



Full wwPDB EM Validation Report ⓘ

Nov 17, 2025 – 05:01 PM JST

PDB ID : 9KMZ / pdb_00009kmz
EMDB ID : EMD-62450
Title : Bat MERsSr-CoV NL140422 Nsp1 bound to the Human 40S Ribosomal subunit-State1
Authors : Yuan, S.; Yan, R.; Wu, M.
Deposited on : 2024-11-18
Resolution : 2.78 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

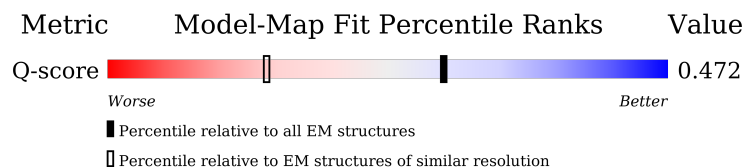
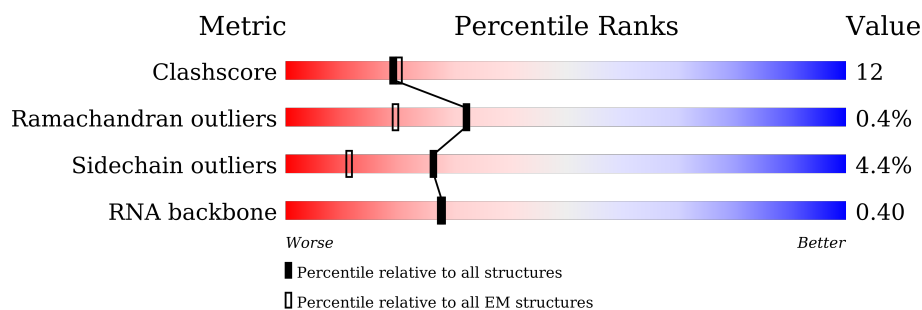
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY




The reported resolution of this entry is 2.78 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.






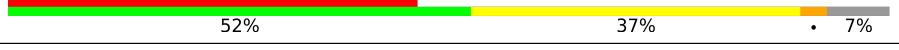


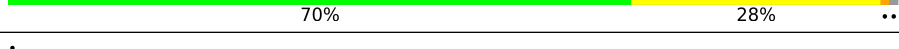
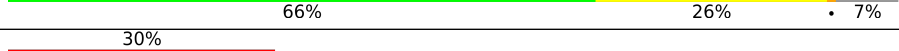
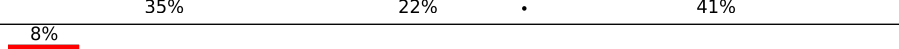

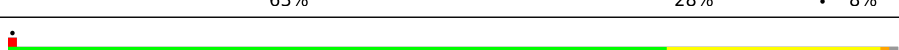

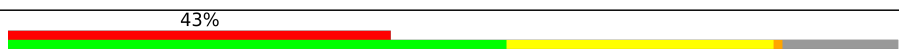
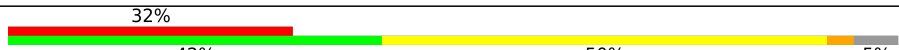
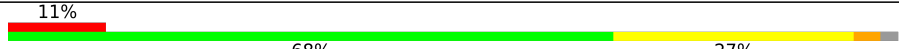
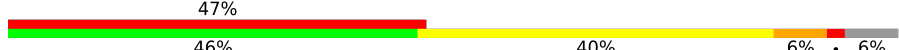




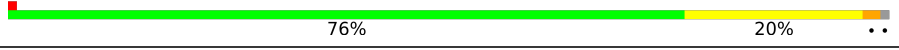
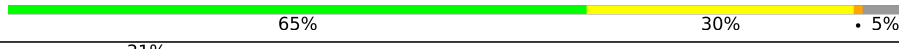
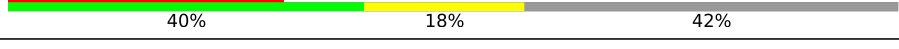


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	10754 (2.28 - 3.28)

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 $\leq 5\%$. 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	2	1869	
2	A	295	
3	B	264	

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Mol	Chain	Length	Quality of chain
4	C	293	
5	D	243	
6	E	263	
7	F	204	
8	G	249	
9	H	194	
10	I	208	
11	J	194	
12	K	165	
13	L	158	
14	M	132	
15	N	151	
16	O	151	
17	P	145	
18	Q	146	
19	R	135	
20	S	152	
21	T	145	
22	U	119	
23	V	83	
24	W	130	
25	X	143	
26	Y	130	
27	Z	125	
28	a	101	

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Mol	Chain	Length	Quality of chain
29	b	82	<div><div><div></div><div></div><div></div></div><div>89%10%</div></div>
30	c	62	<div><div><div></div><div></div><div></div></div><div>55%53%44%</div></div>
31	d	55	<div><div><div></div><div></div><div></div></div><div>15%58%38%</div></div>
32	e	56	<div><div><div></div><div></div><div></div></div><div>12%79%20%</div></div>
33	f	74	<div><div><div></div><div></div><div></div></div><div>81%68%28%</div></div>
34	g	315	<div><div><div></div><div></div><div></div></div><div>63%66%32%</div></div>
35	h	25	<div><div><div></div><div></div><div></div></div><div>64%20%12%</div></div>
36	n	196	<div><div><div></div><div></div><div></div></div><div>12%86%</div></div>

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 74738 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1669	Total	C	N	O	P	0	0
			35610	15907	6400	11643	1660		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	213	Total	C	N	O	S	0	0
			1686	1072	295	311	8		

- Molecule 3 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 5 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	225	Total	C	N	O	S	0	0
			1752	1117	315	313	7		

- Molecule 6 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 8 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	230	Total	C	N	O	S	0	0
			1864	1164	373	320	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	221	ARG	LYS	variant	UNP P62753

- Molecule 9 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	186	Total	C	N	O	S	0	0
			1501	957	276	267	1		

- Molecule 10 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	205	Total	C	N	O	S	0	0
			1682	1056	331	290	5		

- Molecule 11 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 12 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	97	Total	C	N	O	S	0	0
			816	533	144	133	6		

- Molecule 13 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	151	Total	C	N	O	S	0	0
			1229	782	230	211	6		

- Molecule 14 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	121	Total	C	N	O	S	0	0
			935	586	165	175	9		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	135	Total	C	N	O	S	0	0
			1010	618	198	188	6		

- Molecule 17 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	126	Total	C	N	O	S	0	0
			1037	659	196	175	7		

- Molecule 18 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	138	Total	C	N	O	S	0	0
			1097	698	206	190	3		

- Molecule 19 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 20 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	143	Total	C	N	O	S	0	0
			1184	743	240	200	1		

- Molecule 21 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	144	Total	C	N	O	S	0	0
			1123	703	217	200	3		

- Molecule 22 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	101	Total	C	N	O	S	0	0
			803	504	153	142	4		

- Molecule 23 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 24 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 25 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 26 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	124	Total	C	N	O	S	0	0
			1014	641	198	170	5		

- Molecule 27 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 28 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	99	Total	C	N	O	S	0	0
			794	494	165	130	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	78	VAL	ALA	conflict	UNP P62854

- Molecule 29 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	82	Total	C	N	O	S	0	0
			641	402	118	114	7		

- Molecule 30 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	62	Total	C	N	O	S	0	0
			489	297	97	93	2		

- Molecule 31 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 32 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	56	Total	C	N	O	S	0	0
			442	273	96	72	1		

- Molecule 33 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	74	Total	C	N	O	S	0	0
			611	385	117	102	7		

- Molecule 34 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	314	Total	C	N	O	S	0	0
			2441	1537	425	467	12		

- Molecule 35 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	22	Total	C	N	O	S	0	0
			213	130	57	23	3		

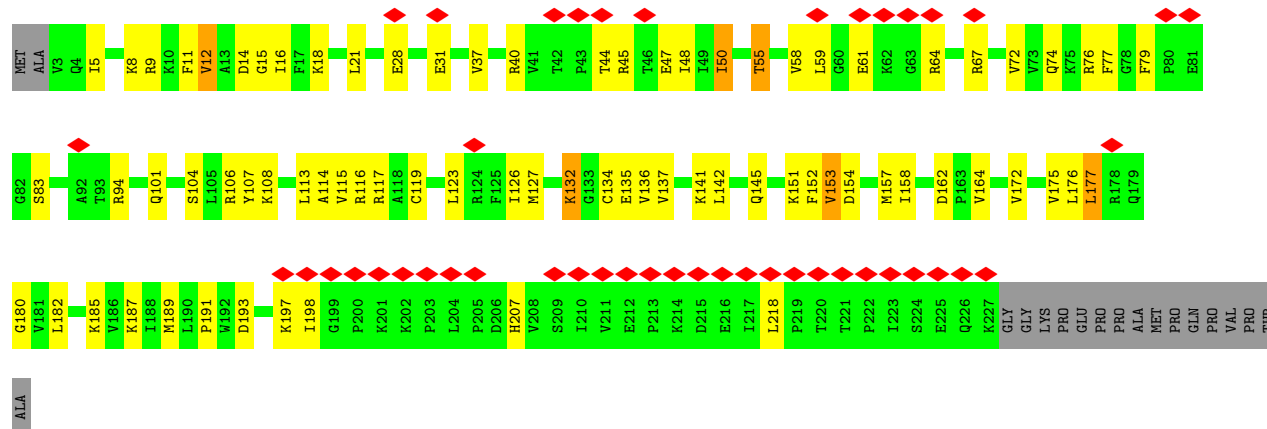
- Molecule 36 is a protein called ORF1ab polyprotein.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	n	27	Total	C	N	O	0	0
			215	140	34	41		

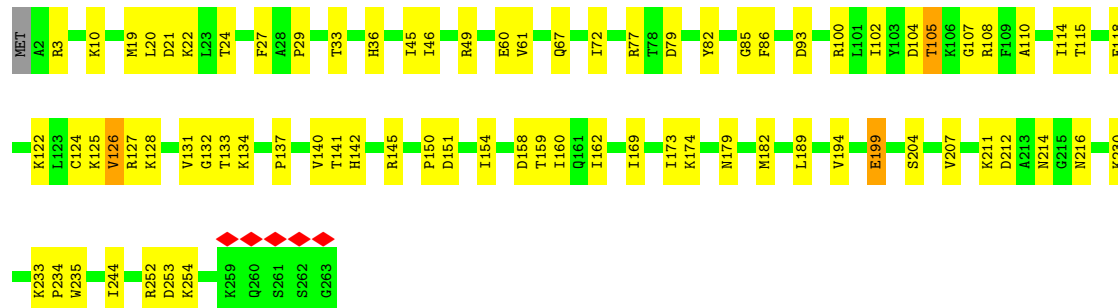




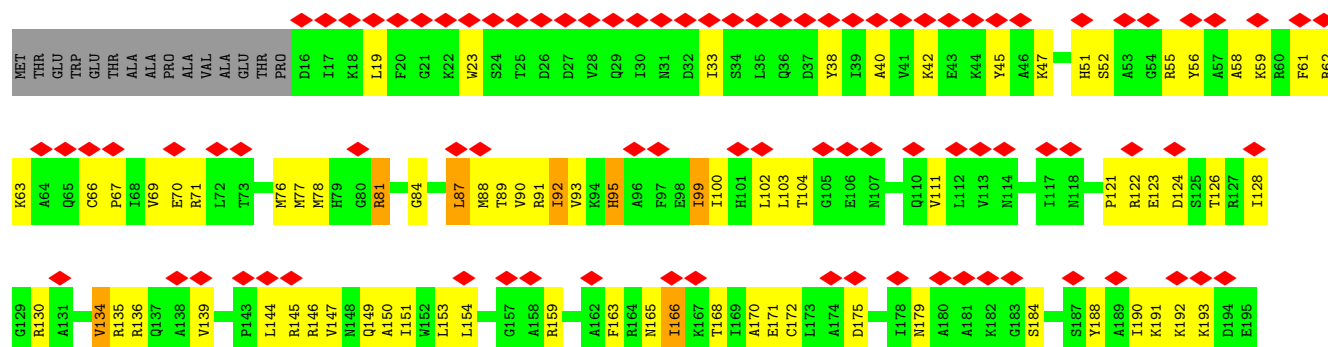
• Molecule 5: Small ribosomal subunit protein uS3

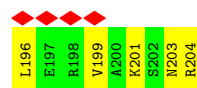


• Molecule 6: Small ribosomal subunit protein eS4, X isoform



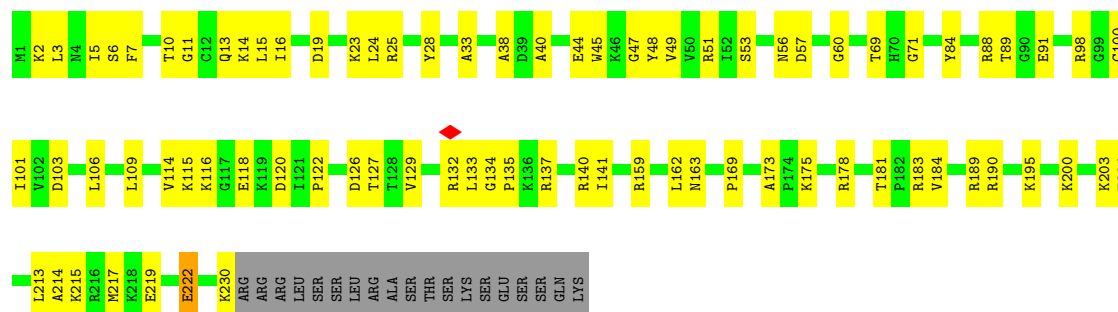
• Molecule 7: Small ribosomal subunit protein uS7





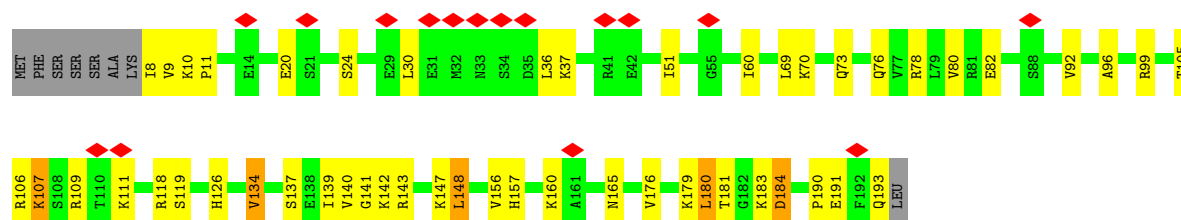
• Molecule 8: Small ribosomal subunit protein eS6

Chain G: 60% 32% 8%



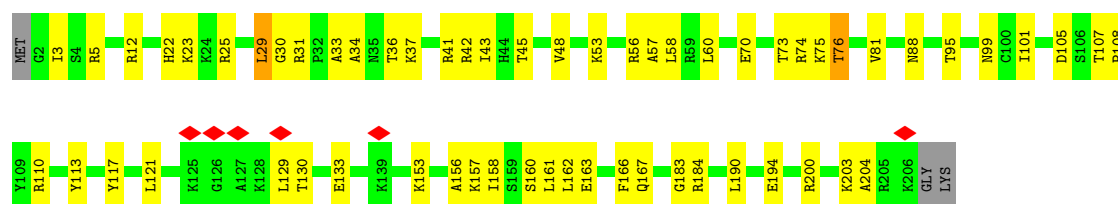
• Molecule 9: Small ribosomal subunit protein eS7

Chain H: 8% 70% 24%



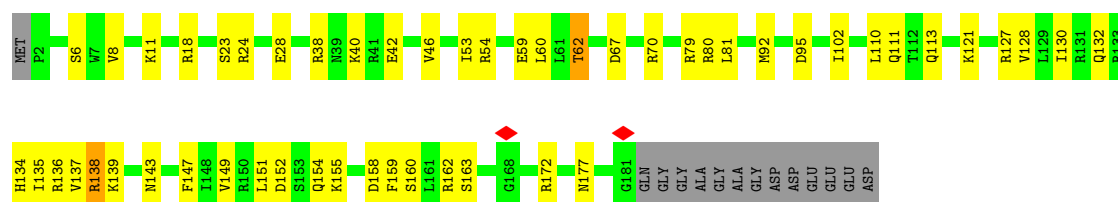
• Molecule 10: Small ribosomal subunit protein eS8

Chain I: 70% 28%

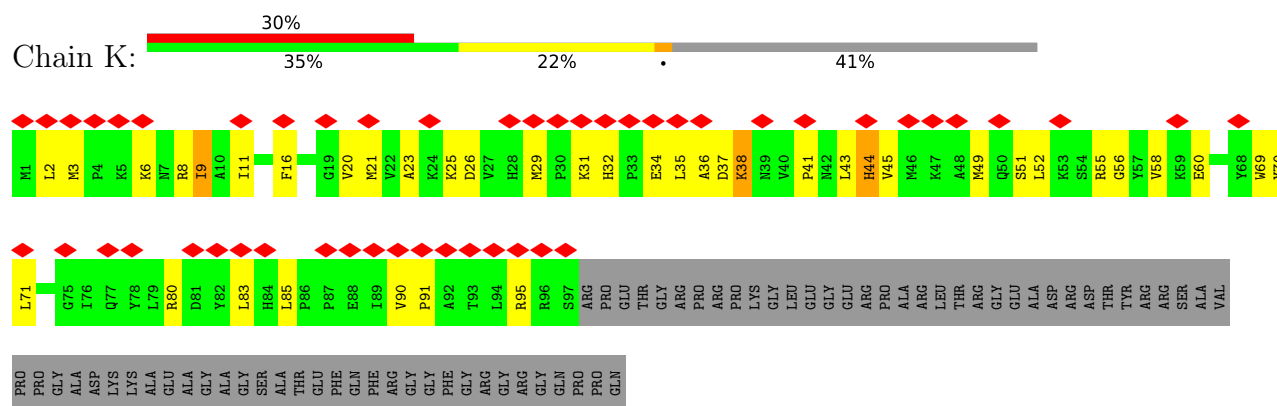


• Molecule 11: Small ribosomal subunit protein uS4

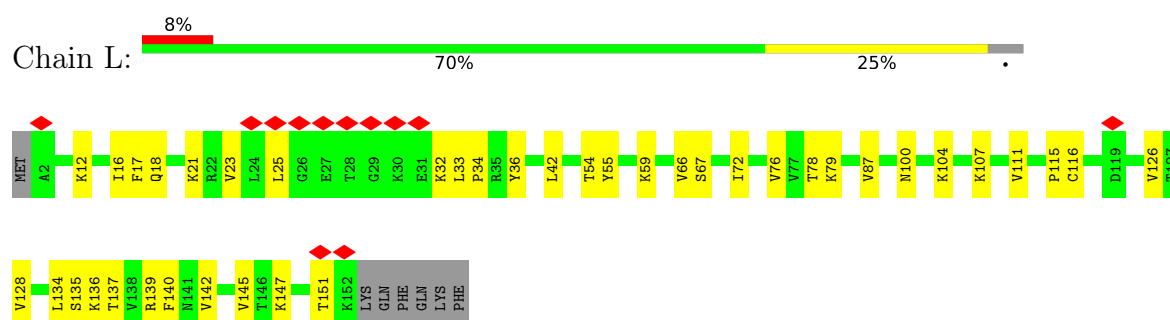
Chain J: 66% 26% 7%



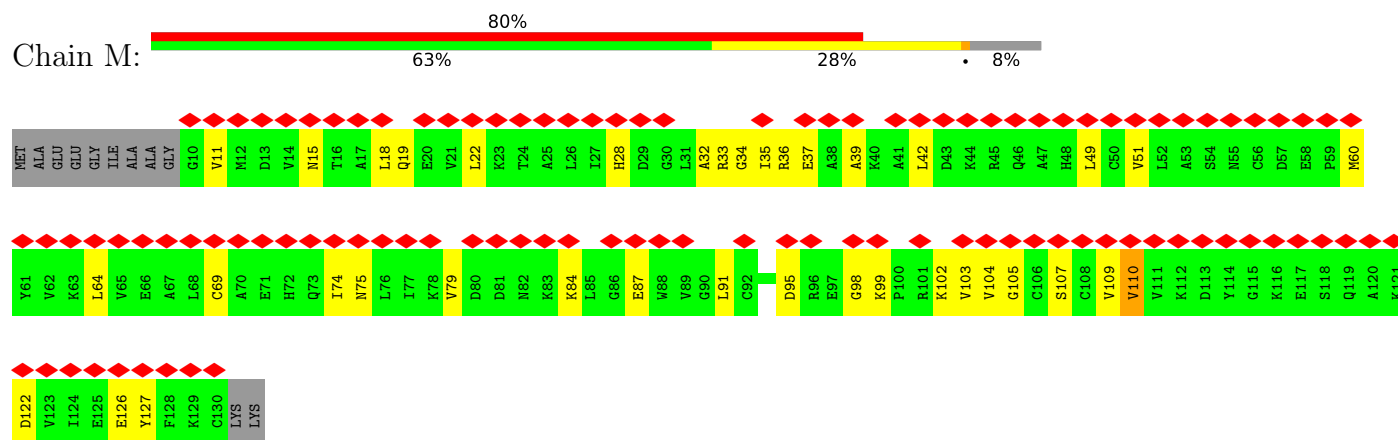
- Molecule 12: Small ribosomal subunit protein eS10



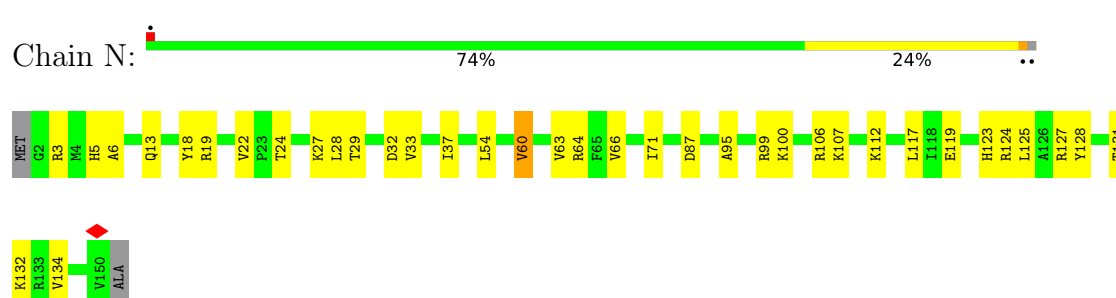
- Molecule 13: Small ribosomal subunit protein uS17



- Molecule 14: Small ribosomal subunit protein eS12

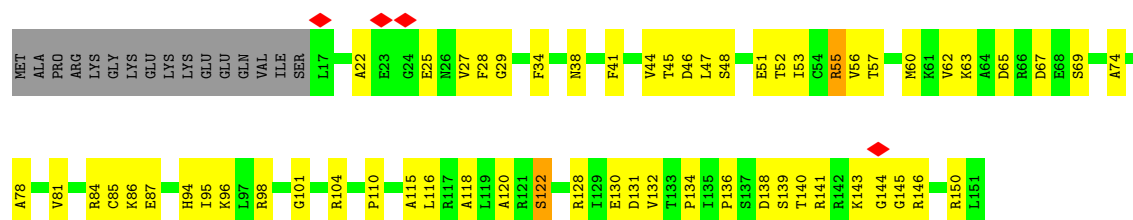


- Molecule 15: Small ribosomal subunit protein uS15




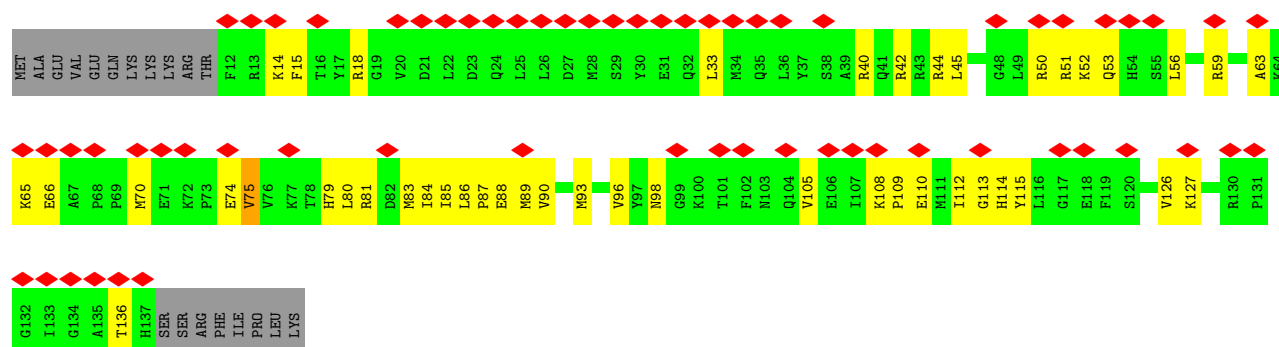
- Molecule 16: Small ribosomal subunit protein uS11

Chain O: 

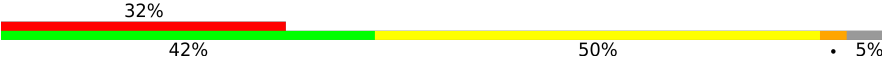


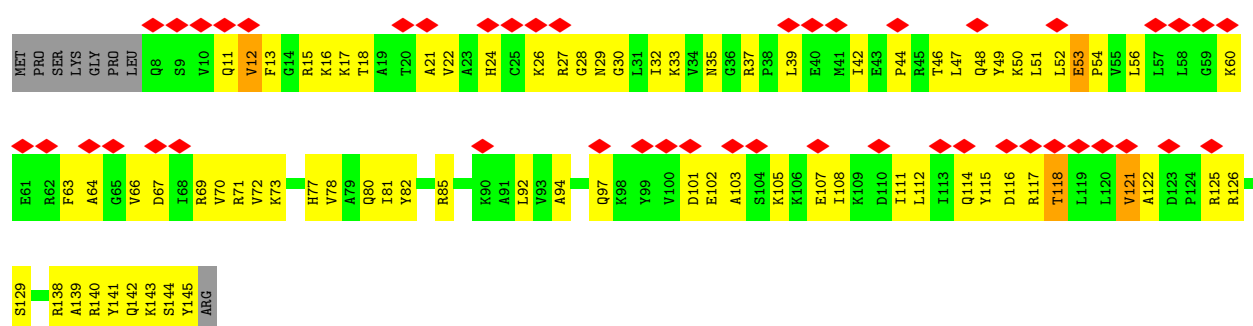
- Molecule 17: Small ribosomal subunit protein uS19

Chain P: 



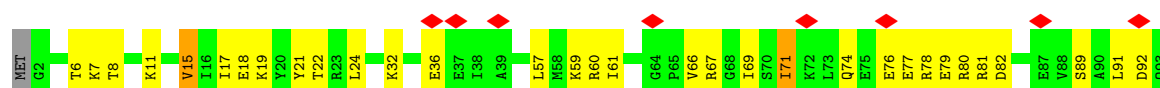
- Molecule 18: Small ribosomal subunit protein uS9

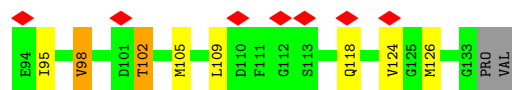
Chain Q: 



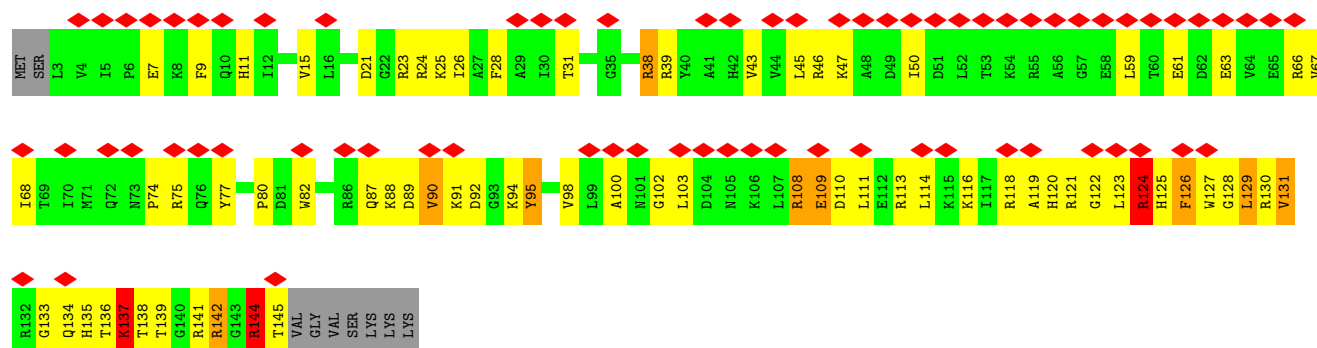
- Molecule 19: Small ribosomal subunit protein eS17

Chain R: 

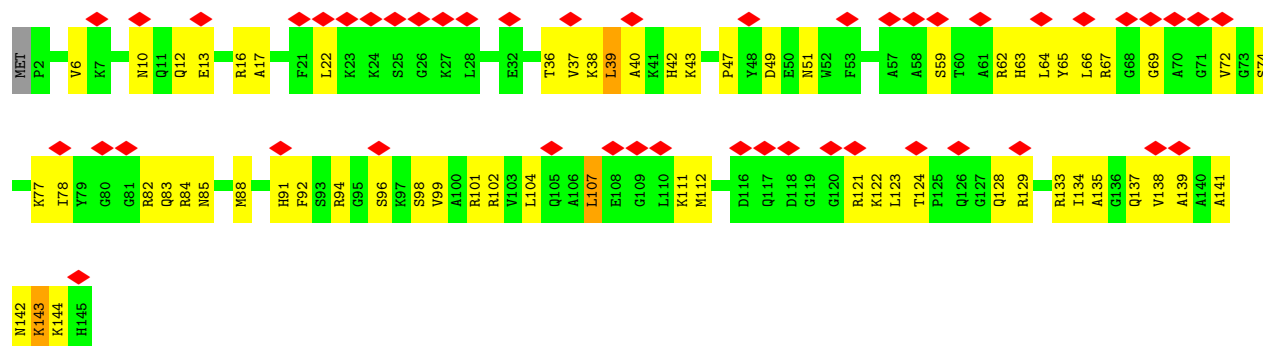




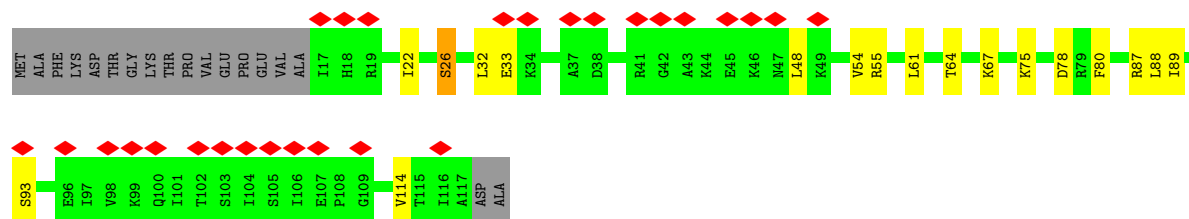
- Molecule 20: Small ribosomal subunit protein uS13



