Full wwPDB EM Validation Report ⓘ

Nov 23, 2022 – 08:45 AM JST

PDB ID	:	7V2P
EMDB ID	:	EMD-31659
Title	:	T.thermophilus 30S ribosome with KsgA, class K5
Authors	:	Raina, R.; Singh, J.; Anand, R.; Vinothkumar, K.R.
Deposited on	:	2021-08-09
Resolution	:	3.30 Å(reported)
Based on initial model	:	4B3R

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:

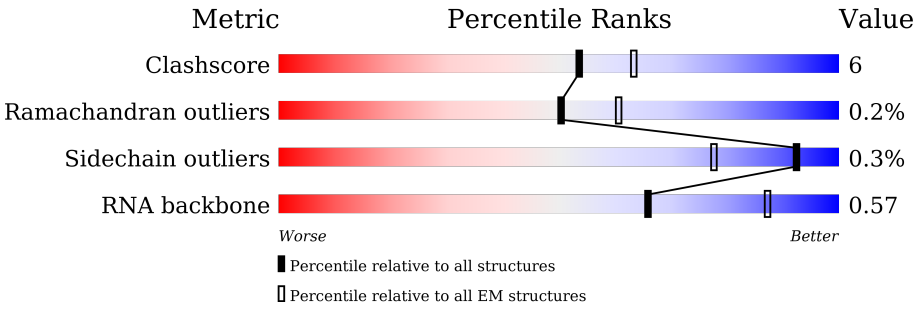
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 3.30 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	1522	59% 27% 6% 8%
2	B	256	73% 13% 14%
3	C	239	72% 14% 14%
4	D	209	88% 11%
5	E	162	79% 14% 7%
6	F	101	6% 84% 16%
7	G	156	83% 16%

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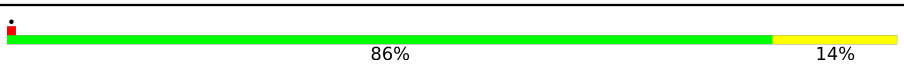
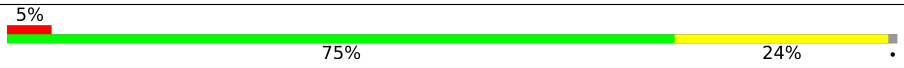
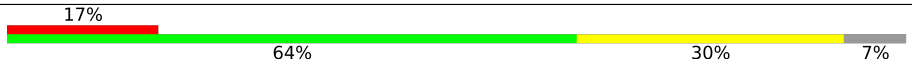
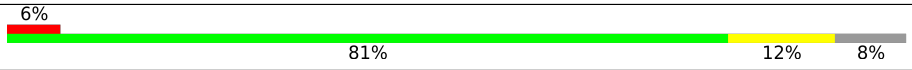
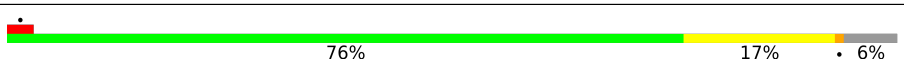
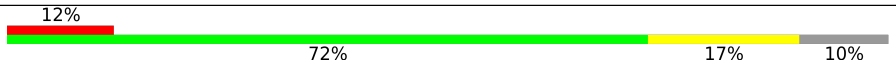
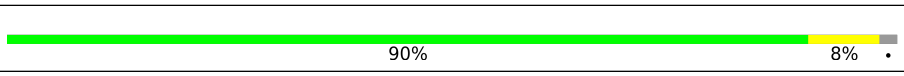
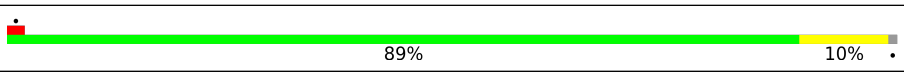
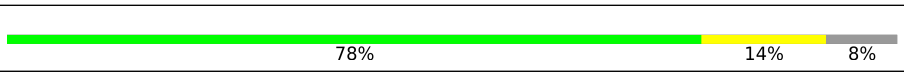
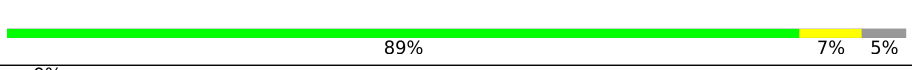
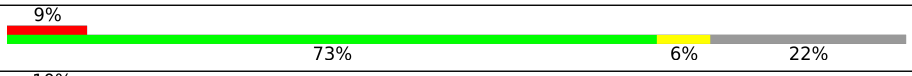
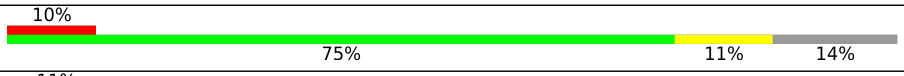
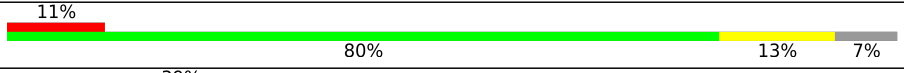
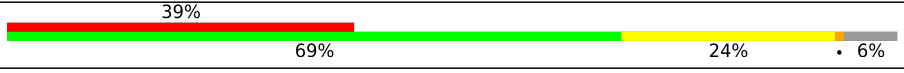
Mol	Chain	Length	Quality of chain
8	H	138	
9	I	128	
10	J	105	
11	K	129	
12	L	132	
13	M	126	
14	N	61	
15	O	89	
16	P	88	
17	Q	105	
18	R	88	
19	S	93	
20	T	106	
21	U	298	
22	V	27	

2 Entry composition (i)

There are 23 unique types of molecules in this entry. The entry contains 51135 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16s ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1394	29962	13336	5547	9685	1394	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	220	1802	1150	326	321	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	206	1612	1016	314	281	1	0	0

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	150	1146	724	217	201	4	0	0

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	127	Total	C	N	O	0	0
			1010	639	197	174		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	98	Total	C	N	O	S	0	0
			794	499	156	138	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	119	Total	C	N	O	S	0	0
			885	549	168	165	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	124	Total	C	N	O	S	0	0
			970	611	195	163	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	113	Total	C	N	O	S	0	0
			905	559	187	157	2		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	81	Total	C	N	O	S	0	0
			682	433	136	112	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	100	Total	C	N	O	S	0	0
			834	534	155	143	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	69	Total	C	N	O	0	0
			565	361	110	94		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	80	Total	C	N	O	S	0	0
			647	414	119	112	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	99	Total	C	N	O	S	0	0
			763	470	162	129	2		

- Molecule 21 is a protein called Ribosomal RNA small subunit methyltransferase A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	279	Total	C	N	O	S	0	0
			2203	1414	366	417	6		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	-5	HIS	-	expression tag	UNP P37468
U	-4	HIS	-	expression tag	UNP P37468
U	-3	HIS	-	expression tag	UNP P37468
U	-2	HIS	-	expression tag	UNP P37468
U	-1	HIS	-	expression tag	UNP P37468
U	0	HIS	-	expression tag	UNP P37468

- Molecule 22 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	V	24	Total	C	N	O	0	0
			208	128	50	30		

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

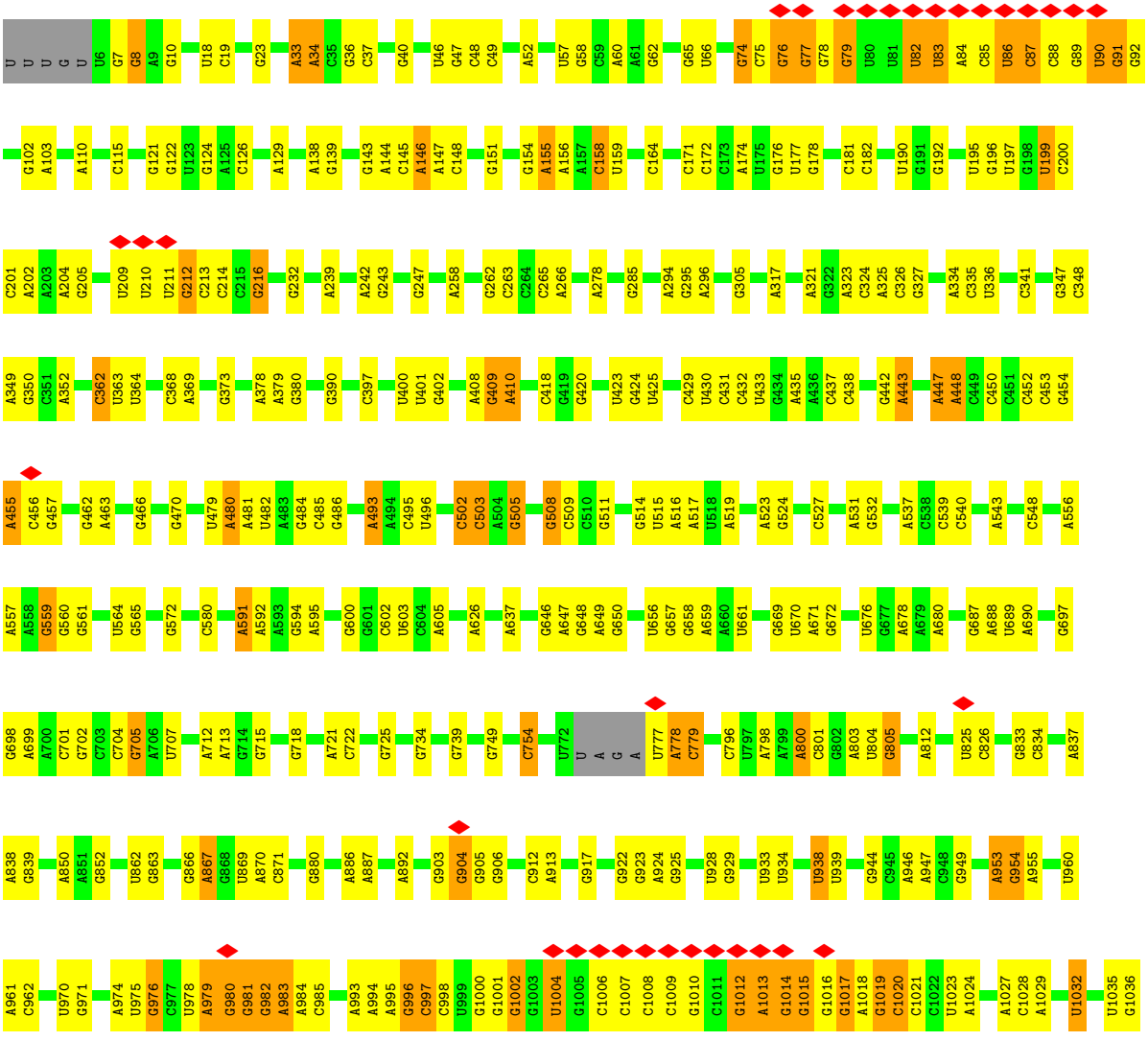
Mol	Chain	Residues	Atoms		AltConf
23	D	1	Total	Zn	0
			1	1	
23	N	1	Total	Zn	0
			1	1	

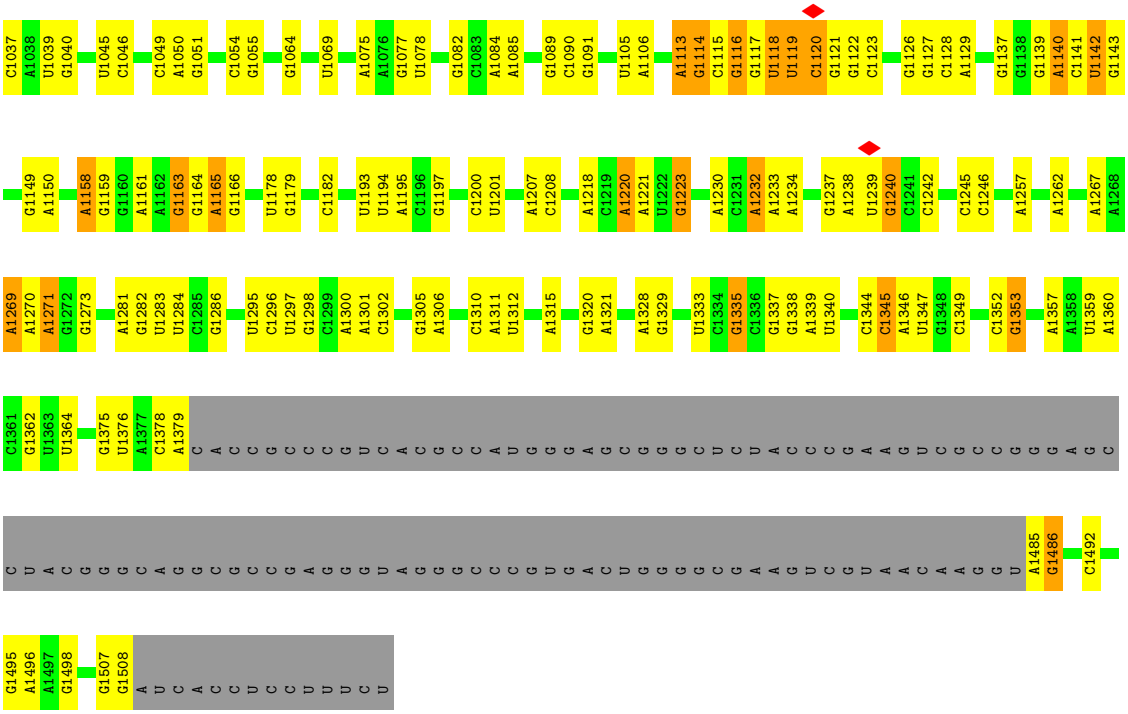
3 Residue-property plots (i)

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

- Molecule 1: 16s ribosomal RNA

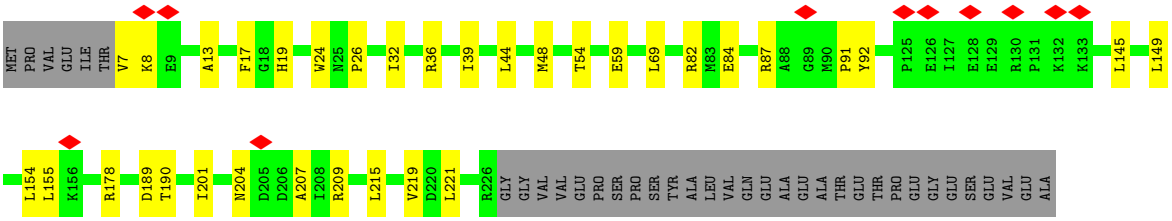
Chain A:





