



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 24, 2014 – 10:45 PM EDT

PDB ID : 4TOW
Title : Crystal structure of the E. coli ribosome bound to flopristin. This file contains the 30S subunit of the second 70S ribosome.
Authors : Noeske, J.; Huang, J.; Olivier, N.B.; Giacobbe, R.A.; Zambrowski, M.; Cate, J.H.D.
Deposited on : 2014-06-06
Resolution : 2.90 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

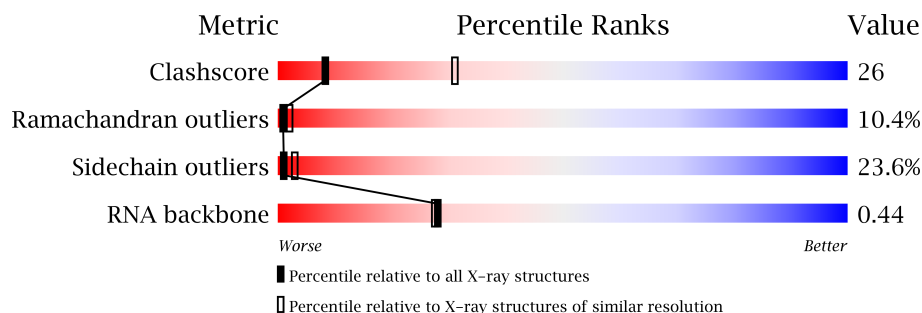
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23489

1 Overall quality at a glance

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RNA backbone	1838	1055 (3.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	1539	
2	B	218	
3	C	206	
4	D	205	
5	E	150	
6	F	100	
7	G	151	
8	H	129	
9	I	127	
10	J	98	
11	K	117	
12	L	123	
13	M	114	
14	N	100	

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Mol	Chain	Length	Quality of chain
15	O	88	
16	P	82	
17	Q	80	
18	R	55	
19	S	79	
20	T	85	
21	U	51	

2 Entry composition

There are 23 unique types of molecules in this entry. The entry contains 51819 atoms, of which 0 are hydrogen and 0 are deuterium.

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

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1539	Total	C	N	O	P	0	0	0
			33015	14725	6052	10699	1539			

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	218	Total	C	N	O	S	0	0	0
			1705	1081	305	312	7			

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	206	Total	C	N	O	S	0	0	0
			1625	1028	305	289	3			

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	205	Total	C	N	O	S	0	0	0
			1643	1026	315	298	4			

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	150	Total	C	N	O	S	0	0	0
			1106	687	211	202	6			

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	100	Total	C	N	O	S	0	0	0
			818	515	148	149	6			

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	151	Total	C	N	O	S	0	0	0
			1182	735	227	216	4			

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	129	Total	C	N	O	S	0	0	0
			979	616	173	184	6			

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	127	Total	C	N	O	S	0	0	0
			1022	634	206	179	3			

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	98	Total	C	N	O	S	0	0	0
			787	493	150	143	1			

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	117	Total	C	N	O	S	0	0	0
			877	540	174	160	3			

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	123	Total	C	N	O	S	0	0	0
			955	590	196	165	4			

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	114	Total	C	N	O	S	0	0	0
			884	546	178	157	3			

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	96	Total	C	N	O	S	0	0	0
			774	483	160	128	3			

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	O	88	Total	C	N	O	S	0	0	0
			710	437	143	129	1			

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	82	Total	C	N	O	S	0	0	0
			649	406	128	114	1			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	80	Total	C	N	O	S	0	0	0
			649	411	121	114	3			

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	R	55	Total	C	N	O	0	0	0
			456	288	86	82			

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	79	Total	C	N	O	S	0	0	0
			638	408	120	108	2			

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	85	Total	C	N	O	S	0	0	0
			665	411	137	114	3			

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	U	51	Total	C	N	O	S	0	0	0
			426	265	86	74	1			

- Molecule 22 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	55	Total	Mg	0	0
			55	55		
22	M	1	Total	Mg	0	0
			1	1		

- Molecule 23 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	A	189	Total	O	0	0
			189	189		
23	L	1	Total	O	0	0
			1	1		
23	N	3	Total	O	0	0
			3	3		
23	T	4	Total	O	0	0
			4	4		
23	U	1	Total	O	0	0
			1	1		

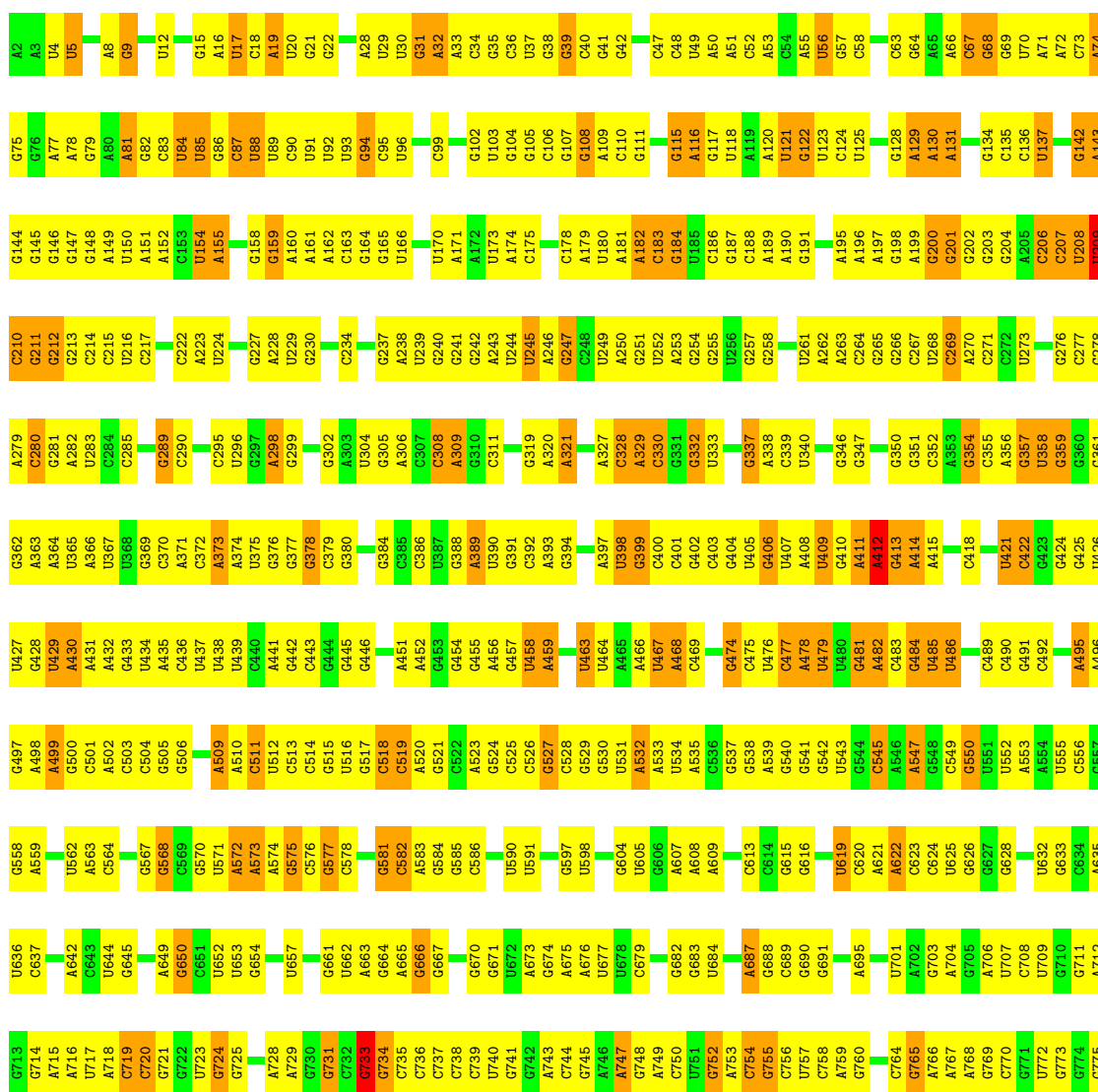
3 Residue-property plots

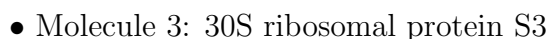
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

Note EDS was not executed.

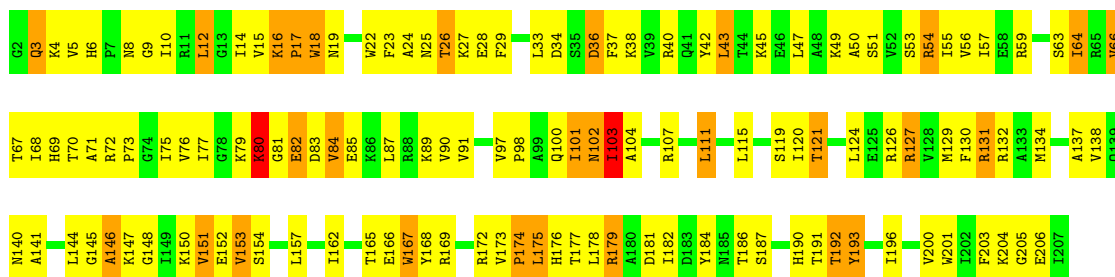
• Molecule 1: 16S rRNA

Chain A:



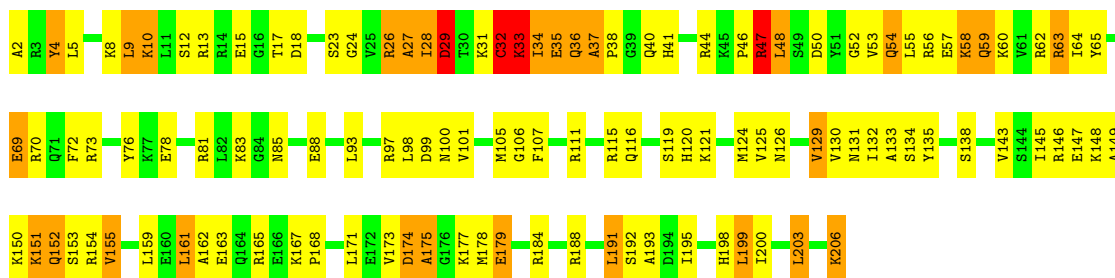


Chain C:



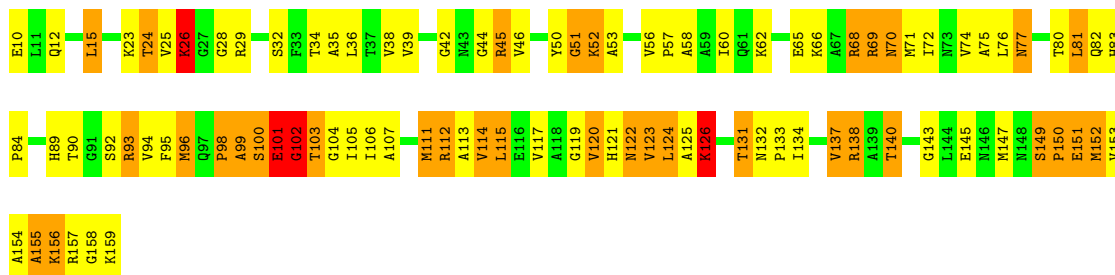
• Molecule 4: 30S ribosomal protein S4

Chain D:



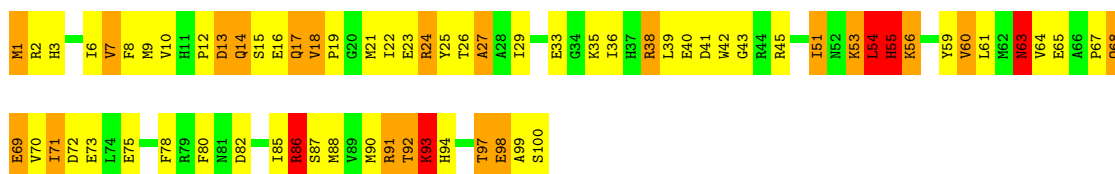
• Molecule 5: 30S ribosomal protein S5

Chain E:



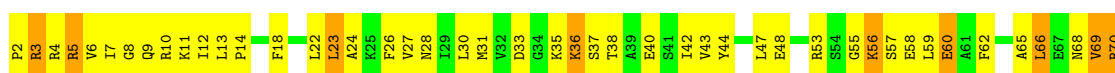
• Molecule 6: 30S ribosomal protein S6

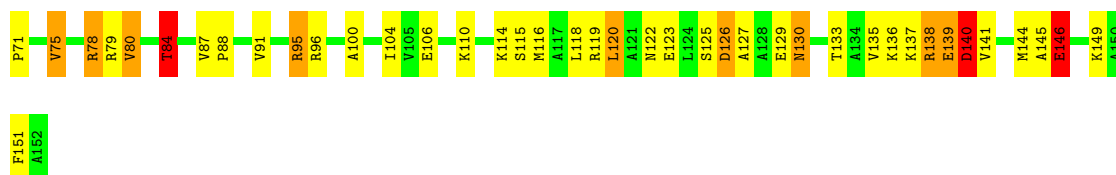
Chain F:



• Molecule 7: 30S ribosomal protein S7

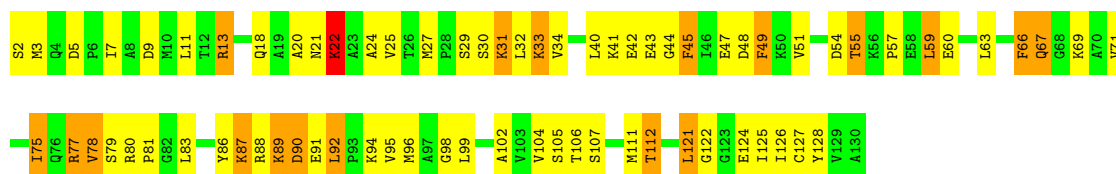
Chain G:





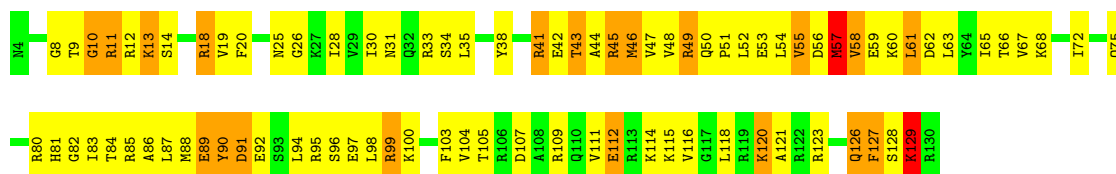
• Molecule 8: 30S ribosomal protein S8

Chain H:



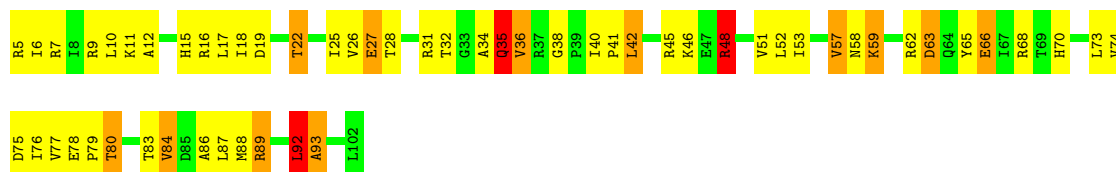
• Molecule 9: 30S ribosomal protein S9

Chain I:



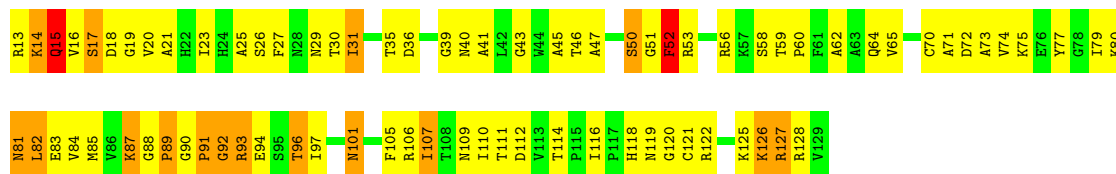
• Molecule 10: 30S ribosomal protein S10

Chain J:



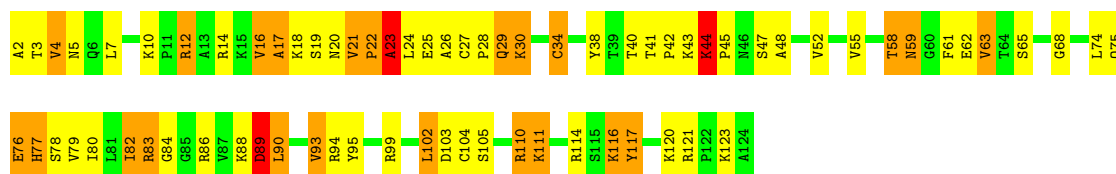
• Molecule 11: 30S ribosomal protein S11

Chain K:



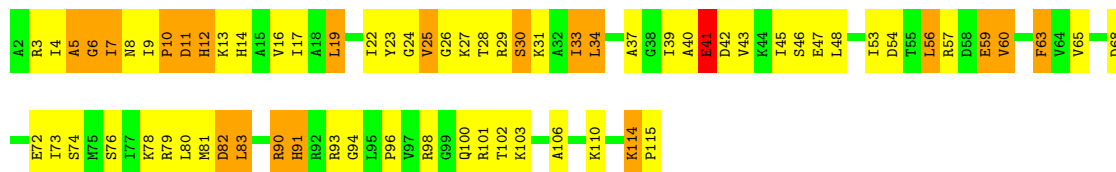
• Molecule 12: 30S ribosomal protein S12

Chain L:



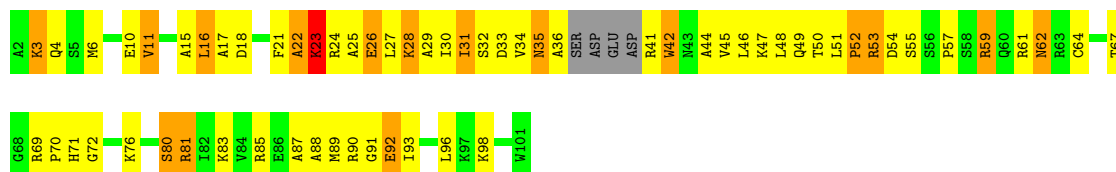
- Molecule 13: 30S ribosomal protein S13

Chain M:



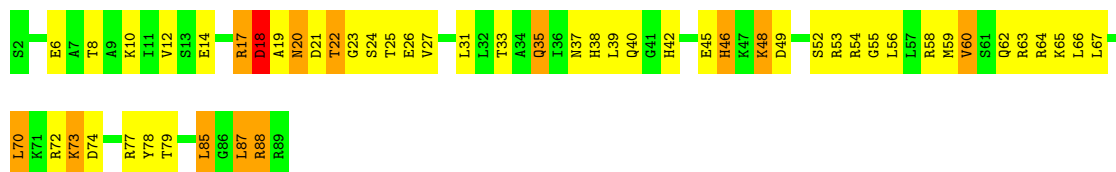
- Molecule 14: 30S ribosomal protein S14

Chain N:



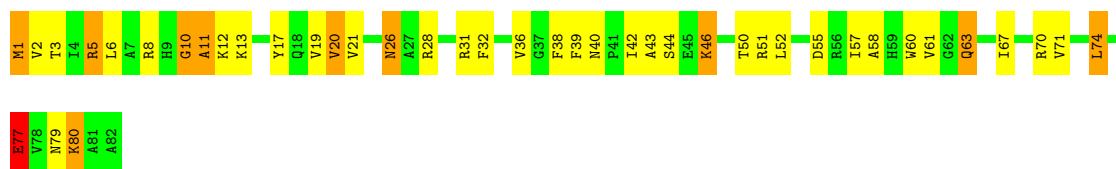
- Molecule 15: 30S ribosomal protein S15

Chain O:



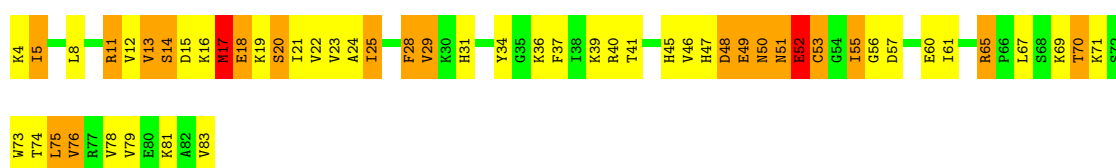
- Molecule 16: 30S ribosomal protein S16

Chain P:



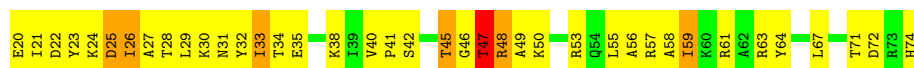
- Molecule 17: 30S ribosomal protein S17

Chain Q:

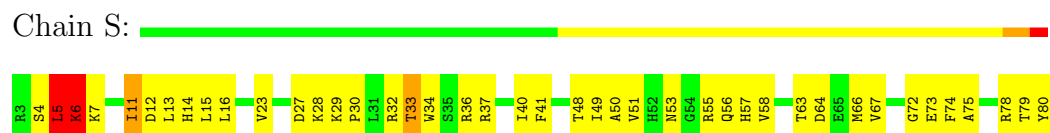


- Molecule 18: 30S ribosomal protein S18

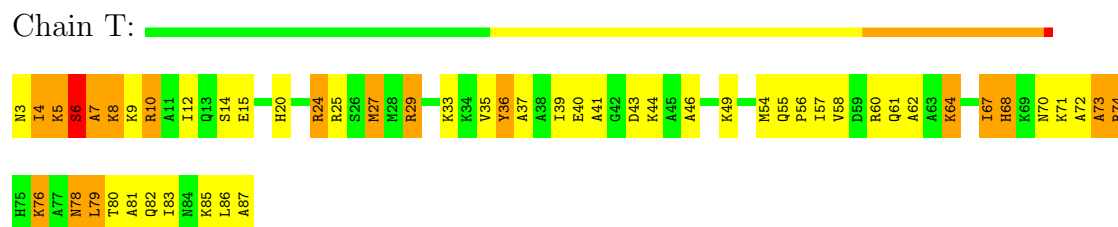
Chain R:



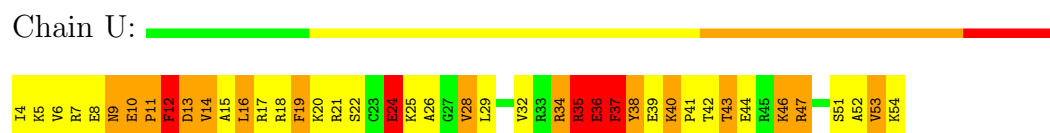
- Molecule 19: 30S ribosomal protein S19



- Molecule 20: 30S ribosomal protein S20



- Molecule 21: 30S ribosomal protein S21



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	211.79Å 433.06Å 623.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.33 – 2.90	Depositor
% Data completeness (in resolution range)	87.4 (69.33-2.90)	Depositor
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.235 , 0.279	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	51819	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.40	0/36966	0.90	9/57666 (0.0%)
2	B	0.33	0/1736	0.60	0/2338
3	C	0.31	0/1652	0.57	0/2225
4	D	0.40	0/1665	0.66	0/2227
5	E	0.36	0/1119	0.70	0/1504
6	F	0.33	0/836	0.63	1/1128 (0.1%)
7	G	0.32	0/1196	0.55	0/1602
8	H	0.32	0/989	0.59	0/1326
9	I	0.32	0/1034	0.62	0/1375
10	J	0.31	0/797	0.62	1/1077 (0.1%)
11	K	0.34	0/893	0.60	0/1205
12	L	0.36	0/969	0.70	0/1300
13	M	0.34	0/893	0.59	0/1193
14	N	0.30	0/785	0.54	0/1043
15	O	0.32	0/718	0.56	0/959
16	P	0.35	0/659	0.58	0/884
17	Q	0.36	0/658	0.61	0/881
18	R	0.32	0/463	0.58	0/621
19	S	0.33	0/653	0.54	0/877
20	T	0.32	0/671	0.57	0/888
21	U	0.45	0/431	0.73	0/570
All	All	0.38	0/55783	0.82	11/82889 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
5	E	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
6	F	0	1
11	K	0	1
12	L	0	1
21	U	0	1
All	All	0	6

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	575	G	N3-C4-C5	7.17	132.19	128.60
1	A	575	G	C4-N9-C1'	-6.69	117.81	126.50
1	A	412	A	O4'-C1'-N9	6.63	113.51	108.20
1	A	575	G	N3-C4-N9	-6.35	122.19	126.00
1	A	209	U	C2-N1-C1'	5.78	124.64	117.70
1	A	1286	U	C2-N1-C1'	5.58	124.39	117.70
1	A	575	G	C8-N9-C1'	5.50	134.15	127.00
1	A	1151	A	O4'-C1'-N9	5.26	112.41	108.20
6	F	86	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	A	733	G	P-O3'-C3'	5.21	125.95	119.70
10	J	48	ARG	NE-CZ-NH1	5.02	122.81	120.30

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	84	ALA	Peptide
5	E	102	GLY	Peptide
6	F	54	LEU	Peptide
11	K	126	LYS	Peptide
12	L	23	ALA	Peptide
21	U	35	ARG	Peptide

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	33015	0	16617	1138	0
2	B	1705	0	1732	148	0
3	C	1625	0	1696	94	0
4	D	1643	0	1707	126	0
5	E	1106	0	1148	115	0
6	F	818	0	808	65	0
7	G	1182	0	1238	57	0
8	H	979	0	1031	54	0
9	I	1022	0	1070	67	0
10	J	787	0	828	48	0
11	K	877	0	887	74	0
12	L	955	0	1016	61	0
13	M	884	0	941	56	0
14	N	774	0	824	55	0
15	O	710	0	728	46	0
16	P	649	0	666	30	0
17	Q	649	0	691	55	0
18	R	456	0	478	39	0
19	S	638	0	665	30	0
20	T	665	0	714	48	0
21	U	426	0	449	54	0
22	A	55	0	0	0	0
22	M	1	0	0	0	0
23	A	189	0	0	19	0
23	L	1	0	0	0	0
23	N	3	0	0	0	0
23	T	4	0	0	0	0
23	U	1	0	0	0	0
All	All	51819	0	35934	2282	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 26.

