4:S2:80:VAL:HA	4:S2:102:VAL:HG22	1.86	0.57
4:S2:38:VAL:HG13	4:S2:39:THR:HG23	1.85	0.57
5:S3:132:LYS:HD3	5:S3:192:PRO:HD2	2.45	0.57
7:S5:152:GLY:O	7:S5:154:ALA:N	2.37	0.57
11:S9:77:ILE:HG23	11:S9:86:LEU:HD23	2.38	0.57
34:SR:28:GLY:N	34:SR:75:ALA:O	2.35	0.57
36:1:1612:A:H5''	74:O8:51:LEU:HD23	1.85	0.57
36:1:2164:A:OP1	39:L2:8:GLN:NE2	2.33	0.57
36:1:3049:A:C2	40:L3:75:ALA:HB2	2.40	0.57
1:2:1111:G:C2	1:2:1112:G:H1'	2.40	0.57
18:C6:6:SER:HB2	18:C6:23:LYS:HB3	2.99	0.57
23:D1:71:ARG:HG2	23:D1:83:TRP:CH2	3.15	0.57
28:D6:38:ARG:O	28:D6:71:LEU:HB2	2.05	0.57
40:L3:46:PHE:HZ	40:L3:83:PRO:HA	1.68	0.57
51:M5:143:ARG:HH21	71:O5:92:LEU:HA	1.70	0.57
36:1:1802:C:O2'	70:O4:59:PRO:O	2.10	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S0:142:PRO:HB3	23:D1:34:ILE:HD13	2.19	0.57
36:1:2571:U:O2'	36:1:2572:C:O2	2.23	0.57
36:1:267:G:O4'	51:M5:50:ARG:HD2	2.04	0.57
36:1:2533:G:N7	87:1:3893:OHX:N4	2.53	0.57
1:2:413:U:H2'	1:2:414:C:C6	2.40	0.57
70:O4:10:ARG:O	36:5:1488:G:O2'	140.04	0.57
36:5:2731:U:OP2	87:5:4137:OHX:N2	2.38	0.57
36:5:1881:A:OP2	87:5:3944:OHX:N4	2.38	0.57
1:6:21:U:H2'	1:6:22:A:H8	1.70	0.57
1:6:895:G:H1	1:6:917:U:H3	1.51	0.57
25:D3:133:LEU:HD11	25:D3:137:LYS:HZ3	1.68	0.57
6:S4:69:HIS:HB3	26:D4:17:LEU:HD23	1.86	0.57
41:L4:64:SER:OG	41:L4:65:TRP:N	2.38	0.57
42:L5:287:ALA:O	42:L5:290:ILE:HG12	2.04	0.57
42:L5:83:LEU:HB3	42:L5:88:ILE:HB	2.10	0.57
52:M6:79:ILE:HG21	52:M6:138:LEU:HD11	2.02	0.57
63:N7:103:GLN:HB3	63:N7:106:GLN:HG3	2.45	0.57
68:O2:61:LYS:HZ3	68:O2:61:LYS:HB2	1.97	0.57
3:S1:36:SER:O	3:S1:38:PHE:N	2.34	0.57
1:2:1437:U:H5'	5:S3:176:LEU:HD23	1.87	0.57
6:S4:57:ASN:HB2	6:S4:60:GLU:H	1.69	0.57
9:S7:74:GLN:HG2	9:S7:131:PHE:CD2	6.22	0.57
36:1:1145:G:OP1	68:O2:44:ARG:NH1	2.33	0.57
36:1:2532:U:H3	36:1:2547:A:H61	1.51	0.57
1:2:1229:G:O2'	1:2:1255:G:N2	2.37	0.57
1:2:330:G:H2'	1:2:331:A:C8	2.40	0.57
1:2:458:G:OP1	26:D4:109:LYS:NZ	2.32	0.57
36:5:3113:A:OP2	87:5:3924:OHX:N4	2.38	0.57
1:6:524:U:N3	1:6:527:A:OP2	2.34	0.57
12:C0:54:TYR:CD2	12:C0:72:GLY:HA2	4.02	0.57
14:C2:54:ARG:O	14:C2:85:LYS:NZ	2.37	0.57
40:L3:211:GLN:NE2	40:L3:283:TYR:O	2.33	0.57
42:L5:183:TRP:CZ3	42:L5:185:PHE:HA	7.61	0.57
47:M0:54:SER:HB2	47:M0:135:ILE:HD11	3.00	0.57
51:M5:13:LYS:O	51:M5:16:SER:OG	2.17	0.57
53:M7:21:TYR:H	53:M7:145:HIS:CE1	2.73	0.57
69:O3:69:GLY:HA3	69:O3:85:PHE:HA	2.37	0.57
4:S2:102:VAL:HG11	4:S2:129:ILE:HG12	1.86	0.57
9:S7:86:GLN:HG3	9:S7:87:ASP:H	1.69	0.57
11:S9:65:LYS:HA	11:S9:70:LEU:HD11	2.42	0.57
36:1:950:G:N1	36:1:1368:U:OP2	2.29	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1677:G:N7	58:N2:74:LYS:HE3	2.20	0.57
36:1:3233:C:H2'	36:1:3234:A:C8	2.40	0.57
36:1:739:G:O6	87:1:3815:OHX:N3	2.38	0.57
36:1:52:A:N3	36:1:811:U:O2'	2.38	0.57
1:2:1132:A:H2'	1:2:1133:A:H8	1.70	0.57
1:2:1483:A:H2'	1:2:1484:G:C8	2.40	0.57
1:2:142:G:H22	1:2:173:A:H2	1.53	0.57
1:2:189:C:H42	1:2:197:A:H2	1.51	0.57
1:2:1237:G:OP2	87:2:2014:OHX:N1	2.37	0.57
1:2:1385:G:N7	87:2:2102:OHX:N3	2.53	0.57
1:2:895:G:H1	1:2:917:U:H3	1.51	0.57
38:4:132:G:N7	87:4:223:OHX:N1	2.53	0.57
36:5:1108:U:H2'	36:5:1109:U:C6	2.40	0.57
36:5:1557:A:N7	36:5:1559:A:N6	2.53	0.57
7:S5:112:ARG:HD2	1:6:1529:C:OP1	375.68	0.57
1:6:1573:A:H4'	1:6:1574:G:H5'	1.86	0.57
1:6:209:U:H2'	1:6:210:A:H8	1.70	0.57
15:C3:54:LEU:HB3	15:C3:60:VAL:HG13	4.16	0.57
15:C3:3:ARG:HB3	15:C3:6:SER:HB2	1.87	0.57
7:S5:37:GLN:HE21	18:C6:46:PHE:HD1	1.53	0.57
20:C8:102:ALA:O	20:C8:104:ASN:N	2.36	0.57
21:C9:15:ILE:HD13	21:C9:60:SER:HA	2.43	0.57
33:E1:144:CYS:HB3	33:E1:147:VAL:HG12	3.14	0.57
36:1:2525:G:OP2	39:L2:37:ARG:NH1	2.38	0.57
41:L4:53:SER:HB3	41:L4:56:ALA:HB2	1.87	0.57
42:L5:85:ARG:HH12	42:L5:254:LYS:H	4.91	0.57
43:L6:105:TYR:CE1	43:L6:134:ARG:HD3	2.67	0.57
51:M5:143:ARG:NH2	71:O5:92:LEU:HD23	2.19	0.57
57:N1:14:MET:HE1	57:N1:55:LYS:HB2	2.99	0.57
76:Q0:110:CYS:SG	76:Q0:111:ARG:N	3.27	0.57
11:S9:75:ALA:HA	11:S9:78:ARG:HB3	4.16	0.57
36:1:381:U:H2'	36:1:382:U:H6	1.70	0.56
1:2:1:U:C4	11:S9:54:ARG:HG3	2.40	0.56
36:5:1365:G:OP2	87:5:3943:OHX:N3	2.38	0.56
36:5:2319:U:O4	87:5:3910:OHX:N2	2.38	0.56
36:5:2916:U:H5	36:5:2935:U:HO2'	1.53	0.56
36:5:3022:G:O2'	36:5:3031:G:O6	2.19	0.56
36:5:248:U:O4	87:5:4129:OHX:N1	2.38	0.56
1:6:1073:G:N7	87:6:2107:OHX:N1	2.53	0.56
13:C1:39:GLY:O	13:C1:41:GLY:N	2.38	0.56
17:C5:123:TYR:HH	20:C8:126:ARG:HH12	1.47	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:D7:2:VAL:O	29:D7:3:LEU:HB2	2.15	0.56
39:L2:54:ARG:HG2	39:L2:55:GLY:O	4.53	0.56
41:L4:60:THR:HG22	41:L4:62:ALA:N	2.20	0.56
42:L5:79:TYR:HB2	42:L5:81:HIS:CD2	4.41	0.56
53:M7:22:LEU:HD12	53:M7:146:ILE:HG13	2.48	0.56
57:N1:48:ILE:HG13	57:N1:94:GLU:HG2	1.87	0.56
62:N6:36:SER:O	62:N6:38:GLU:N	2.38	0.56
63:N7:53:VAL:HG21	63:N7:62:VAL:HG13	1.86	0.56
66:O0:34:LEU:HD21	66:O0:42:ILE:HG21	1.87	0.56
6:S4:176:ASP:N	6:S4:176:ASP:OD2	4.32	0.56
8:S6:164:LYS:HD3	8:S6:167:LYS:HD3	1.87	0.56
9:S7:133:THR:HG22	9:S7:159:VAL:HG12	1.86	0.56
36:1:2094:C:H2'	36:1:2095:G:C8	2.39	0.56
36:1:2150:G:O2'	36:1:2189:U:OP1	2.22	0.56
36:1:2969:A:N7	39:L2:215:ASN:ND2	2.54	0.56
1:2:1374:C:H2'	1:2:1375:A:C8	2.40	0.56
1:2:138:A:OP2	1:2:1706:C:O2'	2.19	0.56
36:5:23:A:H2'	36:5:24:G:H8	1.68	0.56
63:N7:135:ARG:HH22	36:5:2557:A:H5'	197.77	0.56
36:5:3193:C:H2'	36:5:3194:C:H6	1.71	0.56
36:5:891:G:OP1	87:5:3833:OHX:N2	2.38	0.56
17:C5:128:HIS:HA	1:6:1180:C:O2'	336.17	0.56
1:6:550:A:OP2	87:6:2015:OHX:N6	2.37	0.56
1:6:346:G:N7	87:6:2127:OHX:N2	2.53	0.56
26:D4:11:LYS:NZ	1:6:776:G:O6	418.31	0.56
14:C2:60:VAL:HG23	14:C2:87:PRO:HG2	2.03	0.56
15:C3:42:ARG:HG2	15:C3:80:LEU:HD21	5.88	0.56
27:D5:93:SER:HB2	27:D5:100:ILE:HB	1.86	0.56
28:D6:84:VAL:HG13	28:D6:85:ARG:H	1.70	0.56
45:L8:139:VAL:O	45:L8:143:ILE:HG13	2.45	0.56
46:L9:44:THR:HG22	36:5:3186:A:C2	326.44	0.56
55:M9:6:THR:HG23	55:M9:9:ARG:HH21	1.69	0.56
59:N3:89:ASP:OD1	59:N3:91:VAL:HG12	4.69	0.56
71:O5:89:ARG:HH11	71:O5:89:ARG:HG2	1.70	0.56
76:Q0:100:TYR:O	36:5:2895:G:O2'	313.55	0.56
5:S3:192:PRO:HB2	5:S3:201:ALA:HA	2.14	0.56
36:1:1951:C:H3'	36:1:1952:G:H8	1.70	0.56
36:1:2378:C:H2'	36:1:2379:U:H6	1.69	0.56
36:1:773:G:O6	87:1:3783:OHX:N6	2.38	0.56
1:2:1300:A:OP1	4:S2:99:LYS:NZ	2.36	0.56
1:2:1757:G:H4'	36:1:2256:A:N7	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:3:41:G:H1'	37:3:44:C:H42	1.71	0.56
36:1:1831:U:O2'	38:4:114:G:OP1	2.19	0.56
36:5:2859:U:O2'	87:5:3818:OHX:N5	2.39	0.56
36:5:1310:G:O6	87:5:3940:OHX:N4	2.38	0.56
36:5:528:U:H2'	36:5:529:A:H8	1.70	0.56
1:6:1419:G:H2'	1:6:1420:C:O4'	2.06	0.56
3:S1:83:LYS:NZ	16:C4:116:GLU:OE2	2.24	0.56
21:C9:57:ARG:O	21:C9:61:VAL:HG23	2.50	0.56
24:D2:101:TYR:HB2	24:D2:129:VAL:HG23	4.03	0.56
1:2:1251:U:H5'	33:E1:135:HIS:CD2	2.40	0.56
39:L2:95:SER:OG	39:L2:96:LEU:N	2.36	0.56
40:L3:138:ALA:O	40:L3:140:ASP:N	4.47	0.56
42:L5:156:GLY:HA2	42:L5:181:PRO:HD3	1.87	0.56
44:L7:178:ILE:HD11	44:L7:187:GLU:HG2	1.86	0.56
46:L9:49:ASN:O	46:L9:49:ASN:ND2	2.36	0.56
47:M0:36:LEU:HD21	47:M0:69:ARG:HD3	1.87	0.56
36:1:3243:A:C8	52:M6:156:LEU:HD22	2.40	0.56
71:O5:45:LYS:HD2	71:O5:49:LYS:HD3	3.05	0.56
71:O5:82:ALA:HB1	71:O5:84:LYS:HD3	3.40	0.56
4:S2:41:LEU:HD12	4:S2:68:ILE:HD13	1.87	0.56
11:S9:31:ALA:HA	11:S9:36:LEU:HD12	2.00	0.56
36:1:1039:U:H2'	36:1:1040:A:C8	2.40	0.56
36:1:1064:A:H4'	36:1:1065:A:O5'	2.05	0.56
36:1:1196:C:O2	87:1:3889:OHX:N1	2.38	0.56
1:2:1291:G:N2	1:2:1324:G:H22	2.03	0.56
1:2:1352:G:H2'	1:2:1353:U:O4'	2.05	0.56
1:2:1564:U:H2'	1:2:1565:C:H6	1.71	0.56
1:6:86:A:OP2	87:6:2168:OHX:N1	2.38	0.56
12:C0:44:LYS:HA	12:C0:47:GLN:HB3	2.46	0.56
15:C3:7:ALA:O	15:C3:9:LYS:NZ	2.33	0.56
19:C7:20:TYR:CD1	19:C7:38:ILE:HD11	2.40	0.56
40:L3:284:ARG:NH2	40:L3:293:ASN:O	2.56	0.56
42:L5:155:THR:HB	42:L5:179:ARG:HH11	1.69	0.56
47:M0:14:ASN:O	47:M0:128:ARG:NH2	2.44	0.56
57:N1:132:PRO:O	57:N1:134:GLN:NE2	3.71	0.56
58:N2:33:TYR:HE1	58:N2:37:LEU:HD23	6.40	0.56
66:O0:13:LYS:O	66:O0:17:VAL:HG23	2.29	0.56
68:O2:121:ASN:OD1	68:O2:121:ASN:N	2.38	0.56
3:S1:83:LYS:HE2	3:S1:106:THR:HG22	1.87	0.56
4:S2:51:THR:HG22	4:S2:52:THR:HG23	1.87	0.56
5:S3:53:THR:HG21	5:S3:94:ARG:HD3	4.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S4:208:VAL:HG11	6:S4:225:VAL:HG21	1.86	0.56
1:2:140:A:OP2	8:S6:187:LYS:NZ	2.37	0.56
9:S7:69:GLY:HA2	9:S7:72:LYS:HD2	1.85	0.56
36:1:1365:G:OP2	87:1:3863:OHX:N6	2.39	0.56
36:1:2611:U:H2'	36:1:2612:U:C6	2.41	0.56
1:2:1606:C:H2'	1:2:1607:G:C8	2.40	0.56
1:2:1770:U:O2'	87:2:2061:OHX:N5	2.38	0.56
36:5:2683:U:H2'	36:5:2684:C:H6	1.69	0.56
1:6:1239:U:O4	87:6:2063:OHX:N1	2.37	0.56
37:7:112:G:OP2	87:7:218:OHX:N6	2.39	0.56
42:L5:233:ALA:O	42:L5:235:SER:N	2.38	0.56
43:L6:45:GLY:O	43:L6:48:ARG:HG2	2.30	0.56
45:L8:24:ASN:O	45:L8:26:LEU:N	4.02	0.56
53:M7:125:GLN:HB2	53:M7:141:SER:HB2	1.86	0.56
54:M8:96:PHE:CD2	54:M8:97:PRO:HD2	2.41	0.56
56:N0:155:ARG:NH2	56:N0:172:TYR:H	4.44	0.56
56:N0:6:GLU:OE1	56:N0:99:ARG:NH2	3.68	0.56
61:N5:115:ARG:NH1	61:N5:119:THR:OG1	2.40	0.56
49:M3:157:ARG:NH1	64:N8:124:ILE:HG21	3.81	0.56
49:M3:174:ARG:HB2	72:O6:9:ILE:HD12	1.87	0.56
78:Q2:15:LYS:HG3	78:Q2:18:ARG:NH1	5.02	0.56
3:S1:191:GLU:OE1	3:S1:194:ASN:ND2	2.39	0.56
8:S6:21:GLU:HA	8:S6:24:ILE:HG13	2.32	0.56
11:S9:11:THR:O	11:S9:47:PHE:HD2	2.29	0.56
34:SR:38:ARG:HG2	34:SR:67:ILE:HD13	2.26	0.56
36:1:604:G:N7	87:1:4036:OHX:N4	2.53	0.56
1:2:1156:C:C2'	1:2:1157:A:H5'	2.35	0.56
1:2:1290:U:H2'	1:2:1291:G:C8	2.41	0.56
38:4:11:C:H2'	38:4:12:A:C8	2.40	0.56
36:5:3383:G:H2'	36:5:3384:U:H6	1.70	0.56
1:6:1413:U:H4'	1:6:1414:U:OP2	2.05	0.56
22:D0:66:SER:HA	22:D0:81:THR:HA	1.86	0.56
39:L2:204:MET:HB3	39:L2:208:ASP:HB2	3.62	0.56
40:L3:223:GLY:HA2	40:L3:271:GLY:HA3	1.87	0.56
40:L3:5:LYS:HG2	40:L3:6:TYR:CE1	3.35	0.56
44:L7:151:ARG:HD2	44:L7:244:ASN:OD1	2.30	0.56
46:L9:163:GLN:OE1	46:L9:166:ARG:NH1	2.38	0.56
48:M1:155:THR:O	48:M1:159:THR:HG23	5.22	0.56
49:M3:105:ASN:OD1	49:M3:107:GLU:HG2	2.33	0.56
49:M3:166:ALA:N	64:N8:135:GLU:OE1	2.58	0.56
68:O2:97:ALA:HB3	68:O2:100:ILE:HG12	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:O4:80:ARG:HB2	70:O4:85:VAL:HG13	5.04	0.56
74:O8:11:PHE:O	74:O8:15:THR:HG23	2.05	0.56
79:Q3:59:CYS:SG	79:Q3:60:CYS:N	3.14	0.56
2:S0:31:VAL:HG23	2:S0:150:ASP:HA	1.88	0.56
4:S2:109:GLY:HA2	4:S2:139:ILE:HG22	1.87	0.56
4:S2:53:ILE:HD12	4:S2:53:ILE:H	3.88	0.56
7:S5:64:VAL:HG12	7:S5:65:ARG:HD3	1.86	0.56
36:1:1103:A:N7	44:L7:158:LYS:HD3	2.21	0.56
36:1:1240:A:H61	36:1:1244:A:H5''	1.70	0.56
36:1:1336:U:H2'	36:1:1337:A:H8	1.71	0.56
36:1:2771:U:OP2	36:1:2772:C:N4	2.34	0.56
36:1:99:A:OP1	51:M5:194:GLN:NE2	2.38	0.56
1:2:194:U:O2'	1:2:195:G:O4'	2.23	0.56
38:4:11:C:OP2	87:4:229:OHX:N1	2.39	0.56
36:5:1846:C:H5'	36:5:1849:C:N4	2.21	0.56
36:5:3295:A:H2'	36:5:3296:A:C8	2.41	0.56
1:6:1079:U:H2'	1:6:1080:U:O4'	2.05	0.56
20:C8:132:ARG:CZ	1:6:1544:U:H4'	346.82	0.56
1:6:349:U:O4	87:6:2129:OHX:N6	2.39	0.56
38:8:150:G:N7	87:8:215:OHX:N5	2.53	0.56
14:C2:75:VAL:HG21	14:C2:120:VAL:HG21	2.45	0.56
20:C8:20:THR:HG21	20:C8:35:ILE:HG23	4.36	0.56
39:L2:215:ASN:HB2	36:5:2968:G:N7	217.93	0.56
43:L6:56:LYS:HD2	43:L6:98:VAL:HG13	1.88	0.56
43:L6:89:THR:HG21	50:M4:115:PHE:HB2	1.86	0.56
47:M0:46:PHE:CD1	47:M0:140:THR:HA	2.41	0.56
50:M4:22:LEU:HB3	50:M4:64:VAL:HG13	2.36	0.56
58:N2:28:PHE:CE1	58:N2:83:TYR:HE2	2.44	0.56
61:N5:101:GLU:HG2	61:N5:102:LEU:HD23	2.54	0.56
61:N5:135:ILE:HD11	61:N5:138:ARG:HH11	1.70	0.56
63:N7:135:ARG:HH11	36:5:1807:G:H5'	195.63	0.56
1:2:78:A:OP2	87:S6:301:OHX:N3	2.39	0.56
36:1:3365:U:H2'	36:1:3366:G:C8	2.39	0.56
36:1:2310:U:OP1	87:1:4038:OHX:N1	2.39	0.56
1:2:190:C:H42	10:S8:141:ARG:HH22	1.54	0.56
1:2:484:C:N4	1:2:503:G:H22	2.04	0.56
1:2:652:G:H1	1:2:682:C:H42	1.54	0.56
1:2:827:C:H2'	1:2:828:U:C6	2.40	0.56
1:2:222:A:N6	1:2:839:U:H3	2.04	0.56
37:3:4:U:H2'	37:3:5:G:C8	2.41	0.56
36:5:1440:G:N7	87:5:3879:OHX:N4	2.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:3241:G:H2'	36:5:3245:A:C8	2.41	0.56
87:5:4053:OHX:N4	38:8:43:A:OP1	2.39	0.56
36:5:1770:G:N7	87:5:4139:OHX:N1	2.52	0.56
36:5:655:C:H2'	36:5:656:A:C8	2.41	0.56
62:N6:13:ARG:NH1	38:8:24:G:OP2	88.15	0.56
18:C6:12:LYS:HG2	18:C6:17:THR:HA	3.78	0.56
19:C7:35:CYS:HA	19:C7:38:ILE:HG22	1.86	0.56
33:E1:98:VAL:HG12	33:E1:99:LYS:H	3.61	0.56
48:M1:17:LEU:HB3	48:M1:76:ALA:HB1	1.86	0.56
64:N8:22:ILE:HD13	36:5:1114:U:H5''	191.87	0.56
36:1:1738:C:H1'	70:O4:52:GLN:HG3	1.88	0.56
38:4:38:U:C4	71:O5:89:ARG:HD2	2.41	0.56
78:Q2:77:CYS:SG	78:Q2:79:THR:OG1	2.61	0.56
3:S1:77:GLU:OE1	16:C4:114:ARG:NH2	2.39	0.56
6:S4:123:LEU:HA	6:S4:160:VAL:O	2.06	0.56
36:1:1812:G:O3'	36:1:1817:G:O2'	2.24	0.56
36:1:1845:G:O2'	73:O7:5:THR:HG22	2.05	0.56
36:1:2544:U:H2'	36:1:2545:C:C6	2.40	0.56
1:2:240:U:H4'	1:2:241:U:OP2	2.05	0.56
1:2:789:A:O2'	6:S4:106:LYS:NZ	2.39	0.56
36:5:1346:G:H1	36:5:1358:C:H42	1.54	0.56
36:5:748:U:H2'	36:5:749:C:C6	2.41	0.56
1:6:485:A:N6	1:6:486:G:N3	2.53	0.56
1:6:845:G:H2'	1:6:846:G:C8	2.41	0.56
15:C3:18:TYR:HA	24:D2:56:HIS:CD2	2.77	0.56
29:D7:23:THR:HG21	29:D7:29:ARG:NH2	3.79	0.56
29:D7:36:LYS:HB3	29:D7:43:ILE:HG22	1.86	0.56
36:1:860:G:O5'	39:L2:181:LYS:NZ	2.39	0.56
40:L3:142:ALA:O	40:L3:144:ILE:N	3.83	0.56
41:L4:141:ARG:O	41:L4:143:GLU:N	3.85	0.56
42:L5:84:PRO:O	42:L5:86:TYR:N	2.39	0.56
51:M5:65:ARG:HB3	51:M5:127:TYR:HD1	1.69	0.56
62:N6:57:LEU:HB2	62:N6:67:GLU:HB3	1.87	0.56
69:O3:49:ILE:HG23	69:O3:100:ILE:HG13	2.34	0.56
77:Q1:8:LYS:HD3	77:Q1:12:ARG:NH2	2.21	0.56
77:Q1:1:MET:SD	77:Q1:9:ARG:NH1	5.32	0.56
79:Q3:32:GLN:HG2	79:Q3:70:THR:HB	1.88	0.56
34:SR:240:VAL:HG22	34:SR:256:THR:HG22	2.30	0.56
36:1:1711:C:H2'	36:1:1712:G:O4'	2.06	0.56
36:1:2534:G:H22	36:1:2545:C:H42	1.52	0.56
36:1:3019:U:O4	87:1:3884:OHX:N1	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1482:C:OP2	1:2:1521:G:N2	2.33	0.56
36:5:1611:G:H2'	36:5:1612:A:H8	1.71	0.56
36:5:3022:G:O2'	87:5:3995:OHX:N1	2.39	0.56
36:5:595:G:C8	36:5:609:G:C6	2.93	0.56
36:5:595:G:H1	36:5:609:G:H5''	1.71	0.56
25:D3:102:VAL:HG12	25:D3:127:VAL:HG12	1.88	0.56
26:D4:106:GLN:O	26:D4:110:GLN:HB2	2.79	0.56
26:D4:8:ARG:HB2	26:D4:26:ASP:HB3	1.88	0.56
27:D5:43:ASP:O	27:D5:45:GLU:N	3.61	0.56
43:L6:38:THR:HG23	43:L6:90:LYS:HG2	4.42	0.56
45:L8:144:GLU:OE1	72:O6:36:ARG:NH2	2.38	0.56
66:O0:43:ILE:HD11	66:O0:92:ILE:HD11	1.87	0.56
71:O5:85:THR:HG22	71:O5:87:ALA:H	2.60	0.56
79:Q3:24:ARG:NH2	1:6:982:U:O3'	251.75	0.56
2:S0:70:PRO:O	2:S0:95:ALA:N	2.98	0.56
4:S2:243:TYR:HB3	4:S2:246:GLU:HG3	1.88	0.56
8:S6:52:ILE:HG23	8:S6:109:LEU:HD21	2.30	0.56
36:1:2869:U:O2'	36:1:2873:U:OP1	2.20	0.56
36:1:3031:G:O6	87:1:3967:OHX:N2	2.38	0.56
1:2:1374:C:H2'	1:2:1375:A:H8	1.69	0.56
1:6:1572:G:H2'	1:6:1572:G:N3	2.21	0.56
19:C7:104:ASN:O	19:C7:106:THR:N	3.56	0.56
21:C9:42:GLY:HA2	21:C9:84:LYS:HD2	4.58	0.56
40:L3:250:ALA:HB3	36:5:2880:U:H1'	225.20	0.56
44:L7:98:LYS:HB3	44:L7:99:PRO:HD3	2.05	0.56
47:M0:58:GLU:OE2	47:M0:161:GLY:HA3	2.06	0.56
48:M1:90:GLN:NE2	48:M1:170:ASP:OD1	2.93	0.56
55:M9:90:PRO:HB2	55:M9:93:VAL:HG23	1.87	0.56
59:N3:87:ARG:HH22	59:N3:137:VAL:HG22	2.58	0.56
36:1:1508:C:C6	36:1:1880:U:H1'	2.41	0.55
36:1:1919:G:H1'	36:1:1934:G:N2	2.20	0.55
36:1:3199:G:O6	87:1:4027:OHX:N1	2.39	0.55
36:1:715:A:H4'	36:1:716:A:OP1	2.06	0.55
1:2:1523:G:H8	21:C9:79:LEU:HD13	1.72	0.55
36:5:1895:A:O2'	36:5:3053:G:H4'	2.06	0.55
36:5:1919:G:N7	87:5:3983:OHX:N4	2.54	0.55
36:5:21:G:H1	38:8:138:A:H61	1.53	0.55
36:5:3192:U:H2'	36:5:3193:C:C6	2.41	0.55
36:5:3343:G:H21	36:5:3362:A:H2	1.54	0.55
36:5:835:G:O2'	36:5:857:G:N2	2.27	0.55
28:D6:2:PRO:HB3	1:6:1142:A:H5''	349.90	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:973:A:H2'	1:6:974:A:H8	1.70	0.55
15:C3:148:ALA:O	15:C3:150:VAL:N	2.38	0.55
32:E0:37:ARG:O	32:E0:41:THR:OG1	2.88	0.55
45:L8:163:VAL:HG22	45:L8:166:LEU:HD12	2.64	0.55
47:M0:61:SER:OG	47:M0:63:GLU:HG2	2.89	0.55
51:M5:45:PRO:O	51:M5:49:ARG:HB2	4.08	0.55
52:M6:8:VAL:HG22	52:M6:34:VAL:HG13	2.25	0.55
58:N2:19:VAL:HG12	58:N2:105:LEU:HD22	2.38	0.55
62:N6:40:ARG:O	62:N6:44:GLY:N	2.39	0.55
62:N6:5:SER:HB2	62:N6:8:VAL:HG22	6.93	0.55
67:O1:13:THR:HG22	67:O1:72:ARG:HD3	2.17	0.55
77:Q1:6:ARG:NH1	1:6:1114:G:OP2	311.98	0.55
78:Q2:2:VAL:HG23	78:Q2:91:PHE:HD1	1.97	0.55
2:S0:167:LYS:HE3	2:S0:168:HIS:CD2	3.17	0.55
4:S2:118:ALA:HB3	4:S2:124:ALA:HB2	2.15	0.55
7:S5:93:LEU:HD11	7:S5:198:LEU:HD11	3.71	0.55
34:SR:95:ALA:O	34:SR:97:GLY:N	4.96	0.55
36:1:2697:A:H2'	36:1:2698:G:C8	2.41	0.55
36:1:352:A:H61	36:1:365:A:H5''	1.69	0.55
36:1:1930:A:O2'	87:1:3794:OHX:N4	2.40	0.55
36:1:1650:G:O6	87:1:4037:OHX:N2	2.39	0.55
1:2:1282:U:OP1	87:2:2084:OHX:N1	2.39	0.55
36:5:1814:A:OP1	87:5:4095:OHX:N1	2.38	0.55
36:5:2534:G:O6	87:5:3954:OHX:N2	2.40	0.55
71:O5:83:LYS:NZ	38:8:38:U:O2'	72.43	0.55
17:C5:57:MET:HA	17:C5:60:LEU:HG	3.86	0.55
21:C9:108:LEU:HA	21:C9:111:ILE:HG22	1.87	0.55
27:D5:59:TYR:HE2	27:D5:61:SER:HB3	1.71	0.55
39:L2:102:LEU:HD12	39:L2:166:ILE:HD11	1.86	0.55
36:1:2392:C:HO2'	40:L3:266:ARG:NH2	2.04	0.55
44:L7:222:HIS:CE1	44:L7:224:ILE:HG13	2.74	0.55
50:M4:109:ARG:HD3	52:M6:199:TYR:CZ	2.41	0.55
59:N3:108:GLU:HB3	59:N3:128:ARG:HH11	4.86	0.55
63:N7:17:ARG:HA	70:O4:74:ARG:HA	1.88	0.55
65:N9:14:ARG:NH1	65:N9:18:ARG:HD3	2.83	0.55
2:S0:136:ALA:HB1	2:S0:141:ILE:HB	1.87	0.55
3:S1:81:PHE:O	3:S1:83:LYS:N	2.39	0.55
9:S7:154:LEU:HD21	9:S7:183:PHE:HD1	1.72	0.55
19:C7:23:LYS:NZ	34:SR:149:ASP:OD2	4.05	0.55
36:1:2208:A:C6	87:1:3940:OHX:N4	2.74	0.55
36:1:212:G:OP1	36:1:227:G:N2	2.33	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:945:C:H2'	36:1:946:U:C6	2.41	0.55
1:2:1780:G:OP2	87:2:2019:OHX:N3	2.38	0.55
1:2:38:C:H2'	1:2:39:A:H5'	1.88	0.55
1:2:840:U:O2'	1:2:841:U:H5''	2.06	0.55
36:5:1329:U:O2'	36:5:1330:A:H5''	2.07	0.55
36:5:655:C:H2'	36:5:656:A:H8	1.71	0.55
46:L9:137:SER:HB2	46:L9:143:GLU:HB3	3.04	0.55
36:1:2646:C:H4'	47:M0:119:TRP:CE2	2.42	0.55
59:N3:13:ILE:HG13	59:N3:53:SER:HB2	1.89	0.55
70:O4:54:ILE:HD11	70:O4:78:GLY:HA2	2.90	0.55
71:O5:95:PHE:O	71:O5:98:SER:OG	2.17	0.55
3:S1:59:ASP:O	3:S1:62:LYS:NZ	2.39	0.55
5:S3:223:LYS:HD3	34:SR:193:ILE:HD13	3.71	0.55
34:SR:93:ASP:HB3	34:SR:96:THR:HB	1.88	0.55
1:2:1119:G:O6	87:2:2119:OHX:N1	2.39	0.55
1:2:1695:G:H21	1:2:1706:C:N4	2.05	0.55
1:2:196:G:O2'	1:2:197:A:OP2	2.23	0.55
1:2:131:C:OP1	87:2:2041:OHX:N4	2.40	0.55
1:2:990:C:OP2	87:2:2059:OHX:N1	2.39	0.55
38:4:24:G:OP2	62:N6:13:ARG:HD3	2.05	0.55
36:5:1611:G:H2'	36:5:1612:A:C8	2.41	0.55
36:5:2683:U:H2'	36:5:2684:C:C6	2.41	0.55
1:6:986:G:OP2	87:6:2085:OHX:N6	2.39	0.55
15:C3:19:SER:O	15:C3:19:SER:OG	2.19	0.55
17:C5:34:VAL:O	17:C5:42:ARG:HG2	2.07	0.55
24:D2:77:PRO:O	24:D2:79:PHE:N	2.66	0.55
29:D7:49:HIS:CE1	29:D7:70:LYS:HG2	2.41	0.55
41:L4:98:ARG:HG2	41:L4:99:MET:O	2.27	0.55
42:L5:85:ARG:NH1	42:L5:250:ASP:O	2.32	0.55
42:L5:22:ARG:HG2	42:L5:28:THR:OG1	2.06	0.55
46:L9:168:ARG:O	46:L9:170:LYS:HG2	2.06	0.55
52:M6:88:VAL:O	52:M6:90:HIS:N	2.40	0.55
55:M9:7:GLN:HG2	55:M9:32:ILE:HG22	1.88	0.55
37:3:97:A:OP1	56:N0:40:ARG:NH1	2.39	0.55
59:N3:80:ARG:HB2	59:N3:99:ALA:HB3	1.89	0.55
68:O2:23:ASP:OD1	68:O2:23:ASP:N	2.35	0.55
72:O6:70:ARG:HG3	72:O6:87:VAL:HG21	2.90	0.55
2:S0:163:ASN:C	2:S0:165:ARG:H	2.27	0.55
2:S0:9:LEU:HD23	2:S0:54:TRP:CG	2.41	0.55
7:S5:176:THR:O	7:S5:180:ARG:NH1	4.57	0.55
9:S7:155:ASP:OD2	9:S7:156:SER:N	2.77	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1564:U:H2'	36:1:1565:G:C8	2.42	0.55
36:1:2217:U:H2'	36:1:2218:G:C8	2.41	0.55
36:1:2242:A:H5'	39:L2:243:THR:HG23	1.88	0.55
36:1:3365:U:H2'	36:1:3366:G:H8	1.71	0.55
36:1:1778:G:N7	87:1:4029:OHX:N4	2.54	0.55
1:2:1040:G:N2	1:2:1078:C:O2	2.35	0.55
1:2:980:G:O6	87:2:2012:OHX:N1	2.39	0.55
37:3:14:U:H5'	42:L5:24:ARG:NH1	2.22	0.55
36:5:1715:A:H4'	36:5:1716:U:H5'	1.88	0.55
36:5:678:G:O6	87:5:3929:OHX:N5	2.39	0.55
1:6:358:U:O4	87:6:2041:OHX:N2	2.40	0.55
10:S8:50:GLY:HA2	1:6:397:A:O3'	316.17	0.55
14:C2:28:LEU:HD23	14:C2:31:VAL:HB	3.70	0.55
24:D2:8:ALA:HB2	24:D2:74:VAL:HG11	2.55	0.55
26:D4:125:LEU:O	26:D4:128:LYS:HB3	3.43	0.55
47:M0:44:ASP:OD1	47:M0:185:ARG:NH1	2.37	0.55
36:1:744:A:H4'	54:M8:142:GLY:O	2.07	0.55
36:1:3067:C:H5''	55:M9:58:HIS:CD2	2.42	0.55
79:Q3:84:ARG:NH2	79:Q3:88:GLU:OE2	2.39	0.55
3:S1:97:LEU:HB3	3:S1:232:HIS:NE2	3.36	0.55
5:S3:192:PRO:O	5:S3:195:SER:OG	2.54	0.55
5:S3:214:GLU:OE1	34:SR:176:LYS:NZ	2.39	0.55
10:S8:107:THR:HG22	36:1:3354:U:C2	2.40	0.55
36:1:1907:C:O2	40:L3:240:ARG:NH2	2.37	0.55
36:1:2314:U:HO2'	36:1:2315:G:P	2.28	0.55
36:1:2186:U:H5'	36:1:2314:U:OP2	2.06	0.55
36:1:3312:U:H5''	40:L3:25:ILE:HD12	1.87	0.55
36:1:300:G:O6	87:1:4049:OHX:N1	2.40	0.55
1:2:154:G:OP1	8:S6:2:LYS:NZ	2.40	0.55
1:2:580:A:H5''	5:S3:143:ARG:NH1	2.22	0.55
1:2:901:G:OP2	1:2:901:G:N2	2.32	0.55
38:4:126:A:O2'	38:4:128:U:OP1	2.24	0.55
36:5:1238:C:H2'	36:5:1239:C:H6	1.72	0.55
36:5:2921:U:H2'	36:5:2923:U:OP2	2.07	0.55
36:5:3287:U:N3	36:5:3288:G:N7	2.55	0.55
40:L3:174:LYS:N	36:5:3314:A:OP1	205.45	0.55
1:6:1440:C:H2'	1:6:1441:C:O4'	2.06	0.55
17:C5:43:ARG:O	17:C5:47:ARG:HG3	2.06	0.55
21:C9:111:ILE:HG23	21:C9:113:ILE:HG13	1.89	0.55
24:D2:83:ILE:HG13	24:D2:122:SER:HB2	4.14	0.55
41:L4:142:VAL:HB	41:L4:145:ILE:HG21	3.83	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L5:40:HIS:CE1	42:L5:42:ALA:HB3	2.41	0.55
45:L8:100:GLU:OE2	45:L8:108:ARG:NH1	2.40	0.55
47:M0:34:TYR:O	47:M0:88:ARG:HA	2.60	0.55
47:M0:38:LYS:HG2	47:M0:41:ALA:HB2	1.87	0.55
54:M8:30:VAL:O	54:M8:34:THR:HG23	5.04	0.55
61:N5:106:ASP:HB2	61:N5:130:TYR:HE1	2.82	0.55
36:1:1639:C:H5''	70:O4:72:VAL:HG11	1.88	0.55
8:S6:139:ASN:HA	8:S6:142:ARG:HG3	3.13	0.55
36:1:3165:A:H61	36:1:3285:C:H42	1.53	0.55
36:1:770:G:O6	87:1:4096:OHX:N4	2.40	0.55
1:2:1240:U:OP2	87:2:2116:OHX:N1	2.39	0.55
1:2:132:U:H4'	1:2:133:U:H5'	1.87	0.55
1:2:1650:U:H2'	1:2:1651:A:C8	2.41	0.55
1:2:653:C:H2'	1:2:654:C:O4'	2.07	0.55
38:4:155:A:H4'	45:L8:185:ARG:HD3	1.88	0.55
38:4:62:C:H4'	38:4:63:G:O5'	2.07	0.55
36:5:3364:C:OP1	87:5:3857:OHX:N1	2.39	0.55
36:5:1192:C:H5	87:5:4000:OHX:N2	2.05	0.55
1:6:950:C:H2'	1:6:951:A:C8	2.42	0.55
1:2:927:C:O2'	16:C4:125:SER:HB2	2.06	0.55
23:D1:21:ASN:OD1	24:D2:23:ARG:NH2	2.40	0.55
4:S2:143:TYR:O	24:D2:98:GLN:NE2	2.36	0.55
46:L9:120:ASP:OD1	46:L9:124:ARG:NH2	2.35	0.55
48:M1:164:LYS:O	48:M1:168:ASP:HA	3.70	0.55
49:M3:75:PHE:O	49:M3:79:GLU:HB2	2.06	0.55
47:M0:169:LYS:NZ	57:N1:158:THR:O	5.05	0.55
57:N1:83:ARG:HD2	57:N1:85:LEU:HD21	1.88	0.55
61:N5:105:VAL:HG11	61:N5:135:ILE:HG13	1.88	0.55
54:M8:94:PHE:CZ	64:N8:119:PRO:HD3	2.77	0.55
2:S0:126:PRO:HB2	2:S0:152:PRO:HG2	1.89	0.55
36:1:1244:A:N6	36:1:1271:A:OP2	2.40	0.55
36:1:1841:A:O2'	36:1:1842:A:H5''	2.06	0.55
36:1:1874:A:OP1	55:M9:17:VAL:HG12	2.07	0.55
1:2:1538:U:O2'	1:2:1539:G:H8	1.89	0.55
1:2:1657:U:O4	87:2:2058:OHX:N6	2.40	0.55
1:2:237:C:H4'	1:2:238:U:C6	2.42	0.55
1:2:478:A:OP1	32:E0:37:ARG:NH1	2.40	0.55
1:2:480:G:OP1	11:S9:120:LYS:NZ	2.33	0.55
1:2:732:G:H1'	1:2:734:A:H61	1.72	0.55
1:2:74:U:O2'	1:2:75:U:OP2	2.22	0.55
38:4:122:U:H2'	38:4:123:G:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:409:A:H61	38:4:15:G:H1'	1.71	0.55
1:6:1237:G:H2'	1:6:1238:A:H8	1.71	0.55
1:6:927:C:OP1	87:6:2172:OHX:N3	2.40	0.55
1:6:922:G:H2'	1:6:923:A:H8	1.72	0.55
22:D0:30:LYS:HD2	22:D0:111:GLY:HA3	3.19	0.55
22:D0:58:LEU:HD12	22:D0:88:LYS:HD2	1.87	0.55
24:D2:36:LYS:O	24:D2:40:VAL:HG23	2.17	0.55
28:D6:45:VAL:O	28:D6:46:GLU:HG2	3.42	0.55
28:D6:58:VAL:HG22	28:D6:59:TYR:H	4.03	0.55
39:L2:10:LYS:HA	39:L2:16:PHE:CD2	2.41	0.55
41:L4:89:ALA:O	41:L4:91:GLY:N	2.36	0.55
43:L6:158:TYR:CE1	50:M4:115:PHE:HA	2.42	0.55
50:M4:21:VAL:HG12	50:M4:65:LEU:HA	1.89	0.55
51:M5:35:VAL:HG13	51:M5:65:ARG:HB3	3.04	0.55
56:N0:50:LYS:HG2	37:7:77:G:O5'	305.29	0.55
63:N7:33:SER:HB2	63:N7:40:HIS:HE1	1.70	0.55
36:1:1114:U:H5''	64:N8:22:ILE:HD13	1.88	0.55
74:O8:64:LYS:HG3	74:O8:65:LEU:N	4.89	0.55
2:S0:157:ASP:OD1	23:D1:60:ARG:NH2	2.40	0.55
3:S1:151:LYS:HE3	3:S1:154:SER:HA	1.89	0.55
11:S9:60:LEU:HD23	11:S9:93:LEU:HD11	1.88	0.55
34:SR:255:ALA:HB2	34:SR:292:LEU:HD22	1.89	0.55
36:1:2314:U:O4	87:1:3777:OHX:N5	2.40	0.55
36:1:3054:U:H3	36:1:3088:G:H1	1.54	0.55
36:1:2259:A:OP2	87:1:3830:OHX:N2	2.40	0.55
1:2:1228:G:N2	14:C2:68:GLU:OE1	2.40	0.55
1:2:1323:C:H2'	1:2:1324:G:O4'	2.07	0.55
87:2:2003:OHX:N2	10:S8:17:LYS:O	2.40	0.55
1:2:505:A:H3'	1:2:506:A:H5''	1.88	0.55
1:2:979:A:N3	1:2:1775:U:O2'	2.39	0.55
36:5:1899:G:N7	87:5:3860:OHX:N6	2.55	0.55
59:N3:48:ARG:NH2	36:5:3043:C:OP2	252.77	0.55
1:6:1067:C:H2'	1:6:1068:C:H6	1.72	0.55
1:6:1458:G:H5''	1:6:1459:C:OP2	2.07	0.55
13:C1:3:THR:OG1	13:C1:82:ARG:NE	2.40	0.55
15:C3:92:ILE:O	15:C3:96:VAL:HG23	2.07	0.55
21:C9:28:LEU:HD13	21:C9:29:GLU:H	1.72	0.55
40:L3:230:THR:HB	40:L3:247:ARG:NH1	2.21	0.55
41:L4:131:VAL:HB	41:L4:134:LEU:HG	1.89	0.55
41:L4:334:PHE:HA	41:L4:339:LEU:HG	1.88	0.55
43:L6:31:ARG:NH2	43:L6:81:ALA:O	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:L8:54:GLU:HG2	45:L8:57:ARG:NH1	3.44	0.55
51:M5:102:ALA:O	51:M5:106:VAL:HG12	2.07	0.55
5:S3:137:VAL:HG22	5:S3:151:LYS:HG3	3.51	0.55
36:1:1343:A:H2'	36:1:1344:G:H8	1.72	0.55
36:1:1792:C:H2'	36:1:1795:U:C5	2.41	0.55
36:1:2278:C:OP1	87:1:3853:OHX:N3	2.40	0.55
1:2:1685:G:H22	1:2:1716:C:H42	1.55	0.55
1:2:539:G:OP2	1:2:539:G:H8	1.89	0.55
41:L4:186:LYS:NZ	36:5:1388:U:O4	120.03	0.55
36:5:979:U:H1'	36:5:980:A:C4	2.42	0.55
1:6:1472:C:H5'	1:6:1474:G:O4'	2.06	0.55
1:6:55:A:N6	1:6:403:G:H1'	2.21	0.55
20:C8:88:ARG:NH1	20:C8:112:ASP:OD2	3.93	0.55
39:L2:193:ARG:NH1	36:5:2174:G:OP2	191.98	0.55
40:L3:77:THR:HG23	40:L3:326:GLY:O	2.26	0.55
43:L6:109:GLU:N	43:L6:109:GLU:OE1	5.13	0.55
50:M4:24:LYS:HE3	50:M4:25:LYS:HE3	4.12	0.55
59:N3:113:ALA:HA	59:N3:132:ASN:HB3	1.88	0.55
64:N8:47:LYS:HE2	64:N8:48:TYR:CE2	2.89	0.55
70:O4:51:LEU:HD23	70:O4:51:LEU:H	1.71	0.55
2:S0:108:THR:OG1	2:S0:135:GLU:OE1	2.96	0.55
19:C7:37:GLU:HG3	34:SR:150:TRP:HE1	1.70	0.55
36:1:209:A:H4'	36:1:211:A:C8	2.42	0.54
36:1:2445:A:N6	36:1:2502:A:N1	2.55	0.54
44:L7:105:LEU:HD22	36:5:1101:G:H1'	235.65	0.54
39:L2:69:TYR:OH	36:5:2557:A:OP1	192.23	0.54
36:5:3259:U:H5''	36:5:3261:C:H5	1.72	0.54
36:5:528:U:H2'	36:5:529:A:C8	2.43	0.54
20:C8:120:ARG:HE	35:SM:61:ILE:HG21	3.96	0.54
23:D1:71:ARG:HG3	23:D1:83:TRP:CZ2	2.42	0.54
39:L2:51:ASP:HB3	39:L2:54:ARG:HD2	4.24	0.54
40:L3:180:GLU:OE2	36:5:3002:C:O2'	235.87	0.54
42:L5:108:ARG:CZ	42:L5:253:PHE:HB2	2.37	0.54
49:M3:76:THR:HG22	49:M3:101:ARG:HB3	1.88	0.54
70:O4:96:GLU:HA	70:O4:99:LYS:HD2	4.55	0.54
71:O5:45:LYS:O	71:O5:49:LYS:HG2	3.89	0.54
75:O9:8:ARG:O	75:O9:12:LYS:HG3	2.07	0.54
2:S0:124:THR:HG22	2:S0:174:TRP:NE1	2.21	0.54
4:S2:116:LYS:HG2	4:S2:127:ALA:HB3	1.88	0.54
10:S8:36:THR:OG1	10:S8:96:LEU:O	2.24	0.54
36:1:1240:A:H3'	36:1:1241:U:H5'	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1913:A:N3	36:1:2120:A:H2'	2.22	0.54
36:1:2585:G:C8	45:L8:48:ARG:HG3	2.42	0.54
36:1:3152:U:O2	87:1:4044:OHX:N2	2.40	0.54
36:1:501:A:H2'	36:1:502:U:C6	2.42	0.54
36:1:977:C:OP1	54:M8:141:ARG:NH2	2.40	0.54
1:2:1041:G:H2'	1:2:1042:G:C8	2.43	0.54
1:2:67:A:C2	1:2:69:G:H1'	2.42	0.54
1:2:900:A:OP1	16:C4:43:THR:OG1	2.20	0.54
36:5:2904:U:H2'	36:5:2905:U:C6	2.42	0.54
36:5:583:G:OP1	87:5:3820:OHX:N1	2.39	0.54
36:5:799:G:O6	87:5:3942:OHX:N4	2.41	0.54
1:6:1042:G:H22	1:6:1076:A:H2	1.50	0.54
27:D5:74:SER:OG	1:6:1534:G:OP2	345.77	0.54
1:6:1650:U:H2'	1:6:1651:A:C8	2.42	0.54
1:6:816:G:OP1	87:6:2108:OHX:N3	2.41	0.54
40:L3:305:ILE:HG12	40:L3:321:PHE:CZ	2.41	0.54
41:L4:186:LYS:N	41:L4:200:THR:O	2.88	0.54
42:L5:216:GLU:O	42:L5:220:SER:OG	2.18	0.54
44:L7:179:LEU:HD22	44:L7:183:ASP:OD2	2.07	0.54
47:M0:33:ILE:HD11	47:M0:36:LEU:HG	1.88	0.54
50:M4:85:TRP:HE1	50:M4:91:CYS:HB2	1.72	0.54
51:M5:119:TYR:OH	51:M5:131:GLU:OE1	2.28	0.54
36:1:388:G:H4'	53:M7:18:ARG:O	2.07	0.54
36:1:1874:A:N7	55:M9:20:ARG:NH1	2.54	0.54
58:N2:56:VAL:HG22	58:N2:65:VAL:HG22	2.42	0.54
61:N5:117:ASN:HB2	75:O9:18:LYS:HE2	1.88	0.54
75:O9:27:ILE:HD13	38:8:52:A:N6	76.74	0.54
78:Q2:14:GLY:O	78:Q2:16:THR:N	2.38	0.54
2:S0:173:ILE:O	2:S0:177:LEU:HB2	2.52	0.54
3:S1:81:PHE:HD2	3:S1:82:ARG:HG3	1.73	0.54
11:S9:8:TYR:O	87:S9:201:OHX:N4	4.66	0.54
36:1:1445:U:H5''	36:1:1446:A:OP2	2.06	0.54
36:1:3166:C:H42	36:1:3284:G:H1	1.55	0.54
36:1:852:U:H2'	36:1:853:G:H8	1.71	0.54
36:1:873:C:H5''	36:1:874:U:O5'	2.07	0.54
1:2:1664:C:H42	1:2:1737:G:H1	1.56	0.54
36:5:3019:U:O4	87:5:3899:OHX:N2	2.41	0.54
36:5:3041:U:H2'	36:5:3042:U:C6	2.42	0.54
36:5:94:G:H2'	36:5:95:A:C8	2.42	0.54
8:S6:199:GLN:NE2	1:6:127:G:O6	335.64	0.54
1:6:1698:G:H1'	1:6:1699:G:OP1	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:383:G:N7	87:6:2115:OHX:N5	2.54	0.54
38:8:125:U:O2'	38:8:126:A:H5'	2.08	0.54
1:2:918:U:O2'	16:C4:18:ARG:NH1	2.41	0.54
17:C5:28:MET:O	17:C5:32:ASP:HB2	2.08	0.54
18:C6:42:GLU:HG3	18:C6:43:ILE:HD13	5.40	0.54
21:C9:38:LYS:O	21:C9:39:THR:OG1	4.81	0.54
16:C4:113:GLY:HA2	28:D6:59:TYR:HE2	1.72	0.54
30:D8:11:LYS:O	30:D8:31:GLU:N	2.95	0.54
40:L3:113:GLU:HB3	40:L3:176:ALA:HB2	1.89	0.54
42:L5:235:SER:O	42:L5:239:ILE:HG13	2.07	0.54
42:L5:261:THR:H	42:L5:264:GLN:HG3	1.72	0.54
42:L5:34:LYS:HA	57:N1:27:LEU:HD11	2.28	0.54
50:M4:120:VAL:HG22	52:M6:197:LEU:HD13	1.88	0.54
50:M4:40:ASP:O	50:M4:42:LYS:N	3.05	0.54
64:N8:34:MET:HB2	36:5:96:G:OP2	161.09	0.54
64:N8:47:LYS:HE2	64:N8:48:TYR:CZ	3.35	0.54
87:S1:301:OHX:N1	1:6:874:C:OP1	325.29	0.54
9:S7:50:ASP:HB3	9:S7:56:LYS:HE2	3.70	0.54
34:SR:197:SER:OG	34:SR:198:ASN:N	2.38	0.54
36:1:1307:G:H1'	36:1:1308:A:N7	2.21	0.54
36:1:1598:G:OP1	70:O4:25:THR:OG1	2.19	0.54
36:1:1699:A:OP1	87:O4:202:OHX:N2	2.40	0.54
36:1:2178:A:H3'	39:L2:132:ASN:ND2	2.19	0.54
36:1:955:U:H2'	36:1:956:U:C6	2.42	0.54
1:2:1553:G:N2	1:2:1555:A:H3'	2.23	0.54
1:2:16:G:H2'	1:2:17:C:C6	2.43	0.54
1:2:176:C:OP1	87:2:2041:OHX:N3	2.40	0.54
1:2:393:C:OP2	10:S8:2:GLY:N	2.40	0.54
1:2:604:A:OP2	87:2:2079:OHX:N5	2.41	0.54
36:5:1024:G:N2	36:5:1026:A:OP2	2.39	0.54
1:6:1294:G:O2'	1:6:1321:A:N1	2.35	0.54
1:6:127:G:H21	1:6:178:U:H1'	1.71	0.54
1:6:217:A:N6	1:6:845:G:O4'	2.40	0.54
16:C4:31:THR:HB	16:C4:38:THR:HA	1.88	0.54
18:C6:82:ARG:HH21	18:C6:116:LEU:HG	4.52	0.54
22:D0:28:SER:OG	22:D0:29:THR:N	2.39	0.54
40:L3:147:GLU:HA	40:L3:150:ARG:HB3	1.90	0.54
41:L4:337:GLU:HB2	41:L4:339:LEU:CD2	2.38	0.54
46:L9:67:ALA:O	46:L9:71:VAL:HG23	2.08	0.54
49:M3:43:ALA:O	49:M3:137:GLN:NE2	3.21	0.54
49:M3:36:ARG:HG3	49:M3:39:ARG:NH2	3.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:L8:162:LEU:HD23	51:M5:7:LEU:HD11	1.89	0.54
52:M6:18:ARG:O	52:M6:22:VAL:HG12	3.83	0.54
56:N0:28:ARG:HH11	56:N0:99:ARG:NE	2.04	0.54
56:N0:91:TYR:O	56:N0:137:ARG:NH1	2.41	0.54
58:N2:14:THR:HG23	58:N2:66:VAL:HG22	2.68	0.54
36:1:1483:G:O6	70:O4:4:ARG:NH2	2.39	0.54
6:S4:252:ARG:NH2	6:S4:252:ARG:HB3	4.30	0.54
9:S7:50:ASP:N	9:S7:50:ASP:OD1	2.35	0.54
11:S9:57:ARG:HG2	11:S9:97:LEU:HD21	1.90	0.54
11:S9:60:LEU:HD21	11:S9:93:LEU:HB3	6.28	0.54
34:SR:98:GLU:HG2	34:SR:100:TYR:CE2	2.43	0.54
36:1:1168:U:OP1	44:L7:213:GLY:N	2.40	0.54
36:1:2661:G:H1	36:1:2709:C:H42	1.56	0.54
36:1:3056:U:OP2	87:1:3833:OHX:N3	2.40	0.54
1:2:882:U:H2'	1:2:883:C:C6	2.42	0.54
36:5:1597:C:H2'	36:5:1598:G:H8	1.73	0.54
40:L3:247:ARG:NH2	36:5:2341:A:OP1	219.91	0.54
36:5:2396:G:OP1	36:5:2397:A:H4'	2.07	0.54
36:5:1230:G:OP2	87:5:3921:OHX:N6	2.40	0.54
36:5:656:A:H2'	36:5:657:A:C8	2.43	0.54
17:C5:10:ARG:O	17:C5:12:PHE:N	2.40	0.54
24:D2:27:ILE:HD11	24:D2:61:ILE:HD12	1.90	0.54
26:D4:60:PHE:HA	26:D4:70:VAL:O	2.08	0.54
41:L4:271:LYS:HB2	41:L4:274:TYR:HB3	2.36	0.54
42:L5:166:ALA:HB1	42:L5:171:LEU:HD12	1.89	0.54
42:L5:270:LYS:HG3	42:L5:273:ARG:HB3	3.31	0.54
47:M0:35:ASP:OD1	47:M0:86:HIS:NE2	2.79	0.54
59:N3:45:ARG:HD3	59:N3:46:LEU:N	3.56	0.54
63:N7:121:ARG:HG3	63:N7:126:LYS:HB2	1.93	0.54
63:N7:9:LYS:HB3	63:N7:25:ILE:HD12	1.91	0.54
71:O5:47:VAL:O	71:O5:51:ILE:HG13	2.20	0.54
9:S7:44:LYS:HD2	9:S7:63:PRO:HA	1.89	0.54
11:S9:11:THR:HG23	1:6:472:U:H5''	399.62	0.54
34:SR:216:LYS:HA	34:SR:239:GLU:HG3	2.25	0.54
36:1:1528:G:O2'	36:1:1588:A:N3	2.36	0.54
36:1:1778:G:O2'	36:1:1780:G:OP2	2.24	0.54
36:1:186:U:OP1	62:N6:122:LYS:NZ	2.38	0.54
10:S8:162:ALA:HA	36:1:3353:G:H5''	1.89	0.54
36:1:2787:G:OP2	87:1:3847:OHX:N5	2.41	0.54
47:M0:160:PRO:HD3	36:5:2854:U:H4'	295.62	0.54
69:O3:92:LYS:HG2	36:5:3173:G:O6	223.01	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:O1:17:HIS:HD2	36:5:3376:A:H2	187.42	0.54
51:M5:157:LYS:NZ	36:5:58:G:OP1	85.66	0.54
36:5:847:A:H2'	36:5:848:A:C8	2.43	0.54
36:5:92:G:H5''	36:5:94:G:N7	2.23	0.54
1:6:1159:C:N3	87:6:2104:OHX:N5	2.55	0.54
1:6:218:A:H61	1:6:829:A:H2	1.55	0.54
15:C3:132:VAL:HG23	15:C3:134:VAL:HG13	2.02	0.54
23:D1:79:LEU:HD13	23:D1:82:VAL:HG11	1.90	0.54
40:L3:194:TRP:O	40:L3:198:HIS:ND1	2.34	0.54
42:L5:286:VAL:O	42:L5:290:ILE:HG23	2.06	0.54
42:L5:59:ASP:OD2	42:L5:60:ILE:N	3.28	0.54
45:L8:75:ILE:C	45:L8:77:GLN:H	2.09	0.54
47:M0:47:PRO:O	47:M0:178:ARG:NH1	3.20	0.54
52:M6:65:ASN:C	52:M6:67:THR:H	2.10	0.54
53:M7:105:LYS:HD3	53:M7:107:LEU:HD11	3.39	0.54
55:M9:96:ILE:HG22	55:M9:100:ARG:HD2	4.61	0.54
67:O1:13:THR:HG22	67:O1:72:ARG:HH21	6.01	0.54
68:O2:63:THR:HA	68:O2:66:LEU:HD12	1.90	0.54
73:O7:24:ARG:NH1	36:5:361:A:OP1	120.45	0.54
2:S0:101:ARG:HH22	2:S0:104:PRO:HG3	1.72	0.54
2:S0:146:LEU:HD21	2:S0:173:ILE:HG21	2.64	0.54
3:S1:97:LEU:HG	3:S1:232:HIS:CD2	2.43	0.54
5:S3:32:GLU:N	5:S3:32:GLU:OE1	3.62	0.54
6:S4:88:ASP:HB2	6:S4:101:LEU:HD12	2.33	0.54
9:S7:46:ILE:HG12	9:S7:60:ILE:HA	1.94	0.54
10:S8:196:LEU:O	10:S8:200:LYS:HG3	2.07	0.54
34:SR:25:THR:HG21	34:SR:295:SER:HA	3.05	0.54
36:1:135:C:O2	71:O5:94:LYS:N	2.35	0.54
1:2:1798:U:C6	28:D6:97:PRO:HB3	2.43	0.54
1:2:17:C:H2'	1:2:18:C:C6	2.43	0.54
1:2:714:G:O6	1:2:724:C:N4	2.41	0.54
1:2:811:A:C2	1:2:858:G:H1'	2.43	0.54
36:5:123:A:C6	36:5:150:A:C5	2.96	0.54
36:5:595:G:N1	36:5:609:G:H5''	2.23	0.54
10:S8:10:LYS:HE3	1:6:339:C:P	286.87	0.54
1:6:73:U:H2'	1:6:74:U:C6	2.42	0.54
37:7:3:U:H2'	37:7:4:U:C6	2.42	0.54
18:C6:13:LYS:O	18:C6:76:SER:OG	2.26	0.54
20:C8:91:ASP:N	20:C8:96:LYS:O	2.41	0.54
21:C9:28:LEU:O	21:C9:29:GLU:HB2	2.06	0.54
42:L5:183:TRP:CH2	42:L5:188:GLU:HA	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:L9:91:ARG:HD2	46:L9:143:GLU:HA	2.89	0.54
47:M0:36:LEU:CD1	47:M0:87:LEU:HB3	3.21	0.54
47:M0:48:LEU:O	47:M0:139:ARG:HA	2.17	0.54
47:M0:77:THR:O	47:M0:79:VAL:N	2.40	0.54
49:M3:73:ARG:HD2	36:5:76:G:H3'	83.53	0.54
36:1:1603:A:H61	61:N5:71:THR:HG21	1.72	0.54
77:Q1:13:LEU:HD13	77:Q1:17:ARG:HH22	1.72	0.54
8:S6:39:GLU:HG3	8:S6:46:LYS:HE2	5.09	0.54
11:S9:153:GLU:HA	11:S9:156:ILE:HD11	2.20	0.54
36:1:115:A:OP1	51:M5:49:ARG:NE	2.40	0.54
36:1:1898:G:OP2	87:1:3828:OHX:N2	2.40	0.54
36:1:742:G:N7	87:1:3870:OHX:N1	2.56	0.54
87:1:4082:OHX:N2	40:L3:364:LYS:O	2.40	0.54
1:2:1151:A:H4'	1:2:1766:A:N7	2.23	0.54
1:2:400:A:H4'	1:2:401:A:H5'	1.88	0.54
1:2:93:A:H1'	6:S4:3:ARG:HB3	1.89	0.54
36:5:1897:G:H1	36:5:2338:C:H42	1.54	0.54
36:5:3127:A:OP2	87:5:4116:OHX:N1	2.40	0.54
1:6:1087:A:H2'	1:6:1088:A:H8	1.68	0.54
1:6:1237:G:H1	1:6:1248:C:N4	2.05	0.54
1:6:365:G:O6	87:6:2101:OHX:N4	2.41	0.54
1:6:428:A:N3	1:6:440:U:O2'	2.37	0.54
12:C0:8:ARG:O	12:C0:12:HIS:ND1	4.68	0.54
19:C7:57:LEU:O	19:C7:61:ILE:HG13	2.08	0.54
28:D6:75:VAL:O	28:D6:79:ILE:HG13	2.08	0.54
33:E1:106:TYR:HD2	33:E1:116:LYS:HA	1.73	0.54
41:L4:265:GLU:CD	41:L4:265:GLU:H	2.10	0.54
51:M5:160:GLU:OE1	51:M5:160:GLU:N	2.59	0.54
36:1:3182:G:O3'	52:M6:161:LYS:NZ	2.40	0.54
5:S3:210:GLU:OE1	19:C7:19:ARG:NH1	4.04	0.54
5:S3:34:TYR:CE2	5:S3:37:VAL:HG13	2.71	0.54
1:2:1006:C:O2	87:2:2117:OHX:N2	2.41	0.54
1:2:819:G:O6	1:2:853:G:N1	2.40	0.54
36:5:1019:G:H2'	36:5:1020:G:C8	2.43	0.54
36:5:107:A:H2'	36:5:108:A:O4'	2.08	0.54
52:M6:133:ARG:HE	36:5:1189:C:N4	294.41	0.54
36:5:1577:G:N2	36:5:1578:C:N3	2.56	0.54
36:5:1666:G:H2'	36:5:1667:A:C8	2.42	0.54
62:N6:4:GLN:HB2	36:5:229:G:H5''	68.65	0.54
36:5:3245:A:H2	36:5:3246:G:C2	2.26	0.54
25:D3:116:ASP:OD2	1:6:570:A:N6	360.28	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D3:69:ARG:NH1	25:D3:116:ASP:OD1	2.56	0.54
1:2:523:G:H5''	26:D4:59:GLY:O	2.08	0.54
30:D8:19:THR:HG21	30:D8:65:ARG:HA	1.90	0.54
40:L3:221:THR:HB	40:L3:273:HIS:H	1.71	0.54
47:M0:9:TYR:CG	47:M0:97:LEU:HD13	2.43	0.54
49:M3:140:SER:OG	49:M3:143:ALA:N	2.27	0.54
2:S0:59:LEU:HD12	23:D1:79:LEU:HD21	3.94	0.54
3:S1:36:SER:HB3	3:S1:231:LEU:HB3	1.90	0.54
10:S8:67:TRP:CD1	10:S8:183:ILE:HD11	5.27	0.54
11:S9:53:ARG:NH2	11:S9:97:LEU:O	2.39	0.54
36:1:651:G:O2'	36:1:1435:A:OP1	2.24	0.54
36:1:2378:C:H2'	36:1:2379:U:C6	2.41	0.54
36:1:3344:A:H2	36:1:3361:G:H21	1.54	0.54
36:1:1184:A:OP2	87:1:3957:OHX:N3	2.41	0.54
1:2:264:G:N7	87:2:2001:OHX:N3	2.56	0.54
1:2:894:U:H2'	1:2:895:G:C8	2.42	0.54
36:5:1235:U:H4'	36:5:1236:G:H5'	1.89	0.54
12:C0:32:HIS:CD2	12:C0:33:GLU:HG2	5.94	0.54
15:C3:107:LYS:O	15:C3:109:LYS:N	3.34	0.54
23:D1:5:LYS:O	23:D1:7:GLN:N	3.17	0.54
28:D6:79:ILE:HG23	28:D6:84:VAL:HG21	1.90	0.54
42:L5:33:ARG:NH2	37:7:7:G:O3'	272.05	0.54
46:L9:116:ASN:OD1	46:L9:119:GLY:HA2	2.08	0.54
47:M0:169:LYS:NZ	57:N1:159:PHE:H	2.06	0.54
52:M6:14:HIS:NE2	52:M6:124:LEU:HD13	2.23	0.54
63:N7:44:ALA:HB1	63:N7:114:VAL:HG11	1.89	0.54
2:S0:193:GLN:O	2:S0:195:TRP:N	2.42	0.54
4:S2:47:ALA:O	4:S2:49:LYS:N	2.41	0.54
36:1:2707:C:H2'	36:1:2708:C:C6	2.43	0.53
36:1:425:G:O6	87:1:3771:OHX:N6	2.40	0.53
1:2:346:G:H5'	13:C1:79:LYS:HG3	1.89	0.53
1:2:927:C:H2'	1:2:928:U:C6	2.42	0.53
36:5:677:A:H4'	36:5:678:G:O5'	2.08	0.53
3:S1:146:GLN:NE2	1:6:1065:A:N3	344.30	0.53
6:S4:38:LEU:HB2	1:6:298:C:H5''	353.56	0.53
1:6:720:G:O3'	1:6:721:U:H3'	2.07	0.53
14:C2:126:TRP:O	14:C2:128:ALA:N	2.35	0.53
18:C6:82:ARG:HH22	18:C6:114:ARG:HB3	1.72	0.53
1:2:609:U:N3	25:D3:22:ASN:O	2.31	0.53
26:D4:45:ALA:HB2	26:D4:55:VAL:HG11	4.40	0.53
16:C4:114:ARG:HA	28:D6:62:TYR:OH	2.21	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:25:ILE:CD1	40:L3:25:ILE:H	2.21	0.53
41:L4:187:LEU:HD23	41:L4:198:ARG:O	2.70	0.53
46:L9:90:MET:HA	46:L9:182:SER:H	2.44	0.53
50:M4:40:ASP:OD1	50:M4:42:LYS:N	2.36	0.53
70:O4:106:LYS:HD3	70:O4:109:THR:HB	1.90	0.53
36:1:2653:C:P	78:Q2:89:LYS:HG3	2.48	0.53
6:S4:106:LYS:HG3	6:S4:108:ARG:NH1	2.23	0.53
6:S4:247:SER:O	6:S4:251:GLU:HG3	2.46	0.53
8:S6:84:TYR:OH	8:S6:91:GLU:O	3.26	0.53
10:S8:84:HIS:CE1	10:S8:86:SER:HB2	2.42	0.53
36:1:1144:U:H1'	36:1:1145:G:C8	2.44	0.53
36:1:3043:C:OP2	59:N3:48:ARG:NH2	2.39	0.53
36:1:562:C:H2'	36:1:563:U:C6	2.44	0.53
36:1:562:C:H2'	36:1:563:U:H6	1.72	0.53
36:1:568:G:H2'	36:1:569:A:O4'	2.08	0.53
36:1:655:C:H2'	36:1:656:A:C8	2.43	0.53
36:1:656:A:H2'	36:1:657:A:C8	2.42	0.53
1:2:924:A:O2'	1:2:987:G:OP1	2.25	0.53
36:5:1270:A:H2'	36:5:1271:A:C8	2.43	0.53
40:L3:329:PRO:HA	36:5:3047:U:H5'	234.58	0.53
36:5:3164:C:H1'	36:5:3165:A:H5'	1.89	0.53
36:5:712:G:H2'	36:5:713:U:C6	2.42	0.53
36:5:996:A:H2'	36:5:997:A:O4'	2.09	0.53
1:6:827:C:H2'	1:6:828:U:H6	1.73	0.53
37:7:23:A:H2'	37:7:24:A:C8	2.44	0.53
26:D4:20:ARG:HD2	26:D4:74:LEU:HD22	3.05	0.53
27:D5:75:LEU:HA	27:D5:78:ILE:HG22	3.60	0.53
41:L4:148:ILE:HA	41:L4:149:PRO:C	2.46	0.53
42:L5:233:ALA:O	42:L5:236:LEU:N	2.37	0.53
44:L7:33:ARG:O	44:L7:36:ALA:N	2.41	0.53
46:L9:49:ASN:C	46:L9:51:GLN:H	2.11	0.53
47:M0:4:ARG:HG2	47:M0:5:PRO:HD2	1.89	0.53
48:M1:75:LYS:O	48:M1:79:ILE:HG13	2.45	0.53
49:M3:174:ARG:CZ	72:O6:9:ILE:HD13	2.39	0.53
50:M4:94:TRP:CE2	50:M4:100:ALA:HB2	2.43	0.53
57:N1:26:HIS:ND1	57:N1:26:HIS:O	2.41	0.53
36:1:1456:A:N7	67:O1:26:LYS:HE2	2.23	0.53
49:M3:174:ARG:NH1	72:O6:9:ILE:HG21	2.23	0.53
11:S9:179:ARG:HA	11:S9:182:GLU:HG3	3.40	0.53
34:SR:80:ALA:HB3	34:SR:92:TRP:HB2	2.04	0.53
36:1:1596:C:H2'	36:1:1597:C:C6	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2261:G:H21	36:1:2262:A:H61	1.55	0.53
36:1:1450:G:N2	36:1:2354:C:O2	2.42	0.53
36:1:3151:U:H4'	36:1:3294:A:H1'	1.89	0.53
1:2:542:A:N1	32:E0:28:LYS:HD2	2.23	0.53
37:3:49:G:N7	42:L5:58:LYS:HG3	2.24	0.53
64:N8:9:ARG:NH2	36:5:1431:G:N7	149.41	0.53
41:L4:161:LYS:NZ	36:5:209:A:OP1	75.38	0.53
36:5:2659:G:O6	87:5:3824:OHX:N6	2.41	0.53
36:5:3060:C:H1'	36:5:3332:U:H1'	1.90	0.53
36:5:956:U:H2'	36:5:957:C:C6	2.43	0.53
1:6:1645:G:H1	1:6:1756[A]:A:N6	2.07	0.53
1:6:1699:G:N2	1:6:1702:A:O4'	2.40	0.53
1:6:1695:G:H21	1:6:1705:C:H41	1.56	0.53
38:8:82:U:O5'	87:8:228:OHX:N5	2.41	0.53
15:C3:91:LEU:HD12	15:C3:125:LEU:HD12	2.29	0.53
18:C6:86:ALA:HB1	18:C6:109:PHE:CE2	3.03	0.53
28:D6:53:LEU:HD11	28:D6:62:TYR:HD2	1.72	0.53
40:L3:45:SER:HB3	40:L3:339:ARG:HA	1.89	0.53
42:L5:178:ASN:HA	42:L5:183:TRP:CD1	3.16	0.53
42:L5:61:ILE:HD13	42:L5:79:TYR:CE1	2.91	0.53
52:M6:8:VAL:HG12	52:M6:117:ARG:HB3	2.74	0.53
56:N0:13:ARG:NH2	56:N0:51:VAL:HG22	6.44	0.53
63:N7:46:ILE:HD11	63:N7:49:TYR:CG	4.14	0.53
75:O9:21:ARG:NH1	75:O9:24:PRO:HG3	2.23	0.53
3:S1:58:SER:O	3:S1:62:LYS:HB2	4.96	0.53
5:S3:48:VAL:HB	5:S3:86:LEU:HD12	2.03	0.53
6:S4:151:ASP:HB3	6:S4:154:ILE:HG13	1.90	0.53
6:S4:33:ALA:O	1:6:121:U:O2'	354.35	0.53
8:S6:98:ARG:HD3	8:S6:99:GLY:N	2.23	0.53
10:S8:70:GLU:HB3	10:S8:112:TRP:CH2	2.65	0.53
10:S8:36:THR:HG22	10:S8:57:ALA:O	2.34	0.53
36:1:802:C:H2'	36:1:803:C:H6	1.74	0.53
1:2:1464:G:O3'	18:C6:141:SER:OG	2.22	0.53
1:2:149:C:OP1	26:D4:121:THR:OG1	2.26	0.53
36:5:1260:A:O2'	36:5:1279:C:O2	2.26	0.53
36:5:1564:U:H2'	36:5:1565:G:C8	2.43	0.53
66:O0:84:LEU:HD13	36:5:1715:A:C5	261.45	0.53
36:5:825:U:O4	87:5:3878:OHX:N2	2.42	0.53
1:6:867:G:N7	87:6:2023:OHX:N1	2.56	0.53
38:8:83:C:H4'	38:8:85:G:N3	2.23	0.53
13:C1:75:VAL:HG22	13:C1:86:ILE:HG22	1.88	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:C6:60:PHE:CD2	18:C6:63:ILE:HD11	4.63	0.53
4:S2:229:LEU:HD23	23:D1:23:ILE:HD11	3.05	0.53
41:L4:264:SER:O	41:L4:267:VAL:N	2.29	0.53
42:L5:148:ILE:HG12	36:5:2746:A:C6	265.48	0.53
44:L7:156:ILE:HD12	44:L7:161:VAL:HG21	1.89	0.53
47:M0:47:PRO:HB3	47:M0:171:TRP:CZ2	2.44	0.53
47:M0:193:ASP:CG	47:M0:194:GLY:H	2.59	0.53
58:N2:104:ARG:HH22	36:5:1758:G:P	119.26	0.53
61:N5:132:ALA:O	61:N5:136:ALA:N	2.44	0.53
61:N5:67:ILE:HD12	61:N5:83:VAL:HG12	1.90	0.53
68:O2:96:ILE:HG21	68:O2:105:ARG:HG2	1.90	0.53
38:4:69:U:OP2	87:O7:103:OHX:N3	2.42	0.53
1:2:7:G:N7	4:S2:205:ARG:NH1	2.56	0.53
7:S5:42:LEU:HB2	7:S5:46:TRP:O	2.09	0.53
11:S9:8:TYR:O	87:S9:201:OHX:N5	2.42	0.53
34:SR:123:ILE:HG22	34:SR:133:VAL:HG22	1.91	0.53
34:SR:19:TRP:HB2	34:SR:38:ARG:HD2	1.97	0.53
1:2:1233:G:OP1	87:2:2127:OHX:N3	2.40	0.53
1:2:6:G:H2'	1:2:7:G:H8	1.72	0.53
36:5:2211:U:O4	87:5:3877:OHX:N4	2.41	0.53
36:5:856:G:C6	36:5:857:G:N1	2.77	0.53
1:6:1078:C:OP2	87:6:2183:OHX:N5	2.41	0.53
1:6:595:G:OP2	87:6:2069:OHX:N6	2.41	0.53
37:7:3:U:H2'	37:7:4:U:H6	1.72	0.53
38:8:157:U:H3'	38:8:158:U:H3'	1.90	0.53
75:O9:11:GLN:NE2	38:8:45:C:O3'	92.32	0.53
23:D1:40:ASP:HB3	23:D1:46:ILE:HD11	1.89	0.53
40:L3:10:ARG:NH2	40:L3:14:LEU:HD21	2.48	0.53
40:L3:94:GLU:HG3	40:L3:156:SER:OG	2.08	0.53
41:L4:265:GLU:OE2	41:L4:265:GLU:N	2.42	0.53
44:L7:83:LEU:HD23	44:L7:191:VAL:HG22	1.90	0.53
46:L9:44:THR:HG22	36:5:3186:A:N3	325.77	0.53
51:M5:52:GLY:O	51:M5:148:TYR:OH	2.97	0.53
55:M9:28:GLU:HG3	55:M9:49:THR:HG22	4.09	0.53
77:Q1:6:ARG:O	77:Q1:10:THR:HG23	2.09	0.53
39:L2:172:GLY:HA3	79:Q3:68:ALA:H	4.36	0.53
2:S0:88:LYS:HE2	2:S0:201:LEU:HG	5.53	0.53
36:1:1748:G:OP2	74:O8:42:LYS:NZ	2.40	0.53
36:1:543:C:H5''	36:1:544:C:C5	2.44	0.53
1:2:1796:C:OP1	28:D6:87:ARG:NH1	2.42	0.53
1:2:1368:G:O6	87:2:2064:OHX:N5	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:231:U:H3	1:2:234:G:H1	1.54	0.53
37:3:14:U:H5'	42:L5:24:ARG:HH11	1.73	0.53
36:5:821:U:OP2	87:5:3956:OHX:N6	2.42	0.53
1:6:1173:C:H2'	1:6:1174:C:H6	1.73	0.53
1:6:108:A:OP2	87:6:2057:OHX:N4	2.41	0.53
1:6:292:U:H2'	1:6:293:U:C6	2.44	0.53
18:C6:99:GLU:OE1	18:C6:103:ASN:ND2	5.48	0.53
5:S3:11:LEU:HD12	22:D0:86:ILE:HG12	1.90	0.53
41:L4:44:LYS:HB3	41:L4:47:ARG:NH1	3.10	0.53
42:L5:64:ILE:HD12	42:L5:144:VAL:HG21	4.56	0.53
42:L5:61:ILE:HG12	42:L5:79:TYR:HD1	1.74	0.53
36:1:1139:G:OP1	44:L7:97:PRO:HG3	2.09	0.53
45:L8:221:ASN:HA	45:L8:225:LYS:HE3	3.62	0.53
47:M0:210:ILE:HG12	47:M0:217:PHE:CZ	2.44	0.53
47:M0:212:GLU:HB3	47:M0:213:PHE:HD1	2.66	0.53
53:M7:30:ARG:HA	53:M7:119:VAL:HG11	2.16	0.53
41:L4:30:ILE:N	54:M8:25:TYR:OH	2.38	0.53
55:M9:180:LYS:HA	55:M9:183:ALA:HB3	1.89	0.53
57:N1:105:PHE:O	57:N1:109:VAL:HG23	2.37	0.53
36:1:1925:U:O2	79:Q3:19:GLY:HA2	2.09	0.53
79:Q3:8:VAL:HG23	79:Q3:9:GLY:H	3.80	0.53
5:S3:202:LEU:C	5:S3:204:ASP:H	2.39	0.53
7:S5:175:LEU:C	7:S5:177:ILE:H	3.55	0.53
8:S6:50:PHE:HB3	8:S6:111:LEU:HB3	3.16	0.53
34:SR:211:ILE:HD11	34:SR:225:LEU:HD13	1.91	0.53
36:1:2206:G:OP2	36:1:2206:G:H8	1.91	0.53
36:1:2960:C:H2'	36:1:2961:G:H8	1.72	0.53
1:2:1235:C:O2	33:E1:138:ARG:NE	2.36	0.53
1:2:637:C:O2	9:S7:114:ARG:NH2	2.30	0.53
44:L7:158:LYS:HG3	36:5:1103:A:H4'	217.75	0.53
36:5:2794:G:N7	87:5:3903:OHX:N1	2.56	0.53
10:S8:10:LYS:HD3	1:6:338:C:H5''	291.84	0.53
23:D1:77:GLY:O	23:D1:79:LEU:N	2.37	0.53
24:D2:67:GLY:O	24:D2:69:LEU:N	3.74	0.53
40:L3:83:PRO:O	40:L3:165:GLN:NE2	2.42	0.53
36:1:598:A:OP1	44:L7:41:ARG:NH1	2.42	0.53
47:M0:85:PHE:HA	47:M0:140:THR:HG22	1.91	0.53
48:M1:15:GLU:HB2	48:M1:132:ASN:OD1	2.09	0.53
64:N8:46:ASP:N	64:N8:46:ASP:OD1	2.71	0.53
75:O9:44:TRP:CH2	75:O9:45:ARG:HG3	2.44	0.53
3:S1:179:SER:HB3	3:S1:183:GLN:HB2	1.96	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:S2:230:TRP:CD2	24:D2:68:ARG:HD3	2.44	0.53
6:S4:185:GLY:N	6:S4:189:LEU:HD13	2.24	0.53
6:S4:125:LYS:NZ	6:S4:225:VAL:O	2.34	0.53
36:1:844:G:N7	87:1:3819:OHX:N5	2.57	0.53
36:1:744:A:N3	54:M8:141:ARG:NH1	2.56	0.53
36:5:109:A:N1	36:5:322:U:O2'	2.40	0.53
36:5:3194:C:H2'	36:5:3195:U:H3'	1.91	0.53
1:6:1564:U:H2'	1:6:1565:C:C6	2.43	0.53
1:6:871:G:H2'	1:6:872:G:C8	2.44	0.53
36:5:345:G:O2'	38:8:25:G:N3	2.37	0.53
20:C8:136:GLN:NE2	1:6:1544:U:OP1	356.51	0.53
24:D2:111:MET:HG3	24:D2:116:ALA:HB2	1.90	0.53
45:L8:75:ILE:O	45:L8:77:GLN:N	2.41	0.53
46:L9:109:ALA:O	46:L9:110:LYS:HB2	2.37	0.53
54:M8:40:THR:C	54:M8:42:ALA:H	2.12	0.53
63:N7:54:THR:O	63:N7:57:HIS:HB2	2.08	0.53
65:N9:7:HIS:CG	65:N9:8:THR:N	2.76	0.53
75:O9:3:ALA:O	75:O9:5:LYS:HE2	7.35	0.53
76:Q0:83:LYS:NZ	76:Q0:83:LYS:HB3	2.24	0.53
2:S0:29:VAL:HG22	2:S0:150:ASP:HB3	1.90	0.53
4:S2:35:TRP:CE2	4:S2:37:PRO:HB3	2.44	0.53
6:S4:160:VAL:HG13	6:S4:169:ILE:HG23	1.91	0.53
7:S5:110:ALA:HA	7:S5:113:ILE:HB	2.92	0.53
11:S9:154:LYS:HG3	11:S9:155:HIS:CD2	7.46	0.53
11:S9:168:ARG:HG2	11:S9:170:GLY:N	2.24	0.53
36:1:2355:G:H4'	53:M7:139:TYR:CE2	2.44	0.53
36:1:2767:U:OP1	87:1:4032:OHX:N2	2.41	0.53
1:2:134:U:OP1	1:2:136:C:N4	2.42	0.53
1:2:161:U:OP2	8:S6:87:ARG:NH2	2.39	0.53
36:5:1340:G:H1	36:5:1364:C:H42	1.57	0.53
36:5:1725:C:H2'	36:5:1726:C:H6	1.74	0.53
36:5:3178:A:H5''	36:5:3179:U:OP1	2.09	0.53
36:5:1657:C:OP2	87:5:4092:OHX:N2	2.41	0.53
32:E0:14:VAL:HG23	1:6:567:A:H1'	377.96	0.53
25:D3:23:ARG:HB3	25:D3:29:TYR:CE1	2.50	0.53
29:D7:41:LEU:H	29:D7:41:LEU:HD23	3.25	0.53
32:E0:44:PHE:HE1	32:E0:54:ARG:HH22	1.55	0.53
39:L2:145:LYS:O	39:L2:160:SER:OG	2.27	0.53
45:L8:112:GLU:HA	45:L8:115:ALA:HB3	1.89	0.53
45:L8:78:PHE:O	45:L8:80:TYR:N	2.41	0.53
41:L4:106:TRP:HB2	51:M5:199:LEU:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:M7:36:ILE:HG12	53:M7:44:ALA:HB1	1.90	0.53
38:4:71:A:O2'	62:N6:52:ARG:NH2	2.41	0.53
70:O4:96:GLU:O	70:O4:99:LYS:HB2	2.90	0.53
76:Q0:97:ARG:HB2	76:Q0:120:GLN:O	2.64	0.53
4:S2:49:LYS:HE3	4:S2:246:GLU:OE1	2.68	0.53
5:S3:74:GLN:HA	5:S3:79:TYR:HB2	2.14	0.53
6:S4:141:THR:OG1	6:S4:145:ARG:HB2	2.31	0.53
9:S7:97:ARG:HA	9:S7:97:ARG:HH11	4.57	0.53
36:1:2424:A:H2'	36:1:2425:G:O4'	2.08	0.53
36:1:2573:G:O6	87:1:3894:OHX:N3	2.42	0.53
36:1:75:G:H5'	49:M3:58:VAL:HG13	1.90	0.53
36:1:804:C:OP1	41:L4:98:ARG:NH2	2.42	0.53
36:1:915:A:C5	36:1:917:A:H1'	2.44	0.53
36:5:1556:C:O5'	36:5:2169:G:N2	2.41	0.53
36:5:3066:U:O4	87:5:4013:OHX:N3	2.42	0.53
1:6:1360:A:H3'	1:6:1361:U:H4'	1.90	0.53
1:6:151:G:H1	1:6:163:G:H1	1.56	0.53
5:S3:68:GLU:HG2	12:C0:89:ALA:HB1	5.48	0.53
18:C6:40:GLU:C	18:C6:42:GLU:H	3.21	0.53
19:C7:23:LYS:HG2	34:SR:198:ASN:HD21	2.87	0.53
25:D3:107:PHE:CE1	25:D3:114:LYS:HD2	6.18	0.53
33:E1:126:CYS:O	33:E1:128:ALA:N	2.36	0.53
41:L4:118:LYS:O	41:L4:121:ALA:HB3	2.45	0.53
41:L4:144:LYS:CD	41:L4:144:LYS:H	4.84	0.53
41:L4:59:GLN:NE2	73:O7:55:ARG:HH22	2.07	0.53
42:L5:36:LEU:HD13	42:L5:50:ARG:HD2	5.27	0.53
59:N3:87:ARG:HH12	59:N3:137:VAL:HG11	1.92	0.53
66:O0:30:THR:HG22	66:O0:91:SER:HB2	1.91	0.53
78:Q2:3:ASN:HA	78:Q2:92:GLU:O	2.09	0.53
3:S1:90:GLU:OE1	3:S1:91:VAL:N	3.63	0.53
9:S7:50:ASP:HA	9:S7:56:LYS:HA	1.91	0.53
10:S8:11:ARG:O	13:C1:133:LYS:NZ	2.39	0.53
36:1:3000:A:H2'	36:1:3001:C:C6	2.44	0.52
36:1:3055:U:H1'	36:1:3057:U:OP2	2.09	0.52
1:2:868:G:C2	1:2:869:A:C8	2.97	0.52
36:5:2309:A:N3	36:5:2961:G:O2'	2.42	0.52
54:M8:142:GLY:O	36:5:744:A:H4'	169.05	0.52
36:5:980:A:H2'	36:5:981:U:H1'	1.91	0.52
1:6:218:A:H2'	1:6:219:A:H5''	1.91	0.52
1:6:93:A:C6	1:6:398:G:C6	2.98	0.52
37:7:113:C:H2'	37:7:114:U:O4'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:C4:125:SER:OG	16:C4:126:THR:N	2.42	0.52
19:C7:41:ILE:HD13	19:C7:50:ILE:HD12	2.01	0.52
20:C8:24:GLY:HA2	20:C8:58:ALA:HB3	3.17	0.52
22:D0:103:ILE:HA	22:D0:106:ILE:HG22	3.37	0.52
25:D3:62:LYS:HD2	25:D3:118:PRO:HB3	1.90	0.52
27:D5:91:PRO:HB3	27:D5:101:TYR:CE1	2.63	0.52
30:D8:31:GLU:O	30:D8:33:LEU:N	3.71	0.52
40:L3:84:VAL:HG23	40:L3:163:HIS:O	2.67	0.52
41:L4:36:HIS:O	41:L4:40:THR:HG23	2.52	0.52
42:L5:120:LYS:O	42:L5:248:ARG:NH2	3.24	0.52
50:M4:126:GLN:NE2	36:5:3261:C:OP1	296.64	0.52
46:L9:50:ASN:HD21	50:M4:4:ASP:HB3	1.74	0.52
63:N7:108:GLU:O	63:N7:112:LYS:HG3	2.09	0.52
64:N8:22:ILE:H	64:N8:22:ILE:HD12	2.02	0.52
65:N9:23:LYS:CG	65:N9:24:PRO:HD3	2.39	0.52
79:Q3:47:VAL:HA	79:Q3:57:CYS:HA	1.91	0.52
4:S2:225:LEU:HG	23:D1:23:ILE:HG13	1.91	0.52
34:SR:14:GLU:HB3	34:SR:309:VAL:HG22	1.92	0.52
36:1:113:C:OP1	51:M5:147:ARG:NE	2.37	0.52
36:1:2652:U:O2	87:1:4083:OHX:N3	2.42	0.52
36:1:3107:U:O4	36:1:3128:G:N2	2.42	0.52
36:1:3341:U:O2'	36:1:3342:A:H5'	2.09	0.52
1:2:487:G:H3'	1:2:488:G:H5''	1.91	0.52
14:C2:29:LYS:HE2	14:C2:100:TRP:CD1	2.44	0.52
15:C3:66:ILE:HG13	15:C3:67:THR:HG22	2.61	0.52
20:C8:87:ASN:OD1	20:C8:88:ARG:N	2.43	0.52
20:C8:86:LEU:HA	20:C8:99:HIS:ND1	2.82	0.52
22:D0:60:THR:HG1	22:D0:87:HIS:CE1	2.22	0.52
16:C4:92:LYS:NZ	28:D6:69:ASN:HB2	2.24	0.52
40:L3:44:THR:OG1	40:L3:182:GLN:O	2.28	0.52
43:L6:98:VAL:HA	43:L6:101:PHE:HD2	1.74	0.52
45:L8:156:ASP:HB2	45:L8:183:LYS:HD3	1.91	0.52
59:N3:79:VAL:HG22	59:N3:100:GLY:HA2	1.90	0.52
60:N4:50:ALA:HA	60:N4:55:PHE:CG	2.70	0.52
62:N6:56:VAL:HG22	62:N6:105:VAL:O	2.09	0.52
67:O1:30:PRO:HG3	67:O1:60:TRP:CZ2	2.97	0.52
70:O4:82:ALA:O	70:O4:85:VAL:N	2.43	0.52
2:S0:167:LYS:HE3	2:S0:168:HIS:HD2	3.17	0.52
3:S1:129:THR:HA	3:S1:177:GLN:HA	1.92	0.52
5:S3:162:GLN:HG3	1:6:1333:C:O4'	428.54	0.52
11:S9:9:SER:OG	1:6:771:A:OP1	392.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1276:U:OP1	87:1:3979:OHX:N4	2.42	0.52
36:1:2112:U:H4'	36:1:2113:A:H5'	1.92	0.52
36:1:2771:U:H2'	36:1:2772:C:C2	2.44	0.52
36:1:434:U:O4	87:1:4061:OHX:N5	2.43	0.52
36:1:655:C:H2'	36:1:656:A:H8	1.75	0.52
1:2:1307:U:O4	1:2:1319:A:H1'	2.10	0.52
1:2:180:A:H2'	1:2:181:A:O4'	2.08	0.52
1:2:523:G:O6	87:2:2020:OHX:N3	2.43	0.52
36:5:129:U:H2'	36:5:130:A:C8	2.44	0.52
36:5:192:C:H2'	36:5:193:C:C6	2.44	0.52
36:5:2364:G:H22	36:5:2396:G:H1'	1.74	0.52
36:5:962:A:O2'	36:5:963:G:H5'	2.09	0.52
1:6:1029:U:O4	87:6:2153:OHX:N4	2.42	0.52
1:6:151:G:H22	1:6:163:G:N2	2.07	0.52
1:6:41:A:H2'	1:6:438:A:H62	1.74	0.52
12:C0:7:ASP:O	12:C0:11:ILE:HG12	2.09	0.52
19:C7:50:ILE:O	19:C7:54:THR:OG1	2.16	0.52
40:L3:128:LYS:HD2	40:L3:131:THR:HG21	3.92	0.52
40:L3:139:GLN:HG3	40:L3:141:GLY:H	1.75	0.52
40:L3:293:ASN:HB3	40:L3:305:ILE:HG13	1.91	0.52
42:L5:61:ILE:HD13	42:L5:79:TYR:HE1	2.04	0.52
44:L7:203:TRP:CD1	44:L7:204:PRO:HD2	2.73	0.52
46:L9:122:LYS:HD3	46:L9:123:ILE:N	4.80	0.52
51:M5:36:ILE:HG12	51:M5:64:VAL:HG23	2.53	0.52
56:N0:155:ARG:HG3	56:N0:156:VAL:N	2.22	0.52
58:N2:76:LEU:O	58:N2:80:THR:HG23	2.08	0.52
66:O0:39:SER:OG	66:O0:65:THR:HG21	2.10	0.52
64:N8:14:HIS:CE1	68:O2:36:LYS:HE2	2.45	0.52
2:S0:74:VAL:HG23	2:S0:118:PRO:HB3	2.06	0.52
6:S4:246:LEU:HD13	6:S4:251:GLU:HG2	3.56	0.52
8:S6:2:LYS:HB3	8:S6:108:VAL:HG12	5.45	0.52
9:S7:39:ARG:NH2	55:M9:185:LEU:HD22	2.43	0.52
34:SR:221:MET:HG2	34:SR:233:THR:HG23	1.90	0.52
36:1:1651:U:H2'	36:1:1652:G:C8	2.44	0.52
36:1:2366:C:H2'	36:1:2367:A:C8	2.44	0.52
36:1:3317:U:H4'	36:1:3318:G:O5'	2.08	0.52
1:2:1433:G:H2'	1:2:1434:U:C6	2.45	0.52
1:2:602:U:H2'	1:2:603:U:C6	2.45	0.52
36:5:1104:G:H2'	36:5:1105:A:C8	2.44	0.52
36:5:2211:U:H5	36:5:2234:G:H1	1.54	0.52
1:6:37:U:O2'	1:6:770:A:N1	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:7:18:C:O2	37:7:61:G:N2	2.32	0.52
12:C0:14:TYR:CE1	12:C0:18:GLU:HG3	2.80	0.52
16:C4:29:HIS:ND1	16:C4:29:HIS:O	2.43	0.52
23:D1:42:GLU:O	23:D1:42:GLU:HG2	2.98	0.52
13:C1:99:ARG:HB2	25:D3:12:ALA:HB2	2.95	0.52
27:D5:59:TYR:CE2	27:D5:61:SER:HB3	2.45	0.52
40:L3:146:ARG:O	40:L3:150:ARG:N	2.41	0.52
36:1:269:G:H5'	51:M5:120:TRP:CZ3	2.44	0.52
59:N3:27:ASP:OD1	59:N3:27:ASP:N	2.42	0.52
36:1:1433:A:N3	68:O2:27:ARG:NH1	2.57	0.52
3:S1:76:SER:OG	3:S1:78:ASP:OD1	2.26	0.52
7:S5:49:GLU:O	7:S5:51:VAL:N	2.40	0.52
34:SR:91:LEU:HB2	34:SR:103:PHE:HE2	2.29	0.52
36:1:1103:A:H2'	36:1:1103:A:N3	2.25	0.52
36:1:1230:G:N2	36:1:1279:C:N3	2.57	0.52
36:1:132:C:H2'	36:1:133:U:H5''	1.91	0.52
36:1:924:G:OP1	87:1:4043:OHX:N3	2.41	0.52
36:1:517:G:OP1	44:L7:60:ARG:NH1	2.40	0.52
36:1:796:U:H2'	36:1:797:U:C6	2.44	0.52
1:2:1113:A:O2'	87:2:2138:OHX:N6	2.42	0.52
1:2:780:A:C8	26:D4:8:ARG:HB3	2.45	0.52
38:4:124:G:O6	87:4:226:OHX:N2	2.42	0.52
36:5:1232:C:H2'	36:5:1233:G:H8	1.75	0.52
36:5:151:A:H2'	36:5:152:U:O4'	2.09	0.52
36:5:2592:G:H4'	36:5:2594:C:C2	2.45	0.52
36:5:2669:G:N7	87:5:3981:OHX:N2	2.57	0.52
28:D6:10:ARG:NE	1:6:1795:U:O2	329.31	0.52
1:6:654:C:H2'	1:6:655:G:C8	2.45	0.52
36:5:1055:A:H5''	37:7:100:C:O2'	2.10	0.52
38:8:110:C:O2'	38:8:112:U:OP2	2.21	0.52
5:S3:28:GLU:OE1	12:C0:58:GLN:HG3	2.09	0.52
14:C2:56:GLU:HB3	14:C2:124:LYS:HE3	1.91	0.52
17:C5:18:ARG:HH21	17:C5:38:PRO:HG3	2.58	0.52
19:C7:46:LEU:O	19:C7:50:ILE:HG13	2.10	0.52
20:C8:46:VAL:HG11	20:C8:73:MET:HG3	1.91	0.52
40:L3:10:ARG:NH1	40:L3:11:HIS:O	2.56	0.52
42:L5:113:LEU:HB3	42:L5:115:LEU:HD22	1.92	0.52
42:L5:153:THR:HG22	42:L5:179:ARG:HE	1.75	0.52
42:L5:274:GLN:HE22	37:7:60:G:H21	332.99	0.52
46:L9:84:LYS:NZ	46:L9:191:LEU:HD13	2.25	0.52
51:M5:102:ALA:O	51:M5:106:VAL:HG13	3.31	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:M6:185:ALA:O	52:M6:188:SER:OG	3.07	0.52
53:M7:175:ARG:O	53:M7:179:GLN:HB2	2.10	0.52
36:1:1603:A:OP1	55:M9:38:ARG:NH1	2.43	0.52
57:N1:12:ARG:HD3	57:N1:13:TYR:HE2	1.74	0.52
58:N2:89:LEU:HD22	58:N2:93:ILE:HD11	1.90	0.52
1:2:788:A:C4	6:S4:19:LEU:HD13	2.45	0.52
1:2:10:G:H2'	1:2:11:A:C8	2.45	0.52
1:2:1796:C:OP2	28:D6:5:ARG:NH1	2.42	0.52
37:3:38:U:HO2'	37:3:40:C:H5	1.55	0.52
75:O9:10:LYS:NZ	36:5:1834:U:OP2	106.48	0.52
36:5:2943:G:H2'	36:5:2944:U:O4'	2.09	0.52
1:6:1120:U:H2'	1:6:1121:C:C6	2.45	0.52
1:6:1216:C:O2	1:6:1446:A:N6	2.43	0.52
1:6:1334:U:H2'	1:6:1335:U:O4'	2.10	0.52
1:6:1370:U:H4'	1:6:1371:A:H4'	1.92	0.52
16:C4:132:ARG:HB2	16:C4:132:ARG:HH11	2.45	0.52
16:C4:84:ARG:HG3	16:C4:119:THR:HA	1.91	0.52
28:D6:87:ARG:HD2	1:6:1797:A:C6	346.26	0.52
30:D8:8:THR:HB	30:D8:56:LEU:HB2	3.43	0.52
32:E0:55:ARG:HB3	32:E0:58:PRO:HG3	1.90	0.52
40:L3:277:SER:HB3	40:L3:280:HIS:NE2	2.23	0.52
43:L6:76:LEU:HD11	43:L6:141:VAL:HG21	1.92	0.52
44:L7:59:GLU:O	44:L7:63:ILE:HG13	2.10	0.52
46:L9:166:ARG:HD2	46:L9:168:ARG:HH11	12.48	0.52
36:1:2645:G:OP2	47:M0:117:GLY:HA2	2.10	0.52
47:M0:54:SER:O	47:M0:132:GLY:N	3.10	0.52
51:M5:14:LYS:HA	51:M5:19:LEU:HD23	1.91	0.52
53:M7:26:PHE:CE1	53:M7:120:ASN:HA	2.45	0.52
59:N3:136:VAL:HG12	59:N3:137:VAL:HG23	1.91	0.52
63:N7:124:ALA:O	63:N7:126:LYS:N	2.43	0.52
67:O1:44:MET:HB3	67:O1:77:ARG:NH1	3.60	0.52
75:O9:44:TRP:CZ3	75:O9:45:ARG:HG3	2.56	0.52
9:S7:51:VAL:HG23	9:S7:53:GLY:H	1.75	0.52
36:1:1210:U:H3	36:1:1295:G:H1	1.58	0.52
36:1:259:C:H2'	36:1:260:C:C6	2.44	0.52
36:1:398:A:H5''	53:M7:3:ARG:HD2	1.92	0.52
1:2:1107:G:H3'	1:2:1108:G:H21	1.74	0.52
1:2:1621:U:H2'	1:2:1622:G:C8	2.44	0.52
1:2:67:A:O3'	1:2:68:A:H3'	2.09	0.52
36:5:1155:C:H2'	36:5:1156:C:H6	1.74	0.52
56:N0:115:ARG:NH1	36:5:1295:G:O2'	296.84	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:M9:9:ARG:NH2	36:5:1602:A:O3'	108.70	0.52
36:5:2898:G:H5''	36:5:2899:C:H5'	1.91	0.52
36:5:1658:G:O6	87:5:4113:OHX:N3	2.43	0.52
20:C8:36:LYS:NZ	1:6:1568:C:OP2	338.54	0.52
13:C1:90:TYR:OH	1:6:307:G:OP1	327.41	0.52
37:7:11:A:H4'	37:7:13:A:C8	2.45	0.52
38:8:74:U:O2	87:8:216:OHX:N5	2.43	0.52
16:C4:85:ALA:H	16:C4:119:THR:CG2	2.23	0.52
20:C8:87:ASN:OD1	20:C8:99:HIS:HA	2.48	0.52
25:D3:46:SER:OG	25:D3:78:LYS:NZ	2.99	0.52
32:E0:39:LEU:O	32:E0:43:ARG:N	2.85	0.52
40:L3:220:VAL:O	40:L3:334:ARG:NH1	2.42	0.52
41:L4:20:LEU:HD11	41:L4:252:GLU:HG3	1.94	0.52
44:L7:224:ILE:HD13	56:N0:39:SER:HB2	1.92	0.52
45:L8:148:ALA:HB3	45:L8:175:VAL:HG11	3.08	0.52
45:L8:65:LEU:HD12	51:M5:25:VAL:HG13	1.92	0.52
46:L9:21:LYS:HA	50:M4:8:LYS:HG3	1.90	0.52
47:M0:12:GLN:NE2	47:M0:128:ARG:HB3	3.69	0.52
36:1:1048:A:H2'	47:M0:22:TYR:CE1	2.44	0.52
48:M1:82:ARG:HH22	48:M1:114:ILE:HD11	1.75	0.52
50:M4:108:ARG:NH1	50:M4:116:GLU:OE2	3.68	0.52
50:M4:8:LYS:HE2	50:M4:8:LYS:O	6.50	0.52
52:M6:55:HIS:O	52:M6:58:LEU:N	2.41	0.52
59:N3:11:PHE:CD1	59:N3:88:ARG:HD2	2.70	0.52
68:O2:85:LEU:HB2	68:O2:117:ILE:HD13	1.92	0.52
72:O6:57:LEU:O	72:O6:61:ILE:HG13	2.27	0.52
73:O7:2:GLY:O	73:O7:7:SER:HB2	4.17	0.52
74:O8:17:ARG:HG2	74:O8:20:VAL:HG23	3.61	0.52
79:Q3:84:ARG:O	79:Q3:88:GLU:HG2	2.09	0.52
3:S1:70:LEU:HG	3:S1:84:ILE:HD11	3.44	0.52
6:S4:131:LEU:HD11	6:S4:135:GLY:HA2	2.70	0.52
6:S4:28:ALA:O	1:6:448:C:H4'	367.34	0.52
7:S5:136:ALA:O	7:S5:140:THR:OG1	3.03	0.52
7:S5:51:VAL:O	7:S5:65:ARG:NH1	3.32	0.52
11:S9:102:GLU:O	11:S9:106:GLU:N	2.88	0.52
36:1:3228:C:H4'	36:1:3229:G:O5'	2.10	0.52
1:2:1335:U:H2'	1:2:1336:A:H8	1.73	0.52
1:2:1528:U:H2'	1:2:1529:C:H6	1.74	0.52
1:2:446:A:OP1	6:S4:59:ARG:NE	2.36	0.52
1:2:704:C:O2	1:2:705:U:O2'	2.19	0.52
1:2:81:G:OP2	87:2:2112:OHX:N5	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:4:18:U:OP1	87:4:224:OHX:N2	2.42	0.52
36:5:1435:A:H5''	36:5:1436:U:H5''	1.92	0.52
36:5:1554:U:O2'	36:5:1581:C:H2'	2.10	0.52
36:5:1631:C:H5''	36:5:1632:A:H5''	1.92	0.52
55:M9:20:ARG:HD2	36:5:1874:A:OP2	142.61	0.52
36:5:2801:A:O2'	36:5:2802:A:H2'	2.10	0.52
36:5:1829:G:N7	87:5:3960:OHX:N3	2.57	0.52
49:M3:15:ARG:NH2	36:5:96:G:H5'	152.74	0.52
1:6:1031:U:H4'	1:6:1032:G:OP2	2.09	0.52
1:6:1285:U:OP1	87:6:2104:OHX:N2	2.43	0.52
1:6:225:A:N6	1:6:226:A:H62	2.08	0.52
38:8:9:A:H2'	38:8:10:A:C8	2.45	0.52
14:C2:52:LEU:O	14:C2:85:LYS:NZ	2.42	0.52
1:2:1559:A:C6	20:C8:134:ARG:HD2	2.45	0.52
39:L2:47:GLN:HA	39:L2:84:THR:HG22	2.38	0.52
42:L5:106:ALA:HB2	42:L5:166:ALA:HA	1.92	0.52
46:L9:162:GLN:OE1	76:Q0:89:TYR:HE1	1.93	0.52
47:M0:48:LEU:HD23	47:M0:178:ARG:HH12	1.74	0.52
53:M7:129:THR:HG22	53:M7:139:TYR:HB2	1.91	0.52
58:N2:49:ASN:O	58:N2:49:ASN:ND2	2.38	0.52
2:S0:58:VAL:O	2:S0:62:ARG:HG3	4.47	0.52
3:S1:61:LEU:HD11	3:S1:96:LEU:HD13	8.43	0.52
7:S5:43:PHE:HB3	7:S5:46:TRP:HD1	6.29	0.52
7:S5:90:ILE:HD11	7:S5:130:ILE:HG13	2.77	0.52
36:1:1404:G:C6	36:1:1408:G:C6	2.98	0.52
36:1:1824:U:OP1	74:O8:3:ARG:NH1	2.43	0.52
36:1:3003:G:P	40:L3:26:ARG:HH22	2.33	0.52
36:1:374:A:HO2'	36:1:376:G:H8	1.58	0.52
36:1:997:A:H2'	36:1:998:A:O4'	2.10	0.52
1:2:1460:A:O3'	35:SM:72:ARG:NH2	2.43	0.52
1:2:1621:U:H2'	1:2:1622:G:H8	1.74	0.52
1:2:1683:C:O2'	1:2:1684:U:O5'	2.27	0.52
1:2:1649:G:N7	87:2:2018:OHX:N1	2.58	0.52
38:4:121:U:H2'	38:4:122:U:C6	2.45	0.52
38:4:53:A:H4'	75:O9:40:LYS:HD2	1.90	0.52
36:5:1277:C:H2'	36:5:1278:A:C8	2.45	0.52
36:5:188:U:H1'	36:5:208:C:H1'	1.90	0.52
39:L2:226:SER:CA	36:5:2202:C:H5''	209.61	0.52
36:5:2655:U:H4'	36:5:2656:A:O4'	2.10	0.52
21:C9:44:GLU:N	1:6:1477:G:OP1	373.70	0.52
1:6:320:U:OP2	1:6:321:C:H3'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:119:A:H1'	1:6:397:A:C5	2.45	0.52
1:6:846:G:H2'	1:6:847:A:H8	1.74	0.52
1:2:325:G:H4'	13:C1:83:THR:HG21	1.92	0.52
23:D1:12:TYR:CE2	23:D1:14:PRO:HG3	2.44	0.52
25:D3:90:ASP:OD2	32:E0:12:GLY:HA2	2.20	0.52
39:L2:208:ASP:OD2	36:5:912:G:N1	187.51	0.52
39:L2:29:LEU:HA	39:L2:76:PHE:HE1	1.75	0.52
41:L4:31:ARG:NH1	41:L4:34:ILE:HD11	2.24	0.52
42:L5:95:TRP:CH2	42:L5:181:PRO:HD3	5.07	0.52
44:L7:173:LEU:HD21	44:L7:198:ALA:HA	1.94	0.52
47:M0:89:VAL:HG22	47:M0:136:PHE:CE1	3.53	0.52
53:M7:136:ILE:O	53:M7:137:ASN:ND2	2.47	0.52
57:N1:52:MET:HA	57:N1:95:HIS:CD2	2.94	0.52
66:O0:42:ILE:HD11	66:O0:67:VAL:HG22	1.98	0.52
73:O7:22:CYS:SG	73:O7:24:ARG:HG3	2.50	0.52
5:S3:28:GLU:OE2	5:S3:65:ARG:NH1	2.43	0.52
7:S5:105:GLY:O	1:6:1609:U:O2'	378.03	0.52
9:S7:96:ARG:HD2	9:S7:121:VAL:HG13	1.91	0.52
10:S8:189:LEU:O	10:S8:193:LEU:HB2	2.10	0.52
11:S9:27:GLU:OE1	11:S9:39:LYS:NZ	2.51	0.52
36:1:1944:U:H2'	36:1:1945:A:C8	2.45	0.52
36:1:199:A:C4	36:1:201:A:C8	2.98	0.52
36:1:392:G:O2'	62:N6:90:VAL:HG11	2.10	0.52
1:2:1277:G:H2'	1:2:1278:G:O4'	2.10	0.52
1:2:894:U:H2'	1:2:895:G:H8	1.75	0.52
36:5:181:U:H1'	36:5:236:G:N2	2.24	0.52
36:5:2512:C:OP2	87:5:3880:OHX:N6	2.42	0.52
36:5:549:U:H2'	36:5:550:A:H8	1.75	0.52
36:5:59:G:H2'	38:8:33:A:O2'	2.10	0.52
1:6:1584:G:H22	1:6:1611:A:P	2.33	0.52
1:6:264:G:O6	87:6:2024:OHX:N2	2.42	0.52
1:6:26:A:O2'	1:6:27:U:OP2	2.26	0.52
1:6:44:U:OP2	1:6:437:A:N6	2.43	0.52
1:6:507:U:H2'	1:6:508:U:O4'	2.10	0.52
6:S4:187:ARG:NH1	1:6:752:A:H3'	378.27	0.52
33:E1:98:VAL:HG22	33:E1:99:LYS:H	1.74	0.52
39:L2:130:SER:HB2	39:L2:171:GLY:HA3	2.77	0.52
42:L5:122:VAL:C	42:L5:124:GLU:H	3.19	0.52
36:1:1354:G:H4'	43:L6:8:LYS:HE2	1.91	0.52
45:L8:121:SER:O	45:L8:123:GLN:N	2.77	0.52
45:L8:155:ASN:HD21	45:L8:181:LYS:HA	4.36	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:L9:139:ASN:N	46:L9:139:ASN:OD1	3.61	0.52
46:L9:150:SER:HB3	46:L9:153:ASP:HB2	1.91	0.52
47:M0:51:HIS:ND1	47:M0:137:SER:OG	2.40	0.52
49:M3:106:GLN:HB3	72:O6:18:THR:OG1	2.42	0.52
50:M4:37:GLU:HG2	56:N0:72:VAL:HG21	2.45	0.52
53:M7:111:LYS:HB3	53:M7:153:LYS:HB3	1.92	0.52
56:N0:77:VAL:HG11	56:N0:106:LEU:HD13	1.92	0.52
58:N2:89:LEU:HB3	58:N2:93:ILE:HD12	2.41	0.52
60:N4:65:GLU:HA	60:N4:68:ALA:HB3	3.56	0.52
66:O0:92:ILE:HG21	66:O0:100:ILE:HD11	1.92	0.52
3:S1:28:GLU:HG3	3:S1:50:LYS:HG3	7.28	0.52
8:S6:7:TYR:HD2	8:S6:8:PRO:HD2	1.73	0.52
10:S8:76:THR:HB	10:S8:105:ASP:CB	2.49	0.52
11:S9:143:ILE:HG13	1:6:767:U:C5	424.38	0.52
36:1:138:U:H2'	36:1:139:G:H8	1.75	0.51
36:1:1658:G:H2'	36:1:1659:U:C6	2.45	0.51
36:1:180:C:H2'	36:1:181:U:C6	2.44	0.51
36:1:679:U:H2'	36:1:680:G:C8	2.45	0.51
1:2:912:U:H4'	1:2:913:G:O5'	2.09	0.51
38:4:10:A:H2'	38:4:11:C:C6	2.45	0.51
36:5:249:U:O2'	36:5:250:U:H5''	2.09	0.51
36:5:573:C:H2'	36:5:574:U:C6	2.45	0.51
36:5:622:A:H2'	36:5:623:U:O4'	2.10	0.51
33:E1:82:LYS:NZ	1:6:1447:C:N3	382.77	0.51
1:6:1584:G:O2'	1:6:1610:G:O6	2.23	0.51
5:S3:75:LYS:HB3	12:C0:22:VAL:HG22	2.89	0.51
14:C2:62:LEU:HA	14:C2:120:VAL:HA	1.92	0.51
17:C5:128:HIS:N	35:SM:71:ASN:OD1	2.42	0.51
20:C8:140:THR:OG1	20:C8:141:THR:N	2.42	0.51
24:D2:30:SER:HA	24:D2:34:ILE:HD12	1.91	0.51
27:D5:102:THR:HG22	27:D5:103:ARG:H	3.99	0.51
30:D8:51:ASN:ND2	30:D8:51:ASN:O	2.42	0.51
40:L3:19:ARG:HG3	40:L3:273:HIS:CE1	2.46	0.51
40:L3:284:ARG:HG2	40:L3:321:PHE:HE1	2.80	0.51
50:M4:36:VAL:HG11	50:M4:55:ARG:NH2	2.25	0.51
56:N0:109:ASP:OD1	56:N0:113:ARG:NH1	2.43	0.51
64:N8:128:ARG:HB2	72:O6:8:ALA:CB	4.50	0.51
68:O2:16:LYS:HD2	68:O2:18:LYS:HE2	2.22	0.51
72:O6:43:LEU:O	72:O6:47:ILE:HG13	2.10	0.51
76:Q0:92:ASP:O	76:Q0:105:PRO:HG3	2.10	0.51
3:S1:127:VAL:HG11	3:S1:176:VAL:HG21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S1:154:SER:OG	3:S1:154:SER:O	2.28	0.51
3:S1:139:ALA:HB2	3:S1:172:LEU:HD11	2.44	0.51
34:SR:203:THR:OG1	34:SR:204:ALA:N	2.42	0.51
36:1:1385:C:HO2'	43:L6:2:SER:N	2.08	0.51
36:1:1593:A:N3	36:1:1615:C:O2'	2.43	0.51
36:1:173:G:N2	36:1:246:U:H1'	2.26	0.51
36:1:1909:A:H2'	36:1:1910:A:C8	2.45	0.51
36:1:2665:U:H4'	36:1:2666:C:OP1	2.11	0.51
36:1:3009:G:OP1	87:1:4100:OHX:N5	2.42	0.51
36:1:3278:C:H2'	36:1:3278:C:O2	2.09	0.51
36:1:3377:G:OP2	87:1:4077:OHX:N4	2.43	0.51
36:1:3288:G:O2'	87:1:4030:OHX:N1	2.44	0.51
36:1:827:A:H2'	36:1:828:A:H8	1.75	0.51
1:2:549:G:OP2	87:2:1994:OHX:N2	2.43	0.51
1:2:8:U:O2'	87:2:2033:OHX:N1	2.43	0.51
36:5:2344:U:H2'	36:5:2345:A:C8	2.45	0.51
36:5:2623:G:H2'	36:5:2624:G:H8	1.75	0.51
36:5:3276:G:OP2	36:5:3276:G:H2'	2.11	0.51
1:6:1207:C:H42	1:6:1456:C:H5	1.59	0.51
1:6:1405:G:H2'	1:6:1406:A:C8	2.45	0.51
1:6:755:A:HO2'	1:6:756:A:H8	1.58	0.51
1:6:219:A:H2'	1:6:831:U:O2	2.09	0.51
16:C4:115:ILE:HB	28:D6:65:PRO:HG3	6.58	0.51
39:L2:47:GLN:OE1	39:L2:60:LYS:HD2	5.34	0.51
41:L4:93:MET:CE	41:L4:93:MET:H	2.35	0.51
44:L7:138:TYR:CE2	44:L7:233:GLU:HG2	2.44	0.51
45:L8:140:VAL:HA	45:L8:143:ILE:HD12	1.93	0.51
46:L9:92:TYR:HB2	46:L9:142:ASP:HB3	2.02	0.51
48:M1:116:TYR:HD2	48:M1:122:ILE:HD11	1.74	0.51
55:M9:140:GLU:HA	55:M9:143:ILE:HB	1.93	0.51
72:O6:21:THR:O	72:O6:21:THR:OG1	2.55	0.51
36:1:2796:G:O6	78:Q2:63:LYS:HD3	2.09	0.51
2:S0:47:VAL:HG21	19:C7:105:GLN:HB2	1.92	0.51
3:S1:67:GLU:HG3	3:S1:85:LYS:HD2	5.11	0.51
10:S8:193:LEU:HA	10:S8:196:LEU:HD12	5.65	0.51
36:1:999:G:O2'	36:1:1000:C:H5'	2.10	0.51
36:1:1786:G:H2'	36:1:1787:A:C8	2.44	0.51
36:1:2208:A:C6	87:1:3940:OHX:N6	2.76	0.51
1:2:1681:A:H2'	1:2:1682:U:H5'	1.93	0.51
36:5:1135:A:C2	36:5:1136:A:C8	2.98	0.51
36:5:119:U:H4'	36:5:120:G:H3'	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1129:A:N6	36:5:2864:A:O2'	2.43	0.51
36:5:561:C:H2'	36:5:562:C:H6	1.75	0.51
1:6:1686:C:N3	1:6:1716:C:N4	2.58	0.51
15:C3:135:LEU:HD22	15:C3:139:TRP:CD2	2.46	0.51
17:C5:87:PRO:HA	17:C5:90:ILE:HG13	2.84	0.51
21:C9:57:ARG:HH11	21:C9:57:ARG:HB2	1.75	0.51
4:S2:230:TRP:CE2	24:D2:68:ARG:HD3	2.46	0.51
40:L3:171:LEU:HD23	40:L3:172:ALA:H	3.93	0.51
45:L8:133:LYS:HG3	45:L8:201:THR:HG23	2.99	0.51
46:L9:45:PHE:HA	46:L9:54:LYS:O	2.11	0.51
49:M3:75:PHE:O	49:M3:76:THR:OG1	2.25	0.51
54:M8:33:TYR:HA	54:M8:36:LEU:HB2	1.91	0.51
71:O5:28:LEU:HD23	71:O5:47:VAL:HG22	1.91	0.51
75:O9:35:ILE:HD11	38:8:53:A:C2	83.38	0.51
77:Q1:2:ARG:HB3	77:Q1:5:TRP:CD1	2.46	0.51
2:S0:126:PRO:HA	2:S0:133:ILE:HD11	2.12	0.51
2:S0:26:ALA:O	2:S0:46:HIS:ND1	3.38	0.51
3:S1:65:VAL:HG12	3:S1:87:ARG:HA	1.91	0.51
6:S4:57:ASN:OD1	6:S4:59:ARG:NH1	2.43	0.51
8:S6:164:LYS:HB3	8:S6:167:LYS:HB3	1.92	0.51
1:2:858:G:OP1	9:S7:116:ARG:NH2	2.43	0.51
10:S8:39:GLY:O	10:S8:59:ARG:HB3	2.11	0.51
36:1:1352:A:H4'	36:1:1353:U:OP1	2.10	0.51
36:1:2901:G:H5'	46:L9:175:PHE:CZ	2.46	0.51
36:1:415:G:H2'	36:1:416:A:C8	2.45	0.51
1:2:1783:C:H2'	1:2:1784:C:H6	1.74	0.51
1:2:45:U:O2	1:2:434:G:H1'	2.11	0.51
1:2:364:G:O2'	1:2:757:A:N6	2.44	0.51
1:2:75:U:H2'	1:2:76:A:O4'	2.10	0.51
1:2:997:G:H2'	1:2:998:A:O4'	2.11	0.51
70:O4:9:ARG:NH2	36:5:1606:U:O4	141.67	0.51
36:5:2437:G:H2'	36:5:2438:A:O4'	2.10	0.51
36:5:638:C:N4	36:5:647:A:OP1	2.41	0.51
1:6:1625:C:H2'	1:6:1626:U:C6	2.45	0.51
1:6:1672:G:H2'	1:6:1673:G:C8	2.46	0.51
1:6:515:A:H2'	1:6:516:G:O4'	2.09	0.51
1:6:833:U:OP2	87:6:2134:OHX:N5	2.43	0.51
18:C6:109:PHE:HB3	18:C6:116:LEU:HD13	7.00	0.51
5:S3:211:PRO:HG2	19:C7:19:ARG:HB3	4.39	0.51
24:D2:12:ASN:O	24:D2:16:ASN:HB2	2.10	0.51
41:L4:44:LYS:HD3	41:L4:47:ARG:NH1	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:L9:163:GLN:O	46:L9:166:ARG:HG3	2.29	0.51
46:L9:25:VAL:HB	46:L9:78:MET:HE1	3.31	0.51
48:M1:15:GLU:HB3	48:M1:130:VAL:HG13	1.92	0.51
49:M3:180:ARG:O	49:M3:184:GLU:HB2	2.90	0.51
36:1:44:U:OP1	51:M5:84:PRO:HG2	2.10	0.51
52:M6:127:LEU:HD11	56:N0:168:PRO:HG3	1.93	0.51
61:N5:71:THR:HG21	36:5:1603:A:H61	91.41	0.51
68:O2:76:VAL:HG22	68:O2:81:ASP:HB3	1.92	0.51
3:S1:59:ASP:C	3:S1:61:LEU:H	3.88	0.51
8:S6:189:HIS:CE1	8:S6:193:LEU:HD12	2.44	0.51
10:S8:122:GLY:H	10:S8:157:GLU:HG3	1.75	0.51
36:1:2267:C:H2'	36:1:2268:U:O4'	2.10	0.51
36:1:547:G:H1'	36:1:548:G:C8	2.45	0.51
36:1:936:A:OP1	64:N8:28:HIS:ND1	2.40	0.51
1:2:1147:A:H2'	1:2:1148:C:C6	2.46	0.51
1:2:1657:U:H4'	1:2:1658:G:O5'	2.11	0.51
1:2:472:U:H5''	11:S9:11:THR:HG23	1.93	0.51
1:2:532:U:O2'	26:D4:33:ALA:HB1	2.10	0.51
1:2:77:U:O2'	87:S6:301:OHX:N1	2.43	0.51
38:4:104:A:C8	38:4:105:A:C8	2.99	0.51
36:5:2726:C:O2'	36:5:2727:A:H2'	2.10	0.51
38:8:67:U:O4	87:8:222:OHX:N3	2.43	0.51
25:D3:107:PHE:HD2	25:D3:121:ARG:HA	3.29	0.51
25:D3:86:PHE:HB2	25:D3:120:VAL:HG11	1.91	0.51
36:1:2154:U:H4'	39:L2:240:ALA:HB2	1.91	0.51
42:L5:60:ILE:H	42:L5:80:SER:HB3	1.75	0.51
44:L7:47:ARG:NH1	44:L7:183:ASP:OD2	2.44	0.51
45:L8:182:GLY:HA3	45:L8:185:ARG:HB2	2.46	0.51
50:M4:107:GLU:O	50:M4:110:ALA:HB3	2.25	0.51
55:M9:154:ALA:O	55:M9:158:GLU:HG2	2.47	0.51
55:M9:158:GLU:O	55:M9:162:ARG:HG3	4.55	0.51
70:O4:91:ARG:HD3	36:5:2555:G:OP2	215.70	0.51
78:Q2:65:THR:OG1	78:Q2:87:ARG:HD3	2.10	0.51
79:Q3:73:THR:HG22	79:Q3:76:ALA:HB3	1.93	0.51
2:S0:168:HIS:HB3	2:S0:203:PHE:HE2	1.74	0.51
3:S1:105:PHE:H	3:S1:214:LYS:HE2	1.75	0.51
7:S5:177:ILE:HG12	7:S5:180:ARG:HH12	1.75	0.51
11:S9:34:PHE:HD1	11:S9:111:THR:HG21	2.10	0.51
36:1:1176:C:OP1	52:M6:25:LYS:HE3	2.11	0.51
36:1:1782:U:H2'	36:1:1783:U:O4'	2.11	0.51
36:1:2546:C:H5'	36:1:2547:A:OP2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:612:U:H2'	36:1:613:G:H8	1.75	0.51
1:2:47:A:N1	1:2:386:G:H1'	2.26	0.51
1:2:700:C:N4	1:2:738:G:H1	2.08	0.51
36:5:1255:C:H2'	36:5:1256:G:H8	1.76	0.51
36:5:2207:A:H62	36:5:2236:G:H1	1.59	0.51
36:5:1840:U:OP2	87:5:3952:OHX:N4	2.43	0.51
36:5:917:A:OP2	87:5:4132:OHX:N1	2.44	0.51
1:6:1133:A:H2'	1:6:1134:C:O4'	2.10	0.51
1:6:747:C:H2'	1:6:748:U:H6	1.76	0.51
1:6:814:A:C8	1:6:816:G:C8	2.99	0.51
13:C1:67:ARG:NH2	13:C1:128:CYS:O	2.44	0.51
20:C8:16:ARG:NH1	20:C8:19:ASN:O	2.43	0.51
40:L3:361:THR:H	40:L3:371:GLN:NE2	2.09	0.51
41:L4:302:ALA:HB2	54:M8:39:ARG:NH2	2.25	0.51
36:1:596:C:H5'	44:L7:37:ASN:ND2	2.25	0.51
46:L9:87:LYS:N	46:L9:185:GLY:O	2.98	0.51
46:L9:50:ASN:ND2	50:M4:4:ASP:OD1	5.19	0.51
51:M5:53:TYR:HD1	51:M5:133:ILE:HD13	1.75	0.51
56:N0:139:TYR:CD2	56:N0:140:VAL:HG23	2.46	0.51
50:M4:60:LEU:HD22	56:N0:152:LEU:HD11	1.92	0.51
61:N5:33:ARG:HE	36:5:1580:A:H62	154.82	0.51
63:N7:3:LYS:HE2	63:N7:5:LEU:HB2	7.42	0.51
36:1:1162:U:H4'	68:O2:57:TYR:CE1	2.46	0.51
72:O6:98:ARG:H	72:O6:98:ARG:HD2	1.75	0.51
4:S2:144:TRP:HB3	4:S2:152:HIS:CE1	3.15	0.51
9:S7:125:ILE:O	9:S7:129:LEU:HB2	3.34	0.51
5:S3:117:ARG:HG3	35:SM:122:GLU:HB2	1.93	0.51
36:1:1632:A:H2'	36:1:1633:C:C6	2.45	0.51
36:1:1659:U:H2'	36:1:1660:C:C6	2.45	0.51
36:1:2652:U:C5	36:1:2653:C:C5	2.99	0.51
36:1:3049:A:H5'	36:1:3049:A:H8	1.75	0.51
36:1:107:A:H1'	36:1:325:A:N3	2.26	0.51
36:1:2924:U:O4	87:1:3913:OHX:N1	2.43	0.51
36:1:415:G:H2'	36:1:416:A:H8	1.76	0.51
36:1:760:G:H1'	36:1:770:G:N2	2.25	0.51
1:2:1317:C:H2'	1:2:1318:G:O4'	2.11	0.51
1:2:545:A:H4'	1:2:546:U:OP1	2.10	0.51
1:2:751:G:H2'	1:2:752:A:H8	1.75	0.51
1:2:973:A:H2'	1:2:974:A:C8	2.45	0.51
36:5:1284:C:O2'	36:5:1285:G:OP1	2.22	0.51
36:5:1781:C:H2'	36:5:1782:U:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2101:C:H2'	36:5:2102:U:C6	2.45	0.51
36:5:2279:A:O5'	36:5:2280:A:H5'	2.10	0.51
36:5:2400:G:H5''	36:5:2401:A:OP2	2.11	0.51
36:5:2861:U:H2'	36:5:2862:U:O4'	2.11	0.51
36:5:3275:U:H4'	36:5:3276:G:OP2	2.10	0.51
1:6:1263:G:H2'	1:6:1264:G:O4'	2.10	0.51
1:6:1370:U:O4	87:6:2110:OHX:N3	2.44	0.51
1:6:1499:G:C5	1:6:1500:C:C4	2.99	0.51
1:6:1500:C:H2'	1:6:1501:C:C6	2.44	0.51
1:6:1674:C:H2'	1:6:1675:C:C6	2.45	0.51
1:6:222:A:H62	1:6:833:U:H3	1.59	0.51
12:C0:50:THR:HG22	12:C0:55:VAL:HG13	2.10	0.51
12:C0:50:THR:HG21	12:C0:57:THR:OG1	2.20	0.51
13:C1:29:LYS:HD3	13:C1:29:LYS:H	1.75	0.51
1:2:1755:A:H8	25:D3:63:GLN:HG3	1.75	0.51
26:D4:84:LYS:HG3	26:D4:85:PHE:CD2	2.45	0.51
33:E1:144:CYS:SG	33:E1:147:VAL:HG22	2.51	0.51
40:L3:95:THR:C	40:L3:97:ARG:H	2.14	0.51
41:L4:282:SER:OG	41:L4:283:THR:N	2.43	0.51
42:L5:40:HIS:HE1	42:L5:42:ALA:HB3	1.75	0.51
58:N2:33:TYR:CE1	58:N2:37:LEU:HD23	6.60	0.51
62:N6:52:ARG:O	62:N6:70:ILE:HB	2.11	0.51
67:O1:83:GLU:OE2	87:O1:201:OHX:N4	2.44	0.51
75:O9:27:ILE:HG23	75:O9:30:ARG:CZ	2.88	0.51
2:S0:177:LEU:O	2:S0:181:VAL:HG13	2.11	0.51
4:S2:139:ILE:HD12	4:S2:191:ALA:HB1	1.91	0.51
5:S3:140:GLY:HA3	5:S3:182:LEU:HD22	5.08	0.51
6:S4:15:PRO:HG2	6:S4:18:TRP:CE2	2.46	0.51
6:S4:65:LEU:HD23	6:S4:70:VAL:HG11	3.39	0.51
8:S6:67:VAL:HG23	8:S6:100:ALA:H	1.92	0.51
11:S9:102:GLU:HA	11:S9:105:LEU:HB2	2.10	0.51
11:S9:174:ARG:HE	11:S9:174:ARG:HA	1.75	0.51
36:1:1405:U:OP2	68:O2:59:SER:OG	2.29	0.51
36:1:239:G:N7	87:1:3930:OHX:N4	2.58	0.51
36:1:2771:U:O2'	36:1:2772:C:O4'	2.14	0.51
36:1:3393:U:H2'	36:1:3394:U:H6	1.76	0.51
36:1:706:A:H4'	36:1:781:G:O2'	2.11	0.51
1:2:1497:U:C4	1:2:1511:U:C2	2.99	0.51
1:2:926:A:H1'	1:2:988:A:C2	2.45	0.51
64:N8:4:ARG:NH2	36:5:1427:U:OP2	136.37	0.51
36:5:1580:A:P	36:5:2522:G:H1	2.33	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:3081:C:H2'	36:5:3082:C:H6	1.75	0.51
36:5:1071:U:O4	87:5:4018:OHX:N3	2.43	0.51
1:6:1017:U:H2'	1:6:1018:U:C6	2.45	0.51
8:S6:173:PRO:HA	1:6:66:U:O5'	340.71	0.51
25:D3:56:LYS:NZ	25:D3:96:VAL:O	5.41	0.51
26:D4:27:VAL:HG12	26:D4:29:HIS:HD2	2.83	0.51
29:D7:48:SER:O	29:D7:71:ALA:N	2.41	0.51
39:L2:153:GLY:HA3	39:L2:251:LYS:HG2	9.27	0.51
40:L3:58:ARG:HD2	40:L3:354:VAL:HB	1.92	0.51
42:L5:211:LEU:HD13	42:L5:219:PHE:HA	3.55	0.51
45:L8:73:PRO:HG3	45:L8:233:TRP:CD1	2.46	0.51
46:L9:8:GLN:HB2	46:L9:55:VAL:HG23	1.93	0.51
51:M5:118:SER:HB3	51:M5:132:VAL:HG22	3.92	0.51
52:M6:39:GLU:N	52:M6:39:GLU:OE1	2.30	0.51
52:M6:38:ALA:O	52:M6:41:LEU:HB2	2.10	0.51
53:M7:69:ARG:HH21	36:5:2992:U:H1'	193.17	0.51
55:M9:99:LEU:O	55:M9:103:ARG:HB2	2.10	0.51
50:M4:38:ILE:HD11	56:N0:150:PHE:HE2	1.76	0.51
56:N0:44:PHE:C	56:N0:46:GLN:H	2.86	0.51
68:O2:21:HIS:CE1	68:O2:24:ARG:HD2	2.46	0.51
78:Q2:46:LYS:HD3	78:Q2:54:THR:HB	1.91	0.51
3:S1:134:VAL:O	3:S1:218:LEU:HD22	2.11	0.51
4:S2:238:SER:C	4:S2:240:LEU:H	2.14	0.51
6:S4:198:LYS:HD2	6:S4:222:LEU:HD12	4.76	0.51
8:S6:121:LEU:O	8:S6:123:GLY:N	3.67	0.51
8:S6:92:ARG:O	1:6:405:C:O2'	304.46	0.51
9:S7:164:TYR:CZ	9:S7:165:LYS:HE2	3.99	0.51
34:SR:69:GLN:N	34:SR:83:ALA:O	2.84	0.51
36:1:1922:A:H3'	36:1:1923:C:H6	1.76	0.51
1:2:1043:A:H61	1:2:1075:C:N4	2.09	0.51
1:2:1575:G:H2'	1:2:1576:A:C8	2.46	0.51
1:2:918:U:H2'	1:2:919:A:H8	1.74	0.51
65:N9:2:ALA:HB2	36:5:2818:U:H5''	213.12	0.51
36:5:1205:A:H4'	36:5:2835:U:O2'	2.11	0.51
36:5:3120:C:OP2	87:5:3834:OHX:N3	2.44	0.51
36:5:3245:A:H2	36:5:3246:G:N1	2.08	0.51
55:M9:95:TRP:CD2	36:5:855:U:H5''	229.99	0.51
18:C6:11:GLY:HA3	18:C6:80:ALA:O	2.11	0.51
22:D0:70:THR:HG23	1:6:1280:C:O2'	390.76	0.51
24:D2:62:VAL:HG13	29:D7:7:LEU:HD12	1.93	0.51
40:L3:256:HIS:HA	40:L3:257:PRO:C	2.48	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L4:361:HIS:CG	41:L4:362:ASP:N	2.79	0.51
44:L7:123:THR:O	44:L7:127:LEU:HD12	2.11	0.51
59:N3:6:ALA:HB1	59:N3:125:LEU:HD12	2.91	0.51
63:N7:54:THR:HG23	63:N7:57:HIS:H	1.76	0.51
2:S0:22:THR:HG23	2:S0:169:SER:HB3	3.94	0.51
11:S9:47:PHE:CZ	11:S9:51:LYS:HE2	3.60	0.51
36:1:1541:G:H1'	36:1:1557:A:C5	2.46	0.51
36:1:1556:C:H2'	36:1:2169:G:H1	1.76	0.51
36:1:2703:A:OP2	42:L5:23:ARG:NH1	2.43	0.51
36:1:3122:A:O2'	46:L9:63:LYS:HD2	2.10	0.51
1:2:1178:G:H2'	1:2:1179:G:O4'	2.11	0.51
1:2:1191:U:OP2	18:C6:143:ARG:NH2	2.37	0.51
1:2:1637:C:OP2	87:2:2082:OHX:N3	2.44	0.51
1:2:931:C:OP1	28:D6:70:LYS:NZ	2.27	0.51
36:5:872:U:H2'	36:5:873:C:C6	2.46	0.51
22:D0:53:LYS:NZ	1:6:1345:A:OP2	472.39	0.51
1:6:625:C:H2'	1:6:626:U:C6	2.46	0.51
26:D4:120:GLY:HA2	1:6:85:A:O3'	336.71	0.51
1:6:922:G:H2'	1:6:923:A:C8	2.45	0.51
18:C6:47:LYS:HZ1	18:C6:114:ARG:HH21	1.59	0.51
18:C6:109:PHE:HB3	18:C6:117:LEU:HD21	1.92	0.51
23:D1:17:CYS:SG	23:D1:18:SER:N	3.02	0.51
26:D4:91:LEU:O	26:D4:96:LEU:N	3.11	0.51
29:D7:34:ASP:HB3	29:D7:43:ILE:HD12	1.92	0.51
41:L4:74:ILE:HG22	41:L4:75:PRO:HD2	1.93	0.51
42:L5:270:LYS:HG3	42:L5:273:ARG:CB	4.13	0.51
44:L7:33:ARG:NH1	44:L7:34:LYS:HE2	4.68	0.51
45:L8:161:GLU:HA	45:L8:164:VAL:HG22	2.10	0.51
48:M1:166:LYS:O	48:M1:168:ASP:N	2.81	0.51
49:M3:175:SER:O	49:M3:178:LYS:N	2.44	0.51
52:M6:77:SER:HB3	52:M6:106:GLU:OE1	3.20	0.51
54:M8:185:LYS:HD3	54:M8:186:VAL:HG23	2.12	0.51
59:N3:28:ASN:OD1	59:N3:112:SER:N	2.43	0.51
40:L3:73:VAL:HG13	59:N3:89:ASP:O	2.89	0.51
63:N7:27:LYS:HG3	63:N7:29:HIS:CE1	2.40	0.51
66:O0:33:SER:OG	66:O0:39:SER:HB2	2.11	0.51
70:O4:58:ARG:HG3	70:O4:59:PRO:HD2	2.46	0.51
77:Q1:15:ARG:HH12	1:6:1126:G:P	282.37	0.51
2:S0:60:ALA:O	2:S0:64:ILE:HG13	2.10	0.51
3:S1:116:LYS:HG2	3:S1:117:TRP:H	2.16	0.51
3:S1:33:LYS:HE2	3:S1:41:ARG:NH1	3.83	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S4:118:GLU:HA	6:S4:121:TYR:CE1	2.57	0.51
6:S4:130:GLN:HB3	6:S4:138:TYR:CE2	4.91	0.51
6:S4:252:ARG:NH2	6:S4:253:ASP:OD1	3.28	0.51
1:2:810:G:C5	9:S7:111:LYS:HE3	2.45	0.51
36:1:1238:C:H41	36:1:1245:A:P	2.34	0.50
36:1:2214:A:N1	36:1:2429:G:O2'	2.37	0.50
36:1:3081:C:H2'	36:1:3082:C:H6	1.75	0.50
1:2:1737:G:O6	87:2:2008:OHX:N4	2.44	0.50
1:2:872:G:N2	1:2:956:C:O2	2.44	0.50
36:5:1454:A:OP1	87:5:4111:OHX:N4	2.44	0.50
36:5:2222:A:H8	36:5:2222:A:O5'	1.94	0.50
36:5:286:U:H2'	36:5:287:G:C8	2.46	0.50
36:5:2926:A:H2'	36:5:2927:C:C6	2.45	0.50
36:5:3027:A:H2'	36:5:3028:G:O4'	2.10	0.50
36:5:532:A:O2'	36:5:533:A:H5'	2.12	0.50
1:6:1533:C:H4'	1:6:1539:G:C6	2.47	0.50
1:6:1557:U:O2'	1:6:1558:U:H2'	2.11	0.50
1:6:973:A:H2'	1:6:974:A:C8	2.46	0.50
18:C6:109:PHE:O	18:C6:113:ASP:N	2.71	0.50
28:D6:30:ILE:HD11	28:D6:35:ALA:HA	1.93	0.50
32:E0:49:LEU:HD11	32:E0:55:ARG:HB2	1.92	0.50
42:L5:178:ASN:N	42:L5:178:ASN:OD1	2.95	0.50
44:L7:232:ARG:O	44:L7:235:PHE:HB2	2.34	0.50
51:M5:96:ARG:HG2	51:M5:96:ARG:NH1	2.26	0.50
53:M7:51:VAL:HA	53:M7:56:ARG:O	2.11	0.50
56:N0:26:ARG:HH22	56:N0:28:ARG:HD2	1.76	0.50
61:N5:88:MET:HA	61:N5:120:LYS:HE3	1.93	0.50
64:N8:16:SER:HA	36:5:942:U:C4	171.69	0.50
64:N8:74:ASN:HA	64:N8:113:LEU:O	2.39	0.50
65:N9:16:ALA:O	65:N9:20:GLY:HA3	3.87	0.50
67:O1:72:ARG:HB3	67:O1:98:VAL:HG11	1.93	0.50
70:O4:10:ARG:HD2	75:O9:4:GLN:NE2	2.85	0.50
76:Q0:95:VAL:HA	76:Q0:101:ALA:O	2.11	0.50
79:Q3:76:ALA:HA	79:Q3:79:VAL:HB	1.93	0.50
6:S4:31:PRO:HG2	6:S4:38:LEU:HD13	1.94	0.50
7:S5:121:ILE:HD11	7:S5:198:LEU:HD12	1.92	0.50
34:SR:274:LEU:HD13	34:SR:313:TRP:CG	2.46	0.50
36:1:1108:U:H2'	36:1:1109:U:C6	2.46	0.50
36:1:1803:C:H5'	70:O4:63:ALA:HB2	1.92	0.50
1:2:283:U:H5''	8:S6:188:ARG:HD3	1.92	0.50
1:2:832:U:H2'	1:2:833:U:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:3:26:C:H5'	42:L5:56:THR:HB	1.93	0.50
36:5:1366:A:C2	36:5:1367:G:C4	2.99	0.50
36:5:1658:G:H1	36:5:1791:C:H42	1.58	0.50
36:5:1877:U:OP2	87:5:3872:OHX:N3	2.44	0.50
1:6:320:U:H2'	1:6:321:C:O2	2.11	0.50
1:6:647:G:O5'	1:6:647:G:H8	1.94	0.50
15:C3:26:PHE:CE2	15:C3:28:LEU:HB2	3.00	0.50
18:C6:31:VAL:HA	18:C6:67:VAL:HG23	3.98	0.50
1:2:1387:G:OP1	19:C7:33:ARG:NH1	2.43	0.50
21:C9:57:ARG:HG2	21:C9:104:VAL:HG21	1.93	0.50
22:D0:26:LEU:N	22:D0:89:ARG:O	2.90	0.50
23:D1:64:GLU:O	23:D1:68:SER:HB2	2.36	0.50
39:L2:127:ALA:O	39:L2:169:ILE:HD11	2.52	0.50
41:L4:361:HIS:CG	41:L4:362:ASP:H	2.29	0.50
48:M1:108:GLU:HA	48:M1:122:ILE:HG23	2.57	0.50
49:M3:132:ALA:O	49:M3:134:GLU:N	3.40	0.50
49:M3:140:SER:HG	49:M3:143:ALA:H	1.51	0.50
49:M3:57:VAL:HG22	49:M3:147:ILE:HD13	1.93	0.50
51:M5:126:THR:HB	51:M5:127:TYR:CD2	2.46	0.50
52:M6:32:LYS:HA	52:M6:101:ARG:HB3	1.93	0.50
56:N0:82:ASP:OD1	56:N0:87:THR:HB	2.12	0.50
62:N6:89:LYS:HB2	62:N6:91:ASN:OD1	2.93	0.50
63:N7:80:LEU:O	63:N7:82:PRO:HD3	3.07	0.50
68:O2:45:ARG:NH1	36:5:1160:C:N3	206.84	0.50
71:O5:85:THR:HG22	71:O5:87:ALA:N	3.46	0.50
73:O7:65:ARG:HG3	73:O7:65:ARG:NH1	2.27	0.50
74:O8:32:ASN:OD1	74:O8:36:LYS:N	4.24	0.50
2:S0:88:LYS:HB3	2:S0:202:TYR:CZ	2.79	0.50
6:S4:193:GLY:O	6:S4:195:ILE:N	2.45	0.50
9:S7:12:ALA:HB3	9:S7:13:PRO:HD3	1.98	0.50
36:1:1029:G:H2'	36:1:1030:A:C8	2.46	0.50
36:1:2255:A:H5'	36:1:2261:G:H22	1.77	0.50
36:1:2940:A:N7	40:L3:2:SER:N	2.58	0.50
36:1:559:A:OP1	36:1:559:A:H4'	2.11	0.50
36:1:828:A:H2'	36:1:829:U:C6	2.46	0.50
1:2:1175:U:H2'	1:2:1176:G:C8	2.46	0.50
1:2:397:A:O3'	10:S8:50:GLY:HA2	2.12	0.50
36:5:1340:G:H2'	36:5:1341:U:C6	2.46	0.50
36:5:1464:G:N7	87:5:3889:OHX:N3	2.58	0.50
36:5:2836:C:H5	36:5:2852:C:N4	2.04	0.50
36:5:727:G:H2'	36:5:728:G:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:750:G:H2'	36:5:751:A:H8	1.75	0.50
3:S1:151:LYS:NZ	1:6:1066:C:OP1	337.27	0.50
1:6:51:A:OP1	87:6:2034:OHX:N3	2.44	0.50
1:6:234:G:H2'	1:6:235:G:O4'	2.11	0.50
1:6:483:A:H61	1:6:503:G:H22	1.57	0.50
9:S7:104:ARG:NE	1:6:742:U:O2	354.67	0.50
1:6:918:U:H2'	1:6:919:A:C8	2.40	0.50
1:6:982:U:O4	1:6:983:A:N6	2.43	0.50
12:C0:23:ALA:CB	12:C0:64:TYR:HB2	3.95	0.50
22:D0:22:ILE:HD12	22:D0:118:VAL:HA	1.93	0.50
28:D6:20:PRO:HA	28:D6:31:PRO:HA	1.97	0.50
3:S1:108:ASP:HB3	28:D6:66:LYS:O	2.12	0.50
33:E1:86:THR:HG23	33:E1:87:THR:H	3.81	0.50
39:L2:5:ILE:HG22	39:L2:208:ASP:O	2.10	0.50
39:L2:225:ILE:HG21	39:L2:234:LYS:HA	1.93	0.50
40:L3:86:VAL:HG22	40:L3:162:VAL:HG12	1.97	0.50
42:L5:131:LEU:HD22	42:L5:131:LEU:H	1.76	0.50
44:L7:219:LYS:O	44:L7:228:SER:HB2	2.45	0.50
48:M1:133:ARG:HB2	48:M1:152:HIS:NE2	2.26	0.50
49:M3:170:LEU:HD22	72:O6:9:ILE:HG22	5.96	0.50
51:M5:156:HIS:HB3	51:M5:159:ARG:HD2	3.51	0.50
56:N0:8:GLN:HG3	56:N0:26:ARG:NE	2.26	0.50
57:N1:82:ASN:N	57:N1:82:ASN:OD1	2.44	0.50
7:S5:146:THR:HG23	7:S5:157:ARG:HB3	4.69	0.50
8:S6:67:VAL:HG21	8:S6:99:GLY:HA2	2.19	0.50
10:S8:103:GLN:HG2	10:S8:164:ARG:HB3	1.93	0.50
10:S8:61:GLU:O	10:S8:62:THR:OG1	5.15	0.50
18:C6:99:GLU:OE2	34:SR:60:SER:HB2	2.95	0.50
36:1:1000:C:N4	36:1:1046:A:H62	2.10	0.50
36:1:1313:G:H2'	36:1:1314:C:C6	2.46	0.50
36:1:1813:A:H4'	36:1:1817:G:H1'	1.92	0.50
36:1:2369:G:H2'	36:1:2370:G:C8	2.46	0.50
36:1:3218:A:H5''	36:1:3219:G:C5	2.47	0.50
36:1:3319:U:H3'	36:1:3319:U:P	2.51	0.50
36:1:617:G:H4'	53:M7:171:ARG:HE	1.77	0.50
1:2:1756[A]:A:H8	1:2:1756[A]:A:OP2	1.94	0.50
1:2:1014:G:OP1	87:2:1992:OHX:N3	2.44	0.50
1:2:1370:U:O4	87:2:2089:OHX:N3	2.44	0.50
1:2:248:U:H4'	13:C1:36:LYS:HD3	1.91	0.50
1:2:649:U:O2'	1:2:650:U:O5'	2.29	0.50
36:5:2425:G:H2'	36:5:2426:U:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:L6:69:PHE:CZ	36:5:3267:A:H2'	260.56	0.50
17:C5:22:LEU:HA	17:C5:25:LEU:HD12	2.99	0.50
16:C4:92:LYS:HZ3	28:D6:69:ASN:HB2	1.75	0.50
40:L3:160:VAL:HG22	40:L3:183:LEU:HD22	1.92	0.50
41:L4:71:VAL:HG22	41:L4:72:ALA:H	1.77	0.50
44:L7:40:LYS:O	44:L7:44:ILE:HG13	2.12	0.50
46:L9:171:ASP:OD2	46:L9:173:ARG:NH1	3.24	0.50
55:M9:12:ALA:HB1	55:M9:17:VAL:O	2.12	0.50
57:N1:78:LYS:HB3	57:N1:87:LYS:HG3	1.93	0.50
66:O0:25:LEU:HD22	66:O0:90:VAL:HG22	2.82	0.50
67:O1:20:LEU:HD11	67:O1:32:ALA:HB2	1.94	0.50
72:O6:97:SER:C	72:O6:99:ARG:H	2.14	0.50
79:Q3:81:SER:HA	79:Q3:84:ARG:HB2	1.92	0.50
3:S1:212:VAL:O	3:S1:214:LYS:N	2.39	0.50
3:S1:103:MET:HB3	3:S1:215:VAL:HG12	2.52	0.50
5:S3:216:PRO:HG2	5:S3:217:ILE:HG13	1.94	0.50
7:S5:110:ALA:O	7:S5:114:ILE:N	2.90	0.50
10:S8:49:ARG:HD3	1:6:333:A:C8	310.45	0.50
34:SR:117:LYS:H	34:SR:117:LYS:HD2	1.75	0.50
34:SR:49:GLY:HA2	34:SR:54:PHE:CD1	3.84	0.50
36:1:1792:C:H2'	36:1:1795:U:H5	1.77	0.50
36:1:2203:U:H4'	39:L2:241:ARG:HA	1.92	0.50
36:1:2404:A:H5'	36:1:2404:A:C8	2.41	0.50
36:1:2709:C:H2'	36:1:2710:C:C6	2.46	0.50
36:1:3000:A:H2'	36:1:3001:C:H6	1.77	0.50
36:1:317:A:C2	36:1:318:A:C4	2.99	0.50
36:1:414:U:H2'	36:1:415:G:C8	2.45	0.50
36:1:586:C:OP1	69:O3:70:LYS:NZ	2.20	0.50
36:1:701:G:H2'	36:1:702:C:C6	2.47	0.50
1:2:1338:C:H1'	1:2:1410:A:C4	2.46	0.50
1:2:450:U:H2'	1:2:451:A:C8	2.46	0.50
71:O5:95:PHE:CG	36:5:136:G:H5'	62.33	0.50
36:5:1781:C:H2'	36:5:1782:U:H6	1.75	0.50
36:5:2986:U:H2'	36:5:2987:A:C8	2.46	0.50
10:S8:137:LYS:NZ	1:6:192:U:O4	267.08	0.50
1:6:396:G:N2	1:6:398:G:H3'	2.27	0.50
1:6:691:C:OP1	1:6:696:C:N4	2.42	0.50
16:C4:13:VAL:HG13	16:C4:77:THR:H	1.75	0.50
7:S5:28:PRO:HG2	18:C6:37:THR:HG21	3.99	0.50
18:C6:18:ALA:HB2	18:C6:69:VAL:HG13	1.93	0.50
24:D2:47:ILE:HG22	24:D2:65:LEU:HD12	3.89	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D3:109:ARG:O	25:D3:112:LYS:NZ	6.62	0.50
30:D8:22:ARG:NH1	1:6:1619:C:O2	341.30	0.50
39:L2:116:VAL:HG11	39:L2:134:VAL:HG11	2.66	0.50
39:L2:60:LYS:HD3	39:L2:73:GLU:OE2	5.42	0.50
40:L3:296:THR:HG22	40:L3:298:PHE:H	4.63	0.50
42:L5:261:THR:OG1	42:L5:264:GLN:N	2.32	0.50
47:M0:150:GLU:HG3	47:M0:154:ARG:HE	1.76	0.50
47:M0:176:LEU:HD22	47:M0:180:GLU:HG3	1.94	0.50
47:M0:212:GLU:HB3	47:M0:213:PHE:CD1	3.18	0.50
47:M0:4:ARG:HH21	47:M0:99:ILE:HG22	5.83	0.50
52:M6:23:VAL:HG11	52:M6:84:LEU:HD11	1.94	0.50
61:N5:31:THR:HG22	61:N5:33:ARG:HD2	2.85	0.50
63:N7:81:LEU:HG	70:O4:90:ILE:HD12	1.94	0.50
73:O7:84:SER:O	73:O7:85:LYS:HB3	3.65	0.50
74:O8:49:SER:OG	74:O8:50:SER:N	2.45	0.50
4:S2:140:ARG:NH2	23:D1:1:MET:HB3	2.26	0.50
6:S4:153:ASN:O	6:S4:174:LYS:NZ	2.31	0.50
7:S5:40:ILE:HD13	7:S5:42:LEU:HD13	1.92	0.50
11:S9:34:PHE:CE1	11:S9:105:LEU:HB3	2.47	0.50
5:S3:117:ARG:NH1	35:SM:126:ASP:OD2	2.43	0.50
34:SR:295:SER:HB2	34:SR:300:THR:HB	1.93	0.50
36:1:2310:U:OP1	87:1:4038:OHX:N2	2.45	0.50
1:2:1396:U:H2'	1:2:1397:U:C6	2.47	0.50
1:2:205:U:O4	87:2:2035:OHX:N3	2.44	0.50
1:2:704:C:N4	1:2:734:A:O2'	2.45	0.50
37:3:113:C:H2'	37:3:114:U:O4'	2.11	0.50
36:5:1638:A:N1	36:5:1736:G:O2'	2.38	0.50
36:5:1643:A:H4'	36:5:1822:C:H5'	1.94	0.50
36:5:181:U:H1'	36:5:236:G:H22	1.77	0.50
36:5:776:U:H5	36:5:2719:U:O2	1.95	0.50
36:5:60:A:H2'	36:5:61:A:H8	1.77	0.50
1:6:1382:A:O2'	1:6:1383:G:H5''	2.12	0.50
34:SR:282:SER:OG	1:6:1394:G:OP1	417.04	0.50
1:6:289:U:H2'	1:6:290:G:O4'	2.11	0.50
10:S8:51:GLY:H	1:6:397:A:H5''	313.76	0.50
1:6:879:G:H2'	1:6:880:C:C6	2.47	0.50
1:6:946:U:H2'	1:6:947:U:C6	2.47	0.50
13:C1:75:VAL:HG23	13:C1:121:ASP:O	2.61	0.50
13:C1:124:THR:HB	13:C1:141:LYS:HB3	1.93	0.50
1:2:868:G:OP1	15:C3:121:ARG:NH1	2.45	0.50
20:C8:91:ASP:OD2	20:C8:92:ILE:N	4.17	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:D1:27:ASP:HA	23:D1:29:HIS:CE1	2.46	0.50
26:D4:15:ASN:OD1	26:D4:18:LEU:N	2.82	0.50
39:L2:18:SER:OG	39:L2:23:ARG:NH2	5.55	0.50
39:L2:193:ARG:O	39:L2:195:SER:N	3.07	0.50
41:L4:128:ALA:HB1	41:L4:134:LEU:HD12	1.93	0.50
45:L8:152:LEU:HB3	45:L8:180:VAL:HG11	2.05	0.50
56:N0:27:MET:HE3	56:N0:29:ILE:HD11	3.89	0.50
63:N7:50:PRO:HD3	63:N7:68:ILE:HG12	1.93	0.50
67:O1:33:VAL:HG13	67:O1:51:LEU:HD11	2.60	0.50
70:O4:20:ILE:HD11	70:O4:34:HIS:CE1	2.46	0.50
70:O4:96:GLU:OE1	70:O4:99:LYS:NZ	2.96	0.50
39:L2:177:LYS:NZ	79:Q3:33:GLN:OE1	3.23	0.50
79:Q3:77:ALA:O	79:Q3:80:ARG:HB2	2.12	0.50
6:S4:72:VAL:HG22	6:S4:90:ILE:HD13	1.94	0.50
7:S5:32:GLU:HA	7:S5:35:GLN:HB3	1.94	0.50
8:S6:7:TYR:CE1	8:S6:9:VAL:HB	4.44	0.50
8:S6:61:PHE:CE1	8:S6:96:SER:HB2	2.47	0.50
11:S9:146:PHE:HZ	1:6:765:G:N1	432.50	0.50
36:1:2683:U:H2'	36:1:2684:C:C6	2.47	0.50
36:1:305:U:C5	36:1:2776:C:H1'	2.46	0.50
36:1:343:U:O2	41:L4:95:ARG:HD2	2.12	0.50
36:1:84:U:OP1	36:1:701:G:H5''	2.11	0.50
1:2:1297:G:N2	1:2:1300:A:OP2	2.41	0.50
36:5:1301:A:OP1	36:5:1301:A:H8	1.95	0.50
55:M9:134:HIS:HD2	36:5:1947:G:H5'	236.04	0.50
55:M9:104:ARG:NH1	36:5:1949:G:OP1	220.45	0.50
36:5:2202:C:H2'	36:5:2203:U:O4'	2.11	0.50
36:5:2440:G:O2'	36:5:2441:A:OP1	2.27	0.50
36:5:2516:U:O2'	36:5:2595:A:N1	2.38	0.50
36:5:3274:A:H3'	36:5:3275:U:C5'	2.38	0.50
36:5:2752:U:O2	87:5:4158:OHX:N3	2.44	0.50
36:5:754:G:H2'	36:5:755:A:H8	1.77	0.50
1:6:564:G:C2	1:6:578:U:H5''	2.46	0.50
1:6:846:G:H2'	1:6:847:A:C8	2.47	0.50
18:C6:47:LYS:HZ1	18:C6:114:ARG:HD2	1.75	0.50
21:C9:77:ASN:OD1	21:C9:101:ASN:ND2	2.40	0.50
26:D4:58:PHE:HE2	26:D4:72:PHE:HB3	3.09	0.50
30:D8:32:PHE:CE2	30:D8:38:ARG:HB3	2.46	0.50
41:L4:144:LYS:H	41:L4:144:LYS:HD2	4.78	0.50
41:L4:300:ARG:HB2	41:L4:301:PRO:HD2	2.09	0.50
41:L4:42:VAL:O	41:L4:44:LYS:N	3.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L4:63:GLU:HG2	41:L4:64:SER:N	4.35	0.50
42:L5:227:LEU:C	42:L5:229:ASP:H	2.13	0.50
49:M3:154:VAL:HG23	49:M3:156:ALA:H	3.29	0.50
49:M3:60:ALA:HB3	49:M3:65:TYR:O	2.11	0.50
64:N8:75:LEU:HB3	64:N8:118:ILE:HG23	2.09	0.50
77:Q1:16:LYS:O	77:Q1:20:VAL:HG23	2.19	0.50
2:S0:197:ILE:HD12	2:S0:197:ILE:H	1.77	0.50
3:S1:105:PHE:CD2	3:S1:213:ARG:HA	2.47	0.50
6:S4:103:TYR:CE1	6:S4:189:LEU:HD11	2.96	0.50
1:2:448:C:OP1	6:S4:29:PRO:HD3	2.12	0.50
7:S5:142:PRO:HG2	7:S5:170:GLN:OE1	3.95	0.50
7:S5:94:THR:HG22	7:S5:114:ILE:CG1	2.61	0.50
10:S8:184:LEU:HB3	10:S8:189:LEU:HB2	2.49	0.50
6:S4:248:ILE:HB	11:S9:71:PHE:CE2	4.45	0.50
36:1:2898:G:H5''	36:1:2899:C:H5'	1.93	0.50
1:2:57:G:O6	87:2:2013:OHX:N3	2.44	0.50
37:3:11:A:H4'	37:3:13:A:C8	2.47	0.50
38:4:58:G:O6	73:O7:63:ARG:NH2	2.37	0.50
36:5:1232:C:C5	36:5:1261:G:H2'	2.46	0.50
79:Q3:18:TYR:HA	36:5:2131:A:N6	228.49	0.50
40:L3:26:ARG:HH22	36:5:3003:G:P	231.17	0.50
36:5:3299:A:H61	36:5:3315:G:H1	1.59	0.50
1:6:1699:G:H2'	1:6:1700:C:H5'	1.94	0.50
1:6:649:U:H3	1:6:685:A:H61	1.60	0.50
1:6:678:A:H2'	1:6:679:U:O4'	2.12	0.50
42:L5:10:SER:OG	37:7:67:G:H5'	312.76	0.50
13:C1:39:GLY:C	13:C1:41:GLY:H	2.15	0.50
29:D7:56:CYS:HB2	29:D7:61:THR:HG22	1.93	0.50
40:L3:117:ARG:NH2	40:L3:176:ALA:O	2.80	0.50
41:L4:205:PRO:HB3	41:L4:247:PHE:CD2	2.49	0.50
45:L8:51:LYS:HG3	36:5:2523:A:C5	165.88	0.50
45:L8:97:TYR:O	45:L8:132:VAL:HG12	2.11	0.50
47:M0:50:VAL:HG12	47:M0:152:LEU:HD12	2.98	0.50
47:M0:42:THR:HG23	47:M0:45:GLU:HG3	4.08	0.50
52:M6:181:ALA:O	52:M6:184:THR:HG23	2.11	0.50
36:1:1447:G:H3'	53:M7:67:ILE:HD11	1.93	0.50
53:M7:29:THR:HG22	53:M7:87:SER:OG	2.11	0.50
63:N7:111:LYS:HD3	36:5:1629:U:O4	204.94	0.50
70:O4:89:ILE:HG22	70:O4:90:ILE:HD13	1.94	0.50
71:O5:54:VAL:O	71:O5:58:ILE:HG13	3.08	0.50
71:O5:68:GLN:C	71:O5:70:TYR:H	2.14	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:S5:143:ARG:NH1	7:S5:218:GLU:OE2	3.30	0.50
10:S8:21:PHE:CZ	10:S8:22:ARG:HD3	2.47	0.50
34:SR:214:ALA:HB2	34:SR:220:ILE:HA	1.93	0.50
36:1:1440:G:H2'	36:1:1441:G:C8	2.46	0.50
36:1:1674:G:N7	87:1:3844:OHX:N5	2.60	0.50
36:1:2592:G:HO2'	36:1:2593:A:H8	1.58	0.50
36:1:2768:U:H2'	36:1:2769:A:C8	2.47	0.50
36:1:656:A:H2'	36:1:657:A:H8	1.75	0.50
1:2:102:U:O4	1:2:360:A:H2'	2.12	0.50
1:2:1042:G:H2'	1:2:1043:A:O4'	2.12	0.50
1:2:104:A:O2'	87:2:2083:OHX:N6	2.44	0.50
1:2:1238:A:H2'	1:2:1239:U:O4'	2.11	0.50
1:2:1398:U:H4'	1:2:1399:C:OP2	2.12	0.50
1:2:1433:G:H2'	1:2:1434:U:H6	1.77	0.50
1:2:1484:G:H21	1:2:1606:C:H1'	1.77	0.50
1:2:1523:G:N7	21:C9:68:ARG:NH1	2.60	0.50
1:2:1788:G:OP2	16:C4:132:ARG:NH1	2.42	0.50
36:5:1675:G:N7	87:5:3885:OHX:N4	2.59	0.50
36:5:1818:U:H2'	36:5:1819:U:O4'	2.11	0.50
36:5:2255:A:HO2'	36:5:2256:A:P	2.33	0.50
36:5:2533:G:H2'	36:5:2534:G:C8	2.47	0.50
65:N9:2:ALA:HB2	36:5:2818:U:C5'	212.82	0.50
36:5:72:C:C2	36:5:74:G:H1'	2.46	0.50
1:6:526:A:N6	1:6:527:A:C6	2.80	0.50
12:C0:81:ASN:ND2	12:C0:81:ASN:O	2.45	0.50
19:C7:20:TYR:O	19:C7:24:LEU:HD12	2.12	0.50
19:C7:24:LEU:HD23	19:C7:34:LEU:HD12	3.46	0.50
25:D3:23:ARG:O	25:D3:26:GLU:HB2	3.12	0.50
40:L3:165:GLN:OE1	40:L3:167:ARG:NH2	4.88	0.50
40:L3:57:VAL:HG22	40:L3:73:VAL:HG12	2.51	0.50
42:L5:218:ARG:O	42:L5:221:GLU:N	2.45	0.50
42:L5:88:ILE:HD13	42:L5:239:ILE:HG22	5.59	0.50
50:M4:123:LEU:HD23	52:M6:190:VAL:HG13	6.05	0.50
60:N4:4:GLU:OE1	60:N4:4:GLU:N	2.45	0.50
74:O8:42:LYS:HG3	74:O8:55:VAL:HG22	1.94	0.50
75:O9:3:ALA:O	75:O9:4:GLN:HB2	2.12	0.50
3:S1:110:LEU:HA	3:S1:113:MET:HB2	1.94	0.50
9:S7:11:GLN:HG3	9:S7:12:ALA:H	1.76	0.50
11:S9:133:HIS:CD2	11:S9:162:SER:HB2	2.83	0.50
35:SM:58:GLU:OE1	35:SM:62:ARG:NH1	7.01	0.50
35:SM:88:ARG:HG2	35:SM:91:THR:CG2	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2790:A:O2'	87:1:3878:OHX:N1	2.44	0.49
36:1:3296:A:H62	40:L3:124:LYS:NZ	2.10	0.49
1:2:1031:U:H4'	1:2:1032:G:OP2	2.12	0.49
1:2:978:A:H2'	1:2:979:A:O4'	2.11	0.49
36:5:1064:A:H4'	36:5:1065:A:O5'	2.12	0.49
36:5:1121:U:C4	36:5:1122:U:C4	3.00	0.49
36:5:2228:A:H2'	36:5:2229:A:C8	2.47	0.49
36:5:651:G:C6	36:5:652:G:C6	3.00	0.49
64:N8:27:LYS:HB2	36:5:937:G:OP2	168.09	0.49
1:6:1257:U:O2'	1:6:1258:U:O4'	2.30	0.49
1:6:514:G:HO2'	1:6:515:A:H8	1.58	0.49
1:6:647:G:H22	1:6:687:G:H22	1.58	0.49
1:6:763:G:C6	1:6:764:U:C4	3.00	0.49
1:6:109:G:O2'	1:6:796:A:N1	2.39	0.49
1:6:839:U:H2'	1:6:840:U:C6	2.47	0.49
1:6:219:A:N6	1:6:843:U:C2	2.80	0.49
1:6:868:G:H1	1:6:960:U:H3	1.59	0.49
12:C0:55:VAL:HA	12:C0:69:THR:HG23	1.93	0.49
15:C3:91:LEU:HB3	15:C3:122:ILE:HG12	1.98	0.49
7:S5:72:HIS:O	18:C6:79:TYR:OH	2.29	0.49
19:C7:3:ARG:HH22	1:6:1415:U:H5'	409.18	0.49
23:D1:78:LEU:H	23:D1:78:LEU:HD23	1.78	0.49
26:D4:121:THR:HG22	26:D4:123:LYS:HB2	7.63	0.49
39:L2:3:ARG:HG2	39:L2:4:VAL:N	2.55	0.49
40:L3:27:ALA:HB1	40:L3:218:ILE:HG22	3.05	0.49
40:L3:3:HIS:ND1	40:L3:3:HIS:O	2.44	0.49
41:L4:42:VAL:HG12	41:L4:236:LEU:HD21	3.01	0.49
42:L5:140:ARG:HH21	36:5:1080:A:P	231.06	0.49
43:L6:82:ARG:NH1	69:O3:105:SER:O	2.86	0.49
44:L7:140:SER:HB3	44:L7:237:ASN:ND2	2.25	0.49
49:M3:48:PRO:HA	49:M3:137:GLN:HB2	3.55	0.49
51:M5:183:THR:O	51:M5:183:THR:OG1	2.92	0.49
51:M5:149:ASN:OD1	87:M5:303:OHX:N6	2.44	0.49
46:L9:3:TYR:HA	56:N0:142:GLN:OE1	2.12	0.49
59:N3:93:LEU:H	59:N3:93:LEU:HD23	1.76	0.49
36:1:213:A:OP1	62:N6:2:ALA:N	2.45	0.49
62:N6:35:LEU:HA	62:N6:106:ILE:HB	1.92	0.49
67:O1:10:ARG:HH21	36:5:3386:G:H5''	156.26	0.49
72:O6:51:SER:O	72:O6:54:GLU:N	2.42	0.49
6:S4:10:LYS:O	6:S4:12:LEU:N	2.41	0.49
7:S5:151:GLY:HA3	7:S5:155:ALA:HA	3.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:S6:64:LYS:HZ1	8:S6:81:VAL:HG12	3.89	0.49
36:1:1207:G:N7	87:1:3956:OHX:N2	2.60	0.49
36:1:1472:U:H2'	36:1:1473:G:H8	1.77	0.49
36:1:2227:C:H2'	36:1:2228:A:O4'	2.12	0.49
36:1:2240:G:H2'	36:1:2241:U:O4'	2.11	0.49
36:1:2947:G:H4'	36:1:2947:G:OP2	2.12	0.49
1:2:1755:A:C8	25:D3:63:GLN:HG3	2.47	0.49
36:5:2573:G:H3'	36:5:2574:G:H5''	1.94	0.49
36:5:3037:U:H2'	36:5:3038:U:H6	1.77	0.49
40:L3:274:SER:OG	36:5:3139:A:OP1	229.08	0.49
36:5:3074:G:OP1	87:5:4026:OHX:N4	2.44	0.49
36:5:638:C:H2'	36:5:639:G:C8	2.47	0.49
1:6:151:G:N2	1:6:163:G:N2	2.60	0.49
1:6:1533:C:H4'	1:6:1539:G:N1	2.27	0.49
1:6:992:A:OP1	1:6:1786:G:H5'	2.12	0.49
1:6:44:U:H5	1:6:437:A:N1	2.09	0.49
1:6:483:A:H61	1:6:503:G:H1	1.59	0.49
18:C6:31:VAL:O	18:C6:33:GLY:N	2.45	0.49
21:C9:115:GLU:O	21:C9:117:SER:N	2.46	0.49
26:D4:56:SER:O	26:D4:74:LEU:N	2.89	0.49
26:D4:84:LYS:HG3	26:D4:85:PHE:HD2	1.76	0.49
41:L4:126:ILE:HD11	41:L4:233:LEU:HD13	2.53	0.49
41:L4:174:ALA:O	41:L4:176:SER:N	2.45	0.49
41:L4:264:SER:C	41:L4:266:THR:H	2.15	0.49
41:L4:84:ARG:O	41:L4:87:GLN:HG3	2.13	0.49
42:L5:86:TYR:CD1	42:L5:247:ILE:HG12	3.41	0.49
43:L6:170:LYS:HE2	69:O3:34:GLY:HA3	1.94	0.49
44:L7:110:ARG:HB2	44:L7:110:ARG:HH11	4.59	0.49
49:M3:162:ASN:ND2	49:M3:162:ASN:O	3.64	0.49
51:M5:98:LEU:HD13	36:5:290:G:OP1	137.80	0.49
53:M7:22:LEU:HB3	53:M7:90:PHE:CE2	2.47	0.49
54:M8:158:HIS:N	54:M8:186:VAL:HG12	2.23	0.49
56:N0:34:GLU:O	56:N0:38:LYS:HG3	2.11	0.49
63:N7:25:ILE:HG23	63:N7:41:ALA:HB1	2.00	0.49
67:O1:10:ARG:HE	36:5:3386:G:H5'	157.04	0.49
72:O6:79:SER:OG	72:O6:81:THR:HG22	9.39	0.49
2:S0:198:MET:SD	19:C7:88:VAL:HG23	2.80	0.49
11:S9:103:ASP:OD2	11:S9:103:ASP:N	3.74	0.49
11:S9:118:LEU:HD23	11:S9:158:PHE:CE1	3.20	0.49
36:1:1257:C:H42	36:1:1261:G:H22	1.59	0.49
36:1:1472:U:H2'	36:1:1473:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2618:G:O4'	65:N9:3:LYS:NZ	2.41	0.49
36:1:2635:A:H4'	36:1:2636:A:O5'	2.12	0.49
36:1:541:U:O4	87:1:3951:OHX:N2	2.46	0.49
36:1:783:A:OP2	87:1:3997:OHX:N3	2.45	0.49
1:2:1004:U:O4	87:1:3881:OHX:N1	2.45	0.49
1:2:1165:G:O6	1:2:1166:A:N6	2.45	0.49
1:2:1327:C:O2'	5:S3:159:HIS:HD2	1.95	0.49
1:2:1413:U:H4'	1:2:1414:U:OP2	2.11	0.49
1:2:156:A:H2'	1:2:157:A:O4'	2.11	0.49
1:2:741:C:O2	9:S7:107:ARG:NH1	2.45	0.49
1:2:798:C:H2'	1:2:799:A:C8	2.48	0.49
37:3:112:G:H2'	37:3:113:C:C6	2.47	0.49
40:L3:20:LYS:HE3	36:5:3139:A:O3'	219.72	0.49
36:5:3228:C:H4'	36:5:3229:G:O5'	2.12	0.49
1:6:1488:G:H3'	1:6:1515:A:H61	1.77	0.49
1:6:1738:U:H2'	1:6:1739:C:C6	2.48	0.49
6:S4:10:LYS:HD3	1:6:381:C:H5''	360.12	0.49
1:6:913:G:H3'	1:6:914:G:C5'	2.42	0.49
19:C7:85:VAL:HG12	19:C7:87:GLU:H	1.78	0.49
21:C9:125:SER:O	21:C9:129:GLN:HG3	2.12	0.49
23:D1:5:LYS:HD3	23:D1:5:LYS:H	1.76	0.49
25:D3:23:ARG:HD2	25:D3:26:GLU:OE1	2.37	0.49
32:E0:33:ARG:NH1	32:E0:33:ARG:HB3	2.62	0.49
33:E1:106:TYR:HE2	33:E1:116:LYS:HB3	2.99	0.49
41:L4:269:SER:C	41:L4:271:LYS:H	2.34	0.49
41:L4:315:LYS:HD3	41:L4:320:ASN:ND2	2.27	0.49
44:L7:221:LYS:HB2	44:L7:227:GLY:HA3	1.95	0.49
36:1:2618:G:OP1	47:M0:116:ARG:HD3	2.12	0.49
48:M1:94:ARG:C	48:M1:96:PHE:H	2.17	0.49
49:M3:119:TYR:HD1	49:M3:145:PHE:CE2	2.35	0.49
59:N3:79:VAL:HG23	59:N3:80:ARG:HG3	3.00	0.49
63:N7:44:ALA:HB2	63:N7:72:ILE:HG22	2.57	0.49
64:N8:118:ILE:HD13	64:N8:118:ILE:H	1.77	0.49
68:O2:64:LYS:O	68:O2:65:PHE:HB2	2.26	0.49
2:S0:108:THR:O	2:S0:109:ASN:HB3	2.46	0.49
2:S0:49:ASN:HB3	2:S0:52:LYS:HG3	1.92	0.49
4:S2:85:PRO:HG3	4:S2:98:PHE:HD1	2.87	0.49
5:S3:164:VAL:O	5:S3:168:ILE:HG13	2.13	0.49
6:S4:246:LEU:HB2	6:S4:251:GLU:HG2	1.94	0.49
6:S4:49:ARG:HH11	6:S4:50:ASN:HD21	1.60	0.49
11:S9:88:GLU:O	11:S9:91:LYS:HE3	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1631:C:H5''	36:1:1632:A:H5''	1.95	0.49
36:1:269:G:H5''	51:M5:14:LYS:NZ	2.28	0.49
36:1:31:C:OP2	51:M5:188:ARG:NH2	2.45	0.49
36:1:1383:G:O6	87:1:3776:OHX:N4	2.45	0.49
36:1:379:C:H2'	36:1:380:U:H6	1.77	0.49
36:1:435:C:H2'	36:1:436:A:C8	2.47	0.49
1:2:1410:A:H2'	1:2:1411:A:O4'	2.12	0.49
1:2:1417:A:OP1	87:2:2039:OHX:N5	2.46	0.49
1:2:442:C:O2'	1:2:525:A:N1	2.33	0.49
38:4:139:U:H2'	38:4:140:G:C8	2.47	0.49
36:5:879:U:O2	36:5:2357:A:H1'	2.12	0.49
47:M0:157:TYR:CD1	36:5:2836:C:H4'	313.32	0.49
1:6:1690:G:H1	1:6:1711:C:N4	2.08	0.49
1:6:1157:A:OP2	87:6:2109:OHX:N1	2.45	0.49
1:6:555:A:H2'	1:6:556:A:C8	2.47	0.49
14:C2:136:ILE:HA	14:C2:139:HIS:HB3	1.93	0.49
24:D2:77:PRO:HD2	24:D2:79:PHE:CE2	3.38	0.49
23:D1:64:GLU:OE2	29:D7:2:VAL:HG22	2.94	0.49
29:D7:33:LEU:HB3	29:D7:79:PHE:HB2	2.85	0.49
41:L4:60:THR:HG22	41:L4:62:ALA:H	1.76	0.49
47:M0:91:VAL:HG22	47:M0:127:ALA:HB1	3.83	0.49
51:M5:118:SER:HB3	51:M5:132:VAL:HG13	1.94	0.49
87:1:4100:OHX:N3	52:M6:58:LEU:O	2.46	0.49
50:M4:38:ILE:HD13	56:N0:150:PHE:HE2	3.01	0.49
56:N0:27:MET:HG3	57:N1:151:LEU:O	4.12	0.49
62:N6:5:SER:C	62:N6:7:ASP:H	2.43	0.49
67:O1:13:THR:HG23	67:O1:72:ARG:HH11	1.76	0.49
73:O7:55:ARG:HD3	36:5:353:G:N7	108.33	0.49
3:S1:173:THR:O	3:S1:177:GLN:N	5.31	0.49
4:S2:38:VAL:HG22	4:S2:39:THR:H	1.77	0.49
1:2:1514:U:O2'	5:S3:5:ILE:O	2.28	0.49
36:1:108:A:O2'	36:1:109:A:H2'	2.12	0.49
36:1:1723:A:N1	36:1:1788:C:O2'	2.41	0.49
36:1:2376:G:H2'	36:1:2377:G:C8	2.46	0.49
36:1:29:C:H4'	36:1:62:A:H4'	1.93	0.49
1:2:1458:G:H5''	1:2:1459:C:OP2	2.13	0.49
1:2:293:U:OP2	87:2:2105:OHX:N1	2.46	0.49
1:2:733:A:H4'	1:2:734:A:C5	2.47	0.49
36:5:3134:A:OP1	87:5:3841:OHX:N5	2.45	0.49
54:M8:107:THR:HG21	36:5:676:G:H3'	137.57	0.49
1:6:1238:A:C6	1:6:1239:U:H1'	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:660:G:H2'	1:6:661:A:H4'	1.94	0.49
12:C0:54:TYR:CE2	12:C0:75:TYR:HB2	3.75	0.49
16:C4:31:THR:OG1	16:C4:32:ASP:N	2.91	0.49
22:D0:44:ASN:ND2	22:D0:103:ILE:HD11	5.53	0.49
27:D5:59:TYR:HD2	27:D5:60:VAL:N	2.11	0.49
28:D6:41:ILE:HA	28:D6:67:THR:O	2.41	0.49
41:L4:129:THR:HG21	41:L4:238:LEU:HD23	1.94	0.49
42:L5:108:ARG:O	42:L5:111:GLN:HB3	2.12	0.49
43:L6:30:LEU:HD22	43:L6:34:LEU:HD12	1.97	0.49
49:M3:189:GLU:O	49:M3:192:GLU:HG2	2.13	0.49
50:M4:114:ASP:HA	50:M4:117:ARG:CZ	2.43	0.49
51:M5:11:GLN:HE21	51:M5:44:ARG:NH1	3.52	0.49
36:1:1295:G:OP1	56:N0:83:SER:HB2	2.13	0.49
61:N5:46:TYR:HB3	71:O5:75:TYR:HB3	2.62	0.49
62:N6:73:VAL:HA	62:N6:80:VAL:HG22	3.22	0.49
64:N8:73:LEU:HB3	64:N8:112:ILE:HD13	3.37	0.49
66:O0:15:ALA:O	66:O0:18:ILE:HG22	2.12	0.49
68:O2:78:ASN:HA	68:O2:108:ILE:HD11	2.04	0.49
72:O6:45:ARG:NH2	72:O6:54:GLU:OE1	2.45	0.49
4:S2:185:LYS:O	4:S2:189:GLN:HG3	4.70	0.49
6:S4:232:GLY:O	6:S4:234:PRO:HD3	2.13	0.49
7:S5:92:ARG:NH2	7:S5:169:ASN:OD1	2.46	0.49
9:S7:117:THR:HG23	1:6:639:U:OP1	365.91	0.49
10:S8:152:ILE:H	10:S8:152:ILE:HD13	4.83	0.49
36:1:1585:C:H2'	36:1:1586:G:H8	1.77	0.49
36:1:2514:U:OP1	36:1:2514:U:H6	1.96	0.49
36:1:3317:U:O2'	87:1:3919:OHX:N3	2.45	0.49
36:1:3364:C:OP1	87:1:3825:OHX:N5	2.46	0.49
1:2:116:U:H2'	1:2:117:U:C6	2.48	0.49
38:4:81:U:H1'	38:4:82:U:H5''	1.94	0.49
36:5:1632:A:H2'	36:5:1633:C:C6	2.47	0.49
36:5:2207:A:N6	36:5:2236:G:H1	2.10	0.49
36:5:2530:G:H2'	36:5:2531:C:H5''	1.94	0.49
36:5:2523:A:O2'	36:5:2587:U:H1'	2.13	0.49
1:6:1274:C:H4'	1:6:1275:A:O5'	2.13	0.49
1:6:1514:U:H5''	1:6:1515:A:N3	2.28	0.49
1:6:1167:G:H1	1:6:1578:U:H3	1.59	0.49
1:6:1590:G:H2'	1:6:1591:C:H6	1.78	0.49
1:6:83:G:OP2	87:6:2064:OHX:N4	2.45	0.49
1:6:224:C:H2'	1:6:225:A:C8	2.47	0.49
10:S8:5:ARG:NH2	1:6:334:G:O6	305.05	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:C0:38:LYS:HD2	12:C0:41:TYR:CZ	2.48	0.49
14:C2:54:ARG:HD3	14:C2:56:GLU:CD	2.72	0.49
15:C3:34:ILE:O	15:C3:38:VAL:HG23	2.12	0.49
16:C4:51:ASP:CG	1:6:902:G:H1	286.10	0.49
18:C6:46:PHE:CD2	18:C6:49:TYR:HD2	4.67	0.49
18:C6:82:ARG:HH12	18:C6:114:ARG:HB3	1.77	0.49
41:L4:118:LYS:O	41:L4:122:THR:HG23	3.00	0.49
41:L4:191:LYS:HB2	41:L4:194:TYR:CZ	5.22	0.49
41:L4:39:PHE:CD2	41:L4:242:ALA:HB2	3.03	0.49
36:1:1347:U:H4'	41:L4:305:ALA:HB2	1.94	0.49
42:L5:236:LEU:HA	42:L5:239:ILE:HD12	1.93	0.49
43:L6:131:LYS:HD3	43:L6:132:ALA:N	5.42	0.49
43:L6:147:ALA:HA	43:L6:150:LYS:NZ	2.28	0.49
44:L7:177:GLY:O	44:L7:179:LEU:HD13	2.13	0.49
44:L7:110:ARG:NH2	44:L7:206:LYS:HE2	5.75	0.49
47:M0:12:GLN:HA	47:M0:59:GLN:OE1	3.29	0.49
48:M1:92:ARG:HB3	48:M1:94:ARG:HG2	1.94	0.49
67:O1:15:ASN:O	67:O1:19:ARG:HD2	3.29	0.49
71:O5:21:LEU:HB2	71:O5:54:VAL:HG11	2.37	0.49
2:S0:56:LYS:HE2	23:D1:70:ASN:HD21	2.98	0.49
4:S2:139:ILE:HD11	4:S2:191:ALA:HB1	3.16	0.49
5:S3:70:THR:HG23	5:S3:86:LEU:HD13	1.93	0.49
6:S4:125:LYS:NZ	6:S4:157:ASN:HA	4.42	0.49
9:S7:43:PHE:HB2	9:S7:61:PHE:O	2.12	0.49
34:SR:256:THR:N	34:SR:259:GLY:O	2.92	0.49
36:1:1295:G:H2'	36:1:1296:C:C6	2.48	0.49
36:1:1597:C:H2'	36:1:1598:G:C8	2.48	0.49
36:1:3011:A:C8	40:L3:13:HIS:CE1	3.00	0.49
1:2:1171:A:H2'	1:2:1172:G:C8	2.47	0.49
1:2:1251:U:H5'	33:E1:135:HIS:HD2	1.78	0.49
1:2:1657:U:C4	87:2:2058:OHX:N6	2.81	0.49
1:2:484:C:H42	1:2:503:G:H22	1.61	0.49
37:3:11:A:N1	37:3:67:G:O2'	2.38	0.49
1:6:994:G:H2'	1:6:995:A:O4'	2.13	0.49
12:C0:77:ARG:HA	12:C0:82:LEU:HD11	1.93	0.49
16:C4:21:ALA:HB1	16:C4:26:THR:HG22	1.95	0.49
18:C6:6:SER:HA	18:C6:23:LYS:HA	2.38	0.49
20:C8:99:HIS:HD2	20:C8:101:LEU:HD21	1.78	0.49
22:D0:23:ARG:HB3	22:D0:117:VAL:HB	4.53	0.49
24:D2:103:ILE:HG22	24:D2:112:ASP:HA	5.03	0.49
24:D2:23:ARG:HA	24:D2:65:LEU:HB2	5.25	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:C1:101:GLU:HB3	25:D3:12:ALA:HB3	1.95	0.49
36:1:3010:U:O2'	40:L3:13:HIS:HE1	1.95	0.49
40:L3:47:LEU:HG	40:L3:335:ILE:HD11	2.69	0.49
41:L4:3:ARG:NE	41:L4:22:LEU:O	2.39	0.49
41:L4:33:ASP:O	41:L4:37:THR:HG23	2.13	0.49
42:L5:106:ALA:O	42:L5:110:LEU:HD22	3.81	0.49
44:L7:169:ILE:HD12	44:L7:181:ILE:HA	1.94	0.49
44:L7:132:PRO:HA	44:L7:229:PHE:CG	2.73	0.49
50:M4:17:VAL:HG22	50:M4:36:VAL:O	2.13	0.49
54:M8:26:LEU:O	54:M8:30:VAL:HG23	2.12	0.49
54:M8:81:VAL:HG23	54:M8:101:VAL:HG13	1.94	0.49
61:N5:42:ARG:HD2	36:5:14:U:O2	102.66	0.49
38:4:85:G:O6	62:N6:112:ASP:HB3	2.13	0.49
66:O0:43:ILE:HG22	66:O0:70:PHE:HB2	1.95	0.49
68:O2:16:LYS:HD3	68:O2:18:LYS:HG2	1.95	0.49
70:O4:39:ALA:HB1	70:O4:57:LEU:O	2.12	0.49
71:O5:21:LEU:HD21	71:O5:25:LYS:HE3	2.13	0.49
78:Q2:16:THR:C	78:Q2:18:ARG:H	3.93	0.49
78:Q2:14:GLY:C	78:Q2:16:THR:H	2.15	0.49
1:2:1278:G:P	5:S3:185:LYS:HZ3	2.35	0.49
5:S3:35:SER:OG	5:S3:35:SER:O	2.29	0.49
6:S4:137:PRO:HG2	6:S4:150:PRO:HD2	2.62	0.49
8:S6:200:ALA:O	8:S6:203:GLU:HB2	4.23	0.49
9:S7:6:ALA:HB1	9:S7:9:LEU:HD12	1.95	0.49
34:SR:32:LEU:HD11	34:SR:44:SER:HB2	3.23	0.49
36:1:1269:U:N3	36:1:1271:A:H5''	2.28	0.49
36:1:2984:C:H2'	36:1:2985:C:C6	2.45	0.49
36:1:3396:U:O2	87:1:4055:OHX:N3	2.45	0.49
36:1:824:C:H2'	36:1:825:U:H6	1.78	0.49
1:2:122:U:O4	87:2:2016:OHX:N4	2.45	0.49
1:2:990:C:H2'	1:2:991:G:O4'	2.13	0.49
36:5:2207:A:H2'	36:5:2208:A:O4'	2.12	0.49
62:N6:103:LYS:HE3	36:5:221:A:H61	80.71	0.49
53:M7:82:ARG:HB3	36:5:2352:A:OP1	159.41	0.49
36:5:270:U:O2'	36:5:318:A:H1'	2.13	0.49
36:5:3317:U:H1'	87:5:4047:OHX:N6	2.28	0.49
36:5:683:U:H2'	36:5:684:G:O4'	2.13	0.49
41:L4:112:LYS:HG2	36:5:790:U:H5'	120.02	0.49
1:6:1042:G:H2'	1:6:1043:A:H8	1.78	0.49
1:6:1244:A:H3'	1:6:1244:A:N3	2.28	0.49
1:6:840:U:H2'	1:6:841:U:H6	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:C7:66:VAL:HB	19:C7:69:ILE:HD11	1.93	0.49
20:C8:126:ARG:HG3	20:C8:131:LEU:HB2	1.94	0.49
20:C8:91:ASP:OD1	20:C8:92:ILE:N	2.45	0.49
26:D4:121:THR:H	1:6:85:A:H4'	340.08	0.49
39:L2:224:THR:HA	39:L2:237:LEU:O	2.47	0.49
40:L3:122:TRP:CE2	40:L3:127:LYS:HE3	2.48	0.49
40:L3:142:ALA:O	40:L3:145:GLU:N	3.94	0.49
46:L9:13:PRO:HD2	46:L9:16:VAL:HG22	1.93	0.49
48:M1:95:ASN:OD1	48:M1:95:ASN:N	2.73	0.49
54:M8:64:VAL:HG21	54:M8:113:LYS:HD2	1.95	0.49
57:N1:12:ARG:HG3	36:5:2698:G:O2'	260.56	0.49
59:N3:84:SER:HA	59:N3:94:TYR:HB3	1.94	0.49
74:O8:27:ILE:HD13	74:O8:41:THR:HB	1.94	0.49
79:Q3:83:ILE:HG22	79:Q3:87:ARG:HH12	1.78	0.49
4:S2:59:HIS:CD2	4:S2:238:SER:HA	3.16	0.49
5:S3:168:ILE:HD13	5:S3:187:LYS:HE2	1.94	0.49
5:S3:195:SER:HB2	5:S3:200:LYS:HG2	3.51	0.49
6:S4:184:THR:C	6:S4:189:LEU:HD13	2.72	0.49
7:S5:59:VAL:C	7:S5:61:TYR:H	2.16	0.49
10:S8:82:VAL:HG12	10:S8:101:ILE:O	6.30	0.49
11:S9:132:ARG:O	11:S9:134:ILE:N	4.37	0.49
11:S9:151:ASP:OD1	11:S9:151:ASP:N	2.62	0.49
36:1:159:A:H61	36:1:262:U:H3	1.61	0.49
36:1:2522:G:H2'	36:1:2522:G:N3	2.27	0.49
36:1:2816:G:O6	87:1:4076:OHX:N3	2.46	0.49
36:1:899:U:O4	87:1:3834:OHX:N1	2.46	0.49
1:2:1002:G:H2'	1:2:1003:A:H5'	1.94	0.49
1:2:17:C:O2'	1:2:1137:A:N1	2.43	0.49
1:2:1388:A:C5	1:2:1411:A:C6	3.00	0.49
1:2:1731:A:H5''	1:2:1732:A:OP2	2.13	0.49
37:3:7:G:O3'	42:L5:33:ARG:NH2	2.45	0.49
36:5:1087:G:O6	87:5:4018:OHX:N3	2.45	0.49
69:O3:77:ASN:HB2	36:5:1180:A:OP1	264.91	0.49
36:5:151:A:O2'	36:5:152:U:OP1	2.28	0.49
36:5:1540:U:H2'	36:5:1541:G:H8	1.78	0.49
36:5:202:G:N7	87:5:3901:OHX:N5	2.61	0.49
36:5:2665:U:H4'	36:5:2666:C:OP1	2.12	0.49
78:Q2:45:ARG:NH2	36:5:283:G:OP2	147.96	0.49
36:5:2317:A:OP2	87:5:4102:OHX:N2	2.44	0.49
1:6:1395:G:H1	1:6:1403:C:H42	1.61	0.49
13:C1:100:TYR:O	25:D3:10:ASN:HA	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:C6:89:LEU:HG	18:C6:105:LEU:HD23	2.16	0.49
5:S3:209:ILE:HG22	19:C7:38:ILE:O	2.14	0.49
9:S7:141:ARG:HG2	24:D2:51:GLU:HG3	2.59	0.49
28:D6:18:VAL:HG23	28:D6:19:LYS:H	1.77	0.49
1:2:567:A:P	32:E0:10:ARG:HH21	2.36	0.49
33:E1:108:VAL:HG12	33:E1:114:VAL:HG13	4.47	0.49
39:L2:114:SER:O	39:L2:116:VAL:N	2.46	0.49
39:L2:70:ARG:NH1	39:L2:72:ARG:HH21	6.47	0.49
42:L5:184:ASP:HB3	42:L5:187:THR:OG1	4.69	0.49
42:L5:204:VAL:O	42:L5:208:MET:HB2	3.46	0.49
42:L5:85:ARG:NH1	42:L5:254:LYS:H	4.43	0.49
43:L6:137:ASP:O	43:L6:141:VAL:HG23	2.13	0.49
36:1:1362:G:H1'	44:L7:159:GLN:OE1	2.13	0.49
46:L9:83:THR:OG1	46:L9:84:LYS:N	2.45	0.49
36:1:2424:A:H1'	51:M5:77:LYS:O	2.12	0.49
1:2:851:U:OP1	55:M9:172:ARG:NH1	2.46	0.49
78:Q2:39:GLY:HA3	36:5:2765:C:O3'	174.11	0.49
79:Q3:19:GLY:HA2	36:5:1925:U:O2	240.91	0.49
2:S0:119:ARG:NH2	4:S2:238:SER:OG	2.46	0.49
2:S0:88:LYS:O	2:S0:92:HIS:ND1	4.33	0.49
3:S1:109:LYS:HG3	3:S1:113:MET:HE3	1.94	0.49
4:S2:104:VAL:HG22	4:S2:132:ALA:HB1	2.41	0.49
6:S4:112:HIS:ND1	6:S4:239:PRO:HA	3.33	0.49
6:S4:240:LYS:CE	6:S4:240:LYS:H	2.25	0.49
8:S6:139:ASN:HA	8:S6:142:ARG:HB2	1.95	0.49
4:S2:98:PHE:CE1	35:SM:116:GLU:HG3	2.48	0.49
34:SR:249:ARG:NH2	34:SR:315:VAL:HG11	3.53	0.49
36:1:1000:C:H42	36:1:1046:A:H62	1.60	0.49
36:1:1022:U:H2'	36:1:1023:C:O4'	2.12	0.49
36:1:194:U:H2'	36:1:195:U:C6	2.44	0.49
36:1:2203:U:H2'	36:1:2204:C:H6	1.78	0.49
36:1:1009:A:OP2	87:1:3986:OHX:N1	2.46	0.49
36:1:764:U:O4	87:1:3858:OHX:N5	2.45	0.49
1:2:273:G:H1	1:2:283:U:H3	1.61	0.49
1:2:474:A:OP2	11:S9:44:ARG:NH1	2.42	0.49
1:2:502:U:H2'	1:2:503:G:O4'	2.13	0.49
1:2:538:A:H5'	1:2:543:C:H42	1.78	0.49
1:2:563:U:C4	1:2:564:G:C6	3.01	0.49
36:5:1915:A:H2'	36:5:1916:U:C6	2.48	0.49
36:5:314:U:H2'	36:5:315:C:C6	2.48	0.49
36:5:380:U:H2'	36:5:381:U:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:M5:84:PRO:HD2	36:5:44:U:OP1	166.77	0.49
15:C3:3:ARG:NH1	1:6:955:A:OP1	330.90	0.49
13:C1:6:THR:HB	13:C1:9:SER:HB3	1.95	0.49
24:D2:76:SER:HB3	24:D2:77:PRO:HD3	1.94	0.49
25:D3:42:PRO:HA	25:D3:81:LYS:HD2	2.47	0.49
28:D6:84:VAL:HG13	28:D6:85:ARG:N	2.26	0.49
40:L3:92:TYR:CE2	40:L3:101:SER:HB3	2.48	0.49
47:M0:73:ASN:O	47:M0:76:MET:N	3.49	0.49
36:1:2674:A:H5''	48:M1:105:GLY:HA3	1.95	0.49
48:M1:33:ALA:HB2	48:M1:123:PHE:CE1	3.14	0.49
51:M5:172:ARG:HB3	51:M5:174:ILE:HG12	2.80	0.49
52:M6:60:LYS:HE2	36:5:1307:G:H5''	251.74	0.49
53:M7:62:ARG:O	53:M7:64:ASN:N	2.45	0.49
36:1:3308:C:O2	53:M7:69:ARG:HB2	2.13	0.49
55:M9:35:ALA:O	55:M9:37:SER:N	3.71	0.49
58:N2:54:VAL:HG12	58:N2:67:SER:HA	1.94	0.49
67:O1:31:ARG:NH1	67:O1:35:GLU:OE1	2.46	0.49
67:O1:90:PHE:HD2	67:O1:91:SER:O	1.95	0.49
68:O2:11:LYS:O	68:O2:13:HIS:N	2.63	0.49
72:O6:80:PHE:O	72:O6:83:ALA:HB3	2.74	0.49
73:O7:16:HIS:O	73:O7:25:ARG:HD3	2.77	0.49
74:O8:36:LYS:HA	74:O8:37:PRO:HD3	2.29	0.49
2:S0:25:GLY:HA2	2:S0:48:ILE:HD11	1.94	0.49
5:S3:53:THR:HG22	5:S3:91:VAL:HG11	1.95	0.49
6:S4:11:ARG:NH1	6:S4:20:LEU:HB3	3.16	0.49
6:S4:11:ARG:NH2	6:S4:27:TYR:O	3.38	0.49
6:S4:105:VAL:HG22	6:S4:243:GLY:HA2	2.38	0.49
7:S5:184:PHE:C	7:S5:186:ASN:H	2.86	0.49
7:S5:43:PHE:CG	7:S5:44:ASN:N	2.92	0.49
9:S7:74:GLN:HE22	9:S7:92:PHE:HB2	3.01	0.49
10:S8:46:VAL:HG13	10:S8:54:LYS:HB3	1.95	0.49
11:S9:59:LEU:HA	11:S9:62:ARG:HG3	1.94	0.49
36:1:2218:G:H2'	36:1:2219:A:C8	2.47	0.48
36:1:3133:C:H2'	36:1:3134:A:O4'	2.12	0.48
36:1:1192:C:N4	87:1:3945:OHX:N3	2.60	0.48
36:1:602:A:H2'	36:1:603:A:C8	2.48	0.48
36:1:718:G:C2	36:1:721:G:H1'	2.47	0.48
36:1:848:A:H8	36:1:848:A:O5'	1.96	0.48
1:2:1654:G:H2'	1:2:1745:G:N2	2.27	0.48
37:3:48:U:O4	42:L5:58:LYS:HE2	2.13	0.48
37:3:93:C:O2'	37:3:94:C:H5'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1445:U:H5''	36:5:1446:A:OP2	2.13	0.48
36:5:2581:U:H2'	36:5:2582:C:H6	1.78	0.48
36:5:2714:G:N3	36:5:2714:G:H5''	2.28	0.48
36:5:3197:G:H2'	36:5:3198:U:H5''	1.94	0.48
36:5:1122:U:O4	87:5:4055:OHX:N6	2.46	0.48
36:5:750:G:C2	36:5:751:A:C8	3.01	0.48
1:6:1003:A:H4'	1:6:1004:U:O5'	2.13	0.48
1:6:163:G:H8	1:6:163:G:O5'	1.95	0.48
10:S8:16:ALA:HB2	1:6:354:C:H5''	299.11	0.48
1:6:686:C:H2'	1:6:687:G:C8	2.48	0.48
36:5:997:A:O2'	37:7:79:A:N3	2.46	0.48
89:B:101:SPS:H71	89:B:101:SPS:H81	1.68	0.48
17:C5:111:MET:HG2	20:C8:119:ILE:HD11	5.13	0.48
40:L3:46:PHE:CE2	40:L3:205:VAL:HG22	3.08	0.48
40:L3:219:ALA:HB2	40:L3:336:VAL:HG22	2.32	0.48
41:L4:351:PRO:HA	44:L7:71:ALA:HA	1.95	0.48
42:L5:136:GLU:O	42:L5:137:ASP:HB2	2.51	0.48
49:M3:133:PRO:O	49:M3:135:ALA:N	3.20	0.48
50:M4:113:THR:HB	50:M4:116:GLU:H	1.78	0.48
57:N1:130:ARG:O	36:5:1098:A:H4'	255.99	0.48
57:N1:34:TYR:CE1	57:N1:98:HIS:CE1	3.96	0.48
59:N3:120:LYS:HE3	59:N3:124:ASP:OD2	5.06	0.48
62:N6:60:ARG:HG3	62:N6:103:LYS:HD2	1.94	0.48
71:O5:28:LEU:HA	71:O5:31:LEU:HB2	2.50	0.48
51:M5:6:TYR:CD2	72:O6:40:VAL:HG13	2.79	0.48
79:Q3:30:GLU:HA	79:Q3:33:GLN:HG2	2.75	0.48
4:S2:187:LEU:HD21	4:S2:218:ILE:HD11	3.85	0.48
2:S0:110:TYR:HB2	4:S2:38:VAL:HG11	1.95	0.48
5:S3:178:ARG:NE	5:S3:178:ARG:H	2.08	0.48
5:S3:195:SER:O	5:S3:196:ARG:HB3	2.24	0.48
10:S8:97:THR:OG1	10:S8:98:LYS:O	2.72	0.48
36:1:1204:A:H2	36:1:2834:G:N3	2.11	0.48
36:1:533:A:H4'	36:1:534:U:OP1	2.13	0.48
1:2:201:G:H2'	1:2:202:A:C8	2.48	0.48
1:2:542:A:H5''	1:2:544:A:C8	2.48	0.48
38:4:64:U:H3	38:4:96:A:H61	1.62	0.48
36:5:1393:A:N3	36:5:1419:A:O2'	2.42	0.48
36:5:2273:G:N2	36:5:2311:G:H2'	2.28	0.48
36:5:2313:A:H4'	36:5:2314:U:H5'	1.95	0.48
51:M5:68:ARG:NH1	36:5:291:C:OP1	149.09	0.48
36:5:107:A:O2'	36:5:324:A:N3	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:3317:U:H4'	36:5:3318:G:O5'	2.13	0.48
36:5:818:C:N3	36:5:920:A:H5'	2.29	0.48
1:6:1620:C:H2'	1:6:1621:U:H6	1.78	0.48
1:6:802:G:C6	1:6:803:A:C6	3.02	0.48
1:6:914:G:H5'	1:6:914:G:C8	2.48	0.48
56:N0:119:ARG:NH1	37:7:87:G:O2'	279.33	0.48
16:C4:136:ARG:NH1	1:6:1785:U:OP1	299.42	0.48
18:C6:60:PHE:HD2	18:C6:63:ILE:HD11	4.48	0.48
20:C8:86:LEU:O	20:C8:89:GLN:NE2	5.08	0.48
25:D3:86:PHE:CE1	25:D3:88:PRO:HA	2.48	0.48
26:D4:105:ARG:HH22	1:6:459:G:P	363.96	0.48
26:D4:62:THR:HA	26:D4:69:SER:HA	2.17	0.48
29:D7:75:GLU:HB3	29:D7:76:GLY:H	1.48	0.48
7:S5:158:GLN:HG2	30:D8:66:LEU:HD21	1.95	0.48
1:2:1234:A:H4'	33:E1:146:SER:HB3	1.95	0.48
39:L2:42:ARG:HG3	39:L2:89:TYR:CE1	3.07	0.48
41:L4:115:HIS:O	41:L4:119:ARG:HG3	3.21	0.48
41:L4:295:ILE:O	41:L4:299:ILE:HG12	2.13	0.48
47:M0:150:GLU:CG	47:M0:154:ARG:HE	2.26	0.48
50:M4:32:LEU:HD11	50:M4:94:TRP:CG	2.47	0.48
55:M9:4:LEU:HB3	55:M9:24:LEU:HD23	1.95	0.48
58:N2:89:LEU:O	58:N2:93:ILE:HG13	2.14	0.48
59:N3:118:VAL:O	59:N3:137:VAL:N	2.38	0.48
61:N5:58:ASP:O	61:N5:62:VAL:HG23	2.20	0.48
62:N6:40:ARG:HG3	62:N6:45:ILE:O	2.13	0.48
62:N6:27:ARG:NH1	62:N6:75:ARG:O	2.40	0.48
73:O7:39:TYR:CD2	73:O7:40:PRO:HA	2.82	0.48
78:Q2:11:TYR:HE1	78:Q2:13:LYS:HB3	1.77	0.48
79:Q3:17:ARG:HB3	79:Q3:18:TYR:CD1	2.79	0.48
36:1:2554:A:H62	79:Q3:62:LYS:NZ	2.11	0.48
3:S1:131:ASP:N	3:S1:131:ASP:OD1	4.33	0.48
4:S2:59:HIS:HA	23:D1:15:ARG:HE	1.78	0.48
2:S0:139:VAL:HG23	4:S2:62:PRO:HG3	1.94	0.48
5:S3:135:GLU:HB3	5:S3:187:LYS:HB3	2.65	0.48
6:S4:129:VAL:HB	6:S4:139:VAL:HG12	1.96	0.48
1:2:401:A:H1'	6:S4:3:ARG:NH1	2.28	0.48
7:S5:84:LYS:HG2	7:S5:92:ARG:HH12	1.76	0.48
11:S9:157:ASP:OD1	11:S9:158:PHE:N	3.63	0.48
36:1:1278:A:HO2'	36:1:1279:C:H6	1.58	0.48
36:1:1626:U:O4	87:1:4070:OHX:N6	2.46	0.48
36:1:2697:A:H2'	36:1:2698:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:3023:U:H2'	36:1:3024:A:C8	2.48	0.48
36:1:3213:A:N7	50:M4:124:ARG:NH2	2.56	0.48
1:2:1155:G:O2'	87:2:2032:OHX:N2	2.46	0.48
1:2:1260:U:H2'	1:2:1261:G:C8	2.48	0.48
1:2:252:U:H2'	1:2:253:A:H8	1.78	0.48
1:2:415:C:O3'	1:2:416:A:H8	1.96	0.48
36:5:2518:C:OP1	87:5:4120:OHX:N4	2.46	0.48
36:5:252:U:H4'	36:5:253:A:C5'	2.43	0.48
36:5:2877:G:N7	87:5:4048:OHX:N3	2.60	0.48
36:5:1940:G:N2	36:5:3362:A:H8	2.11	0.48
1:6:1067:C:H2'	1:6:1068:C:C6	2.47	0.48
19:C7:52:GLY:HA3	1:6:1389:C:O2'	424.54	0.48
1:6:1793:G:H1'	1:6:1794:A:H2'	1.94	0.48
1:6:646:C:H2'	1:6:647:G:C8	2.48	0.48
38:8:26:U:H2'	38:8:27:U:C6	2.48	0.48
18:C6:120:ASP:OD1	18:C6:121:SER:N	2.45	0.48
18:C6:30:LYS:O	18:C6:66:ARG:HA	2.13	0.48
19:C7:108:ASP:O	19:C7:112:SER:OG	2.19	0.48
22:D0:50:LEU:HD23	22:D0:51:VAL:H	1.77	0.48
2:S0:59:LEU:HD11	23:D1:78:LEU:O	2.13	0.48
24:D2:94:LEU:HD11	24:D2:102:VAL:HG23	3.56	0.48
25:D3:63:GLN:HA	25:D3:65:ASN:N	2.27	0.48
28:D6:11:ASN:O	28:D6:33:ASP:HB2	2.14	0.48
29:D7:56:CYS:HB3	29:D7:59:CYS:O	2.13	0.48
39:L2:104:LEU:O	39:L2:107:VAL:HG22	3.06	0.48
39:L2:204:MET:HE2	39:L2:209:HIS:HB2	1.95	0.48
40:L3:347:SER:O	40:L3:348:ARG:HB3	2.12	0.48
41:L4:281:ILE:HG22	54:M8:25:TYR:HB3	1.94	0.48
47:M0:89:VAL:HG13	47:M0:136:PHE:HE1	1.78	0.48
48:M1:116:TYR:CD2	48:M1:122:ILE:HD11	2.49	0.48
48:M1:16:LYS:HG2	48:M1:130:VAL:CG1	2.43	0.48
48:M1:90:GLN:HG2	48:M1:170:ASP:HB2	1.96	0.48
48:M1:56:THR:OG1	48:M1:56:THR:O	3.48	0.48
52:M6:42:ASN:ND2	52:M6:125:ARG:HD3	3.92	0.48
63:N7:36:HIS:HB3	63:N7:38:PHE:CZ	2.47	0.48
63:N7:53:VAL:HA	63:N7:57:HIS:HD2	2.06	0.48
67:O1:29:ALA:HB3	67:O1:30:PRO:HD3	2.04	0.48
74:O8:16:ARG:NH1	74:O8:70:PRO:HG3	5.59	0.48
77:Q1:4:LYS:HG2	77:Q1:5:TRP:CE3	2.49	0.48
36:1:860:G:P	79:Q3:17:ARG:HH12	2.34	0.48
2:S0:64:ILE:HD13	2:S0:89:PHE:HZ	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:S2:137:ILE:HD13	4:S2:138:PRO:HD2	1.95	0.48
7:S5:149:VAL:HG13	7:S5:156:ARG:HG3	1.96	0.48
7:S5:97:LEU:O	7:S5:99:MET:N	3.35	0.48
10:S8:78:ILE:HA	10:S8:104:ILE:HG22	3.16	0.48
36:1:2443:A:H61	36:1:2504:U:H3	1.61	0.48
36:1:2443:A:O2'	36:1:2444:C:H5'	2.13	0.48
36:1:2544:U:H2'	36:1:2545:C:H6	1.78	0.48
36:1:3203:U:O4	87:1:4085:OHX:N1	2.45	0.48
1:2:1494:C:H2'	1:2:1495:C:H6	1.79	0.48
1:2:190:C:O2'	1:2:191:C:H5'	2.13	0.48
1:2:703:G:H1	1:2:735:C:N4	2.10	0.48
1:2:798:C:H2'	1:2:799:A:H8	1.78	0.48
36:5:1208:U:H6	36:5:3115:C:H42	1.60	0.48
36:5:1595:U:HO2'	36:5:1596:C:H6	1.62	0.48
36:5:2307:G:O2'	36:5:2310:U:OP2	2.28	0.48
51:M5:69:GLY:O	36:5:290:G:H4'	146.50	0.48
36:5:3189:G:H2'	36:5:3190:C:O4'	2.13	0.48
36:5:495:G:H1	36:5:618:C:H42	1.61	0.48
28:D6:89:ARG:N	1:6:1628:U:OP1	359.44	0.48
38:8:29:U:H2'	38:8:30:C:H6	1.79	0.48
1:2:1217:A:H5''	12:C0:1:MET:HG3	1.96	0.48
12:C0:4:PRO:HG2	12:C0:7:ASP:HB2	3.14	0.48
15:C3:96:VAL:O	15:C3:100:LYS:HG2	5.18	0.48
1:2:1579:U:O2'	18:C6:139:GLN:HG3	2.14	0.48
21:C9:132:LEU:O	21:C9:135:ILE:HG13	2.13	0.48
24:D2:8:ALA:HA	24:D2:74:VAL:HG11	1.94	0.48
25:D3:51:GLY:HA2	25:D3:77:ILE:HG13	2.05	0.48
39:L2:226:SER:HA	36:5:2202:C:H5''	210.37	0.48
39:L2:82:VAL:HA	39:L2:86:GLN:OE1	2.35	0.48
40:L3:102:LEU:H	40:L3:102:LEU:HD23	3.03	0.48
41:L4:169:LEU:O	41:L4:172:VAL:HG12	2.14	0.48
43:L6:145:LEU:O	43:L6:149:ILE:N	2.47	0.48
44:L7:41:ARG:NH1	36:5:598:A:OP1	261.22	0.48
47:M0:17:TYR:H	47:M0:95:HIS:CE1	2.31	0.48
50:M4:21:VAL:N	50:M4:33:ALA:O	2.37	0.48
54:M8:133:LYS:HB2	54:M8:135:GLN:NE2	2.29	0.48
36:1:1864:A:OP1	55:M9:88:ARG:NH1	2.46	0.48
57:N1:47:SER:O	57:N1:49:GLN:NE2	4.29	0.48
58:N2:18:ASP:HA	58:N2:62:VAL:HG22	1.95	0.48
58:N2:35:LYS:NZ	58:N2:39:ASP:OD2	4.31	0.48
58:N2:41:ILE:HG12	58:N2:79:LEU:HD13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:N3:87:ARG:HH22	59:N3:137:VAL:HG13	1.78	0.48
63:N7:10:VAL:HB	63:N7:83:THR:CG2	2.42	0.48
66:O0:27:TYR:O	66:O0:30:THR:OG1	2.29	0.48
68:O2:32:TRP:CZ2	68:O2:53:PRO:HD2	2.61	0.48
87:1:3766:OHX:N2	73:O7:44:THR:O	2.45	0.48
74:O8:16:ARG:O	74:O8:18:ALA:N	3.75	0.48
2:S0:101:ARG:NH2	1:6:1320:U:H3'	402.35	0.48
6:S4:246:LEU:HD21	6:S4:254:ARG:CZ	2.43	0.48
8:S6:3:LEU:HD22	8:S6:111:LEU:HD11	2.15	0.48
11:S9:173:ALA:N	1:6:512:A:OP2	459.90	0.48
34:SR:174:ASN:OD1	34:SR:198:ASN:HB3	2.86	0.48
34:SR:242:SER:O	34:SR:292:LEU:HD21	2.12	0.48
36:1:1552:G:OP2	87:1:4034:OHX:N6	2.46	0.48
36:1:2801:A:O2'	36:1:2802:A:H2'	2.13	0.48
87:1:3769:OHX:N1	38:4:2:A:OP2	2.46	0.48
36:1:381:U:H2'	36:1:382:U:C6	2.46	0.48
