



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:09 AM UTC

PDB ID : 6G5H / pdb_00006g5h
EMDB ID : EMD-4352
Title : Cryo-EM structure of a late human pre-40S ribosomal subunit - Mature
Authors : Ameismeier, M.; Cheng, J.; Berninghausen, O.; Beckmann, R.
Deposited on : 2018-03-29
Resolution : 3.60 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

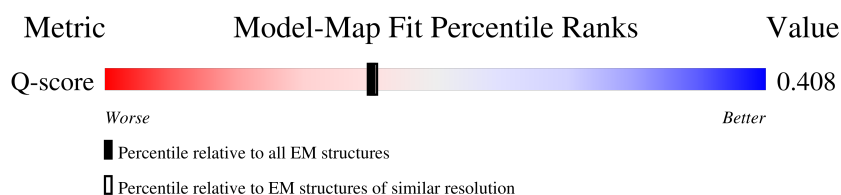
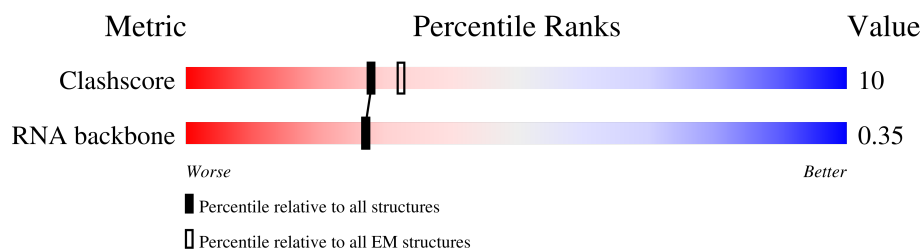
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

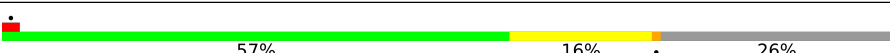
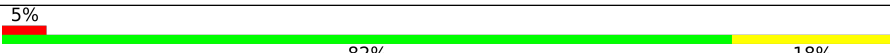
The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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

Mol	Chain	Length	Quality of chain
1	2	1868	
2	A	295	
3	B	264	
4	C	293	
5	E	263	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
6	G	249	
7	H	194	
8	I	208	
9	J	194	
10	L	158	
11	N	151	
12	O	151	
13	V	83	
14	W	130	
15	X	143	
16	Y	133	
17	a	115	
18	b	84	
19	d	56	
20	e	59	
21	h	25	
22	D	243	
23	F	204	
24	K	165	
25	M	132	
26	P	145	
27	Q	146	
28	R	135	
29	S	152	
30	T	145	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
31	U	119	
32	Z	125	
33	c	69	
34	f	156	
35	g	317	

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 74342 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	1665	Total	C	N	O	P	0	0
			35552	15869	6385	11633	1665		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	1772	C	G	conflict	GB 337376

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	206	Total	C	N	O	S	0	0
			1624	1035	287	294	8		

- Molecule 3 is a protein called 40S ribosomal protein S3a.

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

- Molecule 4 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	218	Total	C	N	O	S	0	0
			1682	1090	289	293	10		

- Molecule 5 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 6 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	230	Total	C	N	O	S	0	0
			1862	1164	371	320	7		

- Molecule 7 is a protein called 40S ribosomal protein S7.

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

- Molecule 8 is a protein called 40S ribosomal protein S8.

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

- Molecule 9 is a protein called 40S ribosomal protein S9.

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

- Molecule 10 is a protein called 40S ribosomal protein S11.

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

- Molecule 11 is a protein called 40S ribosomal protein S13.

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

- Molecule 12 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	135	Total	C	N	O	S	0	0
			1006	616	198	186	6		

- Molecule 13 is a protein called 40S ribosomal protein S21.

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

- Molecule 14 is a protein called 40S ribosomal protein S15a.

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

- Molecule 15 is a protein called 40S ribosomal protein S23.

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

- Molecule 16 is a protein called 40S ribosomal protein S24.

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

- Molecule 17 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	a	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 18 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	b	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 19 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	d	54	Total	C	N	O	S	0	0
			455	284	93	73	5		

- Molecule 20 is a protein called 40S ribosomal protein S30.

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

- Molecule 21 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	h	24	Total	C	N	O	S	0	0
			231	140	63	26	2		

- Molecule 22 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	D	225	Total	C	N	O	S	0	0
			1748	1115	315	311	7		

- Molecule 23 is a protein called 40S ribosomal protein S5.

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

- Molecule 24 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	K	95	Total	C	N	O	S	0	0
			800	522	142	131	5		

- Molecule 25 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	M	123	Total	C	N	O	S	0	0
			953	598	169	177	9		

- Molecule 26 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	P	120	Total	C	N	O	S	0	0
			984	625	184	168	7		

- Molecule 27 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Q	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 28 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	R	132	Total	C	N	O	S	0	0
			1066	669	199	194	4		

- Molecule 29 is a protein called 40S ribosomal protein S18.

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

- Molecule 30 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	T	144	Total	C	N	O	S	0	0
			1122	703	217	199	3		

- Molecule 31 is a protein called 40S ribosomal protein S20.

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

- Molecule 32 is a protein called 40S ribosomal protein S25.

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

- Molecule 33 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	61	Total	C	N	O	S	0	0
			479	292	95	90	2		

- Molecule 34 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	72	Total	C	N	O	S	0	0
			585	366	114	97	8		

- Molecule 35 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

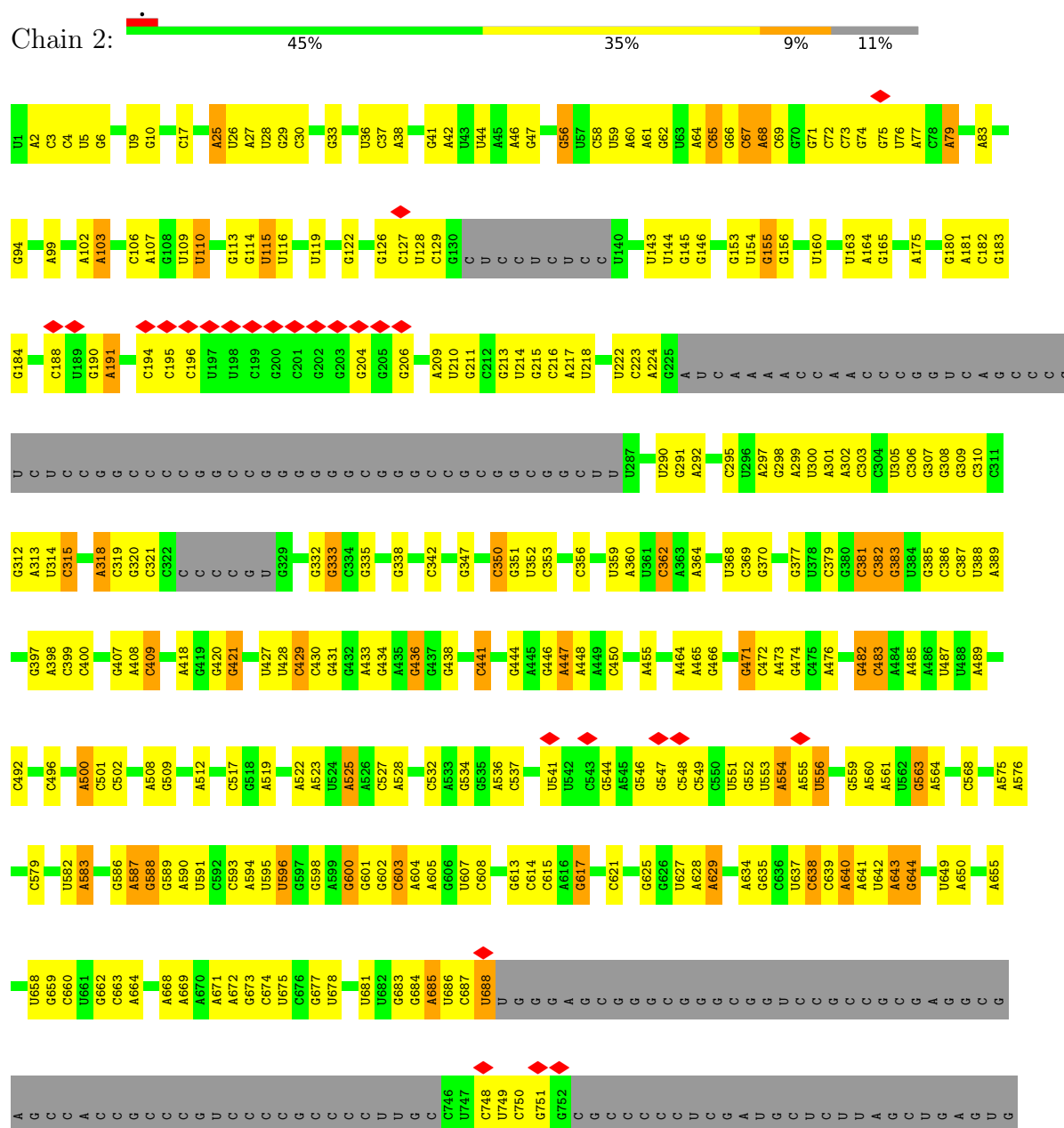
- Molecule 36 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
36	a	1	Total	Zn	0
			1	1	
36	d	1	Total	Zn	0
			1	1	
36	f	1	Total	Zn	0
			1	1	