All (2282) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1385:G:N7	23:A:1870:HOH:O	1.81	1.12
5:E:157:ARG:O	5:E:159:LYS:N	1.95	0.99
14:N:41:ARG:NH1	14:N:42:TRP:O	1.97	0.97
2:B:206:ALA:O	2:B:208:ARG:N	1.98	0.96
1:A:1198:G:N7	23:A:1849:HOH:O	2.01	0.92
1:A:257:G:N7	23:A:1718:HOH:O	2.03	0.90
5:E:101:GLU:O	5:E:103:THR:N	2.04	0.90
6:F:12:PRO:O	6:F:15:SER:OG	1.91	0.89

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:858:G:N7	23:A:1817:HOH:O	2.05	0.89
6:F:91:ARG:O	6:F:92:THR:OG1	1.89	0.88
12:L:116:LYS:O	12:L:117:TYR:CG	2.26	0.88
1:A:1097:C:OP1	2:B:139:ARG:NH2	2.07	0.88
1:A:484:G:H4'	1:A:485:U:O5'	1.74	0.88
2:B:103:ASN:ND2	2:B:106:THR:OG1	2.07	0.87
1:A:687:A:O2'	1:A:701:U:O4	1.92	0.87
1:A:412:A:O2'	1:A:413:G:H4'	1.75	0.86
17:Q:19:LYS:O	17:Q:71:LYS:NZ	2.08	0.86
21:U:10:GLU:HG3	21:U:11:PRO:HD3	1.56	0.85
2:B:221:VAL:O	2:B:223:GLU:N	2.10	0.84
5:E:102:GLY:O	5:E:104:GLY:N	2.11	0.84
5:E:99:ALA:O	5:E:122:ASN:ND2	2.12	0.83
7:G:145:ALA:O	7:G:146:GLU:HB2	1.78	0.81
18:R:25:ASP:O	18:R:27:ALA:N	2.13	0.81
1:A:527:G:C2	1:A:528:C:C6	2.68	0.80
1:A:798:U:O4	23:A:1805:HOH:O	1.99	0.80
1:A:581:G:OP1	15:O:65:LYS:NZ	2.14	0.80
1:A:1001:C:H2'	1:A:1002:G:C8	2.17	0.79
1:A:582:C:N3	1:A:760:G:C6	2.50	0.79
1:A:840:C:N3	1:A:842:U:H4'	1.97	0.79
1:A:32:A:C2	1:A:33:A:C5	2.71	0.79
15:O:19:ALA:O	15:O:20:ASN:HB2	1.85	0.77
1:A:1095:U:OP2	23:A:1852:HOH:O	2.03	0.77
1:A:1124:G:O2'	1:A:1145:A:N6	2.19	0.76
5:E:137:VAL:O	5:E:138:ARG:CB	2.33	0.76
17:Q:21:ILE:N	17:Q:48:ASP:OD1	2.17	0.76
1:A:209:U:H4'	1:A:210:C:OP2	1.85	0.75
1:A:55:A:N7	1:A:56:U:C4	2.54	0.75
4:D:26:ARG:HG3	4:D:27:ALA:N	2.00	0.75
1:A:378:G:C2	1:A:386:C:O2	2.39	0.75
1:A:537:G:OP1	12:L:110:ARG:NH2	2.19	0.75
13:M:6:GLY:O	13:M:8:ASN:N	2.20	0.75
17:Q:48:ASP:N	17:Q:48:ASP:OD2	2.17	0.75
1:A:1101:A:H61	2:B:102:THR:HG21	1.51	0.74
1:A:1266:G:N2	1:A:1269:A:OP2	2.20	0.74
1:A:978:A:OP2	1:A:1362:A:N6	2.20	0.74
1:A:1362:A:H4'	1:A:1362:A:OP1	1.86	0.74
2:B:210:VAL:O	2:B:214:LEU:HB2	1.88	0.74
1:A:919:A:C2	1:A:920:U:C5	2.76	0.74
3:C:175:LEU:HD12	3:C:175:LEU:O	1.88	0.74
5:E:69:ARG:O	5:E:70:ASN:HB2	1.87	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:169:GLU:O	2:B:171:ILE:N	2.21	0.74
1:A:66:A:C6	1:A:67:C:C5	2.76	0.73
10:J:63:ASP:OD1	14:N:85:ARG:NH1	2.22	0.73
1:A:1225:A:H2'	1:A:1226:C:C5	2.22	0.73
1:A:552:U:O2'	12:L:83:ARG:O	2.05	0.73
4:D:145:ILE:HG21	4:D:150:LYS:HA	1.70	0.73
2:B:54:LEU:HA	2:B:57:LEU:HB3	1.69	0.73
1:A:495:A:C2	1:A:496:A:C6	2.77	0.73
1:A:542:G:C2	1:A:543:U:C5	2.76	0.73
12:L:38:TYR:HB2	12:L:52:VAL:HG13	1.70	0.73
1:A:268:U:H2'	1:A:269:C:C6	2.24	0.72
2:B:86:SER:O	2:B:87:CYS:O	2.07	0.72
4:D:100:ASN:OD1	4:D:111:ARG:NH1	2.23	0.72
1:A:55:A:C6	1:A:56:U:C2	2.77	0.72
12:L:34:CYS:HA	12:L:55:VAL:HA	1.71	0.71
16:P:43:ALA:O	16:P:44:SER:OG	2.04	0.71
14:N:91:GLY:O	14:N:93:ILE:N	2.24	0.71
1:A:978:A:HO2'	1:A:1322:C:H5	1.38	0.71
1:A:499:A:C6	1:A:547:A:C8	2.78	0.71
4:D:168:PRO:HB2	4:D:171:LEU:CD1	2.21	0.71
1:A:689:C:OP2	11:K:53:ARG:NH2	2.24	0.71
1:A:405:U:O4	4:D:2:ALA:N	2.23	0.71
1:A:679:C:O2	1:A:712:A:C2	2.43	0.71
4:D:173:VAL:O	4:D:179:GLU:O	2.07	0.71
1:A:1040:U:H2'	1:A:1041:G:C8	2.25	0.70
1:A:374:A:H5''	1:A:452:A:N1	2.06	0.70
1:A:1006:G:H2'	1:A:1007:U:C6	2.26	0.70
1:A:1391:U:H2'	1:A:1392:G:C8	2.25	0.70
1:A:86:G:H1'	1:A:87:C:O4'	1.90	0.70
1:A:319:G:O6	23:A:1734:HOH:O	2.06	0.70
1:A:933:G:N7	7:G:3:ARG:NH2	2.39	0.70
2:B:54:LEU:HD12	2:B:220:THR:HG21	1.74	0.70
8:H:96:MET:HB2	8:H:99:LEU:O	1.92	0.70
4:D:44:ARG:NE	4:D:44:ARG:HA	2.06	0.70
1:A:728:A:C8	15:O:54:ARG:CZ	2.75	0.70
4:D:151:LYS:O	4:D:152:GLN:NE2	2.24	0.70
9:I:84:THR:HG21	9:I:103:PHE:HB3	1.74	0.70
10:J:65:TYR:HB3	14:N:96:LEU:HD11	1.74	0.70
1:A:728:A:H2'	1:A:729:A:C8	2.27	0.70
1:A:568:G:O6	12:L:2:ALA:HB2	1.92	0.69
14:N:54:ASP:OD1	14:N:59:ARG:NH1	2.25	0.69
5:E:24:THR:HA	5:E:29:ARG:HA	1.72	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1408:A:C2	1:A:1494:G:C4	2.81	0.69
10:J:5:ARG:HG3	10:J:6:ILE:HG13	1.74	0.69
1:A:154:U:O4	1:A:155:A:N6	2.26	0.69
1:A:1513:A:H2'	1:A:1514:G:H8	1.58	0.69
11:K:17:SER:O	11:K:80:LYS:N	2.26	0.69
1:A:429:U:H3'	4:D:9:LEU:HD23	1.74	0.69
4:D:198:HIS:CE1	4:D:199:LEU:HD23	2.28	0.69
17:Q:46:VAL:HG21	17:Q:61:ILE:HD11	1.75	0.69
18:R:22:ASP:OD1	18:R:23:TYR:N	2.26	0.69
1:A:527:G:N1	1:A:528:C:C5	2.61	0.68
1:A:1244:G:C6	1:A:1245:C:N4	2.62	0.68
1:A:31:G:N7	1:A:306:A:H1'	2.09	0.68
1:A:505:G:C6	1:A:535:A:C2	2.82	0.68
1:A:718:A:H5'	11:K:119:ASN:ND2	2.08	0.68
14:N:61:ARG:O	14:N:62:ASN:HB2	1.94	0.68
11:K:101:ASN:OD1	11:K:101:ASN:C	2.32	0.67
12:L:21:VAL:O	12:L:23:ALA:N	2.27	0.67
1:A:976:G:OP2	1:A:1358:U:O2'	2.12	0.67
1:A:683:G:N2	11:K:39:GLY:O	2.27	0.67
14:N:21:PHE:O	14:N:23:LYS:N	2.27	0.67
1:A:518:C:H2'	1:A:530:G:C8	2.29	0.67
1:A:72:A:C6	1:A:73:C:N4	2.62	0.67
4:D:174:ASP:O	4:D:175:ALA:CB	2.43	0.67
20:T:6:SER:OG	20:T:7:ALA:N	2.23	0.67
1:A:404:G:O6	4:D:2:ALA:N	2.28	0.67
5:E:101:GLU:O	5:E:101:GLU:CD	2.32	0.67
1:A:111:G:O6	1:A:330:C:N4	2.27	0.67
1:A:1055:A:C6	1:A:1206:G:C5	2.83	0.67
1:A:1298:U:O2	1:A:1298:U:H2'	1.94	0.67
13:M:13:LYS:O	13:M:14:HIS:ND1	2.28	0.67
13:M:40:ALA:O	13:M:42:ASP:N	2.28	0.67
16:P:42:ILE:O	16:P:44:SER:N	2.23	0.67
1:A:1388:C:C2	1:A:1389:C:C5	2.83	0.67
21:U:51:SER:O	21:U:53:VAL:N	2.28	0.66
2:B:73:LYS:O	2:B:75:ALA:N	2.28	0.66
3:C:77:ILE:HA	3:C:84:VAL:HG23	1.76	0.66
1:A:532:A:N6	3:C:192:THR:OG1	2.27	0.66
7:G:12:ILE:HD12	7:G:24:ALA:HB1	1.75	0.66
2:B:99:GLY:O	2:B:101:LEU:N	2.28	0.66
5:E:149:SER:HB2	5:E:152:MET:CG	2.26	0.66
13:M:11:ASP:OD1	13:M:12:HIS:N	2.27	0.66
1:A:1296:C:H4'	1:A:1302:C:N4	2.10	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:50:ASP:O	4:D:53:VAL:HG22	1.95	0.66
1:A:72:A:N6	1:A:73:C:N4	2.43	0.66
9:I:54:LEU:O	9:I:55:VAL:HG22	1.95	0.66
7:G:75:VAL:HG21	7:G:144:MET:HG2	1.77	0.66
14:N:51:LEU:O	14:N:53:ARG:N	2.29	0.65
1:A:495:A:C2	1:A:496:A:N6	2.64	0.65
2:B:83:ALA:O	2:B:86:SER:OG	2.15	0.65
18:R:20:GLU:O	18:R:22:ASP:N	2.29	0.65
12:L:74:LEU:HD11	12:L:80:ILE:HG21	1.78	0.65
1:A:152:A:N6	1:A:170:U:C2	2.65	0.65
5:E:56:VAL:N	5:E:57:PRO:HD2	2.12	0.65
12:L:116:LYS:O	12:L:117:TYR:CD2	2.49	0.65
13:M:33:ILE:HD13	13:M:59:GLU:HB3	1.79	0.65
1:A:736:C:OP1	18:R:61:ARG:NH1	2.30	0.65
1:A:790:A:C6	1:A:791:G:C6	2.85	0.65
12:L:68:GLY:O	12:L:99:ARG:NH1	2.30	0.65
1:A:718:A:C8	1:A:719:C:C5	2.84	0.65
2:B:141:LEU:O	2:B:145:GLU:N	2.30	0.64
1:A:1181:G:O2'	1:A:1182:G:C8	2.50	0.64
1:A:4:U:H5''	1:A:5:U:OP1	1.97	0.64
6:F:9:MET:HG3	6:F:86:ARG:HB2	1.78	0.64
1:A:866:C:C5	1:A:867:G:H1'	2.32	0.64
9:I:90:TYR:O	9:I:91:ASP:CG	2.36	0.64
1:A:1211:U:C2'	1:A:1212:U:OP2	2.46	0.64
8:H:77:ARG:NE	8:H:79:SER:O	2.30	0.64
8:H:94:LYS:HD3	8:H:98:GLY:HA2	1.79	0.64
15:O:62:GLN:O	15:O:66:LEU:HD23	1.97	0.64
20:T:78:ASN:O	20:T:82:GLN:HG2	1.98	0.64
2:B:23:TRP:CG	2:B:23:TRP:O	2.51	0.64
2:B:35:ARG:O	2:B:37:LYS:N	2.31	0.64
9:I:120:LYS:HG2	9:I:123:ARG:HB3	1.79	0.64
17:Q:8:LEU:HD22	17:Q:73:TRP:CH2	2.32	0.64
1:A:1029:U:O2	1:A:1029:U:H2'	1.96	0.64
1:A:980:C:OP2	23:A:1861:HOH:O	2.15	0.64
2:B:135:LEU:O	2:B:137:ARG:N	2.31	0.64
1:A:289:G:C2	1:A:290:C:C5	2.85	0.63
1:A:463:U:H5'	1:A:464:U:OP2	1.98	0.63
1:A:949:A:O2'	1:A:971:G:O6	2.08	0.63
20:T:80:THR:O	20:T:83:ILE:HG13	1.99	0.63
1:A:1181:G:O2'	1:A:1182:G:N7	2.32	0.63
1:A:64:G:C8	1:A:99:C:N4	2.65	0.63
19:S:40:ILE:HB	19:S:66:MET:O	1.98	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:T:81:ALA:O	20:T:85:LYS:HG2	1.98	0.63
1:A:624:C:H2'	1:A:625:U:O4'	1.99	0.63
1:A:909:A:H2'	1:A:910:C:O4'	1.98	0.63
5:E:38:VAL:HG12	5:E:117:VAL:HG21	1.79	0.63
16:P:20:VAL:CG2	16:P:32:PHE:HB2	2.29	0.63
1:A:216:U:H4'	1:A:464:U:H4'	1.80	0.63
1:A:858:G:O6	1:A:869:G:H3'	1.98	0.63
1:A:811:C:O2'	1:A:901:A:N1	2.30	0.63
5:E:155:ALA:HB1	8:H:66:PHE:CD2	2.34	0.63
19:S:4:SER:O	19:S:5:LEU:HB2	1.97	0.63
1:A:66:A:H4'	1:A:173:U:C5	2.34	0.63
13:M:114:LYS:HB2	13:M:115:PRO:HD3	1.80	0.63
1:A:373:A:C2	1:A:374:A:C8	2.87	0.63
1:A:1048:G:OP1	23:A:1846:HOH:O	2.16	0.63
11:K:15:GLN:HA	11:K:77:TYR:HA	1.81	0.63
1:A:1182:G:H4'	1:A:1183:U:H5''	1.79	0.62
1:A:1215:G:C5	1:A:1216:A:N7	2.67	0.62
1:A:1273:C:H2'	1:A:1274:A:O4'	1.99	0.62
1:A:374:A:H5''	1:A:452:A:C2	2.34	0.62
1:A:257:G:C5	23:A:1718:HOH:O	2.49	0.62
12:L:90:LEU:HB2	12:L:93:VAL:HG21	1.80	0.62
3:C:6:HIS:CD2	14:N:89:MET:HB3	2.34	0.62
20:T:29:ARG:O	20:T:33:LYS:HG2	1.98	0.62
1:A:1263:C:H2'	1:A:1264:U:C6	2.34	0.62
1:A:16:A:C2'	1:A:17:U:H5'	2.29	0.62
1:A:32:A:OP1	1:A:398:U:H1'	1.99	0.62
1:A:562:U:H4'	1:A:563:A:O5'	2.00	0.62
2:B:186:ILE:HA	2:B:200:ILE:HB	1.79	0.62
2:B:23:TRP:O	2:B:23:TRP:CD1	2.51	0.62
16:P:20:VAL:HG21	16:P:32:PHE:HB2	1.81	0.62
1:A:1041:G:H2'	1:A:1042:A:C8	2.35	0.62
1:A:55:A:C8	1:A:56:U:C5	2.88	0.62
1:A:866:C:C4	1:A:867:G:H1'	2.35	0.62
4:D:35:GLU:O	4:D:37:ALA:N	2.31	0.62
1:A:435:A:H2'	1:A:436:C:O5'	1.99	0.62
1:A:555:U:H2'	1:A:556:C:C6	2.34	0.62
11:K:27:PHE:CZ	11:K:89:PRO:HG2	2.33	0.62
4:D:59:GLN:O	4:D:63:ARG:HG3	1.99	0.62
1:A:407:U:C2	1:A:408:A:C8	2.87	0.62
1:A:552:U:C4	1:A:553:A:N7	2.68	0.62
4:D:188:ARG:NH1	4:D:191:LEU:CD1	2.63	0.62
1:A:55:A:N7	1:A:56:U:C5	2.68	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:427:U:OP1	4:D:13:ARG:NH2	2.33	0.62
4:D:32:CYS:SG	4:D:33:LYS:N	2.73	0.62
6:F:41:ASP:OD2	6:F:43:GLY:N	2.33	0.62
11:K:125:LYS:O	21:U:34:ARG:NE	2.30	0.62
6:F:45:ARG:O	6:F:56:LYS:HA	2.00	0.62
4:D:26:ARG:O	4:D:27:ALA:HB2	2.00	0.61
12:L:86:ARG:CZ	12:L:88:LYS:HB3	2.30	0.61
1:A:1080:A:OP1	5:E:52:LYS:CE	2.48	0.61
1:A:632:U:O2	1:A:632:U:H2'	1.99	0.61
1:A:955:U:H2'	1:A:956:U:O4'	2.01	0.61
6:F:64:VAL:HG12	6:F:65:GLU:N	2.15	0.61
1:A:978:A:P	1:A:1362:A:N6	2.73	0.61
1:A:990:C:C4	1:A:991:U:O4	2.54	0.61
1:A:115:G:H4'	1:A:116:A:O5'	2.01	0.61
1:A:18:C:C2	1:A:19:A:C8	2.88	0.61
1:A:328:C:H4'	1:A:329:A:H5''	1.83	0.61
1:A:1070:U:H2'	1:A:1071:C:C6	2.35	0.61
1:A:435:A:C2'	1:A:436:C:O5'	2.48	0.61
4:D:48:LEU:HD23	4:D:53:VAL:N	2.16	0.61
1:A:1125:U:H4'	10:J:7:ARG:NH1	2.16	0.61
1:A:378:G:N2	1:A:386:C:O2	2.34	0.61
1:A:790:A:N6	1:A:791:G:C6	2.69	0.61
4:D:4:TYR:O	4:D:5:LEU:HB2	2.00	0.61
20:T:25:ARG:O	20:T:29:ARG:HG2	2.01	0.61
1:A:1169:A:C6	1:A:1170:A:C6	2.89	0.61
1:A:706:A:C5	1:A:707:U:C5	2.89	0.61
1:A:369:G:OP2	1:A:388:G:N1	2.33	0.61
1:A:388:G:O2'	1:A:389:A:OP1	2.14	0.61
2:B:16:PHE:CE1	2:B:18:HIS:CE1	2.89	0.61
3:C:59:ARG:HB2	3:C:63:SER:O	2.00	0.61
6:F:18:VAL:HG12	6:F:19:PRO:N	2.16	0.61
12:L:58:THR:HG22	12:L:59:ASN:N	2.15	0.61
1:A:1211:U:O2'	1:A:1212:U:OP2	2.19	0.60
1:A:409:U:OP1	4:D:24:GLY:HA3	2.01	0.60
1:A:805:C:C2	1:A:806:C:C5	2.89	0.60
1:A:995:C:N3	1:A:1046:A:O2'	2.31	0.60
9:I:52:LEU:HD13	9:I:57:MET:HG2	1.82	0.60
13:M:4:ILE:HA	13:M:57:ARG:CZ	2.31	0.60
1:A:577:G:C8	1:A:816:A:C6	2.89	0.60
1:A:1412:C:H2'	1:A:1413:A:C8	2.37	0.60
5:E:137:VAL:O	5:E:138:ARG:HB2	2.01	0.60
13:M:26:GLY:O	13:M:30:SER:HB2	2.00	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:Q:8:LEU:HB2	17:Q:61:ILE:CG2	2.30	0.60
1:A:1534:A:H5''	1:A:1535:C:OP1	2.01	0.60
1:A:525:C:N4	1:A:526:C:N4	2.49	0.60
2:B:166:ALA:HB2	2:B:187:VAL:HG12	1.82	0.60
1:A:568:G:N2	1:A:883:C:C2	2.70	0.60
2:B:66:LYS:NZ	2:B:154:MET:O	2.33	0.60
4:D:173:VAL:HG13	4:D:174:ASP:N	2.17	0.60
15:O:17:ARG:O	15:O:18:ASP:HB3	2.02	0.60
1:A:1239:A:H2'	1:A:1298:U:O4	2.01	0.60
1:A:411:A:C6	1:A:429:U:C5	2.89	0.60
1:A:515:G:H2'	1:A:516:U:O4'	2.02	0.60
1:A:642:A:C5	8:H:107:SER:HA	2.37	0.60
1:A:778:G:O2'	11:K:121:CYS:HB3	2.01	0.60
5:E:106:ILE:HD11	5:E:124:LEU:HD23	1.83	0.60
1:A:495:A:N1	1:A:496:A:N6	2.49	0.60
12:L:28:PRO:HB2	12:L:29:GLN:OE1	2.02	0.60
1:A:736:C:H2'	1:A:737:C:C6	2.37	0.60
5:E:98:PRO:O	5:E:99:ALA:HB3	2.01	0.60
10:J:6:ILE:HD12	10:J:76:ILE:HB	1.84	0.60
12:L:30:LYS:HA	12:L:30:LYS:HE3	1.83	0.60
1:A:502:A:H2'	1:A:503:C:O4'	2.00	0.60
2:B:206:ALA:C	2:B:208:ARG:N	2.55	0.60
3:C:42:TYR:CE1	3:C:90:VAL:HG21	2.37	0.60
6:F:19:PRO:HA	6:F:22:ILE:HB	1.84	0.60
6:F:64:VAL:HG12	6:F:65:GLU:H	1.67	0.60
19:S:50:ALA:HB1	19:S:57:HIS:HB3	1.83	0.60
1:A:1124:G:C2	1:A:1127:G:N2	2.70	0.59
1:A:203:G:N2	1:A:215:C:C2	2.70	0.59
1:A:38:G:N2	1:A:397:A:C4	2.70	0.59
1:A:406:G:C2	1:A:407:U:C6	2.90	0.59
1:A:583:A:C2	1:A:759:A:C5	2.90	0.59
3:C:36:ASP:O	3:C:40:ARG:HG3	2.02	0.59
16:P:8:ARG:HB3	16:P:28:ARG:NH1	2.17	0.59
2:B:123:ASP:O	2:B:124:GLY:C	2.40	0.59
4:D:168:PRO:HB2	4:D:171:LEU:HD12	1.84	0.59
19:S:66:MET:SD	19:S:74:PHE:CZ	2.95	0.59
21:U:12:PHE:O	21:U:13:ASP:HB2	2.02	0.59
1:A:1286:U:H2'	1:A:1286:U:O2	2.01	0.59
1:A:527:G:C2	1:A:528:C:C5	2.90	0.59
1:A:906:A:N6	23:A:1823:HOH:O	2.35	0.59
3:C:130:PHE:CE2	3:C:131:ARG:HD3	2.37	0.59
14:N:64:CYS:SG	14:N:83:LYS:HG3	2.42	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1028:C:H2'	1:A:1028:C:O2	2.01	0.59
1:A:295:C:C4	1:A:296:U:C4	2.91	0.59
2:B:94:HIS:CD2	2:B:146:ASN:HB2	2.38	0.59
1:A:269:C:H2'	1:A:270:A:C8	2.38	0.59
1:A:542:G:C2	1:A:543:U:C6	2.91	0.59
1:A:570:G:C4	1:A:571:U:C5	2.91	0.59
17:Q:52:GLU:HG2	17:Q:53:CYS:SG	2.42	0.59
1:A:1513:A:H2'	1:A:1514:G:C8	2.38	0.59
4:D:31:LYS:HD3	4:D:31:LYS:N	2.17	0.59
1:A:1219:A:N6	1:A:1220:G:O6	2.36	0.59
1:A:791:G:C6	1:A:792:A:N7	2.71	0.59
6:F:97:THR:O	6:F:98:GLU:HB3	2.02	0.59
1:A:160:A:H2'	1:A:161:A:O4'	2.02	0.59
1:A:202:G:O2'	1:A:468:A:C8	2.56	0.59
2:B:99:GLY:O	2:B:103:ASN:N	2.35	0.59
12:L:74:LEU:HD21	12:L:104:CYS:SG	2.43	0.59
14:N:30:ILE:HG22	14:N:35:ASN:OD1	2.03	0.59
16:P:20:VAL:HG21	16:P:32:PHE:CB	2.32	0.59
1:A:1511:G:C5	1:A:1512:U:C5	2.91	0.59
1:A:441:A:C2	1:A:497:G:C6	2.91	0.59
3:C:173:VAL:O	3:C:175:LEU:N	2.36	0.59
4:D:46:PRO:O	4:D:47:ARG:C	2.41	0.59
5:E:115:LEU:O	5:E:120:VAL:HG23	2.02	0.59
5:E:74:VAL:HB	5:E:76:LEU:HD11	1.85	0.59
12:L:90:LEU:CB	12:L:93:VAL:HG21	2.33	0.59
17:Q:12:VAL:HG23	17:Q:57:ASP:O	2.03	0.59
1:A:1458:G:H5'	20:T:27:MET:HB3	1.85	0.59
1:A:216:U:H2'	1:A:217:C:C6	2.38	0.58
1:A:32:A:H2'	1:A:32:A:N3	2.18	0.58
1:A:657:U:O2	15:O:22:THR:CG2	2.51	0.58
7:G:115:SER:HB3	7:G:118:LEU:HG	1.85	0.58
4:D:124:MET:HG3	4:D:146:ARG:HG2	1.84	0.58
15:O:87:LEU:O	15:O:88:ARG:HB3	2.04	0.58
1:A:228:A:H4'	16:P:63:GLN:HG2	1.85	0.58
20:T:3:ASN:O	20:T:5:LYS:N	2.35	0.58
2:B:208:ARG:O	2:B:212:LEU:N	2.35	0.58
9:I:95:ARG:O	9:I:99:ARG:N	2.32	0.58
18:R:25:ASP:O	18:R:28:THR:N	2.36	0.58
6:F:39:LEU:HD12	6:F:40:GLU:N	2.18	0.58
8:H:59:LEU:HD12	8:H:60:GLU:N	2.18	0.58
1:A:8:A:C6	4:D:206:LYS:HB3	2.39	0.58
3:C:145:GLY:O	3:C:146:ALA:O	2.20	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:O:46:HIS:O	15:O:48:LYS:N	2.36	0.58
20:T:7:ALA:HB1	20:T:10:ARG:HB2	1.86	0.58
1:A:227:G:H2'	1:A:228:A:O4'	2.03	0.58
1:A:829:G:C6	1:A:858:G:N2	2.72	0.58
1:A:511:C:C2	1:A:512:U:C6	2.92	0.58
1:A:841:C:H3'	1:A:843:U:H5''	1.84	0.58
2:B:96:TRP:CE2	2:B:172:ALA:HB2	2.39	0.58
1:A:1036:A:H3'	1:A:1037:C:C6	2.39	0.58
1:A:1201:A:H4'	1:A:1202:U:O5'	2.04	0.58
2:B:163:VAL:HG23	2:B:185:ALA:HB2	1.85	0.58
9:I:25:ASN:O	9:I:62:ASP:HA	2.03	0.58
1:A:206:C:H2'	1:A:207:C:C4'	2.34	0.57
2:B:35:ARG:O	2:B:38:VAL:N	2.35	0.57
5:E:149:SER:O	5:E:153:VAL:HG13	2.03	0.57
1:A:1133:G:C2	1:A:1142:G:C2	2.92	0.57
1:A:475:C:H2'	1:A:476:U:C6	2.39	0.57
10:J:77:VAL:O	10:J:79:PRO:HD3	2.04	0.57
11:K:89:PRO:HD3	21:U:29:LEU:HD11	1.84	0.57
1:A:1330:U:H4'	13:M:23:TYR:CE1	2.39	0.57
1:A:147:G:H2'	1:A:148:G:C8	2.40	0.57
3:C:63:SER:OG	3:C:64:ILE:N	2.36	0.57
11:K:91:PRO:O	11:K:92:GLY:C	2.43	0.57
1:A:1291:U:OP1	7:G:37:SER:HB3	2.04	0.57
1:A:1411:C:H2'	1:A:1412:C:H6	1.69	0.57
1:A:366:A:O2'	1:A:394:G:N2	2.38	0.57
1:A:667:G:C2	1:A:740:U:O2	2.57	0.57
2:B:67:ILE:HG22	2:B:68:LEU:N	2.19	0.57
4:D:32:CYS:O	4:D:33:LYS:CB	2.52	0.57
19:S:11:ILE:HG13	19:S:12:ASP:N	2.19	0.57
19:S:58:VAL:HG11	19:S:75:ALA:HA	1.86	0.57
1:A:1072:G:C5	1:A:1073:U:C4	2.93	0.57
3:C:83:ASP:O	3:C:85:GLU:N	2.38	0.57
7:G:136:LYS:O	7:G:140:ASP:HB2	2.04	0.57
12:L:65:SER:HB2	12:L:82:ILE:HD11	1.85	0.57
1:A:1323:G:H2'	1:A:1324:A:C8	2.39	0.57
1:A:406:G:C2	1:A:407:U:C5	2.92	0.57
1:A:412:A:HO2'	1:A:413:G:H4'	1.68	0.57
18:R:35:GLU:HB2	21:U:19:PHE:CZ	2.40	0.57
1:A:518:C:H4'	1:A:519:C:O5'	2.03	0.57
1:A:822:U:C2	1:A:823:C:C5	2.93	0.57
1:A:890:G:O2'	1:A:891:U:OP2	2.21	0.57
1:A:957:U:O2	1:A:959:A:C8	2.58	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:Q:12:VAL:HG12	17:Q:13:VAL:H	1.67	0.57
19:S:80:TYR:O	19:S:81:ARG:CB	2.52	0.57
21:U:37:PHE:HA	21:U:40:LYS:HE3	1.85	0.57
1:A:577:G:C8	1:A:816:A:N1	2.73	0.57
5:E:57:PRO:O	5:E:60:ILE:HG13	2.04	0.57
1:A:1343:G:O2'	9:I:123:ARG:HD2	2.04	0.57
12:L:44:LYS:HB2	12:L:45:PRO:HD3	1.87	0.57
18:R:33:ILE:HA	18:R:40:VAL:HG23	1.86	0.57
1:A:484:G:C5	1:A:486:U:H1'	2.39	0.57
20:T:43:ASP:HB3	20:T:46:ALA:HB3	1.86	0.57
21:U:24:GLU:HA	21:U:28:VAL:HG22	1.87	0.57
1:A:1072:G:C6	1:A:1073:U:C4	2.93	0.57
1:A:562:U:OP2	12:L:14:ARG:NH2	2.38	0.57
7:G:88:PRO:HD2	7:G:151:PHE:O	2.05	0.57
15:O:19:ALA:O	15:O:20:ASN:CB	2.52	0.57
1:A:1198:G:OP1	23:A:1835:HOH:O	2.17	0.56
5:E:81:LEU:CD1	5:E:120:VAL:HG11	2.35	0.56
7:G:5:ARG:NE	7:G:5:ARG:HA	2.20	0.56
17:Q:19:LYS:HD3	17:Q:49:GLU:HA	1.86	0.56
1:A:1431:A:C6	1:A:1432:G:C6	2.92	0.56
1:A:552:U:C2	1:A:553:A:C8	2.92	0.56
20:T:67:ILE:HD11	20:T:71:LYS:HD3	1.87	0.56
15:O:25:THR:HG23	15:O:66:LEU:HD12	1.86	0.56
18:R:58:ALA:O	18:R:61:ARG:N	2.38	0.56
1:A:1202:U:H2'	1:A:1203:C:O4'	2.04	0.56
1:A:1337:G:H5''	1:A:1338:G:OP1	2.05	0.56
2:B:15:HIS:ND1	2:B:15:HIS:C	2.57	0.56
2:B:91:PHE:O	2:B:150:GLY:HA3	2.05	0.56
1:A:1309:G:C6	1:A:1329:A:C2	2.94	0.56
8:H:9:ASP:OD2	8:H:13:ARG:NH1	2.38	0.56
9:I:120:LYS:CG	9:I:123:ARG:HB3	2.35	0.56
13:M:10:PRO:O	13:M:11:ASP:CB	2.53	0.56
1:A:1361:G:C2	1:A:1362:A:N7	2.73	0.56
1:A:159:G:N2	1:A:162:A:OP2	2.39	0.56
1:A:716:A:N3	11:K:119:ASN:O	2.39	0.56
2:B:210:VAL:CG2	2:B:211:THR:N	2.68	0.56
3:C:40:ARG:HG2	3:C:55:ILE:HD11	1.88	0.56
1:A:1118:U:OP1	9:I:11:ARG:NH1	2.39	0.56
19:S:63:THR:HG22	19:S:64:ASP:N	2.20	0.56
1:A:1302:C:C5	13:M:17:ILE:HD13	2.41	0.56
5:E:82:GLN:OE1	5:E:150:PRO:HD3	2.05	0.56
17:Q:14:SER:C	17:Q:17:MET:HE1	2.26	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1077:G:N2	1:A:1080:A:OP2	2.37	0.56
1:A:804:U:H5''	1:A:805:C:OP2	2.05	0.56
2:B:119:THR:O	2:B:120:GLN:CB	2.54	0.56
2:B:206:ALA:O	2:B:207:ILE:C	2.42	0.56
3:C:72:ARG:HB3	3:C:75:ILE:HG22	1.88	0.56
15:O:18:ASP:C	15:O:18:ASP:OD1	2.44	0.56
20:T:74:ARG:O	20:T:78:ASN:OD1	2.24	0.56
1:A:211:G:O2'	1:A:212:G:C4'	2.53	0.56
1:A:371:A:H1'	1:A:482:A:H1'	1.86	0.56
1:A:511:C:C2	1:A:512:U:C5	2.94	0.56
8:H:78:VAL:N	8:H:126:ILE:O	2.38	0.56
1:A:242:G:N2	1:A:285:C:C2	2.74	0.56
1:A:337:G:H2'	1:A:338:A:C8	2.41	0.56
1:A:302:G:O2'	1:A:556:C:H5''	2.05	0.56
5:E:36:LEU:HD21	5:E:137:VAL:HG11	1.87	0.56
12:L:21:VAL:N	12:L:22:PRO:HD3	2.21	0.56
1:A:1295:U:H2'	1:A:1296:C:C6	2.41	0.56
1:A:1074:G:H4'	2:B:103:ASN:CB	2.35	0.56
2:B:134:ALA:O	2:B:138:THR:N	2.38	0.56
6:F:86:ARG:CG	6:F:86:ARG:HH11	2.19	0.56
6:F:97:THR:O	6:F:98:GLU:CB	2.54	0.56
12:L:25:GLU:O	12:L:26:ALA:C	2.41	0.56
1:A:1481:U:H2'	1:A:1482:G:C8	2.40	0.55
1:A:411:A:C5	1:A:429:U:C5	2.94	0.55
1:A:1377:A:C5	7:G:7:ILE:HD12	2.41	0.55
10:J:80:THR:O	10:J:84:VAL:HB	2.06	0.55
1:A:68:G:C6	1:A:69:G:H1'	2.41	0.55
1:A:833:G:C5	1:A:834:U:C5	2.94	0.55
1:A:987:G:C6	1:A:988:G:C5	2.94	0.55
2:B:102:THR:O	2:B:103:ASN:HB3	2.06	0.55
5:E:25:VAL:O	5:E:28:GLY:N	2.39	0.55
1:A:158:G:H2'	1:A:159:G:H5''	1.87	0.55
1:A:200:G:C3'	1:A:201:G:H5''	2.36	0.55
2:B:27:MET:SD	2:B:193:PRO:HD3	2.47	0.55
5:E:75:ALA:O	5:E:147:MET:HE2	2.06	0.55
20:T:5:LYS:O	20:T:7:ALA:N	2.39	0.55
3:C:179:ARG:O	3:C:206:GLU:O	2.24	0.55
14:N:41:ARG:HG2	14:N:42:TRP:N	2.20	0.55
1:A:542:G:N3	1:A:543:U:C6	2.75	0.55
1:A:585:G:C6	1:A:586:C:C4	2.95	0.55
2:B:135:LEU:O	2:B:138:THR:N	2.40	0.55
2:B:134:ALA:O	2:B:138:THR:HG23	2.07	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:F:88:MET:HE1	18:R:64:TYR:CD2	2.42	0.55
1:A:1068:G:C2'	1:A:1069:C:H5'	2.36	0.55
1:A:1097:C:H2'	1:A:1098:C:C6	2.41	0.55
1:A:1387:G:H2'	1:A:1388:C:H6	1.72	0.55
1:A:243:A:H4'	1:A:244:U:H5''	1.89	0.55
1:A:519:C:OP2	12:L:47:SER:OG	2.24	0.55
1:A:572:A:H5'	1:A:573:A:OP2	2.07	0.55
1:A:661:G:C2	1:A:662:U:C6	2.95	0.55
1:A:991:U:C4	1:A:1212:U:H1'	2.40	0.55
2:B:203:ASN:OD1	2:B:204:ASP:N	2.39	0.55
2:B:52:GLU:HG3	2:B:56:GLU:HG2	1.89	0.55
5:E:101:GLU:HA	5:E:122:ASN:HB2	1.88	0.55
10:J:48:ARG:CG	10:J:48:ARG:HH11	2.20	0.55
1:A:1003:G:C2	1:A:1038:C:C2	2.95	0.55
5:E:137:VAL:O	5:E:138:ARG:HB3	2.06	0.55
1:A:295:C:C4	1:A:296:U:C5	2.95	0.55
1:A:77:A:H2'	1:A:78:A:O4'	2.05	0.55
9:I:57:MET:SD	9:I:58:VAL:N	2.78	0.55
1:A:261:U:OP2	20:T:71:LYS:HD2	2.07	0.55
1:A:1096:C:H2'	1:A:1097:C:C6	2.42	0.55
1:A:16:A:H2'	1:A:17:U:H5'	1.88	0.55
1:A:545:C:H5'	4:D:69:GLU:HG2	1.88	0.55
12:L:22:PRO:O	12:L:24:LEU:N	2.39	0.55
1:A:1170:A:H2'	1:A:1171:A:O4'	2.07	0.55
1:A:1522:U:H2'	1:A:1523:G:H8	1.72	0.55
1:A:477:C:H2'	1:A:478:A:C8	2.41	0.55
1:A:666:G:C6	1:A:741:G:C6	2.95	0.55
1:A:891:U:C5	1:A:906:A:C2	2.95	0.55
4:D:32:CYS:O	4:D:33:LYS:HB2	2.07	0.55
1:A:1166:G:C6	1:A:1168:U:H5''	2.43	0.54
1:A:18:C:N3	1:A:19:A:C8	2.75	0.54
1:A:756:C:O2'	1:A:757:U:H5'	2.06	0.54
11:K:40:ASN:O	11:K:41:ALA:HB3	2.07	0.54
1:A:824:G:H1'	8:H:2:SER:N	2.21	0.54
1:A:403:C:OP1	4:D:134:SER:HB3	2.06	0.54
6:F:6:ILE:HD12	6:F:6:ILE:N	2.22	0.54
8:H:18:GLN:HG2	8:H:63:LEU:HD13	1.88	0.54
9:I:54:LEU:O	9:I:55:VAL:HG13	2.06	0.54
1:A:109:A:C6	1:A:327:A:C6	2.95	0.54
1:A:1439:G:C2	1:A:1463:U:O2	2.60	0.54
1:A:186:C:O4'	20:T:76:LYS:HD2	2.08	0.54
1:A:374:A:C5	1:A:375:U:C5	2.95	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:O:49:ASP:OD1	15:O:52:SER:OG	2.25	0.54
15:O:53:ARG:O	15:O:56:LEU:HB3	2.07	0.54
15:O:70:LEU:HD22	15:O:78:TYR:HB2	1.89	0.54
1:A:1022:A:C6	1:A:1023:U:C4	2.96	0.54
1:A:209:U:H2'	1:A:209:U:O2	2.06	0.54
1:A:451:A:H61	1:A:481:G:H5'	1.73	0.54
2:B:131:LYS:O	2:B:135:LEU:N	2.40	0.54
11:K:25:ALA:N	11:K:87:LYS:O	2.40	0.54
13:M:27:LYS:O	13:M:27:LYS:HD3	2.06	0.54
1:A:115:G:C2	1:A:289:G:N7	2.75	0.54
1:A:577:G:C2	1:A:578:C:C6	2.95	0.54
1:A:620:C:H2'	1:A:621:A:O4'	2.07	0.54
3:C:121:THR:HB	3:C:187:SER:OG	2.07	0.54
4:D:146:ARG:O	4:D:150:LYS:HB2	2.08	0.54
4:D:105:MET:SD	4:D:143:VAL:CG1	2.95	0.54
8:H:7:ILE:HB	8:H:77:ARG:NH1	2.22	0.54
15:O:10:LYS:O	15:O:14:GLU:HG3	2.08	0.54
3:C:181:ASP:O	3:C:203:PHE:HA	2.08	0.54
5:E:38:VAL:HG11	5:E:114:VAL:HA	1.88	0.54
17:Q:16:LYS:C	17:Q:17:MET:SD	2.86	0.54
21:U:34:ARG:NE	21:U:35:ARG:HB2	2.23	0.54
1:A:517:G:O6	23:A:1761:HOH:O	2.18	0.54
2:B:102:THR:HG22	2:B:175:GLU:OE1	2.06	0.54
8:H:32:LEU:HD12	8:H:32:LEU:O	2.08	0.54
11:K:14:LYS:C	11:K:14:LYS:HD2	2.29	0.54
12:L:19:SER:OG	12:L:21:VAL:HG23	2.07	0.54
21:U:39:GLU:HA	21:U:42:THR:OG1	2.08	0.54
1:A:1150:A:N6	1:A:1151:A:H62	2.06	0.54
1:A:1227:A:OP2	13:M:110:LYS:HE3	2.08	0.54
1:A:1317:C:OP1	14:N:57:PRO:HD2	2.07	0.54
1:A:1361:G:H2'	1:A:1362:A:H5''	1.90	0.54
1:A:254:G:OP1	17:Q:69:LYS:O	2.26	0.54
1:A:518:C:H2'	1:A:530:G:H8	1.72	0.54
1:A:773:G:C2	1:A:807:A:C2	2.96	0.54
1:A:920:U:H2'	1:A:921:U:C6	2.43	0.54
3:C:177:THR:HG22	3:C:179:ARG:HG3	1.90	0.54
11:K:16:VAL:O	11:K:17:SER:OG	2.16	0.54
21:U:10:GLU:CG	21:U:11:PRO:HD3	2.33	0.54
1:A:1034:G:H2'	1:A:1035:A:C8	2.43	0.54
1:A:1387:G:H2'	1:A:1388:C:C6	2.42	0.54
9:I:31:ASN:ND2	9:I:38:TYR:OH	2.41	0.54
1:A:104:G:C2	1:A:105:G:C8	2.96	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1070:U:H2'	1:A:1071:C:H6	1.72	0.53
1:A:1309:G:C6	1:A:1329:A:N1	2.77	0.53
5:E:104:GLY:HA3	5:E:122:ASN:HA	1.90	0.53
5:E:122:ASN:O	5:E:123:VAL:O	2.26	0.53
6:F:9:MET:HB2	6:F:85:ILE:HG13	1.89	0.53
9:I:13:LYS:O	9:I:14:SER:HB3	2.07	0.53
1:A:1279:G:OP2	10:J:11:LYS:NZ	2.41	0.53
10:J:26:VAL:HG22	10:J:36:VAL:HG11	1.89	0.53
16:P:44:SER:O	16:P:46:LYS:HG3	2.07	0.53
1:A:1074:G:H4'	2:B:103:ASN:HB3	1.90	0.53
1:A:1416:G:N2	1:A:1485:U:H1'	2.22	0.53
5:E:81:LEU:CD1	5:E:81:LEU:N	2.70	0.53
9:I:120:LYS:O	9:I:121:ALA:HB3	2.09	0.53
1:A:1007:U:H2'	1:A:1008:U:H5''	1.89	0.53
1:A:1055:A:N6	1:A:1206:G:C5	2.76	0.53
1:A:399:G:C6	1:A:400:C:C4	2.97	0.53
1:A:485:U:O2'	1:A:486:U:OP1	2.22	0.53
2:B:53:ALA:C	2:B:54:LEU:HD22	2.29	0.53
7:G:125:SER:C	7:G:127:ALA:H	2.11	0.53
11:K:21:ALA:HB3	11:K:84:VAL:HG13	1.90	0.53
16:P:6:LEU:HD23	16:P:17:TYR:CG	2.43	0.53