1:2:609:U:O2'	25:D3:23:ARG:HD3	2.14	0.48
36:5:1664:G:H2'	36:5:1665:C:C6	2.48	0.48
36:5:1879:A:H2'	36:5:1879:A:N3	2.29	0.48
36:5:2392:C:H5''	36:5:2393:G:OP2	2.14	0.48
52:M6:73:PHE:CD1	36:5:3007:U:H5'	246.01	0.48
36:5:766:U:H4'	36:5:767:U:O5'	2.13	0.48
1:6:1237:G:H2'	1:6:1238:A:C8	2.48	0.48
1:6:363:G:OP1	87:6:2078:OHX:N1	2.47	0.48
38:8:104:A:C8	38:8:105:A:C8	3.00	0.48
38:8:124:G:OP2	87:8:221:OHX:N2	2.45	0.48
12:C0:46:LEU:O	12:C0:50:THR:HG23	2.14	0.48
17:C5:29:SER:OG	17:C5:32:ASP:OD2	3.57	0.48
18:C6:83:GLN:HE22	18:C6:119:ALA:HA	1.77	0.48
19:C7:34:LEU:CD2	19:C7:38:ILE:HD12	2.43	0.48
1:2:1503:A:C6	20:C8:84:TRP:CD1	3.01	0.48
40:L3:159:ARG:HG2	40:L3:182:GLN:HA	1.95	0.48
41:L4:217:LYS:HA	41:L4:220:ARG:HG2	5.27	0.48
41:L4:334:PHE:HA	41:L4:339:LEU:HD11	3.69	0.48
42:L5:277:LEU:HD12	42:L5:282:ARG:HG3	5.31	0.48
43:L6:96:VAL:HG12	43:L6:98:VAL:HB	2.87	0.48
45:L8:156:ASP:OD2	45:L8:156:ASP:N	2.47	0.48
54:M8:18:ALA:HB1	54:M8:19:PRO:HD2	2.11	0.48
56:N0:10:ILE:HG12	56:N0:26:ARG:HB2	2.56	0.48
56:N0:2:ALA:HB3	56:N0:32:SER:HB3	1.95	0.48
58:N2:36:TYR:OH	58:N2:82:LYS:HG2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:N3:17:LEU:HB2	59:N3:52:ALA:HB3	1.95	0.48
60:N4:15:PRO:O	60:N4:17:ARG:HG2	5.69	0.48
61:N5:105:VAL:HG21	61:N5:135:ILE:HG13	3.66	0.48
68:O2:26:HIS:O	68:O2:28:VAL:N	2.46	0.48
70:O4:7:PHE:HD2	70:O4:12:PRO:HA	1.78	0.48
61:N5:46:TYR:HD2	71:O5:75:TYR:HB3	2.09	0.48
76:Q0:97:ARG:HG3	76:Q0:120:GLN:O	2.14	0.48
2:S0:148:ASP:OD2	2:S0:165:ARG:NH1	2.47	0.48
2:S0:195:TRP:CZ2	2:S0:197:ILE:HD13	2.48	0.48
3:S1:168:ILE:O	3:S1:172:LEU:HG	2.52	0.48
3:S1:35:PRO:HG3	3:S1:98:THR:O	2.13	0.48
4:S2:49:LYS:HD2	4:S2:243:TYR:CD1	3.11	0.48
4:S2:85:PRO:HG3	4:S2:98:PHE:CD1	3.15	0.48
5:S3:64:ARG:O	5:S3:66:ILE:N	3.08	0.48
7:S5:107:LYS:O	7:S5:111:VAL:HG23	2.14	0.48
35:SM:57:ASN:O	35:SM:61:ILE:HG22	5.04	0.48
36:1:1120:A:C2	36:1:1139:G:C2	3.02	0.48
36:1:1230:G:H1	36:1:1279:C:N4	2.11	0.48
36:1:1953:G:N2	36:1:2093:A:N7	2.54	0.48
36:1:3005:A:H5''	52:M6:149:TYR:OH	2.14	0.48
36:1:2177:G:O6	87:1:3821:OHX:N2	2.46	0.48
1:2:1528:U:H2'	1:2:1529:C:C6	2.49	0.48
1:2:363:G:OP1	87:2:2046:OHX:N2	2.47	0.48
1:2:93:A:C6	1:2:398:G:C6	3.01	0.48
1:2:625:C:H2'	1:2:626:U:C6	2.49	0.48
1:2:818:C:N4	1:2:819:G:O6	2.47	0.48
36:5:2606:G:H2'	36:5:2606:G:N3	2.29	0.48
1:6:1140:G:C2	1:6:1141:G:C8	3.01	0.48
1:6:1275:A:H8	1:6:1275:A:OP2	1.97	0.48
1:6:1799:U:H4'	1:6:1800:A:H2'	1.96	0.48
1:6:200:A:H2'	1:6:201:G:C8	2.48	0.48
1:6:485:A:H61	1:6:502:U:H3	1.62	0.48
14:C2:59:LEU:HA	14:C2:87:PRO:CB	2.43	0.48
15:C3:129:TYR:HB3	15:C3:135:LEU:HD12	1.96	0.48
16:C4:132:ARG:HB2	16:C4:132:ARG:NH1	2.65	0.48
19:C7:31:ASN:O	19:C7:35:CYS:HB2	2.13	0.48
25:D3:107:PHE:CD2	25:D3:114:LYS:HB2	2.48	0.48
26:D4:5:VAL:O	26:D4:6:THR:HB	2.13	0.48
27:D5:38:HIS:HE1	27:D5:70:LYS:HD3	1.79	0.48
33:E1:121:CYS:HB2	33:E1:132:LEU:HD21	2.35	0.48
40:L3:252:ILE:HG23	40:L3:260:VAL:HG13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:332:ARG:HG2	40:L3:333:LYS:HG3	2.83	0.48
54:M8:67:ILE:HG23	54:M8:81:VAL:HG11	2.12	0.48
55:M9:99:LEU:HD11	55:M9:103:ARG:CZ	2.68	0.48
59:N3:22:ILE:HG12	59:N3:35:TYR:HB2	1.94	0.48
61:N5:71:THR:HG21	36:5:1603:A:N6	92.17	0.48
65:N9:31:SER:OG	65:N9:33:LYS:HB3	2.56	0.48
66:O0:13:LYS:NZ	66:O0:99:ASP:OD2	2.53	0.48
75:O9:7:PHE:HE2	38:8:113:U:C5	98.44	0.48
78:Q2:4:VAL:HG12	78:Q2:93:LEU:HB3	6.00	0.48
5:S3:102:ALA:HB1	5:S3:173:ARG:CG	2.96	0.48
11:S9:61:THR:HA	24:D2:97:ARG:HH12	1.94	0.48
34:SR:278:PHE:O	87:SR:401:OHX:N3	2.81	0.48
36:1:1393:A:N3	36:1:1419:A:O2'	2.40	0.48
36:1:2707:C:H2'	36:1:2708:C:H6	1.79	0.48
36:1:633:C:O2'	69:O3:22:VAL:HA	2.14	0.48
1:2:1470:C:OP1	1:2:1540:G:O2'	2.31	0.48
1:2:1682:U:O2'	1:2:1683:C:H5'	2.13	0.48
1:2:231:U:O2'	1:2:232:U:H5''	2.14	0.48
1:2:463:U:H2'	1:2:464:A:H8	1.78	0.48
1:2:751:G:H2'	1:2:752:A:C8	2.48	0.48
1:2:93:A:H4'	1:2:94:U:OP2	2.14	0.48
38:4:45:C:OP1	75:O9:12:LYS:NZ	2.47	0.48
36:5:1478:C:H2'	36:5:1479:U:H6	1.77	0.48
36:5:1599:G:OP1	87:5:3987:OHX:N3	2.47	0.48
36:5:2772:C:H1'	36:5:2773:C:OP2	2.14	0.48
36:5:3181:C:H2'	36:5:3182:G:C8	2.49	0.48
22:D0:33:GLN:OE1	22:D0:33:GLN:N	2.64	0.48
22:D0:57:ARG:HG2	1:6:1382:A:H4'	446.91	0.48
27:D5:89:ILE:HB	27:D5:101:TYR:HB3	1.95	0.48
14:C2:74:LEU:HD21	33:E1:106:TYR:HB3	3.88	0.48
40:L3:81:THR:OG1	40:L3:321:PHE:HA	2.13	0.48
40:L3:43:LEU:HD11	40:L3:160:VAL:HG21	2.93	0.48
41:L4:136:LEU:O	41:L4:138:ARG:N	2.43	0.48
42:L5:261:THR:HG23	42:L5:264:GLN:HG3	1.95	0.48
44:L7:208:SER:O	44:L7:243:MET:HB3	2.14	0.48
36:1:290:G:H4'	51:M5:69:GLY:O	2.14	0.48
53:M7:24:VAL:HG12	53:M7:86:LYS:HG2	1.94	0.48
36:1:3070:A:OP1	55:M9:62:ARG:HD3	2.13	0.48
56:N0:77:VAL:HG11	56:N0:106:LEU:HG	4.66	0.48
57:N1:157:GLU:CD	57:N1:159:PHE:HE1	3.95	0.48
67:O1:41:LYS:HG3	67:O1:47:ASP:H	5.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:O3:52:VAL:HG21	69:O3:99:ARG:NH1	2.42	0.48
70:O4:71:THR:HG22	70:O4:72:VAL:O	2.14	0.48
2:S0:48:ILE:HG22	2:S0:49:ASN:H	2.36	0.48
6:S4:230:GLU:HB2	6:S4:233:LYS:NZ	6.69	0.48
6:S4:57:ASN:O	6:S4:61:VAL:HG23	2.14	0.48
8:S6:26:VAL:HG21	8:S6:40:ALA:HB1	1.96	0.48
36:1:1386:A:OP2	68:O2:80:LYS:NZ	2.47	0.48
36:1:13:A:OP1	87:1:4018:OHX:N5	2.46	0.48
36:1:2255:A:OP2	36:1:2261:G:N1	2.34	0.48
36:1:2520:A:H2'	36:1:2521:U:C6	2.47	0.48
36:1:2725:U:O4	87:1:3806:OHX:N2	2.47	0.48
36:1:2756:C:O4'	57:N1:49:GLN:HG2	2.14	0.48
36:1:3088:G:H2'	36:1:3089:C:C6	2.49	0.48
36:1:3160:U:H2'	36:1:3161:C:C6	2.48	0.48
1:2:1186:U:OP2	1:2:1456:C:H1'	2.14	0.48
1:2:1199:G:N7	31:D9:40:ARG:HD3	2.29	0.48
1:2:76:A:H8	87:2:2124:OHX:N1	2.11	0.48
1:2:463:U:H2'	1:2:464:A:C8	2.49	0.48
1:2:514:G:N1	1:2:543:C:H5	2.12	0.48
36:5:1560:G:HO2'	36:5:1561:G:P	2.36	0.48
36:5:22:G:H1'	38:8:104:A:N3	2.29	0.48
40:L3:154:TYR:CD1	36:5:3242:G:H2'	262.31	0.48
36:5:546:C:H4'	36:5:547:G:O5'	2.13	0.48
36:5:901:G:H2'	36:5:902:G:C8	2.46	0.48
19:C7:8:THR:HG21	1:6:1330:G:H21	422.08	0.48
1:6:1451:C:H2'	1:6:1452:U:C6	2.47	0.48
1:6:1698:G:O2'	1:6:1699:G:O5'	2.28	0.48
1:6:833:U:O4	87:6:2067:OHX:N2	2.46	0.48
13:C1:83:THR:HA	13:C1:111:VAL:H	2.20	0.48
14:C2:54:ARG:NH1	14:C2:56:GLU:OE2	2.51	0.48
25:D3:73:ARG:HH21	25:D3:84:THR:HG22	4.42	0.48
39:L2:17:THR:OG1	39:L2:18:SER:N	2.44	0.48
40:L3:204:ALA:O	40:L3:207:SER:HB3	4.05	0.48
42:L5:261:THR:N	42:L5:264:GLN:HB2	2.29	0.48
43:L6:52:VAL:CG1	43:L6:65:ILE:HG23	4.87	0.48
51:M5:27:VAL:HB	51:M5:122:ASN:HD21	1.79	0.48
53:M7:92:GLN:HA	53:M7:95:LEU:HB2	1.96	0.48
59:N3:6:ALA:HB1	59:N3:125:LEU:HD11	1.95	0.48
67:O1:80:ASN:OD1	67:O1:81:GLU:N	2.46	0.48
78:Q2:47:GLN:NE2	78:Q2:53:GLN:OE1	2.47	0.48
7:S5:222:LYS:HG3	7:S5:225:ARG:NH2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:S6:57:ASP:OD1	8:S6:72:ARG:NH1	2.47	0.48
34:SR:13:LEU:O	34:SR:309:VAL:HG13	2.13	0.48
34:SR:201:THR:HG21	34:SR:242:SER:HA	2.18	0.48
36:1:1602:A:H5''	55:M9:38:ARG:HG3	1.96	0.48
36:1:3306:U:H2'	36:1:3307:A:H5''	1.95	0.48
36:1:590:G:C2	36:1:610:G:H2'	2.49	0.48
36:1:767:U:H1'	36:1:768:C:C6	2.49	0.48
1:2:1106:U:H2'	1:2:1107:G:H8	1.78	0.48
1:2:1476:C:H2'	1:2:1477:G:H8	1.79	0.48
1:2:1535:U:O2'	1:2:1536:G:H5''	2.12	0.48
1:2:328:A:H2'	1:2:329:G:C8	2.48	0.48
1:2:478:A:O4'	11:S9:127:VAL:HG21	2.13	0.48
37:3:71:G:H2'	37:3:72:A:H8	1.78	0.48
36:5:2157:G:N1	36:5:2178:A:OP2	2.39	0.48
36:5:251:G:H1'	36:5:252:U:C2	2.49	0.48
51:M5:155:VAL:HG12	36:5:58:G:H4'	84.14	0.48
1:6:1054:U:O4	87:6:2181:OHX:N4	2.47	0.48
1:6:198:A:C2'	1:6:199:G:H5'	2.44	0.48
1:6:794:U:H4'	1:6:795:U:OP2	2.13	0.48
37:7:112:G:H2'	37:7:113:C:C6	2.49	0.48
57:N1:28:SER:OG	37:7:9:C:OP1	268.35	0.48
7:S5:26:ALA:HB3	18:C6:28:LEU:N	2.78	0.48
18:C6:52:LEU:HA	18:C6:60:PHE:CE1	3.11	0.48
22:D0:43:LYS:HA	22:D0:43:LYS:NZ	2.28	0.48
25:D3:56:LYS:O	25:D3:57:LEU:HD23	5.53	0.48
28:D6:41:ILE:HD12	28:D6:68:TYR:CD1	5.86	0.48
33:E1:135:HIS:ND1	33:E1:138:ARG:HD3	2.28	0.48
40:L3:339:ARG:NH1	40:L3:342:LEU:HD11	2.28	0.48
41:L4:166:VAL:O	41:L4:170:LYS:HG3	2.14	0.48
41:L4:72:ALA:HB3	41:L4:76:ARG:HH22	1.78	0.48
42:L5:195:LEU:O	42:L5:199:ILE:HG13	2.14	0.48
49:M3:50:PRO:HB2	49:M3:140:SER:O	2.14	0.48
53:M7:108:ASP:OD1	53:M7:111:LYS:HG3	2.13	0.48
53:M7:53:ASP:O	87:M7:205:OHX:N3	2.46	0.48
55:M9:101:VAL:O	55:M9:104:ARG:NH2	2.47	0.48
55:M9:105:LEU:HD12	55:M9:138:LEU:HD12	4.38	0.48
55:M9:7:GLN:HB3	55:M9:24:LEU:HD21	1.95	0.48
66:O0:17:VAL:HG11	66:O0:92:ILE:HD12	2.39	0.48
69:O3:6:ARG:HG3	69:O3:8:TYR:CD1	2.87	0.48
2:S0:50:VAL:O	2:S0:53:THR:HB	2.13	0.48
4:S2:213:ALA:HA	4:S2:216:VAL:HB	2.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S4:6:LYS:HE2	6:S4:6:LYS:HB2	4.44	0.48
8:S6:79:LYS:O	8:S6:80:ASN:HB2	2.48	0.48
36:1:1033:U:H2'	36:1:1034:U:C6	2.48	0.48
36:1:1080:A:OP1	42:L5:140:ARG:HD3	2.14	0.48
36:1:900:G:H1'	36:1:1589:A:H62	1.78	0.48
36:1:945:C:H2'	36:1:946:U:H6	1.79	0.48
36:1:980:A:H2	36:1:1104:G:HO2'	1.59	0.48
1:2:1291:G:H8	1:2:1291:G:O5'	1.96	0.48
1:2:1430:U:H1'	22:D0:72:ASN:HD22	1.78	0.48
1:2:1615:C:H4'	1:2:1616:G:O5'	2.14	0.48
1:2:189:C:N4	1:2:197:A:H2	2.11	0.48
1:2:217:A:OP1	1:2:217:A:H2'	2.14	0.48
1:2:938:G:N2	1:2:941:A:OP2	2.38	0.48
36:5:118:U:C5	36:5:119:U:C4	3.01	0.48
36:5:1667:A:H2'	36:5:1668:G:H8	1.75	0.48
39:L2:227:ARG:NH2	36:5:2155:G:O2'	206.53	0.48
36:5:646:A:C2	36:5:2375:G:C2	3.02	0.48
66:O0:50:VAL:HB	36:5:2553:U:O4'	230.90	0.48
36:5:2754:G:O2'	36:5:2755:C:OP1	2.29	0.48
36:5:1304:A:O2'	36:5:2884:C:O2	2.32	0.48
36:5:2890:A:N1	36:5:2913:C:N3	2.62	0.48
10:S8:172:ARG:NH2	1:6:331:A:N7	286.34	0.48
18:C6:112:TYR:O	18:C6:114:ARG:NH1	3.77	0.48
21:C9:135:ILE:O	21:C9:139:THR:OG1	2.19	0.48
22:D0:87:HIS:ND1	1:6:1383:G:OP1	443.43	0.48
2:S0:36:TYR:OH	23:D1:66:ASP:OD2	3.01	0.48
23:D1:72:LEU:HA	23:D1:75:ASN:HD21	1.79	0.48
26:D4:57:VAL:HB	26:D4:60:PHE:CZ	5.31	0.48
39:L2:44:ILE:HG12	39:L2:87:PHE:HE1	3.92	0.48
39:L2:4:VAL:HG12	39:L2:8:GLN:HG3	3.59	0.48
40:L3:305:ILE:HG12	40:L3:321:PHE:CE2	2.48	0.48
41:L4:292:SER:OG	41:L4:293:SER:N	2.45	0.48
36:1:1362:G:N3	44:L7:158:LYS:HE3	2.28	0.48
44:L7:47:ARG:NH2	44:L7:179:LEU:HD11	3.16	0.48
47:M0:200:LEU:HD12	47:M0:213:PHE:CB	4.57	0.48
49:M3:57:VAL:HG22	49:M3:147:ILE:HG23	1.96	0.48
51:M5:65:ARG:HB3	51:M5:127:TYR:CD1	2.48	0.48
36:1:1764:U:H5''	55:M9:43:LYS:HZ3	1.78	0.48
65:N9:26:THR:O	36:5:1065:A:N6	211.71	0.48
3:S1:124:ASN:HB3	3:S1:138:PHE:CD1	2.49	0.48
4:S2:103:VAL:HG22	4:S2:113:LEU:HD22	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:S2:170:ILE:HD12	1:6:2:A:C2	388.00	0.48
8:S6:12:SER:O	8:S6:13:GLN:HG3	4.40	0.48
9:S7:154:LEU:HD11	9:S7:183:PHE:CD1	2.49	0.48
10:S8:100:ALA:HB3	10:S8:169:ILE:HG12	3.07	0.48
34:SR:106:HIS:CE1	34:SR:126:SER:HB3	2.49	0.48
34:SR:192:PHE:HD1	34:SR:223:TRP:CE3	2.32	0.48
36:1:1027:A:H2'	36:1:1029:G:H5''	1.95	0.47
36:1:123:A:OP1	45:L8:105:LYS:NZ	2.40	0.47
36:1:1675:G:H2'	36:1:1676:A:C8	2.49	0.47
36:1:542:G:H2'	36:1:543:C:C6	2.49	0.47
1:2:1163:A:H2'	1:2:1164:G:O4'	2.13	0.47
1:2:1213:G:O6	87:2:1997:OHX:N3	2.47	0.47
42:L5:140:ARG:NH2	36:5:1080:A:OP2	230.98	0.47
36:5:200:C:H5'	36:5:221:A:C2	2.49	0.47
36:5:2542:U:H1'	36:5:2543:U:C5	2.49	0.47
36:5:3269:U:H5'	36:5:3271:G:O4'	2.14	0.47
87:5:3977:OHX:N5	87:5:4051:OHX:N2	2.62	0.47
64:N8:115:LYS:HD2	36:5:715:A:C8	151.25	0.47
1:6:1468:U:H2'	1:6:1469:A:O4'	2.13	0.47
1:6:27:U:H2'	1:6:28:A:H8	1.79	0.47
15:C3:74:ILE:O	15:C3:78:ASN:HB2	2.77	0.47
20:C8:36:LYS:HB3	20:C8:105:VAL:HG11	2.53	0.47
23:D1:39:VAL:HA	23:D1:45:ALA:HA	1.96	0.47
28:D6:38:ARG:N	28:D6:38:ARG:HD2	2.29	0.47
33:E1:146:SER:HB3	1:6:1234:A:H4'	436.26	0.47
40:L3:137:TYR:O	40:L3:139:GLN:N	2.48	0.47
41:L4:150:LEU:HD11	41:L4:172:VAL:HG22	1.96	0.47
43:L6:107:ALA:HB3	43:L6:109:GLU:OE2	2.13	0.47
47:M0:188:GLY:O	47:M0:190:VAL:N	2.47	0.47
50:M4:22:LEU:HD22	50:M4:94:TRP:CH2	2.70	0.47
50:M4:76:ALA:HB1	50:M4:80:THR:OG1	3.95	0.47
54:M8:158:HIS:H	54:M8:186:VAL:CG1	2.30	0.47
54:M8:72:LYS:HB3	54:M8:72:LYS:NZ	2.58	0.47
55:M9:130:ASN:O	55:M9:132:PHE:N	2.78	0.47
59:N3:10:LYS:NZ	59:N3:56:ASP:OD1	2.44	0.47
61:N5:108:LEU:N	61:N5:125:ARG:O	2.43	0.47
62:N6:71:SER:HB3	62:N6:83:ASP:HB2	3.70	0.47
66:O0:76:GLU:OE1	66:O0:76:GLU:N	2.45	0.47
72:O6:57:LEU:HD11	72:O6:73:ALA:HB2	1.96	0.47
74:O8:57:ASN:OD1	74:O8:57:ASN:N	4.36	0.47
79:Q3:27:LYS:HE2	79:Q3:31:ILE:HD11	4.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:Q3:56:THR:HB	79:Q3:63:THR:OG1	2.84	0.47
2:S0:87:LEU:HA	2:S0:87:LEU:HD12	1.79	0.47
4:S2:140:ARG:HH22	4:S2:228:ASN:HD21	1.62	0.47
4:S2:227:PRO:HA	4:S2:230:TRP:CD2	2.48	0.47
5:S3:101:GLN:O	5:S3:104:SER:HB3	2.13	0.47
8:S6:219:ARG:O	8:S6:223:LYS:HB2	2.13	0.47
10:S8:26:LYS:O	10:S8:29:LEU:HD22	2.40	0.47
34:SR:84:SER:OG	34:SR:85:TRP:N	2.55	0.47
36:1:109:A:H4'	36:1:110:G:OP1	2.14	0.47
36:1:1355:A:H1'	36:1:1356:U:OP2	2.14	0.47
36:1:1653:G:C2	36:1:1654:A:C4	3.02	0.47
36:1:1789:G:O6	87:1:4066:OHX:N4	2.47	0.47
1:2:1583:A:N1	1:2:1611:A:H5''	2.29	0.47
1:2:304:U:H2'	1:2:305:C:C6	2.49	0.47
36:5:2109:U:O2'	36:5:2110:G:H5'	2.14	0.47
36:5:2584:G:H5'	36:5:2585:G:OP2	2.14	0.47
36:5:1536:G:O6	87:5:3838:OHX:N2	2.46	0.47
1:6:1163:A:N3	1:6:1613:U:O2'	2.41	0.47
28:D6:79:ILE:HD11	1:6:1795:U:H5'	336.09	0.47
1:6:27:U:H2'	1:6:28:A:C8	2.49	0.47
24:D2:118:ARG:NH1	1:6:687:G:OP1	400.22	0.47
1:6:993:A:H2'	1:6:994:G:O4'	2.13	0.47
13:C1:75:VAL:HG12	13:C1:119:VAL:HA	1.94	0.47
16:C4:31:THR:HA	16:C4:39:ILE:HG12	2.09	0.47
18:C6:57:LEU:HD12	18:C6:57:LEU:H	4.30	0.47
19:C7:15:ALA:O	19:C7:19:ARG:HG2	2.14	0.47
22:D0:80:GLU:OE2	31:D9:54:LYS:NZ	2.91	0.47
29:D7:61:THR:OG1	29:D7:62:ILE:N	3.22	0.47
42:L5:209:GLU:HG2	42:L5:233:ALA:CB	2.44	0.47
42:L5:4:GLN:N	42:L5:4:GLN:OE1	2.39	0.47
44:L7:198:ALA:O	44:L7:201:PHE:HB3	2.25	0.47
48:M1:54:VAL:HB	48:M1:57:PHE:HB2	2.17	0.47
51:M5:146:ALA:HA	51:M5:149:ASN:ND2	2.39	0.47
51:M5:99:ARG:NH2	51:M5:166:ALA:HB3	2.64	0.47
53:M7:23:ARG:O	53:M7:86:LYS:HE2	2.51	0.47
55:M9:44:LEU:HB3	55:M9:49:THR:HB	1.96	0.47
55:M9:86:GLU:HG2	55:M9:91:SER:H	1.79	0.47
59:N3:37:ILE:HG12	59:N3:59:MET:O	2.14	0.47
59:N3:67:PRO:C	59:N3:69:LEU:H	2.61	0.47
59:N3:67:PRO:O	59:N3:69:LEU:N	3.38	0.47
60:N4:33:ASN:HD21	60:N4:35:LYS:HB3	3.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:N9:17:HIS:O	87:N9:101:OHX:N6	2.47	0.47
70:O4:71:THR:HG23	70:O4:77:GLY:HA3	1.96	0.47
75:O9:21:ARG:HH11	75:O9:24:PRO:HG3	1.77	0.47
2:S0:120:LEU:HD11	2:S0:144:ILE:HG12	3.23	0.47
3:S1:175:GLU:O	3:S1:187:LYS:NZ	2.33	0.47
4:S2:225:LEU:HD13	24:D2:68:ARG:HA	1.96	0.47
6:S4:61:VAL:HG12	6:S4:65:LEU:HD11	3.18	0.47
7:S5:57:SER:C	7:S5:59:VAL:H	2.15	0.47
36:1:1915:A:H5''	55:M9:84:THR:HG22	1.96	0.47
36:1:2881:C:H2'	36:1:2882:U:C6	2.47	0.47
36:1:2892:A:H2'	36:1:2893:C:H6	1.80	0.47
1:2:1474:G:H2'	1:2:1475:A:H8	1.78	0.47
1:2:371:G:O2'	24:D2:88:LYS:NZ	2.36	0.47
1:2:560:U:H2'	1:2:561:G:H8	1.77	0.47
37:3:76:A:OP2	87:3:209:OHX:N5	2.47	0.47
56:N0:90:MET:CG	36:5:1213:G:H4'	318.61	0.47
36:5:1664:G:H2'	36:5:1665:C:H6	1.79	0.47
70:O4:24:LYS:HE2	36:5:1669:C:OP1	157.25	0.47
36:5:1617:G:H1	36:5:1827:C:H42	1.62	0.47
36:5:1436:U:O2'	87:5:3895:OHX:N3	2.47	0.47
36:5:1009:A:OP2	87:5:4023:OHX:N2	2.48	0.47
1:6:319:U:H1'	1:6:323:A:C4	2.50	0.47
1:6:405:C:OP1	87:6:2022:OHX:N5	2.47	0.47
1:6:528:U:C2	1:6:529:A:C8	3.02	0.47
1:6:542:A:H1'	1:6:543:C:OP1	2.14	0.47
14:C2:66:VAL:HG11	14:C2:71:ILE:HD13	3.36	0.47
15:C3:11:ILE:O	15:C3:13:SER:N	2.47	0.47
15:C3:17:PRO:HB3	29:D7:28:PRO:HG3	3.21	0.47
18:C6:113:ASP:O	18:C6:114:ARG:NH1	2.48	0.47
19:C7:41:ILE:HD13	19:C7:47:ARG:HA	1.96	0.47
20:C8:84:TRP:O	1:6:1564:U:O2'	375.66	0.47
24:D2:15:ASN:ND2	24:D2:72:CYS:SG	2.85	0.47
26:D4:56:SER:HB3	26:D4:74:LEU:HD12	1.94	0.47
29:D7:14:SER:HB2	29:D7:17:ARG:HE	1.78	0.47
41:L4:8:VAL:HG22	41:L4:20:LEU:HD11	1.96	0.47
37:3:46:A:P	42:L5:158:ARG:HH11	2.37	0.47
42:L5:274:GLN:HE22	37:7:60:G:N2	332.87	0.47
45:L8:48:ARG:NH2	45:L8:49:TYR:HE2	2.66	0.47
47:M0:207:GLU:HB3	47:M0:211:ARG:HH12	4.90	0.47
47:M0:208:ASN:O	47:M0:212:GLU:HB2	2.47	0.47
48:M1:40:LEU:HD13	48:M1:79:ILE:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:M4:8:LYS:HB3	50:M4:9:ALA:H	1.43	0.47
56:N0:137:ARG:HG2	56:N0:139:TYR:CE1	2.53	0.47
58:N2:67:SER:OG	58:N2:68:THR:N	2.47	0.47
59:N3:3:GLY:HA2	59:N3:40:LYS:HB3	6.32	0.47
61:N5:91:ASN:O	61:N5:95:ILE:HG13	2.15	0.47
67:O1:96:VAL:O	67:O1:98:VAL:HG12	2.14	0.47
36:1:316:U:O2'	72:O6:30:LYS:HG3	2.14	0.47
2:S0:198:MET:SD	2:S0:199:PRO:HD2	2.85	0.47
4:S2:65:GLU:HB3	4:S2:67:GLN:OE1	2.82	0.47
6:S4:246:LEU:H	6:S4:246:LEU:HD12	2.36	0.47
6:S4:72:VAL:HB	6:S4:77:ARG:HG3	4.51	0.47
7:S5:136:ALA:HA	7:S5:201:ALA:O	2.14	0.47
9:S7:126:LEU:HB2	9:S7:173:TYR:CE2	5.13	0.47
9:S7:138:LYS:HD3	9:S7:150:GLN:HE22	7.23	0.47
10:S8:6:ASP:HB3	10:S8:28:GLU:OE2	2.14	0.47
11:S9:174:ARG:HH21	11:S9:177:ALA:HB2	1.79	0.47
36:1:1654:A:O2'	70:O4:59:PRO:HD3	2.15	0.47
36:1:1870:C:H4'	36:1:3076:C:O2	2.14	0.47
36:1:2855:U:OP2	47:M0:6:ALA:HB3	2.15	0.47
36:1:40:A:C2	64:N8:40:HIS:CE1	3.02	0.47
36:1:578:A:H2'	41:L4:334:PHE:CD2	2.49	0.47
1:2:1041:G:OP1	87:2:2123:OHX:N5	2.47	0.47
1:2:1663:G:C2	1:2:1664:C:C2	3.02	0.47
1:2:427:C:H2'	1:2:428:A:O4'	2.15	0.47
35:SM:48:ARG:HH11	36:5:1017:C:H5''	337.25	0.47
36:5:1621:A:H2'	36:5:1622:U:C6	2.49	0.47
36:5:2180:G:H2'	36:5:2181:C:C6	2.49	0.47
53:M7:69:ARG:NH2	36:5:2991:A:N3	195.71	0.47
36:5:832:G:OP1	87:5:3920:OHX:N3	2.48	0.47
1:6:1524:A:H2'	1:6:1525:A:C8	2.50	0.47
20:C8:41:ARG:HG3	1:6:1565:C:OP1	369.94	0.47
37:7:26:C:H2'	37:7:27:A:O4'	2.14	0.47
17:C5:25:LEU:HA	17:C5:28:MET:HE2	3.27	0.47
17:C5:30:THR:O	17:C5:34:VAL:HG13	2.29	0.47
21:C9:118:PRO:O	21:C9:120:GLY:N	2.44	0.47
21:C9:49:ASP:O	21:C9:53:TRP:HD1	4.29	0.47
21:C9:6:VAL:HB	21:C9:14:PHE:CE1	2.59	0.47
25:D3:109:ARG:HB3	25:D3:112:LYS:HB2	1.96	0.47
44:L7:66:LYS:O	44:L7:70:LYS:HB2	2.14	0.47
46:L9:84:LYS:HE2	46:L9:191:LEU:HB3	1.94	0.47
52:M6:113:ASP:OD2	52:M6:114:LYS:HG3	5.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:M7:179:GLN:HA	53:M7:182:ILE:HB	1.96	0.47
61:N5:65:GLN:HE21	71:O5:36:LEU:HD22	8.32	0.47
62:N6:39:LEU:HD22	62:N6:43:TYR:CE2	3.66	0.47
70:O4:81:CYS:SG	70:O4:84:CYS:SG	3.17	0.47
71:O5:38:ARG:HD2	71:O5:41:LEU:HD13	1.94	0.47
71:O5:86:ARG:O	71:O5:90:ARG:HG2	2.14	0.47
74:O8:12:LEU:O	74:O8:15:THR:OG1	2.35	0.47
79:Q3:16:VAL:HA	36:5:1927:G:C8	239.26	0.47
79:Q3:56:THR:HA	79:Q3:63:THR:HA	2.34	0.47
2:S0:185:ARG:HB2	23:D1:45:ALA:HB3	1.96	0.47
4:S2:35:TRP:NE1	4:S2:37:PRO:HB3	2.29	0.47
6:S4:106:LYS:HB2	6:S4:108:ARG:HG3	2.62	0.47
6:S4:29:PRO:O	6:S4:30:ARG:HB3	4.62	0.47
6:S4:92:LEU:HB2	6:S4:95:THR:HG22	5.94	0.47
7:S5:21:THR:OG1	7:S5:21:THR:O	2.32	0.47
9:S7:82:GLU:OE2	9:S7:90:VAL:N	2.46	0.47
10:S8:7:SER:O	10:S8:10:LYS:HB2	3.80	0.47
11:S9:129:ILE:HA	11:S9:134:ILE:HG12	3.03	0.47
36:1:1103:A:N6	36:1:1363:A:H1'	2.30	0.47
36:1:1301:A:H4'	36:1:1302:A:O5'	2.14	0.47
36:1:2592:G:H4'	36:1:2594:C:C2	2.49	0.47
36:1:2993:G:H2'	36:1:3142:A:N6	2.29	0.47
36:1:3275:U:H5'	69:O3:68:TRP:CZ2	2.41	0.47
36:1:2111:G:O6	36:1:3333:G:H3'	2.14	0.47
36:1:544:C:H1'	36:1:548:G:H22	1.78	0.47
36:1:692:A:C4	36:1:693:A:C8	3.03	0.47
36:1:979:U:C2	36:1:980:A:C4	3.02	0.47
1:2:1032:G:C6	1:2:1104:U:C4	3.03	0.47
1:2:1655:A:N1	36:1:2291:A:O2'	2.36	0.47
1:2:1699:G:H2'	1:2:1700:C:H5''	1.97	0.47
1:2:40:A:O2'	87:2:2052:OHX:N5	2.47	0.47
1:2:552:G:C6	1:2:553:G:C6	3.03	0.47
36:5:196:G:N2	36:5:198:A:H3'	2.29	0.47
36:5:212:G:C6	36:5:222:A:C5	3.03	0.47
36:5:3006:A:H2'	36:5:3007:U:O4'	2.15	0.47
36:5:2997:G:H1'	36:5:3396:U:H5'	1.95	0.47
36:5:401:U:O2'	36:5:402:A:OP1	2.29	0.47
36:5:419:G:O3'	36:5:420:G:H5'	2.15	0.47
1:6:1166:A:H2'	1:6:1167:G:O4'	2.14	0.47
2:S0:109:ASN:HB2	1:6:1294:G:H4'	415.66	0.47
1:6:1398:U:H4'	1:6:1399:C:OP2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1638:G:C2	1:6:1639:C:H1'	2.49	0.47
38:8:53:A:H2'	38:8:54:A:H8	1.79	0.47
14:C2:97:LEU:HD11	14:C2:121:VAL:HG22	1.97	0.47
15:C3:67:THR:O	15:C3:69:ASN:N	2.48	0.47
17:C5:21:ASP:O	17:C5:24:LYS:N	2.81	0.47
4:S2:62:PRO:HB3	23:D1:29:HIS:HD2	1.77	0.47
32:E0:49:LEU:H	32:E0:49:LEU:HD22	3.57	0.47
42:L5:144:VAL:HG12	42:L5:173:VAL:HG22	1.94	0.47
42:L5:69:ILE:HD12	42:L5:69:ILE:H	4.95	0.47
45:L8:100:GLU:OE1	45:L8:108:ARG:HD3	2.79	0.47
45:L8:37:GLY:HA3	36:5:2550:U:C6	212.68	0.47
51:M5:11:GLN:HG2	51:M5:44:ARG:HH21	1.80	0.47
36:1:534:U:O2	56:N0:146:LYS:HA	2.15	0.47
56:N0:91:TYR:OH	56:N0:93:GLU:OE2	2.27	0.47
60:N4:36:SER:O	60:N4:40:PHE:N	2.42	0.47
61:N5:50:ALA:HB2	71:O5:79:ASP:HB3	5.63	0.47
63:N7:53:VAL:HA	63:N7:57:HIS:CD2	2.49	0.47
67:O1:10:ARG:HH12	67:O1:44:MET:HG2	4.96	0.47
38:4:49:G:OP2	71:O5:48:ARG:NH1	2.48	0.47
2:S0:14:ALA:O	2:S0:18:LEU:HG	2.15	0.47
3:S1:22:ASP:O	3:S1:25:THR:OG1	4.66	0.47
4:S2:179:VAL:HG12	1:6:3:U:H5'	393.64	0.47
2:S0:110:TYR:HE2	4:S2:64:LYS:HD2	6.12	0.47
5:S3:105:MET:HG2	5:S3:122:VAL:HG21	2.17	0.47
5:S3:217:ILE:C	5:S3:219:ALA:H	4.38	0.47
6:S4:34:GLY:HA3	6:S4:35:PRO:HD3	1.64	0.47
8:S6:137:ARG:O	8:S6:141:ILE:HG13	2.52	0.47
10:S8:114:GLU:HG2	10:S8:120:THR:HA	1.97	0.47
34:SR:224:ASN:O	34:SR:228:LYS:HA	2.81	0.47
36:1:953:G:C8	36:1:1117:G:C8	3.03	0.47
36:1:1346:G:C6	36:1:1347:U:C4	3.02	0.47
36:1:1549:U:H2'	36:1:1550:C:C6	2.49	0.47
36:1:407:A:C2	38:4:17:A:H1'	2.49	0.47
36:1:846:A:H2'	36:1:847:A:O4'	2.14	0.47
1:2:1087:A:H2	1:2:1142:A:H4'	1.79	0.47
1:2:1125:A:C5	1:2:1126:G:H1'	2.50	0.47
1:2:1292:G:H2'	1:2:1293:U:C6	2.50	0.47
1:2:1727:G:H2'	1:2:1728:A:C8	2.49	0.47
37:3:77:G:P	56:N0:50:LYS:HG2	2.55	0.47
36:5:1317:A:O2'	36:5:1318:A:H3'	2.14	0.47
36:5:130:A:H61	36:5:138:U:H3	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L4:44:LYS:NZ	36:5:1427:U:OP1	128.12	0.47
36:5:2628:A:H1'	36:5:2798:C:C2	2.50	0.47
87:5:4001:OHX:N6	87:5:4119:OHX:N4	2.63	0.47
36:5:436:A:H61	36:5:623:U:H3	1.63	0.47
1:6:1639:C:H2'	1:6:1640:C:O4'	2.14	0.47
1:6:1202:A:OP1	87:6:2096:OHX:N1	2.48	0.47
1:6:25:C:H4'	1:6:25:C:OP2	2.15	0.47
1:6:138:A:N6	1:6:266:A:H61	2.11	0.47
1:6:542:A:O2'	1:6:543:C:O5'	2.25	0.47
1:6:582:U:H5'	1:6:582:U:H6	1.80	0.47
61:N5:56:ARG:HG3	38:8:134:G:OP1	79.64	0.47
12:C0:14:TYR:CZ	12:C0:18:GLU:HG3	2.50	0.47
16:C4:25:ASP:OD1	16:C4:26:THR:N	2.55	0.47
17:C5:22:LEU:HD21	17:C5:109:PRO:HB3	1.96	0.47
20:C8:126:ARG:HG2	20:C8:133:VAL:HA	1.96	0.47
22:D0:41:ILE:HG13	22:D0:107:THR:HG21	3.92	0.47
23:D1:9:VAL:HG22	23:D1:10:GLU:H	2.07	0.47
23:D1:16:LYS:HG2	23:D1:21:ASN:HA	1.95	0.47
28:D6:10:ARG:CB	28:D6:34:LYS:HA	2.45	0.47
40:L3:116:ARG:NH2	40:L3:174:LYS:HD3	2.30	0.47
41:L4:219:LEU:O	41:L4:221:ASN:N	3.33	0.47
41:L4:311:HIS:CE1	41:L4:314:LYS:HA	3.00	0.47
42:L5:267:ALA:HA	42:L5:271:LYS:HE3	7.59	0.47
45:L8:54:GLU:HG3	45:L8:57:ARG:NH1	2.30	0.47
45:L8:97:TYR:O	45:L8:132:VAL:HG13	3.67	0.47
47:M0:160:PRO:HB3	36:5:2854:U:O3'	291.04	0.47
37:3:44:C:OP2	48:M1:137:ARG:NH2	2.48	0.47
36:1:560:G:H4'	50:M4:73:PRO:HG2	1.97	0.47
56:N0:46:GLN:HG3	56:N0:51:VAL:O	3.29	0.47
59:N3:129:VAL:O	59:N3:133:SER:OG	2.33	0.47
60:N4:63:ILE:C	60:N4:65:GLU:H	3.08	0.47
62:N6:73:VAL:HA	62:N6:80:VAL:HG23	1.97	0.47
69:O3:26:ASN:HA	69:O3:88:ASN:ND2	2.63	0.47
36:1:1833:G:OP1	75:O9:10:LYS:HD2	2.15	0.47
2:S0:10:THR:OG1	2:S0:13:ASP:OD2	2.33	0.47
2:S0:30:GLN:OE1	2:S0:31:VAL:N	6.07	0.47
2:S0:69:ASN:HB3	2:S0:71:GLU:CD	2.35	0.47
5:S3:220:PRO:O	5:S3:221:SER:OG	2.36	0.47
6:S4:163:ASP:O	6:S4:165:ALA:N	2.38	0.47
6:S4:212:ASP:OD2	6:S4:216:ASN:HB2	2.14	0.47
7:S5:121:ILE:HG13	7:S5:195:ALA:HB1	2.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1897:G:H2'	36:1:1898:G:O4'	2.15	0.47
36:1:1936:A:H2'	36:1:1937:U:O4'	2.15	0.47
36:1:2616:C:C2'	36:1:2617:U:H5'	2.44	0.47
1:2:1524:A:H2'	1:2:1525:A:H8	1.78	0.47
37:3:62:U:O4	37:3:63:A:N6	2.47	0.47
36:5:114:A:N1	36:5:266:A:O2'	2.39	0.47
36:5:1725:C:H2'	36:5:1726:C:C6	2.50	0.47
36:5:289:A:H2'	36:5:290:G:H8	1.79	0.47
36:5:3112:G:O6	36:5:3120:C:H5''	2.14	0.47
36:5:3268:A:O2'	36:5:3269:U:H2'	2.15	0.47
36:5:8:C:H2'	36:5:9:U:O4'	2.14	0.47
1:6:1762:A:H1'	1:6:1783:C:OP1	2.14	0.47
1:6:512:A:H2'	1:6:513:U:H6	1.80	0.47
1:6:675:U:H2'	1:6:676:G:C8	2.50	0.47
8:S6:173:PRO:O	1:6:79:C:H4'	345.64	0.47
12:C0:38:LYS:O	12:C0:41:TYR:HB2	2.66	0.47
21:C9:89:ARG:HB3	21:C9:90:PRO:HD2	1.97	0.47
23:D1:17:CYS:HB2	23:D1:56:SER:HB3	1.97	0.47
25:D3:3:LYS:HB2	25:D3:7:ARG:HH21	9.75	0.47
26:D4:125:LEU:HD12	26:D4:128:LYS:HD2	5.21	0.47
26:D4:29:HIS:CE1	26:D4:34:ASN:H	2.32	0.47
26:D4:50:ALA:O	26:D4:51:GLU:HB3	2.55	0.47
1:2:1236:A:H1'	33:E1:138:ARG:HH12	1.80	0.47
42:L5:84:PRO:O	42:L5:87:GLY:N	2.27	0.47
43:L6:98:VAL:HA	43:L6:101:PHE:CD2	2.51	0.47
51:M5:93:LYS:NZ	36:5:2600:C:OP1	157.02	0.47
36:1:784:A:C6	54:M8:93:ILE:HG22	2.49	0.47
42:L5:42:ALA:HB2	57:N1:67:VAL:HG12	2.53	0.47
70:O4:85:VAL:HA	70:O4:88:ARG:HB2	4.56	0.47
72:O6:55:ARG:O	72:O6:58:ILE:HD13	2.14	0.47
74:O8:38:PHE:CE1	74:O8:57:ASN:HB3	5.69	0.47
79:Q3:49:ARG:HD3	79:Q3:51:ALA:C	3.02	0.47
3:S1:172:LEU:O	3:S1:176:VAL:HG23	2.15	0.47
3:S1:110:LEU:HD11	3:S1:213:ARG:HD2	3.94	0.47
3:S1:140:ILE:HG21	3:S1:213:ARG:HD3	1.96	0.47
7:S5:43:PHE:HD2	7:S5:46:TRP:CD1	6.18	0.47
9:S7:133:THR:HB	9:S7:134:GLU:H	1.56	0.47
34:SR:123:ILE:HD13	34:SR:169:ILE:HG21	2.40	0.47
36:1:2193:U:O2	36:1:2193:U:H2'	2.14	0.47
36:1:224:C:O2	62:N6:103:LYS:NZ	2.48	0.47
36:1:2419:A:H1'	36:1:2804:A:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:728:G:OP1	87:1:3996:OHX:N3	2.47	0.47
1:2:1288:G:H1	1:2:1327:C:H42	1.61	0.47
1:2:1490:C:H4'	1:2:1491:U:OP1	2.15	0.47
1:2:344:A:C6	1:2:345:U:C4	3.02	0.47
1:2:610:G:H2'	1:2:614:C:C5	2.50	0.47
1:2:862:A:H4'	1:2:863:A:O5'	2.15	0.47
56:N0:112:ALA:HB1	36:5:1186:G:N3	298.66	0.47
36:5:1329:U:O2'	36:5:1330:A:OP1	2.30	0.47
36:5:1367:G:HO2'	36:5:1368:U:H6	1.61	0.47
36:5:1856:C:H2'	36:5:1857:C:C6	2.50	0.47
36:5:2581:U:H2'	36:5:2582:C:C6	2.49	0.47
35:SM:33:LYS:HD2	36:5:2667:A:H5''	287.70	0.47
36:5:2677:G:H3'	36:5:2678:A:H5''	1.96	0.47
64:N8:36:GLY:N	36:5:40:A:OP2	174.78	0.47
36:5:65:A:H4'	36:5:66:A:O5'	2.15	0.47
36:5:777:U:O4	87:5:3996:OHX:N1	2.48	0.47
1:6:1688:U:H2'	1:6:1689:A:C8	2.50	0.47
1:6:396:G:N2	1:6:399:A:OP2	2.46	0.47
1:6:84:A:H2'	1:6:85:A:O4'	2.15	0.47
1:6:947:U:H2'	1:6:948:G:H8	1.80	0.47
42:L5:269:SER:CB	37:7:1:G:H21	318.94	0.47
42:L5:272:TYR:CZ	37:7:22:A:H1'	334.72	0.47
56:N0:50:LYS:HE3	37:7:77:G:O4'	301.18	0.47
13:C1:34:TRP:CZ2	13:C1:36:LYS:HB3	3.44	0.47
14:C2:63:VAL:HG11	14:C2:94:ALA:HA	1.97	0.47
24:D2:72:CYS:HB3	24:D2:129:VAL:HG13	1.95	0.47
25:D3:109:ARG:NH2	25:D3:112:LYS:HD2	7.38	0.47
25:D3:109:ARG:NH2	25:D3:114:LYS:O	2.37	0.47
40:L3:122:TRP:CZ2	40:L3:127:LYS:HE3	2.50	0.47
42:L5:181:PRO:HD2	42:L5:195:LEU:HD13	2.81	0.47
44:L7:142:SER:O	44:L7:146:GLN:HG3	2.15	0.47
47:M0:63:GLU:H	47:M0:63:GLU:HG2	1.42	0.47
49:M3:54:LEU:HD22	49:M3:54:LEU:HA	2.67	0.47
50:M4:32:LEU:HD21	50:M4:94:TRP:CE2	2.88	0.47
51:M5:172:ARG:HD2	36:5:30:G:O5'	112.01	0.47
51:M5:84:PRO:HA	51:M5:87:GLN:HB2	2.61	0.47
52:M6:73:PHE:HD1	36:5:3007:U:H5'	246.71	0.47
53:M7:169:THR:HG23	69:O3:60:ARG:NH1	2.30	0.47
61:N5:139:ILE:HD11	61:N5:141:TYR:CE2	2.49	0.47
2:S0:172:LEU:HD22	2:S0:176:LEU:HG	2.23	0.47
2:S0:71:GLU:HA	2:S0:95:ALA:N	3.16	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:S2:87:GLN:HA	4:S2:95:ARG:O	2.14	0.47
6:S4:131:LEU:HD22	6:S4:137:PRO:HB3	1.97	0.47
6:S4:146:THR:HG21	1:6:123:G:N2	342.82	0.47
9:S7:177:THR:OG1	9:S7:178:GLY:N	2.57	0.47
11:S9:44:ARG:HG2	11:S9:45:ILE:HD13	3.07	0.47
11:S9:92:LYS:HB2	11:S9:95:TYR:HD2	8.34	0.47
36:1:993:G:C5	36:1:2637:A:C2	3.03	0.47
36:1:1132:C:H4'	36:1:2865:U:O2'	2.14	0.47
36:1:437:G:H2'	36:1:438:A:C8	2.49	0.47
1:2:1278:G:H2'	1:2:1279:C:O4'	2.15	0.47
1:2:1410:A:H5''	18:C6:118:ILE:HD13	1.96	0.47
1:2:401:A:O2'	1:2:402:C:H4'	2.14	0.47
1:2:740:A:H2'	1:2:741:C:H5''	1.97	0.47
53:M7:139:TYR:CE1	36:5:1507:G:H1'	145.27	0.47
36:5:2267:C:H2'	36:5:2268:U:H6	1.78	0.47
36:5:2674:A:OP2	87:5:4069:OHX:N4	2.48	0.47
1:6:1769:U:OP2	87:6:2111:OHX:N2	2.48	0.47
1:6:345:U:H1'	1:6:346:G:C8	2.50	0.47
1:6:366:A:OP1	1:6:758:U:O2'	2.22	0.47
8:S6:175:ILE:HG12	1:6:78:A:H1'	339.74	0.47
14:C2:81:ASP:O	14:C2:83:GLU:N	2.52	0.47
21:C9:73:VAL:HA	21:C9:76:LEU:HD12	1.96	0.47
25:D3:86:PHE:O	25:D3:124:VAL:HG23	2.14	0.47
25:D3:78:LYS:HG3	25:D3:79:ASN:HD22	2.74	0.47
11:S9:142:ASN:HD21	26:D4:64:PHE:HZ	1.62	0.47
30:D8:15:VAL:HA	30:D8:28:VAL:HG23	2.85	0.47
39:L2:105:GLY:HA2	39:L2:139:HIS:CE1	3.07	0.47
40:L3:183:LEU:O	40:L3:191:LYS:NZ	3.40	0.47
42:L5:201:GLY:O	42:L5:203:HIS:N	2.48	0.47
42:L5:85:ARG:HD3	42:L5:86:TYR:CZ	2.50	0.47
43:L6:52:VAL:HG13	43:L6:67:GLY:HA2	4.71	0.47
44:L7:123:THR:O	44:L7:126:LEU:HB2	2.13	0.47
44:L7:229:PHE:CD1	44:L7:229:PHE:C	3.06	0.47
36:1:517:G:P	44:L7:60:ARG:HH12	2.38	0.47
46:L9:92:TYR:CD1	46:L9:92:TYR:N	2.83	0.47
47:M0:36:LEU:HD13	47:M0:87:LEU:HD13	1.97	0.47
56:N0:23:LYS:O	56:N0:24:LEU:HB2	2.14	0.47
58:N2:20:SER:O	58:N2:24:GLU:HG2	2.14	0.47
59:N3:101:VAL:HG21	59:N3:109:MET:HG2	4.80	0.47
61:N5:106:ASP:HB2	61:N5:130:TYR:CE1	3.16	0.47
61:N5:49:LYS:O	61:N5:51:VAL:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:O3:54:ARG:HG2	69:O3:64:ILE:HD13	5.66	0.47
71:O5:64:GLU:HA	71:O5:67:ARG:HB3	1.97	0.47
39:L2:83:HIS:HB3	79:Q3:64:VAL:HG22	1.95	0.47
2:S0:103:THR:O	2:S0:106:SER:OG	2.31	0.47
3:S1:33:LYS:HD2	3:S1:95:ASN:HD21	1.79	0.47
4:S2:148:LEU:HA	23:D1:4:ASP:HB2	2.35	0.47
5:S3:167:PHE:CE1	5:S3:192:PRO:HB3	2.50	0.47
6:S4:18:TRP:HH2	6:S4:31:PRO:HD3	2.10	0.47
8:S6:58:LYS:HG2	8:S6:105:ASP:O	2.15	0.47
9:S7:133:THR:HG21	9:S7:162:ILE:HD11	1.97	0.47
34:SR:133:VAL:HG12	34:SR:141:LEU:HB2	1.97	0.47
36:1:1571:A:H2'	36:1:1572:U:O4'	2.15	0.47
36:1:2144:A:H1'	36:1:2281:A:N6	2.30	0.47
36:1:2663:G:H4'	42:L5:152:ARG:NH1	2.30	0.47
36:5:1680:G:H2'	36:5:1681:U:C6	2.50	0.47
57:N1:4:SER:HB3	36:5:2631:U:OP2	240.27	0.47
36:5:274:G:H2'	36:5:275:U:O4'	2.14	0.47
36:5:2274:U:OP2	87:5:3898:OHX:N6	2.48	0.47
36:5:359:U:H4'	36:5:817:A:N6	2.30	0.47
28:D6:97:PRO:HG2	1:6:1799:U:H3'	345.48	0.47
1:6:183:U:H2'	1:6:184:C:O4'	2.15	0.47
1:6:217:A:O2'	1:6:218:A:H8	1.97	0.47
1:6:481:A:H61	1:6:507:U:H3	1.63	0.47
1:6:747:C:H2'	1:6:748:U:C6	2.50	0.47
1:6:914:G:H5'	1:6:914:G:H8	1.80	0.47
12:C0:60:SER:O	12:C0:62:GLN:N	2.48	0.47
15:C3:136:PRO:HA	15:C3:137:PRO:HD2	1.67	0.47
15:C3:23:PRO:HG2	15:C3:26:PHE:HB2	2.20	0.47
16:C4:84:ARG:HG2	16:C4:85:ALA:O	2.14	0.47
17:C5:90:ILE:HG21	17:C5:109:PRO:HG3	4.05	0.47
23:D1:18:SER:OG	23:D1:54:ALA:O	2.33	0.47
24:D2:31:SER:O	24:D2:35:ILE:HG12	2.14	0.47
26:D4:57:VAL:HG12	26:D4:73:GLY:HA3	6.48	0.47
41:L4:232:SER:O	41:L4:233:LEU:HB2	2.13	0.47
44:L7:168:ILE:HG13	44:L7:168:ILE:H	2.04	0.47
46:L9:155:SER:O	46:L9:158:ALA:HB3	2.15	0.47
46:L9:169:ASN:O	46:L9:170:LYS:HE3	2.15	0.47
49:M3:131:LYS:HG3	49:M3:132:ALA:H	1.79	0.47
50:M4:127:LYS:O	50:M4:131:VAL:HG23	2.54	0.47
50:M4:20:VAL:HG13	50:M4:68:LEU:O	2.97	0.47
50:M4:108:ARG:NH2	52:M6:196:ALA:O	2.76	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:M7:30:ARG:HA	53:M7:119:VAL:CG1	2.62	0.47
53:M7:97:ASN:O	53:M7:101:ASN:ND2	2.47	0.47
61:N5:129:ASP:HB2	61:N5:130:TYR:CD1	2.50	0.47
68:O2:20:HIS:CG	68:O2:42:VAL:HG21	2.49	0.47
70:O4:41:ARG:HA	70:O4:56:THR:HG22	2.72	0.47
3:S1:105:PHE:HB3	3:S1:110:LEU:HD11	1.97	0.47
3:S1:99:ASN:OD1	3:S1:100:PHE:N	2.48	0.47
4:S2:49:LYS:HD2	4:S2:243:TYR:CE1	3.40	0.47
5:S3:37:VAL:HG12	5:S3:50:ILE:HD13	1.97	0.47
7:S5:62:VAL:HG13	7:S5:89:ILE:HG21	1.96	0.47
8:S6:31:ARG:HH21	8:S6:101:ILE:HD11	4.93	0.47
8:S6:88:ARG:HG3	8:S6:91:GLU:HB2	5.10	0.47
11:S9:136:VAL:O	11:S9:155:HIS:HB3	2.15	0.47
11:S9:59:LEU:HD22	11:S9:69:ARG:HA	2.89	0.47
36:1:1894:U:O2'	36:1:3054:U:OP1	2.31	0.47
36:1:1881:A:OP2	87:1:3900:OHX:N1	2.48	0.47
36:1:3010:U:OP2	87:1:4087:OHX:N5	2.48	0.47
36:1:822:G:H1'	39:L2:15:ILE:HG22	1.96	0.47
36:1:871:U:H2'	36:1:872:U:C6	2.50	0.47
1:2:505:A:H3'	1:2:506:A:C5'	2.44	0.47
1:2:610:G:H2'	1:2:614:C:C6	2.50	0.47
1:2:995:A:H2'	1:2:996:U:O4'	2.15	0.47
38:4:107:G:OP2	87:4:228:OHX:N6	2.48	0.47
67:O1:28:ARG:NH2	36:5:3058:U:OP1	186.19	0.47
36:5:3095:U:H2'	36:5:3096:C:H6	1.80	0.47
36:5:728:G:OP1	87:5:4130:OHX:N4	2.48	0.47
36:5:594:U:H5''	36:5:609:G:O6	2.15	0.47
1:6:138:A:H62	1:6:266:A:N6	2.12	0.47
1:6:1478:G:C4	1:6:1479:A:C8	3.03	0.47
1:6:1648:A:H2'	1:6:1649:G:C8	2.50	0.47
13:C1:91:LEU:HB3	13:C1:100:TYR:HB3	1.96	0.47
13:C1:97:TYR:CD1	25:D3:15:LEU:HB3	2.85	0.47
1:2:917:U:O2	16:C4:41:ARG:NH1	2.46	0.47
39:L2:149:ARG:HH12	39:L2:155:LYS:HD3	1.80	0.47
39:L2:209:HIS:ND1	39:L2:210:PRO:HD2	2.30	0.47
36:1:3137:C:H5''	40:L3:276:THR:HG21	1.96	0.47
40:L3:284:ARG:NH2	40:L3:295:ALA:O	2.46	0.47
41:L4:337:GLU:O	41:L4:339:LEU:N	2.43	0.47
42:L5:95:TRP:CZ2	42:L5:181:PRO:HD3	3.89	0.47
42:L5:209:GLU:HG2	42:L5:233:ALA:HB3	1.97	0.47
44:L7:24:GLU:O	44:L7:26:VAL:N	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:M3:57:VAL:N	49:M3:112:ASN:OD1	2.43	0.47
52:M6:85:ARG:HD3	52:M6:90:HIS:ND1	3.55	0.47
53:M7:67:ILE:HG13	53:M7:82:ARG:CZ	2.45	0.47
36:1:840:C:H4'	55:M9:128:LYS:HD3	1.96	0.47
55:M9:81:ARG:HG2	55:M9:88:ARG:CZ	2.45	0.47
59:N3:109:MET:HG3	59:N3:132:ASN:ND2	2.30	0.47
59:N3:30:GLY:HA3	59:N3:66:LYS:HD2	1.97	0.47
63:N7:3:LYS:O	63:N7:5:LEU:N	2.48	0.47
66:O0:13:LYS:HB3	66:O0:100:ILE:HG22	1.97	0.47
71:O5:85:THR:O	71:O5:89:ARG:HB2	2.14	0.47
73:O7:52:LYS:O	73:O7:55:ARG:HB3	2.14	0.47
79:Q3:6:LYS:HG2	79:Q3:7:LYS:HG3	4.90	0.47
2:S0:33:GLN:NE2	23:D1:63:GLY:O	2.48	0.47
4:S2:143:TYR:CD2	4:S2:147:ASN:HA	4.01	0.47
5:S3:209:ILE:O	19:C7:20:TYR:OH	2.23	0.47
7:S5:20:PHE:CE1	7:S5:34:GLN:HB3	4.23	0.47
36:1:1331:U:H4'	36:1:1332:A:OP2	2.14	0.46
36:1:1577:G:H2'	36:1:1578:C:O4'	2.15	0.46
36:1:1951:C:H3'	36:1:1952:G:C8	2.50	0.46
36:1:216:G:H4'	62:N6:19:TYR:CZ	2.50	0.46
36:1:2618:G:N3	65:N9:3:LYS:NZ	2.63	0.46
36:1:677:A:H4'	36:1:678:G:O5'	2.15	0.46
1:2:1600:A:O2'	1:2:1602:C:N4	2.49	0.46
1:2:365:G:N7	87:2:2074:OHX:N5	2.63	0.46
1:2:802:G:H21	24:D2:107:SER:HB3	1.80	0.46
1:2:851:U:H2'	1:2:852:C:C6	2.51	0.46
1:2:891:A:H2'	1:2:892:A:C8	2.50	0.46
36:5:143:G:OP2	87:5:3932:OHX:N1	2.48	0.46
51:M5:4:TYR:OH	36:5:148:G:OP2	110.74	0.46
36:5:19:U:H3	38:8:140:G:H1	1.63	0.46
36:5:2304:C:C5	36:5:2305:G:C6	3.03	0.46
36:5:2344:U:H2'	36:5:2345:A:H8	1.79	0.46
57:N1:71:SER:OG	36:5:2736:A:O3'	232.05	0.46
54:M8:176:ARG:NH2	36:5:2762:A:O2'	188.03	0.46
36:5:3284:G:OP2	36:5:3284:G:H8	1.98	0.46
36:5:3351:U:H5'	36:5:3352:U:OP2	2.15	0.46
36:5:1947:G:N7	87:5:4104:OHX:N6	2.63	0.46
36:5:979:U:C2	36:5:980:A:C2	3.04	0.46
1:6:1537:C:N3	87:6:2124:OHX:N4	2.62	0.46
11:S9:2:PRO:HB3	1:6:381:C:OP1	361.02	0.46
1:6:460:A:H3'	1:6:461:G:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:504:U:O4	1:6:505:A:N6	2.48	0.46
1:6:539:G:OP2	1:6:539:G:H8	1.98	0.46
37:7:94:C:H2'	37:7:95:A:H8	1.78	0.46
13:C1:8:GLN:OE1	13:C1:14:GLN:N	2.48	0.46
21:C9:105:LEU:HD13	21:C9:122:ARG:HD3	2.22	0.46
2:S0:185:ARG:HG3	23:D1:47:PRO:HD3	1.96	0.46
28:D6:82:ARG:O	28:D6:84:VAL:HG12	2.14	0.46
30:D8:12:VAL:HG22	30:D8:28:VAL:HG11	1.96	0.46
39:L2:113:VAL:HG22	39:L2:134:VAL:HG22	1.96	0.46
41:L4:138:ARG:HH21	41:L4:240:PRO:HG2	2.12	0.46
41:L4:60:THR:HG23	36:5:364:G:OP1	130.28	0.46
43:L6:49:GLY:O	43:L6:163:PHE:N	3.50	0.46
44:L7:216:VAL:HG21	44:L7:219:LYS:HA	1.95	0.46
44:L7:66:LYS:HG3	44:L7:76:TYR:HD2	1.79	0.46
35:SM:39:PRO:HD3	48:M1:52:TYR:CE1	3.17	0.46
49:M3:64:LYS:HD3	49:M3:65:TYR:CE1	3.48	0.46
54:M8:166:LEU:HD23	54:M8:166:LEU:HA	1.84	0.46
70:O4:57:LEU:HD12	70:O4:62:TYR:HD1	3.05	0.46
71:O5:78:LYS:HA	71:O5:81:ARG:HB2	3.47	0.46
36:1:1833:G:O2'	75:O9:4:GLN:HA	2.15	0.46
79:Q3:33:GLN:HE21	79:Q3:49:ARG:NH1	2.13	0.46
3:S1:23:PRO:O	3:S1:26:ARG:HD2	3.79	0.46
4:S2:88:LYS:HE2	4:S2:89:GLN:H	5.26	0.46
6:S4:9:LEU:HD13	6:S4:28:ALA:HB3	4.28	0.46
9:S7:46:ILE:HD11	9:S7:60:ILE:HG12	1.97	0.46
1:2:767:U:H6	11:S9:141:VAL:HA	1.80	0.46
11:S9:83:VAL:HA	11:S9:149:ARG:HA	2.37	0.46
36:1:112:U:O2'	36:1:113:C:P	2.73	0.46
36:1:1345:G:N7	87:1:3856:OHX:N4	2.63	0.46
36:1:2249:G:HO2'	36:1:2250:G:P	2.38	0.46
36:1:297:G:O2'	72:O6:33:ALA:HA	2.15	0.46
36:1:3174:A:C2'	36:1:3175:U:H5'	2.45	0.46
36:1:3218:A:H4'	36:1:3219:G:O5'	2.16	0.46
36:1:3318:G:O3'	36:1:3319:U:H3'	2.15	0.46
36:1:565:U:H2'	36:1:566:G:H8	1.79	0.46
36:1:574:U:H2'	36:1:575:G:C8	2.51	0.46
1:2:1217:A:H8	1:2:1217:A:H5'	1.79	0.46
1:2:1718:G:H2'	1:2:1719:A:H8	1.79	0.46
1:2:1657:U:C2	87:2:2058:OHX:N5	2.83	0.46
1:2:934:C:N3	1:2:1077:C:H4'	2.30	0.46
36:5:1253:U:O2	36:5:1263:A:H5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1452:A:H1'	36:5:2347:U:O5'	2.15	0.46
36:5:2133:U:O4	36:5:2147:A:H2	1.98	0.46
36:5:2342:U:H2'	36:5:2343:C:H6	1.80	0.46
36:5:2423:U:H2'	36:5:2424:A:C8	2.50	0.46
36:5:2697:A:H2'	36:5:2698:G:C8	2.49	0.46
36:5:405:U:H2'	36:5:406:G:H5'	1.97	0.46
72:O6:14:GLY:HA2	36:5:73:C:OP1	108.03	0.46
36:5:913:A:H2	36:5:2134:G:N3	2.13	0.46
1:6:138:A:H5''	1:6:138:A:N3	2.31	0.46
1:6:1680:G:O6	87:6:2170:OHX:N4	2.49	0.46
37:7:94:C:H2'	37:7:95:A:C8	2.50	0.46
38:8:145:U:H2'	38:8:146:U:C6	2.51	0.46
25:D3:14:LYS:O	25:D3:18:HIS:HB2	2.16	0.46
26:D4:104:SER:HB3	26:D4:107:GLN:HG3	1.98	0.46
39:L2:61:VAL:HG12	39:L2:63:PHE:CE1	2.51	0.46
40:L3:250:ALA:HB3	36:5:2880:U:O2	225.06	0.46
42:L5:148:ILE:HD12	42:L5:159:VAL:HG21	5.65	0.46
42:L5:238:ASP:O	42:L5:242:SER:HB3	2.95	0.46
44:L7:140:SER:O	44:L7:144:ILE:HG13	2.16	0.46
45:L8:68:ARG:HA	45:L8:236:GLY:O	4.90	0.46
46:L9:84:LYS:O	46:L9:188:THR:HG23	2.16	0.46
50:M4:103:ILE:O	50:M4:107:GLU:HG3	2.15	0.46
50:M4:20:VAL:HA	50:M4:34:ALA:HA	1.96	0.46
59:N3:104:ASN:ND2	59:N3:106:LYS:H	2.12	0.46
59:N3:6:ALA:HB2	59:N3:126:TRP:CH2	2.60	0.46
62:N6:103:LYS:HA	62:N6:103:LYS:HD3	2.13	0.46
66:O0:25:LEU:HD13	66:O0:87:VAL:HG11	4.87	0.46
68:O2:74:PHE:HB3	68:O2:85:LEU:HD11	3.26	0.46
70:O4:81:CYS:O	70:O4:83:ASN:N	2.58	0.46
72:O6:89:GLU:O	72:O6:93:ILE:HG13	3.74	0.46
5:S3:115:ILE:HD12	5:S3:116:ARG:H	4.56	0.46
5:S3:190:ARG:NH2	5:S3:195:SER:HA	2.30	0.46
6:S4:126:VAL:HA	6:S4:141:THR:HG22	1.96	0.46
8:S6:175:ILE:HB	8:S6:178:LEU:HD13	4.91	0.46
11:S9:129:ILE:HA	11:S9:134:ILE:CG1	3.84	0.46
11:S9:171:ARG:O	11:S9:175:ARG:HB2	2.15	0.46
11:S9:78:ARG:NH2	11:S9:82:ARG:HG3	4.51	0.46
36:1:171:G:H2'	36:1:172:G:O4'	2.16	0.46
36:1:1764:U:H5''	55:M9:43:LYS:NZ	2.30	0.46
36:1:2166:A:O3'	51:M5:72:LYS:NZ	2.48	0.46
36:1:2616:C:H2'	36:1:2617:U:H5'	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:279:U:H2'	36:1:280:U:C6	2.50	0.46
36:1:2904:U:H2'	36:1:2905:U:C6	2.50	0.46
36:1:3096:C:H1'	40:L3:327:CYS:SG	2.56	0.46
36:1:3393:U:H2'	36:1:3394:U:C6	2.50	0.46
36:1:975:C:H2'	36:1:976:U:H6	1.80	0.46
1:2:1208:A:N1	1:2:1455:G:N2	2.59	0.46
1:2:1257:U:H2'	12:C0:2:LEU:HD12	1.97	0.46
1:2:1450:U:H2'	1:2:1451:C:C6	2.50	0.46
1:2:1546:G:OP1	20:C8:123:ARG:HD2	2.15	0.46
1:2:1585:U:H3	1:2:1611:A:H2	1.57	0.46
1:2:158:U:O2'	1:2:159:U:H3'	2.15	0.46
36:5:118:U:H5	36:5:119:U:C4	2.34	0.46
36:5:1340:G:H2'	36:5:1341:U:H6	1.81	0.46
36:5:2261:G:H21	36:5:2262:A:N6	2.13	0.46
36:5:993:G:N3	36:5:2637:A:H2'	2.30	0.46
36:5:3298:C:H2'	36:5:3299:A:O4'	2.15	0.46
36:5:1192:C:C5	87:5:4000:OHX:N6	2.83	0.46
36:5:524:U:H2'	36:5:525:C:H5'	1.97	0.46
1:6:1255:G:H4'	1:6:1256:A:OP1	2.15	0.46
17:C5:122:THR:CG2	1:6:1558:U:H3	368.89	0.46
1:6:271:A:C2	1:6:285:G:C6	3.04	0.46
12:C0:53:GLY:O	12:C0:55:VAL:N	2.42	0.46
14:C2:31:VAL:HG21	14:C2:136:ILE:HD13	1.97	0.46
16:C4:12:GLN:HG3	16:C4:111:ARG:HG3	1.97	0.46
16:C4:82:LYS:HB3	16:C4:118:VAL:HG21	2.64	0.46
26:D4:121:THR:HG1	1:6:149:C:P	335.07	0.46
26:D4:45:ALA:HB1	26:D4:51:GLU:HA	1.96	0.46
26:D4:92:VAL:HG21	26:D4:99:LYS:HG2	1.97	0.46
25:D3:136:TRP:O	32:E0:15:LYS:NZ	2.49	0.46
11:S9:28:LEU:HD11	32:E0:39:LEU:HB3	2.97	0.46
39:L2:59:ALA:HB2	39:L2:78:ALA:HB2	1.96	0.46
40:L3:95:THR:O	40:L3:97:ARG:N	2.48	0.46
46:L9:86:TYR:CD2	46:L9:151:VAL:HG13	2.69	0.46
51:M5:120:TRP:CE3	36:5:269:G:H5'	133.63	0.46
36:1:1316:C:C5	52:M6:130:LYS:HA	2.50	0.46
53:M7:32:THR:HA	53:M7:58:ILE:HG21	1.96	0.46
54:M8:37:ALA:O	54:M8:46:LYS:NZ	2.72	0.46
61:N5:60:TYR:CD1	71:O5:25:LYS:HD3	2.50	0.46
62:N6:88:GLU:HG3	62:N6:94:SER:HB2	1.98	0.46
63:N7:3:LYS:HD3	63:N7:4:PHE:N	6.21	0.46
36:1:2553:U:H5	66:O0:54:SER:HB2	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:O2:14:THR:O	87:5:3999:OHX:N1	184.02	0.46
77:Q1:21:ARG:C	77:Q1:23:ARG:H	2.91	0.46
3:S1:104:ASP:HA	3:S1:214:LYS:HG3	1.97	0.46
4:S2:185:LYS:O	4:S2:189:GLN:N	2.92	0.46
6:S4:71:LYS:HA	6:S4:76:VAL:O	2.15	0.46
9:S7:160:GLN:HA	9:S7:163:ASP:HB2	2.43	0.46
1:2:367:A:OP1	87:S9:201:OHX:N6	2.48	0.46
36:1:1064:A:H5''	36:1:1066:G:O4'	2.16	0.46
36:1:1128:U:OP1	47:M0:4:ARG:NH1	2.42	0.46
36:1:1472:U:H5'	55:M9:4:LEU:HB2	1.98	0.46
36:1:212:G:H2'	41:L4:221:ASN:OD1	2.16	0.46
36:1:3118:C:H4'	76:Q0:106:ARG:NH2	2.28	0.46
36:1:3234:A:H2	36:1:3253:G:H22	1.63	0.46
36:1:1196:C:O2	87:1:3889:OHX:N2	2.49	0.46
36:1:603:A:H2'	36:1:604:G:O4'	2.16	0.46
36:1:665:A:OP1	51:M5:203:ARG:HD2	2.15	0.46
1:2:1503:A:H2'	1:2:1504:G:O4'	2.15	0.46
1:2:1584:G:H22	1:2:1611:A:P	2.39	0.46
1:2:417:A:H4'	1:2:418:G:O5'	2.15	0.46
68:O2:19:ARG:HH22	36:5:1433:A:P	165.41	0.46
36:5:2221:G:N2	36:5:2224:A:OP2	2.34	0.46
64:N8:55:LYS:NZ	36:5:2765:C:OP1	167.65	0.46
36:5:2768:U:H2'	36:5:2769:A:C8	2.51	0.46
36:5:3193:C:H2'	36:5:3194:C:C6	2.51	0.46
36:5:3225:C:C2	36:5:3226:A:C8	3.03	0.46
36:5:873:C:H4'	36:5:874:U:OP2	2.15	0.46
1:6:1442:U:H4'	1:6:1447:C:C5	2.50	0.46
1:6:512:A:H2'	1:6:513:U:C6	2.50	0.46
14:C2:103:LEU:HG	14:C2:116:VAL:HG22	1.98	0.46
17:C5:24:LYS:O	17:C5:28:MET:HG3	3.76	0.46
1:2:1525:A:OP1	21:C9:93:HIS:ND1	2.47	0.46
22:D0:71:PRO:O	22:D0:72:ASN:ND2	5.54	0.46
39:L2:45:VAL:HG22	39:L2:84:THR:HA	1.98	0.46
40:L3:115:LYS:HA	40:L3:118:PHE:HD1	1.80	0.46
40:L3:53:MET:HE3	36:5:3047:U:O2'	236.09	0.46
41:L4:138:ARG:NH1	41:L4:138:ARG:O	2.48	0.46
41:L4:178:LEU:O	41:L4:182:LEU:HD23	2.15	0.46
42:L5:261:THR:OG1	42:L5:264:GLN:HG3	3.46	0.46
45:L8:148:ALA:HA	45:L8:201:THR:HG22	1.98	0.46
46:L9:151:VAL:O	46:L9:155:SER:OG	2.33	0.46
46:L9:163:GLN:HE22	36:5:3108:G:H21	315.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:M0:165:ILE:H	47:M0:165:ILE:HG12	1.45	0.46
50:M4:47:ASP:OD1	50:M4:55:ARG:HB2	3.15	0.46
36:1:1719:G:H5''	55:M9:110:ARG:HH22	1.81	0.46
55:M9:138:LEU:O	55:M9:142:ILE:HG13	2.58	0.46
56:N0:104:GLU:O	56:N0:108:GLN:HG2	2.52	0.46
58:N2:36:TYR:CD2	58:N2:83:TYR:HB2	2.76	0.46
59:N3:104:ASN:HB2	59:N3:105:PRO:HD2	2.19	0.46
59:N3:62:VAL:HG21	59:N3:69:LEU:HB3	1.97	0.46
60:N4:3:VAL:HG12	60:N4:12:LYS:HB3	1.98	0.46
36:1:1117:G:OP1	65:N9:4:SER:HB2	2.16	0.46
64:N8:13:GLY:O	68:O2:36:LYS:HD2	4.44	0.46
79:Q3:33:GLN:HG3	79:Q3:34:HIS:CD2	2.74	0.46
2:S0:148:ASP:OD1	2:S0:149:LEU:N	2.75	0.46
3:S1:113:MET:HE3	3:S1:211:HIS:CD2	4.41	0.46
3:S1:171:ILE:HD12	3:S1:197:ILE:HD13	1.97	0.46
3:S1:71:ALA:C	3:S1:73:LEU:H	3.70	0.46
3:S1:86:LEU:HB3	3:S1:98:THR:OG1	2.15	0.46
4:S2:78:ASP:HA	4:S2:104:VAL:HA	1.97	0.46
4:S2:90:THR:HG21	4:S2:95:ARG:NH1	2.30	0.46
6:S4:106:LYS:HG3	6:S4:108:ARG:CZ	2.88	0.46
7:S5:90:ILE:O	7:S5:94:THR:HG23	2.15	0.46
8:S6:123:GLY:O	8:S6:127:THR:HG22	3.14	0.46
8:S6:64:LYS:O	8:S6:67:VAL:HG22	2.29	0.46
9:S7:31:SER:N	9:S7:32:PRO:HD2	3.05	0.46
11:S9:7:THR:HG23	1:6:772:G:OP1	388.03	0.46
35:SM:70:ASN:O	35:SM:74:LYS:HD3	2.15	0.46
36:1:118:U:C5	36:1:119:U:C4	3.04	0.46
36:1:135:C:N3	71:O5:94:LYS:HB2	2.30	0.46
36:1:1460:A:H2'	36:1:1461:A:C8	2.50	0.46
36:1:1507:G:H2'	36:1:1507:G:N3	2.30	0.46
36:1:1520:G:H2'	36:1:1521:G:O4'	2.15	0.46
36:1:1549:U:H2'	36:1:1550:C:H6	1.81	0.46
36:1:1585:C:H2'	36:1:1586:G:C8	2.49	0.46
36:1:2103:U:H2'	36:1:2104:A:C8	2.50	0.46
36:1:2213:A:N1	36:1:2429:G:H1'	2.31	0.46
36:1:2762:A:H2'	36:1:2763:U:C6	2.51	0.46
36:1:1409:G:OP1	87:1:3849:OHX:N6	2.49	0.46
36:1:994:G:N2	36:1:995:U:O4	2.36	0.46
1:2:1253:U:H5''	33:E1:130:VAL:HB	1.97	0.46
1:2:1274:C:H4'	1:2:1275:A:O5'	2.15	0.46
1:2:1330:G:N1	5:S3:204:ASP:OD1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1428:G:H8	1:2:1428:G:H5'	1.81	0.46
1:2:223:U:H2'	1:2:224:C:C6	2.51	0.46
36:5:1013:G:H2'	36:5:1014:U:O4'	2.15	0.46
36:5:1027:A:O2'	36:5:1029:G:N7	2.43	0.46
36:5:1658:G:H2'	36:5:1659:U:C6	2.49	0.46
36:5:2826:U:O4	87:5:3818:OHX:N6	2.49	0.46
36:5:3298:C:C2	36:5:3299:A:C8	3.04	0.46
36:5:3356:G:C6	36:5:3357:U:C4	3.04	0.46
36:5:348:A:N3	36:5:352:A:O2'	2.48	0.46
1:6:1744:A:N6	1:6:1745:G:C6	2.84	0.46
1:6:417:A:H5'	1:6:418:G:C5	2.50	0.46
25:D3:22:ASN:O	1:6:609:U:C5	339.18	0.46
12:C0:91:TYR:O	12:C0:93:GLN:N	2.44	0.46
17:C5:60:LEU:HD11	17:C5:92:SER:OG	2.16	0.46
20:C8:41:ARG:NH1	1:6:1565:C:OP1	373.05	0.46
23:D1:69:LEU:O	23:D1:73:ALA:N	2.87	0.46
24:D2:89:TRP:O	24:D2:93:LEU:HD23	2.15	0.46
27:D5:73:GLY:O	27:D5:77:ARG:NE	2.48	0.46
14:C2:50:LYS:NZ	33:E1:106:TYR:OH	2.44	0.46
36:1:914:A:C8	39:L2:199:THR:HG21	2.51	0.46
40:L3:116:ARG:HG2	40:L3:175:LYS:HB2	3.71	0.46
40:L3:183:LEU:HA	40:L3:183:LEU:HD12	1.75	0.46
40:L3:79:VAL:HG21	40:L3:338:LEU:HD21	1.96	0.46
41:L4:157:GLU:HG2	41:L4:251:THR:HG21	1.97	0.46
41:L4:157:GLU:HG2	41:L4:209:TYR:HB2	3.00	0.46
41:L4:181:VAL:HG11	41:L4:223:PRO:C	3.11	0.46
42:L5:119:TYR:HE1	42:L5:134:ALA:HA	3.30	0.46
45:L8:166:LEU:HD23	45:L8:166:LEU:HA	1.92	0.46
46:L9:189:GLU:O	46:L9:191:LEU:N	2.48	0.46
46:L9:93:VAL:O	46:L9:177:ASP:HA	2.16	0.46
47:M0:33:ILE:HG23	47:M0:69:ARG:NH2	2.30	0.46
48:M1:93:ASP:OD1	48:M1:156:LYS:NZ	2.37	0.46
63:N7:81:LEU:HA	63:N7:81:LEU:HD22	1.75	0.46
36:1:3173:G:C2	69:O3:96:ALA:HB2	2.51	0.46
71:O5:28:LEU:O	71:O5:32:LYS:HG3	2.15	0.46
72:O6:83:ALA:HA	72:O6:86:LYS:HB3	1.98	0.46
74:O8:54:LEU:HD21	74:O8:56:ILE:HD11	2.04	0.46
79:Q3:13:LYS:HE3	79:Q3:14:TYR:CE2	2.50	0.46
4:S2:83:ILE:HD11	4:S2:125:ILE:HD11	1.98	0.46
8:S6:63:MET:HE2	8:S6:106:LEU:HD13	1.97	0.46
10:S8:49:ARG:HH22	1:6:399:A:P	316.21	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:S9:13:SER:H	11:S9:47:PHE:HB2	1.80	0.46
34:SR:131:ILE:O	34:SR:144:LEU:HB2	2.16	0.46
34:SR:20:VAL:O	34:SR:291:SER:OG	2.15	0.46
36:1:2812:C:H2'	36:1:2813:A:C8	2.50	0.46
36:1:3203:U:O4	87:1:4085:OHX:N3	2.49	0.46
36:1:501:A:H5''	43:L6:28:GLN:HE21	1.80	0.46
36:1:619:A:H4'	36:1:620:U:O4'	2.15	0.46
36:1:619:A:H4'	36:1:620:U:O5'	2.15	0.46
36:1:685:G:N2	36:1:696:C:C2	2.84	0.46
36:1:818:C:N3	36:1:920:A:H5'	2.31	0.46
1:2:1695:G:N2	1:2:1706:C:H41	2.13	0.46
1:2:765:G:O2'	11:S9:149:ARG:NH2	2.49	0.46
38:4:145:U:H2'	38:4:146:U:O4'	2.15	0.46
36:5:1081:U:HO2'	36:5:1082:U:C5'	2.29	0.46
36:5:20:A:C6	36:5:21:G:C6	3.04	0.46
45:L8:33:ASN:HA	36:5:2549:G:N2	212.58	0.46
47:M0:116:ARG:HA	36:5:2618:G:N2	237.95	0.46
36:5:370:U:H4'	36:5:404:G:H5'	1.97	0.46
36:5:386:A:C5	36:5:387:A:H1'	2.50	0.46
1:6:1092:A:O2'	1:6:1093:A:H3'	2.16	0.46
1:6:1360:A:C3'	1:6:1361:U:H4'	2.46	0.46
1:6:200:A:H2'	1:6:201:G:H8	1.81	0.46
1:6:309:C:H2'	1:6:310:C:H6	1.81	0.46
37:7:33:U:H2'	37:7:34:C:O4'	2.15	0.46
61:N5:56:ARG:NH2	38:8:135:G:OP2	82.56	0.46
12:C0:50:THR:HG22	12:C0:55:VAL:HG22	1.97	0.46
14:C2:59:LEU:HD23	14:C2:60:VAL:N	2.29	0.46
23:D1:12:TYR:O	23:D1:14:PRO:HD3	2.16	0.46
25:D3:33:LEU:HD23	25:D3:33:LEU:HA	1.54	0.46
40:L3:47:LEU:HD23	40:L3:164:THR:HG23	2.28	0.46
40:L3:92:TYR:O	40:L3:155:ALA:HA	2.16	0.46
41:L4:222:VAL:O	41:L4:225:VAL:HG23	2.15	0.46
43:L6:170:LYS:HB3	43:L6:172:HIS:CE1	2.51	0.46
36:1:3276:G:H3'	43:L6:48:ARG:NH2	2.31	0.46
47:M0:187:ALA:O	87:M0:303:OHX:N5	2.48	0.46
48:M1:16:LYS:HE2	48:M1:130:VAL:HG11	1.97	0.46
50:M4:24:LYS:HB3	50:M4:24:LYS:HE2	4.55	0.46
51:M5:80:THR:HG21	51:M5:87:GLN:HA	1.96	0.46
52:M6:42:ASN:HD21	52:M6:125:ARG:HH11	3.81	0.46
53:M7:31:GLU:HG2	53:M7:60:PHE:HA	4.33	0.46
41:L4:281:ILE:HG13	54:M8:125:ASP:CG	2.55	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:M8:176:ARG:HA	54:M8:182:LYS:O	2.16	0.46
56:N0:79:VAL:HG21	56:N0:106:LEU:HD11	3.91	0.46
57:N1:15:PHE:CE2	57:N1:44:ALA:HB3	2.50	0.46
61:N5:74:LYS:O	61:N5:78:ASP:HB2	2.92	0.46
62:N6:26:GLN:O	62:N6:30:LEU:HG	2.76	0.46
62:N6:37:LYS:H	62:N6:37:LYS:HD3	2.86	0.46
65:N9:21:ILE:HG22	65:N9:22:LYS:N	3.82	0.46
68:O2:126:LEU:HA	68:O2:126:LEU:HD23	1.84	0.46
49:M3:126:PHE:CD2	71:O5:115:LYS:HG2	2.51	0.46
76:Q0:93:LYS:HG3	76:Q0:102:ARG:HG2	1.97	0.46
2:S0:120:LEU:HD11	2:S0:144:ILE:HG13	1.98	0.46
2:S0:185:ARG:HB3	2:S0:186:GLY:H	4.30	0.46
5:S3:164:VAL:HG13	5:S3:168:ILE:HD11	1.96	0.46
5:S3:66:ILE:O	5:S3:70:THR:HG23	4.52	0.46
6:S4:132:GLY:N	6:S4:136:VAL:O	3.04	0.46
6:S4:11:ARG:NH1	6:S4:21:ASP:OD2	2.77	0.46
7:S5:121:ILE:HD11	7:S5:195:ALA:HA	2.83	0.46
7:S5:166:ARG:NH1	7:S5:170:GLN:OE1	2.49	0.46
9:S7:111:LYS:O	9:S7:112:ARG:HB2	2.16	0.46
10:S8:188:GLU:HG2	13:C1:13:PHE:CD2	2.51	0.46
36:1:1314:C:O5'	36:1:1314:C:H6	1.99	0.46
36:1:1362:G:H2'	36:1:1363:A:C8	2.50	0.46
36:1:3045:G:H2'	36:1:3046:A:O4'	2.16	0.46
36:1:3385:U:H2'	36:1:3386:G:O4'	2.16	0.46
36:1:824:C:H2'	36:1:825:U:C6	2.51	0.46
1:2:1483:A:C6	1:2:1484:G:C6	3.03	0.46
1:2:461:G:H2'	1:2:462:G:H8	1.81	0.46
38:4:156:U:H2'	38:4:157:U:C6	2.50	0.46
36:5:1222:G:OP2	36:5:1222:G:H8	1.98	0.46
36:5:2555:G:H5'	36:5:2556:C:OP2	2.15	0.46
36:5:269:G:O6	87:5:4143:OHX:N6	2.49	0.46
36:5:2882:U:H2'	36:5:2883:U:C6	2.51	0.46
49:M3:58:VAL:CG1	36:5:75:G:H5''	88.54	0.46
1:6:16:G:H2'	1:6:17:C:C6	2.50	0.46
38:8:59:A:H4'	38:8:60:U:H5''	1.98	0.46
18:C6:83:GLN:HG3	18:C6:116:LEU:O	2.16	0.46
28:D6:13:LYS:HB3	1:6:1076:A:O5'	335.11	0.46
30:D8:21:SER:HB2	1:6:1619:C:H5'	343.12	0.46
30:D8:60:GLU:O	30:D8:62:GLU:N	4.88	0.46
39:L2:3:ARG:HD3	36:5:911:C:N4	180.07	0.46
39:L2:48:ILE:HD11	39:L2:83:HIS:HA	6.05	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:278:ILE:HD12	40:L3:279:ASN:CG	4.76	0.46
40:L3:296:THR:OG1	40:L3:357:LYS:O	2.25	0.46
41:L4:23:PRO:HB3	41:L4:259:ASP:OD1	3.04	0.46
41:L4:3:ARG:HA	41:L4:4:PRO:HD2	1.53	0.46
42:L5:216:GLU:HA	42:L5:219:PHE:HB3	1.98	0.46
45:L8:33:ASN:O	45:L8:33:ASN:ND2	4.59	0.46
47:M0:3:ARG:HH22	36:5:2854:U:P	292.25	0.46
47:M0:51:HIS:HB3	47:M0:134:ILE:HG23	1.96	0.46
53:M7:60:PHE:HZ	53:M7:84:PRO:HG3	1.81	0.46
54:M8:44:PHE:CD2	54:M8:134:GLY:HA3	2.51	0.46
55:M9:92:GLN:O	55:M9:96:ILE:HG13	2.22	0.46
57:N1:38:ASP:O	57:N1:64:VAL:HG23	2.20	0.46
59:N3:39:VAL:HG21	59:N3:51:ALA:C	2.55	0.46
64:N8:3:SER:OG	64:N8:4:ARG:N	3.26	0.46
49:M3:138:VAL:HG23	71:O5:118:ILE:HB	1.98	0.46
79:Q3:13:LYS:HD2	79:Q3:14:TYR:CZ	4.38	0.46
79:Q3:56:THR:HG22	79:Q3:63:THR:HG23	1.97	0.46
2:S0:56:LYS:HD2	2:S0:158:VAL:HG23	1.97	0.46
3:S1:65:VAL:HG21	3:S1:85:LYS:HE2	1.97	0.46
4:S2:90:THR:O	4:S2:92:ALA:N	2.68	0.46
1:2:579:A:C2	5:S3:143:ARG:HG2	2.51	0.46
5:S3:54:ARG:HD2	5:S3:57:ASP:CG	3.61	0.46
6:S4:77:ARG:HD2	6:S4:77:ARG:HA	1.73	0.46
9:S7:67:LEU:HD13	9:S7:71:HIS:CE1	3.28	0.46
11:S9:110:GLN:OE1	11:S9:126:ARG:HG2	2.31	0.46
35:SM:51:ARG:CZ	35:SM:52:PRO:HD2	6.26	0.46
34:SR:52:GLN:HG2	34:SR:53:LYS:H	2.54	0.46
36:1:1751:G:H5'	74:O8:26:LYS:NZ	2.31	0.46
36:1:2373:A:N7	36:1:2867:C:H1'	2.31	0.46
36:1:1556:C:O2'	87:1:3809:OHX:N2	2.48	0.46
36:1:506:U:H2'	36:1:507:U:O4'	2.16	0.46
36:1:612:U:H2'	36:1:613:G:C8	2.51	0.46
36:1:95:A:C5	36:1:96:G:H1'	2.51	0.46
1:2:122:U:H5''	6:S4:77:ARG:HH21	1.79	0.46
1:2:1418:G:N7	87:2:1993:OHX:N5	2.63	0.46
1:2:182:A:H2'	1:2:183:U:C6	2.51	0.46
1:2:483:A:H61	1:2:505:A:H1'	1.80	0.46
36:5:112:U:O2'	36:5:113:C:OP2	2.28	0.46
36:5:1471:U:H2'	36:5:1472:U:H6	1.80	0.46
36:5:1728:G:H5''	36:5:1730:G:O4'	2.16	0.46
79:Q3:18:TYR:HA	36:5:2131:A:H61	228.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:241:G:H2'	36:5:242:C:C6	2.51	0.46
36:5:2653:C:H1'	36:5:2694:A:C2	2.51	0.46
51:M5:14:LYS:HE2	36:5:269:G:H5''	133.77	0.46
72:O6:28:TYR:OH	36:5:315:C:OP2	98.62	0.46
1:6:1045:C:C2	1:6:1074:G:C2	3.03	0.46
1:6:179:A:H2'	1:6:180:A:C8	2.51	0.46
1:6:1570:A:OP1	87:6:2124:OHX:N1	2.49	0.46
1:6:282:C:H2'	1:6:283:U:O4'	2.15	0.46
13:C1:64:VAL:HG12	13:C1:129:ARG:NH1	2.31	0.46
16:C4:77:THR:O	16:C4:110:LEU:HD22	2.69	0.46
17:C5:126:VAL:HG11	1:6:1459:C:H4'	342.45	0.46
19:C7:9:VAL:HG13	19:C7:50:ILE:HA	2.48	0.46
21:C9:39:THR:O	21:C9:96:ALA:HB1	2.15	0.46
32:E0:50:VAL:HA	32:E0:53:LYS:O	2.16	0.46
36:1:912:G:OP2	39:L2:9:ARG:NH1	2.48	0.46
44:L7:95:ILE:HA	44:L7:96:PRO:HD3	1.95	0.46
46:L9:118:LEU:HD23	46:L9:118:LEU:HA	1.82	0.46
46:L9:27:VAL:O	46:L9:33:THR:HA	2.59	0.46
47:M0:123:HIS:O	47:M0:123:HIS:CG	2.89	0.46
49:M3:180:ARG:HH11	49:M3:180:ARG:HG2	1.81	0.46
51:M5:11:GLN:HG2	51:M5:44:ARG:NH2	2.30	0.46
51:M5:144:ARG:HD3	71:O5:95:PHE:HE2	1.79	0.46
55:M9:167:ARG:HB3	55:M9:167:ARG:CZ	2.94	0.46
64:N8:73:LEU:O	64:N8:113:LEU:N	3.13	0.46
70:O4:47:CYS:SG	70:O4:81:CYS:SG	3.19	0.46
38:4:41:A:O2'	73:O7:59:THR:HG22	2.16	0.46
4:S2:114:GLY:HA3	4:S2:132:ALA:HB2	1.98	0.46
5:S3:115:ILE:HD13	5:S3:116:ARG:HG3	6.51	0.46
5:S3:38:GLU:HG3	5:S3:49:ILE:HB	1.98	0.46
7:S5:99:MET:HB2	7:S5:180:ARG:CZ	5.22	0.46
7:S5:53:VAL:HB	7:S5:59:VAL:HG22	4.26	0.46
10:S8:11:ARG:HD3	10:S8:15:GLY:O	2.16	0.46
34:SR:149:ASP:HB2	34:SR:175:ASP:HB3	1.97	0.46
36:1:1063:G:C6	36:1:1097:G:C5	3.04	0.46
36:1:2103:U:H2'	36:1:2104:A:H8	1.81	0.46
36:1:2154:U:OP1	39:L2:242:ARG:NH1	2.45	0.46
36:1:2229:A:H2'	36:1:2230:C:O4'	2.16	0.46
36:1:2278:C:C2	36:1:2307:G:C2	3.04	0.46
36:1:2444:C:H3'	36:1:2445:A:H5''	1.97	0.46
36:1:2503:G:H1'	36:1:2504:U:H5	1.81	0.46
36:1:2553:U:H2'	36:1:2553:U:O2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:3245:A:H5'	36:1:3246:G:H5''	1.98	0.46
36:1:3340:G:O6	87:1:4058:OHX:N4	2.48	0.46
36:1:70:A:N1	36:1:313:A:O2'	2.44	0.46
1:2:1111:G:C6	1:2:1112:G:C4	3.04	0.46
1:2:1358:G:OP1	87:2:2109:OHX:N2	2.49	0.46
1:2:1283:U:H3	1:2:1424:A:H61	1.64	0.46
1:2:1619:C:H2'	1:2:1620:C:C6	2.51	0.46
36:5:1440:G:H2'	36:5:1441:G:H8	1.81	0.46
36:5:2541:U:H4'	36:5:2542:U:OP1	2.16	0.46
36:5:2661:G:H2'	36:5:2662:G:C8	2.51	0.46
64:N8:43:ILE:HG23	36:5:2727:A:C2	192.70	0.46
36:5:2947:G:H4'	36:5:2947:G:OP2	2.16	0.46
36:5:3163:A:N1	36:5:3164:C:N4	2.63	0.46
36:5:2273:G:O6	87:5:3893:OHX:N6	2.49	0.46
36:5:541:U:O4	87:5:3927:OHX:N3	2.48	0.46
36:5:850:U:H2'	36:5:851:C:C6	2.50	0.46
1:6:1003:A:H1'	1:6:1005:A:N7	2.30	0.46
21:C9:3:GLY:HA3	1:6:1364:G:N2	432.34	0.46
1:6:95:G:H5'	1:6:96:G:OP2	2.16	0.46
14:C2:71:ILE:O	14:C2:75:VAL:HG23	2.15	0.46
15:C3:85:PRO:HG2	15:C3:129:TYR:CE2	2.76	0.46
21:C9:14:PHE:HZ	21:C9:132:LEU:HD12	4.69	0.46
20:C8:41:ARG:CD	21:C9:46:PRO:HD3	2.46	0.46
25:D3:67:ALA:HB3	25:D3:69:ARG:HH21	1.78	0.46
42:L5:244:HIS:HA	42:L5:247:ILE:HD12	1.98	0.46
46:L9:106:LYS:HA	46:L9:106:LYS:HE3	5.43	0.46
47:M0:56:GLU:HG3	47:M0:162:GLN:N	3.23	0.46
51:M5:136:ASP:OD2	51:M5:138:GLN:HG2	2.36	0.46
52:M6:77:SER:OG	52:M6:106:GLU:OE1	2.21	0.46
61:N5:103:TYR:O	61:N5:138:ARG:NH1	2.83	0.46
63:N7:10:VAL:HG23	63:N7:86:THR:HA	1.98	0.46
70:O4:86:LYS:HE3	70:O4:90:ILE:HD11	3.94	0.46
77:Q1:6:ARG:NH1	77:Q1:10:THR:HG22	2.31	0.46
3:S1:194:ASN:N	3:S1:194:ASN:OD1	2.49	0.46
5:S3:72:LEU:HD22	12:C0:65:TYR:CD1	2.92	0.46
7:S5:140:THR:HA	7:S5:214:LYS:HD2	2.01	0.46
9:S7:168:SER:O	9:S7:172:VAL:HG23	2.34	0.46
10:S8:103:GLN:HG2	10:S8:164:ARG:HG2	1.97	0.46
11:S9:53:ARG:O	11:S9:57:ARG:HG3	2.16	0.46
11:S9:4:ALA:HA	11:S9:5:PRO:HD3	1.73	0.46
11:S9:87:SER:O	11:S9:90:LYS:N	3.05	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SR:182:ASN:HD21	34:SR:184:ASN:ND2	2.14	0.46
36:1:1821:U:C2	70:O4:67:LYS:HB2	2.51	0.46
36:1:2444:C:O4'	72:O6:63:ASN:ND2	2.48	0.46
36:1:2534:G:H2'	36:1:2535:A:C8	2.47	0.46
1:2:1699:G:H22	1:2:1702:A:H5''	1.80	0.46
1:2:1561:U:OP1	87:2:2122:OHX:N3	2.48	0.46
1:2:276:C:O2'	1:2:277:U:H5''	2.15	0.46
1:2:572:C:H6	1:2:572:C:O5'	1.99	0.46
1:2:823:G:H2'	1:2:824:G:C8	2.50	0.46
36:5:1214:U:H2'	36:5:1215:U:C6	2.51	0.46
36:5:126:U:H2'	36:5:127:G:O4'	2.16	0.46
55:M9:5:ARG:NH2	36:5:1471:U:OP1	122.83	0.46
36:5:1817:G:OP2	87:5:4095:OHX:N5	2.49	0.46
36:5:2213:A:N1	36:5:2429:G:H1'	2.30	0.46
36:5:2954:U:O4	89:5:3402:SPS:S15	2.74	0.46
36:5:3226:A:C5	36:5:3227:A:C2	3.04	0.46
36:5:848:A:C5	36:5:849:C:H1'	2.51	0.46
36:5:926:A:H2'	36:5:927:C:C6	2.50	0.46
1:6:1111:G:N7	87:6:2036:OHX:N3	2.64	0.46
1:6:1241:G:H2'	1:6:1242:A:O4'	2.16	0.46
1:6:196:G:O2'	1:6:197:A:OP2	2.29	0.46
1:6:340:U:H2'	1:6:341:A:H8	1.78	0.46
13:C1:97:TYR:O	13:C1:99:ARG:HG2	2.16	0.46
18:C6:132:LYS:HB3	18:C6:138:PHE:CE1	2.51	0.46
18:C6:22:VAL:HG22	18:C6:65:ILE:HG23	1.98	0.46
18:C6:45:ARG:O	18:C6:48:VAL:HG12	2.51	0.46
19:C7:71:PHE:HD1	19:C7:73:LEU:HB3	1.81	0.46
24:D2:106:THR:HG21	24:D2:121:VAL:HG23	5.13	0.46
25:D3:14:LYS:HA	25:D3:17:VAL:HG12	4.26	0.46
39:L2:23:ARG:HA	39:L2:51:ASP:OD1	2.64	0.46
40:L3:328:ILE:HG12	40:L3:329:PRO:HD2	1.98	0.46
41:L4:193:LYS:HB2	41:L4:198:ARG:HA	3.57	0.46
41:L4:299:ILE:HG22	41:L4:300:ARG:O	2.15	0.46
41:L4:48:GLN:NE2	36:5:336:A:N3	94.63	0.46
44:L7:116:PHE:HB2	44:L7:199:ASN:OD1	2.18	0.46
44:L7:29:GLU:O	44:L7:32:ALA:HB3	3.12	0.46
49:M3:108:ILE:O	49:M3:112:ASN:HB2	2.14	0.46
50:M4:104:ALA:HA	50:M4:107:GLU:HB2	3.46	0.46
57:N1:106:LEU:H	57:N1:106:LEU:HG	4.11	0.46
66:O0:45:ALA:HA	66:O0:70:PHE:HB3	3.69	0.46
68:O2:40:SER:O	68:O2:44:ARG:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:O4:74:ARG:HG2	70:O4:75:ALA:H	2.57	0.46
71:O5:86:ARG:HG3	38:8:37:A:OP2	81.25	0.46
71:O5:93:THR:O	71:O5:96:GLU:N	3.10	0.46
75:O9:7:PHE:HB3	38:8:113:U:H5''	108.70	0.46
2:S0:195:TRP:CE2	2:S0:197:ILE:HD13	2.63	0.46
6:S4:175:PHE:HE1	6:S4:225:VAL:HG11	1.80	0.46
7:S5:68:ILE:HD13	7:S5:69:PHE:H	4.98	0.46
9:S7:30:SER:HB2	9:S7:34:LEU:HB2	2.67	0.46
36:1:103:G:OP1	49:M3:70:ARG:NH2	2.49	0.45
36:1:1514:G:HO2'	36:1:1841:A:H2	1.62	0.45
36:1:1841:A:H2	75:O9:45:ARG:NH2	2.10	0.45
36:1:1481:A:H2'	36:1:1858:A:H1'	1.98	0.45
36:1:1863:G:N1	36:1:1866:C:OP2	2.36	0.45
36:1:2221:G:N2	36:1:2223:A:H3'	2.31	0.45
36:1:2633:U:H2'	36:1:2634:U:O4'	2.15	0.45
36:1:3099:C:C5	36:1:3100:U:C4	3.04	0.45
36:1:317:A:H2'	36:1:318:A:C8	2.50	0.45
36:1:27:C:O2'	36:1:327:A:N3	2.40	0.45
36:1:2264:U:OP2	87:1:3881:OHX:N5	2.49	0.45
36:1:631:U:H2'	36:1:632:G:C8	2.51	0.45
38:4:125:U:HO2'	38:4:126:A:P	2.39	0.45
38:4:36:G:OP2	71:O5:85:THR:HG22	2.16	0.45
36:5:1470:U:OP1	87:5:3872:OHX:N2	2.49	0.45
36:5:2881:C:H2'	36:5:2882:U:H6	1.81	0.45
1:6:1766:A:H5''	87:6:2092:OHX:N6	2.31	0.45
1:6:1537:C:O2	87:6:2124:OHX:N4	2.49	0.45
1:6:365:G:H5'	1:6:758:U:O2	2.16	0.45
13:C1:109:VAL:HG11	13:C1:125:VAL:HG11	2.60	0.45
14:C2:42:ALA:HB1	14:C2:47:GLU:HB3	2.45	0.45
18:C6:82:ARG:NH1	18:C6:114:ARG:HB2	3.77	0.45
18:C6:82:ARG:HH12	18:C6:114:ARG:HB2	3.20	0.45
19:C7:46:LEU:HD13	19:C7:50:ILE:HD11	1.98	0.45
20:C8:108:LYS:HA	20:C8:108:LYS:HD2	1.61	0.45
1:2:1523:G:C8	21:C9:79:LEU:HD13	2.49	0.45
23:D1:36:VAL:O	23:D1:51:VAL:N	2.90	0.45
26:D4:20:ARG:CZ	26:D4:74:LEU:HD22	2.46	0.45
27:D5:60:VAL:HA	27:D5:64:VAL:HG11	1.98	0.45
40:L3:293:ASN:HD22	40:L3:304:THR:HG22	1.81	0.45
40:L3:208:VAL:HG12	40:L3:340:LYS:HE2	1.98	0.45
41:L4:145:ILE:HA	41:L4:146:PRO:HD3	2.43	0.45
41:L4:6:VAL:N	41:L4:20:LEU:O	2.53	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:933:A:C6	41:L4:98:ARG:HD2	2.50	0.45
42:L5:48:LYS:NZ	36:5:2748:A:O3'	245.45	0.45
45:L8:159:PRO:HB2	45:L8:162:LEU:HD12	1.97	0.45
47:M0:48:LEU:HD23	47:M0:178:ARG:NH1	2.54	0.45
51:M5:124:ASP:OD2	51:M5:125:SER:N	2.49	0.45
36:1:1316:C:N4	52:M6:131:PRO:HD3	2.31	0.45
53:M7:41:LEU:O	53:M7:45:GLN:HG3	2.16	0.45
53:M7:95:LEU:HA	53:M7:95:LEU:HD23	2.72	0.45
54:M8:184:PHE:CD1	36:5:2730:G:H4'	191.56	0.45
56:N0:28:ARG:HE	56:N0:99:ARG:NH2	3.03	0.45
57:N1:116:ARG:HA	57:N1:126:VAL:HG11	1.99	0.45
57:N1:12:ARG:HD3	57:N1:13:TYR:CE2	2.50	0.45
57:N1:40:VAL:O	57:N1:61:THR:HG23	2.33	0.45
61:N5:105:VAL:HG11	61:N5:126:LEU:HD22	4.09	0.45
75:O9:25:GLN:OE1	75:O9:28:ARG:HG3	2.16	0.45
78:Q2:10:THR:OG1	78:Q2:11:TYR:N	2.45	0.45
6:S4:86:PHE:CD1	6:S4:87:MET:HG2	2.51	0.45
8:S6:78:THR:HG22	8:S6:79:LYS:H	3.19	0.45
6:S4:10:LYS:NZ	11:S9:2:PRO:HB3	3.69	0.45
11:S9:60:LEU:HA	11:S9:60:LEU:HD22	1.81	0.45
36:1:1184:A:O2'	36:1:1185:C:H5'	2.16	0.45
36:1:2100:A:N7	36:1:2101:C:N4	2.64	0.45
36:1:2719:U:O4	87:1:4050:OHX:N3	2.50	0.45
36:1:3006:A:H2'	36:1:3007:U:O4'	2.16	0.45
36:1:31:C:H2'	36:1:32:U:O4'	2.16	0.45
1:2:1068:C:H2'	1:2:1069:A:C8	2.51	0.45
1:2:1594:G:H5'	31:D9:33:LYS:HE3	1.99	0.45
1:2:932:U:O2	28:D6:32:LYS:HE2	2.16	0.45
38:4:1:A:C2	38:4:2:A:C4	3.03	0.45
36:5:1624:G:H2'	36:5:1625:A:O4'	2.16	0.45
36:5:1657:C:O2'	36:5:1797:A:OP2	2.26	0.45
36:5:2353:G:C5	36:5:2354:C:C5	3.04	0.45
36:5:3072:C:H2'	36:5:3073:A:O4'	2.16	0.45
36:5:378:A:H3'	36:5:379:C:H6	1.82	0.45
36:5:789:A:H2'	36:5:790:U:C6	2.51	0.45
1:6:291:G:H2'	1:6:292:U:C6	2.50	0.45
1:6:30:G:H2'	1:6:31:C:C6	2.51	0.45
1:6:700:C:H2'	1:6:701:U:C6	2.51	0.45
1:2:1549:C:OP1	17:C5:42:ARG:NH1	2.49	0.45
19:C7:71:PHE:CD1	19:C7:73:LEU:HB3	2.51	0.45
20:C8:38:VAL:HG12	20:C8:42:TYR:CD2	4.67	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:358:TRP:CZ2	40:L3:360:ASP:HA	2.62	0.45
42:L5:191:ASP:OD2	42:L5:193:GLU:HB2	4.27	0.45
46:L9:112:ILE:HD11	46:L9:134:ILE:HG12	2.06	0.45
36:1:3186:A:O2'	46:L9:42:ASP:HA	2.17	0.45
48:M1:10:ARG:H	48:M1:10:ARG:HG3	1.53	0.45
49:M3:168:ARG:NH1	49:M3:172:LEU:HD11	3.82	0.45
50:M4:128:ARG:O	50:M4:132:LYS:HB2	2.15	0.45
61:N5:109:LYS:HB2	61:N5:109:LYS:HE3	1.70	0.45
63:N7:46:ILE:HD11	63:N7:48:ARG:C	2.37	0.45
63:N7:75:VAL:HG13	63:N7:80:LEU:HD11	2.79	0.45
66:O0:13:LYS:HD3	66:O0:100:ILE:HG22	1.97	0.45
69:O3:16:TYR:CD2	69:O3:25:PRO:HA	3.02	0.45
70:O4:37:LYS:HB2	70:O4:37:LYS:HE3	1.56	0.45
79:Q3:49:ARG:HB2	79:Q3:55:TRP:CZ3	2.50	0.45
3:S1:30:PHE:CD1	3:S1:94:LYS:HA	4.23	0.45
6:S4:100:ARG:O	6:S4:102:VAL:HG12	2.45	0.45
20:C8:125:ILE:HG12	35:SM:61:ILE:HG23	1.99	0.45
35:SM:61:ILE:HG13	35:SM:61:ILE:H	1.61	0.45
34:SR:90:ARG:HE	34:SR:102:ARG:HE	1.63	0.45
1:2:1619:C:H2'	1:2:1620:C:H6	1.82	0.45
1:2:542:A:H5''	1:2:544:A:N9	2.31	0.45
36:5:1078:U:O2	36:5:1082:U:C2	2.69	0.45
36:5:2985:C:H2'	36:5:2986:U:C6	2.51	0.45
36:5:3366:G:H2'	36:5:3367:C:H6	1.81	0.45
36:5:536:U:H1'	36:5:559:A:C8	2.51	0.45
36:5:601:U:H2'	36:5:602:A:C8	2.51	0.45
49:M3:14:PHE:CE1	36:5:665:A:H1'	134.76	0.45
16:C4:136:ARG:HD2	1:6:1769:U:O2	304.46	0.45
10:S8:31:ARG:O	1:6:331:A:H4'	283.16	0.45
1:6:809:A:C6	1:6:810:G:C6	3.04	0.45
14:C2:41:LEU:O	14:C2:43:ARG:HD3	2.16	0.45
21:C9:14:PHE:CZ	21:C9:132:LEU:HD12	5.59	0.45
22:D0:61:LYS:CG	22:D0:86:ILE:HB	2.46	0.45
23:D1:74:GLN:OE1	23:D1:81:ASN:N	3.97	0.45
23:D1:71:ARG:HG2	23:D1:83:TRP:CZ3	3.18	0.45
32:E0:41:THR:O	32:E0:45:VAL:HB	2.97	0.45
40:L3:106:TRP:HB2	40:L3:133:TYR:CE2	2.63	0.45
41:L4:112:LYS:HG2	36:5:790:U:C5'	120.66	0.45
44:L7:176:TYR:CZ	44:L7:197:GLN:HG2	2.51	0.45
47:M0:121:LYS:HB3	47:M0:121:LYS:HE2	1.78	0.45
47:M0:41:ALA:O	47:M0:139:ARG:NH2	2.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:M0:10:ARG:NH2	47:M0:56:GLU:OE1	2.82	0.45
49:M3:157:ARG:HG2	49:M3:158:ALA:H	1.81	0.45
49:M3:187:ALA:HA	49:M3:190:LYS:HE3	6.26	0.45
49:M3:56:PRO:CB	49:M3:112:ASN:HD21	2.30	0.45
51:M5:23:GLN:HG2	51:M5:122:ASN:ND2	2.30	0.45
52:M6:127:LEU:HD22	56:N0:156:VAL:HG12	1.98	0.45
57:N1:85:LEU:HD23	57:N1:85:LEU:HA	1.77	0.45
58:N2:33:TYR:CE2	58:N2:63:VAL:HG21	2.51	0.45
68:O2:126:LEU:HD22	68:O2:127:ALA:H	4.00	0.45
68:O2:16:LYS:O	68:O2:17:PHE:HB2	4.71	0.45
76:Q0:111:ARG:HG3	76:Q0:112:LYS:HD2	2.06	0.45
2:S0:168:HIS:O	2:S0:170:ILE:N	2.50	0.45
2:S0:71:GLU:HA	2:S0:95:ALA:H	3.86	0.45
5:S3:187:LYS:HE3	5:S3:187:LYS:HB2	4.39	0.45
6:S4:193:GLY:O	6:S4:210:ILE:HG23	2.17	0.45
6:S4:49:ARG:HD2	6:S4:50:ASN:ND2	5.29	0.45
6:S4:68:ARG:NH1	6:S4:76:VAL:HG21	2.30	0.45
6:S4:87:MET:O	6:S4:122:LYS:HE3	2.16	0.45
7:S5:161:ASP:O	30:D8:45:LYS:N	3.37	0.45
7:S5:29:ILE:HG22	7:S5:34:GLN:HG3	1.98	0.45
7:S5:57:SER:O	7:S5:59:VAL:HG23	2.16	0.45
9:S7:84:LYS:HD3	9:S7:84:LYS:HA	1.80	0.45
35:SM:64:LYS:O	35:SM:65:THR:OG1	2.30	0.45
34:SR:93:ASP:HB2	34:SR:100:TYR:CE1	2.51	0.45
34:SR:76:ASP:OD1	34:SR:76:ASP:N	2.39	0.45
36:1:1295:G:O2'	56:N0:115:ARG:NH1	2.43	0.45
36:1:1581:C:H2'	36:1:1582:C:C5'	2.47	0.45
36:1:2154:U:H4'	39:L2:240:ALA:CB	2.47	0.45
36:1:2393:G:O2'	36:1:2394:G:OP2	2.34	0.45
36:1:250:U:C5	36:1:251:G:H2'	2.52	0.45
36:1:291:C:H2'	36:1:292:U:H6	1.81	0.45
36:1:3165:A:H2'	36:1:3166:C:C6	2.51	0.45
36:1:76:G:O2'	49:M3:100:ARG:NH1	2.39	0.45
1:2:1147:A:H2'	1:2:1148:C:H6	1.81	0.45
1:2:225:A:H2'	1:2:226:A:O4'	2.17	0.45
1:2:926:A:C2	16:C4:125:SER:HB3	2.51	0.45
38:4:58:G:N2	38:4:100:U:C2	2.84	0.45
36:5:1192:C:C5	87:5:4000:OHX:N2	2.84	0.45
36:5:1439:U:H2'	36:5:1440:G:O4'	2.17	0.45
36:5:1741:A:C6	36:5:1742:U:C2	3.05	0.45
79:Q3:34:HIS:NE2	36:5:1792:C:OP2	220.69	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2943:G:N7	36:5:2944:U:C5	2.84	0.45
1:6:1071:U:H2'	1:6:1072:C:C6	2.52	0.45
1:6:542:A:H3'	1:6:542:A:OP1	2.17	0.45
24:D2:32:LYS:NZ	1:6:638:U:OP2	364.90	0.45
1:6:955:A:H4'	1:6:1073:G:O2'	2.17	0.45
12:C0:1:MET:HG2	12:C0:2:LEU:H	1.81	0.45
15:C3:114:ARG:HD3	15:C3:114:ARG:HA	1.71	0.45
15:C3:22:ALA:HB1	15:C3:23:PRO:CA	2.46	0.45
15:C3:94:LYS:HG2	15:C3:118:ILE:HD13	2.92	0.45
16:C4:107:ARG:O	16:C4:109:GLY:N	2.78	0.45
1:2:1499:G:OP2	21:C9:73:VAL:HG23	2.15	0.45
1:2:687:G:H5'	24:D2:119:LYS:HG2	1.98	0.45
24:D2:50:PHE:HB3	24:D2:63:VAL:HG22	2.13	0.45
28:D6:45:VAL:O	28:D6:49:ALA:HB3	5.04	0.45
39:L2:79:ASN:HD21	39:L2:114:SER:HB3	1.81	0.45
40:L3:347:SER:HB3	40:L3:350:ALA:H	1.81	0.45
41:L4:361:HIS:CD2	41:L4:362:ASP:H	2.35	0.45
44:L7:74:SER:HB3	57:N1:141:VAL:O	2.66	0.45
47:M0:170:LYS:HA	47:M0:177:ASP:HA	1.98	0.45
47:M0:190:VAL:HG13	47:M0:197:VAL:CG2	3.16	0.45
47:M0:38:LYS:HB3	47:M0:46:PHE:HE2	2.71	0.45
51:M5:112:ASN:ND2	51:M5:113:LEU:HD22	2.32	0.45
51:M5:46:ASP:OD1	51:M5:50:ARG:NH2	2.32	0.45
52:M6:108:ILE:HA	52:M6:109:PRO:HD2	1.93	0.45
55:M9:20:ARG:HH11	55:M9:21:LYS:HZ2	3.63	0.45
59:N3:75:PRO:HB2	59:N3:103:ALA:O	2.17	0.45
68:O2:6:HIS:HA	68:O2:7:PRO:HD2	2.50	0.45
73:O7:39:TYR:CG	73:O7:40:PRO:HA	2.70	0.45
2:S0:66:ALA:HB1	23:D1:50:TYR:CD1	2.99	0.45
2:S0:76:ILE:HG12	2:S0:98:ILE:HB	4.20	0.45
5:S3:18:TYR:CE1	5:S3:37:VAL:HG23	2.52	0.45
9:S7:184:GLU:HB3	9:S7:185:ILE:H	1.68	0.45
11:S9:127:VAL:O	11:S9:131:GLN:HB2	2.55	0.45
1:2:1426:C:H5''	35:SM:93:ARG:HH12	1.81	0.45
34:SR:178:VAL:HB	34:SR:192:PHE:HB2	2.17	0.45
36:1:1808:G:OP2	63:N7:133:LYS:NZ	2.49	0.45
36:1:22:G:OP1	73:O7:43:LYS:HE2	2.16	0.45
36:1:2316:G:OP1	87:1:3963:OHX:N6	2.50	0.45
36:1:2808:A:H4'	36:1:2809:C:O5'	2.16	0.45
36:1:2836:C:H5	36:1:2852:C:N4	2.12	0.45
36:1:2883:U:H2'	36:1:2884:C:C6	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:975:C:H2'	36:1:976:U:C6	2.51	0.45
1:2:1237:G:H1	1:2:1248:C:H42	1.65	0.45
1:2:1312:A:C4	1:2:1414:U:C4	3.04	0.45
1:2:514:G:O2'	1:2:515:A:H5'	2.17	0.45
1:2:772:G:N2	1:2:774:A:O2'	2.39	0.45
37:3:3:U:H2'	37:3:4:U:C6	2.51	0.45
38:4:24:G:OP2	62:N6:13:ARG:NH1	2.40	0.45
36:5:1908:A:H2'	36:5:1909:A:O4'	2.17	0.45
36:5:2167:A:H2'	36:5:2168:A:C8	2.51	0.45
36:5:2213:A:C6	36:5:2214:A:C6	3.05	0.45
36:5:230:U:O4	87:5:4040:OHX:N4	2.50	0.45
36:5:2601:A:H2'	36:5:2602:G:C8	2.51	0.45
36:5:2689:A:C8	36:5:2702:A:C6	3.04	0.45
36:5:3279:A:H2'	36:5:3280:U:H5'	1.99	0.45
36:5:3191:G:O6	87:5:4052:OHX:N6	2.49	0.45
43:L6:18:LEU:O	36:5:592:A:H4'	218.07	0.45
64:N8:115:LYS:HD2	36:5:715:A:N7	150.79	0.45
1:6:1080:U:O2'	1:6:1081:A:H5'	2.15	0.45
18:C6:9:THR:HA	1:6:1340:U:O4	436.34	0.45
1:6:1531:G:H2'	1:6:1532:U:C6	2.51	0.45
1:6:1654:G:C6	1:6:1745:G:C6	3.05	0.45
8:S6:186:ARG:NH2	1:6:269:G:N7	350.04	0.45
87:5:3914:OHX:N3	87:7:222:OHX:N6	2.65	0.45
1:2:887:A:H5''	16:C4:120:PRO:HB2	1.97	0.45
17:C5:43:ARG:NH1	1:6:1553:G:O6	400.29	0.45
24:D2:31:SER:O	24:D2:34:ILE:HB	2.86	0.45
28:D6:87:ARG:HD2	1:6:1797:A:N1	347.10	0.45
40:L3:199:PHE:C	40:L3:201:LYS:H	2.46	0.45
40:L3:221:THR:HG22	40:L3:222:LYS:O	2.17	0.45
40:L3:387:LEU:HA	40:L3:387:LEU:HD23	2.71	0.45
42:L5:279:LYS:NZ	42:L5:282:ARG:HH12	2.66	0.45
43:L6:54:TYR:OH	43:L6:57:HIS:HB2	2.56	0.45
44:L7:160:ARG:H	36:5:1362:G:H4'	221.47	0.45
47:M0:171:TRP:O	47:M0:174:THR:HG22	2.17	0.45
47:M0:174:THR:HG23	47:M0:176:LEU:N	2.21	0.45
48:M1:11:ASP:HB3	48:M1:12:LEU:H	1.42	0.45
42:L5:25:GLU:O	48:M1:144:CYS:HA	3.27	0.45
48:M1:63:GLU:O	48:M1:64:LYS:HB2	2.15	0.45
50:M4:102:LYS:HE3	50:M4:102:LYS:HB2	4.21	0.45
50:M4:85:TRP:CD1	50:M4:90:VAL:HG13	2.51	0.45
36:1:3185:U:C6	52:M6:126:VAL:HG21	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:M7:126:ARG:HB3	53:M7:140:GLU:HG2	5.14	0.45
54:M8:96:PHE:CE1	54:M8:114:ILE:HA	2.64	0.45
55:M9:146:LYS:HD3	55:M9:146:LYS:HA	4.58	0.45
55:M9:40:ALA:HA	55:M9:43:LYS:HD2	1.97	0.45
49:M3:165:SER:HB2	64:N8:139:ARG:HH21	1.81	0.45
67:O1:62:ARG:HB2	67:O1:66:GLY:O	2.27	0.45
68:O2:4:LEU:HB2	68:O2:90:LYS:O	2.17	0.45
2:S0:119:ARG:HB3	2:S0:119:ARG:NH1	2.30	0.45
4:S2:203:LYS:HB3	4:S2:206:THR:OG1	2.17	0.45
6:S4:136:VAL:HG11	6:S4:148:ARG:NH2	2.32	0.45
9:S7:173:TYR:CD1	9:S7:181:ILE:HD11	4.22	0.45
10:S8:138:ASN:HA	10:S8:141:ARG:HB2	2.60	0.45
11:S9:172:VAL:HG13	1:6:512:A:OP2	457.31	0.45
36:1:1391:C:C2	68:O2:103:LYS:HD3	2.52	0.45
36:1:1922:A:H2'	36:1:1923:C:O4'	2.17	0.45
36:1:958:C:OP1	36:1:2799:A:H3'	2.16	0.45
36:1:1119:C:OP2	87:1:3850:OHX:N1	2.50	0.45
36:1:507:U:H2'	36:1:508:U:C6	2.52	0.45
1:2:1076:A:H2'	1:2:1077:C:C6	2.52	0.45
1:2:1114:G:HO2'	1:2:1130:G:H1	1.65	0.45
1:2:1275:A:C6	1:2:1438:G:C5	3.05	0.45
1:2:1552:U:H2'	1:2:1553:G:O4'	2.17	0.45
36:5:2203:U:O2'	36:5:2204:C:H5'	2.16	0.45
36:5:172:G:N2	36:5:247:C:N3	2.65	0.45
36:5:2661:G:H2'	36:5:2662:G:H8	1.81	0.45
51:M5:12:ARG:HG3	36:5:268:A:C4	128.56	0.45
36:5:1013:G:O6	87:5:4012:OHX:N6	2.50	0.45
36:5:970:A:H1'	36:5:1112:A:N1	2.32	0.45
1:6:1153:G:H2'	1:6:1154:G:O4'	2.16	0.45
1:6:1213:G:H1	1:6:1450:U:H3	1.65	0.45
7:S5:84:LYS:NZ	1:6:1613:U:OP2	369.06	0.45
1:6:1654:G:H2'	1:6:1745:G:N2	2.32	0.45
1:6:404:G:H2'	1:6:405:C:C6	2.51	0.45
14:C2:83:GLU:C	14:C2:85:LYS:H	4.46	0.45
1:2:1550:A:P	17:C5:42:ARG:NH2	2.89	0.45
17:C5:69:GLU:H	17:C5:69:GLU:CD	4.09	0.45
19:C7:87:GLU:O	19:C7:88:VAL:HB	3.02	0.45
1:2:1459:C:N4	20:C8:139:LYS:HE2	2.32	0.45
29:D7:56:CYS:SG	29:D7:57:GLU:N	2.90	0.45
40:L3:286:GLY:HA3	40:L3:321:PHE:CZ	2.52	0.45
40:L3:2:SER:O	40:L3:3:HIS:HB3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L4:163:LYS:HG3	36:5:209:A:N7	88.01	0.45
41:L4:309:ARG:CZ	41:L4:312:VAL:HG11	2.92	0.45
41:L4:43:ASN:ND2	41:L4:43:ASN:O	4.17	0.45
43:L6:38:THR:HG23	43:L6:90:LYS:HE2	1.97	0.45
45:L8:41:GLN:HG3	45:L8:44:ARG:NH1	2.31	0.45
47:M0:150:GLU:OE1	47:M0:154:ARG:NE	2.49	0.45
48:M1:166:LYS:HE2	48:M1:166:LYS:HB2	1.66	0.45
50:M4:40:ASP:C	50:M4:42:LYS:H	2.42	0.45
36:1:63:A:H5''	51:M5:174:ILE:HG21	1.97	0.45
51:M5:94:TYR:HD1	51:M5:96:ARG:H	1.64	0.45
54:M8:133:LYS:HB2	54:M8:135:GLN:HE22	1.80	0.45
55:M9:103:ARG:HD2	55:M9:124:TYR:CE1	2.52	0.45
55:M9:134:HIS:CD2	36:5:1947:G:H5'	236.43	0.45
64:N8:132:LYS:O	64:N8:136:GLU:HG3	2.38	0.45
76:Q0:94:SER:HA	76:Q0:124:LYS:H	2.10	0.45
76:Q0:88:LYS:HB3	76:Q0:88:LYS:HE3	3.50	0.45
4:S2:227:PRO:O	4:S2:230:TRP:HB2	2.95	0.45
5:S3:31:GLU:O	5:S3:54:ARG:NH2	3.85	0.45
5:S3:7:LYS:HB2	1:6:1515:A:OP2	444.86	0.45
7:S5:61:TYR:CE1	7:S5:165:LEU:HB2	3.03	0.45
8:S6:27:PHE:HB3	8:S6:102:VAL:HG11	2.02	0.45
8:S6:55:GLY:O	8:S6:63:MET:HG3	2.17	0.45
11:S9:105:LEU:HA	11:S9:105:LEU:HD12	2.02	0.45
1:2:768:C:C2	11:S9:143:ILE:HG12	2.52	0.45
11:S9:109:LEU:CB	11:S9:146:PHE:HB3	2.48	0.45
34:SR:235:SER:O	34:SR:237:GLN:NE2	4.24	0.45
36:1:1108:U:H2'	36:1:1109:U:H6	1.82	0.45
36:1:2144:A:C4	36:1:2281:A:C6	3.05	0.45
36:1:2245:C:H4'	39:L2:221:LYS:O	2.17	0.45
36:1:2343:C:H2'	36:1:2344:U:C6	2.47	0.45
36:1:2421:U:H2'	36:1:2422:C:O4'	2.16	0.45
36:1:2443:A:N6	36:1:2504:U:C4	2.85	0.45
36:1:2223:A:N6	36:1:2783:U:O2'	2.48	0.45
36:1:3099:C:H5	36:1:3100:U:C4	2.34	0.45
36:1:3349:C:O5'	36:1:3349:C:H6	2.00	0.45
36:1:565:U:H2'	36:1:566:G:C8	2.52	0.45
36:1:802:C:H2'	36:1:803:C:C6	2.52	0.45
36:1:830:A:H2'	36:1:831:G:O4'	2.16	0.45
1:2:1291:G:N2	1:2:1324:G:N2	2.64	0.45
1:2:1387:G:N7	19:C7:44:LYS:NZ	2.58	0.45
1:2:392:G:H4'	1:2:1672:G:H21	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:553:G:C6	1:2:554:C:N3	2.84	0.45
87:1:3769:OHX:N4	38:4:1:A:OP1	2.50	0.45
38:4:22:U:OP1	62:N6:12:ARG:NH2	2.45	0.45
36:5:1613:A:H2'	36:5:1614:C:C6	2.52	0.45
36:5:998:A:O2'	36:5:999:G:H5'	2.17	0.45
1:6:1227:A:H4'	1:6:1228:G:H5'	1.98	0.45
1:6:194:U:H2'	1:6:194:U:O2	2.15	0.45
25:D3:10:ASN:HB2	1:6:633:U:P	337.70	0.45
1:6:811:A:C4	1:6:858:G:H1'	2.52	0.45
1:2:861:U:O2'	15:C3:20:ARG:NH2	2.50	0.45
15:C3:3:ARG:HB2	15:C3:8:GLY:O	2.17	0.45
20:C8:17:LEU:O	20:C8:20:THR:N	2.92	0.45
1:2:1565:C:OP1	20:C8:41:ARG:HG3	2.17	0.45
22:D0:37:VAL:HG21	22:D0:109:GLU:HB2	1.99	0.45
25:D3:47:SER:HG	25:D3:48:HIS:CE1	4.42	0.45
40:L3:144:ILE:O	40:L3:148:LEU:HB2	2.17	0.45
36:1:3312:U:C5'	40:L3:25:ILE:HD12	2.46	0.45
41:L4:317:PRO:HA	41:L4:323:VAL:HG22	2.73	0.45
42:L5:22:ARG:NH2	42:L5:28:THR:OG1	2.48	0.45
43:L6:145:LEU:O	43:L6:148:GLU:N	2.49	0.45
46:L9:16:VAL:HA	46:L9:28:VAL:O	2.17	0.45
47:M0:87:LEU:HA	47:M0:138:VAL:HG13	1.98	0.45
51:M5:186:GLY:O	51:M5:190:THR:HG23	2.16	0.45
36:1:3007:U:OP1	52:M6:73:PHE:HA	2.16	0.45
54:M8:184:PHE:CG	36:5:2730:G:H4'	191.72	0.45
58:N2:92:TRP:N	58:N2:92:TRP:CD1	4.09	0.45
62:N6:53:ASP:HB2	62:N6:110:HIS:CD2	2.49	0.45
62:N6:83:ASP:OD1	62:N6:84:LYS:N	2.50	0.45
68:O2:103:LYS:O	68:O2:106:VAL:HG22	2.21	0.45
77:Q1:13:LEU:HD22	77:Q1:17:ARG:HG3	4.29	0.45
78:Q2:32:LYS:HA	78:Q2:32:LYS:HD2	4.57	0.45
79:Q3:6:LYS:NZ	79:Q3:7:LYS:HE2	5.69	0.45
5:S3:133:GLY:HA3	5:S3:156:PHE:O	2.16	0.45
5:S3:225:TYR:CE2	34:SR:191:ASP:HB2	2.51	0.45
36:1:1478:C:H2'	36:1:1479:U:C6	2.52	0.45
36:1:1734:G:N7	87:1:3812:OHX:N5	2.65	0.45
36:1:2111:G:H5''	60:N4:48:ARG:HE	1.81	0.45
36:1:2273:G:N2	36:1:2311:G:H2'	2.32	0.45
36:1:3326:G:H2'	36:1:3327:G:H8	1.81	0.45
36:1:595:G:C6	36:1:609:G:H5''	2.52	0.45
1:2:1082:C:H42	1:2:1091:A:N6	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:110:U:O2'	1:2:797:G:H1'	2.17	0.45
1:2:1407:U:H2'	1:2:1408:G:O4'	2.17	0.45
1:2:392:G:H4'	1:2:1672:G:N2	2.31	0.45
1:2:1773:C:C2	1:2:1789:G:C2	3.05	0.45
44:L7:209:ASN:ND2	36:5:1333:C:H1'	242.01	0.45
36:5:1350:A:C5	36:5:1351:U:H1'	2.52	0.45
36:5:145:G:O6	87:5:3932:OHX:N2	2.50	0.45
36:5:1593:A:H2'	36:5:1594:A:C8	2.52	0.45
36:5:2518:C:H2'	36:5:2519:A:C8	2.52	0.45
36:5:3143:C:O2'	87:5:3849:OHX:N3	2.50	0.45
36:5:3152:U:O2	87:5:4147:OHX:N1	2.50	0.45
36:5:329:U:OP2	87:5:3962:OHX:N5	2.50	0.45
18:C6:125:GLU:N	1:6:1585:U:OP1	396.03	0.45
1:6:309:C:H2'	1:6:310:C:C6	2.52	0.45
12:C0:48:SER:HB2	1:6:1220:C:P	438.86	0.45
18:C6:99:GLU:OE1	34:SR:60:SER:N	2.50	0.45
24:D2:68:ARG:HE	24:D2:68:ARG:HB3	4.24	0.45
25:D3:95:PHE:CE1	25:D3:135:LEU:HB3	2.51	0.45
26:D4:58:PHE:CE2	26:D4:72:PHE:HB3	3.08	0.45
39:L2:169:ILE:HG22	39:L2:170:ALA:O	2.72	0.45
41:L4:50:TYR:CD2	41:L4:109:TRP:HH2	2.67	0.45
41:L4:140:HIS:HA	41:L4:177:ASP:OD1	2.17	0.45
41:L4:125:ALA:HB1	41:L4:238:LEU:HB3	1.99	0.45
41:L4:135:VAL:HA	41:L4:245:GLY:O	2.16	0.45
41:L4:285:ASP:O	41:L4:289:ILE:HG13	2.48	0.45
41:L4:341:SER:O	36:5:515:C:O2'	299.73	0.45
36:1:520:U:O4	41:L4:349:THR:HG23	2.16	0.45
41:L4:6:VAL:HG21	41:L4:255:PHE:CZ	2.51	0.45
42:L5:160:PHE:CD2	42:L5:179:ARG:HB3	2.51	0.45
44:L7:125:GLU:HA	44:L7:128:LYS:HB2	1.99	0.45
46:L9:103:ILE:HG13	46:L9:136:PHE:HE2	1.82	0.45
46:L9:94:TYR:CD2	46:L9:98:PRO:HA	2.51	0.45
47:M0:148:VAL:O	47:M0:152:LEU:N	2.97	0.45
47:M0:210:ILE:HG12	47:M0:217:PHE:CE2	2.93	0.45
47:M0:80:SER:O	47:M0:84:ALA:HB2	2.16	0.45
56:N0:99:ARG:NH1	56:N0:126:VAL:O	2.89	0.45
59:N3:28:ASN:ND2	59:N3:112:SER:HB2	2.31	0.45
59:N3:114:ILE:HD12	59:N3:133:SER:HA	3.12	0.45
61:N5:45:LYS:HB2	61:N5:45:LYS:HE2	1.83	0.45
62:N6:57:LEU:HD22	62:N6:58:VAL:N	2.67	0.45
67:O1:72:ARG:O	67:O1:96:VAL:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:O3:69:GLY:HA2	69:O3:85:PHE:HA	1.98	0.45
70:O4:86:LYS:O	70:O4:90:ILE:HG12	2.16	0.45
36:1:359:U:O2'	73:O7:16:HIS:ND1	2.46	0.45
75:O9:2:ALA:N	75:O9:5:LYS:HZ3	6.26	0.45
76:Q0:127:LEU:HD13	76:Q0:128:LYS:HB2	6.16	0.45
39:L2:96:LEU:HD22	79:Q3:83:ILE:HG23	1.98	0.45
3:S1:26:ARG:O	3:S1:50:LYS:HB2	3.89	0.45
7:S5:188:LYS:NZ	27:D5:67:ASP:OD2	2.50	0.45
10:S8:74:LYS:HA	10:S8:74:LYS:HD2	2.58	0.45
34:SR:319:ASN:OD1	34:SR:319:ASN:N	2.81	0.45
36:1:1068:C:H5'	57:N1:110:LYS:HE3	1.98	0.45
36:1:2137:U:C6	36:1:2141:U:C4	3.04	0.45
36:1:2261:G:H21	36:1:2262:A:N6	2.14	0.45
36:1:2794:G:O2'	36:1:2795:U:OP2	2.28	0.45
36:1:3030:G:C6	36:1:3031:G:C4	3.05	0.45
36:1:315:C:OP2	72:O6:28:TYR:OH	2.33	0.45
36:1:2767:U:O4	87:1:3934:OHX:N6	2.50	0.45
36:1:729:C:H2'	36:1:730:C:C6	2.48	0.45
36:1:915:A:H2'	36:1:915:A:N3	2.32	0.45
1:2:1101:G:O3'	24:D2:76:SER:OG	2.28	0.45
1:2:226:A:H2'	1:2:227:U:H5'	1.99	0.45
1:2:495:C:H3'	1:2:496:G:C4'	2.46	0.45
1:2:631:G:H2'	1:2:632:U:C6	2.52	0.45
36:5:1070:U:H2'	36:5:1071:U:O4'	2.17	0.45
36:5:1867:A:H2'	36:5:1868:G:C8	2.52	0.45
36:5:2438:A:H2'	36:5:2439:A:H5''	1.99	0.45
79:Q3:62:LYS:NZ	36:5:2554:A:H62	218.46	0.45
36:5:2846:U:O2'	87:5:3965:OHX:N5	2.49	0.45
36:5:3251:U:H2'	36:5:3252:G:C8	2.52	0.45
36:5:2687:G:N7	87:5:3835:OHX:N1	2.65	0.45
36:5:498:A:H2'	36:5:499:G:H8	1.79	0.45
1:6:1137:A:H2	1:6:1138:A:C5	2.34	0.45
1:6:130:C:O2'	1:6:137:U:N3	2.50	0.45
20:C8:138:THR:OG1	1:6:1459:C:OP2	352.62	0.45
1:6:1620:C:H2'	1:6:1621:U:C6	2.52	0.45
71:O5:7:TYR:OH	38:8:87:G:OP1	16.89	0.45
17:C5:102:PHE:CZ	1:6:1241:G:H5'	386.73	0.45
19:C7:81:LYS:HB2	19:C7:81:LYS:HE3	1.61	0.45
23:D1:71:ARG:HG2	23:D1:83:TRP:CZ2	3.45	0.45
25:D3:79:ASN:HB3	25:D3:81:LYS:HG3	3.97	0.45
30:D8:40:ILE:HG23	30:D8:62:GLU:HB2	2.92	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:E1:103:LEU:HD12	1:6:1252:C:H5'	456.86	0.45
40:L3:231:HIS:CD2	40:L3:270:ARG:CZ	3.35	0.45
42:L5:132:THR:O	42:L5:132:THR:OG1	2.40	0.45
44:L7:160:ARG:HD2	44:L7:203:TRP:CE2	2.51	0.45
44:L7:207:LEU:O	36:5:1334:U:H5'	240.98	0.45
45:L8:195:SER:O	45:L8:197:VAL:N	2.46	0.45
45:L8:244:ALA:HA	45:L8:247:ASP:HB2	2.46	0.45
47:M0:46:PHE:HD2	47:M0:139:ARG:HE	1.65	0.45
55:M9:65:ALA:O	55:M9:68:GLN:HB3	2.35	0.45
36:1:1320:C:O2	56:N0:115:ARG:NH2	2.50	0.45
36:1:1323:G:O3'	56:N0:2:ALA:HA	2.16	0.45
42:L5:17:GLN:HE22	57:N1:22:HIS:N	2.70	0.45
62:N6:112:ASP:H	62:N6:115:ARG:HB2	1.81	0.45
38:4:73:U:OP2	62:N6:75:ARG:HB2	2.17	0.45
67:O1:27:LYS:O	67:O1:30:PRO:HD2	2.16	0.45
70:O4:80:ARG:HD3	70:O4:80:ARG:HA	2.23	0.45
73:O7:58:THR:O	73:O7:60:GLY:N	2.50	0.45
2:S0:77:SER:HB2	2:S0:124:THR:HG21	2.15	0.45
2:S0:31:VAL:N	2:S0:149:LEU:O	2.40	0.45
3:S1:101:HIS:HA	3:S1:217:LEU:HD22	1.99	0.45
7:S5:87:CYS:SG	7:S5:92:ARG:HG3	3.61	0.45
8:S6:137:ARG:NH2	8:S6:177:ARG:HE	2.08	0.45
35:SM:50:ASN:N	35:SM:50:ASN:OD1	3.09	0.45
34:SR:88:THR:HG21	34:SR:102:ARG:HH22	1.93	0.45
36:1:226:C:H4'	62:N6:29:VAL:O	2.17	0.45
36:1:2768:U:H1'	78:Q2:28:TYR:HE1	1.81	0.45
36:1:2892:A:H2'	36:1:2893:C:C6	2.51	0.45
36:1:3045:G:O3'	40:L3:275:ARG:NH1	2.49	0.45
36:1:3215:A:C4	36:1:3259:U:C2	3.05	0.45
36:1:3366:G:H2'	36:1:3367:C:C6	2.52	0.45
36:1:408:A:OP1	87:1:3950:OHX:N3	2.49	0.45
36:1:1070:U:O4	87:1:3993:OHX:N3	2.49	0.45
1:2:420:A:H2'	1:2:421:A:O4'	2.17	0.45
1:2:915:A:H2'	1:2:915:A:N3	2.32	0.45
36:5:1109:U:O4	87:5:3904:OHX:N4	2.50	0.45
36:5:1298:C:OP2	87:5:3928:OHX:N5	2.50	0.45
36:5:2403:G:N7	36:5:2870:C:H4'	2.31	0.45
78:Q2:89:LYS:HG3	36:5:2653:C:P	237.42	0.45
56:N0:170:THR:HG1	36:5:3185:U:HO2'	307.00	0.45
40:L3:309:GLY:HA2	36:5:3328:G:H21	215.76	0.45
1:6:1390:U:H6	1:6:1412:G:H1'	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:S2:164:SER:HB3	1:6:14:C:OP1	375.75	0.45
18:C6:122:ARG:HB3	1:6:1584:G:C8	397.63	0.45
1:6:770:A:OP2	87:6:2105:OHX:N3	2.50	0.45
37:7:102:A:OP1	87:7:221:OHX:N2	2.50	0.45
12:C0:52:LYS:HE3	1:6:1220:C:H5'	444.66	0.45
18:C6:25:GLY:H	18:C6:63:ILE:HA	1.81	0.45
30:D8:54:LEU:HD23	30:D8:56:LEU:HD21	1.99	0.45
32:E0:58:PRO:HB2	32:E0:61:SER:OG	2.17	0.45
33:E1:113:LYS:HE3	33:E1:113:LYS:HB3	1.87	0.45
40:L3:114:VAL:HG13	40:L3:163:HIS:CG	2.73	0.45
41:L4:261:VAL:HG12	41:L4:271:LYS:HE2	1.97	0.45
41:L4:276:LEU:HD12	41:L4:276:LEU:H	1.82	0.45
42:L5:93:THR:HG22	42:L5:158:ARG:HH11	8.98	0.45
42:L5:54:ARG:HG3	37:7:5:G:O3'	282.86	0.45
42:L5:76:ALA:O	42:L5:105:ILE:HD11	3.05	0.45
46:L9:92:TYR:OH	46:L9:101:VAL:HB	2.17	0.45
47:M0:47:PRO:HB3	47:M0:171:TRP:CE2	2.58	0.45
47:M0:36:LEU:HD22	47:M0:73:ASN:CG	2.37	0.45
46:L9:47:LYS:NZ	50:M4:6:ILE:H	2.15	0.45
53:M7:24:VAL:HG13	53:M7:86:LYS:HG2	2.45	0.45
54:M8:42:ALA:HA	54:M8:43:PRO:HD3	1.79	0.45
54:M8:44:PHE:CD1	54:M8:139:ILE:HD11	2.52	0.45
54:M8:57:ILE:HD13	54:M8:147:ARG:CZ	2.47	0.45
55:M9:99:LEU:HD12	36:5:1722:U:H5''	225.21	0.45
58:N2:37:LEU:O	58:N2:41:ILE:HG13	2.18	0.45
61:N5:96:LYS:O	61:N5:100:LYS:HB2	2.62	0.45
66:O0:70:PHE:CD2	66:O0:77:LEU:HD13	2.60	0.45
66:O0:95:ALA:O	66:O0:97:ASP:N	2.47	0.45
36:1:1804:A:O2'	70:O4:78:GLY:O	2.33	0.45
72:O6:74:LYS:HG3	72:O6:80:PHE:HA	1.99	0.45
74:O8:8:ILE:HD12	74:O8:8:ILE:H	2.55	0.45
75:O9:10:LYS:O	75:O9:13:MET:HB2	2.17	0.45
75:O9:20:ASN:ND2	75:O9:20:ASN:O	2.49	0.45
2:S0:172:LEU:O	2:S0:176:LEU:HG	2.17	0.45
2:S0:52:LYS:HD3	23:D1:82:VAL:HA	3.28	0.45
3:S1:229:MET:HA	3:S1:232:HIS:ND1	2.32	0.45
4:S2:61:LEU:HA	4:S2:62:PRO:HD2	1.85	0.45
5:S3:25:PHE:HD2	5:S3:37:VAL:HG11	2.61	0.45
6:S4:195:ILE:HG22	6:S4:196:VAL:H	3.23	0.45
6:S4:211:LYS:O	6:S4:211:LYS:HG3	2.17	0.45
6:S4:112:HIS:CE1	6:S4:239:PRO:HA	2.90	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S4:36:HIS:CG	6:S4:85:GLY:HA3	2.52	0.45
7:S5:175:LEU:O	7:S5:177:ILE:N	3.70	0.45
8:S6:70:PRO:O	8:S6:98:ARG:NH1	2.86	0.45
8:S6:78:THR:HG22	8:S6:92:ARG:HG2	1.99	0.45
9:S7:98:ILE:HG12	9:S7:121:VAL:HG21	1.99	0.45
19:C7:33:ARG:HH22	34:SR:85:TRP:HB3	2.51	0.45
36:1:1148:G:C2	36:1:1156:C:C2	3.04	0.44
36:1:915:A:H8	36:1:2136:C:O2'	2.00	0.44
36:1:2244:A:H5''	39:L2:243:THR:OG1	2.17	0.44
36:1:2280:A:C4	36:1:2282:U:C5	3.05	0.44
36:1:2830:G:H2'	36:1:2831:G:H8	1.81	0.44
36:1:2921:U:H2'	36:1:2923:U:OP2	2.17	0.44
36:1:304:G:N3	36:1:304:G:H2'	2.31	0.44
36:1:534:U:H1'	56:N0:146:LYS:HD2	1.99	0.44
36:1:980:A:OP2	36:1:980:A:H8	2.01	0.44
1:2:1451:C:H2'	1:2:1452:U:H6	1.82	0.44
1:2:453:U:O4	87:2:2005:OHX:N5	2.50	0.44
1:2:776:G:H2'	1:2:777:C:O4'	2.17	0.44
68:O2:44:ARG:NH1	36:5:1145:G:OP1	208.10	0.44
36:5:1456:A:H4'	36:5:1457:U:O5'	2.17	0.44
36:5:1602:A:C6	36:5:1603:A:C6	3.05	0.44
53:M7:139:TYR:CE1	36:5:2355:G:H5'	144.54	0.44
36:5:2924:U:O2'	87:5:4016:OHX:N1	2.51	0.44
36:5:643:U:O4	36:5:644:G:C6	2.70	0.44
1:6:1002:G:C5	1:6:1003:A:N7	2.85	0.44
1:6:1258:U:H5	1:6:1259:U:C4	2.35	0.44
1:6:339:C:O2'	1:6:340:U:H5'	2.17	0.44
3:S1:216:LYS:NZ	1:6:886:U:OP2	277.59	0.44
12:C0:55:VAL:HB	12:C0:68:LEU:HD12	3.16	0.44
15:C3:49:GLN:HA	15:C3:52:VAL:HB	3.32	0.44
16:C4:44:GLY:O	16:C4:59:ALA:HB1	2.34	0.44
39:L2:27:ALA:HB3	39:L2:128:ARG:HH21	1.95	0.44
40:L3:116:ARG:HH21	40:L3:174:LYS:HD3	1.83	0.44
40:L3:43:LEU:HD22	40:L3:203:VAL:HG11	2.00	0.44
41:L4:84:ARG:O	41:L4:84:ARG:HG3	2.96	0.44
42:L5:109:THR:O	42:L5:112:LYS:N	2.97	0.44
42:L5:155:THR:HA	42:L5:179:ARG:HD3	1.99	0.44
43:L6:68:PRO:HB2	43:L6:71:VAL:HG23	1.98	0.44
44:L7:82:LYS:HA	44:L7:119:VAL:HB	1.99	0.44
45:L8:109:LEU:HA	45:L8:109:LEU:HD13	4.19	0.44
46:L9:88:TYR:CZ	46:L9:184:LYS:HD3	3.27	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:M0:74:LYS:O	47:M0:78:THR:HG23	2.95	0.44
48:M1:109:HIS:NE2	48:M1:122:ILE:HA	2.32	0.44
50:M4:32:LEU:HD21	50:M4:94:TRP:CD2	2.83	0.44
53:M7:29:THR:HA	53:M7:32:THR:OG1	2.17	0.44
54:M8:104:LEU:HA	54:M8:104:LEU:HD23	1.79	0.44
54:M8:94:PHE:CE2	64:N8:119:PRO:HD3	2.52	0.44
36:1:841:A:H5'	55:M9:125:LYS:O	2.17	0.44
55:M9:7:GLN:OE1	55:M9:35:ALA:HB3	6.60	0.44
56:N0:161:LYS:HB3	56:N0:161:LYS:NZ	2.32	0.44
57:N1:136:ARG:HD3	57:N1:139:ARG:NH1	2.33	0.44
36:1:213:A:O4'	62:N6:2:ALA:N	2.51	0.44
64:N8:58:MET:SD	36:5:2775:U:H1'	153.62	0.44
64:N8:86:LYS:O	64:N8:90:TYR:HD2	2.02	0.44
3:S1:169:SER:O	3:S1:173:THR:OG1	2.80	0.44
3:S1:35:PRO:HB2	3:S1:38:PHE:HE2	1.82	0.44
2:S0:119:ARG:HH21	4:S2:240:LEU:HB2	1.82	0.44
2:S0:140:ASN:OD1	4:S2:62:PRO:HD3	2.29	0.44
5:S3:115:ILE:HD11	5:S3:138:VAL:HG21	1.98	0.44
7:S5:117:THR:HG21	7:S5:194:LEU:HD13	3.06	0.44
9:S7:10:SER:HB2	9:S7:42:GLN:OE1	2.16	0.44
9:S7:62:VAL:HG13	9:S7:63:PRO:HD2	2.06	0.44
34:SR:18:GLY:O	34:SR:308:ASN:HA	2.17	0.44
36:1:1178:G:O5'	36:1:1178:G:H8	2.00	0.44
36:1:1460:A:H2'	36:1:1461:A:H8	1.81	0.44
36:1:2259:A:H2'	36:1:2260:U:O4'	2.16	0.44
36:1:2988:C:O2'	40:L3:266:ARG:HD3	2.18	0.44
36:1:3043:C:H2'	36:1:3044:G:O4'	2.17	0.44
36:1:3049:A:N6	36:1:3095:U:O4'	2.49	0.44
36:1:270:U:O2'	36:1:318:A:H1'	2.17	0.44
36:1:3266:G:OP2	43:L6:70:LYS:HE3	2.16	0.44
36:1:514:G:N3	41:L4:341:SER:OG	2.40	0.44
36:1:901:G:H2'	36:1:902:G:H8	1.82	0.44
1:2:1340:U:C2	1:2:1378:U:H4'	2.52	0.44
1:2:1209:C:N4	1:2:1454:G:H1	2.16	0.44
1:2:1616:G:N7	87:2:2101:OHX:N4	2.65	0.44
1:2:367:A:C6	1:2:368:U:C4	3.05	0.44
1:2:748:U:H2'	1:2:749:U:H6	1.81	0.44
37:3:42:A:C5	37:3:43:U:C5	3.05	0.44
38:4:139:U:H2'	38:4:140:G:H8	1.80	0.44
38:4:79:A:H2'	38:4:80:A:O2'	2.16	0.44
36:5:2101:C:O2'	36:5:2102:U:OP1	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2651:G:C4	36:5:2796:G:C2	3.05	0.44
36:5:3132:C:H2'	36:5:3133:C:C6	2.51	0.44
40:L3:128:LYS:O	36:5:3150:A:H4'	209.30	0.44
36:5:324:A:H2'	36:5:325:A:C8	2.52	0.44
36:5:3334:U:O2'	36:5:3368:U:O2	2.34	0.44
36:5:3352:U:O2'	87:5:4153:OHX:N1	2.50	0.44
1:6:122:U:O4	87:6:2031:OHX:N6	2.51	0.44
1:6:1170:G:H1	1:6:1469:A:H61	1.66	0.44
1:6:1606:C:H2'	1:6:1607:G:C8	2.53	0.44
1:6:18:C:O4'	1:6:1137:A:N6	2.51	0.44
1:2:895:G:HO2'	16:C4:38:THR:H	1.59	0.44
30:D8:60:GLU:HB3	30:D8:61:ARG:H	4.38	0.44
32:E0:40:TYR:CD2	32:E0:44:PHE:HE1	7.98	0.44
39:L2:79:ASN:HD22	39:L2:165:VAL:HG22	1.82	0.44
42:L5:115:LEU:HD12	42:L5:119:TYR:CD2	4.83	0.44
37:3:7:G:N7	42:L5:21:ARG:NH2	2.65	0.44
42:L5:60:ILE:HB	42:L5:80:SER:HB3	2.98	0.44
44:L7:54:GLU:OE1	44:L7:186:HIS:NE2	3.59	0.44
36:1:1558:A:C8	45:L8:53:PRO:HB3	2.52	0.44
49:M3:6:ASN:O	54:M8:164:ARG:NH1	3.28	0.44
51:M5:37:HIS:NE2	51:M5:63:ARG:HD2	2.46	0.44
53:M7:39:TRP:O	53:M7:113:TYR:HB2	2.18	0.44
53:M7:60:PHE:CZ	53:M7:84:PRO:HG3	2.52	0.44
57:N1:108:ARG:O	57:N1:112:ASN:HB2	2.82	0.44
63:N7:64:LYS:HD3	63:N7:64:LYS:HA	1.80	0.44
66:O0:36:GLN:OE1	66:O0:38:LYS:HD2	2.17	0.44
67:O1:46:THR:HG21	67:O1:91:SER:OG	2.78	0.44
36:1:654:C:OP1	68:O2:27:ARG:NH2	2.50	0.44
68:O2:4:LEU:HD13	68:O2:4:LEU:HA	2.75	0.44
73:O7:28:HIS:CE1	73:O7:30:GLN:HB2	2.76	0.44
76:Q0:127:LEU:HD22	76:Q0:128:LYS:HG2	2.00	0.44
78:Q2:16:THR:O	78:Q2:18:ARG:N	4.09	0.44
79:Q3:44:LYS:HD2	79:Q3:59:CYS:SG	3.00	0.44
3:S1:120:LEU:HG	3:S1:142:PHE:CE1	2.52	0.44
3:S1:171:ILE:HA	3:S1:174:LYS:HE3	1.99	0.44
3:S1:179:SER:O	3:S1:179:SER:OG	2.30	0.44
4:S2:174:ARG:HA	4:S2:195:ASP:OD2	2.86	0.44
4:S2:205:ARG:HD2	1:6:6:G:OP2	380.92	0.44
4:S2:214:ALA:O	4:S2:217:ALA:HB3	2.18	0.44
7:S5:73:THR:O	7:S5:75:GLY:N	2.59	0.44
10:S8:18:ARG:NH1	1:6:105:A:OP1	306.21	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:S8:74:LYS:HB2	10:S8:109:PHE:HE1	3.98	0.44
11:S9:38:ASN:HB2	11:S9:41:GLU:HG3	2.00	0.44
36:1:230:U:H2'	36:1:231:G:O4'	2.17	0.44
36:1:2392:C:H5''	36:1:2393:G:OP2	2.18	0.44
36:1:3242:G:H8	40:L3:154:TYR:CE2	2.34	0.44
36:1:594:U:H2'	36:1:609:G:O6	2.17	0.44
36:1:736:A:C6	36:1:737:G:H1'	2.52	0.44
36:1:884:A:N7	36:1:2139:A:C4	2.86	0.44
1:2:1183:A:C6	1:2:1184:A:N1	2.86	0.44
1:2:131:C:HO2'	1:2:132:U:P	2.40	0.44
1:2:1433:G:C4	31:D9:41:GLN:HB3	2.52	0.44
1:2:1684:U:H2'	1:2:1685:G:O4'	2.17	0.44
1:2:939:A:H2'	1:2:940:A:C8	2.51	0.44
36:5:1070:U:C4	36:5:1071:U:C4	3.06	0.44
45:L8:126:SER:OG	36:5:120:G:N2	91.49	0.44
36:5:498:A:O2'	36:5:3273:A:N1	2.44	0.44
36:5:1659:U:O4	87:5:4113:OHX:N4	2.51	0.44
36:5:83:U:H2'	36:5:84:U:O4'	2.17	0.44
1:6:1388:A:C6	1:6:1411:A:C6	3.06	0.44
1:6:452:A:H3'	1:6:453:U:C5	2.52	0.44
12:C0:29:GLN:O	12:C0:31:LYS:N	2.49	0.44
17:C5:80:MET:HE2	17:C5:80:MET:HB3	1.89	0.44
20:C8:52:VAL:HG13	20:C8:61:LEU:HD21	2.90	0.44
20:C8:96:LYS:HB2	20:C8:96:LYS:HE3	3.65	0.44
21:C9:9:VAL:HG22	21:C9:140:LEU:HD21	1.98	0.44
26:D4:124:ARG:HG3	1:6:150:U:OP2	331.21	0.44
1:2:1617:U:O2'	30:D8:21:SER:O	2.29	0.44
39:L2:118:GLU:HG3	39:L2:126:LEU:HD11	2.00	0.44
39:L2:189:TYR:HA	39:L2:192:LYS:HB2	2.32	0.44
39:L2:3:ARG:HD3	36:5:911:C:H42	180.42	0.44
40:L3:56:ILE:HD11	40:L3:359:ILE:HG12	1.99	0.44
41:L4:29:PRO:HG2	41:L4:277:PRO:HB2	1.99	0.44
42:L5:180:PHE:HB3	42:L5:195:LEU:HD13	2.39	0.44
37:3:49:G:OP1	42:L5:90:HIS:HB3	2.18	0.44
43:L6:105:TYR:HD1	43:L6:105:TYR:O	2.74	0.44
47:M0:127:ALA:O	47:M0:129:VAL:HG23	5.91	0.44
37:3:43:U:H4'	48:M1:140:ARG:O	2.17	0.44
49:M3:178:LYS:HD3	49:M3:179:PHE:CE2	3.20	0.44
50:M4:20:VAL:HG13	50:M4:66:THR:OG1	2.17	0.44
50:M4:27:GLN:CD	50:M4:27:GLN:H	2.21	0.44
51:M5:153:ASP:OD2	51:M5:155:VAL:HG22	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:M8:170:ARG:HA	54:M8:174:ARG:CD	3.39	0.44
60:N4:38:SER:O	60:N4:42:GLN:HG3	2.33	0.44
63:N7:102:GLU:H	63:N7:107:ARG:NH2	2.50	0.44
68:O2:19:ARG:HB2	68:O2:31:ASN:O	3.01	0.44
51:M5:147:ARG:NH1	71:O5:101:THR:OG1	3.09	0.44
72:O6:54:GLU:HA	72:O6:57:LEU:HB2	2.27	0.44
79:Q3:29:LEU:HD22	79:Q3:69:TYR:CD2	2.52	0.44
3:S1:164:ILE:HD13	3:S1:207:LEU:HD11	4.04	0.44
7:S5:25:LEU:HD11	18:C6:57:LEU:HD22	2.00	0.44
8:S6:48:TYR:OH	8:S6:119:GLN:O	2.26	0.44
36:1:1665:C:H2'	36:1:1666:G:C8	2.52	0.44
36:1:1878:G:C2'	36:1:1879:A:H5'	2.47	0.44
36:1:2117:A:N7	36:1:3064:U:O2'	2.40	0.44
36:1:2162:U:OP1	39:L2:234:LYS:NZ	2.47	0.44
36:1:233:C:H2'	36:1:234:G:O4'	2.18	0.44
36:1:3048:A:H5''	40:L3:53:MET:HE3	1.99	0.44
36:1:650:C:O5'	36:1:650:C:H6	2.01	0.44
36:1:954:U:O4	36:1:1115:G:H1'	2.17	0.44
1:2:1537:C:N3	87:2:2131:OHX:N1	2.65	0.44
1:2:477:A:H61	1:2:511:A:N6	2.12	0.44
36:5:1018:G:H2'	36:5:1019:G:O4'	2.16	0.44
36:5:109:A:H4'	36:5:110:G:OP1	2.18	0.44
36:5:1470:U:H2'	36:5:1471:U:C6	2.52	0.44
36:5:2144:A:C4	36:5:2281:A:C6	3.06	0.44
36:5:2568:C:N4	36:5:2574:G:C6	2.85	0.44
36:5:2608:G:H2'	36:5:2609:A:H8	1.82	0.44
36:5:3095:U:H2'	36:5:3096:C:C6	2.52	0.44
1:6:83:G:O5'	1:6:83:G:H8	2.00	0.44
1:6:924:A:H2'	1:6:925:G:C8	2.53	0.44
37:7:114:U:H2'	37:7:115:G:C8	2.53	0.44
38:8:149:A:H2'	38:8:150:G:C8	2.53	0.44
5:S3:72:LEU:HA	12:C0:20:VAL:HG11	2.76	0.44
18:C6:9:THR:HG21	18:C6:87:LYS:O	2.44	0.44
20:C8:105:VAL:HG23	20:C8:106:GLU:N	4.37	0.44
2:S0:63:ILE:HG23	23:D1:35:ASN:O	2.17	0.44
23:D1:35:ASN:OD1	23:D1:52:THR:HB	2.62	0.44
24:D2:55:ASP:C	24:D2:57:ARG:H	2.51	0.44
26:D4:14:SER:HA	26:D4:21:LYS:HG3	2.00	0.44
28:D6:21:VAL:O	28:D6:30:ILE:N	2.50	0.44
28:D6:36:ILE:HG23	28:D6:73:TYR:HB2	1.98	0.44
33:E1:88:PRO:HA	33:E1:89:LYS:HA	4.78	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:87:VAL:HB	40:L3:110:LEU:HD11	1.98	0.44
40:L3:306:THR:HG21	40:L3:316:GLU:HB3	3.56	0.44
40:L3:29:VAL:HG12	40:L3:31:ALA:O	2.17	0.44
40:L3:280:HIS:HB3	40:L3:324:VAL:HG13	2.00	0.44
41:L4:193:LYS:HB2	41:L4:193:LYS:HE3	1.74	0.44
42:L5:231:ILE:HG21	42:L5:239:ILE:HD11	1.99	0.44
42:L5:35:ARG:HG2	36:5:2749:G:O2'	250.70	0.44
45:L8:97:TYR:CZ	45:L8:203:VAL:HG22	4.41	0.44
47:M0:30:LYS:HA	47:M0:30:LYS:HD3	3.34	0.44
50:M4:98:SER:HA	50:M4:101:LYS:HD2	3.15	0.44
53:M7:119:VAL:HA	53:M7:145:HIS:O	2.37	0.44
53:M7:52:LEU:HD12	53:M7:52:LEU:HA	1.82	0.44
54:M8:173:GLU:OE2	64:N8:49:HIS:HD2	6.01	0.44
55:M9:38:ARG:O	55:M9:41:ILE:HB	4.33	0.44
36:1:990:U:H4'	57:N1:100:LYS:HB3	1.99	0.44
58:N2:15:PHE:CE2	58:N2:71:PHE:HD1	2.35	0.44
59:N3:128:ARG:CZ	59:N3:128:ARG:HB3	4.10	0.44
61:N5:63:ILE:HG13	61:N5:84:PHE:CD1	2.52	0.44
64:N8:94:ALA:HB3	64:N8:121:VAL:HG13	1.99	0.44
65:N9:24:PRO:HG2	65:N9:26:THR:HG22	6.93	0.44
66:O0:47:ASN:HD21	66:O0:74:ASN:H	1.65	0.44
67:O1:84:ASP:OD1	67:O1:84:ASP:N	2.49	0.44
69:O3:88:ASN:OD1	69:O3:88:ASN:N	2.83	0.44
75:O9:7:PHE:CE2	38:8:113:U:C4	98.64	0.44
2:S0:112:THR:O	2:S0:115:PHE:HB2	2.17	0.44
2:S0:179:ARG:O	2:S0:183:ARG:HG3	2.17	0.44
3:S1:23:PRO:HB3	3:S1:26:ARG:NH1	2.94	0.44
3:S1:70:LEU:CD1	3:S1:79:HIS:HB3	2.47	0.44
4:S2:84:LYS:NZ	4:S2:208:GLU:HB2	5.42	0.44
6:S4:102:VAL:HG23	6:S4:182:TYR:HE1	1.82	0.44
6:S4:196:VAL:HG12	6:S4:197:HIS:HB2	2.70	0.44
7:S5:113:ILE:O	7:S5:117:THR:OG1	2.28	0.44
8:S6:71:THR:HG22	8:S6:72:ARG:H	3.76	0.44
35:SM:76:VAL:HG12	35:SM:77:THR:O	2.17	0.44
34:SR:33:LEU:O	34:SR:45:TRP:HD1	2.51	0.44
36:1:1195:A:H1'	36:1:1319:G:H4'	1.98	0.44
36:1:1525:G:C5	36:1:1829:G:C6	3.05	0.44
36:1:1641:U:O2'	36:1:1643:A:OP2	2.36	0.44
36:1:2321:A:H2'	36:1:2322:C:O4'	2.17	0.44
36:1:782:U:H2'	36:1:783:A:O4'	2.18	0.44
36:1:945:C:OP1	68:O2:33:ARG:HG3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1471:A:N3	1:2:1474:G:O2'	2.46	0.44
1:2:1729:C:H2'	1:2:1730:A:O4'	2.16	0.44
37:3:36:C:O2	37:3:45:A:H1'	2.18	0.44
37:3:49:G:H4'	37:3:50:U:O5'	2.18	0.44
36:5:142:C:H2'	36:5:143:G:O4'	2.18	0.44
36:5:2258:U:H2'	36:5:2259:A:O4'	2.18	0.44
36:5:230:U:H2'	36:5:231:G:O4'	2.18	0.44
36:5:3045:G:H2'	36:5:3046:A:O4'	2.18	0.44
36:5:3198:U:H4'	36:5:3199:G:OP2	2.17	0.44
36:5:3287:U:C4	36:5:3288:G:N7	2.85	0.44
36:5:380:U:H2'	36:5:381:U:H6	1.82	0.44
87:5:3893:OHX:N2	87:5:4117:OHX:N1	2.65	0.44
36:5:720:A:H2'	36:5:720:A:N3	2.33	0.44
36:5:92:G:H5'	36:5:93:C:C5'	2.48	0.44
1:6:1046:G:N7	87:6:2018:OHX:N1	2.65	0.44
1:6:25:C:O2	87:6:2074:OHX:N6	2.50	0.44
1:6:40:A:H2'	1:6:41:A:O4'	2.17	0.44
38:8:1:A:C2	38:8:2:A:C4	3.06	0.44
12:C0:25:LYS:HB2	12:C0:64:TYR:HE2	1.82	0.44
17:C5:69:GLU:OE1	87:C5:201:OHX:N2	2.51	0.44
18:C6:127:LYS:HA	18:C6:134:ALA:HA	1.97	0.44
1:2:747:C:H4'	24:D2:80:ASN:ND2	2.33	0.44
25:D3:53:VAL:HG13	25:D3:72:VAL:HB	2.78	0.44
28:D6:71:LEU:HD12	28:D6:73:TYR:CZ	2.53	0.44
30:D8:42:ARG:NH1	30:D8:56:LEU:HD22	2.32	0.44
31:D9:33:LYS:O	31:D9:36:LEU:HD23	2.17	0.44
32:E0:13:LYS:O	32:E0:16:SER:OG	2.59	0.44
40:L3:209:PHE:HB3	40:L3:282:ILE:CD1	2.64	0.44
41:L4:135:VAL:O	41:L4:140:HIS:HB2	2.18	0.44
41:L4:13:GLY:O	41:L4:14:GLU:HG2	5.03	0.44
42:L5:119:TYR:OH	42:L5:141:PRO:HD3	2.18	0.44
43:L6:30:LEU:HD23	43:L6:30:LEU:HA	1.74	0.44
43:L6:58:LEU:HA	43:L6:58:LEU:HD23	1.77	0.44
44:L7:119:VAL:HG13	44:L7:124:LEU:CD2	4.27	0.44
45:L8:71:VAL:HA	45:L8:72:PRO:HD2	1.63	0.44
49:M3:16:LYS:O	49:M3:17:HIS:HB2	4.64	0.44
49:M3:54:LEU:HD23	49:M3:141:ALA:HB1	3.83	0.44
50:M4:17:VAL:HG21	50:M4:74:ARG:HB2	1.99	0.44
53:M7:137:ASN:HD22	53:M7:137:ASN:HA	1.58	0.44
54:M8:12:ARG:NH1	36:5:973:A:OP2	181.62	0.44
54:M8:8:LYS:HB2	54:M8:8:LYS:HE3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:N0:2:ALA:HB3	56:N0:32:SER:CB	2.47	0.44
60:N4:58:HIS:CG	60:N4:58:HIS:O	3.00	0.44
63:N7:90:GLU:O	63:N7:92:PHE:N	3.07	0.44
70:O4:100:ILE:H	70:O4:100:ILE:HG13	4.14	0.44
70:O4:54:ILE:HG23	70:O4:70:LYS:HA	2.15	0.44
71:O5:78:LYS:HA	71:O5:81:ARG:CD	2.48	0.44
2:S0:146:LEU:HD12	2:S0:170:ILE:HG22	1.99	0.44
4:S2:66:PHE:CD2	4:S2:130:ILE:HG12	4.59	0.44
4:S2:89:GLN:HB2	1:6:1145:U:O2'	377.03	0.44
6:S4:183:VAL:HG21	6:S4:218:PHE:HE1	1.83	0.44
7:S5:125:THR:O	7:S5:127:GLN:HB2	3.72	0.44
7:S5:225:ARG:HH22	30:D8:57:MET:HB3	3.54	0.44
8:S6:176:GLN:HG3	8:S6:177:ARG:N	2.32	0.44
9:S7:126:LEU:HD13	9:S7:173:TYR:CD2	2.80	0.44
9:S7:184:GLU:HG2	9:S7:185:ILE:H	3.72	0.44
6:S4:26:CYS:SG	11:S9:3:ARG:HG3	3.89	0.44
20:C8:145:ARG:HB2	35:SM:68:ARG:NH2	2.32	0.44
36:1:121:A:C6	45:L8:129:PRO:HG3	2.53	0.44
36:1:1702:U:H1'	36:1:1744:G:N2	2.33	0.44
36:1:2567:C:H2'	36:1:2568:C:H5'	1.99	0.44
36:1:2741:C:H4'	78:Q2:19:LYS:HA	2.00	0.44
36:1:3057:U:O2'	36:1:3059:G:O5'	2.36	0.44
36:1:373:A:N1	36:1:394:G:H4'	2.33	0.44
36:1:827:A:H2'	36:1:828:A:C8	2.51	0.44
1:2:1244:A:HO2'	1:2:1245:G:P	2.39	0.44
1:2:1474:G:H2'	1:2:1475:A:C8	2.52	0.44
1:2:1487:A:H2'	1:2:1488:G:C8	2.53	0.44
1:2:702:G:N7	87:2:2099:OHX:N2	2.65	0.44
1:2:97:C:H2'	1:2:98:U:C6	2.52	0.44
37:3:113:C:C4	37:3:114:U:C4	3.05	0.44
36:5:1276:U:OP2	87:5:3921:OHX:N4	2.50	0.44
36:5:1495:U:H2'	36:5:1842:A:C2	2.53	0.44
36:5:218:G:H2'	36:5:218:G:OP1	2.18	0.44
36:5:2266:U:O5'	36:5:2266:U:H6	2.01	0.44
36:5:2663:G:H2'	36:5:2664:C:O4'	2.17	0.44
36:5:2926:A:H2'	36:5:2927:C:H6	1.83	0.44
60:N4:34:SER:OG	36:5:3085:G:OP1	228.61	0.44
36:5:1940:G:H21	36:5:3362:A:H8	1.65	0.44
36:5:406:G:N2	38:8:16:G:C4	2.86	0.44
36:5:512:U:H2'	36:5:513:G:H8	1.82	0.44
36:5:718:G:N7	36:5:721:G:H1'	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1208:A:N1	1:6:1455:G:N2	2.65	0.44
1:6:1255:G:O2'	1:6:1256:A:O5'	2.30	0.44
1:6:1695:G:N2	1:6:1705:C:H41	2.14	0.44
1:6:1699:G:H1	1:6:1702:A:H5''	1.82	0.44
1:6:419:G:C6	1:6:420:A:C5	3.06	0.44
1:6:52:U:H2'	1:6:53:G:C8	2.53	0.44
12:C0:2:LEU:HB3	12:C0:3:MET:H	4.24	0.44
15:C3:137:PRO:O	15:C3:138:ASN:HB3	2.18	0.44
15:C3:3:ARG:HH21	15:C3:10:GLY:N	2.14	0.44
1:2:1550:A:P	17:C5:42:ARG:HH22	2.41	0.44
18:C6:31:VAL:HG13	18:C6:67:VAL:HB	2.00	0.44
5:S3:203:PRO:HA	19:C7:42:GLN:HB2	1.99	0.44
20:C8:26:ILE:HG13	20:C8:31:ALA:HB2	2.00	0.44
23:D1:60:ARG:HB3	23:D1:60:ARG:CZ	2.47	0.44
23:D1:71:ARG:HA	23:D1:83:TRP:CE3	3.57	0.44
24:D2:126:LEU:HD23	24:D2:126:LEU:HA	1.84	0.44
24:D2:37:PHE:CD2	24:D2:103:ILE:HD12	2.52	0.44
1:2:575:C:N4	25:D3:65:ASN:HD21	2.16	0.44
25:D3:76:LEU:HD23	25:D3:76:LEU:HA	2.13	0.44
1:2:159:U:C6	26:D4:117:LYS:HG2	2.53	0.44
28:D6:4:LYS:HE2	28:D6:5:ARG:HH22	2.58	0.44
28:D6:96:ALA:HA	28:D6:97:PRO:HD3	1.77	0.44
23:D1:64:GLU:OE2	29:D7:3:LEU:HB2	4.53	0.44
29:D7:6:ASP:OD1	29:D7:9:HIS:ND1	2.42	0.44
39:L2:14:SER:OG	39:L2:15:ILE:N	2.90	0.44
40:L3:116:ARG:HD3	40:L3:122:TRP:CG	5.07	0.44
40:L3:84:VAL:HG22	40:L3:162:VAL:HB	2.26	0.44
41:L4:193:LYS:HB3	41:L4:193:LYS:HE3	2.09	0.44
42:L5:86:TYR:CD1	42:L5:247:ILE:HA	2.77	0.44
47:M0:142:ASP:CG	47:M0:178:ARG:HH22	2.21	0.44
47:M0:140:THR:OG1	47:M0:144:ASN:HB3	2.19	0.44
48:M1:50:ALA:HB3	48:M1:61:ARG:HA	2.00	0.44
49:M3:124:ILE:HD11	49:M3:126:PHE:CE1	2.52	0.44
52:M6:25:LYS:HE3	36:5:1176:C:OP1	248.18	0.44
53:M7:10:ASN:O	53:M7:14:SER:HB2	4.03	0.44
53:M7:122:ALA:HB3	53:M7:143:PRO:HB2	2.31	0.44
57:N1:41:ASP:HB2	57:N1:97:LYS:HG2	2.00	0.44
62:N6:111:LEU:HD23	62:N6:116:LYS:HG3	1.99	0.44
62:N6:43:TYR:CD1	62:N6:126:LEU:HA	2.52	0.44
69:O3:45:LEU:HA	69:O3:45:LEU:HD23	2.54	0.44
70:O4:7:PHE:CD2	70:O4:12:PRO:HA	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:O5:77:PRO:O	71:O5:81:ARG:HG3	2.18	0.44
74:O8:5:ILE:HG23	74:O8:10:GLN:OE1	2.18	0.44
36:1:1750:A:H4'	74:O8:26:LYS:HZ1	1.83	0.44
1:2:1642:G:H5'	77:Q1:1:MET:HB3	1.98	0.44
2:S0:168:HIS:HB3	2:S0:203:PHE:CE2	2.52	0.44
4:S2:56:ILE:CG2	4:S2:61:LEU:HB2	2.67	0.44
5:S3:215:GLU:HG2	5:S3:215:GLU:O	2.18	0.44
5:S3:216:PRO:O	5:S3:218:LEU:N	3.53	0.44
6:S4:103:TYR:O	6:S4:182:TYR:OH	2.35	0.44
6:S4:182:TYR:HB2	6:S4:228:ILE:HD13	1.99	0.44
9:S7:137:GLY:HA3	9:S7:153:LEU:HD12	3.26	0.44
9:S7:21:ALA:O	9:S7:25:VAL:HG23	2.34	0.44
10:S8:110:ARG:NH2	36:5:3354:U:O4	241.72	0.44
10:S8:104:ILE:HG13	10:S8:165:LEU:HB2	2.30	0.44
34:SR:222:LEU:HD23	34:SR:234:LEU:HD13	2.45	0.44
36:1:108:A:H2	49:M3:73:ARG:HH22	1.66	0.44
36:1:1293:U:O2'	36:1:1294:A:H5'	2.17	0.44
36:1:1534:A:C8	36:1:1586:G:N2	2.86	0.44
36:1:1668:G:C5	36:1:1669:C:C5	3.05	0.44
36:1:2808:A:N7	36:1:2955:U:H4'	2.33	0.44
36:1:347:G:N7	41:L4:59:GLN:NE2	2.65	0.44
36:1:348:A:N3	36:1:352:A:O2'	2.50	0.44
36:1:397:A:H5'	36:1:398:A:H3'	2.00	0.44
36:1:2814:G:C8	87:1:4071:OHX:N6	2.86	0.44
36:1:742:G:O6	87:1:3870:OHX:N1	2.51	0.44
1:2:1590:G:H2'	1:2:1591:C:H6	1.82	0.44
1:2:885:G:N2	1:2:927:C:O2	2.42	0.44
37:3:28:C:H5''	48:M1:137:ARG:HG2	1.99	0.44
38:4:63:G:O2'	71:O5:49:LYS:HE2	2.17	0.44
36:5:1050:U:O2	36:5:1051:U:H5	2.01	0.44
36:5:2254:U:H2'	36:5:2261:G:H22	1.82	0.44
36:5:3225:C:H2'	36:5:3226:A:H8	1.82	0.44
50:M4:133:LYS:HD3	36:5:3227:A:O2'	301.74	0.44
12:C0:44:LYS:CE	1:6:1217:A:H4'	428.01	0.44
19:C7:4:VAL:HA	1:6:1402:G:OP1	406.06	0.44
1:6:784:C:H2'	1:6:785:U:C6	2.53	0.44
13:C1:56:LYS:HE2	13:C1:56:LYS:HB3	1.83	0.44
14:C2:62:LEU:HD23	14:C2:62:LEU:H	1.83	0.44
15:C3:102:LEU:HD11	15:C3:112:LYS:HA	2.29	0.44
16:C4:104:ALA:HA	16:C4:107:ARG:HB3	2.64	0.44
18:C6:27:GLY:HA2	18:C6:63:ILE:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:C6:99:GLU:OE2	18:C6:102:LYS:NZ	2.40	0.44
23:D1:41:GLU:O	23:D1:44:ARG:NH1	2.41	0.44
24:D2:20:THR:OG1	24:D2:22:LYS:HD3	2.63	0.44
24:D2:82:LYS:O	24:D2:84:GLY:N	2.44	0.44
25:D3:48:HIS:HB3	25:D3:104:LEU:O	2.18	0.44
27:D5:54:VAL:N	27:D5:55:PRO:HD2	2.32	0.44
39:L2:29:LEU:HB2	39:L2:123:ARG:HA	2.13	0.44
40:L3:4:ARG:O	40:L3:5:LYS:HB3	2.17	0.44
37:3:121:U:N3	42:L5:268:GLU:HB3	2.28	0.44
43:L6:52:VAL:HG12	43:L6:53:VAL:H	3.82	0.44
44:L7:47:ARG:HH22	44:L7:179:LEU:HD11	3.05	0.44
36:1:121:A:N1	45:L8:129:PRO:HG3	2.33	0.44
45:L8:82:LEU:HD12	45:L8:82:LEU:HA	1.60	0.44
45:L8:86:THR:HA	45:L8:89:GLU:HB2	3.02	0.44
46:L9:99:ILE:HG21	46:L9:179:ILE:HD11	3.22	0.44
47:M0:172:GLY:C	47:M0:174:THR:H	2.38	0.44
48:M1:26:SER:HB3	48:M1:63:GLU:HG2	2.02	0.44
49:M3:91:ARG:NH2	49:M3:97:VAL:HB	2.33	0.44
52:M6:61:ALA:HA	52:M6:70:PRO:HD2	2.00	0.44
56:N0:26:ARG:NH1	57:N1:150:THR:HG21	2.96	0.44
64:N8:71:PRO:HB2	64:N8:109:TYR:HD2	1.83	0.44
69:O3:59:VAL:HB	69:O3:60:ARG:H	1.52	0.44
71:O5:22:VAL:O	71:O5:26:LYS:HG3	3.67	0.44
74:O8:7:ASP:HB3	74:O8:10:GLN:HB3	2.67	0.44
2:S0:24:LEU:O	2:S0:163:ASN:ND2	2.81	0.44
6:S4:126:VAL:HG22	6:S4:158:ASP:O	5.78	0.44
6:S4:112:HIS:CD2	6:S4:237:SER:HG	2.36	0.44
7:S5:73:THR:N	7:S5:91:GLU:OE2	2.58	0.44
9:S7:48:GLU:HA	9:S7:58:LEU:HD23	1.98	0.44
36:1:1226:G:H2'	36:1:1227:C:C6	2.52	0.44
36:1:1397:C:C2'	36:1:1398:U:H5'	2.47	0.44
36:1:90:C:O2'	36:1:282:G:OP1	2.30	0.44
36:1:2971:A:OP2	87:1:4060:OHX:N1	2.51	0.44
36:1:3279:A:C5	36:1:3280:U:C4	3.05	0.44
36:1:3348:G:H2'	36:1:3349:C:C6	2.53	0.44
36:1:3389:U:O2'	36:1:3390:G:OP2	2.36	0.44
36:1:346:C:C4	36:1:348:A:C8	3.05	0.44
36:1:2983:C:OP1	87:1:4097:OHX:N3	2.51	0.44
36:1:591:G:H21	43:L6:19:LYS:N	2.16	0.44
36:1:972:A:H2'	36:1:973:A:O4'	2.18	0.44
1:2:1064:G:H2'	1:2:1065:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1393:C:H2'	1:2:1394:G:O4'	2.18	0.44
1:2:916:U:H3	16:C4:41:ARG:NH2	2.15	0.44
38:4:31:G:OP2	87:4:217:OHX:N1	2.51	0.44
36:5:2211:U:H5	36:5:2234:G:N1	2.15	0.44
36:5:2234:G:O6	87:5:3877:OHX:N3	2.51	0.44
36:5:2886:U:OP1	87:5:4046:OHX:N1	2.50	0.44
36:5:2754:G:OP2	87:5:3959:OHX:N3	2.51	0.44
36:5:3290:G:O6	87:5:4010:OHX:N3	2.51	0.44
36:5:717:C:H2'	36:5:718:G:O4'	2.17	0.44
1:6:304:U:H2'	1:6:305:C:C6	2.52	0.44
1:6:324:U:O2	1:6:346:G:H1'	2.18	0.44
1:6:514:G:O2'	1:6:515:A:H8	1.99	0.44
38:8:6:U:H2'	38:8:7:U:C6	2.53	0.44
89:B:101:SPS:O1	89:B:101:SPS:H91	2.18	0.44
14:C2:67:THR:C	14:C2:69:ALA:H	2.38	0.44
14:C2:87:PRO:HA	14:C2:140:PHE:CE1	2.46	0.44
15:C3:125:LEU:HD22	15:C3:129:TYR:CE2	3.20	0.44
18:C6:47:LYS:HD2	18:C6:47:LYS:HA	2.00	0.44
18:C6:58:ASP:OD2	18:C6:59:LYS:NZ	2.42	0.44
21:C9:84:LYS:HD2	21:C9:86:ARG:HG2	1.99	0.44
22:D0:72:ASN:HA	1:6:1198:G:O2'	388.74	0.44
22:D0:55:PRO:HG3	22:D0:91:ILE:HD11	1.99	0.44
29:D7:19:HIS:HB3	29:D7:22:LYS:HB2	1.99	0.44
23:D1:85:TYR:CE1	29:D7:6:ASP:HB2	2.53	0.44
1:2:1647:U:O2	32:E0:2:ALA:HA	2.18	0.44
33:E1:100:LEU:C	33:E1:102:VAL:H	2.21	0.44
36:1:2147:A:OP1	39:L2:199:THR:HA	2.16	0.44
39:L2:20:THR:HA	39:L2:23:ARG:HD2	2.00	0.44
39:L2:54:ARG:HG2	39:L2:56:ALA:O	2.18	0.44
40:L3:295:ALA:HB2	40:L3:301:THR:O	2.18	0.44
40:L3:55:THR:O	40:L3:56:ILE:HD12	2.18	0.44
41:L4:162:THR:O	41:L4:166:VAL:HG23	2.18	0.44
41:L4:180:LYS:HZ3	41:L4:202:ARG:HB3	1.83	0.44
46:L9:75:VAL:O	46:L9:78:MET:HB2	2.19	0.44
48:M1:132:ASN:OD1	48:M1:132:ASN:N	2.51	0.44
49:M3:105:ASN:ND2	49:M3:108:ILE:HG12	3.28	0.44
51:M5:148:TYR:O	51:M5:151:ILE:HG22	4.27	0.44
53:M7:29:THR:O	53:M7:119:VAL:HG11	2.18	0.44
53:M7:131:ARG:HA	53:M7:131:ARG:HD2	2.42	0.44
54:M8:90:ASP:O	54:M8:92:ARG:N	2.49	0.44
59:N3:62:VAL:CG2	59:N3:74:MET:HE1	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:N7:124:ALA:O	63:N7:126:LYS:HG3	2.18	0.44
49:M3:159:VAL:HG13	64:N8:144:VAL:HG13	2.00	0.44
64:N8:77:LYS:O	64:N8:79:TRP:N	2.60	0.44
68:O2:122:PRO:C	68:O2:124:GLY:H	2.21	0.44
74:O8:65:LEU:HD23	74:O8:68:SER:HB2	1.98	0.44
75:O9:23:LEU:O	75:O9:25:GLN:NE2	3.13	0.44
79:Q3:8:VAL:HG22	36:5:1927:G:OP1	246.93	0.44
2:S0:57:LEU:HD11	2:S0:173:ILE:HG23	2.00	0.44
3:S1:70:LEU:HD12	3:S1:82:ARG:O	2.17	0.44
4:S2:199:GLN:HG2	1:6:1097:U:H5	381.51	0.44
5:S3:108:LYS:HE2	5:S3:122:VAL:HG23	2.00	0.44
6:S4:148:ARG:HG2	6:S4:148:ARG:H	2.10	0.44
8:S6:7:TYR:CZ	8:S6:125:THR:HG23	3.62	0.44
8:S6:44:GLU:H	8:S6:44:GLU:CD	2.20	0.44
10:S8:195:ARG:HD3	10:S8:195:ARG:HA	1.79	0.44
11:S9:122:VAL:HG23	11:S9:123:HIS:ND1	2.33	0.44
11:S9:126:ARG:O	11:S9:130:THR:HG23	4.43	0.44
35:SM:30:THR:OG1	35:SM:31:SER:N	3.66	0.44
34:SR:41:THR:HG22	34:SR:62:LYS:HG2	2.00	0.44
36:1:1696:A:N6	36:1:1748:G:H2'	2.33	0.44
36:1:2118:C:H6	36:1:2118:C:O5'	2.01	0.44
36:1:2898:G:H5''	36:1:2899:C:C5'	2.48	0.44
36:1:3009:G:C6	36:1:3010:U:C4	3.06	0.44
36:1:3146:G:O3'	40:L3:100:ARG:NH1	2.51	0.44
36:1:996:A:H2'	36:1:997:A:O4'	2.18	0.44
1:2:1375:A:C2	1:2:1376:C:C2	3.05	0.44
1:2:1481:C:O2'	1:2:1482:C:O5'	2.32	0.44
1:2:193:U:H2'	1:2:194:U:H2'	2.00	0.44
1:2:25:C:H4'	1:2:26:A:O5'	2.17	0.44
1:2:560:U:H2'	1:2:561:G:C8	2.52	0.44
1:2:607:G:H4'	1:2:608:U:H5''	2.00	0.44
36:5:1440:G:H2'	36:5:1441:G:C8	2.53	0.44
36:5:1560:G:H2'	36:5:1561:G:C8	2.52	0.44
36:5:1563:C:H2'	36:5:1564:U:O4'	2.17	0.44
36:5:1719:G:H2'	36:5:1720:U:O4'	2.18	0.44
36:5:1807:G:C6	36:5:1808:G:N1	2.86	0.44
53:M7:139:TYR:CE2	36:5:2355:G:H4'	148.49	0.44
36:5:2430:A:H2'	36:5:2431:C:C6	2.53	0.44
57:N1:68:THR:OG1	36:5:2737:C:H4'	224.29	0.44
47:M0:158:LYS:HE3	36:5:2852:C:N3	310.91	0.44
36:5:3333:G:N2	36:5:3369:G:O2'	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:357:A:H2'	36:5:358:G:O4'	2.18	0.44
36:5:986:U:OP2	87:5:4059:OHX:N2	2.51	0.44
36:5:2610:G:O6	87:5:4087:OHX:N6	2.51	0.44
36:5:754:G:C4	36:5:755:A:C8	3.06	0.44
1:6:1078:C:H2'	1:6:1079:U:C6	2.53	0.44
33:E1:95:HIS:ND1	1:6:1248:C:OP2	419.68	0.44
1:6:1614:A:O2'	1:6:1615:C:H5'	2.18	0.44
1:6:1623:C:H2'	1:6:1624:C:C6	2.52	0.44
1:6:1691:A:H2'	1:6:1692:G:C8	2.53	0.44
1:6:1752:U:H2'	1:6:1753:A:C8	2.53	0.44
1:6:310:C:O2'	1:6:311:U:H5'	2.17	0.44
1:6:93:A:H4'	1:6:94:U:OP2	2.17	0.44
15:C3:114:ARG:HD3	15:C3:117:LEU:HD12	2.13	0.44
15:C3:114:ARG:HG2	15:C3:114:ARG:NH1	2.29	0.44
1:2:1553:G:O6	17:C5:43:ARG:HD3	2.17	0.44
20:C8:145:ARG:HG2	35:SM:72:ARG:CZ	8.45	0.44
21:C9:117:SER:HB2	21:C9:123:ARG:HB3	2.00	0.44
21:C9:49:ASP:HB3	21:C9:53:TRP:HB3	1.99	0.44
2:S0:66:ALA:HB2	23:D1:37:ALA:HB2	1.99	0.44
24:D2:30:SER:HB3	24:D2:59:GLY:HA3	4.45	0.44
24:D2:89:TRP:O	24:D2:92:ASN:HB2	2.17	0.44
1:2:533:U:H4'	26:D4:33:ALA:HB3	2.00	0.44
29:D7:31:TYR:CE2	29:D7:48:SER:HB3	2.53	0.44
30:D8:41:VAL:O	30:D8:62:GLU:HB2	2.18	0.44
39:L2:132:ASN:HD22	39:L2:151:PRO:CB	2.31	0.44
39:L2:243:THR:HG22	36:5:2241:U:O2'	232.80	0.44
39:L2:30:ARG:HA	39:L2:74:GLU:OE2	3.80	0.44
40:L3:257:PRO:O	40:L3:259:HIS:N	2.49	0.44
40:L3:386:ASP:HB3	40:L3:387:LEU:H	1.61	0.44
49:M3:100:ARG:HD2	36:5:76:G:O2'	85.78	0.44
49:M3:144:THR:HG21	71:O5:118:ILE:HG21	1.99	0.44
50:M4:8:LYS:HE3	50:M4:8:LYS:HB3	1.68	0.44
51:M5:19:LEU:HA	51:M5:19:LEU:HD12	1.97	0.44
51:M5:99:ARG:HH22	51:M5:166:ALA:HB3	2.25	0.44
52:M6:51:LYS:HE2	52:M6:144:SER:HB2	1.99	0.44
54:M8:82:VAL:HG22	54:M8:127:LEU:HD11	3.39	0.44
55:M9:166:ASN:HD22	55:M9:167:ARG:HG2	7.68	0.44
9:S7:39:ARG:HH22	55:M9:185:LEU:HB3	1.82	0.44
55:M9:8:LYS:HG3	55:M9:22:VAL:CG2	2.47	0.44
36:1:1672:U:P	55:M9:60:LYS:HZ1	2.35	0.44
55:M9:8:LYS:HG3	55:M9:22:VAL:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:L7:75:TYR:HB2	57:N1:141:VAL:HG22	1.99	0.44
61:N5:38:LEU:HD13	61:N5:38:LEU:O	2.18	0.44
62:N6:110:HIS:O	62:N6:115:ARG:NH1	2.57	0.44
64:N8:3:SER:O	64:N8:6:THR:HB	2.18	0.44
65:N9:47:LEU:HA	65:N9:50:THR:HG22	2.55	0.44
66:O0:56:LEU:HA	66:O0:56:LEU:HD23	2.08	0.44
69:O3:30:ILE:HB	69:O3:81:VAL:HG12	2.45	0.44
72:O6:80:PHE:HE1	72:O6:84:LYS:HE3	2.05	0.44
75:O9:2:ALA:N	75:O9:5:LYS:HD3	7.27	0.44
78:Q2:65:THR:HB	78:Q2:66:LYS:H	1.68	0.44
6:S4:71:LYS:HG3	6:S4:91:THR:HB	2.00	0.44
10:S8:67:TRP:CZ2	10:S8:156:VAL:HG11	2.53	0.44
10:S8:184:LEU:HB3	10:S8:189:LEU:HD13	2.00	0.44
10:S8:89:GLU:O	10:S8:93:THR:OG1	2.28	0.44
35:SM:129:ALA:HA	35:SM:132:ALA:HB3	2.91	0.44
34:SR:157:VAL:HB	34:SR:168:THR:HG22	3.65	0.44
34:SR:20:VAL:HG11	34:SR:310:ILE:HG12	2.50	0.44
34:SR:248:ASN:ND2	34:SR:298:GLY:HA3	2.31	0.44
36:1:1140:G:H2'	36:1:1141:C:C6	2.53	0.43
36:1:2350:C:H4'	36:1:3308:C:O2'	2.18	0.43
36:1:2443:A:O2'	36:1:2444:C:OP2	2.31	0.43
36:1:3013:U:H2'	36:1:3014:U:C6	2.53	0.43
36:1:3087:A:H2'	36:1:3088:G:C8	2.53	0.43
36:1:561:C:OP1	50:M4:77:ARG:HG3	2.18	0.43
36:1:692:A:OP1	51:M5:201:ARG:NH2	2.51	0.43
1:2:1122:G:N2	1:2:1125:A:OP2	2.51	0.43
1:2:1441:C:H2'	1:2:1442:U:C6	2.53	0.43
1:2:48:G:C6	1:2:49:C:C4	3.06	0.43
37:3:57:G:H3'	37:3:58:C:C6	2.53	0.43
37:3:58:C:H2'	37:3:59:U:H6	1.83	0.43
36:5:1047:A:C6	36:5:1048:A:C6	3.06	0.43
36:5:1232:C:H2'	36:5:1233:G:C8	2.53	0.43
68:O2:61:LYS:NZ	36:5:1339:C:OP1	194.64	0.43
36:5:122:A:C5	36:5:146:U:C4	3.06	0.43
36:5:1700:G:C6	36:5:1701:C:C4	3.06	0.43
36:5:1733:G:H2'	36:5:1734:G:H8	1.83	0.43
36:5:1821:U:OP2	36:5:1821:U:H4'	2.18	0.43
36:5:2623:G:H2'	36:5:2624:G:C8	2.51	0.43
40:L3:242:THR:HG22	36:5:2948:C:O2'	215.75	0.43
36:5:3346:U:H3	36:5:3359:A:H61	1.66	0.43
87:5:4001:OHX:N3	87:5:4119:OHX:N1	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1362:U:H1'	1:6:1363:U:C5	2.53	0.43
1:6:149:C:H2'	1:6:150:U:H6	1.83	0.43
18:C6:73:GLY:HA3	1:6:1608:U:O3'	398.78	0.43
26:D4:61:ARG:NH2	1:6:530:C:O2	410.59	0.43
1:6:585:A:H2'	1:6:586:G:C8	2.53	0.43
8:S6:171:LYS:NZ	1:6:68:A:OP2	350.76	0.43
1:6:821:U:H2'	1:6:822:U:O4'	2.18	0.43
38:8:125:U:O2	38:8:125:U:H2'	2.18	0.43
73:O7:76:ASN:ND2	38:8:94:C:OP1	47.53	0.43
12:C0:23:ALA:O	12:C0:24:LYS:HB3	4.62	0.43
2:S0:88:LYS:NZ	19:C7:82:ASP:O	6.28	0.43
20:C8:99:HIS:CD2	20:C8:101:LEU:HD21	2.53	0.43
21:C9:86:ARG:HH22	21:C9:90:PRO:HG2	1.83	0.43
22:D0:105:GLN:HG3	22:D0:106:ILE:N	2.33	0.43
2:S0:184:LEU:HD23	23:D1:43:GLY:HA2	1.99	0.43
28:D6:38:ARG:HE	28:D6:83:ILE:HB	1.83	0.43
39:L2:56:ALA:HB2	39:L2:130:SER:HA	2.27	0.43
39:L2:136:ILE:HA	39:L2:148:VAL:HG12	2.00	0.43
39:L2:225:ILE:HG22	39:L2:226:SER:O	2.61	0.43
41:L4:99:MET:SD	41:L4:102:PRO:HA	2.74	0.43
41:L4:288:ARG:O	41:L4:291:ASN:N	3.23	0.43
45:L8:238:LEU:HD23	45:L8:242:ALA:HB1	1.99	0.43
47:M0:116:ARG:HE	47:M0:116:ARG:HB2	1.65	0.43
47:M0:81:GLY:O	47:M0:83:ASP:N	2.63	0.43
47:M0:89:VAL:HG13	47:M0:136:PHE:CE1	2.53	0.43
50:M4:48:GLY:HA3	50:M4:53:VAL:HG13	2.35	0.43
54:M8:55:SER:O	54:M8:58:ASN:N	2.50	0.43
36:1:2294:U:OP2	59:N3:71:LYS:HE2	2.17	0.43
62:N6:70:ILE:HD13	62:N6:82:VAL:HG22	4.61	0.43
64:N8:118:ILE:HG12	64:N8:119:PRO:O	2.17	0.43
64:N8:22:ILE:HG23	36:5:642:U:OP1	193.01	0.43
67:O1:33:VAL:HG13	67:O1:51:LEU:CD1	2.80	0.43
70:O4:5:VAL:HG22	70:O4:6:THR:H	2.68	0.43
72:O6:25:LYS:HB2	72:O6:28:TYR:HD2	1.83	0.43
76:Q0:78:ILE:HG23	76:Q0:83:LYS:HG3	1.99	0.43
3:S1:137:ILE:HD12	3:S1:172:LEU:HD22	2.00	0.43
3:S1:61:LEU:HD22	3:S1:61:LEU:H	1.82	0.43
4:S2:169:LEU:HD12	4:S2:217:ALA:HB1	2.01	0.43
6:S4:106:LYS:HG3	6:S4:108:ARG:HH11	1.83	0.43
11:S9:108:ARG:O	11:S9:111:THR:OG1	2.23	0.43
11:S9:123:HIS:HD2	32:E0:37:ARG:CZ	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SR:10:ARG:HD2	34:SR:10:ARG:HA	1.73	0.43
36:1:1286:A:N3	36:1:1287:A:H1'	2.32	0.43
36:1:274:G:H2'	36:1:275:U:O4'	2.17	0.43
36:1:2972:G:O5'	87:1:4060:OHX:N2	2.52	0.43
36:1:3089:C:H2'	36:1:3090:U:O4'	2.17	0.43
1:2:630:A:H5''	1:2:631:G:OP2	2.18	0.43
1:2:926:A:H1'	1:2:988:A:N1	2.33	0.43
36:5:1192:C:H5	87:5:4000:OHX:N6	2.15	0.43
36:5:1240:A:H2'	36:5:1241:U:H5'	1.99	0.43
36:5:1313:G:N3	36:5:1318:A:H2	2.16	0.43
41:L4:303:GLY:HA3	36:5:1347:U:H5'	201.12	0.43
36:5:2129:U:O2'	36:5:2144:A:N3	2.46	0.43
36:5:2881:C:H2'	36:5:2882:U:C6	2.53	0.43
36:5:3110:C:C4	36:5:3111:U:C4	3.06	0.43
36:5:1808:G:O6	87:5:3938:OHX:N3	2.50	0.43
36:5:79:U:OP2	87:5:3876:OHX:N4	2.51	0.43
1:6:1160:A:H2'	1:6:1161:C:H6	1.82	0.43
1:6:1041:G:OP1	87:6:2145:OHX:N4	2.51	0.43
37:7:46:A:H2'	37:7:47:C:H6	1.83	0.43
12:C0:38:LYS:HB2	12:C0:41:TYR:CD1	2.53	0.43
18:C6:60:PHE:HA	18:C6:63:ILE:HG12	2.92	0.43
24:D2:36:LYS:HB2	24:D2:110:ILE:HD12	2.00	0.43
25:D3:87:VAL:HG12	25:D3:92:CYS:HB3	2.00	0.43
39:L2:15:ILE:HD12	39:L2:15:ILE:HA	4.61	0.43
40:L3:280:HIS:HB3	40:L3:324:VAL:CG1	2.48	0.43
41:L4:42:VAL:C	41:L4:44:LYS:N	3.16	0.43
42:L5:153:THR:HG23	42:L5:160:PHE:CZ	2.53	0.43
42:L5:258:LYS:O	42:L5:258:LYS:HG2	5.05	0.43
44:L7:125:GLU:OE1	44:L7:128:LYS:HD2	3.58	0.43
44:L7:90:LYS:HG3	44:L7:91:GLY:N	2.33	0.43
46:L9:138:THR:C	46:L9:140:VAL:H	2.22	0.43
46:L9:165:CYS:HB3	46:L9:178:GLY:HA2	2.00	0.43
52:M6:171:LYS:O	52:M6:175:THR:HB	3.08	0.43
53:M7:112:LEU:HG	53:M7:150:VAL:HB	2.26	0.43
54:M8:51:ALA:HA	54:M8:54:LEU:HG	1.99	0.43
55:M9:102:LEU:HD22	55:M9:138:LEU:HD12	1.99	0.43
56:N0:44:PHE:O	56:N0:46:GLN:N	3.02	0.43
56:N0:7:TYR:CD1	56:N0:61:ILE:HD11	2.53	0.43
44:L7:74:SER:OG	57:N1:142:SER:HA	2.48	0.43
58:N2:28:PHE:HE1	58:N2:83:TYR:CE2	2.97	0.43
66:O0:45:ALA:HB3	66:O0:48:THR:HB	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1408:G:P	68:O2:33:ARG:HH22	2.41	0.43
3:S1:33:LYS:HB3	3:S1:97:LEU:HD22	1.99	0.43
3:S1:88:VAL:HG11	3:S1:96:LEU:HD12	1.99	0.43
4:S2:100:ALA:O	4:S2:115:ILE:HA	2.18	0.43
1:2:121:U:O2'	6:S4:33:ALA:O	2.25	0.43
8:S6:32:ILE:HG13	8:S6:100:ALA:O	2.18	0.43
9:S7:11:GLN:HE22	9:S7:13:PRO:HD2	5.30	0.43
9:S7:28:GLU:O	9:S7:30:SER:N	2.51	0.43
36:1:2864:A:O3'	47:M0:115:MET:HB2	2.17	0.43
36:1:2871:G:OP2	87:1:4071:OHX:N3	2.51	0.43
36:1:2989:U:H2'	36:1:2990:G:O4'	2.19	0.43
36:1:2107:A:H2	36:1:3344:A:H8	1.66	0.43
36:1:437:G:H2'	36:1:438:A:H8	1.84	0.43
36:1:873:C:H4'	36:1:874:U:OP2	2.17	0.43
1:2:144:U:O2'	1:2:145:A:H8	2.01	0.43
1:2:1487:A:H2'	1:2:1488:G:H8	1.83	0.43
1:2:639:U:OP1	9:S7:117:THR:OG1	2.27	0.43
1:2:68:A:OP1	8:S6:160:ARG:NH2	2.46	0.43
1:2:980:G:H4'	1:2:1776:A:H4'	2.00	0.43
36:5:1094:U:H3'	36:5:1096:U:OP1	2.18	0.43
36:5:1103:A:O5'	36:5:1104:G:H5'	2.17	0.43
51:M5:147:ARG:NH2	36:5:113:C:OP1	77.61	0.43
36:5:117:U:O2	36:5:119:U:H2'	2.19	0.43
36:5:1259:A:N6	36:5:1260:A:N1	2.65	0.43
36:5:1504:A:N1	36:5:1515:A:O2'	2.49	0.43
73:O7:3:LYS:HG3	36:5:2139:A:C5	170.13	0.43
36:5:2174:G:OP1	36:5:2174:G:H8	2.01	0.43
36:5:2316:G:OP1	87:5:4102:OHX:N6	2.51	0.43
36:5:2534:G:H1	36:5:2545:C:N4	2.08	0.43
36:5:736:A:N6	36:5:737:G:N3	2.67	0.43
36:5:781:G:N7	87:5:3906:OHX:N4	2.66	0.43
1:6:1273:G:O5'	1:6:1274:C:H3'	2.19	0.43
1:6:1662:G:O6	87:6:2028:OHX:N2	2.51	0.43
14:C2:27:ALA:HB1	14:C2:132:GLU:HB3	2.00	0.43
14:C2:43:ARG:HG2	14:C2:43:ARG:H	1.85	0.43
87:2:2000:OHX:N3	15:C3:12:SER:O	2.52	0.43
18:C6:102:LYS:HE2	18:C6:102:LYS:HB3	4.06	0.43
20:C8:29:VAL:HG22	20:C8:54:LEU:HD12	2.00	0.43
25:D3:52:ILE:HG13	25:D3:52:ILE:H	2.81	0.43
28:D6:41:ILE:HD13	28:D6:41:ILE:H	1.83	0.43
28:D6:73:TYR:HB3	28:D6:78:ALA:HB2	2.42	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:L2:149:ARG:HH12	39:L2:253:GLN:CB	8.46	0.43
40:L3:170:PRO:HG2	40:L3:314:TYR:OH	2.18	0.43
40:L3:173:GLN:O	40:L3:175:LYS:N	2.51	0.43
40:L3:351:LEU:HD23	40:L3:351:LEU:HA	1.76	0.43
40:L3:4:ARG:HB2	40:L3:4:ARG:HE	4.61	0.43
41:L4:193:LYS:O	41:L4:198:ARG:HG2	3.71	0.43
41:L4:262:TRP:O	41:L4:276:LEU:HD11	2.18	0.43
41:L4:40:THR:O	41:L4:44:LYS:HE3	3.79	0.43
42:L5:60:ILE:HB	42:L5:80:SER:HB2	2.00	0.43
36:1:591:G:N2	43:L6:19:LYS:O	2.50	0.43
44:L7:102:VAL:HG13	44:L7:126:LEU:HD22	2.14	0.43
45:L8:150:LEU:HD21	45:L8:218:ILE:HD13	2.11	0.43
45:L8:41:GLN:CG	45:L8:44:ARG:HH12	2.30	0.43
45:L8:63:LYS:O	45:L8:67:ILE:HG13	2.18	0.43
46:L9:77:ASN:HA	46:L9:80:THR:OG1	2.77	0.43
48:M1:109:HIS:O	48:M1:112:LEU:HG	2.19	0.43
50:M4:21:VAL:HA	50:M4:66:THR:HG23	2.08	0.43
54:M8:103:ALA:HB3	54:M8:106:PHE:CE2	2.65	0.43
55:M9:41:ILE:O	55:M9:45:VAL:HG23	2.27	0.43
57:N1:51:GLY:HA3	57:N1:92:ARG:HG3	2.70	0.43
57:N1:96:ILE:HA	57:N1:96:ILE:HD13	3.05	0.43
58:N2:16:THR:OG1	58:N2:102:GLU:HG2	2.19	0.43
59:N3:48:ARG:HH11	59:N3:48:ARG:CG	2.61	0.43
59:N3:18:PRO:HA	59:N3:51:ALA:HA	1.99	0.43
61:N5:113:LEU:HD12	61:N5:114:VAL:C	2.39	0.43
66:O0:45:ALA:HB2	66:O0:77:LEU:CD2	3.63	0.43
69:O3:10:LYS:HD2	69:O3:33:GLU:OE2	2.18	0.43
87:4:218:OHX:N6	73:O7:62:GLY:O	2.51	0.43
46:L9:93:VAL:HG22	76:Q0:82:LEU:HD13	2.07	0.43
3:S1:158:SER:HA	3:S1:161:ILE:HD12	2.16	0.43
4:S2:156:THR:HG21	4:S2:224:PHE:CD1	2.53	0.43
5:S3:195:SER:OG	5:S3:200:LYS:HA	2.52	0.43
6:S4:19:LEU:HA	6:S4:19:LEU:HD23	1.65	0.43
7:S5:225:ARG:HD3	30:D8:58:GLU:HG2	2.00	0.43
10:S8:191:PHE:HA	10:S8:194:ARG:NH2	2.33	0.43
10:S8:56:ARG:HH22	1:6:332:U:P	288.01	0.43
11:S9:119:ALA:O	11:S9:124:HIS:ND1	4.90	0.43
34:SR:215:GLY:O	34:SR:239:GLU:HG3	2.18	0.43
34:SR:274:LEU:HD13	34:SR:313:TRP:CD2	2.53	0.43
36:1:1317:A:C4	36:1:1319:G:N7	2.86	0.43
1:2:1000:C:H6	1:2:1002:G:C8	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1209:C:H42	1:2:1454:G:H1	1.67	0.43
1:2:1492:A:O2'	1:2:1493:A:H8	1.99	0.43
1:2:195:G:H2'	1:2:196:G:H5'	2.01	0.43
1:2:1655:A:OP1	87:2:2058:OHX:N3	2.51	0.43
1:2:319:U:H1'	1:2:323:A:C4	2.53	0.43
1:2:704:C:H4'	1:2:705:U:OP1	2.18	0.43
36:5:1025:A:N7	36:5:1026:A:O2'	2.51	0.43
36:5:151:A:HO2'	36:5:152:U:P	2.40	0.43
36:5:1564:U:H1'	36:5:1576:G:O6	2.18	0.43
36:5:2101:C:HO2'	36:5:2102:U:P	2.41	0.43
36:5:3200:G:O6	87:5:4052:OHX:N5	2.51	0.43
36:5:378:A:H3'	36:5:379:C:C6	2.54	0.43
1:6:1511:U:H2'	1:6:1512:G:C8	2.53	0.43
1:6:1653:C:N4	1:6:1654:G:C6	2.86	0.43
38:8:53:A:C4	38:8:54:A:C8	3.06	0.43
38:8:78:G:H2'	38:8:79:A:O4'	2.19	0.43
16:C4:22:SER:OG	16:C4:25:ASP:N	5.77	0.43
17:C5:33:PHE:O	17:C5:36:LEU:HD22	4.36	0.43
21:C9:28:LEU:HD21	21:C9:30:VAL:HG13	2.01	0.43
23:D1:80:LYS:HE3	23:D1:80:LYS:HB3	1.57	0.43
9:S7:144:VAL:HG22	24:D2:49:GLU:HB2	1.99	0.43
27:D5:41:ILE:HA	27:D5:41:ILE:HD12	1.83	0.43
16:C4:128:LYS:NZ	28:D6:27:SER:OG	2.48	0.43
23:D1:85:TYR:CD1	29:D7:6:ASP:HB2	2.53	0.43
39:L2:45:VAL:HB	39:L2:61:VAL:HG22	2.00	0.43
41:L4:186:LYS:O	41:L4:200:THR:N	2.83	0.43
37:3:7:G:OP1	42:L5:33:ARG:HD2	2.17	0.43
43:L6:47:PHE:HE2	43:L6:77:ARG:NE	2.75	0.43
46:L9:117:PHE:CE1	46:L9:177:ASP:HB3	2.75	0.43
48:M1:100:GLY:O	48:M1:159:THR:OG1	3.21	0.43
49:M3:60:ALA:HA	49:M3:61:PRO:HD3	1.85	0.43
53:M7:112:LEU:HA	53:M7:151:THR:O	2.37	0.43
53:M7:57:ALA:HB2	53:M7:83:TRP:CE2	2.54	0.43
50:M4:65:LEU:HD11	56:N0:152:LEU:HD12	1.99	0.43
61:N5:72:ALA:O	61:N5:76:VAL:HG23	2.18	0.43
36:1:1629:U:O4	63:N7:111:LYS:HD2	2.18	0.43
77:Q1:6:ARG:NH2	1:6:1112:G:OP1	315.20	0.43
79:Q3:49:ARG:HD3	79:Q3:52:ALA:HA	4.02	0.43
79:Q3:76:ALA:O	79:Q3:80:ARG:HG3	2.54	0.43
79:Q3:83:ILE:HG22	79:Q3:87:ARG:NH1	2.34	0.43
2:S0:98:ILE:HD11	2:S0:116:LYS:HG3	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S1:166:LYS:O	3:S1:170:GLU:HG3	5.66	0.43
4:S2:49:LYS:HD3	4:S2:49:LYS:HA	1.79	0.43
36:1:1355:A:H4'	36:1:1356:U:O5'	2.19	0.43
36:1:1525:G:H5'	36:1:1830:G:OP2	2.17	0.43
36:1:156:G:OP2	72:O6:25:LYS:HB3	2.19	0.43
36:1:1751:G:H5'	74:O8:26:LYS:HZ1	1.83	0.43
36:1:3033:A:H2'	36:1:3034:C:H6	1.84	0.43
36:1:307:A:H2'	36:1:308:A:C8	2.54	0.43
