



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 29, 2016 – 09:20 PM EDT

PDB ID : 5HD1
Title : Crystal structure of antimicrobial peptide Pyrrhocoricin bound to the *Thermus thermophilus* 70S ribosome
Authors : Gagnon, M.G.; Roy, R.N.; Lomakin, I.B.; Florin, T.; Mankin, A.S.; Steitz, T.A.
Deposited on : 2016-01-04
Resolution : 2.70 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-20027107
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-20027107

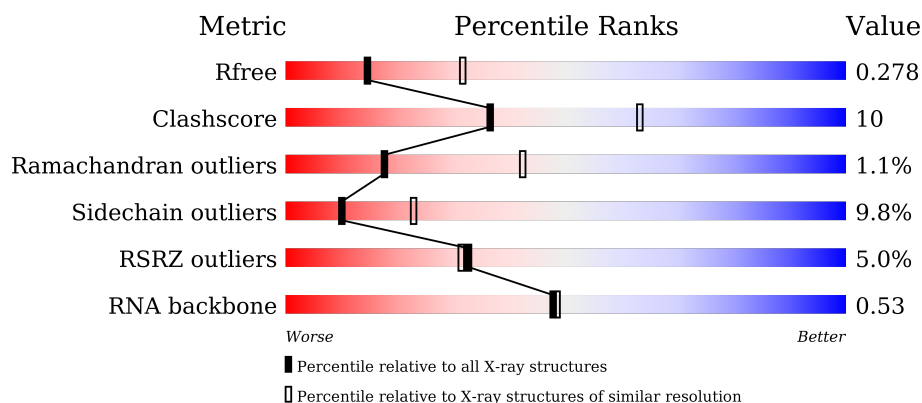
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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))
R_{free}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)
RNA backbone	2183	1069 (3.10-2.30)

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	1A	2915	<div> <div>62%</div> <div>26%</div> <div>6%</div> <div>6%</div> </div>
1	2A	2915	<div> <div>3%</div> <div>52%</div> <div>36%</div> <div>7%</div> <div>.</div> </div>
2	1B	121	<div> <div>74%</div> <div>25%</div> <div>.</div> </div>
2	2B	121	<div> <div>2%</div> <div>37%</div> <div>52%</div> <div>10%</div> <div>.</div> </div>



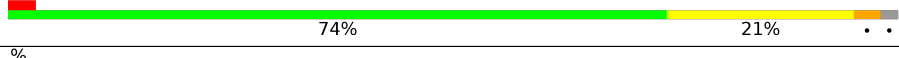

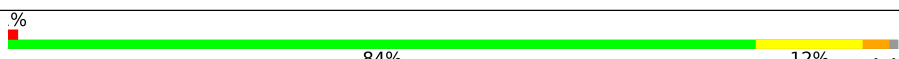

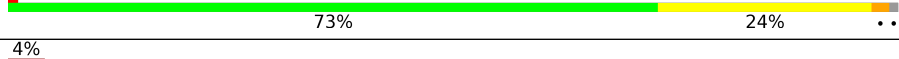

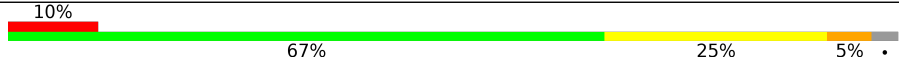


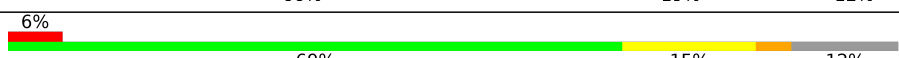




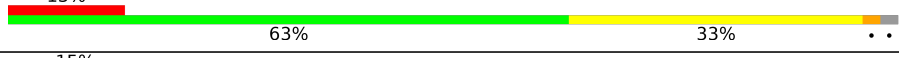






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Mol	Chain	Length	Quality of chain
3	1D	276	
3	2D	276	
4	1E	206	
4	2E	206	
5	1F	210	
5	2F	210	
6	1G	182	
6	2G	182	
7	1H	180	
7	2H	180	
8	1I	148	
8	2I	148	
9	1N	140	
9	2N	140	
10	1O	122	
10	2O	122	
11	1P	150	
11	2P	150	
12	1Q	141	
12	2Q	141	
13	1R	118	
13	2R	118	
14	1S	112	
14	2S	112	
15	1T	146	




















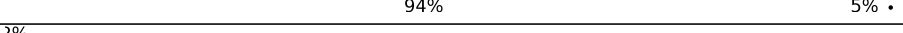
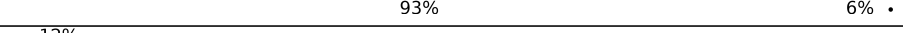




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Mol	Chain	Length	Quality of chain
15	2T	146	
16	1U	118	
16	2U	118	
17	1V	101	
17	2V	101	
18	1W	113	
18	2W	113	
19	1X	96	
19	2X	96	
20	1Y	110	
20	2Y	110	
21	1Z	206	
21	2Z	206	
22	10	85	
22	20	85	
23	11	98	
23	21	98	
24	12	72	
24	22	72	
25	13	60	
25	23	60	
26	14	71	
26	24	71	
27	15	60	
27	25	60	

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Mol	Chain	Length	Quality of chain
28	16	54	
28	26	54	
29	17	49	
29	27	49	
30	18	65	
30	28	65	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	
39	2h	138	
40	1i	128	


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Mol	Chain	Length	Quality of chain
40	2i	128	
41	1j	105	
41	2j	105	
42	1k	129	
42	2k	129	
43	1l	132	
43	2l	132	
44	1m	126	
44	2m	126	
45	1n	61	
45	2n	61	
46	1o	89	
46	2o	89	
47	1p	88	
47	2p	88	
48	1q	105	
48	2q	105	
49	1r	88	
49	2r	88	
50	1s	93	
50	2s	93	
51	1t	106	
51	2t	106	
52	1u	27	
52	2u	27	

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Mol	Chain	Length	Quality of chain
53	1v	24	
53	2v	24	
54	1x	77	
54	2x	77	
55	1z	20	
55	2z	20	

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
56	MG	17	101	-	-	-	X
56	MG	1A	3001	-	-	-	X
56	MG	1A	3009	-	-	-	X
56	MG	1A	3018	-	-	-	X
56	MG	1A	3042	-	-	-	X
56	MG	1A	3053	-	-	-	X
56	MG	1A	3090	-	-	-	X
56	MG	1A	3118	-	-	-	X
56	MG	1A	3126	-	-	-	X
56	MG	1A	3128	-	-	-	X
56	MG	1A	3129	-	-	-	X
56	MG	1A	3147	-	-	-	X
56	MG	1A	3163	-	-	-	X
56	MG	1A	3166	-	-	-	X
56	MG	1A	3173	-	-	-	X
56	MG	1A	3177	-	-	-	X
56	MG	1A	3178	-	-	-	X
56	MG	1A	3179	-	-	-	X
56	MG	1A	3183	-	-	-	X
56	MG	1A	3186	-	-	-	X
56	MG	1A	3191	-	-	-	X
56	MG	1A	3193	-	-	-	X
56	MG	1A	3198	-	-	-	X
56	MG	1A	3203	-	-	-	X
56	MG	1A	3212	-	-	-	X
56	MG	1A	3217	-	-	-	X
56	MG	1A	3229	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	1A	3245	-	-	-	X
56	MG	1A	3262	-	-	-	X
56	MG	1A	3285	-	-	-	X
56	MG	1A	3290	-	-	-	X
56	MG	1A	3305	-	-	-	X
56	MG	1A	3310	-	-	-	X
56	MG	1A	3312	-	-	-	X
56	MG	1A	3324	-	-	-	X
56	MG	1A	3326	-	-	-	X
56	MG	1A	3333	-	-	-	X
56	MG	1A	3336	-	-	-	X
56	MG	1A	3369	-	-	-	X
56	MG	1A	3385	-	-	-	X
56	MG	1A	3386	-	-	-	X
56	MG	1A	3398	-	-	-	X
56	MG	1A	3399	-	-	-	X
56	MG	1A	3409	-	-	-	X
56	MG	1A	3411	-	-	-	X
56	MG	1A	3417	-	-	-	X
56	MG	1A	3418	-	-	-	X
56	MG	1A	3420	-	-	-	X
56	MG	1A	3463	-	-	-	X
56	MG	1A	3485	-	-	-	X
56	MG	1A	3496	-	-	-	X
56	MG	1A	3519	-	-	-	X
56	MG	1A	3525	-	-	-	X
56	MG	1A	3531	-	-	-	X
56	MG	1A	3541	-	-	-	X
56	MG	1A	3553	-	-	-	X
56	MG	1A	3556	-	-	-	X
56	MG	1A	3562	-	-	-	X
56	MG	1A	3571	-	-	-	X
56	MG	1A	3572	-	-	-	X
56	MG	1A	3597	-	-	-	X
56	MG	1A	3607	-	-	-	X
56	MG	1A	3611	-	-	-	X
56	MG	1A	3613	-	-	-	X
56	MG	1A	3618	-	-	-	X
56	MG	1A	3621	-	-	-	X
56	MG	1A	3624	-	-	-	X
56	MG	1A	3634	-	-	-	X
56	MG	1A	3635	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	1A	3636	-	-	-	X
56	MG	1A	3665	-	-	-	X
56	MG	1A	3669	-	-	-	X
56	MG	1A	3670	-	-	-	X
56	MG	1A	3671	-	-	-	X
56	MG	1A	3673	-	-	-	X
56	MG	1A	3680	-	-	-	X
56	MG	1A	3685	-	-	-	X
56	MG	1A	3687	-	-	-	X
56	MG	1A	3694	-	-	-	X
56	MG	1A	3702	-	-	-	X
56	MG	1A	3704	-	-	-	X
56	MG	1A	3708	-	-	-	X
56	MG	1A	3712	-	-	-	X
56	MG	1A	3716	-	-	-	X
56	MG	1A	3728	-	-	-	X
56	MG	1A	3747	-	-	-	X
56	MG	1A	3761	-	-	-	X
56	MG	1A	3762	-	-	-	X
56	MG	1A	3765	-	-	-	X
56	MG	1A	3772	-	-	-	X
56	MG	1A	3788	-	-	-	X
56	MG	1A	3835	-	-	-	X
56	MG	1A	3838	-	-	-	X
56	MG	1A	3842	-	-	-	X
56	MG	1A	3875	-	-	-	X
56	MG	1A	3884	-	-	-	X
56	MG	1A	3896	-	-	-	X
56	MG	1A	3905	-	-	-	X
56	MG	1A	3909	-	-	-	X
56	MG	1A	3918	-	-	-	X
56	MG	1A	3925	-	-	-	X
56	MG	1A	3945	-	-	-	X
56	MG	1A	3948	-	-	-	X
56	MG	1A	3976	-	-	-	X
56	MG	1A	3992	-	-	-	X
56	MG	1A	3995	-	-	-	X
56	MG	1A	4018	-	-	-	X
56	MG	1A	4022	-	-	-	X
56	MG	1A	4052	-	-	-	X
56	MG	1A	4077	-	-	-	X
56	MG	1A	4095	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	1A	4107	-	-	-	X
56	MG	1A	4153	-	-	-	X
56	MG	1A	4165	-	-	-	X
56	MG	1A	4170	-	-	-	X
56	MG	1A	4180	-	-	-	X
56	MG	1A	4185	-	-	-	X
56	MG	1A	4186	-	-	-	X
56	MG	1A	4202	-	-	-	X
56	MG	1A	4207	-	-	-	X
56	MG	1A	4209	-	-	-	X
56	MG	1A	4210	-	-	-	X
56	MG	1A	4219	-	-	-	X
56	MG	1A	4224	-	-	-	X
56	MG	1A	4229	-	-	-	X
56	MG	1A	4230	-	-	-	X
56	MG	1B	203	-	-	-	X
56	MG	1D	301	-	-	-	X
56	MG	1D	302	-	-	-	X
56	MG	1D	303	-	-	-	X
56	MG	1D	304	-	-	-	X
56	MG	1D	306	-	-	-	X
56	MG	1D	309	-	-	-	X
56	MG	1D	312	-	-	-	X
56	MG	1D	313	-	-	-	X
56	MG	1D	314	-	-	-	X
56	MG	1E	304	-	-	-	X
56	MG	1F	304	-	-	-	X
56	MG	1F	307	-	-	-	X
56	MG	1N	202	-	-	-	X
56	MG	1P	205	-	-	-	X
56	MG	1Q	201	-	-	-	X
56	MG	1Q	204	-	-	-	X
56	MG	1R	202	-	-	-	X
56	MG	1U	203	-	-	-	X
56	MG	1U	204	-	-	-	X
56	MG	1U	205	-	-	-	X
56	MG	1U	206	-	-	-	X
56	MG	1V	201	-	-	-	X
56	MG	1X	3001	-	-	-	X
56	MG	1a	1622	-	-	-	X
56	MG	1a	1630	-	-	-	X
56	MG	1a	1642	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	1a	1644	-	-	-	X
56	MG	1a	1648	-	-	-	X
56	MG	1a	1652	-	-	-	X
56	MG	1a	1668	-	-	-	X
56	MG	1a	1675	-	-	-	X
56	MG	1a	1681	-	-	-	X
56	MG	1a	1693	-	-	-	X
56	MG	1a	1696	-	-	-	X
56	MG	1a	1702	-	-	-	X
56	MG	1a	1708	-	-	-	X
56	MG	1a	1713	-	-	-	X
56	MG	1a	1714	-	-	-	X
56	MG	1a	1717	-	-	-	X
56	MG	1a	1720	-	-	-	X
56	MG	1a	1723	-	-	-	X
56	MG	1a	1738	-	-	-	X
56	MG	1a	1741	-	-	-	X
56	MG	1a	1768	-	-	-	X
56	MG	1a	1791	-	-	-	X
56	MG	1a	1798	-	-	-	X
56	MG	1a	1799	-	-	-	X
56	MG	1a	1822	-	-	-	X
56	MG	1a	1825	-	-	-	X
56	MG	1a	1888	-	-	-	X
56	MG	1t	3001	-	-	-	X
56	MG	25	502	-	-	-	X
56	MG	2A	3031	-	-	-	X
56	MG	2A	3032	-	-	-	X
56	MG	2A	3049	-	-	-	X
56	MG	2A	3052	-	-	-	X
56	MG	2A	3053	-	-	-	X
56	MG	2A	3056	-	-	-	X
56	MG	2A	3061	-	-	-	X
56	MG	2A	3062	-	-	-	X
56	MG	2A	3092	-	-	-	X
56	MG	2A	3100	-	-	-	X
56	MG	2A	3101	-	-	-	X
56	MG	2A	3103	-	-	-	X
56	MG	2A	3105	-	-	-	X
56	MG	2A	3108	-	-	-	X
56	MG	2A	3113	-	-	-	X
56	MG	2A	3114	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	2A	3118	-	-	-	X
56	MG	2A	3119	-	-	-	X
56	MG	2A	3128	-	-	-	X
56	MG	2A	3137	-	-	-	X
56	MG	2A	3139	-	-	-	X
56	MG	2A	3144	-	-	-	X
56	MG	2A	3145	-	-	-	X
56	MG	2A	3157	-	-	-	X
56	MG	2A	3158	-	-	-	X
56	MG	2A	3159	-	-	-	X
56	MG	2A	3161	-	-	-	X
56	MG	2A	3182	-	-	-	X
56	MG	2A	3183	-	-	-	X
56	MG	2A	3184	-	-	-	X
56	MG	2A	3186	-	-	-	X
56	MG	2A	3187	-	-	-	X
56	MG	2A	3192	-	-	-	X
56	MG	2A	3196	-	-	-	X
56	MG	2A	3200	-	-	-	X
56	MG	2A	3206	-	-	-	X
56	MG	2A	3207	-	-	-	X
56	MG	2A	3216	-	-	-	X
56	MG	2A	3217	-	-	-	X
56	MG	2A	3219	-	-	-	X
56	MG	2A	3225	-	-	-	X
56	MG	2A	3234	-	-	-	X
56	MG	2A	3236	-	-	-	X
56	MG	2A	3237	-	-	-	X
56	MG	2A	3256	-	-	-	X
56	MG	2A	3260	-	-	-	X
56	MG	2A	3262	-	-	-	X
56	MG	2A	3282	-	-	-	X
56	MG	2A	3283	-	-	-	X
56	MG	2A	3285	-	-	-	X
56	MG	2A	3287	-	-	-	X
56	MG	2A	3289	-	-	-	X
56	MG	2A	3290	-	-	-	X
56	MG	2A	3293	-	-	-	X
56	MG	2A	3294	-	-	-	X
56	MG	2A	3296	-	-	-	X
56	MG	2A	3300	-	-	-	X
56	MG	2A	3302	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	2A	3309	-	-	-	X
56	MG	2A	3310	-	-	-	X
56	MG	2A	3312	-	-	-	X
56	MG	2A	3315	-	-	-	X
56	MG	2A	3319	-	-	-	X
56	MG	2A	3321	-	-	-	X
56	MG	2A	3323	-	-	-	X
56	MG	2A	3325	-	-	-	X
56	MG	2A	3331	-	-	-	X
56	MG	2A	3336	-	-	-	X
56	MG	2A	3337	-	-	-	X
56	MG	2A	3353	-	-	-	X
56	MG	2A	3355	-	-	-	X
56	MG	2A	3361	-	-	-	X
56	MG	2A	3373	-	-	-	X
56	MG	2A	3374	-	-	-	X
56	MG	2A	3383	-	-	-	X
56	MG	2A	3390	-	-	-	X
56	MG	2A	3398	-	-	-	X
56	MG	2A	3408	-	-	-	X
56	MG	2A	3412	-	-	-	X
56	MG	2A	3414	-	-	-	X
56	MG	2A	3418	-	-	-	X
56	MG	2A	3427	-	-	-	X
56	MG	2A	3440	-	-	-	X
56	MG	2A	3447	-	-	-	X
56	MG	2A	3453	-	-	-	X
56	MG	2A	3463	-	-	-	X
56	MG	2A	3467	-	-	-	X
56	MG	2A	3478	-	-	-	X
56	MG	2A	3480	-	-	-	X
56	MG	2A	3528	-	-	-	X
56	MG	2A	3533	-	-	-	X
56	MG	2A	3534	-	-	-	X
56	MG	2A	3535	-	-	-	X
56	MG	2A	3540	-	-	-	X
56	MG	2A	3541	-	-	-	X
56	MG	2A	3543	-	-	-	X
56	MG	2A	3550	-	-	-	X
56	MG	2A	3552	-	-	-	X
56	MG	2A	3559	-	-	-	X
56	MG	2A	3563	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	2A	3567	-	-	-	X
56	MG	2A	3569	-	-	-	X
56	MG	2A	3571	-	-	-	X
56	MG	2A	3573	-	-	-	X
56	MG	2A	3574	-	-	-	X
56	MG	2A	3576	-	-	-	X
56	MG	2A	3581	-	-	-	X
56	MG	2A	3582	-	-	-	X
56	MG	2A	3583	-	-	-	X
56	MG	2A	3585	-	-	-	X
56	MG	2A	3587	-	-	-	X
56	MG	2A	3588	-	-	-	X
56	MG	2A	3590	-	-	-	X
56	MG	2B	3002	-	-	-	X
56	MG	2D	301	-	-	-	X
56	MG	2D	303	-	-	-	X
56	MG	2D	305	-	-	-	X
56	MG	2F	302	-	-	-	X
56	MG	2Q	3003	-	-	-	X
56	MG	2a	1604	-	-	-	X
56	MG	2a	1607	-	-	-	X
56	MG	2a	1613	-	-	-	X
56	MG	2a	1622	-	-	-	X
56	MG	2a	1628	-	-	-	X
56	MG	2a	1631	-	-	-	X
56	MG	2a	1640	-	-	-	X
56	MG	2a	1676	-	-	-	X
56	MG	2a	1682	-	-	-	X
56	MG	2a	1695	-	-	-	X
56	MG	2a	1706	-	-	-	X
56	MG	2a	1707	-	-	-	X
56	MG	2a	1720	-	-	-	X
56	MG	2a	1724	-	-	-	X
56	MG	2a	1739	-	-	-	X
56	MG	2a	1740	-	-	-	X
56	MG	2a	1753	-	-	-	X
56	MG	2a	1764	-	-	-	X
56	MG	2a	1780	-	-	-	X
56	MG	2a	1819	-	-	-	X
56	MG	2a	1827	-	-	-	X
56	MG	2a	1841	-	-	-	X
56	MG	2a	1842	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	2a	1847	-	-	-	X
56	MG	2l	3001	-	-	-	X
56	MG	2x	3004	-	-	-	X

2 Entry composition [i](#)

There are 59 unique types of molecules in this entry. The entry contains 288775 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 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1A	2746	Total	C	N	O	P	0	0	0
			59154	26327	11077	19005	2745			
1	2A	2790	Total	C	N	O	P	0	0	0
			60091	26746	11243	19313	2789			

- Molecule 2 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1B	120	Total	C	N	O	P	0	0	0
			2572	1146	476	831	119			
2	2B	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	1D	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
3	2D	275	Total	C	N	O	S	0	0	0
			2142	1352	426	361	3			

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	1E	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
4	2E	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	1F	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			
5	2F	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	1G	181	Total	C	N	O	S	0	0	0
			1425	914	256	251	4			
6	2G	181	Total	C	N	O	S	0	0	0
			1424	911	258	251	4			

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	1H	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
7	2H	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	1I	146	Total	C	N	O	S	0	0	0
			1085	693	189	202	1			
8	2I	146	Total	C	N	O	S	0	0	0
			1061	680	186	194	1			

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	1N	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			
9	2N	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	1O	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	2O	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	1P	149	Total	C	N	O	S	0	0	0
			1139	709	231	196	3			
11	2P	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	1Q	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
12	2Q	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	1R	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
13	2R	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	1S	110	Total	C	N	O	0	0	0
			877	553	175	149			
14	2S	110	Total	C	N	O	0	0	0
			870	549	173	148			

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	1T	131	Total	C	N	O	0	0	0
			1091	680	225	185	1		
15	2T	131	Total	C	N	O	0	0	0
			1083	675	224	183	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	1U	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
16	2U	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	1V	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			
17	2V	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	1W	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			
18	2W	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	1X	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
19	2X	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	1Y	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			
20	2Y	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	1Z	186	Total	C	N	O	S	0	0	0
			1470	937	262	269	2			
21	2Z	186	Total	C	N	O	S	0	0	0
			1454	929	256	267	2			

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	75	Total	C	N	O	S	0	0	0
			598	370	127	100	1			
22	20	75	Total	C	N	O	S	0	0	0
			598	370	127	100	1			

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	11	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			
23	21	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	12	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			
24	22	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	13	59	Total	C	N	O	0	0	0
			469	298	90	81			
25	23	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	14	69	Total	C	N	O	S	0	0	0
			558	352	102	99	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	24	69	Total	C	N	O	S	0	0	0
			532	339	97	91	5			

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	15	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			
27	25	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	16	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
28	26	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	17	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
29	27	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	18	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			
30	28	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	19	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
31	29	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 32 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	1a	1477	Total	C	N	O	P	0	0	0
			31750	14131	5883	10259	1477			
32	2a	1483	Total	C	N	O	P	0	0	0
			31877	14188	5905	10301	1483			

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	1b	231	Total	C	N	O	S	0	0	0
			1786	1136	321	325	4			
33	2b	231	Total	C	N	O	S	0	0	0
			1697	1079	292	321	5			

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	1c	206	Total	C	N	O	S	0	0	0
			1480	932	281	266	1			
34	2c	206	Total	C	N	O	S	0	0	0
			1412	883	269	259	1			

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	1d	208	Total	C	N	O	S	0	0	0
			1618	1013	312	286	7			
35	2d	208	Total	C	N	O	S	0	0	0
			1630	1022	321	280	7			

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	1e	148	Total	C	N	O	S	0	0	0
			1129	714	213	198	4			
36	2e	148	Total	C	N	O	S	0	0	0
			1095	695	203	193	4			

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	1f	100	Total	C	N	O	S	0	0	0
			806	511	143	149	3			
37	2f	100	Total	C	N	O	S	0	0	0
			817	516	146	152	3			

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	1g	155	Total	C	N	O	S	0	0	0
			1183	732	232	213	6			
38	2g	155	Total	C	N	O	S	0	0	0
			1167	728	220	213	6			

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	1h	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			
39	2h	137	Total	C	N	O	S	0	0	0
			1074	681	202	189	2			

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	1i	127	Total	C	N	O	0	0	0
			976	620	189	167			
40	2i	127	Total	C	N	O	0	0	0
			932	589	177	166			

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
41	1j	97	Total	C	N	O	0	0	0
			682	424	130	128			
41	2j	96	Total	C	N	O	0	0	0
			678	424	126	128			

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	1k	114	Total	C	N	O	S	0	0	0
			826	513	156	154	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	2k	114	Total	C	N	O	S	0	0	0
			829	516	155	155	3			

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	1l	122	Total	C	N	O	S	0	0	0
			920	579	181	159	1			
43	2l	122	Total	C	N	O	S	0	0	0
			918	576	182	159	1			

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	1m	118	Total	C	N	O	S	0	0	0
			923	569	191	161	2			
44	2m	116	Total	C	N	O	S	0	0	0
			903	555	187	159	2			

- Molecule 45 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	1n	60	Total	C	N	O	S	0	0	0
			482	306	100	72	4			
45	2n	60	Total	C	N	O	S	0	0	0
			459	291	93	71	4			

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	1o	88	Total	C	N	O	S	0	0	0
			715	447	140	126	2			
46	2o	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	1p	82	Total	C	N	O	S	0	0	0
			671	424	133	113	1			
47	2p	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	1q	99	Total	C	N	O	S	0	0	0
			811	519	148	142	2			
48	2q	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	1r	68	Total	C	N	O		0	0	0
			555	355	108	92				
49	2r	68	Total	C	N	O		0	0	0
			555	355	108	92				

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	1s	84	Total	C	N	O	S	0	0	0
			642	409	119	112	2			
50	2s	83	Total	C	N	O	S	0	0	0
			646	412	119	113	2			

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	1t	96	Total	C	N	O	S	0	0	0
			712	435	152	123	2			
51	2t	96	Total	C	N	O	S	0	0	0
			731	449	156	124	2			

- Molecule 52 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
52	1u	23	Total	C	N	O	0	0	0
			187	116	42	29			
52	2u	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1v	5	Total	C	N	O	P	0	0	0
			109	49	22	33	5			
53	2v	5	Total	C	N	O	P	0	0	0
			109	49	22	33	5			

- Molecule 54 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
54	1x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			
54	2x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			

- Molecule 55 is a protein called Pyrrhocoricin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
55	1z	16	Total	C	N	O	0	0	0
			126	82	23	21			
55	2z	16	Total	C	N	O	0	0	0
			126	82	23	21			

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	2E	6	Total	Mg	0	0
			6	6		
56	17	3	Total	Mg	0	0
			3	3		
56	2d	1	Total	Mg	0	0
			1	1		
56	1T	4	Total	Mg	0	0
			4	4		
56	1N	7	Total	Mg	0	0
			7	7		
56	20	1	Total	Mg	0	0
			1	1		
56	18	5	Total	Mg	0	0
			5	5		
56	1o	1	Total	Mg	0	0
			1	1		
56	2l	5	Total	Mg	0	0
			5	5		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1Y	1	Total 1	Mg 1	0	0
56	13	1	Total 1	Mg 1	0	0
56	1f	1	Total 1	Mg 1	0	0
56	1P	5	Total 5	Mg 5	0	0
56	2B	9	Total 9	Mg 9	0	0
56	1q	2	Total 2	Mg 2	0	0
56	2a	248	Total 248	Mg 248	0	0
56	1k	2	Total 2	Mg 2	0	0
56	1E	8	Total 8	Mg 8	0	0
56	1b	2	Total 2	Mg 2	0	0
56	25	1	Total 1	Mg 1	0	0
56	2F	2	Total 2	Mg 2	0	0
56	16	2	Total 2	Mg 2	0	0
56	28	2	Total 2	Mg 2	0	0
56	2e	2	Total 2	Mg 2	0	0
56	1W	6	Total 6	Mg 6	0	0
56	1A	1233	Total 1233	Mg 1233	0	0
56	1t	1	Total 1	Mg 1	0	0
56	1n	1	Total 1	Mg 1	0	0
56	1X	1	Total 1	Mg 1	0	0
56	12	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	2p	1	Total 1 Mg 1	0	0
56	1p	1	Total 1 Mg 1	0	0
56	1D	15	Total 15 Mg 15	0	0
56	2N	1	Total 1 Mg 1	0	0
56	1e	3	Total 3 Mg 3	0	0
56	2G	1	Total 1 Mg 1	0	0
56	2f	1	Total 1 Mg 1	0	0
56	1V	2	Total 2 Mg 2	0	0
56	2X	1	Total 1 Mg 1	0	0
56	1a	295	Total 295 Mg 295	0	0
56	2Q	5	Total 5 Mg 5	0	0
56	15	4	Total 4 Mg 4	0	0
56	1x	12	Total 12 Mg 12	0	0
56	1R	8	Total 8 Mg 8	0	0
56	1G	3	Total 3 Mg 3	0	0
56	2O	3	Total 3 Mg 3	0	0
56	11	3	Total 3 Mg 3	0	0
56	1d	1	Total 1 Mg 1	0	0
56	2n	1	Total 1 Mg 1	0	0
56	1H	1	Total 1 Mg 1	0	0
56	2Y	1	Total 1 Mg 1	0	0

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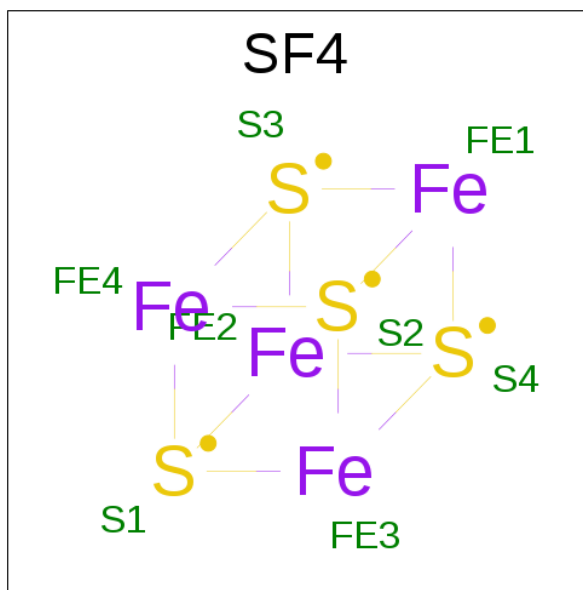
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	23	1	Total 1	Mg 1	0	0
56	2x	4	Total 4	Mg 4	0	0
56	1Z	3	Total 3	Mg 3	0	0
56	2D	6	Total 6	Mg 6	0	0
56	2q	2	Total 2	Mg 2	0	0
56	1U	6	Total 6	Mg 6	0	0
56	1O	3	Total 3	Mg 3	0	0
56	1r	2	Total 2	Mg 2	0	0
56	19	3	Total 3	Mg 3	0	0
56	1l	1	Total 1	Mg 1	0	0
56	1F	9	Total 9	Mg 9	0	0
56	10	7	Total 7	Mg 7	0	0
56	2t	1	Total 1	Mg 1	0	0
56	1Q	5	Total 5	Mg 5	0	0
56	2A	592	Total 592	Mg 592	0	0
56	1h	2	Total 2	Mg 2	0	0
56	2Z	1	Total 1	Mg 1	0	0
56	1B	25	Total 25	Mg 25	0	0
56	2u	1	Total 1	Mg 1	0	0

- Molecule 57 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1Y	1	Total Zn 1 1	0	0
57	14	1	Total Zn 1 1	0	0
57	1n	1	Total Zn 1 1	0	0
57	15	1	Total Zn 1 1	0	0
57	29	1	Total Zn 1 1	0	0
57	19	1	Total Zn 1 1	0	0
57	26	1	Total Zn 1 1	0	0
57	25	1	Total Zn 1 1	0	0
57	24	1	Total Zn 1 1	0	0
57	2n	1	Total Zn 1 1	0	0
57	2Y	1	Total Zn 1 1	0	0
57	16	1	Total Zn 1 1	0	0

- Molecule 58 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
58	1d	1	Total	Fe	S	0	0
			8	4	4		
58	2d	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 59 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	1A	2217	Total	O	0	0
			2217	2217		
59	1B	37	Total	O	0	0
			37	37		
59	1D	23	Total	O	0	0
			23	23		
59	1E	29	Total	O	0	0
			29	29		
59	1F	19	Total	O	0	0
			19	19		
59	1G	2	Total	O	0	0
			2	2		
59	1H	4	Total	O	0	0
			4	4		
59	1I	1	Total	O	0	0
			1	1		
59	1N	6	Total	O	0	0
			6	6		
59	1O	7	Total	O	0	0
			7	7		
59	1P	27	Total	O	0	0
			27	27		
59	1Q	14	Total	O	0	0
			14	14		
59	1R	11	Total	O	0	0
			11	11		
59	1S	2	Total	O	0	0
			2	2		
59	1T	13	Total	O	0	0
			13	13		
59	1U	14	Total	O	0	0
			14	14		
59	1V	7	Total	O	0	0
			7	7		
59	1W	8	Total	O	0	0
			8	8		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	1X	5	Total 5	O 5	0	0
59	1Y	1	Total 1	O 1	0	0
59	1Z	7	Total 7	O 7	0	0
59	10	12	Total 12	O 12	0	0
59	11	5	Total 5	O 5	0	0
59	12	3	Total 3	O 3	0	0
59	13	4	Total 4	O 4	0	0
59	15	9	Total 9	O 9	0	0
59	16	9	Total 9	O 9	0	0
59	17	10	Total 10	O 10	0	0
59	18	12	Total 12	O 12	0	0
59	19	2	Total 2	O 2	0	0
59	1a	338	Total 338	O 338	0	0
59	1b	2	Total 2	O 2	0	0
59	1d	3	Total 3	O 3	0	0
59	1e	7	Total 7	O 7	0	0
59	1f	1	Total 1	O 1	0	0
59	1h	3	Total 3	O 3	0	0
59	1i	1	Total 1	O 1	0	0
59	1j	1	Total 1	O 1	0	0
59	1k	1	Total 1	O 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	1l	3	Total 3	O 3	0	0
59	1m	1	Total 1	O 1	0	0
59	1o	1	Total 1	O 1	0	0
59	1q	1	Total 1	O 1	0	0
59	1r	1	Total 1	O 1	0	0
59	1s	2	Total 2	O 2	0	0
59	1t	1	Total 1	O 1	0	0
59	1v	3	Total 3	O 3	0	0
59	1x	9	Total 9	O 9	0	0
59	2A	809	Total 809	O 809	0	0
59	2B	12	Total 12	O 12	0	0
59	2D	20	Total 20	O 20	0	0
59	2E	11	Total 11	O 11	0	0
59	2F	7	Total 7	O 7	0	0
59	2N	1	Total 1	O 1	0	0
59	2O	3	Total 3	O 3	0	0
59	2P	3	Total 3	O 3	0	0
59	2Q	2	Total 2	O 2	0	0
59	2R	3	Total 3	O 3	0	0
59	2T	3	Total 3	O 3	0	0
59	2U	3	Total 3	O 3	0	0

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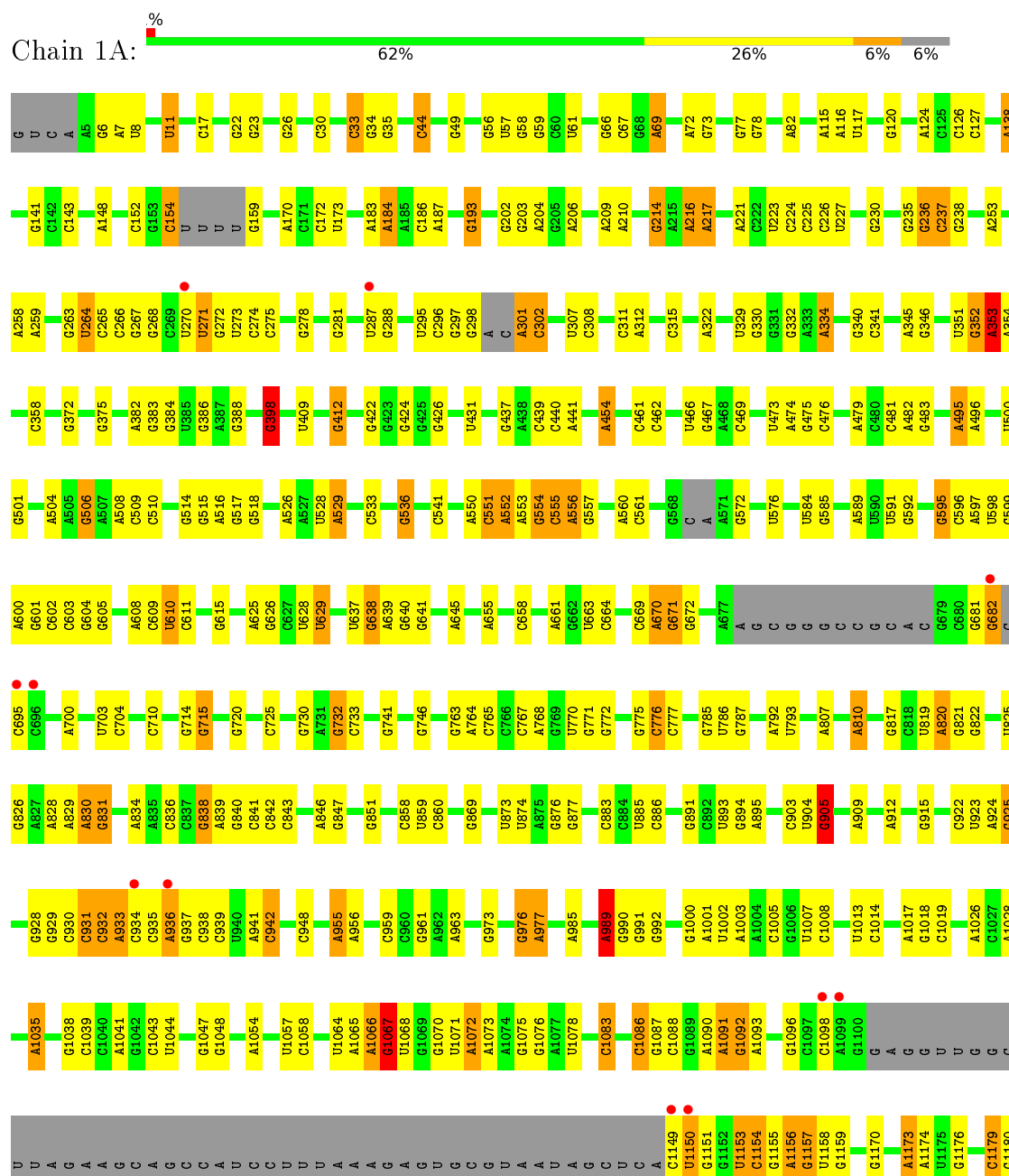
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	2W	1	Total 1	O 1	0	0
59	2X	2	Total 2	O 2	0	0
59	2Y	1	Total 1	O 1	0	0
59	2Z	6	Total 6	O 6	0	0
59	20	4	Total 4	O 4	0	0
59	21	1	Total 1	O 1	0	0
59	23	1	Total 1	O 1	0	0
59	25	1	Total 1	O 1	0	0
59	27	1	Total 1	O 1	0	0
59	28	4	Total 4	O 4	0	0
59	2a	274	Total 274	O 274	0	0
59	2c	2	Total 2	O 2	0	0
59	2d	1	Total 1	O 1	0	0
59	2i	2	Total 2	O 2	0	0
59	2j	2	Total 2	O 2	0	0
59	2l	2	Total 2	O 2	0	0
59	2p	1	Total 1	O 1	0	0
59	2t	3	Total 3	O 3	0	0
59	2v	1	Total 1	O 1	0	0
59	2x	2	Total 2	O 2	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 ($RSRZ > 2$). 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.

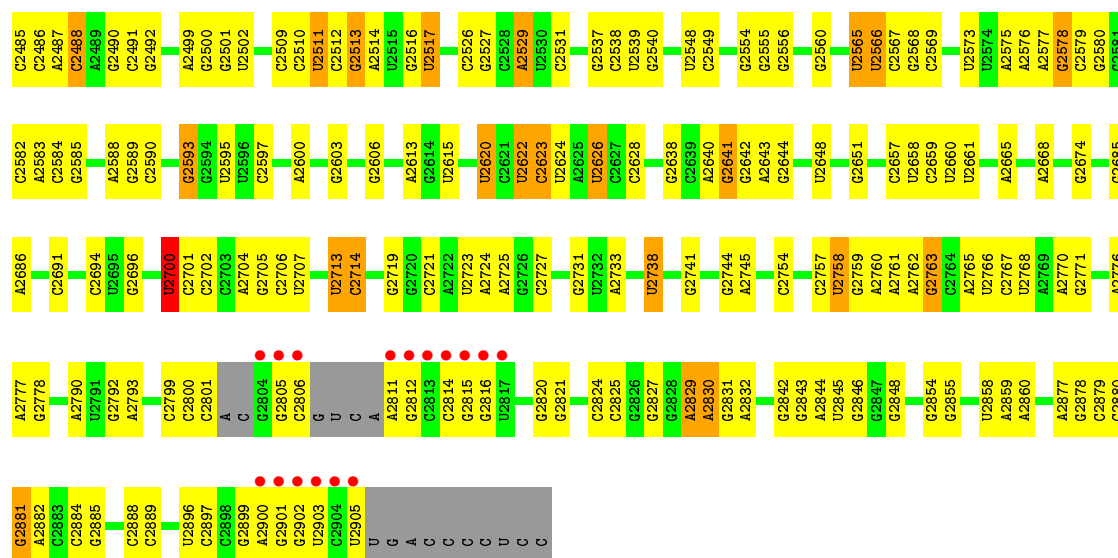
• Molecule 1: 23S Ribosomal RNA



C2801	C2659	G2319	G	G2048	G1920	A1854	A1539	A1429	U1312	G1183
A2802	G2670	A2320	G	U2049	A1921	A1803	A1540	G1430	A1313	C1184
C2803	A2671	A2321	U	A2050	G1924	A1806	A1541	U1435	G1316	U1185
G2804	C2672	A2322	G	A2051	G1924	G1806	A1552	A1435	A1317	U1186
G2805	C2694	U2323	G	G2052	G1927	U1809	A1553	A1440	A1318	A1187
G2806	G2694	U2323	G	A2054	G1927	A1810	C1554	U1441	U1313	A1188
G	G2456	G2330	A	G2059	A1934	G1811	A1555	G1450	A1323	C1198
U	G2457	A2331	C	G2059	C1935	A1812	A1556	U1451	G1328	G1199
C	G2458	G2336	C	U2062	U1936	A1813	U1565	C1452	G1328	A1200
A	A2470	G2337	U	A2063	A1939	A1816	G1566	C1453	U1337	C1198
G2812	G2473	A2338	G	G2064	A1940	A1816	U1571	A1457	C1338	G1199
G2813	U2473	G2340	U	G2064	C1941	A1821	G1572	G1458	U1345	A1201
G2814	U2473	G2341	G	C2076	A1948	G1822	G1572	G1458	U1345	U1210
G2815	G2479	G2342	A	C2077	A1948	U1826	G1578	G1461	U1345	C1211
G2816	A2480	A2342	A	G2077	A1949	C1827	G1578	G1462	U1345	G1216
A2819	G2481	A2342	C	A2081	G1950	U1826	G1578	G1462	A1346	G1217
A2820	G2481	A2342	C	G2082	G1951	U1828	G1578	G1462	A1346	A1218
C2824	C2485	G2345	C	C2083	U1952	G1829	G1583	U1465	A1347	U1219
A2829	A2487	A2346	C	A2083	A1953	G1830	G1583	G1466	A1349	C1221
A2830	C2488	G2347	C	C2086	G1954	A1831	G1583	G1467	C1351	C1222
G2831	A2489	G2348	G	C2087	G1954	A1832	G1583	G1467	C1351	A1221
A2832	G2493	U2355	C	C2087	A1958	A1833	G1583	G1467	C1351	U1219
C2833	G2493	A2356	U	G2090	A1959	C1834	G1583	G1467	C1351	G1220
A2844	G2498	G2357	C	U2095	A1959	C1834	G1583	G1467	C1351	G1221
G2855	A2499	U2244	C	U2095	U1976	A1840	G1583	G1467	C1351	C1222
U2856	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
G2857	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
U2858	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
A2859	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
G2862	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
C2863	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
G2873	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
U2874	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
U2875	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
G2876	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
A2877	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
G2878	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
C2879	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
G2880	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
A2882	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
G2885	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
C2889	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
G2890	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
A2891	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
G2896	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
C2897	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
G2898	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222
A2900	U2502	G2245	C	U2095	U1976	G1841	G1583	G1467	C1351	C1222







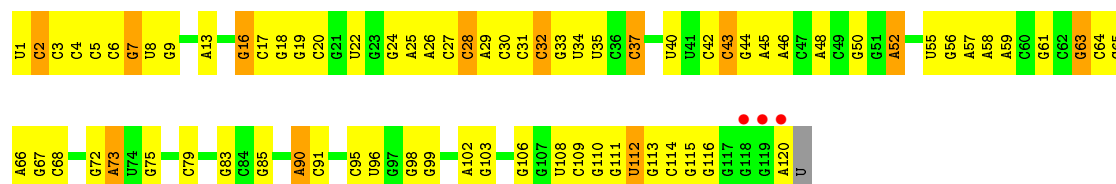
• Molecule 2: 5S Ribosomal RNA

Chain 1B: 74% 25%



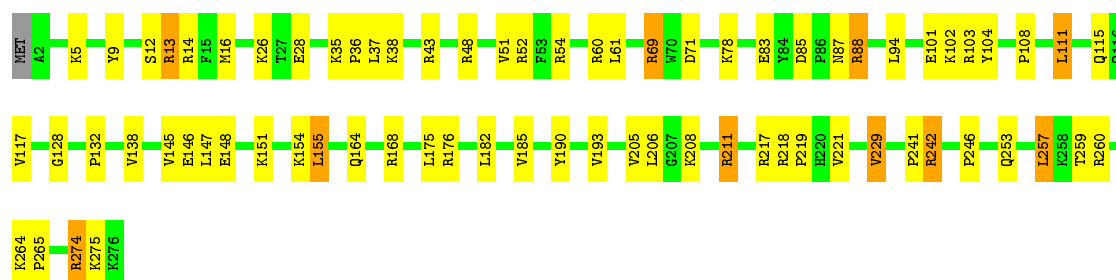
• Molecule 2: 5S Ribosomal RNA

Chain 2B: 2% 37% 52% 10%



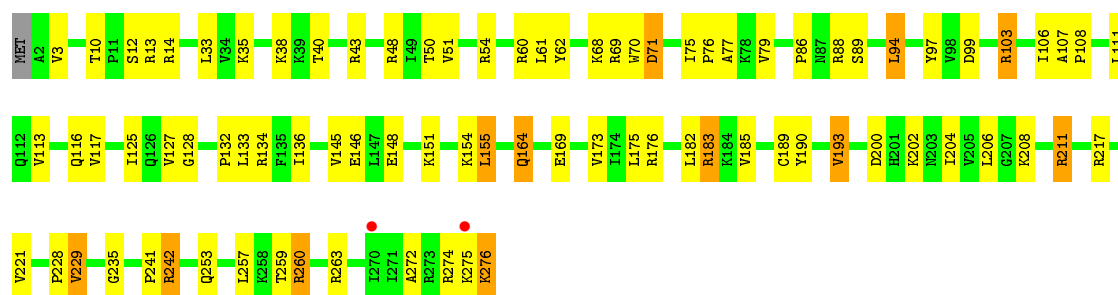
• Molecule 3: 50S ribosomal protein L2

Chain 1D: 73% 23%



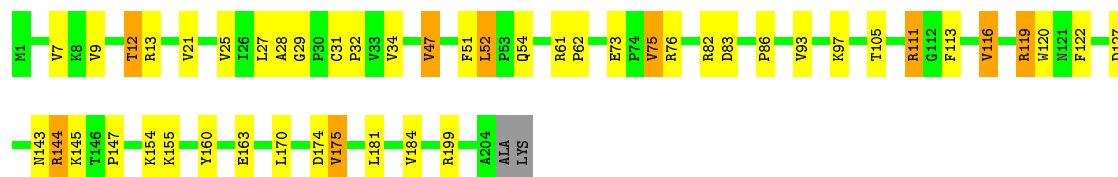
• Molecule 3: 50S ribosomal protein L2

Chain 2D: % 69% 26%



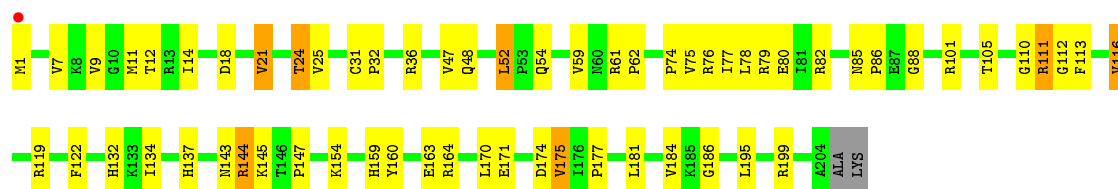
- Molecule 4: 50S ribosomal protein L3

Chain 1E: 76% 19% . .



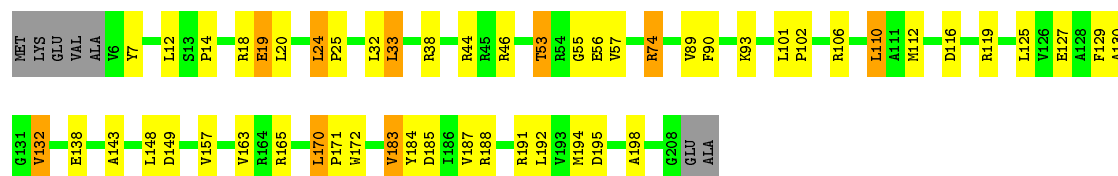
- Molecule 4: 50S ribosomal protein L3

Chain 2E: 69% 27% . .



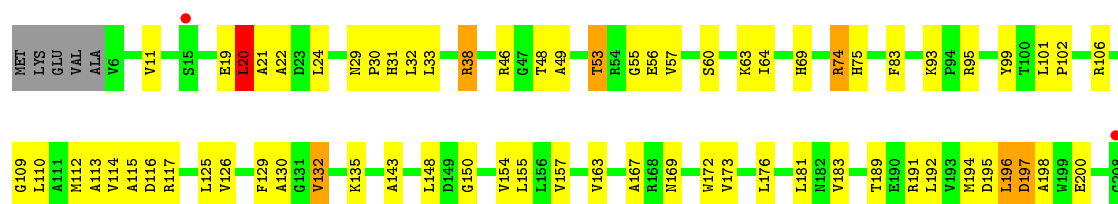
- Molecule 5: 50S ribosomal protein L4

Chain 1F: 71% 21% . .



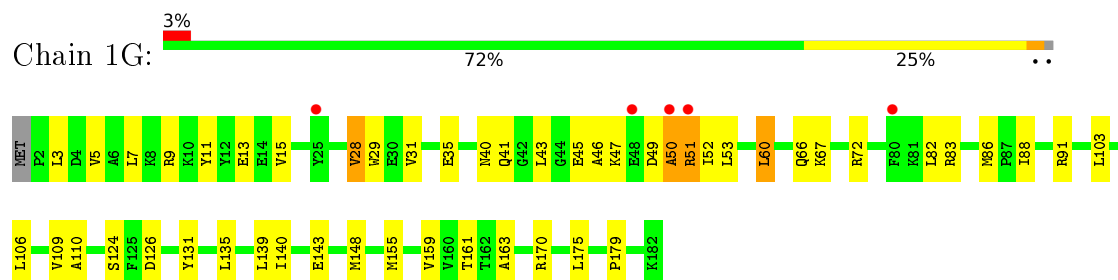
- Molecule 5: 50S ribosomal protein L4

Chain 2F: 64% 30% . .

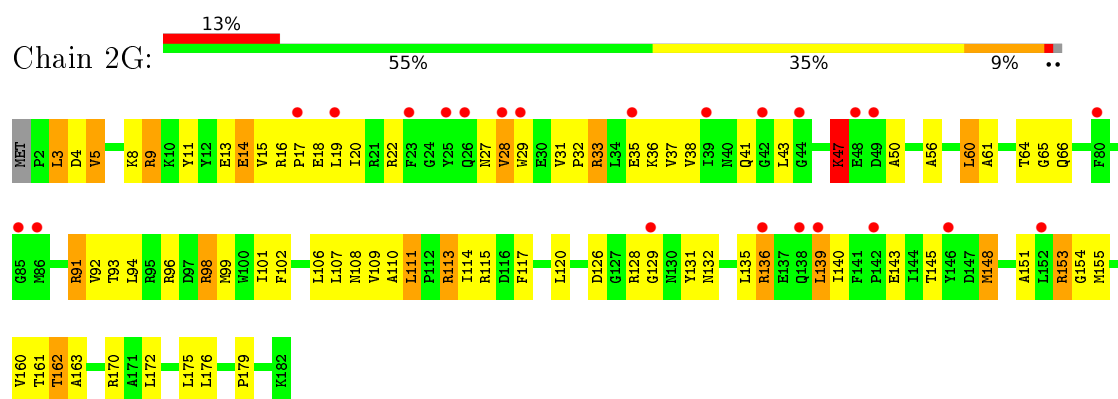


GLU
ALA

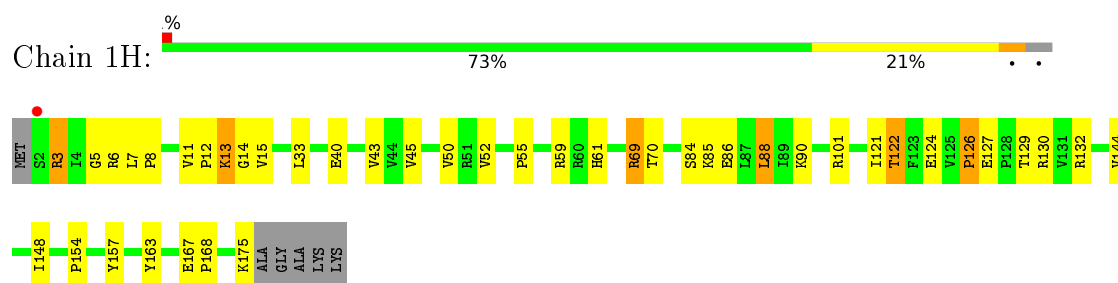
- Molecule 6: 50S ribosomal protein L5



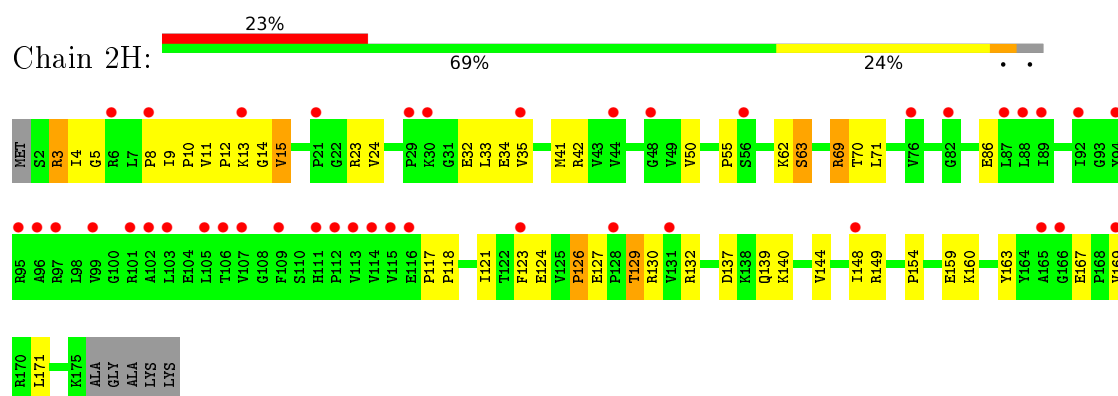
- Molecule 6: 50S ribosomal protein L5



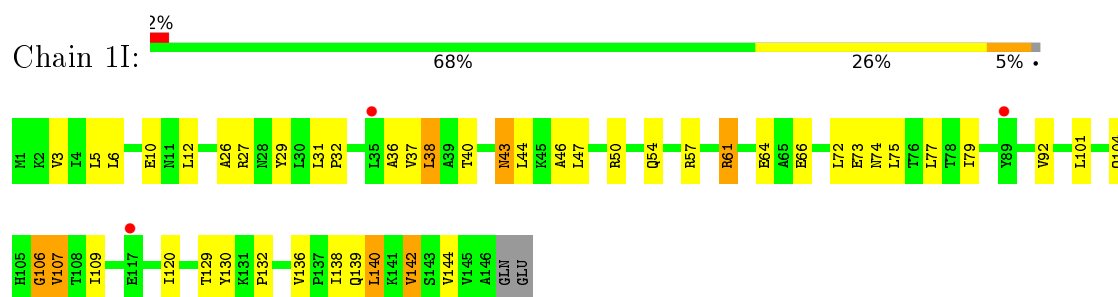
- Molecule 7: 50S ribosomal protein L6



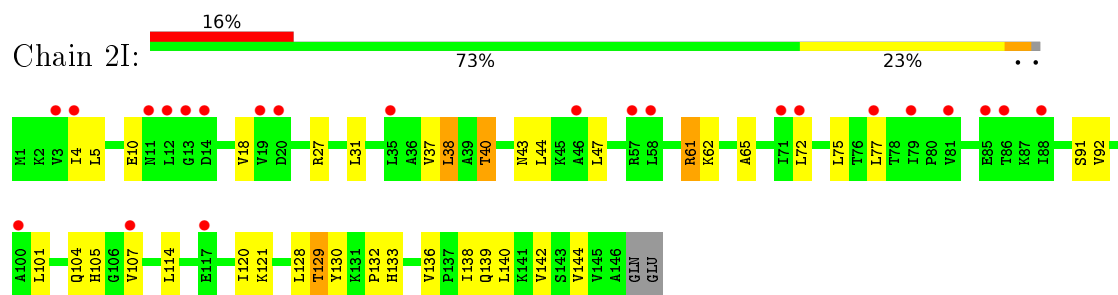
- Molecule 7: 50S ribosomal protein L6



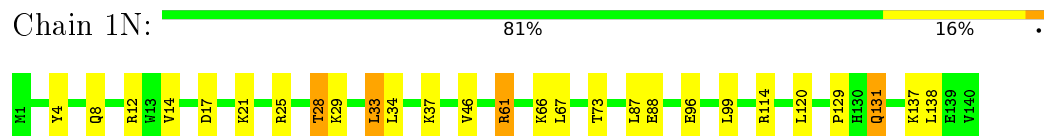
- Molecule 8: 50S ribosomal protein L9



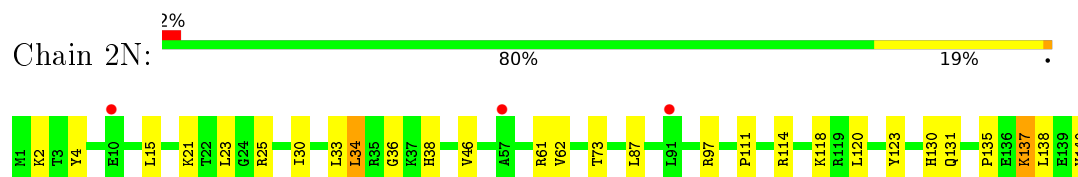
- Molecule 8: 50S ribosomal protein L9



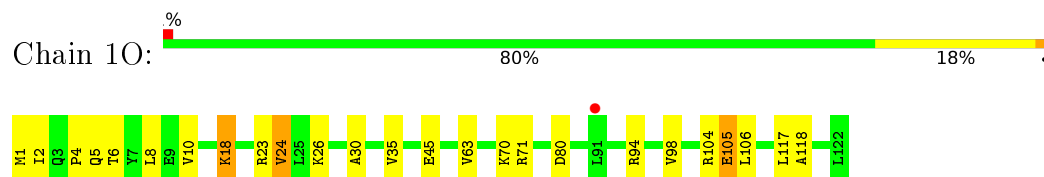
- Molecule 9: 50S ribosomal protein L13



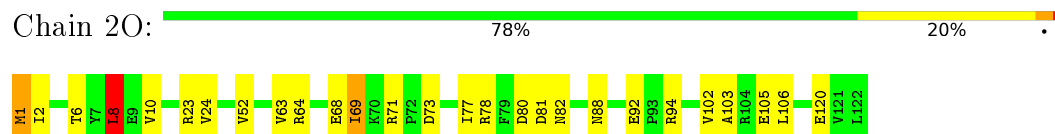
- Molecule 9: 50S ribosomal protein L13



- Molecule 10: 50S ribosomal protein L14

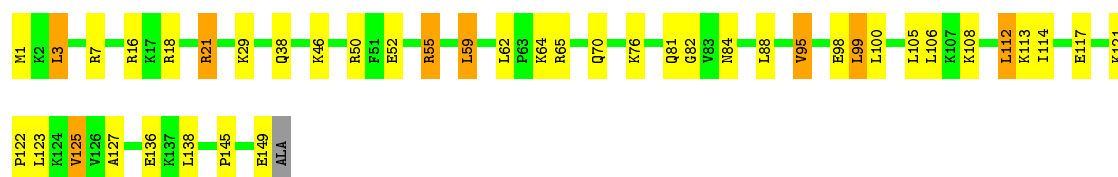


- Molecule 10: 50S ribosomal protein L14

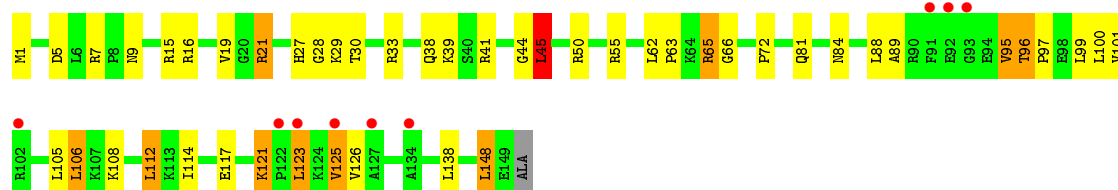


- Molecule 11: 50S ribosomal protein L15

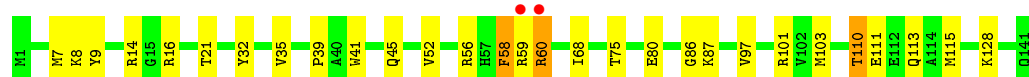
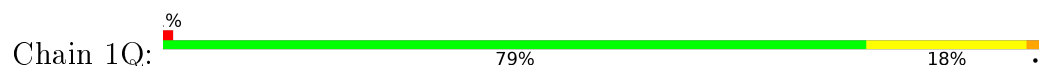




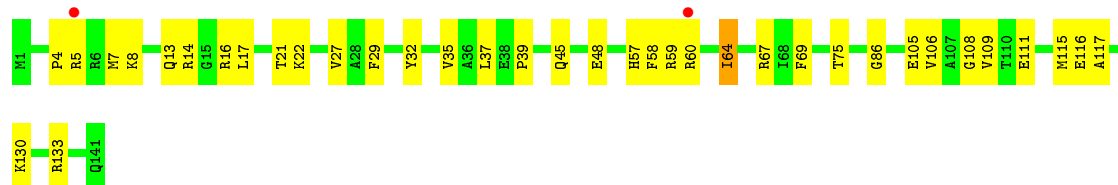
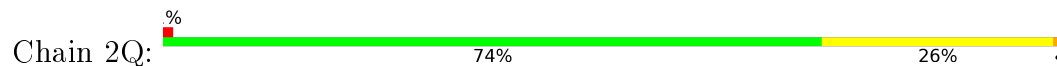
- Molecule 11: 50S ribosomal protein L15



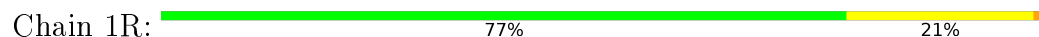
- Molecule 12: 50S ribosomal protein L16



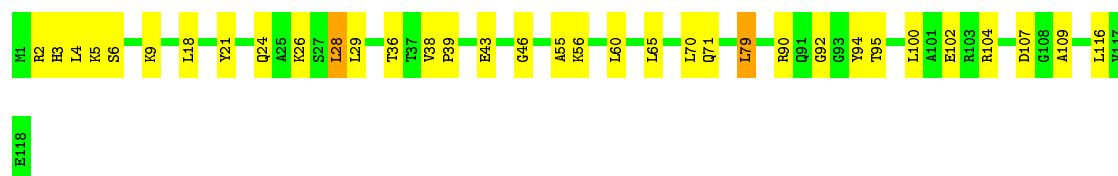
- Molecule 12: 50S ribosomal protein L16



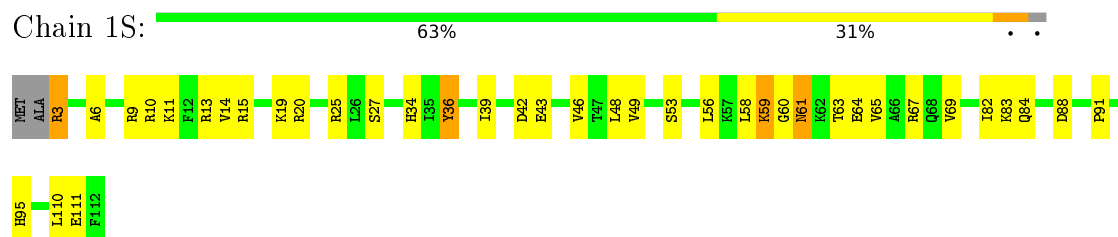
- Molecule 13: 50S ribosomal protein L17



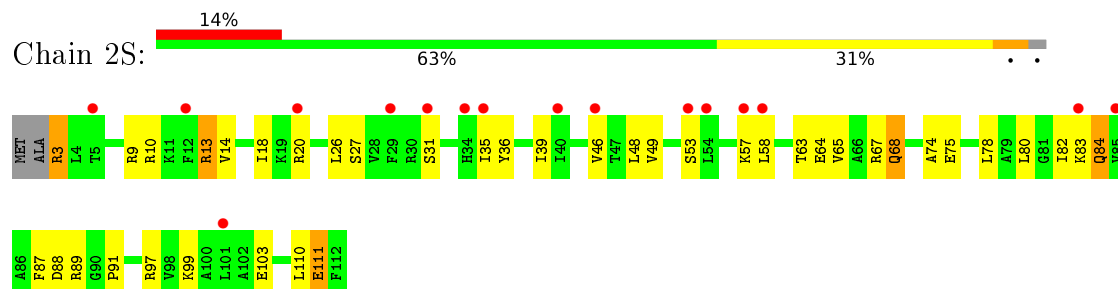
- Molecule 13: 50S ribosomal protein L17



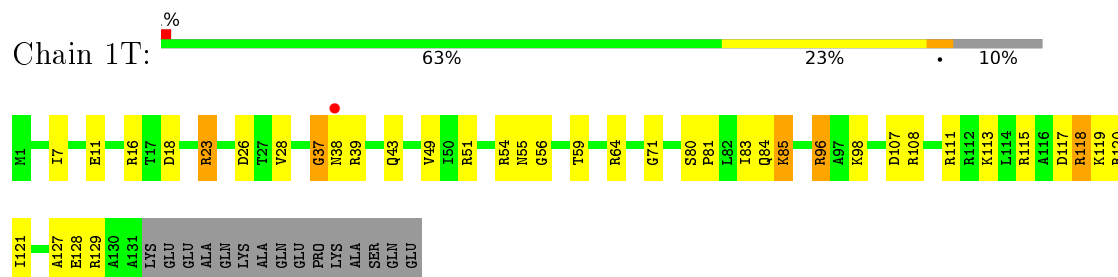
- Molecule 14: 50S ribosomal protein L18



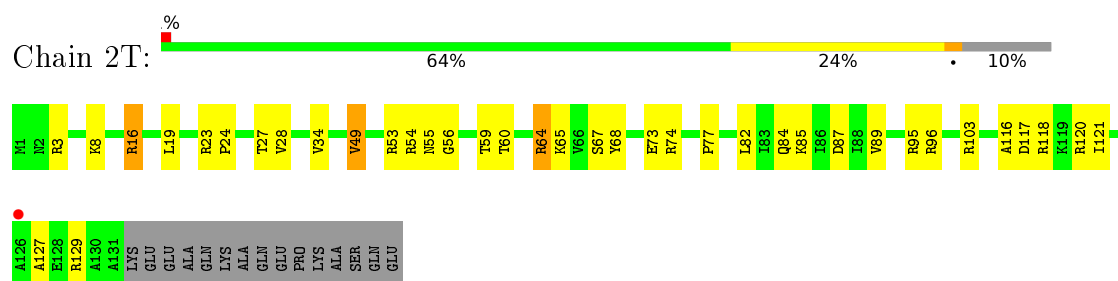
- Molecule 14: 50S ribosomal protein L18



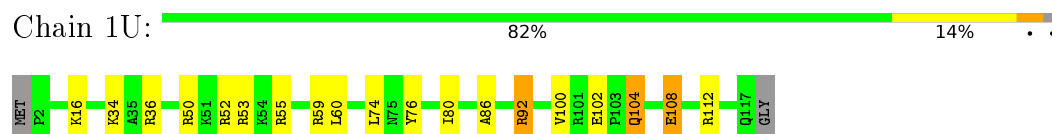
- Molecule 15: 50S ribosomal protein L19



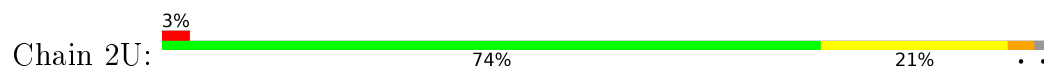
- Molecule 15: 50S ribosomal protein L19

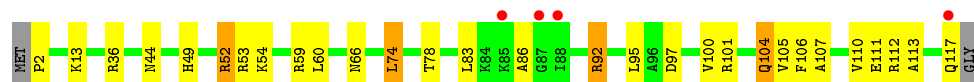


- Molecule 16: 50S ribosomal protein L20

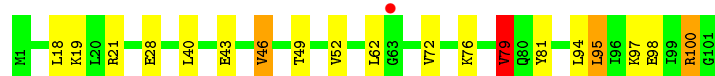
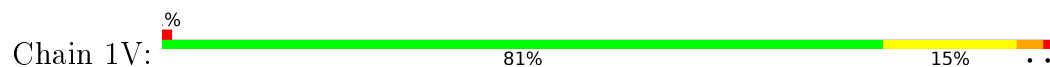


- Molecule 16: 50S ribosomal protein L20

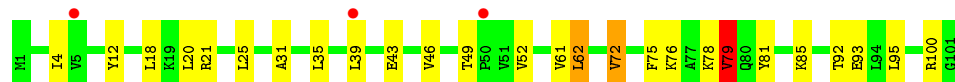
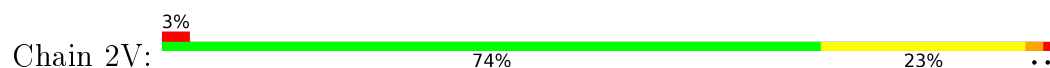




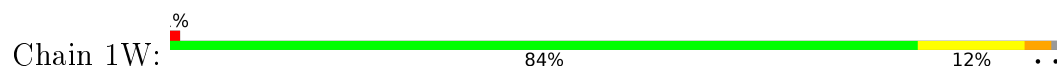
- Molecule 17: 50S ribosomal protein L21



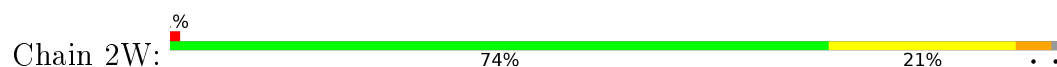
- Molecule 17: 50S ribosomal protein L21



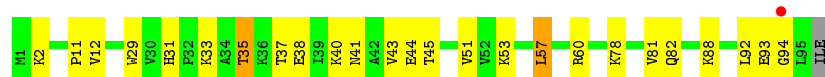
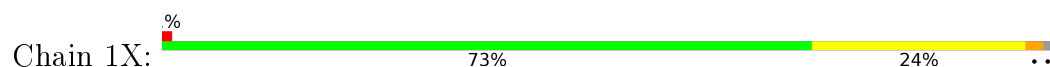
- Molecule 18: 50S ribosomal protein L22



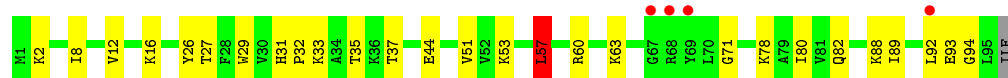
- Molecule 18: 50S ribosomal protein L22



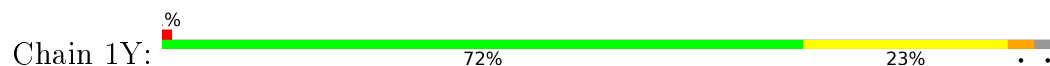
- Molecule 19: 50S ribosomal protein L23



- Molecule 19: 50S ribosomal protein L23

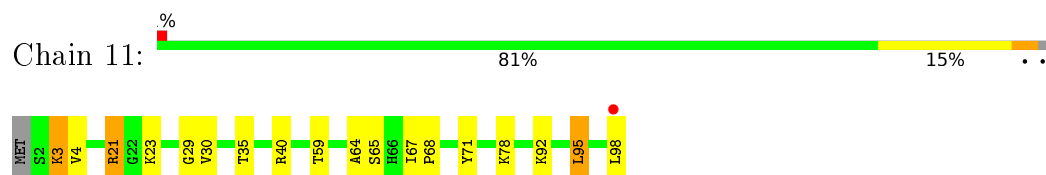


- Molecule 20: 50S ribosomal protein L24

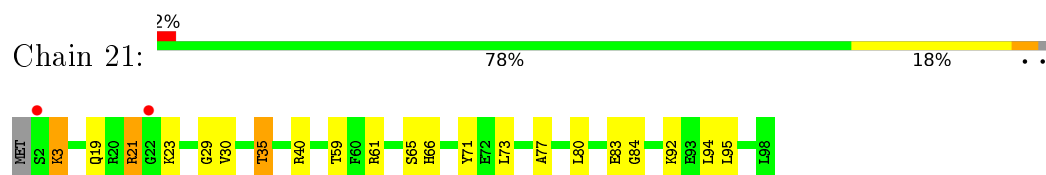




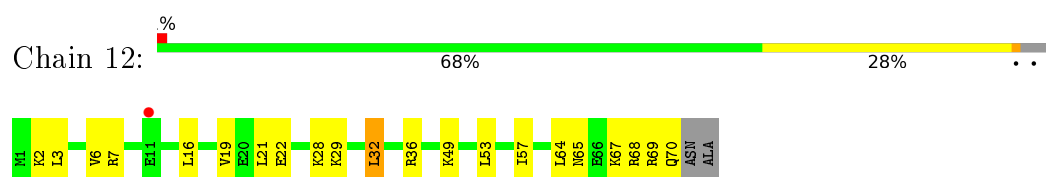
- Molecule 23: 50S ribosomal protein L28



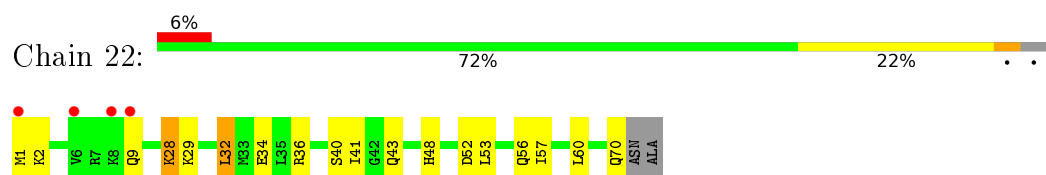
- Molecule 23: 50S ribosomal protein L28



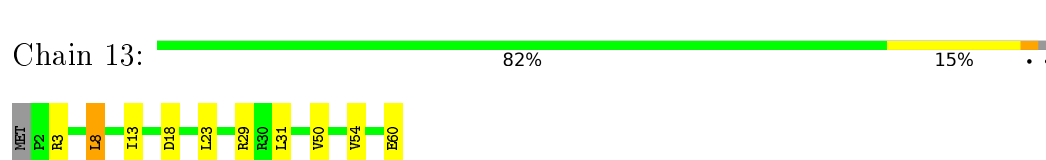
- Molecule 24: 50S ribosomal protein L29



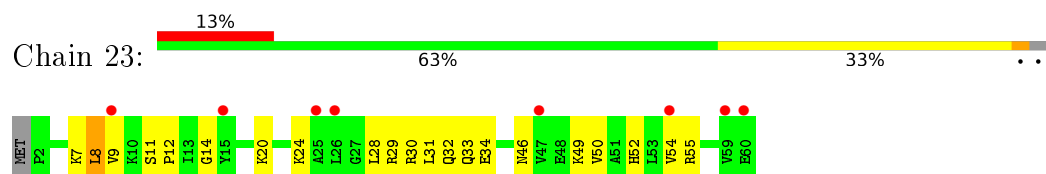
- Molecule 24: 50S ribosomal protein L29



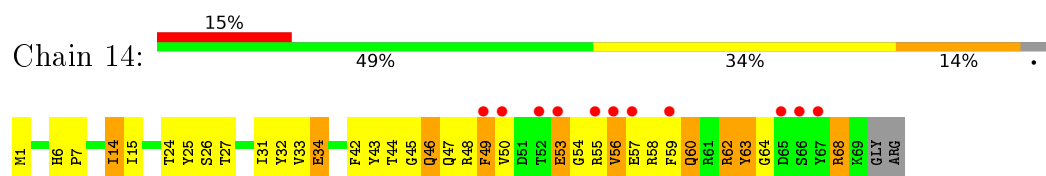
- Molecule 25: 50S ribosomal protein L30



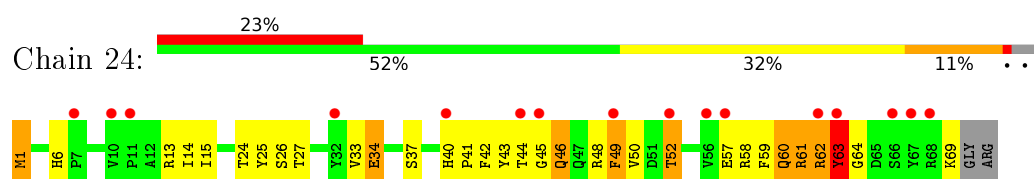
- Molecule 25: 50S ribosomal protein L30



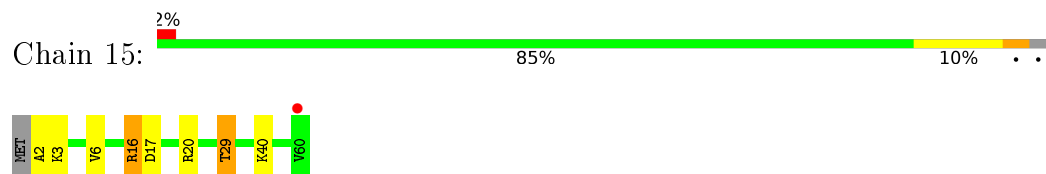
- Molecule 26: 50S ribosomal protein L31



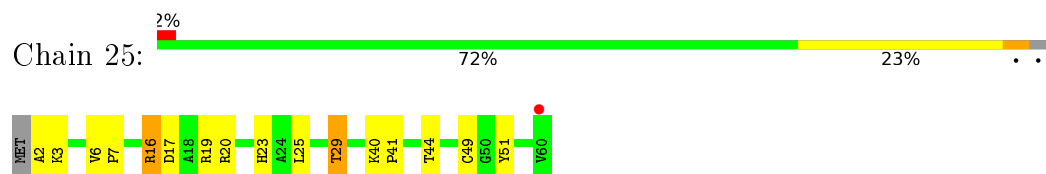
- Molecule 26: 50S ribosomal protein L31



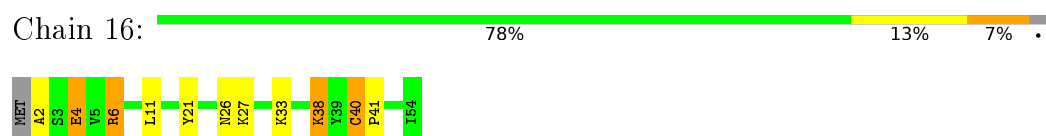
- Molecule 27: 50S ribosomal protein L32



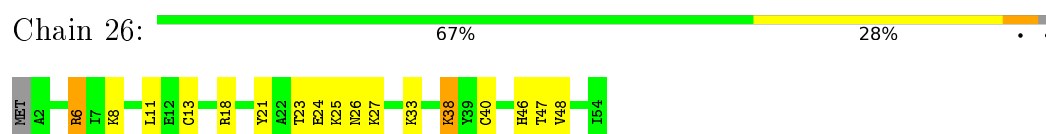
- Molecule 27: 50S ribosomal protein L32



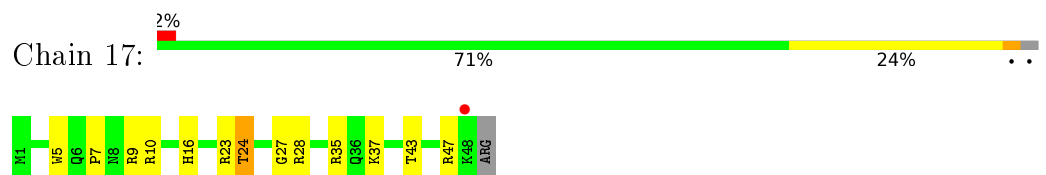
- Molecule 28: 50S ribosomal protein L33



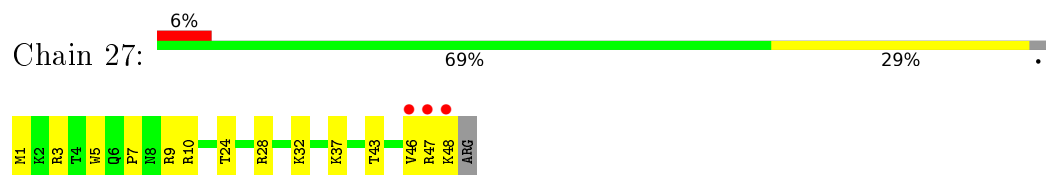
- Molecule 28: 50S ribosomal protein L33



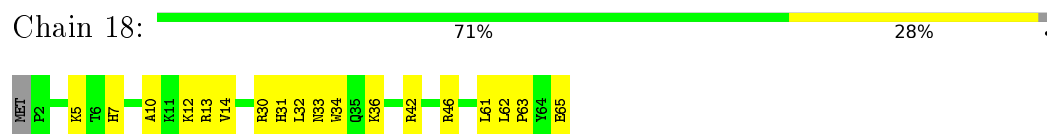
- Molecule 29: 50S ribosomal protein L34



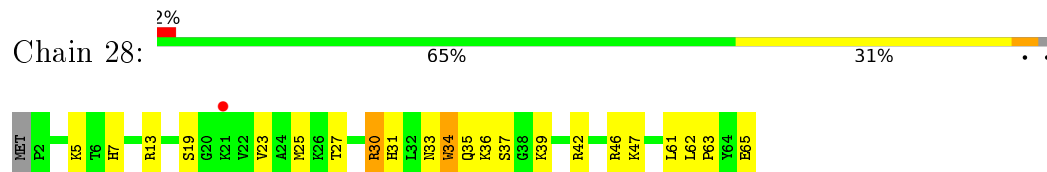
- Molecule 29: 50S ribosomal protein L34



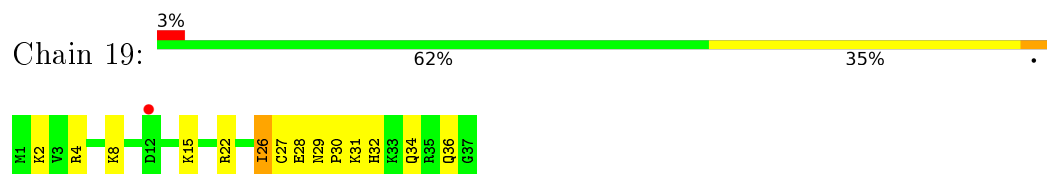
- Molecule 30: 50S ribosomal protein L35



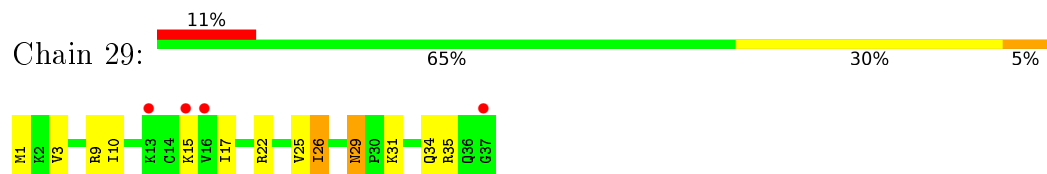
- Molecule 30: 50S ribosomal protein L35



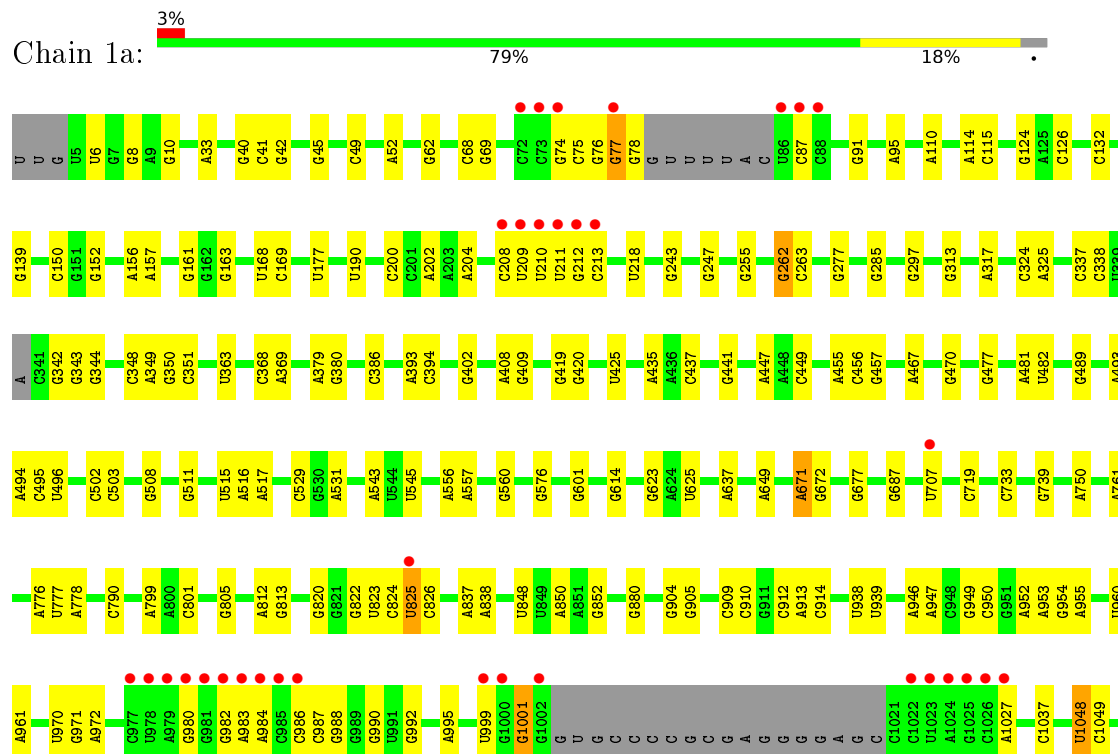
- Molecule 31: 50S ribosomal protein L36

