



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 07:09 AM GMT

PDB ID : 2QBB
Title : Crystal structure of the bacterial ribosome from Escherichia coli in complex with gentamicin. This file contains the 30S subunit of the second 70S ribosome, with gentamicin bound. The entire crystal structure contains two 70S ribosomes and is described in remark 400.
Authors : Borovinskaya, M.A.; Pai, R.D.; Zhang, W.; Schuwirth, B.-S.; Holton, J.M.; Hirokawa, G.; Kaji, H.; Kaji, A.; Cate, J.H.D.
Deposited on : 2007-06-16
Resolution : 3.54 Å(reported)

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

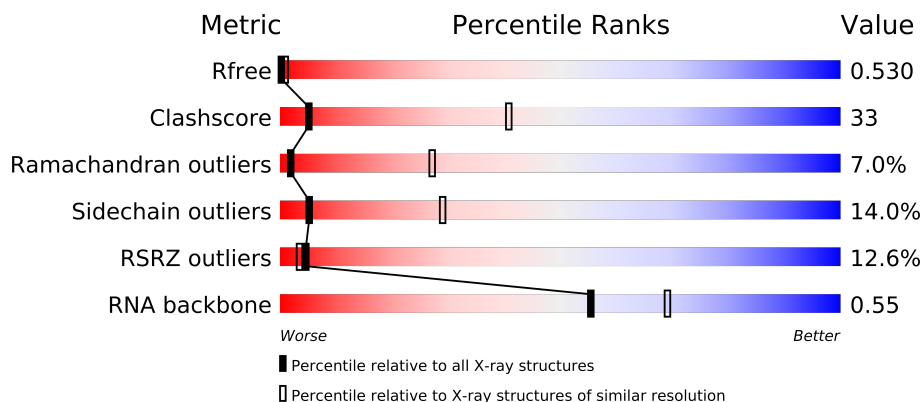
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.54 Å.

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



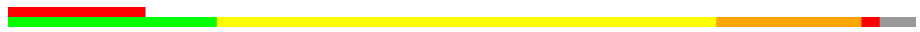
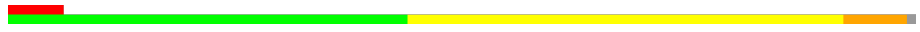


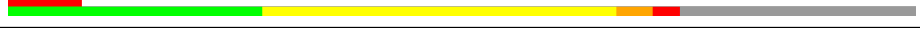
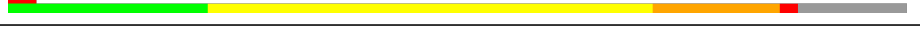
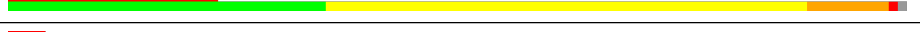


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1270 (3.78-3.30)
Clashscore	79885	1033 (3.70-3.38)
Ramachandran outliers	78287	1067 (3.72-3.36)
Sidechain outliers	78261	1067 (3.72-3.36)
RSRZ outliers	66119	1270 (3.78-3.30)
RNA backbone	1838	1011 (4.30-2.76)

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.

Mol	Chain	Length	Quality of chain
1	A	1542	
2	C	232	
3	D	205	
4	E	166	
5	F	135	
6	G	178	
7	H	129	
8	I	129	
9	J	103	
10	K	128	
11	L	123	
12	M	117	

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Mol	Chain	Length	Quality of chain
13	N	100	
14	O	89	
15	P	82	
16	Q	83	
17	R	74	
18	S	91	
19	T	86	
20	B	240	
21	U	70	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
22	MG	A	2049	-	X
22	MG	A	2056	-	X
22	MG	A	2084	-	X
22	MG	A	2134	-	X
22	MG	A	2161	-	X
22	MG	A	2168	-	X
22	MG	A	2182	-	X
22	MG	A	2196	-	X
22	MG	A	2312	-	X
23	LLL	A	2368	-	X

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 51851 atoms, of which 0 are hydrogen and 0 are deuterium.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1530	Total	C	N	O	P	0	0	0
			32831	14642	6024	10635	1530			

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	206	Total	C	N	O	S	0	0	0
			1624	1028	305	288	3			

- Molecule 3 is a protein called 30S ribosomal protein S4.

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

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	150	Total	C	N	O	S	0	0	0
			1105	687	211	201	6			

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	100	Total	C	N	O	S	0	0	0
			817	515	148	148	6			

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	152	Total	C	N	O	S	0	0	0
			1196	745	230	217	4			

- Molecule 7 is a protein called 30S ribosomal protein S8.

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

- Molecule 8 is a protein called 30S ribosomal protein S9.

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

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	J	98	Total	C	N	O	S	0	0	0
			786	493	150	142	1			

- Molecule 10 is a protein called 30S ribosomal protein S11.

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

- Molecule 11 is a protein called 30S ribosomal protein S12.

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

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	M	113	Total	C	N	O	S	0	0	0
			876	541	177	155	3			

- Molecule 13 is a protein called 30S ribosomal protein S14.

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

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	O	88	Total	C	N	O	S	0	0	0
			714	439	144	130	1			

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	P	80	Total	C	N	O	S	0	0	0
			638	400	126	111	1			

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	Q	81	Total	C	N	O	S	0	0	0
			657	417	122	115	3			

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	R	55	Total	C	N	O	0	0	0
			455	288	86	81			

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	S	80	Total	C	N	O	S	0	0	0
			644	413	121	108	2			

- Molecule 19 is a protein called 30S ribosomal protein S20.

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

- Molecule 20 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	B	218	Total	C	N	O	S	0	0	0
			1704	1081	305	311	7			

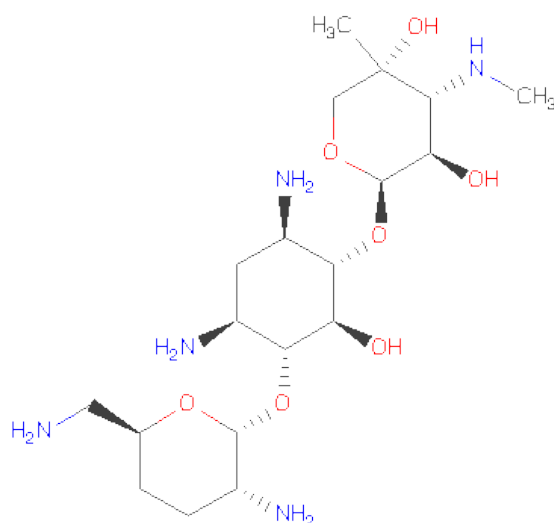
- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	U	51	Total	C	N	O	S	0	0	0
			425	265	86	73	1			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	61	Total	Mg	0	0
			61	61		
22	N	1	Total	Mg	0	0
			1	1		

- Molecule 23 is (2R,3R,4R,5R)-2-(((1S,2S,3R,4S,6R)-4,6-DIAMINO-3-((2R,3R,6S)-3-AMINO-O-6-(AMINOMETHYL)-TETRAHYDRO-2H-PYRAN-2-YLOXY)-2-HYDROXYCYCLOHEXYLOXY)-5-METHYL-4-(METHYLAMINO)-TETRAHYDRO-2H-PYRAN-3,5-DIOL (three-letter code: LLL) (formula: C₁₉H₃₉N₅O₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
23	A	1	Total	C	N	O	0	0
			31	19	5	7		
23	A	1	Total	C	N	O	0	0
			31	19	5	7		
23	A	1	Total	C	N	O	0	0
			31	19	5	7		

- Molecule 24 is water.

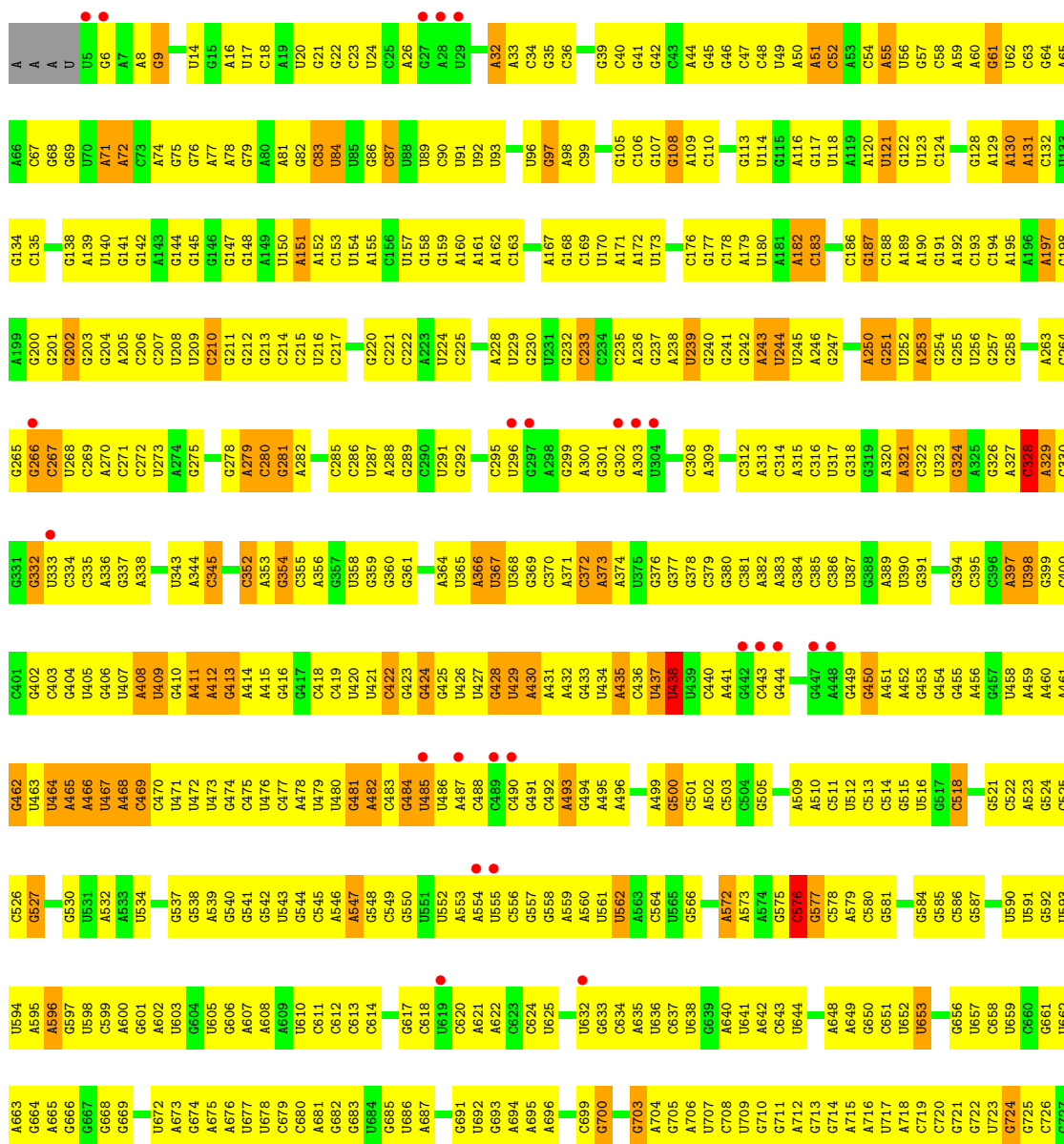
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	A	305	Total 305	O 305	0	0
24	N	3	Total 3	O 3	0	0
24	T	1	Total 1	O 1	0	0

3 Residue-property plots

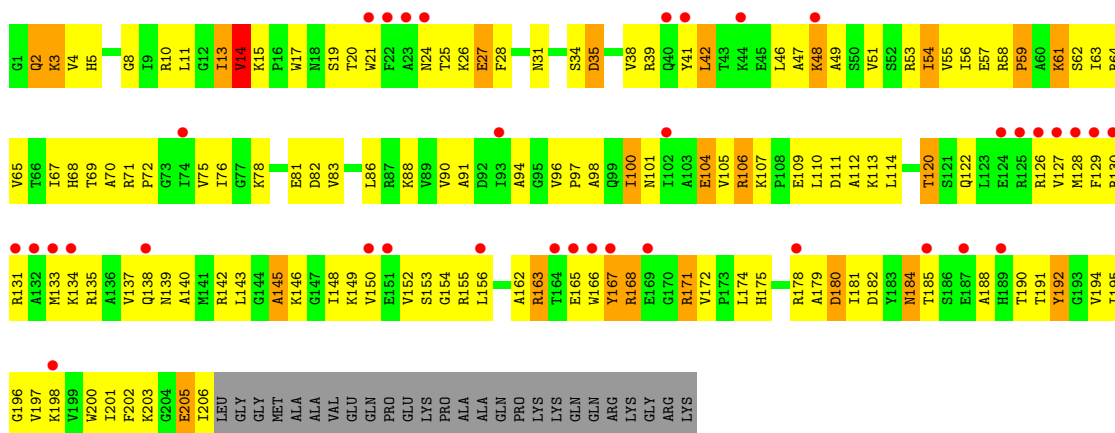
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

- Molecule 1: 16S rRNA

Chain A:

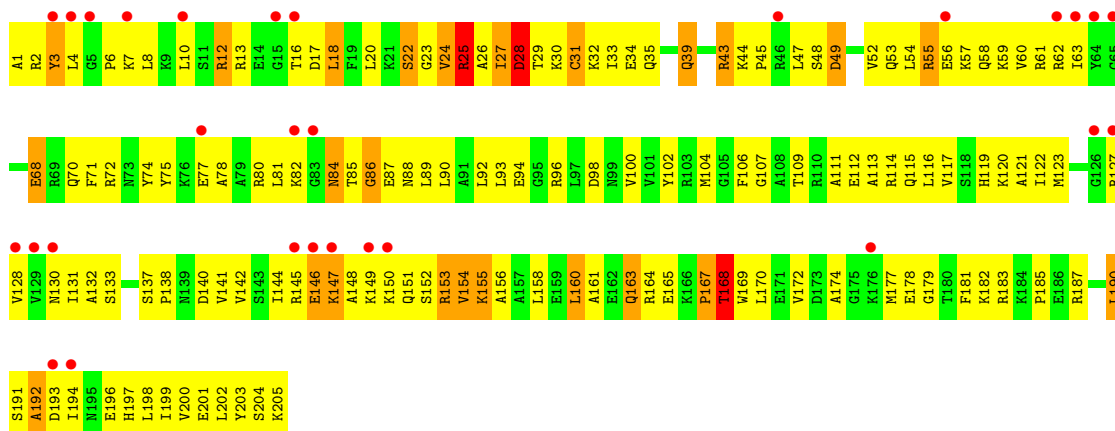






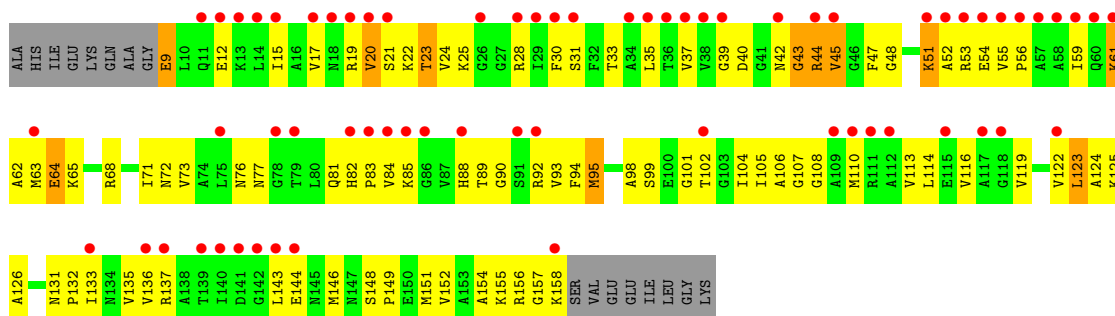
- Molecule 3: 30S ribosomal protein S4

Chain D:



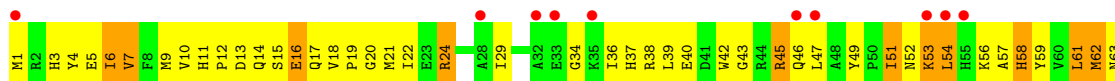
- Molecule 4: 30S ribosomal protein S5

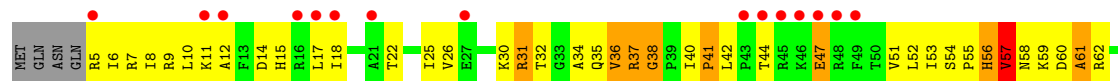
Chain E:



- Molecule 5: 30S ribosomal protein S6

Chain F: 

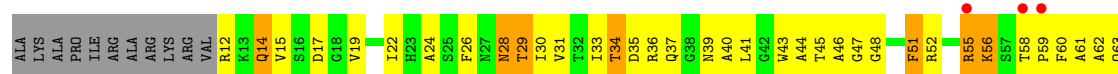






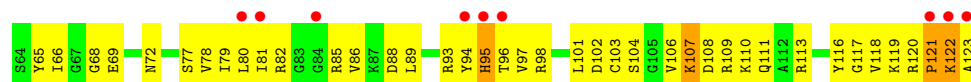
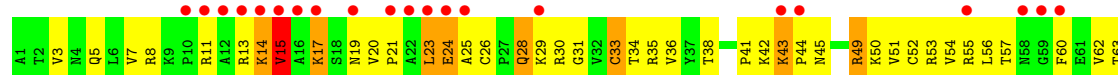
- Molecule 10: 30S ribosomal protein S11

Chain K:



- Molecule 11: 30S ribosomal protein S12

Chain L:



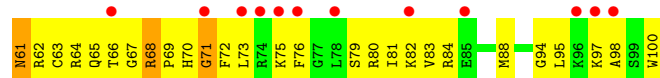
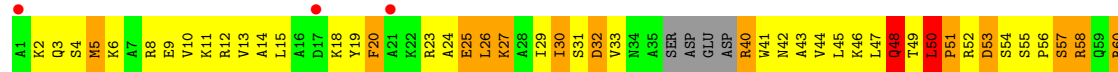
- Molecule 12: 30S ribosomal protein S13

Chain M:



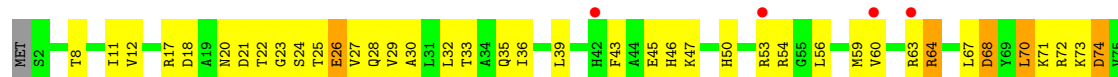
- Molecule 13: 30S ribosomal protein S14

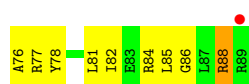
Chain N:



- Molecule 14: 30S ribosomal protein S15

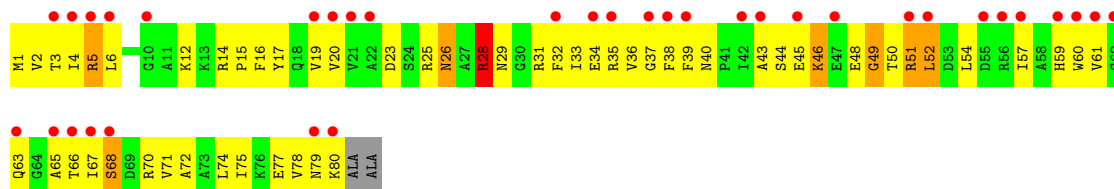
Chain O:





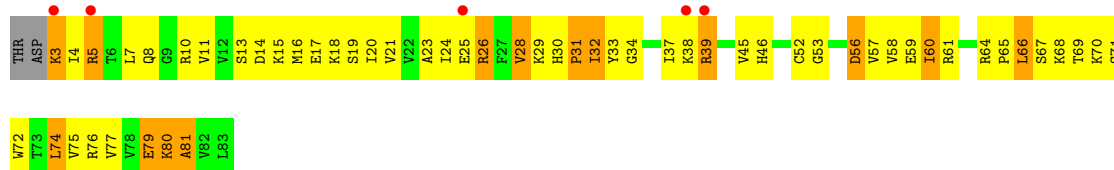
• Molecule 15: 30S ribosomal protein S16

Chain P:



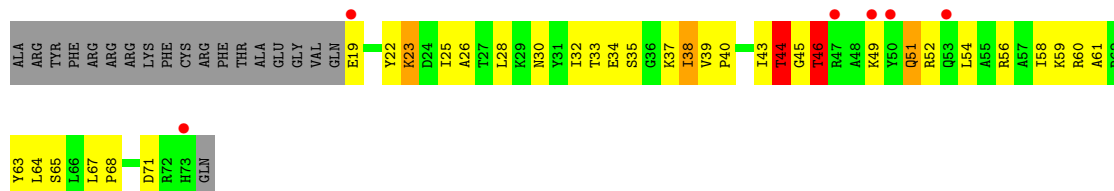
• Molecule 16: 30S ribosomal protein S17

Chain Q:



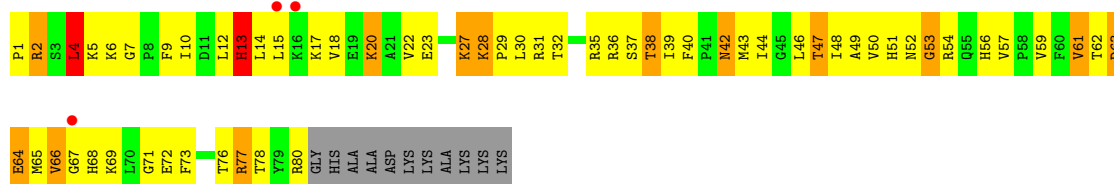
• Molecule 17: 30S ribosomal protein S18

Chain R:



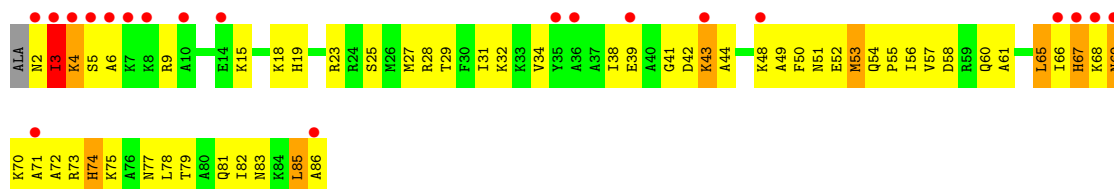
• Molecule 18: 30S ribosomal protein S19

Chain S:



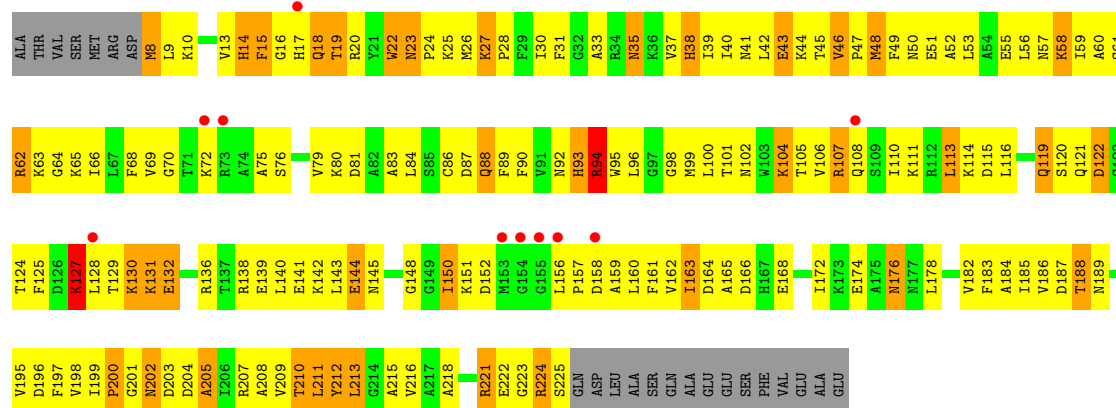
• Molecule 19: 30S ribosomal protein S20

Chain T:



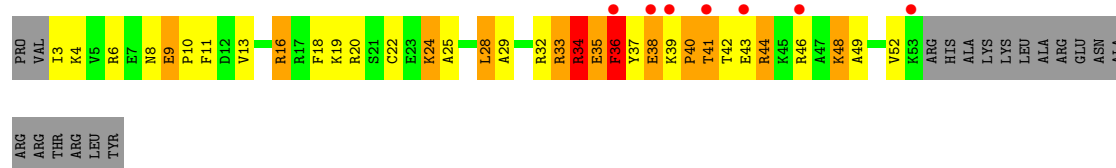
- Molecule 20: 30S ribosomal protein S2

Chain B:



- Molecule 21: 30S ribosomal protein S21

Chain U:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	208.85Å 379.20Å 739.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.00 – 3.54 138.41 – 3.55	Depositor EDS
% Data completeness (in resolution range)	88.8 (70.00-3.54) 89.9 (138.41-3.55)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 3.58Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.281 , 0.320 0.527 , 0.530	Depositor DCC
R_{free} test set	24347 reflections (3.88%)	DCC
Wilson B-factor (Å ²)	125.1	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 24.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 627888 reflections (0.000%)	Xtriage
F_o, F_c correlation	0.61	EDS
Total number of atoms	51851	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	0.26	3/36762 (0.0%)	0.76	23/57350 (0.0%)
2	C	0.23	0/1651	0.44	0/2225
3	D	0.23	0/1665	0.44	0/2227
4	E	0.23	0/1118	0.45	0/1504
5	F	0.24	0/835	0.45	0/1128
6	G	0.23	0/1211	0.45	0/1624
7	H	0.23	0/989	0.44	0/1326
8	I	0.24	0/1034	0.46	0/1375
9	J	0.22	0/796	0.47	0/1077
10	K	0.24	0/893	0.46	0/1205
11	L	0.22	0/969	0.48	0/1300
12	M	0.21	0/884	0.45	0/1181
13	N	0.24	0/785	0.45	0/1043
14	O	0.22	0/722	0.47	0/964
15	P	0.25	0/648	0.46	0/870
16	Q	0.24	0/666	0.46	0/892
17	R	0.23	0/462	0.46	0/621
18	S	0.25	0/660	0.48	0/888
19	T	0.24	0/671	0.39	0/888
20	B	0.25	0/1735	0.45	0/2338
21	U	0.26	0/430	0.47	0/570
All	All	0.25	3/55586 (0.0%)	0.68	23/82596 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	15

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1213	A	P-OP1	-8.98	1.33	1.49
1	A	1128	C	O3'-P	-5.35	1.54	1.61
1	A	495	A	N3-C4	-5.15	1.31	1.34

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1213	A	O5'-P-OP1	-32.89	71.23	110.70
1	A	1212	U	OP1-P-O3'	-10.85	81.34	105.20
1	A	366	A	C2'-C3'-O3'	8.51	128.21	109.50
1	A	1213	A	O5'-P-OP2	8.43	120.82	110.70
1	A	1212	U	OP2-P-O3'	8.26	123.38	105.20
1	A	576	C	O5'-P-OP1	-8.05	98.45	105.70
1	A	765	G	N9-C1'-C2'	-7.56	103.68	112.00
1	A	1424	U	C5'-C4'-C3'	-6.78	105.15	116.00
1	A	1212	U	O3'-P-O5'	6.12	115.64	104.00
1	A	1250	A	C5'-C4'-C3'	5.93	125.50	116.00
1	A	232	G	C5'-C4'-C3'	-5.83	106.67	116.00
1	A	1301	U	N1-C1'-C2'	5.76	121.48	114.00
1	A	438	U	N1-C1'-C2'	-5.65	105.78	112.00
1	A	1432	G	N9-C1'-C2'	-5.63	105.81	112.00
1	A	345	C	C5'-C4'-C3'	-5.51	107.18	116.00
1	A	366	A	C4'-C3'-O3'	5.48	123.96	113.00
1	A	1534	A	C2'-C3'-O3'	-5.32	97.79	109.50
1	A	328	C	C2'-C3'-O3'	5.15	121.94	113.70
1	A	845	A	N9-C1'-C2'	-5.14	106.34	112.00
1	A	1432	G	C5'-C4'-C3'	-5.13	107.79	116.00
1	A	765	G	C4'-C3'-O3'	5.13	123.25	113.00
1	A	40	C	C5'-C4'-C3'	-5.02	107.96	116.00
1	A	814	A	C5'-C4'-C3'	5.02	124.03	116.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	366	A	C3'

All (15) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1331	G	Sidechain
1	A	1405	G	Sidechain

Continued on next page...

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Mol	Chain	Res	Type	Group
1	A	1432	G	Sidechain
1	A	1441	A	Sidechain
1	A	187	G	Sidechain
1	A	281	G	Sidechain
1	A	324	G	Sidechain
1	A	437	U	Sidechain
1	A	438	U	Sidechain
1	A	450	G	Sidechain
1	A	462	G	Sidechain
1	A	481	G	Sidechain
1	A	496	A	Sidechain
1	A	666	G	Sidechain
1	A	703	G	Sidechain

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	32831	0	16521	1239	0
2	C	1624	0	1699	142	0
3	D	1643	0	1710	174	0
4	E	1105	0	1148	93	0
5	F	817	0	808	93	0
6	G	1196	0	1246	98	0
7	H	979	0	1034	79	0
8	I	1022	0	1070	132	0
9	J	786	0	828	86	0
10	K	877	0	887	104	0
11	L	955	0	1019	95	0
12	M	876	0	937	107	0
13	N	774	0	827	110	0
14	O	714	0	734	41	0
15	P	638	0	656	66	0
16	Q	657	0	702	67	0
17	R	455	0	478	44	0
18	S	644	0	675	93	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	T	665	0	714	55	0
20	B	1704	0	1732	205	0
21	U	425	0	449	69	0
22	A	61	0	0	0	0
22	N	1	0	0	0	0
23	A	93	0	117	5	0
24	A	305	0	0	2	0
24	N	3	0	0	0	0
24	T	1	0	0	0	0
All	All	51851	0	35991	2902	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 33.

All (2902) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:3:HIS:HB2	5:F:92:THR:HA	1.30	1.08
13:N:63:CYS:HB3	13:N:67:GLY:H	1.18	1.04
20:B:33:ALA:HA	20:B:38:HIS:HA	1.37	1.04
21:U:36:PHE:HB3	21:U:40:PRO:HD3	1.40	1.04
3:D:116:LEU:HB3	3:D:122:ILE:HD11	1.41	1.02
12:M:71:GLU:HA	12:M:74:MET:HG2	1.41	1.02
9:J:9:ARG:HB2	9:J:99:GLN:HB2	1.41	1.01
21:U:16:ARG:HE	21:U:16:ARG:HA	1.22	1.00
20:B:46:VAL:HG13	20:B:47:PRO:HD3	1.43	0.99
3:D:185:PRO:HB2	3:D:190:LEU:HB2	1.46	0.98
10:K:33:ILE:HB	10:K:73:VAL:HG11	1.47	0.97
8:I:51:LEU:HB3	8:I:56:MET:HG2	1.43	0.97
20:B:198:VAL:HG12	20:B:200:PRO:HD3	1.48	0.95
18:S:30:LEU:H	18:S:48:ILE:HA	1.29	0.95
10:K:124:LYS:HA	21:U:34:ARG:HB3	1.49	0.95
1:A:664:G:H22	1:A:741:G:H1	1.05	0.94
20:B:163:ILE:HG23	20:B:164:ASP:H	1.32	0.94
8:I:25:GLY:HA3	8:I:57:VAL:HA	1.50	0.94
2:C:76:ILE:HA	2:C:83:VAL:HG23	1.47	0.94
19:T:43:LYS:HE2	19:T:44:ALA:H	1.34	0.93
10:K:31:VAL:HG21	10:K:66:ALA:HA	1.47	0.92
1:A:1532:U:H2'	1:A:1533:C:H5''	1.50	0.91
20:B:202:ASN:HD22	20:B:204:ASP:H	1.16	0.91
1:A:243:A:H4'	1:A:244:U:H5'	1.52	0.91
7:H:11:THR:HG22	7:H:14:ARG:HH12	1.36	0.91
1:A:1086:U:H3	1:A:1099:G:H22	0.99	0.90

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:J:53:ILE:HG22	9:J:61:ALA:HB1	1.53	0.90
10:K:91:GLY:HA2	10:K:94:SER:HB3	1.53	0.90
3:D:160:LEU:HD13	3:D:160:LEU:H	1.37	0.90
16:Q:3:LYS:HZ3	16:Q:4:ILE:H	1.20	0.89
3:D:84:ASN:HD22	4:E:101:GLY:HA2	1.36	0.89
4:E:106:ALA:HB1	4:E:110:MET:HB3	1.56	0.88
2:C:128:MET:HB2	2:C:131:ARG:HB2	1.57	0.87
5:F:92:THR:HG22	5:F:94:HIS:H	1.38	0.87
18:S:18:VAL:HG21	18:S:43:MET:HG2	1.57	0.87
1:A:120:A:H2'	1:A:121:U:H5''	1.57	0.86
18:S:51:HIS:HA	18:S:56:HIS:HA	1.56	0.86
3:D:60:VAL:HB	3:D:194:ILE:HD11	1.58	0.86
6:G:104:VAL:HG12	6:G:108:ARG:HD2	1.58	0.86
1:A:522:C:H41	11:L:49:ARG:NH2	1.74	0.86
12:M:21:ILE:HB	12:M:24:VAL:HG22	1.55	0.86
8:I:55:ASP:HB2	8:I:59:LYS:HE3	1.57	0.86
10:K:110:THR:HG22	21:U:4:LYS:HA	1.58	0.85
1:A:1250:A:H4'	8:I:69:GLY:H	1.40	0.85
19:T:60:GLN:HB3	19:T:65:LEU:HD23	1.57	0.85
9:J:17:LEU:HD22	9:J:96:VAL:HG13	1.58	0.85
21:U:43:GLU:HG3	21:U:44:ARG:HH21	1.42	0.85
6:G:130:LYS:H	6:G:134:VAL:HG21	1.40	0.85
20:B:99:MET:HA	20:B:106:VAL:HG21	1.59	0.85
10:K:14:GLN:HA	10:K:77:GLY:HA3	1.57	0.84
10:K:92:ARG:HH11	21:U:20:ARG:HH21	1.26	0.84
5:F:62:MET:HG3	5:F:64:VAL:HG23	1.60	0.84
5:F:90:MET:HG2	17:R:60:ARG:HH21	1.44	0.83
13:N:30:ILE:HG21	13:N:44:VAL:HG21	1.61	0.83
1:A:60:A:H4'	1:A:61:G:H5'	1.58	0.83
20:B:65:LYS:HB2	20:B:158:ASP:H	1.43	0.83
1:A:981:U:H4'	13:N:60:ARG:HD2	1.59	0.82
17:R:51:GLN:HA	17:R:51:GLN:HE21	1.42	0.82
13:N:26:LEU:HD23	13:N:27:LYS:H	1.45	0.82
8:I:19:PHE:HB2	8:I:63:TYR:HB3	1.62	0.82
1:A:617:G:H4'	15:P:46:LYS:HE2	1.60	0.82
1:A:974:A:H4'	1:A:975:A:H5'	1.61	0.82
1:A:1071:C:H2'	1:A:1072:G:H8	1.44	0.82
10:K:52:ARG:HH12	10:K:56:LYS:HE3	1.45	0.82
10:K:86:LYS:HB3	10:K:112:VAL:HG23	1.59	0.82
15:P:28:ARG:HD2	15:P:29:ASN:H	1.43	0.82
21:U:40:PRO:HA	21:U:44:ARG:HD2	1.62	0.81
2:C:126:ARG:HH22	2:C:190:THR:HG23	1.44	0.81

