



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 09:29 AM UTC

PDB ID : 8JSG / pdb_00008jsg
EMDB ID : EMD-36619
Title : Structure of the 30S-IF3 complex from Escherichia coli
Authors : Uday, A.B.; Mishra, R.K.; Hussain, T.
Deposited on : 2023-06-20
Resolution : 4.60 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:

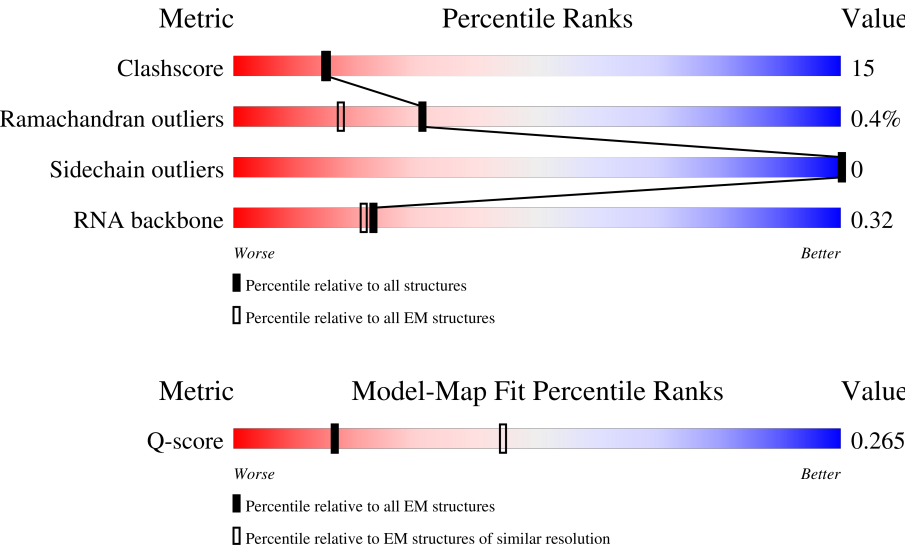
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.60 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	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2407 (4.10 - 5.10)

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	1	73	52% 23% 25%
2	2	53	64% 30% • •
3	3	86	69% 30% •

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Mol	Chain	Length	Quality of chain
4	A	180	 11% 68% 25% 7%
5	P	82	 67% 30%
6	g	1540	 32% 48% 20%
7	k	158	 61% 34% 5%
8	l	205	 70% 30%
9	n	100	 56% 44%
10	p	129	 74% 26%
11	q	128	 60% 31% 9%
12	t	123	 74% 26%
13	u	88	 74% 26%
14	y	82	 76% 24%
15	h	206	 70% 30%
16	m	151	 72% 28%
17	o	129	 60% 38%
18	r	102	 56% 38%
19	s	114	 60% 40%
20	w	100	 53% 43%
21	z	80	 52% 46%
22	j	225	 64% 32%

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 52910 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 protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	1	55	Total	C	N	O	0	0
			456	288	86	82		

- Molecule 2 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	51	Total	C	N	O	S	0	0
			426	265	86	74	1		

- Molecule 3 is a protein called Small ribosomal subunit protein bS20.

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

- Molecule 4 is a protein called Translation initiation factor IF-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	167	Total	C	N	O	S	0	0
			1342	843	241	252	6		

- Molecule 5 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 6 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	1539	Total	C	N	O	P	0	0
			33014	14726	6055	10695	1538		

- Molecule 7 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	k	150	Total	C	N	O	S	0	0
			1106	687	211	202	6		

- Molecule 8 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 9 is a protein called Small ribosomal subunit protein bS6, non-modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	n	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 10 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	q	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	t	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 13 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 14 is a protein called 30S ribosomal protein S16.

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

- Molecule 15 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	h	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 16 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	m	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 17 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 18 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 20 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 21 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	z	79	Total 638	C 408	N 120	O 108	S 2	0	0

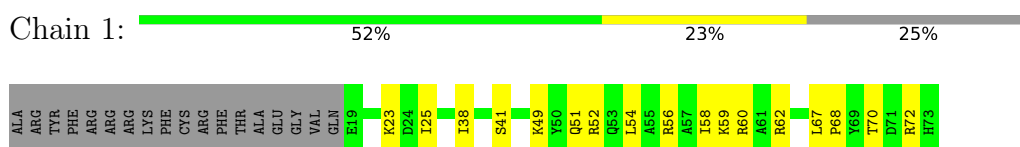
- Molecule 22 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	j	218	Total 1705	C 1081	N 305	O 312	S 7	0	0

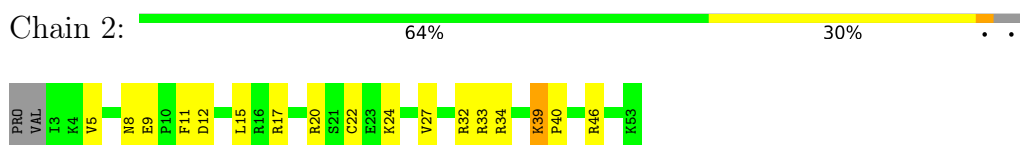
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

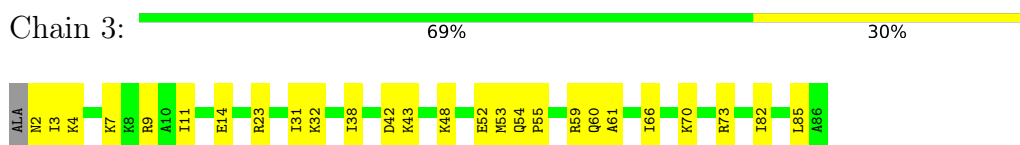
- Molecule 1: Small ribosomal subunit protein bS18



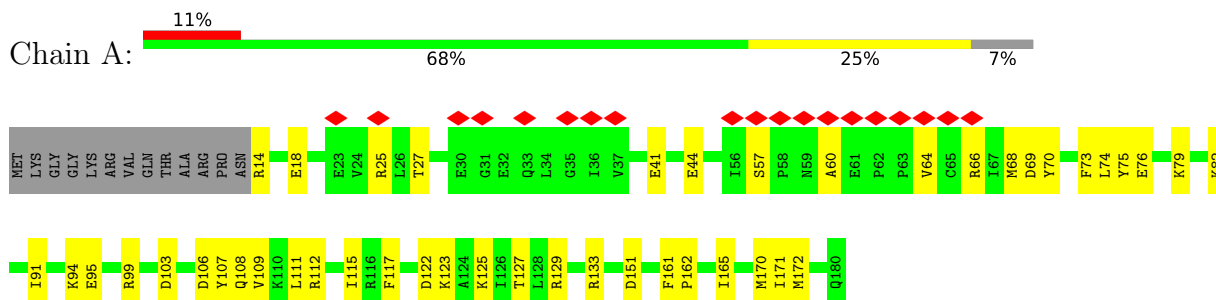
- Molecule 2: Small ribosomal subunit protein bS21



- Molecule 3: Small ribosomal subunit protein bS20

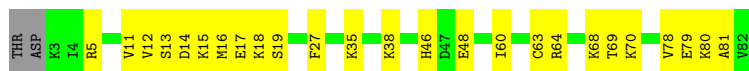


- Molecule 4: Translation initiation factor IF-3



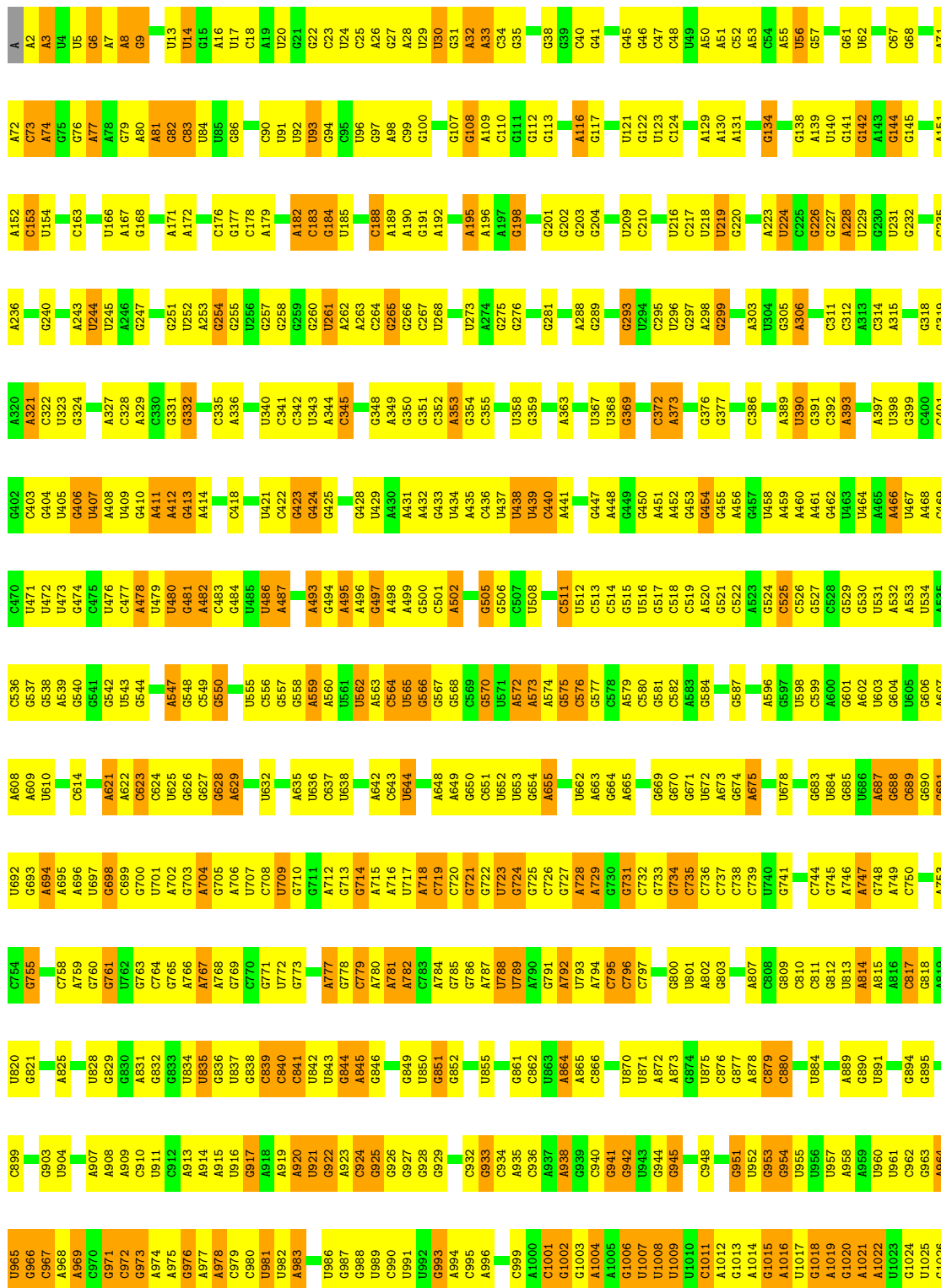
- Molecule 5: Small ribosomal subunit protein uS17



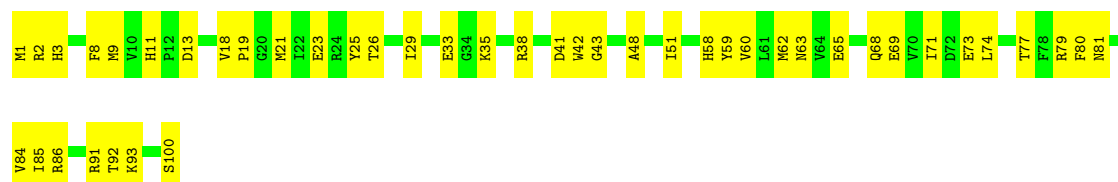


• Molecule 6: 16S ribosomal RNA

Chain g: 32% 48% 20%







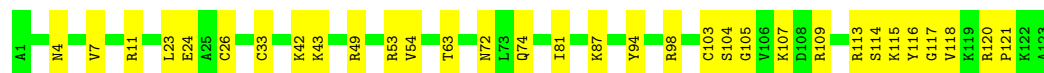
- Molecule 10: Small ribosomal subunit protein uS8



- Molecule 11: Small ribosomal subunit protein uS11



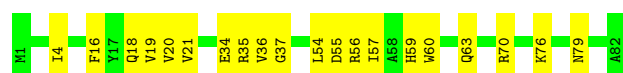
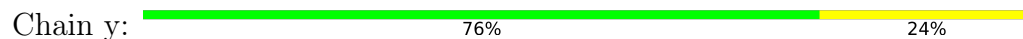
- Molecule 12: Small ribosomal subunit protein uS12



- Molecule 13: Small ribosomal subunit protein uS15

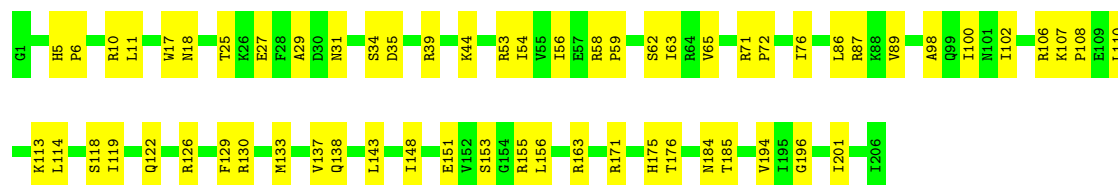


- Molecule 14: 30S ribosomal protein S16



- Molecule 15: Small ribosomal subunit protein uS3





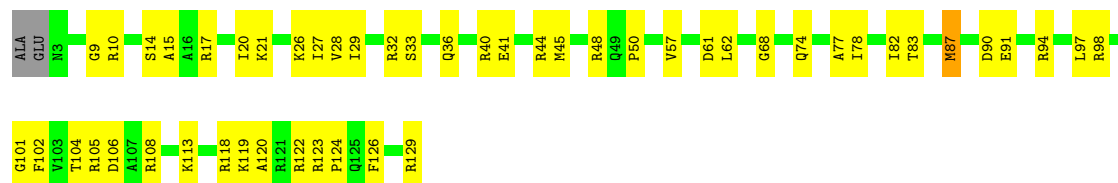
- Molecule 16: Small ribosomal subunit protein uS7

Chain m: 72% 28%



- Molecule 17: Small ribosomal subunit protein uS9

Chain o: 60% 38% ..



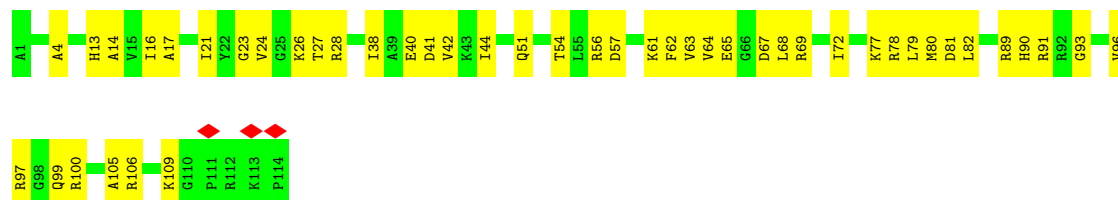
- Molecule 18: Small ribosomal subunit protein uS10

Chain r: 56% 38% . .



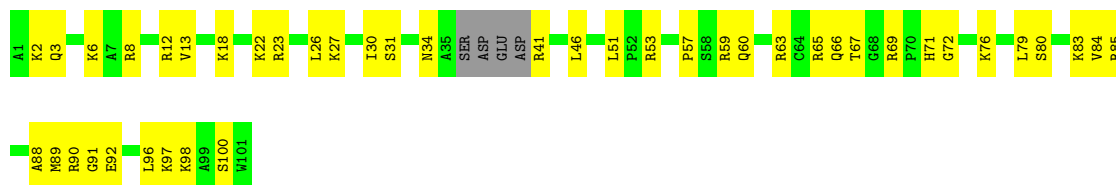
- Molecule 19: Small ribosomal subunit protein uS13

Chain s: 60% 40%



- Molecule 20: Small ribosomal subunit protein uS14

Chain w:  53% 43%



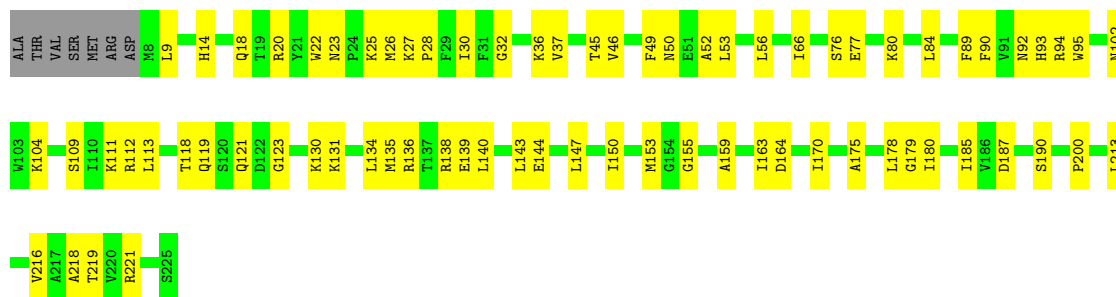
- Molecule 21: Small ribosomal subunit protein uS19

Chain z:  52% 46%



- Molecule 22: Small ribosomal subunit protein uS2

Chain j:  64% 32%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	145664	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	45000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.024	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00126	Depositor
Map size (Å)	384.0, 384.0, 384.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2, 1.2, 1.2	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	1	0.16	0/463	0.39	0/621
2	2	0.15	0/431	0.46	0/570
3	3	0.33	0/671	0.56	0/888
4	A	0.11	0/1356	0.30	0/1807
5	P	0.18	0/658	0.38	0/881
6	g	0.17	0/36966	0.33	0/57667
7	k	0.21	0/1119	0.43	0/1504
8	l	0.17	0/1665	0.34	0/2227
9	n	0.20	0/836	0.58	0/1128
10	p	0.20	0/989	0.38	0/1326
11	q	0.15	0/893	0.43	0/1205
12	t	0.19	0/969	0.40	0/1300
13	u	0.18	0/722	0.39	0/964
14	y	0.19	0/659	0.35	0/884
15	h	0.15	0/1652	0.39	0/2225
16	m	0.17	0/1196	0.41	0/1602
17	o	0.18	0/1034	0.42	1/1375 (0.1%)
18	r	0.14	0/797	0.37	0/1077
19	s	0.13	0/893	0.37	0/1193
20	w	0.11	0/785	0.31	0/1043
21	z	0.11	0/653	0.32	0/877
22	j	0.14	0/1736	0.36	0/2338
All	All	0.17	0/57143	0.35	1/84702 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	o	87	MET	CB-CG-SD	-6.00	94.70	112.70

There are no chirality outliers.

There are no planarity outliers.

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	1	456	0	478	20	0
2	2	426	0	449	20	0
3	3	665	0	714	22	0
4	A	1342	0	1404	32	0
5	P	649	0	691	20	0
6	g	33014	0	16619	806	0
7	k	1106	0	1148	39	0
8	l	1643	0	1710	46	0
9	n	818	0	808	37	0
10	p	979	0	1034	27	0
11	q	877	0	887	40	0
12	t	955	0	1019	27	0
13	u	714	0	737	15	0
14	y	649	0	666	14	0
15	h	1625	0	1699	52	0
16	m	1182	0	1240	39	0
17	o	1022	0	1070	37	0
18	r	787	0	828	28	0
19	s	884	0	944	40	0
20	w	774	0	827	44	0
21	z	638	0	665	39	0
22	j	1705	0	1732	51	0
All	All	52910	0	37369	1314	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 15.

