



wwPDB EM Validation Summary Report ⓘ

Nov 23, 2022 – 08:41 AM JST

PDB ID : 7V2O
EMDB ID : EMD-31658
Title : T.thermophilus 30S ribosome with KsgA, class K4
Authors : Raina, R.; Singh, J.; Anand, R.; Vinothkumar, K.R.
Deposited on : 2021-08-09
Resolution : 3.50 Å (reported)
Based on initial model : 4B3R

This is a wwPDB EM Validation Summary 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:

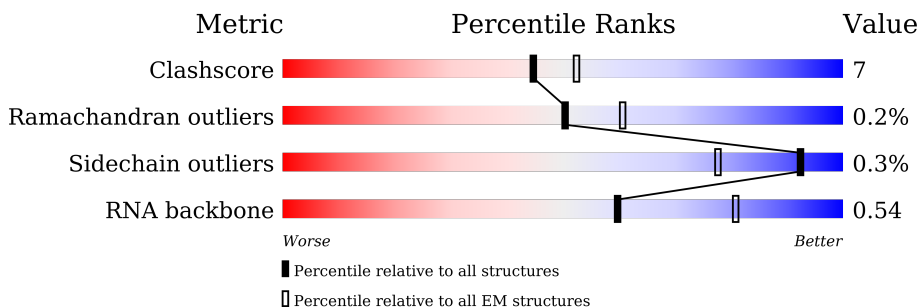
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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 3.50 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 $\leq 5\%$. 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	A	1522	
2	B	256	
3	C	239	
4	D	209	
5	E	162	
6	F	101	
7	G	156	

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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 53005 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	1487	31966	14226	5920	10333	1487	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
			Total	C	N	O	S		
7	G	155	1257	781	252	218	6	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
21	U	264	2069	1321	345	397	6	0	0

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
			Total	C	N	O		
22	V	24	208	128	50	30	0	0

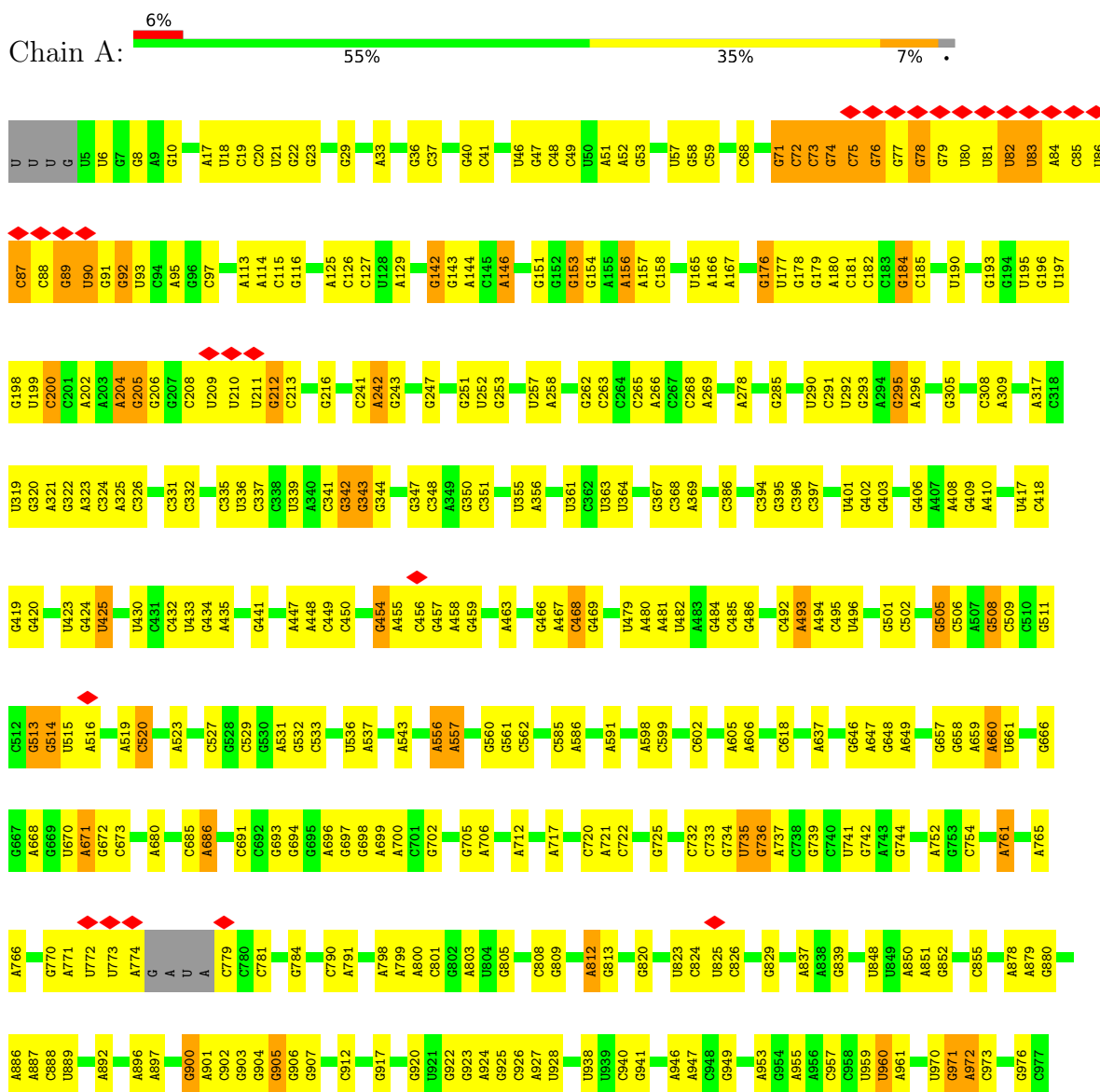
- Molecule 23 is ZINC ION (three-letter code: ZN) (formula: Zn).

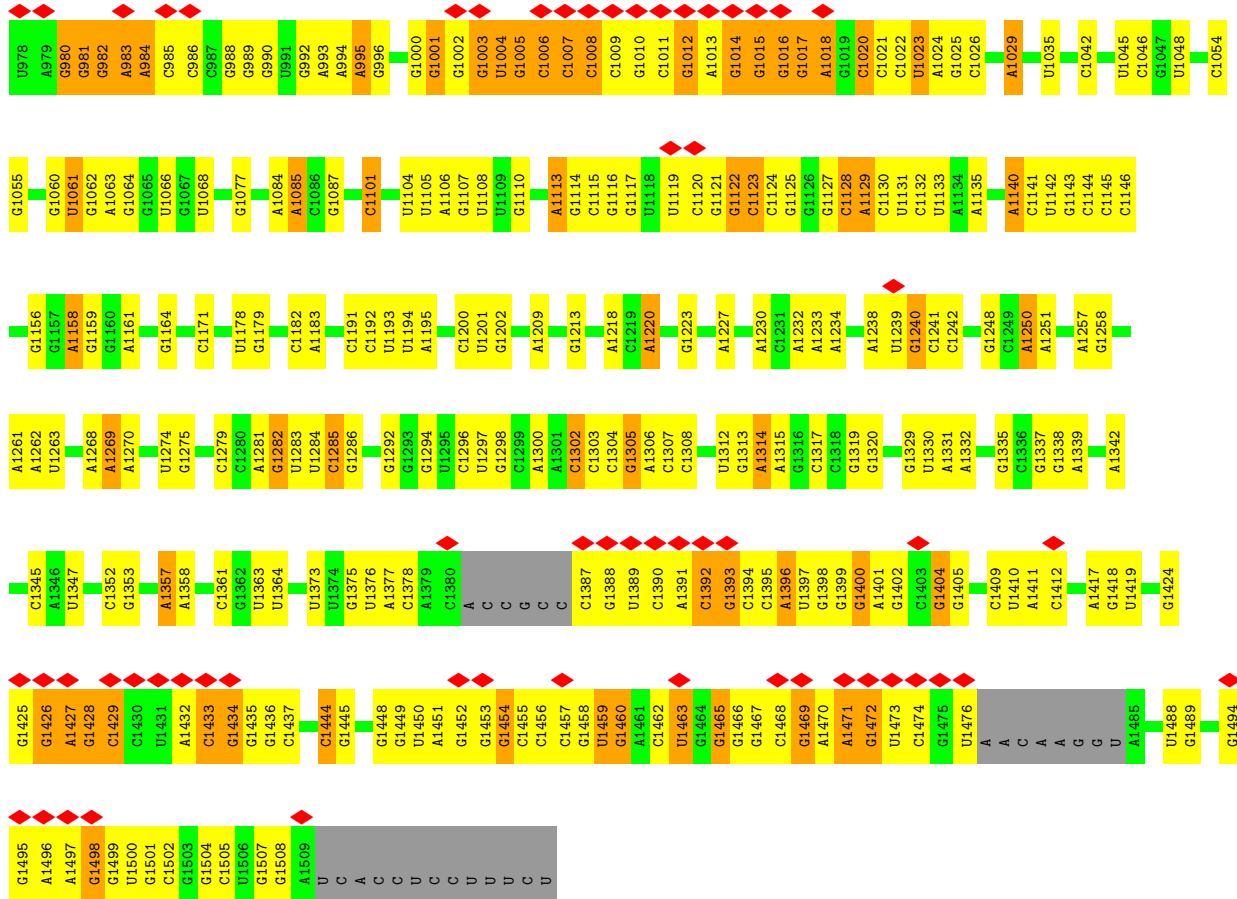
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
23	D	1	1	1	0
23	N	1	1	1	0