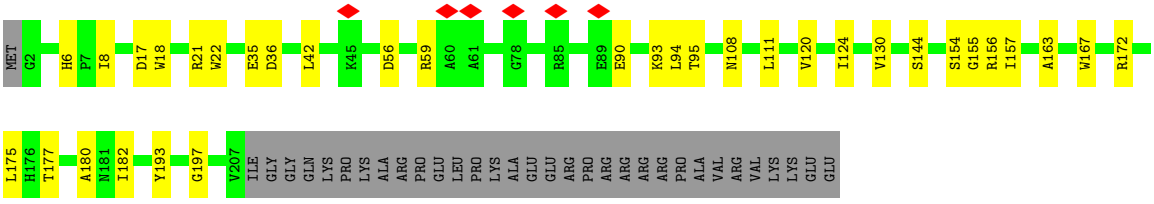
• Molecule 2: 30S ribosomal protein S2

Chain B:



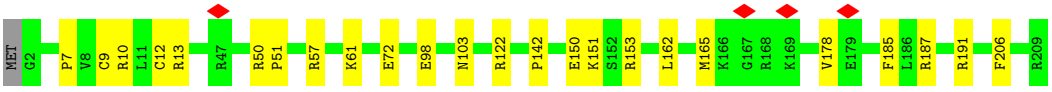
• Molecule 3: 30S ribosomal protein S3

Chain C:



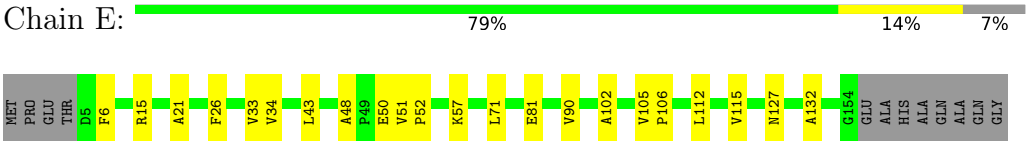
• Molecule 4: 30S ribosomal protein S4

Chain D:



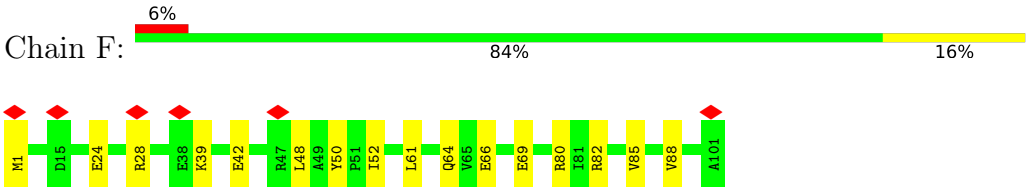
• Molecule 5: 30S ribosomal protein S5

Chain E:



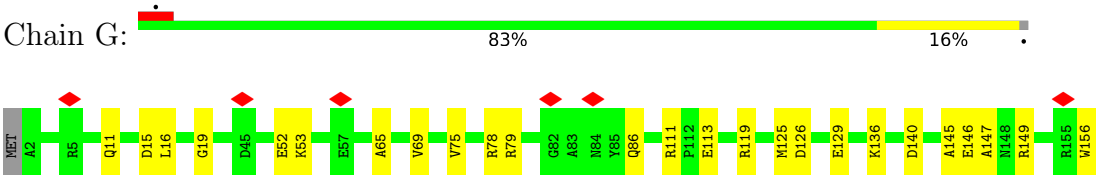
• Molecule 6: 30S ribosomal protein S6

Chain F:



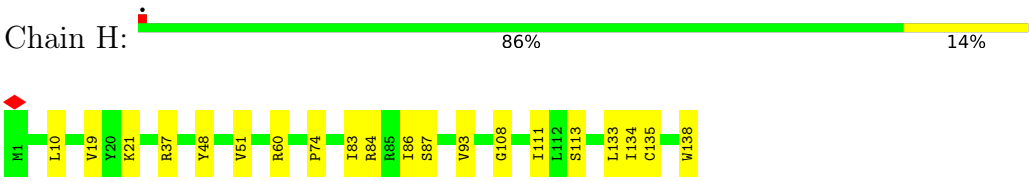
• Molecule 7: 30S ribosomal protein S7

Chain G:



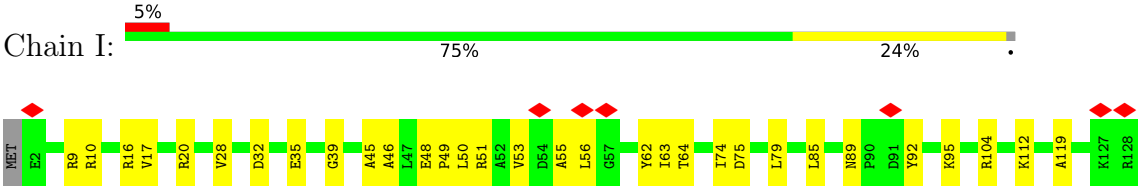
• Molecule 8: 30S ribosomal protein S8

Chain H:



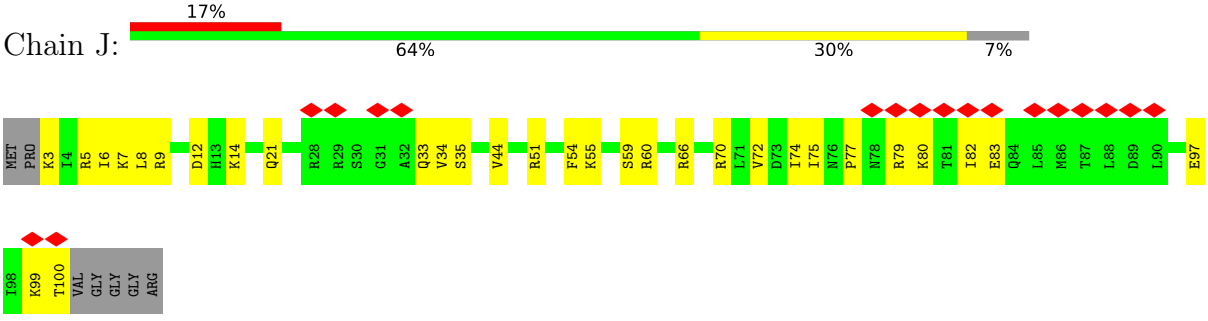
• Molecule 9: 30S ribosomal protein S9

Chain I:



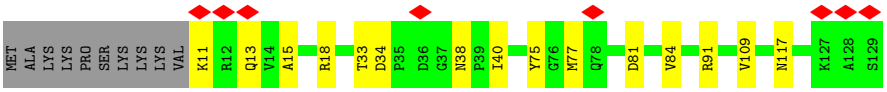
• Molecule 10: 30S ribosomal protein S10

Chain J:



• Molecule 11: 30S ribosomal protein S11

Chain K:

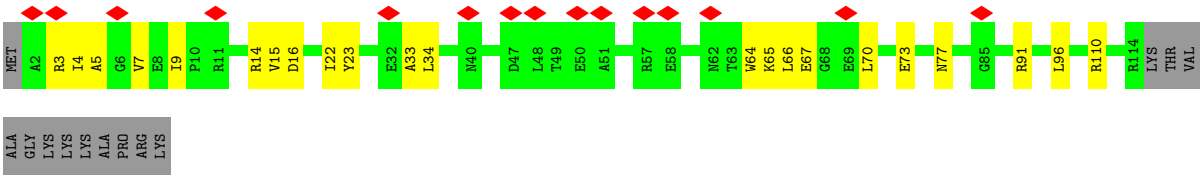


• Molecule 12: 30S ribosomal protein S12

Chain L:

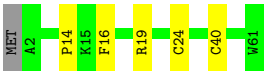
• Molecule 13: 30S ribosomal protein S13

Chain M:



• Molecule 14: 30S ribosomal protein S14 type Z

Chain N:



• Molecule 15: 30S ribosomal protein S15

Chain O:

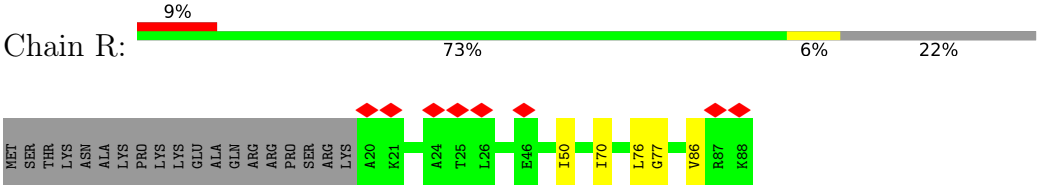
• Molecule 16: 30S ribosomal protein S16

Chain P:

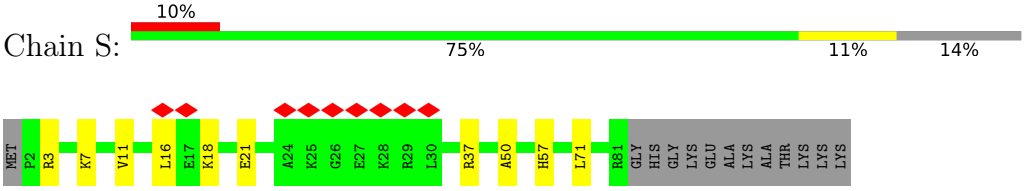
• Molecule 17: 30S ribosomal protein S17

Chain Q:

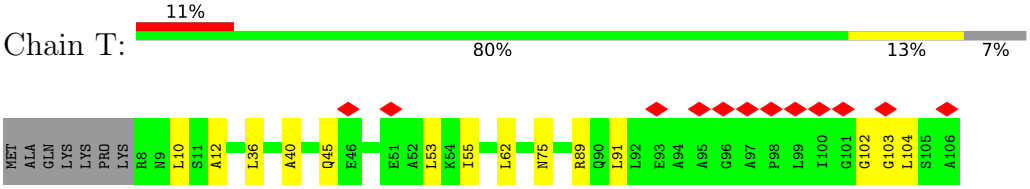
• Molecule 18: 30S ribosomal protein S18



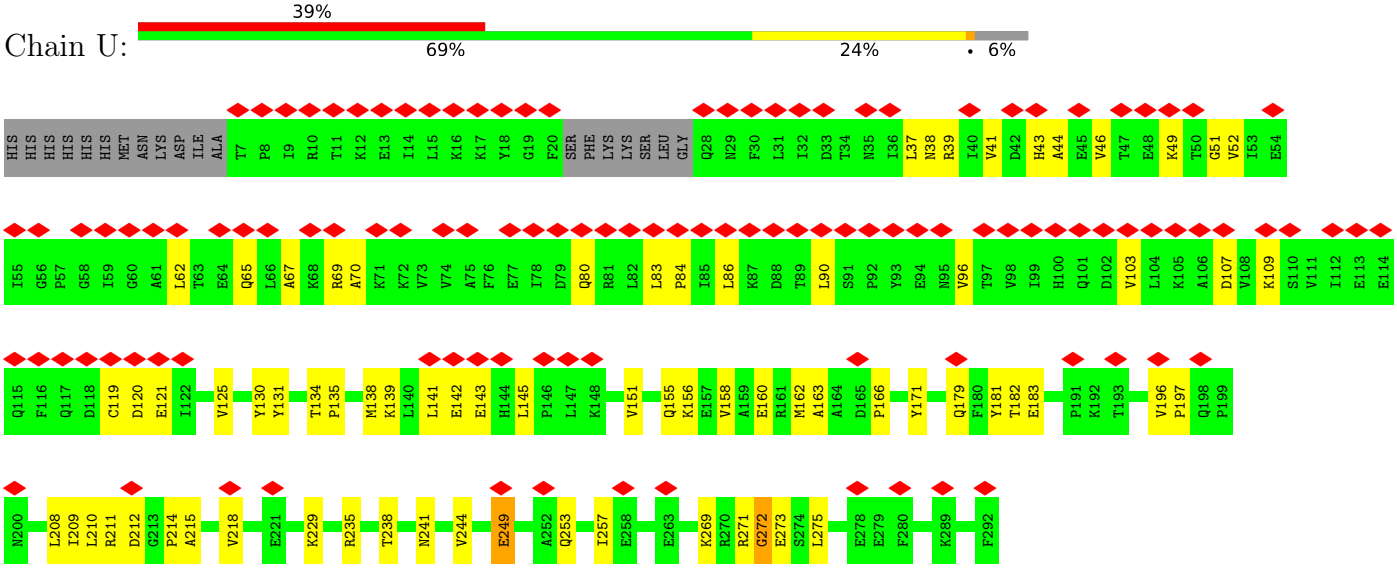
• Molecule 19: 30S ribosomal protein S19



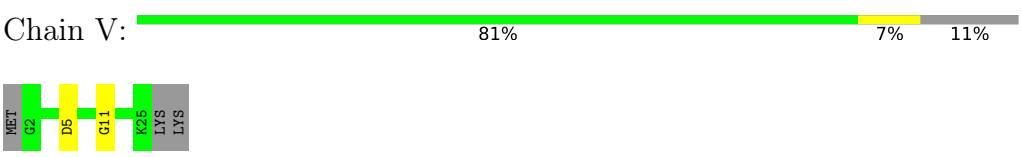
• Molecule 20: 30S ribosomal protein S20



• Molecule 21: Ribosomal RNA small subunit methyltransferase A



• Molecule 22: 30S ribosomal protein Thx



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	102297	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	43.0	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	101449	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.468	Depositor
Minimum map value	-0.148	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.075	Depositor
Map size (Å)	441.6, 441.6, 441.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.55	0/33537	0.80	1/52338 (0.0%)
2	B	0.25	0/1834	0.55	0/2469
3	C	0.26	0/1636	0.56	0/2205
4	D	0.27	0/1733	0.54	0/2318
5	E	0.27	0/1162	0.57	0/1564
6	F	0.25	0/856	0.57	0/1154
7	G	0.25	0/1276	0.57	0/1709
8	H	0.26	0/1136	0.56	0/1527
9	I	0.27	0/1029	0.59	0/1379
10	J	0.26	0/807	0.59	0/1085
11	K	0.27	0/900	0.57	0/1213
12	L	0.26	0/986	0.59	0/1320
13	M	0.26	0/915	0.60	0/1227
14	N	0.26	0/501	0.54	0/664
15	O	0.25	0/745	0.55	0/992
16	P	0.25	0/698	0.56	0/939
17	Q	0.26	0/847	0.54	0/1131
18	R	0.25	0/570	0.56	0/757
19	S	0.26	0/661	0.57	0/890
20	T	0.27	0/765	0.59	0/1007
21	U	0.26	0/2236	0.57	0/3026
22	V	0.31	0/212	0.60	0/277
All	All	0.46	0/55042	0.72	1/81191 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	232	G	C6-N1-C2	-5.01	122.09	125.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	29962	0	15122	223	0
2	B	1802	0	1855	26	0
3	C	1612	0	1677	23	0
4	D	1703	0	1764	14	0
5	E	1146	0	1207	12	0
6	F	843	0	857	9	0
7	G	1257	0	1296	15	0
8	H	1116	0	1177	12	0
9	I	1010	0	1037	20	0
10	J	794	0	840	21	0
11	K	885	0	904	9	0
12	L	970	0	1057	18	0
13	M	905	0	958	18	0
14	N	492	0	529	3	0
15	O	734	0	771	5	0
16	P	682	0	706	7	0
17	Q	834	0	904	4	0
18	R	565	0	631	4	0
19	S	647	0	673	6	0
20	T	763	0	861	10	0
21	U	2203	0	2283	46	0
22	V	208	0	221	1	0
23	D	1	0	0	0	0
23	N	1	0	0	0	0
All	All	51135	0	37330	480	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 6.

