wwPDB EM Map/Model Validation Report (i)

Apr 10, 2016 – 02:35 PM BST

PDB ID	:	4UER
EMDB ID:	:	EMD-2845
Title	:	40S-eIF1-eIF1A-eIF3-eIF3j translation initiation complex from Lachancea kluyveri
Authors	:	Aylett, C.H.S.; Boehringer, D.; Erzberger, J.P.; Schaefer, T.; Ban, N.
Deposited on	:	2014-12-18
Resolution	:	6.47 Å(reported)
Based on PDB ID	:	3U5B

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/EMValidationReportHelp

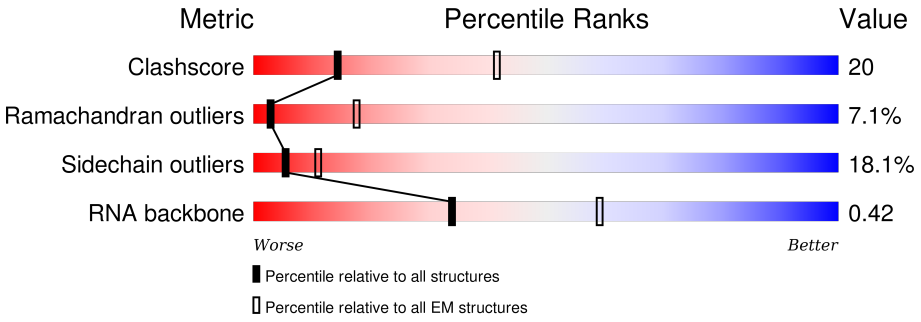
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk27241

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 6.47 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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 <=5%

Mol	Chain	Length	Quality of chain
1	0	100	42% 51% 6% •
2	1	63	27% 49% 24%
3	2	188	56% 31% 12% •
4	3	184	40% 38% 19% •
5	4	214	32% 40% 21% 7%
6	5	97	42% 39% 13% 5%
7	6	81	58% 35% 6% •
8	7	96	42% 39% 18% •

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Mol	Chain	Length	Quality of chain
9	8	70	31% 39% 24% 6%
10	9	71	41% 41% 14% •
11	A	1781	33% 38% 23% 6%
12	B	206	36% 41% 19% •
13	C	223	53% 33% 13% •
14	D	185	51% 33% 15% •
15	E	217	52% 36% 11% •
16	F	83	46% 46% 7% •
17	G	206	50% 38% 10% •
18	H	129	47% 39% 12% •
19	I	141	43% 39% 16% •
20	J	107	42% 39% 19%
21	K	127	49% 36% 10% 5%
22	L	144	49% 38% 10% •
23	M	145	39% 43% 15% •
24	N	53	47% 42% 8% •
25	O	150	53% 33% 12% •
26	P	134	55% 30% 12% •
27	Q	155	52% 38% 8% •
28	R	318	58% 36% 6% •
29	S	124	50% 38% 9% •
30	T	143	39% 45% 15% •
31	U	124	31% 48% 16% 5%
32	V	120	49% 36% 11% •
33	W	260	46% 43% 10% •

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Mol	Chain	Length	Quality of chain
34	X	60	48% 45% 7%
35	Y	226	52% 35% 12%
36	Z	87	49% 28% 21%
37	a	964	47% 53%
38	b	763	73% 25%
39	c	812	65% 33%

2 Entry composition

There are 40 unique types of molecules in this entry. The entry contains 89319 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 protein called EIF1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	100	805	495	148	157	5	0	0

- Molecule 2 is a protein called ES28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	63	497	306	99	91	1	0	0

- Molecule 3 is a protein called ES8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	188	1489	925	298	264	2	0	0

- Molecule 4 is a protein called ES7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	3	184	1481	951	265	265	0	0

- Molecule 5 is a protein called ES1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	214	1709	1084	310	311	4	0	0

- Molecule 6 is a protein called ES26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	5	97	769	475	160	129	5	0	0

- Molecule 7 is a protein called ES27.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 8 is a protein called ES10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	96	Total	C	N	O	S	0	0
			772	499	126	145	2		

- Molecule 9 is a protein called ES25.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	8	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 10 is a protein called ES31.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	71	Total	C	N	O	S	0	0
			516	328	93	91	4		

- Molecule 11 is a RNA chain called 18S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A	1781	Total	C	N	O	P	1	0
			37835	16910	6661	12482	1782		

- Molecule 12 is a protein called US2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	B	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 13 is a protein called US3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	C	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 14 is a protein called US4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	D	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 15 is a protein called US5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	E	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 16 is a protein called EIF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	F	83	Total	C	N	O	S	0	0
			671	423	124	120	4		

- Molecule 17 is a protein called US7.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	G	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 18 is a protein called US8.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	H	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 19 is a protein called US9.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	I	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 20 is a protein called US10.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	J	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 21 is a protein called US11.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	K	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 22 is a protein called US12.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 23 is a protein called US13.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	M	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 24 is a protein called US14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	N	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 25 is a protein called US15.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	O	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 26 is a protein called ES24.

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

- Molecule 27 is a protein called US17.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Q	155	Total	C	N	O	S	0	0
			1213	774	230	206	3		

- Molecule 28 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	R	318	Total	C	N	O	S	0	0
			2437	1541	418	470	8		

- Molecule 29 is a protein called US19.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	S	124	Total	C	N	O	S	0	0
			977	622	182	166	7		

- Molecule 30 is a protein called ES19.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	T	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 31 is a protein called ES12.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	U	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 32 is a protein called ES17.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	V	120	Total	C	N	O	S	0	0
			926	577	177	170	2		

- Molecule 33 is a protein called ES4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	W	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 34 is a protein called ES30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	X	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 35 is a protein called ES6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Y	226	Total	C	N	O	S	0	0
			1799	1129	346	321	3		

- Molecule 36 is a protein called ES21.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Z	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 37 is a protein called EIF3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	449	Total	C	N	O	S	0	0
			3656	2350	616	683	7		

- Molecule 38 is a protein called EIF3B.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	b	572	Total	C	N	O	S	0	92
			3978	2578	667	720	13		

- Molecule 39 is a protein called EIF3C.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	c	544	Total	C	N	O	S	0	0
			4442	2845	736	849	12		

- Molecule 40 is ZINC ION (three-letter code: ZN) (formula: Zn).

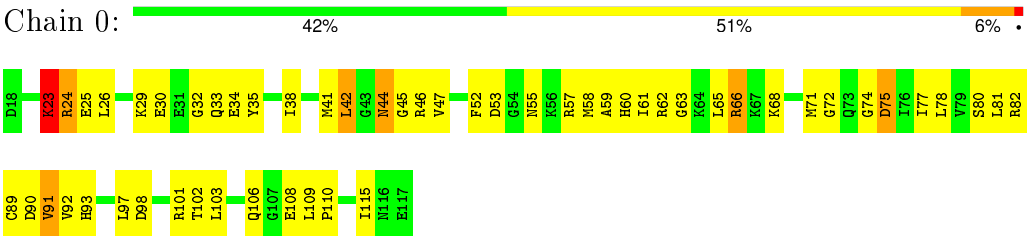
Mol	Chain	Residues	Atoms		AltConf
40	9	1	Total	Zn	0
			1	1	
40	N	1	Total	Zn	0
			1	1	
40	6	1	Total	Zn	0
			1	1	
40	5	1	Total	Zn	0
			1	1	

3 Residue-property plots (i)

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. 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. 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.

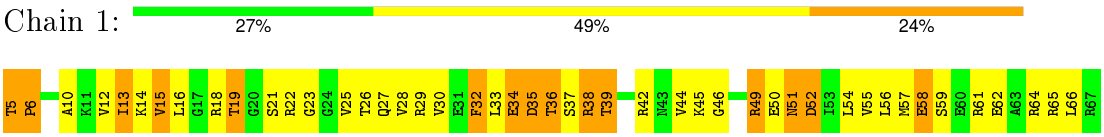
- Molecule 1: EIF1A

Chain 0:



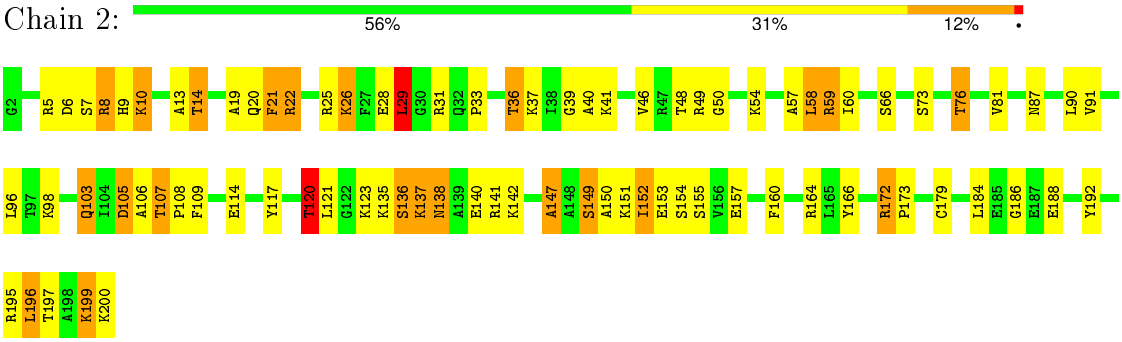
- Molecule 2: ES28

Chain 1:



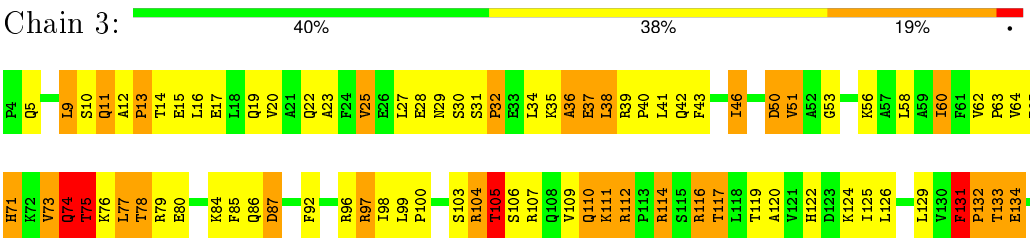
- Molecule 3: ES8

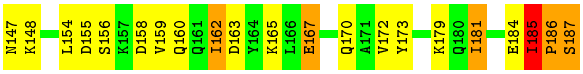
Chain 2:



- Molecule 4: ES7

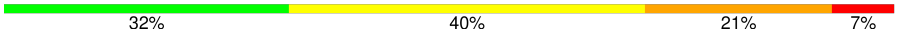
Chain 3:

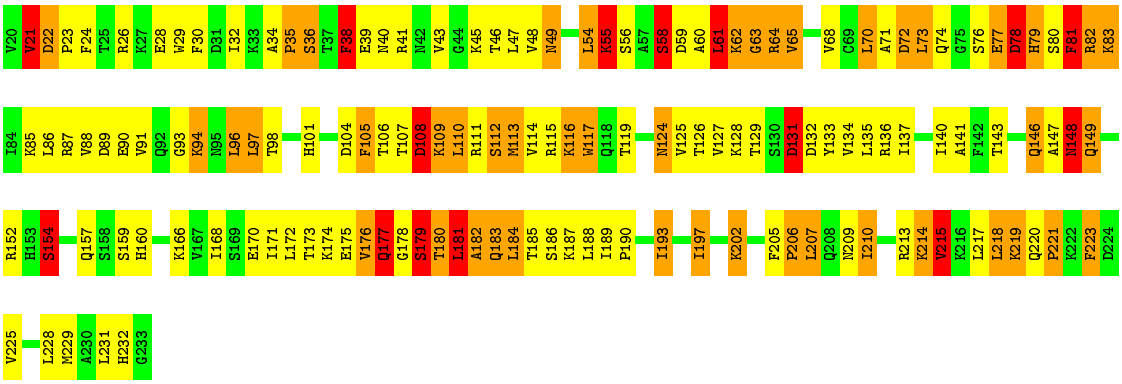




- Molecule 5: ES1

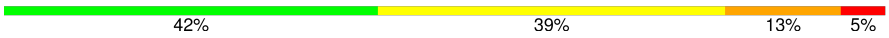
Chain 4:

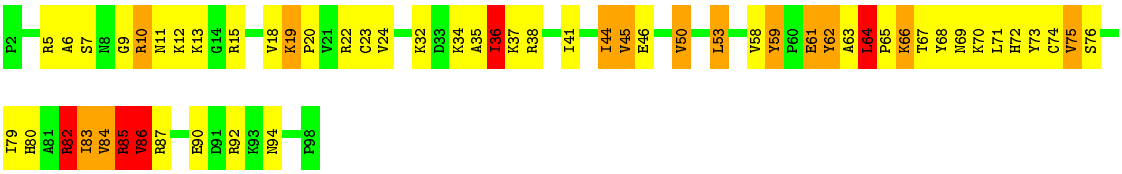




- Molecule 6: ES26

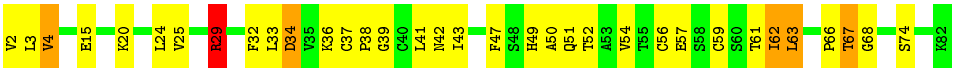
Chain 5:





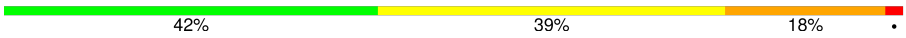
- Molecule 7: ES27

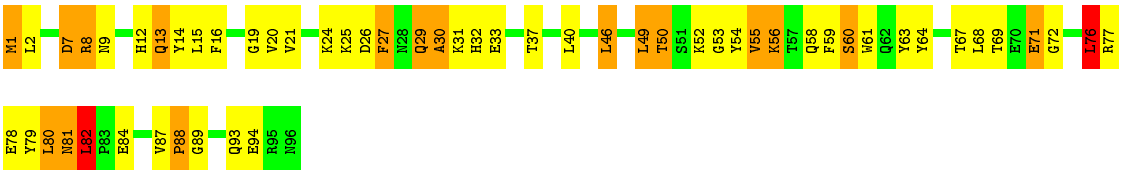
Chain 6:



- Molecule 8: ES10

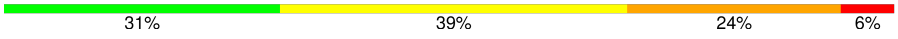
Chain 7:





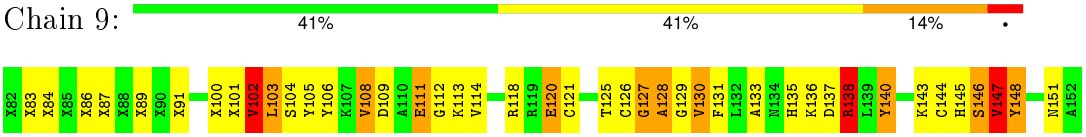
- Molecule 9: ES25

Chain 8:



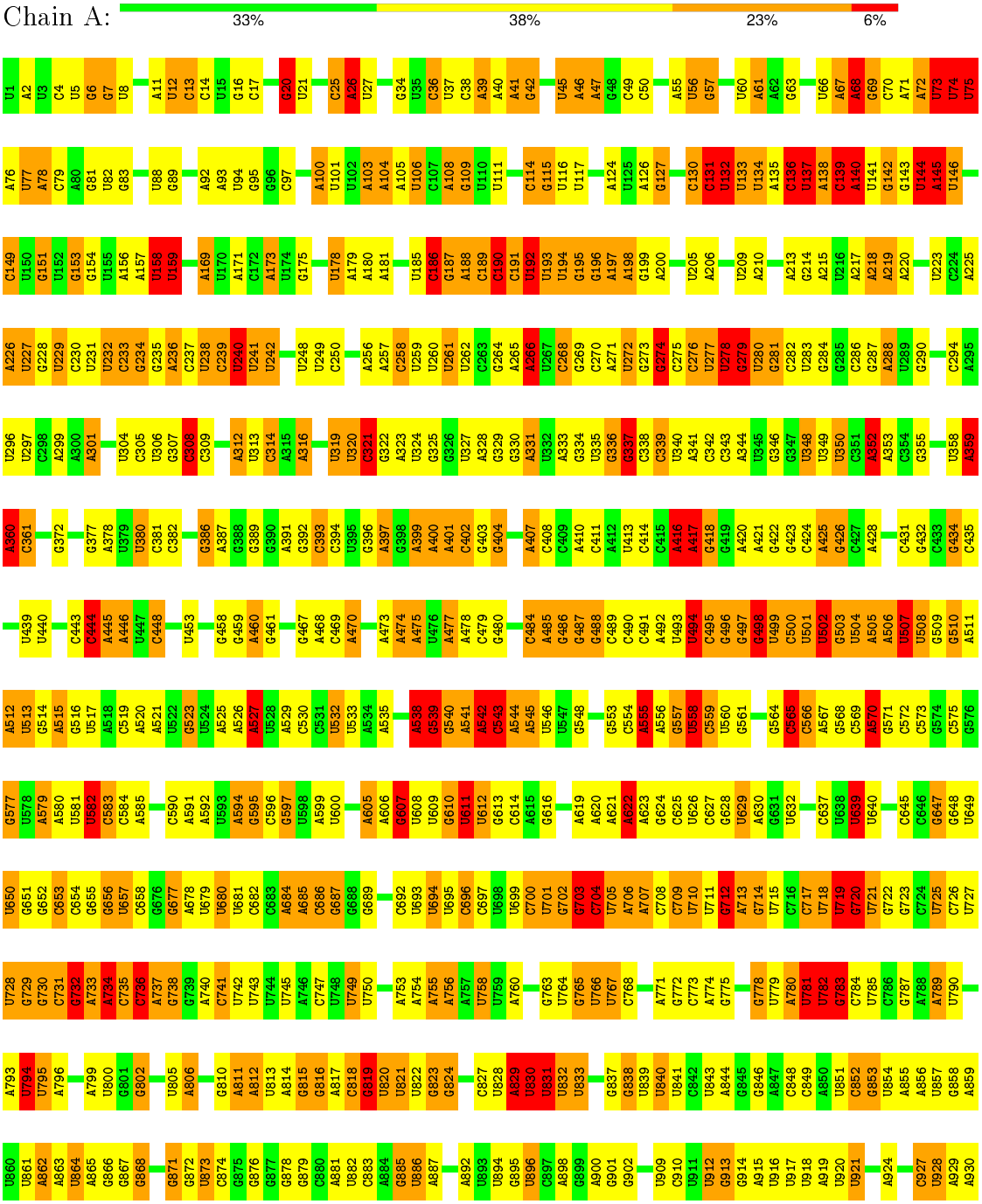
- Molecule 10: ES31

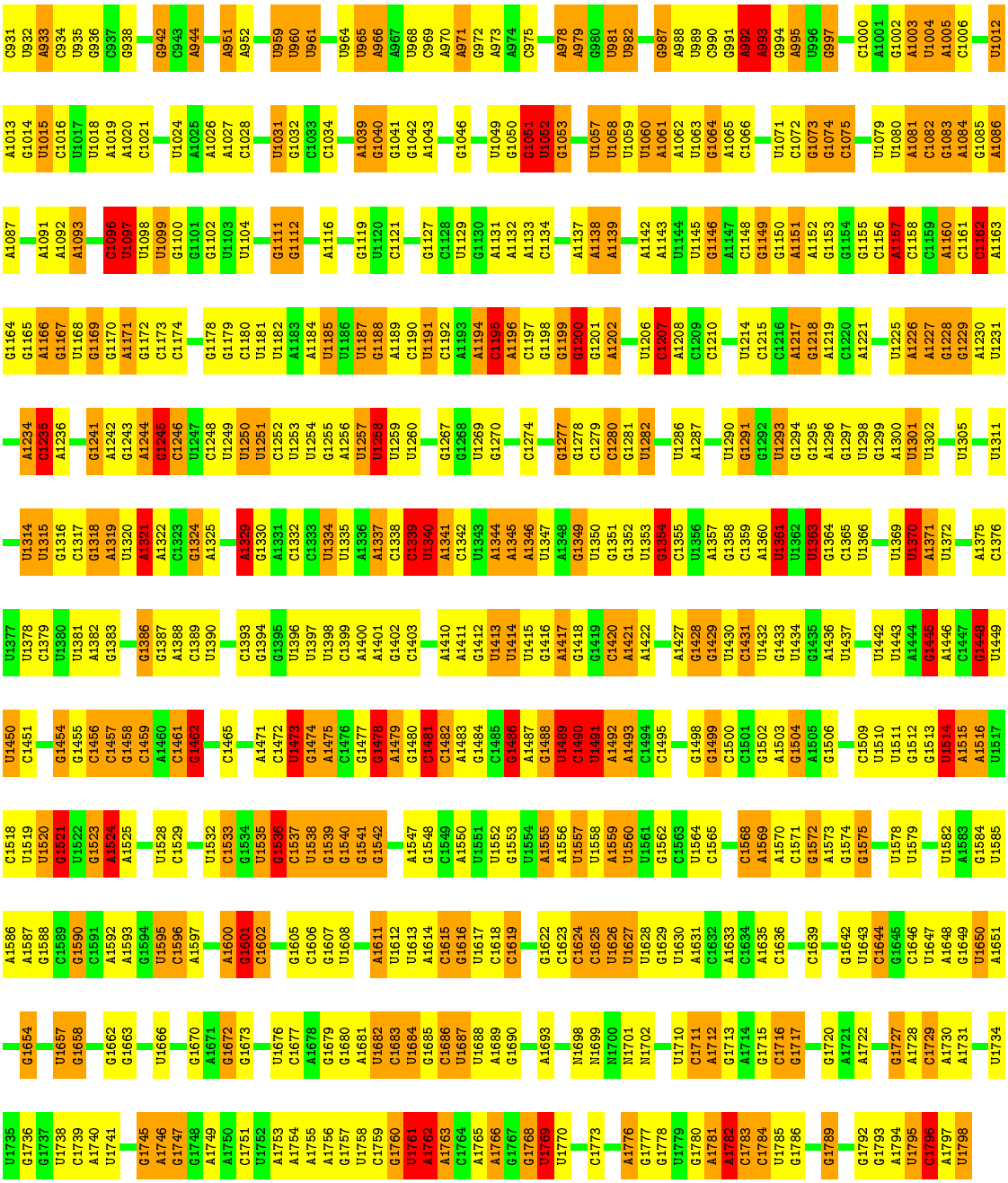
Chain 9:



- Molecule 11: 18S RRNA

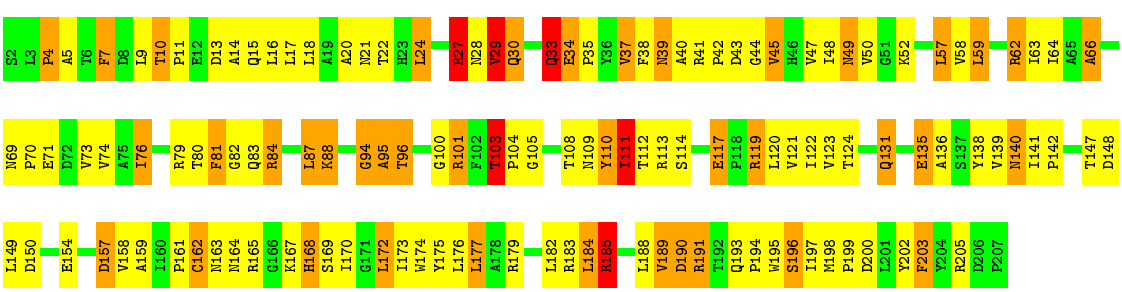
Chain A:





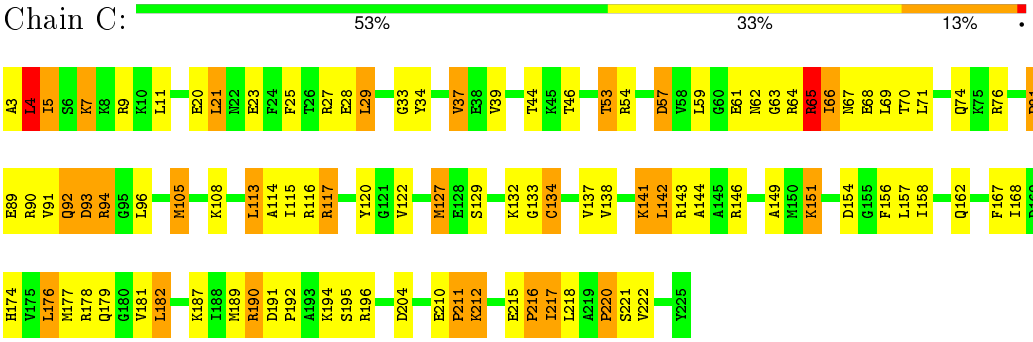
- Molecule 12: US2

Chain B:



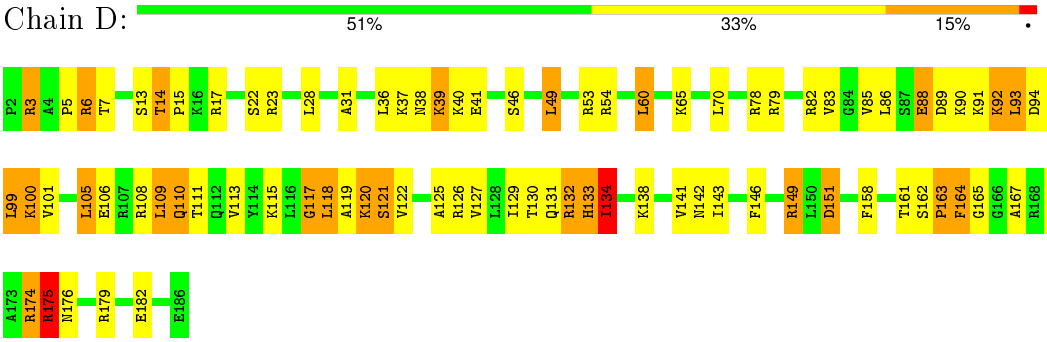
- Molecule 13: US3

Chain C:



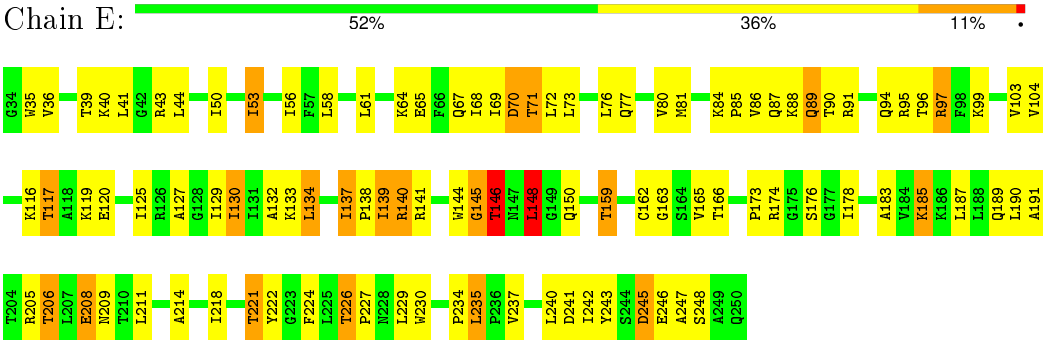
- Molecule 14: US4

Chain D:



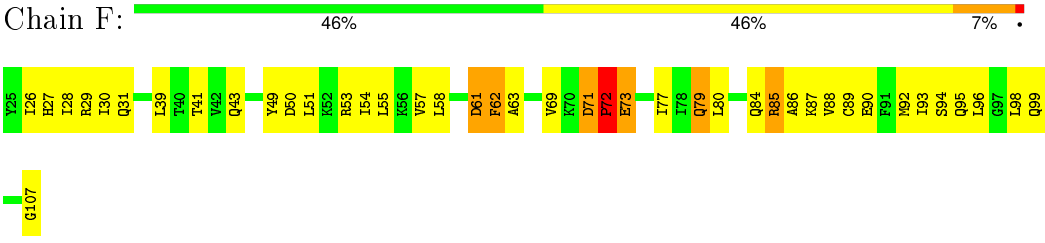
- Molecule 15: US5

Chain E:



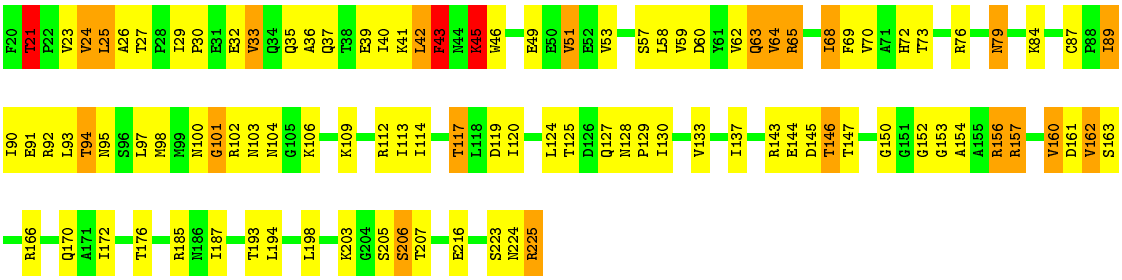
- Molecule 16: EIF1

Chain F:



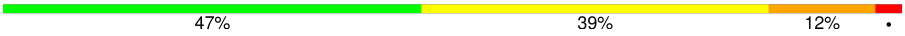
- Molecule 17: US7

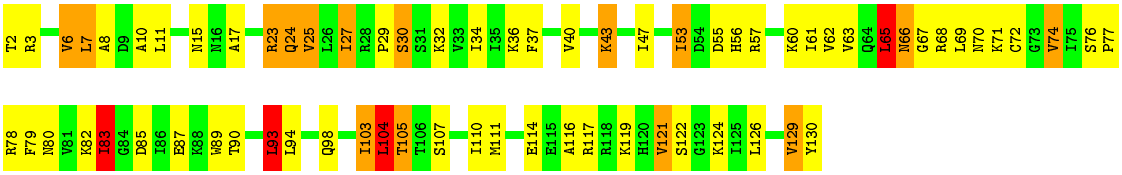
Chain G:



- Molecule 18: US8

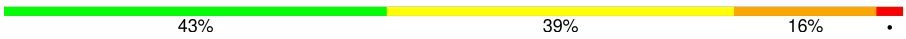
Chain H:

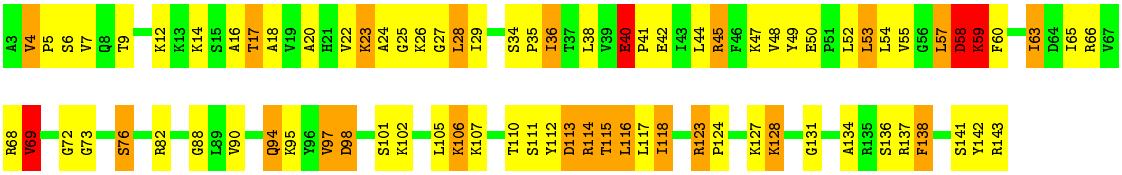




- Molecule 19: US9

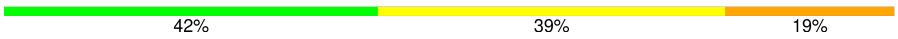
Chain I:

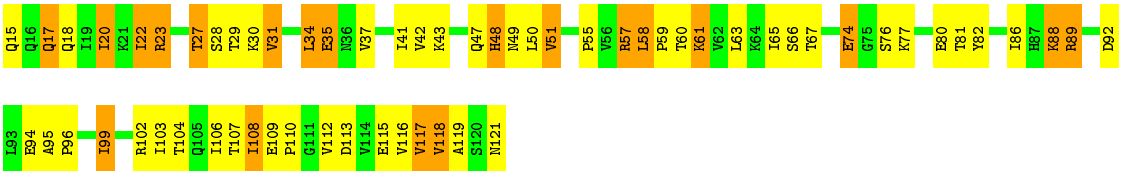




- Molecule 20: US10

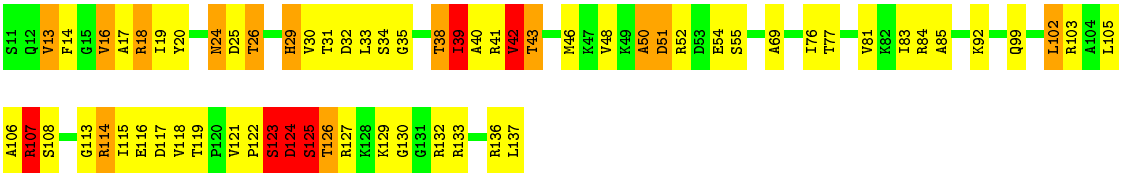
Chain J:





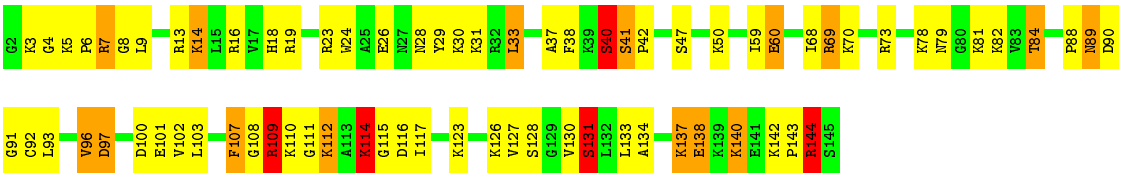
- Molecule 21: US11

Chain K:



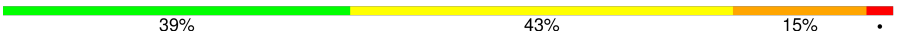
- Molecule 22: US12

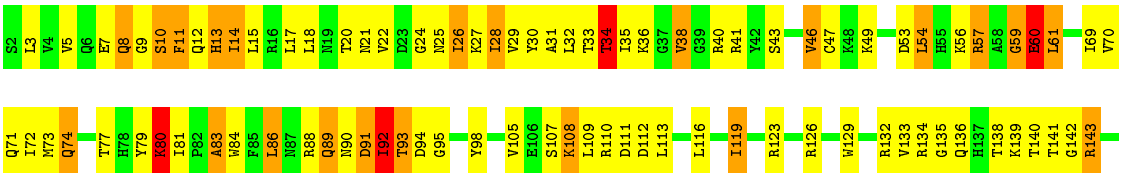
Chain L:



- Molecule 23: US13

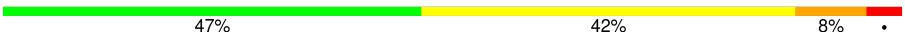
Chain M:





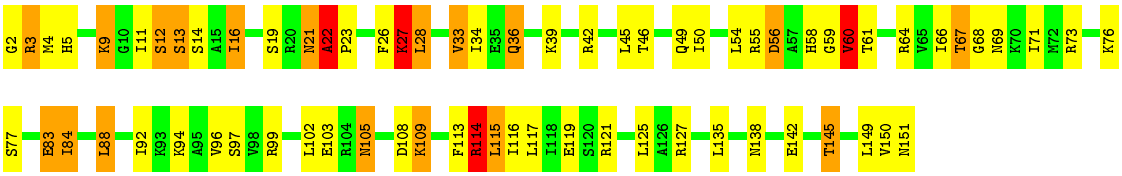
- Molecule 24: US14

Chain N:



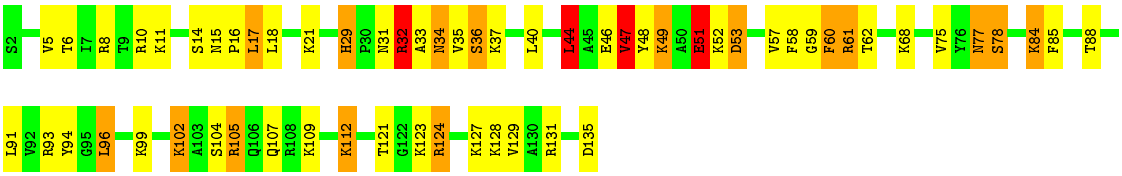
- Molecule 25: US15

Chain O:



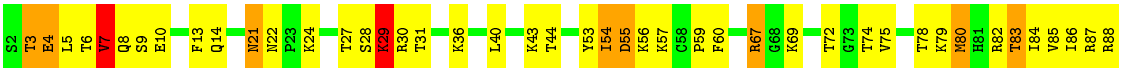
- Molecule 26: ES24

Chain P:



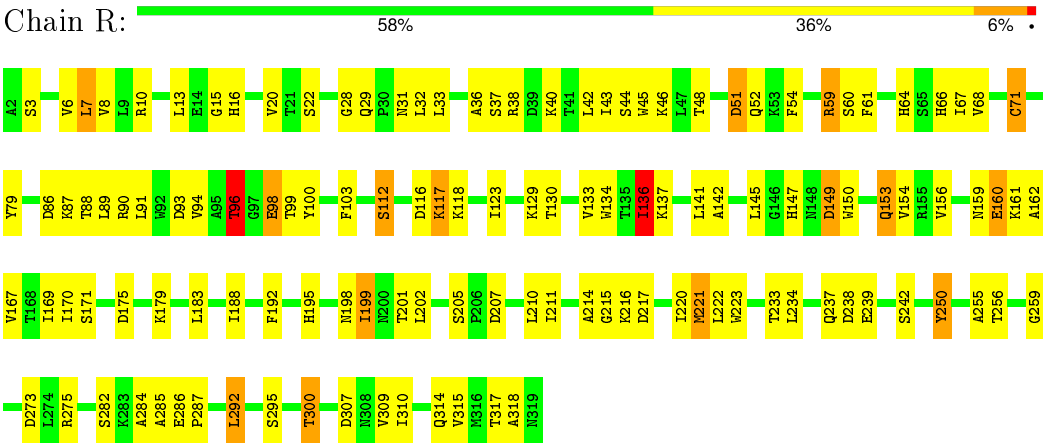
- Molecule 27: US17

Chain Q:



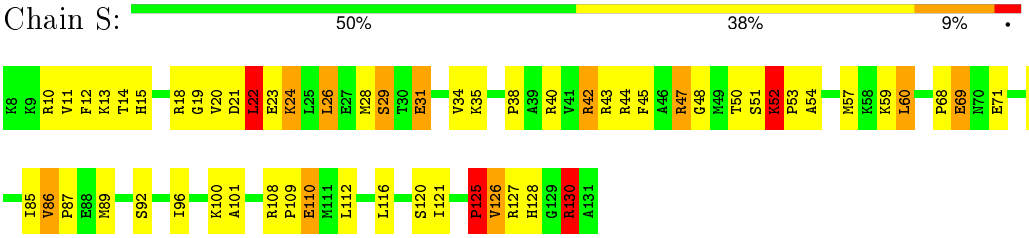
- Molecule 28: RACK1

Chain R:



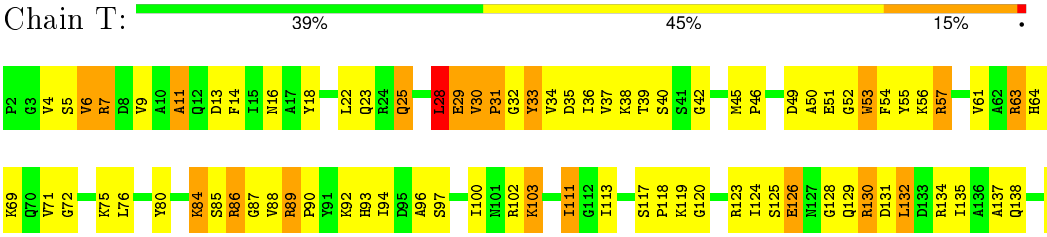
- Molecule 29: US19

Chain S:



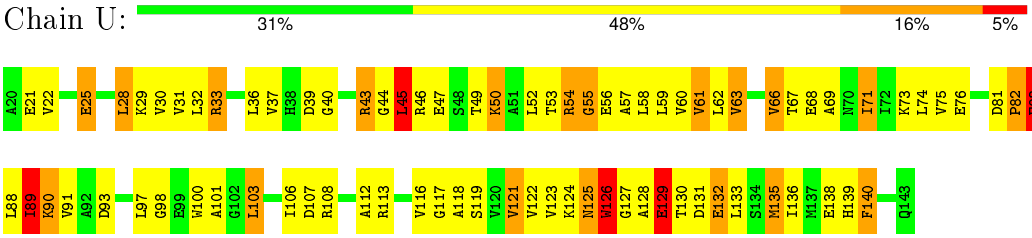
- Molecule 30: ES19

Chain T:



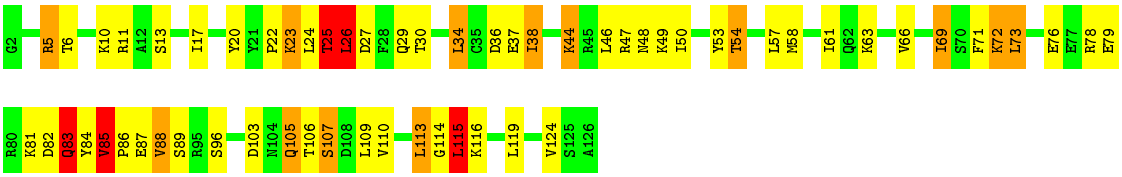
- Molecule 31: ES12

Chain U:



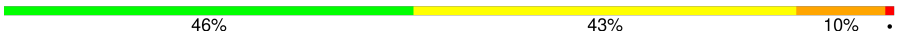
- Molecule 32: ES17

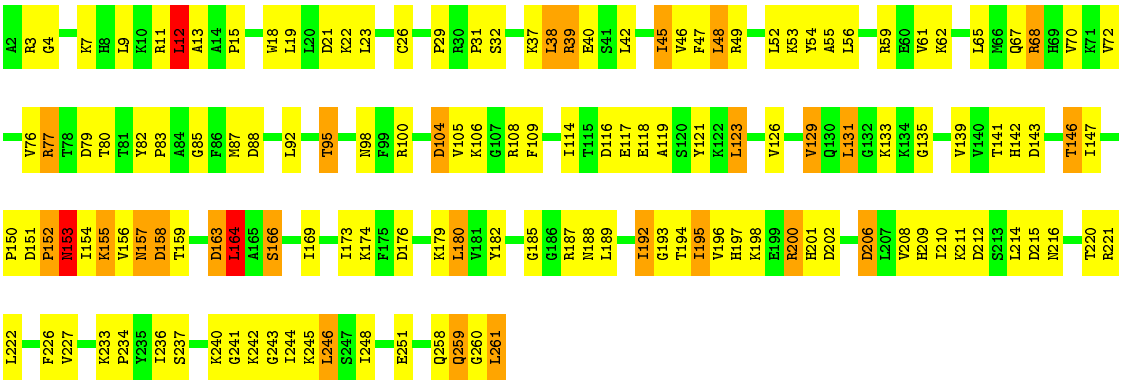
Chain V:



- Molecule 33: ES4

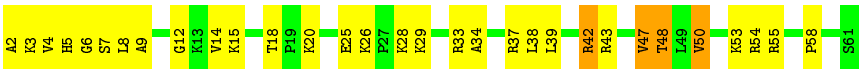
Chain W:





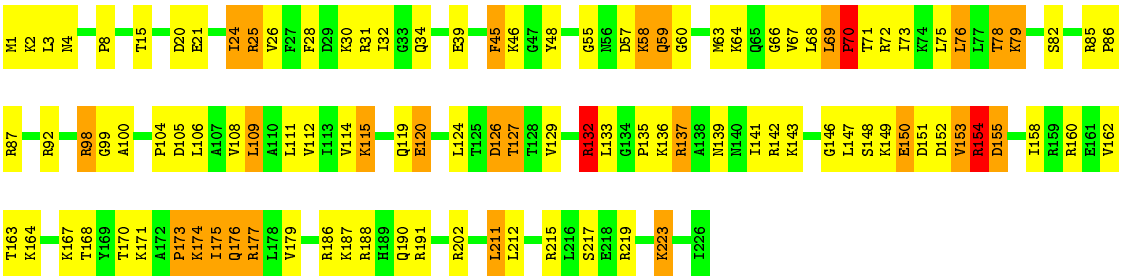
- Molecule 34: ES30

Chain X:



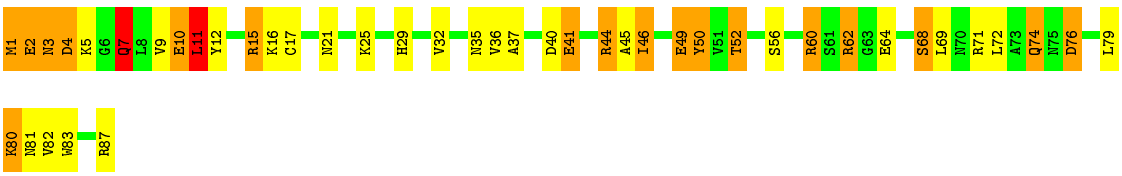
- Molecule 35: ES6

Chain Y:



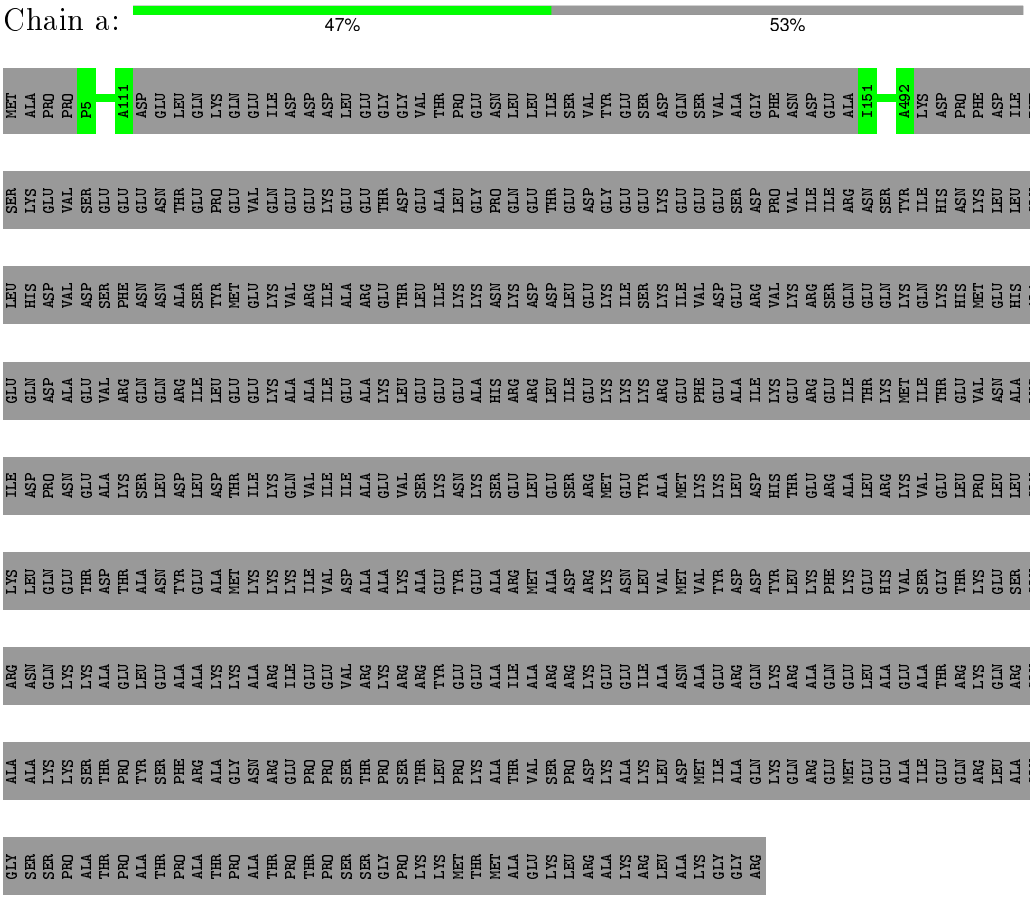
- Molecule 36: ES21

Chain Z:



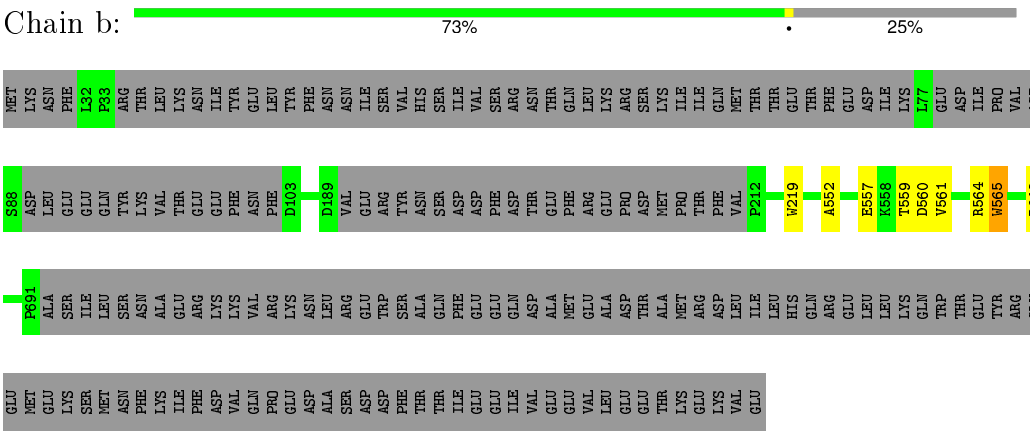
- Molecule 37: EIF3A

Chain a:



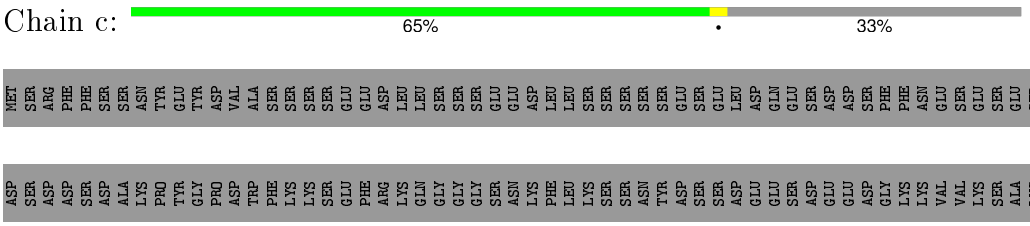
- Molecule 38: EIF3B

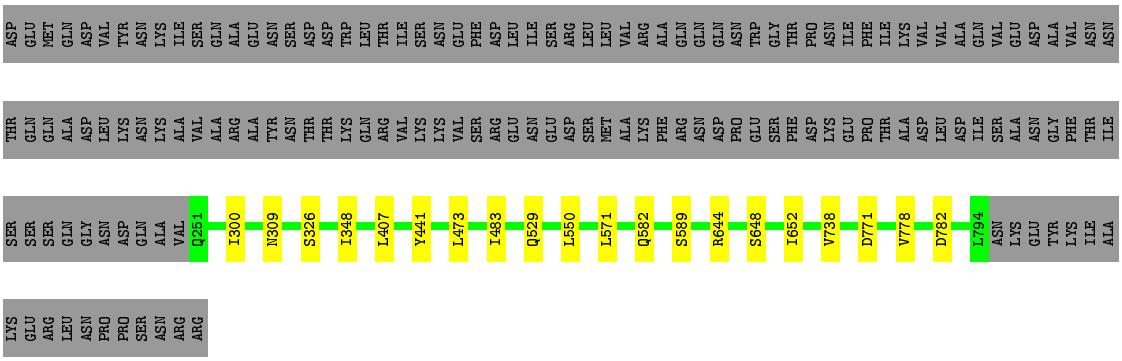
Chain b:



- Molecule 39: EIF3C

Chain c:




ASP GLU MET GLN ASP VAL TYR ASN LYS ILE SER GLN ALA GLU ASN SER ASP ASP TRP LEU THR ILE SER ASN GLU PHE ASP LEU ILE SER ARG LEU LEU VAL ARG ALA GLN GLN GLN ASN TRP GLY THR PRO ASN ILE PHE ILE LYS VAL VAL ALA GLN VAL GLU ASP ALA VAL ASN ASN
THR GLN GLN ALA ASP LEU LYS ASN LYS ALA VAL ALA ARG ALA TYR ASN THR THR LYS GLN ARG VAL LYS LYS VAL SER ARG GLU ASN GLU ASP SER MET ALA LYS PHE ARG ASN ASP PRO GLU SER PHE ASP LYS GLU PRO THR ALA ASP LEU ASP ILE SER ALA ASN GLY PHE THR ILE
SER SER SER GLN GLY ASN ASP GLN ALA VAL Q251 I300 N309 S326 I348 L407 Y441 L473 I483 Q529 L550 L571 Q582 S589 R644 S648 I652 V738 D771 V778 D782 L794 ASN LYS GLU TYR LYS ILE ALA
LYS GLU ARG LEU ASN PRO PRO SER ASN ARG ARG

