



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:42 AM UTC

PDB ID : 7OF1 / pdb_00007of1
EMDB ID : EMD-12866
Title : Nog1-TAP associated immature ribosomal particle population A from *S. cerevisiae*
Authors : Milkereit, P.; Poell, G.
Deposited on : 2021-05-04
Resolution : 3.10 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:

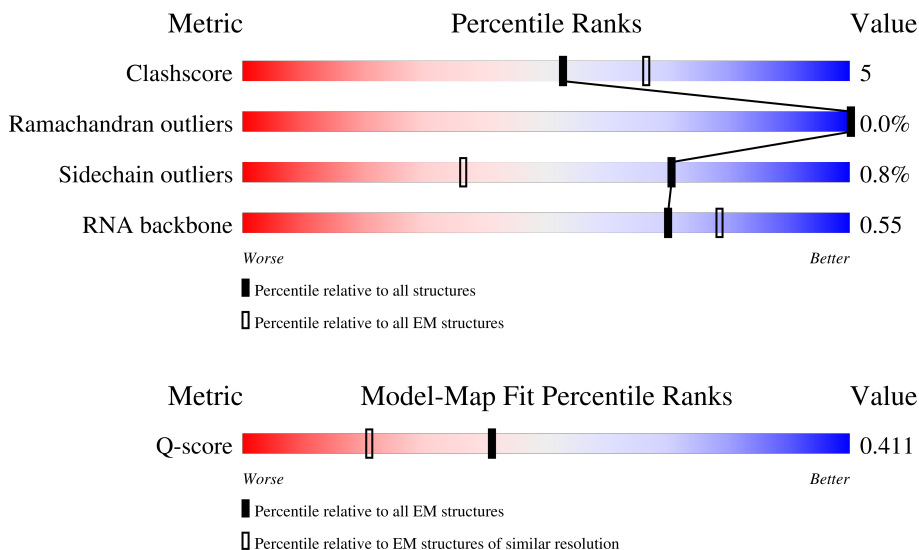
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.10 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.



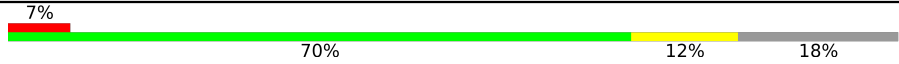
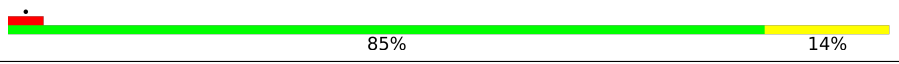
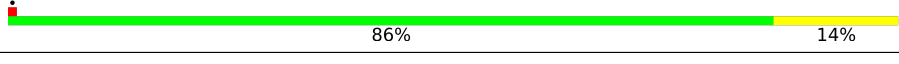


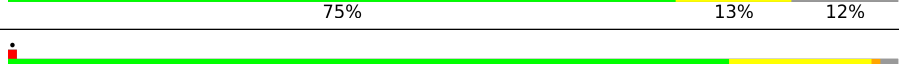
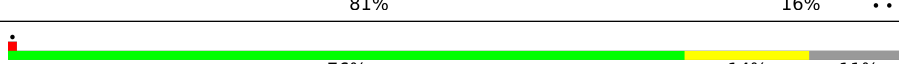
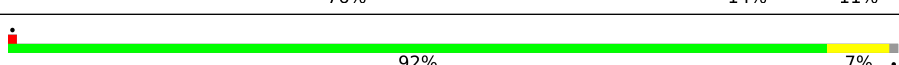
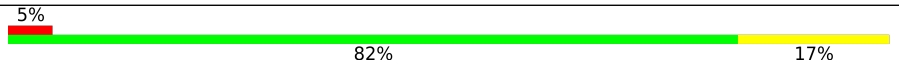
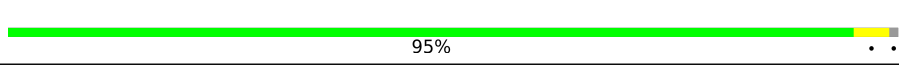

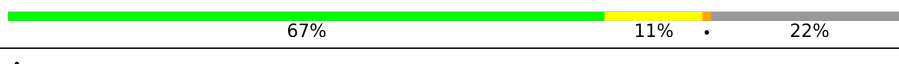
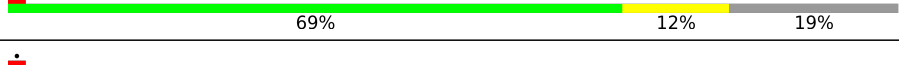
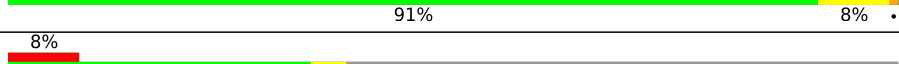
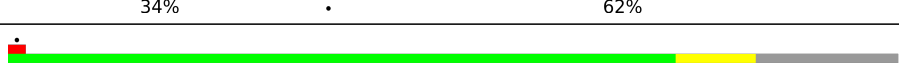



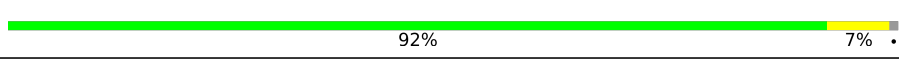






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	A	254	
5	B	387	
6	C	362	
7	E	176	
8	F	244	
9	G	256	
10	H	191	
11	L	199	
12	M	138	
13	N	204	
14	O	199	
15	P	184	
16	Q	186	
17	R	189	
18	S	172	
19	T	160	
20	U	121	
21	V	137	
22	W	236	
23	X	142	
24	Y	127	
25	Z	136	
26	a	149	
27	b	647	
28	c	105	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	d	113	 87% 8%
30	e	130	 90% 7%
31	f	107	 86% 12%
32	g	121	 77% 7% 17%
33	h	120	 93% 6%
34	i	100	 88% 8%
35	j	88	 80% 17%
36	k	78	 8% 95%
37	l	51	 86% 12%
38	m	486	 18% 40% 7% 53%
39	p	92	 11% 85% 7% 9%
40	r	261	 34% 62%
41	u	199	 8% 61% 9% 31%
42	y	245	 72% 19% 9%