All (480) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:749:G:H1	1:A:796:C:HO2'	1.22	0.87
1:A:1114:G:H1	1:A:1126:G:H21	1.28	0.82
1:A:78:G:H1	1:A:86:U:H3	1.30	0.79
1:A:1013:A:H3'	1:A:1014:G:H5"	1.63	0.79
1:A:953:A:H4'	1:A:954:G:H5"	1.69	0.74
2:B:7:VAL:HG13	2:B:8:LYS:HG2	1.70	0.72
17:Q:66:SER:O	17:Q:70:ARG:NH1	2.23	0.72
1:A:352:A:N3	1:A:364:U:O2'	2.24	0.70
1:A:1338:G:H2'	1:A:1339:A:C8	2.27	0.70
20:T:40:ALA:HB2	20:T:55:ILE:HG22	1.72	0.70
1:A:657:G:H2'	1:A:658:G:C8	2.27	0.69
21:U:103:VAL:O	21:U:139:LYS:NZ	2.25	0.69
9:I:20:ARG:HH12	9:I:62:TYR:HB2	1.59	0.68
13:M:7:VAL:HG21	13:M:22:ILE:HG12	1.76	0.68
10:J:5:ARG:HB3	10:J:99:LYS:HB3	1.75	0.67
1:A:658:G:H2'	1:A:659:A:H8	1.60	0.67
3:C:108:ASN:HD21	3:C:144:SER:HB3	1.59	0.67
3:C:156:ARG:H	3:C:163:ALA:HA	1.59	0.66
2:B:54:THR:HG21	2:B:201:ILE:HG12	1.76	0.66
9:I:50:LEU:HD23	9:I:85:LEU:HD11	1.78	0.66
7:G:111:ARG:NH2	7:G:126:ASP:OD2	2.30	0.65
10:J:51:ARG:HD2	10:J:59:SER:HB3	1.79	0.65
5:E:43:LEU:HD11	5:E:132:ALA:HB1	1.78	0.64
1:A:648:G:H22	1:A:725:G:H1	1.44	0.64
21:U:141:LEU:HB3	21:U:181:TYR:HD2	1.62	0.64
1:A:18:U:H2'	1:A:19:C:C6	2.33	0.64
21:U:179:GLN:O	21:U:211:ARG:NH2	2.29	0.63
11:K:15:ALA:HA	11:K:77:MET:HA	1.81	0.63
2:B:24:TRP:CZ3	2:B:26:PRO:HA	2.35	0.62
1:A:1127:G:N2	1:A:1129:A:H62	1.97	0.62
1:A:1492:C:H5'	21:U:235:ARG:HD3	1.82	0.61
21:U:39:ARG:O	21:U:43:HIS:ND1	2.33	0.61
4:D:162:LEU:HG	4:D:178:VAL:HG23	1.82	0.61
13:M:3:ARG:NH1	13:M:5:ALA:O	2.33	0.61
16:P:57:ARG:NH1	16:P:79:VAL:O	2.34	0.61
4:D:191:ARG:O	4:D:191:ARG:NH1	2.33	0.61
8:H:87:SER:HB2	8:H:93:VAL:H	1.65	0.61
1:A:265:C:H2'	1:A:266:A:C8	2.36	0.61
1:A:924:A:H2'	1:A:925:G:C8	2.37	0.60
10:J:77:PRO:O	10:J:79:ARG:NH2	2.34	0.60
19:S:50:ALA:HB1	19:S:57:HIS:HB3	1.83	0.60
17:Q:95:TYR:HA	17:Q:98:LEU:HD12	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:57:ARG:HB3	4:D:206:PHE:HB2	1.84	0.60
12:L:50:ARG:HG3	12:L:90:LEU:HD21	1.82	0.60
1:A:1338:G:H2'	1:A:1339:A:H8	1.68	0.59
9:I:10:ARG:NH1	9:I:75:ASP:OD2	2.36	0.59
1:A:994:A:H2'	1:A:995:A:C8	2.38	0.59
21:U:41:VAL:HG23	21:U:69:ARG:HH21	1.67	0.59
1:A:1114:G:H1	1:A:1126:G:N2	2.01	0.58
13:M:4:ILE:HD13	13:M:9:ILE:HG13	1.84	0.58
1:A:1141:C:C5	1:A:1143:G:H1'	2.38	0.58
7:G:78:ARG:NH1	7:G:79:ARG:O	2.37	0.58
21:U:38:ASN:ND2	21:U:65:GLN:OE1	2.37	0.58
1:A:1298:G:N1	1:A:1301:A:OP2	2.36	0.58
1:A:88:C:H2'	1:A:89:G:H8	1.67	0.58
1:A:1296:C:H2'	1:A:1297:U:C6	2.38	0.58
1:A:705:G:OP1	1:A:705:G:H8	1.85	0.57
20:T:53:LEU:HD13	20:T:102:GLY:H	1.68	0.57
2:B:91:PRO:HG2	2:B:155:LEU:HG	1.86	0.57
7:G:113:GLU:HB2	7:G:119:ARG:HG2	1.85	0.57
9:I:9:ARG:H	9:I:79:LEU:HD23	1.69	0.57
12:L:90:LEU:HB2	12:L:93:VAL:HG12	1.86	0.57
1:A:658:G:H2'	1:A:659:A:C8	2.40	0.57
3:C:177:THR:HG23	3:C:180:ALA:HB2	1.86	0.57
1:A:1233:A:N3	1:A:1352:C:O2'	2.34	0.57
1:A:924:A:O2'	1:A:1315:A:N3	2.35	0.57
1:A:295:G:H2'	1:A:296:A:C8	2.40	0.57
1:A:147:A:H5"	1:A:148:C:H5	1.69	0.56
1:A:265:C:H2'	1:A:266:A:H8	1.69	0.56
1:A:508:G:H2'	1:A:509:C:C6	2.40	0.56
9:I:46:ALA:HB2	9:I:74:ILE:HG23	1.86	0.56
1:A:1245:C:H2'	1:A:1246:C:C6	2.41	0.56
8:H:84:ARG:O	8:H:135:CYS:HB2	2.05	0.56
1:A:401:U:H5"	1:A:480:A:H2	1.70	0.56
2:B:178:ARG:HH22	8:H:74:PRO:HB3	1.71	0.56
1:A:143:G:H2'	1:A:144:A:C8	2.41	0.56
1:A:697:G:H2'	1:A:698:G:C8	2.41	0.56
3:C:130:VAL:HG11	3:C:157:ILE:HD12	1.88	0.56
5:E:105:VAL:HB	5:E:106:PRO:HD3	1.88	0.56
10:J:33:GLN:HB2	10:J:75:ILE:HD11	1.88	0.56
1:A:974:A:H2'	1:A:975:U:C6	2.41	0.56
1:A:1119:U:H1'	1:A:1120:C:C2	2.40	0.56
1:A:1116:G:H3'	1:A:1117:G:H21	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:50:GLU:HG2	5:E:52:PRO:HD2	1.88	0.55
1:A:1113:A:N7	1:A:1114:G:N2	2.51	0.55
6:F:24:GLU:OE1	6:F:28:ARG:NH2	2.38	0.55
8:H:51:VAL:HG21	8:H:60:ARG:HH12	1.70	0.55
1:A:485:C:OP1	12:L:114:ARG:NH2	2.30	0.55
4:D:98:GLU:HA	4:D:103:ASN:HD22	1.71	0.55
6:F:80:ARG:NH1	6:F:88:VAL:O	2.39	0.55
1:A:74:G:O6	1:A:90:U:C2	2.60	0.55
1:A:1142:U:O4'	1:A:1164:G:N2	2.38	0.55
1:A:1232:A:N3	1:A:1353:G:O2'	2.32	0.55
1:A:1296:C:H2'	1:A:1297:U:H6	1.70	0.55
1:A:78:G:O6	1:A:86:U:O4	2.24	0.55
10:J:8:LEU:HB2	10:J:70:ARG:HB2	1.89	0.55
12:L:55:VAL:HG21	12:L:82:ILE:HD11	1.88	0.55
1:A:423:U:OP1	4:D:13:ARG:NH2	2.40	0.55
1:A:564:U:H2'	1:A:565:G:O4'	2.07	0.55
1:A:1164:G:H4'	1:A:1165:A:H5'	1.89	0.55
13:M:65:LYS:HG2	13:M:70:LEU:HD13	1.88	0.55
10:J:6:ILE:HB	10:J:72:VAL:HB	1.89	0.55
1:A:704:C:H3'	1:A:705:G:H5"	1.89	0.54
4:D:50:ARG:HD3	4:D:51:PRO:HD2	1.89	0.54
1:A:144:A:H2'	1:A:145:C:C6	2.43	0.54
9:I:89:ASN:HB3	9:I:92:TYR:HD1	1.73	0.54
10:J:79:ARG:HA	10:J:82:ILE:HG12	1.90	0.54
13:M:23:TYR:HB3	13:M:67:GLU:HG2	1.89	0.54
13:M:65:LYS:CG	13:M:70:LEU:HB2	2.38	0.54
1:A:866:G:H3'	1:A:867:A:H5"	1.89	0.54
1:A:1045:U:H2'	1:A:1046:C:C6	2.43	0.54
1:A:702:G:H5'	11:K:117:ASN:HB2	1.88	0.54
1:A:712:A:H2'	1:A:713:A:C8	2.43	0.54
21:U:37:LEU:O	21:U:65:GLN:NE2	2.40	0.54
1:A:537:A:H5"	12:L:21:VAL:HG21	1.89	0.54
1:A:1237:G:O2'	1:A:1240:G:N3	2.37	0.54
3:C:35:GLU:OE2	3:C:59:ARG:NH1	2.39	0.54
21:U:51:GLY:N	21:U:121:GLU:O	2.28	0.54
13:M:15:VAL:HG13	13:M:34:LEU:HD11	1.90	0.54
21:U:163:ALA:O	21:U:179:GLN:NE2	2.41	0.54
1:A:979:A:O2'	1:A:980:G:H3'	2.08	0.53
21:U:182:THR:HG22	21:U:210:LEU:HA	1.90	0.53
1:A:980:G:H4'	1:A:981:G:OP1	2.07	0.53
21:U:238:THR:HG23	21:U:269:LYS:HA	1.88	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1013:A:H3'	1:A:1014:G:C5'	2.37	0.53
1:A:1220:A:H2	1:A:1223:G:N3	2.06	0.53
15:O:4:THR:OG1	15:O:7:GLU:HG2	2.09	0.53
21:U:90:LEU:HD13	21:U:96:VAL:HG11	1.90	0.53
10:J:34:VAL:HG12	10:J:74:ILE:HD12	1.91	0.53
1:A:505:G:N7	12:L:50:ARG:NH1	2.57	0.53
2:B:84:GLU:OE1	2:B:87:ARG:NH2	2.41	0.53
9:I:55:ALA:O	9:I:56:LEU:HB2	2.09	0.53
13:M:66:LEU:HG	13:M:67:GLU:H	1.74	0.53
8:H:19:VAL:HG23	8:H:21:LYS:HG3	1.90	0.52
1:A:839:G:HO2'	1:A:852:G:HO2'	1.54	0.52
1:A:196:G:H2'	1:A:197:U:C6	2.45	0.52
2:B:7:VAL:HG22	2:B:8:LYS:H	1.74	0.52
2:B:82:ARG:NH1	2:B:92:TYR:OH	2.42	0.52
1:A:602:C:H5'	1:A:603:U:H5"	1.91	0.52
2:B:17:PHE:O	2:B:204:ASN:ND2	2.43	0.52
1:A:87:C:H2'	1:A:88:C:C6	2.45	0.52
1:A:305:G:O2'	1:A:591:A:N1	2.43	0.52
2:B:24:TRP:HZ3	2:B:26:PRO:HA	1.75	0.51
9:I:89:ASN:HB3	9:I:92:TYR:CD1	2.45	0.51
19:S:3:ARG:HH21	19:S:7:LYS:HB3	1.74	0.51
9:I:48:GLU:N	9:I:49:PRO:HD2	2.25	0.51
1:A:1015:G:H2'	1:A:1016:G:H8	1.75	0.51
11:K:40:ILE:HG12	11:K:75:TYR:HD2	1.75	0.51
14:N:16:PHE:HB2	14:N:19:ARG:HG3	1.92	0.51
21:U:83:LEU:O	21:U:86:LEU:HG	2.11	0.51
1:A:502:C:H4'	1:A:503:C:O5'	2.08	0.51
1:A:698:G:H2'	1:A:699:A:C8	2.45	0.51
5:E:81:GLU:HG2	5:E:90:VAL:HG22	1.91	0.51
2:B:7:VAL:N	2:B:48:MET:SD	2.84	0.51
9:I:17:VAL:HG12	9:I:63:ILE:HD12	1.92	0.51
21:U:37:LEU:HD22	21:U:62:LEU:HD13	1.93	0.51
2:B:84:GLU:HG3	2:B:215:LEU:HB3	1.91	0.51
10:J:7:LYS:HB3	10:J:97:GLU:HB3	1.92	0.51
3:C:21:ARG:NH2	3:C:56:ASP:OD2	2.44	0.51
1:A:1245:C:H2'	1:A:1246:C:H6	1.76	0.51
6:F:48:LEU:HD13	6:F:52:ILE:HD12	1.93	0.51
12:L:53:ALA:HB2	12:L:67:ILE:HD11	1.92	0.51
13:M:5:ALA:HB2	13:M:66:LEU:HD11	1.93	0.50
20:T:40:ALA:HB2	20:T:55:ILE:CG2	2.41	0.50
21:U:130:TYR:CD2	21:U:155:GLN:HB2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:107:VAL:HG23	12:L:110:ARG:HG3	1.93	0.50
1:A:928:U:H2'	1:A:929:G:C8	2.47	0.50
3:C:42:LEU:HD13	3:C:94:LEU:HD22	1.92	0.50
7:G:16:LEU:HD21	9:I:45:ALA:HB2	1.92	0.50
11:K:11:LYS:N	11:K:13:GLN:OE1	2.44	0.50
1:A:1006:C:H2'	1:A:1007:C:C5	2.46	0.50
3:C:156:ARG:NH1	3:C:193:TYR:O	2.45	0.50
15:O:82:ILE:HG13	15:O:87:ILE:HB	1.93	0.50
20:T:10:LEU:HG	20:T:12:ALA:H	1.77	0.50
1:A:886:A:H2'	1:A:887:A:H8	1.76	0.50
1:A:397:C:O2'	1:A:605:A:N3	2.43	0.50
5:E:15:ARG:HD3	5:E:26:PHE:CD1	2.47	0.50
21:U:182:THR:OG1	21:U:208:LEU:HD12	2.12	0.50
21:U:183:GLU:HB2	21:U:209:ILE:HG13	1.94	0.50
1:A:57:U:H2'	1:A:58:G:C8	2.46	0.49
1:A:129:A:H1'	1:A:321:A:C5	2.47	0.49
1:A:983:A:H5'	1:A:1004:U:H3	1.76	0.49
3:C:94:LEU:HG	3:C:95:THR:HG23	1.94	0.49
1:A:78:G:H2'	1:A:79:G:C8	2.48	0.49
1:A:1012:G:H1'	1:A:1013:A:C8	2.47	0.49
4:D:98:GLU:HA	4:D:103:ASN:ND2	2.26	0.49
1:A:922:G:N1	1:A:1320:G:OP2	2.39	0.49
1:A:1127:G:H21	1:A:1129:A:H62	1.61	0.49
8:H:86:ILE:HG21	8:H:133:LEU:HD23	1.94	0.49
10:J:99:LYS:NZ	10:J:100:THR:H	2.10	0.49
2:B:178:ARG:NH2	8:H:74:PRO:HB3	2.28	0.49
1:A:1116:G:C2	1:A:1117:G:C6	3.01	0.49
1:A:75:C:H2'	1:A:76:G:H4'	1.95	0.49
1:A:961:A:H5'	1:A:962:C:OP2	2.13	0.49
1:A:1281:A:H2'	1:A:1281:A:N3	2.28	0.49
10:J:44:VAL:HG22	10:J:66:ARG:HB3	1.94	0.49
1:A:523:A:H2'	1:A:524:G:C8	2.48	0.49
5:E:71:LEU:HD21	5:E:115:VAL:HG22	1.94	0.49
21:U:83:LEU:HA	21:U:86:LEU:HD23	1.95	0.49
22:V:5:ASP:O	22:V:11:GLY:HA3	2.13	0.49
1:A:656:U:HO2'	1:A:657:G:H8	1.61	0.49
3:C:36:ASP:OD1	3:C:59:ARG:NH2	2.36	0.49
7:G:145:ALA:C	7:G:147:ALA:H	2.17	0.49
21:U:67:ALA:HA	21:U:70:ALA:HB3	1.94	0.49
1:A:60:A:H3'	1:A:327:G:H22	1.77	0.48
1:A:778:A:H3'	1:A:779:C:H6	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1232:A:H2'	1:A:1233:A:C8	2.48	0.48
7:G:15:ASP:OD1	7:G:16:LEU:N	2.45	0.48
9:I:53:VAL:HG12	9:I:95:LYS:HE2	1.96	0.48
14:N:24:CYS:HB2	14:N:40:CYS:HB3	1.95	0.48
21:U:46:VAL:HG21	21:U:52:VAL:HG23	1.95	0.48
21:U:272:GLY:HA2	21:U:275:LEU:HD13	1.94	0.48
1:A:102:G:H5'	1:A:103:A:H5"	1.95	0.48
1:A:1008:C:H2'	1:A:1009:C:C6	2.47	0.48
8:H:113:SER:HB2	8:H:134:ILE:HD11	1.94	0.48
1:A:1054:C:H2'	1:A:1055:G:H8	1.79	0.48
1:A:1105:U:O4	1:A:1106:A:N6	2.39	0.48
1:A:454:G:H3'	1:A:455:A:C5'	2.44	0.48
1:A:689:U:C2	1:A:690:A:C8	3.02	0.48
1:A:886:A:H2'	1:A:887:A:C8	2.49	0.48
21:U:196:VAL:HB	21:U:197:PRO:HD3	1.95	0.48
1:A:485:C:H2'	1:A:486:G:C8	2.49	0.48
1:A:1090:C:C4	1:A:1091:G:C8	3.02	0.48
1:A:923:G:C2	1:A:924:A:C8	3.01	0.48
10:J:35:SER:HB3	10:J:72:VAL:O	2.14	0.48
16:P:69:THR:HA	16:P:72:ARG:HG2	1.95	0.48
1:A:77:G:H2'	1:A:78:G:O4'	2.14	0.48
1:A:960:U:H4'	1:A:961:A:O4'	2.14	0.48
1:A:1014:G:H1'	1:A:1015:G:O4'	2.13	0.48
1:A:74:G:C6	1:A:91:G:C6	3.02	0.48
1:A:954:G:H5'	1:A:1340:U:O2'	2.13	0.48
1:A:1126:G:H2'	1:A:1127:G:H8	1.78	0.48
1:A:74:G:O6	1:A:90:U:O2	2.31	0.48
6:F:1:MET:HG3	6:F:66:GLU:OE2	2.14	0.48
12:L:107:VAL:HG22	12:L:117:TYR:HB3	1.94	0.48
1:A:212:G:H2'	1:A:213:C:C6	2.49	0.47
1:A:409:G:H1'	1:A:424:G:N2	2.28	0.47
1:A:996:G:O2'	1:A:997:C:OP1	2.31	0.47
1:A:1023:U:H2'	1:A:1024:A:C8	2.49	0.47
9:I:32:ASP:HB3	9:I:35:GLU:HG2	1.95	0.47
21:U:158:VAL:O	21:U:162:MET:HG2	2.14	0.47
9:I:45:ALA:O	9:I:48:GLU:HG2	2.14	0.47
1:A:656:U:O2'	1:A:657:G:H8	1.98	0.47
6:F:1:MET:N	6:F:69:GLU:OE1	2.38	0.47
2:B:69:LEU:HD13	2:B:91:PRO:HB2	1.95	0.47
13:M:5:ALA:C	13:M:7:VAL:H	2.18	0.47
1:A:485:C:H2'	1:A:486:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:82:ARG:HB2	6:F:85:VAL:HG22	1.96	0.47
21:U:138:MET:O	21:U:142:GLU:HG2	2.14	0.47
1:A:1221:A:H62	1:A:1281:A:H62	1.61	0.47
4:D:142:PRO:HA	4:D:185:PHE:HD2	1.80	0.47
11:K:84:VAL:HG21	11:K:91:ARG:HG3	1.95	0.47