4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	BY IMAGE	Depositor
Microscope	OTHER	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4K X 4K)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	#$\|Z\|>2$	RMSZ	#$\|Z\|>2$
1	0	0.64	0/815	1.14	3/1087 (0.3%)
10	9	0.53	0/404	0.99	1/542 (0.2%)
11	A	0.96	38/42127 (0.1%)	1.50	830/65638 (1.3%)
12	B	0.54	0/1617	0.80	0/2215
13	C	0.59	0/1759	0.74	0/2368
14	D	0.60	0/1519	0.82	1/2035 (0.0%)
15	E	0.60	0/1665	0.78	0/2263
16	F	0.64	0/678	1.18	6/903 (0.7%)
17	G	0.49	0/1629	0.72	0/2202
18	H	0.66	0/1038	0.86	3/1395 (0.2%)
19	I	0.57	0/1125	0.85	3/1510 (0.2%)
2	1	0.44	0/499	0.72	0/670
20	J	0.55	0/865	0.76	0/1169
21	K	0.49	0/901	0.82	1/1217 (0.1%)
22	L	0.72	0/1139	0.91	2/1518 (0.1%)
23	M	0.59	0/1211	0.80	0/1628
24	N	0.71	0/452	0.94	1/600 (0.2%)
25	O	0.61	0/1215	0.83	3/1638 (0.2%)
26	P	0.56	0/1087	0.77	1/1449 (0.1%)
27	Q	0.70	0/1239	0.81	0/1673
28	R	0.49	0/2490	0.70	0/3389
29	S	0.60	0/998	0.86	2/1341 (0.1%)
3	2	0.68	0/1514	0.88	2/2021 (0.1%)
30	T	0.57	0/1130	0.81	0/1517
31	U	0.49	0/898	0.76	0/1220
32	V	0.54	0/935	0.81	0/1254
33	W	0.58	0/2109	0.86	1/2839 (0.0%)
34	X	0.50	0/483	0.72	0/643
35	Y	0.55	0/1823	0.75	0/2439
36	Z	0.53	0/693	0.75	0/935
37	a	0.32	0/3729	0.51	0/5041
38	b	0.42	1/3999 (0.0%)	0.57	2/5440 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >2	RMSZ	#|Z| >2
39	c	0.33	0/4525	0.53	0/6120
4	3	0.52	0/1506	0.77	0/2028
5	4	0.45	0/1735	0.81	0/2335
6	5	0.54	0/782	0.77	0/1047
7	6	0.53	0/620	0.82	1/838 (0.1%)
8	7	0.56	0/789	0.83	3/1067 (0.3%)
9	8	0.50	0/571	0.86	1/768 (0.1%)
All	All	0.75	39/94313 (0.0%)	1.18	867/136002 (0.6%)

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
1	0	0	1
10	9	0	2
16	F	0	1
21	K	0	1
27	Q	0	1
32	V	0	2
39	c	0	1
4	3	0	1
5	4	0	1
7	6	0	1
9	8	0	3
All	All	0	15

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	1626	U	O3'-P	48.27	2.19	1.61
11	A	553	G	C6-N1	8.08	1.45	1.39
11	A	377	G	N9-C4	-7.20	1.32	1.38
11	A	1456	C	N3-C4	-7.04	1.29	1.33
11	A	1455	G	C6-O6	6.88	1.30	1.24
11	A	553	G	C6-O6	6.80	1.30	1.24
11	A	1754	A	N9-C4	-6.61	1.33	1.37
11	A	992	A	C2-N3	-6.58	1.27	1.33
11	A	1200	G	C6-N1	6.46	1.44	1.39
11	A	992	A	N9-C4	-6.35	1.34	1.37
11	A	1241	G	N9-C8	6.20	1.42	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	49	C	P-OP2	-6.16	1.38	1.49
11	A	1746	A	N9-C4	-5.99	1.34	1.37
11	A	1555	A	N3-C4	-5.90	1.31	1.34
11	A	1291	G	N3-C4	-5.83	1.31	1.35
11	A	1782	A	C6-N1	-5.81	1.31	1.35
11	A	992	A	N9-C8	5.79	1.42	1.37
38	b	565	TRP	C-N	5.75	1.47	1.34
11	A	1560	U	N3-C4	-5.68	1.33	1.38
11	A	993	A	N7-C5	-5.65	1.35	1.39
11	A	553	G	N1-C2	5.62	1.42	1.37
11	A	538	A	N3-C4	5.60	1.38	1.34
11	A	542	A	N9-C4	-5.53	1.34	1.37
11	A	577	G	C5-C6	-5.53	1.36	1.42
11	A	1084	A	N3-C4	-5.46	1.31	1.34
11	A	331	A	N9-C4	-5.36	1.34	1.37
11	A	973	A	N7-C5	-5.33	1.36	1.39
11	A	865	A	C6-N1	-5.26	1.31	1.35
11	A	377	G	C6-N1	5.21	1.43	1.39
11	A	474	A	N9-C4	-5.19	1.34	1.37
11	A	582	U	P-O5'	-5.16	1.54	1.59
11	A	352	A	N9-C8	-5.14	1.33	1.37
11	A	1758	U	N1-C2	5.11	1.43	1.38
11	A	605	A	N9-C4	-5.08	1.34	1.37
11	A	555	A	N9-C4	5.08	1.40	1.37
11	A	142	G	N9-C4	-5.07	1.33	1.38
11	A	577	G	N9-C4	-5.07	1.33	1.38
11	A	639	U	N1-C2	5.04	1.43	1.38
11	A	944	A	N9-C4	-5.03	1.34	1.37

All (867) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	1626	U	O3'-P-O5'	27.80	156.82	104.00
11	A	1626	U	OP1-P-O3'	-21.44	58.04	105.20
11	A	1626	U	P-O3'-C3'	-19.41	96.41	119.70
11	A	553	G	N1-C6-O6	18.48	130.99	119.90
11	A	1200	G	N1-C6-O6	17.91	130.65	119.90
11	A	577	G	C4-C5-N7	14.78	116.71	110.80
11	A	1200	G	C5-C6-O6	-14.32	120.00	128.60
11	A	1773	C	N3-C4-C5	-14.05	116.28	121.90
11	A	1560	U	C5-C4-O4	13.39	133.93	125.90
11	A	1773	C	C6-N1-C2	-13.34	114.96	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	1541	G	N1-C6-O6	-12.52	112.39	119.90
11	A	577	G	C5-N7-C8	-12.47	98.06	104.30
16	F	72	PRO	CA-N-CD	-12.14	94.50	111.50
11	A	1200	G	N3-C2-N2	-11.90	111.57	119.90
11	A	577	G	C5-C6-O6	-11.78	121.53	128.60
11	A	1782	A	N9-C4-C5	11.66	110.46	105.80
11	A	393	C	C6-N1-C2	11.62	124.95	120.30
11	A	553	G	N3-C2-N2	-11.37	111.94	119.90
11	A	577	G	N1-C6-O6	11.27	126.66	119.90
11	A	1600	A	C2-N3-C4	-11.25	104.97	110.60
11	A	639	U	N3-C2-O2	-11.14	114.40	122.20
11	A	1280	C	N3-C4-C5	-10.97	117.51	121.90
11	A	1782	A	C8-N9-C4	-10.88	101.45	105.80
11	A	144	U	N3-C2-O2	-10.73	114.69	122.20
11	A	1560	U	N3-C2-O2	-10.64	114.75	122.20
11	A	1455	G	C5-C6-N1	-10.55	106.23	111.50
11	A	577	G	C6-C5-N7	-10.48	124.11	130.40
11	A	553	G	C5-C6-N1	-10.39	106.30	111.50
11	A	1782	A	C5-C6-N6	10.37	132.00	123.70
11	A	639	U	N1-C2-O2	10.29	130.00	122.80
11	A	1486	G	C5-N7-C8	-10.06	99.27	104.30
11	A	507	U	N3-C2-O2	-9.98	115.21	122.20
11	A	1096	C	C2-N1-C1'	9.97	129.77	118.80
11	A	1745	G	C5-C6-O6	-9.96	122.62	128.60
11	A	542	A	N7-C8-N9	9.89	118.74	113.80
11	A	553	G	C5-C6-O6	-9.83	122.70	128.60
11	A	1198	G	C8-N9-C4	-9.82	102.47	106.40
11	A	1456	C	N3-C4-N4	-9.81	111.13	118.00
11	A	553	G	C6-C5-N7	-9.75	124.55	130.40
11	A	1782	A	N1-C6-N6	-9.61	112.83	118.60
11	A	1280	C	N3-C4-N4	9.53	124.67	118.00
11	A	1486	G	N7-C8-N9	9.52	117.86	113.10
11	A	139	C	C6-N1-C2	-9.49	116.51	120.30
11	A	1456	C	C5-C4-N4	9.45	126.82	120.20
11	A	1282	U	N3-C2-O2	-9.41	115.61	122.20
11	A	1258	U	N3-C2-O2	-9.40	115.62	122.20
11	A	453	U	N3-C2-O2	-9.29	115.69	122.20
11	A	1654	G	C5-C6-N1	9.22	116.11	111.50
11	A	558	U	N3-C2-O2	-9.14	115.80	122.20
11	A	1761	U	C5-C4-O4	9.12	131.37	125.90
11	A	969	C	C6-N1-C2	9.11	123.94	120.30
11	A	1596	C	C6-N1-C2	-9.11	116.66	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	542	A	C5-N7-C8	-9.10	99.35	103.90
11	A	1169	G	C8-N9-C4	-9.10	102.76	106.40
11	A	402	C	C6-N1-C2	9.02	123.91	120.30
11	A	142	G	N3-C2-N2	-9.01	113.60	119.90
11	A	794	U	N1-C2-O2	8.99	129.09	122.80
8	7	88	PRO	N-CA-CB	8.97	114.07	103.30
11	A	1596	C	N3-C2-O2	-8.94	115.64	121.90
11	A	1455	G	N3-C2-N2	-8.89	113.67	119.90
11	A	1745	G	N3-C4-N9	8.85	131.31	126.00
11	A	507	U	N1-C2-O2	8.85	128.99	122.80
1	0	42	LEU	CB-CG-CD1	-8.84	95.98	111.00
11	A	92	A	C8-N9-C4	-8.83	102.27	105.80
11	A	1749	A	N1-C6-N6	8.80	123.88	118.60
11	A	1654	G	C6-N1-C2	-8.78	119.83	125.10
11	A	992	A	N3-C4-C5	8.74	132.92	126.80
11	A	647	G	N3-C4-N9	-8.73	120.76	126.00
11	A	1503	A	C2-N3-C4	-8.71	106.25	110.60
11	A	1189	A	C8-N9-C4	8.69	109.28	105.80
11	A	453	U	C2-N1-C1'	8.69	128.12	117.70
11	A	558	U	N1-C2-O2	8.68	128.88	122.80
11	A	7	G	N1-C6-O6	-8.66	114.70	119.90
11	A	1745	G	C5-C6-N1	8.66	115.83	111.50
11	A	17	C	C6-N1-C2	-8.62	116.85	120.30
11	A	1291	G	N7-C8-N9	8.58	117.39	113.10
11	A	992	A	C5-C6-N1	-8.58	113.41	117.70
11	A	992	A	N3-C4-N9	-8.55	120.56	127.40
11	A	1387	G	N1-C6-O6	8.45	124.97	119.90
11	A	719	U	C2-N1-C1'	8.44	127.83	117.70
11	A	1782	A	N1-C2-N3	8.41	133.51	129.30
11	A	1131	A	C8-N9-C4	8.41	109.16	105.80
11	A	1773	C	N3-C4-N4	8.40	123.88	118.00
11	A	794	U	N3-C2-O2	-8.39	116.33	122.20
11	A	1486	G	C4-C5-N7	8.37	114.15	110.80
11	A	736	C	C2-N1-C1'	8.35	127.98	118.80
11	A	1200	G	C6-C5-N7	-8.32	125.41	130.40
11	A	136	C	C2-N1-C1'	8.30	127.93	118.80
11	A	966	A	C8-N9-C4	8.29	109.12	105.80
11	A	319	U	N3-C2-O2	8.28	127.99	122.20
11	A	1541	G	C5-C6-O6	8.26	133.56	128.60
11	A	1490	C	C6-N1-C2	-8.21	117.02	120.30
11	A	1773	C	C5-C6-N1	8.20	125.10	121.00
11	A	1291	G	N1-C2-N3	8.20	128.82	123.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	308	C	C5-C6-N1	-8.19	116.91	121.00
11	A	542	A	C4-N9-C1'	8.19	141.04	126.30
11	A	316	A	C8-N9-C4	8.17	109.07	105.80
11	A	1096	C	N1-C2-O2	8.15	123.79	118.90
11	A	577	G	N7-C8-N9	8.14	117.17	113.10
11	A	1119	G	N1-C6-O6	-8.14	115.02	119.90
11	A	992	A	C5-N7-C8	-8.11	99.84	103.90
11	A	1280	C	N1-C2-O2	-8.11	114.03	118.90
11	A	145	A	C8-N9-C4	-8.10	102.56	105.80
11	A	1241	G	C5-N7-C8	-8.09	100.25	104.30
11	A	1387	G	C6-C5-N7	-8.09	125.55	130.40
11	A	1436	A	N1-C6-N6	8.08	123.45	118.60
11	A	1129	U	N3-C4-C5	8.07	119.44	114.60
11	A	1324	G	N3-C4-N9	-8.02	121.19	126.00
11	A	1200	G	N1-C2-N2	8.02	123.42	116.20
11	A	349	U	N3-C2-O2	-7.96	116.62	122.20
11	A	1662	G	N1-C6-O6	-7.96	115.12	119.90
11	A	864	U	N3-C2-O2	-7.96	116.63	122.20
11	A	1455	G	C4-C5-N7	-7.95	107.62	110.80
11	A	1611	A	N7-C8-N9	7.92	117.76	113.80
11	A	1291	G	C8-N9-C4	-7.89	103.24	106.40
11	A	189	C	C2-N1-C1'	7.88	127.47	118.80
11	A	992	A	C6-N1-C2	7.87	123.32	118.60
11	A	581	U	C2-N1-C1'	7.81	127.07	117.70
11	A	1291	G	C2-N3-C4	-7.79	108.00	111.90
11	A	1432	U	C6-N1-C2	7.79	125.67	121.00
11	A	704	C	N1-C2-O2	7.72	123.53	118.90
11	A	1751	C	N3-C4-C5	7.71	124.98	121.90
11	A	142	G	N3-C4-N9	-7.65	121.41	126.00
11	A	555	A	C8-N9-C4	-7.65	102.74	105.80
11	A	334	G	C2-N3-C4	-7.64	108.08	111.90
11	A	1560	U	N3-C4-O4	-7.64	114.05	119.40
11	A	647	G	N9-C4-C5	7.62	108.45	105.40
11	A	594	A	C2-N3-C4	7.62	114.41	110.60
11	A	1305	U	C5-C4-O4	7.60	130.46	125.90
11	A	553	G	C4-C5-C6	7.58	123.35	118.80
11	A	831	U	C5-C6-N1	7.58	126.49	122.70
11	A	1486	G	C8-N9-C4	-7.58	103.37	106.40
1	0	66	ARG	NE-CZ-NH1	7.55	124.08	120.30
11	A	704	C	C2-N1-C1'	7.55	127.11	118.80
11	A	758	U	N3-C2-O2	-7.54	116.92	122.20
11	A	608	U	C2-N3-C4	-7.54	122.48	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	1481	C	C6-N1-C2	-7.53	117.29	120.30
11	A	1758	U	N3-C2-O2	-7.50	116.95	122.20
11	A	89	G	C8-N9-C4	7.50	109.40	106.40
11	A	978	A	C8-N9-C4	7.49	108.80	105.80
11	A	323	A	C8-N9-C4	-7.48	102.81	105.80
11	A	1075	C	N1-C2-O2	-7.47	114.42	118.90
11	A	1241	G	N7-C8-N9	7.47	116.84	113.10
11	A	1389	C	N1-C2-O2	7.47	123.39	118.90
11	A	507	U	C2-N1-C1'	7.47	126.67	117.70
11	A	1280	C	C6-N1-C2	-7.46	117.32	120.30
11	A	1761	U	C6-N1-C2	-7.45	116.53	121.00
11	A	355	G	C5-C6-N1	7.43	115.22	111.50
11	A	1762	A	N1-C6-N6	7.43	123.06	118.60
11	A	871	G	N3-C4-C5	-7.41	124.90	128.60
19	I	40	GLU	C-N-CD	-7.38	104.37	120.60
11	A	583	C	C6-N1-C2	-7.37	117.35	120.30
11	A	1012	U	C2-N3-C4	7.34	131.41	127.00
11	A	1096	C	C6-N1-C1'	-7.34	111.99	120.80
11	A	1274	C	C5-C6-N1	-7.32	117.34	121.00
11	A	1745	G	C4-C5-N7	7.31	113.72	110.80
11	A	1611	A	C2-N3-C4	-7.30	106.95	110.60
11	A	628	G	C2-N3-C4	-7.25	108.28	111.90
11	A	1291	G	C5-N7-C8	-7.24	100.68	104.30
11	A	783	G	C4-C5-N7	7.22	113.69	110.80
11	A	728	U	C2-N1-C1'	7.21	126.36	117.70
11	A	377	G	N3-C2-N2	-7.20	114.86	119.90
11	A	1121	C	C4-C5-C6	7.19	121.00	117.40
11	A	142	G	N3-C4-C5	7.19	132.19	128.60
11	A	1611	A	C5-N7-C8	-7.19	100.31	103.90
11	A	1642	G	C2-N3-C4	7.19	115.49	111.90
11	A	1432	U	C5-C6-N1	-7.14	119.13	122.70
11	A	1329	A	N1-C6-N6	7.11	122.87	118.60
11	A	1456	C	N3-C2-O2	-7.11	116.93	121.90
11	A	1241	G	C4-C5-N7	7.10	113.64	110.80
11	A	1000	C	N3-C4-N4	-7.10	113.03	118.00
11	A	74	U	O4'-C1'-N1	7.08	113.86	108.20
11	A	1057	U	C5-C6-N1	7.07	126.24	122.70
11	A	159	U	C6-N1-C2	7.06	125.24	121.00
11	A	1654	G	C5-C6-O6	-7.06	124.36	128.60
11	A	1747	G	C2-N3-C4	-7.06	108.37	111.90
11	A	1146	G	C8-N9-C4	-7.05	103.58	106.40
11	A	1162	C	C6-N1-C2	-7.05	117.48	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	108	A	N1-C2-N3	7.05	132.82	129.30
11	A	61	A	N7-C8-N9	7.04	117.32	113.80
11	A	610	G	C8-N9-C1'	-7.04	117.85	127.00
11	A	1749	A	N9-C4-C5	-7.04	102.98	105.80
11	A	992	A	C2-N3-C4	-7.03	107.08	110.60
11	A	1533	C	C4-C5-C6	7.02	120.91	117.40
11	A	1462	G	C8-N9-C4	7.00	109.20	106.40
11	A	1749	A	C2-N3-C4	-7.00	107.10	110.60
11	A	313	U	N3-C4-O4	-6.99	114.51	119.40
11	A	1654	G	N3-C4-C5	-6.99	125.11	128.60
11	A	92	A	N9-C4-C5	6.99	108.59	105.80
11	A	1324	G	N3-C2-N2	-6.97	115.02	119.90
11	A	1361	U	N1-C2-O2	6.97	127.68	122.80
25	O	22	ALA	C-N-CD	-6.96	105.30	120.60
11	A	131	C	C6-N1-C2	-6.95	117.52	120.30
11	A	981	U	N3-C2-O2	-6.95	117.33	122.20
11	A	1611	A	N1-C2-N3	6.94	132.77	129.30
11	A	542	A	C8-N9-C1'	-6.92	115.25	127.70
11	A	1548	G	C2-N3-C4	6.91	115.35	111.90
11	A	321	C	C6-N1-C2	-6.90	117.54	120.30
11	A	360	A	N9-C4-C5	-6.89	103.04	105.80
11	A	736	C	C6-N1-C1'	-6.89	112.53	120.80
11	A	1782	A	N7-C8-N9	6.89	117.24	113.80
11	A	305	C	C6-N1-C2	-6.87	117.55	120.30
11	A	1318	G	N1-C6-O6	6.87	124.02	119.90
11	A	410	A	C8-N9-C4	6.87	108.55	105.80
11	A	89	G	N7-C8-N9	-6.86	109.67	113.10
11	A	577	G	N9-C4-C5	-6.84	102.66	105.40
11	A	1297	G	C8-N9-C4	6.84	109.14	106.40
11	A	1206	U	N3-C4-O4	6.83	124.18	119.40
11	A	1174	C	N1-C2-O2	6.83	123.00	118.90
11	A	360	A	C8-N9-C4	6.82	108.53	105.80
11	A	1679	G	N3-C4-C5	-6.80	125.20	128.60
11	A	1319	A	N1-C6-N6	6.79	122.68	118.60
11	A	1210	C	N3-C4-C5	-6.79	119.18	121.90
11	A	240	U	C2-N1-C1'	6.78	125.84	117.70
11	A	453	U	N1-C2-O2	6.78	127.55	122.80
11	A	1773	C	C2-N3-C4	6.78	123.29	119.90
11	A	1600	A	C5-C6-N1	-6.78	114.31	117.70
24	N	36	LEU	CA-CB-CG	6.77	130.88	115.30
11	A	142	G	N1-C2-N2	6.77	122.29	116.20
11	A	192	U	C2-N1-C1'	6.76	125.81	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	1190	C	C6-N1-C2	6.75	123.00	120.30
11	A	1246	C	N3-C2-O2	-6.74	117.18	121.90
11	A	838	G	C8-N9-C4	6.73	109.09	106.40
11	A	73	U	O4'-C1'-N1	6.72	113.58	108.20
11	A	553	G	N1-C2-N2	6.72	122.25	116.20
11	A	566	C	N1-C2-O2	6.72	122.93	118.90
11	A	934	C	C2-N1-C1'	6.72	126.19	118.80
11	A	340	U	N1-C2-O2	6.71	127.50	122.80
11	A	6	G	N1-C2-N3	6.71	127.92	123.90
11	A	1521	G	N3-C4-C5	-6.70	125.25	128.60
11	A	539	G	N7-C8-N9	6.70	116.45	113.10
11	A	607	G	N1-C6-O6	6.70	123.92	119.90
11	A	608	U	N1-C2-N3	6.70	118.92	114.90
11	A	1195	C	C6-N1-C2	-6.68	117.63	120.30
11	A	355	G	C6-N1-C2	-6.68	121.09	125.10
11	A	1455	G	N1-C6-O6	6.68	123.91	119.90
11	A	783	G	N9-C4-C5	-6.66	102.73	105.40
11	A	736	C	C5-C6-N1	6.64	124.32	121.00
11	A	1282	U	C5-C4-O4	6.63	129.88	125.90
11	A	1006	C	C6-N1-C2	-6.63	117.65	120.30
11	A	1258	U	C5-C4-O4	6.62	129.87	125.90
11	A	942	G	N1-C6-O6	-6.61	115.93	119.90
11	A	558	U	C2-N1-C1'	6.60	125.62	117.70
11	A	687	G	N3-C2-N2	-6.59	115.29	119.90
11	A	647	G	N3-C2-N2	-6.58	115.29	119.90
11	A	1000	C	N1-C2-O2	6.58	122.85	118.90
11	A	732	G	N9-C4-C5	-6.58	102.77	105.40
11	A	1503	A	N1-C2-N3	6.57	132.58	129.30
11	A	136	C	N1-C2-O2	6.57	122.84	118.90
11	A	1024	U	N3-C2-O2	-6.56	117.61	122.20
11	A	404	G	C5-C6-O6	-6.56	124.67	128.60
11	A	1611	A	C8-N9-C4	-6.56	103.18	105.80
11	A	1274	C	N3-C4-N4	-6.56	113.41	118.00
11	A	965	U	C5-C6-N1	6.55	125.98	122.70
11	A	1085	G	N3-C2-N2	6.54	124.48	119.90
11	A	1762	A	C8-N9-C4	6.54	108.41	105.80
11	A	75	U	N1-C2-O2	6.53	127.37	122.80
11	A	132	U	C2-N1-C1'	-6.52	109.88	117.70
11	A	1218	G	N1-C6-O6	6.52	123.81	119.90
11	A	1430	U	C5-C4-O4	6.52	129.81	125.90
11	A	75	U	N3-C2-O2	-6.50	117.65	122.20
11	A	557	G	C4-N9-C1'	6.50	134.94	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
16	F	61	ASP	CB-CG-OD2	-6.48	112.47	118.30
16	F	79	GLN	CG-CD-OE1	6.48	134.57	121.60
11	A	1473	U	N3-C2-O2	-6.48	117.66	122.20
11	A	830	U	N3-C2-O2	-6.47	117.67	122.20
11	A	1235	C	N1-C2-O2	-6.47	115.02	118.90
11	A	1462	G	N9-C4-C5	-6.47	102.81	105.40
11	A	627	C	N3-C4-N4	6.46	122.53	118.00
11	A	557	G	C8-N9-C1'	-6.46	118.61	127.00
11	A	1536	G	N3-C4-N9	6.45	129.87	126.00
11	A	377	G	C5-C6-O6	-6.43	124.74	128.60
11	A	554	C	C2-N1-C1'	6.43	125.88	118.80
11	A	1628	U	N3-C2-O2	-6.43	117.70	122.20
11	A	1422	A	C8-N9-C4	6.43	108.37	105.80
11	A	1185	U	C2-N1-C1'	6.41	125.39	117.70
11	A	557	G	C4-C5-C6	6.41	122.64	118.80
3	2	172	ARG	NE-CZ-NH1	6.40	123.50	120.30
11	A	1456	C	C6-N1-C2	-6.40	117.74	120.30
11	A	610	G	C4-N9-C1'	6.39	134.81	126.50
11	A	810	G	C6-C5-N7	-6.39	126.56	130.40
11	A	1749	A	C8-N9-C4	6.39	108.36	105.80
11	A	68	A	C8-N9-C4	-6.39	103.25	105.80
22	L	33	LEU	CA-CB-CG	-6.38	100.62	115.30
11	A	933	A	C8-N9-C4	-6.38	103.25	105.80
11	A	389	G	N3-C4-C5	-6.38	125.41	128.60
11	A	628	G	N3-C2-N2	6.37	124.36	119.90
11	A	404	G	C8-N9-C4	6.37	108.95	106.40
11	A	340	U	N3-C2-O2	-6.36	117.75	122.20
11	A	1096	C	N3-C2-O2	-6.35	117.45	121.90
11	A	1515	A	C8-N9-C4	-6.35	103.26	105.80
11	A	144	U	C6-N1-C2	-6.33	117.20	121.00
11	A	973	A	C2-N3-C4	-6.32	107.44	110.60
11	A	1758	U	C6-N1-C2	-6.32	117.21	121.00
11	A	1246	C	C5-C4-N4	6.31	124.61	120.20
11	A	1363	U	N1-C2-O2	6.31	127.22	122.80
11	A	1200	G	C4-C5-C6	6.30	122.58	118.80
11	A	1454	G	C5-C6-O6	6.30	132.38	128.60
11	A	266	A	N9-C4-C5	-6.30	103.28	105.80
11	A	1745	G	N9-C4-C5	-6.30	102.88	105.40
11	A	767	U	N3-C4-O4	-6.29	115.00	119.40
11	A	1169	G	N7-C8-N9	6.29	116.25	113.10
11	A	1297	G	N7-C8-N9	-6.29	109.95	113.10
11	A	1766	A	C8-N9-C4	6.29	108.31	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	136	C	C6-N1-C1'	-6.28	113.27	120.80
11	A	538	A	N1-C2-N3	-6.28	126.16	129.30
11	A	1670	G	C8-N9-C1'	-6.28	118.84	127.00
11	A	445	A	C2-N3-C4	6.27	113.74	110.60
11	A	543	C	N3-C2-O2	-6.27	117.51	121.90
11	A	407	A	C4-C5-C6	6.27	120.14	117.00
11	A	159	U	C2-N1-C1'	-6.27	110.18	117.70
11	A	1595	U	C5-C4-O4	-6.26	122.14	125.90
11	A	349	U	C4-C5-C6	6.25	123.45	119.70
11	A	1027	A	N7-C8-N9	6.25	116.93	113.80
11	A	868	G	N1-C6-O6	6.25	123.65	119.90
11	A	189	C	N1-C2-O2	6.25	122.65	118.90
11	A	590	C	C2-N1-C1'	6.24	125.67	118.80
11	A	865	A	N1-C6-N6	-6.24	114.86	118.60
11	A	1387	G	C5-C6-O6	-6.24	124.86	128.60
11	A	1329	A	C5-C6-N6	-6.23	118.71	123.70
8	7	76	LEU	CA-CB-CG	6.23	129.63	115.30
11	A	1000	C	C5-C6-N1	-6.23	117.89	121.00
11	A	942	G	C8-N9-C4	-6.22	103.91	106.40
38	b	565	TRP	O-C-N	-6.22	112.74	122.70
11	A	213	A	C8-N9-C4	6.22	108.29	105.80
11	A	557	G	C6-C5-N7	-6.22	126.67	130.40
11	A	1654	G	C8-N9-C4	-6.22	103.91	106.40
11	A	557	G	N3-C4-N9	6.22	129.73	126.00
11	A	874	C	C5-C6-N1	6.21	124.11	121.00
11	A	1670	G	C4-N9-C1'	6.21	134.57	126.50
11	A	393	C	N3-C4-C5	6.21	124.38	121.90
11	A	494	U	N1-C2-O2	6.21	127.15	122.80
11	A	1514	U	N3-C2-O2	-6.21	117.85	122.20
11	A	781	U	C2-N1-C1'	6.21	125.15	117.70
11	A	719	U	N1-C2-O2	6.20	127.14	122.80
11	A	852	C	C5-C6-N1	6.20	124.10	121.00
11	A	186	C	C5-C6-N1	6.20	124.10	121.00
11	A	704	C	C6-N1-C1'	-6.19	113.37	120.80
11	A	1121	C	C5-C6-N1	-6.19	117.91	121.00
11	A	36	C	N3-C4-N4	6.19	122.33	118.00
11	A	1305	U	N1-C2-N3	6.19	118.61	114.90
11	A	1198	G	N9-C4-C5	6.18	107.87	105.40
11	A	189	C	C6-N1-C1'	-6.18	113.38	120.80
11	A	61	A	C8-N9-C4	-6.18	103.33	105.80
11	A	627	C	C5-C4-N4	-6.17	115.88	120.20
11	A	1192	C	N3-C2-O2	6.17	126.22	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	1596	C	C2-N1-C1'	6.17	125.59	118.80
11	A	377	G	N1-C6-O6	6.17	123.60	119.90
11	A	554	C	N1-C2-O2	6.16	122.60	118.90
11	A	1246	C	N3-C4-N4	-6.16	113.69	118.00
18	H	65	LEU	CA-CB-CG	6.16	129.47	115.30
11	A	1490	C	C2-N1-C1'	6.16	125.57	118.80
11	A	192	U	N3-C2-O2	-6.13	117.91	122.20
11	A	1473	U	C5-C4-O4	6.13	129.58	125.90
11	A	719	U	C5-C6-N1	6.13	125.76	122.70
11	A	1745	G	C6-N1-C2	-6.13	121.42	125.10
11	A	266	A	C8-N9-C4	6.12	108.25	105.80
11	A	736	C	N1-C2-O2	6.12	122.57	118.90
11	A	266	A	N1-C6-N6	6.11	122.27	118.60
11	A	932	U	C5-C4-O4	6.11	129.56	125.90
11	A	1796	C	C4-C5-C6	6.10	120.45	117.40
11	A	1346	A	N7-C8-N9	6.10	116.85	113.80
11	A	542	A	C6-C5-N7	-6.10	128.03	132.30
11	A	523	G	N3-C4-C5	-6.10	125.55	128.60
11	A	734	A	N1-C6-N6	6.09	122.25	118.60
11	A	1450	U	C5-C4-O4	6.09	129.55	125.90
11	A	1781	A	C5-C6-N6	6.09	128.57	123.70
11	A	106	U	C6-N1-C2	-6.08	117.35	121.00
11	A	1560	U	N1-C2-N3	6.08	118.55	114.90
11	A	621	A	C8-N9-C4	6.08	108.23	105.80
11	A	1747	G	C8-N9-C4	6.07	108.83	106.40
11	A	1465	C	N3-C4-C5	-6.07	119.47	121.90
11	A	1057	U	C2-N1-C1'	6.06	124.97	117.70
11	A	1776	A	N9-C4-C5	6.06	108.22	105.80
11	A	75	U	C2-N1-C1'	6.05	124.97	117.70
11	A	382	C	C2-N3-C4	-6.05	116.87	119.90
11	A	377	G	N3-C4-C5	6.05	131.62	128.60
11	A	1099	U	C5-C6-N1	6.04	125.72	122.70
11	A	811	A	C8-N9-C4	-6.04	103.38	105.80
11	A	1274	C	C4-C5-C6	6.04	120.42	117.40
11	A	397	A	N1-C6-N6	-6.04	114.98	118.60
11	A	1746	A	C8-N9-C4	6.04	108.22	105.80
11	A	1291	G	N3-C4-N9	-6.03	122.38	126.00
11	A	1339	C	C6-N1-C2	-6.03	117.89	120.30
11	A	1000	C	N3-C2-O2	-6.03	117.68	121.90
11	A	404	G	N9-C4-C5	-6.02	102.99	105.40
1	0	91	VAL	CG1-CB-CG2	-6.02	101.27	110.90
11	A	1258	U	C4-C5-C6	6.01	123.30	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	1521	G	N3-C4-N9	6.01	129.60	126.00
11	A	1455	G	N9-C4-C5	6.00	107.80	105.40
11	A	1537	C	C5-C6-N1	6.00	124.00	121.00
11	A	1314	U	N3-C2-O2	-6.00	118.00	122.20
11	A	279	G	C8-N9-C4	-5.99	104.00	106.40
11	A	1633	A	N9-C4-C5	5.99	108.20	105.80
11	A	274	G	C4-N9-C1'	5.99	134.29	126.50
11	A	831	U	C6-N1-C2	-5.99	117.41	121.00
11	A	1119	G	C5-C6-O6	5.99	132.19	128.60
11	A	542	A	C4-C5-N7	5.99	113.69	110.70
11	A	1157	A	C8-N9-C4	-5.99	103.41	105.80
11	A	1582	U	C6-N1-C2	5.98	124.59	121.00
11	A	1097	U	C2-N1-C1'	5.97	124.87	117.70
11	A	344	A	N1-C6-N6	-5.96	115.02	118.60
11	A	538	A	C4-C5-C6	-5.96	114.02	117.00
11	A	1121	C	N3-C4-C5	-5.96	119.52	121.90
11	A	1601	G	C5-C6-N1	5.96	114.48	111.50
11	A	1768	G	C4-N9-C1'	-5.96	118.76	126.50
11	A	335	U	N1-C2-O2	-5.95	118.63	122.80
11	A	1614	A	C4-C5-C6	5.95	119.97	117.00
11	A	1241	G	C8-N9-C4	-5.94	104.02	106.40
11	A	852	C	C4-C5-C6	-5.94	114.43	117.40
11	A	1436	A	N9-C4-C5	-5.94	103.42	105.80
26	P	44	LEU	CA-CB-CG	5.94	128.96	115.30
11	A	377	G	N3-C4-N9	-5.94	122.44	126.00
11	A	1131	A	N7-C8-N9	-5.93	110.83	113.80
11	A	732	G	C4-C5-N7	5.93	113.17	110.80
11	A	382	C	N3-C4-C5	5.93	124.27	121.90
11	A	1753	A	C8-N9-C4	5.92	108.17	105.80
16	F	71	ASP	CB-CG-OD2	5.92	123.63	118.30
11	A	360	A	N1-C6-N6	5.91	122.15	118.60
11	A	144	U	N1-C2-N3	5.91	118.45	114.90
11	A	997	G	N9-C4-C5	-5.91	103.04	105.40
11	A	1479	A	N1-C6-N6	5.90	122.14	118.60
11	A	1000	C	C5-C4-N4	5.90	124.33	120.20
11	A	1291	G	N3-C2-N2	-5.90	115.77	119.90
11	A	416	A	C8-N9-C4	5.89	108.16	105.80
11	A	1340	U	C5-C4-O4	5.89	129.44	125.90
11	A	1600	A	C5-N7-C8	-5.89	100.95	103.90
11	A	611	U	N1-C2-O2	-5.88	118.68	122.80
11	A	794	U	C2-N1-C1'	5.88	124.76	117.70
11	A	703	G	C8-N9-C4	-5.88	104.05	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	1112	G	C6-N1-C2	-5.88	121.57	125.10
11	A	1503	A	C5-N7-C8	-5.88	100.96	103.90
11	A	151	G	N1-C6-O6	-5.87	116.38	119.90
11	A	460	A	N1-C6-N6	-5.86	115.08	118.60
11	A	1536	G	C4-N9-C1'	5.85	134.11	126.50
11	A	21	U	N3-C2-O2	-5.85	118.11	122.20
11	A	1198	G	N7-C8-N9	5.85	116.02	113.10
11	A	829	A	C8-N9-C4	-5.84	103.47	105.80
11	A	1542	G	C5-C6-O6	5.83	132.10	128.60
11	A	1745	G	C6-C5-N7	-5.83	126.90	130.40
11	A	109	G	C5-C6-O6	-5.83	125.10	128.60
11	A	781	U	N1-C2-O2	5.83	126.88	122.80
11	A	1188	G	C5-C6-O6	-5.83	125.10	128.60
11	A	1421	A	C8-N9-C4	5.83	108.13	105.80
11	A	1169	G	N3-C4-C5	-5.82	125.69	128.60
16	F	61	ASP	CB-CG-OD1	5.82	123.54	118.30
11	A	1643	U	C5-C6-N1	-5.81	119.79	122.70
11	A	144	U	N1-C2-O2	5.81	126.86	122.80
11	A	1274	C	C5-C4-N4	5.81	124.26	120.20
11	A	628	G	N1-C2-N2	-5.80	110.98	116.20
11	A	192	U	N1-C2-O2	5.80	126.86	122.80
11	A	294	C	C6-N1-C2	5.80	122.62	120.30
11	A	628	G	C5-C6-O6	5.80	132.08	128.60
11	A	581	U	C6-N1-C1'	-5.79	113.09	121.20
11	A	1761	U	N3-C4-C5	-5.79	111.12	114.60
11	A	92	A	C6-N1-C2	-5.79	115.13	118.60
11	A	1417	A	N1-C6-N6	5.79	122.07	118.60
11	A	339	C	N1-C2-O2	-5.79	115.43	118.90
11	A	1354	G	N3-C4-C5	-5.78	125.71	128.60
11	A	1129	U	N3-C4-O4	-5.77	115.36	119.40
38	b	552	ALA	C-N-CD	5.77	140.52	128.40
11	A	1798	U	C2-N1-C1'	5.77	124.62	117.70
11	A	1782	A	C4-C5-N7	-5.76	107.82	110.70
11	A	1370	U	N3-C2-O2	-5.76	118.17	122.20
11	A	158	U	N3-C2-O2	-5.75	118.17	122.20
11	A	1602	C	C6-N1-C2	5.75	122.60	120.30
11	A	1626	U	OP2-P-O3'	-5.75	92.54	105.20
11	A	377	G	N1-C2-N2	5.75	121.38	116.20
11	A	444	C	C2-N3-C4	5.75	122.77	119.90
11	A	1324	G	C8-N9-C1'	5.75	134.47	127.00
11	A	971	A	C5-C6-N1	-5.75	114.83	117.70
11	A	342	C	C6-N1-C2	5.74	122.59	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	494	U	N3-C2-O2	-5.74	118.18	122.20
11	A	1633	A	N3-C4-C5	-5.74	122.79	126.80
11	A	810	G	C4-C5-N7	5.73	113.09	110.80
9	8	95	HIS	N-CA-C	5.73	126.47	111.00
11	A	13	C	N3-C4-C5	5.73	124.19	121.90
11	A	92	A	N3-C4-C5	-5.72	122.80	126.80
11	A	1361	U	N3-C2-O2	-5.72	118.19	122.20
11	A	1416	G	C8-N9-C4	-5.72	104.11	106.40
11	A	131	C	C5-C6-N1	5.72	123.86	121.00
11	A	507	U	C6-N1-C2	-5.71	117.57	121.00
11	A	741	C	N1-C2-O2	-5.71	115.47	118.90
11	A	539	G	C5-N7-C8	-5.71	101.44	104.30
11	A	279	G	N7-C8-N9	5.71	115.95	113.10
11	A	308	C	C2-N3-C4	-5.71	117.05	119.90
11	A	1646	C	C6-N1-C2	-5.71	118.02	120.30
11	A	1458	G	C4-N9-C1'	5.70	133.91	126.50
11	A	1279	C	C6-N1-C2	-5.70	118.02	120.30
11	A	380	U	N1-C2-O2	5.69	126.78	122.80
11	A	934	C	C6-N1-C1'	-5.69	113.97	120.80
11	A	1324	G	N9-C4-C5	5.68	107.67	105.40
11	A	393	C	C5-C6-N1	-5.67	118.16	121.00
11	A	831	U	C2-N1-C1'	5.67	124.50	117.70
11	A	1776	A	N1-C6-N6	-5.67	115.20	118.60
11	A	1207	C	C6-N1-C2	5.67	122.57	120.30
11	A	92	A	N1-C6-N6	-5.66	115.20	118.60
11	A	1614	A	C6-C5-N7	-5.66	128.34	132.30
11	A	1052	U	N3-C2-O2	-5.65	118.24	122.20
11	A	1145	U	N1-C2-O2	-5.65	118.84	122.80
11	A	1749	A	C4-C5-N7	5.65	113.53	110.70
11	A	115	G	N1-C6-O6	5.64	123.29	119.90
11	A	864	U	N1-C2-N3	5.64	118.28	114.90
11	A	401	A	N1-C6-N6	5.64	121.98	118.60
11	A	570	A	N3-C4-C5	-5.64	122.85	126.80
11	A	402	C	C2-N1-C1'	-5.63	112.61	118.80
11	A	1666	U	C6-N1-C2	-5.63	117.62	121.00
11	A	498	G	N3-C4-C5	-5.62	125.79	128.60
11	A	1153	G	N1-C6-O6	-5.62	116.53	119.90
11	A	1052	U	N1-C2-O2	5.62	126.73	122.80
11	A	274	G	C8-N9-C4	-5.61	104.16	106.40
11	A	1796	C	C6-N1-C2	-5.61	118.06	120.30
11	A	1075	C	N3-C2-O2	5.61	125.82	121.90
16	F	85	ARG	NE-CZ-NH2	5.61	123.10	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	566	C	N3-C2-O2	-5.60	117.98	121.90
11	A	1282	U	N1-C2-N3	5.59	118.26	114.90
11	A	1745	G	N3-C4-C5	-5.59	125.80	128.60
11	A	628	G	N3-C4-C5	5.59	131.40	128.60
11	A	639	U	N3-C4-O4	-5.59	115.49	119.40
11	A	1662	G	C8-N9-C4	-5.58	104.17	106.40
11	A	36	C	C5-C4-N4	-5.58	116.29	120.20
11	A	995	A	C8-N9-C4	5.58	108.03	105.80
19	I	69	VAL	CB-CA-C	-5.58	100.79	111.40
11	A	972	G	C4-C5-N7	-5.58	108.57	110.80
11	A	1560	U	N1-C2-O2	5.57	126.70	122.80
11	A	258	C	N3-C4-C5	5.57	124.13	121.90
11	A	334	G	N3-C4-C5	5.57	131.38	128.60
11	A	1456	C	N1-C2-N3	5.57	123.09	119.20
11	A	1536	G	C8-N9-C1'	-5.57	119.76	127.00
11	A	966	A	N9-C4-C5	-5.56	103.58	105.80
11	A	1489	U	N3-C2-O2	-5.56	118.31	122.20
11	A	1491	U	N3-C2-O2	-5.56	118.31	122.20
11	A	435	C	C2-N3-C4	5.55	122.68	119.90
11	A	445	A	N1-C2-N3	-5.55	126.53	129.30
11	A	612	U	N3-C4-O4	-5.55	115.52	119.40
11	A	380	U	N3-C2-O2	-5.55	118.32	122.20
11	A	1749	A	N3-C4-C5	5.54	130.68	126.80
11	A	1541	G	N3-C4-C5	-5.54	125.83	128.60
11	A	313	U	C5-C4-O4	5.53	129.22	125.90
11	A	608	U	C5-C6-N1	-5.53	119.93	122.70
11	A	1644	C	N1-C2-O2	-5.53	115.58	118.90
11	A	1781	A	C5-C6-N1	-5.53	114.93	117.70
11	A	829	A	C2-N3-C4	5.53	113.36	110.60
11	A	397	A	C5-C6-N6	5.52	128.12	123.70
11	A	377	G	C4-N9-C1'	-5.52	119.32	126.50
11	A	453	U	C6-N1-C1'	-5.52	113.47	121.20
11	A	1027	A	C5-N7-C8	-5.52	101.14	103.90
7	6	29	ARG	NE-CZ-NH1	5.52	123.06	120.30
11	A	1679	G	C2-N3-C4	5.52	114.66	111.90
11	A	74	U	C1'-O4'-C4'	-5.52	105.49	109.90
11	A	599	A	C5-N7-C8	5.51	106.66	103.90
11	A	1127	G	N9-C4-C5	5.51	107.61	105.40
11	A	1486	G	C6-C5-N7	-5.51	127.09	130.40
11	A	810	G	N1-C6-O6	5.51	123.20	119.90
11	A	1636	C	N3-C4-N4	5.51	121.86	118.00
11	A	145	A	N9-C4-C5	5.50	108.00	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	703	G	N7-C8-N9	5.50	115.85	113.10
11	A	1458	G	C8-N9-C1'	-5.50	119.85	127.00
11	A	142	G	N1-C6-O6	5.49	123.20	119.90
11	A	1633	A	C4-C5-N7	-5.49	107.95	110.70
11	A	74	U	C3'-C2'-C1'	-5.49	97.11	101.50
11	A	453	U	C5-C4-O4	5.49	129.19	125.90
11	A	1119	G	N9-C4-C5	5.49	107.59	105.40
11	A	323	A	N9-C4-C5	5.49	108.00	105.80
11	A	613	G	N1-C6-O6	-5.49	116.61	119.90
11	A	1600	A	C4-C5-N7	5.49	113.44	110.70
11	A	529	A	C8-N9-C4	5.48	107.99	105.80
11	A	355	G	N3-C4-C5	-5.48	125.86	128.60
11	A	1146	G	C4-N9-C1'	5.48	133.63	126.50
11	A	1277	G	N3-C4-N9	-5.48	122.71	126.00
11	A	1503	A	N7-C8-N9	5.48	116.54	113.80
11	A	1280	C	C4-C5-C6	5.47	120.14	117.40
11	A	386	G	C4-C5-N7	-5.47	108.61	110.80
11	A	1185	U	C6-N1-C1'	-5.47	113.54	121.20
11	A	169	A	C8-N9-C4	5.46	107.98	105.80
11	A	557	G	N1-C2-N2	-5.46	111.28	116.20
11	A	712	G	C8-N9-C4	-5.46	104.21	106.40
11	A	1097	U	C6-N1-C1'	-5.46	113.55	121.20
11	A	1462	G	C5-C6-O6	-5.46	125.32	128.60
11	A	1024	U	N1-C2-O2	5.46	126.62	122.80
11	A	838	G	N7-C8-N9	-5.46	110.37	113.10
11	A	1129	U	C2-N3-C4	-5.46	123.72	127.00
11	A	323	A	N7-C8-N9	5.45	116.53	113.80
11	A	951	A	C8-N9-C4	5.45	107.98	105.80
11	A	1330	G	C4-N9-C1'	-5.45	119.41	126.50
11	A	527	A	C8-N9-C4	-5.45	103.62	105.80
11	A	1778	G	N1-C6-O6	-5.45	116.63	119.90
11	A	969	C	N3-C4-C5	5.45	124.08	121.90
11	A	790	U	N1-C2-N3	5.44	118.17	114.90
11	A	1192	C	N1-C2-O2	-5.44	115.63	118.90
11	A	932	U	C6-N1-C1'	5.44	128.82	121.20
11	A	1642	G	N3-C4-C5	-5.44	125.88	128.60
11	A	1170	G	C6-C5-N7	-5.44	127.14	130.40
11	A	627	C	N1-C2-O2	-5.44	115.64	118.90
11	A	1324	G	N1-C2-N2	5.44	121.09	116.20
11	A	938	G	N1-C2-N2	-5.44	111.31	116.20
11	A	308	C	C6-N1-C2	5.43	122.47	120.30
11	A	971	A	N1-C2-N3	5.43	132.02	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	1200	G	N7-C8-N9	5.43	115.82	113.10
11	A	1445	G	N1-C6-O6	5.43	123.16	119.90
11	A	190	C	C6-N1-C2	5.43	122.47	120.30
11	A	1537	C	C5-C4-N4	-5.43	116.40	120.20
11	A	396	G	C5-C6-O6	-5.43	125.34	128.60
11	A	720	G	P-O3'-C3'	5.43	126.21	119.70
11	A	42	G	C8-N9-C4	5.42	108.57	106.40
11	A	639	U	N3-C4-C5	5.42	117.85	114.60
8	7	63	TYR	N-CA-C	5.42	125.64	111.00
11	A	392	G	C5-C6-O6	-5.42	125.35	128.60
11	A	557	G	N3-C4-C5	-5.42	125.89	128.60
11	A	1387	G	C4-C5-N7	5.42	112.97	110.80
11	A	1461	C	C6-N1-C2	5.42	122.47	120.30
11	A	350	U	C5-C6-N1	-5.42	119.99	122.70
11	A	972	G	C5-N7-C8	5.41	107.01	104.30
11	A	1560	U	C6-N1-C2	-5.41	117.75	121.00
11	A	1027	A	C8-N9-C4	-5.41	103.64	105.80
11	A	393	C	C2-N1-C1'	-5.41	112.85	118.80
11	A	1520	U	C5-C6-N1	-5.41	120.00	122.70
11	A	1600	A	N1-C2-N3	5.41	132.00	129.30
11	A	1754	A	C4-C5-C6	-5.41	114.30	117.00
3	2	29	LEU	CA-CB-CG	5.41	127.73	115.30
11	A	393	C	C2-N3-C4	-5.40	117.20	119.90
11	A	1170	G	C5-C6-O6	-5.40	125.36	128.60
11	A	1270	G	C2-N3-C4	5.40	114.60	111.90
11	A	1650	U	C5-C6-N1	-5.40	120.00	122.70
11	A	1148	C	C6-N1-C2	5.40	122.46	120.30
11	A	1762	A	N9-C4-C5	-5.39	103.64	105.80
11	A	268	C	C6-N1-C2	-5.39	118.14	120.30
11	A	767	U	N3-C2-O2	-5.39	118.43	122.20
11	A	1455	G	C4-C5-C6	5.39	122.03	118.80
11	A	1258	U	N1-C2-N3	5.39	118.13	114.90
11	A	1642	G	N3-C4-N9	5.39	129.23	126.00
11	A	264	G	N3-C4-N9	-5.38	122.77	126.00
11	A	1015	U	N1-C2-O2	5.38	126.57	122.80
11	A	1145	U	N3-C2-O2	5.38	125.97	122.20
19	I	40	GLU	C-N-CA	5.38	144.62	122.00
11	A	523	G	N1-C6-O6	-5.38	116.67	119.90
11	A	938	G	N3-C2-N2	5.38	123.66	119.90
11	A	1754	A	N3-C4-C5	5.38	130.56	126.80
11	A	404	G	N1-C6-O6	5.37	123.12	119.90
11	A	1504	G	C5-C6-O6	5.37	131.82	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	426	G	C4-N9-C1'	5.37	133.48	126.50
11	A	696	C	C6-N1-C2	-5.37	118.15	120.30
11	A	554	C	C6-N1-C1'	-5.36	114.36	120.80
11	A	1524	A	N1-C2-N3	5.36	131.98	129.30
11	A	811	A	C4-N9-C1'	5.36	135.95	126.30
11	A	396	G	N1-C6-O6	5.36	123.11	119.90
11	A	1000	C	C6-N1-C2	5.36	122.44	120.30
11	A	1386	G	C4-C5-N7	-5.36	108.66	110.80
11	A	1524	A	N1-C6-N6	-5.36	115.39	118.60
11	A	719	U	C6-N1-C1'	-5.36	113.70	121.20
11	A	7	G	N9-C4-C5	5.35	107.54	105.40
11	A	319	U	N1-C2-N3	-5.35	111.69	114.90
11	A	971	A	C2-N3-C4	-5.35	107.93	110.60
11	A	144	U	C5-C4-O4	5.35	129.11	125.90
11	A	214	G	C8-N9-C1'	5.34	133.95	127.00
11	A	811	A	N3-C4-C5	-5.34	123.06	126.80
11	A	992	A	C4-C5-N7	5.34	113.37	110.70
21	K	107	ARG	NE-CZ-NH1	5.34	122.97	120.30
11	A	1389	C	N3-C2-O2	-5.34	118.16	121.90
11	A	361	C	C5-C6-N1	5.34	123.67	121.00
11	A	469	C	N3-C2-O2	5.34	125.64	121.90
11	A	337	G	N3-C4-C5	-5.33	125.94	128.60
11	A	1672	G	N3-C4-C5	-5.33	125.94	128.60
11	A	42	G	N1-C6-O6	-5.33	116.70	119.90
11	A	1315	U	C5-C4-O4	-5.33	122.70	125.90
11	A	553	G	C2-N3-C4	-5.33	109.23	111.90
11	A	622	A	N9-C4-C5	5.33	107.93	105.80
11	A	1116	A	N1-C6-N6	5.33	121.80	118.60
11	A	1768	G	C8-N9-C1'	5.33	133.92	127.00
18	H	93	LEU	CA-CB-CG	5.32	127.55	115.30
11	A	336	G	C6-C5-N7	-5.32	127.21	130.40
11	A	63	G	C5-C6-O6	5.32	131.79	128.60
11	A	1293	U	N3-C2-O2	-5.32	118.48	122.20
11	A	1297	G	C4-N9-C1'	-5.31	119.59	126.50
29	S	60	LEU	CA-CB-CG	5.31	127.52	115.30
11	A	137	U	N3-C2-O2	-5.31	118.48	122.20
11	A	542	A	C5-C6-N1	-5.31	115.05	117.70
11	A	1052	U	C2-N1-C1'	5.31	124.07	117.70
11	A	1736	G	C8-N9-C4	5.31	108.52	106.40
11	A	1361	U	C2-N1-C1'	5.31	124.07	117.70
11	A	577	G	C2-N3-C4	-5.30	109.25	111.90
11	A	1666	U	C5-C6-N1	5.30	125.35	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	966	A	N7-C8-N9	-5.29	111.15	113.80
11	A	1195	C	P-O3'-C3'	5.29	126.05	119.70
11	A	42	G	N7-C8-N9	-5.29	110.45	113.10
11	A	1334	U	N1-C2-N3	5.29	118.08	114.90
11	A	1614	A	N1-C6-N6	5.29	121.77	118.60
11	A	583	C	C2-N1-C1'	5.29	124.61	118.80
11	A	139	C	C4-C5-C6	5.28	120.04	117.40
11	A	1119	G	N3-C4-C5	-5.28	125.96	128.60
11	A	1086	A	C5-C6-N1	5.28	120.34	117.70
11	A	1148	C	N3-C4-C5	5.28	124.01	121.90
25	O	22	ALA	C-N-CA	5.28	144.16	122.00
11	A	542	A	C8-N9-C4	-5.27	103.69	105.80
11	A	1648	A	N1-C6-N6	-5.27	115.44	118.60
11	A	343	C	C6-N1-C2	-5.27	118.19	120.30
11	A	864	U	C2-N1-C1'	5.27	124.02	117.70
11	A	1611	A	C6-C5-N7	-5.27	128.61	132.30
11	A	647	G	C8-N9-C4	-5.26	104.30	106.40
11	A	1422	A	N7-C8-N9	-5.26	111.17	113.80
11	A	1370	U	C2-N1-C1'	5.26	124.01	117.70
11	A	294	C	N1-C2-N3	-5.26	115.52	119.20
11	A	782	U	P-O3'-C3'	5.25	126.01	119.70
11	A	1270	G	N1-C6-O6	-5.25	116.75	119.90
11	A	815	G	C8-N9-C1'	5.25	133.82	127.00
11	A	139	C	N1-C2-N3	5.25	122.87	119.20
11	A	1363	U	N3-C2-O2	-5.24	118.53	122.20
11	A	927	C	C6-N1-C2	-5.24	118.20	120.30
11	A	1200	G	C8-N9-C4	-5.24	104.30	106.40
11	A	582	U	C5-C6-N1	5.24	125.32	122.70
11	A	1188	G	C8-N9-C4	5.23	108.49	106.40
11	A	6	G	N3-C4-N9	5.23	129.14	126.00
11	A	407	A	C5-N7-C8	5.23	106.52	103.90
11	A	1734	U	C5-C4-O4	5.23	129.04	125.90
11	A	972	G	N1-C6-O6	-5.23	116.76	119.90
11	A	1245	G	N3-C4-N9	-5.23	122.86	126.00
11	A	12	U	N3-C2-O2	-5.22	118.54	122.20
11	A	987	G	C8-N9-C4	5.22	108.49	106.40
11	A	1769	U	C5-C4-O4	5.22	129.03	125.90
11	A	719	U	N3-C2-O2	-5.22	118.55	122.20
11	A	42	G	C5-C6-N1	5.22	114.11	111.50
11	A	1245	G	C4-N9-C1'	-5.22	119.72	126.50
11	A	149	C	C6-N1-C2	5.21	122.39	120.30
11	A	1495	C	C6-N1-C2	5.21	122.39	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	1796	C	C5-C4-N4	5.21	123.85	120.20
11	A	214	G	N3-C4-N9	-5.21	122.88	126.00
11	A	1086	A	N1-C6-N6	-5.21	115.48	118.60
11	A	359	A	C4-C5-C6	-5.20	114.40	117.00
11	A	1761	U	N1-C2-N3	5.20	118.02	114.90
11	A	494	U	C2-N1-C1'	5.20	123.94	117.70
11	A	527	A	N7-C8-N9	5.20	116.40	113.80
11	A	886	U	N3-C2-O2	-5.20	118.56	122.20
11	A	432	G	C5-C6-N1	5.19	114.10	111.50
11	A	1454	G	C5-N7-C8	5.19	106.90	104.30
11	A	1600	A	C6-C5-N7	-5.19	128.66	132.30
11	A	240	U	C5-C6-N1	5.19	125.30	122.70
11	A	1376	C	C6-N1-C2	5.19	122.38	120.30
11	A	572	C	C6-N1-C2	-5.19	118.22	120.30
11	A	1679	G	N1-C6-O6	-5.19	116.79	119.90
11	A	1481	C	C5-C6-N1	5.18	123.59	121.00
11	A	192	U	C5-C6-N1	5.18	125.29	122.70
11	A	1600	A	N3-C4-C5	5.18	130.43	126.80
11	A	1734	U	C4-C5-C6	5.18	122.81	119.70
11	A	111	U	C6-N1-C2	-5.18	117.89	121.00
11	A	417	A	C8-N9-C4	-5.17	103.73	105.80
11	A	1096	C	C6-N1-C2	-5.17	118.23	120.30
11	A	1784	C	N3-C4-C5	5.17	123.97	121.90
11	A	378	A	C4-C5-N7	5.17	113.28	110.70
11	A	749	U	C5-C6-N1	5.17	125.28	122.70
11	A	1648	A	C5-C6-N1	5.17	120.28	117.70
11	A	1431	C	C6-N1-C2	5.16	122.36	120.30
11	A	704	C	N3-C2-O2	-5.16	118.29	121.90
11	A	1763	A	C5-N7-C8	-5.16	101.32	103.90
11	A	387	A	N1-C6-N6	-5.16	115.50	118.60
11	A	240	U	N1-C2-O2	5.16	126.41	122.80
11	A	783	G	C8-N9-C1'	-5.16	120.30	127.00
11	A	597	G	C8-N9-C4	-5.16	104.34	106.40
11	A	1454	G	C4-C5-N7	-5.16	108.74	110.80
11	A	555	A	N9-C4-C5	5.15	107.86	105.80
11	A	132	U	C6-N1-C1'	5.15	128.41	121.20
11	A	266	A	C2-N3-C4	-5.15	108.03	110.60
11	A	68	A	N7-C8-N9	5.14	116.37	113.80
11	A	142	G	C5-C6-N1	-5.14	108.93	111.50
11	A	307	G	C8-N9-C4	5.14	108.46	106.40
11	A	1448	G	N1-C6-O6	-5.14	116.81	119.90
11	A	1462	G	N3-C4-N9	5.14	129.09	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	1542	G	N1-C6-O6	-5.14	116.81	119.90
11	A	378	A	C5-C6-N6	-5.14	119.59	123.70
11	A	885	G	N1-C6-O6	5.14	122.98	119.90
11	A	73	U	C1'-O4'-C4'	-5.13	105.80	109.90
11	A	557	G	C5-C6-N1	-5.13	108.93	111.50
11	A	1330	G	C8-N9-C1'	5.13	133.67	127.00
11	A	1541	G	N9-C4-C5	5.13	107.45	105.40
11	A	810	G	C4-N9-C1'	5.13	133.17	126.50
11	A	1311	U	C6-N1-C2	5.13	124.08	121.00
11	A	192	U	C6-N1-C2	-5.13	117.92	121.00
11	A	1503	A	C5-C6-N1	-5.12	115.14	117.70
11	A	605	A	C8-N9-C4	5.12	107.85	105.80
11	A	1189	A	N7-C8-N9	-5.12	111.24	113.80
11	A	20	G	N1-C2-N2	-5.12	111.59	116.20
11	A	139	C	P-O3'-C3'	5.12	125.84	119.70
11	A	140	A	C4-N9-C1'	5.12	135.51	126.30
11	A	460	A	C4-C5-C6	-5.12	114.44	117.00
11	A	994	G	C4-C5-N7	-5.12	108.75	110.80
11	A	1166	A	C5-C6-N1	5.12	120.26	117.70
11	A	979	A	N1-C2-N3	5.11	131.86	129.30
11	A	380	U	C6-N1-C2	-5.11	117.94	121.00
11	A	1051	G	C8-N9-C1'	-5.11	120.36	127.00
11	A	1148	C	N1-C2-O2	5.11	121.97	118.90
11	A	278	U	C6-N1-C2	-5.11	117.94	121.00
11	A	992	A	N7-C8-N9	5.11	116.35	113.80
11	A	1346	A	C8-N9-C4	-5.11	103.76	105.80
11	A	173	A	C2-N3-C4	-5.10	108.05	110.60
11	A	1258	U	C5-C6-N1	-5.10	120.15	122.70
11	A	1536	G	N3-C4-C5	-5.10	126.05	128.60
11	A	572	C	N3-C2-O2	-5.10	118.33	121.90
18	H	104	LEU	CA-CB-CG	5.10	127.03	115.30
11	A	871	G	N3-C4-N9	5.10	129.06	126.00
29	S	42	ARG	NE-CZ-NH2	-5.09	117.75	120.30
11	A	1782	A	C5-C6-N1	-5.09	115.15	117.70
11	A	7	G	C5-C6-O6	5.09	131.65	128.60
11	A	334	G	N3-C4-N9	-5.09	122.95	126.00
11	A	687	G	N3-C4-N9	-5.09	122.95	126.00
11	A	1605	G	N1-C2-N2	-5.09	111.62	116.20
11	A	26	A	C8-N9-C4	-5.08	103.77	105.80
11	A	819	G	P-O3'-C3'	5.08	125.80	119.70
14	D	175	ARG	NE-CZ-NH1	5.08	122.84	120.30
11	A	973	A	C5-C6-N1	-5.08	115.16	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	1324	G	N3-C4-C5	5.08	131.14	128.60
11	A	647	G	C8-N9-C1'	5.08	133.60	127.00
11	A	1541	G	C5-C6-N1	5.08	114.04	111.50
11	A	564	G	C5-C6-O6	5.07	131.64	128.60
11	A	1093	A	C8-N9-C4	5.07	107.83	105.80
11	A	565	C	N1-C2-O2	5.07	121.94	118.90
11	A	149	C	N3-C4-C5	5.07	123.93	121.90
11	A	312	A	C8-N9-C4	-5.07	103.77	105.80
11	A	431	C	N3-C2-O2	-5.07	118.35	121.90
11	A	573	C	C4-C5-C6	5.07	119.93	117.40
11	A	1171	A	N1-C6-N6	-5.07	115.56	118.60
11	A	766	U	N1-C2-O2	5.06	126.34	122.80
11	A	1722	A	N1-C6-N6	-5.06	115.56	118.60
11	A	1643	U	C2-N3-C4	-5.06	123.97	127.00
11	A	1321	A	N1-C6-N6	-5.06	115.57	118.60
10	9	138	ARG	NE-CZ-NH2	-5.05	117.77	120.30
11	A	270	C	C2-N1-C1'	5.05	124.36	118.80
11	A	611	U	N1-C2-N3	5.05	117.93	114.90
11	A	151	G	C5-C6-N1	5.05	114.03	111.50
11	A	301	A	C4-C5-C6	5.05	119.53	117.00
11	A	1541	G	C2-N3-C4	5.05	114.43	111.90
33	W	164	LEU	CA-CB-CG	5.05	126.92	115.30
11	A	316	A	N7-C8-N9	-5.05	111.28	113.80
11	A	502	U	C5-C6-N1	5.05	125.22	122.70
11	A	56	U	N3-C2-O2	-5.05	118.67	122.20
11	A	440	U	N1-C2-O2	5.05	126.33	122.80
11	A	760	A	N1-C6-N6	5.04	121.63	118.60
11	A	440	U	N3-C4-O4	-5.04	115.87	119.40
11	A	6	G	N1-C2-N2	-5.04	111.66	116.20
11	A	728	U	N1-C2-O2	5.04	126.33	122.80
11	A	1436	A	C6-C5-N7	-5.04	128.77	132.30
11	A	360	A	C5-C6-N6	-5.04	119.67	123.70
22	L	111	GLY	N-CA-C	-5.04	100.50	113.10
11	A	1215	C	N3-C2-O2	-5.04	118.37	121.90
11	A	422	G	C8-N9-C4	-5.04	104.39	106.40
11	A	1051	G	C4-N9-C1'	5.04	133.05	126.50
11	A	49	C	C6-N1-C2	-5.03	118.29	120.30
11	A	965	U	C4-C5-C6	-5.03	116.68	119.70
11	A	391	A	C4-C5-C6	-5.03	114.48	117.00
11	A	1187	U	N3-C2-O2	-5.03	118.68	122.20
11	A	802	G	N3-C4-C5	-5.03	126.08	128.60
25	O	114	ARG	NE-CZ-NH1	5.03	122.81	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	158	U	N1-C2-O2	5.03	126.32	122.80
11	A	100	A	C8-N9-C4	-5.02	103.79	105.80
11	A	1761	U	N3-C2-O2	-5.02	118.69	122.20
11	A	1670	G	N3-C4-C5	-5.02	126.09	128.60
11	A	613	G	N3-C2-N2	5.01	123.41	119.90
11	A	342	C	C5-C6-N1	-5.01	118.49	121.00
11	A	629	U	C5-C6-N1	-5.01	120.19	122.70
11	A	853	G	C4-C5-N7	5.01	112.81	110.80
11	A	1478	G	C8-N9-C4	-5.01	104.40	106.40
11	A	258	C	C6-N1-C2	5.01	122.30	120.30
11	A	349	U	N1-C2-N3	5.01	117.90	114.90
11	A	734	A	P-O3'-C3'	5.01	125.71	119.70
11	A	865	A	N1-C2-N3	5.01	131.80	129.30
11	A	1170	G	N1-C6-O6	5.00	122.90	119.90
11	A	712	G	N7-C8-N9	5.00	115.60	113.10
11	A	1245	G	N3-C4-C5	5.00	131.10	128.60
11	A	1342	C	C4-C5-C6	5.00	119.90	117.40

