



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:14 PM UTC

PDB ID : 6G4W / pdb_00006g4w
EMDB ID : EMD-4349
Title : Cryo-EM structure of a late human pre-40S ribosomal subunit - State A
Authors : Ameismeier, M.; Cheng, J.; Berninghausen, O.; Beckmann, R.
Deposited on : 2018-03-28
Resolution : 4.50 Å(reported)

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

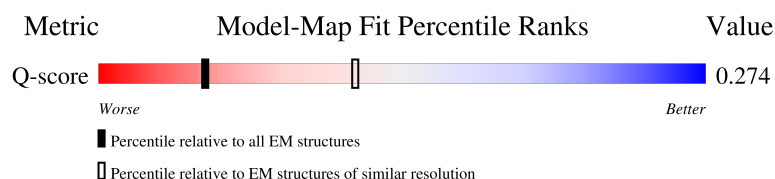
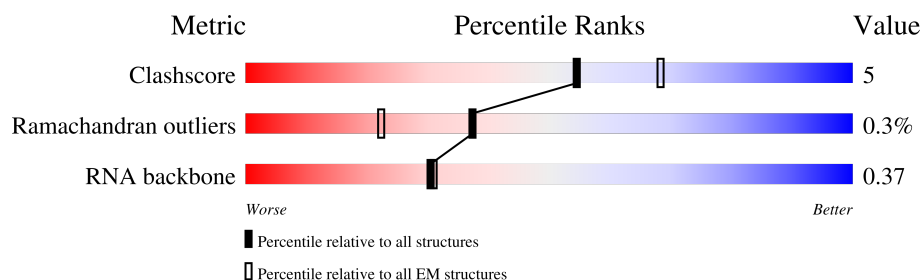
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
RNA backbone	8273	3508	-
Q-score	-	25397	2937 (4.00 - 5.00)

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

Mol	Chain	Length	Quality of chain
1	2	1882	
2	R	135	
3	b	84	
4	B	264	

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Mol	Chain	Length	Quality of chain
5	c	69	
6	E	263	
7	e	59	
8	F	204	
9	H	194	
10	G	249	
11	Z	125	
12	Y	133	
13	x	252	
14	X	143	
15	w	437	
16	W	130	
17	u	804	
18	t	18	
19	T	145	
20	S	152	
21	Q	146	
22	P	145	
23	O	151	
24	N	151	
25	L	158	
26	J	194	
27	I	208	
28	s	800	
29	r	125	

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Mol	Chain	Length	Quality of chain
30	q	281	28% 67% 32%
31	k	19	100%

2 Entry composition

There are 31 unique types of molecules in this entry. The entry contains 45223 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	2	1563	Total	C	O	P	0	0
			18753	7815	9376	1562		

- Molecule 2 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	R	81	Total	C	N	O	0	0
			401	239	81	81		

- Molecule 3 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	b	82	Total	C	N	O	0	0
			405	241	82	82		

- Molecule 4 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	B	213	Total	C	N	O	0	0
			1054	628	213	213		

- Molecule 5 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	c	61	Total	C	N	O	0	0
			300	178	61	61		

- Molecule 6 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	E	262	Total	C	N	O	0	0
			1287	763	262	262		

- Molecule 7 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	e	55	Total	C	N	O	0	0
			270	160	55	55		

- Molecule 8 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	F	189	Total	C	N	O	0	0
			935	557	189	189		

- Molecule 9 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	H	186	Total	C	N	O	0	0
			920	548	186	186		

- Molecule 10 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	G	230	Total	C	N	O	0	0
			1135	675	230	230		

- Molecule 11 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	Z	72	Total	C	N	O	0	0
			358	214	72	72		

- Molecule 12 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	Y	124	Total	C	N	O	0	0
			610	362	124	124		

- Molecule 13 is a protein called RNA-binding protein PNO1.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	x	175	Total	C	N	O	0	0
			865	515	175	175		

- Molecule 14 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	X	141	Total	C	N	O	0	0
			690	408	141	141		

- Molecule 15 is a protein called Bystin.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	w	248	Total	C	N	O	0	0
			1232	736	248	248		

- Molecule 16 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	W	129	Total	C	N	O	0	0
			634	376	129	129		

- Molecule 17 is a protein called Pre-rRNA-processing protein TSR1 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	u	628	Total	C	N	O	0	0
			3106	1850	628	628		

- Molecule 18 is a protein called UNKNOWN.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	t	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 19 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	T	144	Total	C	N	O	0	0
			705	417	144	144		

- Molecule 20 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	S	143	Total	C	N	O	0	0
			704	418	143	143		

- Molecule 21 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Q	139	Total	C	N	O	0	0
			683	405	139	139		

- Molecule 22 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	P	120	Total	C	N	O	0	0
			590	350	120	120		

- Molecule 23 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	O	135	Total	C	N	O	0	0
			659	389	135	135		

- Molecule 24 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	N	149	Total	C	N	O	0	0
			737	439	149	149		

- Molecule 25 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	L	151	Total	C	N	O	0	0
			744	442	151	151		

- Molecule 26 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	J	180	Total	C	N	O	0	0
			888	528	180	180		

- Molecule 27 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	I	205	Total	C	N	O	0	0
			1009	599	205	205		

- Molecule 28 is a protein called RRP12.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	s	768	Total	C	N	O	0	0
			3840	2304	768	768		

- Molecule 29 is a protein called Multifunctional methyltransferase subunit TRM112-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	r	118	Total	C	N	O	0	0
			582	346	118	118		

- Molecule 30 is a protein called Probable 18S rRNA (guanine-N(7))-methyltransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	q	192	Total	C	N	O	0	0
			942	558	192	192		

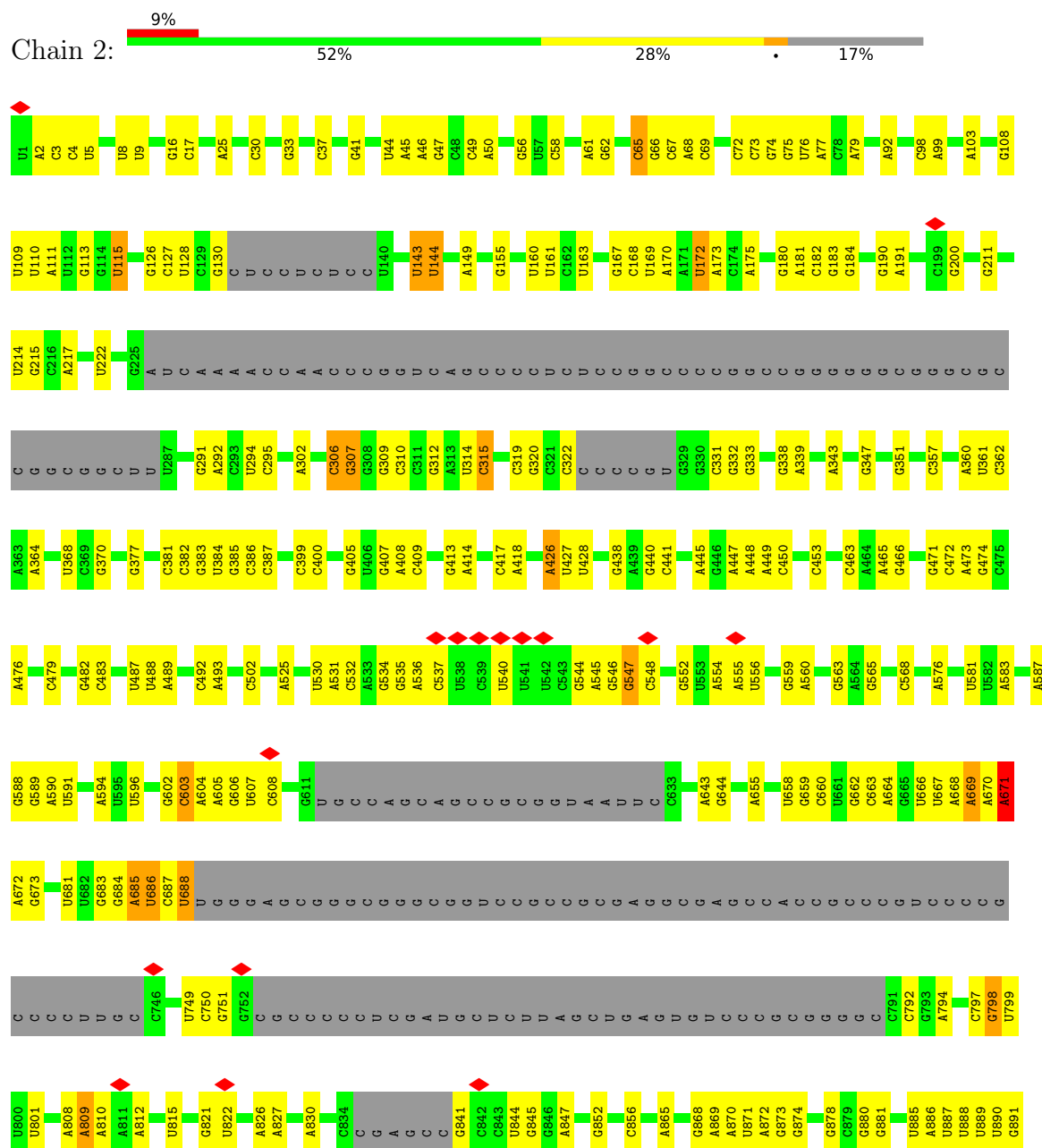
- Molecule 31 is a protein called UNKNOWN HELIX.