3 Residue-property plots

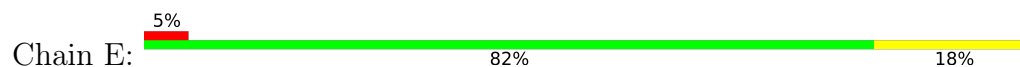
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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



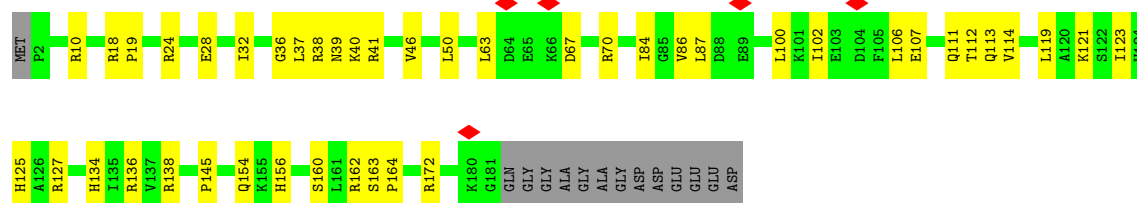


Chain A:



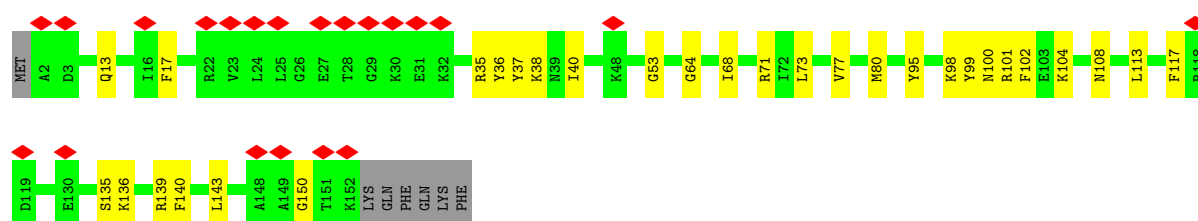
- Molecule 9: 40S ribosomal protein S9

Chain J: 



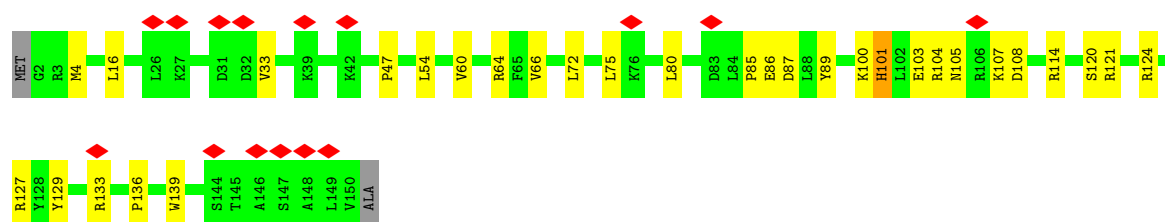
- Molecule 10: 40S ribosomal protein S11

Chain L: 



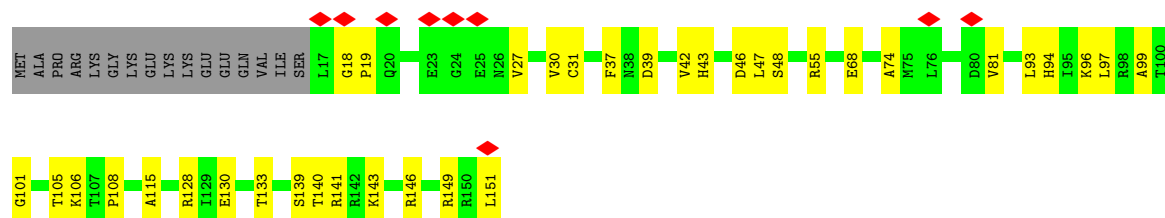
- Molecule 11: 40S ribosomal protein S13

Chain N: 



- Molecule 12: 40S ribosomal protein S14

Chain O: 



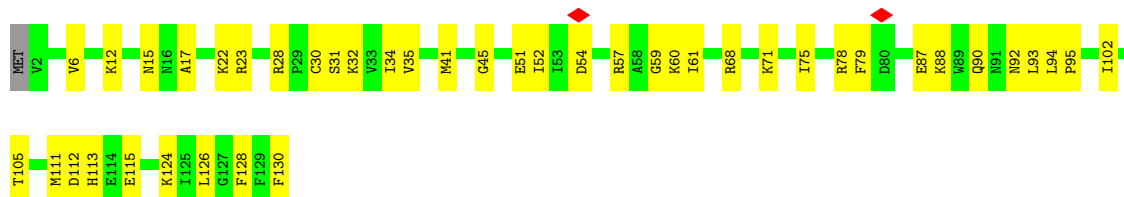
- Molecule 13: 40S ribosomal protein S21

Chain V: 



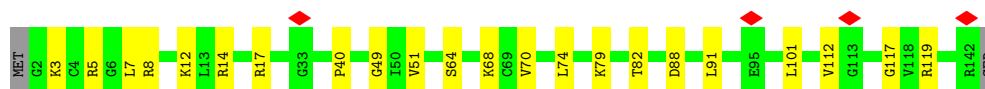
- Molecule 14: 40S ribosomal protein S15a

Chain W: 66% 33%



- Molecule 15: 40S ribosomal protein S23

Chain X: 83% 15%



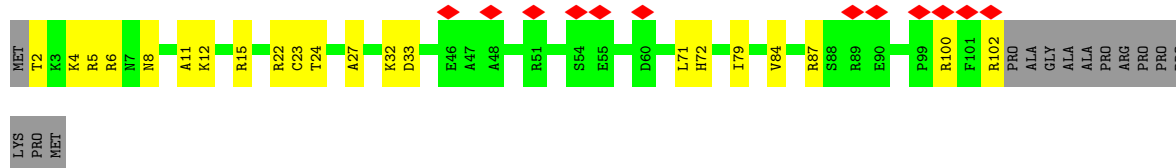
- Molecule 16: 40S ribosomal protein S24

Chain Y: 74% 19% 7%



- Molecule 17: 40S ribosomal protein S26

Chain a: 10% 70% 18% 12%

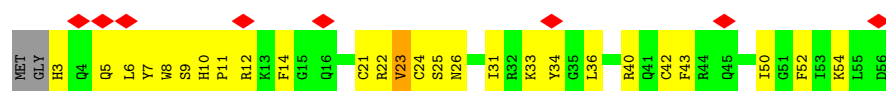


- Molecule 18: 40S ribosomal protein S27

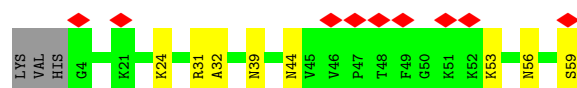
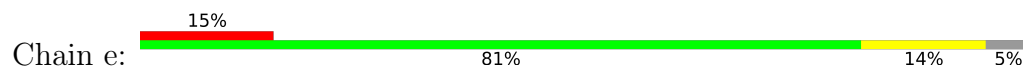
Chain b: 12% 76% 21%



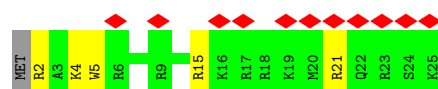
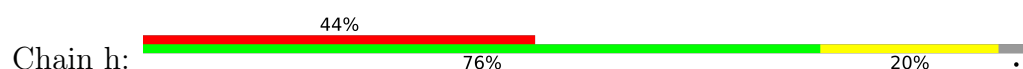
- Molecule 19: 40S ribosomal protein S29



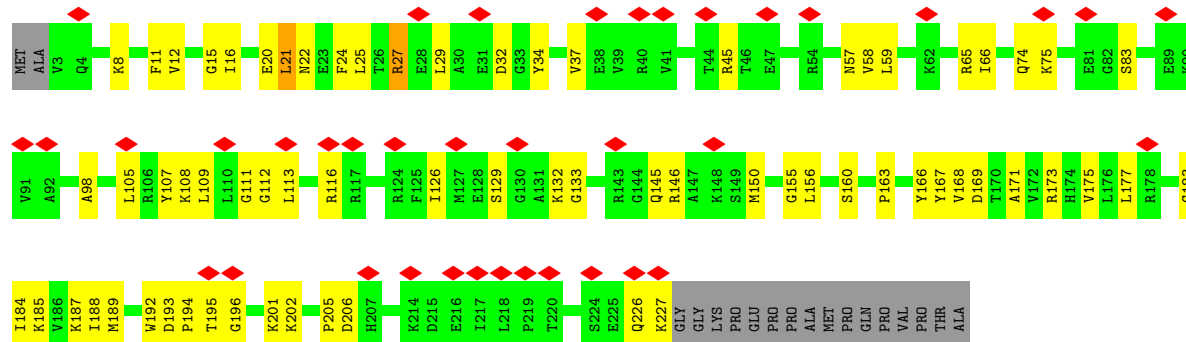
- Molecule 20: 40S ribosomal protein S30