3 Residue-property plots [i](#)

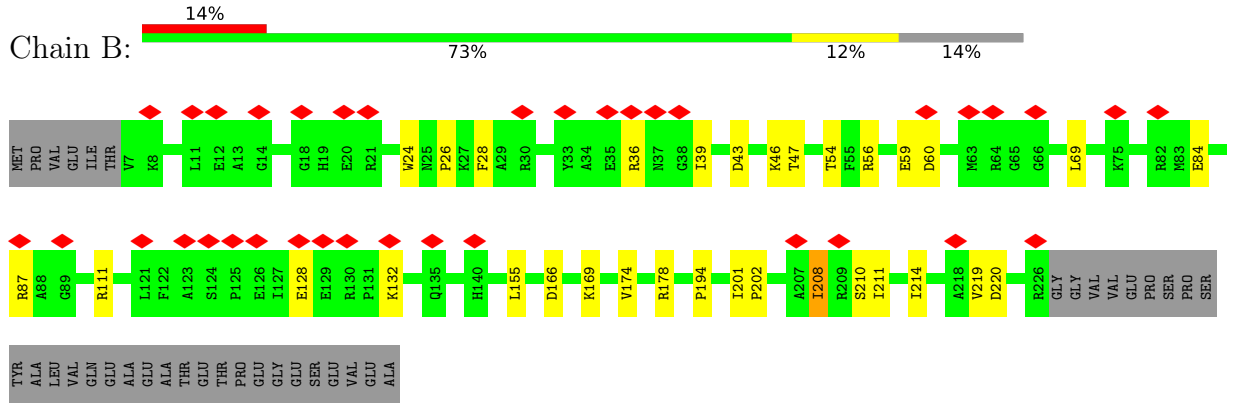
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16s ribosomal RNA

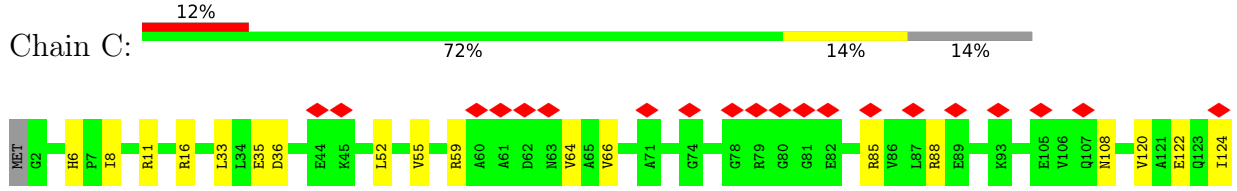


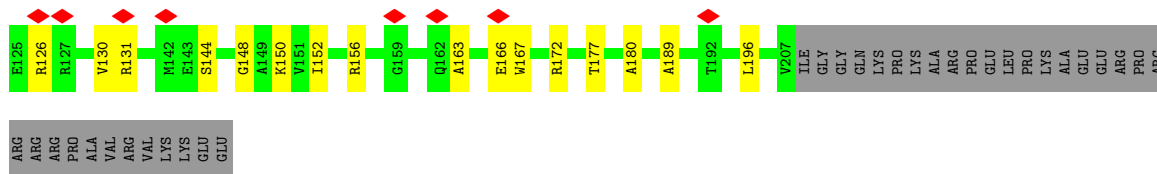


• Molecule 2: 30S ribosomal protein S2

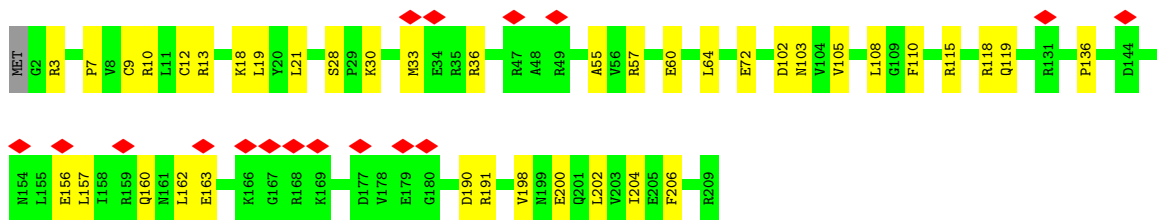
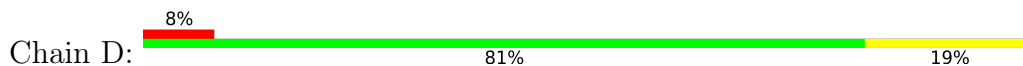


• Molecule 3: 30S ribosomal protein S3

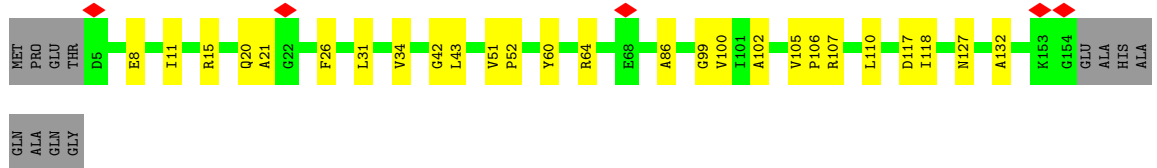
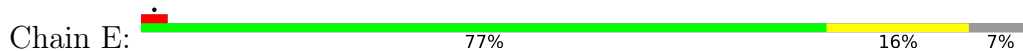




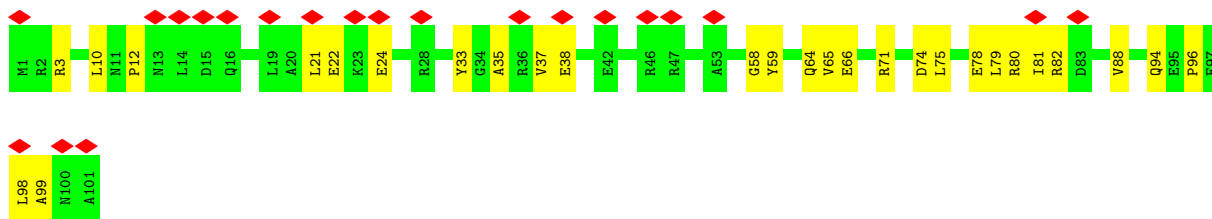
• Molecule 4: 30S ribosomal protein S4



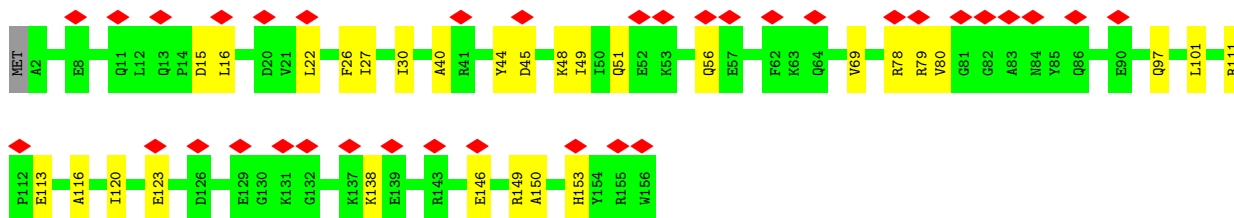
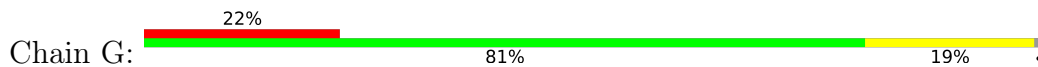
• Molecule 5: 30S ribosomal protein S5