12:L:86:ARG:HA	12:L:94:ARG:HA	1.97	0.47
13:M:14:ARG:NH2	13:M:16:ASP:OD2	2.48	0.47
16:P:4:ILE:HG12	16:P:21:VAL:HG22	1.96	0.47
1:A:155:A:H2'	1:A:156:A:C8	2.49	0.47
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.96	0.47
1:A:65:G:H4'	1:A:66:U:H3'	1.96	0.47
1:A:171:C:H2'	1:A:172:C:H6	1.79	0.47
4:D:61:LYS:NZ	4:D:72:GLU:OE1	2.40	0.47
21:U:143:GLU:HG3	21:U:145:LEU:HG	1.97	0.47
1:A:1270:A:O2'	1:A:1271:A:H8	1.98	0.47
1:A:1329:G:N7	9:I:10:ARG:NH2	2.63	0.47
5:E:102:ALA:HB1	5:E:106:PRO:HB2	1.97	0.47
1:A:76:G:H2'	1:A:77:G:C8	2.50	0.46
1:A:146:A:C2	1:A:147:A:H1'	2.49	0.46
1:A:928:U:H2'	1:A:929:G:H8	1.80	0.46
2:B:91:PRO:HG3	2:B:154:LEU:HB2	1.96	0.46
1:A:453:C:H2'	1:A:454:G:O4'	2.16	0.46
1:A:993:A:H2	1:A:1201:U:H1'	1.81	0.46
1:A:1221:A:H62	1:A:1281:A:N6	2.14	0.46
8:H:108:GLY:HA3	8:H:138:TRP:HB3	1.97	0.46
1:A:373:G:OP1	16:P:3:LYS:HD3	2.14	0.46
1:A:954:G:OP2	1:A:1340:U:O2'	2.30	0.46
10:J:80:LYS:HA	10:J:83:GLU:HG2	1.98	0.46
1:A:57:U:H2'	1:A:58:G:H8	1.81	0.46
1:A:1344:C:O2'	1:A:1345:C:H5'	2.15	0.46
3:C:124:ILE:HD12	3:C:130:VAL:HG22	1.98	0.46
21:U:41:VAL:HA	21:U:44:ALA:HB3	1.98	0.46
1:A:447:A:O2'	1:A:448:A:H8	1.99	0.46
1:A:1300:A:H5"	19:S:3:ARG:HH12	1.80	0.46
1:A:754:C:O2'	21:U:271:ARG:NH2	2.49	0.46
1:A:1040:G:H5"	3:C:154:SER:HB2	1.98	0.46
1:A:1116:G:N1	1:A:1117:G:C6	2.84	0.46
13:M:65:LYS:HG3	13:M:70:LEU:HB2	1.98	0.46
21:U:119:CYS:SG	21:U:120:ASP:N	2.89	0.46
1:A:721:A:H2'	1:A:722:C:C6	2.51	0.46
1:A:1349:C:O2'	10:J:60:ARG:NH2	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:154:SER:OG	3:C:155:GLY:N	2.49	0.46
1:A:258:A:H4'	20:T:75:ASN:HB2	1.97	0.45
1:A:1269:A:H2	1:A:1335:G:H1'	1.81	0.45
2:B:32:ILE:HD11	2:B:190:THR:HG22	1.98	0.45
7:G:146:GLU:HA	7:G:149:ARG:HG3	1.97	0.45
21:U:214:PRO:HG3	21:U:218:VAL:HB	1.99	0.45
1:A:7:G:O2'	1:A:8:G:H5'	2.17	0.45
3:C:111:LEU:HD21	3:C:144:SER:O	2.16	0.45
9:I:112:LYS:HA	9:I:119:ALA:HB2	1.99	0.45
1:A:1019:G:H5"	1:A:1020:C:H5	1.81	0.45
1:A:1015:G:H2'	1:A:1016:G:C8	2.52	0.45
1:A:1117:G:C6	1:A:1118:U:C4	3.05	0.45
12:L:67:ILE:HG12	12:L:97:ILE:HD12	1.98	0.45
1:A:646:G:H2'	1:A:647:A:C8	2.52	0.45
1:A:993:A:C2	1:A:1201:U:H1'	2.52	0.45
13:M:33:ALA:HB2	13:M:64:TRP:CZ2	2.52	0.45
1:A:778:A:H3'	1:A:779:C:C6	2.51	0.45
1:A:1200:C:H2'	1:A:1201:U:C6	2.52	0.45
1:A:838:A:H2'	1:A:839:G:O4'	2.17	0.45
1:A:409:G:H4'	1:A:410:A:H5'	1.98	0.44
2:B:215:LEU:HD23	2:B:215:LEU:HA	1.86	0.44
15:O:37:ASN:O	15:O:41:GLU:HG3	2.18	0.44
21:U:229:LYS:HD3	21:U:229:LYS:HA	1.81	0.44
1:A:195:U:H2'	1:A:196:G:C8	2.51	0.44
1:A:798:A:H2'	1:A:800:A:H5"	1.99	0.44
7:G:15:ASP:O	7:G:19:GLY:HA2	2.18	0.44
1:A:242:A:C2	1:A:278:A:C5	3.05	0.44
1:A:594:G:C4	1:A:595:A:C8	3.06	0.44
1:A:676:U:O2'	1:A:678:A:N7	2.43	0.44
1:A:1089:G:H5"	3:C:172:ARG:HG2	2.00	0.44
1:A:1218:A:H4'	1:A:1286:G:H4'	1.99	0.44
2:B:36:ARG:O	2:B:39:ILE:HG22	2.17	0.44
21:U:80:GLN:O	21:U:84:PRO:HD3	2.18	0.44
1:A:648:G:H2'	1:A:650:G:OP1	2.17	0.44
1:A:671:A:C2	1:A:688:A:C5	3.06	0.44
1:A:777:U:H4'	21:U:131:TYR:CE2	2.52	0.44
1:A:1020:C:H2'	1:A:1021:C:C6	2.52	0.44
2:B:145:LEU:O	2:B:149:LEU:HB2	2.17	0.44
20:T:62:LEU:HD23	20:T:62:LEU:HA	1.87	0.44
1:A:7:G:H4'	1:A:294:A:H4'	2.00	0.44
1:A:442:G:O6	1:A:470:G:O2'	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:53:VAL:HG13	16:P:79:VAL:HG22	2.00	0.44
21:U:156:LYS:O	21:U:160:GLU:HG3	2.17	0.44
1:A:138:A:H2	1:A:216:G:H1	1.66	0.44
1:A:559:G:O2'	1:A:805:G:H5'	2.17	0.44
1:A:934:U:O2	1:A:938:U:H5	2.01	0.44
1:A:1364:U:C4	7:G:156:TRP:HH2	2.36	0.44
1:A:975:U:H2'	1:A:976:G:O4'	2.18	0.44
1:A:1116:G:H3'	1:A:1117:G:N2	2.33	0.44
3:C:120:VAL:O	3:C:124:ILE:HG12	2.18	0.44
3:C:175:LEU:HD23	3:C:182:ILE:HD13	1.99	0.44
10:J:21:GLN:OE1	10:J:21:GLN:HA	2.17	0.44
16:P:43:LYS:HG3	16:P:48:TRP:CG	2.53	0.44
21:U:241:ASN:HA	21:U:244:VAL:HG12	2.00	0.44
1:A:334:A:H2'	1:A:335:C:H6	1.83	0.44
1:A:430:U:H2'	1:A:431:C:C6	2.53	0.44
7:G:125:MET:O	7:G:129:GLU:HG3	2.18	0.44
10:J:3:LYS:HB2	10:J:77:PRO:HD3	2.00	0.44
12:L:110:ARG:NH2	12:L:113:SER:HB2	2.33	0.44
1:A:213:C:H2'	1:A:214:C:C6	2.53	0.43
1:A:1310:C:C2	1:A:1311:A:C8	3.06	0.43
20:T:45:GLN:HB2	20:T:91:LEU:HD13	2.00	0.43
1:A:378:A:H2'	1:A:379:A:C8	2.53	0.43
1:A:981:G:H2'	1:A:982:G:C8	2.53	0.43
1:A:1117:G:H2'	1:A:1118:U:O4'	2.19	0.43
6:F:50:TYR:CE2	18:R:77:GLY:HA2	2.53	0.43
15:O:26:GLU:HG3	15:O:81:LEU:HD22	2.00	0.43
1:A:82:U:H4'	1:A:83:U:OP1	2.18	0.43
1:A:437:C:H2'	1:A:438:C:H6	1.83	0.43
1:A:200:C:H2'	1:A:201:C:C6	2.52	0.43
1:A:1337:G:H2'	1:A:1338:G:H8	1.84	0.43
1:A:734:G:N3	15:O:23:GLY:HA3	2.33	0.43
1:A:1312:U:H4'	13:M:23:TYR:CE2	2.53	0.43
1:A:1485:A:H2'	1:A:1486:G:O4'	2.18	0.43
13:M:91:ARG:HA	13:M:91:ARG:HD2	1.89	0.43
1:A:199:U:H1'	20:T:103:GLY:HA2	2.01	0.43
13:M:5:ALA:HB3	13:M:7:VAL:HG22	2.00	0.43
1:A:661:U:H3	1:A:697:G:H22	1.65	0.43
2:B:59:GLU:HG3	2:B:221:LEU:HD11	1.99	0.43
10:J:99:LYS:HZ3	10:J:100:THR:H	1.67	0.43
11:K:18:ARG:HA	11:K:81:ASP:H	1.84	0.43
4:D:162:LEU:HD12	4:D:165:MET:HG3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:12:ASP:OD1	10:J:14:LYS:N	2.49	0.43
18:R:50:ILE:HG12	18:R:70:ILE:HG21	2.01	0.43
1:A:539:C:H2'	1:A:540:C:C6	2.53	0.43
3:C:22:TRP:CG	3:C:59:ARG:HD2	2.54	0.43
7:G:65:ALA:O	7:G:69:VAL:HG23	2.19	0.43
1:A:1305:G:H2'	1:A:1306:A:C8	2.53	0.43
11:K:18:ARG:HG3	11:K:33:THR:HG23	2.01	0.43
3:C:17:ASP:OD1	3:C:18:TRP:N	2.52	0.42
10:J:99:LYS:HA	10:J:99:LYS:HD2	1.86	0.42
20:T:36:LEU:HD12	20:T:62:LEU:HD12	2.00	0.42
21:U:49:LYS:O	21:U:120:ASP:HB3	2.19	0.42
21:U:80:GLN:HA	21:U:83:LEU:HB2	2.01	0.42
1:A:429:C:H2'	1:A:430:U:C6	2.53	0.42
1:A:1140:A:C2	1:A:1163:G:C4	3.07	0.42
8:H:10:LEU:HD22	8:H:83:ILE:HD11	2.00	0.42
12:L:69:GLY:HA3	12:L:107:VAL:HG11	2.01	0.42
2:B:44:LEU:O	2:B:48:MET:HG2	2.20	0.42
4:D:7:PRO:HB2	4:D:10:ARG:HD2	2.01	0.42
21:U:125:VAL:HG22	21:U:151:VAL:HB	2.00	0.42
1:A:1001:G:O2'	1:A:1002:G:H8	2.02	0.42
5:E:48:ALA:HB2	5:E:57:LYS:HE3	2.02	0.42
21:U:166:PRO:HA	21:U:171:TYR:CG	2.54	0.42
1:A:335:C:H2'	1:A:336:U:C6	2.55	0.42
2:B:69:LEU:HD22	2:B:155:LEU:HD11	2.00	0.42
4:D:9:CYS:O	4:D:12:CYS:HB2	2.19	0.42
12:L:68:PRO:HB2	12:L:117:TYR:HE1	1.83	0.42
17:Q:64:PRO:HB3	17:Q:70:ARG:NH1	2.34	0.42
1:A:362:C:O2'	1:A:390:G:N2	2.50	0.42
1:A:1273:G:H4'	9:I:39:GLY:HA3	2.01	0.42
16:P:20:VAL:HG21	16:P:32:TYR:CG	2.54	0.42
20:T:89:ARG:HB2	20:T:104:LEU:HD21	2.02	0.42
1:A:903:G:H2'	1:A:904:G:N2	2.35	0.42
1:A:1150:A:H8	1:A:1150:A:OP1	2.02	0.42
1:A:1158:A:H2'	1:A:1159:G:C8	2.54	0.42
21:U:109:LYS:HE3	21:U:145:LEU:HD23	2.01	0.42
1:A:36:G:H2'	1:A:37:C:C6	2.55	0.42
7:G:136:LYS:NZ	7:G:140:ASP:OD2	2.52	0.42
12:L:94:ARG:HG3	12:L:95:TYR:CE2	2.55	0.42
13:M:73:GLU:O	13:M:77:ASN:ND2	2.52	0.42
19:S:18:LYS:O	19:S:21:GLU:HG3	2.19	0.42
1:A:335:C:H2'	1:A:336:U:H6	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:979:A:H1'	1:A:980:G:OP1	2.20	0.42
1:A:1023:U:H2'	1:A:1024:A:H8	1.85	0.42
3:C:6:HIS:HE1	3:C:8:ILE:HD12	1.84	0.42
7:G:75:VAL:HB	7:G:86:GLN:HB3	2.02	0.42
21:U:134:THR:CG2	21:U:135:PRO:HD3	2.50	0.42
1:A:144:A:H2'	1:A:145:C:H6	1.84	0.42
1:A:181:C:H2'	1:A:182:C:H6	1.84	0.42
1:A:181:C:H2'	1:A:182:C:C6	2.55	0.42
5:E:33:VAL:HG12	5:E:112:LEU:HD12	2.02	0.42
9:I:28:VAL:HA	9:I:63:ILE:HB	2.01	0.42
19:S:71:LEU:HD23	19:S:71:LEU:HA	1.94	0.41
1:A:91:G:H2'	1:A:92:G:O4'	2.20	0.41
6:F:39:LYS:HG2	6:F:64:GLN:HB3	2.01	0.41
11:K:34:ASP:OD1	11:K:38:ASN:N	2.54	0.41
18:R:76:LEU:HD23	18:R:76:LEU:HA	1.90	0.41
1:A:46:U:H2'	1:A:47:G:C8	2.55	0.41
1:A:158:C:H2'	1:A:159:U:O4'	2.20	0.41
1:A:961:A:O2'	1:A:1032:U:O2'	2.30	0.41
1:A:18:U:H2'	1:A:19:C:H6	1.83	0.41
3:C:130:VAL:HG21	3:C:157:ILE:HG23	2.03	0.41
7:G:11:GLN:OE1	7:G:11:GLN:HA	2.19	0.41
10:J:3:LYS:N	10:J:75:ILE:HA	2.35	0.41
14:N:14:PRO:C	14:N:16:PHE:H	2.23	0.41
1:A:1017:G:H2'	1:A:1018:A:C8	2.56	0.41
13:M:96:LEU:C	13:M:110:ARG:HE	2.24	0.41
1:A:400:U:H2'	1:A:401:U:H6	1.85	0.41
11:K:109:VAL:HG22	18:R:86:VAL:HG12	2.01	0.41
12:L:57:LEU:HD21	12:L:82:ILE:HG13	2.01	0.41
21:U:253:GLN:O	21:U:257:ILE:HG12	2.20	0.41
1:A:19:C:H5"	5:E:127:ASN:ND2	2.35	0.41
1:A:1050:A:H8	1:A:1050:A:OP2	2.04	0.41
1:A:1115:C:H2'	1:A:1116:G:C8	2.55	0.41
7:G:52:GLU:OE1	7:G:53:LYS:HG3	2.20	0.41
21:U:107:ASP:N	21:U:107:ASP:OD1	2.53	0.41
2:B:145:LEU:HD23	2:B:145:LEU:HA	1.91	0.41
4:D:150:GLU:HA	4:D:153:ARG:HD2	2.03	0.41
8:H:111:ILE:HD12	8:H:135:CYS:SG	2.60	0.41
1:A:33:A:H2'	1:A:34:A:C8	2.55	0.41
1:A:493:A:N3	1:A:527:C:O2'	2.46	0.41
1:A:539:C:H2'	1:A:540:C:H6	1.86	0.41
1:A:870:A:H2'	1:A:871:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1054:C:H2'	1:A:1055:G:C8	2.55	0.41
1:A:1115:C:H2'	1:A:1116:G:H8	1.85	0.41
3:C:90:GLU:HA	3:C:93:LYS:HZ3	1.85	0.41
5:E:6:PHE:HB3	5:E:34:VAL:HG13	2.03	0.41
17:Q:45:HIS:NE2	17:Q:47:PRO:HG3	2.36	0.41
1:A:143:G:H2'	1:A:144:A:H8	1.81	0.41
1:A:429:C:H2'	1:A:430:U:H6	1.86	0.41
2:B:13:ALA:HA	2:B:209:ARG:NH1	2.35	0.41
3:C:154:SER:HB3	3:C:197:GLY:H	1.85	0.41
4:D:142:PRO:HB3	4:D:187:ARG:HA	2.02	0.41
1:A:1359:U:H2'	1:A:1360:A:C8	2.56	0.40
1:A:443:A:OP2	1:A:470:G:N2	2.46	0.40
1:A:1014:G:O2'	1:A:1015:G:H5"	2.22	0.40
1:A:1297:U:H2'	1:A:1298:G:O4'	2.21	0.40
1:A:1320:G:H2'	1:A:1321:A:C8	2.56	0.40
9:I:16:ARG:HB2	9:I:64:THR:OG1	2.22	0.40
2:B:19:HIS:NE2	2:B:189:ASP:OD2	2.55	0.40
5:E:51:VAL:HB	5:E:52:PRO:HD3	2.04	0.40
9:I:48:GLU:HA	9:I:51:ARG:HG2	2.03	0.40
10:J:54:PHE:CD2	10:J:55:LYS:HG2	2.56	0.40
19:S:16:LEU:HD12	19:S:16:LEU:HA	1.84	0.40
8:H:37:ARG:NH2	8:H:48:TYR:OH	2.55	0.40
21:U:212:ASP:OD1	21:U:212:ASP:N	2.52	0.40
6:F:42:GLU:OE2	6:F:61:LEU:HD22	2.21	0.40
12:L:29:PHE:CE1	12:L:83:ARG:HG3	2.56	0.40
12:L:44:LYS:HB3	12:L:45:PRO:HD3	2.03	0.40
21:U:211:ARG:NH2	21:U:215:ALA:HB2	2.37	0.40
21:U:271:ARG:O	21:U:273:GLU:N	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	218/256 (85%)	201 (92%)	16 (7%)	1 (0%)	29 61
3	C	204/239 (85%)	187 (92%)	16 (8%)	1 (0%)	29 61
4	D	206/209 (99%)	194 (94%)	12 (6%)	0	100 100
5	E	148/162 (91%)	145 (98%)	2 (1%)	1 (1%)	22 54
6	F	99/101 (98%)	95 (96%)	4 (4%)	0	100 100
7	G	153/156 (98%)	148 (97%)	5 (3%)	0	100 100
8	H	136/138 (99%)	132 (97%)	4 (3%)	0	100 100
9	I	125/128 (98%)	113 (90%)	12 (10%)	0	100 100
10	J	96/105 (91%)	86 (90%)	10 (10%)	0	100 100
11	K	117/129 (91%)	110 (94%)	7 (6%)	0	100 100
12	L	122/132 (92%)	107 (88%)	14 (12%)	1 (1%)	19 51
13	M	111/126 (88%)	97 (87%)	14 (13%)	0	100 100
14	N	58/61 (95%)	54 (93%)	4 (7%)	0	100 100
15	O	86/89 (97%)	85 (99%)	1 (1%)	0	100 100
16	P	79/88 (90%)	78 (99%)	1 (1%)	0	100 100
17	Q	98/105 (93%)	94 (96%)	4 (4%)	0	100 100
18	R	67/88 (76%)	64 (96%)	3 (4%)	0	100 100
19	S	78/93 (84%)	74 (95%)	4 (5%)	0	100 100
20	T	97/106 (92%)	89 (92%)	8 (8%)	0	100 100
21	U	275/298 (92%)	248 (90%)	25 (9%)	2 (1%)	22 54
22	V	22/27 (82%)	22 (100%)	0	0	100 100
All	All	2595/2836 (92%)	2423 (93%)	166 (6%)	6 (0%)	50 77