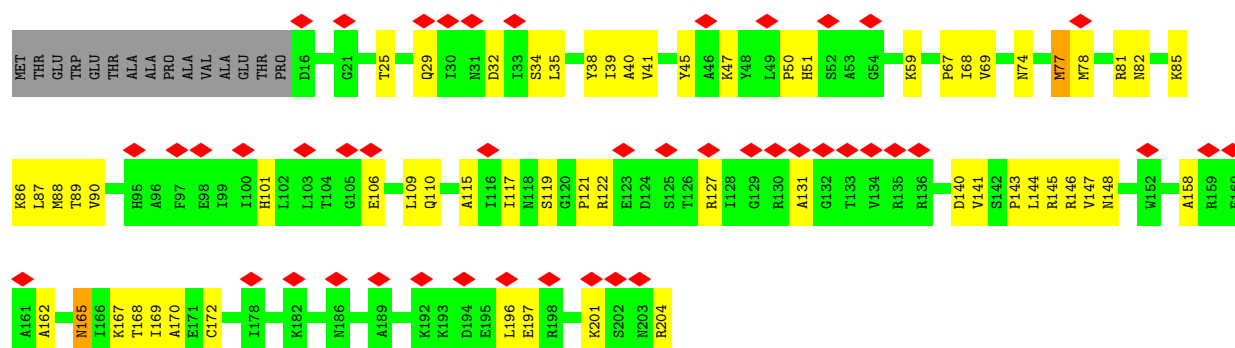
- Molecule 21: 60S ribosomal protein L41



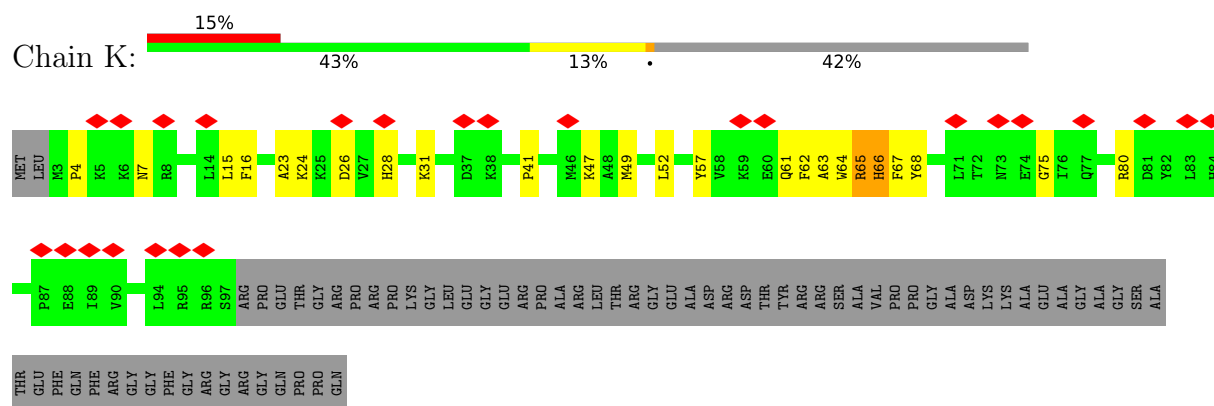
- Molecule 22: 40S ribosomal protein S3



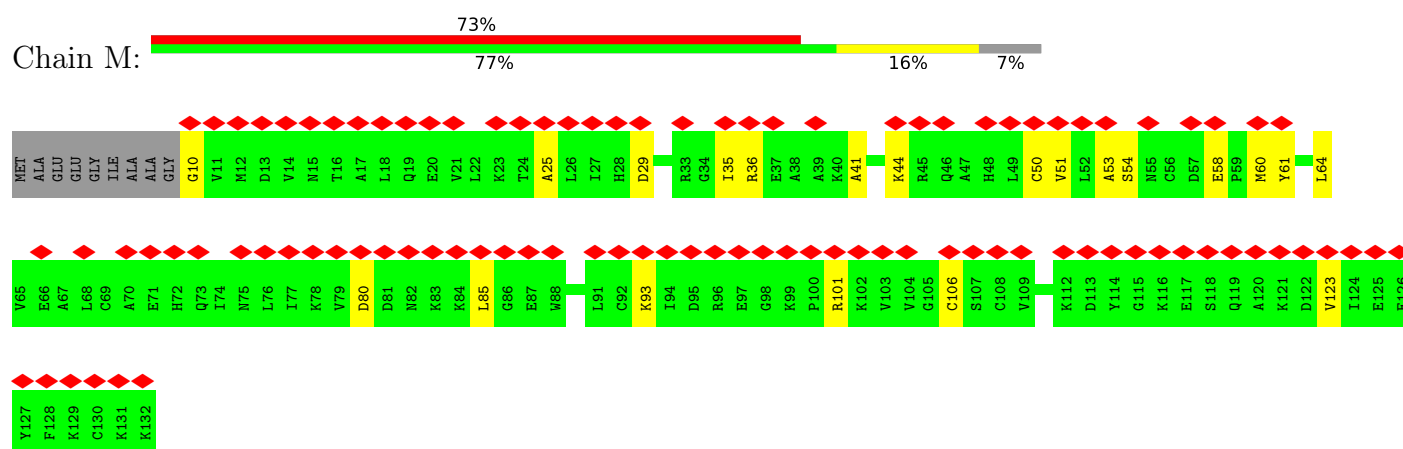
- Molecule 23: 40S ribosomal protein S5



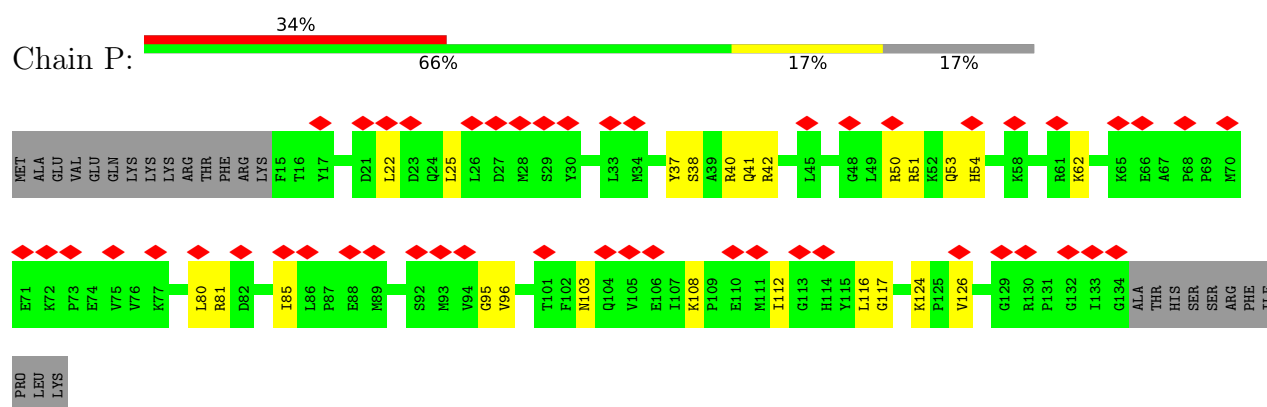
- Molecule 24: 40S ribosomal protein S10



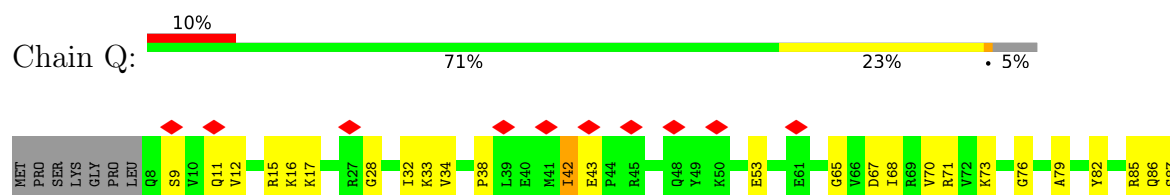
- Molecule 25: 40S ribosomal protein S12

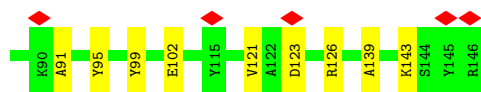


- Molecule 26: 40S ribosomal protein S15

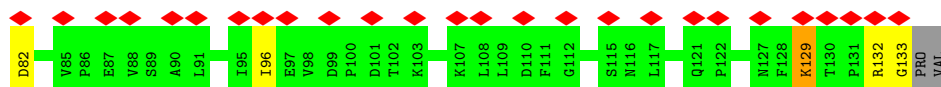
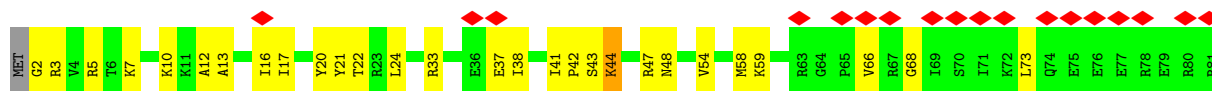
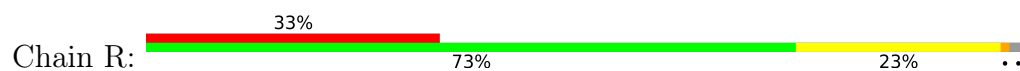