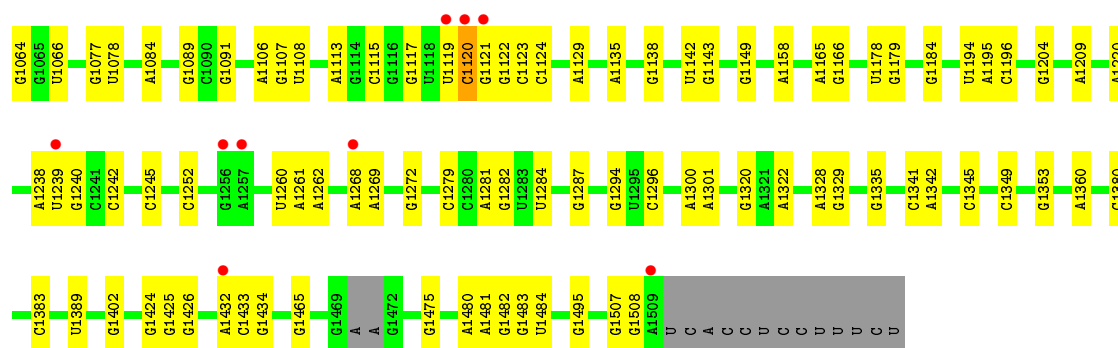


- Molecule 31: 50S ribosomal protein L36

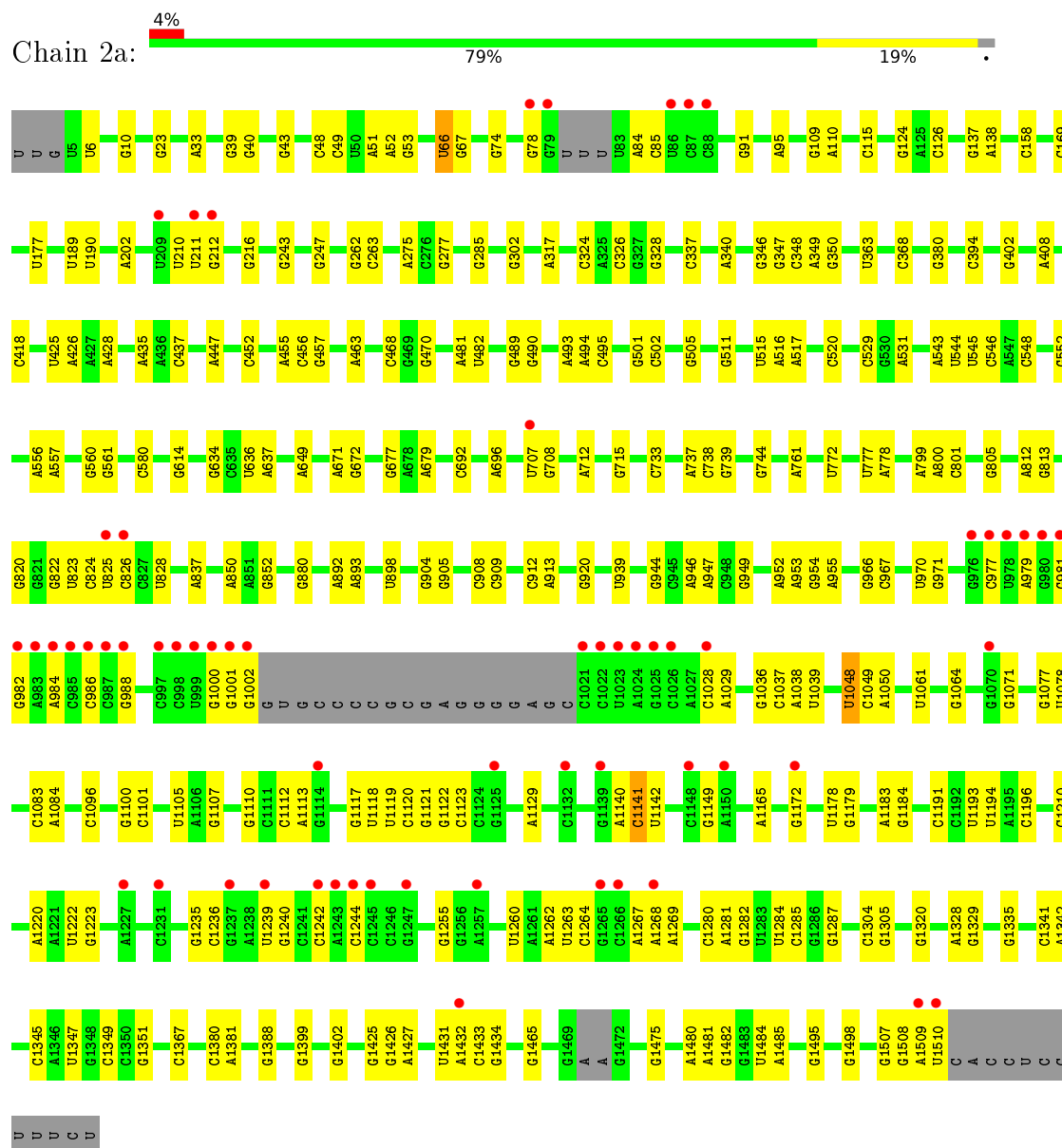


- Molecule 32: 16S Ribosomal RNA

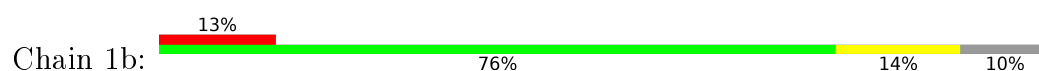


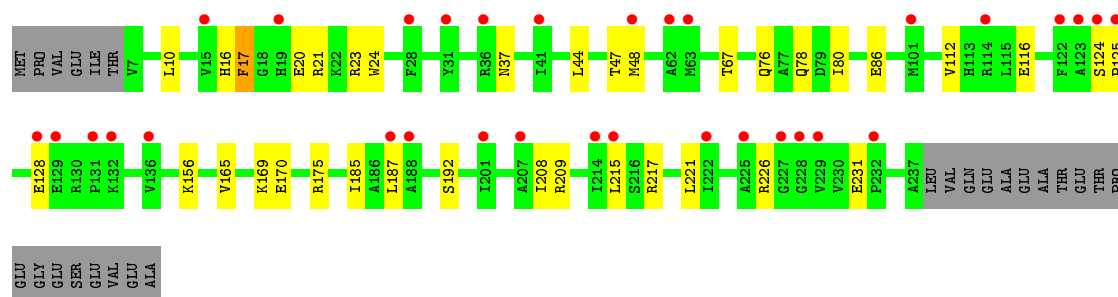


• Molecule 32: 16S Ribosomal RNA

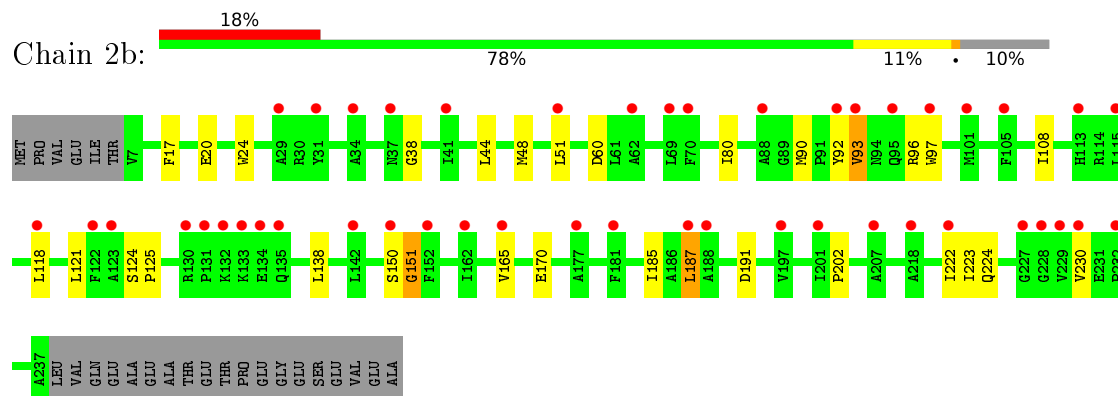


• Molecule 33: 30S ribosomal protein S2

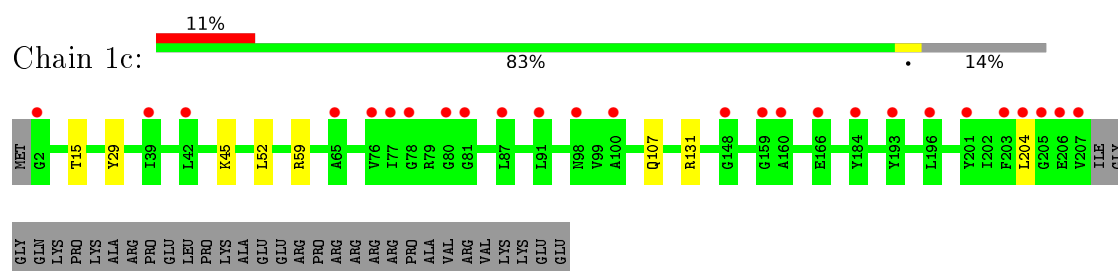




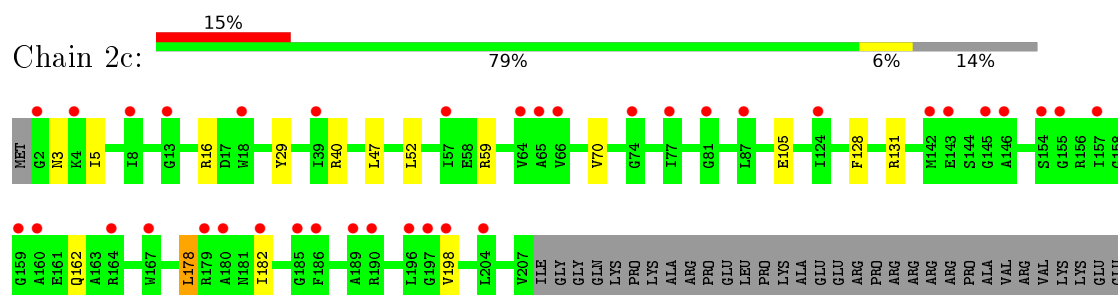
• Molecule 33: 30S ribosomal protein S2



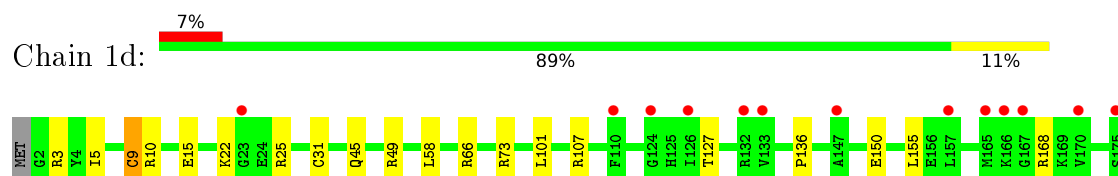
• Molecule 34: 30S ribosomal protein S3

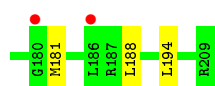


• Molecule 34: 30S ribosomal protein S3

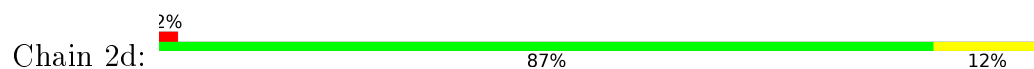


• Molecule 35: 30S ribosomal protein S4

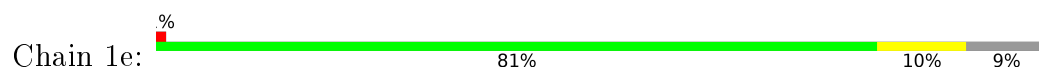




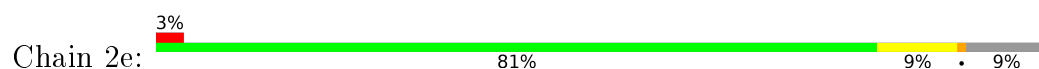
- Molecule 35: 30S ribosomal protein S4



- Molecule 36: 30S ribosomal protein S5



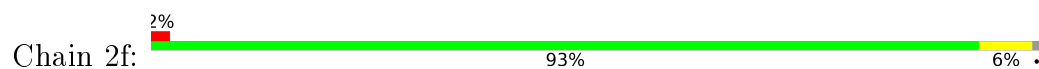
- Molecule 36: 30S ribosomal protein S5



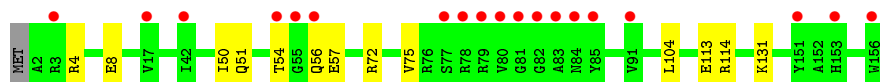
- Molecule 37: 30S ribosomal protein S6



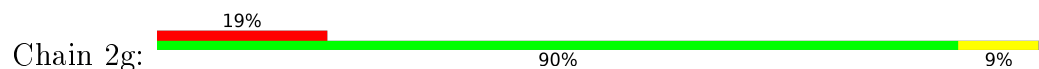
- Molecule 37: 30S ribosomal protein S6

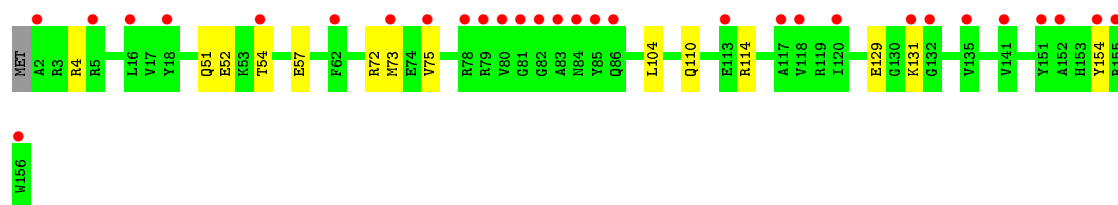


- Molecule 38: 30S ribosomal protein S7



- Molecule 38: 30S ribosomal protein S7





- Molecule 39: 30S ribosomal protein S8

Chain 1h: 93% 7% .



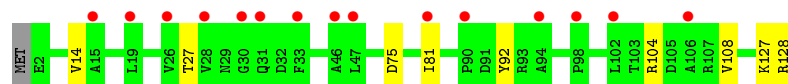
- Molecule 39: 30S ribosomal protein S8

Chain 2h: 8% 92% 7% .



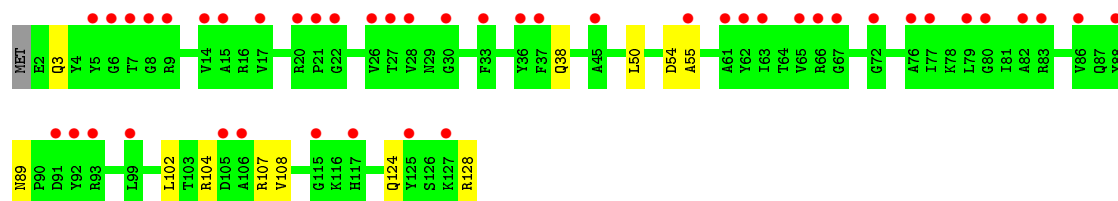
- Molecule 40: 30S ribosomal protein S9

Chain 1i: 12% 92% 7% .



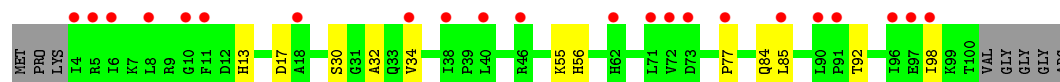
- Molecule 40: 30S ribosomal protein S9

Chain 2i: 35% 90% 9% .



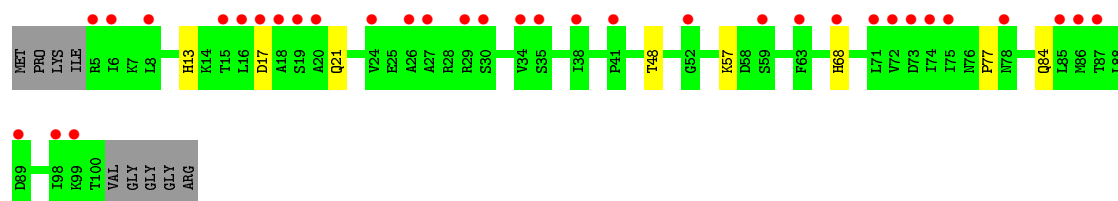
- Molecule 41: 30S ribosomal protein S10

Chain 1j: 21% 81% 11% 8% .

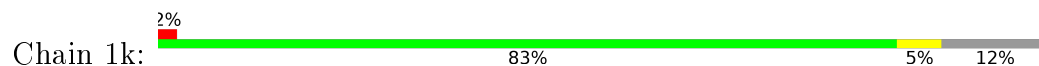


- Molecule 41: 30S ribosomal protein S10

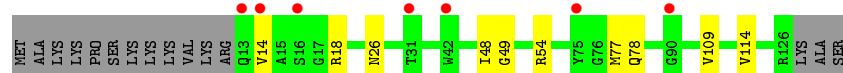
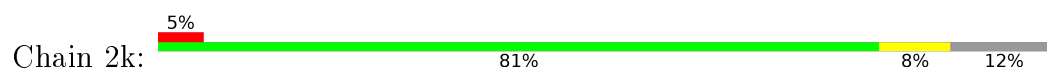
Chain 2j: 32% 84% 8% 9% .



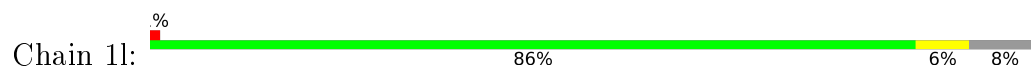
- Molecule 42: 30S ribosomal protein S11



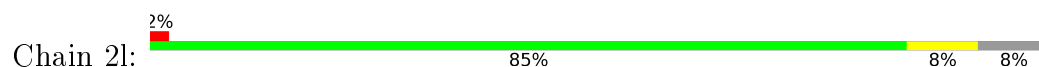
- Molecule 42: 30S ribosomal protein S11



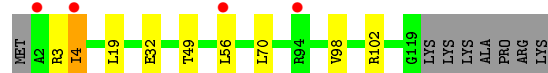
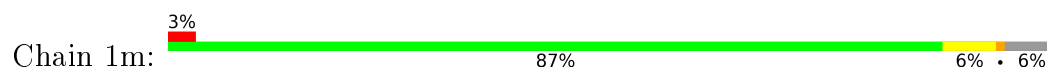
- Molecule 43: 30S ribosomal protein S12



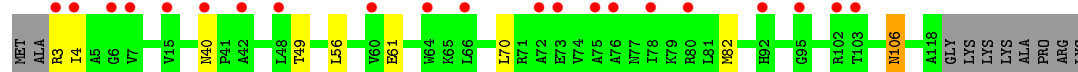
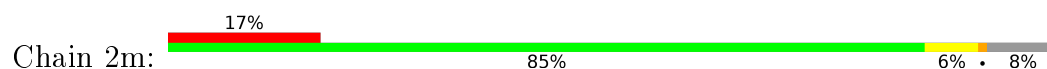
- Molecule 43: 30S ribosomal protein S12



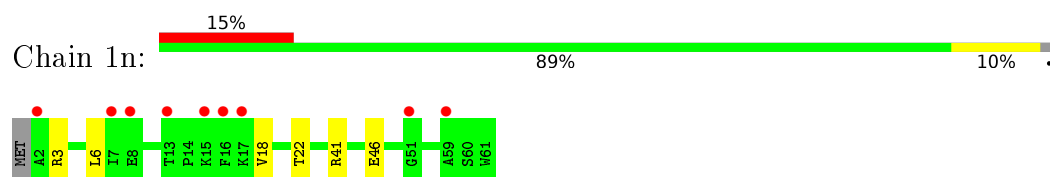
- Molecule 44: 30S ribosomal protein S13



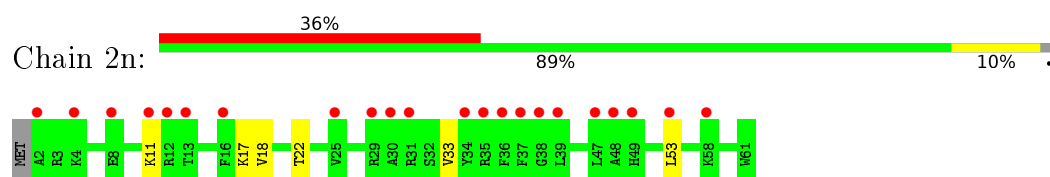
- Molecule 44: 30S ribosomal protein S13



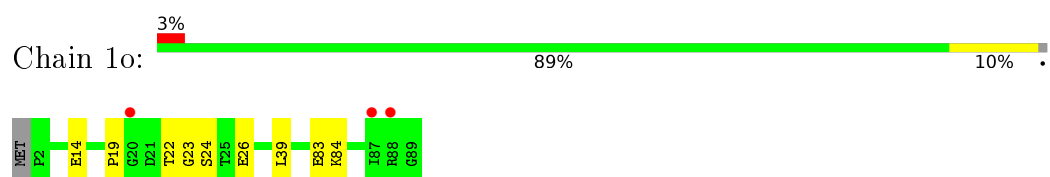
- Molecule 45: 30S ribosomal protein S14 type Z



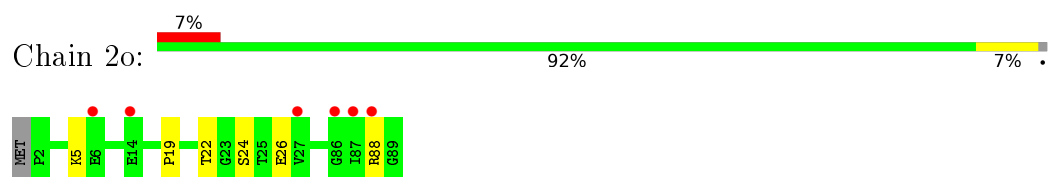
- Molecule 45: 30S ribosomal protein S14 type Z



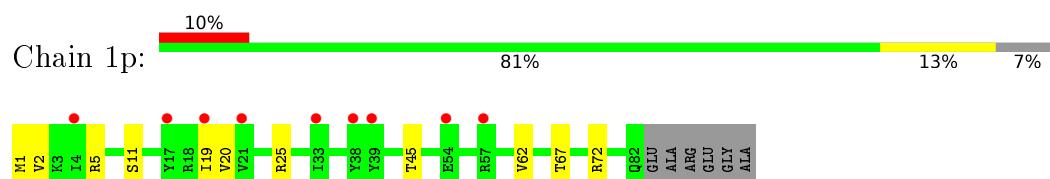
- Molecule 46: 30S ribosomal protein S15



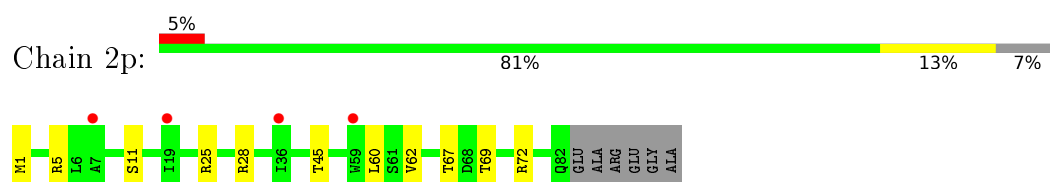
- Molecule 46: 30S ribosomal protein S15



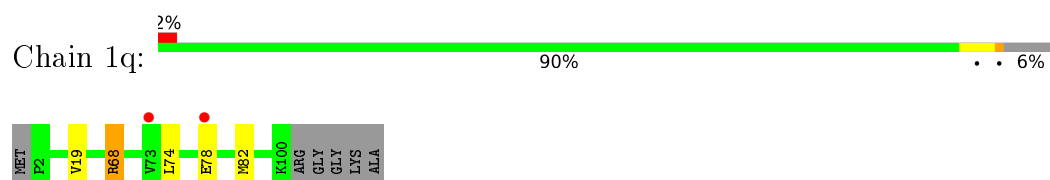
- Molecule 47: 30S ribosomal protein S16



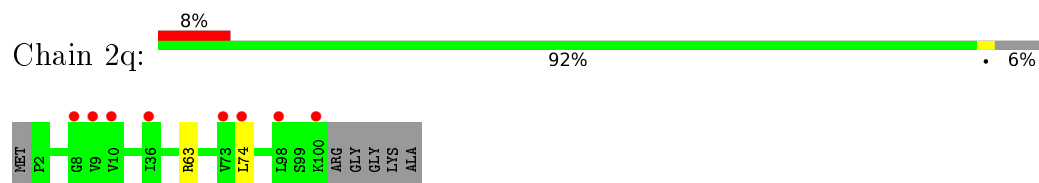
- Molecule 47: 30S ribosomal protein S16



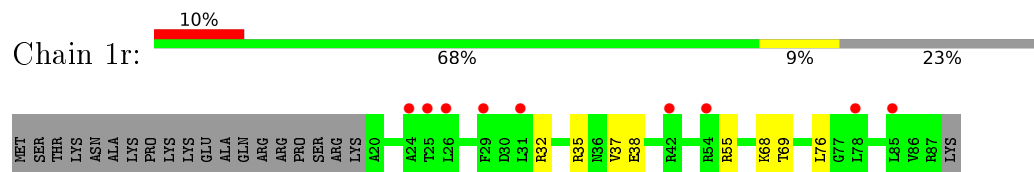
- Molecule 48: 30S ribosomal protein S17



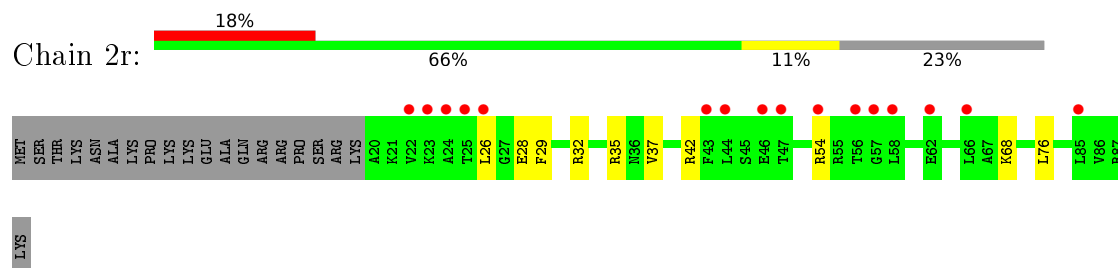
- Molecule 48: 30S ribosomal protein S17



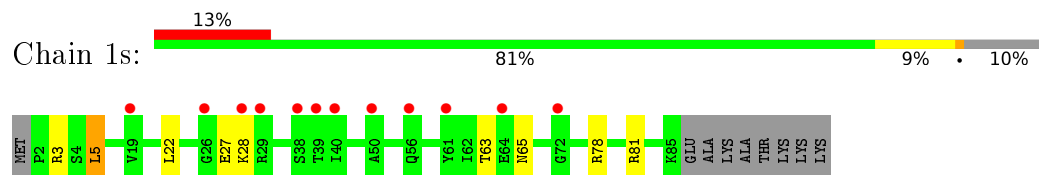
- Molecule 49: 30S ribosomal protein S18



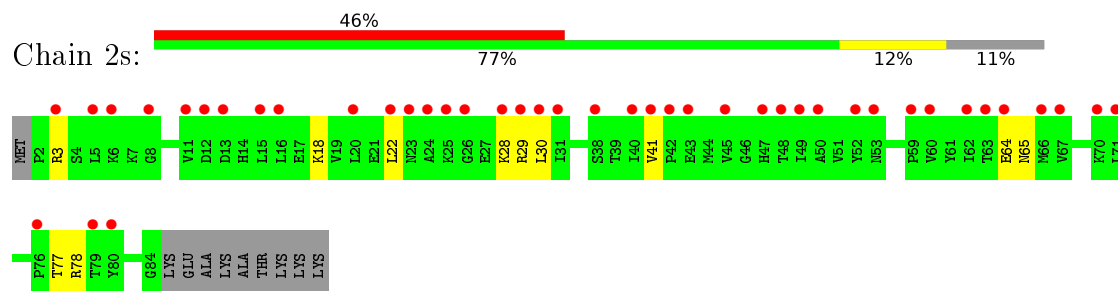
- Molecule 49: 30S ribosomal protein S18



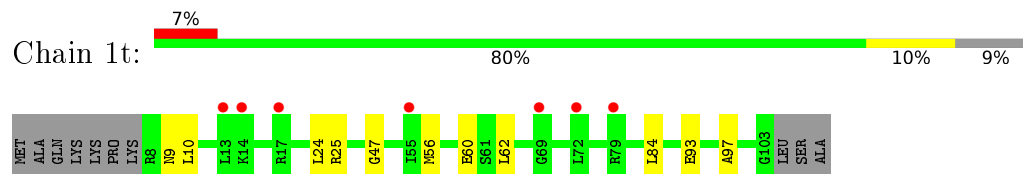
- Molecule 50: 30S ribosomal protein S19



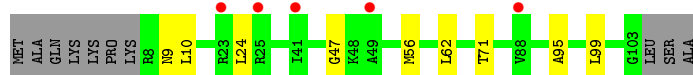
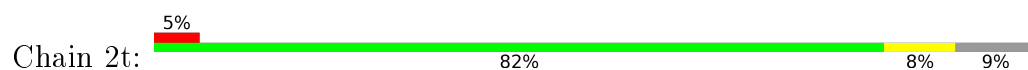
- Molecule 50: 30S ribosomal protein S19



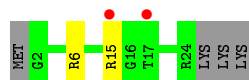
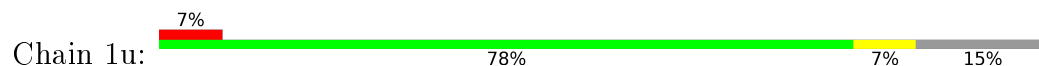
- Molecule 51: 30S ribosomal protein S20



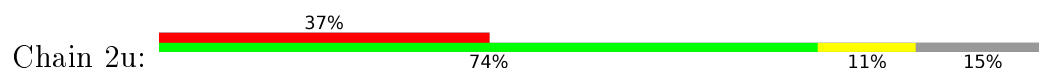
- Molecule 51: 30S ribosomal protein S20



- Molecule 52: 30S ribosomal protein Thx



- Molecule 52: 30S ribosomal protein Thx



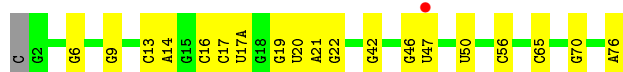
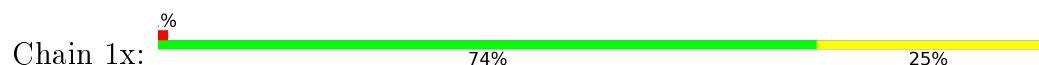
- Molecule 53: mRNA



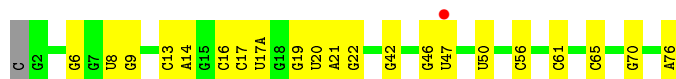
- Molecule 53: mRNA



- Molecule 54: P-site tRNA

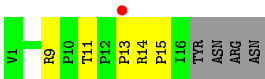


- Molecule 54: P-site tRNA



- Molecule 55: Pyrrhocoricin





● Molecule 55: Pyrrhocoricin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.01Å 450.12Å 622.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.69 – 2.70 49.69 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.4 (49.69-2.70) 99.3 (49.69-2.70)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.14 (at 2.69Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.220 , 0.272 0.229 , 0.278	Depositor DCC
R_{free} test set	79488 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	54.9	Xtriage
Anisotropy	0.097	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 57.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	0 of 1583826 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	288775	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.72% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: 5MU, ZN, SF4, MG, 5MC, 4SU, PSU

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	1A	0.58	4/66249 (0.0%)	0.97	80/103407 (0.1%)
1	2A	0.46	1/67298 (0.0%)	0.94	45/105044 (0.0%)
2	1B	0.45	0/2877	0.85	0/4488
2	2B	0.52	0/2878	0.96	1/4490 (0.0%)
3	1D	0.39	0/2186	0.56	0/2944
3	2D	0.35	0/2192	0.56	0/2951
4	1E	0.40	0/1592	0.57	0/2149
4	2E	0.35	0/1592	0.56	0/2149
5	1F	0.39	0/1619	0.56	0/2193
5	2F	0.34	0/1615	0.56	0/2188
6	1G	0.31	0/1450	0.54	0/1959
6	2G	0.33	0/1449	0.57	0/1958
7	1H	0.34	0/1356	0.53	0/1834
7	2H	0.32	0/1356	0.53	0/1834
8	1I	0.31	0/1100	0.57	0/1501
8	2I	0.30	0/1076	0.55	0/1471
9	1N	0.38	0/1144	0.55	0/1543
9	2N	0.34	0/1144	0.53	0/1543
10	1O	0.42	0/943	0.56	0/1269
10	2O	0.35	0/943	0.58	1/1269 (0.1%)
11	1P	0.37	0/1156	0.59	1/1537 (0.1%)
11	2P	0.36	0/1152	0.60	0/1533
12	1Q	0.38	0/1143	0.53	0/1527
12	2Q	0.36	0/1143	0.58	0/1527
13	1R	0.40	0/982	0.63	0/1312
13	2R	0.33	0/982	0.56	0/1312
14	1S	0.38	0/887	0.55	0/1180
14	2S	0.32	0/880	0.56	0/1172
15	1T	0.37	0/1105	0.56	0/1477
15	2T	0.32	0/1097	0.54	0/1468
16	1U	0.43	0/977	0.54	0/1301
16	2U	0.38	0/977	0.55	1/1301 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	1V	0.39	0/782	0.56	0/1049
17	2V	0.37	0/782	0.56	0/1049
18	1W	0.43	0/897	0.57	0/1205
18	2W	0.38	0/897	0.58	0/1205
19	1X	0.38	0/764	0.54	0/1025
19	2X	0.36	0/764	0.57	1/1025 (0.1%)
20	1Y	0.38	0/819	0.58	0/1095
20	2Y	0.34	0/819	0.55	0/1095
21	1Z	0.32	0/1502	0.51	0/2041
21	2Z	0.33	0/1486	0.51	0/2022
22	10	0.40	0/606	0.58	0/808
22	20	0.35	0/606	0.54	0/808
23	11	0.36	0/762	0.54	0/1014
23	21	0.34	0/762	0.51	0/1014
24	12	0.35	0/590	0.51	0/781
24	22	0.33	0/590	0.47	0/781
25	13	0.37	0/474	0.55	0/635
25	23	0.32	0/469	0.54	0/630
26	14	0.34	0/571	0.66	0/768
26	24	0.35	0/545	0.64	0/737
27	15	0.41	0/469	0.59	0/635
27	25	0.37	0/469	0.54	0/635
28	16	0.38	0/460	0.54	0/613
28	26	0.34	0/456	0.51	0/608
29	17	0.43	0/426	0.54	0/561
29	27	0.37	0/426	0.51	0/561
30	18	0.39	0/525	0.58	0/691
30	28	0.36	0/525	0.55	0/691
31	19	0.43	0/310	0.53	0/407
31	29	0.33	0/310	0.56	0/407
32	1a	0.39	0/35537	0.89	20/55456 (0.0%)
32	2a	0.37	0/35680	0.88	18/55681 (0.0%)
33	1b	0.31	0/1820	0.55	0/2468
33	2b	2.72	8/1728 (0.5%)	0.71	3/2352 (0.1%)
34	1c	0.28	0/1504	0.49	0/2047
34	2c	0.31	0/1435	0.54	1/1960 (0.1%)
35	1d	0.30	0/1648	0.56	1/2222 (0.0%)
35	2d	0.30	0/1659	0.56	0/2230
36	1e	0.31	0/1145	0.53	0/1543
36	2e	0.30	0/1111	0.57	0/1504
37	1f	0.30	0/819	0.49	0/1111
37	2f	0.31	0/830	0.51	0/1125
38	1g	0.28	0/1198	0.47	0/1613

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	2g	0.28	0/1185	0.46	0/1602
39	1h	0.30	0/1108	0.53	0/1494
39	2h	0.29	0/1094	0.52	0/1478
40	1i	0.30	0/995	0.55	0/1339
40	2i	0.30	0/949	0.55	0/1284
41	1j	0.30	0/695	0.56	0/950
41	2j	0.31	0/690	0.56	0/943
42	1k	0.30	0/840	0.53	0/1138
42	2k	0.28	0/844	0.50	0/1145
43	1l	0.32	0/936	0.52	0/1263
43	2l	0.33	0/934	0.59	1/1262 (0.1%)
44	1m	0.29	0/933	0.55	0/1254
44	2m	0.30	0/913	0.53	0/1230
45	1n	0.32	0/491	0.56	0/653
45	2n	0.35	0/467	0.50	0/624
46	1o	0.31	0/726	0.56	1/970 (0.1%)
46	2o	0.31	0/739	0.52	0/985
47	1p	0.26	0/686	0.52	0/926
47	2p	0.30	0/693	0.53	0/935
48	1q	0.32	0/824	0.55	0/1105
48	2q	0.30	0/836	0.48	0/1117
49	1r	0.31	0/560	0.58	0/746
49	2r	0.29	0/560	0.53	0/746
50	1s	0.29	0/657	0.58	1/890 (0.1%)
50	2s	0.32	0/661	0.61	0/893
51	1t	0.30	0/714	0.60	0/948
51	2t	0.29	0/733	0.51	0/969
52	1u	0.26	0/191	0.45	0/252
52	2u	0.33	0/203	0.52	0/266
53	1v	0.66	0/122	1.28	0/188
53	2v	0.48	0/122	0.92	0/188
54	1x	0.53	1/1725 (0.1%)	1.10	16/2689 (0.6%)
54	2x	0.50	0/1725	1.09	11/2689 (0.4%)
55	1z	0.43	0/131	0.67	0/180
55	2z	0.46	0/131	0.67	0/180
All	All	0.49	14/306330 (0.0%)	0.85	203/458260 (0.0%)

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
5	2F	0	1
35	1d	0	1
All	All	0	2

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	2b	92	TYR	CD1-CE1	58.51	2.27	1.39
33	2b	92	TYR	CD2-CE2	54.48	2.21	1.39
33	2b	92	TYR	CE1-CZ	41.36	1.92	1.38
33	2b	92	TYR	CE2-CZ	41.27	1.92	1.38
33	2b	92	TYR	CG-CD1	33.70	1.82	1.39
33	2b	92	TYR	CG-CD2	32.49	1.81	1.39
33	2b	151	GLY	N-CA	22.66	1.80	1.46
33	2b	150	SER	C-N	10.36	1.51	1.33
1	1A	552	A	N9-C4	-6.54	1.33	1.37
1	1A	1187	A	N9-C4	-6.41	1.34	1.37
1	1A	1066	A	N9-C4	-5.90	1.34	1.37
54	1x	22	G	N7-C5	5.61	1.42	1.39
1	2A	1187	A	N9-C4	-5.47	1.34	1.37
1	1A	353	A	N9-C4	-5.26	1.34	1.37

All (203) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	2b	150	SER	C-N-CA	16.36	156.66	122.30
54	1x	46	G	C6-N1-C2	-10.69	118.69	125.10
1	1A	552	A	C2-N3-C4	-9.99	105.61	110.60
54	2x	46	G	C6-N1-C2	-9.61	119.33	125.10
33	2b	151	GLY	N-CA-C	9.25	136.23	113.10
54	2x	14	A	C4-C5-C6	8.71	121.36	117.00
54	1x	14	A	C5-N7-C8	8.42	108.11	103.90
1	1A	1066	A	C2-N3-C4	-8.31	106.45	110.60
1	1A	1806	G	O5'-P-OP2	-8.21	98.31	105.70
1	1A	589	A	O5'-P-OP1	-8.20	98.32	105.70
1	1A	11	U	C2-N1-C1'	8.06	127.37	117.70
54	1x	14	A	C4-C5-C6	8.00	121.00	117.00
54	1x	22	G	C5-N7-C8	-7.94	100.33	104.30
32	2a	738	C	C2-N1-C1'	7.78	127.36	118.80
1	1A	989	A	N1-C6-N6	7.76	123.26	118.60
1	1A	1187	A	C2-N3-C4	-7.75	106.72	110.60
1	1A	353	A	C2-N3-C4	-7.70	106.75	110.60
1	1A	847	G	O5'-P-OP2	-7.62	98.84	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	2484	U	N3-C2-O2	-7.41	117.02	122.20
1	1A	536	G	O4'-C1'-N9	7.39	114.11	108.20
54	2x	22	G	C5-N7-C8	-7.36	100.62	104.30
1	1A	2083	A	O4'-C1'-N9	7.27	114.01	108.20
1	2A	2484	U	C2-N1-C1'	7.13	126.26	117.70
1	2A	2484	U	N1-C2-O2	7.13	127.79	122.80
32	1a	87	C	C2-N3-C4	7.08	123.44	119.90
54	1x	46	G	C5-C6-N1	7.06	115.03	111.50
1	1A	1066	A	C5-N7-C8	-6.98	100.41	103.90
32	1a	87	C	N1-C2-O2	6.95	123.07	118.90
1	1A	2452	C	O5'-P-OP2	-6.93	99.46	105.70
1	1A	138	A	N7-C8-N9	6.92	117.26	113.80
54	2x	46	G	C5-C6-N1	6.91	114.95	111.50
1	1A	1417	U	N3-C4-O4	6.88	124.22	119.40
1	1A	1659	A	O5'-P-OP1	-6.88	99.51	105.70
1	1A	989	A	C2-N3-C4	-6.86	107.17	110.60
1	1A	552	A	N3-C4-N9	-6.68	122.06	127.40
1	1A	552	A	N3-C4-C5	6.67	131.47	126.80
32	1a	825	U	C5-C6-N1	6.65	126.03	122.70
1	1A	1417	U	C5-C4-O4	-6.62	121.93	125.90
1	2A	2260	U	N3-C4-O4	-6.62	114.77	119.40
1	1A	1220	G	OP1-P-O3'	6.61	119.74	105.20
1	1A	1067	G	N3-C4-N9	-6.55	122.07	126.00
1	1A	138	A	C5-N7-C8	-6.52	100.64	103.90
1	2A	536	G	O4'-C1'-N9	6.50	113.40	108.20
32	1a	1048	U	P-O3'-C3'	6.50	127.49	119.70
1	1A	977	A	C5-N7-C8	-6.49	100.65	103.90
1	2A	1302	C	C6-N1-C2	-6.49	117.70	120.30
1	2A	552	A	C2-N3-C4	-6.48	107.36	110.60
1	1A	989	A	C5-N7-C8	-6.48	100.66	103.90
1	2A	596	C	O5'-P-OP1	-6.47	99.88	105.70
1	1A	1248	A	O4'-C1'-N9	6.45	113.36	108.20
1	1A	1066	A	N7-C8-N9	6.40	117.00	113.80
1	1A	2514	A	C8-N9-C4	6.40	108.36	105.80
54	2x	14	A	C5-N7-C8	6.39	107.10	103.90
43	2l	29	GLY	N-CA-C	-6.38	97.14	113.10
1	1A	2083	A	C2-N3-C4	-6.36	107.42	110.60
1	2A	1358	U	C2-N1-C1'	6.36	125.33	117.70
1	1A	989	A	C4-C5-N7	6.33	113.86	110.70
1	1A	2013	G	P-O3'-C3'	6.31	127.27	119.70
1	1A	2857	G	O4'-C1'-N9	6.28	113.22	108.20
54	1x	22	G	C4-C5-C6	-6.23	115.06	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	1x	22	G	N3-C4-N9	-6.20	122.28	126.00
1	1A	214	G	O4'-C1'-N9	6.17	113.13	108.20
34	2c	178	LEU	CA-CB-CG	6.16	129.46	115.30
1	1A	1066	A	N1-C2-N3	6.11	132.35	129.30
1	1A	409	U	C2-N1-C1'	-6.11	110.37	117.70
1	1A	551	C	N3-C2-O2	-6.08	117.64	121.90
32	2a	982	G	C4-N9-C1'	6.08	134.41	126.50
1	2A	1693	G	O4'-C1'-N9	-6.07	103.35	108.20
2	2B	30	C	C6-N1-C2	-6.04	117.88	120.30
32	1a	77	G	C5-C6-O6	5.99	132.19	128.60
1	1A	30	C	O5'-P-OP1	-5.97	100.32	105.70
1	1A	1812	C	OP1-P-O3'	5.97	118.34	105.20
1	1A	1358	U	C2-N1-C1'	5.96	124.85	117.70
19	2X	57	LEU	CA-CB-CG	5.90	128.88	115.30
54	2x	14	A	C5-C6-N1	-5.90	114.75	117.70
32	1a	77	G	N1-C6-O6	-5.89	116.36	119.90
1	1A	839	A	O5'-P-OP2	-5.88	100.41	105.70
1	1A	2514	A	N9-C4-C5	-5.87	103.45	105.80
33	2b	187	LEU	CA-CB-CG	5.84	128.74	115.30
1	1A	138	A	O4'-C1'-N9	5.84	112.87	108.20
1	1A	610	U	O5'-P-OP2	-5.84	100.45	105.70
32	1a	1349	C	C2-N3-C4	5.84	122.82	119.90
32	2a	982	G	N3-C4-C5	-5.82	125.69	128.60
54	1x	22	G	C8-N9-C1'	5.81	134.56	127.00
1	2A	552	A	N3-C4-C5	5.80	130.86	126.80
32	2a	738	C	N1-C2-O2	5.77	122.36	118.90
1	2A	193	G	O5'-P-OP2	-5.77	100.51	105.70
1	2A	829	A	C2-N3-C4	5.77	113.48	110.60
32	2a	1141	C	C2-N1-C1'	5.76	125.14	118.80
10	2O	8	LEU	CA-CB-CG	5.76	128.54	115.30
32	2a	74	G	C5-C6-O6	5.74	132.05	128.60
1	2A	1359	C	C2-N1-C1'	5.74	125.11	118.80
1	2A	1806	G	O5'-P-OP2	-5.74	100.53	105.70
1	2A	1187	A	C2-N3-C4	-5.73	107.74	110.60
1	2A	714	G	N3-C4-C5	5.68	131.44	128.60
32	2a	738	C	C6-N1-C1'	-5.68	113.99	120.80
1	2A	794	G	C4-N9-C1'	-5.68	119.12	126.50
54	1x	22	G	N1-C6-O6	-5.66	116.50	119.90
32	2a	66	U	P-O3'-C3'	5.65	126.48	119.70
32	1a	262	G	P-O3'-C3'	5.63	126.45	119.70
1	2A	88	U	N1-C2-O2	5.62	126.73	122.80
1	2A	2013	G	P-O3'-C3'	5.62	126.44	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	138	A	C8-N9-C4	-5.61	103.56	105.80
1	1A	905	G	N3-C4-C5	5.61	131.40	128.60
1	1A	2083	A	N1-C2-N3	5.60	132.10	129.30
54	1x	22	G	N7-C8-N9	5.60	115.90	113.10
32	1a	150	C	N1-C2-O2	5.60	122.26	118.90
54	1x	14	A	C5-C6-N1	-5.60	114.90	117.70
32	2a	986	C	C2-N3-C4	5.57	122.69	119.90
32	1a	1480	A	N1-C2-N3	5.56	132.08	129.30
1	2A	1248	A	N1-C6-N6	5.55	121.93	118.60
1	2A	2260	U	N3-C4-C5	5.55	117.93	114.60
1	1A	1044	U	O5'-P-OP2	-5.55	100.71	105.70
1	1A	551	C	C5-C4-N4	5.54	124.08	120.20
1	1A	2830	A	N1-C6-N6	5.53	121.92	118.60
1	1A	1693	G	O4'-C1'-N9	-5.52	103.78	108.20
32	2a	982	G	C8-N9-C4	-5.51	104.20	106.40
1	2A	409	U	O4'-C1'-N1	5.49	112.59	108.20
1	1A	2514	A	N1-C2-N3	-5.49	126.55	129.30
32	2a	1141	C	C6-N1-C2	-5.47	118.11	120.30
1	2A	1092	G	C4-N9-C1'	5.46	133.60	126.50
1	2A	33	C	N1-C2-O2	5.45	122.17	118.90
54	1x	14	A	C8-N9-C1'	-5.44	117.90	127.70
32	2a	109	G	P-O3'-C3'	5.44	126.22	119.70
32	1a	986	C	N1-C2-O2	5.42	122.15	118.90
1	1A	1187	A	N3-C4-C5	5.41	130.59	126.80
50	1s	5	LEU	CA-CB-CG	5.39	127.70	115.30
1	2A	989	A	O4'-C1'-N9	5.38	112.51	108.20
35	1d	10	ARG	N-CA-C	-5.37	96.51	111.00
1	2A	2700	U	P-O3'-C3'	5.36	126.13	119.70
54	2x	22	G	C4-C5-C6	-5.36	115.59	118.80
16	2U	74	LEU	CA-CB-CG	5.35	127.60	115.30
32	1a	999	U	C2-N1-C1'	5.34	124.11	117.70
54	2x	46	G	N3-C2-N2	-5.34	116.16	119.90
32	2a	982	G	N7-C8-N9	5.33	115.77	113.10
1	2A	838	G	N3-C4-N9	5.32	129.19	126.00
1	1A	2346	A	O4'-C1'-N9	5.31	112.45	108.20
1	1A	989	A	C6-C5-N7	-5.31	128.59	132.30
11	1P	99	LEU	CA-CB-CG	5.30	127.50	115.30
32	1a	1001	G	N3-C4-N9	5.30	129.18	126.00
32	2a	1349	C	N1-C2-O2	5.30	122.08	118.90
1	1A	1662	C	N1-C2-O2	-5.30	115.72	118.90
1	2A	1248	A	O4'-C1'-N9	5.30	112.44	108.20
1	2A	1440	A	O4'-C1'-N9	5.29	112.43	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	2209	C	N1-C2-O2	5.27	122.06	118.90
54	1x	46	G	N3-C2-N2	-5.26	116.22	119.90
1	2A	1690	C	N1-C2-O2	5.26	122.06	118.90
1	2A	1425	G	O5'-P-OP2	-5.25	100.97	105.70
32	1a	1120	C	C6-N1-C2	-5.25	118.20	120.30
1	1A	977	A	N7-C8-N9	5.24	116.42	113.80
32	2a	1349	C	C2-N3-C4	5.24	122.52	119.90
32	2a	78	G	C5-C6-O6	5.22	131.73	128.60
1	2A	2260	U	C6-N1-C2	5.21	124.13	121.00
1	1A	977	A	O4'-C1'-N9	5.20	112.36	108.20
54	1x	14	A	C4-N9-C1'	5.20	135.65	126.30
1	1A	1461	G	O4'-C1'-N9	5.20	112.36	108.20
1	2A	1920	G	N3-C4-N9	5.20	129.12	126.00
1	1A	353	A	N1-C2-N3	5.19	131.90	129.30
1	1A	1744	A	N1-C6-N6	5.19	121.71	118.60
1	1A	1397	U	O5'-P-OP1	-5.18	101.03	105.70
1	1A	1744	A	C2-N3-C4	-5.18	108.01	110.60
1	1A	2249	G	N3-C4-N9	5.18	129.11	126.00
1	1A	1604	A	C2-N3-C4	-5.18	108.01	110.60
54	2x	46	G	C5-C6-O6	-5.17	125.50	128.60
1	2A	202	G	O4'-C1'-N9	5.17	112.34	108.20
46	1o	23	GLY	N-CA-C	5.17	126.03	113.10
1	2A	88	U	N3-C2-O2	-5.17	118.58	122.20
1	1A	398	G	O4'-C1'-N9	5.17	112.33	108.20
1	2A	1066	A	C2-N3-C4	-5.17	108.02	110.60
1	1A	891	G	O4'-C1'-N9	5.16	112.32	108.20
32	1a	1066	U	N1-C2-O2	-5.15	119.19	122.80
1	1A	11	U	C6-N1-C1'	-5.14	114.01	121.20
1	2A	2013	G	C8-N9-C4	-5.13	104.35	106.40
54	1x	46	G	N9-C4-C5	5.12	107.45	105.40
54	2x	22	G	N7-C8-N9	5.12	115.66	113.10
1	2A	552	A	N3-C4-N9	-5.12	123.31	127.40
1	2A	1114	A	P-O3'-C3'	5.12	125.84	119.70
1	1A	2298	A	C2-N3-C4	-5.11	108.05	110.60
1	1A	820	A	C8-N9-C4	-5.10	103.76	105.80
1	1A	2013	G	O4'-C1'-N9	-5.09	104.13	108.20
1	2A	1297	G	C8-N9-C4	5.09	108.44	106.40
32	2a	1048	U	P-O3'-C3'	5.09	125.80	119.70
1	2A	1187	A	N3-C4-C5	5.08	130.36	126.80
1	2A	714	G	N3-C4-N9	-5.08	122.95	126.00
1	2A	838	G	N3-C4-C5	-5.08	126.06	128.60
32	2a	1183	A	P-O3'-C3'	5.07	125.79	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	2723	U	O4'-C1'-N1	5.07	112.26	108.20
1	1A	2596	U	OP1-P-O3'	5.07	116.34	105.20
54	2x	14	A	C4-N9-C1'	5.06	135.41	126.30
32	1a	671	A	P-O3'-C3'	5.06	125.77	119.70
54	1x	14	A	C4-C5-N7	-5.05	108.18	110.70
1	1A	1176	G	O4'-C1'-N9	5.04	112.24	108.20
1	1A	2514	A	C5-C6-N6	-5.04	119.67	123.70
32	1a	1048	U	OP2-P-O3'	5.04	116.29	105.20
1	1A	2082	G	O5'-P-OP2	-5.03	101.17	105.70
1	1A	1066	A	C8-N9-C4	-5.03	103.79	105.80
1	1A	1744	A	C6-C5-N7	-5.02	128.79	132.30
32	1a	87	C	N3-C4-C5	-5.02	119.89	121.90
32	1a	823	U	P-O3'-C3'	5.01	125.72	119.70
1	1A	977	A	C4-C5-N7	5.01	113.21	110.70
1	1A	2701	C	O5'-P-OP1	-5.01	101.19	105.70
32	1a	1001	G	N3-C2-N2	5.01	123.41	119.90
1	1A	2700	U	N3-C2-O2	-5.00	118.70	122.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
35	1d	9	CYS	Peptide
5	2F	20	LEU	Peptide

5.2 Too-close contacts [i](#)

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	1A	59154	0	29828	579	0
1	2A	60091	0	30297	828	0
2	1B	2572	0	1306	20	0
2	2B	2573	0	1306	52	0
3	1D	2136	0	2218	53	0
3	2D	2142	0	2229	65	0
4	1E	1559	0	1618	30	0
4	2E	1559	0	1618	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	1F	1584	0	1625	30	0
5	2F	1580	0	1619	47	0
6	1G	1425	0	1443	25	0
6	2G	1424	0	1434	61	0
7	1H	1330	0	1407	25	0
7	2H	1330	0	1407	29	0
8	1I	1085	0	1114	27	0
8	2I	1061	0	1080	19	0
9	1N	1117	0	1184	15	0
9	2N	1117	0	1184	15	0
10	1O	933	0	996	17	0
10	2O	933	0	996	20	0
11	1P	1139	0	1223	27	0
11	2P	1135	0	1212	47	0
12	1Q	1122	0	1178	23	0
12	2Q	1122	0	1179	24	0
13	1R	968	0	1033	12	0
13	2R	968	0	1033	18	0
14	1S	877	0	938	28	0
14	2S	870	0	923	25	0
15	1T	1091	0	1151	32	0
15	2T	1083	0	1136	27	0
16	1U	959	0	1019	12	0
16	2U	959	0	1018	21	0
17	1V	771	0	830	9	0
17	2V	771	0	830	15	0
18	1W	886	0	940	9	0
18	2W	886	0	940	19	0
19	1X	750	0	814	19	0
19	2X	750	0	814	21	0
20	1Y	806	0	881	18	0
20	2Y	806	0	881	20	0
21	1Z	1470	0	1478	27	0
21	2Z	1454	0	1452	43	0
22	10	598	0	614	15	0
22	20	598	0	614	12	0
23	11	755	0	826	11	0
23	21	755	0	826	18	0
24	12	588	0	643	11	0
24	22	588	0	643	9	0
25	13	469	0	518	6	0
25	23	464	0	514	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	14	558	0	544	24	0
26	24	532	0	503	22	0
27	15	455	0	465	6	0
27	25	455	0	465	13	0
28	16	453	0	473	8	0
28	26	449	0	469	11	0
29	17	418	0	467	12	0
29	27	418	0	467	10	0
30	18	517	0	582	10	0
30	28	517	0	582	19	0
31	19	307	0	335	10	0
31	29	307	0	335	13	0
32	1a	31750	0	16028	0	0
32	2a	31877	0	16089	0	0
33	1b	1786	0	1744	0	0
33	2b	1697	0	1574	0	0
34	1c	1480	0	1400	0	0
34	2c	1412	0	1246	0	0
35	1d	1618	0	1579	0	0
35	2d	1630	0	1633	0	0
36	1e	1129	0	1185	0	0
36	2e	1095	0	1124	0	0
37	1f	806	0	793	0	0
37	2f	817	0	808	0	0
38	1g	1183	0	1165	0	0
38	2g	1167	0	1119	0	0
39	1h	1088	0	1126	0	0
39	2h	1074	0	1100	0	0
40	1i	976	0	973	0	0
40	2i	932	0	891	0	0
41	1j	682	0	598	0	0
41	2j	678	0	612	0	0
42	1k	826	0	829	0	0
42	2k	829	0	825	0	0
43	1l	920	0	958	0	0
43	2l	918	0	947	0	0
44	1m	923	0	962	0	0
44	2m	903	0	923	0	0
45	1n	482	0	507	0	0
45	2n	459	0	467	0	0
46	1o	715	0	729	0	0
46	2o	728	0	760	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	1p	671	0	679	0	0
47	2p	677	0	686	0	0
48	1q	811	0	858	0	0
48	2q	823	0	891	0	0
49	1r	555	0	618	0	0
49	2r	555	0	618	0	0
50	1s	642	0	629	0	0
50	2s	646	0	644	0	0
51	1t	712	0	759	0	0
51	2t	731	0	807	0	0
52	1u	187	0	186	0	0
52	2u	199	0	208	0	0
53	1v	109	0	55	0	0
53	2v	109	0	55	0	0
54	1x	1625	0	829	0	0
54	2x	1625	0	829	0	0
55	1z	126	0	135	0	0
55	2z	126	0	135	0	0
56	10	7	0	0	0	0
56	11	3	0	0	0	0
56	12	1	0	0	0	0
56	13	1	0	0	0	0
56	15	4	0	0	0	0
56	16	2	0	0	0	0
56	17	3	0	0	0	0
56	18	5	0	0	0	0
56	19	3	0	0	0	0
56	1A	1233	0	0	0	0
56	1B	25	0	0	0	0
56	1D	15	0	0	0	0
56	1E	8	0	0	0	0
56	1F	9	0	0	0	0
56	1G	3	0	0	0	0
56	1H	1	0	0	0	0
56	1N	7	0	0	0	0
56	1O	3	0	0	0	0
56	1P	5	0	0	0	0
56	1Q	5	0	0	0	0
56	1R	8	0	0	0	0
56	1T	4	0	0	0	0
56	1U	6	0	0	0	0
56	1V	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	1W	6	0	0	0	0
56	1X	1	0	0	0	0
56	1Y	1	0	0	0	0
56	1Z	3	0	0	0	0
56	1a	295	0	0	0	0
56	1b	2	0	0	0	0
56	1d	1	0	0	0	0
56	1e	3	0	0	0	0
56	1f	1	0	0	0	0
56	1h	2	0	0	0	0
56	1k	2	0	0	0	0
56	1l	1	0	0	0	0
56	1n	1	0	0	0	0
56	1o	1	0	0	0	0
56	1p	1	0	0	0	0
56	1q	2	0	0	0	0
56	1r	2	0	0	0	0
56	1t	1	0	0	0	0
56	1x	12	0	0	0	0
56	20	1	0	0	0	0
56	23	1	0	0	0	0
56	25	1	0	0	0	0
56	28	2	0	0	0	0
56	2A	592	0	0	0	0
56	2B	9	0	0	0	0
56	2D	6	0	0	0	0
56	2E	6	0	0	0	0
56	2F	2	0	0	0	0
56	2G	1	0	0	0	0
56	2N	1	0	0	0	0
56	2O	3	0	0	0	0
56	2Q	5	0	0	0	0
56	2X	1	0	0	0	0
56	2Y	1	0	0	0	0
56	2Z	1	0	0	0	0
56	2a	248	0	0	0	0
56	2d	1	0	0	0	0
56	2e	2	0	0	0	0
56	2f	1	0	0	0	0
56	2l	5	0	0	0	0
56	2n	1	0	0	0	0
56	2p	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	2q	2	0	0	0	0
56	2t	1	0	0	0	0
56	2u	1	0	0	0	0
56	2x	4	0	0	0	0
57	14	1	0	0	0	0
57	15	1	0	0	0	0
57	16	1	0	0	0	0
57	19	1	0	0	0	0
57	1Y	1	0	0	0	0
57	1n	1	0	0	0	0
57	24	1	0	0	0	0
57	25	1	0	0	0	0
57	26	1	0	0	0	0
57	29	1	0	0	0	0
57	2Y	1	0	0	0	0
57	2n	1	0	0	0	0
58	1d	8	0	0	0	0
58	2d	8	0	0	0	0
59	10	12	0	0	0	0
59	11	5	0	0	0	0
59	12	3	0	0	0	0
59	13	4	0	0	1	0
59	15	9	0	0	0	0
59	16	9	0	0	3	0
59	17	10	0	0	1	0
59	18	12	0	0	1	0
59	19	2	0	0	0	0
59	1A	2217	0	0	122	0
59	1B	37	0	0	4	0
59	1D	23	0	0	1	0
59	1E	29	0	0	4	0
59	1F	19	0	0	1	0
59	1G	2	0	0	0	0
59	1H	4	0	0	0	0
59	1I	1	0	0	1	0
59	1N	6	0	0	2	0
59	1O	7	0	0	0	0
59	1P	27	0	0	0	0
59	1Q	14	0	0	0	0
59	1R	11	0	0	0	0
59	1S	2	0	0	0	0
59	1T	13	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	1U	14	0	0	0	0
59	1V	7	0	0	0	0
59	1W	8	0	0	0	0
59	1X	5	0	0	0	0
59	1Y	1	0	0	0	0
59	1Z	7	0	0	0	0
59	1a	338	0	0	0	0
59	1b	2	0	0	0	0
59	1d	3	0	0	0	0
59	1e	7	0	0	0	0
59	1f	1	0	0	0	0
59	1h	3	0	0	0	0
59	1i	1	0	0	0	0
59	1j	1	0	0	0	0
59	1k	1	0	0	0	0
59	1l	3	0	0	0	0
59	1m	1	0	0	0	0
59	1o	1	0	0	0	0
59	1q	1	0	0	0	0
59	1r	1	0	0	0	0
59	1s	2	0	0	0	0
59	1t	1	0	0	0	0
59	1v	3	0	0	0	0
59	1x	9	0	0	0	0
59	20	4	0	0	0	0
59	21	1	0	0	0	0
59	23	1	0	0	0	0
59	25	1	0	0	0	0
59	27	1	0	0	0	0
59	28	4	0	0	0	0
59	2A	809	0	0	86	0
59	2B	12	0	0	1	0
59	2D	20	0	0	1	0
59	2E	11	0	0	1	0
59	2F	7	0	0	0	0
59	2N	1	0	0	0	0
59	2O	3	0	0	0	0
59	2P	3	0	0	1	0
59	2Q	2	0	0	0	0
59	2R	3	0	0	0	0
59	2T	3	0	0	0	0
59	2U	3	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	2W	1	0	0	0	0
59	2X	2	0	0	1	0
59	2Y	1	0	0	1	0
59	2Z	6	0	0	2	0
59	2a	274	0	0	0	0
59	2c	2	0	0	0	0
59	2d	1	0	0	0	0
59	2i	2	0	0	0	0
59	2j	2	0	0	0	0
59	2l	2	0	0	0	0
59	2p	1	0	0	0	0
59	2t	3	0	0	0	0
59	2v	1	0	0	0	0
59	2x	2	0	0	0	0
All	All	288775	0	190012	2379	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 10.