36:1:629:U:H2'	36:1:630:A:C8	2.53	0.43
1:2:1021:C:H2'	1:2:1022:C:O4'	2.18	0.43
1:2:10:G:H2'	1:2:11:A:H8	1.84	0.43
1:2:1253:U:H2'	1:2:1254:U:C6	2.53	0.43
1:2:629:U:C2	1:2:630:A:C8	3.06	0.43
1:2:733:A:HO2'	1:2:735:C:H5	1.66	0.43
1:2:952:A:H5'	15:C3:98:VAL:HG22	2.00	0.43
1:2:960:U:H1'	15:C3:52:VAL:HG23	2.00	0.43
37:3:52:G:N2	37:3:53:U:C2	2.86	0.43
57:N1:105:PHE:CE2	36:5:1062:A:H4'	245.53	0.43
36:5:1231:A:OP2	87:5:3921:OHX:N5	2.51	0.43
36:5:1483:G:C8	36:5:1485:G:C8	3.07	0.43
36:5:1686:U:O2'	36:5:1688:U:H4'	2.19	0.43
36:5:2572:C:H1'	36:5:2573:G:O4'	2.19	0.43
36:5:3106:A:H2'	36:5:3107:U:O4'	2.18	0.43
36:5:550:A:H2'	36:5:551:A:C8	2.54	0.43
64:N8:111:LYS:NZ	36:5:714:G:N7	139.33	0.43
3:S1:149:GLN:HG3	1:6:1066:C:O3'	346.95	0.43
1:6:1589:C:H2'	1:6:1590:G:C8	2.53	0.43
1:6:525:A:C6	1:6:526:A:C6	3.07	0.43
13:C1:112:SER:C	13:C1:114:ALA:H	2.22	0.43
15:C3:5:HIS:CE1	15:C3:121:ARG:HE	2.36	0.43
17:C5:63:ALA:HA	17:C5:66:ALA:HB3	3.23	0.43
20:C8:48:LYS:HD3	21:C9:35:ASP:HB2	2.01	0.43
20:C8:44:ASN:O	20:C8:48:LYS:HG3	2.50	0.43
20:C8:86:LEU:O	20:C8:89:GLN:HG3	2.18	0.43
22:D0:26:LEU:HA	22:D0:26:LEU:HD23	2.16	0.43
26:D4:10:ARG:HD2	26:D4:26:ASP:HB2	2.00	0.43
22:D0:67:THR:OG1	31:D9:40:ARG:HG3	2.18	0.43
39:L2:92:LYS:HA	39:L2:103:PRO:HD2	2.47	0.43
40:L3:117:ARG:HA	40:L3:175:LYS:HD2	3.93	0.43
36:1:2948:C:O2'	40:L3:242:THR:HG22	2.19	0.43
41:L4:131:VAL:O	41:L4:135:VAL:HG23	2.70	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L4:194:TYR:O	41:L4:195:ARG:HG3	2.17	0.43
44:L7:140:SER:O	44:L7:144:ILE:HG12	3.61	0.43
44:L7:217:PRO:HG2	44:L7:218:ARG:H	1.83	0.43
45:L8:161:GLU:OE2	51:M5:26:ARG:NH1	2.48	0.43
45:L8:162:LEU:HA	51:M5:7:LEU:HD11	2.97	0.43
46:L9:61:GLY:O	46:L9:65:VAL:HG23	2.19	0.43
47:M0:56:GLU:HG3	47:M0:162:GLN:H	2.41	0.43
48:M1:85:LYS:HA	48:M1:89:TYR:CE2	2.53	0.43
49:M3:116:LEU:HD23	49:M3:116:LEU:HA	1.72	0.43
49:M3:46:ILE:HG22	49:M3:49:ARG:CB	2.48	0.43
53:M7:71:ALA:O	53:M7:74:LYS:HB2	2.68	0.43
41:L4:290:ILE:HG23	54:M8:35:PHE:CE2	2.54	0.43
61:N5:54:TYR:O	61:N5:56:ARG:N	3.03	0.43
68:O2:24:ARG:HD3	68:O2:25:TYR:CZ	2.53	0.43
69:O3:60:ARG:HB3	69:O3:60:ARG:CZ	2.48	0.43
71:O5:41:LEU:O	71:O5:44:ILE:HG22	2.39	0.43
73:O7:53:ALA:HA	73:O7:56:ARG:HH11	2.14	0.43
2:S0:162:CYS:HB3	2:S0:173:ILE:HG13	2.92	0.43
5:S3:190:ARG:HH22	5:S3:195:SER:HA	1.84	0.43
6:S4:104:ASP:HB3	6:S4:106:LYS:H	1.84	0.43
7:S5:72:HIS:HA	7:S5:107:LYS:HE2	2.31	0.43
7:S5:76:ARG:C	7:S5:78:ALA:H	2.21	0.43
6:S4:248:ILE:HB	11:S9:71:PHE:CE1	2.54	0.43
35:SM:118:SER:HB3	35:SM:122:GLU:OE2	2.18	0.43
34:SR:130:THR:HG22	34:SR:145:LEU:HD23	2.52	0.43
34:SR:19:TRP:CG	34:SR:38:ARG:HD2	2.88	0.43
34:SR:305:TYR:HE2	34:SR:313:TRP:HH2	2.94	0.43
36:1:1141:C:H2'	36:1:1142:G:O4'	2.19	0.43
36:1:1554:U:C4	36:1:1582:C:H2'	2.53	0.43
36:1:160:G:O6	87:1:4107:OHX:N6	2.52	0.43
36:1:1857:C:C4	36:1:1858:A:C6	3.07	0.43
36:1:2093:A:H2'	36:1:2094:C:O4'	2.18	0.43
36:1:2590:A:C4	36:1:2591:A:C8	3.07	0.43
36:1:2615:G:H2'	36:1:2616:C:C6	2.54	0.43
36:1:2631:U:OP2	57:N1:4:SER:OG	2.32	0.43
36:1:3123:A:C5	36:1:3124:G:C8	3.07	0.43
36:1:535:G:C6	36:1:555:U:N3	2.86	0.43
36:1:856:G:C6	36:1:857:G:N1	2.87	0.43
1:2:1253:U:O2'	33:E1:143:LYS:HA	2.19	0.43
1:2:369:A:O2'	1:2:371:G:OP2	2.30	0.43
1:2:393:C:H2'	1:2:394:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:803:A:C4	9:S7:104:ARG:HG3	2.53	0.43
1:2:958:U:O4	15:C3:12:SER:OG	2.35	0.43
37:3:67:G:C2'	37:3:68:C:H5'	2.48	0.43
38:4:59:A:N1	38:4:100:U:H1'	2.34	0.43
36:5:1940:G:N2	36:5:3362:A:C8	2.87	0.43
36:5:1017:C:N4	36:5:2671:A:OP2	2.50	0.43
36:5:2985:C:H2'	36:5:2986:U:H6	1.83	0.43
36:5:3046:A:H2'	36:5:3047:U:O4'	2.18	0.43
36:5:3362:A:C2	36:5:3363:U:C2	3.07	0.43
1:6:1018:U:H2'	1:6:1019:A:C8	2.54	0.43
1:6:1206:U:H2'	1:6:1207:C:C5	2.54	0.43
1:6:1422:A:H2'	1:6:1423:U:C6	2.53	0.43
1:6:1529:C:H2'	1:6:1530:C:C6	2.54	0.43
1:6:372:G:H1'	1:6:612:U:O2	2.19	0.43
1:6:447:U:C4	1:6:448:C:C4	3.07	0.43
1:6:620:A:C5	1:6:621:A:N1	2.87	0.43
1:6:704:C:H2'	1:6:705:U:O4'	2.18	0.43
13:C1:60:PHE:HB2	13:C1:61:THR:HG23	2.95	0.43
13:C1:80:MET:HB3	13:C1:83:THR:HG23	1.99	0.43
25:D3:103:LEU:HB3	25:D3:126:LYS:HB2	2.23	0.43
1:2:1253:U:H4'	33:E1:143:LYS:N	2.34	0.43
39:L2:65:ASP:HB3	39:L2:68:LYS:O	2.18	0.43
40:L3:13:HIS:HB2	36:5:3044:G:O3'	243.00	0.43
40:L3:287:LYS:HD2	40:L3:287:LYS:HA	4.74	0.43
40:L3:37:ARG:HG3	40:L3:185:GLY:O	2.45	0.43
42:L5:78:ALA:HB3	42:L5:105:ILE:HG12	1.99	0.43
43:L6:152:THR:HA	43:L6:153:PRO:HD3	1.81	0.43
47:M0:153:ARG:O	47:M0:156:ARG:HB2	2.19	0.43
47:M0:30:LYS:HG3	47:M0:63:GLU:HB3	4.53	0.43
50:M4:77:ARG:HG3	36:5:561:C:OP1	349.38	0.43
50:M4:99:TRP:O	50:M4:103:ILE:HG13	3.04	0.43
52:M6:13:GLY:O	52:M6:124:LEU:HD12	2.19	0.43
54:M8:109:GLY:O	54:M8:113:LYS:HB2	2.77	0.43
55:M9:130:ASN:HB3	55:M9:131:ALA:H	1.48	0.43
55:M9:20:ARG:HH11	55:M9:21:LYS:NZ	3.52	0.43
57:N1:101:CYS:SG	57:N1:102:ARG:N	3.15	0.43
60:N4:7:SER:O	60:N4:8:PHE:HB2	2.19	0.43
61:N5:136:ALA:O	61:N5:139:ILE:HG12	2.18	0.43
71:O5:24:LEU:HA	71:O5:27:GLU:HB2	2.00	0.43
72:O6:54:GLU:O	72:O6:58:ILE:HG23	2.19	0.43
76:Q0:107:ALA:O	76:Q0:121:LEU:HD12	3.13	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S0:109:ASN:O	2:S0:112:THR:HG22	2.18	0.43
3:S1:214:LYS:HE3	3:S1:214:LYS:HB2	1.81	0.43
4:S2:139:ILE:CD1	4:S2:191:ALA:HB1	2.77	0.43
6:S4:77:ARG:HG3	6:S4:82:TYR:CE1	2.54	0.43
7:S5:68:ILE:HD13	7:S5:69:PHE:N	5.16	0.43
10:S8:167:ALA:HA	10:S8:183:ILE:HA	2.62	0.43
35:SM:48:ARG:HE	36:1:1017:C:C4'	2.31	0.43
34:SR:127:ARG:C	34:SR:129:LYS:H	2.22	0.43
34:SR:28:GLY:HA3	34:SR:76:ASP:O	2.19	0.43
36:1:1667:A:N6	36:1:1668:G:O6	2.51	0.43
36:1:1949:G:OP1	55:M9:104:ARG:NH2	2.41	0.43
36:1:2339:C:OP2	59:N3:48:ARG:HG2	2.19	0.43
36:1:2659:G:N7	87:1:3775:OHX:N3	2.67	0.43
36:1:3047:U:C2'	36:1:3048:A:H5'	2.48	0.43
36:1:3072:C:H2'	36:1:3073:A:O4'	2.19	0.43
36:1:3126:C:H1'	46:L9:156:GLN:OE1	2.18	0.43
36:1:3318:G:H2'	36:1:3318:G:OP2	2.18	0.43
36:1:563:U:OP1	56:N0:71:LYS:NZ	2.47	0.43
36:1:579:G:C2	36:1:580:C:C2	3.07	0.43
36:1:595:G:C8	36:1:609:G:C6	3.07	0.43
1:2:1200:G:H4'	1:2:1201:G:C5'	2.48	0.43
1:2:1230:A:C2'	1:2:1258:U:H5	2.28	0.43
1:2:129:U:O2	87:2:2001:OHX:N1	2.52	0.43
1:2:1291:G:H22	1:2:1324:G:N2	2.16	0.43
1:2:1357:A:H61	1:2:1366:U:H3	1.67	0.43
1:2:1324:G:OP2	87:2:2051:OHX:N1	2.51	0.43
1:2:281:G:H8	1:2:281:G:P	2.41	0.43
1:2:714:G:N2	1:2:725:U:O4	2.50	0.43
1:2:778:G:H5''	1:2:778:G:N3	2.34	0.43
37:3:96:U:H2'	37:3:97:A:H8	1.84	0.43
38:4:77:A:OP2	87:4:219:OHX:N2	2.52	0.43
38:4:56:G:C2	38:4:57:C:C2	3.06	0.43
36:5:1252:A:C5	36:5:1253:U:C5	3.06	0.43
36:5:2686:A:H2'	36:5:2687:G:O4'	2.19	0.43
36:5:522:A:OP1	87:5:3854:OHX:N4	2.52	0.43
1:6:1537:C:O2'	1:6:1540:G:O6	2.36	0.43
1:6:1784:C:H2'	1:6:1785:U:H6	1.84	0.43
1:6:492:A:H1'	1:6:496:G:H1	1.84	0.43
1:6:592:A:O2'	1:6:596:C:OP1	2.34	0.43
16:C4:37:GLU:HA	1:6:895:G:O2'	260.11	0.43
13:C1:109:VAL:HG11	13:C1:125:VAL:HG21	4.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:C5:54:ALA:C	17:C5:56:PHE:H	2.59	0.43
17:C5:58:LYS:HA	17:C5:61:ARG:HH12	3.23	0.43
17:C5:123:TYR:HH	20:C8:126:ARG:NH1	2.06	0.43
25:D3:57:LEU:HD11	25:D3:73:ARG:HG2	2.01	0.43
26:D4:35:VAL:HG13	26:D4:36:SER:H	1.82	0.43
1:2:525:A:H5''	26:D4:89:TYR:CE1	2.54	0.43
7:S5:124:LEU:HD11	27:D5:59:TYR:HD1	1.83	0.43
28:D6:62:TYR:CG	28:D6:63:ALA:N	2.94	0.43
23:D1:71:ARG:HG3	29:D7:4:VAL:HG11	3.58	0.43
29:D7:58:SER:O	29:D7:60:SER:N	3.47	0.43
40:L3:49:TYR:OH	40:L3:166:ILE:HG13	2.19	0.43
40:L3:283:TYR:CE1	40:L3:354:VAL:HG11	2.73	0.43
36:1:3312:U:OP1	87:L3:402:OHX:N2	2.52	0.43
43:L6:30:LEU:HD11	43:L6:63:LEU:HD21	2.00	0.43
46:L9:150:SER:CB	46:L9:153:ASP:HB2	2.49	0.43
47:M0:140:THR:OG1	47:M0:141:LYS:N	2.47	0.43
36:1:2854:U:O3'	47:M0:160:PRO:HB3	2.18	0.43
50:M4:60:LEU:HA	50:M4:60:LEU:HD23	3.04	0.43
51:M5:103:GLU:O	51:M5:106:VAL:HG13	2.19	0.43
41:L4:108:LYS:HG3	51:M5:203:ARG:HG3	3.40	0.43
52:M6:42:ASN:ND2	52:M6:125:ARG:HH11	3.99	0.43
55:M9:132:PHE:CG	55:M9:138:LEU:HD23	4.63	0.43
55:M9:106:LEU:HD13	55:M9:138:LEU:HD11	2.06	0.43
57:N1:103:GLN:O	57:N1:103:GLN:NE2	5.03	0.43
58:N2:54:VAL:HG13	58:N2:67:SER:HB2	3.98	0.43
59:N3:14:SER:O	59:N3:81:GLN:NE2	2.52	0.43
61:N5:57:LEU:HD23	61:N5:61:LYS:HG2	5.97	0.43
64:N8:84:GLU:O	64:N8:87:ARG:HB2	2.19	0.43
66:O0:41:LEU:O	66:O0:92:ILE:HG12	2.18	0.43
67:O1:13:THR:HG22	67:O1:72:ARG:CD	2.77	0.43
70:O4:10:ARG:HD2	75:O9:4:GLN:CD	3.44	0.43
77:Q1:15:ARG:O	77:Q1:19:LYS:HD3	3.09	0.43
78:Q2:71:ARG:HE	78:Q2:80:ARG:CZ	2.31	0.43
3:S1:124:ASN:N	3:S1:124:ASN:OD1	2.51	0.43
1:2:885:G:OP1	3:S1:136:ARG:NH1	2.51	0.43
4:S2:69:ILE:CG1	4:S2:133:LYS:HB3	3.11	0.43
4:S2:203:LYS:C	4:S2:205:ARG:H	2.43	0.43
4:S2:206:THR:OG1	4:S2:209:ASN:HB2	4.38	0.43
7:S5:128:ASN:O	7:S5:132:VAL:HG23	2.41	0.43
7:S5:216:GLU:O	7:S5:220:VAL:HG23	2.27	0.43
9:S7:63:PRO:O	9:S7:64:VAL:HB	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:S8:92:ARG:NH1	36:1:2107:A:H1'	2.33	0.43
36:1:1080:A:OP2	42:L5:140:ARG:NH2	2.52	0.43
36:1:1245:A:C3'	36:1:1246:G:H5''	2.47	0.43
36:1:1945:A:H2'	36:1:1946:A:H8	1.84	0.43
36:1:2210:G:H8	36:1:2210:G:OP2	2.02	0.43
36:1:2268:U:O2'	36:1:2269:U:H5'	2.19	0.43
36:1:2945:G:H8	36:1:2950:G:O6	2.02	0.43
36:1:3215:A:N3	36:1:3259:U:N3	2.66	0.43
36:1:79:U:OP2	87:1:3816:OHX:N5	2.51	0.43
36:1:566:G:O6	87:1:3898:OHX:N4	2.52	0.43
1:2:1586:A:H2'	1:2:1587:A:O4'	2.19	0.43
37:3:104:A:H3'	37:3:105:C:H6	1.83	0.43
36:5:1213:G:O6	87:5:3961:OHX:N4	2.52	0.43
36:5:1692:U:O4	36:5:1693:C:N4	2.51	0.43
36:5:2148:U:H2'	36:5:2149:A:C4	2.54	0.43
36:5:334:A:H2'	36:5:335:G:H8	1.84	0.43
36:5:573:C:H2'	36:5:574:U:H6	1.82	0.43
1:6:1478:G:C6	1:6:1479:A:C5	3.07	0.43
1:6:1545:A:H2'	1:6:1546:G:C8	2.53	0.43
1:6:1592:A:H2'	1:6:1593:A:C8	2.53	0.43
1:6:301:A:H2'	1:6:302:U:O4'	2.18	0.43
1:6:725:U:H2'	1:6:726:C:C6	2.54	0.43
11:S9:143:ILE:CG1	1:6:767:U:H5	424.32	0.43
1:6:778:G:C4	1:6:780:A:C8	3.07	0.43
1:6:829:A:H61	1:6:843:U:H3	1.67	0.43
1:6:855:A:C2	1:6:857:U:H1'	2.53	0.43
38:8:157:U:H2'	38:8:158:U:C6	2.54	0.43
38:8:77:A:H2'	38:8:78:G:O4'	2.19	0.43
14:C2:81:ASP:HA	14:C2:82:PRO:HD3	1.73	0.43
15:C3:40:TYR:CZ	15:C3:53:LEU:HD23	2.54	0.43
17:C5:122:THR:HG22	17:C5:123:TYR:HD1	5.65	0.43
18:C6:106:LYS:HG2	18:C6:117:LEU:HD11	4.21	0.43
1:2:1316:G:O2'	19:C7:10:LYS:NZ	2.49	0.43
22:D0:60:THR:HG1	22:D0:87:HIS:CG	2.33	0.43
4:S2:140:ARG:NH1	23:D1:10:GLU:OE1	5.71	0.43
2:S0:155:PHE:HE1	23:D1:30:ALA:HB1	3.27	0.43
23:D1:31:SER:HB2	23:D1:56:SER:HA	2.01	0.43
24:D2:104:LEU:HA	24:D2:126:LEU:HB2	2.00	0.43
31:D9:10:HIS:ND1	31:D9:11:PRO:HD2	2.34	0.43
39:L2:20:THR:O	39:L2:23:ARG:HG3	2.19	0.43
36:1:3146:G:O2'	40:L3:100:ARG:NH1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:211:GLN:NE2	40:L3:284:ARG:HA	2.34	0.43
42:L5:50:ARG:HD3	42:L5:65:ILE:HG22	2.01	0.43
87:1:4106:OHX:N4	43:L6:129:GLU:HA	2.34	0.43
45:L8:134:TYR:CG	45:L8:190:VAL:HG11	3.70	0.43
45:L8:63:LYS:O	45:L8:67:ILE:HG12	3.51	0.43
46:L9:163:GLN:NE2	36:5:3108:G:H21	316.41	0.43
46:L9:57:VAL:HG23	46:L9:68:LEU:HG	2.31	0.43
47:M0:45:GLU:O	47:M0:47:PRO:HD3	3.00	0.43
48:M1:91:LEU:HD12	48:M1:163:PHE:CE2	2.54	0.43
48:M1:92:ARG:HA	48:M1:171:VAL:O	2.18	0.43
53:M7:29:THR:HG22	53:M7:87:SER:CB	2.48	0.43
54:M8:125:ASP:O	54:M8:129:VAL:HG23	2.19	0.43
57:N1:45:ASN:ND2	57:N1:48:ILE:HG12	2.33	0.43
57:N1:65:TYR:CE2	57:N1:88:ARG:HB2	2.53	0.43
36:1:3043:C:P	59:N3:48:ARG:HH22	2.42	0.43
61:N5:60:TYR:OH	71:O5:26:LYS:HG3	2.18	0.43
62:N6:19:TYR:HD1	62:N6:20:PHE:CD2	2.36	0.43
64:N8:88:ASP:O	64:N8:92:LYS:HD2	2.19	0.43
65:N9:17:HIS:O	87:N9:101:OHX:N1	5.59	0.43
36:1:1162:U:H4'	68:O2:57:TYR:CD1	2.54	0.43
69:O3:6:ARG:O	69:O3:7:LEU:HD23	3.48	0.43
36:1:1589:A:H4'	70:O4:11:ASN:ND2	2.34	0.43
71:O5:40:SER:HA	38:8:49:G:O2'	55.68	0.43
74:O8:5:ILE:HD13	74:O8:14:LEU:HD12	2.62	0.43
79:Q3:86:LEU:O	79:Q3:90:VAL:HG13	5.14	0.43
2:S0:118:PRO:HG2	2:S0:141:ILE:HD13	2.02	0.43
4:S2:125:ILE:O	4:S2:129:ILE:HG13	2.18	0.43
4:S2:157:LYS:HD3	4:S2:168:ARG:HH21	2.73	0.43
6:S4:121:TYR:HA	6:S4:164:LEU:HD23	2.00	0.43
7:S5:103:ASN:HA	7:S5:106:LYS:HD2	2.01	0.43
7:S5:166:ARG:HB2	30:D8:46:GLY:HA3	2.01	0.43
8:S6:199:GLN:O	8:S6:203:GLU:N	2.97	0.43
9:S7:131:PHE:C	9:S7:133:THR:H	2.21	0.43
9:S7:141:ARG:HH21	9:S7:143:LEU:HD21	1.82	0.43
11:S9:143:ILE:C	11:S9:145:SER:H	2.60	0.43
11:S9:65:LYS:HG2	11:S9:70:LEU:HD11	2.00	0.43
34:SR:35:SER:HB3	34:SR:310:ILE:HD11	2.00	0.43
36:1:1170:A:H2'	36:1:1171:G:O4'	2.19	0.43
36:1:1369:A:H5''	64:N8:21:ARG:HD2	2.01	0.43
36:1:1722:U:C4	36:1:1723:A:N7	2.86	0.43
36:1:2374:C:N4	36:1:2941:A:C4	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:607:A:H4'	36:1:608:A:OP2	2.17	0.43
36:1:663:C:H2'	36:1:664:U:H6	1.84	0.43
36:1:805:G:H1'	41:L4:73:ARG:NH1	2.34	0.43
1:2:1250:U:HO2'	1:2:1251:U:P	2.42	0.43
1:2:1188:G:O2'	1:2:1430:U:OP1	2.30	0.43
1:2:633:U:H2'	1:2:634:G:O4'	2.19	0.43
1:2:71:A:H2'	1:2:72:A:H4'	2.01	0.43
38:4:10:A:C5	38:4:11:C:C4	3.06	0.43
36:5:1006:A:C2	36:5:1045:C:C2	3.06	0.43
67:O1:57:GLN:NE2	36:5:1474:A:O2'	141.17	0.43
36:5:3288:G:O2'	36:5:3289:G:H8	2.02	0.43
36:5:742:G:N7	87:5:3918:OHX:N2	2.67	0.43
36:5:629:U:H2'	36:5:630:A:C8	2.54	0.43
1:6:1394:G:O2'	1:6:1395:G:H5'	2.19	0.43
1:6:5:U:C2	1:6:20:G:N2	2.87	0.43
15:C3:78:ASN:HB3	15:C3:80:LEU:HD13	7.10	0.43
16:C4:85:ALA:N	16:C4:119:THR:HG22	2.29	0.43
17:C5:129:GLY:HA3	35:SM:74:LYS:CG	3.45	0.43
17:C5:74:ALA:HA	17:C5:75:PRO:HD3	1.88	0.43
1:2:1523:G:O6	21:C9:71:VAL:HG11	2.18	0.43
22:D0:44:ASN:HD21	22:D0:103:ILE:HD11	5.86	0.43
24:D2:82:LYS:HE3	1:6:748:U:OP1	361.59	0.43
25:D3:86:PHE:O	25:D3:88:PRO:HD3	2.19	0.43
25:D3:96:VAL:HG23	25:D3:97:ASP:N	2.34	0.43
30:D8:16:LEU:HB2	30:D8:27:GLN:HB2	2.53	0.43
40:L3:11:HIS:HD1	40:L3:235:THR:HA	1.84	0.43
40:L3:283:TYR:CE2	40:L3:325:LYS:HB2	2.53	0.43
40:L3:314:TYR:CG	40:L3:315:GLY:N	2.85	0.43
40:L3:377:HIS:C	40:L3:379:PHE:H	2.20	0.43
42:L5:118:THR:O	42:L5:119:TYR:HB2	2.19	0.43
42:L5:211:LEU:HA	42:L5:211:LEU:HD23	1.89	0.43
44:L7:26:VAL:HG23	44:L7:27:ALA:H	1.84	0.43
45:L8:68:ARG:H	45:L8:68:ARG:HG2	2.08	0.43
46:L9:28:VAL:HG22	46:L9:33:THR:OG1	2.18	0.43
48:M1:139:THR:O	48:M1:145:LYS:HG3	2.19	0.43
48:M1:139:THR:HG22	48:M1:147:THR:HA	2.19	0.43
51:M5:172:ARG:HH22	36:5:63:A:P	102.15	0.43
53:M7:98:ALA:HA	53:M7:101:ASN:HD22	1.84	0.43
54:M8:131:ALA:HB1	54:M8:135:GLN:H	2.22	0.43
36:1:744:A:H1'	54:M8:141:ARG:HD2	2.00	0.43
54:M8:22:ASP:HA	54:M8:27:LYS:HE3	2.29	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:M8:90:ASP:C	54:M8:92:ARG:H	2.21	0.43
55:M9:148:ASP:CG	55:M9:151:ARG:HH21	2.20	0.43
55:M9:40:ALA:O	55:M9:44:LEU:HG	4.86	0.43
55:M9:21:LYS:O	55:M9:53:LYS:HB2	2.59	0.43
55:M9:6:THR:O	55:M9:10:LEU:HB2	2.19	0.43
56:N0:30:PHE:CZ	56:N0:103:VAL:HG21	2.53	0.43
58:N2:48:GLY:C	58:N2:50:LEU:H	2.35	0.43
58:N2:49:ASN:O	58:N2:51:GLY:N	2.88	0.43
62:N6:58:VAL:HA	62:N6:104:LEU:HD23	2.00	0.43
64:N8:21:ARG:NH1	36:5:1369:A:OP1	184.10	0.43
65:N9:14:ARG:HH12	65:N9:18:ARG:HD3	3.16	0.43
67:O1:19:ARG:HD3	67:O1:35:GLU:CG	2.66	0.43
76:Q0:87:SER:O	76:Q0:91:CYS:HB2	2.19	0.43
3:S1:26:ARG:HG2	3:S1:26:ARG:O	2.40	0.43
1:2:920:U:H5''	3:S1:65:VAL:HG22	2.00	0.43
6:S4:58:GLY:HA2	6:S4:61:VAL:HG23	2.60	0.43
7:S5:70:VAL:O	7:S5:72:HIS:N	2.52	0.43
34:SR:52:GLN:HG2	34:SR:53:LYS:N	2.58	0.43
35:SM:48:ARG:HE	36:1:1017:C:H4'	1.84	0.43
36:1:1064:A:N6	36:1:1096:U:C4	2.87	0.43
36:1:2349:U:H5'	36:1:2391:G:OP1	2.19	0.43
36:1:2793:G:H4'	78:Q2:66:LYS:HE3	2.01	0.43
36:1:2887:A:H2'	36:1:2887:A:N3	2.34	0.43
36:1:2911:A:H4'	36:1:2912:G:C8	2.53	0.43
36:1:3019:U:H2'	36:1:3020:U:O4'	2.19	0.43
36:1:1443:G:O6	87:1:3872:OHX:N3	2.52	0.43
1:2:1087:A:C2	1:2:1142:A:H4'	2.53	0.43
1:2:1308:G:H2'	1:2:1309:C:C6	2.53	0.43
1:2:1498:G:O2'	1:2:1499:G:H5'	2.19	0.43
1:2:187:G:C6	1:2:197:A:N6	2.87	0.43
1:2:281:G:H8	1:2:281:G:OP2	2.01	0.43
1:2:372:G:H1'	1:2:612:U:O2	2.19	0.43
1:2:432:G:H2'	1:2:433:C:O4'	2.19	0.43
38:4:49:G:H4'	71:O5:35:LYS:HE2	2.01	0.43
36:5:1262:G:H5''	36:5:1263:A:OP2	2.19	0.43
36:5:1517:G:O2'	36:5:1518:U:H5'	2.19	0.43
36:5:1595:U:H4'	36:5:1595:U:OP1	2.18	0.43
36:5:2436:U:H3	36:5:2511:A:H62	1.67	0.43
36:5:2567:C:N4	36:5:2568:C:H41	2.17	0.43
36:5:614:C:H2'	36:5:615:U:O4'	2.18	0.43
36:5:651:G:H3'	87:5:4083:OHX:N5	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1138:A:H2'	1:6:1139:A:H8	1.84	0.43
20:C8:143:ARG:NH2	1:6:1462:G:N7	340.60	0.43
1:6:145:A:C2	1:6:171:A:H2	2.37	0.43
10:S8:43:ILE:N	1:6:260:U:O4	274.16	0.43
1:6:826:U:O4	87:6:2032:OHX:N3	2.52	0.43
1:6:86:A:H2'	1:6:87:C:H6	1.84	0.43
1:6:94:U:H2'	1:6:95:G:O4'	2.19	0.43
13:C1:86:ILE:HG22	13:C1:88:ARG:HG2	6.50	0.43
13:C1:92:HIS:O	13:C1:100:TYR:HA	2.18	0.43
17:C5:24:LYS:O	17:C5:28:MET:HB2	2.19	0.43
18:C6:87:LYS:HB3	18:C6:87:LYS:HE2	2.51	0.43
18:C6:86:ALA:O	18:C6:90:VAL:HG13	2.18	0.43
19:C7:43:SER:OG	19:C7:46:LEU:HB2	2.41	0.43
20:C8:65:GLU:O	20:C8:69:ILE:HG13	2.18	0.43
22:D0:38:SER:OG	22:D0:39:SER:N	2.51	0.43
24:D2:7:LEU:HD13	24:D2:74:VAL:HB	2.00	0.43
26:D4:35:VAL:HG22	26:D4:36:SER:H	1.84	0.43
27:D5:43:ASP:HB2	27:D5:46:LYS:HD2	2.01	0.43
30:D8:13:ILE:HD11	30:D8:31:GLU:CB	2.49	0.43
30:D8:13:ILE:HG13	30:D8:31:GLU:HB2	3.84	0.43
32:E0:39:LEU:HA	32:E0:39:LEU:HD13	2.58	0.43
39:L2:243:THR:OG1	36:5:2244:A:H5''	229.11	0.43
40:L3:105:VAL:HG11	40:L3:148:LEU:HD13	2.01	0.43
40:L3:252:ILE:HG22	36:5:2394:G:H5'	218.37	0.43
42:L5:143:LYS:HG3	42:L5:172:TYR:HD2	1.84	0.43
42:L5:201:GLY:O	42:L5:204:VAL:N	2.49	0.43
42:L5:257:GLU:O	42:L5:258:LYS:NZ	6.65	0.43
43:L6:102:ASN:ND2	43:L6:105:TYR:H	2.16	0.43
44:L7:223:PHE:HE2	56:N0:35:VAL:HG21	1.84	0.43
44:L7:150:LYS:NZ	44:L7:244:ASN:O	3.42	0.43
45:L8:124:ASP:C	45:L8:126:SER:H	2.20	0.43
45:L8:221:ASN:OD1	45:L8:221:ASN:N	2.52	0.43
45:L8:41:GLN:HG3	45:L8:42:PRO:HD2	2.08	0.43
46:L9:111:PHE:HD1	46:L9:127:PRO:HA	1.84	0.43
46:L9:112:ILE:HG21	46:L9:161:LEU:HD11	2.00	0.43
46:L9:176:LEU:HD23	46:L9:176:LEU:HA	2.07	0.43
47:M0:36:LEU:HD12	47:M0:87:LEU:HB3	2.80	0.43
47:M0:74:LYS:HB2	47:M0:74:LYS:HE3	1.88	0.43
49:M3:47:ALA:HB1	49:M3:48:PRO:CD	2.48	0.43
51:M5:31:ARG:HB2	51:M5:129:TYR:OH	2.18	0.43
51:M5:93:LYS:HG3	36:5:289:A:N3	145.12	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:M7:26:PHE:CD1	53:M7:121:GLN:HG3	4.12	0.43
53:M7:141:SER:O	53:M7:143:PRO:HD3	2.32	0.43
53:M7:46:LYS:HE2	53:M7:46:LYS:HB2	3.41	0.43
58:N2:58:GLU:HB2	58:N2:63:VAL:HG13	3.96	0.43
60:N4:8:PHE:CD2	60:N4:46:PRO:HG3	2.53	0.43
64:N8:90:TYR:CD1	64:N8:100:PRO:HG3	2.54	0.43
69:O3:8:TYR:HB3	69:O3:101:PHE:CD1	2.63	0.43
39:L2:177:LYS:HB2	79:Q3:29:LEU:HD13	2.01	0.43
4:S2:206:THR:HG21	1:6:14:C:OP2	378.82	0.43
4:S2:72:LEU:HD12	4:S2:72:LEU:HA	2.10	0.43
5:S3:44:THR:HG23	5:S3:45:LYS:HG3	4.00	0.43
6:S4:35:PRO:HD2	6:S4:83:PRO:HG2	2.12	0.43
9:S7:31:SER:O	9:S7:35:LYS:HE3	3.37	0.43
10:S8:192:TYR:O	10:S8:196:LEU:HB2	2.19	0.43
10:S8:88:ASN:N	10:S8:88:ASN:OD1	2.51	0.43
11:S9:154:LYS:HG3	11:S9:155:HIS:HD2	8.28	0.43
36:1:1496:C:C2	36:1:1521:G:N2	2.87	0.42
36:1:1597:C:H2'	36:1:1598:G:H8	1.84	0.42
36:1:1598:G:H2'	36:1:1599:G:H8	1.84	0.42
36:1:2197:C:N4	36:1:2241:U:H2'	2.33	0.42
36:1:2347:U:H2'	36:1:2348:A:O4'	2.19	0.42
36:1:2818:U:C6	36:1:2818:U:H5'	2.49	0.42
36:1:290:G:H2'	36:1:291:C:C6	2.54	0.42
36:1:3159:C:H2'	36:1:3160:U:C6	2.51	0.42
36:1:3166:C:H2'	36:1:3167:A:O4'	2.19	0.42
36:1:3205:G:H2'	36:1:3206:C:C5	2.54	0.42
36:1:2107:A:H2	36:1:3344:A:C8	2.37	0.42
36:1:1466:G:O6	87:1:3774:OHX:N4	2.51	0.42
36:1:543:C:H5''	36:1:544:C:H5	1.83	0.42
36:1:549:U:H3'	36:1:550:A:H8	1.84	0.42
36:1:736:A:C5	36:1:737:G:H1'	2.54	0.42
1:2:1018:U:C2	1:2:1019:A:N7	2.87	0.42
1:2:615:A:H2'	1:2:616:G:H8	1.84	0.42
1:2:783:G:H1'	1:2:784:C:C6	2.54	0.42
37:3:35:C:C5	37:3:36:C:C5	3.07	0.42
36:5:2105:G:H2'	36:5:2106:A:H8	1.84	0.42
36:5:2818:U:C6	36:5:2818:U:H5'	2.48	0.42
87:5:3845:OHX:N4	87:5:4083:OHX:N2	2.67	0.42
87:5:4001:OHX:N3	87:5:4119:OHX:N4	2.67	0.42
36:5:98:G:H4'	36:5:281:G:OP1	2.19	0.42
1:6:1160:A:OP2	87:6:2159:OHX:N4	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:S9:161:THR:HG21	87:6:2175:OHX:N2	445.31	0.42
1:6:967:A:C6	1:6:968:U:C4	3.06	0.42
38:8:15:G:C6	38:8:16:G:N1	2.87	0.42
12:C0:44:LYS:HE3	1:6:1217:A:H4'	427.44	0.42
17:C5:78:THR:OG1	17:C5:79:HIS:N	2.52	0.42
18:C6:24:ALA:HB2	18:C6:92:TYR:OH	2.34	0.42
19:C7:104:ASN:N	19:C7:104:ASN:OD1	2.52	0.42
21:C9:138:GLN:HA	21:C9:141:GLU:HG3	3.32	0.42
22:D0:109:GLU:HB3	22:D0:112:VAL:HB	2.01	0.42
22:D0:27:THR:HB	22:D0:88:LYS:HG2	2.73	0.42
24:D2:112:ASP:OD2	24:D2:112:ASP:N	3.05	0.42
25:D3:52:ILE:HG22	25:D3:99:ASN:HA	2.99	0.42
25:D3:89:ASN:HB2	25:D3:92:CYS:SG	2.59	0.42
28:D6:84:VAL:HG22	28:D6:85:ARG:O	2.18	0.42
7:S5:148:ARG:HH11	30:D8:22:ARG:NH2	3.36	0.42
30:D8:33:LEU:HD11	30:D8:53:ILE:HD13	7.57	0.42
31:D9:21:CYS:SG	31:D9:24:CYS:N	3.86	0.42
31:D9:30:LEU:HA	31:D9:39:CYS:HA	2.11	0.42
39:L2:86:GLN:HG3	39:L2:87:PHE:N	3.22	0.42
40:L3:41:VAL:CA	40:L3:185:GLY:HA3	2.36	0.42
40:L3:252:ILE:HD12	40:L3:252:ILE:HA	2.64	0.42
40:L3:360:ASP:OD2	40:L3:364:LYS:NZ	2.77	0.42
41:L4:177:ASP:OD1	41:L4:180:LYS:HE3	2.18	0.42
41:L4:257:LYS:HG2	41:L4:257:LYS:O	2.20	0.42
43:L6:147:ALA:HA	43:L6:150:LYS:HZ2	1.83	0.42
44:L7:80:GLN:HG3	57:N1:136:ARG:H	1.84	0.42
46:L9:117:PHE:CZ	46:L9:165:CYS:HB3	2.99	0.42
49:M3:149:GLN:HA	49:M3:150:PRO:HD3	1.83	0.42
50:M4:15:VAL:HG13	56:N0:150:PHE:O	2.19	0.42
50:M4:21:VAL:HG11	50:M4:65:LEU:HD23	2.00	0.42
55:M9:169:ALA:HA	55:M9:172:ARG:HD2	2.01	0.42
56:N0:106:LEU:HD22	56:N0:123:ILE:HD11	2.01	0.42
57:N1:102:ARG:NH1	57:N1:106:LEU:HD21	4.09	0.42
61:N5:86:VAL:HG11	61:N5:95:ILE:HG12	2.20	0.42
62:N6:117:ALA:O	62:N6:121:ARG:HB2	2.19	0.42
72:O6:37:THR:OG1	72:O6:38:LYS:N	3.13	0.42
75:O9:10:LYS:HA	75:O9:13:MET:CE	2.49	0.42
2:S0:148:ASP:N	2:S0:151:SER:OG	2.42	0.42
1:2:6:G:OP2	4:S2:205:ARG:HD2	2.19	0.42
6:S4:104:ASP:HB3	6:S4:105:VAL:H	1.42	0.42
7:S5:45:LYS:HD3	7:S5:45:LYS:HA	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:S6:178:LEU:HD12	8:S6:178:LEU:HA	2.55	0.42
9:S7:82:GLU:OE2	9:S7:89:HIS:HA	2.37	0.42
11:S9:163:PRO:C	11:S9:165:GLY:H	2.26	0.42
34:SR:37:SER:HG	34:SR:38:ARG:H	2.95	0.42
36:1:1069:C:H2'	36:1:1070:U:O4'	2.19	0.42
36:1:1189:C:C4	52:M6:133:ARG:CZ	3.03	0.42
36:1:1614:C:H2'	36:1:1615:C:H6	1.83	0.42
36:1:2677:G:H2'	36:1:2679:A:H2	1.83	0.42
36:1:2767:U:H2'	36:1:2768:U:C6	2.55	0.42
36:1:654:C:H2'	36:1:655:C:C6	2.54	0.42
36:1:853:G:N7	79:Q3:2:ALA:HB2	2.33	0.42
36:1:873:C:H2'	36:1:875:G:O4'	2.19	0.42
1:2:1182:U:O2	1:2:1184:A:H8	2.02	0.42
1:2:1234:A:H1'	33:E1:140:TYR:OH	2.19	0.42
1:2:1777:G:C6	1:2:1778:G:C6	3.08	0.42
1:2:526:A:H2'	1:2:527:A:O4'	2.19	0.42
36:5:1100:U:H2'	36:5:1101:G:O4'	2.19	0.42
36:5:1171:G:O6	87:5:3917:OHX:N1	2.51	0.42
36:5:1222:G:H1'	36:5:1285:G:N2	2.34	0.42
36:5:144:A:N6	36:5:145:G:C2	2.87	0.42
36:5:1017:C:H42	36:5:2671:A:P	2.42	0.42
51:M5:91:GLU:OE2	36:5:277:G:H5'	162.02	0.42
36:5:2786:G:N7	87:5:4060:OHX:N2	2.66	0.42
36:5:1540:U:OP1	87:5:4001:OHX:N2	2.52	0.42
41:L4:232:SER:HA	36:5:694:C:O2'	96.66	0.42
36:5:958:C:H5'	36:5:2799:A:H2'	2.01	0.42
1:6:1325:A:H2'	1:6:1326:A:H8	1.84	0.42
5:S3:203:PRO:HB3	1:6:1332:C:H4'	429.95	0.42
1:6:1486:G:H1'	1:6:1592:A:O2'	2.19	0.42
21:C9:68:ARG:NH1	1:6:1521:G:O6	415.97	0.42
1:6:1541:G:C6	1:6:1542:G:N1	2.87	0.42
1:6:1563:C:H2'	1:6:1564:U:C6	2.54	0.42
28:D6:84:VAL:HB	1:6:1797:A:N6	339.05	0.42
1:6:279:G:C6	1:6:281:G:C5	3.07	0.42
1:6:766:U:H5'	1:6:767:U:H5''	2.01	0.42
12:C0:27:PHE:CD1	12:C0:40:LEU:HD23	2.55	0.42
14:C2:124:LYS:C	35:SM:169:ALA:HB2	8.45	0.42
14:C2:60:VAL:H	14:C2:87:PRO:HB2	2.47	0.42
17:C5:28:MET:HE3	17:C5:33:PHE:HB2	3.76	0.42
7:S5:69:PHE:CD2	18:C6:50:GLU:HG3	2.53	0.42
18:C6:54:LEU:HD12	18:C6:108:ALA:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:C9:52:GLY:HA2	21:C9:55:TYR:CD2	2.53	0.42
22:D0:66:SER:OG	22:D0:81:THR:HG22	2.20	0.42
24:D2:23:ARG:HD2	24:D2:65:LEU:O	2.18	0.42
24:D2:37:PHE:CE2	24:D2:103:ILE:HD12	2.54	0.42
25:D3:15:LEU:HD13	1:6:611:U:H5'	346.73	0.42
27:D5:62:VAL:O	27:D5:66:VAL:HG23	2.33	0.42
1:2:1532:U:OP2	27:D5:77:ARG:NH1	2.51	0.42
39:L2:49:VAL:HG13	39:L2:58:LEU:HB2	3.79	0.42
36:1:2880:U:H1'	40:L3:250:ALA:HB3	2.01	0.42
40:L3:9:PRO:HD2	59:N3:45:ARG:HE	2.78	0.42
41:L4:170:LYS:HG3	41:L4:175:HIS:HB2	4.43	0.42
41:L4:185:LYS:HE2	41:L4:201:GLN:OE1	2.19	0.42
41:L4:237:GLN:O	41:L4:246:ARG:HG3	2.19	0.42
42:L5:178:ASN:HB3	42:L5:183:TRP:CE2	2.54	0.42
42:L5:55:PHE:CZ	42:L5:158:ARG:HG3	2.54	0.42
47:M0:152:LEU:HA	47:M0:152:LEU:HD23	2.17	0.42
47:M0:7:ARG:HG2	47:M0:7:ARG:H	1.54	0.42
48:M1:36:VAL:HG12	48:M1:37:LEU:HD23	2.01	0.42
43:L6:175:LYS:HE2	50:M4:111:ALA:O	2.19	0.42
51:M5:22:LEU:HD12	51:M5:22:LEU:HA	2.18	0.42
53:M7:108:ASP:OD1	53:M7:111:LYS:HE2	2.19	0.42
53:M7:112:LEU:HA	53:M7:112:LEU:HD12	2.02	0.42
53:M7:60:PHE:HB3	53:M7:64:ASN:HB3	2.30	0.42
56:N0:50:LYS:HB3	56:N0:50:LYS:HE2	3.37	0.42
57:N1:65:TYR:HD2	57:N1:75:ILE:HG22	1.84	0.42
61:N5:67:ILE:CD1	61:N5:121:LYS:HG3	2.49	0.42
62:N6:120:GLN:OE1	62:N6:126:LEU:HA	9.14	0.42
63:N7:24:VAL:HG23	63:N7:44:ALA:O	3.38	0.42
65:N9:12:GLN:NE2	36:5:954:U:H1'	213.11	0.42
69:O3:85:PHE:O	87:O3:202:OHX:N2	4.11	0.42
71:O5:70:TYR:HB3	71:O5:76:GLN:HG2	4.57	0.42
72:O6:34:SER:O	72:O6:37:THR:OG1	2.37	0.42
76:Q0:96:CYS:HB2	76:Q0:110:CYS:HB2	2.86	0.42
77:Q1:4:LYS:O	77:Q1:7:LYS:HB3	2.18	0.42
3:S1:131:ASP:HB3	3:S1:180:THR:OG1	2.18	0.42
3:S1:231:LEU:O	3:S1:231:LEU:HD22	4.36	0.42
4:S2:123:GLY:HA2	4:S2:126:ARG:HD2	2.01	0.42
1:2:579:A:H2	5:S3:143:ARG:HG2	1.84	0.42
7:S5:89:ILE:O	7:S5:92:ARG:HB2	2.18	0.42
8:S6:64:LYS:NZ	8:S6:81:VAL:HG12	4.72	0.42
10:S8:22:ARG:NE	10:S8:25:ARG:HD2	6.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:S9:111:THR:O	11:S9:115:LYS:HB2	2.93	0.42
11:S9:113:VAL:HG21	11:S9:129:ILE:HD11	2.01	0.42
35:SM:68:ARG:O	35:SM:69:ARG:C	2.57	0.42
34:SR:112:SER:HB3	34:SR:154:VAL:HG22	2.01	0.42
36:1:1109:U:H2'	36:1:1110:U:O4'	2.20	0.42
36:1:1235:U:H3	36:1:1263:A:H62	1.67	0.42
36:1:1278:A:O2'	36:1:1279:C:H6	2.02	0.42
36:1:1462:A:H2'	36:1:1463:U:O4'	2.19	0.42
36:1:1526:U:H5'	36:1:1594:A:N6	2.34	0.42
36:1:1573:G:C2	36:1:1574:C:H1'	2.54	0.42
36:1:3205:G:H2'	36:1:3206:C:C4	2.54	0.42
36:1:371:G:H4'	36:1:396:A:N1	2.34	0.42
36:1:431:U:H2'	36:1:432:G:C8	2.54	0.42
36:1:665:A:H1'	49:M3:14:PHE:CZ	2.55	0.42
36:1:748:U:H2'	36:1:749:C:C6	2.54	0.42
36:1:873:C:O3'	36:1:875:G:H5'	2.19	0.42
1:2:1174:C:C4	1:2:1175:U:C4	3.08	0.42
1:2:1325:A:C2	1:2:1326:A:C5	3.08	0.42
1:2:1347:U:OP1	22:D0:90:TYR:OH	2.20	0.42
1:2:770:A:OP2	87:2:2110:OHX:N6	2.53	0.42
1:2:881:A:H2'	1:2:882:U:O4'	2.20	0.42
52:M6:18:ARG:NH2	36:5:1318:A:OP1	277.71	0.42
36:5:1482:A:N7	36:5:1866:C:O2'	2.47	0.42
70:O4:4:ARG:HD2	36:5:1485:G:N2	152.72	0.42
36:5:1506:A:H1'	36:5:1848:G:C6	2.53	0.42
73:O7:9:GLY:HA3	36:5:1852:G:H1'	155.00	0.42
36:5:1856:C:H2'	36:5:1857:C:H6	1.84	0.42
36:5:2175:U:H4'	36:5:2176:U:OP2	2.19	0.42
36:5:2209:U:H1'	36:5:2210:G:H5''	2.01	0.42
36:5:2375:G:N2	36:5:2377:G:C8	2.86	0.42
36:5:2426:U:H2'	36:5:2427:U:C6	2.54	0.42
45:L8:241:LYS:HB2	36:5:2586:G:N7	185.48	0.42
78:Q2:19:LYS:HA	36:5:2741:C:H4'	209.21	0.42
36:5:3115:C:O2'	36:5:3117:C:N4	2.48	0.42
36:5:3181:C:H2'	36:5:3182:G:H8	1.82	0.42
36:5:3376:A:H5'	36:5:3377:G:H5''	2.01	0.42
36:5:33:G:O2'	36:5:51:A:N6	2.50	0.42
36:5:408:A:N6	38:8:15:G:H1'	2.33	0.42
64:N8:67:HIS:NE2	36:5:71:A:OP2	120.16	0.42
36:5:818:C:C2	36:5:920:A:H5'	2.54	0.42
1:6:1081:A:H1'	1:6:1082:C:H5	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1548:G:H2'	1:6:1549:C:H6	1.85	0.42
11:S9:124:HIS:CD2	1:6:478:A:O2'	452.25	0.42
1:6:913:G:H3'	1:6:914:G:H5''	2.01	0.42
1:6:961:U:H2'	1:6:962:C:H6	1.83	0.42
14:C2:44:GLY:HA3	1:6:1227:A:O2'	463.71	0.42
14:C2:45:LEU:HB3	14:C2:46:ARG:H	2.77	0.42
1:2:1590:G:OP1	21:C9:91:TYR:HB2	2.19	0.42
25:D3:97:ASP:O	25:D3:100:ASP:HB2	2.73	0.42
28:D6:19:LYS:HE3	28:D6:19:LYS:HB2	1.85	0.42
28:D6:85:ARG:O	28:D6:86:VAL:HB	2.19	0.42
40:L3:25:ILE:HD13	40:L3:25:ILE:N	2.27	0.42
40:L3:292:ALA:HB1	40:L3:295:ALA:HB3	2.01	0.42
40:L3:32:PHE:CD1	40:L3:182:GLN:HB3	2.55	0.42
40:L3:3:HIS:ND1	40:L3:3:HIS:C	2.88	0.42
41:L4:303:GLY:H	36:5:1347:U:H5''	198.97	0.42
41:L4:74:ILE:HG13	41:L4:75:PRO:HD2	4.68	0.42
42:L5:115:LEU:HD12	42:L5:119:TYR:HD2	4.03	0.42
43:L6:175:LYS:HB2	50:M4:112:LEU:O	2.79	0.42
43:L6:50:LYS:HG2	43:L6:74:VAL:HG21	2.00	0.42
44:L7:103:LEU:N	44:L7:130:ILE:HD11	5.48	0.42
44:L7:119:VAL:HG13	44:L7:124:LEU:HD23	3.40	0.42
44:L7:132:PRO:HA	44:L7:229:PHE:CD1	2.93	0.42
44:L7:139:PRO:HA	44:L7:237:ASN:OD1	2.19	0.42
47:M0:76:MET:HE3	47:M0:148:VAL:HA	2.00	0.42
49:M3:94:GLY:HA3	71:O5:116:TYR:OH	2.20	0.42
51:M5:38:ARG:HH21	51:M5:60:VAL:HG13	1.84	0.42
51:M5:79:ALA:HB1	51:M5:81:TYR:CZ	2.54	0.42
53:M7:70:THR:OG1	53:M7:71:ALA:N	2.95	0.42
41:L4:281:ILE:HB	54:M8:29:LEU:HD21	3.42	0.42
61:N5:45:LYS:HB3	71:O5:75:TYR:HD2	4.60	0.42
36:1:378:A:H1'	62:N6:90:VAL:O	2.20	0.42
63:N7:54:THR:H	63:N7:57:HIS:HB2	1.84	0.42
68:O2:111:ARG:O	68:O2:114:ALA:HB3	2.49	0.42
43:L6:172:HIS:CE1	69:O3:35:VAL:HG22	2.54	0.42
72:O6:15:LYS:HD2	72:O6:16:LYS:H	4.53	0.42
74:O8:12:LEU:HA	74:O8:12:LEU:HD13	2.18	0.42
36:1:1926:C:H3'	79:Q3:7:LYS:HG2	2.00	0.42
2:S0:110:TYR:CE2	4:S2:64:LYS:HD2	6.33	0.42
3:S1:120:LEU:HD23	3:S1:121:ILE:H	1.84	0.42
3:S1:205:PHE:HA	3:S1:206:PRO:HD2	1.87	0.42
4:S2:172:ALA:HA	4:S2:173:PRO:HD3	2.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:S5:77:TYR:HB3	7:S5:84:LYS:HA	2.09	0.42
8:S6:73:ILE:HG22	8:S6:74:LYS:H	3.52	0.42
9:S7:63:PRO:HB2	9:S7:64:VAL:H	2.47	0.42
9:S7:67:LEU:HD23	9:S7:67:LEU:HA	1.92	0.42
11:S9:122:VAL:HG23	11:S9:123:HIS:HD1	1.83	0.42
34:SR:132:LYS:HA	34:SR:142:ALA:O	2.54	0.42
36:1:1252:A:H2'	36:1:1253:U:C5	2.54	0.42
36:1:126:U:H2'	36:1:127:G:O4'	2.20	0.42
36:1:1549:U:O4	87:1:3915:OHX:N1	2.53	0.42
36:1:1836:C:O2'	36:1:1842:A:N1	2.43	0.42
36:1:2389:C:H2'	36:1:2390:A:C8	2.55	0.42
36:1:2403:G:O6	87:1:4076:OHX:N6	2.52	0.42
36:1:2577:C:H2'	36:1:2578:U:O4'	2.19	0.42
36:1:2223:A:N1	36:1:2783:U:H1'	2.33	0.42
36:1:2900:A:H2	36:1:3025:C:O2	2.02	0.42
36:1:384:A:H1'	36:1:1465:A:C8	2.54	0.42
36:1:541:U:H2'	36:1:542:G:C8	2.54	0.42
36:1:551:A:O2'	36:1:552:G:H8	2.02	0.42
36:1:621:A:OP1	53:M7:165:VAL:HG11	2.18	0.42
1:2:1066:C:O3'	3:S1:149:GLN:HG3	2.19	0.42
1:2:1110:G:N2	1:2:1136:U:H1'	2.34	0.42
1:2:1357:A:N6	1:2:1366:U:H3	2.17	0.42
1:2:29:U:H2'	1:2:30:G:C8	2.54	0.42
1:2:988:A:C2	1:2:989:U:H1'	2.55	0.42
36:5:1481:A:O3'	36:5:1858:A:O2'	2.34	0.42
36:5:191:U:H2'	36:5:192:C:C6	2.55	0.42
36:5:626:U:H2'	36:5:627:U:O4'	2.20	0.42
1:6:1207:C:H5''	87:6:2094:OHX:N3	2.35	0.42
1:6:1553:G:N2	1:6:1555:A:H3'	2.35	0.42
13:C1:38:ALA:O	1:6:246:G:N2	324.49	0.42
1:6:386:G:H2'	1:6:387:A:C8	2.54	0.42
42:L5:21:ARG:N	37:7:10:C:O2	286.97	0.42
37:7:47:C:H2'	37:7:48:U:H6	1.84	0.42
61:N5:48:SER:HB2	38:8:136:G:OP1	84.53	0.42
14:C2:59:LEU:HB3	14:C2:123:VAL:HB	3.05	0.42
15:C3:130:ARG:HD3	15:C3:137:PRO:O	4.50	0.42
15:C3:70:LYS:HG2	15:C3:70:LYS:H	2.92	0.42
16:C4:43:THR:OG1	16:C4:46:MET:HG3	3.23	0.42
21:C9:73:VAL:HG21	21:C9:102:ARG:HG3	2.06	0.42
22:D0:33:GLN:O	22:D0:37:VAL:HG23	2.19	0.42
22:D0:53:LYS:HA	22:D0:53:LYS:HD3	2.61	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:D1:80:LYS:NZ	23:D1:80:LYS:O	2.49	0.42
24:D2:95:PRO:HD3	24:D2:130:TYR:CD1	2.86	0.42
26:D4:27:VAL:O	26:D4:68:LYS:HA	2.65	0.42
26:D4:60:PHE:CD1	26:D4:71:GLY:HA3	2.72	0.42
32:E0:14:VAL:O	32:E0:18:THR:HG23	2.19	0.42
32:E0:46:ASN:O	32:E0:47:VAL:HG12	2.29	0.42
40:L3:41:VAL:HA	40:L3:185:GLY:CA	2.39	0.42
41:L4:198:ARG:HD3	41:L4:199:TRP:NE1	2.35	0.42
41:L4:206:LEU:HB3	41:L4:248:VAL:HG22	2.07	0.42
44:L7:239:LEU:HD22	44:L7:243:MET:SD	3.01	0.42
47:M0:140:THR:HG21	47:M0:144:ASN:HD22	1.84	0.42
59:N3:83:LYS:HE2	59:N3:84:SER:N	2.34	0.42
61:N5:71:THR:O	61:N5:75:LYS:HG3	2.37	0.42
67:O1:70:ARG:HE	67:O1:102:LYS:NZ	4.97	0.42
67:O1:75:ILE:HG12	67:O1:93:VAL:HG13	2.28	0.42
67:O1:6:ASP:O	67:O1:8:VAL:HG13	4.14	0.42
67:O1:96:VAL:O	67:O1:98:VAL:N	2.53	0.42
74:O8:10:GLN:HA	74:O8:13:GLU:CD	4.31	0.42
77:Q1:2:ARG:NH1	1:6:1773:C:OP2	310.81	0.42
1:2:1113:A:H5''	77:Q1:6:ARG:HH21	1.83	0.42
78:Q2:31:GLY:HA3	36:5:2767:U:O3'	192.64	0.42
2:S0:41:ARG:HB3	2:S0:45:VAL:O	2.19	0.42
2:S0:59:LEU:O	2:S0:63:ILE:HG13	2.29	0.42
3:S1:24:PHE:HA	3:S1:27:LYS:CG	3.72	0.42
7:S5:63:GLN:HB3	7:S5:88:PRO:HA	2.44	0.42
8:S6:148:SER:O	8:S6:151:ASP:HB2	4.20	0.42
9:S7:35:LYS:HB3	9:S7:35:LYS:HE3	2.00	0.42
9:S7:35:LYS:HZ3	9:S7:39:ARG:HD2	1.84	0.42
11:S9:39:LYS:HB3	11:S9:43:TYR:CZ	3.23	0.42
11:S9:92:LYS:HA	11:S9:92:LYS:HE3	2.00	0.42
34:SR:201:THR:HG21	34:SR:242:SER:CA	2.73	0.42
36:1:1192:C:N3	87:1:3945:OHX:N5	2.67	0.42
36:1:1277:C:O2'	36:1:1278:A:C8	2.72	0.42
36:1:1341:U:H2'	36:1:1342:C:H6	1.84	0.42
36:1:1900:A:N6	36:1:1908:A:H61	2.16	0.42
36:1:209:A:H4'	36:1:211:A:H8	1.82	0.42
36:1:2197:C:C2	36:1:2241:U:C4	3.07	0.42
36:1:2534:G:H22	36:1:2545:C:N4	2.17	0.42
36:1:628:A:H4'	36:1:1399:A:C6	2.55	0.42
1:2:1298:U:H2'	1:2:1299:G:O4'	2.20	0.42
1:2:398:G:H8	1:2:398:G:O5'	2.03	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:703:G:H2'	1:2:704:C:H5'	2.00	0.42
1:2:706:A:H61	1:2:734:A:N6	2.16	0.42
38:4:127:U:C2'	38:4:128:U:H5'	2.48	0.42
38:4:91:C:H2'	38:4:92:A:C8	2.54	0.42
36:5:1390:A:N3	36:5:1390:A:H5'	2.34	0.42
74:O8:42:LYS:NZ	36:5:1750:A:OP2	141.28	0.42
36:5:2828:G:N2	36:5:2863:G:H1'	2.35	0.42
36:5:750:G:N3	36:5:751:A:C8	2.87	0.42
1:6:103:A:OP1	87:6:2033:OHX:N4	2.53	0.42
18:C6:71:GLY:HA2	1:6:1483:A:H4'	412.46	0.42
1:6:1584:G:N2	1:6:1610:G:H2'	2.35	0.42
1:6:824:G:C6	1:6:825:U:O4	2.73	0.42
12:C0:46:LEU:HG	12:C0:66:TYR:CD2	2.53	0.42
13:C1:94:ILE:HA	13:C1:95:PRO:HD3	1.85	0.42
15:C3:100:LYS:O	15:C3:104:ARG:HG3	2.20	0.42
1:2:959:U:H5'	15:C3:15:ALA:O	2.19	0.42
16:C4:41:ARG:O	16:C4:42:VAL:HG22	2.20	0.42
21:C9:40:SER:OG	21:C9:41:SER:N	3.18	0.42
21:C9:70:GLN:O	21:C9:70:GLN:HG2	2.48	0.42
23:D1:83:TRP:CZ2	23:D1:85:TYR:HA	2.76	0.42
24:D2:28:ARG:HG3	24:D2:29:PRO:HA	2.01	0.42
26:D4:88:THR:O	26:D4:92:VAL:HG23	2.20	0.42
27:D5:80:LEU:HD22	27:D5:101:TYR:CE2	3.94	0.42
27:D5:38:HIS:CG	27:D5:39:ALA:N	2.87	0.42
28:D6:58:VAL:HG23	28:D6:59:TYR:CD2	2.54	0.42
39:L2:79:ASN:HA	39:L2:169:ILE:HA	2.00	0.42
40:L3:103:THR:HG21	40:L3:147:GLU:OE2	2.40	0.42
40:L3:241:LYS:HE2	40:L3:241:LYS:HB3	2.51	0.42
41:L4:362:ASP:C	56:N0:26:ARG:HH12	2.22	0.42
42:L5:64:ILE:HG13	42:L5:109:THR:HG21	3.99	0.42
45:L8:67:ILE:HG22	45:L8:237:ILE:HB	2.01	0.42
46:L9:75:VAL:HA	46:L9:78:MET:HE2	2.00	0.42
47:M0:76:MET:HE2	47:M0:76:MET:HB3	2.54	0.42
50:M4:20:VAL:O	50:M4:66:THR:OG1	2.24	0.42
52:M6:19:LEU:O	52:M6:23:VAL:HG23	2.20	0.42
52:M6:41:LEU:HD12	52:M6:41:LEU:HA	1.92	0.42
52:M6:46:GLU:HG2	52:M6:48:PHE:H	1.83	0.42
55:M9:149:ALA:O	55:M9:152:GLU:HB3	2.19	0.42
55:M9:60:LYS:HB2	55:M9:60:LYS:HZ3	1.84	0.42
55:M9:69:SER:HB2	55:M9:74:ARG:CB	3.61	0.42
60:N4:63:ILE:HB	60:N4:64:THR:H	3.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:O4:94:LEU:HA	70:O4:94:LEU:HD23	1.97	0.42
73:O7:84:SER:O	73:O7:85:LYS:HB2	2.20	0.42
61:N5:117:ASN:HA	75:O9:14:ALA:HB1	2.02	0.42
75:O9:4:GLN:HA	36:5:1833:G:O2'	120.23	0.42
77:Q1:5:TRP:O	77:Q1:9:ARG:N	2.49	0.42
2:S0:56:LYS:NZ	2:S0:158:VAL:HA	2.75	0.42
5:S3:134:CYS:SG	5:S3:135:GLU:N	3.03	0.42
5:S3:218:LEU:HD23	5:S3:218:LEU:HA	1.83	0.42
7:S5:30:PRO:O	7:S5:33:VAL:HB	2.20	0.42
7:S5:61:TYR:HE1	7:S5:165:LEU:HB2	2.70	0.42
8:S6:102:VAL:HG13	8:S6:106:LEU:HD12	2.01	0.42
8:S6:137:ARG:HB3	8:S6:140:ASN:HB2	2.35	0.42
8:S6:23:ARG:O	8:S6:26:VAL:HG23	2.20	0.42
9:S7:102:PRO:HD3	9:S7:112:ARG:HD2	2.01	0.42
36:1:1002:A:H2'	36:1:1003:A:H8	1.84	0.42
36:1:1246:G:H8	36:1:1246:G:OP1	2.01	0.42
36:1:2108:C:H1'	36:1:3344:A:C8	2.55	0.42
36:1:2269:U:H2'	36:1:2271:A:OP2	2.20	0.42
36:1:2723:U:H2'	36:1:2724:U:C6	2.54	0.42
36:1:821:U:OP2	87:1:3875:OHX:N3	2.52	0.42
1:2:1291:G:N2	1:2:1325:A:N3	2.66	0.42
1:2:1365:C:O3'	18:C6:30:LYS:NZ	2.52	0.42
1:2:1498:G:H2'	1:2:1499:G:H8	1.84	0.42
1:2:1685:G:H22	1:2:1716:C:N4	2.17	0.42
1:2:351:C:O2'	13:C1:104:HIS:NE2	2.52	0.42
1:2:694:U:H3'	1:2:695:U:C6	2.55	0.42
36:5:1151:U:O4	36:5:1200:A:N6	2.52	0.42
36:5:1510:G:O5'	36:5:1510:G:H8	2.02	0.42
36:5:1559:A:H4'	36:5:1560:G:OP2	2.20	0.42
36:5:1615:C:OP1	87:5:3969:OHX:N5	2.53	0.42
36:5:1658:G:H2'	36:5:1659:U:H6	1.84	0.42
36:5:1658:G:C4	36:5:1796:G:C5	3.08	0.42
63:N7:135:ARG:NH1	36:5:1807:G:H5'	195.26	0.42
36:5:41:G:H4'	36:5:2410:U:H2'	2.01	0.42
36:5:2885:C:N4	36:5:2886:U:O4	2.53	0.42
36:5:952:A:H1'	36:5:1114:U:H1'	2.00	0.42
1:6:1009:U:H2'	1:6:1010:C:H6	1.85	0.42
1:6:1545:A:H2'	1:6:1546:G:H8	1.84	0.42
1:6:1590:G:H2'	1:6:1591:C:C6	2.54	0.42
1:6:1783:C:H2'	1:6:1784:C:C6	2.54	0.42
1:6:383:G:O6	87:6:2115:OHX:N5	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:901:G:N1	1:6:902:G:C6	2.88	0.42
17:C5:51:SER:HB3	17:C5:52:LYS:H	4.20	0.42
18:C6:14:LYS:O	18:C6:123:ARG:NH2	2.51	0.42
1:2:1389:C:O2'	19:C7:52:GLY:HA3	2.18	0.42
20:C8:114:GLU:HA	20:C8:117:LYS:HB2	2.51	0.42
20:C8:123:ARG:HG3	20:C8:133:VAL:HG21	2.00	0.42
20:C8:5:VAL:O	27:D5:42:LEU:HB2	4.22	0.42
22:D0:63:LEU:O	22:D0:83:GLU:HA	2.19	0.42
22:D0:75:GLY:HA2	1:6:1193:A:H4'	375.73	0.42
24:D2:104:LEU:HB3	24:D2:125:ILE:HA	2.01	0.42
29:D7:31:TYR:CD2	29:D7:48:SER:HB3	2.71	0.42
5:S3:12:VAL:HG21	31:D9:34:TYR:HB3	2.64	0.42
40:L3:103:THR:HG21	40:L3:147:GLU:CD	2.40	0.42
40:L3:10:ARG:NH2	40:L3:263:SER:O	2.49	0.42
40:L3:360:ASP:OD2	60:N4:17:ARG:NH2	2.52	0.42
42:L5:278:SER:OG	42:L5:281:GLU:HG3	2.19	0.42
43:L6:131:LYS:HG2	43:L6:133:GLU:H	1.83	0.42
43:L6:176:PHE:CE2	69:O3:107:ILE:HD13	3.70	0.42
48:M1:140:ARG:HD3	48:M1:140:ARG:HA	4.52	0.42
50:M4:16:GLU:OE1	50:M4:19:ARG:NH1	2.48	0.42
50:M4:17:VAL:HG11	50:M4:74:ARG:HA	2.02	0.42
52:M6:106:GLU:H	52:M6:106:GLU:HG2	1.64	0.42
57:N1:154:VAL:HG23	57:N1:155:PRO:O	2.49	0.42
62:N6:55:GLU:HB3	62:N6:108:LYS:HB2	3.15	0.42
63:N7:81:LEU:HD12	70:O4:93:PHE:CE2	3.89	0.42
71:O5:43:LYS:O	71:O5:46:THR:OG1	2.36	0.42
2:S0:75:ALA:HB1	2:S0:174:TRP:CH2	3.14	0.42
4:S2:208:GLU:O	4:S2:212:LYS:HG3	2.63	0.42
4:S2:233:GLN:HA	4:S2:234:PRO:HD3	1.90	0.42
5:S3:113:LEU:HD11	5:S3:117:ARG:NH1	2.34	0.42
5:S3:60:GLY:HA3	5:S3:65:ARG:HB3	3.33	0.42
5:S3:69:LEU:O	5:S3:72:LEU:HB2	2.19	0.42
8:S6:176:GLN:HG3	8:S6:177:ARG:H	1.85	0.42
8:S6:214:LYS:HE3	8:S6:214:LYS:HB2	4.20	0.42
1:2:805:U:O4	9:S7:104:ARG:NH1	2.52	0.42
10:S8:74:LYS:HB2	10:S8:109:PHE:CE1	3.55	0.42
5:S3:115:ILE:HG21	35:SM:110:TRP:HA	2.01	0.42
34:SR:166:SER:HA	34:SR:184:ASN:HD21	1.83	0.42
34:SR:32:LEU:HA	34:SR:45:TRP:O	2.75	0.42
36:1:1598:G:H2'	36:1:1599:G:C8	2.54	0.42
36:1:1604:G:H2'	36:1:1605:A:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2175:U:O2	39:L2:23:ARG:HB2	2.20	0.42
36:1:2357:A:H2'	36:1:2358:A:C8	2.54	0.42
36:1:2416:U:H2'	36:1:2417:U:C6	2.55	0.42
36:1:3107:U:OP1	76:Q0:114:LYS:NZ	2.46	0.42
36:1:1169:A:OP1	87:1:3854:OHX:N3	2.53	0.42
36:1:386:A:C5	36:1:387:A:H1'	2.54	0.42
36:1:2187:G:OP2	87:1:3897:OHX:N5	2.52	0.42
1:2:1054:U:H2'	1:2:1055:U:H6	1.84	0.42
1:2:1229:G:HO2'	1:2:1255:G:N2	2.17	0.42
1:2:1545:A:H2'	1:2:1546:G:H8	1.85	0.42
1:2:1622:G:H2'	1:2:1623:C:C6	2.55	0.42
1:2:1663:G:C6	1:2:1664:C:C4	3.08	0.42
1:2:1783:C:H2'	1:2:1784:C:C6	2.52	0.42
1:2:57:G:OP1	26:D4:112:LYS:NZ	2.47	0.42
1:2:591:A:H5''	11:S9:24:LEU:HD22	2.01	0.42
36:5:627:U:H4'	36:5:1399:A:O2'	2.19	0.42
36:5:1668:G:H2'	36:5:1669:C:O4'	2.20	0.42
36:5:170:G:N7	87:5:4129:OHX:N3	2.68	0.42
36:5:1677:G:N2	36:5:1755:C:O2'	2.40	0.42
55:M9:43:LYS:HG2	36:5:1764:U:OP2	93.98	0.42
36:5:1816:A:O2'	36:5:1817:G:OP1	2.30	0.42
36:5:20:A:N6	36:5:21:G:O6	2.52	0.42
53:M7:138:LYS:O	36:5:2356:A:H4'	150.15	0.42
36:5:2413:A:H2	36:5:2809:C:N4	2.18	0.42
36:5:2437:G:H1	36:5:2510:U:H3	1.67	0.42
36:5:2924:U:C5	36:5:2925:C:C2	3.07	0.42
36:5:334:A:H2'	36:5:335:G:C8	2.54	0.42
36:5:1861:G:OP2	87:5:3909:OHX:N2	2.52	0.42
87:5:3977:OHX:N3	87:5:4051:OHX:N4	2.67	0.42
1:6:1051:G:O2'	1:6:1052:U:OP1	2.36	0.42
1:6:1429:G:H2'	1:6:1430:U:C6	2.55	0.42
7:S5:180:ARG:NH2	1:6:1473:U:O4	354.58	0.42
1:6:1616:G:H2'	1:6:1617:U:C6	2.54	0.42
1:6:363:G:H1	1:6:381:C:H42	1.67	0.42
1:6:565:C:O2	87:6:2123:OHX:N6	2.53	0.42
38:8:126:A:O2'	38:8:128:U:OP2	2.32	0.42
12:C0:48:SER:HA	1:6:1219:A:O2'	436.96	0.42
15:C3:23:PRO:HD2	15:C3:26:PHE:HB3	2.02	0.42
15:C3:65:VAL:C	15:C3:67:THR:H	3.18	0.42
21:C9:28:LEU:HD23	21:C9:111:ILE:CD1	8.96	0.42
1:2:1429:G:C1'	22:D0:74:GLU:HG2	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:S9:123:HIS:CE1	32:E0:37:ARG:HD2	4.27	0.42
39:L2:41:ILE:HG12	39:L2:42:ARG:N	2.35	0.42
40:L3:188:ILE:O	40:L3:191:LYS:HB2	2.43	0.42
40:L3:199:PHE:O	40:L3:200:GLU:HB2	2.20	0.42
40:L3:53:MET:HG2	40:L3:77:THR:HG22	3.06	0.42
41:L4:3:ARG:NH1	41:L4:22:LEU:HD12	2.32	0.42
41:L4:140:HIS:CD2	41:L4:247:PHE:H	2.44	0.42
45:L8:152:LEU:O	45:L8:197:VAL:HA	2.44	0.42
45:L8:64:ILE:O	45:L8:68:ARG:HG2	2.30	0.42
46:L9:1:MET:SD	56:N0:138:GLN:NE2	4.57	0.42
47:M0:38:LYS:HB3	47:M0:46:PHE:CE2	3.25	0.42
47:M0:48:LEU:HA	47:M0:178:ARG:HH12	1.85	0.42
48:M1:109:HIS:HA	48:M1:112:LEU:HD21	2.01	0.42
50:M4:54:PRO:O	50:M4:56:GLN:HG2	2.19	0.42
51:M5:162:ARG:O	36:5:29:C:O2'	107.34	0.42
51:M5:70:ASN:ND2	51:M5:93:LYS:HD3	2.34	0.42
52:M6:179:ALA:HA	52:M6:182:ASN:HB3	3.44	0.42
53:M7:116:HIS:NE2	53:M7:118:GLN:HG2	2.34	0.42
55:M9:110:ARG:HH12	36:5:1720:U:P	232.42	0.42
57:N1:11:THR:HG22	57:N1:14:MET:HB3	2.00	0.42
60:N4:33:ASN:ND2	60:N4:35:LYS:HB3	3.87	0.42
61:N5:38:LEU:HB3	61:N5:39:LYS:H	4.40	0.42
62:N6:37:LYS:CG	62:N6:38:GLU:H	2.32	0.42
64:N8:101:VAL:HG22	64:N8:124:ILE:HB	2.54	0.42
64:N8:128:ARG:HG3	64:N8:128:ARG:O	4.81	0.42
36:1:1431:G:OP2	64:N8:12:ARG:NH1	2.53	0.42
69:O3:12:LYS:HB2	69:O3:31:LYS:HB3	2.02	0.42
63:N7:15:ARG:HH12	70:O4:86:LYS:HZ3	1.67	0.42
72:O6:99:ARG:HB3	72:O6:100:HIS:H	1.57	0.42
74:O8:17:ARG:O	74:O8:18:ALA:HB3	4.59	0.42
4:S2:229:LEU:HD11	23:D1:10:GLU:OE1	8.75	0.42
8:S6:135:PRO:HB2	8:S6:141:ILE:HG12	2.02	0.42
9:S7:30:SER:O	9:S7:31:SER:HB2	2.20	0.42
10:S8:136:SER:HB3	10:S8:139:ALA:HB2	2.00	0.42
11:S9:60:LEU:HD21	11:S9:93:LEU:CB	5.77	0.42
34:SR:5:GLU:HA	34:SR:317:THR:HA	2.69	0.42
36:1:1096:U:OP2	57:N1:116:ARG:NH2	2.53	0.42
36:1:1158:A:O5'	36:1:1158:A:H8	2.02	0.42
36:1:1317:A:C4	36:1:1319:G:C8	3.07	0.42
36:1:1945:A:H2'	36:1:1946:A:C8	2.54	0.42
36:1:258:G:H2'	36:1:259:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2694:A:C6	36:1:2695:A:C6	3.08	0.42
36:1:2877:G:H2'	36:1:2878:G:C8	2.54	0.42
36:1:3294:A:H2'	36:1:3295:A:O4'	2.20	0.42
36:1:3372:A:H2'	36:1:3373:U:C6	2.54	0.42
36:1:39:A:H61	36:1:42:C:H3'	1.85	0.42
36:1:574:U:H2'	36:1:575:G:H8	1.85	0.42
36:1:705:A:H4'	36:1:706:A:OP1	2.19	0.42
1:2:1102:G:OP1	24:D2:76:SER:OG	2.37	0.42
38:4:151:C:C4	61:N5:24:LEU:HD11	2.55	0.42
36:5:130:A:C6	36:5:139:G:C6	3.06	0.42
36:5:1573:G:C6	36:5:1574:C:H1'	2.55	0.42
36:5:1609:C:H2'	36:5:1610:G:C8	2.54	0.42
36:5:1692:U:C4	36:5:1693:C:N4	2.88	0.42
36:5:178:U:H2'	36:5:179:C:O4'	2.20	0.42
36:5:2712:U:H4'	36:5:2743:A:O3'	2.20	0.42
36:5:2971:A:N6	89:5:3402:SPS:O10	2.53	0.42
52:M6:68:ARG:NH1	36:5:2988:C:OP1	218.81	0.42
36:5:3251:U:H2'	36:5:3252:G:H8	1.84	0.42
36:5:3358:U:H2'	36:5:3359:A:H8	1.85	0.42
1:6:1037:C:H2'	1:6:1038:U:H6	1.84	0.42
1:6:11:A:H2'	1:6:12:U:H5'	2.01	0.42
31:D9:45:GLU:CD	1:6:1433:G:H22	411.82	0.42
87:6:2112:OHX:N5	87:6:2151:OHX:N4	2.68	0.42
1:6:792:U:O2'	1:6:793:A:H5'	2.19	0.42
1:6:836:U:H2'	1:6:837:G:C8	2.54	0.42
42:L5:274:GLN:NE2	37:7:60:G:H21	332.76	0.42
15:C3:27:LYS:H	15:C3:27:LYS:CE	2.29	0.42
15:C3:54:LEU:O	15:C3:60:VAL:HB	2.19	0.42
1:2:885:G:N2	16:C4:123:SER:HB2	2.33	0.42
17:C5:18:ARG:HD2	17:C5:36:LEU:O	3.52	0.42
18:C6:79:TYR:HA	18:C6:82:ARG:HD3	2.02	0.42
19:C7:16:LEU:HA	19:C7:16:LEU:HD23	1.86	0.42
19:C7:49:LYS:HA	1:6:1389:C:H4'	424.27	0.42
20:C8:133:VAL:HG23	20:C8:134:ARG:HG3	7.41	0.42
27:D5:42:LEU:H	27:D5:42:LEU:HG	1.50	0.42
30:D8:10:ALA:HB1	30:D8:30:VAL:HB	2.34	0.42
7:S5:61:TYR:OH	30:D8:52:ASP:OD1	4.21	0.42
39:L2:179:LEU:HD12	39:L2:179:LEU:HA	2.46	0.42
40:L3:230:THR:HA	40:L3:235:THR:HB	2.01	0.42
40:L3:303:LYS:NZ	40:L3:359:ILE:O	2.79	0.42
40:L3:9:PRO:HG3	36:5:2914:G:H5'	255.79	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:L6:143:LYS:HB2	43:L6:143:LYS:HE3	4.16	0.42
46:L9:85:GLY:O	46:L9:186:PHE:HB3	3.30	0.42
47:M0:210:ILE:HA	47:M0:217:PHE:CE2	2.55	0.42
48:M1:122:ILE:HA	48:M1:122:ILE:HD13	2.31	0.42
48:M1:21:ILE:HG12	48:M1:125:MET:HB3	4.29	0.42
49:M3:74:GLY:HA3	49:M3:98:ASP:HB2	2.14	0.42
50:M4:38:ILE:HD13	56:N0:150:PHE:CE2	3.87	0.42
51:M5:59:PHE:HZ	51:M5:148:TYR:CE1	2.55	0.42
53:M7:18:ARG:HG2	53:M7:147:GLU:HB3	4.76	0.42
53:M7:40:GLU:HB3	53:M7:43:LYS:HB2	2.01	0.42
54:M8:170:ARG:HA	54:M8:174:ARG:HD2	2.60	0.42
50:M4:38:ILE:CD1	56:N0:150:PHE:HE2	2.33	0.42
56:N0:170:THR:OG1	36:5:3185:U:O2'	306.16	0.42
57:N1:127:GLN:HB3	57:N1:127:GLN:HE21	1.72	0.42
58:N2:94:ARG:O	58:N2:96:VAL:HG23	2.19	0.42
60:N4:52:THR:O	60:N4:56:ARG:HG3	2.25	0.42
70:O4:46:ASP:OD2	70:O4:80:ARG:NH1	3.40	0.42
70:O4:71:THR:HG22	70:O4:78:GLY:N	3.98	0.42
79:Q3:8:VAL:HG23	79:Q3:9:GLY:N	3.49	0.42
2:S0:74:VAL:HG13	2:S0:98:ILE:HG13	3.03	0.42
3:S1:66:VAL:HG13	16:C4:33:LEU:O	2.20	0.42
4:S2:87:GLN:HG2	4:S2:96:THR:CB	3.69	0.42
8:S6:38:GLY:HA3	8:S6:50:PHE:HE2	3.21	0.42
34:SR:103:PHE:CD1	34:SR:138:GLY:HA2	2.55	0.42
34:SR:280:GLY:O	87:SR:401:OHX:N6	2.53	0.42
34:SR:295:SER:HB3	34:SR:302:PHE:HE2	3.40	0.42
34:SR:18:GLY:N	34:SR:308:ASN:OD1	3.33	0.42
36:1:1098:A:C2	36:1:1099:A:C8	3.08	0.42
36:1:1317:A:H3'	36:1:1317:A:OP2	2.19	0.42
36:1:162:G:H2'	36:1:163:C:C6	2.54	0.42
36:1:1805:C:H4'	70:O4:79:SER:HB2	2.01	0.42
36:1:1844:C:H2'	36:1:1845:G:H5''	2.01	0.42
36:1:2376:G:C6	36:1:2377:G:O6	2.73	0.42
36:1:2869:U:H5''	36:1:2870:C:OP2	2.20	0.42
36:1:2948:C:H2'	36:1:2949:U:O4'	2.19	0.42
36:1:2751:G:N7	87:1:4001:OHX:N2	2.68	0.42
1:2:1157:A:H2'	1:2:1160:A:N7	2.34	0.42
1:2:1347:U:OP2	22:D0:23:ARG:NH2	2.45	0.42
1:2:1489:U:O2'	1:2:1490:C:OP2	2.36	0.42
1:2:1535:U:H1'	1:2:1536:G:C2	2.55	0.42
1:2:992:A:OP1	87:2:2002:OHX:N2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:381:C:H1'	1:2:755:A:H61	1.84	0.42
1:2:577:G:H8	1:2:577:G:H3'	1.85	0.42
1:2:795:U:C5	1:2:796:A:C8	3.08	0.42
37:3:36:C:O2'	37:3:37:G:H5'	2.20	0.42
36:5:1120:A:C2	36:5:1139:G:C2	3.07	0.42
36:5:1137:C:H2'	36:5:1138:U:O4'	2.18	0.42
36:5:589:A:H1'	36:5:1337:A:H5''	2.02	0.42
36:5:1671:C:H2'	36:5:1672:U:O4'	2.20	0.42
36:5:1724:U:H4'	36:5:1725:C:OP1	2.20	0.42
36:5:1817:G:OP1	87:5:4095:OHX:N1	2.53	0.42
36:5:1889:G:H2'	36:5:1889:G:N3	2.35	0.42
39:L2:241:ARG:HH22	36:5:2156:C:P	214.89	0.42
36:5:2220:A:H2'	36:5:2221:G:O4'	2.20	0.42
40:L3:26:ARG:NH2	36:5:3003:G:OP2	229.73	0.42
36:5:3319:U:H6	36:5:3319:U:H2'	1.71	0.42
69:O3:53:TYR:OH	36:5:431:U:OP1	213.04	0.42
36:5:914:A:H5'	36:5:915:A:N7	2.35	0.42
36:5:45:A:O2'	36:5:95:A:N1	2.46	0.42
1:6:1234:A:H2'	1:6:1235:C:C5	2.55	0.42
16:C4:132:ARG:HH12	1:6:1788:G:P	295.67	0.42
1:6:495:C:H3'	1:6:496:G:C5'	2.49	0.42
55:M9:172:ARG:NH2	1:6:851:U:OP1	315.97	0.42
38:8:79:A:H2'	38:8:80:A:O4'	2.20	0.42
12:C0:1:MET:HG3	12:C0:2:LEU:H	3.34	0.42
12:C0:59:PHE:CZ	12:C0:62:GLN:HA	2.72	0.42
13:C1:7:VAL:O	13:C1:9:SER:N	3.96	0.42
16:C4:84:ARG:HB2	16:C4:118:VAL:HG23	2.01	0.42
18:C6:10:PHE:CE2	1:6:1379:C:H5'	434.02	0.42
18:C6:126:PRO:O	18:C6:128:LYS:HE3	2.19	0.42
18:C6:5:PRO:HG2	18:C6:24:ALA:HB2	2.02	0.42
5:S3:201:ALA:HB3	19:C7:42:GLN:HE21	3.31	0.42
25:D3:79:ASN:OD1	25:D3:81:LYS:HG3	2.63	0.42
26:D4:26:ASP:OD1	26:D4:68:LYS:HE3	2.20	0.42
39:L2:140:ASN:HA	39:L2:141:PRO:HD2	1.74	0.42
39:L2:86:GLN:HG2	39:L2:87:PHE:N	2.35	0.42
40:L3:232:ARG:HD3	40:L3:268:GLY:H	1.85	0.42
40:L3:231:HIS:HD2	40:L3:270:ARG:NE	2.71	0.42
40:L3:4:ARG:HD2	40:L3:7:GLU:HG3	2.01	0.42
40:L3:96:PRO:HB3	52:M6:153:VAL:HG23	2.02	0.42
42:L5:119:TYR:HE1	42:L5:133:GLU:O	2.03	0.42
42:L5:259:LYS:CE	42:L5:259:LYS:H	5.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:3:22:A:N1	42:L5:269:SER:HA	2.35	0.42
42:L5:92:LEU:HD12	42:L5:92:LEU:H	1.83	0.42
43:L6:176:PHE:HE2	69:O3:107:ILE:HD13	3.73	0.42
44:L7:173:LEU:HA	44:L7:173:LEU:HD12	2.05	0.42
45:L8:202:GLU:O	45:L8:203:VAL:HB	2.66	0.42
45:L8:230:LYS:HE3	45:L8:230:LYS:HB2	4.53	0.42
46:L9:78:MET:HB2	46:L9:78:MET:HE2	1.77	0.42
47:M0:52:LEU:HD23	47:M0:164:LYS:O	3.05	0.42
47:M0:75:TYR:CE2	47:M0:79:VAL:HG21	3.32	0.42
47:M0:81:GLY:C	47:M0:83:ASP:H	2.23	0.42
50:M4:93:LYS:HE3	50:M4:93:LYS:HB2	1.65	0.42
52:M6:23:VAL:O	52:M6:27:LEU:HG	2.19	0.42
53:M7:29:THR:HG22	53:M7:87:SER:HB3	2.33	0.42
53:M7:9:THR:OG1	53:M7:151:THR:OG1	2.37	0.42
55:M9:89:LEU:HA	55:M9:90:PRO:HD2	2.47	0.42
61:N5:38:LEU:HD11	61:N5:40:LEU:HD13	2.01	0.42
68:O2:71:HIS:HB3	68:O2:91:THR:O	3.25	0.42
69:O3:102:LEU:HA	69:O3:102:LEU:HD23	1.74	0.42
76:Q0:85:LEU:O	76:Q0:88:LYS:HB3	2.19	0.42
79:Q3:45:LYS:HE3	79:Q3:45:LYS:HB2	1.82	0.42
3:S1:136:ARG:NH1	1:6:885:G:OP1	276.64	0.42
3:S1:145:LYS:HG2	3:S1:149:GLN:HB3	3.20	0.42
3:S1:101:HIS:O	3:S1:217:LEU:HD13	2.19	0.42
3:S1:35:PRO:HD3	3:S1:98:THR:OG1	4.88	0.42
5:S3:158:ILE:H	5:S3:158:ILE:HD13	2.27	0.42
6:S4:159:THR:OG1	6:S4:227:VAL:HG23	2.20	0.42
6:S4:29:PRO:O	6:S4:31:PRO:HD3	2.20	0.42
1:2:638:U:H1'	9:S7:112:ARG:HH12	1.85	0.42
34:SR:61:PHE:HB3	34:SR:92:TRP:CE3	2.55	0.42
36:1:1488:G:H5''	36:1:1838:G:O6	2.20	0.42
36:1:1618:G:H4'	38:4:129:C:H1'	2.01	0.42
36:1:1742:U:H2'	36:1:1743:G:H8	1.84	0.42
36:1:2336:U:H2'	36:1:2337:C:O4'	2.19	0.42
36:1:2413:A:H2'	36:1:2414:G:C8	2.55	0.42
36:1:2553:U:O4'	66:O0:50:VAL:HB	2.20	0.42
36:1:3181:C:H2'	36:1:3182:G:O4'	2.20	0.42
36:1:364:G:OP1	41:L4:60:THR:HG23	2.19	0.42
36:1:352:A:N6	36:1:365:A:H5''	2.35	0.42
36:1:1650:G:N7	87:1:4037:OHX:N2	2.67	0.42
36:1:3152:U:O2	87:1:4044:OHX:N4	2.53	0.42
36:1:2952:G:O6	87:1:4081:OHX:N2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:3087:A:OP2	87:1:4082:OHX:N5	2.53	0.42
36:1:830:A:H4'	36:1:1866:C:C5	2.54	0.42
1:2:1437:U:O2'	5:S3:181:VAL:HG13	2.19	0.42
1:2:647:G:N2	1:2:687:G:H22	2.18	0.42
1:2:856:A:C4	9:S7:64:VAL:HG11	2.55	0.42
38:4:67:U:H5''	73:O7:84:SER:O	2.19	0.42
36:5:1596:C:H2'	36:5:1597:C:C6	2.55	0.42
45:L8:241:LYS:HD2	36:5:2584:G:N2	187.76	0.42
36:5:2897:A:H2'	36:5:2899:C:C5'	2.50	0.42
89:5:3402:SPS:H81	89:5:3402:SPS:H71	1.67	0.42
36:5:2725:U:O4	87:5:3874:OHX:N1	2.53	0.42
36:5:495:G:H1	36:5:618:C:N4	2.18	0.42
36:5:989:A:H2'	36:5:990:U:O4'	2.19	0.42
24:D2:76:SER:OG	1:6:1102:G:OP1	353.67	0.42
1:6:1171:A:N6	1:6:1467:C:H42	2.17	0.42
1:6:495:C:H3'	1:6:496:G:H5'	2.02	0.42
16:C4:122:PRO:HB3	1:6:887:A:H1'	284.70	0.42
12:C0:15:LEU:HA	12:C0:15:LEU:HD23	4.63	0.42
15:C3:149:LEU:HA	15:C3:149:LEU:HD13	4.51	0.42
16:C4:103:ARG:HH21	16:C4:107:ARG:HH22	1.67	0.42
16:C4:43:THR:OG1	16:C4:44:GLY:N	2.51	0.42
22:D0:41:ILE:HD11	22:D0:107:THR:HG21	2.02	0.42
25:D3:92:CYS:HA	25:D3:95:PHE:CD2	2.41	0.42
25:D3:93:LEU:O	25:D3:96:VAL:HG22	2.20	0.42
27:D5:38:HIS:ND1	27:D5:70:LYS:HG2	6.29	0.42
28:D6:87:ARG:HH21	28:D6:94:ASN:HB3	2.26	0.42
29:D7:23:THR:O	29:D7:25:VAL:N	4.16	0.42
31:D9:14:TYR:OH	1:6:1553:G:O2'	405.09	0.42
39:L2:6:ARG:HH12	39:L2:199:THR:H	1.67	0.42
40:L3:382:THR:HA	40:L3:386:ASP:OD2	2.19	0.42
41:L4:229:ASN:OD1	41:L4:230:VAL:N	2.89	0.42
41:L4:22:LEU:HA	41:L4:23:PRO:HD3	2.08	0.42
42:L5:85:ARG:HD2	42:L5:254:LYS:HE3	6.92	0.42
43:L6:80:ASN:HB2	36:5:3272:C:O2	248.49	0.42
44:L7:88:ARG:HD2	44:L7:90:LYS:O	2.20	0.42
45:L8:72:PRO:HA	45:L8:73:PRO:HD3	1.87	0.42
46:L9:90:MET:HB2	46:L9:144:ILE:HG22	2.02	0.42
46:L9:166:ARG:HD2	46:L9:168:ARG:NH1	12.06	0.42
50:M4:126:GLN:HE21	36:5:3261:C:P	295.69	0.42
51:M5:89:VAL:C	51:M5:92:LEU:HD13	3.30	0.42
52:M6:193:GLN:O	52:M6:196:ALA:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:M6:27:LEU:HD13	52:M6:98:ALA:O	2.38	0.42
53:M7:19:GLY:HA3	53:M7:22:LEU:HD11	2.49	0.42
55:M9:152:GLU:O	55:M9:156:ASN:ND2	2.46	0.42
55:M9:23:TRP:HB3	55:M9:51:VAL:HG22	2.01	0.42
56:N0:46:GLN:HG2	56:N0:51:VAL:O	2.20	0.42
57:N1:124:VAL:HG12	57:N1:125:ALA:H	2.13	0.42
59:N3:104:ASN:HD21	59:N3:106:LYS:HB2	1.85	0.42
63:N7:81:LEU:HD12	70:O4:93:PHE:CD2	3.56	0.42
64:N8:115:LYS:HB3	64:N8:116:GLY:H	1.70	0.42
67:O1:22:GLY:H	67:O1:28:ARG:NH2	2.18	0.42
68:O2:104:ASN:O	68:O2:108:ILE:HG13	2.46	0.42
68:O2:55:ILE:HA	68:O2:55:ILE:HD12	1.94	0.42
74:O8:29:LYS:O	74:O8:30:LYS:HG2	2.20	0.42
78:Q2:17:CYS:SG	78:Q2:77:CYS:HB3	2.30	0.42
2:S0:9:LEU:HD22	2:S0:10:THR:H	1.85	0.42
2:S0:167:LYS:HB3	2:S0:168:HIS:CD2	3.18	0.42
3:S1:188:LEU:HD22	3:S1:212:VAL:HG21	2.01	0.42
4:S2:237:VAL:O	4:S2:238:SER:OG	5.26	0.42
5:S3:14:ASP:O	5:S3:17:PHE:HB3	2.22	0.42
5:S3:175:VAL:CG1	5:S3:182:LEU:HB2	2.45	0.42
1:2:144:U:H5	8:S6:137:ARG:NH1	2.18	0.42
8:S6:14:LYS:HD3	8:S6:16:PHE:CZ	3.29	0.42
10:S8:6:ASP:OD1	10:S8:8:ARG:HB3	2.20	0.42
34:SR:183:LEU:HD12	34:SR:186:PHE:HD1	6.03	0.42
34:SR:52:GLN:H	34:SR:52:GLN:NE2	2.18	0.42
36:1:1100:U:OP2	44:L7:196:LYS:HE3	2.20	0.41
36:1:2113:A:N7	36:1:2114:C:C4	2.88	0.41
36:1:1128:U:C2	36:1:2828:G:O4'	2.73	0.41
36:1:2882:U:H2'	36:1:2883:U:O4'	2.19	0.41
36:1:3266:G:H2'	36:1:3267:A:C8	2.55	0.41
36:1:511:G:H1	36:1:580:C:H42	1.68	0.41
36:1:608:A:H5''	36:1:609:G:OP2	2.19	0.41
36:1:801:A:H4'	36:1:802:C:O5'	2.19	0.41
36:1:929:A:H2'	36:1:930:U:C6	2.55	0.41
36:1:993:G:N3	36:1:2637:A:H2'	2.35	0.41
1:2:1159:C:O2	87:2:2084:OHX:N6	2.52	0.41
1:2:463:U:C2	1:2:464:A:C8	3.08	0.41
1:2:78:A:H1'	8:S6:175:ILE:HG12	2.02	0.41
87:1:3889:OHX:N6	87:3:216:OHX:N3	2.68	0.41
38:4:79:A:O5'	38:4:79:A:H8	2.02	0.41
36:5:1464:G:O2'	87:5:3829:OHX:N5	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:381:U:H2'	36:5:382:U:C6	2.54	0.41
36:5:411:U:H2'	36:5:412:G:H8	1.85	0.41
36:5:48:A:O4'	36:5:50:U:C6	2.72	0.41
36:5:608:A:H5''	36:5:609:G:OP2	2.19	0.41
41:L4:93:MET:HB2	36:5:658:G:N2	146.84	0.41
36:5:699:A:H2'	36:5:700:C:O4'	2.20	0.41
36:5:764:U:H2'	36:5:765:C:H2'	2.02	0.41
1:6:1091:A:H4'	1:6:1092:A:O5'	2.19	0.41
1:6:1196:A:H4'	1:6:1197:C:O5'	2.20	0.41
1:6:142:G:C2	1:6:266:A:C5	3.08	0.41
1:6:485:A:C6	1:6:486:G:H1'	2.55	0.41
1:6:640:U:H2'	1:6:641:G:O4'	2.20	0.41
1:6:940:A:H2'	1:6:941:A:O4'	2.20	0.41
1:6:990:C:H2'	1:6:991:G:O4'	2.20	0.41
1:6:991:G:O2'	1:6:992:A:H5''	2.20	0.41
12:C0:29:GLN:OE1	12:C0:39:ASN:ND2	2.53	0.41
14:C2:66:VAL:HG11	14:C2:71:ILE:HG21	2.02	0.41
15:C3:148:ALA:O	15:C3:151:ASN:N	2.49	0.41
1:2:869:A:H5''	15:C3:90:TYR:CD2	2.55	0.41
20:C8:132:ARG:NH2	1:6:1544:U:H4'	346.16	0.41
25:D3:30:LYS:HE2	25:D3:34:LEU:HD11	4.77	0.41
27:D5:84:GLU:HA	27:D5:87:GLY:HA2	6.08	0.41
33:E1:134:ASN:H	1:6:1251:U:H4'	443.36	0.41
39:L2:66:PRO:HB2	39:L2:67:TYR:CD2	2.55	0.41
40:L3:188:ILE:O	40:L3:192:VAL:HG12	2.29	0.41
40:L3:227:GLU:O	40:L3:267:ALA:HB1	2.19	0.41
43:L6:69:PHE:HB2	43:L6:138:GLN:HE21	2.71	0.41
44:L7:153:PHE:CD2	44:L7:153:PHE:N	2.95	0.41
44:L7:218:ARG:NH1	36:5:1171:G:P	256.37	0.41
44:L7:96:PRO:HA	44:L7:97:PRO:HD3	1.91	0.41
45:L8:90:THR:HA	45:L8:214:LEU:HD21	2.47	0.41
36:1:86:G:C6	49:M3:13:HIS:CD2	3.08	0.41
50:M4:21:VAL:CG1	50:M4:65:LEU:HD23	2.50	0.41
52:M6:108:ILE:HG21	52:M6:108:ILE:HD13	2.09	0.41
54:M8:134:GLY:O	54:M8:137:THR:OG1	2.58	0.41
55:M9:38:ARG:O	55:M9:42:ARG:HB2	2.20	0.41
56:N0:141:LYS:HB2	56:N0:141:LYS:HE3	1.88	0.41
58:N2:36:TYR:O	58:N2:40:HIS:HB2	2.19	0.41
62:N6:109:LEU:HD23	62:N6:109:LEU:HA	2.13	0.41
62:N6:50:ILE:HD11	62:N6:70:ILE:HG13	3.51	0.41
63:N7:72:ILE:H	63:N7:72:ILE:HD13	4.15	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:N8:46:ASP:O	64:N8:47:LYS:HB3	2.47	0.41
68:O2:12:LYS:HD3	68:O2:57:TYR:O	3.14	0.41
71:O5:31:LEU:CD1	71:O5:47:VAL:HG11	2.50	0.41
73:O7:72:ARG:O	73:O7:75:LYS:N	2.52	0.41
78:Q2:40:LYS:HG3	78:Q2:44:ASP:OD2	2.47	0.41
2:S0:120:LEU:HD12	2:S0:121:VAL:H	1.85	0.41
2:S0:185:ARG:HA	23:D1:44:ARG:HA	2.02	0.41
1:2:1066:C:H4'	3:S1:149:GLN:HE21	1.83	0.41
3:S1:23:PRO:O	3:S1:27:LYS:HG2	2.20	0.41
4:S2:238:SER:HA	4:S2:239:PRO:HD2	2.43	0.41
4:S2:87:GLN:HG2	4:S2:96:THR:HB	3.16	0.41
6:S4:103:TYR:CD1	6:S4:189:LEU:HD11	2.82	0.41
6:S4:212:ASP:OD1	6:S4:244:ILE:HG23	2.20	0.41
8:S6:189:HIS:ND1	8:S6:189:HIS:O	2.70	0.41
8:S6:68:LEU:O	8:S6:69:LEU:HB2	2.20	0.41
10:S8:92:ARG:HG3	36:1:3345:G:OP2	2.20	0.41
11:S9:116:LEU:O	11:S9:118:LEU:HD12	3.12	0.41
35:SM:51:ARG:NH2	35:SM:52:PRO:HD2	6.40	0.41
36:1:1230:G:H2'	36:1:1231:A:H8	1.85	0.41
36:1:1381:A:OP1	41:L4:197:ARG:NH1	2.52	0.41
36:1:1478:C:H2'	36:1:1479:U:H6	1.85	0.41
36:1:161:G:H5'	36:1:162:G:OP2	2.21	0.41
36:1:1750:A:H4'	74:O8:26:LYS:NZ	2.34	0.41
36:1:1814:A:OP1	87:1:3984:OHX:N2	2.53	0.41
36:1:2220:A:N6	36:1:2221:G:C6	2.88	0.41
36:1:2358:A:H2'	36:1:2359:C:O4'	2.20	0.41
36:1:2897:A:H2'	36:1:2899:C:H5''	2.01	0.41
36:1:2910:A:O2'	36:1:3130:A:N1	2.44	0.41
36:1:551:A:C2	36:1:552:G:C4	3.08	0.41
36:1:763:G:H2'	36:1:764:U:O4'	2.19	0.41
36:1:776:U:C5	36:1:2719:U:O2	2.74	0.41
36:1:795:G:O6	87:1:3790:OHX:N3	2.52	0.41
1:2:1349:G:H1	1:2:1376:C:N4	2.17	0.41
1:2:1537:C:H4'	1:2:1538:U:H5	1.86	0.41
1:2:542:A:HO2'	1:2:542:A:H8	1.68	0.41
1:2:5:U:H2'	1:2:6:G:C8	2.56	0.41
37:3:67:G:H2'	37:3:68:C:O4'	2.20	0.41
38:4:152:G:H2'	38:4:153:U:O4'	2.21	0.41
36:5:1223:A:N1	36:5:1287:A:O2'	2.39	0.41
36:5:1316:C:H5''	36:5:1317:A:C2	2.55	0.41
72:O6:27:SER:HB3	36:5:156:G:P	90.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:O8:26:LYS:NZ	36:5:1751:G:H5''	129.36	0.41
36:5:1794:G:O2'	36:5:1795:U:H5'	2.20	0.41
36:5:1879:A:OP1	36:5:1879:A:H4'	2.19	0.41
36:5:3112:G:C2	36:5:3121:U:C5	3.08	0.41
36:5:3225:C:H2'	36:5:3226:A:O4'	2.20	0.41
36:5:438:A:H4'	36:5:439:C:OP2	2.21	0.41
36:5:664:U:H2'	36:5:665:A:C8	2.56	0.41
1:6:1175:U:H2'	1:6:1176:G:C8	2.55	0.41
25:D3:13:ARG:NH1	1:6:351:C:O4'	322.28	0.41
1:6:408:C:O2	1:6:1731:A:O2'	2.23	0.41
16:C4:125:SER:HB2	1:6:926:A:H2	282.75	0.41
12:C0:46:LEU:HA	12:C0:46:LEU:HD13	1.80	0.41
1:2:1220:C:OP1	12:C0:48:SER:OG	2.37	0.41
12:C0:52:LYS:HG3	12:C0:54:TYR:CE2	2.55	0.41
13:C1:16:GLN:HE22	13:C1:34:TRP:HE3	1.68	0.41
15:C3:78:ASN:HB3	15:C3:80:LEU:CD1	6.91	0.41
16:C4:121:VAL:O	1:6:886:U:O2'	289.01	0.41
16:C4:13:VAL:HG22	16:C4:76:ILE:HG13	2.01	0.41
16:C4:90:ARG:HA	16:C4:90:ARG:HD3	3.91	0.41
18:C6:123:ARG:HG3	18:C6:124:PRO:HD2	2.02	0.41
21:C9:30:VAL:HA	21:C9:31:PRO:HD2	1.94	0.41
21:C9:23:GLN:HG3	21:C9:55:TYR:CE2	4.61	0.41
22:D0:61:LYS:HG2	22:D0:86:ILE:O	2.20	0.41
22:D0:95:ALA:HB1	22:D0:96:PRO:HD2	2.01	0.41
27:D5:60:VAL:HG11	27:D5:89:ILE:HG21	3.04	0.41
39:L2:230:VAL:O	39:L2:233:GLN:HB2	2.53	0.41
40:L3:116:ARG:NH1	40:L3:122:TRP:CD1	2.88	0.41
41:L4:141:ARG:HD3	41:L4:141:ARG:HA	2.42	0.41
41:L4:219:LEU:HD22	41:L4:222:VAL:HG11	2.34	0.41
42:L5:107:ARG:HH12	42:L5:120:LYS:HA	1.85	0.41
36:1:612:U:OP1	43:L6:21:THR:HB	2.20	0.41
43:L6:52:VAL:HG11	43:L6:65:ILE:HG13	2.03	0.41
43:L6:66:SER:C	43:L6:68:PRO:HA	3.31	0.41
43:L6:39:VAL:HB	43:L6:87:THR:OG1	2.73	0.41
44:L7:109:THR:HB	54:M8:4:ASP:HB3	2.01	0.41
45:L8:186:LEU:HA	45:L8:186:LEU:HD23	1.96	0.41
47:M0:179:PRO:HA	47:M0:182:LEU:HD12	2.02	0.41
48:M1:108:GLU:HA	48:M1:122:ILE:CG2	2.50	0.41
51:M5:106:VAL:O	51:M5:109:ARG:N	2.52	0.41
51:M5:122:ASN:OD1	51:M5:123:GLN:N	2.53	0.41
53:M7:111:LYS:HA	53:M7:153:LYS:HE3	6.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:N0:111:ALA:HA	56:N0:116:ALA:H	2.43	0.41
57:N1:42:ILE:HD11	57:N1:76:ILE:HD11	2.01	0.41
59:N3:10:LYS:NZ	59:N3:54:LEU:O	2.94	0.41
60:N4:27:LYS:HD3	60:N4:29:PHE:CZ	3.46	0.41
61:N5:61:LYS:HB2	61:N5:61:LYS:HE3	1.92	0.41
62:N6:59:VAL:HG12	62:N6:103:LYS:O	2.20	0.41
63:N7:40:HIS:ND1	63:N7:40:HIS:O	4.00	0.41
65:N9:58:LYS:HA	65:N9:58:LYS:NZ	4.44	0.41
73:O7:19:CYS:SG	73:O7:34:CYS:HB2	2.59	0.41
77:Q1:2:ARG:HG3	77:Q1:3:ALA:N	2.35	0.41
2:S0:151:SER:HA	2:S0:152:PRO:HD2	1.89	0.41
3:S1:55:LYS:HD3	3:S1:55:LYS:HA	2.20	0.41
4:S2:101:VAL:HG22	4:S2:115:ILE:HG12	2.02	0.41
4:S2:41:LEU:HD11	4:S2:56:ILE:HD13	2.45	0.41
6:S4:179:LYS:N	6:S4:194:THR:O	2.52	0.41
6:S4:95:THR:HG22	26:D4:16:PRO:HB2	2.01	0.41
7:S5:58:LEU:HD12	7:S5:138:THR:HA	3.70	0.41
8:S6:2:LYS:HE3	8:S6:2:LYS:HB2	1.75	0.41
10:S8:24:LYS:O	1:6:400:A:H5''	308.73	0.41
11:S9:170:GLY:HA3	1:6:512:A:OP1	457.93	0.41
34:SR:183:LEU:HD12	34:SR:186:PHE:CD1	6.13	0.41
36:1:1014:U:H2'	36:1:1015:U:H5''	2.01	0.41
36:1:1344:G:H1	36:1:1360:C:H42	1.69	0.41
36:1:1758:G:N2	36:1:1767:C:N3	2.49	0.41
36:1:2104:A:H2'	36:1:2105:G:H8	1.85	0.41
36:1:2376:G:C6	36:1:2377:G:C6	3.08	0.41
36:1:2550:U:C4	39:L2:40:TYR:CE1	3.07	0.41
36:1:2660:G:O2'	36:1:2744:U:H1'	2.21	0.41
36:1:2794:G:N7	87:1:3831:OHX:N2	2.68	0.41
1:2:1105:C:N4	25:D3:4:GLY:HA2	2.35	0.41
1:2:1202:A:N3	1:2:1202:A:H3'	2.36	0.41
1:2:1488:G:H5'	1:2:1489:U:OP1	2.19	0.41
1:2:1580:C:H2'	1:2:1581:C:C6	2.54	0.41
1:2:1599:C:O2	87:2:2080:OHX:N3	2.53	0.41
1:2:353:A:OP2	87:2:1995:OHX:N4	2.52	0.41
1:2:361:C:H6	1:2:361:C:H5'	1.85	0.41
1:2:591:A:H2'	1:2:592:A:H8	1.85	0.41
1:2:708:C:O2'	1:2:709:C:H5'	2.20	0.41
36:5:1252:A:H2'	36:5:1253:U:H5'	2.01	0.41
68:O2:105:ARG:NH2	36:5:1412:G:OP1	147.21	0.41
36:5:1659:U:H2'	36:5:1660:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1744:G:C6	36:5:1745:C:C4	3.08	0.41
36:5:2971:A:N6	89:5:3402:SPS:C10	2.83	0.41
36:5:3000:A:H2'	36:5:3001:C:C6	2.55	0.41
36:5:3054:U:OP2	87:5:3822:OHX:N6	2.52	0.41
36:5:363:G:H2'	36:5:364:G:O4'	2.20	0.41
36:5:2177:G:O6	87:5:3890:OHX:N1	2.53	0.41
87:5:3976:OHX:N4	87:5:3985:OHX:N2	2.68	0.41
36:5:754:G:C5	36:5:755:A:N7	2.88	0.41
36:5:950:G:C2	36:5:1370:G:C6	3.08	0.41
1:6:1425:A:O2'	1:6:1426:C:H5'	2.20	0.41
1:6:1427:A:O2'	1:6:1428:G:OP1	2.29	0.41
20:C8:39:GLY:H	1:6:1566:U:H5''	355.64	0.41
1:6:38:C:H42	1:6:39:A:N6	2.18	0.41
6:S4:49:ARG:NH1	1:6:447:U:OP1	383.96	0.41
1:6:463:U:H2'	1:6:464:A:C8	2.56	0.41
1:6:939:A:C6	1:6:940:A:C6	3.09	0.41
38:8:104:A:H3'	38:8:105:A:H5''	2.03	0.41
38:8:155:A:H2'	38:8:156:U:O4'	2.19	0.41
13:C1:78:THR:HA	13:C1:84:ILE:HG22	2.11	0.41
13:C1:98:ASN:O	13:C1:98:ASN:ND2	2.50	0.41
17:C5:79:HIS:O	17:C5:81:ARG:N	2.54	0.41
18:C6:93:HIS:HA	18:C6:97:VAL:HB	2.59	0.41
21:C9:66:TYR:HE2	21:C9:129:GLN:HG3	4.44	0.41
30:D8:41:VAL:O	30:D8:42:ARG:HD2	2.20	0.41
1:2:1433:G:C5	31:D9:41:GLN:HB3	2.55	0.41
39:L2:70:ARG:HD2	39:L2:72:ARG:HE	3.29	0.41
41:L4:84:ARG:HA	41:L4:87:GLN:OE1	3.22	0.41
42:L5:279:LYS:HZ3	42:L5:282:ARG:HH12	3.44	0.41
43:L6:46:ARG:HG2	43:L6:47:PHE:CZ	3.04	0.41
45:L8:132:VAL:HG23	45:L8:199:ALA:O	2.20	0.41
46:L9:12:VAL:HG13	46:L9:13:PRO:HD2	2.02	0.41
46:L9:21:LYS:HE2	46:L9:21:LYS:HB3	1.80	0.41
46:L9:77:ASN:HB3	46:L9:151:VAL:HG21	2.02	0.41
47:M0:10:ARG:HG2	47:M0:11:TYR:CE1	2.73	0.41
49:M3:144:THR:C	49:M3:146:PRO:HD3	2.93	0.41
49:M3:32:LYS:O	49:M3:36:ARG:HG3	2.20	0.41
51:M5:178:HIS:HD2	51:M5:179:LYS:N	5.60	0.41
55:M9:115:ILE:HD12	55:M9:115:ILE:HA	1.78	0.41
55:M9:184:LEU:O	55:M9:185:LEU:HD23	2.42	0.41
57:N1:22:HIS:HB3	57:N1:23:GLY:H	1.53	0.41
59:N3:87:ARG:HG3	59:N3:93:LEU:HD21	2.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:N5:43:ALA:HA	61:N5:44:PRO:HD3	2.21	0.41
67:O1:71:LEU:HA	67:O1:71:LEU:HD23	2.03	0.41
70:O4:42:PRO:HD3	70:O4:56:THR:HG22	2.47	0.41
71:O5:119:LYS:O	71:O5:119:LYS:HE3	4.96	0.41
74:O8:44:LYS:HG2	74:O8:53:THR:HB	2.97	0.41
4:S2:188:LEU:HD13	4:S2:196:VAL:HG11	2.28	0.41
4:S2:162:CYS:H	4:S2:213:ALA:HB2	1.85	0.41
6:S4:47:PHE:CE2	6:S4:90:ILE:HG21	2.55	0.41
8:S6:68:LEU:HD13	8:S6:68:LEU:HA	2.06	0.41
35:SM:49:LYS:HG3	35:SM:50:ASN:OD1	4.06	0.41
34:SR:110:VAL:HA	34:SR:126:SER:HB2	2.02	0.41
34:SR:286:GLU:HA	34:SR:287:PRO:HD3	1.88	0.41
36:1:1725:C:H2'	36:1:1726:C:C6	2.56	0.41
36:1:1854:C:O5'	36:1:1854:C:H6	2.03	0.41
36:1:2439:A:H2'	36:1:2440:G:O4'	2.19	0.41
36:1:2576:G:C6	36:1:2577:C:C4	3.09	0.41
36:1:2623:G:H1	36:1:2644:C:H42	1.67	0.41
36:1:2747:A:H5'	42:L5:175:HIS:HA	2.02	0.41
36:1:2984:C:C2	36:1:2985:C:C5	3.08	0.41
36:1:31:C:H5'	51:M5:96:ARG:HD2	2.00	0.41
36:1:3205:G:OP2	36:1:3206:C:N4	2.47	0.41
36:1:527:A:H61	36:1:565:U:H3	1.68	0.41
36:1:717:C:C5	36:1:718:G:C6	3.08	0.41
1:2:1151:A:H4'	1:2:1766:A:C5	2.55	0.41
1:2:1476:C:H2'	1:2:1477:G:C8	2.56	0.41
1:2:138:A:H61	1:2:266:A:H61	1.67	0.41
1:2:516:G:OP2	87:2:2038:OHX:N6	2.54	0.41
1:2:82:U:H2'	1:2:83:G:O4'	2.21	0.41
38:4:149:A:H2'	38:4:150:G:C8	2.56	0.41
36:5:1276:U:H2'	36:5:1277:C:O4'	2.20	0.41
36:5:132:C:HO2'	36:5:133:U:H6	1.65	0.41
70:O4:10:ARG:HD3	36:5:1489:A:OP1	132.53	0.41
36:5:168:U:H3	36:5:254:A:H61	1.69	0.41
36:5:2651:G:H4'	36:5:2652:U:OP2	2.20	0.41
87:5:3977:OHX:N6	87:5:4051:OHX:N2	2.67	0.41
36:5:591:G:N2	36:5:612:U:OP1	2.48	0.41
1:6:1147:A:H2'	1:6:1148:C:O4'	2.20	0.41
17:C5:77:ARG:NH1	1:6:1241:G:OP1	384.09	0.41
1:6:489:C:O2'	1:6:490:C:O5'	2.39	0.41
1:6:546:U:H2'	1:6:547:U:C6	2.55	0.41
14:C2:63:VAL:HG23	14:C2:66:VAL:HG22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:C3:149:LEU:O	87:C3:201:OHX:N5	2.53	0.41
16:C4:106:ALA:HB1	28:D6:56:ALA:HB3	2.01	0.41
18:C6:14:LYS:O	18:C6:123:ARG:NH1	2.52	0.41
19:C7:110:VAL:HA	19:C7:113:LEU:HB2	6.62	0.41
20:C8:35:ILE:HB	20:C8:38:VAL:CG2	2.88	0.41
20:C8:84:TRP:HA	20:C8:89:GLN:HE22	2.88	0.41
2:S0:66:ALA:HB1	23:D1:50:TYR:CE1	2.56	0.41
24:D2:41:MET:HG2	24:D2:129:VAL:HG11	3.03	0.41
31:D9:40:ARG:O	31:D9:43:PHE:HB3	2.62	0.41
1:2:1335:U:H1'	31:D9:56:ARG:NH1	2.35	0.41
32:E0:20:LYS:HD2	32:E0:20:LYS:HA	3.41	0.41
39:L2:134:VAL:CG2	39:L2:148:VAL:HB	4.05	0.41
39:L2:182:ALA:HB2	36:5:2148:U:O2'	212.75	0.41
39:L2:66:PRO:HB2	39:L2:67:TYR:CE2	2.56	0.41
40:L3:361:THR:HG23	40:L3:371:GLN:O	2.52	0.41
41:L4:188:ARG:HG3	41:L4:190:GLY:H	1.85	0.41
42:L5:272:TYR:CE1	37:7:22:A:H1'	335.30	0.41
44:L7:164:SER:O	44:L7:165:ASP:HB2	2.20	0.41
45:L8:153:ILE:HG22	45:L8:154:ALA:O	2.20	0.41
42:L5:286:VAL:HG13	47:M0:206:LEU:HD22	2.19	0.41
48:M1:94:ARG:O	48:M1:96:PHE:HD2	2.24	0.41
48:M1:95:ASN:O	48:M1:102:PHE:HA	2.20	0.41
50:M4:23:ILE:HG22	50:M4:29:ALA:HA	2.02	0.41
50:M4:77:ARG:O	50:M4:81:VAL:HG23	2.20	0.41
51:M5:74:PRO:HB2	51:M5:75:VAL:H	1.70	0.41
50:M4:108:ARG:NH2	52:M6:197:LEU:HA	2.34	0.41
56:N0:40:ARG:HD2	56:N0:40:ARG:HA	1.71	0.41
57:N1:106:LEU:HA	57:N1:106:LEU:HD13	1.75	0.41
58:N2:84:LEU:HD22	58:N2:89:LEU:HB2	2.95	0.41
63:N7:27:LYS:HD2	63:N7:27:LYS:HA	1.68	0.41
63:N7:29:HIS:O	63:N7:31:GLU:N	2.53	0.41
65:N9:10:HIS:O	65:N9:11:ASN:HB3	2.20	0.41
66:O0:43:ILE:O	66:O0:89:VAL:HA	2.21	0.41
67:O1:12:TYR:HD2	67:O1:75:ILE:HG13	1.85	0.41
68:O2:19:ARG:O	68:O2:22:SER:HB3	2.21	0.41
70:O4:11:ASN:HA	70:O4:12:PRO:HD3	1.84	0.41
70:O4:22:VAL:HG12	70:O4:30:LEU:HD22	2.02	0.41
70:O4:8:ARG:HB2	70:O4:34:HIS:NE2	2.62	0.41
70:O4:57:LEU:HG	70:O4:62:TYR:HE1	3.87	0.41
75:O9:5:LYS:HG2	75:O9:5:LYS:H	3.57	0.41
1:2:1113:A:H5''	77:Q1:6:ARG:NH2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:Q3:51:ALA:HA	36:5:1795:U:C4	208.96	0.41
2:S0:172:LEU:HA	2:S0:172:LEU:HD23	2.08	0.41
2:S0:41:ARG:NE	2:S0:45:VAL:HB	2.33	0.41
3:S1:39:GLU:HG3	3:S1:40:ASN:N	2.36	0.41
4:S2:113:LEU:HB2	4:S2:215:PHE:CD1	2.65	0.41
4:S2:218:ILE:O	4:S2:221:THR:OG1	2.43	0.41
4:S2:35:TRP:HE3	4:S2:46:LYS:HE2	1.85	0.41
5:S3:143:ARG:HB3	5:S3:143:ARG:NH2	2.36	0.41
6:S4:57:ASN:OD1	6:S4:57:ASN:N	3.66	0.41
7:S5:222:LYS:HG3	7:S5:225:ARG:CZ	2.50	0.41
10:S8:42:ARG:HH21	10:S8:59:ARG:NH2	2.17	0.41
11:S9:30:LEU:HD22	11:S9:105:LEU:HD23	2.02	0.41
34:SR:170:ILE:HD12	34:SR:211:ILE:HG23	2.02	0.41
36:1:122:A:C2	36:1:145:G:N3	2.88	0.41
36:1:215:G:OP1	62:N6:12:ARG:HD2	2.20	0.41
36:1:2315:G:C2	36:1:2316:G:N7	2.88	0.41
36:1:2538:U:H4'	36:1:2539:C:OP2	2.20	0.41
36:1:2795:U:OP2	78:Q2:63:LYS:NZ	2.53	0.41
36:1:303:G:C2	36:1:313:A:C2	3.09	0.41
36:1:3106:A:H2'	36:1:3107:U:O4'	2.20	0.41
36:1:3344:A:H2	36:1:3361:G:N2	2.18	0.41
36:1:864:G:O6	36:1:893:C:H3'	2.20	0.41
36:1:980:A:C8	36:1:980:A:OP2	2.74	0.41
1:2:1043:A:H61	1:2:1075:C:H42	1.67	0.41
1:2:130:C:O2'	1:2:131:C:OP1	2.34	0.41
1:2:1592:A:H61	1:2:1604:U:H3	1.66	0.41
1:2:711:U:H4'	1:2:712:G:OP1	2.20	0.41
1:2:73:U:O2'	1:2:74:U:C2	2.73	0.41
1:2:819:G:C6	1:2:853:G:C2	3.08	0.41
36:5:1294:A:O2'	36:5:1295:G:H5''	2.20	0.41
36:5:1602:A:C5	36:5:1603:A:C6	3.08	0.41
36:5:3041:U:H2'	36:5:3042:U:H6	1.83	0.41
36:5:3121:U:H1'	36:5:3122:A:H5''	2.02	0.41
36:5:501:A:H2'	36:5:502:U:O4'	2.20	0.41
36:5:792:G:O6	87:5:4101:OHX:N6	2.53	0.41
36:5:852:U:O2'	36:5:853:G:H5'	2.20	0.41
1:6:1026:A:N7	1:6:1772:C:O2'	2.45	0.41
1:6:622:A:C2	1:6:1105:C:C2	3.09	0.41
1:6:1141:G:H2'	1:6:1142:A:C8	2.56	0.41
1:6:277:U:O2'	1:6:278:U:OP1	2.34	0.41
1:6:358:U:O2'	1:6:360:A:OP1	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:601:A:H2'	1:6:602:U:C6	2.55	0.41
1:6:607:G:H5'	1:6:613:G:N2	2.35	0.41
37:7:23:A:C6	37:7:24:A:C6	3.08	0.41
51:M5:109:ARG:NH1	38:8:141:C:OP1	121.03	0.41
14:C2:80:ASN:OD1	14:C2:80:ASN:N	2.53	0.41
19:C7:87:GLU:O	19:C7:88:VAL:HG12	2.21	0.41
20:C8:125:ILE:HD11	35:SM:57:ASN:HB3	2.08	0.41
20:C8:56:LYS:HD3	20:C8:60:GLU:HB2	4.62	0.41
20:C8:41:ARG:NH2	21:C9:36:ILE:O	3.34	0.41
20:C8:41:ARG:HD2	21:C9:46:PRO:HD3	2.03	0.41
29:D7:73:LEU:HD12	29:D7:73:LEU:H	1.85	0.41
30:D8:32:PHE:HB2	30:D8:38:ARG:HB2	6.19	0.41
31:D9:5:ASN:OD1	31:D9:7:TRP:NE1	2.51	0.41
14:C2:73:LYS:HD2	33:E1:108:VAL:HG22	2.82	0.41
39:L2:112:ILE:HD12	79:Q3:79:VAL:HG22	2.02	0.41
40:L3:46:PHE:CD2	40:L3:81:THR:HG22	2.55	0.41
41:L4:144:LYS:CG	41:L4:145:ILE:H	4.17	0.41
43:L6:100:LYS:NZ	43:L6:137:ASP:OD2	3.11	0.41
44:L7:173:LEU:O	44:L7:178:ILE:HB	2.66	0.41
44:L7:134:VAL:O	44:L7:229:PHE:HA	2.71	0.41
45:L8:68:ARG:O	45:L8:69:LEU:HB2	4.58	0.41
37:3:64:A:H3'	47:M0:204:GLY:O	2.20	0.41
47:M0:99:ILE:O	47:M0:99:ILE:HG23	2.19	0.41
48:M1:54:VAL:HG11	48:M1:57:PHE:CG	2.56	0.41
49:M3:132:ALA:HA	49:M3:133:PRO:HD2	1.96	0.41
55:M9:40:ALA:O	55:M9:44:LEU:HD22	2.20	0.41
55:M9:90:PRO:HG2	55:M9:93:VAL:HG21	2.98	0.41
61:N5:102:LEU:HB2	61:N5:103:TYR:CE2	3.18	0.41
63:N7:42:LEU:HD23	63:N7:101:PHE:HE1	2.37	0.41
64:N8:82:ILE:HD11	64:N8:102:ILE:HG12	3.14	0.41
66:O0:19:LYS:HG2	66:O0:19:LYS:H	2.56	0.41
71:O5:115:LYS:HB2	71:O5:115:LYS:HE2	2.94	0.41
73:O7:28:HIS:HE1	73:O7:30:GLN:HB2	2.08	0.41
2:S0:123:VAL:HG12	2:S0:125:ASP:H	1.85	0.41
2:S0:131:GLN:O	2:S0:135:GLU:HB2	3.23	0.41
3:S1:50:LYS:O	3:S1:52:THR:N	2.52	0.41
5:S3:179:GLN:HB3	5:S3:180:GLY:H	2.84	0.41
5:S3:52:ALA:O	5:S3:91:VAL:HB	2.21	0.41
6:S4:131:LEU:HD22	6:S4:131:LEU:HA	1.78	0.41
6:S4:154:ILE:O	6:S4:155:LYS:HE2	2.20	0.41
6:S4:192:ILE:HD12	6:S4:238:LEU:HD13	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S4:157:ASN:CG	6:S4:222:LEU:HD21	2.80	0.41
7:S5:143:ARG:O	7:S5:162:VAL:HG13	3.33	0.41
7:S5:183:ALA:O	7:S5:186:ASN:HB3	2.21	0.41
8:S6:56:ASN:HB2	8:S6:108:VAL:HG12	2.03	0.41
1:2:161:U:O3'	8:S6:83:CYS:HA	2.20	0.41
1:2:337:G:O3'	10:S8:10:LYS:HE2	2.20	0.41
11:S9:146:PHE:HZ	1:6:765:G:H1	433.12	0.41
11:S9:108:ARG:HA	11:S9:147:MET:HA	2.03	0.41
34:SR:266:ASP:HA	34:SR:267:PRO:HA	1.90	0.41
34:SR:284:ALA:C	34:SR:286:GLU:H	2.22	0.41
36:1:1912:U:C4	36:1:1913:A:C6	3.08	0.41
36:1:3258:U:O2'	36:1:3260:G:OP1	2.28	0.41
36:1:1415:U:O4	87:1:4019:OHX:N4	2.53	0.41
36:1:437:G:H22	36:1:622:A:N6	2.14	0.41
1:2:1366:U:O2'	21:C9:7:ARG:HD2	2.21	0.41
1:2:1460:A:C4	17:C5:128:HIS:CD2	3.08	0.41
1:2:1553:G:H22	1:2:1555:A:H3'	1.84	0.41
1:2:872:G:H2'	1:2:873:U:O4'	2.20	0.41
36:5:1034:U:H2'	36:5:1035:G:O4'	2.21	0.41
36:5:1084:A:H2'	36:5:1085:A:O4'	2.20	0.41
36:5:1222:G:H1'	36:5:1285:G:H22	1.85	0.41
36:5:1302:A:H61	36:5:2832:C:H1'	1.85	0.41
36:5:1388:U:OP2	87:5:3925:OHX:N5	2.53	0.41
36:5:1529:A:OP2	36:5:1592:G:N2	2.53	0.41
53:M7:139:TYR:CD2	36:5:2355:G:H4'	147.93	0.41
36:5:2733:A:H2'	36:5:2734:A:O4'	2.21	0.41
59:N3:12:ARG:N	36:5:3040:A:OP1	269.30	0.41
36:5:3163:A:N1	36:5:3164:C:C4	2.89	0.41
36:5:3288:G:O2'	36:5:3289:G:P	2.79	0.41
36:5:394:G:N2	36:5:396:A:H3'	2.36	0.41
68:O2:27:ARG:NH2	36:5:654:C:OP1	170.41	0.41
22:D0:75:GLY:N	1:6:1194:A:OP2	375.75	0.41
22:D0:78:THR:HG21	1:6:1281:G:H5''	388.38	0.41
21:C9:122:ARG:NH2	1:6:1500:C:OP1	420.89	0.41
1:6:1619:C:H2'	1:6:1620:C:H6	1.85	0.41
1:6:452:A:OP2	87:6:2027:OHX:N1	2.54	0.41
1:6:755:A:C2	1:6:756:A:C4	3.08	0.41
1:6:968:U:H2'	1:6:969:C:O4'	2.21	0.41
37:7:22:A:C6	37:7:23:A:C6	3.09	0.41
15:C3:114:ARG:HG3	1:6:952:A:O2'	300.90	0.41
17:C5:18:ARG:NH2	17:C5:38:PRO:HG3	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:C6:116:LEU:HD13	18:C6:116:LEU:HA	1.90	0.41
18:C6:44:LEU:HD12	18:C6:78:VAL:HG21	2.68	0.41
20:C8:50:ALA:HB2	20:C8:72:ILE:HD12	2.70	0.41
21:C9:117:SER:HB2	21:C9:123:ARG:CB	2.51	0.41
22:D0:57:ARG:HG2	1:6:1382:A:C4'	446.35	0.41
26:D4:84:LYS:HB3	26:D4:85:PHE:HD2	4.41	0.41
27:D5:98:GLN:HE21	27:D5:99:ALA:H	3.99	0.41
39:L2:116:VAL:CG1	39:L2:126:LEU:HB2	2.88	0.41
39:L2:202:VAL:HG13	39:L2:217:GLN:HG2	3.57	0.41
39:L2:55:GLY:O	39:L2:56:ALA:HB3	4.62	0.41
40:L3:198:HIS:O	40:L3:201:LYS:HB2	2.60	0.41
40:L3:252:ILE:HD13	40:L3:252:ILE:HA	1.69	0.41
40:L3:305:ILE:H	40:L3:305:ILE:HG13	1.58	0.41
41:L4:146:PRO:O	87:L4:401:OHX:N5	2.54	0.41
41:L4:77:VAL:HG21	41:L4:84:ARG:CZ	2.61	0.41
43:L6:5:LYS:HE3	43:L6:5:LYS:HA	2.02	0.41
45:L8:238:LEU:HB2	45:L8:243:GLN:HG2	2.02	0.41
46:L9:122:LYS:HD3	46:L9:123:ILE:H	5.01	0.41
46:L9:129:ARG:O	46:L9:132:VAL:HG13	2.50	0.41
47:M0:169:LYS:NZ	57:N1:159:PHE:HA	3.21	0.41
47:M0:206:LEU:O	47:M0:210:ILE:HG13	2.20	0.41
48:M1:96:PHE:CE1	48:M1:160:VAL:HG23	3.95	0.41
49:M3:174:ARG:HB2	72:O6:9:ILE:CD1	2.50	0.41
50:M4:113:THR:HG22	50:M4:115:PHE:H	1.85	0.41
51:M5:149:ASN:O	51:M5:152:CYS:HB2	2.85	0.41
51:M5:183:THR:O	51:M5:184:LYS:HB3	4.51	0.41
51:M5:185:ALA:HB3	51:M5:190:THR:HB	5.36	0.41
52:M6:17:GLY:HA3	36:5:1313:G:O3'	267.31	0.41
54:M8:115:VAL:O	54:M8:118:GLY:N	3.17	0.41
55:M9:173:ARG:HE	55:M9:177:VAL:HG21	9.94	0.41
58:N2:107:PHE:HB3	58:N2:108:TYR:H	1.60	0.41
59:N3:87:ARG:HH22	59:N3:137:VAL:CG2	3.23	0.41
60:N4:39:LEU:O	60:N4:44:LYS:HB2	2.21	0.41
62:N6:11:ASP:HB3	62:N6:14:LYS:HB2	2.03	0.41
65:N9:11:ASN:OD1	65:N9:14:ARG:HD3	4.62	0.41
66:O0:14:LEU:O	66:O0:18:ILE:N	2.53	0.41
66:O0:41:LEU:HD22	66:O0:41:LEU:HA	1.84	0.41
68:O2:66:LEU:HD23	68:O2:66:LEU:HA	1.77	0.41
70:O4:61:GLN:C	70:O4:63:ALA:H	2.54	0.41
71:O5:101:THR:CG2	71:O5:104:GLN:H	3.65	0.41
78:Q2:85:LEU:HA	78:Q2:85:LEU:HD12	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S3:31:GLU:HG2	5:S3:107:PHE:CZ	2.55	0.41
5:S3:176:LEU:HD23	1:6:1437:U:H5'	413.90	0.41
6:S4:118:GLU:HA	6:S4:121:TYR:CD1	3.49	0.41
6:S4:125:LYS:HZ3	6:S4:157:ASN:HA	4.96	0.41
6:S4:86:PHE:O	6:S4:87:MET:HB2	2.25	0.41
7:S5:40:ILE:HG12	7:S5:42:LEU:HB3	2.02	0.41
9:S7:39:ARG:N	9:S7:40:PRO:HD2	2.48	0.41
9:S7:97:ARG:HA	9:S7:97:ARG:HD3	3.81	0.41
36:1:1039:U:H2'	36:1:1040:A:H8	1.83	0.41
36:1:1621:A:H2'	36:1:1622:U:C6	2.55	0.41
36:1:1764:U:H3'	36:1:1765:U:H4'	2.01	0.41
36:1:2192:C:C4	36:1:2193:U:C5	3.08	0.41
36:1:2207:A:N6	36:1:2208:A:N7	2.69	0.41
36:1:2636:A:H5''	36:1:2637:A:C5'	2.49	0.41
36:1:291:C:H2'	36:1:292:U:C6	2.56	0.41
36:1:3335:A:N7	36:1:3370:A:O2'	2.36	0.41
36:1:621:A:O2'	87:1:4061:OHX:N1	2.54	0.41
36:1:863:C:H2'	36:1:864:G:O4'	2.20	0.41
36:1:929:A:C6	36:1:930:U:C4	3.09	0.41
1:2:1586:A:H1'	1:2:1611:A:N6	2.35	0.41
1:2:231:U:O2'	1:2:232:U:H3'	2.21	0.41
1:2:728:U:H2'	1:2:728:U:O2	2.21	0.41
1:2:901:G:H22	16:C4:54:GLU:CD	2.19	0.41
54:M8:153:PHE:CE1	36:5:1109:U:H4'	171.27	0.41
36:5:1190:A:C5	36:5:1193:A:H1'	2.55	0.41
36:5:1485:G:N7	87:5:3947:OHX:N2	2.67	0.41
36:5:2953:U:H2'	36:5:2954:U:C6	2.55	0.41
36:5:3084:C:H2'	36:5:3085:G:O4'	2.21	0.41
36:5:3098:G:H5''	36:5:3099:C:OP1	2.20	0.41
36:5:2997:G:C1'	36:5:3396:U:H5'	2.51	0.41
36:5:546:C:H5'	36:5:547:G:OP1	2.20	0.41
73:O7:13:ASN:O	36:5:817:A:C4	140.97	0.41
36:5:863:C:C4	36:5:864:G:C5	3.09	0.41
1:6:1507:G:O6	87:6:2020:OHX:N4	2.54	0.41
1:6:1646:C:H2'	1:6:1647:U:C6	2.56	0.41
1:6:500:C:O2'	1:6:501:U:O5'	2.38	0.41
1:6:705:U:HO2'	1:6:706:A:H8	1.67	0.41
37:7:106:U:H2'	37:7:107:C:C6	2.56	0.41
38:8:57:C:O2'	38:8:58:G:H5'	2.21	0.41
13:C1:78:THR:OG1	13:C1:119:VAL:HG23	2.21	0.41
15:C3:42:ARG:HB2	15:C3:42:ARG:NH1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:C6:114:ARG:O	18:C6:115:THR:HB	4.04	0.41
21:C9:72:GLY:O	21:C9:76:LEU:HG	2.20	0.41
22:D0:102:ARG:O	22:D0:106:ILE:HG22	2.20	0.41
23:D1:72:LEU:O	23:D1:76:ASP:HB2	2.20	0.41
23:D1:79:LEU:HD22	23:D1:82:VAL:HG21	2.03	0.41
23:D1:81:ASN:OD1	23:D1:81:ASN:N	3.12	0.41
25:D3:133:LEU:HD21	25:D3:137:LYS:HZ3	1.85	0.41
26:D4:127:LYS:O	26:D4:131:ARG:HB2	3.52	0.41
26:D4:18:LEU:HD22	26:D4:85:PHE:HD1	1.85	0.41
27:D5:85:LYS:HE3	27:D5:86:GLU:HB3	2.01	0.41
33:E1:149:LYS:HB2	33:E1:149:LYS:HE2	1.71	0.41
39:L2:118:GLU:HG2	39:L2:156:LYS:NZ	2.69	0.41
36:1:2941:A:HO2'	40:L3:255:TRP:HZ3	1.67	0.41
40:L3:281:LYS:NZ	40:L3:351:LEU:H	2.19	0.41
41:L4:257:LYS:O	41:L4:260:GLN:HB2	2.21	0.41
41:L4:309:ARG:NH2	41:L4:312:VAL:HB	2.36	0.41
43:L6:166:LYS:N	43:L6:169:ASP:OD2	2.53	0.41
44:L7:127:LEU:HD13	44:L7:136:TYR:CE2	4.78	0.41
44:L7:53:LYS:HG3	44:L7:57:THR:HG21	2.02	0.41
44:L7:88:ARG:NE	44:L7:103:LEU:HD13	2.36	0.41
47:M0:196:PHE:CG	47:M0:197:VAL:N	3.13	0.41
48:M1:85:LYS:NZ	48:M1:85:LYS:HB2	2.36	0.41
51:M5:174:ILE:HG21	36:5:63:A:H5''	103.08	0.41
53:M7:127:ARG:O	53:M7:139:TYR:N	2.75	0.41
53:M7:5:GLY:HA3	53:M7:118:GLN:OE1	2.20	0.41
56:N0:14:LEU:HD23	56:N0:14:LEU:HA	1.81	0.41
47:M0:169:LYS:HZ2	57:N1:159:PHE:H	1.69	0.41
62:N6:100:HIS:HA	62:N6:101:PRO:HD2	1.66	0.41
62:N6:102:SER:OG	62:N6:103:LYS:NZ	2.66	0.41
63:N7:105:SER:O	63:N7:109:GLU:N	3.47	0.41
63:N7:9:LYS:HD3	63:N7:9:LYS:HA	2.10	0.41
64:N8:64:GLN:HB2	64:N8:67:HIS:CD2	2.56	0.41
65:N9:23:LYS:HB3	65:N9:24:PRO:HD3	2.68	0.41
67:O1:83:GLU:O	67:O1:85:ALA:N	4.07	0.41
68:O2:57:TYR:CE1	36:5:1162:U:H4'	198.95	0.41
69:O3:51:TYR:HD2	69:O3:67:MET:HG3	2.14	0.41
69:O3:67:MET:CE	69:O3:87:ASN:HB2	5.42	0.41
79:Q3:37:TYR:HB2	79:Q3:47:VAL:HB	2.03	0.41
36:1:1926:C:H5'	79:Q3:8:VAL:HG13	2.02	0.41
2:S0:203:PHE:HA	2:S0:203:PHE:HD2	1.74	0.41
2:S0:55:GLU:O	2:S0:58:VAL:HB	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:S2:35:TRP:NE1	4:S2:67:GLN:OE1	3.46	0.41
4:S2:71:THR:O	4:S2:74:PRO:HD3	2.98	0.41
5:S3:108:LYS:HE3	5:S3:118:ALA:HA	2.02	0.41
11:S9:40:LYS:HB2	11:S9:40:LYS:HE3	1.89	0.41
34:SR:159:ASN:ND2	34:SR:163:ASP:HA	2.35	0.41
34:SR:59:ARG:HB3	34:SR:61:PHE:CE2	2.56	0.41
34:SR:22:SER:OG	34:SR:70:ASP:HA	3.01	0.41
36:1:1049:C:H2'	36:1:1050:U:C6	2.56	0.41
36:1:2777:G:H4'	36:1:2778:G:H5''	2.03	0.41
36:1:2987:A:H2'	36:1:2988:C:C6	2.56	0.41
36:1:3180:A:C6	52:M6:114:LYS:HD2	2.55	0.41
1:2:111:U:C2	1:2:304:U:C4	3.08	0.41
1:2:1229:G:OP2	33:E1:102:VAL:HG23	2.20	0.41
1:2:1235:C:C2	33:E1:138:ARG:NH2	2.87	0.41
1:2:123:G:OP1	6:S4:77:ARG:NH2	2.52	0.41
1:2:1458:G:C2	1:2:1459:C:C4	3.09	0.41
1:2:1785:U:H2'	1:2:1786:G:C8	2.51	0.41
1:2:276:C:H1'	1:2:277:U:C5	2.56	0.41
1:2:434:G:N7	87:2:2015:OHX:N2	2.68	0.41
1:2:62:A:OP1	87:2:2034:OHX:N4	2.54	0.41
37:3:108:A:H2'	37:3:109:G:C8	2.56	0.41
36:5:1343:A:C2	36:5:1362:G:C2	3.09	0.41
64:N8:12:ARG:NH1	36:5:1431:G:OP2	148.43	0.41
36:5:1775:G:C2	36:5:1776:G:C8	3.08	0.41
36:5:1934:G:O6	87:5:3832:OHX:N2	2.53	0.41
36:5:1944:U:H3	36:5:2104:A:H61	1.69	0.41
36:5:2117:A:H2'	36:5:2118:C:O4'	2.21	0.41
39:L2:200:ARG:HD2	36:5:2186:U:OP2	217.34	0.41
36:5:2507:C:HO2'	36:5:2508:U:P	2.42	0.41
51:M5:28:TRP:CD1	36:5:2515:A:H5''	160.73	0.41
47:M0:157:TYR:HB3	36:5:2836:C:H1'	309.67	0.41
36:5:2931:C:H2'	36:5:2932:U:O4'	2.21	0.41
36:5:2984:C:H2'	36:5:2985:C:C6	2.55	0.41
36:5:3101:G:H2'	36:5:3102:G:O4'	2.21	0.41
36:5:507:U:H2'	36:5:508:U:H6	1.81	0.41
36:5:59:G:O6	36:5:330:G:N2	2.54	0.41
1:6:1086:A:H2	1:6:1141:G:N3	2.19	0.41
1:6:1214:U:OP1	1:6:1246:C:H1'	2.21	0.41
1:6:1442:U:H2'	1:6:1443:U:C6	2.56	0.41
1:6:1647:U:H2'	1:6:1648:A:C8	2.56	0.41
1:6:1779:U:H2'	1:6:1781:A:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:838:G:O6	87:6:2067:OHX:N3	2.53	0.41
1:6:215:A:H5''	1:6:216:U:OP2	2.21	0.41
1:6:570:A:H8	1:6:570:A:OP2	2.04	0.41
32:E0:24:THR:HG23	1:6:587:C:H5'	420.79	0.41
12:C0:34:GLU:O	12:C0:35:ILE:HB	4.73	0.41
1:2:915:A:N6	16:C4:41:ARG:HH22	2.18	0.41
17:C5:111:MET:HG2	20:C8:119:ILE:CG1	3.56	0.41
17:C5:128:HIS:O	17:C5:130:ARG:NH1	2.54	0.41
17:C5:16:SER:HA	17:C5:20:VAL:O	2.21	0.41
20:C8:36:LYS:HB2	20:C8:102:ALA:HA	2.02	0.41
21:C9:6:VAL:HG13	21:C9:66:TYR:CE1	2.76	0.41
23:D1:15:ARG:O	23:D1:16:LYS:HB2	2.21	0.41
26:D4:125:LEU:HA	26:D4:125:LEU:HD12	1.95	0.41
7:S5:120:ILE:HD11	27:D5:98:GLN:NE2	2.36	0.41
28:D6:10:ARG:HB2	28:D6:34:LYS:HG3	2.02	0.41
29:D7:35:VAL:C	29:D7:36:LYS:HG3	4.59	0.41
29:D7:58:SER:C	29:D7:60:SER:H	4.20	0.41
39:L2:137:ILE:HG23	39:L2:147:ARG:O	4.45	0.41
40:L3:91:GLY:O	40:L3:101:SER:HA	2.51	0.41
40:L3:161:LEU:HD22	40:L3:178:LEU:HD11	2.02	0.41
41:L4:82:THR:HG23	41:L4:84:ARG:H	1.86	0.41
41:L4:93:MET:HE3	41:L4:93:MET:H	1.90	0.41
42:L5:270:LYS:O	42:L5:273:ARG:HB3	3.27	0.41
43:L6:155:LEU:HD22	43:L6:159:LEU:HG	2.95	0.41
43:L6:165:LEU:HD23	43:L6:165:LEU:HA	1.77	0.41
43:L6:97:ASN:O	43:L6:99:GLU:HG3	2.19	0.41
44:L7:126:LEU:O	44:L7:130:ILE:HG12	2.20	0.41
36:1:597:G:OP1	44:L7:37:ASN:HB3	2.20	0.41
44:L7:92:ILE:HA	44:L7:92:ILE:HD13	1.86	0.41
47:M0:3:ARG:NH2	47:M0:63:GLU:HG3	2.35	0.41
47:M0:78:THR:OG1	47:M0:79:VAL:N	3.62	0.41
51:M5:99:ARG:HA	51:M5:130:PHE:CE2	2.56	0.41
52:M6:180:SER:OG	52:M6:181:ALA:N	2.89	0.41
53:M7:67:ILE:CG2	53:M7:68:GLY:N	2.84	0.41
55:M9:144:GLN:HE22	55:M9:151:ARG:HH22	6.01	0.41
61:N5:82:LEU:HB3	61:N5:84:PHE:CE2	2.56	0.41
62:N6:48:LEU:HD13	62:N6:115:ARG:HE	1.86	0.41
63:N7:26:VAL:HG22	63:N7:42:LEU:O	2.21	0.41
64:N8:73:LEU:O	64:N8:112:ILE:HA	2.36	0.41
36:1:952:A:OP1	65:N9:14:ARG:NH2	2.54	0.41
67:O1:52:ALA:HA	67:O1:53:PRO:HD3	1.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:O4:65:VAL:HG13	70:O4:69:HIS:HB2	2.34	0.41
71:O5:77:PRO:HD2	71:O5:80:LEU:HD12	2.55	0.41
72:O6:46:GLU:HG2	72:O6:46:GLU:H	1.68	0.41
73:O7:3:LYS:HG2	36:5:2138:A:O2'	173.61	0.41
2:S0:64:ILE:HD12	2:S0:181:VAL:HG11	2.47	0.41
4:S2:106:ASP:HB2	4:S2:107:SER:H	1.74	0.41
5:S3:191:ASP:OD2	5:S3:193:ALA:HB3	2.94	0.41
5:S3:6:SER:HA	1:6:1514:U:H1'	443.29	0.41
6:S4:150:PRO:HB2	6:S4:154:ILE:HD12	2.02	0.41
6:S4:159:THR:HG21	6:S4:227:VAL:O	2.54	0.41
7:S5:89:ILE:HD12	7:S5:90:ILE:H	1.86	0.41
9:S7:64:VAL:N	9:S7:65:PRO:HD2	2.52	0.41
10:S8:166:TYR:HB3	10:S8:184:LEU:HD22	2.02	0.41
11:S9:99:LEU:HD12	11:S9:99:LEU:HA	1.93	0.41
35:SM:48:ARG:HA	36:5:1019:G:OP1	334.77	0.41
35:SM:84:LYS:HD3	35:SM:86:ASN:HB2	2.03	0.41
34:SR:144:LEU:HD12	34:SR:181:TRP:CZ3	2.56	0.41
34:SR:19:TRP:CD2	34:SR:306:THR:HG22	2.62	0.41
36:1:128:G:H2'	36:1:129:U:O4'	2.21	0.41
36:1:1350:A:H2'	36:1:1351:U:H3'	2.02	0.41
36:1:1668:G:C6	36:1:1669:C:C4	3.09	0.41
36:1:2704:A:C8	36:1:2706:G:C5	3.09	0.41
36:1:2713:U:OP1	78:Q2:9:LYS:HD2	2.21	0.41
36:1:2830:G:H2'	36:1:2831:G:C8	2.55	0.41
36:1:3057:U:C2	36:1:3086:A:C6	3.08	0.41
1:2:1061:A:H2'	1:2:1062:A:H5'	2.01	0.41
1:2:1132:A:H2'	1:2:1133:A:C8	2.52	0.41
1:2:1279:C:H2'	1:2:1280:C:O4'	2.20	0.41
1:2:130:C:HO2'	1:2:131:C:P	2.42	0.41
1:2:845:G:O6	87:2:2036:OHX:N5	2.54	0.41
1:2:256:A:H2'	1:2:257:A:O4'	2.21	0.41
1:2:549:G:C2	1:2:550:A:C8	3.09	0.41
1:2:736:C:C2'	1:2:737:A:H5'	2.51	0.41
38:4:45:C:H2'	38:4:46:G:O4'	2.20	0.41
36:5:1466:G:O6	87:5:3829:OHX:N5	2.54	0.41
36:5:2206:G:N2	36:5:2238:G:H1'	2.36	0.41
36:5:2950:G:C5	36:5:2979:U:C4	3.09	0.41
36:5:3269:U:H4'	36:5:3270:U:O5'	2.21	0.41
36:5:701:G:H2'	36:5:702:C:C6	2.56	0.41
36:5:722:G:C5	36:5:723:U:C5	3.08	0.41
36:5:848:A:C4	36:5:849:C:H1'	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1081:A:N3	1:6:1083:G:C6	2.89	0.41
1:6:1756[A]:A:H8	1:6:1756[A]:A:O5'	2.03	0.41
1:6:984:G:N7	87:6:2014:OHX:N2	2.68	0.41
13:C1:39:GLY:C	13:C1:41:GLY:N	2.74	0.41
15:C3:107:LYS:HB3	15:C3:107:LYS:HE3	5.30	0.41
17:C5:89:MET:H	17:C5:89:MET:HG3	1.74	0.41
18:C6:140:LYS:HB2	18:C6:140:LYS:HE3	1.95	0.41
22:D0:27:THR:HB	22:D0:88:LYS:HG3	2.03	0.41
22:D0:96:PRO:HB2	22:D0:97:VAL:H	1.57	0.41
24:D2:58:SER:OG	1:6:636:A:H1'	356.40	0.41
26:D4:86:GLU:OE1	26:D4:90:ARG:HD2	2.21	0.41
30:D8:5:THR:HA	30:D8:6:PRO:HD3	1.79	0.41
39:L2:188:LYS:HD3	39:L2:189:TYR:CE1	2.56	0.41
39:L2:27:ALA:O	39:L2:128:ARG:NH2	2.53	0.41
41:L4:222:VAL:HG13	41:L4:225:VAL:HB	3.31	0.41
41:L4:354:VAL:O	41:L4:358:THR:HG23	2.75	0.41
42:L5:179:ARG:HA	42:L5:179:ARG:HD3	1.83	0.41
42:L5:259:LYS:H	42:L5:259:LYS:CD	5.01	0.41
44:L7:66:LYS:HG3	44:L7:76:TYR:CD2	2.55	0.41
44:L7:89:ILE:HD13	44:L7:89:ILE:HA	1.73	0.41
45:L8:200:LEU:HA	45:L8:200:LEU:HD23	1.84	0.41
45:L8:36:ILE:HG22	36:5:2550:U:C5	211.70	0.41
47:M0:10:ARG:NH2	47:M0:161:GLY:HA2	2.36	0.41
48:M1:103:GLY:HA3	48:M1:128:TYR:CD2	2.63	0.41
48:M1:132:ASN:HA	48:M1:154:THR:CG2	2.50	0.41
50:M4:24:LYS:HG2	50:M4:62:GLN:O	2.21	0.41
51:M5:53:TYR:O	51:M5:54:LYS:HD2	2.21	0.41
52:M6:23:VAL:CG1	52:M6:84:LEU:HD11	2.50	0.41
55:M9:167:ARG:HG2	55:M9:170:ARG:HD2	2.03	0.41
66:O0:39:SER:O	66:O0:65:THR:OG1	2.29	0.41
68:O2:76:VAL:HG21	68:O2:94:ALA:HB1	2.96	0.41
72:O6:26:ILE:H	72:O6:26:ILE:HG13	1.71	0.41
5:S3:45:LYS:HB2	5:S3:46:THR:H	1.68	0.41
6:S4:21:ASP:OD1	6:S4:24:SER:OG	2.53	0.41
7:S5:168:VAL:O	7:S5:172:ILE:HG13	2.75	0.41
7:S5:62:VAL:CG1	7:S5:89:ILE:HG12	2.66	0.41
8:S6:170:THR:OG1	8:S6:170:THR:O	2.37	0.41
8:S6:201:GLN:HB2	8:S6:201:GLN:HE21	1.65	0.41
9:S7:154:LEU:HD21	9:S7:183:PHE:CD1	2.52	0.41
10:S8:196:LEU:HB3	10:S8:200:LYS:HE2	2.02	0.41
34:SR:88:THR:HG22	34:SR:104:VAL:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1223:A:C6	36:1:1224:C:C4	3.09	0.41
36:1:1500:G:H2'	36:1:1501:U:O4'	2.21	0.41
36:1:1682:U:O2	58:N2:82:LYS:NZ	2.27	0.41
36:1:1716:U:O2'	36:1:1717:U:H4'	2.21	0.41
36:1:1719:G:H4'	36:1:1732:U:H4'	2.03	0.41
36:1:2704:A:C8	36:1:2706:G:C6	3.09	0.41
36:1:2714:G:H4'	36:1:2715:A:O5'	2.20	0.41
36:1:543:C:H3'	36:1:544:C:C6	2.56	0.41
36:1:644:G:H2'	36:1:2372:A:N7	2.36	0.41
36:1:663:C:H2'	36:1:664:U:C6	2.55	0.41
36:1:726:G:H1'	36:1:744:A:N6	2.35	0.41
36:1:911:C:N4	39:L2:3:ARG:HD3	2.36	0.41
36:1:926:A:H2'	36:1:927:C:C6	2.56	0.41
1:2:1178:G:C6	1:2:1179:G:C5	3.09	0.41
1:2:1216:C:C2	1:2:1444:A:N1	2.89	0.41
1:2:249:U:H3'	1:2:250:C:H5'	2.03	0.41
1:2:635:A:H2'	1:2:636:A:C8	2.55	0.41
1:2:773:C:OP1	6:S4:21:ASP:HB2	2.21	0.41
1:2:884:A:H61	1:2:927:C:H42	1.69	0.41
36:5:238:A:H2'	36:5:239:G:C8	2.56	0.41
36:5:260:C:H2'	36:5:261:U:O4'	2.20	0.41
36:5:3156:U:O2'	36:5:3157:U:O4'	2.39	0.41
36:5:2533:G:C6	87:5:3954:OHX:N2	2.89	0.41
1:6:1200:G:H4'	1:6:1201:G:C5'	2.50	0.41
1:6:1562:G:C2	1:6:1563:C:C2	3.09	0.41
1:6:1634:C:H4'	1:6:1635:A:OP2	2.21	0.41
1:6:187:G:O5'	1:6:187:G:H8	2.04	0.41
1:6:957:G:C6	1:6:958:U:C4	3.09	0.41
37:7:110:G:C6	37:7:111:U:C4	3.09	0.41
14:C2:130:THR:O	14:C2:133:LEU:HB2	2.20	0.41
15:C3:36:GLN:NE2	15:C3:39:LYS:HD3	6.25	0.41
15:C3:42:ARG:C	15:C3:44:GLY:H	3.09	0.41
15:C3:88:LEU:HD23	15:C3:88:LEU:HA	1.93	0.41
17:C5:79:HIS:HB2	1:6:1241:G:H1'	392.89	0.41
2:S0:198:MET:SD	19:C7:85:VAL:HG11	2.60	0.41
21:C9:6:VAL:HG13	21:C9:66:TYR:CZ	2.61	0.41
25:D3:96:VAL:HG23	25:D3:97:ASP:H	1.85	0.41
28:D6:51:ARG:O	28:D6:55:GLU:HB2	2.21	0.41
28:D6:88:SER:OG	28:D6:91:ASP:HB2	2.21	0.41
1:2:1596:C:P	31:D9:19:ARG:HH12	2.44	0.41
33:E1:123:ASN:HA	33:E1:124:PRO:HD2	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1253:U:H4'	33:E1:143:LYS:CA	2.51	0.41
41:L4:11:LEU:HD23	41:L4:11:LEU:HA	1.78	0.41
37:3:27:A:OP2	42:L5:57:ASN:HB2	2.20	0.41
44:L7:136:TYR:CE2	44:L7:231:ASN:ND2	4.04	0.41
45:L8:78:PHE:C	45:L8:80:TYR:N	2.68	0.41
46:L9:101:VAL:HG12	46:L9:136:PHE:HZ	1.86	0.41
46:L9:25:VAL:O	46:L9:35:THR:HA	2.62	0.41
47:M0:207:GLU:CD	47:M0:211:ARG:HH22	4.46	0.41
49:M3:107:GLU:OE1	72:O6:18:THR:OG1	3.07	0.41
51:M5:164:LEU:HA	51:M5:164:LEU:HD23	2.26	0.41
52:M6:62:THR:HA	36:5:1306:G:C6	234.40	0.41
53:M7:48:LEU:HA	53:M7:48:LEU:HD23	1.72	0.41
54:M8:165:ILE:HD11	54:M8:172:PHE:HB3	2.26	0.41
56:N0:139:TYR:CE2	56:N0:140:VAL:HG23	2.55	0.41
61:N5:51:VAL:HG12	61:N5:52:PRO:O	2.67	0.41
62:N6:5:SER:C	62:N6:7:ASP:N	3.01	0.41
63:N7:90:GLU:C	63:N7:92:PHE:H	2.71	0.41
67:O1:30:PRO:HG3	67:O1:60:TRP:HZ2	2.51	0.41
73:O7:39:TYR:HA	73:O7:40:PRO:HA	1.75	0.41
75:O9:9:ILE:HG22	75:O9:13:MET:HE2	2.53	0.41
3:S1:27:LYS:HD3	3:S1:27:LYS:HA	1.73	0.41
6:S4:180:LEU:HD23	6:S4:180:LEU:HA	1.85	0.41
6:S4:73:ASP:OD1	6:S4:89:VAL:N	2.53	0.41
34:SR:238:ASP:HB2	34:SR:239:GLU:H	1.59	0.41
34:SR:37:SER:HB3	34:SR:39:ASP:OD1	2.75	0.41
36:1:2162:U:H2'	36:1:2163:C:O4'	2.21	0.41
36:1:2194:G:C6	36:1:2195:C:N4	2.89	0.41
36:1:2338:C:H1'	59:N3:49:LEU:HD12	2.03	0.41
36:1:279:U:H2'	36:1:280:U:H6	1.86	0.41
36:1:3328:G:C2	36:1:3329:U:H1'	2.55	0.41
36:1:503:C:OP1	43:L6:26:ARG:HD2	2.21	0.41
36:1:900:G:H2'	36:1:901:G:C8	2.56	0.41
1:2:1265:G:H2'	1:2:1266:U:O4'	2.20	0.41
87:2:2143:OHX:N1	28:D6:2:PRO:HD3	2.36	0.41
1:2:38:C:C2'	1:2:39:A:H5'	2.50	0.41
38:4:121:U:C2	38:4:122:U:C5	3.09	0.41
38:4:140:G:H2'	38:4:141:C:O4'	2.21	0.41
52:M6:18:ARG:NH1	36:5:1315:U:OP1	278.82	0.41
36:5:1441:G:O2'	36:5:1442:U:H5'	2.21	0.41
36:5:2599:U:H2'	36:5:2600:C:C6	2.56	0.41
36:5:2875:U:C4	87:5:4057:OHX:N3	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:O6:53:TYR:HE2	36:5:295:A:OP1	146.65	0.41
52:M6:68:ARG:NH1	36:5:2988:C:P	217.61	0.41
36:5:3031:G:O6	87:5:3995:OHX:N1	2.54	0.41
36:5:3266:G:C6	36:5:3267:A:C6	3.09	0.41
36:5:3342:A:N6	36:5:3343:G:C6	2.89	0.41
36:5:980:A:H2'	36:5:981:U:C1'	2.50	0.41
1:6:1012:U:H2'	1:6:1013:A:O4'	2.21	0.41
31:D9:41:GLN:HB3	1:6:1433:G:C4	404.85	0.41
1:6:1565:C:H2'	1:6:1566:U:C6	2.56	0.41
37:7:9:C:OP2	37:7:10:C:N4	2.51	0.41
15:C3:20:ARG:HD2	24:D2:56:HIS:NE2	2.35	0.41
3:S1:72:ASP:H	16:C4:114:ARG:HH12	2.69	0.41
1:2:918:U:H5'	16:C4:29:HIS:NE2	2.36	0.41
16:C4:90:ARG:HB3	16:C4:91:THR:H	1.93	0.41
18:C6:103:ASN:O	18:C6:107:LYS:HB2	2.46	0.41
18:C6:82:ARG:NH2	18:C6:116:LEU:HG	4.43	0.41
20:C8:66:LEU:O	20:C8:70:VAL:HG23	2.21	0.41
21:C9:61:VAL:O	21:C9:65:ILE:HG13	2.36	0.41
25:D3:19:ARG:NE	25:D3:19:ARG:HA	2.36	0.41
26:D4:15:ASN:HA	26:D4:16:PRO:HD2	2.58	0.41
26:D4:35:VAL:HG13	26:D4:36:SER:N	2.36	0.41
28:D6:18:VAL:HG21	28:D6:33:ASP:OD1	2.21	0.41
29:D7:3:LEU:HD23	29:D7:3:LEU:HA	1.74	0.41
29:D7:40:CYS:O	29:D7:42:ASN:N	3.86	0.41
1:2:1648:A:H4'	32:E0:4:VAL:HG21	2.03	0.41
33:E1:148:TYR:HA	33:E1:148:TYR:HD1	1.74	0.41
39:L2:183:GLY:O	39:L2:186:PHE:HB3	2.20	0.41
40:L3:131:THR:OG1	40:L3:132:LYS:N	3.83	0.41
40:L3:169:THR:HG22	40:L3:171:LEU:HG	2.02	0.41
42:L5:4:GLN:C	42:L5:6:ASP:H	2.88	0.41
45:L8:95:ASN:HA	45:L8:98:ARG:NH1	6.22	0.41
46:L9:62:ARG:HD3	46:L9:62:ARG:HA	4.41	0.41
48:M1:166:LYS:C	48:M1:168:ASP:N	2.86	0.41
49:M3:165:SER:O	49:M3:167:PHE:N	2.54	0.41
49:M3:32:LYS:HA	49:M3:35:ARG:CZ	3.18	0.41
49:M3:70:ARG:NH2	36:5:75:G:H4'	93.67	0.41
51:M5:114:ARG:NH2	51:M5:157:LYS:HG3	3.49	0.41
51:M5:165:THR:O	51:M5:169:LYS:HG3	2.20	0.41
51:M5:19:LEU:HD12	51:M5:22:LEU:HD23	2.03	0.41
52:M6:25:LYS:HD3	52:M6:25:LYS:HA	1.72	0.41
36:1:2356:A:H4'	53:M7:138:LYS:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:M7:118:GLN:HG3	53:M7:147:GLU:HG2	2.03	0.41
53:M7:24:VAL:CG1	53:M7:86:LYS:HG2	2.50	0.41
56:N0:10:ILE:O	56:N0:59:VAL:N	2.45	0.41
57:N1:79:MET:HB3	57:N1:84:TYR:CE2	2.56	0.41
57:N1:40:VAL:HG21	57:N1:96:ILE:HG13	2.03	0.41
64:N8:147:LEU:HD12	72:O6:7:ILE:HD11	7.38	0.41
57:N1:88:ARG:NH2	65:N9:33:LYS:O	2.86	0.41
68:O2:4:LEU:HD12	68:O2:4:LEU:HA	1.88	0.41
78:Q2:8:ARG:HH11	78:Q2:8:ARG:HG3	1.86	0.41
3:S1:164:ILE:O	3:S1:168:ILE:HG13	2.20	0.41
3:S1:59:ASP:O	3:S1:61:LEU:N	4.00	0.41
4:S2:64:LYS:HA	4:S2:134:LEU:HD11	2.02	0.41
6:S4:41:SER:HB2	6:S4:42:LEU:H	2.03	0.41
6:S4:67:GLN:HB3	6:S4:69:HIS:CD2	3.44	0.41
7:S5:43:PHE:HD2	7:S5:46:TRP:HD1	6.75	0.41
1:2:163:G:H5'	8:S6:54:GLY:HA3	2.03	0.41
9:S7:112:ARG:NH2	9:S7:117:THR:OG1	2.54	0.41
10:S8:118:GLY:HA3	10:S8:143:TRP:CE3	4.12	0.41
11:S9:114:TYR:C	11:S9:116:LEU:H	2.56	0.41
11:S9:171:ARG:CZ	11:S9:174:ARG:HD3	6.57	0.41
11:S9:17:ARG:O	11:S9:23:ARG:NH2	3.41	0.41
36:1:1192:C:C4	87:1:3945:OHX:N5	2.89	0.40
36:1:139:G:H2'	36:1:140:C:C6	2.56	0.40
36:1:2252:A:C2	36:1:2265:C:C2	3.09	0.40
36:1:250:U:H3'	36:1:251:G:C5'	2.50	0.40
36:1:2565:U:H2'	36:1:2566:C:C6	2.55	0.40
36:1:2775:U:H2'	36:1:2776:C:C6	2.56	0.40
36:1:3218:A:OP1	36:1:3218:A:H3'	2.21	0.40
36:1:3174:A:C5	36:1:3279:A:H1'	2.56	0.40
36:1:2910:A:N1	87:1:3770:OHX:N1	2.68	0.40
1:2:1156:C:OP1	87:2:2151:OHX:N2	2.55	0.40
1:2:1317:C:O2'	1:2:1400:A:N3	2.47	0.40
1:2:144:U:C2	1:2:145:A:C8	3.10	0.40
1:2:1533:C:H4'	1:2:1539:G:C2	2.56	0.40
1:2:156:A:H1'	1:2:416:A:C5	2.57	0.40
1:2:103:A:O3'	1:2:308:C:N4	2.54	0.40
1:2:783:G:O2'	1:2:784:C:OP2	2.28	0.40
37:3:53:U:H2'	37:3:54:U:C6	2.56	0.40
38:4:107:G:C2	38:4:116:G:C5	3.09	0.40
36:5:138:U:H2'	36:5:139:G:C8	2.56	0.40
36:5:1595:U:C2	36:5:1596:C:C5	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:3078:U:OP1	36:5:3080:G:H5'	2.22	0.40
52:M6:167:TYR:HE1	36:5:3180:A:H2'	283.26	0.40
36:5:3223:A:C5	36:5:3263:G:C6	3.08	0.40
36:5:1192:C:C5	87:5:4000:OHX:N5	2.90	0.40
50:M4:77:ARG:NH2	36:5:524:U:OP1	342.41	0.40
1:6:1037:C:O2	1:6:1094:G:N2	2.49	0.40
1:6:139:C:H4'	1:6:140:A:O5'	2.21	0.40
1:6:1429:G:C6	1:6:1430:U:C4	3.10	0.40
1:6:1696:G:H2'	1:6:1698:G:O6	2.21	0.40
1:6:30:G:C6	1:6:31:C:C4	3.09	0.40
11:S9:44:ARG:NH1	1:6:474:A:OP2	414.73	0.40
1:6:838:G:C6	1:6:839:U:C4	3.09	0.40
10:S8:69:SER:HB2	13:C1:22:ASN:OD1	2.21	0.40
18:C6:37:THR:HA	18:C6:49:TYR:OH	2.58	0.40
19:C7:104:ASN:C	19:C7:106:THR:H	3.23	0.40
20:C8:31:ALA:CB	20:C8:58:ALA:HB2	2.61	0.40
21:C9:108:LEU:HB3	21:C9:114:VAL:HG22	6.65	0.40
22:D0:24:ILE:HG23	22:D0:116:VAL:HG12	5.42	0.40
24:D2:75:ILE:HG13	24:D2:125:ILE:HD13	2.02	0.40
27:D5:85:LYS:HG3	27:D5:86:GLU:N	2.36	0.40
40:L3:139:GLN:HB2	40:L3:140:ASP:H	1.64	0.40
40:L3:214:MET:HG2	40:L3:214:MET:H	4.13	0.40
40:L3:62:ARG:O	40:L3:64:GLY:N	2.54	0.40
44:L7:205:PHE:N	44:L7:205:PHE:CD2	3.64	0.40
44:L7:93:ASN:O	44:L7:94:LYS:HB2	2.41	0.40
45:L8:24:ASN:C	45:L8:26:LEU:H	4.33	0.40
46:L9:2:LYS:HA	46:L9:2:LYS:HD3	1.89	0.40
36:1:2676:A:N6	48:M1:22:SER:O	2.55	0.40
50:M4:97:SER:O	50:M4:100:ALA:N	3.44	0.40
51:M5:169:LYS:HB3	51:M5:169:LYS:HE2	1.93	0.40
54:M8:19:PRO:HD3	54:M8:53:PHE:CD1	2.56	0.40
54:M8:62:VAL:HG13	54:M8:66:ARG:HD3	2.37	0.40
61:N5:38:LEU:HD13	61:N5:40:LEU:HD21	4.86	0.40
62:N6:37:LYS:H	62:N6:37:LYS:CD	3.53	0.40
62:N6:50:ILE:CD1	62:N6:70:ILE:HG13	4.27	0.40
63:N7:54:THR:HG21	63:N7:56:LYS:NZ	3.85	0.40
63:N7:51:LEU:HB2	63:N7:65:ARG:HH11	1.86	0.40
63:N7:87:LEU:HG	63:N7:88:ASP:N	2.35	0.40
64:N8:65:GLN:HG2	64:N8:65:GLN:H	1.69	0.40
70:O4:3:GLN:HE21	70:O4:3:GLN:HB2	1.64	0.40
70:O4:41:ARG:HA	70:O4:42:PRO:HD3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:O5:10:ARG:NH2	38:8:65:A:O3'	33.44	0.40
73:O7:14:LYS:NZ	75:O9:51:ILE:HD11	2.36	0.40
2:S0:110:TYR:N	2:S0:110:TYR:CD2	3.07	0.40
2:S0:167:LYS:HB3	2:S0:168:HIS:H	1.50	0.40
2:S0:188:LEU:HA	2:S0:188:LEU:HD22	2.48	0.40
3:S1:142:PHE:O	3:S1:208:GLN:N	2.44	0.40
3:S1:71:ALA:O	3:S1:73:LEU:N	4.19	0.40
4:S2:212:LYS:O	4:S2:215:PHE:HB3	2.76	0.40
5:S3:113:LEU:HA	5:S3:113:LEU:HD23	1.88	0.40
6:S4:250:GLU:CD	6:S4:250:GLU:H	3.91	0.40
7:S5:213:LYS:HA	7:S5:213:LYS:HD3	1.83	0.40
8:S6:76:LEU:HA	8:S6:76:LEU:HD23	1.97	0.40
11:S9:112:GLN:HG3	11:S9:148:VAL:HB	2.03	0.40
34:SR:103:PHE:CE1	34:SR:138:GLY:HA2	2.77	0.40
34:SR:24:ALA:HB3	34:SR:34:LEU:HB3	2.58	0.40
34:SR:80:ALA:O	34:SR:92:TRP:N	2.85	0.40
36:1:1369:A:H2'	36:1:1370:G:O4'	2.21	0.40
36:1:1543:G:N2	36:1:1551:C:H1'	2.36	0.40
36:1:1646:G:HO2'	36:1:1647:A:P	2.44	0.40
36:1:1922:A:H3'	36:1:1923:C:C6	2.54	0.40
1:2:1667:A:H4'	36:1:1935:G:O2'	2.21	0.40
36:1:3021:A:C8	36:1:3023:U:C2	3.09	0.40
36:1:3033:A:H2'	36:1:3034:C:C6	2.56	0.40
36:1:3087:A:OP1	87:1:4082:OHX:N1	2.54	0.40
36:1:75:G:H5'	49:M3:58:VAL:CG1	2.51	0.40
1:2:1153:G:H1	1:2:1625:C:N4	2.16	0.40
1:2:1156:C:O2'	1:2:1157:A:H5'	2.21	0.40
1:2:1557:U:OP2	1:2:1559:A:O2'	2.15	0.40
1:2:393:C:H4'	1:2:1673:G:O2'	2.21	0.40
1:2:491:C:N3	1:2:496:G:N2	2.68	0.40
1:2:895:G:O2'	16:C4:38:THR:N	2.33	0.40
38:4:86:U:H5'	38:4:87:G:OP1	2.22	0.40
36:5:1940:G:H2'	36:5:1941:C:O4'	2.21	0.40
36:5:237:G:C2	36:5:238:A:C8	3.09	0.40
36:5:638:C:H2'	36:5:639:G:H8	1.86	0.40
36:5:977:C:O2'	36:5:978:G:H5'	2.22	0.40
1:6:1392:U:H2'	1:6:1393:C:C6	2.56	0.40
1:6:1595:U:N3	1:6:1600:A:H2	2.14	0.40
1:6:1157:A:OP1	87:6:2109:OHX:N4	2.54	0.40
1:6:560:U:H2'	1:6:561:G:C8	2.55	0.40
37:7:95:A:C2	37:7:96:U:C2	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:C0:32:HIS:CG	12:C0:33:GLU:H	3.05	0.40
21:C9:118:PRO:C	21:C9:120:GLY:H	2.58	0.40
22:D0:21:LYS:HB2	22:D0:21:LYS:HE3	1.95	0.40
23:D1:25:LYS:CB	23:D1:28:ASP:HB2	4.50	0.40
24:D2:96:ALA:HB3	24:D2:99:PHE:CE1	2.81	0.40
27:D5:46:LYS:HA	27:D5:49:ARG:HG3	4.99	0.40
28:D6:59:TYR:HA	28:D6:60:PRO:HD3	2.21	0.40
32:E0:53:LYS:HE2	32:E0:53:LYS:HB3	1.82	0.40
40:L3:350:ALA:O	40:L3:351:LEU:HB2	2.21	0.40
40:L3:60:LEU:O	40:L3:69:LYS:N	2.54	0.40
41:L4:300:ARG:HG2	54:M8:39:ARG:O	2.97	0.40
42:L5:190:ILE:HD11	42:L5:195:LEU:HD22	2.67	0.40
43:L6:155:LEU:HD23	50:M4:115:PHE:CE1	3.69	0.40
43:L6:168:GLY:O	43:L6:170:LYS:HE3	2.21	0.40
43:L6:50:LYS:HG2	43:L6:74:VAL:CG2	2.52	0.40
49:M3:15:ARG:CZ	36:5:96:G:H5'	152.25	0.40
52:M6:141:LEU:O	52:M6:145:VAL:HG22	2.20	0.40
53:M7:134:GLY:HA3	36:5:883:A:N7	157.26	0.40
55:M9:130:ASN:C	55:M9:132:PHE:H	2.24	0.40
56:N0:155:ARG:HD3	56:N0:172:TYR:CD2	2.87	0.40
56:N0:75:PHE:O	56:N0:94:ILE:N	2.48	0.40
57:N1:39:ILE:HD12	57:N1:102:ARG:HD3	2.01	0.40
62:N6:111:LEU:CD2	62:N6:116:LYS:HE3	2.51	0.40
62:N6:27:ARG:HB2	62:N6:75:ARG:HD3	2.03	0.40
62:N6:74:TYR:CZ	62:N6:77:LYS:HE3	2.56	0.40
68:O2:81:ASP:O	68:O2:84:THR:OG1	3.34	0.40
72:O6:98:ARG:HB3	72:O6:99:ARG:H	4.35	0.40
75:O9:3:ALA:H	75:O9:5:LYS:NZ	2.19	0.40
2:S0:103:THR:HA	2:S0:104:PRO:HD3	1.92	0.40
2:S0:83:GLN:O	2:S0:87:LEU:HD22	3.45	0.40
3:S1:190:PRO:C	3:S1:191:GLU:HG3	3.00	0.40
3:S1:35:PRO:CB	3:S1:231:LEU:HD11	4.56	0.40
4:S2:243:TYR:O	4:S2:246:GLU:HB2	2.20	0.40
5:S3:103:GLU:HG3	5:S3:106:LYS:HD2	4.45	0.40
5:S3:176:LEU:HD12	5:S3:176:LEU:H	1.85	0.40
6:S4:47:PHE:HE2	6:S4:90:ILE:HG21	1.86	0.40
9:S7:75:THR:HG22	9:S7:161:GLN:OE1	2.46	0.40
1:2:339:C:P	10:S8:10:LYS:HD2	2.61	0.40
10:S8:138:ASN:N	10:S8:138:ASN:OD1	2.63	0.40
11:S9:134:ILE:HD13	11:S9:141:VAL:O	5.19	0.40
36:1:104:G:H2'	36:1:105:C:O4'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1298:C:O3'	76:Q0:113:ARG:NH1	2.54	0.40
36:1:1541:G:H2'	36:1:1542:G:O4'	2.21	0.40
36:1:158:G:H2'	36:1:159:A:H8	1.87	0.40
36:1:2945:G:O2'	36:1:2948:C:OP2	2.39	0.40
36:1:2922:G:H1'	36:1:2951:G:N3	2.36	0.40
36:1:269:G:N2	36:1:295:A:OP2	2.36	0.40
36:1:3011:A:N1	36:1:3043:C:O2'	2.38	0.40
1:2:1195:C:N4	18:C6:143:ARG:HA	2.37	0.40
1:2:1475:A:H2'	1:2:1476:C:O4'	2.22	0.40
1:2:1541:G:C5	1:2:1542:G:C6	3.08	0.40
1:2:1600:A:H4'	1:2:1601:G:OP1	2.22	0.40
1:2:1666:U:C4	1:2:1736:G:C2	3.09	0.40
1:2:1769:U:H1'	16:C4:136:ARG:HG3	2.04	0.40
1:2:372:G:H5'	24:D2:88:LYS:NZ	2.34	0.40
36:5:1033:U:H2'	36:5:1034:U:H5'	2.02	0.40
36:5:1155:C:H6	36:5:1155:C:O5'	2.05	0.40
36:5:1176:C:H2'	36:5:1177:G:N2	2.36	0.40
36:5:1223:A:OP2	36:5:1285:G:N2	2.53	0.40
36:5:1435:A:H5''	36:5:1436:U:C5'	2.51	0.40
36:5:1529:A:P	36:5:1592:G:H22	2.44	0.40
36:5:1650:G:N7	87:5:4096:OHX:N1	2.69	0.40
36:5:192:C:H2'	36:5:193:C:H6	1.87	0.40
36:5:2209:U:H4'	36:5:2210:G:OP1	2.17	0.40
36:5:2898:G:H5''	36:5:2899:C:C5'	2.51	0.40
36:5:313:A:H2'	36:5:314:U:C6	2.57	0.40
36:5:736:A:C5	36:5:737:G:H1'	2.56	0.40
36:5:944:C:H2'	36:5:945:C:H6	1.86	0.40
1:6:1192:C:C4	1:6:1193:A:C5	3.09	0.40
1:6:1535:U:H1'	1:6:1536:G:OP2	2.21	0.40
1:6:420:A:H2'	1:6:421:A:O4'	2.20	0.40
1:6:567:A:H2	1:6:583:C:O2	2.04	0.40
1:6:831:U:C6	1:6:832:U:H5	2.39	0.40
1:6:90:C:H2'	1:6:91:G:C8	2.56	0.40
42:L5:266:ALA:HA	37:7:1:G:C4	315.52	0.40
87:5:3914:OHX:N6	87:7:222:OHX:N6	2.69	0.40
14:C2:31:VAL:HG23	14:C2:132:GLU:HB2	2.02	0.40
14:C2:52:LEU:HA	14:C2:85:LYS:HZ1	1.86	0.40
15:C3:99:ARG:O	15:C3:103:GLU:HG2	2.20	0.40
17:C5:72:LYS:HG2	17:C5:72:LYS:H	3.31	0.40
1:2:1417:A:O2'	18:C6:128:LYS:HE2	2.21	0.40
19:C7:106:THR:O	19:C7:110:VAL:HG23	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:C7:5:ARG:O	19:C7:10:LYS:HE3	2.21	0.40
20:C8:28:ILE:HG13	20:C8:56:LYS:O	5.40	0.40
21:C9:45:MET:HE1	21:C9:46:PRO:HD2	2.02	0.40
22:D0:57:ARG:HG3	22:D0:89:ARG:CZ	2.51	0.40
23:D1:12:TYR:CZ	23:D1:14:PRO:HG3	2.57	0.40
24:D2:44:HIS:CE1	24:D2:101:TYR:CZ	3.82	0.40
24:D2:34:ILE:O	24:D2:38:LEU:HG	2.87	0.40
32:E0:33:ARG:HH11	32:E0:33:ARG:HB3	2.33	0.40
39:L2:145:LYS:HG3	39:L2:157:VAL:HG23	3.61	0.40
39:L2:249:SER:HB3	39:L2:250:GLN:H	4.27	0.40
40:L3:383:LEU:HD23	40:L3:383:LEU:HA	1.97	0.40
41:L4:328:ASN:HA	41:L4:329:PRO:HD2	1.98	0.40
44:L7:102:VAL:O	44:L7:105:LEU:N	2.55	0.40
44:L7:216:VAL:HG11	44:L7:227:GLY:C	2.41	0.40
44:L7:93:ASN:N	44:L7:93:ASN:OD1	2.75	0.40
45:L8:147:LYS:HE2	45:L8:147:LYS:HB3	1.92	0.40
47:M0:65:LEU:HA	47:M0:65:LEU:HD23	1.92	0.40
54:M8:147:ARG:O	54:M8:150:VAL:HG22	2.26	0.40
36:1:1719:G:OP2	55:M9:121:HIS:HB2	2.22	0.40
55:M9:68:GLN:O	55:M9:71:ARG:HG2	4.21	0.40
56:N0:40:ARG:O	56:N0:43:TYR:HB3	2.22	0.40
56:N0:44:PHE:O	56:N0:47:LYS:N	2.50	0.40
58:N2:81:LYS:HD2	58:N2:90:ARG:NH1	2.36	0.40
58:N2:90:ARG:C	58:N2:92:TRP:H	2.25	0.40
59:N3:48:ARG:NH1	59:N3:48:ARG:HG3	2.68	0.40
59:N3:86:ARG:HB2	59:N3:92:PHE:CE1	2.56	0.40
61:N5:47:ALA:HB3	71:O5:77:PRO:HG3	2.02	0.40
62:N6:107:THR:OG1	62:N6:108:LYS:N	2.54	0.40
63:N7:60:LYS:O	63:N7:64:LYS:HG2	2.20	0.40
36:1:715:A:C8	64:N8:115:LYS:HD3	2.57	0.40
36:1:709:A:H1'	64:N8:57:GLY:HA2	2.03	0.40
75:O9:3:ALA:H	75:O9:5:LYS:HZ2	1.69	0.40
36:1:838:G:O6	79:Q3:4:ARG:NH2	2.54	0.40
2:S0:170:ILE:O	2:S0:174:TRP:HD1	2.29	0.40
2:S0:177:LEU:HA	2:S0:177:LEU:HD23	1.91	0.40
2:S0:80:THR:OG1	2:S0:81:PHE:N	3.87	0.40
3:S1:135:LEU:HD23	3:S1:216:LYS:O	5.60	0.40
3:S1:22:ASP:HA	3:S1:23:PRO:HD3	2.28	0.40
6:S4:184:THR:OG1	6:S4:224:ASN:O	2.28	0.40
7:S5:135:ASP:O	7:S5:139:ASN:HB2	2.22	0.40
7:S5:89:ILE:HG13	7:S5:89:ILE:H	1.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:S6:116:LYS:NZ	8:S6:117:GLY:O	4.94	0.40
9:S7:11:GLN:NE2	9:S7:13:PRO:HD2	4.45	0.40
34:SR:232:TYR:OH	34:SR:265:LEU:HD12	2.21	0.40
34:SR:35:SER:OG	34:SR:45:TRP:NE1	2.48	0.40
34:SR:38:ARG:HG2	34:SR:67:ILE:CG2	2.51	0.40
36:1:3102:G:O2'	36:1:3103:A:H5'	2.21	0.40
36:1:3166:C:N3	36:1:3284:G:N2	2.65	0.40
36:1:501:A:H4'	43:L6:61:ASN:ND2	2.37	0.40
36:1:637:C:H1'	36:1:638:C:C6	2.56	0.40
36:1:752:C:H2'	36:1:753:C:C6	2.56	0.40
36:1:891:G:H2'	36:1:892:U:O4'	2.21	0.40
1:2:1456:C:C5'	1:2:1457:C:H5''	2.48	0.40
1:2:1602:C:H2'	1:2:1603:U:O4'	2.21	0.40
1:2:1584:G:N2	1:2:1611:A:OP2	2.35	0.40
1:2:238:U:H2'	1:2:239:C:C6	2.56	0.40
1:2:212:U:C2	1:2:254:A:C2	3.10	0.40
1:2:338:C:H1'	10:S8:5:ARG:HB3	2.02	0.40
1:2:477:A:N6	1:2:511:A:H61	2.16	0.40
1:2:850:A:C2	1:2:851:U:C2	3.10	0.40
36:5:1355:A:H1'	36:5:1356:U:OP2	2.22	0.40
36:5:1478:C:H42	36:5:1875:G:H1	1.68	0.40
36:5:1566:A:H2'	36:5:1567:U:H5'	2.03	0.40
36:5:1641:U:O2'	36:5:1642:A:H3'	2.19	0.40
36:5:2374:C:N4	36:5:2941:A:N3	2.69	0.40
45:L8:48:ARG:NH2	36:5:2526:C:C2	187.73	0.40
36:5:2658:G:C6	36:5:2659:G:N7	2.90	0.40
36:5:2809:C:C4	36:5:2810:C:H1'	2.56	0.40
36:5:2830:G:H1'	36:5:2861:U:C2	2.56	0.40
36:5:2908:G:OP1	87:5:3858:OHX:N1	2.54	0.40
36:5:296:A:H8	36:5:296:A:O5'	2.04	0.40
36:5:32:U:H2'	36:5:33:G:O4'	2.21	0.40
36:5:3316:A:H5''	36:5:3318:G:N2	2.36	0.40
89:5:3402:SPS:H91	89:5:3402:SPS:O1	2.22	0.40
36:5:711:A:N7	36:5:712:G:H1'	2.36	0.40
1:6:1287:A:H4'	1:6:1288:G:OP1	2.20	0.40
1:6:15:U:O5'	1:6:15:U:H6	2.04	0.40
1:6:198:A:O2'	1:6:199:G:H5'	2.21	0.40
1:6:220:A:H3'	1:6:832:U:H1'	2.02	0.40
1:6:526:A:C6	1:6:527:A:C5	3.10	0.40
1:6:542:A:O2'	1:6:543:C:H3'	2.22	0.40
1:6:882:U:H2'	1:6:883:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:C4:51:ASP:HB3	1:6:906:A:OP2	292.24	0.40
38:8:118:C:C2	38:8:136:G:C2	3.10	0.40
61:N5:38:LEU:HD12	38:8:147:U:O4'	122.29	0.40
61:N5:61:LYS:NZ	38:8:59:A:O2'	70.67	0.40
18:C6:43:ILE:H	18:C6:43:ILE:HG12	1.81	0.40
19:C7:11:ARG:HH12	1:6:1325:A:P	421.91	0.40
22:D0:63:LEU:HB3	31:D9:34:TYR:CE1	4.51	0.40
24:D2:106:THR:HB	24:D2:122:SER:O	2.21	0.40
25:D3:67:ALA:O	25:D3:68:ILE:HD13	5.33	0.40
15:C3:15:ALA:CB	29:D7:20:LYS:HD3	5.46	0.40
30:D8:29:ARG:HA	30:D8:41:VAL:HA	2.04	0.40
39:L2:241:ARG:HG2	39:L2:241:ARG:H	1.85	0.40
40:L3:188:ILE:CD1	40:L3:189:SER:H	2.34	0.40
40:L3:231:HIS:CD2	40:L3:270:ARG:NH2	3.28	0.40
41:L4:107:ARG:HG2	41:L4:108:LYS:N	2.49	0.40
42:L5:5:LYS:HE2	87:L5:301:OHX:N2	2.35	0.40
59:N3:16:GLY:O	59:N3:18:PRO:HD3	3.05	0.40
59:N3:49:LEU:HA	59:N3:50:PRO:HD3	2.05	0.40
63:N7:122:HIS:HB2	63:N7:131:PHE:CE2	3.55	0.40
64:N8:25:HIS:CD2	64:N8:25:HIS:C	4.28	0.40
69:O3:89:LEU:HA	69:O3:90:PRO:HD3	1.70	0.40
71:O5:32:LYS:O	71:O5:35:LYS:HB3	2.89	0.40
73:O7:28:HIS:CD2	73:O7:31:LYS:HB2	2.55	0.40
73:O7:81:GLY:O	38:8:95:G:H1'	41.36	0.40
76:Q0:118:THR:OG1	76:Q0:120:GLN:HG3	3.70	0.40
36:1:2802:A:C8	78:Q2:56:PRO:HA	2.56	0.40
2:S0:120:LEU:HD21	2:S0:144:ILE:HD11	2.37	0.40
2:S0:17:LEU:HD23	2:S0:172:LEU:HD13	2.02	0.40
2:S0:200:ASP:HA	2:S0:203:PHE:CD1	3.11	0.40
2:S0:20:ALA:HB3	2:S0:172:LEU:HD12	2.03	0.40
3:S1:131:ASP:CG	3:S1:180:THR:HB	4.95	0.40
6:S4:14:ALA:HA	6:S4:15:PRO:HD2	1.84	0.40
7:S5:77:TYR:CD1	7:S5:87:CYS:HB2	2.57	0.40
7:S5:93:LEU:HA	7:S5:93:LEU:HD22	1.79	0.40
8:S6:67:VAL:O	8:S6:68:LEU:HB2	2.45	0.40
8:S6:84:TYR:O	8:S6:86:PRO:HD3	2.22	0.40
10:S8:117:TYR:CE1	10:S8:150:ALA:HB2	2.56	0.40
11:S9:153:GLU:O	11:S9:156:ILE:HG13	2.21	0.40
11:S9:14:THR:HA	11:S9:15:PRO:HD3	2.34	0.40
34:SR:228:LYS:HE3	34:SR:228:LYS:HB2	4.22	0.40
34:SR:249:ARG:HB3	34:SR:250:TYR:H	1.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1157:G:H2'	36:1:1158:A:O4'	2.21	0.40
36:1:1210:U:H2'	36:1:1211:U:H6	1.87	0.40
36:1:1536:G:C4	36:1:1537:A:C8	3.10	0.40
36:1:1603:A:P	55:M9:38:ARG:HH11	2.44	0.40
36:1:2331:C:H2'	36:1:2332:A:O4'	2.21	0.40
36:1:2656:A:C8	36:1:2658:G:C8	3.10	0.40
36:1:3020:U:H2'	36:1:3033:A:N6	2.37	0.40
36:1:516:A:H4'	44:L7:60:ARG:NH2	2.36	0.40
36:1:678:G:H2'	36:1:679:U:C6	2.56	0.40
1:2:1146:G:C2	1:2:1147:A:C4	3.10	0.40
1:2:1338:C:N4	1:2:1339:C:H41	2.20	0.40
1:2:1395:G:C6	1:2:1396:U:N3	2.89	0.40
1:2:130:C:O2'	87:2:2041:OHX:N4	2.55	0.40
1:2:413:U:H2'	1:2:414:C:H6	1.83	0.40
1:2:513:U:H2'	1:2:514:G:C8	2.57	0.40
1:2:811:A:N7	9:S7:111:LYS:HB2	2.36	0.40
38:4:69:U:H5''	38:4:70:G:OP2	2.21	0.40
38:4:87:G:OP2	71:O5:5:LYS:HE2	2.22	0.40
36:5:1152:G:N2	36:5:1200:A:H61	2.19	0.40
39:L2:241:ARG:NH2	36:5:2156:C:OP2	217.12	0.40
39:L2:226:SER:N	36:5:2202:C:H5''	209.98	0.40
36:5:2278:C:C2	36:5:2307:G:N2	2.90	0.40
36:5:255:A:H2'	36:5:256:G:H8	1.87	0.40
36:5:2619:G:H2'	36:5:2620:G:O4'	2.21	0.40
51:M5:171:SER:HA	36:5:288:C:O3'	125.94	0.40
40:L3:53:MET:HE3	36:5:3048:A:H5'	234.76	0.40
36:5:3223:A:C6	36:5:3263:G:C6	3.10	0.40
69:O3:60:ARG:HD2	36:5:3275:U:N3	216.19	0.40
67:O1:17:HIS:CD2	36:5:3376:A:H2	188.07	0.40
36:5:506:U:H2'	36:5:507:U:O4'	2.22	0.40
36:5:650:C:O5'	36:5:650:C:H6	2.04	0.40
1:6:11:A:C2'	1:6:12:U:H5'	2.52	0.40
1:6:1689:A:O5'	1:6:1689:A:H8	2.05	0.40
1:6:1063:U:O4	87:6:2181:OHX:N3	2.55	0.40
1:6:542:A:H1'	1:6:543:C:P	2.62	0.40
1:6:902:G:O5'	1:6:902:G:H8	2.04	0.40
1:6:926:A:H1'	1:6:988:A:C2	2.56	0.40
37:7:46:A:H2'	37:7:47:C:C6	2.57	0.40
38:8:76:C:H2'	38:8:77:A:O4'	2.22	0.40
13:C1:45:PRO:HG2	13:C1:48:ALA:HB2	3.04	0.40
15:C3:40:TYR:CE2	15:C3:53:LEU:HD23	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:C3:55:ARG:HA	15:C3:60:VAL:O	2.21	0.40
15:C3:64:ARG:HD2	15:C3:70:LYS:HD2	6.75	0.40
15:C3:93:LYS:HA	15:C3:150:VAL:HG21	2.04	0.40
1:2:901:G:N2	16:C4:54:GLU:OE2	2.38	0.40
18:C6:73:GLY:H	18:C6:76:SER:HG	3.77	0.40
20:C8:117:LYS:NZ	35:SM:61:ILE:HD11	11.03	0.40
21:C9:84:LYS:NZ	21:C9:86:ARG:HG2	5.19	0.40
22:D0:23:ARG:HD3	22:D0:92:ASP:OD1	2.20	0.40
4:S2:147:ASN:O	23:D1:4:ASP:N	5.27	0.40
26:D4:92:VAL:HG12	26:D4:97:ALA:O	5.31	0.40
27:D5:74:SER:HA	27:D5:77:ARG:NH2	2.91	0.40
28:D6:86:VAL:HG12	1:6:1795:U:OP1	345.77	0.40
29:D7:29:ARG:HA	29:D7:29:ARG:HD3	2.54	0.40
31:D9:31:ILE:HA	31:D9:31:ILE:HD13	2.31	0.40
32:E0:15:LYS:HG3	1:6:584:C:O3'	388.71	0.40
33:E1:86:THR:C	33:E1:88:PRO:HD2	5.16	0.40
39:L2:200:ARG:O	39:L2:203:ALA:N	2.43	0.40
39:L2:83:HIS:NE2	39:L2:86:GLN:HB2	2.36	0.40
41:L4:143:GLU:HB3	41:L4:144:LYS:HZ2	9.71	0.40
41:L4:9:HIS:O	41:L4:153:SER:N	2.82	0.40
42:L5:107:ARG:NH1	42:L5:120:LYS:O	2.57	0.40
42:L5:5:LYS:HA	42:L5:5:LYS:HD2	1.74	0.40
44:L7:189:ILE:HG23	44:L7:190:THR:HG23	2.03	0.40
45:L8:136:LEU:HD12	45:L8:162:LEU:HD22	2.06	0.40
45:L8:156:ASP:O	45:L8:183:LYS:HE3	7.43	0.40
47:M0:58:GLU:OE2	47:M0:60:LEU:HD23	4.55	0.40
47:M0:77:THR:HG22	47:M0:82:ARG:HA	2.03	0.40
48:M1:109:HIS:CD2	48:M1:109:HIS:H	2.40	0.40
48:M1:10:ARG:HH12	48:M1:133:ARG:NE	2.20	0.40
48:M1:94:ARG:H	48:M1:94:ARG:HG2	1.58	0.40
50:M4:25:LYS:HE2	50:M4:25:LYS:HB3	3.38	0.40
36:1:268:A:C5	51:M5:12:ARG:HG2	2.56	0.40
51:M5:59:PHE:HD1	51:M5:133:ILE:HD11	1.87	0.40
52:M6:140:LYS:HA	52:M6:140:LYS:HD2	1.78	0.40
54:M8:178:ARG:HA	54:M8:178:ARG:HD3	1.77	0.40
55:M9:4:LEU:CA	55:M9:7:GLN:HG2	4.65	0.40
50:M4:16:GLU:HB3	56:N0:149:LYS:HB3	3.20	0.40
56:N0:6:GLU:HB2	56:N0:30:PHE:CE1	2.71	0.40
59:N3:10:LYS:HD2	59:N3:13:ILE:HD11	2.02	0.40
62:N6:22:ALA:O	62:N6:27:ARG:NE	2.94	0.40
62:N6:5:SER:HB2	62:N6:8:VAL:HG13	4.80	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:N7:76:ASN:OD1	63:N7:77:TYR:N	2.68	0.40
64:N8:75:LEU:HB3	64:N8:118:ILE:CG2	2.52	0.40
67:O1:60:TRP:CZ3	67:O1:64:VAL:HG12	2.56	0.40
68:O2:79:VAL:O	68:O2:83:GLU:HG3	2.21	0.40
69:O3:58:GLU:HG3	69:O3:59:VAL:N	2.36	0.40
78:Q2:24:LYS:HD2	78:Q2:75:VAL:HG12	2.04	0.40
78:Q2:22:GLN:O	78:Q2:75:VAL:HG22	2.23	0.40
2:S0:78:SER:HB3	2:S0:100:GLY:O	2.21	0.40
4:S2:140:ARG:HD3	4:S2:222:TYR:CZ	2.56	0.40
4:S2:242:ILE:HD12	4:S2:242:ILE:HA	2.02	0.40
5:S3:114:ALA:HB3	5:S3:117:ARG:HB3	2.03	0.40
6:S4:112:HIS:NE2	6:S4:237:SER:O	3.20	0.40
6:S4:117:GLU:O	6:S4:118:GLU:HB3	4.65	0.40
7:S5:157:ARG:HB2	7:S5:224:ASN:OD1	2.22	0.40
7:S5:161:ASP:OD2	30:D8:42:ARG:NH2	2.55	0.40
9:S7:114:ARG:C	9:S7:116:ARG:H	2.24	0.40
9:S7:114:ARG:O	9:S7:117:THR:HB	2.85	0.40
9:S7:31:SER:HA	9:S7:35:LYS:CB	3.36	0.40
10:S8:44:HIS:O	10:S8:56:ARG:N	2.83	0.40
11:S9:59:LEU:O	11:S9:62:ARG:HB2	2.64	0.40
11:S9:78:ARG:HG3	11:S9:79:ARG:N	2.61	0.40
11:S9:86:LEU:HA	11:S9:86:LEU:HD12	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	S0	204/251 (81%)	157 (77%)	34 (17%)	13 (6%)	2	19
2	s0	204/251 (81%)	148 (72%)	31 (15%)	25 (12%)	0	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	S1	212/254 (84%)	154 (73%)	38 (18%)	20 (9%)	1	10
3	s1	214/254 (84%)	169 (79%)	30 (14%)	15 (7%)	1	16
4	S2	215/253 (85%)	169 (79%)	36 (17%)	10 (5%)	3	28
4	s2	215/253 (85%)	172 (80%)	25 (12%)	18 (8%)	1	12
5	S3	221/239 (92%)	186 (84%)	24 (11%)	11 (5%)	3	25
5	s3	221/239 (92%)	172 (78%)	36 (16%)	13 (6%)	2	21
6	S4	258/260 (99%)	197 (76%)	44 (17%)	17 (7%)	1	18
6	s4	258/260 (99%)	200 (78%)	42 (16%)	16 (6%)	2	19
7	S5	204/224 (91%)	153 (75%)	35 (17%)	16 (8%)	1	13
7	s5	204/224 (91%)	150 (74%)	41 (20%)	13 (6%)	2	19
8	S6	224/236 (95%)	189 (84%)	23 (10%)	12 (5%)	2	23
8	s6	216/236 (92%)	176 (82%)	32 (15%)	8 (4%)	4	35
9	S7	182/189 (96%)	127 (70%)	39 (21%)	16 (9%)	1	11
9	s7	184/189 (97%)	141 (77%)	29 (16%)	14 (8%)	1	14
10	S8	184/200 (92%)	150 (82%)	25 (14%)	9 (5%)	3	26
10	s8	184/200 (92%)	151 (82%)	27 (15%)	6 (3%)	5	37
11	S9	183/196 (93%)	148 (81%)	27 (15%)	8 (4%)	3	29
11	s9	183/196 (93%)	141 (77%)	33 (18%)	9 (5%)	3	26
12	C0	94/105 (90%)	69 (73%)	16 (17%)	9 (10%)	1	10
12	c0	92/105 (88%)	63 (68%)	14 (15%)	15 (16%)	0	2
13	C1	153/155 (99%)	122 (80%)	21 (14%)	10 (6%)	1	18
13	c1	144/155 (93%)	120 (83%)	19 (13%)	5 (4%)	4	36
14	C2	122/142 (86%)	71 (58%)	33 (27%)	18 (15%)	0	3
14	c2	122/142 (86%)	78 (64%)	30 (25%)	14 (12%)	0	7
15	C3	148/150 (99%)	120 (81%)	17 (12%)	11 (7%)	1	15
15	c3	148/150 (99%)	116 (78%)	20 (14%)	12 (8%)	1	12
16	C4	125/136 (92%)	89 (71%)	24 (19%)	12 (10%)	1	10
16	c4	126/136 (93%)	96 (76%)	16 (13%)	14 (11%)	0	7
17	C5	122/141 (86%)	99 (81%)	13 (11%)	10 (8%)	1	12
17	c5	133/141 (94%)	86 (65%)	38 (29%)	9 (7%)	1	17
18	C6	139/142 (98%)	118 (85%)	13 (9%)	8 (6%)	2	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	c6	140/142 (99%)	118 (84%)	13 (9%)	9 (6%)	2	19
19	C7	116/136 (85%)	90 (78%)	18 (16%)	8 (7%)	1	16
19	c7	113/136 (83%)	86 (76%)	18 (16%)	9 (8%)	1	13
20	C8	143/145 (99%)	111 (78%)	25 (18%)	7 (5%)	3	26
20	c8	143/145 (99%)	117 (82%)	19 (13%)	7 (5%)	3	26
21	C9	141/143 (99%)	116 (82%)	18 (13%)	7 (5%)	3	25
21	c9	141/143 (99%)	116 (82%)	21 (15%)	4 (3%)	6	41
22	D0	105/120 (88%)	89 (85%)	12 (11%)	4 (4%)	4	33
22	d0	108/120 (90%)	90 (83%)	13 (12%)	5 (5%)	3	28
23	D1	85/87 (98%)	64 (75%)	8 (9%)	13 (15%)	0	3
23	d1	85/87 (98%)	61 (72%)	17 (20%)	7 (8%)	1	12
24	D2	127/129 (98%)	106 (84%)	16 (13%)	5 (4%)	4	33
24	d2	127/129 (98%)	107 (84%)	17 (13%)	3 (2%)	7	45
25	D3	142/144 (99%)	104 (73%)	22 (16%)	16 (11%)	0	7
25	d3	142/144 (99%)	117 (82%)	24 (17%)	1 (1%)	26	71
26	D4	132/134 (98%)	106 (80%)	16 (12%)	10 (8%)	1	14
26	d4	132/134 (98%)	101 (76%)	20 (15%)	11 (8%)	1	12
27	D5	68/107 (64%)	50 (74%)	12 (18%)	6 (9%)	1	11
27	d5	67/107 (63%)	49 (73%)	16 (24%)	2 (3%)	5	40
28	D6	95/97 (98%)	57 (60%)	24 (25%)	14 (15%)	0	3
28	d6	95/97 (98%)	69 (73%)	14 (15%)	12 (13%)	0	5
29	D7	79/81 (98%)	69 (87%)	7 (9%)	3 (4%)	4	33
29	d7	79/81 (98%)	57 (72%)	16 (20%)	6 (8%)	1	14
30	D8	61/66 (92%)	47 (77%)	10 (16%)	4 (7%)	1	18
30	d8	61/66 (92%)	41 (67%)	11 (18%)	9 (15%)	0	3
31	D9	51/55 (93%)	37 (72%)	11 (22%)	3 (6%)	2	21
31	d9	51/55 (93%)	40 (78%)	8 (16%)	3 (6%)	2	21
32	E0	58/60 (97%)	41 (71%)	15 (26%)	2 (3%)	5	37
33	E1	69/76 (91%)	38 (55%)	19 (28%)	12 (17%)	0	2
33	e1	74/76 (97%)	39 (53%)	12 (16%)	23 (31%)	0	0
34	SR	316/318 (99%)	260 (82%)	43 (14%)	13 (4%)	3	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	sR	316/318 (99%)	264 (84%)	38 (12%)	14 (4%)	3	29
35	SM	155/273 (57%)	107 (69%)	32 (21%)	16 (10%)	1	8
35	sM	98/273 (36%)	66 (67%)	23 (24%)	9 (9%)	1	10
39	L2	250/253 (99%)	217 (87%)	23 (9%)	10 (4%)	4	32
39	l2	250/253 (99%)	204 (82%)	33 (13%)	13 (5%)	2	24
40	L3	384/386 (100%)	315 (82%)	46 (12%)	23 (6%)	2	20
40	l3	384/386 (100%)	337 (88%)	35 (9%)	12 (3%)	5	39
41	L4	359/361 (99%)	285 (79%)	52 (14%)	22 (6%)	2	19
41	l4	359/361 (99%)	288 (80%)	53 (15%)	18 (5%)	3	25
42	L5	294/296 (99%)	229 (78%)	42 (14%)	23 (8%)	1	13
42	l5	292/296 (99%)	250 (86%)	35 (12%)	7 (2%)	7	45
43	L6	152/175 (87%)	132 (87%)	17 (11%)	3 (2%)	9	49
43	l6	153/175 (87%)	123 (80%)	25 (16%)	5 (3%)	5	37
44	L7	220/243 (90%)	173 (79%)	39 (18%)	8 (4%)	4	35
44	l7	221/243 (91%)	193 (87%)	23 (10%)	5 (2%)	8	46
45	L8	231/255 (91%)	184 (80%)	38 (16%)	9 (4%)	4	33
45	l8	229/255 (90%)	167 (73%)	48 (21%)	14 (6%)	2	19
46	L9	189/191 (99%)	159 (84%)	19 (10%)	11 (6%)	2	21
46	l9	189/191 (99%)	163 (86%)	21 (11%)	5 (3%)	7	43
47	M0	207/220 (94%)	167 (81%)	31 (15%)	9 (4%)	3	30
47	m0	209/220 (95%)	165 (79%)	33 (16%)	11 (5%)	2	23
48	M1	167/173 (96%)	134 (80%)	19 (11%)	14 (8%)	1	12
48	m1	167/173 (96%)	137 (82%)	19 (11%)	11 (7%)	1	18
49	M3	191/198 (96%)	153 (80%)	27 (14%)	11 (6%)	2	21
49	m3	192/198 (97%)	153 (80%)	24 (12%)	15 (8%)	1	13
50	M4	134/137 (98%)	114 (85%)	15 (11%)	5 (4%)	4	35
50	m4	135/137 (98%)	115 (85%)	16 (12%)	4 (3%)	5	40
51	M5	201/203 (99%)	176 (88%)	19 (10%)	6 (3%)	5	40
51	m5	201/203 (99%)	174 (87%)	23 (11%)	4 (2%)	9	49
52	M6	195/198 (98%)	173 (89%)	16 (8%)	6 (3%)	5	39
52	m6	195/198 (98%)	182 (93%)	9 (5%)	4 (2%)	9	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	M7	181/183 (99%)	150 (83%)	25 (14%)	6 (3%)	5	37
53	m7	153/183 (84%)	127 (83%)	25 (16%)	1 (1%)	26	71
54	M8	183/185 (99%)	151 (82%)	24 (13%)	8 (4%)	3	29
54	m8	183/185 (99%)	154 (84%)	20 (11%)	9 (5%)	3	26
55	M9	186/188 (99%)	160 (86%)	23 (12%)	3 (2%)	12	53
55	m9	186/188 (99%)	166 (89%)	13 (7%)	7 (4%)	4	33
56	N0	170/172 (99%)	155 (91%)	12 (7%)	3 (2%)	11	51
56	n0	170/172 (99%)	152 (89%)	15 (9%)	3 (2%)	11	51
57	N1	157/159 (99%)	137 (87%)	15 (10%)	5 (3%)	5	38
57	n1	157/159 (99%)	131 (83%)	24 (15%)	2 (1%)	15	58
58	N2	98/120 (82%)	72 (74%)	23 (24%)	3 (3%)	5	39
58	n2	96/120 (80%)	80 (83%)	11 (12%)	5 (5%)	2	24
59	N3	134/136 (98%)	117 (87%)	15 (11%)	2 (2%)	13	54
59	n3	134/136 (98%)	122 (91%)	7 (5%)	5 (4%)	4	35
60	N4	96/155 (62%)	68 (71%)	18 (19%)	10 (10%)	1	8
60	n4	133/155 (86%)	102 (77%)	22 (16%)	9 (7%)	1	17
61	N5	119/141 (84%)	99 (83%)	14 (12%)	6 (5%)	3	25
61	n5	118/141 (84%)	94 (80%)	19 (16%)	5 (4%)	3	31
62	N6	124/126 (98%)	107 (86%)	13 (10%)	4 (3%)	5	38
62	n6	124/126 (98%)	102 (82%)	21 (17%)	1 (1%)	24	69
63	N7	133/135 (98%)	114 (86%)	10 (8%)	9 (7%)	1	17
63	n7	133/135 (98%)	112 (84%)	12 (9%)	9 (7%)	1	17
64	N8	146/148 (99%)	118 (81%)	22 (15%)	6 (4%)	3	32
64	n8	146/148 (99%)	111 (76%)	24 (16%)	11 (8%)	1	14
65	N9	56/58 (97%)	41 (73%)	12 (21%)	3 (5%)	2	23
65	n9	56/58 (97%)	39 (70%)	12 (21%)	5 (9%)	1	11
66	O0	95/104 (91%)	80 (84%)	11 (12%)	4 (4%)	3	31
66	o0	98/104 (94%)	84 (86%)	11 (11%)	3 (3%)	5	39
67	O1	107/112 (96%)	89 (83%)	8 (8%)	10 (9%)	1	10
67	o1	107/112 (96%)	83 (78%)	18 (17%)	6 (6%)	2	22
68	O2	125/129 (97%)	104 (83%)	18 (14%)	3 (2%)	7	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	o2	125/129 (97%)	103 (82%)	16 (13%)	6 (5%)	3	27
69	O3	104/106 (98%)	96 (92%)	7 (7%)	1 (1%)	19	64
69	o3	104/106 (98%)	92 (88%)	9 (9%)	3 (3%)	6	40
70	O4	110/119 (92%)	88 (80%)	17 (16%)	5 (4%)	3	29
70	o4	110/119 (92%)	98 (89%)	11 (10%)	1 (1%)	21	67
71	O5	117/119 (98%)	93 (80%)	22 (19%)	2 (2%)	11	52
71	o5	117/119 (98%)	98 (84%)	14 (12%)	5 (4%)	3	30
72	O6	97/99 (98%)	78 (80%)	13 (13%)	6 (6%)	2	19
72	o6	97/99 (98%)	78 (80%)	14 (14%)	5 (5%)	2	24
73	O7	85/87 (98%)	64 (75%)	16 (19%)	5 (6%)	2	21
73	o7	85/87 (98%)	72 (85%)	11 (13%)	2 (2%)	7	45
74	O8	75/77 (97%)	62 (83%)	9 (12%)	4 (5%)	2	23
74	o8	75/77 (97%)	60 (80%)	12 (16%)	3 (4%)	4	32
75	O9	48/50 (96%)	40 (83%)	7 (15%)	1 (2%)	9	48
75	o9	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
76	Q0	50/52 (96%)	42 (84%)	7 (14%)	1 (2%)	9	49
76	q0	50/52 (96%)	46 (92%)	2 (4%)	2 (4%)	4	32
77	Q1	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
77	q1	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
78	Q2	103/105 (98%)	80 (78%)	17 (16%)	6 (6%)	2	21
78	q2	103/105 (98%)	95 (92%)	7 (7%)	1 (1%)	19	64
79	Q3	89/91 (98%)	71 (80%)	10 (11%)	8 (9%)	1	10
79	q3	89/91 (98%)	74 (83%)	12 (14%)	3 (3%)	5	37
80	e0	60/62 (97%)	38 (63%)	15 (25%)	7 (12%)	0	6
81	m2	144/165 (87%)	67 (46%)	48 (33%)	29 (20%)	0	1
82	p0	139/311 (45%)	110 (79%)	20 (14%)	9 (6%)	1	18
83	p1	45/106 (42%)	26 (58%)	17 (38%)	2 (4%)	3	29
83	p2	44/106 (42%)	33 (75%)	6 (14%)	5 (11%)	0	7
84	f	145/157 (92%)	97 (67%)	34 (23%)	14 (10%)	1	9
All	All	22711/24675 (92%)	18197 (80%)	3231 (14%)	1283 (6%)	2	22

