



Full wwPDB X-ray Structure Validation Report

Jul 11, 2014 – 11:43 PM EDT

PDB ID : 4L6K
Title : Crystal Structure of Blasticidin S Bound to Thermus Thermophilus 70S Ribosome. This file contains the 30S subunit, tRNA and mRNA molecules from the first 70S ribosome.
Authors : Svidritskiy, E.; Ling, C.; Ermolenko, D.N.; Korostelev, A.A.
Deposited on : 2013-06-12
Resolution : 3.40 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>

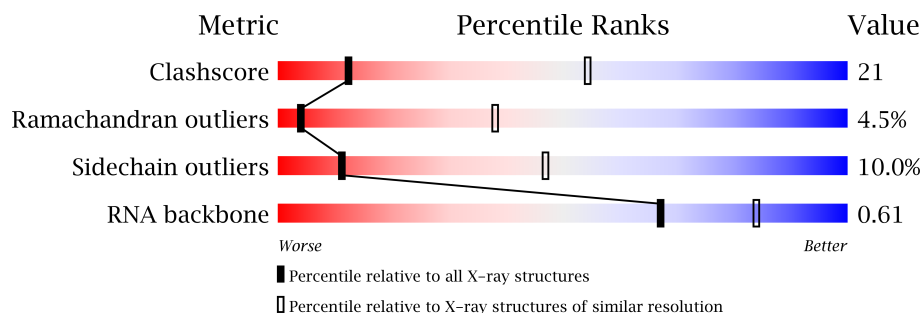
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : **FAILED**
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) : stable23161

1 Overall quality at a glance

The reported resolution of this entry is 3.40 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	1214 (3.50-3.30)
Ramachandran outliers	78287	1177 (3.50-3.30)
Sidechain outliers	78261	1177 (3.50-3.30)
RNA backbone	1838	1002 (4.02-2.76)





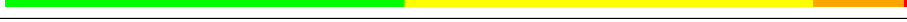

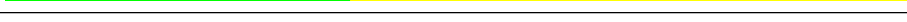

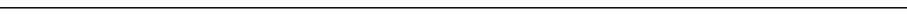

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The 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	1504	
2	B	234	
3	C	206	
4	D	208	
5	E	151	
6	F	101	
7	G	155	
8	H	138	
9	I	127	
10	J	98	
11	K	114	
12	L	122	
13	M	117	
14	N	60	

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Mol	Chain	Length	Quality of chain
15	O	88	
16	P	83	
17	Q	99	
18	R	70	
19	S	78	
20	T	99	
21	U	24	
22	V	77	
22	W	77	
23	X	5	

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 54782 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1504	Total	C	N	O	P	0	0	0
			32336	14391	5994	10447	1504			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	234	Total	C	N	O	S	0	0	0
			1901	1213	341	342	5			

- 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
			1613	1016	314	282	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	151	Total	C	N	O	S	0	0	0
			1156	729	218	205	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

- 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
			1011	639	198	174				

- 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
			795	499	156	139	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	114	Total	C	N	O	S	0	0	0
			843	522	159	159	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	122	Total	C	N	O	S	0	0	0
			957	603	193	160	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	117	Total	C	N	O	S	0	0	0
			934	577	192	163	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	118	ALA	-	EXPRESSION TAG	UNP P62655

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- 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
			734	459	147	126	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	83	Total	C	N	O	S	0	0	0
			701	443	139	118	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	99	Total	C	N	O	S	0	0	0
			824	528	152	142	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	R	70	Total	C	N	O	0	0	0
			574	367	112	95			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	78	Total	C	N	O	S	0	0	0
			630	403	114	111	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	U	24	Total	C	N	O	0	0	0
			209	128	50	31			

- Molecule 22 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	V	77	Total	C	N	O	P	0	0	0
			1640	732	297	535	76			
22	W	77	Total	C	N	O	P	0	0	0
			1640	732	297	535	76			

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	X	5	Total	C	N	O	P	0	0	0
			109	49	22	33	5			

- Molecule 24 is ZINC ION (three-letter code: ZN) (formula: Zn).

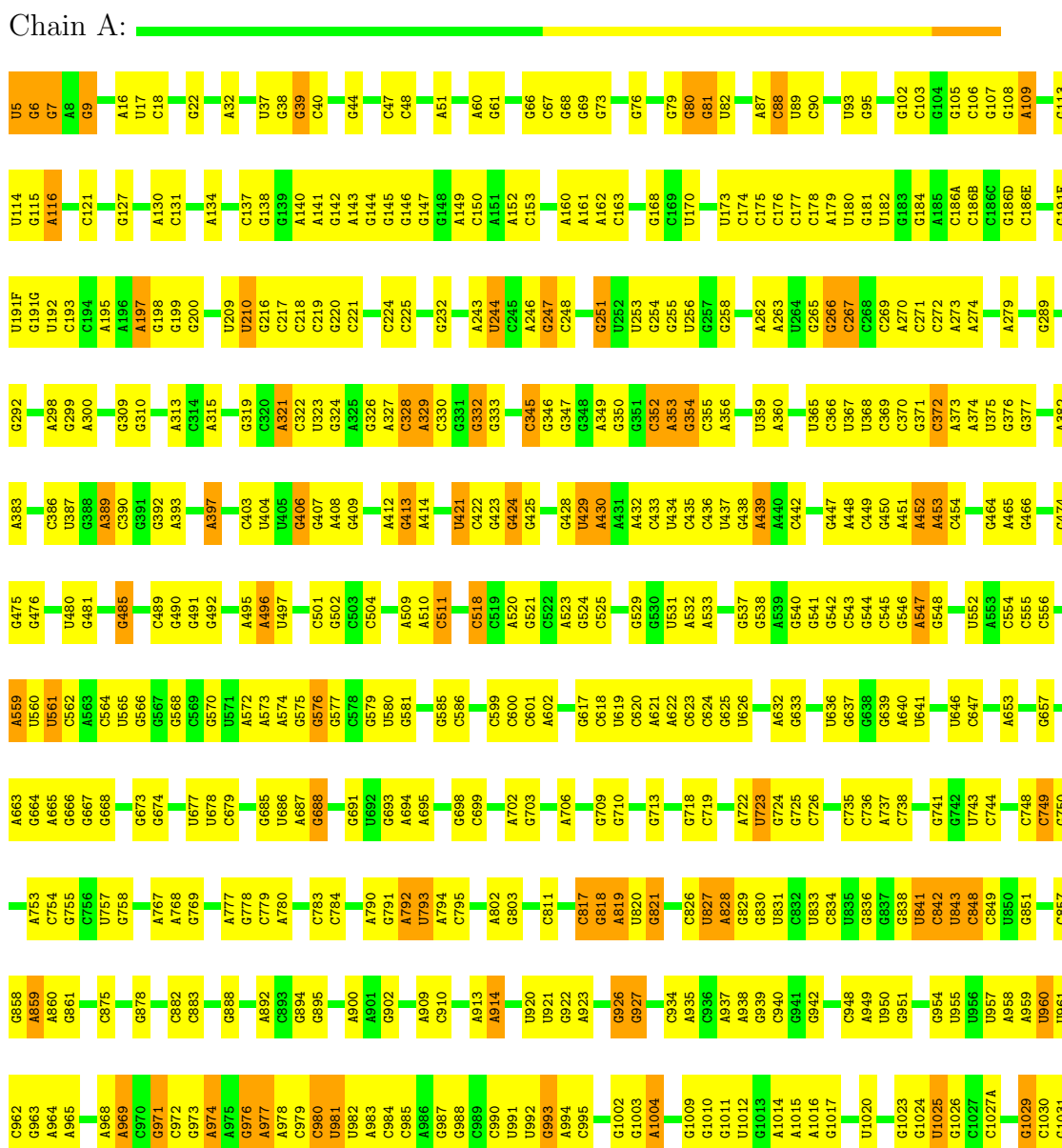
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	D	1	Total	Zn	0	0
			1	1		
24	N	1	Total	Zn	0	0
			1	1		

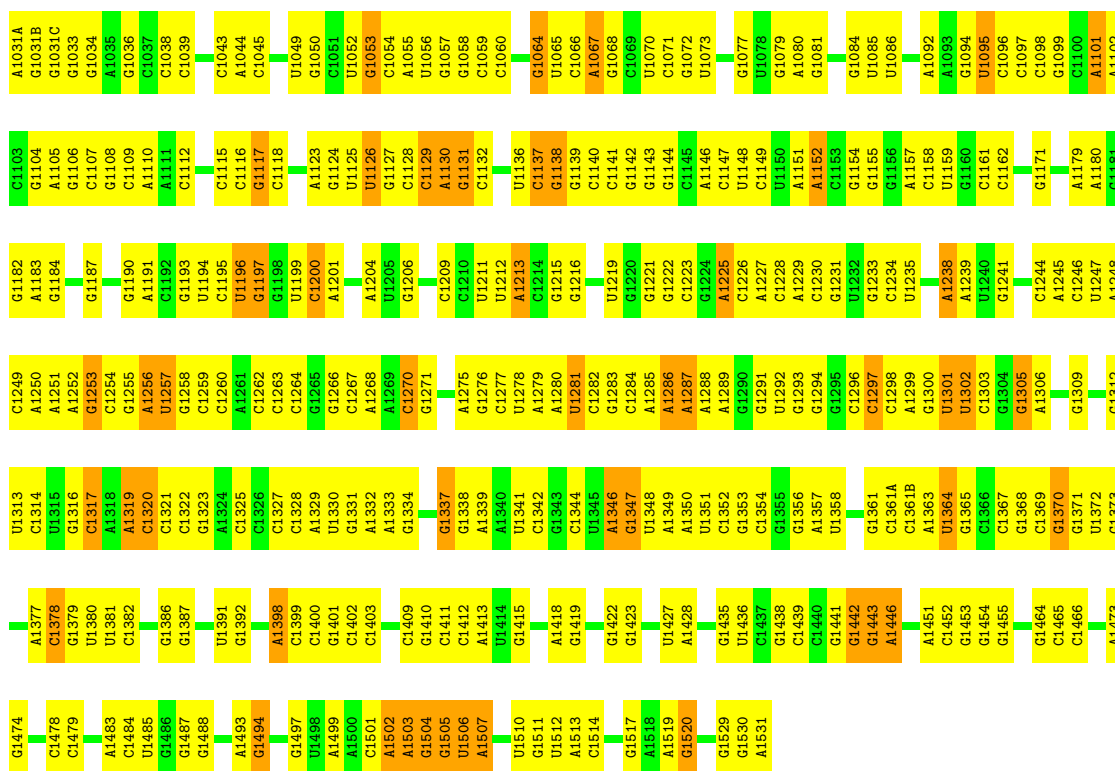
3 Residue-property plots

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

Note EDS was not executed.

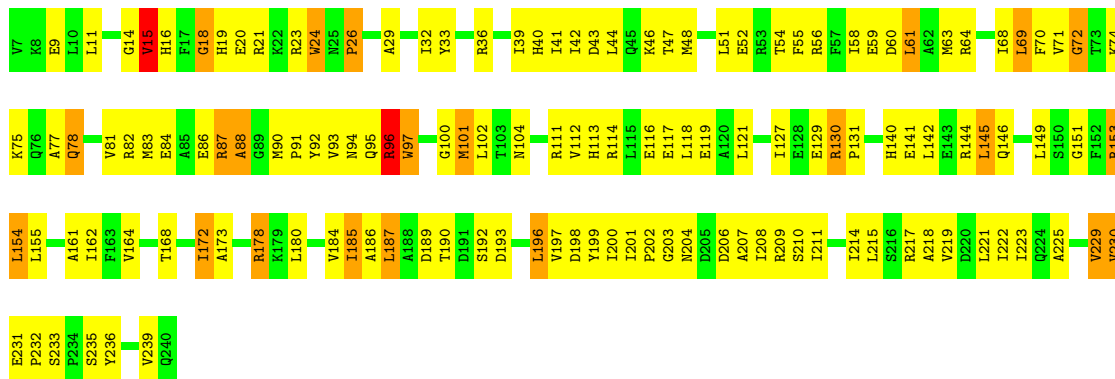
• Molecule 1: 16S ribosomal RNA





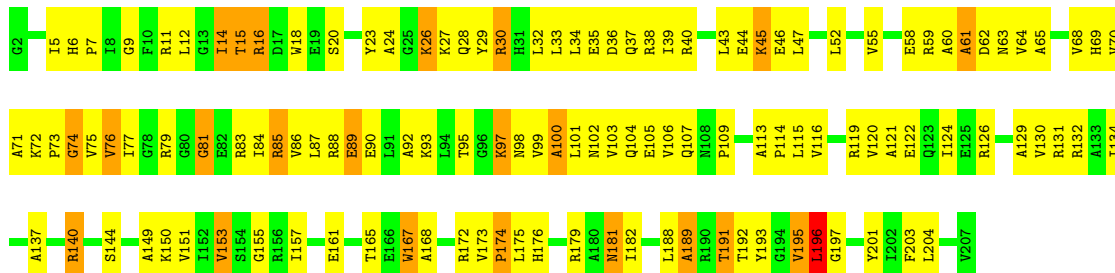
• Molecule 2: 30S ribosomal protein S2

Chain B:

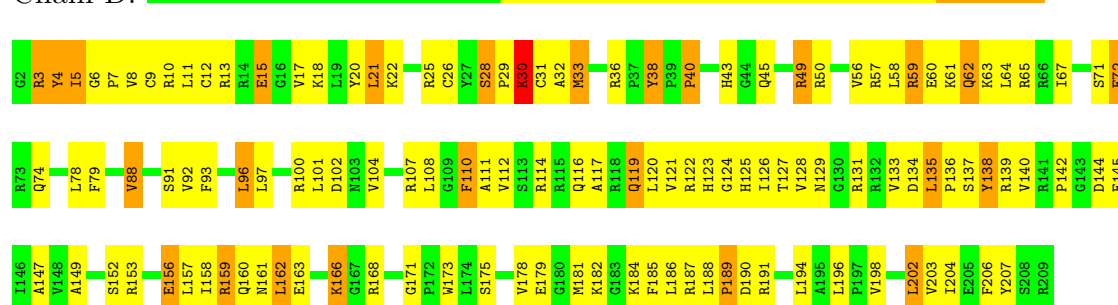


• Molecule 3: 30S ribosomal protein S3

Chain C:



Chain D:



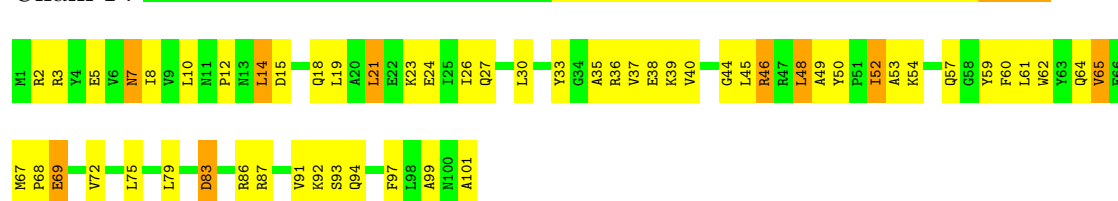
- Molecule 5: 30S ribosomal protein S5

Chain E:



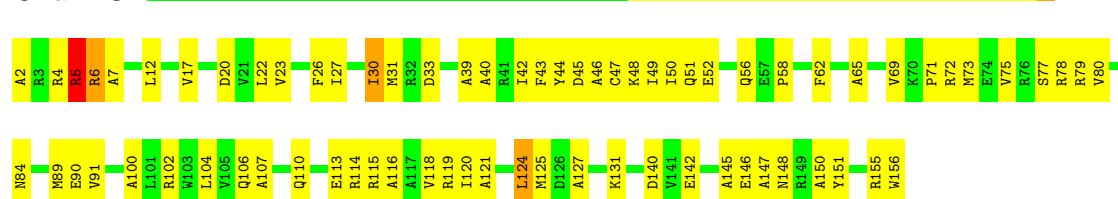
- Molecule 6: 30S ribosomal protein S6

Chain F:



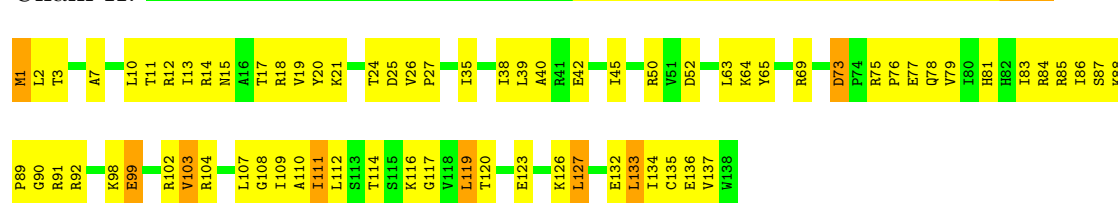
- Molecule 7: 30S ribosomal protein S7

Chain G:



- Molecule 8: 30S ribosomal protein S8

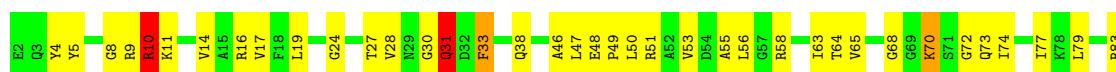
Chain H:



- Molecule 9: 30S ribosomal protein S9

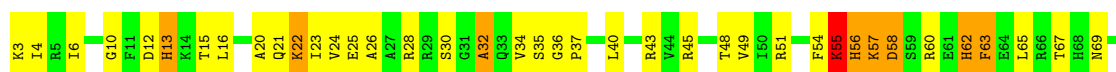
Chain I:





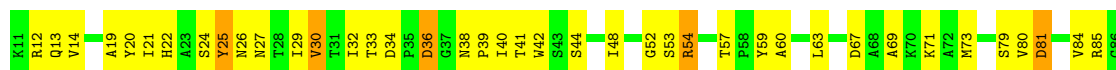
• Molecule 10: 30S ribosomal protein S10

Chain J:



• Molecule 11: 30S ribosomal protein S11

Chain K:



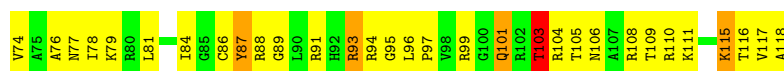
• Molecule 12: 30S ribosomal protein S12

Chain L:



• Molecule 13: 30S ribosomal protein S13

Chain M:



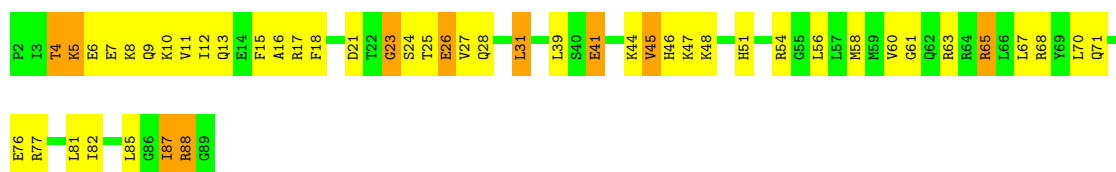
• Molecule 14: 30S ribosomal protein S14

Chain N:



• Molecule 15: 30S ribosomal protein S15

Chain O:



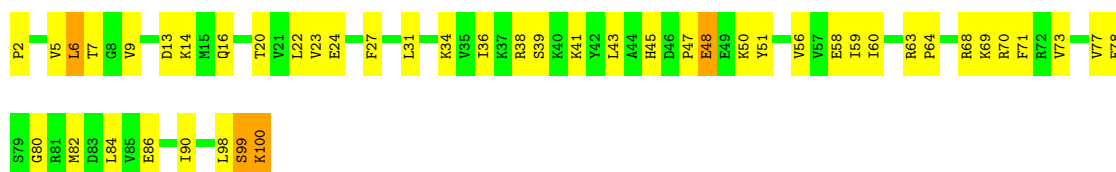
- Molecule 16: 30S ribosomal protein S16

Chain P:



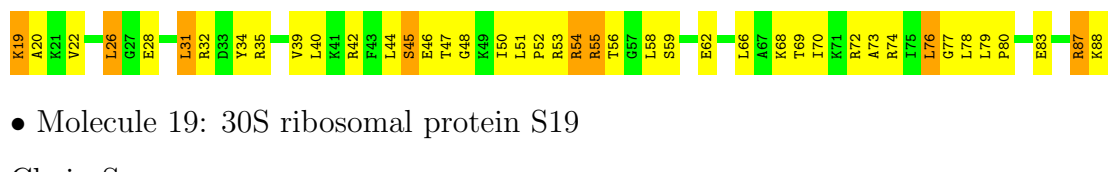
- Molecule 17: 30S ribosomal protein S17

Chain Q:



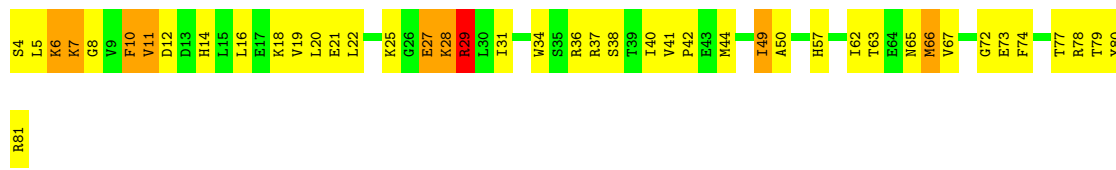
- Molecule 18: 30S ribosomal protein S18

Chain R:



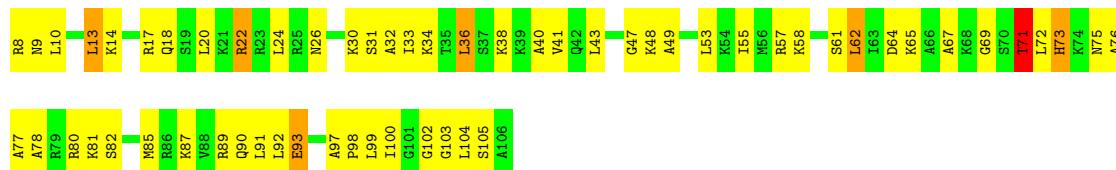
- Molecule 19: 30S ribosomal protein S19

Chain S:



- Molecule 20: 30S ribosomal protein S20

Chain T:



- Molecule 21: 30S ribosomal protein Thx

Chain U:



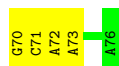
- Molecule 22: tRNA

Chain V:



- Molecule 22: tRNA

Chain W:



- Molecule 23: mRNA

Chain X:



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	211.53Å 454.44Å 620.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.98 – 3.40	Depositor
% Data completeness (in resolution range)	99.8 (49.98-3.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.231 , 0.268	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	54782	wwPDB-VP
Average B, all atoms (Å ²)	108.0	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: ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.28	1/36198 (0.0%)	0.55	0/56497
2	B	0.22	0/1936	0.40	0/2609
3	C	0.22	0/1637	0.40	0/2205
4	D	0.27	0/1733	0.45	0/2318
5	E	0.24	0/1172	0.43	0/1576
6	F	0.24	0/856	0.43	0/1154
7	G	0.22	0/1276	0.36	0/1709
8	H	0.23	0/1136	0.44	0/1527
9	I	0.22	0/1029	0.39	0/1378
10	J	0.21	0/808	0.41	0/1085
11	K	0.23	0/857	0.44	0/1157
12	L	0.25	0/973	0.46	0/1301
13	M	0.21	0/944	0.41	0/1265
14	N	0.24	0/501	0.39	0/664
15	O	0.25	0/745	0.40	0/992
16	P	0.26	0/717	0.45	0/963
17	Q	0.25	0/837	0.42	0/1117
18	R	0.24	0/579	0.44	0/768
19	S	0.20	0/643	0.40	0/865
20	T	0.24	0/764	0.42	0/1006
21	U	0.20	0/213	0.37	0/277
22	V	0.21	0/1832	0.48	0/2855
22	W	0.17	0/1832	0.44	0/2855
23	X	0.26	0/122	0.47	0/188
All	All	0.26	1/59340 (0.0%)	0.51	0/88331

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	5	U	OP3-P	-10.80	1.48	1.61

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	32336	0	16317	769	0
2	B	1901	0	1951	125	0
3	C	1613	0	1677	116	0
4	D	1703	0	1764	134	0
5	E	1156	0	1213	73	0
6	F	843	0	857	62	0
7	G	1257	0	1296	52	0
8	H	1116	0	1177	67	0
9	I	1011	0	1043	95	0
10	J	795	0	840	62	0
11	K	843	0	859	54	0
12	L	957	0	1046	68	0
13	M	934	0	992	74	0
14	N	492	0	531	46	0
15	O	734	0	771	44	0
16	P	701	0	720	51	0
17	Q	824	0	893	42	0
18	R	574	0	644	47	0
19	S	630	0	652	57	0
20	T	762	0	859	45	0
21	U	209	0	221	19	0
22	V	1640	0	837	33	0
22	W	1640	0	837	50	0
23	X	109	0	55	0	0
24	D	1	0	0	0	0
24	N	1	0	0	0	0
All	All	54782	0	38052	1965	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 21.