2 Entry composition [i](#)

There are 43 unique types of molecules in this entry. The entry contains 199300 atoms, of which 84914 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
			Total	C	H	N	O	P		
1	1	2787	89635	26644	29972	10797	19435	2787	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
2	2	158	5048	1500	1695	586	1109	158	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
3	3	43	1388	412	464	170	299	43	0	0

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	A	208	3268	1006	1663	319	279	1	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	B	386	6247	1956	3166	584	533	8	0	0

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	C	361	5613	1730	2864	522	494	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
7	E	160	2637	820	1363	230	223	1	0	0

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

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

- Molecule 9 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
9	G	225	3612	1127	1853	313	316	3	0	0

- Molecule 10 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
10	H	188	3059	948	1566	271	270	4	0	0

- Molecule 11 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
11	L	178	2895	885	1473	296	241	0	0

- Molecule 12 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 13 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
13	N	203	3500	1077	1780	361	281	1	0	0

- Molecule 14 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 15 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
15	P	176	2823	865	1430	278	250		0	0

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
16	Q	146	2335	713	1206	218	197	1	0	0

- Molecule 17 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
17	R	154	2572	772	1331	262	207		0	0

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
18	S	170	2892	916	1467	265	241	3	0	0

- Molecule 19 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
19	T	61	976	295	500	95	85	1	0	0

- Molecule 20 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
20	U	102	1631	524	823	132	152		0	0

- Molecule 21 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
21	V	136	Total	C	H	N	O	S	0	0
			2052	628	1049	189	179	7		

- Molecule 22 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace	
22	W	227	Total	C	H	N	O	S	0	0
			3648	1149	1834	310	350	5		

- Molecule 23 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace	
23	X	120	Total	C	H	N	O	S	0	0
			1984	617	1025	168	172	2		

- Molecule 24 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	126	Total	C	H	N	O	0	0
			2075	625	1082	192	176		

- Molecule 25 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	H	N	O	0	0
			2248	710	1156	202	180		

- Molecule 26 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace	
26	a	94	Total	C	H	N	O	S	0	0
			1528	484	786	131	126	1		

- Molecule 27 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
27	b	497	Total	C	H	N	O	S	0	0
			8098	2554	4075	698	752	19		

- Molecule 28 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
28	c	97	1541	479	798	124	139	1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
29	d	104	1746	539	899	162	145	1	0	0

- Molecule 30 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
30	e	126	2093	641	1081	204	166	1	0	0

- Molecule 31 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 32 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
32	g	101	1652	493	856	164	135	4	0	0

- Molecule 33 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
33	h	119	2048	615	1079	186	167	1	0	0

- Molecule 34 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
34	i	96	1566	465	823	148	128	2	0	0

- Molecule 35 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
35	j	85	1348	408	678	146	111	5	0	0

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
36	k	77	1295	391	683	115	106		0	0

- Molecule 37 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
37	l	50	912	272	476	97	65	2	0	0

- Molecule 38 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
38	m	229	3669	1162	1855	325	322	5	0	0

- Molecule 39 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
39	p	84	1329	397	687	130	110	5	0	0

- Molecule 40 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
40	r	99	1769	531	918	181	136	3	0	0

- Molecule 41 is a protein called Ribosome biogenesis protein RLP24.

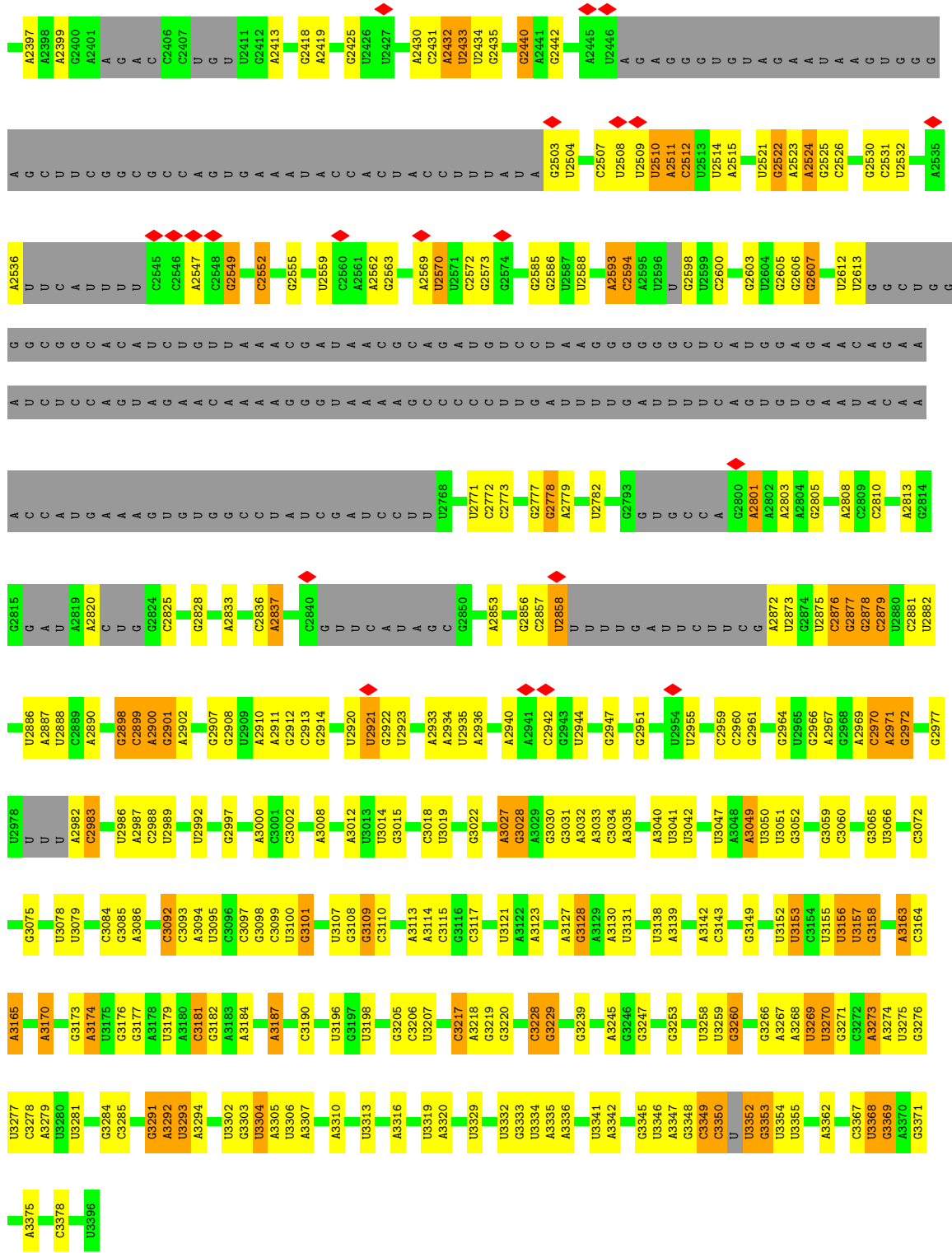
Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
41	u	138	2379	732	1212	235	191	9	0	0