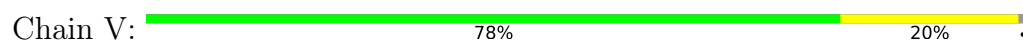
- Molecule 21: Small ribosomal subunit protein eS19

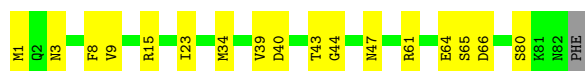


- Molecule 22: Small ribosomal subunit protein uS10



- Molecule 23: Small ribosomal subunit protein eS21





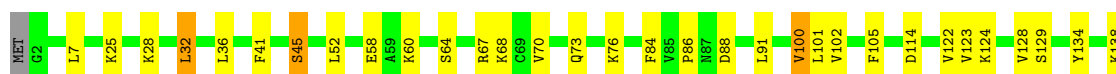
- Molecule 24: Small ribosomal subunit protein uS8

Chain W: 73% 26%



- Molecule 25: Small ribosomal subunit protein uS12

Chain X: 76% 20%



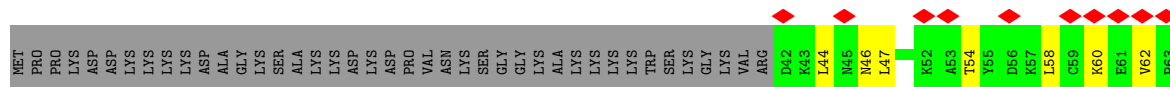
- Molecule 26: Small ribosomal subunit protein eS24

Chain Y: 65% 30% 5%



- Molecule 27: Small ribosomal subunit protein eS25

Chain Z: 31% 40% 18% 42%




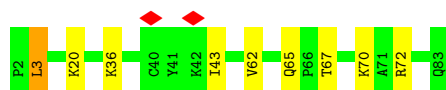
- Molecule 28: Small ribosomal subunit protein eS26

Chain a: 71% 26%



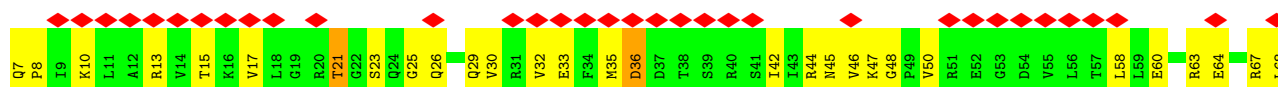
- Molecule 29: Small ribosomal subunit protein eS27

Chain b: 



- Molecule 30: Small ribosomal subunit protein eS28

Chain c: 




- Molecule 31: Small ribosomal subunit protein uS14

Chain d: 




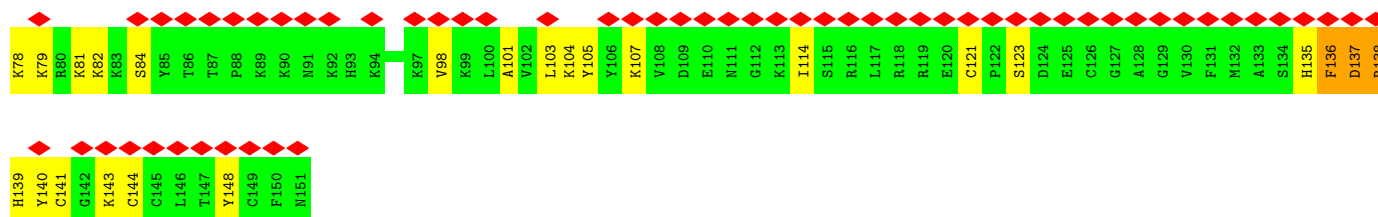
- Molecule 32: Small ribosomal subunit protein eS30

Chain e: 



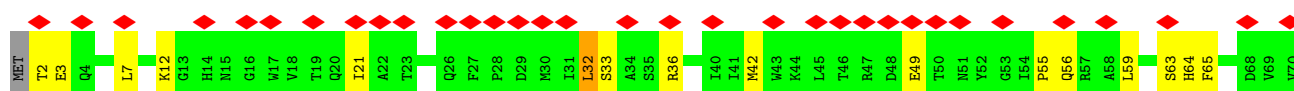
- Molecule 33: Small ribosomal subunit protein eS31

Chain f: 



- Molecule 34: Small ribosomal subunit protein RACK1

Chain g: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	99345	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.866	Depositor
Minimum map value	-0.997	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.049	Depositor
Recommended contour level	0.14	Depositor
Map size (Å)	486.4, 486.4, 486.4	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	2	0.26	0/39823	0.32	5/62066 (0.0%)
2	A	0.21	0/1723	0.30	0/2341
3	B	0.22	0/1756	0.36	0/2350
4	C	0.27	0/1726	0.40	0/2332
5	D	0.25	0/1780	0.43	0/2397
6	E	0.28	0/2118	0.36	0/2849
7	F	0.17	0/1516	0.44	0/2037
8	G	0.26	0/1887	0.52	2/2513 (0.1%)
9	H	0.21	0/1524	0.43	0/2042
10	I	0.23	0/1711	0.35	0/2282
11	J	0.25	0/1524	0.33	0/2035
12	K	0.30	0/840	0.63	1/1133 (0.1%)
13	L	0.24	0/1250	0.30	0/1673
14	M	0.11	0/945	0.30	0/1269
15	N	0.22	0/1226	0.30	0/1649
16	O	0.21	0/1023	0.36	0/1372
17	P	0.17	0/1058	0.48	0/1414
18	Q	0.20	0/1114	0.48	0/1492
19	R	0.17	0/1082	0.38	0/1452
20	S	0.50	0/1202	0.84	4/1610 (0.2%)
21	T	0.20	0/1143	0.51	0/1530
22	U	0.16	0/813	0.32	0/1092
23	V	0.21	0/631	0.29	0/844
24	W	0.28	0/1051	0.35	0/1406
25	X	0.24	0/1116	0.33	0/1490
26	Y	0.23	0/1031	0.29	0/1370
27	Z	0.13	0/580	0.42	0/780
28	a	0.24	0/807	0.36	0/1082
29	b	0.20	0/654	0.33	0/876
30	c	0.15	0/491	0.36	0/656
31	d	0.25	0/470	0.45	0/623
32	e	0.19	0/447	0.33	0/587
33	f	0.26	0/623	0.51	0/822
34	g	0.13	0/2498	0.34	0/3399

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.22	0/214	0.42	0/272
36	n	0.15	0/219	0.21	0/293
All	All	0.25	0/79616	0.37	12/115430 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
20	S	0	2
33	f	0	1
All	All	0	3

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1310	U	O3'-P-O5'	-8.31	91.54	104.00
1	2	1309	C	C1'-C2'-O2'	-7.58	97.03	108.40
20	S	103	LEU	N-CA-C	-6.09	103.09	110.88
1	2	1609	C	C2'-C3'-O3'	5.97	118.45	109.50
20	S	102	GLY	N-CA-C	-5.74	107.39	115.32
1	2	293	C	OP2-P-O3'	5.73	125.19	108.00
8	G	89	THR	N-CA-C	5.47	117.24	111.28
20	S	38	ARG	CB-CA-C	-5.42	110.31	116.54
20	S	59	LEU	N-CA-C	5.28	117.50	110.53
8	G	100	CYS	N-CA-C	5.24	116.99	111.28
1	2	1608	U	C2'-C3'-O3'	5.22	117.33	109.50
12	K	38	LYS	N-CA-C	-5.00	100.24	108.49

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
20	S	124	ARG	Sidechain
20	S	144	ARG	Sidechain
33	f	138	ARG	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of 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	2	35610	0	18000	718	0
2	A	1686	0	1688	44	0
3	B	1729	0	1803	50	0
4	C	1690	0	1777	31	0
5	D	1752	0	1848	55	0
6	E	2076	0	2177	49	0
7	F	1495	0	1549	69	0
8	G	1864	0	2018	63	0
9	H	1501	0	1593	36	0
10	I	1682	0	1769	45	0
11	J	1499	0	1618	30	0
12	K	816	0	841	30	0
13	L	1229	0	1302	22	0
14	M	935	0	964	27	0
15	N	1202	0	1289	28	0
16	O	1010	0	1034	48	0
17	P	1037	0	1082	37	0
18	Q	1097	0	1161	75	0
19	R	1068	0	1121	35	0
20	S	1184	0	1244	78	0
21	T	1123	0	1153	60	0
22	U	803	0	873	14	0
23	V	625	0	628	16	0
24	W	1034	0	1080	28	0
25	X	1098	0	1167	22	0
26	Y	1014	0	1082	28	0
27	Z	574	0	627	14	0
28	a	794	0	849	26	0
29	b	641	0	665	8	0
30	c	489	0	514	27	0
31	d	459	0	452	19	0
32	e	442	0	487	8	0
33	f	611	0	638	50	0
34	g	2441	0	2396	75	0
35	h	213	0	258	6	0
36	n	215	0	220	4	0
All	All	74738	0	58967	1646	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 12.