All (1314) 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)
6:g:1055:A:H62	6:g:1200:C:N4	1.57	1.03
6:g:1055:A:N6	6:g:1200:C:H42	1.58	1.00
6:g:448:A:N6	6:g:486:U:H3	1.61	0.99
6:g:1349:A:N6	6:g:1373:G:H21	1.62	0.98
6:g:321:A:H61	6:g:332:G:H1	1.07	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:440:C:H2'	6:g:441:A:H8	1.28	0.96
16:m:107:ALA:O	16:m:118:ARG:NH1	1.99	0.95
6:g:1160:G:H1	6:g:1176:A:N6	1.62	0.95
6:g:582:C:N4	6:g:759:A:H62	1.62	0.95
6:g:582:C:H42	6:g:759:A:N6	1.65	0.94
6:g:1349:A:H62	6:g:1373:G:N2	1.65	0.94
6:g:1351:U:H3	6:g:1371:G:H1	0.99	0.92
6:g:1349:A:H62	6:g:1373:G:H21	1.13	0.91
6:g:1011:C:H2'	6:g:1012:A:H8	1.36	0.90
16:m:112:ASP:HB3	16:m:118:ARG:HD3	1.54	0.89
6:g:1055:A:N6	6:g:1200:C:N4	2.17	0.89
6:g:1099:G:H5''	22:j:94:ARG:HH21	1.39	0.87
1:l:59:LYS:NZ	6:g:735:C:OP1	2.08	0.86
6:g:1440:U:H3	6:g:1461:G:H1	1.21	0.84
6:g:76:G:H1	6:g:93:U:H3	0.87	0.84
3:3:31:ILE:HD13	3:3:53:MET:HE1	1.58	0.84
6:g:139:A:N1	6:g:224:U:C4	2.46	0.83
6:g:321:A:N6	6:g:332:G:H1	1.76	0.83
6:g:1160:G:H1	6:g:1176:A:H61	1.27	0.82
6:g:203:G:O2'	6:g:204:G:N7	2.13	0.82
6:g:991:U:H1'	6:g:993:G:H8	1.45	0.82
6:g:438:U:H3	6:g:496:A:H62	1.26	0.81
8:l:53:GLN:HG2	8:l:198:LEU:HD11	1.61	0.81
6:g:1503:A:C6	6:g:1532:U:N3	2.49	0.81
17:o:87:MET:SD	17:o:94:ARG:HB2	2.22	0.80
9:n:9:MET:HB3	9:n:85:ILE:HB	1.64	0.80
6:g:694:A:H62	6:g:788:U:H4'	1.44	0.80
6:g:424:G:H2'	6:g:425:G:C8	2.18	0.79
15:h:5:HIS:HD2	15:h:6:PRO:HD2	1.48	0.79
6:g:458:U:H3	6:g:474:G:H1	0.85	0.79
6:g:744:C:H2'	6:g:745:G:H8	1.46	0.79
6:g:235:C:H2'	6:g:236:A:H8	1.46	0.79
1:l:60:ARG:NH1	6:g:736:C:OP1	2.15	0.79
6:g:1160:G:N1	6:g:1176:A:N6	2.31	0.78
8:l:131:ILE:HG22	8:l:133:SER:H	1.48	0.78
18:r:57:VAL:HG22	18:r:58:ASN:H	1.48	0.78
3:3:23:ARG:HH21	3:3:60:GLN:HE22	1.32	0.78
6:g:1331:G:H8	19:s:26:LYS:HD2	1.48	0.78
18:r:27:GLU:HA	18:r:30:LYS:HB2	1.66	0.78
22:j:134:LEU:HD11	22:j:138:ARG:HE	1.48	0.78
6:g:1503:A:N6	6:g:1532:U:C2	2.52	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:116:A:N7	6:g:117:G:N2	2.31	0.77
6:g:673:A:H4'	9:n:86:ARG:HH12	1.49	0.77
6:g:56:U:H2'	6:g:57:G:H8	1.49	0.77
3:3:31:ILE:HD13	3:3:53:MET:CE	2.13	0.77
6:g:1242:G:N2	6:g:1302:C:O2	2.17	0.77
6:g:989:U:O2	6:g:1016:A:N6	2.17	0.77
6:g:994:A:N6	6:g:1046:A:O2'	2.17	0.77
6:g:1294:G:O2'	19:s:41:ASP:OD2	2.03	0.76
6:g:363:A:N6	12:t:26:CYS:SG	2.58	0.76
16:m:110:ARG:CB	16:m:118:ARG:HD2	2.15	0.76
6:g:1328:C:H2'	6:g:1329:A:C8	2.21	0.76
9:n:93:LYS:HA	9:n:93:LYS:HE3	1.67	0.76
22:j:23:ASN:ND2	22:j:190:SER:O	2.19	0.75
6:g:452:A:H1'	14:y:70:ARG:HH22	1.52	0.75
16:m:112:ASP:CB	16:m:118:ARG:HD3	2.18	0.74
6:g:1279:G:H4'	18:r:9:ARG:HH12	1.52	0.74
6:g:983:A:H8	6:g:1049:U:H3	1.36	0.74
6:g:691:G:N1	6:g:696:A:N7	2.35	0.74
20:w:18:LYS:O	20:w:22:LYS:NZ	2.21	0.74
6:g:448:A:N7	6:g:486:U:O4	2.21	0.73
6:g:738:C:OP2	9:n:91:ARG:NH1	2.21	0.73
6:g:1220:G:N2	21:z:53:GLY:O	2.21	0.73
6:g:991:U:H1'	6:g:993:G:C8	2.24	0.73
6:g:825:A:O2'	10:p:12:ARG:NH2	2.22	0.73
9:n:2:ARG:HD2	9:n:68:GLN:HE21	1.53	0.73
6:g:673:A:H2'	6:g:674:G:C8	2.23	0.72
6:g:1056:U:O2'	15:h:155:ARG:NH1	2.20	0.72
6:g:1407:C:H2'	6:g:1408:A:H8	1.54	0.72
6:g:1266:G:N2	6:g:1269:A:OP2	2.22	0.72
9:n:77:THR:HA	9:n:80:PHE:CE1	2.23	0.72
6:g:139:A:N1	6:g:224:U:O4	2.22	0.72
5:P:63:CYS:SG	5:P:64:ARG:N	2.62	0.72
6:g:973:G:H5''	6:g:974:A:H2'	1.72	0.72
6:g:1009:U:O4	6:g:1020:G:O6	2.08	0.72
6:g:243:A:H4'	6:g:244:U:H5'	1.72	0.72
6:g:447:G:H21	6:g:487:A:H62	1.36	0.72
6:g:1011:C:H2'	6:g:1012:A:C8	2.22	0.71
6:g:1060:U:H2'	6:g:1061:G:H8	1.54	0.71
6:g:1425:U:H3	6:g:1475:G:H1	1.36	0.71
3:3:2:ASN:ND2	6:g:332:G:OP2	2.24	0.70
3:3:82:ILE:HD12	3:3:85:LEU:HD21	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:m:37:THR:O	16:m:41:ILE:HG13	1.92	0.70
6:g:1251:A:H3'	6:g:1252:A:H8	1.57	0.70
6:g:1423:G:H1	6:g:1477:U:H3	1.40	0.70
17:o:33:SER:H	17:o:36:GLN:HE22	1.40	0.70
14:y:54:LEU:HD23	14:y:57:ILE:HD11	1.72	0.70
12:t:42:LYS:HG2	12:t:43:LYS:H	1.57	0.70
6:g:9:G:H5'	7:k:107:GLY:HA3	1.73	0.70
6:g:966:G:H21	6:g:967:C:H41	1.40	0.69
6:g:1328:C:H5'	19:s:28:ARG:HA	1.74	0.69
14:y:76:LYS:O	14:y:79:ASN:ND2	2.24	0.69
22:j:131:LYS:HG2	22:j:135:MET:HE2	1.73	0.69
18:r:65:TYR:HB3	20:w:96:LEU:HD11	1.73	0.69
6:g:948:C:OP1	19:s:97:ARG:NH2	2.26	0.69
21:z:57:VAL:HG11	21:z:75:PRO:HD2	1.73	0.69
6:g:920:A:O2'	6:g:921:U:O5'	2.10	0.69
6:g:1318:A:N1	6:g:1320:C:N4	2.40	0.69
1:1:41:SER:HB3	1:1:51:GLN:HG3	1.75	0.68
10:p:5:PRO:HB2	10:p:32:LYS:HZ3	1.57	0.68
6:g:1147:C:O2	17:o:17:ARG:NH1	2.27	0.68
6:g:1269:A:H1'	6:g:1312:G:H21	1.58	0.68
6:g:1126:U:O4	18:r:9:ARG:NH1	2.26	0.68
6:g:1274:A:O2'	6:g:1275:A:OP2	2.11	0.68
6:g:674:G:H2'	6:g:675:A:H8	1.57	0.68
6:g:448:A:H62	6:g:486:U:H3	0.78	0.68
6:g:1238:A:N7	6:g:1301:U:O2	2.26	0.68
7:k:156:ARG:NH1	10:p:42:GLU:OE2	2.27	0.68
16:m:110:ARG:HB2	16:m:118:ARG:HD2	1.74	0.68
22:j:134:LEU:HD21	22:j:138:ARG:HH21	1.59	0.68
15:h:113:LYS:HA	15:h:184:ASN:HD22	1.58	0.68
6:g:582:C:N4	6:g:759:A:N6	2.30	0.67
6:g:936:C:O2'	6:g:1382:C:N4	2.22	0.67
6:g:403:C:H2'	6:g:404:G:H8	1.60	0.67
17:o:44:ARG:O	17:o:48:ARG:NH2	2.27	0.67
19:s:99:GLN:CD	19:s:100:ARG:H	2.03	0.67
6:g:76:G:N2	6:g:93:U:O2	2.27	0.67
6:g:82:G:H2'	6:g:83:C:H4'	1.77	0.67
6:g:791:G:N2	6:g:792:A:N7	2.42	0.67
6:g:7:A:N6	7:k:96:GLN:OE1	2.28	0.67
6:g:522:C:H41	12:t:49:ARG:HH22	1.43	0.67
6:g:786:G:H2'	6:g:787:A:H8	1.58	0.67
6:g:1277:C:O2'	6:g:1279:G:N7	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:996:A:N1	6:g:1045:C:O2'	2.28	0.66
6:g:1263:C:N3	6:g:1273:C:N4	2.43	0.66
8:l:108:ALA:N	8:l:112:GLU:OE2	2.27	0.66
4:A:106:ASP:HA	4:A:109:VAL:HG22	1.76	0.66
6:g:766:A:N6	6:g:767:A:N1	2.43	0.66
6:g:1095:U:OP1	6:g:1108:G:N2	2.25	0.66
22:j:134:LEU:HD11	22:j:138:ARG:NE	2.11	0.66
6:g:512:U:H1'	8:l:39:GLN:HE22	1.61	0.66
6:g:699:C:H2'	6:g:700:G:H8	1.60	0.66
6:g:745:G:H2'	6:g:746:A:H8	1.61	0.66
6:g:1034:G:H2'	6:g:1035:A:H4'	1.78	0.66
6:g:1052:U:O2	6:g:1206:G:O6	2.13	0.66
6:g:1479:C:H2'	6:g:1480:A:H8	1.60	0.66
22:j:119:GLN:OE1	22:j:136:ARG:NH1	2.29	0.66
19:s:79:LEU:HD21	19:s:90:HIS:HB3	1.76	0.66
2:2:32:ARG:HH21	11:q:124:LYS:HA	1.61	0.65
13:u:32:THR:HG22	13:u:62:ARG:HH11	1.61	0.65
16:m:46:LEU:HD13	16:m:49:LEU:HD21	1.77	0.65
6:g:584:G:N2	6:g:880:C:OP1	2.29	0.65
5:P:18:LYS:HZ2	5:P:48:GLU:HA	1.62	0.65
8:l:81:LEU:HD23	8:l:88:ASN:HD21	1.60	0.65
6:g:139:A:C6	6:g:224:U:O4	2.49	0.65
6:g:993:G:H21	6:g:995:C:H42	1.43	0.65
6:g:728:A:H2'	6:g:729:A:C8	2.31	0.65
15:h:87:ARG:NH1	15:h:98:ALA:O	2.28	0.65
6:g:1414:U:H2'	6:g:1415:G:H8	1.62	0.65
3:3:32:LYS:NZ	6:g:1439:G:OP1	2.29	0.65
14:y:18:GLN:OE1	14:y:35:ARG:NE	2.28	0.65
2:2:22:CYS:HG	6:g:1536:C:HO2'	1.44	0.65
6:g:451:A:N7	6:g:481:G:N1	2.45	0.65
21:z:31:ARG:HA	21:z:49:ALA:HB3	1.78	0.65
6:g:1071:C:H2'	6:g:1072:G:H8	1.60	0.65
6:g:1127:G:O2'	6:g:1280:A:N6	2.28	0.65
8:l:161:ALA:HA	8:l:164:ARG:HH21	1.62	0.65
18:r:7:ARG:HD2	18:r:75:ASP:HA	1.79	0.65
6:g:1206:G:H2'	6:g:1207:G:C8	2.32	0.64
6:g:1239:A:N3	6:g:1297:G:N2	2.45	0.64
6:g:1223:C:O2'	6:g:1225:A:N6	2.30	0.64
12:t:53:ARG:HG2	12:t:63:THR:HG22	1.79	0.64
6:g:218:U:H2'	6:g:219:U:C6	2.32	0.64
6:g:745:G:H2'	6:g:746:A:C8	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:1241:G:H2'	6:g:1242:G:H8	1.63	0.64
11:q:21:HIS:HA	11:q:84:MET:HB2	1.80	0.64
15:h:18:ASN:ND2	20:w:90:ARG:O	2.31	0.64
6:g:945:G:O6	6:g:1236:A:N1	2.31	0.64
6:g:1430:A:H2'	6:g:1431:A:H8	1.63	0.64
7:k:81:GLN:H	7:k:146:MET:HE1	1.63	0.64
8:l:10:LEU:HD13	8:l:62:ARG:HG2	1.80	0.64
6:g:952:U:O2'	6:g:953:G:OP1	2.15	0.63
6:g:1317:C:OP2	20:w:27:LYS:NZ	2.27	0.63
7:k:80:LEU:HD11	7:k:146:MET:SD	2.39	0.63
9:n:85:ILE:HG22	9:n:86:ARG:H	1.63	0.63
6:g:1179:A:OP1	17:o:98:ARG:NH1	2.32	0.63
6:g:1254:A:O2'	6:g:1356:G:OP1	2.16	0.63
19:s:23:GLY:HA2	19:s:68:LEU:HD22	1.80	0.63
19:s:64:VAL:HG23	19:s:65:GLU:HG2	1.80	0.63
18:r:5:ARG:N	18:r:76:ILE:O	2.31	0.63
6:g:406:G:O2'	8:l:115:GLN:NE2	2.31	0.63
1:l:59:LYS:NZ	6:g:734:G:O2'	2.31	0.63
6:g:952:U:H2'	6:g:953:G:H8	1.64	0.63
6:g:942:G:N2	6:g:1341:U:O2	2.31	0.63
6:g:253:A:H2'	6:g:254:G:H8	1.62	0.63
16:m:129:ASN:HA	16:m:134:VAL:HG11	1.79	0.62
6:g:689:C:OP2	11:q:28:ASN:ND2	2.32	0.62
6:g:687:A:N3	6:g:705:G:N2	2.48	0.62
7:k:89:THR:OG1	7:k:90:GLY:N	2.24	0.62
6:g:951:G:H2'	6:g:952:U:C6	2.35	0.62
6:g:27:G:N3	6:g:557:G:N2	2.47	0.62
6:g:674:G:H2'	6:g:675:A:C8	2.35	0.62
6:g:1351:U:O4	6:g:1371:G:O6	2.18	0.62
6:g:141:G:H2'	6:g:142:G:C8	2.35	0.62
6:g:675:A:H1'	11:q:117:HIS:HD2	1.65	0.62
6:g:836:G:O2'	6:g:837:U:O4'	2.17	0.62
6:g:1343:G:H4'	17:o:123:ARG:HG2	1.80	0.62
6:g:440:C:H2'	6:g:441:A:C8	2.21	0.62
6:g:458:U:O4	6:g:474:G:O6	2.18	0.62
9:n:38:ARG:NH1	9:n:62:MET:O	2.33	0.62
6:g:746:A:C6	6:g:747:A:N6	2.68	0.61
15:h:35:ASP:OD1	15:h:58:ARG:NH2	2.31	0.61
22:j:163:ILE:HD12	22:j:185:ILE:HD11	1.83	0.61
6:g:684:U:O2'	11:q:40:ALA:O	2.14	0.61
15:h:59:PRO:HG2	15:h:62:SER:HB2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:458:U:O2	6:g:474:G:N2	2.29	0.61
6:g:573:A:N6	6:g:574:A:N1	2.47	0.61
8:l:115:GLN:OE1	8:l:119:HIS:NE2	2.33	0.61
6:g:1330:U:O2	6:g:1331:G:N1	2.34	0.61
7:k:91:SER:OG	7:k:129:SER:O	2.17	0.61
9:n:33:GLU:O	9:n:35:LYS:NZ	2.32	0.61
6:g:502:A:OP1	12:t:114:SER:N	2.31	0.61
6:g:562:U:H4'	6:g:563:A:H5'	1.80	0.61
6:g:988:G:H21	6:g:1015:G:H21	1.46	0.61
16:m:110:ARG:HB3	16:m:118:ARG:HD2	1.80	0.61
6:g:978:A:OP1	6:g:981:U:N3	2.33	0.61
16:m:118:ARG:HH11	16:m:118:ARG:HG2	1.64	0.61
6:g:53:A:OP2	6:g:353:A:N6	2.32	0.61
6:g:235:C:H2'	6:g:236:A:C8	2.34	0.61
14:y:4:ILE:HG12	14:y:21:VAL:HG12	1.83	0.61
4:A:103:ASP:OD2	6:g:1494:G:N2	2.29	0.61
6:g:496:A:O2'	6:g:497:G:H5'	2.01	0.61
6:g:894:G:H2'	6:g:895:G:H8	1.65	0.61
6:g:1134:G:H3'	6:g:1135:U:H5''	1.82	0.61
6:g:539:A:H2'	6:g:540:G:C8	2.36	0.60
6:g:1510:C:H2'	6:g:1511:G:C8	2.36	0.60
10:p:79:ARG:HG3	10:p:81:GLY:H	1.66	0.60
20:w:89:MET:HE2	20:w:89:MET:HA	1.83	0.60
6:g:1293:C:N4	6:g:1294:G:O6	2.34	0.60
5:P:14:ASP:OD1	5:P:15:LYS:N	2.34	0.60
6:g:7:A:N3	6:g:298:A:N6	2.49	0.60
15:h:107:LYS:HB3	15:h:110:LEU:HD13	1.83	0.60
3:3:73:ARG:NH1	6:g:263:A:OP1	2.34	0.60
6:g:981:U:H4'	20:w:63:ARG:HH21	1.66	0.60
6:g:1097:C:H2'	6:g:1098:C:C6	2.36	0.60
16:m:67:ASN:O	16:m:137:ARG:NH1	2.35	0.60
6:g:1269:A:H2'	6:g:1313:U:H1'	1.82	0.60
16:m:63:VAL:O	16:m:67:ASN:ND2	2.31	0.60
22:j:76:SER:O	22:j:80:LYS:HG3	2.02	0.60
6:g:408:A:OP1	8:l:109:THR:OG1	2.13	0.60
6:g:1312:G:OP1	21:z:6:LYS:NZ	2.35	0.60
6:g:1350:A:OP1	17:o:122:ARG:NH1	2.34	0.60
8:l:113:ALA:O	8:l:117:VAL:HG23	2.02	0.60
9:n:77:THR:HA	9:n:80:PHE:HE1	1.63	0.60
6:g:940:C:N4	6:g:941:G:O6	2.34	0.60
6:g:1075:U:H2'	6:g:1076:U:C6	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:j:66:ILE:HG23	22:j:159:ALA:HB3	1.83	0.60
6:g:1472:U:H2'	6:g:1473:G:C8	2.36	0.60
11:q:33:ILE:HG13	11:q:41:LEU:HD21	1.83	0.60
6:g:952:U:H2'	6:g:953:G:C8	2.37	0.59
22:j:18:GLN:HE21	22:j:37:VAL:HG23	1.66	0.59
6:g:1397:C:OP2	7:k:28:ARG:NH2	2.35	0.59
6:g:477:C:H2'	6:g:478:A:C5	2.38	0.59
6:g:544:G:OP1	8:l:58:GLN:NE2	2.35	0.59
6:g:699:C:H2'	6:g:700:G:C8	2.37	0.59
6:g:1057:G:H4'	15:h:196:GLY:HA3	1.83	0.59
20:w:67:THR:H	20:w:83:LYS:HZ3	1.51	0.59
6:g:714:G:H2'	6:g:715:A:C8	2.37	0.59
6:g:714:G:H2'	6:g:715:A:H8	1.67	0.59
6:g:942:G:N1	6:g:1341:U:N3	2.41	0.59
6:g:1440:U:O4	6:g:1461:G:O6	2.21	0.59
20:w:46:LEU:HD22	21:z:9:PHE:HD1	1.67	0.59
6:g:766:A:O2'	6:g:767:A:OP1	2.21	0.59
6:g:348:G:H2'	6:g:349:A:H8	1.67	0.59
6:g:720:C:H3'	6:g:721:G:H5''	1.84	0.59
6:g:782:A:H62	6:g:800:G:H21	1.50	0.59
4:A:27:THR:HB	4:A:66:ARG:HA	1.84	0.59
6:g:875:U:O2	10:p:15:ASN:ND2	2.36	0.59
6:g:1328:C:H5''	19:s:27:THR:HG22	1.84	0.59
7:k:44:ARG:NH1	7:k:70:MET:SD	2.74	0.59
1:1:54:LEU:O	1:1:58:ILE:HG23	2.03	0.59
6:g:1503:A:C6	6:g:1532:U:C2	2.91	0.59
6:g:635:A:H2'	6:g:636:U:H6	1.68	0.58
6:g:1026:G:OP2	6:g:1031:C:N4	2.35	0.58
6:g:1479:C:H2'	6:g:1480:A:C8	2.38	0.58
22:j:36:LYS:O	22:j:36:LYS:HD3	2.03	0.58
6:g:1251:A:N7	6:g:1369:C:O2'	2.32	0.58
6:g:766:A:C6	6:g:767:A:N1	2.72	0.58
6:g:924:C:O2'	6:g:925:G:N3	2.35	0.58
6:g:675:A:H1'	11:q:117:HIS:CD2	2.38	0.58
9:n:11:HIS:ND1	9:n:13:ASP:OD1	2.36	0.58
16:m:69:ARG:HH12	16:m:96:ASN:HA	1.68	0.58
17:o:50:PRO:HA	17:o:102:PHE:HE1	1.67	0.58
19:s:89:ARG:HH21	21:z:77:ARG:HH12	1.52	0.58
11:q:16:SER:HA	11:q:78:ILE:HA	1.85	0.58
16:m:26:VAL:HG12	16:m:42:VAL:HG11	1.85	0.58
4:A:95:GLU:OE2	4:A:127:THR:OG1	2.13	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:1038:C:H2'	6:g:1039:G:C8	2.38	0.58
6:g:9:G:OP2	7:k:125:LYS:HE2	2.03	0.58
6:g:1266:G:O2'	6:g:1268:G:N7	2.36	0.58
18:r:9:ARG:NH2	18:r:99:GLN:OE1	2.37	0.58
2:2:34:ARG:HH21	6:g:1524:C:H3'	1.69	0.58
6:g:116:A:N6	6:g:314:C:O2'	2.30	0.58
16:m:133:ALA:HA	16:m:136:LYS:HE2	1.85	0.58
6:g:965:U:H5''	6:g:969:A:H8	1.68	0.57
6:g:977:A:H2'	6:g:978:A:H5''	1.85	0.57
6:g:1389:C:O2'	6:g:1390:U:O5'	2.22	0.57
6:g:1474:U:H2'	6:g:1475:G:H8	1.69	0.57
5:P:16:MET:HB2	5:P:19:SER:HB3	1.86	0.57
6:g:227:G:H3'	6:g:228:A:H8	1.68	0.57
6:g:539:A:H2'	6:g:540:G:H8	1.69	0.57
11:q:86:LYS:HD2	11:q:114:PRO:HD3	1.87	0.57
6:g:718:A:O5'	11:q:118:ASN:ND2	2.37	0.57
16:m:56:SER:HB2	16:m:59:GLU:HG2	1.86	0.57
2:2:34:ARG:NH2	6:g:1524:C:H3'	2.20	0.57
6:g:1510:C:H2'	6:g:1511:G:H8	1.68	0.57
6:g:460:A:H2'	6:g:461:A:H8	1.70	0.57
13:u:14:PHE:CE2	13:u:25:GLU:HG3	2.40	0.57
6:g:406:G:N2	6:g:437:U:O2	2.37	0.57
6:g:1315:U:H3	6:g:1319:A:H8	1.52	0.57
2:2:17:ARG:HA	2:2:20:ARG:HE	1.69	0.57
6:g:796:C:OP1	11:q:127:ARG:NH1	2.38	0.57
7:k:79:THR:HG21	7:k:99:SER:HA	1.87	0.57
15:h:130:ARG:HA	15:h:133:MET:SD	2.45	0.57
4:A:94:LYS:NZ	6:g:789:U:O4	2.37	0.57
6:g:376:G:H2'	6:g:377:G:H8	1.70	0.57
6:g:1057:G:H2'	6:g:1058:G:C8	2.40	0.57
9:n:71:ILE:HA	9:n:74:LEU:HG	1.87	0.57
10:p:8:ASP:OD2	10:p:12:ARG:NH2	2.24	0.57
20:w:97:LYS:NZ	20:w:98:LYS:O	2.37	0.57
5:P:17:GLU:OE2	6:g:273:U:O2'	2.17	0.56
6:g:424:G:H2'	6:g:425:G:H8	1.68	0.56
9:n:8:PHE:CE1	9:n:60:VAL:HG11	2.40	0.56
22:j:109:SER:O	22:j:112:ARG:HG3	2.05	0.56
11:q:35:ASP:OD1	11:q:37:GLN:NE2	2.38	0.56
12:t:72:ASN:ND2	12:t:104:SER:OG	2.38	0.56
6:g:555:U:H2'	6:g:556:C:C6	2.40	0.56
6:g:916:U:H2'	6:g:917:G:H8	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:m:115:MET:N	16:m:115:MET:SD	2.78	0.56
6:g:432:A:C4	6:g:433:G:C8	2.94	0.56
6:g:575:G:H4'	6:g:576:C:H5''	1.86	0.56
6:g:938:A:O2'	6:g:1376:U:O2	2.22	0.56
6:g:1177:G:OP2	6:g:1177:G:H3'	2.05	0.56
15:h:27:GLU:O	15:h:31:ASN:ND2	2.34	0.56
3:3:38:ILE:HG12	3:3:82:ILE:HD13	1.87	0.56
4:A:70:TYR:O	4:A:74:LEU:HB2	2.05	0.56
6:g:687:A:N6	6:g:701:U:O4'	2.38	0.56
6:g:1038:C:H2'	6:g:1039:G:H8	1.71	0.56
6:g:1257:A:H62	20:w:57:PRO:HG2	1.71	0.56
6:g:1320:C:H1'	21:z:71:GLY:HA3	1.88	0.56
19:s:14:ALA:HA	19:s:44:ILE:HD11	1.88	0.56
6:g:981:U:O3'	20:w:63:ARG:NH2	2.38	0.56
6:g:1464:U:H2'	6:g:1465:A:H8	1.69	0.56
5:P:64:ARG:NH1	6:g:130:A:OP1	2.39	0.56
6:g:522:C:H41	12:t:49:ARG:NH2	2.03	0.56
6:g:763:G:H2'	6:g:764:C:C6	2.40	0.56
6:g:941:G:H2'	6:g:942:G:C8	2.40	0.56
6:g:654:G:C2	6:g:655:A:H1'	2.41	0.56
6:g:1079:G:H2'	6:g:1080:A:H8	1.69	0.56
18:r:10:LEU:HD23	18:r:18:ILE:HG13	1.87	0.56
19:s:69:ARG:O	19:s:72:ILE:HG22	2.06	0.56
6:g:166:U:H2'	6:g:167:A:H8	1.71	0.56
6:g:565:U:H3'	6:g:566:G:H8	1.70	0.56
7:k:12:GLU:N	7:k:12:GLU:OE1	2.38	0.56
17:o:50:PRO:HA	17:o:102:PHE:CE1	2.41	0.56
6:g:1231:G:H2'	6:g:1232:U:C6	2.40	0.56
3:3:2:ASN:O	3:3:7:LYS:NZ	2.28	0.55
6:g:626:G:H2'	6:g:627:G:H8	1.71	0.55
6:g:789:U:O2'	6:g:791:G:N7	2.36	0.55
6:g:1404:C:H2'	6:g:1405:G:C8	2.41	0.55
7:k:141:ASP:N	7:k:141:ASP:OD1	2.36	0.55
14:y:55:ASP:OD2	14:y:55:ASP:N	2.39	0.55
6:g:520:A:H62	6:g:529:G:N2	2.04	0.55
6:g:908:A:H2'	6:g:909:A:H8	1.70	0.55
21:z:31:ARG:HG2	21:z:56:HIS:HB2	1.88	0.55
2:2:33:ARG:HG2	2:2:34:ARG:HD3	1.88	0.55
6:g:1279:G:O2'	6:g:1281:C:OP2	2.17	0.55
18:r:56:HIS:O	18:r:58:ASN:ND2	2.39	0.55
22:j:22:TRP:H	22:j:22:TRP:CD1	2.23	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:j:46:VAL:HA	22:j:49:PHE:CE2	2.41	0.55
6:g:393:A:OP1	6:g:483:C:O2'	2.24	0.55
6:g:936:C:HO2'	6:g:1382:C:H42	1.54	0.55
6:g:1310:G:O5'	19:s:78:ARG:NH2	2.39	0.55
6:g:1458:G:H2'	6:g:1459:G:H8	1.72	0.55
6:g:1514:G:H2'	6:g:1515:G:C8	2.41	0.55
10:p:29:SER:OG	10:p:32:LYS:HG2	2.06	0.55
6:g:1161:C:H2'	6:g:1162:C:C6	2.42	0.55
6:g:1219:A:H4'	21:z:36:ARG:HH22	1.70	0.55
19:s:105:ALA:HB3	19:s:106:ARG:HH11	1.72	0.55
5:P:78:VAL:HG12	5:P:79:GLU:OE1	2.06	0.55
9:n:21:MET:HE3	9:n:25:TYR:CE2	2.41	0.55
14:y:20:VAL:HG23	14:y:35:ARG:HA	1.88	0.55
21:z:69:LYS:HB2	21:z:72:GLU:HG3	1.88	0.55
6:g:1059:C:N4	6:g:1060:U:O4	2.39	0.55
6:g:1074:G:H2'	6:g:1075:U:H6	1.70	0.55
10:p:74:ILE:HD13	10:p:128:VAL:HG22	1.88	0.55
6:g:662:U:H2'	6:g:663:A:C8	2.42	0.55
6:g:903:G:H2'	6:g:904:U:C6	2.42	0.55
2:2:46:ARG:HH21	6:g:1529:G:P	2.30	0.55
6:g:17:U:H2'	6:g:18:C:C6	2.42	0.55
6:g:32:A:H2'	6:g:33:A:H8	1.71	0.55
8:l:7:LYS:HD2	8:l:20:LEU:HD13	1.89	0.55
15:h:5:HIS:CD2	15:h:6:PRO:HD2	2.35	0.55
16:m:90:VAL:HG13	16:m:95:ARG:HB2	1.89	0.55
22:j:178:LEU:HD23	22:j:180:ILE:HD11	1.89	0.55
6:g:746:A:H2'	6:g:747:A:C8	2.42	0.55
6:g:688:G:H2'	6:g:689:C:C6	2.42	0.54
17:o:14:SER:HB3	17:o:77:ALA:HB2	1.88	0.54
6:g:1071:C:H2'	6:g:1072:G:C8	2.43	0.54
6:g:1174:G:H2'	6:g:1175:G:C8	2.42	0.54
6:g:1373:G:OP1	16:m:35:LYS:NZ	2.34	0.54
6:g:1472:U:H2'	6:g:1473:G:H8	1.70	0.54
1:1:49:LYS:HZ3	1:1:52:ARG:HH12	1.55	0.54
5:P:46:HIS:HB2	5:P:70:LYS:HD3	1.88	0.54
6:g:264:C:H2'	6:g:265:G:O4'	2.07	0.54
6:g:614:C:OP1	8:l:82:LYS:NZ	2.40	0.54
6:g:349:A:H2'	6:g:350:G:C8	2.43	0.54
11:q:83:VAL:O	11:q:110:THR:OG1	2.26	0.54
10:p:1:SER:O	10:p:3:GLN:NE2	2.39	0.54
16:m:78:ARG:HA	16:m:78:ARG:NE	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:409:U:OP2	8:l:21:LYS:NZ	2.41	0.54
8:l:187:ARG:NH1	8:l:196:GLU:OE2	2.41	0.54
6:g:928:G:N2	6:g:1390:U:O2	2.40	0.54
6:g:976:G:OP1	20:w:72:GLY:N	2.32	0.54
6:g:993:G:H2'	6:g:995:C:H41	1.72	0.54
16:m:46:LEU:O	16:m:49:LEU:HG	2.08	0.54
6:g:45:G:H2'	6:g:46:G:H8	1.72	0.54
6:g:673:A:H2'	6:g:674:G:H8	1.69	0.54
15:h:148:ILE:HG22	15:h:201:ILE:HG23	1.89	0.54
4:A:14:ARG:N	4:A:18:GLU:OE1	2.41	0.54
6:g:421:U:H3	15:h:126:ARG:HD3	1.72	0.54
6:g:500:G:H2'	6:g:501:C:C6	2.43	0.54
6:g:1309:G:O2'	19:s:78:ARG:NH2	2.38	0.54
19:s:24:VAL:HG13	19:s:28:ARG:HB3	1.89	0.54
6:g:32:A:H2'	6:g:33:A:C8	2.42	0.54
6:g:876:C:H2'	6:g:877:G:H8	1.73	0.54
6:g:715:A:H2'	6:g:716:A:C8	2.43	0.53
14:y:56:ARG:HE	14:y:56:ARG:HA	1.73	0.53
15:h:184:ASN:OD1	15:h:185:THR:N	2.41	0.53
16:m:13:PRO:HB3	16:m:23:ALA:HB2	1.90	0.53
6:g:704:A:O2'	6:g:705:G:O4'	2.19	0.53
6:g:1502:A:H2'	6:g:1504:G:N7	2.22	0.53
18:r:35:GLN:HB3	18:r:37:ARG:HH21	1.72	0.53
6:g:651:C:H2'	6:g:652:U:C6	2.43	0.53
6:g:811:C:H5	6:g:812:G:C5	2.25	0.53
6:g:1018:G:H5'	6:g:1019:A:OP2	2.09	0.53
6:g:1344:C:OP1	17:o:123:ARG:NH2	2.35	0.53
7:k:96:GLN:HG3	7:k:97:PRO:HD2	1.89	0.53
20:w:53:ARG:HH12	21:z:36:ARG:NH1	2.07	0.53
6:g:40:C:H2'	6:g:41:G:C8	2.44	0.53
6:g:662:U:H2'	6:g:663:A:H8	1.73	0.53
6:g:1004:A:OP1	6:g:1025:U:N3	2.40	0.53
6:g:1009:U:C4	6:g:1020:G:O6	2.61	0.53
6:g:1359:C:O2'	6:g:1361:G:OP2	2.19	0.53
17:o:83:THR:HG22	17:o:97:LEU:HD21	1.90	0.53
9:n:19:PRO:O	9:n:23:GLU:HG2	2.08	0.53
11:q:13:LYS:NZ	11:q:14:GLN:O	2.42	0.53
15:h:119:ILE:HA	15:h:122:GLN:OE1	2.09	0.53
19:s:24:VAL:HG22	19:s:28:ARG:HG2	1.90	0.53
1:l:68:PRO:HG3	9:n:48:ALA:HB1	1.90	0.53
6:g:542:G:OP1	8:l:9:LYS:NZ	2.30	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:744:C:H2'	6:g:745:G:C8	2.35	0.53
6:g:1391:U:H2'	6:g:1392:G:C8	2.44	0.53
3:3:59:ARG:NH2	6:g:195:A:OP1	2.37	0.53
6:g:413:G:N2	6:g:428:G:O2'	2.42	0.53
6:g:725:G:H2'	6:g:726:C:H6	1.73	0.53
6:g:825:A:HO2'	10:p:12:ARG:HH22	1.53	0.53
22:j:30:ILE:HG22	22:j:32:GLY:H	1.73	0.53
2:2:8:ASN:OD1	11:q:97:ARG:NE	2.42	0.53
6:g:713:G:H2'	6:g:714:G:C8	2.44	0.53
6:g:1407:C:H2'	6:g:1408:A:C8	2.39	0.53
12:t:105:GLY:HA3	12:t:118:VAL:HG22	1.90	0.53
16:m:118:ARG:NH1	16:m:118:ARG:HG2	2.23	0.53
19:s:105:ALA:HB3	19:s:106:ARG:NH1	2.24	0.53
3:3:11:ILE:O	3:3:14:GLU:HG3	2.09	0.52
6:g:1230:C:H2'	6:g:1231:G:C8	2.43	0.52
6:g:34:C:H2'	6:g:35:G:H8	1.75	0.52
6:g:358:U:H2'	6:g:359:G:H8	1.73	0.52
6:g:520:A:N6	6:g:529:G:H21	2.07	0.52
6:g:626:G:H2'	6:g:627:G:C8	2.44	0.52
6:g:1056:U:HO2'	15:h:155:ARG:HH12	1.55	0.52
6:g:1064:G:O3'	6:g:1190:G:N2	2.41	0.52
4:A:133:ARG:H	4:A:133:ARG:HD3	1.74	0.52
6:g:184:G:H2'	6:g:185:U:C6	2.44	0.52
6:g:13:U:O2'	6:g:14:U:O4'	2.27	0.52
6:g:1060:U:H2'	6:g:1061:G:C8	2.41	0.52
6:g:1316:G:H4'	20:w:59:ARG:CZ	2.40	0.52
11:q:79:LYS:HZ2	11:q:105:ARG:HH22	1.57	0.52
3:3:61:ALA:HA	3:3:66:ILE:HG22	1.92	0.52
6:g:8:A:N7	8:l:204:SER:OG	2.42	0.52
6:g:52:C:H2'	6:g:53:A:C8	2.44	0.52
6:g:296:U:H2'	6:g:297:G:C8	2.45	0.52
6:g:1002:G:H2'	6:g:1003:G:C8	2.44	0.52
6:g:1019:A:H2'	6:g:1020:G:C8	2.44	0.52
6:g:451:A:H2	6:g:480:U:C4	2.28	0.52
6:g:1414:U:H2'	6:g:1415:G:C8	2.42	0.52
6:g:1524:C:OP2	11:q:124:LYS:NZ	2.43	0.52
16:m:110:ARG:HD3	16:m:118:ARG:HG3	1.92	0.52
6:g:305:G:H4'	6:g:306:A:H5''	1.92	0.52
21:z:48:ILE:HD11	21:z:70:LEU:HD21	1.92	0.52
5:P:35:LYS:NZ	10:p:81:GLY:O	2.34	0.52
6:g:459:A:H2'	6:g:460:A:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:1342:C:H4'	17:o:126:PHE:HB3	1.92	0.52
15:h:10:ARG:NH2	15:h:176:THR:O	2.43	0.52
4:A:112:ARG:HA	4:A:115:ILE:HD12	1.91	0.52
6:g:40:C:H2'	6:g:41:G:H8	1.74	0.52
22:j:92:ASN:OD1	22:j:93:HIS:N	2.43	0.52
6:g:796:C:H2'	6:g:797:C:C6	2.45	0.52
6:g:987:G:O2'	21:z:33:TRP:NE1	2.41	0.52
6:g:1013:G:N2	6:g:1015:G:H5''	2.25	0.52
6:g:1485:U:H2'	6:g:1486:G:C8	2.45	0.52
7:k:82:HIS:ND1	7:k:83:PRO:O	2.38	0.52
6:g:231:U:H2'	6:g:232:G:H8	1.75	0.51
6:g:572:A:H62	6:g:864:A:N6	2.09	0.51
6:g:1524:C:H2'	6:g:1525:G:C8	2.44	0.51
15:h:151:GLU:OE2	15:h:153:SER:OG	2.25	0.51
17:o:91:GLU:OE1	17:o:94:ARG:HD3	2.10	0.51
18:r:8:ILE:HD11	18:r:87:LEU:HD13	1.92	0.51
22:j:218:ALA:O	22:j:221:ARG:HG2	2.10	0.51
6:g:840:C:C2	6:g:841:C:H2'	2.46	0.51
11:q:96:ILE:HG13	11:q:97:ARG:HG3	1.91	0.51
19:s:93:GLY:HA3	19:s:109:LYS:HE2	1.91	0.51
6:g:45:G:H2'	6:g:46:G:C8	2.45	0.51
6:g:431:A:C4	6:g:432:A:C8	2.98	0.51
6:g:1033:G:H2'	6:g:1034:G:O4'	2.11	0.51
6:g:1215:G:OP2	6:g:1215:G:H8	1.93	0.51
8:l:201:GLU:O	8:l:204:SER:OG	2.21	0.51
15:h:29:ALA:HB1	20:w:65:ARG:HH22	1.75	0.51
15:h:155:ARG:NH2	15:h:194:VAL:O	2.43	0.51
6:g:1160:G:O2'	6:g:1161:C:O5'	2.29	0.51
6:g:1521:C:H2'	6:g:1522:U:C6	2.45	0.51
12:t:33:CYS:HA	12:t:54:VAL:HA	1.91	0.51
4:A:170:MET:SD	4:A:170:MET:N	2.84	0.51
6:g:1269:A:H1'	6:g:1312:G:N2	2.24	0.51
6:g:1474:U:H2'	6:g:1475:G:C8	2.46	0.51
15:h:56:ILE:HG23	15:h:63:ILE:HD11	1.90	0.51
6:g:81:A:O2'	6:g:82:G:OP1	2.25	0.51
6:g:1035:A:H3'	6:g:1037:C:H41	1.76	0.51
6:g:1361:G:N2	6:g:1362:A:N1	2.58	0.51
15:h:108:PRO:HB2	15:h:114:LEU:CD2	2.41	0.51
4:A:91:ILE:HB	4:A:123:LYS:HE3	1.92	0.51
6:g:580:C:H2'	6:g:581:G:C8	2.46	0.51
6:g:986:U:H2'	6:g:987:G:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:l:33:ILE:HG23	8:l:34:GLU:HG2	1.92	0.51
2:2:11:PHE:CG	2:2:12:ASP:N	2.79	0.51
6:g:779:C:H2'	6:g:780:A:C4	2.46	0.51
6:g:1018:G:O6	6:g:1019:A:N6	2.43	0.51
6:g:1319:A:H3'	21:z:4:LEU:HD11	1.92	0.51
18:r:12:ALA:O	18:r:70:HIS:N	2.39	0.51
3:3:2:ASN:OD1	3:3:3:ILE:N	2.43	0.51
6:g:144:G:H2'	6:g:145:G:H8	1.76	0.51
6:g:369:G:N2	6:g:393:A:H1'	2.25	0.51
6:g:500:G:H2'	6:g:501:C:H6	1.74	0.51
6:g:601:G:H2'	6:g:602:A:H8	1.76	0.51
6:g:1216:A:OP1	20:w:8:ARG:NH2	2.38	0.51
9:n:3:HIS:HB2	9:n:92:THR:HA	1.91	0.51
9:n:43:GLY:HA2	9:n:58:HIS:CE1	2.46	0.51
6:g:438:U:O4	6:g:496:A:N7	2.44	0.50
6:g:1253:G:H2'	6:g:1254:A:O4'	2.11	0.50
13:u:47:LYS:O	13:u:49:HIS:ND1	2.44	0.50
15:h:34:SER:OG	15:h:58:ARG:NH2	2.32	0.50
18:r:46:LYS:HB2	18:r:68:ARG:HH12	1.75	0.50
19:s:4:ALA:O	19:s:56:ARG:NH2	2.44	0.50
1:1:56:ARG:NH2	6:g:736:C:OP1	2.44	0.50
6:g:23:C:H2'	6:g:24:U:H6	1.75	0.50
6:g:642:A:N7	10:p:106:SER:HA	2.25	0.50
6:g:894:G:H2'	6:g:895:G:C8	2.46	0.50
6:g:1077:G:N2	6:g:1079:G:H3'	2.26	0.50
17:o:119:LYS:HG2	17:o:120:ALA:H	1.76	0.50
6:g:1306:A:O2'	19:s:97:ARG:NH1	2.44	0.50
6:g:1526:G:O2'	6:g:1527:U:OP1	2.27	0.50
6:g:116:A:H62	6:g:117:G:H21	1.58	0.50
6:g:1190:G:OP1	15:h:175:HIS:NE2	2.43	0.50
7:k:18:ASN:OD1	7:k:19:ARG:N	2.45	0.50
10:p:115:ALA:O	10:p:119:GLY:N	2.43	0.50
6:g:216:U:H4'	6:g:464:U:H4'	1.94	0.50
6:g:1001:C:O2'	6:g:1002:G:OP1	2.28	0.50
6:g:1489:G:H2'	6:g:1490:U:C6	2.46	0.50
6:g:116:A:H62	6:g:117:G:N2	2.09	0.50
6:g:671:G:O2'	9:n:79:ARG:NH2	2.40	0.50
6:g:1021:A:H3'	6:g:1022:A:H5''	1.92	0.50
6:g:1241:G:H2'	6:g:1242:G:C8	2.46	0.50
8:l:94:GLU:HG2	8:l:185:PRO:HG2	1.93	0.50
12:t:113:ARG:NH2	12:t:118:VAL:HB	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:z:11:ASP:HB2	21:z:14:LEU:HB2	1.94	0.50
1:1:56:ARG:HH22	6:g:736:C:P	2.35	0.50
6:g:107:G:OP1	6:g:134:G:N2	2.45	0.50
17:o:105:ARG:NH1	17:o:106:ASP:O	2.43	0.50
22:j:140:LEU:O	22:j:144:GLU:HB2	2.12	0.50
6:g:20:U:H1'	6:g:572:A:C2	2.47	0.50
6:g:635:A:H2'	6:g:636:U:C6	2.45	0.50
6:g:1161:C:H2'	6:g:1162:C:H6	1.77	0.50
6:g:1187:G:H2'	6:g:1188:A:C8	2.47	0.50
6:g:1436:U:O4	6:g:1437:A:N6	2.44	0.50
6:g:1468:A:H2'	6:g:1469:C:C6	2.47	0.50
19:s:38:ILE:HD11	19:s:54:THR:HG21	1.94	0.50
6:g:1279:G:N3	6:g:1279:G:H2'	2.26	0.50
6:g:191:G:H2'	6:g:192:A:C8	2.47	0.49
6:g:672:U:H5'	9:n:79:ARG:HH12	1.77	0.49
6:g:1040:U:H2'	6:g:1042:A:N6	2.27	0.49
6:g:1117:A:O2'	6:g:1180:A:OP1	2.30	0.49
6:g:1238:A:N7	6:g:1301:U:C2	2.80	0.49
6:g:2:A:N6	6:g:3:A:N1	2.49	0.49
6:g:411:A:H4'	6:g:412:A:H5'	1.93	0.49
6:g:422:C:H4'	6:g:423:G:C4	2.46	0.49
8:l:161:ALA:O	8:l:166:LYS:NZ	2.36	0.49
12:t:98:ARG:NH1	12:t:104:SER:O	2.35	0.49
21:z:11:ASP:O	21:z:15:LEU:N	2.40	0.49
21:z:65:MET:HB3	21:z:68:HIS:HB2	1.94	0.49
6:g:763:G:H2'	6:g:764:C:H6	1.77	0.49
6:g:940:C:H2'	6:g:941:G:C8	2.47	0.49
6:g:981:U:OP1	20:w:8:ARG:NH1	2.46	0.49
6:g:1097:C:H2'	6:g:1098:C:H6	1.77	0.49
6:g:1239:A:O2'	6:g:1297:G:N2	2.44	0.49
6:g:1255:G:N7	6:g:1279:G:N1	2.59	0.49
6:g:1316:G:H3'	6:g:1317:C:H5''	1.94	0.49
11:q:83:VAL:O	11:q:84:MET:HE2	2.12	0.49
5:P:17:GLU:OE1	5:P:17:GLU:N	2.45	0.49
6:g:184:G:H2'	6:g:185:U:H6	1.77	0.49
6:g:1281:C:H2'	6:g:1282:C:C5	2.47	0.49
7:k:148:SER:H	7:k:151:MET:HE2	1.78	0.49
8:l:117:VAL:HG22	8:l:122:ILE:HD13	1.94	0.49
9:n:73:GLU:O	9:n:77:THR:HG23	2.12	0.49
20:w:34:ASN:O	20:w:41:ARG:N	2.46	0.49
21:z:4:LEU:HD21	21:z:69:LYS:HD3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:198:G:N7	6:g:220:G:N2	2.60	0.49
6:g:542:G:O3'	8:l:13:ARG:NH2	2.41	0.49
6:g:1303:C:H3'	6:g:1304:G:H8	1.76	0.49
9:n:21:MET:HE3	9:n:25:TYR:CZ	2.46	0.49
12:t:81:ILE:HD11	12:t:94:TYR:CG	2.47	0.49
18:r:14:ASP:HB3	18:r:17:LEU:HB3	1.95	0.49
22:j:45:THR:HG23	22:j:200:PRO:HD2	1.94	0.49
4:A:171:ILE:O	4:A:172:MET:HE2	2.12	0.49
6:g:607:A:H2'	6:g:608:A:H8	1.78	0.49
6:g:1384:C:N4	6:g:1385:G:O6	2.45	0.49
12:t:120:ARG:HD3	12:t:121:PRO:HD2	1.95	0.49
17:o:40:ARG:O	17:o:44:ARG:NH2	2.46	0.49
17:o:41:GLU:OE1	17:o:41:GLU:N	2.46	0.49
6:g:797:C:OP1	11:q:126:ARG:NH1	2.45	0.49
6:g:1003:G:O6	6:g:1035:A:H8	1.96	0.49
6:g:1082:A:H2'	6:g:1083:U:O4'	2.13	0.49
6:g:1526:G:H2'	6:g:1527:U:C6	2.47	0.49
11:q:33:ILE:HG21	11:q:73:VAL:HG11	1.95	0.49
4:A:76:GLU:OE2	6:g:701:U:O2'	2.31	0.49
6:g:202:G:N2	6:g:466:A:H61	2.11	0.49
6:g:648:A:H2'	6:g:649:A:C8	2.47	0.49
6:g:1520:C:H2'	6:g:1521:C:C6	2.48	0.49
2:2:11:PHE:HB2	2:2:15:LEU:HD12	1.93	0.48
6:g:441:A:C4	6:g:497:G:N2	2.81	0.48
6:g:520:A:H62	6:g:529:G:H21	1.60	0.48
6:g:522:C:N4	12:t:49:ARG:HH22	2.11	0.48
6:g:993:G:N2	6:g:995:C:H42	2.08	0.48
10:p:100:ILE:HG22	10:p:128:VAL:HB	1.95	0.48
19:s:79:LEU:HD12	19:s:82:LEU:HD22	1.94	0.48
2:2:24:LYS:NZ	6:g:1536:C:N3	2.60	0.48
3:3:9:ARG:HG2	6:g:108:G:C6	2.48	0.48
7:k:155:LYS:NZ	10:p:70:VAL:O	2.46	0.48
10:p:14:ARG:NH2	10:p:74:ILE:O	2.42	0.48
11:q:37:GLN:NE2	11:q:39:ASN:OD1	2.46	0.48
20:w:26:LEU:O	20:w:30:ILE:HG12	2.12	0.48
6:g:1316:G:O3'	20:w:59:ARG:NH2	2.45	0.48
20:w:13:VAL:HG12	20:w:60:GLN:NE2	2.28	0.48
6:g:607:A:H2'	6:g:608:A:C8	2.49	0.48
6:g:725:G:H2'	6:g:726:C:C6	2.47	0.48
6:g:745:G:C2	6:g:746:A:C5	3.01	0.48
7:k:93:VAL:HA	7:k:126:ALA:HA	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:l:120:LYS:O	8:l:145:ARG:NH2	2.38	0.48
10:p:5:PRO:HB2	10:p:32:LYS:NZ	2.26	0.48
6:g:974:A:H5'	20:w:71:HIS:HB3	1.94	0.48
6:g:1471:U:H2'	6:g:1472:U:C6	2.47	0.48
15:h:11:LEU:HD11	15:h:17:TRP:HA	1.94	0.48
17:o:118:ARG:HH12	17:o:124:PRO:HA	1.79	0.48