All (1283) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	S0	4	PRO
2	S0	158	VAL
2	S0	169	SER
2	S0	191	ARG
3	S1	82	ARG
3	S1	132	ASP
3	S1	206	PRO
4	S2	48	GLY
5	S3	62	ASN
5	S3	211	PRO
5	S3	220	PRO
6	S4	104	ASP
7	S5	39	GLU
7	S5	43	PHE
7	S5	153	GLY
8	S6	149	LYS
8	S6	153	VAL
8	S6	154	ARG
8	S6	225	GLU
9	S7	29	ASN
9	S7	31	SER
9	S7	64	VAL
9	S7	74	GLN
9	S7	155	ASP
10	S8	149	SER
11	S9	93	LEU
11	S9	98	ALA
11	S9	134	ILE
12	C0	60	SER
12	C0	61	TRP
12	C0	87	VAL
12	C0	88	PRO
13	C1	3	THR
13	C1	7	VAL
13	C1	40	LEU
13	C1	154	ALA
14	C2	22	VAL
14	C2	91	VAL
15	C3	12	SER
15	C3	68	GLY
15	C3	138	ASN
15	C3	149	LEU
16	C4	42	VAL

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Mol	Chain	Res	Type
17	C5	54	ALA
17	C5	125	PRO
17	C5	126	VAL
18	C6	41	PRO
19	C7	85	VAL
19	C7	86	PRO
19	C7	88	VAL
20	C8	14	ILE
20	C8	82	PRO
20	C8	92	ILE
21	C9	53	TRP
21	C9	69	LYS
21	C9	116	ILE
23	D1	7	GLN
23	D1	82	VAL
25	D3	3	LYS
25	D3	92	CYS
25	D3	138	GLU
27	D5	93	SER
28	D6	82	ARG
28	D6	84	VAL
28	D6	86	VAL
32	E0	47	VAL
33	E1	84	VAL
33	E1	94	LYS
33	E1	98	VAL
34	SR	318	ALA
35	SM	42	ALA
35	SM	47	ALA
35	SM	52	PRO
35	SM	167	PRO
35	SM	172	VAL
39	L2	98	VAL
39	L2	115	ASN
39	L2	141	PRO
40	L3	3	HIS
40	L3	4	ARG
40	L3	69	LYS
40	L3	139	GLN
40	L3	187	SER
40	L3	347	SER
41	L4	4	PRO