All (1646) 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)
33:f:141:CYS:SG	33:f:148:TYR:CE2	2.18	1.35
33:f:141:CYS:SG	33:f:148:TYR:CZ	2.39	1.13
33:f:141:CYS:SG	33:f:148:TYR:OH	2.15	1.04
1:2:1521:C:H2'	20:S:136:THR:HB	1.42	0.99
1:2:1033:G:H1	1:2:1080:A:HO2'	1.06	0.96
33:f:141:CYS:SG	33:f:148:TYR:HE2	1.72	0.95
1:2:1407:U:C5	1:2:1428:G:H5'	2.02	0.95
18:Q:97:GLN:HA	18:Q:105:LYS:HG2	1.54	0.87
1:2:334:C:H5	8:G:190:ARG:HH12	1.24	0.86
1:2:1231:C:O2'	1:2:1253:A:N6	2.09	0.85
16:O:34:PHE:HB3	16:O:41:PHE:HB2	1.61	0.82
1:2:1133:A:H4'	28:a:13:LYS:HD3	1.60	0.82
18:Q:73:LYS:H	18:Q:73:LYS:HD2	1.44	0.81
1:2:64:A:H2	1:2:83:A:H62	1.25	0.81
1:2:1407:U:H5	1:2:1428:G:H5'	1.46	0.81
1:2:1680:G:H4'	30:c:25:GLY:HA3	1.63	0.81
20:S:129:LEU:HA	20:S:142:ARG:HB3	1.63	0.80
31:d:53:ILE:HD13	31:d:55:LEU:HD23	1.62	0.80
1:2:1473:G:N1	1:2:1476:A:N6	2.30	0.80
1:2:1227:G:N2	1:2:1639:G:OP2	2.14	0.80
16:O:86:LYS:NZ	16:O:122:SER:O	2.17	0.78
1:2:1073:U:H2'	1:2:1074:C:H6	1.48	0.78
31:d:22:ARG:NH1	31:d:36:LEU:O	2.16	0.78
7:F:66:CYS:SG	7:F:71:ARG:NH1	2.55	0.78
9:H:51:ILE:HG21	9:H:179:LYS:HG3	1.66	0.78
1:2:1231:C:HO2'	1:2:1253:A:N6	1.81	0.77
20:S:124:ARG:HD3	20:S:131:VAL:HA	1.65	0.76
20:S:89:ASP:HB3	20:S:113:ARG:HH12	1.50	0.76
1:2:1228:A:H1'	1:2:1634:A:H1'	1.67	0.76
1:2:1230:C:H5'	20:S:134:GLN:HB2	1.68	0.76
34:g:246:TYR:HB2	34:g:261:LEU:HD21	1.68	0.76
1:2:1516:G:N2	1:2:1516:G:OP2	2.19	0.76
16:O:63:LYS:HE3	16:O:63:LYS:HA	1.68	0.76
1:2:1615:U:OP2	17:P:40:ARG:NH2	2.19	0.75
1:2:1535:U:N3	7:F:78:MET:SD	2.59	0.75
3:B:83:LYS:HD3	3:B:106:THR:HG22	1.68	0.75
1:2:1729:U:H3	1:2:1805:G:H1	1.34	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1274:G:H8	1:2:1324:G:H5''	1.51	0.74
1:2:1589:A:OP2	21:T:84:ARG:NH2	2.18	0.74
25:X:58:GLU:OE2	25:X:58:GLU:N	2.20	0.74
1:2:940:U:H3	1:2:1002:U:H3	1.34	0.74
1:2:1542:C:H42	21:T:82:ARG:HH12	1.35	0.74
1:2:1473:G:O6	7:F:62:ARG:NH1	2.21	0.74
7:F:47:LYS:NZ	18:Q:116:ASP:OD1	2.20	0.74
18:Q:15:ARG:NH1	18:Q:17:LYS:O	2.21	0.74
1:2:1312:G:H5'	12:K:2:LEU:HD13	1.70	0.74
7:F:204:ARG:NH1	30:c:7:GLN:OE1	2.21	0.74
11:J:67:ASP:HB3	11:J:70:ARG:HB3	1.70	0.74
7:F:104:THR:HG21	7:F:111:VAL:HG21	1.70	0.73
7:F:123:GLU:OE1	7:F:204:ARG:NH2	2.21	0.73
20:S:130:ARG:HG2	20:S:134:GLN:HE22	1.51	0.73
4:C:75:ILE:HD11	4:C:265:PRO:HB3	1.70	0.73
6:E:104:ASP:OD1	6:E:105:THR:N	2.21	0.73
12:K:31:LYS:HA	12:K:35:LEU:HD22	1.71	0.73
1:2:1609:C:OP1	20:S:124:ARG:HB3	1.89	0.73
1:2:1294:G:N2	1:2:1295:A:N7	2.37	0.72
1:2:1589:A:H5''	21:T:82:ARG:HG3	1.69	0.72
4:C:200:ARG:O	11:J:54:ARG:NH2	2.23	0.72
5:D:123:LEU:HD11	5:D:152:PHE:HB2	1.72	0.72
1:2:1230:C:H5'	20:S:134:GLN:CB	2.20	0.72
1:2:1499:U:H4'	5:D:176:LEU:HD21	1.70	0.72
9:H:20:GLU:OE2	9:H:20:GLU:N	2.21	0.72
1:2:919:A:OP2	15:N:64:ARG:NH2	2.23	0.71
1:2:1303:C:N4	1:2:1507:G:N7	2.38	0.71
1:2:65:C:N4	8:G:134:GLY:O	2.23	0.71
1:2:1217:A:H2'	1:2:1218:C:H6	1.56	0.71
9:H:36:LEU:HB3	9:H:78:ARG:HH21	1.56	0.71
15:N:37:ILE:HD11	15:N:63:VAL:HG21	1.72	0.71
18:Q:48:GLN:HG2	18:Q:52:LEU:HD23	1.73	0.71
1:2:1865:C:OP2	28:a:5:ARG:NH1	2.24	0.71
8:G:118:GLU:N	8:G:118:GLU:OE2	2.24	0.71
1:2:801:U:O4	9:H:106:ARG:NH2	2.24	0.71
1:2:1642:U:H2'	18:Q:145:TYR:H	1.55	0.71
25:X:28:LYS:HE3	25:X:32:LEU:HD13	1.72	0.70
1:2:1777:G:H21	1:2:1778:C:H5''	1.55	0.70
5:D:172:VAL:HG22	5:D:185:LYS:HG2	1.73	0.70
12:K:52:LEU:O	12:K:56:GLY:N	2.24	0.70
18:Q:16:LYS:HE2	18:Q:82:TYR:HB2	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1718:G:N2	1:2:1719:A:N7	2.40	0.70
1:2:587:A:H5'	1:2:592:C:H41	1.56	0.70
8:G:213:LEU:O	8:G:217:MET:HG3	1.92	0.70
18:Q:77:HIS:O	18:Q:81:ILE:HB	1.92	0.70
21:T:69:GLY:H	21:T:121:ARG:HG3	1.57	0.70
17:P:84:ILE:HG21	17:P:113:GLY:H	1.56	0.69
20:S:142:ARG:HH11	20:S:142:ARG:HB2	1.57	0.69
18:Q:35:ASN:O	18:Q:37:ARG:NH1	2.25	0.69
5:D:157:MET:HE1	5:D:187:LYS:HB2	1.73	0.69
1:2:1451:G:N2	1:2:1452:A:O2'	2.25	0.69
7:F:124:ASP:OD2	7:F:149:GLN:NE2	2.26	0.69
7:F:170:ALA:HB3	27:Z:71:ALA:HB2	1.74	0.69
18:Q:42:ILE:HG23	18:Q:44:PRO:HD2	1.74	0.69
1:2:573:U:H1'	1:2:576:A:H2	1.58	0.69
1:2:1091:C:HO2'	24:W:2:VAL:N	1.91	0.69
1:2:1599:U:OP1	27:Z:46:ASN:ND2	2.26	0.69
26:Y:55:ILE:HD13	26:Y:75:ILE:HG12	1.75	0.69
1:2:957:A:H3'	1:2:958:G:H21	1.58	0.68
27:Z:44:LEU:HD11	27:Z:78:LYS:HE3	1.74	0.68
1:2:104:A:OP1	10:I:12:ARG:NH1	2.25	0.68
18:Q:16:LYS:NZ	18:Q:78:VAL:O	2.22	0.68
34:g:21:ILE:HD11	34:g:33:SER:HA	1.74	0.68
1:2:1673:U:O2'	7:F:84:GLY:N	2.26	0.68
9:H:143:ARG:HD3	24:W:53:ILE:HG13	1.73	0.68
11:J:18:ARG:O	11:J:24:ARG:NH1	2.27	0.68
2:A:191:ARG:HH12	23:V:44:GLY:HA3	1.59	0.68
5:D:21:LEU:HD21	5:D:37:VAL:HG11	1.76	0.68
29:b:36:LYS:HD3	29:b:43:ILE:HG22	1.76	0.68
5:D:175:VAL:HG23	5:D:182:LEU:HB2	1.74	0.68
1:2:1591:C:O2'	7:F:91:ARG:NH2	2.27	0.67
25:X:68:LYS:HB3	25:X:91:LEU:HD22	1.76	0.67
1:2:1308:U:C5	33:f:138:ARG:HG3	2.30	0.67
1:2:1329:U:O2	1:2:1500:G:O6	2.12	0.67
1:2:1629:C:H5''	20:S:38:ARG:HH21	1.58	0.67
1:2:544:G:OP2	1:2:545:A:N6	2.27	0.67
14:M:60:MET:HE1	14:M:64:LEU:HD12	1.75	0.67
1:2:92:A:H1'	6:E:3:ARG:HB2	1.75	0.67
1:2:1441:U:H4'	1:2:1442:U:H5'	1.76	0.67
10:I:57:ALA:HB2	10:I:183:GLY:HA2	1.75	0.67
18:Q:80:GLN:HE22	18:Q:81:ILE:HG12	1.59	0.67
34:g:170:TRP:HA	34:g:195:LEU:HB3	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1474:A:H1'	18:Q:121:VAL:HB	1.76	0.66
4:C:134:ASN:O	4:C:134:ASN:ND2	2.22	0.66
1:2:1298:G:H1'	17:P:79:HIS:HE1	1.61	0.66
1:2:1073:U:H2'	1:2:1074:C:C6	2.28	0.66
1:2:1451:G:N2	1:2:1452:A:HO2'	1.94	0.66
5:D:108:LYS:HB3	5:D:113:LEU:HD23	1.77	0.66
8:G:49:VAL:HG23	8:G:114:VAL:HG23	1.77	0.66
34:g:71:ILE:HD12	34:g:78:ALA:HB2	1.76	0.66
1:2:1399:C:H3'	1:2:1401:A:H5''	1.76	0.66
18:Q:47:LEU:HD23	18:Q:81:ILE:HG21	1.77	0.66
22:U:22:ILE:HD12	22:U:89:ILE:HD11	1.77	0.66
1:2:1450:G:H2'	1:2:1451:G:H8	1.61	0.66
34:g:285:GLN:H	34:g:303:THR:HG22	1.61	0.66
1:2:1024:A:OP2	15:N:124:ARG:NH2	2.25	0.66
1:2:1589:A:N7	21:T:82:ARG:NH2	2.40	0.66
2:A:52:LYS:HG3	19:R:109:LEU:HD22	1.76	0.66
19:R:57:LEU:HD13	19:R:69:ILE:HD11	1.78	0.66
1:2:1615:U:O2	1:2:1620:A:N6	2.30	0.66
1:2:1274:G:OP1	1:2:1276:A:N6	2.28	0.65
16:O:46:ASP:OD1	16:O:47:LEU:N	2.28	0.65
20:S:120:HIS:CE1	20:S:131:VAL:HG23	2.31	0.65
1:2:1273:C:O2'	1:2:1275:G:OP1	2.13	0.65
1:2:1299:A:H1'	17:P:80:LEU:HD11	1.77	0.65
1:2:860:G:H21	24:W:107:SER:HG	1.42	0.65
1:2:860:G:N2	24:W:107:SER:HG	1.95	0.65
27:Z:47:LEU:O	27:Z:80:ARG:NH1	2.30	0.65
1:2:1451:G:H21	1:2:1452:A:HO2'	1.42	0.65
9:H:179:LYS:HD3	9:H:180:LEU:N	2.12	0.65
3:B:34:LYS:O	3:B:98:THR:OG1	2.14	0.65
33:f:144:CYS:SG	33:f:148:TYR:OH	2.54	0.65
1:2:1643:U:H4'	18:Q:144:SER:HB3	1.77	0.65
1:2:1864:U:H5''	28:a:79:ILE:HD11	1.79	0.65
7:F:122:ARG:HH12	7:F:204:ARG:HE	1.43	0.65
18:Q:29:ASN:HA	18:Q:64:ALA:HA	1.77	0.65
6:E:137:PRO:HB2	6:E:150:PRO:HD2	1.77	0.65
19:R:32:LYS:NZ	19:R:36:GLU:OE2	2.29	0.65
30:c:29:GLN:NE2	30:c:45:ASN:OD1	2.28	0.65
1:2:928:G:H2'	1:2:929:G:C8	2.31	0.65
1:2:84:A:N3	1:2:150:A:O2'	2.28	0.65
1:2:1719:A:H61	1:2:1814:G:H2'	1.63	0.65
13:L:111:VAL:HG12	13:L:140:PHE:HB2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:a:78:VAL:HG13	28:a:83:VAL:HB	1.79	0.64
1:2:563:G:N7	11:J:172:ARG:NH2	2.44	0.64
1:2:617:G:H4'	25:X:88:ASP:HB3	1.79	0.64
19:R:126:MET:O	19:R:126:MET:HG2	1.97	0.64
1:2:1247:C:H4'	1:2:1248:U:H4'	1.79	0.64
1:2:1398:G:O6	1:2:1448:A:N1	2.31	0.64
5:D:21:LEU:HD11	5:D:48:ILE:HG21	1.78	0.64
7:F:130:ARG:O	30:c:23:SER:N	2.28	0.64
27:Z:60:LYS:O	27:Z:64:ASN:ND2	2.30	0.64
30:c:32:VAL:HB	30:c:42:ILE:HG22	1.79	0.64
1:2:1060:A:H4'	1:2:1061:U:H5'	1.77	0.64
1:2:1229:G:H3'	20:S:138:THR:HG23	1.80	0.64
5:D:94:ARG:O	5:D:101:GLN:NE2	2.31	0.64
1:2:1507:G:H22	33:f:84:SER:HA	1.63	0.64
1:2:1594:A:N6	21:T:49:ASP:OD2	2.30	0.64
1:2:1587:G:H5'	21:T:77:LYS:HG3	1.79	0.64
5:D:191:PRO:HB2	5:D:197:LYS:HB2	1.78	0.64
1:2:1143:A:H5'	4:C:190:SER:HB3	1.79	0.64
1:2:1398:G:H1	1:2:1448:A:H2	1.46	0.64
7:F:165:ASN:ND2	7:F:172:CYS:SG	2.70	0.64
34:g:304:ASP:O	34:g:305:ASN:ND2	2.31	0.64
1:2:560:A:OP2	11:J:177:ASN:ND2	2.31	0.63
7:F:139:VAL:HA	30:c:44:ARG:NH2	2.13	0.63
21:T:36:THR:HG23	21:T:37:VAL:HG13	1.79	0.63
1:2:925:G:H1	1:2:1017:U:H3	1.46	0.63
1:2:1203:G:H2'	1:2:1204:A:C8	2.33	0.63
1:2:1864:U:O4	28:a:34:LYS:NZ	2.29	0.63
20:S:121:ARG:O	20:S:124:ARG:HB2	1.99	0.63
33:f:121:CYS:HG	33:f:123:SER:HG	1.41	0.63
1:2:1587:G:H2'	21:T:92:PHE:HB2	1.79	0.63
1:2:1607:A:C4	20:S:128:GLY:HA3	2.33	0.63
1:2:1714:U:H2'	1:2:1715:A:C8	2.33	0.63
1:2:609:U:H2'	1:2:610:G:H8	1.63	0.63
1:2:1473:G:N2	1:2:1476:A:N1	2.46	0.63
24:W:28:ARG:HB3	24:W:60:LYS:HG2	1.80	0.63
1:2:78:C:OP1	8:G:159:ARG:NH2	2.32	0.63
6:E:124:CYS:HA	6:E:142:HIS:CE1	2.33	0.63
1:2:1664:A:O2'	1:2:1666:C:N4	2.30	0.63
1:2:1711:U:H2'	1:2:1712:A:H8	1.63	0.63
1:2:1854:U:H2'	1:2:1855:G:H8	1.63	0.63
1:2:1252:C:OP1	22:U:75:LYS:NZ	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:131:ASP:OD2	28:a:67:LEU:HD23	1.99	0.63
33:f:101:ALA:HA	33:f:104:LYS:HE2	1.81	0.63
34:g:89:LEU:HD13	34:g:99:ARG:HB3	1.79	0.63
2:A:181:GLU:O	2:A:185:MET:HG3	1.99	0.62
3:B:164:ILE:O	3:B:168:MET:HG3	1.99	0.62
1:2:1179:G:N2	1:2:1182:A:OP2	2.32	0.62
9:H:9:VAL:HG23	9:H:24:SER:HB3	1.81	0.62
1:2:1215:C:O2'	1:2:1645:C:OP2	2.17	0.62
1:2:1862:G:O2'	28:a:5:ARG:NH2	2.32	0.62
10:I:70:GLU:OE2	13:L:21:LYS:NZ	2.31	0.62
11:J:134:HIS:HB3	11:J:159:PHE:HE1	1.65	0.62
1:2:818:A:P	11:J:80:ARG:HH12	2.23	0.62
14:M:32:ALA:HB2	14:M:37:GLU:HB3	1.80	0.62
1:2:1523:C:H5''	20:S:141:ARG:NH1	2.14	0.62
1:2:1711:U:H2'	1:2:1712:A:C8	2.35	0.62
1:2:1473:G:H1	1:2:1476:A:N6	1.97	0.62
1:2:4:C:H4'	4:C:207:ALA:HB2	1.81	0.62
20:S:116:LYS:O	20:S:118:ARG:NH1	2.28	0.62
1:2:860:G:N2	24:W:107:SER:OG	2.32	0.62
1:2:1013:U:OP1	1:2:1129:G:O2'	2.18	0.62
1:2:1323:U:H5'	1:2:1324:G:C8	2.35	0.62
1:2:1522:A:H5''	20:S:137:LYS:O	2.00	0.62
21:T:59:SER:OG	21:T:62:ARG:NH2	2.29	0.62
24:W:115:GLU:HG3	24:W:118:ARG:HH21	1.65	0.62
3:B:131:ASP:HB3	3:B:180:ASP:HB2	1.82	0.61
21:T:144:LYS:HD2	21:T:144:LYS:O	2.00	0.61
1:2:1523:C:OP1	20:S:141:ARG:HD3	2.00	0.61
21:T:104:LEU:HD22	21:T:107:LEU:HD22	1.82	0.61
1:2:606:G:H5''	32:e:56:ASN:HB3	1.82	0.61
1:2:920:A:OP1	24:W:57:ARG:NE	2.27	0.61
1:2:1736:G:H2'	1:2:1737:G:H8	1.65	0.61
27:Z:68:ILE:HD12	27:Z:111:ARG:HD3	1.82	0.61
1:2:1863:A:OP2	28:a:4:LYS:NZ	2.33	0.61
3:B:36:PRO:HB2	3:B:38:MET:SD	2.39	0.61
1:2:1217:A:H2'	1:2:1218:C:C6	2.36	0.61
1:2:1332:A:O2'	5:D:145:GLN:O	2.16	0.61
10:I:34:ALA:HB2	10:I:56:ARG:HH11	1.66	0.61
1:2:1740:C:H42	1:2:1794:C:H42	1.46	0.61
13:L:42:LEU:HD13	13:L:72:ILE:HD11	1.81	0.61
33:f:138:ARG:HH11	33:f:138:ARG:HB3	1.66	0.61
1:2:1408:U:H5''	1:2:1439:A:H61	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:981:A:H2'	1:2:982:G:C8	2.36	0.61
3:B:190:PRO:O	3:B:195:LYS:NZ	2.34	0.61
15:N:22:VAL:HG23	15:N:66:VAL:HG22	1.81	0.61
1:2:1098:C:H2'	1:2:1099:G:C8	2.36	0.61
1:2:1736:G:H2'	1:2:1737:G:C8	2.36	0.61
34:g:155:ARG:HE	34:g:199:THR:HA	1.64	0.60
1:2:334:C:H5	8:G:190:ARG:NH1	1.98	0.60
1:2:583:A:OP2	11:J:162:ARG:NH2	2.33	0.60
3:B:122:GLU:HG2	3:B:213:ARG:HH12	1.67	0.60
1:2:118:C:H1'	1:2:445:A:C5	2.36	0.60
1:2:220:U:H2'	1:2:221:A:H8	1.64	0.60
1:2:436:G:OP2	1:2:471:G:O2'	2.18	0.60
1:2:889:U:H1'	1:2:890:U:H2'	1.84	0.60
1:2:1275:G:H21	1:2:1277:C:H5''	1.66	0.60
5:D:115:VAL:HG21	5:D:142:LEU:HD22	1.83	0.60
6:E:79:ASP:HB3	6:E:82:TYR:HB2	1.84	0.60
1:2:922:A:N1	1:2:1022:U:C5	2.70	0.60
1:2:1036:A:H4'	1:2:1855:G:N2	2.17	0.60
1:2:1815:A:H2'	1:2:1816:G:O4'	2.01	0.60
15:N:28:LEU:H	15:N:28:LEU:HD12	1.65	0.60
1:2:317:C:OP2	8:G:183:ARG:NH1	2.35	0.60
1:2:953:C:O2	16:O:55:ARG:NH2	2.35	0.60
10:I:157:LYS:NZ	10:I:158:ILE:O	2.35	0.60
1:2:922:A:N1	1:2:1022:U:H5	1.99	0.60
1:2:1298:G:O3'	17:P:59:ARG:NH2	2.34	0.60
1:2:1308:U:H5	33:f:138:ARG:HD3	1.67	0.60
5:D:55:THR:HA	5:D:58:VAL:HG12	1.83	0.60
14:M:49:LEU:O	14:M:107:SER:OG	2.18	0.60
1:2:640:A:H2'	1:2:641:A:C8	2.37	0.60
24:W:83:LEU:HD11	24:W:120:HIS:HA	1.82	0.60
27:Z:80:ARG:HD3	27:Z:83:LEU:HD13	1.84	0.60
1:2:1284:A:H61	14:M:91:LEU:HD22	1.66	0.59
16:O:44:VAL:HG13	16:O:53:ILE:HB	1.84	0.59
1:2:570:C:O2	26:Y:34:THR:OG1	2.17	0.59
1:2:1308:U:C6	33:f:138:ARG:HG3	2.37	0.59
1:2:1060:A:O2'	1:2:1062:A:N7	2.27	0.59
6:E:126:VAL:HA	6:E:141:THR:HA	1.83	0.59
19:R:81:ARG:NH1	19:R:82:ASP:OD1	2.28	0.59
18:Q:92:LEU:HD22	18:Q:112:LEU:HD11	1.84	0.59
19:R:78:ARG:NE	19:R:78:ARG:HA	2.16	0.59
1:2:106:C:H2'	1:2:107:A:H8	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:77:GLU:HG2	19:R:78:ARG:HH21	1.66	0.59
26:Y:114:MET:HG3	26:Y:125:VAL:HG21	1.83	0.59
28:a:24:THR:HG21	28:a:71:LEU:HB3	1.85	0.59
1:2:107:A:H2'	1:2:108:G:C8	2.37	0.59
2:A:34:MET:HE1	2:A:162:PRO:HB3	1.83	0.59
2:A:184:ARG:HG3	2:A:189:ILE:HD11	1.84	0.59
10:I:42:ARG:HG2	10:I:58:LEU:HB2	1.85	0.59
1:2:367:U:H4'	1:2:371:A:C8	2.38	0.59
1:2:1614:A:OP2	17:P:42:ARG:NH2	2.36	0.59
18:Q:30:GLY:N	18:Q:63:PHE:O	2.34	0.59
1:2:1083:A:N7	1:2:1841:C:O2'	2.34	0.59
1:2:1603:G:OP2	20:S:24:ARG:NH2	2.36	0.59
4:C:191:VAL:HG11	4:C:236:PHE:HA	1.84	0.59
1:2:455:A:H2'	1:2:456:C:C6	2.37	0.59
10:I:101:ILE:HD12	10:I:190:LEU:HD11	1.85	0.59
20:S:110:ASP:HA	20:S:113:ARG:HD3	1.84	0.59
1:2:822:U:H2'	1:2:824:C:OP2	2.03	0.59
8:G:200:LYS:O	8:G:204:GLU:HG2	2.02	0.59
33:f:141:CYS:CB	33:f:148:TYR:CE2	2.85	0.59
34:g:12:LYS:NZ	34:g:49:GLU:O	2.31	0.59
21:T:91:HIS:CG	21:T:92:PHE:H	2.21	0.58
1:2:1153:C:OP2	24:W:71:LYS:NZ	2.29	0.58
1:2:1313:A:H61	14:M:35:ILE:HG22	1.67	0.58
21:T:6:VAL:HG11	21:T:65:TYR:HE2	1.66	0.58
1:2:1227:G:N7	1:2:1228:A:N6	2.52	0.58
1:2:1299:A:N7	1:2:1514:G:O2'	2.35	0.58
2:A:76:VAL:HG12	2:A:123:VAL:HB	1.84	0.58
6:E:124:CYS:HA	6:E:142:HIS:HE1	1.68	0.58
9:H:181:THR:HG22	9:H:183:LYS:HG3	1.85	0.58
15:N:29:THR:OG1	15:N:32:ASP:OD2	2.19	0.58
18:Q:77:HIS:HA	18:Q:80:GLN:HE21	1.69	0.58
11:J:113:GLN:OE1	11:J:154:GLN:NE2	2.37	0.58
34:g:59:LEU:HD23	34:g:95:GLY:HA2	1.83	0.58
1:2:1084:A:OP1	1:2:1858:G:O2'	2.21	0.58
1:2:1265:A:H2'	33:f:81:LYS:HD3	1.86	0.58
2:A:122:LEU:HD21	2:A:133:PRO:HB2	1.85	0.58
3:B:125:VAL:HG23	3:B:169:MET:HG2	1.85	0.58
6:E:86:PHE:CE1	6:E:182:MET:HE2	2.38	0.58
1:2:220:U:H2'	1:2:221:A:C8	2.38	0.58
1:2:1521:C:H5''	20:S:136:THR:HG22	1.86	0.58
2:A:188:THR:OG1	2:A:189:ILE:N	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:172:LYS:NZ	34:g:191:HIS:O	2.32	0.58
3:B:28:LYS:HB3	3:B:48:LEU:HD11	1.85	0.58
1:2:1231:C:O2'	1:2:1232:U:OP1	2.21	0.58
5:D:8:LYS:HB2	22:U:61:LEU:HD11	1.84	0.58
7:F:58:ALA:HB2	18:Q:125:ARG:HH22	1.69	0.58
17:P:74:GLU:HG2	17:P:75:VAL:HG22	1.84	0.58
34:g:244:ASN:ND2	34:g:292:SER:O	2.37	0.58
1:2:1424:G:O4'	18:Q:26:LYS:NZ	2.37	0.58
2:A:160:ALA:N	23:V:66:ASP:OD2	2.30	0.58
1:2:1273:C:H5''	1:2:1286:G:H1	1.69	0.57
1:2:1609:C:H1'	1:2:1610:G:OP2	2.04	0.57
7:F:19:LEU:HB3	7:F:23:TRP:HB2	1.84	0.57
12:K:20:VAL:HG12	12:K:69:TRP:HB2	1.85	0.57
1:2:1283:C:H2'	1:2:1284:A:H4'	1.84	0.57
5:D:116:ARG:NE	36:n:172:ASP:OD1	2.37	0.57
9:H:78:ARG:O	9:H:82:GLU:HG2	2.03	0.57
12:K:35:LEU:C	12:K:35:LEU:HD23	2.29	0.57
20:S:119:ALA:O	20:S:123:LEU:HG	2.04	0.57
28:a:78:VAL:CG1	28:a:84:VAL:HG22	2.34	0.57
33:f:121:CYS:SG	33:f:123:SER:OG	2.60	0.57
1:2:1240:A:H2'	1:2:1241:A:H4'	1.86	0.57
1:2:1609:C:H2'	1:2:1609:C:O2	2.05	0.57
18:Q:12:VAL:HG11	18:Q:94:ALA:HB2	1.86	0.57
20:S:130:ARG:H	20:S:142:ARG:NH1	2.02	0.57
1:2:1317:C:H2'	1:2:1317:C:O2	2.04	0.57
8:G:3:LEU:HD13	8:G:109:LEU:HB3	1.86	0.57
13:L:78:THR:HG22	13:L:79:LYS:HG3	1.85	0.57
1:2:145:G:H2'	1:2:146:G:C8	2.40	0.57
1:2:973:C:N3	16:O:55:ARG:NH1	2.53	0.57
7:F:204:ARG:HH12	30:c:60:GLU:HG3	1.70	0.57
14:M:22:LEU:HG	14:M:51:VAL:HG23	1.87	0.57
1:2:104:A:N7	1:2:356:C:N4	2.53	0.57
1:2:493:A:H1'	1:2:574:A:H5''	1.87	0.57
14:M:39:ALA:HA	14:M:42:LEU:HB2	1.87	0.57
20:S:125:HIS:O	20:S:126:PHE:HB3	2.05	0.57
29:b:67:THR:OG1	29:b:70:LYS:O	2.22	0.57
5:D:61:GLU:HB2	5:D:64:ARG:HD2	1.86	0.57
19:R:89:SER:HB3	19:R:92:ASP:HB2	1.85	0.57
21:T:39:LEU:CD2	21:T:43:LYS:HE3	2.35	0.57
1:2:296:U:O2'	6:E:131:VAL:O	2.19	0.56
1:2:1327:G:O2'	1:2:1328:G:O4'	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1618:C:O2	31:d:12:ARG:NH2	2.37	0.56
1:2:1627:C:H4'	1:2:1628:C:OP1	2.04	0.56
3:B:49:VAL:HG21	3:B:62:LEU:HD22	1.87	0.56
11:J:130:ILE:HG13	11:J:135:ILE:HG13	1.87	0.56
2:A:127:PRO:HG2	2:A:152:SER:HB2	1.87	0.56
1:2:952:G:O2'	16:O:52:THR:N	2.37	0.56
1:2:1112:U:O2	1:2:1121:G:O6	2.24	0.56
1:2:1139:C:H2'	1:2:1140:G:O4'	2.04	0.56
9:H:160:LYS:HD2	9:H:191:GLU:HA	1.86	0.56
10:I:3:ILE:O	10:I:30:GLY:N	2.38	0.56
13:L:126:VAL:HG12	13:L:145:VAL:HG22	1.86	0.56
34:g:42:MET:HB3	34:g:56:GLN:H	1.70	0.56
1:2:57:U:OP1	1:2:504:G:O2'	2.22	0.56
7:F:56:TYR:HB3	7:F:63:LYS:HB3	1.87	0.56
18:Q:143:LYS:HD3	18:Q:143:LYS:N	2.20	0.56
21:T:139:ALA:O	21:T:144:LYS:HE2	2.05	0.56
1:2:1573:G:H2'	1:2:1574:C:C6	2.41	0.56
17:P:79:HIS:CD2	17:P:96:VAL:HA	2.40	0.56
18:Q:82:TYR:HA	18:Q:85:ARG:HG3	1.88	0.56
1:2:303:C:O2	10:I:184:ARG:NH1	2.34	0.56
1:2:562:U:H2'	1:2:563:G:C8	2.41	0.56
5:D:137:VAL:HG22	5:D:151:LYS:HB3	1.88	0.56
34:g:198:VAL:HG11	34:g:209:SER:HA	1.88	0.56
1:2:748:C:OP1	1:2:750:C:O2'	2.18	0.56
1:2:1566:G:H21	1:2:1568:C:H3'	1.71	0.56
7:F:51:HIS:NE2	7:F:70:GLU:OE2	2.32	0.56
8:G:49:VAL:HG22	8:G:115:LYS:HB2	1.88	0.56
18:Q:80:GLN:NE2	18:Q:81:ILE:HG12	2.20	0.56
32:e:52:LYS:O	32:e:53:LYS:HE2	2.05	0.56
1:2:1342:U:H4'	1:2:1343:U:O5'	2.06	0.56
21:T:6:VAL:HG11	21:T:65:TYR:CE2	2.41	0.56
1:2:1752:C:H41	1:2:1780:G:H3'	1.71	0.56
7:F:139:VAL:HB	30:c:46:VAL:HG23	1.88	0.56
20:S:130:ARG:HH11	20:S:142:ARG:HD3	1.71	0.56
34:g:85:GLY:HA2	34:g:104:HIS:HB2	1.87	0.56
1:2:527:C:H4'	11:J:121:LYS:HD3	1.88	0.56
1:2:1284:A:O2'	14:M:33:ARG:O	2.18	0.56
6:E:151:ASP:HB3	6:E:154:ILE:HG13	1.87	0.56
12:K:9:ILE:HG13	12:K:83:LEU:HD21	1.87	0.56
19:R:76:GLU:O	19:R:80:ARG:HG3	2.06	0.56
34:g:154:VAL:HG22	34:g:167:SER:HA	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:193:GLY:HA3	34:g:212:LYS:HG2	1.88	0.56
1:2:28:U:H2'	1:2:29:G:H8	1.71	0.55
1:2:433:A:H5''	10:I:22:HIS:HB3	1.88	0.55
3:B:129:THR:HB	3:B:180:ASP:HA	1.86	0.55
5:D:74:GLN:NE2	5:D:79:PHE:O	2.26	0.55
12:K:80:ARG:NH1	12:K:85:LEU:O	2.39	0.55
1:2:1374:C:O2'	1:2:1464:C:O2	2.22	0.55
11:J:110:LEU:HB2	11:J:147:PHE:HB3	1.88	0.55
24:W:70:ASN:ND2	24:W:130:PHE:OXT	2.37	0.55
1:2:1723:G:H2'	1:2:1724:A:H8	1.71	0.55
34:g:65:PHE:HB2	34:g:83:TRP:HE1	1.71	0.55
1:2:1309:C:O2'	33:f:140:TYR:C	2.50	0.55
1:2:1519:U:H4'	20:S:136:THR:CG2	2.36	0.55
3:B:138:PHE:HB3	3:B:213:ARG:HH21	1.72	0.55
9:H:147:LYS:HA	24:W:49:GLU:HG2	1.89	0.55
17:P:87:PRO:HD3	17:P:112:ILE:HD11	1.87	0.55
21:T:40:ALA:HA	21:T:96:SER:N	2.21	0.55
1:2:1399:C:H2'	1:2:1401:A:C8	2.42	0.55
1:2:1628:C:OP1	21:T:85:ASN:ND2	2.40	0.55
1:2:1754:G:O6	1:2:1776:G:O2'	2.23	0.55
9:H:8:ILE:O	9:H:10:LYS:NZ	2.31	0.55
19:R:6:THR:HG22	19:R:8:THR:H	1.71	0.55
26:Y:41:ARG:HG2	26:Y:55:ILE:HG22	1.88	0.55
34:g:42:MET:CB	34:g:56:GLN:H	2.20	0.55
34:g:207:CYS:O	34:g:218:LEU:HA	2.06	0.55
1:2:634:A:H2'	1:2:635:G:H8	1.72	0.55
1:2:1235:G:N2	1:2:1236:G:N3	2.55	0.55
4:C:72:ASP:HB3	4:C:74:LYS:HG2	1.88	0.55
4:C:134:ASN:HD22	4:C:134:ASN:C	2.12	0.55
4:C:220:ASP:N	4:C:220:ASP:OD1	2.37	0.55
8:G:48:TYR:OH	8:G:116:LYS:NZ	2.40	0.55
10:I:130:THR:N	10:I:133:GLU:OE2	2.40	0.55
18:Q:117:ARG:NH1	18:Q:118:THR:OG1	2.39	0.55
34:g:296:GLN:HB3	34:g:312:VAL:HG21	1.88	0.55
1:2:1518:C:H5''	1:2:1519:U:H6	1.72	0.55
16:O:45:THR:HG22	16:O:52:THR:HA	1.89	0.55
20:S:114:LEU:HB3	20:S:122:GLY:HA3	1.89	0.55
21:T:39:LEU:C	21:T:43:LYS:HE2	2.31	0.55
1:2:1317:C:C2'	1:2:1318:G:OP1	2.55	0.55
1:2:1798:C:H2'	1:2:1799:G:O4'	2.07	0.55
3:B:179:ASN:HB3	3:B:183:GLU:HG3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:178:HIS:ND1	4:C:221:ASP:OD2	2.38	0.55
20:S:39:ARG:HB3	20:S:82:TRP:HZ2	1.69	0.55
4:C:198:ALA:HB1	4:C:202:THR:HG21	1.89	0.55
12:K:36:ALA:C	12:K:38:LYS:H	2.14	0.55
17:P:108:LYS:HD2	17:P:109:PRO:HD2	1.87	0.55
20:S:142:ARG:HB2	20:S:142:ARG:NH1	2.21	0.55
1:2:959:G:OP1	16:O:104:ARG:NH2	2.40	0.55
12:K:49:MET:HE3	12:K:58:VAL:HG11	1.88	0.55
26:Y:51:THR:OG1	26:Y:53:ASP:OD1	2.19	0.55
1:2:1010:G:H2'	1:2:1011:A:C8	2.41	0.54
1:2:1566:G:O2'	1:2:1567:G:N2	2.30	0.54
9:H:139:ILE:HG23	9:H:156:VAL:HG13	1.88	0.54
1:2:180:G:O2'	1:2:181:A:OP1	2.24	0.54
1:2:1309:C:O2'	33:f:140:TYR:HA	2.07	0.54
1:2:1797:U:H2'	1:2:1798:C:C6	2.41	0.54
16:O:140:THR:OG1	16:O:141:ARG:N	2.38	0.54
1:2:581:U:H4'	26:Y:66:GLY:HA2	1.88	0.54
2:A:54:THR:HA	2:A:162:PRO:HD2	1.88	0.54
2:A:94:THR:O	2:A:186:ARG:NH2	2.40	0.54
19:R:80:ARG:HH11	19:R:80:ARG:HB3	1.73	0.54
22:U:80:PHE:HB3	31:d:52:PHE:HB3	1.89	0.54
28:a:73:TYR:CB	28:a:78:VAL:HG23	2.37	0.54
1:2:750:C:H2'	1:2:751:G:C8	2.43	0.54
1:2:1253:A:H4'	1:2:1254:C:H5''	1.89	0.54
1:2:1395:C:H4'	18:Q:121:VAL:HG12	1.89	0.54
13:L:33:LEU:HD12	13:L:34:PRO:HD2	1.87	0.54
28:a:11:ALA:HB3	28:a:33:ASP:HB2	1.88	0.54
1:2:870:A:H62	1:2:916:A:H5'	1.73	0.54
1:2:913:A:OP2	9:H:99:ARG:NH1	2.40	0.54
1:2:1397:U:H3	1:2:1442:U:H5''	1.72	0.54
3:B:224:GLU:HB3	3:B:227:LYS:HD3	1.89	0.54
21:T:124:THR:O	21:T:128:GLN:N	2.31	0.54
34:g:186:THR:HG21	34:g:224:GLY:HA3	1.88	0.54
1:2:398:A:OP1	1:2:399:C:O2'	2.19	0.54
1:2:568:C:H2'	1:2:569:A:C8	2.43	0.54
1:2:993:G:OP1	1:2:1131:G:N2	2.29	0.54
7:F:66:CYS:HB3	7:F:71:ARG:HH22	1.70	0.54
7:F:136:ARG:HH21	7:F:199:VAL:HG21	1.73	0.54
14:M:103:VAL:HG23	14:M:104:VAL:HG13	1.89	0.54
16:O:95:ILE:HG13	16:O:116:LEU:HD11	1.89	0.54
16:O:144:GLY:O	28:a:22:ARG:NH2	2.35	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:195:LEU:HD22	34:g:196:ASN:H	1.73	0.54
1:2:448:A:H5''	10:I:25:ARG:HA	1.90	0.54
1:2:1298:G:H1'	17:P:79:HIS:CE1	2.42	0.54
8:G:159:ARG:HG2	8:G:173:ALA:HB2	1.90	0.54
26:Y:23:MET:HE1	26:Y:75:ILE:HG13	1.90	0.54
1:2:532:C:H2'	1:2:533:A:C8	2.43	0.54
1:2:1032:C:OP1	15:N:112:LYS:NZ	2.41	0.54
1:2:1299:A:H62	1:2:1514:G:H4'	1.72	0.54
1:2:1550:G:O2'	1:2:1558:C:O2	2.25	0.54
1:2:1658:G:H5''	31:d:33:LYS:HB2	1.89	0.54
4:C:84:PHE:CE2	4:C:265:PRO:HD3	2.43	0.54
6:E:107:GLY:HA2	6:E:189:LEU:HG	1.89	0.54
9:H:126:HIS:CE1	9:H:181:THR:HG23	2.42	0.54
21:T:98:SER:O	21:T:102:ARG:HG2	2.08	0.54
25:X:60:LYS:HE2	25:X:114:ASP:HA	1.89	0.54
1:2:613:G:N1	1:2:629:A:OP1	2.32	0.54
1:2:980:A:H2'	1:2:981:A:C8	2.43	0.54
1:2:1015:U:O2'	1:2:1017:U:OP2	2.15	0.54
1:2:1076:G:OP1	15:N:106:ARG:NH1	2.38	0.54
1:2:1705:C:H2'	1:2:1706:G:C8	2.43	0.54
12:K:51:SER:OG	12:K:55:ARG:NH1	2.41	0.54
34:g:152:SER:N	34:g:168:CYS:O	2.39	0.54
1:2:630:U:C4	36:n:182:TYR:HD1	2.25	0.54
1:2:1426:U:H1'	21:T:123:LEU:HD22	1.90	0.54
1:2:1618:C:O4'	31:d:10:HIS:NE2	2.41	0.54
1:2:1779:G:H5'	1:2:1780:G:H5''	1.90	0.54
5:D:218:LEU:HD11	34:g:192:THR:HA	1.90	0.54
11:J:111:GLN:NE2	11:J:127:ARG:HB2	2.23	0.54
18:Q:101:ASP:O	18:Q:105:LYS:HG3	2.07	0.54
34:g:173:LEU:HD22	34:g:187:ASN:HD21	1.73	0.54
1:2:575:A:H3'	1:2:576:A:H5''	1.90	0.53
1:2:598:G:O2'	1:2:605:A:N1	2.40	0.53
1:2:1539:U:N3	21:T:47:PRO:HG3	2.23	0.53
1:2:1866:A:N6	28:a:84:VAL:HB	2.23	0.53
15:N:127:ARG:O	15:N:131:THR:HG23	2.07	0.53
25:X:84:PHE:CE2	25:X:86:PRO:HA	2.43	0.53
34:g:172:LYS:HD3	34:g:191:HIS:HB2	1.89	0.53
1:2:12:U:H2'	1:2:13:C:C6	2.43	0.53
1:2:1262:C:N4	31:d:17:GLY:HA3	2.23	0.53
6:E:20:LEU:HD21	6:E:46:ILE:HD12	1.90	0.53
12:K:23:ALA:HA	12:K:34:GLU:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:87:PRO:HB2	17:P:109:PRO:HB2	1.91	0.53
32:e:16:THR:O	32:e:18:LYS:NZ	2.41	0.53
1:2:155:G:H4'	8:G:15:LEU:HG	1.90	0.53
1:2:642:U:H4'	1:2:644:G:H4'	1.89	0.53
1:2:1270:G:H1	33:f:81:LYS:NZ	2.05	0.53
1:2:1309:C:H2'	33:f:141:CYS:O	2.08	0.53
2:A:192:GLU:CD	2:A:192:GLU:H	2.17	0.53
7:F:139:VAL:HA	30:c:44:ARG:HH22	1.72	0.53
19:R:61:ILE:HD11	19:R:71:ILE:HD11	1.91	0.53
27:Z:62:VAL:HG11	27:Z:70:PRO:HB3	1.91	0.53
1:2:150:A:H62	1:2:168:C:H42	1.56	0.53
1:2:582:U:H1'	26:Y:33:ALA:HB2	1.90	0.53
1:2:1228:A:H2'	1:2:1228:A:N3	2.23	0.53
7:F:87:LEU:HD11	7:F:91:ARG:NH2	2.23	0.53
14:M:109:VAL:HG12	14:M:110:VAL:HG23	1.90	0.53
1:2:562:U:H4'	11:J:132:GLN:HB3	1.90	0.53
1:2:1230:C:OP1	20:S:142:ARG:NE	2.41	0.53
7:F:192:LYS:O	7:F:196:LEU:HG	2.09	0.53
10:I:194:GLU:OE2	13:L:12:LYS:HE2	2.09	0.53
19:R:61:ILE:HG13	19:R:66:VAL:HG23	1.89	0.53
21:T:39:LEU:HD23	21:T:43:LYS:HE3	1.88	0.53
34:g:246:TYR:HB3	34:g:261:LEU:HD11	1.90	0.53
34:g:302:TYR:HB3	34:g:304:ASP:H	1.74	0.53
1:2:1022:U:O2	15:N:128:TYR:CZ	2.62	0.53
1:2:1224:G:N2	18:Q:143:LYS:HG2	2.24	0.53
1:2:1665:G:H4'	1:2:1666:C:OP2	2.09	0.53
8:G:49:VAL:HG21	8:G:115:LYS:HD2	1.91	0.53
31:d:19:ARG:CZ	31:d:32:ARG:HH12	2.20	0.53
1:2:344:U:H2'	1:2:345:U:C6	2.44	0.53