All (2379) 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)
15:2T:55:ASN:H	15:2T:59:THR:HG22	1.30	0.96
1:1A:353:A:H2	1:1A:1254:A:HO2'	0.98	0.95
1:2A:1116:G:H1	1:2A:1124:C:H42	15.74	0.93
1:1A:1404:A:H61	1:1A:1417:U:H3	1.16	0.93
1:1A:786:U:OP2	59:1A:4301:HOH:O	1.88	0.92
1:2A:183:A:N7	59:2A:3605:HOH:O	2.04	0.90
1:1A:2510:C:OP1	59:1A:4302:HOH:O	1.88	0.90
1:1A:1735:A:H62	1:1A:1744:A:H2	1.20	0.89
15:1T:55:ASN:H	15:1T:59:THR:HG22	1.41	0.86
21:2Z:130:PRO:HB2	21:2Z:131:ARG:HH21	1.40	0.85
1:1A:776:C:OP2	59:1A:4303:HOH:O	1.94	0.85
1:2A:2831:G:OP2	59:2A:3601:HOH:O	1.96	0.84
1:2A:1116:G:H1	1:2A:1124:C:N4	15.75	0.83
1:2A:621:G:N7	59:2A:3616:HOH:O	2.11	0.83
1:2A:1828:U:H5'	3:2D:259:THR:HG22	1.60	0.83
1:1A:893:U:O4	1:1A:977:A:N6	2.12	0.82
20:1Y:54:LYS:HA	20:1Y:56:PRO:HD3	1.61	0.81
1:1A:1647:U:O4	59:1A:4304:HOH:O	1.97	0.81
1:1A:2298:A:H62	1:1A:2355:U:H3	1.29	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:33:ARG:HH11	6:2G:33:ARG:HB2	1.45	0.80
21:2Z:134:PRO:O	21:2Z:136:PHE:N	2.15	0.80
29:17:24:THR:HG22	29:17:27:GLY:H	1.46	0.80
1:2A:1098:C:H42	1:2A:1151:G:H1	1.28	0.79
16:2U:49:HIS:HA	16:2U:52:ARG:HG2	1.64	0.79
1:1A:829:A:OP2	59:1A:4305:HOH:O	1.99	0.79
1:1A:2330:G:N7	59:1A:4339:HOH:O	2.14	0.79
1:1A:893:U:OP2	59:1A:4306:HOH:O	1.99	0.79
1:1A:1066:A:H62	1:1A:1185:U:H3	1.31	0.78
2:2B:20:C:H42	2:2B:63:G:H1	1.31	0.78
1:1A:426:G:N7	59:1A:4346:HOH:O	2.15	0.78
3:1D:71:ASP:HB3	3:1D:103:ARG:HH22	1.49	0.78
1:1A:807:A:OP1	59:1A:4303:HOH:O	2.02	0.77
17:2V:62:LEU:HD23	17:2V:93:GLU:HG2	1.66	0.77
1:2A:2441:A:OP2	59:2A:3603:HOH:O	2.01	0.77
4:2E:132:HIS:NE2	59:2E:401:HOH:O	2.17	0.76
22:10:11:ARG:O	22:10:14:ARG:NH2	2.19	0.76
1:1A:1355:G:OP2	29:17:9:ARG:NH1	2.18	0.76
1:1A:1828:U:H5'	3:1D:259:THR:HG22	1.66	0.76
1:2A:1355:G:OP2	29:27:9:ARG:NH1	2.19	0.76
1:2A:1735:A:H62	1:2A:1744:A:H2	1.32	0.76
18:2W:71:VAL:HA	18:2W:107:LEU:HD12	1.68	0.76
1:1A:1000:G:O6	59:1A:4309:HOH:O	2.04	0.76
1:1A:1377:G:OP1	59:1A:4307:HOH:O	2.02	0.76
1:2A:929:G:N2	1:2A:948:C:O2	28.16	0.76
1:1A:1619:G:OP2	59:1A:4310:HOH:O	2.04	0.75
1:1A:2111:G:O6	59:1A:4308:HOH:O	2.03	0.75
1:2A:1404:A:N6	1:2A:1417:U:O4	2.16	0.75
14:2S:99:LYS:NZ	14:2S:103:GLU:OE2	2.18	0.75
1:1A:474:A:N7	59:1A:4361:HOH:O	2.18	0.75
1:1A:655:A:OP1	11:1P:65:ARG:NH1	2.20	0.75
1:2A:2816:G:N1	1:2A:2901:G:O6	2.18	0.75
1:1A:550:A:OP1	59:1A:4311:HOH:O	2.05	0.75
1:2A:1989:G:OP1	59:2A:3604:HOH:O	2.04	0.75
1:2A:1214:G:H1	1:2A:1224:C:H42	1.32	0.74
15:1T:16:ARG:NH2	15:1T:83:ILE:O	2.20	0.74
1:2A:2626:U:OP1	59:2A:3606:HOH:O	2.05	0.74
1:1A:830:A:OP2	59:1A:4305:HOH:O	2.03	0.74
15:1T:51:ARG:NH1	59:1T:301:HOH:O	2.13	0.74
1:1A:1360:C:OP2	59:1A:4307:HOH:O	2.05	0.74
1:2A:1056:G:OP2	16:2U:66:ASN:ND2	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:900:G:H2'	1:2A:901:G:H8	1.52	0.74
1:2A:1830:C:OP2	3:2D:183:ARG:NH2	2.21	0.74
1:1A:1354:G:H4'	29:17:7:PRO:HB2	1.68	0.73
3:2D:276:LYS:H	3:2D:276:LYS:HD3	1.50	0.73
1:1A:894:G:OP1	59:1A:4315:HOH:O	2.06	0.73
1:2A:1248:A:H2	1:2A:1286:A:H62	1.33	0.73
1:1A:1846:G:O6	3:1D:35:LYS:NZ	2.16	0.73
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.69	0.73
1:1A:1461:G:N2	1:1A:1628:C:O2	2.16	0.73
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.20	0.73
6:1G:161:THR:HG22	6:1G:163:ALA:H	1.52	0.73
1:2A:1066:A:H62	1:2A:1185:U:H3	1.32	0.73
1:2A:2053:G:N7	59:2A:3665:HOH:O	2.22	0.73
1:2A:1649:C:OP2	59:2A:3609:HOH:O	2.06	0.73
1:2A:2517:U:OP1	4:2E:144:ARG:NH2	2.21	0.73
1:2A:655:A:OP1	11:2P:65:ARG:NH1	2.22	0.73
4:1E:47:VAL:HG11	4:1E:86:PRO:HD2	1.71	0.72
18:1W:25:ARG:NH2	18:1W:74:ALA:O	2.21	0.72
1:2A:2858:U:OP2	15:2T:95:ARG:NH1	2.22	0.72
20:2Y:49:VAL:HG21	20:2Y:61:ILE:HG23	1.70	0.72
1:1A:1075:G:OP2	12:1Q:128:LYS:NZ	2.22	0.72
1:1A:2441:A:OP2	59:1A:4312:HOH:O	2.06	0.72
1:1A:1035:A:OP2	59:1A:4320:HOH:O	2.08	0.72
1:1A:909:A:OP2	59:1A:4313:HOH:O	2.06	0.72
1:2A:396:G:OP2	59:2A:3608:HOH:O	2.06	0.72
3:2D:206:LEU:HD22	3:2D:211:ARG:HG2	1.70	0.72
1:2A:2694:C:OP1	15:2T:53:ARG:NH2	2.21	0.72
1:2A:1064:U:H3	1:2A:1187:A:H62	1.36	0.72
1:2A:816:G:OP2	59:2A:3610:HOH:O	2.07	0.72
1:1A:120:G:OP2	59:1A:4316:HOH:O	2.07	0.72
1:2A:2026:A:OP1	59:2A:3607:HOH:O	2.05	0.72
16:2U:92:ARG:HA	16:2U:95:LEU:HB2	1.71	0.72
1:1A:1098:C:H42	1:1A:1151:G:H1	1.37	0.72
1:1A:439:C:O2	1:1A:475:G:N2	74.37	0.72
1:2A:117:U:OP1	59:2A:3613:HOH:O	2.08	0.72
1:1A:2801:C:O2	1:1A:2902:G:N2	2.22	0.72
1:1A:598:U:OP1	59:1A:4317:HOH:O	2.07	0.72
1:2A:186:C:OP2	59:2A:3605:HOH:O	2.08	0.72
1:1A:1502:G:OP2	59:1A:4318:HOH:O	2.07	0.72
1:1A:2100:U:OP1	23:11:21:ARG:NH2	2.22	0.71
1:1A:1248:A:H2	1:1A:1286:A:H62	1.38	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.24	0.71
1:2A:1377:G:OP1	59:2A:3611:HOH:O	2.07	0.71
1:1A:1649:C:OP2	59:1A:4322:HOH:O	2.08	0.71
1:2A:2338:A:H2'	1:2A:2339:A:C8	2.25	0.71
20:2Y:94:LYS:NZ	59:2Y:601:HOH:O	2.23	0.71
1:1A:1435:U:O2	1:1A:1440:A:N6	2.19	0.71
1:1A:2459:A:OP1	59:1A:4302:HOH:O	2.08	0.71
1:1A:1001:A:OP2	59:1A:4319:HOH:O	2.07	0.71
1:1A:2123:U:H3	1:1A:2208:G:H1	1.37	0.71
1:2A:1828:U:OP2	3:2D:274:ARG:NH2	2.23	0.71
1:2A:2513:G:N7	59:2A:3677:HOH:O	2.23	0.71
1:1A:1007:U:OP2	59:1A:4314:HOH:O	2.06	0.71
1:1A:1991:A:OP1	59:1A:4321:HOH:O	2.08	0.71
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.26	0.71
1:2A:2310:G:H2'	1:2A:2311:G:H8	1.55	0.71
1:2A:2696:G:O6	59:2A:3612:HOH:O	2.08	0.71
1:1A:2014:U:OP2	59:1A:4324:HOH:O	2.08	0.71
1:1A:2648:U:H5''	4:1E:82:ARG:HH21	1.55	0.71
1:2A:2405:C:OP2	30:28:30:ARG:NH1	2.24	0.71
1:2A:152:C:OP2	23:21:92:LYS:NZ	2.24	0.71
31:19:2:LYS:NZ	31:19:31:LYS:O	2.24	0.70
15:1T:84:GLN:HG2	15:1T:85:LYS:HD3	1.72	0.70
1:2A:1367:A:OP1	59:2A:3614:HOH:O	2.09	0.70
1:1A:2586:C:OP2	59:1A:4323:HOH:O	2.08	0.70
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.74	0.70
2:2B:58:A:OP2	59:2B:3101:HOH:O	2.08	0.70
4:1E:127:ASP:OD2	59:1E:401:HOH:O	2.10	0.70
8:1I:3:VAL:HG12	8:1I:38:LEU:HA	1.74	0.70
1:2A:1716:C:OP1	59:2A:3615:HOH:O	2.10	0.70
1:1A:2699:U:O4	59:1A:4326:HOH:O	2.10	0.70
15:1T:115:ARG:NH2	59:1T:303:HOH:O	2.25	0.69
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.57	0.69
1:1A:1316:G:OP2	59:1A:4325:HOH:O	2.09	0.69
2:1B:58:A:OP2	59:1B:301:HOH:O	2.09	0.69
28:16:2:ALA:N	59:16:201:HOH:O	2.26	0.69
1:1A:2250:G:OP2	59:1A:4328:HOH:O	2.10	0.69
1:1A:777:C:OP2	59:1A:4303:HOH:O	2.11	0.69
7:1H:3:ARG:HG2	7:1H:6:ARG:HG2	1.75	0.69
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.74	0.69
19:2X:35:THR:HG22	19:2X:37:THR:H	1.57	0.69
1:1A:1054:A:OP2	59:1A:4331:HOH:O	2.11	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.74	0.69
1:2A:1314:A:OP2	59:2A:3607:HOH:O	2.10	0.69
1:2A:706:G:H5'	5:2F:99:TYR:CE2	2.28	0.69
6:2G:5:VAL:HG13	6:2G:8:LYS:HB3	1.75	0.69
1:1A:1514:C:OP1	59:1A:4330:HOH:O	2.11	0.69
1:1A:8:U:H3	1:1A:2640:A:H2	1.40	0.69
14:2S:84:GLN:HA	14:2S:111:GLU:HB2	1.73	0.69
1:2A:1813:A:OP2	59:2A:3617:HOH:O	2.11	0.68
1:1A:1369:G:OP2	59:1A:4327:HOH:O	2.10	0.68
1:1A:2342:G:N7	59:1A:4428:HOH:O	2.26	0.68
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.75	0.68
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.58	0.68
1:1A:1352:A:N3	59:1A:4422:HOH:O	2.25	0.68
2:2B:55:U:H1'	6:2G:29:TRP:HE1	1.58	0.68
2:2B:22:U:H3	2:2B:61:G:H1	1.40	0.68
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.75	0.68
1:1A:138:A:H8	1:1A:1453:C:HO2'	1.42	0.68
1:1A:710:C:O2'	59:1A:4329:HOH:O	2.11	0.68
6:1G:41:GLN:HB3	6:1G:43:LEU:HD13	1.75	0.68
5:2F:53:THR:HG22	5:2F:56:GLU:HG3	1.76	0.68
1:2A:661:A:H8	11:2P:117:GLU:HG3	1.58	0.68
59:2A:3601:HOH:O	13:2R:3:HIS:NE2	2.26	0.68
1:1A:1000:G:OP2	12:1Q:14:ARG:NH2	2.27	0.68
5:1F:56:GLU:OE2	5:1F:93:LYS:NZ	2.27	0.68
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.74	0.68
1:1A:869:G:OP1	59:1A:4333:HOH:O	2.12	0.68
1:2A:1361:U:H2'	1:2A:1362:A:H8	1.59	0.68
1:2A:877:G:O2'	11:2P:38:GLN:NE2	2.26	0.68
7:2H:86:GLU:OE2	7:2H:132:ARG:NH2	2.26	0.68
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.75	0.68
1:1A:2433:A:N3	59:1A:4437:HOH:O	2.27	0.68
1:2A:777:C:OP1	59:2A:3622:HOH:O	2.12	0.68
2:2B:50:G:OP1	14:2S:63:THR:N	2.27	0.68
7:1H:124:GLU:HB2	7:1H:132:ARG:HB3	1.76	0.67
1:2A:1083:C:H42	1:2A:1162:G:H1	1.42	0.67
1:2A:514:G:N7	18:2W:49:LYS:NZ	2.41	0.67
1:1A:1043:C:OP1	59:1A:4332:HOH:O	2.11	0.67
1:1A:1648:A:OP1	59:1A:4322:HOH:O	2.13	0.67
59:1E:403:HOH:O	13:1R:3:HIS:NE2	2.26	0.67
1:2A:2510:C:OP2	59:2A:3625:HOH:O	2.13	0.67
1:2A:1256:G:N2	1:2A:1257:A:N7	5.71	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2P:126:VAL:HG12	11:2P:148:LEU:HD22	1.76	0.67
1:1A:1387:A:OP2	59:1A:4304:HOH:O	2.12	0.67
1:2A:2043:U:OP1	59:2A:3623:HOH:O	2.12	0.67
21:2Z:77:ASP:OD2	21:2Z:80:ARG:NH1	2.27	0.67
1:2A:785:G:OP1	59:2A:3621:HOH:O	2.12	0.67
1:2A:839:A:O2'	59:2A:3602:HOH:O	1.97	0.67
3:2D:69:ARG:NH2	3:2D:128:GLY:O	2.28	0.67
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.59	0.67
1:2A:1233:A:OP2	59:2A:3628:HOH:O	2.13	0.67
1:1A:1813:A:OP1	59:1A:4301:HOH:O	2.12	0.67
18:2W:4:LYS:HE2	18:2W:6:ILE:HD11	1.77	0.66
3:1D:164:GLN:HE21	3:1D:176:ARG:HH12	1.42	0.66
1:2A:2022:A:H2'	1:2A:2023:G:C8	2.30	0.66
1:2A:795:C:OP2	59:2A:3627:HOH:O	2.13	0.66
6:2G:33:ARG:NH1	6:2G:33:ARG:HB2	2.10	0.66
29:27:5:TRP:NE1	29:27:7:PRO:HG3	2.11	0.66
1:1A:785:G:OP1	59:1A:4335:HOH:O	2.13	0.66
1:2A:1077:A:H2	1:2A:1167:G:H22	1.43	0.66
6:2G:15:VAL:HG22	6:2G:175:LEU:HB3	1.78	0.66
20:2Y:9:LYS:NZ	20:2Y:28:LYS:O	2.21	0.66
1:1A:1220:G:N2	1:1A:1222:C:OP2	2.28	0.66
1:1A:2090:G:OP2	59:1A:4334:HOH:O	2.13	0.66
1:1A:932:C:H2'	1:1A:933:A:H5''	1.77	0.66
26:24:60:GLN:HA	26:24:62:ARG:HG2	1.78	0.66
1:2A:1116:G:N2	1:2A:1124:C:N3	16.98	0.66
1:2A:1802:G:OP1	59:2A:3626:HOH:O	2.13	0.66
1:1A:1499:A:OP2	59:1A:4337:HOH:O	2.13	0.66
1:2A:609:C:OP2	11:2P:21:ARG:NH2	2.28	0.66
1:2A:2643:A:HO2'	1:2A:2820:G:HO2'	1.36	0.66
1:1A:152:C:OP2	23:11:92:LYS:NZ	2.28	0.65
1:1A:1394:A:OP1	59:1A:4341:HOH:O	2.14	0.65
1:1A:2059:G:O6	59:1A:4340:HOH:O	2.14	0.65
1:2A:608:A:N1	1:2A:855:G:O2'	2.27	0.65
30:28:33:ASN:HA	30:28:36:LYS:HD2	1.79	0.65
1:2A:1512:G:HO2'	1:2A:1592:C:HO2'	1.37	0.65
14:1S:59:LYS:HE3	14:1S:59:LYS:H	1.60	0.65
1:2A:1360:C:OP2	59:2A:3611:HOH:O	2.13	0.65
1:2A:2606:G:N7	59:2A:3705:HOH:O	2.29	0.65
25:13:3:ARG:NH1	25:13:60:GLU:OE1	2.29	0.65
1:1A:1298:A:OP1	59:1A:4336:HOH:O	2.13	0.65
1:1A:1358:U:OP1	59:1A:4344:HOH:O	2.15	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1715:A:OP2	59:1A:4342:HOH:O	2.14	0.65
1:1A:2584:C:OP1	59:1A:4323:HOH:O	2.13	0.65
15:1T:108:ARG:HG2	15:1T:111:ARG:HH12	1.62	0.65
1:1A:1039:C:OP1	16:1U:53:ARG:NH2	2.29	0.65
1:1A:1064:U:HO2'	1:1A:1066:A:H2	1.44	0.65
1:1A:2095:U:OP1	59:1A:4343:HOH:O	2.15	0.65
1:1A:2210:U:H2'	1:1A:2211:G:H8	1.61	0.65
1:1A:2800:C:OP1	4:1E:61:ARG:NH2	2.29	0.65
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.70	0.65
1:2A:1026:A:OP1	59:2A:3632:HOH:O	2.14	0.65
1:2A:1625:A:N7	59:2A:3704:HOH:O	2.29	0.65
1:2A:551:C:OP1	59:2A:3631:HOH:O	2.14	0.65
3:2D:145:VAL:HB	3:2D:155:LEU:HB2	1.77	0.65
1:2A:1090:A:N1	1:2A:1155:G:O2'	2.28	0.65
1:2A:2046:C:N4	59:2A:3709:HOH:O	2.30	0.65
1:1A:2323:U:H5'	6:1G:88:ILE:HD11	1.78	0.65
1:2A:673:G:H4'	30:28:46:ARG:HH22	1.62	0.65
1:2A:1815:A:OP1	59:2A:3633:HOH:O	2.14	0.65
1:1A:1068:U:OP2	59:1A:4338:HOH:O	2.13	0.64
59:2A:3601:HOH:O	4:2E:110:GLY:O	2.15	0.64
1:2A:996:G:OP1	12:2Q:16:ARG:NH2	2.30	0.64
1:2A:1992:A:OP1	59:2A:3629:HOH:O	2.13	0.64
1:2A:2595:U:O4	59:2A:3618:HOH:O	2.11	0.64
1:2A:57:U:H2'	1:2A:58:G:H8	5.20	0.64
2:2B:24:G:N2	2:2B:27:C:N3	2.35	0.64
11:2P:19:VAL:HG12	11:2P:27:HIS:HB3	1.77	0.64
21:2Z:152:ALA:O	21:2Z:155:LEU:HB2	1.97	0.64
1:1A:2657:C:OP2	1:1A:2744:G:O2'	2.13	0.64
1:1A:341:C:OP1	15:1T:39:ARG:NH2	167.40	0.64
1:2A:330:G:H21	1:2A:353:A:H62	1.44	0.64
26:24:24:THR:OG1	26:24:25:TYR:N	2.30	0.64
1:2A:1516:G:N2	1:2A:1567:G:OP2	2.31	0.64
1:1A:2634:G:OP1	59:1A:4345:HOH:O	2.15	0.64
1:1A:877:G:O2'	11:1P:38:GLN:NE2	2.31	0.64
19:2X:44:GLU:OE2	59:2X:8101:HOH:O	2.15	0.64
1:1A:2882:A:OP2	59:1A:4347:HOH:O	2.15	0.64
1:2A:2509:C:OP2	59:2A:3625:HOH:O	2.15	0.64
1:2A:322:A:N7	59:2A:3708:HOH:O	2.30	0.64
1:1A:2623:C:OP2	27:15:2:ALA:N	2.30	0.64
1:2A:2100:U:OP1	23:21:21:ARG:NH2	2.31	0.64
5:2F:11:VAL:HG22	5:2F:125:LEU:HB2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1210:U:H2'	1:1A:1211:C:C6	2.32	0.64
8:1I:31:LEU:HD21	8:1I:38:LEU:HG	1.79	0.64
1:2A:1059:U:H2'	1:2A:1060:G:C8	2.32	0.64
1:2A:1102:A:N6	1:2A:1132:G:OP2	2.31	0.64
1:2A:1870:G:OP2	59:2A:3634:HOH:O	2.15	0.64
1:2A:2738:U:H4'	10:2O:1:MET:HE1	1.80	0.64
1:2A:1691:G:H5''	1:2A:1692:C:H5'	1.80	0.63
1:2A:1826:U:H2'	1:2A:1827:C:C6	2.33	0.63
1:2A:2079:A:N7	59:2A:3711:HOH:O	2.30	0.63
2:1B:102:A:N7	59:1B:304:HOH:O	2.30	0.63
6:2G:107:LEU:HA	6:2G:111:LEU:HD22	1.80	0.63
10:2O:2:ILE:HD12	10:2O:6:THR:HG21	1.79	0.63
24:12:29:LYS:HG2	24:12:57:ILE:HD13	1.81	0.63
1:1A:1430:G:O2'	1:1A:1441:U:O2	2.13	0.63
1:1A:807:A:H5'	59:1A:4393:HOH:O	1.97	0.63
1:2A:1060:G:H2'	1:2A:1061:G:H8	1.62	0.63
1:2A:2657:C:OP2	1:2A:2744:G:O2'	2.15	0.63
1:2A:2603:G:OP1	59:2A:3604:HOH:O	2.16	0.63
15:2T:56:GLY:O	15:2T:59:THR:HG23	1.98	0.63
5:2F:116:ASP:OD2	11:2P:1:MET:N	2.26	0.63
8:1I:129:THR:HG22	8:1I:139:GLN:HE22	1.64	0.63
9:1N:67:LEU:HB3	9:1N:88:GLU:HG3	1.80	0.63
1:2A:842:C:H2'	1:2A:843:C:C6	2.34	0.63
21:2Z:70:LEU:HG	21:2Z:91:LEU:HD21	1.81	0.63
26:14:53:GLU:HB2	26:14:54:GLY:HA2	1.81	0.63
2:2B:5:C:OP1	2:2B:61:G:O2'	2.15	0.63
8:2I:65:ALA:HB1	8:2I:136:VAL:HG11	1.79	0.63
11:2P:62:LEU:O	30:28:13:ARG:NH1	2.32	0.63
1:1A:1091:A:H3'	1:1A:1092:G:H5'	1.79	0.63
7:1H:86:GLU:OE2	7:1H:130:ARG:NH1	2.32	0.63
15:1T:54:ARG:HA	15:1T:59:THR:HG22	1.81	0.63
20:1Y:68:HIS:ND1	20:1Y:70:SER:HB3	2.13	0.63
1:2A:1100:G:H3'	1:2A:1101:G:H8	1.64	0.63
1:2A:57:U:H2'	1:2A:58:G:C8	5.23	0.63
1:1A:258:A:H2'	1:1A:259:A:C8	3.12	0.62
1:2A:1846:G:O6	3:2D:35:LYS:NZ	2.26	0.62
1:2A:1039:C:OP1	16:2U:53:ARG:NH2	2.31	0.62
1:2A:2302:U:H2'	1:2A:2303:C:C6	2.34	0.62
1:2A:624:G:O2'	1:2A:701:A:N6	2.33	0.62
21:2Z:70:LEU:O	21:2Z:89:PHE:N	2.26	0.62
1:1A:541:C:OP1	27:15:16:ARG:NH2	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:22:32:LEU:HD22	24:22:36:ARG:HD3	1.80	0.62
23:11:21:ARG:HD3	23:11:35:THR:HG21	1.80	0.62
1:1A:1500:U:OP1	13:1R:77:ARG:NH1	2.32	0.62
1:1A:682:G:H1	1:1A:695:C:H42	1.48	0.62
1:2A:2375:C:OP1	22:20:55:ARG:NH1	2.32	0.62
24:22:29:LYS:HG2	24:22:57:ILE:HD13	1.81	0.62
1:1A:1231:G:H5'	17:1V:81:TYR:CE1	2.34	0.62
1:1A:610:U:H2'	1:1A:611:C:C6	2.34	0.62
14:1S:83:LYS:HG2	14:1S:111:GLU:HG3	1.82	0.62
1:1A:2339:A:H2'	1:1A:2340:G:C8	2.35	0.62
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.47	0.62
21:1Z:70:LEU:HG	21:1Z:91:LEU:HD21	1.82	0.62
6:2G:11:TYR:HB2	6:2G:176:LEU:HD21	1.80	0.62
18:2W:88:ARG:NH1	18:2W:94:ASP:OD2	2.33	0.62
1:2A:332:G:N3	1:2A:352:G:O2'	2.33	0.62
6:2G:13:GLU:O	6:2G:15:VAL:N	2.33	0.62
16:2U:104:GLN:OE1	16:2U:105:VAL:N	2.29	0.62
1:2A:2641:G:H2'	1:2A:2642:G:C8	2.35	0.62
1:2A:590:U:O4	59:2A:3636:HOH:O	2.15	0.62
1:1A:976:G:OP2	25:13:29:ARG:NH2	2.32	0.61
1:2A:1361:U:H2'	1:2A:1362:A:C8	2.35	0.61
1:2A:1735:A:OP2	1:2A:1744:A:N6	2.32	0.61
1:2A:2100:U:O3'	23:21:35:THR:OG1	2.18	0.61
1:2A:483:G:O2'	1:2A:494:G:O6	2.10	0.61
15:2T:24:PRO:HA	15:2T:49:VAL:HG22	1.82	0.61
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.33	0.61
1:1A:2816:G:N1	1:1A:2901:G:O6	2.19	0.61
4:1E:111:ARG:HG3	4:1E:160:TYR:CD2	2.35	0.61
1:1A:2573:U:H1'	10:1O:23:ARG:HH11	1.65	0.61
1:2A:1276:G:H2'	1:2A:1277:G:H8	1.64	0.61
10:2O:68:GLU:HB3	10:2O:78:ARG:HB2	1.83	0.61
1:1A:2694:C:O2	10:1O:70:LYS:NZ	2.29	0.61
15:2T:55:ASN:N	15:2T:59:THR:HG22	2.10	0.61
3:1D:108:PRO:HD2	3:1D:111:LEU:HG	1.82	0.61
1:2A:2588:A:H5'	27:25:3:LYS:HD2	1.81	0.61
1:2A:786:U:H2'	1:2A:787:G:C8	2.35	0.61
16:2U:78:THR:O	16:2U:117:GLN:NE2	2.33	0.61
17:2V:43:GLU:N	17:2V:43:GLU:OE2	2.34	0.61
14:1S:15:ARG:O	14:1S:19:LYS:HG2	1.99	0.61
1:1A:236:G:OP1	59:1A:4348:HOH:O	2.16	0.61
1:1A:2799:C:H1'	4:1E:62:PRO:HG3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:51:ARG:NH2	59:1T:304:HOH:O	2.34	0.61
1:2A:2573:U:H1'	10:2O:23:ARG:HH11	1.65	0.61
26:14:57:GLU:HB3	26:14:58:ARG:HG2	1.80	0.61
1:2A:1121:C:H3'	1:2A:1122:A:H8	1.65	0.61
1:2A:1188:A:OP1	9:2N:25:ARG:NH2	2.34	0.61
1:2A:1906:A:H2'	1:2A:1907:C:O4'	2.00	0.61
11:2P:100:LEU:HD12	11:2P:112:LEU:HD11	1.82	0.61
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.82	0.61
9:2N:21:LYS:NZ	9:2N:140:VAL:O	2.33	0.61
1:1A:271:U:OP1	8:1I:50:ARG:NH2	2.34	0.61
1:2A:2095:U:H2'	1:2A:2096:U:C6	2.36	0.61
3:2D:79:VAL:HG21	3:2D:111:LEU:HD11	1.83	0.61
1:1A:302:C:H42	1:1A:384:G:H1	1.49	0.60
2:1B:8:U:O3'	14:1S:25:ARG:NH2	2.25	0.60
8:2I:114:LEU:HD11	8:2I:128:LEU:HD13	1.84	0.60
28:16:6:ARG:NH2	59:16:202:HOH:O	2.33	0.60
1:1A:1323:A:OP1	13:1R:36:THR:HG23	2.01	0.60
1:1A:1540:A:H2'	1:1A:1541:A:C8	2.35	0.60
1:1A:2441:A:H2'	1:1A:2441:A:N3	2.15	0.60
1:2A:1495:A:O2'	1:2A:1575:G:N2	2.27	0.60
1:1A:2087:C:OP1	59:1A:4349:HOH:O	2.16	0.60
1:2A:2226:G:H5''	1:2A:2227:G:N7	2.15	0.60
1:2A:2622:U:C4	27:25:3:LYS:HG2	2.36	0.60
5:2F:32:LEU:HB3	5:2F:112:MET:HE1	1.81	0.60
1:1A:903:C:H4'	22:10:23:VAL:HG21	1.83	0.60
1:1A:2672:G:OP1	59:1A:4350:HOH:O	2.16	0.60
6:1G:49:ASP:O	6:1G:51:ARG:N	2.31	0.60
1:2A:1647:U:O4	59:2A:3619:HOH:O	2.12	0.60
1:2A:1826:U:H2'	1:2A:1827:C:H6	1.66	0.60
1:1A:1693:G:OP1	59:1A:4325:HOH:O	2.17	0.60
1:2A:706:G:H5'	5:2F:99:TYR:CD2	2.36	0.60
8:2I:27:ARG:HD2	23:21:71:TYR:CE2	2.36	0.60
8:1I:37:VAL:HG13	8:1I:38:LEU:HD12	1.84	0.60
1:2A:82:A:N1	1:2A:96:G:O2'	2.28	0.60
1:2A:867:A:H2'	1:2A:990:G:H5''	1.82	0.60
1:2A:1015:C:OP2	59:2A:3640:HOH:O	2.17	0.60
1:2A:2811:A:H1'	1:2A:2903:U:H1'	1.83	0.60
2:2B:75:G:H22	21:2Z:73:GLN:NE2	1.99	0.60
1:1A:154:C:H42	1:1A:159:G:H1	1.48	0.60
4:1E:174:ASP:OD1	4:1E:175:VAL:N	2.34	0.60
1:2A:1059:U:H2'	1:2A:1060:G:H8	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1738:U:OP2	59:2A:3635:HOH:O	2.15	0.60
1:1A:883:C:N4	59:1A:4499:HOH:O	2.33	0.60
2:1B:66:A:H61	2:1B:108:U:H2'	1.67	0.60
1:2A:2366:C:H1'	22:20:39:ARG:HH21	1.67	0.60
1:2A:552:A:O2'	1:2A:553:A:H5'	2.01	0.60
12:2Q:29:PHE:O	21:2Z:122:ARG:NH2	2.35	0.60
1:2A:757:G:O3'	3:2D:202:LYS:NZ	44.27	0.60
2:2B:31:C:H4'	6:2G:29:TRP:CH2	2.37	0.60
8:2I:62:LYS:HE2	8:2I:133:HIS:HE1	1.67	0.60
14:2S:48:LEU:HD23	14:2S:82:ILE:HD11	1.84	0.60
18:2W:37:ARG:HD2	18:2W:38:TYR:CE2	2.37	0.60
1:1A:2670:G:O2'	7:1H:175:LYS:NZ	2.34	0.59
1:1A:992:G:OP1	59:1A:4314:HOH:O	2.16	0.59
6:1G:72:ARG:HB3	6:1G:72:ARG:HH11	3.77	0.59
7:2H:9:ILE:HB	7:2H:50:VAL:HB	1.84	0.59
2:2B:114:C:H4'	14:2S:46:VAL:HG22	1.83	0.59
1:1A:1090:A:H4'	1:1A:1091:A:H5''	1.84	0.59
1:2A:1198:C:OP2	59:2A:3639:HOH:O	2.17	0.59
1:2A:2815:G:H2'	1:2A:2816:G:C8	2.36	0.59
5:1F:18:ARG:HG2	5:1F:19:GLU:H	1.67	0.59
20:1Y:6:HIS:CD2	20:1Y:6:HIS:H	2.20	0.59
1:2A:2765:A:N3	31:29:15:LYS:NZ	2.48	0.59
1:2A:951:G:O2'	12:2Q:67:ARG:NH2	2.33	0.59
2:2B:1:U:H2'	2:2B:2:C:C5	2.36	0.59
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.34	0.59
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.21	0.59
19:1X:35:THR:HG22	19:1X:38:GLU:H	1.68	0.59
1:2A:80:G:N1	1:2A:100:A:OP2	2.28	0.59
1:2A:2305:C:OP1	14:2S:89:ARG:NH1	2.31	0.59
1:1A:1064:U:H3	1:1A:1187:A:H62	1.49	0.59
1:1A:2044:G:H5'	1:1A:2628:C:H4'	1.84	0.59
1:1A:928:G:H1	1:1A:939:C:H42	1.51	0.59
1:2A:555:C:OP1	1:2A:583:G:N1	2.33	0.59
6:2G:135:LEU:HB2	6:2G:155:MET:HG2	1.83	0.59
1:1A:826:G:OP1	3:1D:218:ARG:NH2	2.36	0.59
14:1S:34:HIS:ND1	14:1S:53:SER:OG	2.28	0.59
1:2A:1295:G:OP2	11:2P:21:ARG:NH1	2.34	0.59
1:2A:2314:G:O2'	6:2G:132:ASN:HB2	2.02	0.59
1:2A:885:U:H2'	1:2A:886:C:C6	2.38	0.59
1:2A:1120:C:O5'	12:2Q:59:ARG:NH1	2.36	0.59
21:2Z:52:SER:OG	21:2Z:53:ILE:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1552:A:O2'	1:1A:1553:A:O5'	2.21	0.59
1:1A:1826:U:H2'	1:1A:1827:C:C6	2.38	0.59
28:26:21:TYR:CE1	28:26:38:LYS:HG2	2.38	0.59
1:2A:2367:C:OP1	22:20:24:LYS:NZ	2.34	0.59
1:2A:721:A:OP1	5:2F:63:LYS:NZ	2.32	0.59
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.21	0.59
19:2X:60:ARG:HH22	29:27:47:ARG:HH12	1.51	0.59
1:1A:1070:G:C4	1:1A:1179:C:H1'	2.38	0.58
1:2A:1154:C:H3'	1:2A:1155:G:C8	2.37	0.58
1:2A:732:G:N2	1:2A:834:A:H61	2.01	0.58
1:2A:757:G:N2	1:2A:766:C:O2	2.34	0.58
1:1A:2206:C:O2'	1:1A:2207:G:H5'	2.04	0.58
1:1A:514:G:N7	18:1W:49:LYS:NZ	2.51	0.58
1:2A:1032:G:O2'	1:2A:1045:A:N3	2.32	0.58
1:2A:1124:C:H41	1:2A:1133:A:H5''	1.69	0.58
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.36	0.58
5:2F:150:GLY:HA2	5:2F:172:TRP:CE3	2.39	0.58
7:2H:149:ARG:NH1	7:2H:167:GLU:OE1	2.36	0.58
1:1A:1201:A:OP2	59:1A:4353:HOH:O	2.17	0.58
1:1A:1844:G:H4'	3:1D:51:VAL:HG21	1.86	0.58
1:1A:1219:U:OP1	1:1A:1221:A:N6	2.34	0.58
1:1A:2210:U:H2'	1:1A:2211:G:C8	2.39	0.58
3:1D:164:GLN:NE2	3:1D:176:ARG:HH12	2.02	0.58
11:1P:121:LYS:O	11:1P:123:LEU:N	2.35	0.58
1:2A:533:C:OP1	59:2A:3642:HOH:O	2.17	0.58
1:1A:929:G:N2	1:1A:948:C:O2	27.31	0.58
1:2A:120:G:O6	59:2A:3638:HOH:O	2.16	0.58
1:2A:298:G:N3	1:2A:540:C:H4'	110.17	0.58
5:2F:110:LEU:HD11	5:2F:181:LEU:HG	1.86	0.58
1:1A:2734:G:OP2	59:1A:4354:HOH:O	2.17	0.58
1:1A:2819:A:N6	1:1A:2899:G:O2'	2.34	0.58
1:2A:1017:A:OP2	59:2A:3636:HOH:O	2.17	0.58
1:2A:2440:G:OP2	59:2A:3603:HOH:O	2.17	0.58
3:2D:242:ARG:N	3:2D:242:ARG:HD3	2.18	0.58
1:1A:172:C:H2'	1:1A:173:U:C6	2.38	0.58
1:1A:550:A:OP1	59:1A:4358:HOH:O	2.18	0.58
1:2A:1078:U:OP1	31:29:9:ARG:NH2	2.36	0.58
18:2W:17:VAL:HG11	18:2W:103:ILE:HD11	1.86	0.58
1:1A:2366:C:H1'	22:10:39:ARG:HH21	1.69	0.57
1:1A:1450:U:H2'	1:1A:1451:U:C6	2.39	0.57
1:1A:1391:G:OP2	59:1A:4352:HOH:O	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:524:G:N1	1:2A:527:A:OP2	2.37	0.57
4:2E:111:ARG:HG3	4:2E:160:TYR:CD2	2.39	0.57
1:2A:2800:C:OP1	4:2E:61:ARG:NH2	2.37	0.57
1:1A:1833:A:H4'	3:1D:259:THR:HG23	1.85	0.57
1:1A:2033:G:OP1	18:1W:11:ARG:NH2	2.37	0.57
1:2A:1833:A:O2'	3:2D:259:THR:HG21	2.03	0.57
6:2G:64:THR:HB	6:2G:94:LEU:HD11	1.85	0.57
1:1A:1088:C:O2	1:1A:1157:G:N2	2.25	0.57
1:1A:1093:A:OP2	1:1A:1154:C:N4	2.37	0.57
1:1A:1426:G:C8	15:1T:118:ARG:HG2	88.56	0.57
1:2A:2548:U:H2'	1:2A:2549:C:C6	2.39	0.57
1:2A:437:G:OP1	59:2A:3643:HOH:O	2.17	0.57
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.20	0.57
1:2A:2226:G:H3'	1:2A:2227:G:C8	2.40	0.57
1:1A:1404:A:N6	1:1A:1417:U:H3	1.95	0.57
1:1A:2254:U:H2'	1:1A:2255:U:C6	2.38	0.57
12:1Q:52:VAL:O	12:1Q:56:ARG:HG3	2.05	0.57
23:21:23:LYS:HB3	23:21:29:GLY:HA3	1.87	0.57
1:2A:1424:A:H4'	1:2A:1425:G:OP2	2.03	0.57
7:2H:124:GLU:HB2	7:2H:132:ARG:HB3	1.85	0.57
1:1A:235:G:H4'	1:1A:412:G:C5	2.40	0.57
1:1A:2395:G:OP2	22:10:55:ARG:NH1	2.38	0.57
1:1A:2450:A:C8	1:1A:2450:A:H5'	2.40	0.57
1:1A:876:G:OP2	59:1A:4355:HOH:O	2.17	0.57
1:1A:629:U:OP1	5:1F:102:PRO:HA	2.04	0.57
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.20	0.57
1:2A:1082:G:H1	1:2A:1163:C:H42	1.49	0.57
1:2A:1309:G:H2'	1:2A:2035:A:N6	2.19	0.57
1:2A:310:C:H42	1:2A:377:G:H1	1.53	0.57
1:1A:1425:G:O2'	1:1A:1426:G:OP1	4.81	0.57
1:1A:1524:G:O2'	1:1A:1604:A:N1	2.37	0.57
1:1A:481:C:H4'	59:1A:5847:HOH:O	2.05	0.57
1:2A:821:G:O3'	59:2A:3644:HOH:O	2.18	0.57
1:2A:1184:C:O3'	9:2N:25:ARG:NH1	2.38	0.57
1:1A:846:A:OP1	1:1A:846:A:H8	1.88	0.57
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.85	0.57
6:2G:16:ARG:HH22	6:2G:28:VAL:HG12	1.69	0.57
8:2I:37:VAL:HG13	8:2I:38:LEU:HD12	1.87	0.57
24:12:65:ASN:OD1	24:12:69:ARG:NH1	2.34	0.57
21:1Z:145:GLU:O	21:1Z:148:ASP:N	2.37	0.57
1:2A:2328:C:H2'	1:2A:2329:G:H8	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:143:ALA:HB1	5:2F:148:LEU:HB2	1.87	0.57
12:2Q:37:LEU:HD21	12:2Q:130:LYS:HG2	1.87	0.57
15:2T:116:ALA:HB1	15:2T:121:ILE:HD11	1.87	0.57
12:1Q:59:ARG:HA	12:1Q:60:ARG:NH2	2.20	0.56
1:2A:1104:G:H3'	1:2A:1105:U:H6	1.67	0.56
1:2A:1588:A:OP2	59:2A:3641:HOH:O	2.17	0.56
1:2A:2297:A:H4'	1:2A:2298:A:O4'	2.05	0.56
5:2F:56:GLU:OE2	5:2F:93:LYS:NZ	2.36	0.56
1:1A:2107:U:H2'	1:1A:2108:G:C8	2.40	0.56
15:1T:56:GLY:O	15:1T:59:THR:HG23	2.05	0.56
22:20:27:GLU:HG3	22:20:68:GLU:HA	1.87	0.56
6:2G:113:ARG:NH2	6:2G:139:LEU:O	2.36	0.56
1:1A:1280:G:OP1	59:1A:4351:HOH:O	2.17	0.56
6:1G:135:LEU:HB2	6:1G:155:MET:HG2	1.87	0.56
1:2A:412:G:OP1	59:2A:3646:HOH:O	2.18	0.56
1:1A:141:G:N2	1:1A:172:C:N3	54.90	0.56
1:1A:2522:U:OP2	59:1A:4357:HOH:O	2.17	0.56
1:1A:2702:C:OP2	59:1A:4356:HOH:O	2.17	0.56
2:2B:55:U:O3'	6:2G:27:ASN:ND2	2.39	0.56
7:2H:159:GLU:HG3	7:2H:169:VAL:HG11	1.87	0.56
1:1A:2257:G:N2	59:1A:4460:HOH:O	2.29	0.56
19:1X:35:THR:HG23	19:1X:37:THR:H	1.71	0.56
1:2A:903:C:H4'	22:20:23:VAL:HG21	1.88	0.56
1:2A:2362:G:HO2'	1:2A:2363:A:H8	1.53	0.56
1:2A:2858:U:O4	15:2T:23:ARG:NH2	2.38	0.56
19:1X:60:ARG:HH22	29:17:47:ARG:HH22	1.53	0.56
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.41	0.56
21:1Z:77:ASP:OD2	21:1Z:80:ARG:NH1	2.34	0.56
27:25:16:ARG:NH1	27:25:17:ASP:OD1	2.35	0.56
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	1.87	0.56
21:2Z:134:PRO:C	21:2Z:136:PHE:H	2.07	0.56
21:2Z:152:ALA:HA	21:2Z:155:LEU:HD22	1.86	0.56
1:2A:1113:G:HO2'	1:2A:1141:A:HO2'	1.54	0.56
1:2A:647:G:H2'	1:2A:648:C:C6	2.41	0.56
7:2H:137:ASP:HB3	7:2H:140:LYS:HB3	1.87	0.56
1:2A:2651:G:OP1	9:2N:97:ARG:NH2	2.39	0.56
1:1A:2022:A:OP1	13:1R:9:LYS:NZ	2.34	0.56
1:1A:330:G:H21	1:1A:353:A:H62	1.54	0.56
2:1B:23:G:O6	59:1B:302:HOH:O	2.17	0.56
1:2A:1835:U:O2	3:2D:50:THR:HB	2.05	0.56
23:11:23:LYS:HB3	23:11:29:GLY:HA3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:14:ILE:HG23	26:14:31:ILE:HB	1.85	0.56
2:1B:12:C:H2'	22:10:73:GLY:HA3	1.87	0.56
4:1E:29:GLY:HA3	59:1E:404:HOH:O	2.06	0.56
14:1S:56:LEU:HB2	14:1S:58:LEU:HG	1.88	0.56
19:1X:88:LYS:HE3	19:1X:93:GLU:HG3	1.86	0.56
1:2A:656:A:H2'	1:2A:657:A:C8	2.41	0.56
14:2S:84:GLN:H	14:2S:111:GLU:HG3	1.70	0.56
24:12:32:LEU:HD22	24:12:36:ARG:HH11	1.70	0.56
1:2A:1404:A:H2'	1:2A:1405:A:H5'	1.88	0.56
1:2A:320:C:H2'	1:2A:321:G:O4'	2.06	0.56
1:1A:1067:G:N2	1:1A:1068:U:O4	2.34	0.56
1:1A:2898:C:OP2	59:1A:4360:HOH:O	2.18	0.56
1:2A:1685:U:H2'	1:2A:1686:C:H5''	1.88	0.56
1:2A:666:G:H21	1:2A:670:A:H2	1.52	0.56
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.88	0.56
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.06	0.56
24:12:32:LEU:HD22	24:12:36:ARG:NH1	2.20	0.55
1:1A:552:A:C2	1:1A:2063:A:H2'	2.41	0.55
5:1F:18:ARG:NH2	5:1F:127:GLU:OE2	2.39	0.55
8:1I:72:LEU:C	8:1I:74:ASN:H	2.07	0.55
14:1S:84:GLN:HA	14:1S:111:GLU:HB2	1.88	0.55
10:1O:80:ASP:OD1	15:1T:64:ARG:NH2	2.39	0.55
25:23:9:VAL:HG12	25:23:32:GLN:HE22	1.71	0.55
1:2A:1924:G:OP1	3:2D:241:PRO:HB2	2.06	0.55
1:2A:957:C:OP1	12:2Q:8:LYS:NZ	2.29	0.55
7:2H:23:ARG:NH1	7:2H:34:GLU:OE2	2.39	0.55
1:1A:1222:C:H2'	1:1A:1223:C:C6	2.41	0.55
1:1A:1845:A:OP2	3:1D:54:ARG:NH2	2.33	0.55
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.07	0.55
21:1Z:144:LEU:HD21	21:1Z:150:LEU:HD13	1.88	0.55
1:2A:1039:C:OP2	16:2U:54:LYS:NZ	2.37	0.55
1:2A:1808:U:H2'	1:2A:1814:A:N6	2.21	0.55
1:2A:2226:G:H8	1:2A:2227:G:N7	2.03	0.55
1:2A:2278:A:H5''	1:2A:2279:A:H5'	1.88	0.55
1:2A:323:A:OP1	20:2Y:86:ARG:NH2	2.39	0.55
1:2A:667:A:N1	1:2A:2380:A:O2'	2.35	0.55
1:2A:78:G:H1	1:2A:103:C:H42	1.53	0.55
2:2B:90:A:C5	2:2B:91:C:H1'	2.41	0.55
11:2P:95:VAL:HG12	11:2P:123:LEU:HD22	1.88	0.55
11:2P:15:ARG:N	11:2P:15:ARG:HD2	2.21	0.55
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1067:G:H22	1:1A:1187:A:H2	1.53	0.55
1:2A:1354:G:H4'	29:27:7:PRO:HB2	1.88	0.55
1:2A:895:A:H2	25:23:24:LYS:HB3	1.71	0.55
1:1A:1066:A:H3'	1:1A:1066:A:C8	2.42	0.55
1:1A:267:G:OP2	59:1A:4362:HOH:O	2.18	0.55
11:2P:16:ARG:NH2	59:2P:5001:HOH:O	2.27	0.55
1:1A:595:G:N1	1:1A:2052:A:OP2	2.30	0.55
22:20:11:ARG:O	22:20:14:ARG:NH2	2.39	0.55
1:2A:1682:C:H2'	1:2A:1683:A:C8	2.42	0.55
5:2F:117:ARG:NH2	5:2F:189:THR:O	2.40	0.55
18:1W:14:PRO:HG2	18:1W:78:GLU:HG2	1.88	0.55
19:1X:43:VAL:HG21	19:1X:81:VAL:HG11	1.88	0.55
1:2A:898:G:H2'	1:2A:899:G:C8	2.42	0.55
1:2A:900:G:H2'	1:2A:901:G:C8	2.36	0.55
2:2B:3:C:H2'	2:2B:4:C:C6	2.41	0.55
1:1A:2648:U:H5''	4:1E:82:ARG:NH2	2.21	0.55
16:1U:86:ALA:O	17:1V:49:THR:HG23	2.07	0.55
1:2A:2044:G:H5'	1:2A:2628:C:H4'	1.89	0.55
1:2A:2845:U:H2'	1:2A:2846:G:C8	2.41	0.55
4:2E:170:LEU:HB3	4:2E:184:VAL:HG22	1.88	0.55
6:2G:114:ILE:HB	6:2G:117:PHE:HB2	1.89	0.55
1:2A:998:G:H5''	12:2Q:13:GLN:HB3	1.88	0.55
1:1A:2319:G:O2'	1:1A:2321:A:N7	2.40	0.55
1:1A:2858:U:O4	15:1T:23:ARG:NH2	2.33	0.55
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.40	0.55
7:2H:8:PRO:O	7:2H:10:PRO:HD3	2.07	0.55
18:2W:14:PRO:HG2	18:2W:78:GLU:HG2	1.88	0.55
1:1A:2207:G:H2'	1:1A:2208:G:C8	2.42	0.55
1:1A:2302:U:H2'	1:1A:2303:C:C6	2.42	0.55
21:1Z:58:VAL:HG12	21:1Z:68:PRO:HA	1.88	0.55
1:2A:1105:U:N3	1:2A:1133:A:N7	2.55	0.55
1:2A:1276:G:H2'	1:2A:1277:G:C8	2.42	0.55
1:2A:1337:U:H2'	1:2A:1338:C:C6	2.42	0.55
4:2E:1:MET:HE3	4:2E:199:ARG:HD2	1.88	0.55
11:2P:89:ALA:O	11:2P:121:LYS:NZ	2.40	0.55
1:1A:1217:G:O2'	1:1A:1218:A:O4'	2.24	0.55
1:2A:1070:G:C4	1:2A:1179:C:H1'	2.42	0.55
6:2G:66:GLN:HB3	6:2G:92:VAL:HG21	1.89	0.55
1:2A:1054:A:H5'	16:2U:59:ARG:HD3	1.89	0.55
23:21:3:LYS:HB2	23:21:61:ARG:HH11	1.73	0.54
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1155:G:H21	1:1A:1156:A:H2	1.54	0.54
1:1A:682:G:N2	1:1A:695:C:N3	2.53	0.54
11:2P:88:LEU:HD11	11:2P:114:ILE:HD12	1.89	0.54
1:1A:1992:A:OP2	3:1D:242:ARG:NH2	2.40	0.54
4:1E:54:GLN:HB2	4:1E:76:ARG:HG2	1.88	0.54
8:1I:77:LEU:HB3	8:1I:142:VAL:HG13	1.89	0.54
8:1I:6:LEU:HG	8:1I:36:ALA:HA	1.88	0.54
1:1A:645:A:OP2	11:1P:108:LYS:NZ	2.38	0.54
26:24:62:ARG:H	26:24:62:ARG:CZ	2.20	0.54
1:2A:622:G:N2	1:2A:627:C:O3'	2.40	0.54
21:2Z:92:SER:O	21:2Z:94:GLU:N	2.33	0.54
1:1A:1813:A:N7	59:1A:4496:HOH:O	2.33	0.54
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.88	0.54
1:2A:2312:C:H2'	1:2A:2313:G:H8	1.73	0.54
11:2P:44:GLY:CA	11:2P:45:LEU:HB2	2.37	0.54
21:2Z:153:SER:HB3	21:2Z:167:PRO:HB3	1.90	0.54
1:1A:1026:A:OP1	59:1A:4365:HOH:O	2.19	0.54
1:1A:885:U:H2'	1:1A:886:C:C6	2.42	0.54
26:24:48:ARG:HB2	26:24:52:THR:OG1	2.08	0.54
1:2A:141:G:H4'	19:2X:35:THR:HG21	1.88	0.54
1:1A:2783:C:H2'	1:1A:2784:C:C6	2.42	0.54
1:2A:1111:U:N3	1:2A:1114:A:OP2	2.23	0.54
1:2A:1450:U:H2'	1:2A:1451:U:C6	2.42	0.54
1:2A:172:C:H2'	1:2A:173:U:C6	2.43	0.54
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.43	0.54
16:2U:44:ASN:ND2	17:2V:75:PHE:HB3	2.22	0.54
26:14:68:ARG:HH21	26:14:68:ARG:HA	1.72	0.54
19:1X:60:ARG:NH2	29:17:47:ARG:HH22	2.05	0.54
1:1A:2052:A:C6	1:1A:2509:C:H1'	2.43	0.54
1:2A:1102:A:O2'	1:2A:1103:G:OP1	2.26	0.54
1:2A:2121:G:H2'	1:2A:2122:G:H8	1.72	0.54
15:2T:27:THR:HB	15:2T:89:VAL:HG22	1.90	0.54
1:1A:1479:A:H61	1:1A:1604:A:H62	1.56	0.54
1:1A:238:G:OP2	30:18:13:ARG:NH2	2.40	0.54
1:1A:2859:A:OP2	1:1A:2875:U:H5	1.91	0.54
8:1I:40:THR:O	8:1I:44:LEU:HB2	2.08	0.54
3:2D:68:LYS:HD2	3:2D:70:TRP:CZ2	2.42	0.54
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.89	0.54
6:2G:15:VAL:HA	6:2G:175:LEU:HD23	1.90	0.54
1:1A:601:G:H2'	1:1A:602:C:C6	2.43	0.54
12:1Q:60:ARG:H	12:1Q:60:ARG:NH1	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:34:HIS:HD1	14:1S:53:SER:HG	1.51	0.54
15:1T:117:ASP:O	15:1T:121:ILE:HG13	2.08	0.54
1:2A:1039:C:O2'	1:2A:1041:A:OP1	2.24	0.54
1:2A:665:C:O2'	1:2A:2361:C:OP1	2.18	0.54
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.07	0.54
1:1A:2529:A:OP2	59:1A:4359:HOH:O	2.18	0.54
4:1E:7:VAL:HG22	4:1E:27:LEU:HB3	1.88	0.54
2:2B:43:C:OP1	26:24:6:HIS:NE2	2.41	0.54
1:2A:905:G:O2'	1:2A:961:G:O6	2.21	0.54
11:2P:84:ASN:OD1	11:2P:117:GLU:HB2	2.08	0.54
8:1I:79:ILE:HB	8:1I:144:VAL:HG12	1.90	0.53
21:1Z:144:LEU:HD11	21:1Z:150:LEU:HD22	1.89	0.53
1:2A:2124:C:H1'	1:2A:2208:G:N2	2.23	0.53
1:2A:586:C:O2'	59:2A:3620:HOH:O	2.12	0.53
1:2A:836:C:OP1	59:2A:3648:HOH:O	2.19	0.53
1:2A:2318:G:N1	6:2G:43:LEU:O	2.34	0.53
1:2A:2760:A:H5'	7:2H:4:ILE:HD12	1.89	0.53
1:1A:57:U:H2'	1:1A:58:G:C8	5.59	0.53
26:24:61:ARG:O	26:24:63:TYR:N	2.42	0.53
1:2A:1713:G:O2'	1:2A:2012:U:O4	2.19	0.53
1:2A:206:A:C2	1:2A:223:U:H4'	2.43	0.53
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	1.91	0.53
20:1Y:23:ARG:HG2	20:1Y:42:VAL:HG22	1.89	0.53
1:2A:1050:C:H2'	1:2A:1051:C:C6	2.43	0.53
1:2A:2759:G:H1	1:2A:2766:U:H2'	1.73	0.53
6:2G:179:PRO:HB2	26:24:42:PHE:HE1	1.73	0.53
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.90	0.53
31:19:27:CYS:SG	31:19:28:GLU:N	2.81	0.53
1:1A:1614:G:H5'	3:1D:60:ARG:HA	1.91	0.53
10:1O:104:ARG:NH2	15:1T:43:GLN:OE1	2.41	0.53
1:2A:1409:G:P	23:21:3:LYS:HG3	2.49	0.53
3:2D:127:VAL:HA	3:2D:193:VAL:HG22	1.91	0.53
21:2Z:48:PHE:HE1	21:2Z:71:VAL:HG21	1.73	0.53
1:2A:2052:A:N3	1:2A:2466:G:O2'	2.33	0.53
1:2A:2226:G:H5''	1:2A:2227:G:C8	2.43	0.53
1:2A:2284:A:H2'	1:2A:2285:A:C8	2.44	0.53
11:2P:121:LYS:O	11:2P:123:LEU:N	2.36	0.53
23:11:64:ALA:HA	23:11:67:ILE:HG13	1.91	0.53
1:1A:1465:U:O2'	1:1A:1466:G:OP1	2.25	0.53
1:1A:720:G:O2'	5:1F:74:ARG:HD3	2.08	0.53
1:2A:330:G:N2	1:2A:333:A:O5'	2.32	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:417:G:O2'	1:2A:436:G:OP1	2.19	0.53
8:2I:31:LEU:HD21	8:2I:38:LEU:HG	1.91	0.53
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.09	0.53
13:2R:21:TYR:CZ	13:2R:43:GLU:HG2	2.43	0.53
1:1A:1064:U:O2'	1:1A:1066:A:H2	1.92	0.53
1:1A:1404:A:N1	1:1A:1417:U:O4	2.42	0.53
1:1A:296:C:H2'	1:1A:297:G:H8	1.74	0.53
1:1A:69:A:N7	19:1X:31:HIS:HE1	2.06	0.53
7:1H:144:VAL:O	7:1H:148:ILE:HG12	2.09	0.53
29:27:24:THR:O	29:27:28:ARG:HG3	2.08	0.53
1:2A:2583:A:OP1	1:2A:2585:G:O2'	2.23	0.53
1:2A:2072:A:H5'	1:2A:2589:G:O4'	2.08	0.53
1:2A:423:G:N7	59:2A:3725:HOH:O	2.34	0.53
1:1A:1218:A:H4'	1:1A:1219:U:OP1	2.08	0.53
3:2D:276:LYS:H	3:2D:276:LYS:CD	2.22	0.53
4:2E:78:LEU:O	4:2E:79:ARG:HG2	2.09	0.53
11:1P:52:GLU:OE1	11:1P:55:ARG:NH1	2.31	0.53
19:1X:2:LYS:NZ	19:1X:38:GLU:OE2	2.40	0.53
1:2A:2573:U:H1'	10:2O:23:ARG:HD3	1.90	0.53
13:2R:55:ALA:HB2	13:2R:79:LEU:HD13	1.90	0.53
26:14:59:PHE:O	26:14:62:ARG:HD3	2.09	0.53
1:1A:1920:G:N3	1:1A:1920:G:H2'	2.23	0.53
1:1A:17:C:O2'	1:1A:576:U:OP1	2.27	0.53
5:1F:143:ALA:HB1	5:1F:148:LEU:HB2	1.91	0.53
1:1A:184:A:H62	11:1P:38:GLN:HE22	1.57	0.53
1:2A:2017:C:H4'	1:2A:2018:G:OP1	2.09	0.53
1:2A:792:A:H2'	1:2A:2623:C:H5''	1.90	0.53
1:2A:2691:C:OP2	4:2E:111:ARG:NH2	2.42	0.53
1:2A:704:C:H2'	1:2A:705:C:C6	2.44	0.53
1:2A:732:G:H21	1:2A:834:A:H61	1.55	0.53
2:2B:32:C:H2'	2:2B:33:G:O4'	2.09	0.53
3:1D:52:ARG:NH2	59:1D:402:HOH:O	2.36	0.52
3:1D:9:TYR:CZ	3:1D:13:ARG:HG2	2.44	0.52
1:2A:2529:A:OP2	59:2A:3652:HOH:O	2.19	0.52
2:2B:75:G:N2	21:2Z:87:ASP:OD1	2.39	0.52
5:2F:155:LEU:HD11	5:2F:176:LEU:HD12	1.91	0.52
1:1A:2120:U:H3	1:1A:2211:G:H1	1.56	0.52
5:1F:195:ASP:HB3	5:1F:198:ALA:H	1.75	0.52
6:1G:179:PRO:HB2	26:14:42:PHE:HE1	1.74	0.52
12:1Q:60:ARG:NH1	21:1Z:180:VAL:HG23	2.24	0.52
25:23:30:ARG:H	25:23:33:GLN:NE2	2.06	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2879:C:H2'	1:2A:2880:C:O4'	2.10	0.52
1:2A:885:U:H2'	1:2A:886:C:H6	1.73	0.52
11:2P:114:ILE:HG13	11:2P:125:VAL:HG21	1.92	0.52
1:1A:1158:U:H2'	1:1A:1159:G:C8	2.44	0.52
1:1A:703:U:H2'	1:1A:704:C:C6	2.44	0.52
14:1S:11:LYS:O	14:1S:15:ARG:HG3	2.09	0.52
15:1T:96:ARG:CZ	15:1T:96:ARG:HB3	2.40	0.52
19:1X:44:GLU:HG3	19:1X:51:VAL:HG23	1.91	0.52
22:20:32:ARG:H	22:20:35:ASN:ND2	2.07	0.52
24:22:41:ILE:HG13	24:22:43:GLN:HB2	1.90	0.52
1:2A:1879:G:H2'	1:2A:1880:G:H8	1.74	0.52
1:2A:635:G:O2'	1:2A:639:A:N1	2.41	0.52
1:2A:675:G:OP1	30:28:19:SER:OG	2.25	0.52
6:2G:16:ARG:NH2	6:2G:28:VAL:HG12	2.24	0.52
15:2T:127:ALA:C	15:2T:129:ARG:H	2.12	0.52
25:13:8:LEU:HD13	25:13:31:LEU:HD23	1.91	0.52
1:1A:2338:A:H2'	1:1A:2339:A:C8	2.43	0.52
6:1G:46:ALA:HB2	6:1G:53:LEU:HD12	1.90	0.52
10:1O:35:VAL:HG21	10:1O:105:GLU:HG3	1.90	0.52
1:2A:1317:A:H3'	1:2A:1318:U:H5''	1.92	0.52
1:2A:181:U:OP2	59:2A:3650:HOH:O	2.19	0.52
1:2A:2307:U:OP2	14:2S:9:ARG:NH2	2.42	0.52
6:2G:61:ALA:HA	6:2G:66:GLN:O	2.09	0.52
1:1A:2226:G:OP2	1:1A:2226:G:H4'	2.07	0.52
1:1A:296:C:H2'	1:1A:297:G:C8	2.44	0.52
1:1A:2583:A:N7	4:1E:144:ARG:HD2	2.23	0.52
25:23:12:PRO:HB2	25:23:20:LYS:HG2	1.92	0.52
1:2A:235:G:H4'	1:2A:412:G:C5	2.44	0.52
1:2A:1174:A:N6	1:2A:2502:U:OP1	2.42	0.52
1:2A:351:U:H4'	20:2Y:68:HIS:CE1	2.45	0.52
1:2A:44:C:H2'	1:2A:45:C:C6	2.45	0.52
21:2Z:150:LEU:HD11	21:2Z:172:ALA:HB3	1.91	0.52
1:1A:924:A:H2'	1:1A:925:G:C8	5.24	0.52
14:1S:63:THR:OG1	14:1S:64:GLU:N	4.41	0.52
1:2A:353:A:HO2'	1:2A:354:A:H8	1.56	0.52
22:10:32:ARG:H	22:10:35:ASN:ND2	2.07	0.52
1:1A:1086:C:H42	1:1A:1159:G:H1	1.56	0.52
4:1E:82:ARG:HG2	4:1E:83:ASP:N	2.24	0.52
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.91	0.52
1:2A:1812:C:H1'	1:2A:2620:U:H5''	1.92	0.52
1:2A:947:C:H2'	1:2A:948:C:C6	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.45	0.52
1:1A:1076:G:H5''	31:19:8:LYS:HE3	1.90	0.52
1:1A:440:C:H2'	1:1A:441:A:C8	2.44	0.52
1:2A:1154:C:H2'	1:2A:1155:G:C8	3.40	0.52
3:2D:71:ASP:CB	3:2D:103:ARG:HH22	2.23	0.52
4:2E:59:VAL:HG21	4:2E:74:PRO:HB3	1.90	0.52
21:2Z:10:ARG:NH1	21:2Z:26:GLY:O	2.42	0.52
12:2Q:60:ARG:NH2	21:2Z:181:GLU:OE2	2.40	0.52
1:2A:117:U:OP2	59:2A:3651:HOH:O	2.19	0.52
1:2A:1291:A:OP1	5:2F:38:ARG:NH1	2.42	0.52
1:2A:2858:U:H4'	1:2A:2877:A:C2	2.45	0.52
1:2A:703:U:H2'	1:2A:704:C:C6	2.45	0.52
1:2A:1828:U:H5''	3:2D:260:ARG:HB3	1.91	0.52
8:2I:104:GLN:HG3	8:2I:105:HIS:CD2	2.45	0.52
1:1A:2347:A:H61	22:10:43:THR:CG2	2.23	0.51
23:21:65:SER:OG	23:21:66:HIS:ND1	2.31	0.51
1:2A:1457:A:H2'	1:2A:1458:G:C8	2.45	0.51
1:1A:1232:U:H4'	17:1V:79:VAL:HG22	1.93	0.51
1:1A:894:G:H2'	1:1A:895:A:C8	2.46	0.51
1:1A:346:G:C8	5:1F:171:PRO:HG3	2.45	0.51
1:2A:846:A:OP1	1:2A:846:A:H8	1.93	0.51
6:2G:38:VAL:HG22	6:2G:93:THR:HG23	1.92	0.51
1:1A:1674:U:H2'	1:1A:1675:G:C8	2.44	0.51
1:1A:904:U:O2	1:1A:2279:A:H2'	2.09	0.51
1:2A:2354:C:HO2'	1:2A:2384:G:HO2'	1.57	0.51
1:2A:2554:G:H2'	1:2A:2555:G:C8	2.45	0.51
1:1A:1312:U:OP1	59:1A:4364:HOH:O	2.19	0.51
1:1A:1328:G:O2'	59:1A:4367:HOH:O	2.19	0.51
1:1A:138:A:H8	1:1A:1453:C:O2'	1.94	0.51
1:1A:1873:C:H5'	3:1D:253:GLN:NE2	2.25	0.51
20:1Y:15:VAL:HG21	20:1Y:42:VAL:HG11	1.93	0.51
1:2A:1476:U:H2'	1:2A:1477:C:C6	2.46	0.51
1:2A:1643:C:H2'	1:2A:1644:C:H6	1.76	0.51
1:2A:1887:G:O6	59:2A:3630:HOH:O	2.14	0.51
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.41	0.51
1:2A:645:A:OP2	11:2P:108:LYS:NZ	2.43	0.51
26:14:63:TYR:N	26:14:64:GLY:HA2	2.25	0.51
1:1A:2622:U:C4	27:15:3:LYS:HG2	2.46	0.51
12:1Q:14:ARG:HG2	12:1Q:41:TRP:HH2	1.75	0.51
1:2A:661:A:H2'	11:2P:117:GLU:OE2	2.10	0.51
27:15:16:ARG:NH1	27:15:17:ASP:OD1	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2795:G:N7	59:1A:4502:HOH:O	2.34	0.51
15:1T:55:ASN:N	15:1T:59:THR:HG22	2.19	0.51
1:2A:2824:C:C5'	27:25:29:THR:HG21	2.41	0.51
1:2A:1227:G:O3'	25:23:29:ARG:NH1	2.37	0.51
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.11	0.51
12:2Q:57:HIS:NE2	12:2Q:116:GLU:HB3	2.25	0.51
26:14:58:ARG:HB3	26:14:58:ARG:HH11	1.75	0.51
28:16:4:GLU:O	28:16:27:LYS:HE2	2.11	0.51
1:1A:2249:G:N3	1:1A:2249:G:H2'	2.25	0.51
1:1A:33:C:H5''	1:1A:34:G:OP2	2.10	0.51
1:1A:6:G:H2'	1:1A:7:A:O4'	2.10	0.51
21:1Z:92:SER:O	21:1Z:94:GLU:N	2.39	0.51
1:2A:1673:G:H2'	1:2A:1674:U:H6	1.76	0.51
1:2A:560:A:H2'	1:2A:561:C:C6	2.46	0.51
1:2A:625:A:H4'	1:2A:626:G:H5'	1.93	0.51
9:2N:36:GLY:HA2	9:2N:38:HIS:CE1	2.45	0.51
1:1A:1803:A:OP2	59:1A:4363:HOH:O	2.18	0.51
1:1A:1816:A:H1'	1:1A:1959:A:N6	2.25	0.51
1:2A:1103:G:H2'	1:2A:1104:G:C8	2.45	0.51
1:2A:1863:U:O2'	1:2A:1990:A:N1	2.40	0.51
1:2A:663:U:H2'	1:2A:664:C:C6	2.45	0.51
1:2A:1739:U:O2'	3:2D:14:ARG:NH2	2.44	0.51
1:2A:552:A:OP2	9:2N:114:ARG:NH1	2.43	0.51
1:1A:2244:U:H2'	1:1A:2245:G:C8	2.45	0.51
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.76	0.51
1:2A:2033:G:OP1	18:2W:11:ARG:NH2	2.43	0.51
1:2A:990:G:N2	1:2A:1016:G:H1'	2.26	0.51
5:2F:197:ASP:O	5:2F:200:GLU:HB2	2.10	0.51
19:2X:57:LEU:HD11	19:2X:78:LYS:HD2	1.92	0.51
1:1A:2315:G:H22	1:1A:2323:U:H3	1.58	0.51
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.75	0.51
8:1I:132:PRO:O	59:1I:5001:HOH:O	2.19	0.51
12:1Q:21:THR:HG21	12:1Q:101:ARG:N	2.26	0.51
13:1R:36:THR:HG22	13:1R:37:THR:H	1.75	0.51
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.92	0.51
1:2A:1765:G:H8	1:2A:1769:A:H62	1.58	0.51
1:2A:2012:U:H2'	1:2A:2013:G:H5''	1.93	0.51
1:2A:2824:C:H2'	1:2A:2825:C:C6	2.45	0.51
5:2F:117:ARG:HH12	11:2P:1:MET:H2	1.58	0.51
6:2G:114:ILE:HG23	6:2G:136:ARG:NH2	2.26	0.51
1:1A:2488:C:O2	31:19:4:ARG:NH2	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	1.92	0.50
7:1H:55:PRO:HG2	7:1H:61:HIS:CE1	2.45	0.50
1:2A:239:A:C5	1:2A:240:G:H1'	2.46	0.50
1:2A:330:G:N1	1:2A:333:A:OP2	2.44	0.50
1:2A:902:C:O2'	1:2A:903:C:OP1	2.25	0.50
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.46	0.50
21:2Z:9:TYR:OH	21:2Z:61:LEU:HD23	2.11	0.50
26:14:24:THR:OG1	26:14:25:TYR:N	2.36	0.50
1:1A:2604:U:H2'	1:1A:2605:C:C6	2.46	0.50
1:1A:2831:G:O2'	1:1A:2833:C:OP2	2.23	0.50
12:1Q:110:THR:HG23	12:1Q:113:GLN:HB2	1.93	0.50
15:1T:51:ARG:HD3	59:1T:302:HOH:O	2.12	0.50
1:2A:1070:G:N2	1:2A:1082:G:H1'	29.93	0.50
1:2A:2043:U:O2'	1:2A:2628:C:H5'	2.12	0.50
1:2A:63:C:O2'	1:2A:481:C:N3	2.41	0.50
1:2A:900:G:N3	1:2A:1381:A:H2	127.24	0.50
10:2O:120:GLU:HB2	15:2T:68:TYR:HE2	1.76	0.50
1:1A:2017:C:H4'	1:1A:2018:G:OP1	2.12	0.50
1:1A:2622:U:H5'	1:1A:2622:U:H6	1.75	0.50
1:2A:75:C:H42	1:2A:106:G:H1	1.58	0.50
1:2A:1673:G:H2'	1:2A:1674:U:C6	2.47	0.50
1:2A:171:C:H2'	1:2A:172:C:C6	3.47	0.50
1:2A:200:G:H2'	1:2A:201:A:O4'	2.11	0.50
1:2A:2565:U:H2'	1:2A:2566:U:C6	2.47	0.50
10:2O:64:ARG:NH1	10:2O:81:ASP:OD1	2.44	0.50
12:2Q:64:ILE:HG22	12:2Q:106:VAL:HG12	1.93	0.50
1:1A:1184:C:O3'	9:1N:25:ARG:NH1	2.43	0.50
1:1A:714:G:H5'	1:1A:715:G:OP2	2.11	0.50
1:1A:725:C:OP1	59:1A:4369:HOH:O	2.19	0.50
1:1A:991:G:H2'	1:1A:992:G:C8	2.47	0.50
7:1H:11:VAL:HG21	7:1H:50:VAL:HG23	1.92	0.50
1:2A:2593:G:OP2	59:2A:3649:HOH:O	2.19	0.50
3:2D:60:ARG:HD3	3:2D:86:PRO:HB2	1.93	0.50
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.94	0.50
8:2I:40:THR:O	8:2I:44:LEU:HB2	2.12	0.50
11:2P:81:GLN:NE2	11:2P:105:LEU:O	2.44	0.50
26:14:46:GLN:HB2	26:14:48:ARG:CZ	2.42	0.50
1:1A:124:A:OP1	59:1A:4370:HOH:O	2.19	0.50
1:1A:894:G:C4	1:1A:977:A:H8	2.30	0.50
1:1A:922:C:H2'	1:1A:923:U:O4'	2.11	0.50
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1050:C:H2'	1:2A:1051:C:H6	1.77	0.50
1:2A:1587:G:H2'	1:2A:1588:A:H8	1.77	0.50
1:2A:466:U:H2'	1:2A:467:G:C8	2.47	0.50
6:2G:151:ALA:O	6:2G:153:ARG:HD3	2.12	0.50
1:1A:2638:G:O2'	1:1A:2793:A:N1	2.37	0.50
8:1I:92:VAL:HG11	8:1I:144:VAL:HG11	1.94	0.50
20:1Y:92:ASN:CB	20:1Y:94:LYS:H	2.23	0.50
1:2A:1302:C:H6	1:2A:1302:C:O5'	1.94	0.50
1:2A:1820:C:H2'	1:2A:1821:A:C5	2.46	0.50
1:2A:2700:U:P	1:2A:2731:G:H22	2.35	0.50
12:2Q:57:HIS:HD2	12:2Q:117:ALA:HB2	1.75	0.50
14:2S:10:ARG:HH21	14:2S:91:PRO:HB2	1.76	0.50
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.93	0.50
26:14:26:SER:OG	26:14:27:THR:N	2.44	0.50
1:1A:1230:G:OP2	59:1A:4320:HOH:O	2.20	0.50
1:1A:1785:A:OP2	15:1T:113:LYS:NZ	2.43	0.50
1:1A:2458:G:OP2	59:1A:4374:HOH:O	2.19	0.50
8:1I:132:PRO:HD2	8:1I:136:VAL:O	2.12	0.50
15:1T:51:ARG:HG3	15:1T:98:LYS:HD2	1.93	0.50
1:2A:26:G:N2	1:2A:536:G:H1'	2.26	0.50
1:2A:70:U:OP2	24:22:29:LYS:NZ	2.41	0.50
1:2A:720:G:H1'	5:2F:74:ARG:HD3	1.94	0.50
1:1A:2297:A:H4'	1:1A:2298:A:O4'	2.11	0.50
21:1Z:19:ARG:NH1	21:1Z:84:GLU:O	2.44	0.50
1:2A:1105:U:O4'	1:2A:1107:G:H5''	2.12	0.50
6:2G:18:GLU:HG2	6:2G:175:LEU:HD21	1.94	0.50
1:1A:358:C:H4'	20:1Y:73:ARG:HD3	1.94	0.50
1:1A:600:A:H3'	59:1A:4647:HOH:O	2.11	0.50
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	1.94	0.50
12:1Q:60:ARG:HD2	21:1Z:179:ASP:OD1	2.12	0.50
26:24:41:PRO:HG3	26:24:49:PHE:CZ	2.47	0.50
1:2A:1406:G:H2'	1:2A:1407:C:C6	2.89	0.50
10:2O:88:ASN:HD21	10:2O:92:GLU:HB2	1.77	0.50
22:10:27:GLU:HB2	22:10:69:PHE:HD1	1.77	0.49
1:1A:2019:G:OP1	59:1A:4375:HOH:O	2.20	0.49
1:1A:2544:A:H2'	1:1A:2545:A:O4'	2.12	0.49
1:1A:2855:G:H2'	1:1A:2856:U:O4'	2.12	0.49
19:1X:57:LEU:CD1	19:1X:78:LYS:HB2	2.41	0.49
1:2A:2375:C:H2'	1:2A:2376:G:O4'	2.11	0.49
1:2A:820:A:H2'	1:2A:820:A:N3	2.27	0.49
1:2A:885:U:H1'	1:2A:1235:G:H1'	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:37:C:N3	2:2B:48:A:O2'	2.45	0.49
21:2Z:157:LEU:HD13	21:2Z:162:GLU:HA	1.94	0.49
1:1A:1073:A:N6	1:1A:1170:G:H2'	2.26	0.49
1:1A:1096:G:H22	1:1A:1153:U:H5	1.60	0.49
1:1A:2341:G:H2'	1:1A:2342:G:O4'	2.12	0.49
1:1A:307:U:H2'	1:1A:308:C:H6	1.76	0.49
1:1A:57:U:H2'	1:1A:58:G:H8	5.60	0.49
5:1F:14:PRO:HD2	5:1F:127:GLU:OE1	2.12	0.49
14:1S:6:ALA:O	14:1S:10:ARG:HG3	2.13	0.49
1:2A:1423:A:O2'	1:2A:1424:A:H3'	2.11	0.49
1:2A:1508:C:H4'	1:2A:2714:C:H5'	1.94	0.49
1:2A:489:U:O4	59:2A:3645:HOH:O	2.18	0.49
1:2A:909:A:H2'	1:2A:910:G:C8	2.48	0.49
1:1A:550:A:O2'	1:1A:2064:C:O2	2.26	0.49
1:1A:77:G:H1'	1:1A:78:G:H8	4.57	0.49
1:2A:1051:C:C2	1:2A:1182:G:N2	2.80	0.49
1:2A:1586:U:C2'	1:2A:1587:G:H5'	2.42	0.49
1:2A:1473:C:N4	1:2A:1616:A:OP2	2.37	0.49
1:2A:168:G:OP2	29:27:32:LYS:HE3	2.13	0.49
1:2A:50:A:OP2	1:2A:114:G:N1	2.40	0.49
6:2G:28:VAL:O	6:2G:31:VAL:HG13	2.11	0.49
6:2G:33:ARG:HH12	6:2G:162:THR:HG21	1.77	0.49
1:1A:2284:A:H2'	1:1A:2285:A:C8	2.47	0.49
1:1A:274:C:H2'	1:1A:275:C:C6	2.47	0.49
1:1A:641:G:N2	1:1A:733:C:O2	75.06	0.49
1:1A:817:G:OP2	59:1A:4372:HOH:O	2.19	0.49
9:1N:17:ASP:O	9:1N:21:LYS:NZ	2.25	0.49
21:1Z:75:ASN:O	21:1Z:84:GLU:HG2	2.13	0.49
1:2A:1397:U:OP2	59:2A:3653:HOH:O	2.19	0.49
1:2A:2054:A:O2'	1:2A:2056:G:OP2	2.29	0.49
1:2A:755:U:H2'	1:2A:756:G:C8	2.47	0.49
1:2A:947:C:H2'	1:2A:948:C:H6	1.78	0.49
3:2D:71:ASP:HB3	3:2D:103:ARG:HH22	1.78	0.49
1:2A:184:A:H62	11:2P:38:GLN:HE22	1.59	0.49
1:2A:1284:G:H2'	1:2A:1285:U:O4'	2.13	0.49
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.78	0.49
1:2A:67:C:H2'	1:2A:68:G:H8	1.78	0.49
7:2H:154:PRO:HB3	7:2H:163:TYR:CZ	2.47	0.49
11:2P:39:LYS:HA	11:2P:45:LEU:HG	1.94	0.49
15:2T:85:LYS:NZ	15:2T:87:ASP:OD2	2.44	0.49
1:1A:2824:C:H5'	27:15:29:THR:HG21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1809:U:H2'	59:1A:4496:HOH:O	2.12	0.49
1:1A:2723:U:H1'	1:1A:2724:A:C8	2.48	0.49
1:1A:584:U:OP2	59:1A:4377:HOH:O	2.20	0.49
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.77	0.49
1:2A:1121:C:H3'	1:2A:1122:A:C8	2.47	0.49
1:2A:1159:G:H2'	1:2A:1160:G:C8	2.48	0.49
1:2A:2121:G:H2'	1:2A:2122:G:C8	2.48	0.49
1:2A:2578:G:H2'	1:2A:2579:C:C6	2.47	0.49
1:2A:628:U:H4'	1:2A:704:C:H4'	1.95	0.49
3:2D:133:LEU:HD23	3:2D:136:ILE:HD12	1.95	0.49
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.47	0.49
1:1A:1616:A:H2'	1:1A:1617:A:C8	2.47	0.49
1:1A:663:U:H2'	1:1A:664:C:C6	2.48	0.49
3:1D:147:LEU:HD13	3:1D:155:LEU:HD11	1.94	0.49
1:2A:466:U:O2	5:2F:46:ARG:NH2	2.40	0.49
10:2O:77:ILE:HB	15:2T:74:ARG:HD3	1.93	0.49
14:2S:3:ARG:HG2	14:2S:3:ARG:HH11	1.77	0.49
16:2U:44:ASN:HD21	17:2V:75:PHE:HB3	1.77	0.49
1:1A:2416:G:O2'	1:1A:2417:U:OP1	2.23	0.49
1:1A:2650:A:OP2	59:1A:4373:HOH:O	2.19	0.49
15:1T:108:ARG:HB3	15:1T:108:ARG:CZ	2.42	0.49
15:1T:23:ARG:HG3	15:1T:120:ARG:NH1	2.26	0.49
1:2A:1643:C:H2'	1:2A:1644:C:C6	2.47	0.49
1:2A:1675:G:H2'	1:2A:1676:C:C6	2.47	0.49
1:2A:1685:U:C2'	1:2A:1686:C:H5''	2.42	0.49
1:2A:1777:G:H2'	1:2A:1778:G:H8	1.78	0.49
1:2A:2080:A:O2'	5:2F:69:HIS:HD2	1.96	0.49
1:2A:322:A:N1	1:2A:345:A:O2'	2.38	0.49
6:2G:36:LYS:HG2	6:2G:160:VAL:HB	1.94	0.49
6:2G:96:ARG:O	6:2G:99:MET:HB3	2.13	0.49
8:2I:92:VAL:HG13	8:2I:120:ILE:HB	1.94	0.49
1:1A:1633:C:H2'	1:1A:1634:C:H6	1.77	0.49
1:1A:466:U:O2	5:1F:46:ARG:NH2	2.41	0.49
7:1H:101:ARG:HH22	7:1H:122:THR:HA	1.78	0.49
10:1O:71:ARG:NH2	10:1O:105:GLU:OE1	2.40	0.49
10:1O:4:PRO:O	10:1O:5:GLN:HB2	2.13	0.49
1:2A:1000:G:OP2	12:2Q:14:ARG:NH2	2.46	0.49
7:2H:3:ARG:HH22	7:2H:5:GLY:H	1.61	0.49
8:1I:27:ARG:HD2	23:11:71:TYR:CE1	2.47	0.48
29:17:5:TRP:NE1	29:17:7:PRO:HG3	2.27	0.48
1:1A:1924:G:OP1	3:1D:241:PRO:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.93	0.48
26:24:59:PHE:HA	26:24:61:ARG:N	2.28	0.48
1:2A:2122:G:O6	1:2A:2209:C:N4	2.45	0.48
1:2A:2660:U:H2'	1:2A:2661:U:C6	2.48	0.48
2:2B:55:U:C1'	6:2G:29:TRP:HE1	2.26	0.48
2:2B:75:G:H22	21:2Z:73:GLN:HE21	1.60	0.48
3:2D:200:ASP:HB2	59:2D:416:HOH:O	2.12	0.48
1:2A:775:G:C5	3:2D:208:LYS:HB2	2.48	0.48
1:1A:1091:A:H8	1:1A:1091:A:OP1	1.96	0.48
1:1A:1337:U:H2'	1:1A:1338:C:C6	2.48	0.48
1:1A:2083:A:C2	1:1A:2514:A:N6	2.81	0.48
1:1A:2579:C:OP1	59:1A:4371:HOH:O	2.19	0.48
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.30	0.48
1:2A:183:A:H5''	1:2A:184:A:O5'	2.12	0.48
1:2A:2120:U:H2'	1:2A:2121:G:H5'	1.93	0.48
1:2A:2762:A:H8	1:2A:2762:A:OP1	1.96	0.48
1:2A:661:A:H5''	11:2P:117:GLU:HG2	1.95	0.48
14:2S:35:ILE:HD11	14:2S:97:ARG:HE	1.77	0.48
1:1A:859:U:H2'	1:1A:860:C:C6	2.48	0.48
3:1D:26:LYS:HB3	3:1D:83:GLU:HG2	1.95	0.48
4:1E:120:TRP:CE3	4:1E:155:LYS:HD3	2.48	0.48
1:1A:2829:A:OP2	13:1R:2:ARG:NH2	2.46	0.48
1:2A:1389:G:O2'	1:2A:1430:G:H2'	2.13	0.48
1:2A:2214:G:H2'	1:2A:2215:G:C8	2.48	0.48
1:2A:2590:C:H4'	4:2E:134:ILE:HG12	1.95	0.48
5:2F:126:VAL:HG21	5:2F:129:PHE:CZ	2.48	0.48
15:2T:16:ARG:HD3	15:2T:19:LEU:HG	1.94	0.48
21:2Z:134:PRO:HG3	21:2Z:161:VAL:HG11	1.95	0.48
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.46	0.48
11:1P:59:LEU:HD21	30:18:10:ALA:HA	1.95	0.48
1:1A:301:A:O2'	1:1A:302:C:OP1	2.29	0.48
3:1D:83:GLU:OE1	3:1D:104:TYR:OH	2.13	0.48
21:1Z:91:LEU:HD11	21:1Z:96:VAL:HG11	1.95	0.48
1:2A:1070:G:O2'	59:2A:3656:HOH:O	2.20	0.48
1:2A:1346:A:C8	1:2A:1348:G:C8	3.01	0.48
1:2A:1789:A:H4'	1:2A:2727:C:O4'	2.13	0.48
1:2A:475:G:OP2	59:2A:3655:HOH:O	2.20	0.48
1:2A:601:G:H2'	1:2A:602:C:C6	2.49	0.48
1:2A:972:G:H2'	1:2A:973:G:O4'	2.13	0.48
2:2B:108:U:H2'	2:2B:109:C:H5''	1.95	0.48
1:2A:1844:G:H5''	3:2D:54:ARG:HH21	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:730:G:OP1	29:17:16:HIS:ND1	2.47	0.48
1:1A:1833:A:O2'	3:1D:259:THR:HG21	2.13	0.48
5:1F:44:ARG:NH1	59:1F:402:HOH:O	2.38	0.48
23:21:77:ALA:HA	23:21:80:LEU:HD13	1.96	0.48
6:2G:108:ASN:HA	26:24:37:SER:HB2	1.95	0.48
1:2A:1451:U:H2'	1:2A:1452:C:C6	2.49	0.48
1:2A:1176:G:O6	1:2A:2061:C:H1'	2.14	0.48
1:2A:830:A:C8	1:2A:838:G:C5	3.02	0.48
24:12:3:LEU:O	24:12:7:ARG:HG3	2.14	0.48
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.27	0.48
14:1S:10:ARG:O	14:1S:14:VAL:HG13	2.13	0.48
25:23:46:ASN:O	25:23:50:VAL:HG22	2.12	0.48
1:2A:1042:G:OP1	16:2U:92:ARG:HG2	2.13	0.48
1:2A:1017:A:C8	1:2A:1232:U:C2	3.01	0.48
1:2A:2117:U:H2'	1:2A:2118:C:C6	2.48	0.48
1:2A:435:C:O2'	1:2A:436:G:H5'	2.14	0.48
1:2A:585:G:OP2	59:2A:3654:HOH:O	2.20	0.48
1:2A:822:G:H4'	1:2A:823:A:O5'	2.13	0.48
3:2D:77:ALA:HB2	3:2D:97:TYR:CD2	2.48	0.48
6:2G:13:GLU:O	6:2G:17:PRO:HD2	2.14	0.48
10:2O:71:ARG:NE	10:2O:105:GLU:OE2	2.42	0.48
12:2Q:58:PHE:CZ	12:2Q:109:VAL:HG21	2.49	0.48
27:15:16:ARG:HD2	27:15:20:ARG:NH1	2.29	0.48
28:16:11:LEU:HB2	28:16:21:TYR:HB2	1.95	0.48
11:1P:62:LEU:O	30:18:13:ARG:HD3	2.14	0.48
1:1A:1475:C:H2'	1:1A:1476:U:C6	2.49	0.48
1:1A:353:A:HO2'	1:1A:354:A:H8	1.58	0.48
4:1E:145:LYS:NZ	59:1E:402:HOH:O	2.22	0.48
15:1T:127:ALA:C	15:1T:129:ARG:H	2.17	0.48
21:1Z:44:PHE:CZ	21:1Z:86:VAL:HG11	2.48	0.48
29:27:46:VAL:HG13	29:27:48:LYS:HE2	1.96	0.48
30:28:34:TRP:CE2	30:28:35:GLN:HB2	2.49	0.48
1:2A:579:U:H2'	1:2A:580:G:H8	1.78	0.48
1:2A:830:A:N6	3:2D:229:VAL:HG11	2.28	0.48
2:2B:72:G:O2'	2:2B:73:A:O4'	2.30	0.48
7:2H:69:ARG:HG3	7:2H:70:THR:N	2.29	0.48
16:2U:86:ALA:O	17:2V:49:THR:HG23	2.13	0.48
19:2X:31:HIS:HD2	19:2X:33:LYS:H	1.59	0.48
21:2Z:44:PHE:CZ	21:2Z:86:VAL:HG11	2.48	0.48
1:1A:1565:U:H2'	1:1A:1566:G:O4'	2.13	0.48
10:1O:98:VAL:HG13	10:1O:117:LEU:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:1Q:32:TYR:OH	12:1Q:111:GLU:OE1	2.19	0.48
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.65	0.48
1:2A:1978:C:H2'	1:2A:1979:C:C6	2.49	0.48
1:2A:2511:U:H5''	1:2A:2512:C:OP2	2.14	0.48
1:2A:2641:G:H2'	1:2A:2642:G:H8	1.78	0.48
15:2T:117:ASP:O	15:2T:121:ILE:HG13	2.13	0.48
1:1A:2723:U:O2'	1:1A:2725:A:H5'	2.14	0.48
1:2A:483:G:C8	29:27:37:LYS:HG2	2.49	0.48
1:2A:2310:G:H2'	1:2A:2311:G:C8	2.41	0.48
1:2A:2312:C:H2'	1:2A:2313:G:C8	2.48	0.48
1:2A:2376:G:O6	30:28:39:LYS:HE3	2.14	0.48
1:2A:724:C:H2'	1:2A:725:C:C6	2.49	0.48
2:2B:44:G:OP1	6:2G:98:ARG:NH2	2.47	0.48
4:2E:11:MET:HG2	4:2E:24:THR:HB	1.96	0.48
15:2T:65:LYS:HE2	15:2T:67:SER:HB2	1.94	0.48
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.14	0.48
1:1A:2878:G:H2'	1:1A:2879:C:O4'	2.13	0.48
1:1A:810:A:H2	3:1D:219:PRO:HG3	1.79	0.48
7:1H:88:LEU:HD22	7:1H:130:ARG:HG2	1.96	0.48
16:1U:76:TYR:CE1	16:1U:80:ILE:HG13	2.49	0.48
1:2A:1699:G:C4	13:2R:9:LYS:HD2	2.49	0.48
1:2A:790:G:OP1	4:2E:132:HIS:ND1	2.45	0.48
2:2B:20:C:N4	2:2B:63:G:H1	2.06	0.48
3:2D:146:GLU:HB2	3:2D:189:CYS:HB3	1.96	0.48
1:1A:1222:C:H2'	1:1A:1223:C:H6	1.78	0.47
1:1A:1555:A:H3'	1:1A:1556:A:H8	1.78	0.47
1:1A:186:C:N3	1:1A:193:G:N1	21.39	0.47
1:1A:2702:C:O3'	1:1A:2880:C:H4'	2.13	0.47
1:1A:2800:C:P	4:1E:61:ARG:HH21	2.37	0.47
9:1N:61:ARG:HA	9:1N:61:ARG:HE	1.78	0.47
14:1S:46:VAL:HG12	14:1S:48:LEU:HD12	1.96	0.47
1:2A:1066:A:H61	1:2A:1187:A:H61	1.62	0.47
1:2A:105:U:H2'	1:2A:106:G:H8	1.78	0.47
1:2A:2854:G:H2'	1:2A:2855:G:C8	2.49	0.47
1:2A:330:G:H2'	1:2A:332:G:OP2	2.13	0.47
1:2A:345:A:OP2	5:2F:169:ASN:HB2	2.14	0.47
1:2A:984:G:N3	1:2A:1235:G:H4'	2.30	0.47
1:2A:917:U:OP1	12:2Q:5:ARG:HD3	2.13	0.47
1:1A:1073:A:H61	1:1A:1170:G:H2'	1.79	0.47
1:1A:1474:G:H2'	1:1A:1475:C:C6	2.48	0.47
1:1A:1783:G:N7	59:1A:4510:HOH:O	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1846:G:OP2	59:1A:4380:HOH:O	2.20	0.47
1:1A:206:A:C2	1:1A:223:U:H4'	2.49	0.47
1:1A:2043:U:O2'	1:1A:2628:C:H5'	2.14	0.47
1:1A:2759:G:O6	1:1A:2767:C:H5''	2.14	0.47
1:2A:172:C:H2'	1:2A:173:U:H6	1.79	0.47
1:2A:2685:G:H2'	1:2A:2686:A:C8	2.48	0.47
1:2A:2824:C:H2'	1:2A:2825:C:H6	1.79	0.47
1:1A:138:A:C8	1:1A:1453:C:O2'	2.66	0.47
1:1A:552:A:N1	1:1A:2063:A:H2'	2.29	0.47
1:1A:529:A:OP2	59:1A:4351:HOH:O	2.20	0.47
1:2A:632:G:H2'	1:2A:633:C:C6	2.49	0.47
7:2H:117:PRO:HG3	7:2H:123:PHE:CD2	2.49	0.47
17:2V:31:ALA:O	17:2V:61:VAL:HG12	2.14	0.47
21:2Z:108:PRO:HG3	21:2Z:141:VAL:HB	1.95	0.47
1:1A:741:G:OP1	1:1A:1425:G:O2'	2.29	0.47
1:2A:1160:G:H2'	1:2A:1161:C:O4'	2.15	0.47
1:2A:1457:A:H2'	1:2A:1458:G:H8	1.78	0.47
1:2A:2091:G:H2'	1:2A:2092:A:H8	1.80	0.47
1:2A:2313:G:C2	1:2A:2314:G:C8	3.03	0.47
1:2A:2582:C:H5''	1:2A:2583:A:H5''	1.97	0.47
2:2B:6:C:H42	2:2B:115:G:H1	1.60	0.47
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.87	0.47
1:1A:1710:A:H2	10:1O:1:MET:HE1	1.78	0.47
12:1Q:86:GLY:HA3	22:10:10:THR:HG21	1.96	0.47
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.66	0.47
1:2A:2216:C:C2'	1:2A:2217:C:H5'	2.45	0.47
1:2A:448:A:H2'	1:2A:449:A:C8	2.49	0.47
1:2A:44:C:H2'	1:2A:45:C:H6	1.80	0.47
6:2G:129:GLY:O	6:2G:161:THR:HB	2.14	0.47
10:2O:2:ILE:HG13	10:2O:8:LEU:HD11	1.97	0.47
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.47	0.47
1:2A:1231:G:H5'	17:2V:81:TYR:CE1	2.49	0.47
20:2Y:44:ILE:HD13	20:2Y:44:ILE:H	1.79	0.47
1:1A:955:A:H2'	1:1A:956:A:H5''	4.63	0.47
4:1E:12:THR:HG22	4:1E:13:ARG:H	1.79	0.47
5:1F:170:LEU:HG	5:1F:172:TRP:NE1	2.30	0.47
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.49	0.47
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.65	0.47
1:2A:1992:A:OP2	3:2D:242:ARG:NH2	2.45	0.47
1:2A:2269:C:O2'	1:2A:2438:C:OP2	2.27	0.47
1:2A:275:C:H2'	1:2A:276:G:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2830:A:C2	1:2A:2831:G:C4	3.03	0.47
1:2A:406:U:H2'	1:2A:407:G:H8	1.80	0.47
1:2A:776:C:H3'	59:2A:3794:HOH:O	2.15	0.47
1:2A:948:C:H2'	1:2A:949:C:C6	2.49	0.47
2:2B:16:G:H1	2:2B:68:C:H42	1.61	0.47
13:2R:2:ARG:NH1	13:2R:5:LYS:O	2.47	0.47
21:2Z:54:HIS:ND1	21:2Z:101:PRO:HG3	2.28	0.47
1:1A:1826:U:H2'	1:1A:1827:C:H6	1.78	0.47
1:1A:2783:C:H2'	1:1A:2784:C:H6	1.80	0.47
1:1A:551:C:C5	1:1A:2791:U:H2'	2.50	0.47
2:1B:66:A:N6	2:1B:108:U:H2'	2.28	0.47
8:1I:72:LEU:O	8:1I:74:ASN:N	2.48	0.47
21:1Z:45:ASP:O	21:1Z:49:ARG:HG3	2.14	0.47
27:25:49:CYS:SG	27:25:51:TYR:HB2	2.55	0.47
1:2A:160:C:H2'	1:2A:161:G:H8	2.00	0.47
1:2A:1777:G:H2'	1:2A:1778:G:C8	2.50	0.47
1:2A:2537:G:H2'	1:2A:2538:C:C6	2.50	0.47
1:2A:592:G:H2'	1:2A:2051:A:C5	2.50	0.47
1:2A:69:A:H5''	1:2A:71:A:C8	2.49	0.47
10:2O:80:ASP:OD2	15:2T:64:ARG:NH2	2.47	0.47
1:2A:1311:G:O5'	18:2W:15:ARG:NH2	2.47	0.47
21:2Z:54:HIS:CG	21:2Z:101:PRO:HG3	2.49	0.47
21:2Z:71:VAL:HG13	21:2Z:88:PHE:CE1	2.50	0.47
1:1A:1173:A:H5''	59:1A:4430:HOH:O	2.13	0.47
1:1A:26:G:N2	1:1A:536:G:H1'	2.29	0.47
5:1F:32:LEU:HB3	5:1F:112:MET:HE1	1.96	0.47
7:1H:101:ARG:NH2	7:1H:122:THR:OG1	2.48	0.47
10:1O:63:VAL:HG12	10:1O:106:LEU:HD11	1.97	0.47
2:1B:91:C:OP1	12:1Q:16:ARG:HG2	2.15	0.47
3:2D:10:THR:OG1	3:2D:13:ARG:HG2	2.14	0.47
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.15	0.47
