



Full wwPDB X-ray Structure Validation Report i

Sep 25, 2014 – 11:10 AM EDT

PDB ID : 4TPE
Title : Crystal structure of the E. coli ribosome bound to flopristin and linopristin.
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 : 2014-06-07
Resolution : 2.80 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>

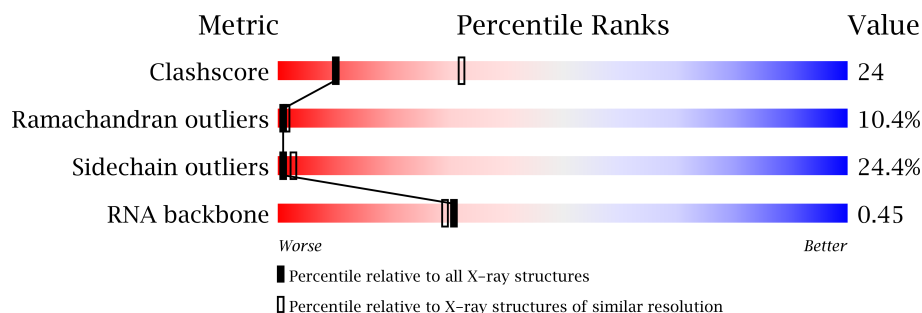
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.80 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	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RNA backbone	1838	1076 (3.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	56	Total	Mg	0	0
			56	56		

- Molecule 23 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	A	192	Total	O	0	0
			192	192		
23	L	1	Total	O	0	0
			1	1		
23	N	3	Total	O	0	0
			3	3		
23	T	1	Total	O	0	0
			1	1		
23	U	1	Total	O	0	0
			1	1		

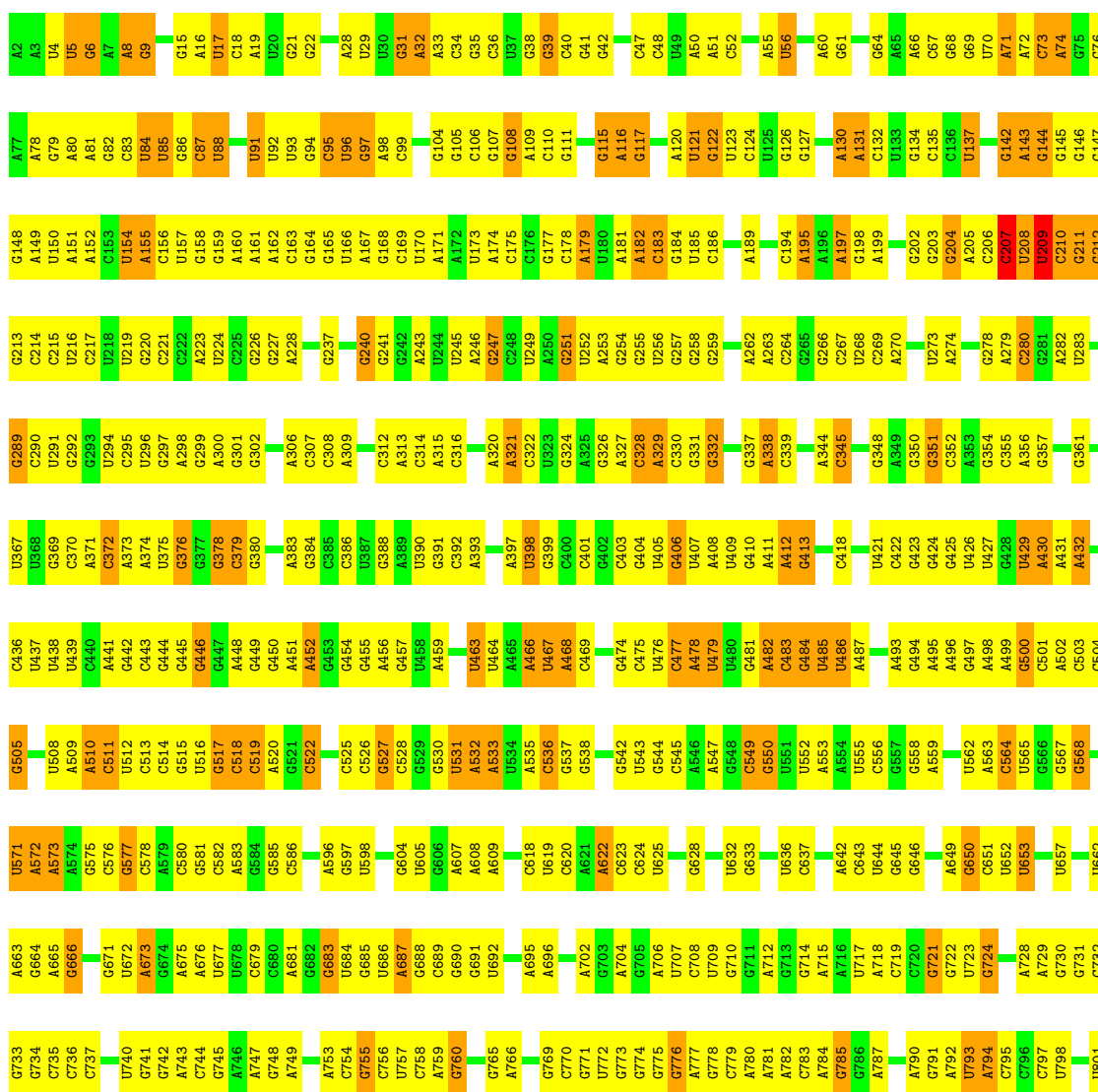
3 Residue-property plots

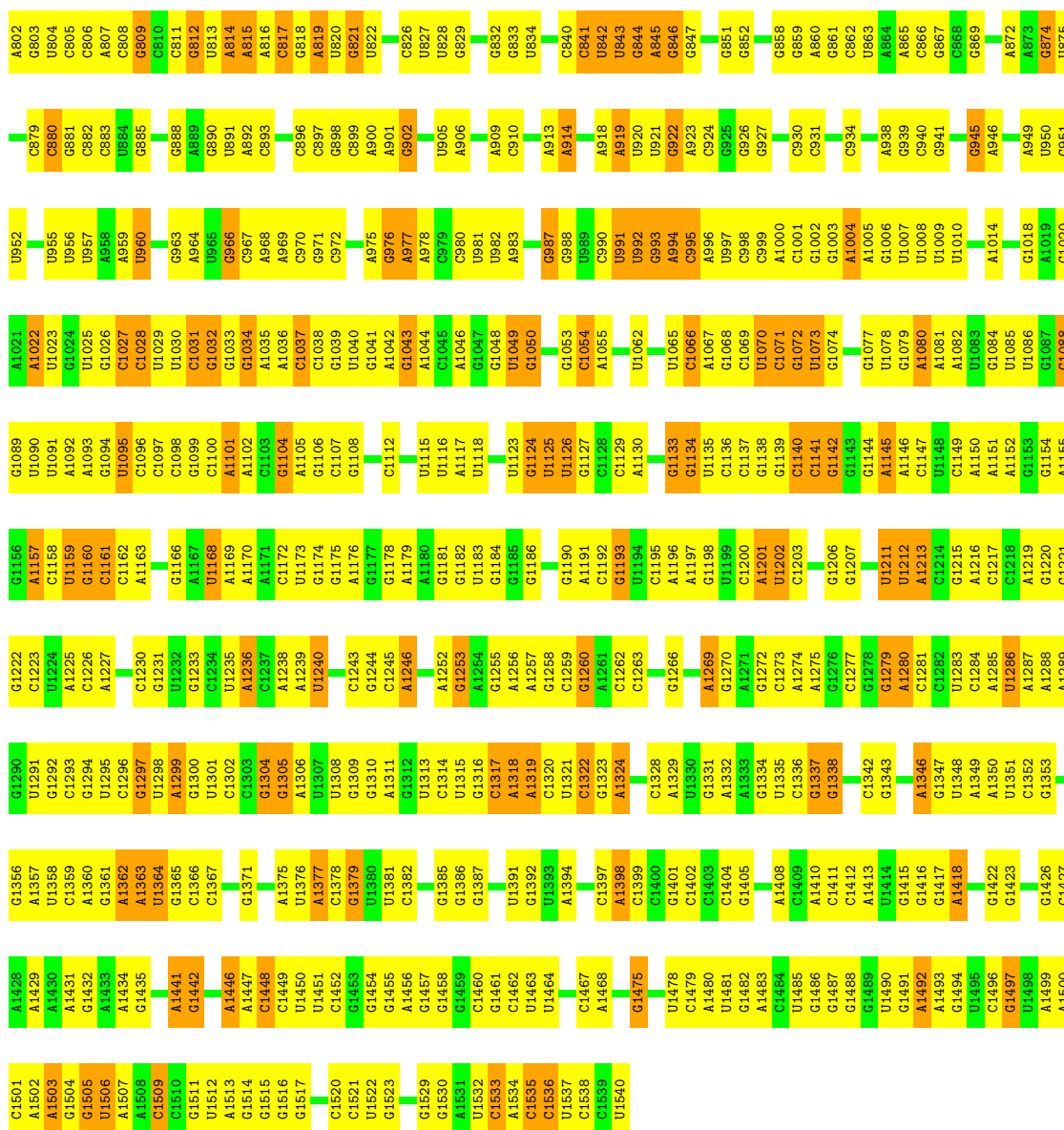
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

• Molecule 1: 16S rRNA

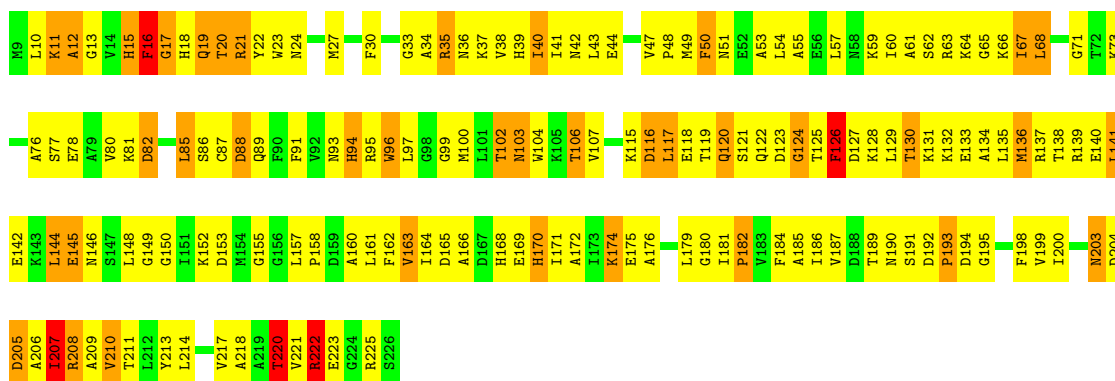
Chain A:





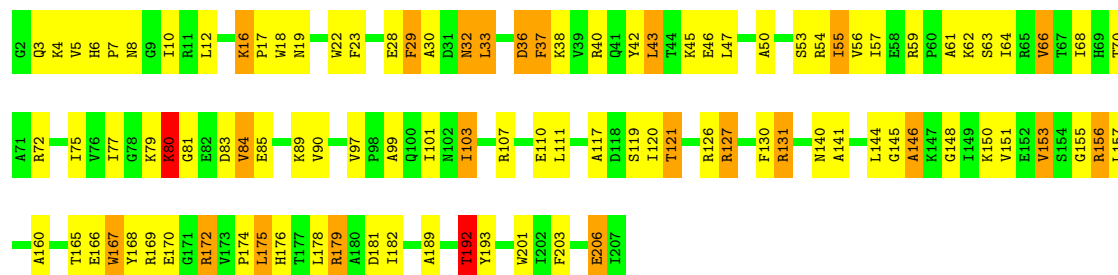
• Molecule 2: 30S ribosomal protein S2

Chain B:



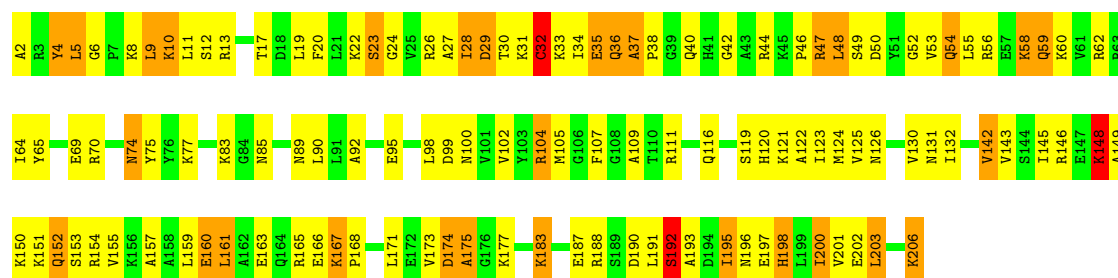
• Molecule 3: 30S ribosomal protein S3

Chain C:



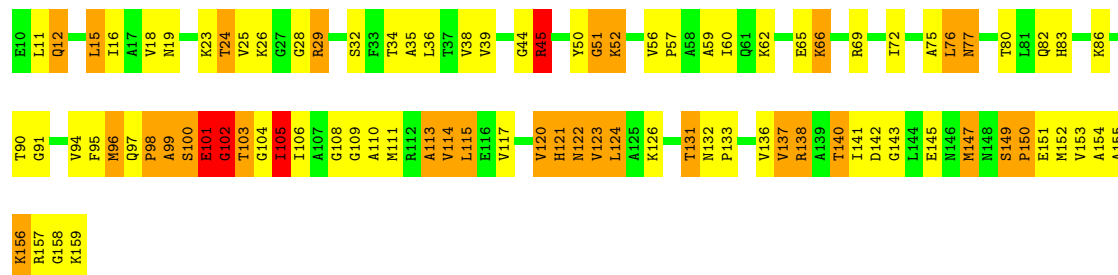
• Molecule 4: 30S ribosomal protein S4

Chain D:



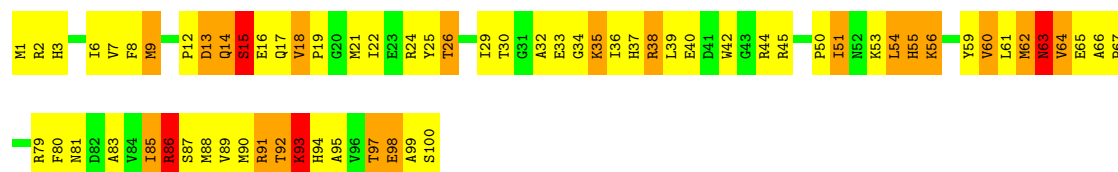
• Molecule 5: 30S ribosomal protein S5

Chain E:



• Molecule 6: 30S ribosomal protein S6

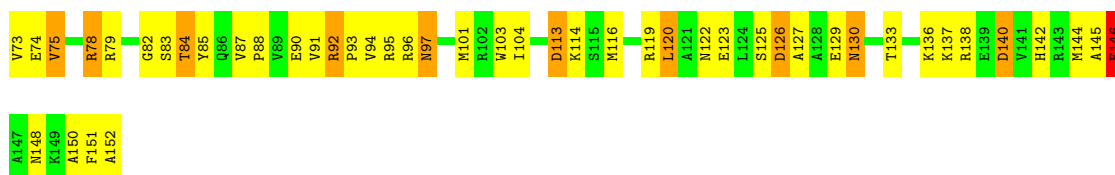
Chain F:



• Molecule 7: 30S ribosomal protein S7

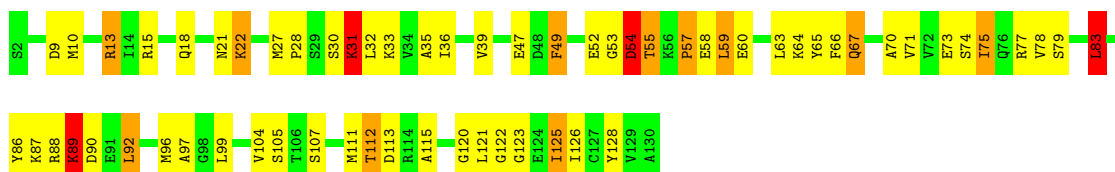
Chain G:





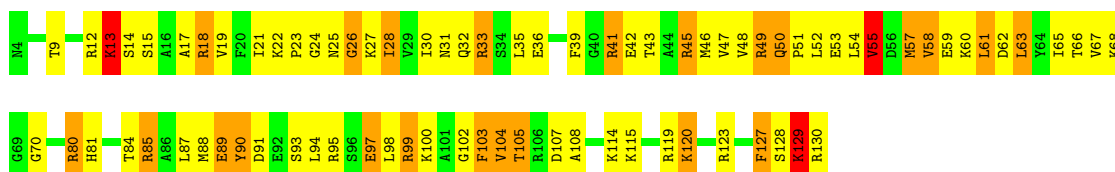
• Molecule 8: 30S ribosomal protein S8

Chain H:



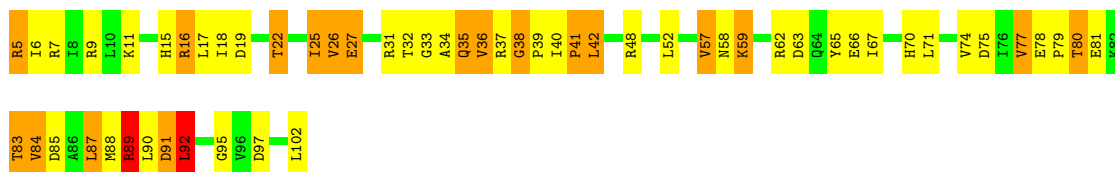
• Molecule 9: 30S ribosomal protein S9

Chain I:



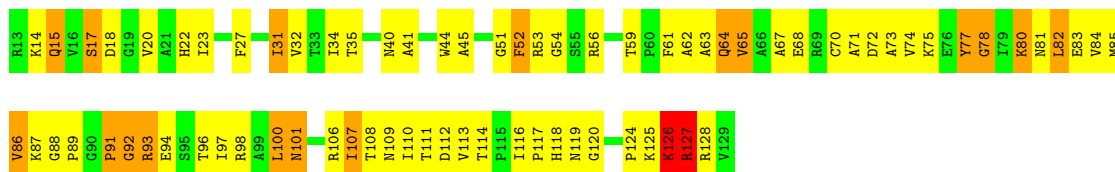
• Molecule 10: 30S ribosomal protein S10

Chain J:



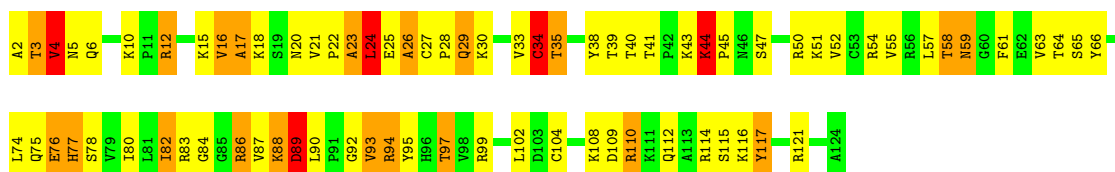
• Molecule 11: 30S ribosomal protein S11

Chain K:



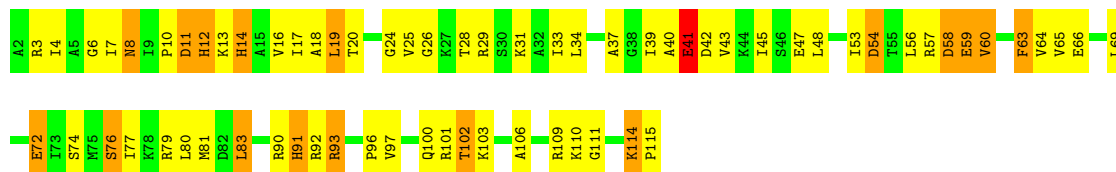
• Molecule 12: 30S ribosomal protein S12

Chain L:



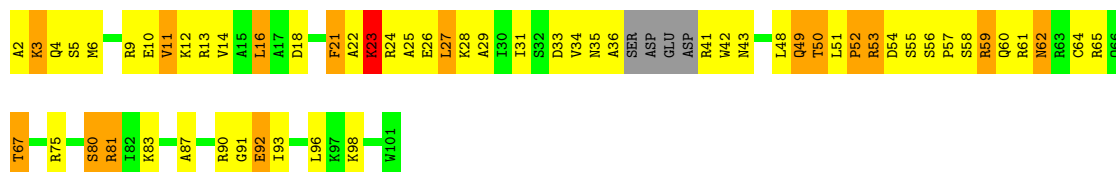
- Molecule 13: 30S ribosomal protein S13

Chain M:



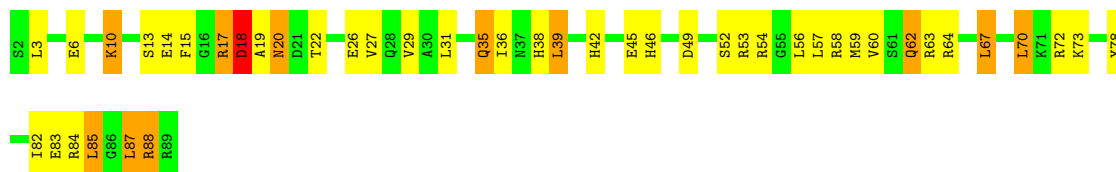
- Molecule 14: 30S ribosomal protein S14

Chain N:



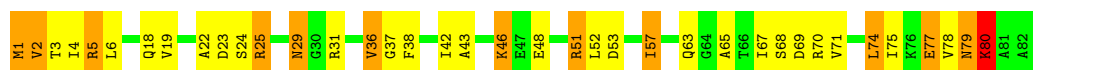
- Molecule 15: 30S ribosomal protein S15

Chain O:



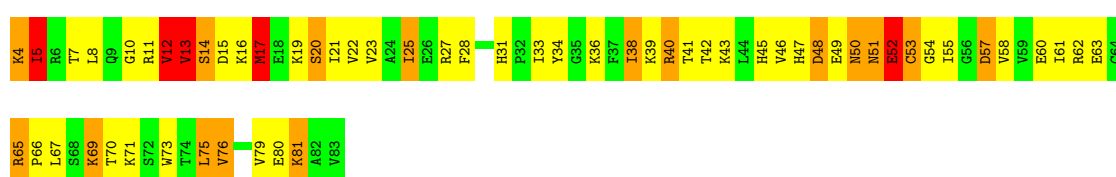
- Molecule 16: 30S ribosomal protein S16

Chain P:



- Molecule 17: 30S ribosomal protein S17

Chain Q:



- Molecule 18: 30S ribosomal protein S18

Chain R:



- Molecule 19: 30S ribosomal protein S19

Chain S:

- Molecule 20: 30S ribosomal protein S20

Chain T:

- Molecule 21: 30S ribosomal protein S21

Chain U:

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	211.97Å 434.65Å 623.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.36 – 2.80	Depositor
% Data completeness (in resolution range)	89.2 (69.36-2.80)	Depositor
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.215 , 0.260	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	0.29	0/36966	0.79	2/57666 (0.0%)
2	B	0.26	0/1736	0.52	0/2338
3	C	0.26	0/1652	0.50	0/2225
4	D	0.32	0/1665	0.57	0/2227
5	E	0.31	0/1119	0.64	0/1504
6	F	0.27	0/836	0.60	1/1128 (0.1%)
7	G	0.26	0/1196	0.50	0/1602
8	H	0.26	0/989	0.50	0/1326
9	I	0.27	0/1034	0.54	0/1375
10	J	0.27	0/797	0.55	0/1077
11	K	0.28	0/893	0.58	0/1205
12	L	0.30	0/969	0.61	0/1300
13	M	0.26	0/893	0.55	0/1193
14	N	0.25	0/785	0.48	0/1043
15	O	0.26	0/718	0.48	0/959
16	P	0.27	0/659	0.52	0/884
17	Q	0.29	0/658	0.54	0/881
18	R	0.28	0/463	0.54	0/621
19	S	0.28	0/653	0.52	0/877
20	T	0.26	0/671	0.51	0/888
21	U	0.35	0/431	0.60	0/570
All	All	0.28	0/55783	0.73	3/82889 (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
5	E	0	1
6	F	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
12	L	0	1
21	U	0	1
All	All	0	4

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	209	U	C2-N1-C1'	6.06	124.97	117.70
6	F	86	ARG	NE-CZ-NH1	5.97	123.28	120.30
1	A	207	C	C2-N1-C1'	5.19	124.51	118.80

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	E	102	GLY	Peptide
6	F	54	LEU	Peptide
12	L	24	LEU	Peptide
21	U	39	GLU	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	978	0
2	B	1705	0	1732	125	0
3	C	1625	0	1696	64	0
4	D	1643	0	1707	121	0
5	E	1106	0	1148	101	0
6	F	818	0	808	56	0
7	G	1182	0	1238	54	0
8	H	979	0	1031	42	0
9	I	1022	0	1070	70	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	787	0	828	59	0
11	K	877	0	887	65	0
12	L	955	0	1016	72	0
13	M	884	0	941	49	0
14	N	774	0	824	45	0
15	O	710	0	728	30	0
16	P	649	0	666	29	0
17	Q	649	0	691	59	0
18	R	456	0	478	40	0
19	S	638	0	665	37	0
20	T	665	0	714	46	0
21	U	426	0	449	59	0
22	A	56	0	0	0	0
23	A	192	0	0	21	0
23	L	1	0	0	0	0
23	N	3	0	0	0	0
23	T	1	0	0	0	0
23	U	1	0	0	1	0
All	All	51819	0	35934	2041	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 24.