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Mol	Chain	Res	Type
41	L4	131	VAL
41	L4	175	HIS
41	L4	270	SER
41	L4	311	HIS
41	L4	339	LEU
42	L5	85	ARG
42	L5	178	ASN
42	L5	228	ALA
42	L5	233	ALA
42	L5	234	ASP
42	L5	296	GLN
43	L6	97	ASN
44	L7	25	GLN
44	L7	163	LEU
45	L8	25	PRO
45	L8	31	PRO
46	L9	50	ASN
46	L9	169	ASN
48	M1	11	ASP
48	M1	115	LYS
48	M1	165	GLN
49	M3	129	ASN
50	M4	9	ALA
50	M4	36	VAL
51	M5	74	PRO
51	M5	75	VAL
51	M5	94	TYR
52	M6	66	LYS
52	M6	110	PRO
52	M6	111	PRO
56	N0	167	ARG
60	N4	8	PHE
60	N4	64	THR
60	N4	81	PRO
61	N5	44	PRO
61	N5	50	ALA
62	N6	37	LYS
63	N7	17	ARG
63	N7	35	SER
63	N7	125	GLY
67	O1	7	VAL
67	O1	84	ASP

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Mol	Chain	Res	Type
68	O2	27	ARG
70	O4	10	ARG
73	O7	59	THR
74	O8	33	LYS
75	O9	4	GLN
76	Q0	78	ILE
78	Q2	30	ALA
78	Q2	34	SER
78	Q2	100	LYS
79	Q3	58	SER
2	s0	4	PRO
2	s0	111	ILE
2	s0	158	VAL
2	s0	164	ASN
2	s0	189	VAL
2	s0	206	ASP
3	s1	106	THR
3	s1	132	ASP
4	s2	92	ALA
4	s2	164	SER
4	s2	176	SER
4	s2	248	SER
5	s3	61	GLU
5	s3	216	PRO
5	s3	220	PRO
6	s4	53	LYS
6	s4	104	ASP
6	s4	196	VAL
7	s5	28	PRO
7	s5	184	PHE
8	s6	122	GLU
8	s6	173	PRO
8	s6	174	LYS
9	s7	63	PRO
9	s7	64	VAL
9	s7	66	SER
9	s7	74	GLN
9	s7	131	PHE
10	s8	153	GLU
11	s9	118	LEU
11	s9	144	PRO
12	c0	32	HIS

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Mol	Chain	Res	Type
12	c0	83	PRO
12	c0	88	PRO
12	c0	97	PRO
13	c1	61	THR
15	c3	12	SER
15	c3	18	TYR
15	c3	66	ILE
15	c3	87	ASP
16	c4	126	THR
16	c4	132	ARG
17	c5	11	VAL
17	c5	51	SER
17	c5	52	LYS
17	c5	125	PRO
18	c6	116	LEU
19	c7	99	VAL
20	c8	14	ILE
23	d1	4	ASP
23	d1	6	GLY
24	d2	68	ARG
26	d4	30	PRO
26	d4	32	ARG
29	d7	12	ALA
29	d7	20	LYS
30	d8	32	PHE
30	d8	59	SER
31	d9	6	VAL
31	d9	7	TRP
80	e0	43	ARG
80	e0	47	VAL
33	e1	83	LYS
33	e1	87	THR
33	e1	92	LYS
33	e1	98	VAL
33	e1	103	LEU
33	e1	110	ALA
34	sR	4	ASN
34	sR	160	GLU
35	sM	50	ASN
35	sM	120	GLU
35	sM	172	VAL
39	l2	144	ASN

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Mol	Chain	Res	Type
39	l2	212	GLY
39	l2	238	ILE
40	l3	140	ASP
40	l3	143	GLY
40	l3	155	ALA
41	l4	14	GLU
41	l4	25	VAL
41	l4	142	VAL
41	l4	145	ILE
41	l4	301	PRO
41	l4	313	LEU
41	l4	353	ALA
42	l5	178	ASN
42	l5	258	LYS
43	l6	98	VAL
44	l7	193	PRO
44	l7	229	PHE
45	l8	25	PRO
45	l8	34	PHE
45	l8	133	LYS
46	l9	62	ARG
47	m0	74	LYS
48	m1	8	PRO
81	m2	11	PRO
81	m2	15	PRO
81	m2	18	VAL
81	m2	87	VAL
81	m2	88	PRO
81	m2	101	PRO
81	m2	102	PRO
81	m2	121	GLU
81	m2	123	ILE
49	m3	47	ALA
49	m3	93	ILE
49	m3	100	ARG
49	m3	101	ARG
49	m3	134	GLU
49	m3	150	PRO
49	m3	162	ASN
51	m5	76	PRO
54	m8	99	THR
55	m9	112	ALA

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Mol	Chain	Res	Type
58	n2	44	GLU
59	n3	42	SER
61	n5	38	LEU
61	n5	44	PRO
61	n5	45	LYS
61	n5	55	ASN
62	n6	84	LYS
63	n7	17	ARG
64	n8	76	ASP
65	n9	21	ILE
65	n9	23	LYS
65	n9	24	PRO
66	o0	38	LYS
67	o1	5	LYS
67	o1	45	GLY
68	o2	6	HIS
69	o3	60	ARG
72	o6	4	LYS
72	o6	98	ARG
73	o7	87	SER
76	q0	78	ILE
78	q2	17	CYS
82	p0	93	LEU
83	p1	35	VAL
83	p2	36	PRO
84	f	18	THR
84	f	64	ILE
84	f	109	THR
84	f	111	ASP
2	S0	39	ASN
2	S0	111	ILE
2	S0	190	ASP
3	S1	21	VAL
3	S1	37	THR
3	S1	63	GLY
3	S1	158	SER
3	S1	176	VAL
3	S1	209	ASN
4	S2	163	GLY
4	S2	182	PRO
5	S3	93	ASP
5	S3	218	LEU

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Mol	Chain	Res	Type
6	S4	11	ARG
6	S4	12	LEU
6	S4	195	ILE
6	S4	200	ARG
7	S5	26	ALA
7	S5	47	SER
7	S5	58	LEU
7	S5	63	GLN
7	S5	71	ALA
7	S5	150	GLY
8	S6	70	PRO
8	S6	122	GLU
8	S6	138	ALA
8	S6	152	ASP
8	S6	165	GLY
8	S6	173	PRO
9	S7	32	PRO
9	S7	36	ALA
9	S7	186	PRO
10	S8	52	ASN
10	S8	152	ILE
11	S9	6	ARG
11	S9	166	GLY
12	C0	30	ALA
12	C0	92	ILE
12	C0	93	GLN
13	C1	6	THR
13	C1	30	ARG
14	C2	69	ALA
14	C2	107	ASP
14	C2	126	TRP
14	C2	127	GLY
15	C3	22	ALA
15	C3	148	ALA
16	C4	48	VAL
16	C4	114	ARG
17	C5	11	VAL
17	C5	48	GLY
17	C5	52	LYS
18	C6	32	ASN
18	C6	39	VAL
18	C6	97	VAL

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Mol	Chain	Res	Type
19	C7	115	LEU
19	C7	124	VAL
20	C8	103	ASN
22	D0	96	PRO
23	D1	4	ASP
23	D1	15	ARG
23	D1	44	ARG
23	D1	78	LEU
25	D3	11	SER
25	D3	112	LYS
25	D3	114	LYS
25	D3	137	LYS
26	D4	4	ALA
26	D4	35	VAL
26	D4	47	VAL
27	D5	42	LEU
27	D5	71	ILE
28	D6	5	ARG
28	D6	35	ALA
28	D6	36	ILE
28	D6	45	VAL
28	D6	46	GLU
28	D6	63	ALA
33	E1	118	ARG
34	SR	98	GLU
34	SR	146	GLY
34	SR	238	ASP
35	SM	69	ARG
35	SM	154	TYR
39	L2	13	GLY
39	L2	143	GLU
39	L2	250	GLN
40	L3	138	ALA
40	L3	155	ALA
40	L3	170	PRO
40	L3	171	LEU
40	L3	175	LYS
40	L3	221	THR
40	L3	351	LEU
40	L3	385	LYS
41	L4	14	GLU
41	L4	15	ALA

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Mol	Chain	Res	Type
41	L4	265	GLU
41	L4	292	SER
41	L4	309	ARG
41	L4	313	LEU
41	L4	317	PRO
42	L5	148	ILE
42	L5	153	THR
42	L5	202	GLY
43	L6	98	VAL
44	L7	55	TYR
44	L7	159	GLN
45	L8	36	ILE
45	L8	39	ALA
45	L8	76	ALA
45	L8	157	VAL
45	L8	190	VAL
46	L9	80	THR
46	L9	139	ASN
47	M0	78	THR
47	M0	117	GLY
47	M0	189	GLU
47	M0	194	GLY
47	M0	207	GLU
48	M1	8	PRO
48	M1	12	LEU
48	M1	94	ARG
48	M1	95	ASN
48	M1	114	ILE
49	M3	47	ALA
49	M3	67	ARG
49	M3	136	GLU
49	M3	141	ALA
49	M3	166	ALA
51	M5	81	TYR
51	M5	158	HIS
52	M6	16	VAL
53	M7	36	ILE
53	M7	157	VAL
53	M7	159	LYS
54	M8	91	ALA
55	M9	130	ASN
56	N0	130	GLU

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Mol	Chain	Res	Type
56	N0	154	HIS
57	N1	22	HIS
57	N1	124	VAL
57	N1	159	PHE
58	N2	11	ILE
58	N2	51	GLY
59	N3	134	GLY
60	N4	76	VAL
60	N4	97	LYS
61	N5	45	LYS
63	N7	4	PHE
63	N7	16	GLY
63	N7	30	ASP
64	N8	27	LYS
64	N8	66	ALA
64	N8	97	GLU
66	O0	27	TYR
66	O0	96	GLY
67	O1	111	GLU
71	O5	119	LYS
74	O8	37	PRO
74	O8	49	SER
79	Q3	3	LYS
79	Q3	9	GLY
79	Q3	59	CYS
2	s0	30	GLN
2	s0	44	GLY
2	s0	68	PRO
2	s0	94	GLY
2	s0	95	ALA
2	s0	110	TYR
3	s1	72	ASP
3	s1	93	GLY
3	s1	200	ALA
3	s1	206	PRO
4	s2	106	ASP
4	s2	149	GLY
5	s3	203	PRO
5	s3	217	ILE
6	s4	194	THR
7	s5	36	ALA
7	s5	43	PHE

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Mol	Chain	Res	Type
8	s6	25	ARG
9	s7	67	LEU
9	s7	73	VAL
10	s8	122	GLY
11	s9	169	PRO
12	c0	23	ALA
12	c0	80	LEU
12	c0	92	ILE
13	c1	6	THR
13	c1	7	VAL
13	c1	55	ASP
14	c2	63	VAL
15	c3	3	ARG
15	c3	108	ASP
16	c4	48	VAL
16	c4	90	ARG
16	c4	124	ASP
17	c5	17	TYR
18	c6	39	VAL
19	c7	88	VAL
21	c9	26	GLY
21	c9	33	TYR
22	d0	96	PRO
23	d1	43	GLY
24	d2	78	ARG
25	d3	46	SER
26	d4	33	ALA
26	d4	35	VAL
26	d4	54	ALA
26	d4	121	THR
27	d5	103	ARG
28	d6	28	LYS
28	d6	63	ALA
29	d7	24	LEU
30	d8	16	LEU
30	d8	33	LEU
30	d8	61	ARG
80	e0	51	ASN
33	e1	79	LYS
33	e1	84	VAL
33	e1	102	VAL
33	e1	105	TYR

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Mol	Chain	Res	Type
33	e1	127	GLY
34	sR	96	THR
34	sR	163	ASP
34	sR	226	ALA
34	sR	271	VAL
35	sM	31	SER
35	sM	47	ALA
39	l2	24	GLN
39	l2	142	ASP
39	l2	194	ASN
39	l2	216	HIS
40	l3	129	ALA
40	l3	139	GLN
40	l3	187	SER
40	l3	258	ALA
40	l3	347	SER
41	l4	15	ALA
41	l4	43	ASN
41	l4	144	LYS
42	l5	127	GLY
42	l5	260	PHE
42	l5	296	GLN
43	l6	140	VAL
44	l7	178	ILE
45	l8	79	GLN
45	l8	121	SER
45	l8	122	LYS
45	l8	203	VAL
45	l8	239	GLY
46	l9	144	ILE
46	l9	167	VAL
47	m0	3	ARG
47	m0	82	ARG
47	m0	204	GLY
48	m1	94	ARG
48	m1	165	GLN
81	m2	22	TYR
81	m2	30	VAL
81	m2	67	LYS
81	m2	97	ALA
81	m2	125	ILE
81	m2	148	THR

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Mol	Chain	Res	Type
50	m4	41	GLN
50	m4	136	ALA
51	m5	183	THR
51	m5	184	LYS
54	m8	112	ALA
54	m8	113	LYS
54	m8	147	ARG
55	m9	131	ALA
56	n0	45	LEU
58	n2	50	LEU
58	n2	51	GLY
60	n4	63	ILE
60	n4	75	THR
60	n4	76	VAL
60	n4	133	THR
63	n7	134	LEU
64	n8	24	LYS
64	n8	65	GLN
64	n8	67	HIS
65	n9	39	PHE
66	o0	46	ALA
67	o1	82	GLU
67	o1	84	ASP
68	o2	62	LYS
68	o2	125	ARG
69	o3	59	VAL
71	o5	37	SER
72	o6	20	MET
82	p0	68	SER
83	p2	16	ASP
83	p2	17	SER
2	S0	30	GLN
3	S1	26	ARG
3	S1	48	VAL
3	S1	54	LEU
3	S1	58	SER
3	S1	62	LYS
3	S1	221	PRO
4	S2	35	TRP
4	S2	136	VAL
5	S3	44	THR
5	S3	216	PRO

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Mol	Chain	Res	Type
5	S3	217	ILE
6	S4	120	SER
6	S4	175	PHE
6	S4	204	GLY
7	S5	50	GLU
7	S5	99	MET
8	S6	148	SER
9	S7	110	GLN
9	S7	112	ARG
9	S7	131	PHE
10	S8	10	LYS
10	S8	19	ALA
11	S9	18	PRO
11	S9	167	ALA
12	C0	64	TYR
13	C1	4	GLU
13	C1	55	ASP
13	C1	146	ALA
14	C2	93	ASP
14	C2	101	ALA
14	C2	106	ILE
14	C2	111	ASN
14	C2	125	ASN
14	C2	131	ASP
15	C3	3	ARG
15	C3	28	LEU
15	C3	137	PRO
16	C4	12	GLN
16	C4	50	ALA
16	C4	75	GLY
17	C5	69	GLU
19	C7	101	ASN
20	C8	91	ASP
21	C9	28	LEU
22	D0	17	GLN
22	D0	73	GLY
23	D1	10	GLU
23	D1	42	GLU
24	D2	83	ILE
25	D3	41	SER
25	D3	110	LYS
25	D3	139	LYS

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Mol	Chain	Res	Type
26	D4	5	VAL
26	D4	54	ALA
27	D5	39	ALA
27	D5	43	ASP
27	D5	94	LYS
28	D6	8	ASN
28	D6	58	VAL
28	D6	97	PRO
29	D7	76	GLY
31	D9	11	PRO
31	D9	20	GLN
33	E1	102	VAL
33	E1	109	ASP
34	SR	49	GLY
34	SR	163	ASP
35	SM	68	ARG
39	L2	125	ALA
39	L2	251	LYS
40	L3	63	PRO
40	L3	174	LYS
40	L3	258	ALA
40	L3	302	LYS
40	L3	378	ALA
40	L3	386	ASP
41	L4	90	PHE
41	L4	140	HIS
42	L5	72	ASP
42	L5	93	THR
42	L5	111	GLN
42	L5	163	LEU
42	L5	253	PHE
42	L5	259	LYS
44	L7	91	GLY
45	L8	79	GLN
46	L9	40	HIS
46	L9	49	ASN
46	L9	79	ILE
46	L9	110	LYS
46	L9	190	ASP
47	M0	82	ARG
48	M1	117	ASP
48	M1	152	HIS

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Mol	Chain	Res	Type
49	M3	130	GLY
49	M3	165	SER
49	M3	176	GLU
50	M4	113	THR
52	M6	89	SER
53	M7	109	ALA
54	M8	41	ASP
54	M8	97	PRO
54	M8	99	THR
55	M9	53	LYS
57	N1	122	GLN
57	N1	146	ASN
58	N2	27	VAL
60	N4	9	SER
60	N4	70	LYS
60	N4	86	SER
61	N5	36	LYS
61	N5	117	ASN
62	N6	125	LYS
63	N7	102	GLU
66	O0	53	LYS
67	O1	21	HIS
67	O1	99	ALA
67	O1	102	LYS
68	O2	62	LYS
69	O3	59	VAL
71	O5	35	LYS
72	O6	21	THR
72	O6	33	ALA
72	O6	64	SER
72	O6	98	ARG
72	O6	99	ARG
78	Q2	95	GLY
2	s0	10	THR
2	s0	65	ALA
2	s0	194	PRO
2	s0	205	ARG
3	s1	60	ALA
3	s1	129	THR
3	s1	147	ALA
3	s1	209	ASN
3	s1	224	ASP

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Mol	Chain	Res	Type
4	s2	88	LYS
4	s2	163	GLY
4	s2	182	PRO
5	s3	76	ARG
5	s3	93	ASP
5	s3	219	ALA
6	s4	51	ARG
6	s4	135	GLY
6	s4	245	LYS
7	s5	74	ALA
7	s5	176	THR
8	s6	70	PRO
8	s6	126	ASP
8	s6	138	ALA
9	s7	10	SER
9	s7	30	SER
11	s9	88	GLU
11	s9	147	MET
12	c0	30	ALA
12	c0	31	LYS
12	c0	82	LEU
12	c0	95	ARG
14	c2	39	ASP
14	c2	54	ARG
15	c3	29	SER
15	c3	139	TRP
15	c3	140	LYS
16	c4	11	SER
16	c4	50	ALA
16	c4	108	SER
16	c4	131	GLY
17	c5	80	MET
18	c6	3	ALA
18	c6	142	TYR
19	c7	63	LYS
19	c7	86	PRO
19	c7	116	LYS
20	c8	55	HIS
20	c8	61	LEU
20	c8	107	SER
21	c9	29	GLU
22	d0	49	ASN

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Mol	Chain	Res	Type
22	d0	52	LYS
22	d0	119	ALA
23	d1	15	ARG
23	d1	42	GLU
26	d4	58	PHE
28	d6	62	TYR
28	d6	94	ASN
29	d7	41	LEU
29	d7	59	CYS
30	d8	60	GLU
30	d8	62	GLU
31	d9	11	PRO
33	e1	85	TYR
33	e1	100	LEU
33	e1	111	GLU
33	e1	131	PHE
33	e1	136	LYS
33	e1	146	SER
34	sR	15	GLY
34	sR	63	GLY
34	sR	105	GLY
35	sM	168	GLU
39	l2	69	TYR
39	l2	80	GLU
41	l4	90	PHE
41	l4	233	LEU
41	l4	311	HIS
41	l4	345	GLU
43	l6	10	TYR
43	l6	138	GLN
44	l7	191	VAL
44	l7	228	SER
45	l8	39	ALA
45	l8	112	GLU
45	l8	237	ILE
47	m0	25	ALA
47	m0	151	GLY
47	m0	220	GLN
48	m1	95	ASN
81	m2	10	PRO
81	m2	58	ASP
81	m2	89	SER

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Mol	Chain	Res	Type
81	m2	119	LEU
49	m3	76	THR
49	m3	129	ASN
49	m3	133	PRO
49	m3	135	ALA
50	m4	60	LEU
50	m4	135	LEU
52	m6	12	LYS
54	m8	8	LYS
54	m8	84	VAL
55	m9	35	ALA
55	m9	36	ASN
55	m9	156	ASN
56	n0	130	GLU
57	n1	117	ALA
59	n3	68	GLU
60	n4	6	ASP
61	n5	47	ALA
63	n7	91	ALA
64	n8	17	ALA
64	n8	48	TYR
64	n8	66	ALA
67	o1	99	ALA
69	o3	90	PRO
70	o4	82	ALA
71	o5	81	ARG
71	o5	110	ALA
74	o8	35	GLY
79	q3	51	ALA
82	p0	21	GLU
82	p0	33	VAL
82	p0	94	THR
83	p1	16	ASP
84	f	15	SER
84	f	16	SER
84	f	17	ALA
2	S0	185	ARG
3	S1	207	LEU
4	S2	145	GLY
4	S2	150	GLN
5	S3	196	ARG
6	S4	22	LYS

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Mol	Chain	Res	Type
6	S4	23	LEU
6	S4	194	THR
6	S4	245	LYS
7	S5	31	GLU
7	S5	45	LYS
7	S5	51	VAL
7	S5	64	VAL
7	S5	65	ARG
8	S6	146	GLY
9	S7	98	ILE
9	S7	111	LYS
9	S7	156	SER
10	S8	120	THR
14	C2	87	PRO
15	C3	19	SER
16	C4	40	ALA
17	C5	80	MET
17	C5	101	ALA
18	C6	40	GLU
18	C6	142	TYR
19	C7	84	TYR
19	C7	87	GLU
21	C9	29	GLU
21	C9	50	ALA
21	C9	119	LYS
22	D0	55	PRO
24	D2	30	SER
24	D2	66	ASN
25	D3	64	PRO
25	D3	109	ARG
25	D3	131	SER
26	D4	34	ASN
29	D7	23	THR
30	D8	36	THR
31	D9	6	VAL
32	E0	51	ASN
33	E1	83	LYS
33	E1	87	THR
33	E1	100	LEU
33	E1	127	GLY
34	SR	51	ASP
34	SR	249	ARG

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Mol	Chain	Res	Type
34	SR	268	GLN
35	SM	12	VAL
35	SM	39	PRO
35	SM	48	ARG
35	SM	88	ARG
35	SM	173	GLU
41	L4	137	ALA
41	L4	268	ALA
42	L5	7	ALA
42	L5	125	VAL
42	L5	177	GLU
42	L5	258	LYS
44	L7	72	ALA
45	L8	113	ALA
46	L9	15	GLY
47	M0	77	THR
48	M1	108	GLU
48	M1	168	ASP
48	M1	172	LEU
49	M3	50	PRO
49	M3	76	THR
51	M5	183	THR
53	M7	164	LYS
54	M8	108	ALA
60	N4	67	VAL
64	N8	47	LYS
64	N8	115	LYS
65	N9	24	PRO
66	O0	97	ASP
67	O1	82	GLU
67	O1	97	LEU
68	O2	110	ALA
70	O4	82	ALA
73	O7	12	HIS
73	O7	85	LYS
73	O7	86	ALA
74	O8	18	ALA
78	Q2	15	LYS
78	Q2	17	CYS
79	Q3	7	LYS
79	Q3	84	ARG
2	s0	14	ALA

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Mol	Chain	Res	Type
2	s0	92	HIS
2	s0	109	ASN
2	s0	127	ARG
2	s0	152	PRO
2	s0	185	ARG
3	s1	55	LYS
3	s1	210	ILE
4	s2	62	PRO
4	s2	155	ALA
4	s2	235	LEU
4	s2	238	SER
5	s3	94	ARG
5	s3	113	LEU
6	s4	30	ARG
6	s4	90	ILE
6	s4	168	LYS
6	s4	195	ILE
6	s4	202	ASP
7	s5	35	GLN
7	s5	37	GLN
7	s5	45	LYS
7	s5	100	ASN
9	s7	11	GLN
9	s7	133	THR
9	s7	151	LYS
10	s8	52	ASN
10	s8	136	SER
11	s9	162	SER
11	s9	167	ALA
12	c0	3	MET
12	c0	35	ILE
12	c0	91	TYR
14	c2	58	LEU
14	c2	87	PRO
14	c2	89	ILE
14	c2	106	ILE
14	c2	131	ASP
14	c2	141	SER
16	c4	37	GLU
16	c4	114	ARG
18	c6	33	GLY
18	c6	97	VAL

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Mol	Chain	Res	Type
18	c6	113	ASP
18	c6	121	SER
26	d4	36	SER
26	d4	51	GLU
28	d6	11	ASN
28	d6	35	ALA
28	d6	82	ARG
33	e1	81	LYS
33	e1	106	TYR
33	e1	112	GLY
33	e1	128	ALA
33	e1	148	TYR
34	sR	231	MET
34	sR	285	ALA
35	sM	43	ASP
39	l2	56	ALA
39	l2	127	ALA
39	l2	180	LEU
40	l3	3	HIS
40	l3	63	PRO
40	l3	236	LYS
40	l3	284	ARG
43	l6	97	ASN
45	l8	69	LEU
45	l8	240	ASN
46	l9	2	LYS
47	m0	173	PHE
47	m0	196	PHE
48	m1	114	ILE
48	m1	167	TYR
48	m1	168	ASP
81	m2	36	ALA
81	m2	55	VAL
81	m2	99	LYS
81	m2	159	LYS
49	m3	44	ALA
49	m3	50	PRO
49	m3	60	ALA
52	m6	65	ASN
56	n0	2	ALA
60	n4	72	SER
63	n7	103	GLN

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Mol	Chain	Res	Type
67	o1	60	TRP
71	o5	3	GLY
71	o5	119	LYS
72	o6	34	SER
72	o6	65	GLY
74	o8	18	ALA
79	q3	10	ILE
79	q3	45	LYS
82	p0	48	ARG
83	p2	35	VAL
84	f	11	ALA
84	f	98	GLY
84	f	113	VAL
84	f	132	LYS
2	S0	103	THR
2	S0	195	TRP
3	S1	61	LEU
3	S1	156	ALA
3	S1	210	ILE
4	S2	39	THR
4	S2	247	ALA
6	S4	45	ILE
9	S7	5	GLN
10	S8	136	SER
11	S9	118	LEU
12	C0	25	LYS
14	C2	112	ALA
16	C4	18	ARG
16	C4	51	ASP
17	C5	109	PRO
20	C8	53	ASP
24	D2	45	GLY
25	D3	27	ASN
25	D3	128	SER
26	D4	6	THR
26	D4	100	VAL
30	D8	35	ASP
33	E1	101	ALA
33	E1	111	GLU
34	SR	15	GLY
34	SR	28	GLY
34	SR	105	GLY

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Mol	Chain	Res	Type
34	SR	135	THR
35	SM	100	THR
39	L2	47	GLN
39	L2	127	ALA
40	L3	68	HIS
40	L3	317	ILE
41	L4	130	ALA
41	L4	146	PRO
41	L4	181	VAL
42	L5	119	TYR
42	L5	260	PHE
42	L5	295	GLY
46	L9	83	THR
47	M0	47	PRO
48	M1	173	ASP
50	M4	10	SER
53	M7	160	ALA
54	M8	149	ALA
54	M8	162	ALA
54	M8	175	ALA
55	M9	129	GLY
59	N3	46	LEU
60	N4	77	LYS
62	N6	49	PRO
63	N7	36	HIS
63	N7	103	GLN
64	N8	117	ARG
65	N9	25	LYS
70	O4	12	PRO
72	O6	3	VAL
3	s1	218	LEU
4	s2	91	ARG
4	s2	150	GLN
4	s2	204	THR
4	s2	234	PRO
5	s3	44	THR
5	s3	45	LYS
6	s4	80	THR
6	s4	150	PRO
7	s5	98	MET
7	s5	151	GLY
9	s7	41	LEU

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Mol	Chain	Res	Type
10	s8	101	ILE
11	s9	5	PRO
14	c2	92	ALA
14	c2	107	ASP
14	c2	108	ARG
14	c2	115	VAL
14	c2	119	SER
16	c4	32	ASP
16	c4	51	ASP
17	c5	6	ASN
17	c5	71	GLU
18	c6	44	LEU
19	c7	19	ARG
19	c7	117	LEU
21	c9	43	ASN
28	d6	8	ASN
29	d7	58	SER
30	d8	20	GLY
80	e0	44	PHE
34	sR	74	THR
34	sR	186	PHE
34	sR	318	ALA
35	sM	36	ASP
39	l2	241	ARG
41	l4	24	ALA
41	l4	272	VAL
41	l4	342	LYS
47	m0	77	THR
48	m1	108	GLU
81	m2	51	PRO
81	m2	105	ARG
49	m3	51	LEU
51	m5	68	ARG
52	m6	16	VAL
54	m8	155	MET
55	m9	130	ASN
60	n4	7	SER
60	n4	96	LEU
63	n7	16	GLY
63	n7	28	PRO
63	n7	36	HIS
64	n8	93	SER

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Mol	Chain	Res	Type
68	o2	5	PRO
68	o2	124	GLY
82	p0	47	GLY
84	f	93	LEU
84	f	121	GLY
84	f	148	ILE
2	S0	5	ALA
2	S0	152	PRO
3	S1	51	SER
5	S3	72	LEU
5	S3	81	PRO
6	S4	35	PRO
6	S4	205	PHE
6	S4	234	PRO
9	S7	109	VAL
10	S8	59	ARG
10	S8	199	LYS
14	C2	108	ARG
14	C2	119	SER
16	C4	125	SER
16	C4	126	THR
18	C6	33	GLY
18	C6	113	ASP
23	D1	12	TYR
23	D1	14	PRO
23	D1	16	LYS
24	D2	67	GLY
28	D6	85	ARG
35	SM	87	THR
35	SM	89	ARG
42	L5	213	ASP
44	L7	158	LYS
50	M4	6	ILE
52	M6	112	TYR
65	N9	29	TYR
67	O1	45	GLY
70	O4	59	PRO
70	O4	77	GLY
79	Q3	51	ALA
2	s0	139	VAL
3	s1	22	ASP
4	s2	151	PRO

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Mol	Chain	Res	Type
5	s3	102	ALA
7	s5	29	ILE
8	s6	152	ASP
9	s7	129	LEU
10	s8	78	ILE
12	c0	24	LYS
16	c4	118	VAL
19	c7	105	GLN
20	c8	145	ARG
22	d0	118	VAL
23	d1	2	GLU
27	d5	44	GLN
28	d6	13	LYS
28	d6	59	TYR
28	d6	86	VAL
80	e0	54	ARG
33	e1	137	ASP
41	l4	302	ALA
42	l5	139	PRO
46	l9	110	LYS
47	m0	176	LEU
48	m1	11	ASP
48	m1	117	ASP
48	m1	153	LYS
81	m2	103	ARG
52	m6	5	PRO
54	m8	91	ALA
54	m8	171	LYS
64	n8	28	HIS
68	o2	127	ALA
73	o7	85	LYS
83	p2	22	SER
4	S2	236	PRO
6	S4	150	PRO
44	L7	26	VAL
6	s4	107	GLY
11	s9	168	ARG
19	c7	121	VAL
23	d1	9	VAL
35	sM	51	ARG
81	m2	86	VAL
55	m9	143	ILE

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Mol	Chain	Res	Type
57	n1	124	VAL
58	n2	60	GLY
59	n3	16	GLY
66	o0	96	GLY
13	C1	113	PRO
14	C2	82	PRO
14	C2	115	VAL
16	C4	96	PRO
23	D1	23	ILE
26	D4	95	GLY
41	L4	66	GLY
41	L4	328	ASN
47	M0	16	PRO
2	s0	199	PRO
6	s4	111	VAL
28	d6	75	VAL
80	e0	50	VAL
45	l8	36	ILE
81	m2	141	VAL
76	q0	80	PRO
20	C8	142	GLY
23	D1	46	ILE
26	D4	29	HIS
40	L3	305	ILE
43	L6	6	ALA
61	N5	35	PRO
62	N6	92	GLY
67	O1	88	PRO
2	s0	118	PRO
13	c1	76	VAL
15	c3	59	GLY
15	c3	82	PRO
20	c8	4	VAL
20	c8	135	GLY
26	d4	29	HIS
80	e0	14	VAL
42	l5	255	PRO
81	m2	59	ILE
53	m7	67	ILE
59	n3	3	GLY
60	n4	67	VAL
63	n7	82	PRO

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Mol	Chain	Res	Type
65	n9	29	TYR
74	o8	37	PRO
82	p0	214	VAL
25	D3	108	GLY
28	D6	18	VAL
30	D8	44	VAL
73	O7	23	GLY
79	Q3	8	VAL
15	c3	22	ALA
17	c5	48	GLY
26	d4	120	GLY
30	d8	47	PRO
59	n3	107	GLY
64	n8	56	VAL
64	n8	70	LYS
15	C3	85	PRO
29	D7	38	PRO
30	D8	6	PRO
58	n2	22	PRO
63	n7	70	PRO
82	p0	80	VAL
24	d2	29	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	S0	164/209 (78%)	140 (85%)	24 (15%)	4	21
2	s0	165/209 (79%)	137 (83%)	28 (17%)	2	14
3	S1	191/223 (86%)	157 (82%)	34 (18%)	2	12
3	s1	192/223 (86%)	160 (83%)	32 (17%)	3	15
4	S2	176/204 (86%)	147 (84%)	29 (16%)	3	15
4	s2	176/204 (86%)	134 (76%)	42 (24%)	1	4
5	S3	182/194 (94%)	146 (80%)	36 (20%)	1	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	s3	182/194 (94%)	158 (87%)	24 (13%)	5	26
6	S4	221/221 (100%)	194 (88%)	27 (12%)	6	28
6	s4	221/221 (100%)	192 (87%)	29 (13%)	5	26
7	S5	173/190 (91%)	146 (84%)	27 (16%)	3	18
7	s5	173/190 (91%)	146 (84%)	27 (16%)	3	18
8	S6	188/201 (94%)	162 (86%)	26 (14%)	4	23
8	s6	187/201 (93%)	162 (87%)	25 (13%)	5	25
9	S7	165/169 (98%)	144 (87%)	21 (13%)	5	27
9	s7	165/169 (98%)	138 (84%)	27 (16%)	3	16
10	S8	150/161 (93%)	128 (85%)	22 (15%)	4	21
10	s8	150/161 (93%)	128 (85%)	22 (15%)	4	21
11	S9	158/165 (96%)	128 (81%)	30 (19%)	2	9
11	s9	158/165 (96%)	128 (81%)	30 (19%)	2	9
12	C0	77/98 (79%)	69 (90%)	8 (10%)	9	38
12	c0	73/98 (74%)	64 (88%)	9 (12%)	6	28
13	C1	129/136 (95%)	110 (85%)	19 (15%)	4	21
13	c1	129/136 (95%)	111 (86%)	18 (14%)	4	23
14	C2	88/118 (75%)	73 (83%)	15 (17%)	2	14
14	c2	88/118 (75%)	74 (84%)	14 (16%)	3	17
15	C3	127/127 (100%)	101 (80%)	26 (20%)	1	7
15	c3	127/127 (100%)	111 (87%)	16 (13%)	5	27
16	C4	81/104 (78%)	65 (80%)	16 (20%)	1	8
16	c4	97/104 (93%)	78 (80%)	19 (20%)	1	8
17	C5	101/117 (86%)	89 (88%)	12 (12%)	6	29
17	c5	103/117 (88%)	87 (84%)	16 (16%)	3	18
18	C6	117/118 (99%)	98 (84%)	19 (16%)	3	16
18	c6	118/118 (100%)	101 (86%)	17 (14%)	4	22
19	C7	94/124 (76%)	77 (82%)	17 (18%)	2	11
19	c7	92/124 (74%)	79 (86%)	13 (14%)	4	22
20	C8	128/128 (100%)	106 (83%)	22 (17%)	2	14
20	c8	128/128 (100%)	106 (83%)	22 (17%)	2	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	C9	115/115 (100%)	95 (83%)	20 (17%)	2	13
21	c9	115/115 (100%)	104 (90%)	11 (10%)	10	42
22	D0	100/113 (88%)	83 (83%)	17 (17%)	2	14
22	d0	103/113 (91%)	84 (82%)	19 (18%)	2	10
23	D1	74/74 (100%)	59 (80%)	15 (20%)	1	7
23	d1	74/74 (100%)	61 (82%)	13 (18%)	2	12
24	D2	110/110 (100%)	89 (81%)	21 (19%)	2	9
24	d2	110/110 (100%)	92 (84%)	18 (16%)	3	16
25	D3	119/119 (100%)	100 (84%)	19 (16%)	3	17
25	d3	119/119 (100%)	98 (82%)	21 (18%)	2	12
26	D4	112/112 (100%)	98 (88%)	14 (12%)	6	28
26	d4	112/112 (100%)	92 (82%)	20 (18%)	2	11
27	D5	61/88 (69%)	50 (82%)	11 (18%)	2	11
27	d5	61/88 (69%)	53 (87%)	8 (13%)	5	26
28	D6	83/83 (100%)	66 (80%)	17 (20%)	1	7
28	d6	83/83 (100%)	74 (89%)	9 (11%)	8	36
29	D7	70/70 (100%)	66 (94%)	4 (6%)	25	65
29	d7	70/70 (100%)	57 (81%)	13 (19%)	2	9
30	D8	56/59 (95%)	45 (80%)	11 (20%)	1	8
30	d8	56/59 (95%)	45 (80%)	11 (20%)	1	8
31	D9	47/48 (98%)	39 (83%)	8 (17%)	2	14
31	d9	47/48 (98%)	37 (79%)	10 (21%)	1	6
32	E0	51/51 (100%)	43 (84%)	8 (16%)	3	18
33	E1	62/66 (94%)	53 (86%)	9 (14%)	4	21
33	e1	66/66 (100%)	54 (82%)	12 (18%)	2	11
34	SR	259/261 (99%)	236 (91%)	23 (9%)	12	46
34	sR	260/261 (100%)	241 (93%)	19 (7%)	17	56
35	SM	97/228 (42%)	78 (80%)	19 (20%)	1	8
35	sM	54/228 (24%)	44 (82%)	10 (18%)	2	10
39	L2	193/195 (99%)	157 (81%)	36 (19%)	2	9
39	l2	192/195 (98%)	157 (82%)	35 (18%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	L3	319/322 (99%)	256 (80%)	63 (20%)	1	8
40	l3	320/322 (99%)	263 (82%)	57 (18%)	2	12
41	L4	288/288 (100%)	242 (84%)	46 (16%)	3	17
41	l4	288/288 (100%)	242 (84%)	46 (16%)	3	17
42	L5	244/244 (100%)	206 (84%)	38 (16%)	3	18
42	l5	243/244 (100%)	193 (79%)	50 (21%)	1	7
43	L6	134/152 (88%)	116 (87%)	18 (13%)	5	25
43	l6	135/152 (89%)	112 (83%)	23 (17%)	2	14
44	L7	186/204 (91%)	162 (87%)	24 (13%)	5	26
44	l7	187/204 (92%)	162 (87%)	25 (13%)	5	25
45	L8	187/207 (90%)	160 (86%)	27 (14%)	4	22
45	l8	177/207 (86%)	153 (86%)	24 (14%)	5	24
46	L9	171/171 (100%)	135 (79%)	36 (21%)	1	6
46	l9	171/171 (100%)	137 (80%)	34 (20%)	1	8
47	M0	177/186 (95%)	146 (82%)	31 (18%)	2	13
47	m0	179/186 (96%)	149 (83%)	30 (17%)	2	14
48	M1	147/150 (98%)	122 (83%)	25 (17%)	2	14
48	m1	147/150 (98%)	120 (82%)	27 (18%)	2	10
49	M3	154/158 (98%)	136 (88%)	18 (12%)	7	30
49	m3	154/158 (98%)	134 (87%)	20 (13%)	5	26
50	M4	107/108 (99%)	88 (82%)	19 (18%)	2	12
50	m4	108/108 (100%)	88 (82%)	20 (18%)	2	10
51	M5	175/175 (100%)	145 (83%)	30 (17%)	2	14
51	m5	175/175 (100%)	150 (86%)	25 (14%)	4	22
52	M6	160/161 (99%)	141 (88%)	19 (12%)	6	29
52	m6	160/161 (99%)	145 (91%)	15 (9%)	11	43
53	M7	140/145 (97%)	108 (77%)	32 (23%)	1	4
53	m7	125/145 (86%)	103 (82%)	22 (18%)	2	12
54	M8	150/150 (100%)	130 (87%)	20 (13%)	5	25
54	m8	150/150 (100%)	130 (87%)	20 (13%)	5	25
55	M9	153/153 (100%)	135 (88%)	18 (12%)	6	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	m9	153/153 (100%)	131 (86%)	22 (14%)	4	22
56	N0	156/156 (100%)	128 (82%)	28 (18%)	2	11
56	n0	156/156 (100%)	122 (78%)	34 (22%)	1	5
57	N1	136/136 (100%)	109 (80%)	27 (20%)	1	8
57	n1	136/136 (100%)	107 (79%)	29 (21%)	1	6
58	N2	87/106 (82%)	74 (85%)	13 (15%)	4	20
58	n2	85/106 (80%)	71 (84%)	14 (16%)	3	15
59	N3	104/104 (100%)	90 (86%)	14 (14%)	5	25
59	n3	104/104 (100%)	92 (88%)	12 (12%)	7	31
60	N4	57/129 (44%)	54 (95%)	3 (5%)	28	67
60	n4	100/129 (78%)	89 (89%)	11 (11%)	8	35
61	N5	104/117 (89%)	82 (79%)	22 (21%)	1	6
61	n5	104/117 (89%)	88 (85%)	16 (15%)	3	19
62	N6	109/109 (100%)	88 (81%)	21 (19%)	2	8
62	n6	109/109 (100%)	94 (86%)	15 (14%)	4	23
63	N7	115/115 (100%)	102 (89%)	13 (11%)	7	32
63	n7	115/115 (100%)	95 (83%)	20 (17%)	2	13
64	N8	118/118 (100%)	97 (82%)	21 (18%)	2	12
64	n8	118/118 (100%)	97 (82%)	21 (18%)	2	12
65	N9	46/46 (100%)	39 (85%)	7 (15%)	3	19
65	n9	46/46 (100%)	40 (87%)	6 (13%)	5	26
66	O0	81/87 (93%)	65 (80%)	16 (20%)	1	8
66	o0	84/87 (97%)	74 (88%)	10 (12%)	6	29
67	O1	92/96 (96%)	79 (86%)	13 (14%)	4	22
67	o1	94/96 (98%)	79 (84%)	15 (16%)	3	17
68	O2	109/110 (99%)	88 (81%)	21 (19%)	2	8
68	o2	109/110 (99%)	85 (78%)	24 (22%)	1	5
69	O3	90/90 (100%)	80 (89%)	10 (11%)	8	34
69	o3	90/90 (100%)	79 (88%)	11 (12%)	6	28
70	O4	95/101 (94%)	82 (86%)	13 (14%)	4	24
70	o4	95/101 (94%)	78 (82%)	17 (18%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	O5	104/104 (100%)	85 (82%)	19 (18%)	2	10
71	o5	103/104 (99%)	84 (82%)	19 (18%)	2	10
72	O6	81/81 (100%)	62 (76%)	19 (24%)	1	4
72	o6	80/81 (99%)	60 (75%)	20 (25%)	1	4
73	O7	70/70 (100%)	57 (81%)	13 (19%)	2	9
73	o7	70/70 (100%)	53 (76%)	17 (24%)	1	4
74	O8	68/68 (100%)	55 (81%)	13 (19%)	2	9
74	o8	67/68 (98%)	57 (85%)	10 (15%)	4	20
75	O9	45/45 (100%)	36 (80%)	9 (20%)	1	7
75	o9	45/45 (100%)	40 (89%)	5 (11%)	8	34
76	Q0	47/47 (100%)	38 (81%)	9 (19%)	2	9
76	q0	47/47 (100%)	36 (77%)	11 (23%)	1	4
77	Q1	23/23 (100%)	17 (74%)	6 (26%)	0	3
77	q1	23/23 (100%)	17 (74%)	6 (26%)	0	3
78	Q2	90/90 (100%)	73 (81%)	17 (19%)	2	9
78	q2	90/90 (100%)	66 (73%)	24 (27%)	0	3
79	Q3	71/71 (100%)	63 (89%)	8 (11%)	7	32
79	q3	71/71 (100%)	57 (80%)	14 (20%)	1	8
80	e0	53/53 (100%)	36 (68%)	17 (32%)	0	2
82	p0	105/253 (42%)	86 (82%)	19 (18%)	2	11
84	f	123/132 (93%)	107 (87%)	16 (13%)	5	26
All	All	18849/20371 (92%)	15796 (84%)	3053 (16%)	3	16

All (3053) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	S0	7	PHE
2	S0	9	LEU
2	S0	22	THR
2	S0	27	ARG
2	S0	32	HIS
2	S0	37	VAL
2	S0	41	ARG
2	S0	49	ASN
2	S0	62	ARG

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Mol	Chain	Res	Type
2	S0	88	LYS
2	S0	101	ARG
2	S0	108	THR
2	S0	114	SER
2	S0	153	SER
2	S0	154	GLU
2	S0	168	HIS
2	S0	170	ILE
2	S0	172	LEU
2	S0	177	LEU
2	S0	188	LEU
2	S0	196	SER
2	S0	198	MET
2	S0	200	ASP
2	S0	203	PHE
3	S1	21	VAL
3	S1	28	GLU
3	S1	29	TRP
3	S1	30	PHE
3	S1	36	SER
3	S1	46	THR
3	S1	61	LEU
3	S1	70	LEU
3	S1	78	ASP
3	S1	81	PHE
3	S1	89	ASP
3	S1	96	LEU
3	S1	97	LEU
3	S1	104	ASP
3	S1	105	PHE
3	S1	108	ASP
3	S1	111	ARG
3	S1	120	LEU
3	S1	124	ASN
3	S1	133	TYR
3	S1	135	LEU
3	S1	148	ASN
3	S1	154	SER
3	S1	176	VAL
3	S1	180	THR
3	S1	181	LEU
3	S1	184	LEU

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Mol	Chain	Res	Type
3	S1	194	ASN
3	S1	195	LYS
3	S1	202	LYS
3	S1	215	VAL
3	S1	218	LEU
3	S1	222	LYS
3	S1	223	PHE
4	S2	41	LEU
4	S2	53	ILE
4	S2	69	ILE
4	S2	70	ASP
4	S2	78	ASP
4	S2	89	GLN
4	S2	95	ARG
4	S2	96	THR
4	S2	97	ARG
4	S2	99	LYS
4	S2	107	SER
4	S2	111	VAL
4	S2	117	THR
4	S2	134	LEU
4	S2	137	ILE
4	S2	139	ILE
4	S2	141	ARG
4	S2	152	HIS
4	S2	166	THR
4	S2	167	VAL
4	S2	182	PRO
4	S2	186	LYS
4	S2	189	GLN
4	S2	206	THR
4	S2	221	THR
4	S2	222	TYR
4	S2	226	THR
4	S2	237	VAL
4	S2	242	ILE
5	S3	4	LEU
5	S3	7	LYS
5	S3	23	GLU
5	S3	37	VAL
5	S3	44	THR
5	S3	45	LYS

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Mol	Chain	Res	Type
5	S3	55	THR
5	S3	65	ARG
5	S3	70	THR
5	S3	76	ARG
5	S3	84	ILE
5	S3	89	GLU
5	S3	91	VAL
5	S3	93	ASP
5	S3	105	MET
5	S3	111	ASN
5	S3	113	LEU
5	S3	124	ARG
5	S3	127	MET
5	S3	128	GLU
5	S3	134	CYS
5	S3	138	VAL
5	S3	142	LEU
5	S3	158	ILE
5	S3	174	HIS
5	S3	175	VAL
5	S3	176	LEU
5	S3	178	ARG
5	S3	179	GLN
5	S3	182	LEU
5	S3	189	MET
5	S3	204	ASP
5	S3	207	THR
5	S3	215	GLU
5	S3	217	ILE
5	S3	223	LYS
6	S4	12	LEU
6	S4	38	LEU
6	S4	39	ARG
6	S4	65	LEU
6	S4	76	VAL
6	S4	77	ARG
6	S4	95	THR
6	S4	115	THR
6	S4	116	ASP
6	S4	131	LEU
6	S4	133	LYS
6	S4	148	ARG

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Mol	Chain	Res	Type
6	S4	160	VAL
6	S4	164	LEU
6	S4	180	LEU
6	S4	182	TYR
6	S4	187	ARG
6	S4	206	ASP
6	S4	211	LYS
6	S4	212	ASP
6	S4	217	THR
6	S4	220	THR
6	S4	227	VAL
6	S4	238	LEU
6	S4	240	LYS
6	S4	248	ILE
6	S4	259	GLN
7	S5	24	VAL
7	S5	25	LEU
7	S5	27	THR
7	S5	32	GLU
7	S5	38	THR
7	S5	41	LYS
7	S5	45	LYS
7	S5	46	TRP
7	S5	48	PHE
7	S5	53	VAL
7	S5	65	ARG
7	S5	70	VAL
7	S5	76	ARG
7	S5	84	LYS
7	S5	89	ILE
7	S5	93	LEU
7	S5	94	THR
7	S5	97	LEU
7	S5	98	MET
7	S5	109	LYS
7	S5	119	ASP
7	S5	128	ASN
7	S5	147	THR
7	S5	156	ARG
7	S5	157	ARG
7	S5	166	ARG
7	S5	219	ARG

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Mol	Chain	Res	Type
8	S6	7	TYR
8	S6	12	SER
8	S6	15	THR
8	S6	18	ILE
8	S6	19	ASP
8	S6	65	GLN
8	S6	76	LEU
8	S6	78	THR
8	S6	81	VAL
8	S6	97	VAL
8	S6	114	VAL
8	S6	115	LYS
8	S6	125	THR
8	S6	126	ASP
8	S6	133	LEU
8	S6	143	LYS
8	S6	150	GLU
8	S6	154	ARG
8	S6	155	ASP
8	S6	169	TYR
8	S6	170	THR
8	S6	177	ARG
8	S6	201	GLN
8	S6	212	LEU
8	S6	216	LEU
8	S6	223	LYS
9	S7	9	LEU
9	S7	15	GLU
9	S7	16	LEU
9	S7	38	LEU
9	S7	46	ILE
9	S7	50	ASP
9	S7	67	LEU
9	S7	70	PHE
9	S7	76	LYS
9	S7	85	PHE
9	S7	95	GLU
9	S7	97	ARG
9	S7	109	VAL
9	S7	110	GLN
9	S7	114	ARG
9	S7	115	SER

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Mol	Chain	Res	Type
9	S7	126	LEU
9	S7	133	THR
9	S7	147	ASN
9	S7	181	ILE
9	S7	185	ILE
10	S8	20	GLN
10	S8	21	PHE
10	S8	29	LEU
10	S8	37	LYS
10	S8	46	VAL
10	S8	56	ARG
10	S8	58	LEU
10	S8	62	THR
10	S8	82	VAL
10	S8	88	ASN
10	S8	103	GLN
10	S8	135	LYS
10	S8	137	LYS
10	S8	151	LYS
10	S8	152	ILE
10	S8	155	SER
10	S8	158	SER
10	S8	164	ARG
10	S8	193	LEU
10	S8	195	ARG
10	S8	197	THR
10	S8	199	LYS
11	S9	3	ARG
11	S9	6	ARG
11	S9	22	SER
11	S9	28	LEU
11	S9	39	LYS
11	S9	54	ARG
11	S9	60	LEU
11	S9	89	ASP
11	S9	92	LYS
11	S9	93	LEU
11	S9	94	ASP
11	S9	96	VAL
11	S9	97	LEU
11	S9	99	LEU
11	S9	105	LEU

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Mol	Chain	Res	Type
11	S9	109	LEU
11	S9	121	SER
11	S9	130	THR
11	S9	134	ILE
11	S9	138	LYS
11	S9	149	ARG
11	S9	150	LEU
11	S9	151	ASP
11	S9	156	ILE
11	S9	161	THR
11	S9	171	ARG
11	S9	172	VAL
11	S9	174	ARG
11	S9	175	ARG
11	S9	182	GLU
12	C0	1	MET
12	C0	20	VAL
12	C0	27	PHE
12	C0	46	LEU
12	C0	55	VAL
12	C0	56	LYS
12	C0	76	LEU
12	C0	82	LEU
13	C1	21	ASN
13	C1	27	THR
13	C1	29	LYS
13	C1	37	ASN
13	C1	40	LEU
13	C1	44	THR
13	C1	56	LYS
13	C1	64	VAL
13	C1	67	ARG
13	C1	69	LYS
13	C1	74	THR
13	C1	79	LYS
13	C1	83	THR
13	C1	88	ARG
13	C1	91	LEU
13	C1	98	ASN
13	C1	99	ARG
13	C1	123	VAL
13	C1	128	CYS

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Mol	Chain	Res	Type
14	C2	28	LEU
14	C2	37	VAL
14	C2	38	HIS
14	C2	43	ARG
14	C2	46	ARG
14	C2	50	LYS
14	C2	52	LEU
14	C2	61	VAL
14	C2	66	VAL
14	C2	71	ILE
14	C2	74	LEU
14	C2	80	ASN
14	C2	103	LEU
14	C2	126	TRP
14	C2	132	GLU
15	C3	3	ARG
15	C3	9	LYS
15	C3	11	ILE
15	C3	19	SER
15	C3	27	LYS
15	C3	32	SER
15	C3	35	GLU
15	C3	39	LYS
15	C3	52	VAL
15	C3	58	HIS
15	C3	64	ARG
15	C3	66	ILE
15	C3	69	ASN
15	C3	78	ASN
15	C3	80	LEU
15	C3	83	GLU
15	C3	88	LEU
15	C3	102	LEU
15	C3	105	ASN
15	C3	110	ASP
15	C3	114	ARG
15	C3	115	LEU
15	C3	125	LEU
15	C3	129	TYR
15	C3	131	THR
15	C3	135	LEU
16	C4	12	GLN

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Mol	Chain	Res	Type
16	C4	13	VAL
16	C4	26	THR
16	C4	29	HIS
16	C4	39	ILE
16	C4	42	VAL
16	C4	43	THR
16	C4	56	SER
16	C4	83	ILE
16	C4	92	LYS
16	C4	99	GLN
16	C4	118	VAL
16	C4	123	SER
16	C4	127	ARG
16	C4	136	ARG
16	C4	137	LEU
17	C5	11	VAL
17	C5	18	ARG
17	C5	20	VAL
17	C5	22	LEU
17	C5	29	SER
17	C5	36	LEU
17	C5	52	LYS
17	C5	69	GLU
17	C5	79	HIS
17	C5	89	MET
17	C5	103	ASN
17	C5	110	GLU
18	C6	26	LYS
18	C6	29	ILE
18	C6	31	VAL
18	C6	52	LEU
18	C6	57	LEU
18	C6	59	LYS
18	C6	66	ARG
18	C6	68	ARG
18	C6	69	VAL
18	C6	74	HIS
18	C6	76	SER
18	C6	98	ASP
18	C6	106	LYS
18	C6	109	PHE
18	C6	114	ARG

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Mol	Chain	Res	Type
18	C6	116	LEU
18	C6	117	LEU
18	C6	127	LYS
18	C6	137	ARG
19	C7	3	ARG
19	C7	5	ARG
19	C7	6	THR
19	C7	8	THR
19	C7	43	SER
19	C7	46	LEU
19	C7	47	ARG
19	C7	49	LYS
19	C7	62	GLN
19	C7	69	ILE
19	C7	71	PHE
19	C7	78	ARG
19	C7	81	LYS
19	C7	83	GLN
19	C7	84	TYR
19	C7	88	VAL
19	C7	104	ASN
20	C8	3	LEU
20	C8	5	VAL
20	C8	6	GLN
20	C8	11	PHE
20	C8	12	GLN
20	C8	14	ILE
20	C8	17	LEU
20	C8	18	LEU
20	C8	26	ILE
20	C8	28	ILE
20	C8	40	ARG
20	C8	53	ASP
20	C8	71	GLN
20	C8	77	THR
20	C8	88	ARG
20	C8	92	ILE
20	C8	93	THR
20	C8	107	SER
20	C8	109	LEU
20	C8	132	ARG
20	C8	136	GLN

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Mol	Chain	Res	Type
20	C8	138	THR
21	C9	6	VAL
21	C9	18	TYR
21	C9	22	LEU
21	C9	28	LEU
21	C9	30	VAL
21	C9	33	TYR
21	C9	35	ASP
21	C9	57	ARG
21	C9	64	HIS
21	C9	67	MET
21	C9	70	GLN
21	C9	71	VAL
21	C9	88	VAL
21	C9	125	SER
21	C9	126	GLU
21	C9	130	ARG
21	C9	131	ASP
21	C9	132	LEU
21	C9	133	ASP
21	C9	144	GLU
22	D0	15	GLN
22	D0	18	GLN
22	D0	20	ILE
22	D0	23	ARG
22	D0	33	GLN
22	D0	41	ILE
22	D0	43	LYS
22	D0	50	LEU
22	D0	51	VAL
22	D0	57	ARG
22	D0	70	THR
22	D0	74	GLU
22	D0	77	LYS
22	D0	103	ILE
22	D0	105	GLN
22	D0	117	VAL
22	D0	120	SER
23	D1	5	LYS
23	D1	7	GLN
23	D1	11	LEU
23	D1	18	SER

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Mol	Chain	Res	Type
23	D1	25	LYS
23	D1	32	VAL
23	D1	33	GLN
23	D1	40	ASP
23	D1	41	GLU
23	D1	44	ARG
23	D1	52	THR
23	D1	60	ARG
23	D1	76	ASP
23	D1	78	LEU
23	D1	80	LYS
24	D2	2	THR
24	D2	3	ARG
24	D2	7	LEU
24	D2	18	GLU
24	D2	24	GLN
24	D2	25	VAL
24	D2	26	LEU
24	D2	30	SER
24	D2	53	ILE
24	D2	65	LEU
24	D2	68	ARG
24	D2	74	VAL
24	D2	81	VAL
24	D2	83	ILE
24	D2	98	GLN
24	D2	103	ILE
24	D2	104	LEU
24	D2	112	ASP
24	D2	121	VAL
24	D2	126	LEU
24	D2	129	VAL
25	D3	7	ARG
25	D3	9	LEU
25	D3	16	ARG
25	D3	28	ASN
25	D3	55	GLU
25	D3	57	LEU
25	D3	65	ASN
25	D3	69	ARG
25	D3	75	GLN
25	D3	79	ASN

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Mol	Chain	Res	Type
25	D3	82	LYS
25	D3	83	VAL
25	D3	84	THR
25	D3	107	PHE
25	D3	109	ARG
25	D3	132	LEU
25	D3	138	GLU
25	D3	140	LYS
25	D3	144	ARG
26	D4	10	ARG
26	D4	29	HIS
26	D4	47	VAL
26	D4	51	GLU
26	D4	57	VAL
26	D4	61	ARG
26	D4	74	LEU
26	D4	102	LYS
26	D4	115	ASP
26	D4	121	THR
26	D4	124	ARG
26	D4	127	LYS
26	D4	128	LYS
26	D4	135	ASP
27	D5	42	LEU
27	D5	54	VAL
27	D5	58	ARG
27	D5	59	TYR
27	D5	60	VAL
27	D5	75	LEU
27	D5	82	HIS
27	D5	85	LYS
27	D5	92	ILE
27	D5	98	GLN
27	D5	100	ILE
28	D6	12	LYS
28	D6	15	ARG
28	D6	18	VAL
28	D6	33	ASP
28	D6	38	ARG
28	D6	39	MET
28	D6	41	ILE
28	D6	44	ILE

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Mol	Chain	Res	Type
28	D6	50	VAL
28	D6	55	GLU
28	D6	61	GLU
28	D6	64	LEU
28	D6	66	LYS
28	D6	69	ASN
28	D6	71	LEU
28	D6	85	ARG
28	D6	91	ASP
29	D7	33	LEU
29	D7	37	CYS
29	D7	61	THR
29	D7	77	THR
30	D8	7	VAL
30	D8	19	THR
30	D8	32	PHE
30	D8	35	ASP
30	D8	38	ARG
30	D8	39	THR
30	D8	48	VAL
30	D8	49	ARG
30	D8	52	ASP
30	D8	58	GLU
30	D8	61	ARG
31	D9	7	TRP
31	D9	10	HIS
31	D9	19	ARG
31	D9	25	SER
31	D9	28	THR
31	D9	30	LEU
31	D9	36	LEU
31	D9	38	ILE
32	E0	20	LYS
32	E0	21	VAL
32	E0	29	LYS
32	E0	39	LEU
32	E0	43	ARG
32	E0	47	VAL
32	E0	49	LEU
32	E0	56	MET
33	E1	83	LYS
33	E1	89	LYS

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Mol	Chain	Res	Type
33	E1	91	ILE
33	E1	93	HIS
33	E1	95	HIS
33	E1	97	LYS
33	E1	103	LEU
33	E1	108	VAL
33	E1	113	LYS
34	SR	16	HIS
34	SR	50	ASP
34	SR	52	GLN
34	SR	56	VAL
34	SR	66	HIS
34	SR	71	CYS
34	SR	76	ASP
34	SR	117	LYS
34	SR	136	ILE
34	SR	137	LYS
34	SR	140	CYS
34	SR	165	ASP
34	SR	193	ILE
34	SR	202	LEU
34	SR	223	TRP
34	SR	232	TYR
34	SR	233	THR
34	SR	238	ASP
34	SR	248	ASN
34	SR	264	SER
34	SR	265	LEU
34	SR	268	GLN
34	SR	290	VAL
35	SM	24	GLU
35	SM	30	THR
35	SM	33	LYS
35	SM	45	SER
35	SM	46	LYS
35	SM	53	ARG
35	SM	64	LYS
35	SM	78	ASP
35	SM	84	LYS
35	SM	89	ARG
35	SM	91	THR
35	SM	92	ASP

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Mol	Chain	Res	Type
35	SM	94	HIS
35	SM	97	THR
35	SM	100	THR
35	SM	102	THR
35	SM	116	GLU
35	SM	131	ILE
35	SM	140	ASP
39	L2	17	THR
39	L2	18	SER
39	L2	19	HIS
39	L2	32	LEU
39	L2	44	ILE
39	L2	45	VAL
39	L2	49	VAL
39	L2	62	VAL
39	L2	72	ARG
39	L2	96	LEU
39	L2	98	VAL
39	L2	101	VAL
39	L2	104	LEU
39	L2	107	VAL
39	L2	114	SER
39	L2	116	VAL
39	L2	143	GLU
39	L2	148	VAL
39	L2	149	ARG
39	L2	157	VAL
39	L2	165	VAL
39	L2	168	VAL
39	L2	179	LEU
39	L2	180	LEU
39	L2	181	LYS
39	L2	191	LEU
39	L2	193	ARG
39	L2	199	THR
39	L2	204	MET
39	L2	207	VAL
39	L2	211	HIS
39	L2	226	SER
39	L2	227	ARG
39	L2	231	SER
39	L2	250	GLN

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Mol	Chain	Res	Type
39	L2	252	THR
40	L3	3	HIS
40	L3	7	GLU
40	L3	19	ARG
40	L3	24	SER
40	L3	25	ILE
40	L3	28	ARG
40	L3	30	LYS
40	L3	44	THR
40	L3	45	SER
40	L3	53	MET
40	L3	54	THR
40	L3	55	THR
40	L3	56	ILE
40	L3	67	PHE
40	L3	72	VAL
40	L3	73	VAL
40	L3	79	VAL
40	L3	81	THR
40	L3	85	VAL
40	L3	97	ARG
40	L3	100	ARG
40	L3	102	LEU
40	L3	103	THR
40	L3	110	LEU
40	L3	112	ASP
40	L3	114	VAL
40	L3	116	ARG
40	L3	157	VAL
40	L3	163	HIS
40	L3	167	ARG
40	L3	187	SER
40	L3	188	ILE
40	L3	192	VAL
40	L3	196	ARG
40	L3	206	ASP
40	L3	212	ASN
40	L3	214	MET
40	L3	226	PHE
40	L3	235	THR
40	L3	238	LEU
40	L3	244	ARG

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Mol	Chain	Res	Type
40	L3	248	LYS
40	L3	252	ILE
40	L3	264	VAL
40	L3	284	ARG
40	L3	289	ASP
40	L3	296	THR
40	L3	301	THR
40	L3	304	THR
40	L3	305	ILE
40	L3	313	HIS
40	L3	319	ASN
40	L3	328	ILE
40	L3	332	ARG
40	L3	343	TYR
40	L3	345	ASN
40	L3	347	SER
40	L3	349	LYS
40	L3	354	VAL
40	L3	355	SER
40	L3	364	LYS
40	L3	372	THR
40	L3	380	MET
41	L4	3	ARG
41	L4	14	GLU
41	L4	20	LEU
41	L4	55	LYS
41	L4	63	GLU
41	L4	74	ILE
41	L4	93	MET
41	L4	98	ARG
41	L4	99	MET
41	L4	105	THR
41	L4	118	LYS
41	L4	120	TYR
41	L4	133	SER
41	L4	138	ARG
41	L4	150	LEU
41	L4	152	VAL
41	L4	153	SER
41	L4	156	LEU
41	L4	194	TYR
41	L4	196	ASN

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Mol	Chain	Res	Type
41	L4	203	ARG
41	L4	206	LEU
41	L4	222	VAL
41	L4	225	VAL
41	L4	230	VAL
41	L4	238	LEU
41	L4	246	ARG
41	L4	256	THR
41	L4	259	ASP
41	L4	265	GLU
41	L4	283	THR
41	L4	288	ARG
41	L4	300	ARG
41	L4	306	THR
41	L4	307	GLN
41	L4	313	LEU
41	L4	316	ASN
41	L4	318	LEU
41	L4	327	LEU
41	L4	332	LYS
41	L4	333	VAL
41	L4	338	LYS
41	L4	339	LEU
41	L4	346	LYS
41	L4	349	THR
41	L4	354	VAL
42	L5	4	GLN
42	L5	9	SER
42	L5	15	ARG
42	L5	22	ARG
42	L5	23	ARG
42	L5	35	ARG
42	L5	41	LYS
42	L5	50	ARG
42	L5	67	SER
42	L5	69	ILE
42	L5	70	THR
42	L5	81	HIS
42	L5	92	LEU
42	L5	105	ILE
42	L5	107	ARG
42	L5	115	LEU

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Mol	Chain	Res	Type
42	L5	131	LEU
42	L5	140	ARG
42	L5	144	VAL
42	L5	146	LEU
42	L5	155	THR
42	L5	159	VAL
42	L5	163	LEU
42	L5	185	PHE
42	L5	187	THR
42	L5	188	GLU
42	L5	189	GLU
42	L5	193	GLU
42	L5	231	ILE
42	L5	236	LEU
42	L5	245	GLU
42	L5	257	GLU
42	L5	259	LYS
42	L5	263	GLU
42	L5	273	ARG
42	L5	278	SER
42	L5	279	LYS
42	L5	293	LEU
43	L6	5	LYS
43	L6	18	LEU
43	L6	21	THR
43	L6	31	ARG
43	L6	52	VAL
43	L6	65	ILE
43	L6	78	ARG
43	L6	79	VAL
43	L6	84	VAL
43	L6	89	THR
43	L6	90	LYS
43	L6	102	ASN
43	L6	129	GLU
43	L6	134	ARG
43	L6	146	ILE
43	L6	154	LEU
43	L6	164	SER
43	L6	173	MET
44	L7	24	GLU
44	L7	25	GLN

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Mol	Chain	Res	Type
44	L7	26	VAL
44	L7	38	LYS
44	L7	46	GLU
44	L7	77	VAL
44	L7	82	LYS
44	L7	83	LEU
44	L7	92	ILE
44	L7	93	ASN
44	L7	100	ARG
44	L7	121	LYS
44	L7	124	LEU
44	L7	128	LYS
44	L7	129	LEU
44	L7	140	SER
44	L7	143	THR
44	L7	157	ASN
44	L7	161	VAL
44	L7	179	LEU
44	L7	181	ILE
44	L7	182	ASP
44	L7	184	LEU
44	L7	239	LEU
45	L8	26	LEU
45	L8	27	THR
45	L8	41	GLN
45	L8	43	LYS
45	L8	71	VAL
45	L8	74	THR
45	L8	77	GLN
45	L8	79	GLN
45	L8	81	THR
45	L8	84	ARG
45	L8	95	ASN
45	L8	110	THR
45	L8	118	GLU
45	L8	126	SER
45	L8	136	LEU
45	L8	149	LYS
45	L8	150	LEU
45	L8	156	ASP
45	L8	157	VAL
45	L8	169	LEU

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Mol	Chain	Res	Type
45	L8	180	VAL
45	L8	185	ARG
45	L8	190	VAL
45	L8	221	ASN
45	L8	229	VAL
45	L8	246	MET
45	L8	248	LYS
46	L9	1	MET
46	L9	5	GLN
46	L9	9	GLN
46	L9	16	VAL
46	L9	18	VAL
46	L9	38	LEU
46	L9	41	ILE
46	L9	42	ASP
46	L9	44	THR
46	L9	48	VAL
46	L9	52	LEU
46	L9	55	VAL
46	L9	68	LEU
46	L9	69	ARG
46	L9	70	THR
46	L9	100	ASN
46	L9	118	LEU
46	L9	124	ARG
46	L9	133	THR
46	L9	139	ASN
46	L9	146	LEU
46	L9	151	VAL
46	L9	152	GLU
46	L9	155	SER
46	L9	157	ASN
46	L9	161	LEU
46	L9	162	GLN
46	L9	164	ILE
46	L9	169	ASN
46	L9	170	LYS
46	L9	172	ILE
46	L9	177	ASP
46	L9	182	SER
46	L9	183	HIS
46	L9	189	GLU

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Mol	Chain	Res	Type
46	L9	191	LEU
47	M0	3	ARG
47	M0	4	ARG
47	M0	7	ARG
47	M0	32	ARG
47	M0	33	ILE
47	M0	42	THR
47	M0	48	LEU
47	M0	52	LEU
47	M0	55	ASN
47	M0	57	LEU
47	M0	63	GLU
47	M0	82	ARG
47	M0	83	ASP
47	M0	87	LEU
47	M0	91	VAL
47	M0	116	ARG
47	M0	121	LYS
47	M0	128	ARG
47	M0	129	VAL
47	M0	133	GLN
47	M0	138	VAL
47	M0	156	ARG
47	M0	163	GLN
47	M0	165	ILE
47	M0	174	THR
47	M0	175	ASN
47	M0	177	ASP
47	M0	197	VAL
47	M0	203	LYS
47	M0	207	GLU
47	M0	209	ASN
48	M1	10	ARG
48	M1	11	ASP
48	M1	12	LEU
48	M1	13	LYS
48	M1	19	LEU
48	M1	22	SER
48	M1	28	ASP
48	M1	39	GLN
48	M1	44	THR
48	M1	46	VAL

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Mol	Chain	Res	Type
48	M1	51	ARG
48	M1	80	LEU
48	M1	82	ARG
48	M1	92	ARG
48	M1	94	ARG
48	M1	106	ILE
48	M1	107	ASP
48	M1	112	LEU
48	M1	137	ARG
48	M1	140	ARG
48	M1	147	THR
48	M1	161	SER
48	M1	166	LYS
48	M1	171	VAL
48	M1	173	ASP
49	M3	13	HIS
49	M3	15	ARG
49	M3	23	LYS
49	M3	24	VAL
49	M3	53	LEU
49	M3	54	LEU
49	M3	55	ARG
49	M3	58	VAL
49	M3	68	LYS
49	M3	69	VAL
49	M3	100	ARG
49	M3	114	GLN
49	M3	124	ILE
49	M3	131	LYS
49	M3	136	GLU
49	M3	138	VAL
49	M3	153	ASP
49	M3	169	THR
50	M4	8	LYS
50	M4	27	GLN
50	M4	28	SER
50	M4	38	ILE
50	M4	50	LYS
50	M4	53	VAL
50	M4	55	ARG
50	M4	58	ILE
50	M4	72	LEU

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Mol	Chain	Res	Type
50	M4	83	LYS
50	M4	90	VAL
50	M4	102	LYS
50	M4	105	GLN
50	M4	108	ARG
50	M4	120	VAL
50	M4	124	ARG
50	M4	128	ARG
50	M4	133	LYS
50	M4	135	LEU
51	M5	12	ARG
51	M5	17	ASP
51	M5	18	VAL
51	M5	22	LEU
51	M5	38	ARG
51	M5	43	THR
51	M5	46	ASP
51	M5	49	ARG
51	M5	62	TYR
51	M5	71	ARG
51	M5	80	THR
51	M5	90	ASN
51	M5	92	LEU
51	M5	94	TYR
51	M5	97	SER
51	M5	99	ARG
51	M5	106	VAL
51	M5	121	VAL
51	M5	132	VAL
51	M5	133	ILE
51	M5	138	GLN
51	M5	151	ILE
51	M5	159	ARG
51	M5	171	SER
51	M5	178	HIS
51	M5	182	ASN
51	M5	187	ARG
51	M5	188	ARG
51	M5	196	THR
51	M5	204	LYS
52	M6	33	ILE
52	M6	34	VAL

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Mol	Chain	Res	Type
52	M6	42	ASN
52	M6	66	LYS
52	M6	67	THR
52	M6	77	SER
52	M6	78	ARG
52	M6	79	ILE
52	M6	85	ARG
52	M6	110	PRO
52	M6	116	LYS
52	M6	124	LEU
52	M6	128	ARG
52	M6	143	THR
52	M6	160	ARG
52	M6	184	THR
52	M6	188	SER
52	M6	189	ASP
52	M6	190	VAL
53	M7	7	THR
53	M7	10	ASN
53	M7	23	ARG
53	M7	24	VAL
53	M7	29	THR
53	M7	36	ILE
53	M7	41	LEU
53	M7	52	LEU
53	M7	55	GLN
53	M7	56	ARG
53	M7	67	ILE
53	M7	69	ARG
53	M7	72	GLN
53	M7	90	PHE
53	M7	95	LEU
53	M7	114	VAL
53	M7	118	GLN
53	M7	119	VAL
53	M7	127	ARG
53	M7	128	ARG
53	M7	129	THR
53	M7	135	ARG
53	M7	137	ASN
53	M7	142	SER
53	M7	144	SER

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Mol	Chain	Res	Type
53	M7	148	LEU
53	M7	157	VAL
53	M7	166	VAL
53	M7	168	LEU
53	M7	171	ARG
53	M7	180	LYS
53	M7	181	ARG
54	M8	3	ILE
54	M8	6	THR
54	M8	11	LYS
54	M8	17	THR
54	M8	21	SER
54	M8	22	ASP
54	M8	26	LEU
54	M8	32	LEU
54	M8	40	THR
54	M8	41	ASP
54	M8	49	LEU
54	M8	111	ARG
54	M8	113	LYS
54	M8	115	VAL
54	M8	135	GLN
54	M8	147	ARG
54	M8	161	LYS
54	M8	174	ARG
54	M8	180	ARG
54	M8	185	LYS
55	M9	5	ARG
55	M9	17	VAL
55	M9	31	GLU
55	M9	44	LEU
55	M9	49	THR
55	M9	51	VAL
55	M9	59	SER
55	M9	74	ARG
55	M9	81	ARG
55	M9	92	GLN
55	M9	104	ARG
55	M9	116	ASP
55	M9	123	LEU
55	M9	134	HIS
55	M9	139	VAL

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Mol	Chain	Res	Type
55	M9	143	ILE
55	M9	164	LEU
55	M9	173	ARG
56	N0	1	MET
56	N0	8	GLN
56	N0	12	ARG
56	N0	16	THR
56	N0	21	GLU
56	N0	45	LEU
56	N0	47	LYS
56	N0	61	ILE
56	N0	70	THR
56	N0	71	LYS
56	N0	79	VAL
56	N0	80	ARG
56	N0	87	THR
56	N0	100	VAL
56	N0	105	THR
56	N0	117	ARG
56	N0	122	HIS
56	N0	125	LYS
56	N0	132	THR
56	N0	136	LYS
56	N0	137	ARG
56	N0	142	GLN
56	N0	155	ARG
56	N0	156	VAL
56	N0	157	GLN
56	N0	162	THR
56	N0	171	PHE
56	N0	172	TYR
57	N1	11	THR
57	N1	26	HIS
57	N1	27	LEU
57	N1	29	THR
57	N1	32	LYS
57	N1	47	SER
57	N1	75	ILE
57	N1	78	LYS
57	N1	79	MET
57	N1	80	VAL
57	N1	88	ARG

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Mol	Chain	Res	Type
57	N1	89	LEU
57	N1	92	ARG
57	N1	93	VAL
57	N1	96	ILE
57	N1	102	ARG
57	N1	104	GLU
57	N1	106	LEU
57	N1	122	GLN
57	N1	126	VAL
57	N1	127	GLN
57	N1	128	LEU
57	N1	131	GLN
57	N1	139	ARG
57	N1	146	ASN
57	N1	149	GLN
57	N1	158	THR
58	N2	10	LYS
58	N2	16	THR
58	N2	19	VAL
58	N2	38	ILE
58	N2	49	ASN
58	N2	50	LEU
58	N2	52	ASN
58	N2	59	ASP
58	N2	61	THR
58	N2	74	LYS
58	N2	93	ILE
58	N2	94	ARG
58	N2	100	THR
59	N3	13	ILE
59	N3	36	ILE
59	N3	48	ARG
59	N3	54	LEU
59	N3	69	LEU
59	N3	83	LYS
59	N3	98	ASN
59	N3	102	ILE
59	N3	104	ASN
59	N3	120	LYS
59	N3	124	ASP
59	N3	132	ASN
59	N3	133	SER

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Mol	Chain	Res	Type
59	N3	135	VAL
60	N4	5	ILE
60	N4	7	SER
60	N4	47	ARG
61	N5	25	LYS
61	N5	26	VAL
61	N5	27	ARG
61	N5	29	SER
61	N5	31	THR
61	N5	34	LEU
61	N5	38	LEU
61	N5	39	LYS
61	N5	59	SER
61	N5	63	ILE
61	N5	73	MET
61	N5	87	SER
61	N5	92	LYS
61	N5	105	VAL
61	N5	112	THR
61	N5	113	LEU
61	N5	115	ARG
61	N5	125	ARG
61	N5	133	LEU
61	N5	135	ILE
61	N5	139	ILE
61	N5	142	ILE
62	N6	3	LYS
62	N6	8	VAL
62	N6	10	SER
62	N6	13	ARG
62	N6	28	ARG
62	N6	37	LYS
62	N6	39	LEU
62	N6	48	LEU
62	N6	57	LEU
62	N6	72	SER
62	N6	74	TYR
62	N6	76	LEU
62	N6	78	PHE
62	N6	87	LYS
62	N6	88	GLU
62	N6	90	VAL

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Mol	Chain	Res	Type
62	N6	105	VAL
62	N6	110	HIS
62	N6	115	ARG
62	N6	125	LYS
62	N6	126	LEU
63	N7	17	ARG
63	N7	34	LYS
63	N7	46	ILE
63	N7	57	HIS
63	N7	75	VAL
63	N7	81	LEU
63	N7	86	THR
63	N7	87	LEU
63	N7	90	GLU
63	N7	92	PHE
63	N7	103	GLN
63	N7	132	SER
63	N7	134	LEU
64	N8	4	ARG
64	N8	6	THR
64	N8	8	THR
64	N8	10	LYS
64	N8	16	SER
64	N8	34	MET
64	N8	42	ARG
64	N8	47	LYS
64	N8	56	VAL
64	N8	60	TYR
64	N8	73	LEU
64	N8	74	ASN
64	N8	88	ASP
64	N8	91	LEU
64	N8	97	GLU
64	N8	104	THR
64	N8	115	LYS
64	N8	118	ILE
64	N8	120	ASN
64	N8	130	VAL
64	N8	139	ARG
65	N9	14	ARG
65	N9	22	LYS
65	N9	23	LYS

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Mol	Chain	Res	Type
65	N9	25	LYS
65	N9	28	LYS
65	N9	50	THR
65	N9	59	LYS
66	O0	16	LEU
66	O0	32	LYS
66	O0	33	SER
66	O0	34	LEU
66	O0	41	LEU
66	O0	43	ILE
66	O0	48	THR
66	O0	52	ARG
66	O0	54	SER
66	O0	55	GLU
66	O0	61	MET
66	O0	79	THR
66	O0	83	LYS
66	O0	97	ASP
66	O0	99	ASP
66	O0	104	LEU
67	O1	8	VAL
67	O1	16	LEU
67	O1	26	LYS
67	O1	31	ARG
67	O1	36	ILE
67	O1	55	LEU
67	O1	68	GLU
67	O1	73	LEU
67	O1	75	ILE
67	O1	79	ARG
67	O1	84	ASP
67	O1	86	LYS
67	O1	89	LEU
68	O2	10	VAL
68	O2	16	LYS
68	O2	19	ARG
68	O2	24	ARG
68	O2	26	HIS
68	O2	27	ARG
68	O2	28	VAL
68	O2	33	ARG
68	O2	50	ILE

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Mol	Chain	Res	Type
68	O2	54	LYS
68	O2	61	LYS
68	O2	62	LYS
68	O2	67	SER
68	O2	73	THR
68	O2	75	LEU
68	O2	79	VAL
68	O2	86	THR
68	O2	87	MET
68	O2	88	HIS
68	O2	109	LEU
68	O2	125	ARG
69	O3	4	SER
69	O3	15	SER
69	O3	22	VAL
69	O3	28	SER
69	O3	37	THR
69	O3	45	LEU
69	O3	59	VAL
69	O3	70	LYS
69	O3	80	VAL
69	O3	98	VAL
70	O4	5	VAL
70	O4	8	ARG
70	O4	22	VAL
70	O4	24	LYS
70	O4	49	SER
70	O4	51	LEU
70	O4	52	GLN
70	O4	58	ARG
70	O4	65	VAL
70	O4	68	THR
70	O4	86	LYS
70	O4	88	ARG
70	O4	102	LYS
71	O5	13	SER
71	O5	15	GLU
71	O5	22	VAL
71	O5	27	GLU
71	O5	28	LEU
71	O5	30	GLU
71	O5	31	LEU

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Mol	Chain	Res	Type
71	O5	43	LYS
71	O5	45	LYS
71	O5	47	VAL
71	O5	49	LYS
71	O5	71	LYS
71	O5	85	THR
71	O5	89	ARG
71	O5	101	THR
71	O5	102	GLU
71	O5	104	GLN
71	O5	111	PHE
71	O5	119	LYS
72	O6	7	ILE
72	O6	11	LEU
72	O6	13	LYS
72	O6	21	THR
72	O6	25	LYS
72	O6	26	ILE
72	O6	34	SER
72	O6	36	ARG
72	O6	44	VAL
72	O6	45	ARG
72	O6	57	LEU
72	O6	58	ILE
72	O6	60	LEU
72	O6	62	ARG
72	O6	68	ARG
72	O6	81	THR
72	O6	87	VAL
72	O6	88	GLU
72	O6	99	ARG
73	O7	13	ASN
73	O7	25	ARG
73	O7	28	HIS
73	O7	33	THR
73	O7	36	SER
73	O7	44	THR
73	O7	45	ARG
73	O7	52	LYS
73	O7	58	THR
73	O7	65	ARG
73	O7	67	LEU

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Mol	Chain	Res	Type
73	O7	76	ASN
73	O7	80	THR
74	O8	31	LEU
74	O8	32	ASN
74	O8	40	GLN
74	O8	41	THR
74	O8	50	SER
74	O8	53	THR
74	O8	57	ASN
74	O8	61	LYS
74	O8	64	LYS
74	O8	65	LEU
74	O8	67	GLN
74	O8	72	THR
74	O8	77	ARG
75	O9	4	GLN
75	O9	9	ILE
75	O9	19	GLN
75	O9	21	ARG
75	O9	23	LEU
75	O9	34	THR
75	O9	37	TYR
75	O9	45	ARG
75	O9	51	ILE
76	Q0	77	ILE
76	Q0	78	ILE
76	Q0	83	LYS
76	Q0	85	LEU
76	Q0	99	CYS
76	Q0	106	ARG
76	Q0	112	LYS
76	Q0	113	ARG
76	Q0	127	LEU
77	Q1	2	ARG
77	Q1	11	ARG
77	Q1	13	LEU
77	Q1	17	ARG
77	Q1	19	LYS
77	Q1	21	ARG
78	Q2	3	ASN
78	Q2	8	ARG
78	Q2	16	THR

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Mol	Chain	Res	Type
78	Q2	17	CYS
78	Q2	24	LYS
78	Q2	26	THR
78	Q2	35	LEU
78	Q2	45	ARG
78	Q2	54	THR
78	Q2	60	LYS
78	Q2	61	LYS
78	Q2	64	THR
78	Q2	78	LYS
78	Q2	83	LEU
78	Q2	84	THR
78	Q2	85	LEU
78	Q2	93	LEU
79	Q3	11	THR
79	Q3	16	VAL
79	Q3	45	LYS
79	Q3	49	ARG
79	Q3	57	CYS
79	Q3	71	VAL
79	Q3	73	THR
79	Q3	91	GLU
2	s0	6	THR
2	s0	9	LEU
2	s0	22	THR
2	s0	24	LEU
2	s0	30	GLN
2	s0	37	VAL
2	s0	39	ASN
2	s0	57	LEU
2	s0	59	LEU
2	s0	87	LEU
2	s0	96	THR
2	s0	101	ARG
2	s0	108	THR
2	s0	110	TYR
2	s0	112	THR
2	s0	119	ARG
2	s0	131	GLN
2	s0	135	GLU
2	s0	138	TYR
2	s0	144	ILE

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Mol	Chain	Res	Type
2	s0	165	ARG
2	s0	172	LEU
2	s0	177	LEU
2	s0	179	ARG
2	s0	185	ARG
2	s0	188	LEU
2	s0	189	VAL
2	s0	198	MET
3	s1	26	ARG
3	s1	36	SER
3	s1	37	THR
3	s1	39	GLU
3	s1	47	LEU
3	s1	51	SER
3	s1	62	LYS
3	s1	68	VAL
3	s1	70	LEU
3	s1	74	GLN
3	s1	78	ASP
3	s1	84	ILE
3	s1	89	ASP
3	s1	95	ASN
3	s1	103	MET
3	s1	105	PHE
3	s1	122	GLU
3	s1	125	VAL
3	s1	126	THR
3	s1	152	ARG
3	s1	173	THR
3	s1	181	LEU
3	s1	184	LEU
3	s1	185	THR
3	s1	191	GLU
3	s1	217	LEU
3	s1	219	LYS
3	s1	222	LYS
3	s1	223	PHE
3	s1	228	LEU
3	s1	231	LEU
3	s1	234	GLU
4	s2	53	ILE
4	s2	54	GLU

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Mol	Chain	Res	Type
4	s2	55	GLU
4	s2	69	ILE
4	s2	70	ASP
4	s2	72	LEU
4	s2	80	VAL
4	s2	82	ASN
4	s2	83	ILE
4	s2	90	THR
4	s2	91	ARG
4	s2	97	ARG
4	s2	102	VAL
4	s2	106	ASP
4	s2	107	SER
4	s2	108	ASN
4	s2	111	VAL
4	s2	113	LEU
4	s2	117	THR
4	s2	126	ARG
4	s2	131	ILE
4	s2	141	ARG
4	s2	146	THR
4	s2	159	THR
4	s2	164	SER
4	s2	166	THR
4	s2	167	VAL
4	s2	170	ILE
4	s2	194	GLU
4	s2	198	THR
4	s2	207	LEU
4	s2	209	ASN
4	s2	218	ILE
4	s2	221	THR
4	s2	224	PHE
4	s2	225	LEU
4	s2	226	THR
4	s2	230	TRP
4	s2	232	GLU
4	s2	237	VAL
4	s2	240	LEU
4	s2	242	ILE
5	s3	4	LEU
5	s3	9	ARG

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Mol	Chain	Res	Type
5	s3	21	LEU
5	s3	44	THR
5	s3	59	LEU
5	s3	67	ASN
5	s3	76	ARG
5	s3	84	ILE
5	s3	91	VAL
5	s3	103	GLU
5	s3	115	ILE
5	s3	117	ARG
5	s3	125	TYR
5	s3	127	MET
5	s3	132	LYS
5	s3	158	ILE
5	s3	162	GLN
5	s3	164	VAL
5	s3	176	LEU
5	s3	179	GLN
5	s3	207	THR
5	s3	212	LYS
5	s3	213	GLU
5	s3	224	ASP
6	s4	6	LYS
6	s4	9	LEU
6	s4	22	LYS
6	s4	38	LEU
6	s4	42	LEU
6	s4	49	ARG
6	s4	51	ARG
6	s4	56	LEU
6	s4	57	ASN
6	s4	65	LEU
6	s4	67	GLN
6	s4	73	ASP
6	s4	78	THR
6	s4	92	LEU
6	s4	113	ARG
6	s4	116	ASP
6	s4	131	LEU
6	s4	148	ARG
6	s4	170	THR
6	s4	176	ASP

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Mol	Chain	Res	Type
6	s4	180	LEU
6	s4	182	TYR
6	s4	191	ARG
6	s4	221	ARG
6	s4	223	ASN
6	s4	237	SER
6	s4	246	LEU
6	s4	254	ARG
6	s4	255	ARG
7	s5	25	LEU
7	s5	27	THR
7	s5	31	GLU
7	s5	38	THR
7	s5	45	LYS
7	s5	46	TRP
7	s5	59	VAL
7	s5	63	GLN
7	s5	66	GLN
7	s5	68	ILE
7	s5	76	ARG
7	s5	86	GLN
7	s5	87	CYS
7	s5	93	LEU
7	s5	112	ARG
7	s5	119	ASP
7	s5	137	ILE
7	s5	157	ARG
7	s5	167	ARG
7	s5	194	LEU
7	s5	199	ILE
7	s5	203	LYS
7	s5	206	SER
7	s5	208	SER
7	s5	213	LYS
7	s5	215	ASP
7	s5	219	ARG
8	s6	19	ASP
8	s6	21	GLU
8	s6	57	ASP
8	s6	67	VAL
8	s6	71	THR
8	s6	73	ILE

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Mol	Chain	Res	Type
8	s6	76	LEU
8	s6	78	THR
8	s6	93	LYS
8	s6	109	LEU
8	s6	119	GLN
8	s6	125	THR
8	s6	128	THR
8	s6	151	ASP
8	s6	157	VAL
8	s6	163	THR
8	s6	168	THR
8	s6	169	TYR
8	s6	170	THR
8	s6	175	ILE
8	s6	177	ARG
8	s6	210	GLN
8	s6	211	LEU
8	s6	212	LEU
8	s6	215	ARG
9	s7	11	GLN
9	s7	24	PHE
9	s7	28	GLU
9	s7	33	GLU
9	s7	35	LYS
9	s7	50	ASP
9	s7	64	VAL
9	s7	67	LEU
9	s7	77	LEU
9	s7	80	GLU
9	s7	86	GLN
9	s7	87	ASP
9	s7	90	VAL
9	s7	95	GLU
9	s7	97	ARG
9	s7	110	GLN
9	s7	114	ARG
9	s7	116	ARG
9	s7	117	THR
9	s7	123	ASP
9	s7	125	ILE
9	s7	129	LEU
9	s7	143	LEU

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Mol	Chain	Res	Type
9	s7	144	VAL
9	s7	160	GLN
9	s7	166	LEU
9	s7	185	ILE
10	s8	4	SER
10	s8	10	LYS
10	s8	17	LYS
10	s8	18	ARG
10	s8	25	ARG
10	s8	29	LEU
10	s8	46	VAL
10	s8	59	ARG
10	s8	60	ILE
10	s8	61	GLU
10	s8	89	GLU
10	s8	105	ASP
10	s8	138	ASN
10	s8	152	ILE
10	s8	153	GLU
10	s8	155	SER
10	s8	165	LEU
10	s8	168	CYS
10	s8	175	GLN
10	s8	176	SER
10	s8	184	LEU
10	s8	199	LYS
11	s9	3	ARG
11	s9	7	THR
11	s9	9	SER
11	s9	14	THR
11	s9	21	SER
11	s9	28	LEU
11	s9	49	LEU
11	s9	53	ARG
11	s9	57	ARG
11	s9	71	PHE
11	s9	78	ARG
11	s9	82	ARG
11	s9	87	SER
11	s9	89	ASP
11	s9	93	LEU
11	s9	101	VAL

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Mol	Chain	Res	Type
11	s9	103	ASP
11	s9	105	LEU
11	s9	109	LEU
11	s9	130	THR
11	s9	133	HIS
11	s9	134	ILE
11	s9	143	ILE
11	s9	149	ARG
11	s9	151	ASP
11	s9	156	ILE
11	s9	172	VAL
11	s9	175	ARG
11	s9	180	LYS
11	s9	182	GLU
12	c0	2	LEU
12	c0	5	LYS
12	c0	15	LEU
12	c0	33	GLU
12	c0	36	ASP
12	c0	47	GLN
12	c0	67	THR
12	c0	77	ARG
12	c0	79	TYR
13	c1	4	GLU
13	c1	5	LEU
13	c1	33	ARG
13	c1	40	LEU
13	c1	44	THR
13	c1	46	LYS
13	c1	47	THR
13	c1	56	LYS
13	c1	60	PHE
13	c1	61	THR
13	c1	67	ARG
13	c1	69	LYS
13	c1	74	THR
13	c1	83	THR
13	c1	87	ARG
13	c1	90	TYR
13	c1	111	VAL
13	c1	129	ARG
14	c2	28	LEU

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Mol	Chain	Res	Type
14	c2	43	ARG
14	c2	45	LEU
14	c2	61	VAL
14	c2	62	LEU
14	c2	71	ILE
14	c2	74	LEU
14	c2	85	LYS
14	c2	89	ILE
14	c2	103	LEU
14	c2	125	ASN
14	c2	136	ILE
14	c2	138	GLU
14	c2	140	PHE
15	c3	6	SER
15	c3	20	ARG
15	c3	37	ILE
15	c3	53	LEU
15	c3	60	VAL
15	c3	64	ARG
15	c3	66	ILE
15	c3	67	THR
15	c3	70	LYS
15	c3	76	LYS
15	c3	84	ILE
15	c3	87	ASP
15	c3	102	LEU
15	c3	115	LEU
15	c3	134	VAL
15	c3	138	ASN
16	c4	13	VAL
16	c4	14	PHE
16	c4	26	THR
16	c4	31	THR
16	c4	51	ASP
16	c4	62	LEU
16	c4	79	VAL
16	c4	89	THR
16	c4	103	ARG
16	c4	107	ARG
16	c4	114	ARG
16	c4	118	VAL
16	c4	123	SER

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Mol	Chain	Res	Type
16	c4	124	ASP
16	c4	127	ARG
16	c4	132	ARG
16	c4	133	ARG
16	c4	136	ARG
16	c4	137	LEU
17	c5	12	PHE
17	c5	21	ASP
17	c5	27	GLU
17	c5	36	LEU
17	c5	40	ARG
17	c5	49	MET
17	c5	51	SER
17	c5	69	GLU
17	c5	71	GLU
17	c5	77	ARG
17	c5	102	PHE
17	c5	106	GLU
17	c5	110	GLU
17	c5	121	ILE
17	c5	122	THR
17	c5	134	THR
18	c6	6	SER
18	c6	17	THR
18	c6	23	LYS
18	c6	28	LEU
18	c6	37	THR
18	c6	43	ILE
18	c6	53	LEU
18	c6	57	LEU
18	c6	62	ASN
18	c6	67	VAL
18	c6	69	VAL
18	c6	110	THR
18	c6	114	ARG
18	c6	118	ILE
18	c6	127	LYS
18	c6	128	LYS
18	c6	137	ARG
19	c7	25	THR
19	c7	30	THR
19	c7	34	LEU

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Mol	Chain	Res	Type
19	c7	46	LEU
19	c7	47	ARG
19	c7	49	LYS
19	c7	54	THR
19	c7	69	ILE
19	c7	76	GLU
19	c7	80	ARG
19	c7	85	VAL
19	c7	110	VAL
19	c7	113	LEU
20	c8	3	LEU
20	c8	6	GLN
20	c8	15	LEU
20	c8	18	LEU
20	c8	19	ASN
20	c8	21	ASN
20	c8	33	THR
20	c8	36	LYS
20	c8	55	HIS
20	c8	63	GLN
20	c8	75	ASN
20	c8	85	PHE
20	c8	94	ASP
20	c8	100	THR
20	c8	104	ASN
20	c8	106	GLU
20	c8	109	LEU
20	c8	116	LEU
20	c8	133	VAL
20	c8	136	GLN
20	c8	138	THR
20	c8	141	THR
21	c9	22	LEU
21	c9	27	LYS
21	c9	28	LEU
21	c9	57	ARG
21	c9	68	ARG
21	c9	103	LYS
21	c9	123	ARG
21	c9	126	GLU
21	c9	131	ASP
21	c9	132	LEU

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Mol	Chain	Res	Type
21	c9	140	LEU
22	d0	13	GLU
22	d0	23	ARG
22	d0	27	THR
22	d0	30	LYS
22	d0	36	ASN
22	d0	41	ILE
22	d0	42	VAL
22	d0	44	ASN
22	d0	57	ARG
22	d0	60	THR
22	d0	63	LEU
22	d0	66	SER
22	d0	70	THR
22	d0	72	ASN
22	d0	74	GLU
22	d0	77	LYS
22	d0	81	THR
22	d0	99	ILE
22	d0	107	THR
23	d1	5	LYS
23	d1	12	TYR
23	d1	25	LYS
23	d1	32	VAL
23	d1	33	GLN
23	d1	42	GLU
23	d1	50	TYR
23	d1	62	ARG
23	d1	68	SER
23	d1	69	LEU
23	d1	76	ASP
23	d1	81	ASN
23	d1	82	VAL
24	d2	7	LEU
24	d2	9	ASP
24	d2	15	ASN
24	d2	24	GLN
24	d2	25	VAL
24	d2	28	ARG
24	d2	31	SER
24	d2	47	ILE
24	d2	55	ASP

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Mol	Chain	Res	Type
24	d2	65	LEU
24	d2	68	ARG
24	d2	88	LYS
24	d2	98	GLN
24	d2	103	ILE
24	d2	112	ASP
24	d2	124	LYS
24	d2	126	LEU
24	d2	129	VAL
25	d3	9	LEU
25	d3	15	LEU
25	d3	16	ARG
25	d3	19	ARG
25	d3	28	ASN
25	d3	31	LYS
25	d3	40	SER
25	d3	52	ILE
25	d3	56	LYS
25	d3	73	ARG
25	d3	79	ASN
25	d3	84	THR
25	d3	96	VAL
25	d3	97	ASP
25	d3	100	ASP
25	d3	103	LEU
25	d3	107	PHE
25	d3	121	ARG
25	d3	125	VAL
25	d3	132	LEU
25	d3	144	ARG
26	d4	3	ASP
26	d4	6	THR
26	d4	26	ASP
26	d4	29	HIS
26	d4	30	PRO
26	d4	31	ASN
26	d4	43	LYS
26	d4	44	LEU
26	d4	47	VAL
26	d4	49	LYS
26	d4	55	VAL
26	d4	58	PHE

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Mol	Chain	Res	Type
26	d4	62	THR
26	d4	78	SER
26	d4	86	GLU
26	d4	88	THR
26	d4	91	LEU
26	d4	110	GLN
26	d4	116	LYS
26	d4	125	LEU
27	d5	40	VAL
27	d5	41	ILE
27	d5	43	ASP
27	d5	54	VAL
27	d5	57	TYR
27	d5	60	VAL
27	d5	71	ILE
27	d5	102	THR
28	d6	10	ARG
28	d6	11	ASN
28	d6	24	VAL
28	d6	25	ASN
28	d6	39	MET
28	d6	41	ILE
28	d6	82	ARG
28	d6	89	ARG
28	d6	90	GLU
29	d7	3	LEU
29	d7	34	ASP
29	d7	36	LYS
29	d7	41	LEU
29	d7	43	ILE
29	d7	46	VAL
29	d7	49	HIS
29	d7	52	THR
29	d7	56	CYS
29	d7	59	CYS
29	d7	67	THR
29	d7	72	LYS
29	d7	77	THR
30	d8	28	VAL
30	d8	33	LEU
30	d8	36	THR
30	d8	39	THR

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Mol	Chain	Res	Type
30	d8	42	ARG
30	d8	49	ARG
30	d8	54	LEU
30	d8	57	MET
30	d8	58	GLU
30	d8	64	ARG
30	d8	65	ARG
31	d9	5	ASN
31	d9	10	HIS
31	d9	22	ARG
31	d9	25	SER
31	d9	26	SER
31	d9	31	ILE
31	d9	36	LEU
31	d9	38	ILE
31	d9	39	CYS
31	d9	49	ASP
80	e0	4	VAL
80	e0	13	LYS
80	e0	15	LYS
80	e0	21	VAL
80	e0	23	LYS
80	e0	24	THR
80	e0	26	LYS
80	e0	28	LYS
80	e0	41	THR
80	e0	44	PHE
80	e0	47	VAL
80	e0	48	THR
80	e0	49	LEU
80	e0	50	VAL
80	e0	54	ARG
80	e0	55	ARG
80	e0	62	VAL
33	e1	86	THR
33	e1	90	LYS
33	e1	97	LYS
33	e1	100	LEU
33	e1	103	LEU
33	e1	106	TYR
33	e1	113	LYS
33	e1	115	THR

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Mol	Chain	Res	Type
33	e1	116	LYS
33	e1	117	LEU
33	e1	147	VAL
33	e1	151	ASN
34	sR	5	GLU
34	sR	25	THR
34	sR	48	THR
34	sR	64	HIS
34	sR	66	HIS
34	sR	74	THR
34	sR	76	ASP
34	sR	135	THR
34	sR	136	ILE
34	sR	145	LEU
34	sR	159	ASN
34	sR	160	GLU
34	sR	164	ASP
34	sR	197	SER
34	sR	245	PHE
34	sR	250	TYR
34	sR	275	ARG
34	sR	286	GLU
34	sR	297	ASP
35	sM	34	LYS
35	sM	37	VAL
35	sM	41	SER
35	sM	48	ARG
35	sM	49	LYS
35	sM	50	ASN
35	sM	68	ARG
35	sM	69	ARG
35	sM	74	LYS
35	sM	75	ASP
39	l2	7	ASN
39	l2	15	ILE
39	l2	23	ARG
39	l2	32	LEU
39	l2	33	ASP
39	l2	45	VAL
39	l2	47	GLN
39	l2	74	GLU
39	l2	79	ASN

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Mol	Chain	Res	Type
39	12	86	GLN
39	12	96	LEU
39	12	101	VAL
39	12	104	LEU
39	12	109	GLU
39	12	112	ILE
39	12	116	VAL
39	12	137	ILE
39	12	147	ARG
39	12	149	ARG
39	12	157	VAL
39	12	158	ILE
39	12	159	SER
39	12	165	VAL
39	12	179	LEU
39	12	180	LEU
39	12	193	ARG
39	12	194	ASN
39	12	216	HIS
39	12	217	GLN
39	12	224	THR
39	12	230	VAL
39	12	241	ARG
39	12	242	ARG
39	12	246	LEU
39	12	249	SER
40	13	3	HIS
40	13	4	ARG
40	13	5	LYS
40	13	10	ARG
40	13	17	LEU
40	13	20	LYS
40	13	24	SER
40	13	37	ARG
40	13	43	LEU
40	13	55	THR
40	13	56	ILE
40	13	70	ARG
40	13	77	THR
40	13	84	VAL
40	13	85	VAL
40	13	103	THR

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Mol	Chain	Res	Type
40	l3	104	THR
40	l3	110	LEU
40	l3	114	VAL
40	l3	116	ARG
40	l3	120	LYS
40	l3	139	GLN
40	l3	148	LEU
40	l3	150	ARG
40	l3	169	THR
40	l3	171	LEU
40	l3	183	LEU
40	l3	187	SER
40	l3	188	ILE
40	l3	192	VAL
40	l3	193	ASP
40	l3	196	ARG
40	l3	205	VAL
40	l3	207	SER
40	l3	208	VAL
40	l3	211	GLN
40	l3	214	MET
40	l3	229	VAL
40	l3	232	ARG
40	l3	246	LEU
40	l3	247	ARG
40	l3	252	ILE
40	l3	266	ARG
40	l3	274	SER
40	l3	284	ARG
40	l3	316	GLU
40	l3	324	VAL
40	l3	328	ILE
40	l3	332	ARG
40	l3	340	LYS
40	l3	341	SER
40	l3	347	SER
40	l3	348	ARG
40	l3	355	SER
40	l3	364	LYS
40	l3	367	LYS
40	l3	382	THR
41	l4	16	THR

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Mol	Chain	Res	Type
41	14	27	SER
41	14	33	ASP
41	14	37	THR
41	14	43	ASN
41	14	47	ARG
41	14	55	LYS
41	14	63	GLU
41	14	67	THR
41	14	69	ARG
41	14	71	VAL
41	14	92	ASN
41	14	93	MET
41	14	99	MET
41	14	112	LYS
41	14	118	LYS
41	14	120	TYR
41	14	136	LEU
41	14	138	ARG
41	14	144	LYS
41	14	148	ILE
41	14	150	LEU
41	14	151	VAL
41	14	160	GLN
41	14	172	VAL
41	14	179	LEU
41	14	187	LEU
41	14	193	LYS
41	14	200	THR
41	14	203	ARG
41	14	206	LEU
41	14	217	LYS
41	14	220	ARG
41	14	222	VAL
41	14	227	THR
41	14	230	VAL
41	14	258	LEU
41	14	283	THR
41	14	313	LEU
41	14	319	LYS
41	14	327	LEU
41	14	333	VAL
41	14	339	LEU

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Mol	Chain	Res	Type
41	14	345	GLU
41	14	347	THR
41	14	359	LEU
42	15	5	LYS
42	15	9	SER
42	15	34	LYS
42	15	38	THR
42	15	41	LYS
42	15	51	LEU
42	15	52	VAL
42	15	61	ILE
42	15	65	ILE
42	15	70	THR
42	15	73	VAL
42	15	75	LEU
42	15	81	HIS
42	15	89	THR
42	15	110	LEU
42	15	111	GLN
42	15	112	LYS
42	15	113	LEU
42	15	118	THR
42	15	122	VAL
42	15	128	GLU
42	15	132	THR
42	15	133	GLU
42	15	135	VAL
42	15	137	ASP
42	15	140	ARG
42	15	146	LEU
42	15	148	ILE
42	15	155	THR
42	15	171	LEU
42	15	185	PHE
42	15	187	THR
42	15	189	GLU
42	15	203	HIS
42	15	206	GLN
42	15	208	MET
42	15	211	LEU
42	15	227	LEU
42	15	230	ASP

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Mol	Chain	Res	Type
42	15	241	THR
42	15	242	SER
42	15	258	LYS
42	15	259	LYS
42	15	260	PHE
42	15	265	TYR
42	15	268	GLU
42	15	273	ARG
42	15	275	THR
42	15	293	LEU
42	15	297	GLN
43	16	4	GLN
43	16	5	LYS
43	16	12	SER
43	16	15	VAL
43	16	21	THR
43	16	31	ARG
43	16	46	ARG
43	16	48	ARG
43	16	50	LYS
43	16	57	HIS
43	16	64	LEU
43	16	65	ILE
43	16	78	ARG
43	16	88	SER
43	16	91	VAL
43	16	94	GLU
43	16	98	VAL
43	16	105	TYR
43	16	109	GLU
43	16	131	LYS
43	16	152	THR
43	16	154	LEU
43	16	155	LEU
44	17	33	ARG
44	17	41	ARG
44	17	83	LEU
44	17	88	ARG
44	17	93	ASN
44	17	110	ARG
44	17	121	LYS
44	17	124	LEU

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Mol	Chain	Res	Type
44	17	130	ILE
44	17	153	PHE
44	17	156	ILE
44	17	158	LYS
44	17	165	ASP
44	17	173	LEU
44	17	175	LYS
44	17	176	TYR
44	17	179	LEU
44	17	184	LEU
44	17	189	ILE
44	17	194	HIS
44	17	196	LYS
44	17	225	GLN
44	17	228	SER
44	17	229	PHE
44	17	239	LEU
45	18	41	GLN
45	18	50	VAL
45	18	68	ARG
45	18	71	VAL
45	18	74	THR
45	18	79	GLN
45	18	109	LEU
45	18	134	TYR
45	18	136	LEU
45	18	149	LYS
45	18	150	LEU
45	18	153	ILE
45	18	160	ILE
45	18	163	VAL
45	18	169	LEU
45	18	172	LYS
45	18	180	VAL
45	18	183	LYS
45	18	185	ARG
45	18	200	LEU
45	18	211	LEU
45	18	232	HIS
45	18	245	LYS
45	18	248	LYS
46	19	1	MET

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Mol	Chain	Res	Type
46	19	5	GLN
46	19	6	THR
46	19	17	THR
46	19	18	VAL
46	19	40	HIS
46	19	44	THR
46	19	52	LEU
46	19	55	VAL
46	19	62	ARG
46	19	68	LEU
46	19	69	ARG
46	19	73	SER
46	19	80	THR
46	19	106	LYS
46	19	107	ASP
46	19	118	LEU
46	19	120	ASP
46	19	122	LYS
46	19	132	VAL
46	19	133	THR
46	19	143	GLU
46	19	144	ILE
46	19	146	LEU
46	19	151	VAL
46	19	157	ASN
46	19	161	LEU
46	19	167	VAL
46	19	173	ARG
46	19	179	ILE
46	19	184	LYS
46	19	186	PHE
46	19	187	ILE
46	19	191	LEU
47	m0	3	ARG
47	m0	4	ARG
47	m0	21	ARG
47	m0	26	VAL
47	m0	35	ASP
47	m0	36	LEU
47	m0	42	THR
47	m0	48	LEU
47	m0	52	LEU

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Mol	Chain	Res	Type
47	m0	55	ASN
47	m0	57	LEU
47	m0	58	GLU
47	m0	63	GLU
47	m0	71	CYS
47	m0	87	LEU
47	m0	121	LYS
47	m0	125	LEU
47	m0	130	ASP
47	m0	137	SER
47	m0	140	THR
47	m0	150	GLU
47	m0	154	ARG
47	m0	156	ARG
47	m0	163	GLN
47	m0	167	LEU
47	m0	169	LYS
47	m0	177	ASP
47	m0	185	ARG
47	m0	205	SER
47	m0	212	GLU
48	m1	7	ASN
48	m1	10	ARG
48	m1	12	LEU
48	m1	46	VAL
48	m1	47	GLN
48	m1	56	THR
48	m1	60	ARG
48	m1	80	LEU
48	m1	87	LYS
48	m1	95	ASN
48	m1	97	SER
48	m1	101	ASN
48	m1	106	ILE
48	m1	107	ASP
48	m1	119	SER
48	m1	130	VAL
48	m1	137	ARG
48	m1	140	ARG
48	m1	142	LYS
48	m1	148	VAL
48	m1	153	LYS

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Mol	Chain	Res	Type
48	m1	155	THR
48	m1	156	LYS
48	m1	159	THR
48	m1	161	SER
48	m1	171	VAL
48	m1	174	LYS
49	m3	4	SER
49	m3	15	ARG
49	m3	46	ILE
49	m3	54	LEU
49	m3	57	VAL
49	m3	58	VAL
49	m3	67	ARG
49	m3	69	VAL
49	m3	73	ARG
49	m3	107	GLU
49	m3	115	ARG
49	m3	118	GLU
49	m3	123	ILE
49	m3	128	ARG
49	m3	131	LYS
49	m3	160	GLN
49	m3	168	ARG
49	m3	183	ARG
49	m3	184	GLU
49	m3	189	GLU
50	m4	4	ASP
50	m4	12	TRP
50	m4	15	VAL
50	m4	25	LYS
50	m4	28	SER
50	m4	37	GLU
50	m4	53	VAL
50	m4	58	ILE
50	m4	62	GLN
50	m4	63	VAL
50	m4	64	VAL
50	m4	70	PHE
50	m4	72	LEU
50	m4	91	CYS
50	m4	107	GLU
50	m4	115	PHE

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Mol	Chain	Res	Type
50	m4	123	LEU
50	m4	126	GLN
50	m4	130	THR
50	m4	135	LEU
51	m5	5	LYS
51	m5	7	LEU
51	m5	10	LEU
51	m5	12	ARG
51	m5	19	LEU
51	m5	22	LEU
51	m5	49	ARG
51	m5	76	PRO
51	m5	80	THR
51	m5	96	ARG
51	m5	105	ARG
51	m5	106	VAL
51	m5	109	ARG
51	m5	117	ASN
51	m5	138	GLN
51	m5	142	ILE
51	m5	152	CYS
51	m5	153	ASP
51	m5	176	LYS
51	m5	178	HIS
51	m5	179	LYS
51	m5	183	THR
51	m5	188	ARG
51	m5	201	ARG
51	m5	204	LYS
52	m6	22	VAL
52	m6	34	VAL
52	m6	43	ILE
52	m6	67	THR
52	m6	78	ARG
52	m6	85	ARG
52	m6	100	GLU
52	m6	106	GLU
52	m6	115	LYS
52	m6	126	VAL
52	m6	130	LYS
52	m6	142	SER
52	m6	143	THR

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Mol	Chain	Res	Type
52	m6	175	THR
52	m6	188	SER
53	m7	7	THR
53	m7	8	SER
53	m7	9	THR
53	m7	14	SER
53	m7	23	ARG
53	m7	24	VAL
53	m7	41	LEU
53	m7	52	LEU
53	m7	55	GLN
53	m7	72	GLN
53	m7	89	LYS
53	m7	114	VAL
53	m7	115	SER
53	m7	119	VAL
53	m7	120	ASN
53	m7	124	LYS
53	m7	126	ARG
53	m7	138	LYS
53	m7	144	SER
53	m7	148	LEU
53	m7	152	GLU
53	m7	155	GLU
54	m8	7	SER
54	m8	17	THR
54	m8	23	ASN
54	m8	24	VAL
54	m8	26	LEU
54	m8	32	LEU
54	m8	57	ILE
54	m8	63	SER
54	m8	69	ARG
54	m8	80	THR
54	m8	111	ARG
54	m8	113	LYS
54	m8	135	GLN
54	m8	147	ARG
54	m8	155	MET
54	m8	161	LYS
54	m8	165	ILE
54	m8	178	ARG

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Mol	Chain	Res	Type
54	m8	180	ARG
54	m8	181	SER
55	m9	6	THR
55	m9	10	LEU
55	m9	13	SER
55	m9	17	VAL
55	m9	20	ARG
55	m9	30	SER
55	m9	31	GLU
55	m9	36	ASN
55	m9	43	LYS
55	m9	63	THR
55	m9	74	ARG
55	m9	88	ARG
55	m9	106	LEU
55	m9	128	LYS
55	m9	134	HIS
55	m9	138	LEU
55	m9	148	ASP
55	m9	152	GLU
55	m9	153	LYS
55	m9	156	ASN
55	m9	173	ARG
55	m9	186	LYS
56	n0	1	MET
56	n0	17	GLU
56	n0	19	VAL
56	n0	21	GLU
56	n0	32	SER
56	n0	34	GLU
56	n0	52	LYS
56	n0	73	LYS
56	n0	80	ARG
56	n0	82	ASP
56	n0	87	THR
56	n0	88	HIS
56	n0	96	ASP
56	n0	97	VAL
56	n0	98	SER
56	n0	99	ARG
56	n0	100	VAL
56	n0	103	VAL

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Mol	Chain	Res	Type
56	n0	104	GLU
56	n0	105	THR
56	n0	117	ARG
56	n0	119	ARG
56	n0	120	SER
56	n0	130	GLU
56	n0	132	THR
56	n0	136	LYS
56	n0	137	ARG
56	n0	142	GLN
56	n0	145	THR
56	n0	148	LEU
56	n0	155	ARG
56	n0	160	THR
56	n0	162	THR
56	n0	172	TYR
57	n1	12	ARG
57	n1	18	ASP
57	n1	25	VAL
57	n1	27	LEU
57	n1	35	LYS
57	n1	71	SER
57	n1	76	ILE
57	n1	78	LYS
57	n1	80	VAL
57	n1	83	ARG
57	n1	86	GLU
57	n1	88	ARG
57	n1	89	LEU
57	n1	93	VAL
57	n1	103	GLN
57	n1	104	GLU
57	n1	112	ASN
57	n1	124	VAL
57	n1	126	VAL
57	n1	127	GLN
57	n1	131	GLN
57	n1	139	ARG
57	n1	141	VAL
57	n1	143	THR
57	n1	144	GLU
57	n1	149	GLN

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Mol	Chain	Res	Type
57	n1	150	THR
57	n1	151	LEU
57	n1	154	VAL
58	n2	16	THR
58	n2	27	VAL
58	n2	37	LEU
58	n2	38	ILE
58	n2	43	VAL
58	n2	49	ASN
58	n2	54	VAL
58	n2	55	THR
58	n2	58	GLU
58	n2	62	VAL
58	n2	68	THR
58	n2	72	SER
58	n2	75	TYR
58	n2	100	THR
59	n3	4	ASN
59	n3	7	GLN
59	n3	9	THR
59	n3	13	ILE
59	n3	14	SER
59	n3	22	ILE
59	n3	48	ARG
59	n3	72	LYS
59	n3	88	ARG
59	n3	98	ASN
59	n3	101	VAL
59	n3	124	ASP
60	n4	1	MET
60	n4	9	SER
60	n4	17	ARG
60	n4	27	LYS
60	n4	54	LEU
60	n4	57	LYS
60	n4	96	LEU
60	n4	109	LEU
60	n4	123	ARG
60	n4	127	LYS
60	n4	133	THR
61	n5	24	LEU
61	n5	27	ARG

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Mol	Chain	Res	Type
61	n5	29	SER
61	n5	37	THR
61	n5	38	LEU
61	n5	39	LYS
61	n5	56	ARG
61	n5	57	LEU
61	n5	63	ILE
61	n5	73	MET
61	n5	109	LYS
61	n5	112	THR
61	n5	115	ARG
61	n5	125	ARG
61	n5	134	ASP
61	n5	135	ILE
62	n6	7	ASP
62	n6	12	ARG
62	n6	13	ARG
62	n6	32	SER
62	n6	37	LYS
62	n6	40	ARG
62	n6	45	ILE
62	n6	50	ILE
62	n6	51	ARG
62	n6	56	VAL
62	n6	59	VAL
62	n6	66	GLN
62	n6	67	GLU
62	n6	74	TYR
62	n6	120	GLN
63	n7	17	ARG
63	n7	24	VAL
63	n7	26	VAL
63	n7	33	SER
63	n7	34	LYS
63	n7	52	LYS
63	n7	54	THR
63	n7	65	ARG
63	n7	66	THR
63	n7	72	ILE
63	n7	81	LEU
63	n7	83	THR
63	n7	85	TYR

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Mol	Chain	Res	Type
63	n7	90	GLU
63	n7	99	GLU
63	n7	100	THR
63	n7	103	GLN
63	n7	114	VAL
63	n7	126	LYS
63	n7	128	GLN
64	n8	6	THR
64	n8	8	THR
64	n8	15	VAL
64	n8	26	ARG
64	n8	27	LYS
64	n8	42	ARG
64	n8	44	ASN
64	n8	46	ASP
64	n8	60	TYR
64	n8	64	GLN
64	n8	67	HIS
64	n8	73	LEU
64	n8	85	ASP
64	n8	91	LEU
64	n8	97	GLU
64	n8	98	THR
64	n8	103	ASP
64	n8	128	ARG
64	n8	130	VAL
64	n8	132	LYS
64	n8	133	LEU
65	n9	19	ASN
65	n9	21	ILE
65	n9	26	THR
65	n9	33	LYS
65	n9	40	ARG
65	n9	59	LYS
66	o0	9	SER
66	o0	19	LYS
66	o0	40	LYS
66	o0	41	LEU
66	o0	50	VAL
66	o0	52	ARG
66	o0	61	MET
66	o0	86	ARG

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Mol	Chain	Res	Type
66	o0	100	ILE
66	o0	104	LEU
67	o1	13	THR
67	o1	16	LEU
67	o1	24	SER
67	o1	31	ARG
67	o1	44	MET
67	o1	46	THR
67	o1	54	GLU
67	o1	55	LEU
67	o1	68	GLU
67	o1	83	GLU
67	o1	90	PHE
67	o1	91	SER
67	o1	93	VAL
67	o1	106	THR
67	o1	107	VAL
68	o2	4	LEU
68	o2	14	THR
68	o2	15	LYS
68	o2	19	ARG
68	o2	24	ARG
68	o2	27	ARG
68	o2	33	ARG
68	o2	35	GLN
68	o2	41	VAL
68	o2	50	ILE
68	o2	61	LYS
68	o2	71	HIS
68	o2	72	LYS
68	o2	73	THR
68	o2	75	LEU
68	o2	81	ASP
68	o2	82	LEU
68	o2	86	THR
68	o2	87	MET
68	o2	109	LEU
68	o2	113	LYS
68	o2	119	VAL
68	o2	125	ARG
68	o2	126	LEU
69	o3	9	VAL

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Mol	Chain	Res	Type
69	o3	10	LYS
69	o3	37	THR
69	o3	49	ILE
69	o3	58	GLU
69	o3	60	ARG
69	o3	70	LYS
69	o3	80	VAL
69	o3	81	VAL
69	o3	88	ASN
69	o3	98	VAL
70	o4	5	VAL
70	o4	6	THR
70	o4	22	VAL
70	o4	25	THR
70	o4	29	ILE
70	o4	30	LEU
70	o4	46	ASP
70	o4	57	LEU
70	o4	58	ARG
70	o4	65	VAL
70	o4	66	SER
70	o4	71	THR
70	o4	80	ARG
70	o4	85	VAL
70	o4	88	ARG
70	o4	100	ILE
70	o4	101	VAL
71	o5	13	SER
71	o5	20	GLN
71	o5	21	LEU
71	o5	27	GLU
71	o5	28	LEU
71	o5	36	LEU
71	o5	38	ARG
71	o5	45	LYS
71	o5	46	THR
71	o5	47	VAL
71	o5	62	GLN
71	o5	68	GLN
71	o5	79	ASP
71	o5	81	ARG
71	o5	84	LYS

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Mol	Chain	Res	Type
71	o5	86	ARG
71	o5	89	ARG
71	o5	107	LYS
71	o5	119	LYS
72	o6	3	VAL
72	o6	7	ILE
72	o6	9	ILE
72	o6	20	MET
72	o6	21	THR
72	o6	29	LYS
72	o6	34	SER
72	o6	35	ASN
72	o6	36	ARG
72	o6	43	LEU
72	o6	44	VAL
72	o6	45	ARG
72	o6	57	LEU
72	o6	58	ILE
72	o6	60	LEU
72	o6	68	ARG
72	o6	74	LYS
72	o6	76	ARG
72	o6	94	ILE
72	o6	98	ARG
73	o7	3	LYS
73	o7	15	SER
73	o7	17	THR
73	o7	21	ARG
73	o7	24	ARG
73	o7	25	ARG
73	o7	26	SER
73	o7	33	THR
73	o7	44	THR
73	o7	55	ARG
73	o7	58	THR
73	o7	59	THR
73	o7	65	ARG
73	o7	67	LEU
73	o7	75	LYS
73	o7	80	THR
73	o7	84	SER
74	o8	8	ILE

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Mol	Chain	Res	Type
74	o8	14	LEU
74	o8	16	ARG
74	o8	22	THR
74	o8	24	THR
74	o8	31	LEU
74	o8	53	THR
74	o8	57	ASN
74	o8	61	LYS
74	o8	64	LYS
75	o9	5	LYS
75	o9	15	LYS
75	o9	21	ARG
75	o9	23	LEU
75	o9	45	ARG
76	q0	79	GLU
76	q0	83	LYS
76	q0	85	LEU
76	q0	88	LYS
76	q0	97	ARG
76	q0	99	CYS
76	q0	108	THR
76	q0	110	CYS
76	q0	112	LYS
76	q0	113	ARG
76	q0	127	LEU
77	q1	2	ARG
77	q1	13	LEU
77	q1	14	LYS
77	q1	17	ARG
77	q1	21	ARG
77	q1	23	ARG
78	q2	2	VAL
78	q2	7	THR
78	q2	8	ARG
78	q2	16	THR
78	q2	21	THR
78	q2	22	GLN
78	q2	26	THR
78	q2	32	LYS
78	q2	35	LEU
78	q2	38	GLN
78	q2	45	ARG

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Mol	Chain	Res	Type
78	q2	47	GLN
78	q2	48	SER
78	q2	61	LYS
78	q2	71	ARG
78	q2	73	GLU
78	q2	78	LYS
78	q2	83	LEU
78	q2	84	THR
78	q2	85	LEU
78	q2	93	LEU
78	q2	104	LEU
78	q2	105	GLN
78	q2	106	PHE
79	q3	3	LYS
79	q3	4	ARG
79	q3	13	LYS
79	q3	16	VAL
79	q3	24	ARG
79	q3	38	ASP
79	q3	42	CYS
79	q3	54	ILE
79	q3	56	THR
79	q3	58	SER
79	q3	64	VAL
79	q3	79	VAL
79	q3	82	THR
79	q3	89	MET
82	p0	4	ILE
82	p0	5	ARG
82	p0	6	GLU
82	p0	39	HIS
82	p0	42	ARG
82	p0	43	LYS
82	p0	48	ARG
82	p0	51	VAL
82	p0	52	LEU
82	p0	66	PHE
82	p0	67	LEU
82	p0	69	ASP
82	p0	70	LEU
82	p0	72	ASP
82	p0	76	LEU

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Mol	Chain	Res	Type
82	p0	81	LYS
82	p0	91	GLU
82	p0	93	LEU
82	p0	97	LYS
84	f	12	ASP
84	f	16	SER
84	f	37	ARG
84	f	49	THR
84	f	52	HIS
84	f	54	HIS
84	f	58	HIS
84	f	78	HIS
84	f	79	ASN
84	f	102	LEU
84	f	105	MET
84	f	106	ASP
84	f	108	ASP
84	f	109	THR
84	f	120	LEU
84	f	133	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (61) such sidechains are listed below:

Mol	Chain	Res	Type
2	S0	23	HIS
3	S1	79	HIS
3	S1	95	ASN
5	S3	159	HIS
7	S5	103	ASN
9	S7	71	HIS
9	S7	180	GLN
12	C0	39	ASN
23	D1	75	ASN
34	SR	52	GLN
34	SR	184	ASN
35	SM	108	GLN
39	L2	132	ASN
40	L3	371	GLN
41	L4	59	GLN
41	L4	328	ASN
41	L4	361	HIS
43	L6	28	GLN

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Mol	Chain	Res	Type
43	L6	57	HIS
44	L7	37	ASN
44	L7	48	ASN
44	L7	159	GLN
46	L9	50	ASN
47	M0	59	GLN
48	M1	109	HIS
51	M5	194	GLN
53	M7	101	ASN
56	N0	138	GLN
57	N1	146	ASN
65	N9	19	ASN
70	O4	18	ASN
73	O7	76	ASN
75	O9	11	GLN
75	O9	19	GLN
7	s5	72	HIS
9	s7	71	HIS
9	s7	74	GLN
10	s8	138	ASN
12	c0	32	HIS
20	c8	89	GLN
23	d1	3	ASN
24	d2	56	HIS
27	d5	44	GLN
28	d6	69	ASN
29	d7	19	HIS
34	sR	237	GLN
40	l3	211	GLN
40	l3	231	HIS
42	l5	81	HIS
44	l7	172	ASN
46	l9	8	GLN
47	m0	12	GLN
51	m5	11	GLN
52	m6	42	ASN
54	m8	5	HIS
56	n0	157	GLN
61	n5	65	GLN
63	n7	57	HIS
64	n8	49	HIS
70	o4	18	ASN

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Mol	Chain	Res	Type
75	o9	4	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1776/1800 (98%)	463 (26%)	42 (2%)
1	6	1791/1800 (99%)	450 (25%)	35 (1%)
36	1	3145/3396 (92%)	683 (21%)	65 (2%)
36	5	3145/3396 (92%)	661 (21%)	65 (2%)
37	3	120/121 (99%)	20 (16%)	1 (0%)
37	7	120/121 (99%)	15 (12%)	1 (0%)
38	4	157/158 (99%)	33 (21%)	3 (1%)
38	8	157/158 (99%)	32 (20%)	1 (0%)
85	B	1/4 (25%)	1 (100%)	0
85	C	1/4 (25%)	0	0
All	All	10413/10958 (95%)	2358 (22%)	213 (2%)

All (2358) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	23	G
1	2	25	C
1	2	26	A
1	2	27	U
1	2	34	G
1	2	45	U
1	2	47	A
1	2	49	C
1	2	50	C
1	2	57	G
1	2	60	U
1	2	63	G
1	2	68	A
1	2	69	G
1	2	72	A
1	2	73	U
1	2	74	U
1	2	75	U
1	2	76	A

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Mol	Chain	Res	Type
1	2	77	U
1	2	90	C
1	2	104	A
1	2	105	A
1	2	114	C
1	2	128	U
1	2	131	C
1	2	132	U
1	2	133	U
1	2	134	U
1	2	135	A
1	2	136	C
1	2	137	U
1	2	140	A
1	2	141	U
1	2	144	U
1	2	145	A
1	2	146	U
1	2	153	G
1	2	158	U
1	2	159	U
1	2	161	U
1	2	178	U
1	2	179	A
1	2	184	C
1	2	185	U
1	2	186	C
1	2	187	G
1	2	190	C
1	2	191	C
1	2	192	U
1	2	193	U
1	2	195	G
1	2	196	G
1	2	197	A
1	2	200	A
1	2	215	A
1	2	217	A
1	2	219	A
1	2	227	U
1	2	228	G
1	2	229	U

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Mol	Chain	Res	Type
1	2	233	C
1	2	234	G
1	2	235	G
1	2	238	U
1	2	240	U
1	2	241	U
1	2	243	G
1	2	249	U
1	2	250	C
1	2	257	A
1	2	260	U
1	2	261	U
1	2	262	U
1	2	265	A
1	2	267	U
1	2	270	C
1	2	271	A
1	2	272	U
1	2	275	C
1	2	276	C
1	2	277	U
1	2	278	U
1	2	279	G
1	2	280	U
1	2	281	G
1	2	288	A
1	2	290	G
1	2	292	U
1	2	299	A
1	2	302	U
1	2	309	C
1	2	314	C
1	2	316	A
1	2	320	U
1	2	321	C
1	2	322	G
1	2	323	A
1	2	333	A
1	2	337	G
1	2	338	C
1	2	341	A
1	2	352	A

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Mol	Chain	Res	Type
1	2	356	G
1	2	359	A
1	2	360	A
1	2	361	C
1	2	380	U
1	2	390	G
1	2	400	A
1	2	402	C
1	2	404	G
1	2	416	A
1	2	418	G
1	2	419	G
1	2	421	A
1	2	424	C
1	2	425	A
1	2	426	G
1	2	428	A
1	2	434	G
1	2	437	A
1	2	439	U
1	2	444	C
1	2	452	A
1	2	455	C
1	2	468	A
1	2	470	A
1	2	475	A
1	2	480	G
1	2	484	C
1	2	485	A
1	2	488	G
1	2	493	U
1	2	495	C
1	2	496	G
1	2	497	G
1	2	498	G
1	2	499	U
1	2	500	C
1	2	502	U
1	2	503	G
1	2	504	U
1	2	505	A
1	2	506	A

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Mol	Chain	Res	Type
1	2	507	U
1	2	510	G
1	2	511	A
1	2	513	U
1	2	515	A
1	2	516	G
1	2	527	A
1	2	532	U
1	2	538	A
1	2	539	G
1	2	540	G
1	2	541	A
1	2	542	A
1	2	543	C
1	2	544	A
1	2	547	U
1	2	548	G
1	2	555	A
1	2	556	A
1	2	557	G
1	2	558	U
1	2	559	C
1	2	565	C
1	2	578	U
1	2	579	A
1	2	580	A
1	2	585	A
1	2	594	A
1	2	595	G
1	2	596	C
1	2	605	A
1	2	606	A
1	2	609	U
1	2	610	G
1	2	611	U
1	2	614	C
1	2	617	U
1	2	619	A
1	2	620	A
1	2	622	A
1	2	623	A
1	2	624	G

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Mol	Chain	Res	Type
1	2	628	G
1	2	630	A
1	2	639	U
1	2	650	U
1	2	653	C
1	2	655	G
1	2	656	G
1	2	657	U
1	2	658	C
1	2	680	U
1	2	684	A
1	2	694	U
1	2	696	C
1	2	697	C
1	2	700	C
1	2	703	G
1	2	704	C
1	2	705	U
1	2	706	A
1	2	707	A
1	2	709	C
1	2	710	U
1	2	711	U
1	2	712	G
1	2	714	G
1	2	717	C
1	2	718	U
1	2	719	U
1	2	720	G
1	2	721	U
1	2	722	G
1	2	723	G
1	2	725	U
1	2	727	U
1	2	731	C
1	2	732	G
1	2	733	A
1	2	734	A
1	2	735	C
1	2	736	C
1	2	737	A
1	2	738	G

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Mol	Chain	Res	Type
1	2	741	C
1	2	742	U
1	2	754	A
1	2	755	A
1	2	756	A
1	2	765	G
1	2	766	U
1	2	774	A
1	2	775	G
1	2	777	C
1	2	778	G
1	2	781	U
1	2	783	G
1	2	784	C
1	2	789	A
1	2	794	U
1	2	807	A
1	2	812	A
1	2	815	G
1	2	816	G
1	2	818	C
1	2	819	G
1	2	820	U
1	2	821	U
1	2	823	G
1	2	824	G
1	2	829	A
1	2	830	U
1	2	831	U
1	2	833	U
1	2	841	U
1	2	846	G
1	2	856	A
1	2	863	A
1	2	864	U
1	2	865	A
1	2	876	G
1	2	886	U
1	2	896	U
1	2	898	A
1	2	912	U
1	2	913	G

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Mol	Chain	Res	Type
1	2	914	G
1	2	915	A
1	2	916	U
1	2	926	A
1	2	933	A
1	2	935	U
1	2	942	G
1	2	951	A
1	2	960	U
1	2	966	A
1	2	970	A
1	2	977	A
1	2	985	G
1	2	988	A
1	2	992	A
1	2	993	A
1	2	997	G
1	2	1003	A
1	2	1004	U
1	2	1005	A
1	2	1024	U
1	2	1025	A
1	2	1026	A
1	2	1028	C
1	2	1040	G
1	2	1043	A
1	2	1053	G
1	2	1058	U
1	2	1059	U
1	2	1060	U
1	2	1061	A
1	2	1062	A
1	2	1073	G
1	2	1081	A
1	2	1082	C
1	2	1087	A
1	2	1091	A
1	2	1092	A
1	2	1096	C
1	2	1097	U
1	2	1098	U
1	2	1100	G

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Mol	Chain	Res	Type
1	2	1109	G
1	2	1138	A
1	2	1139	A
1	2	1143	A
1	2	1146	G
1	2	1150	G
1	2	1151	A
1	2	1157	A
1	2	1158	C
1	2	1159	C
1	2	1160	A
1	2	1164	G
1	2	1167	G
1	2	1185	U
1	2	1191	U
1	2	1194	A
1	2	1196	A
1	2	1199	G
1	2	1200	G
1	2	1202	A
1	2	1207	C
1	2	1208	A
1	2	1217	A
1	2	1218	G
1	2	1227	A
1	2	1228	G
1	2	1229	G
1	2	1243	G
1	2	1244	A
1	2	1245	G
1	2	1251	U
1	2	1258	U
1	2	1275	A
1	2	1276	U
1	2	1285	U
1	2	1286	U
1	2	1301	U
1	2	1314	U
1	2	1315	U
1	2	1316	G
1	2	1321	A
1	2	1337	A

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Mol	Chain	Res	Type
1	2	1340	U
1	2	1341	A
1	2	1344	A
1	2	1345	A
1	2	1350	U
1	2	1355	C
1	2	1361	U
1	2	1362	U
1	2	1363	U
1	2	1364	G
1	2	1370	U
1	2	1371	A
1	2	1372	U
1	2	1390	U
1	2	1398	U
1	2	1400	A
1	2	1412	G
1	2	1413	U
1	2	1414	U
1	2	1415	U
1	2	1420	C
1	2	1424	A
1	2	1427	A
1	2	1428	G
1	2	1432	U
1	2	1435	G
1	2	1436	A
1	2	1446	A
1	2	1456	C
1	2	1458	G
1	2	1459	C
1	2	1460	A
1	2	1462	G
1	2	1464	G
1	2	1471	A
1	2	1473	U
1	2	1474	G
1	2	1478	G
1	2	1482	C
1	2	1485	C
1	2	1486	G
1	2	1489	U