All (1965) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
22:V:74:C:H5''	22:V:75:C:H5''	1.43	1.01
1:A:979:C:H3'	1:A:980:C:H5''	1.40	0.99
1:A:545:C:H5'	4:D:72:GLU:HG3	1.42	0.98
3:C:33:LEU:HD21	14:N:53:LEU:HD22	1.46	0.97
9:I:28:VAL:HG22	9:I:63:ILE:HB	1.42	0.97
1:A:559:A:H4'	1:A:560:U:H3'	1.45	0.96
2:B:204:ASN:HD21	2:B:207:ALA:H	1.07	0.96
12:L:46:LYS:HG3	12:L:47:PRO:HD3	1.49	0.95
16:P:75:ARG:HH11	16:P:75:ARG:HG3	1.33	0.94
17:Q:7:THR:HG22	17:Q:58:GLU:HG2	1.50	0.94
10:J:49:VAL:HG23	14:N:41:ARG:HB2	1.52	0.92
10:J:63:PHE:HA	14:N:59:ALA:H	1.34	0.92
22:W:1:C:H42	22:W:72:A:H61	1.17	0.92
22:W:54:U:H3	22:W:58:A:H62	1.16	0.92
5:E:11:ILE:HD13	5:E:31:LEU:HD12	1.51	0.91
8:H:7:ALA:HB2	8:H:85:ARG:HD3	1.51	0.90
8:H:114:THR:HG23	8:H:116:LYS:H	1.36	0.90
8:H:86:ILE:HG21	8:H:133:LEU:HD13	1.53	0.90
6:F:97:PHE:HD2	18:R:31:LEU:HD21	1.34	0.89
12:L:37:THR:HG23	12:L:38:VAL:HG23	1.54	0.89
1:A:972:C:H4'	10:J:57:LYS:HG3	1.54	0.88
16:P:49:LEU:HD23	16:P:50:LYS:N	1.90	0.87
5:E:50:GLU:HG2	5:E:52:PRO:HD2	1.58	0.85
2:B:16:HIS:HD2	2:B:210:SER:HA	1.40	0.85
7:G:151:TYR:HE2	11:K:54:ARG:HH21	1.24	0.85
11:K:41:THR:HG22	11:K:42:TRP:H	1.43	0.84
15:O:82:ILE:HG23	15:O:87:ILE:HG22	1.58	0.84
1:A:1117:G:H4'	9:I:104:ARG:HH21	1.42	0.83
1:A:436:C:H2'	1:A:437:U:H6	1.42	0.83
9:I:113:LYS:HG2	9:I:119:ALA:HA	1.61	0.82
6:F:35:ALA:HB1	6:F:65:VAL:HG21	1.61	0.82
9:I:125:TYR:HD2	9:I:126:SER:H	1.22	0.82
1:A:501:C:H2'	1:A:502:G:H8	1.45	0.82
12:L:86:GLY:HA2	12:L:97:TYR:HA	1.61	0.82
1:A:841:U:O2'	1:A:842:C:H5''	1.79	0.82
2:B:69:LEU:HB3	2:B:162:ILE:HG22	1.60	0.82
19:S:63:THR:H	19:S:66:MET:HE3	1.40	0.82
1:A:976:G:N2	1:A:1361(A):C:H2'	1.95	0.81
1:A:1281:U:H5'	1:A:1282:C:C5	2.16	0.81
1:A:1268:A:H4'	21:U:20:LYS:HA	1.62	0.81
1:A:818:G:O2'	1:A:819:A:H5''	1.80	0.81
4:D:189:PRO:HB2	4:D:194:LEU:HD21	1.62	0.80