All (2041) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1500:A:OP2	23:A:1883:HOH:O	1.75	1.04
6:F:12:PRO:O	6:F:15:SER:OG	1.78	1.01
1:A:1198:G:N7	23:A:1852:HOH:O	1.94	0.97
14:N:41:ARG:NH1	14:N:42:TRP:O	1.98	0.96
2:B:103:ASN:ND2	2:B:106:THR:OG1	1.98	0.96
18:R:25:ASP:O	18:R:27:ALA:N	1.98	0.96
1:A:515:G:N7	23:A:1766:HOH:O	1.99	0.94
1:A:1097:C:OP1	2:B:139:ARG:NH2	1.99	0.94
1:A:966:G:O2'	9:I:130:ARG:OXT	1.87	0.92
1:A:558:G:OP1	23:A:1730:HOH:O	1.85	0.92
1:A:803:G:OP1	23:A:1802:HOH:O	1.88	0.92
1:A:858:G:N7	23:A:1820:HOH:O	2.04	0.91
1:A:978:A:OP2	1:A:1362:A:N6	2.05	0.88
1:A:532:A:N6	3:C:192:THR:OG1	2.06	0.88
1:A:1211:U:O2'	1:A:1212:U:OP2	1.91	0.88
20:T:5:LYS:O	20:T:7:ALA:N	2.07	0.86
2:B:15:HIS:O	2:B:17:GLY:N	2.09	0.86