There are no chirality outliers.

All (15) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	23	LYS	Peptide
4	3	131	PHE	Peptide
5	4	131	ASP	Peptide
7	6	42	ASN	Peptide
9	8	54	VAL	Peptide
9	8	93	SER	Peptide
9	8	96	SER	Peptide
10	9	105	TYR	Peptide
10	9	138	ARG	Peptide
16	F	62	PHE	Sidechain
21	K	124	ASP	Peptide
27	Q	127	GLN	Peptide
32	V	22	PRO	Peptide
32	V	85	VAL	Peptide
39	c	644	ARG	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	0	805	0	790	147	0
2	1	497	0	535	36	0
3	2	1489	0	1525	59	0
4	3	1481	0	1572	80	0
5	4	1709	0	1784	125	0
6	5	769	0	814	51	0
7	6	610	0	630	24	0
8	7	772	0	727	42	0
9	8	563	0	603	45	0
10	9	516	0	517	42	0
11	A	37835	0	19056	1168	0
12	B	1577	0	1566	221	0
13	C	1734	0	1817	80	0
14	D	1494	0	1573	81	0
15	E	1635	0	1715	88	0
16	F	671	0	707	80	0
17	G	1609	0	1675	70	0
18	H	1021	0	1060	54	0
19	I	1105	0	1166	70	0
20	J	855	0	917	41	0
21	K	891	0	883	63	0
22	L	1121	0	1196	61	0
23	M	1192	0	1222	63	0
24	N	442	0	428	24	0
25	O	1192	0	1255	45	0
26	P	1073	0	1132	41	0
27	Q	1213	0	1257	50	0
28	R	2437	0	2386	77	0
29	S	977	0	1002	41	0
30	T	1112	0	1124	69	0
31	U	890	0	887	43	0
32	V	926	0	930	76	0
33	W	2068	0	2154	71	0
34	X	475	0	523	86	0
35	Y	1799	0	1879	88	0
36	Z	684	0	672	39	0
37	a	3656	0	3708	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	b	3978	0	3768	0	0
39	c	4442	0	4474	0	0
40	5	1	0	0	0	0
40	6	1	0	0	0	0
40	9	1	0	0	0	0
40	N	1	0	0	0	0
All	All	89319	0	71629	2907	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 20.