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:22:HIS:HB3	11:K:29:ILE:HG13	1.63	0.80
11:K:57:THR:HG23	11:K:60:ALA:H	1.46	0.80
4:D:29:PRO:HG2	4:D:30:LYS:HZ1	1.47	0.80
10:J:48:THR:HA	10:J:62:HIS:HB3	1.62	0.80
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.64	0.80
16:P:22:THR:HA	16:P:33:ILE:HG12	1.62	0.79
1:A:1281:U:H4'	1:A:1282:C:OP2	1.82	0.79
14:N:27:CYS:SG	14:N:29:ARG:HG3	2.21	0.79
2:B:208:ILE:HD12	2:B:208:ILE:H	1.48	0.79
3:C:43:LEU:O	3:C:47:LEU:HB3	1.83	0.79
4:D:119:GLN:HG3	4:D:123:HIS:CD2	2.18	0.79
10:J:92:THR:HG23	10:J:93:GLY:H	1.48	0.78
12:L:38:VAL:HB	12:L:56:LYS:HD3	1.65	0.78
1:A:1031(A):A:H5''	1:A:1031(B):G:OP2	1.82	0.78
15:O:16:ALA:HB1	15:O:21:ASP:HB3	1.64	0.78
2:B:154:LEU:HD13	2:B:154:LEU:H	1.49	0.78
10:J:4:ILE:HB	10:J:74:ILE:HB	1.65	0.78
6:F:10:LEU:HD13	6:F:61:LEU:HD13	1.64	0.78
2:B:18:GLY:H	2:B:42:ILE:HG22	1.48	0.78
2:B:172:ILE:HD12	2:B:173:ALA:H	1.48	0.77
19:S:50:ALA:HB1	19:S:57:HIS:HB3	1.64	0.77
1:A:1285:A:H1'	1:A:1286:A:OP2	1.84	0.77
4:D:117:ALA:O	4:D:121:VAL:HG23	1.84	0.77
6:F:7:ASN:HD21	18:R:34:TYR:HE1	1.31	0.77
3:C:47:LEU:HD21	3:C:68:VAL:HG11	1.65	0.77
1:A:624:C:H4'	16:P:10:GLY:HA2	1.67	0.77
1:A:1128:C:H4'	9:I:16:ARG:HH12	1.49	0.76
6:F:33:TYR:HB2	6:F:75:LEU:HD12	1.68	0.76
12:L:51:LEU:HD23	12:L:51:LEU:H	1.50	0.76
1:A:134:A:H61	16:P:25:ARG:HH12	1.31	0.76
7:G:115:ARG:O	7:G:118:VAL:HG22	1.86	0.76
10:J:49:VAL:O	10:J:60:ARG:HB2	1.86	0.76
19:S:31:ILE:HG23	19:S:49:ILE:HA	1.67	0.76
2:B:55:PHE:HE1	2:B:218:ALA:HA	1.51	0.76
1:A:1226:C:H2'	13:M:103:THR:HG22	1.67	0.75
1:A:1301:U:H3'	1:A:1302:U:H5''	1.66	0.75
1:A:1329:A:H62	21:U:7:ARG:NH2	1.85	0.75
1:A:1513:A:H2'	1:A:1514:C:C6	2.22	0.75
1:A:1342:C:H4'	9:I:125:TYR:HB3	1.69	0.75
22:W:9:G:H5'	22:W:46:G:H1'	1.66	0.75
1:A:1348:U:H4'	9:I:120:ARG:HD2	1.67	0.75
9:I:16:ARG:HB2	9:I:64:THR:HG22	1.69	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:45:LYS:HG2	12:L:46:LYS:H	1.52	0.75
13:M:39:ILE:HG13	13:M:56:LEU:HD21	1.69	0.75
12:L:32:ARG:HD3	12:L:61:SER:HB3	1.68	0.74
20:T:20:LEU:O	20:T:24:LEU:HD23	1.87	0.74
3:C:92:ALA:HA	3:C:95:THR:HB	1.69	0.74
21:U:18:TYR:HA	21:U:22:ARG:HE	1.52	0.74
15:O:4:THR:HG23	15:O:7:GLU:HB2	1.68	0.74
8:H:114:THR:HG22	8:H:117:GLY:O	1.87	0.74
8:H:89:PRO:HA	8:H:92:ARG:HH11	1.53	0.74
20:T:72:LEU:HD11	20:T:77:ALA:HA	1.70	0.74
1:A:1004:A:H5''	1:A:1024:G:H22	1.53	0.74
14:N:50:LYS:HD3	14:N:52:GLN:HG3	1.70	0.74
1:A:134:A:N6	16:P:25:ARG:HH12	1.85	0.73
12:L:68:TYR:HB3	12:L:98:HIS:CD2	2.23	0.73
6:F:99:ALA:HB2	18:R:31:LEU:HD22	1.70	0.73
13:M:67:GLU:HG3	13:M:68:GLY:H	1.53	0.73
22:V:62:C:H2'	22:V:63:G:C8	2.22	0.73
2:B:24:TRP:CZ3	2:B:26:PRO:HA	2.22	0.73
1:A:67:C:H2'	1:A:68:G:C8	2.24	0.73
4:D:49:ARG:HA	4:D:49:ARG:CZ	2.19	0.73
2:B:48:MET:HA	2:B:51:LEU:HD12	1.71	0.73
1:A:243:A:H4'	1:A:244:U:O5'	1.88	0.72
1:A:37:U:H2'	1:A:38:G:H8	1.53	0.72
4:D:100:ARG:NH1	4:D:137:SER:HA	2.04	0.72
12:L:31:PHE:HE2	12:L:85:ARG:HG3	1.52	0.72
8:H:24:THR:HG22	8:H:25:ASP:H	1.54	0.72
8:H:12:ARG:HH12	8:H:27:PRO:HD3	1.53	0.72
20:T:30:LYS:HD2	20:T:34:LYS:HE3	1.70	0.72
1:A:1347:G:N2	1:A:1373:G:H2'	2.04	0.72
5:E:43:LEU:HD11	5:E:132:ALA:HB1	1.71	0.72
6:F:23:LYS:O	6:F:27:GLN:HG2	1.88	0.72
2:B:16:HIS:CD2	2:B:210:SER:HA	2.25	0.72
12:L:27:LYS:HE2	12:L:32:ARG:HH22	1.53	0.72
13:M:49:THR:HG22	13:M:51:ALA:H	1.55	0.72
1:A:1327:C:OP1	21:U:20:LYS:HB3	1.90	0.72
1:A:1182:G:H4'	1:A:1183:A:H5''	1.72	0.72
1:A:664:G:H22	1:A:741:G:H1	1.36	0.72
22:V:74:C:H3'	22:V:75:C:H4'	1.69	0.72
1:A:192:U:H4'	20:T:103:GLY:H	1.52	0.72
16:P:49:LEU:HD23	16:P:50:LYS:H	1.53	0.72
3:C:86:VAL:O	3:C:90:GLU:HG2	1.90	0.72
4:D:119:GLN:HG3	4:D:123:HIS:HD2	1.52	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:19:VAL:HG22	8:H:21:LYS:HG2	1.72	0.72
5:E:121:LYS:HG3	5:E:123:LEU:HD13	1.71	0.71
1:A:1238:A:C8	1:A:1303:C:H1'	2.25	0.71
1:A:1004:A:N1	1:A:1025:U:H4'	2.04	0.71
3:C:52:LEU:HD13	3:C:68:VAL:HG13	1.71	0.71
1:A:328:C:H4'	1:A:329:A:H5'	1.71	0.71
7:G:45:ASP:O	7:G:49:ILE:HG13	1.90	0.71
1:A:495:A:H4'	1:A:496:A:OP1	1.91	0.71
20:T:100:ILE:HG22	20:T:102:GLY:H	1.54	0.71
1:A:978:A:OP2	1:A:1361(B):C:N4	2.24	0.70
4:D:9:CYS:HB3	4:D:32:ALA:HB2	1.71	0.70
9:I:97:LYS:HD3	9:I:102:LEU:HD22	1.72	0.70
16:P:20:VAL:HG21	16:P:32:TYR:CG	2.24	0.70
19:S:18:LYS:HG2	19:S:31:ILE:HD13	1.74	0.70
1:A:1296:C:H4'	1:A:1302:U:O4	1.91	0.70
4:D:49:ARG:HH21	4:D:50:ARG:HG2	1.55	0.70
1:A:141:A:H1'	1:A:182:U:O2	1.91	0.70
1:A:833:U:H2'	1:A:834:C:H6	1.55	0.70
1:A:1142:G:H2'	1:A:1143:G:O4'	1.92	0.70
11:K:21:ILE:HB	11:K:84:VAL:HG12	1.73	0.70
4:D:29:PRO:HG2	4:D:30:LYS:NZ	2.06	0.69
5:E:101:ILE:H	5:E:101:ILE:HD13	1.57	0.69
1:A:1004:A:H1'	1:A:1036:G:H22	1.58	0.69
2:B:204:ASN:ND2	2:B:207:ALA:H	1.85	0.69
9:I:4:TYR:HB2	9:I:19:LEU:HB2	1.75	0.69
11:K:79:SER:HA	11:K:104:GLN:HB3	1.73	0.69
13:M:40:ASN:HB3	13:M:43:THR:HG23	1.75	0.69
22:W:21:A:H2'	22:W:46:G:O6	1.92	0.69
3:C:71:ALA:HB2	3:C:115:LEU:HD21	1.73	0.69
19:S:22:LEU:HD13	19:S:27:GLU:HB2	1.74	0.69
16:P:53:VAL:HG12	16:P:79:VAL:HG22	1.74	0.69
1:A:1031:G:H2'	1:A:1031(A):A:O4'	1.91	0.69
1:A:1105:A:H2'	1:A:1106:G:H8	1.56	0.69
17:Q:9:VAL:HG12	17:Q:56:VAL:HG22	1.75	0.69
1:A:1227:A:N3	1:A:1227:A:H2'	2.07	0.69
1:A:1438:G:H2'	1:A:1439:C:H6	1.58	0.69
1:A:748:C:H1'	1:A:749:C:OP2	1.93	0.69
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.73	0.69
2:B:24:TRP:HZ3	2:B:29:ALA:HB2	1.56	0.69
13:M:91:ARG:HD2	19:S:81:ARG:HH22	1.56	0.69
3:C:189:ALA:HB3	3:C:196:LEU:HB3	1.75	0.69
18:R:47:THR:HA	18:R:83:GLU:HB2	1.74	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1363:A:H4'	1:A:1364:U:H5''	1.73	0.68
2:B:21:ARG:HB3	2:B:39:ILE:HA	1.75	0.68
10:J:6:ILE:HD11	10:J:72:VAL:HB	1.74	0.68
18:R:51:LEU:HD22	18:R:55:ARG:HH21	1.56	0.68
15:O:63:ARG:O	15:O:67:LEU:HD13	1.93	0.68
1:A:191(G):G:C4	20:T:105:SER:HB3	2.27	0.68
1:A:436:C:H2'	1:A:437:U:C6	2.27	0.68
3:C:130:VAL:O	3:C:134:ILE:HG13	1.93	0.68
1:A:826:C:H5'	8:H:12:ARG:HH21	1.57	0.68
9:I:70:LYS:O	9:I:74:ILE:HG12	1.94	0.68
17:Q:86:GLU:O	17:Q:90:ILE:HG12	1.93	0.68
6:F:69:GLU:O	6:F:72:VAL:HG12	1.93	0.68
13:M:3:ARG:NH2	13:M:7:VAL:HG12	2.09	0.68
2:B:204:ASN:HD21	2:B:207:ALA:N	1.88	0.68
9:I:127:LYS:NZ	9:I:128:ARG:HH11	1.91	0.68
19:S:16:LEU:O	19:S:20:LEU:HG	1.94	0.68
4:D:7:PRO:HB2	4:D:10:ARG:HD2	1.76	0.68
4:D:61:LYS:HA	4:D:203:VAL:HG22	1.76	0.68
5:E:76:ILE:HG13	5:E:77:PRO:HD2	1.76	0.68
5:E:91:LEU:HA	5:E:120:THR:HG22	1.76	0.68
9:I:125:TYR:HD2	9:I:126:SER:N	1.92	0.68
9:I:48:GLU:N	9:I:49:PRO:HD2	2.08	0.68
1:A:817:C:H1'	1:A:819:A:H5'	1.76	0.68
3:C:20:SER:HB2	3:C:40:ARG:HH22	1.59	0.68
4:D:64:LEU:HD13	4:D:198:VAL:HG21	1.75	0.68
8:H:64:LYS:HG2	8:H:79:VAL:HG21	1.74	0.68
16:P:43:LYS:HG3	16:P:48:TRP:CE3	2.29	0.67
1:A:1238:A:N7	1:A:1303:C:H1'	2.10	0.67
1:A:1438:G:H2'	1:A:1439:C:C6	2.29	0.67
1:A:328:C:H4'	1:A:329:A:C5'	2.23	0.67
1:A:1092:A:H5''	7:G:4:ARG:NH2	2.10	0.67
9:I:103:THR:HG22	9:I:105:ASP:H	1.58	0.67
1:A:501:C:H2'	1:A:502:G:C8	2.27	0.67
2:B:162:ILE:HD11	2:B:184:VAL:HA	1.74	0.67
2:B:61:LEU:HD21	2:B:68:ILE:HD11	1.77	0.67
15:O:39:LEU:HB3	15:O:56:LEU:HD12	1.76	0.67
18:R:50:ILE:HD11	18:R:74:ARG:NH1	2.10	0.67
22:V:74:C:H5'	22:V:75:C:OP2	1.95	0.67
3:C:134:ILE:HG22	3:C:168:ALA:HB3	1.75	0.67
3:C:75:VAL:O	3:C:83:ARG:HG2	1.91	0.67
15:O:9:GLN:O	15:O:13:GLN:HG2	1.94	0.67
18:R:66:LEU:O	18:R:70:ILE:HG12	1.94	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:186(B):C:O2'	20:T:89:ARG:HD2	1.93	0.67
3:C:191:THR:HG21	3:C:193:TYR:CZ	2.29	0.67
1:A:1297:C:OP1	13:M:13:LYS:HE3	1.95	0.67
7:G:27:ILE:HD12	7:G:40:ALA:HA	1.75	0.67
12:L:53:LYS:HD2	12:L:53:LYS:N	2.09	0.67
22:W:54:U:H3	22:W:58:A:N6	1.91	0.67
1:A:974:A:H8	1:A:974:A:OP1	1.77	0.66
9:I:97:LYS:HB3	9:I:98:PRO:HD3	1.76	0.66
14:N:24:CYS:HB3	14:N:29:ARG:H	1.60	0.66
3:C:35:GLU:HA	3:C:38:ARG:HG2	1.77	0.66
11:K:29:ILE:C	11:K:29:ILE:HD12	2.16	0.66
1:A:88:C:H2'	1:A:89:U:O4'	1.96	0.66
3:C:95:THR:HG22	3:C:97:LYS:H	1.60	0.66
12:L:17:VAL:HG23	12:L:18:ARG:H	1.60	0.66
22:W:63:G:H2'	22:W:64:G:C8	2.31	0.66
5:E:136:MET:HB3	5:E:140:ARG:HH21	1.59	0.66
13:M:95:GLY:O	13:M:110:ARG:HB3	1.96	0.66
1:A:1109:C:H2'	1:A:1110:A:O4'	1.96	0.65
18:R:32:ARG:HA	18:R:69:THR:HG21	1.78	0.65
4:D:9:CYS:SG	4:D:32:ALA:HB2	2.35	0.65
15:O:4:THR:OG1	15:O:6:GLU:HG2	1.96	0.65
6:F:97:PHE:CD2	18:R:31:LEU:HD21	2.25	0.65
14:N:3:ARG:O	14:N:7:ILE:HG13	1.97	0.65
1:A:537:G:H2'	1:A:538:G:H8	1.62	0.65
8:H:12:ARG:HH11	8:H:26:VAL:HA	1.61	0.65
1:A:1285:A:H4'	1:A:1286:A:O5'	1.96	0.65
1:A:560:U:H4'	1:A:561:U:O5'	1.96	0.65
1:A:1108:G:H5'	3:C:176:HIS:CD2	2.31	0.65
11:K:41:THR:HG22	11:K:42:TRP:N	2.11	0.65
1:A:757:U:H2'	1:A:758:G:O4'	1.95	0.65
4:D:189:PRO:HB2	4:D:194:LEU:CD2	2.26	0.65
4:D:58:LEU:HD23	4:D:62:GLN:HG3	1.78	0.65
12:L:5:THR:HG23	12:L:8:GLN:NE2	2.10	0.65
16:P:75:ARG:HH11	16:P:75:ARG:CG	2.08	0.65
9:I:46:ALA:HB2	9:I:74:ILE:HG23	1.78	0.65
11:K:54:ARG:O	11:K:57:THR:HG22	1.97	0.64
1:A:1064:G:H21	1:A:1190:G:H2'	1.62	0.64
4:D:139:ARG:HG3	4:D:139:ARG:HH11	1.61	0.64
1:A:1118:C:OP1	9:I:104:ARG:HG3	1.98	0.64
4:D:101:LEU:HB2	4:D:138:TYR:HB3	1.78	0.64
5:E:51:VAL:HB	5:E:52:PRO:HD3	1.78	0.64
16:P:43:LYS:HA	16:P:48:TRP:CB	2.28	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1225:A:N3	1:A:1225:A:H2'	2.11	0.64
9:I:16:ARG:O	9:I:63:ILE:HG23	1.96	0.64
10:J:45:ARG:HB2	10:J:65:LEU:HB3	1.79	0.64
1:A:1004:A:H61	1:A:1025:U:H4'	1.63	0.64
2:B:219:VAL:O	2:B:222:ILE:HG12	1.97	0.64
13:M:27:LYS:HE2	13:M:31:LYS:HE3	1.80	0.64
1:A:1136:U:H5''	1:A:1137:C:OP2	1.97	0.64
12:L:40:ARG:CG	12:L:41:THR:H	2.10	0.64
3:C:134:ILE:CG2	3:C:168:ALA:HB3	2.28	0.64
17:Q:14:LYS:HD2	17:Q:14:LYS:H	1.63	0.64
1:A:1325:C:P	21:U:15:ARG:HH21	2.20	0.64
1:A:1427:U:H2'	1:A:1428:A:C8	2.33	0.63
7:G:113:GLU:HG3	7:G:118:VAL:HG23	1.79	0.63
8:H:69:ARG:HD3	8:H:76:PRO:HA	1.80	0.63
18:R:19:LYS:HE3	18:R:19:LYS:HA	1.80	0.63
22:V:74:C:H3'	22:V:75:C:C4'	2.28	0.63
9:I:113:LYS:H	9:I:119:ALA:HA	1.62	0.63
12:L:40:ARG:HG2	12:L:41:THR:H	1.62	0.63
7:G:77:SER:HB3	7:G:84:ASN:OD1	1.98	0.63
9:I:8:GLY:HA2	9:I:79:LEU:HD12	1.80	0.63
10:J:48:THR:HG22	10:J:62:HIS:ND1	2.14	0.63
12:L:74:HIS:HD2	12:L:76:LEU:H	1.46	0.63
1:A:1502:A:C8	1:A:1505:G:N2	2.66	0.63
1:A:913:A:H4'	1:A:914:A:O5'	1.99	0.63
2:B:59:GLU:HB2	2:B:221:LEU:HD11	1.81	0.63
7:G:73:MET:HA	7:G:91:VAL:HG23	1.79	0.63
8:H:40:ALA:HB2	8:H:45:ILE:HG13	1.80	0.63
9:I:127:LYS:HZ3	9:I:128:ARG:HH11	1.44	0.63
1:A:1302:U:C5	13:M:17:VAL:HG11	2.34	0.63
19:S:28:LYS:HB3	19:S:29:ARG:HH11	1.64	0.63
1:A:1117:G:H5'	1:A:1118:C:OP2	1.98	0.63
1:A:624:C:H2'	1:A:625:G:H8	1.63	0.63
12:L:23:VAL:HG12	12:L:23:VAL:O	1.98	0.63
20:T:26:ASN:OD1	20:T:71:THR:HG23	1.98	0.63
1:A:1057:G:H4'	3:C:197:GLY:H	1.64	0.63
3:C:29:TYR:HE1	3:C:33:LEU:HD22	1.63	0.63
5:E:10:MET:HG3	5:E:13:ILE:HD11	1.81	0.63
6:F:21:LEU:O	6:F:24:GLU:HB3	1.98	0.63
8:H:102:ARG:H	8:H:102:ARG:HD2	1.63	0.63
11:K:32:ILE:O	11:K:32:ILE:HD12	1.99	0.63
15:O:63:ARG:CZ	15:O:87:ILE:HD11	2.28	0.63
8:H:102:ARG:N	8:H:102:ARG:HD2	2.14	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1313:U:OP1	19:S:6:LYS:HG3	1.99	0.62
22:W:63:G:H2'	22:W:64:G:H8	1.62	0.62
22:W:71:C:H2'	22:W:72:A:C8	2.34	0.62
1:A:1435:G:H2'	1:A:1436:U:C6	2.35	0.62
1:A:646:U:H2'	1:A:647:C:C6	2.35	0.62
1:A:922:G:H2'	1:A:923:A:C8	2.34	0.62
2:B:11:LEU:HD12	2:B:217:ARG:HH22	1.65	0.62
4:D:67:ILE:HD13	4:D:196:LEU:HD22	1.81	0.62
5:E:69:VAL:O	5:E:71:LEU:HD12	1.98	0.62
8:H:109:ILE:HG12	8:H:110:ALA:H	1.64	0.62
12:L:23:VAL:HG13	12:L:97:TYR:CE2	2.35	0.62
2:B:95:GLN:HA	2:B:96:ARG:NH2	2.15	0.62
1:A:636:U:H5'	17:Q:2:PRO:HD3	1.81	0.62
22:V:62:C:H2'	22:V:63:G:H8	1.64	0.62
1:A:878:G:H5'	8:H:89:PRO:HG2	1.81	0.62
13:M:14:ARG:HG2	13:M:44:ARG:CZ	2.30	0.62
1:A:1227:A:H2	1:A:1228:C:H1'	1.64	0.62
1:A:1228:C:OP1	13:M:115:LYS:HE3	1.99	0.62
1:A:922:G:N3	1:A:1398:A:H2	1.97	0.62
1:A:1503:A:O2'	1:A:1504:G:O5'	2.17	0.62
1:A:224:C:H2'	1:A:225:C:H6	1.65	0.62
1:A:559:A:C4'	1:A:560:U:H3'	2.25	0.62
1:A:818:G:C2'	1:A:819:A:H5''	2.29	0.62
4:D:58:LEU:CD2	4:D:62:GLN:HG3	2.30	0.62
1:A:1080:A:H5''	5:E:16:THR:HG21	1.82	0.62
10:J:37:PRO:HA	10:J:72:VAL:HG22	1.81	0.62
12:L:81:VAL:O	12:L:105:ASP:HB2	1.99	0.62
1:A:365:U:H5''	1:A:366:C:OP1	1.99	0.62
7:G:51:GLN:HG3	7:G:58:PRO:HD3	1.82	0.62
8:H:109:ILE:HG12	8:H:110:ALA:N	2.15	0.62
9:I:83:ARG:HA	9:I:86:VAL:HG12	1.81	0.62
12:L:6:ILE:O	12:L:10:VAL:HG23	2.00	0.62
14:N:47:LEU:O	14:N:50:LYS:HG3	1.98	0.62
1:A:127:G:O2'	17:Q:2:PRO:HA	2.00	0.61
1:A:555:C:H2'	1:A:556:C:C6	2.35	0.61
20:T:57:ARG:HH12	20:T:100:ILE:HG21	1.64	0.61
1:A:109:A:C6	1:A:326:G:C6	2.89	0.61
6:F:67:MET:HB2	6:F:68:PRO:HD2	1.81	0.61
19:S:18:LYS:O	19:S:22:LEU:HD23	2.00	0.61
1:A:1148:U:H2'	1:A:1149:C:O4'	2.00	0.61
4:D:61:LYS:HD3	4:D:62:GLN:N	2.14	0.61
13:M:67:GLU:HG3	13:M:68:GLY:N	2.14	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:P:28:ARG:HG2	16:P:29:ASP:OD1	2.00	0.61
1:A:979:C:H3'	1:A:980:C:C5'	2.23	0.61
5:E:101:ILE:HG12	5:E:119:LEU:HA	1.83	0.61
9:I:112:LYS:HA	9:I:119:ALA:HB2	1.82	0.61
1:A:269:C:H2'	1:A:270:A:C8	2.36	0.61
2:B:187:LEU:HD23	2:B:201:ILE:O	2.00	0.61
7:G:120:ILE:O	7:G:124:LEU:HB2	2.01	0.61
20:T:72:LEU:HD11	20:T:77:ALA:CA	2.30	0.61
22:W:59:A:H2'	22:W:60:U:H5'	1.81	0.61
1:A:1263:C:H2'	1:A:1264:C:H6	1.66	0.61
5:E:45:PHE:CE2	5:E:47:LYS:HD2	2.36	0.61
1:A:1510:U:H2'	1:A:1511:G:C8	2.36	0.61
1:A:1014:A:C2	1:A:1219:U:H1'	2.36	0.61
3:C:73:PRO:HD3	3:C:105:GLU:HG2	1.82	0.61
8:H:12:ARG:NH1	8:H:26:VAL:HA	2.15	0.61
10:J:34:VAL:HG22	10:J:74:ILE:HG12	1.81	0.61
13:M:50:GLU:HA	13:M:53:VAL:HB	1.82	0.61
2:B:162:ILE:CD1	2:B:184:VAL:HA	2.30	0.60
9:I:9:ARG:HG2	9:I:14:VAL:HG22	1.83	0.60
13:M:10:PRO:HD3	13:M:22:ILE:HD11	1.83	0.60
1:A:1065:U:C5	1:A:1190:G:H1'	2.36	0.60
1:A:67:C:H2'	1:A:68:G:H8	1.65	0.60
2:B:11:LEU:HD12	2:B:217:ARG:NH2	2.17	0.60
2:B:20:GLU:HG3	2:B:189:ASP:OD1	2.00	0.60
3:C:7:PRO:O	3:C:11:ARG:HG2	2.00	0.60
1:A:464:G:O6	1:A:466:G:H5''	2.01	0.60
1:A:542:G:OP1	4:D:10:ARG:NH2	2.33	0.60
2:B:91:PRO:HA	2:B:154:LEU:HD21	1.84	0.60
12:L:6:ILE:HD12	12:L:7:ASN:H	1.66	0.60
1:A:737:A:H2'	1:A:738:C:C6	2.36	0.60
9:I:4:TYR:CE2	9:I:88:TYR:HB3	2.37	0.60
10:J:40:LEU:HB2	10:J:69:ASN:HB2	1.84	0.60
22:W:71:C:H2'	22:W:72:A:H8	1.65	0.60
1:A:922:G:H4'	5:E:20:GLN:HA	1.83	0.60
14:N:41:ARG:HG3	14:N:42:ILE:N	2.16	0.60
17:Q:45:HIS:HE2	17:Q:47:PRO:HB3	1.67	0.60
1:A:960:U:H2'	1:A:1225:A:H62	1.65	0.60
1:A:537:G:H2'	1:A:538:G:C8	2.37	0.60
4:D:57:ARG:HB3	4:D:206:PHE:HB2	1.83	0.60
15:O:5:LYS:HD3	15:O:6:GLU:H	1.66	0.60
6:F:44:GLY:HA2	6:F:59:TYR:CZ	2.37	0.60
7:G:23:VAL:O	7:G:27:ILE:HG12	2.02	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:F:50:TYR:HE1	18:R:74:ARG:O	1.84	0.60
19:S:6:LYS:HD2	19:S:6:LYS:H	1.67	0.60
20:T:49:ALA:HB2	20:T:92:LEU:HD22	1.82	0.60
1:A:1106:G:H2'	1:A:1107:C:C6	2.36	0.60
1:A:677:U:H3	1:A:713:G:H22	1.49	0.60
1:A:913:A:H1'	1:A:914:A:OP2	2.02	0.60
10:J:26:ALA:HB3	10:J:85:LEU:HD21	1.84	0.60
15:O:26:GLU:HA	15:O:81:LEU:HD11	1.84	0.60
2:B:54:THR:HG21	2:B:201:ILE:HD11	1.84	0.59
22:W:23:C:H2'	22:W:24:U:C6	2.37	0.59
1:A:1101:A:H4'	1:A:1102:A:O5'	2.02	0.59
1:A:1301:U:H3'	1:A:1302:U:C5'	2.32	0.59
1:A:1337:G:H5''	1:A:1338:G:OP1	2.01	0.59
1:A:149:A:H2'	1:A:150:C:C6	2.38	0.59
15:O:45:VAL:HG22	15:O:46:HIS:ND1	2.16	0.59
4:D:133:VAL:HG11	4:D:138:TYR:HD2	1.67	0.59
7:G:113:GLU:HG2	7:G:119:ARG:HG2	1.84	0.59
1:A:668:G:H1'	15:O:46:HIS:HD2	1.67	0.59
17:Q:63:ARG:HG2	17:Q:64:PRO:HD2	1.83	0.59
6:F:50:TYR:CE1	18:R:77:GLY:HA2	2.36	0.59
11:K:29:ILE:HG22	11:K:44:SER:CB	2.31	0.59
1:A:1196:U:H5'	1:A:1197:G:C5'	2.33	0.59
1:A:1411:C:H2'	1:A:1412:C:C6	2.37	0.59
1:A:180:U:H2'	1:A:181:G:H5''	1.84	0.59
1:A:209:U:H5''	1:A:210:U:OP1	2.02	0.59
1:A:359:U:H2'	1:A:360:A:C8	2.37	0.59
4:D:29:PRO:O	4:D:30:LYS:HB3	2.01	0.59
22:W:48:C:H5''	22:W:49:G:H5''	1.85	0.59
1:A:987:G:H2'	1:A:988:G:H8	1.67	0.59
2:B:14:GLY:O	2:B:15:VAL:HG13	2.03	0.59
1:A:406:G:C5'	4:D:5:ILE:HD12	2.32	0.59
12:L:100:VAL:O	12:L:103:VAL:HG22	2.02	0.59
1:A:1286:A:H3'	1:A:1287:A:H5''	1.85	0.59
3:C:134:ILE:HG23	3:C:151:VAL:HB	1.84	0.59
7:G:42:ILE:HD13	7:G:116:ALA:HB3	1.84	0.59
14:N:22:THR:OG1	14:N:33:VAL:HG21	2.03	0.59
1:A:833:U:H2'	1:A:834:C:C6	2.36	0.59
2:B:121:LEU:HB3	2:B:127:ILE:HD11	1.85	0.59
13:M:99:ARG:HB2	13:M:101:GLN:HE21	1.67	0.59
2:B:214:ILE:H	2:B:214:ILE:HD12	1.68	0.58
8:H:12:ARG:NH1	8:H:27:PRO:HD3	2.18	0.58
1:A:113:G:H2'	1:A:114:U:H6	1.68	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1441:G:H5''	1:A:1442:G:O5'	2.02	0.58
1:A:7:G:H5'	1:A:298:A:O4'	2.02	0.58
4:D:62:GLN:NE2	4:D:65:ARG:HH12	2.01	0.58
3:C:18:TRP:HZ2	14:N:57:ARG:HG3	1.68	0.58
1:A:1144:G:H21	1:A:1146:A:H62	1.50	0.58
1:A:37:U:H2'	1:A:38:G:C8	2.38	0.58
1:A:547:A:H4'	1:A:548:G:O5'	2.04	0.58
3:C:37:GLN:HE22	14:N:52:GLN:NE2	2.01	0.58
15:O:24:SER:HB3	15:O:27:VAL:HG23	1.83	0.58
1:A:255:G:H1'	17:Q:16:GLN:NE2	2.19	0.58
1:A:332:G:OP2	20:T:10:LEU:HD23	2.02	0.58
2:B:100:GLY:HA3	2:B:104:ASN:HB3	1.86	0.58
4:D:26:CYS:HA	4:D:31:CYS:HA	1.85	0.58
1:A:377:G:OP1	16:P:3:LYS:HD2	2.04	0.58
19:S:6:LYS:CD	19:S:6:LYS:H	2.17	0.58
6:F:7:ASN:ND2	18:R:34:TYR:HE1	2.02	0.58
19:S:49:ILE:HD12	19:S:49:ILE:H	1.67	0.58
22:W:68:C:H2'	22:W:69:C:C6	2.39	0.58
1:A:1144:G:H21	1:A:1146:A:N6	2.01	0.58
7:G:78:ARG:HE	7:G:80:VAL:HG11	1.68	0.58
16:P:43:LYS:HA	16:P:48:TRP:HB3	1.84	0.58
4:D:135:LEU:H	4:D:135:LEU:HD22	1.67	0.58
22:V:19:G:H4'	22:V:20:U:OP2	2.03	0.58
1:A:1010:G:N2	1:A:1020:U:H1'	2.18	0.58
1:A:429:U:H1'	1:A:430:A:H5''	1.86	0.58
5:E:80:ILE:HD11	5:E:91:LEU:HD12	1.85	0.58
13:M:50:GLU:CD	13:M:50:GLU:H	2.06	0.58
1:A:153:C:H42	1:A:168:G:H1	1.52	0.58
1:A:253:U:H2'	1:A:254:G:H8	1.69	0.58
1:A:424:G:H2'	1:A:425:G:H8	1.68	0.58
6:F:48:LEU:H	6:F:48:LEU:HD23	1.69	0.58
6:F:3:ARG:HD3	6:F:64:GLN:OE1	2.04	0.58
8:H:35:ILE:O	8:H:39:LEU:HB2	2.04	0.58
12:L:5:THR:HG23	12:L:8:GLN:HE21	1.68	0.58
22:V:19:G:C2	22:V:57:A:N3	2.72	0.58
1:A:639:G:O2'	1:A:640:A:H5'	2.04	0.58
1:A:843:U:H3'	1:A:848:C:H5'	1.86	0.58
4:D:159:ARG:HH11	4:D:159:ARG:HB3	1.68	0.58
17:Q:6:LEU:HD23	17:Q:6:LEU:N	2.17	0.58
1:A:619:U:C2	4:D:135:LEU:HD21	2.39	0.57
10:J:55:LYS:O	10:J:56:HIS:CG	2.57	0.57
1:A:1268:A:H4'	21:U:20:LYS:CA	2.34	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:104:VAL:HG21	4:D:140:VAL:HG21	1.85	0.57
12:L:82:VAL:HG23	12:L:106:ALA:HB2	1.86	0.57
15:O:4:THR:HG23	15:O:7:GLU:CB	2.33	0.57
4:D:120:LEU:HD21	4:D:157:LEU:HD23	1.86	0.57
9:I:102:LEU:HD12	9:I:102:LEU:N	2.20	0.57
1:A:1031(B):G:H2'	1:A:1031(C):G:O4'	2.04	0.57
1:A:859:A:H2'	1:A:860:A:O4'	2.05	0.57
1:A:89:U:H2'	1:A:90:C:H6	1.68	0.57
1:A:429:U:H2'	4:D:25:ARG:NH1	2.18	0.57
4:D:9:CYS:CB	4:D:32:ALA:HB2	2.32	0.57
1:A:1097:C:H2'	1:A:1098:C:C6	2.39	0.57
1:A:976:G:C8	1:A:1358:U:H2'	2.39	0.57
20:T:32:ALA:O	20:T:36:LEU:HB2	2.04	0.57
4:D:190:ASP:O	4:D:194:LEU:HD23	2.05	0.57
6:F:26:ILE:O	6:F:30:LEU:HD13	2.04	0.57
6:F:52:ILE:HD11	6:F:86:ARG:HB3	1.85	0.57
1:A:977:A:H8	1:A:1223:C:C4	2.22	0.57
1:A:1412:C:H2'	1:A:1413:A:C8	2.40	0.57
4:D:88:VAL:O	4:D:92:VAL:HG23	2.04	0.57
5:E:10:MET:HB3	5:E:32:VAL:HG22	1.87	0.57
9:I:9:ARG:O	9:I:10:ARG:HB2	2.04	0.57
22:W:17:C:H5''	22:W:17(A):U:OP2	2.04	0.57
1:A:262:A:C6	1:A:263:A:C6	2.92	0.57
3:C:20:SER:HB2	3:C:40:ARG:NH2	2.18	0.57
9:I:117:HIS:HB2	9:I:121:ARG:HD2	1.86	0.57
12:L:116:ARG:HB3	12:L:121:THR:HB	1.86	0.57
18:R:52:PRO:O	18:R:56:THR:HG23	2.05	0.57
19:S:63:THR:N	19:S:66:MET:HE3	2.17	0.57
20:T:76:ALA:O	20:T:80:ARG:HG2	2.05	0.57
1:A:1141:C:H2'	1:A:1142:G:H8	1.70	0.57
9:I:125:TYR:CD2	9:I:126:SER:N	2.70	0.57
11:K:59:TYR:CZ	11:K:63:LEU:HD11	2.39	0.57
12:L:5:THR:N	12:L:8:GLN:HE21	2.01	0.57
3:C:18:TRP:CZ2	14:N:57:ARG:HG3	2.39	0.57
1:A:1306:A:H1'	1:A:1332:A:C2	2.40	0.57
1:A:89:U:H2'	1:A:90:C:C6	2.40	0.57
2:B:162:ILE:O	2:B:162:ILE:HD12	2.05	0.56
3:C:119:ARG:HG2	3:C:140:ARG:HH12	1.70	0.56
13:M:14:ARG:HG2	13:M:44:ARG:NH1	2.20	0.56
1:A:115:G:H4'	1:A:116:A:O5'	2.05	0.56
4:D:110:PHE:HD1	4:D:110:PHE:N	2.03	0.56
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.87	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:41:THR:HG21	11:K:71:LYS:HD3	1.87	0.56
20:T:69:GLY:O	20:T:73:HIS:CD2	2.58	0.56
1:A:983:A:H3'	1:A:983:A:N3	2.20	0.56
1:A:1228:C:H2'	1:A:1229:A:H8	1.69	0.56
1:A:265:G:C2'	1:A:266:G:H5'	2.35	0.56
1:A:321:A:N7	1:A:328:C:C6	2.74	0.56
1:A:735:C:H2'	1:A:736:C:H6	1.69	0.56
2:B:187:LEU:HA	2:B:201:ILE:HB	1.88	0.56
3:C:9:GLY:HA2	3:C:12:LEU:HD23	1.87	0.56
8:H:24:THR:HG22	8:H:25:ASP:N	2.20	0.56
22:V:74:C:C5'	22:V:75:C:OP2	2.52	0.56
1:A:1060:C:H5''	10:J:51:ARG:HG2	1.87	0.56
1:A:1267:C:H5	1:A:1268:A:C5	2.23	0.56
3:C:14:ILE:HG23	3:C:15:THR:N	2.21	0.56
1:A:1128:C:H4'	9:I:16:ARG:NH1	2.19	0.56
10:J:43:ARG:HB2	10:J:67:THR:CG2	2.35	0.56
11:K:99:GLN:HB3	11:K:105:VAL:HG21	1.86	0.56
1:A:1246:C:H2'	1:A:1247:U:C6	2.40	0.56
1:A:1347:G:H22	1:A:1373:G:H2'	1.68	0.56
1:A:79:G:H1	1:A:90:C:H42	1.54	0.56
10:J:30:SER:HB2	10:J:80:LYS:HG2	1.87	0.56
1:A:434:U:H2'	1:A:435:C:C6	2.41	0.56
1:A:87:A:H5''	1:A:88:C:OP2	2.05	0.56
2:B:15:VAL:HG21	2:B:209:ARG:HE	1.69	0.56
2:B:87:ARG:NH1	2:B:87:ARG:HB3	2.20	0.56
4:D:168:ARG:HE	4:D:168:ARG:HA	1.69	0.56
4:D:36:ARG:HD3	4:D:38:TYR:CE1	2.40	0.56
1:A:1080:A:C5'	5:E:16:THR:HG21	2.36	0.56
1:A:355:C:C4	1:A:356:A:N7	2.74	0.56
1:A:359:U:H2'	1:A:360:A:H8	1.70	0.56
1:A:376:G:OP2	16:P:67:THR:HG21	2.04	0.56
2:B:185:ILE:HG23	2:B:199:TYR:HB2	1.88	0.56
3:C:35:GLU:O	3:C:39:ILE:HG13	2.05	0.56
5:E:79:GLU:CD	5:E:79:GLU:H	2.07	0.56
1:A:1151:A:O2'	1:A:1152:A:H8	1.89	0.56
1:A:1346:A:H5''	9:I:120:ARG:HH12	1.70	0.56
1:A:687:A:H1'	1:A:688:G:OP2	2.04	0.56
2:B:201:ILE:HG21	2:B:214:ILE:HG21	1.88	0.56
2:B:19:HIS:NE2	2:B:206:ASP:HB2	2.21	0.56
2:B:82:ARG:HA	2:B:92:TYR:CE1	2.41	0.56
4:D:8:VAL:HB	4:D:21:LEU:HD22	1.87	0.56
13:M:84:ILE:HG23	13:M:86:CYS:H	1.71	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1118:C:H1'	1:A:1179:A:C5	2.41	0.56
2:B:184:VAL:HB	2:B:198:ASP:H	1.71	0.56
4:D:74:GLN:O	4:D:78:LEU:HG	2.05	0.56
1:A:976:G:P	14:N:32:SER:H	2.28	0.56
16:P:13:HIS:C	16:P:15:PRO:HD3	2.25	0.56
19:S:63:THR:HG23	19:S:65:ASN:H	1.69	0.56
4:D:110:PHE:CD1	4:D:110:PHE:N	2.73	0.55
4:D:189:PRO:CB	4:D:194:LEU:HD21	2.35	0.55
1:A:407:G:H5'	4:D:3:ARG:NH1	2.21	0.55
5:E:72:GLN:O	5:E:75:THR:HG22	2.06	0.55
10:J:3:LYS:O	10:J:100:THR:HA	2.06	0.55
15:O:87:ILE:HG23	15:O:88:ARG:HG2	1.87	0.55
18:R:44:LEU:HD23	18:R:80:PRO:HD2	1.87	0.55
1:A:224:C:H2'	1:A:225:C:C6	2.41	0.55
1:A:243:A:H1'	1:A:244:U:OP2	2.05	0.55
1:A:251:G:C6	1:A:266:G:C6	2.94	0.55
1:A:523:A:N1	12:L:91:ASP:HB2	2.21	0.55
4:D:163:GLU:O	4:D:166:LYS:HG3	2.07	0.55
15:O:27:VAL:O	15:O:31:LEU:HB2	2.06	0.55
1:A:353:A:H2'	1:A:354:G:OP2	2.06	0.55
1:A:38:G:C2	1:A:397:A:C2	2.94	0.55
10:J:21:GLN:O	10:J:25:GLU:HG3	2.07	0.55
12:L:31:PHE:HB3	12:L:83:LEU:HD11	1.89	0.55
16:P:43:LYS:HG3	16:P:48:TRP:CD2	2.40	0.55
22:V:68:C:H2'	22:V:69:C:C6	2.40	0.55
22:W:70:G:O2'	22:W:71:C:H5'	2.06	0.55
1:A:1002:G:H2'	1:A:1003:G:O4'	2.06	0.55
1:A:1356:G:H2'	1:A:1357:A:C8	2.42	0.55
2:B:69:LEU:HD23	2:B:155:LEU:HD22	1.86	0.55
3:C:86:VAL:O	3:C:89:GLU:HG3	2.05	0.55
4:D:107:ARG:HD3	4:D:173:TRP:CH2	2.41	0.55
7:G:20:ASP:OD2	7:G:22:LEU:HB3	2.06	0.55
8:H:1:MET:HE3	8:H:3:THR:HG23	1.88	0.55
12:L:45:LYS:HB2	12:L:91:ASP:O	2.06	0.55
13:M:19:LEU:HA	13:M:22:ILE:HG12	1.88	0.55
1:A:152:A:N6	1:A:170:U:C2	2.75	0.55
3:C:58:GLU:HB2	3:C:65:ALA:HB3	1.88	0.55
4:D:162:LEU:HD13	4:D:178:VAL:HG13	1.88	0.55
1:A:16:A:O2'	1:A:17:U:H5'	2.07	0.55
1:A:559:A:H5''	1:A:560:U:H3'	1.89	0.55
2:B:51:LEU:O	2:B:55:PHE:HD2	1.90	0.55
6:F:19:LEU:O	6:F:19:LEU:HD23	2.07	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:66:LEU:HA	13:M:70:LEU:HB2	1.87	0.55
13:M:94:ARG:HH12	19:S:81:ARG:HD2	1.71	0.55
22:W:33:U:H2'	22:W:35:A:OP2	2.07	0.55
5:E:121:LYS:HG3	5:E:123:LEU:CD1	2.37	0.55
17:Q:27:PHE:CZ	17:Q:36:ILE:HD11	2.42	0.55
20:T:43:LEU:HD12	20:T:55:ILE:HD12	1.89	0.55
1:A:1157:A:H4'	1:A:1158:C:O5'	2.06	0.55
1:A:1346:A:H5''	9:I:120:ARG:NH1	2.20	0.55
1:A:1493:A:C2'	1:A:1494:G:H5'	2.37	0.55
17:Q:77:VAL:HG12	17:Q:78:GLU:HG2	1.89	0.55
19:S:22:LEU:CD1	19:S:27:GLU:HB2	2.37	0.55
2:B:75:LYS:HA	2:B:78:GLN:HB2	1.89	0.55
3:C:150:LYS:HB3	3:C:201:TYR:HB2	1.89	0.55
7:G:69:VAL:O	7:G:71:PRO:HD3	2.06	0.55
17:Q:14:LYS:HD2	17:Q:14:LYS:N	2.21	0.55
17:Q:43:LEU:HD22	17:Q:68:ARG:HB2	1.89	0.55
1:A:673:G:H2'	1:A:674:G:C8	2.41	0.55
2:B:32:ILE:HD11	2:B:190:THR:HG22	1.88	0.55
3:C:173:VAL:N	3:C:174:PRO:HD3	2.21	0.55
9:I:128:ARG:HD3	22:V:32:C:OP2	2.07	0.55
14:N:24:CYS:SG	14:N:27:CYS:SG	3.05	0.55
1:A:1029:G:HO2'	1:A:1030:C:H5	1.54	0.54
1:A:1106:G:H2'	1:A:1107:C:H6	1.72	0.54
17:Q:5:VAL:HG22	17:Q:60:ILE:HG13	1.89	0.54
1:A:738:C:H5''	6:F:69:GLU:HB2	1.89	0.54
2:B:32:ILE:CD1	2:B:190:THR:HG22	2.38	0.54
15:O:47:LYS:H	15:O:47:LYS:HD2	1.72	0.54
1:A:1367:C:O2'	10:J:48:THR:HG21	2.07	0.54
1:A:386:C:O2'	1:A:387:U:H5'	2.07	0.54
1:A:397:A:N3	1:A:397:A:H3'	2.22	0.54
1:A:678:U:H2'	1:A:679:C:C6	2.43	0.54
1:A:976:G:H22	1:A:1361(A):C:H2'	1.71	0.54
2:B:88:ALA:HB2	2:B:219:VAL:HG13	1.88	0.54
9:I:111:ARG:HH12	9:I:113:LYS:HA	1.73	0.54
9:I:28:VAL:HA	9:I:63:ILE:O	2.06	0.54
12:L:65:VAL:HG11	12:L:97:TYR:CE1	2.42	0.54
15:O:44:LYS:O	15:O:47:LYS:HE3	2.07	0.54
22:W:43:A:H2'	22:W:44:A:C8	2.42	0.54
1:A:818:G:C3'	1:A:819:A:H5''	2.37	0.54
3:C:43:LEU:HD12	3:C:55:VAL:HG21	1.90	0.54
3:C:58:GLU:O	3:C:59:ARG:HG3	2.07	0.54
9:I:104:ARG:O	9:I:104:ARG:HD2	2.07	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:79:SER:HB3	11:K:106:LYS:HE3	1.88	0.54
12:L:83:LEU:HB3	12:L:103:VAL:HG21	1.89	0.54
12:L:82:VAL:HG21	12:L:99:ILE:HG13	1.89	0.54
1:A:390:C:H4'	16:P:28:ARG:HH21	1.73	0.54
1:A:406:G:H2'	1:A:407:G:H8	1.73	0.54
1:A:546:G:P	4:D:72:GLU:HB2	2.47	0.54
4:D:127:THR:HG22	4:D:147:ALA:O	2.07	0.54
6:F:60:PHE:C	6:F:61:LEU:HD12	2.27	0.54
15:O:26:GLU:OE2	15:O:77:ARG:HD2	2.07	0.54
1:A:279:A:C5	17:Q:98:LEU:HD13	2.43	0.54
22:V:48:C:C2	22:V:59:A:H1'	2.42	0.54
1:A:790:A:C6	1:A:791:G:C6	2.95	0.54
1:A:938:A:C6	1:A:939:G:C5	2.96	0.54
3:C:121:ALA:O	3:C:124:ILE:HB	2.07	0.54
3:C:73:PRO:O	3:C:76:VAL:HG22	2.07	0.54
6:F:48:LEU:HB2	18:R:77:GLY:O	2.07	0.54
11:K:44:SER:O	11:K:48:ILE:HG12	2.07	0.54
14:N:26:ARG:HH21	14:N:43:CYS:HB2	1.71	0.54
22:W:50:U:H2'	22:W:51:C:C6	2.42	0.54
3:C:181:ASN:ND2	3:C:204:LEU:HB2	2.22	0.54
5:E:10:MET:CB	5:E:32:VAL:HG22	2.38	0.54
1:A:1057:G:C4	1:A:1204:A:C2	2.96	0.54
1:A:147:G:H1	1:A:175:C:H42	1.55	0.54
1:A:328:C:H1'	1:A:329:A:OP2	2.07	0.54
4:D:21:LEU:HD12	4:D:22:LYS:H	1.73	0.54
7:G:12:LEU:HD23	7:G:12:LEU:N	2.22	0.54
15:O:63:ARG:NH1	15:O:87:ILE:HD11	2.22	0.54
1:A:1256:A:H2	1:A:1277:C:C4	2.25	0.54
3:C:34:LEU:HD22	3:C:38:ARG:HE	1.73	0.54
9:I:73:GLN:O	9:I:77:ILE:HG12	2.08	0.54
1:A:1225:A:H5''	1:A:1226:C:H5	1.73	0.54
1:A:1263:C:H2'	1:A:1264:C:C6	2.43	0.54
1:A:1371:G:OP1	9:I:11:LYS:HG2	2.07	0.54
1:A:179:A:H2'	1:A:180:U:H6	1.73	0.54
1:A:447:G:H2'	1:A:485:G:N2	2.22	0.54
1:A:622:A:C8	1:A:623:C:C6	2.96	0.54
1:A:811:C:H4'	1:A:900:A:N6	2.23	0.54
1:A:942:G:H21	9:I:124:GLN:NE2	2.06	0.54
1:A:954:G:H2'	1:A:955:U:O4'	2.07	0.54
2:B:161:ALA:HB1	2:B:185:ILE:HD11	1.88	0.54
5:E:147:ASP:O	5:E:151:LEU:HG	2.08	0.54
5:E:43:LEU:HD23	5:E:44:GLY:N	2.23	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:10:GLY:HA3	10:J:16:LEU:HD21	1.88	0.54
11:K:84:VAL:HG22	11:K:109:VAL:O	2.08	0.54
11:K:81:ASP:OD1	11:K:106:LYS:HD2	2.07	0.54
12:L:5:THR:H	12:L:8:GLN:HE21	1.55	0.54
1:A:1409:C:H2'	1:A:1410:G:C8	2.43	0.53
1:A:81:G:H5''	1:A:82:U:OP2	2.08	0.53
2:B:219:VAL:O	2:B:223:ILE:HG13	2.08	0.53
3:C:81:GLY:O	3:C:85:ARG:HD3	2.07	0.53
9:I:51:ARG:HG2	9:I:56:LEU:HB2	1.89	0.53
22:W:48:C:C4	22:W:59:A:C8	2.96	0.53
1:A:1296:C:H4'	1:A:1302:U:C4	2.43	0.53
1:A:1352:C:H2'	1:A:1353:G:C8	2.42	0.53