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Mol	Chain	Res	Type
1	2	1490	C
1	2	1491	U
1	2	1492	A
1	2	1493	A
1	2	1506	G
1	2	1515	A
1	2	1516	A
1	2	1517	U
1	2	1518	C
1	2	1521	G
1	2	1523	G
1	2	1524	A
1	2	1526	A
1	2	1535	U
1	2	1536	G
1	2	1537	C
1	2	1538	U
1	2	1539	G
1	2	1540	G
1	2	1542	G
1	2	1557	U
1	2	1559	A
1	2	1569	A
1	2	1572	G
1	2	1573	A
1	2	1574	G
1	2	1584	G
1	2	1590	G
1	2	1601	G
1	2	1614	A
1	2	1616	G
1	2	1619	C
1	2	1631	A
1	2	1657	U
1	2	1658	G
1	2	1680	G
1	2	1682	U
1	2	1683	C
1	2	1684	U
1	2	1698	G
1	2	1699	G
1	2	1700	C

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Mol	Chain	Res	Type
1	2	1701	A
1	2	1702	A
1	2	1712	A
1	2	1713	G
1	2	1731	A
1	2	1734	U
1	2	1740	A
1	2	1754	A
1	2	1760	G
1	2	1762	A
1	2	1766	A
1	2	1769	U
1	2	1770	U
1	2	1777	G
1	2	1780	G
1	2	1782	A
1	2	1783	C
1	2	1792	G
1	2	1793	G
1	2	1794	A
1	2	1795	U
1	2	1796	C
36	1	13	A
36	1	14	U
36	1	16	A
36	1	26	A
36	1	40	A
36	1	43	A
36	1	45	A
36	1	49	A
36	1	59	G
36	1	60	A
36	1	65	A
36	1	66	A
36	1	74	G
36	1	75	G
36	1	92	G
36	1	93	C
36	1	94	G
36	1	99	A
36	1	109	A
36	1	110	G

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Mol	Chain	Res	Type
36	1	111	C
36	1	113	C
36	1	116	A
36	1	117	U
36	1	121	A
36	1	122	A
36	1	130	A
36	1	131	C
36	1	133	U
36	1	136	G
36	1	146	U
36	1	147	U
36	1	156	G
36	1	157	A
36	1	161	G
36	1	166	C
36	1	176	G
36	1	187	A
36	1	190	U
36	1	191	U
36	1	192	C
36	1	205	C
36	1	206	G
36	1	210	U
36	1	213	A
36	1	218	G
36	1	219	A
36	1	240	U
36	1	241	G
36	1	243	G
36	1	249	U
36	1	250	U
36	1	251	G
36	1	252	U
36	1	269	G
36	1	270	U
36	1	286	U
36	1	295	A
36	1	298	U
36	1	315	C
36	1	316	U
36	1	319	A

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Mol	Chain	Res	Type
36	1	323	A
36	1	329	U
36	1	339	C
36	1	349	A
36	1	350	C
36	1	351	A
36	1	376	G
36	1	397	A
36	1	398	A
36	1	399	A
36	1	401	U
36	1	402	A
36	1	403	C
36	1	414	U
36	1	421	G
36	1	422	A
36	1	438	A
36	1	439	C
36	1	440	A
36	1	495	G
36	1	520	U
36	1	521	A
36	1	535	G
36	1	543	C
36	1	544	C
36	1	546	C
36	1	547	G
36	1	548	G
36	1	552	G
36	1	555	U
36	1	556	U
36	1	557	A
36	1	558	U
36	1	559	A
36	1	569	A
36	1	578	A
36	1	579	G
36	1	592	A
36	1	596	C
36	1	597	G
36	1	604	G
36	1	607	A

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Mol	Chain	Res	Type
36	1	609	G
36	1	611	A
36	1	620	U
36	1	621	A
36	1	636	C
36	1	638	C
36	1	649	A
36	1	660	A
36	1	677	A
36	1	681	U
36	1	683	U
36	1	691	A
36	1	705	A
36	1	709	A
36	1	712	G
36	1	715	A
36	1	716	A
36	1	719	U
36	1	720	A
36	1	725	G
36	1	764	U
36	1	765	C
36	1	766	U
36	1	767	U
36	1	776	U
36	1	777	U
36	1	781	G
36	1	785	G
36	1	787	G
36	1	802	C
36	1	806	A
36	1	817	A
36	1	827	A
36	1	830	A
36	1	849	C
36	1	851	C
36	1	861	C
36	1	874	U
36	1	879	U
36	1	890	C
36	1	896	A
36	1	907	G

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Mol	Chain	Res	Type
36	1	908	G
36	1	914	A
36	1	916	G
36	1	917	A
36	1	921	A
36	1	923	C
36	1	924	G
36	1	925	A
36	1	937	G
36	1	944	C
36	1	953	G
36	1	959	C
36	1	960	U
36	1	967	A
36	1	978	G
36	1	979	U
36	1	980	A
36	1	981	U
36	1	982	C
36	1	994	G
36	1	1001	G
36	1	1002	A
36	1	1003	A
36	1	1006	A
36	1	1010	G
36	1	1013	G
36	1	1017	C
36	1	1018	G
36	1	1020	G
36	1	1021	G
36	1	1024	G
36	1	1025	A
36	1	1029	G
36	1	1036	A
36	1	1037	C
36	1	1047	A
36	1	1049	C
36	1	1064	A
36	1	1065	A
36	1	1071	U
36	1	1072	G
36	1	1079	A

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Mol	Chain	Res	Type
36	1	1080	A
36	1	1081	U
36	1	1083	G
36	1	1093	A
36	1	1094	U
36	1	1095	U
36	1	1097	G
36	1	1098	A
36	1	1103	A
36	1	1104	G
36	1	1117	G
36	1	1129	A
36	1	1131	G
36	1	1144	U
36	1	1145	G
36	1	1153	A
36	1	1159	A
36	1	1161	G
36	1	1168	U
36	1	1179	A
36	1	1180	A
36	1	1181	U
36	1	1182	A
36	1	1185	C
36	1	1190	A
36	1	1191	U
36	1	1192	C
36	1	1193	A
36	1	1201	C
36	1	1202	A
36	1	1209	G
36	1	1213	G
36	1	1216	C
36	1	1217	A
36	1	1221	A
36	1	1222	G
36	1	1227	C
36	1	1232	C
36	1	1233	G
36	1	1235	U
36	1	1236	G
36	1	1241	U

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Mol	Chain	Res	Type
36	1	1243	G
36	1	1245	A
36	1	1246	G
36	1	1248	C
36	1	1249	G
36	1	1251	A
36	1	1253	U
36	1	1254	C
36	1	1258	U
36	1	1262	G
36	1	1263	A
36	1	1264	G
36	1	1265	U
36	1	1266	G
36	1	1269	U
36	1	1270	A
36	1	1271	A
36	1	1274	A
36	1	1278	A
36	1	1279	C
36	1	1280	C
36	1	1285	G
36	1	1287	A
36	1	1292	C
36	1	1294	A
36	1	1296	C
36	1	1308	A
36	1	1309	U
36	1	1313	G
36	1	1315	U
36	1	1318	A
36	1	1330	A
36	1	1331	U
36	1	1332	A
36	1	1348	U
36	1	1349	G
36	1	1350	A
36	1	1351	U
36	1	1352	A
36	1	1353	U
36	1	1355	A
36	1	1356	U

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Mol	Chain	Res	Type
36	1	1357	G
36	1	1386	A
36	1	1387	G
36	1	1398	U
36	1	1399	A
36	1	1400	G
36	1	1402	C
36	1	1405	U
36	1	1408	G
36	1	1411	C
36	1	1417	G
36	1	1418	A
36	1	1419	A
36	1	1429	G
36	1	1431	G
36	1	1433	A
36	1	1434	G
36	1	1435	A
36	1	1437	C
36	1	1443	G
36	1	1446	A
36	1	1450	G
36	1	1460	A
36	1	1481	A
36	1	1482	A
36	1	1485	G
36	1	1496	C
36	1	1502	C
36	1	1508	C
36	1	1521	G
36	1	1527	C
36	1	1533	U
36	1	1536	G
36	1	1542	G
36	1	1555	U
36	1	1556	C
36	1	1560	G
36	1	1561	G
36	1	1562	C
36	1	1563	C
36	1	1564	U
36	1	1567	U

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Mol	Chain	Res	Type
36	1	1568	U
36	1	1569	U
36	1	1570	U
36	1	1571	A
36	1	1572	U
36	1	1576	G
36	1	1580	A
36	1	1582	C
36	1	1583	A
36	1	1587	A
36	1	1589	A
36	1	1593	A
36	1	1596	C
36	1	1605	A
36	1	1607	U
36	1	1608	C
36	1	1620	U
36	1	1629	U
36	1	1630	U
36	1	1632	A
36	1	1639	C
36	1	1641	U
36	1	1643	A
36	1	1657	C
36	1	1665	C
36	1	1677	G
36	1	1683	A
36	1	1688	U
36	1	1713	G
36	1	1715	A
36	1	1716	U
36	1	1717	U
36	1	1724	U
36	1	1725	C
36	1	1729	A
36	1	1736	G
36	1	1741	A
36	1	1742	U
36	1	1750	A
36	1	1751	G
36	1	1761	C
36	1	1763	U

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Mol	Chain	Res	Type
36	1	1764	U
36	1	1765	U
36	1	1766	G
36	1	1767	C
36	1	1770	G
36	1	1780	G
36	1	1793	C
36	1	1797	A
36	1	1810	A
36	1	1812	G
36	1	1813	A
36	1	1814	A
36	1	1815	U
36	1	1816	A
36	1	1817	G
36	1	1819	U
36	1	1820	U
36	1	1821	U
36	1	1822	C
36	1	1835	A
36	1	1839	A
36	1	1841	A
36	1	1842	A
36	1	1845	G
36	1	1846	C
36	1	1849	C
36	1	1850	A
36	1	1863	G
36	1	1866	C
36	1	1879	A
36	1	1880	U
36	1	1886	A
36	1	1906	G
36	1	1908	A
36	1	1926	C
36	1	1927	G
36	1	1935	G
36	1	1937	U
36	1	1951	C
36	1	1952	G
36	1	2094	C
36	1	2100	A

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Mol	Chain	Res	Type
36	1	2101	C
36	1	2102	U
36	1	2107	A
36	1	2111	G
36	1	2112	U
36	1	2113	A
36	1	2114	C
36	1	2115	G
36	1	2121	G
36	1	2122	G
36	1	2130	G
36	1	2131	A
36	1	2134	G
36	1	2139	A
36	1	2140	U
36	1	2144	A
36	1	2158	A
36	1	2169	G
36	1	2170	U
36	1	2171	G
36	1	2187	G
36	1	2188	A
36	1	2195	C
36	1	2201	G
36	1	2205	U
36	1	2208	A
36	1	2209	U
36	1	2210	G
36	1	2223	A
36	1	2228	A
36	1	2239	G
36	1	2244	A
36	1	2248	C
36	1	2249	G
36	1	2250	G
36	1	2251	G
36	1	2255	A
36	1	2256	A
36	1	2272	G
36	1	2281	A
36	1	2282	U
36	1	2287	C

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Mol	Chain	Res	Type
36	1	2288	G
36	1	2307	G
36	1	2309	A
36	1	2310	U
36	1	2313	A
36	1	2314	U
36	1	2315	G
36	1	2323	G
36	1	2334	U
36	1	2336	U
36	1	2342	U
36	1	2350	C
36	1	2361	A
36	1	2367	A
36	1	2372	A
36	1	2373	A
36	1	2374	C
36	1	2375	G
36	1	2385	G
36	1	2393	G
36	1	2394	G
36	1	2397	A
36	1	2401	A
36	1	2402	A
36	1	2403	G
36	1	2404	A
36	1	2411	U
36	1	2418	G
36	1	2419	A
36	1	2428	U
36	1	2429	G
36	1	2435	G
36	1	2437	G
36	1	2438	A
36	1	2444	C
36	1	2445	A
36	1	2502	A
36	1	2503	G
36	1	2508	U
36	1	2511	A
36	1	2514	U
36	1	2515	A

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Mol	Chain	Res	Type
36	1	2522	G
36	1	2523	A
36	1	2531	C
36	1	2533	G
36	1	2534	G
36	1	2537	U
36	1	2538	U
36	1	2539	C
36	1	2540	A
36	1	2541	U
36	1	2542	U
36	1	2543	U
36	1	2547	A
36	1	2548	C
36	1	2549	G
36	1	2552	C
36	1	2554	A
36	1	2555	G
36	1	2556	C
36	1	2560	C
36	1	2561	A
36	1	2562	A
36	1	2568	C
36	1	2569	A
36	1	2570	U
36	1	2571	U
36	1	2572	C
36	1	2573	G
36	1	2576	G
36	1	2580	A
36	1	2581	U
36	1	2585	G
36	1	2586	G
36	1	2593	A
36	1	2594	C
36	1	2606	G
36	1	2607	G
36	1	2614	G
36	1	2635	A
36	1	2637	A
36	1	2638	C
36	1	2652	U

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Mol	Chain	Res	Type
36	1	2656	A
36	1	2659	G
36	1	2672	G
36	1	2674	A
36	1	2675	C
36	1	2677	G
36	1	2681	U
36	1	2689	A
36	1	2691	A
36	1	2694	A
36	1	2696	A
36	1	2705	A
36	1	2708	C
36	1	2714	G
36	1	2716	U
36	1	2728	G
36	1	2729	U
36	1	2752	U
36	1	2753	G
36	1	2758	A
36	1	2769	A
36	1	2772	C
36	1	2777	G
36	1	2778	G
36	1	2781	U
36	1	2796	G
36	1	2800	G
36	1	2801	A
36	1	2803	A
36	1	2810	C
36	1	2814	G
36	1	2817	A
36	1	2818	U
36	1	2819	A
36	1	2830	G
36	1	2842	U
36	1	2843	U
36	1	2845	A
36	1	2860	U
36	1	2871	G
36	1	2872	A
36	1	2873	U

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Mol	Chain	Res	Type
36	1	2876	C
36	1	2887	A
36	1	2897	A
36	1	2898	G
36	1	2899	C
36	1	2916	U
36	1	2923	U
36	1	2925	C
36	1	2935	U
36	1	2936	A
36	1	2940	A
36	1	2942	C
36	1	2943	G
36	1	2947	G
36	1	2960	C
36	1	2971	A
36	1	2977	G
36	1	2979	U
36	1	2983	C
36	1	2990	G
36	1	2996	U
36	1	2997	G
36	1	3011	A
36	1	3012	A
36	1	3025	C
36	1	3030	G
36	1	3040	A
36	1	3050	U
36	1	3056	U
36	1	3059	G
36	1	3065	G
36	1	3074	G
36	1	3078	U
36	1	3079	U
36	1	3080	G
36	1	3086	A
36	1	3092	C
36	1	3097	C
36	1	3098	G
36	1	3104	U
36	1	3122	A
36	1	3129	A

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Mol	Chain	Res	Type
36	1	3130	A
36	1	3131	U
36	1	3141	A
36	1	3142	A
36	1	3143	C
36	1	3151	U
36	1	3153	U
36	1	3154	C
36	1	3155	U
36	1	3156	U
36	1	3157	U
36	1	3164	C
36	1	3165	A
36	1	3167	A
36	1	3168	A
36	1	3170	A
36	1	3171	U
36	1	3173	G
36	1	3174	A
36	1	3176	G
36	1	3179	U
36	1	3181	C
36	1	3187	A
36	1	3196	U
36	1	3207	U
36	1	3210	A
36	1	3217	C
36	1	3218	A
36	1	3219	G
36	1	3229	G
36	1	3239	G
36	1	3243	A
36	1	3244	A
36	1	3245	A
36	1	3246	G
36	1	3247	G
36	1	3253	G
36	1	3257	C
36	1	3259	U
36	1	3269	U
36	1	3270	U
36	1	3276	G

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Mol	Chain	Res	Type
36	1	3281	U
36	1	3286	G
36	1	3289	G
36	1	3294	A
36	1	3303	G
36	1	3304	U
36	1	3307	A
36	1	3313	U
36	1	3316	A
36	1	3318	G
36	1	3319	U
36	1	3320	A
36	1	3341	U
36	1	3342	A
36	1	3345	G
36	1	3347	A
36	1	3350	C
36	1	3351	U
36	1	3352	U
36	1	3353	G
36	1	3354	U
36	1	3355	U
36	1	3356	G
36	1	3368	U
36	1	3369	G
36	1	3375	A
36	1	3376	A
36	1	3378	C
36	1	3382	U
36	1	3383	G
36	1	3388	C
36	1	3389	U
36	1	3396	U
37	3	7	G
37	3	10	C
37	3	11	A
37	3	13	A
37	3	22	A
37	3	29	C
37	3	41	G
37	3	53	U
37	3	55	A

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Mol	Chain	Res	Type
37	3	60	G
37	3	65	G
37	3	68	C
37	3	74	C
37	3	76	A
37	3	90	U
37	3	101	G
37	3	102	A
37	3	104	A
37	3	112	G
37	3	121	U
38	4	16	G
38	4	23	U
38	4	34	U
38	4	35	C
38	4	51	G
38	4	59	A
38	4	62	C
38	4	63	G
38	4	69	U
38	4	70	G
38	4	71	A
38	4	75	G
38	4	80	A
38	4	81	U
38	4	82	U
38	4	83	C
38	4	85	G
38	4	86	U
38	4	87	G
38	4	90	U
38	4	95	G
38	4	96	A
38	4	102	U
38	4	104	A
38	4	106	C
38	4	111	A
38	4	113	U
38	4	125	U
38	4	126	A
38	4	128	U
38	4	138	A

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Mol	Chain	Res	Type
38	4	152	G
38	4	155	A
1	6	2	A
1	6	11	A
1	6	17	C
1	6	25	C
1	6	26	A
1	6	27	U
1	6	34	G
1	6	47	A
1	6	57	G
1	6	60	U
1	6	63	G
1	6	65	A
1	6	67	A
1	6	68	A
1	6	69	G
1	6	72	A
1	6	75	U
1	6	76	A
1	6	77	U
1	6	101	U
1	6	104	A
1	6	114	C
1	6	115	G
1	6	132	U
1	6	137	U
1	6	138	A
1	6	140	A
1	6	141	U
1	6	142	G
1	6	143	G
1	6	144	U
1	6	145	A
1	6	146	U
1	6	153	G
1	6	159	U
1	6	161	U
1	6	162	A
1	6	166	C
1	6	178	U
1	6	179	A

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Mol	Chain	Res	Type
1	6	181	A
1	6	184	C
1	6	185	U
1	6	187	G
1	6	188	A
1	6	190	C
1	6	191	C
1	6	192	U
1	6	193	U
1	6	194	U
1	6	195	G
1	6	196	G
1	6	199	G
1	6	200	A
1	6	215	A
1	6	216	U
1	6	217	A
1	6	218	A
1	6	219	A
1	6	220	A
1	6	226	A
1	6	227	U
1	6	228	G
1	6	230	C
1	6	232	U
1	6	233	C
1	6	234	G
1	6	235	G
1	6	238	U
1	6	240	U
1	6	241	U
1	6	250	C
1	6	261	U
1	6	262	U
1	6	265	A
1	6	266	A
1	6	267	U
1	6	270	C
1	6	271	A
1	6	272	U
1	6	273	G
1	6	277	U

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Mol	Chain	Res	Type
1	6	278	U
1	6	280	U
1	6	287	G
1	6	299	A
1	6	302	U
1	6	314	C
1	6	316	A
1	6	319	U
1	6	320	U
1	6	321	C
1	6	322	G
1	6	337	G
1	6	338	C
1	6	341	A
1	6	344	A
1	6	352	A
1	6	359	A
1	6	360	A
1	6	361	C
1	6	378	A
1	6	385	A
1	6	390	G
1	6	400	A
1	6	401	A
1	6	402	C
1	6	404	G
1	6	416	A
1	6	423	G
1	6	424	C
1	6	425	A
1	6	426	G
1	6	434	G
1	6	438	A
1	6	439	U
1	6	444	C
1	6	448	C
1	6	454	U
1	6	468	A
1	6	475	A
1	6	477	A
1	6	480	G
1	6	484	C

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Mol	Chain	Res	Type
1	6	486	G
1	6	488	G
1	6	489	C
1	6	490	C
1	6	492	A
1	6	493	U
1	6	494	U
1	6	496	G
1	6	500	C
1	6	501	U
1	6	504	U
1	6	505	A
1	6	506	A
1	6	508	U
1	6	510	G
1	6	511	A
1	6	512	A
1	6	513	U
1	6	515	A
1	6	519	C
1	6	536	C
1	6	538	A
1	6	539	G
1	6	540	G
1	6	541	A
1	6	542	A
1	6	543	C
1	6	544	A
1	6	548	G
1	6	555	A
1	6	556	A
1	6	557	G
1	6	558	U
1	6	559	C
1	6	565	C
1	6	568	G
1	6	570	A
1	6	574	G
1	6	577	G
1	6	579	A
1	6	580	A
1	6	594	A

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Mol	Chain	Res	Type
1	6	595	G
1	6	597	G
1	6	606	A
1	6	609	U
1	6	610	G
1	6	611	U
1	6	619	A
1	6	620	A
1	6	623	A
1	6	624	G
1	6	637	C
1	6	639	U
1	6	651	G
1	6	652	G
1	6	653	C
1	6	659	C
1	6	660	G
1	6	661	A
1	6	662	U
1	6	665	U
1	6	667	U
1	6	669	G
1	6	670	U
1	6	676	G
1	6	679	U
1	6	681	U
1	6	682	C
1	6	683	C
1	6	684	A
1	6	685	A
1	6	687	G
1	6	690	G
1	6	695	U
1	6	696	C
1	6	697	C
1	6	698	U
1	6	709	C
1	6	710	U
1	6	711	U
1	6	717	C
1	6	719	U
1	6	720	G

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Mol	Chain	Res	Type
1	6	721	U
1	6	722	G
1	6	730	G
1	6	742	U
1	6	743	U
1	6	751	G
1	6	754	A
1	6	755	A
1	6	756	A
1	6	765	G
1	6	766	U
1	6	767	U
1	6	774	A
1	6	775	G
1	6	780	A
1	6	781	U
1	6	782	U
1	6	783	G
1	6	787	G
1	6	789	A
1	6	792	U
1	6	793	A
1	6	794	U
1	6	811	A
1	6	812	A
1	6	814	A
1	6	815	G
1	6	821	U
1	6	823	G
1	6	825	U
1	6	826	U
1	6	829	A
1	6	830	U
1	6	832	U
1	6	833	U
1	6	834	G
1	6	835	U
1	6	842	C
1	6	844	A
1	6	861	U
1	6	862	A
1	6	863	A

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Mol	Chain	Res	Type
1	6	864	U
1	6	865	A
1	6	871	G
1	6	876	G
1	6	886	U
1	6	898	A
1	6	906	A
1	6	911	U
1	6	913	G
1	6	914	G
1	6	933	A
1	6	935	U
1	6	942	G
1	6	944	A
1	6	946	U
1	6	958	U
1	6	959	U
1	6	960	U
1	6	966	A
1	6	969	C
1	6	992	A
1	6	993	A
1	6	997	G
1	6	1003	A
1	6	1004	U
1	6	1005	A
1	6	1020	A
1	6	1021	C
1	6	1026	A
1	6	1028	C
1	6	1029	U
1	6	1032	G
1	6	1039	A
1	6	1040	G
1	6	1052	U
1	6	1053	G
1	6	1057	U
1	6	1058	U
1	6	1059	U
1	6	1060	U
1	6	1061	A
1	6	1063	U

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Mol	Chain	Res	Type
1	6	1071	U
1	6	1081	A
1	6	1082	C
1	6	1091	A
1	6	1092	A
1	6	1096	C
1	6	1097	U
1	6	1098	U
1	6	1099	U
1	6	1100	G
1	6	1137	A
1	6	1138	A
1	6	1149	G
1	6	1151	A
1	6	1154	G
1	6	1155	G
1	6	1158	C
1	6	1159	C
1	6	1160	A
1	6	1164	G
1	6	1167	G
1	6	1185	U
1	6	1191	U
1	6	1194	A
1	6	1196	A
1	6	1197	C
1	6	1199	G
1	6	1200	G
1	6	1202	A
1	6	1207	C
1	6	1217	A
1	6	1218	G
1	6	1227	A
1	6	1228	G
1	6	1229	G
1	6	1230	A
1	6	1235	C
1	6	1239	U
1	6	1240	U
1	6	1243	G
1	6	1244	A
1	6	1245	G

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Mol	Chain	Res	Type
1	6	1246	C
1	6	1256	A
1	6	1257	U
1	6	1258	U
1	6	1273	G
1	6	1275	A
1	6	1284	C
1	6	1285	U
1	6	1286	U
1	6	1288	G
1	6	1291	G
1	6	1293	U
1	6	1314	U
1	6	1315	U
1	6	1316	G
1	6	1320	U
1	6	1321	A
1	6	1335	U
1	6	1344	A
1	6	1345	A
1	6	1354	G
1	6	1361	U
1	6	1362	U
1	6	1363	U
1	6	1364	G
1	6	1367	G
1	6	1370	U
1	6	1371	A
1	6	1388	A
1	6	1390	U
1	6	1398	U
1	6	1399	C
1	6	1400	A
1	6	1402	G
1	6	1413	U
1	6	1414	U
1	6	1415	U
1	6	1427	A
1	6	1428	G
1	6	1445	G
1	6	1446	A
1	6	1448	G

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Mol	Chain	Res	Type
1	6	1458	G
1	6	1459	C
1	6	1461	C
1	6	1469	A
1	6	1471	A
1	6	1473	U
1	6	1481	C
1	6	1482	C
1	6	1486	G
1	6	1490	C
1	6	1491	U
1	6	1492	A
1	6	1493	A
1	6	1494	C
1	6	1506	G
1	6	1514	U
1	6	1515	A
1	6	1516	A
1	6	1517	U
1	6	1521	G
1	6	1523	G
1	6	1524	A
1	6	1535	U
1	6	1536	G
1	6	1537	C
1	6	1538	U
1	6	1540	G
1	6	1554	U
1	6	1557	U
1	6	1559	A
1	6	1569	A
1	6	1574	G
1	6	1582	U
1	6	1584	G
1	6	1600	A
1	6	1601	G
1	6	1603	U
1	6	1621	U
1	6	1634	C
1	6	1636	C
1	6	1637	C
1	6	1638	G

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Mol	Chain	Res	Type
1	6	1657	U
1	6	1658	G
1	6	1697	G
1	6	1698	G
1	6	1699	G
1	6	1700	C
1	6	1701	A
1	6	1702	A
1	6	1712	A
1	6	1713	G
1	6	1716	C
1	6	1717	G
1	6	1736	G
1	6	1754	A
1	6	1755	A
1	6	1760	G
1	6	1762	A
1	6	1766	A
1	6	1767	G
1	6	1769	U
1	6	1780	G
1	6	1782	A
1	6	1783	C
1	6	1788	G
1	6	1789	G
1	6	1791	A
1	6	1792	G
1	6	1793	G
1	6	1794	A
1	6	1796	C
1	6	1799	U
1	6	1800	A
36	5	14	U
36	5	15	C
36	5	26	A
36	5	30	G
36	5	31	C
36	5	40	A
36	5	49	A
36	5	57	A
36	5	59	G
36	5	60	A

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Mol	Chain	Res	Type
36	5	65	A
36	5	66	A
36	5	72	C
36	5	73	C
36	5	74	G
36	5	76	G
36	5	89	A
36	5	92	G
36	5	93	C
36	5	96	G
36	5	99	A
36	5	109	A
36	5	110	G
36	5	111	C
36	5	116	A
36	5	120	G
36	5	121	A
36	5	122	A
36	5	124	U
36	5	133	U
36	5	134	U
36	5	135	C
36	5	136	G
36	5	150	A
36	5	152	U
36	5	156	G
36	5	157	A
36	5	165	A
36	5	166	C
36	5	170	G
36	5	171	G
36	5	173	G
36	5	174	C
36	5	181	U
36	5	182	U
36	5	184	U
36	5	187	A
36	5	190	U
36	5	191	U
36	5	210	U
36	5	213	A
36	5	218	G

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Mol	Chain	Res	Type
36	5	219	A
36	5	221	A
36	5	231	G
36	5	235	A
36	5	236	G
36	5	239	G
36	5	240	U
36	5	243	G
36	5	245	U
36	5	248	U
36	5	249	U
36	5	250	U
36	5	251	G
36	5	252	U
36	5	253	A
36	5	254	A
36	5	269	G
36	5	284	A
36	5	286	U
36	5	295	A
36	5	323	A
36	5	329	U
36	5	334	A
36	5	338	A
36	5	339	C
36	5	349	A
36	5	350	C
36	5	351	A
36	5	374	A
36	5	375	A
36	5	376	G
36	5	382	U
36	5	398	A
36	5	399	A
36	5	401	U
36	5	402	A
36	5	403	C
36	5	421	G
36	5	422	A
36	5	436	A
36	5	437	G
36	5	438	A

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Mol	Chain	Res	Type
36	5	439	C
36	5	441	U
36	5	442	G
36	5	492	U
36	5	496	C
36	5	507	U
36	5	520	U
36	5	521	A
36	5	523	A
36	5	531	G
36	5	532	A
36	5	533	A
36	5	543	C
36	5	546	C
36	5	547	G
36	5	548	G
36	5	553	U
36	5	555	U
36	5	557	A
36	5	559	A
36	5	565	U
36	5	569	A
36	5	578	A
36	5	579	G
36	5	589	A
36	5	592	A
36	5	594	U
36	5	595	G
36	5	600	G
36	5	604	G
36	5	607	A
36	5	609	G
36	5	611	A
36	5	612	U
36	5	619	A
36	5	620	U
36	5	636	C
36	5	649	A
36	5	660	A
36	5	677	A
36	5	681	U
36	5	691	A

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Mol	Chain	Res	Type
36	5	692	A
36	5	705	A
36	5	708	G
36	5	712	G
36	5	715	A
36	5	716	A
36	5	720	A
36	5	726	G
36	5	727	G
36	5	741	U
36	5	742	G
36	5	758	C
36	5	763	G
36	5	766	U
36	5	767	U
36	5	768	C
36	5	776	U
36	5	777	U
36	5	781	G
36	5	785	G
36	5	786	A
36	5	806	A
36	5	817	A
36	5	830	A
36	5	850	U
36	5	861	C
36	5	869	G
36	5	874	U
36	5	879	U
36	5	891	G
36	5	895	A
36	5	896	A
36	5	897	U
36	5	907	G
36	5	908	G
36	5	910	G
36	5	913	A
36	5	914	A
36	5	916	G
36	5	917	A
36	5	924	G
36	5	936	A

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Mol	Chain	Res	Type
36	5	937	G
36	5	944	C
36	5	959	C
36	5	960	U
36	5	963	G
36	5	968	G
36	5	974	G
36	5	979	U
36	5	981	U
36	5	993	G
36	5	994	G
36	5	1001	G
36	5	1002	A
36	5	1006	A
36	5	1010	G
36	5	1014	U
36	5	1015	U
36	5	1016	C
36	5	1017	C
36	5	1018	G
36	5	1019	G
36	5	1021	G
36	5	1024	G
36	5	1025	A
36	5	1026	A
36	5	1028	U
36	5	1029	G
36	5	1032	C
36	5	1035	G
36	5	1047	A
36	5	1049	C
36	5	1064	A
36	5	1065	A
36	5	1072	G
36	5	1081	U
36	5	1082	U
36	5	1085	A
36	5	1093	A
36	5	1095	U
36	5	1097	G
36	5	1098	A
36	5	1103	A

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Mol	Chain	Res	Type
36	5	1104	G
36	5	1117	G
36	5	1131	G
36	5	1152	G
36	5	1153	A
36	5	1159	A
36	5	1160	C
36	5	1161	G
36	5	1174	G
36	5	1180	A
36	5	1181	U
36	5	1191	U
36	5	1192	C
36	5	1193	A
36	5	1196	C
36	5	1201	C
36	5	1202	A
36	5	1209	G
36	5	1222	G
36	5	1223	A
36	5	1232	C
36	5	1235	U
36	5	1236	G
36	5	1237	G
36	5	1239	C
36	5	1241	U
36	5	1242	G
36	5	1245	A
36	5	1246	G
36	5	1248	C
36	5	1253	U
36	5	1258	U
36	5	1262	G
36	5	1263	A
36	5	1264	G
36	5	1265	U
36	5	1266	G
36	5	1281	G
36	5	1285	G
36	5	1305	U
36	5	1307	G
36	5	1308	A

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Mol	Chain	Res	Type
36	5	1309	U
36	5	1313	G
36	5	1324	U
36	5	1330	A
36	5	1331	U
36	5	1349	G
36	5	1351	U
36	5	1352	A
36	5	1353	U
36	5	1355	A
36	5	1356	U
36	5	1357	G
36	5	1368	U
36	5	1380	G
36	5	1385	C
36	5	1386	A
36	5	1387	G
36	5	1399	A
36	5	1400	G
36	5	1419	A
36	5	1421	G
36	5	1431	G
36	5	1433	A
36	5	1434	G
36	5	1437	C
36	5	1438	U
36	5	1446	A
36	5	1450	G
36	5	1481	A
36	5	1482	A
36	5	1508	C
36	5	1527	C
36	5	1536	G
36	5	1548	C
36	5	1554	U
36	5	1555	U
36	5	1556	C
36	5	1557	A
36	5	1560	G
36	5	1561	G
36	5	1562	C
36	5	1567	U

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Mol	Chain	Res	Type
36	5	1568	U
36	5	1570	U
36	5	1571	A
36	5	1572	U
36	5	1574	C
36	5	1575	A
36	5	1576	G
36	5	1577	G
36	5	1578	C
36	5	1579	C
36	5	1580	A
36	5	1581	C
36	5	1582	C
36	5	1583	A
36	5	1587	A
36	5	1589	A
36	5	1605	A
36	5	1607	U
36	5	1620	U
36	5	1629	U
36	5	1639	C
36	5	1643	A
36	5	1644	C
36	5	1645	U
36	5	1675	G
36	5	1677	G
36	5	1683	A
36	5	1713	G
36	5	1716	U
36	5	1724	U
36	5	1725	C
36	5	1736	G
36	5	1750	A
36	5	1751	G
36	5	1761	C
36	5	1762	C
36	5	1764	U
36	5	1765	U
36	5	1766	G
36	5	1770	G
36	5	1775	G
36	5	1780	G

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Mol	Chain	Res	Type
36	5	1793	C
36	5	1797	A
36	5	1810	A
36	5	1813	A
36	5	1814	A
36	5	1815	U
36	5	1816	A
36	5	1817	G
36	5	1818	U
36	5	1821	U
36	5	1839	A
36	5	1841	A
36	5	1842	A
36	5	1846	C
36	5	1849	C
36	5	1850	A
36	5	1863	G
36	5	1864	A
36	5	1878	G
36	5	1879	A
36	5	1880	U
36	5	1893	A
36	5	1906	G
36	5	1926	C
36	5	2100	A
36	5	2101	C
36	5	2102	U
36	5	2111	G
36	5	2112	U
36	5	2113	A
36	5	2114	C
36	5	2121	G
36	5	2122	G
36	5	2129	U
36	5	2131	A
36	5	2134	G
36	5	2144	A
36	5	2149	A
36	5	2158	A
36	5	2169	G
36	5	2170	U
36	5	2187	G

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Mol	Chain	Res	Type
36	5	2188	A
36	5	2192	C
36	5	2201	G
36	5	2203	U
36	5	2205	U
36	5	2206	G
36	5	2208	A
36	5	2210	G
36	5	2222	A
36	5	2223	A
36	5	2229	A
36	5	2244	A
36	5	2249	G
36	5	2250	G
36	5	2251	G
36	5	2252	A
36	5	2253	G
36	5	2255	A
36	5	2256	A
36	5	2269	U
36	5	2270	A
36	5	2273	G
36	5	2276	G
36	5	2279	A
36	5	2280	A
36	5	2288	G
36	5	2301	U
36	5	2307	G
36	5	2310	U
36	5	2313	A
36	5	2315	G
36	5	2318	U
36	5	2335	G
36	5	2336	U
36	5	2338	C
36	5	2347	U
36	5	2372	A
36	5	2373	A
36	5	2374	C
36	5	2375	G
36	5	2385	G
36	5	2392	C

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Mol	Chain	Res	Type
36	5	2393	G
36	5	2394	G
36	5	2397	A
36	5	2401	A
36	5	2402	A
36	5	2403	G
36	5	2404	A
36	5	2405	C
36	5	2411	U
36	5	2418	G
36	5	2419	A
36	5	2438	A
36	5	2439	A
36	5	2441	A
36	5	2443	A
36	5	2444	C
36	5	2505	U
36	5	2506	U
36	5	2507	C
36	5	2508	U
36	5	2510	U
36	5	2511	A
36	5	2512	C
36	5	2514	U
36	5	2515	A
36	5	2522	G
36	5	2523	A
36	5	2524	A
36	5	2525	G
36	5	2526	C
36	5	2531	C
36	5	2532	U
36	5	2535	A
36	5	2538	U
36	5	2539	C
36	5	2540	A
36	5	2541	U
36	5	2543	U
36	5	2544	U
36	5	2549	G
36	5	2552	C
36	5	2555	G

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Mol	Chain	Res	Type
36	5	2567	C
36	5	2568	C
36	5	2569	A
36	5	2570	U
36	5	2571	U
36	5	2572	C
36	5	2573	G
36	5	2574	G
36	5	2584	G
36	5	2585	G
36	5	2587	U
36	5	2589	G
36	5	2593	A
36	5	2594	C
36	5	2606	G
36	5	2607	G
36	5	2614	G
36	5	2638	C
36	5	2652	U
36	5	2656	A
36	5	2657	A
36	5	2674	A
36	5	2675	C
36	5	2676	A
36	5	2677	G
36	5	2678	A
36	5	2680	A
36	5	2689	A
36	5	2690	G
36	5	2691	A
36	5	2694	A
36	5	2696	A
36	5	2705	A
36	5	2714	G
36	5	2719	U
36	5	2720	G
36	5	2727	A
36	5	2728	G
36	5	2729	U
36	5	2752	U
36	5	2753	G
36	5	2762	A

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Mol	Chain	Res	Type
36	5	2772	C
36	5	2773	C
36	5	2776	C
36	5	2777	G
36	5	2778	G
36	5	2779	A
36	5	2782	U
36	5	2796	G
36	5	2799	A
36	5	2800	G
36	5	2801	A
36	5	2802	A
36	5	2803	A
36	5	2804	A
36	5	2810	C
36	5	2814	G
36	5	2816	G
36	5	2817	A
36	5	2818	U
36	5	2829	U
36	5	2844	C
36	5	2845	A
36	5	2847	A
36	5	2849	C
36	5	2853	A
36	5	2865	U
36	5	2871	G
36	5	2872	A
36	5	2875	U
36	5	2887	A
36	5	2889	C
36	5	2899	C
36	5	2900	A
36	5	2922	G
36	5	2923	U
36	5	2928	C
36	5	2935	U
36	5	2936	A
36	5	2942	C
36	5	2945	G
36	5	2947	G
36	5	2960	C

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Mol	Chain	Res	Type
36	5	2964	G
36	5	2971	A
36	5	2979	U
36	5	2983	C
36	5	2990	G
36	5	2996	U
36	5	2997	G
36	5	3012	A
36	5	3049	A
36	5	3056	U
36	5	3057	U
36	5	3059	G
36	5	3078	U
36	5	3079	U
36	5	3086	A
36	5	3092	C
36	5	3098	G
36	5	3102	G
36	5	3113	A
36	5	3119	U
36	5	3122	A
36	5	3130	A
36	5	3131	U
36	5	3142	A
36	5	3143	C
36	5	3150	A
36	5	3153	U
36	5	3155	U
36	5	3156	U
36	5	3157	U
36	5	3158	G
36	5	3162	C
36	5	3164	C
36	5	3165	A
36	5	3168	A
36	5	3172	A
36	5	3173	G
36	5	3174	A
36	5	3176	G
36	5	3177	G
36	5	3178	A
36	5	3179	U

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Mol	Chain	Res	Type
36	5	3181	C
36	5	3185	U
36	5	3187	A
36	5	3195	U
36	5	3196	U
36	5	3206	C
36	5	3207	U
36	5	3217	C
36	5	3218	A
36	5	3219	G
36	5	3224	G
36	5	3227	A
36	5	3229	G
36	5	3234	A
36	5	3238	G
36	5	3239	G
36	5	3244	A
36	5	3245	A
36	5	3246	G
36	5	3247	G
36	5	3259	U
36	5	3260	G
36	5	3265	C
36	5	3266	G
36	5	3269	U
36	5	3270	U
36	5	3275	U
36	5	3276	G
36	5	3277	U
36	5	3278	C
36	5	3280	U
36	5	3281	U
36	5	3282	U
36	5	3284	G
36	5	3285	C
36	5	3286	G
36	5	3287	U
36	5	3288	G
36	5	3289	G
36	5	3290	G
36	5	3293	U
36	5	3304	U

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Mol	Chain	Res	Type
36	5	3313	U
36	5	3316	A
36	5	3317	U
36	5	3318	G
36	5	3320	A
36	5	3341	U
36	5	3342	A
36	5	3345	G
36	5	3348	G
36	5	3351	U
36	5	3352	U
36	5	3353	G
36	5	3354	U
36	5	3355	U
36	5	3356	G
36	5	3358	U
36	5	3368	U
36	5	3369	G
36	5	3378	C
36	5	3389	U
36	5	3396	U
37	7	22	A
37	7	33	U
37	7	41	G
37	7	50	U
37	7	54	U
37	7	60	G
37	7	64	A
37	7	65	G
37	7	73	C
37	7	74	C
37	7	76	A
37	7	93	C
37	7	102	A
37	7	112	G
37	7	121	U
38	8	13	A
38	8	21	C
38	8	34	U
38	8	35	C
38	8	48	A
38	8	50	C

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Mol	Chain	Res	Type
38	8	51	G
38	8	52	A
38	8	59	A
38	8	62	C
38	8	63	G
38	8	79	A
38	8	80	A
38	8	81	U
38	8	82	U
38	8	83	C
38	8	84	C
38	8	85	G
38	8	86	U
38	8	87	G
38	8	95	G
38	8	104	A
38	8	105	A
38	8	106	C
38	8	111	A
38	8	113	U
38	8	116	G
38	8	125	U
38	8	126	A
38	8	156	U
38	8	157	U
38	8	158	U
85	B	75	C

All (213) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	25	C
1	2	68	A
1	2	73	U
1	2	74	U
1	2	130	C
1	2	131	C
1	2	139	C
1	2	158	U
1	2	192	U
1	2	218	A
1	2	240	U

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Mol	Chain	Res	Type
1	2	242	U
1	2	278	U
1	2	322	G
1	2	417	A
1	2	499	U
1	2	501	U
1	2	503	G
1	2	512	A
1	2	555	A
1	2	704	C
1	2	720	G
1	2	721	U
1	2	811	A
1	2	829	A
1	2	913	G
1	2	1058	U
1	2	1081	A
1	2	1157	A
1	2	1207	C
1	2	1244	A
1	2	1250	U
1	2	1344	A
1	2	1481	C
1	2	1489	U
1	2	1568	C
1	2	1573	A
1	2	1615	C
1	2	1657	U
1	2	1698	G
1	2	1711	C
1	2	1761	U
36	1	13	A
36	1	65	A
36	1	210	U
36	1	239	G
36	1	269	G
36	1	285	A
36	1	397	A
36	1	594	U
36	1	619	A
36	1	637	C
36	1	715	A

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Mol	Chain	Res	Type
36	1	763	G
36	1	873	C
36	1	896	A
36	1	916	G
36	1	979	U
36	1	981	U
36	1	993	G
36	1	1064	A
36	1	1094	U
36	1	1097	G
36	1	1103	A
36	1	1196	C
36	1	1273	A
36	1	1329	U
36	1	1331	U
36	1	1352	A
36	1	1355	A
36	1	1481	A
36	1	1484	U
36	1	1507	G
36	1	1562	C
36	1	1582	C
36	1	1716	U
36	1	1820	U
36	1	1841	A
36	1	2101	C
36	1	2112	U
36	1	2208	A
36	1	2209	U
36	1	2249	G
36	1	2281	A
36	1	2372	A
36	1	2400	G
36	1	2404	A
36	1	2418	G
36	1	2513	U
36	1	2537	U
36	1	2541	U
36	1	2554	A
36	1	2585	G
36	1	2593	A
36	1	2801	A

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Mol	Chain	Res	Type
36	1	2818	U
36	1	3078	U
36	1	3121	U
36	1	3195	U
36	1	3218	A
36	1	3228	C
36	1	3269	U
36	1	3319	U
36	1	3350	C
36	1	3351	U
36	1	3353	G
36	1	3375	A
37	3	52	G
38	4	80	A
38	4	85	G
38	4	125	U
1	6	25	C
1	6	75	U
1	6	76	A
1	6	139	C
1	6	158	U
1	6	187	G
1	6	192	U
1	6	217	A
1	6	272	U
1	6	277	U
1	6	512	A
1	6	542	A
1	6	555	A
1	6	558	U
1	6	678	A
1	6	697	C
1	6	755	A
1	6	829	A
1	6	834	G
1	6	1031	U
1	6	1051	G
1	6	1058	U
1	6	1097	U
1	6	1196	A
1	6	1244	A
1	6	1255	G

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Mol	Chain	Res	Type
1	6	1344	A
1	6	1481	C
1	6	1535	U
1	6	1568	C
1	6	1573	A
1	6	1620	C
1	6	1657	U
1	6	1698	G
1	6	1754	A
36	5	43	A
36	5	151	A
36	5	183	G
36	5	238	A
36	5	438	A
36	5	546	C
36	5	588	G
36	5	715	A
36	5	765	C
36	5	816	A
36	5	873	C
36	5	896	A
36	5	916	G
36	5	993	G
36	5	1017	C
36	5	1027	A
36	5	1064	A
36	5	1081	U
36	5	1152	G
36	5	1222	G
36	5	1238	C
36	5	1241	U
36	5	1284	C
36	5	1307	G
36	5	1329	U
36	5	1352	A
36	5	1355	A
36	5	1367	G
36	5	1481	A
36	5	1554	U
36	5	1560	G
36	5	1571	A
36	5	1774	C

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Mol	Chain	Res	Type
36	5	1815	U
36	5	1816	A
36	5	2101	C
36	5	2112	U
36	5	2209	U
36	5	2249	G
36	5	2255	A
36	5	2281	A
36	5	2440	G
36	5	2507	C
36	5	2513	U
36	5	2531	C
36	5	2539	C
36	5	2586	G
36	5	2728	G
36	5	2772	C
36	5	2801	A
36	5	2818	U
36	5	2874	G
36	5	3056	U
36	5	3078	U
36	5	3154	C
36	5	3195	U
36	5	3228	C
36	5	3269	U
36	5	3275	U
36	5	3276	G
36	5	3289	G
36	5	3317	U
36	5	3340	G
36	5	3341	U
36	5	3357	U
37	7	49	G
38	8	156	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length

(or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
85	8AN	B	76	86,85	18,24,25	1.04	1 (5%)	10,35,38	2.26	2 (20%)
85	8AN	C	76	86,85	18,24,25	1.10	1 (5%)	10,35,38	2.18	2 (20%)
84	5CT	f	51	84	12,14,15	2.59	3 (25%)	12,15,17	1.50	3 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
85	8AN	B	76	86,85	-	0/3/25/26	0/3/3/3
85	8AN	C	76	86,85	-	0/3/25/26	0/3/3/3
84	5CT	f	51	84	1/1/2/4	0/12/14/16	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	f	51	5CT	O1-C2	-7.01	1.22	1.43
84	f	51	5CT	C1-NZ	-3.59	1.41	1.47
85	B	76	8AN	C5-C4	2.83	1.46	1.40
85	C	76	8AN	C5-C4	3.06	1.47	1.40
84	f	51	5CT	CB-CA	3.57	1.58	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	C	76	8AN	N3-C2-N1	-6.28	123.94	128.87
85	B	76	8AN	N3-C2-N1	-6.09	124.09	128.87
85	B	76	8AN	C1'-N9-C4	-2.58	123.93	126.81
84	f	51	5CT	C1-NZ-CE	-2.30	108.41	113.83
85	C	76	8AN	N6-C6-N1	2.15	122.13	118.52
84	f	51	5CT	O1-C2-C3	2.22	115.69	109.36
84	f	51	5CT	O1-C2-C1	3.23	120.25	109.08

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
84	f	51	5CT	C2

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
85	C	76	8AN	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2282 ligands modelled in this entry, 1109 are monoatomic - leaving 1173 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
87	OHX	1	3761	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3762	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3763	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3764	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3765	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3766	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3767	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3768	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3769	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3770	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3771	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3772	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3773	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3774	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3775	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	1	3776	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3777	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3778	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3779	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3780	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3781	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3782	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3783	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3784	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3785	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3786	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3787	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3788	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3789	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3790	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3791	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3792	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3793	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3794	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3795	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3796	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3797	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3798	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3799	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3800	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3801	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3802	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3803	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3804	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3805	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3806	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3807	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3808	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3809	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3810	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3811	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3812	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3813	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3814	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3815	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3816	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3817	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3818	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	1	3819	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3820	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3821	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3822	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3823	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3824	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3825	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3826	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3827	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3828	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3829	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3830	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3831	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3832	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3833	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3834	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3835	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3836	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3837	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3838	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3839	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3840	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3841	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3842	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3843	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3844	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3845	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3846	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3847	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3848	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3849	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3850	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3851	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3852	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3853	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3854	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3855	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3856	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3857	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3858	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3859	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3860	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3861	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	1	3862	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3863	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3864	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3865	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3866	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3867	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3868	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3869	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3870	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3871	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3872	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3873	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3874	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3875	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3876	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3877	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3878	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3879	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3880	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3881	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3882	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3883	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3884	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3885	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3886	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3887	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3888	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3889	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3890	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3891	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3892	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3893	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3894	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3895	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3896	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3897	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3898	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3899	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3900	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3901	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3902	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3903	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3904	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	1	3905	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3906	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3907	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3908	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3909	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3910	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3911	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3912	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3913	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3914	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3915	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3916	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3917	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3918	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3919	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3920	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3921	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3922	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3923	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3924	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3925	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3926	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3927	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3928	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3929	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3930	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3931	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3932	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3933	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3934	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3935	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3936	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3937	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3938	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3939	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3940	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3941	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3942	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3943	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3944	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3945	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3946	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3947	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	1	3948	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3949	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3950	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3951	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3952	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3953	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3954	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3955	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3956	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3957	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3958	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3959	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3960	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3961	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3962	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3963	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3964	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3965	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3966	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3967	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3968	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3969	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3970	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3971	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3972	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3973	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3974	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3975	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3976	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3977	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3978	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3979	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3980	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3981	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3982	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3983	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3984	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3985	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3986	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3987	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3988	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3989	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3990	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	1	3991	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3992	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3993	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3994	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3995	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3996	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3997	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3998	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	3999	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4000	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4001	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4002	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4003	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4004	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4005	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4006	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4007	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4008	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4009	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4010	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4011	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4012	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4013	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4014	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4015	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4016	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4017	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4018	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4019	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4020	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4021	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4022	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4023	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4024	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4025	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4026	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4027	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4028	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4029	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4030	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4031	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4032	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4033	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	1	4034	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4035	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4036	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4037	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4038	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4039	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4040	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4041	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4042	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4043	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4044	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4045	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4046	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4047	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4048	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4049	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4050	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4051	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4052	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4053	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4054	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4055	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4056	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4057	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4058	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4059	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4060	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4061	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4062	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4063	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4064	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4065	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4066	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4067	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4068	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4069	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4070	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4071	36	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4072	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4073	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4074	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4075	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4076	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	1	4077	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4078	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4079	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4080	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4081	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4082	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4083	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4084	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4085	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4086	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4087	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4088	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4089	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4090	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4091	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4092	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4093	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4094	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4095	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4096	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4097	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4098	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4099	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4100	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4101	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4102	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4103	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4104	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4105	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4106	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4107	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4108	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4109	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4110	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	1	4111	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	1991	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	1992	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	1993	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	1994	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	1995	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	1996	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	1997	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	1998	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	2	1999	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2000	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2001	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2002	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2003	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2004	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2005	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2006	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2007	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2008	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2009	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2010	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2011	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2012	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2013	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2014	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2015	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2016	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2017	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2018	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2019	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2020	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2021	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2022	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2023	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2024	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2025	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2026	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2027	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2028	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2029	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2030	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2031	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2032	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2033	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2034	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2035	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2036	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2037	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2038	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2039	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2040	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2041	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	2	2042	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2043	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2044	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2045	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2046	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2047	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2048	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2049	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2050	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2051	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2052	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2053	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2054	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2055	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2056	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2057	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2058	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2059	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2060	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2061	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2062	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2063	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2064	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2065	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2066	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2067	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2068	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2069	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2070	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2071	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2072	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2073	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2074	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2075	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2076	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2077	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2078	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2079	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2080	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2081	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2082	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2083	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2084	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	2	2085	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2086	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2087	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2088	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2089	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2090	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2091	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2092	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2093	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2094	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2095	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2096	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2097	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2098	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2099	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2100	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2101	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2102	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2103	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2104	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2105	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2106	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2107	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2108	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2109	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2110	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2111	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2112	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2113	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2114	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2115	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2116	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2117	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2118	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2119	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2120	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2121	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2122	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2123	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2124	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2125	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2126	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2127	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	2	2128	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2129	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2130	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2131	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2132	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2133	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2134	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2135	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2136	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2137	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2138	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2139	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2140	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2141	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2142	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2143	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2144	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2145	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2146	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2147	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2148	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2149	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2150	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2151	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	2	2152	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	3	209	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	3	210	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	3	211	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	3	212	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	3	213	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	3	214	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	3	215	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	3	216	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	3	217	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	3	218	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	3	219	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	215	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	216	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	217	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	218	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	219	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	220	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	221	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	4	222	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	223	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	224	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	225	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	226	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	227	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	228	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	229	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	230	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	231	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	4	232	-	0,6,6	0.00	-	0,15,15	0.00	-
89	SPS	5	3402	-	19,23,23	3.44	10 (52%)	16,30,30	3.20	11 (68%)
87	OHX	5	3816	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3817	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3818	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3819	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3820	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3821	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3822	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3823	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3824	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3825	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3826	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3827	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3828	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3829	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3830	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3831	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3832	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3833	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3834	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3835	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3836	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3837	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3838	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3839	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3840	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3841	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3842	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3843	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3844	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3845	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3846	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	5	3847	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3848	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3849	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3850	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3851	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3852	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3853	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3854	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3855	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3856	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3857	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3858	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3859	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3860	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3861	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3862	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3863	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3864	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3865	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3866	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3867	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3868	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3869	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3870	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3871	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3872	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3873	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3874	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3875	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3876	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3877	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3878	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3879	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3880	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3881	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3882	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3883	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3884	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3885	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3886	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3887	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3888	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3889	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	5	3890	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3891	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3892	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3893	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3894	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3895	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3896	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3897	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3898	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3899	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3900	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3901	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3902	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3903	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3904	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3905	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3906	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3907	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3908	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3909	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3910	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3911	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3912	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3913	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3914	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3915	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3916	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3917	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3918	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3919	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3920	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3921	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3922	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3923	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3924	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3925	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3926	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3927	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3928	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3929	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3930	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3931	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3932	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	5	3933	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3934	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3935	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3936	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3937	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3938	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3939	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3940	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3941	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3942	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3943	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3944	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3945	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3946	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3947	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3948	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3949	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3950	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3951	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3952	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3953	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3954	36	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3955	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3956	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3957	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3958	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3959	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3960	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3961	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3962	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3963	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3964	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3965	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3966	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3967	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3968	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3969	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3970	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3971	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3972	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3973	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3974	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3975	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	5	3976	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3977	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3978	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3979	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3980	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3981	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3982	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3983	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3984	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3985	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3986	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3987	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3988	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3989	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3990	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3991	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3992	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3993	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3994	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3995	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3996	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3997	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3998	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	3999	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4000	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4001	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4002	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4003	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4004	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4005	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4006	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4007	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4008	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4009	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4010	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4011	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4012	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4013	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4014	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4015	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4016	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4017	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4018	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	5	4019	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4020	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4021	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4022	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4023	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4024	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4025	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4026	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4027	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4028	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4029	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4030	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4031	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4032	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4033	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4034	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4035	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4036	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4037	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4038	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4039	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4040	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4041	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4042	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4043	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4044	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4045	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4046	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4047	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4048	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4049	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4050	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4051	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4052	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4053	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4054	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4055	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4056	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4057	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4058	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4059	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4060	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4061	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	5	4062	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4063	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4064	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4065	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4066	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4067	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4068	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4069	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4070	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4071	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4072	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4073	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4074	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4075	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4076	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4077	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4078	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4079	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4080	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4081	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4082	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4083	36	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4084	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4085	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4086	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4087	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4088	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4089	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4090	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4091	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4092	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4093	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4094	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4095	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4096	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4097	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4098	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4099	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4100	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4101	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4102	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4103	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4104	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	5	4105	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4106	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4107	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4108	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4109	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4110	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4111	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4112	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4113	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4114	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4115	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4116	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4117	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4118	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4119	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4120	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4121	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4122	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4123	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4124	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4125	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4126	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4127	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4128	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4129	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4130	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4131	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4132	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4133	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4134	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4135	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4136	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4137	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4138	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4139	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4140	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4141	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4142	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4143	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4144	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4145	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4146	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4147	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	5	4148	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4149	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4150	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4151	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4152	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4153	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4154	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4155	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4156	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4157	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4158	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4159	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4160	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4161	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4162	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4163	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4164	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4165	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4166	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4167	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4168	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4169	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4170	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	5	4171	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2012	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2013	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2014	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2015	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2016	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2017	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2018	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2019	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2020	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2021	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2022	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2023	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2024	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2025	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2026	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2027	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2028	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2029	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2030	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	6	2031	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2032	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2033	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2034	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2035	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2036	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2037	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2038	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2039	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2040	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2041	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2042	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2043	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2044	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2045	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2046	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2047	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2048	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2049	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2050	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2051	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2052	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2053	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2054	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2055	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2056	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2057	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2058	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2059	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2060	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2061	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2062	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2063	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2064	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2065	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2066	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2067	1	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2068	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2069	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2070	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2071	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2072	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2073	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	6	2074	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2075	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2076	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2077	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2078	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2079	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2080	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2081	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2082	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2083	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2084	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2085	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2086	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2087	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2088	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2089	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2090	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2091	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2092	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2093	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2094	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2095	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2096	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2097	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2098	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2099	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2100	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2101	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2102	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2103	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2104	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2105	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2106	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2107	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2108	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2109	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2110	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2111	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2112	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2113	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2114	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2115	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2116	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	6	2117	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2118	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2119	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2120	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2121	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2122	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2123	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2124	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2125	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2126	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2127	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2128	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2129	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2130	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2131	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2132	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2133	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2134	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2135	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2136	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2137	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2138	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2139	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2140	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2141	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2142	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2143	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2144	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2145	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2146	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2147	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2148	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2149	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2150	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2151	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2152	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2153	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2154	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2155	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2156	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2157	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2158	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2159	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	6	2160	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2161	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2162	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2163	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2164	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2165	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2166	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2167	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2168	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2169	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2170	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2171	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2172	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2173	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2174	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2175	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2176	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2177	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2178	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2179	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2180	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2181	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2182	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	6	2183	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	7	214	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	7	215	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	7	216	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	7	217	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	7	218	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	7	219	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	7	220	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	7	221	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	7	222	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	7	223	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	7	224	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	210	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	211	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	212	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	213	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	214	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	215	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	216	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	217	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	8	218	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	219	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	220	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	221	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	222	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	223	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	224	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	225	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	226	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	227	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	228	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	229	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	8	230	-	0,6,6	0.00	-	0,15,15	0.00	-
89	SPS	B	101	86	19,23,23	3.52	11 (57%)	16,30,30	3.09	7 (43%)
90	PRO	B	102	-	5,7,8	0.52	0	7,8,10	1.18	1 (14%)
90	PRO	C	101	-	5,7,8	0.38	0	7,8,10	1.42	1 (14%)
87	OHX	C3	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	C5	201	17	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	C8	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	D9	102	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	L3	402	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	L3	403	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	L3	404	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	L4	401	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	L5	301	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	M0	302	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	M0	303	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	M5	302	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	M5	303	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	M6	203	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	M7	205	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	M8	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	M9	202	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	N8	202	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	N9	101	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	O1	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	O3	202	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	O4	202	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	O7	103	73	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	O9	101	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	Q2	503	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	S1	301	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OHX	S6	301	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	S8	301	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	S9	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	SR	401	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	c3	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	c5	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	c5	202	17	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	c8	202	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	d4	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	d9	102	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	l3	403	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	l3	404	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	l4	402	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	l4	403	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	l5	302	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	l5	303	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	l9	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	m0	301	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	m0	302	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	m1	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	m4	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	m5	303	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	m5	304	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	m5	305	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	m6	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	m7	203	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	m8	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	m9	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	n3	202	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	n9	101	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	o3	202	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	o6	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	o7	502	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	o7	503	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	q2	502	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	s1	301	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	s1	302	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	s4	602	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	s8	303	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	s9	201	-	0,6,6	0.00	-	0,15,15	0.00	-
87	OHX	sR	401	-	0,6,6	0.00	-	0,15,15	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	1	3761	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3762	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3763	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3764	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3765	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3766	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3767	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3768	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3769	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3770	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3771	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3772	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3773	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3774	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3775	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3776	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3777	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3778	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3779	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3780	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3781	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3782	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3783	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3784	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3785	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3786	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3787	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3788	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3789	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3790	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3791	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3792	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3793	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3794	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3795	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3796	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3797	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3798	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3799	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3800	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	1	3801	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3802	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3803	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3804	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3805	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3806	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3807	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3808	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3809	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3810	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3811	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3812	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3813	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3814	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3815	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3816	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3817	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3818	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3819	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3820	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3821	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3822	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3823	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3824	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3825	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3826	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3827	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3828	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3829	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3830	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3831	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3832	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3833	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3834	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3835	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3836	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3837	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3838	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3839	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3840	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3841	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3842	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	1	3843	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3844	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3845	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3846	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3847	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3848	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3849	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3850	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3851	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3852	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3853	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3854	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3855	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3856	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3857	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3858	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3859	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3860	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3861	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3862	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3863	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3864	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3865	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3866	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3867	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3868	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3869	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3870	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3871	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3872	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3873	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3874	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3875	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3876	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3877	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3878	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3879	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3880	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3881	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3882	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3883	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3884	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	1	3885	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3886	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3887	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3888	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3889	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3890	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3891	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3892	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3893	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3894	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3895	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3896	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3897	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3898	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3899	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3900	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3901	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3902	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3903	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3904	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3905	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3906	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3907	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3908	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3909	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3910	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3911	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3912	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3913	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3914	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3915	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3916	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3917	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3918	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3919	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3920	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3921	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3922	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3923	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3924	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3925	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3926	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	1	3927	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3928	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3929	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3930	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3931	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3932	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3933	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3934	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3935	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3936	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3937	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3938	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3939	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3940	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3941	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3942	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3943	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3944	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3945	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3946	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3947	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3948	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3949	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3950	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3951	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3952	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3953	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3954	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3955	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3956	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3957	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3958	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3959	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3960	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3961	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3962	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3963	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3964	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3965	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3966	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3967	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3968	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	1	3969	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3970	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3971	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3972	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3973	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3974	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3975	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3976	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3977	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3978	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3979	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3980	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3981	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3982	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3983	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3984	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3985	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3986	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3987	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3988	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3989	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3990	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3991	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3992	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3993	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3994	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3995	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3996	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3997	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3998	-	-	0/0/0/0	0/0/0/0
87	OHX	1	3999	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4000	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4001	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4002	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4003	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4004	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4005	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4006	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4007	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4008	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4009	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4010	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	1	4011	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4012	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4013	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4014	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4015	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4016	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4017	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4018	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4019	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4020	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4021	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4022	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4023	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4024	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4025	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4026	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4027	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4028	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4029	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4030	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4031	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4032	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4033	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4034	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4035	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4036	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4037	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4038	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4039	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4040	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4041	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4042	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4043	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4044	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4045	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4046	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4047	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4048	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4049	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4050	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4051	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4052	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	1	4053	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4054	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4055	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4056	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4057	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4058	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4059	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4060	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4061	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4062	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4063	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4064	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4065	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4066	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4067	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4068	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4069	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4070	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4071	36	-	0/0/0/0	0/0/0/0
87	OHX	1	4072	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4073	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4074	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4075	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4076	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4077	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4078	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4079	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4080	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4081	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4082	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4083	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4084	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4085	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4086	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4087	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4088	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4089	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4090	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4091	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4092	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4093	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4094	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	1	4095	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4096	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4097	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4098	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4099	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4100	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4101	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4102	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4103	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4104	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4105	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4106	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4107	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4108	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4109	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4110	-	-	0/0/0/0	0/0/0/0
87	OHX	1	4111	-	-	0/0/0/0	0/0/0/0
87	OHX	2	1991	-	-	0/0/0/0	0/0/0/0
87	OHX	2	1992	-	-	0/0/0/0	0/0/0/0
87	OHX	2	1993	-	-	0/0/0/0	0/0/0/0
87	OHX	2	1994	-	-	0/0/0/0	0/0/0/0
87	OHX	2	1995	-	-	0/0/0/0	0/0/0/0
87	OHX	2	1996	-	-	0/0/0/0	0/0/0/0
87	OHX	2	1997	-	-	0/0/0/0	0/0/0/0
87	OHX	2	1998	-	-	0/0/0/0	0/0/0/0
87	OHX	2	1999	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2000	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2001	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2002	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2003	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2004	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2005	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2006	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2007	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2008	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2009	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2010	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2011	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2012	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2013	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2014	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2015	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	2	2016	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2017	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2018	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2019	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2020	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2021	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2022	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2023	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2024	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2025	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2026	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2027	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2028	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2029	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2030	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2031	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2032	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2033	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2034	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2035	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2036	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2037	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2038	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2039	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2040	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2041	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2042	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2043	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2044	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2045	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2046	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2047	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2048	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2049	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2050	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2051	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2052	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2053	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2054	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2055	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2056	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2057	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	2	2058	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2059	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2060	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2061	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2062	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2063	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2064	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2065	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2066	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2067	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2068	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2069	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2070	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2071	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2072	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2073	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2074	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2075	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2076	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2077	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2078	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2079	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2080	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2081	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2082	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2083	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2084	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2085	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2086	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2087	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2088	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2089	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2090	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2091	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2092	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2093	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2094	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2095	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2096	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2097	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2098	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2099	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	2	2100	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2101	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2102	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2103	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2104	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2105	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2106	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2107	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2108	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2109	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2110	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2111	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2112	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2113	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2114	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2115	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2116	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2117	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2118	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2119	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2120	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2121	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2122	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2123	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2124	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2125	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2126	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2127	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2128	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2129	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2130	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2131	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2132	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2133	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2134	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2135	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2136	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2137	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2138	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2139	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2140	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2141	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	2	2142	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2143	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2144	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2145	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2146	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2147	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2148	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2149	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2150	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2151	-	-	0/0/0/0	0/0/0/0
87	OHX	2	2152	-	-	0/0/0/0	0/0/0/0
87	OHX	3	209	-	-	0/0/0/0	0/0/0/0
87	OHX	3	210	-	-	0/0/0/0	0/0/0/0
87	OHX	3	211	-	-	0/0/0/0	0/0/0/0
87	OHX	3	212	-	-	0/0/0/0	0/0/0/0
87	OHX	3	213	-	-	0/0/0/0	0/0/0/0
87	OHX	3	214	-	-	0/0/0/0	0/0/0/0
87	OHX	3	215	-	-	0/0/0/0	0/0/0/0
87	OHX	3	216	-	-	0/0/0/0	0/0/0/0
87	OHX	3	217	-	-	0/0/0/0	0/0/0/0
87	OHX	3	218	-	-	0/0/0/0	0/0/0/0
87	OHX	3	219	-	-	0/0/0/0	0/0/0/0
87	OHX	4	215	-	-	0/0/0/0	0/0/0/0
87	OHX	4	216	-	-	0/0/0/0	0/0/0/0
87	OHX	4	217	-	-	0/0/0/0	0/0/0/0
87	OHX	4	218	-	-	0/0/0/0	0/0/0/0
87	OHX	4	219	-	-	0/0/0/0	0/0/0/0
87	OHX	4	220	-	-	0/0/0/0	0/0/0/0
87	OHX	4	221	-	-	0/0/0/0	0/0/0/0
87	OHX	4	222	-	-	0/0/0/0	0/0/0/0
87	OHX	4	223	-	-	0/0/0/0	0/0/0/0
87	OHX	4	224	-	-	0/0/0/0	0/0/0/0
87	OHX	4	225	-	-	0/0/0/0	0/0/0/0
87	OHX	4	226	-	-	0/0/0/0	0/0/0/0
87	OHX	4	227	-	-	0/0/0/0	0/0/0/0
87	OHX	4	228	-	-	0/0/0/0	0/0/0/0
87	OHX	4	229	-	-	0/0/0/0	0/0/0/0
87	OHX	4	230	-	-	0/0/0/0	0/0/0/0
87	OHX	4	231	-	-	0/0/0/0	0/0/0/0
87	OHX	4	232	-	-	0/0/0/0	0/0/0/0
89	SPS	5	3402	-	-	0/15/18/18	0/1/1/1
87	OHX	5	3816	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	5	3817	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3818	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3819	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3820	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3821	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3822	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3823	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3824	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3825	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3826	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3827	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3828	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3829	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3830	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3831	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3832	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3833	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3834	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3835	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3836	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3837	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3838	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3839	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3840	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3841	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3842	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3843	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3844	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3845	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3846	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3847	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3848	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3849	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3850	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3851	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3852	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3853	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3854	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3855	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3856	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3857	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3858	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	5	3859	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3860	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3861	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3862	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3863	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3864	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3865	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3866	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3867	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3868	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3869	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3870	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3871	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3872	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3873	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3874	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3875	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3876	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3877	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3878	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3879	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3880	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3881	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3882	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3883	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3884	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3885	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3886	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3887	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3888	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3889	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3890	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3891	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3892	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3893	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3894	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3895	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3896	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3897	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3898	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3899	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3900	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	5	3901	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3902	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3903	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3904	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3905	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3906	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3907	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3908	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3909	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3910	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3911	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3912	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3913	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3914	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3915	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3916	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3917	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3918	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3919	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3920	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3921	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3922	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3923	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3924	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3925	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3926	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3927	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3928	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3929	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3930	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3931	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3932	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3933	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3934	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3935	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3936	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3937	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3938	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3939	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3940	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3941	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3942	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	5	3943	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3944	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3945	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3946	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3947	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3948	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3949	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3950	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3951	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3952	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3953	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3954	36	-	0/0/0/0	0/0/0/0
87	OHX	5	3955	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3956	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3957	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3958	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3959	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3960	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3961	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3962	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3963	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3964	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3965	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3966	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3967	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3968	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3969	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3970	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3971	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3972	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3973	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3974	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3975	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3976	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3977	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3978	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3979	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3980	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3981	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3982	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3983	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3984	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	5	3985	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3986	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3987	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3988	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3989	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3990	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3991	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3992	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3993	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3994	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3995	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3996	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3997	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3998	-	-	0/0/0/0	0/0/0/0
87	OHX	5	3999	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4000	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4001	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4002	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4003	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4004	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4005	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4006	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4007	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4008	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4009	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4010	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4011	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4012	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4013	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4014	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4015	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4016	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4017	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4018	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4019	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4020	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4021	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4022	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4023	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4024	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4025	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4026	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	5	4027	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4028	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4029	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4030	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4031	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4032	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4033	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4034	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4035	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4036	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4037	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4038	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4039	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4040	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4041	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4042	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4043	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4044	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4045	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4046	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4047	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4048	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4049	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4050	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4051	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4052	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4053	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4054	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4055	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4056	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4057	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4058	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4059	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4060	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4061	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4062	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4063	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4064	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4065	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4066	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4067	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4068	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	5	4069	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4070	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4071	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4072	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4073	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4074	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4075	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4076	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4077	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4078	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4079	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4080	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4081	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4082	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4083	36	-	0/0/0/0	0/0/0/0
87	OHX	5	4084	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4085	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4086	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4087	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4088	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4089	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4090	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4091	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4092	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4093	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4094	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4095	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4096	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4097	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4098	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4099	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4100	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4101	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4102	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4103	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4104	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4105	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4106	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4107	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4108	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4109	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4110	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	5	4111	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4112	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4113	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4114	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4115	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4116	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4117	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4118	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4119	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4120	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4121	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4122	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4123	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4124	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4125	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4126	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4127	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4128	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4129	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4130	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4131	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4132	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4133	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4134	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4135	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4136	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4137	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4138	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4139	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4140	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4141	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4142	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4143	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4144	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4145	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4146	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4147	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4148	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4149	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4150	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4151	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4152	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	5	4153	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4154	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4155	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4156	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4157	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4158	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4159	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4160	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4161	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4162	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4163	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4164	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4165	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4166	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4167	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4168	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4169	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4170	-	-	0/0/0/0	0/0/0/0
87	OHX	5	4171	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2012	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2013	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2014	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2015	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2016	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2017	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2018	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2019	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2020	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2021	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2022	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2023	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2024	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2025	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2026	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2027	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2028	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2029	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2030	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2031	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2032	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2033	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2034	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	6	2035	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2036	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2037	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2038	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2039	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2040	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2041	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2042	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2043	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2044	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2045	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2046	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2047	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2048	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2049	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2050	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2051	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2052	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2053	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2054	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2055	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2056	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2057	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2058	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2059	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2060	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2061	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2062	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2063	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2064	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2065	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2066	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2067	1	-	0/0/0/0	0/0/0/0
87	OHX	6	2068	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2069	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2070	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2071	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2072	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2073	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2074	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2075	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2076	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	6	2077	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2078	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2079	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2080	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2081	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2082	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2083	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2084	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2085	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2086	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2087	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2088	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2089	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2090	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2091	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2092	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2093	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2094	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2095	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2096	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2097	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2098	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2099	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2100	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2101	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2102	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2103	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2104	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2105	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2106	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2107	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2108	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2109	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2110	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2111	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2112	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2113	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2114	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2115	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2116	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2117	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2118	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	6	2119	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2120	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2121	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2122	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2123	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2124	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2125	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2126	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2127	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2128	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2129	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2130	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2131	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2132	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2133	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2134	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2135	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2136	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2137	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2138	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2139	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2140	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2141	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2142	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2143	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2144	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2145	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2146	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2147	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2148	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2149	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2150	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2151	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2152	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2153	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2154	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2155	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2156	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2157	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2158	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2159	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2160	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	6	2161	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2162	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2163	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2164	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2165	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2166	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2167	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2168	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2169	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2170	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2171	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2172	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2173	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2174	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2175	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2176	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2177	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2178	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2179	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2180	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2181	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2182	-	-	0/0/0/0	0/0/0/0
87	OHX	6	2183	-	-	0/0/0/0	0/0/0/0
87	OHX	7	214	-	-	0/0/0/0	0/0/0/0
87	OHX	7	215	-	-	0/0/0/0	0/0/0/0
87	OHX	7	216	-	-	0/0/0/0	0/0/0/0
87	OHX	7	217	-	-	0/0/0/0	0/0/0/0
87	OHX	7	218	-	-	0/0/0/0	0/0/0/0
87	OHX	7	219	-	-	0/0/0/0	0/0/0/0
87	OHX	7	220	-	-	0/0/0/0	0/0/0/0
87	OHX	7	221	-	-	0/0/0/0	0/0/0/0
87	OHX	7	222	-	-	0/0/0/0	0/0/0/0
87	OHX	7	223	-	-	0/0/0/0	0/0/0/0
87	OHX	7	224	-	-	0/0/0/0	0/0/0/0
87	OHX	8	210	-	-	0/0/0/0	0/0/0/0
87	OHX	8	211	-	-	0/0/0/0	0/0/0/0
87	OHX	8	212	-	-	0/0/0/0	0/0/0/0
87	OHX	8	213	-	-	0/0/0/0	0/0/0/0
87	OHX	8	214	-	-	0/0/0/0	0/0/0/0
87	OHX	8	215	-	-	0/0/0/0	0/0/0/0
87	OHX	8	216	-	-	0/0/0/0	0/0/0/0
87	OHX	8	217	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	8	218	-	-	0/0/0/0	0/0/0/0
87	OHX	8	219	-	-	0/0/0/0	0/0/0/0
87	OHX	8	220	-	-	0/0/0/0	0/0/0/0
87	OHX	8	221	-	-	0/0/0/0	0/0/0/0
87	OHX	8	222	-	-	0/0/0/0	0/0/0/0
87	OHX	8	223	-	-	0/0/0/0	0/0/0/0
87	OHX	8	224	-	-	0/0/0/0	0/0/0/0
87	OHX	8	225	-	-	0/0/0/0	0/0/0/0
87	OHX	8	226	-	-	0/0/0/0	0/0/0/0
87	OHX	8	227	-	-	0/0/0/0	0/0/0/0
87	OHX	8	228	-	-	0/0/0/0	0/0/0/0
87	OHX	8	229	-	-	0/0/0/0	0/0/0/0
87	OHX	8	230	-	-	0/0/0/0	0/0/0/0
89	SPS	B	101	86	-	0/15/18/18	0/1/1/1
90	PRO	B	102	-	-	0/0/9/11	0/1/1/1
90	PRO	C	101	-	-	0/0/9/11	0/1/1/1
87	OHX	C3	201	-	-	0/0/0/0	0/0/0/0
87	OHX	C5	201	17	-	0/0/0/0	0/0/0/0
87	OHX	C8	201	-	-	0/0/0/0	0/0/0/0
87	OHX	D9	102	-	-	0/0/0/0	0/0/0/0
87	OHX	L3	402	-	-	0/0/0/0	0/0/0/0
87	OHX	L3	403	-	-	0/0/0/0	0/0/0/0
87	OHX	L3	404	-	-	0/0/0/0	0/0/0/0
87	OHX	L4	401	-	-	0/0/0/0	0/0/0/0
87	OHX	L5	301	-	-	0/0/0/0	0/0/0/0
87	OHX	M0	302	-	-	0/0/0/0	0/0/0/0
87	OHX	M0	303	-	-	0/0/0/0	0/0/0/0
87	OHX	M5	302	-	-	0/0/0/0	0/0/0/0
87	OHX	M5	303	-	-	0/0/0/0	0/0/0/0
87	OHX	M6	203	-	-	0/0/0/0	0/0/0/0
87	OHX	M7	205	-	-	0/0/0/0	0/0/0/0
87	OHX	M8	201	-	-	0/0/0/0	0/0/0/0
87	OHX	M9	202	-	-	0/0/0/0	0/0/0/0
87	OHX	N8	202	-	-	0/0/0/0	0/0/0/0
87	OHX	N9	101	-	-	0/0/0/0	0/0/0/0
87	OHX	O1	201	-	-	0/0/0/0	0/0/0/0
87	OHX	O3	202	-	-	0/0/0/0	0/0/0/0
87	OHX	O4	202	-	-	0/0/0/0	0/0/0/0
87	OHX	O7	103	73	-	0/0/0/0	0/0/0/0
87	OHX	O9	101	-	-	0/0/0/0	0/0/0/0
87	OHX	Q2	503	-	-	0/0/0/0	0/0/0/0
87	OHX	S1	301	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OHX	S6	301	-	-	0/0/0/0	0/0/0/0
87	OHX	S8	301	-	-	0/0/0/0	0/0/0/0
87	OHX	S9	201	-	-	0/0/0/0	0/0/0/0
87	OHX	SR	401	-	-	0/0/0/0	0/0/0/0
87	OHX	c3	201	-	-	0/0/0/0	0/0/0/0
87	OHX	c5	201	-	-	0/0/0/0	0/0/0/0
87	OHX	c5	202	17	-	0/0/0/0	0/0/0/0
87	OHX	c8	202	-	-	0/0/0/0	0/0/0/0
87	OHX	d4	201	-	-	0/0/0/0	0/0/0/0
87	OHX	d9	102	-	-	0/0/0/0	0/0/0/0
87	OHX	l3	403	-	-	0/0/0/0	0/0/0/0
87	OHX	l3	404	-	-	0/0/0/0	0/0/0/0
87	OHX	l4	402	-	-	0/0/0/0	0/0/0/0
87	OHX	l4	403	-	-	0/0/0/0	0/0/0/0
87	OHX	l5	302	-	-	0/0/0/0	0/0/0/0
87	OHX	l5	303	-	-	0/0/0/0	0/0/0/0
87	OHX	l9	201	-	-	0/0/0/0	0/0/0/0
87	OHX	m0	301	-	-	0/0/0/0	0/0/0/0
87	OHX	m0	302	-	-	0/0/0/0	0/0/0/0
87	OHX	m1	201	-	-	0/0/0/0	0/0/0/0
87	OHX	m4	201	-	-	0/0/0/0	0/0/0/0
87	OHX	m5	303	-	-	0/0/0/0	0/0/0/0
87	OHX	m5	304	-	-	0/0/0/0	0/0/0/0
87	OHX	m5	305	-	-	0/0/0/0	0/0/0/0
87	OHX	m6	201	-	-	0/0/0/0	0/0/0/0
87	OHX	m7	203	-	-	0/0/0/0	0/0/0/0
87	OHX	m8	201	-	-	0/0/0/0	0/0/0/0
87	OHX	m9	201	-	-	0/0/0/0	0/0/0/0
87	OHX	n3	202	-	-	0/0/0/0	0/0/0/0
87	OHX	n9	101	-	-	0/0/0/0	0/0/0/0
87	OHX	o3	202	-	-	0/0/0/0	0/0/0/0
87	OHX	o6	201	-	-	0/0/0/0	0/0/0/0
87	OHX	o7	502	-	-	0/0/0/0	0/0/0/0
87	OHX	o7	503	-	-	0/0/0/0	0/0/0/0
87	OHX	q2	502	-	-	0/0/0/0	0/0/0/0
87	OHX	s1	301	-	-	0/0/0/0	0/0/0/0
87	OHX	s1	302	-	-	0/0/0/0	0/0/0/0
87	OHX	s4	602	-	-	0/0/0/0	0/0/0/0
87	OHX	s8	303	-	-	0/0/0/0	0/0/0/0
87	OHX	s9	201	-	-	0/0/0/0	0/0/0/0
87	OHX	sR	401	-	-	0/0/0/0	0/0/0/0

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	B	101	SPS	C9-C10	-8.74	1.31	1.48
89	5	3402	SPS	C9-C10	-8.57	1.31	1.48
89	5	3402	SPS	O13-C13	-5.26	1.19	1.42
89	B	101	SPS	O13-C13	-5.19	1.19	1.42
89	B	101	SPS	C1-C6	-2.97	1.37	1.44
89	B	101	SPS	C3-N4	-2.83	1.32	1.38
89	5	3402	SPS	O10-C10	-2.82	1.19	1.24
89	B	101	SPS	O10-C10	-2.71	1.19	1.24
89	5	3402	SPS	C3-N4	-2.35	1.33	1.38
89	5	3402	SPS	C1-C6	-2.27	1.39	1.44
89	5	3402	SPS	O1-C1	-2.24	1.18	1.24
89	B	101	SPS	O1-C1	-2.23	1.18	1.24
89	B	101	SPS	C6-C5	-2.15	1.37	1.40
89	B	101	SPS	C6-C8	2.68	1.53	1.47
89	5	3402	SPS	C6-C8	2.69	1.53	1.47
89	5	3402	SPS	C10-N11	3.28	1.44	1.34
89	B	101	SPS	C10-N11	3.45	1.44	1.34
89	5	3402	SPS	O15-S15	4.46	1.64	1.50
89	B	101	SPS	O15-S15	4.82	1.65	1.50
89	B	101	SPS	C9-C8	6.82	1.51	1.32
89	5	3402	SPS	C9-C8	6.97	1.52	1.32

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	5	3402	SPS	C12-N11-C10	-4.86	116.01	122.57
89	5	3402	SPS	N2-C3-N4	-4.71	119.76	127.69
89	B	101	SPS	N2-C3-N4	-4.64	119.88	127.69
89	B	101	SPS	C7-C5-C6	-3.64	119.27	123.63
89	5	3402	SPS	C6-C8-C9	-3.22	116.62	127.08
89	5	3402	SPS	C7-C5-C6	-3.02	120.02	123.63
90	C	101	PRO	O-C-CA	-2.89	117.80	125.69
89	B	101	SPS	C6-C8-C9	-2.87	117.75	127.08
89	B	101	SPS	C12-N11-C10	-2.43	119.29	122.57
89	5	3402	SPS	C8-C9-C10	-2.16	117.25	121.56
89	5	3402	SPS	O10-C10-N11	-2.15	118.95	122.34
90	B	102	PRO	CD-N-CA	2.00	112.08	107.11
89	5	3402	SPS	C7-C5-N4	2.28	119.78	116.32
89	5	3402	SPS	O13-C13-C12	2.69	119.70	112.24
89	5	3402	SPS	C18-S17-C16	2.88	108.95	100.14
89	5	3402	SPS	C9-C10-N11	2.98	120.80	114.14
89	B	101	SPS	O13-C13-C12	3.06	120.73	112.24
89	B	101	SPS	C18-S17-C16	3.39	110.52	100.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	5	3402	SPS	C1-N2-C3	7.15	121.12	115.16
89	B	101	SPS	C1-N2-C3	8.08	121.90	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

560 monomers are involved in 816 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	1	3763	OHX	1	0
87	1	3765	OHX	1	0
87	1	3766	OHX	2	0
87	1	3768	OHX	1	0
87	1	3769	OHX	2	0
87	1	3770	OHX	2	0
87	1	3771	OHX	1	0
87	1	3774	OHX	2	0
87	1	3775	OHX	1	0
87	1	3776	OHX	1	0
87	1	3777	OHX	2	0
87	1	3779	OHX	2	0
87	1	3781	OHX	1	0
87	1	3782	OHX	1	0
87	1	3783	OHX	1	0
87	1	3785	OHX	1	0
87	1	3787	OHX	1	0
87	1	3788	OHX	1	0
87	1	3789	OHX	1	0
87	1	3790	OHX	1	0
87	1	3794	OHX	1	0
87	1	3796	OHX	1	0
87	1	3800	OHX	1	0
87	1	3803	OHX	1	0
87	1	3806	OHX	1	0
87	1	3809	OHX	3	0
87	1	3810	OHX	1	0
87	1	3811	OHX	1	0
87	1	3812	OHX	2	0
87	1	3813	OHX	1	0
87	1	3815	OHX	1	0
87	1	3816	OHX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	1	3819	OHX	1	0
87	1	3821	OHX	1	0
87	1	3823	OHX	1	0
87	1	3824	OHX	1	0
87	1	3825	OHX	1	0
87	1	3826	OHX	1	0
87	1	3828	OHX	1	0
87	1	3830	OHX	2	0
87	1	3831	OHX	1	0
87	1	3833	OHX	1	0
87	1	3834	OHX	1	0
87	1	3837	OHX	1	0
87	1	3838	OHX	1	0
87	1	3839	OHX	1	0
87	1	3840	OHX	1	0
87	1	3844	OHX	1	0
87	1	3847	OHX	1	0
87	1	3849	OHX	1	0
87	1	3850	OHX	1	0
87	1	3853	OHX	2	0
87	1	3854	OHX	4	0
87	1	3855	OHX	1	0
87	1	3856	OHX	1	0
87	1	3858	OHX	2	0
87	1	3859	OHX	1	0
87	1	3860	OHX	1	0
87	1	3863	OHX	1	0
87	1	3868	OHX	1	0
87	1	3870	OHX	2	0
87	1	3872	OHX	1	0
87	1	3873	OHX	1	0
87	1	3875	OHX	1	0
87	1	3877	OHX	2	0
87	1	3878	OHX	1	0
87	1	3881	OHX	2	0
87	1	3884	OHX	3	0
87	1	3887	OHX	1	0
87	1	3889	OHX	4	0
87	1	3893	OHX	2	0
87	1	3894	OHX	1	0
87	1	3897	OHX	3	0
87	1	3898	OHX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	1	3899	OHX	1	0
87	1	3900	OHX	1	0
87	1	3904	OHX	1	0
87	1	3906	OHX	1	0
87	1	3911	OHX	1	0
87	1	3913	OHX	1	0
87	1	3915	OHX	1	0
87	1	3919	OHX	1	0
87	1	3920	OHX	1	0
87	1	3921	OHX	1	0
87	1	3930	OHX	1	0
87	1	3932	OHX	1	0
87	1	3934	OHX	1	0
87	1	3935	OHX	1	0
87	1	3936	OHX	1	0
87	1	3937	OHX	2	0
87	1	3938	OHX	2	0
87	1	3939	OHX	1	0
87	1	3940	OHX	5	0
87	1	3942	OHX	2	0
87	1	3943	OHX	1	0
87	1	3945	OHX	3	0
87	1	3949	OHX	1	0
87	1	3950	OHX	3	0
87	1	3951	OHX	3	0
87	1	3952	OHX	1	0
87	1	3956	OHX	1	0
87	1	3957	OHX	1	0
87	1	3958	OHX	1	0
87	1	3960	OHX	1	0
87	1	3963	OHX	1	0
87	1	3964	OHX	1	0
87	1	3967	OHX	2	0
87	1	3974	OHX	1	0
87	1	3978	OHX	1	0
87	1	3979	OHX	1	0
87	1	3981	OHX	1	0
87	1	3984	OHX	1	0
87	1	3986	OHX	1	0
87	1	3991	OHX	1	0
87	1	3993	OHX	1	0
87	1	3996	OHX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	1	3997	OHX	1	0
87	1	3999	OHX	2	0
87	1	4000	OHX	1	0
87	1	4001	OHX	1	0
87	1	4003	OHX	1	0
87	1	4014	OHX	1	0
87	1	4018	OHX	1	0
87	1	4019	OHX	1	0
87	1	4027	OHX	2	0
87	1	4029	OHX	1	0
87	1	4030	OHX	2	0
87	1	4032	OHX	1	0
87	1	4033	OHX	2	0
87	1	4034	OHX	1	0
87	1	4036	OHX	1	0
87	1	4037	OHX	2	0
87	1	4038	OHX	2	0
87	1	4040	OHX	1	0
87	1	4043	OHX	1	0
87	1	4044	OHX	2	0
87	1	4046	OHX	1	0
87	1	4048	OHX	1	0
87	1	4049	OHX	1	0
87	1	4050	OHX	1	0
87	1	4055	OHX	1	0
87	1	4058	OHX	1	0
87	1	4060	OHX	3	0
87	1	4061	OHX	3	0
87	1	4065	OHX	1	0
87	1	4066	OHX	2	0
87	1	4067	OHX	1	0
87	1	4070	OHX	1	0
87	1	4071	OHX	8	0
87	1	4072	OHX	1	0
87	1	4076	OHX	3	0
87	1	4077	OHX	1	0
87	1	4081	OHX	1	0
87	1	4082	OHX	6	0
87	1	4083	OHX	1	0
87	1	4085	OHX	4	0
87	1	4087	OHX	1	0
87	1	4096	OHX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	1	4097	OHX	2	0
87	1	4098	OHX	1	0
87	1	4100	OHX	2	0
87	1	4102	OHX	1	0
87	1	4106	OHX	1	0
87	1	4107	OHX	1	0
87	1	4110	OHX	1	0
87	2	1991	OHX	1	0
87	2	1992	OHX	1	0
87	2	1993	OHX	1	0
87	2	1994	OHX	2	0
87	2	1995	OHX	1	0
87	2	1997	OHX	1	0
87	2	2000	OHX	1	0
87	2	2001	OHX	2	0
87	2	2002	OHX	2	0
87	2	2003	OHX	1	0
87	2	2005	OHX	1	0
87	2	2006	OHX	1	0
87	2	2008	OHX	3	0
87	2	2012	OHX	1	0
87	2	2013	OHX	1	0
87	2	2014	OHX	1	0
87	2	2015	OHX	1	0
87	2	2016	OHX	1	0
87	2	2018	OHX	1	0
87	2	2019	OHX	1	0
87	2	2020	OHX	1	0
87	2	2026	OHX	1	0
87	2	2027	OHX	1	0
87	2	2032	OHX	1	0
87	2	2033	OHX	1	0
87	2	2034	OHX	2	0
87	2	2035	OHX	1	0
87	2	2036	OHX	1	0
87	2	2038	OHX	2	0
87	2	2039	OHX	3	0
87	2	2041	OHX	3	0
87	2	2042	OHX	1	0
87	2	2046	OHX	1	0
87	2	2049	OHX	1	0
87	2	2050	OHX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	2	2051	OHX	1	0
87	2	2052	OHX	2	0
87	2	2055	OHX	1	0
87	2	2057	OHX	1	0
87	2	2058	OHX	5	0
87	2	2059	OHX	1	0
87	2	2061	OHX	1	0
87	2	2064	OHX	1	0
87	2	2066	OHX	2	0
87	2	2072	OHX	1	0
87	2	2074	OHX	2	0
87	2	2075	OHX	1	0
87	2	2076	OHX	1	0
87	2	2078	OHX	1	0
87	2	2079	OHX	1	0
87	2	2080	OHX	3	0
87	2	2082	OHX	1	0
87	2	2083	OHX	1	0
87	2	2084	OHX	2	0
87	2	2089	OHX	3	0
87	2	2092	OHX	2	0
87	2	2095	OHX	1	0
87	2	2097	OHX	1	0
87	2	2099	OHX	4	0
87	2	2101	OHX	2	0
87	2	2102	OHX	1	0
87	2	2105	OHX	1	0
87	2	2106	OHX	1	0
87	2	2108	OHX	2	0
87	2	2109	OHX	1	0
87	2	2110	OHX	1	0
87	2	2112	OHX	1	0
87	2	2116	OHX	2	0
87	2	2117	OHX	1	0
87	2	2119	OHX	1	0
87	2	2120	OHX	1	0
87	2	2122	OHX	1	0
87	2	2123	OHX	2	0
87	2	2124	OHX	1	0
87	2	2127	OHX	3	0
87	2	2128	OHX	1	0
87	2	2130	OHX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	2	2131	OHX	4	0
87	2	2132	OHX	1	0
87	2	2133	OHX	1	0
87	2	2136	OHX	1	0
87	2	2138	OHX	1	0
87	2	2142	OHX	1	0
87	2	2143	OHX	1	0
87	2	2145	OHX	1	0
87	2	2150	OHX	2	0
87	2	2151	OHX	1	0
87	3	209	OHX	1	0
87	3	214	OHX	1	0
87	3	216	OHX	1	0
87	4	216	OHX	1	0
87	4	217	OHX	1	0
87	4	218	OHX	2	0
87	4	219	OHX	1	0
87	4	220	OHX	1	0
87	4	222	OHX	2	0
87	4	223	OHX	1	0
87	4	224	OHX	1	0
87	4	226	OHX	1	0
87	4	227	OHX	1	0
87	4	228	OHX	1	0
87	4	229	OHX	1	0
89	5	3402	SPS	6	0
87	5	3816	OHX	1	0
87	5	3818	OHX	2	0
87	5	3820	OHX	1	0
87	5	3822	OHX	1	0
87	5	3824	OHX	1	0
87	5	3825	OHX	2	0
87	5	3827	OHX	1	0
87	5	3829	OHX	2	0
87	5	3832	OHX	1	0
87	5	3833	OHX	2	0
87	5	3834	OHX	2	0
87	5	3835	OHX	1	0
87	5	3836	OHX	1	0
87	5	3838	OHX	2	0
87	5	3840	OHX	1	0
87	5	3841	OHX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	5	3845	OHX	1	0
87	5	3848	OHX	1	0
87	5	3849	OHX	1	0
87	5	3854	OHX	1	0
87	5	3855	OHX	1	0
87	5	3857	OHX	1	0
87	5	3858	OHX	1	0
87	5	3860	OHX	1	0
87	5	3861	OHX	1	0
87	5	3868	OHX	1	0
87	5	3869	OHX	2	0
87	5	3872	OHX	3	0
87	5	3874	OHX	1	0
87	5	3875	OHX	1	0
87	5	3876	OHX	1	0
87	5	3877	OHX	3	0
87	5	3878	OHX	2	0
87	5	3879	OHX	1	0
87	5	3880	OHX	1	0
87	5	3884	OHX	1	0
87	5	3885	OHX	1	0
87	5	3887	OHX	1	0
87	5	3889	OHX	1	0
87	5	3890	OHX	1	0
87	5	3893	OHX	3	0
87	5	3894	OHX	1	0
87	5	3895	OHX	1	0
87	5	3898	OHX	1	0
87	5	3899	OHX	1	0
87	5	3900	OHX	1	0
87	5	3901	OHX	2	0
87	5	3903	OHX	2	0
87	5	3904	OHX	1	0
87	5	3905	OHX	2	0
87	5	3906	OHX	1	0
87	5	3909	OHX	1	0
87	5	3910	OHX	1	0
87	5	3911	OHX	1	0
87	5	3914	OHX	4	0
87	5	3917	OHX	4	0
87	5	3918	OHX	1	0
87	5	3920	OHX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	5	3921	OHX	3	0
87	5	3922	OHX	1	0
87	5	3924	OHX	1	0
87	5	3925	OHX	1	0
87	5	3927	OHX	1	0
87	5	3928	OHX	2	0
87	5	3929	OHX	1	0
87	5	3932	OHX	2	0
87	5	3934	OHX	1	0
87	5	3935	OHX	2	0
87	5	3938	OHX	2	0
87	5	3940	OHX	1	0
87	5	3942	OHX	1	0
87	5	3943	OHX	1	0
87	5	3944	OHX	1	0
87	5	3945	OHX	1	0
87	5	3947	OHX	1	0
87	5	3948	OHX	1	0
87	5	3952	OHX	1	0
87	5	3954	OHX	4	0
87	5	3955	OHX	1	0
87	5	3956	OHX	1	0
87	5	3958	OHX	1	0
87	5	3959	OHX	1	0
87	5	3960	OHX	1	0
87	5	3961	OHX	1	0
87	5	3962	OHX	1	0
87	5	3963	OHX	1	0
87	5	3964	OHX	1	0
87	5	3965	OHX	1	0
87	5	3966	OHX	1	0
87	5	3969	OHX	1	0
87	5	3976	OHX	2	0
87	5	3977	OHX	3	0
87	5	3981	OHX	1	0
87	5	3983	OHX	1	0
87	5	3985	OHX	1	0
87	5	3987	OHX	1	0
87	5	3988	OHX	2	0
87	5	3991	OHX	1	0
87	5	3995	OHX	2	0
87	5	3996	OHX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	5	3997	OHX	1	0
87	5	3999	OHX	1	0
87	5	4000	OHX	5	0
87	5	4001	OHX	5	0
87	5	4004	OHX	1	0
87	5	4008	OHX	1	0
87	5	4009	OHX	1	0
87	5	4010	OHX	2	0
87	5	4011	OHX	1	0
87	5	4012	OHX	1	0
87	5	4013	OHX	3	0
87	5	4014	OHX	2	0
87	5	4016	OHX	1	0
87	5	4018	OHX	2	0
87	5	4023	OHX	1	0
87	5	4026	OHX	1	0
87	5	4036	OHX	1	0
87	5	4037	OHX	1	0
87	5	4040	OHX	1	0
87	5	4045	OHX	1	0
87	5	4046	OHX	2	0
87	5	4047	OHX	1	0
87	5	4048	OHX	1	0
87	5	4051	OHX	3	0
87	5	4052	OHX	3	0
87	5	4053	OHX	1	0
87	5	4055	OHX	1	0
87	5	4057	OHX	2	0
87	5	4059	OHX	1	0
87	5	4060	OHX	2	0
87	5	4065	OHX	1	0
87	5	4068	OHX	1	0
87	5	4069	OHX	1	0
87	5	4071	OHX	1	0
87	5	4075	OHX	1	0
87	5	4081	OHX	1	0
87	5	4083	OHX	5	0
87	5	4086	OHX	1	0
87	5	4087	OHX	1	0
87	5	4092	OHX	2	0
87	5	4095	OHX	3	0
87	5	4096	OHX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	5	4100	OHX	1	0
87	5	4101	OHX	1	0
87	5	4102	OHX	2	0
87	5	4103	OHX	1	0
87	5	4104	OHX	1	0
87	5	4111	OHX	1	0
87	5	4113	OHX	3	0
87	5	4116	OHX	2	0
87	5	4117	OHX	3	0
87	5	4119	OHX	3	0
87	5	4120	OHX	1	0
87	5	4124	OHX	1	0
87	5	4128	OHX	1	0
87	5	4129	OHX	2	0
87	5	4130	OHX	1	0
87	5	4132	OHX	1	0
87	5	4137	OHX	1	0
87	5	4139	OHX	2	0
87	5	4140	OHX	1	0
87	5	4143	OHX	2	0
87	5	4147	OHX	1	0
87	5	4148	OHX	1	0
87	5	4151	OHX	1	0
87	5	4152	OHX	1	0
87	5	4153	OHX	2	0
87	5	4156	OHX	1	0
87	5	4158	OHX	1	0
87	5	4163	OHX	1	0
87	5	4165	OHX	1	0
87	5	4169	OHX	2	0
87	5	4170	OHX	2	0
87	5	4171	OHX	1	0
87	6	2014	OHX	2	0
87	6	2015	OHX	1	0
87	6	2018	OHX	1	0
87	6	2020	OHX	1	0
87	6	2022	OHX	2	0
87	6	2023	OHX	1	0
87	6	2024	OHX	1	0
87	6	2027	OHX	2	0
87	6	2028	OHX	2	0
87	6	2031	OHX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	6	2032	OHX	1	0
87	6	2033	OHX	1	0
87	6	2034	OHX	1	0
87	6	2036	OHX	1	0
87	6	2037	OHX	1	0
87	6	2038	OHX	2	0
87	6	2039	OHX	2	0
87	6	2040	OHX	2	0
87	6	2041	OHX	2	0
87	6	2044	OHX	1	0
87	6	2050	OHX	1	0
87	6	2053	OHX	1	0
87	6	2054	OHX	1	0
87	6	2055	OHX	1	0
87	6	2056	OHX	1	0
87	6	2057	OHX	1	0
87	6	2058	OHX	1	0
87	6	2060	OHX	1	0
87	6	2063	OHX	3	0
87	6	2064	OHX	1	0
87	6	2067	OHX	4	0
87	6	2069	OHX	2	0
87	6	2070	OHX	1	0
87	6	2074	OHX	2	0
87	6	2078	OHX	1	0
87	6	2081	OHX	1	0
87	6	2083	OHX	2	0
87	6	2085	OHX	1	0
87	6	2086	OHX	1	0
87	6	2087	OHX	1	0
87	6	2089	OHX	2	0
87	6	2092	OHX	2	0
87	6	2094	OHX	2	0
87	6	2095	OHX	1	0
87	6	2096	OHX	3	0
87	6	2101	OHX	1	0
87	6	2103	OHX	1	0
87	6	2104	OHX	2	0
87	6	2105	OHX	1	0
87	6	2107	OHX	1	0
87	6	2108	OHX	1	0
87	6	2109	OHX	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	6	2110	OHX	3	0
87	6	2111	OHX	2	0
87	6	2112	OHX	1	0
87	6	2115	OHX	2	0
87	6	2123	OHX	2	0
87	6	2124	OHX	5	0
87	6	2127	OHX	2	0
87	6	2129	OHX	1	0
87	6	2131	OHX	1	0
87	6	2132	OHX	1	0
87	6	2134	OHX	1	0
87	6	2138	OHX	1	0
87	6	2141	OHX	1	0
87	6	2145	OHX	1	0
87	6	2149	OHX	1	0
87	6	2150	OHX	1	0
87	6	2151	OHX	1	0
87	6	2153	OHX	1	0
87	6	2156	OHX	2	0
87	6	2157	OHX	1	0
87	6	2159	OHX	1	0
87	6	2168	OHX	1	0
87	6	2170	OHX	3	0
87	6	2172	OHX	1	0
87	6	2173	OHX	1	0
87	6	2175	OHX	1	0
87	6	2180	OHX	1	0
87	6	2181	OHX	3	0
87	6	2183	OHX	1	0
87	7	218	OHX	1	0
87	7	221	OHX	1	0
87	7	222	OHX	2	0
87	8	210	OHX	1	0
87	8	214	OHX	1	0
87	8	215	OHX	1	0
87	8	216	OHX	2	0
87	8	217	OHX	1	0
87	8	221	OHX	1	0
87	8	222	OHX	1	0
87	8	228	OHX	2	0
87	8	230	OHX	1	0
89	B	101	SPS	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	C3	201	OHX	3	0
87	C5	201	OHX	5	0
87	L3	402	OHX	1	0
87	L3	403	OHX	2	0
87	L4	401	OHX	3	0
87	L5	301	OHX	1	0
87	M0	302	OHX	2	0
87	M0	303	OHX	5	0
87	M5	302	OHX	1	0
87	M5	303	OHX	1	0
87	M7	205	OHX	1	0
87	M9	202	OHX	1	0
87	N9	101	OHX	2	0
87	O1	201	OHX	2	0
87	O3	202	OHX	1	0
87	O4	202	OHX	2	0
87	O7	103	OHX	6	0
87	O9	101	OHX	1	0
87	Q2	503	OHX	2	0
87	S1	301	OHX	3	0
87	S6	301	OHX	3	0
87	S8	301	OHX	1	0
87	S9	201	OHX	4	0
87	SR	401	OHX	5	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	2	2
81	m2	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	1716:C	O3'	1717:G	P	5.10

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	m2	23:LEU	C	28:ARG	N	3.71
1	m2	52:LYS	C	54:LYS	N	3.25
1	2	1685:G	O3'	1686:C	P	2.98

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	2	1781/1800 (98%)	0.47	99 (5%) 28 25	58, 100, 190, 245	0
1	6	1795/1800 (99%)	0.23	55 (3%) 52 46	41, 84, 172, 231	0
2	S0	206/251 (82%)	1.44	64 (31%) 1 1	99, 112, 122, 125	0
2	s0	206/251 (82%)	0.72	19 (9%) 11 11	78, 93, 107, 115	0
3	S1	214/254 (84%)	1.78	78 (36%) 0 0	114, 152, 175, 179	0
3	s1	216/254 (85%)	0.92	35 (16%) 3 3	80, 93, 110, 126	0
4	S2	217/253 (85%)	0.31	8 (3%) 45 39	79, 95, 109, 118	0
4	s2	217/253 (85%)	0.63	24 (11%) 7 8	63, 79, 90, 99	0
5	S3	223/239 (93%)	0.92	36 (16%) 3 3	90, 103, 122, 135	0
5	s3	223/239 (93%)	0.99	45 (20%) 1 2	83, 108, 131, 139	0
6	S4	260/260 (100%)	2.36	139 (53%) 0 0	78, 101, 111, 133	0
6	s4	260/260 (100%)	1.62	86 (33%) 0 0	56, 79, 94, 113	0
7	S5	206/224 (91%)	2.20	103 (50%) 0 0	107, 122, 134, 144	0
7	s5	206/224 (91%)	1.90	95 (46%) 0 0	88, 106, 123, 134	0
8	S6	226/236 (95%)	0.98	46 (20%) 1 2	77, 113, 131, 142	0
8	s6	218/236 (92%)	0.69	24 (11%) 7 8	56, 85, 110, 123	0
9	S7	184/189 (97%)	1.14	41 (22%) 1 1	96, 127, 147, 152	0
9	s7	186/189 (98%)	0.36	8 (4%) 39 33	70, 103, 132, 139	0
10	S8	188/200 (94%)	1.30	52 (27%) 1 1	68, 88, 122, 139	0
10	s8	188/200 (94%)	0.77	25 (13%) 4 5	52, 69, 110, 129	0
11	S9	185/196 (94%)	2.38	101 (54%) 0 0	91, 107, 137, 157	0
11	s9	185/196 (94%)	1.29	45 (24%) 1 1	68, 87, 125, 146	0
12	C0	96/105 (91%)	2.05	44 (45%) 0 0	96, 121, 141, 151	0
12	c0	96/105 (91%)	2.10	42 (43%) 0 0	105, 136, 149, 150	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
13	C1	155/155 (100%)	1.01	26 (16%)	2 2	71, 84, 118, 130	0
13	c1	146/155 (94%)	0.60	13 (8%)	12 12	54, 66, 94, 115	0
14	C2	124/142 (87%)	0.93	18 (14%)	3 4	149, 161, 174, 180	0
14	c2	124/142 (87%)	2.60	78 (62%)	0 0	180, 196, 211, 215	0
15	C3	150/150 (100%)	1.14	39 (26%)	1 1	79, 94, 109, 115	0
15	c3	150/150 (100%)	0.26	7 (4%)	35 30	63, 76, 93, 96	0
16	C4	127/136 (93%)	1.85	56 (44%)	0 0	83, 146, 158, 162	0
16	c4	128/136 (94%)	0.95	19 (14%)	3 3	64, 96, 104, 109	0
17	C5	124/141 (87%)	1.10	28 (22%)	1 1	87, 103, 120, 130	0
17	c5	135/141 (95%)	1.36	45 (33%)	0 0	72, 107, 122, 123	0
18	C6	141/142 (99%)	2.40	77 (54%)	0 0	92, 110, 116, 118	0
18	c6	142/142 (100%)	2.01	61 (42%)	0 0	82, 104, 118, 136	0
19	C7	120/136 (88%)	1.24	29 (24%)	1 1	95, 110, 129, 131	0
19	c7	117/136 (86%)	0.63	15 (12%)	5 5	85, 102, 114, 122	0
20	C8	145/145 (100%)	1.33	41 (28%)	1 1	85, 109, 135, 142	0
20	c8	145/145 (100%)	1.35	37 (25%)	1 1	83, 101, 117, 124	0
21	C9	143/143 (100%)	2.44	84 (58%)	0 0	95, 110, 125, 133	0
21	c9	143/143 (100%)	1.10	27 (18%)	2 2	82, 98, 115, 123	0
22	D0	107/120 (89%)	1.02	22 (20%)	1 1	86, 114, 136, 138	0
22	d0	110/120 (91%)	1.08	27 (24%)	1 1	85, 115, 144, 149	0
23	D1	87/87 (100%)	0.75	13 (14%)	3 3	96, 103, 117, 122	0
23	d1	87/87 (100%)	0.15	1 (1%)	82 76	71, 82, 104, 111	0
24	D2	129/129 (100%)	0.82	13 (10%)	9 10	80, 92, 101, 111	0
24	d2	129/129 (100%)	0.29	3 (2%)	64 57	59, 68, 75, 84	0
25	D3	144/144 (100%)	1.29	44 (30%)	1 1	70, 78, 90, 102	0
25	d3	144/144 (100%)	0.75	12 (8%)	14 14	52, 57, 70, 81	0
26	D4	134/134 (100%)	2.20	64 (47%)	0 0	89, 111, 123, 127	0
26	d4	134/134 (100%)	0.42	14 (10%)	8 9	65, 88, 100, 105	0
27	D5	70/107 (65%)	2.43	39 (55%)	0 0	118, 134, 141, 146	0
27	d5	69/107 (64%)	2.38	38 (55%)	0 0	98, 112, 124, 126	0
28	D6	97/97 (100%)	1.79	39 (40%)	0 0	86, 108, 160, 162	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å²)		Q<0.9	
28	d6	97/97 (100%)	0.76	13 (13%)	4	5	67, 84, 111, 116	0
29	D7	81/81 (100%)	1.77	36 (44%)	0	0	95, 113, 139, 143	0
29	d7	81/81 (100%)	1.12	19 (23%)	1	1	72, 89, 127, 128	0
30	D8	63/66 (95%)	1.69	23 (36%)	0	0	114, 131, 139, 144	0
30	d8	63/66 (95%)	1.77	25 (39%)	0	0	105, 118, 125, 128	0
31	D9	53/55 (96%)	1.47	15 (28%)	1	1	85, 90, 108, 114	0
31	d9	53/55 (96%)	2.16	26 (49%)	0	0	82, 92, 128, 145	0
32	E0	60/60 (100%)	2.37	36 (60%)	0	0	80, 110, 134, 137	0
33	E1	71/76 (93%)	1.74	28 (39%)	0	0	115, 142, 155, 157	0
33	e1	76/76 (100%)	2.68	38 (50%)	0	0	117, 168, 186, 187	0
34	SR	318/318 (100%)	1.41	90 (28%)	1	1	109, 122, 138, 156	0
34	sR	318/318 (100%)	2.74	185 (58%)	0	0	112, 127, 141, 153	0
35	SM	159/273 (58%)	1.17	37 (23%)	1	1	58, 100, 159, 163	0
35	sM	104/273 (38%)	1.33	25 (24%)	1	1	51, 115, 188, 197	0
36	1	3149/3396 (92%)	0.17	64 (2%)	68	62	33, 58, 136, 238	0
36	5	3150/3396 (92%)	0.13	35 (1%)	82	76	28, 52, 127, 213	0
37	3	121/121 (100%)	-0.02	0	100	100	42, 77, 90, 98	0
37	7	121/121 (100%)	-0.11	0	100	100	33, 55, 66, 75	0
38	4	158/158 (100%)	0.06	3 (1%)	70	63	42, 63, 102, 146	0
38	8	158/158 (100%)	0.03	1 (0%)	90	86	42, 63, 101, 131	0
39	L2	252/253 (99%)	0.59	15 (5%)	25	22	40, 60, 78, 84	0
39	l2	252/253 (99%)	0.35	6 (2%)	62	55	36, 55, 73, 80	0
40	L3	386/386 (100%)	0.40	20 (5%)	31	27	37, 62, 77, 88	0
40	l3	386/386 (100%)	0.32	17 (4%)	38	32	28, 45, 60, 81	0
41	L4	361/361 (100%)	0.09	3 (0%)	87	81	38, 54, 69, 74	0
41	l4	361/361 (100%)	0.03	2 (0%)	90	86	37, 56, 74, 82	0
42	L5	296/296 (100%)	1.67	118 (39%)	0	0	58, 80, 98, 119	0
42	l5	294/296 (99%)	0.55	19 (6%)	22	20	42, 56, 83, 97	0
43	L6	156/175 (89%)	0.76	16 (10%)	9	9	46, 56, 72, 87	0
43	l6	157/175 (89%)	0.70	13 (8%)	14	14	48, 57, 78, 93	0
44	L7	222/243 (91%)	0.20	0	100	100	38, 47, 77, 104	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	l7	223/243 (91%)	-0.00	1 (0%) 93 90	33, 45, 82, 112	0
45	L8	233/255 (91%)	0.88	37 (15%) 3 3	68, 84, 110, 120	0
45	l8	231/255 (90%)	1.21	54 (23%) 1 1	69, 82, 107, 117	0
46	L9	191/191 (100%)	0.26	5 (2%) 59 52	59, 71, 82, 94	0
46	l9	191/191 (100%)	-0.02	2 (1%) 84 78	41, 51, 68, 78	0
47	M0	211/220 (95%)	0.58	20 (9%) 10 11	44, 63, 94, 105	0
47	m0	213/220 (96%)	0.31	4 (1%) 70 63	39, 54, 78, 94	0
48	M1	169/173 (97%)	1.06	28 (16%) 2 2	68, 85, 97, 103	0
48	m1	169/173 (97%)	0.31	1 (0%) 90 86	47, 66, 77, 81	0
49	M3	193/198 (97%)	0.34	3 (1%) 74 68	36, 63, 101, 122	0
49	m3	194/198 (97%)	0.68	18 (9%) 11 11	38, 67, 104, 119	0
50	M4	136/137 (99%)	-0.07	0 100 100	50, 59, 72, 83	0
50	m4	137/137 (100%)	-0.15	0 100 100	43, 50, 66, 84	0
51	M5	203/203 (100%)	0.66	20 (9%) 9 11	39, 56, 67, 71	0
51	m5	203/203 (100%)	1.29	52 (25%) 1 1	40, 58, 68, 73	0
52	M6	197/198 (99%)	-0.15	2 (1%) 84 78	25, 32, 46, 49	0
52	m6	197/198 (99%)	-0.13	0 100 100	18, 24, 45, 52	0
53	M7	183/183 (100%)	0.77	25 (13%) 4 5	44, 52, 105, 133	0
53	m7	155/183 (84%)	0.09	1 (0%) 90 86	36, 45, 55, 77	0
54	M8	185/185 (100%)	0.18	1 (0%) 91 89	42, 51, 68, 88	0
54	m8	185/185 (100%)	0.29	4 (2%) 65 59	39, 53, 64, 72	0
55	M9	188/188 (100%)	0.89	34 (18%) 2 2	64, 78, 147, 156	0
55	m9	188/188 (100%)	0.21	10 (5%) 30 26	50, 62, 123, 138	0
56	N0	172/172 (100%)	0.48	8 (4%) 35 30	37, 56, 70, 75	0
56	n0	172/172 (100%)	0.02	1 (0%) 90 86	32, 45, 57, 67	0
57	N1	159/159 (100%)	0.33	3 (1%) 70 63	41, 56, 99, 105	0
57	n1	159/159 (100%)	0.21	1 (0%) 90 86	37, 45, 82, 88	0
58	N2	100/120 (83%)	1.43	30 (30%) 1 1	94, 106, 112, 117	0
58	n2	98/120 (81%)	1.12	21 (21%) 1 1	74, 85, 93, 95	0
59	N3	136/136 (100%)	0.47	4 (2%) 55 48	49, 59, 73, 82	0
59	n3	136/136 (100%)	0.16	2 (1%) 76 70	31, 41, 52, 57	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
60	N4	98/155 (63%)	2.28	31 (31%) 1 1	59, 74, 147, 155	0
60	n4	135/155 (87%)	0.87	22 (16%) 2 3	41, 93, 124, 142	0
61	N5	121/141 (85%)	0.89	14 (11%) 6 7	59, 71, 86, 103	0
61	n5	120/141 (85%)	0.72	10 (8%) 14 14	55, 68, 82, 97	0
62	N6	126/126 (100%)	0.62	7 (5%) 28 25	48, 64, 77, 85	0
62	n6	126/126 (100%)	0.45	3 (2%) 62 55	50, 66, 82, 85	0
63	N7	135/135 (100%)	2.30	79 (58%) 0 0	83, 96, 107, 111	0
63	n7	135/135 (100%)	1.25	36 (26%) 1 1	78, 89, 101, 109	0
64	N8	148/148 (100%)	0.46	5 (3%) 49 42	32, 54, 76, 82	0
64	n8	148/148 (100%)	0.68	17 (11%) 6 7	34, 55, 72, 75	0
65	N9	58/58 (100%)	0.08	0 100 100	36, 59, 97, 113	0
65	n9	58/58 (100%)	0.05	0 100 100	36, 55, 76, 82	0
66	O0	97/104 (93%)	1.18	25 (25%) 1 1	83, 90, 106, 111	0
66	o0	100/104 (96%)	0.54	9 (9%) 12 12	69, 79, 98, 105	0
67	O1	109/112 (97%)	1.54	36 (33%) 0 0	60, 73, 94, 101	0
67	o1	109/112 (97%)	1.37	26 (23%) 1 1	44, 56, 89, 97	0
68	O2	127/129 (98%)	0.35	3 (2%) 62 55	34, 48, 63, 79	0
68	o2	127/129 (98%)	0.67	7 (5%) 29 25	32, 52, 67, 78	0
69	O3	106/106 (100%)	0.34	2 (1%) 70 63	39, 46, 70, 82	0
69	o3	106/106 (100%)	0.85	14 (13%) 4 5	36, 44, 71, 82	0
70	O4	112/119 (94%)	1.82	48 (42%) 0 0	57, 74, 110, 117	0
70	o4	112/119 (94%)	1.17	29 (25%) 1 1	50, 66, 101, 108	0
71	O5	119/119 (100%)	0.48	4 (3%) 49 42	56, 73, 80, 83	0
71	o5	119/119 (100%)	0.16	4 (3%) 49 42	58, 71, 86, 96	0
72	O6	99/99 (100%)	1.13	19 (19%) 2 2	59, 70, 100, 111	0
72	o6	99/99 (100%)	0.91	14 (14%) 4 4	62, 72, 91, 110	0
73	O7	87/87 (100%)	0.03	0 100 100	41, 49, 70, 80	0
73	o7	87/87 (100%)	0.03	0 100 100	37, 48, 79, 85	0
74	O8	77/77 (100%)	0.91	7 (9%) 11 11	85, 97, 107, 108	0
74	o8	77/77 (100%)	2.16	44 (57%) 0 0	75, 85, 94, 97	0
75	O9	50/50 (100%)	0.19	0 100 100	51, 57, 61, 62	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
75	o9	50/50 (100%)	-0.01	1 (2%) 68 62	49, 54, 63, 64	0
76	Q0	52/52 (100%)	0.87	6 (11%) 6 7	53, 59, 74, 82	0
76	q0	52/52 (100%)	-0.00	1 (1%) 70 63	38, 42, 52, 57	0
77	Q1	25/25 (100%)	0.27	0 100 100	62, 66, 72, 74	0
77	q1	25/25 (100%)	-0.20	0 100 100	49, 53, 54, 55	0
78	Q2	105/105 (100%)	0.37	7 (6%) 21 19	41, 55, 76, 97	0
78	q2	105/105 (100%)	0.11	1 (0%) 84 78	40, 53, 69, 96	0
79	Q3	91/91 (100%)	0.41	2 (2%) 65 59	49, 65, 79, 85	0
79	q3	91/91 (100%)	0.18	0 100 100	40, 55, 71, 81	0
80	e0	62/62 (100%)	1.55	17 (27%) 1 1	60, 88, 117, 120	0
81	m2	150/165 (90%)	1.38	42 (28%) 1 1	102, 138, 156, 161	0
82	p0	143/311 (45%)	2.15	70 (48%) 0 0	100, 125, 220, 229	0
83	p1	47/106 (44%)	4.36	35 (74%) 0 0	179, 224, 242, 245	0
83	p2	46/106 (43%)	4.94	35 (76%) 0 0	275, 283, 288, 289	0
84	f	147/157 (93%)	2.48	83 (56%) 0 0	47, 99, 167, 169	74 (50%)
85	B	3/4 (75%)	0.55	0 100 100	45, 45, 46, 48	0
85	C	3/4 (75%)	0.35	0 100 100	42, 42, 43, 49	0
All	All	33490/35633 (93%)	0.72	4478 (13%) 4 5	18, 74, 141, 289	74 (0%)

All (4478) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
83	p2	31	ASN	23.0
83	p2	30	THR	19.4
83	p1	17	SER	14.6
83	p2	12	LEU	13.6
83	p2	32	ALA	13.4
83	p1	16	ASP	13.2
83	p1	12	LEU	12.6
83	p2	8	SER	12.3
60	N4	76	VAL	12.2
60	N4	86	SER	12.2
1	2	1694	A	12.1
53	M7	161	ALA	11.8
60	N4	88	ASP	11.8
60	N4	75	THR	11.2

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Mol	Chain	Res	Type	RSRZ
18	C6	20	ALA	11.1
83	p1	1	MET	11.0
33	e1	77	GLY	10.9
1	2	1698	G	10.8
1	2	1695	G	10.8
1	2	1709	C	10.7
1	2	1693	A	10.6
1	2	1702	A	10.3
1	2	1696	G	10.3
84	f	157	ASP	10.2
1	2	1692	G	10.0
34	sR	25	THR	10.0
7	S5	71	ALA	9.6
34	sR	24	ALA	9.6
82	p0	211	SER	9.5
16	C4	15	GLY	9.5
1	2	1710	U	9.4
1	2	1708	U	9.4
14	c2	126	TRP	9.3
83	p2	9	TYR	9.2
1	2	1699	G	9.2
36	5	2505	U	9.1
83	p2	29	LEU	9.0
34	sR	214	ALA	8.9
60	N4	85	ALA	8.9
3	S1	91	VAL	8.9
53	M7	162	GLU	8.8
20	C8	2	SER	8.8
83	p1	15	ALA	8.8
60	N4	90	ILE	8.8
81	m2	91	SER	8.7
36	5	2503	G	8.7
13	C1	147	ALA	8.7
34	sR	303	ALA	8.7
82	p0	212	HIS	8.6
3	S1	20	VAL	8.6
3	S1	47	LEU	8.5
12	c0	25	LYS	8.5
60	N4	89	LEU	8.5
34	sR	313	TRP	8.4
60	N4	83	THR	8.4
1	2	1697	G	8.3

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Mol	Chain	Res	Type	RSRZ
34	sR	252	LEU	8.2
10	S8	152	ILE	8.0
34	sR	202	LEU	8.0
13	c1	3	THR	8.0
12	c0	64	TYR	8.0
34	sR	32	LEU	8.0
33	e1	85	TYR	7.9
16	C4	75	GLY	7.9
60	N4	84	GLY	7.9
1	2	913	G	7.8
53	M7	160	ALA	7.7
84	f	149	SER	7.7
7	S5	70	VAL	7.7
34	sR	314	GLN	7.6
34	sR	302	PHE	7.6
60	N4	78	ALA	7.5
35	SM	85	SER	7.5
83	p1	14	LEU	7.5
35	sM	83	LYS	7.5
17	c5	134	THR	7.4
18	c6	142	TYR	7.4
31	d9	4	GLU	7.3
60	N4	87	LEU	7.3
83	p1	5	SER	7.3
34	sR	212	ALA	7.3
34	sR	244	ALA	7.2
20	c8	146	ALA	7.2
12	c0	22	VAL	7.1
34	sR	292	LEU	7.1
1	6	663	U	7.1
8	S6	78	THR	7.1
36	5	2504	U	7.0
83	p2	33	ALA	7.0
6	S4	54	TYR	7.0
26	D4	31	ASN	7.0
83	p2	11	ALA	6.9
34	sR	168	THR	6.9
3	S1	103	MET	6.9
12	c0	23	ALA	6.9
7	S5	152	GLY	6.9
33	E1	85	TYR	6.9
33	e1	83	LYS	6.9

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Mol	Chain	Res	Type	RSRZ
22	d0	67	THR	6.9
83	p2	19	ILE	6.9
34	sR	33	LEU	6.8
34	sR	71	CYS	6.8
14	c2	123	VAL	6.8
30	d8	9	LEU	6.8
33	e1	80	ARG	6.8
16	C4	76	ILE	6.8
26	D4	6	THR	6.7
35	SM	84	LYS	6.7
34	sR	82	SER	6.7
11	S9	138	LYS	6.7
83	p1	2	SER	6.7
18	C6	21	HIS	6.7
26	D4	70	VAL	6.7
26	D4	34	ASN	6.6
34	sR	167	VAL	6.6
83	p2	5	SER	6.6
11	s9	148	VAL	6.6
35	sM	85	SER	6.6
11	S9	141	VAL	6.6
1	6	1694	A	6.6
27	d5	50	ILE	6.5
34	sR	72	THR	6.5
42	L5	146	LEU	6.5
33	e1	81	LYS	6.5
55	M9	186	LYS	6.5
60	n4	69	LYS	6.5
7	s5	37	GLN	6.5
34	SR	33	LEU	6.5
26	D4	4	ALA	6.5
14	c2	122	VAL	6.5
35	SM	89	ARG	6.5
12	c0	65	TYR	6.4
60	N4	68	ALA	6.4
8	S6	77	LEU	6.4
14	c2	112	ALA	6.4
28	D6	49	ALA	6.4
60	N4	72	SER	6.4
55	M9	181	ARG	6.4
34	SR	79	TYR	6.4
11	S9	140	ILE	6.4

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Mol	Chain	Res	Type	RSRZ
18	c6	139	GLN	6.4
4	s2	88	LYS	6.3
14	C2	41	LEU	6.3
82	p0	88	PHE	6.3
82	p0	209	LEU	6.3
26	D4	26	ASP	6.3
18	C6	66	ARG	6.3
83	p2	4	GLU	6.3
13	c1	4	GLU	6.3
82	p0	205	THR	6.2
18	c6	49	TYR	6.2
21	C9	5	SER	6.2
55	M9	182	ASP	6.2
1	2	1703	C	6.2
60	N4	74	LYS	6.2
12	C0	1	MET	6.2
33	e1	96	LYS	6.2
26	D4	67	GLY	6.2
3	S1	59	ASP	6.2
7	S5	37	GLN	6.1
34	sR	213	SER	6.1
60	n4	68	ALA	6.1
82	p0	218	SER	6.1
83	p1	37	VAL	6.1
20	c8	22	VAL	6.1
3	S1	92	GLN	6.1
11	S9	36	LEU	6.1
83	p1	43	ASP	6.1
1	2	715	U	6.1
34	sR	301	LEU	6.1
56	N0	1	MET	6.1
1	6	1695	G	6.1
34	sR	166	SER	6.0
1	2	1701	A	6.0
34	sR	121	MET	6.0
6	S4	44	LEU	6.0
60	N4	77	LYS	6.0
63	N7	46	ILE	6.0
12	c0	93	GLN	6.0
3	S1	90	GLU	6.0
35	SM	88	ARG	6.0
22	D0	82	TYR	6.0

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Mol	Chain	Res	Type	RSRZ
18	C6	18	ALA	6.0
82	p0	216	ALA	6.0
34	sR	170	ILE	6.0
12	C0	66	TYR	6.0
60	N4	70	LYS	6.0
12	C0	64	TYR	6.0
34	SR	25	THR	6.0
3	S1	86	LEU	5.9
33	E1	87	THR	5.9
22	D0	121	ASN	5.9
34	sR	79	TYR	5.9
6	S4	111	VAL	5.9
35	SM	87	THR	5.9
28	D6	62	TYR	5.9
34	sR	253	ALA	5.9
11	S9	110	GLN	5.9
21	C9	105	LEU	5.9
63	N7	92	PHE	5.9
14	c2	105	LYS	5.9
82	p0	219	THR	5.9
13	C1	145	ALA	5.9
4	s2	87	GLN	5.8
34	SR	45	TRP	5.8
21	C9	4	VAL	5.8
83	p2	28	THR	5.8
34	sR	157	VAL	5.8
33	e1	145	HIS	5.8
18	c6	141	SER	5.8
25	D3	48	HIS	5.8
7	S5	100	ASN	5.8
82	p0	86	PHE	5.8
7	S5	155	ALA	5.8
83	p1	23	SER	5.8
83	p2	3	THR	5.8
26	D4	35	VAL	5.8
34	sR	61	PHE	5.8
1	2	506	A	5.8
42	L5	145	PHE	5.7
84	f	155	ARG	5.7
18	c6	44	LEU	5.7
21	C9	92	LYS	5.7
6	s4	183	VAL	5.7

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Mol	Chain	Res	Type	RSRZ
84	f	115	ALA	5.7
33	E1	86	THR	5.7
84	f	18	THR	5.7
3	S1	50	LYS	5.7
26	D4	69	SER	5.7
6	S4	8	HIS	5.7
21	C9	28	LEU	5.6
3	S1	93	GLY	5.6
31	d9	27	HIS	5.6
12	C0	2	LEU	5.6
18	C6	68	ARG	5.6
84	f	87	ARG	5.6
34	sR	243	LEU	5.6
5	S3	217	ILE	5.6
13	C1	146	ALA	5.6
34	SR	83	ALA	5.6
36	1	2507	C	5.6
74	o8	26	LYS	5.6
34	SR	44	SER	5.6
27	d5	51	LEU	5.6
6	S4	66	MET	5.6
3	S1	46	THR	5.6
34	sR	310	ILE	5.6
33	e1	87	THR	5.6
14	c2	117	GLY	5.6
33	e1	86	THR	5.5
4	s2	90	THR	5.5
20	C8	146	ALA	5.5
6	S4	56	LEU	5.5
1	6	662	U	5.5
81	m2	19	LYS	5.5
1	2	1705	C	5.5
35	sM	84	LYS	5.5
28	D6	44	ILE	5.5
1	2	1690	G	5.5
48	M1	127	PHE	5.5
53	M7	157	VAL	5.5
78	Q2	106	PHE	5.5
83	p2	2	SER	5.5
42	L5	51	LEU	5.5
1	2	1707	A	5.5
83	p1	11	ALA	5.5

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Mol	Chain	Res	Type	RSRZ
3	S1	101	HIS	5.5
15	C3	25	TRP	5.5
26	D4	12	VAL	5.5
30	D8	16	LEU	5.5
34	SR	32	LEU	5.4
15	C3	23	PRO	5.4
27	D5	97	LYS	5.4
14	c2	61	VAL	5.4
21	C9	71	VAL	5.4
28	D6	69	ASN	5.4
34	sR	294	TRP	5.4
6	S4	64	ILE	5.4
7	s5	137	ILE	5.4
80	e0	51	ASN	5.4
6	s4	15	PRO	5.4
6	S4	55	ALA	5.4
3	S1	98	THR	5.4
6	S4	65	LEU	5.4
63	N7	42	LEU	5.4
18	C6	39	VAL	5.4
63	n7	96	VAL	5.4
34	sR	28	GLY	5.3
36	5	2506	U	5.3
32	E0	61	SER	5.3
34	sR	163	ASP	5.3
70	O4	23	VAL	5.3
21	C9	50	ALA	5.3
34	sR	254	ALA	5.3
11	S9	134	ILE	5.3
63	N7	26	VAL	5.3
1	2	1711	C	5.3
63	n7	68	ILE	5.3
16	C4	14	PHE	5.3
70	O4	93	PHE	5.3
1	6	659	C	5.3
7	s5	68	ILE	5.3
34	sR	70	ASP	5.3
81	m2	157	ASP	5.3
34	sR	26	SER	5.3
20	C8	22	VAL	5.3
34	sR	211	ILE	5.3
42	L5	95	TRP	5.3

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Mol	Chain	Res	Type	RSRZ
80	e0	62	VAL	5.3
13	C1	2	SER	5.3
36	5	1567	U	5.3
58	N2	33	TYR	5.2
6	s4	39	ARG	5.2
21	C9	84	LYS	5.2
14	c2	28	LEU	5.2
82	p0	70	LEU	5.2
33	e1	98	VAL	5.2
34	SR	81	LEU	5.2
29	D7	51	GLN	5.2
55	M9	185	LEU	5.2
83	p2	20	GLU	5.2
29	d7	33	LEU	5.2
84	f	90	TYR	5.2
11	S9	144	PRO	5.2
34	sR	23	LEU	5.2
34	sR	34	LEU	5.2
12	C0	24	LYS	5.2
14	c2	20	ALA	5.2
42	L5	64	ILE	5.2
3	S1	55	LYS	5.2
1	2	1686	C	5.2
51	m5	6	TYR	5.2
27	d5	89	ILE	5.2
30	D8	7	VAL	5.2
26	D4	32	ARG	5.2
3	S1	140	ILE	5.2
33	E1	145	HIS	5.2
12	C0	62	GLN	5.2
15	C3	62	GLN	5.2
1	6	658	C	5.2
33	e1	84	VAL	5.1
26	D4	30	PRO	5.1
6	S4	90	ILE	5.1
60	N4	66	GLU	5.1
84	f	148	ILE	5.1
11	S9	130	THR	5.1
16	C4	98	GLY	5.1
47	M0	36	LEU	5.1
14	c2	121	VAL	5.1
30	d8	33	LEU	5.1

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Mol	Chain	Res	Type	RSRZ
81	m2	74	GLN	5.1
18	C6	132	LYS	5.1
17	c5	101	ALA	5.1
2	S0	201	LEU	5.1
6	S4	101	LEU	5.1
34	sR	112	SER	5.1
27	D5	60	VAL	5.1
36	5	2539	C	5.1
60	N4	73	ARG	5.1
22	D0	84	MET	5.1
34	sR	92	TRP	5.1
34	sR	204	ALA	5.1
11	S9	147	MET	5.1
11	S9	181	ALA	5.1
28	D6	20	PRO	5.1
60	N4	69	LYS	5.1
18	C6	96	TYR	5.1
82	p0	191	TYR	5.1
11	S9	128	LEU	5.0
7	S5	69	PHE	5.0
2	S0	98	ILE	5.0
33	e1	90	LYS	5.0
35	SM	16	ASP	5.0
15	C3	54	LEU	5.0
83	p1	6	ALA	5.0
33	E1	88	PRO	5.0
6	S4	123	LEU	5.0
18	C6	15	SER	5.0
34	SR	115	ILE	5.0
81	m2	90	ALA	5.0
84	f	43	ASP	5.0
83	p2	1	MET	5.0
33	e1	146	SER	5.0
3	S1	54	LEU	5.0
83	p2	26	LEU	5.0
18	C6	123	ARG	5.0
21	C9	104	VAL	5.0
3	S1	96	LEU	5.0
12	C0	44	LYS	5.0
70	o4	57	LEU	5.0
36	1	1563	C	5.0
43	l6	129	GLU	5.0

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Mol	Chain	Res	Type	RSRZ
17	c5	52	LYS	5.0
18	C6	13	LYS	5.0
26	D4	61	ARG	5.0
34	sR	241	PHE	5.0
12	c0	57	THR	5.0
18	C6	12	LYS	5.0
60	n4	70	LYS	5.0
14	c2	41	LEU	5.0
30	d8	43	ASN	5.0
11	S9	158	PHE	5.0
18	C6	40	GLU	5.0
3	S1	95	ASN	5.0
31	d9	29	GLY	5.0
27	d5	94	LYS	5.0
60	n4	97	LYS	5.0
11	S9	135	ALA	5.0
42	L5	144	VAL	5.0
34	SR	42	LEU	5.0
28	D6	65	PRO	5.0
6	S4	102	VAL	4.9
18	c6	114	ARG	4.9
28	D6	63	ALA	4.9
34	sR	35	SER	4.9
81	m2	18	VAL	4.9
7	s5	145	ASP	4.9
63	N7	136	PHE	4.9
18	C6	7	VAL	4.9
30	d8	7	VAL	4.9
12	C0	25	LYS	4.9
34	sR	81	LEU	4.9
11	S9	3	ARG	4.9
7	s5	130	ILE	4.9
74	o8	43	PHE	4.9
27	D5	67	ASP	4.9
84	f	136	VAL	4.9
34	SR	43	ILE	4.9
6	S4	99	PHE	4.9
45	l8	192	GLN	4.9
10	S8	151	LYS	4.9
34	sR	227	ALA	4.9
11	S9	156	ILE	4.9
5	S3	25	PHE	4.9

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Mol	Chain	Res	Type	RSRZ
5	s3	148	LYS	4.9
29	D7	41	LEU	4.9
14	c2	63	VAL	4.9
36	1	2506	U	4.9
33	e1	88	PRO	4.9
3	S1	28	GLU	4.9
21	c9	18	TYR	4.9
26	D4	22	GLN	4.9
27	D5	58	ARG	4.9
16	C4	39	ILE	4.9
26	D4	18	LEU	4.9
70	O4	73	SER	4.9
34	sR	203	THR	4.9
6	S4	110	ALA	4.9
83	p1	36	PRO	4.9
13	c1	5	LEU	4.8
21	C9	8	ASP	4.8
84	f	42	VAL	4.8
34	sR	293	ALA	4.8
1	2	1691	A	4.8
11	S9	112	GLN	4.8
28	D6	45	VAL	4.8
26	D4	3	ASP	4.8
14	C2	82	PRO	4.8
6	S4	226	PHE	4.8
36	1	1570	U	4.8
84	f	156	THR	4.8
26	D4	7	ILE	4.8
3	s1	89	ASP	4.8
80	e0	53	LYS	4.8
32	E0	56	MET	4.8
6	S4	38	LEU	4.8
8	S6	175	ILE	4.8
21	C9	94	ILE	4.8
26	D4	72	PHE	4.8
21	C9	3	GLY	4.8
1	2	1700	C	4.8
3	S1	217	LEU	4.8
3	S1	53	GLY	4.8
12	C0	23	ALA	4.8
84	f	105	MET	4.8
14	c2	52	LEU	4.8

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Mol	Chain	Res	Type	RSRZ
1	6	1709	C	4.8
1	2	1704	U	4.8
32	E0	54	ARG	4.8
7	s5	90	ILE	4.8
34	SR	102	ARG	4.8
22	d0	78	THR	4.8
84	f	24	SER	4.8
34	sR	311	ARG	4.8
7	S5	41	LYS	4.8
34	sR	74	THR	4.8
35	sM	82	THR	4.8
74	o8	45	VAL	4.8
6	S4	261	LEU	4.7
42	L5	101	THR	4.7
83	p2	7	LEU	4.7
55	M9	51	VAL	4.7
8	S6	80	ASN	4.7
9	S7	33	GLU	4.7
71	o5	120	ALA	4.7
13	C1	156	PHE	4.7
83	p1	19	ILE	4.7
16	C4	97	GLY	4.7
29	D7	58	SER	4.7
83	p1	31	ASN	4.7
58	N2	108	TYR	4.7
7	s5	198	LEU	4.7
18	C6	52	LEU	4.7
19	C7	101	ASN	4.7
42	L5	131	LEU	4.7
6	S4	143	ASP	4.7
74	o8	2	ALA	4.7
60	N4	81	PRO	4.7
34	sR	123	ILE	4.7
34	sR	73	LEU	4.7
83	p1	34	ASN	4.7
34	sR	116	ASP	4.7
62	N6	127	GLU	4.7
3	S1	100	PHE	4.7
21	C9	9	VAL	4.7
11	S9	126	ARG	4.7
27	D5	88	ILE	4.7
15	C3	59	GLY	4.7

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Mol	Chain	Res	Type	RSRZ
8	S6	79	LYS	4.7
19	C7	60	ARG	4.7
84	f	152	GLU	4.7
7	S5	199	ILE	4.7
51	m5	2	GLY	4.7
34	sR	113	VAL	4.7
21	C9	83	ALA	4.7
30	D8	66	LEU	4.7
14	c2	104	ALA	4.7
11	S9	143	ILE	4.7
34	SR	34	LEU	4.7
8	S6	91	GLU	4.7
33	e1	99	LYS	4.6
11	S9	148	VAL	4.6
33	e1	95	HIS	4.6
27	D5	98	GLN	4.6
16	C4	13	VAL	4.6
1	6	1228	G	4.6
36	5	1569	U	4.6
7	S5	137	ILE	4.6
26	D4	33	ALA	4.6
34	sR	36	ALA	4.6
63	N7	70	PRO	4.6
3	S1	138	PHE	4.6
15	C3	26	PHE	4.6
48	M1	96	PHE	4.6
22	d0	77	LYS	4.6
60	n4	67	VAL	4.6
82	p0	87	VAL	4.6
14	c2	21	GLU	4.6
18	C6	116	LEU	4.6
17	c5	136	SER	4.6
70	O4	72	VAL	4.6
51	m5	55	ALA	4.6
84	f	23	CYS	4.6
33	e1	94	LYS	4.6
70	O4	21	LYS	4.6
18	c6	90	VAL	4.6
26	D4	2	SER	4.6
3	S1	29	TRP	4.6
14	c2	59	LEU	4.6
15	C3	61	THR	4.6

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Mol	Chain	Res	Type	RSRZ
34	sR	201	THR	4.6
26	D4	58	PHE	4.6
21	C9	6	VAL	4.6
34	sR	291	SER	4.6
42	L5	63	GLN	4.6
3	s1	84	ILE	4.6
18	c6	36	ILE	4.6
20	c8	144	ARG	4.6
34	sR	115	ILE	4.6
67	O1	14	ILE	4.6
34	sR	300	THR	4.6
12	C0	41	TYR	4.6
63	N7	23	VAL	4.6
35	sM	52	PRO	4.6
72	O6	100	HIS	4.6
6	S4	52	LEU	4.6
20	C8	145	ARG	4.6
20	c8	18	LEU	4.6
5	s3	150	MET	4.6
19	C7	2	GLY	4.6
2	S0	189	VAL	4.6
31	d9	5	ASN	4.5
55	M9	50	ILE	4.5
83	p1	33	ALA	4.5
81	m2	58	ASP	4.5
7	S5	96	SER	4.5
36	1	2205	U	4.5
16	C4	16	VAL	4.5
27	D5	81	ARG	4.5
81	m2	57	GLU	4.5
82	p0	188	VAL	4.5
28	D6	64	LEU	4.5
18	c6	143	ARG	4.5
22	d0	76	SER	4.5
14	C2	32	LEU	4.5
45	l8	162	LEU	4.5
3	S1	84	ILE	4.5
28	d6	69	ASN	4.5
70	O4	79	SER	4.5
7	s5	43	PHE	4.5
14	c2	106	ILE	4.5
21	C9	2	PRO	4.5

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Mol	Chain	Res	Type	RSRZ
78	q2	106	PHE	4.5
7	s5	36	ALA	4.5
42	L5	89	THR	4.5
33	e1	110	ALA	4.5
42	L5	122	VAL	4.5
5	S3	143	ARG	4.5
7	s5	93	LEU	4.5
45	l8	121	SER	4.5
18	c6	11	GLY	4.5
7	S5	154	ALA	4.5
8	s6	169	TYR	4.5
29	D7	33	LEU	4.5
1	2	261	U	4.5
18	C6	14	LYS	4.5
82	p0	20	GLU	4.5
84	f	151	LYS	4.5
21	C9	108	LEU	4.5
32	E0	55	ARG	4.5
14	c2	40	GLY	4.5
33	e1	82	LYS	4.5
84	f	81	GLU	4.5
6	S4	80	THR	4.5
7	s5	69	PHE	4.5
11	S9	164	PHE	4.5
5	s3	180	GLY	4.5
7	S5	151	GLY	4.5
21	C9	40	SER	4.5
10	S8	109	PHE	4.5
1	6	1217	A	4.5
27	D5	36	ALA	4.5
48	M1	66	ALA	4.5
6	S4	57	ASN	4.5
67	O1	20	LEU	4.5
29	D7	32	PHE	4.5
36	1	1762	C	4.5
12	c0	67	THR	4.4
81	m2	104	ASP	4.4
26	D4	68	LYS	4.4
5	S3	87	TYR	4.4
9	S7	43	PHE	4.4
45	l8	155	ASN	4.4
72	O6	99	ARG	4.4

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Mol	Chain	Res	Type	RSRZ
33	E1	130	VAL	4.4
1	6	1708	U	4.4
84	f	142	MET	4.4
84	f	153	ALA	4.4
7	S5	190	ILE	4.4
17	c5	133	ALA	4.4
12	c0	66	TYR	4.4
42	L5	90	HIS	4.4
3	S1	60	ALA	4.4
56	N0	2	ALA	4.4
1	6	678	A	4.4
43	L6	130	ILE	4.4
5	S3	218	LEU	4.4
18	C6	38	LEU	4.4
18	C6	74	HIS	4.4
25	D3	107	PHE	4.4
33	e1	78	LYS	4.4
3	S1	67	GLU	4.4
32	E0	6	GLY	4.4
84	f	41	ILE	4.4
28	D6	67	THR	4.4
40	L3	387	LEU	4.4
6	S4	45	ILE	4.4
20	c8	15	LEU	4.4
18	C6	16	ALA	4.4
34	sR	90	ARG	4.4
7	S5	68	ILE	4.4
6	S4	79	ASP	4.4
34	sR	134	TRP	4.4
16	C4	77	THR	4.4
34	sR	171	SER	4.4
34	sR	263	PHE	4.4
7	S5	116	HIS	4.4
45	l8	196	ALA	4.4
81	m2	121	GLU	4.4
11	s9	48	GLN	4.4
58	N2	93	ILE	4.3
1	6	1199	G	4.3
32	E0	44	PHE	4.3
80	e0	55	ARG	4.3
42	L5	77	ALA	4.3
84	f	86	LYS	4.3

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Mol	Chain	Res	Type	RSRZ
3	S1	102	GLY	4.3
16	C4	105	LEU	4.3
34	sR	42	LEU	4.3
58	N2	27	VAL	4.3
51	m5	147	ARG	4.3
6	S4	67	GLN	4.3
7	S5	97	LEU	4.3
14	C2	122	VAL	4.3
18	C6	36	ILE	4.3
39	L2	253	GLN	4.3
11	s9	6	ARG	4.3
16	C4	115	ILE	4.3
6	S4	82	TYR	4.3
15	C3	24	ALA	4.3
17	C5	76	VAL	4.3
17	c5	135	THR	4.3
18	c6	46	PHE	4.3
18	c6	132	LYS	4.3
82	p0	26	PHE	4.3
9	S7	98	ILE	4.3
84	f	70	LEU	4.3
16	C4	34	SER	4.3
18	C6	65	ILE	4.3
34	SR	181	TRP	4.3
45	l8	197	VAL	4.3
13	C1	152	GLN	4.3
7	S5	106	LYS	4.3
27	D5	69	LEU	4.3
21	c9	55	TYR	4.3
1	2	1706	C	4.3
36	1	3275	U	4.3
18	c6	29	ILE	4.3
83	p1	13	ILE	4.3
40	L3	49	TYR	4.3
6	S4	9	LEU	4.3
6	S4	23	LEU	4.3
6	S4	167	GLY	4.3
34	sR	240	VAL	4.3
27	D5	61	SER	4.3
33	e1	100	LEU	4.3
16	C4	81	VAL	4.3
34	sR	111	MET	4.3

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Mol	Chain	Res	Type	RSRZ
2	S0	15	GLN	4.3
6	s4	18	TRP	4.3
5	s3	176	LEU	4.3
55	M9	52	LYS	4.2
27	d5	101	TYR	4.2
2	s0	166	GLY	4.2
63	N7	45	GLY	4.2
5	s3	152	PHE	4.2
34	SR	46	LYS	4.2
9	S7	58	LEU	4.2
63	N7	118	PHE	4.2
82	p0	16	ARG	4.2
60	N4	98	PRO	4.2
82	p0	221	ALA	4.2
6	S4	25	GLY	4.2
16	C4	27	PHE	4.2
30	D8	44	VAL	4.2
28	D6	46	GLU	4.2
60	n4	85	ALA	4.2
42	L5	147	ASP	4.2
29	D7	70	LYS	4.2
12	C0	27	PHE	4.2
22	d0	79	TRP	4.2
6	S4	11	ARG	4.2
6	S4	88	ASP	4.2
26	D4	97	ALA	4.2
72	o6	27	SER	4.2
3	S1	89	ASP	4.2
6	s4	102	VAL	4.2
7	S5	111	VAL	4.2
17	C5	104	GLN	4.2
21	C9	44	GLU	4.2
58	N2	92	TRP	4.2
34	SR	74	THR	4.2
7	S5	72	HIS	4.2
12	c0	43	ILE	4.2
63	N7	25	ILE	4.2
76	Q0	128	LYS	4.2
55	M9	187	GLU	4.2
36	1	1239	C	4.2
34	sR	16	HIS	4.2
34	sR	156	VAL	4.2

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Mol	Chain	Res	Type	RSRZ
82	p0	215	SER	4.2
2	S0	122	ILE	4.2
63	N7	2	ALA	4.2
21	C9	80	TYR	4.2
6	S4	60	GLU	4.2
15	C3	50	ILE	4.2
36	5	1568	U	4.2
22	D0	69	LYS	4.2
74	o8	73	LEU	4.2
14	C2	37	VAL	4.2
28	d6	45	VAL	4.2
34	SR	136	ILE	4.2
31	d9	16	LYS	4.1
63	N7	91	ALA	4.1
4	s2	84	LYS	4.1
6	S4	259	GLN	4.1
12	c0	3	MET	4.1
11	S9	146	PHE	4.1
32	E0	60	PRO	4.1
27	D5	100	ILE	4.1
20	c8	20	THR	4.1
7	S5	86	GLN	4.1
14	C2	59	LEU	4.1
34	sR	246	SER	4.1
1	2	719	U	4.1
7	s5	44	ASN	4.1
15	C3	33	VAL	4.1
18	C6	49	TYR	4.1
36	1	2505	U	4.1
20	c8	25	ASN	4.1
30	d8	44	VAL	4.1
34	sR	224	ASN	4.1
60	N4	67	VAL	4.1
27	d5	92	ILE	4.1
16	C4	102	LEU	4.1
74	o8	54	LEU	4.1
34	SR	262	VAL	4.1
2	s0	170	ILE	4.1
7	S5	165	LEU	4.1
9	S7	41	LEU	4.1
17	c5	80	MET	4.1
80	e0	49	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
34	sR	155	ARG	4.1
70	O4	64	THR	4.1
7	s5	48	PHE	4.1
28	d6	59	TYR	4.1
34	SR	213	SER	4.1
34	sR	46	LYS	4.1
83	p1	38	GLU	4.1
6	S4	180	LEU	4.1
14	c2	42	ALA	4.1
63	n7	11	ALA	4.1
16	C4	119	THR	4.1
63	n7	12	VAL	4.1
14	c2	64	SER	4.1
34	sR	158	PRO	4.1
12	c0	24	LYS	4.1
18	c6	138	PHE	4.1
34	sR	27	ALA	4.1
4	s2	96	THR	4.1
6	S4	89	VAL	4.1
16	c4	79	VAL	4.1
25	D3	130	VAL	4.1
80	e0	52	GLY	4.1
27	D5	89	ILE	4.1
3	S1	42	ASN	4.1
5	s3	153	ALA	4.1
68	O2	128	LEU	4.1
11	S9	5	PRO	4.1
31	D9	55	PHE	4.1
84	f	22	GLN	4.1
21	C9	91	TYR	4.1
6	s4	184	THR	4.1
11	S9	37	LYS	4.1
27	D5	71	ILE	4.1
30	d8	66	LEU	4.1
19	C7	120	SER	4.1
11	S9	122	VAL	4.1
21	C9	72	GLY	4.1
11	S9	12	TYR	4.1
27	D5	101	TYR	4.1
70	O4	71	THR	4.1
12	C0	61	TRP	4.1
84	f	72	ASP	4.1

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Mol	Chain	Res	Type	RSRZ
6	S4	181	VAL	4.1
11	s9	5	PRO	4.1
84	f	11	ALA	4.1
16	C4	80	HIS	4.1
21	C9	64	HIS	4.1
6	S4	48	LEU	4.1
36	1	1270	A	4.1
3	S1	30	PHE	4.0
39	L2	252	THR	4.0
6	S4	22	LYS	4.0
11	S9	133	HIS	4.0
63	N7	5	LEU	4.0
82	p0	25	LEU	4.0
14	c2	43	ARG	4.0
3	S1	225	VAL	4.0
22	D0	83	GLU	4.0
34	sR	68	VAL	4.0
45	L8	58	VAL	4.0
4	s2	89	GLN	4.0
6	s4	103	TYR	4.0
10	S8	72	ILE	4.0
32	E0	35	TYR	4.0
34	sR	183	LEU	4.0
34	SR	71	CYS	4.0
30	D8	28	VAL	4.0
32	E0	45	VAL	4.0
19	C7	62	GLN	4.0
20	C8	15	LEU	4.0
27	D5	65	LEU	4.0
29	D7	38	PRO	4.0
84	f	134	LEU	4.0
5	s3	138	VAL	4.0
6	S4	18	TRP	4.0
10	S8	67	TRP	4.0
11	S9	111	THR	4.0
11	S9	116	LEU	4.0
15	c3	40	TYR	4.0
33	E1	90	LYS	4.0
61	N5	24	LEU	4.0
82	p0	19	LEU	4.0
3	s1	141	ALA	4.0
53	M7	163	LYS	4.0

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Mol	Chain	Res	Type	RSRZ
82	p0	220	ILE	4.0
36	5	2507	C	4.0
74	O8	43	PHE	4.0
11	S9	105	LEU	4.0
60	N4	71	ARG	4.0
10	S8	179	CYS	4.0
21	c9	23	GLN	4.0
19	c7	25	THR	4.0
1	2	717	C	4.0
36	1	1243	G	4.0
7	s5	138	THR	4.0
18	C6	17	THR	4.0
18	c6	140	LYS	4.0
72	o6	2	THR	4.0
42	l5	235	SER	4.0
26	D4	40	LEU	4.0
2	S0	97	PRO	4.0
11	S9	6	ARG	4.0
7	s5	70	VAL	4.0
21	c9	37	VAL	4.0
22	D0	81	THR	4.0
18	C6	141	SER	4.0
5	s3	184	ILE	4.0
16	C4	112	ILE	4.0
36	1	1568	U	4.0
84	f	65	PHE	4.0
16	C4	79	VAL	4.0
81	m2	156	VAL	4.0
84	f	38	PRO	4.0
26	d4	18	LEU	4.0
58	N2	80	THR	4.0
2	S0	99	ALA	4.0
2	S0	203	PHE	4.0
4	s2	181	SER	4.0
11	S9	29	LYS	4.0
11	s9	146	PHE	4.0
16	C4	41	ARG	4.0
19	C7	63	LYS	4.0
28	d6	68	TYR	4.0
31	d9	20	GLN	4.0
31	d9	28	THR	4.0
63	N7	49	TYR	3.9

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Mol	Chain	Res	Type	RSRZ
1	2	1687	U	3.9
38	4	158	U	3.9
34	sR	304	GLY	3.9
42	L5	83	LEU	3.9
74	o8	51	LEU	3.9
7	S5	107	LYS	3.9
11	S9	180	LYS	3.9
22	d0	64	LYS	3.9
3	S1	38	PHE	3.9
14	c2	128	ALA	3.9
47	M0	84	ALA	3.9
47	m0	221	ALA	3.9
60	N4	82	ILE	3.9
83	p2	22	SER	3.9
15	C3	27	LYS	3.9
14	c2	23	THR	3.9
6	S4	41	SER	3.9
17	C5	8	LYS	3.9
18	C6	47	LYS	3.9
59	N3	2	SER	3.9
20	c8	123	ARG	3.9
34	sR	7	LEU	3.9
84	f	71	GLU	3.9
45	l8	120	LYS	3.9
58	n2	14	THR	3.9
6	s4	101	LEU	3.9
34	SR	35	SER	3.9
21	C9	62	ALA	3.9
36	1	1764	U	3.9
51	m5	48	ALA	3.9
17	c5	126	VAL	3.9
42	L5	158	ARG	3.9
42	L5	203	HIS	3.9
82	p0	51	VAL	3.9
9	s7	93	LEU	3.9
15	C3	51	GLY	3.9
34	sR	210	LEU	3.9
47	M0	112	GLN	3.9
51	M5	22	LEU	3.9
83	p1	3	THR	3.9
1	2	716	C	3.9
63	N7	132	SER	3.9

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Mol	Chain	Res	Type	RSRZ
14	c2	118	ALA	3.9
21	C9	65	ILE	3.9
1	2	1712	A	3.9
26	D4	25	VAL	3.9
36	1	2502	A	3.9
66	o0	7	GLN	3.9
7	S5	54	LYS	3.9
45	L8	67	ILE	3.9
6	s4	35	PRO	3.9
17	c5	125	PRO	3.9
42	L5	129	TYR	3.9
82	p0	69	ASP	3.9
12	c0	27	PHE	3.9
27	D5	99	ALA	3.9
34	sR	124	SER	3.9
11	S9	2	PRO	3.9
18	c6	19	VAL	3.9
5	s3	151	LYS	3.9
70	o4	33	GLN	3.9
18	C6	29	ILE	3.9
6	S4	15	PRO	3.9
20	c8	129	TRP	3.9
60	n4	95	SER	3.9
82	p0	210	VAL	3.9
16	C4	82	LYS	3.9
7	S5	91	GLU	3.9
14	c2	89	ILE	3.9
34	sR	29	GLN	3.9
42	L5	62	CYS	3.9
72	O6	57	LEU	3.9
1	6	660	G	3.9
22	D0	85	ARG	3.9
31	d9	31	ILE	3.9
35	SM	19	VAL	3.9
33	e1	92	LYS	3.9
1	2	134	U	3.8
6	S4	76	VAL	3.8
6	s4	208	VAL	3.8
7	s5	62	VAL	3.8
34	sR	309	VAL	3.8
35	SM	18	VAL	3.8
21	c9	91	TYR	3.8