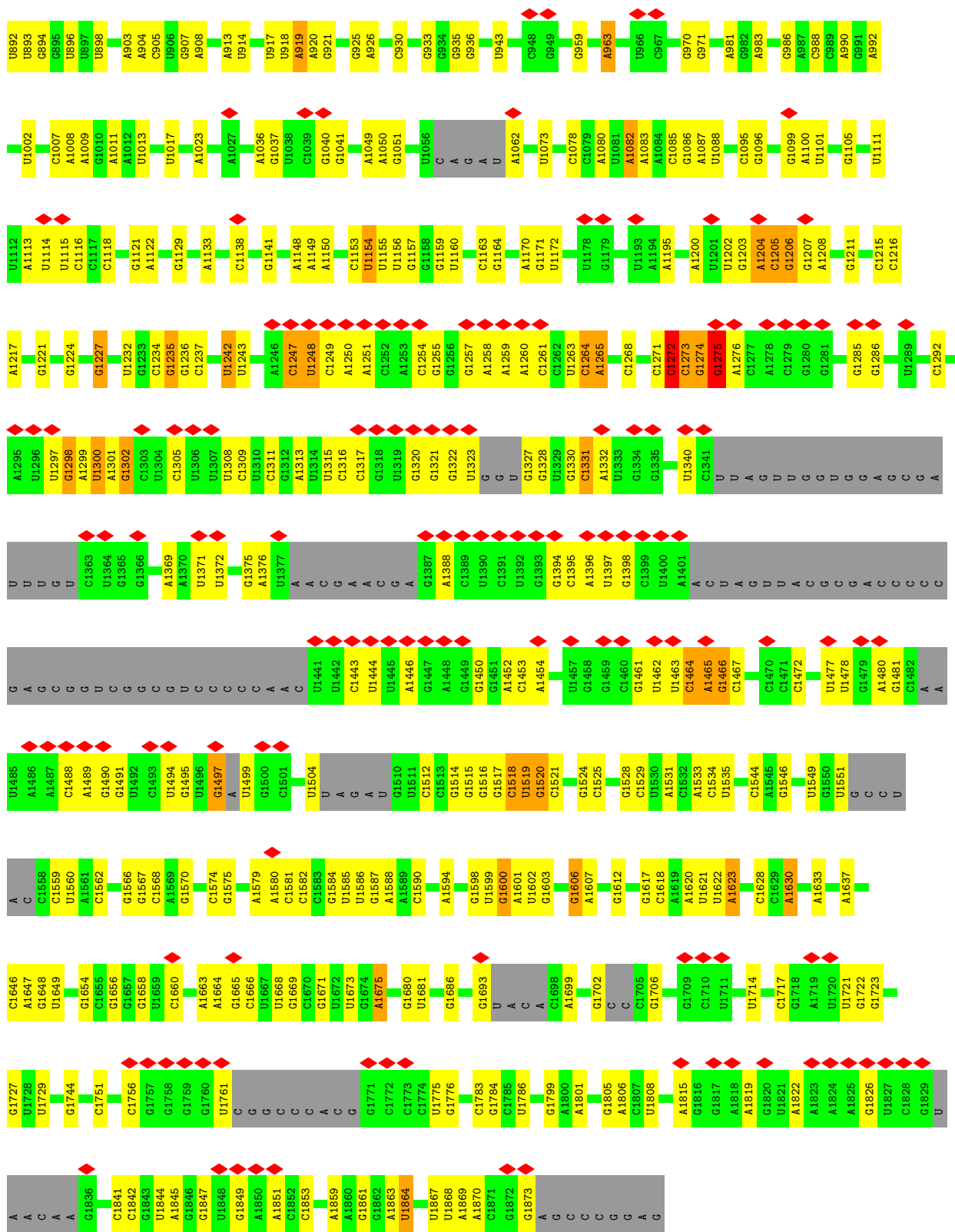
Mol	Chain	Residues	Atoms				AltConf	Trace
31	k	19	Total	C	N	O	0	0
			95	57	19	19		

3 Residue-property plots

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

• Molecule 1: 18S ribosomal RNA

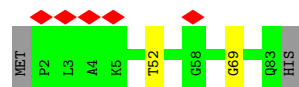




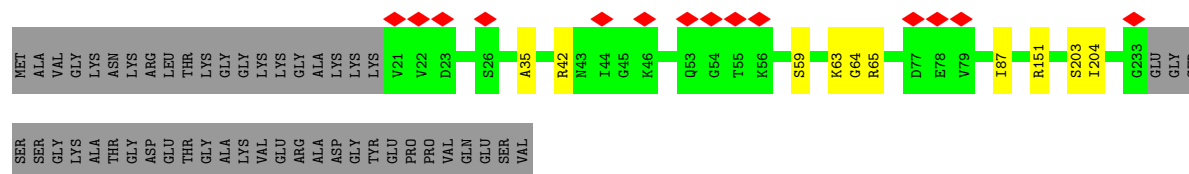
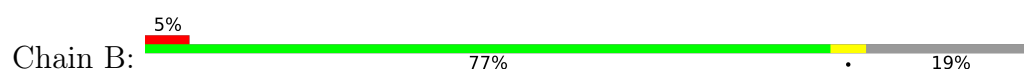
• Molecule 2: 40S ribosomal protein S17

Chain R:

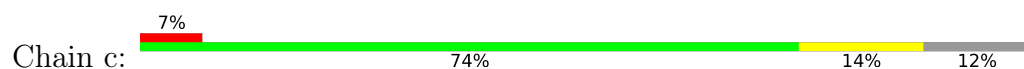
- Molecule 3: 40S ribosomal protein S27



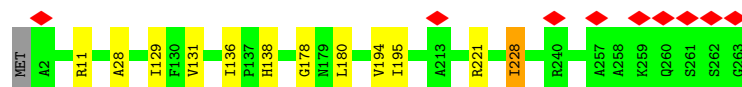
- Molecule 4: 40S ribosomal protein S3a



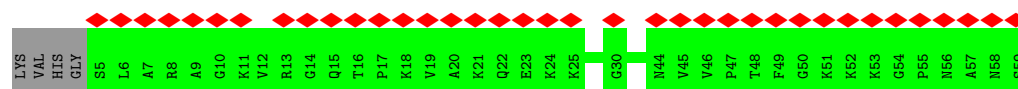
- Molecule 5: 40S ribosomal protein S28



- Molecule 6: 40S ribosomal protein S4, X isoform

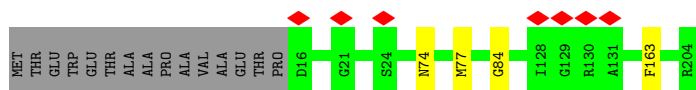


- Molecule 7: 40S ribosomal protein S30

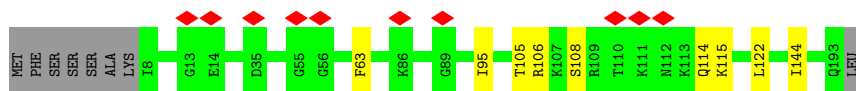
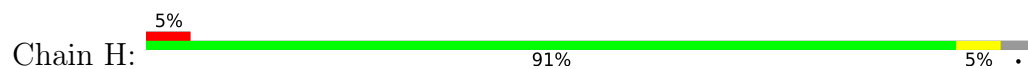


- Molecule 8: 40S ribosomal protein S5

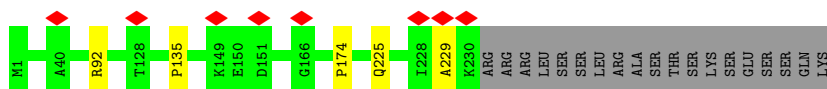




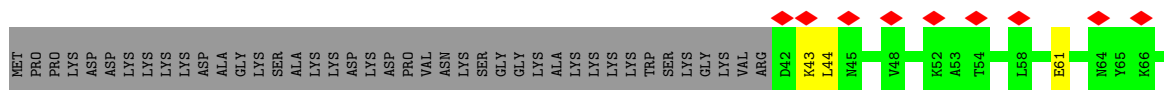
- Molecule 9: 40S ribosomal protein S7



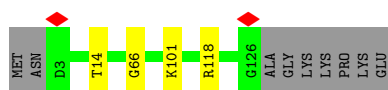
- Molecule 10: 40S ribosomal protein S6



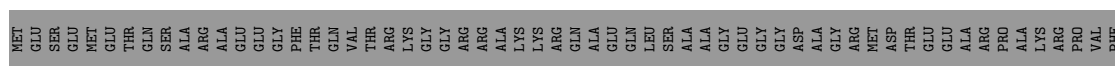
- Molecule 11: 40S ribosomal protein S25