20:S:113:ARG:HG2	20:S:114:LEU:N	2.23	0.53
1:2:1190:A:N3	1:2:1714:U:O2'	2.37	0.53
4:C:194:ARG:HD3	4:C:196:ILE:HD11	1.91	0.53
4:C:255:LEU:HD13	23:V:23:ILE:HD11	1.91	0.53
6:E:128:LYS:HG2	6:E:140:VAL:HB	1.91	0.53
12:K:26:ASP:HB3	12:K:29:MET:HG2	1.90	0.53
16:O:62:VAL:HG21	16:O:67:ASP:HB3	1.91	0.53
18:Q:27:ARG:HA	18:Q:66:VAL:HA	1.91	0.53
34:g:65:PHE:HB2	34:g:83:TRP:NE1	2.24	0.53
1:2:1025:U:H2'	1:2:1026:C:O4'	2.08	0.53
1:2:1617:G:H1	1:2:1620:A:H62	1.57	0.53
1:2:1684:C:H2'	1:2:1684:C:O2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:127:ARG:N	6:E:140:VAL:O	2.39	0.53
19:R:81:ARG:HD3	19:R:81:ARG:C	2.34	0.53
1:2:846:G:H2'	6:E:19:MET:HG2	1.91	0.53
1:2:943:U:H2'	1:2:944:A:H8	1.73	0.53
1:2:1462:U:H5''	1:2:1463:U:H5	1.73	0.53
1:2:1465:A:OP1	19:R:60:ARG:NH1	2.42	0.53
1:2:1471:C:OP1	18:Q:117:ARG:NH2	2.42	0.53
2:A:143:PRO:HB2	23:V:34:MET:HE3	1.91	0.53
17:P:93:MET:HE1	17:P:105:VAL:H	1.74	0.53
18:Q:22:VAL:HG21	18:Q:71:ARG:NH2	2.23	0.53
1:2:455:A:H2'	1:2:456:C:H6	1.74	0.52
1:2:678:U:OP1	15:N:127:ARG:NH2	2.41	0.52
1:2:1394:G:H5'	18:Q:126:ARG:HG2	1.90	0.52
1:2:1845:A:H2'	1:2:1846:G:C8	2.44	0.52
18:Q:97:GLN:HA	18:Q:105:LYS:CG	2.34	0.52
28:a:37:LYS:HG2	28:a:70:LYS:HE2	1.91	0.52
1:2:1546:G:P	18:Q:18:THR:HG21	2.49	0.52
1:2:1642:U:O2'	18:Q:143:LYS:O	2.20	0.52
8:G:44:GLU:OE2	8:G:44:GLU:N	2.23	0.52
30:c:17:VAL:HG22	30:c:30:VAL:HG12	1.91	0.52
34:g:298:LEU:HB3	34:g:310:TRP:HB2	1.91	0.52
1:2:28:U:H2'	1:2:29:G:C8	2.45	0.52
1:2:656:G:N2	1:2:663:C:H5''	2.24	0.52
1:2:1856:C:H2'	1:2:1857:G:H8	1.75	0.52
4:C:273:LEU:HA	4:C:276:THR:HB	1.90	0.52
1:2:944:A:H5''	16:O:134:PRO:HB3	1.90	0.52
1:2:1174:U:H2'	1:2:1175:G:H8	1.75	0.52
1:2:1474:A:C2	1:2:1475:G:H1'	2.44	0.52
16:O:145:GLY:O	28:a:22:ARG:NH2	2.43	0.52
30:c:21:THR:OG1	30:c:29:GLN:OE1	2.23	0.52
33:f:105:TYR:HB2	33:f:107:LYS:HE2	1.90	0.52
1:2:222:U:H5''	13:L:17:PHE:CG	2.44	0.52
1:2:928:G:H1	1:2:1013:U:H3	1.57	0.52
1:2:1717:C:H2'	1:2:1718:G:O4'	2.09	0.52
7:F:121:PRO:HG2	7:F:146:ARG:HG3	1.90	0.52
33:f:135:HIS:C	33:f:137:ASP:H	2.18	0.52
34:g:152:SER:H	34:g:169:GLY:HA2	1.73	0.52
1:2:1354:G:N2	1:2:1357:A:OP2	2.35	0.52
3:B:188:LEU:HD11	3:B:215:VAL:HG21	1.92	0.52
8:G:181:THR:HG22	8:G:184:VAL:HG13	1.90	0.52
14:M:91:LEU:HD13	14:M:102:LYS:HE2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:57:THR:H	16:O:60:MET:HG3	1.75	0.52
30:c:44:ARG:HB3	30:c:44:ARG:CZ	2.40	0.52
1:2:1482:C:OP1	31:d:54:LYS:NZ	2.43	0.52
10:I:163:GLU:O	10:I:167:GLN:HG2	2.10	0.52
34:g:7:LEU:HB3	34:g:272:GLN:HB3	1.92	0.52
34:g:298:LEU:HD23	34:g:310:TRP:HD1	1.74	0.52
1:2:106:C:H2'	1:2:107:A:C8	2.44	0.52
1:2:1430:C:H3'	1:2:1431:G:C8	2.45	0.52
15:N:27:LYS:HE3	15:N:27:LYS:HA	1.91	0.52
1:2:1037:G:H4'	1:2:1845:A:H4'	1.92	0.52
1:2:1138:C:C4	23:V:61:ARG:HD2	2.45	0.52
1:2:1520:G:N2	17:P:127:LYS:O	2.35	0.52
1:2:1567:G:H1'	21:T:37:VAL:HG12	1.92	0.52
1:2:1592:C:H5''	1:2:1593:C:O4'	2.10	0.52
8:G:44:GLU:H	8:G:44:GLU:CD	2.16	0.52
1:2:617:G:N7	25:X:67:ARG:NH1	2.57	0.52
1:2:1308:U:H5	33:f:138:ARG:CD	2.23	0.52
10:I:73:THR:O	10:I:74:ARG:NH1	2.36	0.52
16:O:101:GLY:HA3	16:O:134:PRO:HD2	1.92	0.52
18:Q:108:ILE:HA	18:Q:111:ILE:HG22	1.91	0.52
3:B:29:ASP:OD1	3:B:51:ARG:NE	2.42	0.51
7:F:55:ARG:NE	18:Q:122:ALA:HA	2.25	0.51
7:F:139:VAL:HG12	30:c:44:ARG:HH22	1.75	0.51
1:2:1113:A:H2'	1:2:1114:U:C6	2.46	0.51
1:2:1528:G:H21	1:2:1665:G:H1'	1.75	0.51
1:2:1569:A:OP1	21:T:94:ARG:NH1	2.42	0.51
7:F:134:VAL:O	7:F:135:ARG:HD2	2.10	0.51
9:H:109:ARG:HB3	9:H:111:LYS:HD2	1.92	0.51
18:Q:49:TYR:HA	18:Q:52:LEU:HG	1.91	0.51
1:2:17:C:H2'	1:2:18:C:C6	2.45	0.51
1:2:1410:C:H2'	1:2:1411:G:N7	2.25	0.51
8:G:215:LYS:NZ	8:G:219:GLU:OE1	2.43	0.51
30:c:44:ARG:HB3	30:c:44:ARG:NH1	2.25	0.51
1:2:1242:U:C2	1:2:1518:C:H4'	2.46	0.51
13:L:147:LYS:HG3	13:L:151:THR:HG21	1.92	0.51
19:R:98:VAL:HG13	19:R:102:THR:HG23	1.92	0.51
1:2:1643:U:H3'	18:Q:142:GLN:NE2	2.24	0.51
2:A:2:SER:HB3	2:A:59:LEU:HD12	1.93	0.51
17:P:44:ARG:HB3	17:P:81:ARG:HH12	1.75	0.51
18:Q:13:PHE:CE2	18:Q:15:ARG:HB2	2.46	0.51
20:S:9:PHE:HB3	20:S:11:HIS:CD2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y:27:VAL:HG13	26:Y:69:THR:HB	1.91	0.51
1:2:495:U:H2'	1:2:496:C:O4'	2.11	0.51
1:2:528:A:H2'	1:2:529:A:C8	2.46	0.51
19:R:71:ILE:HD12	19:R:74:GLN:HG2	1.91	0.51
1:2:1267:C:H5'	33:f:82:LYS:HD2	1.93	0.51
1:2:1268:C:O2'	17:P:98:ASN:OD1	2.24	0.51
5:D:116:ARG:HE	36:n:172:ASP:CG	2.19	0.51
5:D:135:GLU:HB2	5:D:153:VAL:HB	1.92	0.51
1:2:51:U:H2'	1:2:52:G:C8	2.46	0.51
1:2:681:U:O2'	1:2:1160:U:OP1	2.24	0.51
1:2:1856:C:H2'	1:2:1857:G:C8	2.45	0.51
3:B:97:LEU:HB3	3:B:228:LEU:HD21	1.92	0.51
10:I:36:THR:HG21	10:I:60:LEU:HD12	1.93	0.51
12:K:32:HIS:HB3	12:K:35:LEU:HB3	1.91	0.51
16:O:22:ALA:H	16:O:25:GLU:HG2	1.75	0.51
18:Q:111:ILE:O	18:Q:114:GLN:HG2	2.11	0.51
24:W:77:PRO:HB2	25:X:7:LEU:HG	1.93	0.51
1:2:656:G:H5'	1:2:662:G:N2	2.26	0.51
1:2:1647:A:OP1	18:Q:138:ARG:NH2	2.44	0.51
2:A:79:SER:OG	2:A:130:ASP:OD1	2.29	0.51
8:G:57:ASP:HA	8:G:106:LEU:HA	1.91	0.51
17:P:86:LEU:HD23	17:P:88:GLU:HB2	1.92	0.51
1:2:30:C:O2'	1:2:596:U:OP1	2.29	0.51
1:2:163:U:OP1	8:G:84:TYR:HA	2.10	0.51
1:2:683:G:H4'	24:W:4:MET:HB3	1.92	0.51
1:2:1603:G:O2'	1:2:1604:G:OP2	2.27	0.51
1:2:1784:G:H2'	1:2:1785:C:C6	2.46	0.51
19:R:21:TYR:HA	19:R:24:LEU:HD12	1.93	0.51
1:2:1096:G:H1	1:2:1136:U:H5	1.58	0.50
1:2:1611:G:H4'	20:S:88:LYS:HB2	1.92	0.50
3:B:138:PHE:O	3:B:213:ARG:N	2.44	0.50
6:E:212:ASP:HB3	6:E:216:ASN:H	1.76	0.50
8:G:162:LEU:O	8:G:169:PRO:HA	2.11	0.50
31:d:31:ILE:N	31:d:38:MET:O	2.41	0.50
1:2:944:A:H1'	16:O:136:PRO:HB3	1.93	0.50
5:D:45:ARG:HH12	5:D:83:SER:HA	1.75	0.50
6:E:125:LYS:HG3	6:E:159:THR:HG22	1.93	0.50
15:N:132:LYS:HB3	15:N:134:VAL:HG23	1.93	0.50
18:Q:102:GLU:HG3	34:g:55:PRO:O	2.10	0.50
1:2:1284:A:H62	14:M:102:LYS:HD3	1.76	0.50
1:2:1714:U:H2'	1:2:1715:A:H8	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:76:THR:HG22	10:I:105:ASP:HB3	1.93	0.50
17:P:18:ARG:HG3	17:P:114:HIS:ND1	2.27	0.50
1:2:625:G:N1	25:X:64:SER:O	2.43	0.50
1:2:1010:G:H2'	1:2:1011:A:H8	1.76	0.50
1:2:1265:A:H8	1:2:1266:C:H4'	1.76	0.50
1:2:1473:G:C6	1:2:1476:A:N6	2.79	0.50
1:2:1598:G:H22	7:F:166:ILE:HA	1.77	0.50
9:H:191:GLU:N	9:H:191:GLU:OE1	2.44	0.50
7:F:38:TYR:CG	7:F:144:LEU:HD13	2.46	0.50
10:I:113:TYR:CE1	10:I:117:TYR:HD2	2.29	0.50
11:J:134:HIS:ND1	11:J:163:SER:HB2	2.27	0.50
16:O:96:LYS:HE2	16:O:132:VAL:HG11	1.93	0.50
34:g:283:PRO:O	34:g:285:GLN:NE2	2.44	0.50
1:2:955:A:H61	1:2:969:U:H5''	1.75	0.50
1:2:1451:G:N2	1:2:1475:G:N7	2.59	0.50
1:2:1614:A:H61	17:P:115:TYR:HE1	1.60	0.50
7:F:47:LYS:HZ2	18:Q:116:ASP:HA	1.76	0.50
9:H:148:LEU:HD23	24:W:49:GLU:HG3	1.94	0.50
10:I:113:TYR:CD2	10:I:121:LEU:HB2	2.46	0.50
18:Q:53:GLU:HG2	18:Q:54:PRO:HD3	1.93	0.50
21:T:88:MET:HE3	21:T:88:MET:HA	1.93	0.50
1:2:946:U:H2'	1:2:947:G:C8	2.47	0.50
1:2:1174:U:H2'	1:2:1175:G:C8	2.46	0.50
1:2:1230:C:OP2	20:S:138:THR:HG23	2.12	0.50
1:2:1519:U:H4'	20:S:136:THR:HG23	1.93	0.50
8:G:2:LYS:HD3	8:G:15:LEU:HD11	1.93	0.50
19:R:7:LYS:HG3	19:R:11:LYS:HG3	1.93	0.50
7:F:179:ASN:ND2	7:F:184:SER:HB3	2.27	0.50
10:I:161:LEU:HD12	10:I:161:LEU:H	1.77	0.50
16:O:98:ARG:HB3	16:O:132:VAL:HG23	1.93	0.50
1:2:377:G:H5'	10:I:99:ASN:HB3	1.94	0.49
21:T:142:ASN:C	21:T:143:LYS:HD2	2.37	0.49
34:g:126:ASP:HB3	34:g:128:THR:HG22	1.94	0.49
1:2:649:U:H1'	25:X:45:SER:HB3	1.93	0.49
4:C:173:LYS:O	23:V:3:ASN:HB2	2.13	0.49
9:H:105:THR:OG1	9:H:107:LYS:O	2.30	0.49
12:K:21:MET:HE1	12:K:45:VAL:HG11	1.93	0.49
1:2:595:U:H2'	1:2:596:U:C6	2.47	0.49
1:2:638:C:O2'	1:2:639:C:H5'	2.12	0.49
1:2:853:C:H5''	1:2:853:C:H6	1.77	0.49
1:2:962:A:N1	1:2:1055:A:O2'	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:232:THR:O	4:C:232:THR:OG1	2.30	0.49
5:D:44:THR:O	5:D:45:ARG:NH1	2.45	0.49
6:E:86:PHE:HE1	6:E:182:MET:HE2	1.77	0.49
10:I:107:THR:HG23	10:I:110:ARG:NH2	2.27	0.49
12:K:3:MET:HE2	12:K:8:ARG:HH12	1.77	0.49
17:P:63:ALA:HA	17:P:66:GLU:HG2	1.95	0.49
20:S:45:LEU:HD23	20:S:50:ILE:HD12	1.94	0.49
3:B:48:LEU:O	16:O:51:GLU:HG3	2.13	0.49
7:F:100:ILE:HA	7:F:103:LEU:HD12	1.94	0.49
15:N:106:ARG:NH1	15:N:107:LYS:HG2	2.27	0.49
21:T:59:SER:HG	21:T:62:ARG:HH21	1.58	0.49
1:2:128:U:H5'	1:2:129:C:H5	1.77	0.49
5:D:158:ILE:H	5:D:189:MET:HE2	1.76	0.49
1:2:293:C:N4	1:2:295:C:H1'	2.27	0.49
1:2:444:G:N2	1:2:447:A:OP2	2.44	0.49
1:2:511:U:O2'	1:2:576:A:N6	2.46	0.49
1:2:867:G:H2'	1:2:868:G:C8	2.47	0.49
1:2:1561:A:H61	1:2:1574:C:N4	2.10	0.49
1:2:1754:G:H2'	1:2:1777:G:H22	1.77	0.49
28:a:78:VAL:HG11	28:a:84:VAL:HG22	1.95	0.49
33:f:141:CYS:CB	33:f:148:TYR:HE2	2.23	0.49
1:2:604:A:O2'	1:2:605:A:O5'	2.28	0.49
1:2:1485:U:H2'	1:2:1486:A:O4'	2.13	0.49
2:A:140:VAL:HG23	2:A:142:LEU:HB2	1.95	0.49
9:H:179:LYS:HD3	9:H:179:LYS:C	2.38	0.49
22:U:33:GLU:OE2	22:U:87:ARG:NH1	2.44	0.49
28:a:25:ASN:O	28:a:25:ASN:ND2	2.45	0.49
34:g:148:SER:H	34:g:175:LYS:HE2	1.78	0.49
1:2:957:A:OP1	16:O:57:THR:OG1	2.20	0.49
1:2:1124:C:O2'	19:R:126:MET:O	2.31	0.49
1:2:1677:U:H2'	1:2:1678:A:C2	2.48	0.49
5:D:162:ASP:O	5:D:164:VAL:N	2.42	0.49
7:F:90:VAL:O	18:Q:50:LYS:NZ	2.45	0.49
34:g:36:ARG:HH21	34:g:83:TRP:HZ2	1.61	0.49
34:g:199:THR:OG1	34:g:200:VAL:N	2.46	0.49
2:A:180:ARG:HD3	2:A:184:ARG:CZ	2.43	0.49
7:F:144:LEU:HG	7:F:145:ARG:N	2.28	0.49
1:2:15:U:H2'	1:2:16:G:O4'	2.13	0.49
1:2:609:U:H2'	1:2:610:G:C8	2.46	0.49
1:2:1266:C:OP1	33:f:81:LYS:NZ	2.45	0.49
1:2:1555:U:O2	1:2:1556:A:N6	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1650:A:H8	1:2:1651:A:C8	2.31	0.49
15:N:5:HIS:HB3	15:N:117:LEU:HD13	1.94	0.49
17:P:33:LEU:HD23	17:P:85:ILE:HD11	1.95	0.49
25:X:41:PHE:O	25:X:76:LYS:NZ	2.33	0.49
1:2:495:U:O2'	6:E:27:PHE:O	2.31	0.48
1:2:1101:U:H2'	1:2:1102:G:H8	1.78	0.48
1:2:1447:G:H21	22:U:55:ARG:HD3	1.78	0.48
1:2:1531:A:N6	7:F:81:ARG:HD2	2.28	0.48
2:A:165:ASN:N	2:A:165:ASN:OD1	2.46	0.48
20:S:15:VAL:HG13	20:S:61:GLU:HG3	1.95	0.48
26:Y:13:MET:SD	26:Y:22:GLN:NE2	2.85	0.48
1:2:1629:C:H6	1:2:1629:C:O5'	1.97	0.48
18:Q:82:TYR:HA	18:Q:85:ARG:CG	2.43	0.48
21:T:91:HIS:CG	21:T:92:PHE:N	2.82	0.48
30:c:13:ARG:HE	30:c:35:MET:HG3	1.78	0.48
34:g:155:ARG:NE	34:g:199:THR:HA	2.28	0.48
1:2:115:U:H2'	1:2:116:U:C6	2.49	0.48
1:2:953:C:H2'	1:2:954:U:C6	2.48	0.48
1:2:1047:C:H5''	16:O:143:LYS:HA	1.95	0.48
1:2:1579:A:O2'	1:2:1581:C:OP2	2.30	0.48
4:C:172:ASN:HB2	11:J:95:ASP:OD2	2.13	0.48
5:D:177:LEU:N	5:D:180:GLY:O	2.46	0.48
6:E:133:THR:O	6:E:134:LYS:HB2	2.12	0.48
18:Q:32:ILE:HG23	18:Q:70:VAL:HB	1.94	0.48
20:S:39:ARG:HB3	20:S:82:TRP:CZ2	2.46	0.48
1:2:996:A:H2'	1:2:997:A:C8	2.49	0.48
1:2:1457:U:H2'	1:2:1458:G:H8	1.77	0.48
1:2:1522:A:H5'	20:S:139:THR:O	2.13	0.48
1:2:1667:U:H2'	1:2:1668:U:C6	2.48	0.48
7:F:150:ALA:HA	7:F:153:LEU:HD12	1.94	0.48
26:Y:28:LEU:HD23	26:Y:68:LYS:HB3	1.94	0.48
34:g:251:ALA:HB3	34:g:286:CYS:HB2	1.95	0.48
4:C:106:VAL:HA	4:C:128:VAL:HG22	1.95	0.48
7:F:203:ASN:O	30:c:63:ARG:HD3	2.14	0.48
12:K:43:LEU:HD12	12:K:44:HIS:N	2.29	0.48
34:g:32:LEU:HD22	34:g:71:ILE:HG22	1.95	0.48
1:2:523:A:OP1	11:J:127:ARG:NE	2.45	0.48
1:2:1203:G:H2'	1:2:1204:A:H8	1.76	0.48
1:2:1608:U:H5'	1:2:1608:U:H6	1.79	0.48
4:C:171:GLY:O	24:W:98:GLN:NE2	2.44	0.48
7:F:52:SER:O	7:F:52:SER:OG	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:44:GLU:OE1	8:G:45:TRP:HD1	1.95	0.48
18:Q:32:ILE:HD12	18:Q:39:LEU:HD13	1.96	0.48
1:2:304:C:OP1	10:I:75:LYS:HE2	2.14	0.48
1:2:929:G:H2'	1:2:930:C:O4'	2.14	0.48
1:2:987:A:C6	3:B:120:MET:HE1	2.49	0.48
1:2:1164:G:O2'	1:2:1165:G:H5'	2.14	0.48
1:2:1451:G:H2'	1:2:1452:A:H2'	1.96	0.48
6:E:214:ASN:ND2	6:E:244:ILE:HG21	2.29	0.48
11:J:53:ILE:HD13	11:J:81:LEU:HD21	1.94	0.48
26:Y:113:ARG:NH2	26:Y:126:GLY:O	2.47	0.48
1:2:809:A:H2'	1:2:810:A:O4'	2.13	0.48
1:2:1658:G:OP2	1:2:1660:C:N4	2.36	0.48
3:B:62:LEU:HD12	3:B:65:ARG:HD2	1.96	0.48
5:D:135:GLU:HB3	5:D:157:MET:CE	2.43	0.48
20:S:130:ARG:HD3	20:S:142:ARG:CD	2.43	0.48
25:X:102:VAL:HG12	25:X:122:VAL:HA	1.96	0.48
34:g:251:ALA:HA	34:g:256:ILE:HA	1.95	0.48
1:2:67:C:C5	8:G:162:LEU:HB3	2.48	0.48
1:2:379:C:H5'	10:I:33:ALA:HA	1.96	0.48
1:2:1331:C:O2'	1:2:1332:A:OP2	2.32	0.48
1:2:1544:C:OP1	18:Q:73:LYS:HB3	2.13	0.48
6:E:60:GLU:OE2	26:Y:20:ARG:NH1	2.39	0.48
9:H:139:ILE:HG22	9:H:141:GLY:H	1.78	0.48
12:K:41:PRO:HB2	12:K:43:LEU:HG	1.96	0.48
27:Z:88:LEU:HD23	27:Z:91:LEU:HD21	1.96	0.48
34:g:106:LYS:HG2	34:g:125:ARG:HB2	1.95	0.48
1:2:895:G:H2'	1:2:895:G:N3	2.29	0.48
1:2:1088:U:H4'	1:2:1089:G:OP2	2.14	0.48
3:B:185:VAL:O	3:B:189:ILE:HG12	2.14	0.48
18:Q:102:GLU:O	18:Q:105:LYS:HB2	2.14	0.48
20:S:144:ARG:O	20:S:145:THR:C	2.56	0.48
30:c:64:GLU:CD	30:c:64:GLU:H	2.21	0.48
1:2:1250:A:C8	1:2:1339:U:H4'	2.49	0.47
1:2:1309:C:O2'	33:f:141:CYS:N	2.47	0.47
1:2:1440:C:O2'	1:2:1441:U:H5'	2.14	0.47
1:2:1473:G:N1	1:2:1476:A:C6	2.82	0.47
8:G:135:PRO:HB3	8:G:140:ARG:HB3	1.96	0.47
20:S:90:VAL:O	20:S:91:LYS:HB2	2.14	0.47
21:T:51:ASN:OD1	21:T:51:ASN:N	2.45	0.47
25:X:134:TYR:O	32:e:13:ARG:NH2	2.44	0.47
34:g:85:GLY:HA3	34:g:104:HIS:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:17:C:H4'	1:2:1166:G:C8	2.48	0.47
1:2:641:A:O2'	1:2:645:C:OP1	2.32	0.47
18:Q:48:GLN:O	18:Q:51:LEU:HG	2.14	0.47
18:Q:77:HIS:HA	18:Q:80:GLN:NE2	2.28	0.47
24:W:111:MET:HE1	24:W:119:LYS:NZ	2.29	0.47
28:a:73:TYR:HB2	28:a:78:VAL:HG23	1.96	0.47
30:c:15:THR:OG1	30:c:33:GLU:OE1	2.32	0.47
34:g:85:GLY:O	34:g:103:GLY:N	2.40	0.47
1:2:221:A:H2'	1:2:222:U:H6	1.80	0.47
1:2:600:G:H2'	1:2:601:G:C8	2.50	0.47
1:2:1148:A:OP1	28:a:6:ARG:NH2	2.48	0.47
14:M:51:VAL:HB	14:M:105:GLY:H	1.79	0.47
34:g:171:ASP:O	34:g:173:LEU:HG	2.14	0.47
1:2:461:U:H2'	1:2:462:C:H6	1.79	0.47
1:2:952:G:C6	1:2:975:G:C6	3.03	0.47
1:2:1101:U:H2'	1:2:1102:G:C8	2.49	0.47
1:2:1402:A:H2'	1:2:1405:A:H61	1.78	0.47
3:B:28:LYS:HD2	3:B:48:LEU:HG	1.96	0.47
8:G:23:LYS:HG3	8:G:40:ALA:O	2.14	0.47
10:I:37:LYS:HE3	10:I:95:THR:HG22	1.96	0.47
13:L:59:LYS:HG2	13:L:134:LEU:HD22	1.96	0.47
1:2:1230:C:H5'	20:S:134:GLN:CG	2.43	0.47
1:2:1551:U:P	5:D:9:ARG:HH12	2.37	0.47
1:2:1569:A:H3'	1:2:1570:G:H8	1.79	0.47
16:O:116:LEU:HD23	28:a:45:VAL:HG12	1.96	0.47
31:d:36:LEU:HD12	31:d:38:MET:HE3	1.95	0.47
34:g:197:THR:HB	34:g:237:ASN:O	2.14	0.47
1:2:180:G:H2'	1:2:181:A:C8	2.49	0.47
1:2:1748:G:O6	1:2:1786:U:O2	2.32	0.47
3:B:83:LYS:HZ2	3:B:106:THR:HA	1.79	0.47
5:D:175:VAL:CG2	5:D:182:LEU:HB2	2.45	0.47
6:E:104:ASP:HB2	6:E:110:ALA:HB2	1.96	0.47
7:F:88:MET:O	7:F:92:ILE:HG12	2.15	0.47
7:F:95:HIS:O	7:F:99:ILE:HB	2.14	0.47
15:N:63:VAL:HG11	15:N:71:ILE:HG12	1.96	0.47
26:Y:5:VAL:HA	26:Y:28:LEU:O	2.13	0.47
31:d:46:TYR:O	31:d:50:ILE:HG22	2.15	0.47
1:2:43:U:OP2	1:2:485:A:N6	2.46	0.47
1:2:441:C:H2'	1:2:442:C:C6	2.50	0.47
1:2:461:U:H2'	1:2:462:C:C6	2.50	0.47
1:2:499:G:C2	1:2:501:C:H1'	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1265:A:C8	1:2:1266:C:H4'	2.50	0.47
1:2:1440:C:H3'	1:2:1441:U:H6	1.80	0.47
1:2:1794:C:H2'	1:2:1795:G:C8	2.50	0.47
1:2:1850:A:H2'	1:2:1851:A:C8	2.50	0.47
8:G:25:ARG:HA	8:G:28:TYR:CD1	2.50	0.47
12:K:26:ASP:HB3	12:K:29:MET:CG	2.44	0.47
18:Q:13:PHE:CZ	18:Q:21:ALA:HB3	2.50	0.47
25:X:123:VAL:HG12	25:X:124:LYS:HG3	1.96	0.47
30:c:29:GLN:HA	30:c:44:ARG:O	2.15	0.47
36:n:185:LYS:NZ	36:n:189:LYS:HE2	2.30	0.47
1:2:1144:A:H2'	1:2:1145:A:C8	2.50	0.47
1:2:1183:A:H2'	1:2:1184:G:H8	1.79	0.47
2:A:4:ALA:H	23:V:80:SER:HB3	1.80	0.47
3:B:110:MET:HA	3:B:113:MET:HE2	1.96	0.47
6:E:233:LYS:HD2	6:E:234:PRO:O	2.15	0.47
1:2:1254:C:H4'	22:U:75:LYS:HE3	1.96	0.47
1:2:1427:C:OP2	1:2:1429:G:H5''	2.14	0.47
10:I:45:THR:CG2	10:I:53:LYS:HD2	2.45	0.47
20:S:74:PRO:HA	20:S:77:TYR:HD2	1.79	0.47
21:T:135:ALA:HA	21:T:138:VAL:HG22	1.97	0.47
26:Y:39:GLU:O	26:Y:43:LYS:HD2	2.15	0.47
31:d:16:GLN:HA	31:d:19:ARG:HH21	1.79	0.47
1:2:880:G:O2'	1:2:881:G:O4'	2.30	0.47
1:2:1232:U:H6	1:2:1233:G:C8	2.33	0.47
1:2:1522:A:H4'	1:2:1523:C:OP2	2.13	0.47
1:2:1546:G:O2'	1:2:1547:C:OP1	2.25	0.47
2:A:54:THR:OG1	2:A:162:PRO:O	2.29	0.47
7:F:201:LYS:HD2	7:F:204:ARG:HD2	1.97	0.47
14:M:69:CYS:HB3	14:M:74:ILE:HB	1.97	0.47
16:O:84:ARG:O	16:O:87:GLU:HG3	2.16	0.47
21:T:63:HIS:CD2	21:T:78:ILE:HD12	2.50	0.47
26:Y:55:ILE:CD1	26:Y:75:ILE:HG12	2.45	0.47
34:g:201:SER:HB2	34:g:206:LEU:HD23	1.97	0.47
1:2:78:C:H1'	8:G:175:LYS:HB2	1.97	0.46
1:2:546:G:H2'	1:2:549:C:C5	2.50	0.46
1:2:946:U:H2'	1:2:947:G:H8	1.80	0.46
1:2:1233:G:H1'	1:2:1252:C:H2'	1.96	0.46
1:2:1261:C:H4'	1:2:1618:C:H42	1.80	0.46
1:2:1858:G:OP2	16:O:146:ARG:NH2	2.48	0.46
5:D:28:GLU:OE1	12:K:70:TYR:OH	2.21	0.46
5:D:76:ARG:HE	5:D:77:PHE:HD1	1.62	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:100:ARG:HB2	6:E:114:ILE:HD13	1.97	0.46
6:E:102:ILE:HG23	6:E:182:MET:HE1	1.97	0.46
8:G:230:LYS:HE3	8:G:230:LYS:HA	1.97	0.46
15:N:29:THR:O	15:N:33:VAL:HG23	2.15	0.46
30:c:8:PRO:HB2	30:c:58:LEU:HD23	1.97	0.46
1:2:1491:G:H2'	1:2:1492:U:C6	2.49	0.46
2:A:134:LEU:CD2	2:A:144:THR:HG21	2.45	0.46
7:F:144:LEU:HG	7:F:145:ARG:H	1.80	0.46
15:N:132:LYS:HD3	15:N:132:LYS:HA	1.75	0.46
16:O:69:SER:O	16:O:110:PRO:HG2	2.16	0.46
27:Z:58:LEU:HD22	27:Z:88:LEU:HG	1.96	0.46
1:2:16:G:H2'	1:2:17:C:C6	2.50	0.46
1:2:297:A:H5'	6:E:132:GLY:HA2	1.98	0.46
1:2:496:C:OP1	6:E:49:ARG:NH2	2.35	0.46
1:2:1019:C:H2'	1:2:1020:A:O4'	2.15	0.46
1:2:1550:G:H3'	1:2:1579:A:H61	1.78	0.46
1:2:1703:C:H2'	1:2:1704:C:O4'	2.16	0.46
2:A:89:LYS:HA	2:A:89:LYS:HD3	1.63	0.46
3:B:83:LYS:NZ	3:B:106:THR:HA	2.30	0.46
4:C:184:VAL:HG23	4:C:195:LEU:HB2	1.97	0.46
8:G:135:PRO:HB2	8:G:141:ILE:HG12	1.97	0.46
9:H:30:LEU:HD23	9:H:30:LEU:HA	1.59	0.46
11:J:59:GLU:O	11:J:62:THR:HG22	2.16	0.46
16:O:44:VAL:HG11	16:O:85:CYS:SG	2.55	0.46
1:2:1232:U:H5''	1:2:1518:C:H41	1.80	0.46
5:D:132:LYS:H	5:D:132:LYS:HG3	1.60	0.46
8:G:88:ARG:HG2	8:G:91:GLU:HB2	1.97	0.46
11:J:42:GLU:O	11:J:46:VAL:HG23	2.15	0.46
16:O:130:GLU:HG3	16:O:131:ASP:N	2.30	0.46
17:P:79:HIS:HD2	17:P:96:VAL:HA	1.80	0.46
1:2:1242:U:N3	1:2:1518:C:H4'	2.30	0.46
4:C:226:ALA:HB1	4:C:230:THR:HG21	1.97	0.46
10:I:29:LEU:HD11	10:I:31:ARG:NH2	2.31	0.46
18:Q:102:GLU:HA	18:Q:105:LYS:HD3	1.97	0.46
1:2:164:A:H3'	1:2:165:G:H21	1.81	0.46
1:2:674:C:H2'	1:2:675:U:C6	2.50	0.46
1:2:685:A:H2'	1:2:686:U:O4'	2.15	0.46
1:2:1294:G:H5'	1:2:1296:U:OP2	2.15	0.46
1:2:1332:A:O2'	5:D:141:LYS:HD3	2.15	0.46
5:D:135:GLU:HB3	5:D:157:MET:HE3	1.97	0.46
9:H:184:ASP:N	9:H:184:ASP:OD1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:3:ARG:HB2	15:N:6:ALA:HB3	1.96	0.46
18:Q:56:LEU:HB3	18:Q:60:LYS:HE3	1.97	0.46
30:c:10:LYS:H	30:c:58:LEU:HB3	1.81	0.46
33:f:137:ASP:C	33:f:138:ARG:HG2	2.40	0.46
34:g:174:VAL:HG21	34:g:207:CYS:SG	2.55	0.46
1:2:1568:C:C2	1:2:1612:G:C2	3.04	0.46
1:2:1723:G:H2'	1:2:1724:A:C8	2.50	0.46
2:A:200:ASP:O	2:A:205:ARG:NH2	2.49	0.46
5:D:126:ILE:HG21	5:D:134:CYS:HB3	1.98	0.46
5:D:197:LYS:HD2	5:D:197:LYS:HA	1.66	0.46
6:E:173:ILE:HD11	6:E:235:TRP:CD2	2.50	0.46
1:2:615:C:O2	32:e:11:LYS:NZ	2.48	0.46
1:2:955:A:H4'	16:O:60:MET:HE1	1.97	0.46
1:2:1289:U:O4	33:f:138:ARG:NH1	2.46	0.46
17:P:108:LYS:HB3	17:P:108:LYS:HE3	1.71	0.46
34:g:217:MET:HE2	34:g:226:HIS:CD2	2.49	0.46
1:2:51:U:H2'	1:2:52:G:H8	1.80	0.46
1:2:205:G:H2'	1:2:206:G:C8	2.50	0.46
1:2:1405:A:O2'	1:2:1406:G:OP1	2.25	0.46
1:2:1654:G:H2'	1:2:1655:C:C6	2.51	0.46
3:B:86:LEU:HB3	3:B:98:THR:HB	1.97	0.46
4:C:244:ILE:O	4:C:247:THR:OG1	2.21	0.46
5:D:15:GLY:HA3	31:d:50:ILE:HG13	1.98	0.46
7:F:136:ARG:HB2	7:F:199:VAL:HG11	1.97	0.46
13:L:16:ILE:HD12	13:L:34:PRO:HB2	1.98	0.46
16:O:29:GLY:O	16:O:94:HIS:N	2.31	0.46
16:O:84:ARG:NH1	16:O:87:GLU:OE2	2.49	0.46
21:T:17:ALA:HB1	21:T:141:ALA:HB3	1.98	0.46
24:W:38:LEU:HD22	24:W:47:ILE:HD13	1.97	0.46
34:g:170:TRP:NE1	34:g:196:ASN:O	2.40	0.46
1:2:329:G:H2'	1:2:330:G:O4'	2.16	0.46
1:2:1199:A:H2'	1:2:1200:A:C8	2.51	0.46
1:2:1329:U:C2	1:2:1500:G:O6	2.69	0.46
1:2:1713:C:H2'	1:2:1714:U:C6	2.51	0.46
2:A:52:LYS:HG2	19:R:109:LEU:HD13	1.98	0.46
9:H:176:VAL:O	9:H:180:LEU:HG	2.16	0.46
1:2:223:C:H2'	1:2:224:A:C8	2.51	0.45
1:2:307:G:N2	10:I:45:THR:O	2.48	0.45
1:2:384:U:O4	10:I:5:ARG:NH2	2.39	0.45
1:2:1112:U:H2'	1:2:1113:A:C8	2.51	0.45
1:2:1311:C:OP2	33:f:143:LYS:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1607:A:H2	1:2:1632:G:H21	1.64	0.45
1:2:1785:C:H2'	1:2:1786:U:O4'	2.15	0.45
1:2:1788:A:H2'	1:2:1789:G:O4'	2.16	0.45
4:C:169:TYR:OH	23:V:9:VAL:HG21	2.16	0.45
8:G:5:ILE:N	8:G:5:ILE:HD12	2.31	0.45
1:2:160:U:O2'	1:2:162:C:OP2	2.29	0.45
1:2:1397:U:N3	1:2:1442:U:H5''	2.31	0.45
7:F:89:THR:O	7:F:93:VAL:HG23	2.16	0.45
8:G:5:ILE:HG21	8:G:45:TRP:HH2	1.80	0.45
9:H:134:VAL:HG22	9:H:137:SER:H	1.80	0.45
11:J:60:LEU:O	11:J:70:ARG:HD2	2.16	0.45
25:X:52:LEU:HD11	25:X:73:GLN:HB2	1.98	0.45
31:d:7:TYR:CG	31:d:8:TRP:N	2.84	0.45
1:2:24:C:OP1	11:J:11:LYS:NZ	2.38	0.45
1:2:600:G:H2'	1:2:601:G:H8	1.81	0.45
1:2:1309:C:O2'	33:f:140:TYR:CA	2.65	0.45
1:2:1450:G:H2'	1:2:1451:G:C8	2.48	0.45
5:D:47:GLU:OE1	5:D:47:GLU:N	2.50	0.45
9:H:165:ASN:OD1	9:H:165:ASN:N	2.50	0.45
11:J:136:ARG:HE	11:J:158:ASP:HB2	1.82	0.45
14:M:60:MET:C	14:M:60:MET:HE3	2.41	0.45
34:g:65:PHE:HB2	34:g:83:TRP:CD1	2.51	0.45
1:2:145:G:O6	8:G:178:ARG:NH2	2.50	0.45
1:2:414:A:OP1	1:2:814:U:O2'	2.27	0.45
1:2:1097:G:H4'	2:A:32:PHE:CD1	2.50	0.45
1:2:1134:G:H2'	1:2:1135:C:C6	2.52	0.45
1:2:1527:C:H2'	1:2:1528:G:O4'	2.17	0.45
1:2:1589:A:P	21:T:84:ARG:HH22	2.36	0.45
1:2:1651:A:O2'	7:F:81:ARG:NH2	2.50	0.45
4:C:83:LEU:O	23:V:15:ARG:NH1	2.42	0.45
5:D:162:ASP:C	5:D:164:VAL:H	2.25	0.45
10:I:157:LYS:HD2	10:I:157:LYS:HA	1.69	0.45
14:M:35:ILE:HG12	33:f:101:ALA:HB3	1.98	0.45
15:N:18:TYR:O	24:W:56:HIS:ND1	2.49	0.45
17:P:40:ARG:H	17:P:42:ARG:NH1	2.14	0.45
20:S:142:ARG:HH11	20:S:142:ARG:CB	2.27	0.45
1:2:1308:U:H4'	1:2:1309:C:OP1	2.17	0.45
12:K:60:GLU:N	12:K:60:GLU:OE2	2.49	0.45
19:R:19:LYS:HB2	19:R:19:LYS:HE3	1.73	0.45
21:T:88:MET:SD	21:T:88:MET:N	2.88	0.45
27:Z:78:LYS:O	27:Z:78:LYS:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:29:G:H2'	1:2:30:C:C6	2.51	0.45
1:2:308:G:H4'	1:2:309:G:OP1	2.17	0.45
1:2:1229:G:H5''	20:S:138:THR:OG1	2.17	0.45
7:F:81:ARG:HA	7:F:81:ARG:HD3	1.61	0.45
13:L:55:TYR:CD1	13:L:115:PRO:HG2	2.52	0.45
16:O:78:ALA:HB3	16:O:118:ALA:HB3	1.99	0.45
26:Y:117:VAL:HG23	26:Y:122:LYS:HG3	1.98	0.45
33:f:141:CYS:HB2	33:f:148:TYR:CE2	2.50	0.45
1:2:352:U:H2'	1:2:353:C:C6	2.51	0.45
1:2:385:G:H3'	13:L:136:LYS:HB2	1.98	0.45
1:2:960:U:O2'	1:2:962:A:N7	2.34	0.45
1:2:988:C:H5''	3:B:116:LYS:HG3	1.98	0.45
1:2:1290:G:C2	33:f:138:ARG:NE	2.82	0.45
1:2:1523:C:H5''	20:S:141:ARG:CZ	2.46	0.45
1:2:1845:A:H2'	1:2:1846:G:H8	1.81	0.45
8:G:19:ASP:OD1	8:G:19:ASP:N	2.47	0.45
21:T:10:ASN:HB3	21:T:13:GLU:HB3	1.97	0.45
22:U:64:THR:HA	22:U:78:ASP:O	2.17	0.45
29:b:62:VAL:HG21	29:b:65:GLN:OE1	2.16	0.45
1:2:1430:C:H3'	1:2:1431:G:H8	1.82	0.45
1:2:1545:A:H5''	1:2:1546:G:C6	2.51	0.45
2:A:42:LYS:HD3	2:A:48:ILE:HD11	1.99	0.45
21:T:66:LEU:HD12	21:T:67:ARG:HG2	1.99	0.45
24:W:85:ASP:OD1	24:W:85:ASP:N	2.50	0.45
1:2:1047:C:H2'	1:2:1048:G:O4'	2.16	0.45
1:2:1103:C:OP1	3:B:157:GLN:NE2	2.48	0.45
1:2:1217:A:P	1:2:1249:C:H41	2.40	0.45
1:2:1313:A:N6	14:M:35:ILE:HG22	2.32	0.45
1:2:1442:U:H1'	18:Q:13:PHE:CD1	2.51	0.45
1:2:1469:A:H5'	7:F:61:PHE:HD2	1.82	0.45
3:B:133:TYR:HD2	3:B:217:MET:SD	2.40	0.45
8:G:69:THR:HG22	8:G:71:GLY:H	1.80	0.45
11:J:155:LYS:HB2	11:J:155:LYS:HE2	1.62	0.45
21:T:37:VAL:HG23	21:T:39:LEU:N	2.31	0.45
23:V:47:ASN:C	23:V:47:ASN:OD1	2.60	0.45
30:c:29:GLN:HE21	30:c:45:ASN:CG	2.21	0.45
34:g:206:LEU:HB2	34:g:218:LEU:HD12	1.99	0.45
1:2:1794:C:H2'	1:2:1795:G:H8	1.81	0.45
10:I:200:ARG:O	10:I:204:ALA:N	2.47	0.45
17:P:56:LEU:HD13	17:P:80:LEU:HD22	1.99	0.45
18:Q:28:GLY:HA3	18:Q:67:ASP:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:57:LEU:O	19:R:61:ILE:HB	2.17	0.45
28:a:64:LEU:HD23	28:a:64:LEU:HA	1.78	0.45
30:c:36:ASP:N	30:c:36:ASP:OD1	2.49	0.45
1:2:1231:C:HO2'	1:2:1253:A:H62	1.43	0.44
1:2:1575:G:H2'	1:2:1576:G:H8	1.82	0.44
1:2:1647:A:H5'	1:2:1649:U:C6	2.52	0.44
1:2:1727:G:H2'	1:2:1728:U:H6	1.82	0.44
1:2:1864:U:OP2	28:a:5:ARG:NH2	2.29	0.44
10:I:153:LYS:HA	10:I:153:LYS:HD2	1.77	0.44
17:P:70:MET:H	17:P:90:VAL:HG12	1.81	0.44
21:T:101:ARG:HB3	21:T:102:ARG:NH1	2.32	0.44
1:2:218:U:H2'	1:2:219:U:C6	2.53	0.44
1:2:1050:A:OP1	1:2:1846:G:N2	2.48	0.44
1:2:1264:C:O2	33:f:78:LYS:N	2.49	0.44
1:2:1290:G:N1	33:f:138:ARG:NE	2.64	0.44
1:2:1308:U:C5	33:f:138:ARG:CG	2.99	0.44
1:2:1308:U:H5	33:f:138:ARG:CG	2.30	0.44
3:B:63:LYS:NZ	3:B:89:GLU:O	2.38	0.44
6:E:29:PRO:HG2	6:E:46:ILE:HD11	2.00	0.44
7:F:159:ARG:O	7:F:163:PHE:HB3	2.17	0.44