1:A:123:U:OP1	1:A:311:C:O2'	2.22	0.53
1:A:1277:C:O2'	1:A:1279:G:H1'	2.07	0.53
1:A:57:G:C6	1:A:58:C:C4	2.96	0.53
1:A:78:A:N6	1:A:79:G:C6	2.76	0.53
21:U:28:VAL:O	21:U:32:VAL:HG23	2.09	0.53
1:A:1201:A:H1'	1:A:1202:U:OP2	2.09	0.53
1:A:818:G:O2'	1:A:819:A:H5'	2.09	0.53
4:D:145:ILE:N	4:D:145:ILE:HD12	2.23	0.53
4:D:29:ASP:C	4:D:31:LYS:H	2.12	0.53
11:K:25:ALA:HA	11:K:30:THR:HG22	1.88	0.53
15:O:70:LEU:HD13	15:O:78:TYR:HA	1.89	0.53
1:A:1124:G:N2	1:A:1127:G:C2	2.76	0.53
1:A:1250:A:C6	1:A:1251:A:C6	2.96	0.53
1:A:1373:G:H5''	7:G:36:LYS:HB2	1.90	0.53
1:A:354:G:C2	1:A:355:C:C5	2.96	0.53
2:B:128:LYS:O	2:B:129:LEU:HB2	2.09	0.53
2:B:20:THR:OG1	2:B:21:ARG:N	2.41	0.53
1:A:1125:U:C6	10:J:40:ILE:HD13	2.44	0.53
21:U:11:PRO:C	21:U:12:PHE:CG	2.80	0.53
1:A:1441:A:C8	1:A:1442:G:C8	2.97	0.53
1:A:1417:G:C6	1:A:1482:G:C6	2.97	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:247:G:C6	1:A:278:G:C2	2.97	0.53
1:A:435:A:C2	1:A:436:C:H1'	2.44	0.53
1:A:657:U:O2	15:O:22:THR:HG23	2.09	0.53
1:A:743:A:C6	1:A:744:C:C4	2.97	0.53
1:A:1101:A:H61	2:B:102:THR:CG2	2.20	0.53
2:B:103:ASN:O	2:B:103:ASN:OD1	2.27	0.53
3:C:64:ILE:HG12	3:C:66:VAL:HG23	1.90	0.53
4:D:48:LEU:HD21	4:D:52:GLY:C	2.29	0.53
5:E:126:LYS:HE2	5:E:126:LYS:HA	1.91	0.53
6:F:88:MET:SD	6:F:90:MET:SD	3.07	0.53
10:J:26:VAL:HG12	10:J:27:GLU:N	2.23	0.53
12:L:16:VAL:O	12:L:17:ALA:O	2.27	0.53
1:A:1486:G:H2'	1:A:1487:G:O4'	2.09	0.53
1:A:247:G:C6	1:A:278:G:N1	2.76	0.53
1:A:527:G:C6	1:A:528:C:C5	2.97	0.53
4:D:145:ILE:HG22	4:D:146:ARG:O	2.08	0.53
5:E:122:ASN:CG	5:E:123:VAL:N	2.62	0.53
11:K:51:GLY:O	11:K:52:PHE:O	2.26	0.53
13:M:14:HIS:HB2	13:M:17:ILE:HD12	1.91	0.53
1:A:976:G:P	1:A:1358:U:O2'	2.67	0.53
1:A:1364:U:O2	1:A:1364:U:H2'	2.08	0.53
1:A:1388:C:H2'	1:A:1389:C:H6	1.74	0.53
2:B:53:ALA:O	2:B:57:LEU:HB2	2.09	0.53
1:A:1080:A:OP1	5:E:52:LYS:HE3	2.09	0.53
6:F:18:VAL:HA	6:F:21:MET:HE2	1.90	0.53
9:I:49:ARG:NH2	9:I:53:GLU:HA	2.24	0.53
12:L:7:LEU:HD22	12:L:12:ARG:CD	2.38	0.53
1:A:485:U:H4'	1:A:485:U:OP2	2.09	0.53
1:A:608:A:H2'	1:A:609:A:O4'	2.09	0.53
4:D:35:GLU:O	4:D:38:PRO:HD3	2.09	0.53
14:N:36:ALA:HB2	14:N:42:TRP:CH2	2.44	0.53
1:A:134:G:H2'	1:A:135:C:O4'	2.09	0.52
9:I:30:ILE:HA	9:I:65:ILE:O	2.08	0.52
12:L:25:GLU:CB	12:L:27:CYS:SG	2.97	0.52
20:T:6:SER:O	20:T:8:LYS:N	2.42	0.52
1:A:1490:U:H2'	1:A:1491:G:C8	2.44	0.52
1:A:238:A:C5	1:A:239:U:C5	2.97	0.52
1:A:847:G:H2'	1:A:848:C:O4'	2.08	0.52
7:G:146:GLU:HA	7:G:149:LYS:HB2	1.91	0.52
16:P:61:VAL:HG21	16:P:67:ILE:HD11	1.89	0.52
18:R:49:ALA:O	18:R:50:LYS:C	2.48	0.52
21:U:12:PHE:O	21:U:13:ASP:CB	2.56	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1067:A:H4'	1:A:1068:G:O5'	2.09	0.52
1:A:108:G:C6	20:T:10:ARG:HG2	2.45	0.52
1:A:1144:G:C2	1:A:1145:A:C2	2.97	0.52
3:C:50:ALA:HB1	3:C:76:VAL:CG2	2.40	0.52
8:H:51:VAL:O	8:H:51:VAL:HG22	2.09	0.52
12:L:25:GLU:HB2	12:L:27:CYS:SG	2.49	0.52
18:R:24:LYS:O	18:R:26:ILE:N	2.39	0.52
1:A:1379:G:N2	1:A:1381:U:O4	2.38	0.52
1:A:206:C:H2'	1:A:207:C:H4'	1.90	0.52
1:A:920:U:C2	1:A:921:U:C5	2.97	0.52
1:A:922:G:H4'	5:E:25:VAL:HA	1.92	0.52
1:A:8:A:C2	5:E:112:ARG:NH2	2.78	0.52
5:E:98:PRO:O	5:E:99:ALA:CB	2.58	0.52
6:F:99:ALA:O	6:F:100:SER:HB3	2.10	0.52
10:J:52:LEU:HD22	10:J:59:LYS:HA	1.91	0.52
1:A:972:C:H4'	10:J:59:LYS:CG	2.39	0.52
1:A:1410:A:H2'	1:A:1411:C:C6	2.45	0.52
1:A:131:A:O2'	1:A:262:A:N3	2.37	0.52
1:A:909:A:C8	1:A:910:C:C5	2.97	0.52
3:C:43:LEU:HD21	3:C:68:ILE:HD11	1.92	0.52
4:D:168:PRO:HB2	4:D:171:LEU:HD13	1.91	0.52
1:A:401:C:OP2	4:D:70:ARG:HD3	2.09	0.52
7:G:71:PRO:HD2	7:G:96:ARG:O	2.09	0.52
20:T:9:LYS:O	20:T:12:ILE:HG12	2.10	0.52
1:A:123:U:H2'	1:A:124:C:H6	1.74	0.52
1:A:1521:C:C2	1:A:1522:U:C6	2.98	0.52
1:A:18:C:C4	1:A:19:A:N7	2.77	0.52
1:A:801:U:H2'	1:A:802:A:H8	1.73	0.52
2:B:80:VAL:HG13	2:B:214:LEU:HD11	1.91	0.52
5:E:76:LEU:HD23	5:E:120:VAL:HG13	1.91	0.52
16:P:38:PHE:CZ	16:P:51:ARG:HB3	2.45	0.52
21:U:53:VAL:HG13	21:U:54:LYS:N	2.25	0.52
1:A:1022:A:C5	1:A:1023:U:C4	2.98	0.52
1:A:1215:G:C6	1:A:1216:A:C5	2.98	0.52
1:A:1300:G:C6	1:A:1335:U:C6	2.97	0.52
1:A:1326:U:H2'	1:A:1327:C:C6	2.45	0.52
1:A:1311:A:C2	1:A:1327:C:N3	2.78	0.52
1:A:295:C:N4	1:A:296:U:O4	2.43	0.52
1:A:545:C:H5'	4:D:69:GLU:CG	2.39	0.52
5:E:52:LYS:O	5:E:53:ALA:HB2	2.09	0.52
17:Q:47:HIS:HB2	17:Q:67:LEU:CD1	2.40	0.52
1:A:407:U:H2'	1:A:408:A:C8	2.45	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:73:C:HO2'	1:A:74:A:C5'	2.23	0.52
1:A:855:U:H2'	1:A:856:C:C6	2.44	0.52
7:G:42:ILE:HD13	7:G:116:MET:HB3	1.91	0.52
13:M:33:ILE:HG23	13:M:59:GLU:HB3	1.91	0.52
1:A:273:U:H1'	17:Q:18:GLU:OE2	2.10	0.52
1:A:369:G:OP2	1:A:388:G:N2	2.39	0.52
1:A:604:G:H2'	1:A:605:U:O4'	2.09	0.52
1:A:632:U:O2	1:A:632:U:C2'	2.58	0.52
1:A:926:G:C6	1:A:1505:G:C5	2.98	0.52
1:A:976:G:N2	1:A:1363:A:C4	2.78	0.52
5:E:101:GLU:HA	5:E:122:ASN:CB	2.40	0.52
5:E:25:VAL:N	5:E:28:GLY:O	2.37	0.52
8:H:89:LYS:HA	8:H:92:LEU:HD12	1.92	0.52
11:K:27:PHE:CE1	11:K:89:PRO:HG2	2.45	0.52
17:Q:61:ILE:HA	17:Q:75:LEU:HA	1.92	0.52
20:T:39:ILE:HD11	20:T:83:ILE:HG22	1.90	0.52
1:A:1082:A:C6	1:A:1083:U:N3	2.78	0.52
1:A:142:G:C2	1:A:143:A:H1'	2.44	0.52
1:A:72:A:C5	1:A:73:C:C5	2.98	0.52
2:B:59:LYS:HA	2:B:62:SER:HB2	1.92	0.52
2:B:82:ASP:N	2:B:82:ASP:OD1	2.43	0.52
5:E:105:ILE:N	5:E:122:ASN:O	2.44	0.52
5:E:131:THR:O	5:E:132:ASN:C	2.48	0.52
5:E:155:ALA:HB1	8:H:66:PHE:CE2	2.44	0.52
11:K:116:ILE:HG22	11:K:116:ILE:O	2.08	0.52
13:M:19:LEU:CB	13:M:30:SER:OG	2.58	0.52
14:N:23:LYS:HG3	14:N:24:ARG:N	2.24	0.52
15:O:56:LEU:O	15:O:59:MET:N	2.43	0.52
15:O:73:LYS:HE2	15:O:73:LYS:HA	1.91	0.52
19:S:29:LYS:CB	19:S:30:PRO:HD2	2.40	0.52
20:T:80:THR:O	20:T:83:ILE:N	2.42	0.52
1:A:1084:G:C5	1:A:1085:U:C4	2.98	0.51
1:A:1087:G:N2	1:A:1099:G:H1'	2.25	0.51
1:A:1202:U:C2'	1:A:1203:C:H5'	2.40	0.51
1:A:102:G:O2'	1:A:151:A:N3	2.34	0.51
1:A:19:A:C2	1:A:20:U:C2	2.98	0.51
1:A:505:G:H2'	1:A:506:G:C8	2.45	0.51
1:A:844:G:H2'	1:A:844:G:N3	2.25	0.51
2:B:206:ALA:O	2:B:209:ALA:N	2.43	0.51
4:D:36:GLN:O	4:D:37:ALA:HB2	2.10	0.51
5:E:149:SER:HB2	5:E:152:MET:HG3	1.92	0.51
1:A:1028:C:C6	1:A:1028:C:OP2	2.63	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:844:G:OP2	1:A:844:G:C8	2.64	0.51
2:B:183:VAL:N	2:B:197:ASP:OD1	2.43	0.51
11:K:52:PHE:CZ	11:K:62:ALA:HA	2.45	0.51
14:N:64:CYS:SG	14:N:80:SER:HB2	2.51	0.51
1:A:476:U:O2'	1:A:477:C:H5'	2.10	0.51
1:A:528:C:O2	1:A:528:C:H2'	2.11	0.51
1:A:73:C:C2	1:A:74:A:C8	2.98	0.51
1:A:878:A:C6	1:A:879:C:C4	2.99	0.51
2:B:47:VAL:HB	2:B:48:PRO:HD3	1.91	0.51
2:B:81:LYS:HG2	2:B:85:LEU:HD23	1.93	0.51
4:D:161:LEU:HD23	4:D:162:ALA:N	2.24	0.51
16:P:10:GLY:O	16:P:11:ALA:HB2	2.11	0.51
1:A:1434:A:N6	1:A:1435:G:C6	2.79	0.51
1:A:1450:U:O2'	1:A:1451:U:H2'	2.11	0.51
1:A:673:A:H2'	1:A:674:G:C8	2.45	0.51
1:A:987:G:N2	1:A:1218:C:O2	2.44	0.51
2:B:102:THR:CG2	2:B:175:GLU:HG2	2.40	0.51
2:B:50:PHE:HB2	2:B:213:TYR:OH	2.10	0.51
3:C:77:ILE:HA	3:C:84:VAL:CG2	2.39	0.51
1:A:1130:A:N9	1:A:1146:A:C2	2.78	0.51
1:A:31:G:O4'	1:A:306:A:C2	2.63	0.51
1:A:756:C:C2'	1:A:757:U:H5'	2.41	0.51
2:B:119:THR:O	2:B:120:GLN:HB3	2.10	0.51
2:B:126:PHE:N	2:B:126:PHE:CD2	2.78	0.51
2:B:225:ARG:O	2:B:226:SER:HB2	2.11	0.51
12:L:90:LEU:CB	12:L:93:VAL:CG2	2.89	0.51
1:A:1071:C:H2'	1:A:1072:G:H8	1.73	0.51
1:A:1491:G:H2'	1:A:1492:A:C8	2.45	0.51
1:A:17:U:C2	1:A:18:C:C6	2.99	0.51
1:A:304:U:H2'	1:A:305:G:C8	2.46	0.51
2:B:57:LEU:HD13	2:B:58:ASN:N	2.26	0.51
10:J:27:GLU:O	10:J:27:GLU:HG2	2.09	0.51
11:K:26:SER:OG	11:K:29:ASN:O	2.17	0.51
12:L:43:LYS:O	12:L:44:LYS:C	2.49	0.51
17:Q:69:LYS:O	17:Q:70:THR:CB	2.58	0.51
20:T:67:ILE:O	20:T:68:HIS:O	2.29	0.51
1:A:1053:G:H4'	1:A:1054:C:H5'	1.93	0.51
1:A:769:G:O2'	1:A:770:C:H5'	2.11	0.51
8:H:5:ASP:OD1	8:H:81:PRO:HD3	2.11	0.51
1:A:1503:A:C8	1:A:1531:A:H1'	2.46	0.51
1:A:258:G:C2	1:A:269:C:O2	2.64	0.51
1:A:56:U:H2'	1:A:57:G:C8	2.46	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:439:U:H5''	4:D:121:LYS:HD2	1.93	0.51
20:T:57:ILE:O	20:T:61:GLN:HG2	2.11	0.51
20:T:73:ALA:O	20:T:74:ARG:C	2.49	0.51
1:A:1540:U:O3'	21:U:18:ARG:NE	2.43	0.51
1:A:1104:G:H2'	1:A:1105:A:O4'	2.10	0.51
4:D:150:LYS:O	4:D:151:LYS:HG2	2.11	0.51
4:D:64:ILE:HG22	4:D:65:TYR:CD1	2.46	0.51
13:M:54:ASP:HA	13:M:57:ARG:HB3	1.93	0.51
14:N:16:LEU:HB3	14:N:55:SER:HA	1.93	0.51
18:R:34:THR:CG2	18:R:38:LYS:HB2	2.41	0.51
21:U:34:ARG:HE	21:U:35:ARG:HB2	1.75	0.51
1:A:1084:G:OP1	1:A:1086:U:C6	2.64	0.51
1:A:1520:C:H2'	1:A:1521:C:C6	2.46	0.51
1:A:724:G:C2	1:A:725:G:C8	2.98	0.51
5:E:150:PRO:O	5:E:153:VAL:HG22	2.11	0.51
5:E:23:LYS:O	5:E:24:THR:CB	2.59	0.51
6:F:70:VAL:HG23	6:F:71:ILE:N	2.26	0.51
10:J:59:LYS:O	10:J:62:ARG:HD2	2.11	0.51
20:T:70:ASN:O	20:T:74:ARG:N	2.43	0.51
1:A:1160:G:O2'	1:A:1161:C:P	2.70	0.50
1:A:425:G:H2'	1:A:426:U:O4'	2.11	0.50
1:A:833:G:C4	1:A:834:U:C6	3.00	0.50
1:A:898:G:O2'	1:A:900:A:N7	2.37	0.50
3:C:97:VAL:HB	3:C:98:PRO:HD2	1.93	0.50
4:D:150:LYS:O	4:D:151:LYS:C	2.47	0.50
8:H:11:LEU:HD22	8:H:75:ILE:HD11	1.93	0.50
11:K:31:ILE:HG12	11:K:31:ILE:O	2.11	0.50
12:L:90:LEU:HB2	12:L:93:VAL:CG2	2.41	0.50
1:A:1505:G:H4'	1:A:1506:U:H5''	1.93	0.50
1:A:1521:C:C4	1:A:1522:U:C5	3.00	0.50
1:A:174:A:C4	1:A:175:C:C6	2.99	0.50
1:A:252:U:H5'	1:A:253:A:OP2	2.10	0.50
1:A:68:G:C5	1:A:69:G:H1'	2.46	0.50
1:A:940:C:N4	1:A:941:G:O6	2.45	0.50
9:I:12:ARG:HD2	9:I:107:ASP:HB3	1.92	0.50
13:M:81:MET:O	13:M:83:LEU:N	2.45	0.50
19:S:36:ARG:HB3	19:S:72:GLY:CA	2.41	0.50
1:A:211:G:O2'	1:A:212:G:H4'	2.12	0.50
1:A:321:A:C8	1:A:328:C:C2	2.99	0.50
1:A:577:G:N3	1:A:578:C:C6	2.80	0.50
1:A:701:U:H4'	1:A:703:G:C8	2.46	0.50
1:A:711:G:O2'	1:A:712:A:H5'	2.11	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:957:U:O2	1:A:959:A:H8	1.94	0.50
1:A:972:C:H4'	10:J:59:LYS:HG2	1.93	0.50
2:B:18:HIS:CD2	2:B:203:ASN:ND2	2.80	0.50
3:C:47:LEU:HB3	3:C:50:ALA:HB3	1.93	0.50
4:D:116:GLN:NE2	4:D:120:HIS:CE1	2.80	0.50
4:D:145:ILE:CG2	4:D:150:LYS:HA	2.41	0.50
11:K:82:LEU:O	11:K:82:LEU:HD23	2.11	0.50
1:A:1089:G:C4	1:A:1090:U:C6	2.99	0.50
1:A:18:C:N3	1:A:19:A:N7	2.59	0.50
2:B:81:LYS:HG3	2:B:91:PHE:CZ	2.46	0.50
4:D:34:ILE:O	4:D:35:GLU:CB	2.59	0.50
7:G:75:VAL:HG11	7:G:144:MET:HG3	1.94	0.50
9:I:57:MET:O	9:I:59:GLU:N	2.45	0.50
15:O:46:HIS:C	15:O:48:LYS:H	2.14	0.50
18:R:34:THR:HG22	18:R:38:LYS:HB2	1.93	0.50
11:K:112:ASP:HB3	21:U:20:LYS:HE3	1.93	0.50
21:U:4:ILE:HG22	21:U:4:ILE:O	2.11	0.50
1:A:1203:C:H4'	14:N:67:THR:HB	1.93	0.50
1:A:237:G:C6	1:A:238:A:C5	3.00	0.50
1:A:649:A:H2'	1:A:650:G:O4'	2.11	0.50
1:A:679:C:C2	1:A:712:A:C2	2.98	0.50
1:A:84:U:O2'	1:A:85:U:H5'	2.12	0.50
4:D:88:GLU:HG2	4:D:188:ARG:HD3	1.93	0.50
1:A:123:U:H2'	1:A:124:C:C6	2.47	0.50
1:A:124:C:N3	1:A:125:U:C4	2.80	0.50
1:A:1288:A:N1	1:A:1371:G:H1'	2.27	0.50
1:A:1267:C:N3	1:A:1327:C:H4'	2.27	0.50
1:A:505:G:H2'	1:A:506:G:H8	1.76	0.50
2:B:142:GLU:HA	2:B:145:GLU:HB2	1.94	0.50
4:D:59:GLN:HA	4:D:59:GLN:OE1	2.11	0.50
6:F:67:PRO:O	6:F:69:GLU:N	2.45	0.50
1:A:1226:C:H2'	13:M:102:THR:HB	1.94	0.50
21:U:14:VAL:O	21:U:16:LEU:HG	2.12	0.50
1:A:183:C:O2'	1:A:184:G:O5'	2.30	0.50
1:A:33:A:H2'	1:A:34:C:C6	2.47	0.50
1:A:421:U:O5'	1:A:422:C:C5	2.65	0.50
1:A:687:A:N3	1:A:688:G:H1'	2.26	0.50
1:A:756:C:H2'	1:A:757:U:C5'	2.42	0.50
1:A:938:A:N6	1:A:939:G:C6	2.80	0.50
5:E:72:ILE:HD13	5:E:145:GLU:CD	2.32	0.50
11:K:107:ILE:O	11:K:107:ILE:HG23	2.11	0.50
20:T:64:LYS:HE3	20:T:64:LYS:HA	1.94	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:213:G:C8	1:A:214:C:C5	2.99	0.50
1:A:485:U:HO2'	1:A:486:U:P	2.34	0.50
3:C:153:VAL:O	3:C:165:THR:O	2.30	0.50
4:D:192:SER:O	4:D:193:ALA:HB3	2.11	0.50
4:D:78:GLU:OE2	4:D:81:ARG:NH1	2.44	0.50
12:L:7:LEU:HD22	12:L:12:ARG:HD2	1.93	0.50
1:A:1105:A:C2	1:A:1106:G:C8	3.00	0.50
1:A:214:C:H2'	1:A:215:C:C6	2.47	0.50
1:A:934:C:H5''	23:A:1825:HOH:O	2.11	0.50
2:B:100:MET:HA	2:B:107:VAL:HG21	1.93	0.50
2:B:36:ASN:O	2:B:37:LYS:HB2	2.12	0.50
5:E:105:ILE:H	5:E:122:ASN:CA	2.25	0.50
5:E:89:HIS:CE1	5:E:90:THR:OG1	2.65	0.50
6:F:99:ALA:O	6:F:100:SER:CB	2.59	0.50
18:R:25:ASP:C	18:R:27:ALA:N	2.63	0.50
18:R:50:LYS:HA	18:R:53:ARG:NH1	2.27	0.50
1:A:1211:U:O2'	1:A:1212:U:P	2.70	0.49
1:A:1255:G:C6	1:A:1279:G:C8	3.00	0.49
1:A:1372:U:OP2	9:I:13:LYS:NZ	2.41	0.49
1:A:363:A:O2'	1:A:364:A:H5'	2.12	0.49
1:A:728:A:H2'	1:A:729:A:H8	1.75	0.49
4:D:151:LYS:HG3	4:D:151:LYS:O	2.12	0.49
5:E:156:LYS:HD2	8:H:71:VAL:HG13	1.93	0.49
9:I:45:ARG:HG3	9:I:46:MET:SD	2.51	0.49
19:S:80:TYR:O	19:S:81:ARG:HB3	2.11	0.49
21:U:29:LEU:O	21:U:29:LEU:HD23	2.12	0.49
1:A:1408:A:C2	1:A:1494:G:C5	3.00	0.49
1:A:577:G:C2	1:A:578:C:C5	3.00	0.49
1:A:951:G:N3	1:A:1231:G:C2	2.79	0.49
2:B:167:ASP:OD2	2:B:191:SER:HA	2.11	0.49
2:B:35:ARG:O	2:B:38:VAL:HG12	2.12	0.49
6:F:14:GLN:C	6:F:16:GLU:H	2.14	0.49
10:J:48:ARG:HH11	10:J:48:ARG:HG3	1.76	0.49
10:J:57:VAL:HG13	10:J:58:ASN:N	2.27	0.49
11:K:90:GLY:O	11:K:91:PRO:O	2.29	0.49
1:A:17:U:C2	1:A:18:C:C5	3.00	0.49
1:A:407:U:H2'	1:A:408:A:H8	1.76	0.49
1:A:582:C:C4	1:A:760:G:C6	3.00	0.49
1:A:748:G:H2'	1:A:749:A:C8	2.47	0.49
2:B:103:ASN:O	2:B:103:ASN:CG	2.50	0.49
2:B:19:GLN:HB3	2:B:189:THR:OG1	2.12	0.49
3:C:141:ALA:O	3:C:146:ALA:HB3	2.11	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:19:ASN:HA	3:C:56:VAL:HG13	1.94	0.49
3:C:57:ILE:HG13	3:C:66:VAL:HG22	1.94	0.49
4:D:124:MET:HE2	4:D:146:ARG:HD2	1.94	0.49
5:E:101:GLU:C	5:E:103:THR:N	2.66	0.49
6:F:85:ILE:O	6:F:86:ARG:O	2.29	0.49
7:G:145:ALA:O	7:G:146:GLU:CB	2.56	0.49
10:J:35:GLN:O	10:J:36:VAL:HB	2.12	0.49
12:L:38:TYR:N	12:L:52:VAL:O	2.42	0.49
14:N:72:GLY:O	14:N:80:SER:HA	2.12	0.49
1:A:1005:A:N7	1:A:1006:G:C4	2.80	0.49
1:A:106:C:O2	1:A:379:C:H4'	2.12	0.49
1:A:951:G:C2	1:A:1231:G:C2	3.01	0.49
1:A:263:A:OP1	20:T:74:ARG:HD3	2.12	0.49
1:A:552:U:N3	1:A:553:A:N7	2.60	0.49
5:E:80:THR:HA	5:E:120:VAL:HG12	1.94	0.49
8:H:75:ILE:HA	8:H:128:TYR:O	2.13	0.49
10:J:84:VAL:O	10:J:88:MET:HG2	2.11	0.49
11:K:16:VAL:HG12	11:K:79:ILE:HG12	1.94	0.49
12:L:77:HIS:O	12:L:78:SER:CB	2.60	0.49
14:N:31:ILE:HG22	14:N:32:SER:N	2.27	0.49
15:O:33:THR:HA	15:O:63:ARG:NH1	2.26	0.49
15:O:37:ASN:O	15:O:40:GLN:HB2	2.13	0.49
17:Q:46:VAL:CG2	17:Q:61:ILE:HD11	2.42	0.49
21:U:43:THR:O	21:U:44:GLU:C	2.51	0.49
1:A:1460:C:N4	1:A:1461:G:C6	2.80	0.49
1:A:583:A:C8	1:A:584:G:C8	3.00	0.49
2:B:210:VAL:HG22	2:B:211:THR:N	2.28	0.49
8:H:11:LEU:HD11	8:H:127:CYS:HB3	1.94	0.49
10:J:92:LEU:O	10:J:93:ALA:HB2	2.12	0.49
1:A:523:A:N1	12:L:89:ASP:HB2	2.27	0.49
15:O:45:GLU:O	15:O:46:HIS:HB2	2.12	0.49
1:A:793:U:HO2'	1:A:1516:G:C1'	2.26	0.49
1:A:182:A:C5	1:A:184:G:N7	2.80	0.49
1:A:635:A:C6	1:A:636:U:C4	3.00	0.49
2:B:43:LEU:HG	2:B:44:GLU:CG	2.43	0.49
2:B:72:THR:HG23	2:B:94:HIS:O	2.11	0.49
3:C:16:LYS:HG3	3:C:17:PRO:HD2	1.95	0.49
4:D:98:LEU:O	4:D:99:ASP:C	2.51	0.49
6:F:88:MET:CE	18:R:64:TYR:CD2	2.95	0.49
1:A:1342:C:H1'	9:I:126:GLN:HG3	1.94	0.49
9:I:30:ILE:HA	9:I:65:ILE:HG13	1.95	0.49
10:J:18:ILE:HG23	10:J:19:ASP:N	2.28	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:N:33:ASP:O	14:N:35:ASN:N	2.42	0.49
14:N:80:SER:O	14:N:83:LYS:N	2.45	0.49
1:A:1144:G:H5''	1:A:1145:A:OP2	2.12	0.49
1:A:978:A:O2'	1:A:1322:C:H5	1.94	0.49
1:A:207:C:H2'	1:A:207:C:O2	2.11	0.49
1:A:32:A:N1	1:A:33:A:C6	2.80	0.49
1:A:509:A:N3	1:A:543:U:O2'	2.41	0.49
1:A:706:A:C1'	11:K:31:ILE:HD11	2.42	0.49
1:A:757:U:OP1	1:A:822:U:O2'	2.24	0.49
4:D:26:ARG:O	4:D:27:ALA:CB	2.61	0.49
4:D:34:ILE:O	4:D:35:GLU:HB3	2.12	0.49
1:A:862:C:H2'	1:A:863:U:H6	1.78	0.49
1:A:890:G:HO2'	1:A:891:U:P	2.36	0.49
1:A:92:U:C4	1:A:93:U:O4	2.66	0.49
3:C:49:LYS:O	3:C:72:ARG:NH1	2.45	0.49
8:H:87:LYS:HG3	8:H:91:GLU:HB3	1.95	0.49
14:N:18:ASP:HA	14:N:22:ALA:HB3	1.95	0.49
1:A:106:C:C2'	1:A:107:G:H5'	2.42	0.49
1:A:247:G:C5	1:A:278:G:N2	2.81	0.49
1:A:743:A:C6	1:A:744:C:C5	3.01	0.49
4:D:151:LYS:CG	4:D:151:LYS:O	2.61	0.49
4:D:203:LEU:O	4:D:203:LEU:HD12	2.11	0.49
1:A:15:G:C4	1:A:16:A:C8	3.01	0.49
1:A:243:A:C2	1:A:246:A:C8	3.01	0.49
1:A:254:G:C4	1:A:255:G:C8	3.00	0.49
1:A:247:G:C5	1:A:278:G:C2	3.00	0.49
1:A:41:G:H2'	1:A:42:G:C8	2.48	0.49
1:A:433:G:C5	1:A:434:U:C5	3.01	0.49
1:A:562:U:H1'	12:L:12:ARG:HG3	1.95	0.49
1:A:834:U:H2'	1:A:835:U:C6	2.48	0.49
2:B:90:PHE:CD2	2:B:150:GLY:O	2.66	0.49
6:F:86:ARG:HH11	6:F:86:ARG:HG2	1.77	0.49
9:I:18:ARG:O	9:I:65:ILE:HA	2.12	0.49
18:R:71:THR:OG1	18:R:72:ASP:N	2.45	0.49
1:A:1068:G:H2'	1:A:1069:C:H5'	1.94	0.48
1:A:165:G:C2	1:A:166:U:C2	3.01	0.48
1:A:200:G:H2'	1:A:201:G:H5''	1.94	0.48
1:A:421:U:C4'	1:A:421:U:OP1	2.61	0.48
1:A:755:G:C2	1:A:756:C:C5	3.01	0.48
6:F:3:HIS:CD2	6:F:94:HIS:HA	2.48	0.48
7:G:42:ILE:O	7:G:42:ILE:HG22	2.13	0.48
11:K:127:ARG:N	21:U:34:ARG:NH2	2.60	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:U:8:GLU:HB3	21:U:12:PHE:CE2	2.47	0.48
1:A:1141:C:C2	1:A:1142:G:C8	3.01	0.48
1:A:1127:G:H5'	1:A:1280:A:O2'	2.12	0.48
1:A:1507:A:C5	1:A:1530:G:C6	3.01	0.48
1:A:636:U:H2'	1:A:637:C:C6	2.47	0.48
1:A:939:G:C2	1:A:940:C:C2	3.01	0.48
1:A:952:U:H2'	1:A:953:G:C8	2.48	0.48
2:B:15:HIS:O	2:B:17:GLY:N	2.46	0.48
3:C:102:ASN:N	3:C:102:ASN:OD1	2.46	0.48
1:A:620:C:C1'	4:D:132:ILE:HD13	2.44	0.48
9:I:127:PHE:C	9:I:127:PHE:CD2	2.87	0.48
10:J:46:LYS:HB3	10:J:66:GLU:OE1	2.13	0.48
12:L:16:VAL:O	12:L:17:ALA:C	2.51	0.48
13:M:106:ALA:O	13:M:110:LYS:HB3	2.13	0.48
18:R:46:GLY:O	18:R:47:THR:O	2.32	0.48
1:A:263:A:P	20:T:74:ARG:NH1	2.86	0.48
1:A:1089:G:N2	1:A:1090:U:H1'	2.28	0.48
1:A:1512:U:O2	1:A:1513:A:C8	2.67	0.48
1:A:445:G:C2	1:A:490:C:C2	3.00	0.48
1:A:66:A:O4'	1:A:173:U:C4	2.66	0.48
1:A:890:G:O2'	1:A:906:A:N6	2.47	0.48
1:A:919:A:N1	1:A:920:U:C5	2.82	0.48
2:B:165:ASP:O	2:B:169:GLU:HG2	2.13	0.48
3:C:64:ILE:CG1	3:C:66:VAL:HG23	2.43	0.48
7:G:57:SER:HB3	7:G:60:GLU:HG3	1.94	0.48
21:U:14:VAL:HG12	21:U:16:LEU:CD2	2.44	0.48
11:K:122:ARG:NH1	21:U:36:GLU:HG2	2.27	0.48
1:A:244:U:H4'	1:A:245:U:C5'	2.44	0.48
1:A:375:U:N3	1:A:376:G:N7	2.61	0.48
1:A:49:U:O4	1:A:365:U:H5	1.96	0.48
1:A:510:A:H5''	1:A:511:C:P	2.53	0.48
1:A:609:A:N7	23:A:1795:HOH:O	2.35	0.48
1:A:747:A:N6	1:A:748:G:C6	2.81	0.48
8:H:67:GLN:C	8:H:69:LYS:N	2.65	0.48
15:O:8:THR:O	15:O:12:VAL:HG23	2.13	0.48
15:O:42:HIS:O	15:O:45:GLU:O	2.31	0.48
1:A:501:C:H1'	1:A:549:C:H1'	1.96	0.48
2:B:139:ARG:C	2:B:139:ARG:CD	2.82	0.48
3:C:148:GLY:O	3:C:203:PHE:N	2.38	0.48
3:C:152:GLU:OE2	3:C:154:SER:HB3	2.14	0.48
6:F:88:MET:HE1	18:R:64:TYR:HD2	1.78	0.48
8:H:86:TYR:CE2	8:H:124:GLU:HB2	2.48	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:93:ARG:NH2	21:U:20:LYS:HD2	2.29	0.48
15:O:35:GLN:NE2	15:O:39:LEU:HD22	2.28	0.48
16:P:50:THR:HG22	16:P:50:THR:O	2.14	0.48
17:Q:45:HIS:ND1	17:Q:70:THR:HG21	2.27	0.48
1:A:1000:A:H2'	1:A:1001:C:O4'	2.13	0.48
1:A:1088:G:C4	1:A:1089:G:C8	3.02	0.48
1:A:1303:C:N4	1:A:1304:G:C6	2.82	0.48
1:A:207:C:O2	1:A:207:C:C2'	2.61	0.48
1:A:55:A:N6	1:A:56:U:N3	2.61	0.48
1:A:960:U:C5	1:A:1225:A:C8	3.01	0.48
3:C:22:TRP:CD1	3:C:57:ILE:HG22	2.49	0.48
4:D:147:GLU:O	4:D:148:LYS:C	2.51	0.48
8:H:88:ARG:O	8:H:122:GLY:HA3	2.13	0.48
14:N:93:ILE:HG21	14:N:96:LEU:HD22	1.95	0.48
11:K:110:ILE:O	21:U:6:VAL:HG22	2.12	0.48
1:A:202:G:H2'	1:A:203:G:O4'	2.13	0.48
1:A:463:U:O2	1:A:463:U:H2'	2.12	0.48
2:B:62:SER:HA	2:B:224:GLY:HA2	1.96	0.48
3:C:83:ASP:O	3:C:84:VAL:C	2.51	0.48
5:E:77:ASN:HB2	5:E:82:GLN:HG2	1.95	0.48
9:I:41:ARG:O	9:I:45:ARG:NH1	2.47	0.48
17:Q:11:ARG:NH2	17:Q:12:VAL:O	2.47	0.48
1:A:644:U:C2	1:A:645:G:C8	3.01	0.48
1:A:756:C:N3	1:A:757:U:C6	2.81	0.48
1:A:767:A:H2'	1:A:768:A:O4'	2.14	0.48
1:A:799:G:C6	1:A:800:G:C4	3.02	0.48
2:B:126:PHE:HD2	2:B:126:PHE:N	2.11	0.48
3:C:184:TYR:CE1	3:C:201:TRP:CE2	3.01	0.48
5:E:153:VAL:O	5:E:157:ARG:N	2.43	0.48
5:E:93:ARG:NH1	5:E:93:ARG:HB3	2.27	0.48
9:I:116:VAL:HG21	10:J:62:ARG:HB2	1.95	0.48
17:Q:17:MET:HE2	17:Q:20:SER:O	2.14	0.48
1:A:1346:A:N6	1:A:1374:A:C8	2.81	0.48
1:A:509:A:C2	1:A:510:A:C2	3.02	0.48
1:A:562:U:OP2	12:L:14:ARG:CZ	2.62	0.48
1:A:666:G:O2'	1:A:667:G:H5'	2.14	0.48
1:A:740:U:O2'	1:A:741:G:H5'	2.13	0.48
1:A:769:G:H4'	1:A:1513:A:H4'	1.95	0.48
3:C:5:VAL:HG21	3:C:10:ILE:HD13	1.94	0.48
7:G:126:ASP:O	7:G:130:ASN:HA	2.13	0.48
7:G:23:LEU:HD23	7:G:26:PHE:HB3	1.96	0.48
11:K:23:ILE:O	11:K:23:ILE:HG13	2.14	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:22:PRO:C	12:L:24:LEU:H	2.16	0.48
18:R:58:ALA:HA	18:R:61:ARG:HD3	1.96	0.48
21:U:14:VAL:HG12	21:U:16:LEU:HD23	1.94	0.48
1:A:1512:U:C2	1:A:1513:A:C8	3.02	0.48
1:A:17:U:N3	1:A:18:C:C5	2.82	0.48
1:A:238:A:O2'	1:A:239:U:H5'	2.14	0.48
1:A:505:G:H5'	1:A:534:U:C2	2.48	0.48
1:A:652:U:C4	1:A:752:G:N3	2.81	0.48
3:C:130:PHE:CE1	3:C:157:LEU:HB3	2.48	0.48
3:C:79:LYS:O	3:C:81:GLY:N	2.47	0.48
3:C:87:LEU:O	3:C:91:VAL:HG23	2.13	0.48
17:Q:52:GLU:HG2	17:Q:53:CYS:H	1.79	0.48
19:S:63:THR:CG2	19:S:64:ASP:N	2.77	0.48
1:A:1255:G:N1	1:A:1279:G:C8	2.82	0.47
1:A:1388:C:N3	1:A:1389:C:C5	2.82	0.47
1:A:1431:A:C6	1:A:1432:G:O6	2.66	0.47
1:A:664:G:N2	1:A:666:G:C8	2.82	0.47
1:A:829:G:C5	1:A:858:G:N2	2.82	0.47
1:A:881:G:C6	1:A:882:C:C4	3.02	0.47
1:A:1101:A:N6	2:B:102:THR:HG21	2.23	0.47
3:C:69:HIS:HA	3:C:104:ALA:HB3	1.95	0.47
6:F:6:ILE:HG22	6:F:7:VAL:N	2.28	0.47
10:J:35:GLN:O	10:J:36:VAL:CB	2.61	0.47
3:C:10:ILE:HD12	14:N:98:LYS:HG3	1.96	0.47
1:A:892:A:O2'	1:A:1415:G:H4'	2.14	0.47
1:A:211:G:N3	1:A:211:G:H2'	2.29	0.47
1:A:57:G:C6	1:A:58:C:N4	2.82	0.47
1:A:661:G:N3	1:A:662:U:C6	2.82	0.47
1:A:8:A:N6	4:D:206:LYS:HB3	2.29	0.47
2:B:85:LEU:O	2:B:85:LEU:HG	2.12	0.47
3:C:81:GLY:O	3:C:82:GLU:C	2.52	0.47
4:D:151:LYS:C	4:D:152:GLN:HE21	2.17	0.47
4:D:78:GLU:HG3	4:D:93:LEU:HD11	1.96	0.47
1:A:1080:A:OP1	5:E:52:LYS:HE2	2.13	0.47
9:I:19:VAL:HG21	9:I:82:GLY:C	2.34	0.47
12:L:111:LYS:O	12:L:114:ARG:HG3	2.14	0.47
13:M:43:VAL:O	13:M:43:VAL:HG23	2.14	0.47
14:N:22:ALA:N	14:N:25:ALA:HB2	2.29	0.47
19:S:15:LEU:HD13	19:S:33:THR:HG21	1.96	0.47
1:A:1053:G:N7	1:A:1200:C:H5''	2.29	0.47
1:A:1252:A:H2'	1:A:1253:G:O4'	2.14	0.47
1:A:1377:A:C5	7:G:7:ILE:CD1	2.96	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1537:U:H5''	1:A:1538:C:OP2	2.14	0.47
1:A:781:A:H2'	1:A:782:A:H5'	1.96	0.47
3:C:138:VAL:O	3:C:141:ALA:HB3	2.14	0.47
5:E:104:GLY:O	5:E:105:ILE:HG22	2.15	0.47
6:F:38:ARG:HG2	6:F:63:ASN:HB3	1.96	0.47
12:L:110:ARG:NE	12:L:117:TYR:CD2	2.82	0.47
15:O:60:VAL:O	15:O:63:ARG:HB3	2.15	0.47
17:Q:14:SER:OG	17:Q:17:MET:CE	2.63	0.47
1:A:1098:C:C2	1:A:1099:G:C8	3.02	0.47
1:A:1157:A:H4'	1:A:1158:C:O5'	2.15	0.47
1:A:1296:C:H5''	1:A:1297:G:OP2	2.14	0.47
1:A:161:A:H2'	1:A:162:A:C8	2.49	0.47
1:A:756:C:C2	1:A:757:U:C6	3.02	0.47
1:A:821:G:H2'	1:A:822:U:H6	1.79	0.47
1:A:881:G:C5	1:A:882:C:C5	3.03	0.47
1:A:439:U:H4'	4:D:121:LYS:HD2	1.96	0.47
6:F:24:ARG:O	6:F:27:ALA:HB3	2.15	0.47
13:M:45:ILE:O	13:M:45:ILE:HG22	2.14	0.47
14:N:36:ALA:HB2	14:N:41:ARG:HG3	1.95	0.47
1:A:332:G:OP2	20:T:5:LYS:HB3	2.14	0.47
1:A:66:A:C4'	1:A:173:U:C4	2.98	0.47
1:A:706:A:C5	1:A:707:U:C4	3.02	0.47
1:A:582:C:C2	1:A:760:G:N1	2.83	0.47
1:A:81:A:H2'	1:A:82:G:C8	2.49	0.47
2:B:104:TRP:CZ2	2:B:156:GLY:N	2.83	0.47
3:C:103:ILE:N	3:C:103:ILE:HD12	2.29	0.47
5:E:81:LEU:O	5:E:98:PRO:HB3	2.15	0.47
1:A:935:A:N1	7:G:3:ARG:NH1	2.62	0.47
17:Q:28:PHE:CE2	17:Q:39:LYS:HG3	2.49	0.47
1:A:1033:G:H3'	1:A:1034:G:H5''	1.97	0.47
1:A:1061:G:C2	1:A:1197:A:C2	3.03	0.47
1:A:1137:C:H1'	1:A:1138:G:N2	2.29	0.47
1:A:1337:G:C5'	1:A:1338:G:OP1	2.62	0.47
1:A:1365:G:H2'	1:A:1366:C:O4'	2.15	0.47
1:A:1492:A:H3'	1:A:1493:A:C8	2.50	0.47
1:A:198:G:O2'	1:A:199:A:H5'	2.15	0.47
1:A:33:A:H2'	1:A:34:C:H6	1.78	0.47
1:A:340:U:C2	1:A:350:G:N2	2.82	0.47
1:A:50:A:H1'	1:A:52:C:O4'	2.15	0.47
2:B:33:GLY:HA2	2:B:40:ILE:H	1.79	0.47
5:E:122:ASN:CG	5:E:123:VAL:H	2.18	0.47
6:F:16:GLU:C	6:F:18:VAL:H	2.17	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:40:THR:HG22	12:L:41:THR:N	2.30	0.47
1:A:1320:C:N3	19:S:36:ARG:NH1	2.63	0.47
21:U:19:PHE:HA	21:U:22:SER:HB3	1.96	0.47
1:A:1184:G:C4	1:A:1185:G:C8	3.01	0.47
1:A:1431:A:N6	1:A:1432:G:O6	2.48	0.47
1:A:280:C:H4'	1:A:281:G:OP2	2.15	0.47
1:A:905:U:C5	1:A:906:A:N7	2.82	0.47
3:C:12:LEU:HD13	3:C:18:TRP:CE2	2.49	0.47
3:C:50:ALA:HB1	3:C:76:VAL:HG22	1.97	0.47
1:A:619:U:H3	4:D:131:ASN:HB3	1.79	0.47