- Molecule 42 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
42	y	224	3379	1051	1686	294	342	6	0	0

- Molecule 43 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

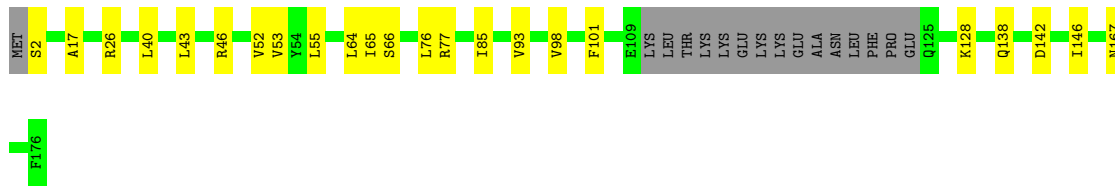
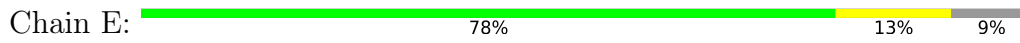
Mol	Chain	Residues	Atoms		AltConf
43	b	1	Total	Mg	0
			1	1	
43	m	1	Total	Mg	0
			1	1	



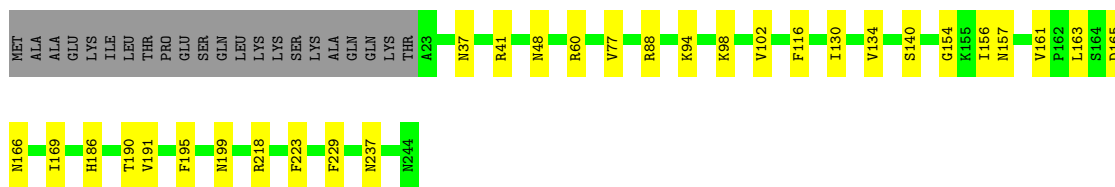
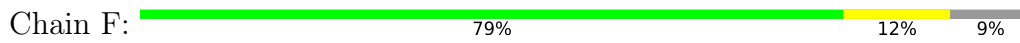
• Molecule 2: 5.8S rRNA



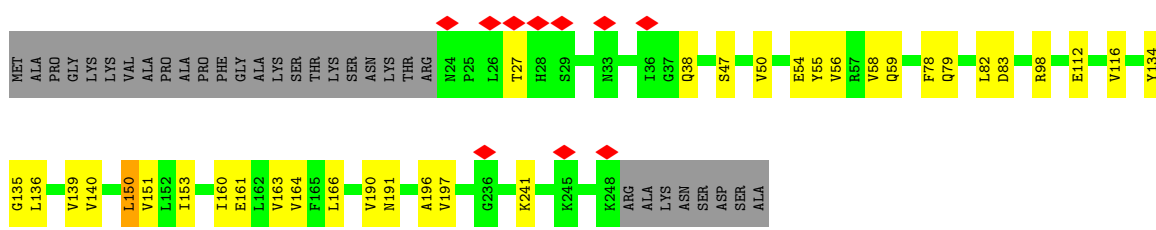
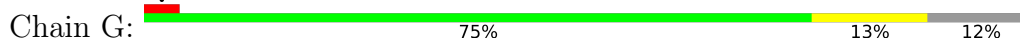
• Molecule 7: 60S ribosomal protein L6-A



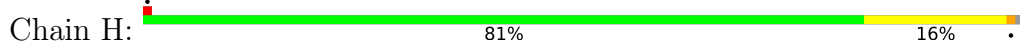
• Molecule 8: 60S ribosomal protein L7-A



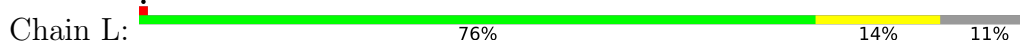
• Molecule 9: 60S ribosomal protein L8-A