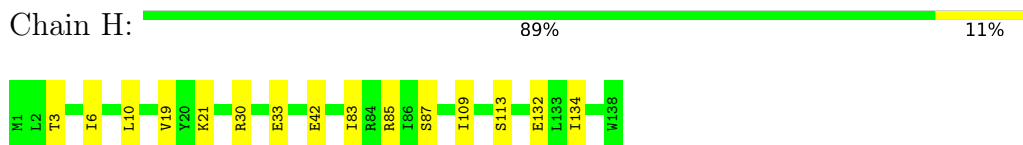
• Molecule 6: 30S ribosomal protein S6



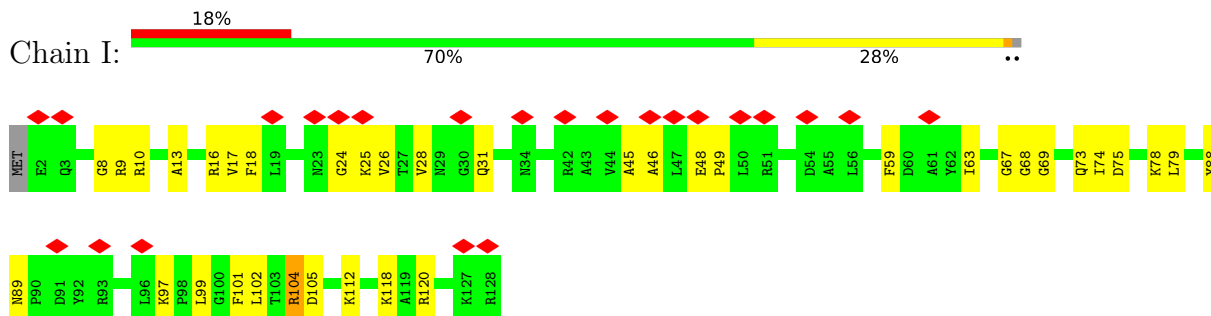
• Molecule 7: 30S ribosomal protein S7



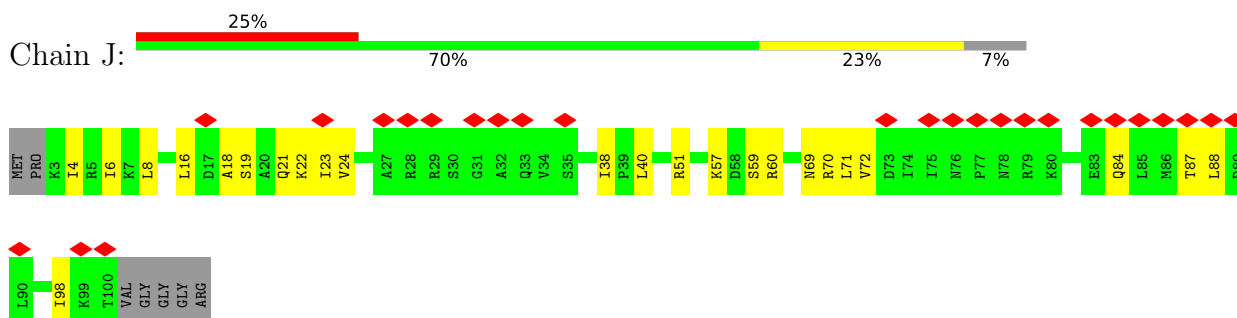
- Molecule 8: 30S ribosomal protein S8



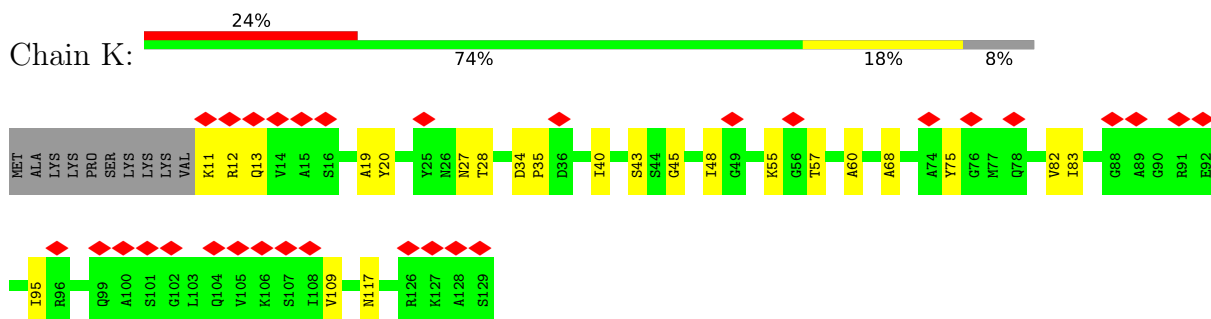
- Molecule 9: 30S ribosomal protein S9



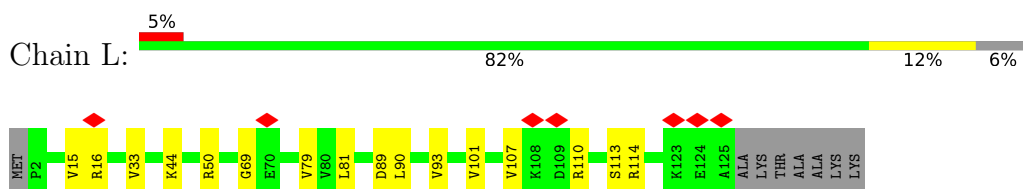
- Molecule 10: 30S ribosomal protein S10



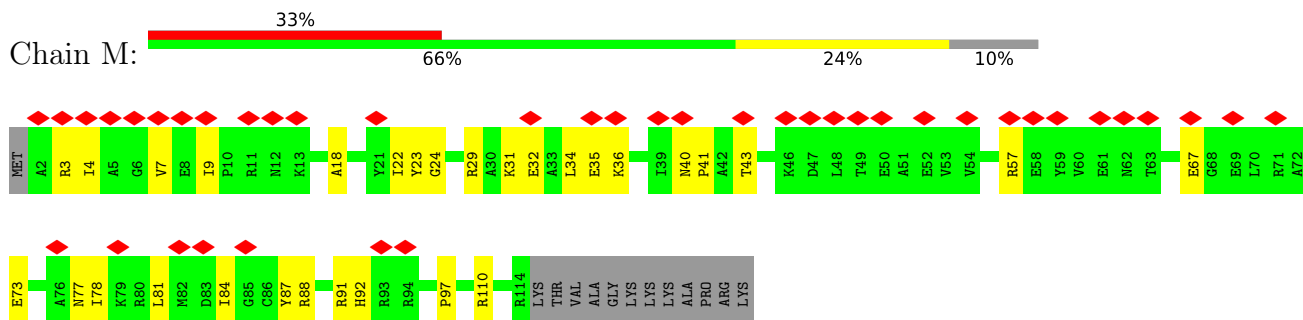
- Molecule 11: 30S ribosomal protein S11



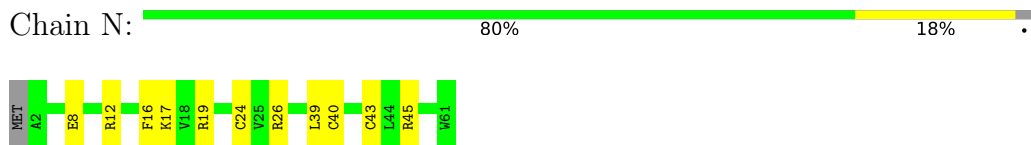
- Molecule 12: 30S ribosomal protein S12



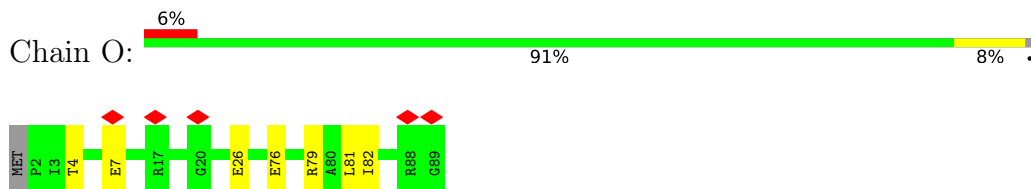
- Molecule 13: 30S ribosomal protein S13



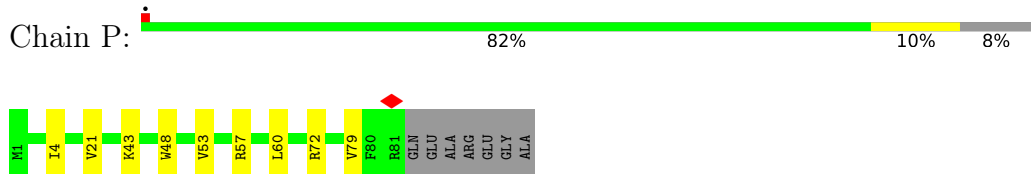
• Molecule 14: 30S ribosomal protein S14 type Z



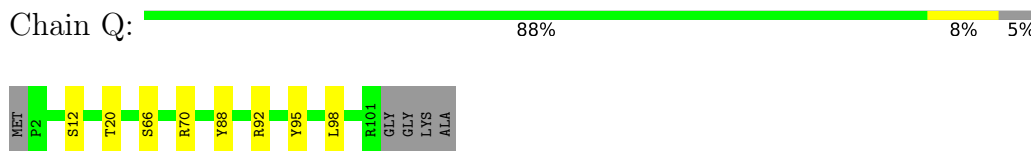
• Molecule 15: 30S ribosomal protein S15



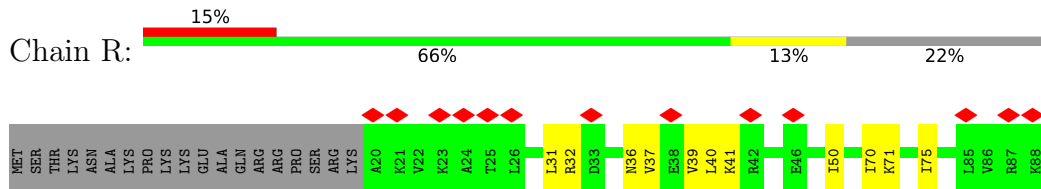
• Molecule 16: 30S ribosomal protein S16