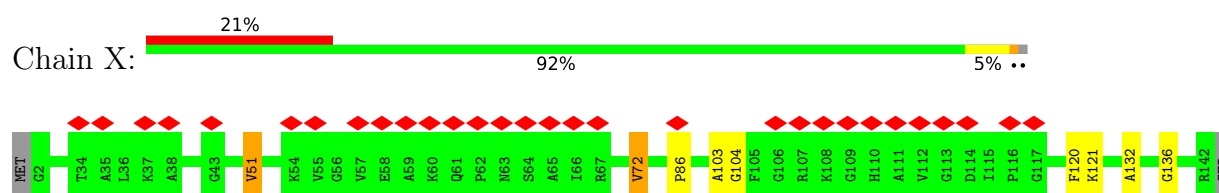
- Molecule 12: 40S ribosomal protein S24



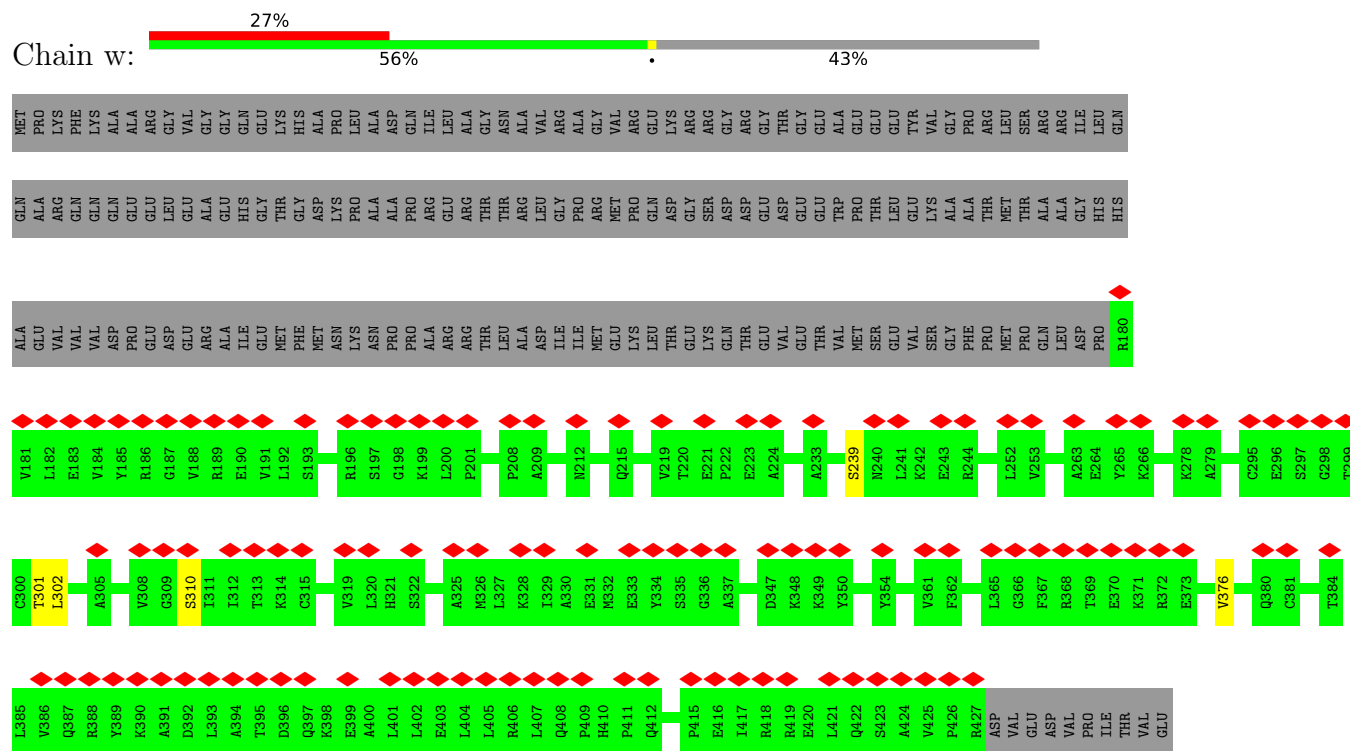
- Molecule 13: RNA-binding protein PNO1



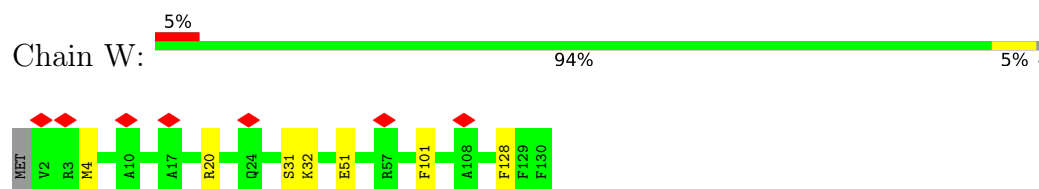
- Molecule 14: 40S ribosomal protein S23



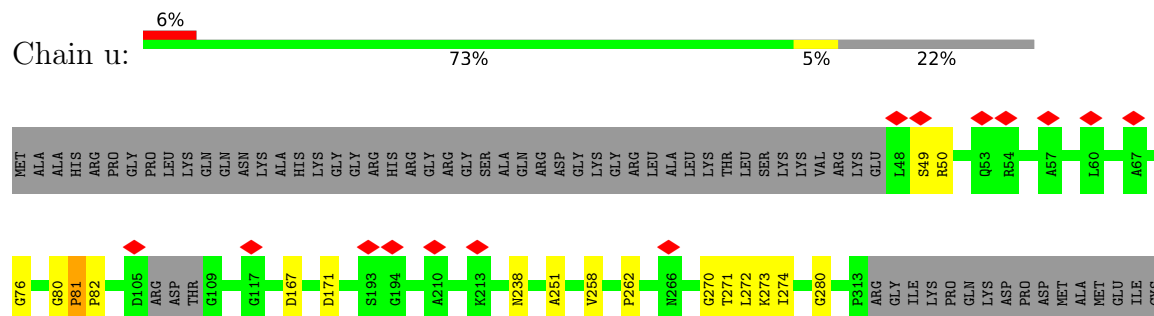
- Molecule 15: Bystin

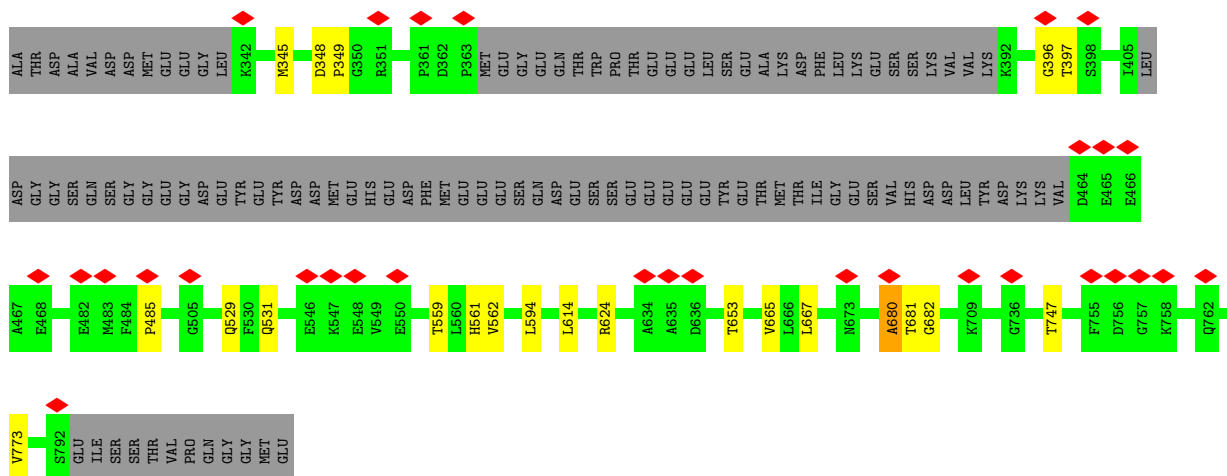


- Molecule 16: 40S ribosomal protein S15a



- Molecule 17: Pre-rRNA-processing protein TSR1 homolog

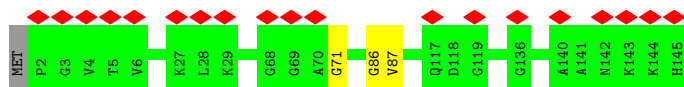




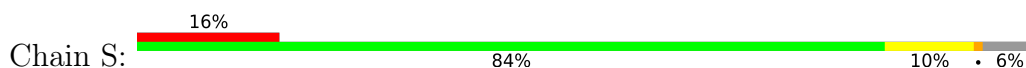
- Molecule 18: UNKNOWN



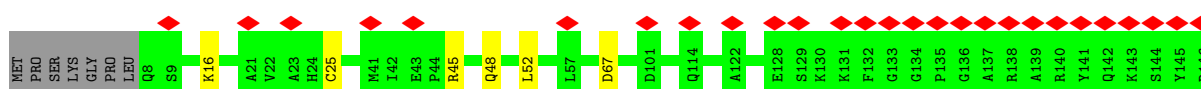
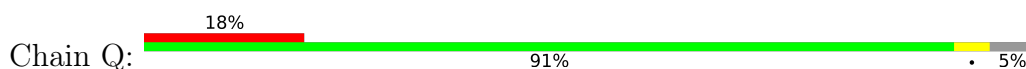
- Molecule 19: 40S ribosomal protein S19