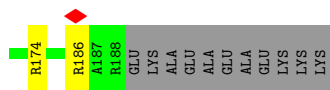


• Molecule 10: 60S ribosomal protein L9-A

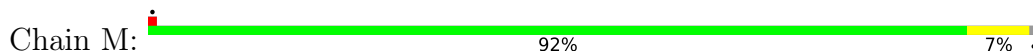


• Molecule 11: 60S ribosomal protein L13-A

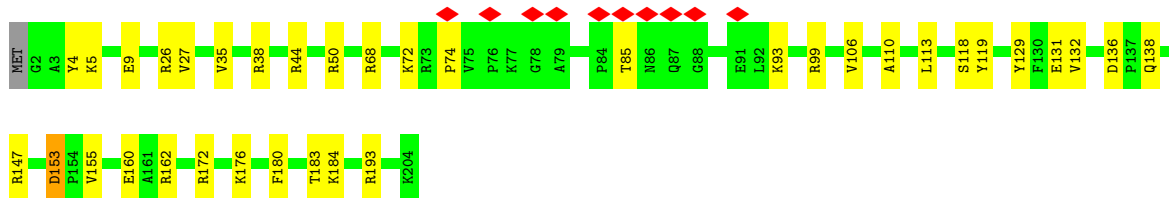
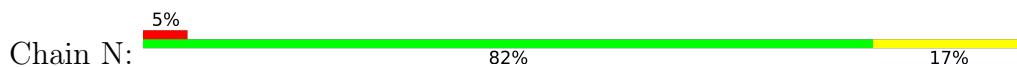




• Molecule 12: 60S ribosomal protein L14-A



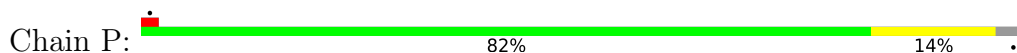
• Molecule 13: 60S ribosomal protein L15-A



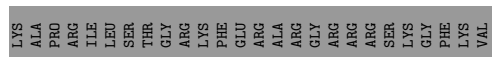
• Molecule 14: 60S ribosomal protein L16-A



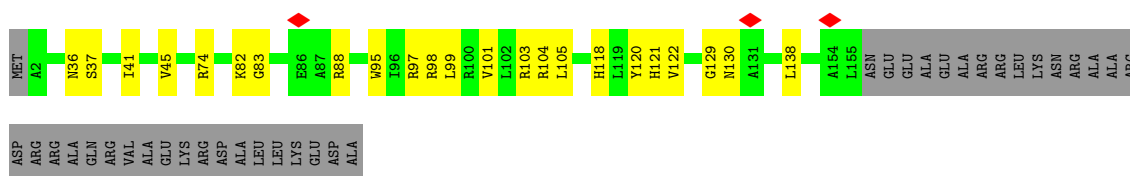
• Molecule 15: 60S ribosomal protein L17-A



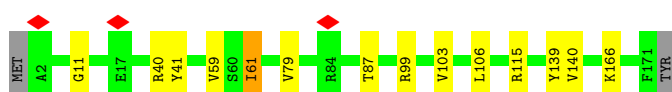
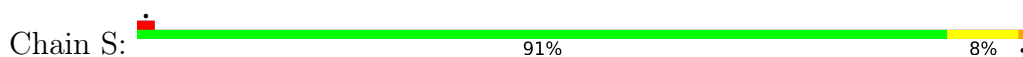
• Molecule 16: 60S ribosomal protein L18-A



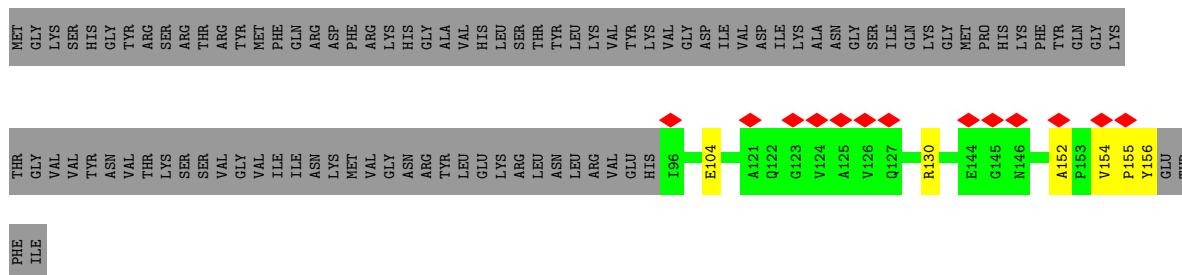
- Molecule 17: 60S ribosomal protein L19-A



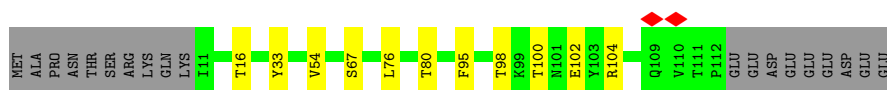
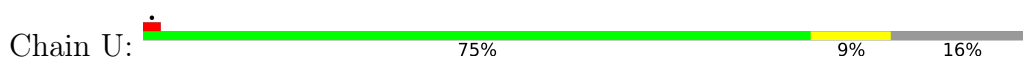
- Molecule 18: 60S ribosomal protein L20-A



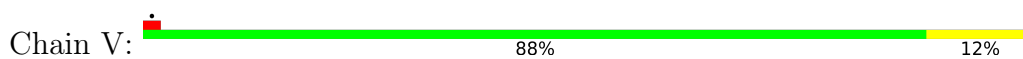
- Molecule 19: 60S ribosomal protein L21-A



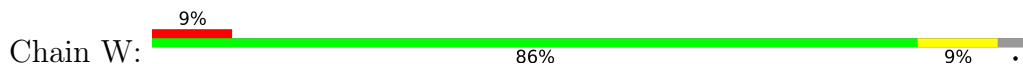
- Molecule 20: 60S ribosomal protein L22-A