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	U	249	GLU
21	U	272	GLY
5	E	21	ALA
12	L	44	LYS
2	B	207	ALA
3	C	167	TRP

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	191/220 (87%)	191 (100%)	0	100 100
3	C	160/188 (85%)	160 (100%)	0	100 100
4	D	180/181 (99%)	178 (99%)	2 (1%)	73 85
5	E	115/123 (94%)	115 (100%)	0	100 100
6	F	90/90 (100%)	90 (100%)	0	100 100
7	G	126/127 (99%)	126 (100%)	0	100 100
8	H	119/119 (100%)	119 (100%)	0	100 100
9	I	98/99 (99%)	97 (99%)	1 (1%)	76 86
10	J	88/92 (96%)	87 (99%)	1 (1%)	73 85
11	K	90/99 (91%)	90 (100%)	0	100 100
12	L	104/109 (95%)	104 (100%)	0	100 100
13	M	91/101 (90%)	91 (100%)	0	100 100
14	N	49/50 (98%)	49 (100%)	0	100 100
15	O	79/80 (99%)	79 (100%)	0	100 100
16	P	70/74 (95%)	70 (100%)	0	100 100
17	Q	95/97 (98%)	95 (100%)	0	100 100
18	R	60/77 (78%)	60 (100%)	0	100 100
19	S	71/80 (89%)	69 (97%)	2 (3%)	43 70
20	T	76/82 (93%)	76 (100%)	0	100 100
21	U	247/264 (94%)	246 (100%)	1 (0%)	91 95
22	V	19/22 (86%)	19 (100%)	0	100 100
All	All	2218/2374 (93%)	2211 (100%)	7 (0%)	92 96

