Full wwPDB EM Validation Report (i)

Apr 16, 2024 – 04:08 am BST

PDB ID	:	7NAU
EMDB ID	:	EMD-12248
Title	:	Bacterial 30S ribosomal subunit assembly complex state C (Consensus Refinement)
Authors	:	Schedlbauer, A.; Iturrioz, I.; Ochoa-Lizarralde, B.; Diercks, T.; Kaminishi, T.; Capuni, R.; Astigarraga, E.; Gil-Carton, D.; Fucini, P.; Connell, S.
Deposited on	:	2021-01-25
Resolution	:	3.78 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

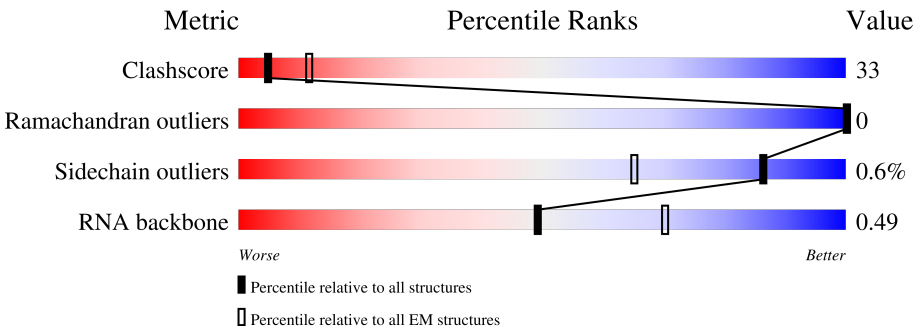
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.78 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1542	19% 60% 19% •
2	B	241	53% 77% 16% 7%
3	C	233	• 37% 53% 9%
4	D	206	53% 46%
5	E	167	• 59% 35% 7%
6	F	135	• 44% 35% 21%
7	G	179	52% 32% 50% 18%

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Mol	Chain	Length	Quality of chain
8	H	130	65% 33%
9	I	130	43% 55%
10	J	103	37% 59%
11	K	129	52% 37% 10%
12	L	124	52% 46%
13	M	118	5% 59% 37%
14	N	101	63% 36%
15	O	89	58% 40%
16	P	82	55% 44%
17	Q	84	50% 44% 5%
18	R	75	63% 24% 13%
19	S	92	41% 48% 11%
20	T	87	48% 51%
21	X	151	53% 47%

2 Entry composition (i)

There are 23 unique types of molecules in this entry. The entry contains 52283 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1522	32664	14573	5988	10581	1522	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	224	1753	1109	315	321	8	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	211	1653	1046	310	293	4	0	0

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	156	1152	717	217	212	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	106	862	545	156	154	7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	146	1143	710	220	209	4	0	0

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	99	795	498	152	144	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	116	866	534	170	159	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	123	957	591	196	165	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	114	883	546	178	156	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	N	100	805	499	164	139	3	0	0

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	Q	80	648	411	121	113	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	R	65	535	339	100	95	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	S	82	658	421	125	110	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	T	86	670	414	138	115	3	0	0

- Molecule 21 is a protein called Ribosome maturation factor RimP.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	X	151	1174	742	197	230	5	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	151	ALA	-	expression tag	UNP P0A8A8

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

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
22	A	57	57	57	0

- Molecule 23 is ZINC ION (three-letter code: ZN) (formula: Zn).

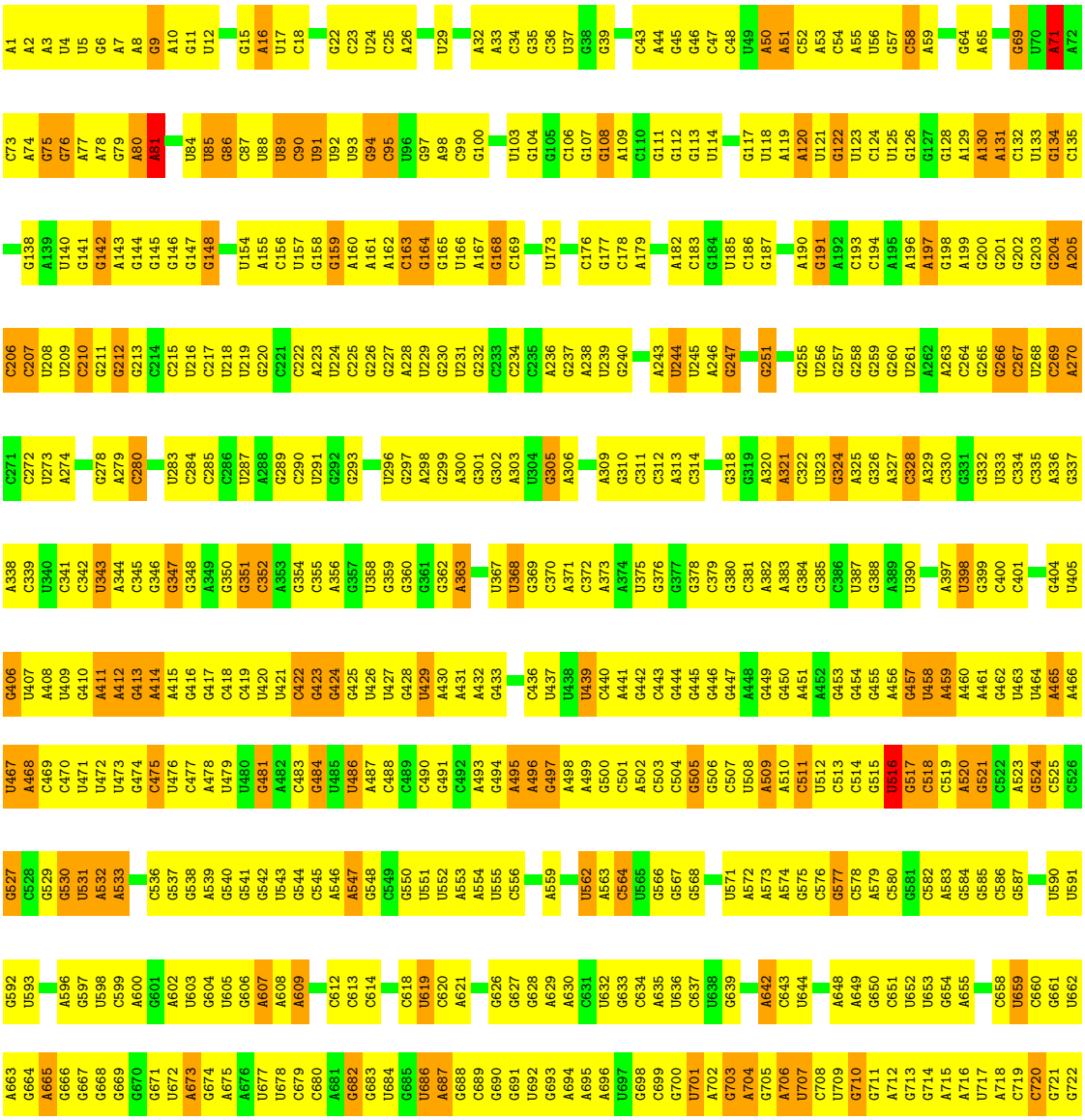
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
23	B	1	1	1	0

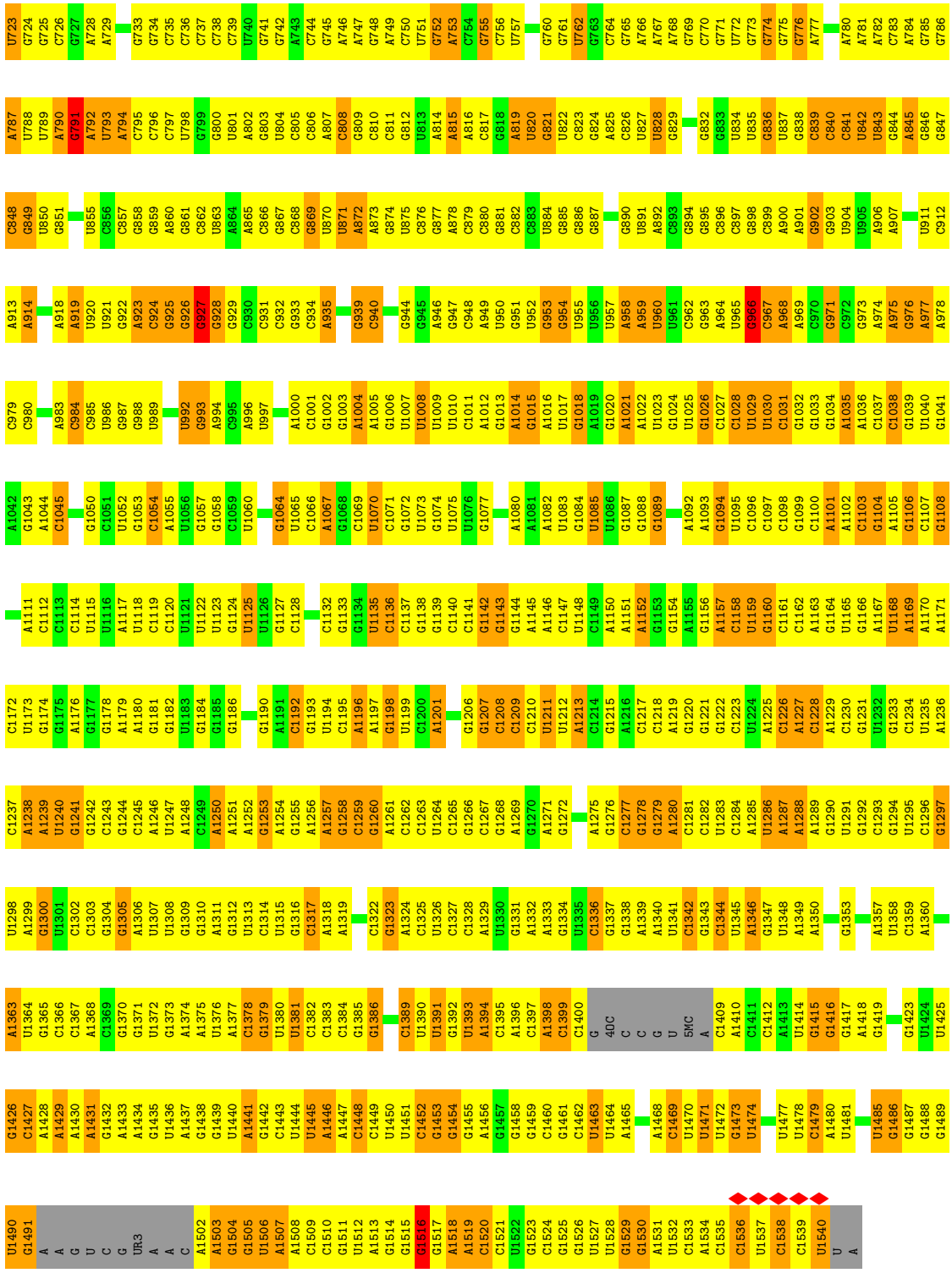
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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

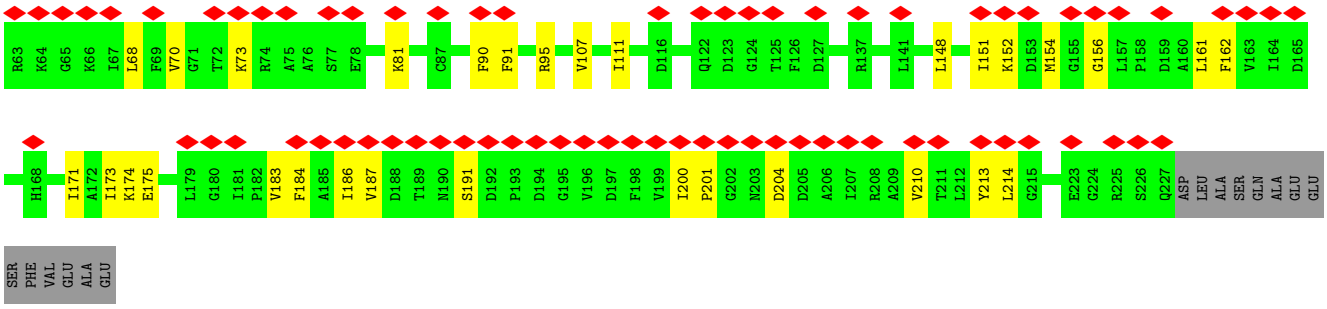
Chain A: 19% 60% 19%





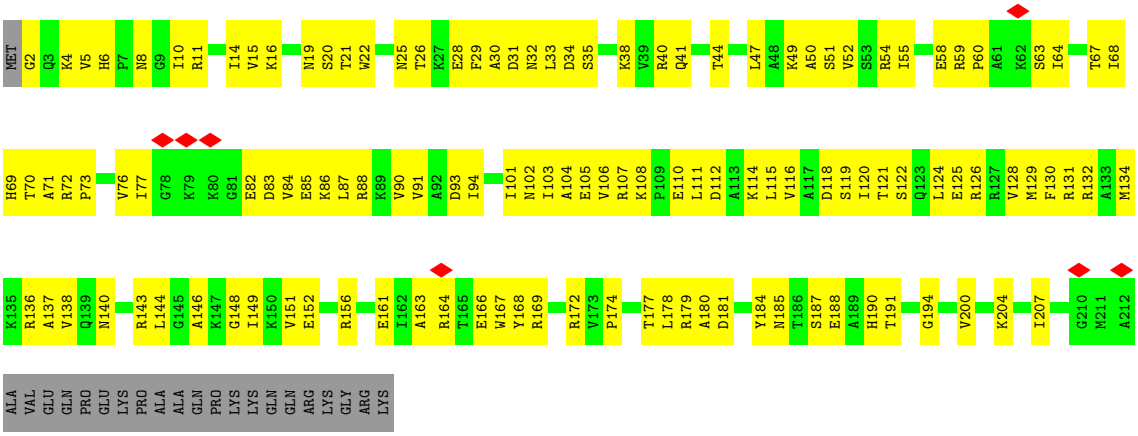
• Molecule 2: 30S ribosomal protein S2

Chain B:



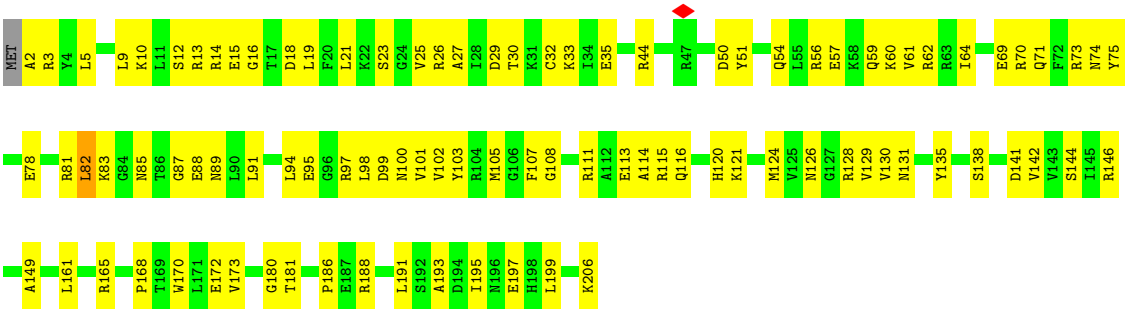
- Molecule 3: 30S ribosomal protein S3

Chain C:



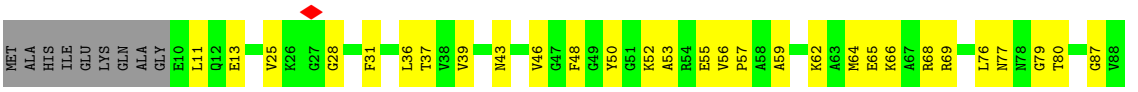
- Molecule 4: 30S ribosomal protein S4

Chain D:



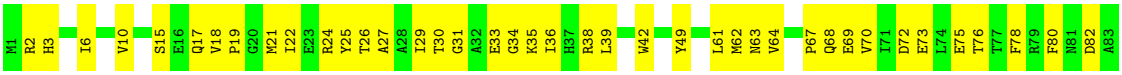
- Molecule 5: 30S ribosomal protein S5

Chain E:



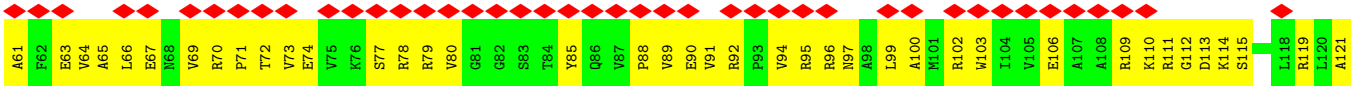
• Molecule 6: 30S ribosomal protein S6

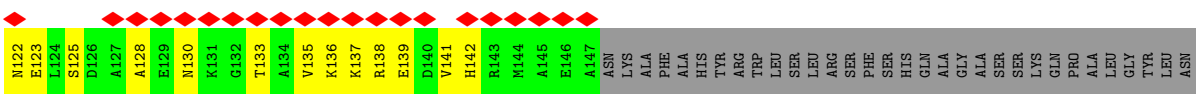
Chain F:



• Molecule 7: 30S ribosomal protein S7

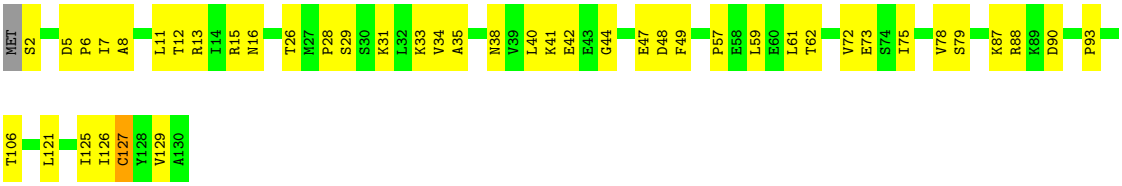
Chain G:





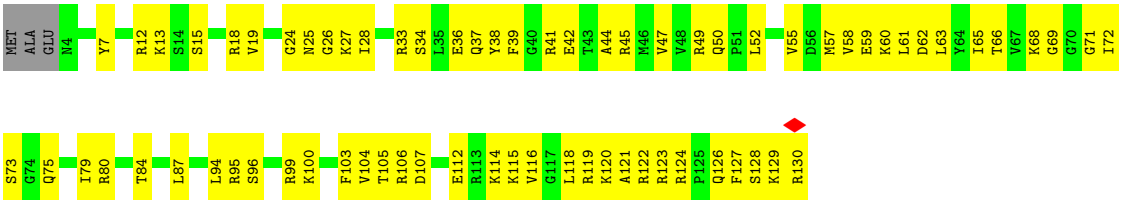
• Molecule 8: 30S ribosomal protein S8

Chain H:



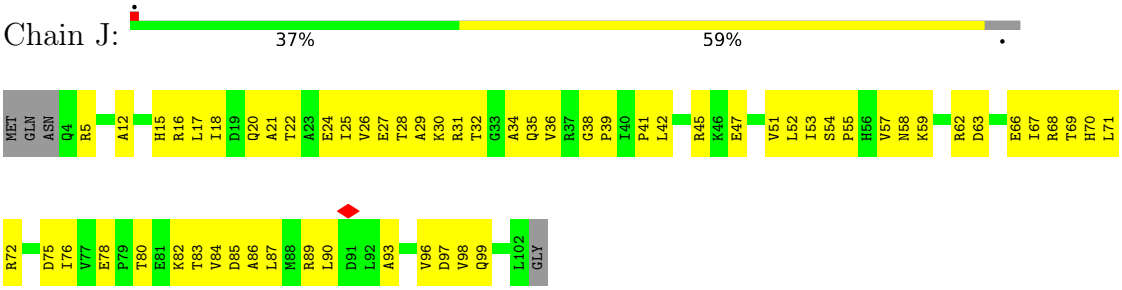
• Molecule 9: 30S ribosomal protein S9

Chain I:



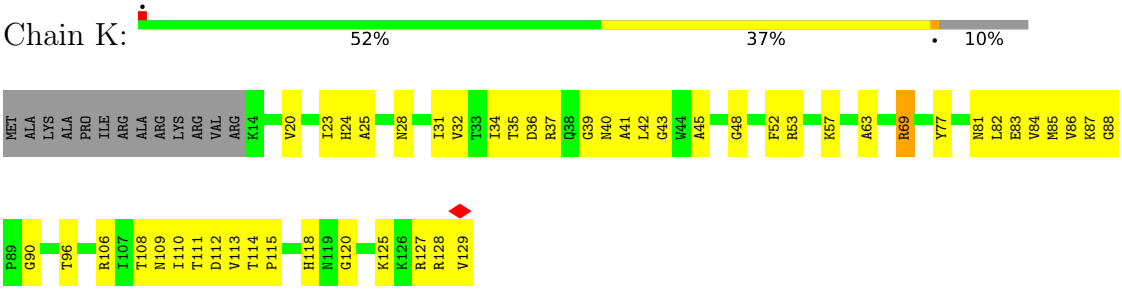
• Molecule 10: 30S ribosomal protein S10

Chain J:



• Molecule 11: 30S ribosomal protein S11

Chain K:

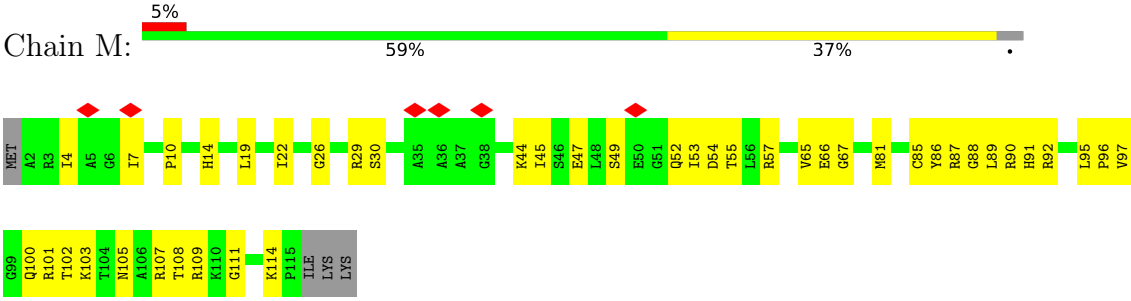


• Molecule 12: 30S ribosomal protein S12

Chain L:

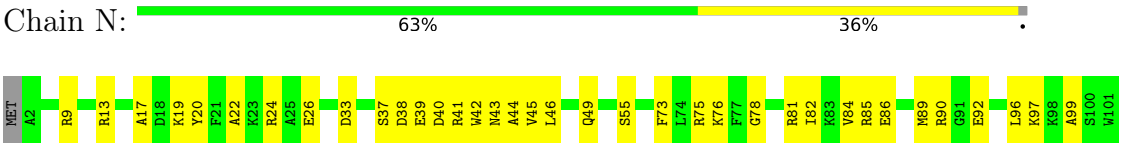
• Molecule 13: 30S ribosomal protein S13

Chain M:



• Molecule 14: 30S ribosomal protein S14

Chain N:

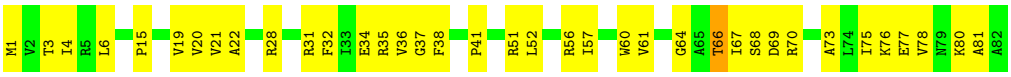


• Molecule 15: 30S ribosomal protein S15

Chain O:

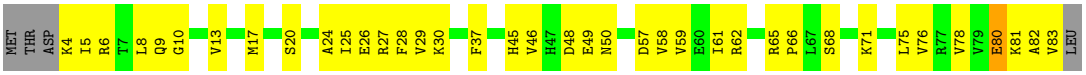
• Molecule 16: 30S ribosomal protein S16

Chain P:



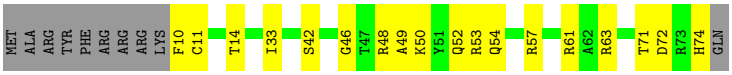
• Molecule 17: 30S ribosomal protein S17

Chain Q:



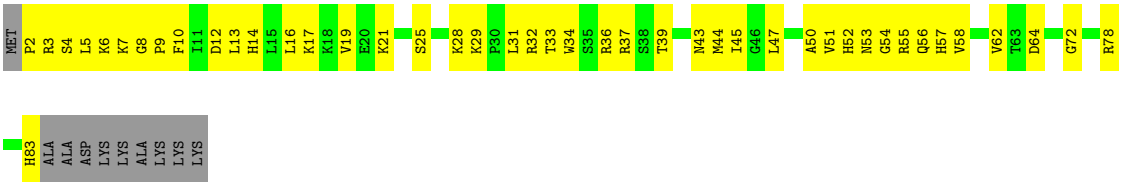
• Molecule 18: 30S ribosomal protein S18

Chain R:



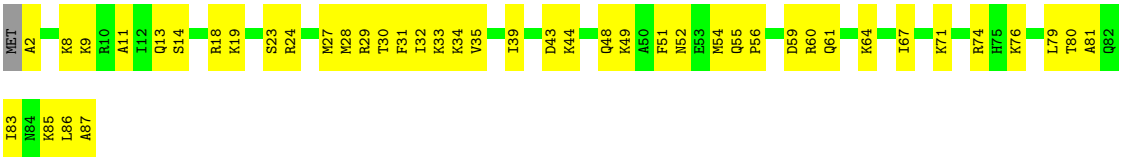
• Molecule 19: 30S ribosomal protein S19

Chain S:



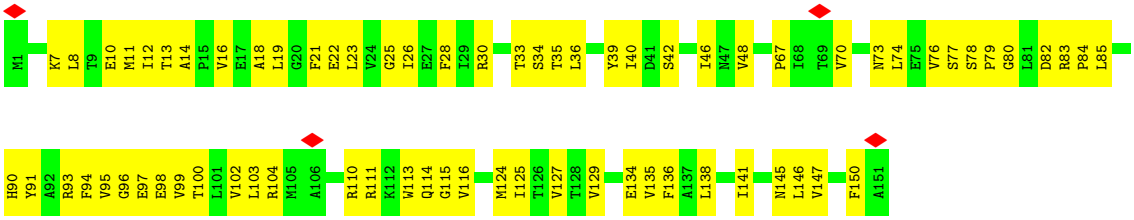
• Molecule 20: 30S ribosomal protein S20

Chain T:



• Molecule 21: Ribosome maturation factor RimP

Chain X:


M1
K7 L8 T9 E10 M11 I12 T13 A14 P15 V16 E17 A18 L19 G20 F21 E22 L23 V24 G25 I26 E27 F28 I29 R30
T33 S34 T35 L36
Y39 I40 D41 S42
I46 N47 V48
P67 I68 T69 V70
N73 L74 E75 V76 S77 S78 P79 G80 L81 D82 R83 P84 L85
H90 Y91 A92 R93 F94 V95 G96 E97 E98 V99 T100 L101 V102 L103 R104 M105 A106
R110 R111 K112 W113 Q114 G115 V116
M124 I125 T126 V127 T128 V129
E134 V135 F136 A137 L138
I141
N145 L146 V147
F150 A151

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	14097	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	46.1	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.100	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	416.64, 416.64, 416.64	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.085, 1.085, 1.085	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, G7M, D2T, 2MG, 5MC, MA6, MG, PSU

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	1.09	6/36363 (0.0%)	1.00	9/56718 (0.0%)
2	B	0.40	0/1784	0.50	0/2403
3	C	0.48	0/1680	0.53	0/2263
4	D	0.55	0/1665	0.55	0/2227
5	E	0.58	0/1165	0.62	0/1568
6	F	0.52	0/881	0.61	0/1189
7	G	0.34	0/1156	0.49	0/1550
8	H	0.58	0/989	0.58	0/1326
9	I	0.45	0/1034	0.61	0/1375
10	J	0.47	0/805	0.57	0/1089
11	K	0.57	0/882	0.76	0/1191
12	L	0.59	0/960	0.62	0/1286
13	M	0.53	0/892	0.59	0/1193
14	N	0.49	0/817	0.50	0/1088
15	O	0.50	0/722	0.53	0/964
16	P	0.57	0/659	0.58	0/884
17	Q	0.60	0/657	0.62	0/881
18	R	0.53	0/544	0.63	0/731
19	S	0.46	0/675	0.54	0/908
20	T	0.46	0/676	0.44	0/895
21	X	0.61	0/1192	0.69	0/1619
All	All	0.93	6/56198 (0.0%)	0.89	9/83348 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	919	A	N9-C4	-5.54	1.34	1.37
1	A	270	A	N9-C4	-5.18	1.34	1.37
1	A	71	A	N9-C4	-5.08	1.34	1.37
1	A	609	A	N9-C4	-5.07	1.34	1.37
1	A	665	A	N9-C4	-5.06	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	642	A	N9-C4	-5.05	1.34	1.37

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	108	G	C2-N3-C4	-6.59	108.60	111.90
1	A	81	A	N9-C4-C5	-6.10	103.36	105.80
1	A	1008	U	C2-N1-C1'	5.87	124.74	117.70
1	A	1008	U	C6-N1-C1'	-5.28	113.81	121.20
1	A	324	G	N3-C4-C5	5.21	131.21	128.60
1	A	791	G	N3-C4-N9	-5.20	122.88	126.00
1	A	841	C	N1-C2-O2	5.16	122.00	118.90
1	A	362	G	N3-C4-C5	5.12	131.16	128.60
1	A	927	G	N1-C6-O6	5.01	122.91	119.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32664	0	16451	1526	0
2	B	1753	0	1780	29	0
3	C	1653	0	1727	117	0
4	D	1643	0	1707	88	0
5	E	1152	0	1193	45	0
6	F	862	0	864	53	0
7	G	1143	0	1200	99	0
8	H	979	0	1031	45	0
9	I	1022	0	1070	103	0
10	J	795	0	836	65	0
11	K	866	0	874	58	0
12	L	957	0	1017	87	0
13	M	883	0	941	62	0
14	N	805	0	844	43	0
15	O	714	0	734	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	P	649	0	666	32	0
17	Q	648	0	691	51	0
18	R	535	0	552	21	0
19	S	658	0	683	54	0
20	T	670	0	719	41	0
21	X	1174	0	1174	92	0
22	A	57	0	0	0	0
23	B	1	0	0	0	0
All	All	52283	0	36754	2498	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 33.