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:932:C:H5''	6:G:3:ARG:HG2	1.61	0.81
2:C:70:ALA:HA	2:C:105:VAL:HG21	1.62	0.80
2:C:182:ASP:HB2	2:C:203:LYS:HE2	1.62	0.80
18:S:31:ARG:HA	18:S:49:ALA:HB3	1.60	0.80
20:B:156:LEU:HD12	20:B:156:LEU:H	1.46	0.79
4:E:81:GLN:HG2	4:E:148:SER:HA	1.63	0.79
10:K:111:ASP:HB2	21:U:19:LYS:HE3	1.64	0.79
1:A:17:U:H2'	1:A:18:C:C6	2.16	0.79
10:K:83:VAL:HB	10:K:109:ILE:HA	1.62	0.79
18:S:10:ILE:HG22	18:S:38:THR:H	1.48	0.79
13:N:55:SER:HB2	13:N:58:ARG:HD2	1.63	0.79
20:B:184:ALA:HB3	20:B:195:VAL:HG21	1.62	0.79
10:K:22:ILE:HG21	10:K:95:THR:HG21	1.63	0.79
13:N:68:ARG:HB3	13:N:68:ARG:HH11	1.47	0.79
6:G:78:ARG:HG2	6:G:83:THR:HG22	1.65	0.78
20:B:16:GLY:HA2	20:B:40:ILE:HG13	1.64	0.78
20:B:61:SER:HB2	20:B:62:ARG:HH11	1.47	0.78
3:D:10:LEU:HB3	3:D:62:ARG:HD3	1.64	0.78
1:A:1328:C:H5''	12:M:27:THR:HG21	1.63	0.78
18:S:30:LEU:HB2	18:S:48:ILE:HG23	1.64	0.78
7:H:87:ARG:H	7:H:90:GLU:HB2	1.49	0.78
18:S:43:MET:HB2	18:S:61:VAL:HG11	1.66	0.78
1:A:1323:G:H2'	1:A:1324:A:C8	2.18	0.78
20:B:61:SER:HB2	20:B:62:ARG:NH1	1.99	0.78
8:I:34:LEU:HD21	8:I:48:ARG:HE	1.46	0.78
18:S:10:ILE:HG22	18:S:37:SER:HB3	1.66	0.78
2:C:26:LYS:HG3	2:C:27:GLU:HG3	1.65	0.78
1:A:817:C:H1'	1:A:819:A:H5'	1.64	0.78
1:A:1399:C:H4'	1:A:1400:C:H5''	1.64	0.77
20:B:19:THR:HG23	20:B:20:ARG:H	1.48	0.77
10:K:28:ASN:HD21	10:K:47:GLY:H	1.31	0.77
3:D:197:HIS:O	3:D:200:VAL:HG22	1.83	0.77
1:A:1412:C:H2'	1:A:1413:A:C8	2.20	0.77
20:B:202:ASN:ND2	20:B:204:ASP:H	1.82	0.77
10:K:80:ASN:N	10:K:80:ASN:HD22	1.82	0.77
12:M:10:ASP:HA	12:M:44:ILE:HD13	1.67	0.77
1:A:1142:G:H2'	1:A:1143:G:O4'	1.85	0.77
20:B:60:ALA:HA	20:B:64:GLY:HA3	1.65	0.77
1:A:1078:U:H4'	4:E:137:ARG:NH1	2.00	0.77
5:F:91:ARG:HG3	5:F:93:LYS:HE3	1.66	0.77
1:A:1151:A:HO2'	1:A:1152:A:H8	1.33	0.76
1:A:524:G:H2'	1:A:525:C:C6	2.20	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:P:61:VAL:HA	15:P:65:ALA:HB3	1.66	0.76
1:A:373:A:H1'	1:A:481:G:N3	2.01	0.76
9:J:12:ALA:HB2	9:J:96:VAL:HG12	1.66	0.76
5:F:88:MET:HG3	5:F:89:VAL:H	1.50	0.76
2:C:190:THR:HG22	2:C:191:THR:H	1.49	0.76
1:A:1009:U:H2'	1:A:1010:U:C6	2.21	0.76
19:T:61:ALA:HA	19:T:67:HIS:H	1.51	0.76
1:A:1236:A:H4'	1:A:1304:G:H4'	1.67	0.76
1:A:518:C:H2'	1:A:530:G:C8	2.21	0.76
1:A:1296:C:H4'	1:A:1302:C:H41	1.51	0.76
18:S:10:ILE:HB	18:S:14:LEU:HD11	1.66	0.75
19:T:4:LYS:HD2	19:T:5:SER:H	1.50	0.75
1:A:1239:A:H4'	1:A:1240:U:H5'	1.67	0.75
1:A:662:U:O2'	1:A:836:G:H5''	1.86	0.75
10:K:34:THR:HA	10:K:41:LEU:HG	1.69	0.75
4:E:114:LEU:HD13	4:E:122:VAL:HG21	1.69	0.75
12:M:14:ALA:HB2	12:M:42:VAL:HG23	1.69	0.74
13:N:63:CYS:HB3	13:N:67:GLY:N	2.00	0.74
1:A:1078:U:H4'	4:E:137:ARG:HH12	1.52	0.74
13:N:50:LEU:H	13:N:51:PRO:HD2	1.51	0.74
2:C:137:VAL:HA	2:C:148:ILE:HD13	1.67	0.74
18:S:17:LYS:HB3	18:S:30:LEU:HD22	1.69	0.74
10:K:88:PRO:HD3	21:U:28:LEU:HD11	1.68	0.74
12:M:79:LEU:HD13	12:M:86:ARG:HB3	1.67	0.74
1:A:1278:G:H4'	1:A:1279:G:H5'	1.70	0.74
6:G:115:MET:HA	6:G:118:ARG:HD2	1.67	0.74
5:F:88:MET:HG3	5:F:89:VAL:N	2.02	0.74
20:B:128:LEU:HD12	20:B:129:THR:H	1.51	0.74
3:D:24:VAL:HG23	3:D:25:ARG:HD2	1.70	0.74
3:D:25:ARG:HD3	3:D:26:ALA:N	2.02	0.74
1:A:505:G:H5'	1:A:534:U:H2'	1.68	0.73
1:A:600:A:H5''	7:H:88:LYS:HD2	1.68	0.73
10:K:92:ARG:NH1	21:U:20:ARG:HH21	1.85	0.73
1:A:1160:G:H4'	20:B:130:LYS:HB2	1.69	0.73
11:L:56:LEU:HD12	11:L:60:PHE:HB2	1.69	0.73
1:A:522:C:H41	11:L:49:ARG:HH22	1.35	0.73
16:Q:56:ASP:HA	16:Q:81:ALA:HB2	1.68	0.73
1:A:859:G:H2'	1:A:860:A:C8	2.24	0.73
1:A:204:G:H21	1:A:466:A:N6	1.85	0.73
19:T:68:LYS:HA	19:T:68:LYS:HE2	1.69	0.73
20:B:187:ASP:OD1	20:B:203:ASP:HB3	1.89	0.73
20:B:218:ALA:HA	20:B:221:ARG:HG2	1.69	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:238:A:H2'	1:A:239:U:H5''	1.71	0.73
12:M:28:ARG:HH12	12:M:59:VAL:HA	1.53	0.73
13:N:51:PRO:HB2	13:N:54:SER:HB3	1.71	0.73
1:A:451:A:H5'	15:P:70:ARG:HH22	1.54	0.73
1:A:1315:U:H5	18:S:5:LYS:HZ1	1.37	0.72
12:M:44:ILE:HD12	12:M:44:ILE:H	1.54	0.72
1:A:264:C:H4'	16:Q:64:ARG:HD2	1.69	0.72
20:B:186:VAL:O	20:B:200:PRO:HA	1.88	0.72
3:D:28:ASP:HA	3:D:33:ILE:HG21	1.72	0.72
3:D:96:ARG:HB3	3:D:98:ASP:OD2	1.89	0.72
5:F:42:TRP:HE1	5:F:61:LEU:HD23	1.52	0.72
11:L:120:ARG:HG2	11:L:121:PRO:HD2	1.71	0.72
20:B:185:ILE:HA	20:B:199:ILE:HB	1.72	0.72
3:D:77:GLU:HA	3:D:80:ARG:HG2	1.71	0.72
15:P:57:ILE:O	15:P:61:VAL:HG23	1.90	0.72
1:A:484:G:H4'	1:A:485:U:O5'	1.87	0.72
7:H:76:ARG:HG3	7:H:77:VAL:N	2.05	0.72
17:R:22:TYR:HB2	17:R:61:ALA:HB2	1.70	0.72
1:A:474:G:H2'	1:A:475:C:C6	2.24	0.72
1:A:781:A:H2'	1:A:782:A:H5'	1.70	0.72
1:A:993:G:H2'	1:A:995:C:H41	1.54	0.72
1:A:269:C:H2'	1:A:270:A:C8	2.24	0.72
1:A:636:U:H2'	1:A:637:C:C6	2.25	0.72
1:A:376:G:H5''	15:P:5:ARG:HB2	1.72	0.72
3:D:146:GLU:HA	3:D:149:LYS:HG2	1.72	0.72
5:F:36:ILE:HG13	5:F:64:VAL:HG22	1.71	0.72
1:A:17:U:H2'	1:A:18:C:H6	1.55	0.71
1:A:523:A:H61	11:L:88:ASP:HB2	1.55	0.71
1:A:1206:G:H4'	2:C:192:TYR:HA	1.71	0.71
6:G:23:ALA:O	6:G:26:VAL:HG22	1.90	0.71
1:A:1314:C:H3'	18:S:5:LYS:HZ2	1.55	0.71
9:J:37:ARG:NE	9:J:37:ARG:HA	2.06	0.71
2:C:48:LYS:H	2:C:48:LYS:HD3	1.55	0.71
1:A:328:C:H4'	1:A:329:A:H5''	1.71	0.71
15:P:6:LEU:HB3	15:P:17:TYR:HB3	1.73	0.71
4:E:156:ARG:HA	4:E:158:LYS:HZ3	1.55	0.70
20:B:45:THR:HA	20:B:48:MET:HG3	1.73	0.70
1:A:239:U:OP1	1:A:239:U:H4'	1.90	0.70
4:E:158:LYS:HZ1	7:H:63:LYS:HD3	1.55	0.70
11:L:35:ARG:NH1	11:L:36:VAL:HG22	2.06	0.70
21:U:24:LYS:HD2	21:U:25:ALA:H	1.56	0.70
3:D:71:PHE:HE1	3:D:89:LEU:HD21	1.57	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:182:A:O2'	1:A:183:C:H3'	1.91	0.70
6:G:130:LYS:N	6:G:134:VAL:HG21	2.06	0.70
20:B:221:ARG:HH11	20:B:221:ARG:HB3	1.56	0.70
12:M:106:ARG:HD3	12:M:111:PRO:HA	1.73	0.70
13:N:63:CYS:HB2	13:N:79:SER:HB3	1.72	0.70
13:N:45:LEU:HD21	18:S:9:PHE:HB2	1.72	0.70
6:G:145:GLU:HA	6:G:148:LYS:HB2	1.73	0.70
1:A:842:U:H2'	1:A:843:U:O3'	1.91	0.70
1:A:1060:U:H4'	9:J:54:SER:HB2	1.72	0.70
6:G:110:ARG:HD2	6:G:122:GLU:HB2	1.74	0.70
20:B:79:VAL:HG12	20:B:90:PHE:HB2	1.71	0.70
2:C:19:SER:HB3	2:C:21:TRP:HE1	1.56	0.70
1:A:337:G:H2'	1:A:338:A:C8	2.26	0.69
1:A:658:C:H2'	1:A:659:U:H6	1.57	0.69
2:C:61:LYS:NZ	2:C:96:VAL:HG11	2.08	0.69
20:B:122:ASP:OD1	20:B:124:THR:HG22	1.93	0.69
5:F:5:GLU:HA	5:F:63:ASN:HA	1.74	0.69
1:A:465:A:H2'	1:A:467:U:OP2	1.93	0.69
4:E:28:ARG:HH12	4:E:30:PHE:HB3	1.57	0.69
1:A:999:C:H2'	1:A:1000:A:C8	2.27	0.69
18:S:5:LYS:C	18:S:6:LYS:HD2	2.13	0.69
1:A:473:U:H2'	1:A:474:G:C8	2.27	0.69
1:A:1343:G:H1'	8:I:122:ARG:HH12	1.57	0.69
1:A:1162:C:H2'	1:A:1163:A:C8	2.27	0.69
13:N:46:LYS:HZ2	18:S:10:ILE:H	1.39	0.69
3:D:25:ARG:NH1	3:D:30:LYS:HE3	2.07	0.69
1:A:909:A:H2'	1:A:910:C:O4'	1.93	0.69
4:E:95:MET:HA	4:E:124:ALA:HB2	1.73	0.69
19:T:43:LYS:HE2	19:T:44:ALA:N	2.08	0.69
1:A:1391:U:H2'	1:A:1392:G:C8	2.28	0.69
21:U:40:PRO:O	21:U:44:ARG:HB2	1.93	0.69
1:A:1250:A:H4'	8:I:69:GLY:N	2.08	0.69
11:L:24:GLU:HB2	11:L:26:CYS:SG	2.32	0.69
16:Q:45:VAL:HG12	16:Q:46:HIS:H	1.58	0.69
20:B:172:ILE:HG22	20:B:176:ASN:HD21	1.57	0.69
9:J:53:ILE:CG2	9:J:61:ALA:HB1	2.22	0.69
1:A:1302:C:OP2	12:M:16:ILE:HD11	1.93	0.69
2:C:69:THR:HG21	2:C:75:VAL:HG21	1.74	0.69
1:A:764:C:H2'	1:A:765:G:H5'	1.75	0.69
19:T:56:ILE:O	19:T:60:GLN:HG2	1.93	0.69
9:J:12:ALA:HB3	9:J:18:ILE:HB	1.73	0.69
1:A:1316:G:N2	1:A:1318:A:H3'	2.08	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:G:12:LEU:HD22	6:G:13:PRO:HD2	1.73	0.69
13:N:14:ALA:HB1	13:N:18:LYS:HE3	1.75	0.69
3:D:153:ARG:HG3	3:D:154:VAL:H	1.57	0.68
3:D:94:GLU:HG2	3:D:190:LEU:HG	1.75	0.68
5:F:42:TRP:NE1	5:F:61:LEU:HD23	2.07	0.68
1:A:673:A:H2'	1:A:674:G:C8	2.29	0.68
10:K:105:ARG:HH21	21:U:10:PRO:HB3	1.59	0.68
13:N:30:ILE:HD12	13:N:30:ILE:H	1.58	0.68
2:C:59:PRO:HG2	2:C:62:SER:OG	1.92	0.68
9:J:53:ILE:HG13	13:N:84:ARG:CZ	2.24	0.68
1:A:279:A:H5''	1:A:280:C:H3'	1.75	0.68
2:C:122:GLN:HB3	2:C:127:VAL:HG21	1.74	0.68
1:A:719:C:H1'	17:R:37:LYS:HB2	1.75	0.68
9:J:65:TYR:OH	13:N:84:ARG:HG3	1.94	0.68
1:A:518:C:H2'	1:A:530:G:H8	1.58	0.68
1:A:764:C:C2'	1:A:765:G:H5'	2.24	0.68
2:C:149:LYS:HB3	2:C:200:TRP:HB2	1.75	0.68
8:I:27:ILE:HB	8:I:34:LEU:HB2	1.74	0.68
5:F:90:MET:HG2	17:R:60:ARG:NH2	2.09	0.68
1:A:499:A:H4'	1:A:500:G:OP1	1.93	0.68
1:A:1026:G:N3	1:A:1026:G:H2'	2.09	0.68
7:H:113:ARG:NH2	7:H:114:ALA:HA	2.09	0.68
2:C:190:THR:HG22	2:C:191:THR:N	2.09	0.67
2:C:61:LYS:HZ2	2:C:96:VAL:HG11	1.57	0.67
8:I:71:ILE:HD12	8:I:71:ILE:H	1.58	0.67
4:E:89:THR:HG22	4:E:90:GLY:H	1.59	0.67
1:A:1477:U:H2'	1:A:1478:U:C6	2.30	0.67
10:K:75:GLU:CD	10:K:75:GLU:H	1.95	0.67
9:J:6:ILE:HB	9:J:76:ILE:HD11	1.76	0.67
1:A:1296:C:H4'	1:A:1302:C:N4	2.09	0.67
1:A:763:G:H2'	1:A:764:C:H6	1.59	0.67
2:C:31:ASN:HD22	2:C:58:ARG:HE	1.41	0.67
6:G:64:ALA:HA	6:G:127:ALA:HA	1.76	0.67
5:F:7:VAL:HG13	5:F:88:MET:HB3	1.77	0.67
16:Q:8:GLN:HA	16:Q:59:GLU:HA	1.76	0.67
13:N:12:ARG:HA	13:N:15:LEU:HD12	1.75	0.67
1:A:312:C:H2'	1:A:313:A:C8	2.30	0.67
8:I:41:GLU:H	8:I:44:ARG:NH1	1.91	0.67
4:E:152:VAL:HG21	7:H:98:LEU:HB3	1.77	0.67
1:A:237:G:H2'	1:A:238:A:H8	1.59	0.67
1:A:473:U:H2'	1:A:474:G:H8	1.59	0.67
1:A:160:A:H2'	1:A:161:A:O4'	1.94	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1218:C:H2'	1:A:1219:A:C8	2.29	0.67
1:A:384:G:H2'	1:A:385:C:C6	2.30	0.67
1:A:632:U:H5''	1:A:633:G:C8	2.29	0.67
1:A:312:C:H2'	1:A:313:A:H8	1.58	0.67
2:C:65:VAL:HG21	2:C:90:VAL:HG11	1.77	0.67
2:C:2:GLN:H	2:C:2:GLN:NE2	1.92	0.67
21:U:38:GLU:C	21:U:40:PRO:HD2	2.15	0.67
1:A:371:A:O2'	1:A:372:C:H5'	1.95	0.67
16:Q:75:VAL:HG23	16:Q:76:ARG:H	1.59	0.67
3:D:145:ARG:HB3	3:D:147:LYS:HD2	1.77	0.67
1:A:882:C:O2'	1:A:883:C:H5'	1.95	0.67
1:A:154:U:H2'	1:A:155:A:C8	2.29	0.67
1:A:8:A:H5'	4:E:105:ILE:HG22	1.76	0.67
3:D:24:VAL:HG23	3:D:25:ARG:H	1.59	0.67
1:A:1202:U:H1'	13:N:68:ARG:HD2	1.76	0.67
10:K:80:ASN:HB3	10:K:105:ARG:HB3	1.77	0.67
2:C:57:GLU:HB2	2:C:64:ARG:HB2	1.77	0.67
12:M:71:GLU:CA	12:M:74:MET:HG2	2.24	0.66
1:A:18:C:H4'	1:A:1078:U:O2	1.95	0.66
12:M:10:ASP:HB2	12:M:11:HIS:ND1	2.10	0.66
1:A:1007:U:H2'	1:A:1008:U:C6	2.30	0.66
1:A:1309:G:H1'	12:M:72:ILE:HD11	1.77	0.66
1:A:35:G:H2'	1:A:36:C:C6	2.31	0.66
3:D:138:PRO:HA	3:D:181:PHE:HD2	1.60	0.66
1:A:590:U:H2'	1:A:591:U:C6	2.30	0.66
20:B:22:TRP:HB3	20:B:38:HIS:NE2	2.10	0.66
5:F:1:MET:SD	5:F:67:PRO:HD3	2.35	0.66
1:A:973:G:H3'	1:A:974:A:H5''	1.76	0.66
16:Q:16:MET:CB	16:Q:19:SER:HB2	2.23	0.66
11:L:82:ARG:HG2	11:L:82:ARG:HH11	1.59	0.66
5:F:9:MET:HB3	5:F:59:TYR:CD2	2.31	0.66
15:P:43:ALA:HA	15:P:46:LYS:HE3	1.76	0.66
1:A:859:G:H2'	1:A:860:A:H8	1.61	0.66
1:A:1348:U:H4'	8:I:121:ARG:HG3	1.76	0.66
4:E:33:THR:HG22	4:E:51:LYS:HB3	1.76	0.66
1:A:1168:U:H4'	1:A:1169:A:OP2	1.96	0.66
1:A:56:U:H2'	1:A:57:G:H8	1.59	0.66
1:A:1018:G:H2'	1:A:1019:A:H8	1.59	0.66
8:I:48:ARG:O	8:I:52:GLU:HG2	1.95	0.66
1:A:285:C:H2'	1:A:286:C:H6	1.60	0.66
2:C:13:ILE:HD13	2:C:13:ILE:H	1.59	0.66
18:S:30:LEU:HD12	18:S:48:ILE:HG12	1.76	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:K:80:ASN:H	10:K:80:ASN:HD22	1.43	0.66
1:A:1238:A:H5'	1:A:1336:C:H41	1.60	0.66
1:A:1018:G:H2'	1:A:1019:A:C8	2.31	0.66
3:D:81:LEU:HB2	3:D:88:ASN:ND2	2.10	0.66
2:C:134:LYS:HA	2:C:167:TYR:HE2	1.60	0.66
8:I:56:MET:C	8:I:58:GLU:H	2.00	0.66
20:B:202:ASN:HD22	20:B:204:ASP:N	1.90	0.66
12:M:33:LEU:HB3	12:M:38:ILE:O	1.95	0.66
1:A:501:C:H2'	1:A:502:A:H8	1.60	0.66
19:T:79:THR:O	19:T:82:ILE:HG13	1.96	0.66
12:M:90:HIS:HA	12:M:108:ARG:HH22	1.61	0.66
1:A:492:C:H2'	1:A:493:A:N3	2.09	0.66
1:A:982:U:H5''	13:N:5:MET:HE3	1.77	0.66
21:U:34:ARG:HH21	21:U:36:PHE:HE2	1.42	0.66
21:U:42:THR:O	21:U:46:ARG:HG3	1.95	0.66
1:A:1144:G:N2	1:A:1146:A:H62	1.94	0.66
1:A:190:A:H2'	1:A:191:G:O4'	1.95	0.66
1:A:957:U:H4'	18:S:78:THR:HB	1.78	0.66
1:A:9:G:H5'	4:E:107:GLY:HA3	1.78	0.66
4:E:61:LYS:O	4:E:65:LYS:HG2	1.94	0.65
20:B:23:ASN:HD22	20:B:24:PRO:HD2	1.61	0.65
13:N:27:LYS:HA	13:N:31:SER:HB2	1.77	0.65
1:A:922:G:H2'	1:A:923:A:C8	2.30	0.65
7:H:45:ILE:HG21	7:H:60:LEU:HD21	1.77	0.65
12:M:78:ARG:O	12:M:82:LEU:HB2	1.97	0.65
2:C:70:ALA:HA	2:C:105:VAL:CG2	2.26	0.65
20:B:162:VAL:HG13	20:B:184:ALA:HB2	1.77	0.65
12:M:18:LEU:HD23	12:M:24:VAL:HG21	1.78	0.65
1:A:452:A:H2'	1:A:453:G:O4'	1.96	0.65
11:L:51:VAL:HG12	11:L:52:CYS:H	1.59	0.65
15:P:3:THR:HB	15:P:66:THR:O	1.95	0.65
1:A:1399:C:H4'	1:A:1400:C:C5'	2.26	0.65
1:A:552:U:H2'	1:A:553:A:C8	2.31	0.65
8:I:83:THR:HA	8:I:86:LEU:HD22	1.77	0.65
13:N:40:ARG:HH11	18:S:6:LYS:HB2	1.62	0.65
20:B:187:ASP:HB3	20:B:201:GLY:O	1.96	0.65
3:D:155:LYS:HA	3:D:158:LEU:HD13	1.79	0.65
20:B:10:LYS:HB3	20:B:211:LEU:HD21	1.79	0.65
4:E:84:VAL:HG11	4:E:146:MET:HB3	1.79	0.65
1:A:285:C:H2'	1:A:286:C:C6	2.31	0.65
1:A:1226:C:H4'	1:A:1227:A:OP1	1.96	0.65
3:D:106:PHE:CG	3:D:144:ILE:HD11	2.32	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:Q:80:LYS:HE3	16:Q:80:LYS:N	2.12	0.65
20:B:101:THR:HA	20:B:178:LEU:HD11	1.77	0.65
1:A:1038:C:H2'	1:A:1039:G:C8	2.31	0.65
1:A:678:U:H2'	1:A:679:C:C6	2.31	0.65
8:I:48:ARG:HA	8:I:51:LEU:HD12	1.77	0.65
2:C:113:LYS:HB2	2:C:184:ASN:OD1	1.97	0.65
1:A:946:A:H2'	1:A:947:G:C8	2.32	0.65
1:A:784:A:H2'	1:A:785:G:H8	1.62	0.65
15:P:3:THR:HG22	15:P:66:THR:HB	1.78	0.65
1:A:382:A:H2'	1:A:383:A:C8	2.31	0.65
10:K:91:GLY:O	10:K:95:THR:HG22	1.95	0.64
7:H:11:THR:HA	7:H:14:ARG:NH1	2.12	0.64
5:F:29:ILE:HD13	5:F:64:VAL:HG21	1.78	0.64
1:A:372:C:H4'	1:A:373:A:H5'	1.79	0.64
6:G:88:VAL:HA	6:G:152:HIS:HB2	1.79	0.64
1:A:1186:G:H21	13:N:100:TRP:C	2.00	0.64
8:I:44:ARG:O	8:I:47:VAL:HG22	1.97	0.64
3:D:25:ARG:HD3	3:D:26:ALA:H	1.62	0.64
1:A:268:U:H2'	1:A:269:C:C6	2.32	0.64
1:A:1343:G:H2'	1:A:1344:C:C6	2.32	0.64
1:A:157:U:O2'	1:A:158:G:H5'	1.96	0.64
1:A:920:U:H2'	1:A:921:U:C6	2.33	0.64
2:C:26:LYS:HG3	2:C:27:GLU:H	1.62	0.64
15:P:59:HIS:O	15:P:63:GLN:HG3	1.97	0.64
8:I:46:VAL:HA	8:I:49:GLN:HG3	1.78	0.64
10:K:17:ASP:HB3	10:K:80:ASN:ND2	2.12	0.64
1:A:1513:A:H2'	1:A:1514:G:C8	2.33	0.64
1:A:266:G:O2'	1:A:267:C:H3'	1.98	0.64
20:B:107:ARG:HH21	20:B:111:LYS:HB2	1.63	0.64
3:D:22:SER:H	3:D:109:THR:HG22	1.62	0.64
1:A:1404:C:H2'	1:A:1405:G:C8	2.32	0.64
1:A:1137:C:H1'	1:A:1138:G:N1	2.13	0.64
1:A:950:U:H2'	1:A:951:G:H8	1.62	0.64
1:A:961:U:H3	1:A:983:A:N6	1.95	0.64
13:N:50:LEU:N	13:N:51:PRO:HD2	2.12	0.64
20:B:86:CYS:HB3	20:B:88:GLN:CD	2.18	0.64
1:A:1238:A:H5'	1:A:1336:C:N4	2.12	0.64
5:F:97:THR:O	5:F:98:GLU:HB3	1.96	0.64
2:C:120:THR:HG22	2:C:188:ALA:HB2	1.80	0.64
19:T:69:ASN:H	19:T:69:ASN:ND2	1.94	0.64
4:E:82:HIS:HB2	4:E:83:PRO:HD2	1.77	0.64
14:O:28:GLN:O	14:O:32:LEU:HD23	1.98	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:I:50:PRO:HD3	8:I:79:ARG:HG3	1.77	0.64
1:A:1323:G:H2'	1:A:1324:A:H8	1.62	0.64
1:A:1144:G:H21	1:A:1146:A:H62	1.44	0.64
1:A:1158:C:O2'	20:B:131:LYS:HB2	1.98	0.64
8:I:32:ARG:HH11	8:I:37:TYR:HD1	1.46	0.64
10:K:124:LYS:O	21:U:33:ARG:NE	2.29	0.64
12:M:48:SER:HB2	12:M:51:GLN:HG3	1.78	0.64
15:P:68:SER:OG	15:P:71:VAL:HG12	1.98	0.64
7:H:37:ASN:O	7:H:41:GLU:HG2	1.97	0.64
8:I:64:ILE:H	8:I:64:ILE:HD12	1.61	0.63
1:A:1343:G:H4'	8:I:123:ARG:O	1.98	0.63
1:A:1171:A:H2'	1:A:1172:C:C6	2.33	0.63
2:C:142:ARG:HH21	2:C:143:LEU:HD11	1.63	0.63
18:S:35:ARG:NH2	18:S:52:ASN:HA	2.13	0.63
1:A:454:G:H2'	1:A:455:G:H8	1.62	0.63
1:A:478:A:H2'	1:A:479:U:O4'	1.97	0.63
1:A:1250:A:H2'	1:A:1251:A:C8	2.33	0.63
2:C:152:VAL:HB	2:C:156:LEU:HD21	1.80	0.63
1:A:269:C:H2'	1:A:270:A:H8	1.63	0.63
1:A:434:U:H3'	1:A:435:A:H8	1.63	0.63
1:A:560:A:H4'	1:A:561:U:H5"	1.80	0.63
6:G:52:ARG:HH22	6:G:121:ASN:HD21	1.44	0.63
5:F:42:TRP:HB2	5:F:59:TYR:HB2	1.80	0.63
1:A:1390:U:H2'	1:A:1391:U:C6	2.33	0.63
16:Q:45:VAL:HG11	16:Q:60:ILE:HG21	1.80	0.63
1:A:56:U:H2'	1:A:57:G:C8	2.34	0.63
6:G:2:ARG:NH1	6:G:2:ARG:HB3	2.13	0.63
1:A:41:G:H2'	1:A:42:G:C8	2.32	0.63
19:T:49:ALA:HA	19:T:52:GLU:OE2	1.99	0.63
1:A:1132:C:H2'	1:A:1133:G:H8	1.63	0.63
10:K:80:ASN:N	10:K:80:ASN:ND2	2.46	0.63
1:A:129:A:H1'	1:A:130:A:C8	2.33	0.63
4:E:156:ARG:HA	4:E:158:LYS:NZ	2.13	0.63
6:G:52:ARG:HH22	6:G:121:ASN:ND2	1.96	0.63
1:A:1134:G:C2	1:A:1135:U:H1'	2.34	0.63
1:A:140:U:H2'	1:A:141:G:H8	1.63	0.63
11:L:35:ARG:HH12	11:L:36:VAL:HG22	1.63	0.63
12:M:90:HIS:HA	12:M:108:ARG:NH2	2.14	0.63
4:E:53:ARG:HE	4:E:54:GLU:HG2	1.63	0.63
1:A:108:G:C6	19:T:9:ARG:HG2	2.34	0.63
13:N:46:LYS:NZ	18:S:10:ILE:H	1.97	0.63
1:A:1314:C:H3'	18:S:5:LYS:NZ	2.13	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:89:LEU:HD13	3:D:199:ILE:HD11	1.81	0.63
1:A:590:U:H2'	1:A:591:U:H6	1.63	0.63
1:A:1227:A:H5''	12:M:113:LYS:NZ	2.14	0.63
1:A:179:A:H2'	1:A:180:U:O4'	1.98	0.63
1:A:237:G:H2'	1:A:238:A:C8	2.33	0.63
1:A:33:A:H2'	1:A:34:C:H6	1.64	0.63
8:I:38:PHE:HZ	8:I:74:GLN:HB3	1.64	0.63
8:I:9:GLY:HA2	8:I:80:HIS:CD2	2.34	0.63
8:I:9:GLY:HA2	8:I:80:HIS:HD2	1.63	0.63
10:K:51:PHE:CZ	10:K:61:ALA:HA	2.33	0.63
4:E:125:LYS:HD2	4:E:126:ALA:H	1.64	0.63
11:L:49:ARG:HH12	11:L:88:ASP:CB	2.10	0.63
3:D:28:ASP:HA	3:D:33:ILE:CG2	2.29	0.63
16:Q:45:VAL:HG12	16:Q:46:HIS:N	2.14	0.63
1:A:501:C:H2'	1:A:502:A:C8	2.33	0.63
16:Q:79:GLU:HG3	16:Q:80:LYS:NZ	2.14	0.63
2:C:140:ALA:HB3	2:C:148:ILE:HD12	1.80	0.62
1:A:1170:A:H2'	1:A:1171:A:O4'	1.99	0.62
1:A:1226:C:H5''	12:M:101:THR:HB	1.80	0.62
4:E:64:GLU:O	4:E:68:ARG:HG2	1.98	0.62
1:A:1320:C:H5''	18:S:2:ARG:NE	2.14	0.62
9:J:66:GLU:HB3	13:N:98:ALA:HB2	1.81	0.62
1:A:176:C:H2'	1:A:177:G:N3	2.14	0.62
4:E:143:LEU:O	4:E:146:MET:HG2	1.99	0.62
16:Q:60:ILE:HG22	16:Q:74:LEU:HA	1.81	0.62
13:N:23:ARG:O	13:N:26:LEU:HD22	2.00	0.62
1:A:524:G:H2'	1:A:525:C:H6	1.65	0.62
15:P:38:PHE:HE2	15:P:51:ARG:HH11	1.47	0.62
1:A:1086:U:H3	1:A:1099:G:N2	1.84	0.62
20:B:86:CYS:HB2	20:B:221:ARG:NH1	2.14	0.62
1:A:539:A:H2'	1:A:540:G:C8	2.35	0.62
19:T:38:ILE:HD11	19:T:82:ILE:HA	1.81	0.62
1:A:244:U:O4	1:A:906:A:H1'	2.00	0.62
12:M:92:ARG:HE	12:M:92:ARG:HA	1.63	0.62
3:D:13:ARG:HG3	3:D:55:ARG:HH12	1.64	0.62
16:Q:79:GLU:HG3	16:Q:80:LYS:HZ2	1.62	0.62
1:A:1053:G:H4'	1:A:1054:C:H5'	1.82	0.62
17:R:34:GLU:HB2	21:U:18:PHE:HZ	1.64	0.62
1:A:429:U:H3'	3:D:8:LEU:HD23	1.82	0.62
8:I:94:ARG:HH11	8:I:94:ARG:HB3	1.64	0.62
3:D:160:LEU:HD22	3:D:161:ALA:N	2.14	0.62
1:A:376:G:H2'	1:A:377:G:H8	1.65	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:I:94:ARG:HA	8:I:97:LEU:HG	1.82	0.62
5:F:53:LYS:NZ	5:F:53:LYS:H	1.97	0.62
7:H:94:VAL:HG23	7:H:101:ALA:HB2	1.82	0.62
1:A:1273:C:H2'	1:A:1274:A:O4'	2.00	0.62
12:M:85:TYR:HA	12:M:88:LEU:HD12	1.79	0.62
14:O:70:LEU:HD11	14:O:77:ARG:HB2	1.82	0.62
1:A:1071:C:H2'	1:A:1072:G:C8	2.30	0.62
20:B:16:GLY:H	20:B:39:ILE:HG23	1.65	0.62
20:B:63:LYS:HG2	20:B:224:ARG:HH22	1.64	0.62
1:A:1218:C:H2'	1:A:1219:A:H8	1.63	0.62
1:A:699:C:H2'	1:A:700:G:H5''	1.82	0.62
20:B:94:ARG:HE	20:B:94:ARG:N	1.98	0.62
9:J:22:THR:OG1	9:J:72:ARG:HG3	2.00	0.62
1:A:453:G:H2'	1:A:454:G:C8	2.35	0.61
6:G:26:VAL:HG12	6:G:42:VAL:HG11	1.81	0.61
2:C:31:ASN:ND2	2:C:58:ARG:HE	1.97	0.61
1:A:1081:A:H5'	4:E:22:LYS:HD2	1.82	0.61
2:C:154:GLY:HA3	2:C:162:ALA:HB1	1.82	0.61
11:L:17:LYS:HE3	11:L:17:LYS:N	2.15	0.61
8:I:33:SER:HB3	8:I:36:GLN:HB2	1.82	0.61
20:B:14:HIS:HB2	20:B:208:ALA:HB2	1.82	0.61
20:B:75:ALA:O	20:B:79:VAL:HG23	2.00	0.61
15:P:52:LEU:HD21	15:P:75:ILE:HG23	1.81	0.61
1:A:1369:C:H2'	1:A:1370:G:C8	2.35	0.61
20:B:53:LEU:HD11	20:B:216:VAL:HG12	1.80	0.61
20:B:205:ALA:HB3	20:B:208:ALA:HB3	1.83	0.61
1:A:193:C:H2'	1:A:194:C:C6	2.34	0.61
1:A:89:U:H2'	1:A:90:C:O4'	2.01	0.61
12:M:22:TYR:HB3	12:M:69:ARG:CZ	2.31	0.61
1:A:1060:U:H5''	9:J:53:ILE:HG12	1.82	0.61
19:T:66:ILE:HG23	19:T:70:LYS:HB3	1.83	0.61
20:B:218:ALA:O	20:B:222:GLU:HG2	2.01	0.61
1:A:1152:A:H2'	1:A:1153:G:H8	1.66	0.61
12:M:95:PRO:N	12:M:108:ARG:HG2	2.14	0.61
1:A:1137:C:H1'	1:A:1138:G:C2	2.34	0.61
1:A:211:G:H2'	1:A:212:G:O4'	2.00	0.61
1:A:109:A:H4'	1:A:110:C:OP2	2.00	0.61
1:A:1450:U:H2'	1:A:1452:C:C4	2.36	0.61
18:S:29:PRO:HA	18:S:47:THR:HB	1.82	0.61
20:B:60:ALA:O	20:B:224:ARG:HD2	2.00	0.61
1:A:270:A:H2'	1:A:271:C:C6	2.35	0.61
1:A:636:U:H2'	1:A:637:C:H6	1.64	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1405:G:O2'	1:A:1406:U:H5'	2.00	0.61
14:O:36:ILE:HD11	14:O:59:MET:HB2	1.83	0.61
20:B:93:HIS:CD2	20:B:145:ASN:HB3	2.35	0.61
1:A:1435:G:H2'	1:A:1436:U:C6	2.35	0.61
1:A:813:U:H5''	1:A:816:A:N6	2.15	0.61
20:B:160:LEU:HD23	20:B:182:VAL:HG22	1.82	0.61
14:O:12:VAL:HG11	14:O:22:THR:HG22	1.83	0.61
1:A:204:G:H21	1:A:466:A:H62	1.47	0.61
1:A:493:A:H5'	1:A:494:G:OP2	2.01	0.61
1:A:1301:U:H2'	1:A:1301:U:O2	1.99	0.61
14:O:24:SER:HB3	14:O:27:VAL:HG23	1.82	0.61
12:M:53:ASP:HA	12:M:56:ARG:NH1	2.15	0.61
1:A:131:A:H2'	1:A:132:C:C6	2.36	0.61
2:C:149:LYS:HB2	2:C:168:ARG:HG3	1.82	0.61
11:L:81:ILE:HG23	11:L:94:TYR:HB3	1.82	0.61
5:F:53:LYS:HZ3	5:F:53:LYS:H	1.48	0.61
9:J:57:VAL:HG22	9:J:58:ASN:H	1.65	0.61
1:A:736:C:H2'	1:A:737:C:C6	2.36	0.61
16:Q:3:LYS:HA	16:Q:3:LYS:HE2	1.82	0.61
12:M:13:HIS:HB2	12:M:16:ILE:HG22	1.82	0.61
1:A:235:C:H2'	1:A:236:A:C8	2.36	0.61
1:A:182:A:HO2'	1:A:183:C:H3'	1.66	0.61
1:A:98:A:H2'	1:A:99:C:O4'	1.99	0.61
11:L:85:ARG:HG3	11:L:86:VAL:N	2.16	0.60
1:A:1278:G:H4'	1:A:1279:G:C5'	2.31	0.60
3:D:104:MET:SD	3:D:179:GLY:HA3	2.41	0.60
15:P:25:ARG:H	15:P:25:ARG:HD3	1.66	0.60
10:K:124:LYS:HA	21:U:34:ARG:CB	2.30	0.60
3:D:185:PRO:HB2	3:D:190:LEU:CB	2.26	0.60
1:A:320:A:H2'	1:A:321:A:C8	2.36	0.60
1:A:806:C:H2'	1:A:807:A:H8	1.66	0.60
1:A:1032:G:H5''	1:A:1032:G:N3	2.16	0.60
1:A:431:A:H2'	1:A:432:A:O4'	2.01	0.60
1:A:607:A:H2'	1:A:608:A:C8	2.37	0.60
11:L:41:PRO:HB3	11:L:49:ARG:NH1	2.14	0.60
13:N:51:PRO:HG2	13:N:52:ARG:H	1.67	0.60
10:K:34:THR:HB	10:K:40:ALA:HA	1.83	0.60
1:A:430:A:OP1	3:D:8:LEU:HB2	2.00	0.60
1:A:723:U:O4'	21:U:48:LYS:HD3	2.00	0.60
6:G:21:LEU:HD23	6:G:21:LEU:H	1.66	0.60
8:I:27:ILE:HG21	8:I:34:LEU:HD13	1.84	0.60
10:K:22:ILE:HG12	10:K:31:VAL:HG12	1.83	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:G:100:MET:O	6:G:104:VAL:HG23	2.02	0.60
4:E:104:ILE:HD11	4:E:114:LEU:HB2	1.84	0.60
1:A:1320:C:N3	18:S:35:ARG:HD3	2.16	0.60
7:H:124:ILE:HG22	7:H:125:ILE:H	1.66	0.60
1:A:472:U:H2'	1:A:473:U:C6	2.36	0.60
2:C:155:ARG:H	2:C:162:ALA:HA	1.66	0.60
1:A:966:G:H21	8:I:129:ARG:HD3	1.66	0.60
9:J:35:GLN:HG2	9:J:77:VAL:HB	1.83	0.60
1:A:662:U:H2'	1:A:663:A:C8	2.36	0.60
12:M:1:ALA:O	12:M:3:ILE:HG13	2.01	0.60
13:N:41:TRP:HD1	13:N:44:VAL:HG23	1.66	0.60
13:N:53:ASP:HA	13:N:58:ARG:HD3	1.83	0.60
3:D:71:PHE:CE1	3:D:89:LEU:HD21	2.37	0.60
1:A:763:G:H2'	1:A:764:C:C6	2.36	0.60
12:M:15:VAL:HG22	12:M:33:LEU:HD11	1.83	0.60
12:M:52:ILE:HD12	12:M:55:LEU:HD12	1.82	0.60
1:A:390:U:H2'	1:A:391:G:C8	2.36	0.60
4:E:28:ARG:NH1	4:E:30:PHE:HB3	2.16	0.60
1:A:1330:U:H2'	1:A:1331:G:H5'	1.83	0.60
17:R:34:GLU:HB2	21:U:18:PHE:CZ	2.37	0.60
1:A:241:G:O2'	1:A:242:G:H5'	2.02	0.60
19:T:4:LYS:HD2	19:T:5:SER:N	2.16	0.60
1:A:1478:U:H2'	1:A:1479:C:C6	2.36	0.60
1:A:33:A:H2'	1:A:34:C:C6	2.36	0.60
11:L:106:VAL:HG23	11:L:116:TYR:HB3	1.83	0.60
21:U:36:PHE:O	21:U:39:LYS:HD2	2.01	0.60
7:H:124:ILE:HG22	7:H:125:ILE:N	2.16	0.60
1:A:1513:A:H2'	1:A:1514:G:H8	1.65	0.60
21:U:24:LYS:HD2	21:U:25:ALA:N	2.16	0.60
16:Q:66:LEU:H	16:Q:66:LEU:HD12	1.65	0.60
20:B:23:ASN:HD22	20:B:24:PRO:CD	2.15	0.60
17:R:34:GLU:H	17:R:34:GLU:CD	2.05	0.59
3:D:93:LEU:O	3:D:96:ARG:HB2	2.02	0.59
4:E:52:ALA:HB2	4:E:61:LYS:HE2	1.84	0.59
1:A:1311:A:N7	18:S:1:PRO:HG3	2.17	0.59
1:A:958:A:H61	18:S:53:GLY:HA3	1.66	0.59
1:A:812:G:N3	1:A:812:G:H2'	2.17	0.59
1:A:602:A:O2'	1:A:603:U:H5'	2.02	0.59
11:L:43:LYS:HE2	11:L:44:PRO:HD3	1.82	0.59
1:A:21:G:H2'	1:A:22:G:C8	2.36	0.59
11:L:5:GLN:HA	11:L:8:ARG:HH21	1.67	0.59
1:A:825:A:H2'	1:A:826:C:H6	1.67	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:163:ILE:HG23	20:B:164:ASP:N	2.10	0.59
8:I:25:GLY:HA3	8:I:57:VAL:CA	2.28	0.59
3:D:90:LEU:HD21	3:D:196:GLU:HB3	1.84	0.59
3:D:77:GLU:OE1	3:D:80:ARG:HD3	2.02	0.59
2:C:13:ILE:O	2:C:14:VAL:HG22	2.02	0.59
13:N:68:ARG:HB3	13:N:68:ARG:NH1	2.17	0.59
19:T:85:LEU:HD23	19:T:86:ALA:H	1.66	0.59
1:A:1070:U:H2'	1:A:1071:C:C6	2.36	0.59
3:D:78:ALA:O	3:D:85:THR:HA	2.03	0.59
1:A:1237:C:H3'	1:A:1336:C:H41	1.67	0.59
1:A:676:A:H1'	10:K:116:PRO:HB3	1.84	0.59
18:S:69:LYS:O	18:S:72:GLU:HG2	2.02	0.59
6:G:110:ARG:CD	6:G:122:GLU:HB2	2.32	0.59
19:T:50:PHE:O	19:T:53:MET:HG3	2.02	0.59
7:H:6:ILE:HB	7:H:76:ARG:NH1	2.17	0.59
1:A:950:U:H2'	1:A:951:G:C8	2.38	0.59
14:O:8:THR:O	14:O:12:VAL:HG23	2.03	0.59
16:Q:30:HIS:CE1	16:Q:32:ILE:HG22	2.37	0.59
18:S:66:VAL:HG23	18:S:67:GLY:H	1.67	0.59
10:K:22:ILE:HD12	10:K:85:VAL:HG22	1.83	0.59
5:F:29:ILE:HG21	5:F:64:VAL:HG11	1.84	0.59
20:B:142:LYS:HA	20:B:145:ASN:OD1	2.03	0.59
8:I:79:ARG:NH2	8:I:102:PHE:HA	2.17	0.59
4:E:64:GLU:HG3	4:E:65:LYS:N	2.17	0.59
8:I:15:ALA:O	8:I:66:VAL:HG23	2.03	0.59
10:K:26:PHE:CE2	21:U:32:ARG:HD3	2.37	0.59
1:A:1030:U:H4'	1:A:1031:C:C4	2.37	0.59
1:A:358:U:H2'	1:A:359:G:C8	2.38	0.59
18:S:44:ILE:HA	18:S:61:VAL:HB	1.84	0.59
7:H:118:ALA:HB3	7:H:120:LEU:HD22	1.85	0.59
12:M:2:ARG:HB3	12:M:6:ILE:HA	1.84	0.59
1:A:86:G:H1'	1:A:87:C:O4'	2.03	0.59
19:T:79:THR:HG22	19:T:83:ASN:HD21	1.68	0.59
1:A:923:A:H2'	1:A:924:C:C6	2.38	0.59
1:A:1343:G:H2'	1:A:1344:C:H6	1.68	0.59
16:Q:16:MET:HB3	16:Q:19:SER:HB2	1.83	0.59
9:J:51:VAL:HG23	13:N:80:ARG:HB2	1.84	0.59
18:S:39:ILE:HB	18:S:66:VAL:O	2.03	0.59
1:A:96:U:H2'	1:A:97:G:C8	2.38	0.59
1:A:1034:G:H2'	1:A:1034:G:N3	2.17	0.59
20:B:42:LEU:O	20:B:46:VAL:HG12	2.02	0.59
21:U:39:LYS:N	21:U:40:PRO:HD2	2.18	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:M:47:LEU:HD22	12:M:51:GLN:HB3	1.85	0.59
11:L:60:PHE:HB3	11:L:62:VAL:HG13	1.85	0.59
16:Q:60:ILE:HG12	16:Q:72:TRP:HE3	1.68	0.59
17:R:38:ILE:HG22	17:R:58:ILE:HG21	1.85	0.59
1:A:806:C:H2'	1:A:807:A:C8	2.38	0.59
1:A:625:U:H4'	15:P:16:PHE:CZ	2.38	0.59
20:B:195:VAL:HG12	20:B:197:PHE:H	1.68	0.59
18:S:62:THR:HG22	18:S:63:ASP:H	1.67	0.59
12:M:52:ILE:HG13	12:M:56:ARG:HH11	1.68	0.59
20:B:65:LYS:HD3	20:B:89:PHE:CZ	2.38	0.59
13:N:20:PHE:CD1	13:N:24:ALA:HB2	2.38	0.59
1:A:1221:G:H4'	18:S:52:ASN:O	2.03	0.59
1:A:41:G:H2'	1:A:42:G:H8	1.66	0.59
9:J:55:PRO:HA	13:N:80:ARG:NH2	2.18	0.59
1:A:736:C:H2'	1:A:737:C:H6	1.67	0.59
1:A:918:A:H2'	1:A:919:A:C8	2.37	0.58
3:D:149:LYS:HD3	3:D:177:MET:HG3	1.84	0.58
1:A:436:C:O2'	1:A:437:U:H5'	2.03	0.58
6:G:46:LEU:O	6:G:57:GLU:HB3	2.02	0.58
1:A:605:U:H2'	1:A:606:G:H8	1.68	0.58
1:A:148:G:N3	1:A:1446:A:H2	2.00	0.58
13:N:5:MET:O	13:N:8:ARG:HB2	2.03	0.58
15:P:28:ARG:CD	15:P:29:ASN:H	2.14	0.58
1:A:409:U:H2'	1:A:410:G:C8	2.37	0.58
1:A:607:A:H2'	1:A:608:A:H8	1.66	0.58
1:A:207:C:H3'	1:A:208:U:C6	2.38	0.58
8:I:23:GLY:O	8:I:25:GLY:N	2.36	0.58
4:E:148:SER:HB2	4:E:149:PRO:HD2	1.84	0.58
1:A:999:C:H2'	1:A:1000:A:H8	1.64	0.58
20:B:168:GLU:O	20:B:172:ILE:HD12	2.03	0.58
4:E:89:THR:HG22	4:E:90:GLY:N	2.18	0.58
1:A:1287:A:H2'	1:A:1288:A:C8	2.39	0.58
1:A:1306:A:N6	1:A:1331:G:H1'	2.18	0.58
4:E:84:VAL:CG1	4:E:146:MET:HB3	2.34	0.58
3:D:29:THR:HB	3:D:30:LYS:HD3	1.84	0.58
1:A:1132:C:H2'	1:A:1133:G:C8	2.38	0.58
5:F:81:ASN:HB3	5:F:84:VAL:HG12	1.84	0.58
1:A:57:G:H2'	1:A:58:C:C6	2.39	0.58
1:A:443:C:H2'	1:A:444:G:C8	2.38	0.58
8:I:57:VAL:HB	8:I:58:GLU:OE2	2.04	0.58
18:S:43:MET:O	18:S:46:LEU:HB2	2.03	0.58
1:A:502:A:H2'	1:A:503:C:H6	1.68	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:117:VAL:O	3:D:130:ASN:HA	2.04	0.58
4:E:55:VAL:N	4:E:56:PRO:HD2	2.18	0.58
1:A:843:U:H5'	1:A:844:G:N7	2.19	0.58
1:A:620:C:N1	3:D:131:ILE:HD13	2.18	0.58
1:A:796:C:H4'	10:K:126:ARG:HH21	1.69	0.58
1:A:398:U:H2'	1:A:399:G:H8	1.68	0.58
6:G:72:VAL:HA	6:G:89:GLU:HA	1.86	0.58
11:L:49:ARG:HG2	11:L:89:LEU:HD21	1.86	0.58
7:H:54:THR:HG23	7:H:55:LYS:HG2	1.85	0.58
16:Q:5:ARG:HE	16:Q:5:ARG:HA	1.69	0.58
1:A:1317:C:H2'	1:A:1318:A:O4'	2.02	0.58
1:A:632:U:H5''	1:A:633:G:H8	1.68	0.58
14:O:35:GLN:O	14:O:39:LEU:HB2	2.03	0.58
1:A:797:C:OP1	10:K:125:LYS:HG2	2.03	0.58
1:A:796:C:OP1	10:K:127:ARG:HB3	2.04	0.58
10:K:95:THR:HG23	10:K:96:ILE:H	1.68	0.58
16:Q:16:MET:HB2	16:Q:19:SER:HB2	1.84	0.58
16:Q:8:GLN:HB3	16:Q:59:GLU:HB2	1.85	0.58
15:P:50:THR:HG22	15:P:51:ARG:N	2.19	0.58
9:J:56:HIS:O	9:J:57:VAL:HG12	2.04	0.58
1:A:1414:U:H2'	1:A:1415:G:H8	1.68	0.57
6:G:52:ARG:HH12	6:G:121:ASN:HD22	1.49	0.57
11:L:98:ARG:HB2	11:L:116:TYR:HA	1.85	0.57
20:B:65:LYS:HB2	20:B:158:ASP:N	2.18	0.57
3:D:31:CYS:O	3:D:32:LYS:HB2	2.03	0.57
11:L:79:ILE:HD12	11:L:96:THR:HG22	1.85	0.57
1:A:135:C:O2	15:P:1:MET:HB2	2.03	0.57
1:A:1186:G:H4'	8:I:111:GLU:OE1	2.04	0.57
1:A:1272:G:H2'	1:A:1273:C:C6	2.39	0.57
19:T:29:THR:HA	19:T:32:LYS:HE3	1.86	0.57
1:A:1292:G:H2'	1:A:1293:C:C6	2.39	0.57
1:A:1085:U:H3'	1:A:1086:U:C5	2.40	0.57
18:S:14:LEU:H	18:S:14:LEU:HD23	1.69	0.57
2:C:156:LEU:HD11	2:C:165:GLU:HB2	1.86	0.57
2:C:57:GLU:O	2:C:63:ILE:HA	2.05	0.57
1:A:1307:U:H2'	1:A:1308:U:C6	2.39	0.57
1:A:715:A:H2'	1:A:716:A:C8	2.40	0.57
4:E:154:ALA:HB1	7:H:65:PHE:CZ	2.39	0.57
20:B:14:HIS:HD2	20:B:202:ASN:H	1.50	0.57
1:A:16:A:O2'	1:A:17:U:H5'	2.04	0.57
1:A:1008:U:H2'	1:A:1009:U:H5''	1.87	0.57
6:G:2:ARG:CB	6:G:2:ARG:HH11	2.18	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1081:A:OP1	4:E:22:LYS:HB2	2.04	0.57
12:M:22:TYR:HB2	12:M:65:GLU:HA	1.86	0.57
1:A:1234:C:O2'	1:A:1235:U:H5'	2.04	0.57
16:Q:25:GLU:HB3	16:Q:38:LYS:HD3	1.85	0.57
1:A:420:U:H2'	1:A:422:C:C5	2.39	0.57
6:G:19:SER:OG	6:G:22:LEU:HB2	2.04	0.57
11:L:38:THR:HG22	11:L:50:LYS:HG2	1.85	0.57
1:A:708:C:H2'	1:A:709:U:C6	2.39	0.57
9:J:26:VAL:HG13	9:J:36:VAL:HG11	1.85	0.57
16:Q:80:LYS:H	16:Q:80:LYS:HE3	1.68	0.57
1:A:429:U:H1'	1:A:430:A:H5''	1.85	0.57
1:A:275:G:H5'	16:Q:15:LYS:HD3	1.86	0.57
5:F:92:THR:HG22	5:F:93:LYS:N	2.20	0.57
8:I:23:GLY:O	8:I:61:ASP:HB3	2.05	0.57
15:P:46:LYS:C	15:P:48:GLU:H	2.08	0.57
10:K:28:ASN:ND2	10:K:46:ALA:HB3	2.20	0.57
9:J:42:LEU:HD11	9:J:73:LEU:HB2	1.85	0.57
16:Q:64:ARG:HG2	16:Q:65:PRO:HD2	1.85	0.57
11:L:78:VAL:HG12	11:L:101:LEU:HD13	1.86	0.57
3:D:137:SER:HB3	3:D:138:PRO:HD2	1.86	0.57
8:I:20:ILE:HD13	8:I:85:ALA:HB3	1.87	0.57
3:D:58:GLN:O	3:D:62:ARG:HG2	2.05	0.57
9:J:8:ILE:HG13	9:J:100:ILE:HG22	1.86	0.57
1:A:254:G:OP1	16:Q:68:LYS:O	2.22	0.57
18:S:27:LYS:HB3	18:S:27:LYS:NZ	2.20	0.57
1:A:1028:C:H2'	1:A:1029:U:O4'	2.04	0.57
8:I:5:TYR:O	8:I:19:PHE:HA	2.05	0.57
18:S:29:PRO:HA	18:S:47:THR:O	2.04	0.57
6:G:108:ARG:HG2	6:G:115:MET:HE3	1.85	0.57
15:P:48:GLU:HG3	15:P:49:GLY:H	1.70	0.57
1:A:1078:U:H2'	1:A:1079:G:O4'	2.04	0.57
4:E:19:ARG:O	4:E:20:VAL:HB	2.04	0.57
1:A:437:U:H2'	1:A:438:U:O4'	2.05	0.57
1:A:1172:C:O2'	1:A:1173:U:H5'	2.04	0.57
1:A:677:U:H2'	1:A:678:U:C6	2.39	0.57
18:S:2:ARG:H	18:S:2:ARG:CZ	2.17	0.57
21:U:16:ARG:NH1	21:U:19:LYS:HE2	2.20	0.57
12:M:78:ARG:NH2	18:S:64:GLU:HB2	2.20	0.57
3:D:146:GLU:HB3	3:D:149:LYS:HE3	1.85	0.57
1:A:1162:C:H2'	1:A:1163:A:H8	1.70	0.57
18:S:35:ARG:HB2	18:S:71:GLY:HA2	1.85	0.57
5:F:81:ASN:OD1	5:F:83:ALA:HB3	2.05	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1212:U:H5'	1:A:1213:A:OP1	2.05	0.57
14:O:29:VAL:HG11	14:O:67:LEU:HD21	1.86	0.57
20:B:31:PHE:HB2	20:B:41:ASN:HA	1.87	0.57
21:U:36:PHE:CB	21:U:40:PRO:HD3	2.26	0.57
1:A:455:G:H2'	1:A:456:A:C8	2.40	0.57
1:A:633:G:H2'	1:A:634:C:C6	2.40	0.57
1:A:1221:G:O3'	18:S:76:THR:HG21	2.05	0.57
1:A:1384:C:H2'	1:A:1385:G:H8	1.70	0.57
19:T:2:ASN:ND2	19:T:3:ILE:HG13	2.20	0.57
1:A:83:C:O2'	1:A:84:U:H2'	2.04	0.57
1:A:919:A:N3	1:A:1080:A:H2	2.03	0.56
1:A:1149:C:H2'	1:A:1150:A:C8	2.40	0.56
8:I:10:ARG:HB3	8:I:15:ALA:HA	1.86	0.56
1:A:1053:G:HO2'	1:A:1199:U:H5	1.53	0.56
2:C:202:PHE:HZ	2:C:205:GLU:HG2	1.69	0.56
12:M:78:ARG:HH12	18:S:64:GLU:HG2	1.70	0.56
12:M:28:ARG:NH2	12:M:62:PHE:HB2	2.20	0.56
2:C:26:LYS:HG3	2:C:27:GLU:N	2.20	0.56
4:E:45:VAL:HG23	4:E:71:ILE:CG2	2.35	0.56
1:A:1527:U:O2'	1:A:1528:U:H5'	2.05	0.56
19:T:19:HIS:O	19:T:23:ARG:HG2	2.05	0.56
7:H:25:THR:O	7:H:26:MET:HB3	2.05	0.56
19:T:53:MET:O	19:T:57:VAL:HG22	2.05	0.56
20:B:102:ASN:O	20:B:106:VAL:HG23	2.05	0.56
5:F:6:ILE:HD12	5:F:7:VAL:N	2.21	0.56
2:C:149:LYS:HG3	2:C:168:ARG:HB2	1.87	0.56
1:A:235:C:H2'	1:A:236:A:H8	1.70	0.56
20:B:172:ILE:HG22	20:B:176:ASN:ND2	2.19	0.56
3:D:153:ARG:HG3	3:D:154:VAL:N	2.19	0.56
1:A:1219:A:H2'	1:A:1220:G:C8	2.40	0.56
2:C:14:VAL:HG11	2:C:178:ARG:HA	1.87	0.56
15:P:67:ILE:HD11	15:P:71:VAL:HG22	1.86	0.56
1:A:625:U:H4'	15:P:16:PHE:CE2	2.39	0.56
1:A:208:U:H2'	1:A:210:C:C4	2.40	0.56
1:A:833:G:H2'	1:A:834:U:C6	2.40	0.56
6:G:77:ARG:HG3	6:G:79:VAL:HG23	1.87	0.56
1:A:63:C:H5'	1:A:64:G:OP2	2.05	0.56
2:C:179:ALA:HB3	2:C:181:ILE:HD11	1.87	0.56
21:U:33:ARG:CZ	21:U:34:ARG:HG2	2.35	0.56
6:G:107:ALA:O	6:G:118:ARG:HB3	2.05	0.56
19:T:66:ILE:HG22	19:T:67:HIS:N	2.20	0.56
20:B:104:LYS:HG3	20:B:105:THR:N	2.21	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:66:ALA:HB1	5:F:67:PRO:HD2	1.87	0.56
1:A:1171:A:H2'	1:A:1172:C:H6	1.71	0.56
12:M:2:ARG:HD3	12:M:2:ARG:H	1.70	0.56
1:A:301:G:H2'	1:A:302:G:H8	1.69	0.56
1:A:412:A:H4'	1:A:413:G:OP1	2.04	0.56
1:A:678:U:H2'	1:A:679:C:H6	1.69	0.56
1:A:1241:G:H2'	1:A:1242:G:H8	1.70	0.56
1:A:408:A:OP1	3:D:111:ALA:HB3	2.04	0.56
1:A:596:A:H2'	1:A:597:G:H8	1.71	0.56
1:A:981:U:H2'	1:A:982:U:C5	2.41	0.56
8:I:82:ILE:O	8:I:86:LEU:HD13	2.05	0.56
1:A:1060:U:H2'	1:A:1061:G:H8	1.70	0.56
5:F:29:ILE:HG23	5:F:66:ALA:HB2	1.88	0.56
7:H:87:ARG:N	7:H:90:GLU:HB2	2.20	0.56
4:E:156:ARG:HD2	7:H:42:GLU:O	2.06	0.56
1:A:1342:C:H2'	1:A:1343:G:C8	2.41	0.56
14:O:43:PHE:CD1	14:O:56:LEU:HD22	2.40	0.56
1:A:107:G:O6	19:T:9:ARG:HD3	2.06	0.56
14:O:8:THR:O	14:O:11:ILE:HG22	2.06	0.56
6:G:99:ALA:O	6:G:103:ILE:HG13	2.06	0.56
10:K:45:THR:HG23	10:K:48:GLY:HA3	1.86	0.56
11:L:107:LYS:H	11:L:107:LYS:NZ	2.04	0.56
1:A:640:A:O2'	1:A:641:U:H5'	2.06	0.56
8:I:49:GLN:N	8:I:50:PRO:HD2	2.20	0.56
1:A:664:G:N2	1:A:741:G:H1	1.89	0.56
11:L:113:ARG:NH2	11:L:120:ARG:HA	2.21	0.56
3:D:123:MET:HB2	3:D:128:VAL:HA	1.87	0.56
10:K:111:ASP:CB	21:U:19:LYS:HE3	2.35	0.56
8:I:25:GLY:HA2	8:I:60:LEU:O	2.06	0.56
10:K:80:ASN:H	10:K:80:ASN:ND2	2.00	0.56
1:A:1391:U:H2'	1:A:1392:G:H8	1.68	0.56
7:H:113:ARG:HA	7:H:116:ARG:NH1	2.20	0.56
1:A:677:U:H2'	1:A:678:U:H6	1.70	0.56
1:A:140:U:H2'	1:A:141:G:C8	2.41	0.56
1:A:1329:A:O2'	1:A:1330:U:H5'	2.05	0.56
9:J:52:LEU:HA	9:J:62:ARG:HA	1.87	0.56
1:A:1367:C:H5'	9:J:62:ARG:NH1	2.21	0.56
5:F:93:LYS:O	5:F:94:HIS:HB2	2.06	0.56
20:B:27:LYS:HA	20:B:30:ILE:HD12	1.87	0.56
5:F:29:ILE:HG22	5:F:34:GLY:HA3	1.85	0.56
1:A:923:A:H2'	1:A:924:C:H6	1.71	0.56
10:K:19:VAL:HG12	10:K:82:GLU:HB2	1.88	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:337:G:H2'	1:A:338:A:H8	1.69	0.56
1:A:188:C:H2'	1:A:189:A:O4'	2.05	0.56
1:A:783:C:O2'	1:A:784:A:H5'	2.06	0.56
4:E:43:GLY:C	4:E:44:ARG:HD3	2.27	0.56
3:D:2:ARG:HB3	3:D:114:ARG:NH2	2.20	0.56
1:A:686:U:O4	1:A:703:G:H1'	2.06	0.56
5:F:88:MET:HE1	17:R:60:ARG:HB3	1.87	0.56
1:A:60:A:H4'	1:A:61:G:OP1	2.05	0.56
20:B:61:SER:HA	20:B:223:GLY:O	2.06	0.56
1:A:839:C:H2'	1:A:840:C:O4'	2.06	0.56
1:A:195:A:H1'	1:A:222:C:O2'	2.06	0.56
1:A:784:A:H2'	1:A:785:G:C8	2.41	0.56
1:A:1321:U:H2'	1:A:1322:C:C5	2.41	0.56
16:Q:31:PRO:O	16:Q:32:ILE:HB	2.06	0.56
1:A:207:C:H2'	1:A:208:U:O4'	2.05	0.56
1:A:709:U:H2'	1:A:710:G:C8	2.41	0.56
1:A:1244:G:H2'	1:A:1245:C:C6	2.41	0.56
13:N:68:ARG:HH12	13:N:70:HIS:HB2	1.71	0.55
8:I:18:VAL:HG13	8:I:64:ILE:HG13	1.88	0.55
20:B:68:PHE:HA	20:B:161:PHE:O	2.06	0.55
9:J:5:ARG:HG2	9:J:79:PRO:HD3	1.88	0.55
1:A:455:G:H2'	1:A:456:A:H8	1.70	0.55
1:A:1338:G:H2'	1:A:1339:A:C8	2.40	0.55
3:D:102:TYR:HE1	3:D:109:THR:HA	1.71	0.55
7:H:101:ALA:HB3	7:H:112:ASP:HB3	1.88	0.55
7:H:28:SER:HB3	7:H:57:GLU:O	2.06	0.55
5:F:79:ARG:NH2	5:F:87:SER:HB3	2.20	0.55
4:E:85:LYS:HE3	4:E:94:PHE:HB2	1.89	0.55
3:D:18:LEU:HB3	3:D:63:ILE:HG12	1.88	0.55
5:F:36:ILE:HD12	5:F:36:ILE:H	1.71	0.55
15:P:67:ILE:HG13	15:P:71:VAL:HG13	1.88	0.55
7:H:110:MET:HG3	7:H:115:ALA:HB2	1.87	0.55
4:E:44:ARG:HA	4:E:71:ILE:O	2.07	0.55
1:A:1069:C:H4'	1:A:1192:C:O2	2.07	0.55
1:A:272:C:H2'	1:A:273:U:C6	2.41	0.55
1:A:201:G:O2'	1:A:202:G:H5'	2.06	0.55
5:F:16:GLU:CD	5:F:16:GLU:H	2.08	0.55
13:N:71:GLY:O	13:N:79:SER:HA	2.05	0.55
12:M:15:VAL:O	12:M:19:THR:HG23	2.07	0.55
6:G:55:LYS:HB2	6:G:59:GLU:OE1	2.07	0.55
3:D:138:PRO:HA	3:D:181:PHE:CD2	2.39	0.55
1:A:1173:U:H2'	1:A:1174:G:C8	2.41	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:U:49:ALA:O	21:U:52:VAL:HG12	2.06	0.55
6:G:76:SER:HA	6:G:84:TYR:O	2.06	0.55
10:K:110:THR:HA	21:U:19:LYS:NZ	2.21	0.55
6:G:59:GLU:O	6:G:63:VAL:HG23	2.06	0.55
1:A:405:U:O4	3:D:1:ALA:HA	2.07	0.55
3:D:43:ARG:HD2	3:D:44:LYS:H	1.70	0.55
1:A:1005:A:H2'	1:A:1006:G:O4'	2.07	0.55
12:M:106:ARG:HA	12:M:106:ARG:HH11	1.72	0.55
5:F:40:GLU:OE1	5:F:100:SER:HB2	2.06	0.55
1:A:1283:U:H2'	1:A:1284:C:C6	2.41	0.55
3:D:98:ASP:HB3	3:D:132:ALA:HB1	1.89	0.55
2:C:134:LYS:HA	2:C:167:TYR:CE2	2.42	0.55
11:L:43:LYS:CE	11:L:44:PRO:HD3	2.37	0.55
1:A:709:U:H2'	1:A:710:G:H8	1.70	0.55
1:A:1347:G:N2	1:A:1373:G:H2'	2.21	0.55
9:J:10:LEU:O	9:J:71:LEU:HA	2.06	0.55
21:U:16:ARG:NE	21:U:16:ARG:HA	2.05	0.55
8:I:23:GLY:H	8:I:61:ASP:H	1.55	0.55
19:T:38:ILE:HD11	19:T:82:ILE:HG22	1.87	0.55
9:J:65:TYR:HB3	13:N:95:LEU:HD11	1.88	0.55
16:Q:68:LYS:C	16:Q:70:LYS:H	2.10	0.55
3:D:22:SER:CB	3:D:109:THR:HG22	2.37	0.55
8:I:94:ARG:HB3	8:I:94:ARG:NH1	2.20	0.55
5:F:79:ARG:HH21	5:F:87:SER:HB3	1.71	0.55
1:A:1254:A:H2'	1:A:1255:G:C8	2.41	0.55
19:T:15:LYS:HA	19:T:18:LYS:HE3	1.87	0.55
18:S:50:VAL:O	18:S:57:VAL:HG22	2.06	0.55
20:B:22:TRP:HZ3	20:B:27:LYS:HB2	1.71	0.55
3:D:194:ILE:HG23	3:D:194:ILE:O	2.06	0.55
1:A:922:G:N3	1:A:1398:A:H2	2.05	0.55
12:M:44:ILE:CD1	12:M:44:ILE:H	2.16	0.55
11:L:56:LEU:HD21	11:L:81:ILE:HG13	1.89	0.55
1:A:335:C:H2'	1:A:336:A:H8	1.72	0.55
2:C:63:ILE:HD11	2:C:94:ALA:CB	2.36	0.55
15:P:4:ILE:O	15:P:71:VAL:HG11	2.07	0.55
17:R:44:THR:HB	17:R:46:THR:HG22	1.89	0.55
10:K:33:ILE:HG12	10:K:69:CYS:SG	2.47	0.55
1:A:415:A:H3'	1:A:416:G:H8	1.71	0.55
1:A:237:G:H5''	16:Q:26:ARG:NH2	2.22	0.55
1:A:1308:U:H3'	12:M:97:ARG:HH11	1.72	0.55
14:O:32:LEU:O	14:O:36:ILE:HG12	2.07	0.55
1:A:398:U:H2'	1:A:399:G:C8	2.42	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:730:G:O2'	1:A:766:A:H5'	2.07	0.55
8:I:98:ARG:NE	8:I:103:VAL:HG21	2.22	0.55
2:C:91:ALA:HB2	2:C:98:ALA:H	1.71	0.55
19:T:54:GLN:N	19:T:55:PRO:HD2	2.21	0.55
13:N:79:SER:OG	13:N:82:LYS:HG2	2.05	0.55
1:A:1239:A:H4'	1:A:1240:U:C5'	2.37	0.55
16:Q:11:VAL:HG23	16:Q:56:ASP:O	2.08	0.55
1:A:1206:G:C4'	2:C:192:TYR:HA	2.37	0.55
1:A:737:C:H2'	1:A:738:C:H6	1.71	0.55
14:O:73:LYS:O	14:O:74:ASP:HB2	2.07	0.55
6:G:15:PRO:HG2	6:G:43:TYR:OH	2.07	0.55
9:J:17:LEU:HD22	9:J:96:VAL:CG1	2.35	0.54
1:A:1288:A:N1	1:A:1371:G:H1'	2.21	0.54
21:U:8:ASN:O	21:U:9:GLU:HB2	2.06	0.54
1:A:1231:G:H5'	8:I:128:LYS:HE2	1.88	0.54
5:F:17:GLN:O	5:F:21:MET:HG3	2.07	0.54
1:A:1494:G:N7	23:A:2367:LLL:N32	2.55	0.54
20:B:207:ARG:HH11	20:B:207:ARG:HA	1.73	0.54
13:N:60:ARG:HG3	13:N:62:ARG:HG3	1.88	0.54
2:C:72:PRO:O	2:C:76:ILE:HG12	2.07	0.54
18:S:10:ILE:HG22	18:S:38:THR:N	2.20	0.54
1:A:1141:C:H2'	1:A:1142:G:H8	1.72	0.54
11:L:31:GLY:HA3	11:L:54:VAL:CG1	2.37	0.54
1:A:1163:A:H2'	1:A:1164:G:H8	1.73	0.54
1:A:254:G:O2'	1:A:255:G:H5'	2.07	0.54
1:A:441:A:H61	1:A:493:A:N6	2.05	0.54
8:I:28:VAL:HA	8:I:32:ARG:O	2.07	0.54
1:A:708:C:H2'	1:A:709:U:H6	1.72	0.54
1:A:77:A:H2'	1:A:78:A:C8	2.43	0.54
1:A:1060:U:C4'	9:J:54:SER:HB2	2.36	0.54
1:A:1252:A:H2'	1:A:1253:G:O4'	2.07	0.54
6:G:134:VAL:HB	6:G:137:ARG:HH21	1.72	0.54
1:A:922:G:H4'	4:E:24:VAL:HA	1.87	0.54
7:H:58:LEU:CD2	7:H:60:LEU:HB2	2.37	0.54
14:O:81:LEU:HD23	14:O:85:LEU:HD13	1.89	0.54
11:L:107:LYS:O	11:L:107:LYS:HD2	2.08	0.54
20:B:204:ASP:O	20:B:209:VAL:HG13	2.07	0.54
19:T:67:HIS:CE1	19:T:68:LYS:HE3	2.42	0.54
1:A:975:A:H4'	1:A:976:G:O5'	2.07	0.54
4:E:37:VAL:HG11	4:E:113:VAL:HG12	1.89	0.54
1:A:1262:C:N4	1:A:1273:C:H42	2.05	0.54
6:G:71:THR:HG22	6:G:141:HIS:CE1	2.42	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:272:C:H2'	1:A:273:U:H6	1.71	0.54
9:J:85:ASP:HA	9:J:88:MET:SD	2.47	0.54
1:A:1432:G:H1'	1:A:1468:A:N6	2.23	0.54
2:C:39:ARG:NH1	2:C:56:ILE:HD12	2.23	0.54
1:A:1148:U:H5'	8:I:6:TYR:OH	2.08	0.54
5:F:46:GLN:HG3	5:F:47:LEU:H	1.72	0.54
9:J:76:ILE:O	9:J:76:ILE:HD12	2.08	0.54
1:A:467:U:O2	1:A:467:U:H2'	2.08	0.54
1:A:770:C:O2'	1:A:771:G:H5'	2.07	0.54
21:U:24:LYS:CD	21:U:25:ALA:H	2.21	0.54
16:Q:74:LEU:HD22	16:Q:75:VAL:N	2.23	0.54
1:A:32:A:H2'	1:A:33:A:C8	2.43	0.54
1:A:1226:C:H5''	12:M:101:THR:CB	2.37	0.54
1:A:1201:A:H8	1:A:1201:A:H5''	1.73	0.54
9:J:55:PRO:HA	13:N:80:ARG:HH21	1.73	0.54
1:A:1028:C:H3'	1:A:1029:U:H6	1.72	0.54
1:A:201:G:O2'	1:A:469:C:H4'	2.07	0.54
6:G:24:LYS:O	6:G:28:ILE:HG12	2.08	0.54
15:P:36:VAL:O	15:P:36:VAL:HG13	2.08	0.54
7:H:76:ARG:HG3	7:H:77:VAL:H	1.72	0.54
1:A:190:A:O5'	1:A:190:A:H8	1.91	0.54
1:A:814:A:H5'	1:A:1511:G:H4'	1.90	0.54
1:A:793:U:O2	1:A:1516:G:H4'	2.07	0.54
1:A:1520:C:H2'	1:A:1521:C:C6	2.42	0.54
1:A:545:C:H5''	3:D:68:GLU:HG2	1.89	0.54