- Molecule 27: 40S ribosomal protein S16

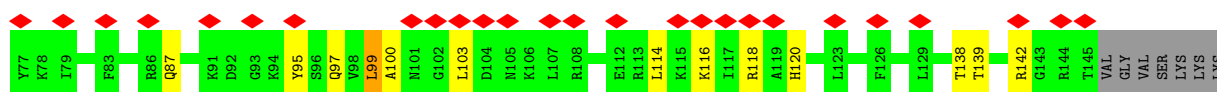
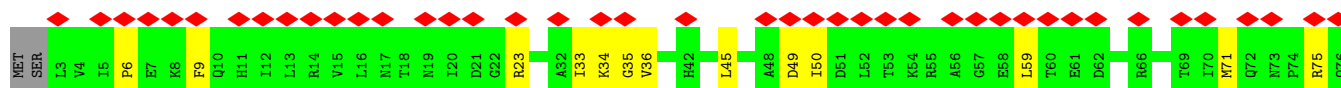
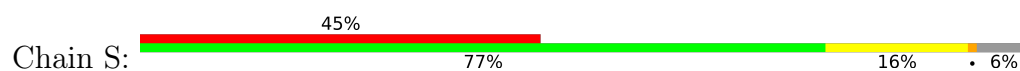




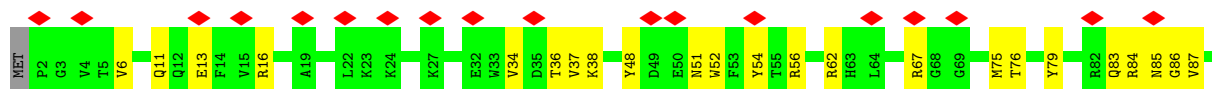
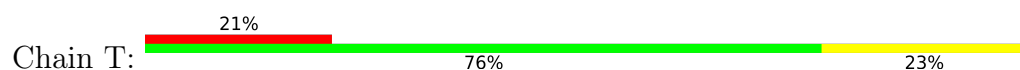
- Molecule 28: 40S ribosomal protein S17



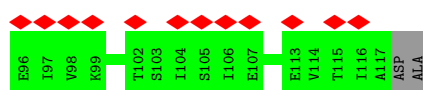
- Molecule 29: 40S ribosomal protein S18



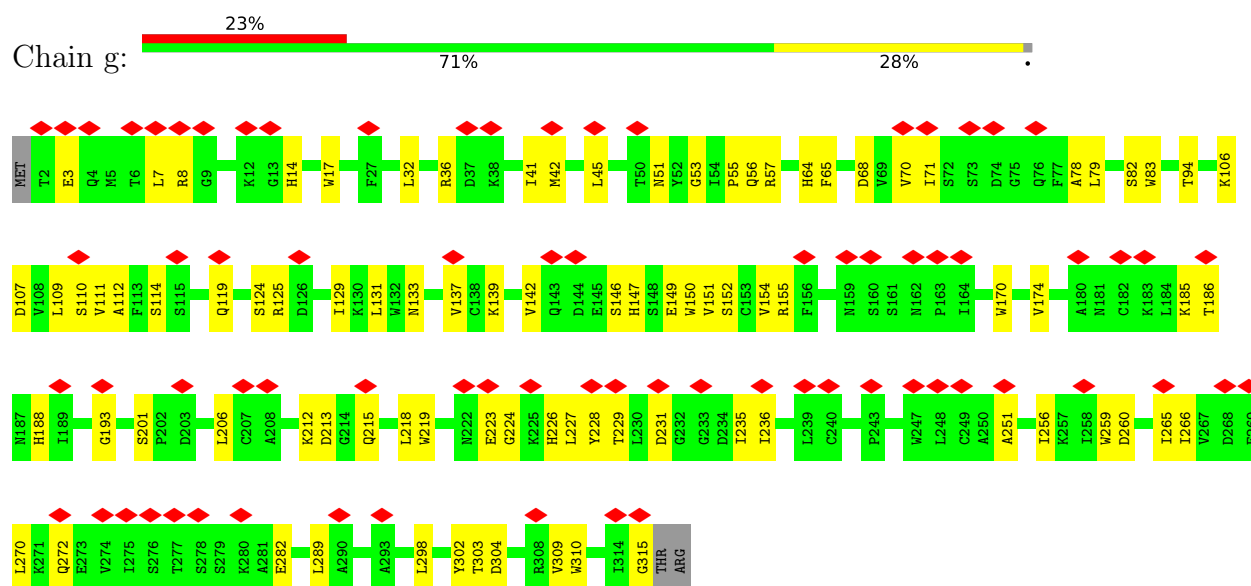
- Molecule 30: 40S ribosomal protein S19



- Molecule 31: 40S ribosomal protein S20



- Molecule 32: 40S ribosomal protein S25



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	70822	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	0.372	Depositor
Minimum map value	-0.186	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	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	2	0.56	0/39755	0.61	16/61954 (0.0%)
2	A	0.57	0/1661	0.89	4/2259 (0.2%)
3	B	0.54	0/1756	0.91	4/2350 (0.2%)
4	C	0.66	0/1718	0.98	7/2322 (0.3%)
5	E	0.67	1/2118 (0.0%)	0.82	1/2849 (0.0%)
6	G	0.49	0/1885	0.88	0/2510
7	H	0.36	0/1524	0.81	1/2042 (0.0%)
8	I	0.55	0/1711	0.87	3/2282 (0.1%)
9	J	0.68	0/1524	0.93	0/2035
10	L	0.63	0/1250	0.83	0/1673
11	N	0.56	0/1226	0.88	0/1649
12	O	0.55	0/1019	0.91	1/1367 (0.1%)
13	V	0.56	0/631	0.83	0/844
14	W	0.65	0/1051	0.93	0/1406
15	X	0.63	0/1116	0.92	0/1490
16	Y	0.60	0/1031	0.88	0/1370
17	a	0.59	0/828	0.83	0/1109
18	b	0.48	0/653	0.79	0/876
19	d	0.51	0/466	0.85	1/618 (0.2%)
20	e	0.52	0/447	0.85	2/587 (0.3%)
21	h	0.45	0/232	1.01	0/295
22	D	0.53	0/1776	0.96	7/2392 (0.3%)
23	F	0.43	0/1516	0.89	2/2037 (0.1%)
24	K	0.43	0/824	0.85	2/1112 (0.2%)
25	M	0.30	0/963	0.76	0/1291
26	P	0.36	0/1003	0.77	0/1341
27	Q	0.49	0/1126	0.89	0/1506
28	R	0.45	0/1080	0.94	6/1449 (0.4%)
29	S	0.33	0/1202	0.80	2/1610 (0.1%)
30	T	0.47	1/1142 (0.1%)	0.80	0/1530
31	U	0.50	0/813	1.01	3/1092 (0.3%)
32	Z	0.34	0/580	0.86	2/780 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.42	0/481	0.86	1/643 (0.2%)
34	f	0.31	0/595	0.70	0/785
35	g	0.39	0/2497	0.74	0/3399
All	All	0.54	2/79200 (0.0%)	0.74	65/114854 (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
8	I	0	1
11	N	0	1
12	O	0	1
15	X	0	1
16	Y	0	1
18	b	0	1
22	D	0	1
23	F	0	4
27	Q	0	1
30	T	0	1
34	f	0	1
All	All	0	14

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	237	SER	C-N	-8.45	1.21	1.33
30	T	87	VAL	C-N	-7.08	1.23	1.33

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	37	C	C1'-C2'-O2'	-10.20	93.10	108.40
19	d	23	VAL	N-CA-C	10.05	120.87	110.72
7	H	85	LYS	N-CA-C	9.34	121.45	111.28
1	2	37	C	C4'-C3'-O3'	8.94	126.41	113.00
3	B	64	GLY	N-CA-C	8.56	123.00	112.73

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	I	101	ILE	Peptide
11	N	101	HIS	Peptide
12	O	93	LEU	Peptide
15	X	112	VAL	Peptide
16	Y	118	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	35552	0	17948	431	0
2	A	1624	0	1634	60	0
3	B	1729	0	1801	63	0
4	C	1682	0	1769	57	0
5	E	2076	0	2177	29	0
6	G	1862	0	2018	28	0
7	H	1501	0	1593	47	0
8	I	1682	0	1769	31	0
9	J	1499	0	1618	34	0
10	L	1229	0	1302	23	0
11	N	1202	0	1289	24	0
12	O	1006	0	1030	23	0
13	V	625	0	628	10	0
14	W	1034	0	1080	44	0
15	X	1098	0	1167	19	0
16	Y	1014	0	1082	21	0
17	a	814	0	864	20	0
18	b	640	0	665	10	0
19	d	455	0	446	86	0
20	e	442	0	487	6	0
21	h	231	0	277	4	0
22	D	1748	0	1844	81	0
23	F	1495	0	1549	40	0
24	K	800	0	818	70	0
25	M	953	0	990	14	0
26	P	984	0	1028	17	0
27	Q	1109	0	1174	27	0
28	R	1066	0	1116	45	0
29	S	1184	0	1244	18	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	T	1122	0	1153	27	0
31	U	803	0	873	48	0
32	Z	574	0	627	10	0
33	c	479	0	507	11	0
34	f	585	0	616	11	0
35	g	2440	0	2396	60	0
36	a	1	0	0	0	0
36	d	1	0	0	0	0
36	f	1	0	0	0	0
All	All	74342	0	58579	1234	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 10.