19:1X:11:PRO:HB3	19:1X:92:LEU:HD11	1.97	0.47
26:24:40:HIS:HB3	26:24:43:TYR:HB2	1.96	0.47
1:2A:1894:U:OP1	1:2A:2421:G:O2'	2.32	0.47
1:2A:2566:U:H5''	1:2A:2567:C:OP2	2.13	0.47
1:2A:298:G:O2'	1:2A:540:C:H5''	109.84	0.47
1:2A:945:A:H2'	1:2A:946:A:O4'	2.15	0.47
3:2D:164:GLN:HE21	3:2D:176:ARG:HH12	1.63	0.47
4:2E:48:GLN:HA	4:2E:80:GLU:HA	1.97	0.47
6:2G:11:TYR:O	6:2G:16:ARG:HG3	2.14	0.47
20:2Y:43:ASN:CG	20:2Y:65:ALA:HB3	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:103:G:H21	21:2Z:73:GLN:NE2	2.13	0.47
1:1A:1462:C:OP2	59:1A:4384:HOH:O	2.21	0.47
1:1A:793:U:O2	1:1A:2035:A:H1'	2.15	0.47
1:1A:820:A:H2'	1:1A:820:A:N3	2.30	0.47
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.48	0.47
1:2A:1883:A:H2'	1:2A:1884:A:C8	2.50	0.47
1:2A:1887:G:C6	1:2A:1888:G:C6	3.03	0.47
1:2A:2416:G:O2'	1:2A:2417:U:OP1	2.21	0.47
1:2A:2509:C:H3'	59:2A:3625:HOH:O	2.15	0.47
14:2S:68:GLN:HA	14:2S:68:GLN:HE21	1.79	0.47
1:1A:830:A:H5'	1:1A:831:G:OP1	2.15	0.47
7:1H:167:GLU:HA	7:1H:168:PRO:HD3	1.80	0.47
11:1P:46:LYS:HB3	11:1P:46:LYS:HE3	1.70	0.47
1:1A:956:A:H2'	12:1Q:9:TYR:OH	2.14	0.47
1:2A:104:C:H2'	1:2A:105:U:H6	1.80	0.47
1:2A:1337:U:H2'	1:2A:1338:C:H6	1.80	0.47
1:2A:990:G:H2'	1:2A:991:G:H8	1.80	0.47
3:2D:145:VAL:HG12	3:2D:146:GLU:O	2.15	0.47
1:2A:1846:G:H3'	3:2D:62:TYR:CE1	2.50	0.47
1:2A:1288:G:O2'	11:2P:7:ARG:NH2	2.47	0.47
29:17:24:THR:O	29:17:28:ARG:HG3	2.16	0.46
31:19:32:HIS:O	31:19:34:GLN:HG3	2.15	0.46
1:1A:1840:A:H2'	1:1A:1841:G:O4'	2.14	0.46
2:1B:57:A:H1'	6:1G:29:TRP:HB2	1.97	0.46
9:1N:114:ARG:NH1	59:1N:3101:HOH:O	2.27	0.46
1:1A:1188:A:OP1	9:1N:25:ARG:NH2	2.48	0.46
1:2A:143:C:H2'	1:2A:144:G:H8	1.80	0.46
1:2A:1603:C:OP2	1:2A:1604:A:O2'	2.26	0.46
1:2A:20:A:H2'	1:2A:21:C:C6	2.50	0.46
1:2A:621:G:H2'	1:2A:622:G:C8	3.20	0.46
1:2A:623:C:O2	1:2A:627:C:H4'	2.15	0.46
10:2O:103:ALA:HB1	10:2O:105:GLU:OE1	2.15	0.46
1:1A:1356:G:O2'	29:17:47:ARG:NH2	2.48	0.46
1:1A:1652:C:H4'	1:1A:1653:A:O5'	2.15	0.46
1:1A:2659:C:H2'	1:1A:2660:U:C6	2.49	0.46
1:1A:515:G:H2'	1:1A:516:A:C8	2.50	0.46
1:1A:842:C:H2'	1:1A:843:C:C6	2.49	0.46
1:1A:894:G:O6	1:1A:973:G:H2'	2.15	0.46
8:1I:29:TYR:O	8:1I:32:PRO:HD2	2.15	0.46
8:1I:61:ARG:HD2	8:1I:61:ARG:HA	1.66	0.46
21:1Z:24:LEU:HB2	21:1Z:41:LEU:HD23	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:22:9:GLN:HE22	24:22:56:GLN:HB3	1.81	0.46
1:2A:1586:U:O2'	1:2A:1587:G:H5'	2.15	0.46
1:2A:2567:C:H2'	1:2A:2568:G:O4'	2.16	0.46
1:2A:862:C:H2'	1:2A:863:C:H6	1.79	0.46
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.98	0.46
6:2G:56:ALA:O	6:2G:60:LEU:HB2	2.15	0.46
13:2R:38:VAL:HB	13:2R:39:PRO:HD3	1.97	0.46
1:1A:1216:G:H3'	1:1A:1217:G:H5'	1.96	0.46
1:1A:2290:G:N7	22:10:14:ARG:NH1	2.63	0.46
1:1A:2299:A:OP2	59:1A:4376:HOH:O	2.20	0.46
1:1A:670:A:H2'	1:1A:671:G:O4'	2.15	0.46
2:1B:102:A:OP2	59:1B:303:HOH:O	2.20	0.46
1:2A:1098:C:N4	1:2A:1151:G:H1	2.07	0.46
1:2A:1467:G:H1'	1:2A:1541:A:N1	2.30	0.46
1:2A:1596:C:H2'	1:2A:1597:C:C6	2.50	0.46
1:2A:1656:C:OP1	59:2A:3659:HOH:O	2.21	0.46
1:2A:2330:G:C2	14:2S:3:ARG:HA	2.50	0.46
1:2A:663:U:H2'	1:2A:664:C:H6	1.79	0.46
4:2E:9:VAL:HG13	4:2E:25:VAL:O	2.15	0.46
10:2O:6:THR:HG22	10:2O:8:LEU:HD22	1.98	0.46
1:1A:1076:G:H21	31:19:36:GLN:HE22	1.62	0.46
1:1A:2505:G:O2'	12:1Q:80:GLU:HA	2.15	0.46
2:1B:33:G:C2	2:1B:50:G:C2	3.04	0.46
27:25:41:PRO:HG2	27:25:44:THR:OG1	2.15	0.46
1:2A:1064:U:HO2'	1:2A:1066:A:H2	1.59	0.46
1:2A:1232:U:H4'	17:2V:79:VAL:HG22	1.96	0.46
1:2A:2067:G:H5'	27:25:19:ARG:HA	1.97	0.46
1:2A:860:C:H2'	1:2A:861:C:H6	1.81	0.46
3:2D:33:LEU:HD11	3:2D:103:ARG:HA	1.97	0.46
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.96	0.46
1:1A:1451:U:H2'	1:1A:1452:C:C6	2.50	0.46
1:1A:230:G:C8	30:18:5:LYS:HG2	2.51	0.46
1:1A:266:C:H3'	59:1A:4362:HOH:O	2.16	0.46
5:1F:129:PHE:CD1	5:1F:163:VAL:HG21	2.50	0.46
1:2A:1625:A:H2'	1:2A:1626:A:C8	2.50	0.46
1:2A:1879:G:H2'	1:2A:1880:G:C8	2.50	0.46
1:2A:2419:U:H2'	1:2A:2420:G:C8	2.51	0.46
1:2A:927:G:H1	1:2A:940:U:H3	1.62	0.46
6:2G:32:PRO:HB3	6:2G:172:LEU:HD22	1.97	0.46
7:2H:118:PRO:HG2	7:2H:121:ILE:HG13	1.97	0.46
1:2A:437:G:C5	11:2P:72:PRO:HB3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1042:G:H5'	16:2U:92:ARG:HH21	1.81	0.46
26:14:46:GLN:O	26:14:48:ARG:HG2	2.15	0.46
1:1A:1788:G:O2'	59:1A:4381:HOH:O	2.20	0.46
1:1A:2758:U:OP1	7:1H:85:LYS:NZ	2.33	0.46
1:1A:307:U:H2'	1:1A:308:C:C6	2.50	0.46
1:1A:508:A:OP1	20:1Y:50:ARG:NH2	2.48	0.46
1:1A:905:G:O2'	1:1A:961:G:O6	2.31	0.46
1:2A:105:U:H2'	1:2A:106:G:C8	2.51	0.46
1:2A:1090:A:O4'	1:2A:1092:G:H8	1.99	0.46
1:2A:1100:G:H3'	1:2A:1101:G:C8	2.45	0.46
1:2A:1104:G:H5''	1:2A:1105:U:H2'	1.97	0.46
1:2A:1402:U:H2'	1:2A:1403:G:O4'	2.16	0.46
1:2A:2227:G:OP1	1:2A:2227:G:H8	1.98	0.46
1:2A:2465:G:H1'	59:2A:3665:HOH:O	2.15	0.46
1:2A:2638:G:N3	1:2A:2793:A:H2	2.14	0.46
1:2A:2884:C:H2'	1:2A:2885:G:O4'	2.16	0.46
1:2A:810:A:N1	1:2A:1819:A:O2'	2.41	0.46
1:2A:990:G:H2'	1:2A:991:G:C8	2.50	0.46
24:12:21:LEU:HD13	24:12:64:LEU:HA	1.98	0.46
1:1A:258:A:C6	1:1A:259:A:C6	3.85	0.46
11:1P:100:LEU:HD12	11:1P:112:LEU:HD11	1.97	0.46
21:1Z:158:PRO:HG2	21:1Z:161:VAL:HG11	1.98	0.46
1:2A:1404:A:H2'	1:2A:1405:A:C5'	2.46	0.46
1:2A:1652:C:H5''	1:2A:1653:A:H5'	1.96	0.46
1:2A:1828:U:H5'	3:2D:259:THR:CG2	2.40	0.46
1:2A:2328:C:O2'	1:2A:2329:G:OP1	2.33	0.46
1:2A:22:G:H2'	1:2A:23:G:C8	3.15	0.46
1:2A:2854:G:H2'	1:2A:2855:G:H8	1.81	0.46
1:2A:863:C:O2'	1:2A:885:U:H5''	2.15	0.46
1:2A:94:G:H4'	24:22:48:HIS:CD2	2.51	0.46
2:2B:40:U:N3	2:2B:43:C:OP2	2.49	0.46
5:2F:20:LEU:HD13	5:2F:21:ALA:H	1.81	0.46
1:2A:2760:A:O2'	7:2H:63:SER:O	2.24	0.46
17:2V:4:ILE:HD12	17:2V:39:LEU:HB3	1.98	0.46
25:13:13:ILE:O	59:13:201:HOH:O	2.20	0.46
1:1A:1833:A:H2'	1:1A:1834:C:O4'	2.16	0.46
1:1A:2440:G:OP2	59:1A:4312:HOH:O	2.21	0.46
1:1A:2862:C:H2'	1:1A:2863:G:C8	2.50	0.46
11:1P:84:ASN:OD1	11:1P:117:GLU:HB2	2.16	0.46
21:1Z:110:GLY:HA3	21:1Z:174:VAL:HG11	1.98	0.46
1:2A:1067:G:N2	1:2A:1068:U:O4	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1139:U:N3	1:2A:1142:U:OP2	2.47	0.46
1:2A:1210:U:H2'	1:2A:1211:C:C6	2.51	0.46
1:2A:2251:C:OP2	59:2A:3660:HOH:O	2.21	0.46
1:2A:2820:G:N2	1:2A:2899:G:H1'	2.31	0.46
1:2A:440:C:H2'	1:2A:441:A:C8	2.51	0.46
1:2A:67:C:H2'	1:2A:68:G:C8	2.50	0.46
15:2T:23:ARG:HG3	15:2T:120:ARG:NH1	2.30	0.46
1:1A:2397:C:H2'	1:1A:2398:U:C6	2.50	0.46
4:1E:170:LEU:HB3	4:1E:184:VAL:HG22	1.97	0.46
1:2A:25:G:C6	1:2A:26:G:N1	2.84	0.46
1:2A:267:G:O2'	1:2A:268:G:H8	1.99	0.46
1:2A:751:A:H2'	1:2A:752:A:O4'	2.30	0.46
13:2R:28:LEU:HD23	13:2R:28:LEU:HA	1.80	0.46
1:1A:628:U:H4'	1:1A:704:C:H4'	1.97	0.46
14:1S:39:ILE:HB	14:1S:49:VAL:HG13	1.97	0.46
26:24:33:VAL:HG12	26:24:34:GLU:H	1.81	0.46
1:2A:2484:U:O2	1:2A:2484:U:H2'	2.16	0.46
1:2A:2733:A:OP1	59:2A:3661:HOH:O	2.21	0.46
2:2B:98:G:H2'	2:2B:99:G:O4'	2.16	0.46
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.16	0.46
1:2A:1322:G:O2'	13:2R:24:GLN:HG2	2.15	0.46
19:2X:27:THR:OG1	19:2X:80:ILE:HG12	2.16	0.46
1:1A:1510:C:H2'	1:1A:1511:G:C8	2.51	0.45
1:1A:2122:G:H2'	1:1A:2123:U:O4'	2.16	0.45
1:1A:2548:U:H2'	1:1A:2549:C:C6	2.52	0.45
1:1A:2543:G:O2'	1:1A:2668:A:N1	2.49	0.45
11:1P:95:VAL:HG13	11:1P:125:VAL:HB	1.96	0.45
26:24:62:ARG:H	26:24:62:ARG:NE	2.13	0.45
26:24:62:ARG:O	26:24:64:GLY:N	2.43	0.45
1:2A:1106:U:O2'	1:2A:1115:A:O4'	2.30	0.45
1:2A:1920:G:N3	1:2A:1920:G:H2'	2.31	0.45
1:2A:2417:U:OP1	1:2A:2422:A:N6	2.49	0.45
1:2A:264:U:H2'	1:2A:265:C:C6	2.51	0.45
1:2A:500:U:C4	1:2A:501:G:C6	3.29	0.45
1:2A:621:G:H2'	1:2A:622:G:H8	2.48	0.45
12:2Q:32:TYR:CE1	12:2Q:133:ARG:HG3	2.51	0.45
13:2R:95:THR:HG22	13:2R:116:LEU:HD23	1.98	0.45
16:2U:97:ASP:OD1	16:2U:101:ARG:HD2	2.17	0.45
21:2Z:127:LYS:O	21:2Z:128:VAL:HG12	2.16	0.45
1:1A:2330:G:N2	14:1S:3:ARG:HA	2.32	0.45
1:1A:2339:A:H2'	1:1A:2340:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:43:GLU:OE1	14:1S:43:GLU:N	6.05	0.45
15:1T:7:ILE:O	15:1T:11:GLU:HG3	2.16	0.45
1:2A:1090:A:H4'	1:2A:1091:A:H5''	1.98	0.45
7:2H:71:LEU:HA	7:2H:71:LEU:HD12	1.72	0.45
11:2P:96:THR:HG23	11:2P:99:LEU:HD23	1.97	0.45
14:2S:3:ARG:NH1	14:2S:3:ARG:HG2	2.31	0.45
1:1A:1399:A:H2'	1:1A:1400:G:O4'	2.16	0.45
1:1A:1520:C:H2'	1:1A:1521:G:C8	2.51	0.45
1:1A:2753:A:OP1	31:19:22:ARG:NH2	2.35	0.45
1:1A:329:U:H2'	1:1A:330:G:O4'	2.16	0.45
1:1A:963:A:H5''	2:1B:98:G:O2'	2.17	0.45
3:1D:37:LEU:HD22	3:1D:87:ASN:ND2	2.32	0.45
9:1N:28:THR:HG22	9:1N:29:LYS:HG3	1.98	0.45
1:1A:1288:G:O2'	11:1P:7:ARG:NH2	2.50	0.45
13:1R:28:LEU:HD12	13:1R:48:VAL:HG21	1.98	0.45
1:2A:1242:U:H2'	1:2A:1243:U:C6	2.51	0.45
1:2A:2488:C:H5''	1:2A:2490:G:O6	2.17	0.45
1:2A:2556:G:N3	1:2A:2576:A:H2	2.14	0.45
1:2A:263:G:H2'	1:2A:264:U:C6	2.51	0.45
1:2A:26:G:O2'	1:2A:27:A:OP2	2.30	0.45
26:14:33:VAL:HG12	26:14:34:GLU:H	1.82	0.45
1:1A:1620:C:N4	59:1A:4310:HOH:O	2.48	0.45
1:1A:1633:C:H2'	1:1A:1634:C:C6	2.51	0.45
1:1A:332:G:N3	1:1A:352:G:O2'	2.48	0.45
19:1X:41:ASN:O	19:1X:45:THR:HG23	2.15	0.45
20:1Y:54:LYS:HA	20:1Y:56:PRO:CD	2.39	0.45
1:2A:555:C:H4'	1:2A:556:A:H5''	1.99	0.45
2:2B:111:G:H2'	2:2B:112:U:O4'	2.17	0.45
4:2E:36:ARG:HD3	4:2E:85:ASN:HD21	1.81	0.45
5:2F:64:ILE:HD11	5:2F:75:HIS:HB2	1.97	0.45
1:2A:1302:C:H4'	5:2F:83:PHE:CD1	2.52	0.45
14:2S:39:ILE:HB	14:2S:49:VAL:HG22	1.98	0.45
1:1A:1217:G:N2	1:1A:1221:A:OP2	2.45	0.45
1:1A:1649:C:H5'	59:1A:4723:HOH:O	2.16	0.45
1:1A:224:C:H2'	1:1A:225:C:C6	2.52	0.45
1:2A:1937:A:H2'	1:2A:1938:U:O4'	2.17	0.45
1:2A:7:A:H2'	1:2A:8:U:H6	1.81	0.45
3:2D:38:LYS:HE3	3:2D:40:THR:HG22	1.98	0.45
2:2B:57:A:C4	6:2G:29:TRP:HB2	2.52	0.45
7:2H:24:VAL:HG22	7:2H:35:VAL:HB	1.97	0.45
19:2X:35:THR:HG22	19:2X:37:THR:N	2.27	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.31	0.45
31:19:26:ILE:H	31:19:26:ILE:HD13	1.81	0.45
1:1A:1013:U:H2'	1:1A:1014:C:C6	2.52	0.45
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.98	0.45
4:1E:9:VAL:HG13	4:1E:25:VAL:O	2.16	0.45
12:1Q:68:ILE:HD13	12:1Q:103:MET:HE3	1.98	0.45
1:1A:1200:A:OP1	16:1U:55:ARG:HD3	2.17	0.45
1:2A:1699:G:C6	13:2R:9:LYS:HB2	2.52	0.45
1:2A:531:A:H4'	1:2A:532:G:O5'	4.11	0.45
1:2A:786:U:H2'	1:2A:787:G:H8	1.79	0.45
3:2D:75:ILE:HG21	3:2D:99:ASP:HB2	1.99	0.45
15:2T:84:GLN:HG2	15:2T:85:LYS:HG2	1.98	0.45
1:2A:470:C:OP1	16:2U:2:PRO:HA	2.16	0.45
18:2W:34:ASN:OD1	18:2W:37:ARG:NH2	2.50	0.45
1:1A:1687:A:H2'	1:1A:1688:G:O4'	2.17	0.45
1:1A:1869:G:C8	1:1A:1948:A:H1'	2.52	0.45
1:1A:2356:G:OP2	28:16:38:LYS:NZ	2.37	0.45
4:1E:144:ARG:HB3	4:1E:145:LYS:H	1.45	0.45
1:2A:1096:G:H5''	1:2A:1097:C:OP2	2.17	0.45
1:2A:2347:A:H61	22:20:43:THR:HG22	1.82	0.45
1:2A:386:G:H2'	1:2A:387:A:C8	2.51	0.45
1:2A:386:G:H2'	1:2A:387:A:H8	1.81	0.45
14:2S:10:ARG:HG2	14:2S:13:ARG:NH2	2.31	0.45
26:14:44:THR:O	26:14:46:GLN:N	2.49	0.45
1:1A:2542:A:H5'	7:1H:157:TYR:CZ	2.52	0.45
1:1A:2600:A:OP2	59:1A:4383:HOH:O	2.20	0.45
3:1D:242:ARG:HG2	3:1D:246:PRO:HG3	1.99	0.45
5:1F:24:LEU:HD12	5:1F:25:PRO:HD2	1.98	0.45
8:1I:140:LEU:HD22	8:1I:140:LEU:HA	1.75	0.45
10:1O:80:ASP:OD2	15:1T:71:GLY:HA3	2.16	0.45
20:1Y:6:HIS:H	20:1Y:6:HIS:HD2	1.65	0.45
21:1Z:102:LEU:HD13	21:1Z:123:ASP:HA	1.99	0.45
1:2A:2431:C:P	30:28:33:ASN:H	2.39	0.45
30:28:62:LEU:HB3	30:28:65:GLU:HG2	1.99	0.45
1:2A:1682:C:OP2	59:2A:3662:HOH:O	2.21	0.45
1:2A:241:C:OP2	30:28:5:LYS:NZ	2.36	0.45
1:2A:2832:A:OP1	4:2E:159:HIS:NE2	2.48	0.45
1:2A:679:G:O6	1:2A:698:C:N4	2.40	0.45
2:2B:2:C:H2'	2:2B:3:C:C6	2.52	0.45
6:2G:61:ALA:O	6:2G:65:GLY:N	2.48	0.45
7:2H:3:ARG:HH12	7:2H:5:GLY:N	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:2Q:59:ARG:NH1	12:2Q:60:ARG:HE	2.15	0.45
1:2A:2287:G:H5'	12:2Q:86:GLY:HA2	1.98	0.45
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.52	0.45
1:1A:1520:C:H2'	1:1A:1521:G:H8	1.82	0.45
1:1A:1603:C:OP2	1:1A:1604:A:O2'	2.23	0.45
1:1A:2345:G:H5'	14:1S:9:ARG:HG2	1.99	0.45
1:1A:2554:G:H2'	1:1A:2555:G:C8	2.51	0.45
2:1B:28:C:H2'	2:1B:29:A:O4'	2.17	0.45
14:1S:36:TYR:CD1	14:1S:36:TYR:N	2.85	0.45
1:1A:2873:G:OP1	15:1T:119:LYS:HD2	2.17	0.45
20:1Y:52:SER:O	20:1Y:54:LYS:N	2.50	0.45
2:2B:83:G:H4'	25:23:52:HIS:CG	2.52	0.45
1:2A:1475:C:H2'	1:2A:1476:U:C6	2.52	0.45
1:2A:1495:A:H8	1:2A:1495:A:OP2	1.99	0.45
1:2A:1702:C:H2'	1:2A:1703:C:H6	1.81	0.45
1:2A:2272:C:O2'	1:2A:2273:U:H5'	2.17	0.45
1:2A:2296:C:OP2	28:26:6:ARG:NH1	2.50	0.45
1:2A:250:A:H2'	1:2A:251:C:O4'	2.17	0.45
1:2A:2623:C:OP2	27:25:2:ALA:N	2.50	0.45
1:2A:323:A:P	20:2Y:86:ARG:HH21	2.40	0.45
1:2A:609:C:O2	11:2P:33:ARG:NH2	2.35	0.45
1:2A:909:A:H2'	1:2A:910:G:H8	1.82	0.45
10:2O:69:ILE:HD11	10:2O:77:ILE:HG23	1.99	0.45
18:2W:4:LYS:HB2	18:2W:106:ILE:HG12	1.97	0.45
21:2Z:91:LEU:HD13	21:2Z:91:LEU:HA	1.76	0.45
1:1A:1091:A:H3'	1:1A:1092:G:C5'	2.45	0.45
1:1A:1017:A:H5'	1:1A:1232:U:H1'	1.98	0.45
1:1A:214:G:H21	1:1A:216:A:H62	1.65	0.45
1:1A:1715:A:H5''	1:1A:2561:G:OP1	2.16	0.45
1:1A:2578:G:H2'	1:1A:2579:C:C6	2.52	0.45
1:1A:603:C:H2'	1:1A:604:G:C8	2.52	0.45
1:1A:775:G:C6	3:1D:208:LYS:HB2	2.51	0.45
7:1H:3:ARG:CG	7:1H:6:ARG:HG2	2.44	0.45
14:1S:48:LEU:HD23	14:1S:82:ILE:HD11	1.97	0.45
15:1T:26:ASP:OD1	15:1T:120:ARG:NH2	2.40	0.45
27:25:16:ARG:HG3	27:25:17:ASP:N	2.32	0.45
1:2A:1587:G:H2'	1:2A:1588:A:C8	2.51	0.45
1:2A:1631:A:H2'	1:2A:1632:A:O4'	2.16	0.45
1:2A:1856:G:H4'	3:2D:242:ARG:CZ	2.47	0.45
1:2A:358:C:H4'	20:2Y:73:ARG:HD2	1.98	0.45
4:2E:79:ARG:HD2	4:2E:195:LEU:HD21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:126:PRO:HD2	7:2H:130:ARG:O	2.17	0.45
2:1B:4:C:H2'	2:1B:5:C:O4'	2.17	0.44
8:1I:104:GLN:O	8:1I:106:GLY:N	2.44	0.44
1:2A:137:G:N3	1:2A:139:A:N6	2.60	0.44
1:2A:173:U:H4'	1:2A:206:A:H4'	1.99	0.44
1:2A:1898:A:H5'	1:2A:1899:G:OP2	2.17	0.44
1:2A:2371:A:H2'	1:2A:2372:A:O4'	2.16	0.44
14:2S:26:LEU:HD22	14:2S:87:PHE:CD1	2.51	0.44
1:2A:594:A:OP2	17:2V:78:LYS:HE2	2.17	0.44
19:2X:44:GLU:HG3	19:2X:51:VAL:HG23	1.99	0.44
6:1G:66:GLN:HG3	26:14:1:MET:HE2	1.99	0.44
1:1A:1844:G:OP1	59:1A:4388:HOH:O	2.21	0.44
1:1A:2730:G:O2'	1:1A:2856:U:OP1	2.25	0.44
1:1A:235:G:H4'	1:1A:412:G:C6	2.52	0.44
1:1A:2649:G:P	4:1E:82:ARG:HH22	2.39	0.44
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.98	0.44
1:2A:2878:G:H2'	1:2A:2879:C:O4'	2.17	0.44
1:2A:2741:G:O2'	4:2E:186:GLY:HA3	2.18	0.44
6:2G:107:LEU:HD23	6:2G:111:LEU:HD21	1.99	0.44
15:2T:54:ARG:HA	15:2T:59:THR:HG22	1.99	0.44
21:2Z:76:LEU:HD12	21:2Z:83:PRO:HA	1.98	0.44
1:1A:1856:G:H2'	1:1A:1857:C:O4'	2.17	0.44
1:1A:2086:C:H2'	1:1A:2087:C:C6	2.52	0.44
1:1A:495:A:H2'	1:1A:496:A:O4'	2.18	0.44
1:1A:598:U:H2'	1:1A:599:G:C8	2.53	0.44
1:2A:1129:A:N3	1:2A:1150:U:O2'	2.41	0.44
1:2A:131:C:O4'	11:2P:1:MET:HG2	97.16	0.44
1:2A:2331:A:H2'	1:2A:2331:A:N3	2.32	0.44
11:2P:28:GLY:O	11:2P:30:THR:N	2.51	0.44
1:2A:2848:G:H5'	13:2R:46:GLY:HA2	1.99	0.44
28:16:40:CYS:HA	28:16:41:PRO:HD3	1.75	0.44
1:1A:885:U:H1'	1:1A:1235:G:H1'	2.00	0.44
1:1A:2480:A:OP2	59:1A:4382:HOH:O	2.20	0.44
1:1A:424:G:O6	59:1A:4378:HOH:O	2.20	0.44
1:1A:552:A:O2'	1:1A:553:A:H5'	2.18	0.44
1:1A:924:A:H2'	1:1A:925:G:H5'	1.99	0.44
1:2A:118:G:H4'	1:2A:148:A:H5'	1.99	0.44
1:2A:2333:A:H2'	1:2A:2334:G:O4'	2.17	0.44
1:2A:2409:U:H2'	1:2A:2410:G:H8	1.82	0.44
1:2A:241:C:O2'	59:2A:3658:HOH:O	2.20	0.44
1:2A:38:C:H2'	1:2A:39:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1844:G:H4'	3:2D:51:VAL:HG21	1.98	0.44
4:2E:144:ARG:HB3	4:2E:145:LYS:H	1.44	0.44
8:2I:61:ARG:HD3	8:2I:61:ARG:HA	1.71	0.44
1:1A:604:G:H2'	1:1A:605:G:C8	2.53	0.44
7:1H:43:VAL:HG13	7:1H:52:VAL:HG22	1.99	0.44
8:1I:43:ASN:HA	8:1I:46:ALA:HB3	1.99	0.44
1:1A:341:C:H5	15:1T:39:ARG:HH21	161.43	0.44
1:2A:1042:G:H2'	1:2A:1042:G:N3	2.32	0.44
1:2A:1227:G:H4'	25:23:29:ARG:HH22	1.83	0.44
1:2A:149:C:H2'	1:2A:150:C:C6	2.52	0.44
1:2A:1659:A:H8	1:2A:1659:A:P	2.40	0.44
2:2B:2:C:H2'	2:2B:3:C:H6	1.81	0.44
7:2H:154:PRO:HB3	7:2H:163:TYR:CE2	2.52	0.44
7:2H:11:VAL:HG13	7:2H:15:VAL:HG22	2.00	0.44
8:2I:91:SER:HB3	8:2I:121:LYS:HE3	1.99	0.44
9:2N:30:ILE:HG22	9:2N:34:LEU:HD22	2.00	0.44
1:2A:593:A:O2'	17:2V:78:LYS:HE3	2.17	0.44
31:19:15:LYS:HD3	31:19:26:ILE:HD11	2.00	0.44
1:1A:2375:C:H2'	1:1A:2376:G:O4'	2.18	0.44
1:1A:2896:U:H2'	1:1A:2897:C:C6	2.52	0.44
1:1A:930:C:H2'	1:1A:931:C:O4'	2.18	0.44
1:1A:609:C:OP2	11:1P:21:ARG:NH2	2.50	0.44
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.61	0.44
1:2A:1268:G:C2	1:2A:1272:G:C5	3.06	0.44
1:2A:267:G:HO2'	1:2A:268:G:H8	1.57	0.44
1:2A:677:A:N3	1:2A:677:A:H2'	2.33	0.44
4:2E:175:VAL:O	4:2E:177:PRO:HD3	2.18	0.44
5:2F:109:GLY:O	5:2F:113:ALA:N	2.46	0.44
10:2O:63:VAL:HG12	10:2O:106:LEU:HD11	2.00	0.44
1:1A:186:C:N4	1:1A:193:G:O6	23.09	0.44
1:1A:517:G:H2'	1:1A:518:G:O4'	2.17	0.44
11:1P:1:MET:SD	11:1P:1:MET:N	4.99	0.44
14:1S:10:ARG:HG2	14:1S:13:ARG:NH2	2.33	0.44
17:1V:98:GLU:OE2	17:1V:100:ARG:NH1	2.51	0.44
22:20:19:LYS:HG2	22:20:41:ARG:HH21	1.82	0.44
26:24:41:PRO:HG3	26:24:49:PHE:CE2	2.53	0.44
1:2A:1474:G:H2'	1:2A:1475:C:C6	2.53	0.44
1:2A:1571:G:H2'	1:2A:1572:G:O4'	2.18	0.44
1:2A:976:G:H4'	1:2A:977:A:O5'	2.18	0.44
4:2E:54:GLN:HB2	4:2E:76:ARG:HG2	2.00	0.44
5:2F:53:THR:CG2	5:2F:55:GLY:H	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:2V:25:LEU:H	17:2V:92:THR:HG1	1.64	0.44
18:2W:18:ARG:NH1	18:2W:76:VAL:O	2.51	0.44
2:1B:12:C:O2'	22:10:74:ARG:HG2	2.18	0.44
1:1A:1090:A:H4'	1:1A:1091:A:C5'	2.48	0.44
1:1A:1198:C:OP1	16:1U:92:ARG:NH1	2.50	0.44
1:1A:2249:G:H5''	59:1A:5557:HOH:O	2.18	0.44
7:1H:11:VAL:HA	7:1H:12:PRO:HD3	1.79	0.44
21:1Z:7:ALA:O	21:1Z:62:PRO:HD3	2.18	0.44
1:2A:1211:C:H2'	1:2A:1212:U:C6	2.53	0.44
1:2A:1315:C:H5''	1:2A:1316:G:O5'	2.18	0.44
1:2A:1693:G:OP2	1:2A:1693:G:H3'	2.17	0.44
1:2A:2302:U:O2'	1:2A:2385:C:O2	2.34	0.44
1:2A:2526:C:H2'	1:2A:2527:G:H8	1.83	0.44
1:2A:2706:C:H2'	1:2A:2707:U:C6	2.53	0.44
1:2A:2799:C:H1'	4:2E:62:PRO:HG3	2.00	0.44
1:2A:330:G:H21	1:2A:353:A:N6	2.14	0.44
4:2E:134:ILE:HA	4:2E:137:HIS:CD2	2.53	0.44
4:2E:163:GLU:HG2	4:2E:164:ARG:N	2.33	0.44
5:2F:196:LEU:HA	5:2F:196:LEU:HD13	1.82	0.44
5:2F:31:HIS:HB2	11:2P:9:ASN:OD1	2.18	0.44
20:2Y:6:HIS:H	20:2Y:6:HIS:CD2	2.36	0.44
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.98	0.44
1:1A:1092:G:H1'	1:1A:1155:G:N2	2.33	0.44
1:1A:1682:C:OP2	59:1A:4387:HOH:O	2.21	0.44
1:1A:2480:A:H2'	1:1A:2481:G:O4'	2.18	0.44
9:1N:138:LEU:HA	9:1N:138:LEU:HD23	1.76	0.44
9:1N:96:GLU:H	9:1N:96:GLU:CD	2.21	0.44
1:1A:2330:G:H22	14:1S:3:ARG:NE	2.16	0.44
26:24:57:GLU:HA	26:24:58:ARG:HA	1.58	0.44
11:2P:65:ARG:HG3	30:28:25:MET:HG3	2.00	0.44
1:2A:179:A:H2'	1:2A:180:C:C6	2.52	0.44
1:2A:2091:G:H2'	1:2A:2092:A:C8	2.53	0.44
1:2A:2411:G:H4'	28:26:18:ARG:HG2	2.00	0.44
1:2A:1684:C:H5''	1:2A:2721:C:O2'	2.18	0.44
8:2I:132:PRO:HD2	8:2I:136:VAL:O	2.18	0.44
11:2P:21:ARG:HA	11:2P:21:ARG:HD3	1.74	0.44
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.99	0.44
14:2S:63:THR:HG23	14:2S:64:GLU:H	1.83	0.44
1:1A:1072:A:C2	1:1A:2499:A:H5'	2.52	0.43
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	2.00	0.43
9:1N:114:ARG:HD2	59:1N:3101:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:1Q:39:PRO:HA	12:1Q:97:VAL:O	2.18	0.43
28:26:13:CYS:SG	28:26:47:THR:HG21	2.58	0.43
1:2A:1214:G:H1	1:2A:1224:C:N4	2.07	0.43
1:2A:1333:U:C2	1:2A:1372:C:O2	2.71	0.43
1:2A:1844:G:O3'	3:2D:54:ARG:NH2	2.51	0.43
1:2A:2356:G:OP2	28:26:38:LYS:NZ	2.26	0.43
1:2A:2626:U:OP1	59:2A:3657:HOH:O	2.20	0.43
1:2A:671:G:H8	1:2A:671:G:O5'	2.01	0.43
2:2B:1:U:H2'	2:2B:2:C:H5	1.81	0.43
2:2B:28:C:H5''	14:2S:31:SER:OG	2.18	0.43
3:2D:71:ASP:HB3	3:2D:103:ARG:NH2	2.33	0.43
1:2A:2327:C:O2'	6:2G:128:ARG:NH2	2.51	0.43
12:2Q:4:PRO:HG3	12:2Q:69:PHE:HE2	1.83	0.43
16:2U:52:ARG:HD3	59:2U:3101:HOH:O	2.18	0.43
21:2Z:11:GLU:O	21:2Z:36:LYS:NZ	2.51	0.43
1:1A:767:C:H2'	1:1A:768:A:H8	1.84	0.43
3:1D:168:ARG:H	3:1D:168:ARG:CD	4.94	0.43
3:1D:175:LEU:HD12	3:1D:185:VAL:HG21	2.01	0.43
23:21:19:GLN:HB3	23:21:35:THR:HG23	1.99	0.43
28:26:23:THR:OG1	28:26:24:GLU:N	2.51	0.43
1:2A:1716:C:C5	1:2A:1717:U:C4	3.06	0.43
1:2A:171:C:H2'	1:2A:172:C:H6	2.68	0.43
1:2A:1960:U:OP1	1:2A:2615:U:O2'	2.36	0.43
1:2A:13:A:C6	1:2A:550:A:C2	3.06	0.43
1:2A:775:G:OP1	3:2D:12:SER:HB2	2.19	0.43
3:2D:164:GLN:HE21	3:2D:176:ARG:HH22	1.67	0.43
20:2Y:68:HIS:ND1	20:2Y:70:SER:HB3	2.33	0.43
30:18:61:LEU:O	30:18:63:PRO:HD3	2.17	0.43
1:1A:1054:A:OP2	9:1N:37:LYS:NZ	2.43	0.43
1:1A:552:A:C2	1:1A:2064:C:H4'	2.53	0.43
1:1A:767:C:H2'	1:1A:768:A:C8	2.53	0.43
1:1A:770:U:H2'	1:1A:771:G:O4'	2.18	0.43
1:1A:2829:A:P	13:1R:2:ARG:HH22	2.41	0.43
22:20:53:MET:HA	22:20:58:THR:O	2.18	0.43
31:29:3:VAL:HA	31:29:35:ARG:O	2.19	0.43
1:2A:2298:A:C5	1:2A:2300:G:C5	3.06	0.43
1:2A:839:A:OP2	1:2A:2092:A:O2'	2.33	0.43
3:2D:117:VAL:HG11	3:2D:128:GLY:HA3	2.00	0.43
6:2G:106:LEU:O	6:2G:110:ALA:HB3	2.18	0.43
6:2G:109:VAL:HG21	26:24:14:ILE:HG21	1.99	0.43
7:2H:12:PRO:O	7:2H:15:VAL:HG13	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:2Y:23:ARG:HG2	20:2Y:42:VAL:HG22	2.00	0.43
1:1A:1403:G:O2'	1:1A:1404:A:H5''	2.19	0.43
1:1A:1587:G:H5''	1:1A:1588:A:OP2	2.18	0.43
1:1A:2217:C:OP1	59:1A:4392:HOH:O	2.21	0.43
1:1A:1067:G:N7	9:1N:66:LYS:HE2	2.33	0.43
17:1V:95:LEU:HD13	17:1V:97:LYS:HD3	2.01	0.43
21:1Z:140:ASP:OD1	21:1Z:142:SER:OG	2.26	0.43
1:2A:160:C:H2'	1:2A:161:G:C8	2.82	0.43
1:2A:2107:U:H2'	1:2A:2108:G:C8	2.54	0.43
1:2A:2272:C:H1'	1:2A:2399:A:N3	2.33	0.43
1:2A:2668:A:O3'	7:2H:160:LYS:NZ	2.52	0.43
1:2A:54:A:H2'	1:2A:55:C:O4'	2.19	0.43
1:2A:1873:C:H5'	3:2D:253:GLN:NE2	2.33	0.43
4:2E:9:VAL:HB	15:2T:3:ARG:HG2	2.00	0.43
1:1A:746:G:O2'	1:1A:1678:A:N3	2.45	0.43
1:1A:1828:U:OP2	3:1D:274:ARG:NH2	2.52	0.43
1:1A:2342:G:O2'	22:10:43:THR:HG22	2.18	0.43
1:1A:554:G:N3	1:1A:554:G:O4'	2.51	0.43
1:1A:671:G:H2'	1:1A:672:G:O4'	2.19	0.43
1:1A:785:G:O6	59:1A:4379:HOH:O	2.20	0.43
3:1D:16:MET:CG	3:1D:211:ARG:HH21	2.32	0.43
5:1F:170:LEU:HD12	5:1F:170:LEU:HA	1.90	0.43
6:1G:11:TYR:HA	6:1G:15:VAL:HB	2.00	0.43
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.53	0.43
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	2.01	0.43
21:1Z:151:HIS:HA	21:1Z:170:THR:HA	1.99	0.43
23:21:23:LYS:HB2	23:21:23:LYS:HE3	1.86	0.43
26:24:46:GLN:OE1	26:24:48:ARG:NH2	2.52	0.43
1:2A:468:A:H1'	1:2A:1245:C:O4'	2.18	0.43
1:2A:346:G:HO2'	1:2A:1249:U:H3	1.62	0.43
1:2A:279:C:H2'	1:2A:280:G:H8	1.83	0.43
1:2A:973:G:O5'	1:2A:973:G:H8	2.00	0.43
15:2T:64:ARG:HB2	15:2T:73:GLU:HG2	1.99	0.43
21:2Z:30:ASN:HB2	59:2Z:5002:HOH:O	2.19	0.43
26:14:58:ARG:HB3	26:14:58:ARG:NH1	2.32	0.43
1:1A:1765:G:H2'	1:1A:1766:A:H2'	2.01	0.43
1:1A:1881:U:H2'	1:1A:1882:C:O4'	2.18	0.43
1:1A:66:G:H2'	1:1A:67:C:O4'	2.17	0.43
1:1A:936:A:H2'	1:1A:937:G:O4'	2.18	0.43
1:1A:894:G:N9	1:1A:977:A:H8	2.17	0.43
4:1E:51:PHE:CD2	4:1E:52:LEU:HG	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:183:VAL:O	5:1F:187:VAL:HG23	2.18	0.43
1:2A:1357:U:OP2	19:2X:63:LYS:NZ	2.34	0.43
1:2A:1755:U:H2'	1:2A:1756:C:C6	2.53	0.43
1:2A:579:U:H2'	1:2A:580:G:C8	2.53	0.43
1:2A:907:A:N3	2:2B:79:C:O2'	2.43	0.43
1:2A:955:A:C6	1:2A:956:A:C6	3.07	0.43
3:2D:146:GLU:OE1	3:2D:190:TYR:N	2.35	0.43
3:2D:75:ILE:HA	3:2D:76:PRO:HD3	1.81	0.43
6:2G:145:THR:N	6:2G:148:MET:SD	2.70	0.43
11:2P:95:VAL:HG13	11:2P:125:VAL:HA	2.01	0.43
16:2U:106:PHE:O	16:2U:110:VAL:HG23	2.19	0.43
23:11:67:ILE:N	23:11:68:PRO:HD2	2.34	0.43
1:1A:592:G:H2'	1:1A:2051:A:C5	2.54	0.43
3:1D:43:ARG:HA	3:1D:48:ARG:O	2.19	0.43
13:1R:21:TYR:OH	13:1R:43:GLU:HG2	2.19	0.43
14:1S:65:VAL:O	14:1S:69:VAL:HG12	2.19	0.43
16:1U:34:LYS:HE2	16:1U:34:LYS:HA	2.00	0.43
1:2A:1194:G:H2'	1:2A:1195:C:C6	2.53	0.43
1:2A:1373:G:H8	1:2A:1373:G:O5'	2.01	0.43
1:2A:149:C:H2'	1:2A:150:C:H6	1.84	0.43
1:2A:2027:C:O5'	1:2A:2027:C:H6	2.01	0.43
1:2A:2227:G:H3'	1:2A:2228:A:H5''	2.00	0.43
1:2A:2418:G:OP1	59:2A:3643:HOH:O	2.21	0.43
1:2A:2761:A:H4'	7:2H:62:LYS:HB3	1.99	0.43
1:2A:338:G:H2'	1:2A:339:C:C6	2.54	0.43
1:2A:352:G:OP1	1:2A:352:G:H8	2.01	0.43
1:2A:504:A:C2	1:2A:505:A:C5	3.07	0.43
1:2A:901:G:C6	1:2A:902:C:N4	2.87	0.43
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.47	0.43
1:2A:1659:A:C2	18:2W:93:ALA:HB2	2.54	0.43
1:1A:1349:C:H2'	1:1A:1350:C:H6	2.56	0.43
1:1A:2044:G:H4'	1:1A:2628:C:O3'	2.17	0.43
1:1A:959:C:OP1	59:1A:4391:HOH:O	2.21	0.43
3:1D:85:ASP:OD2	3:1D:88:ARG:NH1	2.51	0.43
7:1H:69:ARG:HG3	7:1H:70:THR:N	2.34	0.43
18:1W:23:LEU:HD12	18:1W:23:LEU:HA	1.83	0.43
1:2A:1048:G:O2'	1:2A:1055:A:N1	2.41	0.43
1:2A:1443:C:H2'	1:2A:1444:C:O4'	2.71	0.43
1:2A:1553:A:H4'	1:2A:1555:A:C5	2.53	0.43
1:2A:2480:A:H2'	1:2A:2481:G:O4'	2.19	0.43
1:2A:2575:A:C2	1:2A:2658:U:H4'	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:6:G:H2'	1:2A:7:A:C8	2.52	0.43
5:2F:29:ASN:HA	5:2F:30:PRO:HD2	1.86	0.43
6:2G:136:ARG:HA	6:2G:154:GLY:HA3	2.01	0.43
13:2R:92:GLY:HA2	13:2R:94:TYR:CZ	2.53	0.43
18:2W:18:ARG:HG3	18:2W:76:VAL:HB	2.01	0.43
1:1A:1271:A:H2'	1:1A:1272:G:H5'	4.66	0.43
1:1A:2346:A:C8	1:1A:2348:G:C5	3.07	0.43
1:1A:26:G:C2	1:1A:536:G:N3	2.86	0.43
1:2A:1118:A:H3'	1:2A:1119:G:C8	2.54	0.43
1:2A:1176:G:C8	1:2A:2046:C:H4'	2.54	0.43
1:2A:209:A:O4'	1:2A:221:A:H1'	2.18	0.43
11:2P:126:VAL:HG12	11:2P:148:LEU:CD2	2.47	0.43
19:2X:88:LYS:HG2	19:2X:93:GLU:HG3	2.00	0.43
1:1A:2575:A:C2	1:1A:2658:U:H4'	2.54	0.43
5:1F:149:ASP:N	5:1F:149:ASP:OD1	2.51	0.43
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.58	0.43
11:1P:88:LEU:HD11	11:1P:114:ILE:HD12	2.01	0.43
17:1V:49:THR:HG22	17:1V:49:THR:O	2.19	0.43
20:1Y:8:LYS:HD3	20:1Y:97:ARG:NH1	2.34	0.43
1:2A:1386:U:O4	19:2X:16:LYS:HE2	2.18	0.43
1:2A:1638:G:H2'	1:2A:1639:G:C8	2.54	0.43
1:2A:1765:G:H8	1:2A:1769:A:N6	2.17	0.43
1:2A:2239:G:C5	1:2A:2240:C:C4	3.07	0.43
1:2A:2406:C:O2'	23:21:30:VAL:HG22	2.18	0.43
1:2A:2700:U:OP2	1:2A:2731:G:N2	2.50	0.43
1:2A:2767:C:HO2'	1:2A:2768:U:H6	1.66	0.43
1:2A:2770:A:H2'	1:2A:2771:G:O4'	2.18	0.43
1:2A:2896:U:H2'	1:2A:2897:C:C6	2.54	0.43
1:2A:29:G:H2'	1:2A:30:C:C6	2.54	0.43
1:2A:37:A:H2'	1:2A:38:C:C6	2.54	0.43
1:2A:69:A:N7	19:2X:31:HIS:HE1	2.17	0.43
2:2B:26:A:O5'	2:2B:26:A:H8	2.02	0.43
2:2B:66:A:H61	2:2B:108:U:H2'	1.83	0.43
3:2D:43:ARG:HA	3:2D:48:ARG:O	2.19	0.43
9:2N:15:LEU:HB2	9:2N:135:PRO:HB2	2.01	0.43
12:2Q:108:GLY:HA3	21:2Z:116:VAL:HG13	2.01	0.43
1:1A:1739:U:O2'	3:1D:14:ARG:NH2	2.52	0.42
1:1A:1765:G:N7	59:1A:4519:HOH:O	2.36	0.42
1:1A:903:C:N4	1:1A:904:U:O4	2.52	0.42
5:1F:33:LEU:HA	5:1F:33:LEU:HD12	1.94	0.42
7:1H:124:GLU:OE1	7:1H:132:ARG:HD2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2282:G:OP1	22:20:18:ALA:HB1	2.19	0.42
1:2A:2325:C:H2'	1:2A:2326:G:C8	2.54	0.42
1:2A:2589:G:H2'	1:2A:2590:C:C6	2.54	0.42
1:2A:503:A:C6	1:2A:505:A:C6	3.07	0.42
1:2A:548:U:H2'	1:2A:549:U:C6	2.54	0.42
1:2A:875:A:N7	1:2A:2259:C:H5'	2.34	0.42
1:2A:862:C:O2'	1:2A:976:G:O6	2.35	0.42
1:2A:988:G:O3'	59:2A:3666:HOH:O	2.22	0.42
2:2B:19:G:H2'	2:2B:20:C:O4'	2.19	0.42
2:2B:64:C:H2'	2:2B:65:C:C6	2.54	0.42
8:2I:72:LEU:HD22	8:2I:101:LEU:HD11	2.00	0.42
1:2A:655:A:H1'	11:2P:66:GLY:HA2	2.01	0.42
1:2A:2330:G:N1	14:2S:3:ARG:HA	2.33	0.42
15:2T:73:GLU:OE1	15:2T:103:ARG:NE	2.44	0.42
17:2V:12:TYR:CG	17:2V:20:LEU:HD21	2.53	0.42
1:1A:1275:C:H2'	1:1A:1276:G:C8	2.53	0.42
1:1A:1424:A:H4'	1:1A:1425:G:OP2	2.19	0.42
1:1A:2802:A:H2'	1:1A:2802:A:N3	2.33	0.42
3:1D:35:LYS:HB2	3:1D:36:PRO:HD2	2.01	0.42
6:1G:9:ARG:O	6:1G:13:GLU:HG2	2.20	0.42
7:1H:154:PRO:HB3	7:1H:163:TYR:CE2	2.54	0.42
9:1N:33:LEU:HD12	9:1N:33:LEU:HA	1.90	0.42
12:1Q:111:GLU:O	12:1Q:115:MET:HG2	2.19	0.42
31:29:29:ASN:HD22	31:29:31:LYS:H	1.66	0.42
1:2A:2754:C:OP1	31:29:35:ARG:HD3	2.19	0.42
1:2A:1509:C:H2'	1:2A:1510:C:C6	2.54	0.42
1:2A:1823:C:OP1	59:2A:3664:HOH:O	2.21	0.42
1:2A:2059:G:H2'	1:2A:2060:C:O4'	2.18	0.42
1:2A:2101:G:H2'	1:2A:2102:C:C6	2.54	0.42
1:2A:2568:G:H2'	1:2A:2569:C:C6	2.54	0.42
1:2A:2757:C:C4	1:2A:2758:U:C4	3.07	0.42
1:2A:1833:A:H4'	3:2D:259:THR:HG23	2.00	0.42
1:1A:398:G:H8	23:11:65:SER:O	2.02	0.42
24:12:2:LYS:O	24:12:6:VAL:HG23	2.19	0.42
1:1A:141:G:H4'	19:1X:35:THR:HG21	2.01	0.42
1:1A:1822:G:H5'	3:1D:205:VAL:HG13	2.01	0.42
1:1A:2049:U:H2'	1:1A:2050:G:O4'	2.18	0.42
1:1A:216:A:H8	1:1A:217:A:H5'	1.83	0.42
6:1G:83:ARG:N	6:1G:86:MET:SD	2.72	0.42
15:1T:108:ARG:HG2	15:1T:111:ARG:NH1	2.33	0.42
11:2P:63:PRO:HD3	30:28:27:THR:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1561:U:H2'	1:2A:1562:G:H8	1.83	0.42
1:2A:1840:A:H2'	1:2A:1841:G:O4'	2.19	0.42
1:2A:1967:U:H2'	1:2A:1968:C:C6	2.54	0.42
5:2F:195:ASP:HB3	5:2F:198:ALA:H	1.84	0.42
5:2F:24:LEU:HD23	5:2F:115:ALA:HA	2.02	0.42
26:14:57:GLU:HA	26:14:58:ARG:HA	1.44	0.42
11:1P:64:LYS:HE3	30:18:12:LYS:HD3	2.00	0.42
1:1A:1217:G:H22	1:1A:1221:A:P	2.42	0.42
1:1A:1571:G:C6	1:1A:1572:G:C2	3.08	0.42
1:1A:1711:A:H2'	1:1A:1712:G:O4'	2.19	0.42
1:1A:2801:C:O2'	1:1A:2802:A:H4'	2.18	0.42
1:1A:603:C:H2'	1:1A:604:G:H8	1.85	0.42
6:1G:28:VAL:O	6:1G:31:VAL:HG13	2.20	0.42
6:1G:60:LEU:HD22	6:1G:60:LEU:HA	1.79	0.42
8:1I:12:LEU:HD23	8:1I:12:LEU:HA	1.90	0.42
30:28:61:LEU:O	30:28:63:PRO:HD3	2.18	0.42
1:2A:1101:G:H5''	1:2A:1102:A:H5'	2.00	0.42
1:2A:2419:U:H2'	1:2A:2420:G:H8	1.83	0.42
1:2A:2590:C:C4'	4:2E:134:ILE:HG12	2.49	0.42
1:2A:2792:G:OP2	9:2N:118:LYS:HD3	2.19	0.42
1:2A:644:G:N3	1:2A:644:G:H5'	2.35	0.42
1:2A:658:C:H2'	1:2A:659:C:C6	2.55	0.42
1:2A:624:G:N2	1:2A:701:A:OP2	2.42	0.42
1:2A:775:G:H5'	1:2A:776:C:H5''	2.02	0.42
1:2A:921:G:O2'	21:2Z:151:HIS:HE1	2.03	0.42
3:2D:94:LEU:HA	3:2D:94:LEU:HD23	1.92	0.42
13:2R:104:ARG:HD2	13:2R:109:ALA:HB3	2.00	0.42
10:2O:73:ASP:HB2	15:2T:82:LEU:HD13	2.01	0.42
16:2U:107:ALA:O	16:2U:111:GLU:HG2	2.19	0.42
1:1A:1626:A:H8	1:1A:1626:A:OP2	2.03	0.42
1:1A:173:U:H4'	1:1A:206:A:H4'	2.00	0.42
1:1A:1755:U:H2'	1:1A:1756:C:C6	2.55	0.42
1:1A:214:G:N2	1:1A:216:A:H62	2.18	0.42
1:1A:237:C:O2	1:1A:281:G:N2	64.39	0.42
3:1D:71:ASP:CB	3:1D:103:ARG:HH22	2.27	0.42
3:1D:26:LYS:HE2	3:1D:28:GLU:O	2.20	0.42
1:1A:2456:G:OP1	5:1F:74:ARG:NH2	2.52	0.42
6:1G:50:ALA:O	6:1G:52:ILE:N	2.46	0.42
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.19	0.42
21:1Z:91:LEU:HA	21:1Z:91:LEU:HD13	1.80	0.42
24:22:28:LYS:HD3	24:22:60:LEU:HD11	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:24:1:MET:HG2	26:24:6:HIS:CD2	2.55	0.42
1:2A:2824:C:H5'	27:25:29:THR:HG21	2.02	0.42
1:2A:1080:U:H2'	1:2A:1081:G:C8	2.55	0.42
1:2A:1096:G:C5	1:2A:1097:C:C4	3.08	0.42
1:2A:1104:G:H3'	1:2A:1105:U:C6	2.51	0.42
1:2A:142:C:H2'	1:2A:143:C:H6	1.84	0.42
1:2A:1988:C:H2'	1:2A:1989:G:O4'	2.20	0.42
1:2A:2088:G:O2'	1:2A:2090:G:H5''	2.19	0.42
1:2A:2118:C:H2'	1:2A:2119:U:C6	2.54	0.42
1:2A:2713:U:H4'	1:2A:2714:C:OP1	2.20	0.42
1:2A:457:U:H6	1:2A:457:U:O5'	2.02	0.42
1:2A:619:U:H2'	1:2A:620:G:C8	2.54	0.42
19:2X:26:TYR:CE2	19:2X:89:ILE:HG13	2.55	0.42
21:2Z:151:HIS:ND1	21:2Z:168:GLU:O	2.50	0.42
1:1A:1471:G:C6	1:1A:1472:A:C6	3.07	0.42
1:1A:8:U:N3	1:1A:2640:A:H2	2.10	0.42
1:1A:817:G:OP1	29:17:10:ARG:NH1	2.51	0.42
5:1F:89:VAL:HG12	5:1F:90:PHE:CD2	2.55	0.42
7:1H:40:GLU:OE1	7:1H:61:HIS:NE2	2.33	0.42
21:1Z:14:LYS:HA	21:1Z:15:PRO:HD3	1.96	0.42
25:23:11:SER:HA	25:23:31:LEU:HD21	2.01	0.42
27:25:20:ARG:HG2	27:25:23:HIS:ND1	2.34	0.42
1:2A:80:G:N2	1:2A:100:A:OP2	2.51	0.42
1:2A:1047:G:H2'	1:2A:1048:G:O4'	2.20	0.42
1:2A:1364:G:C6	1:2A:1365:C:N4	2.87	0.42
1:2A:2276:U:C4	1:2A:2277:A:C5	3.07	0.42
1:2A:2488:C:N4	31:29:10:ILE:HG23	2.35	0.42
1:2A:40:C:H2'	1:2A:41:G:H8	1.83	0.42
19:2X:31:HIS:HA	19:2X:32:PRO:HD3	1.88	0.42
1:1A:1083:C:OP1	59:1A:4389:HOH:O	2.21	0.42
1:1A:1404:A:H2'	1:1A:1405:A:H5'	2.02	0.42
1:1A:2591:U:C5	1:1A:2592:G:C6	3.08	0.42
1:1A:263:G:H2'	1:1A:264:U:O4'	2.20	0.42
1:1A:2020:C:H4'	1:1A:2735:C:O2	2.20	0.42
2:1B:90:A:N7	2:1B:91:C:H1'	2.35	0.42
6:1G:131:TYR:HB3	6:1G:159:VAL:CG1	2.49	0.42
7:1H:5:GLY:HA2	7:1H:69:ARG:HB3	2.01	0.42
10:1O:26:LYS:O	10:1O:30:ALA:HB2	2.20	0.42
14:1S:15:ARG:NE	14:1S:88:ASP:OD2	2.37	0.42
18:1W:14:PRO:HG2	18:1W:78:GLU:CG	2.50	0.42
31:29:15:LYS:HB3	31:29:26:ILE:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1346:A:H2	1:2A:1671:G:N3	2.17	0.42
1:2A:251:C:H2'	1:2A:252:C:O4'	2.19	0.42
1:2A:2815:G:H2'	1:2A:2816:G:H8	1.82	0.42
1:2A:321:G:H5''	1:2A:322:A:OP1	2.19	0.42
1:2A:367:G:N2	1:2A:368:A:H62	2.18	0.42
1:2A:531:A:H5''	1:2A:532:G:H3'	2.01	0.42
1:2A:901:G:H2'	1:2A:902:C:C6	2.55	0.42
1:2A:933:A:N3	1:2A:933:A:H2'	2.34	0.42
2:2B:17:C:H2'	2:2B:18:G:O4'	2.19	0.42
5:2F:129:PHE:O	5:2F:132:VAL:HG13	2.20	0.42
5:2F:46:ARG:HB3	5:2F:48:THR:HG23	2.02	0.42
6:2G:102:PHE:O	6:2G:106:LEU:HB2	2.20	0.42
6:2G:9:ARG:HD3	6:2G:13:GLU:OE1	2.19	0.42
11:2P:101:VAL:HA	11:2P:106:LEU:O	2.20	0.42
11:2P:125:VAL:HG13	11:2P:138:LEU:HD21	2.01	0.42
1:2A:1384:G:H5''	19:2X:16:LYS:HD2	2.02	0.42
23:11:95:LEU:O	23:11:98:LEU:HB2	2.18	0.42
1:1A:1065:A:N1	1:1A:1185:U:O2'	2.47	0.42
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	2.01	0.42
8:1I:26:ALA:O	8:1I:31:LEU:HB2	2.20	0.42
1:1A:1247:G:H5'	11:1P:3:LEU:HD23	2.01	0.42
12:1Q:87:LYS:HA	12:1Q:87:LYS:HD3	4.26	0.42
25:23:28:LEU:HA	25:23:28:LEU:HD23	1.91	0.42
29:27:3:ARG:HD3	29:27:3:ARG:HA	1.80	0.42
1:2A:1101:G:C5'	1:2A:1102:A:H5'	2.50	0.42
1:2A:1109:C:H42	1:2A:1119:G:H1	1.67	0.42
1:2A:1292:A:OP1	5:2F:95:ARG:NH2	2.51	0.42
1:2A:1332:A:C5	1:2A:1333:U:C4	3.08	0.42
1:2A:2401:U:O2'	1:2A:2402:G:H5'	2.19	0.42
1:2A:488:G:N1	1:2A:492:G:C6	2.87	0.42
4:2E:24:THR:HG22	4:2E:186:GLY:O	2.20	0.42
9:2N:123:TYR:OH	9:2N:130:HIS:NE2	2.48	0.42
18:2W:41:LYS:HE3	27:25:25:LEU:HD11	2.02	0.42
19:2X:8:ILE:O	24:22:36:ARG:NH2	2.52	0.42
1:1A:1313:A:C2	1:1A:2034:A:C4	3.08	0.42
1:1A:1349:C:H2'	1:1A:1350:C:C6	3.22	0.42
1:1A:334:A:C6	1:1A:351:U:C4	3.08	0.42
1:1A:1856:G:H4'	3:1D:242:ARG:CZ	2.49	0.42
6:1G:106:LEU:HD12	6:1G:110:ALA:HB3	2.02	0.42
20:1Y:81:LYS:HE2	20:1Y:81:LYS:HB3	1.74	0.42
26:24:26:SER:OG	26:24:27:THR:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1114:A:H4'	1:2A:1115:A:H5''	2.02	0.42
1:2A:1332:A:H5''	1:2A:1333:U:OP2	2.20	0.42
1:2A:1409:G:OP2	23:21:3:LYS:HG3	2.20	0.42
1:2A:2249:G:H2'	1:2A:2249:G:N3	2.35	0.42
1:2A:417:G:H1'	1:2A:437:G:O4'	2.20	0.42
1:2A:598:U:H2'	1:2A:599:G:C8	2.55	0.42
2:2B:95:C:H2'	2:2B:96:U:C6	2.55	0.42
3:2D:132:PRO:HG3	3:2D:190:TYR:CE1	2.55	0.42
3:2D:228:PRO:HD3	3:2D:235:GLY:HA3	2.02	0.42
3:2D:77:ALA:O	3:2D:116:GLN:HG3	2.19	0.42
4:2E:112:GLY:O	4:2E:159:HIS:HA	2.20	0.42
5:2F:24:LEU:HD21	5:2F:114:VAL:HG12	2.02	0.42
1:2A:493:G:H5''	5:2F:60:SER:HB2	2.01	0.42
6:2G:91:ARG:HE	6:2G:91:ARG:HB3	1.75	0.42
1:1A:1149:C:H2'	1:1A:1150:U:C5	2.54	0.42
1:1A:2046:C:H2'	1:1A:2047:C:C6	2.55	0.42
1:1A:2331:A:N3	1:1A:2331:A:H2'	2.35	0.42
1:1A:2640:A:O2'	1:1A:2641:G:OP2	2.29	0.42
1:1A:509:C:H2'	1:1A:510:C:C6	2.54	0.42
1:1A:989:A:C4	1:1A:2459:A:C2	3.08	0.42
3:1D:132:PRO:HG3	3:1D:190:TYR:CE1	2.54	0.42
10:1O:98:VAL:HG22	10:1O:118:ALA:HA	2.02	0.42
17:1V:19:LYS:HA	17:1V:94:LEU:O	2.19	0.42
19:1X:12:VAL:HG22	19:1X:29:TRP:CE2	2.55	0.42
31:29:17:ILE:HA	31:29:17:ILE:HD12	1.82	0.42
1:2A:1072:A:C2	1:2A:2499:A:H5'	2.55	0.42
1:2A:1181:G:O2'	1:2A:2060:C:H5'	2.19	0.42
1:2A:1374:U:H5''	1:2A:1375:C:H5	1.85	0.42
1:2A:224:C:H2'	1:2A:225:C:C6	2.55	0.42
1:2A:2371:A:C2	1:2A:2372:A:H1'	2.54	0.42
1:2A:769:G:H2'	1:2A:770:U:O4'	2.20	0.42
1:2A:1848:U:O4	3:2D:154:LYS:HD3	2.20	0.42
3:2D:275:LYS:HA	3:2D:275:LYS:HD3	1.63	0.42
4:2E:181:LEU:HA	4:2E:181:LEU:HD12	1.79	0.42
1:2A:469:C:H4'	5:2F:49:ALA:HB2	2.01	0.42
6:2G:37:VAL:O	6:2G:94:LEU:N	2.48	0.42
9:2N:111:PRO:HA	9:2N:114:ARG:NH1	2.35	0.42
30:18:33:ASN:HA	30:18:36:LYS:HD2	2.02	0.41
1:1A:1531:A:H2'	1:1A:1532:G:C8	2.55	0.41
1:1A:315:C:C2	1:1A:372:G:C2	3.08	0.41
1:1A:483:G:C8	29:17:37:LYS:HG2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:182:LEU:HD23	3:1D:182:LEU:HA	1.90	0.41
3:1D:78:LYS:HE2	3:1D:78:LYS:HB3	1.86	0.41
4:1E:51:PHE:H	4:1E:75:VAL:HG11	1.85	0.41
18:1W:9:TYR:HA	18:1W:100:THR:CG2	2.50	0.41
1:2A:2319:G:H5''	1:2A:2321:A:OP2	2.20	0.41
1:2A:2443:A:C6	1:2A:2444:A:C6	3.08	0.41
1:2A:2500:G:C6	1:2A:2501:G:C6	3.08	0.41
1:2A:775:G:C6	3:2D:208:LYS:HB2	2.54	0.41
1:2A:910:G:H4'	2:2B:102:A:H4'	2.03	0.41
22:10:29:GLN:O	22:10:67:VAL:HG23	2.21	0.41
24:12:32:LEU:HD12	24:12:57:ILE:HD12	2.02	0.41
1:1A:143:C:H5'	19:1X:2:LYS:HD3	2.02	0.41
1:1A:2347:A:H61	22:10:43:THR:HG22	1.83	0.41
1:1A:2778:G:N3	1:1A:2778:G:H2'	2.35	0.41
1:1A:840:G:C6	1:1A:841:C:C4	3.08	0.41
3:1D:38:LYS:HA	3:1D:38:LYS:HD2	1.87	0.41
4:1E:119:ARG:HD2	4:1E:120:TRP:CE2	2.54	0.41
1:1A:2583:A:C8	4:1E:144:ARG:HD2	2.55	0.41
7:1H:121:ILE:HA	7:1H:121:ILE:HD13	1.92	0.41
11:1P:123:LEU:HA	11:1P:123:LEU:HD23	1.90	0.41
13:1R:26:LYS:HE2	13:1R:70:LEU:O	2.20	0.41
1:2A:113:C:H2'	1:2A:114:G:O4'	2.21	0.41
1:2A:10:G:H2'	1:2A:11:U:H5''	2.01	0.41
1:2A:1308:U:C4	1:2A:1309:G:C6	3.08	0.41
1:2A:1556:A:H2'	1:2A:1557:G:C8	2.54	0.41
1:2A:2324:C:O2'	1:2A:2325:C:H5'	2.19	0.41
1:2A:2888:C:OP2	59:2A:3670:HOH:O	2.22	0.41
1:2A:485:A:C2	1:2A:495:A:C4	3.08	0.41
1:2A:853:U:OP2	11:2P:41:ARG:NH2	2.50	0.41
4:2E:77:ILE:HD13	4:2E:195:LEU:HD22	2.01	0.41
6:2G:18:GLU:CG	6:2G:175:LEU:HD21	2.50	0.41
10:2O:102:VAL:HB	10:2O:106:LEU:HD12	2.02	0.41
10:2O:64:ARG:O	10:2O:82:ASN:HA	2.20	0.41
11:2P:63:PRO:HG2	30:28:25:MET:HB2	2.02	0.41
23:11:3:LYS:HG2	23:11:4:VAL:HG23	2.02	0.41
24:12:29:LYS:HE2	24:12:57:ILE:HG21	2.01	0.41
26:14:6:HIS:HA	26:14:7:PRO:HD3	1.96	0.41
1:1A:1245:C:H2'	1:1A:1246:C:C6	2.69	0.41
1:1A:1763:G:C6	1:1A:1764:U:C4	3.08	0.41
1:1A:2659:C:H2'	1:1A:2660:U:H6	1.86	0.41
5:1F:132:VAL:HA	5:1F:138:GLU:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:112:LEU:HD13	11:1P:127:ALA:HB2	2.01	0.41
13:1R:38:VAL:HB	13:1R:39:PRO:HD3	2.01	0.41
23:21:73:LEU:HA	23:21:73:LEU:HD23	1.81	0.41
1:2A:1362:A:H2'	1:2A:1363:C:C6	2.56	0.41
1:2A:2657:C:H2'	1:2A:2658:U:O4'	2.21	0.41
1:2A:2658:U:H2'	1:2A:2659:C:C6	2.56	0.41
1:2A:29:G:H2'	1:2A:30:C:O4'	2.20	0.41
4:2E:18:ASP:HB3	15:2T:82:LEU:HD21	2.02	0.41
5:2F:176:LEU:HD23	5:2F:176:LEU:HA	1.95	0.41
6:2G:41:GLN:HB3	6:2G:43:LEU:HD13	2.01	0.41
11:2P:95:VAL:HG13	11:2P:125:VAL:HB	2.01	0.41
1:2A:909:A:P	12:2Q:22:LYS:HG3	2.60	0.41
18:2W:46:PHE:O	18:2W:50:VAL:HG23	2.21	0.41
20:2Y:14:LEU:HD11	20:2Y:22:GLY:HA2	2.03	0.41
8:1I:27:ARG:HD2	23:11:71:TYR:CZ	2.56	0.41
1:1A:1038:G:OP1	16:1U:50:ARG:NH2	2.50	0.41
1:1A:2283:U:H5''	1:1A:2284:A:OP1	2.20	0.41
1:1A:22:G:H2'	1:1A:23:G:C8	3.24	0.41
1:1A:555:C:H4'	1:1A:556:A:H5''	2.02	0.41
1:1A:830:A:C8	1:1A:838:G:C5	3.08	0.41
7:1H:7:LEU:HA	7:1H:8:PRO:HD3	1.88	0.41
18:1W:18:ARG:HG3	18:1W:76:VAL:HB	2.02	0.41
1:2A:2393:G:H21	30:28:42:ARG:NH2	2.19	0.41
1:2A:1000:G:H2'	1:2A:1001:A:H2'	2.02	0.41
1:2A:1013:U:H4'	25:23:14:GLY:O	2.20	0.41
1:2A:1266:C:C2	1:2A:1274:G:C2	3.07	0.41
1:2A:594:A:H5''	1:2A:595:G:OP2	2.20	0.41
1:2A:78:G:H1	1:2A:103:C:N4	2.17	0.41
1:2A:897:U:H5'	25:23:49:LYS:HD2	2.03	0.41
1:2A:948:C:H2'	1:2A:949:C:H6	1.85	0.41
6:2G:47:LYS:HE2	6:2G:47:LYS:HB2	1.68	0.41
10:2O:88:ASN:ND2	10:2O:92:GLU:HB2	2.35	0.41
12:2Q:27:VAL:HG12	12:2Q:29:PHE:H	1.85	0.41
12:2Q:17:LEU:HB3	12:2Q:39:PRO:HB2	2.02	0.41
13:2R:26:LYS:HE2	13:2R:70:LEU:O	2.20	0.41
16:2U:110:VAL:O	16:2U:113:ALA:HB3	2.20	0.41
21:2Z:53:ILE:HA	59:2Z:5006:HOH:O	2.20	0.41
30:18:62:LEU:HB3	30:18:65:GLU:HG2	2.01	0.41
1:1A:1457:A:H2'	1:1A:1458:G:C8	2.55	0.41
1:1A:1903:C:H2'	1:1A:1904:G:O4'	2.20	0.41
1:1A:504:A:N3	1:1A:506:G:H5''	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:764:A:C5	1:1A:765:C:H1'	2.56	0.41
1:1A:885:U:H2'	1:1A:886:C:H6	1.86	0.41
10:1O:18:LYS:HB2	10:1O:45:GLU:HB3	2.02	0.41
11:1P:18:ARG:NH2	11:1P:21:ARG:HD2	2.36	0.41
12:1Q:58:PHE:O	12:1Q:60:ARG:NH1	2.53	0.41
30:28:34:TRP:CG	30:28:35:GLN:N	2.88	0.41
1:2A:865:A:C4	1:2A:1233:A:C2	3.08	0.41
1:2A:1288:G:H2'	1:2A:1289:G:O4'	2.20	0.41
1:2A:2382:G:O2'	28:26:46:HIS:ND1	2.45	0.41
1:2A:2560:G:O6	59:2A:3663:HOH:O	2.21	0.41
1:2A:587:C:H2'	1:2A:588:U:O4'	2.20	0.41
2:2B:28:C:H2'	2:2B:29:A:H8	1.84	0.41
3:2D:204:ILE:H	3:2D:204:ILE:HG12	3.20	0.41
6:2G:153:ARG:HE	6:2G:153:ARG:HB2	1.72	0.41
9:2N:15:LEU:HD12	9:2N:137:LYS:HZ2	1.85	0.41
1:2A:1042:G:C5'	16:2U:92:ARG:HH21	2.34	0.41
1:1A:1465:U:HO2'	1:1A:1466:G:P	2.42	0.41
1:1A:2507:C:H4'	59:1A:5205:HOH:O	2.20	0.41
1:1A:475:G:OP2	59:1A:4390:HOH:O	2.21	0.41
1:1A:786:U:H2'	1:1A:787:G:C8	2.55	0.41
3:1D:16:MET:HG3	3:1D:211:ARG:HH21	1.85	0.41
3:1D:5:LYS:HE3	3:1D:5:LYS:HB3	1.85	0.41
7:1H:126:PRO:HB2	7:1H:127:GLU:H	1.65	0.41
1:1A:1710:A:C2	10:1O:1:MET:HE1	2.55	0.41
11:1P:76:LYS:HE2	11:1P:76:LYS:HB3	1.77	0.41
14:1S:67:ARG:HE	14:1S:67:ARG:HB2	1.72	0.41
21:1Z:92:SER:O	21:1Z:92:SER:OG	2.28	0.41
25:23:8:LEU:HD13	25:23:31:LEU:HD23	2.01	0.41
1:2A:1067:G:C5	1:2A:1184:C:C4	3.08	0.41
1:2A:1350:C:C2	1:2A:1669:G:C2	3.08	0.41
1:2A:1897:A:H2'	1:2A:1898:A:C8	2.55	0.41
1:2A:1958:A:C8	1:2A:1960:U:H2'	2.55	0.41
1:2A:2323:U:C5	1:2A:2324:C:H5	2.39	0.41
1:2A:2341:G:H2'	1:2A:2342:G:O4'	2.20	0.41
1:2A:2409:U:H2'	1:2A:2410:G:C8	2.55	0.41
1:2A:87:G:C6	1:2A:88:U:C4	3.09	0.41
2:2B:28:C:H2'	2:2B:29:A:C8	2.55	0.41
2:2B:8:U:H3	2:2B:113:G:H1	1.67	0.41
7:2H:127:GLU:C	7:2H:129:THR:H	2.22	0.41
8:2I:129:THR:HG23	8:2I:139:GLN:HE22	1.85	0.41
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:53:GLU:HB2	26:14:54:GLY:CA	2.48	0.41
26:14:56:VAL:HA	26:14:60:GLN:CD	2.41	0.41
30:18:42:ARG:NH1	59:18:203:HOH:O	2.42	0.41
1:1A:1067:G:C5	1:1A:1184:C:C4	3.08	0.41
1:1A:1312:U:OP2	1:1A:2033:G:N1	2.40	0.41
1:1A:1939:A:O2'	1:1A:1941:C:N4	2.54	0.41
1:1A:2114:G:C6	1:1A:2236:A:C8	3.09	0.41
1:1A:2118:C:H2'	1:1A:2119:U:C6	2.55	0.41
1:1A:2657:C:H2'	1:1A:2658:U:O4'	2.21	0.41
1:1A:553:A:H62	1:1A:2062:U:H3	1.68	0.41
1:1A:591:U:C4	1:1A:592:G:C6	3.09	0.41
6:1G:103:LEU:HA	6:1G:103:LEU:HD23	1.81	0.41
11:1P:81:GLN:NE2	11:1P:105:LEU:O	2.54	0.41
13:1R:53:HIS:O	13:1R:56:LYS:HB2	2.20	0.41
14:1S:10:ARG:HH21	14:1S:91:PRO:HB2	1.84	0.41
15:1T:80:SER:HA	15:1T:81:PRO:HD3	1.90	0.41
28:26:25:LYS:HE3	28:26:27:LYS:HA	2.02	0.41
1:2A:1073:A:H2'	1:2A:1074:A:C8	2.55	0.41
1:2A:2600:A:OP1	59:2A:3668:HOH:O	2.22	0.41
1:2A:2643:A:C2	1:2A:2799:C:C2	3.09	0.41
1:2A:2648:U:H5''	4:2E:82:ARG:NH1	2.36	0.41
1:2A:488:G:N2	1:2A:491:A:OP2	2.46	0.41
1:2A:703:U:H2'	1:2A:704:C:H6	1.82	0.41
1:2A:917:U:H2'	1:2A:918:A:C8	2.55	0.41
3:2D:175:LEU:HD12	3:2D:185:VAL:HG21	2.03	0.41
1:2A:612:A:OP1	5:2F:95:ARG:NH1	2.54	0.41
18:2W:9:TYR:H	18:2W:102:HIS:CE1	2.38	0.41
18:2W:45:TYR:CZ	18:2W:49:LYS:HE3	2.55	0.41
1:1A:1007:U:H2'	1:1A:1008:C:C6	2.56	0.41
1:1A:1153:U:O2'	1:1A:1154:C:H6	2.04	0.41
1:1A:1225:C:H2'	1:1A:1226:A:O4'	2.21	0.41
1:1A:2890:C:H2'	1:1A:2891:A:O4'	2.21	0.41
1:1A:732:G:N2	1:1A:834:A:H61	2.18	0.41
1:1A:841:C:H2'	1:1A:842:C:C6	2.56	0.41
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	2.02	0.41
4:1E:31:CYS:HA	4:1E:32:PRO:HD2	1.87	0.41
6:1G:109:VAL:HG13	26:14:33:VAL:HG11	2.03	0.41
28:26:11:LEU:HB2	28:26:21:TYR:HB2	2.02	0.41
28:26:8:LYS:HD3	30:28:34:TRP:CG	2.56	0.41
1:2A:1404:A:C6	1:2A:1417:U:O4	2.74	0.41
1:2A:1387:A:C4	1:2A:1442:U:O4'	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2539:U:O2'	1:2A:2540:G:H3'	2.21	0.41
1:2A:29:G:C5	1:2A:30:C:C4	3.09	0.41
1:2A:5:A:H2	1:2A:6:G:N7	2.19	0.41
2:2B:24:G:H4'	2:2B:25:A:C8	2.55	0.41
2:2B:32:C:H42	2:2B:50:G:H1	1.67	0.41
3:2D:107:ALA:HA	3:2D:108:PRO:HD3	1.80	0.41
3:2D:68:LYS:O	3:2D:69:ARG:HB2	2.21	0.41
4:2E:14:ILE:HG13	4:2E:21:VAL:HG13	2.03	0.41
15:2T:65:LYS:CE	15:2T:67:SER:HB2	2.50	0.41
17:2V:72:VAL:HG13	17:2V:85:LYS:HB3	2.02	0.41
28:16:2:ALA:N	59:16:203:HOH:O	2.54	0.41
1:1A:1086:C:H2'	1:1A:1087:G:O4'	2.61	0.41
1:1A:2012:U:H2'	1:1A:2013:G:H5''	2.02	0.41
6:1G:28:VAL:HG23	6:1G:29:TRP:CD1	2.56	0.41
2:1B:31:C:H4'	6:1G:29:TRP:CH2	2.55	0.41
1:2A:1044:U:O2'	1:2A:1045:A:H5'	2.21	0.41
1:2A:2076:C:OP1	1:2A:2077:G:H4'	2.21	0.41
1:2A:209:A:N1	1:2A:253:A:O2'	2.49	0.41
1:2A:2479:G:O2'	1:2A:2492:G:N2	2.53	0.41
1:2A:2644:G:H5''	1:2A:2821:G:H5'	2.03	0.41
1:2A:468:A:H5''	1:2A:469:C:OP1	2.21	0.41
1:2A:530:G:O3'	1:2A:531:A:H8	2.03	0.41
1:2A:842:C:H2'	1:2A:843:C:H6	1.85	0.41
1:2A:910:G:C6	1:2A:911:C:N4	2.89	0.41
1:2A:955:A:N3	1:2A:2275:C:O2'	2.40	0.41
4:2E:143:ASN:HD22	4:2E:147:PRO:HD3	1.85	0.41
13:2R:107:ASP:OD2	13:2R:109:ALA:HB2	2.21	0.41
14:2S:65:VAL:O	14:2S:68:GLN:HB2	2.21	0.41
1:2A:359:C:HO2'	20:2Y:35:TYR:HH	1.65	0.41
1:1A:1067:G:C5	1:1A:1068:U:C4	6.59	0.41
1:1A:1451:U:H2'	1:1A:1452:C:H6	1.86	0.41
1:1A:1670:C:H2'	1:1A:1671:G:O4'	2.21	0.41
1:1A:209:A:N1	1:1A:253:A:O2'	2.46	0.41
1:1A:2342:G:O2'	1:1A:2347:A:N1	2.45	0.41
1:1A:2720:G:H2'	1:1A:2721:C:C6	2.56	0.41
1:1A:322:A:N1	1:1A:345:A:O2'	2.44	0.41
1:1A:382:A:H2'	1:1A:383:G:O4'	2.20	0.41
1:1A:454:A:H8	1:1A:454:A:OP2	2.03	0.41
1:1A:638:G:C5	1:1A:639:A:C8	12.77	0.41
1:1A:830:A:C6	3:1D:229:VAL:HG11	2.56	0.41
15:1T:16:ARG:HD2	15:1T:18:ASP:OD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:1U:16:LYS:HB3	16:1U:16:LYS:HE2	1.86	0.41
1:2A:1313:A:C2	1:2A:2034:A:C4	3.09	0.41
1:2A:2082:G:H5''	1:2A:2514:A:C2	2.56	0.41
1:2A:2626:U:C2	27:25:7:PRO:HA	2.55	0.41
1:2A:418:C:H5''	1:2A:435:C:H5''	2.02	0.41
1:2A:653:G:H1'	1:2A:663:U:O2'	2.21	0.41
1:2A:709:G:C6	1:2A:710:C:C4	3.09	0.41
1:2A:748:G:C2	1:2A:777:C:C2	3.09	0.41
1:2A:788:G:H4'	1:2A:1722:A:H5'	2.03	0.41
1:2A:922:C:H2'	1:2A:923:U:O4'	2.21	0.41
1:2A:924:A:H2'	1:2A:925:G:C8	5.44	0.41
6:2G:120:LEU:HB3	6:2G:131:TYR:OH	2.21	0.41
21:2Z:55:HIS:CE1	21:2Z:135:GLU:HB2	2.56	0.41
1:1A:126:C:H2'	1:1A:127:C:C6	2.83	0.41
1:1A:2367:C:H2'	1:1A:2368:U:O4'	2.21	0.41
1:1A:311:C:H2'	1:1A:312:A:H8	1.86	0.41
1:1A:515:G:H2'	1:1A:516:A:H8	1.85	0.41
1:1A:825:U:H6	1:1A:825:U:OP2	3.60	0.41
1:1A:819:U:O2'	3:1D:48:ARG:HD3	2.20	0.41
10:1O:23:ARG:HG3	10:1O:24:VAL:N	2.36	0.41
12:1Q:52:VAL:HG22	21:1Z:183:LEU:HD21	2.03	0.41
12:1Q:60:ARG:HD3	12:1Q:60:ARG:HA	1.70	0.41
23:21:3:LYS:HB2	23:21:61:ARG:NH1	2.34	0.41
24:22:1:MET:N	24:22:52:ASP:OD2	2.52	0.41
1:2A:140:C:H2'	1:2A:141:G:O4'	2.21	0.41
1:2A:2540:G:O6	31:29:31:LYS:NZ	2.54	0.41
1:2A:504:A:N3	1:2A:506:G:H5''	2.36	0.41
1:2A:825:U:H6	1:2A:825:U:OP1	4.90	0.41
2:2B:18:G:H2'	2:2B:19:G:C8	2.56	0.41
1:2A:2829:A:C5	13:2R:4:LEU:HD11	2.56	0.41
21:2Z:48:PHE:O	21:2Z:52:SER:N	2.46	0.41
1:1A:1047:G:H2'	1:1A:1048:G:O4'	2.21	0.40
1:1A:1222:C:O5'	1:1A:1222:C:H6	2.03	0.40
1:1A:1416:G:H2'	1:1A:1417:U:H5	1.85	0.40
1:1A:1889:A:N6	1:1A:1904:G:O2'	2.54	0.40
1:1A:1953:A:H2'	1:1A:1954:G:O4'	2.21	0.40
1:1A:44:C:OP2	1:1A:203:G:H2'	2.20	0.40
1:1A:637:U:H5''	59:1A:5896:HOH:O	2.21	0.40
1:1A:671:G:H8	1:1A:671:G:O5'	2.03	0.40
3:1D:101:GLU:HG3	3:1D:102:LYS:N	2.36	0.40
5:1F:110:LEU:HD23	5:1F:110:LEU:HA	1.94	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:1I:106:GLY:HA2	8:1I:107:VAL:O	2.22	0.40
23:21:21:ARG:HD2	23:21:35:THR:HG21	2.02	0.40
23:21:94:LEU:HA	23:21:94:LEU:HD23	1.84	0.40
25:23:7:LYS:HE2	25:23:34:GLU:OE2	2.22	0.40
1:2A:1094:C:H42	1:2A:2763:G:H1	1.68	0.40
1:2A:2347:A:H61	22:20:43:THR:CG2	2.34	0.40
1:2A:2537:G:O2'	31:29:1:MET:N	2.34	0.40
1:2A:2704:A:H2'	1:2A:2705:G:C8	2.57	0.40
1:2A:830:A:H5'	1:2A:831:G:OP1	2.21	0.40
1:2A:841:C:H2'	1:2A:842:C:C6	2.56	0.40
1:2A:870:A:H2'	1:2A:871:C:O4'	2.21	0.40
8:2I:62:LYS:HG2	8:2I:133:HIS:CE1	2.56	0.40
1:2A:2719:G:H1'	13:2R:71:GLN:HE22	1.86	0.40
18:2W:72:LYS:N	18:2W:106:ILE:O	2.50	0.40
20:2Y:76:CYS:SG	20:2Y:78:ALA:HB3	2.61	0.40
25:13:23:LEU:HD13	25:13:50:VAL:HG11	2.03	0.40
26:14:15:ILE:HB	26:14:32:TYR:CD2	2.56	0.40
1:1A:264:U:H2'	1:1A:265:C:C6	2.57	0.40
1:1A:2858:U:H4'	1:1A:2877:A:C2	2.56	0.40
1:1A:942:C:O5'	1:1A:942:C:H6	2.03	0.40
3:1D:145:VAL:HB	3:1D:155:LEU:HB2	2.03	0.40
3:1D:257:LEU:HD23	3:1D:257:LEU:HA	1.94	0.40
3:1D:264:LYS:HA	3:1D:265:PRO:HD3	1.94	0.40
1:1A:611:C:P	11:1P:16:ARG:HH12	2.44	0.40
2:1B:50:G:H5''	14:1S:61:ASN:HD22	1.86	0.40
26:24:13:ARG:NH1	26:24:15:ILE:HD11	2.36	0.40
30:28:23:VAL:HG11	30:28:47:LYS:HD3	2.04	0.40
31:29:35:ARG:HH11	31:29:35:ARG:HD3	1.78	0.40
1:2A:1116:G:C8	1:2A:1134:G:C6	3.09	0.40
1:2A:1184:C:OP1	9:2N:23:LEU:HB3	2.22	0.40
1:2A:1425:G:H2'	1:2A:1426:G:C5'	3.37	0.40
1:2A:1539:A:H2'	1:2A:1540:A:C8	2.56	0.40
1:2A:1814:A:N1	59:2A:3745:HOH:O	2.37	0.40
1:2A:224:C:H2'	1:2A:225:C:H6	1.86	0.40
1:2A:2881:G:C2	1:2A:2882:A:N6	2.89	0.40
1:2A:845:G:OP2	1:2A:845:G:H8	3.56	0.40
2:2B:6:C:H2'	2:2B:7:G:H5''	2.04	0.40
4:2E:105:THR:HG21	4:2E:164:ARG:NH1	2.36	0.40
4:2E:31:CYS:HA	4:2E:32:PRO:HD2	1.88	0.40
5:2F:154:VAL:HG22	5:2F:191:ARG:HB2	2.02	0.40
6:2G:19:LEU:HA	6:2G:22:ARG:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2P:5:ASP:HA	11:2P:7:ARG:HH22	1.87	0.40
24:12:16:LEU:O	24:12:67:LYS:NZ	2.54	0.40
1:1A:1066:A:H8	1:1A:1066:A:H3'	1.86	0.40
1:1A:1878:A:H2'	1:1A:1879:G:H8	1.85	0.40
1:1A:226:C:H2'	1:1A:227:U:O4'	2.21	0.40
1:1A:501:G:H4'	1:1A:526:A:N1	2.37	0.40
1:1A:560:A:H2'	1:1A:561:C:C6	2.57	0.40
1:1A:682:G:H1	1:1A:695:C:N4	2.16	0.40
8:1I:72:LEU:C	8:1I:74:ASN:N	2.74	0.40
9:1N:129:PRO:HA	9:1N:131:GLN:HE22	1.87	0.40
12:1Q:58:PHE:O	12:1Q:60:ARG:N	2.52	0.40
20:1Y:56:PRO:C	20:1Y:58:GLY:H	2.24	0.40
31:29:22:ARG:NH1	31:29:35:ARG:HD2	2.36	0.40
1:2A:795:C:O2	1:2A:1663:A:H2'	2.22	0.40
1:2A:2704:A:H2'	1:2A:2705:G:H8	1.86	0.40
1:2A:356:G:N3	1:2A:356:G:H2'	2.36	0.40
1:2A:382:A:H2'	1:2A:383:G:O4'	2.21	0.40
1:2A:702:G:H2'	1:2A:703:U:O4'	2.22	0.40
1:2A:817:G:OP1	29:27:10:ARG:NH1	2.50	0.40
1:2A:919:G:N2	1:2A:950:U:C2	2.89	0.40
1:2A:955:A:H2	1:2A:2275:C:O2	2.05	0.40
1:2A:967:U:H2'	1:2A:968:C:C6	2.56	0.40
3:2D:133:LEU:HD23	3:2D:133:LEU:HA	1.85	0.40
3:2D:182:LEU:HB2	3:2D:272:ALA:HB3	2.02	0.40
4:2E:11:MET:HE2	4:2E:24:THR:HB	2.04	0.40
7:2H:4:ILE:HG22	7:2H:69:ARG:HG2	2.04	0.40
12:2Q:29:PHE:HB2	12:2Q:105:GLU:OE2	2.21	0.40
14:2S:74:ALA:O	14:2S:78:LEU:HG	2.21	0.40
20:2Y:2:ARG:NH2	20:2Y:4:LYS:HD3	2.35	0.40
25:13:18:ASP:OD1	25:13:18:ASP:N	2.50	0.40
29:17:35:ARG:NH1	59:17:202:HOH:O	2.54	0.40
1:1A:2473:U:H1'	1:1A:2502:U:O4	2.22	0.40
1:1A:2723:U:OP1	1:1A:2726:G:H4'	2.22	0.40
1:1A:2898:C:H2'	1:1A:2899:G:O4'	2.21	0.40
1:1A:714:G:C5	1:1A:715:G:H1'	8.75	0.40
16:1U:102:GLU:HB3	16:1U:104:GLN:HE22	1.87	0.40
16:1U:108:GLU:O	16:1U:112:ARG:HG2	2.22	0.40
18:1W:71:VAL:HA	18:1W:107:LEU:HD12	2.03	0.40
1:2A:1176:G:C2	1:2A:1177:A:C4	3.10	0.40
1:2A:1366:A:H2'	1:2A:1367:A:O4'	2.21	0.40
1:2A:1869:G:C8	1:2A:1948:A:H1'	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2483:G:H2'	1:2A:2486:C:H42	1.86	0.40
1:2A:2859:A:H2'	1:2A:2860:A:O4'	2.21	0.40
1:2A:580:G:OP1	9:2N:111:PRO:HD2	2.22	0.40
1:2A:770:U:H2'	1:2A:771:G:O4'	2.21	0.40
1:2A:902:C:H2'	1:2A:903:C:C6	2.57	0.40
1:2A:92:G:H2'	1:2A:93:G:O4'	2.21	0.40
1:2A:2238:A:OP1	3:2D:263:ARG:HD2	2.22	0.40
8:2I:44:LEU:HD12	8:2I:44:LEU:HA	1.83	0.40
1:2A:62:A:O3'	19:2X:71:GLY:HA3	2.20	0.40
21:2Z:61:LEU:HA	21:2Z:62:PRO:HD3	1.93	0.40
31:19:29:ASN:HA	31:19:30:PRO:HD3	1.94	0.40
1:1A:1466:G:C2	1:1A:1467:G:C8	3.10	0.40
1:1A:554:G:C5	1:1A:2043:U:H5''	2.57	0.40
1:1A:461:C:H2'	1:1A:462:C:H5'	2.04	0.40
1:2A:1889:A:C2	1:2A:1905:A:H1'	2.57	0.40
1:2A:644:G:H8	1:2A:646:G:O6	2.04	0.40
2:2B:52:A:H8	2:2B:52:A:OP2	2.04	0.40
4:2E:36:ARG:NH2	4:2E:88:GLY:O	2.53	0.40
6:2G:56:ALA:HA	6:2G:153:ARG:NH2	2.36	0.40
6:2G:3:LEU:HD12	6:2G:4:ASP:O	2.22	0.40
1:2A:2760:A:C2	7:2H:63:SER:HB3	2.56	0.40
14:2S:26:LEU:HD22	14:2S:87:PHE:CE1	2.56	0.40
20:2Y:7:VAL:HG21	20:2Y:72:VAL:HG12	2.03	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	
3	1D	273/276 (99%)	260 (95%)	13 (5%)	0	100	100
3	2D	273/276 (99%)	252 (92%)	19 (7%)	2 (1%)	26	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	1E	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	34	63
4	2E	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	34	63
5	1F	201/210 (96%)	192 (96%)	7 (4%)	2 (1%)	19	45
5	2F	201/210 (96%)	190 (94%)	10 (5%)	1 (0%)	34	63
6	1G	179/182 (98%)	164 (92%)	10 (6%)	5 (3%)	6	15
6	2G	179/182 (98%)	157 (88%)	18 (10%)	4 (2%)	8	22
7	1H	172/180 (96%)	159 (92%)	12 (7%)	1 (1%)	30	59
7	2H	172/180 (96%)	158 (92%)	12 (7%)	2 (1%)	16	39
8	1I	144/148 (97%)	124 (86%)	17 (12%)	3 (2%)	9	23
8	2I	144/148 (97%)	122 (85%)	20 (14%)	2 (1%)	14	35
9	1N	138/140 (99%)	138 (100%)	0	0	100	100
9	2N	138/140 (99%)	135 (98%)	2 (1%)	1 (1%)	26	55
10	1O	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
10	2O	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
11	1P	147/150 (98%)	137 (93%)	8 (5%)	2 (1%)	14	35
11	2P	147/150 (98%)	136 (92%)	9 (6%)	2 (1%)	14	35
12	1Q	139/141 (99%)	132 (95%)	6 (4%)	1 (1%)	26	55
12	2Q	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
13	1R	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
13	2R	116/118 (98%)	110 (95%)	6 (5%)	0	100	100
14	1S	108/112 (96%)	102 (94%)	5 (5%)	1 (1%)	21	49
14	2S	108/112 (96%)	99 (92%)	7 (6%)	2 (2%)	10	25
15	1T	129/146 (88%)	120 (93%)	8 (6%)	1 (1%)	24	51
15	2T	129/146 (88%)	123 (95%)	6 (5%)	0	100	100
16	1U	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
16	2U	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
17	1V	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	19	45
17	2V	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	19	45
18	1W	110/113 (97%)	110 (100%)	0	0	100	100
18	2W	110/113 (97%)	110 (100%)	0	0	100	100
19	1X	93/96 (97%)	89 (96%)	3 (3%)	1 (1%)	17	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	2X	93/96 (97%)	88 (95%)	3 (3%)	2 (2%)	8	22
20	1Y	105/110 (96%)	97 (92%)	6 (6%)	2 (2%)	10	25
20	2Y	105/110 (96%)	98 (93%)	6 (6%)	1 (1%)	19	45
21	1Z	184/206 (89%)	170 (92%)	14 (8%)	0	100	100
21	2Z	184/206 (89%)	168 (91%)	13 (7%)	3 (2%)	12	30
22	10	73/85 (86%)	70 (96%)	2 (3%)	1 (1%)	14	35
22	20	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
23	11	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	17	42
23	21	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	17	42
24	12	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
24	22	68/72 (94%)	65 (96%)	3 (4%)	0	100	100
25	13	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
25	23	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
26	14	67/71 (94%)	50 (75%)	10 (15%)	7 (10%)	1	0
26	24	67/71 (94%)	49 (73%)	12 (18%)	6 (9%)	1	1
27	15	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
27	25	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
28	16	51/54 (94%)	51 (100%)	0	0	100	100
28	26	51/54 (94%)	51 (100%)	0	0	100	100
29	17	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
29	27	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
30	18	62/65 (95%)	62 (100%)	0	0	100	100
30	28	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
31	19	35/37 (95%)	35 (100%)	0	0	100	100
31	29	35/37 (95%)	35 (100%)	0	0	100	100
33	1b	229/256 (90%)	187 (82%)	33 (14%)	9 (4%)	4	8
33	2b	229/256 (90%)	191 (83%)	25 (11%)	13 (6%)	2	3
34	1c	204/239 (85%)	176 (86%)	27 (13%)	1 (0%)	34	63
34	2c	204/239 (85%)	176 (86%)	28 (14%)	0	100	100
35	1d	206/209 (99%)	185 (90%)	19 (9%)	2 (1%)	19	45
35	2d	206/209 (99%)	186 (90%)	18 (9%)	2 (1%)	19	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	1e	146/162 (90%)	129 (88%)	15 (10%)	2 (1%)	14	35
36	2e	146/162 (90%)	133 (91%)	11 (8%)	2 (1%)	14	35
37	1f	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
37	2f	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
38	1g	153/156 (98%)	138 (90%)	13 (8%)	2 (1%)	15	37
38	2g	153/156 (98%)	138 (90%)	13 (8%)	2 (1%)	15	37
39	1h	135/138 (98%)	129 (96%)	6 (4%)	0	100	100
39	2h	135/138 (98%)	130 (96%)	4 (3%)	1 (1%)	26	55
40	1i	125/128 (98%)	109 (87%)	16 (13%)	0	100	100
40	2i	125/128 (98%)	107 (86%)	16 (13%)	2 (2%)	12	30
41	1j	95/105 (90%)	81 (85%)	10 (10%)	4 (4%)	3	7
41	2j	94/105 (90%)	83 (88%)	10 (11%)	1 (1%)	17	42
42	1k	112/129 (87%)	102 (91%)	9 (8%)	1 (1%)	21	49
42	2k	112/129 (87%)	102 (91%)	9 (8%)	1 (1%)	21	49
43	1l	120/132 (91%)	114 (95%)	5 (4%)	1 (1%)	24	51
43	2l	120/132 (91%)	115 (96%)	5 (4%)	0	100	100
44	1m	116/126 (92%)	104 (90%)	11 (10%)	1 (1%)	21	49
44	2m	114/126 (90%)	100 (88%)	12 (10%)	2 (2%)	11	27
45	1n	58/61 (95%)	51 (88%)	6 (10%)	1 (2%)	11	29
45	2n	58/61 (95%)	51 (88%)	7 (12%)	0	100	100
46	1o	86/89 (97%)	79 (92%)	6 (7%)	1 (1%)	16	39
46	2o	86/89 (97%)	77 (90%)	7 (8%)	2 (2%)	8	20
47	1p	80/88 (91%)	73 (91%)	7 (9%)	0	100	100
47	2p	80/88 (91%)	73 (91%)	7 (9%)	0	100	100
48	1q	97/105 (92%)	87 (90%)	9 (9%)	1 (1%)	19	45
48	2q	97/105 (92%)	87 (90%)	10 (10%)	0	100	100
49	1r	66/88 (75%)	61 (92%)	5 (8%)	0	100	100
49	2r	66/88 (75%)	61 (92%)	5 (8%)	0	100	100
50	1s	82/93 (88%)	69 (84%)	13 (16%)	0	100	100
50	2s	81/93 (87%)	66 (82%)	13 (16%)	2 (2%)	7	18
51	1t	94/106 (89%)	82 (87%)	9 (10%)	3 (3%)	5	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	2t	94/106 (89%)	81 (86%)	10 (11%)	3 (3%)	5	12
52	1u	21/27 (78%)	18 (86%)	2 (10%)	1 (5%)	3	5
52	2u	21/27 (78%)	18 (86%)	2 (10%)	1 (5%)	3	5
55	1z	14/20 (70%)	9 (64%)	3 (21%)	2 (14%)	0	0
55	2z	14/20 (70%)	7 (50%)	4 (29%)	3 (21%)	0	0
All	All	11438/12168 (94%)	10532 (92%)	776 (7%)	130 (1%)	17	42

