



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:31 PM UTC

PDB ID : 7OHT / pdb_00007oht
EMDB ID : EMD-12908
Title : Nog1-TAP associated immature ribosomal particles from *S. cerevisiae* after rpL2 expression shut down, population A
Authors : Milkereit, P.; Poell, G.
Deposited on : 2021-05-11
Resolution : 4.70 Å(reported)
Based on initial model : 3JCT

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

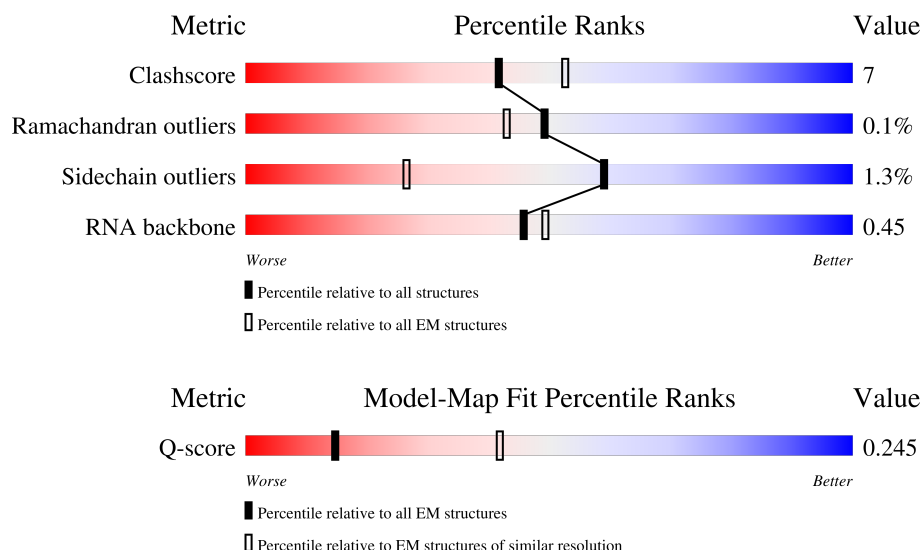
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 Å.

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



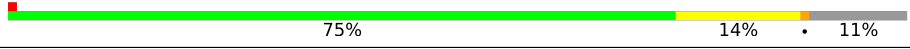
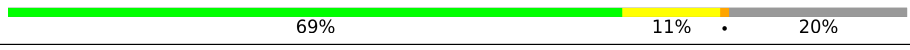
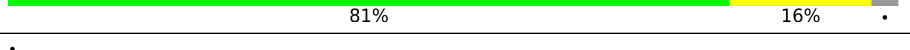
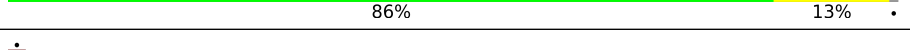
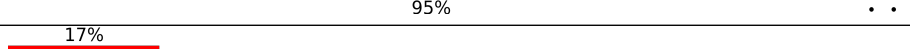
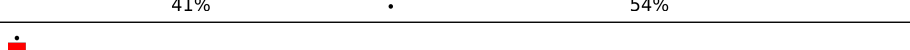
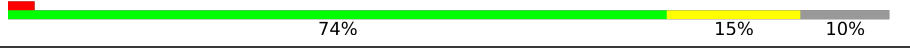
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1989 (4.20 - 5.20)

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

Mol	Chain	Length	Quality of chain
1	1	3396	
2	2	158	
3	3	121	

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Mol	Chain	Length	Quality of chain
4	B	387	
5	C	362	
6	D	297	
7	E	176	
8	F	244	
9	H	191	
10	J	174	
11	M	138	
12	O	199	
13	Q	186	
14	S	172	
15	T	160	
16	V	137	
17	W	236	
18	b	647	
19	e	130	
20	f	107	
21	m	486	
22	r	261	
23	u	199	
24	v	344	
25	w	203	
26	x	515	
27	y	245	

2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 135365 atoms, of which 59714 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 25S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1	1485	Total	C	H	N	O	P	0	0
			47732	14188	15960	5725	10374	1485		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	2	19	Total	C	H	N	O	P	0	0
			605	180	203	69	134	19		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	3	114	Total	C	H	N	O	P	0	0
			3661	1086	1229	436	796	114		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	B	350	Total	C	H	N	O	S	0	0
			5624	1763	2849	516	489	7		

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	C	239	Total	C	H	N	O		0	0
			3813	1178	1961	348	326			

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	D	265	Total	C	H	N	O	S	0	0
			4236	1352	2098	377	407	2		

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	E	141	Total	C	H	N	O	S	0	0
			2338	724	1217	203	193	1		

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	F	222	Total	C	H	N	O	S	0	0
			3647	1151	1863	324	308	1		

- Molecule 9 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	H	191	Total	C	H	N	O	S	0	0
			3105	963	1587	274	277	4		

- Molecule 10 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	169	Total	C	H	N	O	S	0	0
			2738	847	1385	253	249	4		

- Molecule 11 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	M	137	Total	C	H	N	O	S	0	0
			2214	678	1155	200	179	2		

- Molecule 12 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	O	197	Total	C	H	N	O	S	0	0
			3216	1003	1661	289	262	1		

- Molecule 13 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	Q	85	Total	C	H	N	O		0	0
			1357	414	705	123	115			

- Molecule 14 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	S	171	Total	C	H	N	O	S	0	0
			2913	925	1476	266	243	3		

- Molecule 15 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	T	116	Total	C	H	N	O	S	0	0
			1899	583	976	176	161	3		

- Molecule 16 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	V	124	Total	C	H	N	O	S	0	0
			1880	576	963	171	163	7		

- Molecule 17 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	W	234	Total	C	H	N	O	S	0	0
			3806	1194	1921	323	362	6		

- Molecule 18 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	b	453	Total	C	H	N	O	S	0	0
			7406	2340	3727	635	686	18		

- Molecule 19 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	e	39	Total	C	H	N	O	S	0	0
			625	185	331	59	50			

- Molecule 20 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	f	106	Total	C	H	N	O	S	0	0
			1731	540	881	165	144	1		

- Molecule 21 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	m	433	Total	C	H	N	O	S	0	0
			7069	2221	3565	633	641	9		

- Molecule 22 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	r	230	Total	C	H	N	O	S	0	0
			3827	1177	1967	352	324	7		

- Molecule 23 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	u	94	Total	C	H	N	O	S	0	0
			1633	504	833	164	123	9		

- Molecule 24 is a protein called Ribosome biogenesis protein RPF2.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	v	263	Total	C	H	N	O	S	0	0
			4323	1365	2193	372	379	14		

- Molecule 25 is a protein called Regulator of ribosome biosynthesis.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	w	182	Total	C	H	N	O	S	0	0
			2960	911	1512	261	271	5		

- Molecule 26 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	x	488	Total	C	H	N	O	S	0	0
			7606	2398	3799	677	711	21		

- Molecule 27 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	y	225	Total	C	H	N	O	S	0	0
			3398	1056	1697	295	343	7		

- Molecule 28 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

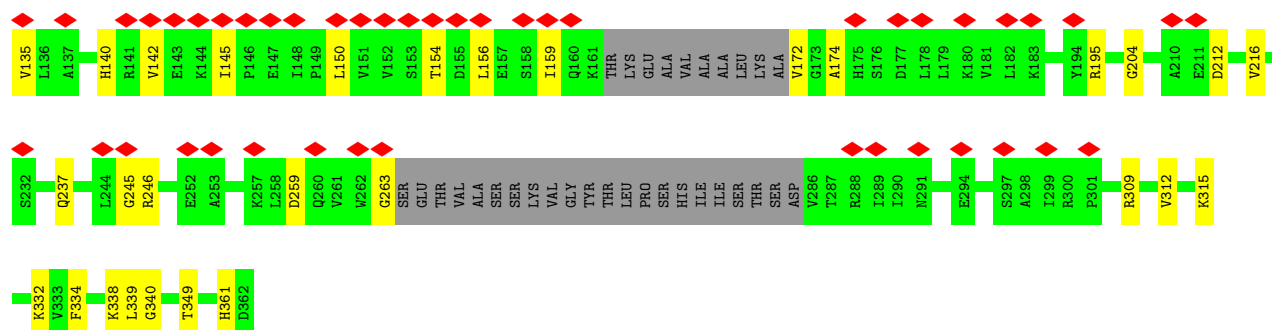
Mol	Chain	Residues	Atoms		AltConf
28	b	1	Total 1	Mg 1	0
28	m	1	Total 1	Mg 1	0

- Molecule 29 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
29	u	1	Total 1	Zn 1	0

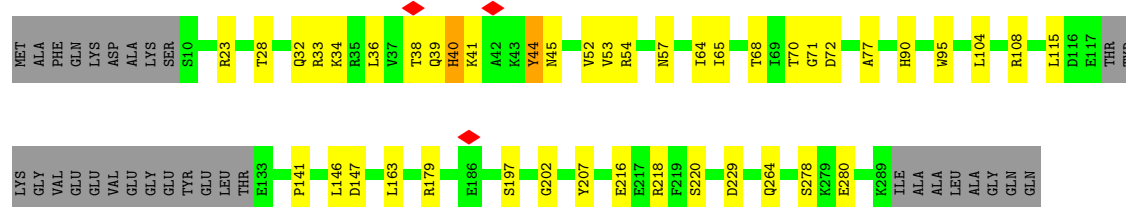






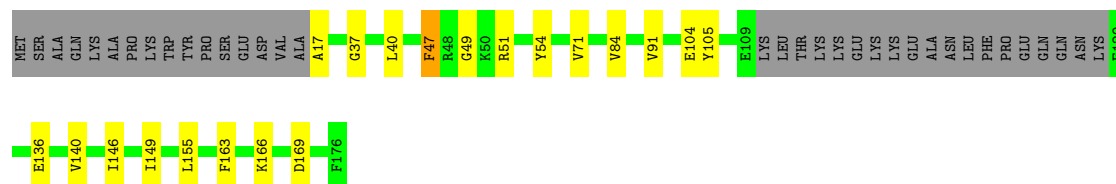
• Molecule 6: 60S ribosomal protein L5

Chain D: 75% 14% 11%



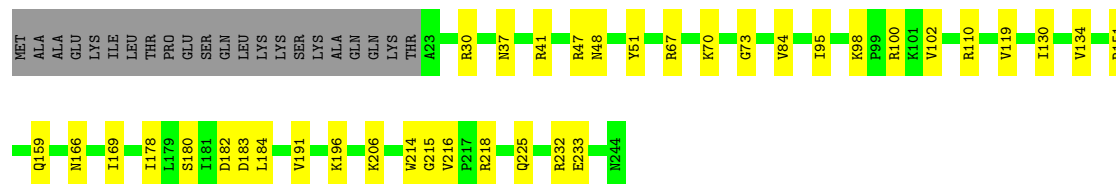
• Molecule 7: 60S ribosomal protein L6-A