4:D:48:LEU:CD2	4:D:53:VAL:N	2.77	0.47
5:E:15:LEU:HD12	5:E:15:LEU:C	2.34	0.47
8:H:30:SER:O	8:H:34:VAL:HG23	2.14	0.47
9:I:92:GLU:HG3	9:I:95:ARG:NH1	2.30	0.47
1:A:135:C:O2	16:P:1:MET:HB2	2.14	0.47
17:Q:15:ASP:N	17:Q:17:MET:HE1	2.30	0.47
17:Q:52:GLU:HG2	17:Q:53:CYS:N	2.30	0.47
21:U:40:LYS:H	21:U:41:PRO:CD	2.27	0.47
1:A:1071:C:H2'	1:A:1072:G:C8	2.50	0.47
1:A:1417:G:N2	1:A:1484:C:C4	2.83	0.47
1:A:158:G:C4	1:A:159:G:C8	3.02	0.47
1:A:289:G:N1	1:A:290:C:C4	2.82	0.47
1:A:512:U:H2'	1:A:513:C:C6	2.50	0.47
1:A:859:G:C8	1:A:869:G:N2	2.83	0.47
2:B:152:LYS:HG3	2:B:153:ASP:N	2.30	0.47
2:B:72:THR:HG22	2:B:73:LYS:N	2.29	0.47
3:C:111:LEU:N	3:C:111:LEU:CD2	2.77	0.47
3:C:150:LYS:HB3	3:C:169:ARG:HG2	1.96	0.47
4:D:134:SER:O	4:D:135:TYR:C	2.53	0.47
4:D:148:LYS:O	4:D:150:LYS:N	2.48	0.47
8:H:89:LYS:HG3	8:H:90:ASP:N	2.29	0.47
16:P:5:ARG:O	16:P:19:VAL:HA	2.15	0.47
20:T:62:ALA:HA	20:T:68:HIS:N	2.30	0.47
20:T:79:LEU:O	20:T:82:GLN:HB2	2.15	0.47
1:A:339:C:O2	1:A:351:G:N2	2.47	0.47
1:A:407:U:O2	1:A:408:A:C8	2.68	0.47
1:A:439:U:H1'	4:D:119:SER:O	2.14	0.47
1:A:822:U:H2'	1:A:823:C:H6	1.79	0.47
5:E:155:ALA:HB3	5:E:156:LYS:HE3	1.97	0.47
1:A:1280:A:C8	10:J:42:LEU:HD23	2.49	0.47
11:K:16:VAL:O	11:K:17:SER:CB	2.62	0.47
11:K:46:THR:O	11:K:50:SER:OG	2.33	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:36:C:OP1	12:L:120:LYS:HE3	2.15	0.47
1:A:675:A:OP1	18:R:74:HIS:CE1	2.67	0.47
1:A:1521:C:C4	1:A:1522:U:C4	3.03	0.47
2:B:45:LYS:O	2:B:45:LYS:HG3	2.15	0.47
7:G:35:LYS:HB2	7:G:38:THR:HG22	1.97	0.47
9:I:87:LEU:C	9:I:89:GLU:H	2.18	0.47
14:N:24:ARG:HG2	14:N:27:LEU:HD12	1.97	0.47
20:T:79:LEU:O	20:T:83:ILE:HG23	2.15	0.47
1:A:1096:C:H2'	1:A:1097:C:H6	1.81	0.47
1:A:1138:G:C2	1:A:1140:C:C5	3.03	0.47
1:A:1163:A:C2	1:A:1174:G:C2	3.04	0.47
1:A:1182:G:H4'	1:A:1183:U:C5'	2.43	0.47
1:A:53:A:C2	1:A:359:G:C2	3.03	0.47
1:A:468:A:N3	1:A:468:A:O4'	2.48	0.47
1:A:542:G:C4	1:A:543:U:C5	3.03	0.47
1:A:575:G:C6	1:A:821:G:C5	3.03	0.47
1:A:866:C:C5	1:A:867:G:C1'	2.98	0.47
1:A:994:A:H2'	1:A:994:A:N3	2.30	0.47
2:B:30:PHE:CD1	2:B:30:PHE:N	2.82	0.47
4:D:174:ASP:O	4:D:175:ALA:HB2	2.14	0.47
1:A:938:A:O3'	7:G:95:ARG:NH2	2.48	0.47
8:H:59:LEU:CD1	8:H:60:GLU:N	2.78	0.47
12:L:79:VAL:O	12:L:103:ASP:HB2	2.15	0.47
13:M:19:LEU:HB3	13:M:30:SER:OG	2.15	0.47
13:M:11:ASP:HA	13:M:45:ILE:HD13	1.97	0.47
13:M:5:ALA:HB2	13:M:57:ARG:CG	2.45	0.47
15:O:17:ARG:O	15:O:18:ASP:CB	2.62	0.47
1:A:1385:G:C6	1:A:1386:G:C5	3.03	0.46
1:A:1443:C:H2'	1:A:1444:U:O4'	2.15	0.46
1:A:158:G:C5	1:A:159:G:N7	2.83	0.46
1:A:828:U:H2'	1:A:829:G:O5'	2.15	0.46
1:A:923:A:H2'	1:A:924:C:O4'	2.15	0.46
3:C:19:ASN:OD1	3:C:54:ARG:NE	2.48	0.46
4:D:107:PHE:CD1	4:D:107:PHE:N	2.81	0.46
14:N:15:ALA:O	14:N:17:ALA:N	2.48	0.46
19:S:55:ARG:NE	19:S:79:THR:CG2	2.78	0.46
1:A:1244:G:C6	1:A:1245:C:C4	3.04	0.46
1:A:158:G:C5	1:A:164:G:C6	3.04	0.46
1:A:37:U:O2'	1:A:500:G:H4'	2.15	0.46
1:A:613:C:C2	1:A:628:G:N2	2.83	0.46
1:A:644:U:H2'	1:A:645:G:O4'	2.15	0.46
2:B:71:GLY:HA3	2:B:164:ILE:CG2	2.45	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:187:VAL:HB	2:B:191:SER:CB	2.45	0.46
3:C:130:PHE:CD2	3:C:157:LEU:HD23	2.49	0.46
6:F:86:ARG:HD3	18:R:64:TYR:CE1	2.50	0.46
7:G:13:LEU:CD1	7:G:14:PRO:HD2	2.46	0.46
13:M:37:ALA:CB	13:M:56:LEU:HG	2.45	0.46
13:M:74:SER:O	13:M:78:LYS:HG3	2.16	0.46
1:A:624:C:H4'	16:P:10:GLY:O	2.14	0.46
1:A:1053:G:C4'	1:A:1054:C:H5'	2.45	0.46
1:A:328:C:C2'	1:A:328:C:O2	2.64	0.46
4:D:48:LEU:CD2	4:D:52:GLY:C	2.84	0.46
14:N:44:ALA:HA	14:N:47:LYS:HG3	1.98	0.46
20:T:33:LYS:O	20:T:36:TYR:CD2	2.69	0.46
1:A:128:G:C2	1:A:234:C:C2	3.03	0.46
1:A:670:G:N2	1:A:737:C:O2	2.49	0.46
4:D:54:GLN:HG2	4:D:203:LEU:HB2	1.97	0.46
7:G:116:MET:HA	7:G:119:ARG:HD3	1.97	0.46
7:G:55:GLY:O	7:G:56:LYS:O	2.33	0.46
11:K:29:ASN:OD1	11:K:47:ALA:HB3	2.15	0.46
1:A:136:C:H2'	1:A:137:U:C6	2.50	0.46
1:A:1521:C:N3	1:A:1522:U:C5	2.83	0.46
1:A:354:G:C2	1:A:355:C:C6	3.03	0.46
1:A:373:A:O2'	1:A:374:A:H5'	2.15	0.46
1:A:496:A:C2	1:A:497:G:C5	3.03	0.46
1:A:841:C:H2'	1:A:843:U:O4'	2.15	0.46
1:A:8:A:O4'	5:E:107:ALA:C	2.54	0.46
2:B:64:LYS:HD3	2:B:64:LYS:C	2.36	0.46
8:H:43:GLU:OE1	8:H:112:THR:HG21	2.15	0.46
18:R:33:ILE:O	18:R:33:ILE:HG12	2.14	0.46
20:T:37:ALA:O	20:T:40:GLU:HB3	2.15	0.46
1:A:223:A:C6	1:A:224:U:C4	3.03	0.46
1:A:445:G:N1	1:A:446:G:C5	2.84	0.46
1:A:484:G:N7	1:A:486:U:H1'	2.31	0.46
1:A:511:C:O2	1:A:512:U:C6	2.69	0.46
3:C:9:GLY:HA2	3:C:12:LEU:HG	1.97	0.46
4:D:9:LEU:O	4:D:10:LYS:C	2.54	0.46
9:I:10:GLY:HA2	9:I:81:HIS:ND1	2.31	0.46
9:I:46:MET:O	9:I:49:ARG:HB3	2.16	0.46
9:I:26:GLY:H	9:I:59:GLU:HA	1.80	0.46
10:J:65:TYR:HB3	14:N:96:LEU:CD1	2.44	0.46
1:A:1260:G:OP1	1:A:1284:C:O2'	2.29	0.46
1:A:1435:G:H2'	1:A:1436:U:C6	2.50	0.46
1:A:414:A:C2	1:A:415:A:H1'	2.51	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:582:C:C2	1:A:760:G:C6	3.04	0.46
1:A:862:C:H2'	1:A:863:U:C6	2.50	0.46
3:C:53:SER:O	3:C:54:ARG:HB2	2.15	0.46
12:L:75:GLN:O	12:L:76:GLU:C	2.53	0.46
15:O:88:ARG:HG3	15:O:88:ARG:O	2.15	0.46
17:Q:21:ILE:HB	17:Q:48:ASP:OD1	2.16	0.46
1:A:110:C:H2'	1:A:111:G:O4'	2.16	0.46
1:A:1402:C:H2'	1:A:1403:C:O4'	2.16	0.46
1:A:289:G:C2	1:A:290:C:C6	3.03	0.46
1:A:563:A:N7	1:A:567:G:H1'	2.31	0.46
1:A:706:A:C6	1:A:707:U:C4	3.04	0.46
1:A:791:G:C5	1:A:792:A:N7	2.84	0.46
1:A:991:U:C4	1:A:1212:U:C1'	2.99	0.46
4:D:62:ARG:HG3	4:D:72:PHE:CD2	2.51	0.46
6:F:18:VAL:O	6:F:21:MET:HB2	2.16	0.46
6:F:93:LYS:C	6:F:94:HIS:CG	2.90	0.46
7:G:42:ILE:CG2	7:G:42:ILE:O	2.64	0.46
14:N:53:ARG:C	14:N:55:SER:H	2.19	0.46
14:N:61:ARG:O	14:N:62:ASN:CB	2.62	0.46
1:A:263:A:OP2	20:T:74:ARG:NH1	2.49	0.46
21:U:14:VAL:HG12	21:U:16:LEU:HG	1.97	0.46
1:A:35:G:C2	1:A:550:G:C2	3.04	0.46
4:D:62:ARG:CG	4:D:72:PHE:CD2	2.99	0.46
5:E:38:VAL:CG1	5:E:117:VAL:HG21	2.46	0.46
15:O:45:GLU:HG2	15:O:46:HIS:N	2.31	0.46
1:A:1053:G:O5'	1:A:1054:C:H3'	2.16	0.46
1:A:1151:A:C2	1:A:1152:A:C5	3.04	0.46
1:A:1298:U:O2	1:A:1298:U:C2'	2.62	0.46
1:A:137:U:H1'	1:A:227:G:N2	2.30	0.46
1:A:1426:G:H2'	1:A:1427:C:O4'	2.16	0.46
1:A:1491:G:C6	1:A:1492:A:C6	3.03	0.46
1:A:158:G:C6	1:A:164:G:C6	3.04	0.46
1:A:457:G:N2	1:A:476:U:C2	2.84	0.46
1:A:485:U:O4'	1:A:485:U:O2	2.32	0.46
1:A:545:C:O2'	1:A:549:C:H5''	2.16	0.46
1:A:570:G:N3	1:A:571:U:C5	2.84	0.46
1:A:623:C:C4	1:A:624:C:C5	3.03	0.46
1:A:853:C:C4	1:A:854:U:C5	3.04	0.46
2:B:141:LEU:O	2:B:144:LEU:N	2.48	0.46
2:B:15:HIS:ND1	2:B:15:HIS:O	2.49	0.46
4:D:29:ASP:C	4:D:31:LYS:N	2.70	0.46
7:G:116:MET:O	7:G:120:LEU:HB2	2.16	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:49:PHE:CD1	8:H:49:PHE:C	2.87	0.46
8:H:95:VAL:HG21	8:H:128:TYR:HB3	1.98	0.46
11:K:58:SER:O	11:K:91:PRO:HG3	2.16	0.46
13:M:79:ARG:O	13:M:83:LEU:HD23	2.16	0.46
1:A:1095:U:P	23:A:1852:HOH:O	2.73	0.45
1:A:1150:A:H1'	1:A:1280:A:N6	2.31	0.45
1:A:137:U:O2	1:A:227:G:C2	2.69	0.45
1:A:485:U:C5'	1:A:485:U:O2	2.65	0.45
1:A:666:G:C2	1:A:667:G:C8	3.03	0.45
1:A:790:A:C5	1:A:791:G:C5	3.04	0.45
1:A:577:G:C8	1:A:816:A:C2	3.03	0.45
2:B:135:LEU:C	2:B:137:ARG:H	2.19	0.45
3:C:153:VAL:CG2	3:C:157:LEU:HD21	2.46	0.45
3:C:186:THR:HG22	3:C:187:SER:N	2.31	0.45
10:J:28:THR:O	10:J:28:THR:HG22	2.16	0.45
12:L:88:LYS:HG3	12:L:88:LYS:O	2.16	0.45
13:M:10:PRO:O	13:M:11:ASP:HB2	2.14	0.45
14:N:10:GLU:O	14:N:11:VAL:C	2.54	0.45
17:Q:70:THR:HG22	17:Q:71:LYS:H	1.82	0.45
1:A:1480:A:H2'	1:A:1481:U:O4'	2.16	0.45
1:A:413:G:O2'	1:A:428:G:N2	2.49	0.45
1:A:542:G:N3	1:A:543:U:C5	2.83	0.45
1:A:682:G:N2	1:A:709:U:C2	2.84	0.45
2:B:140:GLU:O	2:B:141:LEU:C	2.54	0.45
5:E:149:SER:HB2	5:E:152:MET:HG2	1.97	0.45
8:H:24:ALA:O	8:H:25:VAL:HG23	2.17	0.45
13:M:34:LEU:N	13:M:34:LEU:HD23	2.31	0.45
16:P:12:LYS:O	16:P:13:LYS:HB2	2.16	0.45
17:Q:8:LEU:HD23	17:Q:25:ILE:HD12	1.98	0.45
20:T:36:TYR:C	20:T:36:TYR:CD1	2.90	0.45
1:A:106:C:H2'	1:A:107:G:H5'	1.98	0.45
1:A:1343:G:H2'	1:A:1344:C:C6	2.52	0.45
1:A:1387:G:C4	1:A:1388:C:C5	3.04	0.45
1:A:1397:C:O4'	1:A:1397:C:O2	2.32	0.45
1:A:211:G:H21	1:A:212:G:H1'	1.81	0.45
1:A:28:A:C5	1:A:29:U:C5	3.04	0.45
1:A:407:U:C2	1:A:408:A:N7	2.85	0.45
1:A:573:A:C2	1:A:574:A:C2	3.04	0.45
1:A:64:G:C2	1:A:67:C:N4	2.84	0.45
1:A:718:A:H1'	11:K:118:HIS:HA	1.98	0.45
1:A:652:U:C5	1:A:752:G:N3	2.84	0.45
1:A:913:A:H4'	1:A:914:A:OP1	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:47:VAL:O	2:B:50:PHE:CD2	2.70	0.45
9:I:99:ARG:HA	9:I:104:VAL:CG2	2.46	0.45
15:O:18:ASP:CG	15:O:19:ALA:O	2.54	0.45
1:A:1533:C:H4'	1:A:1533:C:OP1	2.16	0.45
1:A:268:U:H2'	1:A:269:C:H6	1.74	0.45
1:A:819:A:H4'	1:A:820:U:OP2	2.17	0.45
1:A:919:A:C6	1:A:920:U:C5	3.04	0.45
2:B:193:PRO:O	2:B:195:GLY:N	2.47	0.45
5:E:115:LEU:HD12	5:E:120:VAL:HG21	1.99	0.45
5:E:150:PRO:C	5:E:152:MET:H	2.20	0.45
5:E:50:TYR:O	5:E:51:GLY:O	2.35	0.45
1:A:1232:U:H5''	9:I:126:GLN:O	2.16	0.45
11:K:110:ILE:HG22	21:U:17:ARG:NH1	2.29	0.45
11:K:35:THR:OG1	11:K:40:ASN:N	2.49	0.45
12:L:84:GLY:HA2	12:L:95:TYR:HA	1.99	0.45
18:R:28:THR:O	18:R:31:ASN:HB2	2.15	0.45
20:T:55:GLN:N	20:T:56:PRO:CD	2.80	0.45
1:A:1198:G:H5''	23:A:1835:HOH:O	2.17	0.45
1:A:145:G:C2	1:A:146:G:C8	3.05	0.45
1:A:1512:U:O2'	1:A:1513:A:H5'	2.16	0.45
1:A:21:G:H2'	1:A:22:G:C8	2.51	0.45
1:A:451:A:C8	1:A:452:A:C6	3.04	0.45
2:B:50:PHE:CD1	2:B:50:PHE:C	2.89	0.45
2:B:72:THR:HG22	2:B:95:ARG:NH1	2.31	0.45
3:C:151:VAL:HG12	3:C:200:VAL:HB	1.98	0.45
5:E:58:ALA:O	5:E:62:LYS:HB2	2.16	0.45
12:L:25:GLU:HB3	12:L:27:CYS:SG	2.57	0.45
13:M:114:LYS:CB	13:M:115:PRO:HD3	2.47	0.45
17:Q:14:SER:OG	17:Q:17:MET:HE1	2.16	0.45
17:Q:50:ASN:O	17:Q:51:ASN:C	2.55	0.45
1:A:1031:C:H4'	1:A:1032:G:C2	2.52	0.45
1:A:1053:G:O5'	1:A:1054:C:H5'	2.17	0.45
1:A:1160:G:O6	1:A:1181:G:C6	2.70	0.45
1:A:1261:A:C6	1:A:1275:A:C4	3.05	0.45
1:A:195:A:C6	1:A:196:A:N1	2.84	0.45
1:A:200:G:C2'	1:A:201:G:H5''	2.47	0.45
1:A:282:A:C8	1:A:283:U:C5	3.04	0.45
1:A:392:C:H2'	1:A:393:A:C8	2.50	0.45
1:A:431:A:H2'	1:A:432:A:O4'	2.16	0.45
1:A:597:G:H2'	1:A:598:U:H5'	1.98	0.45
1:A:691:G:H4'	1:A:798:U:OP1	2.17	0.45
1:A:891:U:C4	1:A:906:A:C2	3.05	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:938:A:C2	1:A:1345:U:O4	2.69	0.45
2:B:17:GLY:O	2:B:39:HIS:O	2.34	0.45
5:E:155:ALA:C	5:E:156:LYS:HG3	2.37	0.45
5:E:68:ARG:O	5:E:71:MET:HE3	2.16	0.45
14:N:52:PRO:O	14:N:53:ARG:HB3	2.16	0.45
1:A:1098:C:H2'	1:A:1099:G:O4'	2.17	0.45
1:A:435:A:C2	1:A:436:C:N1	2.85	0.45
1:A:607:A:C2	1:A:608:A:C4	3.05	0.45
1:A:72:A:C5	1:A:73:C:N4	2.84	0.45
1:A:968:A:C8	1:A:1062:U:H4'	2.51	0.45
4:D:177:LYS:O	4:D:178:MET:HB2	2.16	0.45
11:K:107:ILE:C	11:K:107:ILE:HD13	2.37	0.45
11:K:87:LYS:HA	11:K:114:THR:HG22	1.99	0.45
1:A:1106:G:H2'	1:A:1107:C:C6	2.51	0.45
1:A:121:U:H3'	1:A:122:G:H5'	1.98	0.45
1:A:1314:C:H2'	1:A:1315:U:C6	2.52	0.45
1:A:414:A:C2	1:A:415:A:C4	3.04	0.45
1:A:519:C:H2'	1:A:520:A:O4'	2.17	0.45
1:A:743:A:C5	1:A:744:C:C5	3.05	0.45
1:A:754:C:H3'	1:A:754:C:O2	2.16	0.45
2:B:60:ILE:HD12	2:B:61:ALA:N	2.31	0.45
5:E:102:GLY:C	5:E:104:GLY:N	2.70	0.45
5:E:95:PHE:O	5:E:125:ALA:O	2.35	0.45
6:F:54:LEU:C	6:F:55:HIS:O	2.54	0.45
9:I:50:GLN:N	9:I:51:PRO:HD2	2.32	0.45
9:I:57:MET:O	9:I:60:LYS:HB2	2.16	0.45
13:M:19:LEU:HB2	13:M:30:SER:OG	2.16	0.45
15:O:73:LYS:HA	15:O:73:LYS:CE	2.47	0.45
1:A:1103:C:C4	1:A:1104:G:N7	2.85	0.45
1:A:1118:U:H1'	1:A:1179:A:C5	2.52	0.45
1:A:117:G:H2'	1:A:118:U:O4'	2.17	0.45
1:A:1204:A:P	23:A:1845:HOH:O	2.74	0.45
1:A:158:G:C6	1:A:164:G:C5	3.05	0.45
1:A:376:G:H5''	16:P:5:ARG:HB2	1.98	0.45
1:A:501:C:H2'	1:A:502:A:C8	2.52	0.45
1:A:563:A:H2'	1:A:567:G:C8	2.52	0.45
1:A:64:G:N2	1:A:67:C:C4	2.85	0.45
4:D:129:VAL:CG1	4:D:129:VAL:O	2.64	0.45
5:E:156:LYS:HA	5:E:159:LYS:NZ	2.31	0.45
5:E:66:LYS:O	5:E:69:ARG:O	2.35	0.45
6:F:1:MET:HG2	6:F:65:GLU:HG2	1.98	0.45
6:F:38:ARG:HG2	6:F:63:ASN:CB	2.46	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:F:51:ILE:O	6:F:51:ILE:HG12	2.17	0.45
1:A:1004:A:C2	1:A:1026:G:N3	2.85	0.45
1:A:1126:U:O4	10:J:73:LEU:HD12	2.16	0.45
1:A:1169:A:N6	1:A:1170:A:N6	2.65	0.45
1:A:1215:G:C4	1:A:1216:A:C8	3.05	0.45
1:A:165:G:N2	1:A:166:U:O2	2.50	0.45
1:A:209:U:C4'	1:A:210:C:OP2	2.62	0.45
1:A:295:C:N3	1:A:296:U:C5	2.85	0.45
1:A:575:G:C6	1:A:821:G:N7	2.85	0.45
2:B:111:ILE:O	2:B:114:LEU:HB3	2.17	0.45
3:C:67:THR:OG1	3:C:102:ASN:ND2	2.50	0.45
3:C:147:LYS:HG3	3:C:204:LYS:O	2.17	0.45
7:G:69:VAL:HG21	7:G:104:ILE:HD11	1.98	0.45
9:I:55:VAL:HG23	9:I:55:VAL:O	2.16	0.45
10:J:46:LYS:HG2	10:J:68:ARG:HG2	1.99	0.45
14:N:88:ALA:N	14:N:93:ILE:HD12	2.32	0.45
16:P:6:LEU:CD1	16:P:71:VAL:HG23	2.47	0.45
17:Q:47:HIS:HB3	17:Q:74:THR:OG1	2.16	0.45
1:A:1099:G:H2'	1:A:1100:C:O4'	2.17	0.44
1:A:1195:C:H2'	1:A:1197:A:O4'	2.18	0.44
1:A:1426:G:C4	1:A:1475:G:C2	3.05	0.44
1:A:399:G:C6	1:A:400:C:N4	2.85	0.44
1:A:403:C:H5'	4:D:132:ILE:HG23	2.00	0.44
1:A:839:C:C2'	1:A:840:C:H5'	2.47	0.44
1:A:921:U:H2'	1:A:922:G:O4'	2.16	0.44
1:A:939:G:C6	1:A:940:C:C4	3.05	0.44
4:D:173:VAL:O	4:D:174:ASP:CB	2.65	0.44
8:H:30:SER:O	8:H:33:LYS:HB2	2.17	0.44
11:K:19:GLY:O	11:K:82:LEU:HA	2.17	0.44
13:M:14:HIS:HB2	13:M:17:ILE:CD1	2.46	0.44
13:M:39:ILE:HG13	13:M:56:LEU:HD21	1.99	0.44
18:R:48:ARG:N	18:R:48:ARG:HD2	2.31	0.44
19:S:51:VAL:O	19:S:58:VAL:HG12	2.17	0.44
1:A:1071:C:O2	1:A:1072:G:C8	2.69	0.44
1:A:1346:A:C8	1:A:1348:U:C2	3.05	0.44
1:A:32:A:C2	1:A:33:A:C4	3.05	0.44
1:A:361:G:O6	1:A:362:G:N1	2.50	0.44
1:A:402:G:H4'	1:A:620:C:O2	2.18	0.44
1:A:49:U:C5	1:A:364:A:C6	3.05	0.44
1:A:714:G:H21	1:A:777:A:H1'	1.82	0.44
1:A:840:C:C4	1:A:842:U:C5'	3.01	0.44
1:A:949:A:C2'	1:A:971:G:O6	2.65	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:18:PHE:CZ	7:G:58:GLU:HG2	2.52	0.44
7:G:68:ASN:HB3	7:G:130:ASN:HB3	1.99	0.44
7:G:78:ARG:HD3	7:G:80:VAL:CG2	2.48	0.44
9:I:107:ASP:OD2	9:I:109:ARG:HG3	2.18	0.44
1:A:1078:U:O2	5:E:90:THR:HG21	2.17	0.44
1:A:1328:C:H5''	13:M:28:THR:CG2	2.47	0.44
1:A:1434:A:N6	1:A:1435:G:N1	2.65	0.44
1:A:53:A:N3	1:A:359:G:C2	2.86	0.44
1:A:458:U:H2'	1:A:459:A:C8	2.52	0.44
1:A:708:C:H2'	1:A:709:U:C6	2.53	0.44
3:C:203:PHE:CE1	3:C:205:GLY:O	2.71	0.44
5:E:107:ALA:HA	5:E:125:ALA:HB3	1.98	0.44
5:E:133:PRO:O	5:E:137:VAL:CG1	2.65	0.44
5:E:153:VAL:HG23	5:E:157:ARG:CB	2.47	0.44
7:G:37:SER:OG	9:I:43:THR:HG23	2.16	0.44
10:J:12:ALA:HB3	10:J:18:ILE:HB	1.99	0.44
13:M:83:LEU:N	13:M:83:LEU:CD2	2.79	0.44
20:T:55:GLN:N	20:T:56:PRO:HD2	2.32	0.44
1:A:1098:C:C4	1:A:1099:G:N7	2.85	0.44
1:A:1124:G:N2	1:A:1127:G:N2	2.66	0.44
2:B:131:LYS:HA	2:B:131:LYS:HE2	1.98	0.44
3:C:172:ARG:O	3:C:174:PRO:HD3	2.17	0.44
5:E:103:THR:O	5:E:122:ASN:HA	2.18	0.44
5:E:125:ALA:O	5:E:126:LYS:HB3	2.18	0.44
6:F:21:MET:O	6:F:25:TYR:CG	2.70	0.44
9:I:91:ASP:C	9:I:91:ASP:OD2	2.55	0.44
11:K:122:ARG:CZ	21:U:36:GLU:HG2	2.48	0.44
11:K:27:PHE:CZ	11:K:89:PRO:CG	3.00	0.44
11:K:60:PRO:N	11:K:91:PRO:HB3	2.32	0.44
15:O:87:LEU:C	15:O:87:LEU:HD23	2.37	0.44
19:S:67:VAL:HG12	19:S:67:VAL:O	2.16	0.44
1:A:1000:A:C2	1:A:1041:G:C2	3.05	0.44
1:A:1244:G:C2	1:A:1294:G:C2	3.05	0.44
1:A:1356:G:H2'	1:A:1357:A:C8	2.52	0.44
1:A:53:A:C2	1:A:359:G:C6	3.05	0.44
1:A:391:G:H2'	1:A:392:C:O4'	2.17	0.44
1:A:436:C:C2	1:A:437:U:C5	3.05	0.44
1:A:748:G:H2'	1:A:749:A:H8	1.83	0.44
2:B:213:TYR:O	2:B:217:VAL:HG23	2.18	0.44
4:D:150:LYS:HG2	4:D:151:LYS:N	2.32	0.44
4:D:57:GLU:O	4:D:58:LYS:C	2.55	0.44
5:E:101:GLU:O	5:E:101:GLU:OE2	2.36	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:67:GLN:C	8:H:69:LYS:H	2.19	0.44
10:J:10:LEU:N	10:J:10:LEU:HD12	2.32	0.44
11:K:25:ALA:O	11:K:88:GLY:HA3	2.17	0.44
12:L:61:PHE:N	12:L:61:PHE:CD1	2.85	0.44
18:R:32:TYR:CD2	18:R:55:LEU:HD21	2.52	0.44
19:S:11:ILE:HG21	19:S:41:PHE:CE2	2.52	0.44
20:T:58:VAL:HG13	20:T:72:ALA:HA	2.00	0.44
1:A:1070:U:C2	1:A:1071:C:C5	3.06	0.44
1:A:1074:G:N2	1:A:1075:U:H1'	2.33	0.44
1:A:179:A:H2'	1:A:180:U:C6	2.53	0.44
1:A:29:U:N3	1:A:30:U:C5	2.86	0.44
1:A:28:A:H2'	1:A:29:U:O4'	2.17	0.44
1:A:476:U:C2'	1:A:477:C:H5'	2.48	0.44
1:A:720:C:O2'	18:R:56:ALA:HB2	2.18	0.44
1:A:738:C:H2'	1:A:739:C:H6	1.81	0.44
1:A:745:G:H5''	1:A:851:G:O2'	2.17	0.44
1:A:777:A:C2	1:A:778:G:H1'	2.52	0.44
1:A:874:G:C6	1:A:875:U:C4	3.05	0.44
2:B:91:PHE:CD2	2:B:91:PHE:O	2.71	0.44
4:D:177:LYS:HE2	4:D:177:LYS:HB2	1.82	0.44
7:G:27:VAL:HG12	7:G:43:VAL:HG21	1.99	0.44
8:H:86:TYR:C	8:H:87:LYS:HD2	2.38	0.44
11:K:89:PRO:HD3	21:U:29:LEU:CD1	2.48	0.44
1:A:1329:A:H5''	13:M:25:VAL:HA	2.00	0.44
15:O:74:ASP:CG	15:O:77:ARG:HG3	2.38	0.44
20:T:60:ARG:O	20:T:64:LYS:HB2	2.18	0.44
1:A:1269:A:C2	1:A:1313:U:O4'	2.71	0.44
1:A:1397:C:H3'	1:A:1398:A:H5''	2.00	0.44
1:A:149:A:C2	1:A:150:U:C2	3.06	0.44
1:A:1516:G:C2	1:A:1518:A:OP2	2.71	0.44
1:A:179:A:C5	1:A:180:U:C4	3.06	0.44
1:A:246:A:N3	1:A:279:A:N6	2.66	0.44
1:A:441:A:C2	1:A:497:G:C5	3.06	0.44
3:C:162:ILE:HD12	3:C:162:ILE:O	2.18	0.44
5:E:154:ALA:HA	5:E:157:ARG:HB3	1.99	0.44
6:F:54:LEU:O	6:F:55:HIS:O	2.36	0.44
6:F:38:ARG:NH1	6:F:63:ASN:HB2	2.33	0.44
13:M:22:ILE:HB	13:M:25:VAL:CG1	2.48	0.44
15:O:33:THR:HA	15:O:63:ARG:HH11	1.82	0.44
18:R:35:GLU:HB2	21:U:19:PHE:HZ	1.80	0.44
1:A:1130:A:C1'	1:A:1146:A:C2	3.01	0.44
1:A:1220:G:H4'	19:S:34:TRP:O	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:309:A:H1'	1:A:608:A:C2	2.53	0.44
1:A:375:U:C2	1:A:376:G:C8	3.06	0.44
1:A:429:U:H4'	1:A:430:A:OP1	2.14	0.44
1:A:663:A:H2'	1:A:664:G:O4'	2.17	0.44
3:C:121:THR:CB	3:C:187:SER:OG	2.65	0.44
5:E:150:PRO:C	5:E:152:MET:N	2.71	0.44
8:H:40:LEU:O	8:H:45:PHE:HB2	2.18	0.44
8:H:55:THR:C	8:H:57:PRO:HD3	2.38	0.44
9:I:8:GLY:N	9:I:86:ALA:HB2	2.33	0.44
14:N:30:ILE:O	14:N:33:ASP:HB3	2.16	0.44
17:Q:12:VAL:HG12	17:Q:13:VAL:N	2.32	0.44
18:R:45:THR:OG1	18:R:45:THR:O	2.31	0.44
19:S:53:ASN:HB3	19:S:75:ALA:HB1	1.99	0.44
1:A:1386:G:C2	1:A:1387:G:C8	3.05	0.44
1:A:517:G:C8	1:A:531:U:C5	3.06	0.44
1:A:673:A:O3'	6:F:86:ARG:NH2	2.51	0.44
1:A:728:A:OP1	15:O:54:ARG:NH2	2.51	0.44
1:A:75:G:C2	1:A:96:U:C2	3.06	0.44
1:A:77:A:C2	1:A:93:U:N3	2.86	0.44
3:C:167:TRP:HE3	3:C:167:TRP:C	2.21	0.44
6:F:40:GLU:HB2	6:F:42:TRP:HE1	1.83	0.44
6:F:71:ILE:HG22	6:F:72:ASP:N	2.33	0.44
9:I:49:ARG:C	9:I:51:PRO:HD2	2.38	0.44
17:Q:50:ASN:O	17:Q:52:GLU:N	2.51	0.44
19:S:30:PRO:HA	19:S:48:THR:O	2.18	0.44
1:A:1463:U:H2'	1:A:1464:U:C6	2.54	0.43
1:A:1489:G:C2'	1:A:1490:U:H5'	2.48	0.43
1:A:15:G:C2	1:A:16:A:C4	3.06	0.43
1:A:222:C:C2	1:A:223:A:C8	3.06	0.43
1:A:373:A:N3	1:A:374:A:C8	2.86	0.43
1:A:688:G:O2'	1:A:704:A:N1	2.46	0.43
1:A:772:U:O2'	1:A:773:G:H5'	2.17	0.43
2:B:135:LEU:C	2:B:137:ARG:N	2.71	0.43
2:B:71:GLY:O	2:B:93:ASN:HA	2.17	0.43
4:D:105:MET:SD	4:D:143:VAL:HG13	2.57	0.43
4:D:124:MET:CE	4:D:146:ARG:HD2	2.47	0.43
4:D:188:ARG:O	4:D:191:LEU:HD12	2.18	0.43
5:E:35:ALA:O	5:E:50:TYR:O	2.37	0.43
8:H:88:ARG:O	8:H:89:LYS:HB3	2.18	0.43
17:Q:28:PHE:CE1	17:Q:37:PHE:O	2.71	0.43
17:Q:55:ILE:HG12	17:Q:56:GLY:N	2.33	0.43
1:A:1048:G:H4'	14:N:3:LYS:CE	2.49	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1055:A:C6	1:A:1206:G:C4	3.06	0.43
1:A:1211:U:H1'	1:A:1213:A:C2	2.52	0.43
1:A:190:A:H2'	1:A:191:G:O4'	2.17	0.43
1:A:211:G:O2'	1:A:212:G:O4'	2.36	0.43
1:A:451:A:H4'	1:A:452:A:O5'	2.17	0.43
1:A:575:G:N2	1:A:881:G:H1'	2.33	0.43
1:A:802:A:C2	1:A:803:G:H1'	2.53	0.43
1:A:823:C:O2'	1:A:824:G:H5'	2.18	0.43
1:A:841:C:N3	1:A:843:U:C5	2.86	0.43
1:A:844:G:H3'	1:A:844:G:OP1	2.18	0.43
1:A:926:G:C6	1:A:1505:G:C6	3.05	0.43
1:A:996:A:H2'	1:A:997:U:C6	2.53	0.43
2:B:186:ILE:HA	2:B:200:ILE:O	2.18	0.43
3:C:34:ASP:O	3:C:38:LYS:HB2	2.17	0.43
4:D:73:ARG:O	4:D:76:TYR:N	2.51	0.43
9:I:12:ARG:O	9:I:12:ARG:HG3	2.16	0.43
11:K:92:GLY:O	11:K:94:GLU:N	2.51	0.43
12:L:63:VAL:HG21	12:L:95:TYR:CD2	2.54	0.43
18:R:23:TYR:HA	18:R:58:ALA:HB1	2.00	0.43
19:S:58:VAL:CG1	19:S:75:ALA:HB2	2.48	0.43
21:U:43:THR:O	21:U:46:LYS:HB3	2.17	0.43
21:U:53:VAL:HG13	21:U:54:LYS:H	1.83	0.43
11:K:109:ASN:HB3	21:U:6:VAL:O	2.18	0.43
1:A:1078:U:C5	1:A:1079:G:C5	3.05	0.43
1:A:1169:A:C2	1:A:1170:A:C4	3.06	0.43
1:A:1349:A:C2	1:A:1374:A:C4	3.06	0.43
1:A:198:G:N2	1:A:199:A:H1'	2.33	0.43
1:A:198:G:H2'	1:A:199:A:C5'	2.48	0.43
1:A:111:G:C6	1:A:330:C:N4	2.84	0.43
1:A:541:G:H2'	1:A:542:G:O4'	2.17	0.43
1:A:57:G:C5	1:A:58:C:C4	3.06	0.43
1:A:575:G:O2'	1:A:821:G:OP2	2.13	0.43
1:A:867:G:H2'	1:A:868:C:C6	2.54	0.43
1:A:81:A:C2	1:A:89:U:C2	3.06	0.43
1:A:976:G:C2	1:A:1363:A:C2	3.06	0.43
2:B:133:GLU:O	2:B:137:ARG:HB3	2.18	0.43
4:D:97:ARG:O	4:D:101:VAL:HG23	2.19	0.43
4:D:26:ARG:CG	4:D:27:ALA:N	2.67	0.43
5:E:56:VAL:N	5:E:57:PRO:CD	2.80	0.43
1:A:1078:U:C2	5:E:90:THR:HG21	2.53	0.43
7:G:137:LYS:O	7:G:141:VAL:HG23	2.18	0.43
8:H:66:PHE:C	8:H:66:PHE:CD1	2.89	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:I:28:ILE:HB	9:I:35:LEU:HB2	1.99	0.43
9:I:44:ALA:HB1	9:I:47:VAL:HG21	2.00	0.43
14:N:53:ARG:C	14:N:55:SER:N	2.72	0.43
15:O:27:VAL:O	15:O:31:LEU:HD12	2.18	0.43
17:Q:36:LYS:HG3	17:Q:37:PHE:N	2.33	0.43
18:R:25:ASP:C	18:R:27:ALA:H	2.21	0.43
19:S:80:TYR:CG	19:S:81:ARG:N	2.87	0.43
1:A:1137:C:O2	1:A:1137:C:O4'	2.36	0.43
1:A:1222:G:H5''	19:S:78:ARG:NH1	2.34	0.43
1:A:1359:C:O2'	1:A:1361:G:N7	2.50	0.43
1:A:978:A:P	1:A:1362:A:H61	2.41	0.43
1:A:130:A:C2	1:A:264:C:C2	3.06	0.43
1:A:327:A:N1	1:A:329:A:C2	2.86	0.43
1:A:55:A:N6	1:A:56:U:C2	2.86	0.43
1:A:731:G:H5'	1:A:766:A:H4'	2.00	0.43
1:A:756:C:H2'	1:A:757:U:H5'	2.01	0.43
1:A:745:G:H1'	1:A:836:G:O2'	2.18	0.43
1:A:884:U:H4'	1:A:885:G:H5''	2.01	0.43
2:B:139:ARG:HD2	2:B:140:GLU:N	2.32	0.43
4:D:98:LEU:O	4:D:101:VAL:N	2.51	0.43
4:D:24:GLY:O	4:D:161:LEU:HD11	2.18	0.43
4:D:206:LYS:O	4:D:206:LYS:CD	2.66	0.43
7:G:65:ALA:HB1	7:G:127:ALA:HB3	2.01	0.43
9:I:19:VAL:HG21	9:I:83:ILE:N	2.33	0.43
13:M:3:ARG:HA	13:M:9:ILE:HG12	2.00	0.43
19:S:6:LYS:HB2	19:S:7:LYS:HG2	2.00	0.43
1:A:1261:A:C2	1:A:1262:C:C5	3.06	0.43
1:A:1397:C:C3'	1:A:1398:A:H5''	2.48	0.43
1:A:407:U:N3	1:A:408:A:N7	2.66	0.43
1:A:552:U:C4'	12:L:83:ARG:HD2	2.49	0.43
1:A:590:U:H2'	1:A:591:U:C6	2.54	0.43
1:A:939:G:N1	1:A:940:C:N3	2.67	0.43
1:A:93:U:C2'	1:A:94:G:H5''	2.49	0.43
5:E:157:ARG:C	5:E:159:LYS:N	2.66	0.43
6:F:88:MET:HE3	18:R:64:TYR:CE2	2.54	0.43
6:F:90:MET:O	6:F:91:ARG:O	2.37	0.43
11:K:118:HIS:O	11:K:119:ASN:HB2	2.17	0.43
11:K:52:PHE:CE2	11:K:62:ALA:HB1	2.53	0.43
13:M:73:ILE:HA	13:M:76:SER:OG	2.18	0.43
15:O:70:LEU:CD1	15:O:78:TYR:HA	2.48	0.43
1:A:1151:A:C2	1:A:1152:A:C4	3.07	0.43
1:A:1211:U:H2'	1:A:1212:U:OP2	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1495:U:H2'	1:A:1496:C:O4'	2.18	0.43
1:A:454:G:N2	1:A:479:U:O2	2.50	0.43
1:A:821:G:H2'	1:A:822:U:C6	2.54	0.43
5:E:96:MET:HE3	5:E:111:MET:CE	2.49	0.43
11:K:15:GLN:O	11:K:15:GLN:HG3	2.18	0.43
14:N:17:ALA:HA	14:N:21:PHE:HB2	2.01	0.43
18:R:24:LYS:C	18:R:26:ILE:H	2.20	0.43
21:U:25:LYS:HD3	21:U:26:ALA:H	1.84	0.43
1:A:102:G:H2'	1:A:103:U:H6	1.84	0.43
1:A:1381:U:C5	1:A:1382:C:H5	2.37	0.43
1:A:1484:C:H2'	1:A:1485:U:O4'	2.18	0.43
1:A:1534:A:H4'	1:A:1535:C:H2'	2.01	0.43
1:A:356:A:C2'	1:A:357:G:H5'	2.47	0.43
1:A:875:U:C4	1:A:876:C:C5	3.06	0.43
1:A:878:A:N6	1:A:879:C:N4	2.67	0.43
2:B:208:ARG:O	2:B:211:THR:N	2.52	0.43
2:B:50:PHE:HD1	2:B:54:LEU:HD23	1.84	0.43
5:E:105:ILE:H	5:E:122:ASN:HA	1.84	0.43
1:A:1072:G:OP1	5:E:62:LYS:NZ	2.52	0.43
7:G:114:LYS:HB2	7:G:118:LEU:HD12	2.00	0.43
10:J:18:ILE:CG2	10:J:19:ASP:N	2.82	0.43
11:K:122:ARG:NH1	21:U:36:GLU:CG	2.81	0.43
17:Q:19:LYS:CD	17:Q:49:GLU:HA	2.47	0.43
20:T:24:ARG:O	20:T:27:MET:HG3	2.17	0.43
1:A:1101:A:H4'	1:A:1102:A:O5'	2.18	0.43
1:A:1144:G:N1	1:A:1145:A:C2	2.87	0.43
1:A:1191:A:H5''	3:C:4:LYS:HE3	2.01	0.43
1:A:1399:C:H4'	1:A:1400:C:O5'	2.19	0.43
1:A:158:G:C2'	1:A:159:G:H5''	2.48	0.43
1:A:229:U:H2'	1:A:230:G:O4'	2.19	0.43
1:A:753:A:H4'	1:A:754:C:O5'	2.18	0.43
1:A:764:C:C4	1:A:765:G:C5	3.06	0.43
1:A:867:G:H2'	1:A:868:C:H6	1.83	0.43
1:A:9:G:OP2	5:E:126:LYS:CE	2.67	0.43
2:B:125:THR:O	2:B:126:PHE:HB3	2.19	0.43
2:B:69:PHE:O	2:B:91:PHE:HA	2.19	0.43
3:C:121:THR:CB	3:C:187:SER:HG	2.32	0.43
4:D:40:GLN:OE1	4:D:41:HIS:NE2	2.51	0.43
6:F:17:GLN:O	6:F:21:MET:HG3	2.19	0.43
7:G:100:ALA:O	7:G:104:ILE:HG13	2.18	0.43
8:H:29:SER:HB2	8:H:59:LEU:HB2	2.00	0.43
9:I:99:ARG:HA	9:I:104:VAL:HG21	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:489:C:O2'	1:A:490:C:H5'	2.19	0.43
1:A:869:G:H4'	1:A:872:A:C8	2.54	0.43