All (2498) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:920:U:O4'	1:A:1080:A:C2	2.13	1.00
21:X:21:PHE:CD2	21:X:40:ILE:HG21	1.98	0.98
18:R:11:CYS:O	18:R:14:THR:HG22	1.63	0.97
11:K:81:ASN:HA	11:K:106:ARG:HB2	1.46	0.97
1:A:841:C:N3	1:A:845:A:N6	2.10	0.97
16:P:3:THR:HG22	16:P:66:THR:CG2	1.96	0.96
17:Q:59:VAL:HG22	17:Q:78:VAL:HG13	1.45	0.96
13:M:4:ILE:HD12	13:M:10:PRO:HG3	1.46	0.95
1:A:1415:G:H1	1:A:1485:U:H3	1.14	0.95
1:A:73:C:HO2'	1:A:74:A:H8	1.12	0.94
1:A:363:A:C5'	12:L:31:ARG:HG3	1.98	0.93
11:K:87:LYS:HE2	11:K:113:VAL:CG1	1.99	0.93
1:A:841:C:O2	1:A:845:A:N6	2.03	0.91
1:A:954:G:H21	1:A:1227:A:H62	1.17	0.91
5:E:37:THR:HG21	5:E:64:MET:SD	2.11	0.91
1:A:841:C:C2	1:A:845:A:N6	2.39	0.90
1:A:843:U:H2'	1:A:844:G:H8	1.35	0.90
1:A:1103:C:OP1	2:B:95:ARG:NH2	2.05	0.90
2:B:73:LYS:HE3	2:B:204:ASP:O	1.73	0.89
9:I:55:VAL:HG21	9:I:94:LEU:CD1	2.04	0.88
1:A:447:G:N1	1:A:486:U:OP2	2.06	0.88
15:O:26:GLU:OE1	15:O:26:GLU:N	2.07	0.88
1:A:1162:C:N3	1:A:1174:G:N1	2.21	0.88
6:F:42:TRP:CZ2	6:F:61:LEU:CD1	2.56	0.88
9:I:65:ILE:HG21	9:I:79:ILE:HD12	1.54	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:927:G:O6	1:A:1390:U:O2	1.91	0.87
12:L:80:ILE:HG22	12:L:81:LEU:N	1.88	0.87
16:P:3:THR:HG22	16:P:66:THR:HG23	1.54	0.86
11:K:87:LYS:HE2	11:K:113:VAL:HG11	1.57	0.86
1:A:443:C:N3	1:A:491:G:N1	2.22	0.86
10:J:53:ILE:HG21	10:J:63:ASP:OD2	1.76	0.86
15:O:26:GLU:HB3	15:O:81:LEU:HD22	1.58	0.86
1:A:928:G:N2	1:A:1389:C:O2	2.09	0.86
1:A:786:G:N1	1:A:796:C:N3	2.23	0.85
1:A:920:U:O4'	1:A:1080:A:N1	2.09	0.85
9:I:55:VAL:HG21	9:I:94:LEU:HD13	1.58	0.85
1:A:71:A:N6	1:A:99:C:O2	2.08	0.85
5:E:36:LEU:CD1	5:E:133:PRO:HB2	2.06	0.85
1:A:933:G:N7	7:G:3:ARG:NH1	2.25	0.85
12:L:87:VAL:HG13	12:L:96:HIS:CE1	2.12	0.84
1:A:1510:C:H2'	1:A:1511:G:H8	1.43	0.84
6:F:42:TRP:CZ2	6:F:61:LEU:HD12	2.13	0.84
1:A:660:C:N3	1:A:745:G:N1	2.26	0.83
1:A:1316:G:H22	1:A:1319:A:H5"	1.39	0.83
12:L:39:THR:HG23	21:X:48:VAL:HG13	1.60	0.83
1:A:141:G:N1	1:A:222:C:N3	2.24	0.83
1:A:774:G:N1	1:A:805:C:N3	2.26	0.83
15:O:24:SER:O	15:O:27:VAL:HG12	1.78	0.83
1:A:927:G:C6	1:A:1390:U:O2	2.32	0.82
15:O:26:GLU:O	15:O:29:VAL:HG12	1.80	0.82
1:A:363:A:H5"	12:L:31:ARG:HG3	1.61	0.82
6:F:76:THR:O	6:F:80:PHE:N	2.12	0.82
1:A:591:U:N3	1:A:648:A:N1	2.26	0.82
1:A:837:U:O2	1:A:849:G:N1	2.12	0.82
21:X:67:PRO:HB2	21:X:70:VAL:HB	1.61	0.82
1:A:988:G:N2	1:A:1217:C:O2	2.12	0.81
1:A:1158:C:N3	1:A:1181:G:N1	2.27	0.81
1:A:138:G:N1	1:A:225:C:N3	2.24	0.81
1:A:683:G:H1	1:A:707:U:H3	1.27	0.81
1:A:119:A:N6	1:A:287:U:O2	2.14	0.81
1:A:203:G:O2'	1:A:465:A:N1	2.13	0.81
1:A:689:C:N3	1:A:698:G:N1	2.27	0.81
1:A:925:G:O6	1:A:1391:U:O2	1.96	0.81
1:A:953:G:N1	1:A:1228:C:N3	2.25	0.81
6:F:3:HIS:HB3	6:F:92:THR:OG1	1.78	0.81
3:C:2:GLY:O	3:C:4:LYS:NZ	2.13	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:4:ILE:O	13:M:4:ILE:HG22	1.79	0.81
4:D:170:TRP:CH2	4:D:191:LEU:HD21	2.16	0.81
1:A:806:C:H2'	1:A:807:A:H8	1.44	0.81
21:X:113:TRP:HB3	21:X:129:VAL:HG11	1.61	0.81
21:X:125:ILE:HG22	21:X:127:VAL:HG23	1.63	0.81
1:A:1426:G:N2	1:A:1474:U:O2	2.14	0.80
1:A:138:G:O6	1:A:225:C:N4	2.14	0.80
1:A:927:G:N2	1:A:1391:U:O5'	2.15	0.80
1:A:605:U:O2	1:A:633:G:N1	2.14	0.80
17:Q:62:ARG:CD	17:Q:76:VAL:HG22	2.11	0.80
7:G:91:VAL:O	7:G:96:ARG:NH1	2.14	0.80
9:I:33:ARG:HB3	9:I:37:GLN:HE22	1.47	0.80
1:A:683:G:N2	1:A:707:U:O2	2.15	0.80
2:B:111:ILE:HD12	2:B:152:LYS:HA	1.63	0.80
13:M:65:VAL:O	13:M:66:GLU:HG2	1.82	0.80
14:N:33:ASP:O	14:N:41:ARG:NH2	2.15	0.80
1:A:1038:C:H2'	1:A:1039:G:H8	1.48	0.79
1:A:514:C:N3	1:A:537:G:N1	2.29	0.79
1:A:562:U:H5'	12:L:15:LYS:HZ1	1.46	0.79
1:A:669:G:O6	1:A:737:C:N4	2.16	0.79
13:M:4:ILE:HD12	13:M:10:PRO:CG	2.12	0.79
1:A:517:G:N1	1:A:533:A:OP1	2.16	0.79
18:R:10:PHE:O	18:R:11:CYS:SG	2.40	0.79
2:B:23:TRP:HZ3	2:B:25:PRO:HA	1.48	0.79
12:L:21:VAL:HG13	12:L:95:TYR:CE2	2.17	0.79
1:A:363:A:H5'	12:L:31:ARG:HG3	1.65	0.78
1:A:1160:G:O6	1:A:1182:G:N1	2.16	0.78
1:A:1233:G:OP1	9:I:119:ARG:NH1	2.15	0.78
10:J:26:VAL:HG12	10:J:36:VAL:HG21	1.65	0.78
1:A:157:U:N3	1:A:164:G:O6	2.15	0.78
1:A:25:C:H2'	1:A:26:A:H8	1.46	0.78
1:A:836:G:O6	1:A:850:U:N3	2.15	0.78
11:K:45:ALA:HB1	11:K:69:ARG:HG3	1.64	0.78
1:A:401:C:OP2	4:D:70:ARG:NE	2.15	0.78
1:A:1340:A:O2'	9:I:130:ARG:NH1	2.17	0.78
12:L:80:ILE:HG22	12:L:81:LEU:H	1.47	0.78
1:A:933:G:N2	1:A:1384:C:O2	2.16	0.78
1:A:444:G:N1	1:A:490:C:N3	2.27	0.78
1:A:1179:A:OP2	9:I:95:ARG:NH2	2.17	0.78
13:M:7:ILE:HG12	13:M:66:GLU:OE1	1.84	0.78
1:A:786:G:N2	1:A:796:C:O2	2.16	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1158:C:O2	1:A:1181:G:N2	2.14	0.78
11:K:113:VAL:O	11:K:113:VAL:HG12	1.83	0.78
1:A:1218:C:H2'	1:A:1219:A:H8	1.49	0.78
16:P:77:GLU:O	16:P:81:ALA:N	2.17	0.78
1:A:682:G:O6	1:A:708:C:N4	2.17	0.77
7:G:72:THR:H	7:G:142:HIS:CE1	2.03	0.77
1:A:716:A:H1'	11:K:120:GLY:HA2	1.66	0.77
5:E:153:VAL:HA	5:E:156:LYS:HE2	1.66	0.77
1:A:1118:U:H5'	9:I:106:ARG:HG2	1.64	0.77
6:F:42:TRP:CZ2	6:F:61:LEU:HD13	2.18	0.77
1:A:219:U:H2'	1:A:220:G:H8	1.50	0.77
10:J:36:VAL:HG22	10:J:38:GLY:H	1.49	0.77
10:J:53:ILE:HG21	10:J:63:ASP:CG	2.04	0.77
12:L:37:VAL:HG12	12:L:53:CYS:HB2	1.65	0.77
1:A:517:G:N2	1:A:529:G:O2'	2.18	0.77
1:A:689:C:O2	1:A:698:G:N2	2.17	0.77
1:A:745:G:H2'	1:A:746:A:H8	1.49	0.77
1:A:1297:G:N2	7:G:114:LYS:O	2.18	0.77
5:E:89:HIS:HD2	5:E:90:THR:HG23	1.48	0.77
6:F:29:ILE:HG22	6:F:34:GLY:HA3	1.65	0.76
19:S:50:ALA:HA	19:S:58:VAL:O	1.85	0.76
1:A:404:G:N7	4:D:2:ALA:N	2.34	0.76
1:A:1319:A:OP1	19:S:3:ARG:NE	2.18	0.76
12:L:80:ILE:CG2	12:L:81:LEU:H	1.98	0.76
1:A:158:G:N2	1:A:163:C:O2	2.17	0.76
1:A:1213:A:O2'	1:A:1215:G:N7	2.16	0.76
21:X:33:THR:O	21:X:35:THR:HG23	1.85	0.76
1:A:1166:G:N1	1:A:1169:A:OP2	2.17	0.76
1:A:91:U:H2'	1:A:92:U:C6	2.20	0.76
6:F:6:ILE:HG13	6:F:89:VAL:HG23	1.67	0.76
12:L:29:GLN:HB3	12:L:81:LEU:HD11	1.66	0.76
1:A:156:C:O2	1:A:165:G:N2	2.17	0.76
1:A:692:U:N3	1:A:695:A:OP2	2.14	0.76
1:A:71:A:N1	1:A:99:C:O2'	2.17	0.76
1:A:774:G:O6	1:A:805:C:N4	2.15	0.76
19:S:25:SER:O	19:S:28:LYS:NZ	2.19	0.76
1:A:671:G:O6	1:A:735:C:N4	2.18	0.76
1:A:141:G:O6	1:A:222:C:N4	2.14	0.76
1:A:658:C:N4	1:A:748:G:O6	2.19	0.76
1:A:1346:A:H61	1:A:1374:A:H3'	1.51	0.76
15:O:80:GLN:O	15:O:84:ARG:NH2	2.19	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:835:U:N3	1:A:851:G:O6	2.19	0.75
1:A:1316:G:N1	1:A:1319:A:OP2	2.18	0.75
1:A:1052:U:N3	1:A:1206:G:O6	2.19	0.75
1:A:713:G:H2'	1:A:714:G:C8	2.21	0.75
9:I:25:ASN:O	9:I:61:LEU:N	2.19	0.75
1:A:652:U:O4	1:A:752:G:O2'	2.04	0.75
1:A:1008:U:H5	1:A:1021:A:N1	1.84	0.75
17:Q:46:VAL:HG11	17:Q:61:ILE:HD12	1.66	0.75
1:A:333:U:OP1	20:T:2:ALA:N	2.19	0.75
15:O:26:GLU:CB	15:O:81:LEU:HD22	2.16	0.75
1:A:579:A:N6	1:A:762:U:O4	2.19	0.75
1:A:682:G:N1	1:A:708:C:N3	2.34	0.75
1:A:859:G:OP2	1:A:869:G:N1	2.18	0.75
21:X:102:VAL:HG23	21:X:110:ARG:NH2	2.02	0.75
1:A:246:A:N1	1:A:278:G:O2'	2.19	0.74
17:Q:29:VAL:O	17:Q:37:PHE:HA	1.87	0.74
6:F:17:GLN:OE1	6:F:24:ARG:NH2	2.18	0.74
9:I:65:ILE:HG21	9:I:79:ILE:CD1	2.17	0.74
1:A:890:G:O2'	1:A:906:A:N6	2.20	0.74
1:A:103:U:OP2	20:T:9:LYS:NZ	2.20	0.74
1:A:257:G:N2	1:A:269:C:O2	2.20	0.74
1:A:604:G:N2	1:A:634:C:O2	2.20	0.74
8:H:34:VAL:O	8:H:38:ASN:ND2	2.20	0.74
3:C:40:ARG:NH1	3:C:55:ILE:O	2.19	0.74
1:A:1162:C:O2	1:A:1174:G:N2	2.12	0.74
3:C:19:ASN:ND2	14:N:90:ARG:O	2.19	0.74
1:A:237:G:H5"	17:Q:27:ARG:NH2	2.02	0.74
15:O:6:GLU:OE1	15:O:6:GLU:N	2.21	0.74
1:A:1266:G:N2	1:A:1269:A:OP2	2.19	0.73
3:C:129:MET:HB2	3:C:132:ARG:HG2	1.71	0.73
1:A:604:G:N1	1:A:634:C:N3	2.33	0.73
11:K:23:ILE:HG12	11:K:32:VAL:HG12	1.68	0.73
12:L:39:THR:CG2	21:X:48:VAL:HG13	2.17	0.73
4:D:128:ARG:NH1	4:D:129:VAL:O	2.21	0.73
1:A:122:G:N1	1:A:239:U:O2	2.20	0.73
1:A:955:U:O2'	19:S:83:HIS:ND1	2.17	0.73
1:A:1297:G:O3'	7:G:114:LYS:NZ	2.22	0.73
1:A:947:G:N2	1:A:1234:C:O2	2.20	0.73
3:C:21:THR:OG1	3:C:58:GLU:HG3	1.88	0.73
12:L:80:ILE:CG2	12:L:81:LEU:N	2.51	0.73
15:O:27:VAL:O	15:O:31:LEU:HG	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:15:GLU:OE2	4:D:56:ARG:NH2	2.21	0.73
21:X:10:GLU:O	21:X:13:THR:HG22	1.89	0.73
1:A:539:A:H2'	1:A:540:G:H8	1.53	0.72
1:A:237:G:H5"	17:Q:27:ARG:CZ	2.18	0.72
18:R:11:CYS:HB2	18:R:14:THR:CG2	2.19	0.72
5:E:36:LEU:HD23	5:E:50:TYR:HD1	1.54	0.72
17:Q:10:GLY:HA3	17:Q:25:ILE:HG12	1.72	0.72
1:A:375:U:OP1	16:P:70:ARG:NH1	2.22	0.72
1:A:1358:U:H3	1:A:1363:A:H62	1.36	0.72
5:E:36:LEU:HD23	5:E:50:TYR:CD1	2.24	0.72
21:X:74:LEU:CD2	21:X:76:VAL:HG23	2.20	0.72
1:A:158:G:N1	1:A:163:C:N3	2.27	0.72
1:A:699:C:H2'	1:A:700:G:H8	1.55	0.72
3:C:126:ARG:HB2	3:C:128:VAL:HG23	1.70	0.72
8:H:41:LYS:NZ	8:H:48:ASP:OD1	2.22	0.72
11:K:83:GLU:OE1	11:K:108:THR:OG1	2.08	0.72
1:A:91:U:H2'	1:A:92:U:H6	1.53	0.72
1:A:1343:G:OP2	9:I:129:LYS:NZ	2.22	0.72
9:I:55:VAL:CG2	9:I:94:LEU:HD13	2.20	0.72
1:A:875:U:O2	8:H:16:ASN:ND2	2.18	0.72
14:N:43:ASN:HA	14:N:46:LEU:HD12	1.72	0.72
20:T:44:LYS:HD2	20:T:87:ALA:H	1.55	0.72
1:A:1178:G:H3'	9:I:99:ARG:HH22	1.55	0.72
1:A:1524:C:H2'	1:A:1525:G:H8	1.55	0.72
10:J:27:GLU:OE1	10:J:31:ARG:NH1	2.23	0.72
1:A:679:C:O2	1:A:711:G:N2	2.19	0.71
1:A:245:U:O2	1:A:283:U:N3	2.18	0.71
7:G:49:THR:HG23	7:G:53:ARG:HH12	1.54	0.71
9:I:34:SER:H	9:I:37:GLN:HE21	1.38	0.71
1:A:1312:G:N2	1:A:1325:C:O2	2.19	0.71
1:A:451:A:H61	1:A:481:G:H5'	1.55	0.71
1:A:1163:A:N6	1:A:1173:U:O4	2.16	0.71
3:C:91:VAL:HA	3:C:94:ILE:HG22	1.73	0.71
1:A:257:G:N1	1:A:269:C:N3	2.31	0.71
1:A:1287:A:H2'	1:A:1288:A:C8	2.26	0.71
1:A:1382:C:H1'	7:G:79:ARG:HH11	1.53	0.71
1:A:828:U:O4	1:A:858:G:N2	2.18	0.71
1:A:1524:C:H2'	1:A:1525:G:C8	2.25	0.71
1:A:443:C:N4	1:A:491:G:O6	2.20	0.70
1:A:464:U:N3	1:A:467:U:OP2	2.17	0.70
1:A:841:C:N4	1:A:844:G:OP2	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1513:A:H2'	1:A:1514:G:C8	2.25	0.70
1:A:343:U:O2	1:A:346:G:N1	2.15	0.70
17:Q:62:ARG:HD2	17:Q:76:VAL:CG2	2.21	0.70
1:A:263:A:OP2	20:T:74:ARG:NH1	2.24	0.70
12:L:83:ARG:HG2	12:L:98:VAL:HG22	1.74	0.70
1:A:459:A:N6	1:A:473:U:O4	2.19	0.70
19:S:3:ARG:HG3	19:S:4:SER:H	1.55	0.70
1:A:477:C:H2'	1:A:478:A:C8	2.27	0.70
12:L:87:VAL:HG13	12:L:96:HIS:HE1	1.57	0.70
11:K:48:GLY:HA2	11:K:53:ARG:HH22	1.57	0.70
21:X:40:ILE:CD1	21:X:76:VAL:HG13	2.21	0.70
1:A:210:C:O2	1:A:211:G:N1	2.25	0.70
1:A:785:G:H2'	1:A:786:G:H8	1.55	0.70
15:O:29:VAL:HG21	15:O:67:LEU:HD21	1.74	0.70
1:A:843:U:H2'	1:A:844:G:C8	2.25	0.70
3:C:156:ARG:H	3:C:163:ALA:HA	1.57	0.70
21:X:102:VAL:CG2	21:X:110:ARG:HH22	2.05	0.70
1:A:713:G:H2'	1:A:714:G:H8	1.55	0.70
1:A:1240:U:O4	7:G:109:ARG:NH1	2.24	0.70
1:A:1436:U:H2'	1:A:1437:A:C8	2.27	0.70
8:H:79:SER:OG	8:H:125:ILE:O	2.06	0.70
9:I:47:VAL:HA	9:I:50:GLN:HG2	1.72	0.70
12:L:74:LEU:HD13	12:L:80:ILE:HD11	1.73	0.70
1:A:417:G:N1	1:A:426:U:O2	2.18	0.69
1:A:607:A:H2'	1:A:608:A:C8	2.26	0.69
6:F:78:PHE:HA	6:F:84:VAL:HG11	1.72	0.69
14:N:37:SER:HG	14:N:40:ASP:H	1.37	0.69
6:F:21:MET:HA	6:F:24:ARG:HH12	1.54	0.69
9:I:15:SER:OG	9:I:75:GLN:NE2	2.25	0.69
11:K:20:VAL:HB	11:K:37:ARG:HE	1.55	0.69
3:C:55:ILE:HD13	3:C:68:ILE:HG13	1.72	0.69
1:A:1376:U:H2'	1:A:1377:A:C8	2.27	0.69
17:Q:62:ARG:HG2	17:Q:76:VAL:HG23	1.74	0.69
9:I:57:MET:HA	9:I:60:LYS:HD3	1.74	0.69
13:M:4:ILE:CD1	13:M:10:PRO:CG	2.71	0.69
2:B:187:VAL:HG13	2:B:191:SER:HB2	1.74	0.69
1:A:1307:U:O2'	13:M:109:ARG:NH2	2.26	0.69
1:A:443:C:O2	1:A:491:G:N2	2.21	0.69
1:A:1220:G:N2	19:S:54:GLY:O	2.25	0.69
1:A:1178:G:N2	1:A:1181:G:OP2	2.22	0.69
9:I:42:GLU:OE1	9:I:45:ARG:NH1	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1279:G:OP2	1:A:1279:G:N2	2.25	0.68
4:D:95:GLU:HA	4:D:100:ASN:ND2	2.08	0.68
1:A:404:G:OP2	4:D:115:ARG:NH2	2.26	0.68
1:A:829:G:O6	1:A:857:C:N4	2.13	0.68
10:J:30:LYS:CE	10:J:36:VAL:HG12	2.22	0.68
14:N:92:GLU:OE1	14:N:92:GLU:N	2.26	0.68
19:S:12:ASP:OD1	19:S:14:HIS:N	2.26	0.68
1:A:514:C:N4	1:A:537:G:O6	2.19	0.68
7:G:61:ALA:HA	7:G:64:VAL:HG12	1.75	0.68
9:I:55:VAL:CG2	9:I:94:LEU:CD1	2.71	0.68
13:M:89:LEU:HD23	13:M:92:ARG:HH12	1.56	0.68
21:X:21:PHE:HD2	21:X:40:ILE:HG21	1.58	0.68
1:A:517:G:C2	1:A:530:G:H1'	2.28	0.68
1:A:1304:G:N1	1:A:1332:A:OP2	2.25	0.68
1:A:1436:U:H2'	1:A:1437:A:H8	1.59	0.68
11:K:35:THR:HA	11:K:42:LEU:H	1.59	0.68
15:O:26:GLU:HB3	15:O:81:LEU:CD2	2.23	0.68
6:F:38:ARG:HB2	6:F:97:THR:HA	1.76	0.68
10:J:47:GLU:O	10:J:66:GLU:HA	1.94	0.68
1:A:219:U:H2'	1:A:220:G:C8	2.28	0.68
1:A:881:G:OP1	12:L:9:ARG:NH2	2.26	0.68
17:Q:48:ASP:HA	17:Q:75:LEU:HD22	1.75	0.68
1:A:658:C:N3	1:A:748:G:N1	2.33	0.68
1:A:744:C:H2'	1:A:745:G:C8	2.29	0.68
1:A:1279:G:O2'	1:A:1281:C:OP2	2.09	0.68
21:X:99:VAL:HG22	21:X:146:LEU:HA	1.75	0.68
1:A:591:U:O4	1:A:648:A:N6	2.15	0.68
1:A:607:A:H2'	1:A:608:A:H8	1.58	0.68
1:A:1162:C:N4	1:A:1174:G:O6	2.18	0.68
5:E:87:GLY:O	5:E:94:VAL:HG22	1.94	0.68
7:G:51:ALA:HB2	7:G:58:GLU:HB3	1.75	0.68
9:I:106:ARG:NH1	9:I:107:ASP:O	2.27	0.68
17:Q:62:ARG:HD2	17:Q:76:VAL:HG22	1.76	0.68
21:X:74:LEU:HD21	21:X:76:VAL:HG23	1.75	0.68
1:A:949:A:OP2	13:M:105:ASN:ND2	2.27	0.67
15:O:17:ARG:NH2	15:O:20:ASN:OD1	2.26	0.67
2:B:68:LEU:HB3	2:B:161:LEU:HD23	1.77	0.67
1:A:613:C:H2'	1:A:614:C:H6	1.59	0.67
4:D:102:VAL:HG13	4:D:107:PHE:HB2	1.74	0.67
17:Q:45:HIS:HB3	17:Q:71:LYS:HG2	1.76	0.67
1:A:76:G:N1	1:A:93:U:O2	2.19	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:G:OP1	1:A:605:U:O2'	2.09	0.67
5:E:151:GLU:OE1	5:E:151:GLU:N	2.24	0.67
3:C:25:ASN:N	3:C:28:GLU:OE2	2.28	0.67
12:L:53:CYS:SG	12:L:54:ARG:N	2.68	0.67
18:R:42:SER:O	18:R:46:GLY:N	2.28	0.67
1:A:825:A:O2'	8:H:13:ARG:NH2	2.27	0.67
1:A:947:G:O3'	13:M:108:THR:OG1	2.12	0.67
5:E:11:LEU:HD13	5:E:39:VAL:HB	1.76	0.67
12:L:82:ILE:HA	12:L:97:THR:HA	1.76	0.67
1:A:3:A:O2'	1:A:612:C:O2'	2.13	0.67
1:A:444:G:N2	1:A:490:C:O2	2.17	0.67
1:A:944:G:N1	1:A:1338:G:OP2	2.28	0.67
1:A:1151:A:HO2'	1:A:1152:A:H8	1.42	0.67
1:A:706:A:H2'	1:A:707:U:C6	2.30	0.67
1:A:1014:A:H2'	1:A:1015:G:C8	2.30	0.67
1:A:1513:A:H2'	1:A:1514:G:H8	1.60	0.67
3:C:22:TRP:HB3	3:C:59:ARG:H	1.59	0.67
7:G:92:ARG:HG3	7:G:94:VAL:HG22	1.77	0.67
9:I:28:ILE:HG22	9:I:63:LEU:HB2	1.77	0.67
10:J:27:GLU:HB2	10:J:31:ARG:HH12	1.60	0.67
1:A:193:C:O2'	20:T:59:ASP:OD2	2.14	0.67
18:R:72:ASP:N	18:R:72:ASP:OD1	2.25	0.67
21:X:84:PRO:HA	21:X:145:ASN:HA	1.76	0.67
7:G:5:ARG:NH1	7:G:6:VAL:O	2.28	0.66
21:X:100:THR:HG23	21:X:147:VAL:HG21	1.77	0.66
8:H:48:ASP:O	8:H:62:THR:N	2.19	0.66
1:A:695:A:N6	1:A:797:C:O2'	2.27	0.66
3:C:82:GLU:HG3	3:C:83:ASP:H	1.57	0.66
1:A:1080:A:OP1	5:E:52:LYS:HD2	1.95	0.66
1:A:1248:A:H4'	9:I:33:ARG:HH12	1.60	0.66
8:H:49:PHE:HA	8:H:61:LEU:HA	1.78	0.66
15:O:77:ARG:HA	15:O:80:GLN:HE21	1.59	0.66
1:A:514:C:O2	1:A:537:G:N2	2.27	0.66
3:C:134:MET:HB2	3:C:151:VAL:HG21	1.77	0.66
7:G:111:ARG:HH12	7:G:122:ASN:HB2	1.59	0.66
1:A:459:A:H2'	1:A:460:A:C8	2.30	0.66
1:A:662:U:H2'	1:A:663:A:C8	2.31	0.66
1:A:738:C:OP1	6:F:2:ARG:NH2	2.28	0.66
1:A:1313:U:H2'	1:A:1314:C:H6	1.61	0.66
9:I:84:THR:HG21	9:I:103:PHE:HB3	1.78	0.66
21:X:22:GLU:OE1	21:X:22:GLU:N	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:700:G:N2	1:A:701:U:O4	2.28	0.66
13:M:19:LEU:HB2	13:M:30:SER:HB2	1.78	0.66
1:A:728:A:H2'	1:A:729:A:C8	2.31	0.66
1:A:1440:U:H4'	1:A:1441:A:N1	2.11	0.66
7:G:72:THR:OG1	7:G:142:HIS:NE2	2.26	0.66
18:R:11:CYS:O	18:R:14:THR:CG2	2.42	0.66
18:R:11:CYS:HB2	18:R:14:THR:HG21	1.78	0.66
3:C:70:THR:O	3:C:106:VAL:N	2.23	0.66
1:A:33:A:N3	12:L:29:GLN:NE2	2.44	0.65
3:C:132:ARG:HG3	3:C:136:ARG:HH12	1.60	0.65
1:A:104:G:OP2	20:T:13:GLN:NE2	2.29	0.65
1:A:517:G:O2'	1:A:531:U:O4	2.10	0.65
1:A:1342:C:H5"	9:I:129:LYS:HG3	1.77	0.65
5:E:105:ILE:HD13	5:E:123:VAL:HG12	1.76	0.65
6:F:42:TRP:CH2	6:F:61:LEU:HD12	2.31	0.65
3:C:19:ASN:OD1	3:C:54:ARG:NH2	2.26	0.65
1:A:1031:C:O2	1:A:1032:G:N1	2.29	0.65
1:A:1073:U:H3	1:A:1102:A:H61	1.43	0.65
7:G:67:GLU:HA	7:G:70:ARG:HG2	1.79	0.65
8:H:5:ASP:OD1	8:H:8:ALA:N	2.26	0.65
11:K:48:GLY:HA2	11:K:53:ARG:NH2	2.12	0.65
4:D:85:ASN:OD1	4:D:88:GLU:N	2.20	0.65
4:D:121:LYS:HG2	4:D:131:ASN:HD21	1.61	0.65
13:M:4:ILE:CD1	13:M:10:PRO:HG3	2.24	0.65
1:A:1308:U:H5'	13:M:109:ARG:HH22	1.62	0.65
1:A:1514:G:H2'	1:A:1515:G:C8	2.32	0.65
6:F:29:ILE:HG21	6:F:64:VAL:HG11	1.78	0.65
17:Q:58:VAL:N	17:Q:80:GLU:OE2	2.25	0.65
1:A:544:G:OP1	4:D:59:GLN:NE2	2.29	0.65
1:A:562:U:OP2	12:L:15:LYS:NZ	2.23	0.65
1:A:1038:C:H2'	1:A:1039:G:C8	2.29	0.65
19:S:3:ARG:HG3	19:S:4:SER:N	2.12	0.65
1:A:494:G:O2'	1:A:496:A:H1'	1.97	0.65
3:C:21:THR:OG1	3:C:58:GLU:CG	2.45	0.65
1:A:664:G:H22	1:A:741:G:H1	1.45	0.65
1:A:1310:G:N2	1:A:1327:C:O2	2.17	0.65
17:Q:57:ASP:OD1	17:Q:83:VAL:CG1	2.45	0.65
1:A:996:A:H2'	1:A:997:U:C6	2.32	0.65
9:I:24:GLY:H	9:I:61:LEU:HA	1.61	0.65
12:L:74:LEU:HD13	12:L:80:ILE:CD1	2.26	0.65
1:A:363:A:OP2	12:L:31:ARG:NH2	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:613:C:H2'	1:A:614:C:C6	2.32	0.64
17:Q:62:ARG:CD	17:Q:76:VAL:CG2	2.74	0.64
1:A:344:A:O2'	1:A:346:G:N7	2.29	0.64
1:A:563:A:H61	1:A:884:U:H3	1.46	0.64
3:C:83:ASP:HA	3:C:86:LYS:HG2	1.80	0.64
5:E:43:ASN:O	5:E:43:ASN:OD1	2.14	0.64
1:A:714:G:H2'	1:A:715:A:C8	2.32	0.64
1:A:922:G:H2'	1:A:923:A:H8	1.62	0.64
1:A:1426:G:H2'	1:A:1427:C:C6	2.32	0.64
1:A:1510:C:H2'	1:A:1511:G:C8	2.29	0.64
3:C:122:SER:O	3:C:126:ARG:NH1	2.29	0.64
12:L:75:GLN:O	12:L:78:SER:OG	2.12	0.64
21:X:46:ILE:O	21:X:46:ILE:HG22	1.97	0.64
1:A:273:U:O4	1:A:274:A:N6	2.30	0.64
1:A:721:G:H4'	1:A:722:G:O4'	1.96	0.64
9:I:123:ARG:NH1	9:I:124:ARG:O	2.30	0.64
1:A:380:G:N2	1:A:383:A:OP2	2.29	0.64
1:A:449:G:O6	1:A:484:G:N1	2.19	0.64
17:Q:62:ARG:HG2	17:Q:76:VAL:CG2	2.27	0.64
1:A:571:U:OP1	1:A:819:A:O2'	2.14	0.64
1:A:922:G:H2'	1:A:923:A:C8	2.33	0.64
1:A:337:G:H2'	1:A:338:A:C8	2.33	0.64
1:A:564:C:OP1	12:L:12:ARG:NE	2.20	0.64
1:A:671:G:N1	1:A:735:C:N3	2.41	0.64
1:A:912:C:N3	1:A:913:A:N6	2.45	0.64
1:A:1313:U:H2'	1:A:1314:C:C6	2.33	0.64
6:F:15:SER:HA	6:F:18:VAL:HG13	1.79	0.64
11:K:84:VAL:O	11:K:111:THR:OG1	2.10	0.64
1:A:69:G:H22	1:A:71:A:H62	1.46	0.64
1:A:363:A:H5"	12:L:31:ARG:CG	2.28	0.64
1:A:515:G:H3'	1:A:516:PSU:H6	1.63	0.64
1:A:539:A:H2'	1:A:540:G:C8	2.32	0.64
1:A:1119:C:H2'	1:A:1120:C:C6	2.33	0.64
6:F:69:GLU:OE1	6:F:69:GLU:N	2.31	0.64
10:J:52:LEU:HD21	10:J:59:LYS:HG2	1.80	0.64
7:G:70:ARG:O	7:G:138:ARG:NH2	2.30	0.64
21:X:90:HIS:HA	21:X:93:ARG:HH11	1.62	0.64
21:X:102:VAL:CG2	21:X:110:ARG:NH2	2.60	0.64
1:A:920:U:C1'	1:A:1080:A:C2	2.81	0.63
1:A:924:C:H2'	1:A:925:G:H2'	1.80	0.63
1:A:1310:G:N1	1:A:1327:C:N3	2.37	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:796:C:H2'	1:A:797:C:C6	2.33	0.63
1:A:1112:C:O2'	3:C:179:ARG:NE	2.32	0.63
7:G:20:SER:HB3	7:G:23:LEU:HD12	1.80	0.63
15:O:12:VAL:HG23	15:O:27:VAL:HG21	1.78	0.63
1:A:108:G:H5'	1:A:109:A:H5"	1.79	0.63
1:A:399:G:H2'	1:A:400:C:C6	2.34	0.63
1:A:823:C:HO2'	8:H:2:SER:N	1.96	0.63
1:A:1415:G:N2	1:A:1485:U:O2	2.29	0.63
10:J:29:ALA:O	10:J:34:ALA:N	2.29	0.63
13:M:44:LYS:N	13:M:47:GLU:OE2	2.23	0.63
7:G:111:ARG:HH22	7:G:122:ASN:HD22	1.46	0.63
1:A:750:C:O2'	15:O:21:ASP:OD1	2.12	0.63
1:A:1095:U:OP1	1:A:1108:G:N1	2.25	0.63
10:J:34:ALA:HB1	10:J:76:ILE:HG21	1.79	0.63
1:A:517:G:H1'	1:A:530:G:H8	1.64	0.63
1:A:414:A:H2'	1:A:415:A:H8	1.64	0.63
1:A:898:G:N2	1:A:901:A:OP2	2.31	0.63
1:A:1491:G:H3'	21:X:30:ARG:HB3	1.81	0.63
6:F:21:MET:HA	6:F:24:ARG:NH1	2.14	0.63
1:A:35:G:H2'	1:A:36:C:C6	2.34	0.63
1:A:679:C:N3	1:A:711:G:N1	2.43	0.63
1:A:950:U:H3'	13:M:101:ARG:HH12	1.63	0.63
1:A:1015:G:N2	1:A:1218:C:O2	2.31	0.63
3:C:11:ARG:NH1	3:C:180:ALA:O	2.32	0.63
3:C:28:GLU:OE1	3:C:28:GLU:N	2.27	0.63
5:E:65:GLU:HA	5:E:68:ARG:HG3	1.81	0.63
1:A:789:U:O4	1:A:793:U:N3	2.31	0.63
1:A:1070:U:O2	1:A:1106:G:N2	2.32	0.63
1:A:1160:G:N7	1:A:1182:G:N2	2.38	0.63
10:J:52:LEU:HB2	14:N:81:ARG:HD2	1.81	0.63
13:M:4:ILE:O	13:M:4:ILE:CG2	2.46	0.63
21:X:85:LEU:HD23	21:X:85:LEU:H	1.64	0.63
1:A:80:A:H2'	1:A:81:A:H8	1.63	0.62
1:A:628:G:H2'	1:A:629:A:C8	2.33	0.62
1:A:636:U:H5'	17:Q:6:ARG:HH21	1.63	0.62
1:A:1435:G:H2'	1:A:1436:U:C6	2.34	0.62
11:K:87:LYS:HE2	11:K:113:VAL:HG12	1.80	0.62
1:A:912:C:H2'	1:A:913:A:C8	2.34	0.62
21:X:96:GLY:N	21:X:97:GLU:OE1	2.32	0.62
1:A:1375:A:H5"	7:G:25:LYS:HE3	1.80	0.62
21:X:19:LEU:HG	21:X:19:LEU:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:29:ARG:HA	20:T:32:ILE:HD12	1.82	0.62
21:X:16:VAL:HG11	21:X:23:LEU:HB2	1.80	0.62
1:A:218:U:H2'	1:A:219:U:C6	2.35	0.62
14:N:38:ASP:OD1	14:N:41:ARG:NH1	2.32	0.62
1:A:264:C:O3'	17:Q:65:ARG:NH1	2.33	0.62
1:A:694:A:C2	1:A:695:A:H1'	2.35	0.62
1:A:1077:G:N2	1:A:1080:A:OP2	2.30	0.62
1:A:1104:G:H2'	1:A:1105:A:C8	2.34	0.62
13:M:54:ASP:OD1	13:M:55:THR:N	2.31	0.62
1:A:975:A:N1	1:A:1366:C:O2'	2.27	0.62
12:L:21:VAL:HG13	12:L:95:TYR:HE2	1.60	0.62
14:N:40:ASP:O	14:N:44:ALA:HB2	2.00	0.62
17:Q:8:LEU:HG	17:Q:25:ILE:HD13	1.82	0.62
1:A:363:A:N6	12:L:27:CYS:SG	2.72	0.62
1:A:795:C:H5"	11:K:128:ARG:HH12	1.65	0.62
1:A:1512:U:H2'	1:A:1513:A:H8	1.64	0.62
5:E:36:LEU:HD21	5:E:134:ILE:HG12	1.82	0.62
9:I:26:GLY:N	9:I:59:GLU:OE1	2.33	0.62
11:K:28:ASN:O	11:K:57:LYS:NZ	2.31	0.62
1:A:1158:C:N4	1:A:1181:G:O6	2.24	0.62
21:X:39:TYR:HB3	21:X:79:PRO:HG3	1.81	0.62
1:A:770:C:H2'	1:A:771:G:H8	1.65	0.62
1:A:97:G:C5	1:A:98:A:H1'	2.34	0.61
1:A:255:G:H2'	1:A:256:U:C6	2.34	0.61
1:A:530:G:H2'	1:A:531:U:C4	2.35	0.61
1:A:1527:U:H2'	1:A:1528:U:C6	2.35	0.61
3:C:191:THR:OG1	3:C:194:GLY:N	2.33	0.61
5:E:103:THR:N	5:E:122:ASN:OD1	2.33	0.61
9:I:33:ARG:HB3	9:I:37:GLN:NE2	2.14	0.61
1:A:333:U:H2'	1:A:334:C:H6	1.63	0.61
1:A:542:G:OP1	4:D:10:LYS:NZ	2.18	0.61
1:A:626:G:O2'	16:P:51:ARG:NH2	2.30	0.61
1:A:720:C:O3'	18:R:52:GLN:NE2	2.34	0.61
13:M:4:ILE:CD1	13:M:10:PRO:HG2	2.30	0.61
21:X:111:ARG:HD2	21:X:136:PHE:HA	1.83	0.61
1:A:928:G:N1	1:A:1389:C:N3	2.41	0.61
1:A:1314:C:N4	19:S:2:PRO:O	2.33	0.61
1:A:1512:U:H2'	1:A:1513:A:C8	2.36	0.61
10:J:80:THR:O	10:J:83:THR:OG1	2.10	0.61
19:S:33:THR:O	19:S:52:HIS:ND1	2.33	0.61
21:X:111:ARG:CD	21:X:136:PHE:HA	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:824:G:H2'	1:A:825:A:H8	1.66	0.61
1:A:955:U:HO2'	19:S:83:HIS:CE1	2.17	0.61
3:C:132:ARG:HD3	3:C:136:ARG:HH22	1.65	0.61
1:A:106:C:H2'	1:A:107:G:H8	1.65	0.61
1:A:925:G:H4'	1:A:926:G:H2'	1.83	0.61
1:A:1114:C:N3	1:A:1186:G:N1	2.36	0.61
1:A:1427:C:H2'	1:A:1428:A:C8	2.35	0.61
8:H:48:ASP:OD1	8:H:49:PHE:N	2.33	0.61
1:A:88:U:O2'	1:A:89:U:O5'	2.15	0.61
1:A:132:C:H2'	1:A:133:U:H6	1.64	0.61
1:A:744:C:H2'	1:A:745:G:H8	1.64	0.61
1:A:951:G:OP2	13:M:101:ARG:NH2	2.28	0.61
1:A:1166:G:C5	1:A:1168:U:H5"	2.35	0.61
1:A:1179:A:H5"	9:I:104:VAL:HG12	1.81	0.61
1:A:470:C:H2'	1:A:471:U:H6	1.65	0.61
1:A:792:A:HO2'	1:A:793:U:H6	1.49	0.61
1:A:1342:C:O5'	9:I:129:LYS:NZ	2.34	0.61
1:A:1440:U:O2	1:A:1461:G:O6	2.19	0.61
1:A:25:C:H2'	1:A:26:A:C8	2.33	0.61
1:A:953:G:O6	1:A:1228:C:N4	2.22	0.61
1:A:987:G:H2'	1:A:988:G:H8	1.64	0.61
3:C:20:SER:OG	3:C:40:ARG:NH2	2.34	0.61
3:C:68:ILE:HB	3:C:103:ILE:HG22	1.83	0.61
8:H:106:THR:HB	8:H:121:LEU:HD23	1.82	0.61
9:I:112:GLU:OE2	9:I:115:LYS:NZ	2.33	0.61
1:A:532:A:N1	3:C:161:GLU:OE2	2.33	0.60
1:A:868:C:H2'	1:A:869:G:O4'	2.01	0.60
1:A:1054:C:O5'	1:A:1196:A:O2'	2.18	0.60
10:J:85:ASP:OD1	10:J:86:ALA:N	2.31	0.60
13:M:7:ILE:N	13:M:66:GLU:OE1	2.33	0.60
1:A:255:G:H2'	1:A:256:U:H6	1.67	0.60
1:A:500:G:H2'	1:A:501:C:C6	2.36	0.60
1:A:837:U:H2'	1:A:838:G:H8	1.66	0.60
1:A:1223:C:OP2	19:S:78:ARG:NH2	2.31	0.60
12:L:72:HIS:HB3	12:L:99:ARG:HH12	1.67	0.60
1:A:635:A:O3'	17:Q:6:ARG:NH2	2.35	0.60
1:A:953:G:N2	1:A:1228:C:O2	2.19	0.60
1:A:1409:C:H2'	1:A:1410:A:C8	2.36	0.60
17:Q:28:PHE:CE2	17:Q:37:PHE:HB3	2.37	0.60
1:A:399:G:H2'	1:A:400:C:H6	1.67	0.60
1:A:1458:G:H2'	1:A:1459:G:H8	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1471:U:H2'	1:A:1472:U:C6	2.36	0.60
3:C:120:ILE:HD11	3:C:137:ALA:HB2	1.83	0.60
16:P:69:ASP:OD1	16:P:69:ASP:N	2.32	0.60
1:A:1384:C:H2'	1:A:1385:G:C8	2.36	0.60
10:J:35:GLN:HG2	10:J:78:GLU:HB2	1.82	0.60
1:A:193:C:H2'	1:A:194:C:C6	2.36	0.60
1:A:355:C:O2'	1:A:388:G:N3	2.29	0.60
1:A:673:A:H2'	1:A:674:G:C8	2.37	0.60
1:A:1218:C:H2'	1:A:1219:A:C8	2.35	0.60
1:A:712:A:H2'	1:A:713:G:C8	2.37	0.60
1:A:1114:C:O2	1:A:1186:G:N2	2.18	0.60
1:A:1367:C:O5'	9:I:114:LYS:NZ	2.34	0.60
3:C:41:GLN:O	3:C:44:THR:OG1	2.20	0.60
4:D:26:ARG:NH2	4:D:30:THR:O	2.35	0.60
11:K:109:ASN:OD1	11:K:110:ILE:N	2.35	0.60
20:T:67:ILE:HD12	20:T:71:LYS:HD3	1.84	0.60
1:A:124:C:H2'	1:A:125:U:C6	2.36	0.60
6:F:27:ALA:O	6:F:31:GLY:N	2.24	0.60
1:A:1178:G:O5'	9:I:95:ARG:NH2	2.35	0.60
1:A:1447:A:H5"	1:A:1448:C:H5	1.67	0.60
1:A:1503:A:C6	1:A:1504:G:H1'	2.37	0.60
4:D:95:GLU:HA	4:D:100:ASN:HD22	1.66	0.60
21:X:124:MET:CG	21:X:135:VAL:HG13	2.32	0.60
1:A:781:A:OP2	1:A:800:G:N2	2.31	0.59
9:I:34:SER:N	9:I:37:GLN:HE21	1.99	0.59
1:A:427:U:OP1	4:D:13:ARG:NH1	2.30	0.59
1:A:1071:C:H2'	1:A:1072:G:C8	2.37	0.59
15:O:26:GLU:CG	15:O:81:LEU:HD22	2.32	0.59
20:T:60:ARG:O	20:T:64:LYS:N	2.30	0.59
1:A:335:C:H2'	1:A:336:A:H8	1.68	0.59
1:A:542:G:O3'	4:D:14:ARG:NH1	2.27	0.59
1:A:660:C:N4	1:A:745:G:O6	2.20	0.59
1:A:677:U:H2'	1:A:678:U:H6	1.66	0.59
1:A:1381:U:O2'	7:G:79:ARG:O	2.19	0.59
1:A:310:G:OP1	16:P:31:ARG:N	2.35	0.59
1:A:313:A:H2'	1:A:314:C:C6	2.37	0.59
1:A:373:A:O2'	1:A:451:A:N7	2.35	0.59
1:A:1398:A:N6	1:A:1502:A:OP1	2.32	0.59
3:C:34:ASP:OD1	3:C:38:LYS:NZ	2.31	0.59
12:L:3:THR:N	12:L:6:GLN:OE1	2.35	0.59
1:A:2:A:O2'	4:D:83:LYS:NZ	2.29	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:C:H2'	1:A:313:A:C8	2.37	0.59
1:A:785:G:H2'	1:A:786:G:C8	2.37	0.59
1:A:1256:A:O2'	1:A:1278:G:O6	2.19	0.59
5:E:76:LEU:HD13	5:E:79:GLY:H	1.68	0.59
1:A:147:G:H2'	1:A:148:G:C8	2.38	0.59
1:A:401:C:O2'	1:A:621:A:N3	2.34	0.59
1:A:876:C:O5'	8:H:15:ARG:NH1	2.36	0.59
1:A:1013:G:N2	1:A:1016:A:OP2	2.35	0.59
1:A:1523:G:OP1	11:K:125:LYS:NZ	2.26	0.59
4:D:73:ARG:NH2	4:D:74:ASN:OD1	2.32	0.59
9:I:49:ARG:NH2	9:I:58:VAL:HG11	2.16	0.59
1:A:459:A:H2'	1:A:460:A:H8	1.66	0.59
12:L:83:ARG:HG2	12:L:98:VAL:CG2	2.32	0.59
1:A:85:U:H1'	1:A:86:G:H21	1.68	0.59
1:A:1241:G:H2'	1:A:1242:G:H8	1.67	0.59
4:D:99:ASP:OD1	4:D:100:ASN:N	2.35	0.59
4:D:188:ARG:HH12	4:D:193:ALA:HA	1.68	0.59
14:N:86:GLU:HB3	14:N:90:ARG:HH22	1.67	0.59
6:F:42:TRP:HZ2	6:F:61:LEU:CD1	2.14	0.59
13:M:4:ILE:HD12	13:M:22:ILE:HD11	1.84	0.59
19:S:51:VAL:O	19:S:57:HIS:HA	2.02	0.59
1:A:1223:C:P	19:S:78:ARG:HH21	2.26	0.58
1:A:1226:C:H2'	13:M:102:THR:HB	1.84	0.58
1:A:1350:A:O2'	7:G:33:ASP:OD1	2.18	0.58
1:A:1478:U:H3'	1:A:1479:C:H5"	1.84	0.58
1:A:35:G:H2'	1:A:36:C:H6	1.66	0.58
1:A:269:C:H2'	1:A:270:A:C8	2.38	0.58
1:A:407:U:O2'	4:D:113:GLU:HG2	2.03	0.58
1:A:769:G:N1	1:A:811:C:O2	2.35	0.58
1:A:920:U:H5'	1:A:1080:A:N6	2.18	0.58
7:G:53:ARG:NH2	7:G:125:SER:OG	2.30	0.58
17:Q:28:PHE:CE2	17:Q:37:PHE:CB	2.85	0.58