All (2907) 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)
11:A:1151:A:C2'	11:A:1152:A:H5'	1.10	1.57
11:A:1151:A:C6	11:A:1152:A:C8	1.93	1.57
11:A:1293:U:H1'	12:B:111:ILE:CB	1.21	1.57
11:A:1293:U:H1'	12:B:111:ILE:CG1	1.27	1.56
1:0:46:ARG:CD	34:X:3:LYS:HE3	1.39	1.53
11:A:1151:A:H3'	11:A:1152:A:P	1.49	1.53
1:0:46:ARG:HD3	34:X:3:LYS:CE	1.09	1.52
12:B:42:PRO:CD	32:V:105:GLN:NE2	1.76	1.49
11:A:1151:A:H2'	11:A:1152:A:C5'	0.99	1.47
1:0:82:ARG:NH2	22:L:68:ILE:HD11	1.21	1.44
11:A:1296:A:OP1	12:B:138:TYR:CE2	1.73	1.40
11:A:1151:A:N1	11:A:1152:A:C8	1.84	1.39
11:A:579:A:N6	13:C:143:ARG:HA	1.38	1.37
11:A:1293:U:C1'	12:B:111:ILE:CG1	2.01	1.36
11:A:1151:A:C6	11:A:1152:A:N7	1.90	1.36
1:0:85:GLN:NE2	34:X:6:GLY:N	1.71	1.35
1:0:46:ARG:NE	34:X:3:LYS:HG3	1.03	1.33
1:0:88:GLN:NE2	34:X:5:HIS:H	1.28	1.31
1:0:63:GLY:N	11:A:566:C:OP1	1.65	1.29
12:B:42:PRO:HD3	32:V:105:GLN:NE2	1.39	1.29
11:A:1293:U:C1'	12:B:111:ILE:HG12	1.56	1.29
11:A:1293:U:C1'	12:B:111:ILE:HB	1.64	1.28
11:A:579:A:H61	13:C:143:ARG:CA	1.45	1.28
11:A:1295:G:H5'	12:B:108:THR:OG1	1.21	1.28
11:A:1151:A:C2	11:A:1152:A:C8	2.22	1.27
11:A:1151:A:C2'	11:A:1152:A:C5'	1.78	1.27
11:A:1301:U:OP1	15:E:97:ARG:HD3	1.36	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:579:A:N1	13:C:143:ARG:O	1.66	1.26
1:0:82:ARG:NH2	22:L:68:ILE:CD1	1.99	1.25
11:A:1151:A:C2	11:A:1152:A:N9	2.04	1.25
11:A:1151:A:C2	11:A:1152:A:C1'	2.21	1.24
1:0:46:ARG:CD	34:X:3:LYS:HG3	1.66	1.23
1:0:85:GLN:HE22	34:X:6:GLY:N	1.30	1.22
11:A:1298:U:O2	15:E:209:ASN:OD1	1.53	1.22
1:0:46:ARG:NE	34:X:3:LYS:CG	2.00	1.22
11:A:1686:C:H2'	11:A:1687:U:H6	1.07	1.20
11:A:1151:A:N3	11:A:1152:A:O4'	1.76	1.19
1:0:46:ARG:CD	34:X:3:LYS:CE	2.04	1.17
11:A:579:A:N6	13:C:143:ARG:HG3	1.59	1.16
12:B:41:ARG:HG3	32:V:103:ASP:CB	1.76	1.15
11:A:1295:G:OP1	12:B:108:THR:HB	1.46	1.15
11:A:1152:A:C2	11:A:1627:U:N3	2.15	1.14
1:0:85:GLN:NE2	34:X:5:HIS:C	1.85	1.13
11:A:1151:A:C2'	11:A:1152:A:H5"	1.77	1.12
11:A:1293:U:O3'	12:B:110:TYR:CE1	2.01	1.12
11:A:1320:U:H3'	12:B:101:ARG:NH2	1.64	1.12
11:A:1296:A:OP1	12:B:138:TYR:HE2	0.81	1.12
12:B:38:PHE:CZ	32:V:109:LEU:HA	1.84	1.12
11:A:1151:A:N6	11:A:1152:A:N7	1.97	1.11
11:A:1324:G:O3'	12:B:113:ARG:NH2	1.84	1.11
11:A:1324:G:C5'	12:B:113:ARG:NE	2.13	1.11
11:A:12:U:O2'	11:A:1299:G:N2	1.82	1.11
11:A:1295:G:C5'	12:B:108:THR:OG1	1.99	1.10
16:F:69:VAL:HB	16:F:79:GLN:HE22	1.17	1.09
11:A:1293:U:C1'	12:B:111:ILE:CB	2.14	1.09
11:A:1295:G:P	12:B:108:THR:HB	1.92	1.08
11:A:1151:A:C5	11:A:1152:A:C8	2.39	1.08
1:0:82:ARG:HA	34:X:7:SER:OG	1.54	1.08
11:A:1151:A:C3'	11:A:1152:A:C5'	2.31	1.07
1:0:88:GLN:HB2	34:X:5:HIS:O	1.53	1.07
1:0:88:GLN:CD	34:X:5:HIS:H	1.56	1.07
1:0:88:GLN:CD	34:X:5:HIS:N	2.08	1.07
11:A:1294:G:O2'	12:B:109:ASN:CB	2.02	1.07
1:0:58:MET:HG3	34:X:3:LYS:HE2	1.31	1.07
11:A:1151:A:C3'	11:A:1152:A:P	2.43	1.06
12:B:42:PRO:HD2	32:V:105:GLN:NE2	1.46	1.05
11:A:1302:U:OP1	15:E:88:LYS:NZ	1.90	1.05
11:A:1152:A:N3	11:A:1627:U:C2	2.24	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1293:U:H1'	12:B:111:ILE:HB	1.05	1.03
1:0:46:ARG:CD	34:X:3:LYS:CG	2.37	1.03
1:0:29:LYS:HA	1:0:33:GLN:NE2	1.74	1.02
11:A:1301:U:OP1	15:E:97:ARG:CD	2.06	1.02
1:0:44:ASN:OD1	11:A:1755:A:N6	1.94	1.01
11:A:1152:A:N1	11:A:1627:U:C4	2.27	1.01
11:A:1324:G:H5"	12:B:113:ARG:CZ	1.91	1.01
11:A:1715:G:O6	11:A:1716:C:N4	1.93	1.01
12:B:41:ARG:HA	32:V:105:GLN:CG	1.90	1.00
11:A:1293:U:O3'	12:B:110:TYR:CZ	2.14	1.00
11:A:1151:A:H2'	11:A:1152:A:H5"	1.34	1.00
11:A:1152:A:C2	11:A:1627:U:C4	2.50	1.00
12:B:42:PRO:CD	32:V:105:GLN:HE22	1.52	1.00
11:A:1626:U:O3'	11:A:1627:U:P	2.19	1.00
11:A:1294:G:O2'	12:B:109:ASN:HB2	1.16	0.99
11:A:1686:C:H2'	11:A:1687:U:C6	1.98	0.99
11:A:701:U:H3	11:A:737:A:H61	1.07	0.99
1:0:82:ARG:HB3	34:X:8:LEU:N	1.73	0.98
1:0:46:ARG:HD3	34:X:3:LYS:NZ	1.76	0.98
4:3:9:LEU:HD21	4:3:17:GLU:HB3	1.43	0.98
1:0:82:ARG:CA	34:X:7:SER:OG	2.11	0.98
11:A:1293:U:C2'	12:B:111:ILE:HB	1.94	0.98
11:A:1492:A:HO2'	11:A:1493:A:H8	1.00	0.98
11:A:1152:A:C2	11:A:1627:U:C2	2.51	0.98
1:0:29:LYS:HA	1:0:33:GLN:HE21	1.25	0.97
11:A:1151:A:C2	11:A:1152:A:O4'	2.15	0.97
1:0:46:ARG:HD3	34:X:3:LYS:CD	1.93	0.97
14:D:60:LEU:HD21	14:D:93:LEU:HD21	1.45	0.97
11:A:1300:A:C5'	15:E:117:THR:HG21	1.89	0.97
1:0:82:ARG:CZ	22:L:68:ILE:CD1	2.43	0.97
1:0:88:GLN:NE2	34:X:5:HIS:N	2.13	0.96
11:A:1152:A:N3	11:A:1627:U:N3	2.14	0.96
30:T:57:ARG:HH11	30:T:57:ARG:HG3	1.26	0.96
11:A:1588:G:H1	11:A:1608:U:H3	1.13	0.96
11:A:1324:G:H4'	12:B:113:ARG:HE	1.30	0.95
12:B:38:PHE:CD1	32:V:109:LEU:HB2	2.01	0.95
11:A:1151:A:H2'	11:A:1152:A:C4'	1.97	0.94
1:0:82:ARG:HB3	34:X:8:LEU:H	1.26	0.94
12:B:38:PHE:CE1	32:V:109:LEU:HB2	2.02	0.94
1:0:62:ARG:HD2	1:0:92:VAL:HA	1.47	0.94
17:G:117:THR:HG21	17:G:194:LEU:HD12	1.48	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1152:A:C6	11:A:1627:U:O4	2.21	0.94
12:B:38:PHE:CE1	32:V:109:LEU:HA	2.02	0.94
1:0:63:GLY:HA3	11:A:565:C:C2'	1.98	0.94
11:A:1151:A:N1	11:A:1152:A:N9	2.06	0.94
1:0:85:GLN:CB	34:X:5:HIS:O	2.16	0.93
11:A:579:A:H61	13:C:143:ARG:HA	0.77	0.93
11:A:151:G:O6	26:P:124:ARG:NH2	2.01	0.93
11:A:1294:G:OP1	12:B:110:TYR:HE1	1.50	0.93
11:A:1644:C:H1'	16:F:63:ALA:HB2	1.50	0.93
11:A:1321:A:O5'	12:B:104:PRO:HG2	1.69	0.93
11:A:1324:G:H5'	12:B:113:ARG:NE	1.81	0.92
11:A:1644:C:H1'	16:F:63:ALA:CB	1.98	0.92
1:0:85:GLN:HB3	34:X:5:HIS:O	1.70	0.92
11:A:1324:G:C4'	12:B:113:ARG:HH21	1.82	0.92
11:A:1585:U:H3	11:A:1611:A:H2	0.96	0.92
1:0:61:ILE:HA	1:0:91:VAL:HG12	1.47	0.92
16:F:30:ILE:HG12	16:F:107:GLY:HA2	1.51	0.92
1:0:63:GLY:HA3	11:A:565:C:C3'	2.00	0.91
10:9:86:UNK:O	10:9:87:UNK:HG3	1.69	0.91
11:A:1626:U:O3'	11:A:1627:U:OP1	1.88	0.91
11:A:1300:A:O2'	15:E:86:VAL:HB	1.71	0.91
5:4:129:THR:HB	5:4:180:THR:HA	1.51	0.91
5:4:97:LEU:HD13	5:4:98:THR:H	1.34	0.91
11:A:279:G:H3'	11:A:280:U:H5"	1.50	0.91
11:A:475:A:OP2	14:D:126:ARG:NH1	2.04	0.90
21:K:85:ALA:H	21:K:119:THR:HG22	1.36	0.90
12:B:38:PHE:CE1	32:V:109:LEU:CA	2.54	0.90
11:A:912:U:H4'	11:A:913:G:H3'	1.52	0.89
11:A:1715:G:C6	11:A:1716:C:C4	2.60	0.89
11:A:1295:G:H5"	12:B:108:THR:HG21	1.55	0.89
11:A:1294:G:O3'	12:B:108:THR:CB	2.21	0.89
11:A:1151:A:C1'	11:A:1152:A:H5'	2.03	0.88
12:B:42:PRO:HD3	32:V:105:GLN:CD	1.92	0.88
11:A:1151:A:C5	11:A:1152:A:H8	1.88	0.88
1:0:88:GLN:CD	34:X:5:HIS:CA	2.36	0.88
11:A:1324:G:C3'	12:B:113:ARG:HH21	1.87	0.88
1:0:61:ILE:HA	1:0:91:VAL:CG1	2.04	0.88
16:F:71:ASP:OD1	16:F:72:PRO:HD2	1.72	0.88
11:A:1300:A:H4'	15:E:86:VAL:HG21	1.56	0.87
11:A:1716:C:HO2'	11:A:1717:G:H8	0.89	0.87
14:D:110:GLN:HE22	14:D:126:ARG:HG2	1.39	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1299:G:O3'	15:E:99:LYS:HE3	1.75	0.87
5:4:32:ILE:HD11	5:4:46:THR:HG23	1.55	0.87
22:L:79:ASN:HB3	22:L:81:LYS:H	1.40	0.87
11:A:1324:G:C5'	12:B:113:ARG:CZ	2.52	0.87
11:A:1324:G:H4'	12:B:113:ARG:HH21	1.36	0.87
11:A:1152:A:C4	11:A:1627:U:N3	2.41	0.86
11:A:523:G:OP2	26:P:37:LYS:NZ	2.08	0.86
19:I:58:ASP:O	19:I:60:PHE:N	2.07	0.86
11:A:1324:G:C4'	12:B:113:ARG:HE	1.88	0.86
11:A:579:A:C6	13:C:143:ARG:HA	2.11	0.86
29:S:126:VAL:HG13	29:S:127:ARG:H	1.41	0.86
12:B:49:ASN:HB3	12:B:52:LYS:HG3	1.56	0.86
35:Y:57:ASP:HA	35:Y:106:LEU:HA	1.58	0.86
32:V:25:THR:O	32:V:27:ASP:N	2.07	0.86
11:A:1293:U:H2'	12:B:109:ASN:OD1	1.76	0.86
11:A:1324:G:H4'	12:B:113:ARG:NE	1.91	0.85
15:E:140:ARG:NH1	36:Z:1:MET:SD	2.49	0.85
33:W:139:VAL:HG13	33:W:150:PRO:HG3	1.58	0.85
11:A:1152:A:C6	11:A:1627:U:C4	2.63	0.85
12:B:24:LEU:O	12:B:163:ASN:ND2	2.08	0.85
11:A:1293:U:H4'	12:B:110:TYR:CE2	2.11	0.85
12:B:41:ARG:HA	32:V:105:GLN:HG3	1.59	0.85
1:0:46:ARG:HE	34:X:3:LYS:HG3	1.03	0.85
11:A:1299:G:C4'	15:E:208:GLU:OE2	2.25	0.85
17:G:73:THR:HG23	19:I:114:ARG:HD3	1.58	0.85
11:A:579:A:C2	13:C:143:ARG:O	2.30	0.85
1:0:63:GLY:HA3	11:A:565:C:O2'	1.75	0.85
11:A:132:U:H1'	11:A:133:U:OP2	1.77	0.85
11:A:1300:A:H5"	15:E:117:THR:HG21	1.56	0.84
16:F:98:LEU:HD11	16:F:102:ASN:HB2	1.57	0.84
1:0:82:ARG:HH21	22:L:68:ILE:HD11	1.02	0.84
11:A:1429:G:H1'	20:J:74:GLU:HG2	1.59	0.84
17:G:37:GLN:HG2	19:I:53:LEU:HD13	1.60	0.84
11:A:1151:A:H3'	11:A:1152:A:OP1	1.76	0.83
11:A:1686:C:C2'	11:A:1687:U:H6	1.91	0.83
11:A:1529:C:OP1	17:G:112:ARG:NH1	2.10	0.83
11:A:1324:G:C4'	12:B:113:ARG:NH2	2.41	0.83
11:A:1321:A:O4'	12:B:104:PRO:HB2	1.78	0.83
1:0:88:GLN:OE1	34:X:5:HIS:N	2.10	0.83
11:A:1324:G:H4'	12:B:113:ARG:NH2	1.94	0.83
8:7:27:PHE:HB3	8:7:40:LEU:HD23	1.58	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:D:93:LEU:HA	14:D:96:VAL:HG13	1.59	0.83
11:A:320:U:H2'	11:A:321:C:H2'	1.58	0.83
7:6:29:ARG:HH11	7:6:29:ARG:HG3	1.41	0.83
11:A:1291:G:N2	11:A:1324:G:H22	1.76	0.83
12:B:38:PHE:CD2	32:V:109:LEU:HD13	2.14	0.82
5:4:111:ARG:HG3	6:5:68:TYR:HB2	1.59	0.82
13:C:108:LYS:HG2	13:C:113:LEU:HD12	1.61	0.82
11:A:142:G:H22	11:A:173:A:H2	1.23	0.82
1:0:46:ARG:CD	34:X:3:LYS:CD	2.53	0.82
11:A:1542:G:N2	11:A:1569:A:OP2	2.12	0.82
11:A:829:A:O2'	11:A:830:U:OP2	1.97	0.82
11:A:1300:A:O3'	15:E:86:VAL:HG21	1.79	0.82
11:A:1294:G:P	12:B:110:TYR:CE1	2.72	0.82
16:F:69:VAL:HB	16:F:79:GLN:NE2	1.95	0.82
11:A:1151:A:C4	11:A:1152:A:C8	2.69	0.81
14:D:109:LEU:HB2	14:D:146:PHE:HB3	1.62	0.81
11:A:919:A:H5'	21:K:18:ARG:HH12	1.45	0.81
11:A:1229:G:O2'	11:A:1255:G:N2	2.14	0.81
1:0:83:ASP:OD2	34:X:9:ALA:HA	1.80	0.81
3:2:10:LYS:NZ	11:A:339:C:OP2	2.14	0.81
12:B:38:PHE:CG	32:V:109:LEU:HD13	2.16	0.80
11:A:1294:G:O3'	12:B:108:THR:OG1	1.99	0.80
12:B:38:PHE:CE1	32:V:109:LEU:CB	2.64	0.80
11:A:1644:C:C1'	16:F:63:ALA:HB2	2.11	0.80
21:K:50:ALA:O	21:K:52:ARG:N	2.14	0.80
1:0:106:GLN:HE21	1:0:108:GLU:HG3	1.43	0.80
4:3:131:PHE:O	4:3:133:THR:N	2.14	0.80
11:A:1151:A:C4	11:A:1152:A:H8	2.00	0.80
1:0:88:GLN:HG3	34:X:5:HIS:HB2	1.62	0.80
11:A:1034:C:HO2'	18:H:2:THR:N	1.79	0.80
20:J:27:THR:HG23	20:J:113:ASP:HB3	1.62	0.80
11:A:79:C:H1'	35:Y:174:LYS:HD3	1.62	0.80
12:B:42:PRO:HD2	32:V:105:GLN:HE21	1.43	0.80
11:A:1295:G:P	12:B:108:THR:CB	2.70	0.80
11:A:1151:A:N1	11:A:1152:A:C4	2.50	0.80
1:0:85:GLN:NE2	34:X:6:GLY:O	2.14	0.80
11:A:12:U:HO2'	11:A:1299:G:H21	1.30	0.80
22:L:7:ARG:O	27:Q:99:ARG:NH1	2.14	0.79
11:A:1293:U:O4'	12:B:111:ILE:CD1	2.31	0.79
12:B:179:ARG:HD3	12:B:183:ARG:HH11	1.46	0.79
1:0:82:ARG:CZ	22:L:68:ILE:HD13	2.10	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:K:107:ARG:HG3	21:K:107:ARG:HH11	1.46	0.79
28:R:284:ALA:HB2	32:V:63:LYS:HE2	1.64	0.79
11:A:1681:A:H2'	11:A:1682:U:H5'	1.65	0.79
11:A:579:A:N6	13:C:143:ARG:CG	2.43	0.79
11:A:280:U:O2'	11:A:281:G:OP2	1.99	0.79
11:A:868:G:OP1	25:O:121:ARG:NH1	2.15	0.79
32:V:88:VAL:HG22	32:V:89:SER:H	1.47	0.79
11:A:1229:G:HO2'	11:A:1255:G:N2	1.81	0.79
12:B:41:ARG:CA	32:V:105:GLN:HG3	2.13	0.78
1:0:88:GLN:HB2	34:X:5:HIS:C	2.03	0.78
17:G:62:VAL:HG13	17:G:89:ILE:HG21	1.64	0.78
11:A:187:G:H4'	11:A:188:A:OP1	1.83	0.78
16:F:99:GLN:HG2	16:F:102:ASN:ND2	1.99	0.78
5:4:39:GLU:HG3	5:4:40:ASN:H	1.47	0.78
25:O:114:ARG:HH11	25:O:114:ARG:HG2	1.48	0.78
11:A:1686:C:C2	11:A:1687:U:C6	2.72	0.78
11:A:1686:C:C2'	11:A:1687:U:O5'	2.30	0.78
11:A:734:A:H5"	11:A:735:C:OP1	1.83	0.78
11:A:579:A:H61	13:C:143:ARG:CB	1.96	0.78
11:A:1291:G:O5'	11:A:1291:G:H8	1.67	0.78
1:0:46:ARG:CZ	34:X:3:LYS:HG3	2.09	0.78
15:E:56:ILE:HG23	15:E:61:LEU:HB2	1.63	0.78
11:A:1716:C:O2'	11:A:1717:G:H8	1.67	0.77
31:U:76:GLU:OE2	31:U:90:LYS:NZ	2.17	0.77
11:A:579:A:C6	13:C:143:ARG:HG3	2.19	0.77
1:0:106:GLN:HE21	1:0:108:GLU:CG	1.96	0.77
11:A:136:C:H4'	11:A:137:U:OP1	1.83	0.77
11:A:276:C:O2'	11:A:277:U:H5"	1.84	0.77
11:A:1369:U:OP1	30:T:119:LYS:NZ	2.16	0.77
11:A:1324:G:C4'	12:B:113:ARG:NE	2.47	0.77
11:A:1299:G:H4'	15:E:208:GLU:OE2	1.84	0.77
11:A:40:A:OP1	14:D:3:ARG:NH2	2.18	0.77
22:L:73:ARG:HE	22:L:84:THR:HG22	1.49	0.77
11:A:1057:U:O2'	11:A:1058:U:OP2	2.02	0.77
11:A:1293:U:C1'	12:B:111:ILE:CD1	2.62	0.77
10:9:146:SER:HB3	11:A:1234:A:O2'	1.85	0.77
11:A:1073:G:H2'	11:A:1074:G:H5"	1.66	0.77
11:A:1151:A:C3'	11:A:1152:A:H5'	2.04	0.77
5:4:62:LYS:O	5:4:64:ARG:N	2.17	0.77
11:A:1686:C:H2'	11:A:1687:U:O5'	1.83	0.77
2:1:12:VAL:HG22	2:1:28:VAL:HG11	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:M:84:TRP:HA	23:M:89:GLN:HE22	1.50	0.76
11:A:1151:A:N1	11:A:1152:A:C5	2.53	0.76
12:B:41:ARG:CG	32:V:103:ASP:CB	2.61	0.76
11:A:1626:U:C3'	11:A:1627:U:P	2.72	0.76
3:2:36:THR:HB	3:2:57:ALA:O	1.85	0.76
11:A:1293:U:O4'	12:B:111:ILE:HG12	1.83	0.76
11:A:1587:A:H1'	17:G:104:ASN:HD22	1.50	0.76
35:Y:153:VAL:O	35:Y:155:ASP:N	2.16	0.76
19:I:40:GLU:HA	19:I:42:GLU:N	2.01	0.76
18:H:27:ILE:HD11	18:H:61:ILE:HD12	1.65	0.76
23:M:83:ALA:HA	23:M:86:LEU:HD22	1.66	0.76
36:Z:74:GLN:NE2	36:Z:81:ASN:O	2.18	0.76
11:A:484:C:H42	11:A:503:G:H22	1.33	0.76
11:A:1715:G:C6	11:A:1716:C:N4	2.54	0.76
5:4:181:LEU:O	5:4:184:LEU:N	2.18	0.76
14:D:175:ARG:HG3	14:D:175:ARG:HH11	1.51	0.76
11:A:514:G:H1	11:A:543:C:H5	1.33	0.76
4:3:35:LYS:O	4:3:37:GLU:N	2.18	0.76
28:R:89:LEU:HB2	28:R:103:PHE:HB2	1.68	0.76
11:A:494:U:O2'	11:A:495:C:O5'	2.01	0.75
6:5:35:ALA:HB3	6:5:37:LYS:HE3	1.67	0.75
18:H:30:SER:HA	18:H:34:ILE:HD12	1.67	0.75
1:0:85:GLN:OE1	34:X:4:VAL:O	1.83	0.75
11:A:488:G:H4'	11:A:488:G:OP1	1.86	0.75
11:A:1559:A:H5"	23:M:135:GLY:HA3	1.67	0.75
12:B:42:PRO:CD	32:V:105:GLN:HE21	1.94	0.75
16:F:77:ILE:HG13	16:F:79:GLN:NE2	2.02	0.75
5:4:83:LYS:NZ	21:K:116:GLU:OE2	2.18	0.75
16:F:27:HIS:HB2	16:F:43:GLN:NE2	2.02	0.75
12:B:42:PRO:HD2	32:V:105:GLN:HE22	1.19	0.75
11:A:1550:A:P	29:S:42:ARG:HH22	2.08	0.75
11:A:127:G:N7	35:Y:202:ARG:NH2	2.35	0.74
5:4:109:LYS:HG3	5:4:113:MET:HE3	1.69	0.74
31:U:89:ILE:HG23	31:U:90:LYS:H	1.52	0.74
16:F:27:HIS:O	16:F:43:GLN:HG2	1.87	0.74
11:A:1428:G:H5'	11:A:1428:G:H8	1.53	0.74
19:I:5:PRO:HG2	19:I:24:ALA:HB2	1.69	0.74
13:C:64:ARG:O	13:C:67:ASN:N	2.20	0.74
11:A:1520:U:OP2	30:T:75:LYS:NZ	2.20	0.74
23:M:26:ILE:HD11	23:M:31:ALA:N	2.02	0.74
19:I:12:LYS:HD3	19:I:17:THR:HB	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:G:144:GLU:OE2	17:G:225:ARG:NH2	2.21	0.74
11:A:818:C:N4	11:A:819:G:O6	2.21	0.74
12:B:200:ASP:HB2	32:V:85:VAL:HG21	1.69	0.74
23:M:123:ARG:HG3	23:M:133:VAL:HG21	1.69	0.74
11:A:1324:G:C5'	12:B:113:ARG:HE	1.93	0.73
30:T:57:ARG:NH1	30:T:57:ARG:HG3	2.03	0.73
11:A:1521:G:O6	30:T:68:ARG:NH1	2.21	0.73
4:3:50:ASP:OD1	4:3:50:ASP:N	2.21	0.73
1:0:106:GLN:NE2	1:0:108:GLU:HG3	2.02	0.73
11:A:1151:A:H2	11:A:1152:A:C1'	1.94	0.73
11:A:765:G:C2	14:D:149:ARG:HD2	2.23	0.73
11:A:582:U:C6	11:A:582:U:H5"	2.24	0.73
11:A:1293:U:O4'	12:B:111:ILE:CG1	2.37	0.73
1:0:88:GLN:HG3	34:X:5:HIS:CB	2.18	0.73
1:0:109:LEU:HG	1:0:110:PRO:HD2	1.70	0.73
11:A:1293:U:N1	12:B:111:ILE:HG12	2.02	0.73
11:A:108:A:H2'	11:A:109:G:C8	2.23	0.73
11:A:649:U:O2'	11:A:650:U:O5'	2.07	0.73
17:G:40:ILE:HG23	17:G:42:LEU:HD22	1.71	0.73
13:C:7:LYS:NZ	20:J:115:GLU:OE2	2.21	0.72
21:K:102:LEU:HD22	21:K:105:LEU:HD11	1.71	0.72
17:G:57:SER:O	17:G:59:VAL:N	2.20	0.72
11:A:1686:C:O2'	11:A:1687:U:C5'	2.37	0.72
16:F:80:LEU:HB3	16:F:84:GLN:NE2	2.04	0.72
12:B:4:PRO:HB2	12:B:7:PHE:HB2	1.70	0.72
5:4:202:LYS:NZ	5:4:202:LYS:O	2.23	0.72
19:I:18:ALA:HB2	19:I:69:VAL:HG13	1.71	0.72
28:R:170:ILE:HG21	28:R:211:ILE:HD11	1.70	0.72
1:0:46:ARG:HE	34:X:3:LYS:CG	1.82	0.72
16:F:39:LEU:HD11	16:F:79:GLN:HB3	1.71	0.72
11:A:337:G:H3'	27:Q:133:LYS:HB2	1.69	0.72
11:A:74:U:O2'	11:A:75:U:OP2	2.06	0.72
13:C:65:ARG:HA	13:C:68:GLU:HG3	1.70	0.72
11:A:1542:G:N2	11:A:1568:C:H1'	2.04	0.72
5:4:157:GLN:O	5:4:159:SER:N	2.20	0.72
32:V:82:ASP:O	32:V:83:GLN:NE2	2.20	0.72
12:B:52:LYS:HD2	36:Z:82:VAL:HA	1.72	0.72
11:A:1160:A:H2'	11:A:1161:C:C6	2.25	0.72
10:9:102:VAL:O	10:9:104:SER:N	2.23	0.72
11:A:1683:C:O2'	11:A:1684:U:O5'	2.07	0.72
1:0:88:GLN:CG	34:X:5:HIS:C	2.58	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:D:110:GLN:NE2	14:D:126:ARG:HG2	2.04	0.72
30:T:63:ARG:HG3	30:T:67:MET:HE3	1.70	0.72
11:A:1290:U:H2'	11:A:1291:G:C8	2.25	0.71
30:T:86:ARG:HH11	30:T:86:ARG:HG3	1.55	0.71
6:5:10:ARG:HD2	11:A:1795:U:O2	1.89	0.71
15:E:69:ILE:HD11	15:E:133:LYS:HB3	1.72	0.71
11:A:491:C:N3	11:A:496:G:N2	2.38	0.71
1:0:88:GLN:HE22	34:X:4:VAL:N	1.88	0.71
32:V:20:TYR:CE2	32:V:38:ILE:HD11	2.26	0.71
5:4:173:THR:O	5:4:177:GLN:NE2	2.23	0.71
11:A:1293:U:H1'	12:B:111:ILE:CD1	2.16	0.71
1:0:63:GLY:CA	11:A:565:C:O2'	2.38	0.71
35:Y:24:ILE:O	35:Y:26:VAL:N	2.23	0.71
30:T:49:ASP:HB3	30:T:53:TRP:HB3	1.73	0.71
11:A:584:C:H1'	34:X:18:THR:HG21	1.71	0.71
20:J:106:ILE:HG13	20:J:107:THR:H	1.53	0.71
11:A:717:C:H42	11:A:720:G:H22	1.37	0.71
17:G:113:ILE:O	17:G:117:THR:OG1	2.07	0.71
33:W:79:ASP:HB3	33:W:82:TYR:HB2	1.73	0.71
27:Q:78:THR:HG22	27:Q:84:ILE:HG22	1.72	0.71
11:A:1293:U:O4'	12:B:111:ILE:HD13	1.90	0.71
11:A:614:C:OP2	22:L:5:LYS:NZ	2.24	0.71
11:A:1600:A:H4'	11:A:1601:G:OP1	1.90	0.71
11:A:1151:A:C3'	11:A:1152:A:H5"	2.11	0.71
11:A:1324:G:H4'	12:B:113:ARG:CZ	2.20	0.71
12:B:84:ARG:NH2	32:V:82:ASP:OD1	2.23	0.70
13:C:179:GLN:NE2	13:C:179:GLN:O	2.24	0.70
25:O:84:ILE:HG22	25:O:135:LEU:HD21	1.73	0.70
1:0:38:ILE:HG21	1:0:72:GLY:O	1.90	0.70
13:C:29:LEU:HD21	13:C:69:LEU:HD11	1.73	0.70
21:K:29:HIS:HB3	21:K:41:ARG:HG3	1.72	0.70
11:A:1626:U:HO3'	11:A:1627:U:P	2.11	0.70
16:F:80:LEU:HD13	16:F:84:GLN:OE1	1.92	0.70
11:A:159:U:O2'	35:Y:87:ARG:NH1	2.24	0.70
27:Q:4:GLU:HG3	27:Q:5:LEU:HG	1.74	0.70
14:D:117:GLY:O	14:D:119:ALA:N	2.24	0.70
15:E:203:LYS:O	15:E:206:THR:HG23	1.91	0.70
12:B:185:ARG:HB2	36:Z:45:ALA:HB3	1.72	0.70
11:A:591:A:H2'	11:A:592:A:C8	2.27	0.70
11:A:1300:A:C4'	15:E:86:VAL:HG21	2.21	0.70
4:3:133:THR:HG22	4:3:159:VAL:HG12	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:T:126:GLU:HA	30:T:129:GLN:HG3	1.74	0.70
1:0:46:ARG:CG	34:X:3:LYS:HE3	2.21	0.70
22:L:91:GLY:O	22:L:93:LEU:N	2.25	0.70
6:5:32:LYS:NZ	11:A:930:A:OP1	2.23	0.70
6:5:15:ARG:NH1	11:A:936:G:N7	2.39	0.70
11:A:1294:G:O3'	12:B:108:THR:HB	1.85	0.70
1:0:38:ILE:HG23	1:0:74:GLY:N	2.07	0.70
21:K:29:HIS:O	21:K:29:HIS:ND1	2.24	0.70
13:C:53:THR:O	13:C:53:THR:OG1	2.08	0.70
14:D:60:LEU:CD2	14:D:93:LEU:HD21	2.22	0.70
12:B:167:LYS:HB3	12:B:168:HIS:CD2	2.27	0.70
5:4:154:SER:OG	5:4:154:SER:O	2.09	0.70
1:0:23:LYS:HZ3	1:0:25:GLU:HG2	1.57	0.70
11:A:992:A:H2	11:A:1012:U:H3	1.38	0.69
30:T:28:LEU:HD13	30:T:29:GLU:H	1.56	0.69
1:0:46:ARG:HD3	34:X:3:LYS:HE3	0.70	0.69
11:A:1711:C:H2'	11:A:1712:A:H5"	1.74	0.69
11:A:579:A:H61	13:C:143:ARG:CG	2.03	0.69
12:B:157:ASP:OD1	36:Z:60:ARG:NH1	2.25	0.69
19:I:97:VAL:HG12	19:I:98:ASP:H	1.57	0.69
1:0:88:GLN:CB	34:X:5:HIS:O	2.37	0.69
32:V:50:ILE:O	32:V:54:THR:HG23	1.92	0.69
5:4:176:VAL:O	5:4:178:GLY:N	2.25	0.69
11:A:701:U:H3	11:A:737:A:N6	1.87	0.69
11:A:1564:U:H2'	11:A:1565:C:C6	2.27	0.69
11:A:1533:C:H4'	11:A:1539:G:N1	2.06	0.69
28:R:76:ASP:N	28:R:76:ASP:OD1	2.18	0.69
35:Y:164:LYS:HB3	35:Y:167:LYS:HB3	1.75	0.69
11:A:1321:A:O4'	12:B:104:PRO:CB	2.40	0.69
11:A:867:G:OP2	25:O:3:ARG:NH1	2.24	0.69
31:U:54:ARG:O	31:U:56:GLU:N	2.23	0.69
11:A:1321:A:O5'	12:B:104:PRO:CG	2.40	0.69
8:7:68:LEU:HD11	8:7:76:LEU:HD21	1.73	0.69
3:2:114:GLU:HG2	3:2:120:THR:HA	1.75	0.69
11:A:653:C:H2'	11:A:654:C:O4'	1.92	0.69
11:A:1294:G:OP1	12:B:110:TYR:CE1	2.39	0.68
11:A:1300:A:H4'	15:E:86:VAL:HG11	1.74	0.68
25:O:55:ARG:NH1	25:O:56:ASP:OD2	2.26	0.68
11:A:959:U:C6	25:O:61:THR:HB	2.28	0.68
15:E:116:LYS:HG2	15:E:127:ALA:HB3	1.75	0.68
11:A:226:A:H2'	11:A:227:U:H5'	1.73	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:H:15:ASN:HD21	18:H:71:LYS:HA	1.58	0.68
14:D:163:PRO:O	14:D:165:GLY:N	2.26	0.68
11:A:1296:A:P	12:B:138:TYR:CE2	2.85	0.68
2:1:52:ASP:OD1	2:1:52:ASP:N	2.26	0.68
12:B:193:GLN:O	12:B:195:TRP:N	2.26	0.68
16:F:39:LEU:HD12	16:F:80:LEU:O	1.93	0.68
5:4:28:GLU:OE2	5:4:94:LYS:NZ	2.19	0.68
11:A:1339:C:O2'	11:A:1340:U:OP1	2.12	0.68
22:L:130:VAL:O	22:L:131:SER:HB3	1.93	0.68
11:A:38:C:H2'	11:A:39:A:H5'	1.76	0.68
33:W:85:GLY:N	33:W:88:ASP:OD2	2.27	0.68
1:0:85:GLN:NE2	34:X:6:GLY:CA	2.56	0.68
11:A:1550:A:OP2	29:S:42:ARG:NH2	2.26	0.68
11:A:1267:G:H21	11:A:1448:G:H5"	1.59	0.68
28:R:300:THR:HG23	28:R:314:GLN:HG3	1.76	0.68
11:A:839:U:H2'	11:A:840:U:H5'	1.75	0.68
3:2:50:GLY:HA2	11:A:397:A:O3'	1.94	0.68
11:A:702:G:O6	11:A:736:C:N4	2.19	0.68
7:6:29:ARG:NH1	7:6:29:ARG:HG3	2.09	0.68
11:A:1295:G:C5'	12:B:108:THR:CB	2.72	0.68
14:D:53:ARG:NH1	14:D:97:LEU:O	2.27	0.68
11:A:778:G:H22	26:P:10:ARG:NH2	1.90	0.68
11:A:1298:U:C2	15:E:209:ASN:OD1	2.44	0.67
31:U:61:VAL:HG13	31:U:121:VAL:HG23	1.74	0.67
3:2:25:ARG:NH2	11:A:386:G:OP2	2.27	0.67
11:A:1295:G:H5"	12:B:108:THR:CG2	2.24	0.67
1:0:85:GLN:HB2	34:X:5:HIS:O	1.92	0.67
11:A:1324:G:C3'	12:B:113:ARG:NH2	2.53	0.67
2:1:32:PHE:HE1	2:1:38:ARG:HB3	1.58	0.67
11:A:418:G:O2'	35:Y:59:GLN:NE2	2.27	0.67
1:0:30:GLU:O	1:0:33:GLN:HG2	1.94	0.67
11:A:1300:A:H5"	15:E:117:THR:CG2	2.24	0.67
11:A:959:U:H6	25:O:61:THR:HB	1.59	0.67
35:Y:67:VAL:HG21	35:Y:99:GLY:HA2	1.76	0.67
19:I:50:GLU:OE1	19:I:82:ARG:NH2	2.27	0.67
18:H:27:ILE:HG12	18:H:61:ILE:HB	1.76	0.67
12:B:71:GLU:O	12:B:96:THR:HG22	1.95	0.67
11:A:582:U:H6	11:A:582:U:H5"	1.57	0.67
11:A:1449:U:H2'	11:A:1450:U:C6	2.28	0.67
33:W:31:PRO:HG2	33:W:38:LEU:HD13	1.76	0.67
11:A:533:U:H4'	26:P:33:ALA:HB2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:D:169:PRO:HD2	14:D:174:ARG:HD2	1.76	0.67
5:4:76:SER:OG	5:4:78:ASP:OD1	2.12	0.67
11:A:1294:G:P	12:B:110:TYR:HE1	2.16	0.67
4:3:50:ASP:HA	4:3:56:LYS:HA	1.76	0.67
4:3:50:ASP:HB3	4:3:56:LYS:HG2	1.76	0.67
22:L:96:VAL:HG23	22:L:97:ASP:H	1.60	0.67
11:A:169:A:H5"	35:Y:176:GLN:HG2	1.77	0.67
9:8:41:ILE:HG23	9:8:42:LEU:H	1.59	0.67
19:I:113:ASP:CG	19:I:114:ARG:H	1.98	0.67
11:A:765:G:N3	14:D:149:ARG:NH1	2.42	0.67
12:B:41:ARG:CA	32:V:105:GLN:CG	2.71	0.66
11:A:140:A:N6	11:A:281:G:OP1	2.21	0.66
11:A:131:C:O2'	11:A:132:U:OP1	2.11	0.66
11:A:1199:G:O6	20:J:67:THR:HG23	1.95	0.66
4:3:38:LEU:HD23	4:3:41:LEU:HD12	1.76	0.66
1:0:63:GLY:HA3	11:A:565:C:H3'	1.76	0.66
14:D:109:LEU:HD13	14:D:129:ILE:HD13	1.75	0.66
12:B:185:ARG:HA	36:Z:44:ARG:HA	1.77	0.66
11:A:1789:G:H8	11:A:1789:G:H5"	1.60	0.66
1:0:88:GLN:HE22	34:X:5:HIS:H	1.38	0.66
30:T:117:SER:HB2	30:T:123:ARG:HB2	1.77	0.66
21:K:81:VAL:H	21:K:115:ILE:HG22	1.61	0.66
10:9:126:CYS:O	10:9:128:ALA:N	2.28	0.66
11:A:1254:U:OP2	31:U:46:ARG:NH1	2.28	0.66
12:B:10:THR:OG1	12:B:13:ASP:OD2	2.13	0.66
33:W:13:ALA:O	33:W:39:ARG:NH2	2.28	0.66
11:A:1151:A:C2	11:A:1152:A:H1'	2.25	0.66
11:A:1459:C:OP1	23:M:126:ARG:NH2	2.28	0.66
18:H:47:ILE:HG22	18:H:65:LEU:HB3	1.76	0.66
1:0:46:ARG:HD2	34:X:3:LYS:HE3	1.67	0.66
16:F:77:ILE:HG13	16:F:79:GLN:HE22	1.60	0.66
11:A:711:U:H1'	11:A:712:G:H5'	1.78	0.66
5:4:70:LEU:O	5:4:74:GLN:N	2.28	0.66
13:C:120:TYR:OH	15:E:120:GLU:OE2	2.12	0.66
11:A:1756[B]:A:O2'	11:A:1757:G:H5'	1.95	0.66
16:F:62:PHE:HE2	16:F:84:GLN:HB3	1.60	0.66
11:A:1688:U:H2'	11:A:1689:A:C8	2.31	0.65
24:N:33:LYS:O	24:N:36:LEU:HD23	1.95	0.65
16:F:96:LEU:O	16:F:96:LEU:HD23	1.96	0.65
5:4:206:PRO:O	5:4:207:LEU:HB2	1.95	0.65
18:H:70:ASN:ND2	18:H:130:TYR:O	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:687:G:H5'	18:H:119:LYS:HG2	1.76	0.65
11:A:843:U:H2'	11:A:844:A:C8	2.30	0.65
11:A:1686:C:C2'	11:A:1687:U:O4'	2.45	0.65
2:1:10:ALA:HA	2:1:32:PHE:HA	1.78	0.65
11:A:1041:G:H2'	11:A:1042:G:C8	2.30	0.65
2:1:36:THR:OG1	2:1:37:SER:N	2.28	0.65
11:A:1536:G:C5	11:A:1538:U:H1'	2.32	0.65
16:F:50:ASP:OD2	16:F:53:ARG:HG2	1.96	0.65
11:A:1151:A:C6	11:A:1152:A:C5	2.84	0.65
11:A:1686:C:H2'	11:A:1687:U:O4'	1.96	0.65
11:A:765:G:N1	14:D:149:ARG:HB3	2.11	0.65
32:V:47:ARG:NH1	32:V:48:ASN:OD1	2.29	0.65
33:W:212:ASP:OD2	33:W:216:ASN:HB2	1.97	0.65
16:F:62:PHE:CZ	16:F:87:LYS:HG3	2.31	0.65
14:D:96:VAL:HA	14:D:99:LEU:HD22	1.78	0.65
11:A:819:G:O2'	11:A:820:U:H5'	1.96	0.65
12:B:70:PRO:HB2	12:B:94:GLY:HA3	1.77	0.65
11:A:1606:C:H2'	11:A:1607:G:C8	2.31	0.65
16:F:58:LEU:HD22	16:F:80:LEU:HD22	1.79	0.65
27:Q:6:THR:O	27:Q:8:GLN:N	2.30	0.65
11:A:1339:C:O2'	11:A:1341:A:N7	2.30	0.65
28:R:195:HIS:CD2	28:R:199:ILE:HD13	2.32	0.65
11:A:740:A:H2'	11:A:741:C:H5"	1.77	0.65
11:A:1592:A:H2'	11:A:1593:A:H8	1.61	0.65
14:D:99:LEU:O	14:D:100:LYS:HB3	1.97	0.65
8:7:56:LYS:HG3	8:7:67:THR:HB	1.78	0.65
9:8:59:TYR:HE1	9:8:61:SER:HB3	1.61	0.65
12:B:41:ARG:HA	32:V:105:GLN:NE2	2.12	0.65
1:0:78:LEU:C	1:0:92:VAL:HG12	2.17	0.65
11:A:656:G:O2'	11:A:657:U:O4'	2.15	0.65
11:A:1151:A:N1	11:A:1152:A:N7	2.20	0.65
1:0:82:ARG:CB	34:X:7:SER:OG	2.26	0.64
34:X:14:VAL:O	34:X:18:THR:HG23	1.97	0.64
36:Z:41:GLU:H	36:Z:41:GLU:CD	2.00	0.64
11:A:901:G:N2	21:K:54:GLU:OE1	2.29	0.64
11:A:895:G:H1	11:A:917:U:H3	1.45	0.64
19:I:95:LYS:O	28:R:59:ARG:NH2	2.30	0.64
25:O:27:LYS:H	25:O:27:LYS:HE2	1.61	0.64
17:G:94:THR:HB	17:G:114:ILE:HG13	1.77	0.64
30:T:30:VAL:O	30:T:32:GLY:N	2.29	0.64
11:A:1479:A:OP1	30:T:57:ARG:NH1	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:R:90:ARG:NH1	28:R:99:THR:OG1	2.31	0.64
8:7:8:ARG:HD2	8:7:12:HIS:HE1	1.63	0.64
23:M:11:PHE:CE1	23:M:59:GLY:HA2	2.32	0.64
6:5:37:LYS:O	6:5:38:ARG:HD2	1.98	0.64
11:A:1324:G:C4'	12:B:113:ARG:CZ	2.75	0.64
11:A:1585:U:N3	11:A:1611:A:H2	1.82	0.64
5:4:110:LEU:H	5:4:110:LEU:HD12	1.63	0.64
12:B:168:HIS:HB3	12:B:203:PHE:CZ	2.32	0.64
7:6:62:ILE:HG13	7:6:63:LEU:H	1.62	0.64
11:A:1762:A:H1'	11:A:1783:C:H5'	1.80	0.64
11:A:497:G:H4'	11:A:498:G:OP1	1.97	0.64
11:A:1429:G:C1'	20:J:74:GLU:HG2	2.27	0.64
11:A:66:U:H5	35:Y:173:PRO:HG3	1.63	0.64
11:A:647:G:N2	11:A:687:G:H22	1.95	0.64
25:O:54:LEU:HB3	25:O:60:VAL:HG21	1.79	0.64
11:A:1300:A:C3'	15:E:86:VAL:HG21	2.27	0.64
8:7:8:ARG:HD2	8:7:12:HIS:CE1	2.33	0.64
1:0:58:MET:HG3	34:X:3:LYS:CE	2.18	0.63
11:A:499:U:O2'	11:A:500:C:O4'	2.16	0.63
17:G:152:GLY:O	17:G:154:ALA:N	2.31	0.63
11:A:1597:A:OP2	24:N:32:ARG:NH2	2.31	0.63
12:B:110:TYR:H	12:B:110:TYR:HD1	1.46	0.63
1:0:61:ILE:HG12	1:0:91:VAL:HG11	1.80	0.63
11:A:145:A:O2'	11:A:146:U:O5'	2.16	0.63
1:0:62:ARG:CD	1:0:92:VAL:HA	2.27	0.63
11:A:138:A:O2'	35:Y:149:LYS:NZ	2.31	0.63
30:T:86:ARG:NH1	30:T:90:PRO:O	2.32	0.63
8:7:14:TYR:HE1	8:7:21:VAL:HG22	1.64	0.63
32:V:17:ILE:HG23	32:V:58:MET:HE1	1.80	0.63
12:B:183:ARG:NH2	12:B:191:ARG:O	2.32	0.63
6:5:84:VAL:O	6:5:86:VAL:N	2.30	0.63
11:A:1689:A:H2'	11:A:1690:G:H8	1.64	0.63
11:A:1498:G:C2'	11:A:1499:G:H5'	2.28	0.63
5:4:134:VAL:HB	5:4:219:LYS:HB2	1.80	0.63
4:3:114:ARG:NH2	11:A:637:C:O2	2.30	0.63
11:A:753:A:H5'	33:W:221:ARG:HG3	1.80	0.63
11:A:1151:A:H3'	11:A:1152:A:O5'	1.96	0.63
16:F:62:PHE:CE2	16:F:84:GLN:HB3	2.33	0.63
6:5:59:TYR:HE2	21:K:113:GLY:HA2	1.64	0.63
28:R:216:LYS:HA	28:R:239:GLU:HG3	1.80	0.63
33:W:185:GLY:N	33:W:189:LEU:HD13	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1623:C:H2'	11:A:1624:C:C6	2.34	0.63
8:7:56:LYS:NZ	13:C:28:GLU:OE1	2.29	0.63
33:W:259:GLN:O	33:W:261:LEU:N	2.31	0.63
13:C:114:ALA:HB3	13:C:117:ARG:HB2	1.80	0.63
11:A:1015:U:H5"	11:A:1016:C:OP2	1.98	0.63
1:0:88:GLN:CB	34:X:5:HIS:C	2.66	0.63
11:A:470:A:C8	11:A:470:A:H5"	2.33	0.63
1:0:33:GLN:HE21	1:0:78:LEU:HD11	1.64	0.63
19:I:115:THR:O	19:I:117:LEU:N	2.32	0.63
11:A:158:U:O2'	11:A:159:U:H3'	1.98	0.63
11:A:1592:A:H2'	11:A:1593:A:C8	2.34	0.63
1:0:97:LEU:HG	1:0:115:ILE:HG21	1.80	0.63
5:4:171:ILE:HA	5:4:174:LYS:HE3	1.81	0.63
16:F:62:PHE:CD2	16:F:84:GLN:OE1	2.52	0.63
11:A:498:G:O2'	11:A:499:U:O5'	2.17	0.63
11:A:702:G:HO2'	11:A:703:G:H8	1.47	0.63
17:G:37:GLN:HB3	19:I:53:LEU:HB3	1.80	0.63
15:E:129:ILE:O	15:E:133:LYS:HG2	1.99	0.63
11:A:38:C:C2'	11:A:39:A:H5'	2.29	0.63
28:R:136:ILE:H	28:R:136:ILE:HD13	1.63	0.63
22:L:109:ARG:HB3	22:L:112:LYS:HB2	1.81	0.63
20:J:118:VAL:HG22	20:J:119:ALA:H	1.63	0.63
15:E:144:TRP:CE2	15:E:173:PRO:HG3	2.34	0.63
1:0:62:ARG:HG3	1:0:91:VAL:O	1.98	0.62
28:R:150:TRP:HE1	32:V:37:GLU:HG3	1.64	0.62
11:A:1202:A:N6	11:A:1457:C:H5"	2.13	0.62
23:M:94:ASP:OD2	23:M:98:TYR:OH	2.17	0.62
26:P:91:LEU:HA	26:P:96:LEU:HD12	1.80	0.62
11:A:66:U:C5	35:Y:173:PRO:HG3	2.35	0.62
19:I:34:SER:HB3	19:I:38:LEU:HD12	1.80	0.62
3:2:138:ASN:ND2	11:A:197:A:H61	1.98	0.62
11:A:1151:A:H2	11:A:1152:A:H1'	1.59	0.62
11:A:497:G:O2'	11:A:498:G:O5'	2.17	0.62
11:A:1428:G:H5'	11:A:1428:G:C8	2.35	0.62
16:F:29:ARG:HB2	16:F:41:THR:HB	1.80	0.62
13:C:191:ASP:HB3	13:C:194:LYS:HG3	1.82	0.62
15:E:145:GLY:O	15:E:146:THR:HB	1.98	0.62
11:A:1320:U:H3'	12:B:101:ARG:HH22	1.62	0.62
11:A:1523:G:N7	30:T:64:HIS:HE1	1.98	0.62
2:1:42:ARG:HH11	2:1:56:LEU:HD22	1.63	0.62
11:A:1701:N:H3'	11:A:1702:N:H5"	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1612:U:H2'	11:A:1613:U:H5'	1.79	0.62
32:V:76:GLU:HA	32:V:79:GLU:HB2	1.81	0.62
16:F:49:TYR:O	16:F:51:LEU:HD12	1.98	0.62
18:H:105:THR:HG23	18:H:110:ILE:HG12	1.81	0.62
33:W:11:ARG:O	33:W:12:LEU:HB2	1.98	0.62
2:1:10:ALA:HB1	2:1:30:VAL:HB	1.81	0.62
4:3:145:GLY:O	4:3:147:ASN:ND2	2.31	0.62
11:A:1081:A:H5"	11:A:1082:C:OP1	1.99	0.62
15:E:103:VAL:HG12	15:E:190:LEU:HD12	1.80	0.62
5:4:112:SER:O	5:4:114:VAL:N	2.32	0.62
12:B:41:ARG:N	32:V:105:GLN:HG3	2.15	0.62
16:F:98:LEU:HD21	16:F:102:ASN:HB2	1.81	0.62
5:4:34:ALA:N	5:4:41:ARG:O	2.29	0.62
1:0:85:GLN:HE21	34:X:6:GLY:C	2.00	0.62
11:A:702:G:O2'	11:A:703:G:H8	1.82	0.62
6:5:44:ILE:HD12	6:5:44:ILE:H	1.65	0.62
11:A:794:U:O2	11:A:794:U:H2'	2.00	0.62
11:A:823:G:O2'	11:A:824:G:P	2.57	0.62
30:T:61:VAL:O	30:T:65:ILE:HG13	2.00	0.62
11:A:579:A:N1	13:C:143:ARG:C	2.50	0.61
11:A:1291:G:N2	11:A:1324:G:N2	2.45	0.61
11:A:843:U:H2'	11:A:844:A:H8	1.64	0.61
4:3:11:GLN:HG3	4:3:13:PRO:HD2	1.80	0.61
11:A:1214:U:OP1	11:A:1246:C:H1'	1.99	0.61
18:H:57:ARG:NH2	25:O:16:ILE:HG22	2.15	0.61
1:0:45:GLY:HA3	1:0:66:ARG:HH12	1.64	0.61
4:3:74:GLN:HE22	4:3:92:PHE:HB2	1.65	0.61
11:A:1626:U:H3'	11:A:1627:U:OP2	2.00	0.61
6:5:75:VAL:O	6:5:79:ILE:N	2.27	0.61
20:J:48:HIS:ND1	20:J:48:HIS:O	2.34	0.61
23:M:26:ILE:HD12	23:M:27:LYS:N	2.16	0.61
11:A:820:U:H2'	11:A:821:U:H4'	1.82	0.61
8:7:56:LYS:HE3	8:7:58:GLN:HG2	1.80	0.61
11:A:677:G:H2'	11:A:678:A:C8	2.35	0.61
27:Q:3:THR:OG1	27:Q:82:ARG:NE	2.34	0.61
11:A:1474:G:H2'	11:A:1475:A:C8	2.36	0.61
11:A:1300:A:H4'	15:E:86:VAL:CG2	2.30	0.61
11:A:1657:U:H4'	11:A:1658:G:O5'	1.99	0.61
10:9:138:ARG:NH2	11:A:1236:A:O4'	2.33	0.61
30:T:52:GLY:O	30:T:54:PHE:N	2.25	0.61
11:A:1686:C:N1	11:A:1687:U:C6	2.69	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:38:ILE:HD11	1:0:47:VAL:HB	1.82	0.61
18:H:80:ASN:HD22	18:H:124:LYS:HG2	1.65	0.61
11:A:1524:A:H2'	11:A:1525:A:C8	2.35	0.61
2:1:22:ARG:HH21	11:A:1619:C:H1'	1.64	0.61
11:A:248:U:H4'	27:Q:36:LYS:HD3	1.82	0.61
12:B:41:ARG:HA	32:V:105:GLN:CD	2.20	0.61
5:4:77:GLU:OE2	21:K:114:ARG:NH2	2.30	0.61
11:A:1615:C:H4'	11:A:1616:G:O5'	2.00	0.61
22:L:24:TRP:HE3	22:L:30:LYS:HD3	1.66	0.61
18:H:11:LEU:HD12	18:H:74:VAL:HB	1.82	0.61
11:A:497:G:H2'	11:A:498:G:C8	2.36	0.61
9:8:43:ASP:O	9:8:45:GLU:N	2.34	0.61
11:A:1358:G:H2'	11:A:1359:C:C6	2.35	0.61
11:A:218:A:O2'	11:A:219:A:OP1	2.15	0.61
11:A:1299:G:H4'	15:E:99:LYS:CE	2.31	0.60
19:I:49:TYR:HB3	19:I:53:LEU:HD11	1.82	0.60
11:A:732:G:O2'	11:A:733:A:O4'	2.19	0.60
32:V:20:TYR:CD2	32:V:38:ILE:HD11	2.36	0.60
3:2:25:ARG:HA	11:A:400:A:H5"	1.82	0.60
11:A:1370:U:H4'	11:A:1371:A:C5'	2.32	0.60
14:D:37:LYS:HB3	34:X:33:ARG:HB2	1.81	0.60
16:F:31:GLN:CD	16:F:39:LEU:HD23	2.21	0.60
14:D:146:PHE:CE2	14:D:149:ARG:HD3	2.36	0.60
11:A:1168:U:H2'	11:A:1169:G:H5'	1.82	0.60
11:A:1442:U:H2'	11:A:1443:U:C6	2.37	0.60
11:A:1031:U:H4'	11:A:1032:G:OP2	1.99	0.60
35:Y:114:VAL:HG12	35:Y:115:LYS:HD3	1.81	0.60
5:4:181:LEU:H	5:4:181:LEU:HD13	1.66	0.60
11:A:143:G:N7	35:Y:177:ARG:NH2	2.49	0.60
10:9:100:UNK:C	10:9:102:VAL:H	2.14	0.60
11:A:822:U:H2'	11:A:823:G:H5"	1.83	0.60
11:A:1490:C:H4'	11:A:1491:U:OP1	1.99	0.60
11:A:1542:G:H22	11:A:1568:C:H1'	1.67	0.60
9:8:54:VAL:O	9:8:88:ILE:HG21	2.01	0.60
31:U:56:GLU:HB3	31:U:124:LYS:HG2	1.84	0.60
4:3:13:PRO:HB3	4:3:14:THR:HB	1.82	0.60
15:E:245:ASP:N	15:E:245:ASP:OD1	2.34	0.60
3:2:39:GLY:O	3:2:59:ARG:HB3	2.02	0.60
28:R:93:ASP:HB2	28:R:100:TYR:HE2	1.67	0.60
21:K:19:ILE:HB	21:K:83:ILE:HD12	1.84	0.60
11:A:703:G:H2'	11:A:704:C:H5'	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:765:G:H1	14:D:149:ARG:HB3	1.67	0.60
35:Y:135:PRO:HB2	35:Y:141:ILE:HG12	1.84	0.60
11:A:693:U:H5'	11:A:694:U:H5'	1.83	0.60
6:5:35:ALA:O	6:5:36:ILE:HG22	2.00	0.60
11:A:901:G:H22	21:K:54:GLU:CD	2.04	0.60
25:O:5:HIS:HB3	25:O:117:LEU:HD13	1.84	0.60
11:A:1480:G:H4'	30:T:11:ALA:HB1	1.84	0.60
11:A:1299:G:O3'	15:E:99:LYS:CE	2.49	0.60
16:F:31:GLN:CG	16:F:39:LEU:HB3	2.32	0.60
5:4:137:ILE:HD11	5:4:172:LEU:HB3	1.83	0.60
6:5:87:ARG:NH2	6:5:94:ASN:O	2.34	0.60
8:7:60:SER:HB2	13:C:27:ARG:HD2	1.83	0.60
11:A:1417:A:O3'	19:I:128:LYS:HE2	2.02	0.60
17:G:73:THR:HG23	19:I:114:ARG:CD	2.30	0.60
11:A:543:C:H5'	11:A:543:C:O2	2.02	0.60
11:A:1672:G:H2'	11:A:1673:G:C8	2.37	0.60
11:A:1381:U:H1'	11:A:1516:A:N6	2.17	0.60
11:A:1293:U:O2'	12:B:111:ILE:HB	2.01	0.59
3:2:5:ARG:HD3	3:2:29:LEU:O	2.02	0.59
35:Y:8:PRO:HG3	35:Y:112:VAL:HG13	1.84	0.59
5:4:105:PHE:N	5:4:214:LYS:HZ1	2.00	0.59
5:4:70:LEU:HD21	5:4:79:HIS:CD2	2.36	0.59
1:0:34:GLU:HG2	1:0:53:ASP:HB2	1.83	0.59
12:B:66:ALA:HB2	36:Z:37:ALA:HB2	1.85	0.59
11:A:1324:G:H5'	12:B:113:ARG:CD	2.31	0.59
11:A:498:G:O2'	11:A:499:U:P	2.60	0.59
9:8:42:LEU:HD12	9:8:43:ASP:N	2.17	0.59
18:H:104:LEU:HB2	18:H:124:LYS:O	2.01	0.59
35:Y:219:ARG:O	35:Y:223:LYS:HB2	2.01	0.59
11:A:229:U:H3	11:A:236:A:H61	1.51	0.59
36:Z:17:CYS:HB2	36:Z:56:SER:HB3	1.84	0.59
11:A:1738:U:H2'	11:A:1739:C:C6	2.37	0.59
23:M:54:LEU:H	23:M:54:LEU:HD22	1.66	0.59
11:A:1321:A:C1'	12:B:104:PRO:HB2	2.32	0.59
19:I:40:GLU:HG3	19:I:42:GLU:HB2	1.84	0.59
17:G:145:ASP:OD1	17:G:146:THR:N	2.36	0.59
5:4:193:ILE:O	5:4:197:ILE:HG12	2.03	0.59
11:A:702:G:C6	11:A:737:A:N6	2.71	0.59
11:A:538:A:H8	11:A:543:C:C4	2.20	0.59
9:8:60:VAL:HG22	9:8:101:TYR:HB2	1.83	0.59
13:C:177:MET:SD	13:C:182:LEU:HD11	2.43	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1316:G:HO2'	11:A:1401:A:HO2'	1.50	0.59
35:Y:142:ARG:HA	35:Y:147:LEU:HD12	1.85	0.59
4:3:185:ILE:HG22	4:3:186:PRO:HD3	1.82	0.59
9:8:92:ILE:HG12	9:8:100:ILE:HG22	1.84	0.59
11:A:569:C:H41	22:L:69:ARG:HH12	1.49	0.59
28:R:214:ALA:HB2	28:R:220:ILE:HA	1.85	0.59
11:A:1293:U:C1'	12:B:111:ILE:HD13	2.30	0.59
10:9:144:CYS:HB3	10:9:147:VAL:HG13	1.85	0.59
2:1:45:LYS:HG3	17:G:166:ARG:HD3	1.83	0.59
30:T:111:ILE:HG23	30:T:113:ILE:HG13	1.84	0.59
11:A:470:A:H8	11:A:470:A:H5"	1.67	0.59
11:A:1716:C:O2'	11:A:1717:G:C8	2.47	0.59
28:R:93:ASP:HB2	28:R:100:TYR:CE2	2.37	0.59
7:6:50:ALA:O	7:6:52:THR:N	2.35	0.59
11:A:45:U:O2'	11:A:46:A:H2'	2.03	0.59
2:1:25:VAL:HG11	2:1:66:LEU:HD12	1.85	0.59
11:A:702:G:O2'	11:A:703:G:O4'	2.21	0.59
12:B:150:ASP:OD2	12:B:165:ARG:NH2	2.36	0.59
1:0:83:ASP:CG	34:X:9:ALA:HA	2.23	0.59
3:2:37:LYS:H	3:2:59:ARG:H	1.51	0.59
23:M:46:VAL:HG22	23:M:72:ILE:HG22	1.83	0.59
11:A:407:A:H2'	11:A:408:C:C6	2.38	0.59
4:3:51:VAL:HG23	4:3:53:GLY:H	1.67	0.59
25:O:67:THR:O	25:O:69:ASN:N	2.36	0.59
11:A:501:U:HO2'	11:A:502:U:H6	1.51	0.58
11:A:67:A:O3'	11:A:68:A:H3'	2.03	0.58
33:W:37:LYS:HB2	33:W:40:GLU:HG2	1.84	0.58
23:M:91:ASP:O	23:M:92:ILE:HB	2.03	0.58
11:A:1071:U:H2'	11:A:1072:C:C6	2.38	0.58
6:5:24:VAL:HG11	6:5:71:LEU:HD12	1.85	0.58
28:R:36:ALA:HB2	28:R:71:CYS:HB3	1.85	0.58
11:A:1300:A:O2'	15:E:86:VAL:CB	2.49	0.58
11:A:992:A:C2	11:A:1012:U:N3	2.65	0.58
11:A:1657:U:H1'	11:A:1658:G:OP2	2.02	0.58
33:W:200:ARG:NH1	33:W:202:ASP:OD2	2.36	0.58
11:A:1715:G:H2'	11:A:1716:C:H5'	1.85	0.58
18:H:103:ILE:HD11	18:H:126:LEU:HD12	1.86	0.58
12:B:169:SER:O	12:B:173:ILE:HG12	2.03	0.58
16:F:28:ILE:HD11	16:F:92:MET:HE3	1.86	0.58
11:A:143:G:H2'	11:A:144:U:H5"	1.85	0.58
21:K:38:THR:OG1	21:K:39:ILE:N	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:975:C:H5”	25:O:109:LYS:HE2	1.85	0.58
11:A:1166:A:H5”	17:G:101:GLY:H	1.68	0.58
28:R:74:THR:HG23	28:R:79:TYR:HB2	1.85	0.58
11:A:1300:A:C4’	15:E:86:VAL:HG11	2.33	0.58
21:K:32:ASP:O	21:K:35:GLY:N	2.33	0.58
23:M:26:ILE:HD11	23:M:31:ALA:H	1.68	0.58
30:T:16:ASN:OD1	30:T:56:LYS:NZ	2.35	0.58
11:A:704:C:OP2	11:A:704:C:H3’	2.04	0.58
11:A:1711:C:O2’	11:A:1712:A:OP1	2.14	0.58
26:P:104:SER:HB3	26:P:107:GLN:HB2	1.85	0.58
12:B:121:VAL:HG23	12:B:141:ILE:HG21	1.84	0.58
13:C:127:MET:HE1	13:C:133:GLY:HA2	1.84	0.58
31:U:28:LEU:HD13	31:U:32:LEU:HD11	1.84	0.58
16:F:30:ILE:HG13	16:F:30:ILE:O	2.04	0.58
19:I:55:VAL:HG21	19:I:105:LEU:HG	1.85	0.58
30:T:14:PHE:HZ	30:T:132:LEU:HD23	1.69	0.58
21:K:107:ARG:HG3	21:K:107:ARG:NH1	2.15	0.58
5:4:141:ALA:HB1	5:4:207:LEU:HD23	1.84	0.58
33:W:179:LYS:N	33:W:194:THR:O	2.36	0.58
29:S:28:MET:O	29:S:29:SER:HB3	2.02	0.58
1:0:88:GLN:CB	34:X:6:GLY:HA2	2.33	0.58
22:L:59:ILE:HD12	34:X:4:VAL:HG22	1.85	0.58
6:5:87:ARG:NH1	11:A:1796:C:OP1	2.36	0.58
11:A:380:U:H5	14:D:5:PRO:HA	1.68	0.58
11:A:61:A:H8	11:A:269:G:HO2’	1.49	0.58
35:Y:3:LEU:HD13	35:Y:111:LEU:HD11	1.85	0.58
11:A:1488:G:H3’	11:A:1515:A:H61	1.68	0.58
21:K:85:ALA:H	21:K:119:THR:CG2	2.15	0.58
1:0:52:PHE:CZ	1:0:109:LEU:HD11	2.38	0.58
9:8:88:ILE:HA	9:8:104:ALA:HB2	1.85	0.58
11:A:399:A:H4’	33:W:3:ARG:HG2	1.85	0.58
11:A:1338:C:H1’	11:A:1410:A:C4	2.39	0.58
33:W:49:ARG:HB2	33:W:55:ALA:HB3	1.85	0.58
11:A:1332:C:O2’	13:C:162:GLN:HB3	2.04	0.58
1:0:84:PHE:CZ	34:X:7:SER:O	2.43	0.57
19:I:47:LYS:HZ1	19:I:114:ARG:HD2	1.68	0.57
11:A:918:U:H2’	11:A:919:A:C8	2.39	0.57
3:2:39:GLY:N	3:2:60:ILE:O	2.30	0.57
11:A:1178:G:H2’	11:A:1179:G:O4’	2.04	0.57
28:R:255:ALA:HB2	28:R:292:LEU:HD22	1.86	0.57
29:S:52:LYS:HG3	29:S:53:PRO:HD3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:58:MET:CG	34:X:3:LYS:HE2	2.22	0.57
11:A:1498:G:H2'	11:A:1499:G:H5'	1.85	0.57
4:3:74:GLN:NE2	4:3:92:PHE:HB2	2.19	0.57
33:W:104:ASP:HB3	33:W:106:LYS:H	1.69	0.57
11:A:324:U:OP1	27:Q:133:LYS:NZ	2.36	0.57
11:A:542:A:H2'	11:A:543:C:H3'	1.85	0.57
4:3:143:LEU:HB2	4:3:147:ASN:HB2	1.85	0.57
11:A:625:C:H2'	11:A:626:U:C6	2.39	0.57
3:2:8:ARG:O	3:2:8:ARG:HG3	2.04	0.57
11:A:1595:U:N3	11:A:1600:A:H2	2.02	0.57
11:A:190:C:N4	11:A:196:G:O6	2.37	0.57
34:X:55:ARG:HB3	34:X:58:PRO:HG3	1.87	0.57
30:T:57:ARG:HH11	30:T:57:ARG:CG	2.09	0.57
3:2:10:LYS:HG2	27:Q:133:LYS:HE3	1.85	0.57
22:L:24:TRP:CE3	22:L:30:LYS:HD3	2.39	0.57
27:Q:80:MET:HB2	27:Q:83:THR:HG23	1.86	0.57
11:A:1483:A:H2'	11:A:1484:G:C8	2.39	0.57
33:W:151:ASP:HB3	33:W:154:ILE:HG13	1.87	0.57
36:Z:74:GLN:HB2	36:Z:79:LEU:HB2	1.86	0.57
11:A:495:C:H3'	11:A:496:G:O4'	2.05	0.57
28:R:16:HIS:CE1	28:R:43:ILE:HG12	2.39	0.57
11:A:780:A:C8	26:P:8:ARG:HB3	2.40	0.57
17:G:72:HIS:O	19:I:47:LYS:HE2	2.04	0.57
11:A:68:A:OP1	35:Y:160:ARG:NH1	2.36	0.57
2:1:32:PHE:CE1	2:1:38:ARG:HB3	2.38	0.57
11:A:514:G:N1	11:A:543:C:H5	2.00	0.57
13:C:115:ILE:HG23	13:C:116:ARG:HG3	1.87	0.57
11:A:895:G:HO2'	21:K:38:THR:H	1.53	0.57
6:5:24:VAL:HG12	6:5:72:HIS:O	2.05	0.57
5:4:117:TRP:HE1	5:4:152:ARG:CZ	2.18	0.57
11:A:241:U:H5'	11:A:242:U:OP2	2.04	0.57
11:A:1293:U:C4'	12:B:111:ILE:HD13	2.35	0.57
11:A:1099:U:OP1	18:H:71:LYS:NZ	2.37	0.57
10:9:135:HIS:ND1	10:9:138:ARG:HD2	2.20	0.57
11:A:1169:G:N1	11:A:1575:G:OP2	2.36	0.57
23:M:70:VAL:HG12	23:M:74:GLN:OE1	2.05	0.57
11:A:1242:A:OP1	29:S:59:LYS:NZ	2.37	0.57
11:A:7:G:N7	15:E:205:ARG:NH1	2.51	0.57
11:A:1152:A:N3	11:A:1627:U:O2	2.36	0.57
19:I:116:LEU:H	19:I:116:LEU:HD22	1.70	0.57
11:A:448:C:OP1	33:W:29:PRO:HD3	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6:37:CYS:O	7:6:39:GLY:N	2.38	0.57
12:B:27:ARG:HG3	12:B:44:GLY:O	2.04	0.57
5:4:39:GLU:HB3	5:4:73:LEU:O	2.04	0.57
11:A:735:C:OP2	11:A:735:C:H2'	2.05	0.57
11:A:591:A:H2'	11:A:592:A:H8	1.70	0.57
11:A:116:U:H2'	11:A:117:U:C6	2.40	0.57
11:A:855:A:C2	11:A:857:U:H1'	2.40	0.57
35:Y:186:ARG:O	35:Y:190:GLN:HG2	2.04	0.57
11:A:639:U:H4'	11:A:639:U:OP2	2.04	0.57
5:4:97:LEU:CD1	5:4:98:THR:H	2.11	0.56
17:G:91:GLU:HA	17:G:94:THR:HG23	1.88	0.56
11:A:990:C:H2'	11:A:991:G:O4'	2.04	0.56
11:A:66:U:C4	35:Y:158:ILE:HG21	2.40	0.56
21:K:81:VAL:HG13	21:K:115:ILE:HG21	1.87	0.56
11:A:1226:A:O2'	11:A:1227:A:OP1	2.23	0.56
11:A:1173:C:H3'	23:M:141:THR:HG21	1.87	0.56
14:D:17:ARG:O	14:D:23:ARG:NH2	2.38	0.56
11:A:1300:A:H5'	15:E:99:LYS:HG3	1.87	0.56
1:0:78:LEU:O	1:0:92:VAL:HG12	2.06	0.56
16:F:98:LEU:HD23	16:F:103:ILE:CG1	2.35	0.56
3:2:8:ARG:HH11	3:2:21:PHE:H	1.54	0.56
11:A:1160:A:H2'	11:A:1161:C:H6	1.69	0.56
21:K:81:VAL:HG22	21:K:115:ILE:HB	1.87	0.56
12:B:13:ASP:HA	12:B:16:LEU:HD12	1.87	0.56
4:3:107:ARG:NH2	11:A:741:C:O2	2.38	0.56
11:A:1525:A:OP1	30:T:93:HIS:ND1	2.36	0.56
11:A:93:A:O2'	33:W:4:GLY:HA3	2.05	0.56
11:A:802:G:H21	18:H:107:SER:HB3	1.71	0.56
8:7:2:LEU:HD13	11:A:1258:U:H4'	1.87	0.56
14:D:38:ASN:HB2	14:D:41:GLU:HG3	1.87	0.56
11:A:1413:U:H4'	11:A:1414:U:OP2	2.06	0.56
11:A:885:G:H2'	11:A:886:U:C6	2.40	0.56
11:A:886:U:O2'	21:K:121:VAL:O	2.22	0.56
1:0:59:ALA:HA	1:0:89:CYS:O	2.05	0.56
11:A:104:A:OP2	11:A:308:C:N4	2.37	0.56
12:B:41:ARG:HH11	32:V:103:ASP:CB	2.18	0.56
11:A:717:C:N3	11:A:720:G:N1	2.48	0.56
1:0:38:ILE:HG23	1:0:74:GLY:H	1.70	0.56
10:9:135:HIS:HB2	10:9:138:ARG:CB	2.35	0.56
33:W:152:PRO:O	33:W:154:ILE:N	2.39	0.56
11:A:885:G:H21	21:K:123:SER:HB2	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:149:GLN:NE2	11:A:1066:C:H4'	2.20	0.56
32:V:71:PHE:HE1	32:V:73:LEU:HD22	1.71	0.56
29:S:96:ILE:HD11	29:S:116:LEU:HD22	1.88	0.56
11:A:180:A:H2'	11:A:181:A:O4'	2.05	0.56
21:K:13:VAL:HG22	21:K:76:ILE:HA	1.87	0.56
35:Y:78:THR:HG23	35:Y:92:ARG:HG2	1.86	0.56
11:A:1321:A:N9	12:B:104:PRO:HB2	2.21	0.56
30:T:6:VAL:HG13	30:T:66:TYR:CE2	2.41	0.56
5:4:136:ARG:NH1	11:A:885:G:OP1	2.39	0.56
6:5:23:CYS:HB2	6:5:74:CYS:HB3	1.88	0.56
1:0:84:PHE:CE2	34:X:7:SER:C	2.63	0.56
14:D:175:ARG:HD3	14:D:179:ARG:NH1	2.21	0.56
11:A:823:G:O2'	11:A:824:G:O5'	2.24	0.56
33:W:194:THR:O	33:W:195:ILE:HB	2.05	0.56
11:A:1511:U:H2'	11:A:1512:G:C8	2.41	0.56
26:P:77:ASN:O	26:P:78:SER:HB3	2.05	0.56
31:U:30:VAL:HB	31:U:132:GLU:HG3	1.86	0.56
11:A:513:U:OP1	14:D:133:HIS:NE2	2.38	0.56
11:A:1207:C:H42	11:A:1456:C:H5	1.53	0.56
11:A:577:G:H8	11:A:577:G:H3'	1.71	0.56
32:V:26:LEU:HD23	32:V:26:LEU:H	1.70	0.56
5:4:147:ALA:O	5:4:148:ASN:ND2	2.28	0.56
11:A:312:A:C2	11:A:314:C:H2'	2.40	0.56
1:0:82:ARG:NH2	22:L:68:ILE:CG1	2.66	0.56
16:F:98:LEU:CD1	16:F:102:ASN:HB2	2.31	0.56
16:F:98:LEU:CD1	16:F:102:ASN:HD22	2.19	0.56
16:F:85:ARG:HA	16:F:88:VAL:HG12	1.87	0.56
13:C:64:ARG:O	13:C:66:ILE:N	2.39	0.56
17:G:42:LEU:HB2	17:G:46:TRP:O	2.05	0.56
11:A:717:C:N4	11:A:720:G:H22	2.03	0.56
22:L:102:VAL:HG12	22:L:127:VAL:HG12	1.88	0.56
3:2:138:ASN:O	3:2:141:ARG:HB2	2.06	0.56
21:K:13:VAL:N	21:K:77:THR:OG1	2.38	0.56
11:A:1555:A:OP2	29:S:47:ARG:NH1	2.39	0.56
25:O:12:SER:O	25:O:13:SER:HB3	2.06	0.56
16:F:80:LEU:HB3	16:F:84:GLN:HE22	1.70	0.56
11:A:514:G:O2'	11:A:515:A:H5'	2.06	0.56
11:A:1370:U:O2'	11:A:1371:A:OP2	2.20	0.56