1:A:1381:U:H5	1:A:1382:C:C4	2.27	0.53
1:A:198:G:H2'	1:A:199:G:C8	2.44	0.53
1:A:979:C:C3'	1:A:980:C:H5''	2.26	0.53
2:B:77:ALA:O	2:B:81:VAL:HG23	2.08	0.53
19:S:36:ARG:HB2	19:S:72:GLY:CA	2.38	0.53
3:C:18:TRP:C	3:C:20:SER:H	2.11	0.53
4:D:18:LYS:HD3	4:D:20:TYR:OH	2.08	0.53
7:G:150:ALA:HB1	11:K:57:THR:HG21	1.90	0.53
10:J:4:ILE:O	10:J:73:ASP:HA	2.08	0.53
19:S:40:ILE:HG21	19:S:62:ILE:HD11	1.90	0.53
1:A:1105:A:H2'	1:A:1106:G:C8	2.40	0.53
1:A:1064:G:N2	1:A:1190:G:H2'	2.23	0.53
1:A:1226:C:N4	13:M:104:ARG:HB2	2.23	0.53
1:A:1288:A:H1'	1:A:1352:C:O2'	2.08	0.53
3:C:14:ILE:HG13	3:C:15:THR:H	1.73	0.53
4:D:30:LYS:C	4:D:32:ALA:H	2.11	0.53
5:E:145:LYS:O	5:E:149:GLU:HG2	2.08	0.53
9:I:127:LYS:HZ3	9:I:128:ARG:NH1	2.06	0.53
1:A:372:C:H4'	1:A:373:A:OP1	2.09	0.53
1:A:524:G:H2'	1:A:525:C:C6	2.43	0.53
3:C:64:VAL:O	3:C:100:ALA:HB3	2.08	0.53
10:J:43:ARG:HB2	10:J:67:THR:HG23	1.89	0.53
11:K:85:ARG:HA	11:K:112:THR:OG1	2.08	0.53
22:V:17:C:H5''	22:V:17(A):U:OP2	2.09	0.53
7:G:150:ALA:HA	11:K:59:TYR:HB3	1.90	0.53
13:M:89:GLY:O	13:M:93:ARG:HD2	2.08	0.53
18:R:73:ALA:HB3	18:R:79:LEU:HD12	1.91	0.53
22:W:8:U:H1'	22:W:48:C:H1'	1.89	0.53
4:D:153:ARG:HH11	4:D:181:MET:HE3	1.73	0.53
5:E:80:ILE:HG22	8:H:104:ARG:NH1	2.24	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:I:88:TYR:O	9:I:89:ASN:HB2	2.09	0.53
1:A:736:C:OP1	18:R:68:LYS:HE2	2.08	0.53
1:A:987:G:H2'	1:A:988:G:C8	2.43	0.53
10:J:75:ILE:HG13	10:J:76:ASN:N	2.23	0.53
11:K:29:ILE:HG22	11:K:44:SER:HB3	1.90	0.53
12:L:10:VAL:HG11	17:Q:36:ILE:HG21	1.91	0.53
12:L:46:LYS:CG	12:L:47:PRO:HD3	2.33	0.53
16:P:75:ARG:NH1	16:P:75:ARG:HG3	2.12	0.53
18:R:56:THR:HB	18:R:58:LEU:HD13	1.91	0.53
22:W:48:C:H2'	22:W:59:A:H1'	1.90	0.53
1:A:754:C:H3'	1:A:754:C:O2	2.09	0.53
3:C:36:ASP:HA	3:C:39:ILE:HD12	1.91	0.53
18:R:44:LEU:HD11	18:R:50:ILE:HD13	1.90	0.53
1:A:243:A:C2	1:A:246:A:C8	2.96	0.53
3:C:181:ASN:HD22	3:C:204:LEU:HB2	1.74	0.53
3:C:81:GLY:O	3:C:85:ARG:HB2	2.09	0.53
5:E:36:ASP:O	5:E:37:ARG:HB2	2.09	0.53
9:I:70:LYS:H	9:I:70:LYS:HD3	1.74	0.53
13:M:84:ILE:HG13	19:S:74:PHE:HE1	1.73	0.53
1:A:273:A:N6	1:A:274:A:N6	2.57	0.52
1:A:827:U:H5''	1:A:828:A:OP2	2.09	0.52
4:D:49:ARG:HA	4:D:49:ARG:NH1	2.23	0.52
7:G:46:ALA:O	7:G:50:ILE:HG12	2.08	0.52
12:L:44:PRO:HG3	12:L:52:ARG:HG3	1.91	0.52
6:F:91:VAL:HG11	18:R:72:ARG:NH1	2.24	0.52
1:A:1225:A:H5'	13:M:103:THR:OG1	2.09	0.52
1:A:1427:U:H2'	1:A:1428:A:H8	1.73	0.52
10:J:6:ILE:HD12	10:J:23:ILE:HD12	1.91	0.52
22:V:68:C:H2'	22:V:69:C:H6	1.75	0.52
1:A:1038:C:H2'	1:A:1039:C:C6	2.44	0.52
1:A:1182:G:H4'	1:A:1183:A:C5'	2.38	0.52
1:A:960:U:C5	1:A:1225:A:C8	2.97	0.52
3:C:40:ARG:O	3:C:44:GLU:HG2	2.09	0.52
5:E:102:ALA:HB1	5:E:106:PRO:HG2	1.91	0.52
5:E:80:ILE:HG22	8:H:104:ARG:HH12	1.74	0.52
8:H:73:ASP:C	8:H:75:ARG:H	2.13	0.52
11:K:20:TYR:O	11:K:30:VAL:HA	2.10	0.52
12:L:26:LEU:HD13	12:L:27:LYS:N	2.24	0.52
1:A:1057:G:H4'	3:C:197:GLY:N	2.24	0.52
1:A:1070:U:H2'	1:A:1071:C:H6	1.74	0.52
2:B:229:VAL:HG12	2:B:230:VAL:N	2.25	0.52
1:A:554:C:H2'	1:A:555:C:C6	2.44	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:152:SER:HB3	4:D:158:ILE:CD1	2.40	0.52
1:A:430:A:OP1	4:D:9:CYS:HB2	2.09	0.52
12:L:89:VAL:HG12	12:L:92:LEU:H	1.75	0.52
14:N:12:ARG:HG2	14:N:14:PRO:HD3	1.92	0.52
15:O:15:PHE:CZ	15:O:85:LEU:HD21	2.44	0.52
1:A:197:A:N6	1:A:221:C:H5'	2.24	0.52
1:A:66:G:H4'	1:A:173:U:C5	2.45	0.52
8:H:64:LYS:CG	8:H:79:VAL:HG21	2.39	0.52
10:J:58:ASP:C	10:J:60:ARG:H	2.12	0.52
14:N:26:ARG:NH2	14:N:43:CYS:HB2	2.25	0.52
1:A:976:G:H8	1:A:1358:U:H2'	1.71	0.52
5:E:11:ILE:N	5:E:11:ILE:HD12	2.25	0.52
11:K:29:ILE:HG22	11:K:44:SER:HB2	1.91	0.52
14:N:26:ARG:HH21	14:N:43:CYS:CB	2.22	0.52
17:Q:43:LEU:HB3	17:Q:69:LYS:HG2	1.91	0.52
1:A:116:A:H61	1:A:313:A:H1'	1.75	0.52
1:A:1252:A:H2'	1:A:1253:G:O4'	2.09	0.52
1:A:878:G:OP1	8:H:90:GLY:HA3	2.09	0.52
1:A:973:G:H3'	1:A:974:A:H5''	1.92	0.52
2:B:74:LYS:CB	2:B:74:LYS:HZ2	2.23	0.52
7:G:65:ALA:HB1	7:G:127:ALA:HB3	1.92	0.52
8:H:98:LYS:HB2	8:H:99:GLU:OE2	2.10	0.52
12:L:91:ASP:O	12:L:93:PRO:HD3	2.10	0.52
1:A:1131:G:H2'	1:A:1132:C:C6	2.45	0.52
1:A:1391:U:H2'	1:A:1392:G:C8	2.45	0.52
1:A:1499:A:H1'	1:A:1520:G:H5'	1.91	0.52
3:C:92:ALA:HB2	3:C:99:VAL:HG13	1.91	0.52
4:D:134:ASP:O	4:D:136:PRO:HD3	2.10	0.52
8:H:20:TYR:HD1	8:H:65:TYR:CD2	2.27	0.52
6:F:60:PHE:CE2	18:R:78:LEU:HD21	2.44	0.52
1:A:191(F):U:O2	20:T:105:SER:HB2	2.10	0.52
1:A:1066:C:H5'	1:A:1067:A:OP2	2.10	0.52
1:A:892:A:O2'	1:A:1415:G:H4'	2.09	0.52
1:A:1422:G:H2'	1:A:1423:G:H8	1.75	0.52
1:A:44:G:OP2	16:P:12:LYS:HE3	2.10	0.52
1:A:523:A:H61	12:L:91:ASP:HB2	1.75	0.52
1:A:820:U:H4'	1:A:821:G:OP2	2.10	0.52
3:C:16:ARG:NH1	3:C:16:ARG:HB2	2.24	0.52
3:C:191:THR:HG22	3:C:192:THR:H	1.74	0.52
4:D:88:VAL:HG12	4:D:91:SER:H	1.75	0.52
8:H:89:PRO:HA	8:H:92:ARG:NH1	2.24	0.52
22:W:50:U:H3	22:W:64:G:H1	1.57	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1010:G:H2'	1:A:1011:G:C8	2.45	0.51
1:A:1004:A:N6	1:A:1025:U:H4'	2.24	0.51
1:A:983:A:H1'	1:A:1049:U:O2	2.09	0.51
1:A:691:G:C6	11:K:52:GLY:HA2	2.46	0.51
1:A:838:G:N2	1:A:849:C:C2	2.78	0.51
1:A:977:A:H2'	1:A:978:A:H5''	1.92	0.51
2:B:71:VAL:HG12	2:B:93:VAL:O	2.11	0.51
4:D:206:PHE:HD2	4:D:207:TYR:CD2	2.27	0.51
6:F:50:TYR:CE2	6:F:52:ILE:HG22	2.45	0.51
8:H:42:GLU:HG3	8:H:109:ILE:HD12	1.92	0.51
22:V:74:C:C5'	22:V:75:C:H5''	2.30	0.51
1:A:1009:G:H2'	1:A:1010:G:H8	1.75	0.51
1:A:192:U:H2'	1:A:193:C:C6	2.45	0.51
1:A:300:A:H1'	1:A:565:U:O2	2.10	0.51
1:A:983:A:H5'	1:A:984:C:OP2	2.10	0.51
2:B:200:ILE:H	2:B:200:ILE:HD12	1.74	0.51
2:B:69:LEU:HD22	2:B:91:PRO:HB2	1.92	0.51
15:O:54:ARG:CZ	15:O:58:MET:HE3	2.41	0.51
1:A:564:C:C5	17:Q:31:LEU:HD11	2.46	0.51
18:R:70:ILE:O	18:R:74:ARG:HG3	2.11	0.51
1:A:937:A:H1'	1:A:1379:G:N2	2.26	0.51
3:C:120:VAL:O	3:C:124:ILE:HG12	2.10	0.51
16:P:43:LYS:HA	16:P:48:TRP:HB2	1.92	0.51
1:A:186(A):C:H5'	20:T:78:ALA:HB1	1.92	0.51
1:A:1015:A:H2'	1:A:1016:A:C8	2.45	0.51
1:A:1195:C:H5''	1:A:1196:U:OP2	2.10	0.51
1:A:1221:G:OP1	19:S:36:ARG:HD3	2.10	0.51
1:A:1285:A:H8	1:A:1285:A:OP1	1.93	0.51
1:A:1379:G:N7	7:G:2:ALA:HB3	2.25	0.51
1:A:1478:C:H2'	1:A:1479:C:H6	1.75	0.51
1:A:149:A:O2'	1:A:150:C:H5'	2.10	0.51
1:A:324:G:N2	1:A:327:A:C8	2.79	0.51
1:A:617:G:H5'	16:P:45:THR:HG22	1.92	0.51
1:A:1079:G:O3'	5:E:14:ARG:NH2	2.44	0.51
10:J:6:ILE:CD1	10:J:72:VAL:HB	2.40	0.51
1:A:115:G:H1'	1:A:116:A:OP2	2.11	0.51
8:H:88:LYS:HB3	8:H:89:PRO:HD2	1.92	0.51
9:I:14:VAL:O	9:I:65:VAL:HG23	2.10	0.51
20:T:13:LEU:H	20:T:13:LEU:HD13	1.75	0.51
22:V:19:G:C2	22:V:57:A:C2	2.98	0.51
1:A:802:A:H2'	1:A:803:G:O4'	2.11	0.51
4:D:59:ARG:HE	4:D:59:ARG:HA	1.74	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1329:A:P	13:M:28:ALA:HB3	2.51	0.51
19:S:11:VAL:HG23	19:S:38:SER:OG	2.10	0.51
1:A:664:G:N2	1:A:741:G:H1	2.08	0.51
2:B:15:VAL:HG21	2:B:209:ARG:HH21	1.75	0.51
1:A:673:G:H5''	6:F:87:ARG:NH1	2.26	0.51
8:H:20:TYR:HE2	8:H:75:ARG:NH1	2.09	0.51
8:H:20:TYR:HA	8:H:65:TYR:CE2	2.46	0.51
10:J:12:ASP:OD1	10:J:15:THR:HG23	2.10	0.51
16:P:74:LEU:O	16:P:79:VAL:HG23	2.10	0.51
1:A:145:G:H2'	1:A:146:G:H8	1.76	0.51
1:A:386:C:C2'	1:A:387:U:H5'	2.40	0.51
1:A:489:C:H2'	1:A:490:G:H8	1.76	0.51
4:D:111:ALA:HA	4:D:161:ASN:HD22	1.76	0.51
6:F:83:ASP:N	6:F:83:ASP:OD1	2.41	0.51
1:A:1095:U:H2'	1:A:1096:C:C6	2.46	0.51
1:A:1161:C:H2'	1:A:1162:C:C6	2.46	0.51
1:A:1285:A:C1'	1:A:1286:A:OP2	2.58	0.51
1:A:452:A:HO2'	1:A:453:A:H8	1.58	0.51
1:A:639:G:H2'	1:A:640:A:H8	1.76	0.51
3:C:11:ARG:HB3	3:C:15:THR:HB	1.93	0.51
3:C:18:TRP:HE3	3:C:18:TRP:H	1.59	0.51
6:F:44:GLY:HA2	6:F:59:TYR:CE2	2.46	0.51
10:J:91:PRO:HB3	10:J:94:VAL:HB	1.92	0.51
12:L:81:VAL:HG13	12:L:104:TYR:HB3	1.93	0.51
15:O:25:THR:HG21	15:O:70:LEU:HB2	1.93	0.51
18:R:53:ARG:HE	18:R:59:SER:C	2.15	0.51
1:A:949:A:C4	1:A:1233:G:N2	2.79	0.51
1:A:1275:A:H2'	1:A:1276:G:H8	1.75	0.51
1:A:345:C:H1'	1:A:346:G:N2	2.26	0.51
1:A:429:U:H4'	1:A:430:A:O5'	2.09	0.51
2:B:97:TRP:CH2	2:B:173:ALA:HA	2.46	0.51
9:I:85:LEU:HD12	9:I:86:VAL:N	2.26	0.51
11:K:33:THR:HA	11:K:40:ILE:HG12	1.93	0.51
1:A:979:C:H42	14:N:18:VAL:HG12	1.76	0.51
16:P:22:THR:HG22	16:P:32:TYR:HB2	1.93	0.51
22:W:65:C:H2'	22:W:66:C:H6	1.76	0.51
1:A:1418:A:C2	1:A:1483:A:C2	2.99	0.50
1:A:397:A:N7	1:A:548:G:C8	2.79	0.50
3:C:28:GLN:O	3:C:32:LEU:HG	2.10	0.50
7:G:62:PHE:CD1	7:G:124:LEU:HD21	2.46	0.50
10:J:48:THR:HA	10:J:62:HIS:CB	2.37	0.50
11:K:25:TYR:CD1	11:K:25:TYR:N	2.79	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:Q:7:THR:CG2	17:Q:58:GLU:HG2	2.31	0.50
20:T:33:ILE:CD1	20:T:62:LEU:HD22	2.41	0.50
1:A:428:G:H4'	1:A:429:U:O5'	2.11	0.50
1:A:723:U:H5''	1:A:724:G:OP2	2.11	0.50
1:A:792:A:H4'	1:A:793:U:O5'	2.11	0.50
4:D:173:TRP:C	4:D:186:LEU:HD12	2.32	0.50
13:M:81:LEU:HD11	13:M:88:ARG:HH21	1.76	0.50
20:T:67:ALA:HA	20:T:72:LEU:O	2.10	0.50
1:A:1161:C:H2'	1:A:1162:C:H6	1.76	0.50
2:B:15:VAL:HG23	2:B:16:HIS:CE1	2.46	0.50
4:D:168:ARG:NE	4:D:168:ARG:HA	2.27	0.50
13:M:24:GLY:C	13:M:25:ILE:HD12	2.31	0.50
1:A:1016:A:H2'	1:A:1017:G:O4'	2.11	0.50
1:A:1270:C:H2'	1:A:1271:G:C8	2.47	0.50
1:A:957:U:O2	1:A:959:A:C8	2.65	0.50
4:D:138:TYR:HD1	4:D:139:ARG:N	2.08	0.50
7:G:89:MET:HB3	7:G:155:ARG:HG2	1.93	0.50
9:I:114:TYR:HE1	10:J:60:ARG:O	1.94	0.50
17:Q:59:ILE:O	17:Q:59:ILE:HD12	2.12	0.50
17:Q:59:ILE:HG22	17:Q:73:VAL:HA	1.94	0.50
18:R:40:LEU:HD22	18:R:70:ILE:HD13	1.93	0.50
19:S:6:LYS:HG2	19:S:7:LYS:HD3	1.93	0.50
22:V:74:C:H3'	22:V:75:C:C5'	2.41	0.50
1:A:1023:G:H2'	1:A:1024:G:O4'	2.12	0.50
1:A:192:U:H2'	1:A:193:C:H6	1.77	0.50
1:A:254:G:C2	1:A:255:G:C8	2.99	0.50
2:B:111:ARG:NE	2:B:111:ARG:HA	2.26	0.50
3:C:113:ALA:HB3	3:C:114:PRO:HD3	1.93	0.50
3:C:182:ILE:HG13	3:C:203:PHE:HA	1.92	0.50
1:A:1279:A:H62	3:C:26:LYS:HE2	1.75	0.50
5:E:92:LYS:O	5:E:119:LEU:HD12	2.11	0.50
8:H:11:THR:HA	8:H:14:ARG:NH1	2.26	0.50
9:I:5:TYR:HE2	9:I:16:ARG:HB3	1.77	0.50
10:J:84:GLN:HG3	10:J:88:LEU:HD22	1.93	0.50
13:M:96:LEU:HB3	13:M:97:PRO:HD2	1.93	0.50
1:A:1455:G:H5''	20:T:31:SER:OG	2.12	0.50
1:A:1338:G:C6	1:A:1339:A:C6	3.00	0.50
1:A:451:A:C2	1:A:480:U:C4	2.99	0.50
2:B:72:GLY:O	2:B:94:ASN:HB2	2.11	0.50
5:E:11:ILE:HD11	5:E:33:VAL:HG23	1.93	0.50
9:I:46:ALA:HB2	9:I:74:ILE:CG2	2.41	0.50
12:L:65:VAL:HG11	12:L:97:TYR:HE1	1.76	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:N:25:VAL:HG23	14:N:38:GLY:O	2.10	0.50
15:O:16:ALA:CB	15:O:21:ASP:HB3	2.38	0.50
2:B:54:THR:O	2:B:58:ILE:HG12	2.11	0.50
4:D:28:SER:CB	4:D:29:PRO:HD2	2.42	0.50
10:J:98:ILE:N	10:J:98:ILE:HD12	2.27	0.50
11:K:33:THR:HG22	11:K:39:PRO:HA	1.93	0.50
1:A:179:A:H2'	1:A:180:U:C6	2.47	0.50
1:A:735:C:H6	1:A:735:C:O5'	1.94	0.50
2:B:208:ILE:HD12	2:B:208:ILE:N	2.23	0.50
3:C:191:THR:HG21	3:C:193:TYR:CE2	2.46	0.50
7:G:121:ALA:O	7:G:125:MET:HG3	2.12	0.50
7:G:51:GLN:CG	7:G:58:PRO:HD3	2.42	0.50
19:S:29:ARG:O	19:S:31:ILE:HG22	2.11	0.50
1:A:1138:G:N3	1:A:1138:G:H3'	2.26	0.50
1:A:1401:G:C2	1:A:1402:C:H1'	2.46	0.50
1:A:353:A:C2'	1:A:354:G:OP2	2.60	0.50
1:A:995:C:H5'	14:N:8:GLU:HG2	1.94	0.50
4:D:28:SER:HB2	4:D:29:PRO:HD2	1.94	0.50
9:I:114:TYR:N	9:I:114:TYR:CD2	2.80	0.50
22:W:68:C:H2'	22:W:69:C:H6	1.75	0.50
1:A:1086:U:H3	1:A:1099:G:H22	1.60	0.49
1:A:113:G:H2'	1:A:114:U:C6	2.47	0.49
1:A:1402:C:H2'	1:A:1403:C:O4'	2.12	0.49
5:E:83:GLU:HG2	5:E:88:LYS:HG3	1.94	0.49
1:A:453:A:H5'	16:P:72:ARG:HG3	1.92	0.49
1:A:926:G:C6	1:A:1505:G:C5	3.00	0.49
2:B:87:ARG:HE	2:B:233:SER:H	1.61	0.49
3:C:36:ASP:O	3:C:40:ARG:HG3	2.12	0.49
5:E:6:PHE:HB2	5:E:34:VAL:HG13	1.93	0.49
1:A:673:G:H5''	6:F:87:ARG:HH12	1.77	0.49
15:O:8:LYS:O	15:O:12:ILE:HG13	2.11	0.49
22:V:20:U:H5'	22:V:21:A:OP2	2.12	0.49
22:V:21:A:C2	22:V:46:G:C2	3.00	0.49
22:W:10:G:N2	22:W:26:G:H1'	2.27	0.49
1:A:1049:U:H4'	1:A:1050:G:H5''	1.94	0.49
1:A:216:G:C6	1:A:217:C:N4	2.80	0.49
1:A:894:G:H2'	1:A:895:G:O4'	2.11	0.49
4:D:4:TYR:HE1	4:D:6:GLY:O	1.95	0.49
1:A:1196:U:H5'	1:A:1197:G:O5'	2.12	0.49
4:D:36:ARG:HD3	4:D:38:TYR:OH	2.12	0.49
6:F:2:ARG:HD2	6:F:69:GLU:HB3	1.95	0.49
15:O:7:GLU:HA	15:O:10:LYS:HD2	1.94	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:U:9:ARG:O	21:U:13:ILE:HG13	2.12	0.49
22:W:20:U:C5	22:W:59:A:N6	2.80	0.49
1:A:1287:A:H2'	1:A:1288:A:C8	2.48	0.49
1:A:1370:G:C2	1:A:1371:G:C8	3.00	0.49
2:B:47:THR:HA	2:B:202:PRO:HG2	1.94	0.49
4:D:9:CYS:HB3	4:D:32:ALA:CB	2.41	0.49
8:H:86:ILE:HG22	8:H:87:SER:N	2.28	0.49
11:K:41:THR:CG2	11:K:42:TRP:H	2.21	0.49
19:S:6:LYS:H	19:S:6:LYS:CE	2.26	0.49
1:A:160:A:H2'	1:A:161:A:O4'	2.12	0.49
1:A:349:A:O2'	1:A:350:G:H5'	2.13	0.49
1:A:575:G:H4'	1:A:576:G:H5''	1.94	0.49
3:C:68:VAL:HG12	3:C:70:VAL:HG23	1.93	0.49
4:D:17:VAL:HG12	4:D:18:LYS:N	2.27	0.49
5:E:79:GLU:HB3	5:E:92:LYS:HA	1.93	0.49
1:A:1291:G:H4'	9:I:38:GLN:O	2.13	0.49
10:J:63:PHE:HB3	14:N:57:ARG:O	2.13	0.49
11:K:34:ASP:N	11:K:40:ILE:HD11	2.28	0.49
16:P:20:VAL:HG21	16:P:32:TYR:CB	2.43	0.49
6:F:50:TYR:CE1	18:R:74:ARG:O	2.66	0.49
1:A:1313:U:OP2	19:S:6:LYS:HB3	2.12	0.49
1:A:1316:G:H2'	1:A:1317:C:H5''	1.94	0.49
1:A:722:A:HO2'	1:A:723:U:H6	1.57	0.49
13:M:76:ALA:HA	13:M:79:LYS:CE	2.42	0.49
14:N:22:THR:HB	14:N:33:VAL:HG11	1.94	0.49
16:P:34:GLU:OE2	16:P:55:ARG:HD3	2.12	0.49
22:W:9:G:H5'	22:W:46:G:C1'	2.42	0.49
1:A:184:G:C4'	1:A:224:C:H4'	2.42	0.49
1:A:955:U:H1'	1:A:1227:A:N6	2.28	0.49
2:B:97:TRP:CE2	2:B:101:MET:HG3	2.48	0.49
1:A:545:C:C5'	4:D:72:GLU:HG3	2.29	0.49
8:H:20:TYR:HA	8:H:65:TYR:CZ	2.48	0.49
11:K:26:ASN:O	11:K:27:ASN:HB2	2.13	0.49
15:O:87:ILE:HG23	15:O:88:ARG:N	2.27	0.49
18:R:54:ARG:N	18:R:54:ARG:HD2	2.27	0.49
1:A:748:C:O2	1:A:749:C:H5	1.95	0.49
1:A:438:G:H4'	4:D:123:HIS:ND1	2.27	0.49
5:E:10:MET:HA	5:E:32:VAL:HA	1.95	0.49
1:A:1187:G:H5'	9:I:113:LYS:HE2	1.94	0.49
10:J:51:ARG:HB2	10:J:60:ARG:HA	1.95	0.49
21:U:21:TYR:O	21:U:22:ARG:HG3	2.13	0.49
1:A:1230:C:H2'	1:A:1231:G:H8	1.78	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1328:C:H5''	13:M:28:ALA:HB1	1.94	0.48
1:A:1409:C:H2'	1:A:1410:G:H8	1.77	0.48
1:A:1411:C:H2'	1:A:1412:C:H6	1.76	0.48
4:D:149:ALA:HB3	4:D:152:SER:HG	1.77	0.48
5:E:92:LYS:O	5:E:118:ILE:HG13	2.13	0.48
9:I:99:LEU:HB3	9:I:101:PHE:HE1	1.78	0.48
10:J:51:ARG:H	10:J:60:ARG:HA	1.77	0.48
12:L:17:VAL:HG23	12:L:18:ARG:N	2.26	0.48
13:M:22:ILE:HB	13:M:25:ILE:HD13	1.95	0.48
19:S:12:ASP:HB3	19:S:14:HIS:CE1	2.48	0.48
1:A:1305:G:H1'	1:A:1306:A:C8	2.47	0.48
1:A:1443:G:H3'	1:A:1446:A:H5'	1.94	0.48
6:F:45:LEU:O	6:F:46:ARG:HG2	2.14	0.48
20:T:33:ILE:HD11	20:T:62:LEU:HD22	1.94	0.48
21:U:12:LYS:HB3	21:U:17:THR:O	2.13	0.48
22:W:40:C:H2'	22:W:41:C:C6	2.47	0.48
1:A:1234:C:H4'	1:A:1364:U:H1'	1.96	0.48
1:A:620:C:H2'	1:A:621:A:O4'	2.12	0.48
1:A:939:G:H2'	1:A:940:C:C6	2.49	0.48
2:B:70:PHE:HB2	2:B:92:TYR:HB2	1.94	0.48
4:D:49:ARG:NE	4:D:50:ARG:H	2.12	0.48
6:F:53:ALA:O	6:F:54:LYS:HB2	2.12	0.48
13:M:12:ASN:HA	13:M:46:LYS:HE2	1.94	0.48
1:A:105:G:C6	1:A:106:C:N4	2.81	0.48
1:A:1464:G:O2'	1:A:1465:C:H5'	2.13	0.48
1:A:489:C:H2'	1:A:490:G:C8	2.48	0.48
1:A:841:U:C2'	1:A:842:C:H5''	2.43	0.48
1:A:574:A:N3	1:A:883:C:H1'	2.29	0.48
2:B:19:HIS:CD2	2:B:20:GLU:HG2	2.49	0.48
2:B:69:LEU:HD13	2:B:92:TYR:HA	1.95	0.48
14:N:23:ARG:HD2	14:N:28:GLY:O	2.12	0.48
1:A:1327:C:OP1	21:U:21:TYR:CD1	2.67	0.48
2:B:214:ILE:N	2:B:214:ILE:HD12	2.27	0.48
4:D:15:GLU:HG2	4:D:63:LYS:HG3	1.95	0.48
11:K:12:ARG:HB3	11:K:12:ARG:CZ	2.43	0.48
12:L:40:ARG:HG2	12:L:41:THR:N	2.28	0.48
1:A:1077:G:N2	1:A:1080:A:OP2	2.45	0.48
1:A:559:A:C5'	1:A:560:U:H3'	2.44	0.48
1:A:687:A:H4'	1:A:688:G:O5'	2.14	0.48
1:A:791:G:C5	1:A:792:A:N7	2.81	0.48
2:B:141:GLU:O	2:B:145:LEU:HB2	2.14	0.48
5:E:135:THR:O	5:E:138:ALA:HB3	2.14	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:I:51:ARG:HD3	9:I:56:LEU:HD22	1.95	0.48
11:K:24:SER:HB2	11:K:27:ASN:O	2.13	0.48
1:A:192:U:C4'	20:T:103:GLY:H	2.22	0.48
1:A:818:G:C3'	1:A:819:A:C5'	2.92	0.48
1:A:875:C:H1'	8:H:15:ASN:HD21	1.79	0.48
1:A:80:G:O6	1:A:88:C:N4	2.47	0.48
2:B:172:ILE:HD12	2:B:173:ALA:N	2.25	0.48
5:E:64:ARG:HG3	5:E:65:ASN:N	2.28	0.48
9:I:92:TYR:O	9:I:96:LEU:HB2	2.13	0.48
12:L:45:LYS:HG2	12:L:46:LYS:HG2	1.96	0.48
1:A:719:C:C2	18:R:50:ILE:HG12	2.49	0.48
22:V:58:A:H2	22:V:60:U:HO2'	1.57	0.48
1:A:1275:A:H2'	1:A:1276:G:C8	2.49	0.48
1:A:1312:G:H2'	1:A:1313:U:C6	2.48	0.48
1:A:663:A:O2'	1:A:664:G:H5'	2.13	0.48
1:A:993:G:H4'	1:A:994:A:OP2	2.14	0.48
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.78	0.48
3:C:137:ALA:O	3:C:140:ARG:HD2	2.14	0.48
1:A:1330:U:O4	1:A:1331:G:N1	2.47	0.48
1:A:309:G:O2'	1:A:310:G:H5'	2.14	0.48
1:A:453:A:H2'	1:A:454:C:C6	2.48	0.48
1:A:965:A:C2	1:A:969:A:C2	3.02	0.48
3:C:52:LEU:HD13	3:C:68:VAL:CG1	2.40	0.48
9:I:33:PHE:HE2	9:I:47:LEU:HB2	1.78	0.48
9:I:97:LYS:HA	9:I:102:LEU:CD1	2.44	0.48
1:A:142:G:H2'	1:A:143:A:H8	1.78	0.48
1:A:255:G:O6	1:A:266:G:O6	2.32	0.48
1:A:439:A:C4	1:A:496:A:C2	3.01	0.48
4:D:153:ARG:HH11	4:D:181:MET:CE	2.26	0.48
10:J:22:LYS:HD2	10:J:22:LYS:O	2.14	0.48
10:J:35:SER:O	10:J:72:VAL:HG13	2.14	0.48
12:L:96:ARG:HB2	12:L:97:TYR:CE1	2.47	0.48
1:A:1225:A:H5'	13:M:103:THR:CB	2.44	0.48
13:M:2:ALA:HB1	13:M:57:ARG:NH1	2.29	0.48
14:N:44:LEU:O	14:N:44:LEU:HD12	2.13	0.48
16:P:6:LEU:HG	16:P:19:ILE:HD13	1.96	0.48
22:W:59:A:C5	22:W:60:U:C5	3.02	0.48
1:A:265:G:O2'	1:A:266:G:H5'	2.14	0.47
1:A:407:G:H5'	4:D:3:ARG:HH11	1.79	0.47
2:B:43:ASP:OD2	2:B:46:LYS:HB2	2.14	0.47
2:B:60:ASP:O	2:B:64:ARG:HG2	2.14	0.47
3:C:88:ARG:HG2	3:C:101:LEU:HB3	1.96	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:107:ARG:HH11	5:E:107:ARG:HG3	1.77	0.47
5:E:77:PRO:HD2	5:E:142:LEU:HD22	1.96	0.47
8:H:114:THR:HG23	8:H:116:LYS:N	2.18	0.47
9:I:33:PHE:HE2	9:I:47:LEU:HD22	1.79	0.47
19:S:36:ARG:HB2	19:S:72:GLY:HA2	1.96	0.47
1:A:1329:A:H62	21:U:7:ARG:HH21	1.60	0.47
1:A:253:U:H2'	1:A:254:G:C8	2.47	0.47
1:A:376:G:O2'	1:A:377:G:H5'	2.14	0.47
1:A:403:C:O2'	1:A:404:U:H5'	2.14	0.47
1:A:709:G:H2'	1:A:710:G:H8	1.79	0.47
1:A:878:G:C5'	8:H:89:PRO:HG2	2.44	0.47
1:A:939:G:C6	1:A:940:C:N4	2.82	0.47
2:B:184:VAL:HG12	2:B:197:VAL:HG13	1.96	0.47
3:C:15:THR:HG21	3:C:181:ASN:HA	1.95	0.47
4:D:156:GLU:O	4:D:160:GLN:HB2	2.14	0.47
4:D:30:LYS:C	4:D:32:ALA:N	2.68	0.47
17:Q:69:LYS:C	17:Q:70:ARG:HD2	2.35	0.47
1:A:1505:G:H5''	1:A:1506:U:H5''	1.95	0.47
1:A:948:C:C5	13:M:106:ASN:ND2	2.82	0.47
2:B:208:ILE:H	2:B:208:ILE:CD1	2.23	0.47
2:B:24:TRP:H	2:B:24:TRP:HD1	1.62	0.47
2:B:52:GLU:O	2:B:56:ARG:HG3	2.14	0.47
2:B:75:LYS:C	2:B:77:ALA:H	2.18	0.47
3:C:75:VAL:O	3:C:75:VAL:HG12	2.13	0.47
5:E:79:GLU:N	5:E:79:GLU:CD	2.68	0.47
7:G:27:ILE:HD11	7:G:43:PHE:CD2	2.49	0.47
16:P:20:VAL:HG23	16:P:34:GLU:O	2.14	0.47
16:P:75:ARG:NH1	16:P:75:ARG:CG	2.71	0.47
13:M:86:CYS:HA	19:S:73:GLU:O	2.14	0.47
1:A:352:C:H6	1:A:352:C:OP1	1.97	0.47
1:A:552:U:H5'	12:L:85:ARG:HE	1.78	0.47
1:A:826:C:H2'	1:A:827:U:C6	2.49	0.47
8:H:77:GLU:HG3	8:H:78:GLN:N	2.29	0.47
3:C:30:ARG:HH11	14:N:38:GLY:CA	2.27	0.47
3:C:30:ARG:HH11	14:N:38:GLY:HA3	1.80	0.47
20:T:14:LYS:O	20:T:18:GLN:HG3	2.14	0.47
20:T:87:LYS:O	20:T:91:LEU:HG	2.15	0.47
1:A:1106:G:OP1	3:C:172:ARG:HD3	2.14	0.47
1:A:1258:G:O2'	1:A:1259:C:H5'	2.15	0.47
1:A:69:G:C2	1:A:73:G:C5	3.02	0.47
3:C:15:THR:HG22	3:C:16:ARG:N	2.30	0.47
13:M:14:ARG:HB2	13:M:17:VAL:HG22	1.96	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
22:V:23:C:H2'	22:V:24:U:C6	2.49	0.47
22:W:65:C:H2'	22:W:66:C:C6	2.49	0.47
1:A:1009:G:H2'	1:A:1010:G:C8	2.50	0.47
1:A:1004:A:C6	1:A:1025:U:H4'	2.49	0.47
1:A:1327:C:H2'	1:A:1328:C:C6	2.50	0.47
1:A:272:C:H2'	1:A:273:A:H8	1.79	0.47
1:A:938:A:N6	1:A:939:G:C6	2.83	0.47
2:B:112:VAL:O	2:B:116:GLU:HG2	2.14	0.47
7:G:48:LYS:O	7:G:52:GLU:HG3	2.15	0.47
1:A:1316:G:O6	19:S:5:LEU:HD23	2.14	0.47
1:A:382:A:O2'	1:A:383:A:H5'	2.15	0.47
1:A:722:A:O2'	1:A:723:U:H6	1.97	0.47
1:A:926:G:C6	1:A:1505:G:C6	3.02	0.47
3:C:29:TYR:CE1	3:C:33:LEU:HD22	2.46	0.47
8:H:38:ILE:O	8:H:42:GLU:HG2	2.15	0.47
9:I:110:GLU:HG2	9:I:119:ALA:HB1	1.97	0.47
10:J:24:VAL:HG13	10:J:28:ARG:HD2	1.96	0.47
1:A:1225:A:N3	1:A:1225:A:C2'	2.77	0.47
2:B:142:LEU:HD11	2:B:146:GLN:HE21	1.80	0.47
2:B:75:LYS:C	2:B:75:LYS:HD3	2.35	0.47
1:A:408:A:H4'	4:D:112:VAL:HG21	1.95	0.47
6:F:39:LYS:HB3	6:F:39:LYS:NZ	2.29	0.47
21:U:9:ARG:HH21	21:U:10:ARG:HD2	1.80	0.47
1:A:791:G:C6	1:A:792:A:N7	2.83	0.47
1:A:819:A:H4'	1:A:820:U:OP2	2.15	0.47
5:E:51:VAL:O	5:E:54:ALA:HB3	2.15	0.47
7:G:26:PHE:CE2	7:G:30:ILE:HD11	2.50	0.47
12:L:52:ARG:HB3	12:L:68:TYR:HE1	1.79	0.47
16:P:14:ASN:HD22	16:P:42:ARG:NH2	2.13	0.47
18:R:26:LEU:HG	18:R:42:ARG:NH1	2.29	0.47
1:A:38:G:H22	1:A:397:A:H5'	1.80	0.47
1:A:511:C:C4	1:A:541:G:N2	2.83	0.47
1:A:984:C:H2'	1:A:985:C:C6	2.50	0.47
4:D:187:ARG:HG3	4:D:188:LEU:O	2.15	0.47
5:E:36:ASP:OD2	5:E:38:GLN:HB2	2.15	0.47
9:I:17:VAL:HG22	9:I:63:ILE:HD13	1.96	0.47
16:P:12:LYS:C	16:P:14:ASN:H	2.17	0.47
16:P:3:LYS:O	16:P:21:VAL:HA	2.15	0.47
19:S:21:GLU:HG3	19:S:22:LEU:HD22	1.97	0.47
19:S:6:LYS:HD2	19:S:7:LYS:H	1.79	0.47
20:T:49:ALA:HB3	20:T:99:LEU:HD12	1.96	0.47
7:G:147:ALA:HB1	22:W:40:C:O3'	2.15	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1058:G:H2'	1:A:1059:C:O4'	2.14	0.47
1:A:1127:G:H1'	1:A:1148:U:H3	1.79	0.47
1:A:1285:A:OP1	1:A:1285:A:C8	2.68	0.47
1:A:748:C:H4'	1:A:749:C:O5'	2.15	0.47
1:A:792:A:H4'	1:A:793:U:C5'	2.44	0.47
2:B:33:TYR:HB2	2:B:43:ASP:HA	1.97	0.47
12:L:24:PRO:C	12:L:26:LEU:H	2.17	0.47
12:L:56:LYS:HD2	12:L:56:LYS:N	2.30	0.47
13:M:87:TYR:O	13:M:91:ARG:HG2	2.15	0.47
1:A:1422:G:H2'	1:A:1423:G:C8	2.50	0.46
1:A:1501:C:OP2	1:A:1504:G:H2'	2.14	0.46
7:G:72:ARG:HG3	7:G:142:GLU:OE2	2.16	0.46
9:I:50:LEU:O	9:I:53:VAL:HG22	2.15	0.46
17:Q:99:SER:C	17:Q:100:LYS:HD2	2.35	0.46
22:W:4:G:O2'	22:W:5:G:H5'	2.14	0.46
1:A:106:C:H2'	1:A:107:G:H8	1.80	0.46
1:A:177:C:H2'	1:A:178:C:H6	1.80	0.46
1:A:769:G:H4'	1:A:1513:A:H4'	1.98	0.46
2:B:47:THR:O	2:B:51:LEU:HG	2.15	0.46
4:D:18:LYS:HD3	4:D:20:TYR:CZ	2.50	0.46
9:I:10:ARG:HG2	9:I:104:ARG:O	2.15	0.46
13:M:3:ARG:HH21	13:M:7:VAL:HG12	1.81	0.46
15:O:21:ASP:OD1	15:O:24:SER:HB2	2.15	0.46
1:A:939:G:H1	1:A:1344:C:H42	1.63	0.46
12:L:49:SER:O	12:L:50:ALA:HB2	2.14	0.46
17:Q:24:GLU:HA	17:Q:39:SER:HB3	1.97	0.46
1:A:265:G:H5'	17:Q:64:PRO:O	2.15	0.46
1:A:1504:G:OP1	1:A:1507:A:H4'	2.16	0.46
1:A:657:G:H4'	15:O:28:GLN:HG2	1.97	0.46
1:A:677:U:H2'	1:A:678:U:C6	2.51	0.46
1:A:962:C:H2'	1:A:963:G:O4'	2.15	0.46
2:B:178:ARG:HH22	2:B:196:LEU:HA	1.79	0.46
3:C:97:LYS:HB2	3:C:98:ASN:H	1.54	0.46
7:G:102:ARG:O	7:G:106:GLN:HG3	2.16	0.46
1:A:691:G:N1	11:K:52:GLY:HA2	2.30	0.46
12:L:27:LYS:HE2	12:L:32:ARG:NH2	2.26	0.46
19:S:49:ILE:HD12	19:S:49:ILE:N	2.31	0.46
1:A:685:G:O2'	1:A:686:U:H5'	2.15	0.46
1:A:818:G:H3'	1:A:819:A:C5'	2.46	0.46
4:D:79:PHE:CE1	4:D:204:ILE:HD13	2.50	0.46
9:I:27:THR:HG23	9:I:31:GLN:O	2.15	0.46
17:Q:45:HIS:CD2	17:Q:47:PRO:HD3	2.50	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:555:C:H2'	1:A:556:C:H6	1.77	0.46
1:A:955:U:H1'	1:A:1227:A:H61	1.81	0.46
2:B:168:THR:OG1	2:B:192:SER:HA	2.15	0.46
2:B:83:MET:HE1	2:B:233:SER:HB2	1.98	0.46
3:C:149:ALA:HA	3:C:201:TYR:O	2.16	0.46
4:D:31:CYS:O	4:D:32:ALA:HB3	2.16	0.46
4:D:71:SER:OG	4:D:74:GLN:HB2	2.16	0.46
8:H:119:LEU:HD13	8:H:127:LEU:HD21	1.98	0.46
11:K:36:ASP:N	11:K:36:ASP:OD1	2.48	0.46
11:K:67:ASP:OD1	11:K:71:LYS:HE3	2.15	0.46
12:L:67:ALA:CB	12:L:84:ILE:HD11	2.45	0.46
15:O:21:ASP:OD2	15:O:24:SER:HB2	2.15	0.46
16:P:4:ILE:HA	16:P:20:VAL:O	2.16	0.46
16:P:8:ARG:NH2	16:P:15:PRO:HG3	2.31	0.46
21:U:18:TYR:O	21:U:22:ARG:HB2	2.14	0.46
1:A:1064:G:OP2	1:A:1386:G:H4'	2.16	0.46
1:A:1118:C:H1'	1:A:1179:A:C4	2.51	0.46
1:A:450:G:N7	1:A:481:G:C6	2.84	0.46
2:B:211:ILE:O	2:B:215:LEU:HB2	2.16	0.46
5:E:101:ILE:HG12	5:E:101:ILE:O	2.15	0.46
5:E:11:ILE:CD1	5:E:33:VAL:HG23	2.46	0.46
8:H:123:GLU:O	8:H:126:LYS:HB3	2.15	0.46
1:A:1226:C:C4	13:M:104:ARG:HB2	2.51	0.46
13:M:109:THR:HG22	13:M:109:THR:O	2.16	0.46
14:N:24:CYS:O	14:N:28:GLY:HA2	2.15	0.46
15:O:18:PHE:O	15:O:21:ASP:HB2	2.14	0.46
15:O:56:LEU:O	15:O:60:VAL:HG23	2.16	0.46
1:A:1029:G:N1	1:A:1031(B):G:C6	2.83	0.46
4:D:21:LEU:HD12	4:D:21:LEU:H	1.81	0.46
5:E:59:GLY:O	5:E:63:ARG:HG3	2.16	0.46
17:Q:13:ASP:H	17:Q:14:LYS:HD2	1.80	0.46
1:A:1052:U:C2	1:A:1200:C:N4	2.84	0.46
1:A:1228:C:H4'	13:M:116:THR:O	2.16	0.46
1:A:1372:U:H2'	1:A:1373:G:O4'	2.16	0.46
1:A:1504:G:C4'	1:A:1505:G:OP2	2.64	0.46
1:A:432:A:N7	1:A:433:C:C4	2.84	0.46
1:A:693:G:C6	1:A:694:A:C6	3.04	0.46
1:A:87:A:H3'	1:A:88:C:O4'	2.16	0.46
1:A:950:U:H2'	1:A:951:G:C8	2.51	0.46
2:B:149:LEU:O	2:B:153:ARG:HG2	2.16	0.46
4:D:149:ALA:HB3	4:D:152:SER:OG	2.16	0.46
13:M:74:VAL:HA	13:M:77:ASN:HD22	1.81	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:N:45:ARG:O	14:N:49:HIS:HD2	1.99	0.46
15:O:21:ASP:CG	15:O:24:SER:HB2	2.36	0.46
1:A:375:U:H4'	16:P:17:TYR:CE2	2.51	0.46
19:S:41:VAL:CG1	19:S:42:PRO:HD2	2.46	0.46
1:A:323:U:O3'	20:T:22:ARG:HG2	2.16	0.46
1:A:1049:U:H4'	1:A:1050:G:C5'	2.46	0.46
1:A:1130:A:C2	1:A:1146:A:C5	3.03	0.46
1:A:1128:C:O2'	1:A:1130:A:C8	2.61	0.46
1:A:1129:C:H1'	1:A:1132:C:H5	1.81	0.46
1:A:1225:A:H5''	1:A:1226:C:C5	2.50	0.46
1:A:1381:U:H5	1:A:1382:C:C5	2.34	0.46
1:A:957:U:O2	1:A:959:A:H8	1.97	0.46
2:B:114:ARG:O	2:B:118:LEU:HG	2.15	0.46
5:E:11:ILE:HG21	5:E:105:VAL:HG22	1.98	0.46
8:H:19:VAL:HG23	8:H:19:VAL:O	2.16	0.46
1:A:718:G:H5'	11:K:117:ASN:ND2	2.31	0.46
15:O:56:LEU:C	15:O:56:LEU:HD23	2.37	0.46
19:S:25:LYS:HB3	19:S:27:GLU:CD	2.35	0.46
1:A:1194:U:H2'	1:A:1195:C:C6	2.51	0.45
1:A:1277:C:C2'	1:A:1278:U:H5'	2.46	0.45
1:A:927:G:N2	1:A:1391:U:H1'	2.32	0.45
1:A:321:A:C2	1:A:333:G:C2	3.04	0.45
1:A:560:U:H5'	1:A:566:G:N2	2.30	0.45
4:D:139:ARG:HG3	4:D:139:ARG:NH1	2.29	0.45
4:D:147:ALA:HB2	4:D:182:LYS:HG2	1.96	0.45
1:A:1349:A:H5''	9:I:121:ARG:HB2	1.97	0.45
13:M:91:ARG:HH21	13:M:97:PRO:HG2	1.81	0.45
1:A:1056:U:H2'	1:A:1056:U:O2	2.16	0.45
1:A:1256:A:H5'	1:A:1257:U:OP1	2.15	0.45
1:A:474:G:OP2	16:P:75:ARG:NH1	2.50	0.45
1:A:909:A:H2'	1:A:910:C:O4'	2.15	0.45
1:A:93:U:H2'	1:A:95:G:H8	1.81	0.45
2:B:86:GLU:C	2:B:88:ALA:H	2.20	0.45
4:D:56:VAL:HG12	4:D:202:LEU:HD11	1.97	0.45
1:A:972:C:OP2	10:J:57:LYS:HD3	2.16	0.45
1:A:1031(C):G:H2'	1:A:1033:G:O4'	2.17	0.45
1:A:1084:G:C5	1:A:1085:U:C4	3.04	0.45
1:A:1250:A:H4'	9:I:68:GLY:N	2.32	0.45
1:A:173:U:C6	1:A:197:A:C2	3.04	0.45
1:A:748:C:C1'	1:A:749:C:OP2	2.63	0.45
1:A:836:G:C6	1:A:851:G:C6	3.04	0.45
1:A:93:U:H2'	1:A:95:G:C8	2.52	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1112:C:O2	3:C:179:ARG:HG3	2.15	0.45
4:D:112:VAL:HG13	4:D:116:GLN:OE1	2.16	0.45
5:E:20:GLN:O	5:E:21:ALA:C	2.55	0.45
5:E:30:ALA:O	5:E:45:PHE:HA	2.17	0.45
6:F:10:LEU:HD13	6:F:61:LEU:CD1	2.41	0.45
6:F:12:PRO:HG3	6:F:57:GLN:O	2.16	0.45
15:O:7:GLU:O	15:O:11:VAL:HG23	2.15	0.45
18:R:51:LEU:CD2	18:R:52:PRO:HD2	2.46	0.45
22:W:17(A):U:H1'	22:W:18:G:P	2.57	0.45
1:A:105:G:C6	1:A:106:C:C4	3.05	0.45
1:A:991:U:O2'	1:A:993:G:C8	2.69	0.45
3:C:155:GLY:HA3	3:C:196:LEU:HD22	1.98	0.45
4:D:36:ARG:HD3	4:D:38:TYR:HE1	1.80	0.45
6:F:91:VAL:HG12	6:F:92:LYS:O	2.16	0.45
10:J:6:ILE:CG1	10:J:72:VAL:HB	2.46	0.45
12:L:40:ARG:CG	12:L:41:THR:N	2.80	0.45
20:T:81:LYS:O	20:T:85:MET:HG2	2.15	0.45
1:A:743:U:H2'	1:A:744:C:C6	2.50	0.45
1:A:830:G:H2'	1:A:831:U:O4'	2.17	0.45
5:E:76:ILE:HG13	5:E:77:PRO:CD	2.44	0.45
1:A:1298:C:C5	7:G:114:ARG:HD3	2.52	0.45
9:I:48:GLU:N	9:I:49:PRO:CD	2.78	0.45
9:I:114:TYR:CE1	10:J:60:ARG:O	2.70	0.45
13:M:23:TYR:CZ	13:M:71:ARG:HD3	2.51	0.45
13:M:81:LEU:HD11	13:M:88:ARG:NH2	2.32	0.45
17:Q:36:ILE:O	17:Q:36:ILE:HD12	2.16	0.45
20:T:72:LEU:C	20:T:72:LEU:HD13	2.37	0.45
1:A:1123:A:H4'	10:J:36:GLY:HA3	1.99	0.45
1:A:413:G:H21	1:A:428:G:H1'	1.81	0.45
1:A:5:U:O2'	1:A:6:G:O5'	2.34	0.45
2:B:84:GLU:HA	2:B:87:ARG:HB2	1.97	0.45
4:D:107:ARG:HH21	4:D:114:ARG:NH2	2.14	0.45
4:D:116:GLN:O	4:D:116:GLN:HG2	2.16	0.45
4:D:3:ARG:HD2	4:D:5:ILE:HG12	1.98	0.45
5:E:41:VAL:O	5:E:67:VAL:HG12	2.16	0.45