1:A:337:G:H2'	1:A:338:A:H8	1.67	0.58
1:A:1340:A:O3'	9:I:130:ARG:NH2	2.36	0.58
3:C:47:LEU:HB3	3:C:50:ALA:HB3	1.85	0.58
11:K:88:GLY:N	11:K:114:THR:HG22	2.19	0.58
1:A:666:G:H5'	1:A:726:C:H1'	1.83	0.58
1:A:692:U:O2'	1:A:694:A:N7	2.24	0.58
1:A:1264:U:H2'	1:A:1265:C:H6	1.69	0.58
20:T:35:VAL:O	20:T:39:ILE:HG13	2.02	0.58
1:A:363:A:H5"	12:L:31:ARG:NE	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:17:ARG:NH2	15:O:18:ASP:OD1	2.34	0.58
1:A:745:G:H2'	1:A:746:A:C8	2.36	0.58
1:A:1029:U:H2'	1:A:1031:C:N3	2.18	0.58
7:G:111:ARG:NH1	7:G:123:GLU:OE2	2.36	0.58
17:Q:58:VAL:HB	17:Q:80:GLU:HG3	1.85	0.58
20:T:23:SER:OG	20:T:24:ARG:N	2.36	0.58
1:A:468:A:H3'	1:A:469:C:H6	1.69	0.58
1:A:643:C:H2'	1:A:644:U:H6	1.69	0.58
8:H:29:SER:H	8:H:57:PRO:HB2	1.68	0.58
15:O:82:ILE:O	15:O:86:GLY:N	2.37	0.58
1:A:142:G:H3'	1:A:143:A:H8	1.68	0.58
1:A:517:G:H1'	1:A:530:G:C8	2.38	0.58
12:L:34:CYS:HB2	12:L:53:CYS:SG	2.44	0.58
12:L:52:VAL:HG12	12:L:66:TYR:HA	1.85	0.58
21:X:97:GLU:OE1	21:X:97:GLU:N	2.37	0.58
21:X:98:GLU:HA	21:X:116:VAL:HA	1.85	0.58
1:A:384:G:H2'	1:A:385:C:C6	2.38	0.58
1:A:1070:U:H3	1:A:1106:G:H1	1.50	0.58
4:D:170:TRP:CH2	4:D:191:LEU:CD2	2.87	0.58
19:S:3:ARG:HH21	19:S:10:PHE:HB3	1.69	0.58
19:S:3:ARG:NH1	19:S:9:PRO:HA	2.19	0.58
1:A:946:A:H2'	1:A:947:G:C8	2.39	0.58
3:C:172:ARG:HD2	3:C:174:PRO:HD3	1.85	0.58
4:D:168:PRO:HB3	4:D:170:TRP:CH2	2.39	0.58
4:D:172:GLU:O	4:D:181:THR:N	2.37	0.58
11:K:35:THR:HG23	11:K:37:ARG:H	1.68	0.58
12:L:82:ILE:HG22	12:L:97:THR:HG22	1.86	0.58
17:Q:13:VAL:CG2	17:Q:24:ALA:HB2	2.34	0.58
19:S:17:LYS:O	19:S:21:LYS:HG2	2.04	0.58
1:A:878:A:H2'	1:A:879:C:C6	2.38	0.57
6:F:38:ARG:HB3	6:F:63:ASN:HB2	1.86	0.57
8:H:6:PRO:HB2	8:H:33:LYS:HE3	1.86	0.57
13:M:65:VAL:O	13:M:66:GLU:CG	2.52	0.57
1:A:1032:G:H3'	1:A:1032:G:N3	2.18	0.57
1:A:1118:U:P	9:I:106:ARG:HE	2.26	0.57
10:J:98:VAL:O	10:J:99:GLN:NE2	2.27	0.57
17:Q:62:ARG:CG	17:Q:76:VAL:CG2	2.81	0.57
20:T:44:LYS:HG3	20:T:87:ALA:HB3	1.86	0.57
1:A:705:G:H2'	1:A:706:A:H5'	1.86	0.57
1:A:1002:G:H2'	1:A:1003:G:H8	1.70	0.57
1:A:1471:U:H2'	1:A:1472:U:H6	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:87:LYS:HD2	8:H:93:PRO:HD3	1.87	0.57
12:L:114:ARG:HB2	12:L:119:VAL:O	2.05	0.57
1:A:1367:C:H5"	9:I:116:VAL:HG23	1.87	0.57
1:A:1536:C:O2'	3:C:164:ARG:NH2	2.36	0.57
13:M:4:ILE:HD11	13:M:10:PRO:HG2	1.85	0.57
21:X:124:MET:HG3	21:X:135:VAL:HG13	1.86	0.57
1:A:299:G:H2'	1:A:300:A:C8	2.40	0.57
1:A:939:G:O6	1:A:1344:C:N4	2.37	0.57
1:A:1327:C:H2'	1:A:1328:C:C6	2.38	0.57
4:D:170:TRP:HH2	4:D:191:LEU:HD21	1.70	0.57
7:G:60:GLU:OE1	7:G:60:GLU:N	2.37	0.57
13:M:65:VAL:C	13:M:66:GLU:HG2	2.24	0.57
1:A:313:A:H2'	1:A:314:C:H6	1.68	0.57
1:A:564:C:OP2	12:L:12:ARG:NH2	2.31	0.57
1:A:801:U:H2'	1:A:802:A:C8	2.39	0.57
1:A:947:G:N1	1:A:1234:C:N3	2.32	0.57
1:A:1346:A:OP1	9:I:122:ARG:NH1	2.36	0.57
1:A:1393:U:H3'	1:A:1394:A:H8	1.70	0.57
11:K:85:MET:HG2	11:K:111:THR:OG1	2.04	0.57
15:O:10:LYS:O	15:O:13:SER:OG	2.23	0.57
1:A:363:A:H5'	12:L:31:ARG:H	1.69	0.57
1:A:381:C:H2'	1:A:382:A:O4'	2.03	0.57
1:A:509:A:N3	1:A:543:U:O2'	2.31	0.57
1:A:967:5MC:H3'	1:A:968:A:H2'	1.87	0.57
1:A:1005:A:C2	1:A:1006:G:H1'	2.39	0.57
1:A:1426:G:C2	1:A:1474:U:O2	2.57	0.57
6:F:73:GLU:CD	6:F:73:GLU:H	2.08	0.57
7:G:26:PHE:HA	7:G:29:ILE:HD12	1.86	0.57
1:A:1435:G:H2'	1:A:1436:U:H6	1.69	0.57
1:A:1458:G:H2'	1:A:1459:G:C8	2.39	0.57
7:G:73:VAL:HG12	7:G:142:HIS:CD2	2.40	0.57
8:H:40:LEU:O	8:H:44:GLY:N	2.38	0.57
15:O:63:ARG:HA	15:O:66:LEU:HD12	1.87	0.57
1:A:251:G:O6	1:A:272:C:N4	2.37	0.57
2:B:23:TRP:CZ3	2:B:25:PRO:HA	2.34	0.57
9:I:12:ARG:HG3	9:I:13:LYS:H	1.70	0.57
21:X:90:HIS:HA	21:X:93:ARG:NH1	2.20	0.57
1:A:36:C:H5'	12:L:118:GLY:HA2	1.85	0.57
1:A:341:C:H2'	1:A:342:C:C6	2.40	0.57
1:A:948:C:H2'	1:A:949:A:H8	1.70	0.57
1:A:1160:G:H22	1:A:1176:A:H2	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:13:GLU:HB2	5:E:39:VAL:HG12	1.87	0.57
1:A:384:G:H2'	1:A:385:C:H6	1.70	0.56
1:A:1044:A:N7	1:A:1045:C:H1'	2.19	0.56
1:A:1289:A:N1	1:A:1371:G:O2'	2.34	0.56
4:D:29:ASP:OD1	4:D:30:THR:N	2.37	0.56
1:A:877:G:O6	1:A:878:A:N6	2.38	0.56
3:C:108:LYS:HB2	3:C:111:LEU:HB2	1.87	0.56
3:C:181:ASP:OD2	3:C:204:LYS:NZ	2.38	0.56
15:O:26:GLU:CB	15:O:81:LEU:CD2	2.82	0.56
20:T:44:LYS:NZ	20:T:86:LEU:HB3	2.20	0.56
1:A:142:G:H3'	1:A:143:A:C8	2.40	0.56
1:A:251:G:HO2'	1:A:266:G:H8	1.53	0.56
1:A:564:C:P	12:L:12:ARG:HE	2.27	0.56
1:A:867:G:O2'	1:A:873:A:N1	2.34	0.56
1:A:1275:A:H2'	1:A:1276:G:O4'	2.06	0.56
1:A:1464:U:H2'	1:A:1465:A:C8	2.40	0.56
4:D:12:SER:O	4:D:16:GLY:N	2.38	0.56
4:D:50:ASP:OD1	4:D:51:TYR:N	2.38	0.56
7:G:72:THR:O	7:G:96:ARG:NH2	2.37	0.56
10:J:32:THR:HG21	10:J:83:THR:HA	1.88	0.56
10:J:51:VAL:HG13	14:N:81:ARG:HB2	1.87	0.56
17:Q:10:GLY:CA	17:Q:25:ILE:HG12	2.35	0.56
20:T:44:LYS:HE3	20:T:86:LEU:HD23	1.87	0.56
1:A:829:G:N1	1:A:857:C:N3	2.38	0.56
1:A:973:G:O3'	14:N:81:ARG:NH2	2.33	0.56
7:G:89:VAL:HG12	7:G:90:GLU:H	1.68	0.56
8:H:75:ILE:HD12	8:H:75:ILE:O	2.05	0.56
1:A:413:G:H1'	1:A:428:G:N2	2.20	0.56
1:A:460:A:H2'	1:A:461:A:C8	2.40	0.56
1:A:842:U:H2'	1:A:843:U:C6	2.39	0.56
1:A:1288:A:H2'	1:A:1289:A:C8	2.40	0.56
3:C:108:LYS:HB3	3:C:144:LEU:HD21	1.87	0.56
16:P:34:GLU:OE2	16:P:56:ARG:NH2	2.39	0.56
1:A:187:G:N2	1:A:190:A:OP2	2.35	0.56
1:A:1305:G:N1	1:A:1331:G:O2'	2.33	0.56
3:C:91:VAL:HG21	3:C:101:ILE:HD11	1.87	0.56
4:D:19:LEU:HB2	4:D:21:LEU:HG	1.87	0.56
11:K:34:ILE:CD1	11:K:43:GLY:N	2.68	0.56
1:A:229:U:C2	1:A:230:G:C8	2.94	0.56
1:A:1341:U:O2'	1:A:1342:C:H5'	2.06	0.56
20:T:18:ARG:HH21	20:T:19:LYS:HG2	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:987:G:H2'	1:A:988:G:C8	2.40	0.56
1:A:1250:A:H2'	1:A:1251:A:C8	2.41	0.56
1:A:1380:U:C5	7:G:3:ARG:HA	2.40	0.56
1:A:50:A:O2'	1:A:360:G:N2	2.38	0.56
1:A:80:A:H2'	1:A:81:A:C8	2.40	0.56
13:M:10:PRO:HG3	13:M:22:ILE:HD11	1.87	0.56
21:X:114:GLN:HG3	21:X:114:GLN:O	2.05	0.56
1:A:265:G:N2	1:A:267:C:H5'	2.21	0.56
1:A:284:C:H2'	1:A:285:C:C6	2.41	0.56
1:A:390:U:O3'	16:P:28:ARG:NH2	2.38	0.56
1:A:1128:C:N3	1:A:1145:A:N6	2.54	0.56
14:N:73:PHE:CZ	14:N:78:GLY:HA2	2.41	0.56
21:X:10:GLU:HA	21:X:13:THR:HG22	1.88	0.56
1:A:162:A:C5	1:A:163:C:H1'	2.41	0.55
1:A:263:A:H2'	1:A:264:C:C6	2.41	0.55
1:A:322:C:H2'	1:A:323:U:H6	1.71	0.55
1:A:468:A:H3'	1:A:469:C:C6	2.41	0.55
3:C:73:PRO:HG3	3:C:105:GLU:HB3	1.87	0.55
3:C:191:THR:N	3:C:194:GLY:O	2.39	0.55
9:I:55:VAL:HG21	9:I:94:LEU:HD11	1.86	0.55
19:S:44:MET:SD	19:S:47:LEU:HD12	2.46	0.55
1:A:471:U:H2'	1:A:472:U:C6	2.41	0.55
1:A:966:2MG:H3'	1:A:967:5MC:HM51	1.88	0.55
4:D:124:MET:O	4:D:144:SER:OG	2.16	0.55
5:E:154:ALA:HB2	5:E:164:ILE:HG13	1.87	0.55
1:A:628:G:H2'	1:A:629:A:H8	1.71	0.55
1:A:967:5MC:OP2	1:A:968:A:O2'	2.21	0.55
1:A:980:C:O2'	14:N:13:ARG:NH1	2.38	0.55
1:A:1296:C:H5'	13:M:14:HIS:CE1	2.40	0.55
1:A:1518:MA6:H8	1:A:1518:MA6:O5'	2.06	0.55
19:S:55:ARG:HG3	19:S:56:GLN:HG3	1.88	0.55
1:A:299:G:C6	1:A:300:A:C6	2.95	0.55
1:A:518:C:H5"	1:A:530:G:N7	2.20	0.55
1:A:782:A:H2'	1:A:783:C:O4'	2.06	0.55
1:A:976:G:OP2	1:A:1358:U:O2'	2.25	0.55
1:A:979:C:OP1	1:A:1223:C:N4	2.39	0.55
3:C:85:GLU:OE2	3:C:88:ARG:NE	2.34	0.55
6:F:67:PRO:O	6:F:70:VAL:HG12	2.06	0.55
14:N:84:VAL:HG13	14:N:85:ARG:N	2.21	0.55
1:A:613:C:OP1	4:D:81:ARG:NH1	2.37	0.55
4:D:103:TYR:O	4:D:165:ARG:NH2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:107:ARG:O	13:M:111:GLY:N	2.27	0.55
21:X:124:MET:SD	21:X:135:VAL:HG13	2.46	0.55
1:A:524:G:H2'	1:A:525:C:C6	2.42	0.55
1:A:538:G:H2'	1:A:539:A:H8	1.72	0.55
1:A:714:G:H2'	1:A:715:A:H8	1.70	0.55
1:A:767:A:H2'	1:A:768:A:H8	1.71	0.55
1:A:935:A:O2'	1:A:1383:C:O2	2.24	0.55
1:A:1399:C:H42	1:A:1502:A:H62	1.55	0.55
1:A:1415:G:O6	1:A:1485:U:O4	2.24	0.55
2:B:68:LEU:HD23	2:B:161:LEU:CD2	2.36	0.55
1:A:350:G:H2'	1:A:351:G:C8	2.42	0.55
1:A:774:G:C6	1:A:775:G:C4	2.95	0.55
1:A:806:C:H2'	1:A:807:A:C8	2.34	0.55
1:A:920:U:O4'	1:A:1080:A:C6	2.60	0.55
1:A:925:G:H1	1:A:1391:U:H1'	1.71	0.55
1:A:1317:C:O5'	14:N:24:ARG:NH2	2.38	0.55
4:D:121:LYS:O	4:D:146:ARG:NH1	2.37	0.55
20:T:49:LYS:HA	20:T:52:ASN:HD21	1.71	0.55
1:A:215:C:H2'	1:A:216:U:O4'	2.07	0.55
7:G:5:ARG:HH11	7:G:7:ILE:HG22	1.72	0.55
1:A:606:G:N2	1:A:632:U:OP1	2.31	0.55
1:A:677:U:H2'	1:A:678:U:C6	2.42	0.55
1:A:980:C:O3'	14:N:13:ARG:NH2	2.36	0.55
1:A:1314:C:OP1	19:S:6:LYS:NZ	2.27	0.55
1:A:1340:A:H2'	1:A:1341:U:C6	2.42	0.55
2:B:173:ILE:HG23	2:B:183:VAL:HG21	1.89	0.55
9:I:59:GLU:C	9:I:60:LYS:HD2	2.27	0.55
16:P:19:VAL:HG21	16:P:52:LEU:HD21	1.89	0.55
1:A:11:G:H2'	1:A:12:U:C6	2.42	0.55
1:A:158:G:O6	1:A:163:C:N4	2.33	0.55
1:A:924:C:C2'	1:A:925:G:H2'	2.37	0.55
1:A:1246:A:H2'	1:A:1247:U:C6	2.42	0.55
1:A:1450:U:O2	1:A:1453:G:N1	2.32	0.55
17:Q:28:PHE:CZ	17:Q:37:PHE:HB2	2.42	0.55
1:A:264:C:O2'	17:Q:66:PRO:O	2.25	0.54
2:B:111:ILE:HD13	2:B:148:LEU:HD13	1.89	0.54
1:A:107:G:N7	1:A:108:G:N2	2.55	0.54
1:A:223:A:H2'	1:A:224:U:C6	2.42	0.54
1:A:297:G:N2	1:A:301:G:N7	2.55	0.54
1:A:449:G:H2'	1:A:450:G:C8	2.41	0.54
1:A:555:U:H2'	1:A:556:C:C6	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:865:A:N3	1:A:918:A:O2'	2.39	0.54
7:G:35:LYS:HB3	7:G:38:THR:HG22	1.89	0.54
7:G:70:ARG:NH2	7:G:97:ASN:OD1	2.41	0.54
9:I:57:MET:CA	9:I:60:LYS:HD3	2.36	0.54
14:N:82:ILE:O	14:N:85:ARG:N	2.39	0.54
18:R:49:ALA:HA	18:R:52:GLN:HB3	1.89	0.54
1:A:160:A:H2'	1:A:161:A:O4'	2.08	0.54
1:A:216:U:H2'	1:A:217:C:C6	2.41	0.54
1:A:302:G:H2'	1:A:303:A:H8	1.72	0.54
1:A:414:A:C4	1:A:415:A:C8	2.94	0.54
1:A:508:U:H4'	4:D:51:TYR:CD2	2.41	0.54
1:A:885:G:H2'	1:A:886:G:H8	1.71	0.54
1:A:1470:U:H2'	1:A:1471:U:C6	2.42	0.54
4:D:95:GLU:HG2	4:D:186:PRO:HG3	1.88	0.54
12:L:72:HIS:NE2	21:X:48:VAL:HB	2.21	0.54
13:M:49:SER:O	13:M:53:ILE:HG12	2.07	0.54
1:A:427:U:H3'	1:A:428:G:H2'	1.89	0.54
1:A:1208:C:O2'	1:A:1209:C:OP1	2.23	0.54
1:A:1367:C:H3'	9:I:114:LYS:NZ	2.23	0.54
1:A:1393:U:H3'	1:A:1394:A:C8	2.43	0.54
1:A:1426:G:H1	1:A:1474:U:H3	1.53	0.54
4:D:95:GLU:OE1	4:D:100:ASN:ND2	2.32	0.54
21:X:102:VAL:HG23	21:X:110:ARG:HH22	1.65	0.54
1:A:341:C:H2'	1:A:342:C:H6	1.71	0.54
10:J:66:GLU:HB2	14:N:99:ALA:HB2	1.88	0.54
12:L:54:ARG:NE	12:L:62:GLU:OE1	2.36	0.54
1:A:193:C:O4'	20:T:55:GLN:NE2	2.37	0.54
1:A:826:C:H5'	8:H:13:ARG:CZ	2.37	0.54
1:A:1389:C:C4	1:A:1390:U:C4	2.96	0.54
5:E:93:ARG:HB2	5:E:128:TYR:HB2	1.88	0.54
9:I:19:VAL:HG13	9:I:65:ILE:HG12	1.89	0.54
13:M:66:GLU:HG3	13:M:67:GLY:H	1.73	0.54
1:A:701:U:H4'	1:A:703:G:C8	2.43	0.54
1:A:1095:U:H2'	1:A:1096:C:C6	2.42	0.54
1:A:1329:A:H5"	13:M:26:GLY:H	1.73	0.54
1:A:1350:A:OP2	9:I:120:LYS:NZ	2.33	0.54
9:I:49:ARG:HH21	9:I:58:VAL:HG11	1.72	0.54
1:A:689:C:N4	1:A:698:G:O6	2.37	0.54
4:D:61:VAL:HA	4:D:64:ILE:HG22	1.89	0.54
1:A:94:G:H4'	1:A:95:C:H5'	1.88	0.54
1:A:728:A:C6	1:A:729:A:C6	2.95	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:25:ILE:O	10:J:28:THR:OG1	2.22	0.54
10:J:85:ASP:O	10:J:89:ARG:HG2	2.07	0.54
1:A:598:U:H2'	1:A:599:C:C6	2.42	0.54
1:A:996:A:H2'	1:A:997:U:H6	1.73	0.54
1:A:1328:C:H2'	1:A:1329:A:H8	1.72	0.54
5:E:154:ALA:HB1	5:E:159:LYS:O	2.08	0.54
12:L:37:VAL:N	21:X:78:SER:OG	2.41	0.54
12:L:39:THR:CG2	21:X:48:VAL:CG1	2.84	0.54
13:M:91:HIS:CD2	13:M:97:VAL:HG11	2.43	0.54
16:P:22:ALA:HB2	16:P:32:PHE:HB2	1.90	0.54
16:P:38:PHE:CE1	16:P:51:ARG:HB3	2.43	0.54
1:A:1102:A:H2'	1:A:1103:C:H6	1.73	0.53
1:A:1309:G:OP2	13:M:98:ARG:NH2	2.37	0.53
1:A:1343:G:H3'	9:I:124:ARG:HH21	1.73	0.53
10:J:45:ARG:NE	10:J:47:GLU:OE2	2.41	0.53
1:A:602:A:H2'	1:A:603:U:C6	2.43	0.53
1:A:920:U:C4'	1:A:1080:A:C6	2.91	0.53
1:A:953:G:O6	13:M:103:LYS:NZ	2.34	0.53
1:A:1015:G:C6	1:A:1016:A:C6	2.97	0.53
10:J:30:LYS:HE3	10:J:36:VAL:HG12	1.89	0.53
11:K:34:ILE:HG13	11:K:43:GLY:O	2.08	0.53
1:A:125:U:H2'	1:A:126:G:H8	1.74	0.53
1:A:503:C:H2'	1:A:504:C:C6	2.43	0.53
1:A:713:G:C2	1:A:714:G:C5	2.97	0.53
1:A:878:A:H2'	1:A:879:C:H6	1.74	0.53
7:G:72:THR:H	7:G:142:HIS:HE1	1.52	0.53
1:A:517:G:H21	1:A:529:G:HO2'	1.55	0.53
1:A:604:G:O6	1:A:634:C:N4	2.32	0.53
1:A:954:G:H21	1:A:1227:A:N6	1.96	0.53
1:A:1023:U:H2'	1:A:1024:G:H8	1.74	0.53
1:A:1023:U:C2	1:A:1024:G:C8	2.96	0.53
1:A:1277:C:H1'	1:A:1282:C:H1'	1.90	0.53
1:A:1376:U:O3'	7:G:95:ARG:NH1	2.41	0.53
5:E:36:LEU:CD2	5:E:50:TYR:CD1	2.91	0.53
1:A:51:A:N7	1:A:114:U:O2'	2.41	0.53
1:A:706:A:C5	1:A:707:U:C4	2.96	0.53
1:A:742:G:H5"	15:O:58:ARG:HH11	1.73	0.53
1:A:1278:G:H4'	1:A:1279:G:C4	2.44	0.53
1:A:1515:G:H5"	1:A:1516:2MG:OP2	2.08	0.53
6:F:42:TRP:HZ2	6:F:61:LEU:HD13	1.68	0.53
9:I:15:SER:OG	9:I:69:GLY:O	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:C:H2'	1:A:125:U:H6	1.72	0.53
1:A:822:U:H2'	1:A:823:C:H6	1.74	0.53
1:A:1305:G:H2'	1:A:1331:G:H21	1.74	0.53
3:C:32:ASN:O	3:C:35:SER:OG	2.23	0.53
5:E:142:ASP:O	5:E:145:GLU:HG2	2.09	0.53
10:J:85:ASP:O	10:J:89:ARG:NH1	2.42	0.53
20:T:61:GLN:HA	20:T:64:LYS:HB2	1.90	0.53
21:X:113:TRP:HB3	21:X:129:VAL:CG1	2.37	0.53
1:A:59:A:H5"	1:A:387:U:H5"	1.90	0.53
1:A:1511:G:H2'	1:A:1512:U:H6	1.73	0.53
9:I:25:ASN:HB3	9:I:62:ASP:HB3	1.91	0.53
12:L:56:ARG:HA	12:L:62:GLU:HA	1.90	0.53
1:A:451:A:N6	1:A:481:G:H5'	2.24	0.53
1:A:454:G:H22	1:A:478:A:H2	1.56	0.53
1:A:958:A:C2	19:S:55:ARG:HB3	2.44	0.53
1:A:1118:U:H2'	1:A:1119:C:H6	1.73	0.53
1:A:1533:C:H2'	1:A:1534:A:C8	2.43	0.53
1:A:141:G:N2	1:A:222:C:O2	2.34	0.53
1:A:382:A:H2'	1:A:383:A:C8	2.44	0.53
1:A:1010:U:H2'	1:A:1011:C:H6	1.74	0.53
1:A:1333:A:H2'	1:A:1334:G:O4'	2.09	0.53
1:A:1449:C:C4	1:A:1450:U:C4	2.97	0.53
1:A:1511:G:H2'	1:A:1512:U:C6	2.44	0.53
1:A:660:C:O2	1:A:745:G:N2	2.39	0.53
1:A:1285:A:H4'	1:A:1286:U:C5	2.44	0.53
1:A:1399:C:O3'	1:A:1518:MA6:H2	2.08	0.53
11:K:24:HIS:HB3	11:K:31:ILE:HB	1.91	0.53
1:A:208:U:H2'	1:A:210:C:C4	2.44	0.52
1:A:465:A:C2	1:A:466:A:C4	2.97	0.52
1:A:500:G:O5'	12:L:121:ARG:NH2	2.42	0.52
1:A:767:A:C4	1:A:768:A:C8	2.97	0.52
1:A:978:A:C6	1:A:1318:A:C6	2.98	0.52
10:J:75:ASP:OD1	10:J:76:ILE:N	2.42	0.52
1:A:10:A:H2'	1:A:11:G:H8	1.73	0.52
1:A:735:C:H2'	1:A:736:C:C6	2.44	0.52
1:A:1323:G:H2'	1:A:1324:A:C8	2.44	0.52
2:B:31:ILE:HD13	2:B:39:HIS:CE1	2.44	0.52
3:C:6:HIS:CE1	3:C:8:ASN:HB3	2.44	0.52
4:D:25:VAL:HG13	4:D:26:ARG:HG3	1.91	0.52
10:J:17:LEU:HA	10:J:20:GLN:OE1	2.09	0.52
21:X:30:ARG:HA	21:X:34:SER:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:G:C6	1:A:98:A:H1'	2.45	0.52
1:A:952:U:H2'	1:A:953:G:H8	1.73	0.52
1:A:1073:U:H3	1:A:1102:A:N6	2.06	0.52
4:D:108:GLY:HA3	4:D:114:ALA:HB2	1.90	0.52
1:A:333:U:H2'	1:A:334:C:C6	2.43	0.52
1:A:358:U:H2'	1:A:359:G:H8	1.75	0.52
1:A:590:U:C5'	8:H:31:LYS:HZ1	2.23	0.52
1:A:602:A:H2'	1:A:603:U:H6	1.74	0.52
1:A:1346:A:C8	1:A:1348:U:C2	2.98	0.52
1:A:1519:MA6:OP2	1:A:1519:MA6:H8	2.08	0.52
11:K:35:THR:OG1	11:K:36:ASP:N	2.42	0.52
17:Q:58:VAL:C	17:Q:59:VAL:HG23	2.30	0.52
18:R:50:LYS:O	18:R:54:GLN:NE2	2.42	0.52
19:S:32:ARG:HD2	19:S:57:HIS:CE1	2.44	0.52
1:A:23:C:H2'	1:A:24:U:H6	1.74	0.52
1:A:1009:U:H2'	1:A:1010:U:H6	1.74	0.52
1:A:1034:G:H2'	1:A:1035:A:C8	2.44	0.52
1:A:1505:G:O2'	1:A:1506:U:OP2	2.26	0.52
3:C:114:LYS:HA	3:C:185:ASN:ND2	2.25	0.52
19:S:36:ARG:NH1	19:S:53:ASN:HA	2.25	0.52
19:S:64:ASP:OD1	19:S:64:ASP:N	2.42	0.52
1:A:501:C:O3'	12:L:115:SER:OG	2.28	0.52
1:A:636:U:H2'	1:A:637:C:C6	2.44	0.52
1:A:643:C:H2'	1:A:644:U:C6	2.45	0.52
1:A:773:G:H2'	1:A:774:G:O4'	2.10	0.52
1:A:802:A:H2'	1:A:803:G:O4'	2.10	0.52
1:A:954:G:N2	1:A:1227:A:H62	1.96	0.52
1:A:1296:C:H5'	13:M:14:HIS:HE1	1.75	0.52
1:A:1343:G:O3'	9:I:124:ARG:NE	2.41	0.52
2:B:23:TRP:HB3	2:B:39:HIS:CD2	2.45	0.52
3:C:111:LEU:HG	3:C:144:LEU:HD23	1.91	0.52
11:K:25:ALA:HB3	11:K:88:GLY:O	2.10	0.52
21:X:42:SER:CB	21:X:46:ILE:HG13	2.39	0.52
1:A:756:C:H2'	1:A:757:U:H6	1.74	0.52
1:A:1118:U:H2'	1:A:1119:C:C6	2.45	0.52
2:B:81:LYS:HG3	2:B:91:PHE:CZ	2.45	0.52
3:C:116:VAL:O	3:C:120:ILE:HG12	2.09	0.52
11:K:20:VAL:O	11:K:20:VAL:HG13	2.10	0.52
14:N:90:ARG:NE	14:N:92:GLU:OE2	2.42	0.52
1:A:131:A:H2'	1:A:132:C:C6	2.45	0.52
1:A:297:G:N2	1:A:300:A:OP2	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:G:N2	1:A:326:G:H3'	2.24	0.52
5:E:62:LYS:O	5:E:66:LYS:HG3	2.10	0.52
7:G:71:PRO:HA	7:G:138:ARG:HE	1.75	0.52
11:K:88:GLY:H	11:K:114:THR:HG22	1.73	0.52
20:T:27:MET:HG3	20:T:28:MET:N	2.25	0.52
1:A:144:G:C6	1:A:145:G:C5	2.98	0.52
1:A:230:G:H2'	1:A:231:U:C6	2.45	0.52
1:A:530:G:H2'	1:A:531:U:C5	2.45	0.52
1:A:583:A:C5	1:A:584:G:C8	2.98	0.52
1:A:967:5MC:H2'	1:A:968:A:N7	2.25	0.52
1:A:1299:A:N3	1:A:1299:A:H2'	2.25	0.52
1:A:1444:U:H2'	1:A:1445:U:H6	1.75	0.52
1:A:1463:U:H2'	1:A:1464:U:C6	2.45	0.52
3:C:14:ILE:HG22	3:C:15:VAL:HG13	1.91	0.52
13:M:10:PRO:HB2	13:M:45:ILE:HG13	1.92	0.52
1:A:471:U:H2'	1:A:472:U:H6	1.74	0.52
1:A:673:A:H8	1:A:673:A:OP2	1.93	0.52
1:A:903:G:H2'	1:A:904:U:C6	2.45	0.52
3:C:21:THR:CG2	3:C:58:GLU:HG3	2.40	0.52
6:F:39:LEU:HD12	6:F:62:MET:HG2	1.91	0.52
1:A:138:G:N2	1:A:225:C:O2	2.25	0.51
1:A:190:A:C4	1:A:191:G:H1'	2.45	0.51
1:A:672:U:O2'	1:A:673:A:H5'	2.10	0.51
1:A:900:A:H2'	1:A:901:A:O4'	2.09	0.51
1:A:1002:G:H2'	1:A:1003:G:C8	2.45	0.51
1:A:1025:U:H4'	1:A:1026:G:H8	1.75	0.51
1:A:1057:G:H2'	1:A:1058:G:O4'	2.10	0.51
1:A:1067:A:HO2'	1:A:1093:A:HO2'	1.56	0.51
1:A:1263:C:H2'	1:A:1264:U:C6	2.44	0.51
1:A:1517:G:N7	1:A:1518:MA6:H103	2.25	0.51
3:C:69:HIS:HA	3:C:104:ALA:O	2.10	0.51
3:C:87:LEU:HA	3:C:90:VAL:HG22	1.92	0.51
3:C:115:LEU:HA	3:C:118:ASP:OD2	2.11	0.51
4:D:9:LEU:HD13	4:D:32:CYS:SG	2.51	0.51
11:K:34:ILE:HG13	11:K:43:GLY:CA	2.40	0.51
16:P:57:ILE:HD13	16:P:75:ILE:HD11	1.91	0.51
19:S:47:LEU:O	19:S:62:VAL:N	2.42	0.51
1:A:207:C:H2'	1:A:208:U:O4'	2.10	0.51
1:A:503:C:O2'	1:A:510:A:N1	2.36	0.51
1:A:927:G:C5	1:A:928:G:N7	2.78	0.51
3:C:148:GLY:HA3	3:C:172:ARG:H	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:55:VAL:CG2	9:I:94:LEU:HD11	2.40	0.51
10:J:12:ALA:HB2	10:J:96:VAL:HG23	1.93	0.51
14:N:37:SER:C	14:N:39:GLU:H	2.14	0.51
16:P:57:ILE:O	16:P:61:VAL:HG23	2.10	0.51
19:S:52:HIS:HA	19:S:57:HIS:HA	1.92	0.51
1:A:12:U:O2'	1:A:914:A:OP2	2.27	0.51
1:A:120:A:C4	1:A:122:G:C5	2.98	0.51
1:A:302:G:H2'	1:A:303:A:C8	2.45	0.51
1:A:690:G:C6	1:A:691:G:C6	2.98	0.51
1:A:1009:U:H3	1:A:1020:G:H1	1.58	0.51
1:A:1010:U:H2'	1:A:1011:C:C6	2.46	0.51
1:A:1371:G:O3'	9:I:71:GLY:HA3	2.09	0.51
1:A:157:U:H2'	1:A:158:G:H8	1.75	0.51
1:A:218:U:H2'	1:A:219:U:H6	1.75	0.51
1:A:716:A:C6	1:A:717:U:C4	2.99	0.51
1:A:821:G:C6	1:A:822:U:C4	2.98	0.51
1:A:891:U:OP2	1:A:906:A:N6	2.30	0.51
1:A:1347:G:H1'	1:A:1348:U:H5	1.74	0.51
5:E:37:THR:HG21	5:E:64:MET:CE	2.40	0.51
7:G:135:VAL:O	7:G:139:GLU:HG2	2.10	0.51
1:A:855:U:OP2	1:A:871:U:N3	2.42	0.51
6:F:72:ASP:O	6:F:76:THR:HG23	2.10	0.51
10:J:45:ARG:HB3	10:J:69:THR:OG1	2.09	0.51
12:L:35:THR:N	12:L:54:ARG:O	2.36	0.51
14:N:49:GLN:HE22	19:S:12:ASP:HA	1.75	0.51
1:A:414:A:H2'	1:A:415:A:C8	2.43	0.51
1:A:592:G:C6	1:A:648:A:C6	2.99	0.51
1:A:642:A:C6	1:A:643:C:C4	2.98	0.51
1:A:1178:G:O2'	1:A:1180:A:N7	2.40	0.51
4:D:138:SER:N	4:D:141:ASP:OD2	2.43	0.51
7:G:27:VAL:O	7:G:31:MET:N	2.44	0.51
12:L:110:ARG:HB2	12:L:119:VAL:HG21	1.92	0.51
15:O:29:VAL:HG23	15:O:63:ARG:HB2	1.91	0.51
1:A:119:A:H4'	1:A:120:A:N9	2.26	0.51
1:A:155:A:C6	1:A:156:C:C4	2.99	0.51
1:A:217:C:H2'	1:A:218:U:C6	2.45	0.51
1:A:925:G:O4'	1:A:927:G:C8	2.63	0.51
1:A:1104:G:C6	1:A:1105:A:C6	2.99	0.51
1:A:1317:C:N3	19:S:37:ARG:NH1	2.42	0.51
3:C:54:ARG:HB3	3:C:69:HIS:HB2	1.93	0.51
7:G:63:GLU:O	7:G:67:GLU:HG2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:33:ARG:HD2	9:I:38:TYR:CD1	2.46	0.51
11:K:113:VAL:CG1	11:K:113:VAL:O	2.54	0.51
17:Q:4:LYS:HG3	17:Q:5:ILE:HG23	1.92	0.51
1:A:131:A:C6	1:A:232:G:C6	2.99	0.51
1:A:837:U:H2'	1:A:838:G:C8	2.45	0.51
1:A:1271:A:H2'	1:A:1272:G:H8	1.76	0.51
7:G:103:TRP:HZ3	7:G:138:ARG:HA	1.76	0.51
10:J:42:LEU:HB2	10:J:71:LEU:HG	1.93	0.51
10:J:67:ILE:HG12	14:N:96:LEU:HD13	1.92	0.51
14:N:19:LYS:HG3	14:N:20:TYR:CD1	2.45	0.51
1:A:1087:G:C6	1:A:1099:G:C6	2.99	0.51
1:A:1348:U:H2'	1:A:1349:A:H8	1.76	0.51
1:A:1451:U:O2'	1:A:1452:C:OP1	2.28	0.51
3:C:71:ALA:O	3:C:72:ARG:NH1	2.41	0.51
5:E:36:LEU:HD12	5:E:133:PRO:HB2	1.89	0.51
1:A:771:G:H2'	1:A:772:U:H6	1.76	0.51
1:A:1305:G:H2'	1:A:1331:G:N2	2.26	0.51
1:A:1372:U:H2'	1:A:1373:G:O4'	2.11	0.51
10:J:27:GLU:O	10:J:31:ARG:HG2	2.10	0.51
13:M:53:ILE:O	13:M:57:ARG:HG3	2.11	0.51
14:N:42:TRP:CE2	14:N:46:LEU:HD11	2.46	0.51
1:A:122:G:H2'	1:A:123:U:C6	2.46	0.50
1:A:699:C:H2'	1:A:700:G:C8	2.41	0.50
1:A:1279:G:O2'	1:A:1280:A:OP1	2.29	0.50
7:G:53:ARG:NH2	7:G:121:ALA:O	2.44	0.50
9:I:65:ILE:CG2	9:I:79:ILE:CD1	2.89	0.50
10:J:53:ILE:HD13	10:J:63:ASP:OD1	2.11	0.50
17:Q:49:GLU:HG3	17:Q:50:ASN:N	2.26	0.50
1:A:261:U:H2'	1:A:263:A:OP2	2.11	0.50
1:A:532:A:H3'	1:A:532:A:N3	2.25	0.50
1:A:620:C:H2'	1:A:621:A:O4'	2.12	0.50
1:A:896:C:H2'	1:A:897:C:H6	1.76	0.50
7:G:111:ARG:HH12	7:G:122:ASN:CB	2.24	0.50
11:K:63:ALA:HB1	11:K:96:THR:HB	1.94	0.50
21:X:103:LEU:C	21:X:103:LEU:HD12	2.32	0.50
1:A:400:C:H2'	1:A:401:C:C6	2.46	0.50
1:A:590:U:H2'	1:A:591:U:C6	2.46	0.50
1:A:627:G:OP1	16:P:51:ARG:NH1	2.43	0.50
1:A:879:C:H2'	1:A:880:C:H6	1.75	0.50
6:F:36:ILE:HG23	6:F:64:VAL:HG22	1.92	0.50
9:I:34:SER:OG	9:I:37:GLN:HG3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:35:THR:HA	11:K:42:LEU:N	2.26	0.50
19:S:32:ARG:HG2	19:S:52:HIS:CE1	2.46	0.50
1:A:155:A:H2'	1:A:156:C:C6	2.47	0.50
1:A:165:G:C6	1:A:166:U:C4	2.98	0.50
1:A:532:A:H2'	1:A:533:A:H5"	1.93	0.50
1:A:633:G:H2'	1:A:634:C:H6	1.76	0.50
1:A:1005:A:C4	1:A:1006:G:H1'	2.45	0.50
1:A:1028:C:C4	1:A:1029:U:C4	2.99	0.50
1:A:1057:G:O2'	3:C:188:GLU:OE1	2.28	0.50
1:A:1060:U:OP1	14:N:85:ARG:NH2	2.40	0.50
1:A:1107:C:C5	1:A:1108:G:C8	2.99	0.50
1:A:1400:C:OP1	1:A:1517:G:N1	2.44	0.50
10:J:30:LYS:HE3	10:J:36:VAL:CG1	2.40	0.50
12:L:41:THR:OG1	21:X:74:LEU:N	2.43	0.50
16:P:73:ALA:HA	16:P:76:LYS:HB3	1.93	0.50
19:S:31:LEU:H	19:S:31:LEU:HD23	1.76	0.50
21:X:40:ILE:O	21:X:46:ILE:HG12	2.11	0.50
1:A:567:G:H2'	1:A:568:G:O4'	2.12	0.50
1:A:796:C:H2'	1:A:797:C:H6	1.74	0.50
1:A:844:G:C4	1:A:845:A:H1'	2.47	0.50
1:A:962:C:H1'	1:A:1201:A:C6	2.46	0.50
1:A:1023:U:H2'	1:A:1024:G:C8	2.46	0.50
1:A:1084:G:O2'	1:A:1103:C:N4	2.43	0.50
1:A:1165:U:H3'	1:A:1166:G:C8	2.47	0.50
1:A:1426:G:C2	1:A:1427:C:C2	2.99	0.50
3:C:26:THR:HA	14:N:76:LYS:HE3	1.92	0.50
5:E:105:ILE:CD1	5:E:123:VAL:HG12	2.41	0.50
12:L:63:VAL:HG22	12:L:64:THR:H	1.77	0.50
1:A:122:G:H2'	1:A:123:U:H6	1.76	0.50
1:A:957:U:N3	1:A:960:U:OP2	2.43	0.50
1:A:1074:G:O2'	1:A:1101:A:N1	2.37	0.50
1:A:1305:G:N2	1:A:1332:A:OP2	2.45	0.50
1:A:1346:A:N1	1:A:1374:A:H5"	2.26	0.50
17:Q:29:VAL:C	17:Q:37:PHE:HD1	2.15	0.50
1:A:125:U:H2'	1:A:126:G:C8	2.46	0.50
1:A:552:U:O3'	12:L:84:GLY:HA3	2.11	0.50
1:A:974:A:OP2	14:N:81:ARG:NE	2.24	0.50
3:C:52:VAL:HG23	3:C:68:ILE:HG23	1.94	0.50
7:G:36:LYS:HB3	9:I:41:ARG:HH22	1.76	0.50
7:G:65:ALA:O	7:G:69:VAL:HG23	2.12	0.50
7:G:115:SER:O	7:G:119:ARG:HG3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:28:PHE:CZ	17:Q:37:PHE:CB	2.94	0.50
21:X:100:THR:HG22	21:X:114:GLN:CB	2.42	0.50
1:A:123:U:H2'	1:A:124:C:H6	1.76	0.50
1:A:920:U:H5'	1:A:1080:A:C6	2.47	0.50
3:C:140:ASN:HA	3:C:143:ARG:NH2	2.27	0.50
5:E:36:LEU:HD13	5:E:133:PRO:HB2	1.91	0.50
6:F:2:ARG:CZ	6:F:68:GLN:HE21	2.25	0.50
11:K:32:VAL:HG23	11:K:45:ALA:HB3	1.94	0.50
19:S:36:ARG:HB3	19:S:72:GLY:CA	2.42	0.50
1:A:1209:C:H2'	1:A:1210:C:C6	2.47	0.50
1:A:1288:A:N1	1:A:1371:G:H1'	2.26	0.50
1:A:1346:A:N6	1:A:1374:A:H3'	2.23	0.50
1:A:1360:A:OP2	14:N:75:ARG:NH2	2.44	0.50
1:A:1376:U:OP1	7:G:25:LYS:NZ	2.35	0.50
1:A:1377:A:H2'	7:G:2:PRO:HG3	1.93	0.50
9:I:96:SER:O	9:I:100:LYS:HG2	2.11	0.50
13:M:52:GLN:O	13:M:55:THR:OG1	2.27	0.50
13:M:66:GLU:HG3	13:M:67:GLY:N	2.26	0.50
18:R:11:CYS:HB2	18:R:14:THR:HG22	1.92	0.50
21:X:138:LEU:HA	21:X:141:ILE:HB	1.94	0.50
1:A:296:U:O2'	1:A:556:C:O2	2.23	0.49
1:A:531:U:H4'	1:A:532:A:OP1	2.12	0.49
1:A:925:G:H1	1:A:1391:U:C1'	2.25	0.49
1:A:946:A:H2'	1:A:947:G:H8	1.75	0.49
1:A:1348:U:H2'	1:A:1349:A:C8	2.46	0.49
3:C:72:ARG:NH1	3:C:72:ARG:HA	2.27	0.49
5:E:59:ALA:HA	5:E:62:LYS:HG3	1.93	0.49
6:F:38:ARG:NH2	6:F:63:ASN:OD1	2.39	0.49
9:I:120:LYS:HB2	9:I:123:ARG:HB3	1.94	0.49
21:X:28:PHE:HD1	21:X:36:LEU:HB3	1.77	0.49
1:A:335:C:H2'	1:A:336:A:C8	2.46	0.49
1:A:1308:U:H5'	13:M:109:ARG:NH2	2.26	0.49
1:A:1381:U:H2'	1:A:1382:C:O4'	2.12	0.49
7:G:70:ARG:HA	7:G:100:ALA:HB2	1.94	0.49
7:G:106:GLU:O	7:G:110:LYS:HG2	2.12	0.49
7:G:130:ASN:HA	7:G:135:VAL:HG11	1.94	0.49
1:A:260:G:H2'	1:A:261:U:H6	1.77	0.49
1:A:457:G:H3'	1:A:458:U:C6	2.48	0.49
1:A:470:C:H2'	1:A:471:U:C6	2.47	0.49
1:A:1027:C:H2'	1:A:1028:C:C6	2.47	0.49
1:A:1072:G:H2'	1:A:1073:U:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1151:A:O2'	1:A:1152:A:H8	1.95	0.49
1:A:1291:U:H2'	1:A:1292:G:H8	1.77	0.49
1:A:1292:G:H2'	1:A:1293:C:C6	2.47	0.49
1:A:1444:U:H2'	1:A:1445:U:C6	2.48	0.49
6:F:33:GLU:HB3	6:F:35:LYS:NZ	2.28	0.49
16:P:20:VAL:HA	16:P:35:ARG:HA	1.93	0.49
21:X:91:TYR:HA	21:X:94:PHE:HB2	1.94	0.49
1:A:6:G:H4'	1:A:298:A:H4'	1.95	0.49
1:A:376:G:OP1	16:P:6:LEU:N	2.45	0.49
1:A:415:A:H2'	1:A:416:G:O4'	2.12	0.49
1:A:739:C:O2'	15:O:42:HIS:ND1	2.34	0.49
1:A:784:A:H2'	1:A:785:G:C8	2.46	0.49
1:A:789:U:O4	1:A:1502:A:H2	1.96	0.49
1:A:933:G:N1	1:A:1384:C:N3	2.45	0.49
1:A:1178:G:H3'	9:I:99:ARG:NH2	2.25	0.49
1:A:1284:C:H3'	1:A:1285:A:H8	1.78	0.49
7:G:17:LYS:NZ	9:I:42:GLU:HG2	2.26	0.49
9:I:119:ARG:NH1	9:I:126:GLN:H	2.10	0.49
16:P:60:TRP:O	16:P:64:GLY:N	2.46	0.49
1:A:15:G:C2	1:A:16:A:C4	3.01	0.49
1:A:541:G:H2'	1:A:542:G:H8	1.77	0.49
1:A:841:C:N4	1:A:843:U:H3'	2.27	0.49
9:I:42:GLU:HA	9:I:45:ARG:HG3	1.94	0.49
15:O:87:LEU:O	15:O:89:ARG:HG2	2.11	0.49
17:Q:28:PHE:CE2	17:Q:37:PHE:HB2	2.47	0.49
19:S:33:THR:O	19:S:51:VAL:HA	2.12	0.49
1:A:775:G:C2	1:A:776:G:C4	3.00	0.49
20:T:48:GLN:O	20:T:52:ASN:ND2	2.45	0.49
1:A:123:U:H2'	1:A:124:C:C6	2.48	0.49
1:A:1009:U:H2'	1:A:1010:U:C6	2.47	0.49
6:F:82:ASP:OD1	6:F:82:ASP:N	2.44	0.49
7:G:111:ARG:NH2	7:G:122:ASN:HD22	2.09	0.49
1:A:56:U:H2'	1:A:57:G:H8	1.77	0.49
1:A:77:A:H3'	1:A:78:A:H8	1.78	0.49
1:A:161:A:H2'	1:A:162:A:C8	2.47	0.49
1:A:406:G:H21	4:D:116:GLN:HE22	1.61	0.49
1:A:540:G:H2'	1:A:541:G:H8	1.78	0.49
1:A:1178:G:H21	1:A:1180:A:H3'	1.78	0.49
1:A:1359:C:H3'	14:N:75:ARG:HH22	1.78	0.49
1:A:1366:C:H2'	1:A:1367:C:C6	2.48	0.49
10:J:54:SER:HB2	10:J:58:ASN:HB2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:X:21:PHE:CD2	21:X:40:ILE:CG2	2.86	0.49
1:A:432:A:H2'	1:A:433:G:O4'	2.13	0.49
1:A:439:U:O4'	4:D:120:HIS:HD2	1.96	0.49
1:A:538:G:H2'	1:A:539:A:C8	2.48	0.49
1:A:925:G:C6	1:A:1391:U:O2	2.63	0.49
1:A:988:G:N1	1:A:1217:C:N3	2.47	0.49
1:A:1105:A:N1	1:A:1106:G:N1	2.61	0.49
1:A:1285:A:H4'	1:A:1286:U:C4	2.48	0.49
3:C:118:ASP:OD1	3:C:119:SER:N	2.46	0.49