11:A:1489:U:OP2	13:C:9:ARG:NH1	2.38	0.56
11:A:852:C:H6	11:A:852:C:O5'	1.88	0.56
33:W:246:LEU:HD13	33:W:251:GLU:HG2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:I:22:VAL:HG22	19:I:65:ILE:HD13	1.88	0.56
12:B:38:PHE:CD1	32:V:109:LEU:CB	2.85	0.56
4:3:71:HIS:CG	4:3:131:PHE:HZ	2.24	0.56
32:V:5:ARG:O	32:V:10:LYS:HE2	2.05	0.56
11:A:1097:U:O4	15:E:201:ASN:ND2	2.39	0.56
1:0:82:ARG:CZ	22:L:68:ILE:HD11	2.06	0.55
8:7:15:LEU:HD13	8:7:21:VAL:HG23	1.87	0.55
3:2:192:TYR:O	3:2:196:LEU:HB2	2.05	0.55
11:A:540:G:O3'	11:A:541:A:H3'	2.06	0.55
23:M:83:ALA:O	23:M:89:GLN:NE2	2.39	0.55
11:A:238:U:O2'	11:A:239:C:H5'	2.05	0.55
4:3:117:THR:HG1	11:A:639:U:P	2.28	0.55
14:D:151:ASP:N	14:D:151:ASP:OD1	2.39	0.55
11:A:149:C:O2'	35:Y:132:ARG:NH1	2.39	0.55
5:4:179:SER:OG	5:4:179:SER:O	2.21	0.55
27:Q:59:PRO:HG2	27:Q:60:PHE:CE2	2.41	0.55
11:A:1625:C:C5'	15:E:91:ARG:NH1	2.43	0.55
11:A:1151:A:O3'	11:A:1152:A:H5"	2.07	0.55
11:A:1299:G:H5'	15:E:208:GLU:OE2	2.07	0.55
1:0:33:GLN:NE2	1:0:78:LEU:HD11	2.21	0.55
13:C:141:LYS:HD2	13:C:179:GLN:CG	2.36	0.55
13:C:29:LEU:HB2	13:C:34:TYR:HB2	1.87	0.55
11:A:896:U:O4'	21:K:38:THR:HG21	2.06	0.55
11:A:827:C:H2'	11:A:828:U:C6	2.41	0.55
11:A:489:C:H42	11:A:497:G:H22	1.53	0.55
19:I:50:GLU:OE2	19:I:112:TYR:OH	2.24	0.55
1:0:103:LEU:HD23	1:0:106:GLN:NE2	2.22	0.55
30:T:9:VAL:HG12	30:T:14:PHE:HB2	1.88	0.55
11:A:103:A:H4'	11:A:104:A:OP2	2.06	0.55
3:2:48:THR:HG21	3:2:54:LYS:HB2	1.87	0.55
11:A:706:A:C6	11:A:734:A:N6	2.75	0.55
5:4:110:LEU:HD21	5:4:213:ARG:HD2	1.89	0.55
13:C:34:TYR:OH	13:C:37:VAL:HG22	2.07	0.55
9:8:65:LEU:HB3	9:8:71:ILE:HD13	1.89	0.55
6:5:5:ARG:NH1	11:A:1796:C:OP2	2.39	0.55
19:I:9:THR:HG21	19:I:88:GLY:HA2	1.88	0.55
11:A:1650:U:H2'	11:A:1651:A:C8	2.42	0.55
7:6:36:LYS:HG2	7:6:43:ILE:HG22	1.88	0.55
11:A:749:U:H2'	11:A:750:U:C6	2.41	0.55
28:R:64:HIS:ND1	28:R:86:ASP:OD2	2.35	0.55
1:0:46:ARG:HD3	34:X:3:LYS:HZ2	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:88:GLN:HE22	34:X:4:VAL:H	1.54	0.55
11:A:1291:G:C8	11:A:1291:G:O5'	2.55	0.55
12:B:179:ARG:HD3	12:B:183:ARG:NH1	2.17	0.55
11:A:1157:A:H3'	11:A:1157:A:C8	2.42	0.55
11:A:647:G:N2	11:A:687:G:N2	2.54	0.55
5:4:34:ALA:HB3	5:4:41:ARG:HA	1.89	0.55
35:Y:109:LEU:HD13	35:Y:111:LEU:HD21	1.87	0.55
3:2:188:GLU:HG2	27:Q:13:PHE:CD2	2.42	0.55
1:0:42:LEU:HD11	1:0:58:MET:SD	2.46	0.55
16:F:92:MET:SD	16:F:103:ILE:HG12	2.46	0.55
5:4:39:GLU:HG3	5:4:40:ASN:N	2.21	0.55
6:5:9:GLY:HA3	6:5:34:LYS:HE2	1.89	0.55
11:A:190:C:O2'	11:A:191:C:OP2	2.23	0.55
28:R:93:ASP:OD1	28:R:96:THR:HB	2.06	0.55
33:W:159:THR:HG23	33:W:173:ILE:HD13	1.88	0.55
11:A:652:G:H1	11:A:682:C:N4	2.05	0.55
19:I:47:LYS:HZ1	19:I:114:ARG:HH11	1.55	0.55
11:A:286:C:H2'	11:A:287:G:H5'	1.89	0.55
33:W:158:ASP:OD2	33:W:174:LYS:NZ	2.38	0.55
33:W:192:ILE:HG13	33:W:243:GLY:HA3	1.89	0.55
20:J:57:ARG:HG3	20:J:89:ARG:CZ	2.36	0.55
30:T:42:GLY:HA2	30:T:84:LYS:HB2	1.89	0.55
16:F:98:LEU:HD11	16:F:102:ASN:HD22	1.71	0.55
11:A:1776:A:H2'	11:A:1777:G:C8	2.42	0.55
18:H:8:ALA:HA	18:H:74:VAL:HG11	1.88	0.55
11:A:1760:G:H2'	11:A:1761:U:H5'	1.88	0.55
10:9:91:UNK:HG2	11:A:1445:G:C4	2.41	0.55
9:8:60:VAL:CG2	9:8:101:TYR:HB2	2.37	0.55
11:A:1783:C:H2'	11:A:1784:C:H6	1.72	0.55
11:A:197:A:H2'	11:A:198:A:C8	2.42	0.55
5:4:34:ALA:HB2	5:4:43:VAL:HG23	1.89	0.55
33:W:104:ASP:HB2	33:W:108:ARG:H	1.72	0.55
11:A:1514:U:O2	11:A:1514:U:H5'	2.07	0.55
11:A:425:A:H5'	11:A:425:A:H8	1.72	0.55
1:0:41:MET:HA	1:0:41:MET:HE2	1.88	0.55
31:U:67:THR:O	31:U:69:ALA:N	2.35	0.55
22:L:16:ARG:NH1	27:Q:101:GLU:OE1	2.40	0.55
12:B:147:THR:OG1	12:B:159:ALA:HB1	2.07	0.55
11:A:1433:G:H2'	11:A:1434:U:C6	2.42	0.55
1:0:46:ARG:CD	34:X:3:LYS:HZ2	2.20	0.54
11:A:142:G:O6	35:Y:177:ARG:NH1	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1157:A:H2'	11:A:1160:A:N7	2.21	0.54
11:A:592:A:OP1	14:D:39:LYS:HG2	2.07	0.54
3:2:26:LYS:O	3:2:29:LEU:HB3	2.07	0.54
11:A:1625:C:C5'	15:E:91:ARG:HH12	2.09	0.54
12:B:40:ALA:C	32:V:105:GLN:HG3	2.28	0.54
2:1:32:PHE:HZ	2:1:38:ARG:CZ	2.21	0.54
11:A:896:U:C4'	21:K:38:THR:HG21	2.37	0.54
11:A:558:U:O2'	11:A:559:C:O5'	2.25	0.54
2:1:45:LYS:HB3	17:G:162:VAL:HB	1.90	0.54
36:Z:64:GLU:O	36:Z:68:SER:HB2	2.07	0.54
6:5:13:LYS:O	11:A:1075:C:O2'	2.20	0.54
11:A:1686:C:O2'	11:A:1687:U:H5'	2.06	0.54
16:F:98:LEU:HD11	16:F:102:ASN:CB	2.31	0.54
11:A:1559:A:C6	23:M:134:ARG:HD2	2.42	0.54
9:8:77:ARG:NH2	11:A:1533:C:C5	2.75	0.54
1:0:38:ILE:CG2	1:0:75:ASP:H	2.20	0.54
6:5:6:ALA:H	11:A:1796:C:H5	1.50	0.54
20:J:28:SER:OG	20:J:29:THR:N	2.38	0.54
11:A:970:A:H5'	11:A:971:A:OP2	2.07	0.54
26:P:51:GLU:OE1	26:P:53:ASP:N	2.33	0.54
11:A:178:U:C4	35:Y:191:ARG:HD3	2.43	0.54
12:B:58:VAL:O	12:B:62:ARG:HB2	2.07	0.54
11:A:133:U:H3'	11:A:133:U:OP2	2.07	0.54
11:A:93:A:H4'	11:A:94:U:OP2	2.08	0.54
4:3:122:HIS:HA	4:3:125:ILE:HD12	1.89	0.54
1:0:84:PHE:HZ	34:X:7:SER:O	1.86	0.54
11:A:480:G:N2	11:A:509:G:H1'	2.22	0.54
11:A:1492:A:O2'	11:A:1493:A:H8	1.80	0.54
5:4:180:THR:O	5:4:184:LEU:HB2	2.08	0.54
32:V:20:TYR:CZ	32:V:38:ILE:HD11	2.42	0.54
25:O:114:ARG:HG2	25:O:114:ARG:NH1	2.18	0.54
11:A:711:U:H4'	11:A:712:G:OP1	2.08	0.54
11:A:1354:G:H5'	11:A:1355:C:OP2	2.07	0.54
14:D:65:LYS:HA	14:D:70:LEU:HD11	1.89	0.54
4:3:111:LYS:O	4:3:112:ARG:HB2	2.07	0.54
4:3:73:VAL:HG12	4:3:77:LEU:HB2	1.90	0.54
11:A:1293:U:O2'	12:B:111:ILE:N	2.29	0.54
1:0:45:GLY:HA3	1:0:66:ARG:NH1	2.23	0.54
11:A:133:U:H4'	11:A:134:U:OP2	2.07	0.54
14:D:125:ALA:O	14:D:129:ILE:HG13	2.08	0.54
5:4:61:LEU:HD23	5:4:62:LYS:H	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:D:171:ARG:O	14:D:175:ARG:N	2.36	0.54
11:A:989:U:H2'	11:A:990:C:C6	2.42	0.54
5:4:128:LYS:HE3	5:4:132:ASP:HB3	1.90	0.54
11:A:1352:G:H2'	11:A:1353:U:O4'	2.07	0.54
11:A:1151:A:N6	11:A:1152:A:C5	2.74	0.54
14:D:90:LYS:HB2	14:D:95:TYR:CD2	2.43	0.54
4:3:35:LYS:NZ	4:3:39:ARG:HD2	2.23	0.54
23:M:90:ASN:O	29:S:18:ARG:NH1	2.40	0.54
11:A:1332:C:O5'	11:A:1332:C:H6	1.89	0.54
11:A:1098:U:OP1	15:E:159:THR:HB	2.07	0.54
4:3:46:ILE:HG12	4:3:60:ILE:HG23	1.90	0.54
11:A:542:A:O2'	11:A:543:C:O5'	2.26	0.54
12:B:9:LEU:HD22	12:B:10:THR:H	1.72	0.54
18:H:37:PHE:CD2	18:H:103:ILE:HD12	2.43	0.54
24:N:7:TRP:O	24:N:8:PHE:HB2	2.07	0.54
28:R:160:GLU:O	28:R:162:ALA:N	2.35	0.54
8:7:9:ASN:O	8:7:13:GLN:HB3	2.07	0.54
4:3:16:LEU:HA	4:3:19:GLN:HG3	1.90	0.54
9:8:85:LYS:HG3	9:8:86:GLU:N	2.22	0.54
1:0:88:GLN:HB3	34:X:6:GLY:HA2	1.90	0.54
16:F:27:HIS:HB2	16:F:43:GLN:CD	2.28	0.54
4:3:107:ARG:NH1	11:A:741:C:O2	2.40	0.54
8:7:14:TYR:CE1	8:7:21:VAL:HG22	2.43	0.54
11:A:115:G:OP1	27:Q:67:ARG:NH1	2.39	0.54
11:A:20:G:H5'	11:A:571:G:C5	2.43	0.54
11:A:138:A:N6	11:A:266:A:H61	2.06	0.54
11:A:142:G:N2	11:A:173:A:H2	2.00	0.54
11:A:542:A:H5"	11:A:544:A:C8	2.43	0.54
4:3:30:SER:HB2	4:3:34:LEU:HB2	1.90	0.54
11:A:720:G:H1'	11:A:721:U:H5"	1.90	0.54
11:A:1498:G:H5"	30:T:72:GLY:HA3	1.90	0.54
11:A:1217:A:H8	11:A:1217:A:H5'	1.73	0.54
26:P:36:SER:O	26:P:40:LEU:HG	2.08	0.54
11:A:1299:G:C5'	15:E:208:GLU:OE2	2.57	0.53
1:0:30:GLU:H	1:0:33:GLN:NE2	2.07	0.53
10:9:86:UNK:C	10:9:87:UNK:HG3	2.38	0.53
11:A:1034:C:OP1	25:O:9:LYS:NZ	2.40	0.53
21:K:107:ARG:HH11	21:K:107:ARG:CG	2.19	0.53
27:Q:6:THR:CB	27:Q:9:SER:HB3	2.38	0.53
10:9:130:VAL:HG11	10:9:143:LYS:HG2	1.89	0.53
10:9:136:LYS:H	10:9:138:ARG:HB2	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:C:211:PRO:O	13:C:212:LYS:HB2	2.08	0.53
11:A:832:U:H2'	11:A:833:U:H5"	1.89	0.53
11:A:1294:G:O3'	12:B:109:ASN:N	2.40	0.53
11:A:1528:U:OP1	17:G:109:LYS:HG2	2.09	0.53
23:M:30:TYR:O	23:M:33:THR:OG1	2.15	0.53
5:4:72:ASP:OD1	6:5:59:TYR:OH	2.14	0.53
11:A:1535:U:O2'	11:A:1536:G:N3	2.35	0.53
11:A:237:C:H4'	11:A:238:U:H5'	1.90	0.53
2:1:13:ILE:HG13	2:1:29:ARG:O	2.08	0.53
4:3:167:GLU:O	4:3:170:GLN:HB2	2.07	0.53
20:J:23:ARG:HD3	20:J:92:ASP:OD1	2.09	0.53
5:4:48:VAL:HG13	5:4:61:LEU:HD21	1.89	0.53
23:M:31:ALA:O	23:M:34:THR:HG23	2.08	0.53
11:A:717:C:H2'	11:A:718:U:H5"	1.90	0.53
27:Q:84:ILE:HD12	27:Q:86:ILE:HG23	1.90	0.53
3:2:76:THR:HG22	3:2:108:PRO:HG2	1.90	0.53
24:N:22:ARG:HD2	24:N:38:ILE:HD11	1.90	0.53
11:A:1322:A:C2	12:B:109:ASN:ND2	2.76	0.53
11:A:503:G:O2'	11:A:504:U:P	2.65	0.53
11:A:513:U:H2'	11:A:514:G:C8	2.44	0.53
6:5:79:ILE:HG23	6:5:84:VAL:HG21	1.89	0.53
5:4:172:LEU:O	5:4:176:VAL:HG23	2.08	0.53
32:V:44:LYS:HG2	32:V:48:ASN:HD21	1.74	0.53
11:A:866:G:OP1	25:O:2:GLY:HA2	2.07	0.53
18:H:72:CYS:HB3	18:H:129:VAL:HG13	1.90	0.53
11:A:767:U:H5	14:D:142:ASN:H	1.55	0.53
30:T:57:ARG:NH2	30:T:80:TYR:HB3	2.24	0.53
10:9:86:UNK:O	10:9:87:UNK:CG	2.51	0.53
21:K:117:ASP:OD1	21:K:119:THR:HG23	2.09	0.53
5:4:62:LYS:C	5:4:64:ARG:H	2.12	0.53
11:A:1595:U:H3	11:A:1600:A:H2	1.56	0.53
8:7:12:HIS:NE2	8:7:49:LEU:HD21	2.23	0.53
26:P:94:TYR:HD2	26:P:96:LEU:HD11	1.73	0.53
19:I:35:PRO:HG2	19:I:38:LEU:HG	1.90	0.53
33:W:42:LEU:HD12	33:W:109:PHE:HB2	1.89	0.53
13:C:176:LEU:H	13:C:176:LEU:HD12	1.73	0.53
11:A:1149:G:H1'	11:A:1765:A:C4	2.44	0.53
12:B:109:ASN:O	12:B:112:THR:HG22	2.08	0.53
11:A:240:U:H1'	11:A:241:U:P	2.49	0.53
11:A:1320:U:O2	11:A:1322:A:H5'	2.09	0.53
3:2:8:ARG:HH11	3:2:21:PHE:N	2.06	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:T:117:SER:OG	30:T:118:PRO:O	2.20	0.53
3:2:36:THR:HG21	3:2:173:PRO:HB2	1.90	0.53
11:A:230:C:H2'	11:A:231:U:H5"	1.90	0.53
31:U:67:THR:C	31:U:69:ALA:H	2.11	0.53
18:H:83:ILE:HD12	18:H:122:SER:HB2	1.89	0.53
12:B:81:PHE:HB3	12:B:170:ILE:HD13	1.91	0.53
11:A:981:U:H2'	11:A:982:U:H5'	1.91	0.53
4:3:104:ARG:O	4:3:106:SER:N	2.42	0.53
12:B:14:ALA:O	12:B:18:LEU:HG	2.09	0.53
11:A:1473:U:H2'	11:A:1473:U:O2	2.08	0.53
11:A:765:G:N1	14:D:149:ARG:HD2	2.24	0.53
11:A:226:A:C2'	11:A:227:U:H5'	2.38	0.53
28:R:136:ILE:N	28:R:136:ILE:HD13	2.24	0.53
11:A:283:U:H5"	35:Y:188:ARG:HD3	1.90	0.53
11:A:1241:G:H5"	29:S:77:ARG:HB2	1.90	0.53
22:L:90:ASP:OD1	34:X:12:GLY:HA2	2.08	0.53
3:2:105:ASP:OD2	3:2:107:THR:HG23	2.09	0.53
11:A:799:A:H5"	33:W:201:HIS:CE1	2.44	0.53
11:A:632:U:OP1	27:Q:102:LYS:HG3	2.08	0.53
36:Z:72:LEU:O	36:Z:76:ASP:HB2	2.09	0.53
11:A:1151:A:C3'	11:A:1152:A:O5'	2.55	0.53
11:A:1291:G:H22	11:A:1324:G:N2	2.07	0.53
16:F:98:LEU:HD21	16:F:102:ASN:C	2.30	0.53
12:B:49:ASN:HB3	12:B:52:LYS:CG	2.32	0.53
21:K:16:VAL:O	21:K:30:VAL:HA	2.09	0.53
17:G:94:THR:O	17:G:97:LEU:HB2	2.08	0.53
11:A:420:A:H2'	11:A:421:A:O4'	2.08	0.53
4:3:96:ARG:CZ	4:3:124:LYS:HB3	2.39	0.53
11:A:61:A:H8	11:A:269:G:O2'	1.92	0.53
11:A:851:U:H2'	11:A:852:C:C6	2.42	0.53
25:O:113:PHE:HA	25:O:116:ILE:HD12	1.90	0.53
27:Q:14:GLN:HB3	27:Q:54:ILE:HG21	1.91	0.53
7:6:4:VAL:HA	18:H:24:GLN:NE2	2.24	0.53
16:F:58:LEU:HD23	16:F:58:LEU:C	2.29	0.53
11:A:1062:A:H2'	11:A:1063:U:O4'	2.09	0.53
11:A:765:G:C4	14:D:149:ARG:CZ	2.92	0.53
9:8:43:ASP:O	9:8:46:LYS:N	2.27	0.53
11:A:780:A:H8	26:P:8:ARG:HB3	1.73	0.53
17:G:103:ASN:HA	17:G:106:LYS:HD2	1.91	0.53
11:A:114:C:H6	11:A:114:C:H5'	1.74	0.53
27:Q:57:LYS:HB2	27:Q:110:HIS:NE2	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:F:100:LYS:HA	16:F:103:ILE:HD12	1.91	0.52
28:R:192:PHE:HD2	28:R:223:TRP:CE3	2.27	0.52
5:4:157:GLN:H	5:4:160:HIS:HB2	1.74	0.52
26:P:49:LYS:N	26:P:49:LYS:HD3	2.24	0.52
14:D:88:GLU:HG3	14:D:91:LYS:HE3	1.90	0.52
11:A:918:U:O3'	21:K:18:ARG:NH1	2.42	0.52
11:A:6:G:OP2	15:E:205:ARG:HD2	2.10	0.52
15:E:185:LYS:O	15:E:189:GLN:HG3	2.09	0.52
23:M:26:ILE:HD13	23:M:30:TYR:HB2	1.92	0.52
11:A:325:G:H4'	27:Q:83:THR:HG21	1.91	0.52
8:7:1:MET:HG2	8:7:2:LEU:H	1.73	0.52
11:A:1760:G:C2'	11:A:1761:U:H5'	2.39	0.52
27:Q:75:VAL:HG12	27:Q:119:VAL:HA	1.91	0.52
11:A:1420:C:OP1	24:N:54:LYS:NZ	2.38	0.52
19:I:113:ASP:CG	19:I:115:THR:H	2.12	0.52
28:R:33:LEU:HB3	28:R:45:TRP:HB2	1.90	0.52
10:9:133:ALA:HB2	11:A:1252:C:O4'	2.10	0.52
11:A:359:A:C2	22:L:38:PHE:HB3	2.45	0.52
28:R:7:LEU:HD23	28:R:315:VAL:HG22	1.90	0.52
8:7:61:TRP:CD2	13:C:20:GLU:HG3	2.44	0.52
16:F:69:VAL:CB	16:F:79:GLN:HE22	2.06	0.52
11:A:79:C:H4'	35:Y:173:PRO:O	2.09	0.52
11:A:611:U:OP2	22:L:5:LYS:HE2	2.09	0.52
11:A:1535:U:H4'	11:A:1535:U:OP1	2.10	0.52
5:4:174:LYS:NZ	5:4:174:LYS:HB2	2.25	0.52
2:1:34:GLU:O	2:1:35:ASP:HB2	2.10	0.52
33:W:241:GLY:O	33:W:244:ILE:HG12	2.09	0.52
16:F:85:ARG:NH1	16:F:107:GLY:HA3	2.24	0.52
12:B:167:LYS:HB3	12:B:168:HIS:HD2	1.72	0.52
21:K:29:HIS:HB2	21:K:41:ARG:HA	1.92	0.52
5:4:127:VAL:HG11	5:4:176:VAL:HG21	1.91	0.52
25:O:92:ILE:O	25:O:96:VAL:HG23	2.09	0.52
11:A:927:C:H1'	21:K:125:SER:HB2	1.91	0.52
11:A:579:A:N6	13:C:143:ARG:CA	2.25	0.52
11:A:1061:A:H2'	11:A:1062:A:H5'	1.92	0.52
9:8:94:LYS:HD3	9:8:95:HIS:HB3	1.90	0.52
9:8:77:ARG:NH2	11:A:1533:C:H5	2.08	0.52
9:8:41:ILE:HG13	9:8:42:LEU:HG	1.91	0.52
11:A:1199:G:O6	24:N:31:ILE:HD11	2.10	0.52
11:A:1487:A:H2'	11:A:1488:G:C8	2.44	0.52
23:M:18:LEU:HD21	23:M:70:VAL:HG13	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:I:127:LYS:NZ	19:I:131:GLY:O	2.38	0.52
11:A:1647:U:O2	34:X:2:ALA:HA	2.10	0.52
12:B:189:VAL:HG22	12:B:190:ASP:H	1.75	0.52
11:A:1320:U:C3'	12:B:101:ARG:NH2	2.56	0.52
11:A:1324:G:H5"	12:B:113:ARG:NH2	2.25	0.52
11:A:961:U:H5"	25:O:71:ILE:HD13	1.91	0.52
11:A:929:A:OP2	11:A:931:C:N4	2.43	0.52
5:4:134:VAL:O	5:4:218:LEU:HD22	2.10	0.52
11:A:1474:G:H2'	11:A:1475:A:H8	1.72	0.52
3:2:58:LEU:O	3:2:59:ARG:HB2	2.10	0.52
29:S:29:SER:OG	29:S:31:GLU:HG3	2.10	0.52
11:A:1002:G:H2'	11:A:1003:A:H5'	1.92	0.52
5:4:128:LYS:CE	5:4:132:ASP:HB3	2.40	0.52
11:A:1676:U:O2'	11:A:1677:C:H5'	2.09	0.52
13:C:3:ALA:O	13:C:4:LEU:HB2	2.09	0.52
11:A:520:A:H2'	11:A:521:A:C8	2.45	0.52
11:A:530:C:O2	26:P:61:ARG:NH2	2.43	0.52
15:E:67:GLN:HA	15:E:70:ASP:HB2	1.92	0.52
11:A:487:G:H3'	11:A:488:G:H5"	1.92	0.52
5:4:133:TYR:CD1	5:4:181:LEU:HD11	2.44	0.52
12:B:73:VAL:O	12:B:95:ALA:HA	2.09	0.52
28:R:167:VAL:HG12	28:R:183:LEU:HB2	1.92	0.52
22:L:6:PRO:HG3	22:L:14:LYS:HG2	1.91	0.52
11:A:1334:U:H2'	11:A:1335:U:C6	2.45	0.52
11:A:256:A:H2'	11:A:257:A:O4'	2.09	0.52
27:Q:93:TYR:HB2	27:Q:100:TYR:CE2	2.45	0.52
24:N:21:CYS:SG	24:N:23:VAL:HB	2.50	0.52
22:L:107:PHE:CE2	22:L:114:LYS:HB2	2.44	0.52
15:E:89:GLN:OE1	15:E:94:GLN:NE2	2.41	0.52
11:A:1532:U:O3'	23:M:27:LYS:NZ	2.42	0.52
11:A:710:U:H2'	11:A:711:U:H5'	1.91	0.52
11:A:555:A:C8	11:A:555:A:H3'	2.45	0.52
11:A:872:G:H2'	11:A:873:U:O4'	2.09	0.52
2:1:50:GLU:O	2:1:51:ASN:HB2	2.10	0.52
31:U:52:LEU:HD13	31:U:85:LYS:NZ	2.25	0.52
3:2:117:TYR:CD1	3:2:150:ALA:HB2	2.44	0.52
11:A:1039:A:H5"	36:Z:62:ARG:NH2	2.24	0.52
14:D:105:LEU:O	14:D:108:ARG:HG3	2.09	0.51
35:Y:67:VAL:O	35:Y:68:LEU:HB2	2.10	0.51
35:Y:70:PRO:C	35:Y:98:ARG:HH21	2.14	0.51
28:R:295:SER:HB2	28:R:300:THR:HB	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:9:143:LYS:HA	11:A:1253:U:O2'	2.10	0.51
11:A:647:G:H22	11:A:687:G:N2	2.09	0.51
20:J:117:VAL:HG22	20:J:118:VAL:H	1.75	0.51
11:A:577:G:C8	11:A:577:G:H3'	2.45	0.51
19:I:7:VAL:HG22	19:I:22:VAL:HB	1.92	0.51
27:Q:55:ASP:OD2	27:Q:110:HIS:HE1	1.92	0.51
10:9:108:VAL:HG13	31:U:73:LYS:NZ	2.25	0.51
4:3:63:PRO:C	4:3:65:PRO:HD2	2.29	0.51
1:0:46:ARG:CD	34:X:3:LYS:NZ	2.55	0.51
11:A:497:G:O2'	11:A:498:G:O4'	2.29	0.51
35:Y:57:ASP:OD2	35:Y:72:ARG:NH1	2.43	0.51
11:A:144:U:O2'	11:A:145:A:H5'	2.10	0.51
11:A:55:A:OP1	26:P:112:LYS:NZ	2.43	0.51
11:A:56:U:H4'	11:A:57:G:H5'	1.92	0.51
32:V:13:SER:HA	32:V:54:THR:HG22	1.92	0.51
11:A:1081:A:H4'	11:A:1082:C:O5'	2.10	0.51
35:Y:139:ASN:HA	35:Y:142:ARG:HB2	1.91	0.51
28:R:154:VAL:HG12	28:R:171:SER:HB3	1.93	0.51
16:F:28:ILE:HD11	16:F:92:MET:CE	2.39	0.51
6:5:10:ARG:HB2	6:5:34:LYS:HG3	1.91	0.51
12:B:74:VAL:HG22	12:B:96:THR:HG23	1.91	0.51
11:A:1513:G:O2'	11:A:1515:A:N3	2.38	0.51
31:U:31:VAL:HG21	31:U:136:ILE:HD13	1.92	0.51
11:A:1502:G:O6	30:T:102:ARG:NH2	2.44	0.51
22:L:23:ARG:HA	22:L:26:GLU:OE2	2.10	0.51
5:4:186:SER:O	5:4:190:PRO:HD2	2.10	0.51
6:5:22:ARG:HH12	21:K:127:ARG:HG3	1.75	0.51
16:F:98:LEU:HD23	16:F:103:ILE:HG12	1.93	0.51
11:A:912:U:H4'	11:A:913:G:O5'	2.10	0.51
11:A:523:G:H5"	26:P:59:GLY:O	2.10	0.51
11:A:542:A:O2'	11:A:543:C:P	2.67	0.51
11:A:927:C:H2'	11:A:928:U:C6	2.46	0.51
19:I:106:LYS:O	19:I:110:THR:HB	2.10	0.51
30:T:137:ALA:O	30:T:141:GLU:HG2	2.10	0.51
15:E:40:LYS:HA	15:E:43:ARG:NH1	2.25	0.51
19:I:114:ARG:O	19:I:115:THR:OG1	2.26	0.51
20:J:102:ARG:O	20:J:106:ILE:HG22	2.10	0.51
11:A:647:G:H1	11:A:687:G:H1	1.58	0.51
11:A:902:G:O5'	11:A:902:G:H8	1.93	0.51
11:A:229:U:H2'	11:A:230:C:C6	2.46	0.51
11:A:1410:A:H5"	19:I:118:ILE:HD13	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:779:U:OP2	11:A:780:A:H2	1.93	0.51
12:B:27:ARG:HG2	12:B:28:ASN:H	1.75	0.51
3:2:33:PRO:HA	11:A:331:A:H5'	1.92	0.51
18:H:89:TRP:O	18:H:93:LEU:HD22	2.11	0.51
4:3:10:SER:HB3	4:3:43:PHE:O	2.11	0.51
16:F:54:ILE:HA	16:F:57:VAL:HG12	1.92	0.51
11:A:1572:G:H1'	17:G:185:ARG:HH22	1.74	0.51
11:A:1300:A:H5"	15:E:117:THR:CB	2.41	0.51
11:A:1229:G:H1	31:U:47:GLU:HG3	1.75	0.51
11:A:651:G:C2	11:A:684:A:C6	2.98	0.51
11:A:1267:G:H21	11:A:1448:G:C5'	2.22	0.51
11:A:1433:G:C8	24:N:41:GLN:HG2	2.46	0.51
15:E:234:PRO:O	15:E:235:LEU:HB2	2.09	0.51
11:A:1151:A:N3	11:A:1152:A:C8	2.71	0.51
11:A:868:G:H1	11:A:960:U:H3	1.59	0.51
11:A:677:G:H2'	11:A:678:A:H8	1.73	0.51
11:A:458:G:OP2	26:P:105:ARG:NH2	2.43	0.51
11:A:1686:C:C6	11:A:1687:U:C5	2.99	0.51
2:1:26:THR:H	2:1:44:VAL:HG22	1.76	0.51
13:C:105:MET:HG2	13:C:122:VAL:HG21	1.92	0.51
29:S:87:PRO:HD3	29:S:112:LEU:HD22	1.92	0.51
17:G:205:SER:O	17:G:207:THR:N	2.43	0.51
12:B:59:LEU:HD11	36:Z:79:LEU:HD11	1.91	0.51
21:K:25:ASP:N	21:K:55:SER:HB3	2.26	0.51
9:8:50:ILE:O	9:8:54:VAL:HG23	2.11	0.51
24:N:10:HIS:CG	24:N:11:PRO:HD2	2.46	0.51
17:G:69:PHE:HD2	19:I:50:GLU:HG2	1.75	0.51
4:3:131:PHE:O	4:3:133:THR:OG1	2.27	0.51
11:A:542:A:H5"	11:A:544:A:N7	2.25	0.51
8:7:55:VAL:HA	8:7:69:THR:HG23	1.93	0.51
20:J:22:ILE:HD12	20:J:118:VAL:HA	1.93	0.51
10:9:138:ARG:NH2	11:A:1235:C:H2'	2.26	0.51
3:2:76:THR:CG2	3:2:108:PRO:HG2	2.41	0.51
11:A:1458:G:N3	11:A:1458:G:H2'	2.26	0.51
11:A:859:A:C6	25:O:73:ARG:HD3	2.46	0.51
14:D:106:GLU:OE2	14:D:115:LYS:HE2	2.11	0.51
11:A:279:G:H3'	11:A:279:G:H8	1.75	0.50
23:M:27:LYS:O	23:M:29:VAL:N	2.44	0.50
11:A:1381:U:H4'	20:J:59:PRO:HG3	1.93	0.50
14:D:38:ASN:HB3	14:D:40:LYS:H	1.75	0.50
15:E:178:ILE:HB	15:E:185:LYS:HG3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:124:ASN:OD1	5:4:124:ASN:N	2.43	0.50
5:4:119:THR:HB	5:4:143:THR:HG23	1.92	0.50
11:A:882:U:H2'	11:A:883:C:C6	2.46	0.50
30:T:40:SER:OG	30:T:96:ALA:HA	2.11	0.50
11:A:1300:A:H5'	15:E:99:LYS:NZ	2.26	0.50
11:A:503:G:O2'	11:A:504:U:OP1	2.27	0.50
30:T:113:ILE:O	30:T:124:ILE:HD12	2.11	0.50
11:A:446:A:N6	11:A:461:G:H21	2.08	0.50
11:A:1298:U:H1'	15:E:162:CYS:SG	2.51	0.50
11:A:320:U:H3'	11:A:321:C:H5"	1.94	0.50
9:8:71:ILE:HB	9:8:76:ALA:HB2	1.92	0.50
11:A:425:A:H5'	11:A:425:A:C8	2.46	0.50
11:A:713:A:H61	11:A:725:U:H3	1.58	0.50
11:A:1472:C:OP1	17:G:102:ARG:NH2	2.43	0.50
26:P:31:ASN:O	26:P:32:ARG:HB2	2.11	0.50
1:0:60:HIS:CE1	1:0:66:ARG:HH21	2.29	0.50
2:1:15:VAL:HA	2:1:28:VAL:HG22	1.92	0.50
36:Z:71:ARG:HG3	36:Z:83:TRP:CH2	2.46	0.50
11:A:478:A:OP1	34:X:37:ARG:NH1	2.44	0.50
11:A:393:C:H4'	11:A:1673:G:O2'	2.12	0.50
11:A:220:A:H5"	11:A:832:U:H1'	1.93	0.50
11:A:1572:G:H8	17:G:185:ARG:HH12	1.60	0.50
7:6:34:ASP:N	7:6:34:ASP:OD1	2.43	0.50
20:J:51:VAL:HG13	20:J:94:GLU:HB2	1.92	0.50
3:2:136:SER:OG	3:2:137:LYS:N	2.43	0.50
35:Y:28:PHE:CE2	35:Y:104:PRO:HG3	2.46	0.50
1:0:30:GLU:H	1:0:33:GLN:CD	2.15	0.50
1:0:65:LEU:HD11	1:0:93:HIS:HA	1.93	0.50
1:0:92:VAL:HG22	1:0:93:HIS:CD2	2.46	0.50
11:A:734:A:O2'	11:A:735:C:H5'	2.11	0.50
32:V:82:ASP:O	32:V:83:GLN:HB2	2.12	0.50
14:D:163:PRO:C	14:D:165:GLY:H	2.14	0.50
11:A:1410:A:H2'	11:A:1411:A:O4'	2.11	0.50
28:R:29:GLN:HG3	28:R:32:LEU:HB2	1.93	0.50
11:A:1295:G:H5"	12:B:108:THR:CB	2.41	0.50
11:A:1686:C:O2'	11:A:1687:U:O5'	2.30	0.50
32:V:106:THR:O	32:V:109:LEU:HB3	2.10	0.50
5:4:184:LEU:O	5:4:188:LEU:HG	2.12	0.50
15:E:140:ARG:NH2	15:E:226:THR:HG23	2.27	0.50
11:A:336:G:H5'	27:Q:130:PRO:O	2.11	0.50
6:5:85:ARG:O	6:5:86:VAL:HB	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:J:20:ILE:HG13	20:J:95:ALA:O	2.11	0.50
10:9:135:HIS:HB2	10:9:138:ARG:HB3	1.93	0.50
17:G:43:PHE:HA	17:G:68:ILE:O	2.11	0.50
4:3:23:ALA:O	4:3:27:LEU:HG	2.12	0.50
14:D:120:LYS:O	14:D:121:SER:HB2	2.12	0.50
12:B:41:ARG:HA	32:V:105:GLN:HG2	1.86	0.50
11:A:1686:C:C2'	11:A:1687:U:C6	2.79	0.50
11:A:1716:C:O2'	11:A:1717:G:O5'	2.30	0.50
11:A:279:G:C3'	11:A:280:U:H5"	2.28	0.50
4:3:28:GLU:O	4:3:35:LYS:HB2	2.12	0.50
11:A:818:C:N4	11:A:819:G:C6	2.80	0.50
13:C:33:GLY:O	13:C:53:THR:HG23	2.12	0.50
25:O:54:LEU:HB3	25:O:60:VAL:CG2	2.40	0.50
5:4:126:THR:HG22	5:4:136:ARG:HE	1.76	0.50
15:E:106:ASP:N	15:E:106:ASP:OD1	2.44	0.50
31:U:123:VAL:HG11	31:U:126:TRP:HB3	1.94	0.50
15:E:139:ILE:CD1	15:E:191:ALA:HB1	2.42	0.50
23:M:119:ILE:HD11	29:S:110:GLU:HG3	1.93	0.50
11:A:1325:A:OP2	32:V:11:ARG:NH1	2.45	0.50
1:0:82:ARG:NE	22:L:68:ILE:HD13	2.25	0.50
11:A:498:G:H2'	11:A:499:U:C5	2.47	0.50
1:0:71:MET:HE1	1:0:77:ILE:HG22	1.94	0.50
35:Y:58:LYS:C	35:Y:60:GLY:H	2.15	0.50
9:8:46:LYS:HE2	9:8:70:LYS:HD2	1.94	0.50
11:A:789:A:O2'	33:W:106:LYS:NZ	2.43	0.50
27:Q:72:THR:O	27:Q:88:ARG:HD2	2.11	0.50
11:A:1365:C:H5"	19:I:28:LEU:HD23	1.94	0.50
15:E:148:LEU:O	36:Z:4:ASP:HB2	2.12	0.50
23:M:88:ARG:NH2	23:M:112:ASP:OD1	2.44	0.50
16:F:31:GLN:HG2	16:F:39:LEU:HB3	1.92	0.50
1:0:33:GLN:NE2	1:0:78:LEU:HD21	2.27	0.50
27:Q:6:THR:HB	27:Q:9:SER:HB3	1.92	0.50
11:A:533:U:C4'	26:P:33:ALA:HB2	2.39	0.50
4:3:99:LEU:HD12	4:3:116:ARG:HG2	1.92	0.50
11:A:606:A:H4'	11:A:607:G:H5"	1.94	0.50
11:A:707:A:H2'	11:A:708:C:H5"	1.93	0.50
14:D:93:LEU:HA	14:D:96:VAL:CG1	2.38	0.49
12:B:29:VAL:HG13	12:B:150:ASP:HB3	1.93	0.49
20:J:106:ILE:HD12	20:J:108:ILE:HD11	1.93	0.49
12:B:185:ARG:N	36:Z:45:ALA:H	2.09	0.49
11:A:1132:A:OP1	22:L:30:LYS:HE3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:26:LYS:O	3:2:26:LYS:HG3	2.12	0.49
12:B:136:ALA:HB1	12:B:141:ILE:HB	1.94	0.49
31:U:29:LYS:HE2	31:U:100:TRP:NE1	2.27	0.49
29:S:22:LEU:HD21	29:S:109:PRO:HB3	1.94	0.49
30:T:31:PRO:HG3	30:T:103:LYS:HG2	1.94	0.49
33:W:15:PRO:HG2	33:W:18:TRP:CE2	2.46	0.49
13:C:192:PRO:O	13:C:195:SER:HB2	2.11	0.49
11:A:1324:G:C5'	12:B:113:ARG:NH2	2.75	0.49
4:3:35:LYS:HZ2	4:3:39:ARG:HD2	1.76	0.49
8:7:19:GLY:HA2	8:7:68:LEU:HD23	1.93	0.49
29:S:85:ILE:HD11	29:S:116:LEU:HD23	1.93	0.49
4:3:167:GLU:HG3	4:3:170:GLN:OE1	2.12	0.49
13:C:20:GLU:OE2	13:C:76:ARG:NH2	2.44	0.49
11:A:1049:U:H2'	11:A:1050:G:C8	2.47	0.49
9:8:37:GLN:O	9:8:38:HIS:HB3	2.10	0.49
31:U:98:GLY:C	31:U:103:LEU:HD21	2.32	0.49
5:4:185:THR:O	5:4:189:ILE:HG13	2.12	0.49
19:I:25:GLY:H	19:I:63:ILE:HA	1.76	0.49
19:I:112:TYR:OH	19:I:114:ARG:NH2	2.45	0.49
17:G:37:GLN:CD	19:I:53:LEU:HD22	2.32	0.49
11:A:765:G:C6	14:D:149:ARG:HB3	2.48	0.49
1:0:23:LYS:C	1:0:24:ARG:O	2.50	0.49
10:9:120:GLU:HG3	10:9:128:ALA:HB1	1.94	0.49
11:A:1168:U:C2'	11:A:1169:G:H5'	2.41	0.49
18:H:82:LYS:HB2	18:H:85:ASP:OD2	2.12	0.49
11:A:539:G:H8	11:A:539:G:OP2	1.93	0.49
19:I:73:GLY:H	19:I:76:SER:HB3	1.76	0.49
11:A:489:C:H2'	11:A:490:C:C6	2.48	0.49
14:D:95:TYR:O	14:D:99:LEU:N	2.45	0.49
5:4:86:LEU:HB3	5:4:98:THR:OG1	2.11	0.49
5:4:62:LYS:HD2	5:4:91:VAL:HB	1.94	0.49
11:A:1622:G:H2'	11:A:1623:C:C6	2.47	0.49
11:A:190:C:H1'	11:A:191:C:H5'	1.93	0.49
11:A:749:U:H3	11:A:800:U:H3	1.58	0.49
11:A:881:A:H2'	11:A:882:U:O4'	2.13	0.49
17:G:129:PRO:O	17:G:133:VAL:HG23	2.13	0.49
17:G:24:VAL:HG22	17:G:25:LEU:H	1.78	0.49
11:A:501:U:H4'	11:A:502:U:OP1	2.11	0.49
27:Q:97:TYR:O	27:Q:99:ARG:HG2	2.12	0.49
5:4:61:LEU:HG	5:4:64:ARG:HH21	1.77	0.49
16:F:27:HIS:HB2	16:F:43:GLN:CG	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:125:VAL:HG21	5:4:173:THR:HG22	1.94	0.49
11:A:929:A:N6	11:A:930:A:C6	2.80	0.49
11:A:1459:C:O2	29:S:128:HIS:NE2	2.38	0.49
8:7:53:GLY:O	8:7:55:VAL:N	2.39	0.49
7:6:54:VAL:O	7:6:63:LEU:HB2	2.13	0.49
3:2:138:ASN:N	3:2:138:ASN:OD1	2.42	0.49
11:A:194:U:O2'	11:A:195:G:O4'	2.30	0.49
6:5:23:CYS:SG	6:5:74:CYS:HB3	2.52	0.49
12:B:119:ARG:HD2	15:E:241:ASP:OD1	2.12	0.49
20:J:104:THR:HG21	20:J:116:VAL:HG21	1.93	0.49
5:4:56:SER:OG	5:4:59:ASP:OD1	2.29	0.49
11:A:498:G:C4	11:A:499:U:N3	2.81	0.49
22:L:97:ASP:HB2	22:L:100:ASP:OD2	2.12	0.49
3:2:98:LYS:HB3	11:A:329:G:H5"	1.95	0.49
21:K:124:ASP:O	21:K:125:SER:HB2	2.13	0.49
31:U:60:VAL:HG13	31:U:122:VAL:HG22	1.93	0.49
11:A:879:G:O2'	25:O:105:ASN:HB3	2.13	0.49
19:I:16:ALA:HB2	19:I:72:GLY:HA3	1.94	0.49
11:A:1244:A:O2'	11:A:1245:G:OP1	2.29	0.49
8:7:77:ARG:HD3	8:7:84:GLU:HA	1.94	0.49
11:A:1729:C:H5"	11:A:1730:A:OP2	2.13	0.49
28:R:156:VAL:HG22	28:R:169:ILE:HG22	1.95	0.49
1:0:44:ASN:HB3	1:0:46:ARG:NH1	2.28	0.49
12:B:40:ALA:O	32:V:105:GLN:HG3	2.12	0.49
11:A:1300:A:H4'	15:E:86:VAL:CG1	2.42	0.49
23:M:24:GLY:O	23:M:26:ILE:N	2.45	0.49
11:A:1482:C:OP2	11:A:1521:G:N2	2.46	0.49
30:T:53:TRP:HA	30:T:56:LYS:HB2	1.95	0.49
11:A:778:G:H22	26:P:10:ARG:CZ	2.26	0.49
5:4:81:PHE:HA	5:4:106:THR:HG23	1.93	0.49
11:A:1553:G:N2	11:A:1555:A:H3'	2.28	0.49
33:W:163:ASP:O	33:W:164:LEU:HB2	2.11	0.49
4:3:158:ASP:O	4:3:160:GLN:N	2.46	0.49
29:S:81:ARG:HH12	29:S:120:SER:HB3	1.78	0.49
15:E:183:ALA:HB1	15:E:211:LEU:HD21	1.95	0.49
11:A:1152:A:C5	11:A:1627:U:N3	2.81	0.49
11:A:1686:C:O2'	11:A:1687:U:O4'	2.30	0.49
5:4:131:ASP:CG	5:4:180:THR:HG21	2.33	0.49
6:5:79:ILE:HA	6:5:84:VAL:HG21	1.94	0.49
5:4:109:LYS:HD2	5:4:113:MET:HG3	1.94	0.49
12:B:200:ASP:HB2	32:V:85:VAL:CG2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:K:25:ASP:HA	21:K:54:GLU:O	2.12	0.49
8:7:49:LEU:HB3	8:7:55:VAL:CG1	2.42	0.49
23:M:91:ASP:HB3	23:M:95:GLY:H	1.77	0.49
35:Y:126:ASP:OD1	35:Y:127:THR:HG22	2.13	0.49
17:G:21:THR:O	17:G:21:THR:OG1	2.31	0.49
18:H:36:LYS:O	18:H:40:VAL:HG23	2.13	0.49
31:U:33:ARG:O	31:U:37:VAL:HG23	2.13	0.49
11:A:1321:A:O4'	12:B:104:PRO:HG2	2.13	0.49
5:4:61:LEU:H	5:4:61:LEU:HD13	1.77	0.49
6:5:84:VAL:HG13	6:5:85:ARG:H	1.78	0.49
11:A:70:C:H2'	11:A:71:A:O4'	2.12	0.49
5:4:70:LEU:HD11	5:4:79:HIS:HB3	1.95	0.49
10:9:138:ARG:HH22	11:A:1236:A:C1'	2.26	0.49
11:A:393:C:H2'	11:A:394:C:C6	2.48	0.49
18:H:77:PRO:HD2	18:H:79:PHE:CE1	2.47	0.49
8:7:80:LEU:O	8:7:82:LEU:N	2.41	0.49
1:0:88:GLN:NE2	34:X:4:VAL:H	2.11	0.49
11:A:778:G:H22	26:P:10:ARG:HH22	1.57	0.49
11:A:1253:U:H2'	11:A:1254:U:C6	2.48	0.49
28:R:153:GLN:HG2	28:R:202:LEU:HD23	1.95	0.49
17:G:120:ILE:O	17:G:124:LEU:HD12	2.13	0.49
36:Z:40:ASP:HB3	36:Z:46:ILE:HD11	1.94	0.49
11:A:702:G:O6	11:A:737:A:N6	2.45	0.48
10:9:87:UNK:HG2	10:9:87:UNK:O	2.12	0.48
11:A:484:C:N4	11:A:503:G:H22	2.05	0.48
23:M:22:VAL:CG1	23:M:31:ALA:HB1	2.42	0.48
11:A:1156:C:C2'	11:A:1157:A:H5'	2.43	0.48
30:T:52:GLY:HA2	30:T:55:TYR:CD2	2.48	0.48
11:A:1437:U:H5'	13:C:176:LEU:HD23	1.95	0.48
28:R:130:THR:HG22	28:R:145:LEU:HD22	1.94	0.48
5:4:22:ASP:O	5:4:24:PHE:N	2.46	0.48
26:P:15:ASN:OD1	26:P:17:LEU:HD12	2.12	0.48
11:A:1686:C:C5	11:A:1687:U:C5	3.01	0.48
11:A:487:G:H3'	11:A:488:G:C5'	2.43	0.48
11:A:494:U:HO2'	11:A:495:C:P	2.32	0.48
17:G:59:VAL:O	17:G:60:ASP:HB2	2.12	0.48
11:A:717:C:H42	11:A:720:G:N2	2.09	0.48
25:O:27:LYS:CE	25:O:27:LYS:H	2.26	0.48
11:A:196:G:O2'	11:A:197:A:C8	2.66	0.48
11:A:346:G:O2'	27:Q:80:MET:HG2	2.13	0.48
31:U:132:GLU:O	31:U:136:ILE:HG12	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:G:133:VAL:O	17:G:137:ILE:HG12	2.13	0.48
28:R:123:ILE:HG22	28:R:133:VAL:HG22	1.95	0.48
12:B:41:ARG:HA	32:V:105:GLN:HE21	1.77	0.48
3:2:8:ARG:NH1	3:2:21:PHE:HB3	2.28	0.48
5:4:61:LEU:O	5:4:63:GLY:N	2.47	0.48
23:M:32:LEU:O	23:M:38:VAL:HG21	2.13	0.48
13:C:116:ARG:O	13:C:120:TYR:HB2	2.12	0.48
21:K:16:VAL:HG22	21:K:33:LEU:HA	1.95	0.48
11:A:694:U:H2'	11:A:695:U:H5	1.78	0.48
12:B:120:LEU:HD13	12:B:142:PRO:HB2	1.94	0.48
5:4:146:GLN:H	5:4:149:GLN:NE2	2.11	0.48
11:A:730:G:H21	11:A:731:C:H5"	1.78	0.48
8:7:33:GLU:CD	8:7:33:GLU:H	2.16	0.48
29:S:15:HIS:O	29:S:21:ASP:HA	2.12	0.48
28:R:273:ASP:CG	28:R:275:ARG:HH22	2.17	0.48
28:R:40:LYS:HG2	28:R:66:HIS:O	2.14	0.48
11:A:358:U:O2'	11:A:360:A:H5"	2.13	0.48
11:A:130:C:O2'	11:A:131:C:OP1	2.29	0.48
14:D:122:VAL:O	14:D:125:ALA:HB3	2.14	0.48
11:A:209:U:H2'	11:A:210:A:C8	2.49	0.48
1:0:42:LEU:HD11	1:0:58:MET:CE	2.44	0.48
11:A:279:G:H3'	11:A:279:G:C8	2.48	0.48
6:5:36:ILE:HG23	6:5:73:TYR:HB2	1.95	0.48
31:U:29:LYS:HE2	31:U:100:TRP:HE1	1.78	0.48
11:A:680:U:H2'	11:A:681:U:C6	2.49	0.48
29:S:86:VAL:HG23	29:S:87:PRO:HD2	1.96	0.48
13:C:92:GLN:NE2	13:C:92:GLN:O	2.46	0.48
3:2:197:THR:HA	3:2:200:LYS:HB2	1.96	0.48
11:A:1133:A:OP1	22:L:31:LYS:HE2	2.13	0.48
3:2:96:LEU:HD13	3:2:179:CYS:SG	2.53	0.48
23:M:35:ILE:HB	23:M:38:VAL:HG21	1.96	0.48
30:T:126:GLU:CD	30:T:126:GLU:H	2.17	0.48
32:V:13:SER:OG	32:V:54:THR:HG22	2.14	0.48
9:8:70:LYS:HD3	9:8:70:LYS:HA	1.69	0.48
11:A:1202:A:H61	11:A:1457:C:H5"	1.76	0.48
17:G:205:SER:OG	17:G:205:SER:O	2.25	0.48
6:5:7:SER:HB2	6:5:11:ASN:H	1.78	0.48
11:A:1639:C:O2	11:A:1763:A:N1	2.46	0.48
35:Y:45:PHE:HA	35:Y:48:TYR:HD2	1.79	0.48
11:A:1300:A:O3'	15:E:86:VAL:CG2	2.55	0.48
10:9:144:CYS:O	10:9:146:SER:N	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Y:141:ILE:HG21	35:Y:153:VAL:HG13	1.94	0.48
22:L:127:VAL:O	22:L:130:VAL:HG22	2.14	0.48
11:A:782:U:H4'	11:A:783:G:OP2	2.14	0.48
11:A:190:C:O2'	11:A:191:C:H5'	2.14	0.48
11:A:768:C:C6	14:D:143:ILE:HD13	2.49	0.48
28:R:112:SER:CB	28:R:153:GLN:HA	2.43	0.48
27:Q:22:ASN:OD1	27:Q:24:LYS:HB2	2.14	0.48
11:A:1746:A:H2'	11:A:1747:G:O4'	2.13	0.48
11:A:545:A:H4'	11:A:546:U:OP1	2.14	0.48
5:4:157:GLN:NE2	11:A:1046:G:OP1	2.46	0.48
12:B:184:LEU:HB3	36:Z:45:ALA:HB2	1.96	0.48
11:A:992:A:O2'	11:A:1785:U:O2	2.31	0.48
11:A:794:U:O2'	11:A:795:U:O2	2.27	0.48
20:J:48:HIS:CG	20:J:48:HIS:O	2.67	0.48
11:A:287:G:O2'	11:A:288:A:OP2	2.24	0.48
11:A:1244:A:H3'	11:A:1244:A:N3	2.29	0.48
23:M:93:THR:O	29:S:19:GLY:N	2.47	0.48
11:A:507:U:H3'	11:A:507:U:O2	2.13	0.48
11:A:350:U:O2	11:A:352:A:C6	2.66	0.48
11:A:812:A:OP1	11:A:858:G:N2	2.47	0.48
11:A:772:G:OP1	33:W:22:LYS:NZ	2.29	0.48
30:T:45:MET:HE3	30:T:46:PRO:HD2	1.96	0.48
11:A:143:G:C2'	11:A:144:U:H5"	2.44	0.48
23:M:36:LYS:HB3	23:M:105:VAL:HG11	1.96	0.48
11:A:495:C:H3'	11:A:496:G:C4'	2.43	0.48
11:A:1196:A:H1'	11:A:1602:C:O2'	2.13	0.48
11:A:1486:G:H1'	11:A:1592:A:O2'	2.14	0.48
11:A:558:U:H2'	11:A:558:U:O2	2.14	0.48
8:7:12:HIS:CD2	8:7:79:TYR:CD2	3.02	0.48
7:6:61:THR:HG23	7:6:62:ILE:H	1.79	0.48
11:A:823:G:H2'	11:A:824:G:O4'	2.14	0.48
11:A:1347:U:O2	11:A:1516:A:H5'	2.14	0.48
11:A:1316:G:O2'	11:A:1401:A:O2'	2.25	0.48
11:A:114:C:C6	11:A:114:C:H5'	2.49	0.48
19:I:94:GLN:HB2	19:I:102:LYS:HD2	1.96	0.48
1:0:26:LEU:CD1	1:0:102:THR:HG21	2.44	0.48
1:0:46:ARG:HE	34:X:3:LYS:CB	2.26	0.48
26:P:59:GLY:O	26:P:60:PHE:HB2	2.14	0.48
19:I:112:TYR:CZ	19:I:114:ARG:NH2	2.82	0.48
10:9:147:VAL:O	10:9:148:TYR:HB2	2.14	0.48
12:B:69:ASN:HB3	12:B:71:GLU:CD	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:9:143:LYS:HB2	11:A:1253:U:H4'	1.96	0.48
5:4:179:SER:HB3	5:4:183:GLN:CD	2.34	0.48
14:D:91:LYS:O	14:D:92:LYS:HG2	2.13	0.48
15:E:139:ILE:HD11	15:E:191:ALA:HB1	1.96	0.48
36:Z:9:VAL:HG22	36:Z:10:GLU:H	1.79	0.48
6:5:19:LYS:HG3	6:5:20:PRO:HD2	1.96	0.48
17:G:172:ILE:O	17:G:176:THR:HG23	2.14	0.48
35:Y:67:VAL:HG23	35:Y:68:LEU:O	2.13	0.47
35:Y:63:MET:HG2	35:Y:99:GLY:O	2.14	0.47
11:A:1597:A:C8	24:N:14:TYR:CD2	3.02	0.47
32:V:17:ILE:HG12	32:V:58:MET:HE2	1.96	0.47
18:H:105:THR:HG23	18:H:110:ILE:CG1	2.44	0.47
9:8:92:ILE:HG12	9:8:100:ILE:CG2	2.44	0.47
31:U:82:PRO:O	31:U:83:GLU:HB2	2.13	0.47
11:A:526:A:H2'	11:A:527:A:O4'	2.13	0.47
34:X:53:LYS:HG3	34:X:54:ARG:H	1.78	0.47
3:2:66:SER:HB3	3:2:73:SER:OG	2.14	0.47
11:A:192:U:H2'	11:A:192:U:O2	2.13	0.47
23:M:108:LYS:HD2	23:M:108:LYS:HA	1.63	0.47
1:0:88:GLN:HB2	34:X:6:GLY:HA2	1.97	0.47
11:A:499:U:O2'	11:A:500:C:P	2.72	0.47
16:F:30:ILE:CG1	16:F:107:GLY:HA2	2.35	0.47
4:3:30:SER:O	4:3:32:PRO:HD2	2.14	0.47
11:A:992:A:H2	11:A:1012:U:N3	2.06	0.47
23:M:11:PHE:CD1	23:M:59:GLY:HA2	2.49	0.47
11:A:190:C:N4	11:A:196:G:C6	2.82	0.47
11:A:1480:G:H3'	11:A:1481:C:C6	2.49	0.47
24:N:40:ARG:HG2	24:N:41:GLN:OE1	2.14	0.47
11:A:1064:G:H2'	11:A:1065:A:C8	2.49	0.47
11:A:1321:A:C2	12:B:104:PRO:O	2.67	0.47
16:F:26:ILE:HG13	16:F:98:LEU:HD22	1.96	0.47
5:4:181:LEU:O	5:4:182:ALA:C	2.52	0.47
3:2:8:ARG:HD2	3:2:21:PHE:HD1	1.79	0.47
11:A:68:A:O2'	11:A:69:G:OP2	2.25	0.47
5:4:63:GLY:HA2	5:4:88:VAL:O	2.13	0.47
7:6:47:PHE:CD2	25:O:55:ARG:HD2	2.49	0.47
6:5:44:ILE:CD1	6:5:44:ILE:H	2.24	0.47
28:R:221:MET:HG3	28:R:233:THR:HG23	1.94	0.47
9:8:72:GLY:O	9:8:74:SER:N	2.47	0.47
11:A:700:C:H42	11:A:738:G:H1	1.62	0.47
19:I:60:PHE:HA	19:I:63:ILE:HD11	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:S:125:PRO:O	29:S:126:VAL:HB	2.14	0.47
5:4:61:LEU:CD2	5:4:62:LYS:H	2.28	0.47
5:4:62:LYS:O	5:4:88:VAL:HB	2.15	0.47
11:A:72:A:C3'	11:A:73:U:H5"	2.45	0.47
11:A:74:U:HO2'	11:A:75:U:P	2.33	0.47
11:A:781:U:HO2'	11:A:782:U:H6	1.58	0.47
11:A:1617:U:O2'	11:A:1618:C:H5'	2.14	0.47
9:8:54:VAL:HG22	9:8:57:TYR:CE2	2.50	0.47
17:G:133:VAL:HG22	17:G:198:LEU:HD13	1.96	0.47
36:Z:11:LEU:HG	36:Z:11:LEU:H	1.34	0.47
13:C:46:THR:HB	13:C:84:ILE:HG12	1.96	0.47
18:H:53:ILE:HG12	18:H:60:LYS:HB2	1.96	0.47
12:B:124:THR:HG22	12:B:174:TRP:CZ2	2.49	0.47
17:G:36:ALA:HB3	17:G:45:LYS:NZ	2.29	0.47
11:A:1152:A:N6	11:A:1627:U:O4	2.47	0.47
11:A:1299:G:H4'	15:E:99:LYS:HE3	1.96	0.47
11:A:11:A:C2'	11:A:12:U:H5'	2.44	0.47
11:A:132:U:C1'	11:A:133:U:OP2	2.58	0.47
6:5:38:ARG:HH21	6:5:83:ILE:HG13	1.78	0.47
11:A:39:A:OP1	14:D:6:ARG:NH1	2.47	0.47
20:J:65:ILE:HD11	24:N:36:LEU:HD21	1.96	0.47
30:T:52:GLY:HA2	30:T:55:TYR:HD2	1.80	0.47
8:7:1:MET:O	11:A:1258:U:H5'	2.14	0.47
26:P:102:LYS:H	26:P:102:LYS:HD2	1.79	0.47
11:A:1277:G:O2'	13:C:174:HIS:ND1	2.39	0.47
5:4:101:HIS:HD2	5:4:217:LEU:HD22	1.80	0.47
3:2:87:ASN:O	3:2:90:LEU:HB2	2.14	0.47
8:7:26:ASP:OD2	8:7:29:GLN:HG3	2.15	0.47
16:F:86:ALA:HA	16:F:89:CYS:SG	2.55	0.47
11:A:1299:G:H4'	15:E:99:LYS:HE2	1.95	0.47
16:F:61:ASP:OD2	16:F:62:PHE:CD1	2.67	0.47
4:3:71:HIS:CG	4:3:131:PHE:CZ	3.02	0.47
6:5:73:TYR:CZ	6:5:82:ARG:HD2	2.50	0.47
7:6:63:LEU:O	7:6:74:SER:N	2.48	0.47
20:J:117:VAL:HG13	20:J:118:VAL:N	2.30	0.47
9:8:50:ILE:HG22	9:8:51:LEU:HD12	1.96	0.47
31:U:136:ILE:O	31:U:140:PHE:HB2	2.14	0.47
4:3:16:LEU:O	4:3:20:VAL:HG23	2.14	0.47
25:O:11:ILE:O	25:O:11:ILE:HG13	2.15	0.47
11:A:1349:G:N2	11:A:1350:U:C2	2.83	0.47
33:W:98:ASN:HD22	33:W:119:ALA:HB1	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Q:104:HIS:O	27:Q:105:LYS:HG2	2.15	0.47
10:9:127:GLY:O	10:9:129:GLY:N	2.47	0.47
29:S:126:VAL:CG1	29:S:127:ARG:H	2.19	0.47
18:H:10:ALA:HB1	18:H:27:ILE:HD12	1.97	0.47
6:5:38:ARG:NH2	11:A:1798:U:C5	2.83	0.47
11:A:1533:C:P	23:M:27:LYS:HZ1	2.38	0.47
11:A:819:G:C6	11:A:853:G:N1	2.82	0.47
28:R:211:ILE:HG22	28:R:223:TRP:CD1	2.50	0.47
13:C:179:GLN:NE2	13:C:179:GLN:C	2.68	0.47
11:A:1789:G:C8	11:A:1789:G:H5"	2.46	0.47
11:A:894:U:H2'	11:A:895:G:C8	2.49	0.47
8:7:12:HIS:CD2	8:7:79:TYR:HD2	2.33	0.47
11:A:196:G:HO2'	11:A:197:A:H8	1.61	0.47
11:A:1524:A:N3	11:A:1590:G:O2'	2.44	0.47
11:A:1071:U:H2'	11:A:1072:C:H6	1.79	0.47
30:T:5:SER:HG	30:T:66:TYR:HH	1.62	0.47
5:4:179:SER:HB3	5:4:183:GLN:NE2	2.30	0.47
33:W:42:LEU:HD12	33:W:109:PHE:CB	2.45	0.47
2:1:44:VAL:HA	17:G:161:ASP:O	2.15	0.47
18:H:79:PHE:HD2	27:Q:98:ASN:HD22	1.60	0.47
8:7:33:GLU:OE1	8:7:33:GLU:N	2.47	0.47
12:B:140:ASN:HD21	36:Z:29:HIS:HA	1.80	0.47
26:P:84:LYS:HD2	26:P:85:PHE:CE1	2.50	0.47
23:M:109:LEU:HG	23:M:113:LEU:HD11	1.96	0.47
18:H:111:MET:HE1	18:H:116:ALA:HA	1.95	0.47
8:7:25:LYS:HD3	8:7:59:PHE:CZ	2.50	0.47
5:4:30:PHE:CE1	5:4:96:LEU:HB3	2.50	0.47
11:A:920:U:H2'	11:A:921:U:O4'	2.15	0.47
13:C:21:LEU:HD22	13:C:25:PHE:CE2	2.50	0.47
11:A:1366:U:O2'	30:T:7:ARG:HD2	2.14	0.47
11:A:1152:A:C2	11:A:1627:U:C5	3.02	0.47
11:A:702:G:C6	11:A:737:A:C6	3.03	0.47
12:B:52:LYS:HB3	36:Z:82:VAL:HG22	1.97	0.47
11:A:131:C:HO2'	11:A:132:U:P	2.33	0.47
14:D:175:ARG:HD3	14:D:179:ARG:HH11	1.78	0.47
11:A:538:A:C8	11:A:543:C:C4	3.03	0.47
7:6:47:PHE:CD2	7:6:49:HIS:O	2.68	0.47
11:A:823:G:H2'	11:A:824:G:C8	2.49	0.47
5:4:117:TRP:NE1	5:4:152:ARG:CZ	2.77	0.47
31:U:66:VAL:HG11	31:U:71:ILE:HG21	1.97	0.47
18:H:23:ARG:H	18:H:24:GLN:NE2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:I:123:ARG:HG3	19:I:124:PRO:HD2	1.96	0.47
11:A:1351:G:C2	11:A:1375:A:C2	3.02	0.47
7:6:56:CYS:SG	7:6:57:GLU:N	2.87	0.47
22:L:50:LYS:HD3	22:L:101:GLU:HG2	1.97	0.47
11:A:1477:G:H2'	11:A:1478:G:C8	2.50	0.47
11:A:1626:U:C2'	11:A:1627:U:P	3.03	0.47
30:T:118:PRO:C	30:T:120:GLY:H	2.18	0.47
11:A:840:U:O2'	11:A:841:U:H5"	2.15	0.47
18:H:7:LEU:HD22	18:H:11:LEU:HG	1.97	0.47
11:A:239:C:H3'	11:A:240:U:O4'	2.15	0.47
33:W:42:LEU:HD23	33:W:46:VAL:HB	1.97	0.47
11:A:539:G:C8	11:A:539:G:OP2	2.68	0.47
11:A:629:U:OP1	25:O:127:ARG:NH2	2.47	0.47
11:A:372:G:H1'	11:A:612:U:O2	2.14	0.47
11:A:1715:G:C5	11:A:1716:C:C5	3.03	0.47
19:I:113:ASP:CG	19:I:114:ARG:N	2.66	0.47
19:I:47:LYS:HZ1	19:I:114:ARG:CD	2.26	0.47
20:J:106:ILE:C	20:J:108:ILE:H	2.19	0.47
4:3:14:THR:HG23	4:3:15:GLU:H	1.80	0.47
16:F:93:ILE:HG13	16:F:94:SER:N	2.29	0.47
11:A:78:A:N3	35:Y:175:ILE:HG12	2.29	0.47
11:A:1509:C:H2'	11:A:1510:U:O4'	2.14	0.47
11:A:258:C:N4	11:A:259:U:O4	2.48	0.47
11:A:909:U:H2'	11:A:910:C:H6	1.80	0.47
11:A:1280:C:H2'	11:A:1281:G:H8	1.80	0.47
1:0:88:GLN:CG	34:X:5:HIS:CA	2.93	0.46
5:4:71:ALA:C	5:4:73:LEU:H	2.19	0.46
6:5:84:VAL:HG13	6:5:85:ARG:N	2.30	0.46
23:M:22:VAL:HG13	23:M:31:ALA:HB1	1.96	0.46
6:5:10:ARG:HB3	6:5:34:LYS:HA	1.97	0.46
9:8:42:LEU:O	9:8:46:LYS:HB2	2.16	0.46
11:A:710:U:HO2'	11:A:729:G:H1	1.63	0.46
11:A:269:G:C6	11:A:287:G:C6	3.02	0.46
23:M:108:LYS:HE3	23:M:111:ASP:OD2	2.15	0.46
11:A:705:U:H4'	11:A:705:U:OP1	2.14	0.46
11:A:1786:G:OP1	21:K:136:ARG:NH2	2.44	0.46
27:Q:53:TYR:CD1	27:Q:113:PRO:HG2	2.50	0.46
19:I:47:LYS:HZ1	19:I:114:ARG:NH1	2.13	0.46
2:1:12:VAL:HA	2:1:30:VAL:HG12	1.97	0.46
11:A:542:A:H8	11:A:542:A:HO2'	1.62	0.46
27:Q:5:LEU:O	27:Q:7:VAL:N	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:E:173:PRO:O	15:E:176:SER:OG	2.27	0.46
13:C:133:GLY:HA3	13:C:156:PHE:H	1.79	0.46
11:A:1555:A:P	29:S:47:ARG:HH11	2.38	0.46
11:A:192:U:O2'	11:A:193:U:O4'	2.33	0.46
36:Z:80:LYS:NZ	36:Z:80:LYS:HB3	2.30	0.46
13:C:168:ILE:O	13:C:168:ILE:HD12	2.15	0.46
28:R:149:ASP:HB2	28:R:175:ASP:HB3	1.97	0.46
33:W:196:VAL:N	33:W:209:HIS:O	2.43	0.46
11:A:1629:G:H2'	11:A:1630:U:C6	2.51	0.46
11:A:1629:G:H2'	11:A:1630:U:H6	1.80	0.46
15:E:214:ALA:O	15:E:218:ILE:HG13	2.14	0.46
11:A:1004:U:H4'	11:A:1005:A:OP2	2.15	0.46
12:B:33:GLN:C	12:B:34:GLU:HG2	2.36	0.46
17:G:64:VAL:HG12	17:G:65:ARG:HD3	1.97	0.46
12:B:163:ASN:C	12:B:165:ARG:H	2.19	0.46
1:0:103:LEU:O	1:0:106:GLN:HG2	2.15	0.46
15:E:53:ILE:HG23	15:E:56:ILE:HD12	1.98	0.46
11:A:1459:C:N4	23:M:139:LYS:HG3	2.30	0.46
11:A:747:C:O2'	18:H:80:ASN:ND2	2.47	0.46
11:A:927:C:H1'	21:K:125:SER:CB	2.44	0.46
6:5:18:VAL:O	6:5:19:LYS:HB2	2.16	0.46
13:C:84:ILE:HD13	13:C:85:VAL:H	1.79	0.46
5:4:87:ARG:HE	5:4:87:ARG:HB3	1.49	0.46
12:B:88:LYS:HE2	12:B:88:LYS:HA	1.97	0.46
8:7:71:GLU:H	8:7:71:GLU:HG2	1.46	0.46
11:A:1363:U:H2'	11:A:1363:U:O2	2.16	0.46
11:A:1562:G:OP1	30:T:89:ARG:NH2	2.42	0.46
28:R:13:LEU:HB2	28:R:310:ILE:HB	1.97	0.46
11:A:1396:U:H2'	11:A:1397:U:C6	2.51	0.46
4:3:133:THR:HG21	4:3:162:ILE:HD11	1.96	0.46
11:A:544:A:H5"	11:A:545:A:OP2	2.15	0.46
6:5:85:ARG:HA	6:5:85:ARG:HD3	1.78	0.46
11:A:1450:U:H2'	11:A:1451:C:C6	2.50	0.46
28:R:133:VAL:HB	28:R:142:ALA:HB3	1.96	0.46
17:G:124:LEU:O	17:G:125:THR:OG1	2.29	0.46
12:B:76:ILE:O	12:B:124:THR:HG23	2.15	0.46
19:I:36:ILE:HG12	19:I:36:ILE:O	2.15	0.46
32:V:115:LEU:HD13	32:V:116:LYS:H	1.80	0.46
1:0:42:LEU:CD1	1:0:58:MET:SD	3.03	0.46
14:D:149:ARG:HG2	14:D:149:ARG:H	1.25	0.46
11:A:918:U:H2'	11:A:919:A:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1231:U:O5'	11:A:1259:U:H1'	2.14	0.46
12:B:71:GLU:HA	12:B:95:ALA:N	2.31	0.46
11:A:1317:C:H2'	11:A:1318:G:O4'	2.14	0.46
35:Y:78:THR:HG22	35:Y:79:LYS:H	1.80	0.46
22:L:33:LEU:HD23	22:L:33:LEU:HA	1.70	0.46
11:A:1194:A:H2'	11:A:1195:C:H5'	1.98	0.46
12:B:41:ARG:HE	12:B:45:VAL:CG2	2.29	0.46
1:0:60:HIS:CD2	22:L:60:GLU:OE1	2.69	0.46
14:D:60:LEU:HD23	14:D:93:LEU:HD11	1.98	0.46
16:F:30:ILE:HD13	16:F:85:ARG:NH1	2.30	0.46
11:A:1681:A:H2	11:A:1720:G:H21	1.64	0.46
25:O:114:ARG:HD3	25:O:114:ARG:HA	1.68	0.46
7:6:63:LEU:HD23	7:6:63:LEU:HA	1.72	0.46
3:2:138:ASN:HD22	11:A:197:A:H61	1.63	0.46
3:2:66:SER:HB3	3:2:73:SER:CB	2.46	0.46
11:A:77:U:H4'	11:A:78:A:O5'	2.15	0.46
7:6:66:PRO:HB2	11:A:871:G:O2'	2.16	0.46
11:A:1698:N:O2'	11:A:1699:N:P	2.74	0.46
32:V:113:LEU:HG	32:V:114:GLY:N	2.31	0.46
23:M:41:ARG:NH1	30:T:38:LYS:HG3	2.30	0.46
1:0:55:ASN:HD22	1:0:57:ARG:NH1	2.13	0.46
11:A:1321:A:C4	12:B:104:PRO:HB2	2.51	0.46
11:A:1301:U:H5"	15:E:97:ARG:HH12	1.12	0.46
5:4:38:PHE:HB2	5:4:39:GLU:H	1.47	0.46
28:R:43:ILE:HA	28:R:59:ARG:O	2.16	0.46
3:2:141:ARG:NH2	11:A:195:G:O6	2.34	0.46
11:A:768:C:C2	14:D:143:ILE:HD13	2.49	0.46
17:G:100:ASN:O	17:G:102:ARG:N	2.48	0.46
31:U:45:LEU:O	31:U:49:THR:HG23	2.15	0.46
33:W:32:SER:HB2	33:W:83:PRO:HD3	1.96	0.46
11:A:233:C:HO2'	11:A:234:G:P	2.39	0.46
13:C:216:PRO:HB2	13:C:217:ILE:H	1.59	0.46
29:S:20:VAL:HG13	29:S:24:LYS:HD2	1.98	0.46
12:B:105:GLY:O	12:B:108:THR:O	2.34	0.46
12:B:39:ASN:HB3	32:V:105:GLN:HB3	1.98	0.46
16:F:69:VAL:CB	16:F:79:GLN:NE2	2.73	0.46
35:Y:153:VAL:HG12	35:Y:154:ARG:N	2.31	0.46
11:A:1558:U:H3'	11:A:1559:A:H4'	1.98	0.46
14:D:117:GLY:C	14:D:119:ALA:H	2.17	0.46
21:K:17:ALA:HB3	21:K:81:VAL:HB	1.96	0.46
11:A:711:U:C1'	11:A:712:G:H5'	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:R:44:SER:OG	28:R:59:ARG:HB2	2.16	0.46
11:A:1082:C:H2'	11:A:1083:G:H5'	1.98	0.46
9:8:55:PRO:C	9:8:57:TYR:H	2.19	0.46
3:2:66:SER:HA	3:2:73:SER:HA	1.98	0.46
35:Y:211:LEU:O	35:Y:215:ARG:HB2	2.16	0.46
11:A:25:C:OP2	11:A:26:A:H2'	2.15	0.46
11:A:499:U:O2'	11:A:500:C:OP1	2.24	0.46
11:A:485:A:H2'	11:A:486:G:O4'	2.15	0.46
3:2:8:ARG:C	3:2:9:HIS:O	2.53	0.46
9:8:73:GLY:O	9:8:77:ARG:NH1	2.49	0.46
2:1:22:ARG:O	11:A:1617:U:H1'	2.16	0.46
18:H:37:PHE:CE2	18:H:103:ILE:HD12	2.50	0.46
11:A:149:C:OP1	26:P:121:THR:OG1	2.26	0.46
22:L:107:PHE:CD2	22:L:114:LYS:HB2	2.51	0.46
33:W:163:ASP:HB3	33:W:166:SER:O	2.16	0.46
11:A:1228:G:OP2	31:U:44:GLY:HA2	2.16	0.46
11:A:505:A:H2'	11:A:505:A:N3	2.30	0.46
5:4:107:THR:OG1	5:4:108:ASP:N	2.49	0.46
3:2:81:VAL:HG12	3:2:91:VAL:HG22	1.98	0.46
14:D:14:THR:HA	14:D:15:PRO:HD2	1.69	0.46
11:A:1299:G:C3'	15:E:99:LYS:HE3	2.46	0.46
16:F:61:ASP:OD2	16:F:62:PHE:CE1	2.69	0.46
32:V:44:LYS:HE2	32:V:44:LYS:HB2	1.64	0.46
21:K:25:ASP:OD1	21:K:26:THR:N	2.44	0.46
11:A:1783:C:H2'	11:A:1784:C:C6	2.49	0.46
28:R:91:LEU:O	28:R:100:TYR:N	2.42	0.46