6:F:14:LEU:HD12	6:F:15:ASP:O	2.16	0.45
8:H:38:ILE:HD11	8:H:119:LEU:HA	1.98	0.45
14:N:14:PRO:HG2	14:N:15:LYS:H	1.82	0.45
16:P:20:VAL:CG2	16:P:32:TYR:HB2	2.47	0.45
18:R:55:ARG:HG3	18:R:55:ARG:HH11	1.81	0.45
20:T:8:ARG:C	20:T:10:LEU:H	2.19	0.45
1:A:1350:A:C6	1:A:1351:U:N3	2.85	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:175:SER:HB2	4:D:186:LEU:HD21	1.97	0.45
4:D:78:LEU:HB2	4:D:93:PHE:HE2	1.82	0.45
5:E:76:ILE:HG22	5:E:93:PRO:HB3	1.99	0.45
6:F:36:ARG:O	6:F:65:VAL:HG23	2.17	0.45
6:F:7:ASN:O	6:F:8:ILE:HD13	2.17	0.45
7:G:75:VAL:CG1	7:G:145:ALA:HA	2.46	0.45
10:J:40:LEU:HB2	10:J:69:ASN:CB	2.46	0.45
11:K:12:ARG:HB3	11:K:12:ARG:NH1	2.31	0.45
13:M:19:LEU:O	13:M:22:ILE:HG12	2.16	0.45
13:M:76:ALA:HA	13:M:79:LYS:HE3	1.97	0.45
17:Q:9:VAL:HG11	17:Q:84:LEU:HD12	1.97	0.45
1:A:1014:A:C2	19:S:34:TRP:CD1	3.05	0.45
19:S:62:ILE:HD12	19:S:66:MET:SD	2.57	0.45
22:V:18:G:C2	22:V:58:A:C5	3.04	0.45
1:A:1072:G:C5	1:A:1073:U:C4	3.04	0.45
1:A:174:C:H6	1:A:174:C:O5'	1.99	0.45
1:A:355:C:H5'	1:A:389:A:OP2	2.17	0.45
1:A:922:G:H2'	1:A:923:A:H8	1.80	0.45
5:E:12:LEU:C	5:E:12:LEU:HD22	2.37	0.45
6:F:101:ALA:HA	18:R:28:GLU:CD	2.36	0.45
1:A:1328:C:H5''	13:M:28:ALA:CB	2.46	0.45
13:M:54:VAL:HA	13:M:57:ARG:HB2	1.98	0.45
20:T:85:MET:HB2	20:T:104:LEU:HD21	1.98	0.45
1:A:1442:G:C8	1:A:1446:A:C2	3.04	0.45
1:A:292:G:N2	1:A:309:G:C4	2.84	0.45
1:A:722:A:O2'	1:A:723:U:C6	2.66	0.45
1:A:88:C:H2'	1:A:89:U:C1'	2.47	0.45
3:C:89:GLU:OE2	3:C:93:LYS:HD2	2.16	0.45
5:E:25:ARG:HD2	5:E:25:ARG:N	2.31	0.45
13:M:56:LEU:HA	13:M:59:TYR:HB3	1.99	0.45
20:T:90:GLN:HA	20:T:93:GLU:HB3	1.98	0.45
1:A:1244:C:H2'	1:A:1245:A:C8	2.52	0.45
1:A:1248:A:H2'	1:A:1249:C:H6	1.81	0.45
1:A:232:G:H1'	1:A:262:A:N1	2.32	0.45
1:A:328:C:H4'	1:A:329:A:O5'	2.17	0.45
1:A:520:A:N7	1:A:521:G:C8	2.85	0.45
1:A:950:U:H2'	1:A:951:G:H8	1.81	0.45
2:B:172:ILE:H	2:B:172:ILE:HG13	1.53	0.45
6:F:53:ALA:HB2	6:F:86:ARG:HD2	1.99	0.45
6:F:97:PHE:HB3	18:R:31:LEU:HD23	1.98	0.45
16:P:82:GLN:O	16:P:83:GLU:HB2	2.17	0.45
17:Q:100:LYS:N	17:Q:100:LYS:HD2	2.32	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1152:A:H4'	10:J:13:HIS:CD2	2.52	0.44
1:A:1222:G:H5''	19:S:78:ARG:HE	1.82	0.44
1:A:1386:G:H2'	1:A:1387:G:H8	1.81	0.44
3:C:116:VAL:O	3:C:119:ARG:HB3	2.17	0.44
4:D:124:GLY:C	4:D:126:ILE:H	2.21	0.44
6:F:37:VAL:HG12	6:F:38:GLU:N	2.33	0.44
8:H:112:LEU:HD22	8:H:133:LEU:HA	1.99	0.44
8:H:73:ASP:HB3	8:H:75:ARG:HG2	1.99	0.44
9:I:33:PHE:CE2	9:I:47:LEU:HB2	2.52	0.44
12:L:82:VAL:HG22	12:L:83:LEU:N	2.32	0.44
13:M:25:ILE:HD12	13:M:25:ILE:N	2.31	0.44
22:W:17:C:OP1	22:W:61:C:H5'	2.17	0.44
22:W:5:G:O2'	22:W:6:G:P	2.75	0.44
1:A:1154:G:H2'	1:A:1155:G:H8	1.81	0.44
1:A:216:G:C2	1:A:217:C:N3	2.86	0.44
1:A:920:U:H2'	1:A:921:U:C6	2.52	0.44
2:B:235:SER:O	2:B:239:VAL:HG23	2.16	0.44
3:C:45:LYS:HG3	3:C:46:GLU:HG3	1.98	0.44
3:C:83:ARG:O	3:C:87:LEU:HG	2.16	0.44
5:E:149:GLU:O	5:E:153:LYS:HB2	2.18	0.44
5:E:96:PRO:HA	5:E:117:ASP:OD2	2.17	0.44
9:I:114:TYR:N	9:I:114:TYR:HD2	2.16	0.44
1:A:1226:C:OP2	13:M:103:THR:HG21	2.17	0.44
14:N:15:LYS:HD2	14:N:16:PHE:CD2	2.52	0.44
17:Q:20:THR:HG21	17:Q:41:LYS:HD2	1.98	0.44
1:A:1320:C:C4	19:S:36:ARG:HG3	2.53	0.44
1:A:1511:G:H2'	1:A:1512:U:O4'	2.18	0.44
1:A:272:C:H2'	1:A:273:A:C8	2.52	0.44
1:A:600:C:O2'	1:A:601:C:H5'	2.18	0.44
1:A:646:U:H2'	1:A:647:C:H6	1.81	0.44
2:B:24:TRP:CZ3	2:B:29:ALA:HB2	2.42	0.44
4:D:145:GLU:OE1	4:D:184:LYS:HE2	2.17	0.44
4:D:175:SER:CB	4:D:186:LEU:HD21	2.47	0.44
4:D:63:LYS:HD2	4:D:198:VAL:HG12	1.98	0.44
9:I:30:GLY:O	9:I:31:GLN:O	2.35	0.44
9:I:99:LEU:HB3	9:I:101:PHE:CE1	2.51	0.44
19:S:63:THR:HG22	19:S:66:MET:HG2	1.98	0.44
22:V:51:C:H2'	22:V:52:G:C8	2.52	0.44
22:V:52:G:H2'	22:V:53:G:H8	1.82	0.44
1:A:149:A:H2'	1:A:150:C:H6	1.79	0.44
1:A:79:G:H1	1:A:90:C:N4	2.15	0.44
2:B:236:TYR:HA	2:B:239:VAL:CG2	2.47	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:121:VAL:O	4:D:134:ASP:HA	2.17	0.44
5:E:148:VAL:HG21	8:H:107:LEU:HD22	1.98	0.44
7:G:100:ALA:O	7:G:104:LEU:HD23	2.17	0.44
8:H:114:THR:CG2	8:H:119:LEU:HD21	2.48	0.44
14:N:6:LEU:HB3	14:N:23:ARG:HH22	1.83	0.44
20:T:36:LEU:HA	20:T:36:LEU:HD13	1.60	0.44
1:A:1225:A:H5'	13:M:103:THR:HB	2.00	0.44
1:A:1298:C:C4	7:G:114:ARG:HD3	2.52	0.44
1:A:137:C:H2'	1:A:138:G:H8	1.82	0.44
1:A:186(A):C:C5'	20:T:78:ALA:HB1	2.48	0.44
3:C:167:TRP:O	3:C:168:ALA:HB2	2.17	0.44
4:D:128:VAL:O	4:D:129:ASN:HB2	2.18	0.44
6:F:5:GLU:HB3	6:F:62:TRP:NE1	2.33	0.44
12:L:31:PHE:CE2	12:L:85:ARG:HG3	2.43	0.44
13:M:40:ASN:HB3	13:M:43:THR:CG2	2.42	0.44
16:P:55:ARG:HB3	16:P:55:ARG:NH1	2.33	0.44
22:V:40:C:O2'	22:V:41:C:H5'	2.18	0.44
22:W:58:A:O2'	22:W:60:U:C5	2.67	0.44
1:A:105:G:H2'	1:A:106:C:C6	2.53	0.44
1:A:1268:A:H4'	21:U:20:LYS:CB	2.47	0.44
1:A:176:C:H2'	1:A:177:C:C6	2.52	0.44
1:A:968:A:H4'	1:A:969:A:OP2	2.18	0.44
3:C:71:ALA:HA	3:C:106:VAL:HB	1.99	0.44
5:E:137:GLU:O	5:E:141:GLN:HG3	2.17	0.44
11:K:80:VAL:HG22	11:K:103:LEU:HD12	2.00	0.44
14:N:13:THR:N	14:N:14:PRO:HD3	2.32	0.44
13:M:118:ALA:HB3	22:V:29:G:H5'	1.99	0.44
1:A:1142:G:C2	1:A:1143:G:H1'	2.52	0.44
1:A:1320:C:H2'	1:A:1321:C:O4'	2.17	0.44
1:A:1309:G:C6	1:A:1329:A:C2	3.06	0.44
1:A:374:A:C6	1:A:375:U:C4	3.05	0.44
1:A:509:A:C6	1:A:510:A:N1	2.86	0.44
2:B:87:ARG:NH2	2:B:232:PRO:HA	2.33	0.44
4:D:58:LEU:O	4:D:61:LYS:HB3	2.18	0.44
7:G:44:TYR:HA	7:G:47:CYS:HB2	2.00	0.44
1:A:972:C:C4'	10:J:57:LYS:HG3	2.36	0.44
1:A:667:G:H4'	15:O:51:HIS:ND1	2.32	0.44
16:P:58:TYR:O	16:P:62:VAL:HG22	2.18	0.44
18:R:59:SER:H	18:R:62:GLU:CD	2.20	0.44
1:A:1053:G:N7	1:A:1200:C:H5'	2.32	0.44
1:A:1143:G:H2'	1:A:1144:G:C8	2.53	0.44
1:A:1321:C:H5	1:A:1322:C:O2'	2.00	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:39:G:N7	1:A:547:A:H8	2.16	0.44
1:A:602:A:C2	1:A:637:G:C2	3.06	0.44
7:G:113:GLU:CG	7:G:119:ARG:HG2	2.48	0.44
8:H:84:ARG:O	8:H:135:CYS:HB2	2.17	0.44
9:I:118:LYS:C	9:I:120:ARG:H	2.21	0.44
22:W:36:U:H2'	22:W:37:A:O4'	2.18	0.44
22:W:49:G:C2'	22:W:50:U:H5'	2.48	0.44
1:A:17:U:H2'	1:A:18:C:C6	2.53	0.44
1:A:356:A:H1'	1:A:368:U:O2'	2.18	0.44
1:A:39:G:O2'	1:A:40:C:H5'	2.18	0.44
1:A:464:G:C6	1:A:466:G:H5''	2.53	0.44
1:A:736:C:H2'	1:A:737:A:C8	2.53	0.44
1:A:926:G:H5''	1:A:927:G:O5'	2.17	0.44
7:G:146:GLU:C	7:G:148:ASN:H	2.21	0.44
8:H:111:ILE:O	8:H:112:LEU:HD23	2.18	0.44
1:A:1179:A:O2'	9:I:103:THR:HG23	2.18	0.44
1:A:1254:C:OP1	10:J:45:ARG:HD3	2.18	0.44
1:A:1011:G:C6	1:A:1012:U:C4	3.06	0.43
1:A:1070:U:OP1	5:E:25:ARG:NH1	2.50	0.43
1:A:1399:C:H4'	1:A:1400:C:O5'	2.18	0.43
1:A:977:A:O2'	1:A:981:U:N3	2.49	0.43
3:C:45:LYS:HG3	3:C:46:GLU:N	2.33	0.43
4:D:56:VAL:HG12	4:D:202:LEU:CD1	2.47	0.43
4:D:58:LEU:C	4:D:58:LEU:HD23	2.38	0.43
6:F:61:LEU:HD12	6:F:61:LEU:N	2.33	0.43
11:K:54:ARG:NH1	22:W:39:C:O3'	2.51	0.43
19:S:63:THR:HG22	19:S:66:MET:CE	2.48	0.43
1:A:1226:C:H2'	13:M:103:THR:CG2	2.44	0.43
1:A:6:G:H4'	1:A:298:A:H4'	1.99	0.43
1:A:860:A:H2'	1:A:861:G:O4'	2.18	0.43
2:B:193:ASP:OD1	2:B:196:LEU:HG	2.18	0.43
6:F:33:TYR:CE1	6:F:75:LEU:HA	2.53	0.43
6:F:48:LEU:H	6:F:48:LEU:CD2	2.30	0.43
6:F:7:ASN:OD1	6:F:7:ASN:N	2.51	0.43
8:H:17:THR:HG22	8:H:63:LEU:HD13	1.99	0.43
1:A:1226:C:N4	13:M:104:ARG:HD2	2.34	0.43
16:P:6:LEU:HB3	16:P:17:TYR:HB3	2.00	0.43
1:A:1251:A:H2'	1:A:1252:A:O4'	2.17	0.43
1:A:450:G:H4'	16:P:41:PRO:O	2.19	0.43
1:A:546:G:OP2	4:D:72:GLU:HB2	2.18	0.43
1:A:69:G:C2	1:A:73:G:N7	2.86	0.43
2:B:55:PHE:CE1	2:B:218:ALA:HA	2.42	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:142:PRO:HA	4:D:185:PHE:HD2	1.83	0.43
4:D:188:LEU:HG	4:D:189:PRO:HD2	1.99	0.43
14:N:53:LEU:HA	14:N:54:PRO:HD3	1.87	0.43
1:A:17:U:O2'	1:A:1079:G:H1'	2.18	0.43
1:A:1238:A:N3	1:A:1238:A:H2'	2.32	0.43
1:A:1299:A:N7	1:A:1301:U:N3	2.66	0.43
1:A:518:C:C2	1:A:529:G:C6	3.07	0.43
1:A:882:C:O2'	1:A:883:C:H5'	2.18	0.43
2:B:16:HIS:HA	2:B:210:SER:OG	2.19	0.43
4:D:188:LEU:O	4:D:189:PRO:O	2.36	0.43
9:I:33:PHE:CE2	9:I:47:LEU:HD22	2.53	0.43
9:I:99:LEU:HD12	9:I:101:PHE:HE1	1.83	0.43
12:L:24:PRO:C	12:L:26:LEU:N	2.72	0.43
20:T:47:GLY:O	20:T:49:ALA:N	2.50	0.43
1:A:491:G:H2'	1:A:492:G:H8	1.83	0.43
1:A:685:G:C2	1:A:686:U:C4	3.06	0.43
1:A:9:G:OP2	5:E:121:LYS:HE2	2.18	0.43
2:B:164:VAL:HB	2:B:186:ALA:HB2	2.00	0.43
2:B:36:ARG:H	2:B:41:ILE:HD13	1.83	0.43
3:C:161:GLU:OE1	3:C:161:GLU:HA	2.18	0.43
3:C:61:ALA:O	3:C:62:ASP:HB2	2.18	0.43
4:D:92:VAL:O	4:D:96:LEU:HD22	2.19	0.43
1:A:673:G:H4'	6:F:87:ARG:HH12	1.82	0.43
15:O:6:GLU:O	15:O:10:LYS:HG3	2.19	0.43
1:A:958:A:OP1	19:S:79:THR:HG21	2.18	0.43
20:T:40:ALA:HB2	20:T:55:ILE:CG2	2.47	0.43
1:A:1033:G:H2'	1:A:1034:G:H8	1.83	0.43
1:A:1108:G:N3	1:A:1108:G:H2'	2.34	0.43
1:A:1126:U:H2'	1:A:1127:G:O4'	2.19	0.43
1:A:1465:C:H2'	1:A:1466:C:O4'	2.18	0.43
1:A:200:G:N2	1:A:218:C:C2	2.86	0.43
1:A:544:G:H2'	1:A:545:C:H6	1.83	0.43
1:A:580:U:H2'	1:A:581:G:O4'	2.18	0.43
2:B:63:MET:HG3	2:B:225:ALA:HB1	2.01	0.43
3:C:129:ALA:HB3	3:C:132:ARG:HB3	2.00	0.43
7:G:115:ARG:HB2	7:G:118:VAL:HG13	2.00	0.43
8:H:111:ILE:H	8:H:111:ILE:HD13	1.83	0.43
10:J:54:PHE:CG	10:J:55:LYS:N	2.87	0.43
15:O:41:GLU:HA	15:O:44:LYS:HB2	2.00	0.43
19:S:16:LEU:O	19:S:19:VAL:HG12	2.19	0.43
22:W:1:C:C2	22:W:73:A:C2	3.06	0.43
1:A:1107:C:C4	1:A:1108:G:C8	3.06	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1116:C:H2'	1:A:1117:G:O4'	2.19	0.43
1:A:1286:A:H3'	1:A:1286:A:N3	2.34	0.43
1:A:1333:A:H2'	1:A:1334:G:O4'	2.19	0.43
3:C:77:ILE:HA	3:C:84:ILE:HB	2.01	0.43
4:D:30:LYS:HB2	4:D:33:MET:O	2.18	0.43
6:F:38:GLU:HB2	6:F:64:GLN:HG2	2.00	0.43
7:G:31:MET:HA	7:G:39:ALA:HB2	2.01	0.43
12:L:85:ARG:HB2	12:L:100:VAL:HG22	2.00	0.43
15:O:67:LEU:O	15:O:71:GLN:HB2	2.18	0.43
1:A:137:C:O4'	16:P:63:GLY:HA2	2.19	0.43
19:S:28:LYS:HB3	19:S:29:ARG:NH1	2.32	0.43
1:A:1043:C:H2'	1:A:1044:A:H8	1.84	0.43
1:A:504:C:C2	1:A:542:G:C2	3.06	0.43
1:A:76:G:C6	1:A:95:G:C6	3.07	0.43
1:A:783:C:H2'	1:A:784:C:C6	2.53	0.43
3:C:122:GLU:O	3:C:126:ARG:HG2	2.19	0.43
4:D:111:ALA:HA	4:D:161:ASN:ND2	2.32	0.43
5:E:47:LYS:N	5:E:47:LYS:HD3	2.34	0.43
6:F:5:GLU:HB3	6:F:62:TRP:HE1	1.83	0.43
11:K:32:ILE:HD11	11:K:41:THR:HB	2.00	0.43
1:A:520:A:OP2	12:L:50:ALA:HB1	2.18	0.43
1:A:523:A:N6	12:L:91:ASP:HB2	2.34	0.43
15:O:61:GLY:O	15:O:65:ARG:HD2	2.18	0.43
1:A:102:G:C6	1:A:103:C:C4	3.06	0.43
1:A:1031:G:C2'	1:A:1031(A):A:H5'	2.49	0.43
1:A:1270:C:H2'	1:A:1271:G:H8	1.84	0.43
1:A:1305:G:N2	1:A:1331:G:H1'	2.34	0.43
1:A:1454:G:H2'	1:A:1455:G:H8	1.84	0.43
1:A:1513:A:H2'	1:A:1514:C:H6	1.74	0.43
1:A:623:C:O5'	1:A:623:C:H6	2.02	0.43
1:A:673:G:H4'	6:F:87:ARG:NH1	2.33	0.43
1:A:984:C:H2'	1:A:985:C:H6	1.84	0.43
3:C:103:VAL:CG1	3:C:104:GLN:N	2.82	0.43
3:C:70:VAL:HG12	3:C:71:ALA:N	2.34	0.43
4:D:126:ILE:HG22	4:D:127:THR:N	2.33	0.43
1:A:1227:A:OP2	13:M:111:LYS:HE3	2.19	0.43
16:P:20:VAL:HG22	16:P:21:VAL:N	2.33	0.43
16:P:82:GLN:HG2	16:P:83:GLU:N	2.33	0.43
1:A:1438:G:C4	1:A:1439:C:C5	3.07	0.43
3:C:59:ARG:HA	3:C:63:ASN:O	2.19	0.43
4:D:43:HIS:O	4:D:45:GLN:N	2.49	0.43
5:E:76:ILE:HD12	5:E:76:ILE:HA	1.91	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:I:63:ILE:HG22	9:I:64:THR:N	2.34	0.43
12:L:69:ILE:HA	12:L:70:PRO:HD3	1.86	0.43
14:N:21:TYR:HD2	14:N:22:THR:O	2.01	0.43
16:P:20:VAL:HG21	16:P:32:TYR:HB2	2.01	0.43
1:A:1029:G:N1	1:A:1031(A):A:OP2	2.52	0.42
1:A:406:G:H5'	4:D:5:ILE:HD12	1.99	0.42
8:H:120:THR:OG1	8:H:123:GLU:HG3	2.19	0.42
18:R:45:SER:OG	18:R:46:GLU:N	2.52	0.42
19:S:63:THR:HG22	19:S:66:MET:HE2	2.01	0.42
1:A:1072:G:C6	1:A:1073:U:C4	3.07	0.42
1:A:1195:C:H5''	1:A:1196:U:P	2.59	0.42
1:A:1330:U:O4	1:A:1331:G:C6	2.72	0.42
1:A:1473:A:O2'	1:A:1474:G:H5'	2.19	0.42
1:A:266:G:H4'	1:A:267:C:C5	2.54	0.42
1:A:448:A:H2'	1:A:449:C:C6	2.54	0.42
1:A:978:A:C4	1:A:1319:A:C2	3.06	0.42
2:B:20:GLU:CD	2:B:23:ARG:HH12	2.22	0.42
3:C:12:LEU:HD12	3:C:18:TRP:CZ2	2.54	0.42
10:J:6:ILE:HD13	10:J:23:ILE:HG21	2.01	0.42
10:J:32:ALA:HB3	10:J:76:ASN:HB2	2.00	0.42
11:K:38:ASN:HA	11:K:39:PRO:HD3	1.77	0.42
1:A:1314:C:H41	19:S:4:SER:N	2.17	0.42
19:S:6:LYS:HD2	19:S:6:LYS:N	2.34	0.42
20:T:14:LYS:HA	20:T:17:ARG:HH21	1.84	0.42
20:T:53:LEU:O	20:T:57:ARG:HD3	2.19	0.42
1:A:174:C:H2'	1:A:175:C:H6	1.85	0.42
1:A:370:C:O2'	1:A:371:G:H5'	2.19	0.42
1:A:617:G:N1	1:A:618:C:C4	2.88	0.42
1:A:780:A:C2	1:A:803:G:N1	2.87	0.42
1:A:979:C:C5	1:A:980:C:C6	3.07	0.42
3:C:140:ARG:O	3:C:144:SER:HB2	2.19	0.42
3:C:153:VAL:HG22	3:C:157:ILE:HD11	2.01	0.42
8:H:64:LYS:HD2	8:H:79:VAL:HG11	2.01	0.42
10:J:35:SER:HB3	10:J:73:ASP:HB2	2.00	0.42
12:L:109:VAL:HG23	12:L:119:TYR:HB3	2.00	0.42
17:Q:48:GLU:HG3	17:Q:50:LYS:HG2	2.00	0.42
18:R:58:LEU:HA	18:R:62:GLU:OE1	2.20	0.42
1:A:1147:C:H6	1:A:1147:C:O5'	2.02	0.42
1:A:964:A:OP1	1:A:1199:U:OP1	2.37	0.42
1:A:442:C:O5'	1:A:442:C:H6	2.02	0.42
1:A:575:G:H4'	1:A:576:G:C5'	2.48	0.42
1:A:585:G:C6	1:A:586:C:C4	3.07	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:12:LEU:HB3	14:N:57:ARG:HG2	2.02	0.42
4:D:60:GLU:HG2	4:D:202:LEU:HB2	2.02	0.42
7:G:12:LEU:HD23	7:G:12:LEU:H	1.84	0.42
10:J:32:ALA:CB	10:J:76:ASN:HB2	2.49	0.42
18:R:44:LEU:HG	18:R:48:GLY:HA2	2.01	0.42
18:R:54:ARG:H	18:R:54:ARG:HD2	1.84	0.42
1:A:1266:G:C5	1:A:1268:A:OP2	2.73	0.42
1:A:429:U:C1'	1:A:430:A:H5''	2.50	0.42
1:A:60:A:H4'	1:A:61:G:O5'	2.19	0.42
1:A:968:A:OP1	1:A:968:A:H8	2.03	0.42
3:C:188:LEU:HD22	3:C:188:LEU:N	2.34	0.42
4:D:3:ARG:HD3	4:D:4:TYR:N	2.34	0.42
4:D:93:PHE:O	4:D:97:LEU:HG	2.19	0.42
9:I:10:ARG:HA	9:I:104:ARG:HH11	1.85	0.42
11:K:69:ALA:O	11:K:73:MET:HG2	2.19	0.42
13:M:54:VAL:HG22	13:M:57:ARG:HH21	1.85	0.42
20:T:38:LYS:HA	20:T:41:VAL:HG22	2.01	0.42
1:A:1105:A:O2'	1:A:1106:G:H5'	2.20	0.42
1:A:1154:G:O2'	1:A:1155:G:H5'	2.19	0.42
1:A:1158:C:O2	1:A:1158:C:H3'	2.19	0.42
1:A:1377:A:H2'	7:G:2:ALA:HB2	2.00	0.42
1:A:39:G:C2	1:A:40:C:C6	3.07	0.42
1:A:428:G:O4'	1:A:430:A:C8	2.73	0.42
1:A:937:A:H2	1:A:1377:A:HO2'	1.66	0.42
5:E:43:LEU:CD1	5:E:132:ALA:HB1	2.45	0.42
5:E:15:ARG:HD2	5:E:26:PHE:CD2	2.53	0.42
8:H:117:GLY:O	8:H:119:LEU:HD23	2.20	0.42
8:H:132:GLU:HG2	8:H:134:ILE:HD13	2.00	0.42
9:I:46:ALA:HB1	9:I:77:ILE:HB	2.01	0.42
10:J:98:ILE:H	10:J:98:ILE:HD12	1.85	0.42
10:J:98:ILE:HG22	10:J:99:LYS:N	2.35	0.42
12:L:27:LYS:HE2	12:L:32:ARG:HH12	1.84	0.42
19:S:10:PHE:CD1	19:S:10:PHE:N	2.88	0.42
1:A:1323:G:H4'	1:A:1361(B):C:C2	2.54	0.42
1:A:298:A:C6	1:A:299:G:C2	3.07	0.42
1:A:778:G:H2'	1:A:779:C:O4'	2.18	0.42
4:D:100:ARG:HG2	4:D:102:ASP:OD1	2.20	0.42
9:I:11:LYS:H	9:I:104:ARG:NH1	2.18	0.42
11:K:121:PRO:O	11:K:122:LYS:O	2.37	0.42
13:M:29:ARG:HD3	13:M:64:TRP:CH2	2.54	0.42
22:V:51:C:O2	22:V:64:G:C2	2.73	0.42
22:W:5:G:HO2'	22:W:6:G:P	2.42	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1151:A:O2'	1:A:1152:A:O5'	2.38	0.42
1:A:1255:G:C2	1:A:1283:G:C2	3.08	0.42
1:A:1286:A:H3'	1:A:1287:A:C5'	2.48	0.42
1:A:1347:G:C8	9:I:107:ARG:HB3	2.55	0.42
1:A:209:U:H4'	1:A:216:G:C2	2.55	0.42
1:A:564:C:C6	17:Q:31:LEU:HD11	2.55	0.42
1:A:599:C:H2'	1:A:600:C:H6	1.84	0.42
1:A:624:C:H2'	1:A:625:G:C8	2.50	0.42
1:A:632:A:C2'	1:A:633:G:H5'	2.50	0.42
5:E:53:LEU:O	5:E:57:LYS:HG3	2.20	0.42
7:G:75:VAL:O	7:G:75:VAL:HG23	2.20	0.42
9:I:114:TYR:C	9:I:116:LYS:H	2.22	0.42
1:A:706:A:O2'	11:K:29:ILE:HD11	2.19	0.42
20:T:64:ASP:HA	20:T:67:ALA:HB3	2.02	0.42
1:A:1234:C:O2'	1:A:1235:U:H5'	2.20	0.42
1:A:1292:U:H2'	1:A:1293:G:C8	2.54	0.42
1:A:69:G:H2'	1:A:73:G:H8	1.85	0.42
5:E:142:LEU:O	5:E:143:ARG:HD3	2.20	0.42
1:A:1117:G:O5'	9:I:104:ARG:NH2	2.53	0.42
9:I:88:TYR:HA	9:I:88:TYR:HD2	1.73	0.42
20:T:40:ALA:HB2	20:T:55:ILE:HG22	2.01	0.42
22:V:16:C:O2	22:V:60:U:H4'	2.20	0.42
1:A:1068:G:N2	1:A:1191:A:N3	2.64	0.42
1:A:624:C:O3'	16:P:10:GLY:HA2	2.20	0.42
1:A:710:G:OP1	6:F:54:LYS:HE3	2.20	0.42
1:A:88:C:C2'	1:A:89:U:O4'	2.64	0.42
2:B:154:LEU:HD22	2:B:155:LEU:H	1.85	0.42
3:C:11:ARG:O	3:C:14:ILE:O	2.37	0.42
3:C:95:THR:CG2	3:C:97:LYS:HG2	2.50	0.42
4:D:162:LEU:HA	4:D:162:LEU:HD22	1.75	0.42
4:D:13:ARG:NH2	4:D:40:PRO:HA	2.35	0.42
5:E:79:GLU:O	5:E:80:ILE:HG23	2.20	0.42
7:G:51:GLN:HG2	7:G:56:GLN:O	2.19	0.42
9:I:5:TYR:HA	9:I:17:VAL:O	2.20	0.42
10:J:67:THR:HG23	10:J:67:THR:O	2.20	0.42
12:L:6:ILE:CD1	12:L:7:ASN:H	2.33	0.42
14:N:26:ARG:HH12	14:N:47:LEU:HD21	1.84	0.42
18:R:53:ARG:C	18:R:55:ARG:H	2.23	0.42
22:V:59:A:C8	22:V:60:U:C5	3.08	0.42
1:A:1117:G:H4'	9:I:104:ARG:NH2	2.23	0.41
1:A:977:A:C8	1:A:1223:C:C4	3.05	0.41
1:A:1341:U:H6	1:A:1341:U:H3'	1.85	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:140:A:H2'	1:A:141:A:H8	1.85	0.41
1:A:255:G:H2'	1:A:256:U:C6	2.55	0.41
1:A:270:A:H2'	1:A:271:C:C6	2.55	0.41
1:A:406:G:H2'	1:A:407:G:C8	2.54	0.41
1:A:725:G:H2'	1:A:726:C:H6	1.85	0.41
1:A:976:G:N7	1:A:1358:U:C2	2.87	0.41
1:A:994:A:N3	1:A:994:A:H2'	2.35	0.41
2:B:113:HIS:O	2:B:117:GLU:HG3	2.20	0.41
2:B:32:ILE:HG21	2:B:40:HIS:HD2	1.85	0.41
3:C:11:ARG:HH11	3:C:11:ARG:HG2	1.85	0.41
3:C:34:LEU:HD23	3:C:34:LEU:O	2.20	0.41
8:H:103:VAL:HG12	8:H:108:GLY:HA3	2.02	0.41
9:I:16:ARG:HB2	9:I:64:THR:CG2	2.45	0.41
17:Q:14:LYS:CD	17:Q:14:LYS:H	2.30	0.41
17:Q:50:LYS:HG3	17:Q:51:TYR:CD1	2.55	0.41
20:T:61:SER:O	20:T:65:LYS:HG2	2.19	0.41
1:A:1104:G:C6	1:A:1105:A:C5	3.08	0.41
1:A:1281:U:H5'	1:A:1282:C:H5	1.79	0.41
1:A:191(E):G:H2'	1:A:191(F):U:C6	2.55	0.41
1:A:421:U:O2	1:A:421:U:H5'	2.20	0.41
1:A:625:G:H2'	1:A:626:U:H6	1.85	0.41
3:C:101:LEU:HD23	3:C:102:ASN:N	2.35	0.41
3:C:14:ILE:O	3:C:16:ARG:N	2.52	0.41
6:F:62:TRP:CG	18:R:35:ARG:NH1	2.89	0.41
1:A:673:G:C5'	6:F:87:ARG:HH12	2.33	0.41
6:F:5:GLU:HG3	6:F:93:SER:OG	2.20	0.41
1:A:1372:U:OP1	9:I:72:GLY:N	2.52	0.41
1:A:1123:A:O3'	10:J:36:GLY:HA3	2.20	0.41
1:A:1260:C:H4'	1:A:1284:C:H5'	2.01	0.41
1:A:1353:G:H2'	1:A:1354:C:C6	2.55	0.41
2:B:88:ALA:CB	2:B:222:ILE:HD11	2.50	0.41
7:G:115:ARG:HD3	7:G:115:ARG:HA	1.86	0.41
7:G:26:PHE:O	7:G:30:ILE:HG12	2.21	0.41
1:A:1351:U:O4'	7:G:33:ASP:HB3	2.20	0.41
8:H:13:ILE:O	8:H:17:THR:HG23	2.20	0.41
9:I:97:LYS:HA	9:I:102:LEU:HD13	2.01	0.41
12:L:68:TYR:HB3	12:L:98:HIS:HD2	1.80	0.41
13:M:74:VAL:O	13:M:78:ILE:HD13	2.21	0.41
15:O:76:GLU:HA	15:O:76:GLU:OE2	2.21	0.41
17:Q:59:ILE:HD13	17:Q:71:PHE:CD1	2.55	0.41
19:S:22:LEU:HA	19:S:27:GLU:OE1	2.20	0.41
20:T:61:SER:OG	20:T:62:LEU:N	2.53	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
22:W:17(A):U:H1'	22:W:18:G:O5'	2.21	0.41
1:A:1151:A:C2	1:A:1152:A:C5	3.08	0.41
1:A:1277:C:H2'	1:A:1278:U:H5'	2.01	0.41
1:A:1312:G:H2'	1:A:1313:U:H6	1.85	0.41
1:A:1378:C:C5	1:A:1379:G:N9	2.88	0.41
1:A:678:U:H2'	1:A:679:C:H6	1.83	0.41
1:A:958:A:C6	1:A:959:A:C6	3.08	0.41
2:B:15:VAL:C	2:B:16:HIS:CG	2.93	0.41
2:B:90:MET:HA	2:B:91:PRO:HD3	1.93	0.41
3:C:16:ARG:HB2	3:C:16:ARG:HH11	1.86	0.41
1:A:1057:G:O3'	3:C:197:GLY:HA3	2.20	0.41
4:D:102:ASP:HB3	4:D:136:PRO:HB3	2.02	0.41
13:M:68:GLY:O	13:M:72:ALA:N	2.53	0.41
16:P:81:ARG:HG2	16:P:83:GLU:OE1	2.20	0.41
17:Q:22:LEU:HD11	17:Q:39:SER:HB2	2.01	0.41
17:Q:23:VAL:O	17:Q:23:VAL:HG23	2.20	0.41
19:S:16:LEU:HA	19:S:19:VAL:HG12	2.02	0.41
22:V:72:A:C6	22:V:73:A:C6	3.08	0.41
1:A:1143:G:H2'	1:A:1144:G:H8	1.86	0.41
1:A:1211:U:H1'	1:A:1213:A:C2	2.55	0.41
1:A:1227:A:H2	1:A:1228:C:C1'	2.30	0.41
1:A:1381:U:C5	1:A:1382:C:C5	3.08	0.41
1:A:145:G:H2'	1:A:146:G:C8	2.54	0.41
1:A:599:C:H2'	1:A:600:C:C6	2.55	0.41
1:A:795:C:O5'	1:A:795:C:H6	2.04	0.41
3:C:173:VAL:HG12	3:C:173:VAL:O	2.20	0.41
4:D:11:LEU:O	4:D:12:CYS:C	2.58	0.41
4:D:198:VAL:O	4:D:198:VAL:HG23	2.21	0.41
4:D:63:LYS:O	4:D:67:ILE:HG13	2.21	0.41
6:F:35:ALA:CB	6:F:65:VAL:HG21	2.40	0.41
11:K:87:THR:HG22	11:K:87:THR:O	2.21	0.41
11:K:99:GLN:HB3	11:K:105:VAL:CG2	2.48	0.41
13:M:8:GLU:HG3	13:M:67:GLU:OE1	2.20	0.41
18:R:26:LEU:CD1	18:R:39:VAL:HG13	2.51	0.41
19:S:11:VAL:O	19:S:12:ASP:C	2.59	0.41
20:T:58:LYS:O	20:T:62:LEU:HB2	2.20	0.41
22:W:17(A):U:C1'	22:W:18:G:P	3.09	0.41
1:A:1305:G:C5'	21:U:4:GLY:HA3	2.50	0.41
1:A:130:A:C8	17:Q:63:ARG:HG3	2.56	0.41
1:A:1320:C:N4	19:S:36:ARG:HG3	2.36	0.41
1:A:570:G:H1'	1:A:820:U:C4	2.55	0.41
2:B:42:ILE:HD13	2:B:203:GLY:HA2	2.03	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:102:ALA:HB2	5:E:120:THR:OG1	2.20	0.41
8:H:40:ALA:CB	8:H:45:ILE:HG13	2.49	0.41
9:I:30:GLY:C	9:I:31:GLN:HG2	2.41	0.41
13:M:2:ALA:HB1	13:M:57:ARG:HH12	1.84	0.41
15:O:48:LYS:HA	15:O:48:LYS:HE2	2.03	0.41
19:S:40:ILE:HD13	19:S:62:ILE:CD1	2.51	0.41
1:A:1221:G:H4'	19:S:77:THR:CG2	2.50	0.41
22:V:69:C:H2'	22:V:70:G:C8	2.55	0.41
1:A:1053:G:C6	1:A:1199:U:C2	3.08	0.41
1:A:1369:C:H2'	1:A:1370:G:C8	2.56	0.41
1:A:251:G:N1	1:A:266:G:C6	2.89	0.41
1:A:322:C:H5	1:A:328:C:H5	1.68	0.41
9:I:28:VAL:CG2	9:I:63:ILE:HB	2.31	0.41
10:J:30:SER:HB2	10:J:80:LYS:CG	2.49	0.41
10:J:48:THR:HG22	10:J:62:HIS:HB3	2.02	0.41
10:J:58:ASP:C	10:J:60:ARG:N	2.74	0.41
13:M:31:LYS:O	13:M:35:GLU:HG3	2.20	0.41
13:M:70:LEU:O	13:M:74:VAL:HG23	2.20	0.41
16:P:82:GLN:HB3	16:P:82:GLN:HE21	1.72	0.41
1:A:1050:G:N2	1:A:1209:C:H1'	2.35	0.41
1:A:1144:G:N2	1:A:1146:A:H62	2.16	0.41
1:A:1193:G:N2	1:A:1194:U:C2	2.89	0.41
1:A:1361:G:C2'	1:A:1361(A):C:H5'	2.51	0.41
1:A:1438:G:C5	1:A:1439:C:C5	3.08	0.41
1:A:1484:C:H2'	1:A:1485:U:O4'	2.21	0.41
1:A:219:C:H2'	1:A:220:G:O4'	2.20	0.41
1:A:540:G:H2'	1:A:541:G:O4'	2.20	0.41
1:A:622:A:C8	1:A:623:C:C5	3.09	0.41
1:A:857:C:H2'	1:A:858:G:O4'	2.21	0.41
1:A:878:G:C1'	8:H:3:THR:HG21	2.51	0.41
1:A:89:U:O5'	1:A:89:U:H6	2.02	0.41
9:I:5:TYR:C	9:I:84:ALA:HA	2.40	0.41
1:A:529:G:O6	12:L:48:ASN:ND2	2.54	0.41
13:M:67:GLU:HA	13:M:67:GLU:OE2	2.20	0.41
14:N:26:ARG:NH1	14:N:47:LEU:HD21	2.36	0.41
18:R:40:LEU:HD22	18:R:70:ILE:CD1	2.51	0.41
6:F:7:ASN:ND2	18:R:76:LEU:HD11	2.36	0.41
1:A:1115:C:H1'	14:N:61:TRP:OXT	2.21	0.41
1:A:1179:A:H2'	1:A:1180:A:O4'	2.20	0.41
1:A:1206:G:H4'	3:C:192:THR:O	2.21	0.41
1:A:1262:C:C6	21:U:25:LYS:HE2	2.56	0.41
1:A:1298:C:H4'	1:A:1299:A:O4'	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1503:A:O2'	1:A:1504:G:C5'	2.69	0.41
1:A:542:G:H2'	1:A:543:C:C6	2.56	0.41
1:A:673:G:C5'	6:F:87:ARG:NH1	2.84	0.41
1:A:828:A:H2'	1:A:829:G:O4'	2.21	0.41
1:A:939:G:H2'	1:A:940:C:H6	1.86	0.41
2:B:61:LEU:HD11	2:B:68:ILE:HG13	2.03	0.41
2:B:90:MET:CE	2:B:90:MET:HA	2.51	0.41
7:G:79:ARG:HA	7:G:84:ASN:HA	2.03	0.41
10:J:20:ALA:O	10:J:24:VAL:HG23	2.21	0.41
10:J:51:ARG:HG3	14:N:45:ARG:CZ	2.50	0.41
11:K:13:GLN:O	11:K:14:VAL:HG13	2.20	0.41
19:S:78:ARG:HB2	19:S:81:ARG:HG2	2.02	0.41
21:U:2:GLY:C	21:U:4:GLY:H	2.24	0.41
1:A:1293:G:H2'	1:A:1294:G:C8	2.56	0.41
1:A:1353:G:OP1	21:U:10:ARG:NH2	2.54	0.41
1:A:826:C:H5'	8:H:12:ARG:NH2	2.30	0.41
2:B:231:GLU:HA	2:B:232:PRO:HD3	1.97	0.41
3:C:23:TYR:CG	3:C:24:ALA:N	2.88	0.41
3:C:37:GLN:HE22	14:N:52:GLN:HE21	1.67	0.41
4:D:135:LEU:HD22	4:D:135:LEU:N	2.35	0.41
5:E:18:ARG:O	5:E:18:ARG:HG3	2.21	0.41
11:K:108:ILE:O	18:R:87:ARG:HA	2.21	0.41
11:K:88:GLY:O	11:K:90:GLY:N	2.54	0.41
14:N:15:LYS:HD2	14:N:16:PHE:H	1.86	0.41
14:N:32:SER:OG	14:N:41:ARG:HB3	2.21	0.41
18:R:31:LEU:HD23	18:R:31:LEU:H	1.86	0.41
22:W:17(A):U:O2'	22:W:18:G:O5'	2.39	0.41
22:W:49:G:H2'	22:W:50:U:H5'	2.03	0.41
22:W:6:G:O2'	22:W:7:G:H5'	2.21	0.41
1:A:1026:G:H1	1:A:1036:G:N2	2.18	0.41
1:A:162:A:C5	1:A:163:C:H1'	2.56	0.41
2:B:52:GLU:HG2	2:B:56:ARG:HE	1.86	0.41
4:D:29:PRO:C	4:D:30:LYS:HE3	2.42	0.41
6:F:15:ASP:OD2	6:F:18:GLN:HB2	2.20	0.41
11:K:96:ARG:HA	11:K:96:ARG:HD3	1.81	0.41
12:L:84:ILE:HA	12:L:84:ILE:HD12	1.93	0.41
15:O:26:GLU:HG2	15:O:26:GLU:H	1.58	0.41
1:A:1029:G:N2	1:A:1031(A):A:C8	2.89	0.40
1:A:1316:G:N1	1:A:1319:A:OP2	2.53	0.40
1:A:579:G:C6	1:A:580:U:C4	3.10	0.40
2:B:130:ARG:HA	2:B:131:PRO:HD2	1.97	0.40
2:B:178:ARG:HB2	2:B:178:ARG:HH11	1.86	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:97:TRP:CZ2	2:B:101:MET:HB2	2.55	0.40
3:C:165:THR:O	3:C:165:THR:HG23	2.21	0.40
3:C:18:TRP:C	3:C:20:SER:N	2.74	0.40
3:C:36:ASP:HB3	3:C:40:ARG:HH12	1.85	0.40
4:D:206:PHE:CD2	4:D:207:TYR:CD2	3.08	0.40
7:G:107:ALA:O	7:G:110:GLN:HB2	2.21	0.40
9:I:111:ARG:NH1	9:I:113:LYS:HA	2.34	0.40
9:I:92:TYR:HA	9:I:95:LYS:HD2	2.03	0.40
13:M:34:LEU:HD22	13:M:39:ILE:HB	2.03	0.40
13:M:84:ILE:HD11	19:S:66:MET:SD	2.61	0.40
1:A:1004:A:C1'	1:A:1036:G:H22	2.31	0.40
1:A:888:G:H4'	1:A:1488:G:O2'	2.20	0.40
1:A:1493:A:O2'	1:A:1494:G:H5'	2.21	0.40
1:A:694:A:P	11:K:53:SER:HG	2.45	0.40
1:A:990:C:H2'	1:A:991:U:O4'	2.21	0.40
2:B:102:LEU:HB3	2:B:180:LEU:HD12	2.03	0.40
2:B:151:GLY:O	2:B:154:LEU:HD21	2.21	0.40
3:C:109:PRO:HB3	3:C:115:LEU:HD23	2.02	0.40
8:H:127:LEU:H	8:H:127:LEU:HD22	1.85	0.40
9:I:28:VAL:HG13	9:I:63:ILE:C	2.42	0.40
9:I:83:ARG:HA	9:I:86:VAL:CG1	2.49	0.40
12:L:69:ILE:N	12:L:69:ILE:HD12	2.36	0.40
14:N:12:ARG:HG2	14:N:14:PRO:HG3	2.04	0.40
17:Q:34:LYS:O	17:Q:36:ILE:HG23	2.21	0.40
1:A:1234:C:C4'	1:A:1364:U:H1'	2.51	0.40
1:A:247:G:C2	1:A:248:C:C6	3.08	0.40
1:A:315:A:C2	1:A:330:C:C2	3.10	0.40
1:A:392:G:C4	1:A:393:A:C8	3.09	0.40
1:A:475:G:H2'	1:A:476:G:C8	2.56	0.40
2:B:127:ILE:HG22	2:B:127:ILE:O	2.21	0.40
2:B:164:VAL:HB	2:B:186:ALA:CB	2.50	0.40
3:C:23:TYR:CD2	3:C:24:ALA:N	2.90	0.40
4:D:28:SER:CB	4:D:29:PRO:CD	3.00	0.40
4:D:79:PHE:CZ	4:D:204:ILE:HD13	2.57	0.40
18:R:51:LEU:CD2	18:R:55:ARG:HH21	2.28	0.40
19:S:16:LEU:HA	19:S:16:LEU:HD12	1.96	0.40
22:V:29:G:C4	22:V:30:G:C8	3.09	0.40
22:W:1:C:N3	22:W:72:A:N1	2.69	0.40
22:W:30:G:H2'	22:W:31:G:H8	1.86	0.40
1:A:109:A:N6	1:A:326:G:C6	2.90	0.40
1:A:1262:C:OP2	21:U:25:LYS:NZ	2.41	0.40
1:A:1288:A:C6	1:A:1289:A:C6	3.10	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1291:G:C6	1:A:1292:U:C4	3.10	0.40
1:A:1379:G:C6	1:A:1380:U:O4	2.74	0.40
1:A:186(D):G:C6	1:A:186(E):C:C4	3.10	0.40
1:A:452:A:O2'	1:A:453:A:H8	2.03	0.40
1:A:691:G:O6	11:K:52:GLY:HA2	2.21	0.40
1:A:767:A:H2'	1:A:768:A:O4'	2.21	0.40
1:A:971:G:H1'	1:A:1365:G:O2'	2.21	0.40
3:C:52:LEU:HD21	3:C:55:VAL:HB	2.02	0.40
3:C:6:HIS:HD2	3:C:7:PRO:HD2	1.86	0.40
5:E:110:LEU:O	5:E:113:ALA:HB3	2.21	0.40
1:A:1071:C:H5''	5:E:49:PRO:HG2	2.03	0.40
7:G:69:VAL:O	7:G:69:VAL:HG12	2.21	0.40
14:N:23:ARG:HD3	14:N:29:ARG:O	2.21	0.40
17:Q:78:GLU:HG3	17:Q:78:GLU:O	2.21	0.40
18:R:22:VAL:HG23	18:R:55:ARG:O	2.20	0.40
22:W:17(A):U:C1'	22:W:18:G:OP1	2.70	0.40
1:A:1031:G:C8	1:A:1031:G:H3'	2.57	0.40
1:A:1215:G:H2'	1:A:1216:G:H5'	2.02	0.40
1:A:354:G:H2'	1:A:354:G:N3	2.36	0.40
1:A:409:G:H1	1:A:433:C:H42	1.69	0.40
1:A:545:C:H5'	4:D:72:GLU:CG	2.30	0.40
1:A:698:G:C6	1:A:699:C:C4	3.09	0.40
1:A:81:G:C5'	1:A:82:U:OP2	2.69	0.40
2:B:144:ARG:HG3	2:B:145:LEU:N	2.36	0.40
2:B:19:HIS:HE2	2:B:206:ASP:HB2	1.87	0.40
2:B:81:VAL:HG12	2:B:92:TYR:HD1	1.86	0.40
3:C:72:LYS:HG2	3:C:74:GLY:H	1.87	0.40
7:G:5:ARG:HB3	7:G:6:ARG:H	1.50	0.40
8:H:120:THR:HG23	8:H:123:GLU:OE1	2.22	0.40
11:K:19:ALA:HB2	11:K:32:ILE:HG22	2.04	0.40
1:A:750:G:N3	15:O:23:GLY:HA3	2.36	0.40
22:V:48:C:C4	22:V:59:A:C8	3.09	0.40
22:W:10:G:C6	22:W:26:G:C2	3.10	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	232/234 (99%)	183 (79%)	36 (16%)	13 (6%)	3	30
3	C	204/206 (99%)	159 (78%)	28 (14%)	17 (8%)	1	18
4	D	206/208 (99%)	161 (78%)	34 (16%)	11 (5%)	3	32
5	E	149/151 (99%)	120 (80%)	26 (17%)	3 (2%)	11	62
6	F	99/101 (98%)	88 (89%)	10 (10%)	1 (1%)	22	78
7	G	153/155 (99%)	131 (86%)	17 (11%)	5 (3%)	6	50
8	H	136/138 (99%)	114 (84%)	20 (15%)	2 (2%)	15	68
9	I	125/127 (98%)	92 (74%)	25 (20%)	8 (6%)	2	26
10	J	96/98 (98%)	80 (83%)	11 (12%)	5 (5%)	3	32
11	K	112/114 (98%)	93 (83%)	15 (13%)	4 (4%)	5	47
12	L	120/122 (98%)	94 (78%)	22 (18%)	4 (3%)	6	50
13	M	115/117 (98%)	97 (84%)	15 (13%)	3 (3%)	8	56
14	N	58/60 (97%)	47 (81%)	8 (14%)	3 (5%)	3	32
15	O	86/88 (98%)	75 (87%)	9 (10%)	2 (2%)	10	59
16	P	81/83 (98%)	65 (80%)	13 (16%)	3 (4%)	5	46
17	Q	97/99 (98%)	82 (84%)	12 (12%)	3 (3%)	7	52
18	R	68/70 (97%)	55 (81%)	8 (12%)	5 (7%)	2	22
19	S	76/78 (97%)	57 (75%)	12 (16%)	7 (9%)	1	15
20	T	97/99 (98%)	75 (77%)	16 (16%)	6 (6%)	2	27
21	U	22/24 (92%)	16 (73%)	5 (23%)	1 (4%)	4	38
All	All	2332/2372 (98%)	1884 (81%)	342 (15%)	106 (4%)	4	38