Chain E: 69% 11% 20%



• Molecule 8: 60S ribosomal protein L7-A

Chain F: 76% 15% 9%



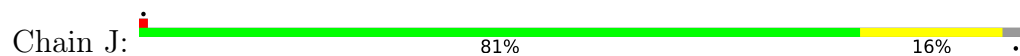
• Molecule 9: 60S ribosomal protein L9-A

Chain H: 83% 17%

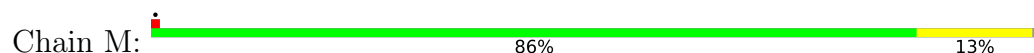




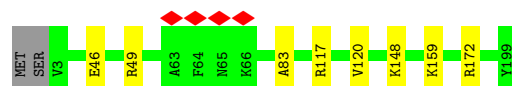
- Molecule 10: 60S ribosomal protein L11-A



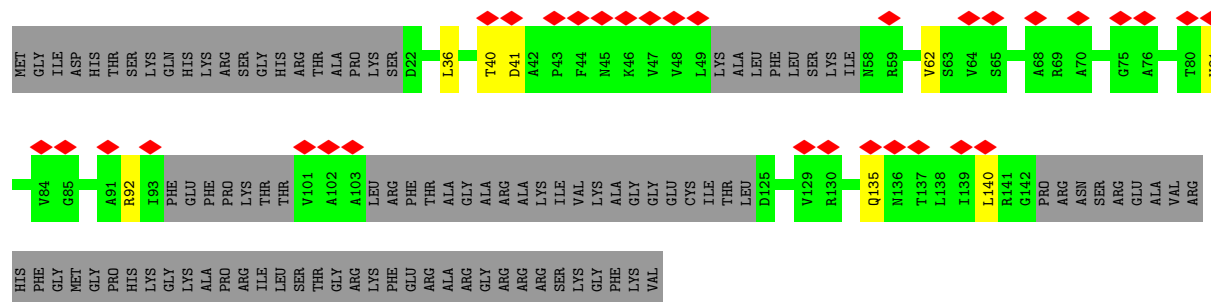
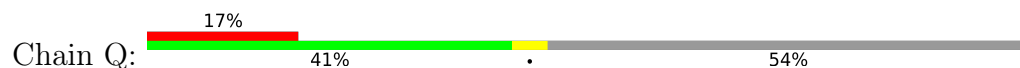
- Molecule 11: 60S ribosomal protein L14-A



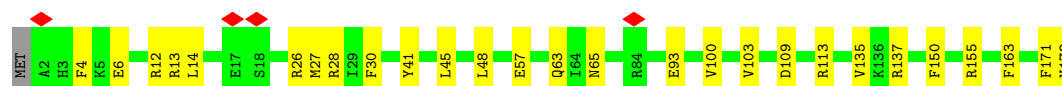
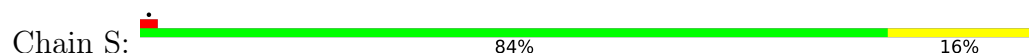
- Molecule 12: 60S ribosomal protein L16-A



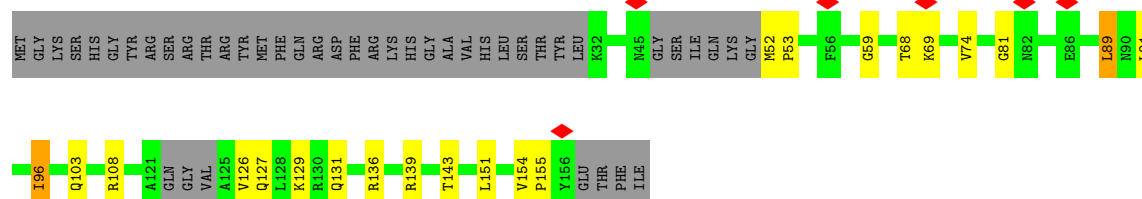
- Molecule 13: 60S ribosomal protein L18-A



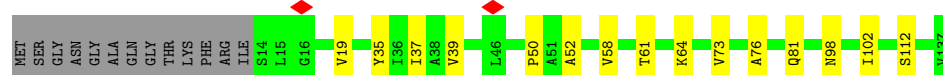
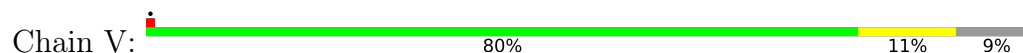
- Molecule 14: 60S ribosomal protein L20-A



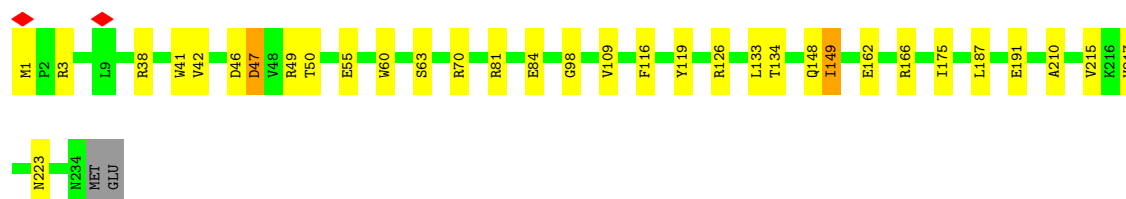
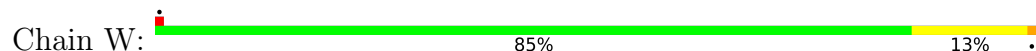
- Molecule 15: 60S ribosomal protein L21-A



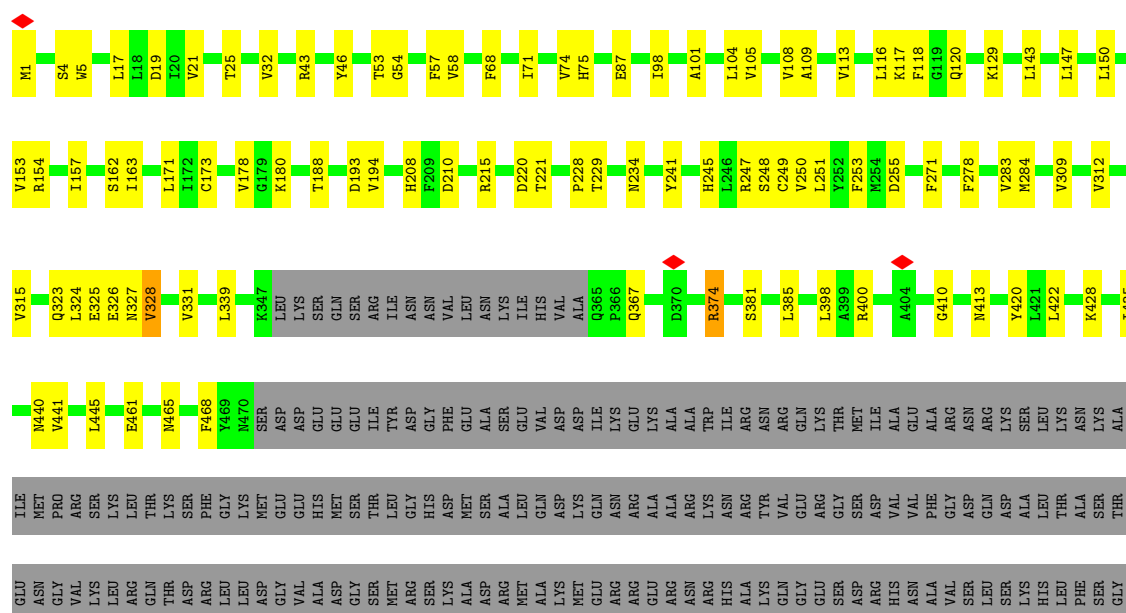
- Molecule 16: 60S ribosomal protein L23-A



- Molecule 17: Ribosome assembly factor MRT4



- Molecule 18: Nucleolar GTP-binding protein 1



LYS
ARG
GLY
VAL
GLY
LYS
THR
ASP
PHE
ARG

• Molecule 19: 60S ribosomal protein L32

Chain e: 15% 29% 70%

MET ALA SER LEU PRO HIS PRO LYS ILE VAL LYS HIS THR LYS LYS PHE LYS ARG ARG HIS HIS SER ASP ARG TVR HIS ARG VAL MET ALA GLU ASN TRP ARG LYS GLN LYS GLY ILE ASP SER VAL VAL ARG ARG ARG PHE ARG GLY ASN ILE SER GLN PRO LYS ILE GLY TYR GLY SER ASN

LYS LYS THR PHE LEU SER PRO LYS HIS VAL LYS HIS THR PHE LEU VAL ALA N78 N79 K80 D81 L82 E83 T84 LEU THR MET HIS THR LYS TYR ALA GLY ILE A97 H98 V106 V107 I108 L109 A110 R111 A112 K113 L114 L115 G116 I117 K118 V119 L126 A127 L128 GLU ALA