15:N:13:GLN:O	29:b:20:LYS:NZ	2.38	0.44
20:S:130:ARG:NH1	20:S:142:ARG:HD3	2.31	0.44
21:T:37:VAL:HG23	21:T:39:LEU:H	1.83	0.44
22:U:22:ILE:HG12	22:U:114:VAL:HG22	1.99	0.44
35:h:2:ARG:HD3	35:h:5:TRP:CD1	2.52	0.44
1:2:945:U:H2'	1:2:946:U:C6	2.53	0.44
1:2:1201:U:H2'	1:2:1202:U:C6	2.52	0.44
3:B:89:GLU:HB2	3:B:228:LEU:HD11	1.99	0.44
3:B:223:PHE:HE1	3:B:228:LEU:HD12	1.82	0.44
9:H:37:LYS:HB3	9:H:37:LYS:HE2	1.85	0.44
11:J:38:ARG:HA	32:e:31:ARG:HB2	2.00	0.44
1:2:641:A:H2'	1:2:642:U:O4'	2.17	0.44
1:2:905:C:H2'	1:2:906:U:O4'	2.18	0.44
1:2:1098:C:H2'	1:2:1099:G:H8	1.81	0.44
1:2:1226:G:OP2	1:2:1523:C:O2'	2.36	0.44
1:2:1692:U:H2'	1:2:1693:G:C8	2.52	0.44
1:2:1713:C:H2'	1:2:1714:U:H6	1.83	0.44
3:B:97:LEU:HD12	3:B:232:HIS:CE1	2.53	0.44
8:G:14:LYS:HG2	8:G:16:ILE:HG23	2.00	0.44
20:S:141:ARG:O	20:S:144:ARG:HG2	2.17	0.44
21:T:129:ARG:HH12	21:T:133:ARG:HG2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:5:ASN:ND2	24:W:8:ALA:HB2	2.32	0.44
1:2:85:A:H2'	1:2:86:C:C6	2.52	0.44
1:2:875:A:N6	1:2:912:C:N3	2.66	0.44
1:2:1092:G:H2'	1:2:1093:A:H8	1.81	0.44
1:2:1453:C:H4'	1:2:1454:A:O5'	2.18	0.44
1:2:1595:U:H5'	1:2:1596:U:C4	2.52	0.44
2:A:102:ARG:HG2	2:A:102:ARG:HH11	1.81	0.44
5:D:106:ARG:HA	5:D:175:VAL:HG11	1.99	0.44
5:D:119:CYS:O	5:D:123:LEU:HG	2.17	0.44
8:G:7:PHE:HD2	8:G:10:THR:HG22	1.82	0.44
8:G:203:LYS:HA	8:G:203:LYS:HD3	1.88	0.44
10:I:88:ASN:HD22	10:I:88:ASN:HA	1.59	0.44
20:S:21:ASP:HB3	20:S:23:ARG:NE	2.33	0.44
21:T:64:LEU:HG	21:T:121:ARG:HD3	1.99	0.44
26:Y:46:LYS:HB2	26:Y:46:LYS:HE3	1.77	0.44
34:g:166:VAL:HG23	34:g:200:VAL:HG11	1.99	0.44
1:2:1046:U:H1'	16:O:140:THR:OG1	2.18	0.44
1:2:1438:A:N3	1:2:1438:A:H2'	2.32	0.44
2:A:109:THR:HG23	2:A:136:GLU:HG2	2.00	0.44
3:B:25:PHE:CD1	3:B:25:PHE:N	2.85	0.44
6:E:174:LYS:O	6:E:179:ASN:ND2	2.50	0.44
7:F:134:VAL:C	7:F:135:ARG:HD2	2.42	0.44
8:G:195:LYS:HZ2	8:G:195:LYS:HG2	1.55	0.44
16:O:63:LYS:HA	16:O:63:LYS:CE	2.40	0.44
18:Q:24:HIS:HB3	18:Q:69:ARG:HB2	2.00	0.44
21:T:128:GLN:HE21	21:T:128:GLN:HB2	1.57	0.44
34:g:218:LEU:O	34:g:227:LEU:HB3	2.17	0.44
1:2:686:U:O2	9:H:118:ARG:NH1	2.45	0.44
1:2:1719:A:C6	1:2:1815:A:C8	3.06	0.44
3:B:117:TRP:CE2	3:B:152:LYS:HE2	2.53	0.44
26:Y:53:ASP:OD1	26:Y:53:ASP:N	2.51	0.44
1:2:630:U:C5	1:2:631:U:H5	2.36	0.44
1:2:678:U:H2'	1:2:679:A:H8	1.83	0.44
1:2:1406:G:C5	1:2:1407:U:C6	3.06	0.44
5:D:67:ARG:HH22	12:K:95:ARG:HE	1.66	0.44
6:E:160:ILE:HB	6:E:169:ILE:HG23	2.00	0.44
18:Q:28:GLY:N	18:Q:67:ASP:H	2.16	0.44
21:T:72:VAL:HG22	21:T:121:ARG:HH21	1.82	0.44
33:f:136:PHE:HD1	33:f:136:PHE:H	1.65	0.44
34:g:248:LEU:O	34:g:258:ILE:HA	2.17	0.44
34:g:268:ASP:HB3	34:g:270:LEU:HG	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:379:C:O2	10:I:5:ARG:NE	2.48	0.44
1:2:442:C:H2'	1:2:443:U:C6	2.53	0.44
1:2:1408:U:H5''	1:2:1439:A:N6	2.33	0.44
1:2:1412:C:H5'	1:2:1413:G:C4	2.53	0.44
5:D:12:VAL:O	5:D:16:ILE:HG23	2.17	0.44
8:G:222:GLU:OE1	8:G:222:GLU:N	2.51	0.44
20:S:43:VAL:O	20:S:47:LYS:HE2	2.17	0.44
22:U:26:SER:OG	22:U:32:LEU:HB2	2.18	0.44
1:2:376:A:H2'	1:2:377:G:O4'	2.18	0.43
1:2:517:C:H2'	1:2:518:G:O4'	2.18	0.43
1:2:604:A:H2'	1:2:605:A:C8	2.53	0.43
1:2:1036:A:H5'	1:2:1856:C:H1'	1.99	0.43
1:2:1134:G:H2'	1:2:1135:C:H6	1.83	0.43
1:2:1313:A:C4	14:M:34:GLY:HA3	2.53	0.43
5:D:67:ARG:HH22	12:K:95:ARG:HB2	1.82	0.43
6:E:72:ILE:HD12	6:E:77:ARG:HG3	1.99	0.43
6:E:100:ARG:HH12	6:E:122:LYS:HA	1.82	0.43
9:H:142:LYS:O	24:W:54:ASP:HB3	2.18	0.43
20:S:130:ARG:HG2	20:S:134:GLN:NE2	2.26	0.43
33:f:138:ARG:HB2	33:f:139:HIS:H	1.46	0.43
1:2:1231:C:O2'	1:2:1232:U:P	2.76	0.43
1:2:1309:C:H3'	1:2:1309:C:H6	1.83	0.43
1:2:1351:G:O2'	1:2:1378:A:N1	2.49	0.43
8:G:69:THR:HG22	8:G:71:GLY:N	2.33	0.43
11:J:151:LEU:HD12	11:J:151:LEU:HA	1.76	0.43
19:R:15:VAL:HA	19:R:18:GLU:HG2	2.00	0.43
34:g:173:LEU:HD22	34:g:187:ASN:ND2	2.33	0.43
1:2:616:A:N3	32:e:12:VAL:HG21	2.33	0.43
1:2:1275:G:C5	1:2:1317:C:OP2	2.71	0.43
1:2:1375:G:H5'	19:R:67:ARG:HH21	1.82	0.43
2:A:163:CYS:SG	2:A:174:MET:HG3	2.58	0.43
4:C:165:VAL:HG21	4:C:217:ALA:HB1	2.00	0.43
5:D:40:ARG:HB3	5:D:47:GLU:HG2	2.00	0.43
14:M:98:GLY:C	14:M:99:LYS:HG2	2.43	0.43
20:S:108:ARG:C	20:S:110:ASP:N	2.75	0.43
20:S:141:ARG:HA	20:S:144:ARG:CZ	2.47	0.43
24:W:36:ARG:HA	24:W:36:ARG:HD3	1.74	0.43
29:b:65:GLN:HB2	29:b:72:ARG:HB3	2.00	0.43
1:2:165:G:H4'	8:G:53:SER:HB3	2.00	0.43
1:2:1406:G:C5	1:2:1407:U:C5	3.07	0.43
2:A:30:LEU:HD21	2:A:35:GLU:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:61:ALA:HB1	2:A:145:ILE:HD13	2.00	0.43
9:H:140:VAL:HG21	9:H:193:GLN:OE1	2.18	0.43
19:R:95:ILE:HD11	19:R:118:GLN:HB2	1.99	0.43
20:S:130:ARG:HD3	20:S:142:ARG:NE	2.34	0.43
21:T:134:ILE:HG23	21:T:137:GLN:HE21	1.83	0.43
1:2:604:A:H4'	1:2:605:A:OP1	2.18	0.43
1:2:820:U:P	11:J:79:ARG:HH22	2.41	0.43
1:2:959:G:OP2	16:O:38:ASN:ND2	2.51	0.43
7:F:193:LYS:HA	7:F:196:LEU:HD12	2.01	0.43
19:R:80:ARG:HB3	19:R:80:ARG:NH1	2.33	0.43
21:T:22:LEU:HD11	21:T:112:MET:HE1	1.99	0.43
1:2:433:A:H2'	1:2:434:G:C8	2.54	0.43
1:2:910:G:H2'	1:2:911:C:O4'	2.18	0.43
1:2:1311:C:OP2	33:f:143:LYS:CG	2.66	0.43
1:2:1457:U:H2'	1:2:1458:G:C8	2.54	0.43
1:2:1828:C:H2'	1:2:1829:G:O4'	2.19	0.43
8:G:10:THR:HA	8:G:129:VAL:HG12	2.01	0.43
9:H:70:LYS:HA	9:H:73:GLN:HG2	2.01	0.43
10:I:113:TYR:OH	10:I:156:ALA:O	2.30	0.43
16:O:74:ALA:HB1	16:O:115:ALA:HB2	1.99	0.43
16:O:78:ALA:O	16:O:81:VAL:HG12	2.18	0.43
20:S:26:ILE:C	20:S:28:PHE:H	2.27	0.43
1:2:29:G:H4'	25:X:129:SER:HB3	2.00	0.43
1:2:293:C:C4	1:2:295:C:H1'	2.53	0.43
1:2:1261:C:H2'	1:2:1262:C:C5	2.53	0.43
1:2:1622:U:O2	20:S:135:HIS:HA	2.18	0.43
5:D:11:PHE:HA	5:D:14:ASP:OD2	2.17	0.43
9:H:76:GLN:O	9:H:80:VAL:HG22	2.18	0.43
18:Q:139:ALA:O	18:Q:140:ARG:NE	2.48	0.43
19:R:17:ILE:HG22	19:R:69:ILE:HG21	2.00	0.43
26:Y:44:LEU:HB3	26:Y:55:ILE:HD12	2.01	0.43
34:g:84:ASP:OD1	34:g:84:ASP:N	2.52	0.43
1:2:85:A:H2'	1:2:86:C:H6	1.83	0.43
1:2:118:C:H1'	1:2:445:A:C4	2.54	0.43
1:2:218:U:O2	10:I:184:ARG:NH2	2.52	0.43
1:2:554:A:H2'	1:2:556:U:C5	2.54	0.43
1:2:1264:C:N4	1:2:1494:U:H3	2.17	0.43
1:2:1308:U:C5	33:f:138:ARG:HD3	2.51	0.43
1:2:1324:G:HO2'	1:2:1325:G:P	2.41	0.43
15:N:27:LYS:HA	15:N:27:LYS:CE	2.48	0.43
20:S:129:LEU:HB2	20:S:142:ARG:NH1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:f:81:LYS:HD2	33:f:81:LYS:HA	1.85	0.43
34:g:200:VAL:HG23	34:g:207:CYS:SG	2.59	0.43
1:2:17:C:O2'	1:2:1194:A:N1	2.40	0.43
1:2:373:G:OP1	13:L:137:THR:OG1	2.35	0.43
1:2:1446:A:H4'	1:2:1447:G:H8	1.84	0.43
1:2:1515:G:H5''	1:2:1621:U:O4	2.19	0.43
1:2:1540:G:H1'	1:2:1594:A:C5	2.54	0.43
1:2:1740:C:H2'	1:2:1741:U:C6	2.54	0.43
3:B:124:HIS:HA	3:B:137:LEU:O	2.19	0.43
5:D:154:ASP:N	5:D:154:ASP:OD1	2.52	0.43
14:M:75:ASN:ND2	14:M:127:TYR:O	2.45	0.43
18:Q:142:GLN:N	18:Q:142:GLN:OE1	2.52	0.43
25:X:25:LYS:HD2	25:X:25:LYS:HA	1.87	0.43
26:Y:32:LYS:HB3	26:Y:32:LYS:HE2	1.74	0.43
26:Y:88:LYS:HB3	26:Y:97:TYR:CE2	2.53	0.43
1:2:1276:A:N3	12:K:44:HIS:HE1	2.17	0.43
1:2:1349:G:H2'	1:2:1350:U:C6	2.53	0.43
2:A:184:ARG:HD3	2:A:191:ARG:HE	1.83	0.43
3:B:179:ASN:HB3	3:B:183:GLU:CG	2.47	0.43
7:F:40:ALA:HB1	7:F:45:TYR:CD2	2.54	0.43
7:F:91:ARG:HE	18:Q:46:THR:HB	1.84	0.43
12:K:6:LYS:NZ	14:M:28:HIS:HA	2.34	0.43
13:L:23:VAL:HG22	13:L:25:LEU:H	1.84	0.43
14:M:84:LYS:O	14:M:87:GLU:HG2	2.19	0.43
22:U:48:LEU:HD11	22:U:93:SER:HB3	2.00	0.43
23:V:1:MET:HE3	23:V:8:PHE:CD2	2.54	0.43
29:b:65:GLN:NE2	29:b:65:GLN:HA	2.34	0.43
33:f:103:LEU:HD12	33:f:104:LYS:HD3	1.99	0.43
34:g:278:SER:OG	34:g:304:ASP:OD1	2.35	0.43
35:h:13:LEU:HD22	35:h:17:ARG:NH2	2.33	0.43
35:h:16:LYS:HE3	35:h:16:LYS:HB3	1.92	0.43
1:2:122:G:H1'	6:E:145:ARG:HA	1.99	0.42
1:2:847:A:OP1	6:E:108:ARG:NH1	2.52	0.42
1:2:1309:C:C2'	33:f:141:CYS:N	2.82	0.42
1:2:1309:C:C3'	1:2:1309:C:C6	3.02	0.42
1:2:1324:G:H21	1:2:1509:U:H2'	1.84	0.42
1:2:1440:C:C2'	1:2:1441:U:H5'	2.49	0.42
1:2:1440:C:C6	1:2:1441:U:H5	2.37	0.42
2:A:158:ASP:OD1	23:V:65:SER:OG	2.32	0.42
8:G:137:ARG:HD3	8:G:178:ARG:NH1	2.34	0.42
9:H:69:LEU:HD22	9:H:96:ALA:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:318:A:H2'	1:2:319:C:O4'	2.19	0.42
1:2:942:G:H2'	1:2:943:U:C6	2.54	0.42
1:2:1155:U:O2	24:W:71:LYS:HB2	2.19	0.42
6:E:36:HIS:CG	6:E:85:GLY:HA3	2.54	0.42
7:F:147:VAL:O	7:F:151:ILE:HG13	2.18	0.42
11:J:28:GLU:OE2	11:J:40:LYS:HD2	2.20	0.42
30:c:67:ARG:HG3	30:c:68:LEU:HG	2.00	0.42
1:2:379:C:H2'	1:2:380:G:O4'	2.20	0.42
1:2:569:A:H2'	1:2:570:C:O4'	2.18	0.42
1:2:1324:G:O2'	1:2:1325:G:O5'	2.37	0.42
1:2:1476:A:OP1	7:F:59:LYS:HG2	2.19	0.42
1:2:1605:G:H3'	1:2:1606:G:O4'	2.19	0.42
1:2:1712:A:H2'	1:2:1713:C:C6	2.54	0.42
1:2:1844:U:H2'	1:2:1845:A:C8	2.54	0.42
17:P:15:PHE:CD2	17:P:87:PRO:HG3	2.55	0.42
19:R:105:MET:HE3	19:R:109:LEU:HD11	2.02	0.42
20:S:125:HIS:O	20:S:126:PHE:CB	2.67	0.42
1:2:388:U:H2'	1:2:389:A:C8	2.54	0.42
1:2:1231:C:HO2'	1:2:1232:U:P	2.41	0.42
1:2:1280:G:N2	1:2:1317:C:O2	2.52	0.42
1:2:1521:C:H6	20:S:136:THR:HB	1.85	0.42
1:2:1650:A:H5''	18:Q:139:ALA:HB2	2.02	0.42
4:C:169:TYR:OH	23:V:3:ASN:HB3	2.20	0.42
6:E:254:LYS:HB3	6:E:254:LYS:HE3	1.78	0.42
7:F:102:LEU:HD22	27:Z:108:ILE:HA	2.00	0.42
8:G:122:PRO:HA	8:G:126:ASP:OD2	2.20	0.42
22:U:54:VAL:HB	22:U:88:LEU:O	2.19	0.42
26:Y:76:TYR:HE2	26:Y:85:ASN:HB2	1.84	0.42
34:g:152:SER:N	34:g:169:GLY:HA2	2.33	0.42
1:2:5:U:H2'	1:2:6:G:H8	1.83	0.42
1:2:39:A:H2'	1:2:40:A:O4'	2.19	0.42
1:2:1004:U:H2'	1:2:1005:G:H8	1.84	0.42
1:2:1022:U:O2	15:N:128:TYR:CE2	2.72	0.42
1:2:1415:C:H2'	1:2:1416:C:C5	2.54	0.42
1:2:1462:U:H5''	1:2:1463:U:C5	2.53	0.42
1:2:1518:C:H5''	1:2:1519:U:C6	2.54	0.42
5:D:123:LEU:HD21	5:D:136:VAL:HG22	2.01	0.42
17:P:50:ARG:O	17:P:53:GLN:HB3	2.20	0.42
21:T:111:LYS:HA	21:T:111:LYS:HD2	1.74	0.42
24:W:104:LEU:HD23	24:W:125:ILE:HA	2.01	0.42
34:g:112:ALA:HA	34:g:154:VAL:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:130:LYS:HB3	34:g:132:TRP:CH2	2.55	0.42
1:2:791:C:H2'	1:2:793:G:OP1	2.19	0.42
1:2:1146:C:O2'	1:2:1150:A:N1	2.45	0.42
1:2:1234:C:H2'	1:2:1235:G:H4'	2.00	0.42
1:2:1406:G:H2'	1:2:1407:U:C5'	2.50	0.42
4:C:132:ASP:OD1	4:C:136:HIS:HB2	2.19	0.42
8:G:11:GLY:O	8:G:13:GLN:NE2	2.52	0.42
8:G:137:ARG:O	8:G:141:ILE:HG13	2.19	0.42
11:J:136:ARG:HG2	11:J:160:SER:H	1.85	0.42
22:U:67:LYS:O	31:d:44:ARG:NH1	2.52	0.42
34:g:201:SER:OG	34:g:203:ASP:OD1	2.37	0.42
1:2:160:U:O2'	1:2:161:U:H3'	2.20	0.42
1:2:216:C:C2	1:2:217:A:C8	3.08	0.42
1:2:454:U:H2'	1:2:455:A:C8	2.54	0.42
1:2:494:C:N4	1:2:509:G:H21	2.18	0.42
1:2:918:U:O2'	24:W:56:HIS:O	2.38	0.42
1:2:984:C:H1'	16:O:138:ASP:O	2.18	0.42
5:D:104:SER:O	5:D:108:LYS:HG2	2.19	0.42
5:D:158:ILE:HG22	5:D:189:MET:HE2	2.02	0.42
6:E:126:VAL:HG13	6:E:158:ASP:O	2.20	0.42
9:H:9:VAL:HG12	9:H:11:PRO:HD3	2.01	0.42
15:N:19:ARG:O	15:N:19:ARG:HG3	2.18	0.42
19:R:59:LYS:HA	19:R:59:LYS:HD3	1.78	0.42
20:S:63:GLU:O	20:S:66:ARG:HG2	2.19	0.42
21:T:37:VAL:HG21	21:T:99:VAL:HG11	2.02	0.42
23:V:64:GLU:HG2	29:b:3:LEU:HG	2.01	0.42
24:W:83:LEU:HD23	24:W:83:LEU:HA	1.79	0.42
1:2:146:G:O6	8:G:137:ARG:NH2	2.50	0.42
1:2:815:U:C2	1:2:816:A:C8	3.07	0.42
1:2:1344:A:N6	1:2:1386:A:H5'	2.35	0.42
1:2:1591:C:H1'	18:Q:77:HIS:CE1	2.55	0.42
8:G:47:GLY:HA3	8:G:118:GLU:OE2	2.20	0.42
8:G:98:ARG:HH21	8:G:103:ASP:CG	2.27	0.42
10:I:203:LYS:HB3	10:I:203:LYS:HE2	1.79	0.42
15:N:119:GLU:O	15:N:123:HIS:ND1	2.53	0.42
21:T:38:LYS:HE2	21:T:38:LYS:HB2	1.80	0.42
24:W:81:VAL:HG11	24:W:86:LEU:HD13	2.01	0.42
34:g:298:LEU:HD23	34:g:310:TRP:CD1	2.54	0.42
1:2:329:G:N3	1:2:329:G:O5'	2.43	0.42
1:2:344:U:H2'	1:2:345:U:H6	1.83	0.42
1:2:1177:U:H2'	1:2:1178:U:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1261:C:H2'	1:2:1262:C:H5	1.85	0.42
1:2:1397:U:H4'	1:2:1398:G:OP2	2.20	0.42
1:2:1816:G:H2'	1:2:1817:G:C8	2.55	0.42
6:E:115:THR:HG23	6:E:118:GLU:H	1.84	0.42
7:F:188:TYR:O	7:F:191:LYS:HG3	2.19	0.42
13:L:32:LYS:HA	13:L:32:LYS:HD2	1.84	0.42
14:M:15:ASN:O	14:M:19:GLN:HG2	2.20	0.42
14:M:64:LEU:HA	14:M:64:LEU:HD23	1.81	0.42
14:M:122:ASP:O	14:M:126:GLU:HG2	2.19	0.42
19:R:105:MET:O	19:R:109:LEU:HG	2.18	0.42
22:U:22:ILE:HB	22:U:89:ILE:HD11	2.02	0.42
34:g:247:TRP:HE1	34:g:260:ASP:HB3	1.85	0.42
1:2:415:A:H2'	1:2:416:U:O4'	2.20	0.42
1:2:496:C:H2'	1:2:497:C:C6	2.54	0.42
1:2:666:U:H2'	1:2:667:U:C6	2.55	0.42
1:2:1308:U:C4	33:f:138:ARG:NH2	2.88	0.42
2:A:203:PHE:HZ	19:R:91:LEU:HD11	1.85	0.42
5:D:50:ILE:O	5:D:50:ILE:HD12	2.19	0.42
6:E:21:ASP:OD1	6:E:24:THR:OG1	2.24	0.42
6:E:252:ARG:NH1	6:E:253:ASP:OD1	2.49	0.42
7:F:76:MET:HG2	7:F:77:MET:N	2.35	0.42
8:G:116:LYS:HZ1	8:G:120:ASP:HA	1.85	0.42
9:H:157:HIS:HB3	9:H:190:PRO:HD3	2.02	0.42
10:I:45:THR:HG22	10:I:53:LYS:CD	2.50	0.42
15:N:95:ALA:O	15:N:99:ARG:HG3	2.18	0.42
17:P:18:ARG:HA	20:S:90:VAL:HG12	2.02	0.42
28:a:36:ILE:HB	28:a:78:VAL:HG21	2.02	0.42
1:2:150:A:H62	1:2:168:C:N4	2.16	0.41
1:2:332:G:N7	8:G:189:ARG:NH1	2.68	0.41
1:2:552:G:N2	1:2:553:U:O4	2.53	0.41
1:2:1183:A:OP2	35:h:18:ARG:NH1	2.44	0.41
1:2:1240:A:H61	1:2:1266:C:H5	1.67	0.41
1:2:1290:G:N2	33:f:138:ARG:HE	2.17	0.41
1:2:1302:G:H4'	1:2:1303:C:O5'	2.20	0.41
1:2:1317:C:O2	1:2:1317:C:C2'	2.68	0.41
1:2:1510:G:N3	1:2:1510:G:H2'	2.35	0.41
1:2:1519:U:OP2	1:2:1521:C:N4	2.53	0.41
1:2:1537:A:N7	1:2:1593:C:H3'	2.35	0.41
3:B:67:PHE:CE2	16:O:48:SER:HB3	2.55	0.41
3:B:67:PHE:HE1	3:B:88:THR:HG23	1.85	0.41
3:B:68:GLU:OE2	3:B:83:LYS:HD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:23:LYS:HB3	10:I:23:LYS:HE2	1.70	0.41
18:Q:107:GLU:H	18:Q:107:GLU:HG2	1.70	0.41
31:d:55:LEU:HD13	31:d:55:LEU:HA	1.91	0.41
1:2:1145:A:C5	1:2:1146:C:H1'	2.55	0.41
1:2:1229:G:OP2	20:S:141:ARG:NH2	2.53	0.41
1:2:1290:G:C2	33:f:138:ARG:CZ	3.03	0.41
1:2:1853:C:N4	35:h:5:TRP:CH2	2.88	0.41
2:A:39:TYR:CG	19:R:105:MET:HG3	2.55	0.41
2:A:191:ARG:NH1	23:V:43:THR:O	2.53	0.41
6:E:199:GLU:HG3	6:E:207:VAL:HB	2.02	0.41
10:I:29:LEU:HD11	10:I:31:ARG:HH21	1.84	0.41
10:I:41:ARG:HD3	10:I:43:ILE:HD12	2.01	0.41
16:O:65:ASP:OD1	16:O:65:ASP:N	2.53	0.41
16:O:120:ALA:HB2	28:a:53:ILE:HD13	2.02	0.41
1:2:96:C:H2'	1:2:97:U:C6	2.55	0.41
1:2:913:A:H61	9:H:119:SER:HB2	1.85	0.41
2:A:84:GLN:HE21	2:A:100:ALA:HB1	1.86	0.41
5:D:127:MET:HE2	5:D:134:CYS:SG	2.61	0.41
7:F:126:THR:HG21	30:c:46:VAL:HA	2.02	0.41
10:I:76:THR:HG23	10:I:108:PRO:HG2	2.01	0.41
15:N:54:LEU:HB3	15:N:60:VAL:HG22	2.02	0.41
17:P:84:ILE:HA	17:P:89:MET:HE3	2.01	0.41
25:X:101:LEU:HB3	25:X:124:LYS:HB2	2.02	0.41
1:2:14:C:OP2	4:C:232:THR:HG21	2.21	0.41
1:2:120:U:H1'	6:E:33:THR:O	2.20	0.41
1:2:496:C:H2'	1:2:497:C:H6	1.85	0.41
1:2:1317:C:O2'	1:2:1318:G:OP1	2.37	0.41
1:2:1668:U:OP2	18:Q:141:TYR:OH	2.39	0.41
5:D:117:ARG:H	5:D:117:ARG:HG3	1.55	0.41
7:F:135:ARG:HH21	7:F:199:VAL:CG2	2.33	0.41
17:P:51:ARG:O	17:P:52:LYS:HB2	2.20	0.41
26:Y:10:ARG:NE	26:Y:26:ASP:OD2	2.53	0.41
32:e:21:LYS:HD3	32:e:21:LYS:N	2.36	0.41
33:f:138:ARG:HB3	33:f:138:ARG:NH1	2.34	0.41
1:2:65:C:H6	1:2:65:C:H2'	1.61	0.41
1:2:157:U:O2'	1:2:159:A:N7	2.37	0.41
1:2:338:G:H2'	1:2:339:A:C8	2.56	0.41
1:2:375:U:H2'	1:2:376:A:C8	2.55	0.41
1:2:964:A:H2'	1:2:965:U:H6	1.84	0.41
1:2:1563:G:C6	1:2:1573:G:N1	2.88	0.41
1:2:1588:A:H5'	21:T:82:ARG:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1854:U:OP1	16:O:150:ARG:NH2	2.53	0.41
3:B:57:ILE:HG23	3:B:59:SER:H	1.86	0.41
7:F:66:CYS:HB3	7:F:71:ARG:NH2	2.35	0.41
17:P:44:ARG:HB3	17:P:81:ARG:NH1	2.35	0.41
18:Q:18:THR:HG22	18:Q:126:ARG:HH21	1.85	0.41
18:Q:70:VAL:HG12	18:Q:72:VAL:HG23	2.02	0.41
19:R:22:THR:HG23	34:g:235:ILE:HB	2.01	0.41
21:T:74:SER:HA	21:T:77:LYS:HB3	2.01	0.41
26:Y:61:ARG:HA	26:Y:61:ARG:HD2	1.89	0.41
1:2:19:A:H2'	1:2:20:G:O4'	2.20	0.41
1:2:931:C:H2'	1:2:932:G:C8	2.55	0.41
1:2:991:G:N1	1:2:1134:G:H4'	2.36	0.41
1:2:1246:A:H1'	1:2:1251:A:C8	2.56	0.41
2:A:68:ILE:HD12	2:A:121:LEU:HB2	2.03	0.41
2:A:104:THR:O	2:A:107:THR:OG1	2.23	0.41
7:F:154:LEU:HD23	7:F:154:LEU:HA	1.86	0.41
7:F:175:ASP:OD1	7:F:175:ASP:C	2.63	0.41
8:G:38:ALA:N	8:G:48:TYR:O	2.47	0.41
13:L:128:VAL:HG12	13:L:142:VAL:HA	2.01	0.41
15:N:87:ASP:OD2	15:N:125:LEU:HD21	2.21	0.41
20:S:26:ILE:HD12	20:S:26:ILE:HA	1.86	0.41
25:X:7:LEU:HD23	25:X:7:LEU:HA	1.89	0.41
1:2:90:G:H2'	1:2:91:A:O4'	2.21	0.41
1:2:1078:C:C4	1:2:1079:C:C5	3.09	0.41
1:2:1470:C:P	7:F:62:ARG:HA	2.61	0.41
1:2:1517:G:H5'	1:2:1518:C:OP2	2.21	0.41
1:2:1552:G:O6	1:2:1557:C:H5''	2.21	0.41
1:2:1560:U:H2'	1:2:1561:A:C8	2.55	0.41
1:2:1597:C:H5'	20:S:25:LYS:HG3	2.03	0.41
1:2:1610:G:H21	20:S:87:GLN:NE2	2.18	0.41
1:2:1837:G:H4'	1:2:1838:U:H5''	2.03	0.41
3:B:87:ILE:HG22	3:B:101:HIS:HB2	2.02	0.41
3:B:196:ASP:O	3:B:199:LYS:HG3	2.21	0.41
13:L:79:LYS:HB2	13:L:87:VAL:HB	2.03	0.41
13:L:135:SER:O	13:L:139:ARG:NH1	2.43	0.41
17:P:65:LYS:HB3	17:P:65:LYS:HE3	1.92	0.41
26:Y:39:GLU:O	26:Y:42:GLU:HG3	2.21	0.41
27:Z:92:LEU:HD21	27:Z:110:THR:HB	2.03	0.41
1:2:963:A:H2'	1:2:964:A:O4'	2.20	0.41
1:2:1467:C:H2'	1:2:1468:C:C6	2.56	0.41
7:F:66:CYS:HA	7:F:67:PRO:HD3	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:116:LYS:NZ	8:G:120:ASP:HA	2.36	0.41
10:I:22:HIS:HD2	10:I:23:LYS:O	2.04	0.41
11:J:137:VAL:O	11:J:139:LYS:N	2.53	0.41
12:K:21:MET:CE	12:K:45:VAL:HG11	2.51	0.41
16:O:28:PHE:HZ	28:a:58:VAL:HG21	1.86	0.41
21:T:101:ARG:HA	21:T:101:ARG:HD3	1.77	0.41
25:X:100:VAL:HG13	25:X:102:VAL:HG13	2.03	0.41
26:Y:11:LYS:H	26:Y:24:VAL:CG1	2.34	0.41
34:g:42:MET:HG3	34:g:56:GLN:HB3	2.02	0.41
34:g:81:GLY:HA3	34:g:104:HIS:NE2	2.36	0.41
1:2:59:U:O5'	1:2:501:C:H4'	2.21	0.41
1:2:205:G:H2'	1:2:206:G:H8	1.84	0.41
1:2:211:G:H2'	1:2:212:C:C6	2.56	0.41
1:2:452:G:H2'	1:2:453:C:H6	1.86	0.41
1:2:629:A:O2'	1:2:631:U:OP1	2.38	0.41
1:2:829:C:OP1	6:E:22:LYS:N	2.42	0.41
1:2:1136:U:H2'	1:2:1137:U:C6	2.55	0.41
1:2:1253:A:C8	1:2:1666:C:H4'	2.55	0.41
1:2:1310:U:O2	1:2:1310:U:C2'	2.68	0.41
1:2:1397:U:C2	18:Q:11:GLN:HB3	2.56	0.41
1:2:1430:C:H6	1:2:1430:C:H2'	1.66	0.41
1:2:1470:C:OP2	7:F:62:ARG:HA	2.21	0.41
1:2:1549:U:H5'	31:d:34:TYR:HE1	1.85	0.41
1:2:1560:U:H2'	1:2:1561:A:H8	1.86	0.41
1:2:1702:G:H2'	1:2:1703:C:O4'	2.20	0.41
3:B:44:ILE:HD13	3:B:69:VAL:HG11	2.02	0.41
3:B:183:GLU:O	3:B:187:LYS:HG2	2.21	0.41
6:E:211:LYS:HB2	6:E:211:LYS:HE2	1.84	0.41
12:K:16:PHE:CZ	12:K:91:PRO:HG3	2.56	0.41
12:K:36:ALA:C	12:K:38:LYS:N	2.79	0.41
18:Q:37:ARG:HA	21:T:10:ASN:OD1	2.20	0.41
20:S:46:ARG:NE	20:S:46:ARG:O	2.53	0.41
20:S:87:GLN:H	20:S:87:GLN:HG2	1.65	0.41
20:S:113:ARG:HA	20:S:116:LYS:HG2	2.02	0.41
20:S:120:HIS:CE1	20:S:124:ARG:HD3	2.56	0.41
21:T:42:HIS:NE2	21:T:43:LYS:NZ	2.68	0.41
21:T:83:GLN:O	21:T:84:ARG:HD3	2.20	0.41
25:X:124:LYS:HG2	25:X:129:SER:HA	2.02	0.41
26:Y:13:MET:HG2	26:Y:22:GLN:HG2	2.02	0.41
29:b:36:LYS:HD2	29:b:36:LYS:HA	1.75	0.41
34:g:2:THR:OG1	34:g:3:GLU:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:263:GLY:O	34:g:265:ILE:HG23	2.21	0.41
1:2:156:G:H5''	8:G:2:LYS:HD2	2.03	0.41
1:2:944:A:H1'	16:O:139:SER:HB3	2.03	0.41
1:2:1008:A:H2'	1:2:1009:A:O4'	2.21	0.41
1:2:1266:C:C6	1:2:1517:G:H8	2.39	0.41
1:2:1350:U:O2	2:A:110:ASN:ND2	2.54	0.41
1:2:1380:C:H2'	1:2:1381:G:O4'	2.21	0.41
1:2:1387:G:H2'	1:2:1388:A:O4'	2.20	0.41
2:A:161:ILE:HA	2:A:162:PRO:HD3	1.97	0.41
3:B:25:PHE:HD1	3:B:25:PHE:H	1.68	0.41
6:E:45:ILE:HA	6:E:61:VAL:HG11	2.02	0.41
7:F:145:ARG:HG3	30:c:48:GLY:HA3	2.02	0.41
8:G:2:LYS:HB3	8:G:2:LYS:HE3	1.79	0.41
12:K:80:ARG:HD3	12:K:85:LEU:O	2.21	0.41
19:R:76:GLU:HA	19:R:79:GLU:HG2	2.02	0.41
20:S:80:PRO:C	20:S:82:TRP:H	2.29	0.41
21:T:64:LEU:HG	21:T:121:ARG:HB2	2.03	0.41
21:T:122:LYS:HD2	21:T:122:LYS:HA	1.64	0.41
25:X:138:LYS:HE2	25:X:138:LYS:HB2	1.93	0.41
34:g:265:ILE:HD12	34:g:266:ILE:O	2.20	0.41
1:2:221:A:H2'	1:2:222:U:C6	2.56	0.40
1:2:920:A:O2'	1:2:922:A:O5'	2.39	0.40
1:2:986:G:OP2	1:2:988:C:N4	2.52	0.40
1:2:1004:U:H2'	1:2:1005:G:C8	2.55	0.40
1:2:1035:A:H2'	1:2:1036:A:O4'	2.21	0.40
1:2:1035:A:O2'	1:2:1856:C:O2	2.38	0.40
1:2:1073:U:C2	1:2:1074:C:C5	3.08	0.40
1:2:1267:C:OP2	33:f:79:LYS:HB2	2.21	0.40
2:A:70:ASN:HB2	4:C:270:THR:OG1	2.21	0.40
5:D:114:ALA:HB3	5:D:117:ARG:CD	2.51	0.40
8:G:132:ARG:HE	8:G:133:LEU:HD13	1.86	0.40
23:V:40:ASP:OD1	23:V:44:GLY:N	2.49	0.40
31:d:36:LEU:HD12	31:d:38:MET:HG3	2.04	0.40
1:2:146:G:H2'	1:2:147:A:O4'	2.22	0.40
1:2:563:G:O2'	1:2:564:A:H8	2.04	0.40
1:2:681:U:OP1	13:L:104:LYS:HD3	2.20	0.40
1:2:943:U:H2'	1:2:944:A:C8	2.55	0.40
1:2:959:G:H2'	1:2:960:U:C6	2.56	0.40
1:2:1139:C:H5	1:2:1149:A:H62	1.67	0.40
1:2:1310:U:O3'	1:2:1310:U:OP1	2.39	0.40
1:2:1855:G:C6	1:2:1856:C:C4	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:228:LEU:O	3:B:232:HIS:HD2	2.04	0.40
6:E:10:LYS:HA	6:E:10:LYS:HD3	1.93	0.40
8:G:3:LEU:CD1	8:G:109:LEU:HB3	2.51	0.40
8:G:214:ALA:HA	8:G:217:MET:HE2	2.03	0.40
12:K:32:HIS:HB3	12:K:35:LEU:CB	2.51	0.40
14:M:22:LEU:HD11	14:M:105:GLY:HA3	2.02	0.40
20:S:75:ARG:HH11	20:S:95:TYR:HB2	1.86	0.40
1:2:152:U:H2'	1:2:153:G:C8	2.56	0.40
1:2:455:A:O2'	1:2:1735:A:N3	2.48	0.40
1:2:587:A:H5'	1:2:592:C:N4	2.32	0.40
1:2:1230:C:OP1	20:S:139:THR:HG22	2.21	0.40
1:2:1232:U:H6	1:2:1233:G:N7	2.19	0.40
1:2:1310:U:C3'	1:2:1310:U:P	3.10	0.40
1:2:1607:A:C6	20:S:128:GLY:N	2.90	0.40
1:2:1690:U:H2'	1:2:1691:U:C6	2.56	0.40
3:B:81:PHE:CD1	3:B:109:LYS:HG2	2.56	0.40
4:C:79:GLU:OE2	4:C:136:HIS:NE2	2.50	0.40
5:D:31:GLU:HA	5:D:107:TYR:HE2	1.86	0.40
8:G:56:ASN:ND2	8:G:60:GLY:O	2.42	0.40
10:I:162:LEU:O	10:I:166:PHE:HD1	2.04	0.40
17:P:15:PHE:HB2	17:P:110:GLU:HG2	2.03	0.40
17:P:45:LEU:HD12	17:P:83:MET:SD	2.61	0.40
18:Q:103:ALA:O	18:Q:107:GLU:HG2	2.21	0.40
20:S:111:LEU:HD11	20:S:125:HIS:CE1	2.56	0.40
27:Z:54:THR:HG23	27:Z:84:ALA:HA	2.02	0.40
30:c:26:GLN:HG3	30:c:47:LYS:HD2	2.02	0.40
1:2:180:G:O2'	1:2:181:A:P	2.79	0.40
1:2:294:U:H5	13:L:36:TYR:CE2	2.40	0.40
1:2:407:G:H5''	1:2:408:A:H5'	2.03	0.40
1:2:1097:G:H4'	2:A:32:PHE:CG	2.57	0.40
1:2:1189:A:H2'	1:2:1190:A:C8	2.56	0.40
1:2:1308:U:C5	33:f:138:ARG:CD	3.03	0.40
1:2:1312:G:O2'	14:M:36:ARG:HB2	2.22	0.40
8:G:33:ALA:HA	8:G:51:ARG:HG3	2.03	0.40
10:I:31:ARG:HH12	10:I:48:VAL:HG12	1.87	0.40
12:K:58:VAL:HG23	12:K:71:LEU:HD12	2.04	0.40
17:P:84:ILE:HD13	17:P:112:ILE:HA	2.03	0.40
20:S:120:HIS:ND1	20:S:131:VAL:HG23	2.36	0.40
21:T:12:GLN:NE2	21:T:16:ARG:HG3	2.37	0.40
35:h:2:ARG:HD3	35:h:5:TRP:NE1	2.37	0.40
1:2:162:C:H2'	1:2:163:U:O4'	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1280:G:H22	1:2:1317:C:H1'	1.86	0.40
1:2:1523:C:O4'	20:S:141:ARG:NH2	2.55	0.40
1:2:1644:C:C1'	18:Q:143:LYS:HD2	2.51	0.40
1:2:1712:A:H2'	1:2:1713:C:H6	1.87	0.40
3:B:62:LEU:HD21	3:B:96:CYS:SG	2.61	0.40
6:E:93:ASP:OD1	6:E:93:ASP:N	2.53	0.40
13:L:55:TYR:OH	13:L:116:CYS:HB3	2.22	0.40
17:P:14:LYS:HD2	17:P:14:LYS:HA	1.88	0.40
18:Q:112:LEU:O	18:Q:115:TYR:HB3	2.22	0.40
20:S:94:LYS:O	20:S:95:TYR:C	2.64	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	A	211/295 (72%)	205 (97%)	5 (2%)	1 (0%)	25	52
3	B	211/264 (80%)	207 (98%)	4 (2%)	0	100	100
4	C	216/293 (74%)	211 (98%)	5 (2%)	0	100	100
5	D	223/243 (92%)	214 (96%)	9 (4%)	0	100	100
6	E	260/263 (99%)	250 (96%)	10 (4%)	0	100	100
7	F	187/204 (92%)	166 (89%)	20 (11%)	1 (0%)	25	52
8	G	228/249 (92%)	220 (96%)	8 (4%)	0	100	100
9	H	184/194 (95%)	177 (96%)	7 (4%)	0	100	100
10	I	203/208 (98%)	194 (96%)	8 (4%)	1 (0%)	25	52
11	J	178/194 (92%)	167 (94%)	10 (6%)	1 (1%)	22	48
12	K	95/165 (58%)	83 (87%)	12 (13%)	0	100	100
13	L	149/158 (94%)	145 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	M	119/132 (90%)	112 (94%)	5 (4%)	2 (2%)	7	23
15	N	147/151 (97%)	147 (100%)	0	0	100	100
16	O	133/151 (88%)	125 (94%)	8 (6%)	0	100	100
17	P	124/145 (86%)	106 (86%)	17 (14%)	1 (1%)	16	41
18	Q	136/146 (93%)	119 (88%)	17 (12%)	0	100	100
19	R	130/135 (96%)	126 (97%)	4 (3%)	0	100	100
20	S	141/152 (93%)	118 (84%)	17 (12%)	6 (4%)	2	6
21	T	142/145 (98%)	128 (90%)	13 (9%)	1 (1%)	19	45
22	U	99/119 (83%)	93 (94%)	6 (6%)	0	100	100
23	V	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
24	W	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
25	X	139/143 (97%)	134 (96%)	5 (4%)	0	100	100
26	Y	122/130 (94%)	119 (98%)	3 (2%)	0	100	100
27	Z	70/125 (56%)	66 (94%)	4 (6%)	0	100	100
28	a	97/101 (96%)	91 (94%)	5 (5%)	1 (1%)	13	36
29	b	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
30	c	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
31	d	53/55 (96%)	48 (91%)	5 (9%)	0	100	100
32	e	54/56 (96%)	48 (89%)	5 (9%)	1 (2%)	6	20
33	f	72/74 (97%)	63 (88%)	8 (11%)	1 (1%)	9	27
34	g	312/315 (99%)	289 (93%)	23 (7%)	0	100	100
35	h	20/25 (80%)	19 (95%)	1 (5%)	0	100	100
36	n	25/196 (13%)	25 (100%)	0	0	100	100
All	All	4827/5583 (86%)	4550 (94%)	260 (5%)	17 (0%)	32	58