1:A:87:C:H2'	1:A:88:U:C6	2.54	0.43
1:A:940:C:H2'	1:A:941:G:C8	2.54	0.43
1:A:976:G:N2	1:A:1363:A:N3	2.67	0.43
1:A:1074:G:H4'	2:B:103:ASN:HB2	1.99	0.43
3:C:102:ASN:C	3:C:103:ILE:HG13	2.39	0.43
4:D:173:VAL:HG13	4:D:174:ASP:H	1.82	0.43
4:D:174:ASP:O	4:D:175:ALA:HB3	2.18	0.43
4:D:17:THR:HG22	4:D:18:ASP:N	2.34	0.43
6:F:22:ILE:HG22	6:F:22:ILE:O	2.18	0.43
9:I:67:VAL:HG13	9:I:67:VAL:O	2.18	0.43
1:A:1308:U:O3'	13:M:91:HIS:HE1	2.01	0.43
14:N:53:ARG:O	14:N:59:ARG:HD2	2.19	0.43
17:Q:29:VAL:O	17:Q:29:VAL:HG22	2.19	0.43
17:Q:47:HIS:HB2	17:Q:67:LEU:HD13	2.01	0.43
1:A:1140:C:O2'	1:A:1141:C:P	2.76	0.43
1:A:1420:U:H2'	1:A:1421:G:O4'	2.19	0.43
1:A:793:U:O2	1:A:1516:G:H4'	2.19	0.43
1:A:282:A:H3'	1:A:283:U:H6	1.84	0.43
1:A:409:U:H2'	1:A:410:G:O4'	2.18	0.43
1:A:585:G:OP1	17:Q:39:LYS:HE3	2.18	0.43
1:A:718:A:N7	1:A:719:C:C5	2.87	0.43
1:A:733:G:H4'	1:A:734:G:OP1	2.19	0.43
1:A:78:A:C6	1:A:79:G:C6	3.06	0.43
5:E:133:PRO:O	5:E:137:VAL:HG13	2.18	0.43
8:H:106:THR:HG21	8:H:121:LEU:HD13	2.00	0.43
8:H:126:ILE:HD12	8:H:126:ILE:N	2.34	0.43
10:J:36:VAL:HG12	10:J:38:GLY:H	1.84	0.43
10:J:48:ARG:NH1	10:J:48:ARG:CG	2.80	0.43
12:L:42:PRO:HA	12:L:89:ASP:O	2.19	0.43
12:L:90:LEU:HB3	12:L:93:VAL:CG2	2.49	0.43
16:P:21:VAL:HG21	16:P:60:TRP:CD1	2.54	0.43
16:P:52:LEU:HD21	16:P:57:ILE:CD1	2.48	0.43
1:A:1182:G:H5'	1:A:1184:G:H5''	2.00	0.42
1:A:1184:G:C2	1:A:1185:G:C8	3.06	0.42
1:A:1491:G:C5	1:A:1492:A:C5	3.07	0.42
1:A:17:U:O2	1:A:18:C:C6	2.72	0.42
1:A:410:G:H5''	1:A:411:A:OP1	2.19	0.42
1:A:504:C:H1'	1:A:510:A:C4	2.53	0.42
1:A:81:A:H61	1:A:87:C:N4	2.17	0.42
1:A:89:U:H2'	1:A:90:C:C6	2.54	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:100:GLN:O	3:C:101:ILE:HB	2.18	0.42
6:F:13:ASP:O	6:F:15:SER:N	2.48	0.42
7:G:146:GLU:OE1	7:G:149:LYS:HE2	2.19	0.42
7:G:31:MET:O	7:G:31:MET:HG2	2.19	0.42
5:E:156:LYS:HG2	8:H:71:VAL:HG22	2.00	0.42
20:T:83:ILE:O	20:T:87:ALA:HB3	2.19	0.42
21:U:6:VAL:HG11	21:U:17:ARG:HG3	2.01	0.42
21:U:53:VAL:HG22	21:U:54:LYS:H	1.83	0.42
1:A:327:A:C2	1:A:329:A:N3	2.87	0.42
1:A:707:U:H2'	1:A:708:C:C6	2.54	0.42
1:A:671:G:N2	1:A:736:C:C2	2.87	0.42
1:A:822:U:N3	1:A:823:C:C5	2.87	0.42
1:A:996:A:H2'	1:A:997:U:C5	2.53	0.42
2:B:102:THR:O	2:B:103:ASN:CB	2.67	0.42
2:B:192:ASP:O	2:B:193:PRO:O	2.36	0.42
2:B:54:LEU:HA	2:B:57:LEU:CB	2.42	0.42
1:A:620:C:C6	4:D:132:ILE:HD13	2.54	0.42
4:D:29:ASP:O	4:D:31:LYS:N	2.46	0.42
5:E:94:VAL:CG1	5:E:111:MET:HE3	2.49	0.42
5:E:42:GLY:O	5:E:119:GLY:HA3	2.19	0.42
6:F:92:THR:O	6:F:93:LYS:C	2.57	0.42
7:G:125:SER:C	7:G:127:ALA:N	2.72	0.42
8:H:11:LEU:HD11	8:H:127:CYS:CB	2.50	0.42
8:H:126:ILE:HG22	8:H:127:CYS:SG	2.59	0.42
11:K:85:MET:HA	11:K:111:THR:O	2.19	0.42
14:N:69:ARG:HA	14:N:70:PRO:HD3	1.90	0.42
17:Q:16:LYS:O	17:Q:17:MET:SD	2.77	0.42
1:A:264:C:H2'	1:A:265:G:O4'	2.18	0.42
1:A:34:C:H2'	1:A:35:G:C8	2.54	0.42
1:A:437:U:C4	1:A:438:U:C5	3.06	0.42
1:A:442:G:C6	1:A:443:C:C4	3.07	0.42
1:A:486:U:OP2	1:A:486:U:C6	2.73	0.42
1:A:73:C:O2'	1:A:74:A:P	2.77	0.42
1:A:769:G:C2'	1:A:770:C:H5'	2.49	0.42
1:A:811:C:H4'	1:A:900:A:N6	2.35	0.42
1:A:983:A:C2'	1:A:983:A:N3	2.81	0.42
1:A:990:C:N3	1:A:991:U:O4	2.52	0.42
1:A:1108:G:H5''	3:C:176:HIS:CD2	2.55	0.42
5:E:100:SER:O	5:E:101:GLU:C	2.57	0.42
6:F:18:VAL:HG12	6:F:19:PRO:CD	2.50	0.42
8:H:27:MET:HG2	8:H:59:LEU:HB3	2.01	0.42
9:I:115:LYS:HB2	9:I:118:LEU:HD22	2.01	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:97:ILE:HD13	11:K:110:ILE:HD11	2.00	0.42
11:K:71:ALA:O	11:K:75:LYS:HG3	2.18	0.42
17:Q:60:GLU:HB3	17:Q:76:VAL:HG23	2.00	0.42
11:K:110:ILE:HG22	21:U:17:ARG:CZ	2.50	0.42
1:A:108:G:C5'	1:A:108:G:N3	2.83	0.42
1:A:1072:G:C6	1:A:1104:G:C2	3.07	0.42
1:A:1139:G:N2	1:A:1143:G:C6	2.87	0.42
1:A:151:A:H2'	1:A:152:A:O4'	2.20	0.42
1:A:252:U:O4	1:A:253:A:N6	2.52	0.42
1:A:282:A:H3'	1:A:283:U:C6	2.55	0.42
1:A:408:A:H2'	1:A:409:U:O4'	2.18	0.42
1:A:583:A:N7	1:A:584:G:N7	2.67	0.42
1:A:676:A:C2	1:A:677:U:C4	3.08	0.42
2:B:43:LEU:HG	2:B:44:GLU:HG3	2.01	0.42
3:C:26:THR:OG1	14:N:76:LYS:HE3	2.20	0.42
6:F:9:MET:HE2	6:F:59:TYR:CD1	2.54	0.42
10:J:74:VAL:HG12	10:J:75:ASP:N	2.34	0.42
14:N:87:ALA:HA	14:N:92:GLU:HG3	2.00	0.42
1:A:1157:A:H5'	1:A:1158:C:C6	2.55	0.42
1:A:1308:U:H2'	1:A:1309:G:C8	2.54	0.42
1:A:1305:G:C6	1:A:1331:G:C2	3.07	0.42
1:A:1446:A:N6	1:A:1447:A:N6	2.68	0.42
1:A:1462:C:H2'	1:A:1463:U:C6	2.54	0.42
1:A:298:A:H2'	1:A:299:G:O4'	2.20	0.42
1:A:328:C:H2'	1:A:328:C:O2	2.20	0.42
1:A:463:U:H3'	1:A:464:U:C6	2.54	0.42
1:A:775:G:C6	1:A:776:G:C5	3.07	0.42
1:A:890:G:N2	1:A:906:A:H2'	2.35	0.42
1:A:929:G:C5	1:A:930:C:C5	3.07	0.42
6:F:19:PRO:HA	6:F:22:ILE:HD12	2.01	0.42
8:H:94:LYS:HD3	8:H:98:GLY:CA	2.49	0.42
10:J:35:GLN:C	10:J:36:VAL:HG23	2.40	0.42
12:L:21:VAL:N	12:L:22:PRO:CD	2.82	0.42
13:M:16:VAL:HG13	13:M:41:GLU:HA	2.02	0.42
15:O:85:LEU:HA	15:O:85:LEU:HD12	1.92	0.42
16:P:52:LEU:HD21	16:P:57:ILE:HD12	2.01	0.42
17:Q:31:HIS:CD2	17:Q:34:TYR:CD1	3.07	0.42
17:Q:47:HIS:HA	17:Q:71:LYS:HE2	2.01	0.42
18:R:59:ILE:O	18:R:63:ARG:HD2	2.19	0.42
19:S:58:VAL:HG11	19:S:75:ALA:CA	2.50	0.42
1:A:1048:G:P	23:A:1846:HOH:O	2.75	0.42
1:A:104:G:H4'	1:A:174:A:O4'	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1105:A:C2	1:A:1106:G:N7	2.87	0.42
1:A:1343:G:C6	1:A:1344:C:N4	2.87	0.42
1:A:1348:U:OP1	9:I:112:GLU:N	2.45	0.42
1:A:1364:U:O2	1:A:1364:U:C2'	2.68	0.42
1:A:1478:U:H2'	1:A:1479:C:C6	2.55	0.42
1:A:68:G:O4'	1:A:171:A:H1'	2.19	0.42
1:A:208:U:C5	1:A:210:C:H6	2.38	0.42
1:A:66:A:H5'	1:A:173:U:O4	2.20	0.42
1:A:728:A:C6	1:A:729:A:C6	3.08	0.42
2:B:222:ARG:NE	2:B:223:GLU:HB2	2.35	0.42
4:D:115:ARG:HG3	4:D:133:ALA:CB	2.49	0.42
4:D:206:LYS:O	4:D:206:LYS:CG	2.64	0.42
4:D:98:LEU:HB2	4:D:135:TYR:HB3	2.02	0.42
5:E:25:VAL:O	5:E:26:LYS:C	2.58	0.42
5:E:96:MET:HE1	5:E:140:THR:HG22	2.02	0.42
6:F:25:TYR:CD2	6:F:25:TYR:N	2.88	0.42
7:G:33:ASP:CB	7:G:35:LYS:HE3	2.50	0.42
9:I:95:ARG:HA	9:I:98:LEU:HB3	2.00	0.42
13:M:46:SER:O	13:M:47:GLU:HB3	2.19	0.42
1:A:375:U:OP1	16:P:70:ARG:HD3	2.20	0.42
18:R:24:LYS:C	18:R:26:ILE:N	2.73	0.42
1:A:1112:C:C4	3:C:178:LEU:HD23	2.54	0.42
1:A:1130:A:C8	1:A:1146:A:N1	2.88	0.42
1:A:1394:A:C5	1:A:1501:C:H4'	2.55	0.42
1:A:1426:G:C5	1:A:1475:G:C2	3.07	0.42
1:A:295:C:C2	1:A:296:U:C6	3.07	0.42
1:A:304:U:O2'	1:A:305:G:H5'	2.19	0.42
1:A:346:G:N3	1:A:346:G:H3'	2.34	0.42
1:A:456:A:C6	1:A:457:G:C5	3.07	0.42
1:A:532:A:N6	3:C:193:TYR:HD2	2.17	0.42
1:A:615:G:C2	1:A:616:G:C8	3.07	0.42
1:A:728:A:C6	1:A:729:A:N6	2.87	0.42
1:A:952:U:O4	13:M:103:LYS:HD3	2.19	0.42
6:F:82:ASP:OD2	6:F:82:ASP:N	2.52	0.42
1:A:684:U:O2'	11:K:40:ASN:O	2.32	0.42
11:K:56:ARG:O	11:K:59:THR:HG23	2.19	0.42
12:L:42:PRO:HD3	12:L:48:ALA:O	2.19	0.42
20:T:83:ILE:O	20:T:87:ALA:CB	2.67	0.42
21:U:12:PHE:CD1	21:U:13:ASP:N	2.88	0.42
1:A:1014:A:N7	1:A:1015:G:C6	2.88	0.42
1:A:1130:A:C4	1:A:1146:A:C2	3.07	0.42
1:A:1306:A:H1'	1:A:1332:A:C5	2.55	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:146:G:N2	1:A:147:G:H1'	2.35	0.42
1:A:418:C:H1'	1:A:540:G:O2'	2.19	0.42
1:A:577:G:C1'	1:A:816:A:H2'	2.49	0.42
1:A:81:A:H2'	1:A:82:G:H8	1.84	0.42
1:A:974:A:OP1	14:N:69:ARG:NH1	2.51	0.42
2:B:187:VAL:HB	2:B:191:SER:HB2	2.02	0.42
2:B:222:ARG:HG2	2:B:223:GLU:N	2.35	0.42
2:B:24:ASN:O	2:B:26:LYS:N	2.52	0.42
4:D:206:LYS:O	4:D:206:LYS:HD3	2.20	0.42
5:E:105:ILE:CG1	5:E:112:ARG:HG3	2.50	0.42
8:H:83:LEU:O	8:H:83:LEU:HD13	2.20	0.42
10:J:12:ALA:CB	10:J:18:ILE:HB	2.50	0.42
11:K:18:ASP:HA	11:K:81:ASN:O	2.19	0.42
13:M:57:ARG:O	13:M:60:VAL:HG13	2.20	0.42
13:M:63:PHE:O	13:M:65:VAL:HG13	2.20	0.42
14:N:87:ALA:HB1	14:N:92:GLU:HB2	2.01	0.42
16:P:38:PHE:CE2	16:P:51:ARG:HD3	2.54	0.42
21:U:47:ARG:HE	21:U:47:ARG:HA	1.85	0.42
1:A:295:C:N4	1:A:296:U:C4	2.88	0.42
1:A:538:G:H2'	1:A:539:A:O4'	2.20	0.42
1:A:63:C:O2'	1:A:380:G:H4'	2.19	0.42
1:A:919:A:C2	1:A:920:U:C6	3.08	0.42
2:B:91:PHE:CD2	2:B:150:GLY:HA3	2.54	0.42
2:B:165:ASP:O	2:B:168:HIS:HB3	2.19	0.42
3:C:101:ILE:O	3:C:101:ILE:HG23	2.20	0.42
4:D:33:LYS:O	4:D:34:ILE:C	2.59	0.42
1:A:15:G:O4'	5:E:29:ARG:NH2	2.52	0.42
6:F:78:PHE:N	6:F:78:PHE:CD2	2.87	0.42
1:A:1377:A:N3	7:G:2:PRO:HG3	2.35	0.42
9:I:57:MET:HA	9:I:60:LYS:HB3	2.02	0.42
10:J:27:GLU:O	10:J:31:ARG:HB3	2.20	0.42
12:L:76:GLU:O	12:L:77:HIS:O	2.37	0.42
13:M:93:ARG:HB3	13:M:93:ARG:CZ	2.50	0.42
16:P:40:ASN:HB3	16:P:43:ALA:HB2	2.02	0.42
1:A:210:C:H5''	1:A:211:G:OP1	2.19	0.42
1:A:436:C:N3	1:A:437:U:C4	2.88	0.42
1:A:12:U:H4'	1:A:526:C:H4'	2.02	0.42
1:A:615:G:C2	1:A:626:G:C5	3.08	0.42
1:A:73:C:O2'	1:A:74:A:O5'	2.31	0.42
1:A:582:C:C4	1:A:760:G:O6	2.72	0.42
1:A:878:A:C5	1:A:879:C:C5	3.08	0.42
1:A:971:G:OP1	1:A:972:C:H5''	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:100:MET:CA	2:B:107:VAL:HG21	2.50	0.42
2:B:96:TRP:CZ3	2:B:175:GLU:OE2	2.72	0.42
2:B:208:ARG:O	2:B:210:VAL:N	2.53	0.42
3:C:84:VAL:HA	3:C:87:LEU:HD12	2.01	0.42
4:D:129:VAL:HG23	4:D:146:ARG:HD3	2.01	0.42
4:D:35:GLU:HG3	4:D:36:GLN:N	2.34	0.42
4:D:59:GLN:OE1	4:D:59:GLN:CA	2.67	0.42
6:F:16:GLU:O	6:F:18:VAL:N	2.52	0.42
6:F:59:TYR:C	6:F:60:VAL:HG23	2.40	0.42
8:H:102:ALA:O	8:H:112:THR:HA	2.19	0.42
9:I:51:PRO:HD3	9:I:80:ARG:HG2	2.02	0.42
11:K:43:GLY:HA3	11:K:74:VAL:HG12	2.02	0.42
13:M:81:MET:O	13:M:82:ASP:C	2.57	0.42
14:N:45:VAL:HG23	14:N:46:LEU:H	1.85	0.42
15:O:46:HIS:C	15:O:48:LYS:N	2.72	0.42
1:A:254:G:O2'	17:Q:18:GLU:O	2.36	0.42
20:T:80:THR:O	20:T:81:ALA:C	2.56	0.42
21:U:9:ASN:N	21:U:12:PHE:HE2	2.18	0.42
1:A:1105:A:N3	1:A:1106:G:C8	2.88	0.41
1:A:1179:A:C2'	1:A:1180:A:H5'	2.50	0.41
1:A:128:G:N1	1:A:129:A:C6	2.88	0.41
1:A:1296:C:H4'	1:A:1302:C:C4	2.54	0.41
1:A:978:A:H4'	1:A:1322:C:C5	2.55	0.41
1:A:1342:C:H2'	1:A:1343:G:C8	2.55	0.41
1:A:270:A:H2'	1:A:271:C:C6	2.54	0.41
1:A:276:G:H2'	1:A:277:C:O4'	2.19	0.41
1:A:406:G:N3	1:A:407:U:C6	2.88	0.41
1:A:502:A:C2	1:A:503:C:C2	3.07	0.41
1:A:716:A:C2'	1:A:717:U:O5'	2.68	0.41
1:A:825:A:O2'	1:A:826:C:H5'	2.19	0.41
3:C:134:MET:SD	3:C:153:VAL:HG13	2.60	0.41
4:D:106:GLY:O	4:D:159:LEU:N	2.53	0.41
4:D:34:ILE:O	4:D:34:ILE:HG23	2.19	0.41
5:E:89:HIS:CE1	5:E:138:ARG:HD3	2.55	0.41
7:G:122:ASN:O	7:G:125:SER:HB2	2.19	0.41
9:I:47:VAL:O	9:I:80:ARG:HG2	2.19	0.41
11:K:23:ILE:HG21	11:K:96:THR:HG21	2.02	0.41
1:A:706:A:O2'	11:K:31:ILE:HD11	2.20	0.41
13:M:39:ILE:HG13	13:M:56:LEU:HD11	2.01	0.41
1:A:1025:U:H5''	1:A:1026:G:OP1	2.20	0.41
1:A:1166:G:H2'	1:A:1168:U:OP2	2.20	0.41
1:A:1319:A:OP2	19:S:5:LEU:HD21	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:435:A:C2	1:A:436:C:C1'	3.03	0.41
1:A:683:G:C6	1:A:708:C:N3	2.88	0.41
1:A:690:G:H2'	1:A:691:G:O4'	2.19	0.41
3:C:53:SER:HB2	3:C:115:LEU:HG	2.01	0.41
3:C:120:ILE:HD11	3:C:137:ALA:CB	2.49	0.41
3:C:124:LEU:HD13	3:C:196:ILE:HG21	2.01	0.41
3:C:184:TYR:CD1	3:C:201:TRP:CD1	3.07	0.41
3:C:50:ALA:O	3:C:51:SER:HB2	2.20	0.41
7:G:13:LEU:HD13	7:G:14:PRO:HD2	2.02	0.41
9:I:26:GLY:HA2	9:I:61:LEU:O	2.19	0.41
12:L:24:LEU:HD22	12:L:59:ASN:OD1	2.20	0.41
15:O:67:LEU:HD23	15:O:78:TYR:CE1	2.55	0.41
16:P:74:LEU:N	16:P:74:LEU:HD23	2.35	0.41
20:T:5:LYS:O	20:T:6:SER:C	2.57	0.41
1:A:1022:A:C5	1:A:1023:U:C5	3.09	0.41
1:A:965:U:OP1	1:A:1198:G:H5''	2.20	0.41
1:A:1240:U:H3'	1:A:1241:G:H5'	2.02	0.41
1:A:39:G:N2	1:A:40:C:C2	2.88	0.41
1:A:790:A:N6	1:A:791:G:N1	2.68	0.41
1:A:991:U:H4'	1:A:992:U:OP1	2.21	0.41
2:B:130:THR:HB	2:B:132:LYS:HB3	2.02	0.41
2:B:154:MET:CE	2:B:158:PRO:HG3	2.51	0.41
2:B:211:THR:HA	2:B:214:LEU:HB2	2.02	0.41
3:C:6:HIS:C	3:C:8:ASN:H	2.23	0.41
4:D:15:GLU:HA	4:D:15:GLU:OE1	2.20	0.41
4:D:195:ILE:CG1	4:D:195:ILE:O	2.68	0.41
9:I:128:SER:O	9:I:129:LYS:C	2.59	0.41
13:M:54:ASP:HA	13:M:57:ARG:CB	2.50	0.41
15:O:45:GLU:O	15:O:46:HIS:CB	2.67	0.41
17:Q:11:ARG:CZ	17:Q:12:VAL:O	2.68	0.41
1:A:1036:A:H5'	1:A:1037:C:OP2	2.20	0.41
1:A:558:G:H8	1:A:558:G:O5'	2.03	0.41
1:A:632:U:H3'	1:A:633:G:H5'	2.03	0.41
1:A:851:G:C2	1:A:852:G:C8	3.08	0.41
1:A:920:U:H2'	1:A:921:U:H6	1.85	0.41
2:B:68:LEU:HD13	2:B:161:LEU:HD11	2.02	0.41
3:C:172:ARG:C	3:C:174:PRO:HD3	2.40	0.41
3:C:64:ILE:HG22	3:C:97:VAL:HG23	2.02	0.41
7:G:106:GLU:O	7:G:110:LYS:HG2	2.20	0.41
8:H:41:LYS:HD2	8:H:48:ASP:HA	2.03	0.41
9:I:114:LYS:HG2	9:I:115:LYS:N	2.35	0.41
9:I:118:LEU:N	9:I:118:LEU:HD12	2.36	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1232:U:OP1	9:I:126:GLN:NE2	2.53	0.41
9:I:57:MET:N	9:I:57:MET:SD	2.94	0.41
11:K:88:GLY:H	11:K:114:THR:HG22	1.85	0.41
12:L:116:LYS:O	12:L:117:TYR:CD1	2.73	0.41
13:M:4:ILE:O	13:M:6:GLY:N	2.53	0.41
1:A:1308:U:OP2	13:M:98:ARG:HG3	2.20	0.41
16:P:39:PHE:CD1	16:P:39:PHE:C	2.92	0.41
16:P:55:ASP:O	16:P:58:ALA:HB3	2.20	0.41
18:R:27:ALA:O	18:R:30:LYS:HG2	2.21	0.41
20:T:44:LYS:HD3	20:T:87:ALA:HA	2.03	0.41
21:U:11:PRO:O	21:U:12:PHE:CB	2.68	0.41
1:A:1036:A:H2'	1:A:1036:A:N3	2.35	0.41
1:A:1089:G:C5	1:A:1090:U:C5	3.09	0.41
1:A:1262:C:C4	1:A:1263:C:C4	3.09	0.41
1:A:1516:G:C2	1:A:1520:C:O2	2.74	0.41
1:A:213:G:C8	1:A:214:C:C6	3.08	0.41
1:A:247:G:O6	1:A:278:G:C6	2.74	0.41
1:A:491:G:O2'	1:A:492:C:H5'	2.20	0.41
1:A:728:A:N1	1:A:729:A:C6	2.88	0.41
2:B:10:LEU:HB2	2:B:43:LEU:HD22	2.03	0.41
3:C:126:ARG:O	3:C:127:ARG:CB	2.67	0.41
3:C:181:ASP:OD2	3:C:204:LYS:HB2	2.19	0.41
3:C:71:ALA:O	3:C:73:PRO:HD3	2.20	0.41
5:E:15:LEU:CD1	5:E:15:LEU:C	2.88	0.41
7:G:40:GLU:HB2	7:G:44:TYR:CE2	2.56	0.41
9:I:18:ARG:HG3	9:I:66:THR:OG1	2.21	0.41
10:J:34:ALA:O	10:J:78:GLU:HB3	2.20	0.41
13:M:96:PRO:HB2	13:M:100:GLN:OE1	2.20	0.41
14:N:36:ALA:CB	14:N:41:ARG:HG3	2.50	0.41
18:R:23:TYR:O	18:R:23:TYR:CD1	2.74	0.41
1:A:1318:A:O2'	19:S:37:ARG:HD3	2.20	0.41
19:S:6:LYS:CB	19:S:7:LYS:HE3	2.50	0.41
1:A:1002:G:H2'	1:A:1003:G:O4'	2.20	0.41
1:A:1271:A:H2'	1:A:1272:G:C8	2.55	0.41
1:A:1375:A:C5	1:A:1376:U:C5	3.08	0.41
1:A:188:C:H2'	1:A:188:C:O2	2.18	0.41
1:A:216:U:C4	1:A:217:C:N4	2.88	0.41
1:A:31:G:C5	1:A:306:A:H1'	2.55	0.41
1:A:652:U:C5	1:A:752:G:C2	3.08	0.41
1:A:942:G:C2	1:A:1342:C:C2	3.09	0.41
3:C:23:PHE:CD2	3:C:24:ALA:N	2.88	0.41
1:A:439:U:H4'	4:D:121:LYS:HG3	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:130:VAL:HG11	4:D:135:TYR:CG	2.55	0.41
5:E:103:THR:O	5:E:121:HIS:O	2.39	0.41
5:E:153:VAL:HG23	5:E:157:ARG:HB2	2.02	0.41
6:F:10:VAL:HG21	6:F:18:VAL:CG2	2.50	0.41
6:F:18:VAL:CG1	6:F:19:PRO:N	2.80	0.41
8:H:21:ASN:O	8:H:22:LYS:C	2.59	0.41
10:J:53:ILE:HG13	14:N:85:ARG:HD2	2.02	0.41
11:K:45:ALA:HB3	11:K:70:CYS:HB2	2.03	0.41
11:K:77:TYR:CD1	11:K:77:TYR:N	2.88	0.41
13:M:5:ALA:O	13:M:7:ILE:N	2.54	0.41
1:A:106:C:O2	1:A:379:C:C5'	2.68	0.41
1:A:1107:C:C4	1:A:1108:G:N7	2.89	0.41
1:A:1202:U:H2'	1:A:1203:C:H5'	2.03	0.41
1:A:483:C:H2'	1:A:484:G:C8	2.56	0.41
1:A:509:A:C6	1:A:510:A:C6	3.09	0.41
1:A:755:G:C2	1:A:756:C:C6	3.09	0.41
1:A:853:C:C2	1:A:854:U:C6	3.08	0.41
1:A:860:A:N6	1:A:861:G:C2	2.89	0.41
8:H:20:ALA:O	8:H:21:ASN:HB2	2.21	0.41
10:J:15:HIS:HB3	10:J:70:HIS:CD2	2.55	0.41
14:N:22:ALA:N	14:N:25:ALA:CB	2.83	0.41
14:N:3:LYS:HB3	14:N:6:MET:HG2	2.01	0.41
15:O:23:GLY:O	15:O:24:SER:C	2.59	0.41
17:Q:24:ALA:HB1	17:Q:41:THR:CG2	2.51	0.41
20:T:35:VAL:HG21	20:T:54:MET:HG2	2.02	0.41
21:U:21:ARG:NH1	21:U:25:LYS:HG3	2.36	0.41
1:A:174:A:C2	1:A:175:C:H1'	2.56	0.41
1:A:250:A:N3	1:A:250:A:H5'	2.36	0.41
1:A:355:C:C2	1:A:356:A:C8	3.08	0.41
1:A:429:U:H3'	4:D:9:LEU:CD2	2.47	0.41
1:A:496:A:N3	1:A:496:A:H2'	2.34	0.41
1:A:509:A:N1	1:A:510:A:N1	2.68	0.41
1:A:622:A:H5''	1:A:623:C:OP2	2.21	0.41
1:A:670:G:N2	1:A:737:C:C2	2.88	0.41
1:A:735:C:H2'	1:A:736:C:C6	2.56	0.41
1:A:73:C:O2	1:A:74:A:C8	2.73	0.41
1:A:899:C:H6	1:A:899:C:OP1	2.04	0.41
2:B:68:LEU:HD12	2:B:158:PRO:CG	2.50	0.41
4:D:124:MET:O	4:D:143:VAL:HA	2.20	0.41
4:D:155:VAL:CG2	4:D:155:VAL:O	2.68	0.41
4:D:173:VAL:CG1	4:D:174:ASP:N	2.83	0.41
6:F:6:ILE:O	6:F:61:LEU:HD12	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:65:ALA:O	7:G:127:ALA:HB1	2.20	0.41
7:G:138:ARG:HB3	7:G:138:ARG:HE	1.69	0.41
7:G:70:ARG:HG3	7:G:96:ARG:HG2	2.03	0.41
10:J:52:LEU:HB2	14:N:81:ARG:HD2	2.03	0.41
15:O:55:GLY:O	15:O:59:MET:HG3	2.21	0.41
16:P:77:GLU:C	16:P:79:ASN:H	2.24	0.41
20:T:44:LYS:NZ	20:T:86:LEU:O	2.47	0.41
21:U:12:PHE:HD1	21:U:13:ASP:N	2.19	0.41
21:U:18:ARG:O	21:U:21:ARG:N	2.54	0.41
1:A:1007:U:C2'	1:A:1008:U:H5''	2.51	0.41
1:A:1061:G:C2	1:A:1197:A:N3	2.89	0.41
1:A:1085:U:C2	1:A:1094:G:O6	2.74	0.41
1:A:1157:A:C5	1:A:1181:G:C6	3.08	0.41
1:A:1181:G:O2'	1:A:1182:G:C5	2.74	0.41
1:A:1399:C:C2	1:A:1401:G:C5	3.09	0.41
1:A:1492:A:H3'	1:A:1493:A:H8	1.86	0.41
1:A:182:A:C8	1:A:184:G:N7	2.89	0.41
1:A:421:U:H4'	1:A:421:U:OP1	2.21	0.41
1:A:503:C:H2'	1:A:504:C:H6	1.86	0.41
1:A:756:C:C4	1:A:757:U:C5	3.08	0.41
1:A:913:A:H4'	1:A:914:A:H4'	2.03	0.41
1:A:977:A:O2'	1:A:1223:C:N4	2.53	0.41
2:B:117:LEU:HB3	2:B:141:LEU:HD11	2.03	0.41
3:C:182:ILE:HD11	3:C:203:PHE:HB2	2.03	0.41
9:I:44:ALA:HB1	9:I:47:VAL:CG2	2.51	0.41
10:J:89:ARG:NH1	10:J:89:ARG:HB2	2.36	0.41
11:K:20:VAL:HB	11:K:35:THR:CG2	2.49	0.41
11:K:72:ASP:O	11:K:73:ALA:HB3	2.21	0.41
12:L:24:LEU:CD2	12:L:59:ASN:OD1	2.68	0.41
13:M:90:ARG:HD2	13:M:96:PRO:O	2.21	0.41
1:A:754:C:OP1	15:O:72:ARG:NH2	2.54	0.41
17:Q:31:HIS:CD2	17:Q:34:TYR:HD1	2.38	0.41
17:Q:51:ASN:O	17:Q:51:ASN:ND2	2.54	0.41
1:A:130:A:OP1	17:Q:65:ARG:HD2	2.21	0.41
18:R:40:VAL:HA	18:R:41:PRO:HD2	1.91	0.41
1:A:1213:A:C5	1:A:1215:G:C4	3.08	0.41
1:A:1361:G:C2'	1:A:1362:A:H5''	2.50	0.41
1:A:358:U:H2'	1:A:359:G:C8	2.56	0.41
1:A:374:A:OP1	1:A:452:A:N1	2.54	0.41
1:A:464:U:N3	1:A:467:U:OP2	2.47	0.41
1:A:619:U:C2	4:D:132:ILE:HD11	2.56	0.41
1:A:642:A:N3	8:H:105:SER:OG	2.50	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:715:A:N6	1:A:716:A:N6	2.69	0.41
2:B:219:ALA:O	2:B:220:THR:HB	2.21	0.41
8:H:43:GLU:OE2	8:H:43:GLU:HA	2.21	0.41
14:N:26:GLU:C	14:N:28:LYS:H	2.23	0.41
14:N:46:LEU:HD12	14:N:49:GLN:HB2	2.03	0.41
16:P:20:VAL:HG21	16:P:32:PHE:CG	2.56	0.41
1:A:1240:U:H5'	1:A:1241:G:C8	2.56	0.41
1:A:978:A:C5	1:A:1318:A:N6	2.89	0.41
1:A:1431:A:C5	1:A:1432:G:C6	3.09	0.41
1:A:1479:C:C2	1:A:1480:A:C8	3.09	0.41
1:A:1493:A:OP2	1:A:1493:A:H8	2.04	0.41
1:A:49:U:C6	1:A:364:A:N6	2.89	0.41
1:A:513:C:H2'	1:A:514:C:C6	2.56	0.41
1:A:55:A:C5	1:A:56:U:C4	3.09	0.41
1:A:570:G:N3	1:A:571:U:C6	2.89	0.41
1:A:57:G:H2'	1:A:58:C:C6	2.56	0.41
1:A:662:U:O2	1:A:662:U:H2'	2.21	0.41
1:A:676:A:N1	1:A:677:U:C4	2.89	0.41
1:A:731:G:OP1	1:A:766:A:H1'	2.21	0.41
1:A:815:A:H4'	1:A:817:C:C5	2.57	0.41
1:A:842:U:O2	1:A:845:A:OP1	2.38	0.41
1:A:857:C:H2'	1:A:858:G:O4'	2.21	0.41
2:B:71:GLY:CA	2:B:164:ILE:CG2	2.99	0.41
2:B:47:VAL:O	2:B:50:PHE:HD2	2.04	0.41
5:E:44:GLY:O	5:E:45:ARG:C	2.59	0.41
7:G:66:LEU:HG	7:G:66:LEU:O	2.20	0.41
10:J:15:HIS:CG	10:J:16:ARG:N	2.88	0.41
10:J:7:ARG:HD3	10:J:75:ASP:OD1	2.21	0.41
1:A:1308:U:O3'	13:M:91:HIS:CE1	2.74	0.41
14:N:51:LEU:HB3	14:N:52:PRO:HD2	2.01	0.41
17:Q:13:VAL:HG12	17:Q:22:VAL:O	2.21	0.41
1:A:951:G:C4	1:A:1231:G:C2	3.09	0.40
1:A:1249:C:O3'	9:I:75:GLN:NE2	2.51	0.40
1:A:1313:U:P	19:S:6:LYS:HB3	2.62	0.40
1:A:22:G:H4'	1:A:885:G:C8	2.56	0.40
1:A:246:A:C4	1:A:279:A:C6	3.08	0.40
1:A:268:U:C4	1:A:269:C:N4	2.89	0.40
1:A:289:G:C2	1:A:290:C:C4	3.09	0.40
1:A:38:G:C2	1:A:397:A:C2	3.09	0.40
1:A:455:G:C2	1:A:478:A:C2	3.09	0.40
1:A:505:G:C2	1:A:506:G:C5	3.10	0.40
1:A:55:A:C6	1:A:56:U:N3	2.89	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:570:G:C2	1:A:571:U:C5	3.09	0.40
1:A:775:G:C2'	1:A:776:G:H5'	2.51	0.40
2:B:211:THR:HA	2:B:214:LEU:CB	2.52	0.40
3:C:80:LYS:HA	3:C:80:LYS:HE3	2.02	0.40
1:A:15:G:H4'	5:E:29:ARG:NH1	2.36	0.40
5:E:34:THR:HB	5:E:50:TYR:CZ	2.56	0.40
7:G:28:ASN:O	7:G:31:MET:HB3	2.21	0.40
7:G:79:ARG:HG2	7:G:84:THR:HG23	2.03	0.40
9:I:20:PHE:O	9:I:63:LEU:HA	2.21	0.40
11:K:35:THR:HG23	11:K:36:ASP:O	2.21	0.40
1:A:750:C:H4'	15:O:21:ASP:HA	2.02	0.40
17:Q:48:ASP:O	17:Q:49:GLU:C	2.59	0.40
1:A:1243:C:N4	1:A:1244:G:O6	2.54	0.40
1:A:1262:C:H2'	1:A:1263:C:O4'	2.22	0.40
1:A:1253:G:C2	1:A:1285:A:N6	2.89	0.40
1:A:1343:G:C5	1:A:1344:C:C4	3.09	0.40
1:A:888:G:H4'	1:A:1488:G:O2'	2.21	0.40
1:A:781:A:H4'	1:A:1522:U:O2'	2.21	0.40
1:A:1527:U:H2'	1:A:1528:U:C6	2.57	0.40
1:A:117:G:O6	1:A:289:G:H1'	2.21	0.40
1:A:805:C:N3	1:A:806:C:C5	2.89	0.40
1:A:931:C:H2'	1:A:932:C:H6	1.87	0.40
2:B:151:ILE:O	2:B:152:LYS:C	2.59	0.40
3:C:12:LEU:HD23	3:C:12:LEU:HA	1.84	0.40
3:C:3:GLN:OE1	3:C:3:GLN:N	2.54	0.40
3:C:56:VAL:O	3:C:66:VAL:HA	2.21	0.40
4:D:58:LYS:HG3	4:D:59:GLN:N	2.33	0.40
5:E:105:ILE:H	5:E:122:ASN:C	2.24	0.40
7:G:125:SER:O	7:G:127:ALA:N	2.54	0.40
17:Q:57:ASP:OD2	17:Q:57:ASP:N	2.55	0.40
1:A:1044:A:N7	1:A:1045:C:H1'	2.37	0.40
1:A:1234:C:O2'	1:A:1235:U:H5'	2.21	0.40
1:A:1291:U:H4'	9:I:42:GLU:HG2	2.04	0.40
1:A:1416:G:C2	1:A:1485:U:O2	2.73	0.40
1:A:1520:C:H2'	1:A:1521:C:H6	1.86	0.40
1:A:178:C:H2'	1:A:179:A:O4'	2.21	0.40
1:A:28:A:N7	1:A:29:U:C5	2.90	0.40
1:A:389:A:C6	1:A:390:U:H1'	2.56	0.40
1:A:409:U:C4	1:A:410:G:C5	3.10	0.40
1:A:652:U:C5	1:A:752:G:C4	3.09	0.40
1:A:805:C:H2'	1:A:806:C:H6	1.87	0.40
2:B:58:ASN:HA	2:B:61:ALA:HB3	2.03	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:99:ASP:OD1	4:D:100:ASN:N	2.53	0.40
5:E:12:GLN:O	5:E:12:GLN:HG3	2.20	0.40
5:E:134:ILE:HD12	5:E:134:ILE:H	1.86	0.40
5:E:25:VAL:HG22	5:E:28:GLY:O	2.22	0.40
5:E:83:HIS:HB2	5:E:84:PRO:HD2	2.02	0.40
6:F:70:VAL:CG2	6:F:71:ILE:N	2.84	0.40
7:G:138:ARG:CZ	7:G:139:GLU:HG2	2.52	0.40
11:K:112:ASP:OD1	11:K:114:THR:HG23	2.21	0.40
1:A:1071:C:C2	1:A:1072:G:C8	3.09	0.40
1:A:1350:A:N6	1:A:1373:G:N2	2.70	0.40
1:A:1443:C:C2	1:A:1444:U:C6	3.09	0.40
1:A:1415:G:C6	1:A:1486:G:C6	3.09	0.40
1:A:1408:A:N1	1:A:1494:G:C5	2.89	0.40
1:A:521:G:O6	1:A:529:G:C6	2.75	0.40
1:A:64:G:C8	1:A:99:C:C4	3.09	0.40
1:A:728:A:N6	1:A:729:A:N6	2.68	0.40
1:A:765:G:C6	1:A:812:G:C4	3.10	0.40
1:A:840:C:C2	1:A:842:U:H4'	2.57	0.40
1:A:931:C:H2'	1:A:932:C:C6	2.56	0.40
2:B:162:PHE:HA	2:B:184:PHE:O	2.22	0.40
2:B:21:ARG:C	2:B:22:TYR:CD1	2.95	0.40
3:C:43:LEU:CD2	3:C:68:ILE:HD11	2.51	0.40
4:D:147:GLU:O	4:D:150:LYS:HB3	2.21	0.40
4:D:57:GLU:OE1	4:D:57:GLU:HA	2.21	0.40
5:E:149:SER:CB	5:E:152:MET:HG3	2.50	0.40
1:A:1348:U:OP1	9:I:111:VAL:HA	2.21	0.40
10:J:22:THR:O	10:J:22:THR:HG23	2.20	0.40
12:L:102:LEU:HB3	12:L:103:ASP:H	1.77	0.40
17:Q:14:SER:HB3	17:Q:22:VAL:CG1	2.52	0.40
18:R:25:ASP:O	18:R:26:ILE:C	2.60	0.40
21:U:15:ALA:O	21:U:16:LEU:C	2.59	0.40
1:A:1540:U:H4'	21:U:18:ARG:HG2	2.04	0.40
11:K:122:ARG:CZ	21:U:36:GLU:CG	3.00	0.40
1:A:1255:G:C6	1:A:1279:G:N7	2.89	0.40
1:A:1306:A:H2'	1:A:1307:U:O4'	2.21	0.40
1:A:1306:A:H1'	1:A:1332:A:N7	2.36	0.40
1:A:308:C:H2'	1:A:309:A:C8	2.56	0.40
1:A:354:G:C4	1:A:355:C:C5	3.10	0.40
1:A:474:G:C6	1:A:475:C:C4	3.10	0.40
1:A:496:A:H2'	1:A:497:G:N7	2.36	0.40
1:A:572:A:H5'	1:A:573:A:P	2.61	0.40
1:A:570:G:C5	1:A:873:A:C6	3.09	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:117:LEU:O	2:B:118:GLU:C	2.59	0.40
5:E:66:LYS:O	5:E:70:ASN:HB2	2.21	0.40
6:F:55:HIS:O	6:F:56:LYS:O	2.40	0.40
6:F:64:VAL:CG1	6:F:65:GLU:N	2.83	0.40
8:H:77:ARG:CZ	8:H:79:SER:O	2.69	0.40
20:T:3:ASN:O	20:T:4:ILE:C	2.59	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	216/218 (99%)	126 (58%)	54 (25%)	36 (17%)	0	0
3	C	204/206 (99%)	146 (72%)	41 (20%)	17 (8%)	1	3
4	D	203/205 (99%)	148 (73%)	35 (17%)	20 (10%)	1	2
5	E	148/150 (99%)	100 (68%)	25 (17%)	23 (16%)	0	0
6	F	98/100 (98%)	65 (66%)	16 (16%)	17 (17%)	0	0
7	G	149/151 (99%)	120 (80%)	19 (13%)	10 (7%)	2	5
8	H	127/129 (98%)	101 (80%)	19 (15%)	7 (6%)	3	8
9	I	125/127 (98%)	91 (73%)	25 (20%)	9 (7%)	2	4
10	J	96/98 (98%)	72 (75%)	15 (16%)	9 (9%)	1	2
11	K	115/117 (98%)	83 (72%)	23 (20%)	9 (8%)	1	3
12	L	121/123 (98%)	92 (76%)	17 (14%)	12 (10%)	1	2
13	M	112/114 (98%)	80 (71%)	21 (19%)	11 (10%)	1	2
14	N	92/100 (92%)	57 (62%)	20 (22%)	15 (16%)	0	0
15	O	86/88 (98%)	63 (73%)	19 (22%)	4 (5%)	4	13
16	P	80/82 (98%)	57 (71%)	18 (22%)	5 (6%)	2	6
17	Q	78/80 (98%)	55 (70%)	14 (18%)	9 (12%)	1	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	R	53/55 (96%)	42 (79%)	7 (13%)	4 (8%)	2	4
19	S	77/79 (98%)	61 (79%)	13 (17%)	3 (4%)	5	18
20	T	83/85 (98%)	62 (75%)	13 (16%)	8 (10%)	1	2
21	U	49/51 (96%)	24 (49%)	12 (24%)	13 (26%)	0	0
All	All	2312/2358 (98%)	1645 (71%)	426 (18%)	241 (10%)	1	2