8:l:197:HIS:O	8:l:201:GLU:HG3	2.13	0.48
4:A:107:TYR:OH	4:A:151:ASP:OD2	2.20	0.48
6:g:28:A:OP1	8:l:72:ARG:NH2	2.46	0.48
6:g:548:G:H2'	6:g:549:C:C6	2.49	0.48
6:g:696:A:H5''	11:q:52:ARG:HH22	1.77	0.48
6:g:920:A:H4'	6:g:921:U:OP1	2.11	0.48
6:g:1087:G:C5	6:g:1099:G:N2	2.81	0.48
6:g:1115:U:H2'	6:g:1116:U:C6	2.49	0.48
6:g:1190:G:H5''	15:h:175:HIS:CE1	2.48	0.48
6:g:1238:A:C8	6:g:1303:C:H1'	2.49	0.48
15:h:138:GLN:OE1	15:h:138:GLN:HA	2.14	0.48
6:g:433:G:H2'	6:g:434:U:C6	2.49	0.48
6:g:736:C:H2'	6:g:737:C:C6	2.49	0.48
6:g:738:C:H2'	6:g:739:C:C6	2.49	0.48
8:l:169:TRP:HD1	8:l:189:ASP:OD2	1.96	0.48
15:h:156:LEU:HB2	15:h:163:ARG:HG3	1.96	0.48
4:A:129:ARG:NH2	6:g:1495:U:OP1	2.39	0.48
5:P:16:MET:SD	6:g:275:G:H4'	2.54	0.48
6:g:178:C:H2'	6:g:179:A:H8	1.78	0.48
6:g:1006:G:H5'	6:g:1006:G:H8	1.79	0.48
6:g:1135:U:N3	6:g:1137:C:O2	2.47	0.48
13:u:86:LEU:O	13:u:88:ARG:N	2.47	0.48
22:j:119:GLN:O	22:j:123:GLY:N	2.47	0.48
6:g:7:A:C4	6:g:298:A:C6	3.02	0.48
11:q:126:ARG:NE	11:q:128:VAL:O	2.46	0.48
6:g:785:G:H2'	6:g:786:G:C8	2.49	0.47
6:g:1319:A:H5'	21:z:4:LEU:HG	1.95	0.47
13:u:35:ILE:HB	13:u:58:MET:HE2	1.96	0.47
15:h:5:HIS:CE1	20:w:89:MET:HB3	2.49	0.47
4:A:82:LYS:HE2	6:g:697:U:H5'	1.96	0.47
6:g:293:G:C4	6:g:305:G:N2	2.83	0.47
6:g:1066:C:N4	6:g:1067:A:N1	2.62	0.47
6:g:1218:C:H2'	6:g:1219:A:C8	2.49	0.47
9:n:26:THR:HA	9:n:29:ILE:HG22	1.96	0.47
6:g:348:G:H2'	6:g:349:A:C8	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:792:A:C8	6:g:794:A:C5	3.02	0.47
6:g:1220:G:O2'	21:z:51:HIS:O	2.32	0.47
19:s:42:VAL:HG21	19:s:51:GLN:NE2	2.30	0.47
6:g:17:U:H2'	6:g:18:C:H6	1.79	0.47
6:g:564:C:OP2	12:t:11:ARG:NH2	2.47	0.47
6:g:627:G:C2	6:g:628:G:C5	3.03	0.47
6:g:636:U:H2'	6:g:637:C:H6	1.79	0.47
6:g:782:A:H62	6:g:800:G:N2	2.13	0.47
6:g:835:U:O2	6:g:851:G:O6	2.31	0.47
6:g:1219:A:H5'	20:w:53:ARG:HH22	1.78	0.47
12:t:4:ASN:HA	12:t:7:VAL:HG22	1.96	0.47
18:r:35:GLN:HB3	18:r:37:ARG:NH2	2.29	0.47
3:3:70:LYS:NZ	6:g:261:U:OP2	2.41	0.47
9:n:23:GLU:HA	9:n:26:THR:HG22	1.96	0.47
6:g:153:C:H2'	6:g:154:U:H6	1.79	0.47
6:g:253:A:H2'	6:g:254:G:C8	2.45	0.47
6:g:494:G:H4'	6:g:495:A:OP1	2.13	0.47
6:g:958:A:C5	21:z:54:ARG:HD2	2.49	0.47
6:g:1083:U:H5''	6:g:1086:U:O4	2.14	0.47
20:w:8:ARG:HB3	20:w:12:ARG:HH21	1.79	0.47
3:3:42:ASP:OD1	3:3:43:LYS:N	2.47	0.47
5:P:27:PHE:HE1	5:P:38:LYS:HG2	1.78	0.47
6:g:24:U:H2'	6:g:25:C:C6	2.50	0.47
6:g:27:G:H2'	6:g:28:A:C8	2.49	0.47
6:g:570:G:H1'	6:g:820:U:C5	2.49	0.47
6:g:601:G:H2'	6:g:602:A:C8	2.49	0.47
6:g:636:U:H2'	6:g:637:C:C6	2.50	0.47
6:g:669:G:H2'	6:g:670:G:C8	2.50	0.47
6:g:786:G:H2'	6:g:787:A:C8	2.46	0.47
6:g:942:G:O6	6:g:1341:U:O4	2.33	0.47
6:g:944:G:H21	6:g:1339:A:H62	1.62	0.47
6:g:954:G:N2	6:g:955:U:C2	2.83	0.47
6:g:991:U:OP2	6:g:1212:U:O2'	2.31	0.47
6:g:1157:A:H4'	6:g:1158:C:O4'	2.15	0.47
6:g:1210:C:O2	6:g:1214:C:O2'	2.26	0.47
7:k:24:VAL:HG22	7:k:25:LYS:H	1.80	0.47
7:k:73:VAL:HG11	7:k:143:LEU:HD13	1.96	0.47
7:k:104:ILE:HG22	7:k:122:VAL:HG12	1.97	0.47
10:p:95:MET:HG3	10:p:95:MET:O	2.15	0.47
14:y:19:VAL:HG13	14:y:36:VAL:HG13	1.96	0.47
18:r:48:ARG:NH1	18:r:66:GLU:OE1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:91:U:H2'	6:g:92:U:C6	2.50	0.47
22:j:77:GLU:HA	22:j:80:LYS:HE2	1.95	0.47
4:A:68:MET:HE3	4:A:74:LEU:HD21	1.97	0.47
6:g:777:A:H3'	6:g:778:G:H8	1.80	0.47
6:g:973:G:O6	6:g:974:A:N6	2.48	0.47
6:g:1268:G:O2'	6:g:1269:A:O4'	2.31	0.47
10:p:63:LYS:O	10:p:64:TYR:HD1	1.98	0.47
16:m:50:ALA:HB2	16:m:57:GLU:HB2	1.97	0.47
19:s:17:ALA:O	19:s:21:ILE:HG13	2.15	0.47
19:s:63:VAL:HG13	19:s:67:ASP:HB3	1.96	0.47
6:g:626:G:C2	6:g:627:G:C5	3.03	0.47
6:g:1106:G:H4'	15:h:171:ARG:HH21	1.80	0.47
15:h:39:ARG:HG2	15:h:54:ILE:HD11	1.97	0.47
5:P:70:LYS:NZ	6:g:254:G:O3'	2.48	0.46
6:g:766:A:HO2'	6:g:767:A:P	2.38	0.46
6:g:1079:G:O2'	6:g:1080:A:OP1	2.27	0.46
6:g:1106:G:H4'	15:h:171:ARG:NH2	2.30	0.46
6:g:1178:G:H5''	6:g:1179:A:H5''	1.97	0.46
6:g:1220:G:H21	21:z:53:GLY:C	2.22	0.46
10:p:26:MET:SD	10:p:27:PRO:HD2	2.55	0.46
14:y:34:GLU:OE2	14:y:60:TRP:NE1	2.36	0.46
4:A:108:GLN:O	4:A:112:ARG:HG3	2.15	0.46
6:g:7:A:H2'	7:k:123:LEU:HD21	1.97	0.46
6:g:580:C:H2'	6:g:581:G:H8	1.80	0.46
6:g:936:C:H41	16:m:1:PRO:HG2	1.80	0.46
6:g:1340:A:H2'	6:g:1341:U:C6	2.50	0.46
19:s:13:HIS:HB2	19:s:16:ILE:HG12	1.96	0.46
21:z:50:VAL:HB	21:z:74:ALA:HB2	1.97	0.46
6:g:34:C:H2'	6:g:35:G:C8	2.50	0.46
6:g:166:U:H2'	6:g:167:A:C8	2.50	0.46
6:g:410:G:H21	6:g:432:A:H62	1.62	0.46
6:g:780:A:H5''	11:q:125:LYS:HD3	1.97	0.46
6:g:1238:A:N3	6:g:1238:A:H2'	2.31	0.46
6:g:1316:G:H2'	6:g:1317:C:C6	2.51	0.46
15:h:17:TRP:H	15:h:17:TRP:CD1	2.33	0.46
6:g:341:C:H2'	6:g:342:C:C6	2.51	0.46
6:g:1201:A:O2'	6:g:1202:U:OP2	2.23	0.46
15:h:118:SER:O	15:h:122:GLN:NE2	2.48	0.46
15:h:137:VAL:HG23	15:h:148:ILE:HD11	1.97	0.46
20:w:27:LYS:O	20:w:31:SER:N	2.49	0.46
1:1:70:THR:HG23	1:1:72:ARG:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:3:ILE:O	3:3:4:LYS:NZ	2.27	0.46
6:g:23:C:H2'	6:g:24:U:C6	2.50	0.46
6:g:96:U:H2'	6:g:97:G:C8	2.50	0.46
6:g:766:A:N6	6:g:814:A:C5	2.84	0.46
6:g:1294:G:O2'	6:g:1295:U:O4'	2.23	0.46
11:q:85:VAL:HG21	11:q:92:ARG:HG3	1.98	0.46
15:h:76:ILE:HD11	15:h:102:ILE:HG21	1.97	0.46
20:w:3:GLN:O	20:w:6:LYS:HG2	2.16	0.46
22:j:164:ASP:OD1	22:j:164:ASP:N	2.48	0.46
6:g:323:U:H2'	6:g:324:G:O4'	2.15	0.46
6:g:643:C:H2'	6:g:644:U:C6	2.50	0.46
6:g:791:G:H21	6:g:792:A:H62	1.64	0.46
6:g:991:U:H5	6:g:1215:G:H21	1.63	0.46
6:g:1004:A:O2'	6:g:1035:A:N7	2.44	0.46
9:n:38:ARG:NH1	9:n:63:ASN:HB2	2.30	0.46
6:g:295:C:H2'	6:g:296:U:H6	1.80	0.46
6:g:517:G:N2	6:g:533:A:OP2	2.44	0.46
6:g:718:A:H2'	6:g:718:A:N3	2.31	0.46
6:g:1460:C:C2	6:g:1461:G:C8	3.04	0.46
15:h:18:ASN:OD1	15:h:53:ARG:NH2	2.34	0.46
21:z:13:HIS:HA	21:z:16:LYS:HD3	1.98	0.46
22:j:27:LYS:HB3	22:j:28:PRO:HD3	1.96	0.46
22:j:153:MET:HE3	22:j:155:GLY:C	2.41	0.46
6:g:372:C:H42	6:g:389:A:H62	1.64	0.46
6:g:543:U:P	8:l:13:ARG:HH21	2.39	0.46
6:g:768:A:C8	6:g:769:G:C8	3.04	0.46
6:g:792:A:H8	6:g:794:A:C5	2.34	0.46
6:g:1009:U:H3	6:g:1020:G:H1	1.58	0.46
15:h:156:LEU:HD12	15:h:163:ARG:HE	1.81	0.46
18:r:72:ARG:HA	18:r:72:ARG:HD3	1.65	0.46
20:w:79:LEU:HB3	20:w:83:LYS:HG3	1.98	0.46
6:g:688:G:H2'	6:g:689:C:H6	1.80	0.46
9:n:69:GLU:O	9:n:73:GLU:OE1	2.34	0.46
6:g:564:C:HO2'	6:g:565:U:P	2.38	0.46
15:h:129:PHE:CG	15:h:156:LEU:HD22	2.51	0.46
6:g:407:U:O4	6:g:436:C:N3	2.49	0.45
6:g:439:U:O2'	6:g:440:C:OP1	2.33	0.45
6:g:723:U:O2'	6:g:724:G:H5''	2.16	0.45
6:g:1218:C:H2'	6:g:1219:A:H8	1.80	0.45
6:g:1309:G:H2'	6:g:1310:G:C8	2.51	0.45
13:u:81:ILE:HD12	13:u:86:LEU:HD23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:r:36:VAL:HG22	18:r:76:ILE:HG23	1.98	0.45
6:g:139:A:C2	6:g:224:U:C5	3.04	0.45
11:q:22:ILE:N	11:q:84:MET:O	2.32	0.45
6:g:3:A:C5	6:g:629:A:H5'	2.50	0.45
6:g:198:G:C5	6:g:220:G:N2	2.84	0.45
6:g:298:A:O2'	6:g:299:G:OP1	2.27	0.45
6:g:335:C:H2'	6:g:336:A:H8	1.81	0.45
6:g:1415:G:O6	6:g:1485:U:O2	2.34	0.45
12:t:113:ARG:O	12:t:113:ARG:NE	2.38	0.45
5:P:15:LYS:C	5:P:16:MET:HE2	2.41	0.45
6:g:1434:A:H2'	6:g:1435:G:O4'	2.16	0.45
13:u:16:ARG:NH2	13:u:76:ARG:HE	2.14	0.45
19:s:89:ARG:HG3	19:s:96:VAL:HG22	1.98	0.45
19:s:91:ARG:HH11	19:s:91:ARG:HG3	1.82	0.45
6:g:925:G:OP1	6:g:926:G:C5	2.69	0.45
6:g:925:G:OP1	6:g:1502:A:N6	2.50	0.45
6:g:1305:G:H4'	6:g:1331:G:C5	2.51	0.45
8:l:49:ASP:N	8:l:49:ASP:OD1	2.49	0.45
5:P:80:LYS:HE3	5:P:81:ALA:HB2	1.99	0.45
6:g:182:A:O2'	6:g:183:C:H5'	2.16	0.45
6:g:455:G:N2	6:g:478:A:N1	2.65	0.45
6:g:727:G:C2	6:g:731:G:C2	3.05	0.45
6:g:948:C:P	19:s:97:ARG:HH22	2.40	0.45
7:k:80:LEU:O	7:k:97:PRO:HB3	2.17	0.45
15:h:18:ASN:HD22	20:w:91:GLY:HA3	1.81	0.45
21:z:52:ASN:HB2	21:z:76:THR:HG22	1.98	0.45
22:j:84:LEU:HD13	22:j:90:PHE:HE1	1.81	0.45
6:g:109:A:N7	6:g:327:A:C4	2.84	0.45
6:g:1201:A:H4'	6:g:1203:C:OP2	2.16	0.45
9:n:93:LYS:HA	9:n:93:LYS:CE	2.38	0.45
2:2:32:ARG:NH2	11:q:126:ARG:O	2.43	0.45
6:g:447:G:N2	6:g:487:A:H62	2.11	0.45
6:g:705:G:C8	6:g:706:A:C8	3.05	0.45
6:g:1478:U:H2'	6:g:1479:C:C5	2.52	0.45
7:k:31:SER:OG	7:k:52:ALA:O	2.34	0.45
6:g:27:G:H2'	6:g:28:A:H8	1.82	0.45
6:g:296:U:H2'	6:g:297:G:H8	1.81	0.45
6:g:549:C:H2'	6:g:550:G:C8	2.52	0.45
6:g:721:G:H8	6:g:721:G:OP1	1.99	0.45
6:g:910:C:H2'	6:g:911:U:C6	2.52	0.45
6:g:987:G:N2	6:g:1014:A:C2	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:1083:U:O4	6:g:1084:G:N1	2.50	0.45
11:q:63:GLN:O	11:q:67:GLU:OE1	2.34	0.45
12:t:109:ARG:HD2	12:t:109:ARG:HA	1.73	0.45
15:h:31:ASN:O	15:h:58:ARG:NH2	2.50	0.45
21:z:48:ILE:HD11	21:z:70:LEU:HD11	1.99	0.45
22:j:216:VAL:HA	22:j:219:THR:HG22	1.99	0.45
6:g:61:G:H2'	6:g:62:U:C6	2.51	0.45
6:g:567:G:H2'	6:g:568:G:O4'	2.17	0.45
6:g:988:G:H21	6:g:1015:G:N2	2.15	0.45
6:g:1146:A:N3	6:g:1146:A:H2'	2.30	0.45
6:g:1188:A:O5'	6:g:1188:A:H8	2.00	0.45
6:g:1416:G:H3'	6:g:1417:G:H8	1.82	0.45
8:l:9:LYS:HE3	8:l:9:LYS:HB3	1.79	0.45
8:l:98:ASP:OD1	8:l:99:ASN:N	2.49	0.45
9:n:1:MET:N	9:n:65:GLU:OE2	2.50	0.45
16:m:52:ARG:HH22	16:m:121:ASN:HA	1.82	0.45
22:j:26:MET:O	22:j:30:ILE:HG12	2.16	0.45
2:2:8:ASN:OD1	2:2:9:GLU:N	2.42	0.44
5:P:68:LYS:HG2	5:P:69:THR:HG23	1.99	0.44
6:g:7:A:C4	6:g:298:A:N6	2.85	0.44
6:g:627:G:H2'	6:g:628:G:H8	1.82	0.44
6:g:865:A:H2'	6:g:866:C:C6	2.52	0.44
6:g:1342:C:H2'	6:g:1343:G:C8	2.52	0.44
8:l:149:LYS:C	8:l:150:LYS:HG3	2.42	0.44
15:h:107:LYS:HA	15:h:107:LYS:HD2	1.74	0.44
19:s:77:LYS:HA	19:s:80:MET:CE	2.46	0.44
22:j:9:LEU:HD11	22:j:14:HIS:CG	2.53	0.44
4:A:99:ARG:HH21	4:A:129:ARG:HG3	1.82	0.44
6:g:663:A:H2'	6:g:664:G:H8	1.82	0.44
6:g:1049:U:C4	20:w:2:LYS:HE2	2.52	0.44
6:g:1140:C:H2'	6:g:1141:C:C6	2.52	0.44
6:g:1160:G:O2'	6:g:1161:C:O4'	2.34	0.44
6:g:1302:C:N3	19:s:40:GLU:HB2	2.32	0.44
6:g:1304:G:H1	6:g:1332:A:P	2.40	0.44
9:n:42:TRP:NE1	9:n:100:SER:OXT	2.50	0.44
9:n:51:ILE:O	9:n:51:ILE:HG13	2.17	0.44
20:w:41:ARG:HH22	21:z:6:LYS:HB2	1.82	0.44
6:g:697:U:H3'	6:g:698:G:C8	2.52	0.44
6:g:971:G:H4'	6:g:972:C:H5''	1.98	0.44
6:g:1073:U:O2'	22:j:102:ASN:HB2	2.17	0.44
6:g:1079:G:HO2'	6:g:1080:A:P	2.39	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:1176:A:N3	6:g:1176:A:H2'	2.33	0.44
6:g:1524:C:C2	6:g:1525:G:C8	3.06	0.44
6:g:1526:G:H2'	6:g:1527:U:H6	1.81	0.44
13:u:28:VAL:O	13:u:32:THR:HG23	2.18	0.44
16:m:74:VAL:HG22	16:m:143:MET:HE1	2.00	0.44
18:r:17:LEU:O	18:r:20:GLN:HG3	2.18	0.44
6:g:38:G:H4'	6:g:547:A:N6	2.32	0.44
6:g:453:G:H2'	6:g:454:G:C8	2.53	0.44
6:g:663:A:H2'	6:g:664:G:C8	2.52	0.44
6:g:784:A:N6	6:g:785:G:O6	2.51	0.44
6:g:922:G:O6	6:g:1396:A:N6	2.51	0.44
6:g:953:G:C6	6:g:954:G:H1'	2.53	0.44
6:g:1300:G:H1'	6:g:1301:U:H5	1.82	0.44
21:z:32:THR:N	21:z:49:ALA:O	2.49	0.44
6:g:61:G:H2'	6:g:62:U:H6	1.82	0.44
6:g:602:A:H2'	6:g:603:U:C6	2.53	0.44
6:g:1304:G:N7	19:s:26:LYS:NZ	2.66	0.44
7:k:32:PHE:CD2	7:k:55:VAL:HG13	2.53	0.44
7:k:88:HIS:ND1	7:k:89:THR:HG23	2.32	0.44
16:m:96:ASN:O	16:m:100:MET:HG3	2.17	0.44
17:o:27:ILE:HG22	17:o:62:LEU:HD21	2.00	0.44
3:3:7:LYS:O	3:3:11:ILE:HG12	2.17	0.44
6:g:98:A:H2'	6:g:99:C:C6	2.52	0.44
6:g:473:U:H2'	6:g:474:G:C8	2.53	0.44
6:g:502:A:P	12:t:114:SER:HG	2.41	0.44
6:g:787:A:O2'	6:g:788:U:OP1	2.31	0.44
16:m:46:LEU:HA	16:m:49:LEU:CD2	2.47	0.44
17:o:90:ASP:CG	17:o:91:GLU:H	2.26	0.44
1:1:56:ARG:HH12	6:g:736:C:P	2.39	0.44
2:2:34:ARG:NE	6:g:1525:G:OP2	2.46	0.44
4:A:165:ILE:HG12	4:A:170:MET:SD	2.58	0.44
6:g:602:A:H2'	6:g:603:U:H6	1.83	0.44
6:g:1052:U:O2	6:g:1206:G:C6	2.70	0.44
6:g:1075:U:H2'	6:g:1076:U:H6	1.83	0.44
6:g:1319:A:O2'	6:g:1323:G:OP2	2.31	0.44
11:q:35:ASP:OD2	11:q:35:ASP:N	2.37	0.44
21:z:32:THR:HG21	21:z:48:ILE:HD12	1.99	0.44
22:j:175:ALA:O	22:j:179:GLY:N	2.33	0.44
2:2:39:LYS:N	2:2:40:PRO:HD2	2.33	0.44
3:3:52:GLU:OE1	3:3:52:GLU:N	2.45	0.44
6:g:112:G:C2	6:g:113:G:C8	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:403:C:H4'	8:l:131:ILE:HD12	2.00	0.44
6:g:455:G:H2'	6:g:456:A:H8	1.83	0.44
6:g:511:C:C2	6:g:512:U:C5	3.06	0.44
6:g:1034:G:C2'	6:g:1035:A:H4'	2.46	0.44
6:g:1097:C:C2	6:g:1098:C:C5	3.06	0.44
6:g:1206:G:O2'	6:g:1207:G:H5'	2.17	0.44
6:g:1246:A:O5'	6:g:1246:A:H8	2.01	0.44
8:l:169:TRP:CE3	8:l:185:PRO:HG3	2.53	0.44
16:m:30:MET:HE1	16:m:35:LYS:HA	2.00	0.44
17:o:29:ILE:N	17:o:32:ARG:O	2.46	0.44
18:r:81:GLU:HA	18:r:84:VAL:HG12	1.99	0.44
20:w:80:SER:O	20:w:84:VAL:HG23	2.17	0.44
22:j:25:LYS:HD2	22:j:25:LYS:HA	1.81	0.44
22:j:134:LEU:CD1	22:j:138:ARG:HG3	2.48	0.44
4:A:107:TYR:CZ	4:A:111:LEU:HD11	2.52	0.44
5:P:11:VAL:O	5:P:13:SER:OG	2.36	0.44
6:g:343:U:H3'	6:g:345:C:C4	2.53	0.44
6:g:460:A:H2'	6:g:461:A:C8	2.51	0.44
6:g:505:G:H2'	6:g:506:G:H8	1.83	0.44
6:g:526:C:OP2	12:t:87:LYS:HE2	2.18	0.44
6:g:708:C:H2'	6:g:709:U:C6	2.53	0.44
6:g:1006:G:H4'	6:g:1007:U:OP1	2.18	0.44
9:n:9:MET:N	9:n:86:ARG:O	2.50	0.44
13:u:16:ARG:CZ	13:u:76:ARG:HH21	2.31	0.44
6:g:154:U:C2	6:g:168:G:N2	2.86	0.43
6:g:637:C:H2'	6:g:638:U:C6	2.52	0.43
6:g:1318:A:C2	21:z:36:ARG:HA	2.53	0.43
6:g:1341:U:O3'	17:o:129:ARG:NH2	2.46	0.43
8:l:36:ALA:O	8:l:41:GLY:HA3	2.17	0.43
13:u:78:THR:HA	13:u:81:ILE:HG22	2.00	0.43
6:g:116:A:N6	6:g:117:G:H21	2.16	0.43
6:g:144:G:H2'	6:g:145:G:C8	2.53	0.43
6:g:153:C:H2'	6:g:154:U:C6	2.53	0.43
6:g:298:A:HO2'	6:g:299:G:P	2.40	0.43
6:g:549:C:H2'	6:g:550:G:H8	1.83	0.43
6:g:1283:U:H2'	6:g:1284:C:C5	2.54	0.43
11:q:85:VAL:HG11	11:q:92:ARG:CZ	2.48	0.43
17:o:9:GLY:O	17:o:15:ALA:HA	2.18	0.43
6:g:409:U:H2'	6:g:410:G:O4'	2.18	0.43
7:k:55:VAL:O	7:k:59:ILE:HG22	2.17	0.43
21:z:33:TRP:HA	21:z:56:HIS:HE1	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:j:118:THR:O	22:j:121:GLN:HG2	2.18	0.43
6:g:73:C:HO2'	6:g:74:A:H8	1.65	0.43
6:g:80:A:H61	6:g:90:C:N4	2.17	0.43
6:g:505:G:H2'	6:g:506:G:C8	2.53	0.43
6:g:1096:C:C2	6:g:1097:C:C5	3.07	0.43
6:g:1157:A:N6	6:g:1180:A:N7	2.66	0.43
6:g:1300:G:N2	6:g:1301:U:O4	2.44	0.43
17:o:101:GLY:O	17:o:104:THR:OG1	2.24	0.43
18:r:40:ILE:HG22	18:r:42:LEU:HD12	2.00	0.43
4:A:75:TYR:OH	6:g:700:G:O6	2.20	0.43
4:A:95:GLU:HG3	4:A:125:LYS:O	2.19	0.43
6:g:254:G:H2'	6:g:255:G:H8	1.84	0.43
6:g:390:U:H2'	6:g:391:G:C8	2.54	0.43
6:g:625:U:H4'	14:y:16:PHE:CZ	2.53	0.43
6:g:1054:C:OP1	6:g:1196:A:H1'	2.18	0.43
6:g:1119:C:P	17:o:10:ARG:HH12	2.41	0.43
10:p:7:ALA:HB2	10:p:76:ARG:HD3	2.00	0.43
2:2:39:LYS:H	2:2:40:PRO:HD2	1.84	0.43
6:g:176:C:H2'	6:g:177:G:N3	2.33	0.43
6:g:433:G:C4	6:g:434:U:C5	3.07	0.43
6:g:1361:G:O2'	6:g:1362:A:OP1	2.28	0.43
16:m:110:ARG:HD3	16:m:118:ARG:CG	2.48	0.43
1:l:38:ILE:HG22	6:g:719:C:O2	2.19	0.43
6:g:1014:A:C2	6:g:1015:G:H1'	2.53	0.43
7:k:17:VAL:HG23	7:k:33:THR:O	2.18	0.43
8:l:187:ARG:HD2	8:l:190:LEU:HD11	2.01	0.43
15:h:25:THR:OG1	20:w:76:LYS:HG3	2.18	0.43
15:h:106:ARG:HG2	15:h:107:LYS:N	2.34	0.43
19:s:77:LYS:HA	19:s:80:MET:HE3	1.99	0.43
20:w:88:ALA:HB1	20:w:96:LEU:HD23	2.00	0.43
1:1:49:LYS:HE3	6:g:835:U:OP1	2.19	0.43
2:2:22:CYS:SG	6:g:1536:C:O2'	2.62	0.43
4:A:117:PHE:HB3	4:A:122:ASP:HB2	2.00	0.43
6:g:142:G:H8	6:g:142:G:OP2	2.02	0.43
6:g:318:G:C6	6:g:336:A:C6	3.07	0.43
6:g:455:G:H2'	6:g:456:A:C8	2.54	0.43
6:g:514:C:H2'	6:g:515:G:H8	1.83	0.43
6:g:524:G:C2	6:g:525:C:C4	3.06	0.43
6:g:683:G:H1	6:g:707:U:H3	1.67	0.43
6:g:780:A:O2'	6:g:781:A:H5''	2.19	0.43
6:g:1246:A:H5''	6:g:1247:U:OP2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:1274:A:HO2'	6:g:1275:A:P	2.37	0.43
8:l:149:LYS:HG3	8:l:150:LYS:N	2.34	0.43
8:l:151:GLN:O	8:l:154:VAL:HG22	2.19	0.43
18:r:91:ASP:OD1	18:r:91:ASP:N	2.51	0.43
19:s:91:ARG:HG3	19:s:91:ARG:NH1	2.34	0.43
6:g:432:A:C5	6:g:433:G:N7	2.87	0.43
6:g:558:G:H3'	6:g:559:A:H5'	2.01	0.43
6:g:1007:U:O2	6:g:1008:U:H5	2.02	0.43
6:g:1074:G:H2'	6:g:1075:U:C6	2.53	0.43
6:g:1081:A:H2'	6:g:1082:A:C8	2.54	0.43
6:g:1331:G:H1'	6:g:1332:A:H2	1.84	0.43
6:g:1356:G:H2'	6:g:1357:A:C8	2.53	0.43
6:g:1380:U:H4'	6:g:1381:U:OP1	2.18	0.43
7:k:81:GLN:HB2	7:k:146:MET:CE	2.49	0.43
11:q:63:GLN:HB3	11:q:94:SER:HB2	2.00	0.43
20:w:46:LEU:HD22	21:z:9:PHE:CD1	2.52	0.43
6:g:405:U:H1'	6:g:498:A:C8	2.54	0.43
6:g:438:U:H5	6:g:494:G:N7	2.17	0.43
6:g:598:U:H2'	6:g:599:C:H6	1.84	0.43
6:g:724:G:C2	6:g:725:G:C8	3.06	0.43
6:g:1184:G:C2	6:g:1185:G:C5	3.07	0.43
6:g:1444:U:H2'	6:g:1445:U:C6	2.54	0.43
7:k:76:ASN:HB2	7:k:81:GLN:HE21	1.83	0.43
20:w:67:THR:N	20:w:83:LYS:HZ3	2.17	0.43
6:g:459:A:H2'	6:g:460:A:H8	1.82	0.42
6:g:1009:U:N3	6:g:1020:G:N1	2.63	0.42
6:g:1027:C:H5''	6:g:1028:C:OP1	2.19	0.42
6:g:1055:A:N6	6:g:1200:C:C4	2.85	0.42
6:g:1458:G:H2'	6:g:1459:G:C8	2.52	0.42
9:n:41:ASP:OD2	9:n:58:HIS:NE2	2.43	0.42
11:q:96:ILE:HG13	11:q:97:ARG:N	2.33	0.42
15:h:133:MET:O	15:h:137:VAL:HG12	2.19	0.42
18:r:9:ARG:HG2	18:r:73:LEU:HD13	2.00	0.42
1:l:58:ILE:HG13	1:l:59:LYS:N	2.34	0.42
6:g:298:A:O2'	6:g:299:G:P	2.77	0.42
6:g:688:G:O2'	6:g:689:C:P	2.78	0.42
6:g:766:A:C6	6:g:814:A:C5	3.07	0.42
6:g:839:C:H2'	6:g:840:C:O4'	2.18	0.42
6:g:964:A:H2'	6:g:969:A:H4'	2.01	0.42
6:g:1347:G:H5''	17:o:108:ARG:HD2	2.01	0.42
22:j:89:PHE:CE2	22:j:153:MET:HB2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:49:LYS:NZ	1:1:52:ARG:HH12	2.17	0.42
3:3:48:LYS:O	3:3:52:GLU:OE1	2.36	0.42
4:A:111:LEU:O	4:A:115:ILE:HG13	2.19	0.42
6:g:275:G:C2	6:g:276:G:C8	3.08	0.42
6:g:851:G:C2	6:g:852:G:C8	3.07	0.42
6:g:993:G:H2'	6:g:993:G:N3	2.34	0.42
10:p:104:SER:HB2	10:p:123:GLU:HB2	2.00	0.42
21:z:49:ALA:HA	21:z:58:PRO:HA	2.01	0.42
2:2:5:VAL:O	11:q:92:ARG:HD3	2.20	0.42
6:g:750:C:O2'	13:u:22:GLY:N	2.49	0.42
6:g:836:G:N2	6:g:851:G:C4	2.86	0.42
6:g:1404:C:H2'	6:g:1405:G:H8	1.83	0.42
7:k:80:LEU:HA	7:k:80:LEU:HD12	1.46	0.42
15:h:71:ARG:HA	15:h:72:PRO:HD3	1.85	0.42
16:m:15:PRO:HG2	17:o:45:MET:HG2	2.00	0.42
19:s:57:ASP:O	19:s:61:LYS:HG3	2.18	0.42
4:A:57:SER:HB3	4:A:60:ALA:HB2	2.02	0.42
6:g:536:C:C4	6:g:537:G:N7	2.88	0.42
6:g:623:C:H2'	6:g:624:C:H6	1.83	0.42
6:g:1158:C:N4	6:g:1160:G:H8	2.18	0.42
6:g:1267:C:H41	6:g:1268:G:N2	2.17	0.42
6:g:1378:C:P	16:m:91:ARG:HH12	2.41	0.42
10:p:6:ILE:O	10:p:10:LEU:HD23	2.19	0.42
16:m:14:ASP:OD1	16:m:14:ASP:N	2.48	0.42
18:r:11:LYS:HA	18:r:71:LEU:HD23	2.02	0.42
2:2:46:ARG:NE	6:g:1529:G:OP2	2.29	0.42
4:A:69:ASP:O	4:A:73:PHE:HB3	2.19	0.42
4:A:79:LYS:NZ	6:g:700:G:OP2	2.46	0.42
6:g:171:A:H2'	6:g:172:A:O4'	2.20	0.42
6:g:216:U:H2'	6:g:217:C:C6	2.55	0.42
6:g:477:C:H2'	6:g:478:A:C4	2.54	0.42
6:g:771:G:H2'	6:g:772:U:H6	1.84	0.42
6:g:1036:A:H5'	6:g:1037:C:OP2	2.20	0.42
6:g:1291:U:O2	17:o:40:ARG:NH2	2.53	0.42
6:g:1343:G:N2	6:g:1349:A:O2'	2.51	0.42
7:k:22:LYS:HE3	7:k:24:VAL:HB	2.02	0.42
10:p:76:ARG:NE	10:p:78:SER:O	2.52	0.42
6:g:603:U:H2'	6:g:604:G:H8	1.84	0.42
6:g:648:A:H2'	6:g:649:A:H8	1.84	0.42
6:g:861:G:H2'	6:g:862:C:H6	1.85	0.42
6:g:1048:G:O2'	6:g:1049:U:H5''	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:1515:G:H2'	6:g:1516:G:C8	2.55	0.42
8:l:48:SER:O	8:l:52:VAL:HG23	2.20	0.42
10:p:13:ILE:HG13	10:p:14:ARG:N	2.34	0.42
12:t:98:ARG:NH1	12:t:103:CYS:SG	2.93	0.42
12:t:98:ARG:HB2	12:t:116:TYR:HA	2.02	0.42
14:y:19:VAL:HG12	14:y:37:GLY:C	2.45	0.42
14:y:59:HIS:O	14:y:63:GLN:HG2	2.20	0.42
22:j:187:ASP:OD1	22:j:190:SER:OG	2.23	0.42
1:l:49:LYS:HZ3	1:l:52:ARG:NH1	2.16	0.42
6:g:228:A:N3	6:g:228:A:H2'	2.35	0.42
6:g:915:A:H2'	6:g:916:U:H5'	2.01	0.42
6:g:1026:G:H2'	6:g:1026:G:N3	2.34	0.42
6:g:1118:U:H2'	6:g:1119:C:C6	2.55	0.42
15:h:44:LYS:HD2	15:h:44:LYS:HA	1.66	0.42
1:l:23:LYS:HZ2	9:n:100:SER:C	2.26	0.42
6:g:495:A:C4	6:g:496:A:C6	3.08	0.42
6:g:777:A:C4	6:g:778:G:C8	3.08	0.42
6:g:1222:G:H5'	6:g:1322:C:H42	1.85	0.42
7:k:39:GLY:HA3	7:k:116:VAL:HB	2.02	0.42
8:l:104:MET:HE2	8:l:170:LEU:HD21	2.02	0.42
11:q:86:LYS:HD3	11:q:113:THR:HA	2.00	0.42
20:w:57:PRO:HA	20:w:60:GLN:HB3	2.01	0.42
22:j:111:LYS:HB2	22:j:111:LYS:HE2	1.87	0.42
5:P:60:ILE:HD12	5:P:60:ILE:HA	1.88	0.42
6:g:71:A:N1	6:g:100:G:C4	2.88	0.42
6:g:297:G:H21	6:g:299:G:H8	1.68	0.42
6:g:505:G:C2	6:g:506:G:C5	3.08	0.42
6:g:718:A:C4	6:g:719:C:C5	3.08	0.42
6:g:1130:A:H2'	6:g:1131:G:O4'	2.20	0.42
6:g:1513:A:N6	6:g:1514:G:O6	2.53	0.42
6:g:1523:G:C5	6:g:1524:C:C5	3.07	0.42
8:l:61:ARG:HH21	8:l:67:LEU:HA	1.85	0.42
12:t:74:GLN:N	12:t:74:GLN:OE1	2.53	0.42
13:u:17:ASP:HB2	13:u:20:ASP:HB2	2.01	0.42
13:u:45:HIS:O	13:u:47:LYS:N	2.53	0.42
18:r:24:GLU:HG3	18:r:25:ILE:N	2.35	0.42
19:s:89:ARG:NH2	21:z:77:ARG:HH12	2.14	0.42
22:j:52:ALA:O	22:j:56:LEU:HD23	2.20	0.42
22:j:147:LEU:O	22:j:150:ILE:HG13	2.20	0.42
1:l:59:LYS:HA	1:l:62:ARG:HD2	2.02	0.41
4:A:161:PHE:CG	4:A:162:PRO:HD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:7:A:C8	7:k:123:LEU:HD21	2.55	0.41
6:g:448:A:N6	6:g:486:U:N3	2.40	0.41
6:g:517:G:N1	6:g:533:A:OP2	2.48	0.41
6:g:802:A:H2'	6:g:803:G:O4'	2.18	0.41
6:g:838:G:O2'	6:g:839:C:OP1	2.30	0.41
6:g:903:G:H2'	6:g:904:U:H6	1.85	0.41
15:h:86:LEU:HA	15:h:89:VAL:HG22	2.01	0.41
22:j:134:LEU:HD12	22:j:138:ARG:HG3	2.01	0.41
2:2:24:LYS:O	2:2:27:VAL:HG22	2.20	0.41
3:3:54:GLN:N	3:3:55:PRO:HD2	2.35	0.41
6:g:484:G:C5	6:g:486:U:H1'	2.55	0.41
6:g:1125:U:C5	6:g:1127:G:H1'	2.55	0.41
6:g:1240:U:C5	16:m:115:MET:HE3	2.54	0.41
6:g:1251:A:H1'	6:g:1370:G:H4'	2.01	0.41
6:g:1300:G:H4'	6:g:1301:U:H5'	2.02	0.41
9:n:42:TRP:HE3	9:n:59:TYR:HD2	1.68	0.41
16:m:24:LYS:HA	16:m:24:LYS:HD2	1.80	0.41
22:j:139:GLU:HG2	22:j:143:LEU:HD23	2.01	0.41
6:g:151:A:H3'	6:g:152:A:H8	1.85	0.41
6:g:737:C:H2'	6:g:738:C:C6	2.55	0.41
6:g:1074:G:H5'	22:j:102:ASN:HB3	2.01	0.41
6:g:1249:C:H1'	17:o:74:GLN:NE2	2.35	0.41
6:g:1431:A:C6	6:g:1432:G:C6	3.09	0.41
11:q:70:ALA:HA	11:q:73:VAL:HG22	2.02	0.41
6:g:532:A:O2'	6:g:533:A:H5''	2.21	0.41
6:g:802:A:C8	6:g:803:G:C8	3.09	0.41
6:g:916:U:H2'	6:g:917:G:C8	2.54	0.41
6:g:1202:U:O4'	20:w:69:ARG:NH1	2.53	0.41
6:g:1302:C:C6	19:s:16:ILE:HD11	2.54	0.41
20:w:85:ARG:HE	20:w:89:MET:HG3	1.85	0.41
4:A:25:ARG:HD2	4:A:64:VAL:HG22	2.02	0.41
5:P:64:ARG:HH11	6:g:130:A:H5'	1.85	0.41
6:g:77:A:N6	6:g:92:U:H3	2.19	0.41
6:g:252:U:O4	6:g:253:A:N6	2.41	0.41
6:g:406:G:C5	6:g:495:A:C2	3.08	0.41
6:g:704:A:H2'	6:g:705:G:C8	2.55	0.41
6:g:844:G:O2'	6:g:845:A:H2'	2.20	0.41
6:g:1076:U:H2'	6:g:1077:G:O4'	2.21	0.41
6:g:1205:U:H2'	6:g:1206:G:C8	2.55	0.41
17:o:45:MET:O	17:o:48:ARG:HG2	2.21	0.41
6:g:512:U:H2'	6:g:513:C:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:1187:G:N3	20:w:100:SER:OG	2.54	0.41
6:g:1523:G:N3	6:g:1523:G:H2'	2.36	0.41
8:l:124:VAL:HG23	8:l:141:VAL:O	2.21	0.41
12:t:23:LEU:C	12:t:24:GLU:OE1	2.64	0.41
12:t:113:ARG:NH1	12:t:118:VAL:HB	2.35	0.41
15:h:87:ARG:HG3	15:h:100:ILE:HG12	2.02	0.41
17:o:78:ILE:O	17:o:82:ILE:HG12	2.21	0.41
21:z:51:HIS:HB2	21:z:56:HIS:ND1	2.35	0.41
6:g:80:A:N6	6:g:90:C:H42	2.19	0.41
6:g:373:A:C2	6:g:482:A:C6	3.09	0.41
6:g:471:U:H2'	6:g:472:U:H6	1.85	0.41
6:g:598:U:H2'	6:g:599:C:C6	2.56	0.41
6:g:794:A:H2'	6:g:795:C:C6	2.56	0.41
6:g:810:C:H1'	6:g:899:C:H41	1.85	0.41
6:g:831:A:OP1	22:j:20:ARG:NH1	2.54	0.41
7:k:125:LYS:NZ	7:k:126:ALA:O	2.53	0.41
20:w:23:ARG:HD2	20:w:51:LEU:HD11	2.01	0.41
6:g:138:G:C6	6:g:226:G:C6	3.08	0.41
6:g:669:G:H2'	6:g:670:G:H8	1.86	0.41
6:g:922:G:C2	6:g:924:C:N4	2.86	0.41
6:g:1488:G:H2'	6:g:1489:G:H8	1.86	0.41
22:j:50:ASN:O	22:j:53:LEU:HG	2.21	0.41
4:A:99:ARG:HH21	4:A:129:ARG:CG	2.34	0.41
5:P:5:ARG:NH2	6:g:636:U:OP1	2.54	0.41
6:g:188:C:H6	6:g:188:C:H2'	1.72	0.41
6:g:515:G:H2'	6:g:516:U:C6	2.56	0.41
6:g:625:U:H4'	14:y:16:PHE:CE1	2.55	0.41
6:g:765:G:C5	6:g:812:G:C2	3.09	0.41
6:g:1047:G:N2	6:g:1214:C:O2'	2.54	0.41
6:g:1150:A:H2'	18:r:41:PRO:HB2	2.03	0.41
6:g:1331:G:H1'	6:g:1332:A:C2	2.55	0.41
6:g:1391:U:H2'	6:g:1392:G:H8	1.85	0.41
6:g:1499:A:C2	6:g:1500:A:C8	3.09	0.41
9:n:81:ASN:OD1	9:n:84:VAL:N	2.54	0.41
10:p:26:MET:HA	10:p:26:MET:HE2	2.03	0.41
10:p:125:ILE:HD13	10:p:125:ILE:HA	1.87	0.41
16:m:43:TYR:HD1	16:m:43:TYR:HA	1.74	0.41
17:o:14:SER:OG	17:o:68:GLY:O	2.38	0.41
17:o:20:ILE:HG12	17:o:62:LEU:HB3	2.03	0.41
19:s:78:ARG:HA	19:s:81:ASP:OD1	2.21	0.41
21:z:3:SER:O	21:z:4:LEU:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:j:84:LEU:HD13	22:j:90:PHE:CE1	2.56	0.41
6:g:6:G:N2	7:k:102:THR:HG21	2.36	0.41
6:g:24:U:H2'	6:g:25:C:H6	1.86	0.41
6:g:29:U:H5'	6:g:30:U:OP2	2.21	0.41
6:g:311:C:H2'	6:g:312:C:H6	1.85	0.41
6:g:533:A:N7	6:g:536:C:C4	2.89	0.41
6:g:1158:C:O2'	22:j:130:LYS:HB2	2.20	0.41
6:g:1307:U:C4	6:g:1330:U:C2	3.09	0.41
6:g:1319:A:O2'	6:g:1320:C:OP2	2.39	0.41
6:g:1443:C:H2'	6:g:1444:U:O4'	2.21	0.41
6:g:1526:G:O2'	6:g:1527:U:P	2.79	0.41
8:l:99:ASN:OD1	8:l:110:ARG:NH1	2.54	0.41
9:n:93:LYS:HE3	9:n:93:LYS:CA	2.41	0.41
11:q:19:VAL:HG12	11:q:82:GLU:HB3	2.03	0.41
13:u:5:GLU:OE1	13:u:5:GLU:N	2.48	0.41
16:m:74:VAL:HG12	16:m:87:PRO:HA	2.02	0.41
22:j:95:TRP:HZ3	22:j:170:ILE:HB	1.86	0.41
3:3:2:ASN:ND2	6:g:331:G:O2'	2.54	0.40
6:g:123:U:C2	6:g:124:C:C5	3.09	0.40
6:g:473:U:H2'	6:g:474:G:H8	1.85	0.40
6:g:621:A:N7	6:g:622:A:C5	2.89	0.40
6:g:791:G:H21	6:g:792:A:N6	2.20	0.40
6:g:968:A:OP2	6:g:1062:U:H4'	2.22	0.40
6:g:1368:A:OP2	17:o:113:LYS:HD2	2.21	0.40
8:l:169:TRP:CZ3	8:l:170:LEU:HB2	2.56	0.40
9:n:18:VAL:N	9:n:19:PRO:HD2	2.36	0.40
15:h:107:LYS:HE3	15:h:143:LEU:HD13	2.02	0.40
17:o:26:LYS:NZ	17:o:28:VAL:HG22	2.36	0.40
21:z:29:PRO:HA	21:z:47:THR:O	2.21	0.40
6:g:482:A:H2'	6:g:483:C:O4'	2.20	0.40
6:g:493:A:H2'	6:g:494:G:O4'	2.20	0.40
6:g:501:C:H2'	6:g:502:A:C8	2.55	0.40
6:g:778:G:C6	6:g:779:C:C4	3.08	0.40
6:g:815:A:O4'	6:g:817:C:N4	2.54	0.40
6:g:878:A:H2'	6:g:879:C:O4'	2.21	0.40
6:g:1073:U:O2'	22:j:104:LYS:HE3	2.21	0.40
6:g:1311:A:H61	6:g:1327:C:N4	2.19	0.40
6:g:1328:C:O2'	19:s:62:PHE:HE2	2.03	0.40
7:k:61:LYS:O	7:k:64:GLU:HG2	2.21	0.40
12:t:115:LYS:C	12:t:117:GLY:H	2.29	0.40
15:h:18:ASN:HB2	20:w:92:GLU:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:w:66:GLN:HB2	20:w:83:LYS:NZ	2.36	0.40
21:z:50:VAL:O	21:z:57:VAL:N	2.48	0.40
22:j:112:ARG:HD2	22:j:113:LEU:N	2.36	0.40
6:g:67:C:H2'	6:g:68:G:C8	2.56	0.40
6:g:123:U:H2'	6:g:124:C:H6	1.86	0.40
6:g:501:C:H2'	6:g:502:A:H8	1.86	0.40
6:g:581:G:C2	6:g:761:G:N1	2.90	0.40
6:g:1430:A:C4	6:g:1431:A:C8	3.10	0.40
6:g:1488:G:C2	6:g:1489:G:C5	3.10	0.40
11:q:22:ILE:O	11:q:86:LYS:N	2.55	0.40
17:o:21:LYS:O	17:o:61:ASP:HB3	2.21	0.40
18:r:46:LYS:HG3	18:r:68:ARG:HH22	1.87	0.40
1:l:25:ILE:HG23	1:l:67:LEU:HD21	2.02	0.40
6:g:191:G:H2'	6:g:192:A:H8	1.85	0.40
6:g:451:A:H1'	6:g:452:A:C8	2.57	0.40
6:g:513:C:C2	6:g:514:C:C5	3.09	0.40
6:g:739:C:O2'	13:u:41:HIS:ND1	2.52	0.40
6:g:1048:G:H4'	6:g:1049:U:C5	2.56	0.40
6:g:1181:G:H1'	6:g:1182:G:C4	2.56	0.40
21:z:18:VAL:HG22	21:z:43:MET:HE1	2.02	0.40
22:j:213:LEU:HA	22:j:216:VAL:HG22	2.03	0.40
1:l:51:GLN:HE21	1:l:51:GLN:HB3	1.73	0.40
4:A:41:GLU:O	4:A:44:GLU:HG3	2.21	0.40
6:g:533:A:O2'	6:g:534:U:H5''	2.21	0.40
6:g:587:G:N2	6:g:755:G:C4	2.89	0.40
6:g:707:U:O3'	11:q:21:HIS:NE2	2.55	0.40
6:g:712:A:H2'	6:g:713:G:O4'	2.21	0.40
6:g:767:A:O2'	6:g:1524:C:O2'	2.19	0.40
6:g:820:U:H4'	6:g:821:G:OP2	2.22	0.40
6:g:834:U:H2'	6:g:835:U:C6	2.57	0.40
6:g:932:C:H2'	6:g:933:G:C8	2.56	0.40
6:g:1052:U:O4	6:g:1200:C:H2'	2.22	0.40
6:g:1214:C:H4'	6:g:1215:G:OP2	2.20	0.40
7:k:95:MET:HG2	7:k:124:ALA:HB2	2.04	0.40
8:l:146:GLU:OE1	8:l:146:GLU:N	2.54	0.40
11:q:37:GLN:HE22	11:q:39:ASN:CG	2.30	0.40
12:t:107:LYS:HE3	12:t:107:LYS:HB3	1.97	0.40
20:w:80:SER:OG	20:w:83:LYS:HE3	2.22	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	
1	1	53/73 (73%)	51 (96%)	2 (4%)	0	100	100
2	2	49/53 (92%)	36 (74%)	12 (24%)	1 (2%)	6	31
3	3	83/86 (96%)	79 (95%)	4 (5%)	0	100	100
4	A	165/180 (92%)	158 (96%)	7 (4%)	0	100	100
5	P	78/82 (95%)	69 (88%)	8 (10%)	1 (1%)	9	41
7	k	148/158 (94%)	132 (89%)	15 (10%)	1 (1%)	18	55
8	l	203/205 (99%)	186 (92%)	17 (8%)	0	100	100
9	n	98/100 (98%)	82 (84%)	16 (16%)	0	100	100
10	p	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
11	q	115/128 (90%)	106 (92%)	9 (8%)	0	100	100
12	t	121/123 (98%)	104 (86%)	17 (14%)	0	100	100
13	u	86/88 (98%)	80 (93%)	4 (5%)	2 (2%)	5	28
14	y	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
15	h	204/206 (99%)	190 (93%)	13 (6%)	1 (0%)	24	63
16	m	149/151 (99%)	141 (95%)	8 (5%)	0	100	100
17	o	125/129 (97%)	114 (91%)	10 (8%)	1 (1%)	16	53
18	r	96/102 (94%)	87 (91%)	6 (6%)	3 (3%)	3	22
19	s	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
20	w	92/100 (92%)	85 (92%)	7 (8%)	0	100	100
21	z	77/80 (96%)	71 (92%)	6 (8%)	0	100	100
22	j	216/225 (96%)	198 (92%)	18 (8%)	0	100	100
All	All	2477/2594 (96%)	2268 (92%)	199 (8%)	10 (0%)	31	67