1:A:1175:G:O2'	1:A:1176:A:H5'	2.08	0.54
2:C:106:ARG:H	2:C:106:ARG:HD2	1.72	0.54
10:K:110:THR:HA	21:U:19:LYS:HZ2	1.73	0.54
12:M:38:ILE:HG13	12:M:55:LEU:HD21	1.89	0.54
1:A:1250:A:O3'	8:I:68:GLY:HA2	2.08	0.54
19:T:66:ILE:HG13	19:T:70:LYS:HE3	1.89	0.54
5:F:67:PRO:O	5:F:70:VAL:HG22	2.07	0.54
11:L:54:VAL:CG2	11:L:79:ILE:HD11	2.38	0.54
1:A:1019:A:H2'	1:A:1020:G:C8	2.43	0.54
12:M:87:GLY:HA2	12:M:90:HIS:HD2	1.72	0.54
1:A:189:A:H2'	1:A:190:A:C8	2.43	0.54
12:M:92:ARG:NE	12:M:92:ARG:HA	2.23	0.54
1:A:1054:C:H1'	1:A:1196:A:C5	2.42	0.54
10:K:12:ARG:N	10:K:76:TYR:HA	2.23	0.54
6:G:45:ALA:O	6:G:49:LEU:HD23	2.07	0.54
1:A:939:G:H5''	6:G:101:ARG:NH1	2.23	0.54
8:I:43:ALA:O	8:I:46:VAL:HG22	2.07	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:522:C:H2'	1:A:523:A:O4'	2.08	0.54
20:B:62:ARG:H	20:B:62:ARG:HD2	1.71	0.54
2:C:148:ILE:O	2:C:168:ARG:HG2	2.08	0.54
1:A:182:A:H1'	1:A:183:C:C5	2.43	0.54
1:A:335:C:H2'	1:A:336:A:C8	2.43	0.54
15:P:52:LEU:HD21	15:P:75:ILE:HG12	1.89	0.54
10:K:70:ALA:C	10:K:72:ALA:H	2.11	0.54
3:D:116:LEU:O	3:D:121:ALA:HB3	2.07	0.54
8:I:34:LEU:HD21	8:I:48:ARG:NE	2.18	0.54
6:G:125:ASP:OD2	6:G:130:LYS:HD2	2.08	0.54
21:U:28:LEU:HD23	21:U:29:ALA:N	2.23	0.54
1:A:1152:A:H2'	1:A:1153:G:C8	2.42	0.54
1:A:813:U:H5''	1:A:816:A:H62	1.74	0.54
1:A:323:U:H2'	1:A:324:G:O4'	2.08	0.54
1:A:512:U:H2'	1:A:513:C:C6	2.43	0.54
12:M:5:GLY:C	12:M:7:ASN:H	2.11	0.54
1:A:470:C:H2'	1:A:471:U:C6	2.42	0.54
20:B:44:LYS:O	20:B:47:PRO:HD2	2.08	0.53
18:S:14:LEU:O	18:S:18:VAL:HG12	2.07	0.53
18:S:62:THR:HB	18:S:64:GLU:OE1	2.08	0.53
19:T:57:VAL:HB	19:T:71:ALA:HB1	1.89	0.53
3:D:25:ARG:HH12	3:D:30:LYS:HE3	1.73	0.53
3:D:29:THR:HG22	3:D:30:LYS:H	1.73	0.53
1:A:465:A:O2'	1:A:466:A:H3'	2.08	0.53
11:L:36:VAL:HA	11:L:52:CYS:HA	1.89	0.53
1:A:840:C:H3'	1:A:842:U:OP2	2.09	0.53
6:G:72:VAL:HG12	6:G:89:GLU:HA	1.90	0.53
1:A:300:A:H2'	1:A:301:G:O4'	2.07	0.53
1:A:939:G:H5''	6:G:101:ARG:HH12	1.73	0.53
8:I:19:PHE:O	8:I:62:LEU:HA	2.08	0.53
10:K:95:THR:HG23	10:K:96:ILE:N	2.23	0.53
3:D:196:GLU:O	3:D:199:ILE:HG12	2.08	0.53
20:B:119:GLN:HA	20:B:122:ASP:HB3	1.89	0.53
3:D:155:LYS:HG2	3:D:156:ALA:N	2.23	0.53
1:A:8:A:H61	3:D:53:GLN:HE22	1.56	0.53
1:A:1308:U:H2'	1:A:1309:G:H8	1.73	0.53
8:I:7:GLY:HA3	8:I:81:GLY:O	2.07	0.53
20:B:13:VAL:HG11	20:B:207:ARG:HG2	1.91	0.53
1:A:418:C:H2'	1:A:419:C:H6	1.72	0.53
8:I:62:LEU:HD23	8:I:64:ILE:HD11	1.91	0.53
1:A:412:A:H61	3:D:29:THR:CG2	2.21	0.53
1:A:204:G:H2'	1:A:205:A:C8	2.43	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:H:6:ILE:HD11	7:H:31:LEU:HD23	1.91	0.53
3:D:53:GLN:HB3	3:D:202:LEU:HB2	1.89	0.53
12:M:96:VAL:C	12:M:98:GLY:H	2.12	0.53
1:A:987:G:O2'	1:A:988:G:H5'	2.08	0.53
10:K:36:ARG:HH11	10:K:36:ARG:HG3	1.74	0.53
19:T:53:MET:HA	19:T:56:ILE:HD12	1.90	0.53
1:A:840:C:C2	1:A:842:U:H4'	2.43	0.53
1:A:1476:A:H2'	1:A:1477:U:O4'	2.08	0.53
1:A:430:A:P	3:D:6:PRO:HA	2.49	0.53
1:A:796:C:H4'	10:K:126:ARG:NH2	2.23	0.53
1:A:512:U:O2'	1:A:513:C:H5'	2.09	0.53
10:K:58:THR:HB	10:K:59:PRO:HD2	1.89	0.53
13:N:9:GLU:OE2	13:N:60:ARG:HG2	2.08	0.53
8:I:5:TYR:HD1	8:I:20:ILE:HG22	1.72	0.53
5:F:6:ILE:HG23	5:F:62:MET:HB3	1.91	0.53
13:N:50:LEU:HG	13:N:51:PRO:HD3	1.89	0.53
18:S:65:MET:HG3	18:S:73:PHE:CZ	2.44	0.53
11:L:81:ILE:CG2	11:L:94:TYR:HB3	2.39	0.53
1:A:1390:U:H2'	1:A:1391:U:H6	1.72	0.53
1:A:212:G:H2'	1:A:213:G:H8	1.72	0.53
17:R:52:ARG:HB3	17:R:56:ARG:NH2	2.24	0.53
1:A:458:U:H2'	1:A:459:A:H8	1.74	0.53
20:B:49:PHE:HA	20:B:212:TYR:OH	2.08	0.53
3:D:27:ILE:O	3:D:28:ASP:HB3	2.08	0.53
1:A:1138:G:N3	1:A:1138:G:H3'	2.24	0.53
1:A:737:C:H2'	1:A:738:C:C6	2.44	0.53
8:I:98:ARG:HA	8:I:103:VAL:HG22	1.90	0.53
1:A:215:C:H2'	1:A:216:U:C6	2.44	0.53
1:A:270:A:H2'	1:A:271:C:H6	1.74	0.53
4:E:156:ARG:HB3	7:H:43:GLY:O	2.09	0.53
3:D:152:SER:HA	3:D:155:LYS:HD3	1.91	0.53
20:B:45:THR:HG23	20:B:200:PRO:HG2	1.91	0.53
8:I:41:GLU:C	8:I:43:ALA:H	2.11	0.53
20:B:14:HIS:CD2	20:B:202:ASN:H	2.27	0.53
3:D:59:LYS:HE3	3:D:194:ILE:HD12	1.90	0.53
1:A:978:A:H5'	1:A:1362:A:N6	2.24	0.53
1:A:484:G:H4'	1:A:485:U:C5'	2.39	0.53
1:A:1020:G:N3	1:A:1020:G:H2'	2.24	0.53
1:A:502:A:H2'	1:A:503:C:C6	2.43	0.53
1:A:766:A:H2	1:A:1525:G:N3	2.06	0.53
3:D:160:LEU:H	3:D:160:LEU:CD1	2.17	0.53
5:F:38:ARG:NH2	5:F:63:ASN:HD21	2.07	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:148:GLY:O	20:B:151:LYS:HG2	2.09	0.53
11:L:54:VAL:HG22	11:L:79:ILE:HD11	1.91	0.53
14:O:78:TYR:CZ	14:O:82:ILE:HD11	2.44	0.53
9:J:52:LEU:HD12	9:J:52:LEU:H	1.74	0.53
1:A:928:G:H2'	1:A:929:G:H8	1.73	0.53
1:A:575:G:H4'	1:A:576:C:O5'	2.08	0.53
8:I:51:LEU:CB	8:I:56:MET:HG2	2.28	0.53
10:K:31:VAL:HG23	10:K:44:ALA:HB3	1.91	0.53
5:F:42:TRP:HE3	5:F:45:ARG:HH12	1.57	0.53
1:A:16:A:O2'	1:A:1080:A:H4'	2.08	0.53
1:A:238:A:C2'	1:A:239:U:H5''	2.38	0.53
11:L:36:VAL:HG12	11:L:52:CYS:HB2	1.91	0.53
1:A:250:A:H1'	1:A:252:U:C5	2.44	0.53
1:A:437:U:H1'	3:D:115:GLN:NE2	2.24	0.53
3:D:43:ARG:NH2	3:D:45:PRO:HA	2.24	0.53
1:A:939:G:H5''	6:G:101:ARG:NH2	2.24	0.53
6:G:74:VAL:HA	6:G:87:PRO:HA	1.89	0.53
10:K:22:ILE:HD13	10:K:95:THR:CG2	2.39	0.52
11:L:85:ARG:HA	11:L:93:ARG:HA	1.91	0.52
19:T:66:ILE:HG21	19:T:71:ALA:HB2	1.90	0.52
1:A:1316:G:H22	1:A:1318:A:H3'	1.70	0.52
1:A:413:G:O6	3:D:32:LYS:HG3	2.09	0.52
2:C:42:LEU:O	2:C:46:LEU:HB2	2.09	0.52
1:A:8:A:C5	3:D:205:LYS:HA	2.43	0.52
9:J:10:LEU:HD11	9:J:25:ILE:HD12	1.91	0.52
3:D:122:ILE:O	3:D:128:VAL:HG23	2.09	0.52
16:Q:3:LYS:NZ	16:Q:4:ILE:H	2.00	0.52
12:M:19:THR:HA	12:M:24:VAL:HG23	1.91	0.52
13:N:50:LEU:N	13:N:51:PRO:CD	2.71	0.52
1:A:1151:A:O2'	1:A:1152:A:H8	1.90	0.52
1:A:1011:C:H2'	1:A:1012:A:C8	2.44	0.52
1:A:412:A:H1'	1:A:413:G:C8	2.44	0.52
1:A:598:U:H2'	1:A:599:C:C6	2.44	0.52
1:A:208:U:H2'	1:A:210:C:N3	2.25	0.52
5:F:86:ARG:HD2	17:R:63:TYR:O	2.08	0.52
2:C:171:ARG:HB2	2:C:171:ARG:NH1	2.24	0.52
8:I:29:ILE:HA	8:I:64:ILE:HB	1.91	0.52
10:K:79:LYS:HB2	10:K:80:ASN:HD22	1.74	0.52
1:A:1314:C:H2'	1:A:1315:U:C6	2.44	0.52
4:E:131:ASN:HD21	4:E:133:ILE:HB	1.74	0.52
1:A:412:A:H1'	1:A:413:G:H8	1.74	0.52
1:A:239:U:C5'	1:A:239:U:H6	2.22	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1001:C:H2'	1:A:1002:G:C8	2.44	0.52
2:C:71:ARG:O	2:C:75:VAL:HG23	2.08	0.52
1:A:384:G:H2'	1:A:385:C:H6	1.72	0.52
1:A:824:G:O2'	1:A:825:A:H5'	2.09	0.52
1:A:624:C:H2'	1:A:625:U:C6	2.44	0.52
10:K:37:GLN:HB2	10:K:39:ASN:HD22	1.75	0.52
7:H:8:ASP:OD1	7:H:12:ARG:HD2	2.09	0.52
20:B:20:ARG:HD2	20:B:37:VAL:HA	1.91	0.52
19:T:70:LYS:HA	19:T:73:ARG:NH1	2.24	0.52
1:A:919:A:O2'	1:A:920:U:H5'	2.09	0.52
1:A:482:A:H2'	1:A:483:C:O4'	2.10	0.52
7:H:103:VAL:HG22	7:H:124:ILE:HA	1.92	0.52
1:A:624:C:H2'	1:A:625:U:H6	1.75	0.52
10:K:126:ARG:HE	10:K:126:ARG:HA	1.73	0.52
2:C:67:ILE:HD12	2:C:100:ILE:HD11	1.91	0.52
2:C:61:LYS:O	2:C:96:VAL:HB	2.09	0.52
12:M:73:SER:O	12:M:77:LYS:HB2	2.09	0.52
4:E:17:VAL:HG23	4:E:33:THR:O	2.08	0.52
1:A:22:G:H2'	1:A:23:C:C6	2.44	0.52
16:Q:32:ILE:HG23	16:Q:33:TYR:CD2	2.45	0.52
1:A:229:U:H2'	1:A:230:G:C8	2.45	0.52
1:A:542:G:O2'	1:A:543:U:H5'	2.09	0.52
8:I:56:MET:SD	8:I:57:VAL:N	2.82	0.52
7:H:125:ILE:HG22	7:H:126:CYS:SG	2.50	0.52
1:A:1342:C:H2'	1:A:1343:G:H8	1.74	0.52
3:D:158:LEU:H	3:D:158:LEU:HD12	1.75	0.52
1:A:1320:C:H41	18:S:36:ARG:HB3	1.72	0.52
1:A:1521:C:H2'	1:A:1522:U:C6	2.44	0.52
3:D:123:MET:HG3	3:D:127:ARG:N	2.25	0.52
1:A:922:G:H2'	1:A:923:A:H8	1.75	0.52
20:B:79:VAL:O	20:B:83:ALA:HB3	2.10	0.52
20:B:115:ASP:O	20:B:119:GLN:HG2	2.09	0.52
3:D:147:LYS:HD3	3:D:148:ALA:N	2.25	0.52
17:R:33:THR:HG22	17:R:39:VAL:HG12	1.90	0.52
1:A:1219:A:H2'	1:A:1220:G:H8	1.74	0.52
1:A:1308:U:H3'	12:M:97:ARG:NH1	2.25	0.52
1:A:833:G:H2'	1:A:834:U:H6	1.73	0.52
1:A:390:U:H2'	1:A:391:G:H8	1.75	0.52
13:N:58:ARG:HH11	13:N:58:ARG:HB3	1.74	0.52
11:L:20:VAL:HG23	11:L:20:VAL:O	2.10	0.52
2:C:49:ALA:O	2:C:71:ARG:HB2	2.10	0.52
1:A:409:U:OP1	3:D:23:GLY:HA3	2.09	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:P:54:LEU:HD21	15:P:75:ILE:HG23	1.92	0.52
1:A:718:A:H5'	10:K:118:ASN:CG	2.30	0.52
1:A:420:U:H2'	1:A:422:C:C4	2.44	0.52
1:A:692:U:O2	1:A:694:A:H5''	2.10	0.52
1:A:1437:A:H2'	1:A:1438:G:H8	1.75	0.52
1:A:105:G:H2'	1:A:106:C:C6	2.45	0.52
1:A:1040:U:H2'	1:A:1041:G:C8	2.45	0.52
8:I:61:ASP:C	8:I:62:LEU:HD13	2.30	0.52
20:B:101:THR:HG22	20:B:174:GLU:OE1	2.09	0.52
1:A:464:U:H2'	1:A:466:A:OP2	2.10	0.52
1:A:1121:U:O2'	1:A:1122:U:H5'	2.08	0.52
1:A:328:C:H4'	1:A:329:A:C5'	2.39	0.52
1:A:674:G:H2'	1:A:675:A:H8	1.75	0.52
1:A:141:G:H2'	1:A:142:G:O4'	2.10	0.52
10:K:51:PHE:HZ	10:K:61:ALA:HA	1.75	0.52
1:A:965:U:OP1	1:A:1198:G:H5''	2.10	0.52
1:A:89:U:H2'	1:A:90:C:C6	2.45	0.52
2:C:91:ALA:CB	2:C:98:ALA:H	2.23	0.52
1:A:1521:C:H2'	1:A:1522:U:H6	1.74	0.52
1:A:216:U:H2'	1:A:217:C:C6	2.45	0.52
20:B:138:ARG:HG3	20:B:141:GLU:OE1	2.10	0.52
1:A:1127:G:H5'	1:A:1280:A:O2'	2.09	0.52
1:A:1289:A:H3'	1:A:1290:G:H8	1.75	0.52
1:A:1014:A:H4'	18:S:13:HIS:CD2	2.45	0.52
5:F:3:HIS:CG	5:F:92:THR:HG23	2.45	0.52
19:T:38:ILE:HD13	19:T:85:LEU:HD13	1.90	0.52
18:S:5:LYS:O	18:S:6:LYS:HD2	2.10	0.52
13:N:52:ARG:NH1	13:N:58:ARG:HH21	2.08	0.52
1:A:373:A:H2'	1:A:374:A:H8	1.73	0.52
12:M:13:HIS:HB2	12:M:16:ILE:CG2	2.39	0.52
4:E:37:VAL:HA	4:E:47:PHE:HA	1.92	0.52
1:A:254:G:H4'	16:Q:19:SER:OG	2.10	0.52
6:G:14:ASP:HB3	6:G:18:GLY:N	2.25	0.52
1:A:1491:G:C5	23:A:2367:LLL:H21	2.44	0.52
4:E:9:GLU:O	4:E:40:ASP:HA	2.10	0.52
1:A:1458:G:H5''	19:T:25:SER:HB2	1.92	0.52
2:C:76:ILE:HA	2:C:83:VAL:CG2	2.31	0.51
2:C:130:ARG:HA	2:C:133:MET:HE2	1.91	0.51
1:A:203:G:N2	1:A:205:A:H61	2.08	0.51
1:A:204:G:N2	1:A:466:A:N6	2.56	0.51
4:E:39:GLY:HA3	4:E:116:VAL:HB	1.92	0.51
10:K:108:ASN:HD21	21:U:6:ARG:HD2	1.74	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:51:ILE:O	5:F:51:ILE:HG23	2.10	0.51
10:K:22:ILE:HD13	10:K:95:THR:HG21	1.93	0.51
4:E:132:PRO:O	4:E:136:VAL:HG12	2.10	0.51
9:J:26:VAL:O	9:J:30:LYS:HG3	2.10	0.51
7:H:77:VAL:HG23	7:H:126:CYS:HA	1.93	0.51
1:A:720:C:H5''	17:R:40:PRO:HA	1.92	0.51
1:A:69:G:N2	1:A:71:A:H62	2.09	0.51
1:A:1028:C:H3'	1:A:1029:U:C6	2.44	0.51
1:A:301:G:H2'	1:A:302:G:C8	2.45	0.51
5:F:100:SER:HA	17:R:23:LYS:CE	2.40	0.51
1:A:586:C:O2'	1:A:878:A:H4'	2.10	0.51
1:A:1073:U:H2'	1:A:1074:G:H8	1.74	0.51
7:H:17:GLN:HE21	7:H:62:LEU:HD23	1.74	0.51
1:A:407:U:O2'	3:D:112:GLU:HG3	2.11	0.51
12:M:24:VAL:HG12	12:M:28:ARG:HD2	1.92	0.51
1:A:947:G:H2'	1:A:948:C:C6	2.45	0.51
2:C:142:ARG:NH2	2:C:143:LEU:HD21	2.25	0.51
1:A:1053:G:N7	1:A:1200:C:H5''	2.25	0.51
3:D:104:MET:SD	3:D:142:VAL:HB	2.50	0.51
7:H:55:LYS:HZ2	7:H:55:LYS:HA	1.75	0.51
1:A:706:A:H4'	10:K:30:ILE:HD11	1.91	0.51
1:A:939:G:H5''	6:G:101:ARG:HH22	1.75	0.51
20:B:26:MET:HE1	20:B:186:VAL:HG23	1.92	0.51
12:M:78:ARG:HH22	18:S:64:GLU:HB2	1.76	0.51
5:F:61:LEU:HD12	5:F:63:ASN:OD1	2.10	0.51
6:G:26:VAL:HA	6:G:42:VAL:HG21	1.93	0.51
1:A:658:C:H2'	1:A:659:U:C6	2.41	0.51
1:A:538:G:OP2	11:L:111:GLN:HB2	2.11	0.51
10:K:127:ARG:HG3	10:K:127:ARG:HH11	1.75	0.51
7:H:74:ILE:HG13	7:H:128:VAL:HG22	1.92	0.51
1:A:74:A:H2'	1:A:75:G:H8	1.75	0.51
1:A:896:C:O2'	1:A:897:C:H5'	2.11	0.51
1:A:728:A:H2'	1:A:729:A:C8	2.45	0.51
20:B:46:VAL:CG1	20:B:47:PRO:HD3	2.30	0.51
1:A:864:A:H2'	1:A:865:A:C8	2.46	0.51
13:N:47:LEU:C	13:N:49:THR:H	2.12	0.51
20:B:130:LYS:HA	20:B:130:LYS:NZ	2.25	0.51
8:I:117:LEU:HD22	8:I:123:ARG:HG2	1.92	0.51
1:A:1163:A:H2'	1:A:1164:G:C8	2.46	0.51
1:A:253:A:H2'	1:A:254:G:H8	1.76	0.51
3:D:145:ARG:HB3	3:D:147:LYS:CD	2.40	0.51
16:Q:30:HIS:ND1	16:Q:32:ILE:HG22	2.26	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:13:VAL:CG1	20:B:207:ARG:HG2	2.40	0.51
1:A:1469:C:H2'	1:A:1470:U:O4'	2.10	0.51
4:E:144:GLU:HG2	4:E:144:GLU:O	2.11	0.51
8:I:56:MET:HG3	8:I:57:VAL:HG23	1.93	0.51
20:B:16:GLY:HA3	20:B:39:ILE:HA	1.93	0.51
20:B:221:ARG:HG3	20:B:222:GLU:OE1	2.10	0.51
1:A:280:C:O2	16:Q:39:ARG:HG3	2.09	0.51
1:A:91:U:H2'	1:A:92:U:H6	1.75	0.51
20:B:95:TRP:HZ2	20:B:100:LEU:HD13	1.75	0.51
1:A:1090:U:H2'	1:A:1091:U:C6	2.46	0.51
1:A:1417:G:N2	1:A:1482:G:H2'	2.25	0.51
1:A:394:G:H2'	1:A:395:C:H6	1.76	0.51
20:B:46:VAL:HA	20:B:49:PHE:HD2	1.76	0.51
21:U:40:PRO:HG2	21:U:41:THR:H	1.74	0.51
6:G:125:ASP:HB3	6:G:130:LYS:HB3	1.92	0.51
5:F:38:ARG:HB3	5:F:63:ASN:HB2	1.91	0.51
8:I:32:ARG:NH1	8:I:37:TYR:HA	2.25	0.51
3:D:13:ARG:CG	3:D:55:ARG:HH12	2.23	0.51
1:A:22:G:H4'	1:A:885:G:C8	2.45	0.51
1:A:418:C:H2'	1:A:419:C:C6	2.45	0.51
5:F:18:VAL:O	5:F:22:ILE:HG13	2.11	0.51
20:B:46:VAL:HA	20:B:49:PHE:CD2	2.46	0.51
15:P:28:ARG:HD3	15:P:29:ASN:HD22	1.76	0.51
2:C:185:THR:HG22	2:C:198:LYS:HA	1.93	0.51
4:E:136:VAL:HG13	4:E:137:ARG:H	1.76	0.51
1:A:1124:G:H3'	9:J:37:ARG:HH12	1.75	0.51
13:N:14:ALA:O	13:N:18:LYS:HG3	2.10	0.51
1:A:1169:A:H2'	1:A:1170:A:C8	2.45	0.51
1:A:956:U:O2'	1:A:957:U:H5'	2.11	0.51
7:H:28:SER:OG	7:H:56:PRO:HB2	2.10	0.51
1:A:860:A:H2'	1:A:861:G:O4'	2.10	0.51
1:A:159:G:H1	1:A:163:C:N4	2.09	0.51
1:A:1308:U:H2'	1:A:1309:G:C8	2.46	0.51
1:A:958:A:N6	18:S:53:GLY:HA3	2.26	0.51
1:A:54:C:H2'	1:A:352:C:H41	1.74	0.51
1:A:642:A:H2'	1:A:643:C:H6	1.76	0.51
20:B:55:GLU:HG3	20:B:197:PHE:CZ	2.46	0.51
8:I:20:ILE:HA	8:I:62:LEU:HB3	1.93	0.51
20:B:86:CYS:HB2	20:B:221:ARG:HH12	1.75	0.51
1:A:958:A:P	18:S:54:ARG:HH22	2.34	0.51
18:S:35:ARG:HB2	18:S:71:GLY:CA	2.40	0.51
1:A:986:U:H2'	1:A:987:G:O4'	2.11	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1073:U:H2'	1:A:1074:G:C8	2.46	0.51
6:G:113:LYS:HB2	6:G:117:LEU:HD12	1.91	0.51
1:A:981:U:H4'	13:N:60:ARG:CD	2.37	0.50
1:A:979:C:H1'	1:A:1317:C:H41	1.76	0.50
1:A:370:C:H2'	1:A:371:A:H8	1.74	0.50
1:A:279:A:C5'	1:A:280:C:H3'	2.41	0.50
1:A:34:C:H2'	1:A:35:G:C8	2.46	0.50
1:A:751:U:H4'	14:O:24:SER:HA	1.93	0.50
1:A:1033:G:C2	1:A:1034:G:H1'	2.46	0.50
1:A:1035:A:H2'	1:A:1036:A:C8	2.45	0.50
9:J:92:LEU:HD22	9:J:92:LEU:H	1.76	0.50
19:T:27:MET:O	19:T:31:ILE:HG13	2.11	0.50
1:A:487:A:H3'	1:A:488:C:H6	1.75	0.50
20:B:26:MET:O	20:B:30:ILE:HG13	2.10	0.50
21:U:3:ILE:CG2	21:U:19:LYS:HD2	2.41	0.50
12:M:52:ILE:HG13	12:M:56:ARG:NH1	2.25	0.50
13:N:50:LEU:H	13:N:51:PRO:CD	2.22	0.50
1:A:769:G:O2'	1:A:770:C:H5'	2.12	0.50
11:L:106:VAL:CG2	11:L:116:TYR:HB3	2.42	0.50
1:A:147:G:H2'	1:A:148:G:C8	2.46	0.50
1:A:1515:G:O2'	1:A:1516:G:H5'	2.12	0.50
1:A:546:A:P	3:D:68:GLU:HB3	2.51	0.50
5:F:86:ARG:NH1	17:R:64:LEU:HD12	2.26	0.50
15:P:19:VAL:HB	15:P:37:GLY:O	2.11	0.50
1:A:317:U:H2'	1:A:318:G:H8	1.76	0.50
12:M:3:ILE:HA	12:M:56:ARG:HG2	1.92	0.50
1:A:336:A:O2'	1:A:337:G:H5'	2.10	0.50
1:A:36:C:H4'	11:L:118:VAL:O	2.10	0.50
1:A:35:G:H2'	1:A:36:C:H6	1.75	0.50
1:A:1017:U:H2'	1:A:1018:G:C8	2.46	0.50
1:A:403:C:O2'	1:A:404:G:H5'	2.11	0.50
1:A:74:A:H2'	1:A:75:G:C8	2.45	0.50
1:A:426:U:H4'	3:D:39:GLN:HA	1.93	0.50
1:A:343:U:O2'	1:A:344:A:H2'	2.10	0.50
11:L:72:ASN:ND2	11:L:104:SER:HB3	2.27	0.50
19:T:43:LYS:HA	19:T:85:LEU:HD11	1.94	0.50
2:C:126:ARG:NH2	2:C:190:THR:HG23	2.19	0.50
8:I:119:LYS:C	8:I:121:ARG:H	2.15	0.50
11:L:26:CYS:SG	11:L:29:LYS:HE2	2.51	0.50
1:A:678:U:H4'	1:A:778:G:OP1	2.12	0.50
1:A:560:A:H5'	1:A:566:G:N2	2.25	0.50
10:K:51:PHE:HB2	10:K:55:ARG:HB3	1.92	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:92:U:H2'	1:A:93:U:C6	2.46	0.50
1:A:208:U:H2'	1:A:210:C:C2	2.46	0.50
1:A:834:U:H2'	1:A:835:U:C6	2.46	0.50
1:A:1483:A:H2'	1:A:1484:C:O4'	2.11	0.50
1:A:858:G:O6	1:A:869:G:H3'	2.12	0.50
21:U:13:VAL:HG13	21:U:13:VAL:O	2.12	0.50
8:I:21:LYS:HG2	8:I:22:PRO:HD2	1.92	0.50
1:A:242:G:H2'	1:A:243:A:H5''	1.93	0.50
11:L:85:ARG:HD2	11:L:93:ARG:HG3	1.92	0.50
1:A:386:C:C2'	1:A:387:U:H5'	2.42	0.50
1:A:908:A:O2'	1:A:909:A:H5'	2.12	0.50
14:O:43:PHE:CE1	14:O:56:LEU:HD22	2.46	0.50
1:A:1272:G:H2'	1:A:1273:C:H6	1.77	0.50
1:A:1033:G:N3	1:A:1034:G:H1'	2.27	0.50
1:A:1091:U:H2'	1:A:1093:A:OP2	2.11	0.50
1:A:1297:G:H1'	1:A:1298:U:H5	1.76	0.50
1:A:295:C:H2'	1:A:296:U:C6	2.46	0.50
20:B:127:LYS:C	20:B:127:LYS:HD2	2.32	0.50
20:B:165:ALA:HB3	20:B:186:VAL:HG12	1.93	0.50
20:B:65:LYS:HA	20:B:89:PHE:HE1	1.77	0.50
2:C:129:PHE:CE2	2:C:156:LEU:HD13	2.46	0.50
1:A:465:A:H2'	1:A:466:A:H3'	1.94	0.50
1:A:438:U:H4'	3:D:119:HIS:HD2	1.76	0.50
1:A:719:C:H2'	17:R:38:ILE:CD1	2.42	0.50
1:A:1336:C:H4'	1:A:1337:G:O5'	2.12	0.50
20:B:95:TRP:CZ2	20:B:100:LEU:HD13	2.46	0.50
1:A:1508:A:H2'	1:A:1509:C:C6	2.46	0.50
1:A:747:A:H2'	1:A:748:G:O4'	2.12	0.50
1:A:1363:A:H2'	1:A:1363:A:N3	2.27	0.50
5:F:3:HIS:N	5:F:3:HIS:CD2	2.79	0.50
20:B:51:GLU:O	20:B:55:GLU:HG2	2.11	0.50
1:A:1313:U:OP2	18:S:5:LYS:HA	2.11	0.50
1:A:1021:A:H2'	1:A:1022:A:O4'	2.12	0.50
1:A:515:G:H2'	1:A:516:U:C6	2.47	0.50
6:G:85:GLN:OE1	6:G:85:GLN:HA	2.11	0.50
20:B:163:ILE:CG2	20:B:164:ASP:H	2.15	0.50
21:U:42:THR:HB	21:U:46:ARG:HH21	1.77	0.50
21:U:42:THR:CB	21:U:46:ARG:HH21	2.25	0.50
13:N:46:LYS:HZ3	18:S:9:PHE:HA	1.77	0.50
20:B:63:LYS:HG2	20:B:224:ARG:NH2	2.26	0.50
1:A:369:G:O2'	1:A:370:C:H5'	2.11	0.50
3:D:115:GLN:HG3	3:D:119:HIS:CE1	2.47	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:155:LYS:H	3:D:155:LYS:HD2	1.77	0.50
3:D:106:PHE:CD1	3:D:144:ILE:HD11	2.47	0.50
1:A:1493:A:H5''	1:A:1494:G:OP2	2.11	0.50
1:A:394:G:H2'	1:A:395:C:C6	2.47	0.50
3:D:169:TRP:CE2	3:D:185:PRO:HB3	2.46	0.50
13:N:51:PRO:CB	13:N:54:SER:HB3	2.40	0.50
2:C:51:VAL:HA	2:C:69:THR:HA	1.94	0.50
1:A:552:U:H4'	11:L:82:ARG:HG2	1.94	0.50
1:A:1370:G:O2'	1:A:1371:G:H5'	2.12	0.50
1:A:825:A:H2'	1:A:826:C:C6	2.47	0.50
18:S:27:LYS:HB3	18:S:27:LYS:HZ2	1.76	0.50
1:A:510:A:N3	1:A:543:U:H1'	2.26	0.50
1:A:868:C:H2'	1:A:869:G:O4'	2.12	0.50
1:A:827:U:H2'	1:A:870:U:O4	2.12	0.50
1:A:1125:U:O2'	1:A:1126:U:H2'	2.12	0.50
6:G:136:LYS:O	6:G:140:VAL:HG23	2.12	0.50
1:A:1049:U:H2'	13:N:2:LYS:HD3	1.93	0.49
20:B:20:ARG:CZ	20:B:20:ARG:HB3	2.41	0.49
5:F:38:ARG:HH21	5:F:63:ASN:HD21	1.60	0.49
1:A:191:G:H2'	1:A:192:A:C8	2.47	0.49
1:A:194:C:O2'	1:A:195:A:H5'	2.12	0.49
1:A:1131:G:O2'	1:A:1132:C:H5'	2.12	0.49
1:A:333:U:H2'	1:A:334:C:C6	2.46	0.49
20:B:69:VAL:HB	20:B:162:VAL:HG23	1.94	0.49
8:I:49:GLN:C	8:I:51:LEU:H	2.15	0.49
20:B:205:ALA:O	20:B:209:VAL:HG22	2.11	0.49
4:E:131:ASN:O	4:E:135:VAL:HG23	2.12	0.49
1:A:204:G:O5'	1:A:204:G:H8	1.96	0.49
16:Q:57:VAL:HB	16:Q:79:GLU:HB3	1.95	0.49
1:A:714:G:N2	1:A:777:A:H1'	2.27	0.49
1:A:91:U:H2'	1:A:92:U:C6	2.47	0.49
6:G:71:THR:HG23	6:G:72:VAL:HG22	1.95	0.49
20:B:76:SER:HA	20:B:92:ASN:HB2	1.94	0.49
16:Q:58:VAL:HG12	16:Q:77:VAL:HG13	1.93	0.49
1:A:836:G:OP2	17:R:49:LYS:HE2	2.11	0.49
1:A:1101:A:H61	20:B:101:THR:HG21	1.76	0.49
19:T:4:LYS:HE3	19:T:6:ALA:H	1.76	0.49
11:L:20:VAL:HB	11:L:94:TYR:CE1	2.47	0.49
6:G:63:VAL:HG12	6:G:127:ALA:HB1	1.94	0.49
18:S:27:LYS:HG3	18:S:28:LYS:HD3	1.94	0.49
1:A:1064:G:OP1	1:A:1386:G:H4'	2.13	0.49
4:E:44:ARG:HD2	4:E:72:ASN:ND2	2.26	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:77:A:H2'	1:A:78:A:H8	1.76	0.49
1:A:802:A:H2'	1:A:803:G:O4'	2.12	0.49
1:A:355:C:O2'	1:A:356:A:H5'	2.12	0.49
1:A:26:A:N6	1:A:558:G:H1'	2.27	0.49
1:A:555:U:H2'	1:A:556:C:H6	1.77	0.49
5:F:69:GLU:O	5:F:73:GLU:HG2	2.12	0.49
8:I:30:ASN:ND2	8:I:65:THR:HA	2.27	0.49
1:A:815:A:H4'	1:A:817:C:C4	2.47	0.49
20:B:83:ALA:HB3	20:B:90:PHE:HB3	1.94	0.49
1:A:963:G:H21	9:J:56:HIS:CE1	2.30	0.49
1:A:26:A:H61	1:A:558:G:H1'	1.76	0.49
1:A:169:C:O2'	1:A:170:U:H5'	2.12	0.49
10:K:106:ILE:HD11	10:K:109:ILE:CG1	2.43	0.49
8:I:4:GLN:HE21	8:I:21:LYS:NZ	2.11	0.49
1:A:162:A:H2'	1:A:163:C:O4'	2.13	0.49
2:C:13:ILE:N	2:C:13:ILE:HD13	2.27	0.49
12:M:89:ARG:NH2	12:M:94:LEU:HD12	2.26	0.49
2:C:188:ALA:HB3	2:C:195:ILE:HB	1.94	0.49
1:A:621:A:H2'	1:A:622:A:C8	2.48	0.49
1:A:653:U:C4	7:H:55:LYS:HE2	2.48	0.49
1:A:643:C:H2'	1:A:644:U:H6	1.76	0.49
1:A:1472:U:H2'	1:A:1473:G:H8	1.78	0.49
20:B:19:THR:O	20:B:37:VAL:HA	2.13	0.49
3:D:169:TRP:CD2	3:D:185:PRO:HB3	2.48	0.49
1:A:1099:G:H2'	1:A:1100:C:O4'	2.13	0.49
1:A:1103:C:H5''	20:B:96:LEU:HD12	1.95	0.49
10:K:19:VAL:HG23	10:K:34:THR:HG23	1.93	0.49
11:L:35:ARG:NH1	11:L:36:VAL:H	2.09	0.49
1:A:1308:U:OP2	12:M:97:ARG:HB2	2.12	0.49
1:A:221:C:O2'	1:A:222:C:H5'	2.12	0.49
20:B:131:LYS:HG3	20:B:132:GLU:N	2.27	0.49
1:A:215:C:H2'	1:A:216:U:H6	1.78	0.49
11:L:49:ARG:HH12	11:L:88:ASP:HB3	1.75	0.49
1:A:132:C:H5''	19:T:68:LYS:NZ	2.28	0.49
9:J:15:HIS:O	9:J:18:ILE:HG22	2.12	0.49
13:N:52:ARG:HH11	13:N:58:ARG:HH21	1.60	0.49
2:C:110:LEU:HD22	2:C:145:ALA:HB2	1.93	0.49
7:H:123:GLU:HG2	7:H:124:ILE:O	2.12	0.49
1:A:1512:U:H2'	1:A:1513:A:H8	1.78	0.49
11:L:23:LEU:O	11:L:25:ALA:N	2.46	0.49
1:A:961:U:H3	1:A:983:A:H62	1.60	0.49
1:A:1053:G:N7	1:A:1199:U:H3'	2.27	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:O:70:LEU:HD12	14:O:78:TYR:HB2	1.94	0.49
1:A:1330:U:C2'	1:A:1331:G:H5'	2.42	0.49
1:A:99:C:H2'	24:A:2620:HOH:O	2.12	0.49
1:A:22:G:H2'	1:A:23:C:H6	1.78	0.49
1:A:1036:A:H2'	1:A:1037:C:O4'	2.13	0.49
14:O:74:ASP:OD1	14:O:76:ALA:HB3	2.12	0.49
1:A:1176:A:H2'	1:A:1177:G:O4'	2.12	0.49
1:A:1203:C:H4'	13:N:66:THR:HG22	1.95	0.49
1:A:1210:C:H1'	1:A:1214:C:O2'	2.12	0.49
1:A:572:A:N3	1:A:917:G:H1'	2.28	0.49
18:S:29:PRO:CA	18:S:47:THR:HB	2.41	0.49
5:F:47:LEU:HD21	5:F:57:ALA:HB3	1.94	0.49
3:D:47:LEU:HD23	3:D:52:VAL:HA	1.93	0.49
4:E:113:VAL:HG23	4:E:114:LEU:N	2.27	0.49
20:B:172:ILE:H	20:B:172:ILE:HD12	1.77	0.49
1:A:220:G:O2'	1:A:221:C:H5'	2.12	0.49
20:B:107:ARG:HG3	20:B:108:GLN:N	2.28	0.49
1:A:560:A:N1	1:A:566:G:H5'	2.27	0.49
1:A:207:C:H3'	1:A:208:U:C5	2.47	0.49
2:C:111:ASP:OD2	2:C:114:LEU:HG	2.12	0.49
9:J:80:THR:HG22	9:J:82:LYS:HG2	1.94	0.49
2:C:8:GLY:HA2	2:C:11:LEU:HG	1.94	0.49
15:P:20:VAL:HG23	15:P:34:GLU:O	2.13	0.49
20:B:20:ARG:HA	20:B:20:ARG:NE	2.27	0.49
8:I:6:TYR:HB2	8:I:19:PHE:CE1	2.48	0.49
1:A:1271:A:H5'	1:A:1314:C:H5''	1.95	0.49
13:N:48:GLN:O	13:N:51:PRO:HD2	2.13	0.49
12:M:44:ILE:HD12	12:M:44:ILE:N	2.25	0.49
1:A:252:U:H2'	1:A:253:A:C8	2.48	0.49
12:M:90:HIS:CE1	12:M:96:VAL:HG21	2.48	0.49
11:L:7:VAL:HG22	16:Q:33:TYR:HD1	1.77	0.49
1:A:1298:U:H2'	6:G:113:LYS:HZ1	1.77	0.49
1:A:1111:A:O2'	1:A:1112:C:H5'	2.13	0.49
13:N:6:LYS:O	13:N:10:VAL:HG23	2.13	0.49
21:U:44:ARG:HG3	21:U:44:ARG:HH11	1.78	0.49
2:C:76:ILE:HD13	2:C:83:VAL:HG21	1.95	0.49
11:L:86:VAL:HG11	11:L:89:LEU:HD23	1.95	0.49
13:N:31:SER:HA	13:N:40:ARG:HA	1.94	0.49
1:A:1343:G:C1'	8:I:122:ARG:HH12	2.24	0.49
16:Q:46:HIS:HB2	16:Q:70:LYS:HE2	1.95	0.49
7:H:113:ARG:HH21	7:H:114:ALA:HA	1.78	0.49
1:A:1149:C:OP2	8:I:10:ARG:NH1	2.46	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:L:68:GLY:HA3	11:L:106:VAL:CG2	2.43	0.49
1:A:379:C:O2'	1:A:380:G:H5'	2.13	0.49
17:R:44:THR:C	17:R:46:THR:H	2.16	0.49
1:A:1062:U:H2'	1:A:1063:C:C6	2.47	0.49
1:A:65:A:H8	1:A:200:G:H4'	1.77	0.49
13:N:9:GLU:O	13:N:13:VAL:HG23	2.13	0.48
3:D:7:LYS:O	3:D:20:LEU:HD12	2.13	0.48
1:A:131:A:H2'	1:A:132:C:H6	1.76	0.48
5:F:61:LEU:HD12	5:F:62:MET:H	1.78	0.48
1:A:279:A:H5'	1:A:281:G:O4'	2.12	0.48
1:A:1319:A:H4'	1:A:1320:C:OP1	2.12	0.48
1:A:1200:C:C3'	1:A:1201:A:H5'	2.43	0.48
5:F:15:SER:HA	5:F:18:VAL:HG23	1.95	0.48
1:A:1299:A:H3'	1:A:1299:A:OP2	2.13	0.48
6:G:68:VAL:CG2	6:G:126:ALA:HB1	2.43	0.48
12:M:23:GLY:HA3	12:M:64:VAL:HG12	1.94	0.48
9:J:87:LEU:H	9:J:87:LEU:HD22	1.78	0.48
13:N:42:ASN:O	13:N:46:LYS:HG2	2.14	0.48
18:S:44:ILE:HD12	18:S:63:ASP:HA	1.95	0.48
13:N:26:LEU:CD2	13:N:27:LYS:H	2.19	0.48
1:A:1077:G:N2	1:A:1079:G:H3'	2.28	0.48
9:J:40:ILE:HD12	9:J:73:LEU:HD12	1.94	0.48
1:A:846:G:H2'	1:A:847:G:C8	2.48	0.48
1:A:1463:U:H2'	1:A:1464:U:C6	2.48	0.48
1:A:692:U:C2	1:A:694:A:H5''	2.48	0.48
1:A:373:A:H1'	1:A:481:G:H1'	1.95	0.48
2:C:156:LEU:CD1	2:C:165:GLU:HB2	2.42	0.48
1:A:599:C:O2'	1:A:600:A:H5'	2.13	0.48
1:A:1123:U:O2'	1:A:1124:G:H5'	2.13	0.48
1:A:252:U:H2'	1:A:253:A:H8	1.78	0.48
1:A:552:U:H2'	1:A:553:A:H8	1.76	0.48
1:A:490:C:H2'	1:A:491:G:C8	2.47	0.48
1:A:955:U:H1'	1:A:1227:A:H62	1.78	0.48
14:O:39:LEU:HD23	14:O:56:LEU:HD13	1.95	0.48
1:A:1319:A:OP2	18:S:4:LEU:HD21	2.13	0.48
14:O:11:ILE:HD11	14:O:30:ALA:HB1	1.95	0.48
1:A:972:C:P	9:J:59:LYS:HD3	2.54	0.48
1:A:618:C:H1'	15:P:14:ARG:NH1	2.28	0.48
12:M:33:LEU:HD22	12:M:38:ILE:HB	1.95	0.48
13:N:26:LEU:O	13:N:30:ILE:N	2.47	0.48
18:S:1:PRO:O	18:S:2:ARG:HB2	2.14	0.48
1:A:435:A:N3	1:A:435:A:H2'	2.29	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:555:U:H2'	1:A:556:C:C6	2.49	0.48
10:K:86:LYS:HB2	10:K:113:THR:HA	1.95	0.48
19:T:67:HIS:ND1	19:T:68:LYS:HG2	2.27	0.48
13:N:30:ILE:HD12	13:N:30:ILE:N	2.28	0.48
13:N:40:ARG:NH1	18:S:6:LYS:HB2	2.27	0.48
1:A:818:G:C3'	1:A:819:A:H5''	2.43	0.48
1:A:370:C:O2'	1:A:371:A:H5'	2.14	0.48
2:C:130:ARG:HD2	2:C:133:MET:HE3	1.94	0.48
2:C:137:VAL:HA	2:C:148:ILE:CD1	2.42	0.48
1:A:464:U:H3'	1:A:466:A:OP1	2.13	0.48
7:H:6:ILE:HD12	7:H:35:ILE:CD1	2.43	0.48
1:A:376:G:OP1	15:P:5:ARG:HB2	2.13	0.48
11:L:35:ARG:O	11:L:53:ARG:N	2.46	0.48
6:G:50:ALA:HA	6:G:55:LYS:O	2.13	0.48
1:A:57:G:H2'	1:A:58:C:H6	1.76	0.48
6:G:2:ARG:CB	6:G:2:ARG:NH1	2.76	0.48
7:H:94:VAL:CG2	7:H:101:ALA:HB2	2.44	0.48
20:B:93:HIS:HD2	20:B:145:ASN:HB3	1.77	0.48
11:L:14:LYS:HG2	11:L:15:VAL:N	2.28	0.48
14:O:68:ASP:O	14:O:72:ARG:HG3	2.14	0.48
1:A:977:A:N6	1:A:1224:U:O5'	2.46	0.48
1:A:960:U:O2'	1:A:1223:C:H4'	2.13	0.48
20:B:19:THR:HG23	20:B:20:ARG:N	2.23	0.48
1:A:465:A:C2'	1:A:466:A:H3'	2.43	0.48
3:D:33:ILE:HG13	3:D:34:GLU:N	2.28	0.48
11:L:79:ILE:C	11:L:101:LEU:HD12	2.33	0.48
2:C:2:GLN:H	2:C:2:GLN:HE21	1.61	0.48
1:A:812:G:O2'	1:A:813:U:H6	1.97	0.48
1:A:49:U:O2'	1:A:50:A:H2'	2.13	0.48
1:A:547:A:H4'	1:A:548:G:O5'	2.13	0.48
1:A:364:A:H2'	1:A:365:U:O2	2.13	0.48
1:A:1181:G:H1'	1:A:1182:G:C5	2.48	0.48
20:B:18:GLN:HB2	20:B:188:THR:OG1	2.13	0.48
1:A:923:A:OP1	4:E:25:LYS:HB3	2.14	0.48
1:A:481:G:O2'	1:A:482:A:H8	1.97	0.48
1:A:1240:U:O4	6:G:29:LEU:HG	2.13	0.48
6:G:144:ALA:C	6:G:146:ALA:H	2.17	0.48
1:A:58:C:O2'	1:A:59:A:H5'	2.13	0.48
1:A:1149:C:H2'	1:A:1150:A:H8	1.77	0.48
1:A:586:C:C2'	1:A:587:G:H5'	2.44	0.48
15:P:20:VAL:HG23	15:P:35:ARG:HA	1.95	0.48
1:A:1246:A:H2'	1:A:1247:U:O4'	2.14	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:M:43:LYS:O	12:M:46:GLU:HG3	2.13	0.48
1:A:113:G:H2'	1:A:114:U:H6	1.79	0.48
1:A:1118:U:H2'	1:A:1119:C:H6	1.78	0.48
20:B:17:HIS:CG	20:B:18:GLN:H	2.31	0.48
20:B:18:GLN:O	20:B:37:VAL:HG23	2.13	0.48
1:A:1092:A:H5''	6:G:3:ARG:NH1	2.29	0.48
20:B:221:ARG:HH11	20:B:221:ARG:CB	2.26	0.48
9:J:6:ILE:O	9:J:75:ASP:HA	2.13	0.48
1:A:598:U:H2'	1:A:599:C:H6	1.79	0.48
1:A:635:A:H2'	1:A:636:U:C6	2.49	0.48
1:A:620:C:C2	3:D:131:ILE:HD13	2.49	0.48
1:A:652:U:H1'	1:A:653:U:C5	2.48	0.48
1:A:1508:A:H2'	1:A:1509:C:H6	1.77	0.48
15:P:20:VAL:HG21	15:P:32:PHE:CG	2.48	0.48
1:A:1057:G:H4'	2:C:196:GLY:H	1.79	0.48
1:A:1095:U:H2'	1:A:1096:C:C6	2.48	0.48
1:A:656:G:O2'	1:A:657:U:H5'	2.14	0.48
1:A:934:C:H5''	24:A:2418:HOH:O	2.14	0.48
20:B:212:TYR:HA	20:B:215:ALA:HB3	1.95	0.48
20:B:20:ARG:HE	20:B:38:HIS:CD2	2.31	0.48
1:A:1060:U:H2'	1:A:1061:G:C8	2.48	0.48
5:F:36:ILE:N	5:F:36:ILE:HD12	2.28	0.48
17:R:51:GLN:CA	17:R:51:GLN:HE21	2.19	0.48
1:A:482:A:C2	1:A:483:C:H1'	2.49	0.48
3:D:151:GLN:HB2	3:D:154:VAL:HG23	1.95	0.48
10:K:30:ILE:HG22	10:K:45:THR:HA	1.96	0.48
1:A:1458:G:H2'	1:A:1459:G:H8	1.79	0.48
11:L:66:ILE:HD12	11:L:66:ILE:N	2.29	0.48
13:N:97:LYS:HB3	13:N:97:LYS:NZ	2.29	0.48
13:N:79:SER:O	13:N:83:VAL:HG23	2.14	0.48
1:A:890:G:O2'	1:A:906:A:N6	2.47	0.48
1:A:1413:A:O2'	1:A:1414:U:H5'	2.14	0.48
2:C:19:SER:HB3	2:C:21:TRP:NE1	2.27	0.48
6:G:88:VAL:HA	6:G:152:HIS:CB	2.42	0.48
15:P:74:LEU:O	15:P:78:VAL:HG12	2.14	0.48
1:A:1034:G:H2'	1:A:1035:A:H5'	1.95	0.48
5:F:100:SER:HA	17:R:23:LYS:HD3	1.95	0.48
1:A:556:C:O2'	1:A:557:G:H5'	2.13	0.48
3:D:191:SER:O	3:D:192:ALA:HB2	2.13	0.48
3:D:169:TRP:HB2	3:D:183:ARG:O	2.14	0.47
3:D:56:GLU:HG2	3:D:198:LEU:HB3	1.95	0.47
11:L:21:PRO:C	11:L:23:LEU:H	2.17	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:255:G:H2'	1:A:256:U:C6	2.49	0.47
2:C:46:LEU:HD12	2:C:75:VAL:HG22	1.96	0.47
9:J:56:HIS:H	13:N:80:ARG:NH2	2.11	0.47
15:P:23:ASP:O	15:P:26:ASN:HB2	2.15	0.47
1:A:1298:U:H4'	1:A:1299:A:C4	2.49	0.47
6:G:109:LYS:HE2	6:G:109:LYS:HA	1.96	0.47
13:N:60:ARG:HE	13:N:62:ARG:HG2	1.78	0.47
18:S:48:ILE:HB	18:S:59:VAL:HG21	1.96	0.47
3:D:160:LEU:HA	3:D:163:GLN:HG3	1.96	0.47
12:M:78:ARG:HB3	12:M:78:ARG:CZ	2.44	0.47
12:M:33:LEU:HD13	12:M:39:ALA:O	2.14	0.47
12:M:52:ILE:HA	12:M:55:LEU:HG	1.96	0.47
19:T:61:ALA:HA	19:T:67:HIS:N	2.24	0.47
2:C:148:ILE:HG12	2:C:149:LYS:N	2.29	0.47
3:D:12:ARG:HA	3:D:33:ILE:HD12	1.94	0.47
2:C:96:VAL:HB	2:C:97:PRO:HD2	1.96	0.47
1:A:731:G:O2'	1:A:732:C:H5'	2.13	0.47
19:T:77:ASN:O	19:T:81:GLN:HG3	2.14	0.47
1:A:952:U:H2'	1:A:953:G:C8	2.49	0.47
3:D:18:LEU:HD22	3:D:18:LEU:H	1.79	0.47
6:G:107:ALA:HA	6:G:110:ARG:HD2	1.96	0.47
20:B:102:ASN:OD1	20:B:105:THR:HB	2.15	0.47
6:G:78:ARG:HA	6:G:83:THR:HA	1.97	0.47
3:D:34:GLU:HG3	3:D:34:GLU:O	2.15	0.47
20:B:185:ILE:HG12	20:B:199:ILE:HG21	1.97	0.47
1:A:1000:A:H2'	1:A:1001:C:C6	2.50	0.47
7:H:113:ARG:HA	7:H:116:ARG:HH12	1.77	0.47
1:A:1248:A:H2	8:I:71:ILE:HD11	1.79	0.47
1:A:955:U:H2'	1:A:956:U:O4'	2.15	0.47
18:S:2:ARG:NH1	18:S:2:ARG:H	2.12	0.47
1:A:715:A:H2'	1:A:716:A:H8	1.79	0.47
1:A:1180:A:OP1	8:I:104:THR:HG22	2.14	0.47
1:A:1180:A:P	8:I:98:ARG:HH22	2.37	0.47
18:S:20:LYS:O	18:S:23:GLU:HG3	2.13	0.47
13:N:60:ARG:NE	13:N:69:PRO:HB3	2.29	0.47
8:I:48:ARG:HB3	8:I:52:GLU:OE1	2.13	0.47
20:B:209:VAL:HG23	20:B:210:THR:H	1.79	0.47
20:B:86:CYS:SG	20:B:87:ASP:N	2.88	0.47
3:D:96:ARG:NH1	3:D:133:SER:HA	2.29	0.47
4:E:157:GLY:O	4:E:158:LYS:HB2	2.14	0.47
1:A:947:G:H2'	1:A:948:C:H6	1.80	0.47
16:Q:66:LEU:O	16:Q:67:SER:HB2	2.15	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:105:G:H2'	1:A:106:C:H6	1.79	0.47
7:H:17:GLN:OE1	7:H:69:ALA:HB1	2.14	0.47
1:A:643:C:OP1	7:H:30:LYS:HD2	2.14	0.47
1:A:333:U:H2'	1:A:334:C:H6	1.78	0.47
5:F:73:GLU:HG2	5:F:73:GLU:H	1.51	0.47
15:P:20:VAL:HG21	15:P:32:PHE:CD2	2.50	0.47
20:B:116:LEU:HB3	20:B:140:LEU:HD11	1.95	0.47
18:S:42:ASN:N	18:S:42:ASN:HD22	2.11	0.47
5:F:3:HIS:CD2	5:F:65:GLU:HG3	2.50	0.47
18:S:48:ILE:HB	18:S:59:VAL:CG2	2.44	0.47
12:M:53:ASP:HA	12:M:56:ARG:CZ	2.44	0.47
1:A:1317:C:OP1	13:N:56:PRO:HD2	2.14	0.47
1:A:1141:C:H2'	1:A:1142:G:C8	2.48	0.47
1:A:484:G:O4'	1:A:486:U:H5'	2.13	0.47
1:A:1033:G:H2'	1:A:1034:G:O4'	2.15	0.47
5:F:100:SER:HA	17:R:23:LYS:CD	2.45	0.47
1:A:562:U:H1'	11:L:11:ARG:HB3	1.97	0.47
9:J:67:ILE:HA	13:N:94:GLY:O	2.15	0.47
1:A:1269:A:H2	1:A:1312:G:N3	2.12	0.47
1:A:1456:A:H2'	1:A:1457:G:O4'	2.15	0.47
1:A:610:U:O2	1:A:610:U:O4'	2.31	0.47
20:B:44:LYS:C	20:B:47:PRO:HD2	2.34	0.47
1:A:130:A:C8	16:Q:64:ARG:HG3	2.49	0.47
5:F:53:LYS:N	5:F:53:LYS:NZ	2.63	0.47
1:A:1384:C:H2'	1:A:1385:G:C8	2.49	0.47
1:A:1462:C:H2'	1:A:1463:U:C6	2.48	0.47
2:C:39:ARG:HE	2:C:54:ILE:HG23	1.80	0.47
1:A:642:A:C5	7:H:106:SER:HA	2.50	0.47
4:E:98:ALA:HB2	4:E:123:LEU:HG	1.95	0.47
8:I:20:ILE:HG23	8:I:60:LEU:HD12	1.97	0.47
16:Q:3:LYS:NZ	16:Q:4:ILE:HD12	2.29	0.47
1:A:1101:A:H4'	1:A:1102:A:O5'	2.15	0.47
5:F:71:ILE:HG13	5:F:72:ASP:N	2.23	0.47
20:B:156:LEU:CD1	20:B:156:LEU:H	2.23	0.47
3:D:71:PHE:O	3:D:74:TYR:HB2	2.15	0.47
9:J:36:VAL:HG22	9:J:76:ILE:HG22	1.97	0.47
1:A:203:G:H21	1:A:205:A:H61	1.63	0.47
11:L:34:THR:O	11:L:35:ARG:HB2	2.15	0.47
4:E:95:MET:HA	4:E:124:ALA:CB	2.42	0.47
1:A:437:U:H5''	3:D:151:GLN:NE2	2.29	0.47
2:C:35:ASP:OD1	2:C:58:ARG:HD2	2.14	0.47
4:E:61:LYS:HB2	4:E:65:LYS:HZ1	1.80	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:777:A:H2'	1:A:778:G:C8	2.48	0.47
15:P:38:PHE:CE2	15:P:51:ARG:HD3	2.50	0.47
5:F:81:ASN:O	5:F:84:VAL:HG12	2.13	0.47
1:A:1292:G:H2'	1:A:1293:C:H6	1.79	0.47
1:A:1386:G:O2'	1:A:1387:G:H5'	2.14	0.47
10:K:30:ILE:HG22	10:K:45:THR:CB	2.45	0.47
1:A:1005:A:N6	1:A:1024:G:H1'	2.29	0.47
1:A:1283:U:H2'	1:A:1284:C:H6	1.80	0.47
1:A:1494:G:OP2	23:A:2367:LLL:N32	2.48	0.47
1:A:1432:G:H1'	1:A:1468:A:H61	1.80	0.47
17:R:63:TYR:N	17:R:63:TYR:CD2	2.82	0.47
20:B:138:ARG:HA	20:B:141:GLU:HG3	1.97	0.47
7:H:17:GLN:CD	7:H:69:ALA:HB1	2.35	0.47
1:A:895:G:H2'	1:A:896:C:C6	2.50	0.47
9:J:92:LEU:HD22	9:J:92:LEU:N	2.29	0.47
1:A:332:G:O2'	1:A:333:U:H5'	2.14	0.47
1:A:356:A:H1'	1:A:368:U:O2'	2.14	0.47
1:A:113:G:H2'	1:A:114:U:C6	2.49	0.47
6:G:61:PHE:O	6:G:65:LEU:HD13	2.15	0.47
5:F:52:ASN:CG	5:F:52:ASN:O	2.52	0.47
1:A:614:C:OP1	3:D:82:LYS:HE2	2.14	0.47
10:K:83:VAL:HG21	10:K:109:ILE:HG12	1.96	0.47
3:D:170:LEU:HD23	3:D:170:LEU:N	2.29	0.47
20:B:151:LYS:HG3	20:B:152:ASP:N	2.30	0.47
20:B:223:GLY:C	20:B:225:SER:H	2.18	0.47
1:A:1412:C:H2'	1:A:1413:A:H8	1.75	0.47
1:A:373:A:C1'	1:A:481:G:H1'	2.44	0.47
20:B:187:ASP:O	20:B:189:ASN:N	2.48	0.47
1:A:993:G:N3	1:A:993:G:H2'	2.30	0.47
1:A:947:G:H4'	12:M:107:THR:OG1	2.15	0.47
20:B:119:GLN:HG3	20:B:136:ARG:NH1	2.29	0.47
17:R:32:ILE:HG22	17:R:33:THR:O	2.14	0.47
2:C:194:VAL:HG12	2:C:195:ILE:N	2.30	0.47
20:B:93:HIS:HB2	20:B:145:ASN:O	2.15	0.47
2:C:172:VAL:O	2:C:174:LEU:HD12	2.15	0.47
13:N:10:VAL:O	13:N:13:VAL:HB	2.15	0.47
1:A:982:U:C5'	13:N:5:MET:HE3	2.45	0.47
1:A:522:C:O2'	1:A:523:A:H5'	2.15	0.47
1:A:389:A:N3	1:A:389:A:H2'	2.30	0.47
1:A:1010:U:O2'	1:A:1011:C:H5'	2.15	0.47
2:C:148:ILE:HA	2:C:200:TRP:O	2.14	0.47
12:M:79:LEU:HB3	12:M:84:CYS:SG	2.55	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1342:C:H5'	8:I:127:SER:HA	1.97	0.47
1:A:96:U:H2'	1:A:97:G:H8	1.78	0.47
6:G:14:ASP:H	6:G:19:SER:H	1.63	0.47
17:R:45:GLY:O	17:R:46:THR:C	2.54	0.47
1:A:586:C:H5''	7:H:81:GLY:HA2	1.97	0.47
12:M:29:SER:O	12:M:32:ILE:HG22	2.15	0.47
3:D:59:LYS:HE3	3:D:194:ILE:CD1	2.45	0.47
20:B:104:LYS:HG3	20:B:105:THR:H	1.80	0.47
13:N:30:ILE:O	13:N:40:ARG:HA	2.15	0.47
2:C:126:ARG:HH22	2:C:190:THR:CG2	2.22	0.47
20:B:86:CYS:HB3	20:B:88:GLN:NE2	2.29	0.47
20:B:124:THR:HG23	20:B:124:THR:O	2.14	0.47
12:M:76:ILE:O	12:M:80:MET:HG3	2.14	0.47
18:S:2:ARG:NE	18:S:2:ARG:HA	2.30	0.47
1:A:1262:C:H2'	1:A:1263:C:O4'	2.15	0.47
14:O:81:LEU:O	14:O:85:LEU:HD13	2.15	0.47
15:P:23:ASP:CG	15:P:25:ARG:HE	2.18	0.47
1:A:1373:G:H5''	6:G:35:LYS:HB2	1.96	0.47
9:J:59:LYS:HG3	9:J:60:ASP:N	2.30	0.47
1:A:656:G:HO2'	1:A:657:U:H5'	1.80	0.47
1:A:171:A:H2'	1:A:172:A:C8	2.49	0.47
1:A:1453:G:H2'	1:A:1454:G:O4'	2.15	0.47
1:A:186:C:H2'	1:A:187:G:O4'	2.15	0.47
1:A:822:U:H2'	1:A:823:C:H6	1.79	0.47
1:A:821:G:O2'	1:A:822:U:H5'	2.15	0.47
1:A:1489:G:H2'	1:A:1490:U:C6	2.50	0.47
1:A:947:G:H5''	12:M:106:ARG:HB2	1.97	0.46
2:C:122:GLN:O	2:C:127:VAL:HG22	2.15	0.46
1:A:410:G:H2'	1:A:429:U:C5	2.50	0.46
1:A:812:G:OP1	1:A:812:G:H4'	2.15	0.46
1:A:735:C:O2'	1:A:736:C:H5'	2.16	0.46
1:A:834:U:H2'	1:A:835:U:H6	1.80	0.46
1:A:1347:G:H8	8:I:108:ARG:HB3	1.80	0.46
5:F:18:VAL:N	5:F:19:PRO:HD2	2.29	0.46
4:E:12:GLU:HB3	4:E:63:MET:CE	2.45	0.46
1:A:308:C:H2'	1:A:309:A:H8	1.79	0.46
1:A:648:A:H2'	1:A:649:A:C8	2.50	0.46
1:A:1281:C:H5'	1:A:1282:C:H5	1.79	0.46
14:O:50:HIS:O	14:O:53:ARG:HB3	2.15	0.46
3:D:182:LYS:NZ	3:D:182:LYS:HB3	2.29	0.46
1:A:663:A:H5''	17:R:49:LYS:HD2	1.96	0.46
10:K:77:GLY:O	10:K:79:LYS:HE3	2.16	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:45:ARG:O	5:F:56:LYS:HA	2.15	0.46
21:U:24:LYS:HZ3	21:U:25:ALA:H	1.63	0.46
6:G:145:GLU:CD	6:G:148:LYS:HD2	2.35	0.46
1:A:253:A:H2'	1:A:254:G:C8	2.49	0.46
7:H:113:ARG:HE	7:H:113:ARG:C	2.18	0.46
2:C:194:VAL:HG12	2:C:195:ILE:H	1.80	0.46
1:A:1053:G:C4'	1:A:1054:C:H5'	2.44	0.46
1:A:1198:G:H2'	1:A:1199:U:C6	2.50	0.46
14:O:82:ILE:O	14:O:86:GLY:N	2.48	0.46
1:A:586:C:H2'	1:A:587:G:H5'	1.96	0.46
19:T:65:LEU:HG	19:T:66:ILE:HD13	1.98	0.46
4:E:81:GLN:NE2	4:E:149:PRO:HD3	2.31	0.46
1:A:920:U:H2'	1:A:921:U:H6	1.77	0.46
3:D:56:GLU:HB2	3:D:198:LEU:HD23	1.97	0.46
1:A:413:G:C6	3:D:32:LYS:HE2	2.51	0.46
1:A:413:G:N1	3:D:32:LYS:HE2	2.30	0.46
1:A:1122:U:H2'	1:A:1123:U:C6	2.50	0.46
1:A:255:G:H1'	16:Q:17:GLU:OE2	2.15	0.46
15:P:71:VAL:HG13	15:P:72:ALA:N	2.31	0.46
1:A:479:U:O2'	1:A:480:U:H5'	2.15	0.46
1:A:735:C:H5'	17:R:59:LYS:HD3	1.97	0.46
1:A:1366:C:H2'	1:A:1367:C:H6	1.79	0.46
6:G:91:ARG:CB	6:G:92:PRO:HD2	2.45	0.46
3:D:75:TYR:CG	3:D:203:TYR:HD1	2.34	0.46
5:F:49:TYR:CE1	17:R:65:SER:HA	2.50	0.46
8:I:22:PRO:HA	8:I:60:LEU:HB2	1.97	0.46
1:A:875:U:O2'	7:H:14:ARG:HD2	2.15	0.46
1:A:204:G:C2	1:A:465:A:H1'	2.51	0.46
1:A:1307:U:H2'	1:A:1308:U:H6	1.80	0.46
9:J:77:VAL:HG12	9:J:78:GLU:HG3	1.97	0.46
10:K:30:ILE:O	10:K:30:ILE:HG13	2.15	0.46
2:C:54:ILE:HG23	2:C:54:ILE:O	2.16	0.46
1:A:928:G:H2'	1:A:929:G:C8	2.50	0.46
1:A:1042:A:H2'	1:A:1043:G:O4'	2.16	0.46
1:A:1058:G:H2'	1:A:1059:C:C6	2.51	0.46
1:A:712:A:O2'	1:A:713:G:H5'	2.15	0.46
20:B:212:TYR:O	20:B:216:VAL:HG22	2.15	0.46
1:A:1085:U:H3'	1:A:1086:U:C6	2.51	0.46
5:F:46:GLN:HG3	5:F:47:LEU:N	2.30	0.46
5:F:70:VAL:HG23	5:F:71:ILE:N	2.31	0.46
1:A:1270:G:H4'	1:A:1313:U:O2'	2.15	0.46
1:A:865:A:H2	1:A:918:A:H4'	1.80	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:L:34:THR:HG23	11:L:55:ARG:HB2	1.97	0.46
1:A:843:U:H4'	1:A:843:U:OP2	2.15	0.46
8:I:118:ARG:HB3	8:I:122:ARG:HG2	1.97	0.46
19:T:49:ALA:O	19:T:52:GLU:HG2	2.15	0.46
14:O:26:GLU:HA	14:O:81:LEU:HD11	1.97	0.46
16:Q:30:HIS:HD2	16:Q:37:ILE:HD11	1.81	0.46
1:A:605:U:H2'	1:A:606:G:C8	2.48	0.46
1:A:640:A:O2'	7:H:107:LYS:HE3	2.14	0.46
3:D:172:VAL:HG23	3:D:178:GLU:O	2.16	0.46
1:A:997:U:H2'	1:A:998:C:C6	2.50	0.46
1:A:1207:G:O2'	1:A:1208:C:H5'	2.16	0.46
10:K:115:ILE:O	10:K:115:ILE:HD12	2.16	0.46
20:B:104:LYS:HB2	20:B:104:LYS:NZ	2.31	0.46
5:F:29:ILE:HG21	5:F:64:VAL:CG1	2.45	0.46
17:R:38:ILE:CG2	17:R:58:ILE:HG21	2.45	0.46
1:A:491:G:O2'	1:A:492:C:H5'	2.15	0.46
3:D:22:SER:N	3:D:109:THR:HG22	2.29	0.46
1:A:20:U:O2'	1:A:21:G:H5'	2.16	0.46
2:C:171:ARG:HB2	2:C:171:ARG:HH11	1.79	0.46
1:A:1438:G:O2'	1:A:1439:G:H5'	2.16	0.46
11:L:65:TYR:HB3	11:L:95:HIS:CD2	2.50	0.46
1:A:1045:C:H2'	1:A:1046:A:O4'	2.16	0.46
21:U:34:ARG:HD3	21:U:39:LYS:HZ3	1.79	0.46
10:K:106:ILE:HD11	10:K:109:ILE:HD11	1.98	0.46
3:D:190:LEU:O	3:D:190:LEU:HD13	2.14	0.46
13:N:26:LEU:HD12	13:N:44:VAL:HG13	1.97	0.46
2:C:190:THR:CG2	2:C:191:THR:H	2.23	0.46
2:C:190:THR:CG2	2:C:191:THR:N	2.79	0.46
6:G:80:GLY:C	6:G:82:SER:H	2.19	0.46
1:A:370:C:H2'	1:A:371:A:C8	2.50	0.46
12:M:84:CYS:HB3	18:S:73:PHE:CE2	2.51	0.46
1:A:451:A:H4'	1:A:452:A:O4'	2.16	0.46
1:A:1161:C:O2'	1:A:1162:C:H5'	2.16	0.46
1:A:1337:G:H5''	1:A:1338:G:OP1	2.16	0.46
11:L:107:LYS:C	11:L:109:ARG:H	2.19	0.46
7:H:17:GLN:NE2	7:H:62:LEU:HB3	2.31	0.46
1:A:1096:C:H2'	1:A:1097:C:C6	2.50	0.46
8:I:62:LEU:N	8:I:62:LEU:HD22	2.30	0.46
20:B:59:ILE:HD12	20:B:60:ALA:N	2.31	0.46
1:A:238:A:C3'	1:A:239:U:H5''	2.46	0.46
1:A:251:G:H4'	1:A:252:U:H5'	1.98	0.46
16:Q:7:LEU:O	16:Q:60:ILE:HD13	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:719:C:O2'	17:R:37:LYS:HB2	2.15	0.46
2:C:13:ILE:C	2:C:15:LYS:H	2.19	0.46
1:A:23:C:O2'	1:A:24:U:H5'	2.16	0.46
3:D:16:THR:HG22	3:D:17:ASP:N	2.30	0.46
12:M:33:LEU:CD2	12:M:38:ILE:HB	2.46	0.46
1:A:1251:A:O2'	1:A:1252:A:H5'	2.16	0.46
5:F:47:LEU:HD21	5:F:57:ALA:CB	2.45	0.46
2:C:180:ASP:OD1	2:C:203:LYS:HB2	2.16	0.46
4:E:81:GLN:H	4:E:146:MET:HE3	1.80	0.46
4:E:88:HIS:CE1	4:E:137:ARG:HH11	2.34	0.46
1:A:1143:G:O2'	1:A:1144:G:H5'	2.15	0.46
9:J:40:ILE:HD12	9:J:73:LEU:HB3	1.97	0.46
1:A:847:G:H2'	1:A:848:C:H6	1.81	0.46
6:G:14:ASP:CB	6:G:19:SER:H	2.29	0.46
1:A:202:G:H1'	1:A:468:A:H8	1.81	0.46
5:F:18:VAL:HG21	5:F:58:HIS:CD2	2.51	0.46
1:A:1159:U:O4'	1:A:1182:G:N2	2.49	0.46
1:A:648:A:O2'	1:A:649:A:H5'	2.16	0.46
1:A:1190:G:OP1	2:C:3:LYS:HA	2.16	0.46
1:A:668:G:O2'	1:A:669:G:H5'	2.16	0.46
1:A:1397:C:H4'	1:A:1398:A:OP2	2.15	0.46
1:A:921:U:H2'	1:A:922:G:C8	2.50	0.46
4:E:136:VAL:HG13	4:E:137:ARG:N	2.30	0.46
2:C:140:ALA:CB	2:C:148:ILE:HD12	2.44	0.46
3:D:22:SER:H	3:D:109:THR:CG2	2.29	0.46
11:L:3:VAL:CG1	16:Q:33:TYR:HB3	2.46	0.46
1:A:1524:C:H2'	1:A:1525:G:C8	2.51	0.46
1:A:766:A:H61	1:A:1511:G:H1'	1.80	0.46
1:A:367:U:OP1	1:A:395:C:H1'	2.16	0.46
1:A:711:G:O2'	1:A:712:A:H5'	2.16	0.46
21:U:40:PRO:O	21:U:42:THR:N	2.49	0.45
3:D:169:TRP:C	3:D:182:LYS:HB2	2.36	0.45
1:A:1533:C:H2'	1:A:1534:A:H3'	1.97	0.45
3:D:197:HIS:O	3:D:201:GLU:HG3	2.16	0.45
7:H:77:VAL:HG12	7:H:84:ILE:HD12	1.98	0.45
1:A:1512:U:H2'	1:A:1513:A:C8	2.51	0.45
1:A:154:U:H2'	1:A:155:A:H8	1.81	0.45
1:A:1201:A:C8	1:A:1201:A:H5''	2.51	0.45
11:L:98:ARG:HD2	11:L:103:CYS:SG	2.56	0.45
1:A:1366:C:H2'	1:A:1367:C:C6	2.50	0.45
1:A:1255:G:O2'	1:A:1258:G:N3	2.42	0.45
1:A:766:A:H2'	1:A:767:A:O4'	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:G:39:GLU:HB3	6:G:43:TYR:CE2	2.51	0.45
6:G:49:LEU:HD21	6:G:120:ALA:O	2.16	0.45
1:A:426:U:H2'	1:A:427:U:C6	2.51	0.45
1:A:171:A:O2'	1:A:172:A:H5'	2.16	0.45
1:A:791:G:C6	1:A:792:A:N7	2.84	0.45
1:A:1332:A:H2'	1:A:1333:A:C8	2.51	0.45
1:A:224:U:H2'	1:A:225:C:C6	2.51	0.45
19:T:85:LEU:HD23	19:T:86:ALA:N	2.30	0.45
18:S:62:THR:HG22	18:S:63:ASP:N	2.30	0.45
12:M:12:LYS:HB3	12:M:13:HIS:H	1.49	0.45
3:D:29:THR:HG22	3:D:30:LYS:N	2.31	0.45
21:U:24:LYS:NZ	21:U:24:LYS:HB3	2.32	0.45
2:C:58:ARG:HA	2:C:62:SER:O	2.16	0.45