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:155:GLY:O	3:C:157:LEU:N	2.08	0.85
1:A:412:A:O2'	1:A:413:G:O5'	1.95	0.85
1:A:1001:C:H2'	1:A:1002:G:C8	2.10	0.85
2:B:206:ALA:O	2:B:208:ARG:N	2.11	0.84
1:A:1124:G:O2'	1:A:1145:A:N6	2.10	0.84
4:D:100:ASN:OD1	4:D:111:ARG:NH1	2.09	0.84
1:A:299:G:O6	23:A:1731:HOH:O	1.96	0.84
12:L:22:PRO:O	12:L:24:LEU:N	2.11	0.84
12:L:116:LYS:O	12:L:117:TYR:CG	2.30	0.83
12:L:66:TYR:O	12:L:97:THR:OG1	1.95	0.83
1:A:484:G:H4'	1:A:485:U:O5'	1.81	0.81
1:A:209:U:H4'	1:A:210:C:OP2	1.80	0.81
11:K:125:LYS:O	21:U:34:ARG:NE	2.13	0.81
1:A:533:A:OP1	23:A:1764:HOH:O	1.97	0.80
4:D:192:SER:OG	4:D:193:ALA:N	2.11	0.80
3:C:16:LYS:NZ	3:C:181:ASP:OD1	2.15	0.80
4:D:70:ARG:O	4:D:74:ASN:ND2	2.14	0.80
1:A:1181:G:O2'	1:A:1182:G:N7	2.15	0.79
1:A:736:C:OP1	18:R:61:ARG:NH1	2.15	0.79
14:N:91:GLY:O	14:N:93:ILE:N	2.15	0.79
7:G:68:ASN:OD1	7:G:130:ASN:ND2	2.16	0.79
12:L:92:GLY:O	12:L:94:ARG:N	2.16	0.79
17:Q:21:ILE:N	17:Q:48:ASP:OD2	2.16	0.79
1:A:1198:G:OP1	23:A:1838:HOH:O	2.01	0.78
5:E:102:GLY:O	5:E:104:GLY:N	2.17	0.78
1:A:537:G:OP1	12:L:110:ARG:NH2	2.17	0.78
5:E:137:VAL:O	5:E:138:ARG:CB	2.32	0.78
6:F:91:ARG:O	6:F:92:THR:OG1	2.01	0.77
11:K:17:SER:O	11:K:80:LYS:N	2.17	0.77
17:Q:8:LEU:HB2	17:Q:61:ILE:CG2	2.14	0.76
1:A:64:G:C8	1:A:99:C:N4	2.53	0.76
1:A:1049:U:OP1	23:A:1846:HOH:O	2.04	0.76
13:M:13:LYS:O	13:M:14:HIS:ND1	2.19	0.76
1:A:1151:A:C2	1:A:1152:A:C5	2.74	0.75
1:A:1004:A:O2'	1:A:1036:A:N1	2.18	0.75
12:L:25:GLU:O	12:L:27:CYS:N	2.21	0.74
1:A:495:A:C2	1:A:496:A:C6	2.75	0.73
1:A:688:G:O2'	1:A:704:A:N1	2.18	0.73
5:E:101:GLU:O	5:E:103:THR:N	2.22	0.73
2:B:169:GLU:O	2:B:171:ILE:N	2.22	0.73
1:A:684:U:O2'	11:K:40:ASN:O	2.04	0.72
1:A:976:G:OP2	1:A:1358:U:O2'	2.06	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:552:U:C4	1:A:553:A:N7	2.57	0.71
15:O:56:LEU:O	15:O:59:MET:N	2.24	0.71
1:A:604:G:H2'	1:A:605:U:O4'	1.91	0.71
2:B:193:PRO:O	2:B:195:GLY:N	2.23	0.71
2:B:54:LEU:HA	2:B:57:LEU:HB3	1.73	0.71
1:A:1266:G:N2	1:A:1269:A:OP2	2.23	0.71
5:E:101:GLU:O	5:E:101:GLU:CD	2.29	0.70
1:A:412:A:HO2'	1:A:413:G:P	2.14	0.70
1:A:485:U:O2'	1:A:486:U:OP1	2.08	0.70
1:A:645:G:N7	23:A:1791:HOH:O	2.23	0.70
1:A:949:A:O2'	1:A:971:G:O6	2.07	0.70
1:A:890:G:O2'	1:A:891:U:OP2	2.09	0.70
9:I:57:MET:SD	9:I:58:VAL:N	2.64	0.70
20:T:48:GLN:O	20:T:52:ASN:ND2	2.25	0.70
1:A:666:G:C6	1:A:741:G:C6	2.80	0.70
6:F:97:THR:O	6:F:98:GLU:HB3	1.91	0.70
8:H:59:LEU:HD12	8:H:60:GLU:N	2.06	0.69
1:A:4:U:H5''	1:A:5:U:OP1	1.92	0.69
1:A:718:A:C5	11:K:118:HIS:CD2	2.80	0.69
12:L:34:CYS:HA	12:L:55:VAL:HA	1.73	0.69
12:L:25:GLU:O	12:L:26:ALA:C	2.30	0.69
1:A:1317:C:OP1	14:N:56:SER:OG	2.08	0.69
9:I:57:MET:O	9:I:59:GLU:N	2.26	0.69
1:A:577:G:C8	1:A:816:A:C6	2.81	0.69
1:A:728:A:H2'	1:A:729:A:C8	2.28	0.68
4:D:4:TYR:O	4:D:5:LEU:HB2	1.93	0.68
1:A:646:G:O6	23:A:1793:HOH:O	2.11	0.68
5:E:137:VAL:O	5:E:138:ARG:HB2	1.93	0.68
2:B:16:PHE:CE2	2:B:18:HIS:CE1	2.82	0.68
9:I:41:ARG:O	9:I:45:ARG:NH1	2.27	0.68
14:N:54:ASP:OD1	14:N:59:ARG:NH1	2.26	0.68
1:A:1133:G:C2	1:A:1142:G:C2	2.81	0.68
1:A:152:A:N6	1:A:170:U:C2	2.62	0.68
1:A:71:A:C2	1:A:72:A:C8	2.82	0.68
5:E:82:GLN:OE1	5:E:150:PRO:HD3	1.94	0.68
6:F:45:ARG:O	6:F:56:LYS:HA	1.93	0.68
9:I:102:GLY:O	9:I:104:VAL:N	2.27	0.68
1:A:1297:G:O2'	7:G:114:LYS:NZ	2.26	0.67
1:A:1000:A:H2'	1:A:1001:C:O4'	1.93	0.67
1:A:1298:U:O2	1:A:1298:U:H2'	1.93	0.67
1:A:568:G:N2	1:A:883:C:C2	2.63	0.67
14:N:61:ARG:O	14:N:62:ASN:HB2	1.93	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:632:U:O2	1:A:632:U:H2'	1.92	0.67
1:A:920:U:H2'	1:A:921:U:C6	2.29	0.67
1:A:1321:U:O3'	19:S:78:ARG:NH2	2.27	0.67
1:A:1361:G:C3'	1:A:1362:A:H5''	2.24	0.67
1:A:939:G:OP1	7:G:95:ARG:NH2	2.27	0.67
9:I:22:LYS:O	9:I:24:GLY:N	2.28	0.67
1:A:1431:A:C6	1:A:1432:G:C6	2.82	0.67
4:D:148:LYS:O	4:D:149:ALA:HB3	1.95	0.67
9:I:84:THR:HG21	9:I:103:PHE:HB3	1.75	0.67
1:A:791:G:C6	1:A:792:A:N7	2.63	0.66
1:A:373:A:C2	1:A:374:A:C8	2.84	0.66
1:A:980:C:N3	23:A:1845:HOH:O	2.28	0.66
5:E:99:ALA:O	5:E:101:GLU:N	2.28	0.66
1:A:405:U:OP1	1:A:406:G:O2'	2.06	0.66
1:A:568:G:O6	12:L:2:ALA:HB2	1.95	0.66
1:A:686:U:O2'	1:A:687:A:OP2	2.12	0.66
1:A:1077:G:N2	1:A:1080:A:OP2	2.29	0.66
7:G:88:PRO:HD2	7:G:151:PHE:O	1.96	0.66
1:A:378:G:C2	1:A:386:C:O2	2.49	0.66
2:B:73:LYS:NZ	2:B:204:ASP:O	2.24	0.65
9:I:120:LYS:HG3	9:I:123:ARG:HB3	1.78	0.65
1:A:1203:C:H4'	14:N:67:THR:HB	1.77	0.65
3:C:150:LYS:HG2	3:C:201:TRP:CE3	2.31	0.65
17:Q:48:ASP:N	17:Q:48:ASP:OD1	2.29	0.65
2:B:82:ASP:N	2:B:82:ASP:OD1	2.28	0.65
1:A:207:C:H2'	1:A:207:C:O2	1.97	0.65
1:A:846:G:C2	1:A:847:G:C8	2.85	0.65
7:G:92:ARG:NE	7:G:93:PRO:HD2	2.11	0.65
1:A:1048:G:OP2	23:A:1849:HOH:O	2.14	0.65
1:A:72:A:N6	1:A:73:C:N4	2.45	0.65
1:A:73:C:O2'	1:A:74:A:O5'	2.14	0.65
2:B:141:LEU:O	2:B:144:LEU:N	2.30	0.65
5:E:56:VAL:N	5:E:57:PRO:HD2	2.11	0.65
10:J:35:GLN:HG2	10:J:77:VAL:HB	1.77	0.65
1:A:1361:G:H3'	1:A:1362:A:H5''	1.78	0.65
1:A:309:A:O2'	1:A:607:A:N1	2.24	0.65
1:A:992:U:C5	1:A:1043:G:C8	2.85	0.65
1:A:536:C:OP1	23:A:1770:HOH:O	2.15	0.64
5:E:155:ALA:HB1	8:H:66:PHE:CD2	2.31	0.64
12:L:38:TYR:HB2	12:L:52:VAL:HG13	1.80	0.64
19:S:55:ARG:CZ	19:S:79:THR:HG22	2.27	0.64
1:A:32:A:OP1	1:A:398:U:H1'	1.97	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:125:ILE:HD11	8:H:128:TYR:CE1	2.31	0.64
1:A:1124:G:N2	1:A:1127:G:C2	2.65	0.64
1:A:1431:A:N6	1:A:1432:G:O6	2.30	0.64
9:I:95:ARG:O	9:I:99:ARG:N	2.30	0.64
8:H:88:ARG:O	8:H:122:GLY:HA3	1.98	0.64
4:D:174:ASP:O	4:D:175:ALA:CB	2.46	0.64
13:M:114:LYS:HB2	13:M:115:PRO:HD3	1.78	0.64
17:Q:19:LYS:O	17:Q:71:LYS:NZ	2.26	0.64
17:Q:12:VAL:HG23	17:Q:57:ASP:O	1.97	0.64
1:A:463:U:H5'	1:A:464:U:OP2	1.98	0.63
6:F:86:ARG:CG	6:F:86:ARG:HH11	2.11	0.63
21:U:53:VAL:HG13	21:U:54:LYS:N	2.14	0.63
1:A:1040:U:H2'	1:A:1041:G:C8	2.34	0.63
1:A:1225:A:H2'	1:A:1226:C:C5	2.34	0.63
2:B:53:ALA:O	2:B:57:LEU:HB2	1.99	0.63
4:D:62:ARG:NH1	4:D:69:GLU:OE1	2.31	0.63
1:A:16:A:H2'	1:A:17:U:H5'	1.80	0.63
2:B:119:THR:O	2:B:120:GLN:CB	2.46	0.63
1:A:149:A:C2	1:A:150:U:C2	2.87	0.63
1:A:1096:C:H2'	1:A:1097:C:H6	1.63	0.63
1:A:55:A:C6	1:A:56:U:C2	2.87	0.63
1:A:1377:A:C5	7:G:7:ILE:HD12	2.33	0.63
1:A:572:A:H5'	1:A:573:A:OP2	1.99	0.62
1:A:32:A:C2	1:A:33:A:C5	2.87	0.62
2:B:141:LEU:O	2:B:145:GLU:N	2.32	0.62
5:E:99:ALA:O	5:E:122:ASN:ND2	2.31	0.62
1:A:1412:C:H2'	1:A:1413:A:C8	2.35	0.62
5:E:141:ILE:O	5:E:143:GLY:N	2.31	0.62
9:I:54:LEU:O	9:I:55:VAL:HG22	1.99	0.62
11:K:101:ASN:OD1	11:K:101:ASN:C	2.38	0.62
21:U:36:GLU:OE1	21:U:36:GLU:HA	1.99	0.62
1:A:1486:G:H2'	1:A:1487:G:O4'	1.98	0.62
1:A:1161:C:O2	1:A:1176:A:C2	2.53	0.62
1:A:1211:U:C2'	1:A:1212:U:OP2	2.47	0.62
1:A:718:A:C8	1:A:719:C:C5	2.88	0.62
13:M:93:ARG:HB3	13:M:93:ARG:CZ	2.28	0.62
18:R:25:ASP:O	18:R:28:THR:N	2.31	0.62
4:D:99:ASP:OD1	4:D:100:ASN:N	2.33	0.62
1:A:1006:G:H2'	1:A:1007:U:C6	2.35	0.62
1:A:475:C:H2'	1:A:476:U:C6	2.34	0.62
4:D:35:GLU:O	4:D:38:PRO:HD3	1.99	0.61
4:D:174:ASP:O	4:D:175:ALA:HB2	2.00	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:33:LYS:HG2	4:D:33:LYS:O	1.99	0.61
13:M:40:ALA:O	13:M:42:ASP:N	2.32	0.61
21:U:4:ILE:N	21:U:19:PHE:CE2	2.68	0.61
1:A:451:A:H4'	1:A:452:A:O5'	2.00	0.61
5:E:136:VAL:O	5:E:140:THR:OG1	2.17	0.61
9:I:26:GLY:N	9:I:61:LEU:O	2.33	0.61
2:B:21:ARG:NH1	2:B:21:ARG:HA	2.16	0.61
2:B:100:MET:HA	2:B:107:VAL:HG21	1.82	0.61
2:B:21:ARG:CZ	2:B:21:ARG:HA	2.29	0.61
4:D:168:PRO:CB	4:D:171:LEU:HD12	2.30	0.61
5:E:98:PRO:O	5:E:99:ALA:HB3	2.00	0.61
21:U:8:GLU:HB3	21:U:12:PHE:CE2	2.36	0.61
1:A:1377:A:C5	7:G:7:ILE:CD1	2.84	0.61
1:A:1490:U:H2'	1:A:1491:G:O4'	1.99	0.61
1:A:170:U:O2'	1:A:171:A:H5'	2.00	0.61
4:D:168:PRO:HB2	4:D:171:LEU:HD12	1.83	0.61
1:A:1151:A:N3	1:A:1152:A:C8	2.69	0.61
2:B:85:LEU:O	2:B:85:LEU:HG	2.00	0.61
1:A:1255:G:C6	1:A:1279:G:C8	2.89	0.61
1:A:72:A:C6	1:A:73:C:C4	2.88	0.61
8:H:55:THR:C	8:H:57:PRO:HD3	2.21	0.61
1:A:1022:A:C5	1:A:1023:U:C4	2.89	0.60
1:A:1138:G:C2	1:A:1140:C:C4	2.89	0.60
2:B:134:ALA:O	2:B:138:THR:OG1	2.16	0.60
5:E:154:ALA:HA	5:E:157:ARG:HB3	1.82	0.60
14:N:80:SER:O	14:N:83:LYS:N	2.33	0.60
1:A:695:A:H2'	1:A:696:A:C8	2.36	0.60
1:A:815:A:N7	1:A:1509:C:O2'	2.25	0.60
7:G:145:ALA:O	7:G:146:GLU:HB2	2.00	0.60
10:J:27:GLU:O	10:J:31:ARG:HB3	2.00	0.60
1:A:794:A:HO2'	1:A:1521:C:HO2'	1.50	0.60
1:A:881:G:C6	1:A:882:C:C4	2.90	0.60
1:A:268:U:H2'	1:A:269:C:C6	2.36	0.60
1:A:990:C:C4	1:A:991:U:O4	2.55	0.60
4:D:146:ARG:O	4:D:150:LYS:N	2.34	0.60
5:E:98:PRO:O	5:E:99:ALA:CB	2.49	0.60
9:I:91:ASP:OD1	9:I:93:SER:N	2.35	0.60
14:N:21:PHE:O	14:N:23:LYS:N	2.34	0.60
1:A:1309:G:C6	1:A:1329:A:C2	2.89	0.60
1:A:16:A:C2'	1:A:17:U:H5'	2.32	0.60
14:N:33:ASP:O	14:N:35:ASN:N	2.35	0.60
1:A:1379:G:N2	1:A:1381:U:O4	2.32	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:533:A:O2'	1:A:535:A:OP2	2.19	0.60
1:A:998:C:H2'	1:A:999:C:C6	2.37	0.60
2:B:210:VAL:O	2:B:214:LEU:HB2	2.02	0.60
4:D:90:LEU:HD21	4:D:200:ILE:HD11	1.84	0.60
6:F:18:VAL:HG12	6:F:19:PRO:N	2.16	0.60
1:A:938:A:N6	1:A:939:G:C6	2.69	0.60
2:B:47:VAL:HB	2:B:48:PRO:HD3	1.83	0.60
4:D:28:ILE:O	4:D:31:LYS:NZ	2.34	0.60
1:A:1041:G:H2'	1:A:1042:A:C8	2.37	0.59
4:D:107:PHE:CG	4:D:145:ILE:HD11	2.37	0.59
4:D:174:ASP:OD2	4:D:175:ALA:N	2.36	0.59
1:A:455:G:N2	1:A:478:A:C2	2.70	0.59
5:E:82:GLN:OE1	5:E:149:SER:HA	2.02	0.59
14:N:41:ARG:HG2	14:N:42:TRP:N	2.18	0.59
14:N:52:PRO:O	14:N:53:ARG:HB3	2.02	0.59
1:A:972:C:H4'	10:J:59:LYS:HG2	1.84	0.59
4:D:74:ASN:HA	4:D:77:LYS:HB2	1.84	0.59
10:J:48:ARG:NH1	10:J:66:GLU:OE1	2.36	0.59
7:G:151:PHE:O	7:G:152:ALA:HB2	2.02	0.59
15:O:87:LEU:O	15:O:88:ARG:HB3	2.02	0.59
1:A:957:U:O3'	19:S:79:THR:OG1	2.19	0.59
1:A:1361:G:H3'	1:A:1362:A:C5'	2.31	0.59
1:A:858:G:O6	1:A:869:G:H3'	2.02	0.59
1:A:227:G:H2'	1:A:228:A:O4'	2.02	0.59
1:A:374:A:H5''	1:A:452:A:N1	2.18	0.59
3:C:16:LYS:HG3	3:C:17:PRO:HD2	1.83	0.59
1:A:131:A:O2'	1:A:262:A:N3	2.32	0.58
15:O:60:VAL:O	15:O:63:ARG:N	2.35	0.58
1:A:513:C:H2'	1:A:514:C:C6	2.39	0.58
19:S:63:THR:HG22	19:S:64:ASP:N	2.18	0.58
5:E:133:PRO:HA	5:E:136:VAL:HG12	1.84	0.58
11:K:127:ARG:HB2	21:U:34:ARG:NH1	2.18	0.58
1:A:1523:G:OP1	11:K:125:LYS:NZ	2.32	0.58
5:E:77:ASN:HB2	5:E:82:GLN:HG2	1.85	0.58
10:J:15:HIS:CE1	10:J:16:ARG:HD3	2.39	0.58
21:U:44:GLU:OE1	21:U:45:ARG:NH1	2.36	0.58
1:A:757:U:OP1	1:A:822:U:O2'	2.16	0.58
2:B:54:LEU:HD12	2:B:220:THR:HG21	1.86	0.58
10:J:22:THR:HA	10:J:25:ILE:HG22	1.84	0.58
13:M:10:PRO:O	13:M:11:ASP:HB2	2.04	0.58
21:U:11:PRO:C	21:U:12:PHE:CG	2.74	0.58
1:A:380:G:N2	1:A:383:A:OP2	2.35	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:495:A:C2	1:A:496:A:N6	2.72	0.58
1:A:955:U:H2'	1:A:956:U:O4'	2.04	0.58
4:D:12:SER:HA	4:D:19:LEU:HD12	1.84	0.58
5:E:105:ILE:HG23	5:E:105:ILE:O	2.04	0.58
5:E:24:THR:HA	5:E:29:ARG:HA	1.85	0.58
7:G:83:SER:O	7:G:85:TYR:N	2.37	0.58
1:A:1004:A:C6	1:A:1005:A:C6	2.91	0.58
1:A:1337:G:H5''	1:A:1338:G:OP1	2.04	0.58
3:C:42:TYR:CE2	3:C:90:VAL:HG21	2.39	0.58
5:E:75:ALA:O	5:E:82:GLN:NE2	2.37	0.58
1:A:1072:G:C6	1:A:1073:U:C4	2.92	0.58
1:A:1296:C:H4'	1:A:1302:C:C4	2.38	0.58
1:A:1323:G:H2'	1:A:1324:A:C8	2.38	0.58
1:A:1521:C:C4	1:A:1522:U:C5	2.92	0.58
1:A:765:G:C6	1:A:812:G:C4	2.92	0.58
1:A:994:A:N3	1:A:994:A:H2'	2.19	0.58
3:C:42:TYR:CZ	3:C:46:GLU:HG3	2.38	0.58
4:D:31:LYS:HD3	4:D:31:LYS:N	2.19	0.58
6:F:85:ILE:O	6:F:86:ARG:O	2.21	0.58
1:A:805:C:C2	1:A:806:C:C5	2.92	0.57
1:A:495:A:N1	1:A:496:A:N6	2.52	0.57
3:C:59:ARG:HB2	3:C:63:SER:O	2.03	0.57
11:K:23:ILE:HD11	11:K:86:VAL:HG13	1.85	0.57
1:A:1359:C:OP2	14:N:75:ARG:NH1	2.37	0.57
1:A:1308:U:OP1	13:M:97:VAL:N	2.37	0.57
1:A:197:A:O2'	1:A:220:G:N2	2.37	0.57
1:A:1080:A:OP1	5:E:52:LYS:HE2	2.05	0.57
10:J:88:MET:O	10:J:89:ARG:CB	2.52	0.57
17:Q:19:LYS:HD3	17:Q:49:GLU:HA	1.86	0.57
1:A:1179:A:O3'	9:I:105:THR:OG1	2.22	0.57
1:A:511:C:C2	1:A:512:U:C5	2.92	0.57
1:A:662:U:H2'	1:A:663:A:C8	2.39	0.57
11:K:107:ILE:O	11:K:107:ILE:HG23	2.04	0.57
12:L:23:ALA:HA	12:L:61:PHE:CD2	2.39	0.57
12:L:90:LEU:HB2	12:L:93:VAL:CG2	2.35	0.57
1:A:1296:C:H4'	1:A:1302:C:N4	2.20	0.57
1:A:256:U:H2'	1:A:257:G:O4'	2.04	0.57
2:B:210:VAL:CG2	2:B:211:THR:N	2.68	0.57
13:M:10:PRO:O	13:M:11:ASP:CB	2.52	0.57
20:T:25:ARG:O	20:T:29:ARG:HG3	2.04	0.57
1:A:134:G:H2'	1:A:135:C:O4'	2.04	0.57
1:A:951:G:N3	1:A:970:C:O2'	2.33	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:148:LYS:O	4:D:149:ALA:CB	2.51	0.57
5:E:35:ALA:O	5:E:50:TYR:O	2.23	0.57
7:G:103:TRP:CD2	7:G:137:LYS:HG2	2.39	0.57
10:J:81:GLU:HA	10:J:84:VAL:HG12	1.85	0.57
1:A:1215:G:C5	1:A:1216:A:N7	2.73	0.57
1:A:1244:G:C6	1:A:1245:C:N4	2.73	0.57
1:A:1408:A:C2	1:A:1494:G:C4	2.92	0.57
1:A:86:G:H1'	1:A:87:C:O4'	2.05	0.57
18:R:58:ALA:O	18:R:61:ARG:N	2.38	0.57
19:S:11:ILE:HG13	19:S:12:ASP:N	2.19	0.57
1:A:254:G:OP1	17:Q:69:LYS:O	2.23	0.57
1:A:409:U:OP1	4:D:24:GLY:CA	2.53	0.57
4:D:19:LEU:HD22	4:D:64:ILE:HG13	1.86	0.57
11:K:17:SER:OG	11:K:18:ASP:N	2.38	0.57
12:L:28:PRO:HB2	12:L:29:GLN:OE1	2.05	0.57
1:A:1041:G:C6	1:A:1042:A:N6	2.73	0.57
4:D:35:GLU:HG3	4:D:36:GLN:HG3	1.87	0.57
6:F:19:PRO:HA	6:F:22:ILE:HB	1.87	0.57
1:A:211:G:O2'	1:A:212:G:H4'	2.05	0.56
2:B:91:PHE:CD1	2:B:150:GLY:HA3	2.40	0.56
6:F:22:ILE:O	6:F:26:THR:OG1	2.22	0.56
1:A:1005:A:O3'	1:A:1037:C:O2'	2.22	0.56
3:C:148:GLY:O	3:C:203:PHE:N	2.36	0.56
4:D:29:ASP:C	4:D:31:LYS:H	2.08	0.56
1:A:404:G:N7	4:D:2:ALA:HB3	2.20	0.56
1:A:401:C:OP2	4:D:70:ARG:HD3	2.05	0.56
1:A:439:U:H4'	4:D:121:LYS:CG	2.35	0.56
1:A:844:G:P	1:A:844:G:O4'	2.63	0.56
3:C:130:PHE:CE1	3:C:131:ARG:HD3	2.40	0.56
1:A:439:U:H4'	4:D:121:LYS:HG3	1.86	0.56
1:A:33:A:H2'	1:A:34:C:C6	2.40	0.56
1:A:968:A:C8	1:A:1062:U:H4'	2.40	0.56
5:E:122:ASN:O	5:E:123:VAL:O	2.23	0.56
21:U:18:ARG:O	21:U:21:ARG:N	2.39	0.56
1:A:412:A:O2'	1:A:413:G:H4'	2.05	0.56
1:A:679:C:O2	1:A:712:A:C2	2.58	0.56
1:A:728:A:C8	15:O:54:ARG:CZ	2.89	0.56
1:A:811:C:N4	1:A:812:G:C6	2.73	0.56
6:F:81:ASN:OD1	6:F:83:ALA:N	2.38	0.56
15:O:19:ALA:O	15:O:20:ASN:HB2	2.03	0.56
15:O:35:GLN:NE2	15:O:39:LEU:HD22	2.19	0.56
1:A:1166:G:H2'	1:A:1168:U:OP2	2.06	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1431:A:C6	1:A:1432:G:O6	2.58	0.56
1:A:706:A:C5	1:A:707:U:C5	2.93	0.56
2:B:205:ASP:N	2:B:205:ASP:OD1	2.37	0.56
4:D:29:ASP:O	4:D:31:LYS:N	2.35	0.56
17:Q:47:HIS:HB2	17:Q:67:LEU:CD1	2.36	0.56
18:R:20:GLU:O	18:R:22:ASP:N	2.38	0.56
20:T:3:ASN:O	20:T:5:LYS:N	2.38	0.56
1:A:1417:G:C6	1:A:1482:G:C6	2.94	0.56
1:A:429:U:O3'	4:D:22:LYS:HE3	2.06	0.56
4:D:22:LYS:O	4:D:23:SER:C	2.43	0.56
1:A:307:C:H5''	1:A:308:C:OP2	2.06	0.56
1:A:313:A:H2'	1:A:314:C:C6	2.41	0.56
1:A:344:A:OP2	1:A:345:C:N4	2.38	0.56
12:L:110:ARG:NE	12:L:117:TYR:CD2	2.73	0.56
12:L:116:LYS:O	12:L:117:TYR:CD2	2.59	0.56
1:A:1226:C:H2'	13:M:102:THR:HB	1.88	0.56
1:A:881:G:C5	1:A:882:C:C5	2.94	0.56
4:D:36:GLN:O	4:D:37:ALA:HB2	2.06	0.56
9:I:120:LYS:CG	9:I:123:ARG:HB3	2.35	0.56
21:U:14:VAL:HG12	21:U:16:LEU:HG	1.88	0.56
1:A:207:C:O2'	1:A:213:G:N2	2.39	0.56
2:B:68:LEU:HD12	2:B:158:PRO:HG2	1.88	0.56
5:E:104:GLY:O	5:E:105:ILE:HG22	2.06	0.56
11:K:52:PHE:CZ	11:K:62:ALA:HA	2.40	0.56
12:L:90:LEU:HB2	12:L:93:VAL:HG21	1.88	0.56
1:A:247:G:C6	1:A:278:G:C2	2.94	0.56
1:A:636:U:H2'	1:A:637:C:C6	2.41	0.56
1:A:1162:C:C2	1:A:1175:G:N2	2.74	0.55
1:A:927:G:O2'	1:A:1503:A:N7	2.37	0.55
1:A:66:A:H4'	1:A:173:U:C5	2.41	0.55
1:A:994:A:C8	1:A:1216:A:H4'	2.41	0.55
3:C:40:ARG:HG2	3:C:55:ILE:HD11	1.88	0.55
19:S:80:TYR:O	19:S:81:ARG:CB	2.53	0.55
1:A:1201:A:H1'	1:A:1202:U:OP2	2.05	0.55
1:A:978:A:C5	1:A:1318:A:N6	2.74	0.55
1:A:455:G:C2	1:A:478:A:N1	2.75	0.55
1:A:976:G:N2	1:A:1363:A:N3	2.54	0.55
2:B:131:LYS:O	2:B:135:LEU:N	2.40	0.55
2:B:35:ARG:O	2:B:38:VAL:HG12	2.07	0.55
5:E:83:HIS:CD2	8:H:96:MET:CE	2.90	0.55
1:A:144:G:C5	1:A:179:A:C2	2.94	0.55
10:J:77:VAL:O	10:J:79:PRO:HD3	2.07	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1316:G:N2	1:A:1318:A:H3'	2.22	0.55
1:A:1361:G:H2'	1:A:1362:A:H5''	1.87	0.55
1:A:1317:C:N4	1:A:1318:A:N3	2.55	0.55
1:A:372:C:O2	23:A:1892:HOH:O	2.08	0.55
1:A:4:U:H2'	1:A:4:U:O2	2.05	0.55
2:B:16:PHE:CZ	2:B:18:HIS:CE1	2.95	0.55
2:B:208:ARG:O	2:B:210:VAL:N	2.40	0.55
5:E:15:LEU:HD12	5:E:15:LEU:C	2.26	0.55
11:K:89:PRO:HD3	21:U:29:LEU:CD1	2.37	0.55
12:L:74:LEU:HD11	12:L:80:ILE:HG21	1.89	0.55
1:A:1089:G:C5	1:A:1090:U:C5	2.95	0.55
1:A:978:A:P	1:A:1362:A:N6	2.79	0.55
2:B:15:HIS:C	2:B:15:HIS:ND1	2.59	0.55
7:G:75:VAL:HG21	7:G:144:MET:HG2	1.89	0.55
12:L:87:VAL:HB	12:L:93:VAL:HG21	1.89	0.55
16:P:23:ASP:O	16:P:25:ARG:N	2.40	0.55
17:Q:60:GLU:HB3	17:Q:76:VAL:CG2	2.37	0.55
19:S:19:VAL:HG21	19:S:44:MET:HG2	1.88	0.55
21:U:40:LYS:N	21:U:41:PRO:CD	2.67	0.55
1:A:106:C:O2	1:A:379:C:H4'	2.07	0.55
1:A:66:A:C6	1:A:67:C:C5	2.95	0.55
19:S:75:ALA:N	19:S:76:PRO:CD	2.69	0.55
1:A:1084:G:C5	1:A:1085:U:C4	2.95	0.55
1:A:1356:G:H2'	1:A:1357:A:C8	2.43	0.55
1:A:960:U:C5	1:A:1225:A:C8	2.95	0.55
4:D:35:GLU:HG3	4:D:36:GLN:N	2.22	0.55
5:E:101:GLU:C	5:E:103:THR:N	2.60	0.55
5:E:96:MET:HE3	5:E:111:MET:CE	2.37	0.55
7:G:126:ASP:N	7:G:126:ASP:OD1	2.38	0.55
1:A:484:G:C5	1:A:486:U:H1'	2.42	0.54
5:E:131:THR:O	5:E:132:ASN:C	2.45	0.54
1:A:671:G:N2	1:A:736:C:C2	2.76	0.54
1:A:960:U:O2'	1:A:1223:C:H4'	2.07	0.54
7:G:74:GLU:O	7:G:88:PRO:HA	2.07	0.54
15:O:17:ARG:O	15:O:18:ASP:HB3	2.07	0.54
1:A:1291:U:H4'	9:I:42:GLU:HG2	1.89	0.54
1:A:1361:G:C2'	1:A:1362:A:H5''	2.36	0.54
5:E:157:ARG:O	5:E:159:LYS:N	2.36	0.54
1:A:174:A:C4	1:A:175:C:C6	2.95	0.54
1:A:406:G:C2	1:A:407:U:C5	2.95	0.54
1:A:76:G:N2	1:A:95:C:C2	2.75	0.54
2:B:94:HIS:CD2	2:B:146:ASN:HB2	2.41	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:133:PRO:HA	5:E:136:VAL:CG1	2.37	0.54
6:F:29:ILE:HG22	6:F:34:GLY:O	2.08	0.54
8:H:9:ASP:OD2	8:H:13:ARG:NH1	2.40	0.54
1:A:718:A:C6	11:K:118:HIS:CD2	2.95	0.54
1:A:1302:C:C5	13:M:17:ILE:HD13	2.43	0.54
1:A:920:U:H2'	1:A:921:U:H6	1.73	0.54
1:A:96:U:O2'	1:A:97:G:P	2.66	0.54
13:M:20:THR:HG22	13:M:26:GLY:C	2.27	0.54
14:N:3:LYS:HB3	14:N:6:MET:HG2	1.90	0.54
1:A:299:G:C6	1:A:300:A:C6	2.95	0.54
2:B:132:LYS:O	2:B:136:MET:HB3	2.07	0.54
3:C:145:GLY:O	3:C:146:ALA:O	2.26	0.54
4:D:167:LYS:HE2	4:D:173:VAL:HG11	1.89	0.54
1:A:401:C:P	4:D:70:ARG:HD3	2.47	0.54
11:K:89:PRO:HD3	21:U:29:LEU:HD11	1.89	0.54
17:Q:16:LYS:C	17:Q:17:MET:SD	2.86	0.54
18:R:72:ASP:C	18:R:73:ARG:HG2	2.28	0.54
20:T:36:TYR:CG	20:T:37:ALA:N	2.76	0.54
8:H:89:LYS:HG3	8:H:90:ASP:N	2.22	0.54
1:A:1149:C:N4	1:A:1150:A:C6	2.75	0.54
1:A:1181:G:O2'	1:A:1182:G:C5	2.60	0.54
1:A:1467:C:H2'	1:A:1468:A:C8	2.43	0.54
1:A:158:G:C5	1:A:164:G:C6	2.96	0.54
1:A:249:U:O2'	1:A:252:U:O2'	2.15	0.54
1:A:442:G:C6	1:A:443:C:C4	2.96	0.54
2:B:62:SER:C	2:B:64:LYS:N	2.60	0.54
3:C:36:ASP:O	3:C:40:ARG:HG3	2.08	0.54
6:F:6:ILE:HD12	6:F:6:ILE:N	2.23	0.54
14:N:16:LEU:HB3	14:N:55:SER:HA	1.90	0.54
15:O:70:LEU:HD13	15:O:78:TYR:HA	1.89	0.54
18:R:63:ARG:HB3	18:R:70:TYR:CZ	2.42	0.54
1:A:429:U:H3'	4:D:9:LEU:HD23	1.90	0.54
1:A:689:C:OP2	11:K:53:ARG:NH2	2.41	0.54
14:N:87:ALA:HB1	14:N:92:GLU:HB2	1.90	0.54
19:S:58:VAL:HG11	19:S:75:ALA:HA	1.90	0.54
1:A:1386:G:C2	1:A:1387:G:C8	2.95	0.54
1:A:1535:C:O2'	1:A:1536:C:C5	2.61	0.54
1:A:207:C:HO2'	1:A:213:G:N2	2.06	0.54
1:A:474:G:C2	1:A:475:C:C2	2.96	0.54
2:B:203:ASN:OD1	2:B:204:ASP:N	2.41	0.54
2:B:206:ALA:O	2:B:207:ILE:C	2.46	0.54
14:N:24:ARG:HG2	14:N:27:LEU:HD12	1.90	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:R:25:ASP:O	18:R:26:ILE:C	2.47	0.54
1:A:1201:A:H4'	1:A:1202:U:O5'	2.07	0.53
1:A:773:G:N3	1:A:807:A:C2	2.76	0.53
17:Q:49:GLU:O	17:Q:50:ASN:CG	2.47	0.53
1:A:1463:U:H2'	1:A:1464:U:C6	2.43	0.53
2:B:81:LYS:HG2	2:B:85:LEU:HD23	1.90	0.53
2:B:88:ASP:N	2:B:88:ASP:OD1	2.41	0.53
11:K:124:PRO:HB2	11:K:126:LYS:HE3	1.90	0.53
20:T:36:TYR:C	20:T:36:TYR:CD1	2.81	0.53
1:A:527:G:C2	1:A:528:C:C6	2.96	0.53
1:A:756:C:H2'	1:A:757:U:H5'	1.90	0.53
4:D:34:ILE:O	4:D:35:GLU:HB3	2.08	0.53
9:I:90:TYR:O	9:I:91:ASP:CG	2.46	0.53
15:O:14:GLU:O	15:O:84:ARG:NH2	2.42	0.53
1:A:409:U:OP1	4:D:24:GLY:HA2	2.08	0.53
1:A:60:A:H4'	1:A:61:G:O5'	2.08	0.53
7:G:93:PRO:O	7:G:97:ASN:ND2	2.41	0.53
9:I:49:ARG:NH2	9:I:52:LEU:O	2.42	0.53
12:L:86:ARG:CZ	12:L:88:LYS:HB3	2.37	0.53
1:A:8:A:C6	4:D:206:LYS:HB3	2.42	0.53
4:D:126:ASN:OD1	4:D:142:VAL:HG23	2.08	0.53
4:D:46:PRO:O	4:D:47:ARG:C	2.46	0.53
5:E:133:PRO:O	5:E:137:VAL:HG13	2.07	0.53
13:M:6:GLY:O	13:M:8:ASN:N	2.42	0.53
15:O:53:ARG:O	15:O:56:LEU:HB3	2.07	0.53
1:A:436:C:C2	1:A:437:U:C5	2.97	0.53
1:A:501:C:H1'	1:A:549:C:H1'	1.91	0.53
1:A:582:C:C2	1:A:760:G:N1	2.77	0.53
4:D:196:ASN:HB3	4:D:198:HIS:CD2	2.43	0.53
19:S:10:PHE:O	19:S:39:THR:OG1	2.26	0.53
1:A:898:G:N2	1:A:901:A:OP2	2.40	0.53
5:E:115:LEU:O	5:E:120:VAL:HG23	2.09	0.53
6:F:18:VAL:O	6:F:21:MET:N	2.41	0.53
1:A:160:A:H2'	1:A:161:A:O4'	2.09	0.53
1:A:223:A:C6	1:A:224:U:C4	2.97	0.53
11:K:51:GLY:O	11:K:52:PHE:O	2.27	0.53
20:T:84:ASN:HA	20:T:87:ALA:HB3	1.90	0.53
1:A:1031:C:H4'	1:A:1032:G:C2	2.43	0.53
1:A:322:C:O2	1:A:332:G:N2	2.41	0.53
1:A:577:G:C8	1:A:816:A:N1	2.77	0.53
2:B:19:GLN:HB3	2:B:189:THR:OG1	2.08	0.53
12:L:102:LEU:HD12	12:L:102:LEU:N	2.24	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:4:TYR:CE2	4:D:11:LEU:HD11	2.44	0.53
7:G:8:GLY:O	7:G:9:GLN:HB3	2.09	0.53
17:Q:52:GLU:HG2	17:Q:53:CYS:H	1.74	0.53
1:A:328:C:O2	1:A:328:C:C2'	2.58	0.52
1:A:714:G:H2'	1:A:715:A:C8	2.43	0.52
10:J:27:GLU:O	10:J:27:GLU:HG2	2.08	0.52
1:A:1314:C:C5	19:S:6:LYS:HE2	2.44	0.52
21:U:12:PHE:O	21:U:13:ASP:CB	2.57	0.52
1:A:1191:A:H5''	3:C:4:LYS:HE3	1.90	0.52
1:A:949:A:C2	1:A:1233:G:N3	2.77	0.52
2:B:68:LEU:HD13	2:B:161:LEU:HD13	1.89	0.52
5:E:38:VAL:HG12	5:E:117:VAL:HG21	1.91	0.52
8:H:105:SER:O	8:H:123:GLY:HA3	2.09	0.52
10:J:35:GLN:O	10:J:36:VAL:HB	2.10	0.52
10:J:85:ASP:HA	10:J:88:MET:HB2	1.90	0.52
1:A:1022:A:C6	1:A:1023:U:C4	2.97	0.52
1:A:1080:A:OP1	5:E:52:LYS:CE	2.57	0.52
1:A:1169:A:H2'	1:A:1170:A:C8	2.44	0.52
1:A:81:A:H2'	1:A:82:G:C8	2.44	0.52
1:A:987:G:C6	1:A:988:G:C5	2.96	0.52
6:F:88:MET:SD	6:F:90:MET:SD	3.08	0.52
16:P:51:ARG:C	16:P:51:ARG:HD3	2.30	0.52
1:A:1095:U:P	23:A:1855:HOH:O	2.67	0.52
1:A:1213:A:C5	1:A:1215:G:C4	2.97	0.52
1:A:1243:C:N4	1:A:1244:G:O6	2.42	0.52
1:A:1286:U:H2'	1:A:1286:U:O2	2.09	0.52
1:A:1480:A:H2'	1:A:1481:U:O4'	2.09	0.52
1:A:425:G:H2'	1:A:426:U:O4'	2.09	0.52
2:B:50:PHE:CD1	2:B:54:LEU:HD23	2.44	0.52
13:M:14:HIS:HB2	13:M:17:ILE:CD1	2.40	0.52
15:O:27:VAL:O	15:O:31:LEU:HD12	2.09	0.52
1:A:1141:C:O2'	1:A:1142:G:OP2	2.23	0.52
1:A:1277:C:O2'	1:A:1279:G:H1'	2.08	0.52
1:A:793:U:O2	1:A:1516:G:H4'	2.10	0.52
1:A:369:G:OP2	1:A:388:G:N1	2.39	0.52
1:A:38:G:C2	1:A:397:A:C2	2.98	0.52
1:A:41:G:H2'	1:A:42:G:C8	2.44	0.52
1:A:485:U:H4'	1:A:485:U:OP2	2.09	0.52
1:A:813:U:H2'	1:A:814:A:H5''	1.91	0.52
5:E:106:ILE:HG13	5:E:123:VAL:O	2.10	0.52
12:L:90:LEU:O	12:L:93:VAL:HG22	2.09	0.52
1:A:1328:C:H5''	13:M:28:THR:HG21	1.90	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:Q:15:ASP:HA	17:Q:21:ILE:HD12	1.90	0.52
1:A:1092:A:C2	1:A:1183:U:O2	2.62	0.52
1:A:1478:U:H2'	1:A:1479:C:C6	2.44	0.52
9:I:30:ILE:HA	9:I:65:ILE:HG13	1.92	0.52
21:U:12:PHE:O	21:U:13:ASP:HB2	2.10	0.52
1:A:1072:G:C5	1:A:1073:U:C4	2.97	0.52
1:A:1364:U:C2'	1:A:1364:U:O2	2.57	0.52
1:A:211:G:N3	1:A:211:G:H2'	2.25	0.52
1:A:409:U:H2'	1:A:410:G:O4'	2.09	0.52
1:A:772:U:O2'	1:A:773:G:H5'	2.09	0.52
1:A:774:G:C5	1:A:775:G:N7	2.77	0.52
1:A:765:G:N1	1:A:812:G:H1'	2.23	0.52
4:D:32:CYS:O	4:D:33:LYS:HB3	2.10	0.52
1:A:115:G:H4'	1:A:116:A:O5'	2.10	0.52
1:A:202:G:H2'	1:A:203:G:O4'	2.10	0.52
1:A:273:U:C2'	1:A:274:A:H5'	2.39	0.52
4:D:107:PHE:CD2	4:D:145:ILE:HD11	2.45	0.52
7:G:40:GLU:O	7:G:44:TYR:CD2	2.63	0.52
1:A:39:G:N2	1:A:40:C:C2	2.78	0.52
1:A:624:C:H2'	1:A:625:U:O4'	2.09	0.52
1:A:756:C:H2'	1:A:757:U:C5'	2.40	0.52
1:A:981:U:H5	1:A:982:U:HO2'	1.57	0.52
4:D:131:ASN:O	4:D:131:ASN:CG	2.48	0.52
12:L:93:VAL:O	12:L:93:VAL:HG23	2.10	0.52
3:C:10:ILE:HD12	14:N:98:LYS:HG3	1.92	0.52
18:R:32:TYR:C	18:R:33:ILE:HG22	2.30	0.52
1:A:1211:U:O2'	1:A:1212:U:P	2.68	0.52
1:A:555:U:H2'	1:A:556:C:C6	2.44	0.52
14:N:52:PRO:O	14:N:53:ARG:CB	2.58	0.52
17:Q:47:HIS:HB2	17:Q:67:LEU:HD13	1.91	0.52
1:A:1034:G:H2'	1:A:1035:A:C8	2.44	0.51
1:A:1273:C:H2'	1:A:1274:A:O4'	2.09	0.51
1:A:780:A:C2	1:A:803:G:N1	2.78	0.51
5:E:106:ILE:HD11	5:E:124:LEU:HD23	1.91	0.51
10:J:25:ILE:HD13	10:J:25:ILE:O	2.11	0.51
6:F:88:MET:HE1	18:R:64:TYR:CD2	2.45	0.51
1:A:451:A:C8	1:A:452:A:C6	2.98	0.51
1:A:575:G:C6	1:A:821:G:N7	2.78	0.51
1:A:872:A:C4	1:A:874:G:C8	2.98	0.51
2:B:103:ASN:O	2:B:103:ASN:CG	2.48	0.51
6:F:97:THR:O	6:F:98:GLU:CB	2.57	0.51
18:R:67:LEU:N	18:R:67:LEU:HD23	2.25	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:T:71:LYS:HE3	20:T:75:HIS:CE1	2.45	0.51
1:A:50:A:N6	1:A:361:G:H4'	2.26	0.51
4:D:105:MET:SD	4:D:143:VAL:HG13	2.51	0.51
4:D:48:LEU:HD23	4:D:53:VAL:N	2.25	0.51
6:F:16:GLU:O	6:F:18:VAL:N	2.43	0.51
17:Q:51:ASN:O	17:Q:52:GLU:O	2.28	0.51
17:Q:60:GLU:HB3	17:Q:76:VAL:HG23	1.92	0.51
1:A:773:G:C2	1:A:807:A:C2	2.99	0.51
2:B:186:ILE:HA	2:B:200:ILE:O	2.10	0.51
2:B:206:ALA:C	2:B:208:ARG:N	2.64	0.51
2:B:91:PHE:O	2:B:150:GLY:HA3	2.11	0.51
4:D:173:VAL:O	4:D:174:ASP:HB3	2.10	0.51
5:E:83:HIS:CD2	8:H:96:MET:HE2	2.45	0.51
20:T:44:LYS:NZ	20:T:86:LEU:O	2.31	0.51
1:A:207:C:O2	1:A:207:C:C2'	2.58	0.51
1:A:72:A:C5	1:A:73:C:C5	2.99	0.51
1:A:811:C:C4	1:A:812:G:C6	2.99	0.51
1:A:991:U:H4'	1:A:992:U:H5''	1.92	0.51
1:A:1074:G:O2'	2:B:102:THR:CG2	2.58	0.51
5:E:101:GLU:HA	5:E:122:ASN:HB2	1.93	0.51
5:E:57:PRO:O	5:E:60:ILE:HG13	2.09	0.51
7:G:116:MET:HA	7:G:119:ARG:HD3	1.92	0.51
9:I:12:ARG:CD	9:I:107:ASP:HB3	2.41	0.51
10:J:35:GLN:HB2	10:J:78:GLU:HB2	1.92	0.51
10:J:87:LEU:HD13	10:J:88:MET:N	2.25	0.51
17:Q:46:VAL:CG2	17:Q:61:ILE:HD11	2.41	0.51
1:A:1288:A:N6	1:A:1289:A:N6	2.59	0.51
1:A:724:G:OP2	1:A:833:G:O2'	2.24	0.51
2:B:99:GLY:O	2:B:103:ASN:N	2.42	0.51
4:D:160:GLU:O	4:D:163:GLU:HB2	2.11	0.51
5:E:19:ASN:HB2	5:E:34:THR:OG1	2.09	0.51
18:R:46:GLY:O	18:R:47:THR:O	2.29	0.51
20:T:54:MET:HE1	20:T:58:VAL:HG21	1.92	0.51
1:A:1071:C:H2'	1:A:1072:G:C8	2.46	0.51
1:A:392:C:C2	1:A:393:A:C8	2.98	0.51
1:A:718:A:H5'	11:K:119:ASN:ND2	2.26	0.51
1:A:72:A:C6	1:A:73:C:N4	2.79	0.51
2:B:102:THR:O	2:B:102:THR:HG23	2.10	0.51
2:B:16:PHE:N	2:B:16:PHE:CD1	2.79	0.51
2:B:20:THR:OG1	2:B:21:ARG:N	2.44	0.51
6:F:13:ASP:O	6:F:15:SER:N	2.43	0.51
7:G:78:ARG:HB2	7:G:85:TYR:HB2	1.93	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:I:45:ARG:HG2	9:I:46:MET:N	2.26	0.51
1:A:1002:G:C4	1:A:1003:G:C8	2.98	0.51
1:A:1192:C:C5	1:A:1193:G:C8	2.99	0.51
1:A:892:A:O2'	1:A:1415:G:H4'	2.10	0.51
1:A:1499:A:H3'	23:A:1883:HOH:O	2.10	0.51
1:A:17:U:H2'	1:A:18:C:C6	2.45	0.51
1:A:406:G:C2	1:A:407:U:C6	2.99	0.51
1:A:940:C:N4	1:A:941:G:O6	2.44	0.51
4:D:157:ALA:O	4:D:161:LEU:HD22	2.11	0.51
5:E:90:THR:HG22	5:E:91:GLY:N	2.25	0.51
14:N:2:ALA:O	14:N:3:LYS:CB	2.58	0.51
19:S:29:LYS:CB	19:S:30:PRO:HD2	2.40	0.51
1:A:920:U:C2	1:A:921:U:C5	2.99	0.51
1:A:427:U:OP1	4:D:13:ARG:NH2	2.44	0.51
5:E:50:TYR:O	5:E:51:GLY:O	2.29	0.51
7:G:68:ASN:O	7:G:138:ARG:NH2	2.44	0.51
18:R:59:ILE:O	18:R:63:ARG:HD2	2.10	0.51
21:U:10:GLU:CB	21:U:11:PRO:HD3	2.41	0.51
1:A:106:C:O2	1:A:379:C:H5'	2.10	0.51
1:A:32:A:H2'	1:A:32:A:N3	2.25	0.51
1:A:502:A:H2'	1:A:503:C:O4'	2.11	0.51
1:A:756:C:C2'	1:A:757:U:H5'	2.41	0.51
9:I:31:ASN:HA	9:I:66:THR:HG22	1.92	0.51
1:A:252:U:O4	1:A:253:A:N6	2.44	0.50
5:E:80:THR:HA	5:E:120:VAL:HG12	1.93	0.50
6:F:38:ARG:HG3	6:F:63:ASN:HB2	1.93	0.50
12:L:39:THR:HA	12:L:50:ARG:O	2.10	0.50
17:Q:47:HIS:HA	17:Q:71:LYS:HE2	1.94	0.50
1:A:1144:G:H5''	1:A:1145:A:OP2	2.11	0.50
1:A:1172:C:H2'	1:A:1173:U:C6	2.46	0.50
1:A:1279:G:O2'	1:A:1281:C:OP2	2.26	0.50
1:A:165:G:N2	1:A:166:U:O2	2.44	0.50
1:A:8:A:N6	4:D:206:LYS:HB3	2.27	0.50
1:A:620:C:C6	4:D:132:ILE:HD13	2.46	0.50
5:E:100:SER:O	5:E:101:GLU:C	2.49	0.50
10:J:19:ASP:HA	10:J:22:THR:HB	1.92	0.50
10:J:41:PRO:O	10:J:42:LEU:HB2	2.11	0.50
12:L:3:THR:O	12:L:6:GLN:N	2.44	0.50
13:M:4:ILE:HA	13:M:57:ARG:CZ	2.42	0.50
1:A:1028:C:C6	1:A:1034:G:N2	2.80	0.50
1:A:1300:G:C6	1:A:1335:U:C6	2.98	0.50
1:A:243:A:C2	1:A:246:A:C8	2.99	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:756:C:C4	1:A:757:U:C5	2.99	0.50
1:A:775:G:C2'	1:A:776:G:H5'	2.41	0.50
1:A:844:G:H2'	1:A:844:G:N3	2.27	0.50
21:U:12:PHE:N	21:U:12:PHE:CD1	2.78	0.50
1:A:68:G:C6	1:A:69:G:H1'	2.46	0.50
1:A:734:G:C6	1:A:735:C:C4	2.99	0.50
2:B:117:LEU:HB3	2:B:141:LEU:HD11	1.92	0.50
8:H:126:ILE:N	8:H:126:ILE:CD1	2.73	0.50
12:L:80:ILE:HD12	12:L:97:THR:CG2	2.41	0.50
14:N:51:LEU:O	14:N:53:ARG:N	2.44	0.50
1:A:666:G:C5	1:A:741:G:C6	3.00	0.50
1:A:96:U:HO2'	1:A:97:G:P	2.35	0.50
2:B:130:THR:HB	2:B:132:LYS:HB3	1.94	0.50