- Molecule 20: 40S ribosomal protein S18



- Molecule 21: 40S ribosomal protein S16

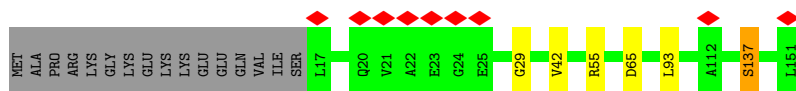
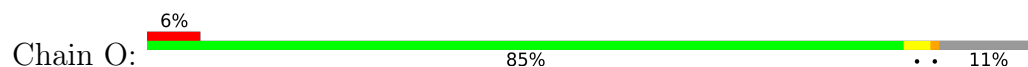


- Molecule 22: 40S ribosomal protein S15





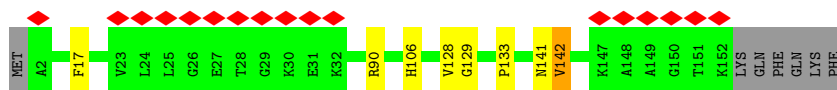
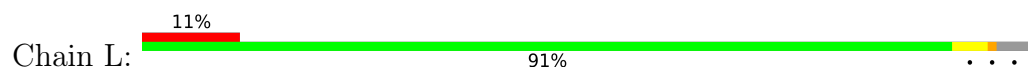
- Molecule 23: 40S ribosomal protein S14



- Molecule 24: 40S ribosomal protein S13



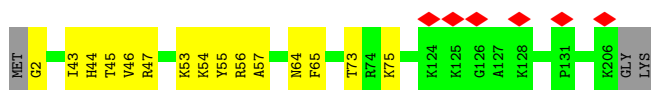
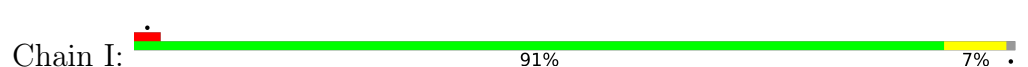
- Molecule 25: 40S ribosomal protein S11



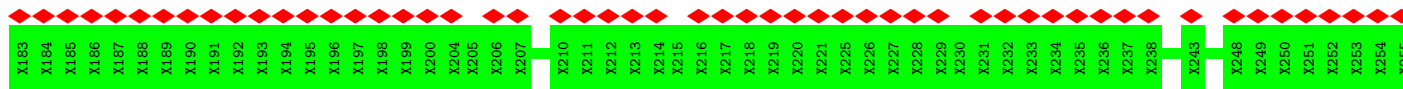
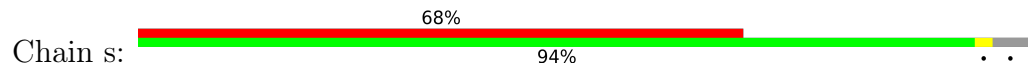
- Molecule 26: 40S ribosomal protein S9



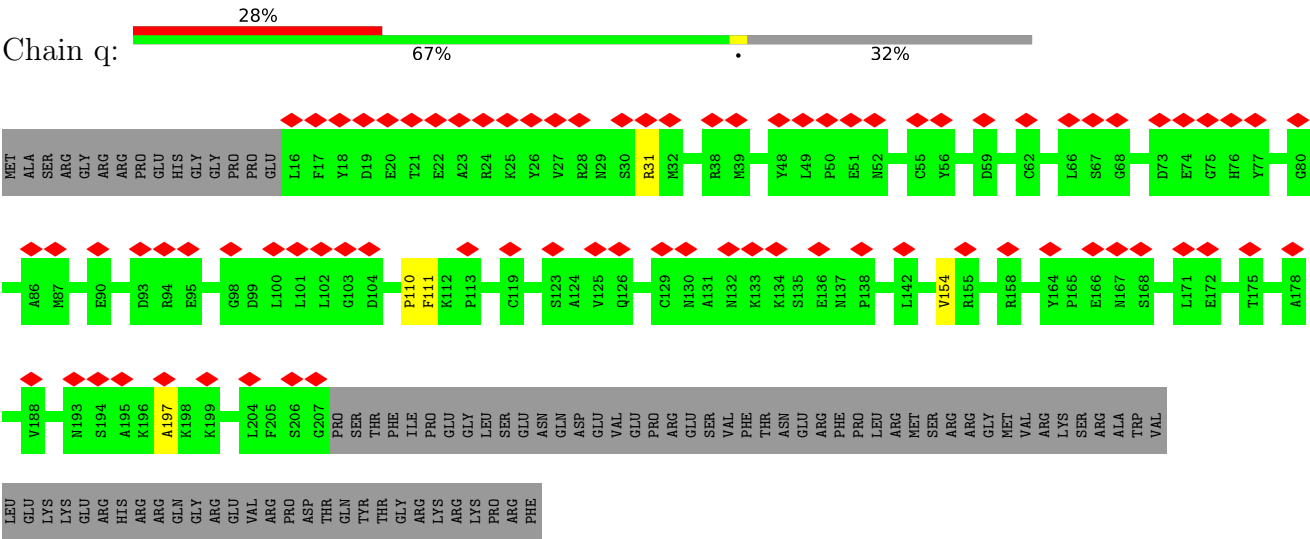
- Molecule 27: 40S ribosomal protein S8



- Molecule 28: RRP12



● Molecule 30: Probable 18S rRNA (guanine-N(7))-methyltransferase



● Molecule 31: UNKNOWN HELIX



There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52414	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 ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.155	Depositor
Minimum map value	-0.042	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	2	0.35	0/20291	0.73	20/31156 (0.1%)
2	R	0.30	0/398	0.98	1/550 (0.2%)
3	b	0.39	0/404	0.78	0/561
4	B	0.35	0/1053	0.78	2/1466 (0.1%)
5	c	0.34	0/299	1.00	4/414 (1.0%)
6	E	0.41	0/1286	0.82	0/1785
7	e	0.33	0/269	0.81	0/372
8	F	0.27	0/934	0.69	2/1300 (0.2%)
9	H	0.31	0/919	0.66	0/1279
10	G	0.32	0/1134	0.68	0/1577
11	Z	0.31	0/357	0.83	2/497 (0.4%)
12	Y	0.36	0/609	0.78	1/845 (0.1%)
13	x	0.37	0/864	0.80	0/1202
14	X	0.43	0/689	0.96	0/954
15	w	0.29	0/1231	0.77	0/1717
16	W	0.50	0/633	0.85	0/878
17	u	0.36	0/3101	0.77	2/4313 (0.0%)
18	t	0.35	0/89	0.82	0/123
19	T	0.29	0/704	0.67	0/975
20	S	0.28	0/703	0.70	0/976
21	Q	0.30	0/682	0.78	2/946 (0.2%)
22	P	0.34	0/589	0.60	0/817
23	O	0.36	0/658	0.75	1/910 (0.1%)
24	N	0.33	0/736	0.60	0/1024
25	L	0.40	0/743	0.76	0/1032
26	J	0.37	0/887	0.78	2/1233 (0.2%)
27	I	0.34	0/1008	0.73	0/1400
29	r	1.03	0/581	1.75	10/807 (1.2%)
30	q	0.98	0/941	1.59	0/1305
31	k	1.05	0/94	1.57	0/130
All	All	0.40	0/42886	0.79	49/62544 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	R	0	2
3	b	0	1
6	E	0	2
12	Y	0	1
14	X	0	1
17	u	0	4
20	S	0	1
22	P	0	1
26	J	0	1
All	All	0	14

There are no bond length outliers.

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	r	46	ILE	CA-C-N	8.31	127.96	119.82
29	r	46	ILE	C-N-CA	8.31	127.96	119.82
1	2	1265	A	C4'-C3'-O3'	8.09	125.13	113.00
1	2	1330	G	C3'-C2'-O2'	7.64	122.16	110.70
1	2	1331	C	C4'-C3'-O3'	7.16	123.73	113.00

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	E	228	ILE	Peptide,Mainchain
2	R	26	ASN	Peptide
2	R	73	LEU	Peptide
12	Y	118	ARG	Peptide
3	b	52	THR	Peptide

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	2	18753	0	9404	246	0
2	R	401	0	170	8	0
3	b	405	0	172	1	0
4	B	1054	0	455	6	0
5	c	300	0	131	8	0
6	E	1287	0	577	7	0
7	e	270	0	126	0	0
8	F	935	0	442	5	0
9	H	920	0	399	14	0
10	G	1135	0	512	5	0
11	Z	358	0	161	24	0
12	Y	610	0	271	2	0
13	x	865	0	394	14	0
14	X	690	0	330	6	0
15	w	1232	0	562	5	0
16	W	634	0	283	13	0
17	u	3106	0	1357	29	0
18	t	90	0	37	4	0
19	T	705	0	343	5	0
20	S	704	0	317	25	0
21	Q	683	0	320	3	0
22	P	590	0	251	37	0
23	O	659	0	321	5	0
24	N	737	0	330	19	0
25	L	744	0	321	6	0
26	J	888	0	389	3	0
27	I	1009	0	451	8	0
28	s	3840	0	848	23	0
29	r	582	0	252	1	0
30	q	942	0	435	7	0
31	k	95	0	97	0	0
All	All	45223	0	20458	336	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 5.