• Molecule 20: 60S ribosomal protein L33-A

Chain f: 92% 7%

MET A2 V9 D40 A41 Q42 V59 R60 G61 S62 K63 I100 I107

• Molecule 21: Nucleolar GTP-binding protein 2

Chain m: 18% 70% 18% 11%

MET G2 E7 R10 R11 R12 R13 E14 G15 D16 T17 K18 N21 L22 R23 V24 K25 Y30 R31 D32 S33 K34 R35 V36 K37 F38 L39 N40 M41 Y42 T43 SER GLY LYS GLU ILE ARG ASN LYS GLY ASN ILE ARG ALA ALA SER F61 Q62 D63 S64 T65 I66 P67 D68

R76 W77 V83 A85 E98 T99 Q100 K101 R109 R110 E120 K121 D122 A123 D124 E125 S126 R130 S136 D139 K144 R147 K148 R149 P150 R151 L157 E158 D159 L160 V161 T164 N165 E166 Y171 Q175 VAL LEU ASP ALA THR LEU LEU MET

GLY ASN GLN GLU ASP LYS GLU ASN GLY W194 S204 S208 K209 R210 I211 W212 N213 E214 L215 V218 S221 S222 D223 V224 V225 I226 H227 V228 D230 A231 R232 D233 P234 L235 G236 T237 R238 K248 K253 H254 Y257 V258 L259 N260 K261 V269 W273 E280

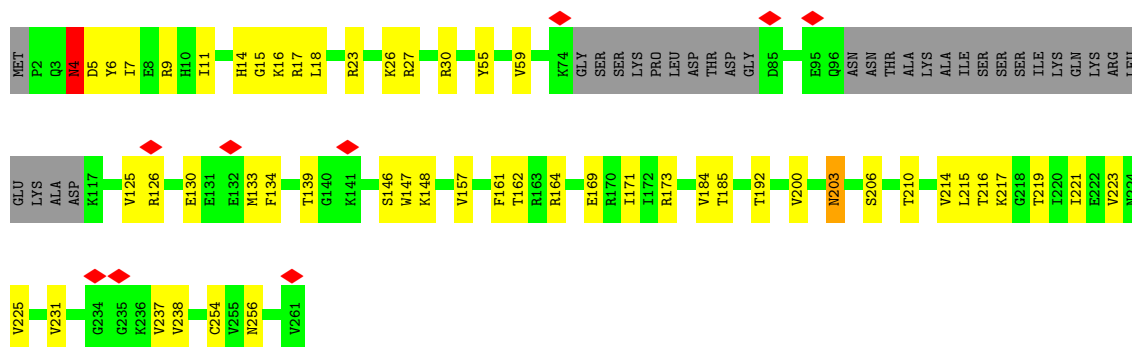
T283 F286 H287 A288 S289 I290 T291 N292 S293 F294 L302 Q308 R313 V318 G319 K328 S329 S330 I331 I332 N333 T334 L335 R336 K337 K338 K339 A344 P345 I346 P347 G348 E349 T350 K351 V352 W353 Q354 Y355 L358 M359 K360 R361 I362 D366 C367 I370 S375 K376

D377 S378 D381 T382 L383 V390 V393 T394 I400 V403 R406 L412 Y416 E417 I418 S419 G420 D423 A424 T425 E426 A432 K440 G441 G442 E443 V449 M458 R459 G460 K461 I462 V466 L467 F468 P469 GLU LYS GLY GLU GLU PRO LYS LYS

LYS
GLU
VAL
GLU
LYS
THR
ALA

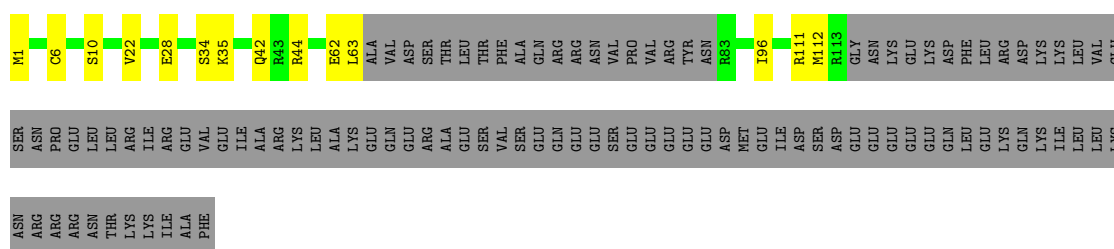
• Molecule 22: Ribosome biogenesis protein NSA2

Chain r: 68% 20% 12%



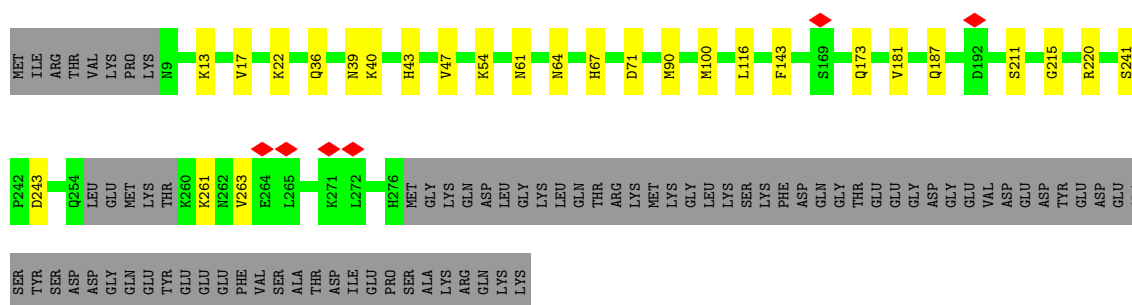
• Molecule 23: Ribosome biogenesis protein RLP24

Chain u: 40% 7% 53%



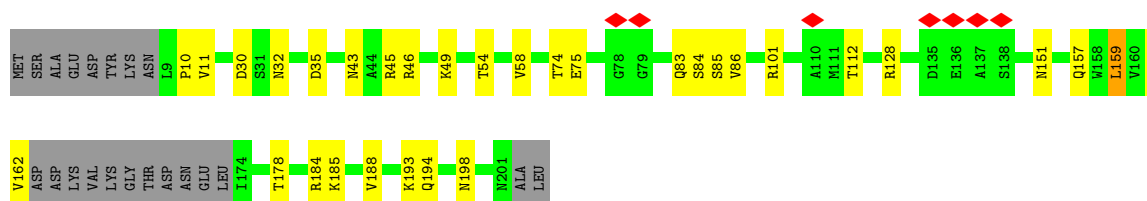
• Molecule 24: Ribosome biogenesis protein RPF2

Chain v: 69% 8% 24%



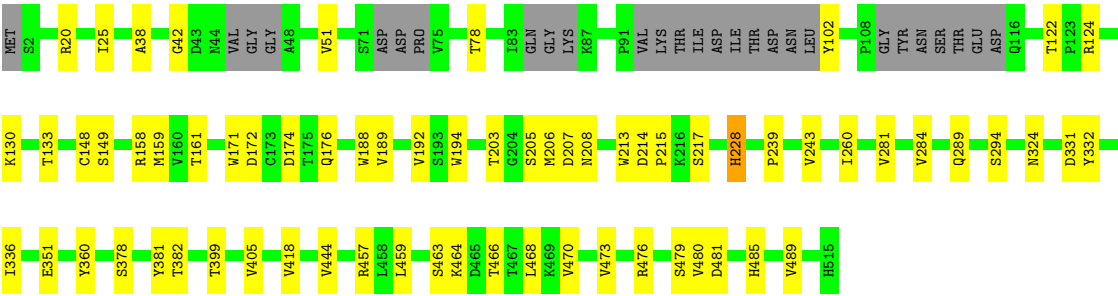
• Molecule 25: Regulator of ribosome biosynthesis

Chain w: 74% 15% 10%

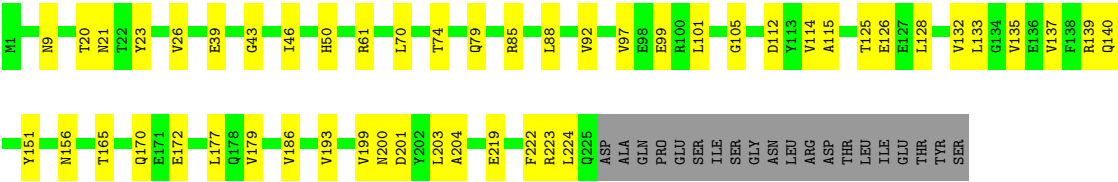


• Molecule 26: Ribosome assembly protein 4

Chain x: 82% 13% 5%



● Molecule 27: Eukaryotic translation initiation factor 6



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21053	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 ($e^-/\text{\AA}^2$)	86.45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.099	Depositor
Minimum map value	-0.026	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	425.40002, 425.40002, 425.40002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0635, 1.0635, 1.0635	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: MG, 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	1	0.08	0/35525	0.25	0/55297
2	2	0.08	0/447	0.28	0/691
3	3	0.07	0/2715	0.22	0/4220
4	B	0.10	0/2833	0.26	0/3806
5	C	0.10	0/1883	0.26	0/2544
6	D	0.10	0/2184	0.25	0/2945
7	E	0.12	0/1137	0.24	0/1525
8	F	0.10	0/1821	0.25	0/2451
9	H	0.09	0/1539	0.26	0/2073
10	J	0.10	0/1374	0.25	0/1842
11	M	0.10	0/1074	0.23	0/1446
12	O	0.10	0/1585	0.21	0/2128
13	Q	0.12	0/656	0.24	0/886
14	S	0.12	0/1473	0.28	0/1980
15	T	0.11	0/936	0.25	0/1255
16	V	0.10	0/931	0.24	0/1254
17	W	0.09	0/1918	0.24	0/2586
18	b	0.10	0/3748	0.29	0/5056
19	e	0.13	0/294	0.23	0/393
20	f	0.11	0/868	0.25	0/1168
21	m	0.10	0/3577	0.29	0/4820
22	r	0.10	0/1892	0.29	0/2528
23	u	0.11	0/816	0.30	0/1078
24	v	0.09	0/2172	0.22	0/2908
25	w	0.10	0/1471	0.23	0/1980
26	x	0.09	0/3897	0.23	0/5282
27	y	0.08	0/1722	0.22	0/2343
All	All	0.09	0/80488	0.25	0/116485