11:A:507:U:H2'	11:A:508:U:O5'	2.16	0.46
23:M:80:LYS:HD2	23:M:80:LYS:HA	1.54	0.46
25:O:99:ARG:O	25:O:103:GLU:HG2	2.16	0.46
11:A:124:A:H1'	33:W:146:THR:HG21	1.98	0.46
12:B:108:THR:HG23	12:B:135:GLU:OE2	2.16	0.45
12:B:39:ASN:HB3	32:V:105:GLN:CB	2.46	0.45
16:F:62:PHE:CZ	16:F:87:LYS:CG	2.98	0.45
14:D:118:LEU:HG	14:D:158:PHE:CZ	2.51	0.45
4:3:159:VAL:O	4:3:162:ILE:HG13	2.16	0.45
28:R:43:ILE:HD13	28:R:60:SER:HA	1.99	0.45
2:1:46:GLY:HA3	17:G:166:ARG:HB2	1.98	0.45
11:A:287:G:O2'	11:A:288:A:P	2.74	0.45
33:W:42:LEU:HD22	33:W:47:PHE:HB2	1.98	0.45
12:B:140:ASN:ND2	36:Z:29:HIS:HA	2.30	0.45
11:A:1111:G:C2'	11:A:1112:G:H5'	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1138:A:H2'	11:A:1139:A:C8	2.51	0.45
29:S:34:VAL:HG21	29:S:45:PHE:HB2	1.99	0.45
16:F:98:LEU:HD12	16:F:98:LEU:HA	1.75	0.45
35:Y:64:LYS:O	35:Y:67:VAL:HG22	2.17	0.45
11:A:1541:G:C6	11:A:1542:G:N1	2.84	0.45
11:A:417:A:H5'	11:A:418:G:C5	2.50	0.45
12:B:71:GLU:N	12:B:71:GLU:OE1	2.37	0.45
17:G:97:LEU:HD23	17:G:97:LEU:HA	1.79	0.45
11:A:240:U:H4'	11:A:240:U:OP1	2.16	0.45
33:W:153:ASN:O	33:W:174:LYS:NZ	2.40	0.45
11:A:725:U:H2'	11:A:726:C:O4'	2.16	0.45
28:R:40:LYS:HA	28:R:68:VAL:HG23	1.98	0.45
4:3:22:GLN:HA	4:3:25:VAL:HG23	1.99	0.45
18:H:25:VAL:O	18:H:62:VAL:HA	2.16	0.45
11:A:1295:G:OP1	12:B:108:THR:CB	2.39	0.45
11:A:1060:U:H5"	11:A:1061:A:OP2	2.16	0.45
14:D:83:VAL:HG23	14:D:85:VAL:HG23	1.99	0.45
35:Y:63:MET:HE2	35:Y:106:LEU:HD22	1.98	0.45
5:4:110:LEU:HA	5:4:113:MET:HB2	1.98	0.45
2:1:49:ARG:HG2	2:1:52:ASP:OD1	2.16	0.45
11:A:417:A:H4'	11:A:418:G:O5'	2.17	0.45
11:A:381:C:H1'	11:A:756:A:C2	2.51	0.45
30:T:124:ILE:HG13	30:T:125:SER:O	2.16	0.45
11:A:273:G:H1	11:A:283:U:H3	1.65	0.45
26:P:35:VAL:O	26:P:36:SER:HB3	2.16	0.45
5:4:101:HIS:O	5:4:217:LEU:HD13	2.17	0.45
18:H:17:ALA:HB2	18:H:25:VAL:HG13	1.97	0.45
20:J:43:LYS:HA	20:J:43:LYS:HD2	1.52	0.45
4:3:173:TYR:HE2	4:3:179:LYS:HB2	1.80	0.45
35:Y:4:ASN:HA	35:Y:15:THR:HG22	1.98	0.45
11:A:960:U:H2'	11:A:961:U:H6	1.81	0.45
11:A:915:A:H5'	11:A:916:U:OP2	2.17	0.45
9:8:59:TYR:HD1	9:8:60:VAL:N	2.13	0.45
11:A:795:U:C5	11:A:796:A:C8	3.04	0.45
3:2:29:LEU:C	3:2:29:LEU:HD23	2.36	0.45
11:A:1166:A:H2'	11:A:1167:G:O4'	2.17	0.45
11:A:767:U:H6	14:D:141:VAL:HA	1.81	0.45
32:V:81:LYS:HB2	32:V:81:LYS:HE3	1.73	0.45
19:I:107:LYS:O	19:I:111:SER:HB2	2.16	0.45
10:9:131:PHE:HE2	31:U:50:LYS:HZ1	1.60	0.45
3:2:8:ARG:NH1	3:2:19:ALA:O	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:66:U:H5'	35:Y:173:PRO:HA	1.98	0.45
11:A:72:A:C2	11:A:73:U:C4	3.05	0.45
11:A:1200:G:H4'	11:A:1201:G:C5'	2.45	0.45
14:D:163:PRO:HG2	14:D:164:PHE:CD2	2.51	0.45
11:A:1281:G:H2'	11:A:1282:U:H6	1.82	0.45
11:A:861:U:H5'	11:A:862:A:OP2	2.16	0.45
11:A:296:U:H2'	11:A:297:U:C6	2.52	0.45
32:V:106:THR:O	32:V:110:VAL:HG23	2.17	0.45
5:4:180:THR:HB	5:4:181:LEU:HD22	1.98	0.45
20:J:27:THR:HB	20:J:88:LYS:CG	2.47	0.45
11:A:491:C:H42	11:A:496:G:H1	1.63	0.45
12:B:84:ARG:HH21	32:V:82:ASP:CG	2.20	0.45
14:D:174:ARG:HA	14:D:174:ARG:HE	1.81	0.45
33:W:19:LEU:HD11	33:W:108:ARG:HD2	1.99	0.45
11:A:779:U:O2'	11:A:780:A:H5"	2.16	0.45
22:L:107:PHE:HA	22:L:107:PHE:HD1	1.68	0.45
13:C:84:ILE:HD13	13:C:85:VAL:N	2.32	0.45
11:A:878:G:O2'	25:O:108:ASP:OD1	2.26	0.45
22:L:40:SER:HB2	22:L:41:SER:H	1.58	0.45
11:A:595:G:H2'	11:A:596:C:C6	2.52	0.45
11:A:1151:A:N9	11:A:1152:A:H5'	2.32	0.45
12:B:131:GLN:O	12:B:135:GLU:HB2	2.17	0.45
16:F:31:GLN:HG3	16:F:39:LEU:HB3	1.97	0.45
17:G:109:LYS:O	17:G:113:ILE:HG13	2.17	0.45
35:Y:70:PRO:O	35:Y:98:ARG:NH2	2.42	0.45
35:Y:137:ARG:HD3	35:Y:177:ARG:HE	1.80	0.45
11:A:1519:U:H2'	11:A:1520:U:C5	2.52	0.45
5:4:205:PHE:HA	5:4:206:PRO:HD2	1.71	0.45
22:L:108:GLY:O	22:L:109:ARG:HG2	2.16	0.45
11:A:196:G:O2'	11:A:197:A:OP2	2.34	0.45
11:A:1612:U:C2'	11:A:1613:U:H5'	2.46	0.45
18:H:55:ASP:C	18:H:57:ARG:H	2.20	0.45
11:A:231:U:O2'	11:A:232:U:H5"	2.17	0.45
12:B:120:LEU:HD12	12:B:142:PRO:O	2.17	0.45
11:A:1402:G:OP1	32:V:10:LYS:NZ	2.49	0.45
11:A:1039:A:O2'	11:A:1040:G:P	2.74	0.45
29:S:22:LEU:HD13	29:S:26:LEU:HD11	1.99	0.45
12:B:124:THR:HG22	12:B:174:TRP:HZ2	1.81	0.45
35:Y:211:LEU:HD11	35:Y:215:ARG:NH2	2.32	0.45
31:U:84:ASN:O	31:U:86:VAL:HG22	2.17	0.45
1:0:88:GLN:CG	34:X:5:HIS:CB	2.94	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:489:C:H6	11:A:489:C:O5'	1.99	0.45
11:A:702:G:OP1	11:A:702:G:H4'	2.17	0.45
11:A:281:G:H2'	11:A:282:C:C6	2.52	0.45
15:E:140:ARG:HB3	15:E:221:THR:HB	1.99	0.45
11:A:66:U:OP1	35:Y:136:LYS:NZ	2.41	0.45
36:Z:71:ARG:HG3	36:Z:83:TRP:CZ2	2.52	0.45
11:A:600:U:H1'	22:L:47:SER:HB3	1.99	0.45
30:T:6:VAL:O	30:T:9:VAL:N	2.39	0.45
11:A:1552:U:H2'	11:A:1553:G:O4'	2.16	0.45
11:A:767:U:C5	14:D:143:ILE:HD12	2.52	0.45
10:9:108:VAL:HB	10:9:114:VAL:HG22	1.98	0.45
17:G:187:ILE:HD12	17:G:187:ILE:H	1.81	0.45
27:Q:91:LEU:HD23	27:Q:91:LEU:HA	1.80	0.45
25:O:115:LEU:O	25:O:119:GLU:HG3	2.16	0.45
11:A:616:G:C2	11:A:622:A:N7	2.84	0.45
11:A:900:A:OP1	21:K:43:THR:OG1	2.20	0.45
17:G:30:PRO:O	17:G:33:VAL:HB	2.16	0.45
5:4:65:VAL:O	21:K:34:SER:HA	2.16	0.45
20:J:82:TYR:HB3	24:N:52:PHE:HB3	1.99	0.45
11:A:1151:A:H2'	11:A:1152:A:H5'	0.46	0.45
1:0:85:GLN:H	34:X:8:LEU:HG	1.82	0.45
11:A:1586:A:H1'	11:A:1611:A:N6	2.32	0.45
11:A:139:C:H4'	11:A:140:A:O5'	2.17	0.45
17:G:25:LEU:HB2	19:I:27:GLY:HA3	1.98	0.45
4:3:39:ARG:N	4:3:40:PRO:HD2	2.32	0.45
30:T:49:ASP:OD2	30:T:53:TRP:N	2.48	0.45
33:W:212:ASP:OD1	33:W:214:LEU:N	2.49	0.45
12:B:142:PRO:HG3	36:Z:32:VAL:HG13	1.99	0.45
11:A:1433:G:H22	24:N:45:GLU:CD	2.20	0.45
22:L:41:SER:HA	22:L:42:PRO:HD3	1.75	0.45
25:O:46:THR:HG23	25:O:49:GLN:OE1	2.17	0.45
14:D:132:ARG:HH11	14:D:132:ARG:HG3	1.82	0.45
7:6:67:THR:HB	7:6:68:GLY:H	1.58	0.45
11:A:1225:U:O2	11:A:1230:A:H4'	2.16	0.45
11:A:1051:G:O2'	11:A:1052:U:P	2.75	0.45
18:H:90:THR:HB	18:H:94:LEU:HD12	1.98	0.45
13:C:11:LEU:HD12	20:J:86:ILE:HG12	1.98	0.45
35:Y:2:LYS:HB3	35:Y:108:VAL:HG22	1.99	0.45
6:5:50:VAL:O	6:5:53:LEU:HB3	2.16	0.45
11:A:1578:U:O2'	11:A:1579:U:H5'	2.17	0.45
12:B:175:TYR:CD2	12:B:199:PRO:HA	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:348:U:OP1	27:Q:85:VAL:HG11	2.17	0.45
14:D:85:VAL:HG12	14:D:99:LEU:HD11	1.98	0.45
14:D:108:ARG:HH11	14:D:110:GLN:HG2	1.82	0.45
12:B:52:LYS:NZ	36:Z:82:VAL:O	2.35	0.45
32:V:23:LYS:HB3	32:V:34:LEU:HD11	1.99	0.45
11:A:1231:U:C4	11:A:1255:G:N2	2.85	0.45
36:Z:71:ARG:HB2	36:Z:83:TRP:CE2	2.51	0.45
6:5:38:ARG:NH2	6:5:83:ILE:HG21	2.32	0.45
11:A:416:A:H4'	11:A:417:A:OP2	2.17	0.45
6:5:5:ARG:HG2	11:A:1796:C:C2	2.52	0.45
11:A:1171:A:H2'	11:A:1172:G:C8	2.52	0.45
5:4:183:GLN:O	5:4:187:LYS:HG3	2.17	0.45
11:A:1217:A:C8	11:A:1217:A:H5'	2.51	0.45
11:A:730:G:H2'	11:A:730:G:N3	2.31	0.45
8:7:25:LYS:HD3	8:7:59:PHE:HZ	1.81	0.45
11:A:1111:G:H2'	11:A:1112:G:H5'	2.00	0.45
16:F:73:GLU:O	16:F:73:GLU:HG3	2.16	0.45
11:A:156:A:H2'	11:A:157:A:O4'	2.17	0.45
11:A:260:U:H5'	11:A:261:U:H5"	1.98	0.45
22:L:134:ALA:HB1	22:L:140:LYS:HB2	1.98	0.45
11:A:1686:C:C2	11:A:1687:U:N1	2.85	0.44
5:4:229:MET:HA	5:4:232:HIS:CE1	2.52	0.44
35:Y:98:ARG:HD3	35:Y:99:GLY:O	2.17	0.44
5:4:110:LEU:CD2	5:4:213:ARG:HD2	2.46	0.44
11:A:782:U:C4'	11:A:783:G:OP2	2.64	0.44
23:M:11:PHE:C	23:M:11:PHE:CD1	2.90	0.44
4:3:12:ALA:HB3	4:3:13:PRO:HD3	1.98	0.44
18:H:78:ARG:CD	18:H:126:LEU:HD23	2.47	0.44
30:T:14:PHE:CZ	30:T:132:LEU:HD23	2.50	0.44
9:8:90:LYS:HE2	9:8:90:LYS:HB3	1.74	0.44
8:7:24:LYS:HB3	8:7:24:LYS:HE2	1.74	0.44
26:P:29:HIS:CE1	26:P:68:LYS:N	2.85	0.44
11:A:579:A:N1	13:C:143:ARG:HA	2.31	0.44
17:G:25:LEU:H	17:G:25:LEU:HD22	1.82	0.44
32:V:24:LEU:O	32:V:25:THR:HG23	2.18	0.44
14:D:129:ILE:HG12	14:D:134:ILE:HD12	2.00	0.44
11:A:277:U:H2'	11:A:278:U:OP1	2.17	0.44
11:A:47:A:N1	11:A:386:G:H1'	2.32	0.44
11:A:413:U:H2'	11:A:414:C:C6	2.52	0.44
9:8:71:ILE:HG13	9:8:71:ILE:H	1.64	0.44
7:6:25:VAL:HG13	18:H:55:ASP:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1617:U:H2'	11:A:1618:C:C6	2.52	0.44
11:A:694:U:H2'	11:A:695:U:C5	2.51	0.44
11:A:707:A:H2	11:A:731:C:H2'	1.81	0.44
13:C:57:ASP:OD1	13:C:57:ASP:N	2.50	0.44
28:R:42:LEU:HB2	28:R:61:PHE:HB2	1.98	0.44
11:A:1727:G:H2'	11:A:1728:A:C8	2.51	0.44
11:A:1057:U:H1'	11:A:1058:U:H2'	1.99	0.44
11:A:477:A:N7	11:A:538:A:N1	2.66	0.44
23:M:29:VAL:O	23:M:43:SER:OG	2.29	0.44
28:R:211:ILE:HG22	28:R:223:TRP:HD1	1.83	0.44
11:A:729:G:N3	11:A:729:G:H2'	2.33	0.44
28:R:16:HIS:CD2	28:R:20:VAL:HG22	2.52	0.44
20:J:50:LEU:CD2	20:J:95:ALA:HB2	2.47	0.44
9:8:54:VAL:HG13	9:8:57:TYR:HD2	1.81	0.44
11:A:1165:G:C6	11:A:1166:A:C6	3.06	0.44
4:3:16:LEU:HD22	4:3:58:LEU:HD21	1.98	0.44
11:A:981:U:C2'	11:A:982:U:H5'	2.47	0.44
35:Y:163:THR:HA	35:Y:168:THR:HA	1.98	0.44
11:A:1256:A:H4'	11:A:1257:U:O5'	2.17	0.44
25:O:142:GLU:HG3	25:O:145:THR:HG23	1.99	0.44
11:A:1393:C:H2'	11:A:1394:G:O4'	2.17	0.44
35:Y:73:ILE:HD12	35:Y:75:LEU:HD21	1.98	0.44
11:A:1321:A:N3	12:B:104:PRO:O	2.51	0.44
12:B:110:TYR:N	12:B:110:TYR:CD1	2.80	0.44
4:3:46:ILE:HD11	4:3:60:ILE:HG12	1.98	0.44
35:Y:72:ARG:HG2	35:Y:98:ARG:HA	1.99	0.44
15:E:140:ARG:NH2	15:E:229:LEU:HD22	2.32	0.44
11:A:57:G:OP1	26:P:112:LYS:HE3	2.17	0.44
12:B:202:TYR:O	12:B:203:PHE:CG	2.70	0.44
11:A:1196:A:OP1	11:A:1196:A:H3'	2.17	0.44
24:N:19:ARG:HD2	24:N:32:ARG:HD2	1.99	0.44
30:T:52:GLY:C	30:T:54:PHE:H	2.15	0.44
28:R:201:THR:HG21	28:R:242:SER:HA	1.98	0.44
33:W:180:LEU:HD22	33:W:192:ILE:HG22	1.99	0.44
18:H:83:ILE:HG13	18:H:117:ARG:HH12	1.80	0.44
2:1:16:LEU:HB2	2:1:27:GLN:HB2	2.00	0.44
22:L:144:ARG:H	22:L:144:ARG:HG3	1.66	0.44
28:R:147:HIS:CE1	28:R:179:LYS:HD2	2.52	0.44
13:C:132:LYS:HB3	13:C:189:MET:HG3	1.99	0.44
3:2:14:THR:HG21	11:A:353:A:O3'	2.17	0.44
12:B:20:ALA:HB3	12:B:22:THR:HG23	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:105:A:H2'	11:A:106:U:O4'	2.17	0.44
22:L:88:PRO:O	22:L:89:ASN:HB2	2.17	0.44
11:A:1300:A:C5'	15:E:99:LYS:HG3	2.47	0.44
14:D:109:LEU:HD22	14:D:113:VAL:HG23	1.98	0.44
6:5:37:LYS:C	6:5:38:ARG:HD2	2.38	0.44
11:A:1536:G:C6	11:A:1538:U:H1'	2.52	0.44
30:T:65:ILE:HG23	30:T:71:VAL:HG22	1.99	0.44
11:A:1316:G:H2'	11:A:1317:C:H6	1.81	0.44
7:6:15:GLU:OE2	7:6:24:LEU:N	2.50	0.44
20:J:31:VAL:O	20:J:35:GLU:HB2	2.18	0.44
19:I:47:LYS:NZ	19:I:114:ARG:HG2	2.32	0.44
11:A:501:U:H2'	11:A:502:U:C6	2.51	0.44
3:2:9:HIS:O	3:2:10:LYS:CB	2.64	0.44
11:A:492:A:H2'	11:A:494:U:H5"	1.98	0.44
23:M:26:ILE:CD1	23:M:30:TYR:HB2	2.48	0.44
11:A:71:A:O3'	11:A:72:A:H4'	2.17	0.44
8:7:29:GLN:O	8:7:30:ALA:HB3	2.18	0.44
27:Q:131:ILE:HA	27:Q:131:ILE:HD13	1.45	0.44
11:A:1250:U:O2'	11:A:1251:U:OP1	2.31	0.44
12:B:48:ILE:HG21	12:B:161:PRO:HB2	1.98	0.44
25:O:22:ALA:HB1	25:O:23:PRO:C	2.38	0.44
16:F:58:LEU:HD21	16:F:84:GLN:OE1	2.17	0.44
14:D:60:LEU:HA	14:D:60:LEU:HD22	1.49	0.44
16:F:98:LEU:HD23	16:F:103:ILE:HG13	1.98	0.44
5:4:77:GLU:C	5:4:79:HIS:H	2.21	0.44
7:6:59:CYS:O	7:6:61:THR:HG22	2.17	0.44
6:5:92:ARG:HD3	11:A:1796:C:OP2	2.17	0.44
17:G:166:ARG:HH12	17:G:170:GLN:HE22	1.64	0.44
11:A:577:G:C8	11:A:577:G:C3'	3.01	0.44
11:A:1244:A:HO2'	11:A:1245:G:P	2.41	0.44
11:A:1277:G:H2'	11:A:1278:G:O4'	2.17	0.44
18:H:111:MET:HE1	18:H:121:VAL:HG23	2.00	0.44
11:A:233:C:O2'	11:A:234:G:P	2.76	0.44
11:A:1418:G:O2'	24:N:56:ARG:O	2.29	0.44
21:K:132:ARG:HH11	21:K:132:ARG:HG3	1.81	0.44
28:R:159:ASN:ND2	28:R:166:SER:O	2.51	0.44
27:Q:21:ASN:HD22	27:Q:31:THR:HA	1.82	0.44
9:8:56:THR:HA	9:8:103:ARG:HH21	1.83	0.44
13:C:137:VAL:HG22	13:C:151:LYS:HG3	1.99	0.44
12:B:182:LEU:HB3	12:B:188:LEU:HD23	2.00	0.44
2:1:19:THR:O	2:1:23:GLY:HA2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1299:G:C3'	15:E:99:LYS:CE	2.96	0.44
11:A:960:U:H2'	11:A:961:U:C6	2.52	0.44
11:A:187:G:C4'	11:A:188:A:OP1	2.61	0.44
23:M:27:LYS:N	23:M:57:ARG:HH21	2.16	0.44
9:8:40:VAL:C	9:8:75:LEU:HD11	2.38	0.44
5:4:81:PHE:HD1	5:4:82:ARG:HG3	1.81	0.44
11:A:1346:A:C8	11:A:1370:U:O2	2.71	0.44
23:M:70:VAL:HA	23:M:73:MET:HE2	2.00	0.44
11:A:268:C:N4	35:Y:186:ARG:HD3	2.33	0.44
24:N:6:VAL:HG23	24:N:7:TRP:CZ3	2.53	0.44
21:K:122:PRO:C	21:K:124:ASP:N	2.71	0.44
2:1:26:THR:O	2:1:44:VAL:HG13	2.18	0.44
16:F:95:GLN:O	16:F:95:GLN:HG2	2.17	0.44
11:A:1248:C:H2'	11:A:1249:U:C6	2.52	0.44
35:Y:31:ARG:H	35:Y:34:GLN:HG3	1.82	0.44
12:B:11:PRO:O	12:B:15:GLN:HG3	2.18	0.44
4:3:86:GLN:CG	4:3:87:ASP:H	2.31	0.44
36:Z:50:TYR:HB2	36:Z:52:THR:HG22	1.99	0.44
12:B:103:THR:HA	12:B:104:PRO:HD3	1.62	0.44
11:A:1686:C:C4	11:A:1687:U:C4	3.05	0.44
35:Y:1:MET:HE2	35:Y:106:LEU:HB2	1.99	0.44
19:I:47:LYS:HZ2	19:I:114:ARG:HG2	1.82	0.44
11:A:67:A:OP1	35:Y:171:LYS:NZ	2.48	0.44
11:A:72:A:O2'	11:A:73:U:H5"	2.18	0.44
12:B:69:ASN:HB3	12:B:71:GLU:OE1	2.18	0.44
14:D:36:LEU:O	34:X:33:ARG:HG3	2.18	0.44
12:B:120:LEU:HD12	12:B:121:VAL:H	1.81	0.44
7:6:36:LYS:HE2	7:6:43:ILE:HG21	1.99	0.44
17:G:29:ILE:HG21	19:I:57:LEU:HD11	2.00	0.44
2:1:55:VAL:HG11	17:G:143:ARG:HD3	1.99	0.44
34:X:39:LEU:HD12	34:X:43:ARG:NH2	2.33	0.44
28:R:286:GLU:HA	28:R:287:PRO:HD3	1.62	0.44
28:R:38:ARG:HG2	28:R:67:ILE:CG2	2.48	0.44
23:M:56:LYS:HD3	23:M:60:GLU:HG3	2.00	0.44
25:O:26:PHE:HE2	25:O:59:GLY:O	2.01	0.44
16:F:28:ILE:HD13	16:F:88:VAL:HG13	1.99	0.43
22:L:79:ASN:HD22	22:L:81:LYS:HB2	1.82	0.43
23:M:129:TRP:CH2	29:S:125:PRO:HG3	2.53	0.43
11:A:1681:A:H1'	35:Y:66:GLY:HA2	2.00	0.43
30:T:64:HIS:CE1	30:T:68:ARG:CZ	3.01	0.43
11:A:712:G:H3'	11:A:712:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:K:30:VAL:HG13	21:K:39:ILE:O	2.18	0.43
4:3:104:ARG:HB2	4:3:105:THR:H	1.45	0.43
11:A:443:C:H2'	11:A:444:C:O4'	2.18	0.43
23:M:49:LYS:NZ	23:M:79:TYR:O	2.51	0.43
12:B:172:LEU:O	12:B:176:LEU:HG	2.17	0.43
33:W:147:ILE:HD13	33:W:169:ILE:HG13	2.00	0.43
16:F:58:LEU:HD23	16:F:58:LEU:O	2.18	0.43
1:0:62:ARG:HH12	1:0:93:HIS:CE1	2.36	0.43
14:D:170:GLY:HA2	14:D:171:ARG:HH21	1.83	0.43
21:K:29:HIS:CB	21:K:41:ARG:HA	2.48	0.43
11:A:839:U:O4	11:A:840:U:C4	2.71	0.43
6:5:61:GLU:O	6:5:62:TYR:HB3	2.18	0.43
4:3:74:GLN:O	4:3:78:THR:HG23	2.18	0.43
6:5:5:ARG:HG2	11:A:1796:C:N1	2.33	0.43
11:A:1318:G:O2'	11:A:1319:A:H5'	2.19	0.43
11:A:1511:U:H2'	11:A:1512:G:H8	1.84	0.43
31:U:66:VAL:HB	31:U:67:THR:H	1.51	0.43
26:P:35:VAL:HG11	26:P:40:LEU:HD11	2.00	0.43
18:H:24:GLN:HA	18:H:63:VAL:O	2.18	0.43
35:Y:215:ARG:HD3	35:Y:215:ARG:HA	1.57	0.43
29:S:78:THR:OG1	29:S:79:HIS:N	2.52	0.43
5:4:55:LYS:HD3	5:4:55:LYS:HA	1.67	0.43
30:T:33:TYR:C	30:T:33:TYR:HD1	2.21	0.43
3:2:31:ARG:NH2	11:A:333:A:OP1	2.51	0.43
11:A:1504:G:OP1	30:T:97:SER:HB2	2.18	0.43
23:M:8:GLN:HB2	23:M:9:GLY:H	1.56	0.43
10:9:83:UNK:O	10:9:84:UNK:HG3	2.18	0.43
11:A:1321:A:O4'	12:B:104:PRO:CG	2.65	0.43
30:T:118:PRO:O	30:T:119:LYS:HB2	2.18	0.43
1:0:24:ARG:O	1:0:25:GLU:C	2.57	0.43
1:0:23:LYS:NZ	1:0:25:GLU:HG2	2.30	0.43
20:J:20:ILE:N	20:J:95:ALA:O	2.50	0.43
11:A:1796:C:H4'	11:A:1797:A:OP2	2.18	0.43
28:R:74:THR:CG2	28:R:79:TYR:HB2	2.48	0.43
30:T:9:VAL:CG1	30:T:14:PHE:HB2	2.48	0.43
11:A:93:A:H1'	33:W:3:ARG:HB3	2.00	0.43
5:4:116:LYS:HD3	5:4:117:TRP:CZ3	2.53	0.43
11:A:886:U:H2'	11:A:887:A:O4'	2.18	0.43
15:E:165:VAL:HA	15:E:201:ASN:O	2.17	0.43
11:A:1142:A:H2'	11:A:1143:A:C8	2.53	0.43
30:T:135:ILE:HG13	30:T:135:ILE:H	1.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:434:G:H5'	22:L:78:LYS:HB3	1.99	0.43
11:A:1149:G:H5"	11:A:1150:G:OP1	2.18	0.43
11:A:12:U:H2'	11:A:13:C:C6	2.54	0.43
11:A:501:U:H2'	11:A:502:U:C5	2.53	0.43
14:D:134:ILE:HA	14:D:158:PHE:HA	2.00	0.43
13:C:70:THR:OG1	13:C:71:LEU:N	2.51	0.43
24:N:33:LYS:HD3	24:N:34:TYR:CE2	2.53	0.43
13:C:28:GLU:HA	13:C:28:GLU:OE1	2.18	0.43
20:J:20:ILE:HD13	20:J:22:ILE:HD13	2.00	0.43
18:H:103:ILE:HD13	18:H:126:LEU:HB2	2.00	0.43
11:A:1002:G:N1	11:A:1761:U:OP1	2.43	0.43
18:H:82:LYS:O	18:H:83:ILE:HG22	2.18	0.43
27:Q:57:LYS:HB2	27:Q:110:HIS:CE1	2.54	0.43
21:K:125:SER:HB3	21:K:126:THR:H	1.45	0.43
8:7:7:ASP:HB3	8:7:37:THR:HG21	2.00	0.43
31:U:129:GLU:O	31:U:133:LEU:HD13	2.18	0.43
34:X:47:VAL:HG22	34:X:48:THR:H	1.82	0.43
11:A:1287:A:N6	11:A:1329:A:H5'	2.32	0.43
27:Q:132:SER:O	27:Q:134:THR:N	2.52	0.43
15:E:227:PRO:HA	15:E:230:TRP:CD1	2.54	0.43
4:3:97:ARG:H	11:A:856:A:H62	1.66	0.43
16:F:77:ILE:CG1	16:F:79:GLN:NE2	2.77	0.43
32:V:34:LEU:O	32:V:38:ILE:HG22	2.18	0.43
19:I:53:LEU:H	19:I:53:LEU:HG	1.47	0.43
11:A:1253:U:H2'	11:A:1254:U:H6	1.83	0.43
5:4:81:PHE:HB2	5:4:82:ARG:H	1.53	0.43
25:O:34:ILE:HD11	25:O:67:THR:HG21	2.00	0.43
11:A:1487:A:H2'	11:A:1488:G:H8	1.83	0.43
19:I:9:THR:OG1	19:I:20:ALA:HB3	2.19	0.43
11:A:719:U:O2	11:A:719:U:H2'	2.18	0.43
33:W:155:LYS:HE2	33:W:155:LYS:HB3	1.76	0.43
26:P:16:PRO:HG2	33:W:95:THR:HG22	2.00	0.43
15:E:137:ILE:HG12	15:E:138:PRO:HD2	2.01	0.43
11:A:1321:A:C4'	12:B:104:PRO:HG2	2.49	0.43
11:A:473:A:C2'	11:A:474:A:H5'	2.49	0.43
21:K:84:ARG:HA	21:K:119:THR:HG22	2.00	0.43
11:A:67:A:C2	11:A:69:G:H1'	2.54	0.43
11:A:66:U:O4	35:Y:158:ILE:HG21	2.19	0.43
14:D:175:ARG:HD2	14:D:176:ASN:N	2.33	0.43
13:C:71:LEU:HD23	13:C:71:LEU:HA	1.85	0.43
17:G:144:GLU:HB2	17:G:160:VAL:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:8:40:VAL:HA	9:8:75:LEU:HD11	2.01	0.43
5:4:70:LEU:HD12	5:4:82:ARG:O	2.18	0.43
20:J:63:LEU:HD22	24:N:34:TYR:CE1	2.53	0.43
11:A:1386:G:OP2	32:V:44:LYS:NZ	2.52	0.43
11:A:1480:G:H3'	11:A:1481:C:H6	1.82	0.43
24:N:42:CYS:O	24:N:45:GLU:N	2.49	0.43
12:B:17:LEU:HD23	12:B:172:LEU:HD13	2.00	0.43
8:7:46:LEU:HD13	8:7:46:LEU:HA	1.66	0.43
17:G:87:CYS:SG	17:G:92:ARG:HG3	2.59	0.43
28:R:282:SER:H	28:R:285:ALA:HB3	1.84	0.43
10:9:111:GLU:HA	10:9:112:GLY:HA2	1.73	0.43
12:B:35:PRO:C	12:B:37:VAL:H	2.22	0.43
11:A:1151:A:C8	11:A:1152:A:P	3.12	0.43
16:F:58:LEU:HD11	16:F:80:LEU:HD11	2.00	0.43
19:I:18:ALA:CB	19:I:69:VAL:HG13	2.46	0.43
5:4:168:ILE:O	5:4:172:LEU:HG	2.19	0.43
11:A:740:A:C2'	11:A:741:C:H5"	2.43	0.43
11:A:1597:A:C8	24:N:14:TYR:HD2	2.36	0.43
33:W:104:ASP:HB3	33:W:106:LYS:N	2.33	0.43
11:A:517:U:H3	11:A:535:A:H61	1.65	0.43
12:B:57:LEU:HD23	12:B:177:LEU:HD23	2.00	0.43
4:3:17:GLU:HG2	4:3:46:ILE:HB	2.01	0.43
16:F:71:ASP:CG	16:F:72:PRO:HD2	2.39	0.43
35:Y:63:MET:HA	35:Y:98:ARG:O	2.18	0.43
4:3:131:PHE:CD1	4:3:132:PRO:N	2.87	0.43
12:B:200:ASP:HA	12:B:203:PHE:CE2	2.54	0.43
30:T:63:ARG:HG3	30:T:67:MET:CE	2.45	0.43
11:A:993:A:H4'	11:A:1777:G:O2'	2.19	0.43
3:2:48:THR:HG21	3:2:54:LYS:HE3	2.00	0.43
22:L:23:ARG:HD2	22:L:26:GLU:OE2	2.18	0.43
32:V:57:LEU:O	32:V:61:ILE:HG13	2.19	0.43
28:R:116:ASP:HB2	28:R:117:LYS:HD2	2.01	0.43
28:R:222:LEU:HD23	28:R:234:LEU:CD1	2.49	0.43
32:V:107:SER:HA	32:V:110:VAL:HG23	2.01	0.43
35:Y:63:MET:HE2	35:Y:106:LEU:CD2	2.49	0.43
11:A:1102:G:OP2	22:L:7:ARG:NH1	2.52	0.43
11:A:186:C:H3'	11:A:187:G:H8	1.82	0.43
5:4:105:PHE:CE1	5:4:213:ARG:HA	2.53	0.43
2:1:58:GLU:HG2	17:G:225:ARG:CZ	2.48	0.43
11:A:720:G:O2'	11:A:721:U:H5'	2.18	0.43
11:A:1600:A:O2'	11:A:1602:C:N4	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:K:24:ASN:O	21:K:25:ASP:HB2	2.19	0.43
23:M:10:SER:OG	23:M:11:PHE:N	2.52	0.43
11:A:823:G:O2'	11:A:824:G:OP1	2.36	0.43
17:G:145:ASP:CG	17:G:146:THR:H	2.17	0.43
11:A:827:C:H2'	11:A:828:U:H6	1.84	0.43
20:J:80:GLU:HG3	24:N:54:LYS:HZ3	1.84	0.43
31:U:125:ASN:O	31:U:126:TRP:CD1	2.72	0.43
11:A:709:C:N4	11:A:730:G:C4	2.87	0.43
22:L:40:SER:O	22:L:41:SER:O	2.36	0.43
30:T:135:ILE:HA	30:T:138:GLN:HG3	1.99	0.43
26:P:14:SER:CB	26:P:21:LYS:HE3	2.49	0.43
17:G:157:ARG:HB2	17:G:224:ASN:OD1	2.19	0.43
11:A:978:A:H2'	11:A:979:A:O4'	2.19	0.43
1:0:32:GLY:O	1:0:81:LEU:HB2	2.19	0.43
10:9:109:ASP:HB2	10:9:113:LYS:HG2	2.00	0.43
11:A:560:U:H2'	11:A:561:G:H8	1.83	0.43
11:A:560:U:H2'	11:A:561:G:C8	2.54	0.43
19:I:6:SER:HA	19:I:23:LYS:HA	2.00	0.43
11:A:1152:A:C6	11:A:1627:U:N3	2.87	0.43
11:A:498:G:H2'	11:A:499:U:C4	2.54	0.43
20:J:58:LEU:HD12	20:J:88:LYS:C	2.38	0.43
1:0:71:MET:SD	1:0:75:ASP:HB2	2.59	0.43
30:T:28:LEU:O	30:T:29:GLU:HB2	2.17	0.43
4:3:114:ARG:C	4:3:116:ARG:H	2.22	0.43
10:9:138:ARG:CZ	11:A:1235:C:O2	2.67	0.43
11:A:1489:U:H2'	11:A:1490:C:OP1	2.19	0.43
22:L:69:ARG:NH1	22:L:116:ASP:OD2	2.52	0.43
11:A:61:A:C8	11:A:269:G:O2'	2.65	0.43
11:A:1769:U:O2	21:K:136:ARG:HD2	2.18	0.43
11:A:506:A:H3'	11:A:506:A:OP1	2.19	0.43
11:A:763:G:C6	11:A:764:U:C4	3.07	0.43
28:R:256:THR:OG1	28:R:259:GLY:O	2.31	0.43
28:R:198:ASN:O	28:R:215:GLY:HA3	2.19	0.43
9:8:97:LYS:HG3	9:8:98:GLN:H	1.84	0.43
16:F:98:LEU:CG	16:F:102:ASN:HB2	2.49	0.42
35:Y:67:VAL:HG23	35:Y:100:ALA:H	1.83	0.42
11:A:1540:G:C6	11:A:1541:G:C4	3.07	0.42
4:3:133:THR:O	4:3:134:GLU:HB2	2.19	0.42
11:A:74:U:H1'	11:A:75:U:O5'	2.19	0.42
11:A:1340:U:N3	11:A:1378:U:H4'	2.34	0.42
11:A:1491:U:H5"	11:A:1491:U:O2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:117:THR:HG23	4:3:120:ALA:H	1.84	0.42
35:Y:76:LEU:HD22	35:Y:92:ARG:HB3	2.01	0.42
22:L:13:ARG:HA	22:L:16:ARG:HD3	2.01	0.42
11:A:768:C:N1	14:D:143:ILE:HD13	2.33	0.42
29:S:108:ARG:HG2	29:S:109:PRO:HD2	2.01	0.42
31:U:129:GLU:HA	31:U:133:LEU:HD22	2.00	0.42
11:A:805:U:H2'	11:A:806:A:H5"	2.01	0.42
4:3:75:THR:OG1	4:3:76:LYS:N	2.52	0.42
12:B:63:ILE:HG12	36:Z:36:VAL:HG22	2.01	0.42
15:E:125:ILE:O	15:E:129:ILE:HG13	2.19	0.42
11:A:14:C:OP2	15:E:206:THR:HG21	2.18	0.42
12:B:69:ASN:HB3	12:B:71:GLU:OE2	2.19	0.42
14:D:31:ALA:HA	14:D:36:LEU:HD12	2.00	0.42
30:T:125:SER:OG	30:T:128:GLY:N	2.45	0.42
19:I:22:VAL:HG22	19:I:65:ILE:CD1	2.49	0.42
11:A:1002:G:C2'	11:A:1003:A:H5'	2.48	0.42
5:4:132:ASP:HB2	5:4:221:PRO:HB3	2.01	0.42
24:N:5:ASN:HB3	24:N:7:TRP:NE1	2.34	0.42
17:G:43:PHE:CZ	17:G:90:ILE:HG21	2.54	0.42
11:A:1133:A:H2'	11:A:1134:C:O4'	2.19	0.42
12:B:87:LEU:HA	12:B:87:LEU:HD12	1.82	0.42
11:A:88:U:H4'	11:A:171:A:O4'	2.19	0.42
11:A:1781:A:H2'	11:A:1782:A:O4'	2.19	0.42
13:C:61:GLU:O	13:C:63:GLY:N	2.52	0.42
11:A:609:U:H4'	11:A:610:G:O5'	2.18	0.42
13:C:142:LEU:O	13:C:144:ALA:N	2.44	0.42
11:A:1013:A:H2'	11:A:1014:G:O4'	2.19	0.42
12:B:162:CYS:HB3	12:B:163:ASN:H	1.34	0.42
27:Q:3:THR:CG2	27:Q:82:ARG:HH21	2.32	0.42
11:A:1490:C:P	11:A:1490:C:O4'	2.78	0.42
11:A:380:U:H5	14:D:5:PRO:CA	2.30	0.42
11:A:1402:G:H2'	11:A:1403:C:C6	2.53	0.42
11:A:1365:C:H5"	19:I:28:LEU:CD2	2.49	0.42
8:7:81:ASN:HB3	31:U:37:VAL:HG11	2.01	0.42
28:R:42:LEU:O	28:R:61:PHE:HD1	2.02	0.42
30:T:33:TYR:C	30:T:33:TYR:CD1	2.93	0.42
8:7:54:TYR:CD1	8:7:54:TYR:N	2.86	0.42
3:2:172:ARG:NH1	11:A:330:G:OP2	2.42	0.42
11:A:36:C:H2'	11:A:37:U:O4'	2.20	0.42
11:A:1740:A:O2'	11:A:1741:U:H5'	2.19	0.42
11:A:1560:U:O2	11:A:1560:U:O4'	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:W:141:THR:O	33:W:143:ASP:N	2.53	0.42
19:I:58:ASP:OD1	19:I:59:LYS:N	2.52	0.42
11:A:484:C:O2'	11:A:485:A:OP1	2.35	0.42
10:9:101:UNK:HA	11:A:1229:G:OP2	2.19	0.42
11:A:542:A:H8	11:A:542:A:O2'	2.01	0.42
11:A:538:A:H8	11:A:543:C:N4	2.16	0.42
5:4:104:ASP:OD1	5:4:214:LYS:NZ	2.43	0.42
12:B:185:ARG:HB2	36:Z:45:ALA:CB	2.47	0.42
8:7:50:THR:HB	8:7:55:VAL:O	2.19	0.42
7:6:61:THR:HG23	7:6:62:ILE:O	2.19	0.42
23:M:95:GLY:HA3	29:S:18:ARG:O	2.20	0.42
11:A:273:G:H2'	11:A:274:G:O4'	2.18	0.42
5:4:146:GLN:CB	5:4:149:GLN:HE22	2.32	0.42
11:A:1456:C:O2	11:A:1456:C:O4'	2.38	0.42
20:J:28:SER:HB2	20:J:112:VAL:HA	2.02	0.42
11:A:1473:U:O2'	17:G:103:ASN:ND2	2.48	0.42
18:H:43:LYS:O	18:H:43:LYS:HG3	2.19	0.42
26:P:47:VAL:HG23	26:P:48:TYR:HD1	1.84	0.42
12:B:83:GLN:HG2	12:B:100:GLY:H	1.84	0.42
13:C:134:CYS:N	13:C:157:LEU:HD11	2.34	0.42
28:R:205:SER:HB3	28:R:210:LEU:HB2	2.02	0.42
11:A:1321:A:C2	12:B:104:PRO:C	2.93	0.42
11:A:579:A:H61	13:C:143:ARG:HG3	1.48	0.42
11:A:1300:A:C5'	15:E:117:THR:CG2	2.77	0.42
11:A:40:A:H2'	11:A:41:A:O4'	2.19	0.42
27:Q:6:THR:OG1	27:Q:7:VAL:N	2.52	0.42
2:1:29:ARG:HG3	2:1:39:THR:OG1	2.20	0.42
22:L:29:TYR:CZ	22:L:33:LEU:HD12	2.54	0.42
11:A:1051:G:HO2'	11:A:1052:U:P	2.43	0.42
27:Q:28:SER:O	27:Q:29:LYS:HB3	2.20	0.42
15:E:44:LEU:HG	15:E:247:ALA:HB2	2.01	0.42
15:E:65:GLU:O	15:E:68:ILE:HB	2.19	0.42
11:A:1150:G:O2'	11:A:1151:A:OP2	2.33	0.42
1:0:85:GLN:NE2	34:X:6:GLY:C	2.66	0.42
1:0:62:ARG:O	1:0:66:ARG:HG3	2.19	0.42
5:4:231:LEU:C	5:4:232:HIS:CD2	2.93	0.42
35:Y:1:MET:CE	35:Y:106:LEU:HB2	2.50	0.42
4:3:159:VAL:HG23	4:3:163:ASP:OD1	2.20	0.42
13:C:66:ILE:O	13:C:70:THR:HG23	2.20	0.42
11:A:1710:U:H2'	11:A:1711:C:C5	2.54	0.42
23:M:69:ILE:HG22	23:M:73:MET:HE2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:460:A:H3'	11:A:461:G:H8	1.84	0.42
27:Q:87:ARG:HH21	27:Q:104:HIS:CE1	2.38	0.42
12:B:20:ALA:O	12:B:21:ASN:HB2	2.19	0.42
26:P:14:SER:HB3	26:P:21:LYS:HE3	2.02	0.42
11:A:81:G:C6	11:A:82:U:N3	2.88	0.42
11:A:714:G:C6	11:A:715:U:C2	3.08	0.42
15:E:104:VAL:HG22	15:E:132:ALA:HB1	2.00	0.42
11:A:1586:A:H2'	11:A:1587:A:C8	2.53	0.42
5:4:97:LEU:HD12	5:4:232:HIS:NE2	2.35	0.42
19:I:53:LEU:HD23	19:I:53:LEU:N	2.34	0.42
4:3:35:LYS:NZ	4:3:36:ALA:H	2.18	0.42
11:A:1595:U:H5	11:A:1596:C:C5	2.37	0.42
11:A:685:A:O2'	11:A:686:C:H5'	2.19	0.42
28:R:201:THR:CB	28:R:242:SER:HA	2.49	0.42
33:W:106:LYS:HG3	33:W:108:ARG:NH2	2.35	0.42
11:A:237:C:C4'	11:A:238:U:H5'	2.49	0.42
35:Y:132:ARG:HG2	35:Y:132:ARG:HH11	1.83	0.42
35:Y:119:GLN:HG3	35:Y:120:GLU:N	2.35	0.42
3:2:157:GLU:O	3:2:160:PHE:HB2	2.19	0.42
11:A:153:G:OP2	26:P:131:ARG:NH2	2.38	0.42
33:W:131:LEU:HD13	33:W:135:GLY:HA2	2.01	0.42
27:Q:127:GLN:HG3	27:Q:137:PHE:CZ	2.54	0.42
21:K:129:LYS:HG3	21:K:130:GLY:N	2.35	0.42
29:S:57:MET:O	29:S:60:LEU:HB3	2.19	0.42
11:A:1321:A:H4'	11:A:1322:A:O5'	2.19	0.42
19:I:27:GLY:HA2	19:I:63:ILE:O	2.19	0.42
11:A:68:A:C8	35:Y:160:ARG:NH1	2.87	0.42
11:A:512:A:HO2'	11:A:513:U:P	2.43	0.42
11:A:1557:U:OP2	11:A:1559:A:O2'	2.33	0.42
11:A:781:U:O2'	11:A:782:U:H6	2.02	0.42
21:K:38:THR:O	21:K:39:ILE:HG23	2.19	0.42
11:A:1346:A:H8	11:A:1370:U:O2	2.03	0.42
13:C:5:ILE:CG2	13:C:9:ARG:HB3	2.50	0.42
35:Y:76:LEU:HA	35:Y:76:LEU:HD23	1.87	0.42
6:5:23:CYS:CB	6:5:74:CYS:HB3	2.50	0.42
15:E:67:GLN:O	15:E:71:THR:HG23	2.20	0.42
11:A:1334:U:H2'	11:A:1335:U:H6	1.83	0.42
28:R:123:ILE:HD11	28:R:156:VAL:HG23	2.01	0.42
23:M:109:LEU:HG	23:M:113:LEU:CD1	2.50	0.42
28:R:38:ARG:HG2	28:R:67:ILE:HG23	2.01	0.42
2:1:5:THR:HA	2:1:6:PRO:HD3	1.79	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:C:167:PHE:HD1	13:C:190:ARG:HD3	1.85	0.42
36:Z:15:ARG:HB3	36:Z:16:LYS:H	1.60	0.42
14:D:127:VAL:HG12	14:D:131:GLN:NE2	2.35	0.42
11:A:579:A:N1	13:C:143:ARG:CA	2.83	0.42
11:A:489:C:N4	11:A:497:G:H22	2.15	0.42
17:G:69:PHE:CD2	19:I:50:GLU:HG2	2.54	0.42
13:C:113:LEU:HD23	13:C:113:LEU:HA	1.66	0.42
11:A:1568:C:OP1	23:M:36:LYS:HE2	2.20	0.42
2:1:32:PHE:CD1	2:1:32:PHE:N	2.87	0.42
11:A:73:U:C2	11:A:74:U:O2	2.73	0.42
8:7:16:PHE:HD2	8:7:76:LEU:HD23	1.84	0.42
10:9:143:LYS:CB	11:A:1253:U:H4'	2.50	0.42
29:S:128:HIS:O	29:S:130:ARG:HG2	2.20	0.42
30:T:65:ILE:HG12	30:T:71:VAL:HG21	2.01	0.42
11:A:1480:G:H4'	30:T:11:ALA:CB	2.49	0.42
11:A:568:G:O2'	11:A:569:C:H5'	2.20	0.42
13:C:127:MET:HG2	13:C:154:ASP:OD2	2.19	0.42
24:N:5:ASN:C	24:N:7:TRP:H	2.23	0.42
31:U:55:GLY:HA2	31:U:85:LYS:CD	2.50	0.42
11:A:812:A:OP1	11:A:814:A:C8	2.72	0.42
11:A:814:A:C5	11:A:816:G:C8	3.08	0.42
32:V:66:VAL:O	32:V:69:ILE:HG12	2.19	0.42
33:W:156:VAL:O	33:W:157:ASN:HB2	2.20	0.42
1:0:88:GLN:CG	34:X:5:HIS:HB2	2.40	0.42
11:A:1686:C:C4	11:A:1687:U:C5	3.08	0.42
11:A:279:G:C3'	11:A:279:G:C8	3.03	0.42
35:Y:55:GLY:C	35:Y:63:MET:HE3	2.39	0.42
10:9:140:TYR:OH	11:A:1234:A:H1'	2.20	0.42
18:H:30:SER:HB2	18:H:61:ILE:CD1	2.50	0.42
11:A:542:A:H8	11:A:543:C:H2'	1.83	0.42
11:A:71:A:C2	11:A:72:A:C2	3.08	0.42
11:A:74:U:O2'	11:A:75:U:H5'	2.20	0.42
9:8:41:ILE:O	9:8:75:LEU:HD13	2.20	0.42
9:8:71:ILE:HG22	9:8:75:LEU:HD12	2.02	0.42
5:4:140:ILE:O	5:4:210:ILE:HA	2.20	0.42
2:1:42:ARG:NH1	2:1:56:LEU:HD22	2.33	0.42
4:3:51:VAL:HG23	4:3:53:GLY:N	2.34	0.42
11:A:681:U:O4	11:A:682:C:N4	2.52	0.42
11:A:328:A:H2'	11:A:329:G:O4'	2.19	0.42
18:H:23:ARG:NH2	36:Z:21:ASN:OD1	2.53	0.42
27:Q:118:GLN:HG3	27:Q:119:VAL:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:I:127:LYS:HA	19:I:134:ALA:HA	2.02	0.42
31:U:98:GLY:CA	31:U:118:ALA:HB2	2.50	0.42
5:4:96:LEU:O	5:4:96:LEU:HD23	2.20	0.42
11:A:505:A:H2'	11:A:506:A:OP1	2.19	0.42
17:G:128:ASN:HD22	17:G:128:ASN:HA	1.74	0.42
35:Y:85:ARG:HA	35:Y:86:PRO:HD3	1.75	0.42
35:Y:148:SER:C	35:Y:150:GLU:H	2.22	0.42
12:B:30:GLN:NE2	12:B:149:LEU:HD13	2.35	0.42
11:A:479:C:O2	11:A:510:G:N2	2.53	0.42
12:B:64:ILE:HG12	12:B:122:ILE:HD11	2.01	0.42
16:F:62:PHE:CD2	16:F:84:GLN:CD	2.93	0.41
5:4:131:ASP:OD2	5:4:180:THR:HG21	2.19	0.41
3:2:21:PHE:O	3:2:22:ARG:HG2	2.20	0.41
4:3:131:PHE:HB3	4:3:132:PRO:HD3	2.02	0.41
5:4:105:PHE:HB2	5:4:214:LYS:HZ1	1.85	0.41
13:C:179:GLN:HE21	13:C:179:GLN:C	2.23	0.41
11:A:839:U:C2'	11:A:840:U:H5'	2.47	0.41
6:5:62:TYR:CZ	21:K:114:ARG:HA	2.54	0.41
11:A:648:G:C4	11:A:687:G:N2	2.88	0.41
28:R:98:GLU:HG3	28:R:99:THR:O	2.20	0.41
10:9:138:ARG:CZ	11:A:1235:C:C2	3.03	0.41
34:X:34:ALA:O	34:X:37:ARG:HB3	2.20	0.41
9:8:54:VAL:HG13	9:8:57:TYR:CD2	2.55	0.41
35:Y:109:LEU:HA	35:Y:109:LEU:HD23	1.84	0.41
4:3:119:THR:HG23	11:A:639:U:OP1	2.19	0.41
11:A:1625:C:H5'	15:E:91:ARG:HH12	1.83	0.41
11:A:425:A:C5'	11:A:425:A:H8	2.32	0.41
14:D:92:LYS:HE3	14:D:92:LYS:HA	2.01	0.41
29:S:108:ARG:HD2	29:S:110:GLU:OE2	2.19	0.41
15:E:111:VAL:HG21	15:E:218:ILE:HD13	2.01	0.41
25:O:83:GLU:H	25:O:83:GLU:HG2	1.55	0.41
5:4:29:TRP:CZ2	5:4:45:LYS:HB3	2.55	0.41
3:2:147:ALA:H	3:2:149:SER:HB3	1.84	0.41
1:0:88:GLN:HB2	34:X:6:GLY:CA	2.50	0.41
21:K:84:ARG:HG3	21:K:119:THR:HA	2.01	0.41
11:A:819:G:HO2'	11:A:820:U:H5'	1.84	0.41
11:A:649:U:HO2'	11:A:650:U:P	2.40	0.41
14:D:49:LEU:HD22	14:D:53:ARG:HG3	2.01	0.41
11:A:778:G:C5	11:A:783:G:N1	2.88	0.41
11:A:781:U:O2'	11:A:782:U:O5'	2.38	0.41
5:4:72:ASP:OD2	21:K:114:ARG:HD2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:R:22:SER:HB3	28:R:36:ALA:HB3	2.02	0.41
31:U:55:GLY:HA2	31:U:85:LYS:HD2	2.02	0.41
11:A:1547:A:H5'	23:M:112:ASP:OD2	2.19	0.41
18:H:111:MET:CE	18:H:116:ALA:HA	2.50	0.41
11:A:1344:A:H4'	11:A:1345:A:OP1	2.19	0.41
13:C:138:VAL:O	13:C:149:ALA:HA	2.20	0.41
15:E:84:LYS:HA	15:E:85:PRO:HD3	1.79	0.41
16:F:98:LEU:CD2	16:F:102:ASN:HB2	2.48	0.41
16:F:85:ARG:NH1	16:F:107:GLY:CA	2.83	0.41
11:A:830:U:O2'	11:A:831:U:OP2	2.34	0.41
35:Y:158:ILE:HA	35:Y:158:ILE:HD12	1.77	0.41
14:D:133:HIS:H	14:D:133:HIS:CD2	2.37	0.41
10:9:143:LYS:CA	11:A:1253:U:H4'	2.50	0.41
11:A:190:C:C4	11:A:196:G:C6	3.09	0.41
4:3:96:ARG:O	11:A:694:U:C5	2.73	0.41
11:A:1553:G:O6	29:S:43:ARG:HD3	2.20	0.41
11:A:1280:C:H2'	11:A:1281:G:C8	2.56	0.41
25:O:21:ASN:HB2	25:O:22:ALA:H	1.66	0.41
15:E:230:TRP:CE2	18:H:68:ARG:HB3	2.55	0.41
26:P:44:LEU:HA	26:P:47:VAL:CG2	2.51	0.41
11:A:205:U:H2'	11:A:206:A:O4'	2.21	0.41
15:E:242:ILE:HG22	15:E:243:TYR:CE2	2.55	0.41
11:A:773:C:OP1	33:W:21:ASP:HB2	2.19	0.41
17:G:95:ASN:O	17:G:98:MET:HG2	2.20	0.41
33:W:61:VAL:HG12	33:W:65:LEU:HD12	2.00	0.41
33:W:68:ARG:NH1	33:W:76:VAL:HG21	2.35	0.41
11:A:1294:G:C2'	12:B:108:THR:HG1	2.29	0.41
1:0:46:ARG:HD2	34:X:3:LYS:CG	2.45	0.41
1:0:61:ILE:HG22	1:0:66:ARG:HG3	2.02	0.41
11:A:1479:A:P	30:T:57:ARG:HH12	2.44	0.41
11:A:336:G:O2'	27:Q:133:LYS:N	2.52	0.41
11:A:68:A:H3'	11:A:68:A:H8	1.84	0.41
23:M:27:LYS:HA	23:M:57:ARG:HE	1.84	0.41
30:T:86:ARG:HH11	30:T:86:ARG:CG	2.29	0.41
5:4:137:ILE:HG22	5:4:215:VAL:CG2	2.50	0.41
11:A:478:A:H5'	34:X:33:ARG:NH2	2.35	0.41
23:M:47:CYS:HB3	23:M:54:LEU:CD1	2.50	0.41
2:1:46:GLY:HA2	17:G:166:ARG:HD2	2.02	0.41
31:U:29:LYS:HA	31:U:32:LEU:HD12	2.00	0.41
31:U:131:ASP:OD1	31:U:132:GLU:N	2.53	0.41
11:A:327:U:O2'	27:Q:10:GLU:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:P:105:ARG:O	26:P:109:LYS:HG3	2.20	0.41
11:A:1244:A:O2'	11:A:1245:G:P	2.78	0.41
3:2:87:ASN:HB3	3:2:90:LEU:HD12	2.02	0.41
12:B:172:LEU:HD13	12:B:176:LEU:HD11	2.01	0.41
12:B:63:ILE:HG23	36:Z:35:ASN:O	2.20	0.41
11:A:82:U:H2'	11:A:83:G:O4'	2.21	0.41
4:3:181:ILE:HA	4:3:181:ILE:HD12	1.72	0.41
4:3:67:LEU:HA	4:3:67:LEU:HD23	1.75	0.41
6:5:64:LEU:HA	6:5:64:LEU:HD22	1.89	0.41
33:W:114:ILE:HB	33:W:118:GLU:OE1	2.20	0.41
20:J:96:PRO:HG2	20:J:99:ILE:HG22	2.02	0.41
15:E:130:ILE:O	15:E:134:LEU:HD22	2.19	0.41
1:0:44:ASN:HB3	1:0:46:ARG:HH12	1.84	0.41
11:A:1324:G:H5"	12:B:113:ARG:NE	1.99	0.41
11:A:499:U:H2'	11:A:500:C:C6	2.55	0.41
11:A:143:G:C2	11:A:173:A:N3	2.88	0.41
11:A:734:A:H4'	11:A:735:C:H5'	2.03	0.41
10:9:144:CYS:CB	10:9:147:VAL:HG13	2.49	0.41
4:3:28:GLU:O	4:3:30:SER:N	2.52	0.41
7:6:32:PHE:CZ	25:O:61:THR:HG22	2.56	0.41
10:9:143:LYS:N	11:A:1253:U:H4'	2.36	0.41
11:A:1756[A]:A:H8	11:A:1756[A]:A:OP2	2.04	0.41
11:A:685:A:HO2'	11:A:686:C:P	2.44	0.41
23:M:11:PHE:HE1	23:M:13:HIS:HA	1.86	0.41
11:A:637:C:OP1	18:H:32:LYS:HG3	2.21	0.41
15:E:81:MET:HE2	15:E:103:VAL:HB	2.03	0.41
10:9:138:ARG:NE	11:A:1235:C:O2	2.53	0.41
29:S:96:ILE:CD1	29:S:116:LEU:HD22	2.51	0.41
32:V:5:ARG:N	32:V:5:ARG:HD3	2.35	0.41
12:B:35:PRO:HG3	36:Z:87:ARG:HH21	1.85	0.41
30:T:130:ARG:HH11	30:T:130:ARG:HG2	1.86	0.41
3:2:195:ARG:HA	3:2:195:ARG:HD3	1.85	0.41
10:9:103:LEU:HA	10:9:103:LEU:HD23	1.71	0.41
33:W:87:MET:SD	33:W:123:LEU:HB2	2.60	0.41
28:R:307:ASP:O	28:R:309:VAL:HG23	2.21	0.41
35:Y:32:ILE:HD12	35:Y:100:ALA:HB1	2.02	0.41
32:V:23:LYS:O	32:V:24:LEU:HB2	2.20	0.41
1:0:52:PHE:CE2	1:0:109:LEU:HD11	2.55	0.41
11:A:916:U:H3	21:K:41:ARG:NH2	2.19	0.41
11:A:959:U:OP2	25:O:14:SER:HA	2.20	0.41
9:8:59:TYR:HE1	9:8:61:SER:CB	2.31	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:196:G:O2'	11:A:197:A:H8	2.02	0.41
11:A:756:A:H1'	33:W:12:LEU:O	2.21	0.41
29:S:52:LYS:HB2	29:S:52:LYS:HE2	1.98	0.41
11:A:240:U:H4'	11:A:241:U:OP2	2.20	0.41
13:C:211:PRO:HB2	13:C:212:LYS:H	1.63	0.41
31:U:125:ASN:C	31:U:127:GLY:H	2.23	0.41
13:C:21:LEU:HD23	13:C:21:LEU:HA	1.82	0.41
11:A:154:G:OP1	35:Y:2:LYS:NZ	2.50	0.41
9:8:69:LEU:HA	9:8:69:LEU:HD22	1.83	0.41
11:A:1570:A:H2'	11:A:1571:C:O4'	2.20	0.41
5:4:90:GLU:HG2	5:4:223:PHE:HZ	1.84	0.41
11:A:1321:A:C5	12:B:105:GLY:N	2.85	0.41
12:B:200:ASP:CB	32:V:85:VAL:CG2	2.99	0.41
11:A:1201:G:H22	11:A:1600:A:H5'	1.85	0.41
11:A:992:A:H2'	11:A:993:A:H5'	2.02	0.41
11:A:901:G:C6	11:A:902:G:C6	3.08	0.41
8:7:14:TYR:C	8:7:14:TYR:CD1	2.93	0.41
11:A:1370:U:H4'	11:A:1371:A:H5'	2.01	0.41
18:H:23:ARG:HA	18:H:23:ARG:HD2	1.80	0.41
11:A:1556:A:C5	11:A:1560:U:C2	3.09	0.41
33:W:131:LEU:HA	33:W:131:LEU:HD22	1.87	0.41
25:O:88:LEU:HD23	25:O:88:LEU:HA	1.88	0.41
20:J:37:VAL:O	20:J:41:ILE:HD13	2.21	0.41
11:A:1162:C:H5"	11:A:1163:A:OP2	2.20	0.41
5:4:35:PRO:HB2	5:4:36:SER:H	1.63	0.41
33:W:208:VAL:HG12	33:W:210:ILE:HD11	2.02	0.41
11:A:1360:A:H2'	11:A:1361:U:C1'	2.51	0.41
1:0:84:PHE:HD2	1:0:85:GLN:HG3	1.86	0.41
36:Z:74:GLN:HE22	36:Z:83:TRP:H	1.68	0.41
8:7:72:GLY:O	8:7:76:LEU:HD22	2.20	0.41
22:L:126:LYS:HA	22:L:131:SER:HA	2.02	0.41
11:A:532:U:H2'	26:P:33:ALA:HB1	2.03	0.41
11:A:794:U:OP2	11:A:794:U:H3'	2.20	0.41
18:H:80:ASN:HD21	18:H:124:LYS:NZ	2.19	0.41
3:2:37:LYS:O	3:2:59:ARG:HA	2.20	0.41
11:A:272:U:HO2'	11:A:273:G:H8	1.66	0.41
11:A:284:G:N7	35:Y:188:ARG:NH1	2.68	0.41
11:A:1337:A:H5'	11:A:1338:C:OP2	2.20	0.41
29:S:89:MET:HB3	29:S:89:MET:HE3	1.92	0.41
11:A:570:A:H5"	11:A:571:G:OP2	2.21	0.41
22:L:114:LYS:HB3	22:L:115:GLY:H	1.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:L:23:ARG:HG3	22:L:23:ARG:HH11	1.85	0.41
11:A:95:G:O2'	11:A:460:A:O2'	2.38	0.41
28:R:29:GLN:C	28:R:31:ASN:H	2.23	0.41
13:C:195:SER:O	13:C:196:ARG:HB3	2.20	0.41
28:R:37:SER:OG	28:R:38:ARG:N	2.54	0.41
11:A:1053:G:H5'	11:A:1053:G:C8	2.56	0.41
11:A:1096:C:O2	11:A:1096:C:H2'	2.20	0.41
19:I:45:ARG:O	19:I:48:VAL:HG12	2.21	0.41
33:W:52:LEU:O	33:W:54:TYR:N	2.54	0.41
4:3:129:LEU:HD21	4:3:172:VAL:HG11	2.02	0.41
11:A:11:A:H2'	11:A:12:U:H5'	2.02	0.41
16:F:77:ILE:CD1	16:F:79:GLN:NE2	2.84	0.41
11:A:1715:G:C2'	11:A:1716:C:H5'	2.51	0.41
11:A:140:A:OP2	35:Y:187:LYS:NZ	2.54	0.41
33:W:129:VAL:HB	33:W:139:VAL:HG12	2.03	0.41
19:I:82:ARG:NH2	19:I:114:ARG:HG2	2.36	0.41
3:2:21:PHE:CZ	3:2:22:ARG:HD3	2.56	0.41
4:3:162:ILE:HA	4:3:165:LYS:HG3	2.02	0.41
1:0:103:LEU:HA	1:0:106:GLN:HG2	2.03	0.41
11:A:68:A:C8	11:A:68:A:H3'	2.55	0.41
11:A:66:U:O2	35:Y:160:ARG:NE	2.52	0.41
6:5:82:ARG:O	6:5:84:VAL:HG12	2.20	0.41
19:I:4:VAL:HG12	19:I:5:PRO:HD2	2.03	0.41
23:M:29:VAL:HA	23:M:32:LEU:HD12	2.03	0.41
11:A:73:U:O2'	11:A:74:U:C6	2.74	0.41
13:C:53:THR:HG22	13:C:91:VAL:HG11	2.03	0.41
9:8:75:LEU:HG	9:8:75:LEU:H	1.46	0.41
11:A:1180:C:O2	29:S:128:HIS:HE1	2.04	0.41
11:A:1535:U:H1'	11:A:1536:G:C2	2.55	0.41
28:R:195:HIS:HD2	28:R:199:ILE:HD13	1.81	0.41
4:3:99:LEU:HD23	4:3:100:PRO:HD2	2.03	0.41
5:4:171:ILE:O	5:4:175:GLU:HG2	2.21	0.41
11:A:755:A:O2'	11:A:756:A:OP1	2.36	0.41
2:1:18:ARG:HA	2:1:25:VAL:O	2.21	0.41
11:A:1167:G:OP1	17:G:101:GLY:HA3	2.21	0.41
31:U:28:LEU:HD22	31:U:32:LEU:HG	2.02	0.41
11:A:5:U:H2'	11:A:6:G:H8	1.86	0.41
32:V:10:LYS:HG2	32:V:53:TYR:CE2	2.56	0.41
11:A:768:C:O2	14:D:143:ILE:HG21	2.21	0.41
21:K:122:PRO:O	21:K:124:ASP:N	2.51	0.41
22:L:107:PHE:CE1	22:L:123:LYS:HB3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:U:52:LEU:HD23	31:U:122:VAL:HG21	2.03	0.41
11:A:458:G:H5"	11:A:459:G:OP1	2.21	0.41
35:Y:28:PHE:CZ	35:Y:104:PRO:HG3	2.56	0.41
20:J:61:LYS:HG3	20:J:86:ILE:HB	2.03	0.41
12:B:198:MET:SD	12:B:199:PRO:HD2	2.61	0.41
28:R:38:ARG:HG2	28:R:67:ILE:HD13	2.03	0.41
28:R:117:LYS:N	28:R:117:LYS:HD2	2.36	0.41
33:W:123:LEU:HD22	33:W:236:ILE:HG23	2.03	0.41
16:F:55:LEU:HD23	16:F:55:LEU:C	2.41	0.41
1:0:80:SER:OG	1:0:90:ASP:HB2	2.21	0.41
11:A:304:U:OP1	27:Q:136:ARG:HD3	2.20	0.41
33:W:100:ARG:NH2	33:W:121:TYR:O	2.54	0.41
11:A:1654:G:H2'	11:A:1745:G:N2	2.35	0.41
1:0:98:ASP:O	1:0:101:ARG:HG2	2.21	0.41
20:J:77:LYS:HG2	20:J:77:LYS:H	1.66	0.41
13:C:94:ARG:H	13:C:94:ARG:HG3	1.51	0.41
6:5:76:SER:O	6:5:80:HIS:N	2.53	0.41
20:J:109:GLU:OE1	20:J:110:PRO:HD2	2.20	0.41
3:2:103:GLN:NE2	3:2:166:TYR:CE1	2.89	0.41
17:G:49:GLU:O	17:G:51:VAL:HG23	2.21	0.41
29:S:68:PRO:HG2	29:S:71:GLU:OE1	2.21	0.41
11:A:1301:U:H2'	11:A:1302:U:O4'	2.21	0.41
16:F:58:LEU:CD2	16:F:80:LEU:HD22	2.48	0.41
11:A:487:G:C6	11:A:488:G:C8	3.08	0.41
11:A:480:G:H22	11:A:509:G:H1'	1.84	0.41
16:F:98:LEU:HD11	16:F:102:ASN:ND2	2.36	0.41
16:F:98:LEU:HG	16:F:99:GLN:O	2.21	0.41
9:8:95:HIS:NE2	17:G:112:ARG:HD3	2.35	0.41
11:A:952:A:O2'	25:O:114:ARG:HG3	2.21	0.41
27:Q:78:THR:HG22	27:Q:84:ILE:CG2	2.45	0.41
11:A:992:A:O4'	11:A:992:A:N3	2.53	0.41
21:K:81:VAL:HG13	21:K:115:ILE:CG2	2.50	0.41
11:A:1042:G:C6	11:A:1043:A:N7	2.89	0.41
23:M:92:ILE:O	23:M:92:ILE:HD13	2.21	0.41
33:W:104:ASP:OD2	33:W:108:ARG:NE	2.41	0.41
22:L:90:ASP:OD2	34:X:15:LYS:N	2.53	0.41
5:4:21:VAL:HG23	5:4:22:ASP:H	1.86	0.41
11:A:1281:G:C5	11:A:1282:U:C5	3.09	0.41
12:B:148:ASP:OD1	12:B:149:LEU:N	2.45	0.41
18:H:6:VAL:HG13	18:H:29:PRO:HD2	2.02	0.41
28:R:266:ASP:HA	28:R:267:PRO:HA	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1182:U:O2	11:A:1184:A:H8	2.04	0.41
11:A:1322:A:H2	12:B:109:ASN:HD21	1.62	0.40
19:I:82:ARG:HH12	19:I:114:ARG:HB3	1.84	0.40
11:A:1568:C:H6	11:A:1568:C:H2'	1.71	0.40
11:A:817:A:C6	11:A:818:C:N4	2.89	0.40
30:T:49:ASP:O	30:T:51:GLU:N	2.54	0.40
11:A:778:G:H1	26:P:10:ARG:HG2	1.86	0.40
35:Y:58:LYS:HB2	35:Y:59:GLN:OE1	2.21	0.40
9:8:65:LEU:HB3	9:8:71:ILE:CD1	2.51	0.40
12:B:13:ASP:O	12:B:16:LEU:HB2	2.21	0.40
5:4:81:PHE:HA	5:4:106:THR:CG2	2.51	0.40
5:4:207:LEU:HB3	5:4:210:ILE:HD11	2.02	0.40
11:A:1474:G:O2'	11:A:1475:A:O5'	2.37	0.40
7:6:2:VAL:HG22	36:Z:64:GLU:OE1	2.21	0.40
27:Q:132:SER:OG	27:Q:132:SER:O	2.39	0.40
11:A:806:A:H8	11:A:806:A:H5'	1.86	0.40
22:L:142:LYS:HA	22:L:143:PRO:HD3	1.88	0.40
11:A:488:G:N7	11:A:498:G:N2	2.68	0.40
11:A:473:A:H2'	11:A:474:A:H5'	2.03	0.40
11:A:1715:G:O6	11:A:1716:C:C4	2.56	0.40
14:D:146:PHE:CZ	14:D:149:ARG:HD3	2.56	0.40
12:B:202:TYR:HD1	12:B:202:TYR:H	1.68	0.40
22:L:4:GLY:O	22:L:5:LYS:C	2.60	0.40
21:K:41:ARG:O	21:K:42:VAL:HG22	2.21	0.40
11:A:1340:U:C2	11:A:1378:U:H4'	2.57	0.40
4:3:124:LYS:HA	4:3:124:LYS:HD3	1.99	0.40
4:3:186:PRO:HB2	4:3:187:SER:H	1.64	0.40
29:S:85:ILE:HA	29:S:89:MET:SD	2.61	0.40
11:A:567:A:O2'	22:L:90:ASP:OD1	2.21	0.40
33:W:98:ASN:HD22	33:W:119:ALA:CB	2.35	0.40
12:B:177:LEU:HA	12:B:177:LEU:HD23	1.94	0.40
11:A:1181:U:H2'	11:A:1182:U:O4'	2.21	0.40
33:W:48:LEU:HA	33:W:48:LEU:HD12	1.89	0.40
33:W:206:ASP:N	33:W:206:ASP:OD1	2.55	0.40
26:P:18:LEU:HA	26:P:18:LEU:HD23	1.89	0.40
11:A:964:U:H4'	11:A:965:U:O5'	2.21	0.40
11:A:1462:G:N7	23:M:143:ARG:NH2	2.69	0.40
3:2:106:ALA:O	3:2:109:PHE:N	2.53	0.40
11:A:1191:U:H5'	19:I:143:ARG:CZ	2.51	0.40
11:A:645:C:H42	11:A:689:G:H1	1.69	0.40
36:Z:3:ASN:OD1	36:Z:7:GLN:HB2	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:O:33:VAL:HA	25:O:36:GLN:HB2	2.02	0.40
1:0:29:LYS:HG2	1:0:35:TYR:CE2	2.56	0.40
17:G:37:GLN:CG	19:I:53:LEU:HD13	2.41	0.40
11:A:919:A:H4'	21:K:35:GLY:HA3	2.03	0.40
5:4:28:GLU:HB3	5:4:49:ASN:H	1.86	0.40
11:A:600:U:OP2	22:L:108:GLY:HA2	2.22	0.40
2:1:21:SER:OG	2:1:22:ARG:N	2.55	0.40
9:8:54:VAL:HG22	9:8:57:TYR:HE2	1.85	0.40
28:R:242:SER:HB3	28:R:292:LEU:HD23	2.03	0.40
11:A:1172:G:C5	11:A:1173:C:C4	3.09	0.40
35:Y:28:PHE:C	35:Y:30:LYS:H	2.25	0.40
16:F:90:GLU:HA	16:F:93:ILE:HG12	2.04	0.40
11:A:1163:A:N6	11:A:1164:G:C6	2.89	0.40
14:D:86:LEU:HD12	14:D:86:LEU:HA	1.85	0.40
13:C:74:GLN:OE1	13:C:81:PRO:HA	2.20	0.40
11:A:1018:U:H2'	11:A:1019:A:C8	2.57	0.40
1:0:62:ARG:NH1	1:0:93:HIS:CE1	2.90	0.40
5:4:58:SER:O	5:4:62:LYS:HG3	2.22	0.40
25:O:28:LEU:HD23	25:O:28:LEU:HA	1.85	0.40
25:O:27:LYS:HD2	25:O:28:LEU:H	1.86	0.40
30:T:72:GLY:O	30:T:76:LEU:HG	2.22	0.40
11:A:1227:A:C2	31:U:43:ARG:HG2	2.56	0.40
31:U:57:ALA:HB3	31:U:85:LYS:NZ	2.36	0.40
8:7:52:LYS:HG3	8:7:54:TYR:CE2	2.57	0.40
26:P:44:LEU:HA	26:P:47:VAL:HG22	2.03	0.40
30:T:85:SER:C	30:T:87:GLY:H	2.24	0.40
28:R:10:ARG:HG2	28:R:54:PHE:CE1	2.56	0.40
12:B:80:THR:C	12:B:82:GLY:H	2.24	0.40
11:A:924:A:O2'	11:A:987:G:OP1	2.36	0.40
29:S:12:PHE:CG	29:S:13:LYS:N	2.88	0.40
34:X:38:LEU:O	34:X:42:ARG:HB2	2.21	0.40
35:Y:39:GLU:HB2	35:Y:46:LYS:HG3	2.03	0.40
4:3:70:PHE:HA	4:3:70:PHE:HD1	1.65	0.40
4:3:62:VAL:HG11	4:3:70:PHE:HD2	1.87	0.40
11:A:1295:G:P	12:B:108:THR:OG1	2.79	0.40
10:9:87:UNK:C	10:9:89:UNK:N	2.84	0.40
5:4:185:THR:HA	5:4:188:LEU:HD12	2.03	0.40
11:A:142:G:C8	11:A:266:A:N1	2.89	0.40
4:3:35:LYS:HB3	4:3:35:LYS:HE3	1.89	0.40
11:A:817:A:H2'	11:A:818:C:C6	2.56	0.40
21:K:105:LEU:HD12	21:K:106:ALA:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:70:LEU:HD21	5:4:79:HIS:CG	2.56	0.40
11:A:686:C:H2'	11:A:687:G:C8	2.56	0.40
11:A:1357:A:C6	11:A:1358:G:C6	3.10	0.40
20:J:34:LEU:HD23	20:J:112:VAL:HG13	2.02	0.40
33:W:42:LEU:CD2	33:W:46:VAL:HB	2.52	0.40
11:A:1138:A:H2'	11:A:1139:A:H8	1.85	0.40
4:3:76:LYS:HE2	4:3:76:LYS:HB3	1.86	0.40
11:A:1361:U:O2	11:A:1361:U:H2'	2.21	0.40
28:R:250:TYR:CD1	28:R:250:TYR:N	2.90	0.40
2:1:54:LEU:HD12	2:1:54:LEU:HA	1.94	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 PDB entries followed by that with respect to all EM entries.