All (241) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	16	PHE
2	B	36	ASN
2	B	73	LYS
2	B	74	ARG
2	B	86	SER
2	B	87	CYS
2	B	100	MET
2	B	126	PHE
2	B	136	MET
2	B	170	HIS
2	B	193	PRO
2	B	207	ILE
2	B	220	THR
2	B	222	ARG
3	C	17	PRO
3	C	146	ALA
4	D	29	ASP
4	D	33	LYS
4	D	35	GLU
4	D	36	GLN
5	E	45	ARG
5	E	98	PRO
5	E	101	GLU
5	E	103	THR
5	E	111	MET
5	E	123	VAL
5	E	158	GLY
6	F	27	ALA
6	F	55	HIS
6	F	56	LYS
6	F	86	ARG
6	F	91	ARG

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Mol	Chain	Res	Type
6	F	92	THR
6	F	93	LYS
6	F	98	GLU
7	G	56	LYS
7	G	130	ASN
7	G	146	GLU
8	H	66	PHE
9	I	41	ARG
9	I	120	LYS
9	I	129	LYS
10	J	57	VAL
10	J	86	ALA
10	J	93	ALA
11	K	52	PHE
11	K	91	PRO
11	K	127	ARG
12	L	4	VAL
12	L	17	ALA
12	L	34	CYS
12	L	44	LYS
12	L	76	GLU
12	L	77	HIS
12	L	89	ASP
12	L	117	TYR
13	M	7	ILE
13	M	11	ASP
13	M	41	GLU
13	M	114	LYS
14	N	22	ALA
14	N	52	PRO
14	N	59	ARG
14	N	92	GLU
17	Q	5	ILE
17	Q	51	ASN
17	Q	52	GLU
17	Q	53	CYS
18	R	21	ILE
18	R	47	THR
19	S	5	LEU
20	T	4	ILE
20	T	6	SER
20	T	41	ALA