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
9	H	0	1
21	m	0	1
22	r	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	H	22	SER	Peptide
21	m	77	TRP	Peptide
22	r	4	ASN	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	1	31772	15960	15999	388	0
2	2	402	203	205	3	0
3	3	2432	1229	1233	25	0
4	B	2775	2849	2846	43	0
5	C	1852	1961	1958	32	0
6	D	2138	2098	2096	35	0
7	E	1121	1217	1215	13	0
8	F	1784	1863	1862	28	0
9	H	1518	1587	1587	22	0
10	J	1353	1385	1383	16	0
11	M	1059	1155	1154	16	0
12	O	1555	1661	1659	7	0
13	Q	652	705	701	8	0
14	S	1437	1476	1475	20	0
15	T	923	976	973	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	V	917	963	962	11	0
17	W	1885	1921	1921	23	0
18	b	3679	3727	3725	65	0
19	e	294	331	329	2	0
20	f	850	881	880	7	0
21	m	3504	3565	3562	71	0
22	r	1860	1967	1965	45	0
23	u	800	833	830	11	0
24	v	2130	2193	2191	19	0
25	w	1448	1512	1510	24	0
26	x	3807	3799	3790	45	0
27	y	1701	1697	1697	38	0
28	b	1	0	0	0	0
28	m	1	0	0	0	0
29	u	1	0	0	0	0
All	All	75651	59714	59708	887	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 887 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)
27:y:186:VAL:HG12	27:y:193:VAL:HG12	1.51	0.92
1:1:1200:A:O2'	1:1:1201:C:O5'	1.85	0.92
1:1:3366:G:OP1	23:u:111:ARG:NH2	2.03	0.91
1:1:3072:C:OP2	1:1:3073:A:N6	2.02	0.90
1:1:2764:C:O2'	1:1:2765:C:OP2	1.89	0.89

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	
4	B	344/387 (89%)	323 (94%)	21 (6%)	0	100	100
5	C	231/362 (64%)	209 (90%)	21 (9%)	1 (0%)	30	67
6	D	261/297 (88%)	249 (95%)	12 (5%)	0	100	100
7	E	137/176 (78%)	135 (98%)	2 (2%)	0	100	100
8	F	220/244 (90%)	211 (96%)	9 (4%)	0	100	100
9	H	189/191 (99%)	180 (95%)	9 (5%)	0	100	100
10	J	167/174 (96%)	160 (96%)	7 (4%)	0	100	100
11	M	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
12	O	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
13	Q	77/186 (41%)	76 (99%)	1 (1%)	0	100	100
14	S	169/172 (98%)	159 (94%)	10 (6%)	0	100	100
15	T	110/160 (69%)	106 (96%)	4 (4%)	0	100	100
16	V	122/137 (89%)	121 (99%)	1 (1%)	0	100	100
17	W	232/236 (98%)	224 (97%)	8 (3%)	0	100	100
18	b	449/647 (69%)	413 (92%)	36 (8%)	0	100	100
19	e	35/130 (27%)	35 (100%)	0	0	100	100
20	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
21	m	427/486 (88%)	386 (90%)	39 (9%)	2 (0%)	24	63
22	r	224/261 (86%)	193 (86%)	29 (13%)	2 (1%)	14	49
23	u	90/199 (45%)	89 (99%)	1 (1%)	0	100	100
24	v	259/344 (75%)	255 (98%)	4 (2%)	0	100	100
25	w	178/203 (88%)	171 (96%)	7 (4%)	0	100	100
26	x	476/515 (92%)	449 (94%)	27 (6%)	0	100	100
27	y	223/245 (91%)	215 (96%)	8 (4%)	0	100	100
All	All	5054/6196 (82%)	4781 (95%)	268 (5%)	5 (0%)	49	83

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	m	209	LYS
22	r	4	ASN
22	r	5	ASP
21	m	210	ARG
5	C	131	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	B	291/323 (90%)	285 (98%)	6 (2%)	47	65
5	C	197/289 (68%)	197 (100%)	0	100	100
6	D	221/245 (90%)	219 (99%)	2 (1%)	70	77
7	E	122/153 (80%)	120 (98%)	2 (2%)	55	69
8	F	186/205 (91%)	186 (100%)	0	100	100
9	H	171/171 (100%)	171 (100%)	0	100	100
10	J	147/150 (98%)	143 (97%)	4 (3%)	39	60
11	M	108/109 (99%)	108 (100%)	0	100	100
12	O	160/162 (99%)	159 (99%)	1 (1%)	78	81
13	Q	70/151 (46%)	70 (100%)	0	100	100
14	S	155/156 (99%)	154 (99%)	1 (1%)	78	81
15	T	100/137 (73%)	97 (97%)	3 (3%)	36	57
16	V	96/105 (91%)	96 (100%)	0	100	100
17	W	211/213 (99%)	209 (99%)	2 (1%)	70	77
18	b	408/573 (71%)	398 (98%)	10 (2%)	42	62
19	e	31/111 (28%)	31 (100%)	0	100	100
20	f	90/91 (99%)	90 (100%)	0	100	100
21	m	385/428 (90%)	373 (97%)	12 (3%)	35	56
22	r	203/229 (89%)	199 (98%)	4 (2%)	48	66
23	u	82/180 (46%)	81 (99%)	1 (1%)	63	74
24	v	238/309 (77%)	238 (100%)	0	100	100
25	w	161/179 (90%)	159 (99%)	2 (1%)	63	74
26	x	428/451 (95%)	421 (98%)	7 (2%)	55	69
27	y	193/211 (92%)	193 (100%)	0	100	100
All	All	4454/5331 (84%)	4397 (99%)	57 (1%)	59	72

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	b	374	ARG
26	x	351	GLU
21	m	210	ARG
26	x	336	ILE
25	w	159	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
24	v	61	ASN
24	v	64	ASN
26	x	402	GLN
14	S	3	HIS
12	O	42	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1458/3396 (42%)	375 (25%)	58 (3%)
2	2	17/158 (10%)	3 (17%)	0
3	3	109/121 (90%)	11 (10%)	1 (0%)
All	All	1584/3675 (43%)	389 (24%)	59 (3%)

5 of 389 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	187	A
1	1	198	A
1	1	200	C
1	1	202	G
1	1	203	G

5 of 59 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1306	G
1	1	3269	U
1	1	2658	G
1	1	3228	C
1	1	3030	G

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 [i](#)

There are no chain breaks in this entry.

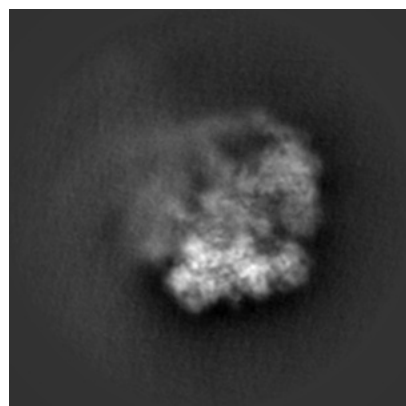
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12908. These allow visual inspection of the internal detail of the map and identification of artifacts.

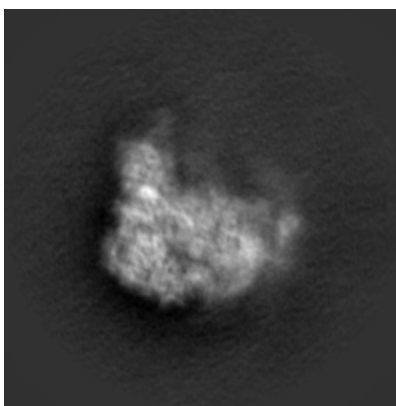
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

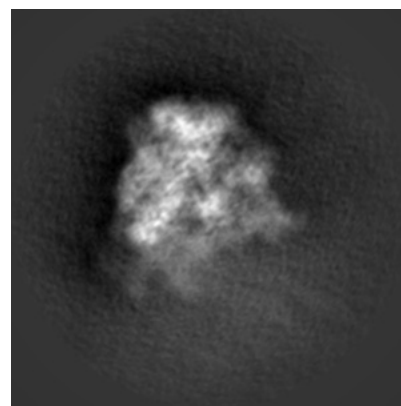
6.1.1 Primary map



X

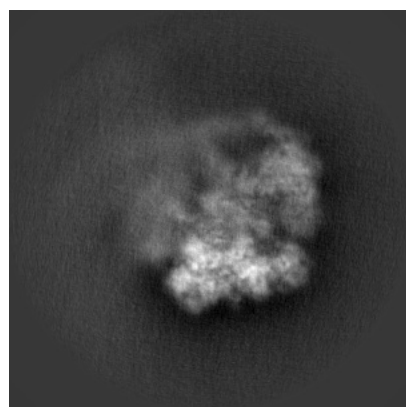


Y

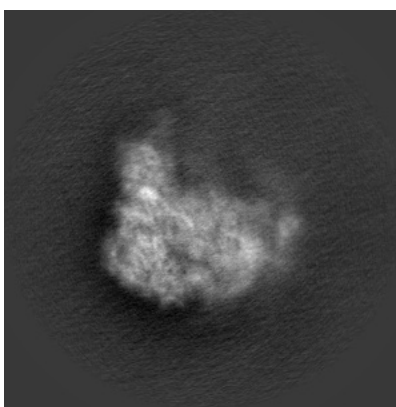


Z

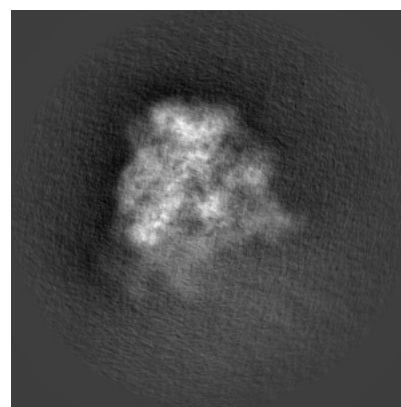
6.1.2 Raw map



X



Y

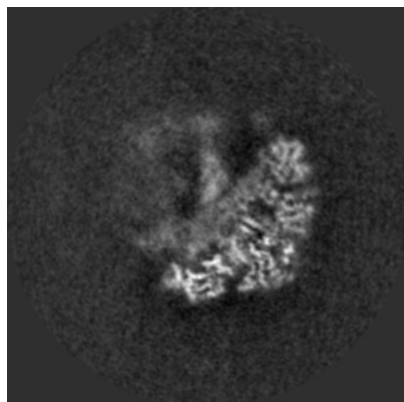


Z

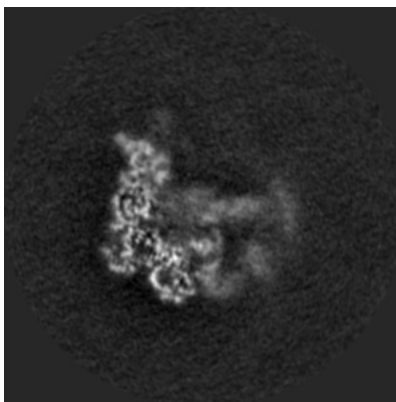
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