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	189	ILE
17	P	75	VAL
20	S	137	LYS
11	J	138	ARG
21	T	143	LYS
14	M	95	ASP

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Mol	Chain	Res	Type
20	S	95	TYR
33	f	136	PHE
20	S	109	GLU
20	S	144	ARG
14	M	110	VAL
20	S	100	ALA
20	S	133	GLY
28	a	63	VAL
10	I	129	LEU
32	e	52	LYS
7	F	33	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	A	179/243 (74%)	174 (97%)	5 (3%)	38	69
3	B	194/231 (84%)	186 (96%)	8 (4%)	26	56
4	C	184/225 (82%)	173 (94%)	11 (6%)	16	40
5	D	189/202 (94%)	176 (93%)	13 (7%)	13	34
6	E	224/225 (100%)	216 (96%)	8 (4%)	30	61
7	F	159/170 (94%)	146 (92%)	13 (8%)	9	26
8	G	200/218 (92%)	194 (97%)	6 (3%)	36	67
9	H	167/174 (96%)	160 (96%)	7 (4%)	25	55
10	I	178/180 (99%)	174 (98%)	4 (2%)	47	76
11	J	160/168 (95%)	149 (93%)	11 (7%)	13	34
12	K	88/136 (65%)	82 (93%)	6 (7%)	13	34
13	L	135/142 (95%)	128 (95%)	7 (5%)	19	47
14	M	102/108 (94%)	99 (97%)	3 (3%)	37	68
15	N	130/131 (99%)	127 (98%)	3 (2%)	45	75
16	O	105/119 (88%)	100 (95%)	5 (5%)	21	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	P	112/130 (86%)	110 (98%)	2 (2%)	54	80
18	Q	114/121 (94%)	108 (95%)	6 (5%)	19	46
19	R	119/122 (98%)	114 (96%)	5 (4%)	25	55
20	S	124/132 (94%)	108 (87%)	16 (13%)	3	10
21	T	114/115 (99%)	112 (98%)	2 (2%)	54	80
22	U	93/107 (87%)	92 (99%)	1 (1%)	70	88
23	V	66/67 (98%)	65 (98%)	1 (2%)	60	84
24	W	112/113 (99%)	109 (97%)	3 (3%)	40	71
25	X	113/115 (98%)	106 (94%)	7 (6%)	15	39
26	Y	108/112 (96%)	105 (97%)	3 (3%)	38	69
27	Z	64/103 (62%)	63 (98%)	1 (2%)	58	83
28	a	87/89 (98%)	84 (97%)	3 (3%)	32	63
29	b	74/74 (100%)	73 (99%)	1 (1%)	62	85
30	c	55/55 (100%)	52 (94%)	3 (6%)	18	44
31	d	48/48 (100%)	44 (92%)	4 (8%)	9	26
32	e	45/45 (100%)	43 (96%)	2 (4%)	24	53
33	f	67/67 (100%)	64 (96%)	3 (4%)	23	52
34	g	272/273 (100%)	259 (95%)	13 (5%)	21	50
35	h	21/24 (88%)	20 (95%)	1 (5%)	21	50
36	n	24/162 (15%)	24 (100%)	0	100	100
All	All	4226/4746 (89%)	4039 (96%)	187 (4%)	26	53