1:A:1477:U:H2'	1:A:1478:U:H6	1.78	0.45
1:A:679:C:H2'	1:A:680:C:C6	2.51	0.45
9:J:56:HIS:H	13:N:80:ARG:HH22	1.63	0.45
1:A:206:C:H2'	1:A:207:C:C6	2.51	0.45
1:A:399:G:H2'	1:A:400:C:C6	2.51	0.45
1:A:201:G:H2'	1:A:202:G:C8	2.51	0.45
1:A:1504:G:H4'	1:A:1505:G:C4	2.51	0.45
1:A:308:C:H2'	1:A:309:A:C8	2.51	0.45
1:A:197:A:H4'	1:A:198:G:O5'	2.14	0.45
13:N:2:LYS:HB3	13:N:5:MET:HB2	1.99	0.45
20:B:184:ALA:H	20:B:195:VAL:HG11	1.80	0.45
20:B:45:THR:CA	20:B:48:MET:HG3	2.45	0.45
6:G:134:VAL:CB	6:G:137:ARG:HH21	2.29	0.45
20:B:96:LEU:HB2	20:B:99:MET:CE	2.46	0.45
10:K:77:GLY:C	10:K:79:LYS:HE3	2.36	0.45
13:N:30:ILE:H	13:N:30:ILE:CD1	2.28	0.45
2:C:126:ARG:HH12	2:C:190:THR:CG2	2.29	0.45
1:A:483:C:H2'	1:A:484:G:N7	2.32	0.45
1:A:847:G:H2'	1:A:848:C:C6	2.51	0.45
1:A:499:A:H4'	1:A:500:G:H5'	1.98	0.45
8:I:38:PHE:HE1	8:I:78:ILE:HD12	1.81	0.45
15:P:74:LEU:HA	15:P:77:GLU:OE2	2.17	0.45
14:O:71:LYS:HB2	14:O:78:TYR:CG	2.52	0.45
11:L:68:GLY:HA3	11:L:106:VAL:HG22	1.98	0.45
5:F:12:PRO:C	5:F:14:GLN:H	2.20	0.45
1:A:620:C:H2'	1:A:621:A:C8	2.51	0.45
2:C:10:ARG:CZ	2:C:181:ILE:HD13	2.46	0.45
1:A:113:G:O4'	1:A:354:G:H4'	2.16	0.45
1:A:1095:U:H5''	1:A:1109:C:O2	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:E:59:ILE:O	4:E:63:MET:HG2	2.16	0.45
13:N:60:ARG:CZ	13:N:62:ARG:CZ	2.94	0.45
20:B:14:HIS:CB	20:B:208:ALA:HB2	2.46	0.45
10:K:17:ASP:HB3	10:K:80:ASN:CG	2.37	0.45
13:N:26:LEU:HA	13:N:30:ILE:HD13	1.98	0.45
4:E:81:GLN:H	4:E:146:MET:CE	2.30	0.45
1:A:203:G:H1'	1:A:465:A:N6	2.31	0.45
1:A:452:A:H1'	15:P:70:ARG:NH1	2.31	0.45
1:A:265:G:H5'	16:Q:65:PRO:O	2.16	0.45
11:L:55:ARG:HH11	11:L:55:ARG:HG3	1.82	0.45
1:A:1249:C:H4'	8:I:37:TYR:OH	2.16	0.45
4:E:125:LYS:HD2	4:E:126:ALA:N	2.30	0.45
1:A:1200:C:H3'	1:A:1201:A:H5'	1.99	0.45
2:C:181:ILE:HD12	2:C:181:ILE:N	2.31	0.45
3:D:43:ARG:HH21	3:D:45:PRO:HA	1.80	0.45
5:F:86:ARG:CZ	17:R:63:TYR:HB3	2.47	0.45
1:A:168:G:O2'	1:A:169:C:H5'	2.16	0.45
20:B:113:LEU:HD11	20:B:144:GLU:HG3	1.98	0.45
1:A:1080:A:H5''	4:E:20:VAL:HG11	1.97	0.45
1:A:412:A:H61	3:D:29:THR:HG22	1.82	0.45
3:D:88:ASN:O	3:D:92:LEU:HD23	2.16	0.45
16:Q:66:LEU:HD13	16:Q:70:LYS:HG2	1.97	0.45
1:A:1234:C:H1'	1:A:1364:U:O2	2.17	0.45
7:H:107:LYS:HA	7:H:107:LYS:HD3	1.83	0.45
1:A:643:C:H2'	1:A:644:U:C6	2.51	0.45
6:G:134:VAL:HB	6:G:137:ARG:NH2	2.31	0.45
9:J:8:ILE:HD12	9:J:75:ASP:HA	1.99	0.45
9:J:7:ARG:O	9:J:100:ILE:HA	2.16	0.45
1:A:191:G:H2'	1:A:192:A:H8	1.82	0.45
1:A:1227:A:H5''	12:M:113:LYS:HZ3	1.81	0.45
1:A:1460:C:H2'	1:A:1461:G:C8	2.51	0.45
3:D:61:ARG:NH2	3:D:68:GLU:H	2.15	0.45
1:A:513:C:H2'	1:A:514:C:H6	1.82	0.45
1:A:425:G:O2'	1:A:426:U:H5'	2.16	0.45
7:H:47:ASP:CG	7:H:48:PHE:H	2.20	0.45
14:O:33:THR:HG23	14:O:63:ARG:NH1	2.32	0.45
20:B:212:TYR:O	20:B:216:VAL:HG13	2.17	0.45
8:I:24:ASN:CG	8:I:25:GLY:N	2.70	0.45
19:T:71:ALA:O	19:T:74:HIS:HB2	2.16	0.45
1:A:1414:U:H2'	1:A:1415:G:C8	2.49	0.45
11:L:20:VAL:HB	11:L:94:TYR:HE1	1.81	0.45
1:A:1124:G:H3'	9:J:37:ARG:NH1	2.31	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:499:A:H1'	1:A:500:G:C8	2.52	0.45
1:A:313:A:O2'	1:A:314:C:H5'	2.17	0.45
1:A:502:A:H2'	1:A:503:C:O4'	2.17	0.45
14:O:26:GLU:HG3	14:O:81:LEU:HD12	1.98	0.45
1:A:1521:C:O2'	1:A:1522:U:H5'	2.16	0.45
6:G:45:ALA:HB3	6:G:119:LEU:HD23	1.99	0.45
1:A:1509:C:O2'	1:A:1510:C:H5'	2.16	0.45
1:A:1472:U:H2'	1:A:1473:G:C8	2.52	0.45
20:B:116:LEU:HB3	20:B:140:LEU:HG	1.99	0.45
4:E:15:ILE:HB	4:E:35:LEU:O	2.17	0.45
1:A:1355:G:O2'	1:A:1356:G:H5'	2.17	0.45
1:A:549:C:H2'	1:A:550:G:C8	2.51	0.45
13:N:29:ILE:HB	13:N:30:ILE:HD12	1.99	0.45
1:A:865:A:C2	1:A:918:A:H4'	2.52	0.45
13:N:49:THR:O	13:N:50:LEU:HB3	2.17	0.45
1:A:411:A:C4	1:A:413:G:H1'	2.52	0.45
7:H:6:ILE:HD12	7:H:35:ILE:HD12	1.97	0.45
1:A:993:G:C2'	1:A:995:C:H41	2.23	0.45
21:U:24:LYS:HZ2	21:U:24:LYS:HB3	1.81	0.45
6:G:144:ALA:O	6:G:145:GLU:HB3	2.17	0.45
8:I:118:ARG:O	8:I:118:ARG:HG2	2.17	0.45
16:Q:17:GLU:O	16:Q:18:LYS:HB2	2.16	0.45
16:Q:39:ARG:HG2	16:Q:39:ARG:HH11	1.81	0.45
1:A:719:C:H3'	1:A:720:C:C6	2.51	0.45
4:E:89:THR:CG2	4:E:90:GLY:H	2.24	0.45
6:G:50:ALA:HB2	6:G:57:GLU:N	2.31	0.45
1:A:714:G:H21	1:A:777:A:H1'	1.82	0.45
1:A:961:U:N3	1:A:983:A:N6	2.65	0.45
1:A:429:U:H4'	1:A:430:A:O5'	2.16	0.45
1:A:620:C:O2	3:D:131:ILE:HG21	2.17	0.45
1:A:707:U:H2'	1:A:708:C:C6	2.51	0.45
7:H:50:VAL:HG23	7:H:57:GLU:O	2.16	0.45
1:A:1056:U:O2'	1:A:1057:G:H5'	2.17	0.45
1:A:1489:G:H2'	1:A:1490:U:H6	1.82	0.45
1:A:1425:U:O2'	1:A:1426:G:H5'	2.17	0.45
1:A:984:C:O2'	1:A:985:C:H5'	2.16	0.45
11:L:80:LEU:HB3	11:L:97:VAL:CG2	2.47	0.45
1:A:682:G:O2'	1:A:683:G:H5'	2.17	0.45
6:G:142:ARG:HG3	6:G:142:ARG:HH11	1.82	0.45
10:K:109:ILE:HG22	21:U:16:ARG:HH12	1.82	0.45
20:B:209:VAL:HG23	20:B:210:THR:N	2.32	0.45
9:J:15:HIS:HA	9:J:18:ILE:HG22	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:J:41:PRO:O	9:J:42:LEU:HB2	2.17	0.45
1:A:598:U:H4'	7:H:85:TYR:CD2	2.52	0.45
1:A:251:G:N2	1:A:266:G:H1	2.14	0.45
16:Q:68:LYS:O	16:Q:70:LYS:N	2.50	0.45
1:A:1248:A:C2	8:I:71:ILE:HD11	2.51	0.45
3:D:202:LEU:HD12	3:D:202:LEU:O	2.16	0.45
8:I:9:GLY:HA3	8:I:81:GLY:N	2.32	0.45
1:A:734:G:H2'	1:A:735:C:C6	2.52	0.45
1:A:738:C:H2'	1:A:739:C:H6	1.82	0.45
4:E:45:VAL:HG23	4:E:71:ILE:HG22	1.98	0.45
1:A:1254:A:OP1	9:J:47:GLU:HG3	2.17	0.45
1:A:1203:C:H2'	1:A:1204:A:O4'	2.17	0.45
1:A:224:U:H2'	1:A:225:C:H6	1.82	0.45
8:I:42:THR:O	8:I:45:MET:HG2	2.17	0.45
8:I:56:MET:C	8:I:58:GLU:N	2.68	0.45
2:C:131:ARG:HG3	2:C:135:ARG:CZ	2.47	0.45
6:G:104:VAL:O	6:G:108:ARG:HG3	2.16	0.45
12:M:14:ALA:O	12:M:18:LEU:HB2	2.17	0.45
12:M:21:ILE:HB	12:M:24:VAL:CG2	2.36	0.45
20:B:65:LYS:HB3	20:B:157:PRO:HA	2.00	0.45
11:L:82:ARG:CG	11:L:82:ARG:HH11	2.30	0.45
1:A:134:G:H2'	1:A:135:C:O4'	2.17	0.45
15:P:1:MET:HG3	15:P:3:THR:CG2	2.47	0.45
14:O:56:LEU:HD12	14:O:59:MET:HE3	1.99	0.45
7:H:118:ALA:HB3	7:H:120:LEU:CD2	2.46	0.45
8:I:126:PHE:O	8:I:128:LYS:N	2.50	0.45
1:A:152:A:H2'	1:A:153:C:O4'	2.17	0.45
11:L:122:LYS:HG3	11:L:123:ALA:H	1.82	0.45
10:K:68:ARG:HG3	10:K:68:ARG:HH11	1.82	0.45
19:T:43:LYS:H	19:T:43:LYS:HD3	1.82	0.44
18:S:18:VAL:O	18:S:22:VAL:HG23	2.18	0.44
18:S:10:ILE:CG2	18:S:37:SER:HB3	2.43	0.44
1:A:521:G:O2'	1:A:522:C:H5'	2.17	0.44
20:B:98:GLY:O	20:B:102:ASN:N	2.47	0.44
2:C:126:ARG:HH12	2:C:190:THR:HG23	1.82	0.44
7:H:87:ARG:HG3	7:H:90:GLU:OE2	2.16	0.44
9:J:73:LEU:HD13	9:J:75:ASP:HB2	1.98	0.44
9:J:6:ILE:HB	9:J:76:ILE:CD1	2.43	0.44
4:E:37:VAL:HG12	4:E:47:PHE:CB	2.46	0.44
1:A:598:U:H4'	7:H:85:TYR:CG	2.52	0.44
1:A:769:G:H4'	1:A:1513:A:H4'	1.98	0.44
1:A:634:C:H2'	1:A:635:A:C8	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:255:G:H2'	1:A:256:U:H6	1.82	0.44
3:D:115:GLN:HG3	3:D:119:HIS:ND1	2.32	0.44
14:O:26:GLU:HG3	14:O:81:LEU:CD1	2.47	0.44
1:A:1287:A:H2'	1:A:1288:A:H8	1.80	0.44
10:K:117:HIS:O	10:K:118:ASN:HB2	2.17	0.44
3:D:48:SER:O	3:D:49:ASP:C	2.54	0.44
1:A:1422:G:O2'	1:A:1423:G:H5'	2.17	0.44
1:A:81:A:H2'	1:A:82:G:H8	1.82	0.44
20:B:185:ILE:HG23	20:B:199:ILE:O	2.17	0.44
1:A:658:C:O2'	1:A:659:U:H5'	2.17	0.44
20:B:119:GLN:HB3	20:B:125:PHE:HB2	2.00	0.44
1:A:1038:C:H2'	1:A:1039:G:H8	1.77	0.44
5:F:37:HIS:O	5:F:97:THR:HG23	2.16	0.44
10:K:55:ARG:NH1	10:K:60:PHE:HD1	2.14	0.44
1:A:89:U:H2'	1:A:90:C:H6	1.82	0.44
9:J:57:VAL:O	9:J:58:ASN:HB2	2.18	0.44
13:N:80:ARG:HG3	13:N:81:ILE:N	2.32	0.44
21:U:48:LYS:HG3	21:U:49:ALA:N	2.33	0.44
1:A:1283:U:O2'	1:A:1284:C:H5'	2.18	0.44
9:J:11:LYS:HB2	9:J:97:ASP:OD1	2.17	0.44
3:D:169:TRP:O	3:D:182:LYS:HB2	2.18	0.44
1:A:121:U:H3'	1:A:121:U:OP1	2.16	0.44
6:G:41:ILE:HG21	6:G:115:MET:HG3	1.98	0.44
9:J:12:ALA:N	9:J:18:ILE:HD12	2.32	0.44
5:F:9:MET:HB3	5:F:59:TYR:CE2	2.53	0.44
5:F:62:MET:HG3	5:F:64:VAL:CG2	2.39	0.44
20:B:10:LYS:CB	20:B:211:LEU:HD21	2.46	0.44
12:M:91:ARG:CZ	12:M:91:ARG:HB2	2.47	0.44
1:A:1305:G:H2'	1:A:1331:G:N2	2.32	0.44
5:F:100:SER:HA	17:R:23:LYS:HE2	1.99	0.44
1:A:642:A:H2'	1:A:643:C:C6	2.52	0.44
1:A:562:U:H1'	11:L:11:ARG:HD2	1.99	0.44
1:A:1047:G:H21	1:A:1215:G:C4'	2.30	0.44
1:A:903:G:H2'	1:A:904:U:C6	2.52	0.44
1:A:577:G:O2'	1:A:578:C:H5'	2.17	0.44
5:F:3:HIS:ND1	5:F:95:ALA:HB2	2.31	0.44
8:I:85:ALA:HA	8:I:88:GLU:OE2	2.17	0.44
1:A:663:A:H2'	1:A:664:G:C8	2.52	0.44
4:E:93:VAL:HG11	4:E:110:MET:SD	2.58	0.44
4:E:81:GLN:CD	4:E:149:PRO:HD3	2.38	0.44
20:B:63:LYS:HA	20:B:224:ARG:CZ	2.47	0.44
4:E:37:VAL:HG12	4:E:47:PHE:HB3	2.00	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:130:LYS:HA	20:B:130:LYS:HZ3	1.82	0.44
17:R:61:ALA:HB3	17:R:67:LEU:HD12	1.98	0.44
1:A:190:A:C4	1:A:191:G:H1'	2.52	0.44
1:A:178:C:O2'	1:A:179:A:H5'	2.17	0.44
15:P:50:THR:CG2	15:P:51:ARG:N	2.80	0.44
1:A:564:C:H1'	16:Q:32:ILE:O	2.17	0.44
1:A:814:A:C5'	1:A:1511:G:H4'	2.47	0.44
1:A:878:A:H5''	7:H:80:PRO:HG2	1.98	0.44
1:A:152:A:H3'	1:A:153:C:H6	1.82	0.44
20:B:139:GLU:HG2	20:B:143:LEU:CD1	2.46	0.44
7:H:29:SER:O	7:H:33:VAL:HG23	2.16	0.44
1:A:62:U:H4'	1:A:378:G:N2	2.33	0.44
1:A:906:A:C2'	1:A:907:A:H5''	2.48	0.44
12:M:14:ALA:HB1	12:M:33:LEU:HD21	2.00	0.44
2:C:112:ALA:HB2	2:C:182:ASP:O	2.17	0.44
1:A:321:A:H5''	1:A:328:C:N4	2.32	0.44
3:D:137:SER:HB2	3:D:140:ASP:OD2	2.18	0.44
16:Q:57:VAL:HB	16:Q:79:GLU:CB	2.47	0.44
9:J:55:PRO:O	9:J:56:HIS:HB3	2.17	0.44
1:A:651:C:H2'	1:A:652:U:C6	2.53	0.44
2:C:34:SER:O	2:C:38:VAL:HG22	2.17	0.44
10:K:108:ASN:ND2	21:U:6:ARG:HB2	2.33	0.44
1:A:46:G:O2'	1:A:365:U:H1'	2.18	0.44
1:A:138:G:O2'	1:A:139:A:H5'	2.17	0.44
1:A:945:G:H21	1:A:1334:G:H4'	1.82	0.44
1:A:44:A:O2'	1:A:45:G:H5'	2.17	0.44
19:T:72:ALA:HA	19:T:75:LYS:HD3	1.99	0.44
2:C:25:THR:HG23	13:N:75:LYS:HE2	1.98	0.44
1:A:1151:A:O4'	9:J:41:PRO:HB2	2.17	0.44
1:A:1348:U:O3'	8:I:121:ARG:HG3	2.16	0.44
10:K:75:GLU:CD	10:K:75:GLU:N	2.68	0.44
1:A:192:A:O2'	1:A:193:C:H5'	2.18	0.44
4:E:64:GLU:CD	4:E:68:ARG:HE	2.20	0.44
15:P:26:ASN:HD22	15:P:26:ASN:HA	1.64	0.44
1:A:693:G:P	10:K:126:ARG:HH12	2.40	0.44
2:C:53:ARG:HG2	2:C:54:ILE:H	1.82	0.44
1:A:822:U:H2'	1:A:823:C:C6	2.53	0.44
1:A:810:C:O2'	1:A:811:C:H5'	2.17	0.44
1:A:593:U:H2'	1:A:594:U:C6	2.53	0.44
13:N:60:ARG:CZ	13:N:69:PRO:HB3	2.48	0.44
10:K:33:ILE:HG13	10:K:73:VAL:HG21	2.00	0.44
8:I:35:GLU:O	8:I:39:GLY:HA3	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1147:C:H4'	8:I:6:TYR:CE1	2.52	0.44
11:L:88:ASP:C	11:L:89:LEU:HD22	2.37	0.44
1:A:1350:A:OP2	8:I:119:LYS:HE3	2.17	0.44
1:A:958:A:N6	1:A:959:A:N1	2.66	0.44
1:A:179:A:O2'	1:A:180:U:H5'	2.17	0.44
5:F:10:VAL:HG12	5:F:11:HIS:N	2.33	0.44
1:A:1291:U:H2'	1:A:1292:G:H8	1.83	0.44
1:A:423:G:H2'	1:A:424:G:O4'	2.18	0.44
4:E:76:ASN:O	4:E:77:ASN:HB3	2.17	0.44
1:A:51:A:H4'	1:A:52:C:OP2	2.18	0.44
1:A:584:G:O2'	1:A:585:G:H5'	2.17	0.44
3:D:72:ARG:HG2	3:D:72:ARG:HH11	1.81	0.44
20:B:69:VAL:O	20:B:163:ILE:HG22	2.18	0.44
21:U:39:LYS:N	21:U:40:PRO:CD	2.81	0.44
1:A:661:G:H2'	1:A:662:U:C6	2.53	0.44
18:S:40:PHE:O	18:S:43:MET:HG3	2.17	0.44
5:F:5:GLU:HG3	5:F:63:ASN:OD1	2.18	0.44
13:N:41:TRP:CD1	13:N:43:ALA:HB3	2.53	0.44
2:C:129:PHE:CG	2:C:130:ARG:N	2.86	0.44
11:L:63:THR:O	11:L:94:TYR:HB2	2.18	0.44
7:H:76:ARG:HG2	7:H:79:ARG:HB3	1.99	0.44
17:R:38:ILE:HD13	17:R:38:ILE:H	1.83	0.44
1:A:1133:G:H2'	1:A:1134:G:O4'	2.18	0.44
1:A:208:U:H6	1:A:208:U:O5'	2.01	0.44
1:A:63:C:O2'	1:A:380:G:H4'	2.18	0.44
1:A:685:G:O2'	1:A:686:U:H5'	2.18	0.44
1:A:768:A:H5'	1:A:1524:C:H1'	2.00	0.44
7:H:80:PRO:C	7:H:82:LEU:H	2.20	0.44
2:C:55:VAL:HG23	2:C:68:HIS:NE2	2.33	0.44
18:S:77:ARG:HG2	18:S:77:ARG:H	1.52	0.44
20:B:47:PRO:O	20:B:51:GLU:HB2	2.18	0.44
18:S:14:LEU:HG	18:S:15:LEU:N	2.33	0.44
6:G:78:ARG:NH1	6:G:82:SER:N	2.66	0.44
2:C:133:MET:HG2	2:C:150:VAL:CG1	2.48	0.44
1:A:327:A:H1'	1:A:329:A:O4'	2.18	0.44
2:C:59:PRO:HB3	9:J:94:ALA:HB2	2.00	0.44
2:C:2:GLN:HE21	2:C:2:GLN:CA	2.31	0.44
2:C:64:ARG:HD3	2:C:64:ARG:HA	1.87	0.44
12:M:93:GLY:O	12:M:108:ARG:HG3	2.17	0.44
1:A:828:U:H2'	1:A:829:G:O5'	2.18	0.44
1:A:1406:U:C2'	1:A:1407:C:H5'	2.47	0.44
1:A:538:G:H2'	1:A:539:A:C8	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:E:55:VAL:N	4:E:56:PRO:CD	2.81	0.44
1:A:299:G:H2'	1:A:300:A:C8	2.53	0.44
1:A:1258:G:O2'	1:A:1259:C:H5'	2.18	0.44
1:A:894:G:H2'	1:A:895:G:H8	1.82	0.44
1:A:1488:G:O2'	1:A:1489:G:H5'	2.17	0.44
1:A:996:A:H2'	1:A:997:U:C6	2.52	0.44
1:A:1356:G:H2'	1:A:1357:A:C8	2.53	0.44
20:B:162:VAL:CG1	20:B:184:ALA:HB2	2.48	0.43
1:A:1098:C:H2'	1:A:1099:G:H8	1.83	0.43
18:S:10:ILE:CG2	18:S:38:THR:H	2.23	0.43
2:C:182:ASP:HB3	2:C:201:ILE:HB	2.00	0.43
13:N:56:PRO:HG2	13:N:57:SER:H	1.83	0.43
15:P:61:VAL:CA	15:P:65:ALA:HB3	2.42	0.43
2:C:133:MET:O	2:C:137:VAL:HG23	2.17	0.43
20:B:185:ILE:HG12	20:B:199:ILE:CG2	2.48	0.43
1:A:844:G:C6	1:A:846:G:H1'	2.53	0.43
1:A:1319:A:OP1	18:S:4:LEU:HD11	2.18	0.43
1:A:601:G:H2'	1:A:602:A:C8	2.52	0.43
3:D:113:ALA:O	3:D:117:VAL:HG23	2.18	0.43
2:C:10:ARG:NH2	2:C:181:ILE:HD13	2.32	0.43
8:I:115:VAL:HG21	9:J:62:ARG:HB2	2.00	0.43
1:A:1005:A:C2	1:A:1006:G:H1'	2.53	0.43
10:K:108:ASN:ND2	21:U:6:ARG:HD2	2.33	0.43
1:A:317:U:H2'	1:A:318:G:C8	2.53	0.43
9:J:80:THR:O	9:J:84:VAL:HG23	2.18	0.43
1:A:1351:U:O2'	1:A:1352:C:H5'	2.17	0.43
15:P:33:ILE:HG21	15:P:60:TRP:CZ2	2.53	0.43
13:N:50:LEU:CD2	13:N:51:PRO:HD3	2.48	0.43
20:B:86:CYS:O	20:B:88:GLN:N	2.50	0.43
3:D:197:HIS:ND1	3:D:198:LEU:N	2.66	0.43
1:A:1000:A:H2'	1:A:1001:C:H6	1.83	0.43
1:A:313:A:H2'	1:A:314:C:C6	2.53	0.43
1:A:34:C:H2'	1:A:35:G:H8	1.81	0.43
1:A:734:G:H2'	1:A:735:C:H6	1.82	0.43
1:A:693:G:OP1	10:K:126:ARG:NH1	2.50	0.43
1:A:301:G:O2'	1:A:302:G:H5'	2.18	0.43
6:G:49:LEU:HD21	6:G:120:ALA:HA	1.99	0.43
1:A:988:G:H2'	1:A:989:U:O4'	2.18	0.43
9:J:82:LYS:HG3	9:J:83:THR:N	2.33	0.43
14:O:21:ASP:C	14:O:23:GLY:H	2.21	0.43
19:T:48:LYS:HA	19:T:51:ASN:HD21	1.82	0.43
21:U:43:GLU:HA	21:U:46:ARG:HD2	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:M:70:ARG:HG3	12:M:74:MET:CE	2.48	0.43
21:U:3:ILE:HG23	21:U:18:PHE:CE2	2.54	0.43
10:K:85:VAL:O	10:K:112:VAL:N	2.51	0.43
1:A:521:G:OP1	11:L:69:GLU:HA	2.16	0.43
11:L:85:ARG:HG3	11:L:86:VAL:H	1.83	0.43
20:B:16:GLY:HA2	20:B:40:ILE:CG1	2.41	0.43
20:B:64:GLY:O	20:B:66:ILE:HG12	2.17	0.43
1:A:815:A:H4'	1:A:817:C:C5	2.53	0.43
3:D:147:LYS:HZ3	3:D:147:LYS:HB2	1.83	0.43
1:A:674:G:O2'	1:A:675:A:H5'	2.18	0.43
1:A:719:C:H2'	17:R:38:ILE:HD13	2.00	0.43
6:G:63:VAL:HA	6:G:66:GLU:OE2	2.18	0.43
8:I:9:GLY:CA	8:I:80:HIS:HB3	2.48	0.43
3:D:100:VAL:HG11	3:D:142:VAL:HG21	2.00	0.43
1:A:358:U:H2'	1:A:359:G:H8	1.81	0.43
12:M:2:ARG:O	12:M:4:ALA:N	2.52	0.43
20:B:116:LEU:HB3	20:B:140:LEU:CD1	2.48	0.43
6:G:65:LEU:O	6:G:69:ARG:HG3	2.17	0.43
1:A:144:G:H2'	1:A:145:G:O4'	2.18	0.43
8:I:87:MET:O	8:I:91:GLU:HG2	2.18	0.43
10:K:111:ASP:N	21:U:19:LYS:HE3	2.34	0.43
1:A:1060:U:C5'	9:J:53:ILE:HG12	2.47	0.43
4:E:132:PRO:HG2	4:E:133:ILE:H	1.84	0.43
3:D:199:ILE:HG13	3:D:200:VAL:N	2.31	0.43
14:O:56:LEU:O	14:O:60:VAL:HG23	2.19	0.43
1:A:1388:C:H2'	1:A:1389:C:H6	1.82	0.43
1:A:1108:G:H5'	2:C:175:HIS:ND1	2.33	0.43
20:B:22:TRP:HB3	20:B:38:HIS:CE1	2.53	0.43
8:I:18:VAL:HG22	8:I:64:ILE:HG23	2.00	0.43
13:N:46:LYS:HZ2	18:S:10:ILE:N	2.10	0.43
12:M:3:ILE:HD12	12:M:9:PRO:HD2	2.00	0.43
3:D:52:VAL:HG12	3:D:198:LEU:HD21	2.00	0.43
2:C:156:LEU:HG	2:C:163:ARG:O	2.19	0.43
1:A:454:G:O2'	1:A:455:G:H5'	2.18	0.43
3:D:12:ARG:HG2	3:D:33:ILE:HD12	2.01	0.43
3:D:78:ALA:HA	3:D:88:ASN:HB3	1.99	0.43
1:A:720:C:H6	1:A:720:C:O5'	2.00	0.43
8:I:71:ILE:N	8:I:71:ILE:HD12	2.28	0.43
1:A:430:A:OP2	3:D:6:PRO:HA	2.18	0.43
1:A:824:G:H2'	1:A:825:A:H8	1.84	0.43
1:A:1410:A:C6	1:A:1491:G:C6	3.07	0.43
1:A:541:G:O2'	3:D:39:GLN:HB3	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:295:C:H2'	1:A:296:U:H6	1.83	0.43
16:Q:52:CYS:HB2	16:Q:58:VAL:HG11	2.00	0.43
15:P:20:VAL:CG2	15:P:32:PHE:HB2	2.49	0.43
1:A:952:U:H2'	1:A:953:G:H8	1.84	0.43
1:A:822:U:O2'	1:A:823:C:H5'	2.17	0.43
2:C:82:ASP:O	2:C:86:LEU:HG	2.18	0.43
1:A:580:C:H2'	1:A:581:G:O4'	2.19	0.43
20:B:52:ALA:O	20:B:56:LEU:HD13	2.17	0.43
14:O:47:LYS:HE3	14:O:47:LYS:HB2	1.80	0.43
6:G:11:ILE:H	6:G:11:ILE:HD12	1.84	0.43
20:B:159:ALA:HB1	20:B:183:PHE:HE1	1.84	0.43
11:L:31:GLY:O	11:L:78:VAL:HA	2.18	0.43
1:A:948:C:O2'	1:A:949:A:H5'	2.18	0.43
6:G:145:GLU:OE2	6:G:148:LYS:HD2	2.19	0.43
1:A:828:U:O2'	20:B:24:PRO:HB3	2.18	0.43
1:A:108:G:O4'	1:A:108:G:N3	2.52	0.43
1:A:537:G:H2'	1:A:538:G:C8	2.53	0.43
1:A:725:G:O2'	1:A:726:C:H5'	2.17	0.43
1:A:291:U:H2'	1:A:292:G:H8	1.83	0.43
1:A:935:A:O2'	1:A:936:C:H5'	2.19	0.43
10:K:124:LYS:CA	21:U:34:ARG:HB3	2.36	0.43
13:N:46:LYS:NZ	18:S:9:PHE:HA	2.33	0.43
1:A:1251:A:H2'	1:A:1252:A:C8	2.53	0.43
4:E:73:VAL:HG11	4:E:143:LEU:HB3	2.01	0.43
4:E:113:VAL:CG2	4:E:114:LEU:N	2.81	0.43
1:A:411:A:N9	1:A:413:G:H1'	2.34	0.43
20:B:83:ALA:CB	20:B:90:PHE:HB3	2.48	0.43
12:M:94:LEU:HB3	12:M:95:PRO:HD2	2.00	0.43
2:C:155:ARG:H	2:C:162:ALA:CA	2.31	0.43
6:G:21:LEU:HD23	6:G:21:LEU:N	2.32	0.43
1:A:586:C:O2'	1:A:587:G:H5'	2.19	0.43
1:A:1096:C:H2'	1:A:1097:C:H6	1.83	0.43
1:A:705:G:N2	10:K:43:TRP:CE3	2.86	0.43
11:L:45:ASN:HD22	11:L:45:ASN:N	2.17	0.43
16:Q:13:SER:HB3	16:Q:21:VAL:CG2	2.48	0.43
1:A:1314:C:H2'	1:A:1315:U:H6	1.83	0.43
13:N:30:ILE:C	13:N:32:ASP:H	2.22	0.43
10:K:28:ASN:HD21	10:K:47:GLY:N	2.07	0.43
1:A:390:U:OP1	15:P:28:ARG:NH2	2.52	0.43
2:C:185:THR:HA	2:C:197:VAL:O	2.18	0.43
1:A:992:U:H1'	1:A:993:G:C2	2.54	0.43
1:A:883:C:O2'	1:A:884:U:H5'	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1380:U:O4	6:G:2:ARG:HB2	2.18	0.43
12:M:4:ALA:C	12:M:6:ILE:H	2.22	0.43
1:A:653:U:C5	7:H:55:LYS:HE2	2.53	0.43
1:A:1178:G:H2'	1:A:1180:A:OP2	2.19	0.43
1:A:1491:G:H5''	1:A:1492:A:OP2	2.19	0.43
9:J:91:ASP:C	9:J:92:LEU:HD13	2.39	0.43
1:A:649:A:H2'	1:A:650:G:O4'	2.19	0.43
1:A:173:U:H5'	1:A:197:A:O4'	2.19	0.43
16:Q:29:LYS:HG3	16:Q:34:GLY:HA2	2.01	0.43
13:N:68:ARG:HB2	13:N:79:SER:HB3	2.01	0.43
13:N:60:ARG:NH2	13:N:69:PRO:HB3	2.33	0.43
13:N:5:MET:SD	13:N:8:ARG:HD2	2.58	0.43
12:M:52:ILE:HA	12:M:55:LEU:CD1	2.49	0.43
10:K:92:ARG:HG2	10:K:92:ARG:HH11	1.84	0.43
20:B:224:ARG:H	20:B:224:ARG:HG2	1.67	0.43
1:A:1130:A:H61	1:A:1144:G:H1'	1.84	0.43
1:A:637:C:O2'	1:A:638:U:H5'	2.19	0.43
2:C:61:LYS:HA	2:C:61:LYS:NZ	2.34	0.43
20:B:107:ARG:HA	20:B:110:ILE:HD12	2.01	0.43
5:F:14:GLN:NE2	5:F:83:ALA:HB2	2.34	0.43
1:A:716:A:N3	10:K:118:ASN:O	2.52	0.43
1:A:83:C:H1'	1:A:84:U:C6	2.53	0.43
1:A:1421:G:O2'	1:A:1422:G:H5'	2.19	0.43
6:G:94:ARG:NE	6:G:98:LEU:HD11	2.33	0.43
3:D:164:ARG:HG3	3:D:165:GLU:N	2.34	0.43
3:D:60:VAL:HA	3:D:63:ILE:HD12	2.00	0.43
12:M:38:ILE:HG13	12:M:55:LEU:CD2	2.48	0.43
1:A:389:A:H3'	1:A:390:U:H6	1.83	0.43
20:B:15:PHE:HD1	20:B:16:GLY:N	2.17	0.43
2:C:48:LYS:HD3	2:C:48:LYS:N	2.28	0.43
3:D:151:GLN:N	3:D:155:LYS:NZ	2.67	0.43
7:H:36:ALA:HA	7:H:39:LEU:HD12	2.00	0.43
1:A:777:A:H2'	1:A:778:G:H8	1.84	0.43
1:A:797:C:O2'	1:A:798:U:H5'	2.18	0.43
1:A:83:C:H6	1:A:83:C:OP2	2.02	0.43
1:A:1461:G:H2'	1:A:1462:C:O4'	2.19	0.43
1:A:1284:C:H2'	1:A:1285:A:C8	2.54	0.43
1:A:1229:A:H2'	1:A:1230:C:C6	2.53	0.43
1:A:543:U:O2'	1:A:544:G:H5'	2.19	0.43
1:A:1118:U:H2'	1:A:1119:C:C6	2.54	0.43
1:A:1388:C:H2'	1:A:1389:C:C6	2.54	0.43
1:A:1216:A:H5''	13:N:4:SER:CB	2.49	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:167:PRO:O	3:D:168:THR:HG23	2.19	0.43
1:A:397:A:H3'	1:A:397:A:N3	2.34	0.43
18:S:29:PRO:HB3	18:S:47:THR:HG22	2.00	0.42
7:H:7:ALA:O	7:H:11:THR:HG23	2.18	0.42
2:C:112:ALA:CB	2:C:184:ASN:HB2	2.49	0.42
20:B:57:ASN:HA	20:B:60:ALA:HB3	1.99	0.42
1:A:475:C:O2'	1:A:476:U:H5'	2.18	0.42
1:A:782:A:H4'	1:A:1514:G:O2'	2.18	0.42
7:H:63:LYS:HG2	7:H:64:TYR:N	2.34	0.42
1:A:314:C:O2'	1:A:315:A:H5'	2.18	0.42
1:A:1225:A:H5''	12:M:101:THR:OG1	2.19	0.42
15:P:4:ILE:HB	15:P:67:ILE:HD12	2.01	0.42
8:I:66:VAL:CG1	8:I:74:GLN:HG3	2.48	0.42
12:M:91:ARG:HG3	12:M:92:ARG:N	2.33	0.42
1:A:402:G:H5'	1:A:621:A:H1'	2.01	0.42
1:A:707:U:H2'	1:A:708:C:H6	1.83	0.42
20:B:95:TRP:HZ2	20:B:100:LEU:HD22	1.83	0.42
9:J:82:LYS:HG3	9:J:83:THR:H	1.83	0.42
18:S:20:LYS:HD2	18:S:20:LYS:O	2.19	0.42
8:I:42:THR:HA	8:I:45:MET:SD	2.59	0.42
1:A:811:C:H4'	1:A:900:A:N6	2.33	0.42
1:A:1346:A:N1	1:A:1374:A:H5''	2.34	0.42
12:M:100:ARG:HG3	12:M:100:ARG:O	2.19	0.42
19:T:38:ILE:HG22	19:T:39:GLU:N	2.33	0.42
1:A:61:G:H4'	1:A:386:C:O2'	2.18	0.42
1:A:1070:U:H2'	1:A:1071:C:H6	1.81	0.42
1:A:476:U:H2'	1:A:477:C:O4'	2.19	0.42
1:A:1001:C:H2'	1:A:1002:G:O4'	2.19	0.42
1:A:1392:G:O2'	1:A:1393:U:H5'	2.18	0.42
4:E:53:ARG:HH21	4:E:54:GLU:CG	2.32	0.42
7:H:94:VAL:HG21	7:H:100:ILE:O	2.19	0.42
1:A:1330:U:H5''	12:M:22:TYR:O	2.19	0.42
1:A:807:A:H2'	1:A:808:C:C6	2.55	0.42
1:A:1385:G:H2'	1:A:1386:G:O4'	2.19	0.42
1:A:1468:A:O2'	1:A:1469:C:H5'	2.17	0.42
5:F:43:GLY:HA2	5:F:58:HIS:CE1	2.54	0.42
1:A:724:G:O2'	1:A:725:G:H5'	2.19	0.42
1:A:663:A:O2'	1:A:664:G:H5'	2.19	0.42
1:A:874:G:O2'	1:A:875:U:H5'	2.19	0.42
12:M:3:ILE:HG12	12:M:52:ILE:HD11	2.00	0.42
1:A:263:A:OP1	19:T:73:ARG:NH1	2.53	0.42
11:L:120:ARG:HG2	11:L:120:ARG:HH11	1.83	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:I:119:LYS:HB3	8:I:122:ARG:HB3	2.02	0.42
12:M:77:LYS:HG2	12:M:81:ASP:OD1	2.18	0.42
15:P:52:LEU:HD22	15:P:75:ILE:HA	2.01	0.42
1:A:812:G:O2'	1:A:813:U:C6	2.72	0.42
1:A:1332:A:H2'	1:A:1333:A:H8	1.84	0.42
1:A:1332:A:H2'	1:A:1333:A:O4'	2.19	0.42
4:E:151:MET:O	4:E:155:LYS:HG3	2.19	0.42
11:L:28:GLN:HE21	11:L:28:GLN:HB3	1.56	0.42
16:Q:23:ALA:C	16:Q:24:ILE:HD12	2.39	0.42
8:I:34:LEU:C	8:I:36:GLN:H	2.23	0.42
1:A:663:A:C5'	17:R:49:LYS:HD2	2.50	0.42
12:M:75:SER:O	12:M:78:ARG:HB2	2.20	0.42
1:A:1313:U:H2'	1:A:1314:C:C6	2.54	0.42
13:N:30:ILE:HG21	13:N:44:VAL:CG2	2.39	0.42
20:B:150:ILE:O	20:B:150:ILE:HG12	2.19	0.42
20:B:68:PHE:CE1	20:B:88:GLN:HB3	2.54	0.42
1:A:771:G:H2'	1:A:772:U:C6	2.55	0.42
11:L:79:ILE:HD12	11:L:96:THR:CG2	2.49	0.42
1:A:1343:G:H1'	8:I:122:ARG:NH1	2.29	0.42
12:M:95:PRO:HB2	12:M:99:GLN:OE1	2.19	0.42
4:E:61:LYS:NZ	4:E:61:LYS:HB3	2.34	0.42
1:A:1379:G:N7	6:G:2:ARG:CZ	2.83	0.42
1:A:177:G:N3	1:A:177:G:O4'	2.51	0.42
1:A:939:G:H5''	6:G:101:ARG:CZ	2.49	0.42
9:J:44:THR:HG23	9:J:70:HIS:HA	2.01	0.42
1:A:841:C:O2	1:A:841:C:H2'	2.18	0.42
13:N:61:ASN:O	13:N:62:ARG:HB2	2.20	0.42
13:N:50:LEU:CG	13:N:51:PRO:HD3	2.49	0.42
1:A:483:C:H2'	1:A:484:G:C8	2.55	0.42
1:A:238:A:H3'	1:A:239:U:H5''	2.02	0.42
3:D:146:GLU:HA	3:D:149:LYS:CG	2.44	0.42
1:A:676:A:H2'	1:A:677:U:C6	2.55	0.42
3:D:141:VAL:HA	3:D:179:GLY:O	2.19	0.42
18:S:68:HIS:HB3	18:S:72:GLU:CD	2.40	0.42
1:A:796:C:O2'	1:A:797:C:H5'	2.20	0.42
1:A:229:U:H2'	1:A:230:G:H8	1.83	0.42
1:A:857:C:H2'	1:A:858:G:O4'	2.19	0.42
1:A:579:A:H2'	1:A:580:C:C6	2.55	0.42
1:A:1264:U:H2'	1:A:1265:C:O4'	2.20	0.42
8:I:44:ARG:HG2	8:I:44:ARG:HH11	1.84	0.42
1:A:663:A:H2'	1:A:664:G:H8	1.83	0.42
10:K:28:ASN:ND2	10:K:56:LYS:HD2	2.35	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:M:79:LEU:CD2	12:M:86:ARG:HE	2.33	0.42
1:A:238:A:H2'	1:A:239:U:C5'	2.47	0.42
1:A:474:G:H2'	1:A:475:C:H6	1.82	0.42
1:A:337:G:O2'	1:A:338:A:H5'	2.19	0.42
1:A:255:G:H5'	16:Q:17:GLU:O	2.19	0.42
12:M:77:LYS:O	12:M:80:MET:HB2	2.20	0.42
8:I:66:VAL:HG22	8:I:67:LYS:N	2.33	0.42
1:A:430:A:O2'	1:A:431:A:H5'	2.20	0.42
2:C:38:VAL:HG23	2:C:39:ARG:N	2.34	0.42
1:A:968:A:H3'	1:A:969:A:C5'	2.49	0.42
1:A:150:U:H2'	1:A:151:A:H8	1.83	0.42
1:A:1358:U:H3'	1:A:1359:C:C6	2.55	0.42
13:N:9:GLU:HB2	13:N:62:ARG:CZ	2.50	0.42
10:K:122:PRO:HB2	21:U:33:ARG:O	2.20	0.42
13:N:76:PHE:CE2	13:N:95:LEU:HD22	2.55	0.42
15:P:28:ARG:HD3	15:P:29:ASN:ND2	2.34	0.42
1:A:128:G:H2'	1:A:129:A:C8	2.55	0.42
17:R:67:LEU:HD23	17:R:68:PRO:HD2	2.01	0.42
3:D:155:LYS:HB3	3:D:155:LYS:HE3	1.91	0.42
1:A:720:C:C5'	17:R:40:PRO:HA	2.49	0.42
18:S:52:ASN:HD22	18:S:76:THR:HA	1.85	0.42
15:P:38:PHE:CD1	15:P:39:PHE:N	2.88	0.42
1:A:213:G:C8	1:A:214:C:C5	3.08	0.42
1:A:1461:G:H2'	1:A:1462:C:H6	1.84	0.42
3:D:187:ARG:O	3:D:191:SER:HB3	2.20	0.42
17:R:28:LEU:C	17:R:30:ASN:H	2.22	0.42
20:B:8:MET:N	20:B:8:MET:SD	2.93	0.42
9:J:53:ILE:HG13	13:N:84:ARG:NE	2.34	0.42
5:F:6:ILE:HG13	5:F:62:MET:HB2	2.01	0.42
4:E:131:ASN:ND2	4:E:133:ILE:HB	2.35	0.42
20:B:161:PHE:HD2	20:B:183:PHE:HB2	1.85	0.42
16:Q:68:LYS:C	16:Q:70:LYS:N	2.73	0.42
7:H:36:ALA:O	7:H:45:ILE:HD11	2.19	0.42
1:A:958:A:N1	18:S:53:GLY:C	2.73	0.42
18:S:2:ARG:NE	18:S:2:ARG:CA	2.83	0.42
18:S:52:ASN:CG	18:S:53:GLY:N	2.73	0.42
14:O:26:GLU:OE2	14:O:77:ARG:HD2	2.19	0.42
1:A:211:G:N3	1:A:211:G:H5''	2.35	0.42
1:A:359:G:O2'	1:A:360:G:H5'	2.20	0.42
1:A:731:G:OP1	1:A:766:A:H1'	2.20	0.42
1:A:513:C:H2'	1:A:514:C:C6	2.55	0.42
15:P:12:LYS:C	15:P:14:ARG:H	2.21	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:681:A:H2'	1:A:682:G:C8	2.55	0.42
1:A:594:U:H2'	1:A:595:A:C8	2.53	0.42
1:A:1352:C:H2'	1:A:1353:G:C8	2.55	0.42
8:I:84:ARG:O	8:I:87:MET:HB3	2.19	0.42
20:B:80:LYS:O	20:B:84:LEU:HB3	2.18	0.42
2:C:109:GLU:OE1	2:C:139:ASN:HB3	2.20	0.42
6:G:30:MET:HA	6:G:38:ALA:HB2	2.01	0.42
1:A:911:U:O2'	1:A:912:C:H5'	2.19	0.42
1:A:287:U:O2'	1:A:288:A:H5'	2.20	0.42
20:B:213:LEU:O	20:B:216:VAL:HG22	2.20	0.42
9:J:41:PRO:HG2	9:J:42:LEU:H	1.85	0.42
1:A:1278:G:OP1	1:A:1279:G:H5'	2.19	0.42
6:G:144:ALA:O	6:G:146:ALA:N	2.48	0.42
6:G:63:VAL:CG1	6:G:127:ALA:HB1	2.50	0.42
1:A:1309:G:H2'	1:A:1310:G:H8	1.85	0.42
18:S:2:ARG:N	18:S:2:ARG:CZ	2.82	0.42
1:A:432:A:H2'	1:A:433:G:H5'	2.02	0.42
1:A:90:C:H2'	1:A:91:U:C6	2.55	0.42
11:L:7:VAL:HG22	16:Q:33:TYR:CD1	2.55	0.42
20:B:43:GLU:HG2	20:B:43:GLU:H	1.31	0.42
3:D:1:ALA:O	3:D:2:ARG:HG2	2.20	0.42
4:E:40:ASP:OD2	4:E:42:ASN:HB3	2.20	0.42
1:A:722:G:H2'	1:A:724:G:C8	2.54	0.42
1:A:611:C:H2'	1:A:612:C:H6	1.83	0.42
10:K:15:VAL:HB	10:K:78:ILE:CD1	2.50	0.42
1:A:940:C:H2'	1:A:941:G:C8	2.55	0.42
10:K:81:LEU:N	10:K:81:LEU:HD23	2.35	0.42
21:U:33:ARG:HH12	21:U:34:ARG:NH1	2.18	0.42
21:U:3:ILE:HG21	21:U:19:LYS:HD2	2.01	0.42
3:D:169:TRP:HB2	3:D:183:ARG:HD2	2.02	0.42
18:S:64:GLU:N	18:S:64:GLU:OE1	2.53	0.42
12:M:56:ARG:O	12:M:59:VAL:HG12	2.19	0.42
5:F:4:TYR:CD2	5:F:71:ILE:HG21	2.54	0.42
13:N:20:PHE:CZ	13:N:51:PRO:HG3	2.55	0.42
3:D:90:LEU:HD21	3:D:196:GLU:CB	2.50	0.42
11:L:33:CYS:HA	11:L:54:VAL:HA	2.02	0.42
16:Q:60:ILE:HA	16:Q:75:VAL:HG22	2.01	0.42
1:A:1166:G:N1	1:A:1169:A:OP2	2.53	0.42
1:A:1237:C:H3'	1:A:1238:A:H5'	2.00	0.42
15:P:39:PHE:CE1	15:P:74:LEU:HD21	2.55	0.42
14:O:84:ARG:C	14:O:85:LEU:HD12	2.40	0.42
2:C:154:GLY:O	2:C:155:ARG:HB2	2.18	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:P:23:ASP:OD1	15:P:25:ARG:HB2	2.20	0.42
11:L:3:VAL:O	11:L:7:VAL:HG23	2.20	0.42
16:Q:28:VAL:HG12	16:Q:37:ILE:O	2.20	0.42
1:A:1260:G:O5'	1:A:1284:C:H4'	2.20	0.42
10:K:35:ASP:OD2	10:K:39:ASN:HB2	2.19	0.42
1:A:1340:A:O2'	1:A:1341:U:H5'	2.20	0.42
16:Q:14:ASP:OD1	16:Q:53:GLY:HA2	2.20	0.42
5:F:74:LEU:HG	5:F:78:PHE:CE1	2.55	0.42
9:J:9:ARG:HE	9:J:99:GLN:NE2	2.18	0.41
12:M:52:ILE:CD1	12:M:55:LEU:HD12	2.48	0.41
19:T:57:VAL:HG23	19:T:58:ASP:N	2.35	0.41
20:B:101:THR:HG22	20:B:174:GLU:CD	2.41	0.41
1:A:921:U:O2	4:E:23:THR:HG23	2.20	0.41
13:N:50:LEU:HG	13:N:51:PRO:CD	2.50	0.41
20:B:87:ASP:CB	20:B:224:ARG:HE	2.33	0.41
3:D:54:LEU:O	3:D:58:GLN:HB2	2.20	0.41
16:Q:17:GLU:C	16:Q:19:SER:H	2.23	0.41
1:A:159:G:N2	1:A:161:A:H3'	2.35	0.41
3:D:2:ARG:O	3:D:3:TYR:HB3	2.20	0.41
1:A:1347:G:C8	8:I:108:ARG:HB3	2.55	0.41
1:A:1493:A:OP1	23:A:2367:LLL:N32	2.47	0.41
9:J:92:LEU:HB2	9:J:93:ALA:H	1.59	0.41
19:T:27:MET:CE	19:T:28:ARG:HG2	2.49	0.41
1:A:1268:G:H2'	1:A:1269:A:C8	2.55	0.41
1:A:1207:G:H2'	1:A:1208:C:C6	2.54	0.41
7:H:72:GLU:CD	7:H:72:GLU:H	2.23	0.41
20:B:42:LEU:HA	20:B:45:THR:HB	2.02	0.41
20:B:46:VAL:O	20:B:49:PHE:HB2	2.20	0.41
21:U:40:PRO:C	21:U:42:THR:N	2.73	0.41
10:K:33:ILE:CB	10:K:73:VAL:HG11	2.34	0.41
8:I:56:MET:HA	8:I:59:LYS:HB2	2.01	0.41
8:I:18:VAL:HG12	8:I:62:LEU:HB2	2.02	0.41
4:E:93:VAL:HG12	4:E:94:PHE:N	2.35	0.41
5:F:72:ASP:HA	5:F:75:GLU:OE1	2.21	0.41
20:B:65:LYS:CB	20:B:157:PRO:HA	2.50	0.41
20:B:224:ARG:HB3	20:B:224:ARG:NH1	2.34	0.41
1:A:203:G:N2	1:A:205:A:N6	2.68	0.41
7:H:63:LYS:CD	7:H:70:VAL:HG21	2.50	0.41
11:L:78:VAL:O	11:L:102:ASP:HB2	2.20	0.41
1:A:840:C:N3	1:A:842:U:H4'	2.36	0.41
3:D:148:ALA:O	3:D:154:VAL:HG21	2.20	0.41
1:A:36:C:O3'	11:L:119:LYS:HA	2.19	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:54:LEU:HD22	5:F:54:LEU:N	2.35	0.41
14:O:25:THR:CG2	14:O:70:LEU:HD23	2.50	0.41
1:A:1492:A:O2'	1:A:1493:A:H5'	2.20	0.41
1:A:692:U:H2'	1:A:694:A:OP2	2.20	0.41
1:A:487:A:H2'	1:A:488:C:O4'	2.21	0.41
1:A:114:U:O4'	1:A:353:A:H1'	2.20	0.41
1:A:1058:G:H2'	1:A:1059:C:H6	1.84	0.41
20:B:113:LEU:HD23	20:B:114:LYS:N	2.35	0.41
2:C:81:GLU:HG3	2:C:82:ASP:N	2.35	0.41
1:A:687:A:C2	1:A:704:A:C5	3.08	0.41
11:L:30:ARG:HB3	11:L:57:THR:CG2	2.50	0.41
20:B:35:ASN:HA	20:B:35:ASN:HD22	1.62	0.41
13:N:68:ARG:HA	13:N:69:PRO:HD2	1.94	0.41
21:U:44:ARG:HG3	21:U:44:ARG:NH1	2.36	0.41
20:B:101:THR:HG23	20:B:102:ASN:N	2.35	0.41
1:A:437:U:H4'	3:D:153:ARG:NH1	2.35	0.41
1:A:1225:A:N3	1:A:1225:A:H2'	2.35	0.41
18:S:35:ARG:O	18:S:71:GLY:N	2.53	0.41
2:C:146:LYS:HB2	2:C:202:PHE:CD2	2.55	0.41
20:B:25:LYS:O	20:B:28:PRO:HD2	2.20	0.41
8:I:18:VAL:HG11	8:I:82:ILE:HG12	2.01	0.41
8:I:24:ASN:ND2	8:I:25:GLY:N	2.68	0.41
3:D:18:LEU:HB2	3:D:20:LEU:HD21	2.02	0.41
20:B:148:GLY:C	20:B:150:ILE:H	2.22	0.41
1:A:1009:U:H1'	1:A:1021:A:C2	2.56	0.41
1:A:130:A:N1	1:A:233:C:H1'	2.36	0.41
11:L:23:LEU:HG	11:L:24:GLU:N	2.35	0.41
1:A:1476:A:O2'	1:A:1477:U:H5'	2.20	0.41
1:A:1479:C:H2'	1:A:1480:A:H8	1.84	0.41
5:F:53:LYS:HB2	5:F:54:LEU:HD22	2.02	0.41
1:A:1081:A:OP1	4:E:21:SER:O	2.38	0.41
18:S:68:HIS:HB3	18:S:72:GLU:OE2	2.20	0.41
5:F:11:HIS:CG	5:F:12:PRO:HD2	2.56	0.41
1:A:302:G:O2'	1:A:303:A:H5'	2.20	0.41
6:G:11:ILE:N	6:G:11:ILE:HD12	2.34	0.41
16:Q:24:ILE:HD12	16:Q:24:ILE:N	2.34	0.41
2:C:5:HIS:ND1	13:N:88:MET:HB3	2.35	0.41
4:E:48:GLY:O	4:E:62:ALA:HB1	2.20	0.41
1:A:123:U:H2'	1:A:124:C:C6	2.56	0.41
1:A:117:G:H2'	1:A:118:U:O4'	2.20	0.41
8:I:6:TYR:HE2	8:I:17:ARG:HB3	1.85	0.41
1:A:889:A:H61	1:A:907:A:H3'	1.85	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:P:40:ASN:OD1	15:P:43:ALA:N	2.53	0.41
13:N:50:LEU:HD23	13:N:51:PRO:HD3	2.03	0.41
13:N:52:ARG:HB3	13:N:53:ASP:H	1.70	0.41
1:A:818:G:C2'	1:A:819:A:H5''	2.51	0.41
2:C:165:GLU:OE2	2:C:165:GLU:HA	2.20	0.41
11:L:54:VAL:HG12	11:L:55:ARG:N	2.36	0.41
1:A:554:A:H5'	11:L:25:ALA:HB1	2.02	0.41
1:A:246:A:N6	1:A:281:G:H1'	2.36	0.41
1:A:961:U:O2	1:A:983:A:N7	2.53	0.41
8:I:94:ARG:HG2	8:I:97:LEU:HD12	2.01	0.41
1:A:1291:U:H2'	1:A:1292:G:C8	2.56	0.41
1:A:716:A:H2'	1:A:717:U:H6	1.85	0.41
1:A:1212:U:C5'	1:A:1213:A:OP1	2.69	0.41
20:B:31:PHE:HB2	20:B:41:ASN:CA	2.50	0.41
1:A:1275:A:H2'	1:A:1276:G:O4'	2.21	0.41
20:B:15:PHE:O	20:B:40:ILE:HD12	2.21	0.41
1:A:1323:G:O2'	1:A:1362:A:O4'	2.39	0.41
11:L:110:LYS:O	11:L:113:ARG:HG3	2.20	0.41
1:A:321:A:O2'	1:A:322:C:H5'	2.19	0.41
1:A:946:A:H2'	1:A:947:G:H8	1.85	0.41
15:P:54:LEU:CD1	15:P:80:LYS:HG2	2.50	0.41
20:B:41:ASN:ND2	20:B:43:GLU:HG3	2.35	0.41
1:A:894:G:O2'	1:A:895:G:H5'	2.20	0.41
1:A:343:U:O3'	1:A:344:A:H8	2.03	0.41
11:L:80:LEU:O	11:L:97:VAL:HG23	2.20	0.41
1:A:291:U:H2'	1:A:292:G:C8	2.56	0.41
20:B:80:LYS:HG3	20:B:81:ASP:OD2	2.21	0.41
10:K:122:PRO:HD2	21:U:35:GLU:HG2	2.01	0.41
21:U:36:PHE:CD2	21:U:39:LYS:HD3	2.55	0.41
1:A:1098:C:O2'	1:A:1099:G:H5'	2.21	0.41
8:I:14:SER:HA	8:I:68:GLY:O	2.20	0.41
19:T:65:LEU:HG	19:T:66:ILE:CD1	2.50	0.41
20:B:65:LYS:HD3	20:B:89:PHE:CE1	2.55	0.41
1:A:1411:C:H2'	1:A:1412:C:C6	2.55	0.41
2:C:110:LEU:CD2	2:C:145:ALA:HB2	2.50	0.41
1:A:413:G:H2'	1:A:428:G:H21	1.85	0.41
1:A:1124:G:H5''	9:J:37:ARG:O	2.20	0.41
1:A:672:U:H2'	1:A:673:A:C8	2.56	0.41
1:A:778:G:H2'	1:A:779:C:C6	2.56	0.41
1:A:1320:C:H5''	18:S:2:ARG:HE	1.83	0.41
9:J:52:LEU:HA	9:J:62:ARG:H	1.86	0.41
1:A:404:G:OP1	3:D:114:ARG:HD3	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1481:U:O2'	1:A:1482:G:H5'	2.21	0.41
1:A:487:A:H3'	1:A:488:C:C6	2.55	0.41
11:L:65:TYR:C	11:L:66:ILE:HD12	2.41	0.41
20:B:139:GLU:HG2	20:B:143:LEU:HD12	2.02	0.41
1:A:397:A:H5''	1:A:397:A:N3	2.36	0.41
17:R:19:GLU:HG3	17:R:54:LEU:HD12	2.02	0.41
1:A:1105:A:H2'	1:A:1106:G:H8	1.85	0.41
21:U:35:GLU:HB3	21:U:36:PHE:H	1.62	0.41
3:D:169:TRP:CD1	3:D:170:LEU:HD22	2.55	0.41
8:I:41:GLU:O	8:I:43:ALA:N	2.54	0.41
10:K:62:ALA:CB	10:K:91:GLY:HA3	2.50	0.41
15:P:28:ARG:HG3	15:P:28:ARG:H	1.63	0.41
2:C:26:LYS:HE3	2:C:26:LYS:HB2	1.95	0.41
1:A:818:G:H3'	1:A:819:A:H5''	2.02	0.41
12:M:44:ILE:O	12:M:47:LEU:HB2	2.20	0.41
9:J:36:VAL:HG12	9:J:38:GLY:H	1.86	0.41
1:A:449:G:H2'	1:A:450:G:C8	2.56	0.41
1:A:861:G:O2'	1:A:862:C:H5'	2.20	0.41
9:J:37:ARG:CZ	9:J:37:ARG:HA	2.50	0.41
11:L:23:LEU:C	11:L:25:ALA:N	2.75	0.41
3:D:22:SER:OG	3:D:109:THR:HG22	2.20	0.41
1:A:1320:C:H2'	1:A:1321:U:O4'	2.20	0.41
8:I:74:GLN:HE21	8:I:74:GLN:N	2.18	0.41
1:A:212:G:H2'	1:A:213:G:C8	2.52	0.41
1:A:1028:C:N3	1:A:1029:U:H1'	2.36	0.41
1:A:545:C:P	3:D:61:ARG:HH12	2.44	0.41
20:B:8:MET:HB2	20:B:9:LEU:H	1.59	0.41
5:F:20:GLY:O	5:F:24:ARG:HD3	2.20	0.41
1:A:526:C:H2'	1:A:527:G:H4'	2.02	0.41
9:J:31:ARG:H	9:J:31:ARG:HG3	1.53	0.41
14:O:64:ARG:NE	14:O:64:ARG:HA	2.36	0.41
6:G:4:ARG:HH11	6:G:4:ARG:HB2	1.86	0.41
14:O:45:GLU:O	14:O:46:HIS:HB2	2.21	0.41
21:U:42:THR:HB	21:U:46:ARG:HE	1.86	0.41
3:D:122:ILE:HG22	3:D:123:MET:H	1.86	0.41
8:I:34:LEU:HD23	8:I:35:GLU:OE1	2.20	0.41
8:I:35:GLU:H	8:I:35:GLU:CD	2.23	0.41
18:S:47:THR:C	18:S:48:ILE:HG13	2.41	0.41
19:T:43:LYS:HB3	19:T:85:LEU:HD21	2.03	0.41
9:J:53:ILE:HG23	9:J:54:SER:N	2.34	0.41
10:K:88:PRO:HA	10:K:92:ARG:HD2	2.03	0.41
5:F:67:PRO:O	5:F:71:ILE:HG23	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:89:PHE:HE2	20:B:152:ASP:O	2.03	0.41
1:A:389:A:C6	1:A:390:U:H1'	2.56	0.41
7:H:95:MET:SD	7:H:98:LEU:HB2	2.61	0.41
20:B:87:ASP:CG	20:B:224:ARG:HH21	2.24	0.41
20:B:59:ILE:O	20:B:62:ARG:HD2	2.20	0.41
1:A:817:C:H1'	1:A:819:A:C5'	2.45	0.41
1:A:1411:C:H2'	1:A:1412:C:H6	1.85	0.41
1:A:1008:U:H2'	1:A:1009:U:C5'	2.50	0.41
3:D:81:LEU:HB2	3:D:88:ASN:HD22	1.81	0.41
1:A:1120:C:H2'	1:A:1121:U:C6	2.56	0.41
1:A:182:A:H5''	1:A:182:A:N3	2.36	0.41
1:A:845:A:N7	1:A:846:G:O4'	2.53	0.41
2:C:42:LEU:O	2:C:46:LEU:HD23	2.21	0.41
2:C:2:GLN:N	2:C:2:GLN:HE21	2.19	0.41
2:C:13:ILE:HG12	2:C:14:VAL:HG13	2.02	0.41
1:A:560:A:H4'	1:A:561:U:C5'	2.50	0.41
1:A:431:A:O2'	1:A:432:A:H5'	2.21	0.41
1:A:1306:A:H8	1:A:1306:A:O5'	2.04	0.41
14:O:17:ARG:HG2	14:O:24:SER:HB2	2.02	0.41
11:L:107:LYS:O	11:L:108:ASP:HB2	2.21	0.41
1:A:1005:A:N6	1:A:1024:G:O2'	2.54	0.41
1:A:1260:G:OP1	1:A:1284:C:H4'	2.21	0.41
18:S:50:VAL:O	18:S:57:VAL:N	2.54	0.41
1:A:1256:A:H4'	1:A:1258:G:C8	2.56	0.41
1:A:1493:A:O5'	1:A:1493:A:H8	2.04	0.41
1:A:78:A:H2'	1:A:79:G:O4'	2.21	0.41
1:A:77:A:O2'	1:A:78:A:H5'	2.20	0.41
1:A:55:A:OP2	1:A:352:C:N4	2.52	0.41
1:A:169:C:C2'	1:A:170:U:H5'	2.51	0.41
1:A:1356:G:N2	1:A:1357:A:C2	2.89	0.41
1:A:228:A:O2'	15:P:60:TRP:HZ3	2.03	0.41
1:A:1264:U:O5'	1:A:1264:U:H6	2.03	0.41
1:A:612:C:H2'	1:A:613:C:C6	2.56	0.41
1:A:611:C:H2'	1:A:612:C:C6	2.56	0.41
1:A:1530:G:H2'	1:A:1531:A:C8	2.56	0.41
7:H:38:VAL:CG1	7:H:111:THR:HG22	2.51	0.41
19:T:34:VAL:HG11	19:T:78:LEU:HD13	2.03	0.41
1:A:6:G:O6	4:E:99:SER:HB2	2.21	0.41
21:U:36:PHE:HA	21:U:36:PHE:HD2	1.73	0.41
7:H:14:ARG:HG3	7:H:15:ASN:N	2.35	0.41
13:N:29:ILE:O	13:N:32:ASP:HB3	2.21	0.41
2:C:184:ASN:HD22	2:C:185:THR:H	1.69	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:E:19:ARG:HG3	4:E:31:SER:O	2.20	0.41
1:A:236:A:H2'	1:A:237:G:H8	1.86	0.41
15:P:15:PRO:HB2	15:P:17:TYR:CE1	2.56	0.41
12:M:111:PRO:HG2	12:M:112:ARG:H	1.84	0.41
1:A:674:G:H2'	1:A:675:A:C8	2.55	0.41
1:A:1309:G:C5'	12:M:76:ILE:HG12	2.50	0.41
10:K:63:GLN:HG3	10:K:98:ALA:HB2	2.03	0.41
1:A:50:A:N6	1:A:361:G:H4'	2.36	0.41
6:G:101:ARG:O	6:G:105:GLU:HG3	2.21	0.41
1:A:75:G:H2'	1:A:76:G:H8	1.86	0.41
1:A:903:G:H2'	1:A:904:U:O4'	2.21	0.41
2:C:78:LYS:HE3	2:C:81:GLU:HG2	2.03	0.41
1:A:691:G:H1'	1:A:696:A:N6	2.35	0.41
17:R:25:ILE:HG13	17:R:26:ALA:N	2.36	0.41
1:A:743:A:H2'	1:A:744:C:H6	1.86	0.41
1:A:1486:G:H2'	1:A:1487:G:O4'	2.20	0.41
1:A:1395:C:O2'	1:A:1396:A:H5'	2.21	0.41
3:D:94:GLU:HG2	3:D:185:PRO:HG3	2.02	0.40
9:J:5:ARG:NH1	9:J:5:ARG:HB2	2.36	0.40
9:J:5:ARG:N	9:J:76:ILE:O	2.54	0.40
2:C:129:PHE:CD2	2:C:156:LEU:HD22	2.56	0.40
3:D:80:ARG:HH12	3:D:81:LEU:HD23	1.86	0.40
20:B:119:GLN:HG3	20:B:136:ARG:HH11	1.85	0.40
2:C:2:GLN:N	2:C:2:GLN:NE2	2.65	0.40
1:A:591:U:O2'	1:A:592:G:H5'	2.21	0.40
11:L:82:ARG:HG2	11:L:82:ARG:NH1	2.29	0.40
14:O:12:VAL:CG1	14:O:22:THR:HG22	2.49	0.40
1:A:1300:G:H1'	1:A:1301:U:C5	2.55	0.40
1:A:926:G:N2	1:A:1505:G:H2'	2.36	0.40
1:A:557:G:H2'	1:A:558:G:O4'	2.21	0.40
2:C:4:VAL:HG22	2:C:5:HIS:N	2.35	0.40
1:A:278:G:O4'	1:A:282:A:H1'	2.21	0.40
1:A:754:C:H3'	1:A:754:C:O2	2.20	0.40
13:N:72:PHE:O	13:N:73:LEU:HD23	2.20	0.40
20:B:186:VAL:CG2	20:B:198:VAL:HG13	2.51	0.40
8:I:44:ARG:O	8:I:48:ARG:HG3	2.22	0.40
7:H:4:ASP:OD1	7:H:7:ALA:HB2	2.20	0.40
1:A:386:C:H2'	1:A:387:U:H5'	2.03	0.40
15:P:2:VAL:O	15:P:65:ALA:HA	2.22	0.40
1:A:236:A:H2'	1:A:237:G:C8	2.56	0.40
3:D:150:LYS:HA	3:D:155:LYS:HZ1	1.86	0.40
6:G:64:ALA:HA	6:G:127:ALA:CA	2.46	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:440:C:O2'	1:A:441:A:H5'	2.21	0.40
1:A:1226:C:N4	12:M:102:LYS:HG3	2.37	0.40
1:A:833:G:O2'	1:A:834:U:H5'	2.21	0.40
1:A:202:G:H4'	1:A:469:C:H5'	2.03	0.40
1:A:75:G:H2'	1:A:76:G:C8	2.56	0.40
1:A:1298:U:H2'	6:G:113:LYS:NZ	2.36	0.40
10:K:24:ALA:HA	10:K:29:THR:CG2	2.51	0.40
21:U:16:ARG:CA	21:U:16:ARG:HE	2.04	0.40
8:I:6:TYR:OH	8:I:8:THR:HG22	2.21	0.40
1:A:1532:U:C2'	1:A:1533:C:H5''	2.37	0.40
12:M:10:ASP:HB2	12:M:11:HIS:CE1	2.57	0.40
3:D:138:PRO:C	3:D:140:ASP:H	2.24	0.40
8:I:66:VAL:CG2	8:I:67:LYS:N	2.84	0.40
12:M:85:TYR:CA	12:M:88:LEU:HD12	2.51	0.40
1:A:1450:U:H2'	1:A:1452:C:C5	2.56	0.40
14:O:24:SER:HB3	14:O:27:VAL:CG2	2.48	0.40
7:H:115:ALA:O	7:H:120:LEU:HD23	2.22	0.40
11:L:107:LYS:HD2	11:L:107:LYS:C	2.42	0.40
1:A:167:A:O2'	1:A:168:G:H5'	2.22	0.40
20:B:164:ASP:OD2	20:B:166:ASP:HB2	2.21	0.40
3:D:120:LYS:HB3	3:D:128:VAL:HG21	2.04	0.40
8:I:24:ASN:O	8:I:60:LEU:N	2.55	0.40
8:I:56:MET:O	8:I:57:VAL:HB	2.22	0.40
21:U:20:ARG:HD2	21:U:20:ARG:N	2.37	0.40
13:N:23:ARG:C	13:N:25:GLU:H	2.25	0.40
15:P:46:LYS:C	15:P:48:GLU:N	2.75	0.40
10:K:28:ASN:HD22	10:K:28:ASN:HA	1.66	0.40
4:E:149:PRO:HA	7:H:98:LEU:HD22	2.03	0.40
2:C:110:LEU:HD21	2:C:140:ALA:O	2.22	0.40
1:A:633:G:H2'	1:A:634:C:H6	1.85	0.40
16:Q:75:VAL:HG23	16:Q:76:ARG:N	2.31	0.40
8:I:66:VAL:HG11	8:I:74:GLN:HG3	2.03	0.40
1:A:109:A:H2'	1:A:326:G:N2	2.37	0.40
1:A:201:G:HO2'	1:A:469:C:H4'	1.86	0.40
1:A:1230:C:H2'	1:A:1231:G:H8	1.86	0.40
1:A:1493:A:OP1	23:A:2367:LLL:H51	2.21	0.40
9:J:59:LYS:HE3	9:J:60:ASP:OD1	2.22	0.40
13:N:11:LYS:HD3	13:N:11:LYS:HA	1.83	0.40
1:A:116:A:H8	1:A:116:A:O5'	2.04	0.40
1:A:1148:U:H5'	8:I:6:TYR:HH	1.87	0.40
3:D:84:ASN:ND2	3:D:86:GLY:H	2.18	0.40
12:M:53:ASP:HA	12:M:56:ARG:HH12	1.84	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:9:MET:HB2	5:F:57:ALA:HB1	2.03	0.40
2:C:104:GLU:O	2:C:105:VAL:HG13	2.21	0.40
20:B:57:ASN:OD1	20:B:58:LYS:N	2.54	0.40
1:A:415:A:N1	1:A:428:G:O6	2.54	0.40
3:D:78:ALA:C	3:D:85:THR:HG23	2.42	0.40
1:A:719:C:O2	17:R:37:LYS:HA	2.21	0.40
17:R:33:THR:HG23	17:R:37:LYS:O	2.22	0.40
10:K:60:PHE:O	10:K:63:GLN:HB3	2.22	0.40
15:P:52:LEU:HD23	15:P:54:LEU:HG	2.02	0.40
1:A:735:C:H2'	1:A:736:C:H6	1.86	0.40
1:A:71:A:O2'	1:A:72:A:H8	2.05	0.40
15:P:26:ASN:OD1	15:P:31:ARG:HD3	2.21	0.40
1:A:360:G:O2'	1:A:361:G:H5'	2.22	0.40
1:A:443:C:H2'	1:A:444:G:H8	1.82	0.40
20:B:41:ASN:CG	20:B:43:GLU:HG3	2.42	0.40
1:A:596:A:H2'	1:A:597:G:C8	2.54	0.40
7:H:105:THR:C	7:H:107:LYS:H	2.25	0.40
1:A:1484:C:O2'	1:A:1485:U:H5'	2.22	0.40
1:A:173:U:H6	1:A:198:G:HO2'	1.70	0.40
8:I:45:MET:N	8:I:45:MET:SD	2.93	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	C	204/232 (88%)	156 (76%)	35 (17%)	13 (6%)	2	30
3	D	203/205 (99%)	143 (70%)	45 (22%)	15 (7%)	2	25
4	E	148/166 (89%)	115 (78%)	29 (20%)	4 (3%)	8	57
5	F	98/135 (73%)	70 (71%)	19 (19%)	9 (9%)	1	18
6	G	150/178 (84%)	121 (81%)	18 (12%)	11 (7%)	2	26
7	H	127/129 (98%)	99 (78%)	23 (18%)	5 (4%)	5	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	I	125/129 (97%)	86 (69%)	29 (23%)	10 (8%)	1	22
9	J	96/103 (93%)	70 (73%)	15 (16%)	11 (12%)	1	13
10	K	115/128 (90%)	84 (73%)	25 (22%)	6 (5%)	3	36
11	L	121/123 (98%)	79 (65%)	34 (28%)	8 (7%)	2	29
12	M	111/117 (95%)	77 (69%)	26 (23%)	8 (7%)	2	26
13	N	92/100 (92%)	58 (63%)	24 (26%)	10 (11%)	1	13
14	O	86/89 (97%)	64 (74%)	19 (22%)	3 (4%)	6	51
15	P	78/82 (95%)	55 (70%)	18 (23%)	5 (6%)	2	30
16	Q	79/83 (95%)	56 (71%)	17 (22%)	6 (8%)	2	24
17	R	53/74 (72%)	40 (76%)	10 (19%)	3 (6%)	3	34
18	S	78/91 (86%)	61 (78%)	11 (14%)	6 (8%)	1	24
19	T	83/86 (96%)	64 (77%)	14 (17%)	5 (6%)	2	32
20	B	216/240 (90%)	149 (69%)	51 (24%)	16 (7%)	2	25
21	U	49/70 (70%)	27 (55%)	15 (31%)	7 (14%)	0	7
All	All	2312/2560 (90%)	1674 (72%)	477 (21%)	161 (7%)	2	27