2:B:163:VAL:HG23	2:B:185:ALA:HB2	1.93	0.50
14:N:21:PHE:CD2	14:N:25:ALA:HB2	2.45	0.50
17:Q:50:ASN:O	17:Q:52:GLU:N	2.44	0.50
17:Q:12:VAL:HG21	17:Q:54:GLY:O	2.11	0.50
20:T:24:ARG:O	20:T:27:MET:HG3	2.12	0.50
1:A:1391:U:H2'	1:A:1392:G:C8	2.46	0.50
3:C:174:PRO:O	3:C:176:HIS:N	2.45	0.50
12:L:25:GLU:CD	12:L:27:CYS:SG	2.90	0.50
1:A:135:C:O2	16:P:1:MET:HB2	2.10	0.50
17:Q:8:LEU:HB2	17:Q:61:ILE:HG21	1.90	0.50
18:R:59:ILE:HG22	18:R:63:ARG:HD2	1.93	0.50
1:A:1360:A:C2	1:A:1361:G:H1'	2.47	0.50
1:A:324:G:N2	1:A:327:A:C8	2.80	0.50
1:A:411:A:C6	1:A:429:U:C5	3.00	0.50
1:A:644:U:C2	1:A:645:G:C8	2.99	0.50
1:A:784:A:H2'	1:A:785:G:C8	2.47	0.50
20:T:58:VAL:HG13	20:T:72:ALA:CB	2.42	0.50
21:U:32:VAL:O	21:U:32:VAL:HG12	2.11	0.50
1:A:1163:A:C2	1:A:1174:G:C2	3.00	0.50
1:A:563:A:N7	1:A:567:G:H1'	2.26	0.50
1:A:582:C:N3	1:A:760:G:C6	2.80	0.50
7:G:90:GLU:OE1	7:G:90:GLU:N	2.44	0.50
12:L:44:LYS:HB2	12:L:45:PRO:HD3	1.94	0.50
16:P:52:LEU:HD21	16:P:57:ILE:CD1	2.41	0.50
1:A:1213:A:C6	1:A:1215:G:N3	2.80	0.50
1:A:515:G:H2'	1:A:516:U:O4'	2.11	0.50
1:A:774:G:C5	1:A:775:G:C8	3.00	0.50
1:A:840:C:N3	1:A:842:U:H4'	2.26	0.50
2:B:123:ASP:O	2:B:124:GLY:O	2.29	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:82:LEU:O	11:K:82:LEU:HD23	2.12	0.50
1:A:1206:G:C6	1:A:1207:G:C5	3.01	0.49
1:A:162:A:H2'	1:A:163:C:O4'	2.11	0.49
3:C:64:ILE:HG22	3:C:97:VAL:HG23	1.94	0.49
5:E:38:VAL:HG12	5:E:39:VAL:N	2.27	0.49
9:I:28:ILE:HB	9:I:35:LEU:HB2	1.92	0.49
17:Q:69:LYS:O	17:Q:70:THR:CB	2.59	0.49
1:A:206:C:H2'	1:A:207:C:C5'	2.42	0.49
2:B:119:THR:O	2:B:120:GLN:HB3	2.12	0.49
1:A:8:A:N6	4:D:54:GLN:OE1	2.45	0.49
12:L:3:THR:O	12:L:4:VAL:C	2.50	0.49
13:M:3:ARG:C	13:M:4:ILE:HG12	2.32	0.49
1:A:1365:G:H2'	1:A:1366:C:O4'	2.13	0.49
1:A:182:A:C5	1:A:184:G:N7	2.81	0.49
1:A:321:A:C8	1:A:328:C:C2	3.00	0.49
1:A:33:A:C2	1:A:34:C:C2	3.00	0.49
2:B:35:ARG:O	2:B:37:LYS:N	2.45	0.49
2:B:96:TRP:CE3	2:B:97:LEU:O	2.65	0.49
4:D:22:LYS:O	4:D:24:GLY:N	2.46	0.49
9:I:13:LYS:O	9:I:14:SER:HB3	2.12	0.49
1:A:1096:C:C2	1:A:1097:C:C5	3.01	0.49
1:A:949:A:C2	1:A:1233:G:C4	3.00	0.49
1:A:448:A:C4	1:A:487:A:C2	3.01	0.49
1:A:558:G:P	23:A:1730:HOH:O	2.65	0.49
1:A:811:C:C5	1:A:812:G:C6	3.00	0.49
1:A:1190:G:H5'	3:C:176:HIS:CE1	2.46	0.49
1:A:1279:G:H4'	1:A:1280:A:OP1	2.12	0.49
3:C:42:TYR:CZ	3:C:90:VAL:HG21	2.47	0.49
7:G:60:GLU:HA	7:G:63:GLU:HB3	1.94	0.49
9:I:12:ARG:HG3	9:I:12:ARG:O	2.13	0.49
17:Q:13:VAL:HG12	17:Q:22:VAL:HG13	1.94	0.49
1:A:1221:G:O3'	19:S:77:THR:HG21	2.11	0.49
1:A:1219:A:N6	1:A:1220:G:O6	2.46	0.49
1:A:203:G:N2	1:A:215:C:C2	2.80	0.49
6:F:38:ARG:HB3	6:F:97:THR:HG23	1.95	0.49
8:H:52:GLU:O	8:H:58:GLU:N	2.46	0.49
10:J:40:ILE:HG22	10:J:42:LEU:HG	1.94	0.49
18:R:22:ASP:OD1	18:R:23:TYR:N	2.45	0.49
1:A:1211:U:O4'	1:A:1213:A:C2	2.65	0.49
1:A:1222:G:OP2	1:A:1322:C:N4	2.46	0.49
1:A:154:U:C2'	1:A:155:A:H5'	2.42	0.49
1:A:429:U:H4'	1:A:430:A:OP1	2.11	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:572:A:H5'	1:A:573:A:P	2.53	0.49
1:A:992:U:C6	1:A:1043:G:N7	2.81	0.49
2:B:190:ASN:OD1	2:B:191:SER:N	2.45	0.49
4:D:192:SER:O	4:D:193:ALA:HB3	2.13	0.49
8:H:126:ILE:N	8:H:126:ILE:HD12	2.27	0.49
1:A:972:C:H4'	10:J:59:LYS:CG	2.43	0.49
21:U:35:ARG:NH2	23:U:101:HOH:O	2.44	0.49
21:U:9:ASN:N	21:U:12:PHE:HE2	2.11	0.49
1:A:158:G:C6	1:A:164:G:C6	3.00	0.49
1:A:246:A:C4	1:A:279:A:C6	3.00	0.49
1:A:748:G:H2'	1:A:749:A:C8	2.47	0.49
9:I:25:ASN:O	9:I:27:LYS:N	2.45	0.49
10:J:15:HIS:HB3	10:J:70:HIS:CD2	2.47	0.49
17:Q:46:VAL:HG22	17:Q:61:ILE:HD11	1.94	0.49
1:A:1002:G:C5	1:A:1003:G:C8	3.01	0.49
1:A:130:A:O2'	1:A:131:A:O5'	2.31	0.49
1:A:355:C:C4	1:A:356:A:N7	2.80	0.49
1:A:451:A:H61	1:A:481:G:H5'	1.77	0.49
11:K:126:LYS:O	11:K:127:ARG:HB2	2.13	0.49
11:K:65:VAL:O	11:K:68:GLU:HB2	2.12	0.49
15:O:19:ALA:O	15:O:20:ASN:CB	2.61	0.49
19:S:80:TYR:O	19:S:81:ARG:HB2	2.13	0.49
1:A:1014:A:H5''	19:S:14:HIS:CD2	2.47	0.49
1:A:1055:A:C6	1:A:1206:G:C5	3.01	0.49
1:A:577:G:C2	1:A:578:C:C6	3.01	0.49
1:A:671:G:O2'	1:A:672:U:H5'	2.13	0.49
2:B:185:ALA:O	2:B:200:ILE:HB	2.13	0.49
4:D:145:ILE:CG2	4:D:150:LYS:HA	2.43	0.49
6:F:8:PHE:CE1	6:F:60:VAL:HB	2.48	0.49
8:H:13:ARG:HD3	8:H:27:MET:HB3	1.94	0.49
9:I:127:PHE:C	9:I:127:PHE:CD1	2.86	0.49
1:A:1092:A:N1	1:A:1183:U:O2	2.46	0.48
1:A:1215:G:C6	1:A:1216:A:C5	3.00	0.48
1:A:454:G:N2	1:A:479:U:O2	2.44	0.48
1:A:755:G:C2	1:A:756:C:C5	3.01	0.48
1:A:977:A:N3	1:A:977:A:H3'	2.28	0.48
10:J:6:ILE:HD11	10:J:79:PRO:HA	1.95	0.48
14:N:36:ALA:HB2	14:N:42:TRP:CH2	2.47	0.48
1:A:1157:A:H4'	1:A:1158:C:O5'	2.13	0.48
1:A:295:C:C4	1:A:296:U:C5	3.00	0.48
1:A:31:G:O4'	1:A:306:A:C2	2.66	0.48
1:A:806:C:O2'	1:A:807:A:H5'	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:84:U:O2'	1:A:85:U:H5'	2.13	0.48
6:F:37:HIS:O	6:F:38:ARG:HB3	2.13	0.48
21:U:11:PRO:O	21:U:12:PHE:CB	2.62	0.48
1:A:1160:G:O2'	1:A:1161:C:P	2.71	0.48
1:A:198:G:O2'	1:A:199:A:H5'	2.12	0.48
1:A:254:G:H4'	17:Q:20:SER:HB2	1.96	0.48
1:A:525:C:N4	1:A:526:C:N4	2.61	0.48
1:A:992:U:O4'	1:A:993:G:N2	2.46	0.48
2:B:152:LYS:HG3	2:B:153:ASP:N	2.28	0.48
6:F:99:ALA:O	6:F:100:SER:CB	2.61	0.48
6:F:38:ARG:CG	6:F:63:ASN:HB2	2.43	0.48
10:J:57:VAL:HG22	10:J:58:ASN:H	1.78	0.48
19:S:40:ILE:HA	19:S:44:MET:SD	2.53	0.48
21:U:10:GLU:N	21:U:12:PHE:CE2	2.81	0.48
1:A:409:U:OP1	4:D:24:GLY:HA3	2.12	0.48
4:D:148:LYS:H	4:D:148:LYS:CD	2.26	0.48
4:D:90:LEU:CD2	4:D:200:ILE:HD11	2.43	0.48
6:F:93:LYS:HG2	6:F:93:LYS:O	2.13	0.48
7:G:78:ARG:O	7:G:79:ARG:HB2	2.13	0.48
12:L:61:PHE:N	12:L:61:PHE:CD1	2.82	0.48
13:M:79:ARG:O	13:M:83:LEU:HD23	2.13	0.48
1:A:1144:G:C2	1:A:1145:A:C2	3.01	0.48
1:A:1302:C:C4	13:M:17:ILE:CD1	2.97	0.48
1:A:209:U:H2'	1:A:209:U:O2	2.13	0.48
1:A:291:U:H2'	1:A:291:U:O2	2.14	0.48
1:A:643:C:H5'	8:H:32:LEU:HD13	1.95	0.48
1:A:690:G:H2'	1:A:691:G:O4'	2.13	0.48
1:A:734:G:C2	1:A:735:C:C6	3.02	0.48
1:A:945:G:H2'	1:A:945:G:N3	2.29	0.48
1:A:945:G:C2	1:A:946:A:C8	3.00	0.48
9:I:51:PRO:HB3	9:I:84:THR:HG23	1.95	0.48
16:P:36:VAL:O	16:P:36:VAL:HG13	2.13	0.48
17:Q:14:SER:C	17:Q:17:MET:HE1	2.33	0.48
17:Q:52:GLU:HG2	17:Q:53:CYS:SG	2.53	0.48
1:A:1000:A:C2	1:A:1041:G:N2	2.82	0.48
1:A:950:U:H2'	1:A:951:G:C8	2.48	0.48
1:A:976:G:C2	1:A:1363:A:C2	3.02	0.48
9:I:50:GLN:N	9:I:51:PRO:HD2	2.29	0.48
13:M:58:ASP:OD1	13:M:58:ASP:C	2.51	0.48
1:A:1003:G:C2	1:A:1038:C:N3	2.82	0.48
1:A:1422:G:C2	1:A:1423:G:C8	3.01	0.48
1:A:1533:C:H4'	1:A:1534:A:OP1	2.14	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:206:C:H2'	1:A:207:C:C4'	2.44	0.48
1:A:350:G:C6	1:A:351:G:C6	3.02	0.48
1:A:485:U:O2	1:A:485:U:O4'	2.32	0.48
1:A:73:C:HO2'	1:A:74:A:C5'	2.25	0.48
1:A:811:C:H4'	1:A:900:A:N6	2.28	0.48
1:A:1379:G:N7	7:G:2:PRO:HB2	2.28	0.48
7:G:42:ILE:HG21	7:G:116:MET:HG3	1.95	0.48
7:G:4:ARG:HG3	7:G:5:ARG:N	2.28	0.48
8:H:96:MET:HB2	8:H:99:LEU:O	2.13	0.48
11:K:45:ALA:HB3	11:K:70:CYS:HB2	1.96	0.48
13:M:11:ASP:O	13:M:12:HIS:HB2	2.14	0.48
21:U:12:PHE:CD1	21:U:13:ASP:N	2.82	0.48
1:A:1066:C:C4	1:A:1067:A:C6	3.02	0.48
1:A:145:G:C2	1:A:146:G:C8	3.01	0.48
1:A:754:C:OP1	15:O:72:ARG:NH2	2.47	0.48
1:A:803:G:C5	1:A:804:U:C4	3.02	0.48
4:D:173:VAL:HG13	4:D:174:ASP:N	2.28	0.48
6:F:86:ARG:HH11	6:F:86:ARG:HG2	1.78	0.48
10:J:18:ILE:HG23	10:J:19:ASP:N	2.29	0.48
10:J:52:LEU:HB2	14:N:81:ARG:HD2	1.94	0.48
1:A:1490:U:H2'	1:A:1491:G:C8	2.48	0.48
1:A:240:G:H4'	1:A:240:G:OP1	2.14	0.48
1:A:649:A:H2'	1:A:650:G:O4'	2.14	0.48
1:A:735:C:H2'	1:A:736:C:C6	2.49	0.48
3:C:153:VAL:CG2	3:C:157:LEU:HD21	2.44	0.48
6:F:14:GLN:C	6:F:16:GLU:H	2.16	0.48
9:I:129:LYS:O	9:I:130:ARG:CD	2.61	0.48
11:K:23:ILE:HG22	11:K:32:VAL:HG22	1.95	0.48
12:L:92:GLY:O	12:L:93:VAL:C	2.51	0.48
18:R:25:ASP:C	18:R:27:ALA:N	2.65	0.48
19:S:4:SER:O	19:S:5:LEU:HB2	2.12	0.48
19:S:67:VAL:HG12	19:S:67:VAL:O	2.13	0.48
1:A:1295:U:H2'	1:A:1296:C:C6	2.49	0.48
1:A:463:U:H3'	1:A:464:U:C6	2.48	0.48
2:B:164:ILE:HG23	2:B:165:ASP:N	2.29	0.48
2:B:199:VAL:C	2:B:200:ILE:HD12	2.33	0.48
3:C:155:GLY:O	3:C:156:ARG:C	2.53	0.48
3:C:172:ARG:NH1	3:C:174:PRO:HG3	2.29	0.48
4:D:192:SER:HB2	4:D:195:ILE:CG1	2.44	0.48
19:S:50:ALA:HB1	19:S:57:HIS:HB3	1.95	0.48
20:T:51:PHE:CD2	20:T:51:PHE:C	2.87	0.48
20:T:65:GLY:CA	20:T:68:HIS:CE1	2.97	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:216:U:H2'	1:A:217:C:C6	2.49	0.47
1:A:123:U:O2'	1:A:290:C:H1'	2.14	0.47
1:A:373:A:N3	1:A:374:A:C8	2.82	0.47
3:C:30:ALA:HB1	14:N:65:ARG:NH2	2.29	0.47
4:D:26:ARG:HG3	4:D:27:ALA:N	2.28	0.47
5:E:72:ILE:HD13	5:E:145:GLU:HG3	1.96	0.47
11:K:112:ASP:OD1	11:K:114:THR:HG23	2.14	0.47
12:L:55:VAL:HG12	12:L:57:LEU:HD23	1.96	0.47
20:T:83:ILE:HD12	20:T:84:ASN:N	2.29	0.47
1:A:104:G:C2	1:A:105:G:C8	3.02	0.47
1:A:1117:A:O2'	9:I:108:ALA:HB2	2.15	0.47
1:A:1491:G:C6	1:A:1492:A:C6	3.01	0.47
1:A:211:G:O2'	1:A:212:G:C4'	2.62	0.47
1:A:64:G:C2	1:A:67:C:N4	2.82	0.47
1:A:826:C:H2'	1:A:827:U:C6	2.49	0.47
2:B:211:THR:HA	2:B:214:LEU:HB2	1.95	0.47
4:D:145:ILE:N	4:D:145:ILE:HD12	2.29	0.47
4:D:20:PHE:CD1	4:D:20:PHE:N	2.81	0.47
7:G:26:PHE:HB2	7:G:101:MET:SD	2.54	0.47
7:G:8:GLY:O	7:G:9:GLN:CB	2.62	0.47
7:G:92:ARG:HB3	7:G:93:PRO:HD2	1.97	0.47
1:A:1125:U:C6	10:J:40:ILE:HD13	2.48	0.47
11:K:20:VAL:O	11:K:35:THR:HG22	2.14	0.47
13:M:54:ASP:HA	13:M:57:ARG:CB	2.44	0.47
15:O:27:VAL:HG13	15:O:31:LEU:CD1	2.44	0.47
15:O:56:LEU:O	15:O:59:MET:HB2	2.13	0.47
1:A:1002:G:H2'	1:A:1003:G:O4'	2.14	0.47
1:A:1147:C:O2	9:I:18:ARG:NH2	2.47	0.47
1:A:1166:G:O2'	1:A:1169:A:N6	2.46	0.47
1:A:1288:A:O2'	1:A:1352:C:O3'	2.32	0.47
1:A:174:A:C2	1:A:175:C:H1'	2.49	0.47
1:A:819:A:H4'	1:A:820:U:OP2	2.15	0.47
5:E:137:VAL:O	5:E:138:ARG:HB3	2.09	0.47
6:F:66:ALA:HB1	6:F:67:PRO:HD2	1.96	0.47
10:J:88:MET:O	10:J:89:ARG:HB2	2.14	0.47
1:A:1028:C:OP2	1:A:1028:C:C6	2.67	0.47
1:A:1260:G:OP1	1:A:1284:C:O2'	2.21	0.47
1:A:369:G:OP2	1:A:388:G:N2	2.47	0.47
1:A:302:G:O2'	1:A:556:C:H5''	2.15	0.47
5:E:109:GLY:O	5:E:110:ALA:HB3	2.14	0.47
5:E:149:SER:OG	5:E:152:MET:HG3	2.15	0.47
8:H:49:PHE:CD1	8:H:49:PHE:C	2.88	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:63:ALA:CB	11:K:92:GLY:HA2	2.44	0.47
11:K:97:ILE:HG13	11:K:98:ARG:N	2.29	0.47
1:A:1317:C:O2'	14:N:49:GLN:HG2	2.14	0.47
16:P:3:THR:HG22	16:P:4:ILE:N	2.29	0.47
17:Q:11:ARG:HA	17:Q:58:VAL:HA	1.97	0.47
17:Q:4:LYS:HG2	17:Q:5:ILE:N	2.28	0.47
1:A:263:A:P	20:T:74:ARG:NH1	2.88	0.47
20:T:78:ASN:O	20:T:82:GLN:HG2	2.14	0.47
1:A:1002:G:C6	1:A:1003:G:C5	3.03	0.47
1:A:146:G:N2	1:A:147:G:H1'	2.29	0.47
1:A:255:G:P	17:Q:71:LYS:HZ2	2.38	0.47
1:A:728:A:C6	1:A:729:A:C6	3.02	0.47
1:A:756:C:C2	1:A:757:U:C6	3.03	0.47
1:A:841:C:H2'	1:A:843:U:O4'	2.14	0.47
2:B:96:TRP:CE2	2:B:172:ALA:HB2	2.50	0.47
6:F:15:SER:CB	6:F:44:ARG:NH1	2.78	0.47
11:K:87:LYS:HA	11:K:114:THR:HG22	1.97	0.47
12:L:38:TYR:HB2	12:L:52:VAL:CG1	2.43	0.47
17:Q:38:ILE:CG2	17:Q:39:LYS:N	2.78	0.47
19:S:75:ALA:N	19:S:76:PRO:HD3	2.29	0.47
21:U:51:SER:O	21:U:52:ALA:C	2.51	0.47
1:A:1255:G:N1	1:A:1279:G:C8	2.82	0.47
1:A:1298:U:O2	1:A:1298:U:C2'	2.62	0.47
1:A:1299:A:O2'	1:A:1301:U:O4'	2.23	0.47
1:A:888:G:H4'	1:A:1488:G:O2'	2.14	0.47
1:A:328:C:H4'	1:A:329:A:H5''	1.97	0.47
1:A:483:C:H2'	1:A:484:G:C8	2.50	0.47
1:A:734:G:N3	1:A:735:C:C6	2.83	0.47
1:A:829:G:C6	1:A:858:G:N2	2.82	0.47
2:B:128:LYS:O	2:B:129:LEU:HB2	2.14	0.47
6:F:88:MET:CE	18:R:64:TYR:CD2	2.97	0.47
7:G:151:PHE:O	7:G:152:ALA:CB	2.62	0.47
11:K:85:MET:HA	11:K:111:THR:O	2.14	0.47
12:L:29:GLN:O	12:L:30:LYS:HG2	2.15	0.47
12:L:24:LEU:HB2	12:L:59:ASN:OD1	2.14	0.47
13:M:40:ALA:O	13:M:41:GLU:C	2.52	0.47
13:M:54:ASP:HA	13:M:57:ARG:HB3	1.96	0.47
14:N:41:ARG:NH2	14:N:43:ASN:OD1	2.47	0.47
17:Q:27:ARG:CG	17:Q:40:ARG:HB3	2.45	0.47
1:A:1027:C:N4	1:A:1034:G:N1	2.62	0.47
1:A:269:C:H2'	1:A:270:A:C8	2.49	0.47
1:A:496:A:C2	1:A:497:G:C5	3.02	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:44:TRP:CE3	11:K:44:TRP:O	2.68	0.47
16:P:79:ASN:O	16:P:80:LYS:HB2	2.15	0.47
1:A:1266:G:N1	1:A:1270:G:C6	2.83	0.47
1:A:1397:C:O2'	1:A:1398:A:OP1	2.29	0.47
1:A:622:A:H5''	1:A:623:C:OP2	2.15	0.47
1:A:801:U:H2'	1:A:802:A:C8	2.49	0.47
1:A:851:G:C2	1:A:852:G:C8	3.03	0.47
7:G:113:ASP:HB2	7:G:119:ARG:HG3	1.96	0.47
10:J:65:TYR:HB3	14:N:96:LEU:HD11	1.96	0.47
12:L:51:LYS:HD2	12:L:51:LYS:N	2.30	0.47
1:A:309:A:H5''	16:P:29:ASN:O	2.15	0.47
1:A:1512:U:O2'	1:A:1513:A:H5'	2.14	0.47
1:A:412:A:HO2'	1:A:413:G:C5'	2.20	0.47
1:A:818:G:O2'	1:A:819:A:H5'	2.12	0.47
1:A:861:G:C5	1:A:862:C:C5	3.03	0.47
2:B:134:ALA:O	2:B:138:THR:HG23	2.15	0.47
5:E:104:GLY:HA3	5:E:122:ASN:HA	1.97	0.47
6:F:59:TYR:HE2	18:R:67:LEU:HD22	1.80	0.47
8:H:78:VAL:HG12	8:H:79:SER:N	2.30	0.47
10:J:84:VAL:O	10:J:88:MET:HB2	2.15	0.47
12:L:25:GLU:C	12:L:27:CYS:N	2.65	0.47
13:M:63:PHE:O	13:M:65:VAL:HG13	2.15	0.47
16:P:52:LEU:HD23	16:P:53:ASP:N	2.29	0.47
1:A:1410:A:H2'	1:A:1411:C:C6	2.49	0.47
1:A:1418:A:C2	1:A:1483:A:C2	3.03	0.47
1:A:403:C:O2'	1:A:404:G:H5'	2.15	0.47
1:A:517:G:C5'	1:A:519:C:C2	2.98	0.47
1:A:790:A:C6	1:A:791:G:C6	3.02	0.47
1:A:970:C:OP1	10:J:59:LYS:NZ	2.40	0.47
2:B:20:THR:O	2:B:21:ARG:NH1	2.48	0.47
9:I:28:ILE:CG2	9:I:35:LEU:HB2	2.45	0.47
9:I:84:THR:HA	9:I:87:LEU:HD12	1.96	0.47
1:A:1159:U:C4	1:A:1182:G:C5	3.03	0.47
1:A:976:G:N2	1:A:1363:A:C2	2.83	0.47
1:A:632:U:O2	1:A:632:U:C2'	2.62	0.47
1:A:679:C:C2	1:A:712:A:C2	3.03	0.47
1:A:734:G:C4	1:A:735:C:C5	3.03	0.47
1:A:78:A:N6	1:A:79:G:C6	2.84	0.47
4:D:37:ALA:HA	4:D:42:GLY:HA3	1.97	0.47
6:F:38:ARG:HG3	6:F:62:MET:O	2.14	0.47
9:I:57:MET:O	9:I:60:LYS:N	2.47	0.47
9:I:30:ILE:HA	9:I:65:ILE:O	2.15	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:35:GLN:O	10:J:36:VAL:CB	2.62	0.47
12:L:61:PHE:HD1	12:L:61:PHE:N	2.13	0.47
19:S:15:LEU:HD13	19:S:33:THR:HG21	1.96	0.47
19:S:6:LYS:HB2	19:S:7:LYS:HE3	1.97	0.47
1:A:1394:A:C5	1:A:1501:C:H4'	2.50	0.46
1:A:919:A:C2	1:A:920:U:C5	3.03	0.46
12:L:74:LEU:HD21	12:L:104:CYS:SG	2.55	0.46
12:L:116:LYS:O	12:L:117:TYR:CB	2.62	0.46
20:T:30:THR:O	20:T:34:LYS:HG2	2.14	0.46
1:A:1105:A:C2	1:A:1106:G:C5	3.03	0.46
1:A:1259:C:N4	1:A:1260:G:C4	2.83	0.46
1:A:182:A:C8	1:A:184:G:N7	2.83	0.46
6:F:15:SER:HB2	6:F:44:ARG:NH1	2.30	0.46
12:L:80:ILE:HD12	12:L:97:THR:HG22	1.97	0.46
14:N:3:LYS:HD3	14:N:6:MET:HG2	1.96	0.46
15:O:67:LEU:HD23	15:O:78:TYR:CE2	2.49	0.46
21:U:40:LYS:HB3	21:U:41:PRO:HD3	1.98	0.46
1:A:1010:U:C2	1:A:1020:G:N1	2.83	0.46
1:A:1003:G:N2	1:A:1038:C:C2	2.83	0.46
1:A:1126:U:C6	1:A:1281:C:C4	3.03	0.46
1:A:445:G:C2	1:A:446:G:C8	3.04	0.46
1:A:496:A:H2'	1:A:497:G:N7	2.29	0.46
4:D:26:ARG:HD2	4:D:31:LYS:CE	2.46	0.46
9:I:26:GLY:CA	9:I:61:LEU:O	2.63	0.46
16:P:78:VAL:O	16:P:80:LYS:N	2.47	0.46
21:U:20:LYS:HZ3	21:U:20:LYS:HA	1.79	0.46
1:A:109:A:C6	1:A:327:A:C6	3.03	0.46
1:A:1149:C:C4	1:A:1150:A:C6	3.03	0.46
1:A:1342:C:H2'	1:A:1343:G:C8	2.50	0.46
1:A:941:G:C2	1:A:1343:G:C2	3.03	0.46
1:A:1533:C:H4'	1:A:1533:C:OP1	2.15	0.46
1:A:439:U:H4'	4:D:121:LYS:CD	2.45	0.46
1:A:683:G:H2'	1:A:684:U:O4'	2.15	0.46
1:A:666:G:C5	1:A:741:G:N1	2.84	0.46
1:A:756:C:N3	1:A:757:U:C6	2.83	0.46
1:A:775:G:O2'	1:A:776:G:H5'	2.16	0.46
2:B:221:VAL:O	2:B:223:GLU:N	2.48	0.46
9:I:81:HIS:O	9:I:85:ARG:HB2	2.16	0.46
11:K:34:ILE:HG13	11:K:70:CYS:SG	2.54	0.46
11:K:77:TYR:CD1	11:K:77:TYR:N	2.83	0.46
13:M:43:VAL:HG23	13:M:43:VAL:O	2.16	0.46
16:P:6:LEU:CD1	16:P:71:VAL:HG23	2.46	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:R:33:ILE:HA	18:R:40:VAL:HG23	1.96	0.46
1:A:503:C:H2'	1:A:504:C:C6	2.51	0.46
1:A:598:U:H4'	8:H:86:TYR:CD1	2.51	0.46
2:B:30:PHE:CD1	2:B:30:PHE:N	2.82	0.46
4:D:119:SER:O	4:D:131:ASN:OD1	2.34	0.46
8:H:30:SER:OG	8:H:33:LYS:HG3	2.15	0.46
9:I:114:LYS:HG3	9:I:120:LYS:HA	1.97	0.46
10:J:65:TYR:CB	14:N:96:LEU:HD11	2.46	0.46
15:O:27:VAL:HG13	15:O:31:LEU:HD11	1.97	0.46
16:P:1:MET:HG2	16:P:2:VAL:N	2.31	0.46
20:T:43:ASP:HB3	20:T:46:ALA:HB3	1.96	0.46
1:A:1133:G:H2'	1:A:1133:G:N3	2.30	0.46
1:A:1151:A:C2	1:A:1152:A:C4	3.04	0.46
1:A:1259:C:O2'	1:A:1283:U:O2	2.30	0.46
1:A:178:C:H2'	1:A:179:A:O4'	2.15	0.46
1:A:754:C:H3'	1:A:754:C:O2	2.15	0.46
2:B:85:LEU:CG	2:B:85:LEU:O	2.64	0.46
3:C:156:ARG:HD3	3:C:160:ALA:O	2.15	0.46
5:E:155:ALA:HB1	8:H:66:PHE:CE2	2.51	0.46
11:K:40:ASN:O	11:K:41:ALA:HB3	2.15	0.46
1:A:186:C:O4'	20:T:76:LYS:HD2	2.15	0.46
1:A:21:G:H2'	1:A:22:G:C8	2.51	0.46
1:A:73:C:O2'	1:A:74:A:P	2.73	0.46
1:A:821:G:H2'	1:A:822:U:H6	1.80	0.46
2:B:17:GLY:O	2:B:40:ILE:HA	2.15	0.46
2:B:60:ILE:O	2:B:65:GLY:N	2.48	0.46
4:D:64:ILE:HG22	4:D:65:TYR:CD1	2.50	0.46
5:E:137:VAL:HA	5:E:140:THR:OG1	2.15	0.46
9:I:28:ILE:HG21	9:I:35:LEU:HB2	1.97	0.46
11:K:35:THR:OG1	11:K:40:ASN:N	2.48	0.46
1:A:1491:G:H5''	12:L:44:LYS:HD2	1.98	0.46
12:L:77:HIS:O	12:L:78:SER:OG	2.33	0.46
13:M:106:ALA:O	13:M:110:LYS:HB3	2.16	0.46
11:K:113:VAL:HB	18:R:73:ARG:NH2	2.30	0.46
1:A:1118:U:H1'	1:A:1179:A:C5	2.51	0.46
1:A:1323:G:H2'	1:A:1324:A:O4'	2.16	0.46
1:A:157:U:O2'	1:A:158:G:H5'	2.16	0.46
1:A:181:A:C5	1:A:194:C:C5	3.04	0.46
1:A:216:U:H5''	1:A:464:U:H4'	1.98	0.46
1:A:296:U:C2	1:A:297:G:C8	3.03	0.46
1:A:518:C:H4'	1:A:519:C:O5'	2.15	0.46
1:A:597:G:C8	1:A:598:U:C5	3.03	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:692:U:H1'	1:A:695:A:N7	2.30	0.46
2:B:99:GLY:HA2	2:B:102:THR:HG22	1.98	0.46
11:K:27:PHE:CZ	11:K:89:PRO:HG2	2.51	0.46
16:P:19:VAL:HG12	16:P:37:GLY:C	2.37	0.46
17:Q:51:ASN:O	17:Q:51:ASN:ND2	2.49	0.46
19:S:55:ARG:CZ	19:S:79:THR:CG2	2.93	0.46
1:A:1042:A:H2'	1:A:1043:G:C1'	2.46	0.46
1:A:1089:G:C4	1:A:1090:U:C6	3.04	0.46
1:A:1115:U:H2'	1:A:1116:U:H6	1.80	0.46
1:A:110:C:C4	1:A:111:G:C5	3.04	0.46
1:A:1225:A:N3	1:A:1225:A:C2'	2.79	0.46
1:A:951:G:C2	1:A:1231:G:C2	3.04	0.46
1:A:1239:A:H4'	1:A:1240:U:H5''	1.96	0.46
1:A:137:U:H1'	1:A:227:G:N2	2.29	0.46
1:A:158:G:C6	1:A:159:G:C5	3.04	0.46
1:A:212:G:C2	1:A:213:G:C8	3.04	0.46
1:A:295:C:C2	1:A:296:U:C6	3.04	0.46
1:A:585:G:C6	1:A:586:C:C4	3.04	0.46
1:A:6:G:H2'	5:E:124:LEU:CD2	2.46	0.46
1:A:583:A:C2	1:A:759:A:C5	3.04	0.46
1:A:940:C:H2'	1:A:941:G:C8	2.51	0.46
4:D:166:GLU:O	4:D:167:LYS:HB2	2.14	0.46
12:L:110:ARG:NE	12:L:117:TYR:CE2	2.84	0.46
15:O:10:LYS:O	15:O:14:GLU:HG3	2.16	0.46
18:R:45:THR:OG1	18:R:45:THR:O	2.33	0.46
21:U:24:GLU:HG3	21:U:28:VAL:HG21	1.96	0.46
1:A:1272:G:N2	1:A:1273:C:H1'	2.31	0.46
1:A:457:G:N2	1:A:476:U:C2	2.84	0.46
1:A:527:G:N1	1:A:528:C:C5	2.84	0.46
1:A:597:G:H2'	1:A:598:U:H5'	1.96	0.46
1:A:772:U:C2'	1:A:773:G:H5'	2.45	0.46
1:A:951:G:C6	1:A:1231:G:C6	3.04	0.46
2:B:67:ILE:HG22	2:B:68:LEU:N	2.31	0.46
2:B:71:GLY:O	2:B:93:ASN:HA	2.16	0.46
1:A:1108:G:H5''	3:C:176:HIS:CD2	2.50	0.46
4:D:102:VAL:HG13	4:D:107:PHE:HB2	1.98	0.46
7:G:11:LYS:O	7:G:12:ILE:C	2.55	0.46
9:I:28:ILE:HG23	9:I:63:LEU:HD11	1.98	0.46
11:K:88:GLY:H	11:K:114:THR:HG22	1.81	0.46
13:M:96:PRO:HA	13:M:109:ARG:HG2	1.97	0.46
17:Q:19:LYS:CD	17:Q:49:GLU:HA	2.46	0.46
20:T:55:GLN:N	20:T:56:PRO:HD2	2.31	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1244:G:C2	1:A:1294:G:C2	3.04	0.45
1:A:1255:G:C6	1:A:1279:G:N7	2.84	0.45
1:A:142:G:C2	1:A:143:A:H1'	2.51	0.45
1:A:729:A:C4	1:A:730:G:C8	3.04	0.45
1:A:755:G:C2	1:A:756:C:C6	3.05	0.45
1:A:774:G:C6	1:A:775:G:C5	3.03	0.45
3:C:22:TRP:CH2	3:C:29:PHE:CE1	3.04	0.45
5:E:103:THR:O	5:E:122:ASN:HA	2.16	0.45
5:E:99:ALA:HB2	5:E:124:LEU:CD1	2.45	0.45
6:F:50:PRO:CD	18:R:74:HIS:HB3	2.46	0.45
12:L:108:LYS:O	12:L:109:ASP:HB2	2.16	0.45
13:M:37:ALA:CB	13:M:56:LEU:HG	2.47	0.45
20:T:69:LYS:HB2	20:T:70:ASN:OD1	2.17	0.45
1:A:1069:C:H2'	1:A:1070:U:O4'	2.16	0.45
1:A:1309:G:C6	1:A:1329:A:N1	2.84	0.45
1:A:255:G:C2	1:A:256:U:C5	3.05	0.45
1:A:537:G:H2'	1:A:538:G:C8	2.51	0.45
2:B:200:ILE:HG22	2:B:200:ILE:O	2.16	0.45
2:B:53:ALA:C	2:B:54:LEU:HD22	2.37	0.45
11:K:23:ILE:HG22	11:K:32:VAL:HG13	1.98	0.45
12:L:75:GLN:O	12:L:76:GLU:C	2.54	0.45
19:S:36:ARG:HG2	19:S:51:VAL:HG13	1.98	0.45
19:S:51:VAL:O	19:S:58:VAL:HG12	2.16	0.45
1:A:1323:G:H4'	1:A:1362:A:C2	2.50	0.45
1:A:890:G:O2'	1:A:891:U:P	2.74	0.45
1:A:938:A:N6	1:A:939:G:C5	2.84	0.45
2:B:60:ILE:HD12	2:B:61:ALA:N	2.31	0.45
2:B:67:ILE:HD13	2:B:160:ALA:HB3	1.99	0.45
5:E:115:LEU:HG	5:E:123:VAL:HG21	1.98	0.45
5:E:82:GLN:OE1	5:E:150:PRO:CD	2.64	0.45
7:G:2:PRO:O	7:G:3:ARG:C	2.54	0.45
17:Q:70:THR:HG22	17:Q:71:LYS:H	1.80	0.45
21:U:14:VAL:O	21:U:16:LEU:HG	2.16	0.45
1:A:1536:C:H2'	1:A:1537:U:O4'	2.16	0.45
1:A:258:G:H2'	1:A:259:G:O4'	2.16	0.45
1:A:510:A:H5''	1:A:511:C:P	2.56	0.45
1:A:577:G:C2	1:A:578:C:C5	3.05	0.45
1:A:731:G:H5'	1:A:766:A:H4'	1.96	0.45
1:A:879:C:H2'	1:A:880:C:O5'	2.16	0.45
1:A:909:A:H2'	1:A:910:C:O4'	2.16	0.45
2:B:87:CYS:O	2:B:89:GLN:N	2.48	0.45
5:E:15:LEU:CD1	5:E:15:LEU:C	2.84	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:F:9:MET:HB2	6:F:85:ILE:HG13	1.98	0.45
7:G:53:ARG:NH2	7:G:122:ASN:OD1	2.44	0.45
10:J:33:GLY:O	10:J:34:ALA:HB2	2.17	0.45
10:J:52:LEU:HD23	10:J:62:ARG:HG3	1.98	0.45
14:N:57:PRO:O	14:N:59:ARG:N	2.49	0.45
15:O:15:PHE:CZ	15:O:85:LEU:HD11	2.51	0.45
1:A:1028:C:O2	1:A:1028:C:H2'	2.16	0.45
1:A:110:C:N4	1:A:111:G:C6	2.84	0.45
1:A:1134:G:C2	1:A:1135:U:H1'	2.51	0.45
1:A:1140:C:O2'	1:A:1141:C:P	2.74	0.45
1:A:1496:C:H2'	1:A:1497:G:O4'	2.17	0.45
1:A:169:C:H2'	1:A:170:U:C6	2.52	0.45
1:A:355:C:H2'	1:A:356:A:O4'	2.17	0.45
1:A:522:C:O2	1:A:522:C:H2'	2.16	0.45
2:B:217:VAL:HG12	2:B:218:ALA:N	2.31	0.45
4:D:187:GLU:N	4:D:190:ASP:OD2	2.50	0.45
4:D:29:ASP:C	4:D:31:LYS:N	2.69	0.45
5:E:96:MET:HB3	5:E:96:MET:HE3	1.71	0.45
7:G:22:LEU:HA	7:G:25:LYS:NZ	2.30	0.45
7:G:70:ARG:HG3	7:G:96:ARG:HG2	1.97	0.45
9:I:49:ARG:NH2	9:I:53:GLU:HA	2.31	0.45
11:K:59:THR:HA	11:K:91:PRO:HB3	1.99	0.45
19:S:79:THR:OG1	19:S:79:THR:O	2.33	0.45
21:U:24:GLU:N	21:U:24:GLU:OE1	2.49	0.45
1:A:320:A:H2'	1:A:321:A:C1'	2.47	0.45
1:A:451:A:OP2	16:P:70:ARG:NH1	2.48	0.45
1:A:543:U:O2'	1:A:544:G:H5'	2.16	0.45
1:A:797:C:O2'	1:A:798:U:H5'	2.17	0.45
1:A:82:G:N2	1:A:88:U:O2	2.50	0.45
2:B:162:PHE:HA	2:B:184:PHE:O	2.17	0.45
3:C:126:ARG:O	3:C:127:ARG:CB	2.64	0.45
3:C:165:THR:OG1	3:C:166:GLU:N	2.47	0.45
3:C:72:ARG:HB3	3:C:75:ILE:HG22	1.99	0.45
6:F:13:ASP:C	6:F:15:SER:H	2.19	0.45
6:F:25:TYR:CD1	6:F:25:TYR:N	2.85	0.45
11:K:72:ASP:O	11:K:73:ALA:HB3	2.15	0.45
1:A:35:G:O2'	12:L:115:SER:O	2.33	0.45
21:U:35:ARG:CG	21:U:36:GLU:N	2.80	0.45
1:A:1151:A:N3	1:A:1152:A:N7	2.65	0.45
1:A:774:G:C4	1:A:775:G:C8	3.04	0.45
1:A:983:A:OP1	14:N:9:ARG:NH2	2.50	0.45
7:G:103:TRP:CE3	7:G:137:LYS:HG2	2.52	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:65:TYR:CD1	8:H:65:TYR:N	2.84	0.45
10:J:34:ALA:O	10:J:78:GLU:HB3	2.17	0.45
1:A:1280:A:C8	10:J:42:LEU:HD23	2.51	0.45
12:L:16:VAL:O	12:L:17:ALA:O	2.35	0.45
14:N:49:GLN:C	14:N:51:LEU:H	2.20	0.45
16:P:67:ILE:HG23	16:P:71:VAL:CG1	2.47	0.45
17:Q:7:THR:HG21	17:Q:60:GLU:OE1	2.17	0.45
17:Q:80:GLU:O	17:Q:81:LYS:HG3	2.17	0.45
1:A:1049:U:H4'	1:A:1050:G:O5'	2.16	0.45
1:A:1108:G:N3	1:A:1108:G:H2'	2.31	0.45
1:A:1181:G:O2'	1:A:1182:G:C8	2.56	0.45
1:A:449:G:H2'	1:A:450:G:C8	2.52	0.45
5:E:121:HIS:O	5:E:122:ASN:HB3	2.16	0.45
5:E:76:LEU:HD12	5:E:76:LEU:H	1.81	0.45
7:G:148:ASN:C	7:G:150:ALA:H	2.20	0.45
7:G:68:ASN:O	7:G:138:ARG:CZ	2.65	0.45
12:L:3:THR:HB	12:L:6:GLN:HG3	1.99	0.45
17:Q:57:ASP:OD1	17:Q:57:ASP:N	2.49	0.45
1:A:131:A:H2'	1:A:132:C:C6	2.52	0.45
1:A:1416:G:N2	1:A:1485:U:H1'	2.31	0.45
1:A:642:A:C5	8:H:107:SER:HA	2.52	0.45
1:A:791:G:C5	1:A:792:A:N7	2.85	0.45
1:A:899:C:OP1	1:A:899:C:H6	1.99	0.45
1:A:993:G:H2'	1:A:995:C:H41	1.81	0.45
3:C:19:ASN:HA	3:C:56:VAL:HG13	1.99	0.45
4:D:27:ALA:O	4:D:31:LYS:NZ	2.50	0.45
4:D:35:GLU:O	4:D:37:ALA:N	2.47	0.45
4:D:59:GLN:HA	4:D:59:GLN:OE1	2.17	0.45
4:D:9:LEU:HG	4:D:32:CYS:SG	2.57	0.45
5:E:101:GLU:OE2	5:E:103:THR:HA	2.17	0.45
6:F:51:ILE:O	6:F:51:ILE:HG12	2.17	0.45
9:I:13:LYS:O	9:I:13:LYS:HG2	2.17	0.45
17:Q:10:GLY:HA3	17:Q:25:ILE:HD13	1.99	0.45
20:T:68:HIS:HB3	20:T:69:LYS:HG3	1.99	0.45
1:A:1074:G:H4'	2:B:103:ASN:HB3	1.98	0.45
1:A:292:G:O2'	1:A:608:A:N6	2.45	0.45
1:A:33:A:H2'	1:A:34:C:H6	1.82	0.45
1:A:477:C:H2'	1:A:478:A:C8	2.52	0.45
1:A:564:C:C4	1:A:565:U:C4	3.05	0.45
1:A:664:G:H2'	1:A:666:G:OP1	2.17	0.45
1:A:794:A:C5	1:A:795:C:C4	3.05	0.45
4:D:116:GLN:HG3	4:D:120:HIS:CE1	2.52	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:183:LYS:HB2	4:D:183:LYS:HE2	1.89	0.45
5:E:15:LEU:HD12	5:E:15:LEU:O	2.17	0.45
9:I:129:LYS:O	9:I:130:ARG:HD2	2.16	0.45
15:O:70:LEU:HD22	15:O:78:TYR:HB2	1.97	0.45
16:P:43:ALA:O	16:P:46:LYS:CG	2.65	0.45
18:R:24:LYS:C	18:R:26:ILE:H	2.20	0.45
1:A:1446:A:N6	1:A:1447:A:H62	2.14	0.44
1:A:268:U:N3	1:A:269:C:C4	2.85	0.44
1:A:374:A:OP1	1:A:452:A:N1	2.50	0.44
1:A:4:U:C2'	1:A:4:U:O2	2.64	0.44
1:A:898:G:O2'	1:A:900:A:N7	2.35	0.44
3:C:121:THR:OG1	3:C:189:ALA:N	2.49	0.44
1:A:401:C:OP2	4:D:70:ARG:CD	2.64	0.44
7:G:66:LEU:HD23	7:G:70:ARG:NE	2.32	0.44
11:K:59:THR:CA	11:K:91:PRO:HB3	2.48	0.44
11:K:84:VAL:HG11	11:K:97:ILE:HG22	1.99	0.44
18:R:34:THR:CG2	18:R:38:LYS:HB2	2.47	0.44
1:A:151:A:H2'	1:A:152:A:O4'	2.18	0.44
1:A:237:G:OP1	17:Q:42:THR:OG1	2.31	0.44
1:A:296:U:C4	1:A:297:G:N7	2.86	0.44
1:A:337:G:H2'	1:A:338:A:C8	2.51	0.44
1:A:493:A:C6	1:A:494:G:N1	2.86	0.44
1:A:571:U:H5'	1:A:819:A:C5	2.52	0.44
1:A:879:C:C2'	1:A:880:C:O5'	2.64	0.44
3:C:83:ASP:O	3:C:85:GLU:N	2.50	0.44
1:A:1072:G:OP1	5:E:62:LYS:NZ	2.50	0.44
5:E:66:LYS:O	5:E:69:ARG:O	2.35	0.44
6:F:3:HIS:O	6:F:92:THR:HA	2.17	0.44
7:G:11:LYS:HD2	7:G:11:LYS:N	2.31	0.44
8:H:53:GLY:C	8:H:54:ASP:CG	2.76	0.44
9:I:49:ARG:C	9:I:49:ARG:HD3	2.37	0.44
1:A:1029:U:O2	1:A:1029:U:H2'	2.16	0.44
1:A:1071:C:H2'	1:A:1072:G:H8	1.80	0.44
1:A:1404:C:H2'	1:A:1405:G:C8	2.51	0.44
1:A:177:G:C6	1:A:178:C:N4	2.85	0.44
1:A:38:G:N2	1:A:397:A:C4	2.84	0.44
1:A:518:C:H2'	1:A:530:G:C8	2.52	0.44
1:A:651:C:N4	1:A:753:A:OP2	2.51	0.44
4:D:38:PRO:HD2	4:D:42:GLY:CA	2.47	0.44
6:F:86:ARG:CG	6:F:86:ARG:NH1	2.75	0.44
8:H:27:MET:HB2	8:H:28:PRO:HD2	2.00	0.44
12:L:64:THR:HG23	12:L:93:VAL:HA	1.99	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:N:61:ARG:O	14:N:62:ASN:CB	2.62	0.44
1:A:1078:U:C5	1:A:1079:G:C5	3.05	0.44
1:A:1084:G:H5'	1:A:1102:A:OP2	2.18	0.44
1:A:1101:A:H4'	1:A:1102:A:O5'	2.17	0.44
1:A:1479:C:C2	1:A:1480:A:C8	3.05	0.44
1:A:517:G:H5'	1:A:519:C:C2	2.51	0.44
1:A:607:A:C2	1:A:608:A:C4	3.05	0.44
1:A:632:U:H3'	1:A:633:G:H5'	1.99	0.44
1:A:866:C:H4'	1:A:919:A:H5'	1.98	0.44
3:C:103:ILE:N	3:C:103:ILE:HD12	2.33	0.44
5:E:104:GLY:O	5:E:105:ILE:CB	2.65	0.44
8:H:78:VAL:N	8:H:126:ILE:O	2.50	0.44
8:H:64:LYS:HB3	8:H:71:VAL:HG21	1.99	0.44
12:L:86:ARG:HD2	12:L:88:LYS:N	2.32	0.44
10:J:67:ILE:HG13	14:N:96:LEU:HD13	1.99	0.44
16:P:29:ASN:OD1	16:P:29:ASN:N	2.50	0.44
21:U:28:VAL:O	21:U:32:VAL:HG23	2.18	0.44
1:A:181:A:N6	1:A:195:A:OP2	2.51	0.44
1:A:39:G:N1	1:A:40:C:C4	2.86	0.44
1:A:444:G:C6	1:A:445:G:N7	2.86	0.44
1:A:468:A:N3	1:A:468:A:O4'	2.50	0.44
1:A:474:G:N1	1:A:475:C:C2	2.85	0.44
1:A:505:G:C6	1:A:535:A:C2	3.05	0.44
1:A:681:A:C2	1:A:710:G:C4	3.05	0.44
3:C:43:LEU:HD21	3:C:68:ILE:HD11	2.00	0.44
4:D:23:SER:CB	4:D:109:ALA:O	2.66	0.44
7:G:25:LYS:O	7:G:29:ILE:HG12	2.17	0.44
9:I:46:MET:O	9:I:49:ARG:HB3	2.18	0.44
9:I:52:LEU:HD13	9:I:57:MET:HG2	1.98	0.44
9:I:57:MET:O	9:I:60:LYS:HB2	2.18	0.44
9:I:87:LEU:C	9:I:89:GLU:H	2.21	0.44
1:A:1302:C:C4	13:M:17:ILE:HD11	2.53	0.44
1:A:1350:A:N1	1:A:1351:U:C2	2.85	0.44
1:A:1450:U:O2'	1:A:1451:U:H2'	2.17	0.44
1:A:1502:A:H5'	1:A:1504:G:N7	2.33	0.44
1:A:40:C:H2'	1:A:41:G:O4'	2.17	0.44
1:A:519:C:H2'	1:A:520:A:O4'	2.18	0.44
1:A:608:A:H2'	1:A:609:A:O4'	2.17	0.44
1:A:731:G:O2'	1:A:732:C:H5'	2.18	0.44
2:B:117:LEU:HD23	2:B:141:LEU:HG	1.99	0.44
1:A:1112:C:N4	3:C:178:LEU:HD23	2.33	0.44
5:E:156:LYS:HD3	8:H:71:VAL:HG22	2.00	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:116:MET:O	7:G:120:LEU:N	2.49	0.44
7:G:55:GLY:O	7:G:56:LYS:O	2.35	0.44
8:H:18:GLN:NE2	8:H:70:ALA:HB1	2.32	0.44
9:I:47:VAL:O	9:I:80:ARG:HG2	2.18	0.44
12:L:99:ARG:HD2	12:L:104:CYS:SG	2.58	0.44
14:N:23:LYS:HG3	14:N:24:ARG:N	2.33	0.44
1:A:1036:A:H2'	1:A:1036:A:N3	2.32	0.44
1:A:1088:G:C4	1:A:1089:G:C8	3.05	0.44
1:A:1141:C:O2'	1:A:1142:G:P	2.76	0.44
1:A:1216:A:OP1	14:N:5:SER:HB2	2.18	0.44
1:A:1346:A:O3'	1:A:1347:G:H4'	2.17	0.44
1:A:216:U:H4'	1:A:464:U:H4'	2.00	0.44
1:A:995:C:N3	1:A:1046:A:O2'	2.46	0.44
4:D:116:GLN:HG3	4:D:120:HIS:ND1	2.33	0.44
5:E:56:VAL:N	5:E:57:PRO:CD	2.80	0.44
9:I:128:SER:O	9:I:129:LYS:C	2.56	0.44
12:L:87:VAL:O	12:L:89:ASP:N	2.51	0.44
20:T:33:LYS:O	20:T:36:TYR:CD2	2.70	0.44
1:A:1244:G:C6	1:A:1245:C:C4	3.06	0.44
1:A:1521:C:N3	1:A:1522:U:C5	2.85	0.44
1:A:1536:C:C5	1:A:1537:U:C5	3.06	0.44
1:A:254:G:C4	1:A:255:G:C8	3.06	0.44
1:A:50:A:H1'	1:A:52:C:O4'	2.18	0.44
1:A:769:G:H4'	1:A:1513:A:H4'	2.00	0.44
11:K:52:PHE:CE1	11:K:62:ALA:HB1	2.52	0.44
16:P:5:ARG:O	16:P:19:VAL:HA	2.17	0.44