All (106) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	15	VAL
3	C	14	ILE
3	C	79	ARG
3	C	100	ALA
4	D	28	SER
4	D	189	PRO
6	F	49	ALA
7	G	5	ARG

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Mol	Chain	Res	Type
10	J	91	PRO
11	K	122	LYS
14	N	14	PRO
17	Q	99	SER
19	S	11	VAL
19	S	28	LYS
19	S	80	TYR
20	T	71	THR
2	B	9	GLU
2	B	24	TRP
2	B	96	ARG
3	C	15	THR
3	C	60	ALA
3	C	181	ASN
3	C	195	VAL
4	D	5	ILE
4	D	88	VAL
4	D	171	GLY
4	D	179	GLU
8	H	2	LEU
8	H	103	VAL
9	I	31	GLN
10	J	56	HIS
10	J	92	THR
11	K	89	ALA
12	L	50	ALA
13	M	101	GLN
13	M	117	VAL
16	P	28	ARG
17	Q	80	GLY
18	R	87	ARG
19	S	27	GLU
20	T	48	LYS
21	U	24	ARG
2	B	129	GLU
3	C	27	LYS
3	C	61	ALA
3	C	81	GLY
3	C	196	LEU
4	D	4	TYR
4	D	30	LYS
4	D	33	MET