• Molecule 17: 30S ribosomal protein S17

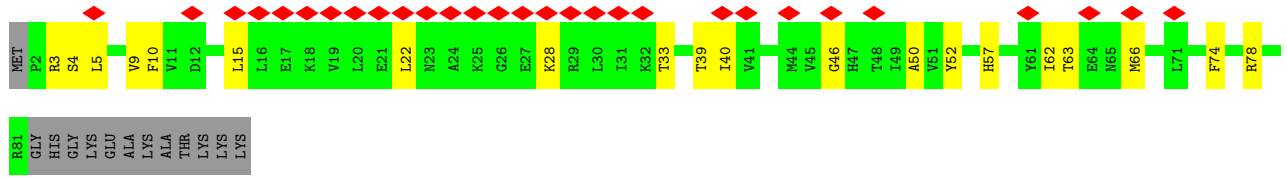


• Molecule 18: 30S ribosomal protein S18

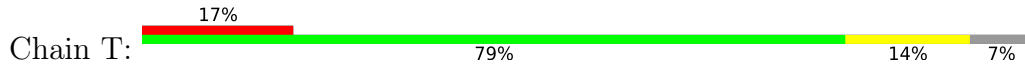


• Molecule 19: 30S ribosomal protein S19

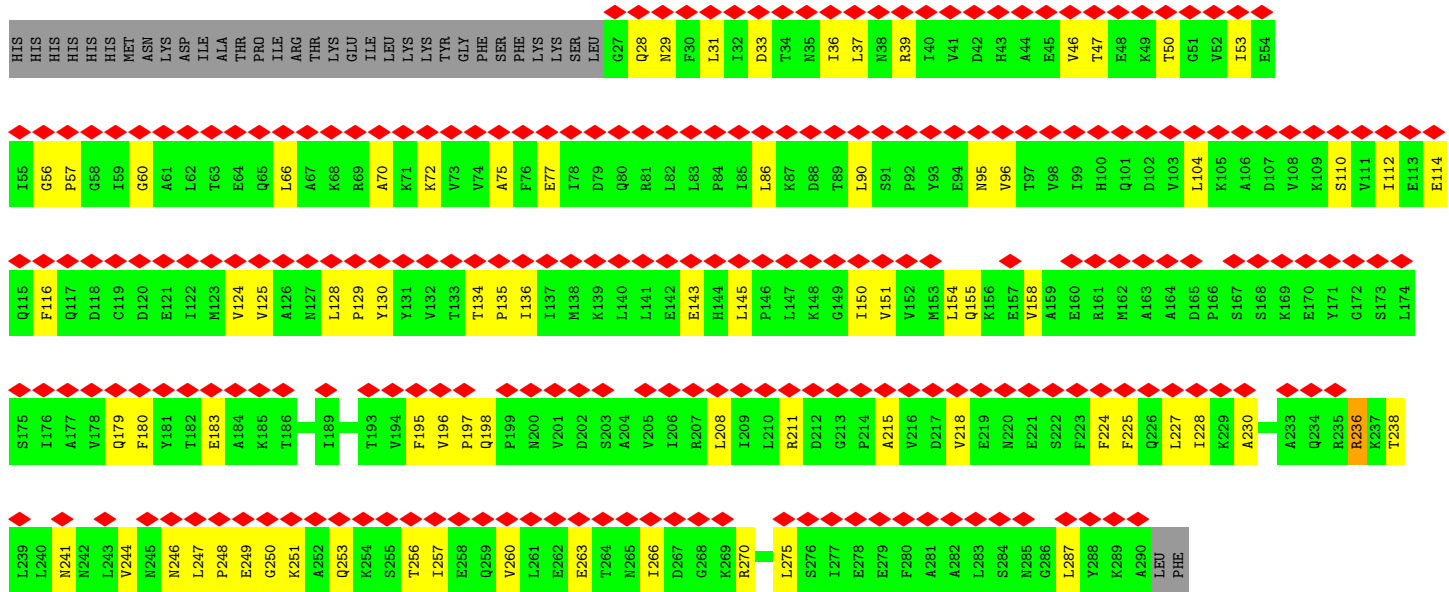
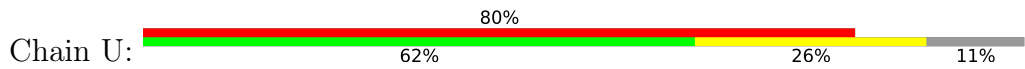




• Molecule 20: 30S ribosomal protein S20



• Molecule 21: Ribosomal RNA small subunit methyltransferase A



• Molecule 22: 30S ribosomal protein Thx



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	64307	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 ($e^-/\text{\AA}^2$)	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	0.373	Depositor
Minimum map value	-0.107	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	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 [i](#)

5.1 Standard geometry [i](#)

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	0.56	0/35779	0.78	2/55837 (0.0%)
2	B	0.25	0/1834	0.56	0/2469
3	C	0.26	0/1636	0.58	0/2205
4	D	0.27	0/1733	0.57	0/2318
5	E	0.27	0/1162	0.58	0/1564
6	F	0.25	0/856	0.61	0/1154
7	G	0.25	0/1276	0.60	0/1709
8	H	0.26	0/1136	0.56	0/1527
9	I	0.27	0/1029	0.61	0/1379
10	J	0.26	0/807	0.62	0/1085
11	K	0.27	0/900	0.60	0/1213
12	L	0.25	0/986	0.61	0/1320
13	M	0.26	0/915	0.65	0/1227
14	N	0.26	0/501	0.55	0/664
15	O	0.25	0/745	0.59	0/992
16	P	0.26	0/698	0.60	0/939
17	Q	0.25	0/847	0.56	0/1131
18	R	0.26	0/570	0.59	0/757
19	S	0.26	0/661	0.57	0/890
20	T	0.27	0/765	0.61	0/1007
21	U	0.25	0/2099	0.56	0/2844
22	V	0.32	0/212	0.57	0/277
All	All	0.47	0/57147	0.72	2/84508 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1061	U	C2'-C3'-O3'	5.21	122.04	113.70
1	A	156	A	C2'-C3'-O3'	5.03	121.75	113.70

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	A	31966	0	16134	323	0
2	B	1802	0	1855	17	0
3	C	1612	0	1677	18	0
4	D	1703	0	1763	27	0
5	E	1146	0	1207	17	0
6	F	843	0	857	16	0
7	G	1257	0	1296	20	0
8	H	1116	0	1177	8	0
9	I	1010	0	1037	21	0
10	J	794	0	840	14	0
11	K	885	0	904	15	0
12	L	970	0	1057	10	0
13	M	905	0	958	19	0
14	N	492	0	529	7	0
15	O	734	0	771	5	0
16	P	682	0	706	5	0
17	Q	834	0	904	5	0
18	R	565	0	631	7	0
19	S	647	0	673	12	0
20	T	763	0	861	13	0
21	U	2069	0	2134	48	0
22	V	208	0	221	2	0
23	D	1	0	0	0	0
23	N	1	0	0	0	0
All	All	53005	0	38192	600	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 7.

The worst 5 of 600 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)
19:S:22:LEU:HD11	19:S:28:LYS:HB3	1.60	0.83
1:A:1398:G:H1	1:A:1463:U:H3	1.29	0.80
1:A:982:G:H1'	1:A:983:A:H4'	1.63	0.78
1:A:905:G:H1	1:A:1373:U:H3	1.28	0.78
1:A:648:G:H22	1:A:725:G:H1	1.34	0.75

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%)	199 (91%)	18 (8%)	1 (0%)	29	68
3	C	204/239 (85%)	189 (93%)	14 (7%)	1 (0%)	29	68
4	D	206/209 (99%)	200 (97%)	6 (3%)	0	100	100
5	E	148/162 (91%)	143 (97%)	5 (3%)	0	100	100
6	F	99/101 (98%)	94 (95%)	5 (5%)	0	100	100
7	G	153/156 (98%)	148 (97%)	5 (3%)	0	100	100
8	H	136/138 (99%)	131 (96%)	5 (4%)	0	100	100
9	I	125/128 (98%)	115 (92%)	10 (8%)	0	100	100
10	J	96/105 (91%)	88 (92%)	8 (8%)	0	100	100
11	K	117/129 (91%)	110 (94%)	7 (6%)	0	100	100
12	L	122/132 (92%)	111 (91%)	10 (8%)	1 (1%)	19	58
13	M	111/126 (88%)	104 (94%)	7 (6%)	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%)	75 (95%)	4 (5%)	0	100	100
17	Q	98/105 (93%)	94 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	92 (95%)	5 (5%)	0	100	100
21	U	262/298 (88%)	248 (95%)	12 (5%)	2 (1%)	19	58
22	V	22/27 (82%)	22 (100%)	0	0	100	100
All	All	2582/2836 (91%)	2440 (94%)	137 (5%)	5 (0%)	50	81

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	L	44	LYS
3	C	167	TRP
21	U	198	GLN
2	B	208	ILE
21	U	266	ILE

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%)	190 (100%)	1 (0%)	88	94
3	C	160/188 (85%)	160 (100%)	0	100	100
4	D	180/181 (99%)	180 (100%)	0	100	100
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	88
10	J	88/92 (96%)	88 (100%)	0	100	100
11	K	90/99 (91%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	48 (98%)	1 (2%)	55	79
15	O	79/80 (99%)	79 (100%)	0	100	100
16	P	70/74 (95%)	69 (99%)	1 (1%)	67	85
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	72
20	T	76/82 (93%)	76 (100%)	0	100	100
21	U	232/264 (88%)	231 (100%)	1 (0%)	91	96
22	V	19/22 (86%)	19 (100%)	0	100	100
All	All	2203/2374 (93%)	2196 (100%)	7 (0%)	92	97

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	P	72	ARG
19	S	5	LEU
21	U	236	ARG
19	S	78	ARG
14	N	17	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
10	J	13	HIS
11	K	13	GLN
21	U	242	ASN
13	M	40	ASN
6	F	64	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1483/1522 (97%)	338 (22%)	21 (1%)

5 of 338 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	U
1	A	8	G
1	A	10	G
1	A	33	A
1	A	40	G

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1061	U
1	A	1363	U
1	A	1497	A
1	A	1400	G
1	A	1284	U

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

There are no chain breaks in this entry.

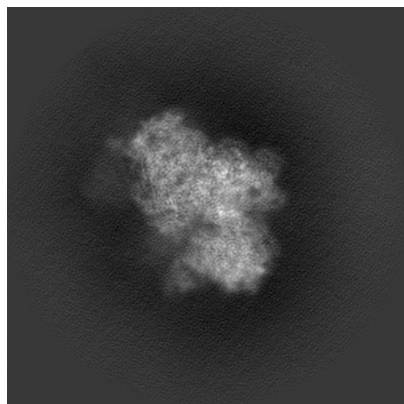
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31658. These allow visual inspection of the internal detail of the map and identification of artifacts.