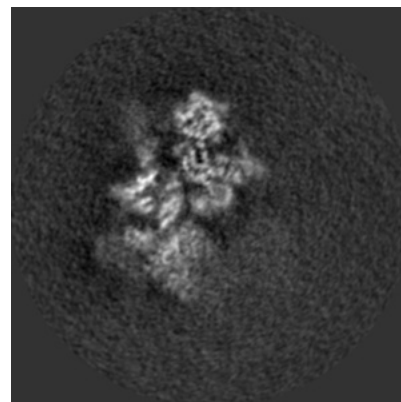
6.2.1 Primary map



X Index: 200

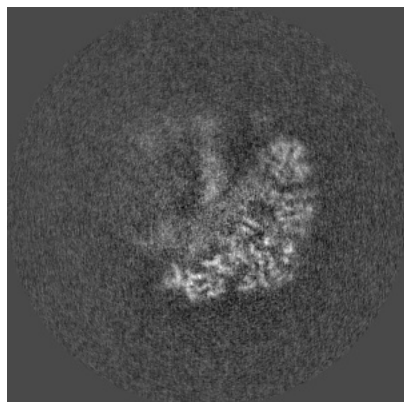


Y Index: 200

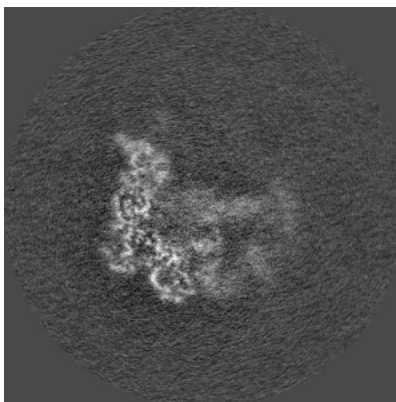


Z Index: 200

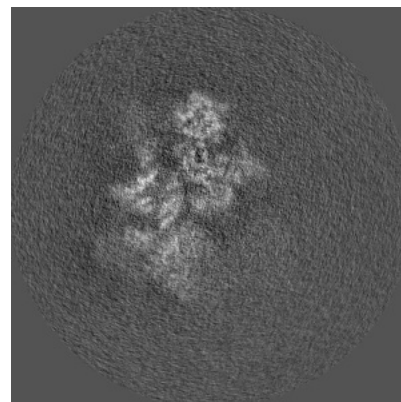
6.2.2 Raw map



X Index: 200



Y Index: 200

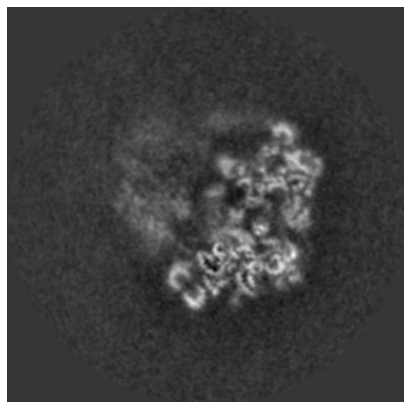


Z Index: 200

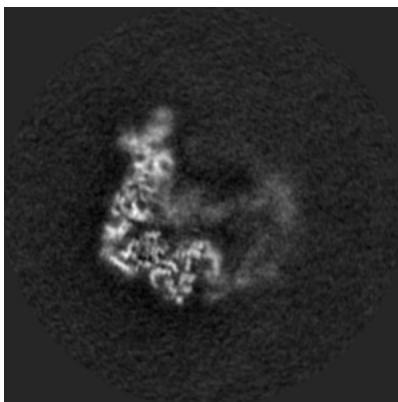
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

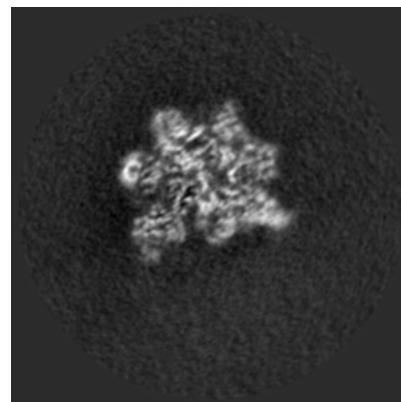
6.3.1 Primary map



X Index: 171

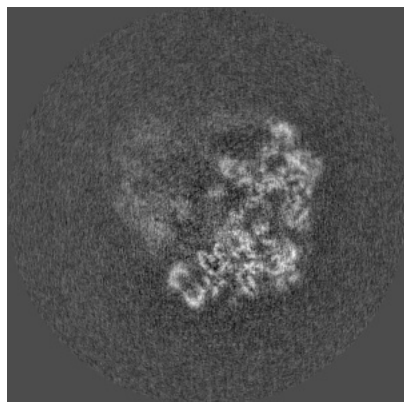


Y Index: 193

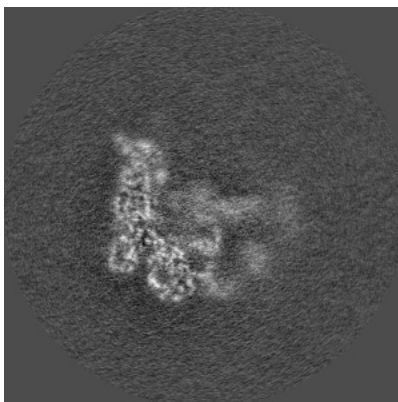


Z Index: 142

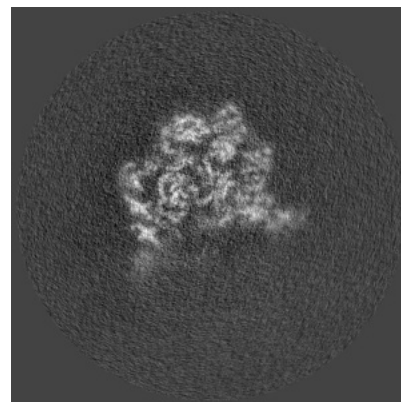
6.3.2 Raw map



X Index: 172



Y Index: 203

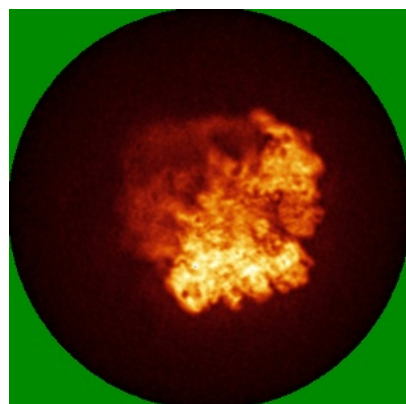


Z Index: 150

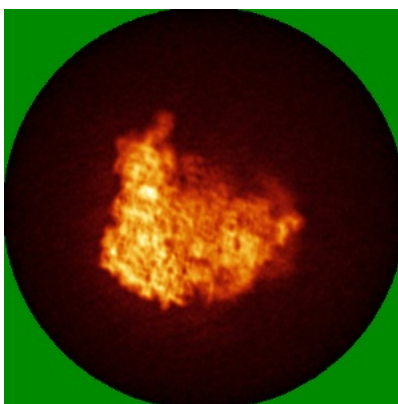
The images above show the largest variance slices of the map in three orthogonal directions.