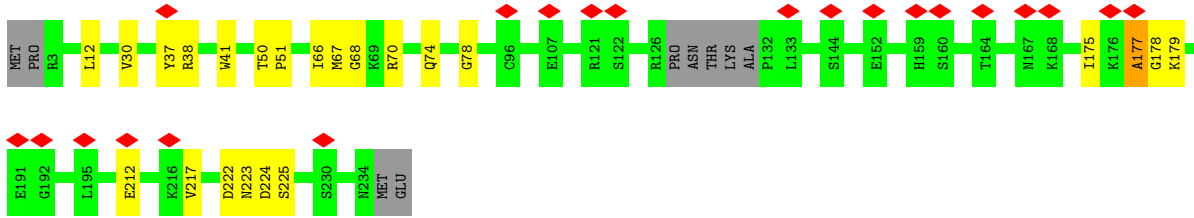


- Molecule 21: 60S ribosomal protein L23-A

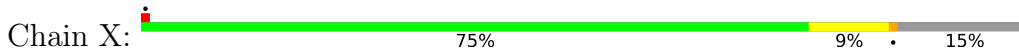


- Molecule 22: Ribosome assembly factor MRT4

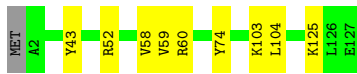




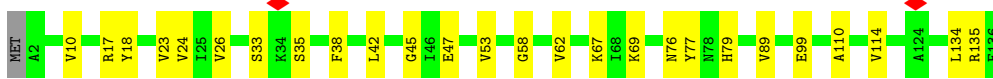
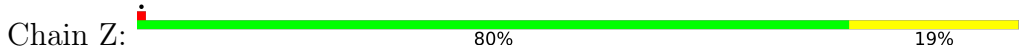
• Molecule 23: 60S ribosomal protein L25



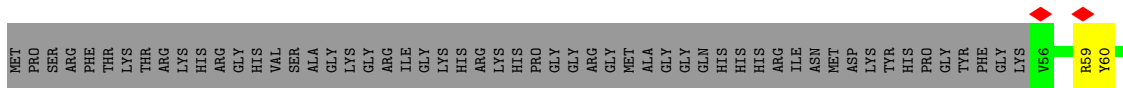
• Molecule 24: 60S ribosomal protein L26-A



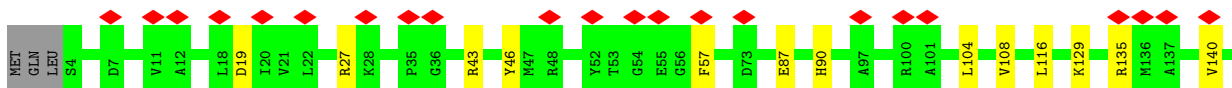
• Molecule 25: 60S ribosomal protein L27-A

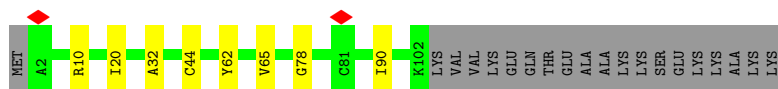
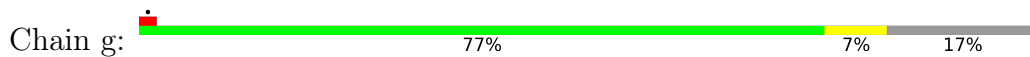


• Molecule 26: 60S ribosomal protein L28



• Molecule 27: Nucleolar GTP-binding protein 1

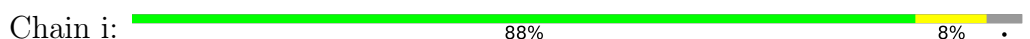




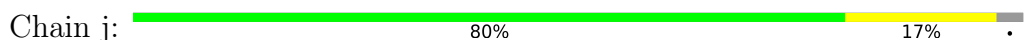
• Molecule 33: 60S ribosomal protein L35-A



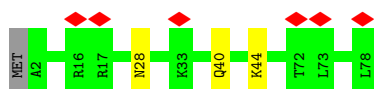
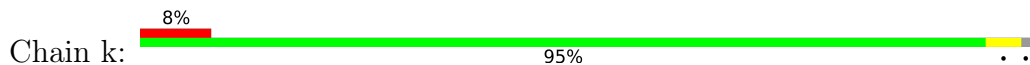
• Molecule 34: 60S ribosomal protein L36-A



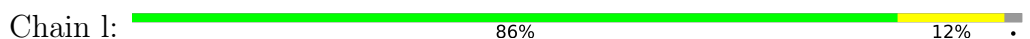
• Molecule 35: 60S ribosomal protein L37-A



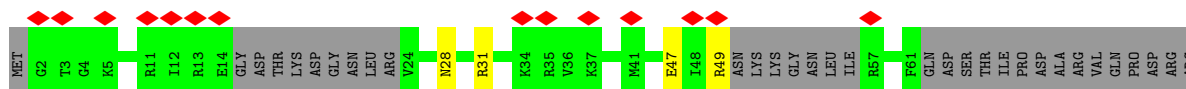
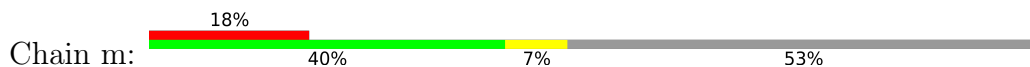
• Molecule 36: 60S ribosomal protein L38



• Molecule 37: 60S ribosomal protein L39



• Molecule 38: Nucleolar GTP-binding protein 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	95319	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 ($e^-/\text{\AA}^2$)	84.67	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	0.113	Depositor
Minimum map value	-0.029	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.016	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