All (130) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
6	1G	126	ASP
7	1H	126	PRO
26	14	49	PHE
26	14	53	GLU
26	14	68	ARG
33	1b	17	PHE
33	1b	125	PRO
36	1e	98	THR
38	1g	4	ARG
41	1j	55	LYS
41	1j	56	HIS
42	1k	49	GLY
44	1m	4	ILE
45	1n	3	ARG
46	1o	19	PRO
48	1q	68	ARG
5	2F	130	ALA
6	2G	14	GLU
6	2G	47	LYS
7	2H	126	PRO
8	2I	10	GLU
21	2Z	127	LYS
21	2Z	128	VAL
21	2Z	135	GLU
26	24	45	GLY
26	24	49	PHE
26	24	62	ARG
33	2b	17	PHE
33	2b	97	TRP

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Mol	Chain	Res	Type
33	2b	125	PRO
33	2b	165	VAL
33	2b	230	VAL
35	2d	20	TYR
36	2e	37	ARG
40	2i	54	ASP
42	2k	49	GLY
46	2o	19	PRO
50	2s	30	LEU
5	1F	7	TYR
8	1I	106	GLY
12	1Q	58	PHE
17	1V	79	VAL
19	1X	94	GLY
22	10	13	GLY
26	14	45	GLY
26	14	50	VAL
33	1b	16	HIS
34	1c	107	GLN
35	1d	9	CYS
43	1l	29	GLY
51	1t	47	GLY
52	1u	6	ARG
7	2H	55	PRO
17	2V	79	VAL
19	2X	94	GLY
20	2Y	54	LYS
26	24	63	TYR
33	2b	93	VAL
33	2b	96	ARG
33	2b	121	LEU
36	2e	98	THR
41	2j	77	PRO
44	2m	106	ASN
51	2t	99	LEU
52	2u	6	ARG
55	2z	13	PRO
6	1G	47	LYS
6	1G	50	ALA
6	1G	51	ARG
8	1I	73	GLU
20	1Y	53	PRO

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Mol	Chain	Res	Type
23	1l	3	LYS
33	1b	20	GLU
38	1g	54	THR
55	1z	13	PRO
55	1z	15	PRO
6	2G	50	ALA
6	2G	126	ASP
8	2I	40	THR
9	2N	2	LYS
11	2P	29	LYS
14	2S	57	LYS
38	2g	4	ARG
40	2i	55	ALA
44	2m	4	ILE
51	2t	47	GLY
55	2z	2	ASP
4	1E	52	LEU
11	1P	29	LYS
20	1Y	54	LYS
33	1b	37	ASN
33	1b	128	GLU
33	1b	231	GLU
4	2E	52	LEU
11	2P	45	LEU
14	2S	84	GLN
26	24	46	GLN
33	2b	124	SER
38	2g	54	THR
50	2s	29	ARG
55	2z	3	LYS
8	1I	107	VAL
26	14	47	GLN
33	1b	124	SER
33	1b	165	VAL
51	1t	10	LEU
51	1t	97	ALA
3	2D	3	VAL
19	2X	2	LYS
23	21	3	LYS
33	2b	20	GLU
35	2d	136	PRO
46	2o	88	ARG

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Mol	Chain	Res	Type
6	1G	124	SER
26	14	46	GLN
41	1j	32	ALA
51	2t	95	ALA
33	2b	38	GLY
14	1S	60	GLY
41	1j	77	PRO
33	2b	151	GLY
3	2D	125	ILE
26	24	50	VAL
39	2h	73	ASP
11	1P	122	PRO
35	1d	136	PRO
15	1T	37	GLY
36	1e	77	PRO
33	2b	202	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	
3	1D	215/218 (99%)	194 (90%)	21 (10%)	10	23
3	2D	216/218 (99%)	193 (89%)	23 (11%)	8	19
4	1E	164/166 (99%)	148 (90%)	16 (10%)	10	23
4	2E	164/166 (99%)	151 (92%)	13 (8%)	15	34
5	1F	160/166 (96%)	142 (89%)	18 (11%)	7	16
5	2F	159/166 (96%)	145 (91%)	14 (9%)	12	28
6	1G	143/156 (92%)	127 (89%)	16 (11%)	7	17
6	2G	142/156 (91%)	120 (84%)	22 (16%)	3	8
7	1H	144/148 (97%)	132 (92%)	12 (8%)	14	31
7	2H	144/148 (97%)	133 (92%)	11 (8%)	16	37
8	1I	110/124 (89%)	95 (86%)	15 (14%)	5	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	2I	104/124 (84%)	93 (89%)	11 (11%)	8	19
9	1N	118/119 (99%)	104 (88%)	14 (12%)	6	15
9	2N	118/119 (99%)	107 (91%)	11 (9%)	11	25
10	1O	100/100 (100%)	94 (94%)	6 (6%)	24	50
10	2O	100/100 (100%)	93 (93%)	7 (7%)	19	42
11	1P	116/116 (100%)	103 (89%)	13 (11%)	7	17
11	2P	115/116 (99%)	103 (90%)	12 (10%)	9	20
12	1Q	111/111 (100%)	104 (94%)	7 (6%)	22	48
12	2Q	111/111 (100%)	104 (94%)	7 (6%)	22	48
13	1R	101/101 (100%)	88 (87%)	13 (13%)	5	12
13	2R	101/101 (100%)	91 (90%)	10 (10%)	10	22
14	1S	87/88 (99%)	80 (92%)	7 (8%)	15	33
14	2S	85/88 (97%)	72 (85%)	13 (15%)	3	8
15	1T	115/127 (91%)	107 (93%)	8 (7%)	19	42
15	2T	113/127 (89%)	105 (93%)	8 (7%)	18	41
16	1U	93/94 (99%)	85 (91%)	8 (9%)	13	29
16	2U	93/94 (99%)	84 (90%)	9 (10%)	10	23
17	1V	80/82 (98%)	69 (86%)	11 (14%)	4	10
17	2V	80/82 (98%)	70 (88%)	10 (12%)	6	13
18	1W	90/92 (98%)	83 (92%)	7 (8%)	16	35
18	2W	90/92 (98%)	85 (94%)	5 (6%)	26	54
19	1X	77/78 (99%)	75 (97%)	2 (3%)	54	83
19	2X	77/78 (99%)	75 (97%)	2 (3%)	54	83
20	1Y	85/91 (93%)	78 (92%)	7 (8%)	14	32
20	2Y	85/91 (93%)	76 (89%)	9 (11%)	8	19
21	1Z	159/179 (89%)	148 (93%)	11 (7%)	19	43
21	2Z	156/179 (87%)	143 (92%)	13 (8%)	14	31
22	10	60/67 (90%)	55 (92%)	5 (8%)	14	31
22	20	60/67 (90%)	57 (95%)	3 (5%)	30	60
23	11	80/83 (96%)	74 (92%)	6 (8%)	17	38
23	21	80/83 (96%)	75 (94%)	5 (6%)	22	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	12	65/67 (97%)	59 (91%)	6 (9%)	11	25
24	22	65/67 (97%)	58 (89%)	7 (11%)	8	18
25	13	51/52 (98%)	49 (96%)	2 (4%)	39	70
25	23	50/52 (96%)	47 (94%)	3 (6%)	24	50
26	14	60/63 (95%)	52 (87%)	8 (13%)	5	11
26	24	53/63 (84%)	45 (85%)	8 (15%)	3	9
27	15	50/52 (96%)	46 (92%)	4 (8%)	15	33
27	25	50/52 (96%)	46 (92%)	4 (8%)	15	33
28	16	51/52 (98%)	46 (90%)	5 (10%)	10	23
28	26	50/52 (96%)	45 (90%)	5 (10%)	9	22
29	17	41/42 (98%)	38 (93%)	3 (7%)	17	39
29	27	41/42 (98%)	39 (95%)	2 (5%)	31	61
30	18	54/55 (98%)	48 (89%)	6 (11%)	8	17
30	28	54/55 (98%)	50 (93%)	4 (7%)	17	39
31	19	34/34 (100%)	33 (97%)	1 (3%)	50	80
31	29	34/34 (100%)	32 (94%)	2 (6%)	24	51
33	1b	177/220 (80%)	149 (84%)	28 (16%)	3	8
33	2b	158/220 (72%)	140 (89%)	18 (11%)	7	16
34	1c	127/188 (68%)	120 (94%)	7 (6%)	27	55
34	2c	108/188 (57%)	92 (85%)	16 (15%)	4	9
35	1d	161/181 (89%)	141 (88%)	20 (12%)	6	13
35	2d	164/181 (91%)	140 (85%)	24 (15%)	4	9
36	1e	113/123 (92%)	99 (88%)	14 (12%)	6	13
36	2e	106/123 (86%)	91 (86%)	15 (14%)	4	10
37	1f	83/90 (92%)	78 (94%)	5 (6%)	24	50
37	2f	86/90 (96%)	80 (93%)	6 (7%)	19	42
38	1g	111/127 (87%)	100 (90%)	11 (10%)	10	22
38	2g	107/127 (84%)	95 (89%)	12 (11%)	7	17
39	1h	114/119 (96%)	105 (92%)	9 (8%)	15	34
39	2h	111/119 (93%)	102 (92%)	9 (8%)	15	33
40	1i	89/99 (90%)	80 (90%)	9 (10%)	9	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	2i	80/99 (81%)	70 (88%)	10 (12%)	6	13
41	1j	60/92 (65%)	52 (87%)	8 (13%)	5	11
41	2j	62/92 (67%)	55 (89%)	7 (11%)	7	16
42	1k	82/99 (83%)	76 (93%)	6 (7%)	17	39
42	2k	82/99 (83%)	73 (89%)	9 (11%)	8	18
43	1l	95/109 (87%)	88 (93%)	7 (7%)	17	39
43	2l	94/109 (86%)	85 (90%)	9 (10%)	10	24
44	1m	90/101 (89%)	81 (90%)	9 (10%)	9	22
44	2m	87/101 (86%)	79 (91%)	8 (9%)	11	25
45	1n	47/50 (94%)	42 (89%)	5 (11%)	8	19
45	2n	43/50 (86%)	37 (86%)	6 (14%)	4	10
46	1o	75/80 (94%)	68 (91%)	7 (9%)	11	25
46	2o	78/80 (98%)	74 (95%)	4 (5%)	29	59
47	1p	67/74 (90%)	56 (84%)	11 (16%)	3	7
47	2p	68/74 (92%)	57 (84%)	11 (16%)	3	7
48	1q	91/97 (94%)	86 (94%)	5 (6%)	27	55
48	2q	94/97 (97%)	92 (98%)	2 (2%)	61	87
49	1r	59/77 (77%)	51 (86%)	8 (14%)	5	11
49	2r	59/77 (77%)	49 (83%)	10 (17%)	2	6
50	1s	65/80 (81%)	56 (86%)	9 (14%)	4	10
50	2s	67/80 (84%)	58 (87%)	9 (13%)	5	11
51	1t	66/82 (80%)	58 (88%)	8 (12%)	6	14
51	2t	71/82 (87%)	65 (92%)	6 (8%)	13	30
52	1u	16/22 (73%)	15 (94%)	1 (6%)	22	48
52	2u	18/22 (82%)	16 (89%)	2 (11%)	8	17
55	1z	15/19 (79%)	12 (80%)	3 (20%)	1	4
55	2z	15/19 (79%)	12 (80%)	3 (20%)	1	4
All	All	9165/10104 (91%)	8268 (90%)	897 (10%)	10	23

All (897) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	13	ARG

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Mol	Chain	Res	Type
3	1D	61	LEU
3	1D	69	ARG
3	1D	88	ARG
3	1D	94	LEU
3	1D	111	LEU
3	1D	115	GLN
3	1D	117	VAL
3	1D	138	VAL
3	1D	154	LYS
3	1D	155	LEU
3	1D	193	VAL
3	1D	211	ARG
3	1D	217	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	257	LEU
3	1D	260	ARG
3	1D	274	ARG
3	1D	275	LYS
4	1E	12	THR
4	1E	21	VAL
4	1E	34	VAL
4	1E	47	VAL
4	1E	73	GLU
4	1E	75	VAL
4	1E	97	LYS
4	1E	111	ARG
4	1E	113	PHE
4	1E	116	VAL
4	1E	119	ARG
4	1E	144	ARG
4	1E	154	LYS
4	1E	163	GLU
4	1E	175	VAL
4	1E	181	LEU
5	1F	12	LEU
5	1F	19	GLU
5	1F	20	LEU
5	1F	24	LEU
5	1F	33	LEU
5	1F	38	ARG

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Mol	Chain	Res	Type
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	106	ARG
5	1F	110	LEU
5	1F	125	LEU
5	1F	132	VAL
5	1F	165	ARG
5	1F	170	LEU
5	1F	183	VAL
5	1F	191	ARG
5	1F	192	LEU
6	1G	3	LEU
6	1G	5	VAL
6	1G	7	LEU
6	1G	28	VAL
6	1G	35	GLU
6	1G	40	ASN
6	1G	45	GLU
6	1G	60	LEU
6	1G	82	LEU
6	1G	91	ARG
6	1G	139	LEU
6	1G	140	ILE
6	1G	143	GLU
6	1G	148	MET
6	1G	170	ARG
6	1G	175	LEU
7	1H	3	ARG
7	1H	13	LYS
7	1H	15	VAL
7	1H	33	LEU
7	1H	45	VAL
7	1H	59	ARG
7	1H	69	ARG
7	1H	84	SER
7	1H	88	LEU
7	1H	90	LYS
7	1H	122	THR
7	1H	129	THR
8	1I	5	LEU
8	1I	10	GLU

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Mol	Chain	Res	Type
8	1I	38	LEU
8	1I	43	ASN
8	1I	47	LEU
8	1I	54	GLN
8	1I	57	ARG
8	1I	61	ARG
8	1I	64	GLU
8	1I	66	GLU
8	1I	75	LEU
8	1I	101	LEU
8	1I	109	ILE
8	1I	140	LEU
8	1I	142	VAL
9	1N	8	GLN
9	1N	12	ARG
9	1N	14	VAL
9	1N	28	THR
9	1N	33	LEU
9	1N	34	LEU
9	1N	46	VAL
9	1N	61	ARG
9	1N	73	THR
9	1N	87	LEU
9	1N	99	LEU
9	1N	120	LEU
9	1N	131	GLN
9	1N	137	LYS
10	1O	8	LEU
10	1O	10	VAL
10	1O	18	LYS
10	1O	24	VAL
10	1O	94	ARG
10	1O	105	GLU
11	1P	3	LEU
11	1P	21	ARG
11	1P	55	ARG
11	1P	59	LEU
11	1P	70	GLN
11	1P	95	VAL
11	1P	98	GLU
11	1P	99	LEU
11	1P	106	LEU

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Mol	Chain	Res	Type
11	1P	112	LEU
11	1P	125	VAL
11	1P	136	GLU
11	1P	149	GLU
12	1Q	7	MET
12	1Q	8	LYS
12	1Q	35	VAL
12	1Q	45	GLN
12	1Q	60	ARG
12	1Q	75	THR
12	1Q	110	THR
13	1R	6	SER
13	1R	18	LEU
13	1R	28	LEU
13	1R	29	LEU
13	1R	33	ARG
13	1R	36	THR
13	1R	44	LEU
13	1R	60	LEU
13	1R	65	LEU
13	1R	67	LEU
13	1R	79	LEU
13	1R	100	LEU
13	1R	111	LEU
14	1S	3	ARG
14	1S	20	ARG
14	1S	36	TYR
14	1S	42	ASP
14	1S	59	LYS
14	1S	61	ASN
14	1S	110	LEU
15	1T	23	ARG
15	1T	28	VAL
15	1T	49	VAL
15	1T	85	LYS
15	1T	96	ARG
15	1T	107	ASP
15	1T	118	ARG
15	1T	128	GLU
16	1U	36	ARG
16	1U	52	ARG
16	1U	59	ARG

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Mol	Chain	Res	Type
16	1U	60	LEU
16	1U	74	LEU
16	1U	92	ARG
16	1U	104	GLN
16	1U	108	GLU
17	1V	18	LEU
17	1V	21	ARG
17	1V	28	GLU
17	1V	43	GLU
17	1V	46	VAL
17	1V	52	VAL
17	1V	62	LEU
17	1V	72	VAL
17	1V	79	VAL
17	1V	95	LEU
17	1V	100	ARG
18	1W	11	ARG
18	1W	15	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	23	LEU
18	1W	83	LYS
18	1W	107	LEU
19	1X	35	THR
19	1X	57	LEU
20	1Y	2	ARG
20	1Y	9	LYS
20	1Y	23	ARG
20	1Y	43	ASN
20	1Y	72	VAL
20	1Y	85	VAL
20	1Y	107	ASP
21	1Z	18	LEU
21	1Z	31	ARG
21	1Z	86	VAL
21	1Z	107	THR
21	1Z	135	GLU
21	1Z	150	LEU
21	1Z	155	LEU
21	1Z	161	VAL
21	1Z	170	THR
21	1Z	183	LEU

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Mol	Chain	Res	Type
21	1Z	185	GLU
22	10	11	ARG
22	10	20	ARG
22	10	49	LYS
22	10	55	ARG
22	10	68	GLU
23	11	21	ARG
23	11	30	VAL
23	11	40	ARG
23	11	59	THR
23	11	78	LYS
23	11	95	LEU
24	12	19	VAL
24	12	28	LYS
24	12	32	LEU
24	12	49	LYS
24	12	53	LEU
24	12	70	GLN
25	13	8	LEU
25	13	54	VAL
26	14	14	ILE
26	14	34	GLU
26	14	49	PHE
26	14	55	ARG
26	14	56	VAL
26	14	60	GLN
26	14	62	ARG
26	14	63	TYR
27	15	6	VAL
27	15	16	ARG
27	15	29	THR
27	15	40	LYS
28	16	4	GLU
28	16	6	ARG
28	16	33	LYS
28	16	38	LYS
28	16	40	CYS
29	17	23	ARG
29	17	24	THR
29	17	43	THR
30	18	14	VAL
30	18	30	ARG

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Mol	Chain	Res	Type
30	18	31	HIS
30	18	32	LEU
30	18	34	TRP
30	18	46	ARG
31	19	26	ILE
33	1b	10	LEU
33	1b	17	PHE
33	1b	21	ARG
33	1b	23	ARG
33	1b	24	TRP
33	1b	44	LEU
33	1b	47	THR
33	1b	48	MET
33	1b	67	THR
33	1b	76	GLN
33	1b	78	GLN
33	1b	80	ILE
33	1b	86	GLU
33	1b	112	VAL
33	1b	116	GLU
33	1b	156	LYS
33	1b	169	LYS
33	1b	170	GLU
33	1b	175	ARG
33	1b	185	ILE
33	1b	187	LEU
33	1b	192	SER
33	1b	208	ILE
33	1b	209	ARG
33	1b	215	LEU
33	1b	217	ARG
33	1b	221	LEU
33	1b	226	ARG
34	1c	15	THR
34	1c	29	TYR
34	1c	45	LYS
34	1c	52	LEU
34	1c	59	ARG
34	1c	131	ARG
34	1c	204	LEU
35	1d	3	ARG
35	1d	5	ILE

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Mol	Chain	Res	Type
35	1d	15	GLU
35	1d	22	LYS
35	1d	25	ARG
35	1d	31	CYS
35	1d	45	GLN
35	1d	49	ARG
35	1d	58	LEU
35	1d	66	ARG
35	1d	73	ARG
35	1d	101	LEU
35	1d	107	ARG
35	1d	127	THR
35	1d	150	GLU
35	1d	155	LEU
35	1d	168	ARG
35	1d	181	MET
35	1d	188	LEU
35	1d	194	LEU
36	1e	12	LEU
36	1e	18	ARG
36	1e	41	VAL
36	1e	47	LYS
36	1e	51	VAL
36	1e	73	ASN
36	1e	75	THR
36	1e	78	HIS
36	1e	79	GLU
36	1e	81	GLU
36	1e	91	LEU
36	1e	120	THR
36	1e	137	GLU
36	1e	152	ARG
37	1f	45	LEU
37	1f	46	ARG
37	1f	69	GLU
37	1f	74	ASP
37	1f	79	LEU
38	1g	8	GLU
38	1g	50	ILE
38	1g	51	GLN
38	1g	56	GLN
38	1g	57	GLU

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Mol	Chain	Res	Type
38	1g	72	ARG
38	1g	75	VAL
38	1g	104	LEU
38	1g	113	GLU
38	1g	114	ARG
38	1g	131	LYS
39	1h	21	LYS
39	1h	50	ARG
39	1h	54	ASP
39	1h	63	LEU
39	1h	75	ARG
39	1h	78	GLN
39	1h	91	ARG
39	1h	98	LYS
39	1h	137	VAL
40	1i	14	VAL
40	1i	27	THR
40	1i	75	ASP
40	1i	81	ILE
40	1i	92	TYR
40	1i	104	ARG
40	1i	108	VAL
40	1i	127	LYS
40	1i	128	ARG
41	1j	13	HIS
41	1j	17	ASP
41	1j	30	SER
41	1j	34	VAL
41	1j	84	GLN
41	1j	85	LEU
41	1j	92	THR
41	1j	98	ILE
42	1k	14	VAL
42	1k	31	THR
42	1k	48	ILE
42	1k	96	ARG
42	1k	109	VAL
42	1k	114	VAL
43	1l	10	LEU
43	1l	23	LYS
43	1l	27	LEU
43	1l	33	ARG

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Mol	Chain	Res	Type
43	1l	54	LYS
43	1l	67	THR
43	1l	83	VAL
44	1m	3	ARG
44	1m	4	ILE
44	1m	19	LEU
44	1m	32	GLU
44	1m	49	THR
44	1m	56	LEU
44	1m	70	LEU
44	1m	98	VAL
44	1m	102	ARG
45	1n	6	LEU
45	1n	18	VAL
45	1n	22	THR
45	1n	41	ARG
45	1n	46	GLU
46	1o	14	GLU
46	1o	22	THR
46	1o	24	SER
46	1o	26	GLU
46	1o	39	LEU
46	1o	83	GLU
46	1o	84	LYS
47	1p	1	MET
47	1p	2	VAL
47	1p	5	ARG
47	1p	11	SER
47	1p	19	ILE
47	1p	20	VAL
47	1p	25	ARG
47	1p	45	THR
47	1p	62	VAL
47	1p	67	THR
47	1p	72	ARG
48	1q	19	VAL
48	1q	68	ARG
48	1q	74	LEU
48	1q	78	GLU
48	1q	82	MET
49	1r	32	ARG
49	1r	35	ARG

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Mol	Chain	Res	Type
49	1r	37	VAL
49	1r	38	GLU
49	1r	55	ARG
49	1r	68	LYS
49	1r	69	THR
49	1r	76	LEU
50	1s	3	ARG
50	1s	5	LEU
50	1s	22	LEU
50	1s	27	GLU
50	1s	28	LYS
50	1s	63	THR
50	1s	65	ASN
50	1s	78	ARG
50	1s	81	ARG
51	1t	9	ASN
51	1t	24	LEU
51	1t	25	ARG
51	1t	56	MET
51	1t	60	GLU
51	1t	62	LEU
51	1t	84	LEU
51	1t	93	GLU
52	1u	15	ARG
55	1z	9	ARG
55	1z	11	THR
55	1z	14	ARG
3	2D	61	LEU
3	2D	71	ASP
3	2D	88	ARG
3	2D	89	SER
3	2D	94	LEU
3	2D	103	ARG
3	2D	106	ILE
3	2D	113	VAL
3	2D	134	ARG
3	2D	155	LEU
3	2D	164	GLN
3	2D	169	GLU
3	2D	173	VAL
3	2D	183	ARG
3	2D	193	VAL

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Mol	Chain	Res	Type
3	2D	211	ARG
3	2D	217	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
3	2D	257	LEU
3	2D	260	ARG
3	2D	276	LYS
4	2E	7	VAL
4	2E	12	THR
4	2E	21	VAL
4	2E	24	THR
4	2E	52	LEU
4	2E	75	VAL
4	2E	111	ARG
4	2E	113	PHE
4	2E	116	VAL
4	2E	119	ARG
4	2E	144	ARG
4	2E	154	LYS
4	2E	175	VAL
5	2F	19	GLU
5	2F	20	LEU
5	2F	33	LEU
5	2F	38	ARG
5	2F	53	THR
5	2F	57	VAL
5	2F	74	ARG
5	2F	106	ARG
5	2F	132	VAL
5	2F	135	LYS
5	2F	183	VAL
5	2F	192	LEU
5	2F	196	LEU
5	2F	197	ASP
6	2G	3	LEU
6	2G	5	VAL
6	2G	9	ARG
6	2G	14	GLU
6	2G	28	VAL
6	2G	33	ARG
6	2G	35	GLU

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Mol	Chain	Res	Type
6	2G	47	LYS
6	2G	60	LEU
6	2G	91	ARG
6	2G	98	ARG
6	2G	111	LEU
6	2G	113	ARG
6	2G	115	ARG
6	2G	136	ARG
6	2G	139	LEU
6	2G	140	ILE
6	2G	143	GLU
6	2G	148	MET
6	2G	153	ARG
6	2G	162	THR
6	2G	170	ARG
7	2H	3	ARG
7	2H	15	VAL
7	2H	32	GLU
7	2H	33	LEU
7	2H	41	MET
7	2H	42	ARG
7	2H	63	SER
7	2H	69	ARG
7	2H	129	THR
7	2H	139	GLN
7	2H	171	LEU
8	2I	5	LEU
8	2I	38	LEU
8	2I	43	ASN
8	2I	47	LEU
8	2I	61	ARG
8	2I	75	LEU
8	2I	77	LEU
8	2I	129	THR
8	2I	140	LEU
8	2I	142	VAL
8	2I	144	VAL
9	2N	33	LEU
9	2N	34	LEU
9	2N	46	VAL
9	2N	61	ARG
9	2N	62	VAL

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Mol	Chain	Res	Type
9	2N	73	THR
9	2N	87	LEU
9	2N	120	LEU
9	2N	131	GLN
9	2N	137	LYS
9	2N	138	LEU
10	2O	1	MET
10	2O	8	LEU
10	2O	10	VAL
10	2O	24	VAL
10	2O	52	VAL
10	2O	69	ILE
10	2O	94	ARG
11	2P	21	ARG
11	2P	45	LEU
11	2P	55	ARG
11	2P	65	ARG
11	2P	95	VAL
11	2P	96	THR
11	2P	106	LEU
11	2P	112	LEU
11	2P	121	LYS
11	2P	123	LEU
11	2P	125	VAL
11	2P	148	LEU
12	2Q	7	MET
12	2Q	21	THR
12	2Q	35	VAL
12	2Q	45	GLN
12	2Q	48	GLU
12	2Q	64	ILE
12	2Q	75	THR
13	2R	6	SER
13	2R	18	LEU
13	2R	28	LEU
13	2R	29	LEU
13	2R	36	THR
13	2R	60	LEU
13	2R	65	LEU
13	2R	79	LEU
13	2R	100	LEU
13	2R	102	GLU

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Mol	Chain	Res	Type
14	2S	3	ARG
14	2S	13	ARG
14	2S	20	ARG
14	2S	36	TYR
14	2S	53	SER
14	2S	58	LEU
14	2S	67	ARG
14	2S	68	GLN
14	2S	75	GLU
14	2S	80	LEU
14	2S	83	LYS
14	2S	110	LEU
14	2S	111	GLU
15	2T	8	LYS
15	2T	16	ARG
15	2T	28	VAL
15	2T	34	VAL
15	2T	49	VAL
15	2T	64	ARG
15	2T	96	ARG
15	2T	118	ARG
16	2U	13	LYS
16	2U	36	ARG
16	2U	52	ARG
16	2U	60	LEU
16	2U	74	LEU
16	2U	83	LEU
16	2U	92	ARG
16	2U	104	GLN
16	2U	112	ARG
17	2V	18	LEU
17	2V	21	ARG
17	2V	35	LEU
17	2V	46	VAL
17	2V	52	VAL
17	2V	62	LEU
17	2V	72	VAL
17	2V	79	VAL
17	2V	95	LEU
17	2V	100	ARG
18	2W	11	ARG
18	2W	15	ARG

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Mol	Chain	Res	Type
18	2W	17	VAL
18	2W	27	LYS
18	2W	107	LEU
19	2X	57	LEU
19	2X	92	LEU
20	2Y	9	LYS
20	2Y	43	ASN
20	2Y	44	ILE
20	2Y	49	VAL
20	2Y	67	LEU
20	2Y	72	VAL
20	2Y	85	VAL
20	2Y	92	ASN
20	2Y	107	ASP
21	2Z	71	VAL
21	2Z	86	VAL
21	2Z	107	THR
21	2Z	128	VAL
21	2Z	131	ARG
21	2Z	135	GLU
21	2Z	136	PHE
21	2Z	150	LEU
21	2Z	154	ASP
21	2Z	155	LEU
21	2Z	161	VAL
21	2Z	170	THR
21	2Z	185	GLU
22	20	19	LYS
22	20	55	ARG
22	20	68	GLU
23	21	21	ARG
23	21	35	THR
23	21	40	ARG
23	21	59	THR
23	21	95	LEU
24	22	2	LYS
24	22	28	LYS
24	22	32	LEU
24	22	34	GLU
24	22	40	SER
24	22	53	LEU
24	22	70	GLN

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Mol	Chain	Res	Type
25	23	8	LEU
25	23	54	VAL
25	23	55	ARG
26	24	1	MET
26	24	34	GLU
26	24	44	THR
26	24	52	THR
26	24	60	GLN
26	24	61	ARG
26	24	63	TYR
26	24	69	LYS
27	25	6	VAL
27	25	16	ARG
27	25	29	THR
27	25	40	LYS
28	26	6	ARG
28	26	33	LYS
28	26	38	LYS
28	26	40	CYS
28	26	48	VAL
29	27	1	MET
29	27	43	THR
30	28	30	ARG
30	28	31	HIS
30	28	34	TRP
30	28	37	SER
31	29	26	ILE
31	29	29	ASN
33	2b	24	TRP
33	2b	44	LEU
33	2b	48	MET
33	2b	51	LEU
33	2b	60	ASP
33	2b	80	ILE
33	2b	90	MET
33	2b	93	VAL
33	2b	108	ILE
33	2b	118	LEU
33	2b	138	LEU
33	2b	170	GLU
33	2b	185	ILE
33	2b	187	LEU

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Mol	Chain	Res	Type
33	2b	191	ASP
33	2b	222	ILE
33	2b	223	ILE
33	2b	224	GLN
34	2c	3	ASN
34	2c	5	ILE
34	2c	16	ARG
34	2c	29	TYR
34	2c	40	ARG
34	2c	47	LEU
34	2c	52	LEU
34	2c	59	ARG
34	2c	70	VAL
34	2c	105	GLU
34	2c	128	PHE
34	2c	131	ARG
34	2c	162	GLN
34	2c	178	LEU
34	2c	182	ILE
34	2c	198	VAL
35	2d	3	ARG
35	2d	5	ILE
35	2d	25	ARG
35	2d	26	CYS
35	2d	34	GLU
35	2d	38	TYR
35	2d	47	ARG
35	2d	58	LEU
35	2d	61	LYS
35	2d	66	ARG
35	2d	73	ARG
35	2d	96	LEU
35	2d	101	LEU
35	2d	122	ARG
35	2d	135	LEU
35	2d	150	GLU
35	2d	157	LEU
35	2d	170	VAL
35	2d	179	GLU
35	2d	181	MET
35	2d	182	LYS
35	2d	187	ARG

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Mol	Chain	Res	Type
35	2d	188	LEU
35	2d	194	LEU
36	2e	11	ILE
36	2e	12	LEU
36	2e	24	ARG
36	2e	27	ARG
36	2e	31	LEU
36	2e	37	ARG
36	2e	41	VAL
36	2e	47	LYS
36	2e	50	GLU
36	2e	51	VAL
36	2e	68	GLU
36	2e	71	LEU
36	2e	78	HIS
36	2e	91	LEU
36	2e	121	LYS
37	2f	17	SER
37	2f	23	LYS
37	2f	27	GLN
37	2f	28	ARG
37	2f	46	ARG
37	2f	75	LEU
38	2g	51	GLN
38	2g	52	GLU
38	2g	57	GLU
38	2g	72	ARG
38	2g	73	MET
38	2g	75	VAL
38	2g	104	LEU
38	2g	110	GLN
38	2g	114	ARG
38	2g	129	GLU
38	2g	131	LYS
38	2g	154	TYR
39	2h	21	LYS
39	2h	26	VAL
39	2h	63	LEU
39	2h	77	GLU
39	2h	78	GLN
39	2h	91	ARG
39	2h	111	ILE

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Mol	Chain	Res	Type
39	2h	120	THR
39	2h	137	VAL
40	2i	3	GLN
40	2i	38	GLN
40	2i	50	LEU
40	2i	89	ASN
40	2i	102	LEU
40	2i	104	ARG
40	2i	107	ARG
40	2i	108	VAL
40	2i	124	GLN
40	2i	128	ARG
41	2j	13	HIS
41	2j	17	ASP
41	2j	21	GLN
41	2j	48	THR
41	2j	57	LYS
41	2j	68	HIS
41	2j	84	GLN
42	2k	14	VAL
42	2k	18	ARG
42	2k	26	ASN
42	2k	48	ILE
42	2k	54	ARG
42	2k	77	MET
42	2k	78	GLN
42	2k	109	VAL
42	2k	114	VAL
43	2l	27	LEU
43	2l	28	LYS
43	2l	33	ARG
43	2l	53	ARG
43	2l	54	LYS
43	2l	55	VAL
43	2l	67	THR
43	2l	83	VAL
43	2l	97	ARG
44	2m	3	ARG
44	2m	40	ASN
44	2m	49	THR
44	2m	56	LEU
44	2m	61	GLU

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Mol	Chain	Res	Type
44	2m	70	LEU
44	2m	82	MET
44	2m	106	ASN
45	2n	11	LYS
45	2n	17	LYS
45	2n	18	VAL
45	2n	22	THR
45	2n	33	VAL
45	2n	53	LEU
46	2o	5	LYS
46	2o	22	THR
46	2o	24	SER
46	2o	26	GLU
47	2p	1	MET
47	2p	5	ARG
47	2p	11	SER
47	2p	25	ARG
47	2p	28	ARG
47	2p	45	THR
47	2p	60	LEU
47	2p	62	VAL
47	2p	67	THR
47	2p	69	THR
47	2p	72	ARG
48	2q	63	ARG
48	2q	74	LEU
49	2r	26	LEU
49	2r	28	GLU
49	2r	29	PHE
49	2r	32	ARG
49	2r	35	ARG
49	2r	37	VAL
49	2r	42	ARG
49	2r	54	ARG
49	2r	68	LYS
49	2r	76	LEU
50	2s	3	ARG
50	2s	18	LYS
50	2s	22	LEU
50	2s	28	LYS
50	2s	41	VAL
50	2s	64	GLU

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Mol	Chain	Res	Type
50	2s	65	ASN
50	2s	77	THR
50	2s	78	ARG
51	2t	9	ASN
51	2t	10	LEU
51	2t	24	LEU
51	2t	56	MET
51	2t	62	LEU
51	2t	71	THR
52	2u	10	ARG
52	2u	15	ARG
55	2z	9	ARG
55	2z	14	ARG
55	2z	16	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (152) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
3	1D	126	GLN
3	1D	164	GLN
3	1D	253	GLN
5	1F	8	GLN
5	1F	69	HIS
5	1F	169	ASN
5	1F	203	GLN
6	1G	40	ASN
8	1I	43	ASN
8	1I	139	GLN
9	1N	8	GLN
9	1N	131	GLN
11	1P	38	GLN
11	1P	70	GLN
14	1S	95	HIS
15	1T	123	GLN
16	1U	81	HIS
16	1U	104	GLN
18	1W	111	HIS
19	1X	31	HIS
19	1X	55	ASN
20	1Y	6	HIS
20	1Y	43	ASN

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Mol	Chain	Res	Type
21	1Z	55	HIS
21	1Z	73	GLN
21	1Z	151	HIS
22	10	35	ASN
24	12	38	GLN
24	12	70	GLN
26	14	46	GLN
31	19	36	GLN
33	1b	16	HIS
33	1b	19	HIS
33	1b	95	GLN
34	1c	118	GLN
34	1c	170	GLN
34	1c	181	ASN
35	1d	43	HIS
35	1d	45	GLN
35	1d	123	HIS
35	1d	160	GLN
36	1e	38	GLN
36	1e	73	ASN
36	1e	141	GLN
37	1f	100	ASN
38	1g	13	GLN
38	1g	56	GLN
38	1g	86	GLN
38	1g	97	GLN
40	1i	31	GLN
40	1i	58	HIS
40	1i	73	GLN
40	1i	89	ASN
40	1i	117	HIS
40	1i	124	GLN
41	1j	56	HIS
41	1j	68	HIS
41	1j	84	GLN
42	1k	93	GLN
43	1l	78	GLN
43	1l	80	HIS
43	1l	99	HIS
45	1n	52	GLN
46	1o	28	GLN
48	1q	16	GLN

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Mol	Chain	Res	Type
48	1q	26	GLN
50	1s	56	GLN
50	1s	65	ASN
50	1s	69	HIS
51	1t	9	ASN
51	1t	26	ASN
51	1t	45	GLN
3	2D	164	GLN
3	2D	253	GLN
4	2E	85	ASN
5	2F	69	HIS
5	2F	169	ASN
5	2F	203	GLN
6	2G	26	GLN
6	2G	40	ASN
6	2G	66	GLN
6	2G	108	ASN
8	2I	133	HIS
8	2I	139	GLN
11	2P	38	GLN
12	2Q	12	GLN
14	2S	68	GLN
14	2S	95	HIS
15	2T	123	GLN
16	2U	44	ASN
16	2U	72	HIS
17	2V	64	HIS
18	2W	60	ASN
19	2X	31	HIS
19	2X	82	GLN
20	2Y	92	ASN
21	2Z	55	HIS
21	2Z	73	GLN
22	20	35	ASN
23	21	56	GLN
24	22	38	GLN
25	23	32	GLN
25	23	33	GLN
28	26	32	ASN
31	29	29	ASN
31	29	36	GLN
33	2b	16	HIS

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Mol	Chain	Res	Type
33	2b	19	HIS
33	2b	45	GLN
33	2b	146	GLN
34	2c	6	HIS
34	2c	176	HIS
34	2c	181	ASN
35	2d	74	GLN
35	2d	123	HIS
35	2d	125	HIS
35	2d	160	GLN
35	2d	201	GLN
36	2e	20	GLN
36	2e	38	GLN
36	2e	141	GLN
37	2f	27	GLN
38	2g	86	GLN
38	2g	97	GLN
38	2g	110	GLN
38	2g	153	HIS
39	2h	78	GLN
40	2i	38	GLN
40	2i	58	HIS
40	2i	73	GLN
40	2i	89	ASN
41	2j	13	HIS
41	2j	33	GLN
41	2j	56	HIS
41	2j	62	HIS
42	2k	26	ASN
42	2k	93	GLN
42	2k	104	GLN
43	2l	75	HIS
43	2l	78	GLN
43	2l	80	HIS
43	2l	99	HIS
44	2m	40	ASN
46	2o	28	GLN
46	2o	62	GLN
47	2p	16	HIS
48	2q	16	GLN
50	2s	56	GLN
50	2s	69	HIS

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Mol	Chain	Res	Type
50	2s	83	HIS
51	2t	42	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2737/2915 (93%)	374 (13%)	22 (0%)
1	2A	2781/2915 (95%)	476 (17%)	23 (0%)
2	1B	119/121 (98%)	10 (8%)	0
2	2B	119/121 (98%)	26 (21%)	2 (1%)
32	1a	1472/1521 (96%)	272 (18%)	0
32	2a	1479/1521 (97%)	278 (18%)	0
53	1v	4/24 (16%)	1 (25%)	0
53	2v	4/24 (16%)	1 (25%)	0
54	1x	75/77 (97%)	16 (21%)	0
54	2x	75/77 (97%)	18 (24%)	0
All	All	8865/9316 (95%)	1472 (16%)	47 (0%)

All (1472) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	11	U
1	1A	33	C
1	1A	35	G
1	1A	44	C
1	1A	49	G
1	1A	56	G
1	1A	59	G
1	1A	61	U
1	1A	69	A
1	1A	72	A
1	1A	73	G
1	1A	82	A
1	1A	115	A
1	1A	116	A
1	1A	117	U
1	1A	148	A
1	1A	154	C
1	1A	170	A
1	1A	184	A
1	1A	193	G

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Mol	Chain	Res	Type
1	1A	202	G
1	1A	204	A
1	1A	210	A
1	1A	216	A
1	1A	217	A
1	1A	221	A
1	1A	236	G
1	1A	237	C
1	1A	264	U
1	1A	268	G
1	1A	271	U
1	1A	272	G
1	1A	273	U
1	1A	278	G
1	1A	287	U
1	1A	288	G
1	1A	295	U
1	1A	298	G
1	1A	302	C
1	1A	334	A
1	1A	340	G
1	1A	352	G
1	1A	353	A
1	1A	375	G
1	1A	386	G
1	1A	388	G
1	1A	398	G
1	1A	412	G
1	1A	422	G
1	1A	431	U
1	1A	437	G
1	1A	454	A
1	1A	467	G
1	1A	469	C
1	1A	473	U
1	1A	476	C
1	1A	479	A
1	1A	482	A
1	1A	495	A
1	1A	500	U
1	1A	506	G
1	1A	528	U

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Mol	Chain	Res	Type
1	1A	529	A
1	1A	533	C
1	1A	554	G
1	1A	555	C
1	1A	556	A
1	1A	557	G
1	1A	572	G
1	1A	585	G
1	1A	595	G
1	1A	596	C
1	1A	597	A
1	1A	608	A
1	1A	615	G
1	1A	625	A
1	1A	626	G
1	1A	629	U
1	1A	638	G
1	1A	640	G
1	1A	658	C
1	1A	661	A
1	1A	669	C
1	1A	670	A
1	1A	671	G
1	1A	681	G
1	1A	682	G
1	1A	700	A
1	1A	715	G
1	1A	732	G
1	1A	763	G
1	1A	772	G
1	1A	776	C
1	1A	810	A
1	1A	821	G
1	1A	822	G
1	1A	828	A
1	1A	830	A
1	1A	831	G
1	1A	836	C
1	1A	838	G
1	1A	851	G
1	1A	858	C
1	1A	873	U

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Mol	Chain	Res	Type
1	1A	874	U
1	1A	905	G
1	1A	912	A
1	1A	915	G
1	1A	925	G
1	1A	931	C
1	1A	932	C
1	1A	933	A
1	1A	934	C
1	1A	935	C
1	1A	936	A
1	1A	938	C
1	1A	941	A
1	1A	942	C
1	1A	955	A
1	1A	976	G
1	1A	985	A
1	1A	989	A
1	1A	990	G
1	1A	1002	U
1	1A	1003	A
1	1A	1005	C
1	1A	1018	G
1	1A	1019	C
1	1A	1028	A
1	1A	1035	A
1	1A	1041	A
1	1A	1057	U
1	1A	1058	C
1	1A	1067	G
1	1A	1071	U
1	1A	1072	A
1	1A	1078	U
1	1A	1083	C
1	1A	1086	C
1	1A	1091	A
1	1A	1092	G
1	1A	1150	U
1	1A	1153	U
1	1A	1154	C
1	1A	1156	A
1	1A	1157	G

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Mol	Chain	Res	Type
1	1A	1173	A
1	1A	1174	A
1	1A	1179	C
1	1A	1180	G
1	1A	1183	G
1	1A	1216	G
1	1A	1217	G
1	1A	1218	A
1	1A	1219	U
1	1A	1220	G
1	1A	1221	A
1	1A	1264	A
1	1A	1285	U
1	1A	1286	A
1	1A	1289	G
1	1A	1298	A
1	1A	1301	G
1	1A	1316	G
1	1A	1317	A
1	1A	1318	U
1	1A	1345	U
1	1A	1346	A
1	1A	1348	G
1	1A	1350	C
1	1A	1351	C
1	1A	1353	A
1	1A	1397	U
1	1A	1404	A
1	1A	1405	A
1	1A	1410	A
1	1A	1424	A
1	1A	1429	A
1	1A	1430	G
1	1A	1440	A
1	1A	1461	G
1	1A	1462	C
1	1A	1465	U
1	1A	1466	G
1	1A	1473	C
1	1A	1482	C
1	1A	1490	A
1	1A	1495	A

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Mol	Chain	Res	Type
1	1A	1496	G
1	1A	1513	C
1	1A	1524	G
1	1A	1528	G
1	1A	1539	A
1	1A	1541	A
1	1A	1552	A
1	1A	1553	A
1	1A	1554	C
1	1A	1555	A
1	1A	1578	C
1	1A	1588	A
1	1A	1589	C
1	1A	1600	A
1	1A	1604	A
1	1A	1612	A
1	1A	1615	A
1	1A	1624	U
1	1A	1627	G
1	1A	1630	C
1	1A	1631	A
1	1A	1632	A
1	1A	1653	A
1	1A	1654	A
1	1A	1694	C
1	1A	1700	A
1	1A	1710	A
1	1A	1720	G
1	1A	1746	A
1	1A	1766	A
1	1A	1767	U
1	1A	1786	G
1	1A	1792	A
1	1A	1793	G
1	1A	1794	G
1	1A	1803	A
1	1A	1810	A
1	1A	1816	A
1	1A	1821	A
1	1A	1830	C
1	1A	1831	G
1	1A	1832	A

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Mol	Chain	Res	Type
1	1A	1846	G
1	1A	1847	G
1	1A	1858	G
1	1A	1859	A
1	1A	1869	G
1	1A	1877	A
1	1A	1878	A
1	1A	1898	A
1	1A	1899	G
1	1A	1910	A
1	1A	1921	A
1	1A	1927	G
1	1A	1934	A
1	1A	1936	U
1	1A	1940	A
1	1A	1948	A
1	1A	1950	G
1	1A	1951	G
1	1A	1958	A
1	1A	1959	A
1	1A	1976	U
1	1A	1981	A
1	1A	1984	U
1	1A	1986	C
1	1A	1988	C
1	1A	1991	A
1	1A	1992	A
1	1A	1993	A
1	1A	2013	G
1	1A	2014	U
1	1A	2018	G
1	1A	2044	G
1	1A	2052	A
1	1A	2054	A
1	1A	2064	C
1	1A	2076	C
1	1A	2077	G
1	1A	2081	A
1	1A	2082	G
1	1A	2083	A
1	1A	2090	G
1	1A	2114	G

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Mol	Chain	Res	Type
1	1A	2205	G
1	1A	2207	G
1	1A	2208	G
1	1A	2209	C
1	1A	2213	G
1	1A	2219	A
1	1A	2226	G
1	1A	2227	G
1	1A	2228	A
1	1A	2229	U
1	1A	2236	A
1	1A	2250	G
1	1A	2279	A
1	1A	2280	A
1	1A	2284	A
1	1A	2286	C
1	1A	2289	A
1	1A	2294	C
1	1A	2298	A
1	1A	2300	G
1	1A	2316	A
1	1A	2331	A
1	1A	2336	G
1	1A	2338	A
1	1A	2345	G
1	1A	2347	A
1	1A	2358	C
1	1A	2361	C
1	1A	2365	G
1	1A	2394	G
1	1A	2396	C
1	1A	2411	G
1	1A	2417	U
1	1A	2433	A
1	1A	2434	U
1	1A	2436	A
1	1A	2439	G
1	1A	2440	G
1	1A	2441	A
1	1A	2442	U
1	1A	2443	A
1	1A	2446	A

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Mol	Chain	Res	Type
1	1A	2450	A
1	1A	2452	C
1	1A	2459	A
1	1A	2470	A
1	1A	2473	U
1	1A	2479	G
1	1A	2485	C
1	1A	2487	A
1	1A	2489	A
1	1A	2493	G
1	1A	2498	G
1	1A	2513	G
1	1A	2516	G
1	1A	2517	U
1	1A	2529	A
1	1A	2536	G
1	1A	2540	G
1	1A	2565	U
1	1A	2577	A
1	1A	2578	G
1	1A	2584	C
1	1A	2590	C
1	1A	2593	G
1	1A	2596	U
1	1A	2613	A
1	1A	2620	U
1	1A	2622	U
1	1A	2623	C
1	1A	2640	A
1	1A	2641	G
1	1A	2665	A
1	1A	2700	U
1	1A	2701	C
1	1A	2702	C
1	1A	2713	U
1	1A	2714	C
1	1A	2724	A
1	1A	2725	A
1	1A	2726	G
1	1A	2738	U
1	1A	2745	A
1	1A	2770	A

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Mol	Chain	Res	Type
1	1A	2776	A
1	1A	2777	A
1	1A	2778	G
1	1A	2781	C
1	1A	2790	A
1	1A	2802	A
1	1A	2812	G
1	1A	2829	A
1	1A	2830	A
1	1A	2844	A
1	1A	2881	G
1	1A	2882	A
1	1A	2885	G
1	1A	2889	C
1	1A	2900	A
1	1A	2901	G
1	1A	2902	G
1	1A	2903	U
2	1B	2	C
2	1B	13	A
2	1B	25	A
2	1B	52	A
2	1B	56	G
2	1B	59	A
2	1B	60	C
2	1B	73	A
2	1B	85	G
2	1B	110	G
32	1a	6	U
32	1a	8	G
32	1a	10	G
32	1a	33	A
32	1a	40	G
32	1a	41	C
32	1a	42	G
32	1a	45	G
32	1a	49	C
32	1a	52	A
32	1a	62	G
32	1a	68	C
32	1a	69	G
32	1a	74	G

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Mol	Chain	Res	Type
32	1a	75	C
32	1a	76	G
32	1a	77	G
32	1a	78	G
32	1a	91	G
32	1a	95	A
32	1a	110	A
32	1a	114	A
32	1a	115	C
32	1a	124	G
32	1a	126	C
32	1a	132	C
32	1a	139	G
32	1a	152	G
32	1a	156	A
32	1a	157	A
32	1a	161	G
32	1a	163	G
32	1a	168	U
32	1a	169	C
32	1a	177	U
32	1a	190	U
32	1a	200	C
32	1a	202	A
32	1a	204	A
32	1a	208	C
32	1a	209	U
32	1a	210	U
32	1a	211	U
32	1a	212	G
32	1a	213	C
32	1a	218	U
32	1a	243	G
32	1a	247	G
32	1a	255	G
32	1a	262	G
32	1a	263	C
32	1a	277	G
32	1a	285	G
32	1a	297	G
32	1a	313	G
32	1a	317	A

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Mol	Chain	Res	Type
32	1a	324	C
32	1a	325	A
32	1a	337	C
32	1a	338	C
32	1a	342	G
32	1a	343	G
32	1a	344	G
32	1a	348	C
32	1a	349	A
32	1a	350	G
32	1a	351	C
32	1a	363	U
32	1a	368	C
32	1a	369	A
32	1a	379	A
32	1a	380	G
32	1a	386	C
32	1a	393	A
32	1a	394	C
32	1a	402	G
32	1a	408	A
32	1a	409	G
32	1a	419	G
32	1a	420	G
32	1a	425	U
32	1a	435	A
32	1a	437	C
32	1a	441	G
32	1a	447	A
32	1a	449	C
32	1a	455	A
32	1a	456	C
32	1a	457	G
32	1a	467	A
32	1a	470	G
32	1a	477	G
32	1a	481	A
32	1a	482	U
32	1a	489	G
32	1a	493	A
32	1a	494	A
32	1a	495	C

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Mol	Chain	Res	Type
32	1a	496	U
32	1a	502	C
32	1a	503	C
32	1a	508	G
32	1a	511	G
32	1a	515	U
32	1a	516	A
32	1a	517	A
32	1a	529	C
32	1a	531	A
32	1a	543	A
32	1a	545	U
32	1a	556	A
32	1a	557	A
32	1a	560	G
32	1a	576	G
32	1a	601	G
32	1a	614	G
32	1a	623	G
32	1a	625	U
32	1a	637	A
32	1a	649	A
32	1a	671	A
32	1a	672	G
32	1a	677	G
32	1a	687	G
32	1a	707	U
32	1a	719	C
32	1a	733	C
32	1a	739	G
32	1a	750	A
32	1a	761	A
32	1a	776	A
32	1a	777	U
32	1a	778	A
32	1a	790	C
32	1a	799	A
32	1a	801	C
32	1a	805	G
32	1a	812	A
32	1a	813	G
32	1a	820	G

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Mol	Chain	Res	Type
32	1a	822	G
32	1a	824	C
32	1a	825	U
32	1a	826	C
32	1a	837	A
32	1a	838	A
32	1a	848	U
32	1a	850	A
32	1a	852	G
32	1a	880	G
32	1a	904	G
32	1a	905	G
32	1a	909	C
32	1a	910	C
32	1a	912	C
32	1a	913	A
32	1a	914	C
32	1a	938	U
32	1a	939	U
32	1a	946	A
32	1a	947	A
32	1a	949	G
32	1a	950	C
32	1a	952	A
32	1a	953	A
32	1a	954	G
32	1a	955	A
32	1a	960	U
32	1a	961	A
32	1a	970	U
32	1a	971	G
32	1a	972	A
32	1a	980	G
32	1a	982	G
32	1a	983	A
32	1a	984	A
32	1a	987	C
32	1a	988	G
32	1a	990	G
32	1a	992	G
32	1a	995	A
32	1a	1001	G

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Mol	Chain	Res	Type
32	1a	1027	A
32	1a	1037	C
32	1a	1048	U
32	1a	1049	C
32	1a	1064	G
32	1a	1077	G
32	1a	1078	U
32	1a	1084	A
32	1a	1089	G
32	1a	1091	G
32	1a	1106	A
32	1a	1107	G
32	1a	1108	U
32	1a	1113	A
32	1a	1115	C
32	1a	1117	G
32	1a	1119	U
32	1a	1120	C
32	1a	1121	G
32	1a	1122	G
32	1a	1123	C
32	1a	1124	C
32	1a	1129	A
32	1a	1135	A
32	1a	1138	G
32	1a	1142	U
32	1a	1143	G
32	1a	1149	G
32	1a	1158	A
32	1a	1165	A
32	1a	1166	G
32	1a	1178	U
32	1a	1179	G
32	1a	1184	G
32	1a	1194	U
32	1a	1195	A
32	1a	1196	C
32	1a	1204	G
32	1a	1209	A
32	1a	1220	A
32	1a	1238	A
32	1a	1239	U

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Mol	Chain	Res	Type
32	1a	1240	G
32	1a	1242	C
32	1a	1245	C
32	1a	1252	C
32	1a	1260	U
32	1a	1261	A
32	1a	1262	A
32	1a	1268	A
32	1a	1269	A
32	1a	1272	G
32	1a	1279	C
32	1a	1281	A
32	1a	1282	G
32	1a	1284	U
32	1a	1287	G
32	1a	1294	G
32	1a	1296	C
32	1a	1300	A
32	1a	1301	A
32	1a	1320	G
32	1a	1322	A
32	1a	1328	A
32	1a	1329	G
32	1a	1335	G
32	1a	1341	C
32	1a	1342	A
32	1a	1345	C
32	1a	1353	G
32	1a	1360	A
32	1a	1380	C
32	1a	1383	C
32	1a	1389	U
32	1a	1402	G
32	1a	1424	G
32	1a	1425	G
32	1a	1426	G
32	1a	1432	A
32	1a	1433	C
32	1a	1434	G
32	1a	1465	G
32	1a	1475	G
32	1a	1481	A

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Mol	Chain	Res	Type
32	1a	1482	G
32	1a	1483	G
32	1a	1484	U
32	1a	1495	G
32	1a	1507	G
32	1a	1508	G
53	1v	15	A
54	1x	6	G
54	1x	9	G
54	1x	13	C
54	1x	16	C
54	1x	17	C
54	1x	17(A)	U
54	1x	19	G
54	1x	20	U
54	1x	21	A
54	1x	42	G
54	1x	47	U
54	1x	50	U
54	1x	56	C
54	1x	65	C
54	1x	70	G
54	1x	76	A
1	2A	9	G
1	2A	11	U
1	2A	12	A
1	2A	13	A
1	2A	14	G
1	2A	33	C
1	2A	35	G
1	2A	44	C
1	2A	47	A
1	2A	49	G
1	2A	56	G
1	2A	61	U
1	2A	68	G
1	2A	69	A
1	2A	72	A
1	2A	73	G
1	2A	77	G
1	2A	81	G
1	2A	82	A

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Mol	Chain	Res	Type
1	2A	86	G
1	2A	88	U
1	2A	91	C
1	2A	93	G
1	2A	99	G
1	2A	115	A
1	2A	116	A
1	2A	117	U
1	2A	130	C
1	2A	138	A
1	2A	154	C
1	2A	155	U
1	2A	161	G
1	2A	169	A
1	2A	170	A
1	2A	184	A
1	2A	187	A
1	2A	193	G
1	2A	203	G
1	2A	204	A
1	2A	209	A
1	2A	210	A
1	2A	211	A
1	2A	212	G
1	2A	217	A
1	2A	221	A
1	2A	227	U
1	2A	236	G
1	2A	237	C
1	2A	254	G
1	2A	268	G
1	2A	270	U
1	2A	271	U
1	2A	272	G
1	2A	273	U
1	2A	274	C
1	2A	287	U
1	2A	288	G
1	2A	300	C
1	2A	301	A
1	2A	317	A
1	2A	321	G

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Mol	Chain	Res	Type
1	2A	334	A
1	2A	347	A
1	2A	350	G
1	2A	352	G
1	2A	353	A
1	2A	356	G
1	2A	357	C
1	2A	361	G
1	2A	365	G
1	2A	368	A
1	2A	375	G
1	2A	377	G
1	2A	385	U
1	2A	386	G
1	2A	412	G
1	2A	422	G
1	2A	425	G
1	2A	431	U
1	2A	436	G
1	2A	437	G
1	2A	438	A
1	2A	441	A
1	2A	448	A
1	2A	454	A
1	2A	461	C
1	2A	468	A
1	2A	469	C
1	2A	480	C
1	2A	481	C
1	2A	482	A
1	2A	495	A
1	2A	506	G
1	2A	507	A
1	2A	516	A
1	2A	528	U
1	2A	529	A
1	2A	533	C
1	2A	552	A
1	2A	553	A
1	2A	555	C
1	2A	556	A
1	2A	557	G

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Mol	Chain	Res	Type
1	2A	568	G
1	2A	573	G
1	2A	585	G
1	2A	595	G
1	2A	596	C
1	2A	597	A
1	2A	608	A
1	2A	625	A
1	2A	626	G
1	2A	629	U
1	2A	639	A
1	2A	640	G
1	2A	641	G
1	2A	651	A
1	2A	658	C
1	2A	661	A
1	2A	669	C
1	2A	670	A
1	2A	671	G
1	2A	678	A
1	2A	697	G
1	2A	699	A
1	2A	732	G
1	2A	772	G
1	2A	776	C
1	2A	811	G
1	2A	821	G
1	2A	822	G
1	2A	828	A
1	2A	830	A
1	2A	831	G
1	2A	836	C
1	2A	838	G
1	2A	851	G
1	2A	858	C
1	2A	865	A
1	2A	873	U
1	2A	874	U
1	2A	893	U
1	2A	903	C
1	2A	905	G
1	2A	913	C

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Mol	Chain	Res	Type
1	2A	915	G
1	2A	926	G
1	2A	930	C
1	2A	932	C
1	2A	933	A
1	2A	934	C
1	2A	935	C
1	2A	936	A
1	2A	938	C
1	2A	941	A
1	2A	942	C
1	2A	955	A
1	2A	960	C
1	2A	962	A
1	2A	968	C
1	2A	976	G
1	2A	982	G
1	2A	985	A
1	2A	989	A
1	2A	990	G
1	2A	1001	A
1	2A	1003	A
1	2A	1005	C
1	2A	1018	G
1	2A	1019	C
1	2A	1028	A
1	2A	1041	A
1	2A	1042	G
1	2A	1044	U
1	2A	1050	C
1	2A	1051	C
1	2A	1057	U
1	2A	1058	C
1	2A	1062	G
1	2A	1065	A
1	2A	1066	A
1	2A	1067	G
1	2A	1070	G
1	2A	1071	U
1	2A	1072	A
1	2A	1078	U
1	2A	1083	C

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Mol	Chain	Res	Type
1	2A	1084	G
1	2A	1086	C
1	2A	1088	C
1	2A	1090	A
1	2A	1091	A
1	2A	1092	G
1	2A	1096	G
1	2A	1100	G
1	2A	1103	G
1	2A	1104	G
1	2A	1105	U
1	2A	1106	U
1	2A	1107	G
1	2A	1108	G
1	2A	1110	U
1	2A	1115	A
1	2A	1116	G
1	2A	1118	A
1	2A	1120	C
1	2A	1121	C
1	2A	1126	U
1	2A	1128	U
1	2A	1131	A
1	2A	1133	A
1	2A	1142	U
1	2A	1143	A
1	2A	1149	C
1	2A	1150	U
1	2A	1156	A
1	2A	1157	G
1	2A	1158	U
1	2A	1160	G
1	2A	1161	C
1	2A	1167	G
1	2A	1175	U
1	2A	1179	C
1	2A	1180	G
1	2A	1183	G
1	2A	1187	A
1	2A	1200	A
1	2A	1216	G
1	2A	1249	U

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Mol	Chain	Res	Type
1	2A	1254	A
1	2A	1264	A
1	2A	1289	G
1	2A	1298	A
1	2A	1301	G
1	2A	1316	G
1	2A	1317	A
1	2A	1332	A
1	2A	1337	U
1	2A	1345	U
1	2A	1346	A
1	2A	1348	G
1	2A	1359	C
1	2A	1364	G
1	2A	1372	C
1	2A	1374	U
1	2A	1387	A
1	2A	1390	C
1	2A	1404	A
1	2A	1405	A
1	2A	1410	A
1	2A	1413	G
1	2A	1415	C
1	2A	1423	A
1	2A	1425	G
1	2A	1429	A
1	2A	1430	G
1	2A	1431	C
1	2A	1436	U
1	2A	1445	G
1	2A	1448	C
1	2A	1461	G
1	2A	1462	C
1	2A	1465	U
1	2A	1466	G
1	2A	1473	C
1	2A	1490	A
1	2A	1491	C
1	2A	1495	A
1	2A	1496	G
1	2A	1505	G
1	2A	1506	A

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Mol	Chain	Res	Type
1	2A	1513	C
1	2A	1517	A
1	2A	1528	G
1	2A	1534	U
1	2A	1535	A
1	2A	1538	C
1	2A	1542	U
1	2A	1554	C
1	2A	1555	A
1	2A	1570	G
1	2A	1587	G
1	2A	1588	A
1	2A	1589	C
1	2A	1590	A
1	2A	1591	A
1	2A	1604	A
1	2A	1605	G
1	2A	1612	A
1	2A	1615	A
1	2A	1624	U
1	2A	1630	C
1	2A	1631	A
1	2A	1640	G
1	2A	1652	C
1	2A	1653	A
1	2A	1654	A
1	2A	1655	A
1	2A	1663	A
1	2A	1686	C
1	2A	1694	C
1	2A	1700	A
1	2A	1715	A
1	2A	1720	G
1	2A	1721	C
1	2A	1746	A
1	2A	1765	G
1	2A	1766	A
1	2A	1767	U
1	2A	1775	G
1	2A	1786	G
1	2A	1788	G
1	2A	1792	A

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Mol	Chain	Res	Type
1	2A	1793	G
1	2A	1794	G
1	2A	1799	G
1	2A	1803	A
1	2A	1810	A
1	2A	1820	C
1	2A	1821	A
1	2A	1830	C
1	2A	1831	G
1	2A	1842	A
1	2A	1846	G
1	2A	1859	A
1	2A	1877	A
1	2A	1889	A
1	2A	1891	G
1	2A	1898	A
1	2A	1899	G
1	2A	1905	A
1	2A	1921	A
1	2A	1927	G
1	2A	1934	A
1	2A	1935	C
1	2A	1936	U
1	2A	1950	G
1	2A	1951	G
1	2A	1957	A
1	2A	1959	A
1	2A	1976	U
1	2A	1984	U
1	2A	1987	A
1	2A	1988	C
1	2A	1991	A
1	2A	1992	A
1	2A	1993	A
1	2A	2005	G
1	2A	2014	U
1	2A	2018	G
1	2A	2041	A
1	2A	2044	G
1	2A	2052	A
1	2A	2054	A
1	2A	2060	C

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Mol	Chain	Res	Type
1	2A	2064	C
1	2A	2067	G
1	2A	2073	G
1	2A	2076	C
1	2A	2077	G
1	2A	2081	A
1	2A	2082	G
1	2A	2083	A
1	2A	2090	G
1	2A	2120	U
1	2A	2125	G
1	2A	2209	C
1	2A	2213	G
1	2A	2217	C
1	2A	2219	A
1	2A	2226	G
1	2A	2227	G
1	2A	2228	A
1	2A	2236	A
1	2A	2246	G
1	2A	2250	G
1	2A	2278	A
1	2A	2280	A
1	2A	2286	C
1	2A	2289	A
1	2A	2291	G
1	2A	2294	C
1	2A	2298	A
1	2A	2300	G
1	2A	2308	C
1	2A	2316	A
1	2A	2318	G
1	2A	2319	G
1	2A	2320	A
1	2A	2328	C
1	2A	2329	G
1	2A	2330	G
1	2A	2331	A
1	2A	2332	G
1	2A	2336	G
1	2A	2345	G
1	2A	2354	C

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Mol	Chain	Res	Type
1	2A	2358	C
1	2A	2361	C
1	2A	2387	A
1	2A	2394	G
1	2A	2396	C
1	2A	2417	U
1	2A	2421	G
1	2A	2424	G
1	2A	2425	G
1	2A	2433	A
1	2A	2434	U
1	2A	2436	A
1	2A	2439	G
1	2A	2440	G
1	2A	2441	A
1	2A	2446	A
1	2A	2450	A
1	2A	2452	C
1	2A	2459	A
1	2A	2476	C
1	2A	2485	C
1	2A	2487	A
1	2A	2488	C
1	2A	2491	C
1	2A	2511	U
1	2A	2513	G
1	2A	2516	G
1	2A	2517	U
1	2A	2529	A
1	2A	2531	C
1	2A	2565	U
1	2A	2566	U
1	2A	2577	A
1	2A	2578	G
1	2A	2580	G
1	2A	2584	C
1	2A	2593	G
1	2A	2597	C
1	2A	2613	A
1	2A	2620	U
1	2A	2622	U
1	2A	2623	C

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Mol	Chain	Res	Type
1	2A	2624	U
1	2A	2626	U
1	2A	2640	A
1	2A	2641	G
1	2A	2665	A
1	2A	2674	G
1	2A	2700	U
1	2A	2701	C
1	2A	2702	C
1	2A	2713	U
1	2A	2714	C
1	2A	2724	A
1	2A	2725	A
1	2A	2738	U
1	2A	2745	A
1	2A	2758	U
1	2A	2763	G
1	2A	2776	A
1	2A	2777	A
1	2A	2778	G
1	2A	2790	A
1	2A	2801	C
1	2A	2805	G
1	2A	2806	C
1	2A	2812	G
1	2A	2814	C
1	2A	2827	G
1	2A	2829	A
1	2A	2830	A
1	2A	2842	G
1	2A	2843	G
1	2A	2844	A
1	2A	2881	G
1	2A	2889	C
1	2A	2900	A
1	2A	2902	G
1	2A	2905	U
2	2B	2	C
2	2B	7	G
2	2B	9	G
2	2B	13	A
2	2B	16	G

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Mol	Chain	Res	Type
2	2B	28	C
2	2B	32	C
2	2B	34	U
2	2B	35	U
2	2B	37	C
2	2B	43	C
2	2B	45	A
2	2B	46	A
2	2B	52	A
2	2B	56	G
2	2B	59	A
2	2B	63	G
2	2B	67	G
2	2B	73	A
2	2B	85	G
2	2B	90	A
2	2B	106	G
2	2B	110	G
2	2B	112	U
2	2B	116	G
2	2B	120	A
32	2a	6	U
32	2a	10	G
32	2a	23	G
32	2a	33	A
32	2a	39	G
32	2a	40	G
32	2a	43	G
32	2a	48	C
32	2a	49	C
32	2a	51	A
32	2a	52	A
32	2a	53	G
32	2a	66	U
32	2a	67	G
32	2a	84	A
32	2a	85	C
32	2a	91	G
32	2a	95	A
32	2a	110	A
32	2a	115	C
32	2a	124	G

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Mol	Chain	Res	Type
32	2a	126	C
32	2a	137	G
32	2a	138	A
32	2a	158	C
32	2a	169	C
32	2a	177	U
32	2a	189	U
32	2a	190	U
32	2a	202	A
32	2a	210	U
32	2a	211	U
32	2a	212	G
32	2a	216	G
32	2a	243	G
32	2a	247	G
32	2a	262	G
32	2a	263	C
32	2a	275	A
32	2a	277	G
32	2a	285	G
32	2a	302	G
32	2a	317	A
32	2a	324	C
32	2a	326	C
32	2a	328	G
32	2a	337	C
32	2a	340	A
32	2a	346	G
32	2a	347	G
32	2a	348	C
32	2a	349	A
32	2a	350	G
32	2a	363	U
32	2a	368	C
32	2a	380	G
32	2a	394	C
32	2a	402	G
32	2a	408	A
32	2a	418	C
32	2a	425	U
32	2a	426	A
32	2a	428	A

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Mol	Chain	Res	Type
32	2a	435	A
32	2a	437	C
32	2a	447	A
32	2a	452	C
32	2a	455	A
32	2a	456	C
32	2a	457	G
32	2a	463	A
32	2a	468	C
32	2a	470	G
32	2a	481	A
32	2a	482	U
32	2a	489	G
32	2a	490	G
32	2a	493	A
32	2a	494	A
32	2a	495	C
32	2a	501	G
32	2a	502	C
32	2a	505	G
32	2a	511	G
32	2a	515	U
32	2a	516	A
32	2a	517	A
32	2a	520	C
32	2a	529	C
32	2a	531	A
32	2a	543	A
32	2a	544	U
32	2a	545	U
32	2a	546	C
32	2a	548	C
32	2a	552	G
32	2a	556	A
32	2a	557	A
32	2a	560	G
32	2a	561	G
32	2a	580	C
32	2a	614	G
32	2a	634	G
32	2a	636	U
32	2a	637	A

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Mol	Chain	Res	Type
32	2a	649	A
32	2a	671	A
32	2a	672	G
32	2a	677	G
32	2a	679	A
32	2a	692	C
32	2a	696	A
32	2a	707	U
32	2a	708	G
32	2a	712	A
32	2a	715	G
32	2a	733	C
32	2a	737	A
32	2a	739	G
32	2a	744	G
32	2a	761	A
32	2a	772	U
32	2a	777	U
32	2a	778	A
32	2a	799	A
32	2a	800	A
32	2a	801	C
32	2a	805	G
32	2a	812	A
32	2a	813	G
32	2a	820	G
32	2a	822	G
32	2a	823	U
32	2a	824	C
32	2a	825	U
32	2a	826	C
32	2a	828	U
32	2a	837	A
32	2a	850	A
32	2a	852	G
32	2a	880	G
32	2a	892	A
32	2a	893	A
32	2a	898	U
32	2a	904	G
32	2a	905	G
32	2a	908	C

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Mol	Chain	Res	Type
32	2a	909	C
32	2a	912	C
32	2a	913	A
32	2a	920	G
32	2a	939	U
32	2a	944	G
32	2a	946	A
32	2a	947	A
32	2a	949	G
32	2a	952	A
32	2a	953	A
32	2a	954	G
32	2a	955	A
32	2a	966	G
32	2a	967	C
32	2a	970	U
32	2a	971	G
32	2a	977	C
32	2a	979	A
32	2a	981	G
32	2a	984	A
32	2a	988	G
32	2a	1000	G
32	2a	1001	G
32	2a	1002	G
32	2a	1028	C
32	2a	1029	A
32	2a	1036	G
32	2a	1037	C
32	2a	1038	A
32	2a	1039	U
32	2a	1048	U
32	2a	1049	C
32	2a	1050	A
32	2a	1061	U
32	2a	1064	G
32	2a	1071	G
32	2a	1077	G
32	2a	1078	U
32	2a	1083	C
32	2a	1084	A
32	2a	1096	C

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Mol	Chain	Res	Type
32	2a	1100	G
32	2a	1101	C
32	2a	1105	U
32	2a	1107	G
32	2a	1110	G
32	2a	1112	C
32	2a	1113	A
32	2a	1117	G
32	2a	1118	U
32	2a	1119	U
32	2a	1120	C
32	2a	1121	G
32	2a	1122	G
32	2a	1123	C
32	2a	1129	A
32	2a	1140	A
32	2a	1141	C
32	2a	1142	U
32	2a	1149	G
32	2a	1165	A
32	2a	1172	G
32	2a	1178	U
32	2a	1179	G
32	2a	1184	G
32	2a	1191	C
32	2a	1193	U
32	2a	1194	U
32	2a	1196	C
32	2a	1210	C
32	2a	1220	A
32	2a	1222	U
32	2a	1223	G
32	2a	1235	G
32	2a	1236	C
32	2a	1239	U
32	2a	1240	G
32	2a	1242	C
32	2a	1244	C
32	2a	1255	G
32	2a	1260	U
32	2a	1262	A
32	2a	1263	U

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Mol	Chain	Res	Type
32	2a	1264	C
32	2a	1267	A
32	2a	1268	A
32	2a	1269	A
32	2a	1280	C
32	2a	1281	A
32	2a	1282	G
32	2a	1284	U
32	2a	1285	C
32	2a	1287	G
32	2a	1304	C
32	2a	1305	G
32	2a	1320	G
32	2a	1328	A
32	2a	1329	G
32	2a	1335	G
32	2a	1341	C
32	2a	1342	A
32	2a	1345	C
32	2a	1347	U
32	2a	1351	G
32	2a	1367	C
32	2a	1380	C
32	2a	1381	A
32	2a	1388	G
32	2a	1399	G
32	2a	1402	G
32	2a	1425	G
32	2a	1426	G
32	2a	1427	A
32	2a	1431	U
32	2a	1432	A
32	2a	1433	C
32	2a	1434	G
32	2a	1465	G
32	2a	1475	G
32	2a	1480	A
32	2a	1481	A
32	2a	1482	G
32	2a	1484	U
32	2a	1485	A
32	2a	1495	G

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Mol	Chain	Res	Type
32	2a	1498	G
32	2a	1507	G
32	2a	1508	G
32	2a	1509	A
32	2a	1510	U
53	2v	15	A
54	2x	6	G
54	2x	8	4SU
54	2x	9	G
54	2x	13	C
54	2x	16	C
54	2x	17	C
54	2x	17(A)	U
54	2x	19	G
54	2x	20	U
54	2x	21	A
54	2x	42	G
54	2x	47	U
54	2x	50	U
54	2x	56	C
54	2x	61	C
54	2x	65	C
54	2x	70	G
54	2x	76	A

All (47) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	183	A
1	1A	184	A
1	1A	187	A
1	1A	270	U
1	1A	301	A
1	1A	715	G
1	1A	792	A
1	1A	810	A
1	1A	1002	U
1	1A	1018	G
1	1A	1153	U
1	1A	1220	G
1	1A	1285	U
1	1A	1425	G

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Mol	Chain	Res	Type
1	1A	1465	U
1	1A	1653	A
1	1A	1709	C
1	1A	2013	G
1	1A	2417	U
1	1A	2433	A
1	1A	2441	A
1	1A	2700	U
1	2A	11	U
1	2A	183	A
1	2A	184	A
1	2A	300	C
1	2A	516	A
1	2A	670	A
1	2A	810	A
1	2A	902	C
1	2A	1047	G
1	2A	1071	U
1	2A	1102	A
1	2A	1114	A
1	2A	1238	A
1	2A	1424	A
1	2A	1465	U
1	2A	1604	A
1	2A	1820	C
1	2A	1934	A
1	2A	2013	G
1	2A	2328	C
1	2A	2353	C
1	2A	2450	A
1	2A	2700	U
2	2B	42	C
2	2B	45	A

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

8 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	$\# Z > 2$
54	5MC	1x	32	54	14,22,23	1.35	1 (7%)	17,32,35	0.96	1 (5%)
54	5MU	1x	54	54	13,22,23	0.59	0	16,32,35	2.87	2 (12%)
54	PSU	1x	55	54,56	15,21,22	1.43	1 (6%)	16,30,33	2.31	4 (25%)
54	4SU	1x	8	54	12,21,22	1.03	1 (8%)	15,30,33	1.51	1 (6%)
54	5MC	2x	32	54	14,22,23	1.27	1 (7%)	17,32,35	0.96	1 (5%)
54	5MU	2x	54	54	13,22,23	0.55	0	16,32,35	2.63	2 (12%)
54	PSU	2x	55	54	15,21,22	1.32	1 (6%)	16,30,33	2.32	4 (25%)
54	4SU	2x	8	54	12,21,22	0.71	1 (8%)	15,30,33	1.63	1 (6%)

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
54	5MC	1x	32	54	-	0/3/25/26	0/2/2/2
54	5MU	1x	54	54	-	0/3/25/26	0/2/2/2
54	PSU	1x	55	54,56	-	0/7/25/26	0/2/2/2
54	4SU	1x	8	54	-	0/3/25/26	0/2/2/2
54	5MC	2x	32	54	-	0/3/25/26	0/2/2/2
54	5MU	2x	54	54	-	0/3/25/26	0/2/2/2
54	PSU	2x	55	54	-	0/7/25/26	0/2/2/2
54	4SU	2x	8	54	-	0/3/25/26	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	1x	55	PSU	C5-C1'	-4.47	1.48	1.52
54	2x	55	PSU	C5-C1'	-4.18	1.48	1.52
54	1x	8	4SU	C2-N3	-3.30	1.31	1.38
54	2x	8	4SU	C2-N3	-2.04	1.33	1.38
54	2x	32	5MC	C5-C4	4.48	1.48	1.41
54	1x	32	5MC	C5-C4	4.78	1.48	1.41

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	1x	54	5MU	C5-C4-N3	-8.03	118.61	125.35
54	2x	54	5MU	C5-C4-N3	-7.69	118.89	125.35
54	2x	8	4SU	C5-C4-N3	-5.77	117.45	123.56
54	1x	8	4SU	C5-C4-N3	-5.42	117.81	123.56
54	2x	55	PSU	C5-C6-N1	-3.99	118.82	124.38
54	1x	55	PSU	C5-C1'-C2'	-3.48	109.52	115.44
54	2x	55	PSU	C5-C1'-C2'	-3.35	109.74	115.44
54	1x	55	PSU	C5-C6-N1	-3.27	119.83	124.38
54	1x	32	5MC	N4-C4-N3	2.19	120.13	116.92
54	2x	32	5MC	N4-C4-N3	2.24	120.21	116.92
54	1x	55	PSU	O4'-C1'-C2'	2.48	107.37	104.69
54	2x	55	PSU	O4'-C1'-C2'	2.74	107.66	104.69
54	2x	55	PSU	C4-N3-C2	6.75	120.79	115.16
54	2x	54	5MU	C4-N3-C2	6.81	120.83	115.16
54	1x	55	PSU	C4-N3-C2	7.11	121.09	115.16
54	1x	54	5MU	C4-N3-C2	7.83	121.69	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2615 ligands modelled in this entry, 2613 are monoatomic - leaving 2 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	$\# Z > 2$
58	SF4	1d	501	35	0,12,12	0.00	-	0,24,24	0.00	-
58	SF4	2d	501	35	0,12,12	0.00	-	0,24,24	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
58	SF4	1d	501	35	-	0/0/48/48	0/6/5/5
58	SF4	2d	501	35	-	0/0/48/48	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