The worst 5 of 1234 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)
3:B:62:LEU:HD11	3:B:91:VAL:CG2	1.37	1.53
19:d:23:VAL:HG23	24:K:64:TRP:CD1	1.42	1.50
28:R:12:ALA:O	28:R:16:ILE:HG22	1.29	1.31
19:d:21:CYS:SG	19:d:23:VAL:HG12	1.73	1.28
7:H:58:LYS:HD2	7:H:90:LYS:NZ	1.50	1.25

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1654/1868 (88%)	530 (32%)	0

5 of 530 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	C
1	2	4	C
1	2	9	U
1	2	10	G

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](#)

Of 3 ligands modelled in this entry, 3 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.

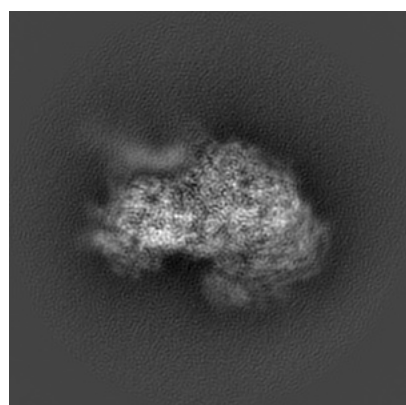
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4352. These allow visual inspection of the internal detail of the map and identification of artifacts.

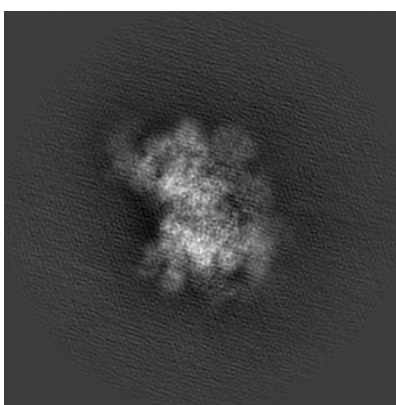
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

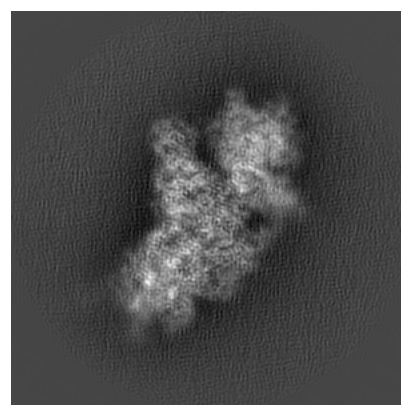
6.1.1 Primary map



X



Y

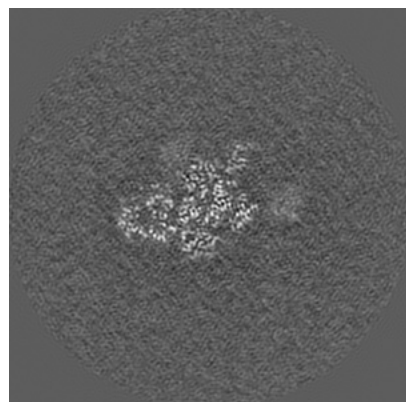


Z

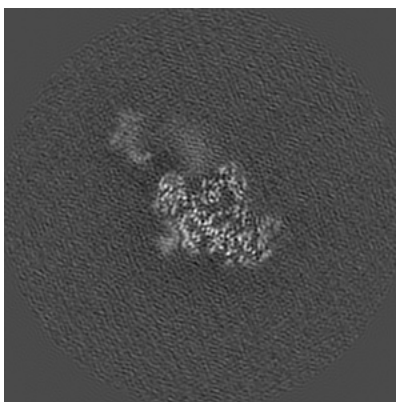
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

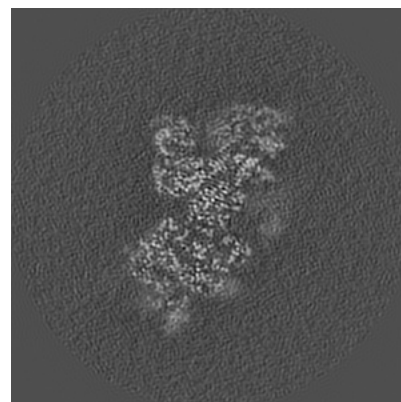
6.2.1 Primary map



X Index: 180



Y Index: 180

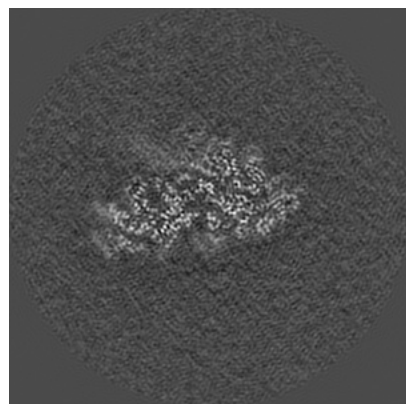


Z Index: 180

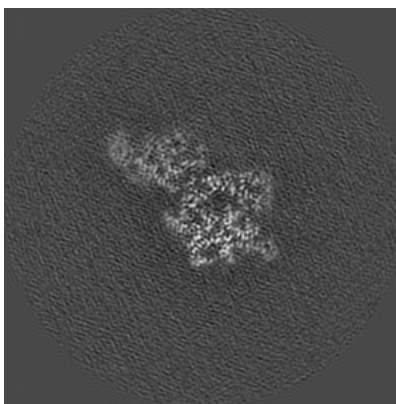
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

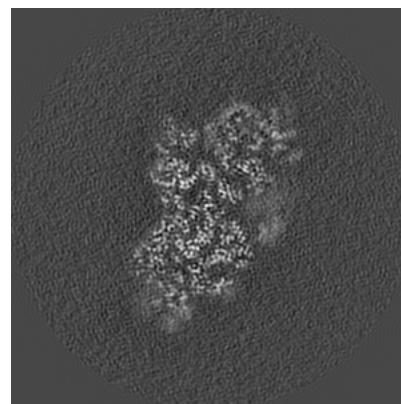
6.3.1 Primary map



X Index: 154



Y Index: 203

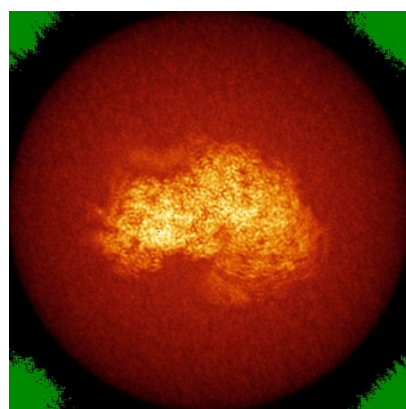


Z Index: 175

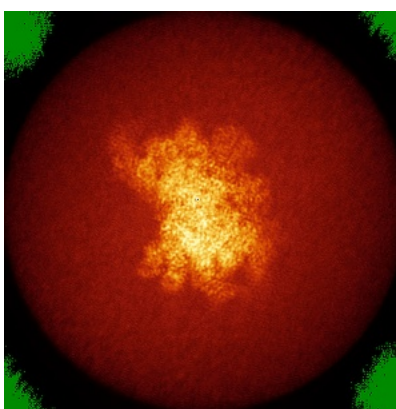
The images above show the largest variance slices of the map in three orthogonal directions.