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	2	39	LYS
18	r	57	VAL
13	u	46	LYS
17	o	57	VAL
18	r	36	VAL
7	k	100	GLU
13	u	87	ARG
15	h	65	VAL
5	P	12	VAL
18	r	6	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	
1	1	48/63 (76%)	48 (100%)	0	100	100
2	2	44/46 (96%)	44 (100%)	0	100	100
3	3	65/65 (100%)	65 (100%)	0	100	100
4	A	146/156 (94%)	146 (100%)	0	100	100
5	P	74/76 (97%)	74 (100%)	0	100	100
7	k	113/118 (96%)	113 (100%)	0	100	100
8	l	172/172 (100%)	172 (100%)	0	100	100
9	n	87/87 (100%)	87 (100%)	0	100	100
10	p	104/104 (100%)	104 (100%)	0	100	100
11	q	90/98 (92%)	90 (100%)	0	100	100
12	t	103/103 (100%)	103 (100%)	0	100	100
13	u	76/76 (100%)	76 (100%)	0	100	100
14	y	65/65 (100%)	65 (100%)	0	100	100
15	h	170/170 (100%)	170 (100%)	0	100	100
16	m	124/124 (100%)	124 (100%)	0	100	100
17	o	105/106 (99%)	105 (100%)	0	100	100
18	r	86/90 (96%)	86 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	s	92/92 (100%)	92 (100%)	0	100	100
20	w	79/83 (95%)	79 (100%)	0	100	100
21	z	70/71 (99%)	70 (100%)	0	100	100
22	j	180/186 (97%)	180 (100%)	0	100	100
All	All	2093/2151 (97%)	2093 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
3	3	12	GLN
3	3	47	GLN
3	3	60	GLN
7	k	120	HIS
8	l	58	GLN
8	l	88	ASN
11	q	37	GLN
11	q	39	ASN
12	t	95	HIS
14	y	9	HIS
15	h	139	ASN
16	m	27	ASN
16	m	51	GLN
16	m	96	ASN
18	r	58	ASN
18	r	70	HIS
19	s	90	HIS
20	w	66	GLN
21	z	51	HIS
21	z	56	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	g	1538/1540 (99%)	563 (36%)	0