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Mol	Chain	Res	Type
20	T	68	HIS
21	U	9	ASN
21	U	12	PHE
21	U	24	GLU
21	U	36	GLU
21	U	37	PHE
21	U	40	LYS
21	U	46	LYS
21	U	52	ALA
2	B	33	GLY
2	B	34	ALA
2	B	51	ASN
2	B	82	ASP
2	B	103	ASN
2	B	120	GLN
2	B	124	GLY
2	B	141	LEU
3	C	80	LYS
3	C	82	GLU
3	C	84	VAL
3	C	101	ILE
3	C	127	ARG
4	D	4	TYR
4	D	27	ALA
4	D	32	CYS
4	D	34	ILE
4	D	47	ARG
4	D	85	ASN
4	D	174	ASP
4	D	175	ALA
5	E	51	GLY
5	E	70	ASN
5	E	99	ALA
5	E	102	GLY
5	E	138	ARG
5	E	150	PRO
6	F	14	GLN
6	F	68	GLN
7	G	9	GLN
7	G	140	ASP
8	H	89	LYS
9	I	55	VAL

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Mol	Chain	Res	Type
9	I	72	ILE
10	J	17	LEU
10	J	35	GLN
10	J	36	VAL
11	K	17	SER
11	K	92	GLY
11	K	93	ARG
12	L	102	LEU
12	L	123	LYS
13	M	6	GLY
13	M	82	ASP
14	N	11	VAL
14	N	16	LEU
14	N	23	LYS
14	N	29	ALA
14	N	31	ILE
14	N	62	ASN
16	P	77	GLU
16	P	80	LYS
18	R	25	ASP
18	R	26	ILE
19	S	6	LYS
20	T	7	ALA
21	U	13	ASP
2	B	21	ARG
2	B	75	ALA
2	B	102	THR
2	B	129	LEU
2	B	135	LEU
3	C	54	ARG
3	C	89	LYS
3	C	166	GLU
4	D	10	LYS
4	D	26	ARG
4	D	154	ARG
4	D	165	ARG
5	E	24	THR
5	E	26	LYS
5	E	68	ARG
5	E	100	SER
5	E	155	ALA
6	F	13	ASP