All (161) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	14	VAL
2	C	54	ILE
2	C	205	GLU
3	D	24	VAL
4	E	102	THR
5	F	92	THR
6	G	3	ARG
6	G	71	THR
8	I	8	THR
8	I	127	SER
9	J	57	VAL
9	J	61	ALA
10	K	126	ARG
11	L	13	ARG
11	L	24	GLU
11	L	121	PRO
11	L	122	LYS
12	M	6	ILE

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Mol	Chain	Res	Type
12	M	111	PRO
13	N	50	LEU
14	O	74	ASP
15	P	28	ARG
15	P	44	SER
16	Q	32	ILE
20	B	19	THR
20	B	22	TRP
20	B	94	ARG
20	B	188	THR
2	C	104	GLU
2	C	153	SER
2	C	180	ASP
3	D	154	VAL
3	D	168	THR
3	D	192	ALA
4	E	20	VAL
4	E	108	GLY
5	F	54	LEU
5	F	85	ILE
5	F	98	GLU
6	G	88	VAL
8	I	24	ASN
8	I	42	THR
8	I	57	VAL
8	I	106	ASP
9	J	36	VAL
9	J	74	VAL
9	J	100	ILE
10	K	88	PRO
11	L	117	GLY
12	M	15	VAL
12	M	22	TYR
13	N	33	VAL
13	N	61	ASN
13	N	71	GLY
14	O	88	ARG
15	P	52	LEU
17	R	44	THR
18	S	4	LEU
19	T	3	ILE
20	B	14	HIS