All (563) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	g	3	A
6	g	5	U
6	g	6	G
6	g	8	A
6	g	9	G
6	g	14	U
6	g	16	A
6	g	22	G
6	g	26	A
6	g	30	U
6	g	31	G
6	g	32	A
6	g	33	A
6	g	47	C
6	g	48	C
6	g	50	A
6	g	51	A
6	g	55	A
6	g	56	U
6	g	72	A
6	g	73	C
6	g	74	A
6	g	77	A
6	g	79	G
6	g	81	A
6	g	82	G
6	g	83	C
6	g	84	U
6	g	86	G
6	g	93	U
6	g	94	G
6	g	108	G
6	g	110	C
6	g	116	A
6	g	121	U
6	g	122	G
6	g	129	A
6	g	131	A
6	g	134	G
6	g	140	U
6	g	142	G
6	g	144	G
6	g	153	C

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Mol	Chain	Res	Type
6	g	163	C
6	g	182	A
6	g	183	C
6	g	184	G
6	g	188	C
6	g	189	A
6	g	190	A
6	g	195	A
6	g	196	A
6	g	198	G
6	g	201	G
6	g	209	U
6	g	210	C
6	g	219	U
6	g	223	A
6	g	224	U
6	g	226	G
6	g	228	A
6	g	229	U
6	g	240	G
6	g	244	U
6	g	245	U
6	g	247	G
6	g	251	G
6	g	254	G
6	g	257	G
6	g	258	G
6	g	260	G
6	g	261	U
6	g	262	A
6	g	265	G
6	g	266	G
6	g	267	C
6	g	268	U
6	g	281	G
6	g	288	A
6	g	289	G
6	g	293	G
6	g	299	G
6	g	303	A
6	g	306	A
6	g	315	A