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
1	0	98/100 (98%)	89 (91%)	6 (6%)	3 (3%)	5 42
2	1	61/63 (97%)	47 (77%)	9 (15%)	5 (8%)	1 18
3	2	184/188 (98%)	155 (84%)	14 (8%)	15 (8%)	1 18
4	3	182/184 (99%)	128 (70%)	27 (15%)	27 (15%)	0 5
5	4	212/214 (99%)	132 (62%)	42 (20%)	38 (18%)	0 4
6	5	95/97 (98%)	58 (61%)	20 (21%)	17 (18%)	0 4
7	6	79/81 (98%)	62 (78%)	13 (16%)	4 (5%)	2 30
8	7	94/96 (98%)	66 (70%)	18 (19%)	10 (11%)	0 11
9	8	68/70 (97%)	46 (68%)	11 (16%)	11 (16%)	0 5
10	9	50/71 (70%)	30 (60%)	9 (18%)	11 (22%)	0 2
12	B	204/206 (99%)	143 (70%)	35 (17%)	26 (13%)	0 8
13	C	221/223 (99%)	180 (81%)	28 (13%)	13 (6%)	2 26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
14	D	183/185 (99%)	153 (84%)	18 (10%)	12 (7%)	1 24
15	E	215/217 (99%)	187 (87%)	16 (7%)	12 (6%)	2 28
16	F	81/83 (98%)	75 (93%)	5 (6%)	1 (1%)	16 61
17	G	204/206 (99%)	154 (76%)	31 (15%)	19 (9%)	1 16
18	H	127/129 (98%)	114 (90%)	10 (8%)	3 (2%)	7 47
19	I	139/141 (99%)	114 (82%)	14 (10%)	11 (8%)	1 19
20	J	105/107 (98%)	87 (83%)	13 (12%)	5 (5%)	3 31
21	K	125/127 (98%)	94 (75%)	16 (13%)	15 (12%)	0 8
22	L	142/144 (99%)	111 (78%)	13 (9%)	18 (13%)	0 8
23	M	143/145 (99%)	110 (77%)	19 (13%)	14 (10%)	1 14
24	N	51/53 (96%)	42 (82%)	7 (14%)	2 (4%)	4 36
25	O	148/150 (99%)	125 (84%)	15 (10%)	8 (5%)	2 29
26	P	132/134 (98%)	106 (80%)	13 (10%)	13 (10%)	1 14
27	Q	153/155 (99%)	125 (82%)	19 (12%)	9 (6%)	2 26
28	R	316/318 (99%)	273 (86%)	30 (10%)	13 (4%)	3 35
29	S	122/124 (98%)	92 (75%)	15 (12%)	15 (12%)	0 8
30	T	141/143 (99%)	111 (79%)	18 (13%)	12 (8%)	1 18
31	U	122/124 (98%)	66 (54%)	23 (19%)	33 (27%)	0 1
32	V	116/120 (97%)	87 (75%)	17 (15%)	12 (10%)	1 12
33	W	258/260 (99%)	202 (78%)	36 (14%)	20 (8%)	1 20
34	X	58/60 (97%)	49 (84%)	7 (12%)	2 (3%)	5 40
35	Y	224/226 (99%)	190 (85%)	22 (10%)	12 (5%)	2 29
36	Z	85/87 (98%)	64 (75%)	11 (13%)	10 (12%)	0 9
37	a	445/964 (46%)	438 (98%)	7 (2%)	0	100 100
38	b	478/763 (63%)	452 (95%)	24 (5%)	2 (0%)	39 80
39	c	542/812 (67%)	507 (94%)	35 (6%)	0	100 100
All	All	6403/7570 (85%)	5264 (82%)	686 (11%)	453 (7%)	3 22