18:R:49:ALA:O	18:R:50:LYS:C	2.56	0.44
20:T:62:ALA:HA	20:T:67:ILE:HG22	2.00	0.44
1:A:126:G:C2'	1:A:127:G:O5'	2.66	0.44
1:A:1288:A:N1	1:A:1371:G:H1'	2.33	0.44
1:A:1375:A:C5	1:A:1376:U:C5	3.06	0.44
1:A:158:G:C5	1:A:159:G:N7	2.86	0.44
1:A:770:C:O2'	1:A:771:G:H5'	2.18	0.44
1:A:983:A:N3	1:A:983:A:C2'	2.81	0.44
2:B:222:ARG:CZ	2:B:223:GLU:HB2	2.48	0.44
4:D:38:PRO:HD2	4:D:42:GLY:HA3	2.00	0.44
6:F:42:TRP:CZ2	6:F:61:LEU:HB2	2.52	0.44
6:F:64:VAL:HG12	6:F:65:GLU:H	1.82	0.44
10:J:37:ARG:O	10:J:38:GLY:O	2.36	0.44
1:A:695:A:OP2	11:K:54:GLY:HA2	2.17	0.44
12:L:82:ILE:HD11	12:L:95:TYR:HB2	1.99	0.44
13:M:11:ASP:HA	13:M:45:ILE:HB	2.00	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:T:47:ALA:HB1	20:T:83:ILE:HG22	1.99	0.44
20:T:79:LEU:O	20:T:83:ILE:HG23	2.18	0.44
21:U:14:VAL:HG12	21:U:16:LEU:HD23	1.99	0.44
21:U:26:ALA:HB1	21:U:30:ALA:HB2	2.00	0.44
1:A:1133:G:O6	1:A:1141:C:N4	2.50	0.43
1:A:1300:G:O6	1:A:1334:G:H3'	2.18	0.43
1:A:446:G:N3	1:A:446:G:H2'	2.33	0.43
1:A:657:U:O2	15:O:22:THR:HG23	2.18	0.43
1:A:930:C:C4	1:A:931:C:C5	3.05	0.43
2:B:181:ILE:N	2:B:181:ILE:HD13	2.33	0.43
6:F:14:GLN:O	6:F:16:GLU:N	2.51	0.43
18:R:51:TYR:O	18:R:53:ARG:N	2.51	0.43
6:F:59:TYR:HE2	18:R:67:LEU:CD2	2.31	0.43
1:A:1053:G:O5'	1:A:1054:C:H3'	2.18	0.43
1:A:1144:G:N2	1:A:1145:A:C2	2.86	0.43
1:A:1160:G:O6	1:A:1181:G:C6	2.71	0.43
1:A:121:U:H3'	1:A:122:G:H5'	2.00	0.43
1:A:1532:U:N3	1:A:1533:C:C5	2.86	0.43
1:A:194:C:O2'	1:A:195:A:H5'	2.17	0.43
1:A:66:A:C4'	1:A:173:U:C4	3.01	0.43
3:C:79:LYS:O	3:C:81:GLY:N	2.51	0.43
6:F:42:TRP:N	6:F:42:TRP:CD1	2.82	0.43
7:G:69:VAL:HG21	7:G:104:ILE:HD11	1.99	0.43
15:O:29:VAL:HG13	15:O:63:ARG:HG3	2.01	0.43
1:A:1029:U:O2	1:A:1031:C:O2	2.36	0.43
1:A:1077:G:N1	1:A:1081:A:C6	2.87	0.43
1:A:1258:G:H2'	1:A:1259:C:C6	2.52	0.43
1:A:1318:A:O2'	19:S:37:ARG:HD3	2.17	0.43
1:A:963:G:O2'	1:A:964:A:H5'	2.18	0.43
2:B:174:LYS:HG2	2:B:175:GLU:N	2.31	0.43
10:J:74:VAL:HG12	10:J:75:ASP:N	2.32	0.43
12:L:58:THR:CG2	12:L:59:ASN:N	2.81	0.43
14:N:93:ILE:HG21	14:N:96:LEU:HD22	1.99	0.43
15:O:56:LEU:O	15:O:57:LEU:C	2.55	0.43
17:Q:50:ASN:O	17:Q:51:ASN:C	2.56	0.43
21:U:53:VAL:HG22	21:U:54:LYS:H	1.82	0.43
1:A:1104:G:C6	1:A:1105:A:C5	3.06	0.43
1:A:1124:G:N2	1:A:1127:G:N2	2.65	0.43
1:A:1138:G:N2	1:A:1140:C:N4	2.66	0.43
1:A:1347:G:O2'	1:A:1348:U:P	2.75	0.43
1:A:165:G:C2	1:A:166:U:C2	3.06	0.43
1:A:456:A:C6	1:A:457:G:C5	3.06	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:706:A:C1'	11:K:31:ILE:HD11	2.48	0.43
1:A:898:G:C6	1:A:902:G:O6	2.71	0.43
6:F:35:LYS:HG3	6:F:37:HIS:NE2	2.33	0.43
12:L:59:ASN:N	12:L:59:ASN:HD22	2.16	0.43
17:Q:49:GLU:C	17:Q:50:ASN:CG	2.76	0.43
1:A:1397:C:O2	1:A:1397:C:O4'	2.37	0.43
1:A:464:U:C2	1:A:466:A:OP2	2.71	0.43
1:A:652:U:O2'	1:A:653:U:OP2	2.30	0.43
1:A:721:G:H4'	1:A:722:G:O5'	2.18	0.43
1:A:748:G:H2'	1:A:749:A:H8	1.84	0.43
1:A:862:C:C4	1:A:863:U:C5	3.06	0.43
1:A:892:A:C6	1:A:893:C:C4	3.06	0.43
3:C:141:ALA:O	3:C:146:ALA:HB3	2.19	0.43
3:C:29:PHE:O	3:C:33:LEU:HB2	2.19	0.43
3:C:42:TYR:CE1	3:C:46:GLU:CG	3.02	0.43
7:G:30:LEU:HD11	7:G:116:MET:HE2	2.01	0.43
9:I:120:LYS:O	9:I:120:LYS:HG3	2.18	0.43
10:J:25:ILE:O	10:J:25:ILE:HG23	2.18	0.43
13:M:39:ILE:HG13	13:M:56:LEU:HD21	2.00	0.43
13:M:72:GLU:O	13:M:76:SER:OG	2.36	0.43
15:O:82:ILE:HG13	15:O:83:GLU:N	2.33	0.43
1:A:280:C:N3	17:Q:40:ARG:HA	2.33	0.43
21:U:10:GLU:HB2	21:U:11:PRO:HD3	1.99	0.43
1:A:1067:A:H4'	1:A:1068:G:O5'	2.18	0.43
1:A:1127:G:H5'	1:A:1280:A:O2'	2.18	0.43
1:A:407:U:H2'	1:A:408:A:C8	2.54	0.43
2:B:184:PHE:CE2	2:B:198:PHE:CD2	3.05	0.43
2:B:23:TRP:O	2:B:23:TRP:CD1	2.71	0.43
3:C:28:GLU:OE1	3:C:28:GLU:N	2.52	0.43
3:C:47:LEU:HB3	3:C:50:ALA:HB3	1.99	0.43
4:D:12:SER:HA	4:D:19:LEU:CD1	2.48	0.43
6:F:39:LEU:HD12	6:F:40:GLU:N	2.33	0.43
9:I:19:VAL:HG22	9:I:65:ILE:HG22	2.00	0.43
15:O:58:ARG:O	15:O:62:GLN:HB2	2.19	0.43
16:P:38:PHE:CE2	16:P:51:ARG:HD2	2.53	0.43
1:A:991:U:C4	1:A:1212:U:O4'	2.72	0.43
1:A:1252:A:H2'	1:A:1253:G:O4'	2.18	0.43
1:A:976:G:P	1:A:1358:U:O2'	2.76	0.43
1:A:183:C:O2'	1:A:184:G:O5'	2.36	0.43
1:A:247:G:C6	1:A:278:G:N1	2.86	0.43
1:A:28:A:H2'	1:A:29:U:O4'	2.19	0.43
1:A:9:G:H5'	5:E:108:GLY:HA3	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:133:PRO:CA	5:E:136:VAL:HG12	2.48	0.43
5:E:154:ALA:O	5:E:155:ALA:C	2.57	0.43
5:E:36:LEU:HD23	5:E:133:PRO:HB2	2.01	0.43
9:I:119:ARG:O	9:I:120:LYS:HB3	2.19	0.43
9:I:28:ILE:CB	9:I:35:LEU:HB2	2.49	0.43
11:K:22:HIS:CE1	11:K:35:THR:HG21	2.54	0.43
21:U:14:VAL:HG12	21:U:16:LEU:CD2	2.49	0.43
21:U:14:VAL:HG12	21:U:16:LEU:CG	2.47	0.43
21:U:47:ARG:HE	21:U:47:ARG:HA	1.84	0.43
1:A:1092:A:C6	1:A:1183:U:O2	2.72	0.43
1:A:116:A:C2	1:A:117:G:H1'	2.54	0.43
1:A:1269:A:C2	1:A:1313:U:O4'	2.72	0.43
1:A:252:U:H5'	1:A:253:A:OP2	2.19	0.43
1:A:476:U:C2'	1:A:477:C:H5'	2.48	0.43
1:A:805:C:H2'	1:A:806:C:H6	1.84	0.43
1:A:807:A:N7	1:A:808:C:C4	2.87	0.43
1:A:76:G:C2	1:A:95:C:N3	2.87	0.43
2:B:82:ASP:H	2:B:85:LEU:HB3	1.83	0.43
2:B:89:GLN:OE1	2:B:221:VAL:HB	2.19	0.43
3:C:111:LEU:HD21	3:C:144:LEU:HB2	2.01	0.43
3:C:182:ILE:HD13	3:C:203:PHE:HA	2.01	0.43
3:C:23:PHE:CD1	10:J:97:ASP:HB2	2.53	0.43
3:C:61:ALA:O	3:C:62:LYS:HB2	2.18	0.43
4:D:145:ILE:HG21	4:D:150:LYS:HA	2.00	0.43
5:E:94:VAL:CG1	5:E:111:MET:CE	2.97	0.43
12:L:21:VAL:HG12	12:L:95:TYR:CE1	2.52	0.43
19:S:55:ARG:NE	19:S:79:THR:HG22	2.34	0.43
19:S:6:LYS:CB	19:S:7:LYS:HE3	2.49	0.43
20:T:58:VAL:HG13	20:T:72:ALA:HB1	2.01	0.43
1:A:107:G:H2'	1:A:108:G:H5''	2.00	0.43
1:A:1222:G:O6	23:A:1864:HOH:O	2.21	0.43
1:A:158:G:C4	1:A:159:G:C8	3.07	0.43
1:A:207:C:H5''	1:A:208:U:OP2	2.18	0.43
1:A:436:C:O2	1:A:436:C:H2'	2.18	0.43
1:A:68:G:C5	1:A:69:G:H1'	2.53	0.43
2:B:144:LEU:N	2:B:144:LEU:HD23	2.34	0.43
5:E:83:HIS:NE2	8:H:96:MET:HE3	2.34	0.43
10:J:52:LEU:CD2	10:J:59:LYS:HA	2.49	0.43
1:A:228:A:H4'	16:P:63:GLN:HG2	2.01	0.43
20:T:3:ASN:O	20:T:4:ILE:C	2.57	0.43
1:A:1296:C:H5''	1:A:1297:G:OP2	2.18	0.43
1:A:1317:C:O2'	14:N:49:GLN:CG	2.67	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1513:A:H2'	1:A:1514:G:C8	2.54	0.43
1:A:793:U:HO2'	1:A:1516:G:C1'	2.31	0.43
1:A:1537:U:C4	1:A:1538:C:N4	2.87	0.43
1:A:282:A:C8	1:A:283:U:C5	3.07	0.43
1:A:301:G:H2'	1:A:302:G:C8	2.54	0.43
1:A:927:G:H4'	1:A:927:G:OP2	2.18	0.43
2:B:123:ASP:O	2:B:124:GLY:C	2.58	0.43
2:B:23:TRP:CG	2:B:23:TRP:O	2.72	0.43
4:D:202:GLU:OE1	5:E:105:ILE:CG2	2.67	0.43
5:E:133:PRO:O	5:E:137:VAL:CG1	2.67	0.43
1:A:15:G:O4'	5:E:29:ARG:NH2	2.52	0.43
13:M:19:LEU:HG	13:M:34:LEU:HD21	2.00	0.43
13:M:47:GLU:HG3	13:M:47:GLU:O	2.18	0.43
13:M:77:ILE:O	13:M:81:MET:HG3	2.18	0.43
19:S:55:ARG:NH2	19:S:79:THR:HG22	2.34	0.43
21:U:36:GLU:CG	21:U:37:PHE:H	2.31	0.43
1:A:121:U:H3'	1:A:122:G:C5'	2.48	0.42
1:A:1361:G:C2	1:A:1362:A:N7	2.87	0.42
1:A:1385:G:H2'	1:A:1386:G:O4'	2.18	0.42
1:A:109:A:O2'	1:A:326:G:N2	2.51	0.42
1:A:905:U:C5	1:A:906:A:C5	3.07	0.42
1:A:922:G:H4'	5:E:25:VAL:HA	2.01	0.42
1:A:923:A:H2'	1:A:924:C:O4'	2.18	0.42
2:B:21:ARG:C	2:B:22:TYR:CD1	2.92	0.42
4:D:100:ASN:O	4:D:104:ARG:HG2	2.19	0.42
4:D:150:LYS:O	4:D:151:LYS:C	2.57	0.42
5:E:102:GLY:O	5:E:104:GLY:CA	2.66	0.42
5:E:157:ARG:C	5:E:159:LYS:N	2.72	0.42
7:G:148:ASN:C	7:G:150:ALA:N	2.72	0.42
8:H:30:SER:O	8:H:31:LYS:C	2.56	0.42
10:J:7:ARG:HD3	10:J:75:ASP:OD2	2.18	0.42
11:K:71:ALA:O	11:K:75:LYS:HG3	2.19	0.42
15:O:42:HIS:O	15:O:45:GLU:O	2.37	0.42
16:P:2:VAL:HA	16:P:22:ALA:O	2.19	0.42
17:Q:45:HIS:O	17:Q:71:LYS:HA	2.18	0.42
20:T:9:LYS:O	20:T:12:ILE:HG12	2.19	0.42
18:R:35:GLU:HB2	21:U:19:PHE:CZ	2.54	0.42
21:U:24:GLU:HG3	21:U:28:VAL:CG2	2.49	0.42
21:U:4:ILE:N	21:U:4:ILE:HD13	2.34	0.42
1:A:1097:C:C2	1:A:1098:C:C6	3.07	0.42
1:A:1245:C:H2'	1:A:1246:A:H8	1.83	0.42
1:A:130:A:C2	1:A:264:C:C6	3.07	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:519:C:OP2	12:L:47:SER:OG	2.37	0.42
1:A:571:U:H5''	1:A:572:A:OP2	2.19	0.42
1:A:865:A:H2	1:A:918:A:H4'	1.84	0.42
2:B:115:LYS:O	2:B:117:LEU:N	2.52	0.42
2:B:140:GLU:C	2:B:144:LEU:HG	2.39	0.42
2:B:180:GLY:O	2:B:182:PRO:HD3	2.19	0.42
3:C:19:ASN:OD1	3:C:54:ARG:NE	2.50	0.42
4:D:19:LEU:HD21	4:D:60:LYS:HG2	2.01	0.42
6:F:32:ALA:O	6:F:33:GLU:C	2.57	0.42
9:I:17:ALA:HB2	9:I:67:VAL:HB	2.01	0.42
9:I:91:ASP:OD1	9:I:91:ASP:C	2.58	0.42
10:J:52:LEU:HD23	10:J:62:ARG:CG	2.49	0.42
11:K:93:ARG:HB3	11:K:94:GLU:H	1.72	0.42
12:L:40:THR:HG22	12:L:41:THR:N	2.33	0.42
14:N:80:SER:O	14:N:81:ARG:C	2.56	0.42
17:Q:14:SER:OG	17:Q:22:VAL:HG12	2.20	0.42
20:T:57:ILE:O	20:T:61:GLN:HG2	2.20	0.42
20:T:67:ILE:HD12	20:T:67:ILE:HA	1.77	0.42
1:A:1099:G:H2'	1:A:1100:C:O4'	2.19	0.42
1:A:1426:G:H2'	1:A:1427:C:O4'	2.20	0.42
1:A:1490:U:C2'	1:A:1491:G:O4'	2.65	0.42
1:A:223:A:H2'	1:A:224:U:C6	2.54	0.42
1:A:374:A:H5''	1:A:452:A:C2	2.54	0.42
1:A:511:C:C2	1:A:512:U:C6	3.07	0.42
1:A:597:G:N7	1:A:598:U:C5	2.87	0.42
1:A:604:G:N7	1:A:605:U:C5	2.87	0.42
1:A:618:C:H5''	1:A:619:U:H5''	2.00	0.42
1:A:740:U:H4'	15:O:42:HIS:CD2	2.54	0.42
1:A:778:G:C6	1:A:779:C:N3	2.88	0.42
1:A:833:G:C4	1:A:834:U:C6	3.08	0.42
1:A:892:A:C5	1:A:893:C:C5	3.07	0.42
1:A:992:U:O4'	1:A:993:G:C2	2.72	0.42
4:D:98:LEU:HD22	4:D:130:VAL:HG12	2.01	0.42
6:F:88:MET:HE3	18:R:64:TYR:CE2	2.54	0.42
12:L:110:ARG:NH1	12:L:112:GLN:O	2.53	0.42
17:Q:63:GLU:N	17:Q:73:TRP:CE3	2.87	0.42
1:A:1220:G:H2'	1:A:1221:G:O4'	2.18	0.42
1:A:1235:U:H2'	1:A:1236:A:O4'	2.20	0.42
1:A:1262:C:O2'	1:A:1263:C:H5'	2.19	0.42
1:A:1328:C:C5'	13:M:28:THR:HG21	2.49	0.42
1:A:1328:C:OP1	13:M:28:THR:HG21	2.19	0.42
1:A:144:G:C6	1:A:179:A:C2	3.08	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1537:U:C5	1:A:1538:C:N4	2.88	0.42
1:A:289:G:N1	1:A:290:C:C4	2.87	0.42
1:A:438:U:C2	1:A:494:G:C6	3.07	0.42
1:A:582:C:C4	1:A:760:G:C6	3.07	0.42
1:A:872:A:C5	1:A:874:G:C8	3.07	0.42
2:B:117:LEU:O	2:B:118:GLU:C	2.57	0.42
3:C:77:ILE:HA	3:C:84:VAL:HG23	2.00	0.42
7:G:31:MET:O	7:G:31:MET:HG2	2.20	0.42
8:H:83:LEU:C	8:H:83:LEU:HD22	2.39	0.42
9:I:13:LYS:CG	9:I:13:LYS:O	2.67	0.42
9:I:13:LYS:O	9:I:14:SER:CB	2.68	0.42
9:I:49:ARG:C	9:I:51:PRO:HD2	2.40	0.42
16:P:67:ILE:HG22	16:P:68:SER:O	2.19	0.42
20:T:64:LYS:HE3	20:T:64:LYS:HA	2.00	0.42
1:A:1133:G:C6	1:A:1142:G:C6	3.08	0.42
1:A:1202:U:C2'	1:A:1203:C:H5'	2.50	0.42
1:A:145:G:N1	1:A:146:G:N7	2.68	0.42
1:A:375:U:N3	1:A:376:G:N7	2.67	0.42
1:A:375:U:C2	1:A:376:G:C8	3.07	0.42
1:A:405:U:O4	4:D:2:ALA:N	2.52	0.42
1:A:455:G:C6	1:A:456:A:C6	3.07	0.42
1:A:484:G:N7	1:A:486:U:H1'	2.34	0.42
1:A:55:A:N7	1:A:56:U:C5	2.87	0.42
1:A:745:G:H5''	1:A:851:G:O2'	2.19	0.42
2:B:115:LYS:C	2:B:117:LEU:N	2.73	0.42
2:B:133:GLU:O	2:B:137:ARG:HB3	2.19	0.42
2:B:169:GLU:O	2:B:170:HIS:C	2.56	0.42
4:D:107:PHE:N	4:D:107:PHE:CD1	2.86	0.42
4:D:29:ASP:O	4:D:31:LYS:NZ	2.43	0.42
11:K:61:PHE:O	11:K:65:VAL:HG12	2.20	0.42
1:A:1006:G:OP1	1:A:1038:C:H5'	2.19	0.42
1:A:1123:U:H2'	1:A:1124:G:C8	2.55	0.42
1:A:1053:G:N7	1:A:1200:C:H5''	2.34	0.42
1:A:1399:C:C2	1:A:1401:G:C5	3.07	0.42
1:A:1491:G:H2'	1:A:1492:A:C8	2.55	0.42
1:A:1408:A:C2	1:A:1494:G:C5	3.06	0.42
1:A:803:G:C6	1:A:804:U:N3	2.88	0.42
1:A:957:U:O2	1:A:959:A:C8	2.72	0.42
1:A:96:U:O2'	1:A:97:G:O5'	2.37	0.42
4:D:58:LYS:CB	4:D:200:ILE:HB	2.50	0.42
4:D:89:ASN:O	4:D:92:ALA:HB3	2.19	0.42
4:D:9:LEU:HD13	4:D:9:LEU:HA	1.81	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:94:VAL:HG13	5:E:111:MET:CE	2.49	0.42
5:E:113:ALA:O	5:E:114:VAL:C	2.58	0.42
7:G:15:ASP:OD1	7:G:44:TYR:OH	2.31	0.42
10:J:35:GLN:CG	10:J:77:VAL:HB	2.49	0.42
12:L:23:ALA:O	12:L:24:LEU:O	2.36	0.42
13:M:19:LEU:HD11	13:M:33:ILE:HG21	2.01	0.42
1:A:675:A:OP1	18:R:74:HIS:CE1	2.72	0.42
1:A:1107:C:OP1	3:C:172:ARG:HG3	2.20	0.42
1:A:1213:A:C8	1:A:1215:G:C6	3.07	0.42
1:A:1288:A:O2'	1:A:1352:C:O2'	2.31	0.42
1:A:1431:A:C5	1:A:1432:G:C6	3.08	0.42
1:A:1491:G:C5	1:A:1492:A:C6	3.08	0.42
1:A:197:A:C5	1:A:221:C:H4'	2.54	0.42
1:A:338:A:C5	1:A:339:C:C5	3.08	0.42
1:A:390:U:C2	1:A:391:G:C8	3.08	0.42
1:A:676:A:C2	1:A:677:U:C2	3.07	0.42
1:A:728:A:N1	1:A:729:A:C6	2.87	0.42
1:A:673:A:C2	1:A:734:G:C2	3.08	0.42
1:A:952:U:OP1	1:A:972:C:N4	2.52	0.42
2:B:62:SER:O	2:B:64:LYS:N	2.53	0.42
9:I:57:MET:HB3	9:I:61:LEU:HD21	2.01	0.42
10:J:11:LYS:HG2	10:J:71:LEU:CD1	2.50	0.42
1:A:1226:C:C4	13:M:103:LYS:HA	2.54	0.42
13:M:16:VAL:CG1	13:M:41:GLU:HB3	2.50	0.42
13:M:40:ALA:O	13:M:43:VAL:HG22	2.19	0.42
13:M:45:ILE:HG22	13:M:45:ILE:O	2.20	0.42
16:P:70:ARG:O	16:P:74:LEU:HD23	2.19	0.42
17:Q:31:HIS:CD2	17:Q:34:TYR:CD2	3.08	0.42
19:S:40:ILE:HB	19:S:66:MET:O	2.20	0.42
19:S:73:GLU:HB2	19:S:74:PHE:CD2	2.54	0.42
1:A:1082:A:OP2	5:E:23:LYS:HE2	2.20	0.42
1:A:1162:C:C2	1:A:1175:G:C2	3.08	0.42
1:A:1202:U:H2'	1:A:1203:C:H5'	2.01	0.42
1:A:1216:A:H2'	1:A:1217:C:C6	2.55	0.42
1:A:204:G:H2'	1:A:205:A:O4'	2.20	0.42
1:A:666:G:C6	1:A:741:G:C5	3.08	0.42
4:D:4:TYR:CZ	4:D:6:GLY:HA3	2.55	0.42
5:E:122:ASN:CG	5:E:123:VAL:N	2.73	0.42
5:E:25:VAL:HG22	5:E:28:GLY:O	2.19	0.42
6:F:38:ARG:NH2	6:F:98:GLU:O	2.50	0.42
9:I:28:ILE:HG23	9:I:63:LEU:CD1	2.50	0.42
10:J:25:ILE:O	10:J:25:ILE:CD1	2.68	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:78:GLU:CD	10:J:80:THR:HG1	2.23	0.42
13:M:16:VAL:HG13	13:M:34:LEU:HD12	2.02	0.42
14:N:27:LEU:C	14:N:31:ILE:HD13	2.40	0.42
18:R:33:ILE:HG12	18:R:33:ILE:O	2.19	0.42
21:U:34:ARG:CD	21:U:35:ARG:HB2	2.50	0.42
1:A:1072:G:C2	1:A:1104:G:C2	3.07	0.42
1:A:1133:G:N3	1:A:1142:G:C2	2.87	0.42
1:A:1130:A:C1'	1:A:1146:A:C2	3.02	0.42
1:A:1401:G:C2	1:A:1402:C:H1'	2.55	0.42
1:A:1441:A:C8	1:A:1442:G:C8	3.08	0.42
1:A:143:A:H5'	1:A:144:G:C5'	2.50	0.42
1:A:1520:C:H2'	1:A:1521:C:C6	2.55	0.42
1:A:794:A:O2'	1:A:1521:C:O2'	2.26	0.42
1:A:499:A:H4'	1:A:500:G:OP1	2.19	0.42
1:A:549:C:H2'	1:A:550:G:O5'	2.20	0.42
1:A:880:C:C2'	1:A:881:G:H5'	2.50	0.42
1:A:865:A:C2	1:A:918:A:H4'	2.55	0.42
1:A:921:U:H2'	1:A:922:G:O4'	2.20	0.42
2:B:102:THR:HB	2:B:175:GLU:HG2	2.02	0.42
2:B:64:LYS:HD3	2:B:64:LYS:C	2.41	0.42
3:C:40:ARG:HA	3:C:55:ILE:CD1	2.50	0.42
3:C:64:ILE:HG23	3:C:99:ALA:HB2	2.02	0.42
4:D:148:LYS:H	4:D:148:LYS:CE	2.33	0.42
5:E:11:LEU:HG	5:E:12:GLN:N	2.35	0.42
5:E:12:GLN:OE1	5:E:12:GLN:HA	2.19	0.42
10:J:26:VAL:HG21	10:J:39:PRO:HG3	2.01	0.42
11:K:35:THR:HG1	11:K:40:ASN:H	1.68	0.42
11:K:91:PRO:O	11:K:92:GLY:O	2.38	0.42
1:A:278:G:OP2	17:Q:43:LYS:NZ	2.53	0.42
17:Q:75:LEU:C	17:Q:75:LEU:CD1	2.88	0.42
20:T:39:ILE:HD11	20:T:83:ILE:HG22	2.01	0.42
21:U:34:ARG:HE	21:U:35:ARG:HB2	1.85	0.42
1:A:1125:U:H4'	10:J:7:ARG:NH1	2.34	0.42
1:A:116:A:C4	1:A:117:G:C8	3.08	0.42
1:A:1456:A:H2'	1:A:1457:G:O4'	2.20	0.42
1:A:273:U:H2'	1:A:274:A:H5'	2.02	0.42
1:A:562:U:H1'	12:L:12:ARG:HG3	2.02	0.42
1:A:582:C:O2	1:A:760:G:C2	2.73	0.42
1:A:821:G:C4	1:A:822:U:C5	3.08	0.42
2:B:119:THR:O	2:B:120:GLN:HB2	2.20	0.42
4:D:95:GLU:OE2	4:D:100:ASN:ND2	2.46	0.42
7:G:123:GLU:O	7:G:127:ALA:HB2	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:5:ARG:HA	10:J:5:ARG:HD3	1.89	0.42
11:K:67:ALA:HB1	11:K:100:LEU:HD13	2.02	0.42
13:M:11:ASP:HA	13:M:45:ILE:HD13	2.01	0.42
14:N:10:GLU:O	14:N:11:VAL:C	2.58	0.42
16:P:19:VAL:CG1	16:P:37:GLY:CA	2.98	0.42
1:A:1014:A:C4	19:S:34:TRP:CH2	3.08	0.42
21:U:14:VAL:HG13	21:U:15:ALA:N	2.35	0.42
1:A:1540:U:H4'	21:U:18:ARG:HG2	2.02	0.42
21:U:36:GLU:OE2	21:U:38:TYR:CD2	2.73	0.42
1:A:108:G:C6	20:T:10:ARG:HG2	2.55	0.41
1:A:1138:G:O2'	1:A:1140:C:H5'	2.20	0.41
1:A:1302:C:C4	13:M:17:ILE:HD13	2.54	0.41
1:A:1319:A:OP2	19:S:5:LEU:HD22	2.20	0.41
1:A:78:A:C2	1:A:92:U:O2	2.73	0.41
2:B:210:VAL:HG22	2:B:211:THR:H	1.85	0.41
5:E:147:MET:O	5:E:147:MET:HG2	2.20	0.41
7:G:71:PRO:HD2	7:G:96:ARG:O	2.20	0.41
8:H:35:ALA:O	8:H:39:VAL:HG23	2.19	0.41
10:J:34:ALA:O	10:J:35:GLN:CB	2.68	0.41
16:P:4:ILE:HD11	16:P:65:ALA:HB1	2.02	0.41
20:T:8:LYS:O	20:T:11:ALA:HB3	2.20	0.41
20:T:43:ASP:HB3	20:T:46:ALA:CB	2.50	0.41
1:A:1461:G:H2'	1:A:1462:C:O4'	2.20	0.41
1:A:147:G:H2'	1:A:148:G:C8	2.55	0.41
1:A:174:A:C2	1:A:175:C:C1'	3.03	0.41
1:A:211:G:H21	1:A:212:G:H1'	1.83	0.41
1:A:247:G:C5	1:A:278:G:C2	3.08	0.41
1:A:463:U:O2	1:A:463:U:H2'	2.19	0.41
1:A:577:G:N3	1:A:578:C:C6	2.89	0.41
1:A:833:G:C5	1:A:834:U:C5	3.08	0.41
1:A:79:G:N2	1:A:91:U:C2	2.88	0.41
1:A:98:A:C2	1:A:99:C:C2	3.09	0.41
2:B:126:PHE:CD1	2:B:126:PHE:C	2.91	0.41
2:B:207:ILE:HG12	2:B:208:ARG:N	2.34	0.41
3:C:179:ARG:O	3:C:206:GLU:O	2.38	0.41
4:D:188:ARG:HA	4:D:188:ARG:HD2	1.80	0.41
4:D:33:LYS:O	4:D:34:ILE:C	2.58	0.41
11:K:77:TYR:O	11:K:78:GLY:C	2.59	0.41
12:L:94:ARG:HB2	12:L:95:TYR:CE2	2.55	0.41
15:O:49:ASP:OD2	15:O:52:SER:OG	2.37	0.41
1:A:1216:A:H2'	1:A:1217:C:H6	1.86	0.41
1:A:1514:G:C4	1:A:1515:G:C8	3.09	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:219:U:C2	1:A:220:G:C8	3.09	0.41
1:A:130:A:C2	1:A:264:C:N1	2.88	0.41
1:A:743:A:C6	1:A:744:C:C4	3.08	0.41
1:A:773:G:C2	1:A:807:A:N1	2.89	0.41
1:A:939:G:P	7:G:95:ARG:NH2	2.94	0.41
1:A:976:G:H5''	1:A:1358:U:O2'	2.19	0.41
2:B:104:TRP:CH2	2:B:155:GLY:C	2.93	0.41
3:C:101:ILE:CG2	3:C:101:ILE:O	2.68	0.41
4:D:124:MET:HG3	4:D:146:ARG:HG2	2.02	0.41
4:D:24:GLY:O	4:D:161:LEU:HD11	2.19	0.41
4:D:40:GLN:O	4:D:40:GLN:HG2	2.20	0.41
5:E:44:GLY:O	5:E:45:ARG:O	2.39	0.41
7:G:33:ASP:HB3	7:G:35:LYS:HE3	2.01	0.41
11:K:64:GLN:O	11:K:68:GLU:HG3	2.20	0.41
12:L:33:VAL:O	12:L:34:CYS:CB	2.68	0.41
15:O:36:ILE:HG23	15:O:56:LEU:HD11	2.03	0.41
16:P:4:ILE:CD1	16:P:65:ALA:HB1	2.50	0.41
21:U:29:LEU:C	21:U:29:LEU:HD23	2.40	0.41
1:A:1140:C:O2'	1:A:1141:C:O5'	2.36	0.41
1:A:1314:C:H2'	1:A:1315:U:C6	2.54	0.41
1:A:575:G:O2'	1:A:821:G:OP2	2.25	0.41
2:B:21:ARG:HA	2:B:21:ARG:NE	2.33	0.41
1:A:598:U:H4'	8:H:86:TYR:CG	2.56	0.41
13:M:33:ILE:HG23	13:M:59:GLU:CB	2.51	0.41
18:R:20:GLU:HG3	18:R:55:LEU:HD13	2.01	0.41
18:R:58:ALA:O	18:R:59:ILE:C	2.58	0.41
1:A:110:C:C4	1:A:111:G:C6	3.09	0.41
1:A:167:A:C2'	1:A:168:G:O5'	2.68	0.41
1:A:439:U:H4'	4:D:121:LYS:HD2	2.03	0.41
1:A:508:U:O3'	23:A:1759:HOH:O	2.22	0.41
1:A:577:G:O2'	1:A:578:C:H5'	2.21	0.41
1:A:624:C:C2	1:A:625:U:C6	3.07	0.41
1:A:66:A:H4'	1:A:173:U:C4	2.55	0.41
1:A:708:C:O2'	1:A:709:U:H5'	2.20	0.41
1:A:782:A:C8	1:A:783:C:C5	3.08	0.41
1:A:814:A:H4'	1:A:1511:G:C4'	2.51	0.41
2:B:118:GLU:HA	2:B:121:SER:HB2	2.02	0.41
2:B:165:ASP:HB3	2:B:168:HIS:HB3	2.02	0.41
5:E:44:GLY:O	5:E:45:ARG:C	2.59	0.41
9:I:19:VAL:HA	9:I:65:ILE:HG22	2.01	0.41
10:J:52:LEU:HD22	10:J:59:LYS:HA	2.01	0.41
12:L:38:TYR:O	12:L:39:THR:HG23	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:Q:12:VAL:CG1	17:Q:21:ILE:HD11	2.51	0.41
17:Q:17:MET:CE	17:Q:20:SER:O	2.69	0.41
19:S:63:THR:CG2	19:S:64:ASP:N	2.83	0.41
1:A:1304:G:N1	1:A:1305:G:N2	2.69	0.41
1:A:154:U:H2'	1:A:155:A:H5'	2.03	0.41
1:A:308:C:N4	1:A:309:A:N6	2.68	0.41
1:A:36:C:O2'	12:L:114:ARG:NH2	2.53	0.41
1:A:369:G:C2	1:A:370:C:C6	3.09	0.41
1:A:431:A:H2'	1:A:432:A:O4'	2.21	0.41
1:A:66:A:C6	1:A:67:C:C4	3.08	0.41
1:A:72:A:C5	1:A:73:C:C4	3.08	0.41
1:A:811:C:O2'	1:A:901:A:N1	2.44	0.41
5:E:149:SER:O	5:E:153:VAL:HG13	2.21	0.41
6:F:93:LYS:C	6:F:94:HIS:CG	2.93	0.41
7:G:37:SER:HA	7:G:40:GLU:HG2	2.03	0.41
8:H:112:THR:HG23	8:H:115:ALA:HB2	2.03	0.41
8:H:92:LEU:HD22	8:H:113:ASP:HB2	2.03	0.41
10:J:19:ASP:HA	10:J:22:THR:CB	2.50	0.41
11:K:116:ILE:HG22	11:K:116:ILE:O	2.20	0.41
12:L:35:THR:N	12:L:54:ARG:O	2.54	0.41
1:A:552:U:O2'	12:L:83:ARG:O	2.38	0.41
17:Q:25:ILE:HG12	17:Q:42:THR:O	2.21	0.41
17:Q:27:ARG:HG2	17:Q:40:ARG:HB3	2.02	0.41
1:A:1073:U:H5'	1:A:1074:G:OP2	2.21	0.41
1:A:1279:G:OP1	10:J:9:ARG:NH2	2.54	0.41
1:A:1434:A:N6	1:A:1435:G:C6	2.88	0.41
1:A:144:G:C4	1:A:179:A:C2	3.08	0.41
1:A:552:U:N3	1:A:553:A:N7	2.69	0.41
1:A:790:A:C6	1:A:791:G:N1	2.89	0.41
1:A:851:G:N3	1:A:851:G:H2'	2.34	0.41
1:A:881:G:C4	1:A:882:C:C6	3.09	0.41
2:B:96:TRP:CZ3	2:B:175:GLU:OE2	2.73	0.41
3:C:37:PHE:HZ	14:N:90:ARG:NH1	2.19	0.41
3:C:66:VAL:O	3:C:66:VAL:HG12	2.21	0.41
3:C:6:HIS:C	3:C:8:ASN:H	2.24	0.41
4:D:151:LYS:O	4:D:152:GLN:OE1	2.39	0.41
4:D:197:GLU:O	4:D:201:VAL:HG23	2.20	0.41
5:E:122:ASN:O	5:E:123:VAL:C	2.59	0.41
6:F:3:HIS:ND1	6:F:65:GLU:HG3	2.36	0.41
9:I:28:ILE:HG21	9:I:35:LEU:HD13	2.03	0.41
11:K:118:HIS:O	11:K:119:ASN:HB2	2.20	0.41
13:M:64:VAL:O	13:M:69:LEU:HD13	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:Q:8:LEU:N	17:Q:8:LEU:CD1	2.83	0.41
20:T:25:ARG:HD2	20:T:29:ARG:NH1	2.34	0.41
1:A:1088:G:C6	1:A:1089:G:N7	2.89	0.41
1:A:1138:G:C6	1:A:1140:C:C2	3.09	0.41
1:A:116:A:C8	1:A:116:A:OP2	2.73	0.41
1:A:1310:G:H2'	1:A:1311:A:O4'	2.21	0.41
1:A:1505:G:H4'	1:A:1506:U:H5''	2.03	0.41
1:A:376:G:H5'	16:P:5:ARG:HB2	2.03	0.41
1:A:423:G:H3'	1:A:423:G:N3	2.36	0.41
1:A:444:G:C4	1:A:445:G:C8	3.08	0.41
1:A:736:C:H2'	1:A:737:C:C6	2.56	0.41
1:A:771:G:C4	1:A:809:G:N2	2.89	0.41
1:A:875:U:O2'	8:H:15:ARG:NH1	2.54	0.41
2:B:18:HIS:CG	2:B:203:ASN:ND2	2.88	0.41
2:B:55:ALA:O	2:B:59:LYS:HB2	2.20	0.41
3:C:56:VAL:C	3:C:57:ILE:HD12	2.41	0.41
3:C:6:HIS:O	3:C:8:ASN:N	2.53	0.41
4:D:173:VAL:O	4:D:174:ASP:CB	2.67	0.41
4:D:49:SER:O	4:D:53:VAL:HG13	2.21	0.41
9:I:24:GLY:H	9:I:61:LEU:HA	1.85	0.41
9:I:84:THR:HB	9:I:98:LEU:HD21	2.02	0.41
1:A:718:A:H5'	11:K:119:ASN:CG	2.41	0.41
11:K:52:PHE:HB3	11:K:56:ARG:NH2	2.36	0.41
12:L:25:GLU:HB3	12:L:27:CYS:SG	2.60	0.41
13:M:60:VAL:HG23	13:M:65:VAL:HG21	2.02	0.41
20:T:73:ALA:O	20:T:77:ALA:HB2	2.20	0.41
21:U:5:LYS:HD2	21:U:5:LYS:O	2.20	0.41
1:A:1158:C:C2'	1:A:1158:C:O2	2.69	0.41
1:A:1163:A:N3	1:A:1174:G:C2	2.88	0.41
1:A:1534:A:H4'	1:A:1535:C:H2'	2.02	0.41
1:A:64:G:C8	1:A:99:C:C4	3.08	0.41
1:A:66:A:O4'	1:A:173:U:C4	2.74	0.41
1:A:842:U:O2	1:A:845:A:OP1	2.38	0.41
1:A:913:A:H4'	1:A:914:A:H4'	2.03	0.41
3:C:130:PHE:CZ	3:C:131:ARG:CD	3.04	0.41
3:C:150:LYS:HB2	3:C:169:ARG:CG	2.51	0.41
3:C:5:VAL:HG21	3:C:10:ILE:HD13	2.02	0.41
4:D:44:ARG:NE	4:D:44:ARG:HA	2.36	0.41
4:D:48:LEU:HD23	4:D:52:GLY:C	2.41	0.41
5:E:149:SER:OG	5:E:152:MET:CG	2.69	0.41
8:H:10:MET:HE1	8:H:36:ILE:HB	2.03	0.41
9:I:33:ARG:HD3	9:I:33:ARG:HA	1.86	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:126:LYS:C	21:U:34:ARG:CZ	2.89	0.41
12:L:65:SER:OG	12:L:97:THR:HG23	2.20	0.41
1:A:1216:A:OP1	14:N:5:SER:CB	2.69	0.41
1:A:1366:C:H2'	1:A:1367:C:C6	2.55	0.41
1:A:1408:A:N1	1:A:1494:G:C5	2.89	0.41
1:A:1448:C:H2'	1:A:1449:C:C6	2.55	0.41
1:A:1467:C:H2'	1:A:1468:A:H8	1.84	0.41
1:A:251:G:H4'	1:A:252:U:O5'	2.20	0.41
1:A:781:A:H4'	1:A:1522:U:O2'	2.21	0.41
1:A:997:U:H2'	1:A:998:C:O4'	2.21	0.41
2:B:11:LYS:O	2:B:12:ALA:C	2.59	0.41
2:B:120:GLN:O	2:B:120:GLN:HG2	2.21	0.41
2:B:71:GLY:HA2	2:B:164:ILE:HG22	2.03	0.41
2:B:17:GLY:O	2:B:39:HIS:O	2.38	0.41
8:H:88:ARG:O	8:H:122:GLY:CA	2.69	0.41
9:I:15:SER:OG	9:I:70:GLY:HA3	2.21	0.41
10:J:11:LYS:HG2	10:J:71:LEU:HD13	2.02	0.41
11:K:88:GLY:N	11:K:114:THR:HG22	2.36	0.41
13:M:91:HIS:HA	13:M:109:ARG:HH21	1.86	0.41
14:N:50:THR:CG2	19:S:13:LEU:HG	2.51	0.41
21:U:11:PRO:O	21:U:12:PHE:CG	2.74	0.41
21:U:4:ILE:HA	21:U:20:LYS:HZ1	1.86	0.41
11:K:126:LYS:O	21:U:34:ARG:CZ	2.68	0.41
21:U:6:VAL:C	21:U:7:ARG:HG2	2.40	0.41
1:A:1022:A:C4	1:A:1023:U:C5	3.09	0.41
1:A:1093:A:C5	1:A:1095:U:O4'	2.74	0.41
1:A:1401:G:C4	1:A:1402:C:C6	3.09	0.41
1:A:246:A:N3	1:A:279:A:N6	2.69	0.41
1:A:552:U:C2	1:A:553:A:C8	3.09	0.41
1:A:756:C:O2'	1:A:757:U:H5'	2.21	0.41
1:A:866:C:C4	1:A:867:G:H1'	2.56	0.41
3:C:117:ALA:O	3:C:121:THR:HB	2.21	0.41
4:D:125:VAL:HG22	4:D:130:VAL:HB	2.02	0.41
5:E:95:PHE:CG	5:E:96:MET:N	2.88	0.41
8:H:18:GLN:HG2	8:H:63:LEU:HD13	2.03	0.41
9:I:26:GLY:HA2	9:I:61:LEU:O	2.21	0.41
9:I:97:GLU:N	9:I:97:GLU:OE2	2.54	0.41
10:J:35:GLN:HG2	10:J:77:VAL:CB	2.47	0.41
13:M:18:ALA:HB2	13:M:45:ILE:HD11	2.03	0.41
14:N:12:LYS:O	14:N:14:VAL:N	2.54	0.41
16:P:6:LEU:HD12	16:P:6:LEU:N	2.35	0.41
17:Q:14:SER:OG	17:Q:17:MET:CE	2.69	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:R:32:TYR:CG	18:R:55:LEU:HD21	2.56	0.41
19:S:38:SER:HB2	19:S:71:LEU:HG	2.03	0.41
20:T:54:MET:HG3	20:T:55:GLN:N	2.36	0.41
20:T:65:GLY:HA2	20:T:68:HIS:CE1	2.56	0.41
1:A:960:U:C4	1:A:1225:A:C8	3.09	0.40
1:A:1458:G:O2'	20:T:23:SER:HB3	2.21	0.40
1:A:517:G:C8	1:A:531:U:C5	3.09	0.40
1:A:76:G:N2	1:A:95:C:N3	2.70	0.40
2:B:42:ASN:OD1	2:B:44:GLU:HB2	2.21	0.40
9:I:54:LEU:O	9:I:55:VAL:HG13	2.21	0.40
11:K:107:ILE:HD13	11:K:107:ILE:C	2.42	0.40
17:Q:65:ARG:HA	17:Q:66:PRO:HD3	1.96	0.40
18:R:48:ARG:N	18:R:48:ARG:HD2	2.35	0.40
18:R:51:TYR:C	18:R:53:ARG:N	2.73	0.40
18:R:67:LEU:O	18:R:68:LEU:HG	2.21	0.40
20:T:51:PHE:HA	20:T:54:MET:HG2	2.03	0.40
21:U:8:GLU:OE2	21:U:12:PHE:CD2	2.73	0.40
21:U:9:ASN:HB3	21:U:10:GLU:HG3	2.02	0.40
1:A:1195:C:H2'	1:A:1197:A:O4'	2.20	0.40
1:A:1306:A:H1'	1:A:1332:A:N7	2.36	0.40
1:A:1537:U:H2'	1:A:1538:C:C6	2.56	0.40
1:A:159:G:N2	1:A:161:A:H3'	2.35	0.40
1:A:213:G:C5	1:A:214:C:C2	3.09	0.40
1:A:437:U:C2'	1:A:438:U:H5'	2.51	0.40
1:A:676:A:H2'	1:A:677:U:C6	2.57	0.40
1:A:866:C:C4'	1:A:919:A:H5'	2.52	0.40
3:C:22:TRP:CH2	3:C:32:ASN:HB3	2.56	0.40
3:C:80:LYS:HE3	3:C:80:LYS:HA	2.03	0.40
4:D:122:ALA:C	4:D:123:ILE:HG12	2.41	0.40
5:E:156:LYS:HA	5:E:159:LYS:NZ	2.35	0.40
18:R:25:ASP:HB3	18:R:28:THR:HB	2.04	0.40
18:R:34:THR:HG21	18:R:38:LYS:HB2	2.04	0.40
11:K:112:ASP:HB3	21:U:4:ILE:HG22	2.04	0.40
1:A:1262:C:C2'	1:A:1263:C:H5'	2.51	0.40
1:A:542:G:C2	1:A:543:U:C5	3.10	0.40
1:A:685:G:O2'	1:A:686:U:H5'	2.22	0.40
1:A:718:A:C6	11:K:118:HIS:NE2	2.90	0.40
1:A:790:A:N6	1:A:791:G:N1	2.69	0.40
2:B:140:GLU:O	2:B:141:LEU:C	2.59	0.40
2:B:161:LEU:HD23	2:B:176:ALA:HB2	2.04	0.40
5:E:94:VAL:CG1	5:E:111:MET:HE3	2.51	0.40
6:F:99:ALA:O	6:F:100:SER:HB3	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:21:ASN:O	8:H:22:LYS:C	2.58	0.40
10:J:19:ASP:HA	10:J:22:THR:HG22	2.03	0.40
12:L:65:SER:HB2	12:L:82:ILE:HD11	2.03	0.40
12:L:84:GLY:HA2	12:L:95:TYR:HD1	1.86	0.40
12:L:94:ARG:C	12:L:95:TYR:CG	2.95	0.40
15:O:3:LEU:HD13	15:O:35:GLN:HG2	2.02	0.40
16:P:75:ILE:O	16:P:78:VAL:HG12	2.21	0.40
17:Q:7:THR:O	17:Q:7:THR:HG23	2.21	0.40
11:K:127:ARG:CB	21:U:34:ARG:NH1	2.82	0.40
1:A:143:A:H5'	1:A:144:G:O5'	2.21	0.40
1:A:1515:G:C2	1:A:1516:G:C5	3.10	0.40
1:A:184:G:N2	1:A:185:U:C2	2.89	0.40
1:A:312:C:H2'	1:A:313:A:O4'	2.21	0.40
1:A:423:G:N2	1:A:424:G:C8	2.90	0.40
1:A:467:U:H3'	1:A:468:A:H5''	2.04	0.40
1:A:687:A:N3	1:A:688:G:H1'	2.36	0.40
1:A:773:G:C4	1:A:807:A:N1	2.90	0.40
1:A:821:G:H2'	1:A:822:U:C6	2.56	0.40
1:A:860:A:N6	1:A:861:G:C2	2.90	0.40
2:B:19:GLN:O	2:B:38:VAL:HG23	2.21	0.40
4:D:202:GLU:O	4:D:203:LEU:C	2.60	0.40
4:D:28:ILE:O	4:D:29:ASP:O	2.39	0.40
5:E:16:ILE:N	5:E:16:ILE:HD12	2.37	0.40
5:E:56:VAL:O	5:E:59:ALA:HB3	2.21	0.40
6:F:6:ILE:HG22	6:F:7:VAL:N	2.36	0.40
10:J:83:THR:HG23	10:J:83:THR:O	2.21	0.40
1:A:1458:G:H5'	20:T:27:MET:HB3	2.02	0.40
20:T:37:ALA:O	20:T:40:GLU:HB3	2.22	0.40
20:T:55:GLN:N	20:T:56:PRO:CD	2.84	0.40
1:A:1426:G:C4	1:A:1475:G:C2	3.09	0.40
1:A:1460:C:N4	1:A:1461:G:C6	2.90	0.40
1:A:371:A:H1'	1:A:482:A:H1'	2.02	0.40
1:A:583:A:C6	1:A:759:A:N7	2.90	0.40
1:A:717:U:O2'	1:A:734:G:O4'	2.30	0.40
1:A:741:G:C4	1:A:742:G:C8	3.10	0.40
1:A:78:A:C6	1:A:79:G:C5	3.09	0.40
1:A:815:A:H4'	1:A:817:C:C4	2.56	0.40
1:A:890:G:HO2'	1:A:891:U:P	2.39	0.40
1:A:896:C:H2'	1:A:897:C:H5'	2.03	0.40
2:B:10:LEU:HD21	2:B:12:ALA:O	2.21	0.40
3:C:167:TRP:HE3	3:C:167:TRP:C	2.25	0.40
1:A:619:U:C2	4:D:132:ILE:HD12	2.57	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:156:LYS:CD	8:H:71:VAL:HG13	2.51	0.40
6:F:32:ALA:O	6:F:34:GLY:N	2.53	0.40
6:F:3:HIS:CE1	6:F:65:GLU:HG3	2.56	0.40
10:J:91:ASP:O	10:J:92:LEU:HG	2.22	0.40
17:Q:17:MET:N	17:Q:17:MET:SD	2.94	0.40
17:Q:21:ILE:HG23	17:Q:21:ILE:O	2.20	0.40
18:R:71:THR:OG1	18:R:72:ASP:N	2.55	0.40
21:U:26:ALA:HA	21:U:29:LEU:HB3	2.03	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%)	137 (63%)	46 (21%)	33 (15%)	0	1
3	C	204/206 (99%)	149 (73%)	44 (22%)	11 (5%)	3	8
4	D	203/205 (99%)	150 (74%)	32 (16%)	21 (10%)	1	1
5	E	148/150 (99%)	92 (62%)	36 (24%)	20 (14%)	0	1
6	F	98/100 (98%)	66 (67%)	17 (17%)	15 (15%)	0	1
7	G	149/151 (99%)	119 (80%)	18 (12%)	12 (8%)	1	3
8	H	127/129 (98%)	102 (80%)	16 (13%)	9 (7%)	2	4
9	I	125/127 (98%)	86 (69%)	28 (22%)	11 (9%)	1	2
10	J	96/98 (98%)	70 (73%)	15 (16%)	11 (12%)	1	1
11	K	115/117 (98%)	81 (70%)	25 (22%)	9 (8%)	1	3
12	L	121/123 (98%)	88 (73%)	18 (15%)	15 (12%)	1	1
13	M	112/114 (98%)	81 (72%)	23 (20%)	8 (7%)	2	4
14	N	92/100 (92%)	60 (65%)	15 (16%)	17 (18%)	0	0
15	O	86/88 (98%)	72 (84%)	10 (12%)	4 (5%)	4	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	P	80/82 (98%)	61 (76%)	14 (18%)	5 (6%)	2	5
17	Q	78/80 (98%)	56 (72%)	13 (17%)	9 (12%)	1	1
18	R	53/55 (96%)	34 (64%)	12 (23%)	7 (13%)	0	1
19	S	77/79 (98%)	60 (78%)	12 (16%)	5 (6%)	2	5
20	T	83/85 (98%)	62 (75%)	16 (19%)	5 (6%)	2	6
21	U	49/51 (96%)	24 (49%)	12 (24%)	13 (26%)	0	0
All	All	2312/2358 (98%)	1650 (71%)	422 (18%)	240 (10%)	1	1