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	122	ARG

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Mol	Chain	Res	Type
4	D	151	LYS
9	I	104	ARG
10	J	9	ARG
19	S	11	VAL
19	S	37	ARG
21	U	249	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	108	ASN
7	G	96	GLN
9	I	58	HIS
11	K	13	GLN
21	U	38	ASN
21	U	65	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1391/1522 (91%)	284 (20%)	14 (1%)

All (284) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	G
1	A	10	G
1	A	23	G
1	A	33	A
1	A	34	A
1	A	40	G
1	A	48	C
1	A	49	C
1	A	52	A
1	A	62	G
1	A	74	G
1	A	76	G
1	A	77	G
1	A	79	G
1	A	82	U

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Mol	Chain	Res	Type
1	A	83	U
1	A	84	A
1	A	85	C
1	A	86	U
1	A	87	C
1	A	90	U
1	A	91	G
1	A	110	A
1	A	115	C
1	A	121	G
1	A	122	G
1	A	124	G
1	A	126	C
1	A	139	G
1	A	146	A
1	A	151	G
1	A	154	G
1	A	155	A
1	A	158	C
1	A	164	C
1	A	174	A
1	A	176	G
1	A	177	U
1	A	178	G
1	A	190	U
1	A	192	G
1	A	199	U
1	A	202	A
1	A	204	A
1	A	205	G
1	A	209	U
1	A	210	U
1	A	211	U
1	A	212	G
1	A	216	G
1	A	239	A
1	A	243	G
1	A	247	G
1	A	262	G
1	A	263	C
1	A	285	G
1	A	317	A

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Mol	Chain	Res	Type
1	A	323	A
1	A	324	C
1	A	325	A
1	A	326	C
1	A	341	C
1	A	347	G
1	A	348	C
1	A	349	A
1	A	350	G
1	A	362	C
1	A	363	U
1	A	368	C
1	A	369	A
1	A	380	G
1	A	402	G
1	A	408	A
1	A	409	G
1	A	410	A
1	A	418	C
1	A	420	G
1	A	425	U
1	A	432	C
1	A	433	U
1	A	435	A
1	A	443	A
1	A	447	A
1	A	448	A
1	A	450	C
1	A	452	C
1	A	455	A
1	A	456	C
1	A	457	G
1	A	462	G
1	A	463	A
1	A	466	G
1	A	479	U
1	A	480	A
1	A	481	A
1	A	482	U
1	A	484	G
1	A	493	A
1	A	495	C

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Mol	Chain	Res	Type
1	A	496	U
1	A	502	C
1	A	503	C
1	A	505	G
1	A	508	G
1	A	511	G
1	A	514	G
1	A	515	U
1	A	516	A
1	A	517	A
1	A	519	A
1	A	531	A
1	A	532	G
1	A	543	A
1	A	548	C
1	A	556	A
1	A	557	A
1	A	559	G
1	A	560	G
1	A	561	G
1	A	572	G
1	A	580	C
1	A	591	A
1	A	592	A
1	A	600	G
1	A	626	A
1	A	637	A
1	A	649	A
1	A	669	G
1	A	670	U
1	A	672	G
1	A	680	A
1	A	687	G
1	A	701	C
1	A	705	G
1	A	707	U
1	A	715	G
1	A	718	G
1	A	739	G
1	A	754	C
1	A	778	A
1	A	779	C

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Mol	Chain	Res	Type
1	A	800	A
1	A	801	C
1	A	803	A
1	A	804	U
1	A	805	G
1	A	812	A
1	A	825	U
1	A	826	C
1	A	833	G
1	A	834	C
1	A	837	A
1	A	850	A
1	A	862	U
1	A	863	G
1	A	867	A
1	A	869	U
1	A	880	G
1	A	892	A
1	A	904	G
1	A	905	G
1	A	906	G
1	A	912	C
1	A	913	A
1	A	917	G
1	A	933	U
1	A	938	U
1	A	939	U
1	A	944	G
1	A	946	A
1	A	947	A
1	A	949	G
1	A	953	A
1	A	954	G
1	A	955	A
1	A	970	U
1	A	971	G
1	A	976	G
1	A	978	U
1	A	979	A
1	A	980	G
1	A	981	G
1	A	982	G

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Mol	Chain	Res	Type
1	A	983	A
1	A	984	A
1	A	985	C
1	A	997	C
1	A	998	C
1	A	1000	G
1	A	1002	G
1	A	1004	U
1	A	1010	G
1	A	1012	G
1	A	1013	A
1	A	1014	G
1	A	1015	G
1	A	1017	G
1	A	1019	G
1	A	1020	C
1	A	1027	A
1	A	1028	C
1	A	1029	A
1	A	1032	U
1	A	1035	U
1	A	1036	G
1	A	1037	C
1	A	1039	U
1	A	1049	C
1	A	1051	G
1	A	1064	G
1	A	1069	U
1	A	1075	A
1	A	1077	G
1	A	1078	U
1	A	1082	G
1	A	1084	A
1	A	1085	A
1	A	1113	A
1	A	1114	G
1	A	1116	G
1	A	1118	U
1	A	1119	U
1	A	1120	C
1	A	1121	G
1	A	1122	G

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Mol	Chain	Res	Type
1	A	1123	C
1	A	1128	C
1	A	1137	G
1	A	1139	G
1	A	1140	A
1	A	1142	U
1	A	1149	G
1	A	1158	A
1	A	1161	A
1	A	1163	G
1	A	1165	A
1	A	1166	G
1	A	1178	U
1	A	1179	G
1	A	1182	C
1	A	1193	U
1	A	1194	U
1	A	1195	A
1	A	1197	G
1	A	1207	A
1	A	1208	C
1	A	1220	A
1	A	1223	G
1	A	1230	A
1	A	1232	A
1	A	1234	A
1	A	1238	A
1	A	1239	U
1	A	1240	G
1	A	1242	C
1	A	1257	A
1	A	1262	A
1	A	1267	A
1	A	1269	A
1	A	1271	A
1	A	1282	G
1	A	1283	U
1	A	1284	U
1	A	1295	U
1	A	1302	C
1	A	1328	A
1	A	1333	U

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Mol	Chain	Res	Type
1	A	1335	G
1	A	1345	C
1	A	1346	A
1	A	1347	U
1	A	1353	G
1	A	1357	A
1	A	1362	G
1	A	1375	G
1	A	1376	U
1	A	1378	C
1	A	1379	A
1	A	1486	G
1	A	1495	G
1	A	1496	A
1	A	1498	G
1	A	1507	G
1	A	1508	G

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	82	U
1	A	409	G
1	A	480	A
1	A	502	C
1	A	862	U
1	A	970	U
1	A	979	A
1	A	980	G
1	A	996	G
1	A	997	C
1	A	1036	G
1	A	1084	A
1	A	1118	U
1	A	1120	C

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

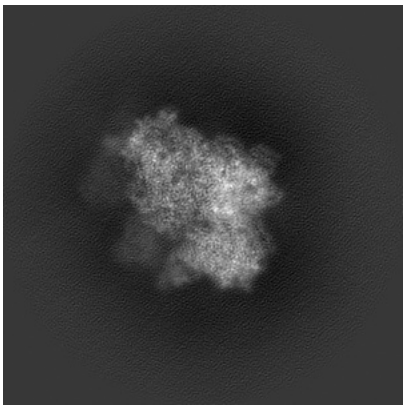
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-31659. These allow visual inspection of the internal detail of the map and identification of artifacts.

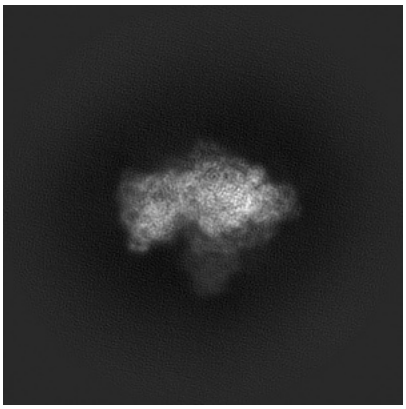
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

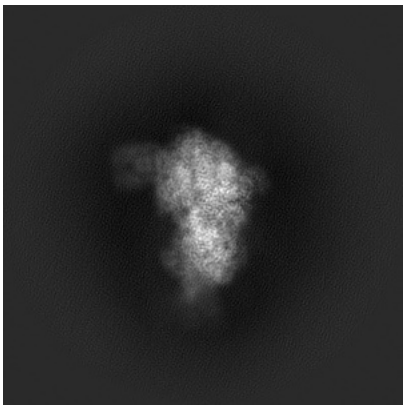
6.1.1 Primary map



X

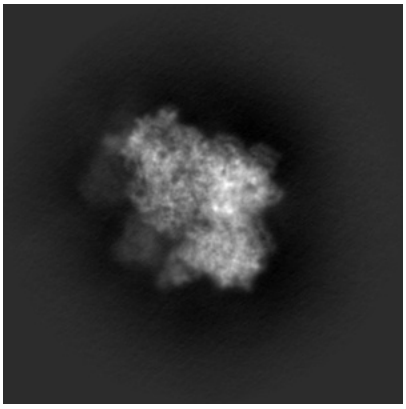


Y

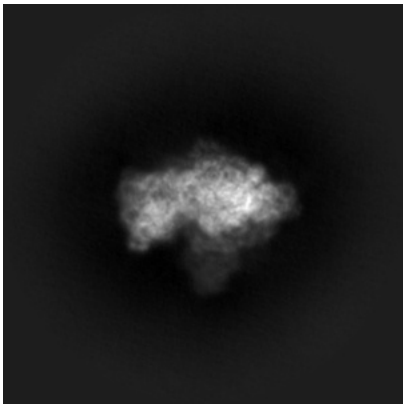


Z

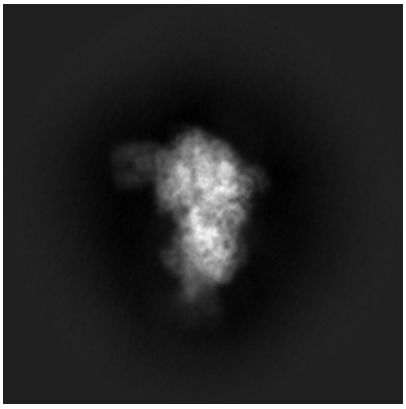
6.1.2 Raw map



X



Y

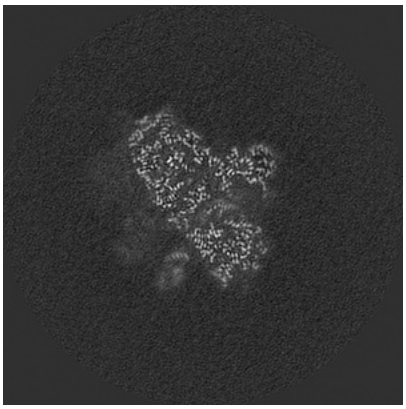


Z

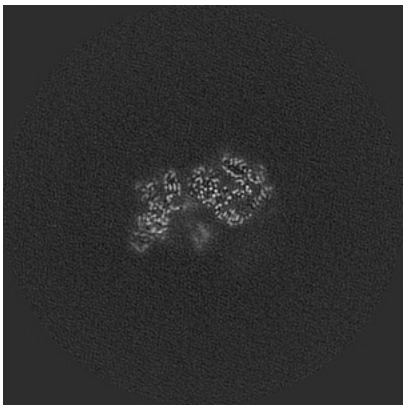
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

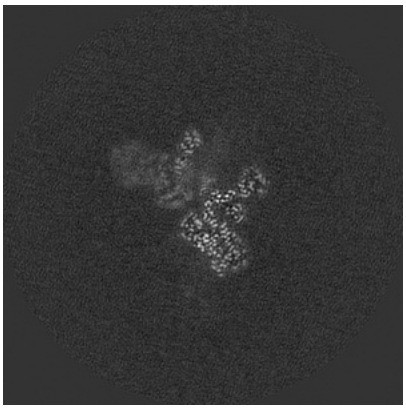
6.2.1 Primary map



X Index: 160

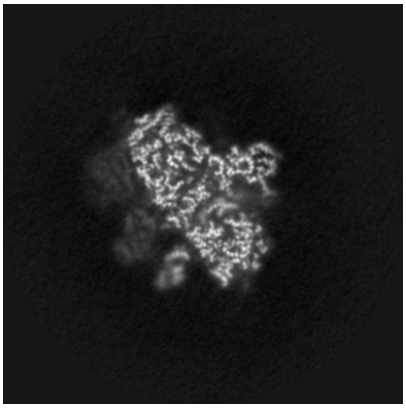


Y Index: 160

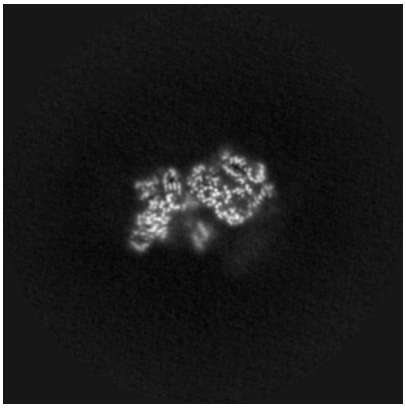


Z Index: 160

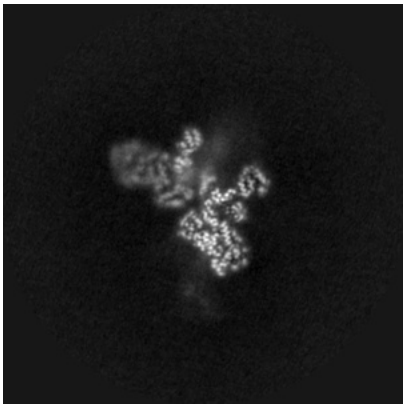
6.2.2 Raw map



X Index: 160



Y Index: 160

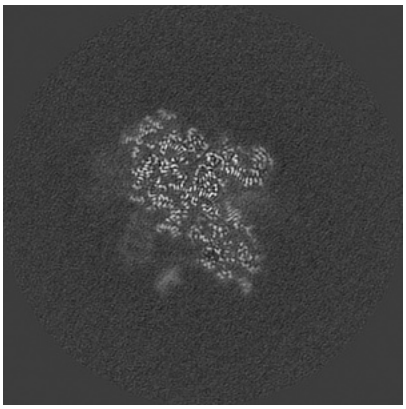


Z Index: 160

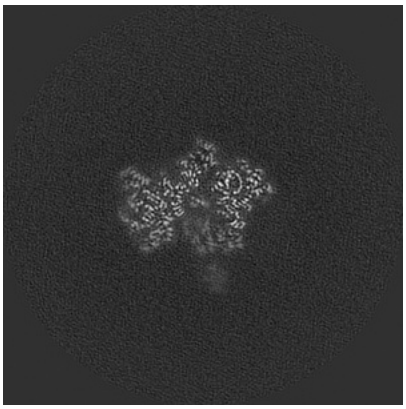
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