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	0.07	0/66772	0.22	0/104061
2	2	0.08	0/3746	0.21	0/5832
3	3	0.06	0/1034	0.19	0/1611
4	A	0.12	0/1635	0.25	0/2199
5	B	0.12	0/3152	0.28	0/4239
6	C	0.10	0/2801	0.27	0/3792
7	E	0.11	0/1295	0.25	0/1740
8	F	0.10	0/1821	0.24	0/2451
9	G	0.10	0/1791	0.24	0/2418
10	H	0.10	0/1514	0.28	0/2039
11	L	0.12	0/1446	0.29	0/1943
12	M	0.11	0/1074	0.23	0/1446
13	N	0.12	0/1757	0.25	0/2354
14	O	0.11	0/1585	0.22	0/2128
15	P	0.10	0/1415	0.25	0/1900
16	Q	0.10	0/1146	0.22	0/1546
17	R	0.11	0/1258	0.27	0/1679
18	S	0.10	0/1460	0.24	0/1962
19	T	0.15	0/483	0.34	0/650
20	U	0.11	0/825	0.26	0/1120
21	V	0.14	0/1018	0.25	0/1369
22	W	0.11	0/1843	0.26	0/2483
23	X	0.10	0/974	0.22	0/1314
24	Y	0.11	0/1004	0.26	0/1341
25	Z	0.10	0/1118	0.22	0/1497
26	a	0.10	0/758	0.21	0/1023
27	b	0.09	0/4094	0.26	0/5515
28	c	0.10	0/751	0.20	0/1008
29	d	0.11	0/861	0.25	0/1156
30	e	0.11	0/1033	0.22	0/1383
31	f	0.12	0/868	0.26	0/1168
32	g	0.12	0/806	0.28	0/1078

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.11	0/978	0.22	0/1301
34	i	0.12	0/749	0.23	0/995
35	j	0.14	0/685	0.26	0/908
36	k	0.10	0/618	0.24	0/826
37	l	0.15	0/443	0.31	0/588
38	m	0.10	0/1847	0.24	0/2483
39	p	0.12	0/649	0.24	0/865
40	r	0.12	0/864	0.29	0/1133
41	u	0.10	0/1189	0.28	0/1581
42	y	0.09	0/1714	0.23	0/2333
All	All	0.09	0/122874	0.23	0/180458

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
10	H	0	1
22	W	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	H	22	SER	Peptide
22	W	177	ALA	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	59663	29972	29997	614	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	2	3353	1695	1695	45	0
3	3	924	464	465	8	0
4	A	1605	1663	1662	19	0
5	B	3081	3166	3165	41	0
6	C	2749	2864	2863	35	0
7	E	1274	1363	1361	16	0
8	F	1784	1863	1862	23	0
9	G	1759	1853	1852	24	0
10	H	1493	1566	1566	26	0
11	L	1422	1473	1472	22	0
12	M	1059	1155	1154	10	0
13	N	1720	1780	1779	29	0
14	O	1555	1661	1659	9	0
15	P	1393	1430	1428	19	0
16	Q	1129	1206	1205	14	0
17	R	1241	1331	1330	18	0
18	S	1425	1467	1466	10	0
19	T	476	500	499	8	0
20	U	808	823	822	9	0
21	V	1003	1049	1048	9	0
22	W	1814	1834	1833	13	0
23	X	959	1025	1023	11	0
24	Y	993	1082	1081	6	0
25	Z	1092	1156	1155	16	0
26	a	742	786	785	7	0
27	b	4023	4075	4071	31	0
28	c	743	798	797	14	0
29	d	847	899	898	4	0
30	e	1012	1081	1079	7	0
31	f	850	881	880	12	0
32	g	796	856	855	4	0
33	h	969	1079	1078	4	0
34	i	743	823	822	6	0
35	j	670	678	677	13	0
36	k	612	683	682	3	0
37	l	436	476	475	8	0
38	m	1814	1855	1848	25	0
39	p	642	687	685	5	0
40	r	851	918	916	10	0
41	u	1167	1212	1212	11	0
42	y	1693	1686	1685	30	0
43	b	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	m	1	0	0	0	0
All	All	114386	84914	84887	1016	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 1016 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)
2:2:13:A:O2'	15:P:121:GLN:O	1.83	0.94
1:1:3149:G:O2'	5:B:129:ALA:O	1.86	0.92
1:1:2234:G:HO2'	1:1:2603:G:HO2'	1.09	0.91
1:1:1268:G:O2'	1:1:1269:U:OP1	1.90	0.90
1:1:408:A:N3	1:1:655:C:O2'	2.06	0.88

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	A	206/254 (81%)	200 (97%)	6 (3%)	0	100	100
5	B	384/387 (99%)	364 (95%)	20 (5%)	0	100	100
6	C	359/362 (99%)	341 (95%)	18 (5%)	0	100	100
7	E	156/176 (89%)	152 (97%)	4 (3%)	0	100	100
8	F	220/244 (90%)	215 (98%)	5 (2%)	0	100	100
9	G	223/256 (87%)	216 (97%)	7 (3%)	0	100	100
10	H	186/191 (97%)	179 (96%)	7 (4%)	0	100	100
11	L	176/199 (88%)	167 (95%)	9 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	M	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
13	N	201/204 (98%)	197 (98%)	4 (2%)	0	100	100
14	O	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
15	P	172/184 (94%)	170 (99%)	2 (1%)	0	100	100
16	Q	144/186 (77%)	141 (98%)	3 (2%)	0	100	100
17	R	152/189 (80%)	146 (96%)	6 (4%)	0	100	100
18	S	168/172 (98%)	157 (94%)	11 (6%)	0	100	100
19	T	59/160 (37%)	54 (92%)	5 (8%)	0	100	100
20	U	100/121 (83%)	96 (96%)	4 (4%)	0	100	100
21	V	134/137 (98%)	134 (100%)	0	0	100	100
22	W	223/236 (94%)	215 (96%)	7 (3%)	1 (0%)	30	61
23	X	118/142 (83%)	115 (98%)	3 (2%)	0	100	100
24	Y	124/127 (98%)	121 (98%)	3 (2%)	0	100	100
25	Z	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
26	a	92/149 (62%)	89 (97%)	3 (3%)	0	100	100
27	b	489/647 (76%)	466 (95%)	22 (4%)	1 (0%)	43	73
28	c	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
29	d	102/113 (90%)	101 (99%)	1 (1%)	0	100	100
30	e	124/130 (95%)	120 (97%)	4 (3%)	0	100	100
31	f	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
32	g	99/121 (82%)	96 (97%)	3 (3%)	0	100	100
33	h	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
34	i	94/100 (94%)	93 (99%)	1 (1%)	0	100	100
35	j	83/88 (94%)	82 (99%)	1 (1%)	0	100	100
36	k	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
37	l	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
38	m	215/486 (44%)	207 (96%)	8 (4%)	0	100	100
39	p	82/92 (89%)	81 (99%)	1 (1%)	0	100	100
40	r	93/261 (36%)	86 (92%)	7 (8%)	0	100	100
41	u	136/199 (68%)	134 (98%)	2 (2%)	0	100	100
42	y	222/245 (91%)	217 (98%)	5 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	6238/7492 (83%)	6036 (97%)	200 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	b	399	ALA
22	W	178	GLY