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

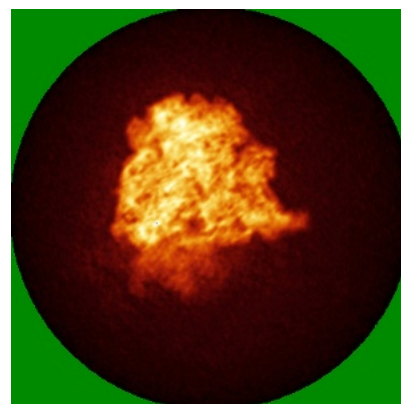
6.4.1 Primary map



X

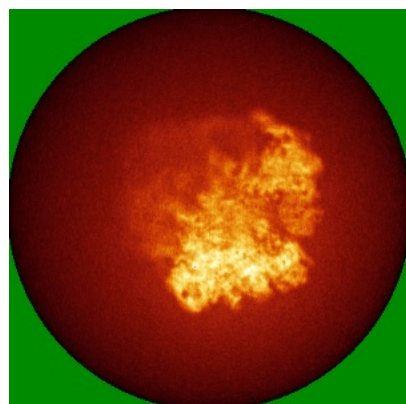


Y

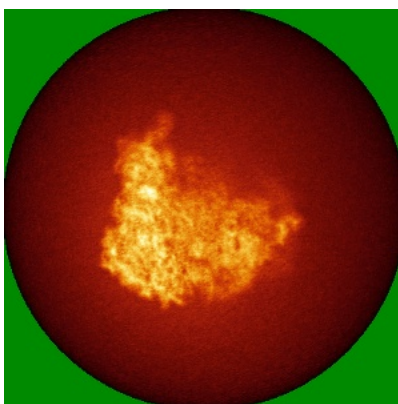


Z

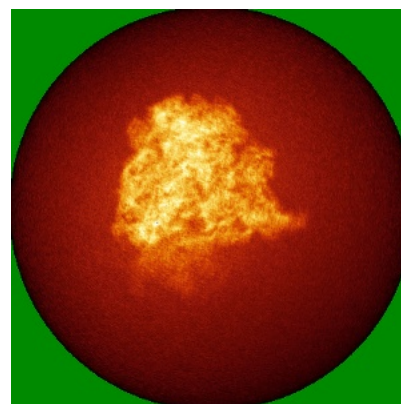
6.4.2 Raw map



X



Y

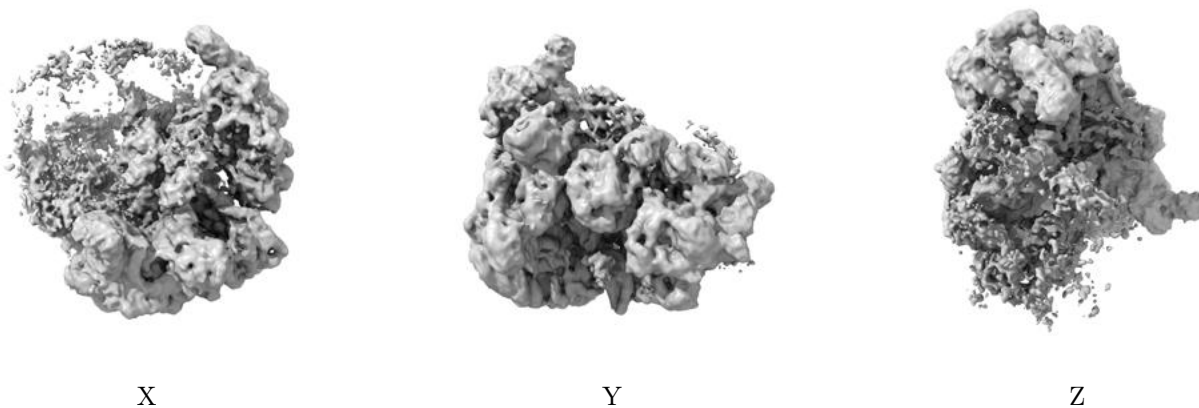


Z

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

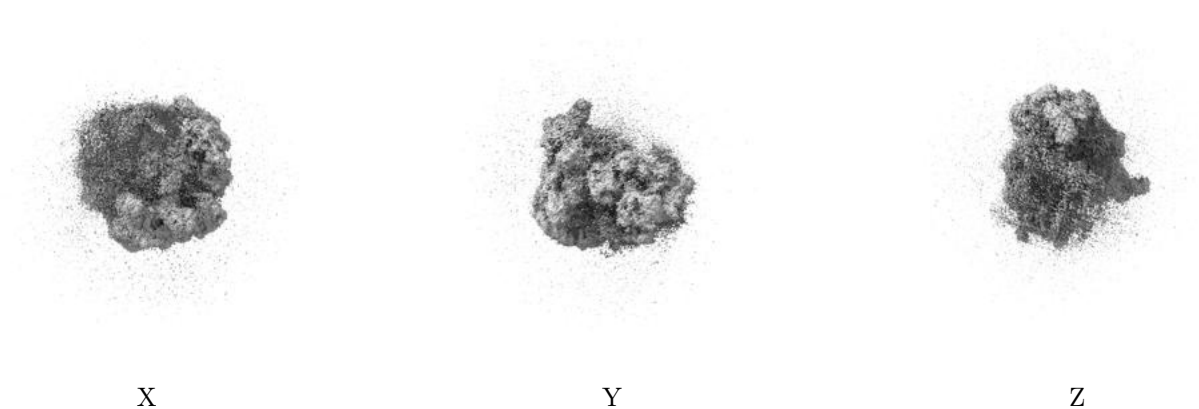
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 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.

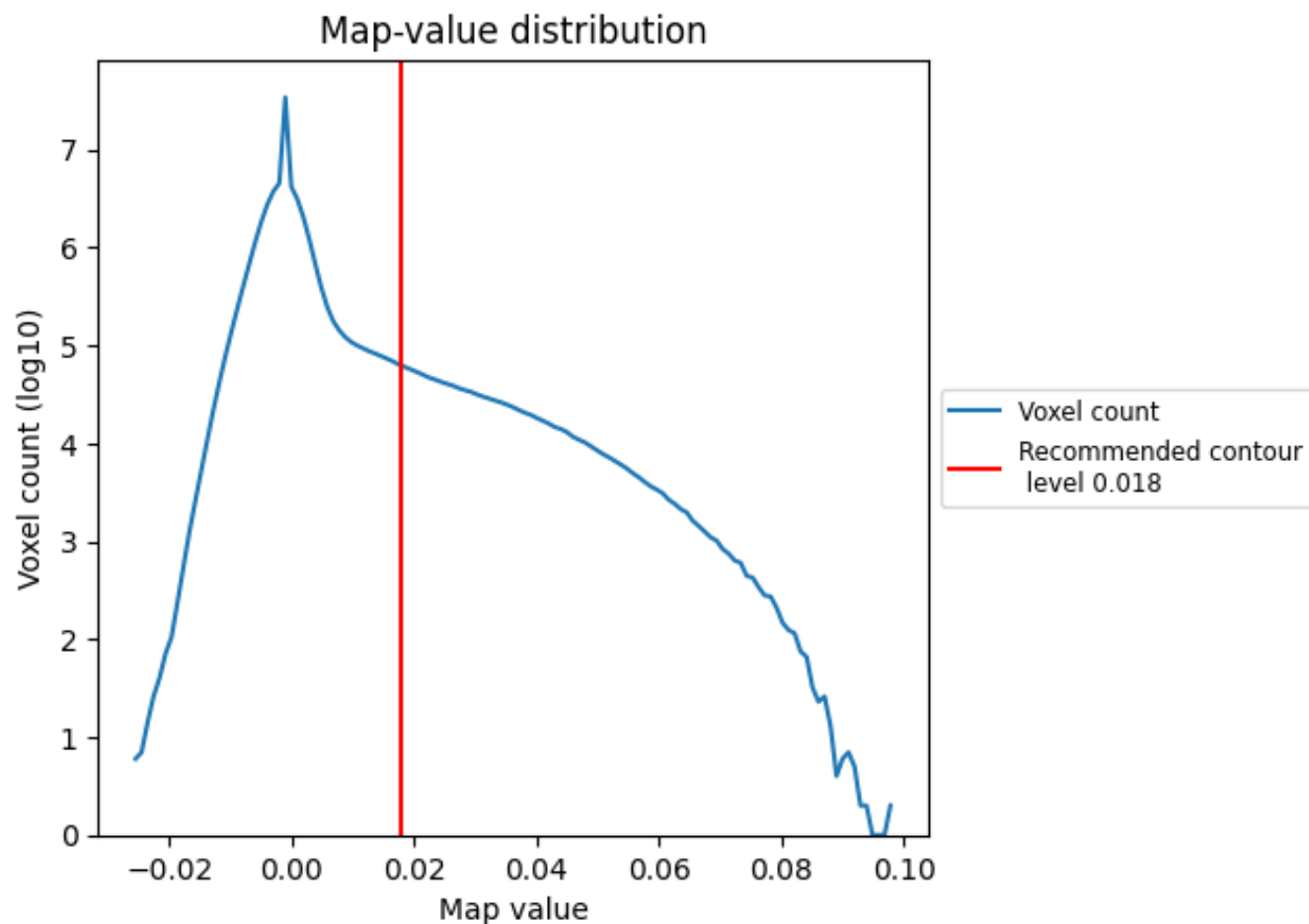
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

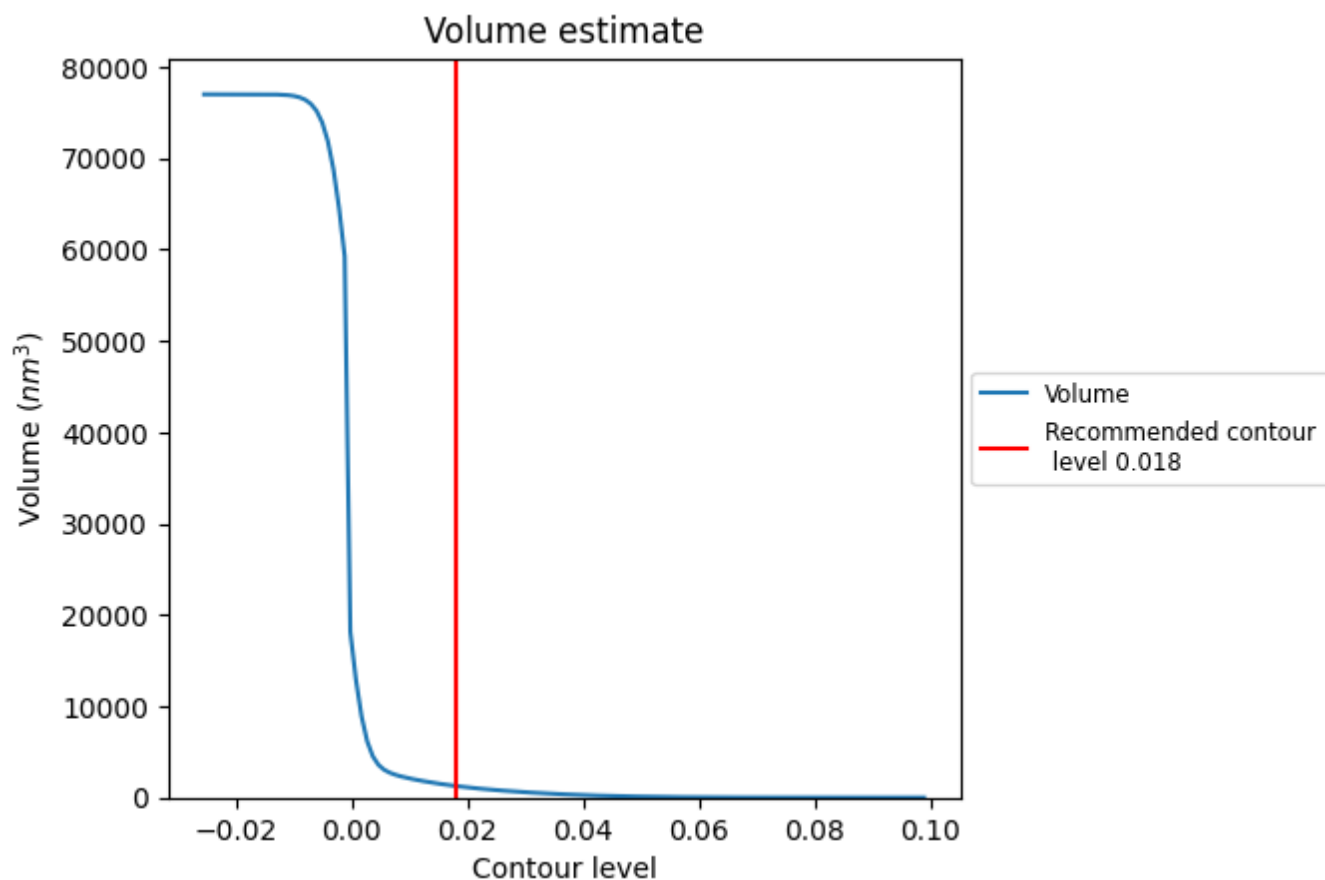
This section contains the results of statistical analysis of the map.