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Mol	Chain	Res	Type	RSRZ
18	C6	5	PRO	3.8
18	C6	6	SER	3.8
34	SR	313	TRP	3.8
48	M1	104	PHE	3.8
18	c6	13	LYS	3.8
15	C3	53	LEU	3.8
18	c6	39	VAL	3.8
18	c6	89	LEU	3.8
27	d5	69	LEU	3.8
63	n7	13	VAL	3.8
45	L8	182	GLY	3.8
6	S4	228	ILE	3.8
21	C9	41	SER	3.8
13	C1	154	ALA	3.8
42	L5	162	ALA	3.8
53	M7	165	VAL	3.8
53	M7	184	ALA	3.8
33	e1	79	LYS	3.8
23	D1	34	ILE	3.8
45	l8	194	THR	3.8
60	n4	83	THR	3.8
63	N7	82	PRO	3.8
1	2	656	G	3.8
58	N2	89	LEU	3.8
6	s4	54	TYR	3.8
12	C0	75	TYR	3.8
29	D7	42	ASN	3.8
10	S8	141	ARG	3.8
29	d7	57	GLU	3.8
7	s5	165	LEU	3.8
36	1	1569	U	3.8
18	c6	18	ALA	3.8
33	E1	93	HIS	3.8
35	sM	67	GLY	3.8
70	O4	24	LYS	3.8
16	C4	18	ARG	3.8
2	s0	173	ILE	3.8
6	S4	91	THR	3.8
7	s5	129	PRO	3.8
14	C2	42	ALA	3.8
18	C6	19	VAL	3.8
31	d9	36	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
53	M7	158	ALA	3.8
6	S4	252	ARG	3.8
14	c2	127	GLY	3.8
5	S3	216	PRO	3.8
14	c2	116	VAL	3.8
21	c9	25	GLN	3.8
23	D1	39	VAL	3.8
51	m5	45	PRO	3.8
83	p1	8	SER	3.8
9	S7	134	GLU	3.8
11	S9	106	GLU	3.8
51	m5	30	TYR	3.8
27	d5	88	ILE	3.8
1	6	1700	C	3.8
7	S5	122	ASN	3.8
25	D3	89	ASN	3.8
18	c6	124	PRO	3.8
58	n2	27	VAL	3.8
83	p2	41	TRP	3.8
42	L5	55	PHE	3.8
80	e0	63	GLN	3.8
20	c8	140	THR	3.8
21	C9	66	TYR	3.8
8	s6	147	LEU	3.8
42	L5	150	LEU	3.8
26	D4	90	ARG	3.8
34	sR	45	TRP	3.8
60	n4	104	ASN	3.8
34	sR	80	ALA	3.8
35	SM	60	ALA	3.8
6	S4	182	TYR	3.8
55	M9	49	THR	3.8
67	o1	82	GLU	3.8
1	2	1059	U	3.8
34	sR	169	ILE	3.8
7	S5	43	PHE	3.8
12	C0	3	MET	3.8
28	D6	21	VAL	3.8
3	S1	45	LYS	3.8
11	s9	20	GLU	3.8
17	c5	104	GLN	3.8
3	s1	140	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
9	S7	77	LEU	3.8
10	s8	176	SER	3.8
33	E1	91	ILE	3.8
3	S1	66	VAL	3.8
6	S4	208	VAL	3.8
66	O0	59	TYR	3.8
2	S0	170	ILE	3.8
66	o0	6	SER	3.8
6	S4	86	PHE	3.8
82	p0	197	PHE	3.8
7	s5	141	GLY	3.7
34	SR	80	ALA	3.7
55	M9	183	ALA	3.7
84	f	106	ASP	3.7
14	c2	96	GLN	3.7
22	d0	98	GLN	3.7
67	O1	71	LEU	3.7
21	C9	39	THR	3.7
26	D4	9	THR	3.7
82	p0	59	VAL	3.7
10	S8	66	SER	3.7
26	D4	66	GLY	3.7
28	D6	59	TYR	3.7
42	L5	247	ILE	3.7
84	f	120	LEU	3.7
33	E1	99	LYS	3.7
70	O4	70	LYS	3.7
1	6	1473	U	3.7
3	S1	207	LEU	3.7
14	c2	103	LEU	3.7
15	C3	37	ILE	3.7
20	C8	21	ASN	3.7
21	C9	14	PHE	3.7
58	N2	28	PHE	3.7
63	N7	113	VAL	3.7
6	S4	260	GLY	3.7
3	S1	58	SER	3.7
9	s7	58	LEU	3.7
11	s9	19	TYR	3.7
27	D5	51	LEU	3.7
30	D8	9	LEU	3.7
36	1	1240	A	3.7

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Mol	Chain	Res	Type	RSRZ
51	m5	53	TYR	3.7
6	S4	26	CYS	3.7
2	S0	23	HIS	3.7
6	S4	87	MET	3.7
27	D5	82	HIS	3.7
27	d5	37	GLN	3.7
34	sR	251	TRP	3.7
7	S5	95	ASN	3.7
21	c9	92	LYS	3.7
84	f	53	GLY	3.7
2	S0	146	LEU	3.7
14	c2	62	LEU	3.7
34	sR	47	LEU	3.7
45	l8	200	LEU	3.7
70	O4	52	GLN	3.7
76	Q0	77	ILE	3.7
11	S9	136	VAL	3.7
14	c2	113	ARG	3.7
45	L8	131	ALA	3.7
84	f	58	HIS	3.7
16	C4	31	THR	3.7
27	d5	59	TYR	3.7
36	1	2503	G	3.7
70	O4	62	TYR	3.7
14	c2	25	GLU	3.7
63	N7	133	LYS	3.7
2	s0	164	ASN	3.7
74	o8	69	LEU	3.7
7	S5	53	VAL	3.7
34	sR	245	PHE	3.7
70	O4	55	SER	3.7
84	f	137	THR	3.7
30	D8	6	PRO	3.7
82	p0	85	GLY	3.7
34	sR	83	ALA	3.7
15	C3	66	ILE	3.7
36	1	2504	U	3.7
36	5	1764	U	3.7
7	S5	87	CYS	3.7
2	S0	161	PRO	3.7
82	p0	60	ARG	3.7
6	S4	162	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
3	S1	215	VAL	3.7
6	S4	27	TYR	3.7
42	L5	119	TYR	3.7
83	p2	45	PHE	3.7
34	SR	72	THR	3.7
5	s3	142	LEU	3.7
25	D3	132	LEU	3.7
53	M7	180	LYS	3.7
55	M9	23	TRP	3.7
2	S0	197	ILE	3.7
3	S1	121	ILE	3.7
63	N7	72	ILE	3.7
82	p0	18	TYR	3.7
42	L5	124	GLU	3.7
74	o8	44	LYS	3.6
29	D7	44	THR	3.6
29	D7	45	THR	3.6
7	s5	89	ILE	3.6
80	e0	2	ALA	3.6
7	s5	156	ARG	3.6
7	s5	72	HIS	3.6
2	S0	192	THR	3.6
30	d8	32	PHE	3.6
34	sR	30	PRO	3.6
6	S4	53	LYS	3.6
16	C4	113	GLY	3.6
17	c5	132	GLY	3.6
11	S9	132	ARG	3.6
12	C0	45	ALA	3.6
34	SR	61	PHE	3.6
81	m2	82	ALA	3.6
84	f	147	ALA	3.6
6	S4	225	VAL	3.6
7	S5	94	THR	3.6
14	c2	30	VAL	3.6
27	d5	90	LYS	3.6
33	E1	146	SER	3.6
42	L5	153	THR	3.6
14	c2	56	GLU	3.6
63	n7	21	LYS	3.6
84	f	133	ASP	3.6
11	S9	97	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
31	d9	40	ARG	3.6
6	S4	71	LYS	3.6
7	S5	212	LYS	3.6
42	L5	52	VAL	3.6
32	E0	48	THR	3.6
11	S9	32	GLY	3.6
81	m2	89	SER	3.6
84	f	131	GLY	3.6
34	sR	69	GLN	3.6
69	o3	60	ARG	3.6
7	s5	71	ALA	3.6
6	s4	92	LEU	3.6
20	C8	40	ARG	3.6
63	N7	65	ARG	3.6
13	C1	155	LYS	3.6
7	s5	31	GLU	3.6
18	c6	48	VAL	3.6
18	c6	85	ILE	3.6
34	sR	67	ILE	3.6
82	p0	100	ILE	3.6
82	p0	214	VAL	3.6
82	p0	217	VAL	3.6
17	c5	10	ARG	3.6
32	E0	38	LEU	3.6
12	c0	26	ASP	3.6
34	sR	165	ASP	3.6
84	f	139	ILE	3.6
4	S2	144	TRP	3.6
7	S5	108	LEU	3.6
33	e1	97	LYS	3.6
3	s1	100	PHE	3.6
21	C9	131	ASP	3.6
82	p0	192	ASP	3.6
1	6	1601	G	3.6
7	S5	132	VAL	3.6
22	d0	68	ARG	3.6
35	SM	53	ARG	3.6
11	S9	95	TYR	3.6
45	l8	238	LEU	3.6
7	s5	79	ASN	3.6
2	S0	106	SER	3.6
7	S5	121	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
22	D0	67	THR	3.6
28	D6	50	VAL	3.6
30	D8	67	ARG	3.6
34	sR	20	VAL	3.6
6	s4	84	ALA	3.6
14	c2	124	LYS	3.6
35	SM	90	ALA	3.6
36	1	1579	C	3.6
74	o8	42	LYS	3.6
1	6	1697	G	3.6
2	S0	182	LEU	3.6
28	D6	68	TYR	3.6
26	D4	85	PHE	3.6
32	E0	46	ASN	3.6
10	S8	73	SER	3.6
19	C7	99	VAL	3.6
31	D9	4	GLU	3.6
35	SM	97	THR	3.6
35	sM	123	ALA	3.6
84	f	12	ASP	3.6
11	S9	86	LEU	3.6
19	c7	26	LEU	3.6
21	C9	42	GLY	3.6
7	S5	92	ARG	3.6
21	c9	24	ARG	3.6
29	d7	38	PRO	3.6
42	L5	181	PRO	3.6
51	m5	26	ARG	3.6
2	S0	198	MET	3.6
16	C4	47	LYS	3.6
19	C7	110	VAL	3.6
63	N7	95	VAL	3.6
6	s4	164	LEU	3.6
14	c2	36	LEU	3.6
28	D6	71	LEU	3.6
34	sR	41	THR	3.6
63	N7	80	LEU	3.6
82	p0	24	SER	3.6
34	sR	53	LYS	3.5
1	6	1466	G	3.5
6	S4	220	THR	3.5
63	N7	79	HIS	3.5

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Mol	Chain	Res	Type	RSRZ
10	S8	168	CYS	3.5
24	D2	60	LYS	3.5
70	o4	21	LYS	3.5
16	c4	112	ILE	3.5
20	c8	73	MET	3.5
84	f	57	VAL	3.5
17	C5	101	ALA	3.5
20	c8	17	LEU	3.5
23	D1	55	LEU	3.5
30	d8	10	ALA	3.5
34	sR	44	SER	3.5
6	S4	199	GLU	3.5
2	S0	199	PRO	3.5
11	S9	129	ILE	3.5
45	L8	116	VAL	3.5
82	p0	63	ILE	3.5
11	S9	4	ALA	3.5
11	s9	80	LEU	3.5
18	C6	54	LEU	3.5
22	d0	72	ASN	3.5
22	d0	121	ASN	3.5
63	N7	101	PHE	3.5
6	S4	78	THR	3.5
6	S4	70	VAL	3.5
7	S5	181	GLU	3.5
10	s8	46	VAL	3.5
22	d0	80	GLU	3.5
36	5	1350	A	3.5
61	N5	124	VAL	3.5
2	S0	11	PRO	3.5
74	O8	5	ILE	3.5
18	C6	44	LEU	3.5
21	C9	70	GLN	3.5
34	SR	27	ALA	3.5
34	sR	236	ALA	3.5
47	M0	87	LEU	3.5
45	L8	130	TYR	3.5
74	o8	52	TYR	3.5
29	D7	43	ILE	3.5
18	c6	54	LEU	3.5
81	m2	75	LEU	3.5
5	S3	183	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
11	s9	4	ALA	3.5
16	c4	15	GLY	3.5
32	E0	32	GLY	3.5
70	o4	62	TYR	3.5
7	s5	83	ARG	3.5
3	S1	137	ILE	3.5
26	D4	17	LEU	3.5
34	SR	252	LEU	3.5
55	M9	24	LEU	3.5
5	s3	149	ALA	3.5
10	S8	181	GLY	3.5
58	N2	107	PHE	3.5
63	N7	117	ALA	3.5
18	c6	79	TYR	3.5
10	s8	200	LYS	3.5
33	E1	98	VAL	3.5
42	L5	254	LYS	3.5
84	f	85	VAL	3.5
6	s4	207	LEU	3.5
7	S5	153	GLY	3.5
20	C8	73	MET	3.5
27	D5	102	THR	3.5
42	L5	92	LEU	3.5
35	SM	15	ALA	3.5
63	n7	136	PHE	3.5
6	S4	77	ARG	3.5
7	s5	133	VAL	3.5
16	C4	29	HIS	3.5
6	S4	47	PHE	3.5
7	S5	75	GLY	3.5
84	f	135	MET	3.5
8	s6	145	PHE	3.5
9	S7	4	PRO	3.5
23	D1	33	GLN	3.5
33	E1	96	LYS	3.5
6	S4	112	HIS	3.5
21	C9	95	ASP	3.5
42	L5	168	ASP	3.5
28	D6	66	LYS	3.5
42	L5	180	PHE	3.5
63	N7	135	ARG	3.5
63	n7	20	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
16	C4	12	GLN	3.5
9	S7	32	PRO	3.5
29	D7	37	CYS	3.5
23	D1	53	TYR	3.5
42	L5	126	GLU	3.5
60	N4	65	GLU	3.5
11	S9	28	LEU	3.5
25	D3	133	LEU	3.5
42	L5	148	ILE	3.5
1	2	1527	C	3.5
20	c8	137	HIS	3.5
26	D4	15	ASN	3.5
26	D4	71	GLY	3.5
60	n4	132	GLY	3.5
2	s0	97	PRO	3.5
25	d3	60	GLU	3.5
43	L6	135	VAL	3.5
42	L5	50	ARG	3.5
42	l5	236	LEU	3.5
7	s5	152	GLY	3.5
16	C4	88	GLY	3.5
11	S9	20	GLU	3.4
29	D7	50	ALA	3.5
63	N7	11	ALA	3.5
42	L5	79	TYR	3.4
24	D2	25	VAL	3.4
30	D8	5	THR	3.4
84	f	82	VAL	3.4
2	S0	84	ARG	3.4
3	S1	41	ARG	3.4
21	C9	15	ILE	3.4
21	C9	100	ILE	3.4
27	D5	94	LYS	3.4
7	s5	159	ALA	3.4
17	c5	127	ARG	3.4
42	L5	226	TYR	3.4
45	l8	134	TYR	3.4
81	m2	11	PRO	3.4
21	c9	15	ILE	3.4
58	n2	11	ILE	3.4
5	s3	25	PHE	3.4
36	5	1566	A	3.4

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Mol	Chain	Res	Type	RSRZ
42	L5	200	PHE	3.4
10	S8	145	ALA	3.4
21	C9	29	GLU	3.4
22	D0	80	GLU	3.4
51	m5	37	HIS	3.4
70	O4	63	ALA	3.4
6	s4	121	TYR	3.4
27	D5	40	VAL	3.4
58	n2	33	TYR	3.4
30	D8	43	ASN	3.4
35	SM	54	PRO	3.4
48	M1	95	ASN	3.4
48	M1	65	ILE	3.4
70	O4	51	LEU	3.4
7	s5	94	THR	3.4
36	5	620	U	3.4
40	L3	48	GLY	3.4
6	S4	59	ARG	3.4
35	sM	119	ALA	3.4
12	C0	22	VAL	3.4
18	C6	117	LEU	3.4
18	c6	55	VAL	3.4
35	SM	106	VAL	3.4
20	C8	142	GLY	3.4
29	d7	32	PHE	3.4
25	D3	47	SER	3.4
81	m2	140	SER	3.4
42	L5	100	ALA	3.4
6	S4	69	HIS	3.4
8	S6	75	LEU	3.4
27	d5	40	VAL	3.4
27	d5	54	VAL	3.4
42	L5	240	TYR	3.4
26	D4	13	ILE	3.4
6	s4	37	LYS	3.4
70	o4	58	ARG	3.4
23	D1	65	SER	3.4
42	L5	123	GLU	3.4
1	6	1710	U	3.4
84	f	25	ALA	3.4
8	S6	84	TYR	3.4
8	s6	216	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
20	C8	101	LEU	3.4
5	S3	184	ILE	3.4
72	o6	9	ILE	3.4
7	s5	180	ARG	3.4
14	c2	125	ASN	3.4
26	D4	16	PRO	3.4
34	SR	121	MET	3.4
45	l8	137	ASN	3.4
11	S9	125	ALA	3.4
34	SR	214	ALA	3.4
31	D9	20	GLN	3.4
51	m5	129	TYR	3.4
51	m5	148	TYR	3.4
67	o1	12	TYR	3.4
35	SM	86	ASN	3.4
20	c8	4	VAL	3.4
21	C9	132	LEU	3.4
36	1	1025	A	3.4
83	p2	6	ALA	3.4
12	C0	63	TYR	3.4
34	sR	305	TYR	3.4
10	S8	43	ILE	3.4
16	C4	83	ILE	3.4
35	SM	83	LYS	3.4
33	e1	93	HIS	3.4
42	l5	200	PHE	3.4
51	m5	54	LYS	3.4
51	m5	52	GLY	3.4
34	sR	239	GLU	3.4
19	C7	86	PRO	3.4
58	n2	89	LEU	3.4
30	D8	27	GLN	3.4
34	SR	263	PHE	3.4
42	L5	65	ILE	3.4
51	M5	30	TYR	3.4
63	N7	131	PHE	3.4
81	m2	85	SER	3.4
84	f	16	SER	3.4
1	6	1701	A	3.4
3	s1	217	LEU	3.4
6	s4	111	VAL	3.4
21	C9	79	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
25	D3	104	LEU	3.4
34	SR	78	ALA	3.4
34	sR	181	TRP	3.4
74	o8	74	LYS	3.4
7	S5	184	PHE	3.4
13	C1	3	THR	3.4
18	C6	140	LYS	3.4
36	1	1028	U	3.4
48	M1	125	MET	3.4
10	S8	143	TRP	3.4
26	D4	19	ALA	3.4
74	o8	55	VAL	3.4
82	p0	187	VAL	3.4
83	p1	41	TRP	3.4
27	d5	71	ILE	3.4
69	o3	64	ILE	3.4
84	f	138	ILE	3.4
11	S9	87	SER	3.4
21	C9	27	LYS	3.4
26	D4	56	SER	3.4
36	1	1349	G	3.4
83	p1	20	GLU	3.4
70	O4	67	LYS	3.4
11	s9	147	MET	3.4
8	S6	100	ALA	3.3
49	m3	191	ALA	3.3
67	O1	60	TRP	3.3
28	d6	44	ILE	3.3
31	d9	17	GLY	3.3
51	M5	15	GLN	3.3
84	f	88	ASN	3.3
81	m2	92	SER	3.3
6	S4	61	VAL	3.3
34	sR	13	LEU	3.3
1	6	1699	G	3.3
9	S7	70	PHE	3.3
11	s9	104	PHE	3.3
16	C4	40	ALA	3.3
45	L8	198	ALA	3.3
6	S4	103	TYR	3.3
22	D0	65	ILE	3.3
35	sM	61	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
36	1	1955	U	3.3
42	L5	61	ILE	3.3
30	D8	56	LEU	3.3
53	M7	168	LEU	3.3
82	p0	68	SER	3.3
11	S9	104	PHE	3.3
12	c0	59	PHE	3.3
18	c6	129	PHE	3.3
18	C6	124	PRO	3.3
51	m5	3	ALA	3.3
53	M7	156	ALA	3.3
67	o1	75	ILE	3.3
70	o4	42	PRO	3.3
83	p2	25	LYS	3.3
83	p2	18	GLU	3.3
9	S7	42	GLN	3.3
11	S9	139	GLN	3.3
6	S4	42	LEU	3.3
32	E0	49	LEU	3.3
39	L2	104	LEU	3.3
45	L8	152	LEU	3.3
11	S9	11	THR	3.3
63	n7	41	ALA	3.3
14	c2	87	PRO	3.3
63	N7	18	TYR	3.3
40	L3	386	ASP	3.3
6	S4	127	LYS	3.3
21	c9	84	LYS	3.3
18	c6	74	HIS	3.3
7	S5	90	ILE	3.3
17	c5	84	ILE	3.3
27	d5	102	THR	3.3
34	sR	284	ALA	3.3
83	p1	32	ALA	3.3
60	n4	84	GLY	3.3
11	S9	118	LEU	3.3
3	s1	68	VAL	3.3
18	C6	122	ARG	3.3
26	D4	8	ARG	3.3
30	d8	45	LYS	3.3
67	O1	61	LYS	3.3
1	2	1370	U	3.3

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Mol	Chain	Res	Type	RSRZ
51	m5	130	PHE	3.3
63	N7	71	PHE	3.3
2	S0	168	HIS	3.3
20	C8	44	ASN	3.3
28	D6	17	HIS	3.3
55	M9	174	ALA	3.3
7	S5	140	THR	3.3
11	s9	184	SER	3.3
36	5	2540	A	3.3
74	o8	53	THR	3.3
2	S0	174	TRP	3.3
7	s5	41	LYS	3.3
18	C6	105	LEU	3.3
58	N2	105	LEU	3.3
61	N5	82	LEU	3.3
16	c4	27	PHE	3.3
21	C9	67	MET	3.3
63	N7	4	PHE	3.3
5	s3	134	CYS	3.3
66	o0	105	ALA	3.3
7	S5	61	TYR	3.3
6	S4	24	SER	3.3
34	SR	137	LYS	3.3
59	n3	2	SER	3.3
84	f	74	SER	3.3
14	c2	82	PRO	3.3
21	C9	47	PRO	3.3
1	2	474	A	3.3
8	S6	97	VAL	3.3
9	S7	74	GLN	3.3
34	sR	6	VAL	3.3
42	L5	133	GLU	3.3
6	S4	34	GLY	3.3
6	s4	107	GLY	3.3
9	S7	69	GLY	3.3
12	c0	63	TYR	3.3
26	D4	29	HIS	3.3
35	SM	105	LYS	3.3
42	L5	27	LYS	3.3
31	d9	30	LEU	3.3
55	M9	173	ARG	3.3
3	s1	98	THR	3.3

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Mol	Chain	Res	Type	RSRZ
7	S5	207	THR	3.3
4	s2	94	GLN	3.3
5	S3	144	ALA	3.3
8	S6	73	ILE	3.3
13	C1	68	GLY	3.3
17	c5	129	GLY	3.3
20	c8	121	ALA	3.3
33	e1	89	LYS	3.3
34	SR	36	ALA	3.3
34	SR	63	GLY	3.3
82	p0	49	ALA	3.3
18	C6	79	TYR	3.3
26	D4	28	LEU	3.3
1	2	658	C	3.3
42	L5	53	VAL	3.3
12	c0	62	GLN	3.3
51	m5	5	LYS	3.3
22	D0	68	ARG	3.3
55	M9	188	ASP	3.3
1	6	1227	A	3.3
20	c8	116	LEU	3.3
7	s5	168	VAL	3.3
34	sR	104	VAL	3.3
11	s9	2	PRO	3.3
67	o1	60	TRP	3.3
70	O4	33	GLN	3.3
72	O6	97	SER	3.3
84	f	76	SER	3.3
8	S6	92	ARG	3.3
16	C4	89	THR	3.3
33	E1	129	GLY	3.3
34	sR	255	ALA	3.3
34	SR	73	LEU	3.3
61	N5	123	TYR	3.3
5	S3	185	LYS	3.3
18	c6	26	LYS	3.3
82	p0	73	PHE	3.3
6	s4	41	SER	3.2
19	C7	74	GLN	3.2
35	SM	58	GLU	3.2
53	M7	181	ARG	3.2
83	p1	21	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
45	l8	154	ALA	3.2
14	C2	52	LEU	3.2
70	O4	76	TYR	3.2
6	s4	36	HIS	3.2
29	d7	47	PHE	3.2
6	S4	192	ILE	3.2
1	6	794	U	3.2
7	s5	140	THR	3.2
20	c8	141	THR	3.2
30	d8	8	THR	3.2
36	5	3275	U	3.2
42	L5	28	THR	3.2
6	S4	7	LYS	3.2
6	S4	51	ARG	3.2
29	D7	46	VAL	3.2
6	s4	17	HIS	3.2
33	E1	95	HIS	3.2
6	S4	173	ILE	3.2
66	O0	88	GLY	3.2
6	s4	14	ALA	3.2
16	C4	101	ALA	3.2
21	C9	96	ALA	3.2
1	2	718	U	3.2
11	s9	7	THR	3.2
18	c6	115	THR	3.2
29	d7	52	THR	3.2
3	S1	88	VAL	3.2
26	D4	64	PHE	3.2
6	s4	173	ILE	3.2
11	s9	109	LEU	3.2
32	E0	39	LEU	3.2
40	l3	178	LEU	3.2
51	m5	58	GLY	3.2
6	S4	191	ARG	3.2
12	C0	28	ASN	3.2
35	sM	69	ARG	3.2
34	sR	205	SER	3.2
83	p1	9	TYR	3.2
70	O4	65	VAL	3.2
83	p1	30	THR	3.2
84	f	32	VAL	3.2
3	S1	85	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
15	C3	58	HIS	3.2
6	S4	256	ARG	3.2
18	c6	38	LEU	3.2
61	n5	90	ALA	3.2
4	s2	121	VAL	3.2
12	c0	28	ASN	3.2
34	SR	103	PHE	3.2
27	D5	93	SER	3.2
6	S4	6	LYS	3.2
6	s4	122	LYS	3.2
21	C9	103	LYS	3.2
18	C6	10	PHE	3.2
34	sR	247	PRO	3.2
45	l8	159	PRO	3.2
58	n2	106	ALA	3.2
18	C6	127	LYS	3.2
42	L5	130	GLU	3.2
20	C8	41	ARG	3.2
51	m5	43	THR	3.2
5	S3	142	LEU	3.2
9	S7	129	LEU	3.2
19	C7	100	LEU	3.2
34	sR	43	ILE	3.2
66	O0	100	ILE	3.2
72	O6	59	ASP	3.2
7	S5	36	ALA	3.2
68	o2	93	ALA	3.2
1	6	1707	A	3.2
34	sR	154	VAL	3.2
42	L5	125	VAL	3.2
45	l8	140	VAL	3.2
34	sR	14	GLU	3.2
28	D6	82	ARG	3.2
58	N2	94	ARG	3.2
79	Q3	58	SER	3.2
12	c0	1	MET	3.2
17	c5	83	MET	3.2
29	d7	24	LEU	3.2
39	L2	71	LEU	3.2
22	D0	15	GLN	3.2
5	s3	185	LYS	3.2
7	s5	33	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
8	S6	95	LYS	3.2
34	sR	75	ALA	3.2
21	c9	9	VAL	3.2
74	o8	70	PRO	3.2
81	m2	10	PRO	3.2
81	m2	20	TYR	3.2
7	S5	112	ARG	3.2
34	sR	189	GLU	3.2
84	f	89	GLU	3.2
2	S0	144	ILE	3.2
9	S7	38	LEU	3.2
12	C0	19	GLY	3.2
27	d5	80	LEU	3.2
34	sR	234	LEU	3.2
42	L5	127	GLY	3.2
53	M7	176	ILE	3.2
6	s4	143	ASP	3.2
34	sR	54	PHE	3.2
58	N2	106	ALA	3.2
1	2	1362	U	3.2
12	c0	94	GLU	3.2
3	s1	47	LEU	3.2
7	s5	190	ILE	3.2
9	S7	93	LEU	3.2
12	c0	68	LEU	3.2
21	c9	22	LEU	3.2
33	e1	91	ILE	3.2
83	p2	13	ILE	3.2
32	E0	7	SER	3.2
2	S0	187	ALA	3.2
6	s4	149	TYR	3.2
6	s4	182	TYR	3.2
12	C0	65	TYR	3.2
14	c2	26	ASP	3.2
31	d9	14	TYR	3.2
42	L5	86	TYR	3.2
61	n5	110	VAL	3.2
63	N7	77	TYR	3.2
82	p0	80	VAL	3.2
34	SR	92	TRP	3.2
66	O0	42	ILE	3.2
83	p1	44	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
5	s3	143	ARG	3.2
10	S8	160	PHE	3.2
5	s3	179	GLN	3.2
12	c0	21	VAL	3.2
12	c0	60	SER	3.2
6	s4	26	CYS	3.2
13	C1	4	GLU	3.2
17	C5	78	THR	3.2
42	L5	98	ALA	3.2
18	C6	92	TYR	3.2
9	S7	126	LEU	3.1
13	C1	148	LYS	3.1
22	d0	63	LEU	3.1
29	D7	69	GLY	3.1
34	sR	223	TRP	3.1
45	L8	93	LEU	3.1
74	o8	36	LYS	3.1
4	s2	208	GLU	3.1
15	C3	60	VAL	3.1
40	l3	85	VAL	3.1
10	S8	149	SER	3.1
18	C6	120	ASP	3.1
18	c6	37	THR	3.1
30	d8	54	LEU	3.1
7	s5	102	ARG	3.1
31	D9	44	ARG	3.1
2	S0	107	PHE	3.1
36	5	1565	G	3.1
36	1	1351	U	3.1
5	S3	186	VAL	3.1
14	c2	115	VAL	3.1
13	c1	2	SER	3.1
27	d5	42	LEU	3.1
55	M9	171	ASP	3.1
82	p0	93	LEU	3.1
4	S2	145	GLY	3.1
34	sR	125	GLY	3.1
1	6	679	U	3.1
6	S4	84	ALA	3.1
7	S5	191	ALA	3.1
10	S8	185	GLU	3.1
17	C5	105	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
32	E0	31	LYS	3.1
33	E1	82	LYS	3.1
34	SR	62	LYS	3.1
36	1	1242	G	3.1
36	1	1564	U	3.1
18	c6	94	GLN	3.1
6	s4	23	LEU	3.1
7	s5	169	ASN	3.1
14	c2	65	SER	3.1
33	e1	134	ASN	3.1
42	L5	163	LEU	3.1
17	C5	99	GLY	3.1
28	D6	41	ILE	3.1
17	c5	119	PHE	3.1
3	S1	65	VAL	3.1
29	d7	46	VAL	3.1
33	e1	102	VAL	3.1
40	l3	179	ALA	3.1
8	S6	182	GLN	3.1
18	C6	57	LEU	3.1
70	o4	51	LEU	3.1
84	f	92	LEU	3.1
28	D6	83	ILE	3.1
35	sM	57	ASN	3.1
26	d4	68	LYS	3.1
34	sR	94	VAL	3.1
4	s2	95	ARG	3.1
7	s5	167	ARG	3.1
11	S9	43	TYR	3.1
21	C9	25	GLN	3.1
2	S0	92	HIS	3.1
11	s9	74	ASN	3.1
21	c9	101	ASN	3.1
26	d4	72	PHE	3.1
31	D9	52	PHE	3.1
31	d9	38	ILE	3.1
39	l2	164	GLY	3.1
84	f	45	SER	3.1
29	D7	55	THR	3.1
80	e0	54	ARG	3.1
14	c2	110	ALA	3.1
32	E0	2	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
60	n4	131	ALA	3.1
2	S0	188	LEU	3.1
9	S7	81	LEU	3.1
22	D0	86	ILE	3.1
7	S5	134	VAL	3.1
17	c5	103	ASN	3.1
28	D6	31	PRO	3.1
30	D8	59	SER	3.1
34	sR	31	ASN	3.1
34	sR	114	ASP	3.1
45	L8	197	VAL	3.1
1	6	1469	A	3.1
3	s1	86	LEU	3.1
3	s1	94	LYS	3.1
14	c2	57	ALA	3.1
36	1	1581	C	3.1
53	M7	164	LYS	3.1
42	L5	151	GLN	3.1
70	O4	61	GLN	3.1
15	c3	16	ILE	3.1
5	S3	90	ARG	3.1
7	S5	102	ARG	3.1
31	D9	56	ARG	3.1
81	m2	155	ARG	3.1
6	S4	83	PRO	3.1
20	C8	25	ASN	3.1
34	SR	308	ASN	3.1
27	d5	97	LYS	3.1
84	f	83	PRO	3.1
10	s8	117	TYR	3.1
47	M0	152	LEU	3.1
60	n4	96	LEU	3.1
81	m2	96	THR	3.1
3	S1	212	VAL	3.1
17	c5	11	VAL	3.1
3	S1	216	LYS	3.1
18	c6	12	LYS	3.1
67	O1	34	LYS	3.1
3	s1	61	LEU	3.1
20	C8	129	TRP	3.1
25	D3	49	ALA	3.1
28	D6	52	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
34	sR	159	ASN	3.1
40	l3	387	LEU	3.1
58	N2	91	ASP	3.1
7	s5	153	GLY	3.1
7	s5	158	GLN	3.1
10	S8	159	GLN	3.1
33	e1	112	GLY	3.1
51	m5	49	ARG	3.1
66	O0	35	ARG	3.1
20	c8	125	ILE	3.1
34	sR	188	ILE	3.1
61	n5	142	ILE	3.1
14	c2	22	VAL	3.1
19	C7	116	LYS	3.1
82	p0	28	VAL	3.1
18	C6	51	PRO	3.1
30	d8	49	ARG	3.1
34	sR	180	ALA	3.1
34	sR	122	ILE	3.1
11	S9	186	GLU	3.1
15	C3	39	LYS	3.1
25	D3	124	VAL	3.1
30	d8	48	VAL	3.1
33	e1	108	VAL	3.1
7	S5	175	LEU	3.1
34	SR	225	LEU	3.1
36	5	1580	A	3.1
58	N2	84	LEU	3.1
67	O1	10	ARG	3.1
84	f	93	LEU	3.1
81	m2	126	ALA	3.1
6	s4	226	PHE	3.0
12	C0	11	ILE	3.0
17	c5	98	ASN	3.0
21	C9	21	PHE	3.0
35	SM	98	GLY	3.0
84	f	31	PHE	3.0
3	S1	32	ILE	3.0
9	S7	91	ILE	3.0
35	SM	99	LYS	3.0
45	l8	153	ILE	3.0
63	n7	72	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
1	2	238	U	3.0
7	S5	133	VAL	3.0
7	s5	181	GLU	3.0
30	d8	55	VAL	3.0
42	L5	159	VAL	3.0
20	c8	32	LEU	3.0
78	Q2	104	LEU	3.0
11	S9	31	ALA	3.0
17	c5	128	HIS	3.0
42	L5	78	ALA	3.0
83	p2	15	ALA	3.0
84	f	54	HIS	3.0
7	S5	172	ILE	3.0
8	S6	86	PRO	3.0
27	d5	78	ILE	3.0
30	D8	17	GLY	3.0
66	O0	23	TYR	3.0
9	S7	155	ASP	3.0
11	S9	142	ASN	3.0
42	L5	60	ILE	3.0
11	s9	152	SER	3.0
22	d0	120	SER	3.0
11	S9	113	VAL	3.0
3	S1	64	ARG	3.0
58	N2	37	LEU	3.0
3	s1	142	PHE	3.0
9	S7	84	LYS	3.0
19	c7	59	LYS	3.0
5	S3	50	ILE	3.0
8	S6	66	GLY	3.0
20	C8	30	TYR	3.0
47	M0	136	PHE	3.0
30	d8	24	GLY	3.0
43	l6	11	PRO	3.0
6	S4	129	VAL	3.0
30	d8	65	ARG	3.0
7	s5	58	LEU	3.0
7	s5	176	THR	3.0
20	C8	3	LEU	3.0
27	d5	105	THR	3.0
7	s5	179	ALA	3.0
18	c6	20	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
29	D7	47	PHE	3.0
48	M1	102	PHE	3.0
61	n5	23	ALA	3.0
63	N7	44	ALA	3.0
6	s4	162	ILE	3.0
5	s3	178	ARG	3.0
7	S5	129	PRO	3.0
22	D0	71	PRO	3.0
45	l8	144	GLU	3.0
17	c5	93	VAL	3.0
18	C6	67	VAL	3.0
60	N4	79	GLN	3.0
8	S6	96	SER	3.0
12	c0	44	LYS	3.0
18	c6	116	LEU	3.0
31	D9	5	ASN	3.0
34	sR	117	LYS	3.0
84	f	114	LYS	3.0
14	c2	67	THR	3.0
36	5	1571	A	3.0
7	S5	182	ALA	3.0
28	d6	40	ALA	3.0
45	L8	91	PHE	3.0
8	S6	101	ILE	3.0
13	c1	117	VAL	3.0
35	SM	17	VAL	3.0
7	s5	126	ASP	3.0
40	l3	106	TRP	3.0
51	m5	7	LEU	3.0
82	p0	76	LEU	3.0
15	C3	14	SER	3.0
31	d9	37	ASN	3.0
21	C9	63	ARG	3.0
63	n7	7	ALA	3.0
72	O6	68	ARG	3.0
74	o8	22	THR	3.0
82	p0	48	ARG	3.0
7	S5	209	TYR	3.0
11	s9	33	GLU	3.0
25	D3	72	VAL	3.0
5	s3	182	LEU	3.0
22	D0	63	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
3	S1	142	PHE	3.0
32	E0	42	ARG	3.0
81	m2	13	PHE	3.0
22	d0	82	TYR	3.0
26	D4	62	THR	3.0
31	D9	28	THR	3.0
40	L3	294	GLY	3.0
53	M7	183	ALA	3.0
74	o8	15	THR	3.0
80	e0	40	TYR	3.0
83	p2	10	ALA	3.0
12	C0	42	VAL	3.0
33	e1	147	VAL	3.0
21	C9	31	PRO	3.0
42	L5	175	HIS	3.0
2	s0	162	CYS	3.0
63	N7	130	PHE	3.0
17	c5	97	TYR	3.0
19	C7	69	ILE	3.0
18	C6	31	VAL	3.0
63	N7	83	THR	3.0
3	S1	211	HIS	3.0
6	S4	92	LEU	3.0
14	C2	36	LEU	3.0
42	L5	75	LEU	3.0
12	c0	74	GLU	3.0
7	S5	162	VAL	3.0
7	s5	57	SER	3.0
14	C2	128	ALA	3.0
18	C6	81	ILE	3.0
8	S6	67	VAL	3.0
42	L5	172	TYR	3.0
55	M9	177	VAL	3.0
58	n2	54	VAL	3.0
63	n7	18	TYR	3.0
5	S3	54	ARG	3.0
7	S5	93	LEU	3.0
11	S9	24	LEU	3.0
12	C0	40	LEU	3.0
16	C4	33	LEU	3.0
21	C9	7	ARG	3.0
66	O0	101	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
3	s1	83	LYS	3.0
13	C1	153	PHE	3.0
21	C9	38	LYS	3.0
42	L5	3	PHE	3.0
27	D5	59	TYR	3.0
34	sR	172	ALA	3.0
45	l8	179	ILE	3.0
3	S1	51	SER	3.0
5	S3	173	ARG	3.0
16	c4	33	LEU	3.0
1	2	1610	G	3.0
63	N7	122	HIS	3.0
70	O4	42	PRO	3.0
2	S0	166	GLY	3.0
20	C8	124	GLY	3.0
22	D0	54	GLY	3.0
1	2	657	U	3.0
1	6	232	U	3.0
1	6	1059	U	3.0
30	d8	13	ILE	3.0
34	SR	131	ILE	3.0
3	S1	97	LEU	3.0
7	S5	25	LEU	3.0
7	S5	62	VAL	3.0
75	o9	2	ALA	3.0
10	S8	21	PHE	3.0
34	SR	196	ASN	3.0
84	f	39	CYS	3.0
11	S9	137	GLY	2.9
19	C7	118	PRO	3.0
15	C3	16	ILE	2.9
3	s1	110	LEU	2.9
8	s6	162	VAL	2.9
15	C3	40	TYR	2.9
63	N7	124	ALA	2.9
72	O6	96	ALA	2.9
27	d5	93	SER	2.9
36	1	1016	C	2.9
29	d7	55	THR	2.9
53	M7	167	ARG	2.9
63	N7	17	ARG	2.9
70	O4	78	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
82	p0	58	MET	2.9
17	c5	85	ILE	2.9
2	S0	54	TRP	2.9
6	S4	128	LYS	2.9
6	s4	9	LEU	2.9
12	C0	5	LYS	2.9
17	c5	5	VAL	2.9
21	C9	114	VAL	2.9
42	L5	99	TYR	2.9
51	m5	22	LEU	2.9
76	Q0	121	LEU	2.9
43	l6	176	PHE	2.9
3	s1	64	ARG	2.9
10	s8	61	GLU	2.9
31	d9	18	SER	2.9
34	SR	82	SER	2.9
42	L5	82	GLU	2.9
1	2	1481	C	2.9
3	S1	219	LYS	2.9
3	s1	97	LEU	2.9
6	s4	123	LEU	2.9
11	S9	85	VAL	2.9
13	c1	59	PRO	2.9
18	C6	9	THR	2.9
40	L3	50	LYS	2.9
53	M7	169	THR	2.9
67	O1	102	LYS	2.9
19	c7	24	LEU	2.9
63	N7	96	VAL	2.9
1	2	959	U	2.9
36	5	1763	U	2.9
6	s4	185	GLY	2.9
48	m1	108	GLU	2.9
51	m5	56	LYS	2.9
11	S9	123	HIS	2.9
11	S9	150	LEU	2.9
18	C6	41	PRO	2.9
19	c7	38	ILE	2.9
47	M0	31	ILE	2.9
9	S7	154	LEU	2.9
35	sM	60	ALA	2.9
70	O4	68	THR	2.9

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Mol	Chain	Res	Type	RSRZ
82	p0	50	VAL	2.9
10	S8	166	TYR	2.9
83	p2	46	ALA	2.9
1	6	754	A	2.9
36	1	1271	A	2.9
6	S4	62	LYS	2.9
7	s5	161	ASP	2.9
8	S6	93	LYS	2.9
29	D7	57	GLU	2.9
34	sR	105	GLY	2.9
84	f	129	ASP	2.9
6	s4	225	VAL	2.9
7	s5	162	VAL	2.9
14	c2	45	LEU	2.9
34	sR	222	LEU	2.9
45	l8	65	LEU	2.9
48	M1	17	LEU	2.9
66	O0	9	SER	2.9
67	O1	33	VAL	2.9
67	o1	95	PRO	2.9
1	6	1696	G	2.9
8	s6	88	ARG	2.9
42	L5	160	PHE	2.9
67	o1	90	PHE	2.9
70	O4	60	ARG	2.9
74	O8	6	THR	2.9
11	S9	39	LYS	2.9
18	c6	14	LYS	2.9
30	D8	45	LYS	2.9
35	sM	75	ASP	2.9
5	s3	136	VAL	2.9
8	s6	76	LEU	2.9
45	l8	152	LEU	2.9
10	S8	167	ALA	2.9
42	L5	242	SER	2.9
82	p0	22	TYR	2.9
2	S0	22	THR	2.9
6	s4	71	LYS	2.9
6	s4	159	THR	2.9
48	M1	153	LYS	2.9
7	s5	144	GLU	2.9
10	S8	140	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	2	714	G	2.9
9	s7	154	LEU	2.9
18	c6	52	LEU	2.9
21	C9	124	ILE	2.9
32	E0	43	ARG	2.9
45	L8	61	GLN	2.9
58	n2	105	LEU	2.9
66	o0	42	ILE	2.9
4	s2	85	PRO	2.9
7	s5	61	TYR	2.9
41	l4	26	PHE	2.9
74	o8	32	ASN	2.9
34	sR	12	THR	2.9
60	n4	66	GLU	2.9
20	c8	124	GLY	2.9
6	s4	90	ILE	2.9
7	S5	194	LEU	2.9
34	sR	220	ILE	2.9
2	s0	20	ALA	2.9
8	S6	149	LYS	2.9
19	C7	83	GLN	2.9
14	c2	92	ALA	2.9
16	C4	78	ALA	2.9
25	D3	140	LYS	2.9
48	M1	64	LYS	2.9
1	2	1584	G	2.9
18	C6	109	PHE	2.9
14	c2	68	GLU	2.9
29	D7	49	HIS	2.9
42	L5	94	ASN	2.9
2	S0	195	TRP	2.9
34	SR	90	ARG	2.9
35	SM	96	ARG	2.9
48	M1	83	GLY	2.9
74	o8	35	GLY	2.9
2	S0	50	VAL	2.9
18	C6	48	VAL	2.9
63	N7	75	VAL	2.9
66	O0	90	VAL	2.9
21	C9	107	ALA	2.9
27	d5	47	TYR	2.9
45	l8	113	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
66	o0	59	TYR	2.9
83	p2	43	ASP	2.9
83	p1	18	GLU	2.9
6	S4	39	ARG	2.9
9	s7	2	SER	2.9
27	D5	68	ARG	2.9
1	2	1685	G	2.9
1	6	1702	A	2.9
6	s4	42	LEU	2.9
14	c2	95	LYS	2.9
34	SR	23	LEU	2.9
36	1	1241	U	2.9
63	N7	22	LYS	2.9
11	S9	96	VAL	2.9
15	C3	65	VAL	2.9
16	C4	42	VAL	2.9
17	c5	96	ILE	2.9
35	sM	25	ILE	2.9
82	p0	94	THR	2.9
84	f	26	LEU	2.9
8	S6	198	ALA	2.9
42	L5	142	PHE	2.9
7	S5	55	ASP	2.9
28	D6	73	TYR	2.9
2	S0	113	ARG	2.9
42	l5	126	GLU	2.9
72	O6	98	ARG	2.9
25	D3	106	GLY	2.9
2	S0	158	VAL	2.9
3	S1	99	ASN	2.9
5	s3	177	MET	2.9
12	c0	35	ILE	2.9
28	D6	8	ASN	2.9
36	1	1238	C	2.9
66	O0	89	VAL	2.9
74	O8	56	ILE	2.9
84	f	80	MET	2.9
20	C8	141	THR	2.9
67	o1	39	PHE	2.9
6	S4	33	ALA	2.9
2	S0	157	ASP	2.9
19	c7	3	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
21	C9	57	ARG	2.9
33	E1	116	LYS	2.9
6	S4	58	GLY	2.9
16	c4	102	LEU	2.9
27	d5	91	PRO	2.9
51	M5	10	LEU	2.9
5	s3	50	ILE	2.8
17	C5	84	ILE	2.8
3	s1	38	PHE	2.8
6	S4	50	ASN	2.8
7	S5	158	GLN	2.8
32	E0	18	THR	2.8
55	M9	170	ARG	2.8
10	S8	70	GLU	2.8
11	S9	8	TYR	2.8
17	C5	123	TYR	2.8
48	M1	142	LYS	2.8
72	O6	53	TYR	2.8
3	S1	110	LEU	2.8
8	s6	193	LEU	2.8
14	c2	102	GLY	2.8
25	D3	57	LEU	2.8
5	s3	186	VAL	2.8
7	S5	211	ILE	2.8
7	s5	29	ILE	2.8
25	D3	102	VAL	2.8
42	l5	125	VAL	2.8
59	N3	137	VAL	2.8
11	S9	121	SER	2.8
51	m5	63	ARG	2.8
70	o4	31	ARG	2.8
21	C9	55	TYR	2.8
21	c9	17	ALA	2.8
1	6	664	U	2.8
36	1	1269	U	2.8
58	N2	88	GLN	2.8
1	6	668	C	2.8
64	n8	104	THR	2.8
21	C9	82	GLY	2.8
34	SR	93	ASP	2.8
35	SM	67	GLY	2.8
40	L3	47	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
16	C4	120	PRO	2.8
20	c8	5	VAL	2.8
34	sR	288	HIS	2.8
63	N7	10	VAL	2.8
63	n7	10	VAL	2.8
5	S3	24	PHE	2.8
6	s4	22	LYS	2.8
9	S7	24	PHE	2.8
39	L2	63	PHE	2.8
70	o4	93	PHE	2.8
6	S4	138	TYR	2.8
7	s5	34	GLN	2.8
10	S8	144	ALA	2.8
43	l6	2	SER	2.8
72	O6	48	ALA	2.8
84	f	15	SER	2.8
11	S9	35	GLY	2.8
11	S9	80	LEU	2.8
3	S1	26	ARG	2.8
9	S7	62	VAL	2.8
45	L8	68	ARG	2.8
17	C5	75	PRO	2.8
19	c7	28	PHE	2.8
45	l8	94	PHE	2.8
53	M7	159	LYS	2.8
7	S5	74	ALA	2.8
29	D7	31	TYR	2.8
51	m5	15	GLN	2.8
3	S1	213	ARG	2.8
5	s3	37	VAL	2.8
5	s3	175	VAL	2.8
6	S4	109	PHE	2.8
9	S7	73	VAL	2.8
11	S9	77	ILE	2.8
18	C6	22	VAL	2.8
20	C8	125	ILE	2.8
27	D5	64	VAL	2.8
45	l8	78	PHE	2.8
47	M0	148	VAL	2.8
21	c9	90	PRO	2.8
35	sM	122	GLU	2.8
28	d6	63	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
68	O2	127	ALA	2.8
68	o2	2	ALA	2.8
7	S5	185	ARG	2.8
1	6	1693	A	2.8
8	s6	79	LYS	2.8
13	c1	138	ASN	2.8
18	c6	130	GLY	2.8
43	L6	8	LYS	2.8
43	L6	55	LEU	2.8
46	l9	191	LEU	2.8
5	S3	208	ILE	2.8
7	s5	82	PHE	2.8
34	sR	178	VAL	2.8
45	l8	74	THR	2.8
51	m5	121	VAL	2.8
63	n7	23	VAL	2.8
70	o4	25	THR	2.8
72	O6	9	ILE	2.8
34	sR	221	MET	2.8
6	S4	17	HIS	2.8
17	c5	114	HIS	2.8
25	d3	71	CYS	2.8
34	SR	24	ALA	2.8
5	s3	21	LEU	2.8
11	S9	120	LYS	2.8
34	sR	38	ARG	2.8
70	o4	16	ARG	2.8
18	c6	28	LEU	2.8
42	L5	201	GLY	2.8
72	O6	50	LEU	2.8
3	S1	48	VAL	2.8
3	S1	114	VAL	2.8
7	S5	89	ILE	2.8
10	S8	64	ASN	2.8
17	c5	86	VAL	2.8
29	D7	62	ILE	2.8
40	L3	78	VAL	2.8
43	l6	130	ILE	2.8
49	m3	182	ILE	2.8
74	o8	25	VAL	2.8
35	sM	168	GLU	2.8
11	s9	51	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
12	C0	26	ASP	2.8
34	SR	66	HIS	2.8
6	s4	34	GLY	2.8
14	C2	28	LEU	2.8
25	D3	103	LEU	2.8
51	m5	10	LEU	2.8
7	s5	64	VAL	2.8
27	D5	92	ILE	2.8
83	p1	22	SER	2.8
3	S1	49	ASN	2.8
21	C9	45	MET	2.8
3	S1	31	ASP	2.8
27	d5	38	HIS	2.8
27	d5	82	HIS	2.8
36	1	1352	A	2.8
36	5	1352	A	2.8
6	s4	124	GLY	2.8
16	c4	42	VAL	2.8
18	c6	60	PHE	2.8
26	D4	5	VAL	2.8
26	D4	106	GLN	2.8
34	sR	85	TRP	2.8
47	m0	124	GLY	2.8
63	N7	123	GLN	2.8
14	c2	24	ILE	2.8
34	sR	186	PHE	2.8
7	S5	139	ASN	2.8
83	p1	4	GLU	2.8
3	s1	46	THR	2.8
3	s1	104	ASP	2.8
6	S4	13	ALA	2.8
6	s4	65	LEU	2.8
7	S5	67	PRO	2.8
26	D4	44	LEU	2.8
67	O1	104	LEU	2.8
1	2	132	U	2.8
6	S4	130	GLN	2.8
21	C9	54	PHE	2.8
30	D8	55	VAL	2.8
51	M5	60	VAL	2.8
11	S9	108	ARG	2.8
13	c1	116	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
14	c2	85	LYS	2.8
63	n7	115	LYS	2.8
43	l6	66	SER	2.8
53	M7	170	SER	2.8
2	S0	18	LEU	2.8
13	C1	22	ASN	2.8
8	s6	78	THR	2.8
34	sR	9	LEU	2.8
36	5	1579	C	2.8
63	N7	87	LEU	2.8
11	S9	124	HIS	2.8
17	C5	128	HIS	2.8
25	D3	51	GLY	2.8
34	sR	287	PRO	2.8
45	L8	226	TYR	2.8
5	s3	164	VAL	2.8
6	s4	228	ILE	2.8
10	S8	56	ARG	2.8
55	M9	175	GLN	2.8
70	O4	80	ARG	2.8
82	p0	208	GLU	2.8
1	2	1689	A	2.8
26	D4	74	LEU	2.8
29	D7	73	LEU	2.8
83	p2	23	SER	2.8
21	C9	90	PRO	2.8
28	d6	62	TYR	2.8
69	o3	65	ARG	2.8
74	o8	46	ARG	2.8
49	m3	147	ILE	2.7
66	O0	43	ILE	2.7
21	C9	53	TRP	2.7
36	1	1572	U	2.7
66	O0	14	LEU	2.7
67	O1	73	LEU	2.7
4	s2	64	LYS	2.7
6	S4	10	LYS	2.7
11	s9	149	ARG	2.7
17	c5	100	LYS	2.7
8	S6	197	ASN	2.7
18	C6	45	ARG	2.7
34	sR	226	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
51	m5	41	ARG	2.7
61	N5	107	VAL	2.7
63	n7	74	VAL	2.7
67	O1	12	TYR	2.7
7	S5	131	GLN	2.7
10	s8	60	ILE	2.7
16	C4	38	THR	2.7
34	sR	136	ILE	2.7
45	L8	99	PRO	2.7
18	c6	98	ASP	2.7
61	N5	81	ILE	2.7
74	o8	27	ILE	2.7
11	S9	174	ARG	2.7
57	N1	27	LEU	2.7
1	2	1601	G	2.7
1	6	1229	G	2.7
4	s2	93	GLY	2.7
36	1	1265	U	2.7
20	c8	42	TYR	2.7
34	sR	290	VAL	2.7
42	L5	246	ALA	2.7
67	O1	66	GLY	2.7
7	s5	103	ASN	2.7
26	D4	81	GLU	2.7
28	d6	67	THR	2.7
34	sR	52	GLN	2.7
36	1	1605	A	2.7
70	O4	20	ILE	2.7
70	o4	26	PRO	2.7
6	s4	73	ASP	2.7
58	n2	98	THR	2.7
8	S6	154	ARG	2.7
67	O1	72	ARG	2.7
81	m2	127	ARG	2.7
1	2	239	C	2.7
10	S8	63	GLY	2.7
6	S4	46	VAL	2.7
15	C3	52	VAL	2.7
34	SR	20	VAL	2.7
51	m5	39	ALA	2.7
53	M7	178	ALA	2.7
9	S7	31	SER	2.7

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Mol	Chain	Res	Type	RSRZ
15	c3	37	ILE	2.7
67	o1	76	SER	2.7
13	C1	16	GLN	2.7
8	S6	74	LYS	2.7
11	S9	171	ARG	2.7
32	E0	37	ARG	2.7
33	e1	125	THR	2.7
18	C6	89	LEU	2.7
34	SR	47	LEU	2.7
4	s2	98	PHE	2.7
6	s4	2	ALA	2.7
13	C1	38	ALA	2.7
16	C4	74	VAL	2.7
20	c8	133	VAL	2.7
21	C9	61	VAL	2.7
39	l2	59	ALA	2.7
42	L5	96	ALA	2.7
1	6	1232	U	2.7
5	s3	103	GLU	2.7
16	c4	83	ILE	2.7
28	D6	61	GLU	2.7
36	5	1016	C	2.7
32	E0	20	LYS	2.7
36	1	1765	U	2.7
70	O4	95	ILE	2.7
20	C8	54	LEU	2.7
55	m9	24	LEU	2.7
18	C6	46	PHE	2.7
11	s9	141	VAL	2.7
34	sR	312	VAL	2.7
63	n7	49	TYR	2.7
6	S4	100	ARG	2.7
7	S5	144	GLU	2.7
19	C7	38	ILE	2.7
22	D0	64	LYS	2.7
22	d0	83	GLU	2.7
27	D5	78	ILE	2.7
70	o4	41	ARG	2.7
1	2	31	C	2.7
20	c8	54	LEU	2.7
23	D1	69	LEU	2.7
34	sR	184	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
7	S5	150	GLY	2.7
34	sR	50	ASP	2.7
51	m5	46	ASP	2.7
84	f	150	PHE	2.7
8	s6	172	ALA	2.7
16	C4	118	VAL	2.7
27	d5	60	VAL	2.7
34	sR	58	VAL	2.7
22	d0	65	ILE	2.7
24	D2	53	ILE	2.7
42	L5	190	ILE	2.7
60	n4	94	ARG	2.7
1	6	1196	A	2.7
1	2	1199	G	2.7
7	s5	42	LEU	2.7
14	C2	78	LEU	2.7
18	c6	83	GLN	2.7
20	C8	113	LEU	2.7
80	e0	30	PRO	2.7
36	1	3154	C	2.7
80	e0	56	MET	2.7
7	S5	79	ASN	2.7
8	s6	144	PHE	2.7
8	s6	156	PHE	2.7
49	M3	98	ASP	2.7
55	M9	22	VAL	2.7
66	O0	40	LYS	2.7
67	O1	39	PHE	2.7
3	s1	225	VAL	2.7
8	s6	163	THR	2.7
9	S7	90	VAL	2.7
11	S9	98	ALA	2.7
16	C4	28	VAL	2.7
18	C6	85	ILE	2.7
18	C6	142	TYR	2.7
18	C6	143	ARG	2.7
34	SR	114	ASP	2.7
7	S5	113	ILE	2.7
81	m2	101	PRO	2.7
11	S9	101	VAL	2.7
30	D8	48	VAL	2.7
42	L5	161	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
53	M7	174	GLY	2.7
81	m2	79	ASN	2.7
6	S4	149	TYR	2.7
6	S4	159	THR	2.7
42	L5	231	ILE	2.7
48	M1	21	ILE	2.7
49	M3	95	ILE	2.7
83	p1	10	ALA	2.7
61	n5	82	LEU	2.7
74	o8	31	LEU	2.7
7	s5	80	LYS	2.7
11	S9	154	LYS	2.7
18	C6	77	GLN	2.7
11	S9	117	GLY	2.7
26	D4	10	ARG	2.7
58	N2	9	GLN	2.7
82	p0	66	PHE	2.7
22	d0	28	SER	2.7
4	s2	178	ILE	2.7
6	s4	163	ASP	2.7
7	S5	161	ASP	2.7
24	D2	27	ILE	2.7
25	D3	59	ILE	2.7
1	2	1534	G	2.7
3	s1	52	THR	2.7
8	s6	133	LEU	2.7
27	D5	75	LEU	2.7
6	s4	175	PHE	2.7
7	S5	101	GLY	2.7
31	d9	52	PHE	2.7
42	L5	223	PHE	2.7
26	D4	86	GLU	2.7
32	E0	27	PRO	2.7
63	N7	12	VAL	2.7
63	N7	47	GLU	2.7
6	S4	169	ILE	2.7
27	D5	41	ILE	2.7
70	o4	39	ALA	2.7
81	m2	125	ILE	2.7
1	2	781	U	2.7
6	s4	238	LEU	2.7
7	S5	125	THR	2.7

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Mol	Chain	Res	Type	RSRZ
7	S5	176	THR	2.7
10	S8	62	THR	2.7
10	S8	121	LEU	2.7
23	D1	40	ASP	2.7
25	D3	50	LYS	2.7
33	E1	94	LYS	2.7
34	SR	261	LYS	2.7
51	m5	51	LEU	2.7
55	M9	44	LEU	2.7
61	n5	111	ASN	2.7
42	L5	54	ARG	2.7
70	o4	68	THR	2.7
7	s5	184	PHE	2.7
58	n2	15	PHE	2.7
3	s1	215	VAL	2.7
6	S4	85	GLY	2.7
17	C5	95	GLY	2.7
45	l8	157	VAL	2.7
51	m5	186	GLY	2.7
17	C5	125	PRO	2.7
7	s5	183	ALA	2.7
9	S7	135	ILE	2.7
27	d5	52	LYS	2.6
40	L3	51	ALA	2.7
66	O0	38	LYS	2.6
63	n7	42	LEU	2.6
20	c8	21	ASN	2.6
5	S3	152	PHE	2.6
29	d7	61	THR	2.6
45	L8	90	THR	2.6
1	2	1337	A	2.6
17	C5	41	VAL	2.6
26	D4	73	GLY	2.6
36	1	1026	A	2.6
36	1	2207	A	2.6
60	n4	79	GLN	2.6
3	S1	94	LYS	2.6
6	s4	127	LYS	2.6
6	s4	145	ARG	2.6
21	c9	64	HIS	2.6
23	D1	23	ILE	2.6
70	O4	37	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
47	M0	68	ALA	2.6
51	m5	4	TYR	2.6
84	f	34	ILE	2.6
34	SR	65	SER	2.6
14	c2	111	ASN	2.6
51	m5	59	PHE	2.6
7	s5	35	GLN	2.6
10	s8	156	VAL	2.6
11	S9	182	GLU	2.6
35	sM	64	LYS	2.6
63	N7	43	VAL	2.6
6	S4	236	ILE	2.6
19	C7	24	LEU	2.6
25	D3	135	LEU	2.6
31	d9	11	PRO	2.6
42	L5	134	ALA	2.6
67	O1	59	ILE	2.6
70	O4	75	ALA	2.6
76	Q0	78	ILE	2.6
13	C1	13	PHE	2.6
34	SR	186	PHE	2.6
45	l8	230	LYS	2.6
10	S8	111	GLN	2.6
1	2	194	U	2.6
5	s3	69	LEU	2.6
17	c5	116	LEU	2.6
20	C8	69	ILE	2.6
24	d2	86	ILE	2.6
28	D6	35	ALA	2.6
29	d7	59	CYS	2.6
12	C0	12	HIS	2.6
20	C8	127	HIS	2.6
3	S1	44	GLY	2.6
11	S9	162	SER	2.6
14	c2	29	LYS	2.6
14	c2	119	SER	2.6
18	c6	2	SER	2.6
25	D3	139	LYS	2.6
29	D7	36	LYS	2.6
63	N7	52	LYS	2.6
34	sR	315	VAL	2.6
51	m5	122	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
2	S0	85	ALA	2.6
7	S5	114	ILE	2.6
11	S9	45	ILE	2.6
14	c2	133	LEU	2.6
30	d8	26	THR	2.6
35	sM	66	ALA	2.6
40	L3	328	ILE	2.6
42	L5	103	LEU	2.6
55	M9	169	ALA	2.6
61	N5	30	ALA	2.6
58	N2	30	PRO	2.6
6	S4	36	HIS	2.6
72	o6	25	LYS	2.6
82	p0	81	LYS	2.6
1	2	1217	A	2.6
2	S0	181	VAL	2.6
3	S1	21	VAL	2.6
10	S8	112	TRP	2.6
18	c6	75	VAL	2.6
31	D9	40	ARG	2.6
31	d9	44	ARG	2.6
34	sR	60	SER	2.6
47	M0	50	VAL	2.6
70	o4	23	VAL	2.6
8	S6	199	GLN	2.6
18	C6	8	GLN	2.6
6	s4	38	LEU	2.6
12	c0	49	LEU	2.6
43	L6	65	ILE	2.6
34	sR	21	THR	2.6
42	L5	118	THR	2.6
2	S0	126	PRO	2.6
31	d9	12	ARG	2.6
42	L5	185	PHE	2.6
10	S8	2	GLY	2.6
10	S8	30	GLY	2.6
11	s9	85	VAL	2.6
18	C6	69	VAL	2.6
26	d4	67	GLY	2.6
29	D7	40	CYS	2.6
30	D8	15	VAL	2.6
51	M5	58	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
81	m2	154	CYS	2.6
42	L5	167	SER	2.6
1	2	1471	A	2.6
45	L8	64	ILE	2.6
57	N1	127	GLN	2.6
16	C4	17	ALA	2.6
20	C8	56	LYS	2.6
21	C9	78	LYS	2.6
60	n4	87	LEU	2.6
66	o0	22	LYS	2.6
3	s1	111	ARG	2.6
12	C0	37	THR	2.6
29	D7	67	THR	2.6
74	o8	72	THR	2.6
8	S6	36	VAL	2.6
18	C6	133	GLY	2.6
19	C7	85	VAL	2.6
58	N2	65	VAL	2.6
64	n8	116	GLY	2.6
70	o4	28	GLY	2.6
3	s1	54	LEU	2.6
7	S5	130	ILE	2.6
7	s5	118	LEU	2.6
10	s8	58	LEU	2.6
18	C6	43	ILE	2.6
21	C9	60	SER	2.6
42	L5	39	GLN	2.6
45	l8	150	LEU	2.6
64	N8	126	LYS	2.6
66	o0	100	ILE	2.6
21	C9	130	ARG	2.6
27	d5	68	ARG	2.6
63	n7	130	PHE	2.6
67	o1	92	TYR	2.6
34	sR	135	THR	2.6
5	S3	37	VAL	2.6
14	c2	120	VAL	2.6
16	c4	28	VAL	2.6
3	s1	188	LEU	2.6
7	S5	46	TRP	2.6
15	C3	43	LYS	2.6
21	C9	113	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
24	D2	61	ILE	2.6
72	o6	99	ARG	2.6
81	m2	118	GLN	2.6
6	s4	27	TYR	2.6
14	C2	57	ALA	2.6
31	d9	34	TYR	2.6
58	N2	12	ALA	2.6
7	s5	24	VAL	2.6
13	C1	151	LYS	2.6
16	C4	95	GLY	2.6
35	sM	50	ASN	2.6
32	E0	14	VAL	2.6
42	L5	182	GLY	2.6
64	n8	120	ASN	2.6
42	l5	159	VAL	2.6
15	c3	25	TRP	2.6
42	L5	113	LEU	2.6
45	l8	142	LEU	2.6
30	D8	10	ALA	2.6
49	m3	179	PHE	2.6
18	C6	121	SER	2.6
51	m5	62	TYR	2.6
84	f	17	ALA	2.6
2	S0	104	PRO	2.6
7	S5	128	ASN	2.6
16	C4	67	VAL	2.6
17	C5	94	VAL	2.6
18	C6	33	GLY	2.6
32	E0	25	GLU	2.6
20	C8	29	VAL	2.6
22	D0	62	VAL	2.6
8	S6	186	ARG	2.6
11	S9	7	THR	2.6
18	C6	28	LEU	2.6
25	d3	103	LEU	2.6
29	D7	52	THR	2.6
60	n4	133	THR	2.6
20	c8	14	ILE	2.6
12	c0	58	GLN	2.6
14	c2	35	ALA	2.6
21	C9	33	TYR	2.6
53	m7	55	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
11	S9	27	GLU	2.6
29	d7	58	SER	2.6
58	n2	17	VAL	2.6
81	m2	133	SER	2.6
74	o8	39	ARG	2.6
13	C1	21	ASN	2.6
12	C0	67	THR	2.6
17	c5	89	MET	2.6
42	L5	104	LEU	2.6
45	L8	65	LEU	2.6
45	L8	69	LEU	2.6
51	m5	42	PRO	2.6
57	n1	66	ASN	2.6
30	d8	5	THR	2.6
58	N2	38	ILE	2.6
72	O6	58	ILE	2.6
82	p0	89	THR	2.6
84	f	44	MET	2.6
3	s1	30	PHE	2.5
9	S7	92	PHE	2.5
31	d9	8	PHE	2.5
8	s6	208	TYR	2.5
25	D3	137	LYS	2.5
33	e1	107	LYS	2.5
71	O5	120	ALA	2.5
1	6	1445	G	2.5
6	S4	254	ARG	2.5
6	s4	46	VAL	2.5
17	c5	137	ARG	2.5
18	C6	114	ARG	2.5
11	S9	145	SER	2.5
18	c6	121	SER	2.5
36	1	1268	G	2.5
47	M0	138	VAL	2.5
67	o1	91	SER	2.5
82	p0	27	VAL	2.5
6	S4	12	LEU	2.5
10	S8	165	LEU	2.5
2	s0	22	THR	2.5
5	s3	24	PHE	2.5
5	s3	141	LYS	2.5
6	s4	109	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
6	s4	153	ASN	2.5
11	s9	91	LYS	2.5
45	l8	70	LYS	2.5
58	n2	13	LYS	2.5
63	N7	126	LYS	2.5
72	o6	100	HIS	2.5
74	o8	11	PHE	2.5
5	s3	3	ALA	2.5
6	s4	100	ARG	2.5
7	S5	196	GLU	2.5
10	s8	166	TYR	2.5
16	c4	85	ALA	2.5
42	L5	76	ALA	2.5
63	N7	99	GLU	2.5
40	l3	162	VAL	2.5
67	O1	23	VAL	2.5
6	S4	253	ASP	2.5
12	c0	36	ASP	2.5
20	C8	23	ASP	2.5
36	1	1567	U	2.5
48	M1	91	LEU	2.5
63	N7	94	SER	2.5
70	O4	66	SER	2.5
6	s4	86	PHE	2.5
12	C0	43	ILE	2.5
45	l8	122	LYS	2.5
2	s0	23	HIS	2.5
15	C3	69	ASN	2.5
34	SR	198	ASN	2.5
7	S5	76	ARG	2.5
8	S6	88	ARG	2.5
13	C1	116	ARG	2.5
51	m5	31	ARG	2.5
59	N3	32	ARG	2.5
60	n4	103	ALA	2.5
6	S4	243	GLY	2.5
34	sR	55	GLY	2.5
82	p0	190	VAL	2.5
7	s5	45	LYS	2.5
43	l6	8	LYS	2.5
45	l8	166	LEU	2.5
1	6	667	U	2.5

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Mol	Chain	Res	Type	RSRZ
1	6	718	U	2.5
6	S4	147	ILE	2.5
13	C1	42	PHE	2.5
34	sR	242	SER	2.5
46	l9	190	ASP	2.5
7	S5	225	ARG	2.5
67	O1	62	ARG	2.5
34	sR	17	ASN	2.5
84	f	78	HIS	2.5
6	S4	95	THR	2.5
1	2	175	G	2.5
1	2	1713	G	2.5
14	C2	123	VAL	2.5
42	L5	204	VAL	2.5
70	O4	6	THR	2.5
74	o8	75	VAL	2.5
27	d5	46	LYS	2.5
34	SR	117	LYS	2.5
34	sR	274	LEU	2.5
11	S9	34	PHE	2.5
14	C2	108	ARG	2.5
40	L3	332	ARG	2.5
8	s6	135	PRO	2.5
35	sM	79	SER	2.5
72	O6	51	SER	2.5
6	S4	190	GLY	2.5
8	s6	134	GLY	2.5
25	D3	96	VAL	2.5
29	D7	54	VAL	2.5
29	d7	53	ALA	2.5
25	D3	123	LYS	2.5
36	1	1580	A	2.5
60	n4	102	LYS	2.5
11	S9	76	LEU	2.5
24	D2	26	LEU	2.5
66	O0	41	LEU	2.5
2	S0	102	PHE	2.5
25	D3	71	CYS	2.5
39	L2	72	ARG	2.5
47	M0	153	ARG	2.5
51	m5	61	ILE	2.5
64	n8	124	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	6	493	U	2.5
4	s2	118	ALA	2.5
5	S3	137	VAL	2.5
6	S4	142	HIS	2.5
8	S6	102	VAL	2.5
21	C9	110	LYS	2.5
51	m5	47	LYS	2.5
59	n3	3	GLY	2.5
63	N7	29	HIS	2.5
63	N7	106	GLN	2.5
64	n8	121	VAL	2.5
66	o0	90	VAL	2.5
67	o1	93	VAL	2.5
80	e0	3	LYS	2.5
6	s4	187	ARG	2.5
10	s8	67	TRP	2.5
19	c7	104	ASN	2.5
35	sM	70	ASN	2.5
22	d0	70	THR	2.5
43	l6	9	TRP	2.5
6	S4	210	ILE	2.5
51	m5	142	ILE	2.5
82	p0	213	PHE	2.5
10	S8	200	LYS	2.5
35	SM	175	ASP	2.5
42	L5	143	LYS	2.5
63	N7	21	LYS	2.5
4	s2	105	GLY	2.5
6	S4	14	ALA	2.5
6	S4	28	ALA	2.5
11	S9	163	PRO	2.5
30	D8	41	VAL	2.5
34	SR	194	GLY	2.5
45	L8	132	VAL	2.5
51	M5	135	VAL	2.5
63	n7	75	VAL	2.5
82	p0	11	TYR	2.5
10	S8	96	LEU	2.5
20	C8	45	LEU	2.5
21	C9	134	ARG	2.5
11	S9	38	ASN	2.5
16	c4	23	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
47	M0	46	PHE	2.5
34	sR	261	LYS	2.5
1	2	1583	A	2.5
1	6	1711	C	2.5
45	L8	161	GLU	2.5
21	C9	88	VAL	2.5
31	d9	6	VAL	2.5
27	D5	83	LEU	2.5
39	L2	69	TYR	2.5
51	M5	6	TYR	2.5
70	O4	5	VAL	2.5
6	s4	44	LEU	2.5
11	S9	109	LEU	2.5
14	c2	74	LEU	2.5
70	O4	32	ALA	2.5
2	s0	46	HIS	2.5
26	D4	63	GLN	2.5
1	2	1340	U	2.5
1	6	1474	G	2.5
4	S2	178	ILE	2.5
8	s6	175	ILE	2.5
6	s4	87	MET	2.5
25	D3	84	THR	2.5
26	d4	102	LYS	2.5
36	1	1763	U	2.5
34	sR	48	THR	2.5
58	N2	13	LYS	2.5
2	S0	51	GLY	2.5
17	C5	81	ARG	2.5
51	m5	60	VAL	2.5
55	M9	178	ALA	2.5
59	N3	3	GLY	2.5
74	o8	3	ARG	2.5
2	s0	146	LEU	2.5
5	S3	21	LEU	2.5
6	S4	35	PRO	2.5
6	s4	82	TYR	2.5
6	s4	83	PRO	2.5
16	C4	20	TYR	2.5
29	d7	50	ALA	2.5
9	S7	158	ASP	2.5
27	d5	44	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
34	SR	76	ASP	2.5
63	N7	28	PRO	2.5
3	S1	56	SER	2.5
7	s5	96	SER	2.5
9	S7	187	SER	2.5
19	C7	70	SER	2.5
82	p0	195	GLN	2.5
25	D3	86	PHE	2.5
34	SR	302	PHE	2.5
42	L5	244	HIS	2.5
43	L6	131	LYS	2.5
11	S9	42	ILE	2.5
70	o4	90	ILE	2.5
6	s4	60	GLU	2.5
2	s0	165	ARG	2.5
19	C7	123	ASN	2.5
36	1	1267	U	2.5
36	5	1351	U	2.5
45	l8	161	GLU	2.5
28	D6	85	ARG	2.5
1	2	765	G	2.5
1	2	914	G	2.5
3	S1	141	ALA	2.5
12	c0	54	TYR	2.5
21	C9	18	TYR	2.5
26	d4	57	VAL	2.5
33	E1	148	TYR	2.5
63	N7	114	VAL	2.5
67	O1	32	ALA	2.5
69	o3	50	ALA	2.5
70	O4	85	VAL	2.5
27	d5	48	ASP	2.5
63	N7	128	GLN	2.5
64	n8	126	LYS	2.5
67	o1	61	LYS	2.5
70	O4	7	PHE	2.5
63	N7	68	ILE	2.5
51	M5	28	TRP	2.5
1	2	280	U	2.5
7	s5	128	ASN	2.5
10	S8	95	THR	2.5
21	C9	37	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
26	D4	55	VAL	2.5
29	D7	68	GLY	2.5
36	5	1353	U	2.5
11	S9	115	LYS	2.5
42	L5	30	TYR	2.5
43	l6	128	LYS	2.5
71	O5	2	ALA	2.5
72	o6	28	TYR	2.5
3	S1	105	PHE	2.5
11	S9	169	PRO	2.5
12	c0	16	PHE	2.5
17	c5	102	PHE	2.5
19	c7	62	GLN	2.5
6	S4	197	HIS	2.5
10	s8	78	ILE	2.5
12	C0	78	GLU	2.5
23	D1	10	GLU	2.5
47	M0	80	SER	2.5
64	n8	146	GLU	2.5
70	o4	29	ILE	2.5
1	2	769	A	2.4
5	S3	69	LEU	2.4
20	c8	142	GLY	2.4
21	c9	105	LEU	2.4
42	L5	164	LYS	2.4
63	N7	27	LYS	2.4
67	O1	37	LYS	2.4
82	p0	23	LYS	2.4
1	2	174	U	2.4
3	S1	156	ALA	2.4
15	c3	15	ALA	2.4
26	D4	82	ALA	2.4
27	D5	79	ALA	2.4
42	L5	132	THR	2.4
6	S4	145	ARG	2.4
10	s8	159	GLN	2.4
19	c7	60	ARG	2.4
25	d3	42	PRO	2.4
34	sR	260	ILE	2.4
63	n7	107	ARG	2.4
4	s2	120	GLU	2.4
6	S4	251	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
2	S0	196	SER	2.4
7	s5	46	TRP	2.4
20	C8	131	LEU	2.4
26	D4	125	LEU	2.4
42	L5	173	VAL	2.4
55	M9	53	LYS	2.4
79	Q3	86	LEU	2.4
6	S4	63	ALA	2.4
11	s9	8	TYR	2.4
21	C9	58	ALA	2.4
68	o2	92	TYR	2.4
70	o4	2	ALA	2.4
36	5	2538	U	2.4
46	L9	31	ARG	2.4
83	p1	28	THR	2.4
7	s5	199	ILE	2.4
12	C0	6	GLU	2.4
15	C3	71	ILE	2.4
27	d5	100	ILE	2.4
39	L2	47	GLN	2.4
42	L5	88	ILE	2.4
64	n8	112	ILE	2.4
14	c2	114	LYS	2.4
5	s3	137	VAL	2.4
7	s5	123	VAL	2.4
34	SR	156	VAL	2.4
34	sR	120	SER	2.4
54	m8	2	GLY	2.4
21	c9	33	TYR	2.4
28	D6	42	ARG	2.4
45	l8	198	ALA	2.4
63	N7	48	ARG	2.4
84	f	146	ALA	2.4
7	s5	84	LYS	2.4
7	s5	172	ILE	2.4
17	C5	9	LYS	2.4
21	c9	111	ILE	2.4
34	SR	99	THR	2.4
46	L9	144	ILE	2.4
51	M5	61	ILE	2.4
35	SM	21	PRO	2.4
42	L5	139	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
70	o4	43	LYS	2.4
12	C0	15	LEU	2.4
18	c6	117	LEU	2.4
34	SR	85	TRP	2.4
34	sR	11	GLY	2.4
39	L2	85	GLY	2.4
45	l8	136	LEU	2.4
45	l8	246	MET	2.4
67	o1	55	LEU	2.4
84	f	84	VAL	2.4
45	l8	80	TYR	2.4
80	e0	11	ALA	2.4
7	S5	170	GLN	2.4
7	s5	122	ASN	2.4
9	S7	76	LYS	2.4
18	C6	70	THR	2.4
67	O1	75	ILE	2.4
14	c2	58	LEU	2.4
22	d0	73	GLY	2.4
25	D3	125	VAL	2.4
34	SR	89	LEU	2.4
45	L8	26	LEU	2.4
58	n2	76	LEU	2.4
63	N7	14	VAL	2.4
63	n7	135	ARG	2.4
66	O0	67	VAL	2.4
67	o1	109	VAL	2.4
16	C4	32	ASP	2.4
34	SR	195	HIS	2.4
7	s5	85	ALA	2.4
15	C3	57	ALA	2.4
26	D4	11	LYS	2.4
48	M1	167	TYR	2.4
51	M5	148	TYR	2.4
9	S7	181	ILE	2.4
16	C4	116	GLU	2.4
60	N4	92	GLU	2.4
82	p0	44	GLU	2.4
12	C0	8	ARG	2.4
13	C1	23	PRO	2.4
21	C9	46	PRO	2.4
24	D2	129	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
27	D5	105	THR	2.4
28	D6	18	VAL	2.4
67	o1	20	LEU	2.4
74	o8	71	PRO	2.4
3	s1	153	HIS	2.4
12	c0	41	TYR	2.4
26	d4	99	LYS	2.4
28	D6	70	LYS	2.4
33	E1	89	LYS	2.4
61	N5	32	PHE	2.4
14	c2	94	ALA	2.4
61	N5	60	TYR	2.4
34	sR	5	GLU	2.4
45	L8	202	GLU	2.4
21	C9	123	ARG	2.4
4	S2	63	VAL	2.4
32	E0	50	VAL	2.4
63	n7	26	VAL	2.4
82	p0	15	LEU	2.4
14	c2	49	THR	2.4
34	sR	233	THR	2.4
39	l2	84	THR	2.4
43	L6	68	PRO	2.4
74	o8	37	PRO	2.4
83	p2	34	ASN	2.4
9	s7	92	PHE	2.4
63	N7	3	LYS	2.4
1	2	558	U	2.4
1	2	1528	U	2.4
24	D2	52	TYR	2.4
34	SR	296	ALA	2.4
35	SM	176	ALA	2.4
48	M1	111	ASP	2.4
58	n2	108	TYR	2.4
1	6	495	C	2.4
6	S4	49	ARG	2.4
20	C8	16	ARG	2.4
43	L6	92	SER	2.4
66	O0	92	ILE	2.4
8	S6	178	LEU	2.4
30	d8	56	LEU	2.4
31	D9	23	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
34	sR	89	LEU	2.4
36	1	1027	A	2.4
74	O8	54	LEU	2.4
5	s3	108	LYS	2.4
63	n7	22	LYS	2.4
7	s5	76	ARG	2.4
14	c2	33	ARG	2.4
30	D8	60	GLU	2.4
32	E0	33	ARG	2.4
67	O1	82	GLU	2.4
36	5	124	U	2.4
9	S7	72	LYS	2.4
15	C3	75	LEU	2.4
20	c8	108	LYS	2.4
34	sR	118	LYS	2.4
35	SM	46	LYS	2.4
45	l8	181	LYS	2.4
72	o6	11	LEU	2.4
72	o6	50	LEU	2.4
19	c7	2	GLY	2.4
27	D5	37	GLN	2.4
53	M7	172	GLN	2.4
1	2	135	A	2.4
11	s9	47	PHE	2.4
81	m2	32	GLY	2.4
32	E0	58	PRO	2.4
36	1	1571	A	2.4
6	S4	119	ALA	2.4
8	S6	71	THR	2.4
14	c2	99	GLU	2.4
25	D3	105	ALA	2.4
34	SR	253	ALA	2.4
34	sR	130	THR	2.4
53	M7	177	ALA	2.4
1	6	1255	G	2.4
36	5	1349	G	2.4
35	SM	170	LYS	2.4
70	O4	54	ILE	2.4
7	S5	198	LEU	2.4
17	C5	116	LEU	2.4
3	S1	43	VAL	2.4
33	E1	84	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
66	O0	31	VAL	2.4
4	S2	66	PHE	2.4
26	D4	60	PHE	2.4
60	N4	8	PHE	2.4
74	o8	40	GLN	2.4
16	C4	114	ARG	2.4
17	C5	127	ARG	2.4
18	c6	68	ARG	2.4
6	s4	64	ILE	2.4
6	s4	220	THR	2.4
11	S9	159	ALA	2.4
27	D5	76	ALA	2.4
45	L8	223	ALA	2.4
45	L8	240	ASN	2.4
42	l5	148	ILE	2.4
45	L8	86	THR	2.4
47	M0	33	ILE	2.4
83	p1	40	ILE	2.4
6	S4	131	LEU	2.4
6	s4	56	LEU	2.4
17	c5	112	LEU	2.4
20	c8	112	ASP	2.4
24	D2	104	LEU	2.4
25	D3	136	TRP	2.4
8	s6	153	VAL	2.4
49	m3	69	VAL	2.4
55	m9	22	VAL	2.4
70	O4	22	VAL	2.4
1	2	1364	G	2.4
7	s5	143	ARG	2.4
12	c0	48	SER	2.4
35	sM	28	SER	2.4
48	M1	131	MET	2.4
82	p0	53	MET	2.4
6	S4	31	PRO	2.4
17	c5	4	ALA	2.4
70	o4	19	LYS	2.4
25	D3	52	ILE	2.4
36	1	1805	C	2.4
42	l5	247	ILE	2.4
72	o6	93	ILE	2.4
3	s1	101	HIS	2.4

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Mol	Chain	Res	Type	RSRZ
8	s6	77	LEU	2.4
22	D0	87	HIS	2.4
51	M5	19	LEU	2.4
6	s4	181	VAL	2.3
17	c5	130	ARG	2.3
18	c6	73	GLY	2.3
26	D4	41	ARG	2.3
26	d4	27	VAL	2.3
55	m9	51	VAL	2.3
58	n2	56	VAL	2.3
43	L6	101	PHE	2.3
69	O3	60	ARG	2.3
16	C4	99	GLN	2.3
51	m5	57	GLN	2.3
1	2	767	U	2.3
10	S8	69	SER	2.3
40	L3	24	SER	2.3
42	L5	235	SER	2.3
14	c2	72	ILE	2.3
21	c9	66	TYR	2.3
25	D3	85	ALA	2.3
42	L5	49	TYR	2.3
42	L5	239	ILE	2.3
51	M5	40	ALA	2.3
70	O4	92	ALA	2.3
2	s0	17	LEU	2.3
3	S1	73	LEU	2.3
11	s9	53	ARG	2.3
11	s9	101	VAL	2.3
15	C3	78	ASN	2.3
20	C8	18	LEU	2.3
21	c9	108	LEU	2.3
70	o4	38	LEU	2.3
2	S0	143	VAL	2.3
7	s5	219	ARG	2.3
22	d0	81	THR	2.3
30	d8	67	ARG	2.3
61	N5	31	THR	2.3
63	n7	79	HIS	2.3
67	O1	79	ARG	2.3
7	s5	20	PHE	2.3
12	C0	53	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
25	d3	86	PHE	2.3
42	l5	169	GLY	2.3
72	O6	49	GLY	2.3
82	p0	29	GLY	2.3
6	S4	245	LYS	2.3
6	s4	125	LYS	2.3
34	SR	221	MET	2.3
63	N7	61	LYS	2.3
36	1	1804	A	2.3
9	S7	115	SER	2.3
38	4	82	U	2.3
11	S9	107	ARG	2.3
14	c2	32	LEU	2.3
51	m5	151	ILE	2.3
56	n0	2	ALA	2.3
81	m2	122	ILE	2.3
28	D6	51	ARG	2.3
35	sM	68	ARG	2.3
6	S4	160	VAL	2.3
3	S1	119	THR	2.3
3	S1	126	THR	2.3
20	c8	55	HIS	2.3
45	L8	70	LYS	2.3
45	L8	94	PHE	2.3
48	M1	54	VAL	2.3
49	m3	80	VAL	2.3
51	M5	37	HIS	2.3
62	N6	82	VAL	2.3
69	o3	59	VAL	2.3
81	m2	142	THR	2.3
36	1	1248	C	2.3
42	l5	151	GLN	2.3
7	S5	77	TYR	2.3
15	C3	74	ILE	2.3
54	m8	67	ILE	2.3
55	M9	54	ALA	2.3
69	o3	51	TYR	2.3
1	2	493	U	2.3
1	2	494	U	2.3
25	D3	42	PRO	2.3
70	O4	30	LEU	2.3
76	Q0	81	SER	2.3

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Mol	Chain	Res	Type	RSRZ
2	S0	156	VAL	2.3
2	s0	82	GLY	2.3
7	s5	53	VAL	2.3
30	d8	28	VAL	2.3
34	sR	62	LYS	2.3
40	l3	86	VAL	2.3
2	s0	96	THR	2.3
18	C6	50	GLU	2.3
39	L2	79	ASN	2.3
58	N2	87	ASN	2.3
63	N7	129	TRP	2.3
48	M1	11	ASP	2.3
8	S6	177	ARG	2.3
18	c6	45	ARG	2.3
27	d5	81	ARG	2.3
5	S3	145	ALA	2.3
5	s3	171	ALA	2.3
14	c2	136	ILE	2.3
34	SR	244	ALA	2.3
34	sR	91	LEU	2.3
36	5	1762	C	2.3
45	l8	237	ILE	2.3
6	s4	43	PRO	2.3
7	S5	88	PRO	2.3
12	c0	20	VAL	2.3
18	C6	76	SER	2.3
20	c8	107	SER	2.3
42	L5	66	SER	2.3
82	p0	199	SER	2.3
1	2	1410	A	2.3
17	c5	113	GLY	2.3
9	S7	78	THR	2.3
12	C0	29	GLN	2.3
2	S0	116	LYS	2.3
10	S8	184	LEU	2.3
34	sR	228	LYS	2.3
35	SM	61	ILE	2.3
40	L3	166	ILE	2.3
41	L4	249	ILE	2.3
43	l6	76	LEU	2.3
51	m5	145	ASP	2.3
11	s9	183	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
15	C3	15	ALA	2.3
20	c8	92	ILE	2.3
21	c9	10	ALA	2.3
25	D3	117	ILE	2.3
66	O0	62	LEU	2.3
6	s4	47	PHE	2.3
7	s5	163	SER	2.3
9	s7	43	PHE	2.3
42	L5	141	PRO	2.3
67	O1	67	VAL	2.3
11	S9	184	SER	2.3
25	D3	131	SER	2.3
18	c6	40	GLU	2.3
38	4	81	U	2.3
67	O1	50	ARG	2.3
70	O4	34	HIS	2.3
7	S5	200	ASN	2.3
20	C8	32	LEU	2.3
26	D4	113	ASN	2.3
27	d5	75	LEU	2.3
42	l5	198	TYR	2.3
43	L6	64	LEU	2.3
68	o2	72	LYS	2.3
82	p0	98	ASN	2.3
11	S9	94	ASP	2.3
26	d4	26	ASP	2.3
58	N2	41	ILE	2.3
26	D4	59	GLY	2.3
40	l3	88	GLY	2.3
1	6	239	C	2.3
2	s0	2	SER	2.3
21	C9	24	ARG	2.3
30	d8	42	ARG	2.3
58	n2	97	SER	2.3
64	n8	119	PRO	2.3
81	m2	161	PRO	2.3
5	s3	105	MET	2.3
18	C6	30	LYS	2.3
35	SM	27	LYS	2.3
40	l3	163	HIS	2.3
55	m9	21	LYS	2.3
67	O1	27	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
74	o8	30	LYS	2.3
20	C8	8	GLN	2.3
31	D9	36	LEU	2.3
47	m0	206	LEU	2.3
62	N6	99	LEU	2.3
63	N7	51	LEU	2.3
64	n8	79	TRP	2.3
70	O4	3	GLN	2.3
1	6	1226	A	2.3
11	s9	14	THR	2.3
36	1	2445	A	2.3
42	L5	56	THR	2.3
83	p2	44	ILE	2.3
2	S0	81	PHE	2.3
8	s6	27	PHE	2.3
10	S8	113	PHE	2.3
7	s5	157	ARG	2.3
29	d7	39	GLY	2.3
67	O1	28	ARG	2.3
14	C2	56	GLU	2.3
17	c5	109	PRO	2.3
15	C3	32	SER	2.3
29	D7	30	SER	2.3
20	C8	55	HIS	2.3
25	d3	104	LEU	2.3
49	m3	170	LEU	2.3
64	N8	73	LEU	2.3
66	O0	44	ILE	2.3
3	s1	105	PHE	2.3
6	S4	175	PHE	2.3
10	S8	138	ASN	2.3
14	c2	66	VAL	2.3
18	C6	32	ASN	2.3
21	C9	89	ARG	2.3
21	c9	21	PHE	2.3
34	sR	285	ALA	2.3
47	M0	139	ARG	2.3
49	m3	57	VAL	2.3
63	n7	2	ALA	2.3
3	s1	235	GLY	2.3
60	n4	88	ASP	2.3
67	O1	19	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	2	545	A	2.3
1	6	1435	G	2.3
11	S9	40	LYS	2.3
21	C9	109	GLU	2.3
36	1	1565	G	2.3
60	N4	91	LYS	2.3
61	n5	36	LYS	2.3
24	D2	111	MET	2.3
35	SM	22	PRO	2.3
8	S6	76	LEU	2.3
17	C5	51	SER	2.3
27	d5	65	LEU	2.3
29	D7	64	CYS	2.3
74	o8	65	LEU	2.3
11	S9	52	ILE	2.3
3	S1	68	VAL	2.3
4	s2	92	ALA	2.3
6	s4	227	VAL	2.3
16	C4	104	ALA	2.3
18	c6	109	PHE	2.3
20	C8	46	VAL	2.3
34	sR	190	ALA	2.3
42	l5	240	TYR	2.3
47	M0	149	VAL	2.3
63	N7	24	VAL	2.3
2	s0	49	ASN	2.3
14	c2	107	ASP	2.3
16	c4	119	THR	2.3
36	1	3156	U	2.3
46	L9	178	GLY	2.3
63	N7	66	THR	2.3
1	2	195	G	2.3
5	S3	110	LEU	2.3
19	C7	26	LEU	2.3
25	D3	88	PRO	2.3
34	SR	91	LEU	2.3
36	1	1350	A	2.3
8	S6	183	ARG	2.3
5	s3	174	HIS	2.3
12	C0	93	GLN	2.3
31	D9	38	ILE	2.3
64	n8	117	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
66	O0	91	SER	2.3
68	o2	96	ILE	2.3
80	e0	43	ARG	2.3
10	s8	179	CYS	2.3
11	s9	37	LYS	2.3
12	c0	79	TYR	2.3
17	C5	56	PHE	2.3
20	C8	133	VAL	2.3
31	d9	23	VAL	2.3
62	N6	125	LYS	2.3
12	C0	34	GLU	2.3
24	D2	59	GLY	2.3
1	2	768	C	2.3
39	L2	115	ASN	2.3
42	L5	109	THR	2.3
81	m2	72	THR	2.3
6	S4	5	PRO	2.3
55	m9	184	LEU	2.3
63	N7	81	LEU	2.3
2	S0	38	PHE	2.3
5	S3	75	LYS	2.3
6	s4	161	LYS	2.3
17	c5	138	PHE	2.3
21	C9	69	LYS	2.3
1	2	473	A	2.3
3	S1	139	ALA	2.3
6	s4	33	ALA	2.3
8	S6	208	TYR	2.3
20	C8	5	VAL	2.3
33	e1	106	TYR	2.3
34	SR	309	VAL	2.3
55	M9	59	SER	2.3
60	N4	95	SER	2.3
72	o6	53	TYR	2.3
1	2	133	U	2.2
5	S3	27	ARG	2.2
10	S8	195	ARG	2.2
12	c0	46	LEU	2.2
15	C3	42	ARG	2.2
16	C4	103	ARG	2.2
44	l7	202	LEU	2.2
58	N2	64	THR	2.2

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Mol	Chain	Res	Type	RSRZ
70	O4	88	ARG	2.2
11	s9	45	ILE	2.2
32	E0	30	PRO	2.2
51	M5	137	PRO	2.2
51	m5	14	LYS	2.2
2	S0	83	GLN	2.2
12	C0	13	GLN	2.2
15	C3	38	VAL	2.2
74	O8	11	PHE	2.2
5	s3	114	ALA	2.2
51	M5	23	GLN	2.2
66	O0	12	GLN	2.2
6	s4	24	SER	2.2
25	D3	141	GLU	2.2
27	D5	87	GLY	2.2
34	sR	147	HIS	2.2
51	m5	118	SER	2.2
39	L2	241	ARG	2.2
58	N2	90	ARG	2.2
82	p0	104	ARG	2.2
6	s4	189	LEU	2.2
20	c8	23	ASP	2.2
34	SR	165	ASP	2.2
36	1	2522	G	2.2
39	l2	60	LYS	2.2
49	m3	95	ILE	2.2
53	M7	29	THR	2.2
72	o6	92	ASN	2.2
8	S6	32	ILE	2.2
28	D6	30	ILE	2.2
10	S8	117	TYR	2.2
10	s8	102	VAL	2.2
29	d7	54	VAL	2.2
54	m8	81	VAL	2.2
58	n2	66	VAL	2.2
22	d0	14	GLN	2.2
42	L5	121	GLY	2.2
61	N5	23	ALA	2.2
55	M9	172	ARG	2.2
6	S4	134	LYS	2.2
6	S4	242	LYS	2.2
67	o1	73	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	2	599	A	2.2
5	S3	26	THR	2.2
7	S5	44	ASN	2.2
33	E1	115	THR	2.2
33	e1	151	ASN	2.2
34	SR	122	ILE	2.2
43	L6	146	ILE	2.2
56	N0	4	PHE	2.2
1	2	1480	G	2.2
2	S0	19	ALA	2.2
7	s5	39	GLU	2.2
10	S8	110	ARG	2.2
19	c7	105	GLN	2.2
28	d6	46	GLU	2.2
36	5	1570	U	2.2
55	M9	72	GLU	2.2
63	n7	44	ALA	2.2
7	s5	106	LYS	2.2
18	c6	47	LYS	2.2
25	D3	114	LYS	2.2
82	p0	14	LYS	2.2
6	S4	189	LEU	2.2
10	s8	184	LEU	2.2
11	s9	21	SER	2.2
23	D1	68	SER	2.2
34	SR	134	TRP	2.2
40	l3	47	LEU	2.2
43	L6	76	LEU	2.2
51	m5	19	LEU	2.2
58	n2	37	LEU	2.2
71	O5	50	SER	2.2
74	o8	14	LEU	2.2
21	c9	67	MET	2.2
10	S8	102	VAL	2.2
63	n7	43	VAL	2.2
67	O1	64	VAL	2.2
82	p0	96	ILE	2.2
18	c6	64	ASP	2.2
2	S0	56	LYS	2.2
2	S0	175	TYR	2.2
3	s1	53	GLY	2.2
7	s5	127	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
10	S8	142	LYS	2.2
11	S9	160	PRO	2.2
32	E0	53	LYS	2.2
34	sR	206	PRO	2.2
63	N7	15	ARG	2.2
74	o8	28	ASN	2.2
61	N5	50	ALA	2.2
1	2	547	U	2.2
2	S0	17	LEU	2.2
2	S0	184	LEU	2.2
10	S8	44	HIS	2.2
10	s8	44	HIS	2.2
16	C4	110	LEU	2.2
17	c5	79	HIS	2.2
49	m3	54	LEU	2.2
1	2	127	G	2.2
55	m9	23	TRP	2.2
7	S5	177	ILE	2.2
32	E0	4	VAL	2.2
39	L2	70	ARG	2.2
67	O1	36	ILE	2.2
70	O4	4	ARG	2.2
72	o6	36	ARG	2.2
6	s4	243	GLY	2.2
14	C2	81	ASP	2.2
13	c1	145	ALA	2.2
19	C7	106	THR	2.2
20	c8	98	TYR	2.2
51	M5	131	GLU	2.2
56	N0	76	GLY	2.2
49	m3	152	THR	2.2
62	n6	43	TYR	2.2
63	N7	116	LYS	2.2
63	n7	73	LYS	2.2
78	Q2	100	LYS	2.2
35	SM	91	THR	2.2
35	sM	54	PRO	2.2
63	N7	127	ASN	2.2
84	f	66	THR	2.2
9	S7	34	LEU	2.2
24	D2	126	LEU	2.2
36	1	2514	U	2.2

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Mol	Chain	Res	Type	RSRZ
3	S1	130	SER	2.2
4	S2	86	VAL	2.2
5	S3	138	VAL	2.2
5	S3	188	ILE	2.2
8	S6	137	ARG	2.2
30	d8	59	SER	2.2
42	L5	16	PHE	2.2
14	C2	60	VAL	2.2
45	L8	40	VAL	2.2
45	l8	195	SER	2.2
55	M9	41	ILE	2.2
63	n7	89	VAL	2.2
67	O1	76	SER	2.2
67	o1	38	LYS	2.2
69	o3	100	ILE	2.2
81	m2	73	VAL	2.2
1	2	298	C	2.2
7	s5	75	GLY	2.2
17	c5	17	TYR	2.2
16	c4	99	GLN	2.2
21	C9	59	ALA	2.2
21	C9	127	ASN	2.2
25	d3	118	PRO	2.2
42	L5	192	PRO	2.2
42	l5	129	TYR	2.2
68	o2	77	ALA	2.2
81	m2	102	PRO	2.2
29	D7	65	THR	2.2
40	l3	164	THR	2.2
1	2	126	A	2.2
1	6	194	U	2.2
12	C0	59	PHE	2.2
2	S0	160	ILE	2.2
5	s3	208	ILE	2.2
22	d0	69	LYS	2.2
27	D5	52	LYS	2.2
33	E1	149	LYS	2.2
36	1	1820	U	2.2
45	L8	232	HIS	2.2
45	l8	91	PHE	2.2
64	n8	137	LYS	2.2
67	O1	17	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
40	L3	359	ILE	2.2
7	S5	105	GLY	2.2
26	D4	39	GLU	2.2
29	D7	48	SER	2.2
30	D8	21	SER	2.2
40	l3	105	VAL	2.2
34	sR	194	GLY	2.2
48	M1	136	ALA	2.2
58	N2	36	TYR	2.2
1	2	584	C	2.2
1	2	1379	C	2.2
11	s9	76	LEU	2.2
14	c2	39	ASP	2.2
21	c9	79	LEU	2.2
28	D6	98	PRO	2.2
42	L5	6	ASP	2.2
66	O0	34	LEU	2.2
26	D4	117	LYS	2.2
28	D6	11	ASN	2.2
29	D7	82	LYS	2.2
45	l8	57	ARG	2.2
45	l8	110	THR	2.2
4	s2	86	VAL	2.2
8	S6	52	ILE	2.2
16	C4	19	ILE	2.2
16	c4	19	ILE	2.2
19	C7	121	VAL	2.2
27	d5	84	GLU	2.2
40	l3	84	VAL	2.2
41	L4	250	TRP	2.2
15	c3	14	SER	2.2
21	C9	85	SER	2.2
11	s9	3	ARG	2.2
11	s9	28	LEU	2.2
68	O2	2	ALA	2.2
31	D9	54	LYS	2.2
34	SR	283	LYS	2.2
42	L5	120	LYS	2.2
45	l8	133	LYS	2.2
64	N8	111	LYS	2.2
70	O4	31	ARG	2.2
7	S5	48	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
8	S6	27	PHE	2.2
32	E0	24	THR	2.2
33	E1	131	PHE	2.2
6	S4	72	VAL	2.2
17	C5	121	ILE	2.2
17	c5	106	GLU	2.2
18	C6	55	VAL	2.2
25	d3	72	VAL	2.2
30	D8	30	VAL	2.2
46	L9	10	ILE	2.2
48	M1	79	ILE	2.2
55	M9	118	HIS	2.2
20	C8	130	GLY	2.2
11	s9	12	TYR	2.2
15	C3	28	LEU	2.2
22	D0	26	LEU	2.2
33	E1	92	LYS	2.2
33	E1	117	LEU	2.2
42	L5	35	ARG	2.2
42	L5	207	TYR	2.2
45	L8	166	LEU	2.2
63	n7	65	ARG	2.2
66	O0	66	LYS	2.2
74	o8	12	LEU	2.2
76	q0	128	LYS	2.2
14	c2	93	ASP	2.2
6	s4	236	ILE	2.2
18	c6	69	VAL	2.2
23	D1	32	VAL	2.2
27	D5	66	VAL	2.2
34	SR	310	ILE	2.2
34	sR	200	ASN	2.2
45	l8	180	VAL	2.2
51	m5	117	ASN	2.2
56	N0	74	ASN	2.2
69	o3	67	MET	2.2
25	D3	58	GLY	2.2
28	d6	17	HIS	2.2
34	SR	55	GLY	2.2
42	l5	87	GLY	2.2
7	s5	92	ARG	2.2
11	s9	10	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
31	d9	56	ARG	2.2
32	E0	28	LYS	2.2
43	l6	77	ARG	2.2
45	L8	231	LYS	2.2
70	O4	74	ARG	2.2
74	o8	17	ARG	2.2
74	o8	78	LEU	2.2
84	f	40	LYS	2.2
18	C6	24	ALA	2.2
1	6	657	U	2.2
12	c0	13	GLN	2.2
36	1	1821	U	2.2
34	sR	191	ASP	2.2
42	L5	251	PRO	2.2
45	l8	165	PHE	2.2
11	s9	83	VAL	2.2
11	s9	134	ILE	2.2
12	c0	11	ILE	2.2
34	SR	58	VAL	2.2
42	L5	189	GLU	2.2
48	M1	138	VAL	2.2
68	o2	95	GLU	2.2
5	s3	106	LYS	2.2
18	c6	27	GLY	2.2
22	D0	70	THR	2.2
25	D3	91	GLY	2.2
40	L3	337	THR	2.2
51	M5	20	ARG	2.2
67	O1	103	GLY	2.2
67	o1	74	ARG	2.2
2	S0	24	LEU	2.1
5	s3	113	LEU	2.1
10	S8	55	TYR	2.1
84	f	73	LEU	2.1
25	d3	85	ALA	2.1
34	SR	212	ALA	2.1
8	S6	201	GLN	2.1
10	S8	103	GLN	2.1
20	c8	85	PHE	2.1
25	D3	95	PHE	2.1
17	c5	111	MET	2.1
40	L3	336	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
54	m8	101	VAL	2.1
61	n5	124	VAL	2.1
48	M1	75	LYS	2.1
49	m3	192	GLU	2.1
19	c7	35	CYS	2.1
84	f	37	ARG	2.1
36	1	1573	G	2.1
1	2	1360	A	2.1
10	s8	165	LEU	2.1
28	D6	72	HIS	2.1
34	SR	7	LEU	2.1
40	l3	137	TYR	2.1
42	L5	171	LEU	2.1
42	L5	222	LEU	2.1
48	M1	128	TYR	2.1
48	M1	147	THR	2.1
63	N7	40	HIS	2.1
69	o3	68	TRP	2.1
84	f	104	ASN	2.1
13	C1	144	ALA	2.1
16	C4	63	ALA	2.1
21	C9	10	ALA	2.1
28	D6	48	ALA	2.1
83	p2	42	ALA	2.1
6	S4	172	PHE	2.1
26	d4	23	PHE	2.1
58	n2	71	PHE	2.1
33	E1	83	LYS	2.1
34	SR	40	LYS	2.1
34	SR	84	SER	2.1
34	sR	161	LYS	2.1
35	SM	95	SER	2.1
70	o4	61	GLN	2.1
78	Q2	105	GLN	2.1
1	2	531	C	2.1
3	s1	121	ILE	2.1
5	s3	116	ARG	2.1
7	S5	187	ILE	2.1
8	s6	215	ARG	2.1
10	s8	77	ARG	2.1
15	C3	55	ARG	2.1
19	C7	78	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
22	d0	35	GLU	2.1
25	d3	125	VAL	2.1
49	m3	190	LYS	2.1
51	M5	14	LYS	2.1
67	o1	108	VAL	2.1
1	2	546	U	2.1
1	6	1604	U	2.1
10	s8	39	GLY	2.1
18	C6	11	GLY	2.1
40	L3	80	ASP	2.1
45	l8	187	GLY	2.1
84	f	21	MET	2.1
14	c2	88	LEU	2.1
18	c6	53	LEU	2.1
60	N4	96	LEU	2.1
63	n7	80	LEU	2.1
67	O1	16	LEU	2.1
76	Q0	85	LEU	2.1
13	C1	149	ALA	2.1
16	c4	59	ALA	2.1
20	C8	42	TYR	2.1
34	SR	241	PHE	2.1
43	l6	47	PHE	2.1
47	M0	72	ALA	2.1
5	S3	89	GLU	2.1
8	S6	31	ARG	2.1
10	s8	199	LYS	2.1
12	C0	38	LYS	2.1
6	s4	140	VAL	2.1
19	c7	87	GLU	2.1
36	1	621	A	2.1
36	5	1025	A	2.1
26	d4	12	VAL	2.1
27	D5	50	ILE	2.1
45	l8	135	GLY	2.1
49	M3	74	GLY	2.1
67	o1	44	MET	2.1
67	o1	45	GLY	2.1
84	f	20	PRO	2.1
40	l3	110	LEU	2.1
42	l5	51	LEU	2.1
42	l5	146	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
45	L8	156	ASP	2.1
67	o1	112	ASP	2.1
11	s9	17	ARG	2.1
11	s9	29	LYS	2.1
13	c1	146	ALA	2.1
18	c6	82	ARG	2.1
23	D1	45	ALA	2.1
33	E1	118	ARG	2.1
34	sR	78	ALA	2.1
43	L6	105	TYR	2.1
34	sR	229	LYS	2.1
35	SM	66	ALA	2.1
35	SM	141	ALA	2.1
45	l8	102	ALA	2.1
67	o1	40	ALA	2.1
72	O6	55	ARG	2.1
9	S7	5	GLN	2.1
9	S7	60	ILE	2.1
34	SR	113	VAL	2.1
42	L5	37	VAL	2.1
46	L9	187	ILE	2.1
62	N6	88	GLU	2.1
1	6	661	A	2.1
6	S4	43	PRO	2.1
7	S5	98	MET	2.1
22	d0	84	MET	2.1
6	s4	261	LEU	2.1
26	D4	87	PRO	2.1
29	D7	74	SER	2.1
36	5	1696	A	2.1
55	M9	48	GLY	2.1
56	N0	90	MET	2.1
62	n6	48	LEU	2.1
72	O6	27	SER	2.1
1	2	711	U	2.1
11	s9	16	LYS	2.1
13	C1	60	PHE	2.1
13	c1	69	LYS	2.1
18	c6	120	ASP	2.1
34	sR	162	ALA	2.1
39	L2	68	LYS	2.1
47	M0	142	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
70	O4	2	ALA	2.1
71	o5	111	PHE	2.1
82	p0	79	PHE	2.1
84	f	27	ARG	2.1
2	S0	74	VAL	2.1
3	s1	114	VAL	2.1
6	s4	169	ILE	2.1
7	s5	160	VAL	2.1
34	sR	88	THR	2.1
40	l3	87	VAL	2.1
51	m5	149	ASN	2.1
12	c0	17	GLN	2.1
22	d0	17	GLN	2.1
63	N7	13	VAL	2.1
10	s8	177	GLY	2.1
24	d2	123	GLY	2.1
34	SR	301	LEU	2.1
34	sR	144	LEU	2.1
42	L5	170	GLY	2.1
7	s5	67	PRO	2.1
48	M1	112	LEU	2.1
8	s6	217	SER	2.1
10	s8	45	SER	2.1
34	sR	278	PHE	2.1
35	SM	51	ARG	2.1
39	L2	147	ARG	2.1
74	o8	48	SER	2.1
2	S0	75	ALA	2.1
7	S5	136	ALA	2.1
32	E0	40	TYR	2.1
84	f	19	TYR	2.1
1	6	666	U	2.1
10	S8	153	GLU	2.1
5	S3	165	ASN	2.1
7	s5	121	ILE	2.1
17	C5	93	VAL	2.1
26	D4	57	VAL	2.1
10	s8	62	THR	2.1
36	5	3154	C	2.1
18	c6	8	GLN	2.1
54	M8	88	THR	2.1
64	n8	138	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
3	S1	231	LEU	2.1
8	S6	68	LEU	2.1
41	L4	263	GLY	2.1
63	N7	16	GLY	2.1
21	C9	86	ARG	2.1
45	l8	193	LYS	2.1
49	m3	131	LYS	2.1
13	c1	115	PHE	2.1
19	C7	107	SER	2.1
22	d0	66	SER	2.1
24	d2	122	SER	2.1
7	S5	119	ASP	2.1
20	c8	53	ASP	2.1
63	N7	7	ALA	2.1
71	o5	110	ALA	2.1
5	S3	174	HIS	2.1
7	s5	23	VAL	2.1
10	s8	38	ILE	2.1
14	c2	31	VAL	2.1
64	n8	101	VAL	2.1
32	E0	29	LYS	2.1
36	5	3155	U	2.1
69	o3	49	ILE	2.1
3	S1	214	LYS	2.1
4	s2	209	ASN	2.1
6	S4	20	LEU	2.1
7	s5	175	LEU	2.1
16	c4	62	LEU	2.1
17	C5	59	LYS	2.1
17	C5	103	ASN	2.1
20	c8	90	ASN	2.1
26	D4	43	LYS	2.1
39	l2	58	LEU	2.1
42	L5	48	LYS	2.1
43	L6	70	LYS	2.1
45	L8	230	LYS	2.1
81	m2	16	ASN	2.1
8	S6	145	PHE	2.1
17	c5	87	PRO	2.1
55	m9	26	PRO	2.1
11	S9	13	SER	2.1
16	c4	108	SER	2.1

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Mol	Chain	Res	Type	RSRZ
20	C8	47	CYS	2.1
55	M9	35	ALA	2.1
61	n5	123	TYR	2.1
80	e0	61	SER	2.1
2	S0	141	ILE	2.1
4	s2	179	VAL	2.1
5	s3	181	VAL	2.1
7	s5	134	VAL	2.1
12	c0	55	VAL	2.1
7	S5	81	ARG	2.1
15	c3	66	ILE	2.1
20	C8	27	LYS	2.1
31	D9	16	LYS	2.1
49	m3	70	ARG	2.1
49	m3	183	ARG	2.1
62	N6	113	LYS	2.1
63	n7	61	LYS	2.1
70	o4	22	VAL	2.1
74	o8	21	LYS	2.1
9	s7	153	LEU	2.1
12	C0	46	LEU	2.1
12	c0	29	GLN	2.1
16	c4	98	GLY	2.1
1	6	793	A	2.1
15	C3	72	MET	2.1
40	L3	165	GLN	2.1
47	m0	112	GLN	2.1
61	n5	40	LEU	2.1
62	N6	35	LEU	2.1
66	O0	104	LEU	2.1
82	p0	52	LEU	2.1
9	S7	183	PHE	2.1
40	L3	365	PHE	2.1
52	M6	184	THR	2.1
2	S0	202	TYR	2.1
12	C0	79	TYR	2.1
69	o3	90	PRO	2.1
56	N0	133	ALA	2.1
64	N8	146	GLU	2.1
58	N2	17	VAL	2.1
64	N8	63	LYS	2.1
67	O1	101	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
70	O4	50	ALA	2.1
71	o5	2	ALA	2.1
4	s2	184	VAL	2.1
40	l3	335	ILE	2.1
42	L5	199	ILE	2.1
43	L6	74	VAL	2.1
60	n4	82	ILE	2.1
69	o3	54	ARG	2.1
69	o3	107	ILE	2.1
5	S3	72	LEU	2.1
5	S3	182	LEU	2.1
6	S4	164	LEU	2.1
11	s9	150	LEU	2.1
34	SR	144	LEU	2.1
62	n6	57	LEU	2.1
70	o4	34	HIS	2.1
81	m2	56	GLY	2.1
83	p2	27	LEU	2.1
15	C3	36	GLN	2.1
18	c6	10	PHE	2.1
12	C0	57	THR	2.1
42	l5	109	THR	2.1
45	l8	81	THR	2.1
14	c2	27	ALA	2.1
14	c2	46	ARG	2.1
16	C4	96	PRO	2.1
28	D6	10	ARG	2.1
35	sM	40	PRO	2.1
29	D7	35	VAL	2.1
45	l8	114	ALA	2.1
51	m5	146	ALA	2.1
55	M9	168	ALA	2.1
80	e0	47	VAL	2.1
7	s5	120	ILE	2.1
16	C4	108	SER	2.1
26	d4	13	ILE	2.1
34	sR	131	ILE	2.1
10	S8	177	GLY	2.1
23	d1	43	GLY	2.1
34	SR	64	HIS	2.1
21	c9	14	PHE	2.1
6	S4	198	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
6	s4	199	GLU	2.1
18	C6	82	ARG	2.1
19	C7	59	LYS	2.1
6	s4	31	PRO	2.1
7	s5	30	PRO	2.1
9	S7	136	VAL	2.1
17	C5	66	ALA	2.1
57	N1	34	TYR	2.1
34	sR	151	VAL	2.1
51	m5	66	VAL	2.1
74	o8	23	ALA	2.1
1	6	39	A	2.1
3	s1	189	ILE	2.1
5	s3	109	LEU	2.1
7	s5	97	LEU	2.1
19	C7	34	LEU	2.1
38	8	80	A	2.1
67	o1	51	LEU	2.1
72	O6	61	ILE	2.1
63	N7	105	SER	2.1
71	O5	3	GLY	2.1
9	s7	24	PHE	2.0
11	s9	110	GLN	2.0
36	1	1272	C	2.1
27	D5	77	ARG	2.0
31	d9	33	LYS	2.0
42	L5	20	PHE	2.0
42	L5	221	GLU	2.0
43	L6	134	ARG	2.0
45	l8	183	LYS	2.0
67	O1	25	PHE	2.0
11	S9	41	GLU	2.0
29	d7	56	CYS	2.0
2	S0	103	THR	2.0
7	S5	147	THR	2.0
8	S6	180	THR	2.0
56	N0	31	ALA	2.0
63	n7	95	VAL	2.0
6	s4	192	ILE	2.0
7	s5	217	LEU	2.0
13	c1	40	LEU	2.0
45	l8	26	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
61	N5	142	ILE	2.0
63	N7	134	LEU	2.0
72	o6	24	PRO	2.0
1	2	1524	A	2.0
5	s3	77	PHE	2.0
12	c0	56	LYS	2.0
25	D3	126	LYS	2.0
6	S4	30	ARG	2.0
29	d7	51	GLN	2.0
34	sR	185	GLN	2.0
39	l2	72	ARG	2.0
51	M5	63	ARG	2.0
63	n7	17	ARG	2.0
69	O3	56	SER	2.0
70	o4	7	PHE	2.0
81	m2	158	PHE	2.0
45	L8	28	HIS	2.0
36	5	1597	C	2.0
10	S8	192	TYR	2.0
11	S9	127	VAL	2.0
13	C1	64	VAL	2.0
27	d5	39	ALA	2.0
33	e1	148	TYR	2.0
34	SR	6	VAL	2.0
34	sR	289	ALA	2.0
55	M9	55	VAL	2.0
84	f	55	ALA	2.0
7	S5	104	ASN	2.0
12	C0	35	ILE	2.0
29	d7	21	LEU	2.0
34	SR	199	ILE	2.0
34	SR	202	LEU	2.0
48	M1	12	LEU	2.0
58	N2	98	THR	2.0
58	n2	16	THR	2.0
66	o0	56	LEU	2.0
72	O6	26	ILE	2.0
1	2	123	G	2.0
36	1	1555	U	2.0
63	N7	67	LYS	2.0
70	O4	99	LYS	2.0
74	O8	30	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
78	Q2	15	LYS	2.0
10	s8	65	PHE	2.0
21	c9	93	HIS	2.0
26	d4	135	ASP	2.0
55	m9	59	SER	2.0
7	S5	64	VAL	2.0
11	s9	156	ILE	2.0
17	C5	63	ALA	2.0
18	C6	112	TYR	2.0
27	d5	76	ALA	2.0
30	d8	25	VAL	2.0
49	m3	173	ALA	2.0
55	m9	183	ALA	2.0
58	N2	83	TYR	2.0
2	s0	177	LEU	2.0
4	S2	64	LYS	2.0
28	d6	53	LEU	2.0
45	L8	46	LEU	2.0
67	o1	71	LEU	2.0
81	m2	54	LYS	2.0
84	f	59	LEU	2.0
17	C5	82	ASN	2.0
21	C9	101	ASN	2.0
70	o4	56	THR	2.0
70	o4	59	PRO	2.0
74	o8	47	GLY	2.0
25	d3	107	PHE	2.0
1	2	1435	G	2.0
14	c2	132	GLU	2.0
16	c4	80	HIS	2.0
17	c5	92	SER	2.0
22	D0	79	TRP	2.0
53	M7	16	SER	2.0
6	S4	105	VAL	2.0
25	d3	120	VAL	2.0
28	d6	73	TYR	2.0
28	D6	53	LEU	2.0
29	D7	71	ALA	2.0
31	D9	46	LYS	2.0
49	m3	177	LYS	2.0
52	M6	185	ALA	2.0
55	m9	35	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
61	N5	103	TYR	2.0
63	N7	89	VAL	2.0
5	S3	29	LEU	2.0
15	C3	41	ALA	2.0
19	c7	69	ILE	2.0
21	C9	128	GLY	2.0
24	D2	68	ARG	2.0
25	D3	93	LEU	2.0
34	SR	123	ILE	2.0
64	n8	102	ILE	2.0
42	l5	180	PHE	2.0
78	Q2	3	ASN	2.0
84	f	79	ASN	2.0
19	C7	75	GLU	2.0
33	e1	111	GLU	2.0
2	S0	72	ASP	2.0
2	s0	50	VAL	2.0
4	S2	78	ASP	2.0
6	s4	51	ARG	2.0
7	S5	143	ARG	2.0
11	S9	63	ASP	2.0
19	C7	89	SER	2.0
25	D3	145	SER	2.0
40	L3	86	VAL	2.0
45	L8	55	TYR	2.0
64	n8	91	LEU	2.0
64	n8	109	TYR	2.0
67	o1	72	ARG	2.0
74	o8	19	ASP	2.0
82	p0	196	VAL	2.0
36	1	1237	G	2.0
36	5	3276	G	2.0
63	n7	45	GLY	2.0
47	M0	173	PHE	2.0
1	2	475	A	2.0
3	S1	33	LYS	2.0
6	S4	184	THR	2.0
8	S6	63	MET	2.0
22	d0	74	GLU	2.0
36	1	1802	C	2.0
58	n2	101	ASN	2.0
45	l8	243	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
2	S0	16	LEU	2.0
2	S0	177	LEU	2.0
5	s3	85	VAL	2.0
7	S5	118	LEU	2.0
20	C8	17	LEU	2.0
26	D4	93	ARG	2.0
26	d4	35	VAL	2.0
41	l4	244	LEU	2.0
42	l5	36	LEU	2.0
43	l6	64	LEU	2.0
69	o3	89	LEU	2.0
78	Q2	2	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
85	8AN	B	76	22/23	0.97	0.20	-	44,44,45,45	0
84	5CT	f	51	15/16	0.70	0.37	-	44,44,44,44	15
85	8AN	C	76	22/23	0.95	0.24	-	40,42,43,43	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	5	3735	1/1	0.94	0.74	66.32	35,35,35,35	1
86	MG	5	3507	1/1	0.95	0.72	64.49	31,31,31,31	0
86	MG	6	1966	1/1	0.97	0.44	56.19	56,56,56,56	0
86	MG	1	3501	1/1	0.90	0.56	50.20	26,26,26,26	0
86	MG	1	3437	1/1	0.89	0.74	47.55	44,44,44,44	0
86	MG	1	3507	1/1	0.98	0.75	47.00	30,30,30,30	0
86	MG	1	3580	1/1	0.97	0.69	46.72	35,35,35,35	0
86	MG	1	3561	1/1	0.95	0.75	46.36	22,22,22,22	0
86	MG	1	3454	1/1	0.97	0.90	45.32	31,31,31,31	0
86	MG	1	3582	1/1	0.98	0.77	43.93	27,27,27,27	0
86	MG	5	3556	1/1	0.94	0.79	41.67	29,29,29,29	0
86	MG	8	203	1/1	0.94	0.84	41.49	44,44,44,44	0
86	MG	5	3505	1/1	0.92	0.76	41.43	27,27,27,27	0
86	MG	N3	201	1/1	0.96	0.61	40.76	36,36,36,36	0
86	MG	1	3495	1/1	0.94	0.84	40.55	34,34,34,34	0
86	MG	5	3560	1/1	0.93	0.65	39.81	26,26,26,26	0
86	MG	5	3563	1/1	0.96	0.68	39.31	27,27,27,27	0
86	MG	1	3465	1/1	0.93	0.69	38.93	28,28,28,28	0
86	MG	1	3557	1/1	0.88	0.67	38.60	55,55,55,55	0
86	MG	1	3448	1/1	0.93	0.89	38.49	49,49,49,49	0
86	MG	5	3582	1/1	0.99	0.62	37.74	23,23,23,23	0
86	MG	1	3681	1/1	0.95	0.91	36.09	37,37,37,37	0
86	MG	5	3527	1/1	0.96	0.77	36.04	21,21,21,21	0
86	MG	1	3467	1/1	0.83	0.58	35.05	42,42,42,42	0
86	MG	5	3656	1/1	0.97	0.54	34.78	33,33,33,33	0
86	MG	1	3560	1/1	0.96	0.69	34.52	46,46,46,46	0
86	MG	5	3593	1/1	0.93	0.64	34.17	35,35,35,35	0
86	MG	5	3501	1/1	0.85	0.86	33.90	31,31,31,31	0
86	MG	2	1911	1/1	0.88	0.84	33.82	77,77,77,77	0
87	OHX	2	2120	7/7	0.91	0.50	33.36	87,87,87,87	3
86	MG	1	3696	1/1	0.93	0.65	32.44	30,30,30,30	0
86	MG	1	3506	1/1	0.99	0.63	31.55	32,32,32,32	0
86	MG	1	3497	1/1	0.94	0.83	31.22	25,25,25,25	0
86	MG	7	203	1/1	0.96	0.54	30.55	54,54,54,54	0
86	MG	1	3414	1/1	0.96	0.74	30.37	43,43,43,43	0
86	MG	6	1901	1/1	0.98	0.59	29.70	52,52,52,52	0
86	MG	5	3686	1/1	0.87	0.67	29.21	37,37,37,37	0
86	MG	6	1981	1/1	0.92	0.61	29.20	54,54,54,54	0
86	MG	5	3537	1/1	0.97	0.70	29.14	32,32,32,32	0
86	MG	1	3477	1/1	0.96	0.62	28.92	41,41,41,41	0
86	MG	5	3508	1/1	0.96	0.57	28.24	25,25,25,25	0
86	MG	6	1933	1/1	0.84	0.64	28.20	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	1	3509	1/1	0.99	0.64	28.02	33,33,33,33	0
86	MG	5	3581	1/1	0.97	0.56	27.95	31,31,31,31	0
86	MG	5	3541	1/1	0.94	0.64	27.66	46,46,46,46	0
86	MG	5	3599	1/1	0.80	0.45	27.64	37,37,37,37	0
86	MG	5	3522	1/1	0.90	0.51	27.17	29,29,29,29	0
86	MG	1	3498	1/1	0.93	0.67	26.99	45,45,45,45	0
86	MG	1	3516	1/1	0.91	0.62	26.23	33,33,33,33	0
86	MG	5	3513	1/1	0.94	0.59	26.07	35,35,35,35	0
86	MG	5	3457	1/1	0.96	0.76	25.91	28,28,28,28	0
86	MG	1	3407	1/1	0.61	0.56	25.80	33,33,33,33	0
86	MG	1	3562	1/1	0.94	0.91	25.71	33,33,33,33	0
86	MG	1	3538	1/1	0.95	0.64	25.19	39,39,39,39	0
86	MG	1	3422	1/1	0.91	0.45	24.81	32,32,32,32	0
87	OHX	2	2141	7/7	0.88	0.50	24.71	90,90,90,90	6
87	OHX	6	2131	7/7	0.92	0.29	24.71	89,89,89,89	6
87	OHX	5	4033	7/7	0.89	0.29	24.65	66,66,66,66	4
86	MG	1	3555	1/1	0.97	0.62	24.13	26,26,26,26	0
87	OHX	1	3939	7/7	0.95	0.26	24.09	54,54,54,54	3
86	MG	1	3587	1/1	0.97	0.63	23.51	35,35,35,35	0
86	MG	2	1910	1/1	0.83	0.61	23.01	69,69,69,69	0
86	MG	1	3573	1/1	0.81	0.71	22.98	40,40,40,40	0
86	MG	1	3585	1/1	0.97	0.81	22.85	20,20,20,20	0
86	MG	1	3756	1/1	0.88	0.77	22.68	53,53,53,53	0
86	MG	1	3546	1/1	0.95	0.61	22.64	36,36,36,36	0
86	MG	5	3585	1/1	0.94	0.48	22.35	29,29,29,29	0
86	MG	1	3530	1/1	0.96	0.60	22.14	41,41,41,41	0
86	MG	1	3464	1/1	0.94	0.50	22.14	38,38,38,38	0
86	MG	1	3469	1/1	0.94	0.59	21.76	41,41,41,41	0
87	OHX	1	3875	7/7	0.97	0.56	21.70	53,53,53,53	3
86	MG	5	3544	1/1	0.81	0.49	21.69	57,57,57,57	0
86	MG	2	1989	1/1	0.68	0.52	21.60	65,65,65,65	0
86	MG	5	3677	1/1	0.95	0.56	21.59	37,37,37,37	0
86	MG	5	3617	1/1	0.92	0.49	21.30	34,34,34,34	0
87	OHX	2	2121	7/7	0.95	0.62	21.07	94,94,94,94	4
86	MG	6	1923	1/1	0.89	0.64	21.00	46,46,46,46	0
86	MG	5	3416	1/1	0.91	0.61	20.87	64,64,64,64	0
86	MG	1	3482	1/1	0.94	0.51	20.83	33,33,33,33	0
86	MG	5	3644	1/1	0.86	0.54	20.32	31,31,31,31	0
86	MG	1	3524	1/1	0.90	0.51	20.05	44,44,44,44	0
87	OHX	5	4053	7/7	0.85	0.67	20.02	50,50,50,50	2
86	MG	5	3594	1/1	0.93	0.51	19.90	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	5	3472	1/1	0.98	0.52	19.88	30,30,30,30	0
86	MG	1	3527	1/1	0.95	0.66	19.28	31,31,31,31	0
86	MG	5	3419	1/1	0.89	0.69	19.26	26,26,26,26	0
86	MG	5	3601	1/1	0.90	0.47	18.93	30,30,30,30	0
86	MG	1	3496	1/1	0.95	0.54	18.82	41,41,41,41	0
86	MG	1	3642	1/1	0.74	0.57	18.62	32,32,32,32	0
87	OHX	5	4132	7/7	0.85	0.53	18.43	34,34,34,34	3
87	OHX	1	4000	7/7	0.92	0.42	18.10	55,55,55,55	3
86	MG	1	3490	1/1	0.94	0.66	18.07	34,34,34,34	0
86	MG	M7	202	1/1	0.96	0.89	18.01	40,40,40,40	0
86	MG	5	3428	1/1	0.95	0.42	17.72	31,31,31,31	0
86	MG	n3	201	1/1	0.93	0.42	17.57	25,25,25,25	0
87	OHX	1	3971	7/7	0.81	0.37	17.55	47,47,47,47	4
86	MG	1	3488	1/1	0.98	0.54	17.12	37,37,37,37	0
86	MG	5	3643	1/1	0.97	0.54	16.96	34,34,34,34	0
86	MG	1	3757	1/1	0.92	0.43	16.71	55,55,55,55	0
86	MG	5	3744	1/1	0.95	0.52	16.60	34,34,34,34	0
86	MG	1	3570	1/1	0.93	0.50	16.60	46,46,46,46	0
87	OHX	6	2127	7/7	0.94	0.40	16.43	58,58,58,58	5
86	MG	5	3497	1/1	0.94	0.52	16.39	32,32,32,32	0
86	MG	5	3719	1/1	0.95	0.44	16.29	34,34,34,34	0
86	MG	5	3455	1/1	0.83	0.56	16.00	31,31,31,31	0
87	OHX	7	220	7/7	0.97	0.37	15.90	73,73,73,73	1
86	MG	2	1932	1/1	0.81	0.64	15.82	64,64,64,64	0
86	MG	1	3413	1/1	0.93	0.57	15.79	41,41,41,41	0
86	MG	1	3583	1/1	0.97	0.64	15.59	31,31,31,31	0
87	OHX	5	3956	7/7	0.95	0.40	15.48	46,46,46,46	3
86	MG	1	3627	1/1	0.96	0.81	15.41	41,41,41,41	0
87	OHX	6	2155	7/7	0.94	0.40	15.36	71,71,71,71	3
87	OHX	5	4076	7/7	0.97	0.36	15.34	32,32,32,32	3
86	MG	1	3415	1/1	0.90	0.37	15.31	43,43,43,43	0
86	MG	m7	201	1/1	0.97	0.63	15.26	33,33,33,33	0
86	MG	5	3545	1/1	0.90	0.59	15.20	46,46,46,46	0
86	MG	1	3559	1/1	0.94	0.50	15.13	22,22,22,22	0
86	MG	5	3550	1/1	0.97	0.48	14.93	32,32,32,32	0
86	MG	5	3451	1/1	0.95	0.41	14.89	29,29,29,29	0
86	MG	1	3575	1/1	0.98	0.46	14.80	32,32,32,32	0
86	MG	5	3440	1/1	0.95	0.48	14.46	30,30,30,30	0
86	MG	1	3588	1/1	0.92	0.40	14.38	39,39,39,39	0
86	MG	4	207	1/1	0.94	0.44	14.17	37,37,37,37	0
86	MG	5	3592	1/1	0.98	0.55	14.10	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	5	3517	1/1	0.86	0.43	14.08	38,38,38,38	0
86	MG	5	3586	1/1	0.96	0.46	14.00	30,30,30,30	0
86	MG	5	3566	1/1	0.97	0.46	13.73	37,37,37,37	0
86	MG	O7	102	1/1	0.90	0.38	13.61	49,49,49,49	0
86	MG	2	1920	1/1	0.95	0.57	13.56	76,76,76,76	0
87	OHX	1	3985	7/7	0.97	0.40	13.51	38,38,38,38	2
86	MG	1	3705	1/1	0.98	0.46	13.49	33,33,33,33	0
86	MG	5	3651	1/1	0.98	0.44	13.46	35,35,35,35	0
87	OHX	1	3983	7/7	0.89	0.47	13.22	77,77,77,77	2
86	MG	1	3517	1/1	0.95	0.40	13.22	46,46,46,46	0
86	MG	1	3670	1/1	0.92	0.41	13.18	38,38,38,38	0
86	MG	5	3597	1/1	0.79	0.38	13.00	48,48,48,48	0
86	MG	6	2006	1/1	0.94	0.62	12.89	67,67,67,67	0
86	MG	5	3589	1/1	0.94	0.53	12.82	35,35,35,35	0
87	OHX	7	222	7/7	0.95	0.40	12.80	38,38,38,38	4
86	MG	1	3742	1/1	0.53	0.69	12.78	44,44,44,44	0
86	MG	1	3540	1/1	0.99	0.51	12.66	41,41,41,41	0
87	OHX	5	4126	7/7	0.89	0.50	12.66	44,44,44,44	3
86	MG	5	3553	1/1	0.87	0.61	12.57	32,32,32,32	0
86	MG	5	3543	1/1	0.95	0.67	12.54	48,48,48,48	0
86	MG	1	3531	1/1	0.97	0.57	12.51	40,40,40,40	0
87	OHX	5	4019	7/7	0.98	0.39	12.49	47,47,47,47	1
86	MG	5	3584	1/1	0.94	0.58	12.37	35,35,35,35	0
86	MG	5	3570	1/1	0.94	0.52	12.35	34,34,34,34	0
86	MG	5	3465	1/1	0.96	0.43	12.31	37,37,37,37	0
86	MG	5	3521	1/1	0.89	0.36	12.28	36,36,36,36	0
86	MG	5	3674	1/1	0.94	0.43	12.13	34,34,34,34	1
87	OHX	5	3940	7/7	0.91	0.41	11.96	34,34,34,34	4
86	MG	1	3609	1/1	0.96	0.47	11.90	44,44,44,44	0
86	MG	1	3732	1/1	0.94	0.38	11.76	35,35,35,35	0
87	OHX	2	2119	7/7	0.94	0.36	11.73	62,62,62,62	3
87	OHX	5	4008	7/7	0.96	0.37	11.63	41,41,41,41	3
87	OHX	1	3963	7/7	0.90	0.42	11.51	51,51,51,51	3
86	MG	5	3588	1/1	0.92	0.60	11.45	28,28,28,28	0
86	MG	1	3545	1/1	0.93	0.38	11.41	31,31,31,31	0
86	MG	5	3519	1/1	0.94	0.40	11.33	30,30,30,30	0
87	OHX	5	4088	7/7	0.95	0.28	11.32	47,47,47,47	3
87	OHX	1	3899	7/7	0.91	0.34	11.26	52,52,52,52	4
86	MG	C	102	1/1	0.94	0.58	11.17	39,39,39,39	0
86	MG	1	3433	1/1	0.89	0.45	11.15	34,34,34,34	0
87	OHX	5	3947	7/7	0.83	0.41	10.96	49,49,49,49	2

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	5	3493	1/1	0.92	0.37	10.85	45,45,45,45	0
87	OHX	1	4004	7/7	0.94	0.34	10.85	75,75,75,75	5
87	OHX	5	3912	7/7	0.98	0.22	10.84	77,77,77,77	3
87	OHX	1	3856	7/7	0.90	0.34	10.83	76,76,76,76	3
87	OHX	6	2102	7/7	0.93	0.39	10.75	97,97,97,97	4
87	OHX	7	216	7/7	0.97	0.33	10.73	62,62,62,62	3
86	MG	5	3783	1/1	0.73	0.34	10.61	35,35,35,35	0
86	MG	5	3421	1/1	0.90	0.46	10.58	44,44,44,44	0
86	MG	5	3407	1/1	0.86	0.42	10.55	40,40,40,40	0
86	MG	1	3735	1/1	0.95	0.36	10.54	49,49,49,49	0
87	OHX	1	4064	7/7	0.97	0.39	10.50	39,39,39,39	3
87	OHX	1	4074	7/7	0.92	0.42	10.48	38,38,38,38	3
86	MG	5	3767	1/1	0.98	0.41	10.29	34,34,34,34	0
86	MG	5	3436	1/1	0.97	0.30	10.27	34,34,34,34	0
86	MG	5	4174	1/1	0.92	1.22	10.22	56,56,56,56	0
86	MG	5	3495	1/1	0.99	0.40	10.21	35,35,35,35	0
87	OHX	2	2010	7/7	0.95	0.30	10.19	101,101,101,101	4
86	MG	6	1990	1/1	0.48	0.53	10.17	79,79,79,79	0
86	MG	5	3413	1/1	0.86	0.33	10.14	33,33,33,33	0
87	OHX	2	2106	7/7	0.95	0.34	10.10	78,78,78,78	3
86	MG	5	3420	1/1	0.91	0.41	10.08	38,38,38,38	0
87	OHX	6	2051	7/7	0.93	0.37	10.04	131,131,131,131	5
86	MG	1	3653	1/1	0.84	1.15	9.98	55,55,55,55	0
86	MG	5	4172	1/1	0.90	0.39	9.94	43,43,43,43	0
86	MG	5	4176	1/1	0.94	0.55	9.78	43,43,43,43	1
86	MG	1	3743	1/1	0.70	0.37	9.74	50,50,50,50	0
86	MG	2	1909	1/1	0.80	0.48	9.70	83,83,83,83	0
87	OHX	5	4072	7/7	0.96	0.32	9.68	44,44,44,44	4
87	OHX	1	4058	7/7	0.91	0.31	9.54	100,100,100,100	4
86	MG	5	3720	1/1	0.90	0.29	9.50	36,36,36,36	0
86	MG	5	3737	1/1	0.85	0.31	9.45	42,42,42,42	0
87	OHX	1	3871	7/7	0.86	0.51	9.42	61,61,61,61	2
86	MG	5	3555	1/1	0.97	0.37	9.38	33,33,33,33	0
87	OHX	1	3883	7/7	0.95	0.27	9.34	71,71,71,71	1
86	MG	5	3565	1/1	0.97	0.66	9.32	31,31,31,31	0
87	OHX	1	4043	7/7	0.98	0.34	9.30	39,39,39,39	2
86	MG	1	3576	1/1	0.93	0.44	9.27	46,46,46,46	0
87	OHX	1	3879	7/7	0.97	0.39	9.24	44,44,44,44	2
87	OHX	5	4077	7/7	0.89	0.35	9.23	68,68,68,68	3
87	OHX	5	3995	7/7	0.98	0.26	9.10	52,52,52,52	3
87	OHX	5	3899	7/7	0.97	0.26	9.06	52,52,52,52	3

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	2	2022	7/7	0.96	0.36	8.98	78,78,78,78	4
87	OHX	6	2162	7/7	0.93	0.40	8.97	114,114,114,114	5
87	OHX	5	4099	7/7	0.93	0.31	8.93	46,46,46,46	5
87	OHX	3	210	7/7	0.97	0.33	8.91	51,51,51,51	5
86	MG	1	3664	1/1	0.93	0.27	8.90	39,39,39,39	0
86	MG	5	3412	1/1	0.99	0.40	8.82	36,36,36,36	0
86	MG	3	204	1/1	0.95	0.58	8.79	33,33,33,33	0
87	OHX	8	225	7/7	0.94	0.28	8.77	47,47,47,47	3
87	OHX	7	221	7/7	0.96	0.29	8.74	50,50,50,50	4
87	OHX	5	4164	7/7	0.88	0.37	8.68	51,51,51,51	3
86	MG	5	3403	1/1	0.98	0.32	8.56	33,33,33,33	0
86	MG	1	3554	1/1	0.96	0.37	8.54	37,37,37,37	0
87	OHX	1	4062	7/7	0.83	0.40	8.51	51,51,51,51	3
87	OHX	5	3974	7/7	0.94	0.46	8.49	85,85,85,85	3
86	MG	6	1943	1/1	0.91	0.55	8.44	70,70,70,70	0
87	OHX	1	4038	7/7	0.91	0.32	8.34	56,56,56,56	4
86	MG	5	3561	1/1	0.98	0.32	8.34	27,27,27,27	0
87	OHX	6	2097	7/7	0.97	0.54	8.33	49,49,49,49	1
87	OHX	3	212	7/7	0.97	0.27	8.30	86,86,86,86	3
86	MG	5	3577	1/1	0.96	0.41	8.27	35,35,35,35	0
87	OHX	6	2153	7/7	0.93	0.32	8.14	67,67,67,67	3
87	OHX	5	4025	7/7	0.93	0.30	8.08	54,54,54,54	4
86	MG	5	3654	1/1	0.93	0.31	8.08	42,42,42,42	0
86	MG	1	3466	1/1	0.98	0.37	8.07	37,37,37,37	0
86	MG	L7	302	1/1	0.91	0.74	8.06	50,50,50,50	0
87	OHX	1	3992	7/7	0.97	0.29	8.03	52,52,52,52	3
86	MG	1	3539	1/1	0.90	0.44	8.01	44,44,44,44	0
86	MG	1	3523	1/1	0.64	0.44	7.95	54,54,54,54	0
87	OHX	6	2161	7/7	0.80	0.35	7.92	84,84,84,84	6
86	MG	5	3794	1/1	0.82	0.30	7.89	41,41,41,41	0
86	MG	12	301	1/1	0.96	0.58	7.87	37,37,37,37	0
86	MG	5	3426	1/1	0.97	0.53	7.85	40,40,40,40	0
86	MG	5	3774	1/1	0.87	0.74	7.72	40,40,40,40	0
87	OHX	1	3838	7/7	0.99	0.30	7.70	52,52,52,52	3
87	OHX	2	2151	7/7	0.84	0.31	7.69	112,112,112,112	7
86	MG	5	3512	1/1	0.96	0.35	7.57	37,37,37,37	0
86	MG	2	1937	1/1	0.95	0.39	7.47	80,80,80,80	0
87	OHX	8	224	7/7	0.97	0.29	7.39	40,40,40,40	3
87	OHX	5	4158	7/7	0.77	0.37	7.29	48,48,48,48	4
86	MG	1	3715	1/1	0.97	0.49	7.28	46,46,46,46	0
87	OHX	5	3962	7/7	0.95	0.29	7.17	62,62,62,62	5

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	B	103	1/1	0.98	0.55	7.17	38,38,38,38	0
87	OHX	1	4105	7/7	0.94	0.29	7.16	46,46,46,46	5
86	MG	6	1918	1/1	0.90	0.40	7.15	41,41,41,41	0
86	MG	1	3472	1/1	0.97	0.39	7.12	42,42,42,42	0
87	OHX	5	3931	7/7	0.94	0.26	7.04	139,139,139,139	5
87	OHX	5	3923	7/7	0.97	0.32	7.03	43,43,43,43	5
86	MG	1	3687	1/1	0.93	0.38	7.00	46,46,46,46	0
87	OHX	1	3968	7/7	0.96	0.27	6.99	72,72,72,72	3
87	OHX	8	218	7/7	0.96	0.22	6.98	80,80,80,80	2
86	MG	1	4112	1/1	0.80	0.34	6.90	36,36,36,36	0
86	MG	1	3419	1/1	0.89	0.25	6.89	36,36,36,36	0
87	OHX	5	3915	7/7	0.96	0.32	6.86	77,77,77,77	3
87	OHX	5	3868	7/7	0.95	0.31	6.84	35,35,35,35	4
86	MG	6	1904	1/1	0.91	0.54	6.84	59,59,59,59	0
87	OHX	1	3920	7/7	0.94	0.35	6.83	43,43,43,43	3
87	OHX	5	4042	7/7	0.88	0.36	6.79	38,38,38,38	4
87	OHX	5	4169	7/7	0.97	0.34	6.79	71,71,71,71	3
87	OHX	1	3897	7/7	0.96	0.30	6.76	49,49,49,49	5
87	OHX	5	4106	7/7	0.91	0.23	6.75	81,81,81,81	5
86	MG	2	1922	1/1	0.92	0.56	6.67	85,85,85,85	0
87	OHX	1	4027	7/7	0.94	0.29	6.64	75,75,75,75	3
86	MG	5	3682	1/1	0.91	0.52	6.63	38,38,38,38	0
87	OHX	6	2146	7/7	0.91	0.48	6.62	48,48,48,48	4
86	MG	5	3506	1/1	0.94	0.39	6.59	38,38,38,38	0
87	OHX	1	4005	7/7	0.97	0.35	6.59	40,40,40,40	4
87	OHX	2	2095	7/7	0.97	0.34	6.56	75,75,75,75	5
86	MG	1	3572	1/1	0.86	0.70	6.54	57,57,57,57	0
87	OHX	5	4083	7/7	0.96	0.30	6.41	35,35,35,35	6
87	OHX	6	2110	7/7	0.92	0.32	6.38	112,112,112,112	6
87	OHX	6	2025	7/7	0.97	0.32	6.38	62,62,62,62	2
86	MG	5	3705	1/1	0.84	0.42	6.36	32,32,32,32	0
87	OHX	1	3820	7/7	0.97	0.38	6.29	47,47,47,47	4
86	MG	5	3717	1/1	0.96	0.52	6.24	26,26,26,26	1
86	MG	5	3491	1/1	0.94	0.46	6.24	30,30,30,30	0
87	OHX	3	211	7/7	0.96	0.33	6.24	64,64,64,64	3
87	OHX	5	4142	7/7	0.83	0.33	6.22	50,50,50,50	4
86	MG	2	1975	1/1	0.88	0.41	6.21	60,60,60,60	0
87	OHX	2	2011	7/7	0.90	0.32	6.18	83,83,83,83	3
86	MG	5	4175	1/1	0.95	0.40	6.18	36,36,36,36	0
87	OHX	5	3903	7/7	0.98	0.28	6.15	49,49,49,49	2
86	MG	8	206	1/1	0.75	0.44	6.12	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	5	3729	1/1	0.82	0.50	6.11	41,41,41,41	0
87	OHX	7	218	7/7	0.98	0.29	6.10	67,67,67,67	3
87	OHX	1	3791	7/7	0.98	0.30	6.08	41,41,41,41	2
86	MG	5	3779	1/1	0.95	0.28	5.97	30,30,30,30	0
87	OHX	1	4010	7/7	0.95	0.27	5.96	44,44,44,44	5
87	OHX	5	4115	7/7	0.87	0.33	5.93	52,52,52,52	4
86	MG	1	3586	1/1	0.88	0.29	5.92	45,45,45,45	0
87	OHX	5	3984	7/7	0.96	0.19	5.92	55,55,55,55	2
87	OHX	2	2097	7/7	0.95	0.37	5.84	73,73,73,73	5
87	OHX	5	3875	7/7	0.96	0.32	5.82	43,43,43,43	3
87	OHX	1	3793	7/7	0.98	0.27	5.81	68,68,68,68	4
86	MG	1	3426	1/1	0.95	0.48	5.77	52,52,52,52	0
86	MG	5	3569	1/1	0.98	0.41	5.77	29,29,29,29	0
86	MG	1	4115	1/1	0.96	0.28	5.75	42,42,42,42	0
87	OHX	1	3915	7/7	0.85	0.40	5.73	66,66,66,66	4
87	OHX	1	3906	7/7	0.96	0.33	5.68	65,65,65,65	4
87	OHX	1	3807	7/7	0.97	0.33	5.68	73,73,73,73	2
86	MG	1	3618	1/1	0.88	0.37	5.63	39,39,39,39	0
87	OHX	1	3859	7/7	0.96	0.28	5.63	53,53,53,53	2
87	OHX	1	3846	7/7	0.98	0.22	5.60	119,119,119,119	3
87	OHX	5	3844	7/7	0.99	0.25	5.59	48,48,48,48	2
87	OHX	5	3845	7/7	0.98	0.28	5.54	37,37,37,37	3
86	MG	1	3406	1/1	0.86	0.28	5.51	44,44,44,44	0
86	MG	6	1952	1/1	0.95	0.66	5.48	53,53,53,53	0
87	OHX	5	4101	7/7	0.94	0.23	5.48	45,45,45,45	5
87	OHX	5	4007	7/7	0.94	0.30	5.47	66,66,66,66	3
87	OHX	1	3887	7/7	0.95	0.20	5.42	131,131,131,131	5
87	OHX	1	3876	7/7	0.98	0.30	5.36	41,41,41,41	2
87	OHX	6	2122	7/7	0.95	0.33	5.32	77,77,77,77	4
87	OHX	5	3942	7/7	0.97	0.29	5.32	44,44,44,44	2
86	MG	1	3476	1/1	0.90	0.29	5.31	43,43,43,43	0
86	MG	5	3530	1/1	0.98	0.24	5.31	55,55,55,55	0
87	OHX	1	3955	7/7	0.90	0.27	5.30	71,71,71,71	3
87	OHX	1	4095	7/7	0.91	0.25	5.29	55,55,55,55	5
86	MG	1	3511	1/1	0.97	0.51	5.20	36,36,36,36	0
86	MG	6	1910	1/1	0.90	0.30	5.16	91,91,91,91	0
86	MG	2	1926	1/1	0.95	0.31	5.14	76,76,76,76	0
86	MG	1	3589	1/1	0.98	0.31	5.14	40,40,40,40	0
86	MG	6	1974	1/1	0.45	0.36	5.11	94,94,94,94	0
87	OHX	2	2108	7/7	0.96	0.24	5.08	79,79,79,79	5
86	MG	1	3556	1/1	0.98	0.41	5.04	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	6	2043	7/7	0.95	0.32	5.03	90,90,90,90	5
87	OHX	8	222	7/7	0.92	0.27	5.00	75,75,75,75	5
87	OHX	5	4086	7/7	0.88	0.27	4.98	39,39,39,39	5
87	OHX	4	231	7/7	0.85	0.31	4.97	73,73,73,73	5
87	OHX	6	2126	7/7	0.95	0.31	4.94	53,53,53,53	3
86	MG	5	3471	1/1	0.94	0.37	4.92	39,39,39,39	0
87	OHX	6	2158	7/7	0.87	0.30	4.91	131,131,131,131	7
86	MG	m5	301	1/1	0.87	0.35	4.84	46,46,46,46	0
87	OHX	6	2020	7/7	0.97	0.22	4.82	100,100,100,100	4
87	OHX	5	3851	7/7	0.99	0.28	4.80	55,55,55,55	2
86	MG	5	3678	1/1	0.98	0.47	4.79	31,31,31,31	1
87	OHX	1	3815	7/7	0.98	0.24	4.76	85,85,85,85	3
86	MG	4	233	1/1	0.81	0.51	4.74	62,62,62,62	0
87	OHX	1	4072	7/7	0.94	0.30	4.72	47,47,47,47	3
86	MG	2	1981	1/1	0.96	0.48	4.69	79,79,79,79	0
86	MG	5	3638	1/1	0.96	0.29	4.69	36,36,36,36	0
86	MG	1	3563	1/1	0.93	0.29	4.69	41,41,41,41	0
87	OHX	4	224	7/7	0.96	0.25	4.69	44,44,44,44	3
86	MG	5	3456	1/1	0.94	0.30	4.68	38,38,38,38	0
86	MG	12	302	1/1	0.92	0.46	4.64	45,45,45,45	0
86	MG	5	3590	1/1	0.96	0.38	4.63	42,42,42,42	0
87	OHX	5	4027	7/7	0.96	0.24	4.54	72,72,72,72	4
87	OHX	1	3778	7/7	0.99	0.27	4.54	64,64,64,64	1
87	OHX	1	3825	7/7	0.94	0.28	4.54	91,91,91,91	5
87	OHX	6	2107	7/7	0.93	0.27	4.52	81,81,81,81	5
87	OHX	1	3853	7/7	0.96	0.32	4.52	54,54,54,54	3
87	OHX	1	3849	7/7	0.94	0.27	4.51	48,48,48,48	5
87	OHX	5	3904	7/7	0.98	0.28	4.50	51,51,51,51	4
87	OHX	5	3965	7/7	0.96	0.23	4.50	50,50,50,50	4
86	MG	1	3429	1/1	0.93	0.29	4.45	36,36,36,36	0
87	OHX	1	3936	7/7	0.97	0.31	4.41	54,54,54,54	3
87	OHX	5	4052	7/7	0.94	0.21	4.39	65,65,65,65	5
86	MG	5	3591	1/1	0.93	0.46	4.37	35,35,35,35	0
87	OHX	5	3976	7/7	0.96	0.24	4.36	58,58,58,58	4
87	OHX	5	3914	7/7	0.97	0.27	4.31	39,39,39,39	4
87	OHX	2	2129	7/7	0.92	0.27	4.29	87,87,87,87	5
86	MG	2	1950	1/1	0.73	0.30	4.27	108,108,108,108	0
87	OHX	5	4012	7/7	0.90	0.20	4.25	119,119,119,119	4
87	OHX	1	3843	7/7	0.98	0.26	4.24	55,55,55,55	2
87	OHX	6	2073	7/7	0.96	0.33	4.22	69,69,69,69	5
87	OHX	1	4030	7/7	0.91	0.23	4.22	130,130,130,130	6