The worst 5 of 336 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)
1:2:1227:G:H4'	30:q:31:ARG:CB	1.42	1.46
1:2:1515:G:H5'	22:P:79:HIS:CB	1.53	1.38
17:u:529:GLN:O	18:t:366:LEU:HA	1.15	1.32

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1525:C:H5''	30:q:197:ALA:CB	1.60	1.31
1:2:1369:A:H5'	28:s:293:UNK:C	1.62	1.28

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	R	75/135 (56%)	63 (84%)	12 (16%)	0	100	100
3	b	80/84 (95%)	72 (90%)	8 (10%)	0	100	100
4	B	211/264 (80%)	196 (93%)	15 (7%)	0	100	100
5	c	59/69 (86%)	53 (90%)	6 (10%)	0	100	100
6	E	260/263 (99%)	235 (90%)	24 (9%)	1 (0%)	30	67
7	e	53/59 (90%)	41 (77%)	12 (23%)	0	100	100
8	F	187/204 (92%)	173 (92%)	14 (8%)	0	100	100
9	H	184/194 (95%)	172 (94%)	12 (6%)	0	100	100
10	G	228/249 (92%)	210 (92%)	18 (8%)	0	100	100
11	Z	70/125 (56%)	63 (90%)	7 (10%)	0	100	100
12	Y	122/133 (92%)	111 (91%)	11 (9%)	0	100	100
13	x	173/252 (69%)	165 (95%)	8 (5%)	0	100	100
14	X	139/143 (97%)	129 (93%)	8 (6%)	2 (1%)	9	39
15	w	246/437 (56%)	226 (92%)	20 (8%)	0	100	100
16	W	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
17	u	618/804 (77%)	550 (89%)	64 (10%)	4 (1%)	21	58
18	t	16/18 (89%)	8 (50%)	5 (31%)	3 (19%)	0	2
19	T	142/145 (98%)	136 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	S	141/152 (93%)	131 (93%)	10 (7%)	0	100	100
21	Q	137/146 (94%)	118 (86%)	19 (14%)	0	100	100
22	P	118/145 (81%)	111 (94%)	7 (6%)	0	100	100
23	O	133/151 (88%)	120 (90%)	13 (10%)	0	100	100
24	N	147/151 (97%)	138 (94%)	9 (6%)	0	100	100
25	L	149/158 (94%)	137 (92%)	11 (7%)	1 (1%)	18	55
26	J	178/194 (92%)	163 (92%)	14 (8%)	1 (1%)	21	58
27	I	203/208 (98%)	184 (91%)	19 (9%)	0	100	100
29	r	116/125 (93%)	110 (95%)	5 (4%)	1 (1%)	14	49
30	q	190/281 (68%)	186 (98%)	2 (1%)	2 (1%)	11	45
31	k	17/19 (90%)	17 (100%)	0	0	100	100
All	All	4519/5438 (83%)	4135 (92%)	369 (8%)	15 (0%)	37	71

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	u	81	PRO
18	t	353	ILE
26	J	161	LEU
29	r	111	ARG
30	q	110	PRO

5.3.2 Protein sidechains ⓘ

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

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1541/1882 (81%)	495 (32%)	0

5 of 495 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	C

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Mol	Chain	Res	Type
1	2	4	C
1	2	5	U
1	2	8	U

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
28	s	39
1	2	4

The worst 5 of 43 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	s	915:UNK	C	919:UNK	N	17.96
1	s	688:UNK	C	692:UNK	N	17.29
1	s	358:UNK	C	360:UNK	N	16.52
1	s	803:UNK	C	807:UNK	N	16.48
1	s	381:UNK	C	383:UNK	N	15.07

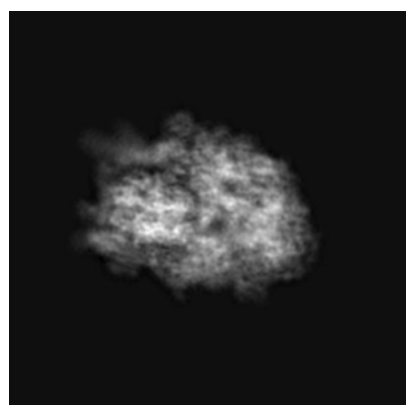
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4349. These allow visual inspection of the internal detail of the map and identification of artifacts.

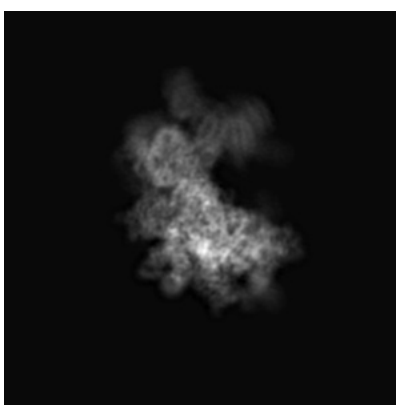
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

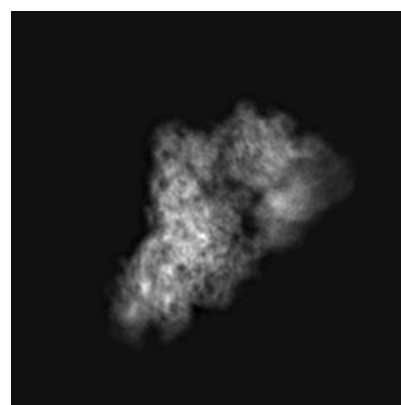
6.1.1 Primary map



X



Y

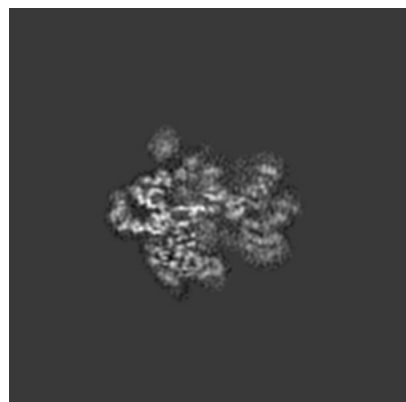


Z

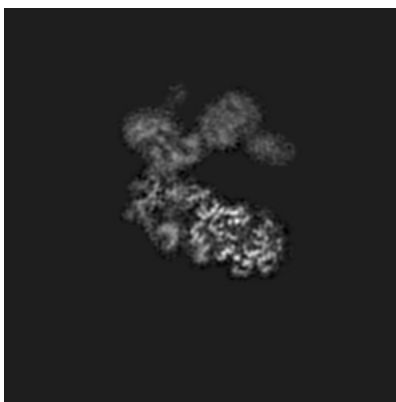
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

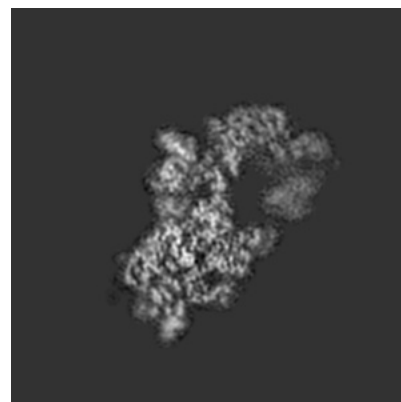
6.2.1 Primary map



X Index: 180



Y Index: 180

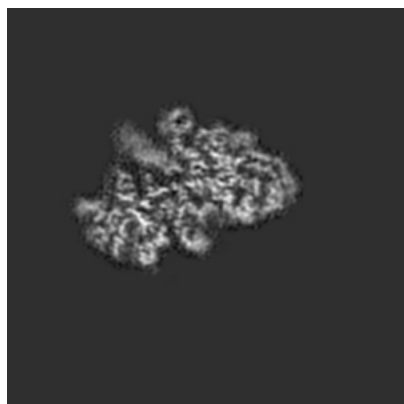


Z Index: 180

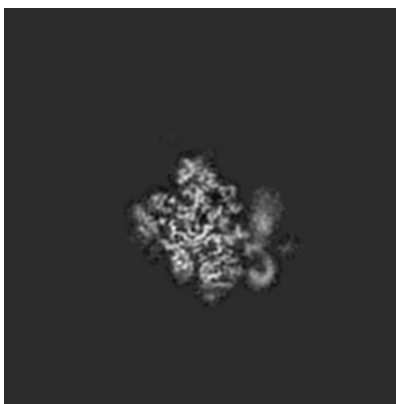
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

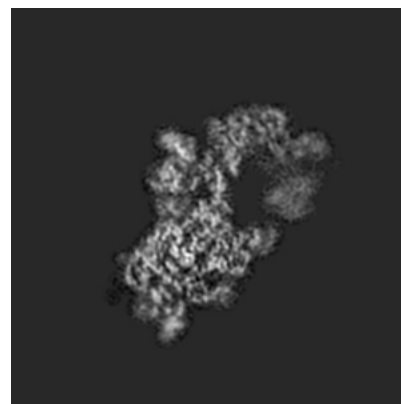
6.3.1 Primary map



X Index: 144



Y Index: 136

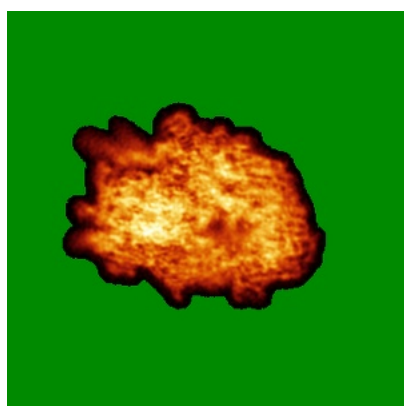


Z Index: 181

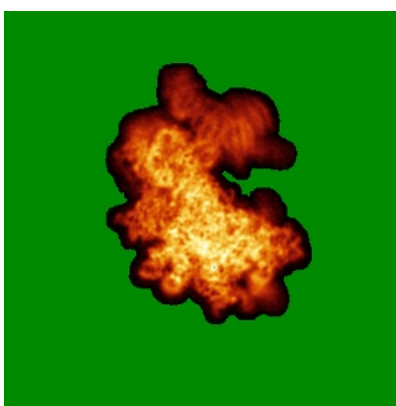
The images above show the largest variance slices of the map in three orthogonal directions.