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.

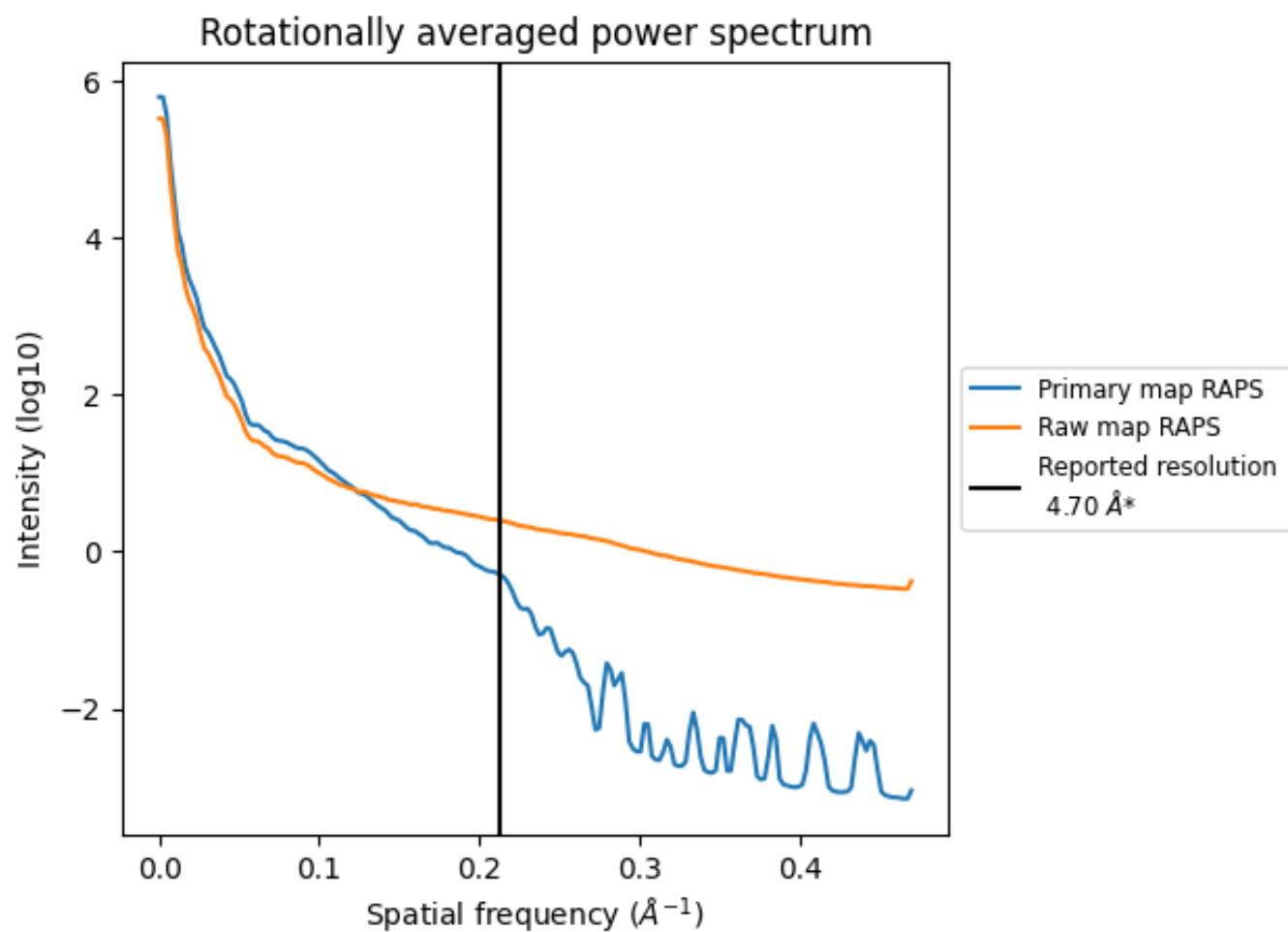
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1261 nm³; this corresponds to an approximate mass of 1139 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 ⓘ

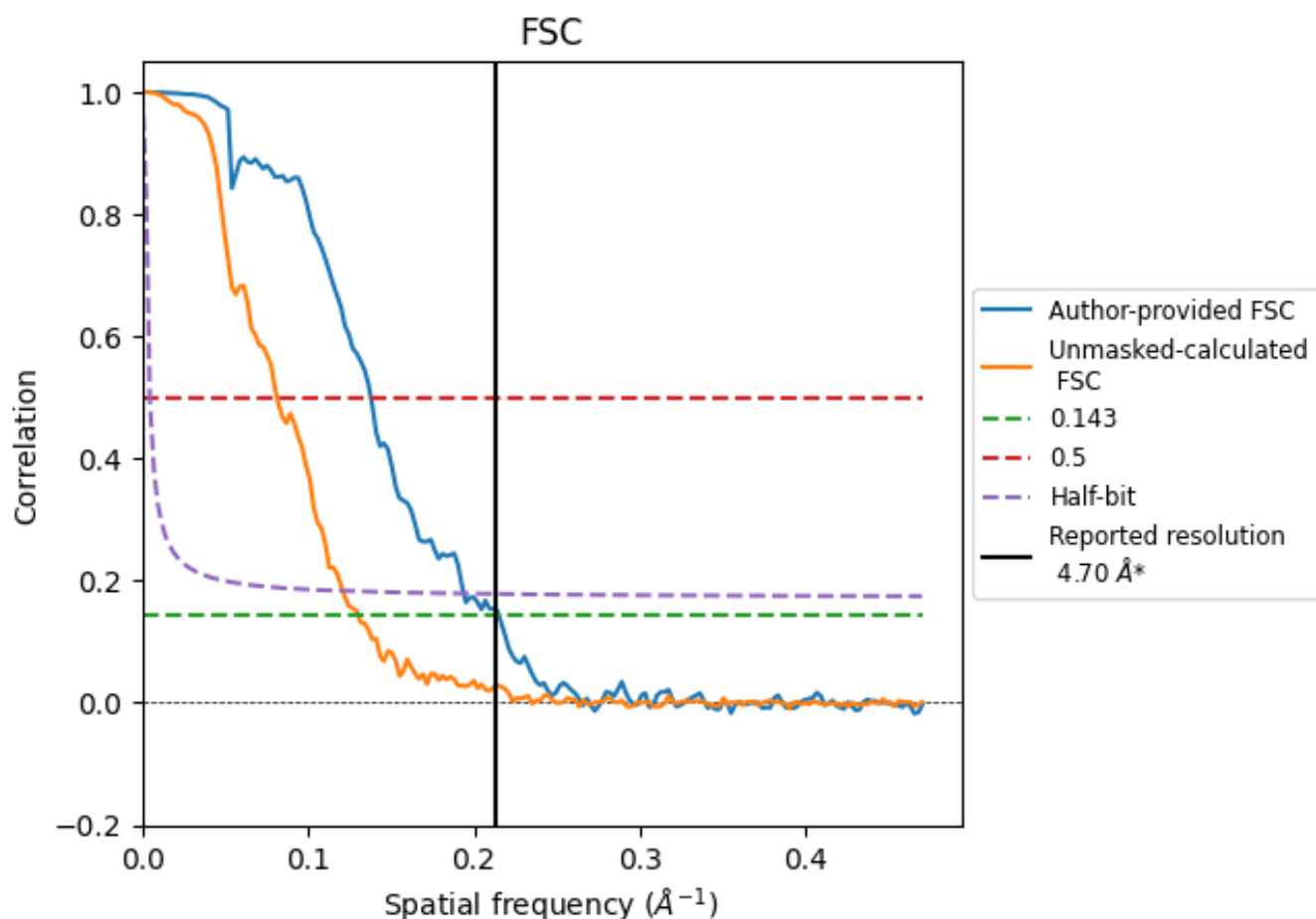


*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

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 0.213 Å⁻¹

8.2 Resolution estimates [i](#)

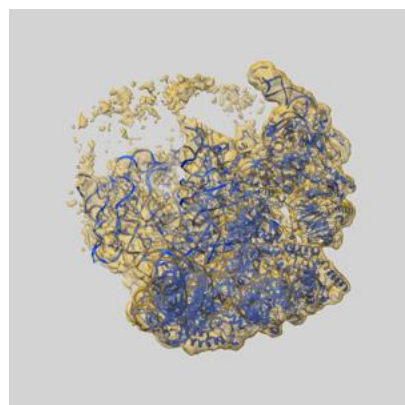
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.65	7.26	5.16
Unmasked-calculated*	7.68	12.30	8.27