6:F:18:VAL:HG22	6:F:19:PRO:HD3	1.95	0.49
8:H:38:ASN:HB2	8:H:42:GLU:OE2	2.13	0.49
20:T:29:ARG:HB3	20:T:33:LYS:HZ1	1.78	0.49
21:X:40:ILE:HD13	21:X:76:VAL:HG13	1.92	0.49
21:X:103:LEU:H	21:X:110:ARG:HH21	1.59	0.49
1:A:34:C:H2'	1:A:35:G:C8	2.48	0.49
1:A:363:A:OP2	12:L:31:ARG:NE	2.45	0.49
1:A:897:C:H2'	1:A:898:G:C8	2.48	0.49
1:A:1385:G:H2'	1:A:1386:G:C8	2.48	0.49
1:A:1518:MA6:H2'	1:A:1519:MA6:H8	1.95	0.49
1:A:1536:C:H5'	5:E:31:PHE:CZ	2.48	0.49
5:E:160:SER:N	5:E:163:GLU:OE1	2.44	0.49
6:F:67:PRO:HB2	6:F:69:GLU:OE2	2.12	0.49
12:L:21:VAL:HG11	12:L:24:LEU:HD12	1.95	0.49
21:X:83:ARG:HD2	21:X:94:PHE:CZ	2.48	0.49
21:X:100:THR:HG22	21:X:114:GLN:HB3	1.95	0.49
1:A:178:C:H2'	1:A:179:A:H8	1.78	0.48
1:A:513:C:H2'	1:A:514:C:C6	2.48	0.48
1:A:1107:C:H5	1:A:1108:G:C8	2.31	0.48
1:A:1525:G:H2'	1:A:1526:G:H8	1.78	0.48
9:I:34:SER:H	9:I:37:GLN:NE2	2.09	0.48
15:O:63:ARG:O	15:O:67:LEU:HG	2.12	0.48
1:A:484:G:O4'	1:A:486:U:H5'	2.13	0.48
1:A:543:U:H5'	4:D:14:ARG:NH2	2.28	0.48
1:A:774:G:H3'	1:A:775:G:H8	1.78	0.48
1:A:911:U:H2'	1:A:912:C:C6	2.48	0.48
1:A:1103:C:H2'	1:A:1104:G:O4'	2.13	0.48
1:A:1398:A:N1	1:A:1503:A:N6	2.61	0.48
6:F:18:VAL:HA	6:F:21:MET:HB3	1.95	0.48
12:L:3:THR:O	12:L:6:GLN:N	2.41	0.48
1:A:592:G:H2'	1:A:593:U:C6	2.47	0.48
1:A:677:U:H3	1:A:713:G:H22	1.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:795:C:H5"	11:K:128:ARG:HH22	1.79	0.48
1:A:824:G:H2'	1:A:825:A:C8	2.46	0.48
1:A:1460:C:H2'	1:A:1461:G:O4'	2.13	0.48
4:D:170:TRP:HH2	4:D:191:LEU:CD2	2.26	0.48
6:F:6:ILE:HG13	6:F:89:VAL:CG2	2.42	0.48
9:I:60:LYS:HD2	9:I:60:LYS:N	2.28	0.48
9:I:127:PHE:CZ	9:I:129:LYS:HA	2.48	0.48
1:A:739:C:HO2'	15:O:42:HIS:CE1	2.27	0.48
1:A:926:G:H1	1:A:1395:C:H1'	1.78	0.48
1:A:1317:C:O2	19:S:37:ARG:NH2	2.42	0.48
1:A:255:G:C2	1:A:272:C:C2	3.02	0.48
1:A:257:G:O6	1:A:269:C:N4	2.31	0.48
1:A:958:A:O2'	1:A:959:A:H5'	2.13	0.48
1:A:1030:U:OP2	1:A:1031:C:N4	2.46	0.48
1:A:1098:C:H2'	1:A:1099:G:H8	1.78	0.48
1:A:1258:G:C2	1:A:1259:C:C2	3.02	0.48
1:A:1287:A:C6	1:A:1288:A:C6	3.02	0.48
1:A:1308:U:H3'	13:M:98:ARG:HH21	1.78	0.48
3:C:21:THR:HG23	3:C:58:GLU:HG3	1.96	0.48
9:I:36:GLU:H	9:I:36:GLU:CD	2.11	0.48
10:J:52:LEU:HB2	14:N:81:ARG:CD	2.42	0.48
17:Q:81:LYS:HD3	17:Q:81:LYS:HA	1.68	0.48
1:A:629:A:H2'	1:A:630:A:O4'	2.14	0.48
1:A:748:G:C2	1:A:749:A:C4	3.01	0.48
9:I:44:ALA:HA	9:I:47:VAL:HG12	1.94	0.48
17:Q:26:GLU:OE2	17:Q:27:ARG:N	2.47	0.48
20:T:48:GLN:OE1	20:T:52:ASN:ND2	2.46	0.48
21:X:134:GLU:HG3	21:X:136:PHE:CE2	2.48	0.48
1:A:128:G:C2	1:A:234:C:C2	3.02	0.48
1:A:309:A:H2'	1:A:310:G:H8	1.78	0.48
1:A:427:U:OP2	1:A:428:G:O2'	2.28	0.48
1:A:505:G:H2'	1:A:506:G:H8	1.78	0.48
1:A:540:G:H2'	1:A:541:G:C8	2.49	0.48
1:A:574:A:HO2'	1:A:882:C:HO2'	1.60	0.48
1:A:598:U:H2'	1:A:599:C:H6	1.79	0.48
1:A:683:G:N2	11:K:39:GLY:O	2.47	0.48
1:A:692:U:OP1	11:K:127:ARG:NH2	2.45	0.48
1:A:765:G:C6	1:A:812:G:C4	3.02	0.48
1:A:1244:G:C6	1:A:1294:G:C6	3.01	0.48
3:C:83:ASP:OD1	3:C:84:VAL:N	2.46	0.48
4:D:173:VAL:HA	4:D:180:GLY:HA2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:41:LYS:HZ3	8:H:48:ASP:CG	2.16	0.48
13:M:98:ARG:HB2	13:M:100:GLN:HE22	1.78	0.48
1:A:300:A:H2'	1:A:301:G:O4'	2.14	0.48
1:A:363:A:P	12:L:30:LYS:HZ2	2.37	0.48
1:A:554:A:H2'	1:A:555:U:C6	2.49	0.48
1:A:827:U:H2'	1:A:870:U:O4	2.14	0.48
1:A:957:U:H2'	1:A:959:A:OP2	2.14	0.48
1:A:1102:A:H2'	1:A:1103:C:C6	2.48	0.48
1:A:1158:C:H5"	1:A:1159:U:OP2	2.14	0.48
1:A:1329:A:H5'	13:M:29:ARG:NE	2.28	0.48
1:A:1450:U:O2	1:A:1454:G:C2	2.67	0.48
7:G:111:ARG:NE	7:G:113:ASP:OD2	2.47	0.48
12:L:37:VAL:HG12	12:L:53:CYS:CB	2.37	0.48
16:P:20:VAL:HG12	16:P:35:ARG:CB	2.44	0.48
20:T:56:PRO:O	20:T:59:ASP:HB2	2.13	0.48
21:X:42:SER:HB2	21:X:46:ILE:HG13	1.95	0.48
1:A:54:C:H2'	1:A:352:C:H41	1.78	0.48
1:A:199:A:H2'	1:A:200:G:H8	1.78	0.48
1:A:439:U:H4'	4:D:121:LYS:HG3	1.96	0.48
1:A:553:A:O2'	12:L:26:ALA:O	2.32	0.48
1:A:654:G:H2'	1:A:655:A:O4'	2.14	0.48
1:A:691:G:H2'	1:A:692:U:C6	2.48	0.48
1:A:984:C:H2'	1:A:985:C:C6	2.49	0.48
1:A:1099:G:C6	1:A:1100:C:C2	3.02	0.48
1:A:1179:A:H2'	1:A:1180:A:O4'	2.14	0.48
3:C:116:VAL:O	3:C:119:SER:OG	2.28	0.48
7:G:103:TRP:HH2	7:G:141:VAL:HG11	1.78	0.48
21:X:14:ALA:O	21:X:18:ALA:HB2	2.14	0.48
1:A:211:G:C6	1:A:212:G:C4	3.02	0.48
1:A:212:G:C4	1:A:213:G:C8	3.02	0.48
1:A:257:G:C6	1:A:270:A:C6	3.02	0.48
1:A:1172:C:H2'	1:A:1173:U:C6	2.49	0.48
1:A:1269:A:N3	1:A:1326:U:H1'	2.28	0.48
1:A:1397:C:O2'	1:A:1398:A:O5'	2.30	0.48
1:A:1398:A:C2	1:A:1503:A:N6	2.82	0.48
3:C:67:THR:HA	3:C:102:ASN:O	2.13	0.48
3:C:138:VAL:HG21	3:C:168:TYR:CE2	2.49	0.48
10:J:96:VAL:HG22	10:J:97:ASP:H	1.79	0.48
1:A:140:U:H2'	1:A:141:G:O4'	2.14	0.47
1:A:204:G:H2'	1:A:205:A:C1'	2.43	0.47
1:A:229:U:H2'	1:A:230:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:G:H2'	1:A:261:U:C6	2.48	0.47
1:A:540:G:C4	1:A:541:G:C8	3.02	0.47
1:A:542:G:H2'	1:A:543:U:H6	1.79	0.47
1:A:1074:G:H2'	1:A:1075:U:C6	2.49	0.47
1:A:1376:U:H5"	7:G:95:ARG:HH12	1.79	0.47
1:A:1450:U:H3'	1:A:1452:C:N4	2.28	0.47
2:B:187:VAL:O	2:B:201:PRO:HA	2.14	0.47
7:G:95:ARG:O	7:G:99:LEU:HG	2.14	0.47
9:I:71:GLY:O	9:I:75:GLN:NE2	2.36	0.47
10:J:35:GLN:O	10:J:76:ILE:HA	2.14	0.47
19:S:10:PHE:O	19:S:39:THR:OG1	2.12	0.47
21:X:95:VAL:HG23	21:X:96:GLY:H	1.79	0.47
1:A:204:G:C6	1:A:205:A:C6	3.02	0.47
1:A:205:A:C2'	1:A:206:C:H5'	2.44	0.47
1:A:660:C:H2'	1:A:661:G:O4'	2.14	0.47
1:A:747:A:H2'	1:A:748:G:O4'	2.15	0.47
1:A:790:A:OP2	1:A:791:G:H3'	2.14	0.47
1:A:967:5MC:H2'	1:A:968:A:C8	2.49	0.47
1:A:1128:C:H4'	1:A:1148:U:O2	2.15	0.47
1:A:1308:U:H3'	13:M:98:ARG:NH2	2.28	0.47
7:G:74:GLU:O	7:G:88:PRO:HA	2.14	0.47
11:K:85:MET:HA	11:K:111:THR:O	2.14	0.47
13:M:81:MET:HE3	13:M:92:ARG:HE	1.78	0.47
17:Q:17:MET:HB3	17:Q:20:SER:HB2	1.96	0.47
20:T:29:ARG:HB3	20:T:33:LYS:NZ	2.28	0.47
21:X:21:PHE:HB3	21:X:40:ILE:HG23	1.94	0.47
1:A:311:C:H2'	1:A:312:C:H6	1.79	0.47
1:A:472:U:H2'	1:A:473:U:C6	2.49	0.47
1:A:1246:A:C5	1:A:1247:U:C4	3.03	0.47
8:H:78:VAL:HG23	8:H:79:SER:H	1.80	0.47
9:I:18:ARG:HB3	9:I:66:THR:HB	1.96	0.47
20:T:79:LEU:O	20:T:83:ILE:N	2.44	0.47
21:X:35:THR:HG22	21:X:73:ASN:HB3	1.95	0.47
1:A:154:U:H2'	1:A:155:A:C8	2.48	0.47
1:A:1105:A:C6	1:A:1106:G:C6	3.02	0.47
1:A:1297:G:N2	1:A:1298:U:O4	2.45	0.47
4:D:57:GLU:HG2	4:D:199:LEU:HB2	1.95	0.47
4:D:130:VAL:HG11	4:D:135:TYR:CD1	2.49	0.47
1:A:456:A:C6	1:A:457:G:C5	3.02	0.47
1:A:636:U:H2'	1:A:637:C:H6	1.79	0.47
1:A:784:A:H2'	1:A:785:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:892:A:C6	1:A:907:A:C8	3.03	0.47
1:A:944:G:H1'	1:A:1339:A:H61	1.79	0.47
1:A:986:U:H1'	19:S:55:ARG:HA	1.96	0.47
1:A:1440:U:H4'	1:A:1441:A:C6	2.49	0.47
3:C:152:GLU:HG2	3:C:166:GLU:O	2.15	0.47
10:J:15:HIS:CD2	10:J:16:ARG:HD3	2.50	0.47
10:J:45:ARG:O	10:J:68:ARG:HA	2.14	0.47
1:A:217:C:H2'	1:A:218:U:H6	1.80	0.47
1:A:738:C:OP1	6:F:91:ARG:NH1	2.47	0.47
1:A:921:U:H2'	1:A:922:G:C8	2.49	0.47
1:A:1118:U:C5'	9:I:106:ARG:HG2	2.41	0.47
1:A:1148:U:H5'	9:I:7:TYR:OH	2.15	0.47
7:G:14:PRO:HA	7:G:21:GLU:HA	1.97	0.47
15:O:26:GLU:H	15:O:26:GLU:CD	2.09	0.47
16:P:66:THR:OG1	16:P:67:ILE:N	2.46	0.47
1:A:123:U:H5"	1:A:311:C:O2'	2.15	0.47
1:A:197:A:N1	1:A:220:G:O2'	2.37	0.47
1:A:224:U:H2'	1:A:225:C:C6	2.50	0.47
1:A:922:G:C2	1:A:923:A:C5	3.02	0.47
1:A:926:G:P	1:A:926:G:H8	2.37	0.47
1:A:1152:A:P	10:J:72:ARG:HH22	2.38	0.47
1:A:1271:A:H2'	1:A:1272:G:C8	2.50	0.47
1:A:1308:U:H5"	13:M:97:VAL:HG22	1.96	0.47
1:A:1486:G:H3'	1:A:1487:G:H8	1.79	0.47
3:C:112:ASP:CG	3:C:115:LEU:H	2.14	0.47
6:F:84:VAL:HG13	6:F:84:VAL:O	2.13	0.47
10:J:15:HIS:O	10:J:18:ILE:HG22	2.14	0.47
15:O:29:VAL:O	15:O:33:THR:OG1	2.23	0.47
15:O:76:ALA:O	15:O:79:THR:OG1	2.29	0.47
19:S:3:ARG:HD2	19:S:8:GLY:O	2.15	0.47
1:A:487:A:H3'	1:A:488:C:C6	2.50	0.47
1:A:542:G:H2'	1:A:543:U:C6	2.49	0.47
1:A:542:G:N2	1:A:543:U:C2	2.83	0.47
1:A:599:C:H2'	1:A:600:A:H8	1.79	0.47
1:A:751:U:C5	1:A:752:G:C5	3.03	0.47
1:A:865:A:H2'	1:A:866:C:C6	2.50	0.47
1:A:1111:A:N1	3:C:177:THR:HG22	2.29	0.47
1:A:1169:A:H2'	1:A:1170:A:C8	2.50	0.47
1:A:1452:C:H4'	1:A:1453:G:O5'	2.15	0.47
3:C:146:ALA:HB3	3:C:149:ILE:HD11	1.97	0.47
5:E:65:GLU:O	5:E:68:ARG:N	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:33:ARG:HD2	9:I:38:TYR:HD1	1.79	0.47
9:I:128:SER:O	9:I:128:SER:OG	2.28	0.47
14:N:49:GLN:NE2	19:S:13:LEU:H	2.12	0.47
16:P:75:ILE:HA	16:P:78:VAL:HG12	1.97	0.47
19:S:36:ARG:HB3	19:S:72:GLY:HA2	1.97	0.47
20:T:24:ARG:NH1	20:T:27:MET:SD	2.87	0.47
1:A:279:A:OP1	1:A:280:C:O2'	2.25	0.47
1:A:462:G:H3'	1:A:463:U:C6	2.50	0.47
1:A:689:C:H2'	1:A:690:G:O4'	2.15	0.47
1:A:861:G:O2'	1:A:874:G:O2'	2.30	0.47
1:A:974:A:P	14:N:81:ARG:HH21	2.37	0.47
2:B:107:VAL:O	2:B:111:ILE:HG12	2.15	0.47
9:I:115:LYS:HB2	9:I:118:LEU:HD12	1.96	0.47
1:A:6:G:O2'	1:A:7:A:O5'	2.31	0.47
1:A:343:U:H3'	1:A:345:C:N4	2.30	0.47
1:A:715:A:H2'	1:A:716:A:H8	1.80	0.47
1:A:965:U:OP1	1:A:1198:G:H5"	2.15	0.47
1:A:1064:G:O6	1:A:1193:G:N1	2.48	0.47
1:A:1179:A:O2'	9:I:106:ARG:HB3	2.15	0.47
1:A:1260:G:OP1	1:A:1284:C:O2'	2.20	0.47
2:B:148:LEU:CD2	2:B:151:ILE:HD11	2.44	0.47
7:G:49:THR:OG1	7:G:52:GLN:NE2	2.48	0.47
8:H:11:LEU:HB3	8:H:75:ILE:CD1	2.45	0.47
8:H:12:THR:O	8:H:16:ASN:N	2.46	0.47
15:O:9:ALA:HA	15:O:12:VAL:HG12	1.96	0.47
1:A:126:G:C6	1:A:236:A:N1	2.83	0.46
1:A:363:A:H5"	12:L:31:ARG:CD	2.45	0.46
1:A:746:A:H2'	1:A:747:A:C8	2.50	0.46
1:A:932:C:N4	1:A:933:G:O6	2.48	0.46
1:A:939:G:P	7:G:102:ARG:HH12	2.38	0.46
1:A:1014:A:C5	1:A:1015:G:C6	3.03	0.46
1:A:1398:A:H2	1:A:1502:A:N6	2.13	0.46
3:C:125:GLU:HB2	3:C:126:ARG:HH12	1.80	0.46
8:H:88:ARG:NH1	8:H:90:ASP:OD2	2.48	0.46
10:J:80:THR:H	10:J:83:THR:CG2	2.28	0.46
21:X:90:HIS:O	21:X:94:PHE:N	2.24	0.46
1:A:263:A:H2'	1:A:264:C:H6	1.80	0.46
1:A:358:U:H2'	1:A:359:G:C8	2.49	0.46
1:A:673:A:C6	1:A:734:G:C6	3.03	0.46
1:A:800:G:H2'	1:A:801:U:C5	2.50	0.46
1:A:1415:G:O6	1:A:1485:U:C4	2.68	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1460:C:C2	1:A:1461:G:C8	3.03	0.46
1:A:1524:C:N4	1:A:1525:G:O6	2.49	0.46
3:C:112:ASP:OD2	3:C:115:LEU:N	2.24	0.46
4:D:18:ASP:OD1	4:D:19:LEU:N	2.48	0.46
5:E:66:LYS:HA	5:E:69:ARG:HH21	1.79	0.46
12:L:23:ALA:HA	12:L:61:PHE:HD2	1.80	0.46
1:A:442:G:C6	1:A:443:C:C4	3.03	0.46
1:A:608:A:H2'	1:A:609:A:O4'	2.15	0.46
1:A:632:U:H5"	1:A:633:G:C8	2.51	0.46
1:A:708:C:O4'	11:K:39:GLY:HA3	2.15	0.46
1:A:921:U:H2'	1:A:922:G:H8	1.80	0.46
1:A:1166:G:N7	1:A:1168:U:H5"	2.30	0.46
3:C:82:GLU:HG3	3:C:83:ASP:N	2.29	0.46
5:E:55:GLU:HG2	5:E:57:PRO:HD2	1.97	0.46
6:F:10:VAL:HA	6:F:84:VAL:HA	1.97	0.46
7:G:47:LEU:HB2	7:G:58:GLU:HG3	1.96	0.46
9:I:71:GLY:O	9:I:75:GLN:HG2	2.16	0.46
10:J:80:THR:OG1	10:J:83:THR:HG23	2.15	0.46
12:L:54:ARG:HH11	12:L:64:THR:HB	1.81	0.46
12:L:83:ARG:NH1	12:L:84:GLY:O	2.48	0.46
15:O:7:ALA:HA	15:O:10:LYS:HB2	1.97	0.46
1:A:37:U:O2'	1:A:547:A:N1	2.43	0.46
1:A:243:A:C2	1:A:245:U:H2'	2.50	0.46
1:A:260:G:C4	1:A:261:U:C5	3.04	0.46
1:A:309:A:O2'	1:A:607:A:N1	2.41	0.46
1:A:409:U:H2'	1:A:410:G:O4'	2.15	0.46
1:A:585:G:C6	1:A:586:C:C4	3.04	0.46
1:A:842:U:H2'	1:A:843:U:N1	2.29	0.46
1:A:1259:C:H5"	1:A:1260:G:OP2	2.16	0.46
1:A:1470:U:H2'	1:A:1471:U:H6	1.77	0.46
8:H:35:ALA:HA	8:H:38:ASN:HD21	1.79	0.46
11:K:34:ILE:HD12	11:K:42:LEU:CB	2.45	0.46
12:L:42:PRO:HG2	12:L:46:ASN:O	2.16	0.46
1:A:94:G:H4'	1:A:95:C:C5'	2.45	0.46
1:A:669:G:O6	1:A:738:C:N4	2.49	0.46
1:A:790:A:N6	1:A:1400:C:N3	2.63	0.46
1:A:1013:G:H2'	1:A:1015:G:OP2	2.14	0.46
5:E:77:ASN:N	5:E:80:THR:O	2.40	0.46
21:X:23:LEU:HD11	21:X:26:ILE:HD11	1.98	0.46
1:A:50:A:H1'	1:A:52:C:C6	2.51	0.46
1:A:325:A:H2'	1:A:326:G:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:G:H5'	4:D:5:LEU:HD22	1.97	0.46
1:A:718:A:C5	1:A:719:C:N3	2.83	0.46
1:A:911:U:H2'	1:A:912:C:H6	1.81	0.46
1:A:1035:A:H2'	1:A:1036:A:O4'	2.14	0.46
1:A:1178:G:H2'	1:A:1180:A:OP2	2.15	0.46
1:A:1211:U:O2'	1:A:1213:A:N3	2.42	0.46
1:A:1359:C:H3'	14:N:75:ARG:NH2	2.30	0.46
3:C:76:VAL:O	3:C:84:VAL:HG23	2.15	0.46
8:H:5:ASP:OD1	8:H:7:ILE:N	2.49	0.46
8:H:47:GLU:HB3	8:H:62:THR:HG22	1.98	0.46
11:K:34:ILE:HD11	11:K:43:GLY:N	2.31	0.46
13:M:44:LYS:HE2	13:M:44:LYS:HB3	1.71	0.46
16:P:20:VAL:HG12	16:P:35:ARG:HB3	1.97	0.46
17:Q:81:LYS:HG3	17:Q:82:ALA:H	1.80	0.46
1:A:88:U:HO2'	1:A:89:U:P	2.36	0.46
1:A:119:A:H4'	1:A:120:A:C4	2.51	0.46
1:A:419:C:C2	1:A:425:G:C2	3.04	0.46
1:A:964:A:O2'	10:J:57:VAL:HG21	2.15	0.46
1:A:974:A:H8	1:A:974:A:OP1	1.99	0.46
1:A:1166:G:O2'	1:A:1169:A:N6	2.49	0.46
1:A:1279:G:H3'	1:A:1279:G:N3	2.31	0.46
1:A:1306:A:H2'	1:A:1307:U:O4'	2.16	0.46
12:L:35:THR:O	12:L:76:GLU:HG2	2.15	0.46
13:M:81:MET:O	13:M:92:ARG:NH2	2.49	0.46
1:A:342:C:H2'	1:A:343:U:C6	2.50	0.46
1:A:411:A:H4'	1:A:412:A:H5'	1.96	0.46
1:A:474:G:OP1	16:P:80:LYS:NZ	2.37	0.46
1:A:765:G:H3'	1:A:812:G:H22	1.80	0.46
1:A:899:C:H2'	1:A:900:A:O4'	2.15	0.46
1:A:1040:U:H2'	1:A:1041:G:C8	2.51	0.46
1:A:1119:C:H2'	1:A:1120:C:H6	1.80	0.46
1:A:1314:C:H2'	1:A:1315:U:C6	2.50	0.46
7:G:40:GLU:HA	7:G:43:VAL:HG22	1.98	0.46
10:J:84:VAL:O	10:J:87:LEU:HG	2.15	0.46
21:X:98:GLU:HA	21:X:115:GLY:O	2.16	0.46
1:A:71:A:O4'	1:A:100:G:N2	2.49	0.46
1:A:780:A:N6	1:A:801:U:OP2	2.48	0.46
1:A:803:G:H2'	1:A:804:U:O4'	2.15	0.46
1:A:811:C:O2'	1:A:901:A:N1	2.44	0.46
1:A:971:G:OP2	1:A:1231:G:N2	2.49	0.46
1:A:1427:C:H2'	1:A:1428:A:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:11:ARG:NH1	3:C:177:THR:O	2.43	0.46
3:C:40:ARG:HH11	3:C:55:ILE:HG23	1.80	0.46
19:S:12:ASP:OD1	19:S:13:LEU:N	2.49	0.46
1:A:2:A:C6	1:A:3:A:C6	3.04	0.46
1:A:155:A:H2'	1:A:156:C:H6	1.80	0.46
1:A:156:C:C4	1:A:157:U:C4	3.04	0.46
1:A:201:G:H2'	1:A:202:G:C8	2.51	0.46
1:A:439:U:H5"	4:D:121:LYS:HD2	1.97	0.46
1:A:566:G:H8	1:A:566:G:OP1	1.99	0.46
1:A:734:G:C6	1:A:735:C:C4	3.04	0.46
1:A:771:G:C6	1:A:809:G:C6	3.03	0.46
1:A:796:C:OP2	11:K:128:ARG:NH2	2.48	0.46
1:A:954:G:O6	13:M:103:LYS:NZ	2.48	0.46
1:A:1207:2MG:C6	1:A:1208:C:C4	3.04	0.46
1:A:1327:C:H2'	1:A:1328:C:H6	1.80	0.46
1:A:1416:G:H3'	1:A:1417:G:C8	2.50	0.46
3:C:110:GLU:H	3:C:110:GLU:CD	2.20	0.46
6:F:75:GLU:O	6:F:78:PHE:HB2	2.16	0.46
12:L:57:LEU:HD13	12:L:57:LEU:HA	1.76	0.46
15:O:17:ARG:NH2	15:O:21:ASP:HB2	2.31	0.46
20:T:30:THR:HA	20:T:33:LYS:HZ3	1.81	0.46
1:A:111:G:O6	1:A:330:C:N4	2.43	0.45
1:A:129:A:O2'	1:A:130:A:H5"	2.16	0.45
1:A:417:G:C6	1:A:418:C:C4	3.05	0.45
1:A:766:A:C4	1:A:767:A:C8	3.04	0.45
1:A:896:C:H2'	1:A:897:C:C6	2.51	0.45
1:A:1015:G:OP2	1:A:1015:G:H8	2.00	0.45
1:A:1040:U:H2'	1:A:1041:G:H8	1.81	0.45
1:A:1451:U:OP2	1:A:1452:C:N4	2.49	0.45
3:C:28:GLU:O	3:C:32:ASN:HB2	2.16	0.45
7:G:17:LYS:HG3	7:G:18:PHE:CE2	2.51	0.45
1:A:633:G:H2'	1:A:634:C:C6	2.51	0.45
1:A:807:A:H2'	1:A:808:C:C6	2.51	0.45
1:A:826:C:H5'	8:H:13:ARG:NH2	2.30	0.45
1:A:1237:C:H4'	1:A:1300:G:H22	1.82	0.45
3:C:6:HIS:HE1	3:C:8:ASN:HB3	1.80	0.45
6:F:101:PRO:HA	6:F:104:LYS:HE3	1.98	0.45
7:G:47:LEU:HD13	7:G:58:GLU:HG3	1.98	0.45
7:G:60:GLU:HA	7:G:63:GLU:CD	2.36	0.45
9:I:12:ARG:HA	9:I:12:ARG:HD2	1.74	0.45
20:T:8:LYS:HB3	20:T:8:LYS:HE2	1.73	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:X:85:LEU:HG	21:X:91:TYR:CE2	2.51	0.45
1:A:34:C:H2'	1:A:35:G:H8	1.81	0.45
1:A:76:G:H3'	1:A:77:A:C8	2.51	0.45
1:A:129:A:H1'	1:A:130:A:C8	2.51	0.45
1:A:629:A:C4	1:A:630:A:C8	3.04	0.45
1:A:684:U:O2	11:K:41:ALA:N	2.45	0.45
1:A:920:U:H5'	1:A:1080:A:H61	1.81	0.45
1:A:1178:G:C5	9:I:99:ARG:NH1	2.85	0.45
1:A:1198:G:H2'	1:A:1199:U:C6	2.51	0.45
3:C:86:LYS:HG3	3:C:87:LEU:N	2.32	0.45
7:G:5:ARG:NH1	7:G:7:ILE:HG22	2.29	0.45
15:O:12:VAL:HG21	15:O:22:THR:HG22	1.98	0.45
17:Q:30:LYS:N	17:Q:37:PHE:CD1	2.84	0.45
20:T:81:ALA:O	20:T:85:LYS:HG2	2.16	0.45
1:A:259:G:C6	1:A:260:G:C5	3.04	0.45
1:A:416:G:C4	1:A:417:G:C8	3.04	0.45
1:A:444:G:H2'	1:A:445:G:H8	1.81	0.45
1:A:604:G:H2'	1:A:605:U:O4'	2.16	0.45
1:A:628:G:H2'	1:A:629:A:O4'	2.17	0.45
1:A:679:C:H2'	1:A:680:C:C6	2.51	0.45
1:A:1052:U:O2'	1:A:1055:A:OP2	2.27	0.45
1:A:1167:A:H2'	1:A:1169:A:C8	2.51	0.45
1:A:1221:G:OP1	19:S:36:ARG:HD3	2.17	0.45
1:A:1377:A:OP1	7:G:95:ARG:NH1	2.50	0.45
9:I:15:SER:HA	9:I:68:LYS:O	2.17	0.45
9:I:47:VAL:HA	9:I:50:GLN:CG	2.42	0.45
21:X:23:LEU:HD21	21:X:26:ILE:HD11	1.98	0.45
1:A:227:G:C6	1:A:228:A:C5	3.04	0.45
1:A:325:A:H2'	1:A:326:G:C8	2.52	0.45
1:A:355:C:H2'	1:A:356:A:O4'	2.15	0.45
1:A:953:G:HO2'	1:A:954:G:P	2.38	0.45
1:A:1069:C:H2'	1:A:1070:U:O4'	2.16	0.45
1:A:1070:U:O4	1:A:1094:G:N1	2.50	0.45
1:A:1342:C:O2'	1:A:1343:G:H5'	2.15	0.45
1:A:1377:A:C6	7:G:7:ILE:HG13	2.51	0.45
1:A:1377:A:N7	7:G:8:GLY:HA2	2.32	0.45
3:C:184:TYR:HA	3:C:200:VAL:O	2.16	0.45
5:E:48:PHE:CZ	5:E:50:TYR:HB2	2.52	0.45
7:G:95:ARG:HA	7:G:95:ARG:HD2	1.66	0.45
8:H:47:GLU:HB3	8:H:62:THR:CG2	2.47	0.45
9:I:52:LEU:HD21	9:I:87:LEU:HD21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:75:GLN:O	9:I:79:ILE:HG12	2.16	0.45
9:I:123:ARG:HD2	9:I:124:ARG:H	1.82	0.45
10:J:24:GLU:O	10:J:27:GLU:HG3	2.17	0.45
16:P:36:VAL:HG21	16:P:57:ILE:HG13	1.98	0.45
1:A:73:C:O2'	1:A:74:A:H5"	2.17	0.45
1:A:75:G:H3'	1:A:76:G:H8	1.80	0.45
1:A:117:G:H2'	1:A:118:U:O4'	2.16	0.45
1:A:156:C:H2'	1:A:157:U:C6	2.51	0.45
1:A:204:G:O6	1:A:205:A:N6	2.50	0.45
1:A:229:U:H2'	1:A:230:G:C8	2.51	0.45
1:A:370:C:H2'	1:A:371:A:C8	2.51	0.45
1:A:546:A:P	4:D:69:GLU:HB3	2.57	0.45
1:A:695:A:H2'	1:A:696:A:C8	2.51	0.45
1:A:841:C:H5"	1:A:843:U:OP2	2.16	0.45
1:A:846:G:H2'	1:A:847:G:H8	1.80	0.45
1:A:1074:G:OP1	5:E:69:ARG:NH1	2.43	0.45
1:A:1095:U:C4	1:A:1096:C:C4	3.05	0.45
1:A:1106:G:C5	1:A:1107:C:N3	2.85	0.45
1:A:1210:C:H5"	1:A:1211:U:OP2	2.16	0.45
1:A:1228:C:P	13:M:107:ARG:HH12	2.39	0.45
1:A:1255:G:C6	1:A:1279:G:N7	2.85	0.45
1:A:1410:A:N6	1:A:1490:U:O2'	2.46	0.45
3:C:90:VAL:HA	3:C:93:ASP:OD2	2.16	0.45
4:D:62:ARG:HD2	4:D:69:GLU:HA	1.98	0.45
7:G:66:LEU:HD23	7:G:70:ARG:HB3	1.99	0.45
9:I:24:GLY:N	9:I:60:LYS:O	2.50	0.45
9:I:25:ASN:O	9:I:60:LYS:N	2.49	0.45
18:R:10:PHE:CG	18:R:46:GLY:HA3	2.52	0.45
1:A:682:G:N2	1:A:708:C:O2	2.45	0.45
1:A:742:G:H5"	15:O:58:ARG:NH1	2.32	0.45
1:A:795:C:C5'	11:K:128:ARG:HH22	2.30	0.45
1:A:1253:G:C2	1:A:1254:A:C4	3.05	0.45
1:A:1286:U:O2'	1:A:1287:A:OP1	2.32	0.45
1:A:1338:G:C2	1:A:1339:A:C4	3.05	0.45
1:A:1539:C:O2'	1:A:1540:U:H5"	2.17	0.45
3:C:148:GLY:HA3	3:C:172:ARG:O	2.16	0.45
10:J:5:ARG:NE	10:J:75:ASP:OD2	2.43	0.45
1:A:76:G:N3	1:A:76:G:H2'	2.32	0.45
1:A:146:G:H2'	1:A:147:G:H8	1.82	0.45
1:A:177:G:C8	1:A:178:C:C6	3.05	0.45
1:A:178:C:H2'	1:A:179:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:426:U:OP1	4:D:33:LYS:NZ	2.41	0.45
1:A:427:U:C4	1:A:428:G:C5	3.05	0.45
1:A:663:A:H5'	1:A:836:G:OP1	2.17	0.45
1:A:1014:A:C2	1:A:1219:A:H1'	2.52	0.45
1:A:1192:C:OP2	3:C:4:LYS:HE3	2.17	0.45
1:A:1241:G:H2'	1:A:1242:G:C8	2.49	0.45
1:A:1250:A:C5	1:A:1287:A:C5	3.05	0.45
1:A:1428:A:C6	1:A:1473:G:C6	3.05	0.45
3:C:49:LYS:HE2	3:C:49:LYS:HB2	1.80	0.45
4:D:23:SER:HB3	4:D:161:LEU:HD21	1.98	0.45
4:D:97:ARG:O	4:D:101:VAL:HG23	2.17	0.45
4:D:98:LEU:HD22	4:D:135:TYR:HD1	1.81	0.45
7:G:51:ALA:O	7:G:56:LYS:HD2	2.16	0.45
8:H:61:LEU:HD12	8:H:61:LEU:O	2.16	0.45
1:A:79:G:H8	1:A:79:G:O5'	1.99	0.45
1:A:186:C:H2'	1:A:187:G:O4'	2.16	0.45
1:A:312:C:H2'	1:A:313:A:H8	1.79	0.45
1:A:468:A:H5'	1:A:469:C:OP2	2.16	0.45
1:A:974:A:H4'	1:A:975:A:H3'	1.98	0.45
1:A:1222:G:OP2	1:A:1322:C:N4	2.34	0.45
1:A:1430:A:H3'	1:A:1431:A:H8	1.82	0.45
1:A:1533:C:H2'	1:A:1534:A:H8	1.82	0.45
3:C:8:ASN:OD1	3:C:16:LYS:NZ	2.43	0.45
4:D:121:LYS:HG2	4:D:131:ASN:ND2	2.30	0.45
7:G:2:PRO:HB3	7:G:6:VAL:HA	1.97	0.45
14:N:42:TRP:O	14:N:45:VAL:HG12	2.17	0.45
18:R:11:CYS:C	18:R:14:THR:HG22	2.35	0.45
1:A:55:A:H61	1:A:368:U:H3	1.64	0.45
1:A:90:C:C2	1:A:91:U:C6	3.05	0.45
1:A:582:C:N3	1:A:760:G:C6	2.85	0.45
1:A:584:G:C4	1:A:585:G:C8	3.05	0.45
1:A:663:A:H2'	1:A:664:G:C8	2.52	0.45
1:A:712:A:H2'	1:A:713:G:H8	1.82	0.45
1:A:767:A:H2'	1:A:768:A:C8	2.51	0.45
1:A:791:G:C5	1:A:792:A:C6	3.05	0.45
1:A:947:G:O6	1:A:1234:C:N4	2.41	0.45
1:A:1106:G:C4	1:A:1107:C:N3	2.85	0.45
1:A:1217:C:H2'	1:A:1218:C:C6	2.52	0.45
1:A:1340:A:H2'	1:A:1341:U:H6	1.82	0.45
4:D:101:VAL:O	4:D:105:MET:N	2.33	0.45
7:G:59:LEU:H	7:G:59:LEU:HD12	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:77:SER:HA	7:G:85:TYR:O	2.17	0.45
17:Q:9:GLN:HE21	17:Q:58:VAL:HG12	1.82	0.45
20:T:32:ILE:HA	20:T:35:VAL:HG12	1.99	0.45
1:A:571:U:H5"	1:A:819:A:C2	2.52	0.44
1:A:705:G:H2'	1:A:706:A:C5'	2.46	0.44
1:A:707:U:OP1	11:K:24:HIS:ND1	2.49	0.44
1:A:875:U:H1'	8:H:16:ASN:ND2	2.32	0.44
1:A:986:U:H2'	1:A:987:G:O4'	2.17	0.44
1:A:1087:G:C4	1:A:1099:G:C2	3.05	0.44
1:A:1147:C:H2'	1:A:1148:U:C6	2.52	0.44
1:A:1261:A:H2'	1:A:1262:C:O4'	2.17	0.44
12:L:36:ARG:HB3	21:X:80:GLY:CA	2.47	0.44
13:M:86:TYR:CZ	13:M:90:ARG:HD2	2.51	0.44
17:Q:28:PHE:CE1	17:Q:37:PHE:O	2.71	0.44
20:T:35:VAL:O	20:T:39:ILE:CG1	2.65	0.44
1:A:154:U:H2'	1:A:155:A:H8	1.82	0.44
1:A:318:G:C6	1:A:336:A:C6	3.05	0.44
1:A:423:G:C2	1:A:424:G:C8	3.05	0.44
1:A:465:A:H2'	1:A:466:A:O4'	2.17	0.44
1:A:776:G:H8	1:A:776:G:OP2	2.00	0.44
1:A:1011:C:H2'	1:A:1012:A:C8	2.51	0.44
1:A:1026:G:C2	1:A:1027:C:C6	3.05	0.44
7:G:138:ARG:HA	7:G:141:VAL:HG12	1.99	0.44
11:K:82:LEU:N	11:K:106:ARG:O	2.50	0.44
12:L:66:TYR:HB3	12:L:96:HIS:ND1	2.32	0.44
19:S:43:ASN:OD1	19:S:43:ASN:N	2.49	0.44
1:A:50:A:N1	1:A:360:G:O2'	2.37	0.44
1:A:375:U:H2'	1:A:376:G:O4'	2.18	0.44
1:A:620:C:C2	1:A:621:A:C8	3.05	0.44
1:A:642:A:C5	1:A:643:C:C5	3.05	0.44
1:A:691:G:C2	1:A:692:U:C4	3.05	0.44
1:A:738:C:H2'	1:A:739:C:H6	1.83	0.44
1:A:803:G:C5	1:A:804:U:C4	3.05	0.44
1:A:809:G:C6	1:A:810:C:C4	3.05	0.44
1:A:1012:A:C6	1:A:1018:G:C6	3.05	0.44
1:A:1088:G:H2'	1:A:1089:G:O4'	2.18	0.44
1:A:1193:G:H2'	1:A:1194:U:H6	1.82	0.44
8:H:41:LYS:HD3	8:H:48:ASP:HA	1.98	0.44
9:I:28:ILE:HG22	9:I:63:LEU:HD13	1.99	0.44
13:M:4:ILE:CD1	13:M:22:ILE:HD11	2.48	0.44
13:M:100:GLN:N	13:M:100:GLN:OE1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:37:GLY:HA3	16:P:52:LEU:HD23	1.99	0.44
21:X:36:LEU:C	21:X:36:LEU:HD12	2.38	0.44
1:A:678:U:C4	1:A:679:C:C4	3.05	0.44
1:A:958:A:OP1	19:S:55:ARG:NH1	2.50	0.44
1:A:1114:C:H2'	1:A:1115:U:O4'	2.18	0.44
1:A:1179:A:O2'	9:I:105:THR:O	2.26	0.44
1:A:1429:A:H3'	1:A:1430:A:H8	1.82	0.44
5:E:25:VAL:HB	5:E:28:GLY:O	2.18	0.44
6:F:10:VAL:HG21	6:F:18:VAL:HG12	1.99	0.44
7:G:106:GLU:HB2	7:G:110:LYS:NZ	2.32	0.44
12:L:54:ARG:HE	12:L:62:GLU:CD	2.17	0.44
17:Q:17:MET:CB	17:Q:20:SER:HB2	2.47	0.44
17:Q:28:PHE:CZ	17:Q:37:PHE:O	2.71	0.44
17:Q:30:LYS:HB2	17:Q:37:PHE:CE1	2.52	0.44
1:A:328:C:H4'	1:A:329:A:H5'	2.00	0.44
1:A:401:C:P	4:D:70:ARG:HE	2.36	0.44
1:A:597:G:C2	1:A:644:U:C2	3.06	0.44
1:A:814:A:H5'	1:A:815:A:P	2.58	0.44
1:A:1092:A:H2'	1:A:1093:A:C8	2.53	0.44
1:A:1190:G:OP1	3:C:5:VAL:N	2.50	0.44
1:A:1237:C:O2'	1:A:1300:G:N1	2.41	0.44
1:A:1365:G:H2'	1:A:1366:C:H6	1.82	0.44
1:A:1505:G:C2	1:A:1506:U:C2	3.05	0.44
12:L:3:THR:HG1	12:L:6:GLN:CD	2.20	0.44
1:A:75:G:C6	1:A:76:G:C5	3.06	0.44
1:A:103:U:H2'	1:A:104:G:O4'	2.17	0.44
1:A:520:A:OP1	1:A:520:A:H4'	2.17	0.44
1:A:734:G:C2	1:A:735:C:C2	3.06	0.44
1:A:1105:A:C2	1:A:1106:G:C2	3.06	0.44
1:A:1206:G:C6	1:A:1207:2MG:C5	3.05	0.44
1:A:1222:G:C2	1:A:1223:C:C2	3.06	0.44
1:A:1277:C:O2'	1:A:1279:G:H8	2.01	0.44
1:A:1328:C:H2'	1:A:1329:A:C8	2.51	0.44
1:A:1357:A:H2	1:A:1365:G:H22	1.64	0.44
2:B:171:ILE:O	2:B:175:GLU:HG3	2.18	0.44
3:C:69:HIS:HD2	3:C:104:ALA:HB3	1.83	0.44
3:C:71:ALA:O	3:C:73:PRO:HD3	2.17	0.44
3:C:169:ARG:HH22	3:C:172:ARG:HA	1.83	0.44
6:F:72:ASP:HA	6:F:75:GLU:HG3	2.00	0.44
1:A:15:G:H2'	1:A:16:A:C8	2.53	0.44
1:A:64:G:H4'	1:A:65:A:H5"	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:457:G:H3'	1:A:458:U:H6	1.83	0.44
1:A:510:A:N3	1:A:543:U:H1'	2.32	0.44
1:A:518:C:C5	1:A:530:G:C4	3.06	0.44
1:A:664:G:P	18:R:53:ARG:HH21	2.40	0.44
1:A:846:G:C4	1:A:847:G:C8	3.05	0.44
1:A:872:A:C4	1:A:874:G:C8	3.06	0.44
1:A:1004:A:C4	1:A:1026:G:C5	3.06	0.44
1:A:1070:U:C2	1:A:1106:G:N2	2.85	0.44
1:A:1306:A:C6	1:A:1307:U:C2	3.06	0.44
1:A:1308:U:H5'	13:M:109:ARG:HH12	1.83	0.44
1:A:1349:A:H1'	1:A:1374:A:N6	2.33	0.44
1:A:1458:G:C2	1:A:1459:G:C4	3.06	0.44
1:A:1518:MA6:H2'	1:A:1519:MA6:C8	2.47	0.44
3:C:10:ILE:HD12	3:C:10:ILE:HA	1.88	0.44
3:C:60:PRO:HD2	3:C:63:SER:O	2.17	0.44
4:D:146:ARG:O	4:D:149:ALA:N	2.50	0.44
8:H:73:GLU:OE1	8:H:73:GLU:N	2.51	0.44
10:J:87:LEU:HA	10:J:90:LEU:HG	1.99	0.44
11:K:87:LYS:CE	11:K:113:VAL:HG11	2.39	0.44
17:Q:57:ASP:OD1	17:Q:83:VAL:HG12	2.17	0.44
19:S:32:ARG:HG3	19:S:57:HIS:CD2	2.53	0.44
21:X:36:LEU:HD11	21:X:74:LEU:HG	1.98	0.44
1:A:17:U:H2'	1:A:18:C:C6	2.53	0.44
1:A:134:G:C5	1:A:135:C:C4	3.05	0.44
1:A:251:G:C6	1:A:266:G:O6	2.70	0.44
1:A:501:C:H2'	1:A:502:A:H8	1.83	0.44
1:A:563:A:N6	1:A:884:U:H3	2.15	0.44
1:A:959:A:H2'	1:A:960:U:O4'	2.18	0.44
1:A:987:G:C4	1:A:988:G:C8	3.06	0.44
1:A:1122:U:H2'	1:A:1123:U:C6	2.53	0.44
1:A:1453:G:N1	1:A:1454:G:C4	2.86	0.44
3:C:51:SER:O	3:C:51:SER:OG	2.31	0.44
4:D:172:GLU:HB2	4:D:181:THR:HB	2.00	0.44
10:J:18:ILE:HD13	10:J:72:ARG:HG2	2.00	0.44
11:K:83:GLU:OE2	11:K:84:VAL:N	2.51	0.44
21:X:28:PHE:CD1	21:X:36:LEU:HB3	2.51	0.44
1:A:45:G:H2'	1:A:46:G:H8	1.83	0.44
1:A:78:A:C4	1:A:79:G:C8	3.06	0.44
1:A:212:G:H2'	1:A:213:G:O4'	2.17	0.44
1:A:243:A:H2	1:A:245:U:H2'	1.83	0.44
1:A:251:G:N1	1:A:266:G:C6	2.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:U:H2'	1:A:269:C:C6	2.53	0.44
1:A:409:U:C4	1:A:410:G:C5	3.06	0.44
1:A:415:A:C4	1:A:416:G:C8	3.06	0.44
1:A:440:C:C2	1:A:441:A:C8	3.06	0.44
1:A:468:A:C8	1:A:469:C:C6	3.05	0.44
1:A:775:G:C6	1:A:776:G:C6	3.06	0.44
1:A:1112:C:N3	3:C:178:LEU:HG	2.32	0.44
10:J:22:THR:HB	10:J:39:PRO:HB3	1.99	0.44
13:M:44:LYS:HG2	13:M:47:GLU:OE1	2.17	0.44
19:S:28:LYS:HA	19:S:28:LYS:HD3	1.82	0.44
21:X:10:GLU:HA	21:X:13:THR:CG2	2.48	0.44
21:X:98:GLU:HG3	21:X:147:VAL:HB	2.00	0.44
1:A:8:A:H4'	1:A:9:G:OP1	2.18	0.43
1:A:23:C:H2'	1:A:24:U:C6	2.52	0.43
1:A:56:U:H2'	1:A:57:G:C8	2.53	0.43
1:A:487:A:H3'	1:A:488:C:H6	1.83	0.43
1:A:511:C:H4'	4:D:44:ARG:HH22	1.82	0.43
1:A:720:C:O2'	18:R:52:GLN:NE2	2.51	0.43
1:A:803:G:C6	1:A:804:U:C4	3.06	0.43
1:A:924:C:H3'	1:A:925:G:H3'	2.00	0.43
1:A:953:G:N2	1:A:954:G:H1'	2.33	0.43
1:A:1310:G:C6	1:A:1311:A:C5	3.07	0.43
1:A:1365:G:H2'	1:A:1366:C:C6	2.53	0.43
1:A:1426:G:C6	1:A:1427:C:C4	3.06	0.43
1:A:1510:C:N4	1:A:1511:G:O6	2.51	0.43
2:B:154:MET:HG2	2:B:156:GLY:O	2.18	0.43
10:J:17:LEU:HD21	10:J:93:ALA:HB3	1.99	0.43
21:X:83:ARG:HD2	21:X:94:PHE:HZ	1.82	0.43
1:A:155:A:C6	1:A:167:A:C6	3.05	0.43
1:A:293:G:C4	1:A:305:G:N2	2.86	0.43
1:A:410:G:H2'	1:A:429:U:C5	2.53	0.43
1:A:457:G:C6	1:A:458:U:N3	2.86	0.43
1:A:695:A:C6	1:A:696:A:C5	3.06	0.43
1:A:755:G:C6	1:A:756:C:C4	3.06	0.43
1:A:842:U:C2	1:A:843:U:C4	3.07	0.43
1:A:872:A:C4	1:A:874:G:N7	2.86	0.43