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	164/196 (84%)	162 (99%)	2 (1%)	63	78
5	B	322/323 (100%)	318 (99%)	4 (1%)	63	78
6	C	288/289 (100%)	285 (99%)	3 (1%)	68	79
7	E	138/153 (90%)	137 (99%)	1 (1%)	76	82
8	F	186/205 (91%)	186 (100%)	0	100	100
9	G	185/208 (89%)	183 (99%)	2 (1%)	65	78
10	H	168/171 (98%)	167 (99%)	1 (1%)	78	83
11	L	140/159 (88%)	139 (99%)	1 (1%)	76	82
12	M	108/109 (99%)	108 (100%)	0	100	100
13	N	175/176 (99%)	174 (99%)	1 (1%)	78	83
14	O	160/162 (99%)	160 (100%)	0	100	100
15	P	141/146 (97%)	141 (100%)	0	100	100
16	Q	120/151 (80%)	119 (99%)	1 (1%)	73	81
17	R	127/154 (82%)	126 (99%)	1 (1%)	73	81
18	S	154/156 (99%)	153 (99%)	1 (1%)	78	83
19	T	50/137 (36%)	50 (100%)	0	100	100
20	U	89/107 (83%)	89 (100%)	0	100	100
21	V	104/105 (99%)	103 (99%)	1 (1%)	68	79

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	W	201/213 (94%)	199 (99%)	2 (1%)	68	79
23	X	104/118 (88%)	103 (99%)	1 (1%)	68	79
24	Y	109/110 (99%)	109 (100%)	0	100	100
25	Z	115/116 (99%)	114 (99%)	1 (1%)	70	80
26	a	77/119 (65%)	76 (99%)	1 (1%)	61	77
27	b	443/573 (77%)	440 (99%)	3 (1%)	76	82
28	c	81/88 (92%)	80 (99%)	1 (1%)	63	78
29	d	91/97 (94%)	90 (99%)	1 (1%)	65	78
30	e	108/111 (97%)	107 (99%)	1 (1%)	70	80
31	f	90/91 (99%)	89 (99%)	1 (1%)	65	78
32	g	86/103 (84%)	84 (98%)	2 (2%)	44	70
33	h	104/105 (99%)	102 (98%)	2 (2%)	50	73
34	i	78/82 (95%)	77 (99%)	1 (1%)	61	77
35	j	69/71 (97%)	68 (99%)	1 (1%)	59	76
36	k	68/69 (99%)	68 (100%)	0	100	100
37	l	45/46 (98%)	45 (100%)	0	100	100
38	m	197/428 (46%)	195 (99%)	2 (1%)	68	79
39	p	66/72 (92%)	65 (98%)	1 (2%)	57	75
40	r	90/229 (39%)	90 (100%)	0	100	100
41	u	123/180 (68%)	123 (100%)	0	100	100
42	y	192/211 (91%)	191 (100%)	1 (0%)	81	85
All	All	5356/6339 (84%)	5315 (99%)	41 (1%)	70	81

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	d	89	LEU
34	i	43	LEU
30	e	21	HIS
32	g	90	ILE
38	m	370	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
14	O	42	ASN
38	m	392	HIS
22	W	205	GLN
37	l	33	ASN
30	e	31	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2762/3396 (81%)	434 (15%)	31 (1%)
2	2	157/158 (99%)	25 (15%)	1 (0%)
3	3	42/121 (34%)	3 (7%)	0
All	All	2961/3675 (80%)	462 (15%)	32 (1%)

5 of 462 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	13	A
1	1	14	U
1	1	26	A
1	1	43	A
1	1	49	A

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	3292	A
1	1	3349	C
1	1	1097	G
1	1	1064	A
1	1	3352	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

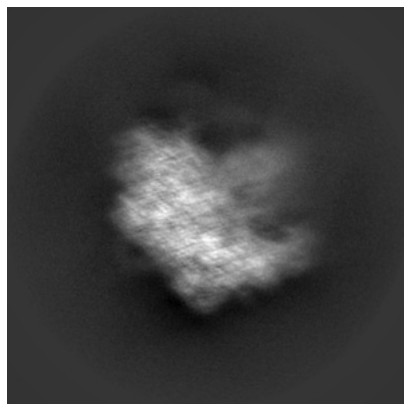
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12866. These allow visual inspection of the internal detail of the map and identification of artifacts.