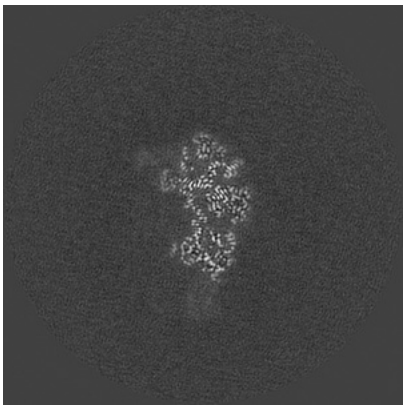
6.3.1 Primary map



X Index: 166

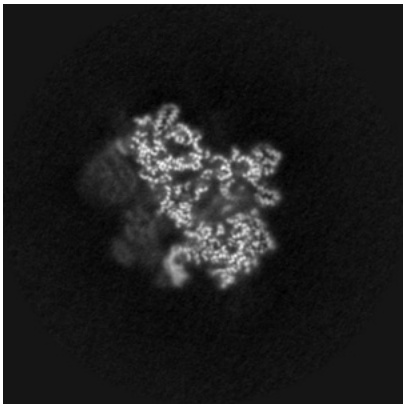


Y Index: 173

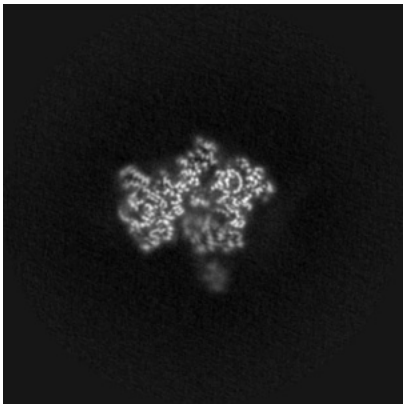


Z Index: 188

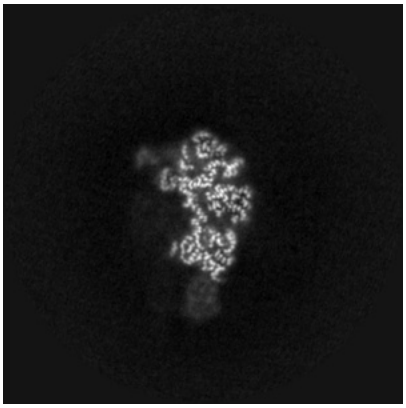
6.3.2 Raw map



X Index: 156



Y Index: 173

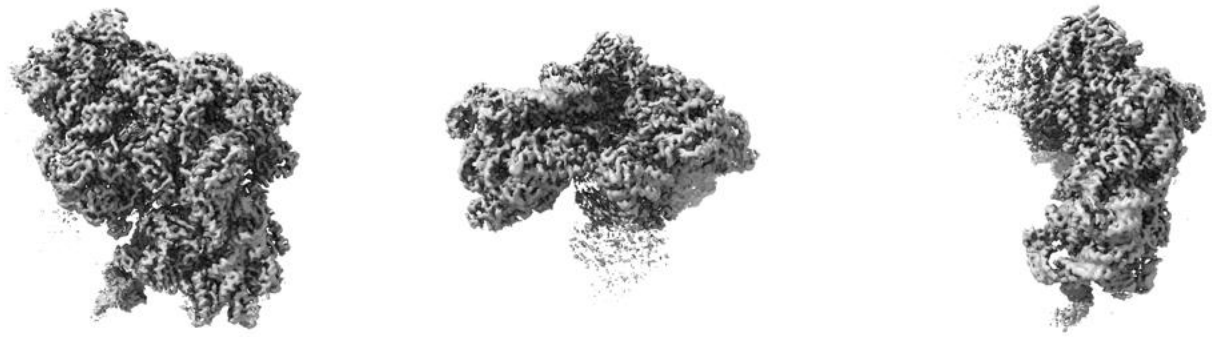


Z Index: 188

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.075. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map

X Y Z

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

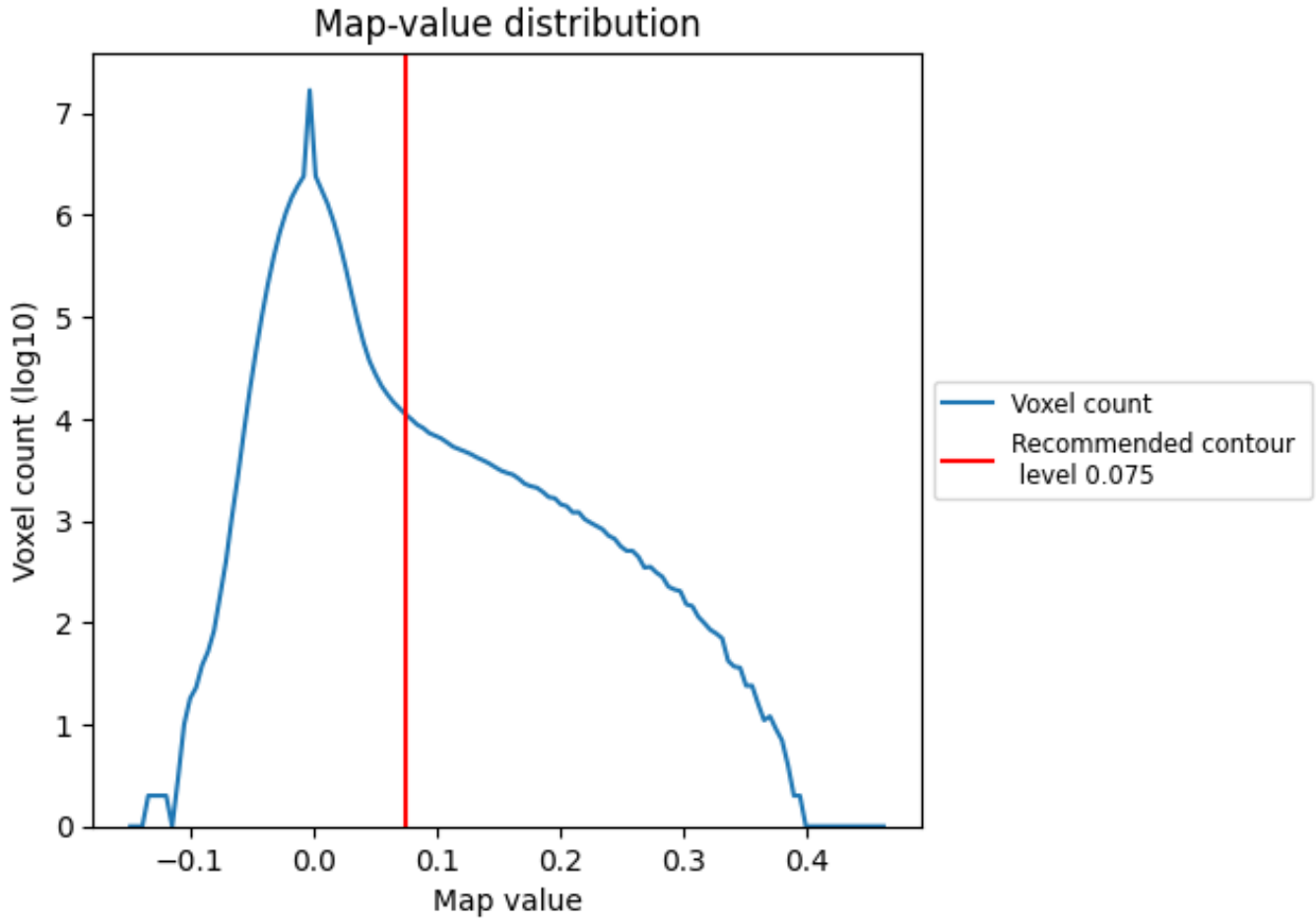
6.5 Mask visualisation (i)

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

7 Map analysis

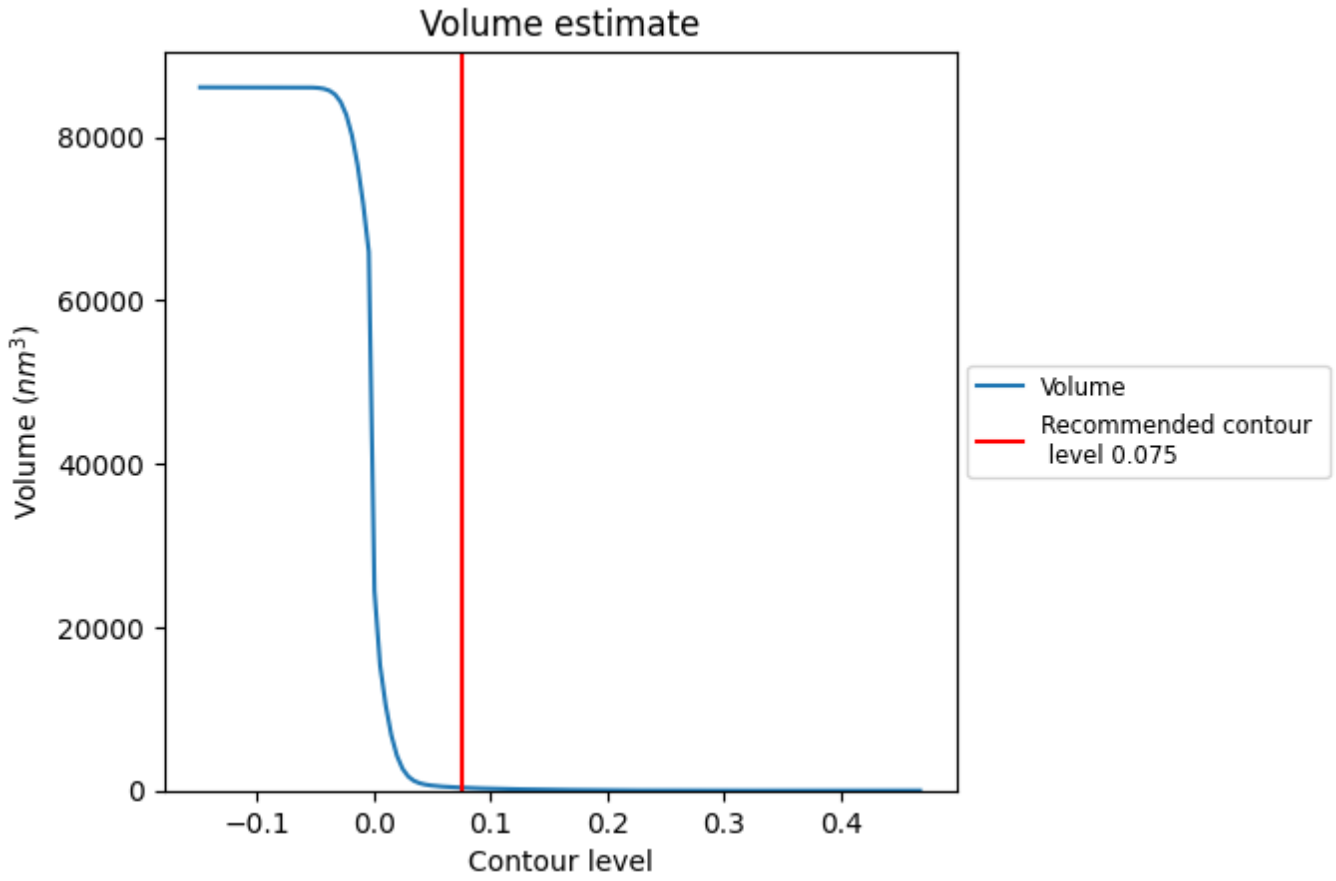
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

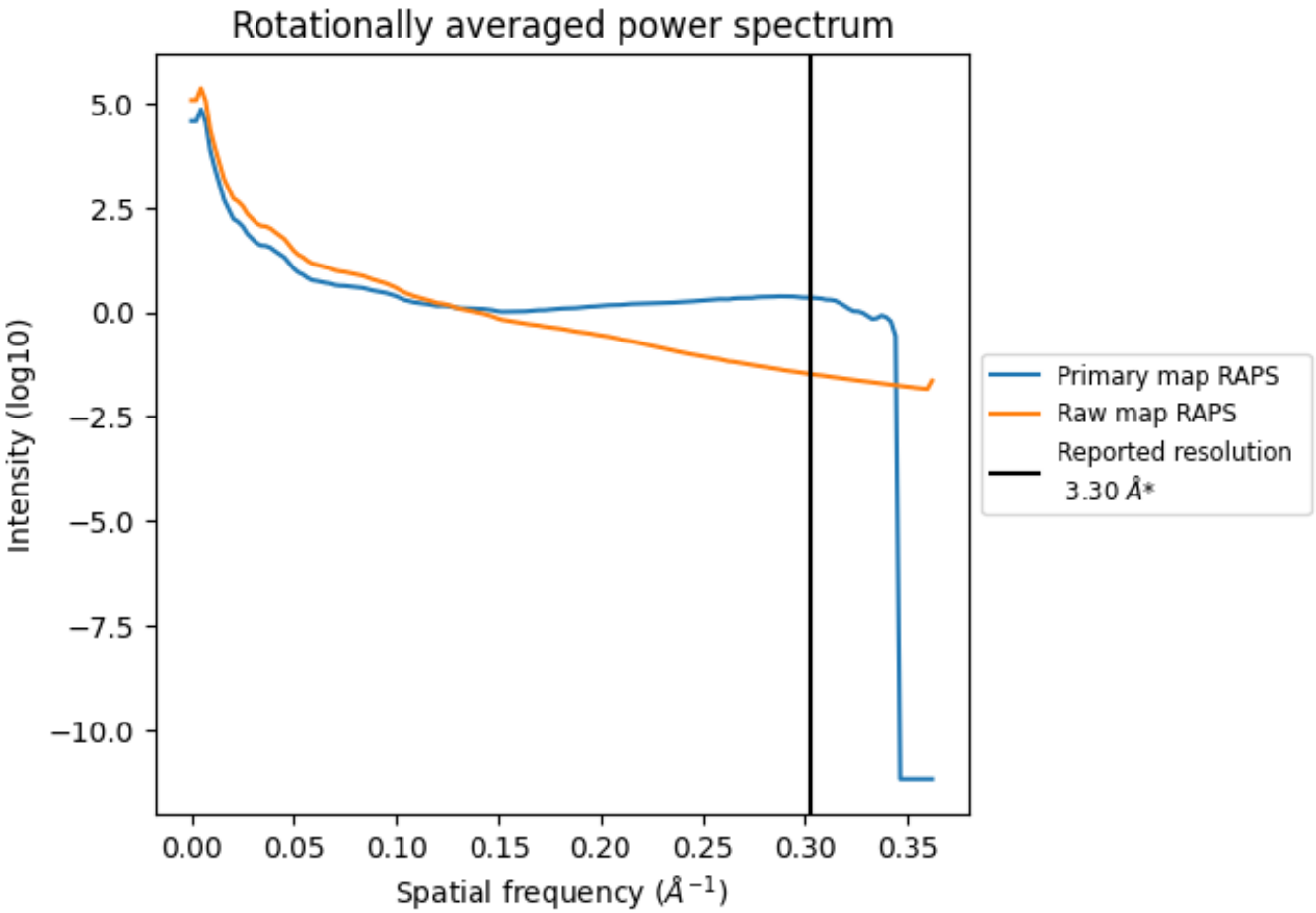
7.2 Volume estimate



The volume at the recommended contour level is 360 nm^3; this corresponds to an approximate mass of 325 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)