1:A:1014:A:H4'	19:S:14:HIS:NE2	2.33	0.43
1:A:1379:G:C6	1:A:1380:U:O4	2.71	0.43
1:A:1491:G:H3'	21:X:30:ARG:CB	2.46	0.43
3:C:125:GLU:OE2	3:C:190:HIS:N	2.51	0.43
5:E:53:ALA:HB3	5:E:59:ALA:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:67:ILE:HG22	16:P:68:SER:O	2.18	0.43
1:A:71:A:H61	1:A:99:C:C2'	2.31	0.43
1:A:76:G:H3'	1:A:77:A:H8	1.82	0.43
1:A:90:C:HO2'	1:A:91:U:H5	1.63	0.43
1:A:211:G:C2	1:A:212:G:C8	3.06	0.43
1:A:299:G:C5	1:A:300:A:C6	3.06	0.43
1:A:483:C:C4	1:A:484:G:C5	3.06	0.43
1:A:698:G:C5	1:A:699:C:C4	3.06	0.43
1:A:1002:G:C6	1:A:1039:G:C6	3.07	0.43
1:A:1022:A:C2	1:A:1023:U:C2	3.06	0.43
1:A:1161:C:H2'	1:A:1162:C:H6	1.82	0.43
1:A:1292:G:H2'	1:A:1293:C:H6	1.82	0.43
1:A:1399:C:N4	1:A:1502:A:H62	2.16	0.43
1:A:1449:C:H2'	1:A:1450:U:O4'	2.17	0.43
1:A:1459:G:H2'	1:A:1460:C:H6	1.82	0.43
1:A:1505:G:H3'	11:K:129:VAL:O	2.18	0.43
2:B:68:LEU:HA	2:B:90:PHE:O	2.19	0.43
4:D:29:ASP:OD1	4:D:29:ASP:N	2.51	0.43
13:M:85:CYS:SG	13:M:88:GLY:N	2.86	0.43
15:O:26:GLU:HG3	15:O:81:LEU:HD22	2.00	0.43
21:X:7:LYS:O	21:X:11:MET:HG2	2.18	0.43
1:A:53:A:H2'	1:A:54:C:O4'	2.17	0.43
1:A:204:G:C5	1:A:465:A:C6	3.06	0.43
1:A:504:C:C2	1:A:542:G:C2	3.06	0.43
1:A:704:A:H3'	1:A:705:G:H8	1.84	0.43
1:A:819:A:N7	1:A:1529:G:C2	2.87	0.43
1:A:900:A:N6	1:A:901:A:N1	2.66	0.43
1:A:1070:U:O2	1:A:1106:G:C2	2.72	0.43
10:J:30:LYS:HE2	10:J:34:ALA:O	2.17	0.43
12:L:54:ARG:HD2	12:L:54:ARG:HA	1.62	0.43
17:Q:62:ARG:HD3	17:Q:76:VAL:HG22	1.98	0.43
1:A:164:G:C6	1:A:165:G:C5	3.06	0.43
1:A:247:G:C5	1:A:278:G:C2	3.05	0.43
1:A:405:U:OP2	4:D:3:ARG:NH2	2.31	0.43
1:A:520:A:C2	1:A:536:C:H1'	2.54	0.43
1:A:792:A:O2'	1:A:793:U:H6	2.01	0.43
1:A:822:U:H2'	1:A:823:C:C6	2.53	0.43
1:A:1306:A:C5	1:A:1332:A:C2	3.06	0.43
1:A:1326:U:H2'	1:A:1327:C:C6	2.53	0.43
1:A:1538:C:C2	5:E:56:VAL:HG21	2.52	0.43
1:A:120:A:O2'	1:A:122:G:N7	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:455:G:C6	1:A:456:A:C5	3.06	0.43
1:A:579:A:H2'	1:A:580:C:C6	2.54	0.43
1:A:1004:A:N6	1:A:1026:G:H1'	2.33	0.43
1:A:1294:G:H2'	1:A:1295:U:C6	2.54	0.43
4:D:82:LEU:HB2	4:D:89:ASN:HD22	1.84	0.43
7:G:58:GLU:OE1	7:G:58:GLU:N	2.49	0.43
21:X:99:VAL:O	21:X:114:GLN:HA	2.17	0.43
1:A:79:G:H21	1:A:90:C:H41	1.66	0.43
1:A:168:G:C6	1:A:169:C:N4	2.87	0.43
1:A:185:U:H2'	1:A:186:C:H6	1.82	0.43
1:A:263:A:H2'	1:A:264:C:C5	2.53	0.43
1:A:310:G:H2'	1:A:311:C:H6	1.83	0.43
1:A:324:G:N1	1:A:327:A:OP2	2.49	0.43
1:A:347:G:C6	1:A:348:G:C5	3.07	0.43
1:A:404:G:C5	4:D:2:ALA:N	2.86	0.43
1:A:648:A:H2'	1:A:649:A:C8	2.54	0.43
1:A:674:G:H21	11:K:118:HIS:HD2	1.65	0.43
1:A:686:U:HO2'	1:A:687:A:H8	1.63	0.43
1:A:709:U:H2'	1:A:710:G:H8	1.84	0.43
1:A:750:C:H4'	15:O:21:ASP:HA	1.99	0.43
1:A:862:C:H2'	1:A:863:U:C6	2.54	0.43
1:A:952:U:H2'	1:A:953:G:C8	2.52	0.43
1:A:1069:C:N3	1:A:1070:U:N3	2.67	0.43
1:A:1172:C:H2'	1:A:1173:U:H6	1.83	0.43
1:A:1503:A:C5	1:A:1504:G:H1'	2.53	0.43
2:B:9:MET:HB3	2:B:14:VAL:HB	2.00	0.43
6:F:49:TYR:HB2	18:R:74:HIS:CD2	2.53	0.43
7:G:78:ARG:HH21	7:G:80:VAL:HG21	1.83	0.43
7:G:102:ARG:O	7:G:106:GLU:HG3	2.19	0.43
8:H:47:GLU:HB3	8:H:62:THR:HB	2.01	0.43
9:I:39:PHE:O	9:I:45:ARG:NH2	2.51	0.43
12:L:21:VAL:HG12	12:L:24:LEU:HB2	2.01	0.43
12:L:33:VAL:O	12:L:55:VAL:HG23	2.18	0.43
12:L:99:ARG:NH2	12:L:105:SER:O	2.52	0.43
20:T:67:ILE:HD13	20:T:67:ILE:HA	1.80	0.43
1:A:43:C:H2'	1:A:44:A:O4'	2.19	0.43
1:A:493:A:H2'	1:A:494:G:C8	2.53	0.43
1:A:538:G:C2	1:A:539:A:C5	3.07	0.43
1:A:690:G:H1'	1:A:698:G:N2	2.34	0.43
1:A:834:U:H2'	1:A:835:U:C6	2.53	0.43
1:A:939:G:C2	1:A:940:C:C2	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:959:A:OP2	1:A:959:A:H8	2.02	0.43
1:A:1033:G:H2'	1:A:1034:G:O4'	2.19	0.43
1:A:1346:A:N6	1:A:1374:A:C8	2.87	0.43
7:G:49:THR:O	7:G:52:GLN:NE2	2.52	0.43
8:H:72:VAL:HG23	8:H:129:VAL:HG23	2.00	0.43
10:J:30:LYS:HA	10:J:30:LYS:HD3	1.68	0.43
1:A:109:A:C6	1:A:327:A:C6	3.06	0.43
1:A:537:G:C4	1:A:538:G:C8	3.06	0.43
1:A:568:G:O2'	1:A:574:A:N1	2.44	0.43
1:A:575:G:O2'	1:A:821:G:H5'	2.19	0.43
1:A:592:G:H2'	1:A:593:U:H6	1.83	0.43
1:A:668:G:C2	1:A:669:G:C8	3.07	0.43
1:A:712:A:C6	1:A:713:G:C6	3.07	0.43
1:A:902:G:C2	1:A:903:G:C8	3.07	0.43
1:A:1208:C:H2'	1:A:1209:C:H6	1.83	0.43
1:A:1246:A:C6	1:A:1247:U:C4	3.07	0.43
3:C:31:ASP:OD1	3:C:32:ASN:N	2.52	0.43
4:D:126:ASN:HA	4:D:142:VAL:HG23	2.00	0.43
10:J:21:ALA:O	10:J:25:ILE:HG12	2.19	0.43
11:K:20:VAL:O	11:K:34:ILE:HA	2.19	0.43
18:R:33:ILE:HD11	18:R:63:ARG:HH21	1.84	0.43
19:S:3:ARG:NH2	19:S:10:PHE:HB3	2.31	0.43
1:A:71:A:C5	1:A:100:G:C5	3.07	0.43
1:A:142:G:C5	1:A:143:A:C5	3.07	0.43
1:A:154:U:C2	1:A:155:A:C8	3.06	0.43
1:A:200:G:C2	1:A:201:G:C8	3.07	0.43
1:A:204:G:O6	1:A:215:C:H1'	2.19	0.43
1:A:455:G:C4	1:A:456:A:C8	3.07	0.43
1:A:584:G:H2'	1:A:585:G:H8	1.84	0.43
1:A:879:C:H2'	1:A:880:C:C6	2.53	0.43
1:A:903:G:C6	1:A:904:U:C4	3.07	0.43
2:B:174:LYS:HE2	2:B:174:LYS:HB2	1.78	0.43
9:I:45:ARG:O	9:I:49:ARG:HG2	2.19	0.43
13:M:54:ASP:HA	13:M:57:ARG:CZ	2.49	0.43
20:T:51:PHE:O	20:T:54:MET:N	2.52	0.43
20:T:76:LYS:O	20:T:80:THR:HG23	2.19	0.43
21:X:115:GLY:HA3	21:X:129:VAL:HG22	2.01	0.43
1:A:872:A:C8	1:A:874:G:C8	3.06	0.42
1:A:1034:G:H2'	1:A:1035:A:H8	1.84	0.42
3:C:77:ILE:HD13	3:C:84:VAL:HG21	2.01	0.42
6:F:3:HIS:HB3	6:F:92:THR:HG1	1.78	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:24:LEU:HD23	12:L:24:LEU:HA	1.70	0.42
14:N:39:GLU:OE2	14:N:43:ASN:ND2	2.52	0.42
14:N:40:ASP:O	14:N:44:ALA:CB	2.67	0.42
20:T:31:PHE:HA	20:T:34:LYS:HD2	2.00	0.42
1:A:158:G:H2'	1:A:159:G:C8	2.54	0.42
1:A:265:G:H21	1:A:267:C:H5'	1.84	0.42
1:A:321:A:H2'	1:A:322:C:C6	2.54	0.42
1:A:408:A:H2'	1:A:409:U:O4'	2.19	0.42
1:A:422:C:H4'	1:A:423:G:O5'	2.19	0.42
1:A:520:A:H2'	1:A:521:G:O4'	2.19	0.42
1:A:592:G:C2	1:A:593:U:C2	3.07	0.42
1:A:749:A:C6	1:A:750:C:C4	3.07	0.42
1:A:761:G:C2	1:A:762:U:C2	3.07	0.42
1:A:787:A:N3	1:A:787:A:H2'	2.34	0.42
1:A:885:G:H2'	1:A:886:G:C8	2.52	0.42
1:A:925:G:O3'	1:A:926:G:H2'	2.19	0.42
1:A:1107:C:H5'	3:C:169:ARG:HH21	1.84	0.42
1:A:1159:U:C2	1:A:1182:G:C2	3.08	0.42
1:A:1459:G:H2'	1:A:1460:C:C6	2.53	0.42
2:B:186:ILE:HG21	2:B:213:TYR:CE2	2.54	0.42
6:F:6:ILE:CG1	6:F:89:VAL:HG23	2.41	0.42
9:I:127:PHE:CE2	9:I:129:LYS:HA	2.54	0.42
20:T:11:ALA:O	20:T:14:SER:OG	2.36	0.42
1:A:44:A:C4	1:A:45:G:C8	3.08	0.42
1:A:113:G:H2'	1:A:114:U:C6	2.54	0.42
1:A:141:G:C2	1:A:223:A:C5	3.07	0.42
1:A:696:A:N3	1:A:786:G:O2'	2.41	0.42
1:A:844:G:C2	1:A:845:A:H1'	2.55	0.42
1:A:860:A:H2'	1:A:861:G:O4'	2.19	0.42
1:A:886:G:C4	1:A:887:G:C8	3.07	0.42
1:A:1070:U:H2'	1:A:1071:C:H6	1.84	0.42
1:A:1144:G:O6	1:A:1145:A:N6	2.46	0.42
1:A:1276:G:C6	1:A:1277:C:C4	3.07	0.42
1:A:1278:G:H4'	1:A:1279:G:N3	2.34	0.42
3:C:167:TRP:CZ3	3:C:169:ARG:HB2	2.55	0.42
3:C:207:ILE:HA	3:C:207:ILE:HD13	1.78	0.42
4:D:78:GLU:O	4:D:81:ARG:N	2.53	0.42
6:F:15:SER:O	6:F:18:VAL:HG22	2.19	0.42
9:I:114:LYS:HA	9:I:121:ALA:HA	2.01	0.42
17:Q:62:ARG:HD2	17:Q:76:VAL:HG21	1.99	0.42
18:R:10:PHE:CD1	18:R:46:GLY:HA3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:A:C6	1:A:339:C:C4	3.06	0.42
1:A:563:A:O2'	1:A:566:G:O3'	2.36	0.42
1:A:764:C:H2'	1:A:765:G:O4'	2.20	0.42
1:A:792:A:C8	1:A:793:U:C5	3.07	0.42
1:A:1096:C:H2'	1:A:1097:C:C6	2.54	0.42
1:A:1256:A:C6	1:A:1278:G:C2	3.07	0.42
1:A:1257:A:H3'	1:A:1258:G:H5'	2.02	0.42
1:A:1289:A:H2'	1:A:1290:G:H5'	2.01	0.42
3:C:6:HIS:CG	14:N:89:MET:HB3	2.55	0.42
3:C:30:ALA:O	3:C:33:LEU:HG	2.19	0.42
8:H:26:THR:HA	8:H:59:LEU:O	2.19	0.42
8:H:87:LYS:HB2	8:H:125:ILE:HD11	2.01	0.42
9:I:80:ARG:HD2	9:I:103:PHE:CE1	2.54	0.42
19:S:16:LEU:HA	19:S:19:VAL:HG12	2.01	0.42
19:S:29:LYS:H	19:S:29:LYS:HE2	1.84	0.42
21:X:36:LEU:CD1	21:X:74:LEU:HA	2.50	0.42
21:X:46:ILE:CG2	21:X:78:SER:HB3	2.49	0.42
21:X:85:LEU:HB2	21:X:90:HIS:CB	2.48	0.42
1:A:415:A:C6	1:A:416:G:C5	3.07	0.42
1:A:508:U:H4'	4:D:51:TYR:CE2	2.54	0.42
1:A:683:G:C2	1:A:684:U:C2	3.07	0.42
1:A:791:G:H2'	1:A:792:A:C4	2.54	0.42
1:A:1151:A:O4'	10:J:41:PRO:HB2	2.20	0.42
1:A:1237:C:H3'	1:A:1336:C:N4	2.34	0.42
1:A:1239:A:H3'	7:G:119:ARG:HH22	1.85	0.42
1:A:1244:G:C6	1:A:1245:C:C4	3.07	0.42
4:D:60:LYS:NZ	4:D:195:ILE:HA	2.35	0.42
21:X:46:ILE:HG21	21:X:78:SER:HB3	2.00	0.42
1:A:1:A:C6	1:A:2:A:C6	3.08	0.42
1:A:57:G:H2'	1:A:58:C:C6	2.55	0.42
1:A:79:G:H2'	1:A:80:A:C8	2.54	0.42
1:A:128:G:H2'	1:A:129:A:C8	2.55	0.42
1:A:661:G:N3	1:A:745:G:C2	2.87	0.42
1:A:841:C:C4	1:A:846:G:N1	2.88	0.42
1:A:1014:A:C8	1:A:1015:G:N7	2.87	0.42
1:A:1157:A:H8	1:A:1157:A:OP1	2.03	0.42
1:A:1222:G:C6	1:A:1223:C:C4	3.08	0.42
1:A:1229:A:H2'	1:A:1230:C:C6	2.54	0.42
1:A:1235:U:H2'	1:A:1236:A:O4'	2.19	0.42
1:A:1278:G:H4'	1:A:1279:G:C2	2.54	0.42
1:A:1293:C:C2	1:A:1294:G:C8	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1318:A:OP1	19:S:7:LYS:HE3	2.19	0.42
1:A:1371:G:H2'	1:A:1372:U:O4'	2.19	0.42
1:A:1433:A:N6	1:A:1434:A:C6	2.88	0.42
1:A:1433:A:C5	1:A:1434:A:C5	3.08	0.42
6:F:25:TYR:O	6:F:29:ILE:HG12	2.19	0.42
10:J:15:HIS:HB3	10:J:70:HIS:CD2	2.53	0.42
12:L:21:VAL:HG12	12:L:21:VAL:O	2.20	0.42
1:A:10:A:H2'	1:A:11:G:C8	2.52	0.42
1:A:93:U:H2'	1:A:95:C:C6	2.55	0.42
1:A:507:C:H2'	1:A:508:U:H5	1.85	0.42
1:A:963:G:H21	10:J:57:VAL:HB	1.85	0.42
1:A:1217:C:OP2	14:N:9:ARG:NH2	2.53	0.42
1:A:1264:U:H2'	1:A:1265:C:C6	2.53	0.42
1:A:1338:G:H2'	1:A:1339:A:C8	2.55	0.42
1:A:1375:A:C6	1:A:1376:U:C4	3.07	0.42
3:C:59:ARG:HG3	3:C:64:ILE:HD13	2.00	0.42
3:C:83:ASP:OD1	3:C:83:ASP:N	2.53	0.42
4:D:102:VAL:CG1	4:D:107:PHE:HB2	2.48	0.42
6:F:73:GLU:C	6:F:76:THR:HG1	2.23	0.42
12:L:76:GLU:OE2	21:X:78:SER:HB2	2.20	0.42
15:O:6:GLU:O	15:O:10:LYS:HG3	2.20	0.42
18:R:71:THR:OG1	18:R:72:ASP:OD1	2.37	0.42
1:A:75:G:N3	1:A:75:G:H2'	2.34	0.42
1:A:160:A:H8	1:A:160:A:OP1	2.03	0.42
1:A:197:A:H4'	1:A:198:G:O5'	2.19	0.42
1:A:209:U:OP2	1:A:210:C:N4	2.52	0.42
1:A:244:U:C2	1:A:894:G:N3	2.88	0.42
1:A:461:A:H2'	1:A:462:G:O4'	2.19	0.42
1:A:597:G:C8	1:A:598:U:C5	3.07	0.42
1:A:684:U:H1'	11:K:40:ASN:HA	2.01	0.42
1:A:847:G:C6	1:A:848:C:C4	3.08	0.42
1:A:891:U:N3	1:A:907:A:N7	2.67	0.42
1:A:895:G:C6	1:A:896:C:C4	3.08	0.42
1:A:921:U:C2	1:A:922:G:C8	3.08	0.42
1:A:933:G:C2	1:A:1385:G:C2	3.08	0.42
1:A:1088:G:C2	1:A:1098:C:C2	3.08	0.42
1:A:1238:A:OP1	1:A:1336:C:N4	2.42	0.42
1:A:1242:G:C6	1:A:1243:C:C4	3.07	0.42
1:A:1255:G:N2	1:A:1283:U:C2	2.88	0.42
1:A:1378:C:OP2	7:G:6:VAL:HG11	2.20	0.42
1:A:1400:C:H4'	1:A:1517:G:N1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:108:LYS:CB	3:C:111:LEU:HB2	2.48	0.42
3:C:111:LEU:HD23	3:C:111:LEU:HA	1.91	0.42
3:C:130:PHE:CG	3:C:131:ARG:N	2.88	0.42
7:G:53:ARG:HH21	7:G:125:SER:HG	1.59	0.42
11:K:25:ALA:HB1	11:K:90:GLY:H	1.85	0.42
19:S:5:LEU:HA	19:S:5:LEU:HD23	1.77	0.42
1:A:107:G:C5	1:A:108:G:N2	2.88	0.42
1:A:112:G:N2	1:A:113:G:H1'	2.35	0.42
1:A:227:G:C4	1:A:228:A:C8	3.08	0.42
1:A:415:A:H3'	1:A:416:G:H8	1.85	0.42
1:A:475:C:H2'	1:A:476:U:H6	1.85	0.42
1:A:487:A:H2'	1:A:488:C:O4'	2.20	0.42
1:A:495:A:C2	1:A:496:A:C6	3.08	0.42
1:A:501:C:H2'	1:A:502:A:C8	2.54	0.42
1:A:505:G:H2'	1:A:506:G:C8	2.55	0.42
1:A:619:U:H1'	4:D:128:ARG:HH12	1.85	0.42
1:A:723:U:N3	1:A:855:U:O3'	2.49	0.42
1:A:1166:G:C6	1:A:1168:U:H5"	2.55	0.42
1:A:1304:G:H21	1:A:1333:A:H62	1.68	0.42
1:A:1317:C:H3'	1:A:1318:A:H8	1.84	0.42
5:E:105:ILE:CD1	5:E:123:VAL:CG1	2.97	0.42
5:E:119:GLY:O	5:E:121:HIS:NE2	2.52	0.42
10:J:27:GLU:O	10:J:31:ARG:NH1	2.52	0.42
21:X:12:ILE:HD11	21:X:26:ILE:HD12	2.01	0.42
21:X:85:LEU:HG	21:X:91:TYR:CZ	2.55	0.42
1:A:238:A:C6	1:A:239:U:C4	3.08	0.42
1:A:453:G:H8	1:A:453:G:OP2	2.03	0.42
1:A:551:U:H2'	1:A:552:U:H6	1.85	0.42
1:A:587:G:C2	1:A:755:G:C5	3.08	0.42
1:A:635:A:H2'	1:A:636:U:C6	2.55	0.42
1:A:675:A:H1'	11:K:118:HIS:CE1	2.55	0.42
1:A:751:U:H1'	15:O:23:GLY:O	2.20	0.42
1:A:903:G:H2'	1:A:904:U:H6	1.85	0.42
1:A:958:A:C8	19:S:55:ARG:CZ	3.03	0.42
1:A:984:C:H2'	1:A:985:C:H6	1.83	0.42
1:A:993:G:N7	1:A:1213:A:N6	2.68	0.42
1:A:1157:A:H4'	1:A:1158:C:O5'	2.18	0.42
1:A:1212:U:H5"	1:A:1213:A:O5'	2.20	0.42
1:A:1228:C:H5'	13:M:107:ARG:HH22	1.84	0.42
1:A:1237:C:H3'	1:A:1336:C:H41	1.84	0.42
1:A:1326:U:H2'	1:A:1327:C:H6	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1382:C:H2'	1:A:1383:C:H6	1.84	0.42
1:A:1428:A:N1	1:A:1473:G:C6	2.88	0.42
5:E:138:ARG:O	5:E:141:ILE:HG22	2.20	0.42
9:I:72:ILE:HG13	9:I:73:SER:N	2.35	0.42
9:I:72:ILE:HA	9:I:75:GLN:HG2	2.02	0.42
17:Q:13:VAL:HG21	17:Q:24:ALA:HB2	2.01	0.42
18:R:57:ARG:HD2	18:R:61:ARG:HH21	1.85	0.42
1:A:3:A:N3	1:A:613:C:H1'	2.35	0.41
1:A:166:U:C2	1:A:167:A:C8	3.08	0.41
1:A:477:C:H2'	1:A:478:A:H8	1.81	0.41
1:A:518:C:H41	1:A:530:G:P	2.43	0.41
1:A:714:G:C2	1:A:715:A:C4	3.08	0.41
1:A:725:G:H2'	1:A:726:C:C6	2.55	0.41
1:A:789:U:C4	1:A:792:A:N7	2.88	0.41
1:A:1117:A:O3'	9:I:106:ARG:NE	2.53	0.41
1:A:1142:G:C6	1:A:1143:G:H1'	2.55	0.41
1:A:1245:C:H2'	1:A:1246:A:O4'	2.20	0.41
1:A:1396:A:O5'	1:A:1396:A:C8	2.73	0.41
1:A:1415:G:C6	1:A:1416:G:C5	3.08	0.41
1:A:1439:G:H2'	1:A:1440:U:O4'	2.20	0.41
1:A:1446:A:C6	1:A:1447:A:C6	3.08	0.41
1:A:1520:C:H2'	1:A:1521:C:C6	2.55	0.41
4:D:124:MET:HB2	4:D:144:SER:OG	2.19	0.41
7:G:15:ASP:OD1	7:G:44:TYR:OH	2.38	0.41
12:L:89:D2T:H7	12:L:89:D2T:H4	1.89	0.41
16:P:4:ILE:HG12	16:P:21:VAL:HG22	2.02	0.41
1:A:176:C:C2	1:A:177:G:C2	3.08	0.41
1:A:301:G:N3	1:A:302:G:C8	2.88	0.41
1:A:440:C:H2'	1:A:441:A:O4'	2.20	0.41
1:A:810:C:H2'	1:A:811:C:O4'	2.20	0.41
1:A:839:C:O2'	1:A:840:C:H5'	2.20	0.41
1:A:901:A:C5	1:A:902:G:H1'	2.55	0.41
1:A:902:G:N3	1:A:903:G:C8	2.88	0.41
1:A:1000:A:C6	1:A:1041:G:C6	3.09	0.41
1:A:1255:G:C6	1:A:1279:G:C5	3.08	0.41
1:A:1283:U:H2'	1:A:1284:C:C6	2.55	0.41
1:A:1478:U:H3'	1:A:1479:C:C5'	2.50	0.41
5:E:46:VAL:HG23	5:E:117:VAL:HG23	2.02	0.41
8:H:28:PRO:HA	8:H:57:PRO:O	2.20	0.41
17:Q:29:VAL:C	17:Q:37:PHE:CD1	2.92	0.41
1:A:145:G:C2	1:A:146:G:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:298:A:C6	1:A:299:G:C2	3.07	0.41
1:A:478:A:H2'	1:A:479:U:O4'	2.20	0.41
1:A:765:G:C5	1:A:812:G:C2	3.08	0.41
1:A:797:C:H5'	11:K:127:ARG:HH21	1.85	0.41
1:A:838:G:C5	1:A:849:G:C2	3.08	0.41
1:A:847:G:H2'	1:A:848:C:O4'	2.20	0.41
1:A:1219:A:H2'	1:A:1220:G:C8	2.56	0.41
1:A:1288:A:H8	1:A:1288:A:OP2	2.03	0.41
7:G:70:ARG:O	7:G:70:ARG:HG3	2.20	0.41
11:K:52:PHE:O	11:K:57:LYS:HB3	2.20	0.41
11:K:114:THR:HA	11:K:115:PRO:HD3	1.83	0.41
1:A:79:G:H2'	1:A:80:A:N7	2.36	0.41
1:A:247:G:C6	1:A:278:G:N1	2.88	0.41
1:A:290:C:H2'	1:A:291:U:H6	1.85	0.41
1:A:378:G:C5	1:A:379:C:C4	3.08	0.41
1:A:517:G:N2	1:A:529:G:HO2'	2.12	0.41
1:A:946:A:C6	1:A:947:G:C6	3.08	0.41
1:A:1206:G:H2'	1:A:1207:2MG:O4'	2.21	0.41
1:A:1267:C:C4	1:A:1268:G:C6	3.08	0.41
2:B:210:VAL:O	2:B:214:LEU:HG	2.19	0.41
3:C:129:MET:CG	3:C:132:ARG:HE	2.33	0.41
4:D:111:ARG:O	4:D:115:ARG:N	2.46	0.41
10:J:54:SER:HA	10:J:55:PRO:HD3	1.91	0.41
12:L:30:LYS:HB3	12:L:30:LYS:HE3	1.89	0.41
1:A:269:C:H2'	1:A:270:A:H8	1.84	0.41
1:A:407:U:O2'	4:D:113:GLU:CG	2.66	0.41
1:A:431:A:C6	1:A:432:A:C4	3.09	0.41
1:A:445:G:H2'	1:A:446:G:O4'	2.21	0.41
1:A:546:A:H4'	1:A:548:G:O3'	2.20	0.41
1:A:591:U:H2'	1:A:592:G:H8	1.86	0.41
1:A:958:A:C6	1:A:959:A:N1	2.88	0.41
1:A:1135:U:O3'	1:A:1136:C:H6	2.03	0.41
1:A:1276:G:C2	1:A:1277:C:C2	3.09	0.41
1:A:1340:A:C2	1:A:1341:U:C2	3.08	0.41
1:A:1379:G:N7	7:G:2:PRO:HG2	2.35	0.41
1:A:1396:A:H2'	1:A:1397:C:C6	2.56	0.41
1:A:1399:C:O2'	1:A:1518:MA6:H93	2.20	0.41
1:A:1416:G:H3'	1:A:1417:G:H8	1.83	0.41
20:T:9:LYS:HE3	20:T:13:GLN:NE2	2.35	0.41
21:X:111:ARG:HD2	21:X:136:PHE:CD1	2.56	0.41
1:A:176:C:H2'	1:A:177:G:N3	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:G:C6	1:A:231:U:C4	3.07	0.41
1:A:642:A:C5	1:A:643:C:C4	3.09	0.41
1:A:739:C:O2	15:O:42:HIS:HE1	2.03	0.41
1:A:801:U:H2'	1:A:802:A:H8	1.81	0.41
1:A:803:G:C6	1:A:804:U:N3	2.89	0.41
1:A:861:G:C6	1:A:862:C:C4	3.09	0.41
1:A:885:G:C2	1:A:886:G:C5	3.09	0.41
1:A:923:A:C5	1:A:924:C:C4	3.09	0.41
1:A:992:U:C4	1:A:1045:C:C2	3.08	0.41
1:A:1164:G:C6	1:A:1165:U:C4	3.08	0.41
1:A:1219:A:C6	1:A:1220:G:C6	3.09	0.41
1:A:1309:G:C6	1:A:1310:G:C5	3.09	0.41
1:A:1349:A:H61	1:A:1373:G:H1'	1.86	0.41
1:A:1384:C:H2'	1:A:1385:G:H8	1.81	0.41
1:A:1423:G:H1	1:A:1477:U:H3	1.68	0.41
1:A:1455:G:H2'	1:A:1456:A:O4'	2.21	0.41
1:A:1468:A:C5	1:A:1469:C:C4	3.09	0.41
2:B:187:VAL:N	2:B:200:ILE:O	2.45	0.41
3:C:50:ALA:O	3:C:70:THR:OG1	2.38	0.41
4:D:27:ALA:O	4:D:30:THR:OG1	2.25	0.41
5:E:132:ASN:ND2	5:E:133:PRO:HD2	2.35	0.41
6:F:18:VAL:O	6:F:22:ILE:HG13	2.20	0.41
7:G:17:LYS:HZ3	9:I:42:GLU:HG2	1.86	0.41
7:G:47:LEU:HA	7:G:50:LEU:HD12	2.02	0.41
10:J:86:ALA:O	10:J:89:ARG:N	2.52	0.41
12:L:83:ARG:HG3	12:L:96:HIS:O	2.20	0.41
21:X:8:LEU:HD21	21:X:67:PRO:HB3	2.03	0.41
1:A:132:C:H2'	1:A:133:U:C6	2.50	0.41
1:A:409:U:P	4:D:23:SER:HG	2.43	0.41
1:A:417:G:C5	1:A:418:C:C4	3.08	0.41
1:A:429:U:O2	1:A:430:A:C8	2.73	0.41
1:A:436:C:H2'	1:A:437:U:C6	2.56	0.41
1:A:1004:A:C2	1:A:1005:A:H1'	2.56	0.41
1:A:1054:C:C2	1:A:1196:A:C5	3.08	0.41
1:A:1142:G:N1	1:A:1143:G:H1'	2.36	0.41
1:A:1427:C:C2	1:A:1428:A:C8	3.09	0.41
4:D:188:ARG:NH2	4:D:195:ILE:O	2.53	0.41
7:G:18:PHE:HB3	7:G:59:LEU:HD21	2.01	0.41
8:H:126:ILE:HD13	8:H:126:ILE:HA	1.78	0.41
9:I:55:VAL:HG13	9:I:57:MET:HG2	2.02	0.41
10:J:82:LYS:HE2	10:J:82:LYS:HB2	1.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:22:ALA:O	14:N:26:GLU:HG3	2.21	0.41
16:P:1:MET:HG2	16:P:3:THR:HG23	2.02	0.41
21:X:91:TYR:CE2	21:X:125:ILE:CD1	3.04	0.41
1:A:202:G:O2'	1:A:468:A:C8	2.73	0.41
1:A:265:G:H8	1:A:265:G:O5'	2.04	0.41
1:A:363:A:H5"	12:L:31:ARG:HE	1.82	0.41
1:A:447:G:O2'	1:A:487:A:N6	2.52	0.41
1:A:503:C:OP1	12:L:116:LYS:NZ	2.47	0.41
1:A:532:A:C2'	1:A:533:A:H5"	2.50	0.41
1:A:540:G:C2	1:A:541:G:C4	3.09	0.41
1:A:669:G:C6	1:A:738:C:N3	2.88	0.41
1:A:790:A:N7	1:A:791:G:C6	2.88	0.41
1:A:819:A:H4'	1:A:820:U:OP2	2.20	0.41
1:A:1092:A:C6	1:A:1093:A:C6	3.08	0.41
1:A:1170:A:H2'	1:A:1171:A:O4'	2.20	0.41
2:B:90:PHE:CZ	2:B:154:MET:HA	2.56	0.41
1:A:80:A:OP2	1:A:80:A:H8	2.03	0.41
1:A:134:G:C6	1:A:135:C:N3	2.89	0.41
1:A:158:G:C4	1:A:164:G:C2	3.08	0.41
1:A:208:U:H2'	1:A:210:C:N3	2.36	0.41
1:A:210:C:H1'	1:A:211:G:C2	2.56	0.41
1:A:228:A:C6	1:A:229:U:C4	3.08	0.41
1:A:236:A:H2'	1:A:237:G:C8	2.55	0.41
1:A:320:A:C2	1:A:321:A:C4	3.09	0.41
1:A:413:G:H1'	1:A:428:G:H22	1.85	0.41
1:A:469:C:H2'	1:A:470:C:O4'	2.21	0.41
1:A:497:G:H2'	1:A:498:A:C8	2.55	0.41
1:A:577:G:C2	1:A:578:C:C2	3.09	0.41
1:A:667:G:C2	1:A:668:G:C8	3.09	0.41
1:A:841:C:N4	1:A:846:G:C6	2.89	0.41
1:A:875:U:H1'	8:H:16:ASN:HD21	1.85	0.41
1:A:881:G:P	12:L:9:ARG:HH22	2.43	0.41
1:A:1000:A:N6	1:A:1040:U:H3	2.18	0.41
1:A:1055:A:C6	1:A:1206:G:C5	3.08	0.41
1:A:1084:G:C5	1:A:1085:U:C4	3.09	0.41
1:A:1181:G:O2'	1:A:1182:G:N7	2.45	0.41
1:A:1233:G:H2'	1:A:1234:C:C6	2.56	0.41
1:A:1398:A:C8	1:A:1504:G:N1	2.89	0.41
1:A:1502:A:C2	1:A:1503:A:C5	3.08	0.41
2:B:20:THR:O	2:B:23:TRP:HD1	2.04	0.41
2:B:90:PHE:CE2	2:B:154:MET:HA	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:162:PHE:HA	2:B:184:PHE:O	2.20	0.41
3:C:105:GLU:OE1	3:C:107:ARG:HD2	2.21	0.41
3:C:121:THR:HA	3:C:124:LEU:HD12	2.02	0.41
3:C:121:THR:HG21	3:C:187:SER:OG	2.20	0.41
4:D:54:GLN:H	4:D:54:GLN:HG3	1.74	0.41
6:F:15:SER:HA	6:F:18:VAL:CG1	2.49	0.41
6:F:17:GLN:O	6:F:21:MET:N	2.50	0.41
6:F:30:THR:HA	6:F:34:GLY:H	1.84	0.41
7:G:5:ARG:HD3	7:G:6:VAL:O	2.21	0.41
7:G:65:ALA:HA	7:G:128:ALA:HA	2.03	0.41
10:J:34:ALA:HB2	10:J:83:THR:HG22	2.02	0.41
12:L:63:VAL:HG21	12:L:95:TYR:HE1	1.86	0.41
14:N:96:LEU:HD12	14:N:97:LYS:H	1.85	0.41
15:O:24:SER:O	15:O:28:GLN:HG3	2.21	0.41
17:Q:78:VAL:HG12	17:Q:80:GLU:O	2.21	0.41
19:S:36:ARG:NH2	19:S:72:GLY:O	2.54	0.41
19:S:45:ILE:O	19:S:47:LEU:HG	2.20	0.41
20:T:49:LYS:HA	20:T:52:ASN:ND2	2.34	0.41
1:A:420:U:C2	1:A:422:C:N3	2.89	0.41
1:A:514:C:C2	1:A:515:G:C8	3.08	0.41
1:A:748:G:C4	1:A:749:A:C8	3.09	0.41
1:A:793:U:C4	1:A:794:A:C5	3.08	0.41
1:A:1106:G:O3'	3:C:172:ARG:HG2	2.21	0.41
1:A:1127:G:C6	1:A:1128:C:C4	3.09	0.41
1:A:1305:G:C5	1:A:1331:G:C2	3.09	0.41
1:A:1345:U:C2	1:A:1377:A:N1	2.89	0.41
1:A:1419:G:H1	1:A:1481:U:H3	1.68	0.41
1:A:1507:A:C4	1:A:1530:G:N2	2.88	0.41
4:D:71:GLN:HG2	4:D:75:TYR:HE2	1.86	0.41
7:G:103:TRP:CG	7:G:137:LYS:HD3	2.56	0.41
8:H:72:VAL:HG21	8:H:75:ILE:CG2	2.50	0.41
8:H:78:VAL:HG22	8:H:127:CYS:HA	2.02	0.41
10:J:51:VAL:O	10:J:62:ARG:HD3	2.21	0.41
11:K:86:VAL:HG13	11:K:112:ASP:HA	2.02	0.41
16:P:15:PRO:HB2	16:P:41:PRO:HG3	2.03	0.41
21:X:10:GLU:C	21:X:13:THR:HG22	2.41	0.41
21:X:39:TYR:HA	21:X:77:SER:O	2.21	0.41
1:A:6:G:HO2'	1:A:7:A:P	2.44	0.40
1:A:36:C:H2'	1:A:37:U:H6	1.85	0.40
1:A:144:G:C6	1:A:145:G:C6	3.09	0.40
1:A:257:G:H2'	1:A:258:G:H8	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:429:U:H1'	1:A:430:A:H5"	2.03	0.40
3:C:16:LYS:HD2	3:C:16:LYS:HA	1.85	0.40
3:C:169:ARG:NH2	3:C:172:ARG:HA	2.36	0.40
4:D:87:GLY:HA3	4:D:197:GLU:HG3	2.03	0.40
6:F:26:THR:O	6:F:30:THR:N	2.33	0.40
6:F:33:GLU:HB3	6:F:35:LYS:HZ3	1.85	0.40
7:G:69:VAL:HG22	7:G:135:VAL:HG13	2.03	0.40
7:G:73:VAL:HG12	7:G:142:HIS:CG	2.55	0.40
9:I:24:GLY:N	9:I:61:LEU:HA	2.32	0.40
9:I:119:ARG:HH12	9:I:126:GLN:H	1.69	0.40
16:P:34:GLU:OE2	16:P:56:ARG:CZ	2.70	0.40
18:R:11:CYS:HB3	18:R:48:ARG:NH1	2.36	0.40
20:T:34:LYS:H	20:T:34:LYS:HG2	1.58	0.40
1:A:8:A:C6	4:D:206:LYS:HB2	2.56	0.40
1:A:35:G:C6	1:A:36:C:N4	2.90	0.40
1:A:142:G:C2	1:A:222:C:C2	3.09	0.40
1:A:579:A:H2'	1:A:580:C:H6	1.86	0.40
1:A:807:A:C6	1:A:808:C:C4	3.10	0.40
1:A:849:G:C2	1:A:850:U:H1'	2.56	0.40
1:A:932:C:C5	7:G:3:ARG:HD3	2.56	0.40
1:A:978:A:O2'	1:A:1322:C:N3	2.54	0.40
1:A:1105:A:O2'	1:A:1106:G:H5'	2.20	0.40
1:A:1251:A:H2'	1:A:1252:A:C8	2.56	0.40
1:A:1275:A:C2	1:A:1276:G:H1'	2.56	0.40
1:A:1282:C:H2'	1:A:1283:U:H6	1.86	0.40
1:A:1345:U:OP1	9:I:122:ARG:HD3	2.22	0.40
1:A:1365:G:C2	1:A:1366:C:C2	3.10	0.40
1:A:1462:C:H2'	1:A:1463:U:C6	2.57	0.40
4:D:19:LEU:HB3	4:D:64:ILE:HD12	2.03	0.40
7:G:57:SER:HB2	7:G:60:GLU:OE1	2.21	0.40
7:G:70:ARG:HH12	7:G:97:ASN:ND2	2.19	0.40
7:G:112:GLY:O	7:G:119:ARG:NE	2.52	0.40
9:I:27:LYS:HE2	9:I:27:LYS:HB3	1.83	0.40
10:J:68:ARG:HG3	10:J:70:HIS:HE1	1.86	0.40
14:N:17:ALA:HA	14:N:55:SER:HA	2.03	0.40
14:N:84:VAL:CG1	14:N:85:ARG:N	2.84	0.40
14:N:86:GLU:HB3	14:N:90:ARG:HH12	1.87	0.40
15:O:7:ALA:O	15:O:11:ILE:N	2.53	0.40
1:A:412:A:H2'	1:A:414:A:H5'	2.03	0.40
1:A:414:A:H2'	1:A:415:A:O4'	2.21	0.40
1:A:577:G:C8	1:A:816:A:N1	2.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:692:U:C2	1:A:695:A:C8	3.10	0.40
1:A:927:G:H21	1:A:1391:U:C5'	2.35	0.40
1:A:947:G:H2'	1:A:948:C:C6	2.56	0.40
1:A:1032:G:C2	1:A:1033:G:C8	3.08	0.40
1:A:1263:C:H2'	1:A:1264:U:H6	1.87	0.40
1:A:1458:G:C4	1:A:1459:G:C8	3.09	0.40
8:H:41:LYS:HZ3	8:H:48:ASP:HA	1.86	0.40
10:J:53:ILE:HD13	10:J:63:ASP:CG	2.42	0.40
12:L:56:ARG:HG2	12:L:57:LEU:O	2.21	0.40
13:M:44:LYS:HG2	13:M:47:GLU:OE2	2.21	0.40
16:P:76:LYS:HE2	16:P:76:LYS:HB2	1.84	0.40
21:X:10:GLU:CA	21:X:13:THR:HG22	2.51	0.40
1:A:77:A:H3'	1:A:78:A:C8	2.55	0.40
1:A:144:G:H2'	1:A:145:G:C8	2.56	0.40
1:A:550:G:H2'	1:A:551:U:C6	2.57	0.40
1:A:651:C:N4	1:A:753:A:OP2	2.54	0.40
1:A:659:U:OP1	15:O:5:THR:HG22	2.22	0.40
1:A:886:G:H2'	1:A:887:G:O4'	2.22	0.40
1:A:977:A:O3'	1:A:980:C:N4	2.54	0.40
1:A:1054:C:C2	1:A:1196:A:C6	3.10	0.40
1:A:1125:U:C2	1:A:1127:G:C8	3.09	0.40
1:A:1292:G:C2	1:A:1293:C:C2	3.09	0.40
3:C:40:ARG:NH1	3:C:55:ILE:HG23	2.36	0.40
3:C:40:ARG:O	3:C:44:THR:HG23	2.21	0.40
4:D:9:LEU:HD23	4:D:9:LEU:HA	1.83	0.40
4:D:88:GLU:O	4:D:91:LEU:N	2.54	0.40
5:E:143:GLY:HA2	5:E:146:ASN:ND2	2.36	0.40
7:G:133:THR:HA	7:G:136:LYS:HE3	2.03	0.40
9:I:118:LEU:HB3	9:I:123:ARG:O	2.21	0.40
12:L:31:ARG:HA	12:L:81:LEU:HA	2.04	0.40
12:L:37:VAL:HG12	12:L:53:CYS:SG	2.61	0.40
17:Q:62:ARG:CG	17:Q:76:VAL:HG22	2.51	0.40
19:S:34:TRP:HA	19:S:52:HIS:HD1	1.86	0.40
20:T:44:LYS:O	20:T:48:GLN:N	2.29	0.40
20:T:80:THR:OG1	20:T:81:ALA:N	2.55	0.40
21:X:25:GLY:HA3	21:X:39:TYR:CD2	2.57	0.40
1:A:168:G:N3	1:A:168:G:H2'	2.37	0.40
1:A:322:C:H2'	1:A:323:U:C6	2.53	0.40
1:A:398:U:C2	1:A:399:G:C8	3.10	0.40
1:A:678:U:H2'	1:A:679:C:O4'	2.22	0.40
1:A:793:U:C4	1:A:794:A:C6	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1082:A:H2'	1:A:1083:U:C6	2.57	0.40
1:A:1227:A:O3'	13:M:114:LYS:HB2	2.21	0.40
1:A:1229:A:H2'	1:A:1230:C:H6	1.87	0.40
1:A:1304:G:H1'	1:A:1334:G:N2	2.37	0.40
1:A:1438:G:C6	1:A:1439:G:C5	3.10	0.40
2:B:70:VAL:N	2:B:162:PHE:O	2.50	0.40
3:C:25:ASN:O	3:C:29:PHE:HB2	2.21	0.40
3:C:87:LEU:HA	3:C:87:LEU:HD23	1.80	0.40
4:D:94:LEU:HD23	4:D:94:LEU:HA	1.84	0.40
8:H:78:VAL:HG23	8:H:125:ILE:O	2.22	0.40
11:K:32:VAL:CG2	11:K:45:ALA:HB3	2.51	0.40
13:M:85:CYS:SG	13:M:87:ARG:HG3	2.62	0.40
13:M:95:LEU:HB3	13:M:96:PRO:HD2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	222/241 (92%)	217 (98%)	5 (2%)	0	100	100
3	C	209/233 (90%)	195 (93%)	14 (7%)	0	100	100
4	D	203/206 (98%)	194 (96%)	9 (4%)	0	100	100
5	E	154/167 (92%)	139 (90%)	15 (10%)	0	100	100
6	F	104/135 (77%)	89 (86%)	15 (14%)	0	100	100
7	G	144/179 (80%)	134 (93%)	10 (7%)	0	100	100
8	H	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
9	I	125/130 (96%)	107 (86%)	18 (14%)	0	100	100
10	J	97/103 (94%)	92 (95%)	5 (5%)	0	100	100
11	K	114/129 (88%)	99 (87%)	15 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	L	120/124 (97%)	107 (89%)	13 (11%)	0	100	100
13	M	112/118 (95%)	101 (90%)	11 (10%)	0	100	100
14	N	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
15	O	86/89 (97%)	77 (90%)	9 (10%)	0	100	100
16	P	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
17	Q	78/84 (93%)	73 (94%)	5 (6%)	0	100	100
18	R	63/75 (84%)	62 (98%)	1 (2%)	0	100	100
19	S	80/92 (87%)	68 (85%)	12 (15%)	0	100	100
20	T	84/87 (97%)	71 (84%)	13 (16%)	0	100	100
21	X	149/151 (99%)	134 (90%)	15 (10%)	0	100	100
All	All	2449/2656 (92%)	2244 (92%)	205 (8%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	186/199 (94%)	186 (100%)	0	100	100
3	C	172/190 (90%)	172 (100%)	0	100	100
4	D	172/173 (99%)	170 (99%)	2 (1%)	71	84
5	E	119/126 (94%)	119 (100%)	0	100	100
6	F	92/116 (79%)	92 (100%)	0	100	100
7	G	121/147 (82%)	121 (100%)	0	100	100
8	H	104/105 (99%)	103 (99%)	1 (1%)	76	86
9	I	105/107 (98%)	105 (100%)	0	100	100
10	J	87/90 (97%)	87 (100%)	0	100	100
11	K	89/99 (90%)	87 (98%)	2 (2%)	52	73
12	L	102/103 (99%)	102 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	M	92/96 (96%)	92 (100%)	0	100	100
14	N	83/84 (99%)	83 (100%)	0	100	100
15	O	76/77 (99%)	76 (100%)	0	100	100
16	P	65/65 (100%)	64 (98%)	1 (2%)	65	81
17	Q	74/78 (95%)	72 (97%)	2 (3%)	44	69
18	R	56/65 (86%)	56 (100%)	0	100	100
19	S	72/79 (91%)	72 (100%)	0	100	100
20	T	65/66 (98%)	64 (98%)	1 (2%)	65	81
21	X	130/130 (100%)	127 (98%)	3 (2%)	50	72
All	All	2062/2195 (94%)	2050 (99%)	12 (1%)	86	92