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

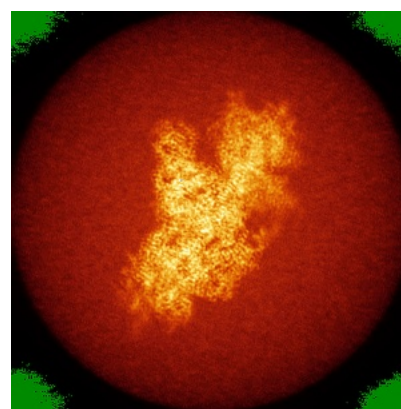
6.4.1 Primary map



X



Y

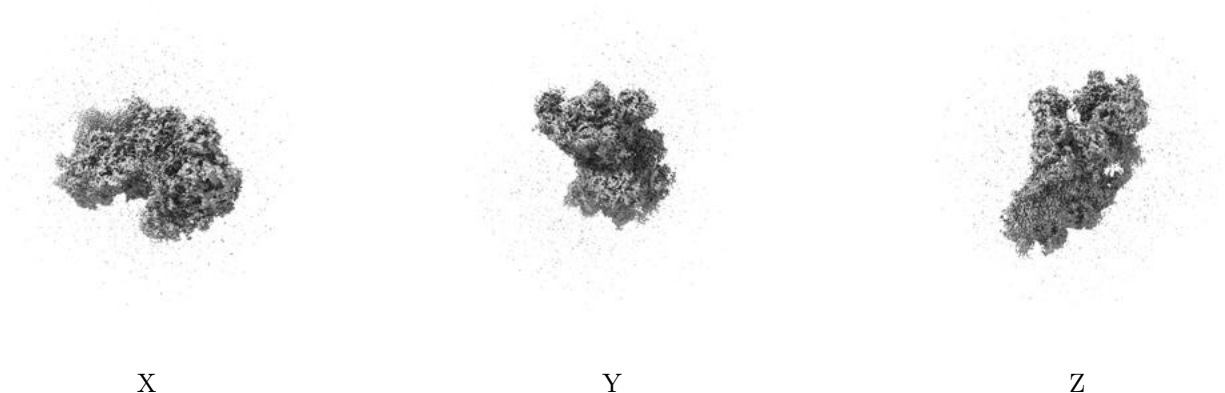


Z

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 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

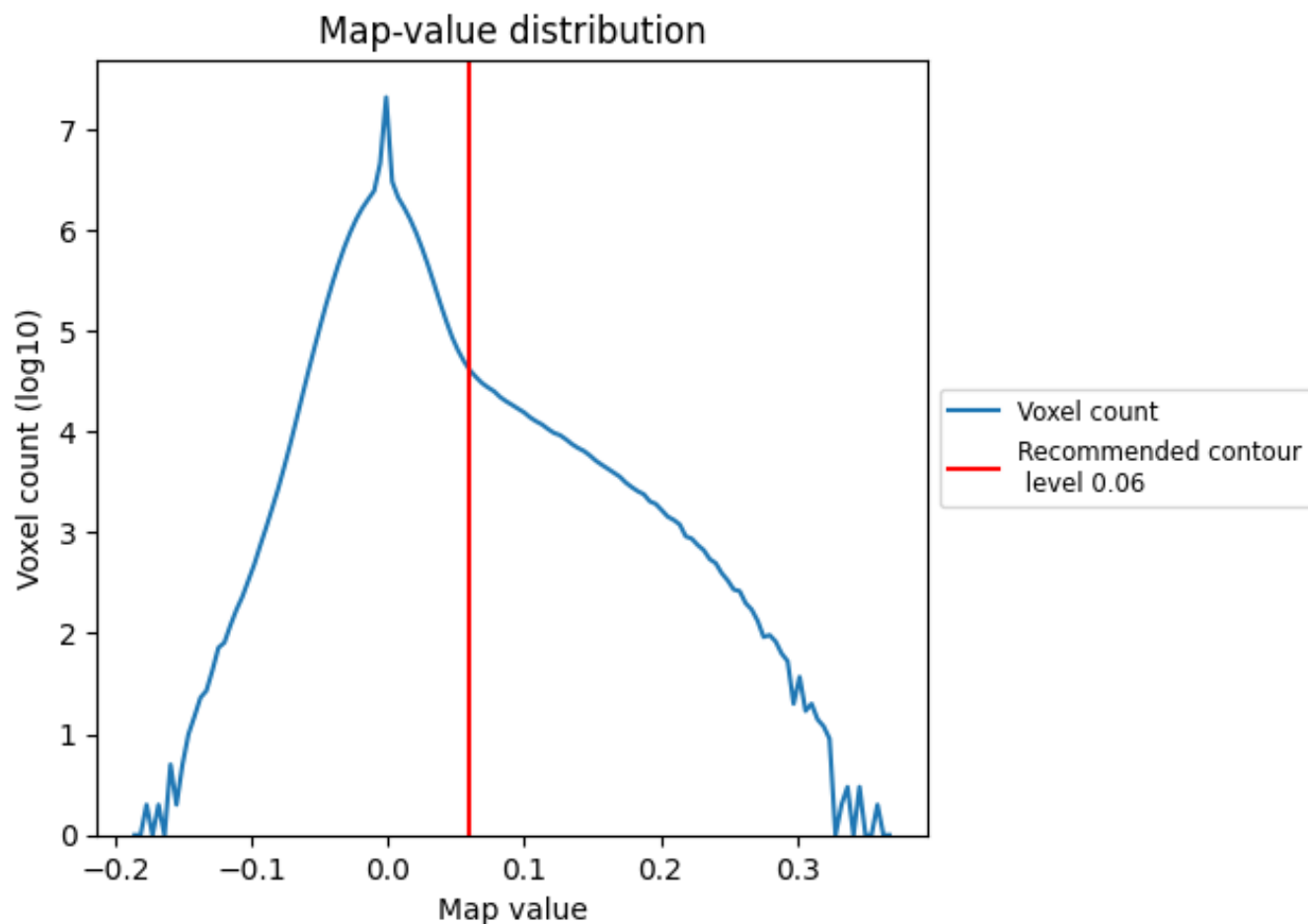
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

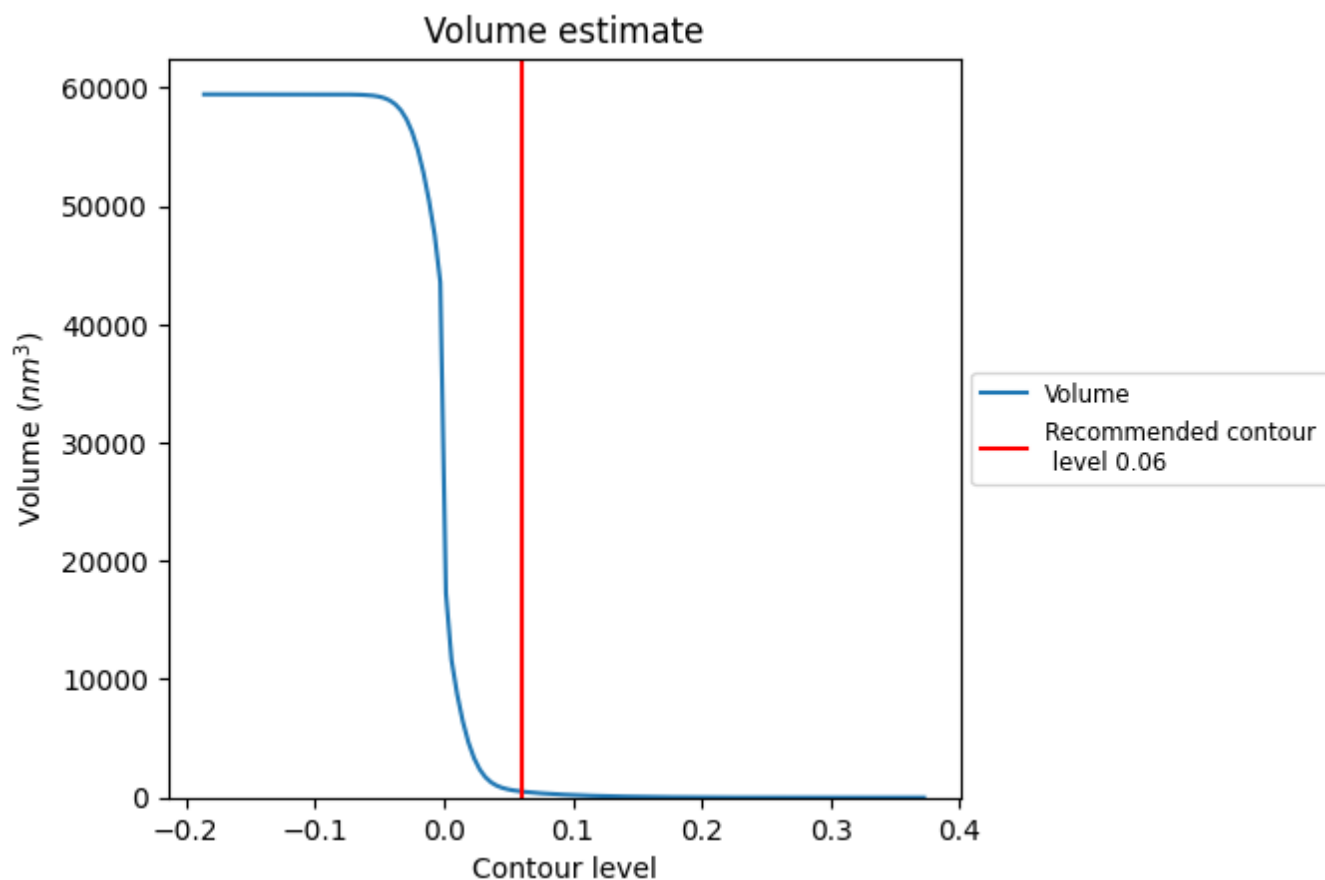
This section contains the results of statistical analysis of the map.

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.