All (240) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	16	PHE
2	B	36	ASN
2	B	124	GLY
2	B	170	HIS
2	B	193	PRO
2	B	194	ASP
2	B	207	ILE
2	B	208	ARG
2	B	220	THR
3	C	66	VAL
3	C	146	ALA
3	C	156	ARG
4	D	23	SER
4	D	29	ASP
4	D	32	CYS
4	D	153	SER
5	E	45	ARG
5	E	98	PRO
5	E	100	SER
5	E	103	THR
5	E	105	ILE
5	E	123	VAL
5	E	138	ARG
6	F	55	HIS
6	F	56	LYS
6	F	86	ARG
6	F	91	ARG
6	F	92	THR
6	F	93	LYS

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Mol	Chain	Res	Type
6	F	98	GLU
7	G	9	GLN
7	G	56	LYS
7	G	130	ASN
9	I	41	ARG
9	I	103	PHE
9	I	120	LYS
10	J	35	GLN
10	J	38	GLY
10	J	57	VAL
10	J	89	ARG
10	J	92	LEU
11	K	52	PHE
11	K	127	ARG
12	L	4	VAL
12	L	15	LYS
12	L	23	ALA
12	L	24	LEU
12	L	26	ALA
12	L	43	LYS
12	L	44	LYS
12	L	76	GLU
12	L	77	HIS
12	L	89	ASP
12	L	93	VAL
12	L	117	TYR
13	M	11	ASP
13	M	41	GLU
14	N	29	ALA
14	N	34	VAL
14	N	52	PRO
14	N	53	ARG
14	N	92	GLU
15	O	73	LYS
17	Q	13	VAL
17	Q	51	ASN
17	Q	52	GLU
18	R	26	ILE
18	R	47	THR
19	S	5	LEU
20	T	4	ILE
20	T	6	SER