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	35	GLU
4	D	82	LEU
8	H	127	CYS
11	K	69	ARG
11	K	77	TYR
16	P	66	THR
17	Q	68	SER
17	Q	80	GLU
20	T	43	ASP
21	X	82	ASP
21	X	104	ARG
21	X	150	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	122	GLN
3	C	140	ASN
3	C	185	ASN
4	D	131	ASN
4	D	136	GLN
4	D	196	ASN
5	E	83	HIS
5	E	89	HIS

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Mol	Chain	Res	Type
5	E	132	ASN
5	E	135	ASN
6	F	14	GLN
7	G	52	GLN
7	G	68	ASN
7	G	122	ASN
8	H	76	GLN
8	H	118	GLN
9	I	37	GLN
9	I	75	GLN
10	J	70	HIS
11	K	28	ASN
11	K	40	ASN
11	K	81	ASN
11	K	118	HIS
12	L	75	GLN
14	N	4	GLN
14	N	49	GLN
15	O	28	GLN
15	O	40	GLN
15	O	62	GLN
15	O	80	GLN
17	Q	9	GLN
18	R	19	GLN
18	R	52	GLN
20	T	13	GLN
20	T	52	ASN
20	T	70	ASN
21	X	47	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1517/1542 (98%)	388 (25%)	10 (0%)