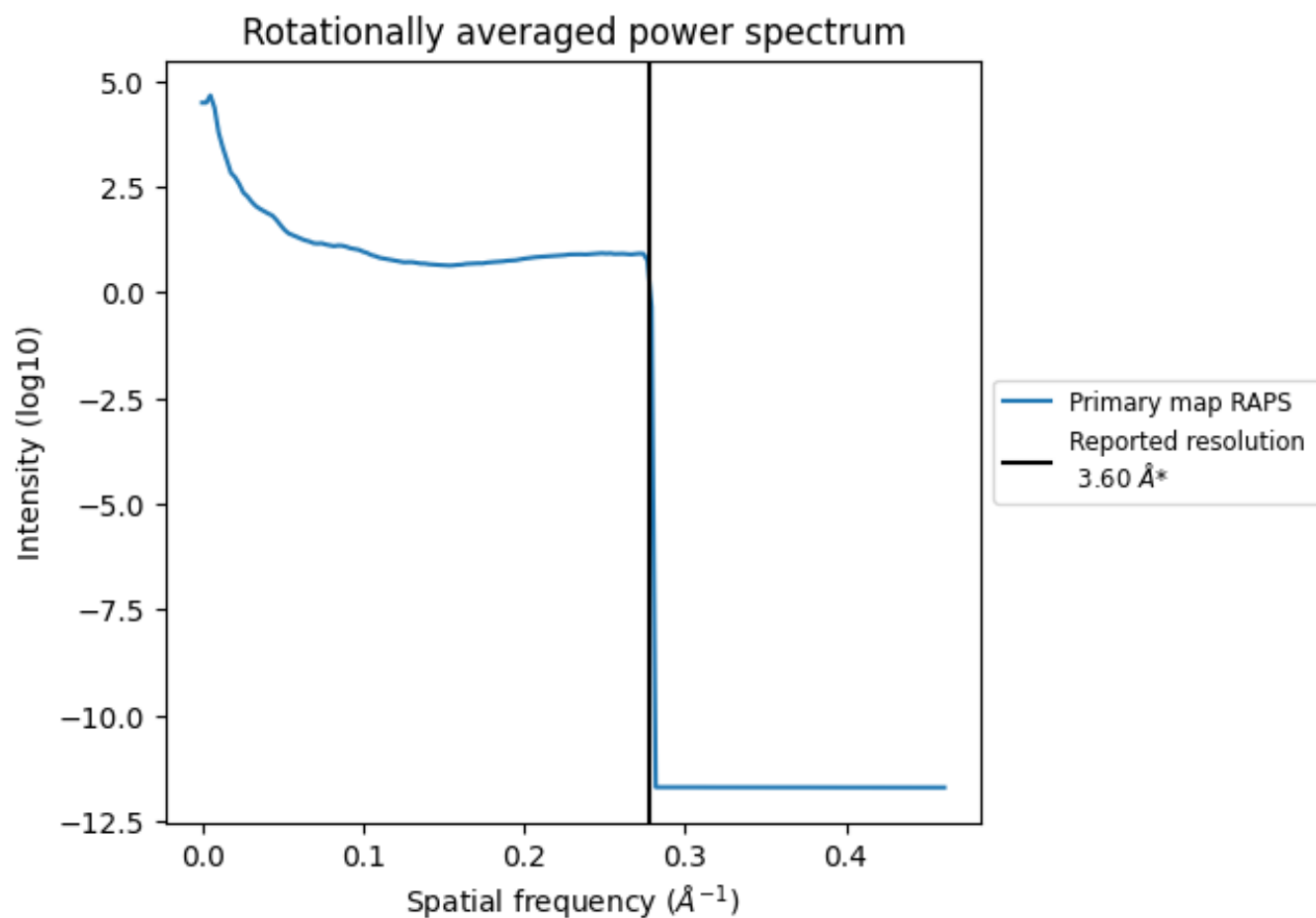
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 517 nm³; this corresponds to an approximate mass of 467 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 ⓘ

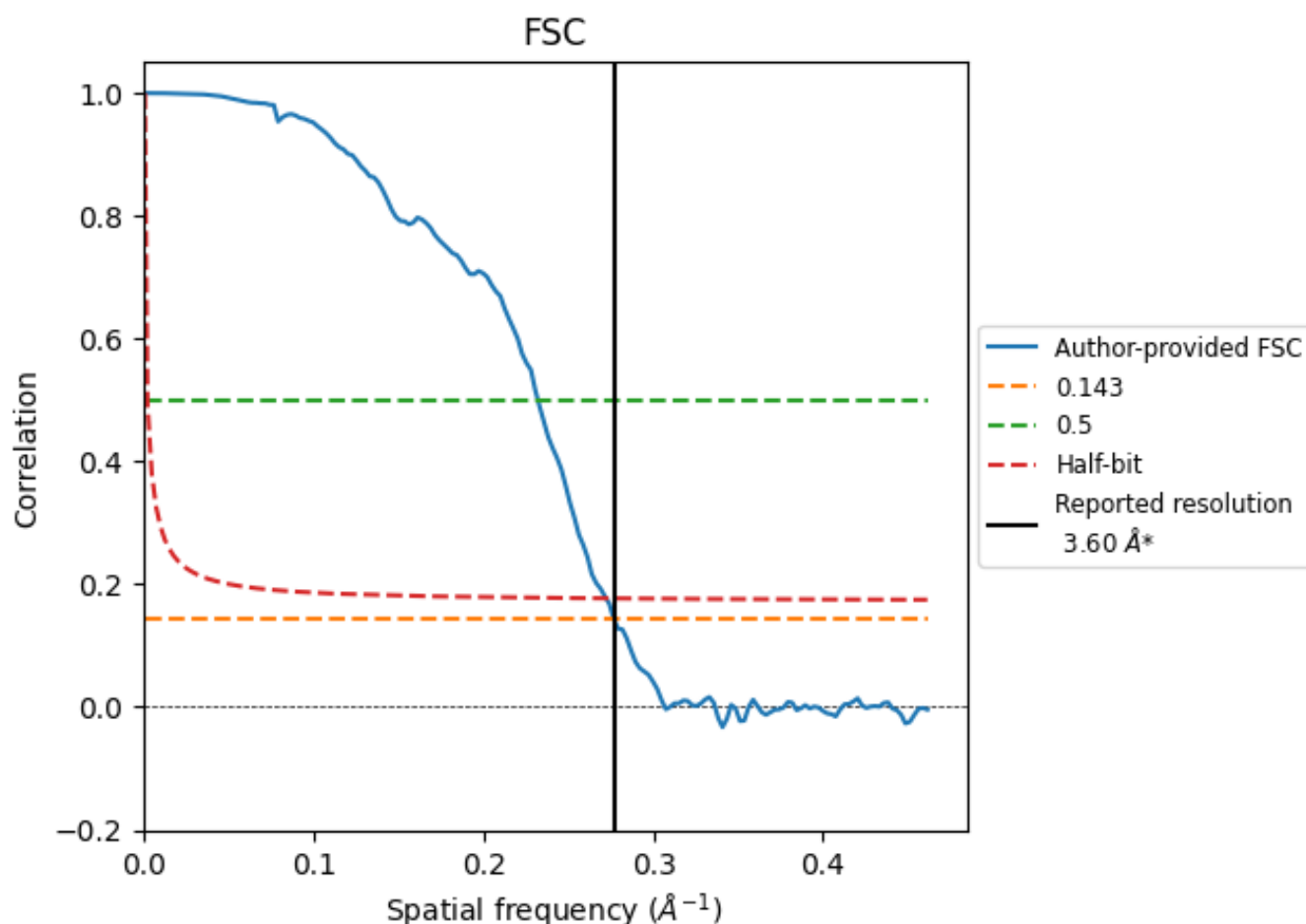


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

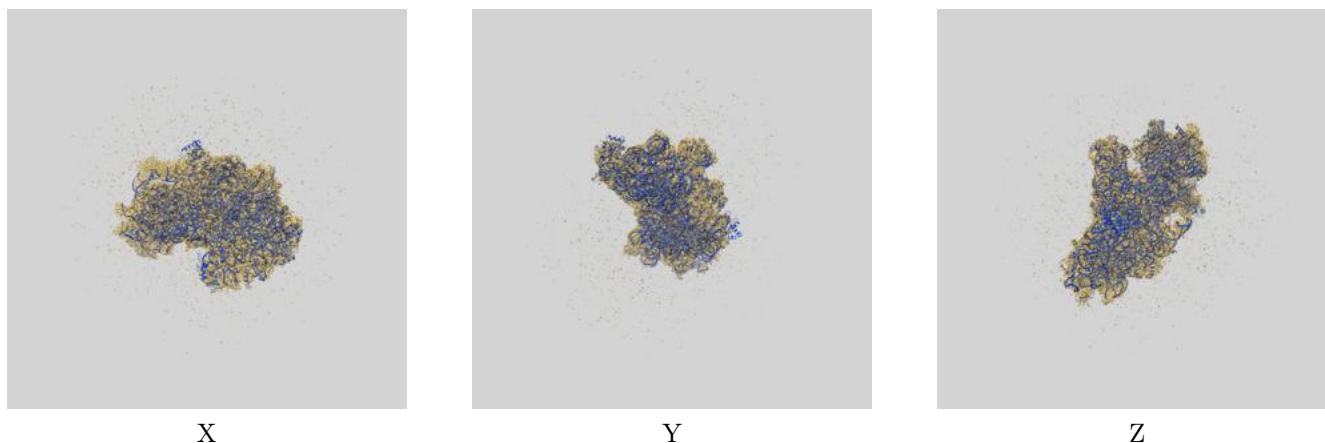
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.61	4.31	3.67
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