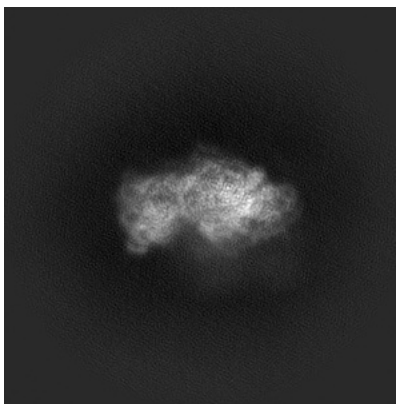
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

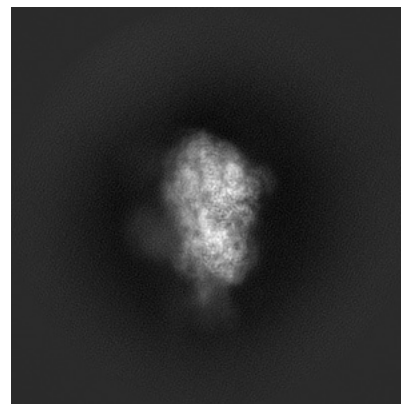
6.1.1 Primary map



X

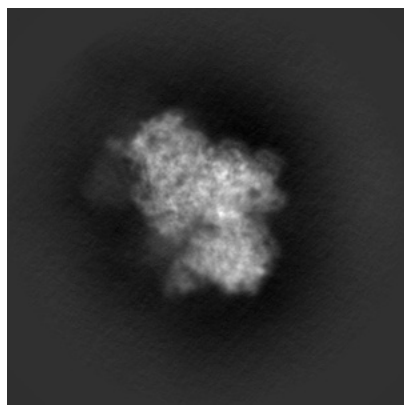


Y

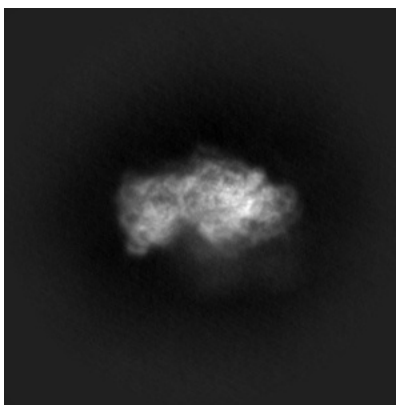


Z

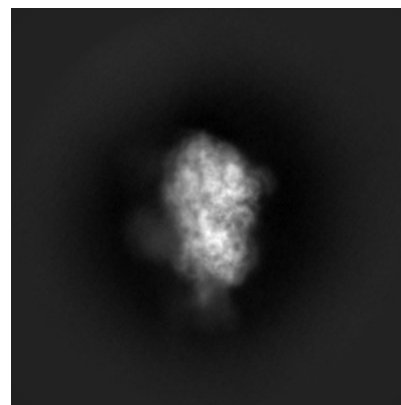
6.1.2 Raw map



X



Y

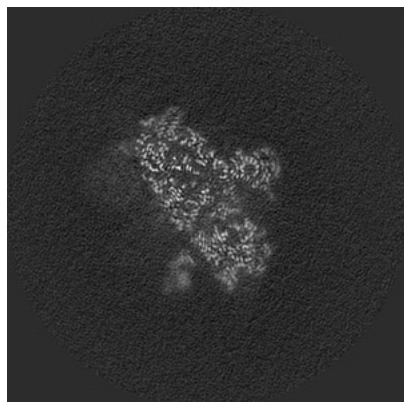


Z

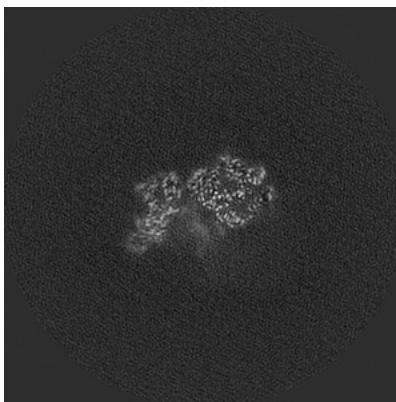
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

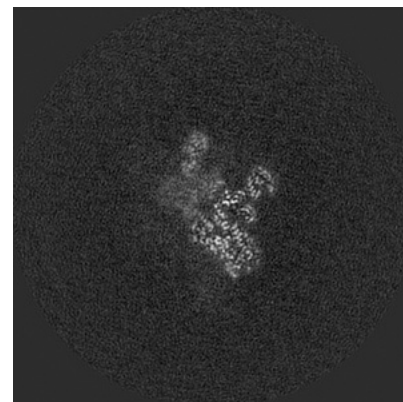
6.2.1 Primary map



X Index: 160

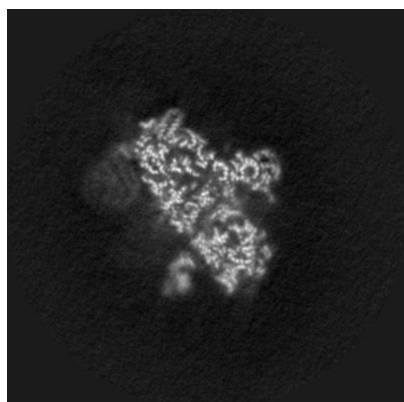


Y Index: 160

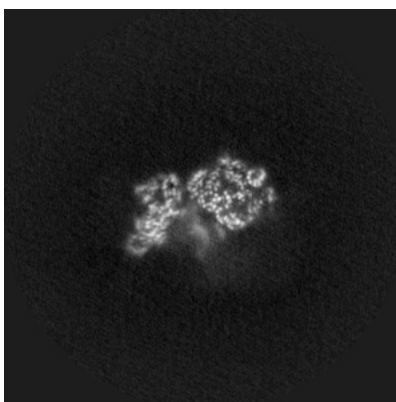


Z Index: 160

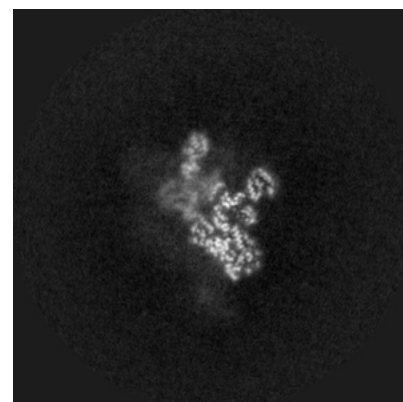
6.2.2 Raw map



X Index: 160



Y Index: 160

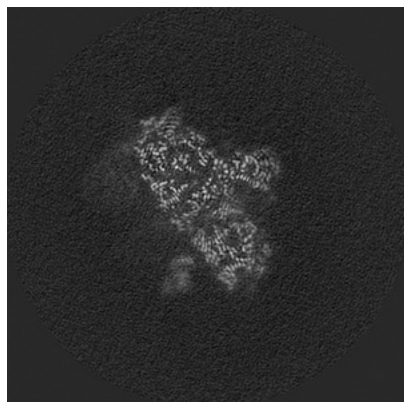


Z Index: 160

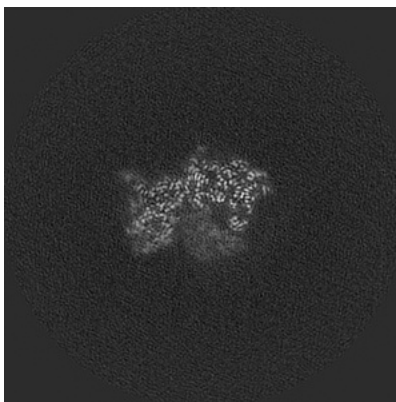
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