All (388) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	5	U
1	A	9	G

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Mol	Chain	Res	Type
1	A	16	A
1	A	22	G
1	A	29	U
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	50	A
1	A	51	A
1	A	58	C
1	A	69	G
1	A	71	A
1	A	75	G
1	A	76	G
1	A	80	A
1	A	81	A
1	A	84	U
1	A	85	U
1	A	86	G
1	A	87	C
1	A	89	U
1	A	90	C
1	A	91	U
1	A	94	G
1	A	95	C
1	A	120	A
1	A	121	U
1	A	122	G
1	A	130	A
1	A	131	A
1	A	134	G
1	A	142	G
1	A	148	G
1	A	159	G
1	A	163	C
1	A	164	G
1	A	168	G
1	A	173	U
1	A	182	A
1	A	183	C
1	A	191	G
1	A	196	A

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Mol	Chain	Res	Type
1	A	197	A
1	A	204	G
1	A	205	A
1	A	206	C
1	A	207	C
1	A	210	C
1	A	212	G
1	A	226	G
1	A	240	G
1	A	244	U
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	269	C
1	A	280	C
1	A	289	G
1	A	305	G
1	A	306	A
1	A	321	A
1	A	328	C
1	A	332	G
1	A	343	U
1	A	347	G
1	A	351	G
1	A	352	C
1	A	354	G
1	A	363	A
1	A	367	U
1	A	368	U
1	A	369	G
1	A	372	C
1	A	397	A
1	A	398	U
1	A	406	G
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	423	G

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Mol	Chain	Res	Type
1	A	424	G
1	A	429	U
1	A	439	U
1	A	457	G
1	A	458	U
1	A	459	A
1	A	465	A
1	A	467	U
1	A	468	A
1	A	475	C
1	A	481	G
1	A	484	G
1	A	486	U
1	A	495	A
1	A	496	A
1	A	497	G
1	A	499	A
1	A	505	G
1	A	509	A
1	A	511	C
1	A	512	U
1	A	516	PSU
1	A	517	G
1	A	518	C
1	A	519	C
1	A	520	A
1	A	521	G
1	A	523	A
1	A	524	G
1	A	527	G7M
1	A	530	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	545	C
1	A	547	A
1	A	559	A
1	A	562	U
1	A	564	C
1	A	572	A
1	A	573	A
1	A	576	C

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Mol	Chain	Res	Type
1	A	577	G
1	A	596	A
1	A	607	A
1	A	618	C
1	A	619	U
1	A	639	G
1	A	650	G
1	A	653	U
1	A	659	U
1	A	665	A
1	A	673	A
1	A	682	G
1	A	686	U
1	A	687	A
1	A	688	G
1	A	693	G
1	A	701	U
1	A	702	A
1	A	703	G
1	A	704	A
1	A	706	A
1	A	707	U
1	A	710	G
1	A	720	C
1	A	723	U
1	A	724	G
1	A	733	G
1	A	752	G
1	A	753	A
1	A	755	G
1	A	762	U
1	A	774	G
1	A	776	G
1	A	777	A
1	A	787	A
1	A	788	U
1	A	790	A
1	A	791	G
1	A	792	A
1	A	793	U
1	A	794	A
1	A	798	U

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Mol	Chain	Res	Type
1	A	808	C
1	A	815	A
1	A	817	C
1	A	819	A
1	A	820	U
1	A	821	G
1	A	828	U
1	A	832	G
1	A	836	G
1	A	839	C
1	A	840	C
1	A	842	U
1	A	843	U
1	A	845	A
1	A	848	C
1	A	849	G
1	A	869	G
1	A	871	U
1	A	872	A
1	A	902	G
1	A	914	A
1	A	919	A
1	A	923	A
1	A	924	C
1	A	925	G
1	A	926	G
1	A	927	G
1	A	928	G
1	A	929	G
1	A	931	C
1	A	934	C
1	A	935	A
1	A	939	G
1	A	940	C
1	A	954	G
1	A	958	A
1	A	959	A
1	A	960	U
1	A	966	2MG
1	A	968	A
1	A	969	A
1	A	971	G

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Mol	Chain	Res	Type
1	A	975	A
1	A	976	G
1	A	977	A
1	A	983	A
1	A	984	C
1	A	989	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1001	C
1	A	1004	A
1	A	1007	U
1	A	1014	A
1	A	1015	G
1	A	1017	U
1	A	1018	G
1	A	1021	A
1	A	1026	G
1	A	1028	C
1	A	1029	U
1	A	1030	U
1	A	1031	C
1	A	1035	A
1	A	1037	C
1	A	1038	C
1	A	1043	G
1	A	1045	C
1	A	1050	G
1	A	1053	G
1	A	1054	C
1	A	1064	G
1	A	1065	U
1	A	1066	C
1	A	1067	A
1	A	1070	U
1	A	1085	U
1	A	1089	G
1	A	1094	G
1	A	1101	A
1	A	1104	G
1	A	1106	G
1	A	1108	G

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Mol	Chain	Res	Type
1	A	1124	G
1	A	1125	U
1	A	1132	C
1	A	1133	G
1	A	1135	U
1	A	1136	C
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1140	C
1	A	1141	C
1	A	1142	G
1	A	1143	G
1	A	1146	A
1	A	1150	A
1	A	1152	A
1	A	1154	G
1	A	1156	G
1	A	1157	A
1	A	1158	C
1	A	1159	U
1	A	1160	G
1	A	1168	U
1	A	1169	A
1	A	1184	G
1	A	1192	C
1	A	1195	C
1	A	1196	A
1	A	1197	A
1	A	1198	G
1	A	1201	A
1	A	1209	C
1	A	1211	U
1	A	1213	A
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1228	C
1	A	1238	A
1	A	1239	A
1	A	1240	U
1	A	1241	G

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Mol	Chain	Res	Type
1	A	1250	A
1	A	1253	G
1	A	1257	A
1	A	1258	G
1	A	1259	C
1	A	1260	G
1	A	1277	C
1	A	1278	G
1	A	1280	A
1	A	1286	U
1	A	1287	A
1	A	1288	A
1	A	1297	G
1	A	1300	G
1	A	1302	C
1	A	1303	C
1	A	1305	G
1	A	1317	C
1	A	1323	G
1	A	1336	C
1	A	1337	G
1	A	1342	C
1	A	1344	C
1	A	1346	A
1	A	1353	G
1	A	1363	A
1	A	1364	U
1	A	1368	A
1	A	1370	G
1	A	1378	C
1	A	1379	G
1	A	1381	U
1	A	1386	G
1	A	1389	C
1	A	1391	U
1	A	1392	G
1	A	1393	U
1	A	1394	A
1	A	1398	A
1	A	1399	C
1	A	1412	C
1	A	1414	U

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Mol	Chain	Res	Type
1	A	1415	G
1	A	1416	G
1	A	1418	A
1	A	1425	U
1	A	1426	G
1	A	1427	C
1	A	1429	A
1	A	1431	A
1	A	1432	G
1	A	1441	A
1	A	1442	G
1	A	1443	C
1	A	1445	U
1	A	1446	A
1	A	1448	C
1	A	1452	C
1	A	1453	G
1	A	1454	G
1	A	1463	U
1	A	1469	C
1	A	1471	U
1	A	1473	G
1	A	1474	U
1	A	1479	C
1	A	1480	A
1	A	1485	U
1	A	1486	G
1	A	1488	G
1	A	1489	G
1	A	1490	U
1	A	1491	G
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1507	A
1	A	1508	A
1	A	1509	C
1	A	1516	2MG
1	A	1520	C
1	A	1529	G
1	A	1530	G

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Mol	Chain	Res	Type
1	A	1531	A
1	A	1532	U
1	A	1535	C
1	A	1536	C
1	A	1537	U
1	A	1538	C
1	A	1540	U

All (10) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	531	U
1	A	686	U
1	A	753	A
1	A	953	G
1	A	983	A
1	A	1103	C
1	A	1208	C
1	A	1279	G
1	A	1286	U
1	A	1531	A

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

9 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\#\|Z\| > 2$
1	2MG	A	966	1	18,26,27	0.98	1 (5%)	16,38,41	1.20	3 (18%)
1	MA6	A	1519	1	18,26,27	0.93	1 (5%)	19,38,41	1.60	5 (26%)
1	2MG	A	1516	1	18,26,27	0.90	1 (5%)	16,38,41	1.22	3 (18%)
1	PSU	A	516	1	18,21,22	1.46	3 (16%)	22,30,33	2.13	5 (22%)
1	5MC	A	967	1	18,22,23	0.91	2 (11%)	26,32,35	1.16	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	2MG	A	1207	1	18,26,27	1.03	1 (5%)	16,38,41	1.17	3 (18%)
12	D2T	L	89	12	7,9,10	1.07	1 (14%)	6,11,13	1.69	1 (16%)
1	G7M	A	527	1	20,26,27	1.05	1 (5%)	17,39,42	1.37	4 (23%)
1	MA6	A	1518	1	18,26,27	0.91	1 (5%)	19,38,41	1.61	5 (26%)

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
1	2MG	A	966	1	-	2/5/27/28	0/3/3/3
1	MA6	A	1519	1	-	5/7/29/30	0/3/3/3
1	2MG	A	1516	1	-	3/5/27/28	0/3/3/3
1	PSU	A	516	1	-	2/7/25/26	0/2/2/2
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
1	2MG	A	1207	1	-	0/5/27/28	0/3/3/3
12	D2T	L	89	12	-	3/7/12/14	-
1	G7M	A	527	1	-	3/3/25/26	0/3/3/3
1	MA6	A	1518	1	-	6/7/29/30	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	516	PSU	C4-N3	-3.34	1.32	1.38
1	A	1207	2MG	C6-N1	-3.03	1.33	1.37
1	A	966	2MG	C6-N1	-2.96	1.33	1.37
1	A	967	5MC	C6-N1	-2.77	1.33	1.38
12	L	89	D2T	O-C	2.73	1.30	1.19
1	A	527	G7M	C8-N9	2.58	1.37	1.33
1	A	1516	2MG	C6-N1	-2.44	1.34	1.37
1	A	516	PSU	C2-N3	-2.38	1.33	1.37
1	A	1519	MA6	C5-C4	2.33	1.47	1.40
1	A	1518	MA6	C5-C4	2.31	1.47	1.40
1	A	516	PSU	O4'-C1'	-2.13	1.40	1.43
1	A	967	5MC	C6-C5	2.01	1.37	1.34

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	516	PSU	N1-C2-N3	6.55	122.55	115.13
1	A	516	PSU	C4-N3-C2	-4.61	119.70	126.34
1	A	967	5MC	C5-C6-N1	-3.68	119.55	123.34
1	A	1519	MA6	C9-N6-C6	-3.62	108.54	119.51
1	A	1518	MA6	C9-N6-C6	-3.37	109.32	119.51
1	A	516	PSU	O2-C2-N1	-3.22	119.25	122.79
1	A	1518	MA6	N3-C2-N1	-3.22	123.64	128.68
1	A	1519	MA6	N3-C2-N1	-3.18	123.71	128.68
1	A	1519	MA6	C4-C5-N7	-3.14	106.13	109.40
12	L	89	D2T	O-C-CA	-3.03	116.84	124.78
1	A	516	PSU	C5-C6-N1	-3.00	117.61	122.11
1	A	1518	MA6	C4-C5-N7	-2.95	106.32	109.40
1	A	1516	2MG	CM2-N2-C2	-2.68	117.95	123.86
1	A	1518	MA6	C10-N6-C9	-2.54	107.95	116.12
1	A	527	G7M	C3'-C2'-C1'	-2.53	97.17	100.98
1	A	966	2MG	CM2-N2-C2	-2.52	118.30	123.86
1	A	1207	2MG	C5-C6-N1	2.49	118.35	113.95
1	A	1518	MA6	N1-C6-N6	2.38	119.56	117.06
1	A	966	2MG	C5-C6-N1	2.36	118.12	113.95
1	A	1207	2MG	C8-N7-C5	2.35	107.46	102.99
1	A	966	2MG	C8-N7-C5	2.32	107.40	102.99
1	A	527	G7M	O4'-C4'-C3'	-2.25	100.67	105.11
1	A	1516	2MG	C5-C6-N1	2.19	117.81	113.95
1	A	527	G7M	O6-C6-N1	-2.17	118.09	120.65
1	A	967	5MC	C5-C4-N3	-2.16	119.34	121.67
1	A	1519	MA6	C10-N6-C6	-2.11	113.11	119.51
1	A	1519	MA6	C10-N6-C9	-2.09	109.40	116.12
1	A	1207	2MG	CM2-N2-C2	-2.05	119.33	123.86
1	A	516	PSU	O4'-C1'-C2'	2.05	108.04	105.14
1	A	527	G7M	O4'-C1'-C2'	-2.05	103.93	106.93
1	A	967	5MC	O2-C2-N3	-2.04	119.02	122.33
1	A	1516	2MG	C8-N7-C5	2.03	106.86	102.99

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	L	89	D2T	CA-CB-SB-CB1
12	L	89	D2T	CG-CB-SB-CB1
12	L	89	D2T	SB-CB-CG-OD2
1	A	527	G7M	C3'-C4'-C5'-O5'
1	A	966	2MG	N1-C2-N2-CM2
1	A	966	2MG	N3-C2-N2-CM2

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Mol	Chain	Res	Type	Atoms
1	A	1516	2MG	O4'-C4'-C5'-O5'
1	A	1516	2MG	C3'-C4'-C5'-O5'
1	A	1518	MA6	C5-C6-N6-C10
1	A	1519	MA6	O4'-C4'-C5'-O5'
1	A	1519	MA6	C3'-C4'-C5'-O5'
1	A	1519	MA6	C5-C6-N6-C9
1	A	1519	MA6	C5-C6-N6-C10
1	A	1518	MA6	O4'-C4'-C5'-O5'
1	A	1518	MA6	C3'-C4'-C5'-O5'
1	A	1519	MA6	N1-C6-N6-C9
1	A	527	G7M	O4'-C4'-C5'-O5'
1	A	1518	MA6	C5-C6-N6-C9
1	A	516	PSU	C3'-C4'-C5'-O5'
1	A	516	PSU	O4'-C4'-C5'-O5'
1	A	527	G7M	C4'-C5'-O5'-P
1	A	1516	2MG	C4'-C5'-O5'-P
1	A	1518	MA6	C4'-C5'-O5'-P
1	A	1518	MA6	N1-C6-N6-C9

There are no ring outliers.

8 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	966	2MG	1	0
1	A	1519	MA6	3	0
1	A	1516	2MG	1	0
1	A	516	PSU	1	0
1	A	967	5MC	5	0
1	A	1207	2MG	3	0
12	L	89	D2T	1	0
1	A	1518	MA6	6	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 58 ligands modelled in this entry, 58 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

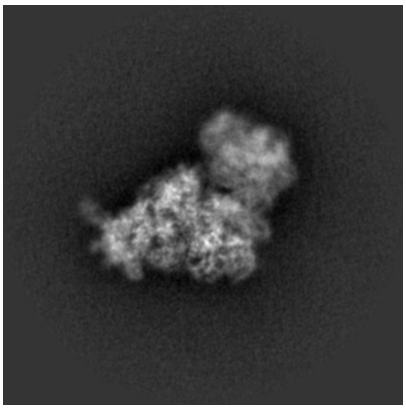
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-12248. These allow visual inspection of the internal detail of the map and identification of artifacts.

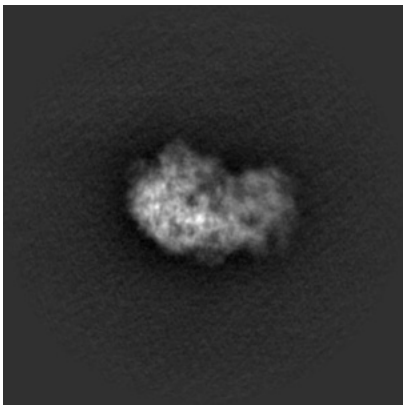
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

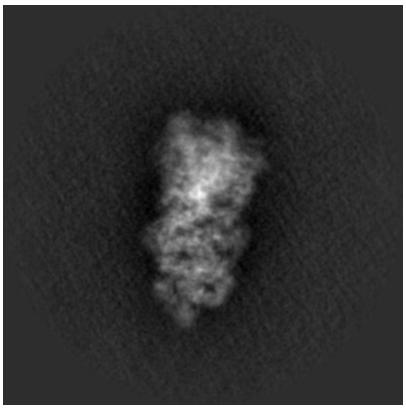
6.1.1 Primary map



X

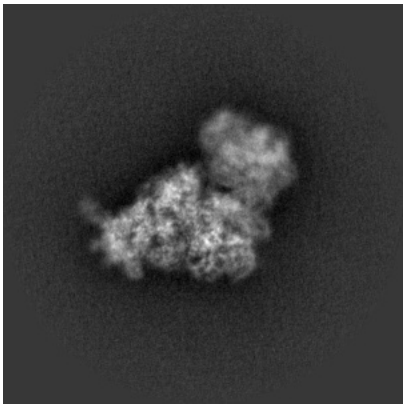


Y

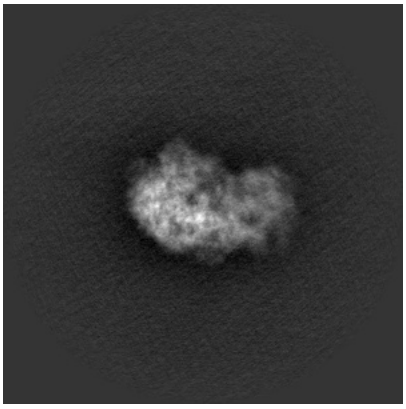


Z

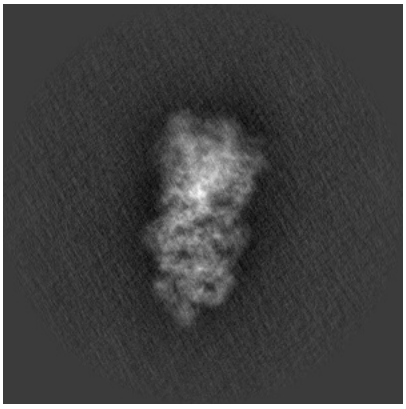
6.1.2 Raw map



X



Y

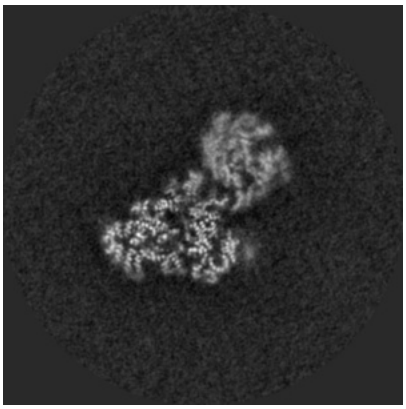


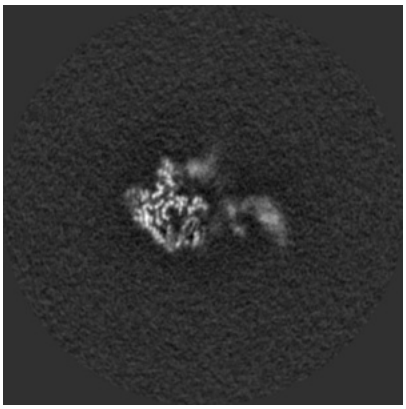
Z

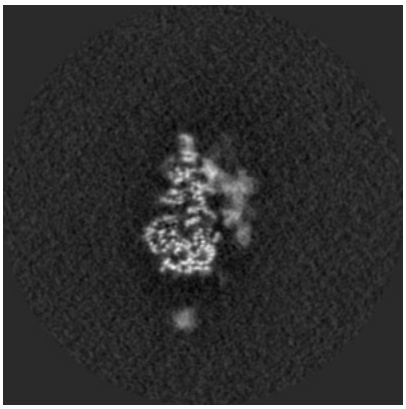
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

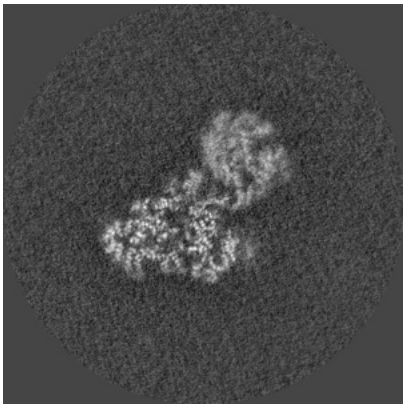
6.2.1 Primary map

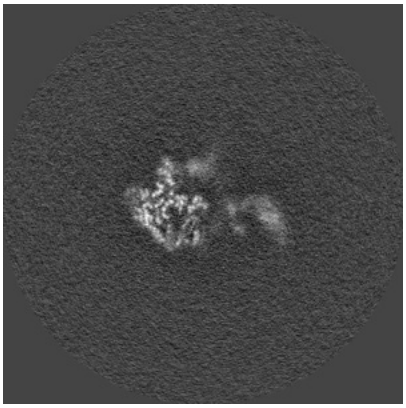

X Index: 192

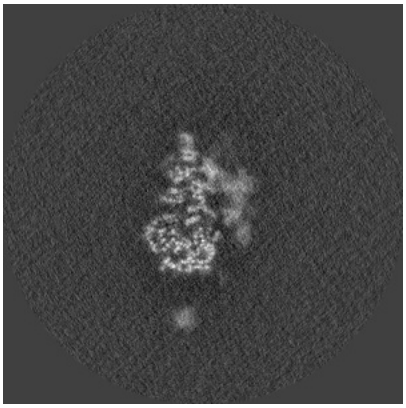

Y Index: 192


Z Index: 192

6.2.2 Raw map


X Index: 192

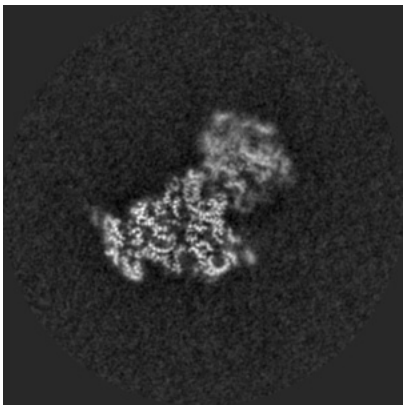

Y Index: 192

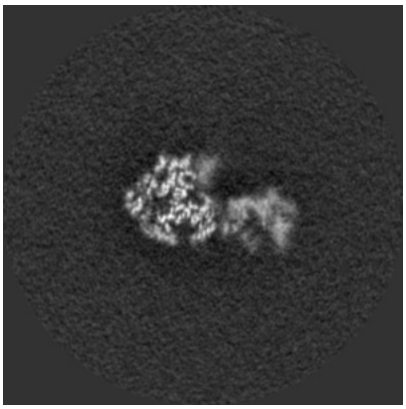

Z Index: 192

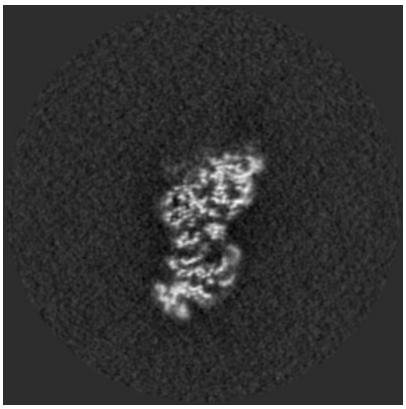
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