All (453) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	24	ARG
2	1	36	THR

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Mol	Chain	Res	Type
2	1	51	ASN
3	2	13	ALA
3	2	22	ARG
3	2	147	ALA
3	2	149	SER
4	3	31	SER
4	3	36	ALA
4	3	64	VAL
4	3	67	LEU
4	3	98	ILE
4	3	104	ARG
4	3	105	THR
4	3	111	LYS
4	3	112	ARG
4	3	131	PHE
4	3	133	THR
4	3	134	GLU
4	3	155	ASP
5	4	21	VAL
5	4	26	ARG
5	4	49	ASN
5	4	58	SER
5	4	60	ALA
5	4	63	GLY
5	4	113	MET
5	4	116	LYS
5	4	176	VAL
5	4	177	GLN
5	4	179	SER
5	4	182	ALA
5	4	206	PRO
5	4	221	PRO
6	5	19	LYS
6	5	45	VAL
6	5	46	GLU
6	5	62	TYR
6	5	65	PRO
6	5	82	ARG
6	5	84	VAL
6	5	85	ARG
7	6	38	PRO
7	6	62	ILE

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Mol	Chain	Res	Type
8	7	60	SER
8	7	81	ASN
8	7	87	VAL
8	7	88	PRO
8	7	93	GLN
9	8	38	HIS
9	8	39	ALA
9	8	43	ASP
9	8	44	GLN
9	8	54	VAL
9	8	71	ILE
9	8	88	ILE
10	9	102	VAL
10	9	103	LEU
10	9	106	TYR
10	9	111	GLU
10	9	128	ALA
10	9	148	TYR
12	B	4	PRO
12	B	29	VAL
12	B	30	GLN
12	B	39	ASN
12	B	66	ALA
12	B	95	ALA
12	B	111	ILE
12	B	191	ARG
12	B	203	PHE
12	B	205	ARG
13	C	4	LEU
13	C	62	ASN
13	C	65	ARG
13	C	93	ASP
13	C	211	PRO
13	C	212	LYS
13	C	216	PRO
13	C	220	PRO
14	D	98	ALA
14	D	100	LYS
14	D	118	LEU
14	D	121	SER
14	D	164	PHE
15	E	146	THR

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Mol	Chain	Res	Type
15	E	148	LEU
16	F	72	PRO
17	G	26	ALA
17	G	39	GLU
17	G	43	PHE
17	G	63	GLN
17	G	101	GLY
17	G	153	GLY
17	G	206	SER
19	I	41	PRO
19	I	58	ASP
19	I	59	LYS
19	I	114	ARG
19	I	116	LEU
19	I	138	PHE
20	J	17	GLN
20	J	118	VAL
21	K	38	THR
21	K	39	ILE
21	K	124	ASP
21	K	125	SER
21	K	126	THR
22	L	3	LYS
22	L	41	SER
22	L	96	VAL
22	L	114	LYS
22	L	128	SER
22	L	131	SER
22	L	137	LYS
22	L	138	GLU
22	L	144	ARG
23	M	14	ILE
23	M	25	ASN
23	M	28	ILE
23	M	60	GLU
23	M	91	ASP
23	M	92	ILE
24	N	8	PHE
25	O	19	SER
25	O	22	ALA
26	P	32	ARG
26	P	36	SER

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Mol	Chain	Res	Type
26	P	78	SER
27	Q	7	VAL
27	Q	29	LYS
27	Q	133	LYS
28	R	51	ASP
28	R	160	GLU
28	R	318	ALA
29	S	29	SER
29	S	54	ALA
29	S	125	PRO
29	S	126	VAL
30	T	31	PRO
30	T	53	TRP
30	T	69	LYS
31	U	21	GLU
31	U	25	GLU
31	U	45	LEU
31	U	55	GLY
31	U	83	GLU
31	U	87	PRO
31	U	89	ILE
31	U	90	LYS
31	U	93	ASP
31	U	126	TRP
32	V	6	THR
32	V	26	LEU
32	V	85	VAL
32	V	86	PRO
32	V	88	VAL
32	V	96	SER
32	V	124	VAL
33	W	104	ASP
33	W	142	HIS
33	W	153	ASN
33	W	164	LEU
33	W	260	GLY
34	X	47	VAL
35	Y	20	ASP
35	Y	25	ARG
35	Y	154	ARG
35	Y	173	PRO
35	Y	174	LYS

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Mol	Chain	Res	Type
36	Z	4	ASP
36	Z	7	GLN
36	Z	11	LEU
38	b	557	GLU
38	b	661	GLU
2	1	35	ASP
2	1	61	ARG
3	2	40	ALA
3	2	105	ASP
3	2	120	THR
3	2	136	SER
3	2	199	LYS
4	3	32	PRO
4	3	156	SER
4	3	186	PRO
5	4	23	PRO
5	4	55	LYS
5	4	72	ASP
5	4	79	HIS
5	4	82	ARG
5	4	93	GLY
5	4	108	ASP
5	4	148	ASN
5	4	181	LEU
5	4	207	LEU
6	5	36	ILE
6	5	63	ALA
6	5	75	VAL
6	5	86	VAL
7	6	63	LEU
8	7	30	ALA
8	7	64	TYR
8	7	82	LEU
9	8	73	GLY
10	9	118	ARG
10	9	127	GLY
12	B	5	ALA
12	B	49	ASN
12	B	81	PHE
12	B	94	GLY
12	B	190	ASP
12	B	194	PRO

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Mol	Chain	Res	Type
12	B	196	SER
13	C	44	THR
13	C	218	LEU
14	D	134	ILE
14	D	167	ALA
14	D	171	ARG
15	E	35	TRP
15	E	203	LYS
15	E	248	SER
17	G	35	GLN
17	G	45	LYS
17	G	58	LEU
17	G	127	GLN
17	G	150	GLY
17	G	223	SER
18	H	66	ASN
19	I	40	GLU
19	I	113	ASP
21	K	40	ALA
21	K	42	VAL
21	K	46	MET
21	K	50	ALA
21	K	51	ASP
21	K	114	ARG
22	L	8	GLY
22	L	97	ASP
23	M	59	GLY
23	M	61	LEU
23	M	142	GLY
24	N	34	TYR
25	O	13	SER
25	O	28	LEU
25	O	68	GLY
26	P	5	VAL
26	P	11	LYS
28	R	3	SER
28	R	28	GLY
28	R	161	LYS
28	R	217	ASP
29	S	48	GLY
29	S	51	SER
29	S	101	ALA

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Mol	Chain	Res	Type
30	T	11	ALA
30	T	28	LEU
30	T	50	ALA
31	U	54	ARG
31	U	63	VAL
31	U	66	VAL
31	U	84	ASN
31	U	91	VAL
31	U	113	ARG
31	U	128	ALA
32	V	25	THR
33	W	12	LEU
33	W	152	PRO
33	W	157	ASN
33	W	195	ILE
33	W	245	LYS
35	Y	24	ILE
35	Y	146	GLY
35	Y	152	ASP
35	Y	153	VAL
36	Z	12	TYR
3	2	41	LYS
3	2	153	GLU
4	3	5	GLN
4	3	29	ASN
4	3	74	GLN
4	3	75	THR
4	3	110	GLN
5	4	35	PRO
5	4	38	PHE
5	4	62	LYS
5	4	209	ASN
6	5	66	LYS
9	8	41	ILE
9	8	55	PRO
9	8	97	LYS
10	9	138	ARG
12	B	27	ARG
12	B	103	THR
13	C	54	ARG
14	D	163	PRO
15	E	106	ASP

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Mol	Chain	Res	Type
15	E	150	GLN
15	E	235	LEU
17	G	33	VAL
17	G	156	ARG
20	J	55	PRO
21	K	18	ARG
21	K	123	SER
22	L	37	ALA
22	L	40	SER
22	L	89	ASN
23	M	10	SER
23	M	80	LYS
23	M	83	ALA
25	O	27	LYS
26	P	34	ASN
26	P	51	GLU
26	P	53	ASP
27	Q	4	GLU
27	Q	55	ASP
27	Q	146	ALA
27	Q	153	PHE
27	Q	154	ALA
28	R	15	GLY
28	R	96	THR
28	R	98	GLU
29	S	11	VAL
29	S	22	LEU
29	S	52	LYS
30	T	25	GLN
31	U	22	VAL
31	U	81	ASP
31	U	82	PRO
31	U	85	LYS
31	U	112	ALA
31	U	135	MET
32	V	83	GLN
32	V	115	LEU
33	W	200	ARG
36	Z	2	GLU
36	Z	10	GLU
36	Z	15	ARG
1	0	23	LYS

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Mol	Chain	Res	Type
2	1	6	PRO
3	2	59	ARG
3	2	152	ILE
4	3	13	PRO
4	3	84	LYS
4	3	132	PRO
5	4	54	LEU
5	4	61	LEU
5	4	81	PHE
5	4	112	SER
5	4	154	SER
5	4	215	VAL
6	5	64	LEU
8	7	94	GLU
10	9	145	HIS
12	B	33	GLN
12	B	158	VAL
12	B	164	ASN
12	B	185	ARG
12	B	189	VAL
13	C	217	ILE
15	E	39	THR
17	G	51	VAL
17	G	79	ASN
19	I	142	TYR
21	K	69	ALA
22	L	92	CYS
22	L	109	ARG
22	L	112	LYS
25	O	138	ASN
26	P	60	PHE
27	Q	145	ALA
28	R	136	ILE
28	R	163	ASP
28	R	237	GLN
30	T	7	ARG
30	T	23	GLN
30	T	39	THR
31	U	39	ASP
31	U	68	GLU
31	U	106	ILE
31	U	107	ASP

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Mol	Chain	Res	Type
31	U	108	ARG
31	U	129	GLU
31	U	130	THR
32	V	23	LYS
32	V	72	LYS
33	W	77	ARG
33	W	80	THR
33	W	163	ASP
33	W	188	ASN
33	W	193	GLY
34	X	50	VAL
35	Y	69	LEU
36	Z	44	ARG
1	0	68	LYS
4	3	73	VAL
4	3	185	ILE
5	4	64	ARG
7	6	51	GLN
13	C	59	LEU
14	D	162	SER
15	E	36	VAL
17	G	21	THR
17	G	64	VAL
18	H	67	GLY
18	H	83	ILE
20	J	49	ASN
22	L	70	LYS
26	P	6	THR
26	P	47	VAL
26	P	77	ASN
29	S	38	PRO
30	T	29	GLU
31	U	101	ALA
33	W	233	LYS
36	Z	46	ILE
36	Z	49	GLU
3	2	10	LYS
3	2	186	GLY
4	3	11	GLN
5	4	78	ASP
5	4	210	ILE
6	5	10	ARG

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Mol	Chain	Res	Type
12	B	139	VAL
14	D	132	ARG
20	J	117	VAL
23	M	7	GLU
23	M	34	THR
25	O	60	VAL
26	P	58	PHE
29	S	10	ARG
29	S	23	GLU
29	S	69	GLU
29	S	130	ARG
33	W	53	LYS
33	W	234	PRO
35	Y	132	ARG
14	D	117	GLY
19	I	97	VAL
21	K	48	VAL
6	5	59	TYR
12	B	117	GLU
31	U	40	GLY
5	4	197	ILE
6	5	50	VAL
10	9	147	VAL
15	E	145	GLY
19	I	29	ILE
30	T	100	ILE
8	7	89	GLY
31	U	117	GLY
33	W	45	ILE
35	Y	70	PRO
15	E	163	GLY

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	0	86/86 (100%)	84 (98%)	2 (2%)	58 82
2	1	56/56 (100%)	38 (68%)	18 (32%)	0 2
3	2	150/150 (100%)	118 (79%)	32 (21%)	1 9
4	3	165/165 (100%)	124 (75%)	41 (25%)	1 6
5	4	191/191 (100%)	137 (72%)	54 (28%)	0 3
6	5	83/83 (100%)	65 (78%)	18 (22%)	1 9
7	6	70/70 (100%)	62 (89%)	8 (11%)	7 32
8	7	77/89 (86%)	58 (75%)	19 (25%)	1 6
9	8	61/61 (100%)	43 (70%)	18 (30%)	0 3
10	9	43/43 (100%)	32 (74%)	11 (26%)	0 6
12	B	164/173 (95%)	122 (74%)	42 (26%)	0 6
13	C	182/182 (100%)	137 (75%)	45 (25%)	1 6
14	D	158/158 (100%)	117 (74%)	41 (26%)	0 5
15	E	176/176 (100%)	130 (74%)	46 (26%)	0 5
16	F	74/74 (100%)	73 (99%)	1 (1%)	74 89
17	G	173/173 (100%)	137 (79%)	36 (21%)	1 10
18	H	110/110 (100%)	84 (76%)	26 (24%)	1 7
19	I	117/117 (100%)	84 (72%)	33 (28%)	0 3
20	J	100/100 (100%)	71 (71%)	29 (29%)	0 3
21	K	81/96 (84%)	57 (70%)	24 (30%)	0 3
22	L	119/119 (100%)	96 (81%)	23 (19%)	2 13
23	M	128/128 (100%)	87 (68%)	41 (32%)	0 2
24	N	47/47 (100%)	38 (81%)	9 (19%)	2 13
25	O	127/127 (100%)	91 (72%)	36 (28%)	0 3
26	P	112/112 (100%)	84 (75%)	28 (25%)	1 6
27	Q	129/136 (95%)	105 (81%)	24 (19%)	2 14
28	R	259/261 (99%)	222 (86%)	37 (14%)	4 25
29	S	101/104 (97%)	82 (81%)	19 (19%)	2 13
30	T	115/115 (100%)	84 (73%)	31 (27%)	0 5
31	U	88/100 (88%)	55 (62%)	33 (38%)	0 1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
32	V	94/109 (86%)	70 (74%)	24 (26%)	1 6
33	W	221/221 (100%)	166 (75%)	55 (25%)	1 6
34	X	51/51 (100%)	43 (84%)	8 (16%)	3 21
35	Y	188/193 (97%)	149 (79%)	39 (21%)	1 10
36	Z	74/74 (100%)	56 (76%)	18 (24%)	1 6
37	a	404/846 (48%)	404 (100%)	0	100 100
38	b	430/693 (62%)	421 (98%)	9 (2%)	61 84
39	c	506/749 (68%)	487 (96%)	19 (4%)	40 73
All	All	5510/6538 (84%)	4513 (82%)	997 (18%)	5 15

All (997) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	44	ASN
1	0	75	ASP
2	1	5	THR
2	1	13	ILE
2	1	14	LYS
2	1	15	VAL
2	1	19	THR
2	1	32	PHE
2	1	33	LEU
2	1	34	GLU
2	1	38	ARG
2	1	39	THR
2	1	49	ARG
2	1	52	ASP
2	1	57	MET
2	1	58	GLU
2	1	59	SER
2	1	62	GLU
2	1	64	ARG
2	1	65	ARG
3	2	6	ASP
3	2	7	SER
3	2	8	ARG
3	2	14	THR
3	2	20	GLN
3	2	21	PHE

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Mol	Chain	Res	Type
3	2	26	LYS
3	2	28	GLU
3	2	29	LEU
3	2	36	THR
3	2	46	VAL
3	2	49	ARG
3	2	58	LEU
3	2	76	THR
3	2	103	GLN
3	2	107	THR
3	2	120	THR
3	2	121	LEU
3	2	123	LYS
3	2	135	LYS
3	2	137	LYS
3	2	138	ASN
3	2	140	GLU
3	2	142	LYS
3	2	151	LYS
3	2	152	ILE
3	2	154	SER
3	2	155	SER
3	2	164	ARG
3	2	184	LEU
3	2	196	LEU
3	2	199	LYS
4	3	9	LEU
4	3	25	VAL
4	3	37	GLU
4	3	38	LEU
4	3	42	GLN
4	3	46	ILE
4	3	50	ASP
4	3	51	VAL
4	3	60	ILE
4	3	66	SER
4	3	67	LEU
4	3	70	PHE
4	3	71	HIS
4	3	74	GLN
4	3	75	THR
4	3	77	LEU

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Mol	Chain	Res	Type
4	3	78	THR
4	3	79	ARG
4	3	80	GLU
4	3	85	PHE
4	3	87	ASP
4	3	97	ARG
4	3	103	SER
4	3	105	THR
4	3	109	VAL
4	3	110	GLN
4	3	114	ARG
4	3	116	ARG
4	3	117	THR
4	3	126	LEU
4	3	131	PHE
4	3	143	LEU
4	3	144	VAL
4	3	148	LYS
4	3	154	LEU
4	3	162	ILE
4	3	167	GLU
4	3	181	ILE
4	3	184	GLU
4	3	185	ILE
4	3	187	SER
5	4	21	VAL
5	4	22	ASP
5	4	36	SER
5	4	38	PHE
5	4	47	LEU
5	4	54	LEU
5	4	55	LYS
5	4	58	SER
5	4	61	LEU
5	4	65	VAL
5	4	68	VAL
5	4	70	LEU
5	4	73	LEU
5	4	77	GLU
5	4	78	ASP
5	4	80	SER
5	4	81	PHE

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Mol	Chain	Res	Type
5	4	83	LYS
5	4	85	LYS
5	4	89	ASP
5	4	94	LYS
5	4	96	LEU
5	4	97	LEU
5	4	105	PHE
5	4	108	ASP
5	4	109	LYS
5	4	110	LEU
5	4	115	ARG
5	4	117	TRP
5	4	124	ASN
5	4	131	ASP
5	4	135	LEU
5	4	146	GLN
5	4	148	ASN
5	4	149	GLN
5	4	154	SER
5	4	166	LYS
5	4	170	GLU
5	4	177	GLN
5	4	179	SER
5	4	180	THR
5	4	181	LEU
5	4	183	GLN
5	4	184	LEU
5	4	193	ILE
5	4	202	LYS
5	4	214	LYS
5	4	215	VAL
5	4	218	LEU
5	4	219	LYS
5	4	220	GLN
5	4	223	PHE
5	4	225	VAL
5	4	228	LEU
6	5	12	LYS
6	5	36	ILE
6	5	41	ILE
6	5	44	ILE
6	5	45	VAL

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Mol	Chain	Res	Type
6	5	53	LEU
6	5	58	VAL
6	5	61	GLU
6	5	64	LEU
6	5	66	LYS
6	5	67	THR
6	5	69	ASN
6	5	70	LYS
6	5	82	ARG
6	5	83	ILE
6	5	85	ARG
6	5	86	VAL
6	5	90	GLU
7	6	3	LEU
7	6	4	VAL
7	6	20	LYS
7	6	29	ARG
7	6	33	LEU
7	6	34	ASP
7	6	41	LEU
7	6	67	THR
8	7	1	MET
8	7	7	ASP
8	7	8	ARG
8	7	13	GLN
8	7	20	VAL
8	7	27	PHE
8	7	29	GLN
8	7	31	LYS
8	7	32	HIS
8	7	46	LEU
8	7	49	LEU
8	7	50	THR
8	7	55	VAL
8	7	56	LYS
8	7	71	GLU
8	7	76	LEU
8	7	78	GLU
8	7	80	LEU
8	7	82	LEU
9	8	38	HIS
9	8	42	LEU

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Mol	Chain	Res	Type
9	8	49	ARG
9	8	50	ILE
9	8	58	ARG
9	8	59	TYR
9	8	69	LEU
9	8	71	ILE
9	8	75	LEU
9	8	77	ARG
9	8	80	LEU
9	8	85	LYS
9	8	92	ILE
9	8	93	SER
9	8	95	HIS
9	8	96	SER
9	8	100	ILE
9	8	105	THR
10	9	102	VAL
10	9	108	VAL
10	9	120	GLU
10	9	121	CYS
10	9	125	THR
10	9	130	VAL
10	9	137	ASP
10	9	140	TYR
10	9	146	SER
10	9	147	VAL
10	9	151	ASN
12	B	7	PHE
12	B	10	THR
12	B	24	LEU
12	B	27	ARG
12	B	29	VAL
12	B	33	GLN
12	B	34	GLU
12	B	37	VAL
12	B	43	ASP
12	B	45	VAL
12	B	47	VAL
12	B	50	VAL
12	B	57	LEU
12	B	59	LEU
12	B	62	ARG

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Mol	Chain	Res	Type
12	B	76	ILE
12	B	79	ARG
12	B	84	ARG
12	B	87	LEU
12	B	88	LYS
12	B	96	THR
12	B	101	ARG
12	B	103	THR
12	B	110	TYR
12	B	111	ILE
12	B	114	SER
12	B	117	GLU
12	B	119	ARG
12	B	123	VAL
12	B	131	GLN
12	B	135	GLU
12	B	140	ASN
12	B	154	GLU
12	B	157	ASP
12	B	162	CYS
12	B	168	HIS
12	B	172	LEU
12	B	177	LEU
12	B	184	LEU
12	B	185	ARG
12	B	196	SER
12	B	197	ILE
13	C	4	LEU
13	C	5	ILE
13	C	7	LYS
13	C	21	LEU
13	C	23	GLU
13	C	29	LEU
13	C	37	VAL
13	C	39	VAL
13	C	53	THR
13	C	57	ASP
13	C	65	ARG
13	C	66	ILE
13	C	81	PRO
13	C	84	ILE
13	C	89	GLU

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Mol	Chain	Res	Type
13	C	90	ARG
13	C	92	GLN
13	C	93	ASP
13	C	94	ARG
13	C	96	LEU
13	C	105	MET
13	C	113	LEU
13	C	117	ARG
13	C	127	MET
13	C	129	SER
13	C	134	CYS
13	C	141	LYS
13	C	142	LEU
13	C	146	ARG
13	C	151	LYS
13	C	158	ILE
13	C	170	THR
13	C	172	THR
13	C	176	LEU
13	C	178	ARG
13	C	181	VAL
13	C	182	LEU
13	C	187	LYS
13	C	190	ARG
13	C	204	ASP
13	C	210	GLU
13	C	215	GLU
13	C	220	PRO
13	C	221	SER
13	C	222	VAL
14	D	3	ARG
14	D	6	ARG
14	D	7	THR
14	D	13	SER
14	D	14	THR
14	D	22	SER
14	D	28	LEU
14	D	39	LYS
14	D	46	SER
14	D	49	LEU
14	D	54	ARG
14	D	60	LEU

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Mol	Chain	Res	Type
14	D	78	ARG
14	D	79	ARG
14	D	82	ARG
14	D	88	GLU
14	D	89	ASP
14	D	92	LYS
14	D	93	LEU
14	D	94	ASP
14	D	96	VAL
14	D	97	LEU
14	D	99	LEU
14	D	101	VAL
14	D	105	LEU
14	D	109	LEU
14	D	110	GLN
14	D	111	THR
14	D	120	LYS
14	D	130	THR
14	D	133	HIS
14	D	134	ILE
14	D	138	LYS
14	D	149	ARG
14	D	151	ASP
14	D	161	THR
14	D	171	ARG
14	D	172	VAL
14	D	174	ARG
14	D	175	ARG
14	D	182	GLU
15	E	41	LEU
15	E	50	ILE
15	E	53	ILE
15	E	58	LEU
15	E	64	LYS
15	E	70	ASP
15	E	71	THR
15	E	72	LEU
15	E	73	LEU
15	E	76	LEU
15	E	77	GLN
15	E	80	VAL
15	E	87	GLN

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Mol	Chain	Res	Type
15	E	89	GLN
15	E	90	THR
15	E	95	ARG
15	E	96	THR
15	E	97	ARG
15	E	106	ASP
15	E	111	VAL
15	E	117	THR
15	E	119	LYS
15	E	130	ILE
15	E	134	LEU
15	E	137	ILE
15	E	139	ILE
15	E	140	ARG
15	E	141	ARG
15	E	146	THR
15	E	148	LEU
15	E	159	THR
15	E	166	THR
15	E	174	ARG
15	E	185	LYS
15	E	187	LEU
15	E	201	ASN
15	E	206	THR
15	E	208	GLU
15	E	221	THR
15	E	222	TYR
15	E	224	PHE
15	E	226	THR
15	E	237	VAL
15	E	240	LEU
15	E	245	ASP
15	E	246	GLU
16	F	73	GLU
17	G	21	THR
17	G	23	VAL
17	G	24	VAL
17	G	25	LEU
17	G	27	THR
17	G	32	GLU
17	G	41	LYS
17	G	42	LEU

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Mol	Chain	Res	Type
17	G	43	PHE
17	G	45	LYS
17	G	53	VAL
17	G	63	GLN
17	G	65	ARG
17	G	68	ILE
17	G	70	VAL
17	G	76	ARG
17	G	79	ASN
17	G	84	LYS
17	G	89	ILE
17	G	93	LEU
17	G	94	THR
17	G	117	THR
17	G	119	ASP
17	G	130	ILE
17	G	146	THR
17	G	147	THR
17	G	156	ARG
17	G	157	ARG
17	G	160	VAL
17	G	162	VAL
17	G	163	SER
17	G	193	THR
17	G	203	LYS
17	G	206	SER
17	G	216	GLU
17	G	225	ARG
18	H	3	ARG
18	H	6	VAL
18	H	7	LEU
18	H	23	ARG
18	H	24	GLN
18	H	25	VAL
18	H	27	ILE
18	H	30	SER
18	H	43	LYS
18	H	53	ILE
18	H	56	HIS
18	H	65	LEU
18	H	66	ASN
18	H	69	LEU

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Mol	Chain	Res	Type
18	H	74	VAL
18	H	76	SER
18	H	83	ILE
18	H	87	GLU
18	H	93	LEU
18	H	98	GLN
18	H	103	ILE
18	H	104	LEU
18	H	105	THR
18	H	114	GLU
18	H	121	VAL
18	H	129	VAL
19	I	4	VAL
19	I	14	LYS
19	I	17	THR
19	I	23	LYS
19	I	26	LYS
19	I	28	LEU
19	I	36	ILE
19	I	44	LEU
19	I	45	ARG
19	I	52	LEU
19	I	53	LEU
19	I	54	LEU
19	I	57	LEU
19	I	58	ASP
19	I	59	LYS
19	I	63	ILE
19	I	66	ARG
19	I	68	ARG
19	I	69	VAL
19	I	76	SER
19	I	90	VAL
19	I	94	GLN
19	I	98	ASP
19	I	101	SER
19	I	106	LYS
19	I	115	THR
19	I	118	ILE
19	I	123	ARG
19	I	128	LYS
19	I	136	SER

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Mol	Chain	Res	Type
19	I	137	ARG
19	I	138	PHE
19	I	141	SER
20	J	15	GLN
20	J	17	GLN
20	J	18	GLN
20	J	20	ILE
20	J	22	ILE
20	J	23	ARG
20	J	27	THR
20	J	30	LYS
20	J	31	VAL
20	J	34	LEU
20	J	35	GLU
20	J	42	VAL
20	J	47	GLN
20	J	48	HIS
20	J	51	VAL
20	J	57	ARG
20	J	58	LEU
20	J	60	THR
20	J	61	LYS
20	J	66	SER
20	J	74	GLU
20	J	76	SER
20	J	81	THR
20	J	88	LYS
20	J	89	ARG
20	J	99	ILE
20	J	103	ILE
20	J	108	ILE
20	J	121	ASN
21	K	13	VAL
21	K	14	PHE
21	K	16	VAL
21	K	20	TYR
21	K	24	ASN
21	K	26	THR
21	K	29	HIS
21	K	31	THR
21	K	39	ILE
21	K	42	VAL

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Mol	Chain	Res	Type
21	K	43	THR
21	K	51	ASP
21	K	92	LYS
21	K	99	GLN
21	K	102	LEU
21	K	103	ARG
21	K	107	ARG
21	K	108	SER
21	K	118	VAL
21	K	123	SER
21	K	124	ASP
21	K	125	SER
21	K	133	ARG
21	K	137	LEU
22	L	7	ARG
22	L	9	LEU
22	L	14	LYS
22	L	18	HIS
22	L	19	ARG
22	L	28	ASN
22	L	40	SER
22	L	60	GLU
22	L	69	ARG
22	L	82	LYS
22	L	84	THR
22	L	103	LEU
22	L	107	PHE
22	L	109	ARG
22	L	110	LYS
22	L	114	LYS
22	L	117	ILE
22	L	131	SER
22	L	133	LEU
22	L	137	LYS
22	L	138	GLU
22	L	140	LYS
22	L	144	ARG
23	M	3	LEU
23	M	5	VAL
23	M	8	GLN
23	M	11	PHE
23	M	12	GLN

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Mol	Chain	Res	Type
23	M	13	HIS
23	M	14	ILE
23	M	15	LEU
23	M	17	LEU
23	M	20	THR
23	M	21	ASN
23	M	26	ILE
23	M	28	ILE
23	M	34	THR
23	M	38	VAL
23	M	40	ARG
23	M	46	VAL
23	M	53	ASP
23	M	54	LEU
23	M	57	ARG
23	M	60	GLU
23	M	61	LEU
23	M	71	GLN
23	M	74	GLN
23	M	77	THR
23	M	80	LYS
23	M	81	ILE
23	M	86	LEU
23	M	89	GLN
23	M	92	ILE
23	M	93	THR
23	M	107	SER
23	M	108	LYS
23	M	110	ARG
23	M	116	LEU
23	M	119	ILE
23	M	132	ARG
23	M	136	GLN
23	M	138	THR
23	M	140	THR
23	M	143	ARG
24	N	6	VAL
24	N	8	PHE
24	N	22	ARG
24	N	25	SER
24	N	30	LEU
24	N	32	ARG

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Mol	Chain	Res	Type
24	N	36	LEU
24	N	39	CYS
24	N	48	ASN
25	O	3	ARG
25	O	4	MET
25	O	9	LYS
25	O	12	SER
25	O	16	ILE
25	O	21	ASN
25	O	27	LYS
25	O	33	VAL
25	O	36	GLN
25	O	39	LYS
25	O	42	ARG
25	O	45	LEU
25	O	50	ILE
25	O	56	ASP
25	O	58	HIS
25	O	60	VAL
25	O	64	ARG
25	O	66	ILE
25	O	67	THR
25	O	76	LYS
25	O	77	SER
25	O	83	GLU
25	O	84	ILE
25	O	88	LEU
25	O	94	LYS
25	O	97	SER
25	O	102	LEU
25	O	105	ASN
25	O	109	LYS
25	O	114	ARG
25	O	115	LEU
25	O	125	LEU
25	O	145	THR
25	O	149	LEU
25	O	150	VAL
25	O	151	ASN
26	P	17	LEU
26	P	29	HIS
26	P	32	ARG

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Mol	Chain	Res	Type
26	P	34	ASN
26	P	44	LEU
26	P	46	GLU
26	P	47	VAL
26	P	49	LYS
26	P	51	GLU
26	P	52	LYS
26	P	57	VAL
26	P	61	ARG
26	P	62	THR
26	P	75	VAL
26	P	84	LYS
26	P	88	THR
26	P	93	ARG
26	P	96	LEU
26	P	99	LYS
26	P	102	LYS
26	P	105	ARG
26	P	112	LYS
26	P	123	LYS
26	P	124	ARG
26	P	127	LYS
26	P	128	LYS
26	P	129	VAL
26	P	135	ASP
27	Q	3	THR
27	Q	7	VAL
27	Q	21	ASN
27	Q	27	THR
27	Q	29	LYS
27	Q	30	ARG
27	Q	40	LEU
27	Q	43	LYS
27	Q	44	THR
27	Q	54	ILE
27	Q	56	LYS
27	Q	67	ARG
27	Q	69	LYS
27	Q	74	THR
27	Q	79	LYS
27	Q	80	MET
27	Q	83	THR

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Mol	Chain	Res	Type
27	Q	99	ARG
27	Q	109	VAL
27	Q	123	VAL
27	Q	131	ILE
27	Q	136	ARG
27	Q	140	VAL
27	Q	141	LYS
28	R	6	VAL
28	R	7	LEU
28	R	8	VAL
28	R	46	LYS
28	R	48	THR
28	R	51	ASP
28	R	52	GLN
28	R	59	ARG
28	R	71	CYS
28	R	76	ASP
28	R	87	LYS
28	R	88	THR
28	R	94	VAL
28	R	96	THR
28	R	112	SER
28	R	117	LYS
28	R	118	LYS
28	R	129	LYS
28	R	134	TRP
28	R	136	ILE
28	R	137	LYS
28	R	141	LEU
28	R	149	ASP
28	R	153	GLN
28	R	165	ASP
28	R	166	SER
28	R	188	ILE
28	R	199	ILE
28	R	207	ASP
28	R	221	MET
28	R	238	ASP
28	R	250	TYR
28	R	266	ASP
28	R	268	GLN
28	R	292	LEU

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Mol	Chain	Res	Type
28	R	300	THR
28	R	317	THR
29	S	14	THR
29	S	22	LEU
29	S	24	LYS
29	S	26	LEU
29	S	31	GLU
29	S	35	LYS
29	S	40	ARG
29	S	44	ARG
29	S	47	ARG
29	S	50	THR
29	S	52	LYS
29	S	69	GLU
29	S	86	VAL
29	S	92	SER
29	S	100	LYS
29	S	110	GLU
29	S	121	ILE
29	S	125	PRO
29	S	130	ARG
30	T	4	VAL
30	T	6	VAL
30	T	13	ASP
30	T	18	TYR
30	T	22	LEU
30	T	25	GLN
30	T	28	LEU
30	T	30	VAL
30	T	33	TYR
30	T	34	VAL
30	T	35	ASP
30	T	36	ILE
30	T	37	VAL
30	T	57	ARG
30	T	63	ARG
30	T	67	MET
30	T	68	ARG
30	T	84	LYS
30	T	86	ARG
30	T	88	VAL
30	T	89	ARG

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Mol	Chain	Res	Type
30	T	92	LYS
30	T	94	ILE
30	T	103	LYS
30	T	111	ILE
30	T	126	GLU
30	T	130	ARG
30	T	131	ASP
30	T	132	LEU
30	T	134	ARG
30	T	144	GLU
31	U	25	GLU
31	U	28	LEU
31	U	33	ARG
31	U	36	LEU
31	U	43	ARG
31	U	45	LEU
31	U	50	LYS
31	U	53	THR
31	U	58	LEU
31	U	59	LEU
31	U	61	VAL
31	U	62	LEU
31	U	63	VAL
31	U	71	ILE
31	U	74	LEU
31	U	75	VAL
31	U	83	GLU
31	U	85	LYS
31	U	88	LEU
31	U	89	ILE
31	U	97	LEU
31	U	103	LEU
31	U	116	VAL
31	U	119	SER
31	U	121	VAL
31	U	125	ASN
31	U	126	TRP
31	U	129	GLU
31	U	132	GLU
31	U	135	MET
31	U	138	GLU
31	U	139	HIS

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Mol	Chain	Res	Type
31	U	140	PHE
32	V	5	ARG
32	V	25	THR
32	V	26	LEU
32	V	29	GLN
32	V	30	THR
32	V	34	LEU
32	V	36	ASP
32	V	38	ILE
32	V	44	LYS
32	V	46	LEU
32	V	49	LYS
32	V	54	THR
32	V	69	ILE
32	V	72	LYS
32	V	73	LEU
32	V	78	ARG
32	V	83	GLN
32	V	84	TYR
32	V	87	GLU
32	V	105	GLN
32	V	107	SER
32	V	113	LEU
32	V	115	LEU
32	V	119	LEU
33	W	7	LYS
33	W	9	LEU
33	W	12	LEU
33	W	23	LEU
33	W	26	CYS
33	W	38	LEU
33	W	39	ARG
33	W	45	ILE
33	W	48	LEU
33	W	56	LEU
33	W	59	ARG
33	W	62	LYS
33	W	67	GLN
33	W	68	ARG
33	W	70	VAL
33	W	72	VAL
33	W	77	ARG

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Mol	Chain	Res	Type
33	W	92	LEU
33	W	95	THR
33	W	105	VAL
33	W	116	ASP
33	W	117	GLU
33	W	123	LEU
33	W	126	VAL
33	W	129	VAL
33	W	131	LEU
33	W	133	LYS
33	W	146	THR
33	W	153	ASN
33	W	155	LYS
33	W	158	ASP
33	W	164	LEU
33	W	166	SER
33	W	176	ASP
33	W	180	LEU
33	W	182	TYR
33	W	187	ARG
33	W	192	ILE
33	W	197	HIS
33	W	198	LYS
33	W	206	ASP
33	W	211	LYS
33	W	215	ASP
33	W	220	THR
33	W	222	LEU
33	W	226	PHE
33	W	227	VAL
33	W	237	SER
33	W	240	LYS
33	W	242	LYS
33	W	246	LEU
33	W	248	ILE
33	W	258	GLN
33	W	259	GLN
33	W	261	LEU
34	X	20	LYS
34	X	25	GLU
34	X	26	LYS
34	X	28	LYS

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Mol	Chain	Res	Type
34	X	29	LYS
34	X	42	ARG
34	X	48	THR
34	X	50	VAL
35	Y	21	GLU
35	Y	25	ARG
35	Y	45	PHE
35	Y	58	LYS
35	Y	59	GLN
35	Y	69	LEU
35	Y	70	PRO
35	Y	71	THR
35	Y	76	LEU
35	Y	78	THR
35	Y	79	LYS
35	Y	82	SER
35	Y	98	ARG
35	Y	105	ASP
35	Y	109	LEU
35	Y	115	LYS
35	Y	120	GLU
35	Y	124	LEU
35	Y	126	ASP
35	Y	127	THR
35	Y	129	VAL
35	Y	132	ARG
35	Y	133	LEU
35	Y	137	ARG
35	Y	143	LYS
35	Y	150	GLU
35	Y	151	ASP
35	Y	154	ARG
35	Y	155	ASP
35	Y	162	VAL
35	Y	170	THR
35	Y	175	ILE
35	Y	176	GLN
35	Y	177	ARG
35	Y	179	VAL
35	Y	211	LEU
35	Y	212	LEU
35	Y	217	SER

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Mol	Chain	Res	Type
35	Y	223	LYS
36	Z	1	MET
36	Z	2	GLU
36	Z	3	ASN
36	Z	5	LYS
36	Z	7	GLN
36	Z	11	LEU
36	Z	25	LYS
36	Z	41	GLU
36	Z	49	GLU
36	Z	50	TYR
36	Z	52	THR
36	Z	60	ARG
36	Z	62	ARG
36	Z	68	SER
36	Z	69	LEU
36	Z	74	GLN
36	Z	76	ASP
36	Z	80	LYS
38	b	219	TRP
38	b	559	THR
38	b	560	ASP
38	b	561	VAL
38	b	564	ARG
38	b	565	TRP
38	b	643	ASP
38	b	659	LYS
38	b	660	VAL
39	c	300	ILE
39	c	309	ASN
39	c	326	SER
39	c	348	ILE
39	c	407	LEU
39	c	441	TYR
39	c	473	LEU
39	c	483	ILE
39	c	529	GLN
39	c	550	LEU
39	c	571	LEU
39	c	582	GLN
39	c	589	SER
39	c	648	SER

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Mol	Chain	Res	Type
39	c	652	ILE
39	c	738	VAL
39	c	771	ASP
39	c	778	VAL
39	c	782	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (45) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	33	GLN
1	0	55	ASN
1	0	106	GLN
3	2	64	ASN
3	2	103	GLN
5	4	101	HIS
5	4	149	GLN
5	4	177	GLN
9	8	95	HIS
13	C	179	GLN
14	D	110	GLN
14	D	131	GLN
15	E	89	GLN
15	E	94	GLN
16	F	27	HIS
16	F	79	GLN
16	F	84	GLN
16	F	99	GLN
16	F	102	ASN
16	F	106	HIS
17	G	104	ASN
17	G	128	ASN
17	G	170	GLN
18	H	24	GLN
18	H	80	ASN
19	I	62	ASN
19	I	74	HIS
20	J	18	GLN
23	M	19	ASN
23	M	89	GLN
24	N	48	ASN
24	N	53	ASN
27	Q	110	HIS

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Mol	Chain	Res	Type
30	T	64	HIS
31	U	125	ASN
32	V	105	GLN
33	W	98	ASN
35	Y	22	HIS
36	Z	74	GLN
38	b	459	ASN
39	c	495	ASN
39	c	529	GLN
39	c	564	HIS
39	c	582	GLN
39	c	611	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	1763/1781 (98%)	544 (30%)	86 (4%)

All (544) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	2	A
11	A	4	C
11	A	8	U
11	A	16	G
11	A	20	G
11	A	25	C
11	A	26	A
11	A	27	U
11	A	34	G
11	A	39	A
11	A	41	A
11	A	42	G
11	A	45	U
11	A	46	A
11	A	47	A
11	A	50	C
11	A	57	G
11	A	60	U
11	A	67	A
11	A	68	A

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Mol	Chain	Res	Type
11	A	69	G
11	A	72	A
11	A	73	U
11	A	74	U
11	A	75	U
11	A	76	A
11	A	77	U
11	A	78	A
11	A	97	C
11	A	100	A
11	A	101	U
11	A	104	A
11	A	114	C
11	A	126	A
11	A	127	G
11	A	131	C
11	A	132	U
11	A	133	U
11	A	134	U
11	A	135	A
11	A	136	C
11	A	137	U
11	A	138	A
11	A	139	C
11	A	140	A
11	A	141	U
11	A	144	U
11	A	145	A
11	A	146	U
11	A	153	G
11	A	158	U
11	A	159	U
11	A	175	G
11	A	178	U
11	A	179	A
11	A	185	U
11	A	186	C
11	A	187	G
11	A	188	A
11	A	189	C
11	A	190	C
11	A	191	C

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Mol	Chain	Res	Type
11	A	192	U
11	A	193	U
11	A	194	U
11	A	195	G
11	A	196	G
11	A	197	A
11	A	198	A
11	A	199	G
11	A	200	A
11	A	215	A
11	A	218	A
11	A	219	A
11	A	223	U
11	A	225	A
11	A	226	A
11	A	227	U
11	A	228	G
11	A	229	U
11	A	233	C
11	A	234	G
11	A	235	G
11	A	236	A
11	A	238	U
11	A	239	C
11	A	240	U
11	A	241	U
11	A	242	U
11	A	249	U
11	A	250	C
11	A	261	U
11	A	262	U
11	A	265	A
11	A	266	A
11	A	271	A
11	A	272	U
11	A	274	G
11	A	275	C
11	A	276	C
11	A	277	U
11	A	278	U
11	A	279	G
11	A	280	U

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Mol	Chain	Res	Type
11	A	281	G
11	A	288	A
11	A	290	G
11	A	299	A
11	A	301	A
11	A	306	U
11	A	308	C
11	A	309	C
11	A	314	C
11	A	316	A
11	A	319	U
11	A	320	U
11	A	321	C
11	A	322	G
11	A	337	G
11	A	338	C
11	A	341	A
11	A	348	U
11	A	352	A
11	A	359	A
11	A	360	A
11	A	361	C
11	A	399	A
11	A	400	A
11	A	401	A
11	A	402	C
11	A	403	G
11	A	404	G
11	A	411	C
11	A	416	A
11	A	418	G
11	A	423	G
11	A	424	C
11	A	425	A
11	A	426	G
11	A	428	A
11	A	434	G
11	A	439	U
11	A	444	C
11	A	445	A
11	A	446	A
11	A	448	C

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Mol	Chain	Res	Type
11	A	467	G
11	A	468	A
11	A	470	A
11	A	475	A
11	A	477	A
11	A	484	C
11	A	485	A
11	A	486	G
11	A	487	G
11	A	488	G
11	A	493	U
11	A	494	U
11	A	495	C
11	A	496	G
11	A	497	G
11	A	498	G
11	A	499	U
11	A	500	C
11	A	502	U
11	A	503	G
11	A	504	U
11	A	505	A
11	A	506	A
11	A	507	U
11	A	508	U
11	A	510	G
11	A	511	A
11	A	512	A
11	A	513	U
11	A	515	A
11	A	516	G
11	A	519	C
11	A	525	A
11	A	527	A
11	A	532	U
11	A	538	A
11	A	539	G
11	A	540	G
11	A	541	A
11	A	542	A
11	A	543	C
11	A	544	A

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Mol	Chain	Res	Type
11	A	545	A
11	A	548	G
11	A	555	A
11	A	556	A
11	A	557	G
11	A	558	U
11	A	559	C
11	A	565	C
11	A	570	A
11	A	575	C
11	A	579	A
11	A	580	A
11	A	582	U
11	A	583	C
11	A	585	A
11	A	594	A
11	A	595	G
11	A	597	G
11	A	605	A
11	A	607	G
11	A	611	U
11	A	619	A
11	A	620	A
11	A	622	A
11	A	623	A
11	A	624	G
11	A	630	A
11	A	639	U
11	A	640	U
11	A	650	U
11	A	653	C
11	A	655	G
11	A	656	G
11	A	657	U
11	A	658	C
11	A	677	G
11	A	679	U
11	A	680	U
11	A	684	A
11	A	685	A
11	A	686	C
11	A	692	C

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Mol	Chain	Res	Type
11	A	694	U
11	A	696	C
11	A	697	C
11	A	699	U
11	A	700	C
11	A	701	U
11	A	702	G
11	A	703	G
11	A	704	C
11	A	705	U
11	A	706	A
11	A	707	A
11	A	709	C
11	A	710	U
11	A	712	G
11	A	713	A
11	A	714	G
11	A	717	C
11	A	718	U
11	A	719	U
11	A	720	G
11	A	721	U
11	A	722	G
11	A	723	G
11	A	725	U
11	A	727	U
11	A	728	U
11	A	729	G
11	A	730	G
11	A	731	C
11	A	732	G
11	A	733	A
11	A	734	A
11	A	735	C
11	A	736	C
11	A	737	A
11	A	738	G
11	A	742	U
11	A	743	U
11	A	745	U
11	A	754	A
11	A	755	A

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Mol	Chain	Res	Type
11	A	756	A
11	A	758	U
11	A	765	G
11	A	766	U
11	A	771	A
11	A	774	A
11	A	775	G
11	A	778	G
11	A	780	A
11	A	781	U
11	A	782	U
11	A	783	G
11	A	784	C
11	A	785	U
11	A	787	G
11	A	789	A
11	A	793	A
11	A	794	U
11	A	795	U
11	A	806	A
11	A	811	A
11	A	812	A
11	A	813	U
11	A	815	G
11	A	816	G
11	A	818	C
11	A	819	G
11	A	820	U
11	A	821	U
11	A	823	G
11	A	824	G
11	A	829	A
11	A	830	U
11	A	831	U
11	A	832	U
11	A	833	U
11	A	837	G
11	A	838	G
11	A	840	U
11	A	846	G
11	A	848	C
11	A	849	C

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Mol	Chain	Res	Type
11	A	854	U
11	A	862	A
11	A	863	A
11	A	864	U
11	A	873	U
11	A	876	G
11	A	892	A
11	A	896	U
11	A	898	A
11	A	912	U
11	A	913	G
11	A	914	G
11	A	921	U
11	A	928	U
11	A	933	A
11	A	935	U
11	A	942	G
11	A	944	A
11	A	951	A
11	A	959	U
11	A	960	U
11	A	961	U
11	A	966	A
11	A	968	U
11	A	982	U
11	A	988	A
11	A	992	A
11	A	993	A
11	A	995	A
11	A	997	G
11	A	1003	A
11	A	1004	U
11	A	1005	A
11	A	1020	A
11	A	1021	C
11	A	1026	A
11	A	1028	C
11	A	1031	U
11	A	1039	A
11	A	1040	G
11	A	1052	U
11	A	1053	G

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Mol	Chain	Res	Type
11	A	1058	U
11	A	1059	U
11	A	1060	U
11	A	1061	A
11	A	1064	G
11	A	1073	G
11	A	1074	G
11	A	1079	U
11	A	1080	U
11	A	1082	C
11	A	1083	G
11	A	1084	A
11	A	1086	A
11	A	1087	A
11	A	1091	A
11	A	1092	A
11	A	1093	A
11	A	1096	C
11	A	1097	U
11	A	1100	G
11	A	1104	U
11	A	1111	G
11	A	1138	A
11	A	1139	A
11	A	1146	G
11	A	1149	G
11	A	1151	A
11	A	1155	G
11	A	1157	A
11	A	1158	C
11	A	1160	A
11	A	1162	C
11	A	1167	G
11	A	1185	U
11	A	1188	G
11	A	1191	U
11	A	1194	A
11	A	1196	A
11	A	1197	C
11	A	1199	G
11	A	1200	G
11	A	1202	A

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Mol	Chain	Res	Type
11	A	1207	C
11	A	1208	A
11	A	1217	A
11	A	1218	G
11	A	1219	A
11	A	1221	A
11	A	1226	A
11	A	1227	A
11	A	1228	G
11	A	1229	G
11	A	1235	C
11	A	1243	G
11	A	1244	A
11	A	1245	G
11	A	1250	U
11	A	1251	U
11	A	1257	U
11	A	1258	U
11	A	1260	U
11	A	1269	U
11	A	1286	U
11	A	1301	U
11	A	1314	U
11	A	1315	U
11	A	1321	A
11	A	1329	A
11	A	1337	A
11	A	1339	C
11	A	1340	U
11	A	1341	A
11	A	1344	A
11	A	1345	A
11	A	1349	G
11	A	1354	G
11	A	1361	U
11	A	1363	U
11	A	1364	G
11	A	1370	U
11	A	1371	A
11	A	1372	U
11	A	1379	C
11	A	1382	A

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Mol	Chain	Res	Type
11	A	1383	G
11	A	1388	A
11	A	1390	U
11	A	1398	U
11	A	1399	C
11	A	1400	A
11	A	1412	G
11	A	1413	U
11	A	1414	U
11	A	1415	U
11	A	1420	C
11	A	1421	A
11	A	1427	A
11	A	1428	G
11	A	1429	G
11	A	1431	C
11	A	1445	G
11	A	1446	A
11	A	1448	G
11	A	1454	G
11	A	1457	C
11	A	1459	C
11	A	1461	C
11	A	1462	G
11	A	1471	A
11	A	1473	U
11	A	1474	G
11	A	1475	A
11	A	1478	G
11	A	1482	C
11	A	1486	G
11	A	1488	G
11	A	1489	U
11	A	1490	C
11	A	1491	U
11	A	1492	A
11	A	1493	A
11	A	1499	G
11	A	1500	C
11	A	1506	G
11	A	1514	U
11	A	1516	A

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Mol	Chain	Res	Type
11	A	1518	C
11	A	1521	G
11	A	1523	G
11	A	1524	A
11	A	1535	U
11	A	1536	G
11	A	1537	C
11	A	1538	U
11	A	1539	G
11	A	1540	G
11	A	1557	U
11	A	1559	A
11	A	1569	A
11	A	1573	A
11	A	1574	G
11	A	1575	G
11	A	1584	G
11	A	1590	G
11	A	1601	G
11	A	1616	G
11	A	1619	C
11	A	1624	C
11	A	1625	C
11	A	1627	U
11	A	1631	A
11	A	1635	A
11	A	1649	G
11	A	1657	U
11	A	1658	G
11	A	1663	G
11	A	1680	G
11	A	1682	U
11	A	1683	C
11	A	1684	U
11	A	1685	G
11	A	1686	C
11	A	1687	U
11	A	1693	A
11	A	1712	A
11	A	1713	G
11	A	1716	C
11	A	1717	G

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Mol	Chain	Res	Type
11	A	1727	G
11	A	1729	C
11	A	1731	A
11	A	1759	C
11	A	1760	G
11	A	1761	U
11	A	1762	A
11	A	1766	A
11	A	1768	G
11	A	1769	U
11	A	1770	U
11	A	1780	G
11	A	1782	A
11	A	1783	C
11	A	1789	G
11	A	1792	G
11	A	1793	G
11	A	1794	A
11	A	1795	U
11	A	1796	C

All (86) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	2	A
11	A	25	C
11	A	45	U
11	A	68	A
11	A	73	U
11	A	74	U
11	A	76	A
11	A	103	A
11	A	114	C
11	A	126	A
11	A	130	C
11	A	131	C
11	A	132	U
11	A	133	U
11	A	136	C
11	A	139	C
11	A	144	U
11	A	158	U

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Mol	Chain	Res	Type
11	A	187	G
11	A	217	A
11	A	218	A
11	A	232	U
11	A	239	C
11	A	240	U
11	A	278	U
11	A	280	U
11	A	320	U
11	A	400	A
11	A	417	A
11	A	484	C
11	A	495	C
11	A	497	G
11	A	498	G
11	A	499	U
11	A	501	U
11	A	503	G
11	A	507	U
11	A	512	A
11	A	542	A
11	A	543	C
11	A	555	A
11	A	558	U
11	A	582	U
11	A	685	A
11	A	704	C
11	A	720	G
11	A	721	U
11	A	734	A
11	A	755	A
11	A	781	U
11	A	782	U
11	A	794	U
11	A	811	A
11	A	815	G
11	A	819	G
11	A	823	G
11	A	829	A
11	A	913	G
11	A	1051	G
11	A	1058	U

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Mol	Chain	Res	Type
11	A	1081	A
11	A	1137	A
11	A	1157	A
11	A	1187	U
11	A	1195	C
11	A	1196	A
11	A	1207	C
11	A	1226	A
11	A	1234	A
11	A	1244	A
11	A	1250	U
11	A	1339	C
11	A	1344	A
11	A	1370	U
11	A	1428	G
11	A	1481	C
11	A	1489	U
11	A	1490	C
11	A	1521	G
11	A	1568	C
11	A	1572	G
11	A	1573	A
11	A	1615	C
11	A	1657	U
11	A	1711	C
11	A	1761	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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 (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.