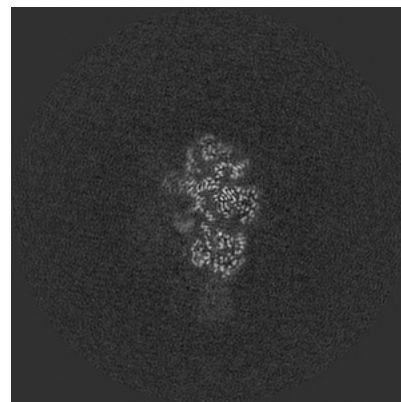
6.3.1 Primary map



X Index: 161

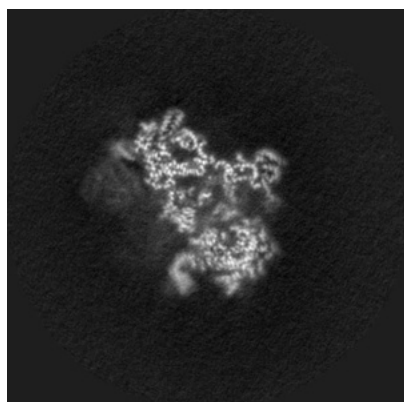


Y Index: 170

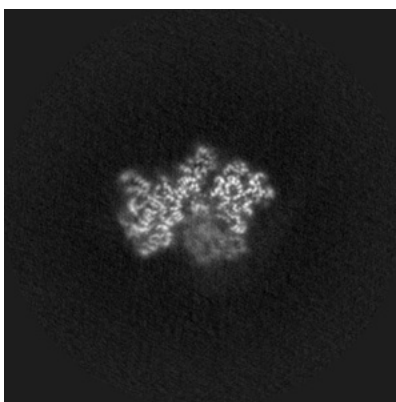


Z Index: 187

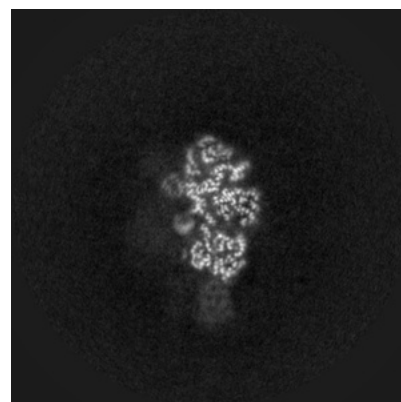
6.3.2 Raw map



X Index: 157



Y Index: 173

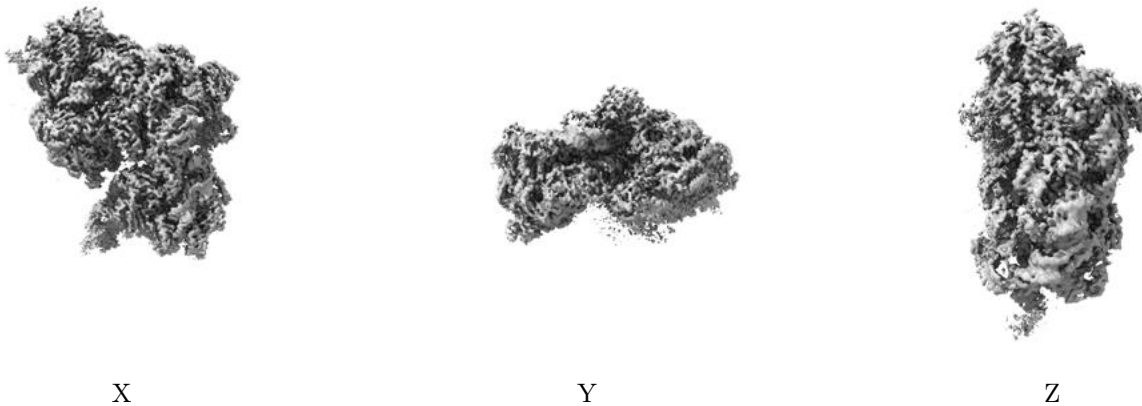


Z Index: 187

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

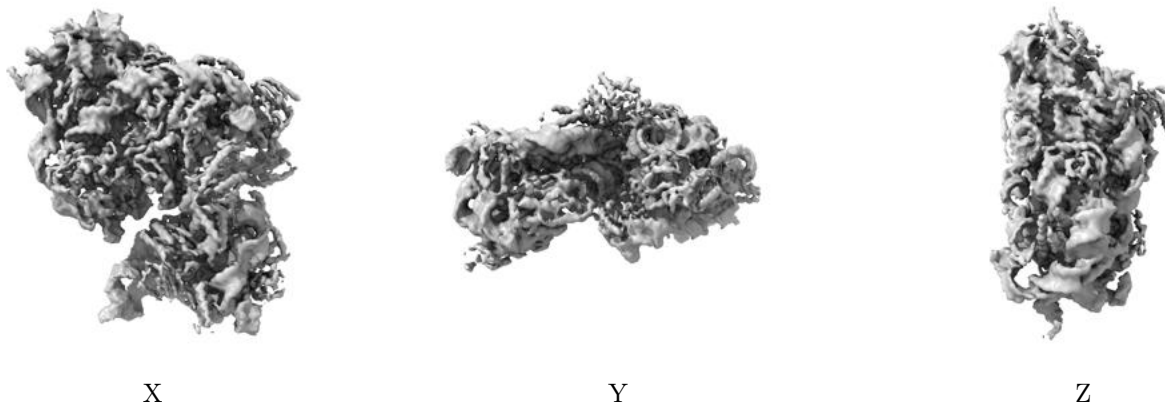
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



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



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.

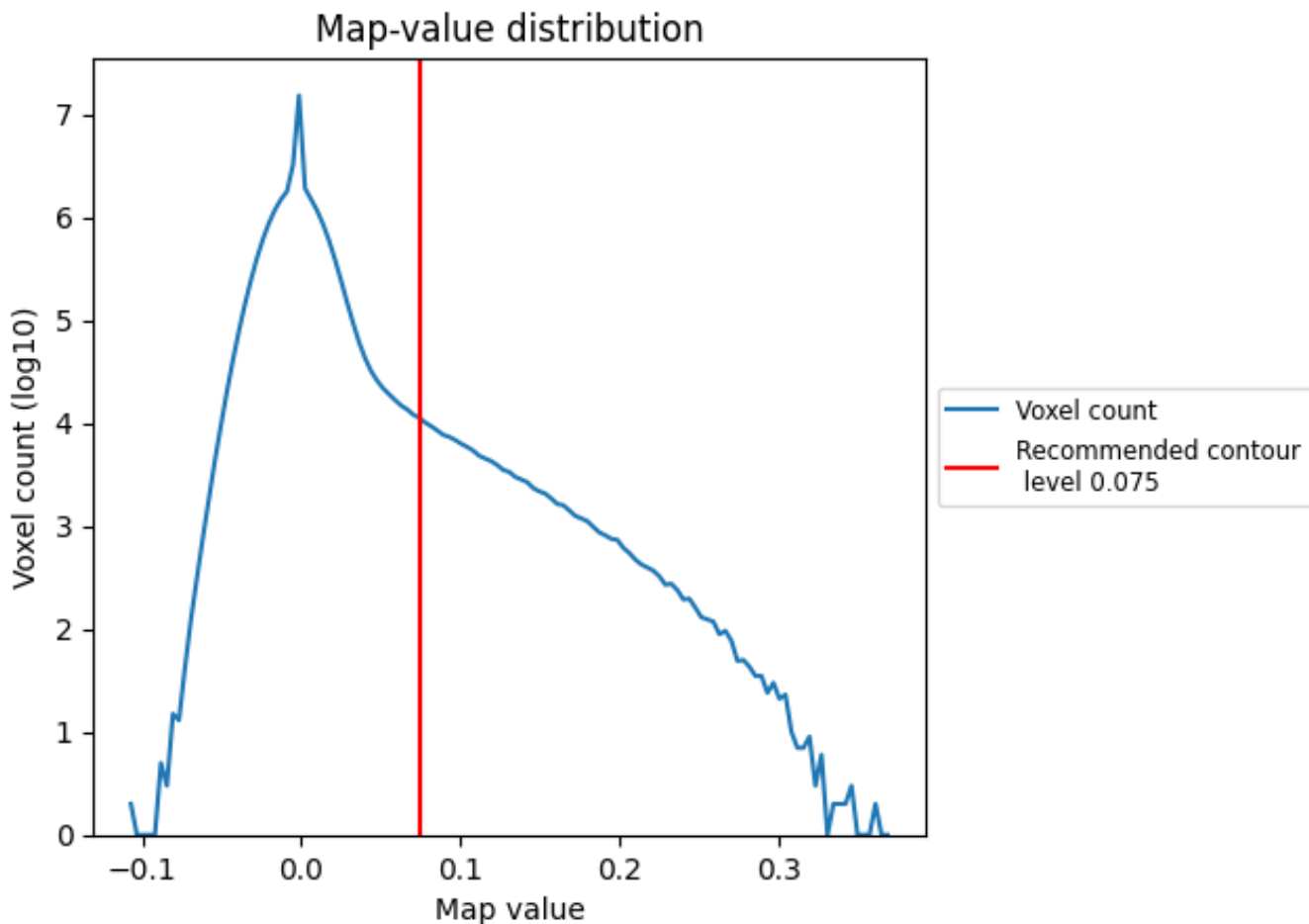
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

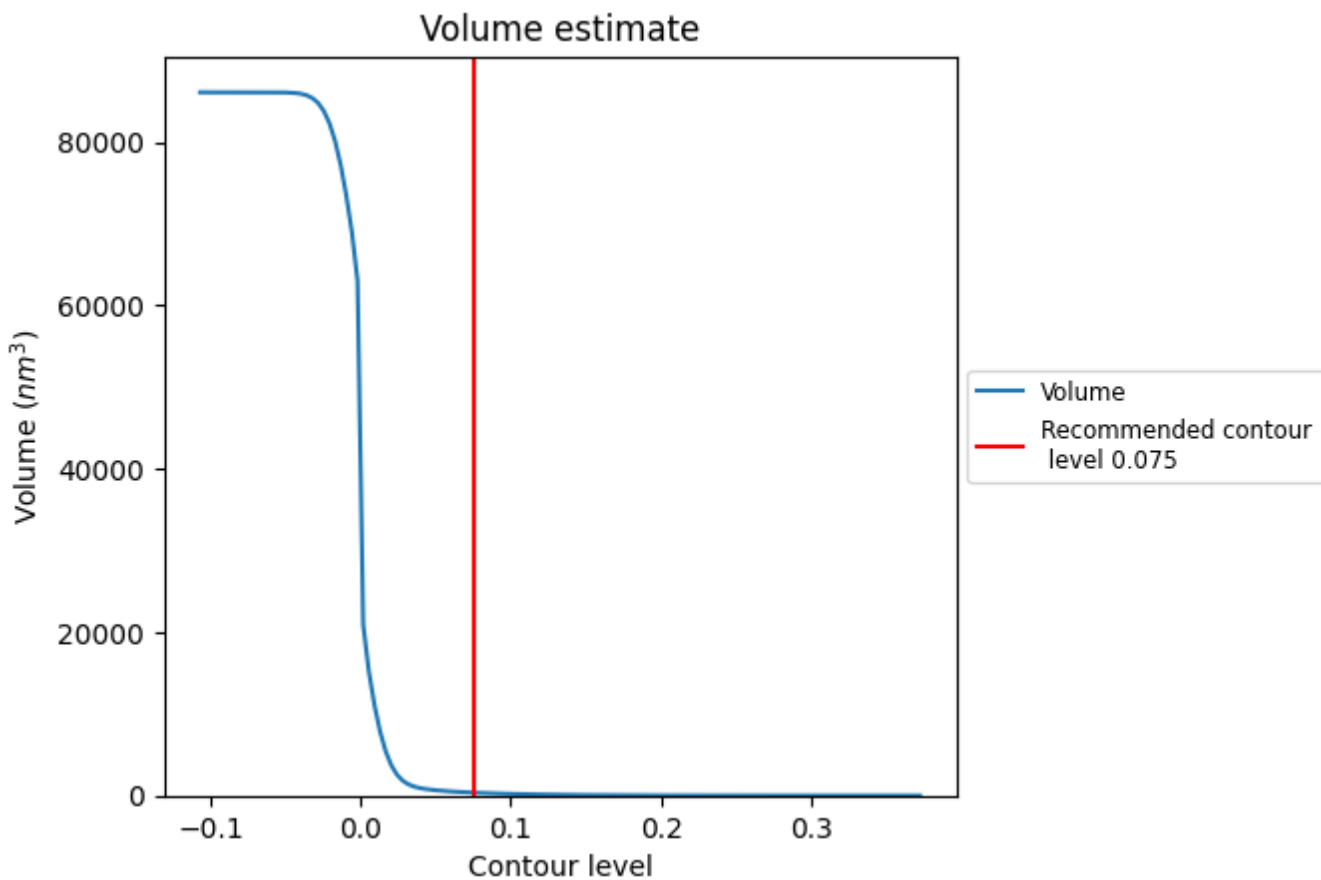
This section contains the results of statistical analysis of the map.