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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	40	LYS
21	U	53	VAL
2	B	13	GLY
2	B	17	GLY
2	B	34	ALA
2	B	35	ARG
2	B	41	ILE
2	B	116	ASP
2	B	120	GLN
2	B	166	ALA
2	B	222	ARG
3	C	12	LEU
3	C	127	ARG
3	C	175	LEU
3	C	192	THR
4	D	4	TYR
4	D	28	ILE
4	D	35	GLU
4	D	175	ALA
5	E	12	GLN
5	E	51	GLY
5	E	99	ALA
5	E	101	GLU
5	E	142	ASP
6	F	14	GLN
6	F	15	SER
7	G	84	THR
7	G	146	GLU
8	H	31	LYS
8	H	89	LYS
9	I	26	GLY
10	J	36	VAL
10	J	41	PRO
11	K	78	GLY
11	K	92	GLY
12	L	17	ALA
12	L	34	CYS
13	M	12	HIS

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Mol	Chain	Res	Type
13	M	25	VAL
13	M	111	GLY
14	N	22	ALA
14	N	59	ARG
14	N	62	ASN
15	O	20	ASN
16	P	24	SER
16	P	77	GLU
16	P	80	LYS
17	Q	5	ILE
17	Q	20	SER
17	Q	76	VAL
18	R	21	ILE
18	R	71	THR
20	T	67	ILE
21	U	10	GLU
21	U	13	ASP
21	U	52	ALA
2	B	12	ALA
2	B	19	GLN
2	B	51	ASN
2	B	126	PHE
2	B	203	ASN
2	B	209	ALA
3	C	80	LYS
3	C	89	LYS
4	D	5	LEU
4	D	36	GLN
4	D	47	ARG
4	D	148	LYS
4	D	154	ARG
4	D	174	ASP
5	E	24	THR
5	E	113	ALA
5	E	122	ASN
5	E	147	MET
6	F	13	ASP
6	F	17	GLN
7	G	3	ARG
8	H	54	ASP
8	H	83	LEU
9	I	23	PRO