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

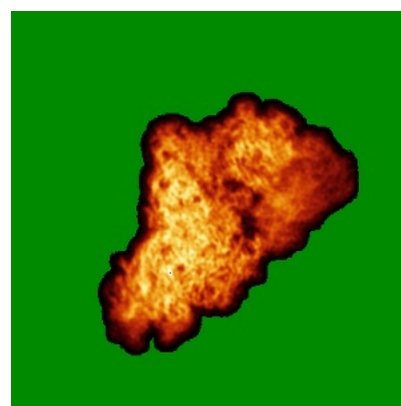
6.4.1 Primary map



X



Y

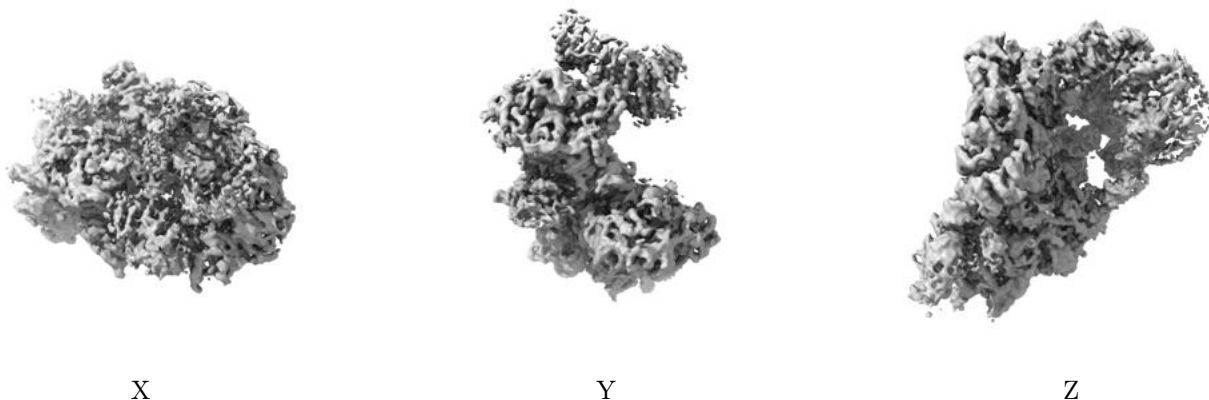


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

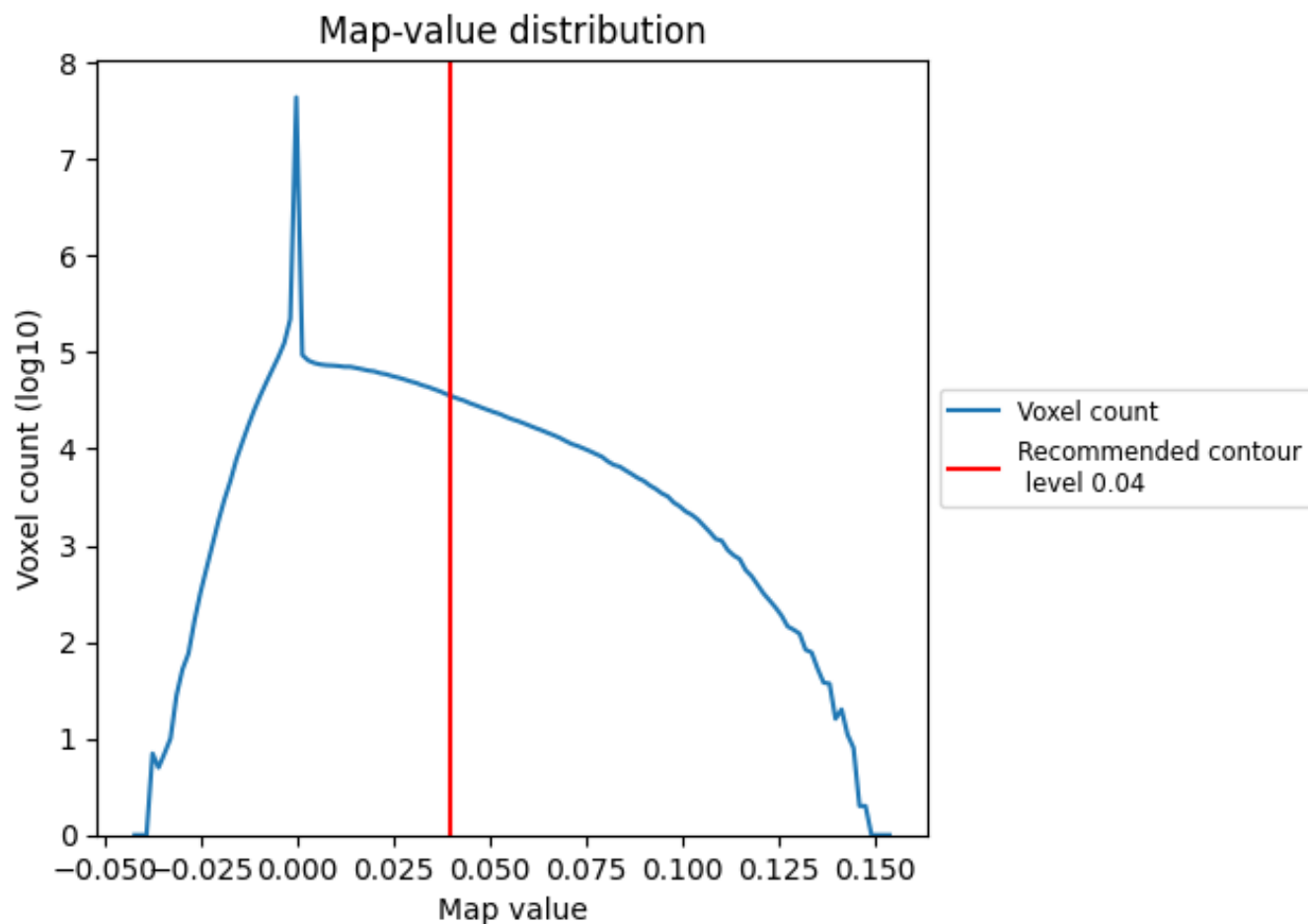
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