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	1A	2746/2915 (94%)	-0.15	31 (1%) 82 83	20, 40, 84, 109	0
1	2A	2790/2915 (95%)	-0.50	81 (2%) 55 55	24, 44, 91, 107	0
2	1B	120/121 (99%)	-0.29	0 100 100	34, 63, 78, 92	0
2	2B	120/121 (99%)	-0.07	3 (2%) 61 61	40, 69, 80, 94	0
3	1D	275/276 (99%)	-0.08	0 100 100	19, 39, 57, 76	0
3	2D	275/276 (99%)	-0.21	2 (0%) 89 90	20, 41, 59, 76	0
4	1E	204/206 (99%)	-0.01	0 100 100	19, 42, 63, 80	0
4	2E	204/206 (99%)	-0.13	1 (0%) 91 93	22, 45, 65, 81	0
5	1F	203/210 (96%)	0.06	0 100 100	19, 48, 74, 86	0
5	2F	203/210 (96%)	-0.09	2 (0%) 84 85	22, 52, 76, 88	0
6	1G	181/182 (99%)	0.06	5 (2%) 56 57	53, 69, 81, 95	0
6	2G	181/182 (99%)	0.82	23 (12%) 5 4	58, 72, 83, 97	0
7	1H	174/180 (96%)	0.11	1 (0%) 90 91	45, 63, 75, 85	0
7	2H	174/180 (96%)	1.25	41 (23%) 1 1	53, 68, 78, 86	0
8	1I	146/148 (98%)	0.39	3 (2%) 67 68	48, 74, 83, 89	0
8	2I	146/148 (98%)	0.79	23 (15%) 3 2	50, 75, 83, 87	0
9	1N	140/140 (100%)	0.02	0 100 100	28, 44, 65, 78	0
9	2N	140/140 (100%)	0.14	3 (2%) 67 68	31, 49, 68, 79	0
10	1O	122/122 (100%)	-0.03	1 (0%) 87 88	30, 42, 61, 66	0
10	2O	122/122 (100%)	-0.23	0 100 100	33, 46, 62, 67	0
11	1P	149/150 (99%)	0.15	0 100 100	21, 53, 74, 86	0
11	2P	149/150 (99%)	0.47	9 (6%) 25 24	24, 56, 75, 84	0
12	1Q	141/141 (100%)	0.21	2 (1%) 78 77	33, 47, 63, 80	0
12	2Q	141/141 (100%)	-0.13	2 (1%) 78 77	36, 51, 66, 79	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	0.08	0 100 100	27, 38, 54, 60	0
13	2R	118/118 (100%)	-0.19	0 100 100	29, 40, 56, 61	0
14	1S	110/112 (98%)	-0.08	0 100 100	33, 50, 63, 71	0
14	2S	110/112 (98%)	0.98	16 (14%) 3 2	44, 77, 85, 92	0
15	1T	131/146 (89%)	-0.16	1 (0%) 87 88	27, 40, 70, 83	0
15	2T	131/146 (89%)	-0.06	1 (0%) 87 88	43, 56, 77, 87	0
16	1U	116/118 (98%)	0.14	0 100 100	21, 35, 54, 71	0
16	2U	116/118 (98%)	-0.03	4 (3%) 49 49	28, 41, 59, 72	0
17	1V	101/101 (100%)	-0.04	1 (0%) 84 85	25, 47, 65, 79	0
17	2V	101/101 (100%)	0.27	3 (2%) 54 54	29, 52, 70, 79	0
18	1W	112/113 (99%)	-0.06	1 (0%) 85 86	25, 33, 56, 86	0
18	2W	112/113 (99%)	-0.22	1 (0%) 85 86	27, 37, 57, 88	0
19	1X	95/96 (98%)	0.08	1 (1%) 82 83	30, 45, 65, 77	0
19	2X	95/96 (98%)	0.18	4 (4%) 40 39	34, 49, 67, 78	0
20	1Y	107/110 (97%)	0.19	1 (0%) 85 86	39, 57, 74, 84	0
20	2Y	107/110 (97%)	0.71	11 (10%) 9 6	44, 60, 76, 86	0
21	1Z	186/206 (90%)	-0.08	0 100 100	48, 67, 80, 87	0
21	2Z	186/206 (90%)	0.79	20 (10%) 8 6	53, 70, 81, 89	0
22	10	75/85 (88%)	0.06	0 100 100	28, 45, 60, 67	0
22	20	75/85 (88%)	0.44	5 (6%) 21 19	31, 50, 63, 70	0
23	11	97/98 (98%)	0.07	1 (1%) 84 85	28, 47, 73, 80	0
23	21	97/98 (98%)	0.09	2 (2%) 67 68	31, 49, 73, 79	0
24	12	70/72 (97%)	0.22	1 (1%) 78 77	43, 55, 69, 78	0
24	22	70/72 (97%)	0.23	4 (5%) 27 26	46, 59, 71, 77	0
25	13	59/60 (98%)	0.08	0 100 100	29, 42, 62, 73	0
25	23	59/60 (98%)	0.79	8 (13%) 4 3	34, 47, 66, 79	0
26	14	69/71 (97%)	0.48	11 (15%) 3 2	60, 81, 93, 96	0
26	24	69/71 (97%)	1.17	16 (23%) 1 1	68, 83, 95, 101	0
27	15	59/60 (98%)	-0.02	1 (1%) 73 74	19, 36, 52, 71	0
27	25	59/60 (98%)	-0.12	1 (1%) 73 74	23, 38, 56, 72	0
28	16	53/54 (98%)	-0.09	0 100 100	37, 48, 65, 69	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	26	53/54 (98%)	-0.04	0 100 100	38, 51, 61, 69	0
29	17	48/49 (97%)	0.08	1 (2%) 67 68	24, 30, 63, 75	0
29	27	48/49 (97%)	0.12	3 (6%) 23 22	26, 32, 66, 75	0
30	18	64/65 (98%)	0.10	0 100 100	30, 39, 50, 58	0
30	28	64/65 (98%)	0.18	1 (1%) 74 75	33, 42, 54, 59	0
31	19	37/37 (100%)	0.41	1 (2%) 58 58	38, 48, 65, 67	0
31	29	37/37 (100%)	0.51	4 (10%) 8 6	42, 52, 66, 71	0
32	1a	1477/1521 (97%)	-0.19	43 (2%) 55 55	29, 71, 95, 112	0
32	2a	1483/1521 (97%)	-0.06	61 (4%) 41 41	43, 77, 98, 110	0
33	1b	231/256 (90%)	0.72	32 (13%) 4 3	65, 81, 91, 101	0
33	2b	231/256 (90%)	1.14	46 (19%) 1 1	67, 86, 94, 102	0
34	1c	206/239 (86%)	0.71	26 (12%) 5 4	66, 82, 89, 95	0
34	2c	206/239 (86%)	1.04	37 (17%) 2 1	66, 83, 90, 96	0
35	1d	208/209 (99%)	0.42	15 (7%) 18 16	57, 76, 87, 95	0
35	2d	208/209 (99%)	0.27	5 (2%) 62 62	58, 73, 84, 89	0
36	1e	148/162 (91%)	0.04	1 (0%) 89 90	43, 66, 77, 86	0
36	2e	148/162 (91%)	0.18	5 (3%) 49 49	60, 74, 84, 91	0
37	1f	100/101 (99%)	0.01	1 (1%) 84 85	57, 72, 81, 84	0
37	2f	100/101 (99%)	0.00	2 (2%) 68 69	61, 74, 82, 87	0
38	1g	155/156 (99%)	0.65	19 (12%) 5 4	60, 74, 89, 97	0
38	2g	155/156 (99%)	1.26	30 (19%) 1 1	70, 83, 91, 96	0
39	1h	137/138 (99%)	0.17	0 100 100	49, 66, 76, 78	0
39	2h	137/138 (99%)	0.66	11 (8%) 15 13	62, 75, 82, 88	0
40	1i	127/128 (99%)	1.00	15 (11%) 6 5	60, 80, 90, 94	0
40	2i	127/128 (99%)	1.89	45 (35%) 0 0	69, 89, 96, 102	0
41	1j	97/105 (92%)	1.17	22 (22%) 1 1	61, 85, 93, 97	0
41	2j	96/105 (91%)	1.58	34 (35%) 0 0	76, 89, 97, 102	0
42	1k	114/129 (88%)	0.10	2 (1%) 71 72	40, 67, 79, 92	0
42	2k	114/129 (88%)	0.52	7 (6%) 25 23	52, 76, 85, 90	0
43	1l	122/132 (92%)	0.08	1 (0%) 87 88	42, 62, 72, 81	0
43	2l	122/132 (92%)	0.20	3 (2%) 61 61	55, 67, 77, 83	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	118/126 (93%)	0.35	4 (3%) 49 49	66, 79, 85, 91	0
44	2m	116/126 (92%)	0.96	21 (18%) 2 1	69, 81, 87, 92	0
45	1n	60/61 (98%)	0.82	9 (15%) 3 2	69, 81, 86, 92	0
45	2n	60/61 (98%)	1.71	22 (36%) 0 0	71, 82, 87, 92	0
46	1o	88/89 (98%)	0.28	3 (3%) 49 49	47, 64, 78, 85	0
46	2o	88/89 (98%)	0.51	6 (6%) 20 19	59, 71, 82, 89	0
47	1p	82/88 (93%)	0.89	9 (10%) 7 5	61, 77, 87, 93	0
47	2p	82/88 (93%)	0.60	4 (4%) 33 32	60, 70, 82, 89	0
48	1q	99/105 (94%)	0.28	2 (2%) 68 69	45, 65, 76, 78	0
48	2q	99/105 (94%)	0.42	8 (8%) 15 12	53, 71, 80, 86	0
49	1r	68/88 (77%)	0.59	9 (13%) 4 4	53, 68, 81, 87	0
49	2r	68/88 (77%)	1.07	16 (23%) 1 1	62, 74, 82, 90	0
50	1s	84/93 (90%)	0.92	12 (14%) 4 3	66, 80, 91, 94	0
50	2s	83/93 (89%)	2.21	43 (51%) 0 0	77, 90, 98, 104	0
51	1t	96/106 (90%)	0.68	7 (7%) 18 16	56, 73, 82, 88	0
51	2t	96/106 (90%)	0.59	5 (5%) 31 30	55, 72, 82, 86	0
52	1u	23/27 (85%)	0.85	2 (8%) 13 10	69, 75, 80, 81	0
52	2u	23/27 (85%)	1.84	10 (43%) 0 0	68, 78, 82, 82	0
53	1v	5/24 (20%)	0.49	0 100 100	61, 64, 86, 94	0
53	2v	5/24 (20%)	1.62	2 (40%) 0 0	65, 67, 86, 94	0
54	1x	72/77 (93%)	-0.16	1 (1%) 78 77	37, 67, 85, 95	0
54	2x	72/77 (93%)	0.21	1 (1%) 78 77	39, 71, 87, 97	0
55	1z	16/20 (80%)	0.72	1 (6%) 23 22	30, 49, 74, 79	0
55	2z	16/20 (80%)	0.89	5 (31%) 1 0	32, 52, 76, 77	0
All	All	20528/21484 (95%)	0.11	1023 (4%) 32 31	19, 61, 90, 112	0

All (1023) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
32	1a	980	G	9.4
38	2g	83	ALA	8.5
32	1a	981	G	8.4
40	2i	15	ALA	7.9
32	2a	979	A	7.8

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Mol	Chain	Res	Type	RSRZ
32	2a	980	G	7.7
32	2a	981	G	7.7
32	1a	979	A	7.4
38	2g	82	GLY	7.3
34	2c	155	GLY	7.1
1	2A	2812	G	7.0
50	2s	12	ASP	6.3
38	1g	79	ARG	6.2
40	2i	21	PRO	6.1
38	2g	156	TRP	6.1
40	2i	61	ALA	6.1
26	24	45	GLY	6.1
7	2H	111	HIS	6.0
38	2g	78	ARG	6.0
1	2A	2813	C	6.0
6	2G	19	LEU	5.9
32	1a	211	U	5.9
32	2a	1510	U	5.9
32	1a	982	G	5.8
34	2c	189	ALA	5.8
20	2Y	1	MET	5.7
40	2i	30	GLY	5.7
32	1a	978	U	5.6
50	2s	80	TYR	5.6
38	1g	156	TRP	5.6
26	24	68	ARG	5.6
33	1b	227	GLY	5.5
40	2i	9	ARG	5.5
40	2i	66	ARG	5.5
38	1g	78	ARG	5.4
20	1Y	1	MET	5.4
41	1j	85	LEU	5.4
1	1A	2815	G	5.4
38	1g	80	VAL	5.4
33	2b	131	PRO	5.3
38	2g	80	VAL	5.3
32	1a	1023	U	5.2
34	2c	145	GLY	5.2
45	2n	25	VAL	5.2
41	2j	26	ALA	5.2
1	2A	1128	U	5.2
40	1i	15	ALA	5.2

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Mol	Chain	Res	Type	RSRZ
1	1A	1554	C	5.2
38	2g	84	ASN	5.1
50	2s	31	ILE	5.1
40	2i	62	TYR	5.0
32	2a	1509	A	5.0
1	2A	2805	G	5.0
40	2i	36	TYR	5.0
40	2i	76	ALA	4.9
1	2A	678	A	4.9
50	2s	24	ALA	4.9
7	2H	101	ARG	4.9
40	2i	7	THR	4.9
34	2c	186	PHE	4.8
7	2H	112	PRO	4.8
50	2s	49	ILE	4.8
26	24	49	PHE	4.8
7	2H	95	ARG	4.8
38	2g	79	ARG	4.8
38	1g	84	ASN	4.8
50	2s	20	LEU	4.8
38	1g	81	GLY	4.7
41	2j	72	VAL	4.7
34	2c	39	ILE	4.7
32	2a	982	G	4.6
32	2a	1239	U	4.6
32	2a	1024	A	4.6
7	2H	103	LEU	4.6
6	2G	48	GLU	4.6
41	1j	98	ILE	4.6
1	2A	2811	A	4.6
1	2A	2904	C	4.6
1	2A	2815	G	4.5
32	2a	1268	A	4.5
51	1t	55	ILE	4.5
33	2b	70	PHE	4.5
52	2u	14	TRP	4.5
40	2i	20	ARG	4.5
1	2A	1091	A	4.5
51	1t	69	GLY	4.5
33	1b	228	GLY	4.5
50	2s	41	VAL	4.5
41	2j	18	ALA	4.4

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Mol	Chain	Res	Type	RSRZ
34	2c	159	GLY	4.4
26	24	67	TYR	4.4
44	2m	78	ILE	4.4
14	2S	34	HIS	4.4
7	2H	102	ALA	4.4
41	2j	6	ILE	4.4
1	2A	2816	G	4.4
32	2a	1025	G	4.4
1	2A	1149	C	4.4
12	1Q	59	ARG	4.3
1	1A	2813	C	4.3
1	1A	2905	U	4.3
1	2A	1130	A	4.3
44	1m	2	ALA	4.3
49	2r	46	GLU	4.3
38	1g	83	ALA	4.3
49	2r	66	LEU	4.3
32	2a	1000	G	4.3
38	2g	154	TYR	4.3
38	2g	16	LEU	4.2
50	2s	8	GLY	4.2
50	1s	40	ILE	4.2
55	2z	16	ILE	4.2
1	2A	1132	G	4.2
41	2j	75	ILE	4.2
40	1i	19	LEU	4.2
14	2S	58	LEU	4.2
21	2Z	5	LEU	4.2
33	2b	152	PHE	4.2
1	2A	217	A	4.2
32	1a	1024	A	4.2
34	2c	124	ILE	4.2
39	2h	96	GLY	4.2
45	2n	39	LEU	4.2
7	2H	114	VAL	4.1
34	2c	154	SER	4.1
44	2m	95	GLY	4.1
1	2A	1129	A	4.1
41	1j	18	ALA	4.1
44	2m	75	ALA	4.1
33	2b	31	TYR	4.1
1	2A	2814	C	4.1

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Mol	Chain	Res	Type	RSRZ
33	2b	101	MET	4.1
33	2b	187	LEU	4.1
47	1p	39	TYR	4.1
33	2b	165	VAL	4.1
50	2s	76	PRO	4.1
34	2c	180	ALA	4.1
38	1g	153	HIS	4.0
40	2i	8	GLY	4.0
46	1o	20	GLY	4.0
40	1i	33	PHE	4.0
40	2i	5	TYR	4.0
41	2j	85	LEU	4.0
47	1p	19	ILE	4.0
50	2s	11	VAL	4.0
40	2i	67	GLY	4.0
19	2X	68	ARG	4.0
38	2g	81	GLY	4.0
29	17	48	LYS	4.0
1	2A	1131	A	4.0
49	1r	24	ALA	4.0
34	2c	13	GLY	3.9
21	2Z	96	VAL	3.9
26	24	66	SER	3.9
53	2v	14	A	3.9
7	2H	115	VAL	3.9
1	1A	2206	C	3.9
1	1A	2814	C	3.9
49	2r	85	LEU	3.9
36	1e	22	GLY	3.9
41	1j	10	GLY	3.9
1	1A	1220	G	3.9
32	1a	977	C	3.9
47	2p	19	ILE	3.9
6	2G	86	MET	3.9
22	20	76	GLY	3.9
50	2s	42	PRO	3.8
33	2b	93	VAL	3.8
33	2b	232	PRO	3.8
1	2A	1554	C	3.8
7	2H	106	THR	3.8
45	2n	38	GLY	3.8
39	2h	122	ARG	3.8

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Mol	Chain	Res	Type	RSRZ
40	1i	90	PRO	3.8
40	1i	106	ALA	3.8
34	1c	193	TYR	3.7
1	1A	1098	C	3.7
32	1a	1022	C	3.7
33	2b	37	ASN	3.7
21	2Z	64	GLY	3.7
35	2d	146	ILE	3.7
33	1b	136	VAL	3.7
33	1b	124	SER	3.7
33	2b	227	GLY	3.7
45	2n	37	PHE	3.7
19	2X	92	LEU	3.7
40	2i	99	LEU	3.7
6	2G	25	TYR	3.7
41	1j	4	ILE	3.7
44	2m	60	VAL	3.7
33	2b	97	TRP	3.7
26	14	57	GLU	3.7
50	2s	52	TYR	3.7
50	2s	53	ASN	3.7
52	2u	6	ARG	3.7
34	1c	78	GLY	3.7
14	2S	12	PHE	3.7
25	23	60	GLU	3.7
45	2n	8	GLU	3.7
41	2j	63	PHE	3.6
7	2H	97	ARG	3.6
1	2A	2902	G	3.6
33	2b	132	LYS	3.6
11	2P	91	PHE	3.6
32	2a	1265	G	3.6
32	1a	1026	C	3.6
32	1a	1120	C	3.6
41	2j	74	ILE	3.6
1	2A	1135	U	3.6
7	2H	105	LEU	3.6
32	1a	212	G	3.6
32	2a	985	C	3.6
45	2n	34	TYR	3.6
50	2s	16	LEU	3.6
1	2A	2121	G	3.6

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Mol	Chain	Res	Type	RSRZ
1	1A	2904	C	3.6
14	2S	54	LEU	3.6
34	1c	207	VAL	3.5
1	1A	2205	G	3.5
1	2A	2806	C	3.5
32	2a	1021	C	3.5
38	1g	82	GLY	3.5
38	2g	85	TYR	3.5
1	1A	2811	A	3.5
50	2s	50	ALA	3.5
32	1a	999	U	3.5
14	2S	20	ARG	3.5
33	2b	197	VAL	3.5
40	2i	14	VAL	3.5
50	2s	45	VAL	3.5
32	2a	1026	C	3.5
40	2i	79	LEU	3.5
41	2j	20	ALA	3.5
49	2r	58	LEU	3.5
45	2n	49	HIS	3.5
54	2x	47	U	3.4
27	25	60	VAL	3.4
32	2a	1022	C	3.4
42	2k	13	GLN	3.4
6	1G	51	ARG	3.4
32	1a	1121	G	3.4
33	2b	201	ILE	3.4
41	1j	6	ILE	3.4
50	2s	40	ILE	3.4
7	2H	166	GLY	3.4
32	2a	707	U	3.4
8	2I	77	LEU	3.4
7	2H	13	LYS	3.4
31	29	16	VAL	3.4
40	2i	45	ALA	3.4
34	2c	87	LEU	3.4
32	2a	984	A	3.4
7	2H	113	VAL	3.4
20	2Y	51	VAL	3.4
32	2a	986	C	3.4
26	14	50	VAL	3.4
33	2b	162	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
36	2e	109	ILE	3.3
1	2A	2905	U	3.3
35	1d	175	SER	3.3
32	2a	978	U	3.3
34	2c	146	ALA	3.3
38	2g	86	GLN	3.3
41	1j	97	GLU	3.3
45	1n	15	LYS	3.3
41	2j	68	HIS	3.3
31	29	13	LYS	3.3
33	1b	36	ARG	3.3
34	1c	80	GLY	3.3
32	1a	825	U	3.3
40	2i	88	TYR	3.3
33	2b	150	SER	3.3
1	1A	2805	G	3.3
1	2A	1089	G	3.3
32	2a	212	G	3.3
38	2g	155	ARG	3.3
55	2z	14	ARG	3.3
40	2i	6	GLY	3.3
44	2m	6	GLY	3.3
44	2m	42	ALA	3.3
1	2A	1105	U	3.3
1	2A	1106	U	3.3
1	2A	1127	U	3.3
34	2c	143	GLU	3.3
33	2b	122	PHE	3.3
45	2n	30	ALA	3.3
40	1i	102	LEU	3.3
50	2s	23	ASN	3.3
40	2i	33	PHE	3.3
50	2s	26	GLY	3.3
52	2u	16	GLY	3.3
33	2b	29	ALA	3.3
32	2a	999	U	3.2
50	2s	6	LYS	3.2
1	2A	1104	G	3.2
32	1a	1000	G	3.2
32	2a	998	C	3.2
32	2a	1001	G	3.2
33	2b	133	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
23	21	22	GLY	3.2
26	24	52	THR	3.2
33	1b	114	ARG	3.2
26	14	59	PHE	3.2
32	2a	983	A	3.2
38	2g	2	ALA	3.2
32	1a	1025	G	3.2
1	2A	946	A	3.2
41	2j	27	ALA	3.2
6	2G	17	PRO	3.2
1	1A	2806	C	3.2
1	2A	2206	C	3.2
1	2A	1134	G	3.2
26	24	44	THR	3.2
49	2r	24	ALA	3.2
33	1b	28	PHE	3.2
32	1a	72	C	3.1
39	2h	131	GLY	3.1
1	2A	2125	G	3.1
21	2Z	62	PRO	3.1
41	2j	87	THR	3.1
45	1n	13	THR	3.1
1	1A	2209	C	3.1
26	14	66	SER	3.1
34	1c	87	LEU	3.1
34	1c	206	GLU	3.1
7	2H	48	GLY	3.1
49	2r	57	GLY	3.1
39	2h	95	VAL	3.1
1	2A	2804	G	3.1
11	2P	93	GLY	3.1
1	2A	2903	U	3.1
1	1A	934	C	3.1
1	2A	669	C	3.1
1	2A	680	C	3.1
32	1a	87	C	3.1
32	2a	1266	C	3.1
49	2r	43	PHE	3.1
35	1d	180	GLY	3.1
34	1c	201	TYR	3.1
52	1u	15	ARG	3.1
34	1c	81	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
39	2h	128	GLY	3.1
38	1g	17	VAL	3.1
7	2H	88	LEU	3.1
45	2n	47	LEU	3.1
12	1Q	60	ARG	3.1
32	1a	707	U	3.1
8	2I	107	VAL	3.1
33	2b	123	ALA	3.1
46	1o	87	ILE	3.1
32	1a	1239	U	3.0
40	2i	27	THR	3.0
1	1A	2804	G	3.0
14	2S	31	SER	3.0
33	1b	41	ILE	3.0
26	24	63	TYR	3.0
7	2H	123	PHE	3.0
7	2H	107	VAL	3.0
1	1A	2208	G	3.0
35	2d	148	VAL	3.0
45	2n	29	ARG	3.0
52	2u	15	ARG	3.0
7	2H	96	ALA	3.0
1	2A	697	G	3.0
1	2A	934	C	3.0
33	1b	101	MET	3.0
22	20	75	LEU	3.0
33	1b	207	ALA	3.0
34	1c	65	ALA	3.0
7	2H	128	PRO	3.0
50	2s	43	GLU	3.0
34	1c	184	TYR	3.0
32	2a	1132	C	3.0
20	2Y	90	LEU	3.0
44	2m	72	ALA	3.0
44	2m	76	ALA	3.0
55	2z	15	PRO	3.0
6	2G	152	LEU	3.0
33	2b	118	LEU	3.0
1	1A	695	C	3.0
1	1A	1149	C	3.0
32	1a	985	C	3.0
26	14	55	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
29	27	47	ARG	3.0
35	1d	170	VAL	3.0
32	1a	208	C	2.9
32	2a	1002	G	2.9
32	1a	983	A	2.9
33	2b	92	TYR	2.9
34	1c	2	GLY	2.9
33	2b	177	ALA	2.9
34	1c	39	ILE	2.9
40	2i	105	ASP	2.9
50	2s	64	GLU	2.9
1	1A	2812	G	2.9
38	2g	151	TYR	2.9
50	2s	48	THR	2.9
20	2Y	5	MET	2.9
32	1a	1027	A	2.9
8	2I	14	ASP	2.9
40	2i	91	ASP	2.9
47	2p	36	ILE	2.9
38	2g	62	PHE	2.9
40	2i	37	PHE	2.9
14	2S	53	SER	2.9
19	2X	67	GLY	2.9
49	1r	31	LEU	2.9
40	1i	98	PRO	2.9
44	2m	64	TRP	2.9
20	2Y	41	GLY	2.9
33	2b	228	GLY	2.9
6	2G	139	LEU	2.9
50	2s	71	LEU	2.9
52	2u	17	THR	2.9
33	2b	88	ALA	2.9
32	2a	1023	U	2.9
41	1j	5	ARG	2.9
6	2G	138	GLN	2.9
41	2j	19	SER	2.9
7	2H	94	TYR	2.9
8	2I	11	ASN	2.9
33	1b	62	ALA	2.9
33	1b	222	ILE	2.8
41	2j	71	LEU	2.8
8	2I	86	THR	2.8

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Mol	Chain	Res	Type	RSRZ
38	2g	5	ARG	2.8
25	23	47	VAL	2.8
47	1p	21	VAL	2.8
1	1A	2207	G	2.8
1	2A	1136	G	2.8
16	2U	88	ILE	2.8
33	1b	132	LYS	2.8
45	1n	2	ALA	2.8
32	1a	209	U	2.8
33	1b	122	PHE	2.8
32	1a	1268	A	2.8
49	2r	56	THR	2.8
50	1s	64	GLU	2.8
11	2P	122	PRO	2.8
31	29	37	GLY	2.8
20	2Y	91	GLU	2.8
33	1b	187	LEU	2.8
50	2s	30	LEU	2.8
49	1r	25	THR	2.8
6	2G	129	GLY	2.8
52	2u	11	GLY	2.8
7	2H	29	PRO	2.8
32	2a	88	C	2.8
6	1G	48	GLU	2.8
6	2G	42	GLY	2.8
7	2H	82	GLY	2.8
40	1i	30	GLY	2.8
7	2H	6	ARG	2.8
29	27	48	LYS	2.8
34	2c	190	ARG	2.8
40	1i	31	GLN	2.8
34	2c	167	TRP	2.8
50	2s	13	ASP	2.8
20	2Y	106	LEU	2.8
34	2c	182	ILE	2.8
35	1d	126	ILE	2.8
41	1j	96	ILE	2.8
45	2n	11	LYS	2.8
32	2a	79	G	2.8
51	1t	13	LEU	2.8
33	1b	125	PRO	2.7
41	1j	77	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
45	2n	48	ALA	2.7
44	1m	94	ARG	2.7
33	2b	105	PHE	2.7
35	1d	124	GLY	2.7
38	1g	85	TYR	2.7
40	2i	92	TYR	2.7
41	1j	38	ILE	2.7
22	20	69	PHE	2.7
1	2A	5	A	2.7
8	2I	13	GLY	2.7
38	2g	113	GLU	2.7
44	2m	102	ARG	2.7
1	2A	2901	G	2.7
21	2Z	125	LEU	2.7
25	23	26	LEU	2.7
19	2X	69	TYR	2.7
22	20	45	PHE	2.7
38	1g	56	GLN	2.7
38	2g	18	TYR	2.7
49	2r	23	LYS	2.7
26	14	52	THR	2.7
7	2H	131	VAL	2.7
26	24	56	VAL	2.7
42	2k	14	VAL	2.7
52	2u	5	ASP	2.7
33	1b	128	GLU	2.7
46	2o	6	GLU	2.7
52	2u	22	ARG	2.7
50	1s	26	GLY	2.7
45	1n	16	PHE	2.7
1	2A	1088	C	2.7
6	2G	39	ILE	2.7
32	1a	984	A	2.7
50	2s	79	THR	2.7
40	2i	55	ALA	2.7
35	1d	167	GLY	2.7
40	2i	72	GLY	2.7
49	1r	26	LEU	2.7
41	2j	38	ILE	2.7
8	2I	20	ASP	2.7
26	14	65	ASP	2.7
46	1o	88	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
1	2A	1112	A	2.7
50	2s	38	SER	2.7
8	2I	100	ALA	2.7
48	1q	73	VAL	2.7
4	2E	1	MET	2.7
41	2j	86	MET	2.7
41	1j	71	LEU	2.7
47	1p	33	ILE	2.7
32	2a	211	U	2.6
32	2a	825	U	2.6
18	2W	111	HIS	2.6
38	2g	118	VAL	2.6
40	2i	26	VAL	2.6
1	2A	2900	A	2.6
32	1a	1432	A	2.6
48	1q	78	GLU	2.6
26	24	62	ARG	2.6
6	2G	26	GLN	2.6
34	2c	77	ILE	2.6
33	2b	34	ALA	2.6
40	2i	115	GLY	2.6
40	1i	26	VAL	2.6
44	2m	7	VAL	2.6
32	2a	977	C	2.6
21	2Z	24	LEU	2.6
30	28	21	LYS	2.6
34	2c	196	LEU	2.6
32	2a	1257	A	2.6
34	2c	164	ARG	2.6
1	2A	2122	G	2.6
14	2S	40	ILE	2.6
32	1a	77	G	2.6
42	2k	90	GLY	2.6
1	2A	1071	U	2.6
33	1b	215	LEU	2.6
50	2s	15	LEU	2.6
32	2a	997	C	2.6
34	1c	205	GLY	2.6
39	2h	106	GLY	2.6
2	2B	118	G	2.6
33	1b	15	VAL	2.6
39	2h	127	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
48	2q	74	LEU	2.6
45	2n	16	PHE	2.6
5	2F	15	SER	2.6
51	1t	14	LYS	2.6
33	2b	62	ALA	2.6
34	2c	160	ALA	2.6
50	2s	59	PRO	2.6
44	2m	80	ARG	2.6
47	1p	57	ARG	2.6
14	2S	29	PHE	2.6
1	1A	1150	U	2.6
1	2A	8	U	2.6
7	1H	2	SER	2.6
1	2A	33	C	2.6
1	2A	1120	C	2.6
6	2G	136	ARG	2.6
40	2i	77	ILE	2.6
33	1b	63	MET	2.6
50	2s	66	MET	2.6
26	14	49	PHE	2.6
48	2q	8	GLY	2.6
1	2A	10	G	2.6
32	1a	86	U	2.6
32	2a	1114	G	2.6
40	2i	93	ARG	2.6
45	2n	12	ARG	2.6
6	2G	142	PRO	2.6
7	2H	92	ILE	2.6
34	1c	100	ALA	2.6
7	2H	44	VAL	2.6
40	2i	28	VAL	2.6
33	1b	129	GLU	2.6
40	1i	47	LEU	2.6
21	2Z	6	LYS	2.5
41	2j	41	PRO	2.5
54	1x	47	U	2.5
20	2Y	55	TYR	2.5
26	24	32	TYR	2.5
32	2a	976	G	2.5
41	2j	16	LEU	2.5
23	21	2	SER	2.5
40	2i	127	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
44	2m	40	ASN	2.5
34	2c	57	ILE	2.5
6	2G	29	TRP	2.5
44	2m	92	HIS	2.5
20	2Y	42	VAL	2.5
48	2q	9	VAL	2.5
34	2c	179	ARG	2.5
50	2s	47	HIS	2.5
8	2I	19	VAL	2.5
10	1O	91	LEU	2.5
23	11	98	LEU	2.5
40	1i	28	VAL	2.5
21	2Z	65	GLN	2.5
21	2Z	142	SER	2.5
35	1d	110	PHE	2.5
1	2A	679	G	2.5
32	1a	1002	G	2.5
7	2H	89	ILE	2.5
14	2S	57	LYS	2.5
33	2b	51	LEU	2.5
41	1j	40	LEU	2.5
50	2s	60	VAL	2.5
24	22	1	MET	2.5
21	2Z	140	ASP	2.5
44	2m	103	THR	2.5
55	2z	12	PRO	2.5
32	1a	88	C	2.5
32	1a	213	C	2.5
32	2a	87	C	2.5
40	2i	22	GLY	2.5
8	2I	72	LEU	2.5
11	2P	92	GLU	2.5
33	2b	134	GLU	2.5
33	1b	48	MET	2.5
32	1a	1509	A	2.5
19	1X	94	GLY	2.5
34	2c	2	GLY	2.5
52	2u	13	ILE	2.5
8	1I	35	LEU	2.5
8	2I	58	LEU	2.5
47	2p	59	TRP	2.5
8	2I	3	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
14	2S	46	VAL	2.5
38	1g	151	TYR	2.5
45	2n	35	ARG	2.5
50	1s	29	ARG	2.5
34	1c	148	GLY	2.5
50	1s	39	THR	2.5
1	2A	1553	A	2.5
7	2H	30	LYS	2.5
7	2H	169	VAL	2.5
14	2S	85	VAL	2.5
1	2A	300	C	2.5
26	24	57	GLU	2.4
44	2m	73	GLU	2.4
11	2P	134	ALA	2.4
33	2b	218	ALA	2.4
44	1m	4	ILE	2.4
46	2o	87	ILE	2.4
7	2H	99	VAL	2.4
21	2Z	153	SER	2.4
27	15	60	VAL	2.4
32	2a	1432	A	2.4
50	1s	19	VAL	2.4
33	1b	31	TYR	2.4
43	1l	64	TYR	2.4
7	2H	21	PRO	2.4
11	2P	127	ALA	2.4
20	2Y	6	HIS	2.4
32	2a	988	G	2.4
21	2Z	175	VAL	2.4
25	23	59	VAL	2.4
29	27	46	VAL	2.4
48	2q	10	VAL	2.4
6	2G	44	GLY	2.4
16	2U	85	LYS	2.4
35	1d	165	MET	2.4
9	2N	91	LEU	2.4
11	2P	123	LEU	2.4
45	2n	53	LEU	2.4
50	2s	29	ARG	2.4
51	1t	17	ARG	2.4
26	14	53	GLU	2.4
37	2f	95	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
41	2j	24	VAL	2.4
43	2l	18	VAL	2.4
49	2r	62	GLU	2.4
47	1p	38	TYR	2.4
11	2P	102	ARG	2.4
32	2a	1227	A	2.4
41	2j	5	ARG	2.4
44	2m	66	LEU	2.4
51	2t	49	ALA	2.4
41	2j	98	ILE	2.4
45	2n	4	LYS	2.4
6	2G	49	ASP	2.4
7	2H	76	VAL	2.4
33	2b	229	VAL	2.4
34	1c	98	ASN	2.4
40	2i	125	TYR	2.4
47	1p	17	TYR	2.4
55	1z	13	PRO	2.4
9	2N	57	ALA	2.4
48	2q	100	LYS	2.4
50	2s	70	LYS	2.4
48	2q	98	LEU	2.4
42	2k	16	SER	2.4
1	2A	933	A	2.4
1	2A	1121	C	2.4
32	2a	209	U	2.4
35	1d	23	GLY	2.4
38	1g	55	GLY	2.4
38	2g	132	GLY	2.4
35	2d	47	ARG	2.4
45	2n	31	ARG	2.4
1	2A	1101	G	2.4
32	2a	78	G	2.4
32	2a	1237	G	2.4
52	1u	17	THR	2.4
33	1b	214	ILE	2.4
45	1n	7	ILE	2.4
6	2G	28	VAL	2.4
38	2g	75	VAL	2.4
51	2t	88	VAL	2.4
41	1j	91	PRO	2.4
6	1G	50	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
47	2p	7	ALA	2.4
22	20	11	ARG	2.4
38	2g	141	VAL	2.4
52	2u	10	ARG	2.4
42	2k	75	TYR	2.3
34	1c	42	LEU	2.3
35	1d	157	LEU	2.3
38	1g	54	THR	2.3
40	1i	94	ALA	2.3
40	2i	80	GLY	2.3
33	2b	222	ILE	2.3
33	2b	230	VAL	2.3
34	2c	198	VAL	2.3
40	2i	17	VAL	2.3
1	2A	2817	U	2.3
21	2Z	155	LEU	2.3
1	2A	677	A	2.3
14	2S	5	THR	2.3
39	2h	99	GLU	2.3
45	2n	13	THR	2.3
50	2s	63	THR	2.3
1	2A	2330	G	2.3
6	2G	35	GLU	2.3
32	1a	1256	G	2.3
34	1c	91	LEU	2.3
35	2d	4	TYR	2.3
12	2Q	5	ARG	2.3
35	2d	164	ALA	2.3
38	1g	77	SER	2.3
41	2j	8	LEU	2.3
44	1m	56	LEU	2.3
49	2r	25	THR	2.3
1	1A	936	A	2.3
8	2I	4	ILE	2.3
8	2I	88	ILE	2.3
38	2g	120	ILE	2.3
34	2c	64	VAL	2.3
40	2i	65	VAL	2.3
41	1j	72	VAL	2.3
41	2j	35	SER	2.3
21	2Z	7	ALA	2.3
49	2r	47	THR	2.3

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Mol	Chain	Res	Type	RSRZ
2	2B	119	G	2.3
7	2H	148	ILE	2.3
1	2A	931	C	2.3
50	2s	67	VAL	2.3
40	2i	83	ARG	2.3
51	2t	25	ARG	2.3
14	2S	101	LEU	2.3
25	23	25	ALA	2.3
33	2b	188	ALA	2.3
36	2e	94	ALA	2.3
50	2s	62	ILE	2.3
1	2A	1103	G	2.3
32	2a	1070	G	2.3
50	2s	3	ARG	2.3
50	1s	72	GLY	2.3
34	2c	4	LYS	2.3
45	2n	58	LYS	2.3
8	2I	12	LEU	2.3
34	1c	160	ALA	2.3
1	2A	1111	U	2.3
8	2I	79	ILE	2.3
34	1c	77	ILE	2.3
11	2P	125	VAL	2.3
38	2g	131	LYS	2.3
33	1b	232	PRO	2.3
41	1j	62	HIS	2.3
41	2j	30	SER	2.3
50	2s	5	LEU	2.3
1	2A	1124	C	2.3
32	2a	1244	C	2.3
33	1b	123	ALA	2.3
47	1p	54	GLU	2.3
1	2A	1140	A	2.3
3	2D	275	LYS	2.3
6	2G	23	PHE	2.3
35	1d	132	ARG	2.3
45	1n	17	LYS	2.3
45	2n	36	PHE	2.3
49	1r	54	ARG	2.3
38	2g	135	VAL	2.3
40	2i	86	VAL	2.3
41	1j	73	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
46	2o	86	GLY	2.2
41	2j	59	SER	2.2
34	1c	204	LEU	2.2
37	1f	1	MET	2.2
49	1r	78	LEU	2.2
7	2H	116	GLU	2.2
33	1b	188	ALA	2.2
38	2g	117	ALA	2.2
38	2g	54	THR	2.2
1	2A	1092	G	2.2
32	2a	1148	C	2.2
35	1d	166	LYS	2.2
1	2A	1143	A	2.2
1	2A	1148	A	2.2
8	2l	81	VAL	2.2
39	2h	61	VAL	2.2
41	2j	34	VAL	2.2
46	2o	14	GLU	2.2
44	2m	48	LEU	2.2
51	1t	72	LEU	2.2
7	2H	165	ALA	2.2
38	2g	73	MET	2.2
49	2r	54	ARG	2.2
6	2G	146	TYR	2.2
1	1A	696	C	2.2
1	2A	696	C	2.2
6	1G	80	PHE	2.2
33	1b	201	ILE	2.2
34	2c	66	VAL	2.2
53	2v	18	G	2.2
1	2A	1090	A	2.2
1	2A	1102	A	2.2
26	24	40	HIS	2.2
50	1s	50	ALA	2.2
42	1k	87	THR	2.2
41	2j	89	ASP	2.2
34	2c	197	GLY	2.2
50	1s	61	TYR	2.2
9	2N	10	GLU	2.2
7	2H	35	VAL	2.2
1	1A	2204	C	2.2
32	1a	73	C	2.2

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Mol	Chain	Res	Type	RSRZ
32	1a	986	C	2.2
17	2V	50	PRO	2.2
1	1A	1099	A	2.2
21	2Z	164	ALA	2.2
24	22	9	GLN	2.2
7	2H	109	PHE	2.2
34	1c	203	PHE	2.2
3	2D	270	ILE	2.2
36	2e	148	VAL	2.2
15	1T	38	ASN	2.2
38	1g	3	ARG	2.2
42	1k	98	LEU	2.2
32	2a	987	C	2.2
8	2I	46	ALA	2.2
1	2A	9	G	2.2
1	2A	1150	U	2.2
17	1V	63	GLY	2.2
41	2j	17	ASP	2.2
32	2a	1150	A	2.2
25	23	54	VAL	2.2
21	2Z	61	LEU	2.2
43	2l	93	LEU	2.2
50	2s	22	LEU	2.2
36	2e	20	GLN	2.2
41	2j	99	LYS	2.2
40	1i	46	ALA	2.2
49	1r	29	PHE	2.2
17	2V	5	VAL	2.2
21	2Z	146	ILE	2.2
33	2b	41	ILE	2.2
35	1d	133	VAL	2.2
49	2r	22	VAL	2.2
51	2t	41	ILE	2.2
18	1W	111	HIS	2.2
33	2b	142	LEU	2.2
31	19	12	ASP	2.2
42	2k	42	TRP	2.2
21	2Z	4	ARG	2.2
39	2h	91	ARG	2.2
49	1r	42	ARG	2.2
50	1s	28	LYS	2.1
8	1I	117	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
8	2I	85	GLU	2.1
8	2I	117	GLU	2.1
21	2Z	150	LEU	2.1
33	1b	19	HIS	2.1
33	2b	115	LEU	2.1
34	2c	18	TRP	2.1
35	1d	147	ALA	2.1
40	2i	82	ALA	2.1
41	1j	11	PHE	2.1
8	2I	71	ILE	2.1
14	2S	35	ILE	2.1
50	1s	56	GLN	2.1
17	2V	39	LEU	2.1
41	2j	73	ASP	2.1
51	2t	23	ARG	2.1
32	2a	1139	G	2.1
50	2s	28	LYS	2.1
7	2H	56	SER	2.1
24	22	6	VAL	2.1
26	14	56	VAL	2.1
26	24	10	VAL	2.1
32	2a	1231	C	2.1
34	2c	185	GLY	2.1
51	1t	79	ARG	2.1
34	2c	142	MET	2.1
45	1n	8	GLU	2.1
1	2A	2207	G	2.1
8	2I	35	LEU	2.1
14	2S	83	LYS	2.1
25	23	9	VAL	2.1
41	1j	90	LEU	2.1
1	1A	270	U	2.1
32	1a	210	U	2.1
32	2a	1242	C	2.1
33	2b	207	ALA	2.1
55	2z	11	THR	2.1
50	2s	25	LYS	2.1
8	2I	57	ARG	2.1
34	1c	76	VAL	2.1
41	2j	52	GLY	2.1
44	2m	3	ARG	2.1
1	2A	1138	G	2.1

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Mol	Chain	Res	Type	RSRZ
1	2A	1215	G	2.1
26	14	67	TYR	2.1
40	2i	63	ILE	2.1
26	24	7	PRO	2.1
34	1c	166	GLU	2.1
43	2l	64	TYR	2.1
32	1a	1257	A	2.1
1	2A	1126	U	2.1
32	2a	86	U	2.1
34	2c	65	ALA	2.1
1	2A	698	C	2.1
20	2Y	43	ASN	2.1
24	22	8	LYS	2.1
12	2Q	60	ARG	2.1
41	2j	29	ARG	2.1
7	2H	87	LEU	2.1
6	1G	25	TYR	2.1
8	1I	89	TYR	2.1
25	23	15	TYR	2.1
34	2c	157	ILE	2.1
40	1i	81	ILE	2.1
47	1p	4	ILE	2.1
1	1A	682	G	2.1
1	1A	2121	G	2.1
1	2A	681	G	2.1
1	2A	1133	A	2.1
31	29	15	LYS	2.1
38	2g	152	ALA	2.1
32	1a	1119	U	2.1
37	2f	89	MET	2.1
41	2j	78	ASN	2.1
5	2F	208	GLY	2.1
6	2G	85	GLY	2.1
16	2U	87	GLY	2.1
32	2a	1245	C	2.1
34	1c	159	GLY	2.1
35	1d	186	LEU	2.1
40	2i	117	HIS	2.1
41	1j	34	VAL	2.1
49	2r	44	LEU	2.1
7	2H	8	PRO	2.1
15	2T	126	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
45	2n	2	ALA	2.1
32	2a	1243	A	2.1
32	2a	1247	G	2.0
33	2b	69	LEU	2.0
33	2b	113	HIS	2.0
33	2b	135	GLN	2.0
44	2m	15	VAL	2.0
38	1g	42	ILE	2.0
44	2m	4	ILE	2.0
48	2q	36	ILE	2.0
33	1b	225	ALA	2.0
45	1n	59	ALA	2.0
39	2h	130	GLY	2.0
45	1n	51	GLY	2.0
33	2b	181	PHE	2.0
1	1A	287	U	2.0
16	2U	117	GLN	2.0
34	1c	196	LEU	2.0
34	2c	204	LEU	2.0
41	1j	8	LEU	2.0
49	2r	26	LEU	2.0
2	2B	120	A	2.0
1	2A	2205	G	2.0
21	2Z	57	ILE	2.0
32	1a	74	G	2.0
32	2a	1125	G	2.0
1	2A	2124	C	2.0
24	12	11	GLU	2.0
32	2a	826	C	2.0
33	2b	130	ARG	2.0
41	1j	46	ARG	2.0
46	2o	88	ARG	2.0
40	2i	106	ALA	2.0
50	1s	38	SER	2.0
36	2e	12	LEU	2.0
49	1r	85	LEU	2.0
38	1g	91	VAL	2.0
46	2o	27	VAL	2.0
34	2c	8	ILE	2.0
1	1A	2901	G	2.0
32	2a	1028	C	2.0
32	2a	1172	G	2.0