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Mol	Chain	Res	Type
20	B	15	PHE
20	B	150	ILE
20	B	163	ILE
21	U	34	ARG
21	U	35	GLU
21	U	36	PHE
2	C	3	LYS
2	C	59	PRO
3	D	31	CYS
3	D	167	PRO
4	E	43	GLY
5	F	89	VAL
6	G	70	PRO
6	G	92	PRO
6	G	112	ASP
8	I	122	ARG
9	J	32	THR
9	J	38	GLY
9	J	56	HIS
10	K	125	LYS
11	L	42	LYS
12	M	3	ILE
12	M	49	GLU
12	M	97	ARG
13	N	20	PHE
13	N	48	GLN
16	Q	81	ALA
17	R	43	ILE
17	R	46	THR
18	S	7	GLY
18	S	53	GLY
18	S	63	ASP
20	B	18	GLN
20	B	127	LYS
20	B	131	LYS
20	B	205	ALA
21	U	41	THR
2	C	47	ALA
2	C	107	LYS
2	C	145	ALA
3	D	22	SER
3	D	27	ILE

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Mol	Chain	Res	Type
3	D	28	ASP
3	D	68	GLU
5	F	58	HIS
5	F	62	MET
7	H	52	GLY
7	H	65	PHE
7	H	82	LEU
8	I	55	ASP
9	J	75	ASP
10	K	14	GLN
10	K	71	ASP
11	L	15	VAL
11	L	23	LEU
15	P	49	GLY
16	Q	26	ARG
16	Q	28	VAL
16	Q	69	THR
18	S	13	HIS
19	T	42	ASP
19	T	65	LEU
19	T	67	HIS
20	B	120	SER
21	U	9	GLU
3	D	3	TYR
3	D	25	ARG
3	D	174	ALA
5	F	82	ASP
6	G	66	GLU
6	G	129	ASN
7	H	2	MET
9	J	34	ALA
12	M	66	GLY
13	N	30	ILE
14	O	18	ASP
15	P	46	LYS
21	U	37	TYR
21	U	40	PRO
2	C	167	TYR
3	D	86	GLY
5	F	51	ILE
6	G	38	ALA
6	G	151	ALA