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	6	1915	1/1	0.64	0.36	4.22	75,75,75,75	0
86	MG	6	1978	1/1	0.81	0.59	4.21	77,77,77,77	0
87	OHX	2	2148	7/7	0.92	0.29	4.21	69,69,69,69	6
87	OHX	2	2134	7/7	0.86	0.30	4.21	74,74,74,74	4
87	OHX	7	219	7/7	0.99	0.24	4.14	67,67,67,67	2
87	OHX	5	4049	7/7	0.92	0.32	4.13	45,45,45,45	3
86	MG	5	3796	1/1	0.96	0.28	4.12	39,39,39,39	0
87	OHX	2	1998	7/7	0.97	0.20	4.12	116,116,116,116	2
86	MG	2	1931	1/1	0.96	0.38	4.10	65,65,65,65	0
86	MG	1	3401	1/1	0.96	0.31	4.08	43,43,43,43	0
86	MG	6	1938	1/1	0.93	0.30	4.04	60,60,60,60	0
87	OHX	1	4066	7/7	0.89	0.27	4.03	63,63,63,63	6
87	OHX	6	2088	7/7	0.92	0.28	4.03	99,99,99,99	3
87	OHX	5	3916	7/7	0.94	0.34	4.02	49,49,49,49	3
87	OHX	1	3896	7/7	0.99	0.33	4.00	49,49,49,49	2
87	OHX	6	2089	7/7	0.96	0.24	3.99	56,56,56,56	4
87	OHX	6	2044	7/7	0.96	0.25	3.99	46,46,46,46	2
86	MG	1	3567	1/1	0.83	0.37	3.96	48,48,48,48	0
87	OHX	5	4124	7/7	0.90	0.35	3.96	48,48,48,48	5
86	MG	1	3479	1/1	0.98	0.29	3.94	45,45,45,45	0
87	OHX	5	3822	7/7	0.99	0.23	3.92	53,53,53,53	2
87	OHX	1	4071	7/7	0.95	0.31	3.90	42,42,42,42	3
86	MG	1	4116	1/1	0.99	0.38	3.89	33,33,33,33	0
87	OHX	5	4048	7/7	0.95	0.24	3.88	37,37,37,37	3
86	MG	13	402	1/1	0.97	0.53	3.86	39,39,39,39	1
87	OHX	6	2150	7/7	0.89	0.30	3.85	78,78,78,78	6
86	MG	5	3596	1/1	0.91	0.26	3.85	44,44,44,44	0
87	OHX	5	3855	7/7	0.98	0.26	3.83	65,65,65,65	3
87	OHX	5	4011	7/7	0.95	0.27	3.81	41,41,41,41	4
87	OHX	5	4010	7/7	0.90	0.26	3.79	120,120,120,120	3
87	OHX	2	2027	7/7	0.96	0.28	3.79	75,75,75,75	4
89	SPS	5	3402	23/23	0.95	0.35	3.77	35,38,52,54	23
87	OHX	1	3903	7/7	0.98	0.21	3.77	53,53,53,53	3
87	OHX	5	3881	7/7	0.97	0.20	3.72	89,89,89,89	3
87	OHX	1	3874	7/7	0.97	0.27	3.71	50,50,50,50	3
87	OHX	5	3909	7/7	0.97	0.27	3.68	57,57,57,57	3
87	OHX	5	3928	7/7	0.98	0.29	3.66	41,41,41,41	4
87	OHX	1	3993	7/7	0.95	0.21	3.66	94,94,94,94	7
87	OHX	5	3833	7/7	0.99	0.27	3.65	51,51,51,51	1
87	OHX	1	4024	7/7	0.91	0.29	3.64	42,42,42,42	3
87	OHX	6	2106	7/7	0.96	0.25	3.62	85,85,85,85	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	5	3843	7/7	1.00	0.23	3.62	62,62,62,62	2
87	OHX	5	3894	7/7	0.97	0.22	3.61	63,63,63,63	3
86	MG	1	3481	1/1	0.95	0.34	3.61	40,40,40,40	0
86	MG	2	1912	1/1	0.74	0.53	3.59	88,88,88,88	0
87	OHX	4	216	7/7	0.98	0.24	3.52	61,61,61,61	3
87	OHX	6	2041	7/7	0.98	0.26	3.52	56,56,56,56	4
87	OHX	1	4006	7/7	0.95	0.26	3.50	48,48,48,48	5
86	MG	6	1944	1/1	0.80	0.29	3.48	63,63,63,63	0
86	MG	1	3719	1/1	0.85	0.48	3.48	65,65,65,65	0
86	MG	5	3564	1/1	0.96	0.33	3.46	32,32,32,32	0
87	OHX	1	3947	7/7	0.96	0.28	3.45	80,80,80,80	3
87	OHX	6	2164	7/7	0.86	0.37	3.44	44,44,44,44	5
87	OHX	1	4048	7/7	0.88	0.23	3.42	116,116,116,116	5
87	OHX	2	2057	7/7	0.94	0.29	3.39	79,79,79,79	1
87	OHX	5	3839	7/7	0.99	0.24	3.39	65,65,65,65	2
87	OHX	5	3937	7/7	0.96	0.20	3.39	50,50,50,50	3
87	OHX	6	2065	7/7	0.94	0.17	3.39	138,138,138,138	5
86	MG	d6	102	1/1	0.81	0.60	3.37	68,68,68,68	0
87	OHX	5	3998	7/7	0.97	0.28	3.37	38,38,38,38	5
87	OHX	5	3865	7/7	0.97	0.26	3.37	60,60,60,60	3
87	OHX	1	3830	7/7	0.98	0.21	3.36	99,99,99,99	3
87	OHX	1	3923	7/7	0.98	0.24	3.35	40,40,40,40	3
86	MG	6	1925	1/1	0.83	0.30	3.34	49,49,49,49	0
87	OHX	8	220	7/7	0.97	0.25	3.32	62,62,62,62	3
87	OHX	1	3966	7/7	0.92	0.28	3.31	35,35,35,35	3
87	OHX	6	2058	7/7	0.98	0.23	3.31	72,72,72,72	2
87	OHX	3	214	7/7	0.97	0.25	3.29	83,83,83,83	4
87	OHX	6	2092	7/7	0.97	0.27	3.28	69,69,69,69	4
87	OHX	M0	302	7/7	0.94	0.41	3.27	55,55,55,55	4
87	OHX	5	3893	7/7	0.98	0.25	3.26	50,50,50,50	2
87	OHX	8	214	7/7	0.98	0.27	3.24	60,60,60,60	3
86	MG	6	1951	1/1	0.90	0.57	3.22	43,43,43,43	0
87	OHX	5	3989	7/7	0.97	0.24	3.22	44,44,44,44	4
87	OHX	1	3898	7/7	0.96	0.21	3.21	89,89,89,89	5
87	OHX	2	1995	7/7	0.99	0.30	3.21	76,76,76,76	2
87	OHX	1	3911	7/7	0.97	0.22	3.20	61,61,61,61	3
86	MG	1	3403	1/1	0.91	0.27	3.18	42,42,42,42	0
87	OHX	1	4032	7/7	0.91	0.28	3.18	52,52,52,52	3
86	MG	5	3672	1/1	0.82	0.29	3.18	78,78,78,78	0
87	OHX	6	2128	7/7	0.97	0.36	3.17	53,53,53,53	4
87	OHX	1	3835	7/7	0.98	0.29	3.16	62,62,62,62	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	1	4003	7/7	0.96	0.19	3.14	63,63,63,63	3
87	OHX	5	4046	7/7	0.91	0.33	3.11	28,28,28,28	1
87	OHX	5	3935	7/7	0.94	0.22	3.10	49,49,49,49	3
87	OHX	1	3885	7/7	0.98	0.26	3.10	53,53,53,53	3
87	OHX	1	3962	7/7	0.97	0.34	3.08	59,59,59,59	2
86	MG	6	1929	1/1	0.96	0.30	3.08	49,49,49,49	0
87	OHX	5	3986	7/7	0.99	0.25	3.06	41,41,41,41	3
86	MG	5	3741	1/1	0.93	0.33	3.05	31,31,31,31	1
87	OHX	5	3900	7/7	0.99	0.26	3.04	43,43,43,43	3
87	OHX	3	219	7/7	0.77	0.25	3.03	82,82,82,82	5
87	OHX	2	2117	7/7	0.85	0.33	3.02	93,93,93,93	4
87	OHX	5	3877	7/7	0.99	0.21	3.02	73,73,73,73	3
86	MG	6	1906	1/1	0.93	0.35	3.00	76,76,76,76	0
86	MG	5	3462	1/1	0.90	0.27	3.00	39,39,39,39	0
87	OHX	5	3818	7/7	0.99	0.25	2.98	51,51,51,51	3
87	OHX	6	2137	7/7	0.89	0.21	2.93	95,95,95,95	4
86	MG	1	3739	1/1	0.81	0.36	2.93	72,72,72,72	0
86	MG	6	1968	1/1	0.97	0.26	2.91	48,48,48,48	0
87	OHX	1	3886	7/7	0.95	0.23	2.90	56,56,56,56	4
87	OHX	5	4024	7/7	0.97	0.28	2.88	50,50,50,50	2
87	OHX	7	224	7/7	0.90	0.24	2.84	54,54,54,54	5
87	OHX	2	2051	7/7	0.95	0.26	2.83	101,101,101,101	5
87	OHX	1	4015	7/7	0.97	0.27	2.82	47,47,47,47	2
87	OHX	5	4117	7/7	0.97	0.26	2.82	49,49,49,49	4
87	OHX	1	3800	7/7	0.99	0.28	2.81	44,44,44,44	3
87	OHX	5	4082	7/7	0.93	0.29	2.81	53,53,53,53	3
87	OHX	5	3888	7/7	0.95	0.46	2.79	42,42,42,42	3
86	MG	5	3405	1/1	0.88	0.26	2.79	47,47,47,47	0
87	OHX	1	3976	7/7	0.96	0.30	2.78	41,41,41,41	4
87	OHX	5	3939	7/7	0.97	0.26	2.78	62,62,62,62	2
86	MG	n6	201	1/1	0.86	0.43	2.76	56,56,56,56	0
86	MG	1	3441	1/1	0.97	0.45	2.76	52,52,52,52	0
87	OHX	1	3841	7/7	0.97	0.20	2.76	70,70,70,70	3
87	OHX	5	3949	7/7	0.95	0.19	2.74	95,95,95,95	4
87	OHX	2	2056	7/7	0.98	0.25	2.74	99,99,99,99	4
86	MG	2	1962	1/1	0.94	0.36	2.73	88,88,88,88	0
86	MG	5	3409	1/1	0.83	0.29	2.72	29,29,29,29	0
87	OHX	5	4054	7/7	0.93	0.30	2.72	56,56,56,56	4
87	OHX	5	4120	7/7	0.92	0.25	2.72	68,68,68,68	7
87	OHX	6	2029	7/7	0.96	0.24	2.70	68,68,68,68	2
87	OHX	6	2032	7/7	0.98	0.20	2.66	117,117,117,117	2

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	1	4008	7/7	0.96	0.27	2.65	47,47,47,47	5
87	OHX	1	4016	7/7	0.93	0.34	2.65	56,56,56,56	3
87	OHX	6	2072	7/7	0.95	0.30	2.63	76,76,76,76	3
87	OHX	1	3784	7/7	0.99	0.26	2.62	73,73,73,73	2
87	OHX	5	4159	7/7	0.90	0.37	2.62	37,37,37,37	5
86	MG	6	2010	1/1	0.91	0.25	2.60	53,53,53,53	0
87	OHX	5	3943	7/7	0.98	0.23	2.60	42,42,42,42	3
87	OHX	19	201	7/7	0.92	0.31	2.60	61,61,61,61	2
87	OHX	2	2132	7/7	0.96	0.32	2.58	87,87,87,87	3
87	OHX	5	3910	7/7	0.98	0.22	2.58	44,44,44,44	4
87	OHX	5	4123	7/7	0.94	0.30	2.57	51,51,51,51	6
87	OHX	2	2037	7/7	0.97	0.27	2.57	73,73,73,73	4
87	OHX	1	3834	7/7	0.97	0.28	2.56	62,62,62,62	3
87	OHX	5	3966	7/7	0.97	0.24	2.56	49,49,49,49	5
86	MG	1	3661	1/1	0.78	0.26	2.55	51,51,51,51	0
87	OHX	1	3798	7/7	0.99	0.21	2.55	69,69,69,69	1
86	MG	5	3680	1/1	0.81	0.34	2.54	43,43,43,43	0
87	OHX	1	3884	7/7	0.97	0.20	2.52	74,74,74,74	4
87	OHX	5	3854	7/7	0.98	0.23	2.52	71,71,71,71	3
87	OHX	5	3873	7/7	0.97	0.23	2.50	62,62,62,62	3
87	OHX	5	4134	7/7	0.93	0.24	2.49	54,54,54,54	4
87	OHX	5	4093	7/7	0.96	0.29	2.49	36,36,36,36	3
87	OHX	1	3808	7/7	0.98	0.24	2.49	74,74,74,74	3
86	MG	5	3800	1/1	0.87	0.36	2.48	44,44,44,44	0
87	OHX	2	2008	7/7	0.98	0.22	2.47	89,89,89,89	5
86	MG	5	3769	1/1	0.98	0.30	2.46	47,47,47,47	0
87	OHX	2	2032	7/7	0.97	0.23	2.46	102,102,102,102	6
87	OHX	2	2136	7/7	0.97	0.24	2.45	74,74,74,74	6
86	MG	1	3738	1/1	0.97	0.25	2.43	41,41,41,41	0
87	OHX	1	3822	7/7	0.99	0.22	2.43	50,50,50,50	4
86	MG	1	3668	1/1	0.98	0.24	2.41	38,38,38,38	1
87	OHX	o7	503	7/7	0.99	0.29	2.40	62,62,62,62	1
87	OHX	6	2178	7/7	0.68	0.28	2.38	145,145,145,145	6
86	MG	n8	201	1/1	0.93	0.32	2.37	37,37,37,37	0
86	MG	d2	201	1/1	0.98	0.31	2.36	59,59,59,59	0
87	OHX	5	4162	7/7	0.94	0.30	2.35	36,36,36,36	4
87	OHX	2	2047	7/7	0.95	0.23	2.34	80,80,80,80	4
87	OHX	1	3890	7/7	0.95	0.30	2.34	48,48,48,48	3
87	OHX	1	3888	7/7	0.98	0.27	2.33	71,71,71,71	3
86	MG	6	1975	1/1	0.95	0.21	2.31	90,90,90,90	0
86	MG	5	3785	1/1	0.98	0.27	2.29	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	L2	302	1/1	0.97	0.30	2.29	41,41,41,41	0
87	OHX	5	3911	7/7	0.99	0.17	2.28	107,107,107,107	2
87	OHX	1	4084	7/7	0.94	0.25	2.26	42,42,42,42	5
87	OHX	N9	101	7/7	1.00	0.22	2.26	64,64,64,64	1
87	OHX	1	3938	7/7	0.97	0.24	2.26	53,53,53,53	3
86	MG	1	3578	1/1	0.94	0.30	2.24	60,60,60,60	0
87	OHX	O9	101	7/7	0.81	0.37	2.20	51,51,51,51	6
87	OHX	1	3782	7/7	0.99	0.23	2.16	71,71,71,71	4
86	MG	1	3737	1/1	0.76	0.42	2.14	63,63,63,63	0
87	OHX	5	3941	7/7	0.92	0.28	2.12	50,50,50,50	5
86	MG	5	3546	1/1	0.95	0.34	2.11	53,53,53,53	0
87	OHX	2	2091	7/7	0.97	0.27	2.11	89,89,89,89	5
86	MG	s8	302	1/1	0.83	0.45	2.10	49,49,49,49	0
87	OHX	5	3862	7/7	0.98	0.20	2.09	85,85,85,85	3
87	OHX	1	4107	7/7	0.89	0.17	2.09	91,91,91,91	6
86	MG	5	3606	1/1	0.95	0.26	2.09	36,36,36,36	0
87	OHX	1	4083	7/7	0.92	0.20	2.08	45,45,45,45	4
87	OHX	6	2045	7/7	0.97	0.23	2.07	91,91,91,91	5
87	OHX	5	3922	7/7	0.99	0.26	2.07	41,41,41,41	1
86	MG	2	1938	1/1	0.72	0.26	2.05	72,72,72,72	0
87	OHX	1	3786	7/7	0.99	0.20	2.04	94,94,94,94	3
87	OHX	5	3948	7/7	0.95	0.22	2.04	56,56,56,56	4
87	OHX	1	3794	7/7	0.99	0.30	2.04	69,69,69,69	2
87	OHX	5	4038	7/7	0.97	0.21	2.03	72,72,72,72	4
87	OHX	2	2125	7/7	0.90	0.24	2.02	147,147,147,147	6
87	OHX	5	3964	7/7	0.97	0.20	2.00	49,49,49,49	4
87	OHX	5	3840	7/7	1.00	0.20	1.99	51,51,51,51	1
86	MG	1	3409	1/1	0.89	0.28	1.96	52,52,52,52	0
87	OHX	6	2014	7/7	0.99	0.25	1.96	76,76,76,76	3
87	OHX	6	2151	7/7	0.96	0.24	1.94	65,65,65,65	4
87	OHX	1	3868	7/7	0.99	0.19	1.94	53,53,53,53	4
87	OHX	1	3799	7/7	0.99	0.22	1.93	78,78,78,78	3
87	OHX	5	3968	7/7	0.96	0.20	1.91	105,105,105,105	5
87	OHX	8	219	7/7	0.98	0.23	1.88	44,44,44,44	3
87	OHX	1	3872	7/7	0.98	0.25	1.86	44,44,44,44	4
87	OHX	m8	201	7/7	0.95	0.29	1.85	47,47,47,47	3
86	MG	2	1966	1/1	0.90	0.24	1.84	74,74,74,74	0
87	OHX	1	3902	7/7	0.97	0.24	1.83	53,53,53,53	3
87	OHX	5	3972	7/7	0.99	0.25	1.82	39,39,39,39	4
87	OHX	1	3773	7/7	0.99	0.26	1.81	49,49,49,49	2
86	MG	2	1967	1/1	0.79	0.29	1.80	93,93,93,93	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	6	2019	7/7	0.99	0.24	1.79	79,79,79,79	2
87	OHX	1	3826	7/7	0.98	0.19	1.79	84,84,84,84	4
87	OHX	5	3878	7/7	0.98	0.26	1.79	59,59,59,59	3
87	OHX	5	3857	7/7	0.98	0.22	1.78	72,72,72,72	3
87	OHX	2	2079	7/7	0.98	0.34	1.78	82,82,82,82	3
87	OHX	1	4040	7/7	0.97	0.25	1.77	52,52,52,52	4
87	OHX	6	2119	7/7	0.96	0.25	1.76	60,60,60,60	3
87	OHX	6	2017	7/7	0.99	0.23	1.75	59,59,59,59	2
87	OHX	1	3840	7/7	0.98	0.19	1.74	85,85,85,85	3
87	OHX	6	2066	7/7	0.94	0.17	1.74	162,162,162,162	3
87	OHX	5	3898	7/7	0.98	0.21	1.73	49,49,49,49	3
87	OHX	5	3874	7/7	0.98	0.25	1.73	49,49,49,49	2
87	OHX	1	3996	7/7	0.95	0.24	1.72	64,64,64,64	5
87	OHX	5	4156	7/7	0.87	0.27	1.72	44,44,44,44	5
87	OHX	1	4092	7/7	0.92	0.26	1.72	47,47,47,47	3
87	OHX	2	2122	7/7	0.83	0.38	1.71	91,91,91,91	7
87	OHX	1	3787	7/7	0.97	0.22	1.69	72,72,72,72	3
87	OHX	6	2070	7/7	0.98	0.22	1.68	87,87,87,87	3
87	OHX	5	4055	7/7	0.97	0.21	1.67	40,40,40,40	6
87	OHX	6	2147	7/7	0.94	0.25	1.65	64,64,64,64	4
87	OHX	5	4018	7/7	0.96	0.17	1.63	76,76,76,76	6
87	OHX	6	2093	7/7	0.97	0.20	1.62	45,45,45,45	2
87	OHX	4	223	7/7	0.97	0.17	1.61	86,86,86,86	3
87	OHX	2	2045	7/7	0.94	0.26	1.61	95,95,95,95	4
86	MG	1	3478	1/1	0.89	0.20	1.60	60,60,60,60	0
87	OHX	1	4018	7/7	0.93	0.24	1.59	69,69,69,69	3
86	MG	1	3474	1/1	0.86	0.32	1.58	48,48,48,48	0
87	OHX	2	2058	7/7	0.95	0.31	1.57	67,67,67,67	4
87	OHX	5	4065	7/7	0.96	0.26	1.55	38,38,38,38	4
86	MG	1	3592	1/1	0.85	0.21	1.53	61,61,61,61	0
87	OHX	5	3901	7/7	0.97	0.21	1.52	72,72,72,72	3
87	OHX	5	3831	7/7	0.99	0.23	1.52	56,56,56,56	2
86	MG	2	1942	1/1	0.88	0.26	1.51	69,69,69,69	0
87	OHX	M6	203	7/7	0.98	0.35	1.50	43,43,43,43	2
87	OHX	1	3767	7/7	0.99	0.19	1.49	77,77,77,77	2
87	OHX	5	3830	7/7	1.00	0.21	1.48	61,61,61,61	1
86	MG	1	3758	1/1	0.90	0.24	1.48	48,48,48,48	0
87	OHX	2	2012	7/7	0.98	0.23	1.46	87,87,87,87	3
87	OHX	6	2061	7/7	0.97	0.25	1.46	86,86,86,86	4
87	OHX	6	2172	7/7	0.90	0.39	1.42	69,69,69,69	3
87	OHX	4	217	7/7	0.98	0.25	1.42	55,55,55,55	2
87	OHX	5	4096	7/7	0.93	0.20	1.42	75,75,75,75	6

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	2	2036	7/7	0.89	0.18	1.42	145,145,145,145	5
87	OHX	5	3993	7/7	0.96	0.23	1.41	42,42,42,42	4
87	OHX	6	2149	7/7	0.88	0.28	1.40	95,95,95,95	6
87	OHX	1	3929	7/7	0.97	0.22	1.38	53,53,53,53	4
87	OHX	5	3944	7/7	0.96	0.27	1.36	46,46,46,46	3
86	MG	5	3422	1/1	0.69	0.23	1.36	43,43,43,43	0
87	OHX	m0	301	7/7	0.95	0.37	1.35	49,49,49,49	3
87	OHX	5	4103	7/7	0.93	0.42	1.33	68,68,68,68	6
86	MG	1	3693	1/1	0.88	0.20	1.32	49,49,49,49	0
87	OHX	2	2150	7/7	0.76	0.15	1.32	151,151,151,151	7
86	MG	1	3733	1/1	0.99	0.27	1.31	40,40,40,40	0
87	OHX	1	3827	7/7	0.99	0.26	1.31	45,45,45,45	4
87	OHX	1	3833	7/7	0.98	0.25	1.31	71,71,71,71	4
87	OHX	1	3958	7/7	0.95	0.28	1.30	45,45,45,45	4
87	OHX	5	4074	7/7	0.92	0.23	1.29	47,47,47,47	3
87	OHX	1	4085	7/7	0.91	0.19	1.26	61,61,61,61	6
87	OHX	1	3817	7/7	0.98	0.19	1.25	109,109,109,109	5
87	OHX	6	2112	7/7	0.97	0.28	1.25	66,66,66,66	4
87	OHX	5	3913	7/7	0.96	0.22	1.25	74,74,74,74	4
87	OHX	1	3821	7/7	0.96	0.28	1.24	66,66,66,66	5
87	OHX	5	4069	7/7	0.96	0.20	1.24	73,73,73,73	3
87	OHX	6	2108	7/7	0.96	0.16	1.23	109,109,109,109	6
87	OHX	5	3936	7/7	0.98	0.24	1.23	53,53,53,53	2
87	OHX	1	3981	7/7	0.96	0.34	1.23	53,53,53,53	3
87	OHX	1	4029	7/7	0.86	0.28	1.22	82,82,82,82	3
86	MG	5	3418	1/1	0.94	0.22	1.21	36,36,36,36	0
87	OHX	1	3944	7/7	0.98	0.23	1.21	48,48,48,48	4
87	OHX	2	2074	7/7	0.92	0.26	1.18	85,85,85,85	3
87	OHX	5	4058	7/7	0.94	0.26	1.18	47,47,47,47	3
87	OHX	q2	502	7/7	0.98	0.25	1.17	47,47,47,47	2
86	MG	6	1973	1/1	0.91	0.32	1.17	51,51,51,51	0
87	OHX	5	4163	7/7	0.88	0.28	1.16	61,61,61,61	7
87	OHX	5	4017	7/7	0.98	0.27	1.15	48,48,48,48	4
87	OHX	6	2049	7/7	0.98	0.20	1.14	97,97,97,97	3
87	OHX	1	3889	7/7	0.98	0.23	1.13	48,48,48,48	2
87	OHX	8	211	7/7	0.99	0.24	1.13	57,57,57,57	3
87	OHX	6	2035	7/7	0.98	0.24	1.11	82,82,82,82	3
87	OHX	1	3766	7/7	0.99	0.23	1.11	61,61,61,61	2
87	OHX	2	2093	7/7	0.93	0.23	1.11	110,110,110,110	5
87	OHX	5	3826	7/7	0.99	0.20	1.11	80,80,80,80	1
87	OHX	5	3892	7/7	0.99	0.24	1.10	59,59,59,59	2
86	MG	1	3440	1/1	0.93	0.51	1.09	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	M0	303	7/7	0.82	0.27	1.07	101,101,101,101	6
87	OHX	1	3775	7/7	0.99	0.18	1.07	66,66,66,66	2
87	OHX	6	2116	7/7	0.98	0.24	1.06	61,61,61,61	2
87	OHX	2	2002	7/7	0.97	0.23	1.05	101,101,101,101	3
86	MG	1	3480	1/1	0.90	0.38	1.05	46,46,46,46	0
87	OHX	7	214	7/7	0.99	0.28	1.05	70,70,70,70	1
87	OHX	1	3892	7/7	0.96	0.23	1.02	65,65,65,65	3
87	OHX	1	4019	7/7	0.87	0.29	1.01	47,47,47,47	2
87	OHX	5	4137	7/7	0.96	0.25	1.01	44,44,44,44	5
87	OHX	2	2123	7/7	0.85	0.33	1.00	121,121,121,121	5
87	OHX	4	232	7/7	0.94	0.25	1.00	65,65,65,65	5
87	OHX	5	3832	7/7	1.00	0.21	0.99	59,59,59,59	2
87	OHX	4	218	7/7	0.98	0.25	0.97	60,60,60,60	4
87	OHX	6	2021	7/7	0.99	0.23	0.96	69,69,69,69	3
87	OHX	5	4037	7/7	0.96	0.17	0.96	106,106,106,106	4
87	OHX	1	3900	7/7	0.95	0.25	0.95	57,57,57,57	3
87	OHX	6	2091	7/7	0.97	0.25	0.94	83,83,83,83	3
87	OHX	M5	302	7/7	0.99	0.21	0.94	61,61,61,61	2
87	OHX	1	3763	7/7	0.99	0.24	0.94	58,58,58,58	2
87	OHX	1	3867	7/7	0.85	0.32	0.93	51,51,51,51	4
87	OHX	1	3831	7/7	0.98	0.21	0.91	48,48,48,48	3
87	OHX	1	3991	7/7	0.97	0.27	0.90	57,57,57,57	3
87	OHX	6	2028	7/7	0.99	0.20	0.88	63,63,63,63	2
87	OHX	4	215	7/7	0.99	0.20	0.87	59,59,59,59	3
87	OHX	5	4097	7/7	0.90	0.20	0.87	106,106,106,106	5
87	OHX	6	2078	7/7	0.96	0.23	0.86	60,60,60,60	5
87	OHX	5	3985	7/7	0.97	0.26	0.85	58,58,58,58	5
87	OHX	2	2024	7/7	0.97	0.25	0.85	100,100,100,100	6
86	MG	1	3676	1/1	0.94	0.25	0.84	52,52,52,52	0
86	MG	n8	202	1/1	0.89	0.31	0.83	50,50,50,50	0
87	OHX	2	2115	7/7	0.94	0.24	0.83	91,91,91,91	6
87	OHX	1	3928	7/7	0.87	0.28	0.80	49,49,49,49	3
87	OHX	6	2103	7/7	0.91	0.26	0.79	67,67,67,67	4
87	OHX	1	3880	7/7	0.98	0.22	0.78	47,47,47,47	5
87	OHX	2	2053	7/7	0.95	0.25	0.76	107,107,107,107	4
88	ZN	d7	101	1/1	0.88	0.41	0.76	147,147,147,147	0
87	OHX	5	3821	7/7	1.00	0.20	0.76	61,61,61,61	2
87	OHX	2	2147	7/7	0.91	0.21	0.75	116,116,116,116	6
87	OHX	5	4057	7/7	0.94	0.24	0.75	36,36,36,36	6
87	OHX	1	3829	7/7	0.97	0.23	0.75	59,59,59,59	2
86	MG	5	3548	1/1	0.85	0.32	0.74	43,43,43,43	0
87	OHX	3	215	7/7	0.96	0.15	0.72	90,90,90,90	3

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	1	4007	7/7	0.97	0.20	0.72	43,43,43,43	4
87	OHX	5	3816	7/7	0.99	0.19	0.71	53,53,53,53	4
87	OHX	1	4020	7/7	0.96	0.25	0.70	47,47,47,47	3
87	OHX	1	3948	7/7	0.98	0.21	0.70	37,37,37,37	2
87	OHX	1	3789	7/7	0.99	0.19	0.69	74,74,74,74	2
86	MG	5	3595	1/1	0.94	0.22	0.68	47,47,47,47	0
87	OHX	5	4056	7/7	0.94	0.24	0.67	50,50,50,50	2
87	OHX	8	213	7/7	0.98	0.21	0.64	62,62,62,62	4
86	MG	1	3615	1/1	0.85	0.30	0.63	68,68,68,68	0
87	OHX	5	4068	7/7	0.93	0.23	0.63	58,58,58,58	5
87	OHX	1	4059	7/7	0.96	0.29	0.63	72,72,72,72	4
87	OHX	2	2003	7/7	0.99	0.24	0.63	76,76,76,76	5
87	OHX	1	4080	7/7	0.91	0.25	0.63	57,57,57,57	4
87	OHX	5	3829	7/7	0.99	0.17	0.62	67,67,67,67	0
86	MG	c8	201	1/1	0.72	0.34	0.61	84,84,84,84	0
87	OHX	1	4100	7/7	0.93	0.27	0.59	38,38,38,38	3
87	OHX	m5	303	7/7	1.00	0.19	0.57	61,61,61,61	2
87	OHX	2	2077	7/7	0.91	0.23	0.55	108,108,108,108	7
87	OHX	5	3886	7/7	0.99	0.23	0.55	44,44,44,44	2
87	OHX	1	3845	7/7	0.97	0.15	0.55	123,123,123,123	3
87	OHX	2	2133	7/7	0.73	0.20	0.53	214,214,214,214	6
87	OHX	1	4022	7/7	0.93	0.22	0.51	71,71,71,71	6
87	OHX	5	3890	7/7	0.97	0.26	0.50	66,66,66,66	4
87	OHX	1	3940	7/7	0.96	0.20	0.49	77,77,77,77	5
87	OHX	5	3925	7/7	0.88	0.27	0.48	60,60,60,60	4
87	OHX	6	2083	7/7	0.96	0.22	0.48	94,94,94,94	7
87	OHX	5	3879	7/7	0.99	0.20	0.48	47,47,47,47	3
87	OHX	6	2095	7/7	0.95	0.20	0.47	99,99,99,99	3
87	OHX	1	3847	7/7	0.99	0.18	0.47	56,56,56,56	3
87	OHX	1	3777	7/7	0.99	0.21	0.46	61,61,61,61	3
87	OHX	5	3887	7/7	0.98	0.21	0.46	43,43,43,43	3
87	OHX	6	2033	7/7	0.99	0.24	0.46	56,56,56,56	5
87	OHX	1	3774	7/7	0.99	0.17	0.45	71,71,71,71	3
86	MG	5	3539	1/1	0.92	0.31	0.44	62,62,62,62	0
86	MG	d3	201	1/1	0.94	0.37	0.43	50,50,50,50	0
87	OHX	2	1992	7/7	0.99	0.19	0.43	98,98,98,98	1
87	OHX	6	2018	7/7	0.99	0.19	0.42	90,90,90,90	2
87	OHX	1	4031	7/7	0.93	0.23	0.41	65,65,65,65	6
87	OHX	2	2144	7/7	0.90	0.49	0.41	103,103,103,103	6
87	OHX	2	2064	7/7	0.90	0.19	0.41	135,135,135,135	5
86	MG	SM	301	1/1	0.93	0.20	0.40	58,58,58,58	0
87	OHX	m7	203	7/7	0.92	0.37	0.39	47,47,47,47	5

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	1	3848	7/7	0.97	0.22	0.38	76,76,76,76	3
87	OHX	1	4076	7/7	0.89	0.26	0.36	45,45,45,45	5
87	OHX	d4	201	7/7	0.91	0.27	0.35	90,90,90,90	6
87	OHX	5	4014	7/7	0.95	0.23	0.34	36,36,36,36	4
87	OHX	2	1993	7/7	0.98	0.22	0.32	96,96,96,96	2
86	MG	6	1948	1/1	0.92	0.27	0.32	85,85,85,85	0
86	MG	3	207	1/1	0.91	0.35	0.31	66,66,66,66	0
87	OHX	5	4060	7/7	0.91	0.22	0.31	55,55,55,55	4
87	OHX	n3	202	7/7	0.97	0.19	0.31	60,60,60,60	3
86	MG	1	3601	1/1	0.90	0.21	0.30	72,72,72,72	0
87	OHX	1	3901	7/7	0.99	0.18	0.29	62,62,62,62	4
87	OHX	1	3780	7/7	0.99	0.25	0.29	75,75,75,75	1
87	OHX	2	2061	7/7	0.98	0.22	0.29	88,88,88,88	5
87	OHX	o7	502	7/7	0.93	0.26	0.29	83,83,83,83	4
87	OHX	1	4044	7/7	0.87	0.25	0.27	108,108,108,108	4
87	OHX	M8	201	7/7	0.94	0.23	0.25	47,47,47,47	3
87	OHX	5	3819	7/7	1.00	0.19	0.23	52,52,52,52	3
87	OHX	5	3927	7/7	0.96	0.14	0.21	146,146,146,146	3
87	OHX	5	4000	7/7	0.96	0.21	0.21	41,41,41,41	4
87	OHX	2	2059	7/7	0.94	0.23	0.21	101,101,101,101	4
87	OHX	1	3914	7/7	0.94	0.23	0.20	79,79,79,79	3
87	OHX	2	2075	7/7	0.96	0.21	0.20	80,80,80,80	6
87	OHX	4	228	7/7	0.98	0.18	0.19	60,60,60,60	3
87	OHX	5	3920	7/7	0.98	0.21	0.19	57,57,57,57	2
87	OHX	5	4040	7/7	0.96	0.20	0.19	73,73,73,73	4
87	OHX	6	2057	7/7	0.96	0.22	0.19	58,58,58,58	2
87	OHX	c5	202	7/7	0.90	0.45	0.19	109,109,109,109	6
87	OHX	5	3979	7/7	0.98	0.20	0.18	55,55,55,55	3
87	OHX	2	2072	7/7	0.86	0.20	0.18	187,187,187,187	7
87	OHX	1	3762	7/7	1.00	0.19	0.18	55,55,55,55	3
87	OHX	1	4109	7/7	0.94	0.20	0.17	48,48,48,48	4
87	OHX	5	3953	7/7	0.99	0.19	0.17	49,49,49,49	2
86	MG	6	2005	1/1	0.99	0.42	0.16	88,88,88,88	0
87	OHX	1	3861	7/7	0.99	0.20	0.15	60,60,60,60	3
87	OHX	5	3823	7/7	1.00	0.20	0.15	62,62,62,62	2
87	OHX	5	3959	7/7	0.98	0.21	0.15	44,44,44,44	3
86	MG	5	3554	1/1	0.86	0.24	0.15	54,54,54,54	0
87	OHX	6	2056	7/7	0.98	0.18	0.14	73,73,73,73	3
87	OHX	6	2012	7/7	1.00	0.21	0.14	70,70,70,70	3
87	OHX	Q2	503	7/7	0.99	0.20	0.14	46,46,46,46	2
87	OHX	5	4073	7/7	0.96	0.17	0.14	77,77,77,77	6
87	OHX	1	3790	7/7	0.99	0.22	0.13	48,48,48,48	3

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	1	3571	1/1	0.98	0.27	0.13	53,53,53,53	0
87	OHX	3	209	7/7	0.99	0.21	0.12	76,76,76,76	4
87	OHX	2	2021	7/7	0.97	0.19	0.12	99,99,99,99	5
87	OHX	5	3884	7/7	0.98	0.16	0.10	78,78,78,78	3
86	MG	2	1954	1/1	0.94	0.26	0.10	105,105,105,105	0
87	OHX	5	3945	7/7	0.98	0.18	0.09	109,109,109,109	4
87	OHX	7	217	7/7	0.99	0.20	0.07	40,40,40,40	1
86	MG	6	1936	1/1	0.95	0.33	0.06	76,76,76,76	0
87	OHX	5	3880	7/7	0.98	0.19	0.06	96,96,96,96	2
87	OHX	1	3842	7/7	0.98	0.21	0.06	80,80,80,80	3
87	OHX	6	2144	7/7	0.96	0.21	0.04	85,85,85,85	7
87	OHX	1	3771	7/7	0.99	0.20	0.04	59,59,59,59	2
87	OHX	6	2123	7/7	0.93	0.21	0.04	70,70,70,70	4
87	OHX	5	4020	7/7	0.98	0.22	0.04	36,36,36,36	2
87	OHX	2	2094	7/7	0.97	0.23	0.03	87,87,87,87	5
87	OHX	1	3770	7/7	0.99	0.18	0.02	61,61,61,61	2
87	OHX	2	2112	7/7	0.88	0.19	0.02	121,121,121,121	6
86	MG	2	1934	1/1	0.96	0.24	0.02	80,80,80,80	0
86	MG	1	3549	1/1	0.99	0.22	0.00	59,59,59,59	0
87	OHX	2	2009	7/7	0.98	0.18	-0.01	89,89,89,89	4
87	OHX	1	3806	7/7	0.99	0.23	-0.01	52,52,52,52	2
87	OHX	4	221	7/7	0.95	0.19	-0.02	61,61,61,61	3
87	OHX	1	3878	7/7	0.98	0.19	-0.02	58,58,58,58	3
87	OHX	5	3926	7/7	0.98	0.18	-0.02	64,64,64,64	5
87	OHX	5	4119	7/7	0.97	0.21	-0.03	64,64,64,64	5
87	OHX	1	3832	7/7	0.97	0.19	-0.04	80,80,80,80	3
87	OHX	5	3825	7/7	1.00	0.20	-0.05	46,46,46,46	1
87	OHX	2	1999	7/7	0.96	0.16	-0.05	113,113,113,113	2
87	OHX	6	2181	7/7	0.90	0.19	-0.05	117,117,117,117	7
87	OHX	5	3896	7/7	0.99	0.20	-0.05	46,46,46,46	5
87	OHX	5	3952	7/7	0.99	0.20	-0.06	45,45,45,45	3
87	OHX	2	2046	7/7	0.96	0.22	-0.06	83,83,83,83	7
87	OHX	5	4001	7/7	0.97	0.20	-0.06	70,70,70,70	4
87	OHX	1	3779	7/7	1.00	0.19	-0.07	49,49,49,49	4
87	OHX	1	3860	7/7	0.99	0.21	-0.08	38,38,38,38	2
87	OHX	6	2175	7/7	0.89	0.18	-0.08	100,100,100,100	6
87	OHX	s8	303	7/7	0.93	0.23	-0.09	105,105,105,105	3
87	OHX	1	3934	7/7	0.97	0.19	-0.09	54,54,54,54	3
87	OHX	5	3824	7/7	0.99	0.18	-0.10	58,58,58,58	1
87	OHX	5	3841	7/7	0.99	0.19	-0.10	38,38,38,38	3
87	OHX	6	2138	7/7	0.93	0.26	-0.11	120,120,120,120	7
87	OHX	1	4054	7/7	0.95	0.22	-0.11	77,77,77,77	6

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	6	2135	7/7	0.87	0.29	-0.12	94,94,94,94	7
87	OHX	2	2007	7/7	0.96	0.20	-0.12	94,94,94,94	5
87	OHX	2	2067	7/7	0.97	0.17	-0.12	132,132,132,132	4
87	OHX	1	3813	7/7	0.98	0.25	-0.12	52,52,52,52	2
86	MG	2	1953	1/1	0.62	0.22	-0.13	89,89,89,89	0
87	OHX	5	3885	7/7	0.99	0.18	-0.13	79,79,79,79	3
87	OHX	1	3776	7/7	0.99	0.20	-0.14	55,55,55,55	1
87	OHX	5	4021	7/7	0.98	0.23	-0.15	37,37,37,37	1
86	MG	1	3651	1/1	0.97	0.23	-0.17	49,49,49,49	0
87	OHX	5	3834	7/7	0.99	0.19	-0.19	54,54,54,54	1
86	MG	L2	301	1/1	0.93	0.24	-0.21	37,37,37,37	0
87	OHX	C8	201	7/7	0.97	0.20	-0.21	111,111,111,111	4
86	MG	1	3669	1/1	0.92	0.15	-0.21	59,59,59,59	0
87	OHX	1	3990	7/7	0.95	0.15	-0.22	92,92,92,92	6
87	OHX	6	2145	7/7	0.92	0.21	-0.22	92,92,92,92	4
87	OHX	5	4043	7/7	0.96	0.22	-0.22	51,51,51,51	3
87	OHX	5	3967	7/7	0.99	0.20	-0.23	47,47,47,47	4
87	OHX	3	216	7/7	0.97	0.20	-0.24	49,49,49,49	5
87	OHX	6	2169	7/7	0.90	0.19	-0.24	89,89,89,89	4
87	OHX	S1	301	7/7	0.96	0.17	-0.24	121,121,121,121	2
86	MG	1	3595	1/1	0.91	0.30	-0.24	78,78,78,78	0
87	OHX	5	3863	7/7	0.99	0.16	-0.24	88,88,88,88	3
87	OHX	1	3765	7/7	0.99	0.17	-0.25	65,65,65,65	2
87	OHX	1	3912	7/7	0.94	0.19	-0.25	126,126,126,126	4
87	OHX	s1	301	7/7	0.98	0.19	-0.25	95,95,95,95	2
87	OHX	1	3907	7/7	0.96	0.23	-0.25	71,71,71,71	3
87	OHX	5	3848	7/7	0.99	0.17	-0.26	100,100,100,100	3
87	OHX	6	2159	7/7	0.92	0.22	-0.27	93,93,93,93	5
87	OHX	M5	303	7/7	0.98	0.22	-0.27	72,72,72,72	4
87	OHX	6	2034	7/7	0.99	0.18	-0.28	66,66,66,66	5
87	OHX	1	4101	7/7	0.89	0.25	-0.28	66,66,66,66	4
87	OHX	5	4147	7/7	0.90	0.19	-0.28	100,100,100,100	6
87	OHX	1	3812	7/7	0.98	0.15	-0.29	88,88,88,88	3
87	OHX	2	2062	7/7	0.95	0.20	-0.29	109,109,109,109	6
87	OHX	1	3969	7/7	0.98	0.17	-0.30	65,65,65,65	4
87	OHX	5	3954	7/7	0.96	0.13	-0.30	149,149,149,149	4
87	OHX	5	4064	7/7	0.99	0.21	-0.30	39,39,39,39	3
87	OHX	2	1991	7/7	0.99	0.18	-0.31	88,88,88,88	0
87	OHX	2	2035	7/7	0.89	0.22	-0.31	116,116,116,116	5
87	OHX	2	2073	7/7	0.97	0.20	-0.31	63,63,63,63	6
87	OHX	1	3951	7/7	0.97	0.15	-0.32	159,159,159,159	7
87	OHX	d9	102	7/7	0.95	0.31	-0.32	106,106,106,106	6

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	1	3974	7/7	0.93	0.25	-0.32	63,63,63,63	5
86	MG	6	1949	1/1	0.95	0.23	-0.33	77,77,77,77	0
87	OHX	1	3769	7/7	0.99	0.20	-0.33	64,64,64,64	2
87	OHX	2	2030	7/7	0.97	0.18	-0.34	98,98,98,98	5
87	OHX	6	2059	7/7	0.98	0.19	-0.34	61,61,61,61	3
88	ZN	o7	501	1/1	0.99	0.18	-0.34	45,45,45,45	0
87	OHX	s9	201	7/7	0.94	0.26	-0.37	71,71,71,71	5
87	OHX	5	4050	7/7	0.93	0.20	-0.38	64,64,64,64	6
87	OHX	1	3783	7/7	0.99	0.17	-0.38	83,83,83,83	2
86	MG	o4	201	1/1	0.92	0.28	-0.39	53,53,53,53	0
87	OHX	2	2124	7/7	0.84	0.18	-0.39	128,128,128,128	6
87	OHX	6	2031	7/7	0.98	0.18	-0.40	80,80,80,80	4
87	OHX	1	4051	7/7	0.97	0.21	-0.41	58,58,58,58	3
87	OHX	5	4081	7/7	0.90	0.14	-0.41	92,92,92,92	3
87	OHX	s1	302	7/7	0.89	0.22	-0.42	99,99,99,99	6
87	OHX	6	2030	7/7	0.99	0.20	-0.42	57,57,57,57	2
87	OHX	6	2121	7/7	0.91	0.27	-0.43	86,86,86,86	5
87	OHX	5	4111	7/7	0.94	0.20	-0.44	51,51,51,51	6
87	OHX	1	4047	7/7	0.92	0.15	-0.44	101,101,101,101	5
87	OHX	S9	201	7/7	0.95	0.25	-0.45	94,94,94,94	6
87	OHX	1	3839	7/7	0.99	0.19	-0.47	64,64,64,64	3
87	OHX	1	3931	7/7	0.98	0.21	-0.48	43,43,43,43	4
87	OHX	1	4082	7/7	0.92	0.20	-0.48	63,63,63,63	5
87	OHX	1	3932	7/7	0.97	0.20	-0.49	57,57,57,57	5
87	OHX	1	3863	7/7	0.99	0.20	-0.49	42,42,42,42	3
87	OHX	2	2031	7/7	0.98	0.18	-0.50	81,81,81,81	4
87	OHX	1	3764	7/7	1.00	0.18	-0.51	65,65,65,65	2
87	OHX	5	4143	7/7	0.90	0.24	-0.51	65,65,65,65	5
87	OHX	1	3792	7/7	0.98	0.21	-0.51	74,74,74,74	3
87	OHX	5	3987	7/7	0.92	0.21	-0.51	64,64,64,64	5
87	OHX	2	2101	7/7	0.91	0.18	-0.51	110,110,110,110	5
87	OHX	5	3820	7/7	0.99	0.18	-0.52	64,64,64,64	2
87	OHX	6	2084	7/7	0.95	0.22	-0.53	104,104,104,104	5
87	OHX	6	2027	7/7	0.99	0.18	-0.53	76,76,76,76	2
87	OHX	2	2065	7/7	0.92	0.20	-0.53	106,106,106,106	5
87	OHX	5	3856	7/7	0.99	0.19	-0.54	54,54,54,54	1
87	OHX	1	4061	7/7	0.90	0.21	-0.54	72,72,72,72	4
87	OHX	L3	404	7/7	0.81	0.27	-0.55	84,84,84,84	6
87	OHX	1	3866	7/7	0.97	0.20	-0.55	69,69,69,69	3
87	OHX	8	223	7/7	0.96	0.14	-0.55	95,95,95,95	7
86	MG	2	1969	1/1	0.56	0.26	-0.56	108,108,108,108	0
86	MG	5	3423	1/1	0.89	0.23	-0.56	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	m0	302	7/7	0.95	0.23	-0.57	96,96,96,96	5
87	OHX	6	2040	7/7	0.99	0.15	-0.57	123,123,123,123	5
87	OHX	5	4127	7/7	0.92	0.22	-0.57	47,47,47,47	4
87	OHX	2	2105	7/7	0.87	0.24	-0.59	87,87,87,87	3
87	OHX	5	3870	7/7	0.96	0.23	-0.59	72,72,72,72	2
87	OHX	8	228	7/7	0.89	0.19	-0.59	101,101,101,101	6
87	OHX	2	2034	7/7	0.95	0.17	-0.59	119,119,119,119	4
87	OHX	1	3952	7/7	0.92	0.16	-0.60	140,140,140,140	5
86	MG	1	3631	1/1	0.97	0.22	-0.60	42,42,42,42	0
87	OHX	2	2084	7/7	0.96	0.18	-0.61	95,95,95,95	5
87	OHX	1	4081	7/7	0.93	0.22	-0.61	43,43,43,43	5
87	OHX	O4	202	7/7	0.92	0.25	-0.62	82,82,82,82	5
87	OHX	5	3846	7/7	0.99	0.20	-0.64	48,48,48,48	1
87	OHX	1	3978	7/7	0.96	0.16	-0.64	77,77,77,77	3
87	OHX	6	2142	7/7	0.94	0.31	-0.66	95,95,95,95	7
87	OHX	5	4026	7/7	0.97	0.18	-0.67	49,49,49,49	3
87	OHX	5	4148	7/7	0.85	0.15	-0.67	145,145,145,145	7
86	MG	M0	301	1/1	0.93	0.21	-0.67	50,50,50,50	0
87	OHX	O3	202	7/7	0.98	0.22	-0.69	52,52,52,52	4
87	OHX	2	2066	7/7	0.97	0.13	-0.69	160,160,160,160	7
87	OHX	4	226	7/7	0.97	0.15	-0.69	103,103,103,103	6
86	MG	2	1914	1/1	0.93	0.24	-0.70	83,83,83,83	0
87	OHX	O7	103	7/7	0.97	0.18	-0.71	78,78,78,78	4
87	OHX	2	2127	7/7	0.93	0.17	-0.71	128,128,128,128	7
87	OHX	1	3761	7/7	1.00	0.19	-0.72	57,57,57,57	1
87	OHX	L5	301	7/7	0.96	0.18	-0.72	88,88,88,88	6
87	OHX	S6	301	7/7	0.86	0.15	-0.72	117,117,117,117	7
87	OHX	1	4011	7/7	0.95	0.20	-0.73	62,62,62,62	3
87	OHX	6	2022	7/7	0.99	0.19	-0.73	67,67,67,67	2
86	MG	1	3421	1/1	0.93	0.21	-0.74	58,58,58,58	0
87	OHX	6	2067	7/7	0.98	0.11	-0.75	154,154,154,154	3
87	OHX	1	3802	7/7	0.99	0.18	-0.75	60,60,60,60	2
87	OHX	1	3926	7/7	0.98	0.18	-0.76	57,57,57,57	4
87	OHX	5	3869	7/7	0.98	0.19	-0.76	76,76,76,76	5
87	OHX	6	2023	7/7	0.99	0.19	-0.76	80,80,80,80	3
87	OHX	1	3988	7/7	0.95	0.17	-0.77	87,87,87,87	5
87	OHX	5	4113	7/7	0.96	0.18	-0.78	55,55,55,55	4
87	OHX	5	3917	7/7	0.98	0.19	-0.80	36,36,36,36	2
87	OHX	1	3935	7/7	0.97	0.15	-0.80	71,71,71,71	2
87	OHX	6	2170	7/7	0.96	0.14	-0.81	83,83,83,83	7
89	SPS	B	101	23/23	0.97	0.21	-0.81	39,42,55,58	0
87	OHX	6	2055	7/7	0.99	0.13	-0.81	113,113,113,113	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
87	OHX	6	2141	7/7	0.86	0.19	-0.82	151,151,151,151	7
87	OHX	1	3785	7/7	0.99	0.20	-0.82	59,59,59,59	2
87	OHX	1	4001	7/7	0.97	0.16	-0.82	61,61,61,61	4
87	OHX	2	2014	7/7	0.98	0.10	-0.82	130,130,130,130	7
86	MG	6	1922	1/1	0.97	0.18	-0.83	55,55,55,55	0
87	OHX	5	4029	7/7	0.97	0.14	-0.83	70,70,70,70	5
87	OHX	6	2134	7/7	0.94	0.13	-0.85	163,163,163,163	7
87	OHX	2	2068	7/7	0.93	0.20	-0.85	103,103,103,103	7
87	OHX	6	2099	7/7	0.96	0.19	-0.86	81,81,81,81	5
87	OHX	6	2090	7/7	0.96	0.20	-0.86	91,91,91,91	7
87	OHX	8	212	7/7	0.99	0.17	-0.87	57,57,57,57	2
86	MG	1	3543	1/1	0.82	0.15	-0.87	58,58,58,58	0
87	OHX	5	3938	7/7	0.97	0.16	-0.87	92,92,92,92	2
87	OHX	1	4049	7/7	0.97	0.15	-0.87	61,61,61,61	5
87	OHX	5	3842	7/7	0.98	0.20	-0.88	64,64,64,64	1
87	OHX	6	2094	7/7	0.98	0.18	-0.89	109,109,109,109	6
86	MG	sM	301	1/1	0.76	0.21	-0.90	53,53,53,53	0
87	OHX	1	4033	7/7	0.94	0.18	-0.91	66,66,66,66	5
87	OHX	5	3906	7/7	0.98	0.18	-0.92	63,63,63,63	3
87	OHX	2	2000	7/7	0.98	0.20	-0.93	105,105,105,105	3
87	OHX	2	2100	7/7	0.97	0.13	-0.93	83,83,83,83	4
87	OHX	5	3907	7/7	0.99	0.19	-0.93	45,45,45,45	4
87	OHX	5	3932	7/7	0.98	0.14	-0.94	94,94,94,94	4
87	OHX	6	2104	7/7	0.94	0.17	-0.94	91,91,91,91	5
87	OHX	l5	303	7/7	0.95	0.19	-0.94	90,90,90,90	6
87	OHX	6	2050	7/7	0.97	0.18	-0.95	87,87,87,87	5
87	OHX	5	3996	7/7	0.96	0.16	-0.95	62,62,62,62	5
86	MG	M6	201	1/1	0.94	0.17	-0.95	34,34,34,34	0
87	OHX	5	3991	7/7	0.97	0.17	-0.97	80,80,80,80	5
87	OHX	2	2139	7/7	0.92	0.18	-0.98	114,114,114,114	6
88	ZN	q3	501	1/1	1.00	0.15	-0.98	62,62,62,62	0
87	OHX	1	3964	7/7	0.94	0.17	-0.99	71,71,71,71	4
87	OHX	2	2088	7/7	0.95	0.18	-0.99	91,91,91,91	6
87	OHX	2	2048	7/7	0.98	0.13	-1.01	141,141,141,141	5
87	OHX	2	2004	7/7	0.96	0.12	-1.01	135,135,135,135	5
87	OHX	2	2096	7/7	0.94	0.17	-1.01	108,108,108,108	6
87	OHX	1	3925	7/7	0.95	0.19	-1.02	96,96,96,96	5
87	OHX	1	3973	7/7	0.96	0.17	-1.03	63,63,63,63	5
87	OHX	1	3943	7/7	0.98	0.12	-1.04	97,97,97,97	6
87	OHX	1	3824	7/7	0.99	0.17	-1.04	68,68,68,68	3
87	OHX	1	3854	7/7	0.99	0.17	-1.05	43,43,43,43	4
87	OHX	1	3977	7/7	0.97	0.15	-1.07	72,72,72,72	7

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	5	4139	7/7	0.94	0.15	-1.08	88,88,88,88	7
88	ZN	O7	101	1/1	0.99	0.16	-1.08	47,47,47,47	0
87	OHX	5	3905	7/7	0.99	0.18	-1.08	60,60,60,60	4
87	OHX	5	4003	7/7	0.98	0.15	-1.12	55,55,55,55	2
87	OHX	5	3872	7/7	0.98	0.17	-1.13	58,58,58,58	4
87	OHX	o6	201	7/7	0.92	0.23	-1.13	68,68,68,68	4
87	OHX	1	3844	7/7	0.98	0.13	-1.14	98,98,98,98	5
87	OHX	1	3908	7/7	0.94	0.17	-1.14	91,91,91,91	3
86	MG	5	3771	1/1	0.93	0.17	-1.15	37,37,37,37	0
87	OHX	6	2053	7/7	0.97	0.17	-1.16	92,92,92,92	5
87	OHX	D9	102	7/7	0.95	0.14	-1.17	97,97,97,97	6
87	OHX	5	4108	7/7	0.96	0.18	-1.17	53,53,53,53	5
87	OHX	1	3809	7/7	0.98	0.18	-1.18	80,80,80,80	2
87	OHX	5	4109	7/7	0.93	0.13	-1.18	133,133,133,133	5
87	OHX	2	2052	7/7	0.97	0.15	-1.18	90,90,90,90	5
87	OHX	5	3827	7/7	0.99	0.19	-1.18	50,50,50,50	3
87	OHX	1	3797	7/7	1.00	0.18	-1.18	54,54,54,54	2
87	OHX	2	2085	7/7	0.96	0.17	-1.19	103,103,103,103	4
86	MG	2	1944	1/1	0.96	0.11	-1.21	102,102,102,102	0
87	OHX	1	4053	7/7	0.95	0.19	-1.22	43,43,43,43	3
87	OHX	2	2026	7/7	0.95	0.21	-1.23	103,103,103,103	4
87	OHX	5	4145	7/7	0.95	0.20	-1.23	71,71,71,71	5
87	OHX	5	3997	7/7	0.98	0.18	-1.24	43,43,43,43	5
86	MG	6	1931	1/1	0.83	0.15	-1.24	92,92,92,92	0
87	OHX	2	2113	7/7	0.93	0.12	-1.25	152,152,152,152	7
87	OHX	6	2115	7/7	0.96	0.17	-1.25	58,58,58,58	2
87	OHX	6	2013	7/7	0.99	0.18	-1.26	87,87,87,87	2
86	MG	1	3616	1/1	0.95	0.10	-1.26	58,58,58,58	0
86	MG	2	1983	1/1	0.97	0.17	-1.27	84,84,84,84	0
87	OHX	1	3982	7/7	0.97	0.20	-1.27	47,47,47,47	5
87	OHX	5	4102	7/7	0.96	0.19	-1.27	40,40,40,40	5
87	OHX	6	2068	7/7	0.98	0.13	-1.27	103,103,103,103	4
87	OHX	5	3850	7/7	0.99	0.17	-1.27	55,55,55,55	4
87	OHX	2	2082	7/7	0.97	0.16	-1.28	90,90,90,90	5
87	OHX	l3	404	7/7	0.93	0.15	-1.29	72,72,72,72	4
87	OHX	1	3967	7/7	0.94	0.16	-1.29	82,82,82,82	3
87	OHX	5	3836	7/7	1.00	0.17	-1.29	71,71,71,71	0
87	OHX	1	3891	7/7	0.91	0.17	-1.30	103,103,103,103	5
87	OHX	5	4009	7/7	0.96	0.17	-1.30	72,72,72,72	5
87	OHX	5	3852	7/7	0.99	0.17	-1.32	56,56,56,56	3
87	OHX	2	2063	7/7	0.96	0.09	-1.33	153,153,153,153	7
87	OHX	6	2130	7/7	0.88	0.16	-1.35	153,153,153,153	7

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
88	ZN	E1	501	1/1	0.97	0.05	-1.37	145,145,145,145	0
87	OHX	5	3853	7/7	0.99	0.14	-1.37	78,78,78,78	2
87	OHX	2	2099	7/7	0.91	0.11	-1.40	185,185,185,185	7
87	OHX	2	2089	7/7	0.95	0.13	-1.40	116,116,116,116	7
87	OHX	1	3877	7/7	0.98	0.12	-1.42	95,95,95,95	2
87	OHX	1	3781	7/7	0.99	0.18	-1.42	76,76,76,76	2
87	OHX	1	3950	7/7	0.97	0.17	-1.44	41,41,41,41	4
86	MG	6	1960	1/1	0.73	0.11	-1.45	65,65,65,65	0
87	OHX	2	2078	7/7	0.97	0.13	-1.45	115,115,115,115	7
87	OHX	1	3917	7/7	0.98	0.18	-1.47	54,54,54,54	4
87	OHX	5	4013	7/7	0.97	0.19	-1.47	48,48,48,48	3
86	MG	6	1903	1/1	0.93	0.13	-1.48	88,88,88,88	0
88	ZN	d9	101	1/1	0.99	0.10	-1.49	91,91,91,91	0
88	ZN	q0	500	1/1	0.99	0.13	-1.49	42,42,42,42	0
87	OHX	sR	401	7/7	0.95	0.14	-1.49	129,129,129,129	6
86	MG	5	3608	1/1	0.95	0.17	-1.52	35,35,35,35	0
88	ZN	Q2	501	1/1	0.98	0.06	-1.52	77,77,77,77	0
87	OHX	2	2013	7/7	0.98	0.14	-1.55	94,94,94,94	4
88	ZN	q2	501	1/1	0.97	0.07	-1.56	71,71,71,71	0
87	OHX	5	4135	7/7	0.86	0.14	-1.58	180,180,180,180	7
86	MG	5	3732	1/1	0.95	0.12	-1.61	50,50,50,50	0
86	MG	6	2185	1/1	0.87	0.18	-1.62	83,83,83,83	0
87	OHX	2	2040	7/7	0.98	0.14	-1.63	89,89,89,89	3
87	OHX	2	2029	7/7	0.97	0.13	-1.63	98,98,98,98	5
87	OHX	5	3999	7/7	0.99	0.16	-1.67	45,45,45,45	2
87	OHX	2	2005	7/7	0.97	0.16	-1.68	99,99,99,99	3
86	MG	O4	201	1/1	0.85	0.13	-1.70	77,77,77,77	0
87	OHX	l3	403	7/7	0.99	0.14	-1.71	50,50,50,50	3
87	OHX	2	2006	7/7	0.98	0.13	-1.71	93,93,93,93	3
87	OHX	C5	201	7/7	0.96	0.10	-1.72	122,122,122,122	7
87	OHX	5	3897	7/7	0.99	0.15	-1.73	58,58,58,58	4
87	OHX	2	2028	7/7	0.99	0.12	-1.73	108,108,108,108	5
87	OHX	1	4086	7/7	0.95	0.19	-1.75	65,65,65,65	4
87	OHX	5	3929	7/7	0.98	0.17	-1.77	55,55,55,55	2
86	MG	2	1980	1/1	0.96	0.11	-1.78	104,104,104,104	0
88	ZN	Q0	500	1/1	0.98	0.11	-1.79	54,54,54,54	0
87	OHX	SR	401	7/7	0.96	0.11	-1.80	144,144,144,144	6
87	OHX	1	3803	7/7	0.99	0.17	-1.81	73,73,73,73	3
87	OHX	1	3937	7/7	0.95	0.10	-1.81	110,110,110,110	6
87	OHX	5	4084	7/7	0.95	0.11	-1.82	143,143,143,143	7
87	OHX	6	2109	7/7	0.98	0.12	-1.84	99,99,99,99	6
86	MG	5	3478	1/1	0.95	0.11	-1.84	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	5	4100	7/7	0.97	0.17	-1.85	69,69,69,69	3
87	OHX	6	2038	7/7	0.99	0.17	-1.85	61,61,61,61	5
87	OHX	S8	301	7/7	0.94	0.12	-1.86	115,115,115,115	7
86	MG	6	2184	1/1	0.99	0.12	-1.87	91,91,91,91	0
87	OHX	2	2114	7/7	0.90	0.17	-1.90	103,103,103,103	4
87	OHX	6	2101	7/7	0.98	0.18	-1.91	62,62,62,62	2
87	OHX	m5	305	7/7	0.99	0.14	-1.95	76,76,76,76	3
87	OHX	4	220	7/7	0.97	0.17	-1.95	84,84,84,84	3
87	OHX	L3	403	7/7	0.97	0.15	-1.95	72,72,72,72	5
87	OHX	6	2039	7/7	0.95	0.12	-1.96	126,126,126,126	5
87	OHX	1	3788	7/7	0.99	0.20	-1.96	58,58,58,58	4
87	OHX	5	3951	7/7	0.96	0.12	-1.99	100,100,100,100	2
87	OHX	1	3942	7/7	0.96	0.12	-2.00	94,94,94,94	4
86	MG	5	3523	1/1	0.95	0.13	-2.04	48,48,48,48	0
87	OHX	2	2020	7/7	0.96	0.13	-2.04	117,117,117,117	3
88	ZN	D9	101	1/1	0.99	0.06	-2.05	89,89,89,89	0
87	OHX	o3	202	7/7	0.98	0.17	-2.10	52,52,52,52	3
87	OHX	2	2080	7/7	0.97	0.14	-2.10	91,91,91,91	4
88	ZN	Q3	501	1/1	0.99	0.09	-2.11	78,78,78,78	0
86	MG	s4	601	1/1	0.86	0.13	-2.17	66,66,66,66	0
87	OHX	2	2071	7/7	0.98	0.18	-2.17	72,72,72,72	6
86	MG	5	3500	1/1	0.98	0.17	-2.20	42,42,42,42	0
87	OHX	6	2074	7/7	0.97	0.15	-2.22	70,70,70,70	2
87	OHX	2	2055	7/7	0.96	0.16	-2.25	63,63,63,63	5
87	OHX	1	3823	7/7	0.99	0.11	-2.25	111,111,111,111	4
87	OHX	5	4107	7/7	0.95	0.18	-2.26	66,66,66,66	3
88	ZN	e1	501	1/1	0.94	0.04	-2.26	173,173,173,173	0
87	OHX	6	2063	7/7	0.98	0.08	-2.26	147,147,147,147	6
87	OHX	c5	201	7/7	0.90	0.15	-2.28	129,129,129,129	6
87	OHX	5	3828	7/7	0.99	0.21	-2.28	44,44,44,44	5
86	MG	2	1941	1/1	0.92	0.09	-2.31	100,100,100,100	0
87	OHX	2	1994	7/7	0.99	0.14	-2.32	97,97,97,97	2
87	OHX	1	4056	7/7	0.96	0.14	-2.33	85,85,85,85	5
87	OHX	2	2038	7/7	0.98	0.10	-2.33	119,119,119,119	6
87	OHX	6	2082	7/7	0.97	0.14	-2.34	99,99,99,99	5
87	OHX	2	2001	7/7	0.99	0.13	-2.35	120,120,120,120	2
87	OHX	5	4087	7/7	0.98	0.17	-2.37	39,39,39,39	4
87	OHX	2	2110	7/7	0.95	0.14	-2.37	112,112,112,112	5
90	PRO	B	102	7/8	0.94	0.19	-2.38	41,41,51,51	0
87	OHX	5	4067	7/7	0.99	0.14	-2.40	49,49,49,49	3
87	OHX	14	402	7/7	0.97	0.19	-2.45	69,69,69,69	5
86	MG	5	3702	1/1	0.98	0.09	-2.48	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	5	3838	7/7	1.00	0.16	-2.53	64,64,64,64	2
87	OHX	5	3866	7/7	0.99	0.10	-2.57	126,126,126,126	2
86	MG	5	3463	1/1	0.72	0.15	-2.63	125,125,125,125	0
87	OHX	2	1997	7/7	0.99	0.11	-2.65	107,107,107,107	5
87	OHX	6	2105	7/7	0.95	0.17	-2.73	81,81,81,81	4
86	MG	5	3630	1/1	0.88	0.20	-2.74	52,52,52,52	0
87	OHX	L4	401	7/7	0.96	0.14	-2.76	67,67,67,67	7
86	MG	5	3758	1/1	0.89	0.11	-2.77	46,46,46,46	0
87	OHX	6	2069	7/7	0.97	0.17	-2.77	73,73,73,73	4
88	ZN	d6	101	1/1	0.98	0.05	-2.82	84,84,84,84	0
87	OHX	1	3895	7/7	0.97	0.16	-2.83	57,57,57,57	4
87	OHX	5	3817	7/7	0.99	0.17	-2.85	57,57,57,57	0
87	OHX	6	2100	7/7	0.99	0.14	-2.88	71,71,71,71	3
86	MG	1	3633	1/1	0.88	0.15	-2.88	59,59,59,59	0
87	OHX	2	2070	7/7	0.96	0.11	-3.01	108,108,108,108	5
86	MG	2	1946	1/1	0.87	0.08	-3.02	108,108,108,108	0
86	MG	1	3484	1/1	0.98	0.12	-3.05	52,52,52,52	0
87	OHX	2	2016	7/7	0.98	0.14	-3.18	96,96,96,96	4
87	OHX	6	2026	7/7	0.99	0.19	-3.22	66,66,66,66	1
86	MG	6	1908	1/1	0.93	0.13	-3.25	109,109,109,109	0
87	OHX	1	3933	7/7	0.97	0.14	-3.26	91,91,91,91	4
87	OHX	1	3894	7/7	0.98	0.09	-3.50	132,132,132,132	7
86	MG	2	1976	1/1	0.88	0.09	-3.81	77,77,77,77	0
87	OHX	1	3999	7/7	0.93	0.06	-3.90	215,215,215,215	2
87	OHX	1	3941	7/7	0.97	0.16	-4.00	51,51,51,51	3
86	MG	6	2003	1/1	0.97	0.10	-4.11	96,96,96,96	0
88	ZN	D6	500	1/1	0.98	0.07	-4.56	103,103,103,103	0
87	OHX	l5	302	7/7	0.92	0.12	-4.67	105,105,105,105	4
90	PRO	C	101	7/8	0.95	0.17	-4.70	35,35,45,45	0
86	MG	6	1977	1/1	0.97	0.10	-4.81	57,57,57,57	0
87	OHX	5	3963	7/7	0.97	0.09	-5.25	107,107,107,107	2
87	OHX	6	2015	7/7	0.99	0.14	-5.92	78,78,78,78	3
86	MG	1	3683	1/1	0.94	0.15	-8.18	39,39,39,39	1
86	MG	5	3580	1/1	0.96	0.59	-	24,24,24,24	0
86	MG	1	3579	1/1	0.98	0.69	-	35,35,35,35	0
86	MG	1	3427	1/1	0.97	0.85	-	42,42,42,42	0
86	MG	5	3798	1/1	0.97	0.42	-	42,42,42,42	0
86	MG	6	1992	1/1	0.80	0.33	-	61,61,61,61	0
86	MG	6	1997	1/1	0.95	0.48	-	53,53,53,53	0
87	OHX	c8	202	7/7	0.95	0.23	-	99,99,99,99	5
86	MG	5	3787	1/1	0.89	0.31	-	68,68,68,68	0
87	OHX	1	4028	7/7	0.94	0.19	-	58,58,58,58	3

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	1	3598	1/1	0.92	0.34	-	39,39,39,39	0
86	MG	1	3584	1/1	0.95	0.75	-	33,33,33,33	0
87	OHX	1	4108	7/7	0.87	0.23	-	59,59,59,59	5
86	MG	2	1902	1/1	0.83	0.98	-	49,49,49,49	0
87	OHX	1	3864	7/7	0.98	0.35	-	104,104,104,104	3
87	OHX	1	3927	7/7	0.94	0.33	-	51,51,51,51	3
86	MG	5	3764	1/1	0.94	0.14	-	39,39,39,39	0
86	MG	2	1971	1/1	0.95	0.19	-	81,81,81,81	0
86	MG	5	3442	1/1	0.98	0.61	-	44,44,44,44	0
87	OHX	2	2126	7/7	0.94	0.52	-	64,64,64,64	4
87	OHX	5	4034	7/7	0.97	0.29	-	40,40,40,40	3
86	MG	1	3674	1/1	0.86	0.36	-	68,68,68,68	0
86	MG	1	3423	1/1	0.75	0.47	-	46,46,46,46	0
86	MG	M7	204	1/1	0.92	0.46	-	46,46,46,46	0
87	OHX	2	2086	7/7	0.93	0.25	-	112,112,112,112	5
87	OHX	6	2152	7/7	0.88	0.14	-	107,107,107,107	5
86	MG	1	3558	1/1	0.89	0.52	-	35,35,35,35	0
86	MG	1	3698	1/1	0.96	0.25	-	42,42,42,42	0
86	MG	1	3714	1/1	0.70	0.70	-	46,46,46,46	0
87	OHX	5	4131	7/7	0.89	0.47	-	45,45,45,45	4
86	MG	5	3697	1/1	0.75	0.62	-	42,42,42,42	0
86	MG	1	3521	1/1	0.97	0.66	-	43,43,43,43	0
86	MG	5	3509	1/1	0.93	0.66	-	39,39,39,39	0
86	MG	6	2002	1/1	0.90	0.32	-	66,66,66,66	0
86	MG	1	3449	1/1	0.78	0.40	-	57,57,57,57	0
87	OHX	6	2052	7/7	0.98	0.17	-	67,67,67,67	3
86	MG	1	3749	1/1	0.94	0.55	-	17,17,17,17	0
87	OHX	1	3979	7/7	0.93	0.09	-	197,197,197,197	5
86	MG	5	3777	1/1	0.79	0.31	-	115,115,115,115	0
86	MG	1	3700	1/1	0.75	0.33	-	51,51,51,51	0
87	OHX	5	4094	7/7	0.81	0.39	-	41,41,41,41	2
87	OHX	2	2049	7/7	0.87	0.28	-	100,100,100,100	4
86	MG	5	3666	1/1	0.90	0.46	-	86,86,86,86	0
86	MG	1	3499	1/1	0.98	0.54	-	37,37,37,37	0
86	MG	6	1954	1/1	0.80	0.63	-	64,64,64,64	0
86	MG	5	3600	1/1	0.98	0.71	-	26,26,26,26	0
87	OHX	1	3837	7/7	0.99	0.21	-	60,60,60,60	2
86	MG	5	3515	1/1	0.94	0.57	-	21,21,21,21	0
86	MG	m5	302	1/1	0.92	0.27	-	67,67,67,67	0
86	MG	1	3405	1/1	0.93	0.55	-	132,132,132,132	0
86	MG	1	3605	1/1	0.89	0.30	-	44,44,44,44	0
87	OHX	5	3978	7/7	0.98	0.32	-	67,67,67,67	3

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
87	OHX	2	2146	7/7	0.93	0.18	-	87,87,87,87	7
86	MG	2	1958	1/1	0.64	0.54	-	104,104,104,104	0
86	MG	1	3750	1/1	0.84	0.82	-	48,48,48,48	0
86	MG	1	3652	1/1	0.89	0.32	-	48,48,48,48	0
87	OHX	5	4032	7/7	0.94	0.15	-	98,98,98,98	7
87	OHX	5	4151	7/7	0.94	0.29	-	76,76,76,76	5
87	OHX	5	4149	7/7	0.92	0.21	-	62,62,62,62	5
86	MG	D3	201	1/1	0.69	0.40	-	54,54,54,54	0
87	OHX	6	2179	7/7	0.89	0.24	-	61,61,61,61	7
87	OHX	6	2165	7/7	0.93	0.31	-	74,74,74,74	6
86	MG	5	3685	1/1	0.78	0.34	-	92,92,92,92	0
86	MG	1	3483	1/1	0.81	0.81	-	54,54,54,54	0
86	MG	1	3637	1/1	0.89	0.67	-	46,46,46,46	0
87	OHX	5	3883	7/7	0.98	0.18	-	63,63,63,63	3
86	MG	1	3682	1/1	0.86	0.30	-	36,36,36,36	0
86	MG	5	3628	1/1	0.90	0.29	-	35,35,35,35	0
86	MG	5	3797	1/1	0.93	0.39	-	42,42,42,42	0
86	MG	5	3815	1/1	0.56	0.44	-	39,39,39,39	0
87	OHX	1	4091	7/7	0.94	0.32	-	42,42,42,42	4
86	MG	5	3477	1/1	0.95	0.83	-	21,21,21,21	0
86	MG	5	3434	1/1	0.93	0.32	-	33,33,33,33	0
86	MG	5	3650	1/1	0.78	0.41	-	42,42,42,42	0
86	MG	M7	203	1/1	0.87	0.40	-	46,46,46,46	0
86	MG	5	3516	1/1	0.93	0.40	-	28,28,28,28	0
86	MG	s8	301	1/1	0.89	0.40	-	52,52,52,52	0
86	MG	5	3806	1/1	0.74	0.27	-	54,54,54,54	0
86	MG	5	3427	1/1	0.95	0.51	-	45,45,45,45	0
86	MG	1	3455	1/1	0.97	0.52	-	29,29,29,29	0
87	OHX	1	4002	7/7	0.96	0.35	-	65,65,65,65	7
87	OHX	5	4028	7/7	0.97	0.13	-	76,76,76,76	4
87	OHX	5	4128	7/7	0.95	0.31	-	37,37,37,37	3
86	MG	6	1909	1/1	0.90	0.30	-	53,53,53,53	0
86	MG	2	1929	1/1	0.83	0.36	-	83,83,83,83	0
86	MG	6	1994	1/1	0.94	0.73	-	49,49,49,49	0
86	MG	7	205	1/1	0.97	0.53	-	26,26,26,26	0
86	MG	5	3562	1/1	0.88	0.50	-	44,44,44,44	0
86	MG	5	3470	1/1	0.94	0.25	-	51,51,51,51	0
87	OHX	1	3918	7/7	0.98	0.14	-	91,91,91,91	5
87	OHX	5	4044	7/7	0.96	0.42	-	48,48,48,48	2
87	OHX	1	3805	7/7	0.99	0.16	-	93,93,93,93	4
86	MG	5	3668	1/1	0.85	0.20	-	36,36,36,36	1
86	MG	o3	201	1/1	0.69	0.36	-	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	5	3454	1/1	0.97	0.58	-	31,31,31,31	0
86	MG	1	3657	1/1	0.85	0.66	-	49,49,49,49	0
87	OHX	1	3873	7/7	0.98	0.22	-	53,53,53,53	5
86	MG	5	3401	1/1	0.84	0.08	-	54,54,54,54	0
86	MG	6	1995	1/1	0.89	0.51	-	47,47,47,47	0
87	OHX	4	229	7/7	0.95	0.21	-	45,45,45,45	3
86	MG	5	3479	1/1	0.91	0.10	-	47,47,47,47	0
87	OHX	5	4146	7/7	0.84	0.26	-	89,89,89,89	7
86	MG	1	3436	1/1	0.93	0.98	-	39,39,39,39	0
86	MG	1	3528	1/1	0.92	0.52	-	47,47,47,47	0
87	OHX	5	4039	7/7	0.92	0.33	-	149,149,149,149	6
87	OHX	5	3934	7/7	0.99	0.18	-	45,45,45,45	1
87	OHX	5	4059	7/7	0.95	0.37	-	45,45,45,45	5
86	MG	1	3673	1/1	0.83	0.58	-	39,39,39,39	0
87	OHX	5	4157	7/7	0.87	0.40	-	35,35,35,35	3
87	OHX	1	3984	7/7	0.96	0.10	-	127,127,127,127	7
87	OHX	6	2177	7/7	0.89	0.14	-	141,141,141,141	7
86	MG	2	1928	1/1	0.97	0.30	-	71,71,71,71	0
86	MG	1	3428	1/1	0.84	0.34	-	52,52,52,52	0
87	OHX	1	3956	7/7	0.97	0.15	-	57,57,57,57	5
87	OHX	5	4161	7/7	0.77	0.37	-	100,100,100,100	7
86	MG	1	3701	1/1	0.86	0.28	-	52,52,52,52	0
86	MG	1	3702	1/1	0.83	0.52	-	45,45,45,45	0
86	MG	1	3574	1/1	0.92	0.95	-	30,30,30,30	0
86	MG	5	3726	1/1	0.86	0.58	-	44,44,44,44	0
86	MG	1	3623	1/1	0.90	0.20	-	57,57,57,57	0
86	MG	5	3701	1/1	0.83	0.32	-	54,54,54,54	0
86	MG	2	1913	1/1	0.94	0.28	-	79,79,79,79	0
86	MG	5	3414	1/1	0.94	0.27	-	44,44,44,44	0
87	OHX	5	4090	7/7	0.89	0.35	-	45,45,45,45	2
86	MG	1	3663	1/1	0.78	1.03	-	44,44,44,44	0
87	OHX	6	2160	7/7	0.97	0.18	-	69,69,69,69	5
87	OHX	5	4035	7/7	0.95	0.29	-	38,38,38,38	5
87	OHX	5	3994	7/7	0.95	0.24	-	88,88,88,88	5
86	MG	5	3693	1/1	0.81	0.31	-	55,55,55,55	0
86	MG	1	3412	1/1	0.97	0.27	-	68,68,68,68	0
86	MG	5	3607	1/1	0.90	0.47	-	50,50,50,50	0
87	OHX	1	4079	7/7	0.86	0.24	-	108,108,108,108	6
86	MG	5	3646	1/1	0.85	0.25	-	55,55,55,55	0
87	OHX	8	216	7/7	0.95	0.23	-	78,78,78,78	5
87	OHX	2	2041	7/7	0.97	0.09	-	141,141,141,141	6
87	OHX	8	210	7/7	1.00	0.18	-	64,64,64,64	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	6	1969	1/1	0.97	0.44	-	55,55,55,55	0
87	OHX	5	4031	7/7	0.95	0.20	-	71,71,71,71	4
86	MG	5	3532	1/1	0.96	0.71	-	28,28,28,28	0
86	MG	1	3614	1/1	0.90	0.55	-	54,54,54,54	0
86	MG	5	3716	1/1	0.96	0.67	-	16,16,16,16	0
87	OHX	5	4170	7/7	0.89	0.19	-	90,90,90,90	5
87	OHX	2	2090	7/7	0.98	0.23	-	94,94,94,94	6
86	MG	3	203	1/1	0.79	0.77	-	42,42,42,42	0
87	OHX	2	2042	7/7	0.98	0.21	-	68,68,68,68	5
86	MG	1	3704	1/1	0.91	0.38	-	59,59,59,59	0
86	MG	1	3662	1/1	0.68	0.79	-	101,101,101,101	0
86	MG	5	3552	1/1	0.91	0.54	-	26,26,26,26	0
86	MG	1	3671	1/1	0.94	0.49	-	47,47,47,47	0
87	OHX	5	4150	7/7	0.93	0.24	-	53,53,53,53	4
86	MG	1	3624	1/1	0.94	0.35	-	33,33,33,33	0
86	MG	5	3805	1/1	0.96	0.61	-	37,37,37,37	0
86	MG	2	1957	1/1	0.77	0.55	-	99,99,99,99	0
87	OHX	6	2124	7/7	0.96	0.11	-	103,103,103,103	6
86	MG	m7	202	1/1	0.95	0.36	-	34,34,34,34	0
86	MG	5	3655	1/1	0.95	0.60	-	41,41,41,41	0
86	MG	5	3464	1/1	0.92	0.80	-	44,44,44,44	0
87	OHX	2	2069	7/7	0.95	0.19	-	115,115,115,115	4
86	MG	1	3457	1/1	0.85	0.65	-	32,32,32,32	0
86	MG	1	3590	1/1	0.99	0.30	-	43,43,43,43	0
87	OHX	2	2098	7/7	0.95	0.24	-	111,111,111,111	6
86	MG	5	3429	1/1	0.94	0.36	-	36,36,36,36	0
87	OHX	1	4103	7/7	0.92	0.25	-	53,53,53,53	5
86	MG	5	3699	1/1	0.89	0.30	-	43,43,43,43	0
86	MG	5	3574	1/1	0.91	0.53	-	36,36,36,36	0
86	MG	2	1916	1/1	0.81	0.71	-	63,63,63,63	0
86	MG	5	3804	1/1	0.96	0.26	-	37,37,37,37	0
87	OHX	5	4114	7/7	0.92	0.20	-	63,63,63,63	6
86	MG	1	3740	1/1	0.98	0.26	-	62,62,62,62	0
87	OHX	6	2174	7/7	0.92	0.31	-	92,92,92,92	6
86	MG	1	3613	1/1	0.89	0.81	-	58,58,58,58	0
86	MG	5	3404	1/1	0.81	0.73	-	49,49,49,49	0
87	OHX	6	2079	7/7	0.98	0.26	-	51,51,51,51	3
87	OHX	C3	201	7/7	0.93	0.27	-	100,100,100,100	5
86	MG	5	3715	1/1	0.97	0.33	-	34,34,34,34	0
86	MG	5	3484	1/1	0.87	0.50	-	38,38,38,38	0
86	MG	1	3620	1/1	0.92	0.36	-	32,32,32,32	0
87	OHX	5	4125	7/7	0.92	0.21	-	98,98,98,98	3

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	5	3669	1/1	0.82	0.41	-	35,35,35,35	0
86	MG	1	3729	1/1	0.77	0.40	-	69,69,69,69	0
87	OHX	2	2087	7/7	0.96	0.14	-	89,89,89,89	5
86	MG	1	3568	1/1	0.88	0.46	-	36,36,36,36	0
87	OHX	5	3969	7/7	0.95	0.21	-	80,80,80,80	3
86	MG	5	3486	1/1	0.82	0.67	-	37,37,37,37	0
87	OHX	5	3908	7/7	0.97	0.19	-	77,77,77,77	4
87	OHX	1	3870	7/7	0.95	0.28	-	67,67,67,67	3
86	MG	m3	201	1/1	0.86	0.51	-	40,40,40,40	0
86	MG	n0	201	1/1	0.85	0.34	-	41,41,41,41	0
87	OHX	1	3836	7/7	0.98	0.17	-	98,98,98,98	3
87	OHX	1	4104	7/7	0.86	0.24	-	73,73,73,73	6
86	MG	1	3608	1/1	0.71	0.44	-	46,46,46,46	0
86	MG	5	3722	1/1	0.78	0.40	-	52,52,52,52	0
87	OHX	1	4098	7/7	0.82	0.34	-	61,61,61,61	5
86	MG	5	3639	1/1	0.83	0.16	-	50,50,50,50	0
86	MG	4	202	1/1	0.54	0.67	-	57,57,57,57	0
86	MG	5	3667	1/1	0.87	0.44	-	33,33,33,33	0
86	MG	5	3640	1/1	0.81	1.16	-	55,55,55,55	0
86	MG	6	1945	1/1	0.95	0.55	-	51,51,51,51	0
87	OHX	5	4130	7/7	0.92	0.19	-	64,64,64,64	5
86	MG	1	3500	1/1	0.96	0.84	-	30,30,30,30	0
86	MG	1	3619	1/1	0.92	0.43	-	53,53,53,53	0
86	MG	1	3748	1/1	0.89	0.44	-	67,67,67,67	0
86	MG	1	3536	1/1	0.95	0.58	-	29,29,29,29	0
86	MG	N6	201	1/1	0.81	0.47	-	70,70,70,70	0
86	MG	5	3604	1/1	0.96	0.47	-	33,33,33,33	0
87	OHX	14	403	7/7	0.97	0.14	-	51,51,51,51	7
86	MG	5	3748	1/1	0.97	0.57	-	30,30,30,30	0
86	MG	1	3504	1/1	0.95	0.65	-	42,42,42,42	0
86	MG	5	3728	1/1	0.92	0.19	-	47,47,47,47	0
86	MG	1	3462	1/1	0.92	0.73	-	44,44,44,44	0
86	MG	5	3749	1/1	0.79	0.41	-	37,37,37,37	0
87	OHX	1	3818	7/7	0.99	0.26	-	62,62,62,62	2
86	MG	2	1979	1/1	0.86	0.44	-	70,70,70,70	0
86	MG	6	1956	1/1	0.98	0.38	-	44,44,44,44	0
87	OHX	1	3922	7/7	0.98	0.21	-	82,82,82,82	3
87	OHX	5	4015	7/7	0.95	0.19	-	62,62,62,62	7
87	OHX	5	4166	7/7	0.96	0.29	-	38,38,38,38	3
86	MG	5	3504	1/1	0.94	0.85	-	25,25,25,25	0
86	MG	1	3706	1/1	0.98	0.23	-	38,38,38,38	0
87	OHX	5	4095	7/7	0.97	0.12	-	119,119,119,119	7

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	1	3688	1/1	0.93	0.74	-	39,39,39,39	0
87	OHX	5	3891	7/7	0.98	0.31	-	63,63,63,63	3
87	OHX	2	2023	7/7	0.97	0.11	-	106,106,106,106	4
87	OHX	6	2133	7/7	0.91	0.35	-	125,125,125,125	6
87	OHX	8	227	7/7	0.88	0.46	-	73,73,73,73	5
86	MG	1	3439	1/1	0.96	0.31	-	60,60,60,60	0
86	MG	1	3736	1/1	0.95	0.11	-	50,50,50,50	0
86	MG	1	4117	1/1	0.95	0.98	-	47,47,47,47	0
87	OHX	5	4110	7/7	0.95	0.21	-	74,74,74,74	7
86	MG	1	3726	1/1	0.85	0.27	-	64,64,64,64	0
87	OHX	1	3953	7/7	0.97	0.27	-	58,58,58,58	2
87	OHX	2	2143	7/7	0.87	0.34	-	84,84,84,84	5
86	MG	1	3596	1/1	0.90	0.37	-	46,46,46,46	0
86	MG	2	1919	1/1	0.87	0.33	-	62,62,62,62	0
86	MG	1	3553	1/1	0.96	0.53	-	24,24,24,24	0
87	OHX	5	4116	7/7	0.94	0.35	-	40,40,40,40	5
86	MG	5	3614	1/1	0.86	0.51	-	35,35,35,35	0
86	MG	5	3458	1/1	0.97	0.49	-	34,34,34,34	0
86	MG	6	1972	1/1	0.53	0.34	-	81,81,81,81	0
86	MG	5	3417	1/1	0.76	0.51	-	36,36,36,36	0
86	MG	5	3766	1/1	0.85	0.32	-	43,43,43,43	0
87	OHX	1	3994	7/7	0.97	0.20	-	54,54,54,54	5
87	OHX	5	3864	7/7	0.98	0.18	-	86,86,86,86	1
86	MG	4	203	1/1	0.86	0.63	-	64,64,64,64	0
87	OHX	5	4061	7/7	0.80	0.46	-	56,56,56,56	3
86	MG	5	3518	1/1	0.98	0.79	-	35,35,35,35	0
86	MG	1	3404	1/1	0.94	0.57	-	57,57,57,57	0
87	OHX	1	4070	7/7	0.88	0.18	-	111,111,111,111	6
86	MG	1	3537	1/1	0.93	0.45	-	57,57,57,57	0
86	MG	1	3508	1/1	0.87	0.59	-	38,38,38,38	0
87	OHX	4	219	7/7	0.97	0.17	-	81,81,81,81	2
86	MG	5	3559	1/1	0.99	0.70	-	27,27,27,27	0
86	MG	6	1991	1/1	0.96	0.15	-	77,77,77,77	0
86	MG	2	1963	1/1	0.79	0.17	-	83,83,83,83	0
86	MG	5	3747	1/1	0.91	0.07	-	124,124,124,124	0
86	MG	5	3778	1/1	0.96	0.63	-	35,35,35,35	0
86	MG	5	3467	1/1	0.76	0.43	-	47,47,47,47	0
86	MG	1	3632	1/1	0.93	0.67	-	47,47,47,47	0
87	OHX	4	222	7/7	0.96	0.20	-	61,61,61,61	3
86	MG	5	3529	1/1	0.96	0.50	-	31,31,31,31	0
86	MG	5	3535	1/1	0.97	0.81	-	29,29,29,29	0
86	MG	6	1942	1/1	0.93	0.41	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	3	217	7/7	0.91	0.36	-	78,78,78,78	4
87	OHX	5	4071	7/7	0.96	0.34	-	40,40,40,40	4
86	MG	1	3626	1/1	0.89	0.47	-	46,46,46,46	0
87	OHX	1	3965	7/7	0.94	0.32	-	56,56,56,56	3
86	MG	1	3678	1/1	0.92	0.41	-	53,53,53,53	0
86	MG	5	3610	1/1	0.95	0.46	-	38,38,38,38	0
86	MG	1	3602	1/1	0.93	0.33	-	58,58,58,58	0
86	MG	1	3646	1/1	0.92	0.29	-	39,39,39,39	0
86	MG	1	3519	1/1	0.95	0.87	-	49,49,49,49	0
86	MG	1	3744	1/1	0.95	0.34	-	44,44,44,44	0
86	MG	5	3664	1/1	0.94	0.25	-	43,43,43,43	0
87	OHX	1	4094	7/7	0.89	0.20	-	77,77,77,77	4
86	MG	5	3793	1/1	0.91	0.19	-	45,45,45,45	0
86	MG	5	3411	1/1	0.80	0.24	-	47,47,47,47	0
87	OHX	1	4097	7/7	0.93	0.20	-	42,42,42,42	6
87	OHX	1	4099	7/7	0.87	0.35	-	53,53,53,53	3
86	MG	6	1959	1/1	0.94	0.35	-	98,98,98,98	0
86	MG	5	3619	1/1	0.89	0.67	-	39,39,39,39	0
87	OHX	5	4089	7/7	0.95	0.26	-	51,51,51,51	4
86	MG	5	3631	1/1	0.85	0.72	-	36,36,36,36	0
86	MG	1	3718	1/1	0.93	0.62	-	52,52,52,52	0
86	MG	1	3747	1/1	0.75	0.34	-	48,48,48,48	0
87	OHX	5	4140	7/7	0.89	0.41	-	49,49,49,49	4
86	MG	1	3710	1/1	0.84	0.24	-	46,46,46,46	0
87	OHX	5	3961	7/7	0.96	0.25	-	47,47,47,47	4
86	MG	5	3468	1/1	0.78	0.47	-	38,38,38,38	1
86	MG	5	3538	1/1	0.97	0.52	-	33,33,33,33	0
87	OHX	1	4023	7/7	0.95	0.38	-	73,73,73,73	3
86	MG	5	3707	1/1	0.90	0.15	-	50,50,50,50	0
86	MG	1	3647	1/1	0.94	0.47	-	64,64,64,64	0
87	OHX	2	2131	7/7	0.93	0.12	-	109,109,109,109	5
86	MG	2	1961	1/1	0.95	0.53	-	86,86,86,86	0
86	MG	5	3743	1/1	0.85	0.45	-	57,57,57,57	0
87	OHX	8	230	7/7	0.93	0.28	-	62,62,62,62	5
86	MG	1	3475	1/1	0.87	0.51	-	44,44,44,44	0
87	OHX	5	3859	7/7	0.98	0.20	-	88,88,88,88	3
86	MG	5	3723	1/1	0.95	0.35	-	35,35,35,35	0
86	MG	1	3534	1/1	0.85	0.25	-	69,69,69,69	0
87	OHX	1	4060	7/7	0.98	0.27	-	65,65,65,65	4
86	MG	5	3439	1/1	0.93	0.38	-	36,36,36,36	0
86	MG	5	3802	1/1	0.87	0.36	-	35,35,35,35	0
87	OHX	8	215	7/7	0.98	0.20	-	85,85,85,85	3

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	5	3453	1/1	0.90	0.49	-	59,59,59,59	0
86	MG	5	3629	1/1	0.84	0.37	-	56,56,56,56	0
86	MG	1	3649	1/1	0.92	0.43	-	37,37,37,37	0
87	OHX	6	2154	7/7	0.94	0.30	-	49,49,49,49	3
87	OHX	6	2016	7/7	0.98	0.22	-	83,83,83,83	4
87	OHX	5	4075	7/7	0.94	0.20	-	43,43,43,43	3
87	OHX	2	2135	7/7	0.67	0.15	-	188,188,188,188	6
86	MG	5	3689	1/1	0.76	0.64	-	75,75,75,75	0
87	OHX	1	3945	7/7	0.94	0.28	-	57,57,57,57	5
86	MG	1	3658	1/1	0.86	0.54	-	42,42,42,42	0
86	MG	5	3780	1/1	0.89	0.52	-	43,43,43,43	0
86	MG	5	4173	1/1	0.97	0.41	-	33,33,33,33	0
86	MG	5	3481	1/1	0.95	0.72	-	37,37,37,37	0
87	OHX	5	3882	7/7	0.99	0.25	-	53,53,53,53	1
86	MG	5	3437	1/1	0.89	0.60	-	39,39,39,39	0
87	OHX	2	2033	7/7	0.98	0.26	-	78,78,78,78	3
86	MG	2	1960	1/1	0.74	0.27	-	76,76,76,76	0
86	MG	1	3577	1/1	0.87	0.67	-	39,39,39,39	0
87	OHX	4	225	7/7	0.95	0.19	-	106,106,106,106	5
86	MG	6	1912	1/1	0.94	0.71	-	39,39,39,39	0
86	MG	5	3670	1/1	0.94	0.35	-	84,84,84,84	0
87	OHX	5	3981	7/7	0.95	0.20	-	58,58,58,58	3
87	OHX	2	2107	7/7	0.89	0.50	-	66,66,66,66	4
86	MG	1	3684	1/1	0.96	0.29	-	52,52,52,52	0
86	MG	1	3526	1/1	0.92	0.51	-	45,45,45,45	0
86	MG	2	1978	1/1	0.59	0.32	-	74,74,74,74	0
86	MG	5	3763	1/1	0.97	0.32	-	43,43,43,43	0
86	MG	1	3435	1/1	0.98	0.90	-	25,25,25,25	0
87	OHX	2	2015	7/7	0.99	0.13	-	90,90,90,90	4
86	MG	6	1965	1/1	0.80	0.38	-	48,48,48,48	0
87	OHX	2	2043	7/7	0.92	0.25	-	100,100,100,100	4
86	MG	1	3514	1/1	0.97	0.43	-	35,35,35,35	0
87	OHX	5	4141	7/7	0.90	0.29	-	58,58,58,58	4
86	MG	5	3431	1/1	0.87	0.30	-	32,32,32,32	0
86	MG	1	3434	1/1	0.87	0.54	-	62,62,62,62	0
86	MG	1	3759	1/1	0.92	0.29	-	48,48,48,48	0
86	MG	5	3740	1/1	0.67	0.50	-	66,66,66,66	0
87	OHX	5	4154	7/7	0.93	0.14	-	97,97,97,97	7
86	MG	1	3727	1/1	0.90	0.35	-	48,48,48,48	0
86	MG	5	3757	1/1	0.94	0.32	-	36,36,36,36	0
86	MG	5	3452	1/1	0.89	0.98	-	33,33,33,33	0
86	MG	1	3606	1/1	0.97	0.21	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	2	1990	1/1	0.95	0.53	-	49,49,49,49	0
87	OHX	6	2143	7/7	0.91	0.38	-	51,51,51,51	3
87	OHX	8	217	7/7	0.91	0.36	-	63,63,63,63	4
86	MG	5	3756	1/1	0.56	0.17	-	73,73,73,73	0
86	MG	5	3557	1/1	0.91	0.56	-	31,31,31,31	0
86	MG	1	3565	1/1	0.89	0.50	-	40,40,40,40	0
86	MG	1	3635	1/1	0.93	0.25	-	88,88,88,88	0
86	MG	1	3629	1/1	0.81	0.98	-	33,33,33,33	0
87	OHX	6	2183	7/7	0.73	0.61	-	76,76,76,76	5
86	MG	5	3657	1/1	0.91	0.34	-	27,27,27,27	0
86	MG	1	3461	1/1	0.83	0.41	-	57,57,57,57	0
87	OHX	6	2048	7/7	0.98	0.19	-	65,65,65,65	4
87	OHX	1	3975	7/7	0.84	0.25	-	88,88,88,88	3
86	MG	6	1982	1/1	0.77	1.00	-	53,53,53,53	0
86	MG	5	3609	1/1	0.85	0.19	-	49,49,49,49	0
86	MG	5	3558	1/1	0.98	0.58	-	22,22,22,22	0
86	MG	1	3610	1/1	0.94	0.65	-	45,45,45,45	0
86	MG	6	1986	1/1	0.68	0.96	-	93,93,93,93	0
86	MG	1	3640	1/1	0.96	0.47	-	62,62,62,62	0
86	MG	6	1967	1/1	0.85	0.35	-	76,76,76,76	0
87	OHX	1	3850	7/7	0.98	0.28	-	47,47,47,47	3
87	OHX	6	2096	7/7	0.97	0.14	-	94,94,94,94	5
87	OHX	1	4102	7/7	0.88	0.26	-	65,65,65,65	3
86	MG	1	3679	1/1	0.71	0.30	-	59,59,59,59	0
86	MG	5	3704	1/1	0.94	0.14	-	66,66,66,66	0
86	MG	5	3461	1/1	0.39	0.22	-	109,109,109,109	0
86	MG	1	3494	1/1	0.95	0.42	-	42,42,42,42	0
86	MG	2	1908	1/1	0.81	0.30	-	90,90,90,90	0
87	OHX	5	3971	7/7	0.96	0.19	-	89,89,89,89	1
86	MG	2	1923	1/1	0.84	0.88	-	45,45,45,45	0
87	OHX	6	2046	7/7	0.98	0.35	-	60,60,60,60	2
86	MG	1	3425	1/1	0.99	0.90	-	27,27,27,27	0
86	MG	2	1904	1/1	0.67	0.42	-	90,90,90,90	0
87	OHX	1	4096	7/7	0.90	0.21	-	80,80,80,80	4
86	MG	1	3518	1/1	0.95	0.66	-	31,31,31,31	0
87	OHX	2	2076	7/7	0.92	0.23	-	87,87,87,87	5
86	MG	5	3605	1/1	0.96	0.16	-	39,39,39,39	1
86	MG	5	3408	1/1	0.82	0.53	-	45,45,45,45	0
87	OHX	1	3995	7/7	0.93	0.56	-	50,50,50,50	2
87	OHX	6	2139	7/7	0.97	0.18	-	86,86,86,86	3
87	OHX	1	4009	7/7	0.86	0.22	-	131,131,131,131	7
87	OHX	5	4006	7/7	0.98	0.23	-	40,40,40,40	3

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	5	3958	7/7	0.99	0.17	-	61,61,61,61	4
86	MG	5	3579	1/1	0.90	0.64	-	38,38,38,38	0
86	MG	5	3620	1/1	0.85	0.47	-	36,36,36,36	0
86	MG	1	3564	1/1	0.97	0.41	-	30,30,30,30	0
86	MG	L3	401	1/1	0.98	0.30	-	41,41,41,41	0
86	MG	1	3722	1/1	0.96	0.23	-	43,43,43,43	0
86	MG	4	204	1/1	0.70	0.61	-	58,58,58,58	0
86	MG	2	1987	1/1	0.36	0.29	-	104,104,104,104	0
87	OHX	6	2087	7/7	0.92	0.26	-	109,109,109,109	6
86	MG	1	3544	1/1	0.85	0.53	-	55,55,55,55	0
86	MG	6	1979	1/1	0.85	0.33	-	101,101,101,101	0
86	MG	5	3549	1/1	0.96	0.84	-	44,44,44,44	0
86	MG	7	209	1/1	0.96	0.13	-	54,54,54,54	0
86	MG	6	2004	1/1	0.54	0.80	-	74,74,74,74	0
86	MG	6	1905	1/1	0.91	0.35	-	51,51,51,51	0
87	OHX	6	2075	7/7	0.98	0.25	-	76,76,76,76	3
86	MG	5	3782	1/1	0.90	0.29	-	38,38,38,38	0
86	MG	5	3634	1/1	0.85	0.17	-	50,50,50,50	0
86	MG	5	3627	1/1	0.88	0.49	-	92,92,92,92	0
86	MG	6	1970	1/1	0.81	1.02	-	64,64,64,64	0
86	MG	1	3741	1/1	0.91	0.42	-	46,46,46,46	0
86	MG	5	3688	1/1	0.91	0.43	-	40,40,40,40	0
86	MG	5	3473	1/1	0.95	0.31	-	63,63,63,63	0
87	OHX	5	4121	7/7	0.87	0.29	-	52,52,52,52	3
86	MG	2	1973	1/1	0.67	0.38	-	80,80,80,80	0
86	MG	5	3755	1/1	0.90	0.56	-	42,42,42,42	0
86	MG	5	3624	1/1	0.79	0.41	-	51,51,51,51	0
86	MG	5	3480	1/1	0.69	0.21	-	76,76,76,76	0
86	MG	5	3445	1/1	0.66	0.48	-	64,64,64,64	0
86	MG	5	3524	1/1	0.97	0.69	-	31,31,31,31	0
87	OHX	5	4062	7/7	0.95	0.30	-	39,39,39,39	3
86	MG	1	3650	1/1	0.89	0.25	-	47,47,47,47	0
86	MG	1	3634	1/1	0.77	0.65	-	41,41,41,41	0
86	MG	5	3496	1/1	0.97	0.46	-	36,36,36,36	0
87	OHX	3	218	7/7	0.94	0.30	-	54,54,54,54	5
86	MG	2	1982	1/1	0.97	0.74	-	46,46,46,46	0
86	MG	5	3784	1/1	0.91	0.26	-	57,57,57,57	0
87	OHX	1	3869	7/7	0.98	0.20	-	92,92,92,92	3
87	OHX	1	3893	7/7	0.94	0.17	-	155,155,155,155	6
86	MG	6	1985	1/1	0.71	0.44	-	55,55,55,55	0
87	OHX	5	3950	7/7	0.96	0.43	-	67,67,67,67	5
86	MG	1	3672	1/1	0.88	0.44	-	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	5	3583	1/1	0.96	0.44	-	27,27,27,27	0
86	MG	5	3714	1/1	0.73	0.29	-	62,62,62,62	0
86	MG	7	208	1/1	0.88	0.26	-	45,45,45,45	0
86	MG	1	3593	1/1	0.98	0.24	-	50,50,50,50	0
86	MG	5	3618	1/1	0.97	0.32	-	47,47,47,47	0
86	MG	5	3611	1/1	0.91	0.32	-	40,40,40,40	0
86	MG	1	3486	1/1	0.99	0.61	-	39,39,39,39	0
86	MG	1	3703	1/1	0.93	0.43	-	40,40,40,40	0
86	MG	5	3443	1/1	0.72	0.43	-	34,34,34,34	0
86	MG	2	1970	1/1	0.88	0.56	-	65,65,65,65	0
86	MG	7	206	1/1	0.98	0.39	-	34,34,34,34	0
87	OHX	1	3998	7/7	0.97	0.26	-	107,107,107,107	4
86	MG	1	3452	1/1	0.85	0.74	-	55,55,55,55	0
86	MG	1	3492	1/1	0.91	0.62	-	32,32,32,32	0
86	MG	7	210	1/1	0.84	0.28	-	43,43,43,43	0
87	OHX	1	3972	7/7	0.97	0.21	-	55,55,55,55	4
87	OHX	1	4013	7/7	0.93	0.34	-	54,54,54,54	3
87	OHX	5	3876	7/7	0.99	0.17	-	62,62,62,62	3
86	MG	7	212	1/1	0.87	0.81	-	51,51,51,51	0
86	MG	5	3613	1/1	0.95	0.65	-	41,41,41,41	0
86	MG	2	1948	1/1	0.86	0.56	-	72,72,72,72	0
87	OHX	2	2116	7/7	0.93	0.18	-	127,127,127,127	7
87	OHX	5	3975	7/7	0.96	0.16	-	115,115,115,115	3
86	MG	1	3510	1/1	0.94	0.36	-	39,39,39,39	0
87	OHX	6	2166	7/7	0.93	0.30	-	66,66,66,66	4
87	OHX	5	3919	7/7	0.98	0.21	-	36,36,36,36	2
86	MG	1	3547	1/1	0.95	0.94	-	32,32,32,32	0
86	MG	5	3696	1/1	0.81	0.18	-	61,61,61,61	0
87	OHX	2	2092	7/7	0.91	0.41	-	73,73,73,73	5
86	MG	1	3644	1/1	0.91	0.31	-	52,52,52,52	0
87	OHX	2	2060	7/7	0.96	0.30	-	89,89,89,89	6
87	OHX	6	2062	7/7	0.97	0.13	-	117,117,117,117	4
86	MG	1	3451	1/1	0.97	0.46	-	53,53,53,53	0
86	MG	2	1927	1/1	0.60	0.21	-	85,85,85,85	0
87	OHX	5	3895	7/7	0.98	0.27	-	42,42,42,42	4
86	MG	5	3663	1/1	0.87	0.31	-	62,62,62,62	0
86	MG	1	3445	1/1	0.94	0.79	-	57,57,57,57	0
87	OHX	1	3852	7/7	0.98	0.25	-	70,70,70,70	3
87	OHX	1	3768	7/7	1.00	0.23	-	52,52,52,52	2
87	OHX	n9	101	7/7	0.99	0.20	-	62,62,62,62	2
87	OHX	1	4039	7/7	0.87	0.09	-	278,278,278,278	6
87	OHX	2	2142	7/7	0.82	0.16	-	132,132,132,132	7

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	5	4152	7/7	0.78	0.49	-	35,35,35,35	4
87	OHX	4	227	7/7	0.88	0.55	-	51,51,51,51	4
86	MG	1	3535	1/1	0.83	0.51	-	39,39,39,39	0
86	MG	6	1939	1/1	0.94	0.33	-	34,34,34,34	0
86	MG	5	3791	1/1	0.87	0.34	-	55,55,55,55	0
86	MG	5	3731	1/1	0.96	0.32	-	30,30,30,30	0
87	OHX	6	2077	7/7	0.94	0.24	-	98,98,98,98	5
87	OHX	1	3997	7/7	0.95	0.24	-	55,55,55,55	5
87	OHX	1	3804	7/7	0.99	0.19	-	62,62,62,62	1
87	OHX	1	4073	7/7	0.83	0.46	-	71,71,71,71	5
86	MG	1	3417	1/1	0.89	0.38	-	78,78,78,78	0
86	MG	5	3661	1/1	0.89	0.63	-	42,42,42,42	0
86	MG	2	1935	1/1	0.98	0.27	-	70,70,70,70	0
86	MG	5	3665	1/1	0.96	0.40	-	54,54,54,54	0
86	MG	1	3680	1/1	0.90	0.69	-	45,45,45,45	0
86	MG	2	1956	1/1	0.92	0.87	-	70,70,70,70	0
86	MG	8	205	1/1	0.97	0.30	-	47,47,47,47	0
86	MG	1	3645	1/1	0.91	0.27	-	51,51,51,51	0
86	MG	1	3566	1/1	0.88	0.30	-	47,47,47,47	0
86	MG	7	201	1/1	0.91	0.54	-	41,41,41,41	0
87	OHX	6	2054	7/7	0.98	0.12	-	87,87,87,87	3
87	OHX	5	4047	7/7	0.86	0.23	-	69,69,69,69	3
87	OHX	1	3959	7/7	0.98	0.23	-	112,112,112,112	3
86	MG	5	3671	1/1	0.72	0.57	-	62,62,62,62	0
86	MG	5	3692	1/1	0.90	0.40	-	38,38,38,38	0
86	MG	5	3441	1/1	0.93	0.28	-	32,32,32,32	0
87	OHX	6	2071	7/7	0.92	0.40	-	58,58,58,58	4
87	OHX	5	4133	7/7	0.93	0.10	-	157,157,157,157	7
87	OHX	5	3921	7/7	0.95	0.14	-	119,119,119,119	6
86	MG	5	3753	1/1	0.91	0.47	-	51,51,51,51	0
86	MG	6	1926	1/1	0.92	0.20	-	65,65,65,65	0
87	OHX	6	2111	7/7	0.94	0.24	-	73,73,73,73	5
87	OHX	2	2149	7/7	0.70	0.28	-	137,137,137,137	6
86	MG	3	205	1/1	0.90	0.52	-	68,68,68,68	0
86	MG	6	1935	1/1	0.85	0.87	-	44,44,44,44	0
86	MG	1	3660	1/1	0.89	0.15	-	82,82,82,82	0
86	MG	5	3812	1/1	0.84	0.61	-	31,31,31,31	0
86	MG	5	3653	1/1	0.97	0.55	-	31,31,31,31	0
87	OHX	5	3860	7/7	0.99	0.20	-	46,46,46,46	3
87	OHX	1	3881	7/7	0.98	0.17	-	86,86,86,86	4
86	MG	5	3466	1/1	0.90	0.44	-	47,47,47,47	0
87	OHX	6	2114	7/7	0.91	0.24	-	66,66,66,66	3

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	1	3713	1/1	0.87	1.07	-	40,40,40,40	0
87	OHX	6	2081	7/7	0.97	0.21	-	74,74,74,74	6
86	MG	L6	201	1/1	0.81	0.19	-	57,57,57,57	0
86	MG	5	3435	1/1	0.83	0.43	-	44,44,44,44	0
86	MG	1	3447	1/1	0.97	0.50	-	51,51,51,51	0
86	MG	5	3648	1/1	0.75	0.65	-	47,47,47,47	0
87	OHX	1	4012	7/7	0.95	0.26	-	64,64,64,64	1
86	MG	1	3430	1/1	0.93	0.17	-	57,57,57,57	0
87	OHX	1	3904	7/7	0.94	0.45	-	59,59,59,59	3
86	MG	5	3788	1/1	0.90	0.24	-	49,49,49,49	0
86	MG	5	3712	1/1	0.88	0.38	-	38,38,38,38	0
87	OHX	1	3857	7/7	0.98	0.27	-	54,54,54,54	4
86	MG	M6	202	1/1	0.79	0.29	-	40,40,40,40	0
87	OHX	2	2111	7/7	0.90	0.28	-	112,112,112,112	5
87	OHX	2	2039	7/7	0.98	0.17	-	103,103,103,103	7
86	MG	5	3641	1/1	0.94	0.44	-	39,39,39,39	0
87	OHX	1	3924	7/7	0.89	0.26	-	71,71,71,71	4
86	MG	1	3491	1/1	0.79	0.62	-	51,51,51,51	0
87	OHX	2	2018	7/7	0.98	0.16	-	74,74,74,74	5
87	OHX	1	3957	7/7	0.97	0.24	-	49,49,49,49	5
86	MG	5	3575	1/1	0.96	0.48	-	28,28,28,28	0
86	MG	5	3573	1/1	0.89	0.29	-	37,37,37,37	0
87	OHX	5	4112	7/7	0.96	0.28	-	52,52,52,52	6
86	MG	5	3679	1/1	0.46	0.42	-	70,70,70,70	0
86	MG	6	1953	1/1	0.84	0.42	-	63,63,63,63	0
86	MG	17	2201	1/1	0.91	0.27	-	46,46,46,46	0
87	OHX	5	4167	7/7	0.93	0.26	-	64,64,64,64	5
86	MG	5	3649	1/1	0.86	0.59	-	29,29,29,29	0
86	MG	M9	201	1/1	0.81	0.31	-	75,75,75,75	0
86	MG	2	1940	1/1	0.87	0.68	-	80,80,80,80	0
86	MG	5	3568	1/1	0.92	0.60	-	38,38,38,38	0
86	MG	4	209	1/1	0.98	0.46	-	63,63,63,63	0
86	MG	4	208	1/1	0.94	0.41	-	51,51,51,51	0
87	OHX	6	2157	7/7	0.91	0.23	-	90,90,90,90	7
86	MG	5	3676	1/1	0.95	0.35	-	29,29,29,29	0
86	MG	5	3450	1/1	0.86	0.48	-	40,40,40,40	0
86	MG	7	204	1/1	0.94	0.69	-	44,44,44,44	0
86	MG	5	3459	1/1	0.70	0.51	-	36,36,36,36	0
86	MG	1	3542	1/1	0.94	0.43	-	50,50,50,50	0
86	MG	5	3542	1/1	0.76	0.54	-	41,41,41,41	0
86	MG	1	3569	1/1	0.96	0.72	-	39,39,39,39	0
86	MG	N8	201	1/1	0.91	0.32	-	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	5	4080	7/7	0.94	0.42	-	35,35,35,35	3
86	MG	1	3581	1/1	0.97	0.81	-	29,29,29,29	0
86	MG	7	202	1/1	0.94	0.78	-	19,19,19,19	0
87	OHX	1	4046	7/7	0.93	0.36	-	50,50,50,50	2
87	OHX	1	4090	7/7	0.87	0.32	-	47,47,47,47	4
87	OHX	2	2152	7/7	0.87	0.31	-	122,122,122,122	6
86	MG	8	202	1/1	0.80	0.36	-	57,57,57,57	0
86	MG	1	3690	1/1	0.87	0.49	-	63,63,63,63	0
87	OHX	2	2118	7/7	0.94	0.15	-	143,143,143,143	7
86	MG	5	3684	1/1	0.71	0.92	-	48,48,48,48	0
87	OHX	1	4057	7/7	0.95	0.10	-	109,109,109,109	5
86	MG	2	1925	1/1	0.87	0.26	-	67,67,67,67	0
87	OHX	5	3889	7/7	0.97	0.20	-	69,69,69,69	3
86	MG	8	201	1/1	0.95	0.29	-	42,42,42,42	0
86	MG	1	3550	1/1	0.97	0.70	-	33,33,33,33	0
87	OHX	6	2168	7/7	0.86	0.26	-	76,76,76,76	3
87	OHX	1	3865	7/7	0.99	0.13	-	75,75,75,75	2
86	MG	5	3727	1/1	0.88	0.42	-	44,44,44,44	0
86	MG	6	1940	1/1	0.95	0.52	-	36,36,36,36	0
87	OHX	1	4045	7/7	0.95	0.31	-	54,54,54,54	1
86	MG	M7	201	1/1	0.69	0.58	-	71,71,71,71	0
86	MG	6	1962	1/1	0.95	0.15	-	93,93,93,93	0
86	MG	2	1988	1/1	0.95	0.13	-	88,88,88,88	0
87	OHX	5	3849	7/7	0.98	0.26	-	51,51,51,51	2
86	MG	1	3416	1/1	0.91	1.00	-	43,43,43,43	0
87	OHX	1	4026	7/7	0.90	0.37	-	52,52,52,52	5
87	OHX	5	3982	7/7	0.95	0.36	-	46,46,46,46	3
86	MG	1	3548	1/1	0.98	0.66	-	30,30,30,30	0
87	OHX	5	3930	7/7	0.99	0.26	-	54,54,54,54	4
87	OHX	5	4005	7/7	0.93	0.48	-	109,109,109,109	5
86	MG	2	1930	1/1	0.74	0.39	-	72,72,72,72	0
87	OHX	m5	304	7/7	0.98	0.28	-	54,54,54,54	3
86	MG	1	3463	1/1	0.86	0.34	-	39,39,39,39	0
86	MG	1	3541	1/1	0.96	0.65	-	28,28,28,28	0
86	MG	5	3598	1/1	0.74	0.57	-	39,39,39,39	0
86	MG	5	3647	1/1	0.95	0.32	-	37,37,37,37	0
87	OHX	5	3980	7/7	0.98	0.23	-	69,69,69,69	3
86	MG	2	1939	1/1	0.56	0.55	-	130,130,130,130	0
86	MG	6	1988	1/1	0.86	0.30	-	80,80,80,80	0
87	OHX	5	4165	7/7	0.78	0.54	-	49,49,49,49	4
86	MG	2	1974	1/1	0.67	0.38	-	83,83,83,83	0
86	MG	5	3636	1/1	0.67	0.57	-	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	1	3410	1/1	0.82	0.57	-	39,39,39,39	0
86	MG	1	3442	1/1	0.90	0.18	-	52,52,52,52	0
86	MG	1	3724	1/1	0.97	0.37	-	55,55,55,55	0
87	OHX	7	215	7/7	0.98	0.20	-	60,60,60,60	5
86	MG	5	3673	1/1	0.58	0.23	-	65,65,65,65	0
87	OHX	5	3858	7/7	0.99	0.24	-	55,55,55,55	1
86	MG	5	3801	1/1	0.84	0.76	-	44,44,44,44	0
86	MG	1	3456	1/1	0.99	0.41	-	32,32,32,32	0
86	MG	6	1927	1/1	0.91	0.34	-	63,63,63,63	0
86	MG	1	3712	1/1	0.94	0.53	-	44,44,44,44	0
87	OHX	5	4155	7/7	0.93	0.20	-	49,49,49,49	6
86	MG	L7	303	1/1	0.91	0.23	-	50,50,50,50	0
86	MG	1	3709	1/1	0.91	0.21	-	48,48,48,48	0
86	MG	5	3662	1/1	0.83	0.26	-	48,48,48,48	0
86	MG	6	1993	1/1	0.74	0.31	-	66,66,66,66	0
87	OHX	5	4171	7/7	0.87	0.65	-	45,45,45,45	3
87	OHX	5	3861	7/7	0.98	0.25	-	47,47,47,47	2
86	MG	6	1957	1/1	0.95	0.11	-	94,94,94,94	0
87	OHX	M9	202	7/7	0.86	0.20	-	77,77,77,77	3
87	OHX	1	3882	7/7	0.99	0.21	-	64,64,64,64	3
86	MG	1	3529	1/1	0.89	0.54	-	34,34,34,34	0
86	MG	5	3742	1/1	0.96	0.46	-	32,32,32,32	0
86	MG	5	3754	1/1	0.86	0.96	-	55,55,55,55	0
86	MG	6	2000	1/1	0.94	0.89	-	48,48,48,48	0
86	MG	1	3460	1/1	0.89	0.32	-	49,49,49,49	0
87	OHX	6	2148	7/7	0.95	0.30	-	54,54,54,54	3
86	MG	2	1985	1/1	0.58	0.53	-	86,86,86,86	0
86	MG	5	3659	1/1	0.97	0.62	-	46,46,46,46	0
87	OHX	5	4079	7/7	0.94	0.27	-	55,55,55,55	3
86	MG	6	1937	1/1	0.57	0.89	-	98,98,98,98	0
87	OHX	5	3973	7/7	0.95	0.30	-	53,53,53,53	4
86	MG	5	3547	1/1	0.88	0.59	-	25,25,25,25	0
87	OHX	2	2025	7/7	0.97	0.21	-	79,79,79,79	5
87	OHX	c3	201	7/7	0.93	0.26	-	84,84,84,84	4
87	OHX	1	3855	7/7	0.97	0.30	-	87,87,87,87	3
86	MG	5	3415	1/1	0.94	0.64	-	31,31,31,31	0
86	MG	5	3733	1/1	0.84	0.27	-	45,45,45,45	0
86	MG	1	3446	1/1	0.95	0.44	-	41,41,41,41	0
86	MG	5	3446	1/1	0.98	0.40	-	31,31,31,31	0
87	OHX	6	2118	7/7	0.91	0.35	-	89,89,89,89	5
86	MG	2	1903	1/1	0.89	0.66	-	43,43,43,43	0
86	MG	1	3695	1/1	0.65	0.40	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	1	3599	1/1	0.92	0.49	-	32,32,32,32	0
86	MG	5	3578	1/1	0.94	0.40	-	17,17,17,17	0
87	OHX	2	2081	7/7	0.95	0.20	-	120,120,120,120	6
87	OHX	1	3814	7/7	0.98	0.22	-	76,76,76,76	3
87	OHX	5	4118	7/7	0.90	0.35	-	52,52,52,52	3
86	MG	2	1901	1/1	0.82	0.25	-	87,87,87,87	0
86	MG	1	3525	1/1	0.93	0.69	-	35,35,35,35	0
87	OHX	1	3910	7/7	0.95	0.17	-	81,81,81,81	4
86	MG	1	3746	1/1	0.83	0.46	-	43,43,43,43	0
86	MG	1	4114	1/1	0.95	0.34	-	41,41,41,41	0
86	MG	1	3612	1/1	0.78	0.31	-	55,55,55,55	0
86	MG	5	3444	1/1	0.92	0.45	-	38,38,38,38	0
86	MG	5	3751	1/1	0.94	0.33	-	40,40,40,40	0
86	MG	5	3768	1/1	0.82	0.90	-	50,50,50,50	0
87	OHX	2	2130	7/7	0.87	0.32	-	84,84,84,84	4
87	OHX	5	3902	7/7	0.99	0.33	-	91,91,91,91	2
86	MG	5	3474	1/1	0.96	0.58	-	51,51,51,51	0
86	MG	4	205	1/1	0.82	0.74	-	44,44,44,44	0
86	MG	5	3533	1/1	0.97	0.54	-	25,25,25,25	0
86	MG	5	3759	1/1	0.86	0.22	-	53,53,53,53	0
86	MG	1	3677	1/1	0.84	0.34	-	46,46,46,46	0
86	MG	5	3721	1/1	0.95	0.69	-	41,41,41,41	0
87	OHX	5	4153	7/7	0.90	0.21	-	111,111,111,111	6
86	MG	1	3493	1/1	0.93	0.71	-	42,42,42,42	0
87	OHX	5	4092	7/7	0.96	0.18	-	55,55,55,55	6
86	MG	5	3799	1/1	0.96	0.28	-	70,70,70,70	0
86	MG	1	3745	1/1	0.79	0.48	-	53,53,53,53	0
87	OHX	5	4085	7/7	0.81	0.47	-	70,70,70,70	4
87	OHX	1	4106	7/7	0.85	0.20	-	72,72,72,72	4
87	OHX	2	2050	7/7	0.93	0.21	-	129,129,129,129	6
87	OHX	M7	205	7/7	0.93	0.19	-	57,57,57,57	5
86	MG	4	213	1/1	0.79	0.50	-	41,41,41,41	0
87	OHX	L3	402	7/7	0.98	0.19	-	59,59,59,59	4
86	MG	O3	201	1/1	0.93	0.56	-	37,37,37,37	0
87	OHX	6	2163	7/7	0.83	0.38	-	61,61,61,61	4
87	OHX	5	3990	7/7	0.94	0.47	-	37,37,37,37	3
86	MG	5	3494	1/1	0.93	0.38	-	33,33,33,33	0
87	OHX	1	3819	7/7	0.98	0.29	-	81,81,81,81	3
87	OHX	1	4088	7/7	0.93	0.21	-	92,92,92,92	7
87	OHX	1	3862	7/7	0.96	0.18	-	83,83,83,83	3
87	OHX	1	4089	7/7	0.80	0.38	-	55,55,55,55	6
87	OHX	1	4093	7/7	0.89	0.49	-	64,64,64,64	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	5	3807	1/1	0.95	0.23	-	36,36,36,36	0
86	MG	1	3721	1/1	0.93	0.47	-	43,43,43,43	0
87	OHX	O1	201	7/7	0.96	0.20	-	93,93,93,93	3
87	OHX	5	3988	7/7	0.94	0.22	-	158,158,158,158	5
86	MG	5	3483	1/1	0.96	0.65	-	28,28,28,28	0
86	MG	5	3713	1/1	0.78	0.41	-	36,36,36,36	0
86	MG	5	3809	1/1	0.94	0.36	-	50,50,50,50	0
86	MG	1	3622	1/1	0.89	0.64	-	44,44,44,44	0
86	MG	5	3703	1/1	0.97	0.69	-	2,2,2,2	0
86	MG	4	212	1/1	0.93	0.41	-	64,64,64,64	0
86	MG	1	3711	1/1	0.82	0.34	-	54,54,54,54	0
86	MG	6	1916	1/1	0.97	0.62	-	66,66,66,66	0
87	OHX	5	3983	7/7	0.97	0.30	-	56,56,56,56	4
86	MG	5	3612	1/1	0.69	0.54	-	42,42,42,42	0
87	OHX	1	3851	7/7	0.99	0.22	-	46,46,46,46	3
86	MG	5	3625	1/1	0.88	0.39	-	42,42,42,42	0
87	OHX	2	2140	7/7	0.93	0.29	-	85,85,85,85	5
87	OHX	6	2076	7/7	0.98	0.17	-	52,52,52,52	5
86	MG	6	2011	1/1	0.81	0.74	-	48,48,48,48	0
87	OHX	6	2132	7/7	0.95	0.24	-	94,94,94,94	6
86	MG	1	3424	1/1	0.94	0.44	-	59,59,59,59	0
87	OHX	2	2104	7/7	0.79	0.21	-	119,119,119,119	5
86	MG	5	3587	1/1	0.96	0.70	-	29,29,29,29	0
87	OHX	1	4037	7/7	0.93	0.35	-	84,84,84,84	7
86	MG	6	1950	1/1	0.90	0.36	-	66,66,66,66	0
86	MG	1	3666	1/1	0.88	0.49	-	65,65,65,65	0
87	OHX	1	4035	7/7	0.96	0.15	-	65,65,65,65	4
86	MG	6	1964	1/1	0.92	0.25	-	82,82,82,82	0
87	OHX	2	2145	7/7	0.87	0.22	-	103,103,103,103	4
86	MG	5	3734	1/1	0.96	0.22	-	37,37,37,37	0
86	MG	5	3433	1/1	0.99	0.51	-	33,33,33,33	0
87	OHX	2	2102	7/7	0.95	0.18	-	118,118,118,118	5
86	MG	1	3617	1/1	0.78	0.56	-	41,41,41,41	0
87	OHX	2	2103	7/7	0.92	0.38	-	118,118,118,118	4
87	OHX	1	3961	7/7	0.96	0.33	-	45,45,45,45	5
87	OHX	5	4122	7/7	0.86	0.40	-	76,76,76,76	5
86	MG	5	3602	1/1	0.87	0.27	-	50,50,50,50	0
86	MG	6	1998	1/1	0.91	0.69	-	42,42,42,42	0
86	MG	2	1965	1/1	0.55	0.86	-	76,76,76,76	0
86	MG	1	3753	1/1	0.91	0.79	-	107,107,107,107	0
87	OHX	N8	202	7/7	0.90	0.37	-	90,90,90,90	7
86	MG	2	1936	1/1	0.73	0.16	-	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	m4	201	7/7	0.96	0.70	-	108,108,108,108	7
87	OHX	6	2176	7/7	0.91	0.27	-	62,62,62,62	7
86	MG	1	3402	1/1	0.99	0.70	-	36,36,36,36	0
86	MG	5	3520	1/1	0.90	0.49	-	44,44,44,44	0
87	OHX	5	3835	7/7	0.99	0.19	-	65,65,65,65	3
86	MG	5	3642	1/1	0.88	0.68	-	64,64,64,64	0
86	MG	6	1921	1/1	0.92	0.45	-	66,66,66,66	0
86	MG	1	3411	1/1	0.94	0.55	-	43,43,43,43	0
86	MG	5	3660	1/1	0.85	0.36	-	64,64,64,64	0
87	OHX	6	2117	7/7	0.96	0.21	-	65,65,65,65	3
86	MG	1	3752	1/1	0.84	0.19	-	64,64,64,64	0
86	MG	1	3512	1/1	0.91	0.70	-	31,31,31,31	0
86	MG	1	3655	1/1	0.96	0.84	-	44,44,44,44	0
86	MG	6	1996	1/1	0.60	0.63	-	70,70,70,70	0
86	MG	6	2008	1/1	0.76	0.96	-	61,61,61,61	0
86	MG	1	3551	1/1	0.86	0.54	-	38,38,38,38	0
86	MG	5	3687	1/1	0.95	0.18	-	47,47,47,47	0
86	MG	5	3738	1/1	0.95	0.42	-	109,109,109,109	0
86	MG	1	3468	1/1	0.94	0.75	-	39,39,39,39	0
86	MG	2	1943	1/1	0.36	0.40	-	115,115,115,115	0
87	OHX	1	4063	7/7	0.89	0.13	-	159,159,159,159	7
87	OHX	5	3970	7/7	0.92	0.29	-	41,41,41,41	7
86	MG	5	3739	1/1	0.94	0.33	-	45,45,45,45	0
87	OHX	1	4077	7/7	0.90	0.23	-	62,62,62,62	4
87	OHX	6	2080	7/7	0.92	0.41	-	82,82,82,82	1
86	MG	7	213	1/1	0.96	0.19	-	49,49,49,49	0
86	MG	6	1983	1/1	0.88	0.89	-	57,57,57,57	0
86	MG	5	3792	1/1	0.94	0.68	-	37,37,37,37	0
87	OHX	1	3816	7/7	0.98	0.28	-	62,62,62,62	5
86	MG	1	3594	1/1	0.94	0.41	-	48,48,48,48	0
86	MG	5	3571	1/1	0.91	0.44	-	21,21,21,21	0
86	MG	5	3551	1/1	0.76	0.53	-	52,52,52,52	0
87	OHX	3	213	7/7	0.95	0.19	-	82,82,82,82	5
87	OHX	6	2024	7/7	0.99	0.15	-	99,99,99,99	3
86	MG	2	1906	1/1	0.83	0.38	-	68,68,68,68	0
87	OHX	5	4002	7/7	0.97	0.19	-	54,54,54,54	3
86	MG	1	3522	1/1	0.96	0.53	-	31,31,31,31	0
86	MG	1	3686	1/1	0.93	0.69	-	35,35,35,35	0
87	OHX	1	4041	7/7	0.93	0.23	-	46,46,46,46	4
87	OHX	2	2137	7/7	0.89	0.18	-	219,219,219,219	7
86	MG	1	3459	1/1	0.79	0.70	-	60,60,60,60	0
87	OHX	1	4036	7/7	0.94	0.15	-	83,83,83,83	6

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	1	3828	7/7	0.98	0.27	-	63,63,63,63	2
86	MG	1	3432	1/1	0.95	0.36	-	49,49,49,49	0
87	OHX	6	2113	7/7	0.97	0.27	-	67,67,67,67	3
86	MG	3	208	1/1	0.84	0.82	-	42,42,42,42	0
86	MG	5	3637	1/1	0.55	0.43	-	50,50,50,50	0
86	MG	1	3667	1/1	0.90	0.48	-	58,58,58,58	0
86	MG	5	3492	1/1	0.94	0.71	-	42,42,42,42	0
87	OHX	2	2109	7/7	0.84	0.29	-	105,105,105,105	6
87	OHX	2	2019	7/7	0.97	0.22	-	81,81,81,81	3
87	OHX	1	3916	7/7	0.96	0.42	-	54,54,54,54	4
86	MG	5	3410	1/1	0.86	0.51	-	44,44,44,44	0
86	MG	5	3488	1/1	0.91	0.56	-	39,39,39,39	0
86	MG	1	3654	1/1	0.94	0.43	-	39,39,39,39	0
86	MG	5	3425	1/1	0.74	0.47	-	45,45,45,45	0
87	OHX	5	4036	7/7	0.94	0.18	-	93,93,93,93	5
86	MG	5	3511	1/1	0.97	0.60	-	28,28,28,28	0
87	OHX	1	3905	7/7	0.97	0.22	-	57,57,57,57	1
86	MG	4	211	1/1	0.82	0.36	-	60,60,60,60	0
86	MG	2	1968	1/1	0.96	0.14	-	101,101,101,101	0
86	MG	5	3789	1/1	0.78	0.33	-	69,69,69,69	0
87	OHX	5	4022	7/7	0.97	0.24	-	39,39,39,39	2
86	MG	Q2	502	1/1	0.90	0.12	-	63,63,63,63	0
87	OHX	5	4136	7/7	0.90	0.42	-	50,50,50,50	4
86	MG	5	3525	1/1	0.97	0.47	-	29,29,29,29	0
86	MG	5	3406	1/1	0.93	0.59	-	35,35,35,35	0
86	MG	2	1955	1/1	0.86	0.96	-	62,62,62,62	0
87	OHX	5	3933	7/7	0.98	0.22	-	38,38,38,38	2
87	OHX	1	3960	7/7	0.95	0.20	-	42,42,42,42	4
87	OHX	1	4017	7/7	0.94	0.31	-	46,46,46,46	2
86	MG	5	3750	1/1	0.94	0.73	-	53,53,53,53	0
86	MG	8	208	1/1	0.79	0.67	-	55,55,55,55	0
86	MG	1	3630	1/1	0.88	0.38	-	76,76,76,76	0
86	MG	6	1955	1/1	0.88	0.42	-	60,60,60,60	0
87	OHX	5	3992	7/7	0.94	0.31	-	38,38,38,38	4
86	MG	1	3453	1/1	0.99	0.81	-	39,39,39,39	0
87	OHX	1	3909	7/7	0.98	0.37	-	73,73,73,73	4
87	OHX	2	2054	7/7	0.93	0.26	-	103,103,103,103	5
86	MG	5	3534	1/1	0.91	0.51	-	36,36,36,36	0
86	MG	6	1932	1/1	0.67	0.48	-	72,72,72,72	0
86	MG	6	1902	1/1	0.91	0.90	-	40,40,40,40	0
86	MG	1	3754	1/1	0.70	0.46	-	71,71,71,71	0
86	MG	2	1907	1/1	0.89	0.55	-	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	5	4144	7/7	0.96	0.22	-	70,70,70,70	7
87	OHX	5	4070	7/7	0.96	0.23	-	45,45,45,45	3
86	MG	1	3656	1/1	0.84	0.60	-	46,46,46,46	0
86	MG	5	3510	1/1	0.94	0.26	-	43,43,43,43	0
87	OHX	5	4066	7/7	0.95	0.36	-	34,34,34,34	4
87	OHX	5	3957	7/7	0.98	0.28	-	42,42,42,42	2
86	MG	6	1980	1/1	0.38	0.27	-	76,76,76,76	0
86	MG	S2	301	1/1	0.89	0.80	-	62,62,62,62	0
86	MG	1	3734	1/1	0.96	0.59	-	35,35,35,35	1
86	MG	1	3730	1/1	0.94	0.14	-	36,36,36,36	0
86	MG	1	3552	1/1	0.97	0.74	-	37,37,37,37	0
86	MG	5	3645	1/1	0.84	0.53	-	56,56,56,56	0
87	OHX	6	2036	7/7	0.98	0.21	-	58,58,58,58	3
86	MG	5	3623	1/1	0.96	0.38	-	31,31,31,31	0
86	MG	1	3716	1/1	0.96	0.33	-	65,65,65,65	0
86	MG	5	3762	1/1	0.83	0.65	-	38,38,38,38	0
86	MG	1	3420	1/1	0.82	0.41	-	45,45,45,45	0
86	MG	5	3438	1/1	0.90	0.46	-	30,30,30,30	0
86	MG	1	3699	1/1	0.94	0.29	-	49,49,49,49	0
86	MG	1	3755	1/1	0.84	0.35	-	45,45,45,45	0
87	OHX	6	2047	7/7	0.98	0.20	-	67,67,67,67	5
86	MG	1	3760	1/1	0.80	0.14	-	62,62,62,62	0
86	MG	1	3443	1/1	0.85	0.55	-	46,46,46,46	0
86	MG	1	3458	1/1	0.88	0.64	-	51,51,51,51	0
86	MG	l3	401	1/1	0.92	0.50	-	27,27,27,27	0
87	OHX	8	229	7/7	0.82	0.36	-	68,68,68,68	3
86	MG	5	3752	1/1	0.97	0.64	-	30,30,30,30	0
87	OHX	7	223	7/7	0.93	0.35	-	54,54,54,54	4
88	ZN	D7	101	1/1	0.69	0.39	-	161,161,161,161	0
87	OHX	1	4065	7/7	0.91	0.36	-	59,59,59,59	5
87	OHX	5	3918	7/7	0.95	0.29	-	73,73,73,73	3
87	OHX	5	4041	7/7	0.97	0.29	-	43,43,43,43	3
86	MG	7	211	1/1	0.89	0.48	-	57,57,57,57	0
86	MG	5	3658	1/1	0.86	0.37	-	39,39,39,39	0
86	MG	5	3652	1/1	0.97	0.29	-	47,47,47,47	0
86	MG	5	3795	1/1	0.97	0.45	-	42,42,42,42	0
86	MG	5	3475	1/1	0.98	0.30	-	42,42,42,42	0
86	MG	l5	301	1/1	0.93	0.15	-	63,63,63,63	0
87	OHX	2	2044	7/7	0.94	0.19	-	98,98,98,98	6
86	MG	5	3576	1/1	0.81	0.45	-	31,31,31,31	0
86	MG	1	3438	1/1	0.98	0.34	-	33,33,33,33	0
86	MG	5	3808	1/1	0.86	0.42	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	1	3611	1/1	0.93	0.27	-	41,41,41,41	0
86	MG	8	209	1/1	0.92	0.19	-	48,48,48,48	0
86	MG	1	3503	1/1	0.93	0.54	-	37,37,37,37	0
86	MG	5	3449	1/1	0.89	0.81	-	45,45,45,45	0
86	MG	1	3708	1/1	0.72	0.51	-	42,42,42,42	0
87	OHX	6	2173	7/7	0.87	0.27	-	64,64,64,64	5
87	OHX	6	2156	7/7	0.93	0.09	-	150,150,150,150	5
87	OHX	5	4104	7/7	0.90	0.28	-	84,84,84,84	4
86	MG	6	1930	1/1	0.96	0.72	-	45,45,45,45	0
87	OHX	1	4014	7/7	0.92	0.26	-	60,60,60,60	3
87	OHX	5	4004	7/7	0.95	0.20	-	82,82,82,82	3
86	MG	5	3675	1/1	0.87	0.27	-	51,51,51,51	0
86	MG	6	1914	1/1	0.82	0.77	-	62,62,62,62	0
86	MG	5	3482	1/1	0.72	0.86	-	52,52,52,52	0
86	MG	6	1928	1/1	0.90	0.38	-	57,57,57,57	0
86	MG	5	3681	1/1	0.86	0.45	-	45,45,45,45	0
87	OHX	1	4050	7/7	0.88	0.27	-	58,58,58,58	5
87	OHX	1	3772	7/7	0.99	0.20	-	67,67,67,67	2
86	MG	3	201	1/1	0.95	0.21	-	80,80,80,80	0
87	OHX	m9	201	7/7	0.92	0.22	-	61,61,61,61	6
87	OHX	1	4055	7/7	0.94	0.27	-	81,81,81,81	5
86	MG	5	3528	1/1	0.93	0.59	-	45,45,45,45	0
87	OHX	1	3987	7/7	0.96	0.22	-	73,73,73,73	5
86	MG	5	3710	1/1	0.94	0.47	-	32,32,32,32	0
86	MG	5	3531	1/1	0.93	0.66	-	35,35,35,35	0
86	MG	1	3639	1/1	0.77	0.70	-	56,56,56,56	0
87	OHX	4	230	7/7	0.95	0.19	-	75,75,75,75	5
86	MG	6	1961	1/1	0.75	0.16	-	95,95,95,95	0
86	MG	2	1977	1/1	0.91	0.99	-	72,72,72,72	0
86	MG	5	3786	1/1	0.92	0.27	-	33,33,33,33	0
86	MG	5	3698	1/1	0.95	0.32	-	39,39,39,39	0
87	OHX	5	3977	7/7	0.95	0.19	-	69,69,69,69	4
86	MG	5	3536	1/1	0.97	0.65	-	26,26,26,26	0
86	MG	5	3765	1/1	0.95	0.41	-	27,27,27,27	0
87	OHX	1	3796	7/7	0.98	0.27	-	57,57,57,57	4
86	MG	5	3691	1/1	0.93	0.32	-	38,38,38,38	0
86	MG	5	3770	1/1	0.86	0.42	-	36,36,36,36	0
87	OHX	m6	201	7/7	0.99	0.27	-	36,36,36,36	3
87	OHX	6	2182	7/7	0.91	0.34	-	113,113,113,113	7
86	MG	2	1952	1/1	0.92	0.45	-	64,64,64,64	0
86	MG	5	3622	1/1	0.83	0.46	-	42,42,42,42	0
87	OHX	5	3837	7/7	1.00	0.16	-	58,58,58,58	2

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	4	206	1/1	0.92	0.25	-	41,41,41,41	0
86	MG	6	1924	1/1	0.92	0.53	-	48,48,48,48	0
86	MG	1	3641	1/1	0.87	0.47	-	49,49,49,49	0
86	MG	1	3470	1/1	0.95	0.61	-	46,46,46,46	0
86	MG	5	3803	1/1	0.85	0.28	-	49,49,49,49	0
86	MG	6	1958	1/1	0.99	0.62	-	44,44,44,44	0
86	MG	5	3567	1/1	0.97	0.63	-	22,22,22,22	0
86	MG	1	3444	1/1	0.87	0.50	-	35,35,35,35	0
86	MG	8	207	1/1	0.83	0.49	-	51,51,51,51	0
87	OHX	1	3930	7/7	0.96	0.35	-	118,118,118,118	2
86	MG	1	3728	1/1	0.94	0.61	-	47,47,47,47	0
87	OHX	1	4034	7/7	0.97	0.31	-	75,75,75,75	3
86	MG	5	3469	1/1	0.91	0.18	-	56,56,56,56	0
86	MG	1	3717	1/1	0.90	0.57	-	59,59,59,59	0
86	MG	1	3665	1/1	0.78	0.70	-	48,48,48,48	0
86	MG	5	3711	1/1	0.82	0.32	-	67,67,67,67	0
86	MG	5	3730	1/1	0.93	0.45	-	55,55,55,55	0
86	MG	2	1917	1/1	0.90	0.54	-	54,54,54,54	0
87	OHX	5	3847	7/7	0.99	0.21	-	54,54,54,54	1
86	MG	5	3708	1/1	0.86	0.67	-	51,51,51,51	0
86	MG	5	3736	1/1	0.94	0.77	-	40,40,40,40	0
87	OHX	5	4016	7/7	0.89	0.39	-	36,36,36,36	2
86	MG	5	3460	1/1	0.89	0.28	-	57,57,57,57	0
86	MG	1	3707	1/1	0.84	0.56	-	48,48,48,48	0
86	MG	1	3697	1/1	0.91	0.31	-	42,42,42,42	0
87	OHX	1	4087	7/7	0.95	0.26	-	44,44,44,44	6
86	MG	14	401	1/1	0.77	0.49	-	42,42,42,42	0
86	MG	6	1941	1/1	0.92	0.52	-	57,57,57,57	0
86	MG	6	2001	1/1	0.89	0.42	-	48,48,48,48	0
86	MG	5	3761	1/1	0.89	0.65	-	38,38,38,38	0
86	MG	1	3473	1/1	0.89	0.30	-	56,56,56,56	0
86	MG	5	3626	1/1	0.88	0.24	-	47,47,47,47	0
86	MG	2	1984	1/1	0.96	0.37	-	67,67,67,67	0
86	MG	5	3694	1/1	0.89	0.58	-	54,54,54,54	0
87	OHX	8	221	7/7	0.95	0.15	-	100,100,100,100	5
87	OHX	1	4068	7/7	0.92	0.27	-	39,39,39,39	3
86	MG	5	3540	1/1	0.98	0.53	-	41,41,41,41	0
87	OHX	6	2086	7/7	0.92	0.27	-	70,70,70,70	5
87	OHX	5	3955	7/7	0.98	0.21	-	40,40,40,40	2
86	MG	f	1001	1/1	0.92	0.32	-	53,53,53,53	0
86	MG	4	201	1/1	0.92	0.21	-	44,44,44,44	0
86	MG	1	3505	1/1	0.83	0.80	-	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	1	3751	1/1	0.87	0.89	-	67,67,67,67	0
87	OHX	1	4111	7/7	0.91	0.15	-	104,104,104,104	7
86	MG	1	3607	1/1	0.85	0.55	-	85,85,85,85	0
87	OHX	1	4078	7/7	0.88	0.11	-	167,167,167,167	7
86	MG	1	3489	1/1	0.83	0.74	-	67,67,67,67	0
86	MG	1	3533	1/1	0.84	0.77	-	49,49,49,49	0
87	OHX	6	2060	7/7	0.95	0.20	-	96,96,96,96	1
86	MG	1	3431	1/1	0.96	0.39	-	47,47,47,47	0
86	MG	1	3694	1/1	0.94	0.20	-	46,46,46,46	0
86	MG	4	214	1/1	0.81	0.85	-	55,55,55,55	0
86	MG	6	1989	1/1	0.88	0.32	-	57,57,57,57	0
86	MG	1	3603	1/1	0.87	0.27	-	63,63,63,63	0
86	MG	1	3621	1/1	0.93	0.38	-	52,52,52,52	0
86	MG	5	3690	1/1	0.87	0.69	-	38,38,38,38	0
86	MG	5	3772	1/1	0.77	0.72	-	52,52,52,52	0
86	MG	1	3675	1/1	0.81	0.35	-	49,49,49,49	0
86	MG	5	3810	1/1	0.98	0.16	-	30,30,30,30	0
87	OHX	6	2042	7/7	0.99	0.28	-	62,62,62,62	3
86	MG	5	3615	1/1	0.89	0.22	-	42,42,42,42	0
87	OHX	1	4075	7/7	0.91	0.23	-	75,75,75,75	5
87	OHX	6	2098	7/7	0.96	0.22	-	87,87,87,87	5
86	MG	5	3760	1/1	0.96	0.19	-	38,38,38,38	0
86	MG	2	1951	1/1	0.85	0.37	-	71,71,71,71	0
86	MG	6	1984	1/1	0.44	0.35	-	109,109,109,109	0
87	OHX	1	3913	7/7	0.96	0.21	-	54,54,54,54	3
86	MG	1	3604	1/1	0.88	0.66	-	39,39,39,39	0
86	MG	3	202	1/1	0.81	0.44	-	56,56,56,56	0
87	OHX	1	3980	7/7	0.94	0.32	-	51,51,51,51	1
86	MG	6	1999	1/1	0.94	0.72	-	36,36,36,36	0
86	MG	q3	502	1/1	0.96	0.52	-	48,48,48,48	0
87	OHX	s4	602	7/7	0.95	0.19	-	76,76,76,76	3
86	MG	1	3628	1/1	0.94	0.64	-	41,41,41,41	0
86	MG	1	3600	1/1	0.47	0.35	-	60,60,60,60	0
87	OHX	1	4069	7/7	0.86	0.34	-	58,58,58,58	5
86	MG	5	3633	1/1	0.88	0.41	-	36,36,36,36	0
87	OHX	1	3811	7/7	0.98	0.30	-	79,79,79,79	2
87	OHX	8	226	7/7	0.97	0.19	-	59,59,59,59	3
86	MG	6	1934	1/1	0.97	0.34	-	43,43,43,43	0
87	OHX	5	4168	7/7	0.86	0.27	-	81,81,81,81	7
87	OHX	1	3810	7/7	0.98	0.28	-	62,62,62,62	3
87	OHX	6	2064	7/7	0.96	0.21	-	98,98,98,98	5
86	MG	1	4113	1/1	0.93	0.16	-	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	5	3487	1/1	0.86	0.35	-	44,44,44,44	0
86	MG	5	3476	1/1	0.98	0.43	-	27,27,27,27	0
86	MG	5	3695	1/1	0.81	0.55	-	45,45,45,45	0
87	OHX	6	2167	7/7	0.91	0.21	-	73,73,73,73	7
87	OHX	1	3986	7/7	0.94	0.21	-	76,76,76,76	3
86	MG	5	3485	1/1	0.90	0.35	-	51,51,51,51	0
86	MG	2	1924	1/1	0.94	0.53	-	100,100,100,100	0
86	MG	1	3591	1/1	0.75	0.29	-	53,53,53,53	0
87	OHX	2	1996	7/7	0.97	0.26	-	101,101,101,101	5
86	MG	2	1933	1/1	0.89	0.44	-	70,70,70,70	0
86	MG	2	1905	1/1	0.92	0.94	-	63,63,63,63	0
86	MG	2	1915	1/1	0.95	0.74	-	57,57,57,57	0
86	MG	1	3659	1/1	0.93	0.84	-	78,78,78,78	0
86	MG	6	1911	1/1	0.92	0.51	-	49,49,49,49	0
87	OHX	6	2171	7/7	0.91	0.37	-	53,53,53,53	7
86	MG	2	1918	1/1	0.98	0.36	-	68,68,68,68	0
87	OHX	6	2120	7/7	0.92	0.21	-	70,70,70,70	3
86	MG	1	3408	1/1	0.92	0.46	-	25,25,25,25	0
86	MG	6	2007	1/1	0.85	0.97	-	51,51,51,51	0
87	OHX	5	4091	7/7	0.95	0.45	-	33,33,33,33	2
87	OHX	5	4105	7/7	0.93	0.30	-	32,32,32,32	4
86	MG	5	3781	1/1	0.86	0.21	-	48,48,48,48	0
87	OHX	5	3867	7/7	0.98	0.24	-	74,74,74,74	2
86	MG	5	3526	1/1	0.97	0.43	-	32,32,32,32	0
86	MG	6	1919	1/1	0.82	1.06	-	64,64,64,64	0
87	OHX	m1	201	7/7	0.80	0.35	-	78,78,78,78	3
86	MG	5	3514	1/1	0.88	0.34	-	42,42,42,42	0
86	MG	1	3625	1/1	0.98	0.41	-	41,41,41,41	0
86	MG	5	3447	1/1	0.68	0.45	-	36,36,36,36	0
86	MG	6	1913	1/1	0.90	0.27	-	79,79,79,79	0
86	MG	1	3689	1/1	0.96	0.31	-	44,44,44,44	0
86	MG	2	1921	1/1	0.81	0.73	-	63,63,63,63	0
86	MG	1	3597	1/1	0.96	0.38	-	47,47,47,47	0
87	OHX	1	3801	7/7	0.99	0.18	-	71,71,71,71	3
87	OHX	1	4110	7/7	0.92	0.25	-	55,55,55,55	5
86	MG	5	3706	1/1	0.91	0.39	-	64,64,64,64	0
87	OHX	5	3871	7/7	0.97	0.27	-	82,82,82,82	3
86	MG	1	3485	1/1	0.92	0.28	-	58,58,58,58	0
86	MG	1	3418	1/1	0.92	0.69	-	47,47,47,47	0
86	MG	5	3448	1/1	0.87	0.43	-	32,32,32,32	0
86	MG	5	3632	1/1	0.98	0.42	-	34,34,34,34	0
86	MG	5	3489	1/1	0.95	0.33	-	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
86	MG	1	3520	1/1	0.89	0.49	-	35,35,35,35	0
87	OHX	6	2180	7/7	0.95	0.15	-	97,97,97,97	6
87	OHX	1	4052	7/7	0.94	0.36	-	58,58,58,58	4
87	OHX	6	2125	7/7	0.92	0.33	-	52,52,52,52	5
86	MG	M5	301	1/1	0.94	0.77	-	47,47,47,47	0
87	OHX	5	4129	7/7	0.86	0.16	-	171,171,171,171	7
86	MG	5	3814	1/1	0.85	0.75	-	44,44,44,44	0
86	MG	4	210	1/1	0.91	0.32	-	54,54,54,54	0
86	MG	5	3746	1/1	0.94	0.70	-	51,51,51,51	0
86	MG	2	1964	1/1	0.83	0.33	-	92,92,92,92	0
86	MG	L7	301	1/1	0.92	0.28	-	38,38,38,38	0
87	OHX	2	2083	7/7	0.95	0.47	-	87,87,87,87	2
86	MG	5	3776	1/1	0.81	0.42	-	41,41,41,41	0
87	OHX	5	4030	7/7	0.94	0.23	-	85,85,85,85	4
86	MG	1	3720	1/1	0.95	0.52	-	48,48,48,48	0
86	MG	1	3725	1/1	0.91	0.29	-	38,38,38,38	0
86	MG	1	3502	1/1	0.97	0.90	-	30,30,30,30	0
87	OHX	5	4063	7/7	0.97	0.31	-	52,52,52,52	3
86	MG	5	3709	1/1	0.94	0.38	-	55,55,55,55	0
86	MG	5	3790	1/1	0.89	0.20	-	46,46,46,46	0
86	MG	5	3773	1/1	0.82	0.69	-	55,55,55,55	0
86	MG	5	3603	1/1	0.88	0.37	-	33,33,33,33	0
87	OHX	1	4042	7/7	0.94	0.18	-	70,70,70,70	5
86	MG	1	3513	1/1	0.96	0.30	-	34,34,34,34	0
87	OHX	6	2037	7/7	0.98	0.23	-	101,101,101,101	3
86	MG	3	206	1/1	0.88	0.19	-	65,65,65,65	0
87	OHX	1	3921	7/7	0.98	0.13	-	82,82,82,82	3
87	OHX	5	4023	7/7	0.94	0.23	-	66,66,66,66	5
86	MG	5	3498	1/1	0.90	0.41	-	42,42,42,42	0
86	MG	1	3691	1/1	0.89	0.23	-	64,64,64,64	0
86	MG	1	3636	1/1	0.87	0.78	-	53,53,53,53	0
86	MG	2	1972	1/1	0.89	0.51	-	57,57,57,57	0
86	MG	q1	101	1/1	0.96	0.28	-	50,50,50,50	0
87	OHX	1	3949	7/7	0.92	0.46	-	111,111,111,111	7
86	MG	5	3424	1/1	0.95	0.26	-	41,41,41,41	0
87	OHX	5	4160	7/7	0.88	0.26	-	123,123,123,123	7
87	OHX	6	2085	7/7	0.99	0.32	-	76,76,76,76	2
87	OHX	1	3970	7/7	0.96	0.14	-	68,68,68,68	1
86	MG	6	1963	1/1	0.90	0.46	-	80,80,80,80	0
86	MG	1	3731	1/1	0.94	0.47	-	57,57,57,57	0
86	MG	1	3471	1/1	0.85	0.52	-	45,45,45,45	0
87	OHX	6	2136	7/7	0.91	0.33	-	62,62,62,62	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	5	4138	7/7	0.86	0.17	-	108,108,108,108	5
87	OHX	5	4098	7/7	0.93	0.23	-	73,73,73,73	5
87	OHX	1	3946	7/7	0.96	0.21	-	69,69,69,69	3
87	OHX	1	4067	7/7	0.87	0.29	-	107,107,107,107	7
87	OHX	5	4051	7/7	0.98	0.16	-	67,67,67,67	5
86	MG	6	1971	1/1	0.85	0.46	-	90,90,90,90	0
86	MG	1	3638	1/1	0.81	0.98	-	48,48,48,48	0
86	MG	2	1959	1/1	0.72	0.29	-	87,87,87,87	0
86	MG	1	3648	1/1	0.88	0.42	-	42,42,42,42	0
86	MG	5	3718	1/1	0.91	0.29	-	63,63,63,63	1
86	MG	1	3450	1/1	0.93	0.42	-	31,31,31,31	0
87	OHX	2	2128	7/7	0.95	0.11	-	115,115,115,115	7
86	MG	5	3503	1/1	0.97	0.53	-	28,28,28,28	0
87	OHX	1	3989	7/7	0.96	0.20	-	94,94,94,94	5
86	MG	5	3572	1/1	0.77	0.26	-	48,48,48,48	0
86	MG	5	3725	1/1	0.82	0.62	-	46,46,46,46	0
87	OHX	5	4078	7/7	0.94	0.26	-	54,54,54,54	5
86	MG	5	3724	1/1	0.96	0.26	-	51,51,51,51	0
86	MG	1	3692	1/1	0.71	0.55	-	61,61,61,61	0
86	MG	5	3499	1/1	0.81	0.46	-	40,40,40,40	0
87	OHX	1	3919	7/7	0.95	0.12	-	106,106,106,106	3
87	OHX	5	4045	7/7	0.92	0.18	-	53,53,53,53	5
86	MG	5	3683	1/1	0.90	0.28	-	62,62,62,62	0
87	OHX	1	3858	7/7	0.97	0.15	-	98,98,98,98	4
86	MG	5	3430	1/1	0.93	0.40	-	41,41,41,41	0
86	MG	2	1949	1/1	0.79	1.01	-	86,86,86,86	0
86	MG	5	3775	1/1	0.97	0.13	-	75,75,75,75	0
86	MG	5	3502	1/1	0.74	0.50	-	57,57,57,57	0
87	OHX	5	3924	7/7	0.99	0.20	-	56,56,56,56	3
86	MG	6	2009	1/1	0.84	0.68	-	64,64,64,64	0
87	OHX	6	2140	7/7	0.92	0.27	-	74,74,74,74	6
86	MG	17	2200	1/1	0.58	0.31	-	50,50,50,50	0
87	OHX	2	2017	7/7	0.97	0.37	-	74,74,74,74	4
87	OHX	1	3795	7/7	0.98	0.16	-	85,85,85,85	2
86	MG	6	1947	1/1	0.90	0.46	-	50,50,50,50	0
87	OHX	2	2138	7/7	0.90	0.27	-	67,67,67,67	5
87	OHX	1	3954	7/7	0.97	0.22	-	122,122,122,122	3
87	OHX	6	2129	7/7	0.98	0.34	-	58,58,58,58	5
86	MG	6	1917	1/1	0.84	0.44	-	64,64,64,64	0
86	MG	2	1947	1/1	0.96	0.21	-	76,76,76,76	0
87	OHX	5	3946	7/7	0.98	0.26	-	45,45,45,45	3
86	MG	5	3432	1/1	0.94	0.33	-	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
87	OHX	5	3960	7/7	0.98	0.14	-	74,74,74,74	1
87	OHX	1	4025	7/7	0.96	0.21	-	56,56,56,56	3
86	MG	5	3621	1/1	0.89	0.36	-	62,62,62,62	0
86	MG	6	1987	1/1	0.90	0.51	-	77,77,77,77	0
86	MG	5	3813	1/1	0.88	1.03	-	42,42,42,42	0
86	MG	8	204	1/1	0.93	0.32	-	43,43,43,43	0
87	OHX	1	4021	7/7	0.91	0.41	-	58,58,58,58	3
86	MG	1	3643	1/1	0.88	0.83	-	38,38,38,38	0
86	MG	5	3635	1/1	0.95	0.55	-	43,43,43,43	0
86	MG	1	3685	1/1	0.85	0.30	-	43,43,43,43	0
86	MG	1	3723	1/1	0.76	0.55	-	67,67,67,67	0
86	MG	5	3700	1/1	0.95	0.37	-	38,38,38,38	0
86	MG	6	1920	1/1	0.89	0.43	-	46,46,46,46	0
86	MG	1	3515	1/1	0.94	0.40	-	28,28,28,28	0
86	MG	5	3745	1/1	0.71	0.46	-	76,76,76,76	0
86	MG	1	3532	1/1	0.92	0.32	-	42,42,42,42	0
86	MG	5	3811	1/1	0.96	0.39	-	32,32,32,32	0
86	MG	6	1976	1/1	0.95	0.19	-	32,32,32,32	0
86	MG	6	1946	1/1	0.89	0.69	-	53,53,53,53	0
86	MG	5	3490	1/1	0.82	0.69	-	41,41,41,41	0
86	MG	2	1945	1/1	0.80	0.23	-	107,107,107,107	0
86	MG	6	1907	1/1	0.87	0.42	-	51,51,51,51	0
86	MG	2	1986	1/1	0.40	0.40	-	118,118,118,118	0
86	MG	7	207	1/1	0.76	0.44	-	55,55,55,55	0
86	MG	5	3616	1/1	0.95	0.83	-	35,35,35,35	0
86	MG	1	3487	1/1	0.87	0.41	-	49,49,49,49	0
86	MG	o2	201	1/1	0.92	0.61	-	35,35,35,35	1

6.5 Other polymers [i](#)

There are no such residues in this entry.