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Mol	Chain	Res	Type
6	g	319	G
6	g	321	A
6	g	322	C
6	g	328	C
6	g	329	A
6	g	332	G
6	g	340	U
6	g	344	A
6	g	345	C
6	g	351	G
6	g	352	C
6	g	353	A
6	g	354	G
6	g	355	C
6	g	367	U
6	g	368	U
6	g	369	G
6	g	372	C
6	g	373	A
6	g	386	C
6	g	390	U
6	g	392	C
6	g	393	A
6	g	397	A
6	g	398	U
6	g	399	G
6	g	401	C
6	g	406	G
6	g	407	U
6	g	411	A
6	g	412	A
6	g	413	G
6	g	414	A
6	g	418	C
6	g	423	G
6	g	424	G
6	g	429	U
6	g	435	A
6	g	438	U
6	g	439	U
6	g	440	C
6	g	450	G

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Mol	Chain	Res	Type
6	g	454	G
6	g	462	G
6	g	466	A
6	g	467	U
6	g	468	A
6	g	469	C
6	g	476	U
6	g	478	A
6	g	479	U
6	g	480	U
6	g	481	G
6	g	482	A
6	g	486	U
6	g	487	A
6	g	493	A
6	g	495	A
6	g	497	G
6	g	499	A
6	g	502	A
6	g	505	G
6	g	508	U
6	g	511	C
6	g	518	C
6	g	519	C
6	g	521	G
6	g	525	C
6	g	527	G
6	g	530	G
6	g	531	U
6	g	538	G
6	g	547	A
6	g	550	G
6	g	559	A
6	g	560	A
6	g	562	U
6	g	564	C
6	g	565	U
6	g	566	G
6	g	570	G
6	g	572	A
6	g	573	A
6	g	575	G

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Mol	Chain	Res	Type
6	g	576	C
6	g	577	G
6	g	579	A
6	g	596	A
6	g	606	G
6	g	609	A
6	g	610	U
6	g	621	A
6	g	623	C
6	g	628	G
6	g	629	A
6	g	632	U
6	g	644	U
6	g	650	G
6	g	653	U
6	g	655	A
6	g	665	A
6	g	675	A
6	g	678	U
6	g	685	G
6	g	687	A
6	g	688	G
6	g	689	C
6	g	690	G
6	g	691	G
6	g	692	U
6	g	693	G
6	g	694	A
6	g	695	A
6	g	698	G
6	g	702	A
6	g	703	G
6	g	704	A
6	g	709	U
6	g	710	G
6	g	714	G
6	g	717	U
6	g	718	A
6	g	719	C
6	g	721	G
6	g	722	G
6	g	723	U

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Mol	Chain	Res	Type
6	g	724	G
6	g	728	A
6	g	729	A
6	g	731	G
6	g	732	C
6	g	733	G
6	g	734	G
6	g	735	C
6	g	741	G
6	g	747	A
6	g	748	G
6	g	749	A
6	g	753	A
6	g	755	G
6	g	758	C
6	g	760	G
6	g	761	G
6	g	767	A
6	g	773	G
6	g	777	A
6	g	779	C
6	g	781	A
6	g	782	A
6	g	788	U
6	g	789	U
6	g	792	A
6	g	793	U
6	g	795	C
6	g	796	C
6	g	801	U
6	g	807	A
6	g	809	G
6	g	813	U
6	g	814	A
6	g	817	C
6	g	818	G
6	g	828	U
6	g	829	G
6	g	832	G
6	g	835	U
6	g	839	C
6	g	840	C

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Mol	Chain	Res	Type
6	g	841	C
6	g	842	U
6	g	843	U
6	g	844	G
6	g	845	A
6	g	846	G
6	g	849	G
6	g	850	U
6	g	851	G
6	g	855	U
6	g	864	A
6	g	870	U
6	g	871	U
6	g	872	A
6	g	873	A
6	g	879	C
6	g	880	C
6	g	884	U
6	g	889	A
6	g	890	G
6	g	891	U
6	g	907	A
6	g	913	A
6	g	914	A
6	g	917	G
6	g	919	A
6	g	920	A
6	g	921	U
6	g	922	G
6	g	923	A
6	g	924	C
6	g	925	G
6	g	927	G
6	g	929	G
6	g	933	G
6	g	934	C
6	g	935	A
6	g	938	A
6	g	941	G
6	g	942	G
6	g	945	G
6	g	951	G

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Mol	Chain	Res	Type
6	g	953	G
6	g	954	G
6	g	957	U
6	g	960	U
6	g	961	U
6	g	962	C
6	g	963	G
6	g	964	A
6	g	965	U
6	g	966	G
6	g	967	C
6	g	969	A
6	g	971	G
6	g	972	C
6	g	973	G
6	g	975	A
6	g	976	G
6	g	978	A
6	g	979	C
6	g	980	C
6	g	981	U
6	g	982	U
6	g	983	A
6	g	990	C
6	g	993	G
6	g	999	C
6	g	1001	C
6	g	1002	G
6	g	1004	A
6	g	1006	G
6	g	1007	U
6	g	1008	U
6	g	1009	U
6	g	1011	C
6	g	1015	G
6	g	1016	A
6	g	1017	U
6	g	1018	G
6	g	1019	A
6	g	1020	G
6	g	1021	A
6	g	1022	A

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Mol	Chain	Res	Type
6	g	1024	G
6	g	1027	C
6	g	1028	C
6	g	1029	U
6	g	1031	C
6	g	1032	G
6	g	1033	G
6	g	1034	G
6	g	1035	A
6	g	1036	A
6	g	1037	C
6	g	1042	A
6	g	1044	A
6	g	1045	C
6	g	1046	A
6	g	1047	G
6	g	1048	G
6	g	1049	U
6	g	1054	C
6	g	1056	U
6	g	1057	G
6	g	1058	G
6	g	1059	C
6	g	1060	U
6	g	1064	G
6	g	1070	U
6	g	1078	U
6	g	1079	G
6	g	1080	A
6	g	1081	A
6	g	1082	A
6	g	1084	G
6	g	1091	U
6	g	1094	G
6	g	1095	U
6	g	1096	C
6	g	1100	C
6	g	1101	A
6	g	1122	U
6	g	1124	G
6	g	1126	U
6	g	1127	G