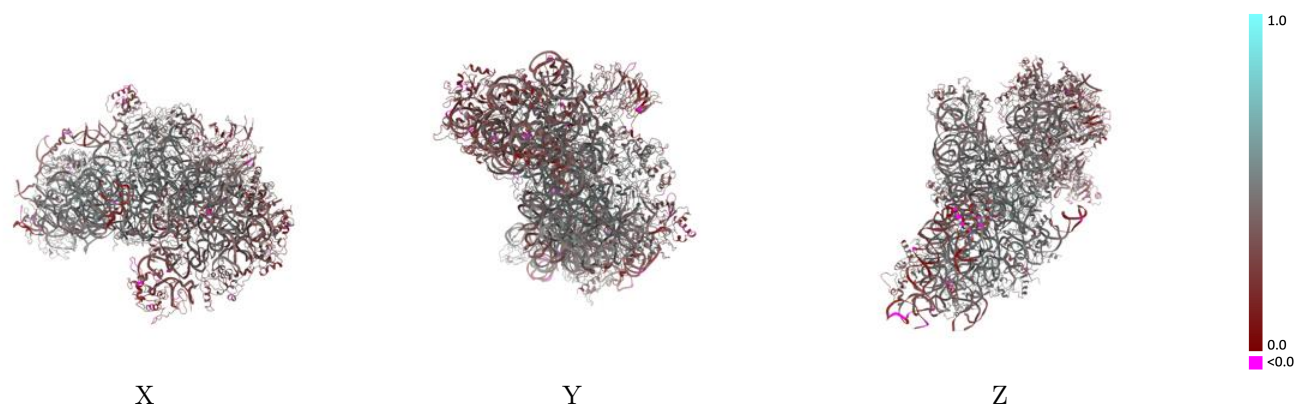
This section contains information regarding the fit between EMDB map EMD-4352 and PDB model 6G5H. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



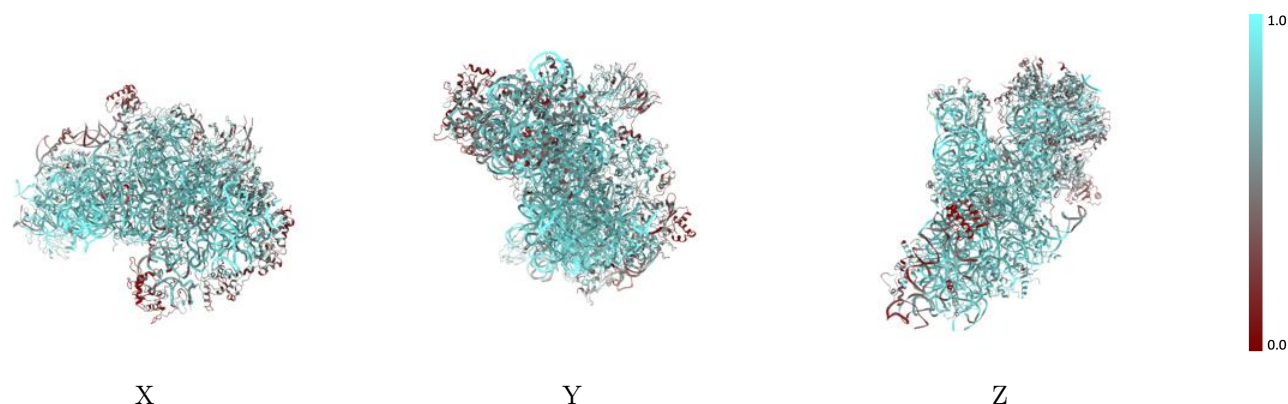
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



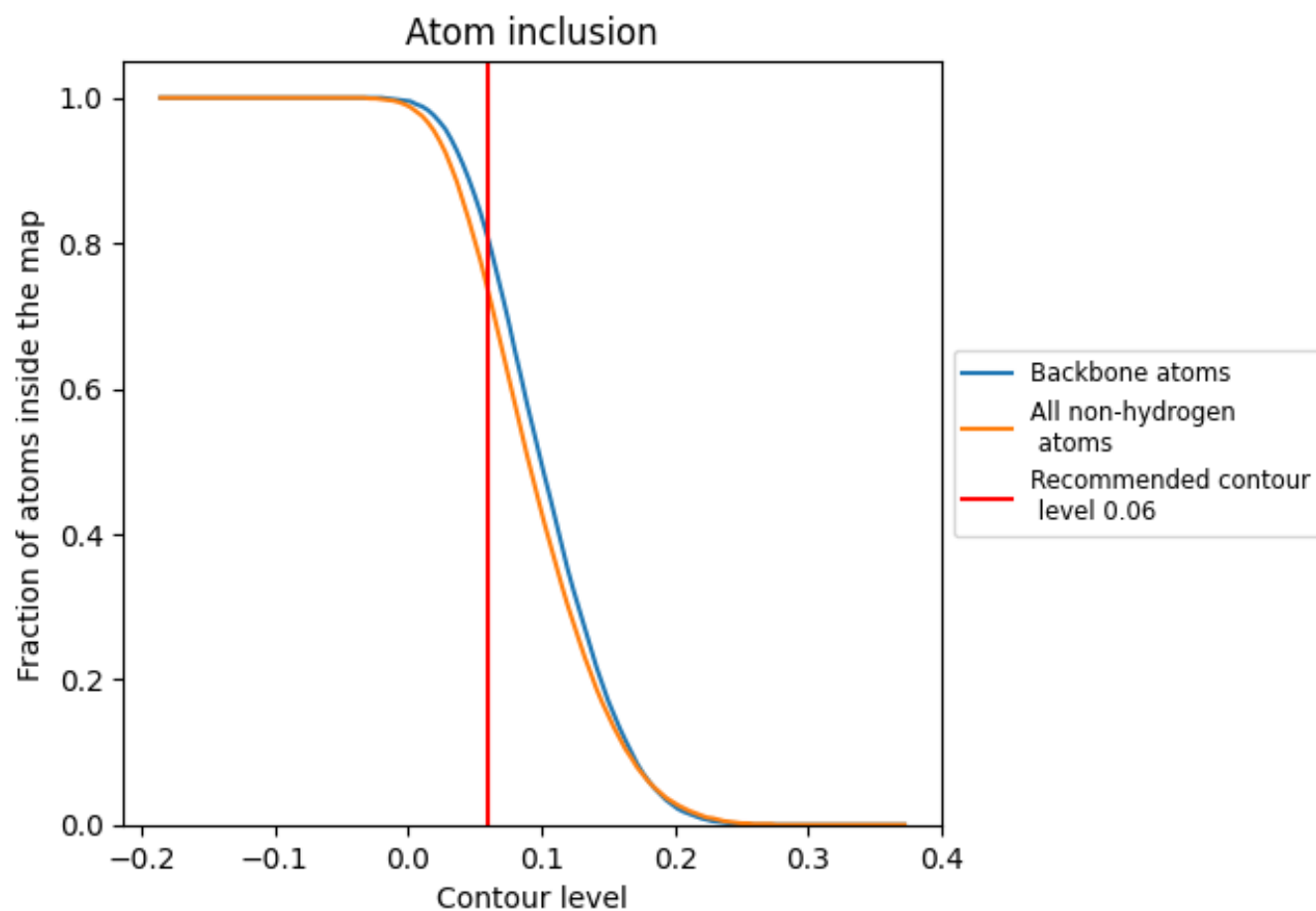
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 73% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7340	 0.4080
2	 0.8500	 0.4210
A	 0.7190	 0.4440
B	 0.6950	 0.4180
C	 0.7560	 0.4730
D	 0.6010	 0.3750
E	 0.7450	 0.4740
F	 0.5610	 0.3440
G	 0.7000	 0.4190
H	 0.3080	 0.2870
I	 0.6990	 0.4310
J	 0.7940	 0.4690
K	 0.5820	 0.3390
L	 0.7010	 0.4600
M	 0.2150	 0.2100
N	 0.7070	 0.4380
O	 0.7070	 0.4280
P	 0.4600	 0.3250
Q	 0.6290	 0.3780
R	 0.5240	 0.3770
S	 0.4440	 0.2990
T	 0.5660	 0.3400
U	 0.5880	 0.3890
V	 0.7400	 0.4640
W	 0.7610	 0.4890
X	 0.7670	 0.4900
Y	 0.7720	 0.4620
Z	 0.4010	 0.2570
a	 0.7110	 0.4550
b	 0.6150	 0.4260
c	 0.5050	 0.3770
d	 0.6370	 0.3480
e	 0.6700	 0.4400
f	 0.3090	 0.2460
g	 0.5750	 0.3320
h	 0.4430	 0.3480