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Mol	Chain	Res	Type
9	I	58	VAL
10	J	17	LEU
10	J	95	GLY
11	K	15	GLN
12	L	88	LYS
13	M	7	ILE
13	M	114	LYS
14	N	13	ARG
14	N	23	LYS
14	N	58	SER
16	P	79	ASN
19	S	6	LYS
19	S	28	LYS
19	S	32	ARG
2	B	63	ARG
2	B	86	SER
2	B	136	MET
2	B	141	LEU
4	D	30	THR
4	D	165	ARG
4	D	192	SER
5	E	102	GLY
6	F	63	ASN
7	G	82	GLY
8	H	67	GLN
9	I	55	VAL
9	I	129	LYS
10	J	90	LEU
11	K	126	LYS
13	M	24	GLY
14	N	3	LYS
14	N	81	ARG
15	O	46	HIS
17	Q	12	VAL
17	Q	53	CYS
18	R	34	THR
20	T	7	ALA
21	U	11	PRO
21	U	36	GLU
2	B	76	ALA
2	B	149	GLY
3	C	7	PRO

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Mol	Chain	Res	Type
3	C	84	VAL
4	D	10	LYS
4	D	37	ALA
4	D	85	ASN
6	F	95	ALA
7	G	8	GLY
7	G	12	ILE
7	G	113	ASP
7	G	140	ASP
9	I	13	LYS
10	J	42	LEU
14	N	50	THR
14	N	64	CYS
15	O	18	ASP
17	Q	17	MET
18	R	25	ASP
18	R	52	GLN
21	U	51	SER
2	B	33	GLY
2	B	82	ASP
4	D	167	LYS
5	E	126	LYS
6	F	18	VAL
8	H	57	PRO
8	H	97	ALA
14	N	11	VAL
14	N	27	LEU
21	U	39	GLU
21	U	41	PRO
9	I	104	VAL
11	K	120	GLY
16	P	42	ILE
5	E	158	GLY
8	H	75	ILE
11	K	91	PRO
6	F	60	VAL
7	G	14	PRO
8	H	120	GLY
2	B	182	PRO
5	E	150	PRO
9	I	50	GLN
19	S	30	PRO

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Mol	Chain	Res	Type
11	K	117	PRO

5.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	180/180 (100%)	131 (73%)	49 (27%)	0	2
3	C	170/170 (100%)	136 (80%)	34 (20%)	2	6
4	D	172/172 (100%)	140 (81%)	32 (19%)	2	7
5	E	113/113 (100%)	86 (76%)	27 (24%)	1	3
6	F	87/87 (100%)	63 (72%)	24 (28%)	0	1
7	G	124/124 (100%)	86 (69%)	38 (31%)	0	1
8	H	104/104 (100%)	82 (79%)	22 (21%)	1	4
9	I	105/105 (100%)	73 (70%)	32 (30%)	0	1
10	J	86/86 (100%)	68 (79%)	18 (21%)	1	5
11	K	90/90 (100%)	65 (72%)	25 (28%)	0	1
12	L	103/103 (100%)	81 (79%)	22 (21%)	1	4
13	M	92/92 (100%)	66 (72%)	26 (28%)	0	1
14	N	79/83 (95%)	67 (85%)	12 (15%)	4	12
15	O	75/76 (99%)	59 (79%)	16 (21%)	1	4
16	P	65/65 (100%)	49 (75%)	16 (25%)	1	3
17	Q	74/74 (100%)	49 (66%)	25 (34%)	0	1
18	R	48/48 (100%)	38 (79%)	10 (21%)	2	5
19	S	70/70 (100%)	57 (81%)	13 (19%)	2	7
20	T	65/65 (100%)	48 (74%)	17 (26%)	1	2
21	U	44/44 (100%)	27 (61%)	17 (39%)	0	0
All	All	1946/1951 (100%)	1471 (76%)	475 (24%)	1	3

All (475) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	11	LYS
2	B	15	HIS
2	B	16	PHE
2	B	20	THR
2	B	21	ARG
2	B	24	ASN
2	B	27	MET
2	B	40	ILE
2	B	43	LEU
2	B	49	MET
2	B	50	PHE
2	B	66	LYS
2	B	67	ILE
2	B	68	LEU
2	B	77	SER
2	B	78	GLU
2	B	80	VAL
2	B	85	LEU
2	B	88	ASP
2	B	94	HIS
2	B	95	ARG
2	B	96	TRP
2	B	102	THR
2	B	103	ASN
2	B	106	THR
2	B	116	ASP
2	B	117	LEU
2	B	122	GLN
2	B	125	THR
2	B	126	PHE
2	B	127	ASP
2	B	130	THR
2	B	142	GLU
2	B	144	LEU
2	B	145	GLU
2	B	148	LEU
2	B	157	LEU
2	B	163	VAL
2	B	174	LYS
2	B	179	LEU
2	B	187	VAL
2	B	192	ASP
2	B	205	ASP

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Mol	Chain	Res	Type
2	B	207	ILE
2	B	210	VAL
2	B	213	TYR
2	B	220	THR
2	B	222	ARG
2	B	225	ARG
3	C	3	GLN
3	C	16	LYS
3	C	18	TRP
3	C	29	PHE
3	C	32	ASN
3	C	33	LEU
3	C	36	ASP
3	C	37	PHE
3	C	38	LYS
3	C	43	LEU
3	C	45	LYS
3	C	53	SER
3	C	55	ILE
3	C	70	THR
3	C	80	LYS
3	C	103	ILE
3	C	107	ARG
3	C	110	GLU
3	C	119	SER
3	C	120	ILE
3	C	121	THR
3	C	131	ARG
3	C	140	ASN
3	C	151	VAL
3	C	153	VAL
3	C	167	TRP
3	C	168	TYR
3	C	170	GLU
3	C	172	ARG
3	C	175	LEU
3	C	179	ARG
3	C	192	THR
3	C	193	TYR
3	C	206	GLU
4	D	8	LYS
4	D	9	LEU

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Mol	Chain	Res	Type
4	D	10	LYS
4	D	17	THR
4	D	32	CYS
4	D	48	LEU
4	D	50	ASP
4	D	54	GLN
4	D	55	LEU
4	D	56	ARG
4	D	58	LYS
4	D	59	GLN
4	D	74	ASN
4	D	75	TYR
4	D	83	LYS
4	D	104	ARG
4	D	142	VAL
4	D	148	LYS
4	D	152	GLN
4	D	155	VAL
4	D	159	LEU
4	D	160	GLU
4	D	161	LEU
4	D	177	LYS
4	D	183	LYS
4	D	191	LEU
4	D	192	SER
4	D	195	ILE
4	D	198	HIS
4	D	200	ILE
4	D	203	LEU
4	D	206	LYS
5	E	15	LEU
5	E	18	VAL
5	E	26	LYS
5	E	29	ARG
5	E	32	SER
5	E	45	ARG
5	E	52	LYS
5	E	65	GLU
5	E	66	LYS
5	E	76	LEU
5	E	77	ASN
5	E	86	LYS

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Mol	Chain	Res	Type
5	E	96	MET
5	E	97	GLN
5	E	101	GLU
5	E	105	ILE
5	E	114	VAL
5	E	115	LEU
5	E	120	VAL
5	E	121	HIS
5	E	124	LEU
5	E	131	THR
5	E	137	VAL
5	E	140	THR
5	E	149	SER
5	E	151	GLU
5	E	156	LYS
6	F	1	MET
6	F	2	ARG
6	F	9	MET
6	F	15	SER
6	F	24	ARG
6	F	26	THR
6	F	30	THR
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	62	MET
6	F	63	ASN
6	F	64	VAL
6	F	79	ARG
6	F	80	PHE
6	F	85	ILE
6	F	87	SER
6	F	89	VAL
6	F	93	LYS
6	F	97	THR
7	G	3	ARG
7	G	4	ARG
7	G	6	VAL

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Mol	Chain	Res	Type
7	G	10	ARG
7	G	11	LYS
7	G	12	ILE
7	G	22	LEU
7	G	23	LEU
7	G	30	LEU
7	G	38	THR
7	G	45	SER
7	G	47	LEU
7	G	48	GLU
7	G	53	ARG
7	G	59	LEU
7	G	62	PHE
7	G	67	GLU
7	G	69	VAL
7	G	70	ARG
7	G	72	THR
7	G	73	VAL
7	G	75	VAL
7	G	78	ARG
7	G	84	THR
7	G	87	VAL
7	G	91	VAL
7	G	92	ARG
7	G	94	VAL
7	G	97	ASN
7	G	120	LEU
7	G	125	SER
7	G	126	ASP
7	G	129	GLU
7	G	133	THR
7	G	136	LYS
7	G	140	ASP
7	G	142	HIS
7	G	146	GLU
8	H	13	ARG
8	H	22	LYS
8	H	31	LYS
8	H	47	GLU
8	H	49	PHE
8	H	54	ASP
8	H	55	THR

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Mol	Chain	Res	Type
8	H	59	LEU
8	H	67	GLN
8	H	73	GLU
8	H	74	SER
8	H	75	ILE
8	H	77	ARG
8	H	83	LEU
8	H	87	LYS
8	H	89	LYS
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	13	LYS
9	I	18	ARG
9	I	21	ILE
9	I	28	ILE
9	I	32	GLN
9	I	33	ARG
9	I	36	GLU
9	I	39	PHE
9	I	43	THR
9	I	45	ARG
9	I	48	VAL
9	I	49	ARG
9	I	55	VAL
9	I	57	MET
9	I	61	LEU
9	I	62	ASP
9	I	63	LEU
9	I	68	LYS
9	I	80	ARG
9	I	85	ARG
9	I	88	MET
9	I	89	GLU
9	I	90	TYR
9	I	94	LEU
9	I	97	GLU
9	I	99	ARG

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Mol	Chain	Res	Type
9	I	100	LYS
9	I	105	THR
9	I	115	LYS
9	I	127	PHE
9	I	129	LYS
10	J	5	ARG
10	J	16	ARG
10	J	22	THR
10	J	25	ILE
10	J	26	VAL
10	J	27	GLU
10	J	32	THR
10	J	59	LYS
10	J	63	ASP
10	J	77	VAL
10	J	80	THR
10	J	83	THR
10	J	84	VAL
10	J	87	LEU
10	J	89	ARG
10	J	91	ASP
10	J	92	LEU
10	J	102	LEU
11	K	14	LYS
11	K	15	GLN
11	K	17	SER
11	K	31	ILE
11	K	64	GLN
11	K	65	VAL
11	K	74	VAL
11	K	77	TYR
11	K	80	LYS
11	K	81	ASN
11	K	82	LEU
11	K	83	GLU
11	K	86	VAL
11	K	93	ARG
11	K	96	THR
11	K	100	LEU
11	K	101	ASN
11	K	106	ARG
11	K	107	ILE

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Mol	Chain	Res	Type
11	K	108	THR
11	K	109	ASN
11	K	110	ILE
11	K	126	LYS
11	K	127	ARG
11	K	128	ARG
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	29	GLN
12	L	34	CYS
12	L	35	THR
12	L	44	LYS
12	L	58	THR
12	L	59	ASN
12	L	63	VAL
12	L	82	ILE
12	L	86	ARG
12	L	89	ASP
12	L	94	ARG
12	L	97	THR
12	L	110	ARG
12	L	121	ARG
13	M	8	ASN
13	M	14	HIS
13	M	19	LEU
13	M	29	ARG
13	M	31	LYS
13	M	41	GLU
13	M	48	LEU
13	M	53	ILE
13	M	54	ASP
13	M	58	ASP
13	M	59	GLU
13	M	60	VAL
13	M	63	PHE
13	M	66	GLU

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Mol	Chain	Res	Type
13	M	72	GLU
13	M	74	SER
13	M	76	SER
13	M	80	LEU
13	M	83	LEU
13	M	90	ARG
13	M	91	HIS
13	M	92	ARG
13	M	93	ARG
13	M	100	GLN
13	M	101	ARG
13	M	102	THR
14	N	4	GLN
14	N	16	LEU
14	N	18	ASP
14	N	21	PHE
14	N	23	LYS
14	N	26	GLU
14	N	28	LYS
14	N	48	LEU
14	N	49	GLN
14	N	60	GLN
14	N	67	THR
14	N	80	SER
15	O	6	GLU
15	O	10	LYS
15	O	13	SER
15	O	17	ARG
15	O	18	ASP
15	O	26	GLU
15	O	35	GLN
15	O	38	HIS
15	O	39	LEU
15	O	62	GLN
15	O	64	ARG
15	O	67	LEU
15	O	70	LEU
15	O	85	LEU
15	O	87	LEU
15	O	88	ARG
16	P	1	MET
16	P	2	VAL

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Mol	Chain	Res	Type
16	P	5	ARG
16	P	18	GLN
16	P	25	ARG
16	P	29	ASN
16	P	31	ARG
16	P	36	VAL
16	P	46	LYS
16	P	48	GLU
16	P	51	ARG
16	P	57	ILE
16	P	69	ASP
16	P	74	LEU
16	P	77	GLU
16	P	80	LYS
17	Q	4	LYS
17	Q	5	ILE
17	Q	12	VAL
17	Q	13	VAL
17	Q	14	SER
17	Q	17	MET
17	Q	23	VAL
17	Q	25	ILE
17	Q	28	PHE
17	Q	33	ILE
17	Q	36	LYS
17	Q	38	ILE
17	Q	40	ARG
17	Q	41	THR
17	Q	48	ASP
17	Q	50	ASN
17	Q	52	GLU
17	Q	55	ILE
17	Q	57	ASP
17	Q	62	ARG
17	Q	65	ARG
17	Q	69	LYS
17	Q	75	LEU
17	Q	79	VAL
17	Q	81	LYS
18	R	20	GLU
18	R	26	ILE
18	R	29	LEU

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Mol	Chain	Res	Type
18	R	33	ILE
18	R	45	THR
18	R	47	THR
18	R	57	ARG
18	R	61	ARG
18	R	63	ARG
18	R	67	LEU
19	S	5	LEU
19	S	6	LYS
19	S	11	ILE
19	S	14	HIS
19	S	19	VAL
19	S	21	LYS
19	S	23	VAL
19	S	33	THR
19	S	36	ARG
19	S	39	THR
19	S	43	ASN
19	S	49	ILE
19	S	56	GLN
20	T	6	SER
20	T	8	LYS
20	T	12	ILE
20	T	15	GLU
20	T	23	SER
20	T	24	ARG
20	T	27	MET
20	T	29	ARG
20	T	36	TYR
20	T	49	LYS
20	T	54	MET
20	T	58	VAL
20	T	64	LYS
20	T	67	ILE
20	T	69	LYS
20	T	70	ASN
20	T	76	LYS
21	U	5	LYS
21	U	7	ARG
21	U	10	GLU
21	U	12	PHE
21	U	14	VAL

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Mol	Chain	Res	Type
21	U	16	LEU
21	U	19	PHE
21	U	20	LYS
21	U	24	GLU
21	U	25	LYS
21	U	28	VAL
21	U	31	GLU
21	U	34	ARG
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 (8) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	15	HIS
2	B	103	ASN
3	C	176	HIS
4	D	74	ASN
7	G	130	ASN
10	J	70	HIS
18	R	74	HIS
20	T	68	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1538/1539 (99%)	340 (22%)	9 (0%)

All (340) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	5	U
1	A	6	G
1	A	8	A
1	A	9	G
1	A	17	U
1	A	19	A
1	A	31	G

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Mol	Chain	Res	Type
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	70	U
1	A	71	A
1	A	73	C
1	A	74	A
1	A	80	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
1	A	93	U
1	A	94	G
1	A	95	C
1	A	97	G
1	A	108	G
1	A	116	A
1	A	117	G
1	A	120	A
1	A	121	U
1	A	122	G
1	A	124	C
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	156	C
1	A	179	A
1	A	182	A
1	A	183	C
1	A	189	A
1	A	195	A

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Mol	Chain	Res	Type
1	A	197	A
1	A	204	G
1	A	207	C
1	A	208	U
1	A	210	C
1	A	211	G
1	A	212	G
1	A	226	G
1	A	240	G
1	A	241	G
1	A	245	U
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	280	C
1	A	289	G
1	A	294	U
1	A	298	A
1	A	315	A
1	A	316	C
1	A	321	A
1	A	328	C
1	A	329	A
1	A	330	C
1	A	331	G
1	A	332	G
1	A	338	A
1	A	345	C
1	A	348	G
1	A	351	G
1	A	352	C
1	A	354	G
1	A	357	G
1	A	367	U
1	A	372	C
1	A	376	G
1	A	378	G
1	A	379	C
1	A	384	G
1	A	398	U
1	A	399	G

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Mol	Chain	Res	Type
1	A	406	G
1	A	412	A
1	A	413	G
1	A	418	C
1	A	421	U
1	A	422	C
1	A	429	U
1	A	430	A
1	A	432	A
1	A	441	A
1	A	446	G
1	A	452	A
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	477	C
1	A	478	A
1	A	479	U
1	A	482	A
1	A	483	C
1	A	484	G
1	A	485	U
1	A	486	U
1	A	498	A
1	A	500	G
1	A	505	G
1	A	509	A
1	A	510	A
1	A	511	C
1	A	517	G
1	A	518	C
1	A	519	C
1	A	522	C
1	A	527	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	536	C
1	A	545	C

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Mol	Chain	Res	Type
1	A	547	A
1	A	549	C
1	A	550	G
1	A	559	A
1	A	564	C
1	A	568	G
1	A	571	U
1	A	572	A
1	A	573	A
1	A	576	C
1	A	577	G
1	A	580	C
1	A	581	G
1	A	596	A
1	A	622	A
1	A	628	G
1	A	650	G
1	A	653	U
1	A	665	A
1	A	666	G
1	A	673	A
1	A	683	G
1	A	687	A
1	A	702	A
1	A	721	G
1	A	723	U
1	A	724	G
1	A	733	G
1	A	747	A
1	A	755	G
1	A	758	C
1	A	760	G
1	A	776	G
1	A	777	A
1	A	785	G
1	A	787	A
1	A	793	U
1	A	794	A
1	A	809	G
1	A	812	G
1	A	814	A
1	A	815	A

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Mol	Chain	Res	Type
1	A	817	C
1	A	819	A
1	A	821	G
1	A	828	U
1	A	832	G
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	859	G
1	A	874	G
1	A	880	C
1	A	885	G
1	A	902	G
1	A	914	A
1	A	919	A
1	A	922	G
1	A	926	G
1	A	934	C
1	A	945	G
1	A	960	U
1	A	966	G
1	A	967	C
1	A	969	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	987	G
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	995	C
1	A	996	A
1	A	1004	A
1	A	1008	U
1	A	1009	U
1	A	1018	G
1	A	1022	A
1	A	1025	U

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Mol	Chain	Res	Type
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	1050	G
1	A	1054	C
1	A	1065	U
1	A	1066	C
1	A	1070	U
1	A	1071	C
1	A	1072	G
1	A	1073	U
1	A	1080	A
1	A	1086	U
1	A	1088	G
1	A	1091	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1104	G
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1129	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

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Mol	Chain	Res	Type
1	A	1155	A
1	A	1157	A
1	A	1159	U
1	A	1160	G
1	A	1161	C
1	A	1168	U
1	A	1178	G
1	A	1184	G
1	A	1186	G
1	A	1193	G
1	A	1196	A
1	A	1202	U
1	A	1212	U
1	A	1213	A
1	A	1227	A
1	A	1230	C
1	A	1236	A
1	A	1238	A
1	A	1240	U
1	A	1246	A
1	A	1253	G
1	A	1256	A
1	A	1257	A
1	A	1260	G
1	A	1269	A
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	1297	G
1	A	1299	A
1	A	1304	G
1	A	1305	G
1	A	1317	C
1	A	1318	A
1	A	1319	A
1	A	1320	C
1	A	1322	C
1	A	1324	A

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Mol	Chain	Res	Type
1	A	1331	G
1	A	1336	C
1	A	1337	G
1	A	1338	G
1	A	1346	A
1	A	1349	A
1	A	1353	G
1	A	1362	A
1	A	1363	A
1	A	1364	U
1	A	1377	A
1	A	1378	C
1	A	1379	G
1	A	1382	C
1	A	1398	A
1	A	1418	A
1	A	1429	A
1	A	1441	A
1	A	1442	G
1	A	1446	A
1	A	1448	C
1	A	1452	C
1	A	1454	G
1	A	1455	G
1	A	1475	G
1	A	1492	A
1	A	1493	A
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	1529	G
1	A	1530	G
1	A	1533	C
1	A	1535	C
1	A	1536	C

All (9) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	96	U
1	A	115	G
1	A	209	U
1	A	429	U
1	A	723	U
1	A	1049	U
1	A	1201	A
1	A	1211	U
1	A	1279	G

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.