All (187) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	41	ARG
2	A	75	SER
2	A	79	SER
2	A	121	LEU
2	A	188	THR
3	B	49	VAL
3	B	125	VAL
3	B	131	ASP
3	B	143	THR
3	B	173	THR

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Mol	Chain	Res	Type
3	B	180	ASP
3	B	203	SER
3	B	225	LEU
4	C	98	LEU
4	C	116	THR
4	C	134	ASN
4	C	162	ILE
4	C	184	VAL
4	C	206	SER
4	C	213	LEU
4	C	230	THR
4	C	232	THR
4	C	260	VAL
4	C	274	VAL
5	D	5	ILE
5	D	12	VAL
5	D	18	LYS
5	D	50	ILE
5	D	55	THR
5	D	59	LEU
5	D	72	VAL
5	D	132	LYS
5	D	153	VAL
5	D	177	LEU
5	D	193	ASP
5	D	198	ILE
5	D	207	HIS
6	E	67	GLN
6	E	105	THR
6	E	126	VAL
6	E	162	ILE
6	E	194	VAL
6	E	199	GLU
6	E	204	SER
6	E	230	LYS
7	F	42	LYS
7	F	69	VAL
7	F	81	ARG
7	F	87	LEU
7	F	92	ILE
7	F	95	HIS
7	F	99	ILE

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Mol	Chain	Res	Type
7	F	128	ILE
7	F	134	VAL
7	F	166	ILE
7	F	168	THR
7	F	171	GLU
7	F	190	ILE
8	G	6	SER
8	G	24	LEU
8	G	101	ILE
8	G	127	THR
8	G	163	ASN
8	G	222	GLU
9	H	60	ILE
9	H	92	VAL
9	H	107	LYS
9	H	134	VAL
9	H	148	LEU
9	H	180	LEU
9	H	184	ASP
10	I	29	LEU
10	I	76	THR
10	I	81	VAL
10	I	160	SER
11	J	6	SER
11	J	8	VAL
11	J	23	SER
11	J	62	THR
11	J	92	MET
11	J	102	ILE
11	J	128	VAL
11	J	138	ARG
11	J	143	ASN
11	J	149	VAL
11	J	152	ASP
12	K	9	ILE
12	K	11	ILE
12	K	25	LYS
12	K	37	ASP
12	K	44	HIS
12	K	90	VAL
13	L	18	GLN
13	L	54	THR

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Mol	Chain	Res	Type
13	L	66	VAL
13	L	67	SER
13	L	76	VAL
13	L	100	ASN
13	L	107	LYS
14	M	11	VAL
14	M	18	LEU
14	M	79	VAL
15	N	24	THR
15	N	60	VAL
15	N	100	LYS
16	O	27	VAL
16	O	55	ARG
16	O	56	VAL
16	O	122	SER
16	O	128	ARG
17	P	126	VAL
17	P	136	THR
18	Q	12	VAL
18	Q	33	LYS
18	Q	53	GLU
18	Q	118	THR
18	Q	121	VAL
18	Q	129	SER
19	R	15	VAL
19	R	71	ILE
19	R	98	VAL
19	R	102	THR
19	R	124	VAL
20	S	7	GLU
20	S	31	THR
20	S	67	VAL
20	S	68	ILE
20	S	90	VAL
20	S	92	ASP
20	S	98	VAL
20	S	108	ARG
20	S	109	GLU
20	S	124	ARG
20	S	126	PHE
20	S	127	TRP
20	S	129	LEU

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Mol	Chain	Res	Type
20	S	131	VAL
20	S	137	LYS
20	S	142	ARG
21	T	39	LEU
21	T	107	LEU
22	U	26	SER
23	V	39	VAL
24	W	30	CYS
24	W	74	VAL
24	W	80	ASP
25	X	32	LEU
25	X	36	LEU
25	X	45	SER
25	X	70	VAL
25	X	100	VAL
25	X	105	PHE
25	X	128	VAL
26	Y	6	THR
26	Y	14	THR
26	Y	27	VAL
27	Z	96	LEU
28	a	57	SER
28	a	78	VAL
28	a	81	SER
29	b	3	LEU
30	c	21	THR
30	c	36	ASP
30	c	50	VAL
31	d	14	PHE
31	d	30	LEU
31	d	53	ILE
31	d	55	LEU
32	e	29	THR
32	e	44	ASN
33	f	98	VAL
33	f	114	ILE
33	f	137	ASP
34	g	32	LEU
34	g	63	SER
34	g	64	HIS
34	g	87	LEU
34	g	102	VAL

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Mol	Chain	Res	Type
34	g	151	VAL
34	g	166	VAL
34	g	168	CYS
34	g	198	VAL
34	g	242	SER
34	g	274	VAL
34	g	277	THR
34	g	305	ASN
35	h	13	LEU

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

Mol	Chain	Res	Type
2	A	29	ASN
2	A	50	ASN
3	B	148	ASN
4	C	172	ASN
5	D	174	HIS
5	D	207	HIS
5	D	226	GLN
6	E	112	HIS
6	E	142	HIS
6	E	214	ASN
7	F	79	HIS
7	F	149	GLN
7	F	165	ASN
8	G	13	GLN
8	G	70	HIS
8	G	81	HIS
8	G	105	ASN
9	H	114	GLN
10	I	165	GLN
11	J	111	GLN
11	J	143	ASN
12	K	44	HIS
13	L	18	GLN
13	L	19	ASN
13	L	39	ASN
13	L	83	GLN
15	N	49	GLN
16	O	38	ASN
17	P	79	HIS

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Mol	Chain	Res	Type
18	Q	48	GLN
18	Q	80	GLN
19	R	48	ASN
19	R	121	GLN
20	S	97	GLN
20	S	120	HIS
21	T	63	HIS
25	X	97	ASN
26	Y	15	ASN
26	Y	63	HIS
27	Z	64	ASN
32	e	15	GLN
33	f	139	HIS
34	g	196	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1658/1869 (88%)	541 (32%)	26 (1%)

All (541) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	33	G
1	2	41	G
1	2	44	U
1	2	46	A
1	2	49	C
1	2	56	G
1	2	60	A
1	2	61	A
1	2	67	C
1	2	68	A
1	2	73	C
1	2	75	G
1	2	76	U
1	2	77	A
1	2	103	A
1	2	113	G

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Mol	Chain	Res	Type
1	2	114	G
1	2	115	U
1	2	126	G
1	2	128	U
1	2	129	C
1	2	130	G
1	2	142	C
1	2	143	U
1	2	155	G
1	2	158	A
1	2	160	U
1	2	162	C
1	2	163	U
1	2	168	C
1	2	170	A
1	2	175	A
1	2	181	A
1	2	182	C
1	2	184	G
1	2	186	C
1	2	191	A
1	2	196	C
1	2	198	U
1	2	200	G
1	2	202	G
1	2	215	G
1	2	293	C
1	2	295	C
1	2	301	A
1	2	305	U
1	2	306	C
1	2	307	G
1	2	308	G
1	2	310	C
1	2	314	U
1	2	321	C
1	2	332	G
1	2	333	G
1	2	351	G
1	2	357	C
1	2	362	C
1	2	364	A

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Mol	Chain	Res	Type
1	2	368	U
1	2	370	G
1	2	377	G
1	2	385	G
1	2	386	C
1	2	388	U
1	2	400	C
1	2	409	C
1	2	428	U
1	2	436	G
1	2	437	G
1	2	447	A
1	2	448	A
1	2	449	A
1	2	450	C
1	2	464	A
1	2	470	G
1	2	471	G
1	2	472	C
1	2	473	A
1	2	474	G
1	2	482	G
1	2	487	U
1	2	492	C
1	2	493	A
1	2	523	A
1	2	525	A
1	2	531	A
1	2	536	A
1	2	537	C
1	2	540	U
1	2	541	U
1	2	543	C
1	2	545	A
1	2	547	G
1	2	548	C
1	2	549	C
1	2	554	A
1	2	555	A
1	2	556	U
1	2	559	G
1	2	560	A

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Mol	Chain	Res	Type
1	2	563	G
1	2	564	A
1	2	568	C
1	2	570	C
1	2	574	A
1	2	576	A
1	2	579	C
1	2	587	A
1	2	589	G
1	2	590	A
1	2	591	U
1	2	604	A
1	2	605	A
1	2	606	G
1	2	607	U
1	2	608	C
1	2	614	C
1	2	615	C
1	2	626	G
1	2	628	A
1	2	629	A
1	2	630	U
1	2	631	U
1	2	632	C
1	2	639	C
1	2	640	A
1	2	643	A
1	2	644	G
1	2	655	A
1	2	660	C
1	2	666	U
1	2	668	A
1	2	669	A
1	2	671	A
1	2	672	A
1	2	673	G
1	2	688	U
1	2	748	C
1	2	750	C
1	2	752	G
1	2	792	C
1	2	795	A

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Mol	Chain	Res	Type
1	2	796	G
1	2	797	C
1	2	798	G
1	2	799	U
1	2	811	A
1	2	821	G
1	2	822	U
1	2	823	U
1	2	824	C
1	2	830	A
1	2	844	U
1	2	847	A
1	2	852	G
1	2	853	C
1	2	872	A
1	2	874	G
1	2	880	G
1	2	882	U
1	2	883	U
1	2	886	A
1	2	889	U
1	2	890	U
1	2	891	G
1	2	894	G
1	2	895	G
1	2	896	U
1	2	897	U
1	2	898	U
1	2	899	U
1	2	900	C
1	2	901	G
1	2	902	G
1	2	903	A
1	2	904	A
1	2	907	G
1	2	909	G
1	2	913	A
1	2	914	U
1	2	916	A
1	2	919	A
1	2	920	A
1	2	922	A

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Mol	Chain	Res	Type
1	2	933	G
1	2	943	U
1	2	953	C
1	2	954	U
1	2	955	A
1	2	956	G
1	2	961	G
1	2	962	A
1	2	970	G
1	2	971	G
1	2	990	A
1	2	992	A
1	2	999	G
1	2	1001	A
1	2	1002	U
1	2	1009	A
1	2	1016	U
1	2	1017	U
1	2	1023	A
1	2	1026	C
1	2	1045	U
1	2	1049	A
1	2	1050	A
1	2	1055	A
1	2	1058	A
1	2	1061	U
1	2	1062	A
1	2	1067	C
1	2	1080	A
1	2	1083	A
1	2	1085	C
1	2	1089	G
1	2	1100	A
1	2	1115	U
1	2	1116	C
1	2	1119	A
1	2	1121	G
1	2	1126	G
1	2	1130	G
1	2	1133	A
1	2	1153	C
1	2	1154	U

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Mol	Chain	Res	Type
1	2	1157	G
1	2	1170	A
1	2	1171	G
1	2	1195	A
1	2	1207	G
1	2	1208	A
1	2	1215	C
1	2	1221	G
1	2	1224	G
1	2	1226	G
1	2	1227	G
1	2	1228	A
1	2	1229	G
1	2	1231	C
1	2	1232	U
1	2	1235	G
1	2	1236	G
1	2	1237	C
1	2	1239	U
1	2	1241	A
1	2	1242	U
1	2	1243	U
1	2	1244	U
1	2	1246	A
1	2	1248	U
1	2	1249	C
1	2	1250	A
1	2	1251	A
1	2	1253	A
1	2	1256	G
1	2	1257	G
1	2	1259	A
1	2	1262	C
1	2	1263	U
1	2	1264	C
1	2	1266	C
1	2	1267	C
1	2	1269	G
1	2	1270	G
1	2	1272	C
1	2	1274	G
1	2	1275	G

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Mol	Chain	Res	Type
1	2	1276	A
1	2	1277	C
1	2	1280	G
1	2	1281	G
1	2	1282	A
1	2	1284	A
1	2	1285	G
1	2	1286	G
1	2	1287	A
1	2	1288	U
1	2	1289	U
1	2	1290	G
1	2	1291	A
1	2	1292	C
1	2	1293	A
1	2	1295	A
1	2	1297	U
1	2	1300	U
1	2	1301	A
1	2	1302	G
1	2	1303	C
1	2	1304	U
1	2	1306	U
1	2	1308	U
1	2	1309	C
1	2	1310	U
1	2	1311	C
1	2	1312	G
1	2	1313	A
1	2	1315	U
1	2	1317	C
1	2	1318	G
1	2	1319	U
1	2	1320	G
1	2	1321	G
1	2	1322	G
1	2	1323	U
1	2	1324	G
1	2	1325	G
1	2	1327	G
1	2	1330	G
1	2	1331	C

Continued on next page...

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Mol	Chain	Res	Type
1	2	1332	A
1	2	1341	C
1	2	1343	U
1	2	1348	G
1	2	1358	U
1	2	1367	U
1	2	1368	U
1	2	1371	U
1	2	1375	G
1	2	1378	A
1	2	1382	A
1	2	1393	G
1	2	1394	G
1	2	1395	C
1	2	1397	U
1	2	1398	G
1	2	1399	C
1	2	1400	U
1	2	1401	A
1	2	1402	A
1	2	1403	C
1	2	1405	A
1	2	1406	G
1	2	1407	U
1	2	1408	U
1	2	1410	C
1	2	1411	G
1	2	1412	C
1	2	1413	G
1	2	1414	A
1	2	1415	C
1	2	1426	U
1	2	1427	C
1	2	1428	G
1	2	1430	C
1	2	1431	G
1	2	1439	A
1	2	1440	C
1	2	1441	U
1	2	1442	U
1	2	1444	U
1	2	1446	A

Continued on next page...

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Mol	Chain	Res	Type
1	2	1450	G
1	2	1453	C
1	2	1454	A
1	2	1455	A
1	2	1456	G
1	2	1462	U
1	2	1463	U
1	2	1474	A
1	2	1475	G
1	2	1476	A
1	2	1477	U
1	2	1489	A
1	2	1490	G
1	2	1494	U
1	2	1497	G
1	2	1501	C
1	2	1502	C
1	2	1503	C
1	2	1504	U
1	2	1506	A
1	2	1507	G
1	2	1508	A
1	2	1509	U
1	2	1510	G
1	2	1511	U
1	2	1514	G
1	2	1515	G
1	2	1517	G
1	2	1518	C
1	2	1519	U
1	2	1520	G
1	2	1521	C
1	2	1523	C
1	2	1524	G
1	2	1527	C
1	2	1528	G
1	2	1529	C
1	2	1531	A
1	2	1532	C
1	2	1533	A
1	2	1534	C
1	2	1535	U

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Mol	Chain	Res	Type
1	2	1537	A
1	2	1538	C
1	2	1539	U
1	2	1540	G
1	2	1541	G
1	2	1542	C
1	2	1543	U
1	2	1544	C
1	2	1546	G
1	2	1547	C
1	2	1552	G
1	2	1555	U
1	2	1557	C
1	2	1560	U
1	2	1563	G
1	2	1566	G
1	2	1567	G
1	2	1568	C
1	2	1569	A
1	2	1578	U
1	2	1579	A
1	2	1580	A
1	2	1585	U
1	2	1587	G
1	2	1588	A
1	2	1589	A
1	2	1590	C
1	2	1591	C
1	2	1592	C
1	2	1593	C
1	2	1594	A
1	2	1595	U
1	2	1596	U
1	2	1597	C
1	2	1599	U
1	2	1600	G
1	2	1601	A
1	2	1602	U
1	2	1603	G
1	2	1604	G
1	2	1605	G
1	2	1606	G

Continued on next page...

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Mol	Chain	Res	Type
1	2	1607	A
1	2	1609	C
1	2	1610	G
1	2	1612	G
1	2	1613	G
1	2	1614	A
1	2	1615	U
1	2	1616	U
1	2	1617	G
1	2	1622	U
1	2	1623	A
1	2	1624	U
1	2	1625	U
1	2	1626	C
1	2	1627	C
1	2	1628	C
1	2	1629	C
1	2	1631	U
1	2	1632	G
1	2	1633	A
1	2	1634	A
1	2	1635	C
1	2	1636	G
1	2	1639	G
1	2	1640	A
1	2	1641	A
1	2	1643	U
1	2	1644	C
1	2	1648	G
1	2	1649	U
1	2	1650	A
1	2	1652	G
1	2	1663	A
1	2	1665	G
1	2	1666	C
1	2	1671	G
1	2	1672	U
1	2	1673	U
1	2	1674	G
1	2	1676	U
1	2	1677	U
1	2	1678	A

Continued on next page...

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Mol	Chain	Res	Type
1	2	1679	A
1	2	1680	G
1	2	1695	A
1	2	1698	C
1	2	1720	U
1	2	1721	U
1	2	1722	G
1	2	1723	G
1	2	1725	U
1	2	1726	G
1	2	1728	U
1	2	1729	U
1	2	1730	U
1	2	1732	G
1	2	1733	U
1	2	1744	G
1	2	1748	G
1	2	1749	G
1	2	1751	C
1	2	1753	C
1	2	1754	G
1	2	1755	C
1	2	1756	C
1	2	1757	G
1	2	1758	G
1	2	1759	G
1	2	1760	G
1	2	1761	U
1	2	1772	C
1	2	1774	C
1	2	1775	U
1	2	1776	G
1	2	1779	G
1	2	1780	G
1	2	1781	A
1	2	1782	G
1	2	1783	C
1	2	1787	G
1	2	1805	G
1	2	1806	A
1	2	1810	U
1	2	1813	A

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Mol	Chain	Res	Type
1	2	1814	G
1	2	1815	A
1	2	1819	A
1	2	1822	A
1	2	1824	A
1	2	1825	A
1	2	1826	G
1	2	1831	A
1	2	1835	A
1	2	1838	U
1	2	1849	G
1	2	1851	A
1	2	1852	C
1	2	1861	G
1	2	1862	G
1	2	1863	A
1	2	1864	U
1	2	1865	C
1	2	1867	U

All (26) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	60	A
1	2	102	A
1	2	180	G
1	2	332	G
1	2	604	A
1	2	954	U
1	2	1016	U
1	2	1231	C
1	2	1309	C
1	2	1310	U
1	2	1317	C
1	2	1342	U
1	2	1397	U
1	2	1405	A
1	2	1440	C
1	2	1453	C
1	2	1522	A
1	2	1527	C
1	2	1546	G

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Mol	Chain	Res	Type
1	2	1589	A
1	2	1590	C
1	2	1609	C
1	2	1613	G
1	2	1627	C
1	2	1643	U
1	2	1675	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

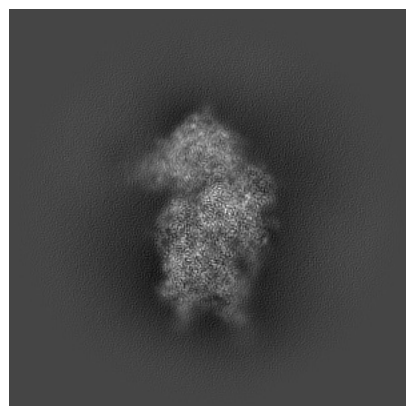
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62450. These allow visual inspection of the internal detail of the map and identification of artifacts.

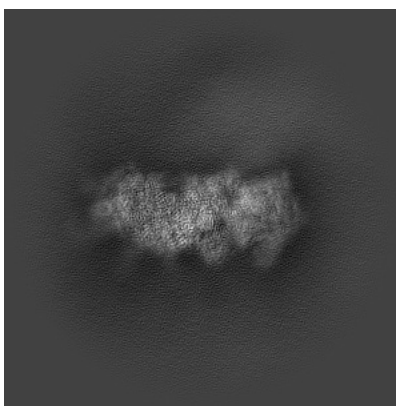
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

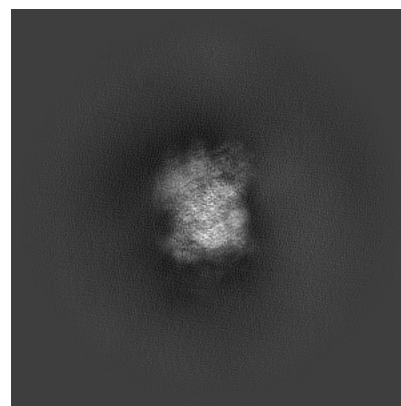
6.1.1 Primary map



X

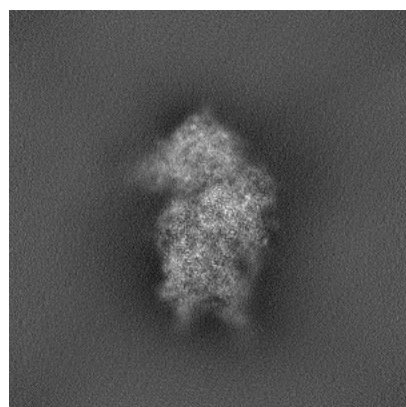


Y

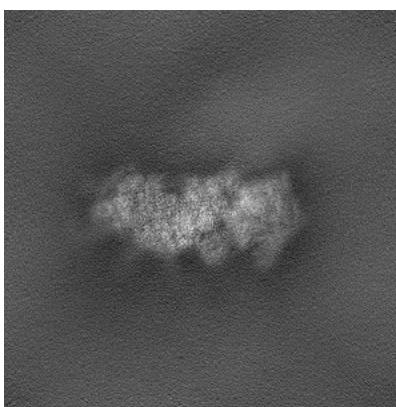


Z

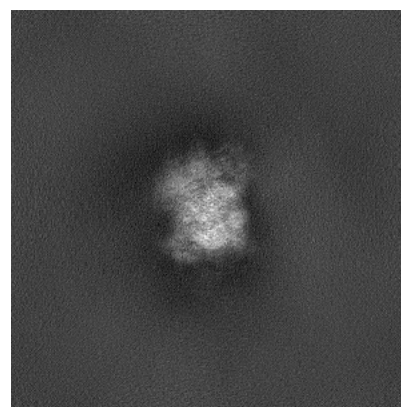
6.1.2 Raw map



X



Y

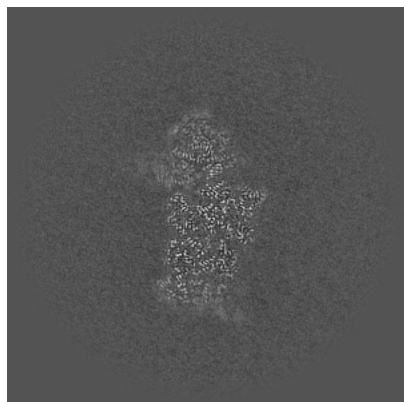


Z

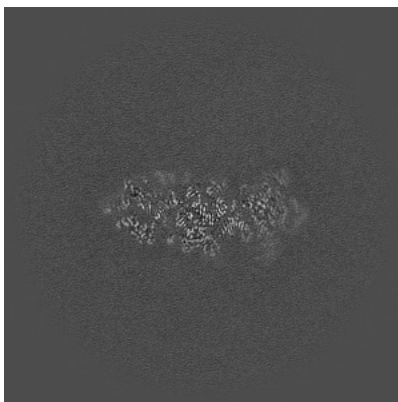
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

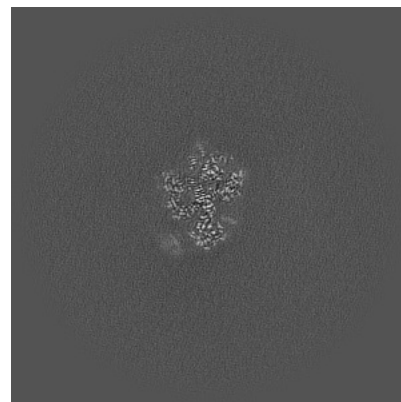
6.2.1 Primary map



X Index: 256

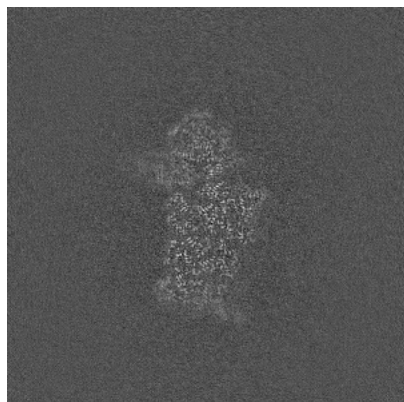


Y Index: 256

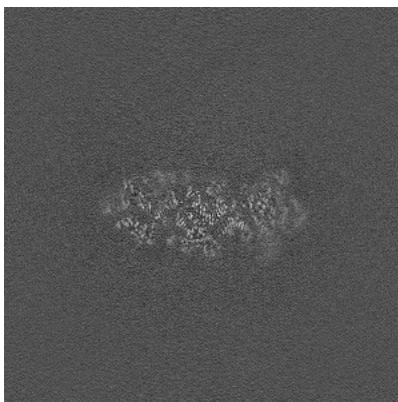


Z Index: 256

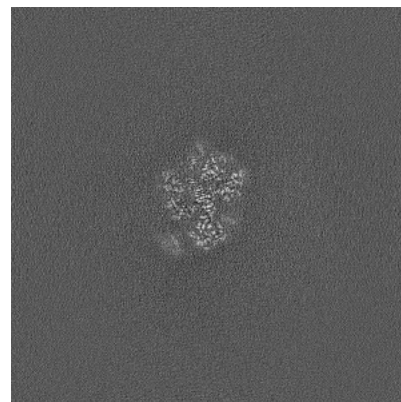
6.2.2 Raw map



X Index: 256



Y Index: 256

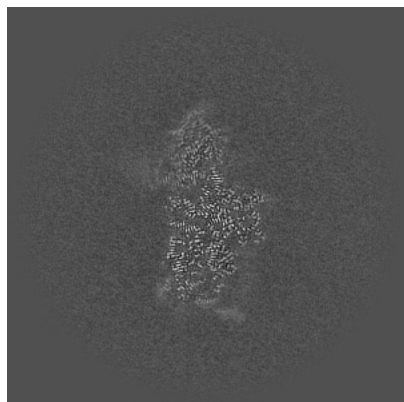


Z Index: 256

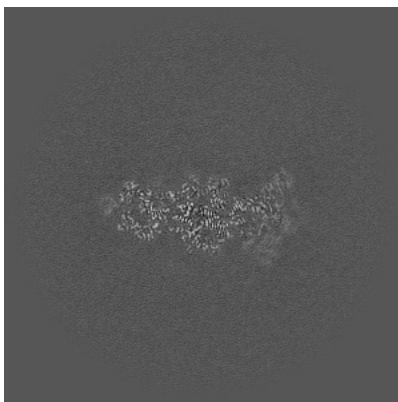
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

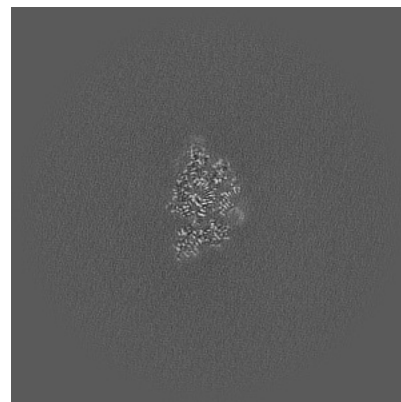
6.3.1 Primary map



X Index: 251

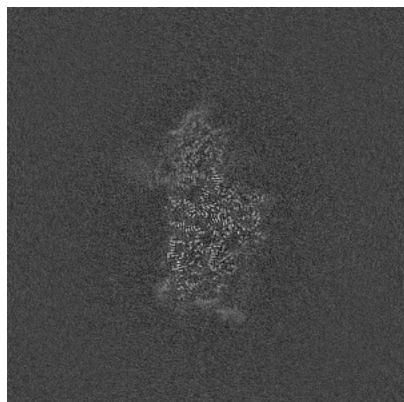


Y Index: 261

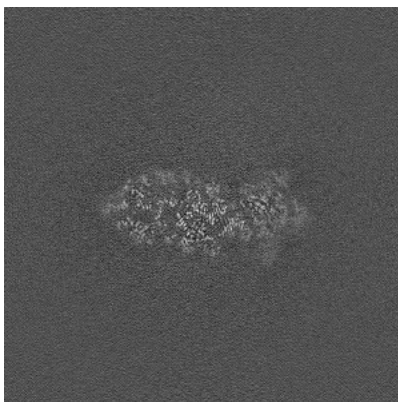


Z Index: 236

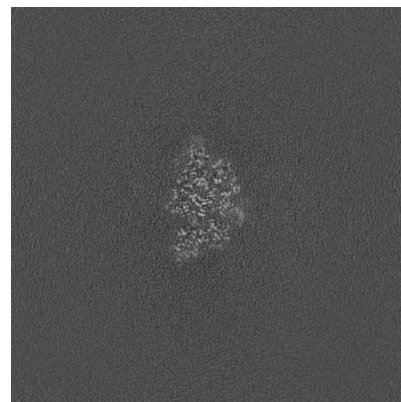
6.3.2 Raw map



X Index: 251



Y Index: 255

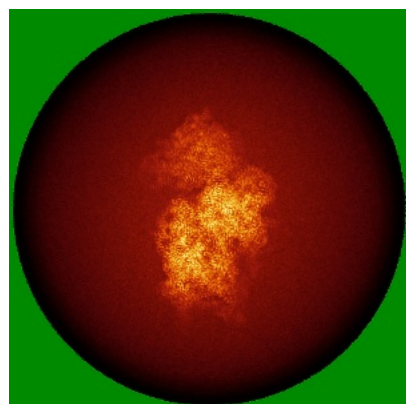


Z Index: 236

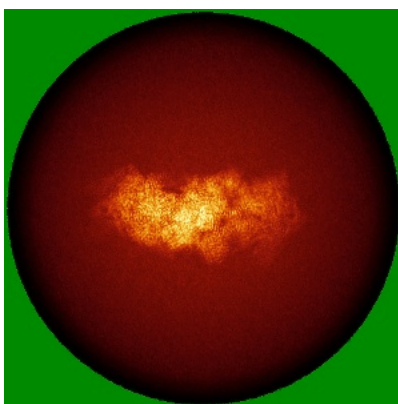
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

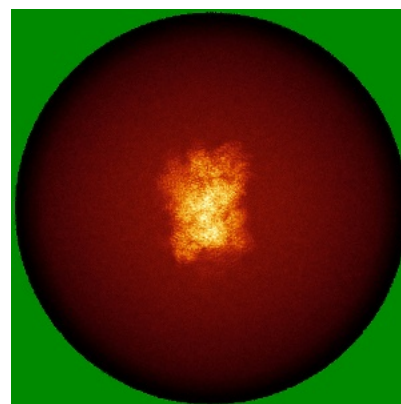
6.4.1 Primary map



X

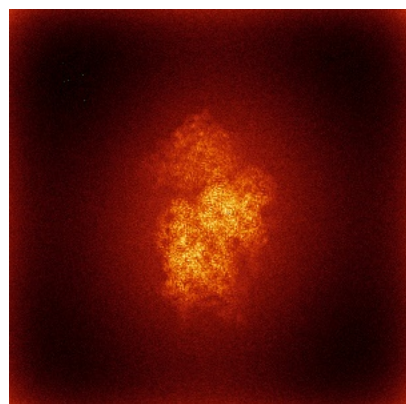


Y

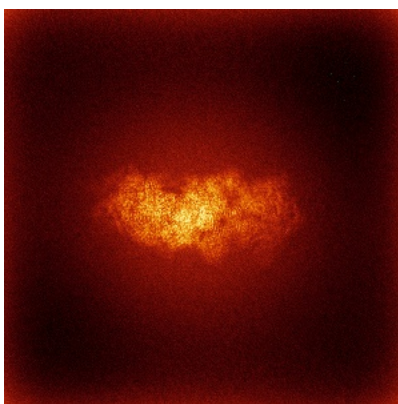


Z

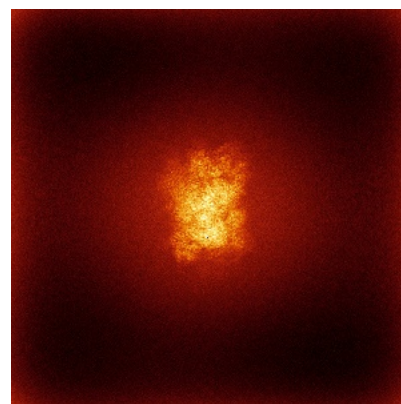
6.4.2 Raw map



X



Y



Z

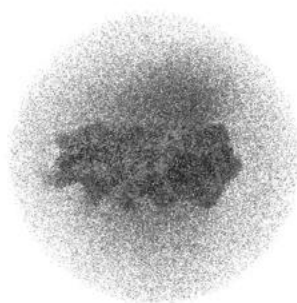
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

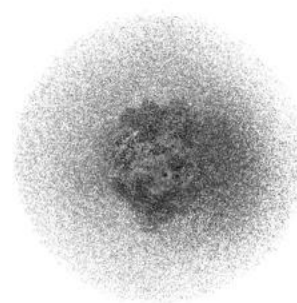
6.5.1 Primary map



X



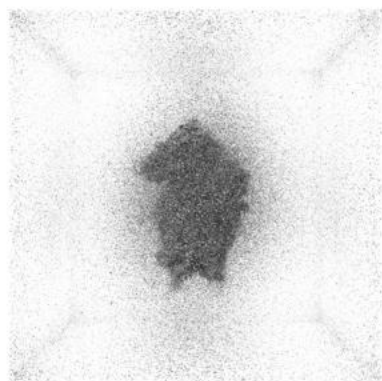
Y



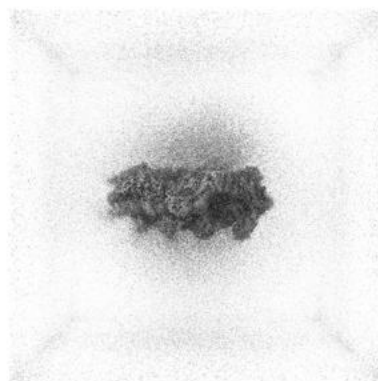
Z

The images above show the 3D surface view of the map at the recommended contour level 0.14. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

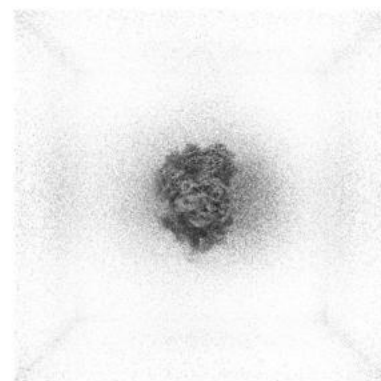
6.5.2 Raw map



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.