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Mol	Chain	Res	Type
8	I	25	GLY
8	I	120	ALA
13	N	19	TYR
13	N	57	SER
19	T	41	GLY
20	B	58	LYS
20	B	200	PRO
3	D	107	GLY
9	J	41	PRO
13	N	51	PRO
10	K	119	GLY
7	H	26	MET
20	B	70	GLY
2	C	100	ILE
6	G	81	GLY
16	Q	31	PRO
18	S	61	VAL

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	C	170/189 (90%)	145 (85%)	25 (15%)	4	27
3	D	172/172 (100%)	148 (86%)	24 (14%)	5	29
4	E	113/125 (90%)	102 (90%)	11 (10%)	12	51
5	F	87/116 (75%)	70 (80%)	17 (20%)	2	12
6	G	125/146 (86%)	114 (91%)	11 (9%)	14	57
7	H	104/104 (100%)	97 (93%)	7 (7%)	23	71
8	I	105/106 (99%)	89 (85%)	16 (15%)	4	25
9	J	86/90 (96%)	75 (87%)	11 (13%)	6	33
10	K	90/98 (92%)	77 (86%)	13 (14%)	5	27
11	L	103/103 (100%)	92 (89%)	11 (11%)	10	45
12	M	91/95 (96%)	79 (87%)	12 (13%)	6	32
13	N	79/83 (95%)	64 (81%)	15 (19%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	O	76/77 (99%)	69 (91%)	7 (9%)	13	54
15	P	65/65 (100%)	58 (89%)	7 (11%)	9	44
16	Q	75/77 (97%)	62 (83%)	13 (17%)	3	17
17	R	48/64 (75%)	41 (85%)	7 (15%)	5	27
18	S	71/78 (91%)	56 (79%)	15 (21%)	1	9
19	T	65/65 (100%)	58 (89%)	7 (11%)	9	44
20	B	180/198 (91%)	147 (82%)	33 (18%)	2	14
21	U	44/60 (73%)	33 (75%)	11 (25%)	1	6
All	All	1949/2111 (92%)	1676 (86%)	273 (14%)	5	29

All (273) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	2	GLN
2	C	13	ILE
2	C	14	VAL
2	C	17	TRP
2	C	20	THR
2	C	24	ASN
2	C	27	GLU
2	C	28	PHE
2	C	35	ASP
2	C	41	TYR
2	C	42	LEU
2	C	48	LYS
2	C	61	LYS
2	C	88	LYS
2	C	101	ASN
2	C	106	ARG
2	C	120	THR
2	C	138	GLN
2	C	163	ARG
2	C	166	TRP
2	C	168	ARG
2	C	171	ARG
2	C	184	ASN
2	C	192	TYR
2	C	206	ILE
3	D	4	LEU

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Mol	Chain	Res	Type
3	D	12	ARG
3	D	18	LEU
3	D	25	ARG
3	D	28	ASP
3	D	35	GLN
3	D	39	GLN
3	D	43	ARG
3	D	49	ASP
3	D	55	ARG
3	D	57	LYS
3	D	70	GLN
3	D	84	ASN
3	D	87	GLU
3	D	146	GLU
3	D	147	LYS
3	D	153	ARG
3	D	155	LYS
3	D	160	LEU
3	D	163	GLN
3	D	168	THR
3	D	190	LEU
3	D	193	ASP
3	D	204	SER
4	E	9	GLU
4	E	23	THR
4	E	44	ARG
4	E	45	VAL
4	E	51	LYS
4	E	61	LYS
4	E	64	GLU
4	E	92	ARG
4	E	95	MET
4	E	119	VAL
4	E	123	LEU
5	F	6	ILE
5	F	7	VAL
5	F	13	ASP
5	F	16	GLU
5	F	24	ARG
5	F	39	LEU
5	F	45	ARG
5	F	53	LYS

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Mol	Chain	Res	Type
5	F	61	LEU
5	F	65	GLU
5	F	69	GLU
5	F	73	GLU
5	F	86	ARG
5	F	88	MET
5	F	96	VAL
5	F	98	GLU
5	F	100	SER
6	G	10	LYS
6	G	55	LYS
6	G	57	GLU
6	G	62	GLU
6	G	78	ARG
6	G	89	GLU
6	G	94	ARG
6	G	109	LYS
6	G	110	ARG
6	G	125	ASP
6	G	132	THR
7	H	55	LYS
7	H	57	GLU
7	H	72	GLU
7	H	76	ARG
7	H	79	ARG
7	H	111	THR
7	H	113	ARG
8	I	26	LYS
8	I	36	GLN
8	I	45	MET
8	I	58	GLU
8	I	59	LYS
8	I	62	LEU
8	I	64	ILE
8	I	67	LYS
8	I	74	GLN
8	I	87	MET
8	I	92	SER
8	I	93	LEU
8	I	109	GLN
8	I	122	ARG
8	I	123	ARG