*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 7.68 differs from the reported value 4.7 by more than 10 %

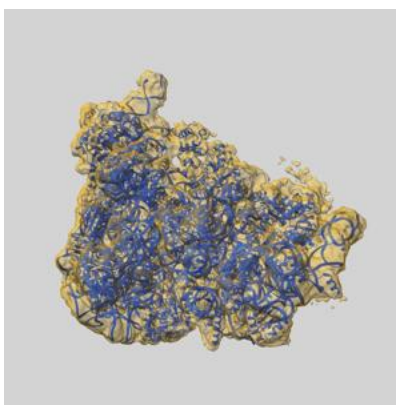
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12908 and PDB model 7OHT. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

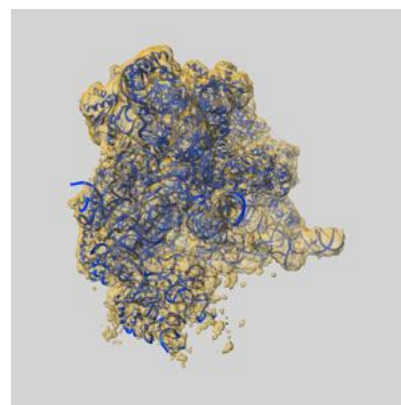
9.1 Map-model overlay [i](#)



X



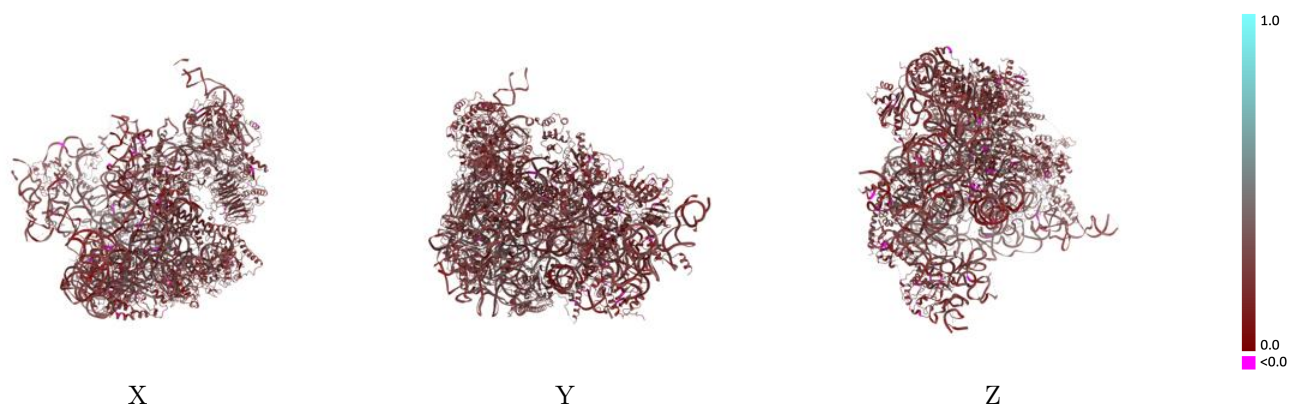
Y



Z

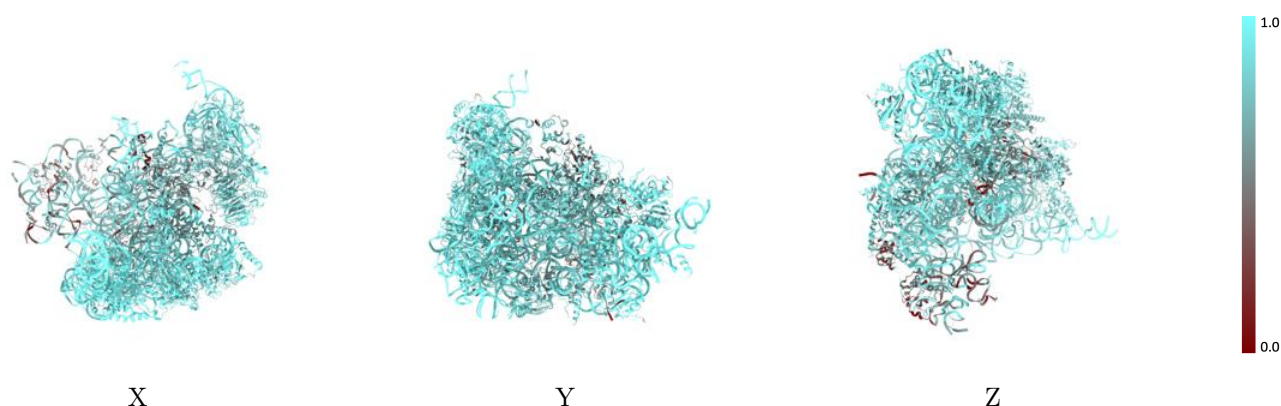
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



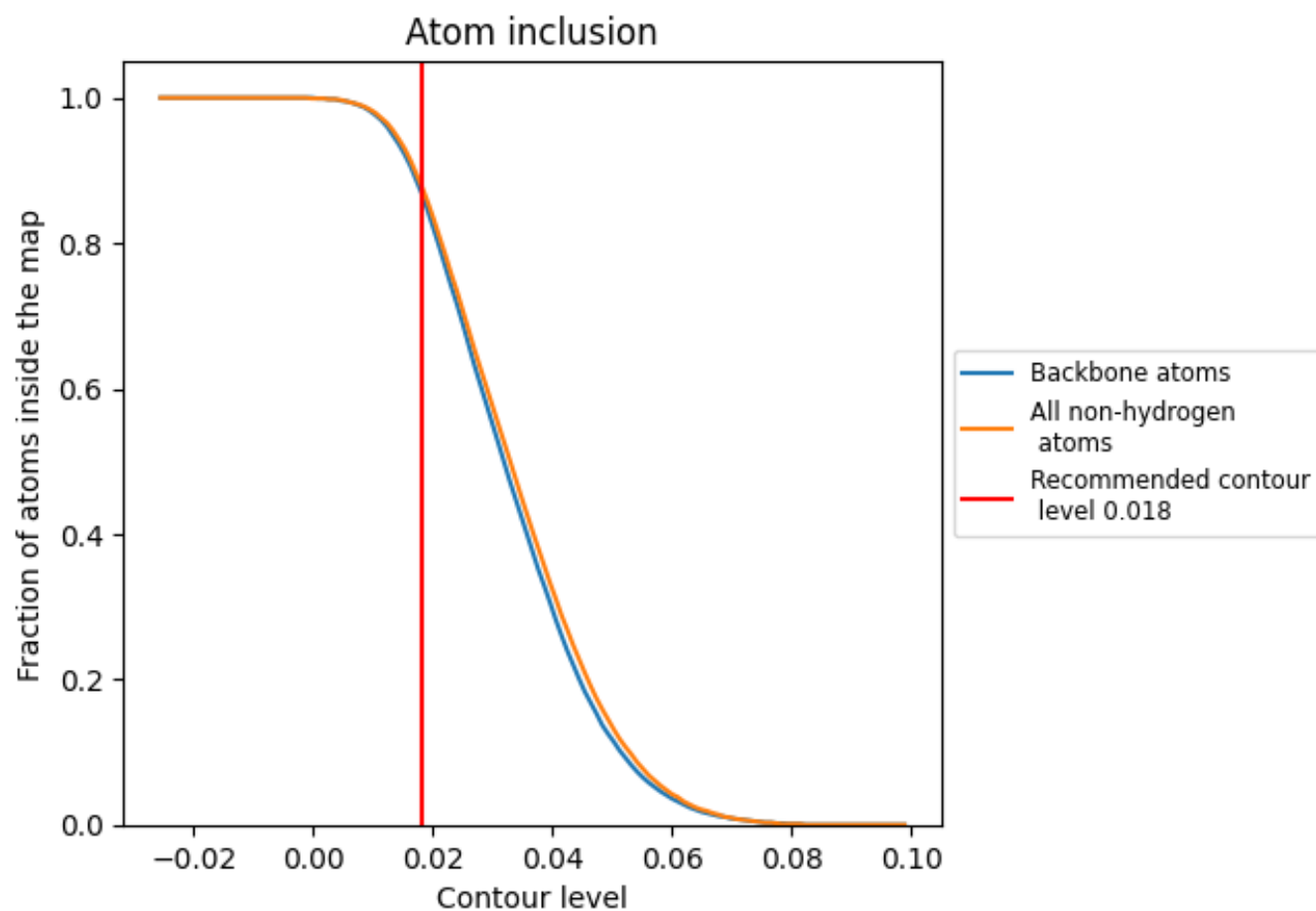
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.018).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 88% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8810	 0.2450
1	 0.9150	 0.2400
2	 0.5550	 0.2080
3	 0.9990	 0.2450
B	 0.9260	 0.2660
C	 0.6310	 0.2350
D	 0.9040	 0.2240
E	 0.9200	 0.2720
F	 0.8660	 0.2730
H	 0.8860	 0.2880
J	 0.9340	 0.2000
M	 0.8890	 0.2870
O	 0.8480	 0.2890
Q	 0.4970	 0.2190
S	 0.8720	 0.2880
T	 0.7790	 0.2650
V	 0.9030	 0.2320
W	 0.9320	 0.2480
b	 0.8810	 0.2300
e	 0.3990	 0.2760
f	 0.8650	 0.3130
m	 0.6400	 0.2240
r	 0.7660	 0.2480
u	 0.9690	 0.2030
v	 0.8910	 0.2470
w	 0.8270	 0.2340
x	 0.8830	 0.2520
y	 0.9470	 0.2340