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Mol	Chain	Res	Type
7	G	7	ALA
9	I	10	ARG
9	I	24	GLY
9	I	103	THR
12	L	18	ARG
14	N	60	SER
15	O	23	GLY
16	P	11	SER
17	Q	48	GLU
18	R	45	SER
20	T	98	PRO
2	B	88	ALA
2	B	130	ARG
3	C	26	LYS
3	C	30	ARG
4	D	40	PRO
7	G	6	ARG
9	I	58	ARG
10	J	55	LYS
15	O	88	ARG
18	R	55	ARG
19	S	8	GLY
20	T	9	ASN
20	T	82	SER
2	B	78	GLN
2	B	230	VAL
3	C	45	LYS
4	D	125	HIS
5	E	49	PRO
7	G	131	LYS
9	I	55	ALA
12	L	5	THR
12	L	45	LYS
13	M	103	THR
16	P	29	ASP
18	R	20	ALA
18	R	54	ARG
19	S	29	ARG
2	B	18	GLY
3	C	189	ALA
5	E	85	GLY
9	I	100	GLY

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Mol	Chain	Res	Type
10	J	32	ALA
11	K	90	GLY
14	N	16	PHE
20	T	97	ALA
2	B	26	PRO
11	K	118	GLY
19	S	67	VAL
2	B	72	GLY
2	B	229	VAL
3	C	74	GLY
3	C	174	PRO
7	G	17	VAL
9	I	89	ASN
5	E	118	ILE