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Mol	Chain	Res	Type
6	g	1128	C
6	g	1130	A
6	g	1132	C
6	g	1133	G
6	g	1135	U
6	g	1137	C
6	g	1138	G
6	g	1139	G
6	g	1142	G
6	g	1143	G
6	g	1144	G
6	g	1145	A
6	g	1146	A
6	g	1151	A
6	g	1152	A
6	g	1157	A
6	g	1159	U
6	g	1160	G
6	g	1161	C
6	g	1166	G
6	g	1167	A
6	g	1168	U
6	g	1176	A
6	g	1177	G
6	g	1178	G
6	g	1179	A
6	g	1180	A
6	g	1181	G
6	g	1183	U
6	g	1184	G
6	g	1193	G
6	g	1194	U
6	g	1197	A
6	g	1198	G
6	g	1201	A
6	g	1202	U
6	g	1205	U
6	g	1206	G
6	g	1207	G
6	g	1208	C
6	g	1211	U
6	g	1212	U

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Mol	Chain	Res	Type
6	g	1213	A
6	g	1214	C
6	g	1215	G
6	g	1217	C
6	g	1221	G
6	g	1222	G
6	g	1224	U
6	g	1226	C
6	g	1227	A
6	g	1235	U
6	g	1238	A
6	g	1240	U
6	g	1241	G
6	g	1243	C
6	g	1246	A
6	g	1247	U
6	g	1248	A
6	g	1250	A
6	g	1251	A
6	g	1252	A
6	g	1254	A
6	g	1255	G
6	g	1256	A
6	g	1257	A
6	g	1258	G
6	g	1260	G
6	g	1268	G
6	g	1270	G
6	g	1272	G
6	g	1274	A
6	g	1275	A
6	g	1276	G
6	g	1278	G
6	g	1279	G
6	g	1280	A
6	g	1281	C
6	g	1282	C
6	g	1283	U
6	g	1284	C
6	g	1285	A
6	g	1287	A
6	g	1289	A

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Mol	Chain	Res	Type
6	g	1294	G
6	g	1295	U
6	g	1297	G
6	g	1298	U
6	g	1299	A
6	g	1300	G
6	g	1301	U
6	g	1302	C
6	g	1305	G
6	g	1306	A
6	g	1307	U
6	g	1308	U
6	g	1311	A
6	g	1313	U
6	g	1315	U
6	g	1317	C
6	g	1318	A
6	g	1319	A
6	g	1320	C
6	g	1322	C
6	g	1326	U
6	g	1327	C
6	g	1329	A
6	g	1330	U
6	g	1331	G
6	g	1334	G
6	g	1336	C
6	g	1338	G
6	g	1340	A
6	g	1346	A
6	g	1347	G
6	g	1348	U
6	g	1349	A
6	g	1350	A
6	g	1355	G
6	g	1359	C
6	g	1360	A
6	g	1361	G
6	g	1362	A
6	g	1364	U
6	g	1373	G
6	g	1375	A

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Mol	Chain	Res	Type
6	g	1379	G
6	g	1380	U
6	g	1381	U
6	g	1382	C
6	g	1386	G
6	g	1390	U
6	g	1392	G
6	g	1394	A
6	g	1395	C
6	g	1398	A
6	g	1399	C
6	g	1401	G
6	g	1403	C
6	g	1404	C
6	g	1406	U
6	g	1410	A
6	g	1415	G
6	g	1419	G
6	g	1421	G
6	g	1423	G
6	g	1427	C
6	g	1440	U
6	g	1446	A
6	g	1448	C
6	g	1451	U
6	g	1453	G
6	g	1463	U
6	g	1470	U
6	g	1471	U
6	g	1477	U
6	g	1479	C
6	g	1487	G
6	g	1490	U
6	g	1491	G
6	g	1493	A
6	g	1496	C
6	g	1497	G
6	g	1498	U
6	g	1499	A
6	g	1502	A
6	g	1503	A
6	g	1504	G

Continued on next page...

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Mol	Chain	Res	Type
6	g	1505	G
6	g	1506	U
6	g	1507	A
6	g	1508	A
6	g	1516	G
6	g	1517	G
6	g	1520	C
6	g	1525	G
6	g	1527	U
6	g	1529	G
6	g	1530	G
6	g	1531	A
6	g	1533	C
6	g	1534	A
6	g	1537	U
6	g	1538	C

There are no RNA pucker outliers to report.

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.

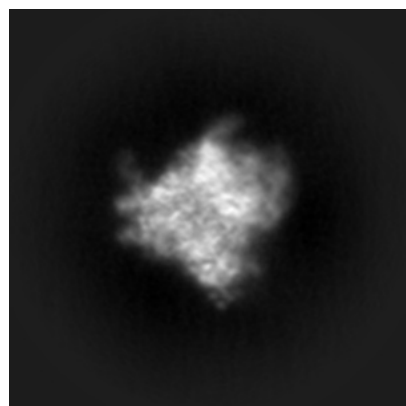
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36619. These allow visual inspection of the internal detail of the map and identification of artifacts.

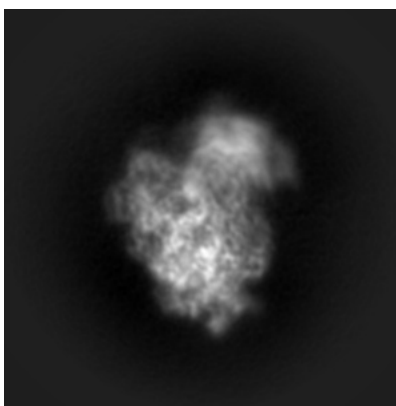
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

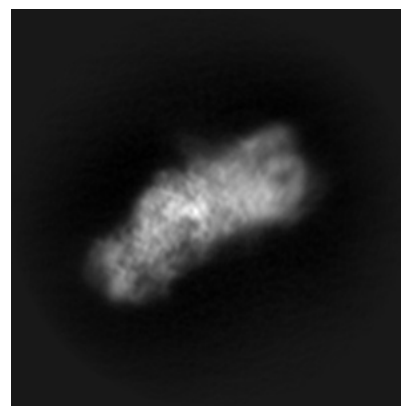
6.1.1 Primary map



X

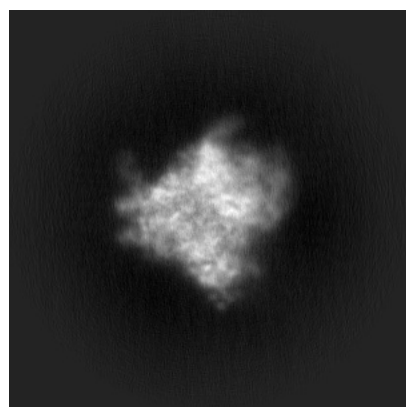


Y

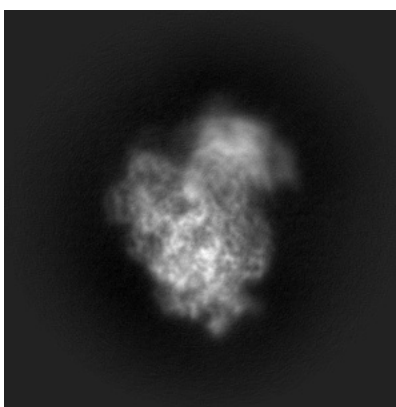


Z

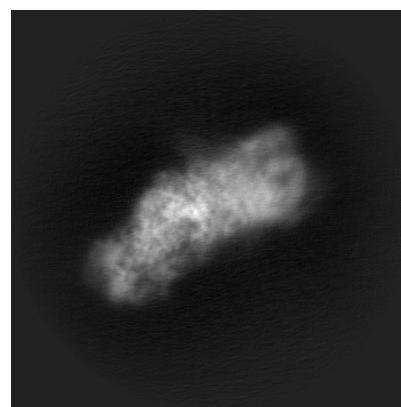
6.1.2 Raw map



X



Y

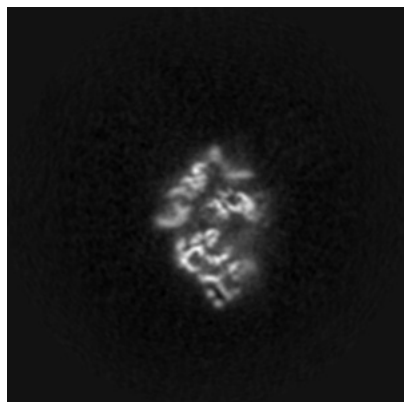


Z

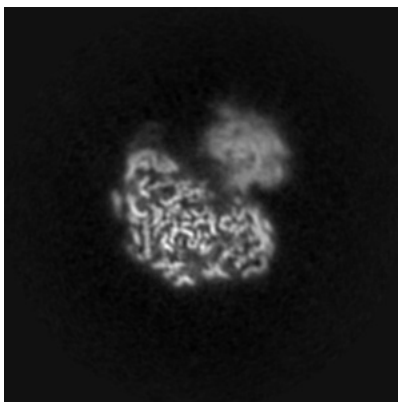
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

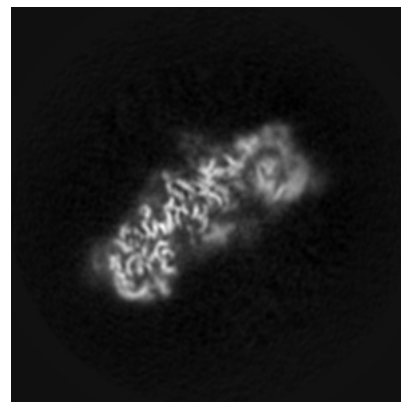
6.2.1 Primary map



X Index: 160



Y Index: 160

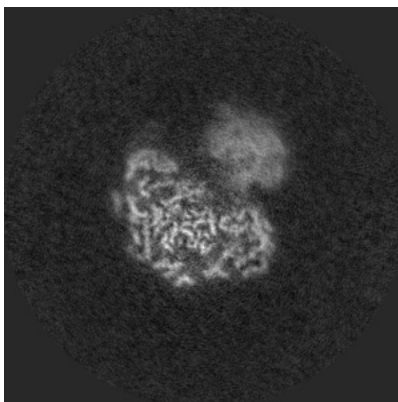


Z Index: 160

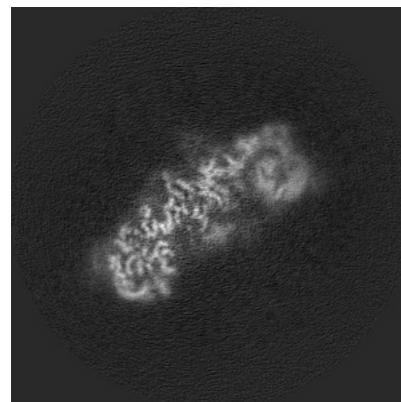
6.2.2 Raw map



X Index: 160



Y Index: 160

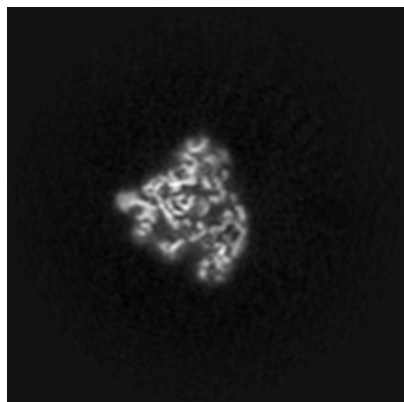


Z Index: 160

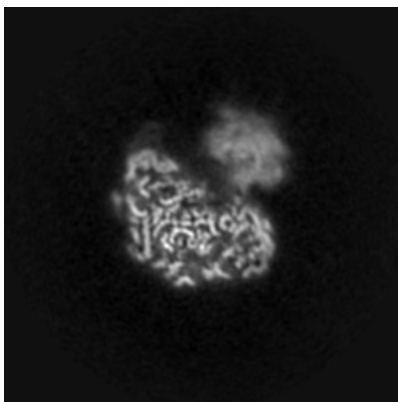
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

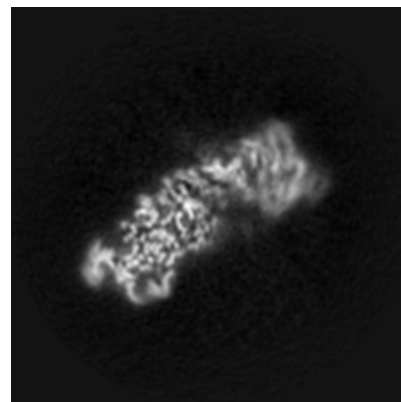
6.3.1 Primary map



X Index: 122

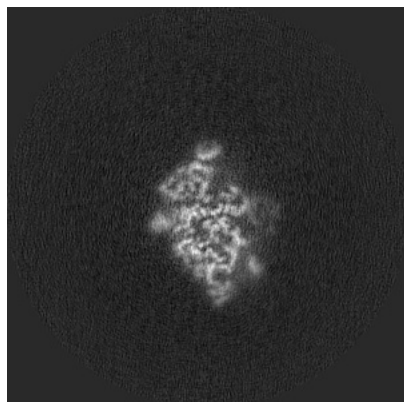


Y Index: 159

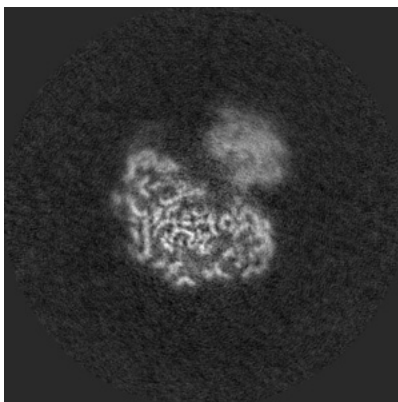


Z Index: 167

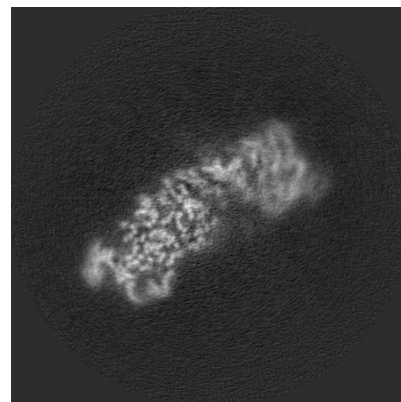
6.3.2 Raw map



X Index: 152



Y Index: 159

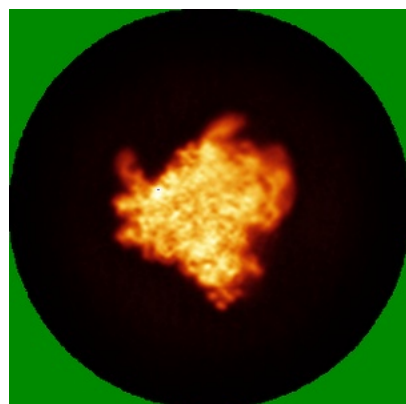


Z Index: 167

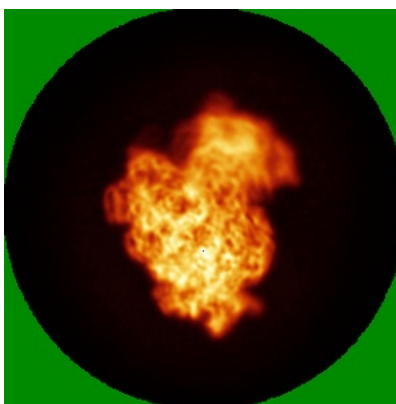
The images above show the largest variance slices of the map in three orthogonal directions.

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

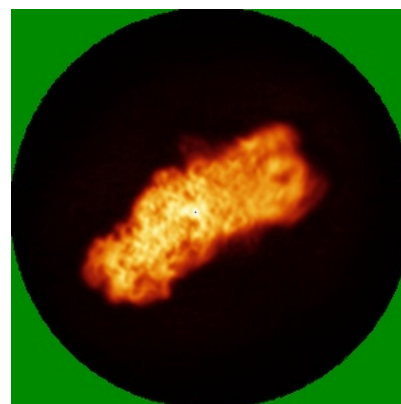
6.4.1 Primary map



X

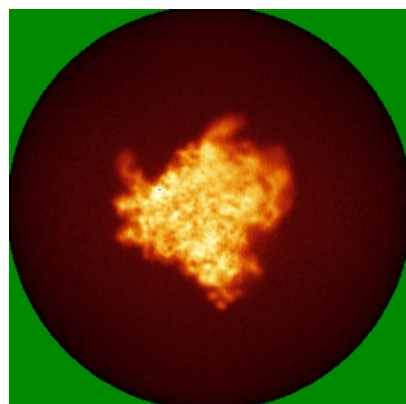


Y

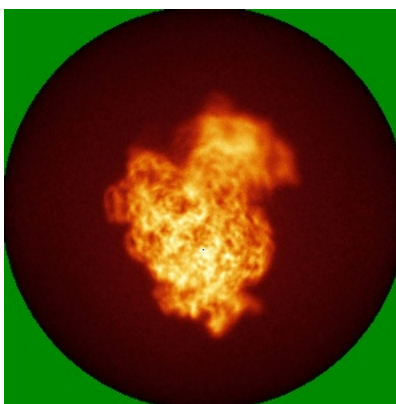


Z

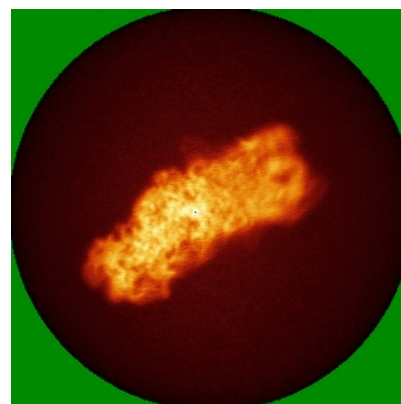
6.4.2 Raw map



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](#)

This section was not generated.

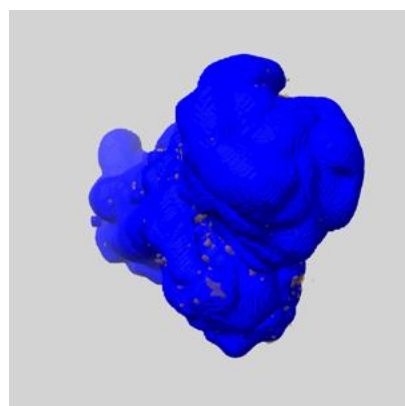
6.6 Mask visualisation [i](#)

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

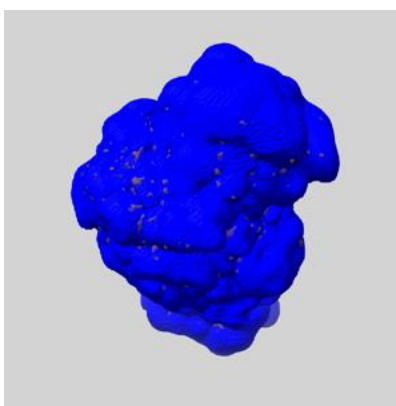
A mask typically either:

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

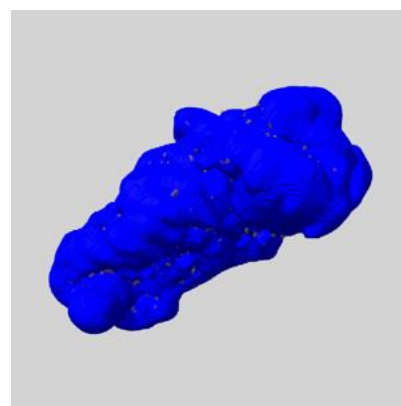
6.6.1 emd_36619_msk_1.map [i](#)