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Mol	Chain	Res	Type	RSRZ
34	2c	74	GLY	2.0
34	2c	81	GLY	2.0
33	2b	95	GLN	2.0
41	2j	15	THR	2.0
42	2k	31	THR	2.0
6	2G	80	PHE	2.0
26	24	11	PRO	2.0
33	1b	131	PRO	2.0
33	1b	229	VAL	2.0
48	2q	73	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
54	4SU	1x	8	20/21	0.97	0.13	-	47,59,71,71	0
54	5MC	1x	32	21/22	0.95	0.19	-	47,63,73,74	0
54	5MU	2x	54	21/22	0.92	0.20	-	68,77,85,100	0
54	5MC	2x	32	21/22	0.91	0.23	-	65,77,87,92	0
54	PSU	1x	55	20/21	0.94	0.16	-	63,69,80,81	0
54	PSU	2x	55	20/21	0.86	0.16	-	68,72,83,84	0
54	4SU	2x	8	20/21	0.93	0.13	-	69,79,87,88	0
54	5MU	1x	54	21/22	0.94	0.14	-	57,69,77,82	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(Å ²)	Q<0.9
56	MG	1A	3128	1/1	0.88	0.84	103.08	46,46,46,46	0
56	MG	1A	3884	1/1	0.95	0.59	55.80	37,37,37,37	0
56	MG	1A	4018	1/1	0.95	0.34	51.68	27,27,27,27	0
56	MG	1a	1717	1/1	0.90	0.77	43.65	62,62,62,62	0
56	MG	1A	3525	1/1	0.92	0.45	40.16	56,56,56,56	0
56	MG	1R	202	1/1	0.82	0.56	37.34	56,56,56,56	0
56	MG	1A	3531	1/1	0.93	0.64	36.75	51,51,51,51	0
56	MG	2A	3478	1/1	0.98	0.28	36.67	49,49,49,49	0
56	MG	2A	3414	1/1	0.69	0.45	35.82	56,56,56,56	0
56	MG	1A	3485	1/1	0.85	0.41	32.97	51,51,51,51	0
56	MG	1F	307	1/1	0.89	0.56	32.25	51,51,51,51	0
56	MG	1A	3613	1/1	0.83	0.45	31.58	51,51,51,51	0
56	MG	1E	304	1/1	0.93	0.43	30.28	53,53,53,53	0
56	MG	2A	3144	1/1	0.96	0.43	29.77	45,45,45,45	0
56	MG	2A	3480	1/1	0.93	0.25	29.46	39,39,39,39	0
56	MG	1A	3186	1/1	0.93	0.46	27.41	39,39,39,39	0
56	MG	1A	3009	1/1	0.93	0.34	25.89	31,31,31,31	0
56	MG	2A	3576	1/1	0.97	0.37	24.61	39,39,39,39	0
56	MG	25	502	1/1	0.86	0.31	24.28	54,54,54,54	0
56	MG	1a	1741	1/1	0.97	0.45	23.40	47,47,47,47	0
56	MG	2A	3571	1/1	0.78	0.41	22.78	43,43,43,43	0
56	MG	1A	4185	1/1	0.97	0.33	22.09	41,41,41,41	0
56	MG	2a	1780	1/1	0.96	0.33	21.97	56,56,56,56	0
56	MG	2A	3108	1/1	0.98	0.34	21.72	30,30,30,30	0
56	MG	2A	3052	1/1	0.86	0.26	21.08	31,31,31,31	0
56	MG	1A	3607	1/1	0.94	0.47	20.44	53,53,53,53	0
56	MG	2A	3331	1/1	0.92	0.36	20.27	55,55,55,55	0
56	MG	2A	3200	1/1	0.96	0.48	19.85	40,40,40,40	0
56	MG	2A	3321	1/1	0.97	0.33	18.55	43,43,43,43	0
56	MG	1A	3386	1/1	0.90	0.34	18.43	43,43,43,43	0
56	MG	2A	3559	1/1	0.89	0.35	18.36	42,42,42,42	0
56	MG	2A	3534	1/1	0.95	0.39	18.04	57,57,57,57	0
56	MG	2A	3355	1/1	0.95	0.26	17.45	34,34,34,34	0
56	MG	2A	3139	1/1	0.99	0.36	17.42	37,37,37,37	0
56	MG	1A	3761	1/1	0.90	0.41	17.35	50,50,50,50	0
56	MG	2a	1640	1/1	0.94	0.85	16.96	72,72,72,72	0
56	MG	2A	3390	1/1	0.94	0.41	16.80	56,56,56,56	0
56	MG	2A	3192	1/1	0.92	0.38	16.77	36,36,36,36	0
56	MG	1a	1708	1/1	0.92	0.52	16.73	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3412	1/1	0.81	0.29	16.57	44,44,44,44	0
56	MG	1A	3747	1/1	0.93	0.30	16.56	22,22,22,22	0
56	MG	2A	3049	1/1	0.85	0.40	16.48	64,64,64,64	0
56	MG	2A	3440	1/1	0.96	0.30	16.43	37,37,37,37	0
56	MG	2a	1819	1/1	0.94	0.47	16.27	56,56,56,56	0
56	MG	1A	3562	1/1	0.67	0.40	16.09	41,41,41,41	0
56	MG	1A	3519	1/1	0.92	0.34	16.05	51,51,51,51	0
56	MG	1A	3420	1/1	0.92	0.27	16.00	57,57,57,57	0
56	MG	1A	3178	1/1	0.97	0.46	15.82	39,39,39,39	0
56	MG	2a	1739	1/1	0.98	0.32	15.79	39,39,39,39	0
56	MG	1A	3945	1/1	0.97	0.33	15.69	33,33,33,33	0
56	MG	1A	3369	1/1	0.95	0.39	15.67	32,32,32,32	0
56	MG	1A	3409	1/1	0.96	0.40	15.46	33,33,33,33	0
56	MG	1A	4107	1/1	0.97	0.41	14.93	35,35,35,35	0
56	MG	2a	1604	1/1	0.91	0.41	14.50	47,47,47,47	0
56	MG	2A	3103	1/1	0.94	0.40	14.41	39,39,39,39	0
56	MG	1A	3418	1/1	0.76	0.36	14.29	52,52,52,52	0
56	MG	2A	3294	1/1	0.97	0.23	14.14	34,34,34,34	0
56	MG	2A	3383	1/1	0.88	0.30	14.13	44,44,44,44	0
56	MG	1a	1702	1/1	0.96	0.27	14.03	41,41,41,41	0
56	MG	1N	202	1/1	0.92	0.42	13.87	54,54,54,54	0
56	MG	2A	3145	1/1	0.96	0.21	13.82	32,32,32,32	0
56	MG	1A	4186	1/1	0.97	0.33	13.76	17,17,17,17	0
56	MG	1A	3398	1/1	0.94	0.31	13.71	46,46,46,46	0
56	MG	1D	301	1/1	0.91	0.30	13.66	37,37,37,37	0
56	MG	2A	3398	1/1	0.98	0.24	13.63	54,54,54,54	0
56	MG	2A	3447	1/1	0.94	0.31	13.54	61,61,61,61	0
56	MG	2A	3312	1/1	0.91	0.24	13.47	35,35,35,35	0
56	MG	1A	3118	1/1	0.92	0.32	13.30	44,44,44,44	0
56	MG	1U	205	1/1	0.95	0.33	13.22	35,35,35,35	0
56	MG	2a	1842	1/1	0.89	0.39	13.21	54,54,54,54	0
56	MG	1A	3572	1/1	0.95	0.35	13.21	35,35,35,35	0
56	MG	2A	3237	1/1	0.92	0.31	13.08	67,67,67,67	0
56	MG	1A	4229	1/1	0.95	0.49	13.05	33,33,33,33	0
56	MG	2a	1724	1/1	0.94	0.35	13.02	58,58,58,58	0
56	MG	1A	4022	1/1	0.94	0.33	12.96	45,45,45,45	0
56	MG	1A	3704	1/1	0.88	0.29	12.81	24,24,24,24	0
56	MG	1a	1696	1/1	0.86	0.42	12.78	61,61,61,61	0
56	MG	2D	305	1/1	0.90	0.34	12.76	29,29,29,29	0
56	MG	1D	303	1/1	0.93	0.29	12.70	45,45,45,45	0
56	MG	2A	3062	1/1	0.97	0.22	12.57	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3336	1/1	0.94	0.26	12.42	56,56,56,56	0
56	MG	1A	3193	1/1	0.97	0.28	12.39	23,23,23,23	0
56	MG	2a	1827	1/1	0.96	0.59	12.24	83,83,83,83	0
56	MG	1A	3948	1/1	0.96	0.38	12.11	39,39,39,39	0
56	MG	2A	3196	1/1	0.74	0.23	11.93	50,50,50,50	0
56	MG	2A	3157	1/1	0.98	0.24	11.91	23,23,23,23	0
56	MG	2A	3550	1/1	0.78	0.30	11.64	49,49,49,49	0
56	MG	1A	3463	1/1	0.96	0.34	11.55	39,39,39,39	0
56	MG	1A	3772	1/1	0.92	0.25	11.53	35,35,35,35	0
56	MG	2A	3092	1/1	0.90	0.35	11.36	34,34,34,34	0
56	MG	1A	3090	1/1	0.93	0.29	11.35	30,30,30,30	0
56	MG	1A	3129	1/1	0.83	0.33	11.20	40,40,40,40	0
56	MG	1A	3326	1/1	0.97	0.28	11.17	46,46,46,46	0
56	MG	1A	4207	1/1	0.97	0.36	11.09	30,30,30,30	0
56	MG	2a	1622	1/1	0.96	0.33	11.01	70,70,70,70	0
56	MG	1U	203	1/1	0.95	0.35	10.61	42,42,42,42	0
56	MG	2A	3325	1/1	0.96	0.26	10.56	28,28,28,28	0
56	MG	1B	203	1/1	0.56	0.42	10.55	66,66,66,66	0
56	MG	2A	3552	1/1	0.88	0.25	10.52	59,59,59,59	0
56	MG	2A	3588	1/1	0.98	0.44	10.31	42,42,42,42	0
56	MG	2A	3541	1/1	0.94	0.28	10.30	51,51,51,51	0
56	MG	2a	1607	1/1	0.94	0.40	10.24	45,45,45,45	0
56	MG	2A	3567	1/1	0.90	0.26	10.20	49,49,49,49	0
56	MG	2A	3217	1/1	0.98	0.30	10.08	36,36,36,36	0
56	MG	2A	3574	1/1	0.96	0.20	9.95	30,30,30,30	0
56	MG	2l	3001	1/1	0.77	0.45	9.86	66,66,66,66	0
56	MG	1A	3571	1/1	0.96	0.26	9.83	52,52,52,52	0
56	MG	2A	3118	1/1	0.95	0.24	9.72	32,32,32,32	0
56	MG	1D	309	1/1	0.82	0.62	9.72	56,56,56,56	0
56	MG	1a	1675	1/1	0.95	0.19	9.68	63,63,63,63	0
56	MG	1U	206	1/1	0.97	0.30	9.44	32,32,32,32	0
56	MG	2A	3543	1/1	0.96	0.23	9.30	47,47,47,47	0
56	MG	2A	3583	1/1	0.83	0.38	9.29	39,39,39,39	0
56	MG	1A	3285	1/1	0.91	0.27	9.23	30,30,30,30	0
56	MG	1a	1720	1/1	0.95	0.28	8.99	58,58,58,58	0
56	MG	2A	3587	1/1	0.96	0.52	8.99	44,44,44,44	0
56	MG	1A	3788	1/1	0.97	0.22	8.98	34,34,34,34	0
56	MG	1A	3324	1/1	0.84	0.28	8.92	38,38,38,38	0
56	MG	1A	3053	1/1	0.97	0.38	8.91	54,54,54,54	0
56	MG	1A	3708	1/1	0.98	0.26	8.90	30,30,30,30	0
56	MG	1a	1738	1/1	0.94	0.35	8.78	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3842	1/1	0.87	0.29	8.74	79,79,79,79	0
56	MG	1A	3635	1/1	0.92	0.25	8.66	18,18,18,18	0
56	MG	2A	3535	1/1	0.91	0.30	8.65	39,39,39,39	0
56	MG	2a	1720	1/1	0.97	0.27	8.63	65,65,65,65	0
56	MG	2A	3207	1/1	0.97	0.36	8.63	60,60,60,60	0
56	MG	1A	3624	1/1	0.97	0.27	8.57	43,43,43,43	0
56	MG	2A	3137	1/1	0.91	0.26	8.52	42,42,42,42	0
56	MG	1A	3909	1/1	0.92	0.27	8.50	34,34,34,34	0
56	MG	1A	3385	1/1	0.96	0.28	8.44	43,43,43,43	0
56	MG	1A	3553	1/1	0.88	0.31	8.30	43,43,43,43	0
56	MG	2A	3540	1/1	0.94	0.24	8.29	36,36,36,36	0
56	MG	1A	3835	1/1	0.99	0.26	8.17	33,33,33,33	0
56	MG	1A	3217	1/1	0.91	0.23	8.15	43,43,43,43	0
56	MG	2a	1847	1/1	0.97	0.36	8.12	46,46,46,46	0
56	MG	2A	3418	1/1	0.88	0.32	8.07	58,58,58,58	0
56	MG	1A	3611	1/1	0.89	0.29	8.03	40,40,40,40	0
56	MG	1A	4224	1/1	0.98	0.29	8.03	23,23,23,23	0
56	MG	2A	3101	1/1	0.95	0.20	7.97	48,48,48,48	0
56	MG	2A	3206	1/1	0.96	0.24	7.95	39,39,39,39	0
56	MG	17	101	1/1	0.96	0.38	7.89	35,35,35,35	0
56	MG	1A	3229	1/1	0.95	0.27	7.87	23,23,23,23	0
56	MG	1F	304	1/1	0.91	0.35	7.80	21,21,21,21	0
56	MG	1A	3191	1/1	0.96	0.32	7.79	35,35,35,35	0
56	MG	2D	301	1/1	0.94	0.21	7.72	51,51,51,51	0
56	MG	2A	3183	1/1	0.83	0.22	7.66	50,50,50,50	0
56	MG	1A	4165	1/1	0.94	0.26	7.62	26,26,26,26	0
56	MG	2A	3296	1/1	0.98	0.21	7.59	32,32,32,32	0
56	MG	1A	3001	1/1	0.93	0.32	7.45	37,37,37,37	0
56	MG	1A	4095	1/1	0.94	0.22	7.42	34,34,34,34	0
56	MG	1A	3556	1/1	0.95	0.28	7.25	49,49,49,49	0
56	MG	2A	3285	1/1	0.96	0.21	7.22	38,38,38,38	0
56	MG	2a	1706	1/1	0.86	0.43	7.21	63,63,63,63	0
56	MG	2a	1707	1/1	0.87	0.31	7.21	52,52,52,52	0
56	MG	1A	3875	1/1	0.94	0.27	7.16	28,28,28,28	0
56	MG	1A	3245	1/1	0.97	0.32	7.06	30,30,30,30	0
56	MG	1a	1723	1/1	0.81	0.26	6.95	69,69,69,69	0
56	MG	1A	3042	1/1	0.90	0.26	6.92	47,47,47,47	0
56	MG	1A	3976	1/1	0.89	0.23	6.89	41,41,41,41	0
56	MG	2A	3056	1/1	0.93	0.31	6.88	45,45,45,45	0
56	MG	2A	3282	1/1	0.80	0.25	6.77	43,43,43,43	0
56	MG	1A	3618	1/1	0.95	0.22	6.75	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	1764	1/1	0.92	0.34	6.72	69,69,69,69	0
56	MG	1a	1714	1/1	0.91	0.26	6.71	53,53,53,53	0
56	MG	1D	314	1/1	0.97	0.28	6.69	43,43,43,43	0
56	MG	1A	3183	1/1	0.96	0.26	6.65	35,35,35,35	0
56	MG	1A	3305	1/1	0.88	0.27	6.64	44,44,44,44	0
56	MG	1A	3541	1/1	0.80	0.30	6.53	56,56,56,56	0
56	MG	2A	3105	1/1	0.90	0.23	6.52	45,45,45,45	0
56	MG	2A	3336	1/1	0.97	0.21	6.42	36,36,36,36	0
56	MG	2A	3161	1/1	0.97	0.26	6.41	48,48,48,48	0
56	MG	1A	3018	1/1	0.84	0.25	6.40	56,56,56,56	0
56	MG	1A	3716	1/1	0.70	0.26	6.37	37,37,37,37	0
56	MG	1a	1652	1/1	0.89	0.22	6.35	54,54,54,54	0
56	MG	2A	3573	1/1	0.97	0.25	6.34	42,42,42,42	0
56	MG	2A	3408	1/1	0.94	0.21	6.31	57,57,57,57	0
56	MG	2A	3453	1/1	0.89	0.21	6.31	49,49,49,49	0
56	MG	2A	3219	1/1	0.94	0.19	6.19	42,42,42,42	0
56	MG	2A	3182	1/1	0.90	0.33	6.14	49,49,49,49	0
56	MG	1A	4202	1/1	0.90	0.35	5.99	67,67,67,67	0
56	MG	1A	3198	1/1	0.99	0.21	5.95	33,33,33,33	0
56	MG	2A	3581	1/1	0.88	0.24	5.94	46,46,46,46	0
56	MG	1a	1798	1/1	0.96	0.23	5.89	59,59,59,59	0
56	MG	2x	3004	1/1	0.93	0.23	5.86	62,62,62,62	0
56	MG	2A	3309	1/1	0.98	0.27	5.78	35,35,35,35	0
56	MG	1a	1768	1/1	0.96	0.20	5.74	32,32,32,32	0
56	MG	1A	3163	1/1	0.94	0.19	5.69	52,52,52,52	0
56	MG	2A	3031	1/1	0.94	0.26	5.67	46,46,46,46	0
56	MG	1A	4230	1/1	0.97	0.27	5.62	47,47,47,47	0
56	MG	2A	3374	1/1	0.91	0.21	5.60	43,43,43,43	0
56	MG	1a	1888	1/1	0.95	0.37	5.57	73,73,73,73	0
56	MG	2a	1676	1/1	0.70	0.23	5.47	64,64,64,64	0
56	MG	2A	3582	1/1	0.93	0.31	5.47	38,38,38,38	0
56	MG	2A	3100	1/1	0.95	0.22	5.47	38,38,38,38	0
56	MG	2A	3300	1/1	0.96	0.25	5.47	37,37,37,37	0
56	MG	1A	3496	1/1	0.85	0.29	5.46	46,46,46,46	0
56	MG	1A	4210	1/1	0.89	0.30	5.39	43,43,43,43	0
56	MG	2A	3225	1/1	0.89	0.19	5.38	43,43,43,43	0
56	MG	2F	302	1/1	0.97	0.23	5.37	41,41,41,41	0
56	MG	1a	1825	1/1	0.88	0.18	5.28	59,59,59,59	0
56	MG	2A	3289	1/1	0.68	0.19	5.27	49,49,49,49	0
56	MG	2A	3293	1/1	0.97	0.22	5.13	37,37,37,37	0
56	MG	1a	1630	1/1	0.94	0.18	5.13	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
56	MG	1a	1713	1/1	0.84	0.29	5.11	67,67,67,67	0
56	MG	1U	204	1/1	0.96	0.33	5.05	55,55,55,55	0
56	MG	1A	3669	1/1	0.93	0.26	5.05	27,27,27,27	0
56	MG	1a	1822	1/1	0.84	0.27	5.04	76,76,76,76	0
56	MG	2A	3463	1/1	0.97	0.17	5.03	40,40,40,40	0
56	MG	2A	3533	1/1	0.98	0.23	4.98	49,49,49,49	0
56	MG	1A	3685	1/1	0.98	0.19	4.95	17,17,17,17	0
56	MG	1A	3179	1/1	0.93	0.21	4.92	36,36,36,36	0
56	MG	2A	3563	1/1	0.93	0.23	4.91	42,42,42,42	0
56	MG	1A	3687	1/1	0.98	0.25	4.91	21,21,21,21	0
56	MG	2A	3187	1/1	0.96	0.23	4.79	44,44,44,44	0
56	MG	1D	306	1/1	0.93	0.27	4.78	13,13,13,13	0
56	MG	1A	3905	1/1	0.89	0.22	4.75	32,32,32,32	0
56	MG	2A	3569	1/1	0.92	0.24	4.74	32,32,32,32	0
56	MG	1A	4052	1/1	0.87	0.24	4.69	24,24,24,24	0
56	MG	1A	3712	1/1	0.93	0.25	4.64	28,28,28,28	0
56	MG	1D	302	1/1	0.91	0.24	4.64	71,71,71,71	0
56	MG	1a	1791	1/1	0.85	0.21	4.59	64,64,64,64	0
56	MG	2a	1628	1/1	0.95	0.26	4.57	66,66,66,66	0
56	MG	1A	3417	1/1	0.94	0.25	4.56	30,30,30,30	0
56	MG	2a	1841	1/1	0.96	0.23	4.55	42,42,42,42	0
56	MG	1Q	204	1/1	0.96	0.31	4.52	42,42,42,42	0
56	MG	1a	1681	1/1	0.97	0.25	4.45	39,39,39,39	0
56	MG	1A	3694	1/1	0.93	0.25	4.43	29,29,29,29	0
56	MG	1A	3634	1/1	0.72	0.23	4.42	29,29,29,29	0
56	MG	2A	3323	1/1	0.94	0.21	4.41	35,35,35,35	0
56	MG	1A	3212	1/1	0.93	0.17	4.40	63,63,63,63	0
56	MG	1A	4209	1/1	0.97	0.37	4.39	27,27,27,27	0
56	MG	2A	3290	1/1	0.96	0.20	4.38	26,26,26,26	0
56	MG	1A	3765	1/1	0.88	0.24	4.37	19,19,19,19	0
56	MG	1A	3992	1/1	0.84	0.20	4.37	54,54,54,54	0
56	MG	2A	3260	1/1	0.95	0.19	4.36	41,41,41,41	0
56	MG	2A	3114	1/1	0.91	0.21	4.35	46,46,46,46	0
56	MG	1A	3762	1/1	0.97	0.22	4.32	10,10,10,10	0
56	MG	1D	312	1/1	0.97	0.34	4.29	41,41,41,41	0
56	MG	2A	3113	1/1	0.97	0.18	4.26	40,40,40,40	0
56	MG	2A	3159	1/1	0.94	0.20	4.26	37,37,37,37	0
56	MG	2A	3310	1/1	0.76	0.20	4.24	38,38,38,38	0
56	MG	1A	3621	1/1	0.98	0.22	4.17	42,42,42,42	0
56	MG	1D	304	1/1	0.92	0.25	4.15	42,42,42,42	0
56	MG	2A	3353	1/1	0.88	0.22	4.08	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3256	1/1	0.89	0.20	4.03	53,53,53,53	0
56	MG	1a	1648	1/1	0.93	0.19	4.01	52,52,52,52	0
56	MG	1a	1668	1/1	0.92	0.16	3.99	44,44,44,44	0
56	MG	1A	3670	1/1	0.95	0.22	3.99	37,37,37,37	0
56	MG	2a	1753	1/1	0.92	0.23	3.96	76,76,76,76	0
56	MG	2D	303	1/1	0.94	0.22	3.96	44,44,44,44	0
56	MG	1A	3411	1/1	0.90	0.20	3.95	43,43,43,43	0
56	MG	1A	3728	1/1	0.95	0.19	3.95	41,41,41,41	0
56	MG	2A	3262	1/1	0.89	0.21	3.92	36,36,36,36	0
56	MG	1A	4153	1/1	0.93	0.22	3.86	68,68,68,68	0
56	MG	1V	201	1/1	0.98	0.25	3.84	44,44,44,44	0
56	MG	1A	3995	1/1	0.94	0.23	3.83	32,32,32,32	0
56	MG	2a	1631	1/1	0.85	0.23	3.79	49,49,49,49	0
56	MG	2A	3236	1/1	0.96	0.18	3.79	45,45,45,45	0
56	MG	1A	3262	1/1	0.89	0.20	3.72	52,52,52,52	0
56	MG	2A	3216	1/1	0.97	0.17	3.70	33,33,33,33	0
56	MG	1A	4170	1/1	0.98	0.23	3.66	10,10,10,10	0
56	MG	1A	3173	1/1	0.98	0.24	3.62	40,40,40,40	0
56	MG	1A	3399	1/1	1.00	0.21	3.60	5,5,5,5	0
56	MG	1A	3290	1/1	0.89	0.22	3.60	15,15,15,15	0
56	MG	2A	3283	1/1	0.95	0.21	3.59	51,51,51,51	0
56	MG	2A	3373	1/1	0.96	0.19	3.56	35,35,35,35	0
56	MG	2A	3427	1/1	0.90	0.16	3.50	41,41,41,41	0
56	MG	1A	3166	1/1	0.96	0.22	3.36	21,21,21,21	0
56	MG	2A	3032	1/1	0.89	0.18	3.34	45,45,45,45	0
56	MG	1D	313	1/1	0.90	0.26	3.28	43,43,43,43	0
56	MG	2a	1695	1/1	0.93	0.25	3.25	62,62,62,62	0
56	MG	1A	4219	1/1	0.94	0.26	3.24	25,25,25,25	0
56	MG	1A	3702	1/1	0.96	0.22	3.24	25,25,25,25	0
56	MG	2A	3467	1/1	0.88	0.19	3.23	60,60,60,60	0
56	MG	2A	3234	1/1	0.97	0.17	3.20	50,50,50,50	0
56	MG	2Q	3003	1/1	0.97	0.24	3.20	50,50,50,50	0
56	MG	1A	3147	1/1	0.92	0.31	3.18	50,50,50,50	0
56	MG	1A	3665	1/1	0.96	0.22	3.18	40,40,40,40	0
56	MG	1A	3671	1/1	0.95	0.18	3.16	30,30,30,30	0
56	MG	2B	3002	1/1	0.93	0.20	3.14	54,54,54,54	0
56	MG	1A	3636	1/1	0.95	0.25	3.13	29,29,29,29	0
56	MG	2A	3186	1/1	0.99	0.20	3.06	46,46,46,46	0
56	MG	1Q	201	1/1	0.95	0.25	3.05	60,60,60,60	0
56	MG	1a	1693	1/1	0.98	0.24	3.02	49,49,49,49	0
56	MG	2A	3053	1/1	0.98	0.19	3.02	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	1682	1/1	0.96	0.23	2.95	54,54,54,54	0
56	MG	1A	3126	1/1	0.87	0.24	2.93	31,31,31,31	0
56	MG	2A	3158	1/1	0.97	0.20	2.89	37,37,37,37	0
56	MG	2A	3128	1/1	0.95	0.18	2.87	47,47,47,47	0
56	MG	2A	3061	1/1	0.85	0.17	2.86	46,46,46,46	0
56	MG	1A	3918	1/1	0.86	0.23	2.85	27,27,27,27	0
56	MG	1A	3310	1/1	0.97	0.25	2.84	37,37,37,37	0
56	MG	1a	1644	1/1	0.95	0.22	2.81	54,54,54,54	0
56	MG	2A	3528	1/1	0.99	0.16	2.77	38,38,38,38	0
56	MG	2A	3119	1/1	0.93	0.23	2.75	53,53,53,53	0
56	MG	2A	3315	1/1	0.76	0.17	2.73	41,41,41,41	0
56	MG	1A	4180	1/1	0.98	0.22	2.70	33,33,33,33	0
56	MG	1A	3597	1/1	0.90	0.23	2.68	49,49,49,49	0
56	MG	2a	1613	1/1	0.94	0.19	2.67	65,65,65,65	0
56	MG	1A	3673	1/1	0.89	0.25	2.66	38,38,38,38	0
56	MG	1P	205	1/1	0.97	0.25	2.60	41,41,41,41	0
56	MG	1A	3177	1/1	0.99	0.18	2.58	14,14,14,14	0
56	MG	2A	3361	1/1	0.94	0.16	2.53	53,53,53,53	0
56	MG	1A	3333	1/1	0.91	0.19	2.46	63,63,63,63	0
56	MG	2A	3585	1/1	0.94	0.18	2.45	35,35,35,35	0
56	MG	1a	1622	1/1	0.95	0.16	2.38	43,43,43,43	0
56	MG	2a	1740	1/1	0.99	0.22	2.36	31,31,31,31	0
56	MG	2A	3319	1/1	0.98	0.22	2.34	38,38,38,38	0
56	MG	1A	3312	1/1	0.96	0.29	2.30	42,42,42,42	0
56	MG	2A	3337	1/1	0.87	0.20	2.28	56,56,56,56	0
56	MG	1A	4077	1/1	0.92	0.19	2.28	62,62,62,62	0
56	MG	1a	1799	1/1	0.87	0.20	2.26	60,60,60,60	0
56	MG	1X	3001	1/1	0.92	0.24	2.24	44,44,44,44	0
56	MG	2A	3302	1/1	0.84	0.19	2.23	30,30,30,30	0
56	MG	1A	3896	1/1	0.84	0.20	2.22	55,55,55,55	0
56	MG	1A	3925	1/1	0.93	0.21	2.20	39,39,39,39	0
56	MG	1A	3838	1/1	0.96	0.22	2.18	54,54,54,54	0
56	MG	1A	3680	1/1	0.95	0.23	2.17	20,20,20,20	0
56	MG	2A	3184	1/1	0.96	0.16	2.16	29,29,29,29	0
56	MG	2A	3287	1/1	0.91	0.16	2.13	55,55,55,55	0
56	MG	1a	1642	1/1	0.98	0.20	2.10	47,47,47,47	0
56	MG	2A	3590	1/1	0.97	0.27	2.06	55,55,55,55	0
56	MG	1A	3203	1/1	0.91	0.18	2.03	30,30,30,30	0
56	MG	2A	3358	1/1	0.87	0.17	2.00	58,58,58,58	0
56	MG	2A	3013	1/1	0.84	0.31	1.99	66,66,66,66	0
56	MG	2A	3174	1/1	0.95	0.17	1.98	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2t	3001	1/1	0.94	0.29	1.97	50,50,50,50	0
56	MG	2A	3462	1/1	0.94	0.16	1.96	60,60,60,60	0
56	MG	2a	1807	1/1	0.97	0.22	1.95	50,50,50,50	0
56	MG	1a	1819	1/1	0.99	0.21	1.92	32,32,32,32	0
56	MG	2e	3001	1/1	0.73	0.26	1.90	67,67,67,67	0
56	MG	1A	3174	1/1	0.90	0.21	1.90	40,40,40,40	0
56	MG	1A	4179	1/1	0.97	0.23	1.87	34,34,34,34	0
56	MG	2A	3503	1/1	0.96	0.19	1.84	32,32,32,32	0
56	MG	2A	3381	1/1	0.92	0.17	1.82	51,51,51,51	0
56	MG	1q	201	1/1	0.76	0.27	1.81	65,65,65,65	0
56	MG	1A	3289	1/1	0.95	0.19	1.80	24,24,24,24	0
56	MG	1A	3678	1/1	0.93	0.19	1.80	27,27,27,27	0
56	MG	2A	3286	1/1	0.97	0.15	1.80	41,41,41,41	0
56	MG	1A	3780	1/1	0.86	0.19	1.80	24,24,24,24	0
56	MG	2q	3002	1/1	0.95	0.21	1.78	48,48,48,48	0
56	MG	2E	303	1/1	0.94	0.22	1.78	44,44,44,44	0
56	MG	2A	3243	1/1	0.86	0.15	1.78	59,59,59,59	0
56	MG	1A	3216	1/1	0.92	0.21	1.77	35,35,35,35	0
56	MG	1a	1894	1/1	0.96	0.23	1.77	65,65,65,65	0
56	MG	2A	3291	1/1	0.94	0.18	1.75	30,30,30,30	0
56	MG	1a	1639	1/1	0.91	0.19	1.73	77,77,77,77	0
56	MG	1D	305	1/1	0.92	0.21	1.73	35,35,35,35	0
56	MG	2a	1664	1/1	0.90	0.24	1.68	84,84,84,84	0
56	MG	2A	3352	1/1	0.90	0.18	1.67	31,31,31,31	0
56	MG	1A	3882	1/1	0.98	0.19	1.67	29,29,29,29	0
56	MG	1A	4192	1/1	0.94	0.23	1.66	40,40,40,40	0
56	MG	1E	308	1/1	0.95	0.23	1.65	29,29,29,29	0
56	MG	1A	3617	1/1	0.97	0.22	1.59	11,11,11,11	0
56	MG	1a	1800	1/1	0.96	0.17	1.57	37,37,37,37	0
56	MG	2A	3411	1/1	0.94	0.17	1.56	55,55,55,55	0
56	MG	2A	3530	1/1	0.95	0.18	1.54	31,31,31,31	0
56	MG	1D	311	1/1	0.92	0.18	1.54	41,41,41,41	0
56	MG	2A	3175	1/1	0.95	0.17	1.51	37,37,37,37	0
56	MG	2A	3580	1/1	0.97	0.18	1.37	40,40,40,40	0
56	MG	2a	1696	1/1	0.89	0.18	1.35	53,53,53,53	0
56	MG	1A	3739	1/1	0.97	0.23	1.31	22,22,22,22	0
56	MG	1A	3660	1/1	0.94	0.17	1.29	46,46,46,46	0
56	MG	1A	3237	1/1	0.90	0.18	1.27	24,24,24,24	0
56	MG	1t	3001	1/1	0.96	0.42	1.27	47,47,47,47	0
56	MG	1A	3674	1/1	0.90	0.24	1.27	43,43,43,43	0
56	MG	1A	4216	1/1	0.97	0.21	1.26	46,46,46,46	0
56	MG	2q	3001	1/1	0.93	0.30	1.26	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3506	1/1	0.94	0.14	1.25	52,52,52,52	0
56	MG	1a	1826	1/1	0.95	0.14	1.23	53,53,53,53	0
56	MG	1A	3643	1/1	0.99	0.20	1.21	12,12,12,12	0
56	MG	1a	1682	1/1	0.84	0.20	1.21	57,57,57,57	0
56	MG	1A	3642	1/1	0.93	0.23	1.21	26,26,26,26	0
56	MG	1A	4188	1/1	0.95	0.23	1.21	40,40,40,40	0
56	MG	2A	3021	1/1	0.89	0.18	1.20	50,50,50,50	0
56	MG	2a	1779	1/1	0.96	0.21	1.17	62,62,62,62	0
56	MG	2a	1757	1/1	0.97	0.19	1.14	61,61,61,61	0
56	MG	2a	1626	1/1	0.89	0.20	1.13	74,74,74,74	0
56	MG	2A	3195	1/1	0.96	0.17	1.13	46,46,46,46	0
56	MG	2A	3222	1/1	0.98	0.15	1.11	29,29,29,29	0
56	MG	1A	4031	1/1	0.95	0.20	1.11	39,39,39,39	0
56	MG	1B	208	1/1	0.94	0.18	1.10	38,38,38,38	0
56	MG	1A	3538	1/1	0.92	0.17	1.08	57,57,57,57	0
56	MG	2A	3512	1/1	0.97	0.14	1.08	36,36,36,36	0
56	MG	1a	1617	1/1	0.89	0.15	1.05	61,61,61,61	0
56	MG	1a	1646	1/1	0.91	0.16	1.00	53,53,53,53	0
57	ZN	15	101	1/1	0.98	0.17	0.98	60,60,60,60	0
56	MG	20	101	1/1	0.97	0.16	0.98	56,56,56,56	0
56	MG	1A	3811	1/1	0.98	0.20	0.97	37,37,37,37	0
56	MG	1A	3791	1/1	0.96	0.17	0.95	53,53,53,53	0
56	MG	2A	3254	1/1	0.95	0.16	0.94	43,43,43,43	0
56	MG	2a	1803	1/1	0.98	0.17	0.93	72,72,72,72	0
56	MG	2A	3320	1/1	0.83	0.13	0.91	45,45,45,45	0
56	MG	1R	207	1/1	0.94	0.25	0.89	49,49,49,49	0
56	MG	1A	3768	1/1	0.96	0.21	0.88	17,17,17,17	0
56	MG	1A	3200	1/1	0.97	0.16	0.83	35,35,35,35	0
56	MG	1a	1760	1/1	0.89	0.17	0.79	49,49,49,49	0
56	MG	1W	3003	1/1	0.97	0.21	0.78	32,32,32,32	0
56	MG	2a	1647	1/1	0.95	0.23	0.76	82,82,82,82	0
56	MG	1h	202	1/1	0.92	0.21	0.76	65,65,65,65	0
56	MG	2A	3153	1/1	0.98	0.15	0.73	29,29,29,29	0
56	MG	1A	3277	1/1	0.90	0.16	0.73	39,39,39,39	0
56	MG	1A	3371	1/1	0.92	0.17	0.72	41,41,41,41	0
56	MG	2A	3255	1/1	0.93	0.17	0.70	49,49,49,49	0
56	MG	1A	3760	1/1	0.94	0.17	0.68	58,58,58,58	0
56	MG	1A	4163	1/1	0.88	0.16	0.66	61,61,61,61	0
56	MG	2a	1639	1/1	0.85	0.26	0.64	71,71,71,71	0
56	MG	2A	3516	1/1	0.93	0.15	0.63	32,32,32,32	0
56	MG	2A	3210	1/1	0.98	0.16	0.63	50,50,50,50	0
56	MG	1p	101	1/1	0.93	0.20	0.63	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3511	1/1	0.95	0.15	0.62	40,40,40,40	0
56	MG	2A	3022	1/1	0.98	0.16	0.60	44,44,44,44	0
56	MG	2A	3504	1/1	0.97	0.15	0.57	39,39,39,39	0
56	MG	2A	3484	1/1	0.92	0.15	0.56	43,43,43,43	0
56	MG	2A	3330	1/1	0.96	0.14	0.55	41,41,41,41	0
56	MG	1n	502	1/1	0.85	0.22	0.55	59,59,59,59	0
56	MG	1a	1649	1/1	0.83	0.16	0.54	83,83,83,83	0
56	MG	1R	203	1/1	0.95	0.21	0.54	59,59,59,59	0
56	MG	1N	204	1/1	0.92	0.19	0.54	44,44,44,44	0
56	MG	1A	3693	1/1	0.96	0.16	0.53	26,26,26,26	0
56	MG	1a	1684	1/1	0.96	0.17	0.44	52,52,52,52	0
56	MG	2D	302	1/1	0.80	0.15	0.44	52,52,52,52	0
56	MG	1B	218	1/1	0.96	0.16	0.43	27,27,27,27	0
56	MG	2a	1792	1/1	0.90	0.17	0.42	62,62,62,62	0
56	MG	1A	3414	1/1	0.83	0.17	0.40	55,55,55,55	0
56	MG	1a	1643	1/1	0.87	0.17	0.37	64,64,64,64	0
56	MG	1Q	203	1/1	0.80	0.23	0.35	64,64,64,64	0
56	MG	1A	3169	1/1	0.87	0.20	0.31	40,40,40,40	0
56	MG	1A	4231	1/1	0.98	0.18	0.26	17,17,17,17	0
56	MG	1A	3470	1/1	0.94	0.17	0.25	47,47,47,47	0
56	MG	1D	308	1/1	0.95	0.21	0.22	29,29,29,29	0
56	MG	1A	3820	1/1	0.98	0.17	0.20	17,17,17,17	0
56	MG	2O	202	1/1	0.93	0.17	0.18	44,44,44,44	0
56	MG	1A	3404	1/1	0.93	0.16	0.18	32,32,32,32	0
56	MG	1A	3620	1/1	0.94	0.15	0.17	37,37,37,37	0
56	MG	2A	3577	1/1	0.92	0.16	0.15	40,40,40,40	0
56	MG	1A	3308	1/1	0.96	0.20	0.13	43,43,43,43	0
56	MG	1A	3676	1/1	0.93	0.16	0.10	38,38,38,38	0
56	MG	1A	3699	1/1	0.97	0.19	0.07	20,20,20,20	0
56	MG	1A	3284	1/1	0.91	0.16	0.06	37,37,37,37	0
56	MG	1A	3689	1/1	0.91	0.17	0.04	26,26,26,26	0
56	MG	1A	3210	1/1	0.97	0.14	0.01	48,48,48,48	0
56	MG	1A	3188	1/1	0.92	0.18	-0.07	37,37,37,37	0
56	MG	1A	3610	1/1	0.95	0.20	-0.07	36,36,36,36	0
56	MG	1A	4214	1/1	0.98	0.20	-0.12	19,19,19,19	0
56	MG	2a	1697	1/1	0.93	0.16	-0.13	53,53,53,53	0
56	MG	19	103	1/1	0.94	0.22	-0.14	51,51,51,51	0
56	MG	1A	3802	1/1	0.99	0.20	-0.17	20,20,20,20	0
56	MG	1A	3222	1/1	0.98	0.18	-0.17	30,30,30,30	0
56	MG	1A	3427	1/1	0.76	0.15	-0.18	67,67,67,67	0
56	MG	2E	301	1/1	0.93	0.14	-0.18	23,23,23,23	0
56	MG	1a	1886	1/1	0.97	0.16	-0.18	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	1744	1/1	0.97	0.22	-0.22	69,69,69,69	0
56	MG	1a	1637	1/1	0.81	0.17	-0.22	60,60,60,60	0
56	MG	1a	1712	1/1	0.86	0.15	-0.22	75,75,75,75	0
56	MG	1D	315	1/1	0.90	0.14	-0.24	39,39,39,39	0
56	MG	1W	3005	1/1	0.96	0.18	-0.25	24,24,24,24	0
56	MG	2a	1831	1/1	0.98	0.15	-0.36	60,60,60,60	0
56	MG	2A	3324	1/1	0.95	0.14	-0.36	47,47,47,47	0
56	MG	15	103	1/1	0.98	0.14	-0.40	34,34,34,34	0
56	MG	1A	3265	1/1	0.97	0.16	-0.44	12,12,12,12	0
56	MG	1A	3989	1/1	0.84	0.17	-0.45	20,20,20,20	0
56	MG	2a	1653	1/1	0.65	0.21	-0.46	85,85,85,85	0
56	MG	1A	4201	1/1	0.95	0.17	-0.47	41,41,41,41	0
56	MG	2a	1742	1/1	0.85	0.15	-0.47	56,56,56,56	0
56	MG	2a	1627	1/1	0.93	0.15	-0.48	63,63,63,63	0
56	MG	1b	3002	1/1	0.91	0.14	-0.49	88,88,88,88	0
56	MG	2l	3002	1/1	0.91	0.20	-0.49	74,74,74,74	0
56	MG	2a	1790	1/1	0.95	0.16	-0.49	53,53,53,53	0
56	MG	2A	3387	1/1	0.91	0.14	-0.50	52,52,52,52	0
56	MG	1A	3771	1/1	0.92	0.18	-0.51	21,21,21,21	0
56	MG	1E	301	1/1	0.86	0.17	-0.52	23,23,23,23	0
56	MG	1A	3158	1/1	0.95	0.17	-0.52	18,18,18,18	0
56	MG	1B	206	1/1	0.78	0.15	-0.53	54,54,54,54	0
56	MG	1A	3168	1/1	0.96	0.19	-0.54	29,29,29,29	0
56	MG	1a	1887	1/1	0.87	0.15	-0.63	49,49,49,49	0
56	MG	2A	3379	1/1	0.98	0.15	-0.65	31,31,31,31	0
56	MG	1A	3567	1/1	0.91	0.16	-0.66	49,49,49,49	0
56	MG	2A	3090	1/1	0.92	0.13	-0.67	38,38,38,38	0
56	MG	1A	3807	1/1	0.96	0.18	-0.68	18,18,18,18	0
56	MG	2a	1786	1/1	0.92	0.15	-0.69	58,58,58,58	0
56	MG	2A	3205	1/1	0.98	0.13	-0.70	23,23,23,23	0
56	MG	2A	3501	1/1	0.94	0.12	-0.70	48,48,48,48	0
57	ZN	25	501	1/1	0.99	0.13	-0.71	55,55,55,55	0
56	MG	1A	3653	1/1	0.98	0.17	-0.75	30,30,30,30	0
56	MG	1a	1638	1/1	0.95	0.14	-0.76	18,18,18,18	0
56	MG	1A	3622	1/1	0.98	0.15	-0.82	32,32,32,32	0
56	MG	1A	3778	1/1	0.96	0.17	-0.86	30,30,30,30	0
56	MG	1A	4211	1/1	0.94	0.17	-0.86	31,31,31,31	0
56	MG	1D	310	1/1	0.96	0.12	-0.89	46,46,46,46	0
56	MG	2a	1812	1/1	0.86	0.13	-0.89	75,75,75,75	0
56	MG	2A	3307	1/1	0.95	0.13	-0.90	35,35,35,35	0
56	MG	1A	3748	1/1	0.95	0.18	-0.90	30,30,30,30	0
56	MG	1A	3623	1/1	0.99	0.15	-0.93	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	1629	1/1	0.92	0.16	-1.00	60,60,60,60	0
56	MG	1A	3256	1/1	0.98	0.11	-1.06	63,63,63,63	0
56	MG	1A	3054	1/1	0.98	0.18	-1.07	45,45,45,45	0
56	MG	1a	1879	1/1	0.79	0.12	-1.08	78,78,78,78	0
56	MG	1A	4181	1/1	0.97	0.16	-1.08	27,27,27,27	0
56	MG	2A	3521	1/1	0.98	0.11	-1.08	42,42,42,42	0
56	MG	2A	3545	1/1	0.88	0.12	-1.14	54,54,54,54	0
56	MG	2A	3502	1/1	0.96	0.11	-1.16	30,30,30,30	0
56	MG	2A	3265	1/1	0.92	0.13	-1.18	44,44,44,44	0
57	ZN	26	501	1/1	0.97	0.10	-1.20	55,55,55,55	0
56	MG	1A	3773	1/1	0.93	0.17	-1.22	31,31,31,31	0
56	MG	1R	205	1/1	0.96	0.17	-1.23	49,49,49,49	0
56	MG	2A	3450	1/1	0.97	0.12	-1.26	30,30,30,30	0
56	MG	1a	1709	1/1	0.94	0.15	-1.29	75,75,75,75	0
56	MG	1a	1807	1/1	0.97	0.14	-1.30	60,60,60,60	0
56	MG	2a	1681	1/1	0.92	0.16	-1.31	47,47,47,47	0
56	MG	1A	3182	1/1	0.96	0.17	-1.31	33,33,33,33	0
56	MG	1A	3242	1/1	0.99	0.16	-1.37	22,22,22,22	0
57	ZN	29	501	1/1	0.97	0.06	-1.37	61,61,61,61	0
56	MG	1A	3654	1/1	0.96	0.15	-1.40	24,24,24,24	0
56	MG	2A	3591	1/1	0.96	0.12	-1.43	44,44,44,44	0
56	MG	1A	3779	1/1	0.97	0.16	-1.47	26,26,26,26	0
56	MG	2A	3083	1/1	0.95	0.10	-1.48	38,38,38,38	0
56	MG	1A	3154	1/1	0.98	0.14	-1.50	21,21,21,21	0
56	MG	1A	4205	1/1	0.95	0.11	-1.50	36,36,36,36	0
56	MG	2A	3589	1/1	0.94	0.10	-1.51	43,43,43,43	0
58	SF4	2d	501	8/8	0.97	0.09	-1.53	62,78,83,91	0
56	MG	2A	3168	1/1	0.90	0.12	-1.53	48,48,48,48	0
56	MG	1A	3836	1/1	0.92	0.17	-1.54	33,33,33,33	0
56	MG	1A	4196	1/1	0.96	0.14	-1.56	50,50,50,50	0
56	MG	1a	1746	1/1	0.94	0.13	-1.59	81,81,81,81	0
56	MG	1A	4172	1/1	0.92	0.17	-1.60	22,22,22,22	0
56	MG	1A	3252	1/1	0.96	0.16	-1.61	48,48,48,48	0
56	MG	1a	1891	1/1	0.88	0.12	-1.62	68,68,68,68	0
56	MG	2A	3220	1/1	0.99	0.13	-1.63	38,38,38,38	0
56	MG	2a	1778	1/1	0.92	0.11	-1.64	61,61,61,61	0
57	ZN	19	102	1/1	0.98	0.09	-1.64	36,36,36,36	0
56	MG	2a	1617	1/1	0.93	0.11	-1.65	69,69,69,69	0
56	MG	1A	3637	1/1	0.93	0.17	-1.67	48,48,48,48	0
56	MG	1A	3946	1/1	0.95	0.17	-1.68	28,28,28,28	0
56	MG	2A	3586	1/1	0.98	0.13	-1.68	33,33,33,33	0
56	MG	1a	1895	1/1	0.93	0.15	-1.68	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3749	1/1	0.98	0.16	-1.71	15,15,15,15	0
56	MG	1a	1893	1/1	0.88	0.10	-1.72	59,59,59,59	0
56	MG	1A	3963	1/1	0.95	0.14	-1.74	45,45,45,45	0
56	MG	1a	1657	1/1	0.94	0.14	-1.76	54,54,54,54	0
56	MG	2a	1691	1/1	0.96	0.13	-1.76	45,45,45,45	0
56	MG	1A	4206	1/1	0.94	0.15	-1.79	29,29,29,29	0
56	MG	1A	3735	1/1	0.94	0.15	-1.80	57,57,57,57	0
56	MG	1A	3789	1/1	0.90	0.17	-1.80	30,30,30,30	0
57	ZN	2Y	501	1/1	0.94	0.05	-1.80	83,83,83,83	0
58	SF4	1d	501	8/8	0.98	0.11	-1.81	62,69,78,87	0
56	MG	1A	3849	1/1	0.88	0.13	-1.83	29,29,29,29	0
56	MG	2a	1728	1/1	0.95	0.11	-1.84	52,52,52,52	0
56	MG	1A	3137	1/1	0.94	0.17	-1.86	44,44,44,44	0
56	MG	1a	1619	1/1	0.97	0.14	-1.88	31,31,31,31	0
57	ZN	2n	102	1/1	0.70	0.09	-1.88	100,100,100,100	0
56	MG	1a	1677	1/1	0.97	0.12	-1.91	48,48,48,48	0
56	MG	1A	3184	1/1	0.96	0.16	-1.91	44,44,44,44	0
56	MG	1A	3299	1/1	0.95	0.13	-1.96	34,34,34,34	0
57	ZN	1n	501	1/1	0.97	0.10	-1.98	93,93,93,93	0
56	MG	1A	3894	1/1	0.96	0.12	-2.01	27,27,27,27	0
56	MG	1A	3679	1/1	0.93	0.18	-2.07	24,24,24,24	0
56	MG	1A	4118	1/1	0.98	0.12	-2.07	37,37,37,37	0
56	MG	1a	1686	1/1	0.92	0.14	-2.07	45,45,45,45	0
56	MG	1U	202	1/1	0.97	0.16	-2.11	25,25,25,25	0
56	MG	2a	1709	1/1	0.83	0.11	-2.12	78,78,78,78	0
57	ZN	16	102	1/1	0.99	0.09	-2.14	32,32,32,32	0
56	MG	2B	3009	1/1	0.88	0.11	-2.16	65,65,65,65	0
56	MG	2G	3001	1/1	0.85	0.09	-2.24	61,61,61,61	0
56	MG	1A	3274	1/1	0.96	0.14	-2.25	29,29,29,29	0
56	MG	1A	4227	1/1	0.93	0.13	-2.27	34,34,34,34	0
56	MG	1R	206	1/1	0.98	0.15	-2.27	42,42,42,42	0
57	ZN	24	501	1/1	0.78	0.06	-2.30	122,122,122,122	0
56	MG	1A	3924	1/1	0.98	0.14	-2.31	19,19,19,19	0
56	MG	1A	3630	1/1	0.93	0.12	-2.33	40,40,40,40	0
56	MG	1x	106	1/1	0.96	0.09	-2.34	52,52,52,52	0
56	MG	1A	3327	1/1	0.96	0.17	-2.34	29,29,29,29	0
56	MG	2A	3372	1/1	0.97	0.13	-2.34	34,34,34,34	0
56	MG	1A	3796	1/1	0.97	0.11	-2.35	46,46,46,46	0
56	MG	1A	3801	1/1	0.97	0.16	-2.38	40,40,40,40	0
56	MG	2A	3057	1/1	0.91	0.11	-2.39	34,34,34,34	0
56	MG	1D	307	1/1	0.96	0.08	-2.40	27,27,27,27	0
57	ZN	1Y	501	1/1	0.97	0.10	-2.42	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1G	201	1/1	0.89	0.10	-2.43	40,40,40,40	0
56	MG	2A	3292	1/1	0.95	0.12	-2.45	32,32,32,32	0
56	MG	1A	3403	1/1	0.87	0.07	-2.47	72,72,72,72	0
57	ZN	14	501	1/1	0.94	0.08	-2.47	104,104,104,104	0
56	MG	2A	3135	1/1	0.86	0.12	-2.47	48,48,48,48	0
56	MG	1a	1666	1/1	0.94	0.12	-2.53	51,51,51,51	0
56	MG	1A	3998	1/1	0.91	0.15	-2.53	51,51,51,51	0
56	MG	1A	3156	1/1	0.98	0.12	-2.56	29,29,29,29	0
56	MG	1F	302	1/1	0.93	0.18	-2.56	39,39,39,39	0
56	MG	1N	205	1/1	0.97	0.14	-2.57	37,37,37,37	0
56	MG	1A	3072	1/1	0.99	0.14	-2.64	32,32,32,32	0
56	MG	2A	3482	1/1	0.90	0.11	-2.67	34,34,34,34	0
56	MG	2a	1646	1/1	0.90	0.15	-2.67	63,63,63,63	0
56	MG	1A	3631	1/1	0.94	0.12	-2.67	47,47,47,47	0
56	MG	1A	4212	1/1	0.91	0.14	-2.72	40,40,40,40	0
56	MG	2A	3122	1/1	0.89	0.08	-2.72	57,57,57,57	0
56	MG	2A	3099	1/1	0.93	0.09	-2.77	54,54,54,54	0
56	MG	2A	3178	1/1	0.97	0.10	-2.78	43,43,43,43	0
56	MG	1A	4225	1/1	0.97	0.14	-2.81	23,23,23,23	0
56	MG	1A	3987	1/1	0.93	0.17	-2.82	12,12,12,12	0
56	MG	1a	1645	1/1	0.94	0.13	-2.83	53,53,53,53	0
56	MG	1a	1661	1/1	0.90	0.13	-2.86	34,34,34,34	0
56	MG	2a	1775	1/1	0.95	0.13	-2.89	62,62,62,62	0
56	MG	1a	1604	1/1	0.90	0.09	-3.00	79,79,79,79	0
56	MG	1A	3313	1/1	0.98	0.12	-3.02	56,56,56,56	0
56	MG	1A	3938	1/1	0.99	0.15	-3.04	16,16,16,16	0
56	MG	1a	1872	1/1	0.91	0.13	-3.05	47,47,47,47	0
56	MG	2A	3509	1/1	0.94	0.08	-3.07	35,35,35,35	0
56	MG	1A	3666	1/1	0.94	0.10	-3.09	30,30,30,30	0
56	MG	1A	4208	1/1	0.96	0.13	-3.10	29,29,29,29	0
56	MG	1A	3857	1/1	0.96	0.13	-3.12	36,36,36,36	0
56	MG	2a	1703	1/1	0.98	0.08	-3.18	60,60,60,60	0
56	MG	1A	3967	1/1	0.96	0.15	-3.19	20,20,20,20	0
56	MG	2a	1672	1/1	0.96	0.07	-3.21	59,59,59,59	0
56	MG	1A	3032	1/1	0.88	0.08	-3.22	50,50,50,50	0
56	MG	1A	3257	1/1	0.95	0.13	-3.24	35,35,35,35	0
56	MG	2A	3362	1/1	0.95	0.11	-3.25	42,42,42,42	0
56	MG	1A	3547	1/1	0.97	0.08	-3.29	38,38,38,38	0
56	MG	1A	3283	1/1	0.94	0.15	-3.30	25,25,25,25	0
56	MG	1a	1837	1/1	0.95	0.11	-3.34	43,43,43,43	0
56	MG	2A	3277	1/1	0.95	0.11	-3.38	38,38,38,38	0
56	MG	2a	1656	1/1	0.84	0.06	-3.38	94,94,94,94	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3278	1/1	0.91	0.13	-3.42	44,44,44,44	0
56	MG	2A	3364	1/1	0.86	0.10	-3.47	44,44,44,44	0
56	MG	2A	3027	1/1	0.94	0.12	-3.48	47,47,47,47	0
56	MG	1A	3814	1/1	0.87	0.13	-3.50	24,24,24,24	0
56	MG	2A	3072	1/1	0.95	0.08	-3.50	39,39,39,39	0
56	MG	1a	1676	1/1	0.93	0.07	-3.54	69,69,69,69	0
56	MG	1A	4182	1/1	0.91	0.12	-3.58	42,42,42,42	0
56	MG	1A	3723	1/1	0.98	0.14	-3.60	11,11,11,11	0
56	MG	2A	3201	1/1	0.97	0.12	-3.64	25,25,25,25	0
56	MG	1A	4221	1/1	0.94	0.10	-3.73	32,32,32,32	0
56	MG	1a	1835	1/1	0.94	0.11	-3.77	36,36,36,36	0
56	MG	1A	3534	1/1	0.96	0.11	-3.77	43,43,43,43	0
56	MG	1A	3641	1/1	0.90	0.10	-3.78	51,51,51,51	0
56	MG	1A	3684	1/1	0.88	0.13	-3.81	29,29,29,29	0
56	MG	2A	3437	1/1	0.96	0.09	-3.84	41,41,41,41	0
56	MG	1A	3176	1/1	0.89	0.12	-3.85	29,29,29,29	0
56	MG	1A	3189	1/1	0.98	0.12	-3.86	26,26,26,26	0
56	MG	1a	1627	1/1	0.96	0.09	-3.87	70,70,70,70	0
56	MG	1B	219	1/1	0.95	0.11	-3.90	60,60,60,60	0
56	MG	15	105	1/1	0.95	0.16	-3.94	35,35,35,35	0
56	MG	1A	3552	1/1	0.96	0.09	-4.06	42,42,42,42	0
56	MG	1E	302	1/1	0.98	0.13	-4.08	50,50,50,50	0
56	MG	2A	3444	1/1	0.96	0.09	-4.08	30,30,30,30	0
56	MG	2A	3176	1/1	0.98	0.11	-4.16	23,23,23,23	0
56	MG	1a	1689	1/1	0.98	0.10	-4.21	62,62,62,62	0
56	MG	1a	1722	1/1	0.98	0.06	-4.23	48,48,48,48	0
56	MG	1P	203	1/1	0.96	0.14	-4.34	26,26,26,26	0
56	MG	2a	1711	1/1	0.96	0.09	-4.42	38,38,38,38	0
56	MG	1A	3881	1/1	0.99	0.11	-4.48	16,16,16,16	0
56	MG	1A	3243	1/1	0.99	0.14	-4.52	24,24,24,24	0
56	MG	1A	3667	1/1	0.97	0.13	-4.58	23,23,23,23	0
56	MG	2A	3093	1/1	0.97	0.09	-4.69	51,51,51,51	0
56	MG	2a	1684	1/1	0.92	0.11	-4.72	44,44,44,44	0
56	MG	1A	3968	1/1	0.98	0.10	-4.77	34,34,34,34	0
56	MG	2a	1669	1/1	0.98	0.07	-4.83	69,69,69,69	0
56	MG	1A	3647	1/1	0.97	0.06	-4.98	47,47,47,47	0
56	MG	2A	3154	1/1	0.98	0.09	-5.12	41,41,41,41	0
56	MG	1a	1659	1/1	0.92	0.10	-5.27	58,58,58,58	0
56	MG	1A	4023	1/1	0.87	0.06	-5.27	73,73,73,73	0
56	MG	1A	3920	1/1	0.95	0.10	-5.31	48,48,48,48	0
56	MG	2a	1793	1/1	0.86	0.09	-5.38	67,67,67,67	0
56	MG	1A	3167	1/1	0.90	0.13	-5.47	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3752	1/1	0.98	0.13	-5.52	34,34,34,34	0
56	MG	2A	3045	1/1	0.84	0.08	-5.57	53,53,53,53	0
56	MG	1A	4220	1/1	0.97	0.14	-5.66	27,27,27,27	0
56	MG	1A	3220	1/1	0.98	0.16	-5.68	30,30,30,30	0
56	MG	2a	1686	1/1	0.94	0.09	-5.73	44,44,44,44	0
56	MG	2a	1741	1/1	0.81	0.06	-5.89	80,80,80,80	0
56	MG	1A	4183	1/1	0.98	0.08	-6.15	35,35,35,35	0
56	MG	1A	3238	1/1	0.97	0.15	-6.28	35,35,35,35	0
56	MG	1A	3846	1/1	0.96	0.11	-6.30	23,23,23,23	0
56	MG	1A	3055	1/1	0.97	0.10	-6.33	54,54,54,54	0
56	MG	1A	3757	1/1	0.99	0.12	-6.45	30,30,30,30	0
56	MG	1A	3950	1/1	0.98	0.08	-6.58	16,16,16,16	0
56	MG	1a	1863	1/1	0.94	0.07	-6.73	73,73,73,73	0
56	MG	1A	3845	1/1	0.97	0.10	-6.84	22,22,22,22	0
56	MG	2A	3431	1/1	0.98	0.07	-7.24	48,48,48,48	0
56	MG	2A	3392	1/1	0.85	0.08	-7.56	41,41,41,41	0
56	MG	1A	3164	1/1	0.97	0.12	-7.63	35,35,35,35	0
56	MG	1A	3934	1/1	0.91	0.09	-7.77	27,27,27,27	0
56	MG	1A	3794	1/1	0.94	0.09	-8.30	43,43,43,43	0
56	MG	2A	3270	1/1	0.97	0.07	-8.60	23,23,23,23	0
56	MG	1A	3830	1/1	0.95	0.13	-8.97	36,36,36,36	0
56	MG	1A	3267	1/1	0.99	0.08	-9.07	23,23,23,23	0
56	MG	1B	211	1/1	0.94	0.07	-18.47	34,34,34,34	0
56	MG	2A	3213	1/1	0.96	0.15	-	40,40,40,40	0
56	MG	2a	1725	1/1	0.89	0.18	-	63,63,63,63	0
56	MG	1A	3388	1/1	0.86	0.50	-	65,65,65,65	0
56	MG	2A	3421	1/1	0.98	0.05	-	40,40,40,40	0
56	MG	1A	4121	1/1	0.93	0.18	-	55,55,55,55	0
56	MG	1a	1766	1/1	0.88	0.11	-	73,73,73,73	0
56	MG	1A	3415	1/1	0.95	0.13	-	46,46,46,46	0
56	MG	1a	1606	1/1	0.90	0.24	-	65,65,65,65	0
56	MG	1a	1774	1/1	0.95	0.30	-	63,63,63,63	0
56	MG	1A	4013	1/1	0.93	0.23	-	56,56,56,56	0
56	MG	2A	3442	1/1	0.95	0.22	-	59,59,59,59	0
56	MG	2A	3579	1/1	0.75	0.24	-	69,69,69,69	0
56	MG	1A	3803	1/1	0.92	0.27	-	62,62,62,62	0
56	MG	1A	4123	1/1	0.96	0.27	-	31,31,31,31	0
56	MG	1a	1629	1/1	0.89	0.26	-	85,85,85,85	0
56	MG	1h	201	1/1	0.98	0.30	-	60,60,60,60	0
56	MG	1A	4103	1/1	0.94	0.37	-	35,35,35,35	0
56	MG	1A	3268	1/1	0.98	0.05	-	34,34,34,34	0
56	MG	2A	3464	1/1	0.98	0.21	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1802	1/1	0.98	0.23	-	59,59,59,59	0
56	MG	2A	3127	1/1	0.96	0.19	-	49,49,49,49	0
56	MG	1A	3159	1/1	0.93	0.22	-	26,26,26,26	0
56	MG	2D	304	1/1	0.94	0.12	-	39,39,39,39	0
56	MG	1A	4112	1/1	0.92	0.25	-	29,29,29,29	0
56	MG	2a	1662	1/1	0.97	0.09	-	71,71,71,71	0
56	MG	1A	4046	1/1	0.89	0.28	-	61,61,61,61	0
56	MG	1A	3594	1/1	0.80	0.25	-	61,61,61,61	0
56	MG	2A	3359	1/1	0.96	0.23	-	39,39,39,39	0
56	MG	1A	3378	1/1	0.95	0.20	-	50,50,50,50	0
56	MG	1a	1614	1/1	0.98	0.14	-	59,59,59,59	0
56	MG	1a	1883	1/1	0.93	0.12	-	62,62,62,62	0
56	MG	1a	1697	1/1	0.81	0.09	-	73,73,73,73	0
56	MG	2A	3150	1/1	0.84	0.19	-	46,46,46,46	0
56	MG	1A	3782	1/1	0.90	0.22	-	28,28,28,28	0
56	MG	2a	1754	1/1	0.85	0.26	-	74,74,74,74	0
56	MG	1A	3548	1/1	0.79	0.12	-	62,62,62,62	0
56	MG	1A	3883	1/1	0.95	0.19	-	49,49,49,49	0
56	MG	1A	3513	1/1	0.92	0.28	-	44,44,44,44	0
56	MG	2a	1710	1/1	0.97	0.09	-	47,47,47,47	0
56	MG	2A	3166	1/1	0.95	0.27	-	50,50,50,50	0
56	MG	2A	3378	1/1	0.96	0.24	-	55,55,55,55	0
56	MG	2A	3004	1/1	0.97	0.10	-	51,51,51,51	0
56	MG	2A	3297	1/1	0.98	0.15	-	33,33,33,33	0
56	MG	2a	1749	1/1	0.94	0.35	-	68,68,68,68	0
56	MG	1A	4108	1/1	0.93	0.18	-	44,44,44,44	0
56	MG	1A	3799	1/1	0.97	0.07	-	38,38,38,38	0
56	MG	1a	1853	1/1	0.98	0.15	-	53,53,53,53	0
56	MG	1A	3393	1/1	0.79	0.40	-	59,59,59,59	0
56	MG	1A	3043	1/1	0.85	0.31	-	44,44,44,44	0
56	MG	2a	1643	1/1	0.85	0.21	-	65,65,65,65	0
56	MG	1a	1763	1/1	0.94	0.12	-	88,88,88,88	0
56	MG	2A	3489	1/1	0.91	0.15	-	46,46,46,46	0
56	MG	1A	3236	1/1	0.94	0.17	-	63,63,63,63	0
56	MG	1A	3413	1/1	0.95	0.18	-	40,40,40,40	0
56	MG	2A	3241	1/1	0.90	0.12	-	41,41,41,41	0
56	MG	1A	3600	1/1	0.93	0.57	-	54,54,54,54	0
56	MG	1A	3510	1/1	0.81	0.18	-	42,42,42,42	0
56	MG	1A	3211	1/1	0.96	0.26	-	39,39,39,39	0
56	MG	2A	3266	1/1	0.86	0.26	-	60,60,60,60	0
56	MG	1A	3916	1/1	0.91	0.19	-	35,35,35,35	0
56	MG	1A	3705	1/1	0.95	0.23	-	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3424	1/1	0.89	0.17	-	42,42,42,42	0
56	MG	1A	3619	1/1	0.96	0.13	-	50,50,50,50	0
56	MG	2a	1733	1/1	0.87	0.30	-	80,80,80,80	0
56	MG	1A	3138	1/1	0.93	0.15	-	49,49,49,49	0
56	MG	1A	3979	1/1	0.98	0.30	-	39,39,39,39	0
56	MG	1A	3038	1/1	0.97	0.17	-	48,48,48,48	0
56	MG	1A	3806	1/1	0.95	0.08	-	66,66,66,66	0
56	MG	1T	202	1/1	0.94	0.07	-	39,39,39,39	0
56	MG	1a	1749	1/1	0.95	0.13	-	78,78,78,78	0
56	MG	2A	3575	1/1	0.96	0.38	-	46,46,46,46	0
56	MG	2A	3017	1/1	0.92	0.14	-	50,50,50,50	0
56	MG	1A	3498	1/1	0.91	0.11	-	46,46,46,46	0
56	MG	1A	4049	1/1	0.96	0.09	-	37,37,37,37	0
56	MG	1A	3481	1/1	0.96	0.28	-	33,33,33,33	0
56	MG	2A	3040	1/1	0.93	0.24	-	52,52,52,52	0
56	MG	2a	1829	1/1	0.96	0.06	-	53,53,53,53	0
56	MG	1A	3922	1/1	0.91	0.22	-	47,47,47,47	0
56	MG	1A	3130	1/1	0.91	0.39	-	49,49,49,49	0
56	MG	2A	3085	1/1	0.93	0.15	-	55,55,55,55	0
56	MG	2a	1633	1/1	0.72	0.31	-	70,70,70,70	0
56	MG	1E	306	1/1	0.90	0.26	-	47,47,47,47	0
56	MG	1A	3148	1/1	0.98	0.28	-	40,40,40,40	0
56	MG	1A	3863	1/1	0.90	0.19	-	58,58,58,58	0
56	MG	1W	3001	1/1	0.95	0.22	-	45,45,45,45	0
56	MG	2A	3235	1/1	0.89	0.23	-	44,44,44,44	0
56	MG	2a	1769	1/1	0.89	0.26	-	76,76,76,76	0
56	MG	1A	3030	1/1	0.94	0.09	-	53,53,53,53	0
56	MG	1A	3003	1/1	0.87	0.24	-	60,60,60,60	0
56	MG	1a	1820	1/1	0.92	0.18	-	69,69,69,69	0
56	MG	1A	4029	1/1	0.92	0.14	-	64,64,64,64	0
56	MG	2A	3203	1/1	0.92	0.28	-	51,51,51,51	0
56	MG	1A	4117	1/1	0.88	0.24	-	51,51,51,51	0
56	MG	1A	4177	1/1	0.97	0.13	-	34,34,34,34	0
56	MG	2A	3476	1/1	0.92	0.18	-	56,56,56,56	0
56	MG	1E	307	1/1	0.92	0.14	-	53,53,53,53	0
56	MG	2A	3198	1/1	0.95	0.06	-	44,44,44,44	0
56	MG	1A	3382	1/1	0.92	0.22	-	49,49,49,49	0
56	MG	2A	3564	1/1	0.90	0.15	-	35,35,35,35	0
56	MG	1a	1672	1/1	0.89	0.21	-	68,68,68,68	0
56	MG	1A	3580	1/1	0.98	0.17	-	46,46,46,46	0
56	MG	2a	1644	1/1	0.96	0.29	-	60,60,60,60	0
56	MG	1a	1636	1/1	0.87	0.20	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3505	1/1	0.94	0.12	-	47,47,47,47	0
56	MG	1A	3662	1/1	0.77	0.22	-	36,36,36,36	0
56	MG	1A	3914	1/1	0.83	0.20	-	40,40,40,40	0
56	MG	2A	3333	1/1	0.92	0.17	-	55,55,55,55	0
56	MG	1A	3690	1/1	0.93	0.16	-	28,28,28,28	0
56	MG	2A	3275	1/1	0.85	0.32	-	65,65,65,65	0
56	MG	1A	4162	1/1	0.94	0.24	-	37,37,37,37	0
56	MG	2A	3132	1/1	0.94	0.17	-	45,45,45,45	0
56	MG	2A	3441	1/1	0.94	0.20	-	58,58,58,58	0
56	MG	1A	4086	1/1	0.93	0.37	-	61,61,61,61	0
56	MG	1A	3869	1/1	0.92	0.16	-	64,64,64,64	0
56	MG	2a	1732	1/1	0.85	0.23	-	57,57,57,57	0
56	MG	2A	3208	1/1	0.92	0.18	-	49,49,49,49	0
56	MG	2A	3347	1/1	0.93	0.07	-	46,46,46,46	0
56	MG	2A	3033	1/1	0.78	0.40	-	64,64,64,64	0
56	MG	1A	3412	1/1	0.97	0.38	-	37,37,37,37	0
56	MG	23	101	1/1	0.95	0.15	-	56,56,56,56	0
56	MG	1B	207	1/1	0.95	0.16	-	52,52,52,52	0
56	MG	1A	4053	1/1	0.95	0.12	-	43,43,43,43	0
56	MG	1A	4189	1/1	0.84	0.18	-	43,43,43,43	0
56	MG	2A	3313	1/1	0.94	0.23	-	39,39,39,39	0
56	MG	2A	3079	1/1	0.93	0.36	-	47,47,47,47	0
56	MG	1A	3516	1/1	0.93	0.09	-	59,59,59,59	0
56	MG	1A	3422	1/1	0.95	0.13	-	50,50,50,50	0
56	MG	2A	3212	1/1	0.76	0.31	-	50,50,50,50	0
56	MG	2D	306	1/1	0.83	0.15	-	65,65,65,65	0
56	MG	1A	3235	1/1	0.98	0.39	-	36,36,36,36	0
56	MG	1A	3741	1/1	0.97	0.18	-	44,44,44,44	0
56	MG	1A	3462	1/1	0.96	0.12	-	64,64,64,64	0
56	MG	1A	3467	1/1	0.96	0.39	-	55,55,55,55	0
56	MG	2a	1761	1/1	0.90	0.13	-	69,69,69,69	0
56	MG	1A	4035	1/1	0.89	0.29	-	78,78,78,78	0
56	MG	2A	3410	1/1	0.98	0.09	-	36,36,36,36	0
56	MG	1A	3937	1/1	0.96	0.20	-	47,47,47,47	0
56	MG	2A	3523	1/1	0.95	0.11	-	27,27,27,27	0
56	MG	1b	3001	1/1	0.90	0.18	-	78,78,78,78	0
56	MG	1a	1615	1/1	0.95	0.10	-	52,52,52,52	0
56	MG	2A	3281	1/1	0.89	0.34	-	58,58,58,58	0
56	MG	2A	3096	1/1	0.89	0.20	-	50,50,50,50	0
56	MG	1A	3731	1/1	0.84	0.44	-	53,53,53,53	0
56	MG	1A	4104	1/1	0.78	0.20	-	63,63,63,63	0
56	MG	1A	3045	1/1	0.88	0.15	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3146	1/1	0.91	0.18	-	46,46,46,46	0
56	MG	1a	1829	1/1	0.91	0.14	-	60,60,60,60	0
56	MG	1A	3287	1/1	0.85	0.15	-	40,40,40,40	0
56	MG	1A	3809	1/1	0.81	0.15	-	16,16,16,16	0
56	MG	1A	3253	1/1	0.98	0.18	-	29,29,29,29	0
56	MG	1A	3657	1/1	0.97	0.41	-	39,39,39,39	0
56	MG	1R	208	1/1	0.89	0.15	-	45,45,45,45	0
56	MG	1A	4075	1/1	0.88	0.09	-	59,59,59,59	0
56	MG	1k	3002	1/1	0.72	0.14	-	68,68,68,68	0
56	MG	1a	1850	1/1	0.97	0.06	-	54,54,54,54	0
56	MG	2A	3134	1/1	0.92	0.18	-	49,49,49,49	0
56	MG	2A	3338	1/1	0.96	0.11	-	61,61,61,61	0
56	MG	2a	1687	1/1	0.91	0.30	-	54,54,54,54	0
56	MG	1a	1789	1/1	0.88	0.20	-	62,62,62,62	0
56	MG	1A	3082	1/1	0.90	0.36	-	45,45,45,45	0
56	MG	1A	3929	1/1	0.96	0.21	-	55,55,55,55	0
56	MG	1A	3187	1/1	0.97	0.20	-	38,38,38,38	0
56	MG	1A	3595	1/1	0.87	0.18	-	65,65,65,65	0
56	MG	1A	3435	1/1	0.98	0.09	-	44,44,44,44	0
56	MG	1A	3384	1/1	0.89	0.18	-	55,55,55,55	0
56	MG	1A	3877	1/1	0.84	0.20	-	56,56,56,56	0
56	MG	2A	3068	1/1	0.95	0.15	-	46,46,46,46	0
56	MG	1A	3501	1/1	0.94	0.20	-	36,36,36,36	0
56	MG	1A	3397	1/1	0.94	0.06	-	57,57,57,57	0
56	MG	1A	3575	1/1	0.89	0.10	-	65,65,65,65	0
56	MG	1a	1788	1/1	0.96	0.23	-	46,46,46,46	0
56	MG	2A	3514	1/1	0.95	0.09	-	54,54,54,54	0
56	MG	1a	1884	1/1	0.79	0.49	-	58,58,58,58	0
56	MG	2a	1848	1/1	0.95	0.10	-	57,57,57,57	0
56	MG	2a	1729	1/1	0.89	0.12	-	70,70,70,70	0
56	MG	1A	3792	1/1	0.97	0.20	-	21,21,21,21	0
56	MG	1A	3151	1/1	0.96	0.17	-	31,31,31,31	0
56	MG	1A	4062	1/1	0.81	0.16	-	63,63,63,63	0
56	MG	1f	3001	1/1	0.89	0.25	-	47,47,47,47	0
56	MG	2a	1621	1/1	0.98	0.14	-	47,47,47,47	0
56	MG	1a	1810	1/1	0.92	0.17	-	74,74,74,74	0
56	MG	1A	3069	1/1	0.87	0.20	-	50,50,50,50	0
56	MG	1A	3011	1/1	0.74	0.25	-	49,49,49,49	0
56	MG	1a	1827	1/1	0.94	0.16	-	44,44,44,44	0
56	MG	1A	3449	1/1	0.93	0.12	-	55,55,55,55	0
56	MG	1A	3343	1/1	0.93	0.23	-	41,41,41,41	0
56	MG	1a	1608	1/1	0.89	0.20	-	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	1817	1/1	0.94	0.15	-	61,61,61,61	0
56	MG	1A	3302	1/1	0.95	0.14	-	15,15,15,15	0
56	MG	1A	3201	1/1	0.98	0.39	-	17,17,17,17	0
56	MG	2d	502	1/1	0.86	0.38	-	48,48,48,48	0
56	MG	1A	3136	1/1	0.96	0.23	-	37,37,37,37	0
56	MG	1A	3484	1/1	0.98	0.13	-	34,34,34,34	0
56	MG	17	103	1/1	0.95	0.11	-	40,40,40,40	0
56	MG	1a	1830	1/1	0.98	0.12	-	36,36,36,36	0
56	MG	2A	3038	1/1	0.96	0.18	-	45,45,45,45	0
56	MG	1W	3006	1/1	0.94	0.07	-	35,35,35,35	0
56	MG	1A	4160	1/1	0.87	0.33	-	45,45,45,45	0
56	MG	1A	3494	1/1	0.99	0.17	-	59,59,59,59	0
56	MG	1A	3085	1/1	0.94	0.24	-	43,43,43,43	0
56	MG	1A	3160	1/1	0.89	0.09	-	42,42,42,42	0
56	MG	2A	3428	1/1	0.80	0.09	-	62,62,62,62	0
56	MG	1W	3004	1/1	0.97	0.17	-	31,31,31,31	0
56	MG	1A	4063	1/1	0.95	0.17	-	64,64,64,64	0
56	MG	1A	3755	1/1	0.88	0.11	-	52,52,52,52	0
56	MG	1A	3902	1/1	0.98	0.20	-	38,38,38,38	0
56	MG	2a	1605	1/1	0.89	0.38	-	74,74,74,74	0
56	MG	1a	1651	1/1	0.92	0.32	-	48,48,48,48	0
56	MG	1A	3350	1/1	0.92	0.18	-	45,45,45,45	0
56	MG	1A	3502	1/1	0.85	0.11	-	67,67,67,67	0
56	MG	1A	3964	1/1	0.95	0.25	-	41,41,41,41	0
56	MG	10	101	1/1	0.95	0.20	-	48,48,48,48	0
56	MG	2A	3493	1/1	0.95	0.24	-	40,40,40,40	0
56	MG	2a	1767	1/1	0.57	0.10	-	88,88,88,88	0
56	MG	1A	3785	1/1	0.88	0.17	-	45,45,45,45	0
56	MG	2a	1615	1/1	0.96	0.87	-	63,63,63,63	0
56	MG	2A	3497	1/1	0.92	0.07	-	52,52,52,52	0
56	MG	1a	1716	1/1	0.69	0.29	-	79,79,79,79	0
56	MG	1a	1739	1/1	0.97	0.06	-	64,64,64,64	0
56	MG	1a	1678	1/1	0.94	0.15	-	41,41,41,41	0
56	MG	2a	1641	1/1	0.77	0.14	-	60,60,60,60	0
56	MG	2A	3314	1/1	0.94	0.06	-	63,63,63,63	0
56	MG	2A	3369	1/1	0.96	0.25	-	42,42,42,42	0
56	MG	2A	3149	1/1	0.95	0.19	-	35,35,35,35	0
56	MG	1A	3362	1/1	0.90	0.27	-	45,45,45,45	0
56	MG	1a	1815	1/1	0.96	0.16	-	43,43,43,43	0
56	MG	1A	3526	1/1	0.93	0.22	-	70,70,70,70	0
56	MG	1A	3366	1/1	0.88	0.22	-	37,37,37,37	0
56	MG	2a	1843	1/1	0.98	0.20	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	1750	1/1	0.93	0.24	-	54,54,54,54	0
56	MG	2A	3123	1/1	0.89	0.30	-	58,58,58,58	0
56	MG	1A	4069	1/1	0.97	0.15	-	37,37,37,37	0
56	MG	1A	3389	1/1	0.71	0.15	-	72,72,72,72	0
56	MG	1B	214	1/1	0.93	0.11	-	37,37,37,37	0
56	MG	1A	3218	1/1	0.95	0.32	-	35,35,35,35	0
56	MG	1A	3150	1/1	0.98	0.12	-	22,22,22,22	0
56	MG	2A	3341	1/1	0.95	0.14	-	54,54,54,54	0
56	MG	2a	1634	1/1	0.74	0.51	-	64,64,64,64	0
56	MG	1a	1751	1/1	0.85	0.10	-	70,70,70,70	0
56	MG	1A	3865	1/1	0.96	0.17	-	50,50,50,50	0
56	MG	2A	3409	1/1	0.85	0.23	-	59,59,59,59	0
56	MG	1A	3912	1/1	0.93	0.19	-	54,54,54,54	0
56	MG	2B	3004	1/1	0.97	0.17	-	41,41,41,41	0
56	MG	2A	3592	1/1	0.95	0.20	-	51,51,51,51	0
56	MG	1A	3509	1/1	0.92	0.20	-	50,50,50,50	0
56	MG	1A	3656	1/1	0.90	0.22	-	43,43,43,43	0
56	MG	2A	3420	1/1	0.94	0.14	-	46,46,46,46	0
56	MG	1A	3632	1/1	0.88	0.08	-	63,63,63,63	0
56	MG	2A	3278	1/1	0.94	0.29	-	44,44,44,44	0
56	MG	1A	3447	1/1	0.94	0.14	-	43,43,43,43	0
56	MG	1A	3805	1/1	0.90	0.12	-	54,54,54,54	0
56	MG	1A	3720	1/1	0.94	0.09	-	47,47,47,47	0
56	MG	2A	3403	1/1	0.90	0.10	-	62,62,62,62	0
56	MG	1A	3826	1/1	0.96	0.19	-	37,37,37,37	0
56	MG	2F	301	1/1	0.91	0.11	-	38,38,38,38	0
56	MG	1A	3542	1/1	0.97	0.13	-	37,37,37,37	0
56	MG	1A	3046	1/1	0.95	0.17	-	51,51,51,51	0
56	MG	2A	3558	1/1	0.93	0.19	-	42,42,42,42	0
56	MG	2A	3162	1/1	0.85	0.13	-	60,60,60,60	0
56	MG	1A	3318	1/1	0.75	0.40	-	63,63,63,63	0
56	MG	2A	3519	1/1	0.97	0.04	-	45,45,45,45	0
56	MG	1A	3091	1/1	0.89	0.37	-	50,50,50,50	0
56	MG	1A	3926	1/1	0.99	0.07	-	15,15,15,15	0
56	MG	2A	3295	1/1	0.88	0.07	-	47,47,47,47	0
56	MG	1A	3344	1/1	0.95	0.18	-	41,41,41,41	0
56	MG	1A	4199	1/1	0.90	0.24	-	53,53,53,53	0
56	MG	2A	3438	1/1	0.98	0.10	-	26,26,26,26	0
56	MG	2a	1619	1/1	0.84	0.42	-	91,91,91,91	0
56	MG	1a	1769	1/1	0.92	0.13	-	66,66,66,66	0
56	MG	1A	3269	1/1	0.92	0.18	-	20,20,20,20	0
56	MG	2a	1635	1/1	0.93	0.17	-	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1e	201	1/1	0.94	0.14	-	63,63,63,63	0
56	MG	1a	1881	1/1	0.83	0.23	-	69,69,69,69	0
56	MG	1B	209	1/1	0.90	0.25	-	68,68,68,68	0
56	MG	1a	1778	1/1	0.92	0.24	-	83,83,83,83	0
56	MG	1A	3012	1/1	0.89	0.14	-	49,49,49,49	0
56	MG	1a	1613	1/1	0.95	0.34	-	61,61,61,61	0
56	MG	1A	4105	1/1	0.94	0.29	-	45,45,45,45	0
56	MG	2A	3269	1/1	0.96	0.28	-	34,34,34,34	0
56	MG	1A	3971	1/1	0.91	0.07	-	47,47,47,47	0
56	MG	1a	1824	1/1	0.98	0.20	-	59,59,59,59	0
56	MG	1A	3649	1/1	0.97	0.11	-	26,26,26,26	0
56	MG	1A	3395	1/1	0.87	0.26	-	51,51,51,51	0
56	MG	1A	3451	1/1	0.98	0.12	-	38,38,38,38	0
56	MG	2A	3172	1/1	0.94	0.24	-	49,49,49,49	0
56	MG	1A	3492	1/1	0.97	0.34	-	52,52,52,52	0
56	MG	1A	3424	1/1	0.85	0.12	-	53,53,53,53	0
56	MG	1A	3588	1/1	0.93	0.13	-	51,51,51,51	0
56	MG	1A	3533	1/1	0.92	0.59	-	75,75,75,75	0
56	MG	1A	3079	1/1	0.98	0.24	-	63,63,63,63	0
56	MG	1A	3059	1/1	0.89	0.19	-	38,38,38,38	0
56	MG	10	102	1/1	0.78	0.24	-	54,54,54,54	0
56	MG	1A	3504	1/1	0.75	0.23	-	61,61,61,61	0
56	MG	1A	3279	1/1	0.94	0.14	-	41,41,41,41	0
56	MG	1A	3337	1/1	0.91	0.20	-	46,46,46,46	0
56	MG	2a	1798	1/1	0.90	0.10	-	47,47,47,47	0
56	MG	2A	3041	1/1	0.95	0.39	-	49,49,49,49	0
56	MG	2A	3048	1/1	0.94	0.29	-	43,43,43,43	0
56	MG	1A	4066	1/1	0.94	0.15	-	71,71,71,71	0
56	MG	2a	1620	1/1	0.84	0.49	-	51,51,51,51	0
56	MG	2A	3349	1/1	0.81	0.15	-	64,64,64,64	0
56	MG	1A	3730	1/1	0.94	0.22	-	44,44,44,44	0
56	MG	19	104	1/1	0.97	0.09	-	59,59,59,59	0
56	MG	1A	4166	1/1	0.92	0.24	-	36,36,36,36	0
56	MG	2A	3524	1/1	0.84	0.29	-	75,75,75,75	0
56	MG	1A	3512	1/1	0.92	0.09	-	41,41,41,41	0
56	MG	12	3001	1/1	0.93	0.18	-	52,52,52,52	0
56	MG	1A	3338	1/1	0.96	0.24	-	32,32,32,32	0
56	MG	1a	1633	1/1	0.98	0.16	-	64,64,64,64	0
56	MG	2a	1655	1/1	0.88	0.09	-	92,92,92,92	0
56	MG	2a	1685	1/1	0.77	0.12	-	83,83,83,83	0
56	MG	2A	3194	1/1	0.93	0.12	-	50,50,50,50	0
56	MG	2a	1731	1/1	0.90	0.10	-	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3698	1/1	0.97	0.30	-	51,51,51,51	0
56	MG	1A	3906	1/1	0.94	0.16	-	34,34,34,34	0
56	MG	2A	3012	1/1	0.97	0.35	-	53,53,53,53	0
56	MG	1V	202	1/1	0.93	0.09	-	51,51,51,51	0
56	MG	1A	3589	1/1	0.81	0.57	-	56,56,56,56	0
56	MG	1A	3840	1/1	0.89	0.14	-	69,69,69,69	0
56	MG	2a	1828	1/1	0.95	0.33	-	48,48,48,48	0
56	MG	1B	205	1/1	0.83	0.20	-	57,57,57,57	0
56	MG	2A	3382	1/1	0.93	0.26	-	43,43,43,43	0
56	MG	2A	3076	1/1	0.92	0.12	-	44,44,44,44	0
56	MG	1a	1809	1/1	0.98	0.14	-	41,41,41,41	0
56	MG	1a	1848	1/1	0.97	0.28	-	53,53,53,53	0
56	MG	2A	3416	1/1	0.88	0.12	-	58,58,58,58	0
56	MG	2A	3400	1/1	0.89	0.26	-	52,52,52,52	0
56	MG	2A	3490	1/1	0.91	0.20	-	45,45,45,45	0
56	MG	1A	3847	1/1	0.96	0.13	-	33,33,33,33	0
56	MG	1A	4080	1/1	0.91	0.18	-	56,56,56,56	0
56	MG	2A	3475	1/1	0.90	0.17	-	57,57,57,57	0
56	MG	1A	3972	1/1	0.86	0.27	-	59,59,59,59	0
56	MG	2A	3448	1/1	0.98	0.05	-	44,44,44,44	0
56	MG	2A	3001	1/1	0.84	0.24	-	38,38,38,38	0
56	MG	2A	3073	1/1	0.90	0.54	-	48,48,48,48	0
56	MG	1A	3036	1/1	0.89	0.19	-	66,66,66,66	0
56	MG	2a	1704	1/1	0.97	0.09	-	67,67,67,67	0
56	MG	1A	4154	1/1	0.96	0.15	-	33,33,33,33	0
56	MG	1A	3104	1/1	0.95	0.13	-	60,60,60,60	0
56	MG	1A	4174	1/1	0.73	0.39	-	62,62,62,62	0
56	MG	1A	3334	1/1	0.91	0.26	-	51,51,51,51	0
56	MG	1A	3441	1/1	0.73	0.20	-	62,62,62,62	0
56	MG	1A	3293	1/1	0.94	0.09	-	42,42,42,42	0
56	MG	1A	3627	1/1	0.95	0.13	-	59,59,59,59	0
56	MG	2A	3537	1/1	0.92	0.14	-	49,49,49,49	0
56	MG	2l	3005	1/1	0.93	0.07	-	48,48,48,48	0
56	MG	1A	3558	1/1	0.94	0.18	-	49,49,49,49	0
56	MG	1A	3307	1/1	0.92	0.22	-	37,37,37,37	0
56	MG	1A	4190	1/1	0.91	0.35	-	51,51,51,51	0
56	MG	1A	3466	1/1	0.79	0.15	-	63,63,63,63	0
56	MG	1A	3957	1/1	0.90	0.22	-	46,46,46,46	0
56	MG	1A	3426	1/1	0.86	0.19	-	65,65,65,65	0
56	MG	1l	102	1/1	0.96	0.18	-	34,34,34,34	0
56	MG	1A	3181	1/1	0.96	0.14	-	37,37,37,37	0
56	MG	1A	3852	1/1	0.91	0.07	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	4116	1/1	0.97	0.22	-	17,17,17,17	0
56	MG	1A	4094	1/1	0.94	0.26	-	34,34,34,34	0
56	MG	1A	3025	1/1	0.84	0.22	-	52,52,52,52	0
56	MG	1R	204	1/1	0.79	0.27	-	56,56,56,56	0
56	MG	1A	3363	1/1	0.74	0.32	-	71,71,71,71	0
56	MG	1a	1817	1/1	0.93	0.34	-	59,59,59,59	0
56	MG	2A	3380	1/1	0.97	0.13	-	47,47,47,47	0
56	MG	1A	3854	1/1	0.91	0.15	-	36,36,36,36	0
56	MG	2A	3522	1/1	0.95	0.08	-	32,32,32,32	0
56	MG	1A	3117	1/1	0.95	0.40	-	43,43,43,43	0
56	MG	1A	3872	1/1	0.96	0.22	-	16,16,16,16	0
56	MG	1A	3941	1/1	0.88	0.33	-	32,32,32,32	0
56	MG	1a	1635	1/1	0.89	0.20	-	87,87,87,87	0
56	MG	2A	3518	1/1	0.76	0.10	-	58,58,58,58	0
56	MG	2A	3303	1/1	0.97	0.48	-	56,56,56,56	0
56	MG	2a	1719	1/1	0.96	0.32	-	43,43,43,43	0
56	MG	2a	1679	1/1	0.92	0.30	-	61,61,61,61	0
56	MG	1A	4128	1/1	0.95	0.17	-	53,53,53,53	0
56	MG	1A	3400	1/1	0.83	0.23	-	44,44,44,44	0
56	MG	2A	3109	1/1	0.91	0.14	-	55,55,55,55	0
56	MG	1A	4156	1/1	0.90	0.20	-	59,59,59,59	0
56	MG	1A	3943	1/1	0.64	0.27	-	74,74,74,74	0
56	MG	1A	3715	1/1	0.94	0.17	-	22,22,22,22	0
56	MG	1a	1755	1/1	0.96	0.32	-	65,65,65,65	0
56	MG	2a	1652	1/1	0.89	0.12	-	86,86,86,86	0
56	MG	1A	3026	1/1	0.96	0.24	-	56,56,56,56	0
56	MG	1A	3638	1/1	0.98	0.21	-	17,17,17,17	0
56	MG	10	105	1/1	0.95	0.06	-	43,43,43,43	0
56	MG	1x	111	1/1	0.87	0.24	-	61,61,61,61	0
56	MG	1A	3787	1/1	0.94	0.15	-	33,33,33,33	0
56	MG	2a	1846	1/1	0.82	0.28	-	78,78,78,78	0
56	MG	1a	1758	1/1	0.91	0.14	-	53,53,53,53	0
56	MG	2A	3345	1/1	0.93	0.12	-	55,55,55,55	0
56	MG	1A	3432	1/1	0.92	0.17	-	52,52,52,52	0
56	MG	1U	201	1/1	0.85	0.13	-	32,32,32,32	0
56	MG	1A	3086	1/1	0.99	0.38	-	43,43,43,43	0
56	MG	1A	3487	1/1	0.89	0.18	-	46,46,46,46	0
56	MG	1A	3543	1/1	0.91	0.35	-	46,46,46,46	0
56	MG	1A	3609	1/1	0.91	0.19	-	31,31,31,31	0
56	MG	1A	3524	1/1	0.89	0.18	-	51,51,51,51	0
56	MG	2a	1830	1/1	0.97	0.19	-	56,56,56,56	0
56	MG	1B	224	1/1	0.98	0.30	-	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1866	1/1	0.98	0.10	-	72,72,72,72	0
56	MG	1A	4019	1/1	0.88	0.25	-	75,75,75,75	0
56	MG	2a	1756	1/1	0.94	0.10	-	62,62,62,62	0
56	MG	1A	4040	1/1	0.92	0.17	-	67,67,67,67	0
56	MG	1a	1844	1/1	0.69	0.14	-	56,56,56,56	0
56	MG	2A	3279	1/1	0.91	0.14	-	72,72,72,72	0
56	MG	2A	3405	1/1	0.88	0.14	-	64,64,64,64	0
56	MG	1A	3858	1/1	0.94	0.28	-	48,48,48,48	0
56	MG	2B	3003	1/1	0.95	0.23	-	51,51,51,51	0
56	MG	1a	1859	1/1	0.94	0.07	-	67,67,67,67	0
56	MG	2A	3015	1/1	0.72	0.39	-	55,55,55,55	0
56	MG	1A	4161	1/1	0.93	0.19	-	45,45,45,45	0
56	MG	1A	3743	1/1	0.98	0.14	-	45,45,45,45	0
56	MG	1A	3034	1/1	0.95	0.37	-	71,71,71,71	0
56	MG	1A	3804	1/1	0.93	0.17	-	71,71,71,71	0
56	MG	1A	3550	1/1	0.94	0.29	-	40,40,40,40	0
56	MG	1A	3777	1/1	0.98	0.20	-	31,31,31,31	0
56	MG	2A	3030	1/1	0.94	0.20	-	44,44,44,44	0
56	MG	1A	4014	1/1	0.95	0.08	-	39,39,39,39	0
56	MG	2a	1722	1/1	0.83	0.27	-	71,71,71,71	0
56	MG	28	102	1/1	0.85	0.36	-	60,60,60,60	0
56	MG	2A	3454	1/1	0.87	0.13	-	30,30,30,30	0
56	MG	2A	3429	1/1	0.96	0.30	-	43,43,43,43	0
56	MG	1A	4004	1/1	0.76	0.22	-	68,68,68,68	0
56	MG	1a	1632	1/1	0.93	0.24	-	72,72,72,72	0
56	MG	1A	3298	1/1	0.89	0.21	-	57,57,57,57	0
56	MG	1A	4083	1/1	0.93	0.13	-	45,45,45,45	0
56	MG	1a	1762	1/1	0.94	0.17	-	67,67,67,67	0
56	MG	1A	3195	1/1	0.91	0.23	-	37,37,37,37	0
56	MG	2A	3376	1/1	0.95	0.11	-	48,48,48,48	0
56	MG	2A	3481	1/1	0.88	0.22	-	48,48,48,48	0
56	MG	1A	3077	1/1	0.89	0.12	-	43,43,43,43	0
56	MG	1A	3758	1/1	0.96	0.08	-	46,46,46,46	0
56	MG	1a	1691	1/1	0.85	0.23	-	59,59,59,59	0
56	MG	1A	4043	1/1	0.75	0.29	-	62,62,62,62	0
56	MG	1A	3152	1/1	0.89	0.14	-	45,45,45,45	0
56	MG	1A	3977	1/1	0.88	0.14	-	58,58,58,58	0
56	MG	2A	3180	1/1	0.86	0.11	-	43,43,43,43	0
56	MG	1A	3579	1/1	0.95	0.19	-	38,38,38,38	0
56	MG	2A	3459	1/1	0.94	0.11	-	33,33,33,33	0
56	MG	2a	1810	1/1	0.91	0.32	-	59,59,59,59	0
56	MG	1A	3300	1/1	0.93	0.10	-	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3185	1/1	0.95	0.16	-	24,24,24,24	0
56	MG	1A	3410	1/1	0.92	0.34	-	22,22,22,22	0
56	MG	1A	4003	1/1	0.73	0.26	-	92,92,92,92	0
56	MG	2A	3143	1/1	0.98	0.06	-	47,47,47,47	0
56	MG	1A	3109	1/1	0.96	0.24	-	62,62,62,62	0
56	MG	1A	3309	1/1	0.90	0.77	-	65,65,65,65	0
56	MG	2a	1668	1/1	0.86	0.30	-	69,69,69,69	0
56	MG	2A	3439	1/1	0.86	0.15	-	48,48,48,48	0
56	MG	1A	3029	1/1	0.95	0.39	-	55,55,55,55	0
56	MG	1A	3551	1/1	0.90	0.19	-	53,53,53,53	0
56	MG	2A	3259	1/1	0.84	0.26	-	34,34,34,34	0
56	MG	1a	1842	1/1	0.89	0.25	-	49,49,49,49	0
56	MG	2A	3554	1/1	0.95	0.13	-	35,35,35,35	0
56	MG	2a	1762	1/1	0.88	0.12	-	64,64,64,64	0
56	MG	1A	3028	1/1	0.96	0.27	-	39,39,39,39	0
56	MG	1A	4027	1/1	0.96	0.15	-	72,72,72,72	0
56	MG	1A	3980	1/1	0.93	0.13	-	42,42,42,42	0
56	MG	1a	1653	1/1	0.93	0.11	-	52,52,52,52	0
56	MG	1a	1840	1/1	0.92	0.13	-	51,51,51,51	0
56	MG	1a	1640	1/1	0.96	0.14	-	62,62,62,62	0
56	MG	1A	3259	1/1	0.96	0.20	-	46,46,46,46	0
56	MG	1B	201	1/1	0.90	0.21	-	64,64,64,64	0
56	MG	2A	3026	1/1	0.83	0.18	-	47,47,47,47	0
56	MG	1A	3706	1/1	0.93	0.14	-	25,25,25,25	0
56	MG	1A	3921	1/1	0.94	0.22	-	23,23,23,23	0
56	MG	1A	3133	1/1	0.94	0.12	-	55,55,55,55	0
56	MG	1A	3295	1/1	0.97	0.32	-	45,45,45,45	0
56	MG	1A	3294	1/1	0.96	0.14	-	52,52,52,52	0
56	MG	2A	3018	1/1	0.87	0.11	-	58,58,58,58	0
56	MG	1A	3843	1/1	0.96	0.18	-	46,46,46,46	0
56	MG	1A	3978	1/1	0.86	0.47	-	38,38,38,38	0
56	MG	1A	4097	1/1	0.98	0.30	-	27,27,27,27	0
56	MG	1A	4145	1/1	0.97	0.17	-	63,63,63,63	0
56	MG	1A	3131	1/1	0.93	0.25	-	43,43,43,43	0
56	MG	2A	3326	1/1	0.96	0.17	-	53,53,53,53	0
56	MG	1a	1796	1/1	0.94	0.07	-	55,55,55,55	0
56	MG	1A	3993	1/1	0.98	0.14	-	32,32,32,32	0
56	MG	2A	3075	1/1	0.99	0.34	-	24,24,24,24	0
56	MG	1A	3834	1/1	0.96	0.25	-	36,36,36,36	0
56	MG	1A	3368	1/1	0.91	0.17	-	65,65,65,65	0
56	MG	1a	1832	1/1	0.93	0.22	-	52,52,52,52	0
56	MG	1a	1735	1/1	0.97	0.25	-	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3586	1/1	0.96	0.26	-	54,54,54,54	0
56	MG	2a	1808	1/1	0.83	0.15	-	65,65,65,65	0
56	MG	1A	3224	1/1	0.97	0.06	-	41,41,41,41	0
56	MG	2A	3245	1/1	0.96	0.10	-	58,58,58,58	0
56	MG	1A	3270	1/1	0.97	0.20	-	26,26,26,26	0
56	MG	1A	3172	1/1	0.90	0.20	-	28,28,28,28	0
56	MG	2a	1781	1/1	0.81	0.08	-	56,56,56,56	0
56	MG	2B	3006	1/1	0.95	0.37	-	57,57,57,57	0
56	MG	1A	4106	1/1	0.97	0.20	-	45,45,45,45	0
56	MG	2A	3199	1/1	0.91	0.14	-	34,34,34,34	0
56	MG	1A	4042	1/1	0.98	0.04	-	50,50,50,50	0
56	MG	1a	1855	1/1	0.84	0.21	-	57,57,57,57	0
56	MG	2A	3094	1/1	0.95	0.23	-	49,49,49,49	0
56	MG	1A	3014	1/1	0.92	0.34	-	51,51,51,51	0
56	MG	2A	3553	1/1	0.95	0.21	-	44,44,44,44	0
56	MG	1A	4158	1/1	0.96	0.32	-	23,23,23,23	0
56	MG	1A	3359	1/1	0.97	0.30	-	43,43,43,43	0
56	MG	2A	3551	1/1	0.93	0.14	-	40,40,40,40	0
56	MG	1B	213	1/1	0.98	0.30	-	59,59,59,59	0
56	MG	1A	3335	1/1	0.95	0.19	-	36,36,36,36	0
56	MG	1A	3645	1/1	0.94	0.09	-	59,59,59,59	0
56	MG	1A	3387	1/1	0.93	0.13	-	54,54,54,54	0
56	MG	2a	1654	1/1	0.74	0.09	-	80,80,80,80	0
56	MG	2A	3202	1/1	0.93	0.15	-	40,40,40,40	0
56	MG	2a	1743	1/1	0.92	0.28	-	64,64,64,64	0
56	MG	1A	3770	1/1	0.91	0.27	-	25,25,25,25	0
56	MG	1A	3080	1/1	0.81	0.10	-	51,51,51,51	0
56	MG	2A	3067	1/1	0.95	0.44	-	54,54,54,54	0
56	MG	1A	4133	1/1	0.98	0.28	-	47,47,47,47	0
56	MG	2A	3126	1/1	0.93	0.49	-	47,47,47,47	0
56	MG	1A	3461	1/1	0.88	0.26	-	62,62,62,62	0
56	MG	2A	3363	1/1	0.94	0.20	-	30,30,30,30	0
56	MG	1a	1730	1/1	0.94	0.19	-	56,56,56,56	0
56	MG	2a	1690	1/1	0.87	0.27	-	58,58,58,58	0
56	MG	2A	3138	1/1	0.90	0.21	-	55,55,55,55	0
56	MG	2A	3356	1/1	0.93	0.15	-	49,49,49,49	0
56	MG	1A	4194	1/1	0.92	0.16	-	41,41,41,41	0
56	MG	1a	1889	1/1	0.96	0.25	-	39,39,39,39	0
56	MG	1A	3149	1/1	0.82	0.21	-	58,58,58,58	0
56	MG	1A	3108	1/1	0.92	0.46	-	46,46,46,46	0
56	MG	1a	1839	1/1	0.95	0.19	-	54,54,54,54	0
56	MG	1a	1770	1/1	0.92	0.37	-	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	4057	1/1	0.95	0.11	-	71,71,71,71	0
56	MG	1A	4056	1/1	0.78	0.41	-	74,74,74,74	0
56	MG	1a	1612	1/1	0.86	0.26	-	82,82,82,82	0
56	MG	2A	3446	1/1	0.92	0.12	-	53,53,53,53	0
56	MG	1A	4016	1/1	0.94	0.15	-	65,65,65,65	0
56	MG	2A	3193	1/1	0.91	0.23	-	48,48,48,48	0
56	MG	2A	3536	1/1	0.89	0.28	-	66,66,66,66	0
56	MG	1A	3066	1/1	0.92	0.18	-	41,41,41,41	0
56	MG	2a	1813	1/1	0.96	0.27	-	74,74,74,74	0
56	MG	1A	3692	1/1	0.93	0.38	-	37,37,37,37	0
56	MG	2A	3070	1/1	0.90	0.17	-	45,45,45,45	0
56	MG	10	107	1/1	0.99	0.10	-	52,52,52,52	0
56	MG	1a	1715	1/1	0.88	0.20	-	51,51,51,51	0
56	MG	1A	4167	1/1	0.96	0.47	-	44,44,44,44	0
56	MG	1A	3536	1/1	0.92	0.07	-	67,67,67,67	0
56	MG	2A	3430	1/1	0.93	0.12	-	54,54,54,54	0
56	MG	1A	4073	1/1	0.90	0.16	-	58,58,58,58	0
56	MG	1A	4144	1/1	0.97	0.28	-	67,67,67,67	0
56	MG	1A	3876	1/1	0.88	0.11	-	64,64,64,64	0
56	MG	1a	1777	1/1	0.86	0.59	-	72,72,72,72	0
56	MG	1B	216	1/1	0.99	0.19	-	54,54,54,54	0
56	MG	1A	3928	1/1	0.83	0.17	-	51,51,51,51	0
56	MG	2a	1680	1/1	0.86	0.20	-	70,70,70,70	0
56	MG	1A	3208	1/1	0.97	0.28	-	17,17,17,17	0
56	MG	1A	3745	1/1	0.98	0.04	-	43,43,43,43	0
56	MG	1A	3190	1/1	0.97	0.30	-	25,25,25,25	0
56	MG	2A	3095	1/1	0.91	0.33	-	48,48,48,48	0
56	MG	1A	4129	1/1	0.96	0.19	-	56,56,56,56	0
56	MG	1A	3523	1/1	0.98	0.06	-	50,50,50,50	0
56	MG	1A	3425	1/1	0.92	0.13	-	62,62,62,62	0
56	MG	1A	3767	1/1	0.98	0.10	-	36,36,36,36	0
56	MG	1A	4217	1/1	0.81	0.30	-	72,72,72,72	0
56	MG	1a	1703	1/1	0.90	0.36	-	61,61,61,61	0
56	MG	1a	1857	1/1	0.98	0.04	-	70,70,70,70	0
56	MG	1A	3816	1/1	0.81	0.27	-	48,48,48,48	0
56	MG	1a	1885	1/1	0.94	0.11	-	66,66,66,66	0
56	MG	1A	3465	1/1	0.78	0.17	-	71,71,71,71	0
56	MG	2A	3474	1/1	0.89	0.14	-	62,62,62,62	0
56	MG	10	104	1/1	0.97	0.38	-	61,61,61,61	0
56	MG	2A	3003	1/1	0.88	0.17	-	67,67,67,67	0
56	MG	1A	4067	1/1	0.66	0.19	-	71,71,71,71	0
56	MG	1A	3392	1/1	0.90	0.27	-	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	4124	1/1	0.94	0.28	-	33,33,33,33	0
56	MG	2X	8001	1/1	0.94	0.19	-	37,37,37,37	0
56	MG	2a	1730	1/1	0.95	0.07	-	66,66,66,66	0
56	MG	2A	3375	1/1	0.95	0.19	-	32,32,32,32	0
56	MG	1A	3851	1/1	0.97	0.21	-	33,33,33,33	0
56	MG	1A	3206	1/1	0.87	0.26	-	46,46,46,46	0
56	MG	1A	3751	1/1	0.95	0.38	-	43,43,43,43	0
56	MG	2A	3499	1/1	0.84	0.23	-	60,60,60,60	0
56	MG	1A	3297	1/1	0.89	0.29	-	37,37,37,37	0
56	MG	1A	3511	1/1	0.96	0.15	-	35,35,35,35	0
56	MG	18	104	1/1	0.89	0.18	-	63,63,63,63	0
56	MG	2A	3555	1/1	0.89	0.12	-	47,47,47,47	0
56	MG	2A	3006	1/1	0.90	0.20	-	66,66,66,66	0
56	MG	1A	3093	1/1	0.98	0.20	-	35,35,35,35	0
56	MG	2A	3415	1/1	0.91	0.09	-	61,61,61,61	0
56	MG	1A	3457	1/1	0.96	0.09	-	22,22,22,22	0
56	MG	1A	3557	1/1	0.93	0.12	-	53,53,53,53	0
56	MG	1A	4193	1/1	0.87	0.45	-	51,51,51,51	0
56	MG	2A	3426	1/1	0.89	0.13	-	51,51,51,51	0
56	MG	1A	3915	1/1	0.92	0.08	-	44,44,44,44	0
56	MG	2A	3407	1/1	0.96	0.23	-	46,46,46,46	0
56	MG	2A	3163	1/1	0.94	0.18	-	36,36,36,36	0
56	MG	2A	3284	1/1	0.92	0.14	-	42,42,42,42	0