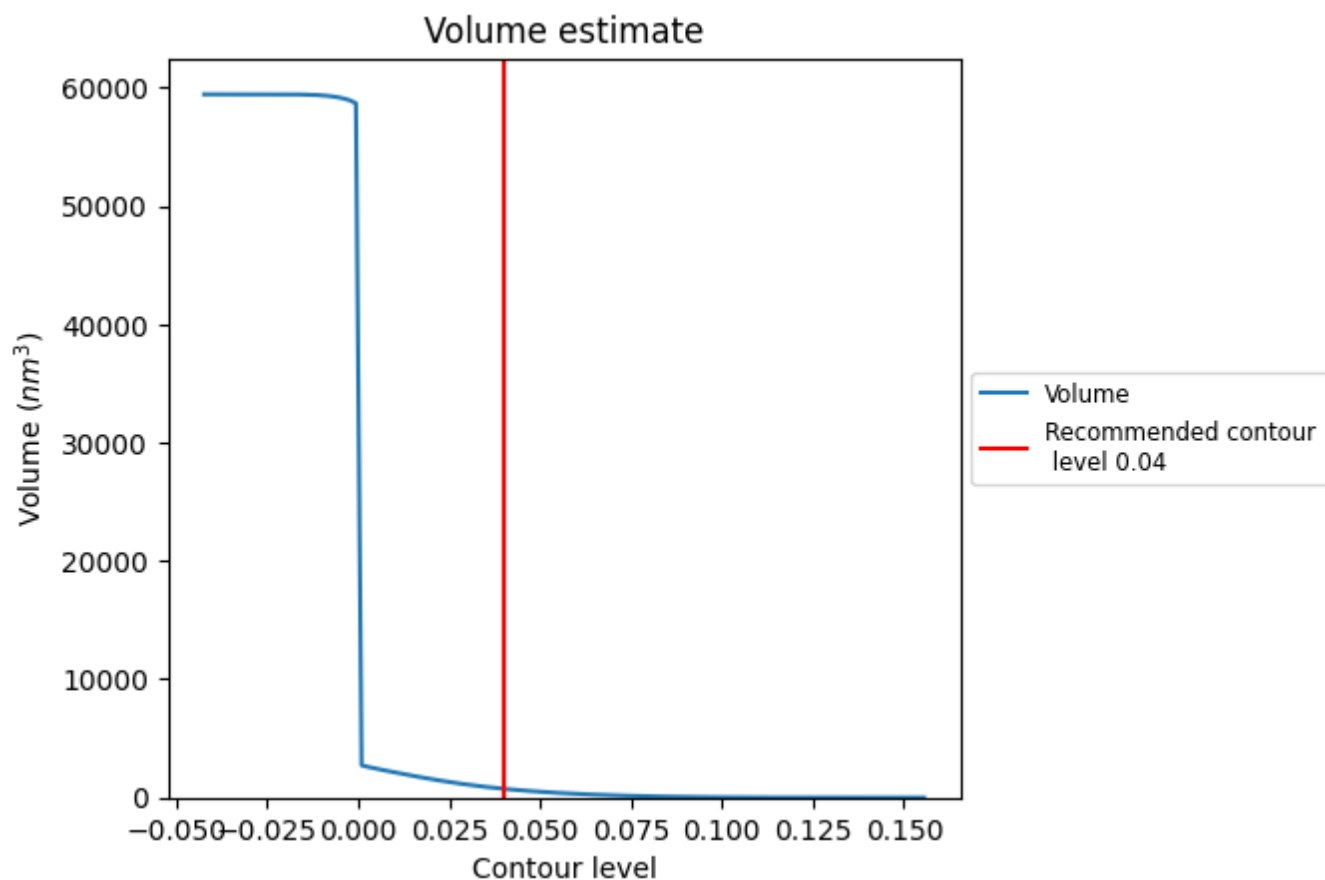
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

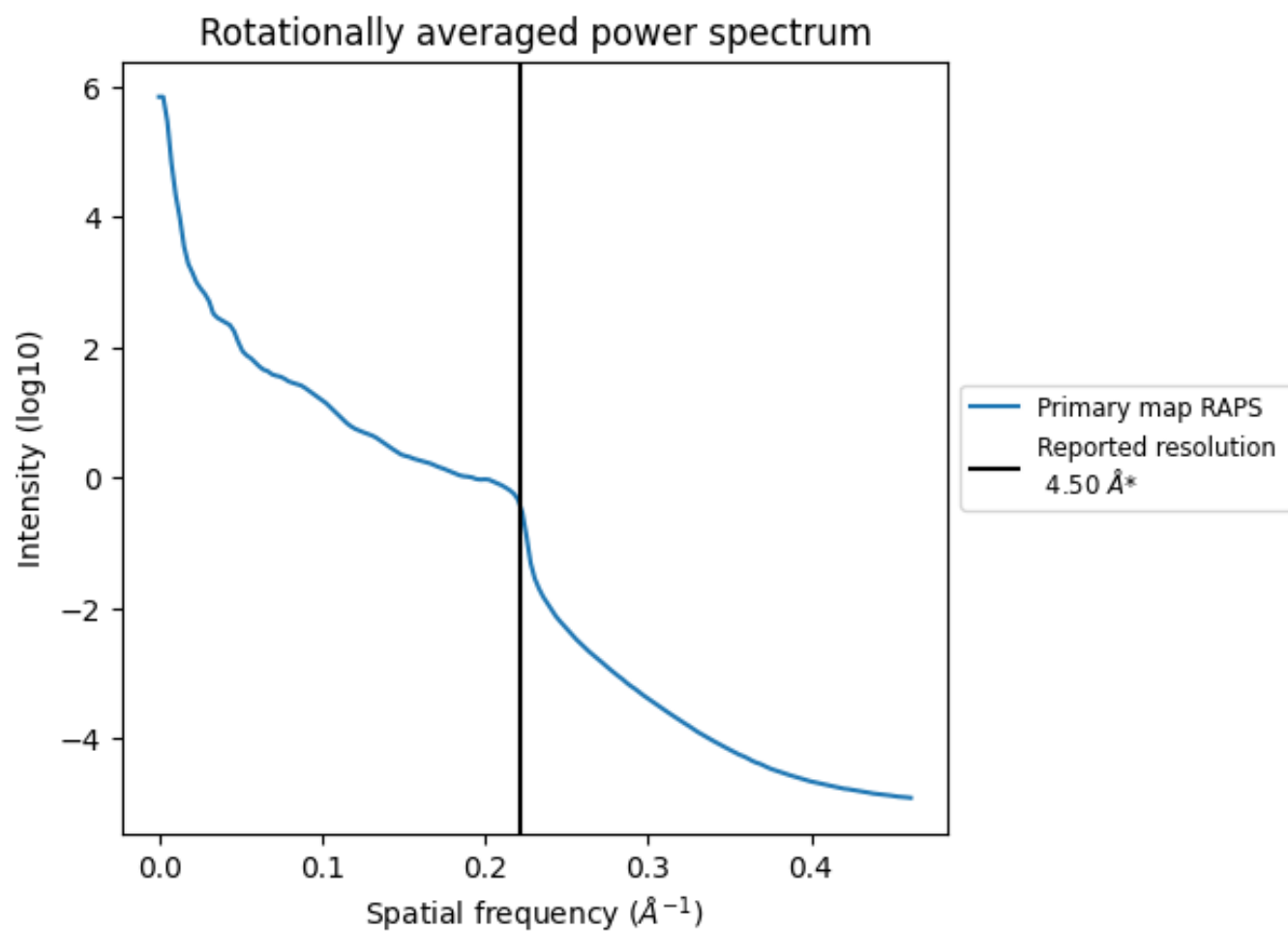
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 742 nm³; this corresponds to an approximate mass of 670 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

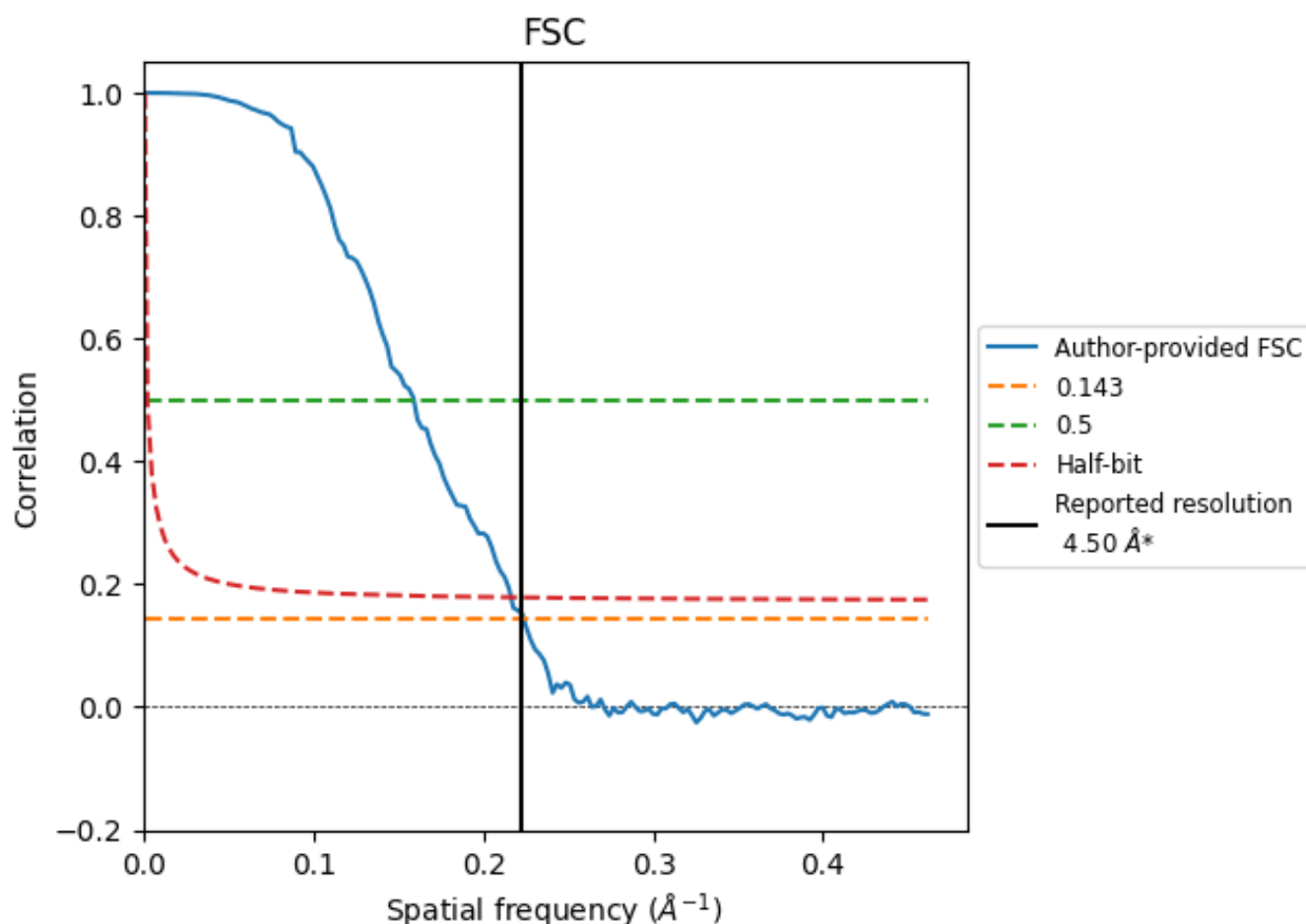


*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

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 0.222 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.47	6.28	4.62
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