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.

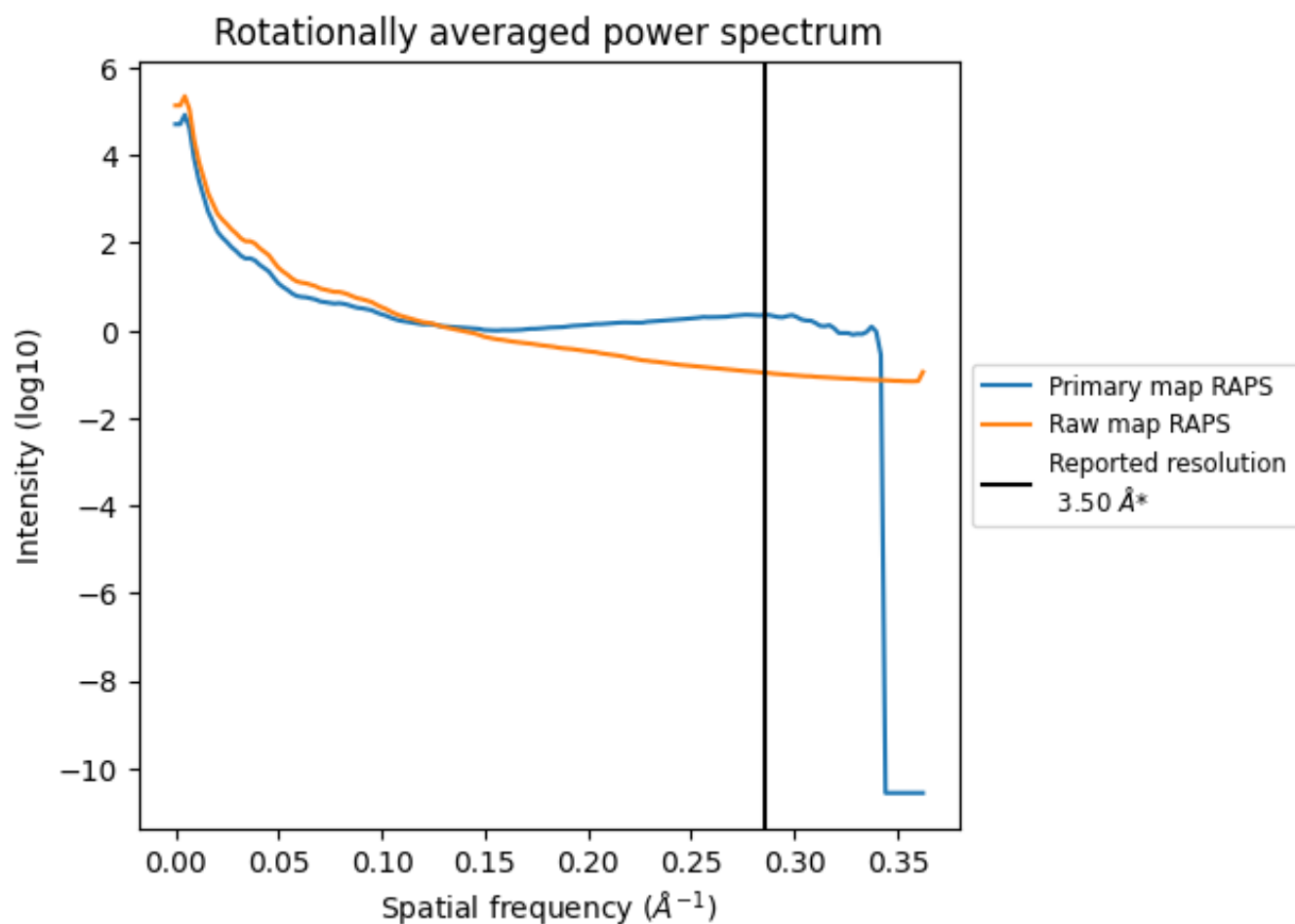
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 358 nm³; this corresponds to an approximate mass of 323 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](#)

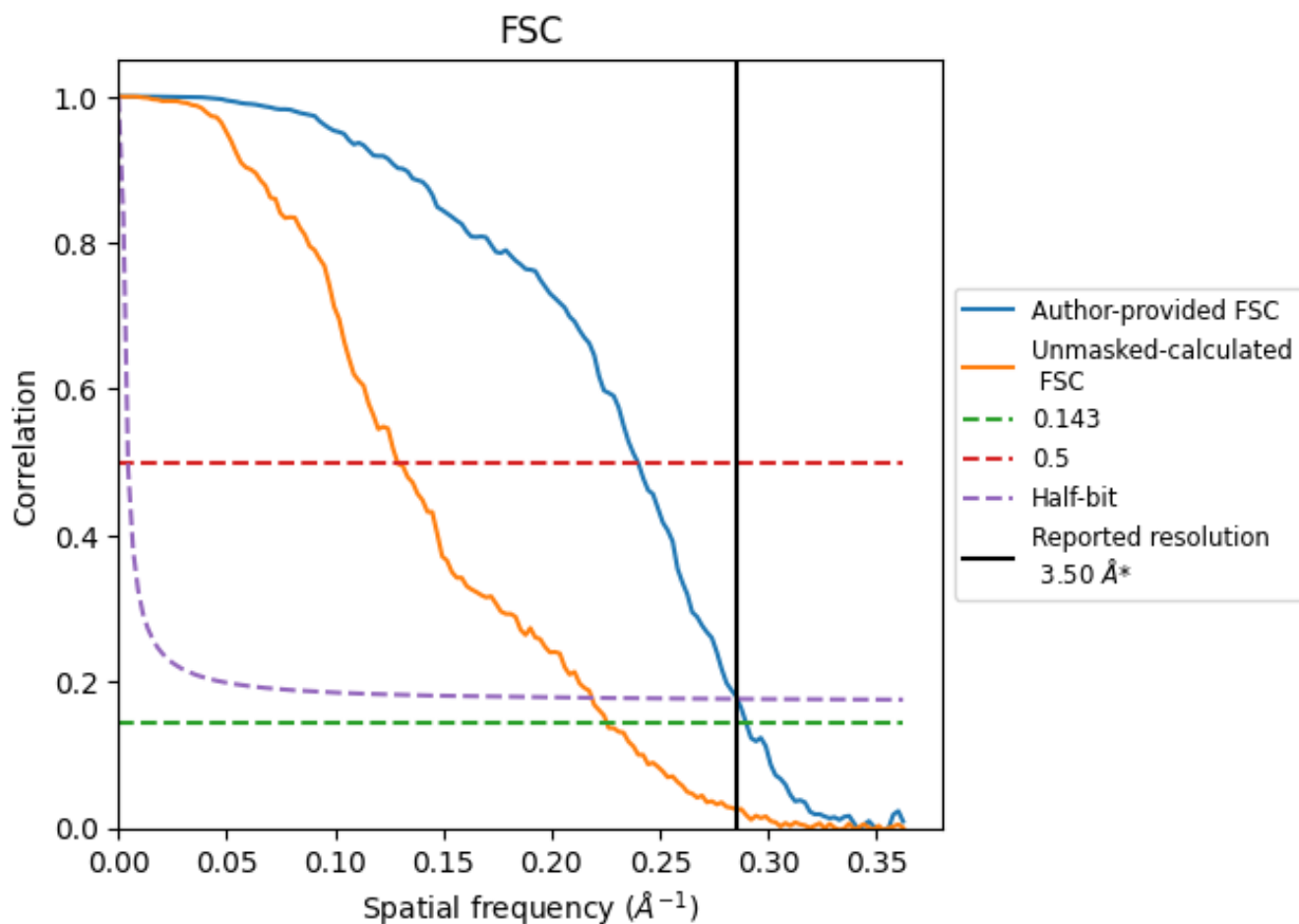


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

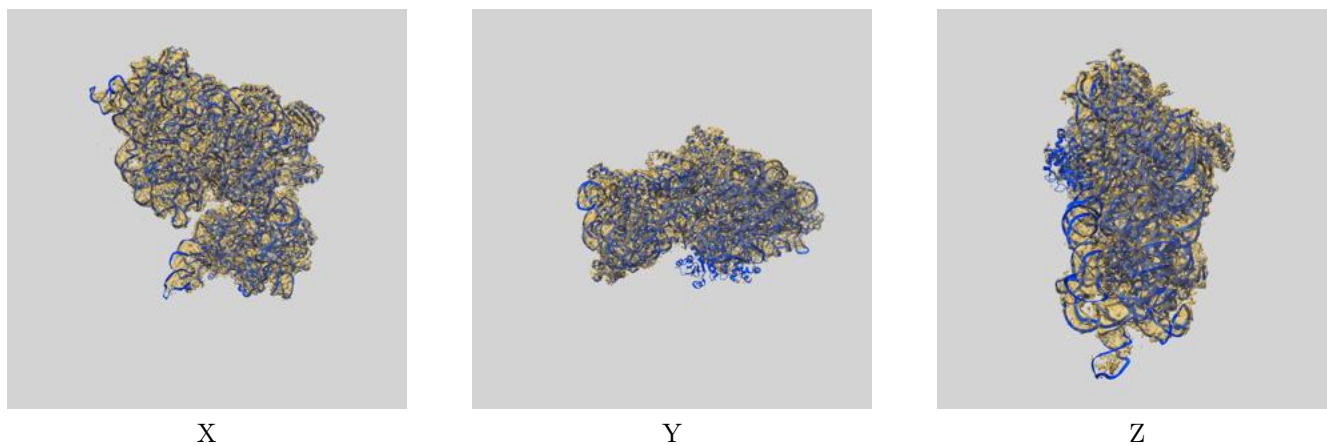
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.45	4.17	3.50
Unmasked-calculated*	4.43	7.76	4.58