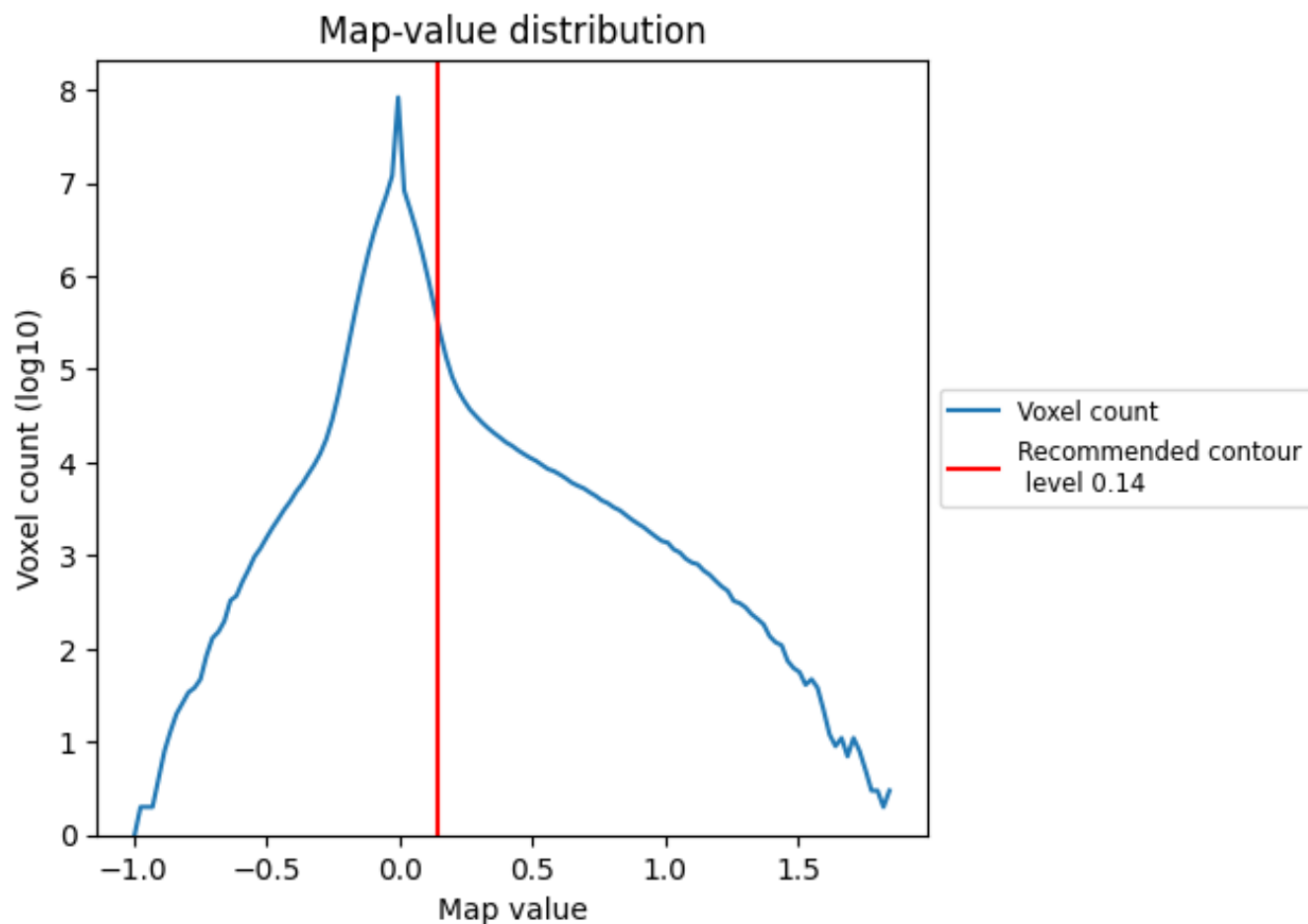
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

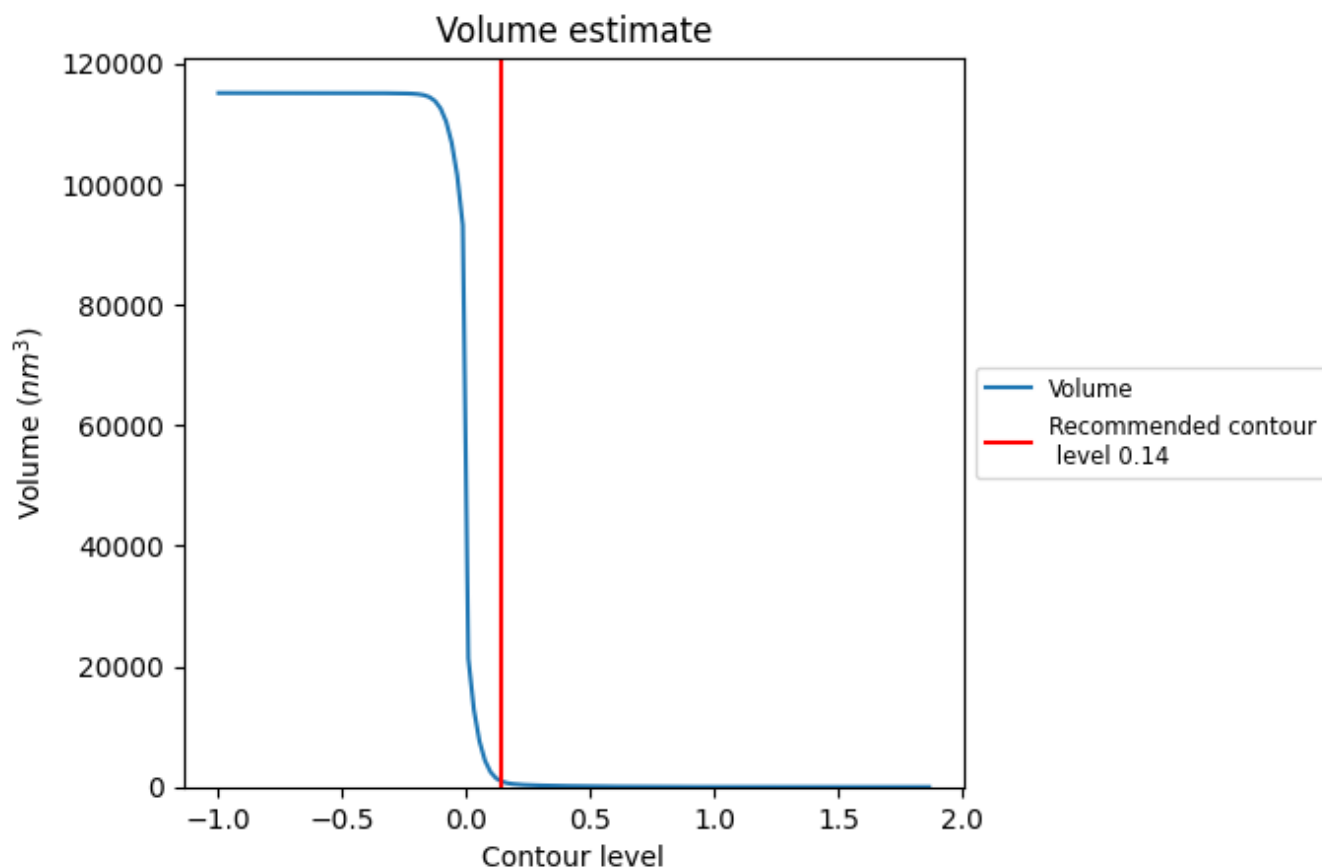
This section contains the results of statistical analysis of the map.

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.

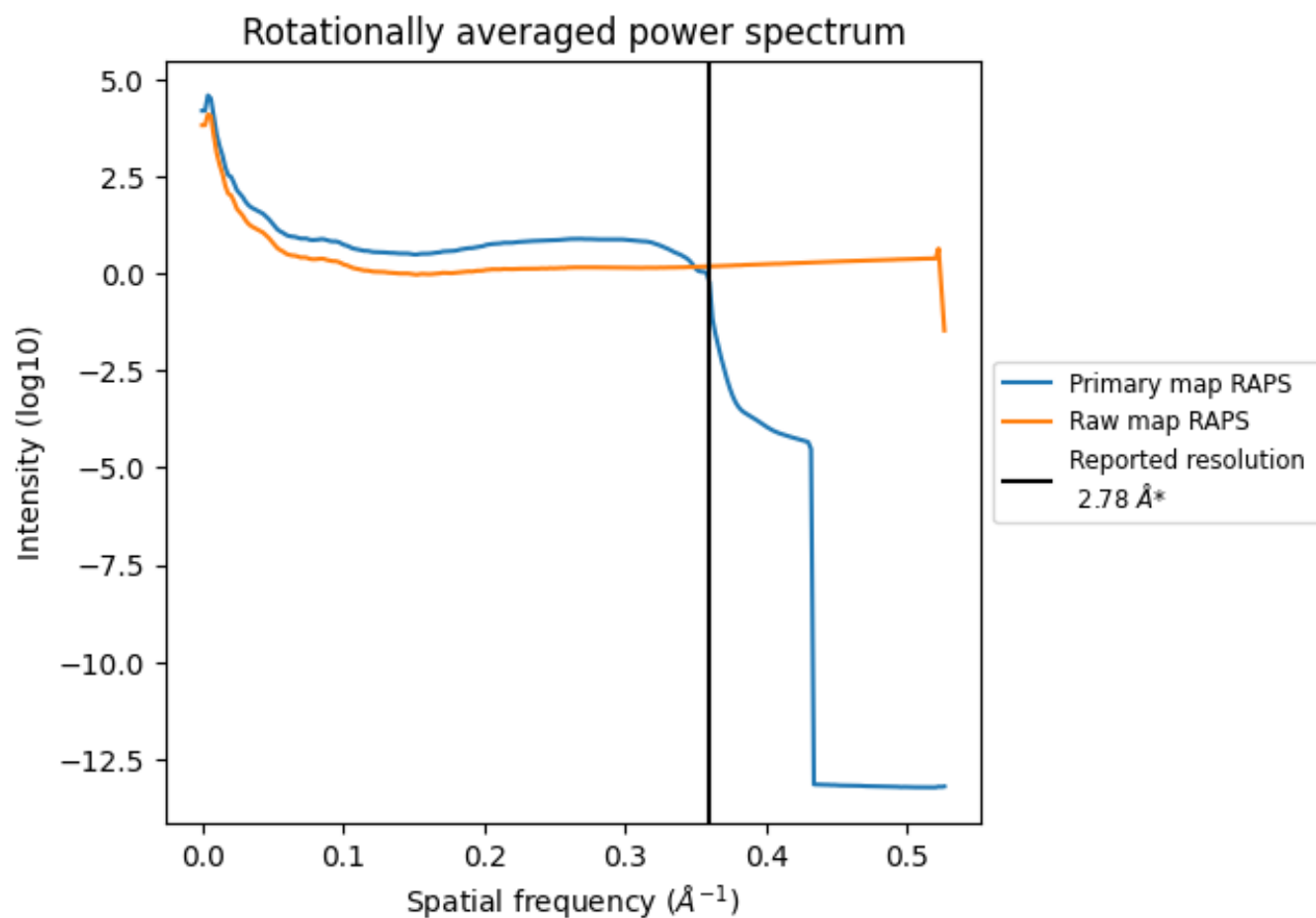
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1008 nm³; this corresponds to an approximate mass of 911 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 ⓘ

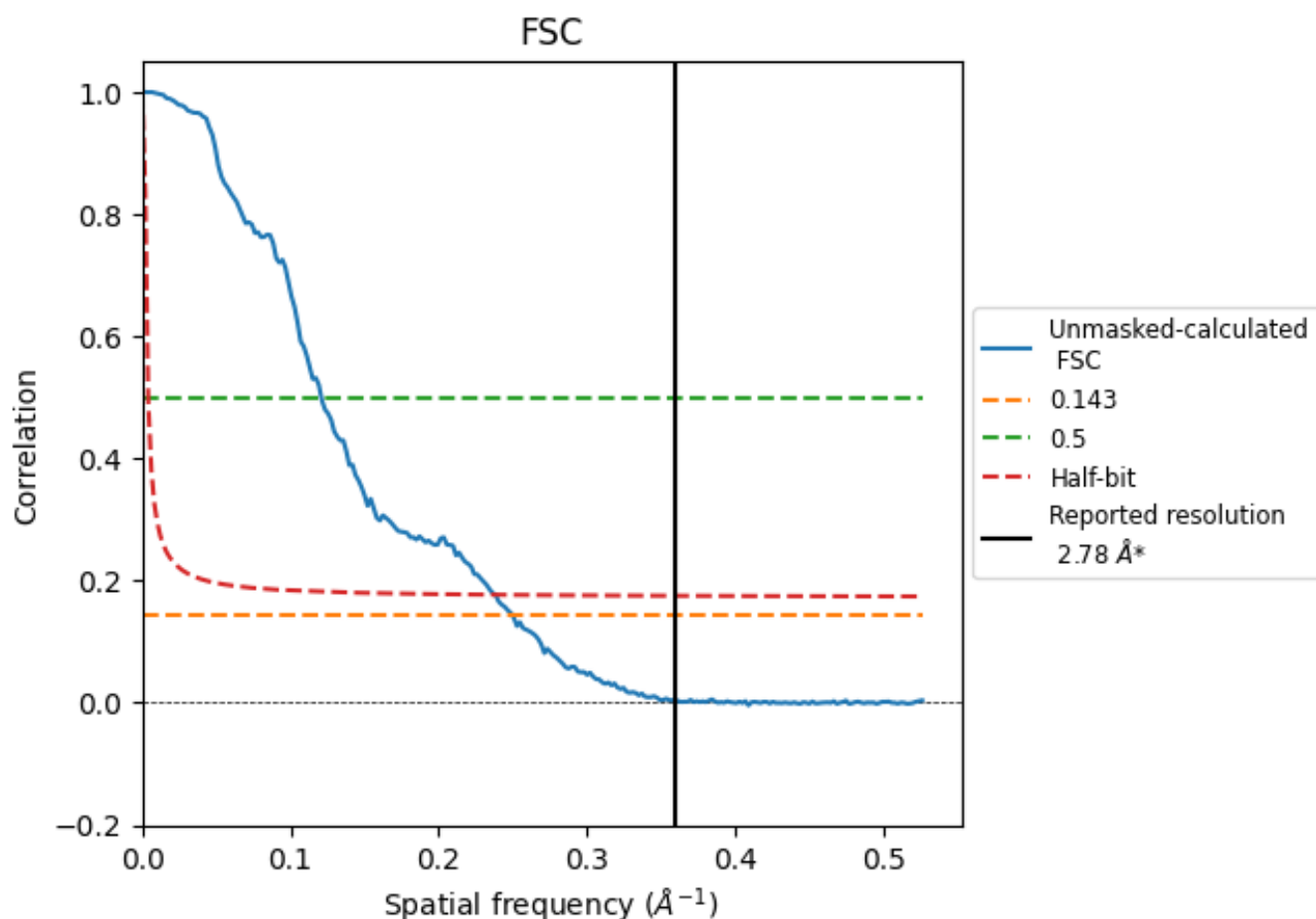


*Reported resolution corresponds to spatial frequency of 0.360 Å⁻¹

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 0.360 Å⁻¹

8.2 Resolution estimates [i](#)

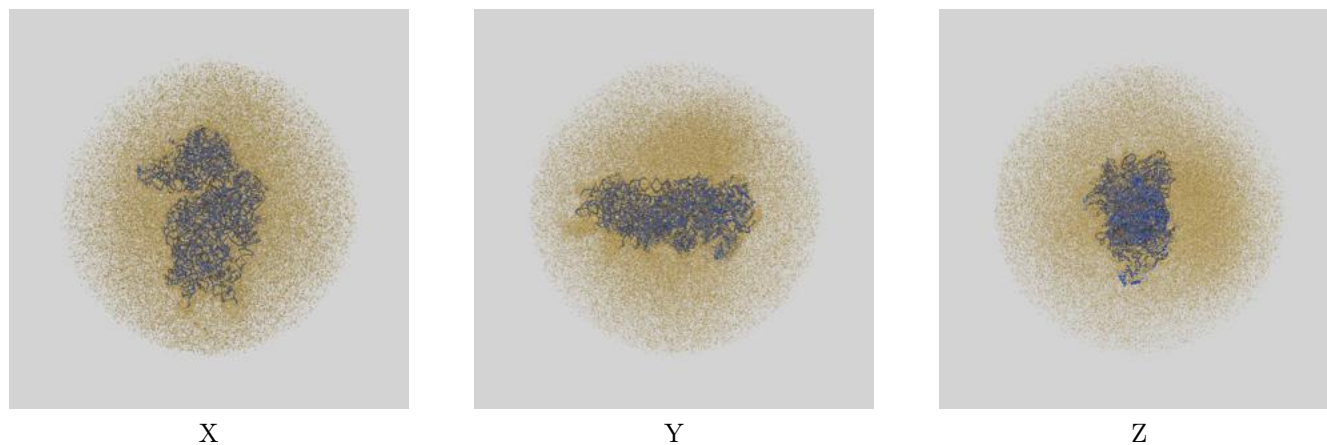
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.78	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.00	8.28	4.20

*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 4.00 differs from the reported value 2.78 by more than 10 %

9 Map-model fit [i](#)

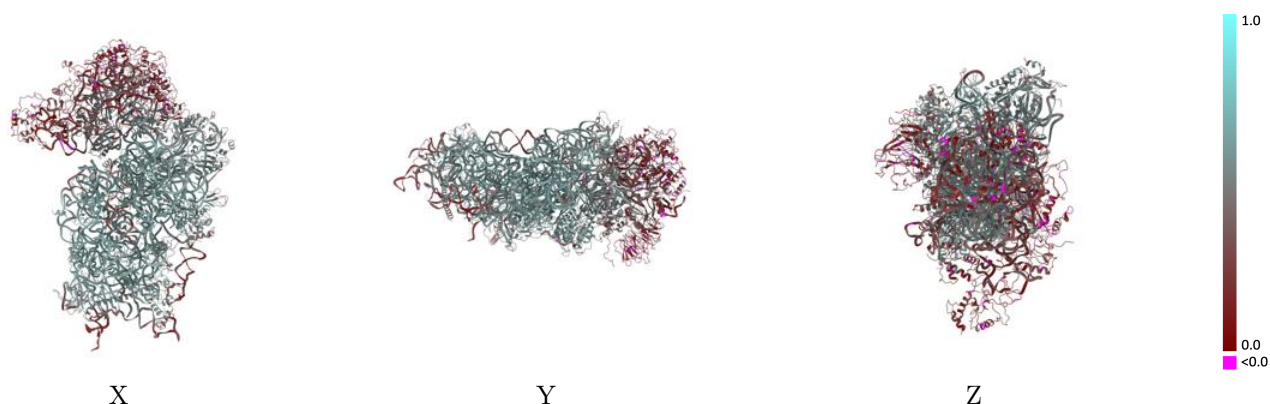
This section contains information regarding the fit between EMDB map EMD-62450 and PDB model 9KMZ. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



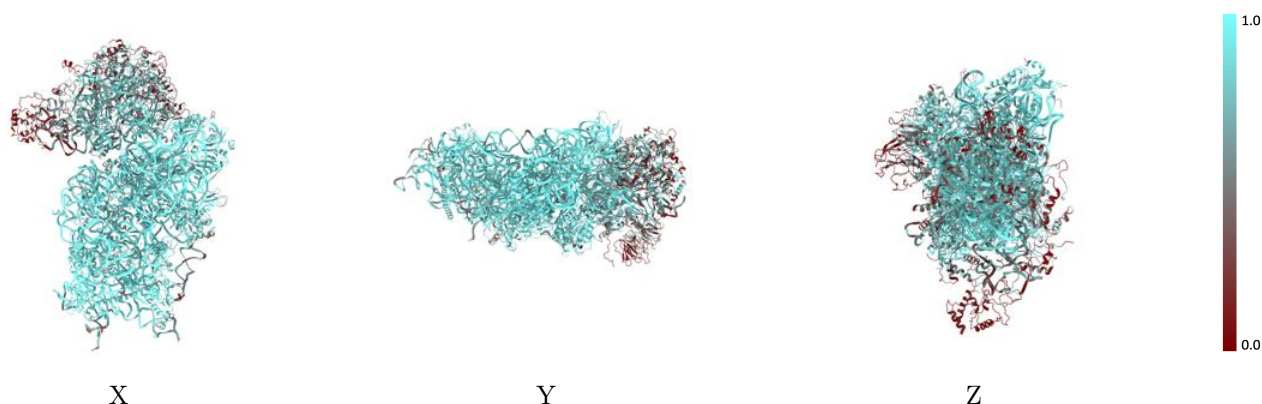
The images above show the 3D surface view of the map at the recommended contour level 0.14 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



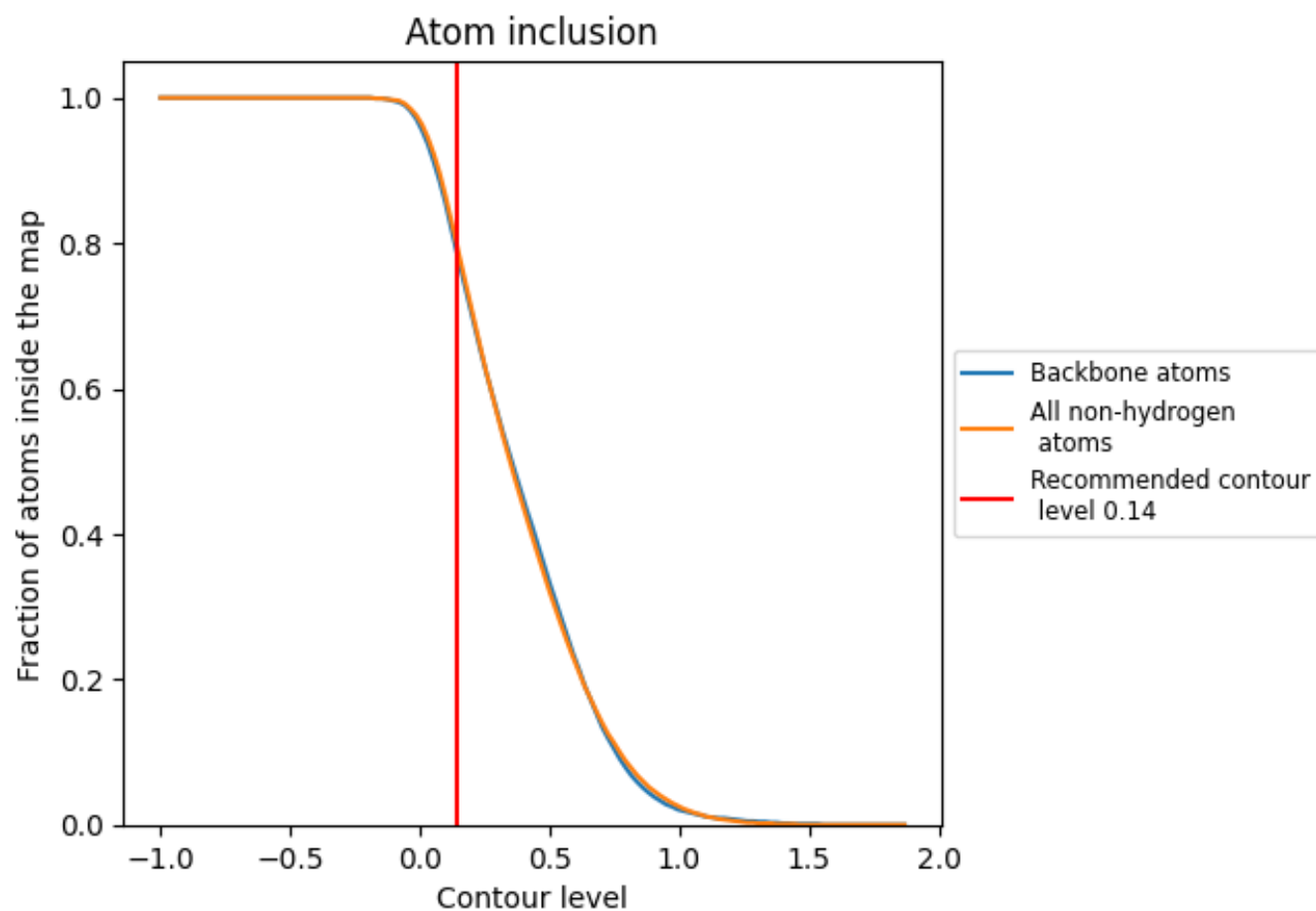
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



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 (0.14).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





The table lists the average atom inclusion at the recommended contour level (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8040	 0.4720
2	 0.8830	 0.4970
A	 0.9320	 0.5750
B	 0.9120	 0.5320
C	 0.9220	 0.5800
D	 0.6250	 0.3900
E	 0.9510	 0.6060
F	 0.4180	 0.2290
G	 0.9070	 0.5340
H	 0.7710	 0.4850
I	 0.8940	 0.5400
J	 0.9380	 0.5860
K	 0.4330	 0.2490
L	 0.9020	 0.5790
M	 0.1690	 0.2200
N	 0.9300	 0.5720
O	 0.8860	 0.5300
P	 0.4000	 0.2530
Q	 0.5870	 0.3020
R	 0.7440	 0.4640
S	 0.4160	 0.1990
T	 0.5650	 0.2300
U	 0.6200	 0.4080
V	 0.9390	 0.5870
W	 0.9670	 0.6130
X	 0.9630	 0.6050
Y	 0.9570	 0.5920
Z	 0.3720	 0.2200
a	 0.9270	 0.5770
b	 0.8700	 0.5350
c	 0.3690	 0.2830
d	 0.7480	 0.4400
e	 0.8410	 0.5410
f	 0.1670	 0.2160
g	 0.3230	 0.2180



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Chain	Atom inclusion	Q-score
h	 0.9120	 0.5590
n	 0.8500	 0.5340