56	MG	2A	3066	1/1	0.84	0.41	-	60,60,60,60	0
56	MG	1A	3061	1/1	0.94	0.16	-	58,58,58,58	0
56	MG	1A	3377	1/1	0.86	0.18	-	48,48,48,48	0
56	MG	1A	3047	1/1	0.93	0.25	-	69,69,69,69	0
56	MG	1a	1609	1/1	0.82	0.09	-	64,64,64,64	0
56	MG	2a	1746	1/1	0.93	0.28	-	43,43,43,43	0
56	MG	1A	3867	1/1	0.94	0.32	-	52,52,52,52	0
56	MG	1a	1625	1/1	0.69	0.33	-	74,74,74,74	0
56	MG	2A	3078	1/1	0.95	0.38	-	51,51,51,51	0
56	MG	1a	1781	1/1	0.97	0.07	-	58,58,58,58	0
56	MG	1A	3856	1/1	0.94	0.36	-	56,56,56,56	0
56	MG	1A	3942	1/1	0.92	0.21	-	44,44,44,44	0
56	MG	2A	3473	1/1	0.94	0.20	-	53,53,53,53	0
56	MG	1A	3306	1/1	0.92	0.34	-	41,41,41,41	0
56	MG	2A	3249	1/1	0.95	0.15	-	29,29,29,29	0
56	MG	1a	1783	1/1	0.94	0.27	-	57,57,57,57	0
56	MG	1A	4138	1/1	0.85	0.18	-	57,57,57,57	0
56	MG	1A	3890	1/1	0.84	0.18	-	45,45,45,45	0
56	MG	1A	3592	1/1	0.97	0.11	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	4000	1/1	0.76	0.34	-	53,53,53,53	0
56	MG	1A	3419	1/1	0.84	0.13	-	75,75,75,75	0
56	MG	2A	3539	1/1	0.93	0.13	-	43,43,43,43	0
56	MG	2A	3329	1/1	0.93	0.11	-	55,55,55,55	0
56	MG	1A	4099	1/1	0.88	0.11	-	33,33,33,33	0
56	MG	1A	3554	1/1	0.91	0.26	-	61,61,61,61	0
56	MG	2A	3273	1/1	0.94	0.30	-	56,56,56,56	0
56	MG	2A	3264	1/1	0.81	0.25	-	47,47,47,47	0
56	MG	1A	3281	1/1	0.98	0.19	-	31,31,31,31	0
56	MG	1A	3468	1/1	0.96	0.17	-	57,57,57,57	0
56	MG	1A	3560	1/1	0.97	0.10	-	44,44,44,44	0
56	MG	1A	3355	1/1	0.94	0.29	-	47,47,47,47	0
56	MG	1A	3142	1/1	0.84	0.13	-	61,61,61,61	0
56	MG	1F	306	1/1	0.92	0.15	-	35,35,35,35	0
56	MG	1A	3898	1/1	0.96	0.09	-	52,52,52,52	0
56	MG	1P	201	1/1	0.91	0.31	-	52,52,52,52	0
56	MG	1a	1742	1/1	0.95	0.25	-	52,52,52,52	0
56	MG	1a	1628	1/1	0.91	0.50	-	55,55,55,55	0
56	MG	1A	4044	1/1	0.93	0.08	-	72,72,72,72	0
56	MG	1e	202	1/1	0.88	0.22	-	62,62,62,62	0
56	MG	2A	3020	1/1	0.91	0.15	-	44,44,44,44	0
56	MG	1A	4233	1/1	0.81	0.21	-	88,88,88,88	0
56	MG	1A	3500	1/1	0.94	0.16	-	55,55,55,55	0
56	MG	1A	4089	1/1	0.95	0.05	-	61,61,61,61	0
56	MG	1A	3207	1/1	0.98	0.14	-	50,50,50,50	0
56	MG	1A	4025	1/1	0.87	0.13	-	69,69,69,69	0
56	MG	1A	3048	1/1	0.94	0.16	-	42,42,42,42	0
56	MG	1A	3591	1/1	0.79	0.23	-	55,55,55,55	0
56	MG	1A	3314	1/1	0.83	0.19	-	38,38,38,38	0
56	MG	1A	3322	1/1	0.96	0.14	-	45,45,45,45	0
56	MG	1A	3241	1/1	0.64	0.42	-	70,70,70,70	0
56	MG	1A	4204	1/1	0.83	0.27	-	56,56,56,56	0
56	MG	2A	3146	1/1	0.94	0.31	-	50,50,50,50	0
56	MG	1A	3180	1/1	0.95	0.10	-	45,45,45,45	0
56	MG	2A	3160	1/1	0.96	0.09	-	46,46,46,46	0
56	MG	2A	3197	1/1	0.81	0.11	-	49,49,49,49	0
56	MG	2a	1603	1/1	0.92	0.39	-	59,59,59,59	0
56	MG	2A	3343	1/1	0.77	0.29	-	55,55,55,55	0
56	MG	1a	1620	1/1	0.96	0.24	-	38,38,38,38	0
56	MG	1B	215	1/1	0.97	0.19	-	31,31,31,31	0
56	MG	1a	1611	1/1	0.82	0.18	-	72,72,72,72	0
56	MG	1A	3913	1/1	0.62	0.53	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3226	1/1	0.94	0.16	-	38,38,38,38	0
56	MG	2A	3229	1/1	0.97	0.14	-	38,38,38,38	0
56	MG	1A	3405	1/1	0.94	0.24	-	45,45,45,45	0
56	MG	1a	1662	1/1	0.95	0.20	-	42,42,42,42	0
56	MG	1A	4007	1/1	0.91	0.16	-	49,49,49,49	0
56	MG	1a	1654	1/1	0.95	0.34	-	51,51,51,51	0
56	MG	2A	3141	1/1	0.94	0.47	-	53,53,53,53	0
56	MG	1A	3878	1/1	0.95	0.19	-	68,68,68,68	0
56	MG	1A	3888	1/1	0.91	0.20	-	29,29,29,29	0
56	MG	1A	4142	1/1	0.94	0.25	-	39,39,39,39	0
56	MG	1x	109	1/1	0.94	0.21	-	47,47,47,47	0
56	MG	2A	3261	1/1	0.81	0.18	-	41,41,41,41	0
56	MG	2A	3433	1/1	0.97	0.06	-	48,48,48,48	0
56	MG	1A	4176	1/1	0.96	0.28	-	41,41,41,41	0
56	MG	1A	3105	1/1	0.87	0.26	-	43,43,43,43	0
56	MG	1A	3261	1/1	0.96	0.30	-	22,22,22,22	0
56	MG	1A	3709	1/1	0.97	0.19	-	29,29,29,29	0
56	MG	1A	3380	1/1	0.84	0.21	-	43,43,43,43	0
56	MG	1A	3868	1/1	0.98	0.21	-	59,59,59,59	0
56	MG	1A	4119	1/1	0.91	0.19	-	35,35,35,35	0
56	MG	1A	3455	1/1	0.96	0.15	-	58,58,58,58	0
56	MG	1A	3141	1/1	0.92	0.08	-	46,46,46,46	0
56	MG	2A	3332	1/1	0.94	0.12	-	51,51,51,51	0
56	MG	2a	1737	1/1	0.76	0.15	-	64,64,64,64	0
56	MG	1A	3015	1/1	0.97	0.21	-	42,42,42,42	0
56	MG	1A	4038	1/1	0.92	0.08	-	81,81,81,81	0
56	MG	1A	3539	1/1	0.91	0.07	-	41,41,41,41	0
56	MG	1A	3900	1/1	0.94	0.13	-	45,45,45,45	0
56	MG	2a	1818	1/1	0.92	0.16	-	63,63,63,63	0
56	MG	1A	3944	1/1	0.85	0.20	-	77,77,77,77	0
56	MG	2A	3051	1/1	0.83	0.18	-	51,51,51,51	0
56	MG	2A	3510	1/1	0.92	0.19	-	61,61,61,61	0
56	MG	1A	3101	1/1	0.88	0.05	-	54,54,54,54	0
56	MG	1a	1880	1/1	0.91	0.15	-	46,46,46,46	0
56	MG	2A	3011	1/1	0.92	0.21	-	49,49,49,49	0
56	MG	1a	1786	1/1	0.81	0.14	-	64,64,64,64	0
56	MG	1A	3471	1/1	0.91	0.23	-	47,47,47,47	0
56	MG	1A	3568	1/1	0.86	0.15	-	52,52,52,52	0
56	MG	2A	3432	1/1	0.95	0.08	-	28,28,28,28	0
56	MG	1A	3897	1/1	0.90	0.13	-	32,32,32,32	0
56	MG	1a	1784	1/1	0.90	0.30	-	64,64,64,64	0
56	MG	2x	3002	1/1	0.81	0.20	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1634	1/1	0.84	0.17	-	61,61,61,61	0
56	MG	2A	3434	1/1	0.95	0.10	-	58,58,58,58	0
56	MG	1A	3493	1/1	0.87	0.21	-	58,58,58,58	0
56	MG	1A	3769	1/1	0.92	0.17	-	45,45,45,45	0
56	MG	2A	3570	1/1	0.96	0.24	-	53,53,53,53	0
56	MG	1A	3477	1/1	0.96	0.15	-	26,26,26,26	0
56	MG	2a	1702	1/1	0.96	0.16	-	51,51,51,51	0
56	MG	1A	3873	1/1	0.94	0.27	-	49,49,49,49	0
56	MG	1A	3917	1/1	0.95	0.12	-	37,37,37,37	0
56	MG	1A	3439	1/1	0.94	0.08	-	38,38,38,38	0
56	MG	1a	1834	1/1	0.94	0.10	-	59,59,59,59	0
56	MG	1A	3908	1/1	0.96	0.36	-	37,37,37,37	0
56	MG	1A	4001	1/1	0.81	0.13	-	46,46,46,46	0
56	MG	1a	1761	1/1	0.90	0.15	-	57,57,57,57	0
56	MG	2a	1727	1/1	0.70	0.25	-	70,70,70,70	0
56	MG	1A	3577	1/1	0.94	0.20	-	56,56,56,56	0
56	MG	2a	1637	1/1	0.90	0.23	-	60,60,60,60	0
56	MG	2A	3086	1/1	0.85	0.28	-	48,48,48,48	0
56	MG	2a	1674	1/1	0.97	0.18	-	46,46,46,46	0
56	MG	18	103	1/1	0.87	0.23	-	46,46,46,46	0
56	MG	2a	1751	1/1	0.90	0.12	-	57,57,57,57	0
56	MG	1A	4120	1/1	0.94	0.34	-	50,50,50,50	0
56	MG	1A	3383	1/1	0.94	0.32	-	42,42,42,42	0
56	MG	1P	202	1/1	0.92	0.26	-	49,49,49,49	0
56	MG	1A	3225	1/1	0.96	0.21	-	35,35,35,35	0
56	MG	2A	3007	1/1	0.87	0.24	-	72,72,72,72	0
56	MG	2A	3253	1/1	0.91	0.29	-	58,58,58,58	0
56	MG	2a	1752	1/1	0.97	0.19	-	51,51,51,51	0
56	MG	1A	3376	1/1	0.80	0.13	-	69,69,69,69	0
56	MG	1A	3358	1/1	0.91	0.22	-	46,46,46,46	0
56	MG	2A	3299	1/1	0.86	0.20	-	25,25,25,25	0
56	MG	1A	3111	1/1	0.97	0.16	-	59,59,59,59	0
56	MG	1A	3776	1/1	0.97	0.18	-	25,25,25,25	0
56	MG	2a	1789	1/1	0.65	0.22	-	69,69,69,69	0
56	MG	1A	3453	1/1	0.85	0.16	-	51,51,51,51	0
56	MG	2A	3170	1/1	0.89	0.16	-	46,46,46,46	0
56	MG	2A	3107	1/1	0.91	0.07	-	65,65,65,65	0
56	MG	1A	4015	1/1	0.96	0.21	-	15,15,15,15	0
56	MG	2a	1630	1/1	0.98	0.12	-	60,60,60,60	0
56	MG	1A	3076	1/1	0.85	0.31	-	60,60,60,60	0
56	MG	2A	3136	1/1	0.88	0.17	-	56,56,56,56	0
56	MG	2a	1801	1/1	0.95	0.36	-	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3949	1/1	0.96	0.12	-	37,37,37,37	0
56	MG	1A	4017	1/1	0.86	0.44	-	70,70,70,70	0
56	MG	1A	3275	1/1	0.93	0.17	-	48,48,48,48	0
56	MG	1A	3522	1/1	0.90	0.08	-	52,52,52,52	0
56	MG	1A	3933	1/1	0.98	0.14	-	29,29,29,29	0
56	MG	15	104	1/1	0.96	0.18	-	53,53,53,53	0
56	MG	2A	3542	1/1	0.96	0.33	-	33,33,33,33	0
56	MG	1A	4096	1/1	0.96	0.29	-	22,22,22,22	0
56	MG	2a	1821	1/1	0.96	0.23	-	66,66,66,66	0
56	MG	1a	1875	1/1	0.76	0.14	-	57,57,57,57	0
56	MG	1A	3246	1/1	0.97	0.10	-	13,13,13,13	0
56	MG	2a	1636	1/1	0.84	0.14	-	50,50,50,50	0
56	MG	1a	1664	1/1	0.96	0.12	-	56,56,56,56	0
56	MG	1A	3328	1/1	0.93	0.11	-	44,44,44,44	0
56	MG	1A	4068	1/1	0.95	0.17	-	37,37,37,37	0
56	MG	2a	1712	1/1	0.78	0.30	-	62,62,62,62	0
56	MG	2A	3443	1/1	0.97	0.04	-	39,39,39,39	0
56	MG	2A	3280	1/1	0.98	0.18	-	55,55,55,55	0
56	MG	1B	221	1/1	0.92	0.16	-	44,44,44,44	0
56	MG	1A	3956	1/1	0.95	0.16	-	53,53,53,53	0
56	MG	1A	3880	1/1	0.95	0.17	-	52,52,52,52	0
56	MG	1A	4111	1/1	0.95	0.30	-	32,32,32,32	0
56	MG	2A	3456	1/1	0.89	0.15	-	65,65,65,65	0
56	MG	1A	3144	1/1	0.94	0.12	-	49,49,49,49	0
56	MG	2A	3147	1/1	0.86	0.27	-	47,47,47,47	0
56	MG	2A	3028	1/1	0.94	0.42	-	63,63,63,63	0
56	MG	1A	3110	1/1	0.90	0.12	-	43,43,43,43	0
56	MG	2A	3385	1/1	0.99	0.22	-	36,36,36,36	0
56	MG	2A	3513	1/1	0.89	0.13	-	53,53,53,53	0
56	MG	1A	3113	1/1	0.91	0.31	-	49,49,49,49	0
56	MG	2a	1826	1/1	0.97	0.22	-	53,53,53,53	0
56	MG	2a	1698	1/1	0.87	0.23	-	62,62,62,62	0
56	MG	1A	3672	1/1	0.93	0.18	-	28,28,28,28	0
56	MG	2a	1658	1/1	0.95	0.20	-	79,79,79,79	0
56	MG	1A	3903	1/1	0.97	0.08	-	41,41,41,41	0
56	MG	1A	3681	1/1	0.82	0.21	-	37,37,37,37	0
56	MG	1a	1877	1/1	0.97	0.28	-	59,59,59,59	0
56	MG	1A	3175	1/1	0.93	0.13	-	40,40,40,40	0
56	MG	1A	3364	1/1	0.98	0.14	-	43,43,43,43	0
56	MG	1A	3374	1/1	0.87	0.37	-	53,53,53,53	0
56	MG	1A	3039	1/1	0.96	0.16	-	48,48,48,48	0
56	MG	1A	3521	1/1	0.95	0.26	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1849	1/1	0.96	0.11	-	55,55,55,55	0
56	MG	1a	1719	1/1	0.71	0.48	-	58,58,58,58	0
56	MG	1a	1767	1/1	0.64	0.28	-	72,72,72,72	0
56	MG	1a	1794	1/1	0.98	0.16	-	24,24,24,24	0
56	MG	2A	3248	1/1	0.90	0.21	-	55,55,55,55	0
56	MG	1A	3831	1/1	0.82	0.16	-	53,53,53,53	0
56	MG	1A	4215	1/1	0.96	0.11	-	44,44,44,44	0
56	MG	1A	4155	1/1	0.96	0.17	-	37,37,37,37	0
56	MG	1a	1683	1/1	0.97	0.06	-	52,52,52,52	0
56	MG	1A	4088	1/1	0.91	0.15	-	76,76,76,76	0
56	MG	1E	305	1/1	0.95	0.28	-	35,35,35,35	0
56	MG	2a	1795	1/1	0.94	0.20	-	54,54,54,54	0
56	MG	1A	3734	1/1	0.97	0.09	-	42,42,42,42	0
56	MG	1A	4169	1/1	0.82	0.33	-	57,57,57,57	0
56	MG	2A	3010	1/1	0.86	0.30	-	53,53,53,53	0
56	MG	1a	1813	1/1	0.93	0.25	-	59,59,59,59	0
56	MG	2A	3386	1/1	0.88	0.32	-	52,52,52,52	0
56	MG	1x	107	1/1	0.90	0.17	-	55,55,55,55	0
56	MG	1a	1710	1/1	0.92	0.39	-	58,58,58,58	0
56	MG	2A	3102	1/1	0.91	0.08	-	68,68,68,68	0
56	MG	2E	304	1/1	0.97	0.21	-	40,40,40,40	0
56	MG	1A	4054	1/1	0.86	0.13	-	56,56,56,56	0
56	MG	2a	1802	1/1	0.91	0.19	-	53,53,53,53	0
56	MG	2A	3435	1/1	0.85	0.19	-	54,54,54,54	0
56	MG	1a	1727	1/1	0.82	0.19	-	80,80,80,80	0
56	MG	1A	3099	1/1	0.88	0.18	-	46,46,46,46	0
56	MG	1A	3244	1/1	0.92	0.22	-	45,45,45,45	0
56	MG	2A	3404	1/1	0.92	0.13	-	58,58,58,58	0
56	MG	2A	3230	1/1	0.92	0.13	-	57,57,57,57	0
56	MG	1A	3593	1/1	0.94	0.19	-	49,49,49,49	0
56	MG	2a	1760	1/1	0.71	0.20	-	67,67,67,67	0
56	MG	1a	1801	1/1	0.96	0.19	-	36,36,36,36	0
56	MG	1A	3990	1/1	0.93	0.12	-	53,53,53,53	0
56	MG	1A	3348	1/1	0.76	0.15	-	57,57,57,57	0
56	MG	1A	4059	1/1	0.90	0.14	-	60,60,60,60	0
56	MG	1A	3084	1/1	0.86	0.60	-	53,53,53,53	0
56	MG	2A	3091	1/1	0.95	0.14	-	39,39,39,39	0
56	MG	2a	1768	1/1	0.69	0.74	-	86,86,86,86	0
56	MG	1A	4226	1/1	0.88	0.37	-	45,45,45,45	0
56	MG	1A	4050	1/1	0.94	0.11	-	53,53,53,53	0
56	MG	1A	3850	1/1	0.95	0.17	-	40,40,40,40	0
56	MG	1A	3008	1/1	0.89	0.31	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3345	1/1	0.94	0.14	-	25,25,25,25	0
56	MG	1A	3456	1/1	0.95	0.10	-	41,41,41,41	0
56	MG	1A	3546	1/1	0.98	0.11	-	46,46,46,46	0
56	MG	1A	3050	1/1	0.93	0.17	-	48,48,48,48	0
56	MG	1A	3817	1/1	0.96	0.10	-	45,45,45,45	0
56	MG	1a	1775	1/1	0.93	0.18	-	55,55,55,55	0
56	MG	1A	3696	1/1	0.93	0.25	-	45,45,45,45	0
56	MG	2A	3189	1/1	0.96	0.11	-	33,33,33,33	0
56	MG	2A	3089	1/1	0.84	0.28	-	51,51,51,51	0
56	MG	2A	3538	1/1	0.96	0.12	-	42,42,42,42	0
56	MG	1a	1663	1/1	0.96	0.17	-	61,61,61,61	0
56	MG	1A	3797	1/1	0.95	0.16	-	41,41,41,41	0
56	MG	1A	3973	1/1	0.89	0.15	-	55,55,55,55	0
56	MG	2A	3365	1/1	0.93	0.23	-	46,46,46,46	0
56	MG	1A	4146	1/1	0.96	0.21	-	40,40,40,40	0
56	MG	1A	3002	1/1	0.92	0.12	-	54,54,54,54	0
56	MG	1A	3581	1/1	0.84	0.20	-	62,62,62,62	0
56	MG	1H	8001	1/1	0.96	0.17	-	72,72,72,72	0
56	MG	1A	3959	1/1	0.95	0.18	-	47,47,47,47	0
56	MG	2A	3371	1/1	0.96	0.19	-	50,50,50,50	0
56	MG	1a	1607	1/1	0.96	0.10	-	73,73,73,73	0
56	MG	1A	3288	1/1	0.97	0.11	-	13,13,13,13	0
56	MG	1a	1861	1/1	0.82	0.19	-	50,50,50,50	0
56	MG	1A	4065	1/1	0.98	0.11	-	43,43,43,43	0
56	MG	1a	1841	1/1	0.95	0.23	-	49,49,49,49	0
56	MG	1a	1870	1/1	0.86	0.07	-	67,67,67,67	0
56	MG	2a	1693	1/1	0.87	0.28	-	50,50,50,50	0
56	MG	2E	302	1/1	0.96	0.23	-	27,27,27,27	0
56	MG	1A	3710	1/1	0.96	0.23	-	37,37,37,37	0
56	MG	2a	1689	1/1	0.92	0.24	-	60,60,60,60	0
56	MG	1a	1605	1/1	0.93	0.13	-	66,66,66,66	0
56	MG	1A	3367	1/1	0.87	0.12	-	56,56,56,56	0
56	MG	1A	3555	1/1	0.90	0.13	-	51,51,51,51	0
56	MG	2a	1614	1/1	0.95	0.07	-	68,68,68,68	0
56	MG	2x	3003	1/1	0.91	0.07	-	65,65,65,65	0
56	MG	1A	3824	1/1	0.95	0.14	-	56,56,56,56	0
56	MG	1A	4110	1/1	0.94	0.14	-	75,75,75,75	0
56	MG	1A	3784	1/1	0.95	0.10	-	65,65,65,65	0
56	MG	2a	1799	1/1	0.87	0.19	-	65,65,65,65	0
56	MG	1A	4078	1/1	0.75	0.63	-	62,62,62,62	0
56	MG	1A	4036	1/1	0.97	0.17	-	30,30,30,30	0
56	MG	2A	3221	1/1	0.91	0.28	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	1721	1/1	0.93	0.17	-	52,52,52,52	0
56	MG	1A	3612	1/1	0.98	0.27	-	41,41,41,41	0
56	MG	1A	3919	1/1	0.92	0.12	-	16,16,16,16	0
56	MG	2a	1774	1/1	0.96	0.38	-	57,57,57,57	0
56	MG	1a	1688	1/1	0.89	0.12	-	74,74,74,74	0
56	MG	1A	3629	1/1	0.93	0.09	-	33,33,33,33	0
56	MG	1A	3234	1/1	0.95	0.52	-	31,31,31,31	0
56	MG	1A	3112	1/1	0.82	0.25	-	63,63,63,63	0
56	MG	2A	3357	1/1	0.97	0.17	-	29,29,29,29	0
56	MG	1a	1865	1/1	0.86	0.22	-	55,55,55,55	0
56	MG	2A	3227	1/1	0.97	0.11	-	51,51,51,51	0
56	MG	1A	4184	1/1	0.90	0.10	-	58,58,58,58	0
56	MG	2A	3133	1/1	0.89	0.14	-	55,55,55,55	0
56	MG	1A	4084	1/1	0.92	0.33	-	73,73,73,73	0
56	MG	1A	3342	1/1	0.94	0.13	-	30,30,30,30	0
56	MG	2A	3104	1/1	0.96	0.07	-	49,49,49,49	0
56	MG	2A	3562	1/1	0.91	0.27	-	44,44,44,44	0
56	MG	2A	3058	1/1	0.75	0.18	-	58,58,58,58	0
56	MG	1A	3740	1/1	0.96	0.32	-	32,32,32,32	0
56	MG	1A	3094	1/1	0.96	0.09	-	45,45,45,45	0
56	MG	1A	3707	1/1	0.93	0.12	-	68,68,68,68	0
56	MG	1A	3260	1/1	0.87	0.26	-	50,50,50,50	0
56	MG	1A	3786	1/1	0.96	0.18	-	18,18,18,18	0
56	MG	1a	1623	1/1	0.98	0.12	-	51,51,51,51	0
56	MG	1A	3215	1/1	0.79	0.15	-	51,51,51,51	0
56	MG	1A	3827	1/1	0.93	0.17	-	70,70,70,70	0
56	MG	1a	1728	1/1	0.84	0.34	-	48,48,48,48	0
56	MG	1A	3127	1/1	0.86	0.24	-	54,54,54,54	0
56	MG	2a	1611	1/1	0.93	0.23	-	48,48,48,48	0
56	MG	1A	3962	1/1	0.89	0.13	-	55,55,55,55	0
56	MG	2A	3024	1/1	0.86	0.17	-	51,51,51,51	0
56	MG	2A	3366	1/1	0.96	0.15	-	45,45,45,45	0
56	MG	2A	3396	1/1	0.90	0.24	-	55,55,55,55	0
56	MG	1a	1744	1/1	0.95	0.16	-	44,44,44,44	0
56	MG	2A	3394	1/1	0.98	0.49	-	61,61,61,61	0
56	MG	2e	3002	1/1	0.90	0.08	-	68,68,68,68	0
56	MG	1A	4152	1/1	0.98	0.21	-	54,54,54,54	0
56	MG	2a	1758	1/1	0.96	0.07	-	89,89,89,89	0
56	MG	1A	3464	1/1	0.93	0.37	-	50,50,50,50	0
56	MG	2A	3130	1/1	0.86	0.08	-	52,52,52,52	0
56	MG	1A	3020	1/1	0.93	0.32	-	38,38,38,38	0
56	MG	1A	3204	1/1	0.95	0.20	-	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3121	1/1	0.99	0.24	-	49,49,49,49	0
56	MG	1a	1698	1/1	0.78	0.14	-	57,57,57,57	0
56	MG	2A	3117	1/1	0.85	0.20	-	52,52,52,52	0
56	MG	1A	3450	1/1	0.95	0.13	-	53,53,53,53	0
56	MG	1A	3429	1/1	0.95	0.07	-	43,43,43,43	0
56	MG	2A	3009	1/1	0.95	0.35	-	35,35,35,35	0
56	MG	2A	3209	1/1	0.79	0.10	-	56,56,56,56	0
56	MG	1A	3444	1/1	0.95	0.11	-	54,54,54,54	0
56	MG	2l	3004	1/1	0.90	0.07	-	61,61,61,61	0
56	MG	1A	3628	1/1	0.98	0.16	-	25,25,25,25	0
56	MG	1a	1797	1/1	0.94	0.47	-	49,49,49,49	0
56	MG	1A	3482	1/1	0.93	0.49	-	49,49,49,49	0
56	MG	1A	3353	1/1	0.71	0.21	-	51,51,51,51	0
56	MG	2A	3335	1/1	0.98	0.21	-	39,39,39,39	0
56	MG	1A	3062	1/1	0.90	0.34	-	49,49,49,49	0
56	MG	1A	3518	1/1	0.90	0.12	-	53,53,53,53	0
56	MG	1A	3170	1/1	0.98	0.12	-	31,31,31,31	0
56	MG	1A	3596	1/1	0.96	0.29	-	32,32,32,32	0
56	MG	2A	3466	1/1	0.93	0.17	-	50,50,50,50	0
56	MG	1A	4009	1/1	0.93	0.10	-	65,65,65,65	0
56	MG	1A	3022	1/1	0.90	0.23	-	54,54,54,54	0
56	MG	1A	3988	1/1	0.89	0.23	-	53,53,53,53	0
56	MG	2A	3188	1/1	0.97	0.10	-	34,34,34,34	0
56	MG	1a	1701	1/1	0.93	0.35	-	47,47,47,47	0
56	MG	1A	3800	1/1	0.96	0.15	-	50,50,50,50	0
56	MG	2A	3508	1/1	0.87	0.21	-	41,41,41,41	0
56	MG	1A	3717	1/1	0.94	0.23	-	59,59,59,59	0
56	MG	1A	3871	1/1	0.93	0.12	-	55,55,55,55	0
56	MG	1a	1736	1/1	0.84	0.19	-	76,76,76,76	0
56	MG	1A	3446	1/1	0.89	0.35	-	45,45,45,45	0
56	MG	1A	3303	1/1	0.93	0.10	-	44,44,44,44	0
56	MG	2A	3156	1/1	0.95	0.17	-	49,49,49,49	0
56	MG	2a	1777	1/1	0.95	0.09	-	53,53,53,53	0
56	MG	17	102	1/1	0.94	0.09	-	42,42,42,42	0
56	MG	1A	3406	1/1	0.89	0.26	-	42,42,42,42	0
56	MG	1A	3812	1/1	0.95	0.25	-	34,34,34,34	0
56	MG	1A	4006	1/1	0.94	0.16	-	36,36,36,36	0
56	MG	2A	3317	1/1	0.91	0.29	-	35,35,35,35	0
56	MG	1A	3766	1/1	0.90	0.26	-	45,45,45,45	0
56	MG	2a	1784	1/1	0.64	0.26	-	80,80,80,80	0
56	MG	1a	1726	1/1	0.87	0.18	-	56,56,56,56	0
56	MG	2A	3263	1/1	0.93	0.19	-	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3273	1/1	0.97	0.09	-	18,18,18,18	0
56	MG	1A	3587	1/1	0.94	0.07	-	59,59,59,59	0
56	MG	2A	3425	1/1	0.97	0.16	-	27,27,27,27	0
56	MG	1A	4134	1/1	0.96	0.16	-	38,38,38,38	0
56	MG	2a	1840	1/1	0.89	0.13	-	58,58,58,58	0
56	MG	1A	3718	1/1	0.85	0.29	-	39,39,39,39	0
56	MG	1A	3271	1/1	0.97	0.27	-	38,38,38,38	0
56	MG	1a	1828	1/1	0.95	0.28	-	57,57,57,57	0
56	MG	2B	3005	1/1	0.80	0.18	-	79,79,79,79	0
56	MG	2A	3014	1/1	0.84	0.37	-	54,54,54,54	0
56	MG	2A	3354	1/1	0.98	0.15	-	54,54,54,54	0
56	MG	1A	3955	1/1	0.94	0.27	-	54,54,54,54	0
56	MG	1A	3480	1/1	0.95	0.27	-	35,35,35,35	0
56	MG	2n	101	1/1	0.95	0.53	-	65,65,65,65	0
56	MG	2A	3556	1/1	0.94	0.21	-	33,33,33,33	0
56	MG	2a	1675	1/1	0.92	0.27	-	57,57,57,57	0
56	MG	1A	3005	1/1	0.88	0.30	-	49,49,49,49	0
56	MG	2A	3252	1/1	0.98	0.13	-	56,56,56,56	0
56	MG	1A	4011	1/1	0.96	0.10	-	41,41,41,41	0
56	MG	1A	3052	1/1	0.94	0.18	-	54,54,54,54	0
56	MG	1A	4173	1/1	0.97	0.16	-	21,21,21,21	0
56	MG	1A	3199	1/1	0.95	0.39	-	35,35,35,35	0
56	MG	2A	3023	1/1	0.91	0.41	-	48,48,48,48	0
56	MG	1A	3936	1/1	0.97	0.30	-	55,55,55,55	0
56	MG	1A	3060	1/1	0.96	0.14	-	52,52,52,52	0
56	MG	1a	1846	1/1	0.77	0.32	-	75,75,75,75	0
56	MG	1A	3795	1/1	0.93	0.19	-	58,58,58,58	0
56	MG	2A	3131	1/1	0.95	0.11	-	43,43,43,43	0
56	MG	2A	3572	1/1	0.95	0.12	-	43,43,43,43	0
56	MG	1A	3197	1/1	0.97	0.25	-	50,50,50,50	0
56	MG	1A	3396	1/1	0.87	0.27	-	49,49,49,49	0
56	MG	1A	3103	1/1	0.86	0.25	-	54,54,54,54	0
56	MG	1A	3107	1/1	0.94	0.28	-	52,52,52,52	0
56	MG	2A	3487	1/1	0.86	0.21	-	42,42,42,42	0
56	MG	1A	3663	1/1	0.95	0.08	-	51,51,51,51	0
56	MG	1A	3372	1/1	0.91	0.18	-	56,56,56,56	0
56	MG	1A	3434	1/1	0.91	0.25	-	53,53,53,53	0
56	MG	1A	3102	1/1	0.90	0.12	-	51,51,51,51	0
56	MG	1a	1747	1/1	0.90	0.14	-	68,68,68,68	0
56	MG	1A	4143	1/1	0.95	0.23	-	34,34,34,34	0
56	MG	1A	4147	1/1	0.98	0.11	-	40,40,40,40	0
56	MG	2Q	3005	1/1	0.93	0.12	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3650	1/1	0.98	0.19	-	50,50,50,50	0
56	MG	1a	1704	1/1	0.94	0.63	-	55,55,55,55	0
56	MG	2A	3500	1/1	0.97	0.09	-	47,47,47,47	0
56	MG	1A	3472	1/1	0.92	0.13	-	47,47,47,47	0
56	MG	1A	3067	1/1	0.97	0.29	-	37,37,37,37	0
56	MG	1A	4002	1/1	0.95	0.08	-	82,82,82,82	0
56	MG	2A	3477	1/1	0.80	0.18	-	39,39,39,39	0
56	MG	2A	3171	1/1	0.97	0.18	-	39,39,39,39	0
56	MG	1A	3861	1/1	0.93	0.16	-	43,43,43,43	0
56	MG	1A	3282	1/1	0.96	0.10	-	73,73,73,73	0
56	MG	1A	3507	1/1	0.97	0.16	-	34,34,34,34	0
56	MG	2a	1824	1/1	0.96	0.17	-	41,41,41,41	0
56	MG	1A	3292	1/1	0.94	0.23	-	35,35,35,35	0
56	MG	2A	3173	1/1	0.87	0.44	-	53,53,53,53	0
56	MG	1A	3339	1/1	0.95	0.70	-	48,48,48,48	0
56	MG	1A	4045	1/1	0.98	0.16	-	49,49,49,49	0
56	MG	2A	3367	1/1	0.96	0.21	-	63,63,63,63	0
56	MG	2a	1661	1/1	0.92	0.04	-	64,64,64,64	0
56	MG	2a	1694	1/1	0.86	0.51	-	60,60,60,60	0
56	MG	1A	3606	1/1	0.96	0.18	-	28,28,28,28	0
56	MG	1T	203	1/1	0.94	0.09	-	44,44,44,44	0
56	MG	1A	3490	1/1	0.95	0.09	-	59,59,59,59	0
56	MG	2A	3316	1/1	0.95	0.20	-	60,60,60,60	0
56	MG	2Y	502	1/1	0.96	0.17	-	47,47,47,47	0
56	MG	1Y	502	1/1	0.95	0.23	-	45,45,45,45	0
56	MG	1A	3889	1/1	0.99	0.14	-	29,29,29,29	0
56	MG	2A	3311	1/1	0.94	0.11	-	57,57,57,57	0
56	MG	1a	1876	1/1	0.85	0.16	-	37,37,37,37	0
56	MG	1A	3744	1/1	0.98	0.14	-	49,49,49,49	0
56	MG	1A	3984	1/1	0.96	0.14	-	52,52,52,52	0
56	MG	2A	3112	1/1	0.97	0.18	-	34,34,34,34	0
56	MG	1a	1858	1/1	0.81	0.10	-	78,78,78,78	0
56	MG	1x	101	1/1	0.73	0.44	-	67,67,67,67	0
56	MG	1a	1752	1/1	0.90	0.10	-	73,73,73,73	0
56	MG	1A	3194	1/1	0.97	0.12	-	35,35,35,35	0
56	MG	1a	1773	1/1	0.98	0.16	-	25,25,25,25	0
56	MG	1a	1601	1/1	0.84	0.15	-	68,68,68,68	0
56	MG	1A	3983	1/1	0.95	0.12	-	51,51,51,51	0
56	MG	2A	3492	1/1	0.90	0.15	-	40,40,40,40	0
56	MG	1A	4125	1/1	0.95	0.22	-	48,48,48,48	0
56	MG	2A	3469	1/1	0.93	0.05	-	45,45,45,45	0
56	MG	2A	3472	1/1	0.93	0.10	-	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3361	1/1	0.94	0.26	-	35,35,35,35	0
56	MG	1A	3024	1/1	0.89	0.36	-	48,48,48,48	0
56	MG	1A	3578	1/1	0.96	0.32	-	53,53,53,53	0
56	MG	1A	3738	1/1	0.96	0.22	-	32,32,32,32	0
56	MG	2A	3406	1/1	0.93	0.20	-	48,48,48,48	0
56	MG	1a	1833	1/1	0.97	0.15	-	43,43,43,43	0
56	MG	2a	1815	1/1	0.92	0.29	-	63,63,63,63	0
56	MG	1A	3402	1/1	0.92	0.20	-	48,48,48,48	0
56	MG	1A	3454	1/1	0.92	0.17	-	56,56,56,56	0
56	MG	2a	1713	1/1	0.87	0.23	-	56,56,56,56	0
56	MG	1a	1687	1/1	0.90	0.21	-	51,51,51,51	0
56	MG	2a	1796	1/1	0.86	0.15	-	80,80,80,80	0
56	MG	1A	3442	1/1	0.91	0.09	-	50,50,50,50	0
56	MG	1A	3540	1/1	0.91	0.31	-	45,45,45,45	0
56	MG	1A	3822	1/1	0.88	0.29	-	56,56,56,56	0
56	MG	16	103	1/1	0.96	0.06	-	50,50,50,50	0
56	MG	1a	1818	1/1	0.90	0.39	-	58,58,58,58	0
56	MG	1G	202	1/1	0.91	0.08	-	51,51,51,51	0
56	MG	1a	1821	1/1	0.88	0.13	-	51,51,51,51	0
56	MG	2A	3584	1/1	0.92	0.14	-	55,55,55,55	0
56	MG	1A	4026	1/1	0.95	0.17	-	44,44,44,44	0
56	MG	2a	1800	1/1	0.80	0.45	-	65,65,65,65	0
56	MG	1W	3002	1/1	0.94	0.38	-	41,41,41,41	0
56	MG	1A	3520	1/1	0.92	0.19	-	47,47,47,47	0
56	MG	1A	3041	1/1	0.91	0.20	-	44,44,44,44	0
56	MG	2A	3529	1/1	0.96	0.11	-	43,43,43,43	0
56	MG	1A	3584	1/1	0.93	0.07	-	50,50,50,50	0
56	MG	2A	3129	1/1	0.93	0.16	-	56,56,56,56	0
56	MG	1A	3982	1/1	0.96	0.18	-	42,42,42,42	0
56	MG	2A	3271	1/1	0.97	0.26	-	41,41,41,41	0
56	MG	1a	1806	1/1	0.86	0.11	-	69,69,69,69	0
56	MG	2a	1806	1/1	0.79	0.18	-	67,67,67,67	0
56	MG	2a	1671	1/1	0.88	0.44	-	58,58,58,58	0
56	MG	2a	1770	1/1	0.93	0.21	-	71,71,71,71	0
56	MG	1A	3866	1/1	0.97	0.07	-	41,41,41,41	0
56	MG	2A	3561	1/1	0.96	0.22	-	46,46,46,46	0
56	MG	1A	3250	1/1	0.96	0.26	-	45,45,45,45	0
56	MG	1A	3044	1/1	0.94	0.13	-	53,53,53,53	0
56	MG	2a	1816	1/1	0.81	0.14	-	74,74,74,74	0
56	MG	2A	3246	1/1	0.85	0.17	-	45,45,45,45	0
56	MG	1A	3301	1/1	0.94	0.12	-	77,77,77,77	0
56	MG	2A	3226	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
56	MG	1A	3123	1/1	0.92	0.13	-	55,55,55,55	0
56	MG	1A	3325	1/1	0.97	0.15	-	37,37,37,37	0
56	MG	1A	3833	1/1	0.94	0.25	-	54,54,54,54	0
56	MG	1A	3473	1/1	0.88	0.13	-	45,45,45,45	0
56	MG	1A	3065	1/1	0.89	0.14	-	48,48,48,48	0
56	MG	1A	3981	1/1	0.92	0.09	-	59,59,59,59	0
56	MG	16	101	1/1	0.83	0.32	-	47,47,47,47	0
56	MG	2a	1773	1/1	0.85	0.20	-	65,65,65,65	0
56	MG	1A	3781	1/1	0.92	0.20	-	25,25,25,25	0
56	MG	2A	3548	1/1	0.92	0.14	-	53,53,53,53	0
56	MG	1A	3360	1/1	0.81	0.14	-	53,53,53,53	0
56	MG	2A	3507	1/1	0.85	0.19	-	48,48,48,48	0
56	MG	1a	1655	1/1	0.94	0.37	-	47,47,47,47	0
56	MG	2A	3368	1/1	0.84	0.15	-	49,49,49,49	0
56	MG	1A	3272	1/1	0.89	0.25	-	46,46,46,46	0
56	MG	2A	3304	1/1	0.97	0.24	-	51,51,51,51	0
56	MG	2A	3494	1/1	0.94	0.28	-	39,39,39,39	0
56	MG	1A	3291	1/1	0.83	0.26	-	57,57,57,57	0
56	MG	1A	4195	1/1	0.95	0.13	-	32,32,32,32	0
56	MG	1a	1811	1/1	0.87	0.13	-	72,72,72,72	0
56	MG	1a	1847	1/1	0.79	0.14	-	72,72,72,72	0
56	MG	2a	1660	1/1	0.83	0.23	-	86,86,86,86	0
56	MG	2a	1814	1/1	0.96	0.11	-	44,44,44,44	0
56	MG	2A	3039	1/1	0.92	0.24	-	43,43,43,43	0
56	MG	2A	3164	1/1	0.95	0.29	-	43,43,43,43	0
56	MG	2A	3272	1/1	0.97	0.08	-	50,50,50,50	0
56	MG	1B	222	1/1	0.93	0.07	-	64,64,64,64	0
56	MG	1A	4034	1/1	0.96	0.27	-	54,54,54,54	0
56	MG	1A	3140	1/1	0.76	0.12	-	43,43,43,43	0
56	MG	2A	3238	1/1	0.90	0.28	-	59,59,59,59	0
56	MG	1a	1782	1/1	0.85	0.17	-	63,63,63,63	0
56	MG	2A	3485	1/1	0.94	0.14	-	48,48,48,48	0
56	MG	1A	3058	1/1	0.94	0.10	-	49,49,49,49	0
56	MG	2Q	3004	1/1	0.94	0.28	-	45,45,45,45	0
56	MG	1Q	202	1/1	0.92	0.35	-	35,35,35,35	0
56	MG	2A	3517	1/1	0.99	0.04	-	43,43,43,43	0
56	MG	2A	3488	1/1	0.96	0.15	-	40,40,40,40	0
56	MG	1A	3430	1/1	0.92	0.19	-	44,44,44,44	0
56	MG	2a	1723	1/1	0.94	0.18	-	61,61,61,61	0
56	MG	2A	3019	1/1	0.94	0.15	-	59,59,59,59	0
56	MG	1A	3974	1/1	0.92	0.20	-	54,54,54,54	0
56	MG	1A	3688	1/1	0.97	0.20	-	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3677	1/1	0.91	0.22	-	30,30,30,30	0
56	MG	1R	201	1/1	0.98	0.32	-	26,26,26,26	0
56	MG	1A	3722	1/1	0.97	0.08	-	38,38,38,38	0
56	MG	1A	4200	1/1	0.96	0.23	-	47,47,47,47	0
56	MG	1A	4198	1/1	0.90	0.12	-	42,42,42,42	0
56	MG	1A	3017	1/1	0.93	0.35	-	50,50,50,50	0
56	MG	2a	1683	1/1	0.94	0.13	-	67,67,67,67	0
56	MG	1A	3686	1/1	0.97	0.26	-	27,27,27,27	0
56	MG	2A	3223	1/1	0.98	0.21	-	31,31,31,31	0
56	MG	2A	3401	1/1	0.90	0.14	-	60,60,60,60	0
56	MG	1A	3311	1/1	0.94	0.21	-	35,35,35,35	0
56	MG	1A	3864	1/1	0.97	0.16	-	38,38,38,38	0
56	MG	1A	3239	1/1	0.96	0.19	-	33,33,33,33	0
56	MG	1G	203	1/1	0.92	0.12	-	61,61,61,61	0
56	MG	2A	3495	1/1	0.96	0.10	-	38,38,38,38	0
56	MG	1A	3153	1/1	0.92	0.26	-	49,49,49,49	0
56	MG	2A	3244	1/1	0.90	0.16	-	49,49,49,49	0
56	MG	2A	3455	1/1	0.89	0.14	-	47,47,47,47	0
56	MG	1r	3002	1/1	0.88	0.13	-	48,48,48,48	0
56	MG	1A	3231	1/1	0.95	0.43	-	53,53,53,53	0
56	MG	1A	4024	1/1	0.92	0.11	-	46,46,46,46	0
56	MG	1A	3703	1/1	0.96	0.30	-	38,38,38,38	0
56	MG	1A	3901	1/1	0.93	0.09	-	35,35,35,35	0
56	MG	1a	1700	1/1	0.89	0.39	-	48,48,48,48	0
56	MG	18	101	1/1	0.95	0.12	-	40,40,40,40	0
56	MG	2a	1673	1/1	0.84	1.03	-	76,76,76,76	0
56	MG	1a	1725	1/1	0.90	0.09	-	75,75,75,75	0
56	MG	1A	3763	1/1	0.97	0.30	-	53,53,53,53	0
56	MG	2A	3124	1/1	0.94	0.52	-	58,58,58,58	0
56	MG	1A	4109	1/1	0.94	0.19	-	37,37,37,37	0
56	MG	1A	3171	1/1	0.96	0.14	-	30,30,30,30	0
56	MG	1A	3394	1/1	0.94	0.19	-	45,45,45,45	0
56	MG	1A	3391	1/1	0.93	0.24	-	29,29,29,29	0
56	MG	1A	3614	1/1	0.90	0.20	-	27,27,27,27	0
56	MG	2a	1677	1/1	0.94	0.09	-	54,54,54,54	0
56	MG	1A	3121	1/1	0.84	0.10	-	54,54,54,54	0
56	MG	1A	3483	1/1	0.96	0.12	-	38,38,38,38	0
56	MG	1A	3428	1/1	0.95	0.10	-	52,52,52,52	0
56	MG	1A	3437	1/1	0.97	0.24	-	33,33,33,33	0
56	MG	1A	4033	1/1	0.76	0.13	-	56,56,56,56	0
56	MG	1a	1745	1/1	0.94	0.39	-	55,55,55,55	0
56	MG	1A	4139	1/1	0.97	0.32	-	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	4213	1/1	0.87	0.10	-	49,49,49,49	0
56	MG	2a	1738	1/1	0.99	0.35	-	36,36,36,36	0
56	MG	1A	4055	1/1	0.92	0.16	-	42,42,42,42	0
56	MG	1a	1772	1/1	0.96	0.14	-	39,39,39,39	0
56	MG	1a	1860	1/1	0.87	0.18	-	68,68,68,68	0
56	MG	1A	3078	1/1	0.96	0.25	-	54,54,54,54	0
56	MG	1A	3986	1/1	0.93	0.11	-	70,70,70,70	0
56	MG	1A	3683	1/1	0.94	0.15	-	44,44,44,44	0
56	MG	2A	3544	1/1	0.93	0.16	-	48,48,48,48	0
56	MG	1a	1816	1/1	0.94	0.12	-	60,60,60,60	0
56	MG	2a	1805	1/1	0.91	0.18	-	73,73,73,73	0
56	MG	1A	3408	1/1	0.87	0.25	-	53,53,53,53	0
56	MG	1A	3927	1/1	0.94	0.12	-	30,30,30,30	0
56	MG	1A	3904	1/1	0.96	0.12	-	52,52,52,52	0
56	MG	2A	3274	1/1	0.95	0.24	-	56,56,56,56	0
56	MG	1A	3035	1/1	0.90	0.20	-	53,53,53,53	0
56	MG	2A	3268	1/1	0.95	0.12	-	33,33,33,33	0
56	MG	1A	3443	1/1	0.93	0.14	-	59,59,59,59	0
56	MG	1A	3497	1/1	0.98	0.13	-	55,55,55,55	0
56	MG	2A	3397	1/1	0.96	0.33	-	45,45,45,45	0
56	MG	1x	103	1/1	0.90	0.18	-	64,64,64,64	0
56	MG	2A	3211	1/1	0.90	0.16	-	40,40,40,40	0
56	MG	2A	3035	1/1	0.92	0.12	-	57,57,57,57	0
56	MG	1A	3569	1/1	0.92	0.26	-	56,56,56,56	0
56	MG	1A	4178	1/1	0.91	0.10	-	54,54,54,54	0
56	MG	1A	3027	1/1	0.84	0.43	-	36,36,36,36	0
56	MG	1B	212	1/1	0.61	0.31	-	53,53,53,53	0
56	MG	1A	3157	1/1	0.98	0.18	-	42,42,42,42	0
56	MG	1a	1856	1/1	0.93	0.15	-	64,64,64,64	0
56	MG	1a	1724	1/1	0.96	0.08	-	70,70,70,70	0
56	MG	1A	4093	1/1	0.92	0.30	-	29,29,29,29	0
56	MG	1a	1671	1/1	0.94	0.32	-	55,55,55,55	0
56	MG	2A	3578	1/1	0.97	0.30	-	45,45,45,45	0
56	MG	2a	1822	1/1	0.92	0.13	-	71,71,71,71	0
56	MG	1a	1764	1/1	0.89	0.17	-	73,73,73,73	0
56	MG	1A	3319	1/1	0.84	0.16	-	58,58,58,58	0
56	MG	1A	3910	1/1	0.95	0.20	-	24,24,24,24	0
56	MG	1A	3495	1/1	0.96	0.11	-	41,41,41,41	0
56	MG	1A	3583	1/1	0.97	0.17	-	46,46,46,46	0
56	MG	1A	3828	1/1	0.92	0.28	-	44,44,44,44	0
56	MG	1A	3280	1/1	0.98	0.10	-	40,40,40,40	0
56	MG	2Q	3001	1/1	0.80	0.34	-	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	4187	1/1	0.97	0.21	-	27,27,27,27	0
56	MG	2A	3081	1/1	0.97	0.20	-	45,45,45,45	0
56	MG	2A	3318	1/1	0.97	0.11	-	37,37,37,37	0
56	MG	2a	1759	1/1	0.92	0.15	-	58,58,58,58	0
56	MG	1a	1787	1/1	0.98	0.27	-	51,51,51,51	0
56	MG	1l	101	1/1	0.89	0.16	-	42,42,42,42	0
56	MG	1a	1862	1/1	0.95	0.36	-	50,50,50,50	0
56	MG	1A	3255	1/1	0.94	0.29	-	68,68,68,68	0
56	MG	1A	3320	1/1	0.97	0.07	-	57,57,57,57	0
56	MG	1A	3961	1/1	0.94	0.15	-	34,34,34,34	0
56	MG	1A	3010	1/1	0.89	0.20	-	57,57,57,57	0
56	MG	2a	1834	1/1	0.96	0.31	-	52,52,52,52	0
56	MG	2A	3546	1/1	0.97	0.15	-	51,51,51,51	0
56	MG	2a	1692	1/1	0.96	0.14	-	59,59,59,59	0
56	MG	1A	3347	1/1	0.80	0.15	-	61,61,61,61	0
56	MG	1A	3228	1/1	0.93	0.25	-	25,25,25,25	0
56	MG	2A	3098	1/1	0.86	0.26	-	48,48,48,48	0
56	MG	2A	3348	1/1	0.90	0.10	-	35,35,35,35	0
56	MG	1O	3003	1/1	0.89	0.14	-	56,56,56,56	0
56	MG	2A	3305	1/1	0.91	0.17	-	53,53,53,53	0
56	MG	1a	1838	1/1	0.94	0.20	-	41,41,41,41	0
56	MG	2a	1623	1/1	0.85	0.17	-	92,92,92,92	0
56	MG	1a	1804	1/1	0.99	0.12	-	42,42,42,42	0
56	MG	2a	1833	1/1	0.75	0.18	-	94,94,94,94	0
56	MG	1A	4175	1/1	0.89	0.32	-	53,53,53,53	0
56	MG	1a	1694	1/1	0.97	0.19	-	48,48,48,48	0
56	MG	1A	3070	1/1	0.90	0.18	-	48,48,48,48	0
56	MG	1A	3162	1/1	0.89	0.21	-	50,50,50,50	0
56	MG	1A	3155	1/1	0.98	0.20	-	24,24,24,24	0
56	MG	2a	1625	1/1	0.81	0.23	-	61,61,61,61	0
56	MG	1A	3095	1/1	0.84	0.17	-	47,47,47,47	0
56	MG	1A	4092	1/1	0.92	0.17	-	69,69,69,69	0
56	MG	1A	3051	1/1	0.95	0.15	-	57,57,57,57	0
56	MG	1a	1711	1/1	0.69	0.10	-	75,75,75,75	0
56	MG	1A	3240	1/1	0.96	0.13	-	66,66,66,66	0
56	MG	1a	1873	1/1	0.95	0.16	-	42,42,42,42	0
56	MG	1A	3530	1/1	0.96	0.08	-	61,61,61,61	0
56	MG	1A	3286	1/1	0.83	0.23	-	40,40,40,40	0
56	MG	1A	3598	1/1	0.95	0.35	-	57,57,57,57	0
56	MG	1a	1705	1/1	0.96	0.12	-	46,46,46,46	0
56	MG	1A	3479	1/1	0.93	0.24	-	44,44,44,44	0
56	MG	1a	1731	1/1	0.72	0.35	-	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1F	308	1/1	0.86	0.24	-	61,61,61,61	0
56	MG	1a	1878	1/1	0.98	0.18	-	50,50,50,50	0
56	MG	1A	3132	1/1	0.92	0.15	-	52,52,52,52	0
56	MG	2A	3395	1/1	0.98	0.13	-	48,48,48,48	0
56	MG	1A	3375	1/1	0.93	0.23	-	57,57,57,57	0
56	MG	2A	3327	1/1	0.92	0.32	-	50,50,50,50	0
56	MG	1A	3923	1/1	0.92	0.10	-	53,53,53,53	0
56	MG	2a	1642	1/1	0.65	0.13	-	85,85,85,85	0
56	MG	1A	3486	1/1	0.97	0.10	-	32,32,32,32	0
56	MG	1A	4071	1/1	0.92	0.23	-	79,79,79,79	0
56	MG	2A	3002	1/1	0.95	0.28	-	58,58,58,58	0
56	MG	2A	3340	1/1	0.97	0.07	-	57,57,57,57	0
56	MG	2A	3452	1/1	0.98	0.12	-	50,50,50,50	0
56	MG	1a	1660	1/1	0.92	0.54	-	47,47,47,47	0
56	MG	1a	1610	1/1	0.96	0.08	-	57,57,57,57	0
56	MG	2A	3306	1/1	0.94	0.17	-	55,55,55,55	0
56	MG	28	101	1/1	0.94	0.36	-	40,40,40,40	0
56	MG	2a	1651	1/1	0.96	0.14	-	54,54,54,54	0
56	MG	1a	1814	1/1	0.92	0.17	-	56,56,56,56	0
56	MG	1A	3841	1/1	0.99	0.24	-	46,46,46,46	0
56	MG	1A	3783	1/1	0.92	0.94	-	58,58,58,58	0
56	MG	1A	3832	1/1	0.96	0.15	-	47,47,47,47	0
56	MG	2A	3486	1/1	0.94	0.14	-	47,47,47,47	0
56	MG	2a	1624	1/1	0.95	0.46	-	61,61,61,61	0
56	MG	2A	3232	1/1	0.84	0.16	-	72,72,72,72	0
56	MG	2a	1836	1/1	0.68	0.24	-	72,72,72,72	0
56	MG	1A	3732	1/1	0.52	0.15	-	59,59,59,59	0
56	MG	1A	3823	1/1	0.97	0.12	-	11,11,11,11	0
56	MG	1B	225	1/1	0.94	0.09	-	33,33,33,33	0
56	MG	2A	3267	1/1	0.93	0.23	-	62,62,62,62	0
56	MG	1A	3599	1/1	0.85	0.13	-	60,60,60,60	0
56	MG	1e	203	1/1	0.97	0.08	-	54,54,54,54	0
56	MG	10	106	1/1	0.93	0.15	-	73,73,73,73	0
56	MG	2a	1785	1/1	0.95	0.14	-	71,71,71,71	0
56	MG	1A	3899	1/1	0.86	0.16	-	36,36,36,36	0
56	MG	1a	1616	1/1	0.87	0.12	-	74,74,74,74	0
56	MG	1A	4114	1/1	0.89	0.12	-	47,47,47,47	0
56	MG	2a	1745	1/1	0.92	0.23	-	52,52,52,52	0
56	MG	1A	3469	1/1	0.87	0.15	-	57,57,57,57	0
56	MG	1A	3859	1/1	0.82	0.21	-	44,44,44,44	0
56	MG	1A	3115	1/1	0.85	0.32	-	46,46,46,46	0
56	MG	1A	3965	1/1	0.93	0.18	-	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	1783	1/1	0.97	0.19	-	47,47,47,47	0
56	MG	1A	4159	1/1	0.91	0.35	-	50,50,50,50	0
56	MG	1A	3016	1/1	0.80	0.15	-	55,55,55,55	0
56	MG	1A	3532	1/1	0.81	0.22	-	55,55,55,55	0
56	MG	1a	1669	1/1	0.90	0.12	-	54,54,54,54	0
56	MG	2A	3389	1/1	0.94	0.17	-	46,46,46,46	0
56	MG	1a	1851	1/1	0.93	0.49	-	60,60,60,60	0
56	MG	1A	3994	1/1	0.95	0.12	-	62,62,62,62	0
56	MG	1A	3460	1/1	0.97	0.23	-	58,58,58,58	0
56	MG	1A	4151	1/1	0.88	0.34	-	57,57,57,57	0
56	MG	1a	1867	1/1	0.94	0.51	-	54,54,54,54	0
56	MG	1A	3329	1/1	0.98	0.18	-	62,62,62,62	0
56	MG	1A	3605	1/1	0.83	0.14	-	40,40,40,40	0
56	MG	1A	3549	1/1	0.95	0.10	-	45,45,45,45	0
56	MG	1B	217	1/1	0.93	0.13	-	36,36,36,36	0
56	MG	2A	3471	1/1	0.96	0.09	-	38,38,38,38	0
56	MG	1B	223	1/1	0.93	0.11	-	66,66,66,66	0
56	MG	2a	1700	1/1	0.91	0.10	-	55,55,55,55	0
56	MG	2A	3115	1/1	0.74	0.20	-	51,51,51,51	0
56	MG	2a	1771	1/1	0.90	0.35	-	50,50,50,50	0
56	MG	1F	303	1/1	0.97	0.09	-	37,37,37,37	0
56	MG	2f	3001	1/1	0.91	0.15	-	49,49,49,49	0
56	MG	1A	3124	1/1	0.69	0.27	-	55,55,55,55	0
56	MG	2A	3106	1/1	0.96	0.18	-	48,48,48,48	0
56	MG	1A	3839	1/1	0.98	0.13	-	56,56,56,56	0
56	MG	1a	1740	1/1	0.82	0.47	-	72,72,72,72	0
56	MG	2A	3461	1/1	0.92	0.24	-	52,52,52,52	0
56	MG	1A	3724	1/1	0.91	0.19	-	61,61,61,61	0
56	MG	2A	3080	1/1	0.86	0.17	-	51,51,51,51	0
56	MG	2B	3008	1/1	0.79	0.15	-	63,63,63,63	0
56	MG	2A	3496	1/1	0.93	0.29	-	35,35,35,35	0
56	MG	1A	3056	1/1	0.93	0.21	-	38,38,38,38	0
56	MG	1A	3664	1/1	0.96	0.27	-	42,42,42,42	0
56	MG	2a	1705	1/1	0.98	0.15	-	60,60,60,60	0
56	MG	1a	1750	1/1	0.94	0.10	-	70,70,70,70	0
56	MG	1A	3582	1/1	0.96	0.11	-	46,46,46,46	0
56	MG	2A	3520	1/1	0.97	0.09	-	50,50,50,50	0
56	MG	1A	3947	1/1	0.99	0.17	-	13,13,13,13	0
56	MG	1Z	303	1/1	0.92	0.12	-	64,64,64,64	0
56	MG	2A	3419	1/1	0.93	0.13	-	66,66,66,66	0
56	MG	1A	4041	1/1	0.89	0.21	-	65,65,65,65	0
56	MG	10	103	1/1	0.94	0.17	-	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3232	1/1	0.98	0.11	-	40,40,40,40	0
56	MG	1A	3616	1/1	0.85	0.14	-	42,42,42,42	0
56	MG	1A	3870	1/1	0.95	0.27	-	41,41,41,41	0
56	MG	1A	3096	1/1	0.85	0.22	-	50,50,50,50	0
56	MG	2A	3342	1/1	0.96	0.32	-	59,59,59,59	0
56	MG	2A	3344	1/1	0.98	0.28	-	47,47,47,47	0
56	MG	2A	3005	1/1	0.92	0.17	-	52,52,52,52	0
56	MG	1A	3448	1/1	0.98	0.21	-	35,35,35,35	0
56	MG	2a	1606	1/1	0.87	0.14	-	69,69,69,69	0
56	MG	1A	4051	1/1	0.96	0.24	-	49,49,49,49	0
56	MG	2A	3557	1/1	0.89	0.14	-	32,32,32,32	0
56	MG	1A	4127	1/1	0.93	0.13	-	29,29,29,29	0
56	MG	1A	3818	1/1	0.80	0.15	-	32,32,32,32	0
56	MG	1A	3561	1/1	0.94	0.12	-	51,51,51,51	0
56	MG	1A	4203	1/1	0.46	0.64	-	71,71,71,71	0
56	MG	1A	4032	1/1	0.73	0.26	-	77,77,77,77	0
56	MG	1A	4064	1/1	0.84	0.23	-	78,78,78,78	0
56	MG	1A	3423	1/1	0.95	0.17	-	48,48,48,48	0
56	MG	2a	1650	1/1	0.87	0.18	-	82,82,82,82	0
56	MG	1A	3529	1/1	0.84	0.15	-	61,61,61,61	0
56	MG	1A	3021	1/1	0.89	0.13	-	46,46,46,46	0
56	MG	2a	1791	1/1	0.94	0.34	-	64,64,64,64	0
56	MG	2A	3214	1/1	0.90	0.12	-	37,37,37,37	0
56	MG	1A	3958	1/1	0.95	0.10	-	58,58,58,58	0
56	MG	2A	3190	1/1	0.85	0.27	-	46,46,46,46	0
56	MG	1A	3576	1/1	0.94	0.13	-	50,50,50,50	0
56	MG	2A	3532	1/1	0.97	0.09	-	36,36,36,36	0
56	MG	1a	1743	1/1	0.88	0.12	-	47,47,47,47	0
56	MG	2A	3334	1/1	0.94	0.21	-	48,48,48,48	0
56	MG	1A	4048	1/1	0.93	0.11	-	50,50,50,50	0
56	MG	1A	4072	1/1	0.81	0.17	-	52,52,52,52	0
56	MG	1a	1734	1/1	0.93	0.34	-	67,67,67,67	0
56	MG	2A	3470	1/1	0.97	0.31	-	40,40,40,40	0
56	MG	2A	3054	1/1	0.94	0.20	-	41,41,41,41	0
56	MG	1a	1756	1/1	0.73	0.26	-	80,80,80,80	0
56	MG	13	101	1/1	0.91	0.20	-	50,50,50,50	0
56	MG	1A	3855	1/1	0.89	0.14	-	62,62,62,62	0
56	MG	1Q	205	1/1	0.98	0.13	-	42,42,42,42	0
56	MG	1A	3223	1/1	0.89	0.21	-	40,40,40,40	0
56	MG	1A	3196	1/1	0.84	0.12	-	48,48,48,48	0
56	MG	2A	3515	1/1	0.67	0.33	-	55,55,55,55	0
56	MG	2a	1659	1/1	0.66	0.23	-	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	1648	1/1	0.68	0.24	-	79,79,79,79	0
56	MG	1Z	301	1/1	0.91	0.12	-	63,63,63,63	0
56	MG	1A	3221	1/1	0.95	0.17	-	36,36,36,36	0
56	MG	1x	104	1/1	0.95	0.10	-	42,42,42,42	0
56	MG	1a	1647	1/1	0.95	0.19	-	45,45,45,45	0
56	MG	1A	4197	1/1	0.90	0.12	-	72,72,72,72	0
56	MG	1A	3564	1/1	0.90	0.25	-	41,41,41,41	0
56	MG	2A	3047	1/1	0.97	0.27	-	41,41,41,41	0
56	MG	1E	303	1/1	0.96	0.28	-	26,26,26,26	0
56	MG	1A	3633	1/1	0.94	0.20	-	29,29,29,29	0
56	MG	2B	3007	1/1	0.97	0.20	-	49,49,49,49	0
56	MG	1A	3476	1/1	0.86	0.47	-	61,61,61,61	0
56	MG	1A	3049	1/1	0.96	0.20	-	39,39,39,39	0
56	MG	1A	3315	1/1	0.90	0.30	-	55,55,55,55	0
56	MG	1A	3911	1/1	0.98	0.11	-	25,25,25,25	0
56	MG	1A	4135	1/1	0.94	0.22	-	28,28,28,28	0
56	MG	1A	3503	1/1	0.95	0.15	-	48,48,48,48	0
56	MG	1A	3251	1/1	0.97	0.17	-	36,36,36,36	0
56	MG	1a	1795	1/1	0.96	0.14	-	60,60,60,60	0
56	MG	2a	1782	1/1	0.97	0.34	-	51,51,51,51	0
56	MG	2A	3568	1/1	0.92	0.08	-	51,51,51,51	0
56	MG	1A	3537	1/1	0.91	0.16	-	55,55,55,55	0
56	MG	1a	1892	1/1	0.96	0.15	-	54,54,54,54	0
56	MG	2A	3351	1/1	0.92	0.17	-	50,50,50,50	0
56	MG	1A	3459	1/1	0.94	0.28	-	43,43,43,43	0
56	MG	1A	3122	1/1	0.87	0.18	-	50,50,50,50	0
56	MG	1A	3517	1/1	0.82	0.18	-	58,58,58,58	0
56	MG	1A	4130	1/1	0.98	0.18	-	38,38,38,38	0
56	MG	1A	3750	1/1	0.81	0.23	-	43,43,43,43	0
56	MG	1a	1845	1/1	0.99	0.38	-	48,48,48,48	0
56	MG	1A	3844	1/1	0.99	0.08	-	33,33,33,33	0
56	MG	2A	3063	1/1	0.93	0.34	-	46,46,46,46	0
56	MG	2A	3527	1/1	0.96	0.23	-	44,44,44,44	0
56	MG	1A	3652	1/1	0.93	0.14	-	48,48,48,48	0
56	MG	1A	3615	1/1	0.97	0.21	-	50,50,50,50	0
56	MG	2a	1667	1/1	0.92	0.25	-	60,60,60,60	0
56	MG	2a	1616	1/1	0.83	0.34	-	60,60,60,60	0
56	MG	1A	3713	1/1	0.93	0.15	-	26,26,26,26	0
56	MG	1A	4082	1/1	0.85	0.15	-	85,85,85,85	0
56	MG	1A	3276	1/1	0.94	0.56	-	34,34,34,34	0
56	MG	1a	1729	1/1	0.90	0.59	-	49,49,49,49	0
56	MG	1A	3330	1/1	0.87	0.16	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3436	1/1	0.67	0.27	-	55,55,55,55	0
56	MG	1a	1680	1/1	0.80	0.18	-	70,70,70,70	0
56	MG	1A	3891	1/1	0.94	0.36	-	61,61,61,61	0
56	MG	2A	3360	1/1	0.98	0.18	-	32,32,32,32	0
56	MG	1A	3088	1/1	0.95	0.30	-	57,57,57,57	0
56	MG	1a	1621	1/1	0.90	0.35	-	64,64,64,64	0
56	MG	1A	3351	1/1	0.92	0.23	-	59,59,59,59	0
56	MG	1A	3081	1/1	0.94	0.21	-	47,47,47,47	0
56	MG	1A	3651	1/1	0.95	0.22	-	52,52,52,52	0
56	MG	2A	3204	1/1	0.87	0.26	-	59,59,59,59	0
56	MG	1B	204	1/1	0.89	0.19	-	49,49,49,49	0
56	MG	1A	3357	1/1	0.93	0.12	-	49,49,49,49	0
56	MG	1A	3527	1/1	0.95	0.11	-	48,48,48,48	0
56	MG	2A	3034	1/1	0.89	0.08	-	58,58,58,58	0
56	MG	1A	3304	1/1	0.92	0.20	-	51,51,51,51	0
56	MG	1A	3545	1/1	0.89	0.28	-	56,56,56,56	0
56	MG	2a	1609	1/1	0.89	0.09	-	55,55,55,55	0
56	MG	1A	3999	1/1	0.96	0.23	-	55,55,55,55	0
56	MG	2A	3457	1/1	0.95	0.20	-	54,54,54,54	0
56	MG	1A	3106	1/1	0.81	0.20	-	47,47,47,47	0
56	MG	1A	3733	1/1	0.92	0.16	-	42,42,42,42	0
56	MG	2A	3111	1/1	0.87	0.27	-	48,48,48,48	0
56	MG	1a	1673	1/1	0.90	0.25	-	54,54,54,54	0
56	MG	1A	3848	1/1	0.98	0.13	-	23,23,23,23	0
56	MG	2a	1844	1/1	0.96	0.14	-	64,64,64,64	0
56	MG	2A	3288	1/1	0.84	0.23	-	46,46,46,46	0
56	MG	2a	1665	1/1	0.80	0.51	-	65,65,65,65	0
56	MG	1A	3655	1/1	0.95	0.09	-	30,30,30,30	0
56	MG	1A	3997	1/1	0.88	0.22	-	25,25,25,25	0
56	MG	1A	4137	1/1	0.93	0.06	-	64,64,64,64	0
56	MG	18	102	1/1	0.90	0.16	-	40,40,40,40	0
56	MG	1a	1650	1/1	0.96	0.24	-	52,52,52,52	0
56	MG	2a	1735	1/1	0.92	0.47	-	73,73,73,73	0
56	MG	1A	3775	1/1	0.94	0.15	-	33,33,33,33	0
56	MG	1A	3746	1/1	0.87	0.40	-	38,38,38,38	0
56	MG	1a	1754	1/1	0.58	0.20	-	89,89,89,89	0
56	MG	1A	3659	1/1	0.94	0.12	-	58,58,58,58	0
56	MG	1a	1624	1/1	0.95	0.29	-	44,44,44,44	0
56	MG	1A	3421	1/1	0.96	0.12	-	64,64,64,64	0
56	MG	1a	1656	1/1	0.94	0.30	-	53,53,53,53	0
56	MG	2A	3399	1/1	0.94	0.15	-	60,60,60,60	0
56	MG	1A	4037	1/1	0.93	0.20	-	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1882	1/1	0.94	0.30	-	59,59,59,59	0
56	MG	2A	3422	1/1	0.93	0.23	-	51,51,51,51	0
56	MG	1N	203	1/1	0.88	0.18	-	44,44,44,44	0
56	MG	1A	3508	1/1	0.90	0.20	-	48,48,48,48	0
56	MG	1A	3793	1/1	0.99	0.20	-	47,47,47,47	0
56	MG	2A	3460	1/1	0.87	0.13	-	74,74,74,74	0
56	MG	2a	1825	1/1	0.96	0.13	-	63,63,63,63	0
56	MG	2a	1845	1/1	0.85	0.25	-	63,63,63,63	0
56	MG	2A	3391	1/1	0.95	0.28	-	55,55,55,55	0
56	MG	1A	3601	1/1	0.84	0.53	-	54,54,54,54	0
56	MG	1a	1618	1/1	0.95	0.14	-	42,42,42,42	0
56	MG	1A	4070	1/1	0.92	0.27	-	55,55,55,55	0
56	MG	1A	3969	1/1	0.95	0.15	-	58,58,58,58	0
56	MG	1A	3691	1/1	0.92	0.34	-	43,43,43,43	0
56	MG	1A	3658	1/1	0.94	0.17	-	60,60,60,60	0
56	MG	1A	4168	1/1	0.97	0.27	-	26,26,26,26	0
56	MG	1A	3401	1/1	0.97	0.12	-	30,30,30,30	0
56	MG	1A	3837	1/1	0.92	0.15	-	50,50,50,50	0
56	MG	2A	3301	1/1	0.95	0.40	-	40,40,40,40	0
56	MG	2A	3231	1/1	0.74	0.23	-	81,81,81,81	0
56	MG	1A	3083	1/1	0.92	0.21	-	44,44,44,44	0
56	MG	2A	3251	1/1	0.94	0.24	-	22,22,22,22	0
56	MG	1A	3254	1/1	0.92	0.08	-	51,51,51,51	0
56	MG	1a	1780	1/1	0.95	0.25	-	57,57,57,57	0
56	MG	1A	3213	1/1	0.99	0.19	-	23,23,23,23	0
56	MG	2a	1747	1/1	0.94	0.49	-	67,67,67,67	0
56	MG	2A	3250	1/1	0.96	0.19	-	58,58,58,58	0
56	MG	2A	3142	1/1	0.96	0.29	-	56,56,56,56	0
56	MG	2A	3491	1/1	0.93	0.12	-	56,56,56,56	0
56	MG	1A	4021	1/1	0.95	0.17	-	33,33,33,33	0
56	MG	1A	3727	1/1	0.97	0.17	-	48,48,48,48	0
56	MG	2a	1645	1/1	0.94	0.21	-	73,73,73,73	0
56	MG	1A	4115	1/1	0.90	0.15	-	36,36,36,36	0
56	MG	1a	1759	1/1	0.96	0.18	-	58,58,58,58	0
56	MG	1a	1868	1/1	0.92	0.23	-	63,63,63,63	0
56	MG	1B	220	1/1	0.93	0.05	-	44,44,44,44	0
56	MG	1A	3202	1/1	0.92	0.14	-	26,26,26,26	0
56	MG	2a	1787	1/1	0.85	0.37	-	65,65,65,65	0
56	MG	2a	1716	1/1	0.89	0.07	-	70,70,70,70	0
56	MG	2A	3350	1/1	0.93	0.21	-	54,54,54,54	0
56	MG	1A	3004	1/1	0.86	0.33	-	47,47,47,47	0
56	MG	1T	201	1/1	0.88	0.27	-	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3152	1/1	0.88	0.37	-	52,52,52,52	0
56	MG	1A	3940	1/1	0.74	0.34	-	70,70,70,70	0
56	MG	1A	3887	1/1	0.94	0.11	-	40,40,40,40	0
56	MG	2a	1835	1/1	0.93	0.32	-	58,58,58,58	0
56	MG	2A	3526	1/1	0.91	0.14	-	37,37,37,37	0
56	MG	1a	1808	1/1	0.96	0.27	-	33,33,33,33	0
56	MG	2A	3046	1/1	0.99	0.23	-	33,33,33,33	0
56	MG	2a	1670	1/1	0.91	0.23	-	62,62,62,62	0
56	MG	1A	3064	1/1	0.92	0.30	-	41,41,41,41	0
56	MG	1A	3602	1/1	0.93	0.12	-	52,52,52,52	0
56	MG	1A	3023	1/1	0.81	0.25	-	49,49,49,49	0
56	MG	2O	201	1/1	0.91	0.14	-	57,57,57,57	0
56	MG	1A	4228	1/1	0.77	0.25	-	58,58,58,58	0
56	MG	1a	1871	1/1	0.95	0.18	-	55,55,55,55	0
56	MG	2A	3082	1/1	0.87	0.11	-	44,44,44,44	0
56	MG	1A	3570	1/1	0.94	0.35	-	49,49,49,49	0
56	MG	1x	105	1/1	0.98	0.13	-	61,61,61,61	0
56	MG	2a	1794	1/1	0.98	0.36	-	46,46,46,46	0
56	MG	2A	3228	1/1	0.90	0.07	-	63,63,63,63	0
56	MG	1A	3416	1/1	0.85	0.24	-	60,60,60,60	0
56	MG	2a	1832	1/1	0.96	0.09	-	59,59,59,59	0
56	MG	1A	3590	1/1	0.72	0.31	-	54,54,54,54	0
56	MG	2A	3531	1/1	0.95	0.27	-	52,52,52,52	0
56	MG	1F	305	1/1	0.86	0.35	-	69,69,69,69	0
56	MG	1A	3661	1/1	0.98	0.19	-	40,40,40,40	0
56	MG	2a	1726	1/1	0.99	0.24	-	61,61,61,61	0
56	MG	1A	3544	1/1	0.97	0.17	-	10,10,10,10	0
56	MG	1a	1793	1/1	0.94	0.15	-	58,58,58,58	0
56	MG	1A	3952	1/1	0.98	0.10	-	41,41,41,41	0
56	MG	1a	1737	1/1	0.94	0.14	-	67,67,67,67	0
56	MG	1A	3092	1/1	0.88	0.24	-	39,39,39,39	0
56	MG	1A	4030	1/1	0.84	0.38	-	59,59,59,59	0
56	MG	2A	3498	1/1	0.86	0.19	-	48,48,48,48	0
56	MG	1A	4149	1/1	0.91	0.20	-	52,52,52,52	0
56	MG	1A	4098	1/1	0.87	0.22	-	24,24,24,24	0
56	MG	2a	1610	1/1	0.88	0.08	-	74,74,74,74	0
56	MG	1A	4141	1/1	0.91	0.23	-	68,68,68,68	0
56	MG	1A	3874	1/1	0.94	0.20	-	53,53,53,53	0
56	MG	1a	1695	1/1	0.95	0.11	-	56,56,56,56	0
56	MG	2A	3169	1/1	0.93	0.15	-	40,40,40,40	0
56	MG	1A	3165	1/1	0.95	0.23	-	42,42,42,42	0
56	MG	2a	1776	1/1	0.95	0.26	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2E	306	1/1	0.95	0.10	-	42,42,42,42	0
56	MG	2N	8001	1/1	0.96	0.13	-	55,55,55,55	0
56	MG	2a	1772	1/1	0.96	0.17	-	57,57,57,57	0
56	MG	1A	3316	1/1	0.95	0.13	-	41,41,41,41	0
56	MG	1a	1831	1/1	0.98	0.27	-	51,51,51,51	0
56	MG	1A	4039	1/1	0.86	0.21	-	67,67,67,67	0
56	MG	1A	3756	1/1	0.80	0.09	-	52,52,52,52	0
56	MG	2a	1699	1/1	0.93	0.25	-	46,46,46,46	0
56	MG	1A	3985	1/1	0.66	0.41	-	60,60,60,60	0
56	MG	1a	1790	1/1	0.96	0.12	-	48,48,48,48	0
56	MG	1A	4102	1/1	0.87	0.10	-	63,63,63,63	0
56	MG	2a	1734	1/1	0.80	0.17	-	80,80,80,80	0
56	MG	1A	3098	1/1	0.95	0.13	-	51,51,51,51	0
56	MG	1A	3119	1/1	0.87	0.24	-	54,54,54,54	0
56	MG	2x	3001	1/1	0.92	0.08	-	68,68,68,68	0
56	MG	1A	4223	1/1	0.96	0.14	-	47,47,47,47	0
56	MG	2A	3449	1/1	0.95	0.11	-	37,37,37,37	0
56	MG	2A	3069	1/1	0.96	0.21	-	58,58,58,58	0
56	MG	1a	1603	1/1	0.95	0.17	-	59,59,59,59	0
56	MG	1A	4232	1/1	0.86	0.21	-	68,68,68,68	0
56	MG	1A	4222	1/1	0.95	0.16	-	68,68,68,68	0
56	MG	2A	3465	1/1	0.97	0.11	-	39,39,39,39	0
56	MG	1A	3726	1/1	0.94	0.18	-	57,57,57,57	0
56	MG	1A	3233	1/1	0.97	0.15	-	28,28,28,28	0
56	MG	2A	3050	1/1	0.96	0.21	-	44,44,44,44	0
56	MG	1A	3682	1/1	0.92	0.12	-	43,43,43,43	0
56	MG	1A	3639	1/1	0.98	0.25	-	38,38,38,38	0
56	MG	2A	3065	1/1	0.86	0.20	-	38,38,38,38	0
56	MG	1A	3932	1/1	0.98	0.20	-	48,48,48,48	0
56	MG	1A	3893	1/1	0.92	0.11	-	61,61,61,61	0
56	MG	1a	1836	1/1	0.72	0.16	-	78,78,78,78	0
56	MG	1A	3565	1/1	0.95	0.13	-	53,53,53,53	0
56	MG	2a	1601	1/1	0.91	0.28	-	67,67,67,67	0
56	MG	1A	3006	1/1	0.57	0.21	-	64,64,64,64	0
56	MG	1N	206	1/1	0.95	0.11	-	29,29,29,29	0
56	MG	2A	3257	1/1	0.92	0.12	-	57,57,57,57	0
56	MG	1x	110	1/1	0.87	0.16	-	68,68,68,68	0
56	MG	1A	3966	1/1	0.95	0.22	-	49,49,49,49	0
56	MG	2a	1823	1/1	0.90	0.47	-	76,76,76,76	0
56	MG	2A	3074	1/1	0.87	0.16	-	47,47,47,47	0
56	MG	1A	3514	1/1	0.90	0.18	-	59,59,59,59	0
56	MG	1A	3736	1/1	0.95	0.10	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3625	1/1	0.94	0.10	-	47,47,47,47	0
56	MG	1A	3810	1/1	0.92	0.17	-	35,35,35,35	0
56	MG	2A	3240	1/1	0.94	0.21	-	59,59,59,59	0
56	MG	2a	1755	1/1	0.87	0.26	-	68,68,68,68	0
56	MG	2a	1649	1/1	0.81	0.20	-	77,77,77,77	0
56	MG	1a	1757	1/1	0.94	0.11	-	70,70,70,70	0
56	MG	1a	1803	1/1	0.78	0.36	-	60,60,60,60	0
56	MG	1A	3433	1/1	0.95	0.18	-	66,66,66,66	0
56	MG	2Z	3001	1/1	0.81	0.07	-	62,62,62,62	0
56	MG	2A	3151	1/1	0.97	0.31	-	38,38,38,38	0
56	MG	1A	3574	1/1	0.86	0.11	-	62,62,62,62	0
56	MG	2A	3185	1/1	0.92	0.13	-	52,52,52,52	0
56	MG	1A	3640	1/1	1.00	0.38	-	53,53,53,53	0
56	MG	2A	3155	1/1	0.98	0.25	-	37,37,37,37	0
56	MG	1A	4090	1/1	0.90	0.16	-	76,76,76,76	0
56	MG	2A	3413	1/1	0.96	0.19	-	54,54,54,54	0
56	MG	1A	4085	1/1	0.91	0.33	-	53,53,53,53	0
56	MG	1a	1721	1/1	0.84	0.22	-	78,78,78,78	0
56	MG	2A	3044	1/1	0.97	0.14	-	39,39,39,39	0
56	MG	1A	3719	1/1	0.96	0.12	-	64,64,64,64	0
56	MG	1A	3219	1/1	0.96	0.16	-	24,24,24,24	0
56	MG	1A	4012	1/1	0.96	0.25	-	40,40,40,40	0
56	MG	2a	1748	1/1	0.91	0.12	-	51,51,51,51	0
56	MG	1A	3499	1/1	0.86	0.14	-	58,58,58,58	0
56	MG	1A	3227	1/1	0.97	0.28	-	27,27,27,27	0
56	MG	2A	3140	1/1	0.98	0.22	-	41,41,41,41	0
56	MG	1A	4191	1/1	0.80	0.28	-	39,39,39,39	0
56	MG	1a	1874	1/1	0.98	0.19	-	31,31,31,31	0
56	MG	2A	3224	1/1	0.88	0.17	-	38,38,38,38	0
56	MG	1A	3114	1/1	0.94	0.32	-	39,39,39,39	0
56	MG	1A	3341	1/1	0.98	0.11	-	25,25,25,25	0
56	MG	1A	3352	1/1	0.48	0.18	-	82,82,82,82	0
56	MG	2a	1608	1/1	0.47	0.37	-	75,75,75,75	0
56	MG	1a	1765	1/1	0.85	0.12	-	71,71,71,71	0
56	MG	1a	1805	1/1	0.97	0.16	-	66,66,66,66	0
56	MG	1a	1864	1/1	0.99	0.09	-	74,74,74,74	0
56	MG	1a	1733	1/1	0.97	0.14	-	49,49,49,49	0
56	MG	1A	3488	1/1	0.91	0.17	-	44,44,44,44	0
56	MG	1A	3100	1/1	0.92	0.19	-	47,47,47,47	0
56	MG	18	105	1/1	0.93	0.27	-	37,37,37,37	0
56	MG	1A	3603	1/1	0.96	0.10	-	60,60,60,60	0
56	MG	1A	3931	1/1	0.94	0.14	-	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1812	1/1	0.90	0.17	-	62,62,62,62	0
56	MG	2A	3308	1/1	0.93	0.12	-	56,56,56,56	0
56	MG	2a	1839	1/1	0.90	0.18	-	48,48,48,48	0
56	MG	1A	3559	1/1	0.97	0.13	-	41,41,41,41	0
56	MG	2u	101	1/1	0.96	0.23	-	60,60,60,60	0
56	MG	1a	1674	1/1	0.89	0.20	-	63,63,63,63	0
56	MG	1A	3491	1/1	0.96	0.12	-	63,63,63,63	0
56	MG	2A	3479	1/1	0.90	0.20	-	51,51,51,51	0
56	MG	1A	3349	1/1	0.93	0.28	-	32,32,32,32	0
56	MG	2a	1638	1/1	0.82	0.11	-	73,73,73,73	0
56	MG	2A	3059	1/1	0.91	0.25	-	59,59,59,59	0
56	MG	1A	3813	1/1	0.95	0.10	-	39,39,39,39	0
56	MG	2A	3084	1/1	0.94	0.38	-	49,49,49,49	0
56	MG	1A	3057	1/1	0.97	0.12	-	57,57,57,57	0
56	MG	1a	1748	1/1	0.95	0.11	-	51,51,51,51	0
56	MG	2A	3384	1/1	0.95	0.10	-	48,48,48,48	0
56	MG	1A	3646	1/1	0.91	0.12	-	53,53,53,53	0
56	MG	2A	3560	1/1	0.97	0.21	-	41,41,41,41	0
56	MG	1A	3721	1/1	0.89	0.21	-	47,47,47,47	0
56	MG	1A	4005	1/1	0.96	0.32	-	47,47,47,47	0
56	MG	2a	1678	1/1	0.99	0.25	-	60,60,60,60	0
56	MG	2A	3328	1/1	0.91	0.17	-	59,59,59,59	0
56	MG	1A	3075	1/1	0.93	0.08	-	46,46,46,46	0
56	MG	1A	3774	1/1	0.98	0.09	-	23,23,23,23	0
56	MG	1a	1785	1/1	0.95	0.24	-	43,43,43,43	0
56	MG	2A	3181	1/1	0.86	0.22	-	40,40,40,40	0
56	MG	2a	1765	1/1	0.87	0.21	-	65,65,65,65	0
56	MG	1A	3996	1/1	0.91	0.12	-	43,43,43,43	0
56	MG	2a	1715	1/1	1.00	0.15	-	65,65,65,65	0
56	MG	2a	1632	1/1	0.41	0.21	-	86,86,86,86	0
56	MG	2a	1701	1/1	0.76	0.15	-	66,66,66,66	0
56	MG	2A	3322	1/1	0.93	0.16	-	39,39,39,39	0
56	MG	1O	3002	1/1	0.95	0.19	-	51,51,51,51	0
56	MG	1A	4079	1/1	0.95	0.16	-	28,28,28,28	0
56	MG	1A	3506	1/1	0.77	0.26	-	37,37,37,37	0
56	MG	2A	3218	1/1	0.98	0.18	-	36,36,36,36	0
56	MG	1A	3608	1/1	0.95	0.07	-	62,62,62,62	0
56	MG	2A	3377	1/1	0.95	0.24	-	38,38,38,38	0
56	MG	2A	3549	1/1	0.94	0.28	-	47,47,47,47	0
56	MG	1A	4113	1/1	0.91	0.15	-	39,39,39,39	0
56	MG	1N	207	1/1	0.97	0.08	-	41,41,41,41	0
56	MG	1r	3001	1/1	0.24	0.20	-	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3205	1/1	0.94	0.33	-	35,35,35,35	0
56	MG	1A	3573	1/1	0.93	0.14	-	44,44,44,44	0
56	MG	19	101	1/1	0.92	0.22	-	38,38,38,38	0
56	MG	2a	1688	1/1	0.97	0.27	-	49,49,49,49	0
56	MG	1a	1641	1/1	0.96	0.17	-	58,58,58,58	0
56	MG	2A	3060	1/1	0.80	0.26	-	46,46,46,46	0
56	MG	1A	3438	1/1	0.84	0.29	-	60,60,60,60	0
56	MG	2A	3120	1/1	0.92	0.15	-	40,40,40,40	0
56	MG	1q	202	1/1	0.92	0.21	-	55,55,55,55	0
56	MG	2A	3370	1/1	0.93	0.09	-	60,60,60,60	0
56	MG	2A	3451	1/1	0.95	0.05	-	41,41,41,41	0
56	MG	1l	201	1/1	0.81	0.13	-	50,50,50,50	0
56	MG	1A	4100	1/1	0.97	0.23	-	22,22,22,22	0
56	MG	1A	3892	1/1	0.92	0.16	-	50,50,50,50	0
56	MG	1A	3007	1/1	0.95	0.17	-	69,69,69,69	0
56	MG	2A	3029	1/1	0.96	0.21	-	54,54,54,54	0
56	MG	2A	3215	1/1	0.96	0.16	-	38,38,38,38	0
56	MG	1A	3790	1/1	0.95	0.17	-	29,29,29,29	0
56	MG	1A	3895	1/1	0.93	0.14	-	33,33,33,33	0
56	MG	2a	1766	1/1	0.90	0.15	-	60,60,60,60	0
56	MG	2A	3483	1/1	0.88	0.17	-	40,40,40,40	0
56	MG	1a	1707	1/1	0.96	0.45	-	45,45,45,45	0
56	MG	1a	1753	1/1	0.87	0.75	-	76,76,76,76	0
56	MG	2Q	3002	1/1	0.92	0.16	-	53,53,53,53	0
56	MG	1A	3626	1/1	0.95	0.18	-	55,55,55,55	0
56	MG	1Z	302	1/1	0.89	0.21	-	50,50,50,50	0
56	MG	1A	3407	1/1	0.93	0.24	-	48,48,48,48	0
56	MG	1A	3266	1/1	0.94	0.17	-	31,31,31,31	0
56	MG	2A	3276	1/1	0.98	0.44	-	48,48,48,48	0
56	MG	1A	3143	1/1	0.85	0.14	-	52,52,52,52	0
56	MG	1A	3379	1/1	0.93	0.23	-	26,26,26,26	0
56	MG	1A	4010	1/1	0.64	0.17	-	76,76,76,76	0
56	MG	1A	3074	1/1	0.94	0.26	-	41,41,41,41	0
56	MG	1A	3332	1/1	0.89	0.17	-	45,45,45,45	0
56	MG	2a	1809	1/1	0.91	0.13	-	69,69,69,69	0
56	MG	2A	3165	1/1	0.93	0.11	-	33,33,33,33	0
56	MG	2A	3191	1/1	0.94	0.43	-	48,48,48,48	0
56	MG	2A	3064	1/1	0.91	0.25	-	34,34,34,34	0
56	MG	1a	1718	1/1	0.78	0.67	-	72,72,72,72	0
56	MG	1A	3317	1/1	0.92	0.12	-	73,73,73,73	0
56	MG	2A	3423	1/1	0.91	0.13	-	60,60,60,60	0
56	MG	1A	3489	1/1	0.82	0.15	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3043	1/1	0.72	0.28	-	61,61,61,61	0
56	MG	1a	1779	1/1	0.66	0.19	-	80,80,80,80	0
56	MG	1A	3031	1/1	0.86	0.13	-	50,50,50,50	0
56	MG	2a	1838	1/1	0.98	0.14	-	54,54,54,54	0
56	MG	1A	4150	1/1	0.94	0.14	-	47,47,47,47	0
56	MG	2A	3036	1/1	0.90	0.11	-	48,48,48,48	0
56	MG	1O	3001	1/1	0.92	0.17	-	40,40,40,40	0
56	MG	1A	3825	1/1	0.89	0.23	-	62,62,62,62	0
56	MG	1T	204	1/1	0.97	0.14	-	49,49,49,49	0
56	MG	1A	3991	1/1	0.93	0.17	-	64,64,64,64	0
56	MG	1N	201	1/1	0.90	0.18	-	54,54,54,54	0
56	MG	1A	3668	1/1	0.95	0.23	-	38,38,38,38	0
56	MG	2A	3505	1/1	0.98	0.14	-	45,45,45,45	0
56	MG	1A	4091	1/1	0.91	0.20	-	71,71,71,71	0
56	MG	2A	3417	1/1	0.96	0.15	-	51,51,51,51	0
56	MG	1A	3475	1/1	0.96	0.26	-	50,50,50,50	0
56	MG	2A	3071	1/1	0.88	0.20	-	66,66,66,66	0
56	MG	1A	4061	1/1	0.88	0.15	-	89,89,89,89	0
56	MG	1A	3960	1/1	0.98	0.20	-	48,48,48,48	0
56	MG	1A	3725	1/1	0.98	0.17	-	34,34,34,34	0
56	MG	1A	3566	1/1	0.92	0.26	-	44,44,44,44	0
56	MG	1A	4028	1/1	0.82	0.11	-	74,74,74,74	0
56	MG	1A	3808	1/1	0.94	0.20	-	14,14,14,14	0
56	MG	2A	3042	1/1	0.95	0.20	-	50,50,50,50	0
56	MG	1A	3935	1/1	0.79	0.27	-	29,29,29,29	0
56	MG	1A	3331	1/1	0.91	0.20	-	43,43,43,43	0
56	MG	1A	3644	1/1	0.89	0.18	-	66,66,66,66	0
56	MG	1A	3040	1/1	0.77	0.25	-	46,46,46,46	0
56	MG	1A	3819	1/1	0.96	0.19	-	38,38,38,38	0
56	MG	2a	1666	1/1	0.96	0.19	-	62,62,62,62	0
56	MG	1A	3585	1/1	0.83	0.09	-	56,56,56,56	0
56	MG	1A	3087	1/1	0.92	0.25	-	51,51,51,51	0
56	MG	1a	1665	1/1	0.84	0.14	-	74,74,74,74	0
56	MG	1A	3247	1/1	0.98	0.25	-	27,27,27,27	0
56	MG	1A	3440	1/1	0.94	0.15	-	52,52,52,52	0
56	MG	2A	3346	1/1	0.92	0.12	-	76,76,76,76	0
56	MG	2A	3025	1/1	0.89	0.26	-	59,59,59,59	0
56	MG	1a	1852	1/1	0.94	0.21	-	62,62,62,62	0
56	MG	1F	301	1/1	0.80	0.34	-	56,56,56,56	0
56	MG	1A	3365	1/1	0.79	0.26	-	74,74,74,74	0
56	MG	1A	3697	1/1	0.91	0.20	-	47,47,47,47	0
56	MG	1A	3975	1/1	0.92	0.21	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	1602	1/1	0.89	0.45	-	54,54,54,54	0
56	MG	1a	1854	1/1	0.97	0.13	-	49,49,49,49	0
56	MG	1A	3089	1/1	0.99	0.13	-	53,53,53,53	0
56	MG	1A	3815	1/1	0.97	0.14	-	32,32,32,32	0
56	MG	2a	1714	1/1	0.93	0.08	-	61,61,61,61	0
56	MG	2A	3097	1/1	0.85	0.18	-	42,42,42,42	0
56	MG	1A	3474	1/1	0.83	0.19	-	61,61,61,61	0
56	MG	2A	3077	1/1	0.86	0.19	-	61,61,61,61	0
56	MG	1a	1631	1/1	0.90	0.20	-	58,58,58,58	0
56	MG	1A	3346	1/1	0.85	0.17	-	38,38,38,38	0
56	MG	1A	3073	1/1	0.76	0.18	-	69,69,69,69	0
56	MG	1A	3097	1/1	0.97	0.42	-	48,48,48,48	0
56	MG	2a	1657	1/1	0.83	0.20	-	58,58,58,58	0
56	MG	1A	3381	1/1	0.92	0.30	-	44,44,44,44	0
56	MG	1A	3753	1/1	0.95	0.16	-	44,44,44,44	0
56	MG	1A	4164	1/1	0.91	0.23	-	66,66,66,66	0
56	MG	1A	3033	1/1	0.96	0.09	-	53,53,53,53	0
56	MG	1A	3700	1/1	0.86	0.21	-	28,28,28,28	0
56	MG	1k	3001	1/1	0.77	0.41	-	66,66,66,66	0
56	MG	1A	3821	1/1	0.95	0.12	-	49,49,49,49	0
56	MG	1A	3953	1/1	0.92	0.25	-	65,65,65,65	0
56	MG	1A	3135	1/1	0.96	0.26	-	49,49,49,49	0
56	MG	1A	3954	1/1	0.97	0.11	-	53,53,53,53	0
56	MG	2l	3003	1/1	0.92	0.12	-	71,71,71,71	0
56	MG	1x	108	1/1	0.75	0.35	-	56,56,56,56	0
56	MG	1A	3604	1/1	0.94	0.10	-	66,66,66,66	0
56	MG	1A	3853	1/1	0.98	0.14	-	35,35,35,35	0
56	MG	2A	3565	1/1	0.96	0.11	-	33,33,33,33	0
56	MG	1A	3071	1/1	0.95	0.10	-	60,60,60,60	0
56	MG	1A	3120	1/1	0.92	0.28	-	37,37,37,37	0
56	MG	1A	4131	1/1	0.94	0.28	-	32,32,32,32	0
56	MG	1A	3296	1/1	0.92	0.43	-	56,56,56,56	0
56	MG	1A	3563	1/1	0.94	0.14	-	46,46,46,46	0
56	MG	2A	3177	1/1	0.95	0.09	-	42,42,42,42	0
56	MG	1a	1792	1/1	0.94	0.23	-	34,34,34,34	0
56	MG	2A	3393	1/1	0.89	0.19	-	35,35,35,35	0
56	MG	2a	1663	1/1	0.91	0.13	-	74,74,74,74	0
56	MG	1A	3370	1/1	0.97	0.18	-	47,47,47,47	0
56	MG	1A	3798	1/1	0.94	0.19	-	31,31,31,31	0
56	MG	1A	3452	1/1	0.96	0.18	-	48,48,48,48	0
56	MG	1A	3356	1/1	0.89	0.20	-	61,61,61,61	0
56	MG	2A	3468	1/1	0.92	0.10	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3862	1/1	0.93	0.10	-	34,34,34,34	0
56	MG	1a	1690	1/1	0.88	0.33	-	57,57,57,57	0
56	MG	1a	1679	1/1	0.97	0.33	-	52,52,52,52	0
56	MG	1A	4058	1/1	0.94	0.20	-	50,50,50,50	0
56	MG	1A	3139	1/1	0.79	0.33	-	52,52,52,52	0
56	MG	2A	3388	1/1	0.78	0.35	-	56,56,56,56	0
56	MG	2a	1612	1/1	0.93	0.18	-	59,59,59,59	0
56	MG	1a	1706	1/1	0.93	0.17	-	51,51,51,51	0
56	MG	2a	1736	1/1	0.88	0.16	-	66,66,66,66	0
56	MG	1A	4148	1/1	0.93	0.17	-	47,47,47,47	0
56	MG	2a	1837	1/1	0.81	0.13	-	75,75,75,75	0
56	MG	1A	3214	1/1	0.95	0.18	-	38,38,38,38	0
56	MG	1A	3729	1/1	0.98	0.28	-	44,44,44,44	0
56	MG	1A	3764	1/1	0.93	0.23	-	46,46,46,46	0
56	MG	1d	502	1/1	0.92	0.33	-	68,68,68,68	0
56	MG	2A	3087	1/1	0.93	0.17	-	41,41,41,41	0
56	MG	1A	3737	1/1	0.96	0.20	-	18,18,18,18	0
56	MG	1A	3939	1/1	0.81	0.20	-	34,34,34,34	0
56	MG	2A	3402	1/1	0.93	0.21	-	47,47,47,47	0
56	MG	1A	3445	1/1	0.65	0.21	-	57,57,57,57	0
56	MG	2E	305	1/1	0.96	0.18	-	48,48,48,48	0
56	MG	2a	1820	1/1	0.94	0.31	-	68,68,68,68	0
56	MG	1A	3648	1/1	0.93	0.33	-	46,46,46,46	0
56	MG	1A	3323	1/1	0.74	0.33	-	58,58,58,58	0
56	MG	1a	1699	1/1	0.90	0.23	-	61,61,61,61	0
56	MG	2A	3055	1/1	0.88	0.25	-	60,60,60,60	0
56	MG	2A	3547	1/1	0.95	0.24	-	54,54,54,54	0
56	MG	1A	3535	1/1	0.97	0.11	-	26,26,26,26	0
56	MG	2A	3242	1/1	0.97	0.14	-	46,46,46,46	0
56	MG	1A	3263	1/1	0.98	0.11	-	31,31,31,31	0
56	MG	1A	3431	1/1	0.93	0.37	-	56,56,56,56	0
56	MG	1A	3829	1/1	0.98	0.14	-	54,54,54,54	0
56	MG	1P	204	1/1	0.96	0.19	-	46,46,46,46	0
56	MG	1A	3037	1/1	0.88	0.31	-	43,43,43,43	0
56	MG	2A	3179	1/1	0.90	0.20	-	31,31,31,31	0
56	MG	1F	309	1/1	0.87	0.15	-	57,57,57,57	0
56	MG	1A	4008	1/1	0.92	0.16	-	47,47,47,47	0
56	MG	1A	3879	1/1	0.90	0.19	-	25,25,25,25	0
56	MG	1A	3478	1/1	0.92	0.42	-	41,41,41,41	0
56	MG	1A	3930	1/1	0.86	0.15	-	47,47,47,47	0
56	MG	11	103	1/1	0.98	0.06	-	36,36,36,36	0
56	MG	1a	1823	1/1	0.93	0.16	-	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3192	1/1	0.93	0.28	-	46,46,46,46	0
56	MG	1a	1692	1/1	0.89	0.10	-	64,64,64,64	0
56	MG	1o	3001	1/1	0.88	0.22	-	47,47,47,47	0
56	MG	1a	1890	1/1	0.93	0.17	-	49,49,49,49	0
56	MG	1A	4047	1/1	0.82	0.19	-	79,79,79,79	0
56	MG	1A	4171	1/1	0.95	0.17	-	41,41,41,41	0
56	MG	1a	1602	1/1	0.89	0.32	-	58,58,58,58	0
56	MG	1A	3885	1/1	0.93	0.15	-	46,46,46,46	0
56	MG	2A	3239	1/1	0.85	0.27	-	64,64,64,64	0
56	MG	1A	4140	1/1	0.81	0.55	-	77,77,77,77	0
56	MG	1A	3013	1/1	0.90	0.26	-	62,62,62,62	0
56	MG	1A	3701	1/1	0.92	0.18	-	47,47,47,47	0
56	MG	2A	3458	1/1	0.97	0.10	-	43,43,43,43	0
56	MG	2a	1797	1/1	0.93	0.09	-	62,62,62,62	0
56	MG	1a	1626	1/1	0.89	0.12	-	61,61,61,61	0
56	MG	2a	1788	1/1	0.89	0.18	-	59,59,59,59	0
56	MG	1A	4157	1/1	0.92	0.15	-	53,53,53,53	0
56	MG	2A	3016	1/1	0.86	0.22	-	56,56,56,56	0
56	MG	2B	3001	1/1	0.89	0.08	-	62,62,62,62	0
56	MG	2a	1763	1/1	0.91	0.09	-	69,69,69,69	0
56	MG	1A	3134	1/1	0.94	0.27	-	52,52,52,52	0
56	MG	1A	3019	1/1	0.96	0.53	-	49,49,49,49	0
56	MG	2a	1618	1/1	0.91	0.27	-	63,63,63,63	0
56	MG	2O	203	1/1	0.96	0.14	-	47,47,47,47	0
56	MG	1A	3209	1/1	0.89	0.15	-	46,46,46,46	0
56	MG	1A	3063	1/1	0.61	0.38	-	49,49,49,49	0
56	MG	1A	4132	1/1	0.92	0.29	-	52,52,52,52	0
56	MG	1A	3515	1/1	0.81	0.17	-	64,64,64,64	0
56	MG	1A	3458	1/1	0.97	0.11	-	28,28,28,28	0
56	MG	1a	1776	1/1	0.93	0.12	-	64,64,64,64	0
56	MG	1A	3711	1/1	0.87	0.08	-	31,31,31,31	0
56	MG	1A	3258	1/1	0.90	0.21	-	46,46,46,46	0
56	MG	2a	1708	1/1	0.84	0.37	-	63,63,63,63	0
56	MG	2a	1804	1/1	0.93	0.24	-	63,63,63,63	0
56	MG	2a	1718	1/1	0.86	0.18	-	54,54,54,54	0
56	MG	1A	4218	1/1	0.87	0.19	-	36,36,36,36	0
56	MG	2A	3110	1/1	0.81	0.46	-	64,64,64,64	0
56	MG	1A	3373	1/1	0.92	0.23	-	43,43,43,43	0
56	MG	2A	3008	1/1	0.91	0.14	-	59,59,59,59	0
56	MG	1a	1685	1/1	0.96	0.16	-	61,61,61,61	0
56	MG	2A	3258	1/1	0.98	0.20	-	34,34,34,34	0
56	MG	2A	3088	1/1	0.93	0.12	-	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3339	1/1	0.91	0.08	-	76,76,76,76	0
56	MG	2a	1811	1/1	0.84	0.23	-	60,60,60,60	0
56	MG	1A	4126	1/1	0.88	0.17	-	56,56,56,56	0
56	MG	1A	4060	1/1	0.96	0.07	-	52,52,52,52	0
56	MG	1A	4074	1/1	0.88	0.09	-	66,66,66,66	0
56	MG	1A	4136	1/1	0.93	0.22	-	38,38,38,38	0
56	MG	1A	4087	1/1	0.95	0.24	-	66,66,66,66	0
56	MG	1a	1670	1/1	0.87	0.12	-	68,68,68,68	0
56	MG	1A	3907	1/1	0.51	0.25	-	53,53,53,53	0
56	MG	1x	112	1/1	0.87	0.07	-	78,78,78,78	0
56	MG	1A	3161	1/1	0.84	0.26	-	47,47,47,47	0
56	MG	2A	3298	1/1	0.97	0.20	-	47,47,47,47	0
56	MG	1a	1771	1/1	0.92	0.15	-	56,56,56,56	0
56	MG	1A	4076	1/1	0.79	0.12	-	71,71,71,71	0
56	MG	2A	3525	1/1	0.86	0.25	-	49,49,49,49	0
56	MG	1A	3714	1/1	0.95	0.17	-	53,53,53,53	0
56	MG	1A	3754	1/1	0.98	0.13	-	32,32,32,32	0
56	MG	2A	3125	1/1	0.95	0.12	-	41,41,41,41	0
56	MG	2a	1717	1/1	0.95	0.35	-	71,71,71,71	0
56	MG	2A	3566	1/1	0.95	0.17	-	32,32,32,32	0
56	MG	1A	3886	1/1	0.88	0.18	-	60,60,60,60	0
56	MG	1a	1658	1/1	0.97	0.22	-	44,44,44,44	0
56	MG	1x	102	1/1	0.90	0.23	-	69,69,69,69	0
56	MG	1a	1732	1/1	0.89	0.23	-	54,54,54,54	0
56	MG	1A	3528	1/1	0.85	0.21	-	60,60,60,60	0
56	MG	2A	3037	1/1	0.96	0.13	-	51,51,51,51	0
56	MG	1a	1843	1/1	0.88	0.16	-	63,63,63,63	0
56	MG	1A	3249	1/1	0.93	0.15	-	44,44,44,44	0
56	MG	1A	4122	1/1	0.96	0.31	-	26,26,26,26	0
56	MG	2A	3167	1/1	0.94	0.14	-	31,31,31,31	0
56	MG	1A	3068	1/1	0.92	0.38	-	54,54,54,54	0
56	MG	1A	3436	1/1	0.86	0.18	-	52,52,52,52	0
56	MG	1A	3145	1/1	0.76	0.21	-	59,59,59,59	0
56	MG	1A	3340	1/1	0.88	0.29	-	38,38,38,38	0
56	MG	1A	3970	1/1	0.96	0.10	-	54,54,54,54	0
56	MG	1A	4020	1/1	0.93	0.17	-	69,69,69,69	0
56	MG	1B	202	1/1	0.94	0.17	-	41,41,41,41	0
56	MG	2A	3247	1/1	0.88	0.19	-	34,34,34,34	0
56	MG	2A	3148	1/1	0.85	0.20	-	65,65,65,65	0
56	MG	1A	3321	1/1	0.96	0.19	-	47,47,47,47	0
56	MG	1a	1869	1/1	0.93	0.15	-	62,62,62,62	0
56	MG	2p	101	1/1	0.94	0.21	-	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3951	1/1	0.96	0.22	-	36,36,36,36	0
56	MG	1A	3860	1/1	0.53	0.58	-	62,62,62,62	0
56	MG	1A	3759	1/1	0.89	0.18	-	56,56,56,56	0
56	MG	2A	3233	1/1	0.83	0.29	-	68,68,68,68	0
56	MG	1A	3695	1/1	0.97	0.13	-	40,40,40,40	0
56	MG	1A	3230	1/1	0.96	0.23	-	40,40,40,40	0
56	MG	1A	3116	1/1	0.86	0.20	-	39,39,39,39	0
56	MG	1A	3264	1/1	0.89	0.21	-	48,48,48,48	0
56	MG	1A	4101	1/1	0.93	0.19	-	39,39,39,39	0
56	MG	1A	3354	1/1	0.93	0.17	-	34,34,34,34	0
56	MG	1A	3248	1/1	0.93	0.14	-	31,31,31,31	0
56	MG	1a	1667	1/1	0.92	0.07	-	47,47,47,47	0
56	MG	1A	3125	1/1	0.79	0.19	-	58,58,58,58	0
56	MG	2A	3116	1/1	0.81	0.39	-	48,48,48,48	0
56	MG	1A	4081	1/1	0.89	0.15	-	73,73,73,73	0
56	MG	15	102	1/1	0.94	0.16	-	45,45,45,45	0
56	MG	1A	3675	1/1	0.87	0.16	-	55,55,55,55	0
56	MG	2A	3445	1/1	0.88	0.15	-	51,51,51,51	0
56	MG	1A	3390	1/1	0.95	0.10	-	46,46,46,46	0
56	MG	1A	3742	1/1	0.90	0.10	-	47,47,47,47	0
56	MG	1B	210	1/1	0.81	0.16	-	50,50,50,50	0

6.5 Other polymers

There are no such residues in this entry.