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Mol	Chain	Res	Type
8	I	129	ARG
9	J	14	ASP
9	J	31	ARG
9	J	37	ARG
9	J	47	GLU
9	J	57	VAL
9	J	78	GLU
9	J	87	LEU
9	J	88	MET
9	J	89	ARG
9	J	92	LEU
9	J	97	ASP
10	K	28	ASN
10	K	29	THR
10	K	34	THR
10	K	51	PHE
10	K	55	ARG
10	K	56	LYS
10	K	76	TYR
10	K	80	ASN
10	K	82	GLU
10	K	84	MET
10	K	100	ASN
10	K	105	ARG
10	K	126	ARG
11	L	14	LYS
11	L	15	VAL
11	L	17	LYS
11	L	19	ASN
11	L	28	GLN
11	L	33	CYS
11	L	43	LYS
11	L	49	ARG
11	L	77	SER
11	L	95	HIS
11	L	107	LYS
12	M	2	ARG
12	M	10	ASP
12	M	28	ARG
12	M	40	GLU
12	M	44	ILE
12	M	46	GLU

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Mol	Chain	Res	Type
12	M	65	GLU
12	M	70	ARG
12	M	79	LEU
12	M	81	ASP
12	M	82	LEU
12	M	91	ARG
13	N	3	GLN
13	N	5	MET
13	N	25	GLU
13	N	26	LEU
13	N	27	LYS
13	N	32	ASP
13	N	40	ARG
13	N	48	GLN
13	N	50	LEU
13	N	53	ASP
13	N	58	ARG
13	N	60	ARG
13	N	64	ARG
13	N	65	GLN
13	N	68	ARG
14	O	20	ASN
14	O	26	GLU
14	O	54	ARG
14	O	64	ARG
14	O	68	ASP
14	O	70	LEU
14	O	88	ARG
15	P	5	ARG
15	P	26	ASN
15	P	28	ARG
15	P	45	GLU
15	P	51	ARG
15	P	68	SER
15	P	79	ASN
16	Q	3	LYS
16	Q	5	ARG
16	Q	10	ARG
16	Q	20	ILE
16	Q	39	ARG
16	Q	56	ASP
16	Q	60	ILE

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Mol	Chain	Res	Type
16	Q	61	ARG
16	Q	66	LEU
16	Q	71	SER
16	Q	74	LEU
16	Q	79	GLU
16	Q	80	LYS
17	R	23	LYS
17	R	35	SER
17	R	38	ILE
17	R	44	THR
17	R	46	THR
17	R	51	GLN
17	R	71	ASP
18	S	2	ARG
18	S	4	LEU
18	S	12	LEU
18	S	13	HIS
18	S	20	LYS
18	S	27	LYS
18	S	28	LYS
18	S	32	THR
18	S	38	THR
18	S	42	ASN
18	S	47	THR
18	S	64	GLU
18	S	66	VAL
18	S	77	ARG
18	S	80	ARG
19	T	3	ILE
19	T	4	LYS
19	T	43	LYS
19	T	53	MET
19	T	69	ASN
19	T	74	HIS
19	T	85	LEU
20	B	8	MET
20	B	23	ASN
20	B	27	LYS
20	B	35	ASN
20	B	38	HIS
20	B	43	GLU
20	B	46	VAL

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Mol	Chain	Res	Type
20	B	48	MET
20	B	50	ASN
20	B	62	ARG
20	B	72	LYS
20	B	88	GLN
20	B	93	HIS
20	B	94	ARG
20	B	104	LYS
20	B	107	ARG
20	B	113	LEU
20	B	119	GLN
20	B	121	GLN
20	B	122	ASP
20	B	127	LYS
20	B	130	LYS
20	B	132	GLU
20	B	144	GLU
20	B	176	ASN
20	B	196	ASP
20	B	202	ASN
20	B	210	THR
20	B	211	LEU
20	B	212	TYR
20	B	213	LEU
20	B	221	ARG
20	B	224	ARG
21	U	11	PHE
21	U	16	ARG
21	U	22	CYS
21	U	24	LYS
21	U	28	LEU
21	U	33	ARG
21	U	34	ARG
21	U	36	PHE
21	U	38	GLU
21	U	44	ARG
21	U	48	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (63) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	2	GLN

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Mol	Chain	Res	Type
2	C	31	ASN
2	C	101	ASN
2	C	139	ASN
3	D	35	GLN
3	D	39	GLN
3	D	53	GLN
3	D	84	ASN
3	D	135	GLN
3	D	151	GLN
3	D	163	GLN
4	E	42	ASN
4	E	131	ASN
5	F	46	GLN
5	F	68	GLN
6	G	8	GLN
6	G	67	ASN
6	G	121	ASN
7	H	3	GLN
7	H	37	ASN
7	H	117	GLN
8	I	4	GLN
8	I	30	ASN
8	I	36	GLN
8	I	49	GLN
8	I	80	HIS
9	J	20	GLN
9	J	56	HIS
9	J	99	GLN
10	K	21	HIS
10	K	28	ASN
10	K	39	ASN
10	K	80	ASN
10	K	100	ASN
10	K	118	ASN
11	L	19	ASN
11	L	28	GLN
11	L	45	ASN
11	L	111	GLN
12	M	7	ASN
12	M	90	HIS
14	O	28	GLN
14	O	40	GLN

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Mol	Chain	Res	Type
14	O	62	GLN
15	P	9	HIS
15	P	29	ASN
15	P	63	GLN
17	R	51	GLN
17	R	53	GLN
18	S	42	ASN
18	S	52	ASN
18	S	55	GLN
19	T	2	ASN
19	T	20	ASN
19	T	69	ASN
19	T	83	ASN
20	B	14	HIS
20	B	23	ASN
20	B	35	ASN
20	B	88	GLN
20	B	119	GLN
20	B	121	GLN
20	B	202	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1529/1542 (99%)	231 (15%)	19 (1%)

All (231) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	14	U
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	52	C
1	A	55	A
1	A	61	G
1	A	67	C
1	A	68	G

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Mol	Chain	Res	Type
1	A	71	A
1	A	72	A
1	A	83	C
1	A	84	U
1	A	87	C
1	A	97	G
1	A	108	G
1	A	121	U
1	A	122	G
1	A	130	A
1	A	131	A
1	A	151	A
1	A	182	A
1	A	183	C
1	A	197	A
1	A	202	G
1	A	209	U
1	A	210	C
1	A	233	C
1	A	239	U
1	A	240	G
1	A	243	A
1	A	244	U
1	A	245	U
1	A	247	G
1	A	250	A
1	A	251	G
1	A	253	A
1	A	257	G
1	A	258	G
1	A	266	G
1	A	267	C
1	A	280	C
1	A	289	G
1	A	316	C
1	A	321	A
1	A	328	C
1	A	329	A
1	A	330	C
1	A	332	G
1	A	345	C
1	A	352	C

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Mol	Chain	Res	Type
1	A	354	G
1	A	367	U
1	A	373	A
1	A	381	C
1	A	397	A
1	A	398	U
1	A	406	G
1	A	408	A
1	A	409	U
1	A	411	A
1	A	412	A
1	A	413	G
1	A	414	A
1	A	421	U
1	A	422	C
1	A	424	G
1	A	429	U
1	A	430	A
1	A	435	A
1	A	438	U
1	A	460	A
1	A	461	A
1	A	462	G
1	A	463	U
1	A	464	U
1	A	465	A
1	A	466	A
1	A	467	U
1	A	468	A
1	A	469	C
1	A	482	A
1	A	484	G
1	A	485	U
1	A	493	A
1	A	500	G
1	A	509	A
1	A	511	C
1	A	518	C
1	A	527	G
1	A	532	A
1	A	547	A
1	A	559	A

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Mol	Chain	Res	Type
1	A	562	U
1	A	572	A
1	A	573	A
1	A	576	C
1	A	577	G
1	A	596	A
1	A	653	U
1	A	665	A
1	A	695	A
1	A	700	G
1	A	721	G
1	A	724	G
1	A	731	G
1	A	733	G
1	A	747	A
1	A	748	G
1	A	755	G
1	A	777	A
1	A	781	A
1	A	782	A
1	A	787	A
1	A	793	U
1	A	794	A
1	A	812	G
1	A	813	U
1	A	815	A
1	A	817	C
1	A	818	G
1	A	819	A
1	A	821	G
1	A	828	U
1	A	829	G
1	A	841	C
1	A	842	U
1	A	843	U
1	A	844	G
1	A	846	G
1	A	847	G
1	A	907	A
1	A	914	A
1	A	926	G
1	A	927	G

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Mol	Chain	Res	Type
1	A	934	C
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	975	A
1	A	976	G
1	A	977	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1009	U
1	A	1020	G
1	A	1025	U
1	A	1026	G
1	A	1027	C
1	A	1028	C
1	A	1030	U
1	A	1031	C
1	A	1034	G
1	A	1035	A
1	A	1050	G
1	A	1053	G
1	A	1065	U
1	A	1066	C
1	A	1085	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1136	C
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1158	C
1	A	1159	U
1	A	1168	U
1	A	1169	A
1	A	1181	G

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Mol	Chain	Res	Type
1	A	1183	U
1	A	1184	G
1	A	1196	A
1	A	1197	A
1	A	1201	A
1	A	1202	U
1	A	1212	U
1	A	1213	A
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1240	U
1	A	1241	G
1	A	1256	A
1	A	1257	A
1	A	1261	A
1	A	1278	G
1	A	1279	G
1	A	1280	A
1	A	1281	C
1	A	1286	U
1	A	1299	A
1	A	1300	G
1	A	1305	G
1	A	1316	G
1	A	1317	C
1	A	1318	A
1	A	1320	C
1	A	1323	G
1	A	1336	C
1	A	1364	U
1	A	1381	U
1	A	1398	A
1	A	1400	C
1	A	1401	G
1	A	1419	G
1	A	1432	G
1	A	1446	A
1	A	1452	C
1	A	1475	G
1	A	1492	A
1	A	1497	G

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Mol	Chain	Res	Type
1	A	1503	A
1	A	1506	U
1	A	1517	G
1	A	1519	A
1	A	1520	C
1	A	1529	G
1	A	1530	G
1	A	1533	C
1	A	1534	A

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	51	A
1	A	239	U
1	A	243	A
1	A	266	G
1	A	279	A
1	A	328	C
1	A	366	A
1	A	372	C
1	A	428	G
1	A	429	U
1	A	484	G
1	A	975	A
1	A	1049	U
1	A	1065	U
1	A	1168	U
1	A	1201	A
1	A	1226	C
1	A	1397	C
1	A	1451	U

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 65 ligands modelled in this entry, 62 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
23	LLL	A	2367	-	33,33,33	3.13	13 (39%)	49,49,49	1.41	5 (10%)
23	LLL	A	2368	-	33,33,33	3.21	16 (48%)	49,49,49	1.52	5 (10%)
23	LLL	A	2369	-	33,33,33	3.08	14 (42%)	49,49,49	1.45	4 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	LLL	A	2367	-	-	0/12/65/65	0/3/3/3
23	LLL	A	2368	-	-	0/12/65/65	0/3/3/3
23	LLL	A	2369	-	-	0/12/65/65	0/3/3/3

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	A	2368	LLL	C22-C32	8.96	1.59	1.52
23	A	2369	LLL	C22-C32	8.80	1.59	1.52
23	A	2367	LLL	C22-C32	8.76	1.59	1.52
23	A	2368	LLL	C22-C12	7.41	1.58	1.52
23	A	2367	LLL	C22-C12	7.12	1.57	1.52
23	A	2369	LLL	C22-C12	6.88	1.57	1.52
23	A	2368	LLL	O53-C53	6.21	1.52	1.43
23	A	2367	LLL	O53-C53	5.99	1.52	1.43
23	A	2369	LLL	O53-C53	5.91	1.51	1.43
23	A	2368	LLL	C43-C33	4.98	1.63	1.54
23	A	2367	LLL	C43-C33	4.80	1.63	1.54
23	A	2368	LLL	C42-C32	4.80	1.59	1.52
23	A	2369	LLL	C42-C32	4.80	1.59	1.52
23	A	2368	LLL	O53-C13	4.69	1.52	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	A	2369	LLL	C43-C33	4.66	1.63	1.54
23	A	2367	LLL	O53-C13	4.64	1.51	1.41
23	A	2367	LLL	C42-C32	4.60	1.59	1.52
23	A	2369	LLL	O53-C13	4.54	1.51	1.41
23	A	2367	LLL	C53-C43	3.82	1.56	1.52
23	A	2368	LLL	O51-C11	3.68	1.51	1.41
23	A	2369	LLL	C53-C43	3.63	1.56	1.52
23	A	2367	LLL	O51-C11	3.61	1.51	1.41
23	A	2367	LLL	C41-C51	3.53	1.60	1.51
23	A	2368	LLL	C53-C43	3.49	1.56	1.52
23	A	2369	LLL	C41-C51	3.47	1.60	1.51
23	A	2368	LLL	C41-C51	3.46	1.60	1.51
23	A	2369	LLL	O51-C11	3.42	1.50	1.41
23	A	2368	LLL	C23-C33	2.84	1.60	1.52
23	A	2367	LLL	C23-C33	2.83	1.60	1.52
23	A	2368	LLL	C52-C42	2.78	1.60	1.52
23	A	2369	LLL	C23-C33	2.63	1.59	1.52
23	A	2367	LLL	C52-C42	2.43	1.59	1.52
23	A	2367	LLL	C31-C21	2.37	1.59	1.52
23	A	2368	LLL	C31-C21	2.36	1.59	1.52
23	A	2367	LLL	C62-C12	2.29	1.56	1.52
23	A	2369	LLL	C31-C21	2.26	1.58	1.52
23	A	2368	LLL	C52-C62	2.19	1.58	1.52
23	A	2369	LLL	C52-C42	2.19	1.58	1.52
23	A	2368	LLL	O62-C13	2.16	1.47	1.41
23	A	2368	LLL	C62-C12	2.08	1.55	1.52
23	A	2368	LLL	C41-C31	2.05	1.58	1.52
23	A	2369	LLL	O11-C42	-2.04	1.38	1.43
23	A	2369	LLL	C62-C12	2.02	1.55	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	2368	LLL	C93-N33-C33	6.02	117.27	113.85
23	A	2369	LLL	C93-N33-C33	5.52	116.99	113.85
23	A	2368	LLL	C53-O53-C13	4.80	118.06	111.22
23	A	2367	LLL	C93-N33-C33	4.71	116.53	113.85
23	A	2367	LLL	C53-O53-C13	4.66	117.85	111.22
23	A	2369	LLL	C53-O53-C13	4.39	117.48	111.22
23	A	2367	LLL	C83-C43-C33	2.85	116.88	112.15
23	A	2368	LLL	C83-C43-C33	2.81	116.82	112.15
23	A	2369	LLL	O43-C43-C83	-2.59	102.36	108.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	2368	LLL	O43-C43-C83	-2.58	102.38	108.08
23	A	2367	LLL	O43-C43-C83	-2.45	102.68	108.08
23	A	2369	LLL	C83-C43-C33	2.44	116.20	112.15
23	A	2367	LLL	C13-O62-C62	2.26	123.76	117.99
23	A	2368	LLL	C13-O62-C62	2.06	123.24	117.99

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1530/1542 (99%)	-0.14	58 (3%) 38 18	5, 60, 120, 167	0
2	C	206/232 (88%)	0.94	36 (17%) 2 2	5, 74, 103, 160	0
3	D	205/205 (100%)	0.68	29 (14%) 3 3	8, 65, 107, 121	0
4	E	150/166 (90%)	2.12	66 (44%) 1 1	5, 59, 96, 125	0
5	F	100/135 (74%)	0.40	11 (11%) 6 4	12, 72, 109, 123	0
6	G	152/178 (85%)	1.40	41 (26%) 1 2	29, 80, 115, 134	0
7	H	129/129 (100%)	1.65	50 (38%) 1 1	5, 56, 91, 112	0
8	I	127/129 (98%)	0.17	11 (8%) 10 6	35, 84, 118, 157	0
9	J	98/103 (95%)	1.55	28 (28%) 1 1	33, 84, 110, 125	0
10	K	117/128 (91%)	-0.24	4 (3%) 43 20	5, 56, 101, 119	0
11	L	123/123 (100%)	1.00	30 (24%) 1 2	5, 47, 103, 123	0
12	M	113/117 (96%)	1.15	26 (23%) 1 2	48, 89, 116, 135	0
13	N	96/100 (96%)	0.77	15 (15%) 3 3	40, 87, 114, 142	0
14	O	88/89 (98%)	0.27	5 (5%) 23 10	5, 56, 107, 128	0
15	P	80/82 (97%)	1.97	35 (43%) 1 1	11, 59, 109, 147	0
16	Q	81/83 (97%)	0.01	5 (6%) 20 9	9, 58, 99, 121	0
17	R	55/74 (74%)	0.23	6 (10%) 6 5	19, 68, 119, 131	0
18	S	80/91 (87%)	0.15	3 (3%) 38 18	48, 94, 127, 153	0
19	T	85/86 (98%)	0.91	20 (23%) 1 2	19, 61, 106, 125	0
20	B	218/240 (90%)	0.03	10 (4%) 31 14	29, 89, 118, 144	0
21	U	51/70 (72%)	0.59	7 (13%) 4 3	46, 78, 116, 132	0
All	All	3884/4102 (94%)	0.44	496 (12%) 4 3	5, 69, 116, 167	0

All (496) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	E	54	GLU	11.4
6	G	9	ARG	10.3
1	A	5	U	9.7
2	C	167	TYR	9.6
6	G	8	GLN	9.5
4	E	13	LYS	9.5
15	P	80	LYS	8.8
4	E	12	GLU	8.6
4	E	11	GLN	8.1
1	A	1346	A	7.9
1	A	1492	A	7.9
12	M	11	HIS	7.9
2	C	165	GLU	7.8
6	G	4	ARG	7.7
4	E	56	PRO	7.7
6	G	10	LYS	7.2
4	E	53	ARG	7.1
2	C	133	MET	6.8
6	G	12	LEU	6.8
20	B	154	GLY	6.7
7	H	90	GLU	6.7
11	L	14	LYS	6.7
1	A	1534	A	6.6
2	C	151	GLU	6.5
15	P	6	LEU	6.5
4	E	14	LEU	6.5
1	A	6	G	6.4
6	G	11	ILE	6.4
6	G	105	GLU	6.2
1	A	485	U	6.2
4	E	60	GLN	6.2
1	A	1257	A	6.2
11	L	58	ASN	6.1
11	L	13	ARG	6.1
9	J	68	ARG	6.0
4	E	57	ALA	6.0
7	H	68	LYS	6.0
8	I	129	ARG	6.0
2	C	134	LYS	5.9
1	A	1344	C	5.9
11	L	43	LYS	5.9
7	H	89	ASP	5.8
4	E	28	ARG	5.8

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Mol	Chain	Res	Type	RSRZ
1	A	1204	A	5.8
19	T	68	LYS	5.8
4	E	52	ALA	5.7
15	P	35	ARG	5.7
4	E	55	VAL	5.6
1	A	443	C	5.5
6	G	153	TYR	5.4
7	H	69	ALA	5.4
12	M	9	PRO	5.3
7	H	75	GLN	5.3
11	L	15	VAL	5.3
7	H	127	TYR	5.2
12	M	47	LEU	5.2
19	T	7	LYS	5.2
6	G	73	GLU	5.2
4	E	19	ARG	5.1
1	A	1374	A	5.1
6	G	106	ALA	5.1
2	C	166	TRP	5.1
2	C	189	HIS	5.0
6	G	108	ARG	5.0
20	B	155	GLY	5.0
13	N	82	LYS	4.9
3	D	82	LYS	4.9
7	H	72	GLU	4.9
7	H	2	MET	4.9
7	H	93	LYS	4.9
2	C	130	ARG	4.8
11	L	12	ALA	4.8
1	A	773	G	4.8
4	E	144	GLU	4.8
1	A	962	C	4.8
4	E	30	PHE	4.7
4	E	86	GLY	4.7
7	H	4	ASP	4.7
4	E	59	ILE	4.7
7	H	63	LYS	4.7
4	E	85	LYS	4.6
3	D	127	ARG	4.5
6	G	80	GLY	4.5
9	J	44	THR	4.5
6	G	81	GLY	4.5

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Mol	Chain	Res	Type	RSRZ
4	E	31	SER	4.5
2	C	128	MET	4.5
9	J	18	ILE	4.5
3	D	46	ARG	4.4
7	H	70	VAL	4.4
7	H	76	ARG	4.4
8	I	123	ARG	4.4
17	R	50	TYR	4.4
7	H	67	GLY	4.4
1	A	1397	C	4.4
2	C	124	GLU	4.3
11	L	123	ALA	4.3
9	J	47	GLU	4.3
9	J	17	LEU	4.3
11	L	16	ALA	4.3
6	G	7	GLY	4.3
15	P	67	ILE	4.3
15	P	61	VAL	4.2
2	C	131	ARG	4.2
2	C	40	GLN	4.2
15	P	47	GLU	4.2
11	L	21	PRO	4.2
15	P	34	GLU	4.2
14	O	89	ARG	4.2
9	J	45	ARG	4.2
19	T	3	ILE	4.2
4	E	84	VAL	4.1
15	P	62	GLY	4.1
15	P	4	ILE	4.1
8	I	121	ARG	4.1
13	N	1	ALA	4.1
1	A	1187	G	4.1
4	E	110	MET	4.1
17	R	19	GLU	4.1
12	M	112	ARG	4.1
2	C	138	GLN	4.0
13	N	76	PHE	4.0
2	C	125	ARG	4.0
15	P	59	HIS	4.0
20	B	153	MET	4.0
9	J	70	HIS	3.9
4	E	92	ARG	3.9

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Mol	Chain	Res	Type	RSRZ
6	G	117	LEU	3.9
1	A	554	A	3.9
12	M	10	ASP	3.9
9	J	46	LYS	3.9
13	N	97	LYS	3.9
3	D	62	ARG	3.9
15	P	22	ALA	3.9
1	A	1202	U	3.9
2	C	22	PHE	3.9
2	C	129	PHE	3.8
7	H	71	VAL	3.8
7	H	126	CYS	3.8
11	L	59	GLY	3.8
7	H	84	ILE	3.8
3	D	4	LEU	3.8
4	E	58	ALA	3.8
11	L	80	LEU	3.8
2	C	156	LEU	3.8
6	G	152	HIS	3.7
1	A	940	C	3.7
9	J	5	ARG	3.7
9	J	12	ALA	3.7
3	D	63	ILE	3.7
1	A	632	U	3.7
11	L	11	ARG	3.7
7	H	9	MET	3.7
19	T	35	TYR	3.7
6	G	21	LEU	3.7
17	R	53	GLN	3.7
1	A	304	U	3.6
5	F	35	LYS	3.6
6	G	107	ALA	3.6
15	P	5	ARG	3.6
4	E	21	SER	3.5
18	S	15	LEU	3.5
2	C	198	LYS	3.5
19	T	67	HIS	3.5
6	G	79	VAL	3.5
1	A	555	U	3.5
11	L	24	GLU	3.5
3	D	16	THR	3.5
12	M	12	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
21	U	46	ARG	3.5
11	L	122	LYS	3.4
4	E	83	PRO	3.4
15	P	43	ALA	3.4
7	H	40	LYS	3.4
1	A	444	G	3.4
11	L	81	ILE	3.4
14	O	63	ARG	3.4
1	A	1349	A	3.4
7	H	77	VAL	3.4
9	J	79	PRO	3.4
11	L	17	LYS	3.3
13	N	96	LYS	3.3
7	H	92	PRO	3.3
15	P	52	LEU	3.3
3	D	130	ASN	3.3
10	K	59	PRO	3.3
19	T	86	ALA	3.3
1	A	1203	C	3.3
6	G	84	TYR	3.3
2	C	126	ARG	3.3
9	J	66	GLU	3.3
17	R	47	ARG	3.3
4	E	44	ARG	3.3
11	L	60	PHE	3.3
2	C	44	LYS	3.3
4	E	143	LEU	3.2
13	N	98	ALA	3.2
2	C	74	ILE	3.2
1	A	619	U	3.2
1	A	447	G	3.2
4	E	51	LYS	3.2
9	J	49	PHE	3.2
12	M	43	LYS	3.2
7	H	17	GLN	3.2
12	M	44	ILE	3.2
6	G	24	LYS	3.2
3	D	128	VAL	3.2
12	M	1	ALA	3.2
6	G	13	PRO	3.2
9	J	11	LYS	3.2
10	K	58	THR	3.2

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Mol	Chain	Res	Type	RSRZ
20	B	73	ARG	3.2
21	U	43	GLU	3.2
4	E	91	SER	3.2
11	L	94	TYR	3.2
19	T	43	LYS	3.2
1	A	489	C	3.2
6	G	29	LEU	3.2
9	J	27	GLU	3.1
1	A	1245	C	3.1
4	E	79	THR	3.1
4	E	109	ALA	3.1
3	D	145	ARG	3.1
11	L	55	ARG	3.1
6	G	85	GLN	3.1
20	B	108	GLN	3.1
4	E	29	ILE	3.1
21	U	39	LYS	3.1
20	B	156	LEU	3.1
21	U	41	THR	3.1
19	T	2	ASN	3.1
7	H	43	GLY	3.1
7	H	45	ILE	3.1
12	M	81	ASP	3.1
7	H	91	LEU	3.1
6	G	109	LYS	3.1
1	A	1185	G	3.1
1	A	1186	G	3.1
7	H	96	ALA	3.1
1	A	1533	C	3.1
12	M	51	GLN	3.1
3	D	64	TYR	3.1
2	C	169	GLU	3.0
1	A	772	U	3.0
6	G	86	VAL	3.0
15	P	57	ILE	3.0
12	M	8	ILE	3.0
19	T	10	ALA	3.0
8	I	108	ARG	3.0
16	Q	3	LYS	3.0
1	A	442	G	3.0
1	A	963	G	3.0
3	D	126	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
15	P	79	ASN	3.0
7	H	97	GLY	3.0
15	P	45	GLU	3.0
14	O	53	ARG	3.0
11	L	10	PRO	3.0
20	B	72	LYS	3.0
13	N	85	GLU	3.0
21	U	53	LYS	3.0
3	D	3	TYR	2.9
2	C	187	GLU	2.9
4	E	15	ILE	2.9
11	L	25	ALA	2.9
6	G	20	GLU	2.9
2	C	48	LYS	2.9
19	T	4	LYS	2.9
11	L	29	LYS	2.9
13	N	74	ARG	2.9
1	A	303	A	2.9
4	E	140	ILE	2.9
12	M	61	LYS	2.9
11	L	23	LEU	2.9
9	J	16	ARG	2.9
11	L	22	ALA	2.9
4	E	35	LEU	2.9
15	P	19	VAL	2.9
7	H	5	PRO	2.9
6	G	74	VAL	2.9
19	T	8	LYS	2.9
1	A	1201	A	2.8
4	E	141	ASP	2.8
2	C	41	TYR	2.8
7	H	95	MET	2.8
7	H	44	PHE	2.8
1	A	27	G	2.8
3	D	193	ASP	2.8
16	Q	39	ARG	2.8
4	E	139	THR	2.8
19	T	14	GLU	2.8
13	N	78	LEU	2.8
12	M	45	SER	2.8
1	A	1528	U	2.8
4	E	37	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
7	H	8	ASP	2.8
7	H	83	ARG	2.8
9	J	69	THR	2.8
5	F	47	LEU	2.8
9	J	87	LEU	2.8
15	P	51	ARG	2.8
7	H	35	ILE	2.8
19	T	36	ALA	2.8
15	P	38	PHE	2.8
4	E	20	VAL	2.8
4	E	36	THR	2.8
4	E	34	ALA	2.8
9	J	102	LEU	2.8
20	B	128	LEU	2.8
13	N	75	LYS	2.8
9	J	21	ALA	2.8
4	E	75	LEU	2.7
4	E	111	ARG	2.7
20	B	17	HIS	2.7
4	E	142	GLY	2.7
4	E	117	ALA	2.7
8	I	117	LEU	2.7
3	D	56	GLU	2.7
15	P	63	GLN	2.7
9	J	91	ASP	2.7
2	C	164	THR	2.7
3	D	5	GLY	2.7
19	T	69	ASN	2.7
15	P	20	VAL	2.7
9	J	48	ARG	2.7
1	A	825	A	2.7
13	N	21	ALA	2.7
1	A	1375	A	2.7
7	H	129	ALA	2.7
21	U	36	PHE	2.7
7	H	14	ARG	2.7
6	G	28	ILE	2.7
7	H	7	ALA	2.7
4	E	17	VAL	2.6
4	E	45	VAL	2.6
12	M	95	PRO	2.6
2	C	132	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
6	G	112	ASP	2.6
3	D	194	ILE	2.6
6	G	94	ARG	2.6
7	H	13	ILE	2.6
3	D	77	GLU	2.6
6	G	89	GLU	2.6
1	A	1343	G	2.6
14	O	60	VAL	2.6
1	A	941	G	2.6
6	G	6	ILE	2.6
1	A	333	U	2.6
7	H	38	VAL	2.6
6	G	143	MET	2.6
15	P	60	TRP	2.6
17	R	73	HIS	2.6
12	M	46	GLU	2.6
4	E	82	HIS	2.6
5	F	55	HIS	2.6
6	G	5	VAL	2.6
2	C	102	ILE	2.5
12	M	48	SER	2.5
3	D	129	VAL	2.5
9	J	67	ILE	2.5
10	K	55	ARG	2.5
19	T	71	ALA	2.5
3	D	65	GLY	2.5
18	S	16	LYS	2.5
4	E	133	ILE	2.5
4	E	18	ASN	2.5
9	J	84	VAL	2.5
4	E	112	ALA	2.4
5	F	46	GLN	2.4
19	T	39	GLU	2.4
1	A	302	G	2.4
12	M	82	LEU	2.4
1	A	1246	A	2.4
19	T	48	LYS	2.4
4	E	137	ARG	2.4
15	P	37	GLY	2.4
1	A	1115	U	2.4
12	M	57	ASP	2.4
8	I	124	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	29	U	2.4
4	E	38	VAL	2.4
3	D	83	GLY	2.4
15	P	55	ASP	2.4
1	A	296	U	2.4
7	H	32	LYS	2.4
15	P	42	ILE	2.4
13	N	71	GLY	2.4
15	P	10	GLY	2.3
15	P	65	ALA	2.3
9	J	43	PRO	2.3
19	T	6	ALA	2.3
20	B	158	ASP	2.3
7	H	39	LEU	2.3
3	D	149	LYS	2.3
6	G	119	LEU	2.3
13	N	73	LEU	2.3
8	I	11	ARG	2.3
2	C	23	ALA	2.3
6	G	27	ASN	2.3
8	I	125	GLN	2.3
4	E	63	MET	2.3
12	M	70	ARG	2.3
8	I	99	LYS	2.3
3	D	147	LYS	2.3
1	A	448	A	2.3
7	H	124	ILE	2.3
7	H	81	GLY	2.3
21	U	38	GLU	2.3
4	E	78	GLY	2.3
12	M	109	LYS	2.3
1	A	1286	U	2.3
7	H	42	GLU	2.3
1	A	28	A	2.3
15	P	66	THR	2.3
1	A	1345	U	2.3
16	Q	25	GLU	2.3
6	G	101	ARG	2.3
6	G	150	PHE	2.3
3	D	7	LYS	2.3
5	F	32	ALA	2.3
4	E	61	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
4	E	88	HIS	2.2
14	O	42	HIS	2.2
2	C	185	THR	2.2
4	E	136	VAL	2.2
3	D	150	LYS	2.2
5	F	53	LYS	2.2
5	F	79	ARG	2.2
1	A	490	C	2.2
11	L	44	PRO	2.2
4	E	122	VAL	2.2
7	H	79	ARG	2.2
3	D	146	GLU	2.2
8	I	38	PHE	2.2
15	P	56	ARG	2.2
7	H	98	LEU	2.2
2	C	93	ILE	2.2
11	L	121	PRO	2.2
15	P	32	PHE	2.2
1	A	1339	A	2.2
2	C	24	ASN	2.2
12	M	111	PRO	2.2
15	P	21	VAL	2.2
19	T	5	SER	2.2
2	C	178	ARG	2.2
16	Q	38	LYS	2.2
12	M	6	ILE	2.2
1	A	266	G	2.2
4	E	42	ASN	2.2
9	J	82	LYS	2.2
18	S	67	GLY	2.2
5	F	1	MET	2.2
15	P	39	PHE	2.2
5	F	33	GLU	2.1
3	D	176	LYS	2.1
16	Q	5	ARG	2.1
17	R	49	LYS	2.1
7	H	125	ILE	2.1
7	H	112	ASP	2.1
13	N	66	THR	2.1
7	H	78	SER	2.1
11	L	19	ASN	2.1
13	N	17	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
4	E	26	GLY	2.1
4	E	39	GLY	2.1
8	I	96	GLU	2.1
1	A	487	A	2.1
11	L	96	THR	2.1
6	G	42	VAL	2.1
3	D	10	LEU	2.1
6	G	77	ARG	2.1
2	C	127	VAL	2.1
9	J	90	LEU	2.1
2	C	150	VAL	2.1
11	L	95	HIS	2.1
1	A	1188	A	2.1
4	E	102	THR	2.1
1	A	297	G	2.1
3	D	15	GLY	2.0
2	C	21	TRP	2.0
4	E	118	GLY	2.0
5	F	28	ALA	2.0
11	L	84	GLY	2.0
15	P	3	THR	2.0
5	F	54	LEU	2.0
4	E	115	GLU	2.0
7	H	94	VAL	2.0
7	H	74	ILE	2.0
12	M	58	GLU	2.0
19	T	66	ILE	2.0
10	K	128	VAL	2.0
12	M	80	MET	2.0
4	E	158	LYS	2.0
9	J	65	TYR	2.0
12	M	77	LYS	2.0
15	P	68	SER	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
22	MG	A	2168	1/1	1.12	26.78	55,55,55,55	1
22	MG	A	2182	1/1	1.98	26.67	57,57,57,57	1
22	MG	A	2134	1/1	0.44	9.53	105,105,105,105	0
22	MG	A	2056	1/1	0.91	6.95	59,59,59,59	0
22	MG	A	2312	1/1	0.36	6.55	66,66,66,66	0
22	MG	A	2161	1/1	0.33	5.40	40,40,40,40	1
23	LLL	A	2368	31/31	0.29	3.00	70,70,70,70	0
22	MG	A	2196	1/1	0.48	2.96	37,37,37,37	0
22	MG	A	2084	1/1	0.20	2.34	108,108,108,108	0
22	MG	A	2049	1/1	0.31	2.13	84,84,84,84	0
22	MG	A	2062	1/1	0.27	1.57	82,82,82,82	0
22	MG	A	2042	1/1	0.41	1.53	86,86,86,86	0
22	MG	A	2273	1/1	0.27	1.09	77,77,77,77	0
23	LLL	A	2369	31/31	0.25	1.08	41,41,41,41	31
22	MG	A	2107	1/1	0.18	1.05	60,60,60,60	0
22	MG	A	2114	1/1	0.11	0.89	63,63,63,63	0
22	MG	A	2155	1/1	0.42	0.79	72,72,72,72	0
22	MG	A	2346	1/1	0.16	0.73	63,63,63,63	0
22	MG	A	2189	1/1	0.12	0.64	31,31,31,31	0
22	MG	A	2334	1/1	0.19	0.43	32,32,32,32	0
22	MG	A	2330	1/1	0.20	0.23	31,31,31,31	0
22	MG	A	2213	1/1	0.20	0.08	15,15,15,15	0
22	MG	A	2016	1/1	0.23	-0.05	13,13,13,13	0
22	MG	A	2236	1/1	0.13	-0.09	77,77,77,77	0
22	MG	A	2141	1/1	0.25	-0.16	54,54,54,54	0
22	MG	A	2324	1/1	0.18	-0.17	91,91,91,91	0
22	MG	A	2128	1/1	0.16	-0.18	70,70,70,70	0
22	MG	A	2360	1/1	0.13	-0.19	55,55,55,55	0
23	LLL	A	2367	31/31	0.14	-0.33	9,9,9,9	0
22	MG	A	2148	1/1	0.22	-0.34	23,23,23,23	0
22	MG	A	2231	1/1	0.18	-0.50	69,69,69,69	0
22	MG	A	2077	1/1	0.25	-0.74	72,72,72,72	0
22	MG	A	2218	1/1	0.17	-0.85	85,85,85,85	0
22	MG	A	2366	1/1	0.18	-0.85	25,25,25,25	0
22	MG	A	2036	1/1	0.07	-0.98	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	2023	1/1	0.12	-1.20	10,10,10,10	0
22	MG	A	2175	1/1	0.12	-1.24	77,77,77,77	0
22	MG	A	2007	1/1	0.08	-1.34	27,27,27,27	0
22	MG	A	2340	1/1	0.10	-1.44	61,61,61,61	0
22	MG	N	2091	1/1	0.06	-1.46	50,50,50,50	0
22	MG	A	2319	1/1	0.08	-1.48	51,51,51,51	0
22	MG	A	2121	1/1	0.10	-1.61	85,85,85,85	0
22	MG	A	2302	1/1	0.15	-1.62	5,5,5,5	0
22	MG	A	2353	1/1	0.08	-1.65	51,51,51,51	0
22	MG	A	2250	1/1	0.09	-1.73	69,69,69,69	0
22	MG	A	2101	1/1	0.07	-1.77	5,5,5,5	0
22	MG	A	2288	1/1	0.07	-2.12	65,65,65,65	0
22	MG	A	2001	1/1	0.08	-2.22	5,5,5,5	0
22	MG	A	2073	1/1	0.07	-2.23	48,48,48,48	0
22	MG	A	2225	1/1	0.07	-2.37	74,74,74,74	0
22	MG	A	2267	1/1	0.04	-2.40	67,67,67,67	0
22	MG	A	2245	1/1	0.08	-2.45	12,12,12,12	0
22	MG	A	2011	1/1	0.06	-2.62	44,44,44,44	0
22	MG	A	2068	1/1	0.06	-2.76	49,49,49,49	0
22	MG	A	2283	1/1	0.10	-2.95	74,74,74,74	0
22	MG	A	2097	1/1	0.10	-2.98	10,10,10,10	0
22	MG	A	2208	1/1	0.06	-3.01	57,57,57,57	0
22	MG	A	2256	1/1	0.07	-3.10	66,66,66,66	0
22	MG	A	2202	1/1	0.11	-3.51	22,22,22,22	0
22	MG	A	2306	1/1	0.05	-3.81	38,38,38,38	0
22	MG	A	2278	1/1	0.04	-4.03	70,70,70,70	0
22	MG	A	2261	1/1	0.03	-4.28	31,31,31,31	0
22	MG	A	2239	1/1	0.03	-5.43	19,19,19,19	0
22	MG	A	2295	1/1	0.05	-5.89	63,63,63,63	0
22	MG	A	2029	1/1	0.08	-8.96	73,73,73,73	0

6.5 Other polymers ⓘ

There are no such residues in this entry.