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.43 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

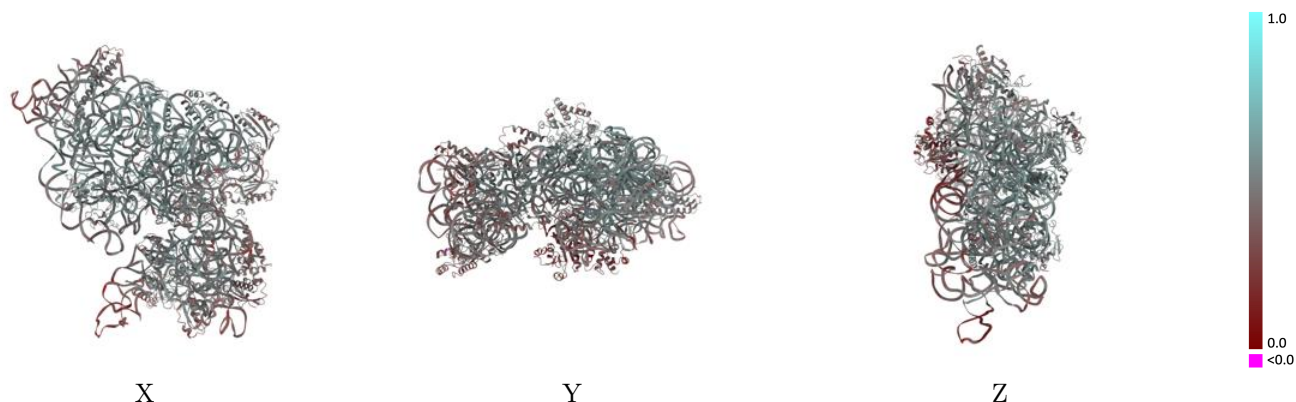
This section contains information regarding the fit between EMDB map EMD-31658 and PDB model 7V2O. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



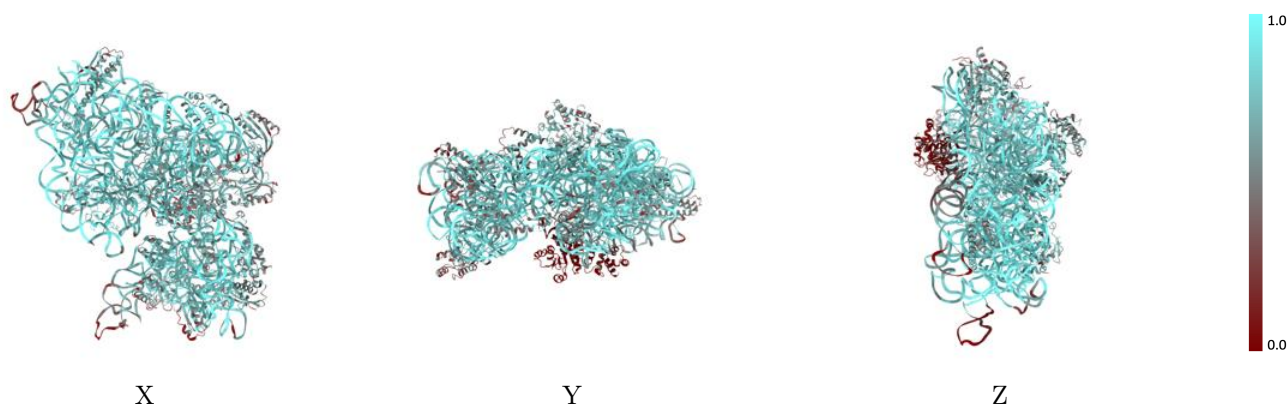
The images above show the 3D surface view of the map at the recommended contour level 0.075 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



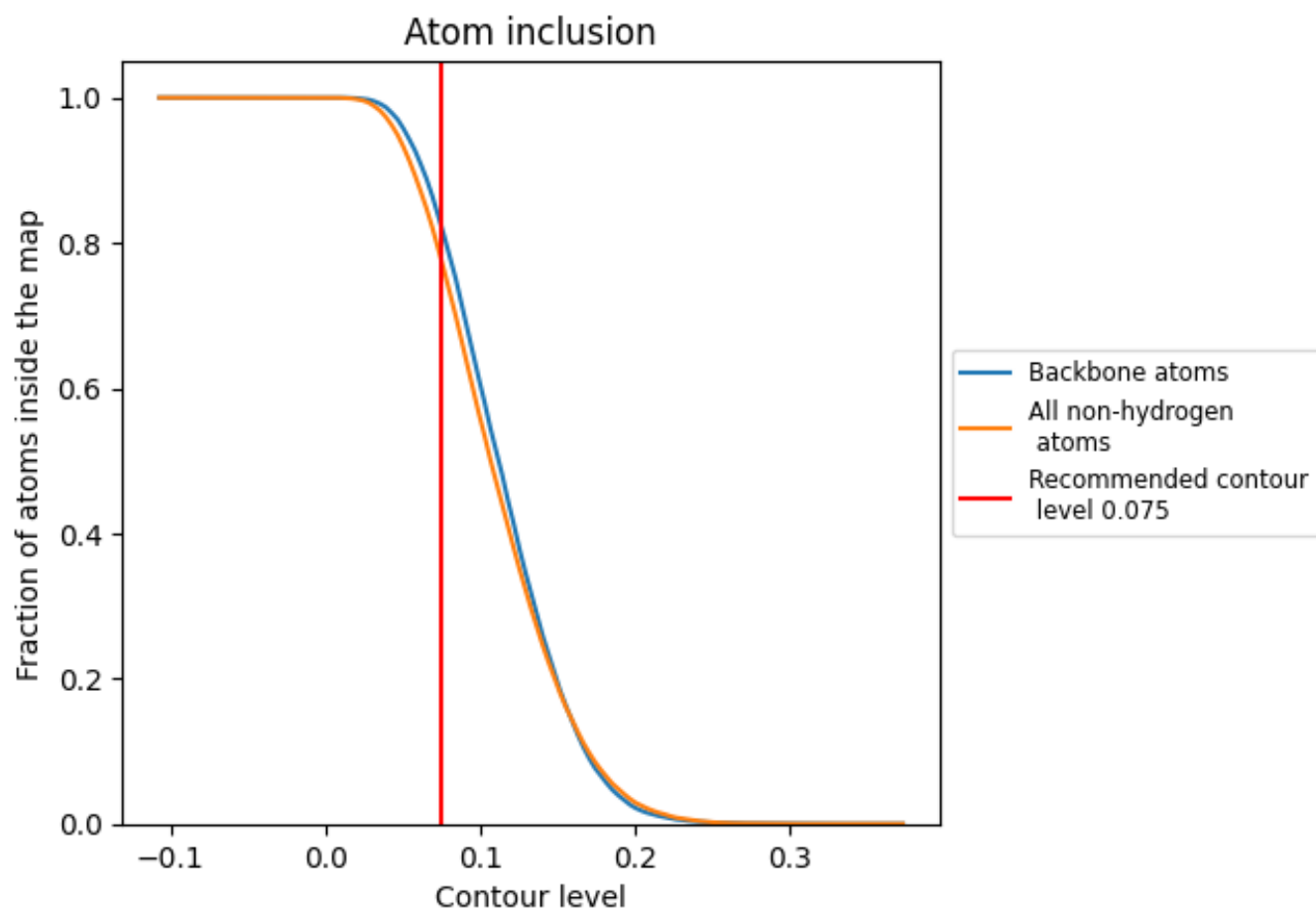
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.075).















































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 78% 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	 0.7761	 0.4660
A	 0.8693	 0.4740
B	 0.6117	 0.4620
C	 0.6814	 0.4690
D	 0.7564	 0.4980
E	 0.8092	 0.5280
F	 0.5941	 0.4560
G	 0.5960	 0.4210
H	 0.8297	 0.5460
I	 0.6440	 0.4210
J	 0.6117	 0.4350
K	 0.5655	 0.4190
L	 0.7812	 0.5050
M	 0.4896	 0.3560
N	 0.8504	 0.4940
O	 0.7641	 0.5080
P	 0.8382	 0.5320
Q	 0.8116	 0.5440
R	 0.6452	 0.4830
S	 0.5151	 0.3730
T	 0.6333	 0.4500
U	 0.1312	 0.3140
V	 0.7958	 0.4720