5.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	202/202 (100%)	184 (91%)	18 (9%)	14	55
3	C	160/160 (100%)	144 (90%)	16 (10%)	11	47
4	D	180/180 (100%)	156 (87%)	24 (13%)	6	30
5	E	116/116 (100%)	103 (89%)	13 (11%)	9	39
6	F	90/90 (100%)	78 (87%)	12 (13%)	6	30
7	G	126/126 (100%)	120 (95%)	6 (5%)	35	80
8	H	119/119 (100%)	105 (88%)	14 (12%)	8	36
9	I	98/98 (100%)	87 (89%)	11 (11%)	9	39
10	J	88/88 (100%)	79 (90%)	9 (10%)	11	46
11	K	86/86 (100%)	77 (90%)	9 (10%)	10	44
12	L	103/103 (100%)	93 (90%)	10 (10%)	12	49
13	M	94/94 (100%)	83 (88%)	11 (12%)	8	37
14	N	49/49 (100%)	46 (94%)	3 (6%)	26	73
15	O	79/79 (100%)	69 (87%)	10 (13%)	6	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	P	72/72 (100%)	65 (90%)	7 (10%)	12	49
17	Q	94/94 (100%)	90 (96%)	4 (4%)	40	83
18	R	61/61 (100%)	56 (92%)	5 (8%)	17	60
19	S	69/69 (100%)	61 (88%)	8 (12%)	8	37
20	T	76/76 (100%)	68 (90%)	8 (10%)	10	44
21	U	19/19 (100%)	19 (100%)	0	100	100
All	All	1981/1981 (100%)	1783 (90%)	198 (10%)	11	47

All (198) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	15	VAL
2	B	44	LEU
2	B	61	LEU
2	B	69	LEU
2	B	87	ARG
2	B	96	ARG
2	B	97	TRP
2	B	101	MET
2	B	119	GLU
2	B	140	HIS
2	B	145	LEU
2	B	153	ARG
2	B	154	LEU
2	B	172	ILE
2	B	178	ARG
2	B	185	ILE
2	B	187	LEU
2	B	196	LEU
3	C	5	ILE
3	C	16	ARG
3	C	69	HIS
3	C	76	VAL
3	C	85	ARG
3	C	89	GLU
3	C	97	LYS
3	C	107	GLN
3	C	131	ARG
3	C	140	ARG
3	C	153	VAL

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Mol	Chain	Res	Type
3	C	167	TRP
3	C	175	LEU
3	C	191	THR
3	C	195	VAL
3	C	196	LEU
4	D	3	ARG
4	D	15	GLU
4	D	21	LEU
4	D	30	LYS
4	D	38	TYR
4	D	49	ARG
4	D	59	ARG
4	D	62	GLN
4	D	72	GLU
4	D	96	LEU
4	D	108	LEU
4	D	110	PHE
4	D	119	GLN
4	D	122	ARG
4	D	131	ARG
4	D	135	LEU
4	D	138	TYR
4	D	144	ASP
4	D	156	GLU
4	D	159	ARG
4	D	162	LEU
4	D	166	LYS
4	D	191	ARG
4	D	202	LEU
5	E	12	LEU
5	E	20	GLN
5	E	25	ARG
5	E	31	LEU
5	E	41	VAL
5	E	72	GLN
5	E	78	HIS
5	E	79	GLU
5	E	101	ILE
5	E	119	LEU
5	E	121	LYS
5	E	123	LEU
5	E	147	ASP

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Mol	Chain	Res	Type
6	F	7	ASN
6	F	14	LEU
6	F	21	LEU
6	F	40	VAL
6	F	46	ARG
6	F	48	LEU
6	F	52	ILE
6	F	65	VAL
6	F	69	GLU
6	F	79	LEU
6	F	83	ASP
6	F	94	GLN
7	G	5	ARG
7	G	30	ILE
7	G	90	GLU
7	G	124	LEU
7	G	140	ASP
7	G	156	TRP
8	H	1	MET
8	H	18	ARG
8	H	50	ARG
8	H	52	ASP
8	H	73	ASP
8	H	81	HIS
8	H	91	ARG
8	H	99	GLU
8	H	111	ILE
8	H	119	LEU
8	H	127	LEU
8	H	133	LEU
8	H	136	GLU
8	H	137	VAL
9	I	10	ARG
9	I	31	GLN
9	I	33	PHE
9	I	70	LYS
9	I	88	TYR
9	I	95	LYS
9	I	99	LEU
9	I	114	TYR
9	I	117	HIS
9	I	121	ARG

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Mol	Chain	Res	Type
9	I	125	TYR
10	J	13	HIS
10	J	22	LYS
10	J	55	LYS
10	J	57	LYS
10	J	58	ASP
10	J	62	HIS
10	J	63	PHE
10	J	78	ASN
10	J	92	THR
11	K	25	TYR
11	K	30	VAL
11	K	36	ASP
11	K	54	ARG
11	K	81	ASP
11	K	91	ARG
11	K	92	GLU
11	K	103	LEU
11	K	116	HIS
12	L	5	THR
12	L	6	ILE
12	L	19	LYS
12	L	22	LYS
12	L	26	LEU
12	L	41	THR
12	L	51	LEU
12	L	54	VAL
12	L	91	ASP
12	L	98	HIS
13	M	9	ILE
13	M	50	GLU
13	M	64	TRP
13	M	65	LYS
13	M	66	LEU
13	M	87	TYR
13	M	93	ARG
13	M	103	THR
13	M	105	THR
13	M	108	ARG
13	M	115	LYS
14	N	31	ARG
14	N	33	VAL

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Mol	Chain	Res	Type
14	N	50	LYS
15	O	4	THR
15	O	5	LYS
15	O	17	ARG
15	O	26	GLU
15	O	31	LEU
15	O	41	GLU
15	O	45	VAL
15	O	65	ARG
15	O	68	ARG
15	O	87	ILE
16	P	2	VAL
16	P	4	ILE
16	P	22	THR
16	P	47	ASP
16	P	69	THR
16	P	75	ARG
16	P	82	GLN
17	Q	6	LEU
17	Q	38	ARG
17	Q	82	MET
17	Q	100	LYS
18	R	19	LYS
18	R	26	LEU
18	R	31	LEU
18	R	76	LEU
18	R	88	LYS
19	S	6	LYS
19	S	7	LYS
19	S	10	PHE
19	S	29	ARG
19	S	37	ARG
19	S	44	MET
19	S	49	ILE
19	S	66	MET
20	T	13	LEU
20	T	22	ARG
20	T	36	LEU
20	T	62	LEU
20	T	71	THR
20	T	73	HIS
20	T	75	ASN

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Mol	Chain	Res	Type
20	T	93	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	40	HIS
2	B	95	GLN
2	B	146	GLN
2	B	204	ASN
3	C	28	GLN
3	C	136	GLN
3	C	170	GLN
3	C	176	HIS
4	D	45	GLN
4	D	62	GLN
4	D	77	ASN
4	D	119	GLN
4	D	125	HIS
4	D	201	GLN
6	F	27	GLN
6	F	94	GLN
7	G	13	GLN
7	G	86	GLN
7	G	110	GLN
8	H	82	HIS
10	J	56	HIS
11	K	26	ASN
11	K	38	ASN
11	K	117	ASN
12	L	7	ASN
12	L	8	GLN
12	L	74	HIS
13	M	77	ASN
13	M	92	HIS
13	M	101	GLN
14	N	49	HIS
14	N	52	GLN
15	O	37	ASN
15	O	42	HIS
15	O	46	HIS
16	P	76	GLN
16	P	82	GLN

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Mol	Chain	Res	Type
17	Q	16	GLN
19	S	14	HIS
19	S	23	ASN
19	S	47	HIS
20	T	73	HIS
20	T	75	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1503/1504 (99%)	204 (13%)	0
22	V	76/77 (98%)	11 (14%)	0
22	W	76/77 (98%)	12 (15%)	0
23	X	4/5 (80%)	1 (25%)	0
All	All	1659/1663 (99%)	228 (13%)	0

All (228) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	G
1	A	9	G
1	A	22	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	80	G
1	A	81	G
1	A	88	C
1	A	108	G
1	A	109	A
1	A	116	A
1	A	121	C
1	A	131	C
1	A	144	G
1	A	195	A
1	A	197	A
1	A	210	U
1	A	244	U

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Mol	Chain	Res	Type
1	A	247	G
1	A	251	G
1	A	258	G
1	A	266	G
1	A	267	C
1	A	289	G
1	A	319	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	332	G
1	A	345	C
1	A	347	G
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	369	C
1	A	372	C
1	A	389	A
1	A	397	A
1	A	406	G
1	A	412	A
1	A	413	G
1	A	414	A
1	A	421	U
1	A	422	C
1	A	423	G
1	A	424	G
1	A	429	U
1	A	430	A
1	A	439	A
1	A	452	A
1	A	453	A
1	A	465	A
1	A	485	G
1	A	496	A
1	A	497	U
1	A	511	C
1	A	518	C
1	A	531	U
1	A	532	A

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Mol	Chain	Res	Type
1	A	533	A
1	A	547	A
1	A	559	A
1	A	561	U
1	A	562	C
1	A	568	G
1	A	572	A
1	A	573	A
1	A	576	G
1	A	577	G
1	A	641	U
1	A	653	A
1	A	665	A
1	A	666	G
1	A	688	G
1	A	695	A
1	A	702	A
1	A	703	G
1	A	723	U
1	A	749	C
1	A	753	A
1	A	755	G
1	A	777	A
1	A	792	A
1	A	793	U
1	A	794	A
1	A	817	C
1	A	818	G
1	A	819	A
1	A	821	G
1	A	827	U
1	A	828	A
1	A	841	U
1	A	842	C
1	A	843	U
1	A	848	C
1	A	859	A
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C

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Mol	Chain	Res	Type
1	A	935	A
1	A	960	U
1	A	961	U
1	A	969	A
1	A	971	G
1	A	974	A
1	A	976	G
1	A	977	A
1	A	980	C
1	A	981	U
1	A	982	U
1	A	992	U
1	A	993	G
1	A	1004	A
1	A	1025	U
1	A	1027(A)	C
1	A	1029	G
1	A	1045	C
1	A	1053	G
1	A	1054	C
1	A	1055	A
1	A	1064	G
1	A	1067	A
1	A	1081	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1117	G
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1140	C
1	A	1152	A
1	A	1159	U
1	A	1171	G
1	A	1184	G

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Mol	Chain	Res	Type
1	A	1196	U
1	A	1197	G
1	A	1200	C
1	A	1201	A
1	A	1212	U
1	A	1213	A
1	A	1225	A
1	A	1238	A
1	A	1239	A
1	A	1241	G
1	A	1253	G
1	A	1256	A
1	A	1257	U
1	A	1270	C
1	A	1280	A
1	A	1281	U
1	A	1286	A
1	A	1287	A
1	A	1297	C
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1305	G
1	A	1317	C
1	A	1319	A
1	A	1320	C
1	A	1337	G
1	A	1346	A
1	A	1347	G
1	A	1364	U
1	A	1368	G
1	A	1370	G
1	A	1378	C
1	A	1398	A
1	A	1419	G
1	A	1442	G
1	A	1443	G
1	A	1446	A
1	A	1451	A
1	A	1452	C
1	A	1453	G
1	A	1487	G

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Mol	Chain	Res	Type
1	A	1494	G
1	A	1497	G
1	A	1502	A
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1507	A
1	A	1517	G
1	A	1519	A
1	A	1520	G
1	A	1529	G
1	A	1530	G
1	A	1531	A
22	V	8	U
22	V	17(A)	U
22	V	19	G
22	V	20	U
22	V	21	A
22	V	31	G
22	V	47	U
22	V	48	C
22	V	74	C
22	V	75	C
22	V	76	A
22	W	6	G
22	W	10	G
22	W	17(A)	U
22	W	18	G
22	W	19	G
22	W	20	U
22	W	37	A
22	W	47	U
22	W	48	C
22	W	49	G
22	W	50	U
22	W	52	G
23	X	16	A

There are no RNA pucker outliers to report.

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

Mogul failed to run properly - this section will therefore be empty.

5.5 Carbohydrates ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.6 Ligand geometry ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.7 Other polymers ⓘ

Mogul failed to run properly - this section will therefore be empty.

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.