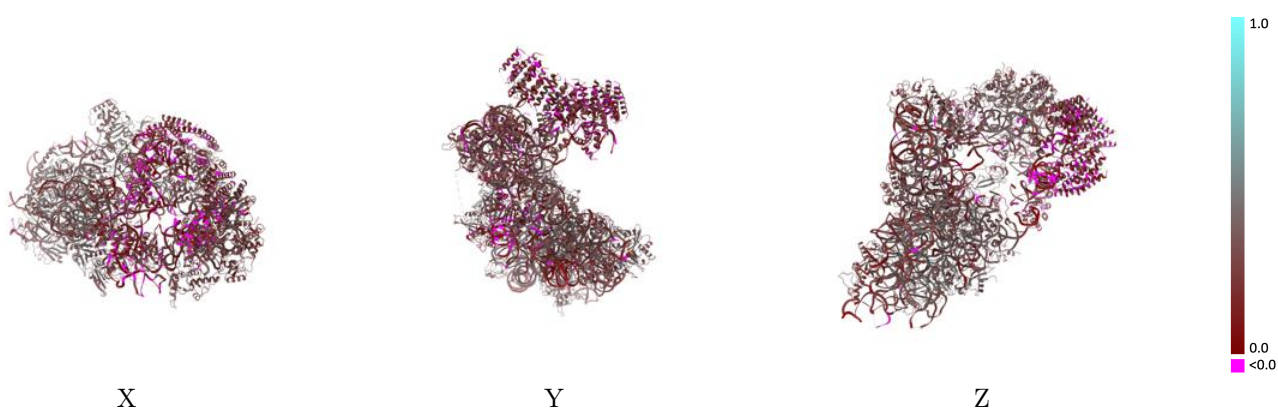
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4349 and PDB model 6G4W. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)

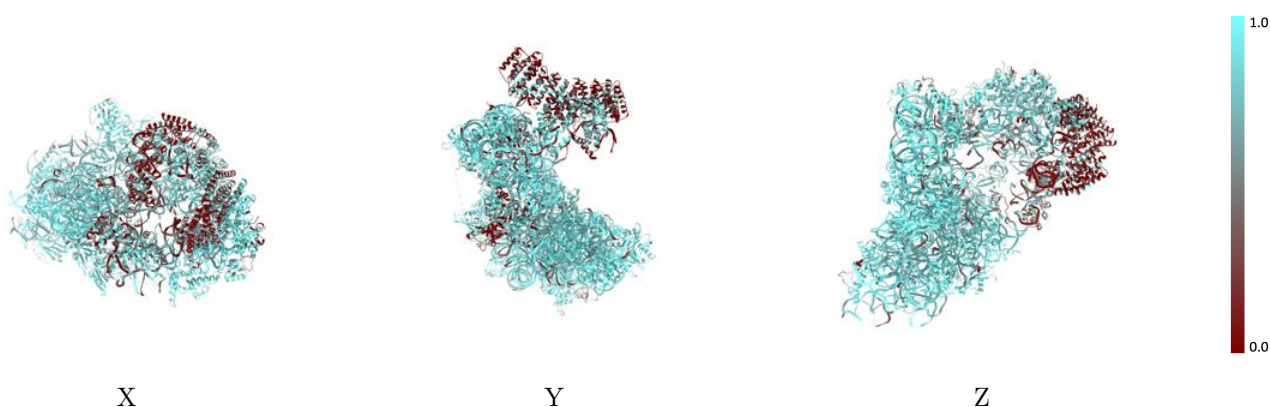
This section was not generated.

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



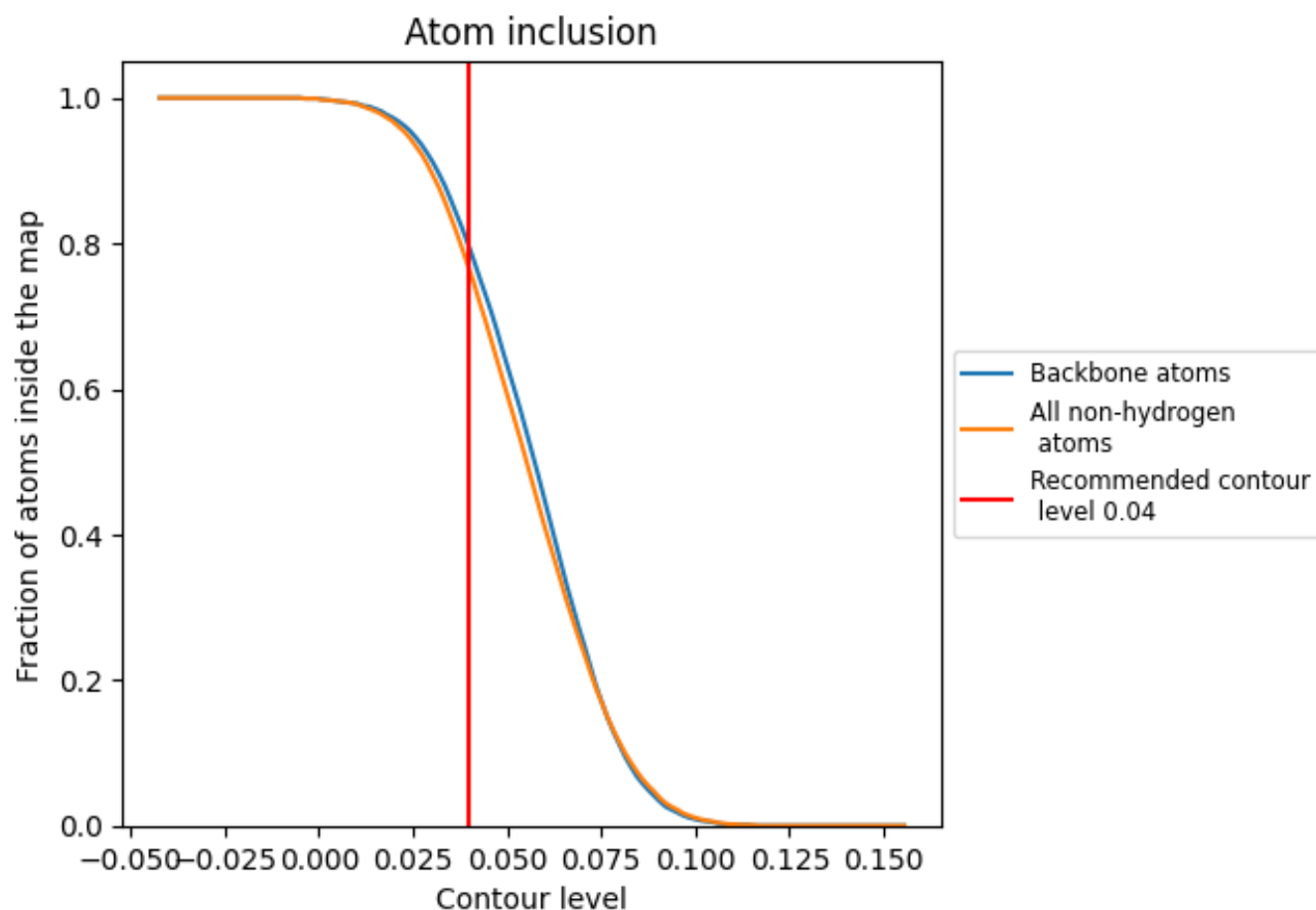
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 76% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7640	 0.2740
2	 0.8110	 0.2600
B	 0.8800	 0.3300
E	 0.8930	 0.3940
F	 0.8900	 0.3150
G	 0.8960	 0.3210
H	 0.8970	 0.3380
I	 0.9110	 0.3300
J	 0.9090	 0.3640
L	 0.8410	 0.4020
N	 0.8510	 0.3040
O	 0.8380	 0.3230
P	 0.8910	 0.3170
Q	 0.7310	 0.2720
R	 0.5140	 0.1740
S	 0.7770	 0.2600
T	 0.8240	 0.3110
W	 0.8830	 0.3280
X	 0.7300	 0.2720
Y	 0.9480	 0.3750
Z	 0.6540	 0.2350
b	 0.8960	 0.3580
c	 0.8270	 0.3220
e	 0.3220	 0.1030
k	 0.8740	 0.3300
q	 0.5470	 0.1810
r	 0.2890	 0.1390
s	 0.3170	 0.1490
t	 0.8440	 0.3910
u	 0.8540	 0.3460
w	 0.5050	 0.1700
x	 0.9030	 0.3370