X



Y

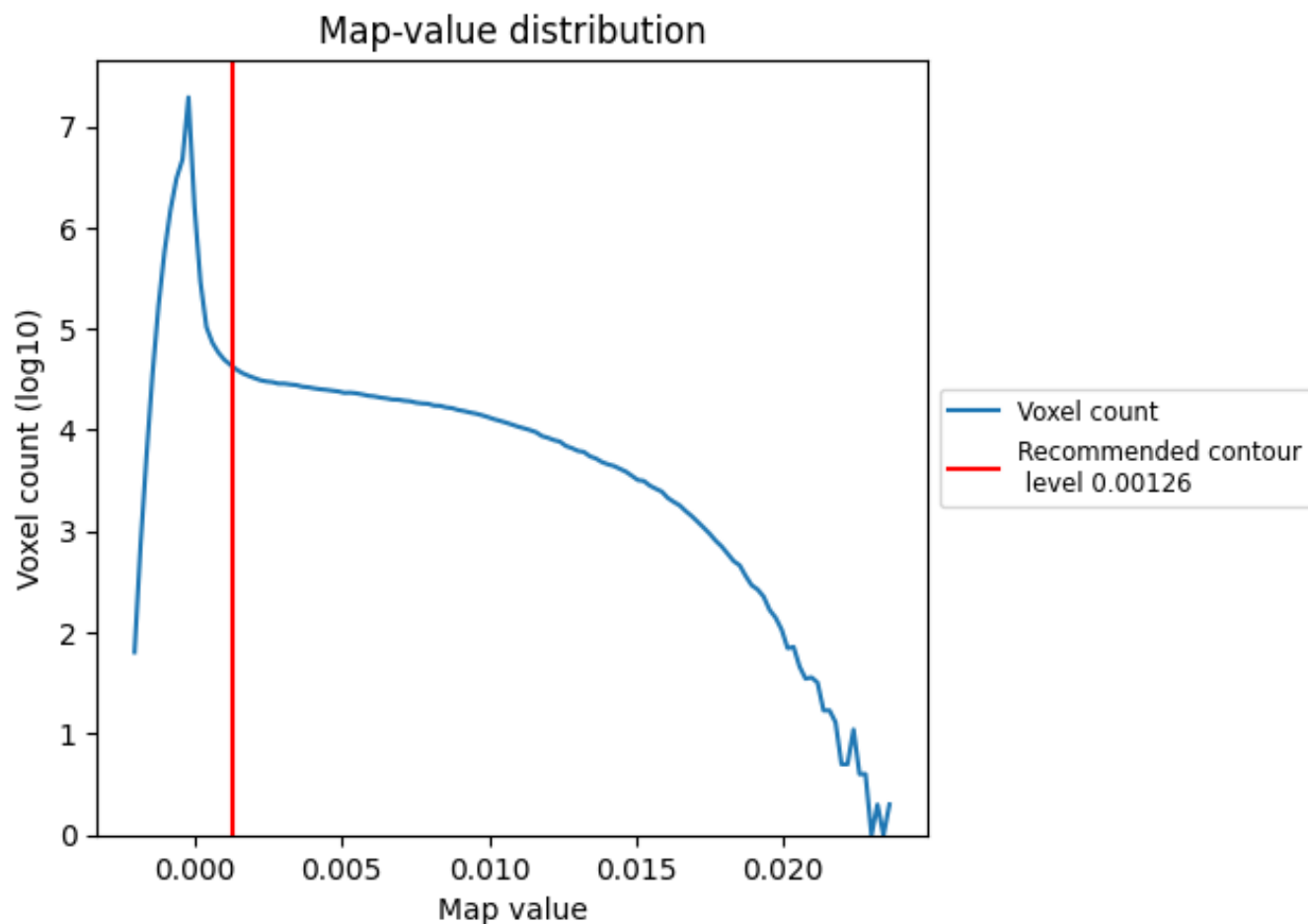


Z

7 Map analysis [i](#)

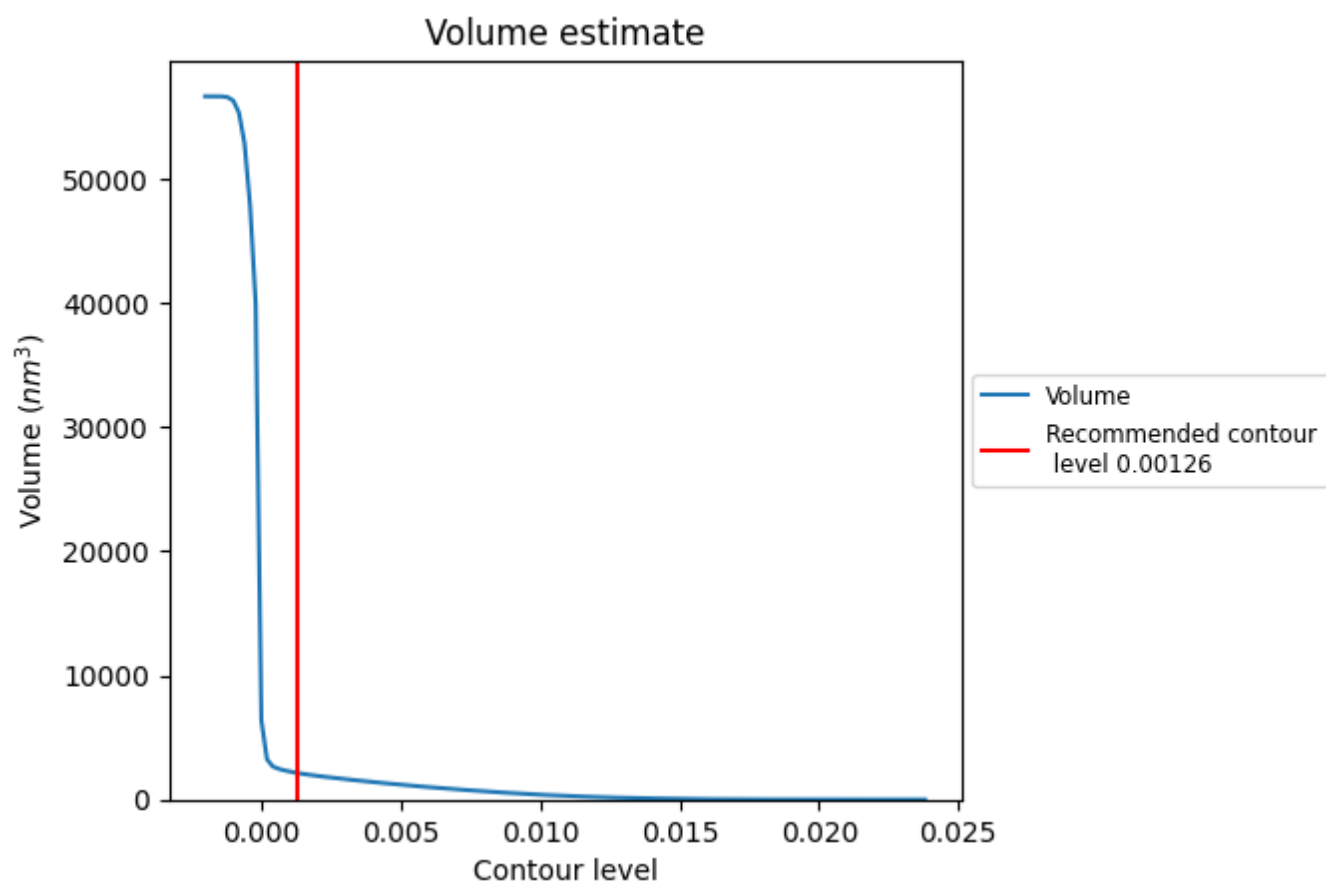
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

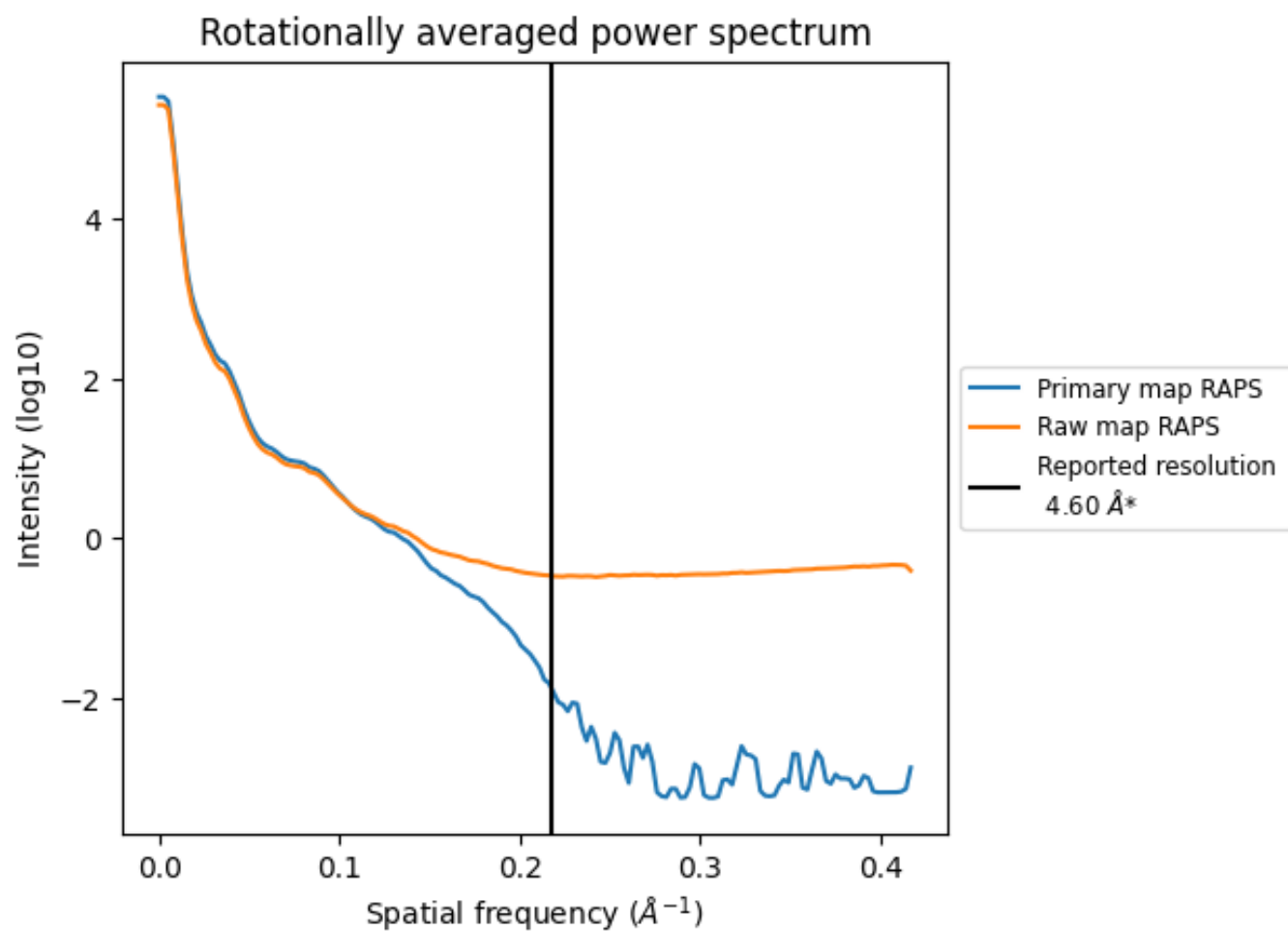
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2144 nm^3 ; this corresponds to an approximate mass of 1937 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

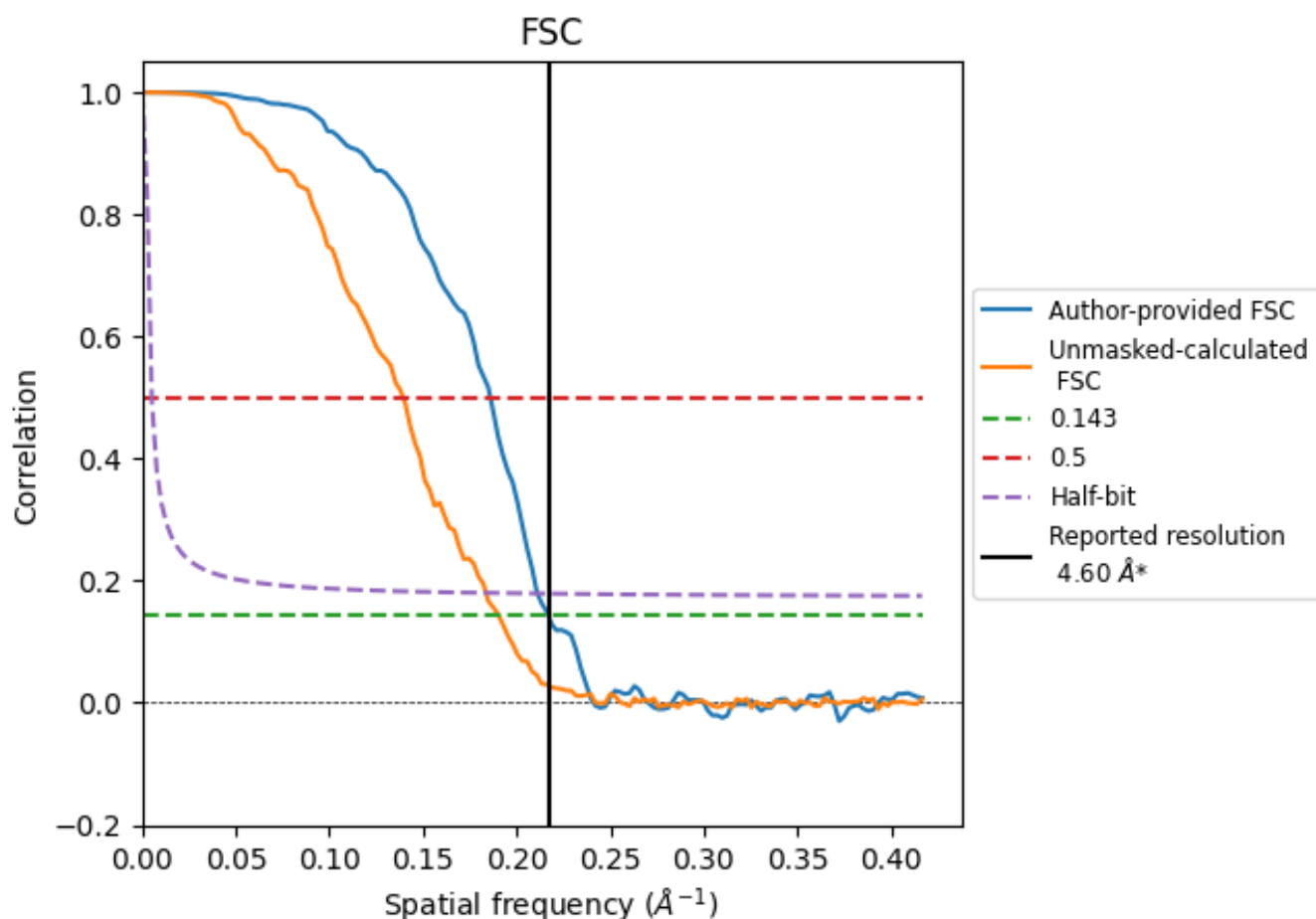


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

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 0.217 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

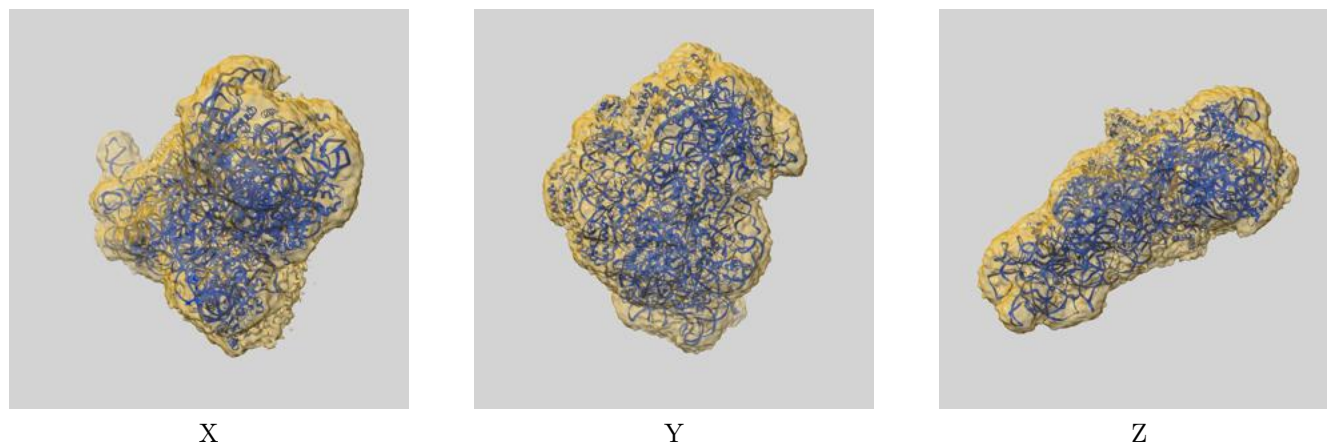
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.61	5.38	4.73
Unmasked-calculated*	5.25	7.17	5.44

*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 5.25 differs from the reported value 4.6 by more than 10 %

9 Map-model fit [i](#)

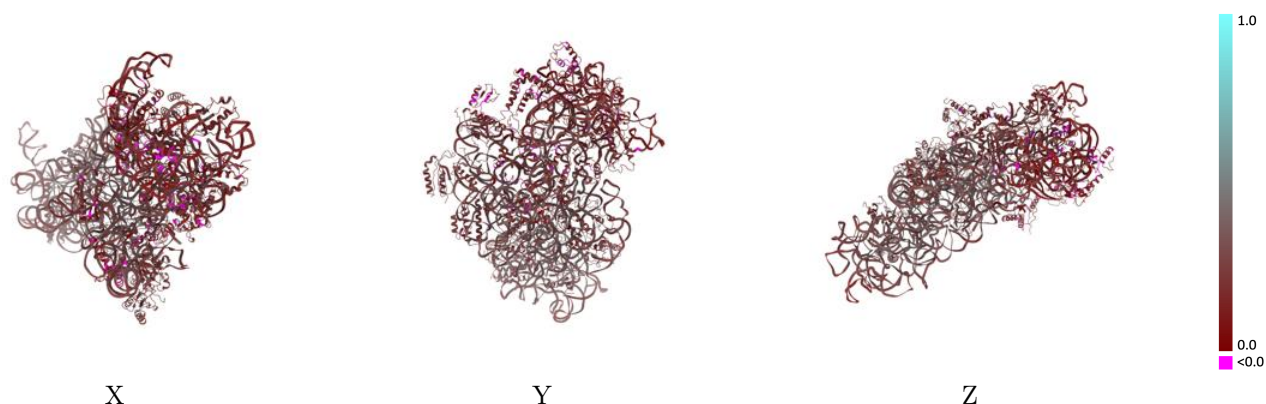
This section contains information regarding the fit between EMDB map EMD-36619 and PDB model 8JSG. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



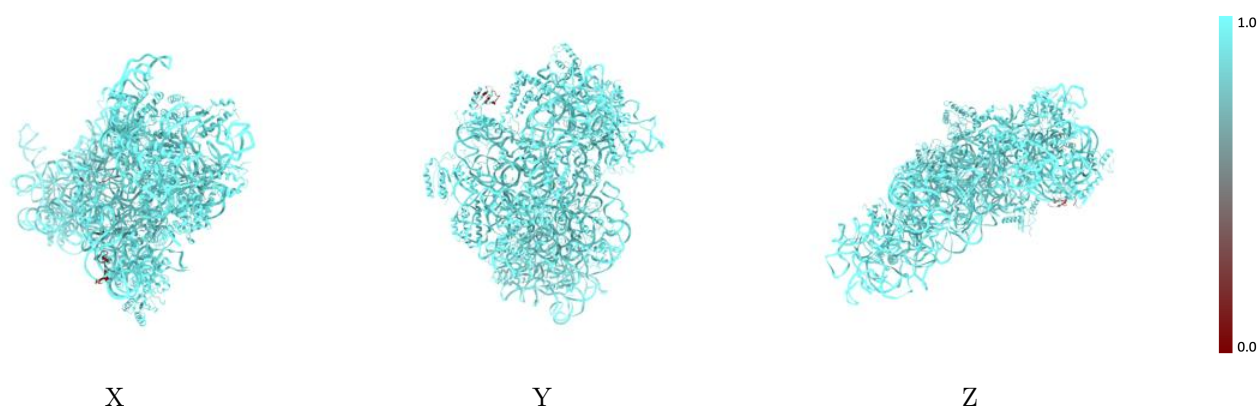
The images above show the 3D surface view of the map at the recommended contour level 0.00126 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



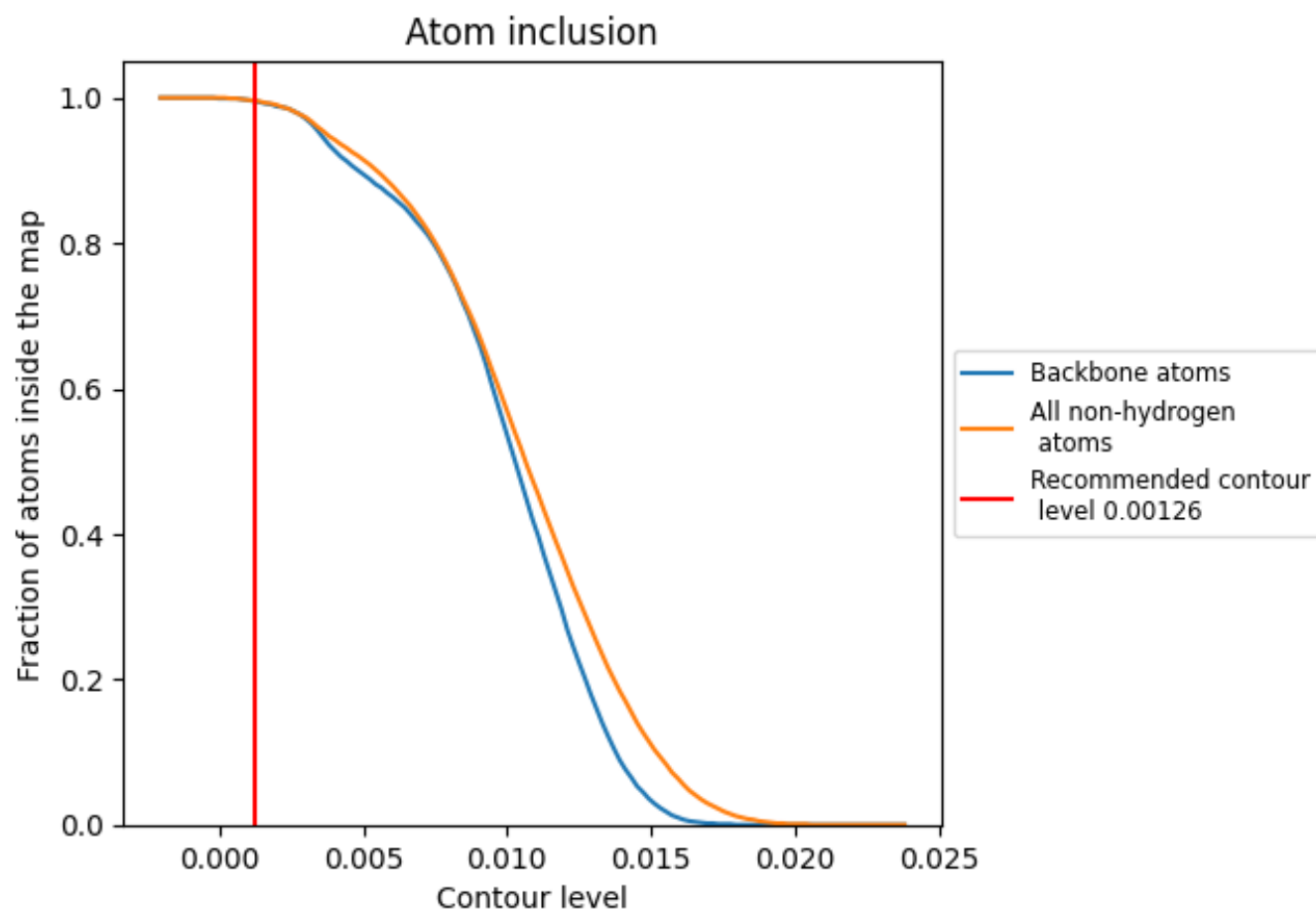
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00126).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.00126) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9960	 0.2650
1	 1.0000	 0.2820
2	 1.0000	 0.0730
3	 1.0000	 0.2600
A	 0.8590	 0.1680
P	 1.0000	 0.3160
g	 1.0000	 0.2870
h	 1.0000	 0.2420
j	 0.9970	 0.2110
k	 1.0000	 0.3070
l	 1.0000	 0.2700
m	 1.0000	 0.1540
n	 1.0000	 0.2640
o	 1.0000	 0.1680
p	 1.0000	 0.2920
q	 1.0000	 0.2560
r	 1.0000	 0.2070
s	 0.9640	 0.1120
t	 1.0000	 0.3230
u	 1.0000	 0.2580
w	 1.0000	 0.1770
y	 1.0000	 0.3020
z	 1.0000	 0.1170