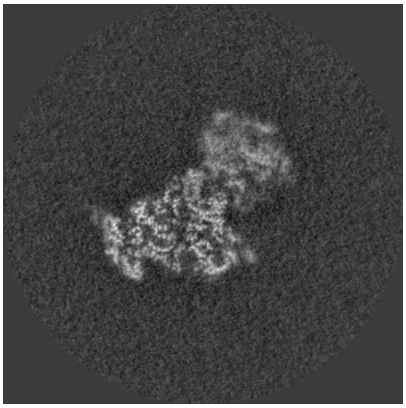
6.3.1 Primary map

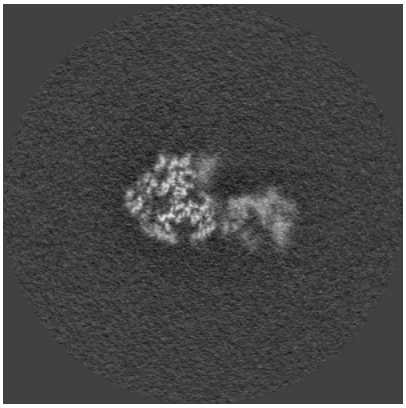

X Index: 188

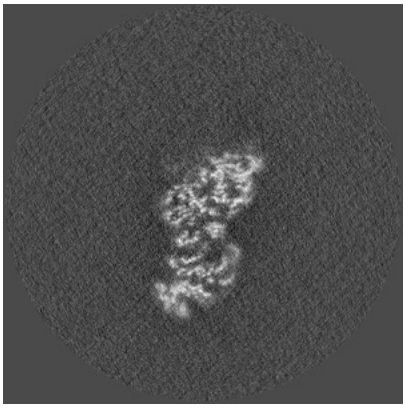

Y Index: 203


Z Index: 155

6.3.2 Raw map


X Index: 188

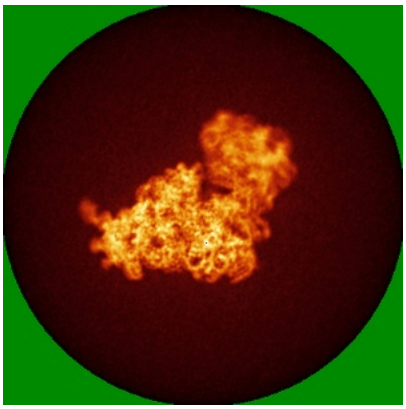

Y Index: 203

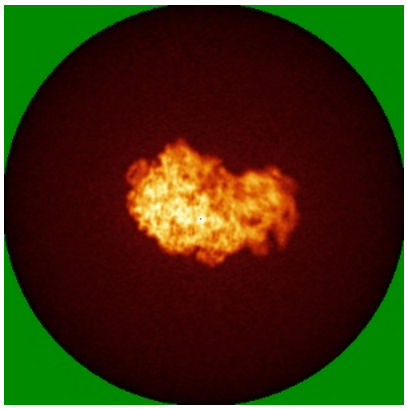

Z Index: 155

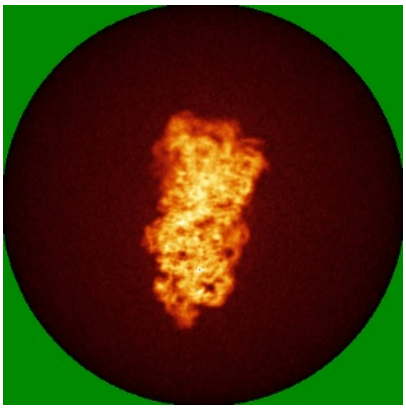
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

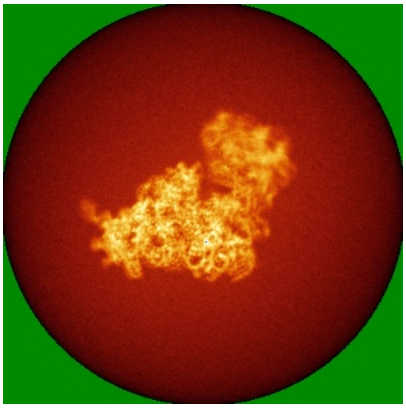
6.4.1 Primary map

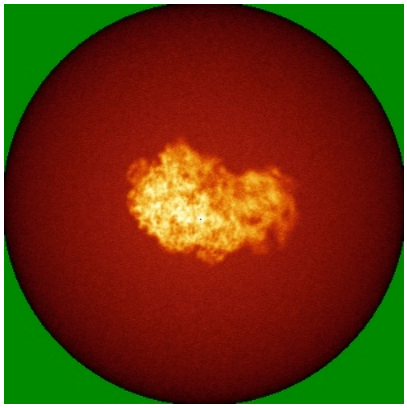

X

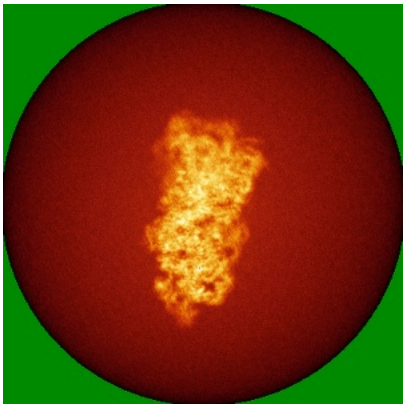

Y


Z

6.4.2 Raw map


X


Y


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

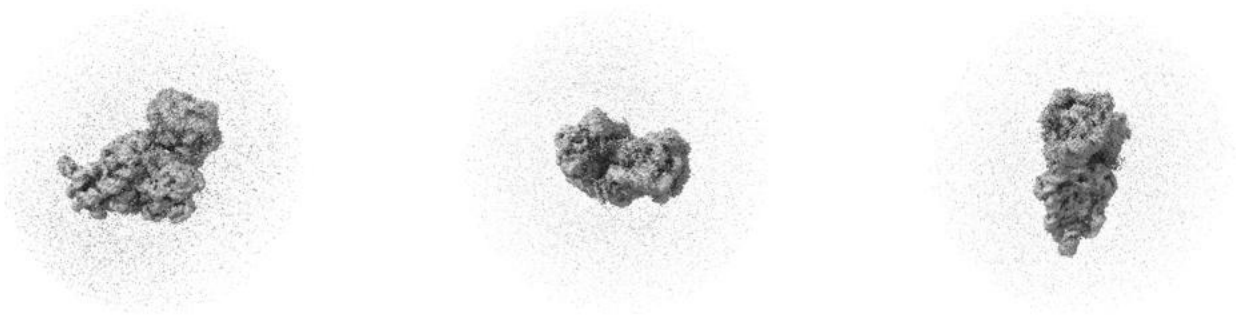
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.016. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

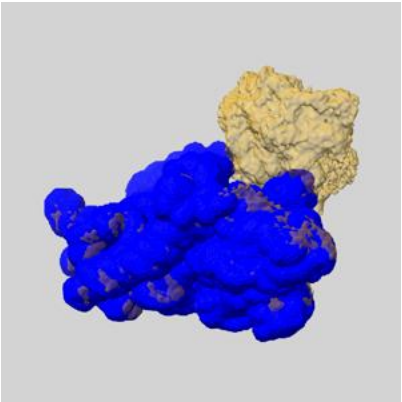
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

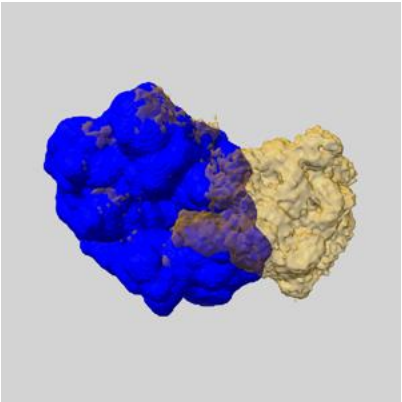
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

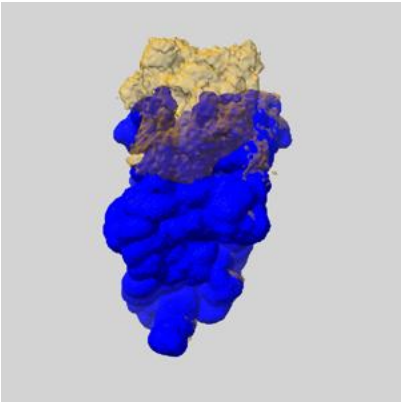
6.6.1 emd_12248_msk_1.map (i)



X

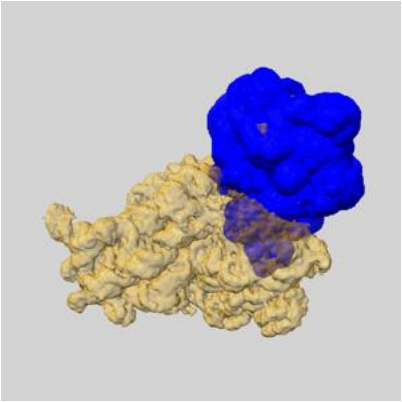


Y

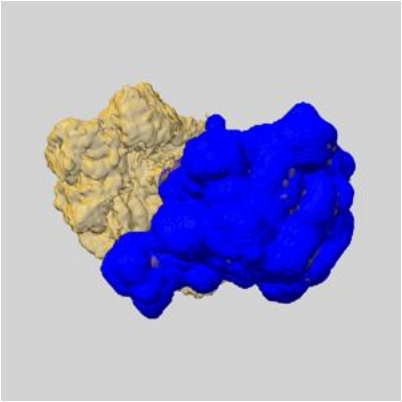


Z

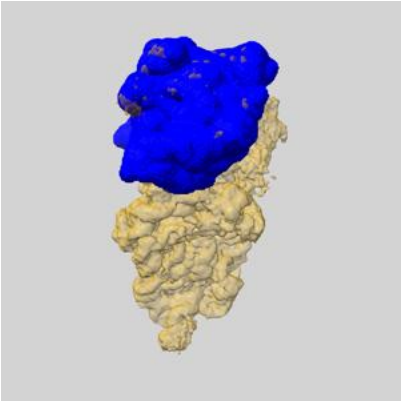
6.6.2 emd_12248_msk_2.map (i)



X



Y

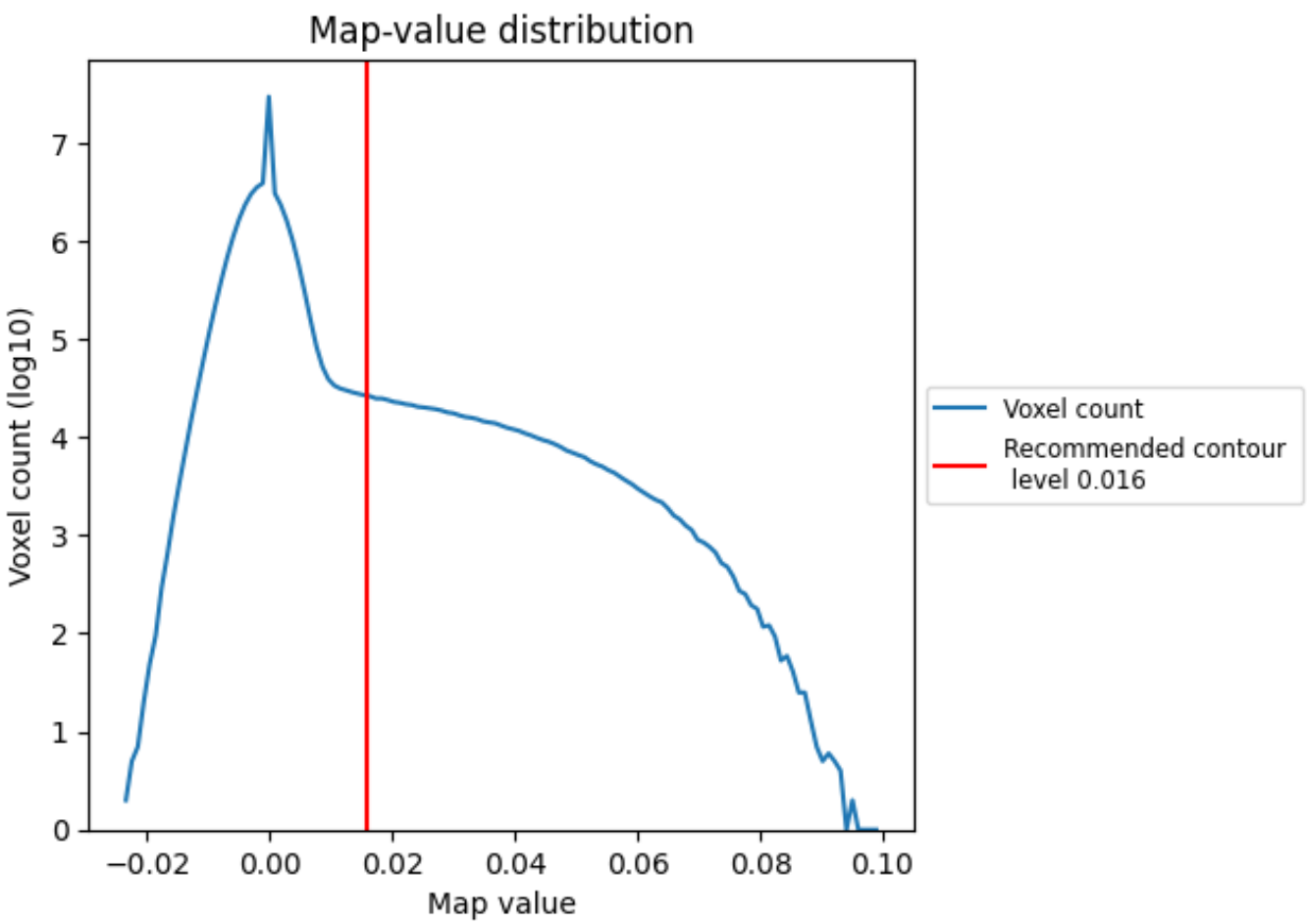


Z

7 Map analysis (i)

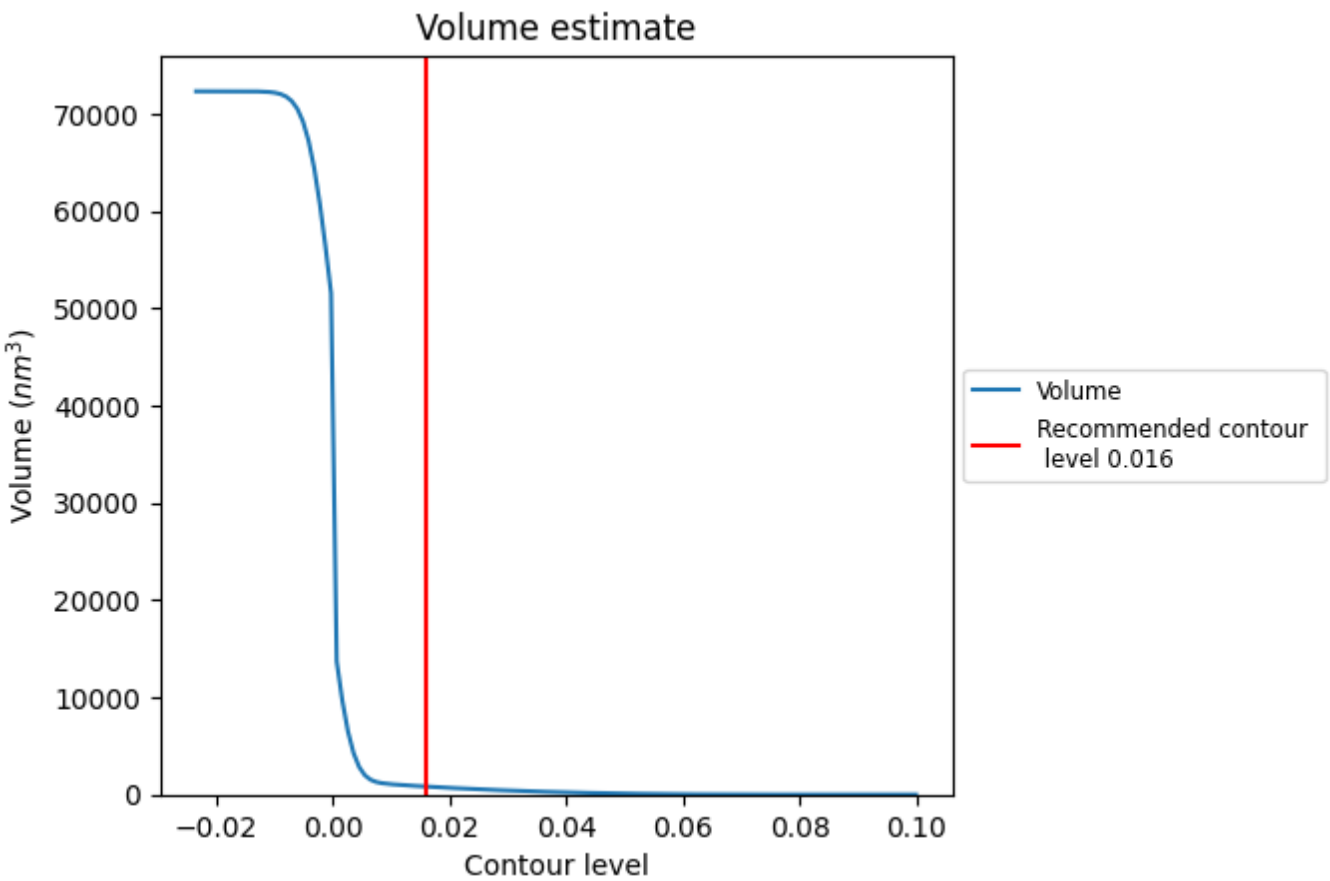
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

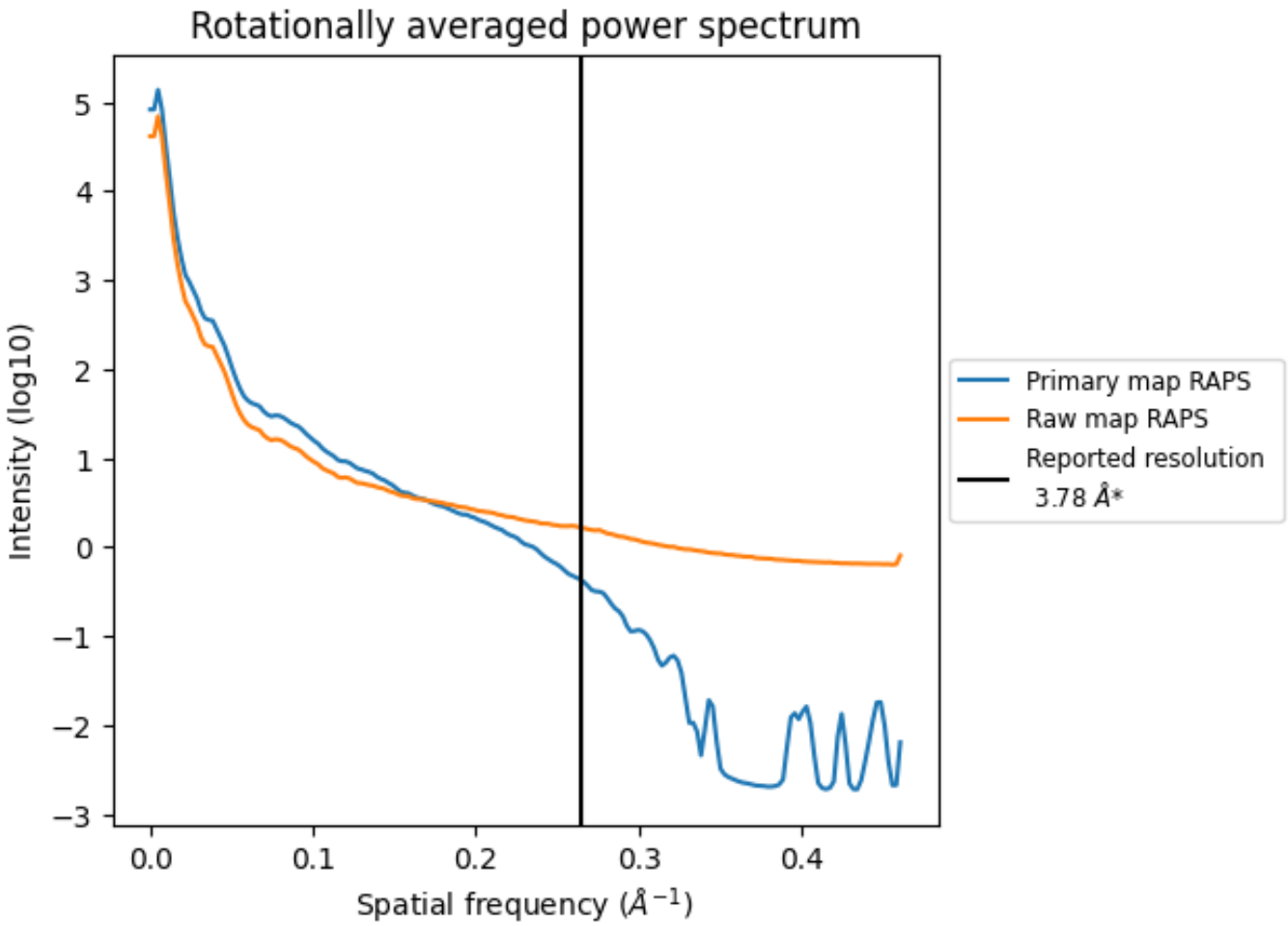
7.2 Volume estimate (i)



The volume at the recommended contour level is 821 nm^3; this corresponds to an approximate mass of 742 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

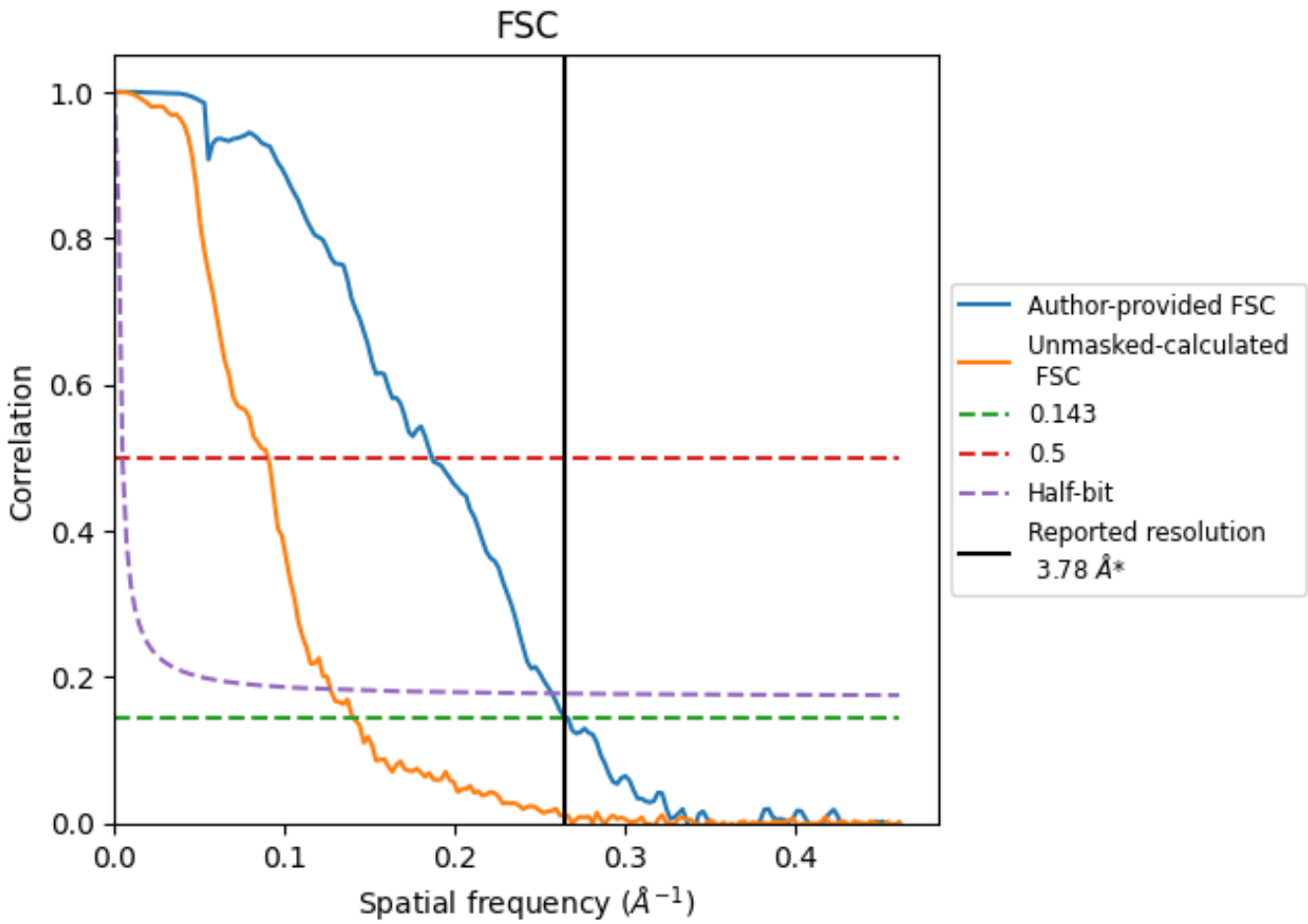


*Reported resolution corresponds to spatial frequency of 0.265 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.265 Å^{-1}

8.2 Resolution estimates (i)

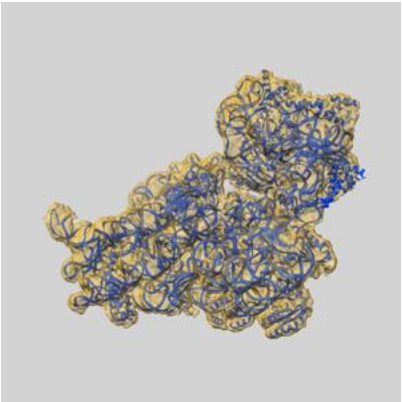
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.78	-	-
Author-provided FSC curve	3.76	5.36	3.89
Unmasked-calculated*	7.11	11.11	7.88

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.11 differs from the reported value 3.78 by more than 10 %

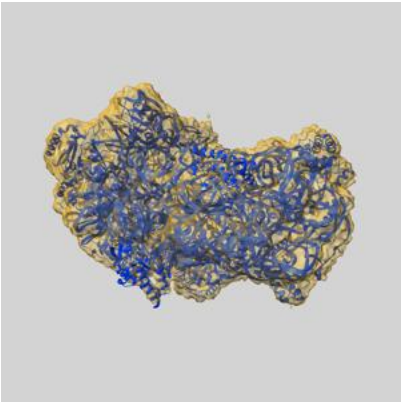
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-12248 and PDB model 7NAU. Per-residue inclusion information can be found in section 3 on page 8.

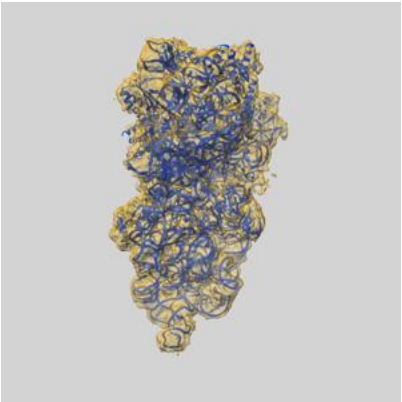
9.1 Map-model overlay (i)



X



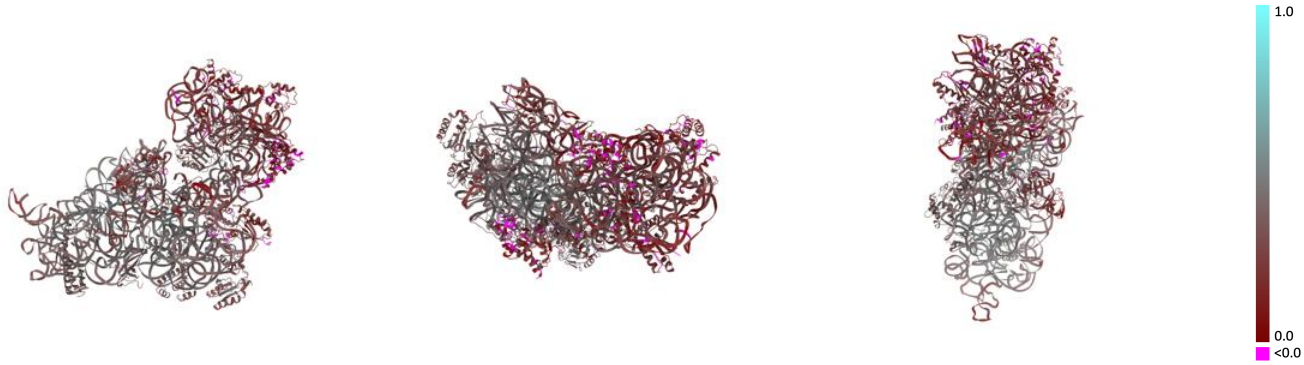
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

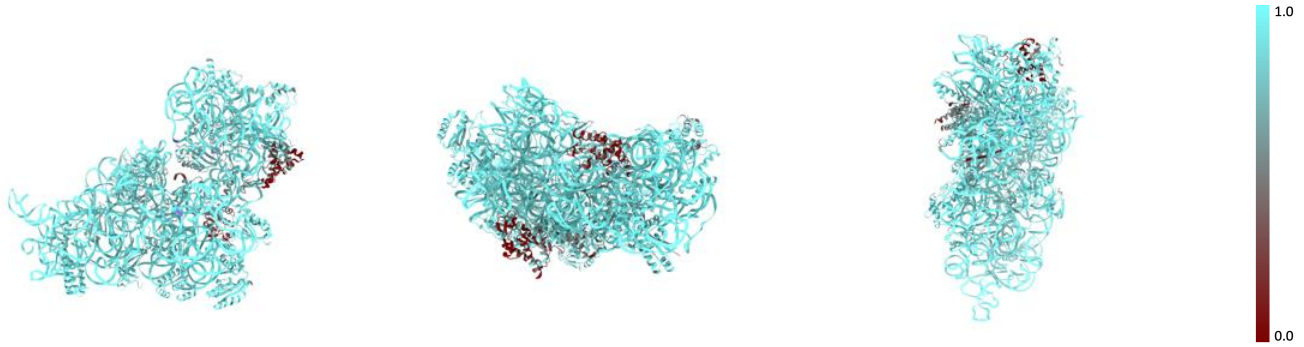
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

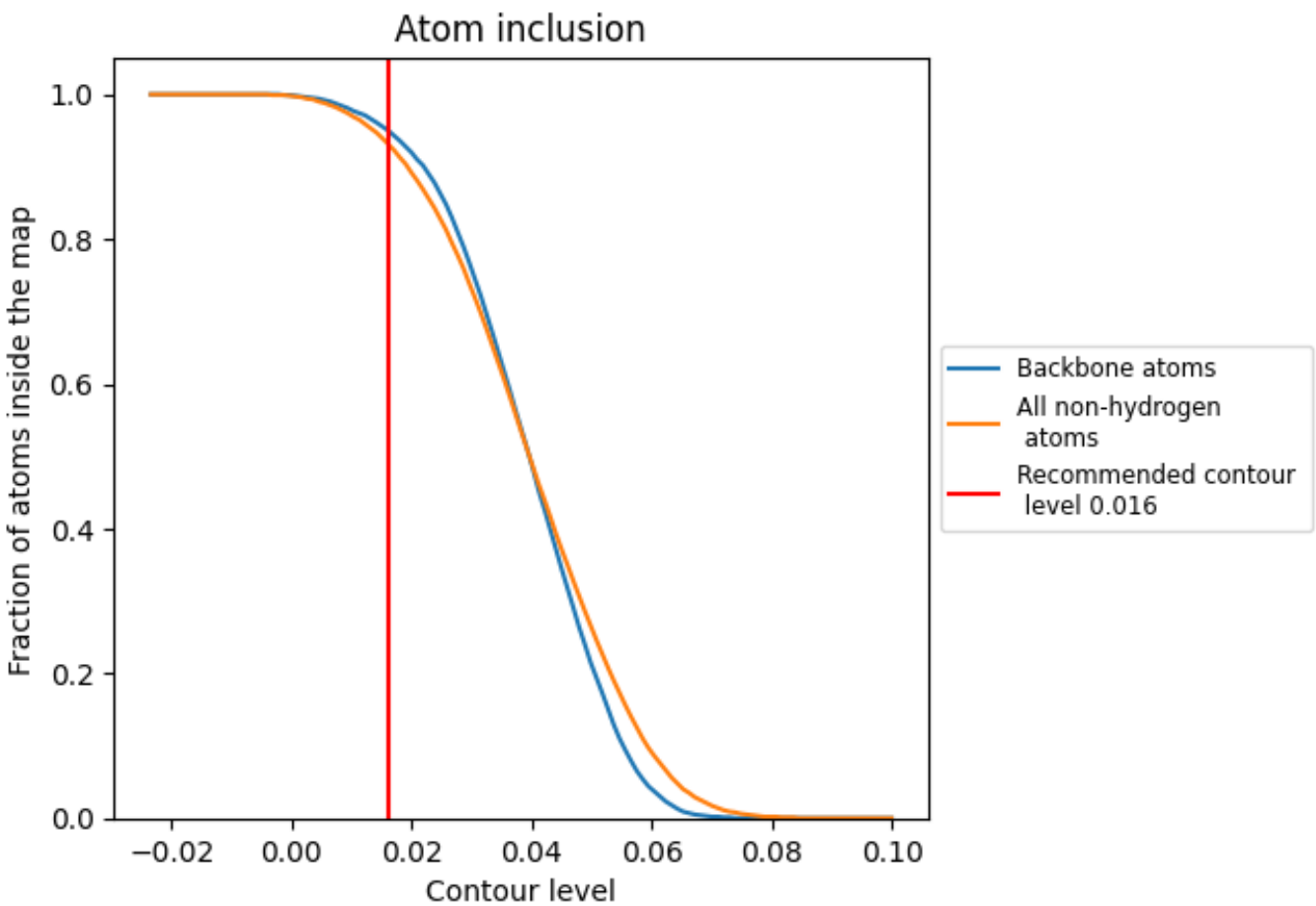
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.016).

9.4 Atom inclusion (i)



At the recommended contour level, 95% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9320	0.3310
A	0.9940	0.3640
B	0.3320	0.1500
C	0.8630	0.2480
D	0.9380	0.3940
E	0.9120	0.3870
F	0.9270	0.3430
G	0.3220	0.1000
H	0.9180	0.3920
I	0.9230	0.1780
J	0.8790	0.1960
K	0.9250	0.2490
L	0.8750	0.3550
M	0.8870	0.1620
N	0.9290	0.2450
O	0.9320	0.3590
P	0.9330	0.4090
Q	0.9350	0.3770
R	0.9300	0.3440
S	0.9490	0.1630
T	0.9850	0.3940
X	0.8730	0.2220