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Mol	Chain	Res	Type
6	F	17	GLN
6	F	53	LYS
6	F	54	LEU
6	F	63	ASN
7	G	10	ARG
7	G	84	THR
8	H	22	LYS
8	H	31	LYS
9	I	91	ASP
10	J	92	LEU
11	K	15	GLN
12	L	22	PRO
12	L	23	ALA
13	M	24	GLY
14	N	34	VAL
14	N	42	TRP
15	O	18	ASP
15	O	20	ASN
15	O	46	HIS
15	O	60	VAL
16	P	10	GLY
16	P	26	ASN
17	Q	13	VAL
19	S	32	ARG
20	T	20	HIS
21	U	11	PRO
2	B	88	ASP
2	B	152	LYS
2	B	166	ALA
2	B	205	ASP
3	C	12	LEU
3	C	191	THR
5	E	151	GLU
6	F	60	VAL
9	I	57	MET
9	I	58	VAL
10	J	41	PRO
13	M	12	HIS
14	N	3	LYS
17	Q	20	SER
17	Q	49	GLU
20	T	73	ALA

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Mol	Chain	Res	Type
20	T	74	ARG
21	U	35	ARG
21	U	53	VAL
2	B	134	ALA
2	B	209	ALA
3	C	14	ILE
4	D	149	ALA
5	E	113	ALA
5	E	122	ASN
5	E	126	LYS
5	E	143	GLY
7	G	126	ASP
8	H	67	GLN
11	K	89	PRO
13	M	5	ALA
13	M	94	GLY
14	N	50	THR
14	N	81	ARG
16	P	11	ALA
17	Q	17	MET
17	Q	70	THR
21	U	38	TYR
2	B	17	GLY
2	B	19	GLN
6	F	33	GLU
7	G	8	GLY
7	G	80	VAL
8	H	44	GLY
13	M	10	PRO
3	C	66	VAL
3	C	103	ILE
9	I	10	GLY
11	K	120	GLY
2	B	180	GLY
4	D	37	ALA
4	D	167	LYS
8	H	78	VAL
10	J	42	LEU
3	C	64	ILE
3	C	174	PRO
4	D	28	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	180/180 (100%)	130 (72%)	50 (28%)	0	2
3	C	170/170 (100%)	134 (79%)	36 (21%)	1	5
4	D	172/172 (100%)	136 (79%)	36 (21%)	1	5
5	E	113/113 (100%)	85 (75%)	28 (25%)	1	3
6	F	87/87 (100%)	61 (70%)	26 (30%)	0	1
7	G	124/124 (100%)	91 (73%)	33 (27%)	1	2
8	H	104/104 (100%)	81 (78%)	23 (22%)	1	4
9	I	105/105 (100%)	76 (72%)	29 (28%)	0	2
10	J	86/86 (100%)	68 (79%)	18 (21%)	1	5
11	K	90/90 (100%)	71 (79%)	19 (21%)	1	5
12	L	103/103 (100%)	76 (74%)	27 (26%)	1	2
13	M	92/92 (100%)	71 (77%)	21 (23%)	1	3
14	N	79/83 (95%)	69 (87%)	10 (13%)	6	18
15	O	75/76 (99%)	59 (79%)	16 (21%)	1	5
16	P	65/65 (100%)	52 (80%)	13 (20%)	2	6
17	Q	74/74 (100%)	52 (70%)	22 (30%)	0	1
18	R	48/48 (100%)	39 (81%)	9 (19%)	2	7
19	S	70/70 (100%)	57 (81%)	13 (19%)	2	7
20	T	65/65 (100%)	49 (75%)	16 (25%)	1	3
21	U	44/44 (100%)	29 (66%)	15 (34%)	0	1
All	All	1946/1951 (100%)	1486 (76%)	460 (24%)	1	3

All (460) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	9	MET
2	B	14	VAL
2	B	15	HIS
2	B	16	PHE

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Mol	Chain	Res	Type
2	B	18	HIS
2	B	19	GLN
2	B	20	THR
2	B	23	TRP
2	B	24	ASN
2	B	27	MET
2	B	28	LYS
2	B	35	ARG
2	B	40	ILE
2	B	43	LEU
2	B	49	MET
2	B	50	PHE
2	B	62	SER
2	B	66	LYS
2	B	67	ILE
2	B	68	LEU
2	B	77	SER
2	B	88	ASP
2	B	89	GLN
2	B	91	PHE
2	B	94	HIS
2	B	95	ARG
2	B	96	TRP
2	B	103	ASN
2	B	106	THR
2	B	117	LEU
2	B	122	GLN
2	B	125	THR
2	B	126	PHE
2	B	130	THR
2	B	133	GLU
2	B	136	MET
2	B	139	ARG
2	B	140	GLU
2	B	143	LYS
2	B	144	LEU
2	B	163	VAL
2	B	164	ILE
2	B	174	LYS
2	B	188	ASP
2	B	205	ASP
2	B	207	ILE

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Mol	Chain	Res	Type
2	B	210	VAL
2	B	220	THR
2	B	222	ARG
2	B	223	GLU
3	C	3	GLN
3	C	15	VAL
3	C	16	LYS
3	C	18	TRP
3	C	25	ASN
3	C	26	THR
3	C	27	LYS
3	C	28	GLU
3	C	29	PHE
3	C	33	LEU
3	C	36	ASP
3	C	37	PHE
3	C	43	LEU
3	C	45	LYS
3	C	70	THR
3	C	80	LYS
3	C	102	ASN
3	C	103	ILE
3	C	107	ARG
3	C	111	LEU
3	C	119	SER
3	C	121	THR
3	C	129	MET
3	C	131	ARG
3	C	132	ARG
3	C	140	ASN
3	C	144	LEU
3	C	151	VAL
3	C	153	VAL
3	C	167	TRP
3	C	168	TYR
3	C	175	LEU
3	C	179	ARG
3	C	190	HIS
3	C	192	THR
3	C	193	TYR
4	D	8	LYS
4	D	9	LEU

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Mol	Chain	Res	Type
4	D	12	SER
4	D	23	SER
4	D	28	ILE
4	D	29	ASP
4	D	32	CYS
4	D	33	LYS
4	D	47	ARG
4	D	48	LEU
4	D	54	GLN
4	D	55	LEU
4	D	56	ARG
4	D	58	LYS
4	D	59	GLN
4	D	60	LYS
4	D	63	ARG
4	D	69	GLU
4	D	83	LYS
4	D	125	VAL
4	D	126	ASN
4	D	129	VAL
4	D	138	SER
4	D	151	LYS
4	D	152	GLN
4	D	153	SER
4	D	155	VAL
4	D	161	LEU
4	D	163	GLU
4	D	179	GLU
4	D	184	ARG
4	D	191	LEU
4	D	199	LEU
4	D	200	ILE
4	D	203	LEU
4	D	206	LYS
5	E	10	GLU
5	E	15	LEU
5	E	26	LYS
5	E	32	SER
5	E	39	VAL
5	E	46	VAL
5	E	52	LYS
5	E	65	GLU

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Mol	Chain	Res	Type
5	E	69	ARG
5	E	77	ASN
5	E	81	LEU
5	E	92	SER
5	E	93	ARG
5	E	96	MET
5	E	101	GLU
5	E	112	ARG
5	E	114	VAL
5	E	115	LEU
5	E	120	VAL
5	E	124	LEU
5	E	126	LYS
5	E	131	THR
5	E	137	VAL
5	E	140	THR
5	E	149	SER
5	E	151	GLU
5	E	152	MET
5	E	156	LYS
6	F	1	MET
6	F	2	ARG
6	F	7	VAL
6	F	8	PHE
6	F	18	VAL
6	F	23	GLU
6	F	24	ARG
6	F	26	THR
6	F	29	ILE
6	F	35	LYS
6	F	36	ILE
6	F	38	ARG
6	F	51	ILE
6	F	53	LYS
6	F	54	LEU
6	F	55	HIS
6	F	63	ASN
6	F	68	GLN
6	F	69	GLU
6	F	71	ILE
6	F	73	GLU
6	F	75	GLU

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Mol	Chain	Res	Type
6	F	80	PHE
6	F	87	SER
6	F	93	LYS
6	F	97	THR
7	G	3	ARG
7	G	4	ARG
7	G	5	ARG
7	G	6	VAL
7	G	11	LYS
7	G	22	LEU
7	G	23	LEU
7	G	30	LEU
7	G	36	LYS
7	G	47	LEU
7	G	48	GLU
7	G	53	ARG
7	G	59	LEU
7	G	60	GLU
7	G	62	PHE
7	G	66	LEU
7	G	69	VAL
7	G	70	ARG
7	G	75	VAL
7	G	78	ARG
7	G	84	THR
7	G	87	VAL
7	G	91	VAL
7	G	95	ARG
7	G	120	LEU
7	G	123	GLU
7	G	129	GLU
7	G	133	THR
7	G	135	VAL
7	G	138	ARG
7	G	139	GLU
7	G	140	ASP
7	G	146	GLU
8	H	3	MET
8	H	13	ARG
8	H	22	LYS
8	H	31	LYS
8	H	33	LYS

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Mol	Chain	Res	Type
8	H	42	GLU
8	H	45	PHE
8	H	47	GLU
8	H	49	PHE
8	H	54	ASP
8	H	55	THR
8	H	59	LEU
8	H	75	ILE
8	H	77	ARG
8	H	80	ARG
8	H	87	LYS
8	H	90	ASP
8	H	92	LEU
8	H	104	VAL
8	H	111	MET
8	H	112	THR
8	H	121	LEU
8	H	125	ILE
9	I	9	THR
9	I	11	ARG
9	I	13	LYS
9	I	18	ARG
9	I	33	ARG
9	I	34	SER
9	I	43	THR
9	I	45	ARG
9	I	46	MET
9	I	48	VAL
9	I	49	ARG
9	I	56	ASP
9	I	57	MET
9	I	61	LEU
9	I	68	LYS
9	I	85	ARG
9	I	88	MET
9	I	89	GLU
9	I	90	TYR
9	I	94	LEU
9	I	96	SER
9	I	97	GLU
9	I	99	ARG
9	I	100	LYS

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Mol	Chain	Res	Type
9	I	105	THR
9	I	112	GLU
9	I	126	GLN
9	I	127	PHE
9	I	129	LYS
10	J	9	ARG
10	J	22	THR
10	J	25	ILE
10	J	27	GLU
10	J	32	THR
10	J	35	GLN
10	J	45	ARG
10	J	48	ARG
10	J	51	VAL
10	J	59	LYS
10	J	63	ASP
10	J	66	GLU
10	J	80	THR
10	J	83	THR
10	J	84	VAL
10	J	87	LEU
10	J	89	ARG
10	J	92	LEU
11	K	13	ARG
11	K	14	LYS
11	K	15	GLN
11	K	31	ILE
11	K	50	SER
11	K	52	PHE
11	K	64	GLN
11	K	65	VAL
11	K	81	ASN
11	K	82	LEU
11	K	83	GLU
11	K	87	LYS
11	K	96	THR
11	K	101	ASN
11	K	105	PHE
11	K	106	ARG
11	K	107	ILE
11	K	126	LYS
11	K	128	ARG

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Mol	Chain	Res	Type
12	L	3	THR
12	L	4	VAL
12	L	5	ASN
12	L	10	LYS
12	L	12	ARG
12	L	16	VAL
12	L	18	LYS
12	L	20	ASN
12	L	21	VAL
12	L	29	GLN
12	L	30	LYS
12	L	44	LYS
12	L	58	THR
12	L	59	ASN
12	L	62	GLU
12	L	63	VAL
12	L	82	ILE
12	L	83	ARG
12	L	89	ASP
12	L	90	LEU
12	L	93	VAL
12	L	94	ARG
12	L	105	SER
12	L	110	ARG
12	L	111	LYS
12	L	116	LYS
12	L	121	ARG
13	M	19	LEU
13	M	25	VAL
13	M	29	ARG
13	M	30	SER
13	M	31	LYS
13	M	33	ILE
13	M	34	LEU
13	M	41	GLU
13	M	48	LEU
13	M	53	ILE
13	M	56	LEU
13	M	59	GLU
13	M	60	VAL
13	M	63	PHE
13	M	68	ASP

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Mol	Chain	Res	Type
13	M	72	GLU
13	M	80	LEU
13	M	83	LEU
13	M	90	ARG
13	M	91	HIS
13	M	101	ARG
14	N	4	GLN
14	N	23	LYS
14	N	26	GLU
14	N	28	LYS
14	N	35	ASN
14	N	48	LEU
14	N	53	ARG
14	N	71	HIS
14	N	80	SER
14	N	90	ARG
15	O	6	GLU
15	O	17	ARG
15	O	18	ASP
15	O	22	THR
15	O	26	GLU
15	O	35	GLN
15	O	38	HIS
15	O	48	LYS
15	O	58	ARG
15	O	64	ARG
15	O	70	LEU
15	O	73	LYS
15	O	79	THR
15	O	85	LEU
15	O	87	LEU
15	O	88	ARG
16	P	1	MET
16	P	2	VAL
16	P	3	THR
16	P	5	ARG
16	P	20	VAL
16	P	26	ASN
16	P	31	ARG
16	P	36	VAL
16	P	46	LYS
16	P	63	GLN

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Mol	Chain	Res	Type
16	P	74	LEU
16	P	77	GLU
16	P	80	LYS
17	Q	4	LYS
17	Q	5	ILE
17	Q	11	ARG
17	Q	14	SER
17	Q	17	MET
17	Q	18	GLU
17	Q	23	VAL
17	Q	25	ILE
17	Q	28	PHE
17	Q	29	VAL
17	Q	40	ARG
17	Q	48	ASP
17	Q	50	ASN
17	Q	52	GLU
17	Q	55	ILE
17	Q	65	ARG
17	Q	75	LEU
17	Q	76	VAL
17	Q	78	VAL
17	Q	79	VAL
17	Q	81	LYS
17	Q	83	VAL
18	R	29	LEU
18	R	33	ILE
18	R	42	SER
18	R	45	THR
18	R	47	THR
18	R	48	ARG
18	R	57	ARG
18	R	59	ILE
18	R	67	LEU
19	S	5	LEU
19	S	6	LYS
19	S	11	ILE
19	S	13	LEU
19	S	14	HIS
19	S	16	LEU
19	S	23	VAL
19	S	27	ASP

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Mol	Chain	Res	Type
19	S	28	LYS
19	S	33	THR
19	S	49	ILE
19	S	56	GLN
19	S	73	GLU
20	T	5	LYS
20	T	6	SER
20	T	8	LYS
20	T	10	ARG
20	T	14	SER
20	T	15	GLU
20	T	24	ARG
20	T	27	MET
20	T	29	ARG
20	T	36	TYR
20	T	49	LYS
20	T	64	LYS
20	T	67	ILE
20	T	76	LYS
20	T	78	ASN
20	T	79	LEU
21	U	5	LYS
21	U	7	ARG
21	U	10	GLU
21	U	12	PHE
21	U	14	VAL
21	U	16	LEU
21	U	19	PHE
21	U	24	GLU
21	U	28	VAL
21	U	34	ARG
21	U	36	GLU
21	U	37	PHE
21	U	38	TYR
21	U	43	THR
21	U	47	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	18	HIS
2	B	103	ASN

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Mol	Chain	Res	Type
2	B	177	ASN
3	C	6	HIS
3	C	176	HIS
4	D	152	GLN
5	E	89	HIS
10	J	70	HIS
13	M	91	HIS
13	M	105	ASN
15	O	40	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1538/1539 (99%)	331 (21%)	9 (0%)

All (331) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	5	U
1	A	9	G
1	A	17	U
1	A	19	A
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	56	U
1	A	67	C
1	A	68	G
1	A	70	U
1	A	71	A
1	A	74	A
1	A	81	A
1	A	83	C
1	A	84	U
1	A	85	U
1	A	87	C
1	A	88	U
1	A	91	U

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Mol	Chain	Res	Type
1	A	94	G
1	A	95	C
1	A	108	G
1	A	116	A
1	A	120	A
1	A	121	U
1	A	122	G
1	A	129	A
1	A	130	A
1	A	131	A
1	A	137	U
1	A	142	G
1	A	143	A
1	A	144	G
1	A	154	U
1	A	155	A
1	A	159	G
1	A	163	C
1	A	181	A
1	A	182	A
1	A	183	C
1	A	184	G
1	A	187	G
1	A	189	A
1	A	197	A
1	A	200	G
1	A	201	G
1	A	204	G
1	A	206	C
1	A	207	C
1	A	208	U
1	A	210	C
1	A	211	G
1	A	212	G
1	A	240	G
1	A	241	G
1	A	245	U
1	A	247	G
1	A	249	U
1	A	251	G
1	A	266	G
1	A	267	C

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Mol	Chain	Res	Type
1	A	269	C
1	A	280	C
1	A	289	G
1	A	298	A
1	A	308	C
1	A	309	A
1	A	320	A
1	A	321	A
1	A	328	C
1	A	329	A
1	A	330	C
1	A	332	G
1	A	333	U
1	A	337	G
1	A	347	G
1	A	352	C
1	A	354	G
1	A	357	G
1	A	358	U
1	A	359	G
1	A	367	U
1	A	370	C
1	A	372	C
1	A	373	A
1	A	377	G
1	A	378	G
1	A	384	G
1	A	389	A
1	A	398	U
1	A	399	G
1	A	406	G
1	A	409	U
1	A	411	A
1	A	412	A
1	A	413	G
1	A	414	A
1	A	421	U
1	A	422	C
1	A	424	G
1	A	429	U
1	A	430	A
1	A	458	U

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Mol	Chain	Res	Type
1	A	459	A
1	A	463	U
1	A	466	A
1	A	467	U
1	A	468	A
1	A	469	C
1	A	474	G
1	A	477	C
1	A	478	A
1	A	479	U
1	A	481	G
1	A	482	A
1	A	484	G
1	A	485	U
1	A	486	U
1	A	495	A
1	A	498	A
1	A	499	A
1	A	509	A
1	A	511	C
1	A	518	C
1	A	519	C
1	A	524	G
1	A	527	G
1	A	532	A
1	A	533	A
1	A	545	C
1	A	547	A
1	A	550	G
1	A	559	A
1	A	564	C
1	A	568	G
1	A	572	A
1	A	573	A
1	A	576	C
1	A	577	G
1	A	581	G
1	A	582	C
1	A	619	U
1	A	622	A
1	A	650	G
1	A	653	U

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Mol	Chain	Res	Type
1	A	654	G
1	A	665	A
1	A	666	G
1	A	687	A
1	A	695	A
1	A	719	C
1	A	720	C
1	A	721	G
1	A	723	U
1	A	724	G
1	A	731	G
1	A	734	G
1	A	747	A
1	A	752	G
1	A	754	C
1	A	755	G
1	A	758	C
1	A	765	G
1	A	777	A
1	A	778	G
1	A	785	G
1	A	793	U
1	A	794	A
1	A	802	A
1	A	804	U
1	A	809	G
1	A	814	A
1	A	815	A
1	A	817	C
1	A	821	G
1	A	827	U
1	A	828	U
1	A	841	C
1	A	842	U
1	A	843	U
1	A	844	G
1	A	845	A
1	A	846	G
1	A	874	G
1	A	876	C
1	A	914	A
1	A	922	G

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Mol	Chain	Res	Type
1	A	926	G
1	A	931	C
1	A	934	C
1	A	935	A
1	A	960	U
1	A	966	G
1	A	969	A
1	A	971	G
1	A	975	A
1	A	976	G
1	A	977	A
1	A	983	A
1	A	987	G
1	A	989	U
1	A	993	G
1	A	994	A
1	A	995	C
1	A	996	A
1	A	1004	A
1	A	1005	A
1	A	1008	U
1	A	1009	U
1	A	1017	U
1	A	1018	G
1	A	1022	A
1	A	1025	U
1	A	1026	G
1	A	1027	C
1	A	1028	C
1	A	1030	U
1	A	1031	C
1	A	1032	G
1	A	1033	G
1	A	1034	G
1	A	1037	C
1	A	1039	G
1	A	1043	G
1	A	1044	A
1	A	1047	G
1	A	1050	G
1	A	1054	C
1	A	1055	A

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Mol	Chain	Res	Type
1	A	1056	U
1	A	1065	U
1	A	1072	G
1	A	1073	U
1	A	1084	G
1	A	1086	U
1	A	1088	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1124	G
1	A	1125	U
1	A	1129	C
1	A	1132	C
1	A	1133	G
1	A	1134	G
1	A	1136	C
1	A	1137	C
1	A	1139	G
1	A	1140	C
1	A	1141	C
1	A	1142	G
1	A	1145	A
1	A	1154	G
1	A	1155	A
1	A	1156	G
1	A	1157	A
1	A	1159	U
1	A	1160	G
1	A	1161	C
1	A	1167	A
1	A	1183	U
1	A	1184	G
1	A	1192	C
1	A	1196	A
1	A	1202	U
1	A	1203	C
1	A	1212	U
1	A	1213	A
1	A	1227	A
1	A	1238	A
1	A	1240	U

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Mol	Chain	Res	Type
1	A	1243	C
1	A	1253	G
1	A	1260	G
1	A	1275	A
1	A	1280	A
1	A	1285	A
1	A	1286	U
1	A	1287	A
1	A	1292	G
1	A	1293	C
1	A	1299	A
1	A	1300	G
1	A	1302	C
1	A	1304	G
1	A	1305	G
1	A	1317	C
1	A	1318	A
1	A	1322	C
1	A	1324	A
1	A	1331	G
1	A	1337	G
1	A	1338	G
1	A	1346	A
1	A	1362	A
1	A	1363	A
1	A	1364	U
1	A	1370	G
1	A	1377	A
1	A	1378	C
1	A	1379	G
1	A	1394	A
1	A	1398	A
1	A	1419	G
1	A	1440	U
1	A	1441	A
1	A	1442	G
1	A	1446	A
1	A	1452	C
1	A	1454	G
1	A	1480	A
1	A	1491	G
1	A	1492	A

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Mol	Chain	Res	Type
1	A	1497	G
1	A	1503	A
1	A	1505	G
1	A	1506	U
1	A	1507	A
1	A	1509	C
1	A	1517	G
1	A	1528	U
1	A	1529	G
1	A	1530	G
1	A	1531	A
1	A	1533	C
1	A	1535	C
1	A	1537	U

All (9) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	115	G
1	A	209	U
1	A	429	U
1	A	559	A
1	A	733	G
1	A	793	U
1	A	1049	U
1	A	1201	A
1	A	1211	U

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 56 ligands modelled in this entry, 56 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.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.