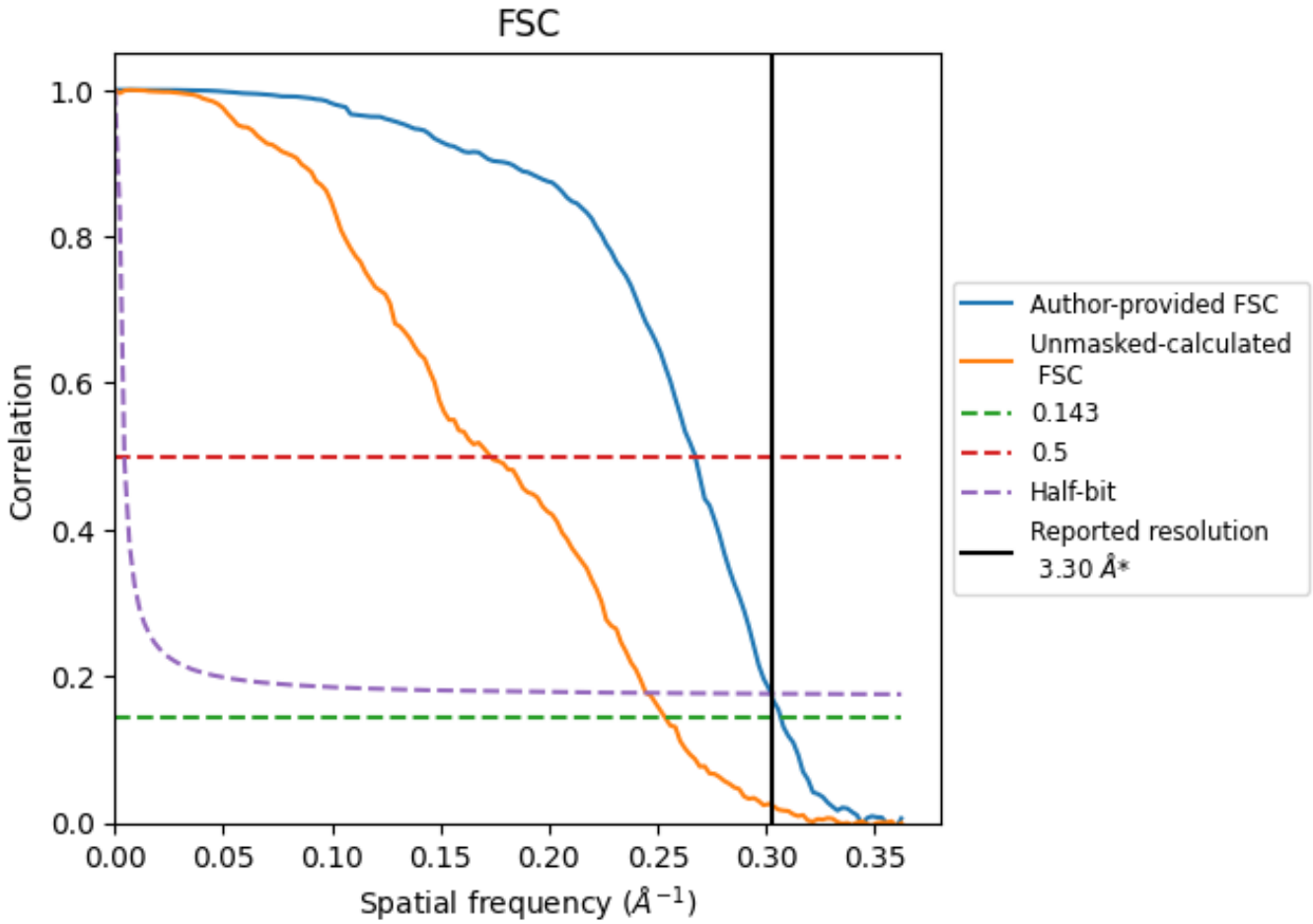


*Reported resolution corresponds to spatial frequency of 0.303 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

8.2 Resolution estimates (i)

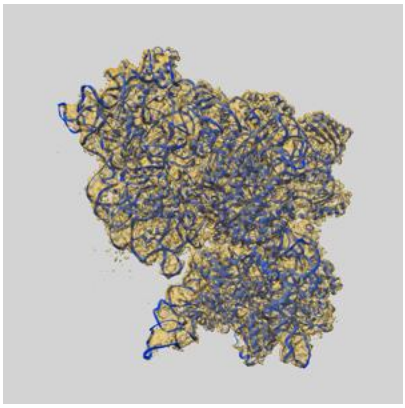
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.26	3.74	3.31
Unmasked-calculated*	3.94	5.78	4.09

*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 3.94 differs from the reported value 3.3 by more than 10 %

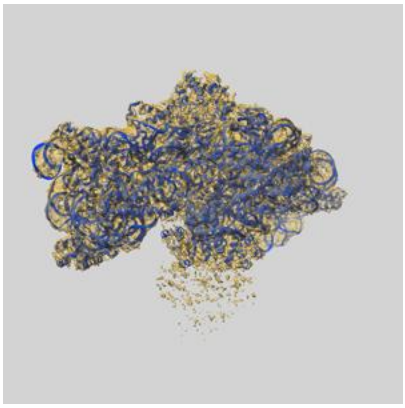
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-31659 and PDB model 7V2P. Per-residue inclusion information can be found in section 3 on page 8.

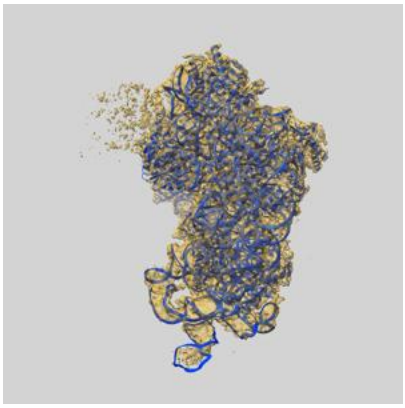
9.1 Map-model overlay



X



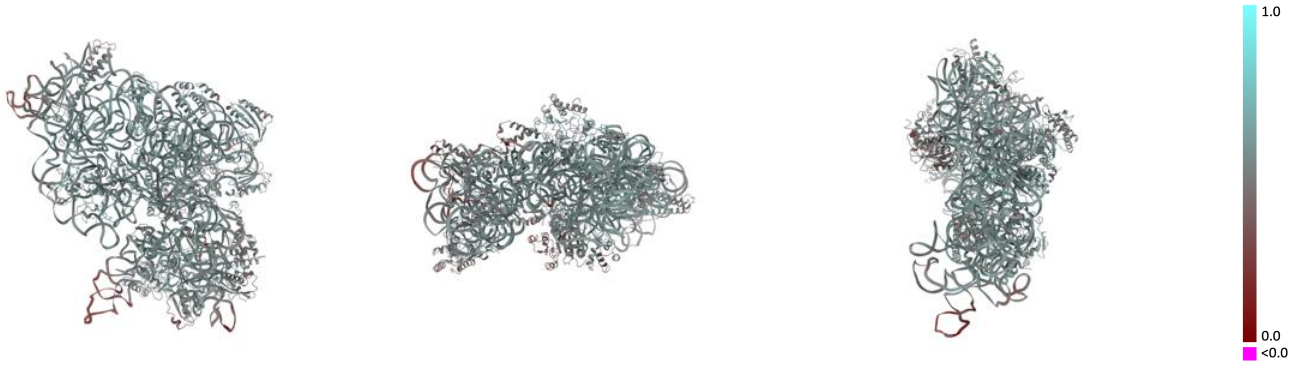
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.075 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.

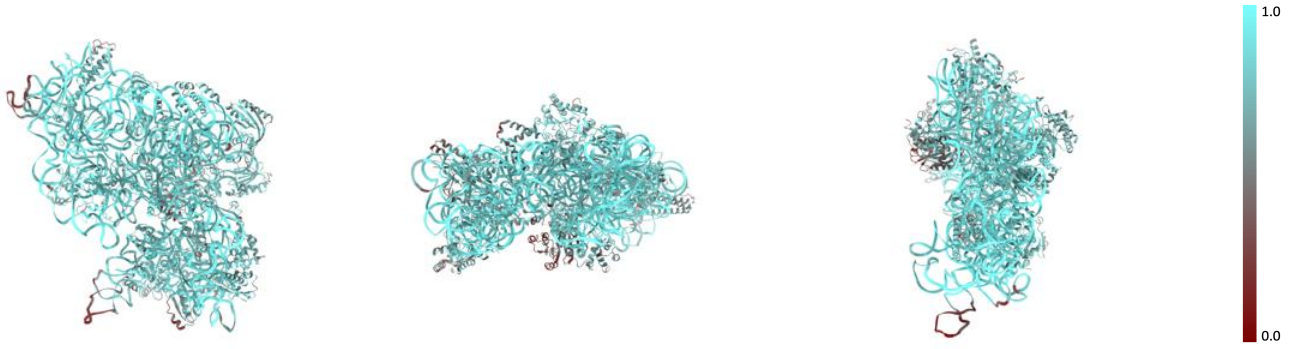
9.2 Q-score mapped to coordinate model



X Y Z

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

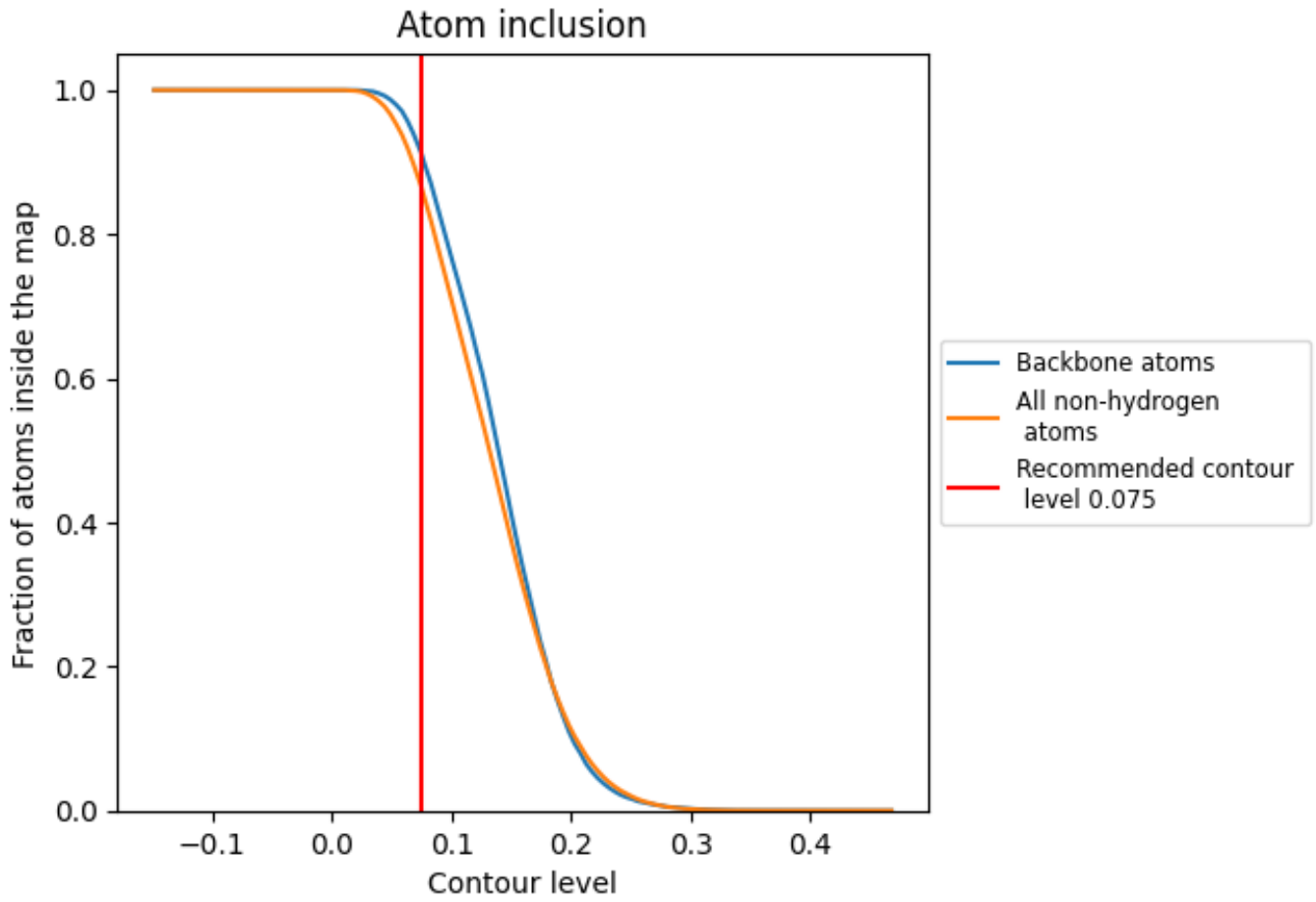
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.075).

9.4 Atom inclusion (i)



At the recommended contour level, 91% of all backbone atoms, 87% 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 (0.075) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8651	0.5300
A	0.9365	0.5370
B	0.7299	0.5160
C	0.7990	0.5320
D	0.8337	0.5440
E	0.8749	0.5610
F	0.7491	0.5250
G	0.7790	0.5100
H	0.8765	0.5680
I	0.7922	0.5140
J	0.6883	0.4930
K	0.7486	0.5200
L	0.8442	0.5540
M	0.6949	0.4730
N	0.9274	0.5710
O	0.8291	0.5370
P	0.9060	0.5710
Q	0.8686	0.5700
R	0.7665	0.5320
S	0.7068	0.4780
T	0.7091	0.5000
U	0.4637	0.4180
V	0.9162	0.5670