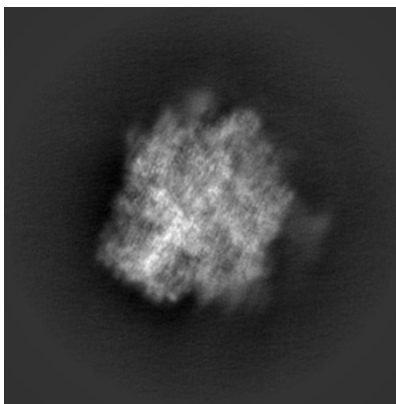
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

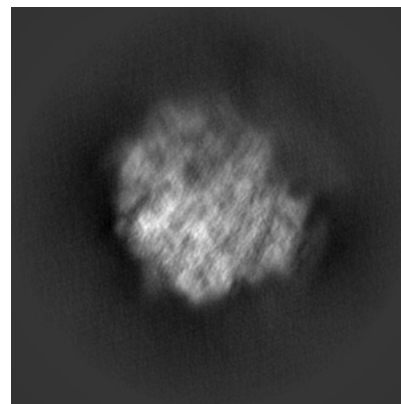
6.1.1 Primary map



X

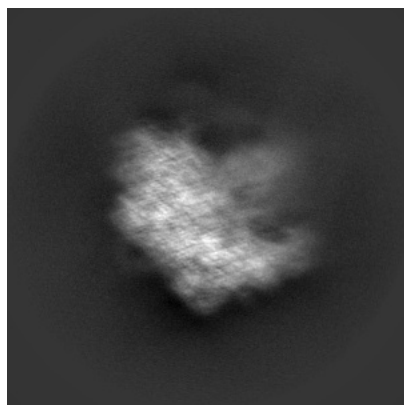


Y

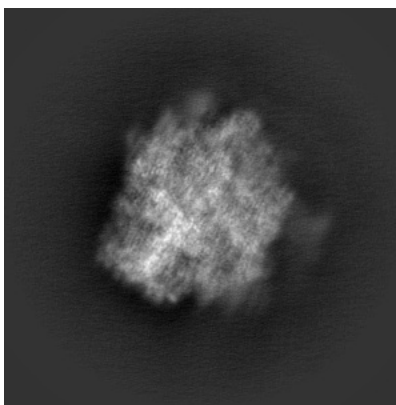


Z

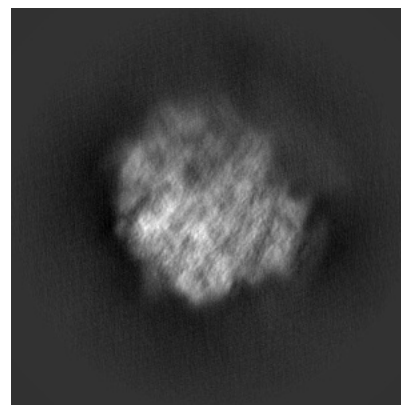
6.1.2 Raw map



X



Y

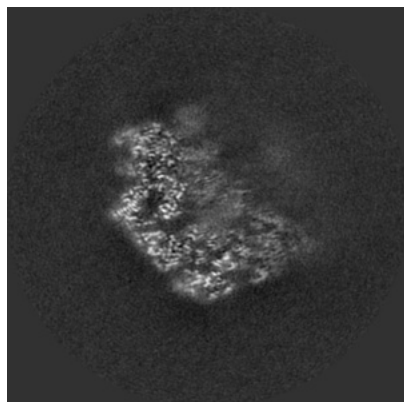


Z

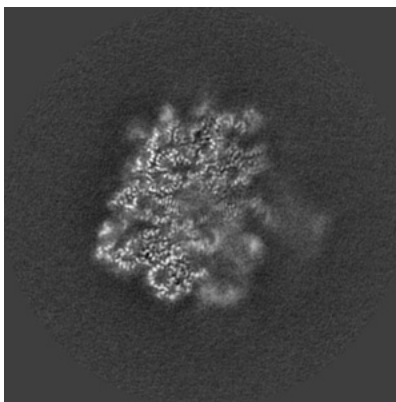
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

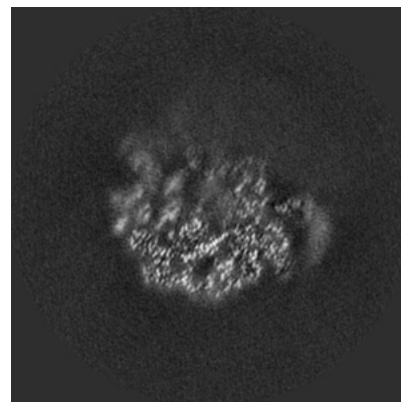
6.2.1 Primary map



X Index: 200

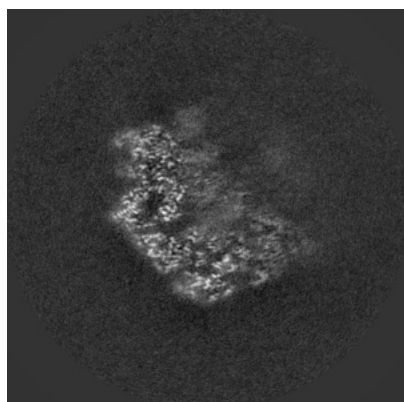


Y Index: 200

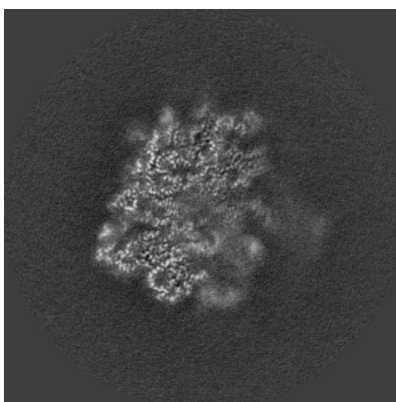


Z Index: 200

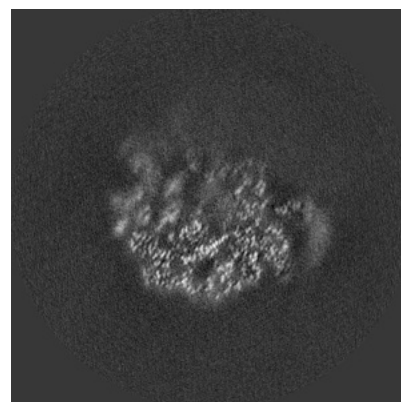
6.2.2 Raw map



X Index: 200



Y Index: 200

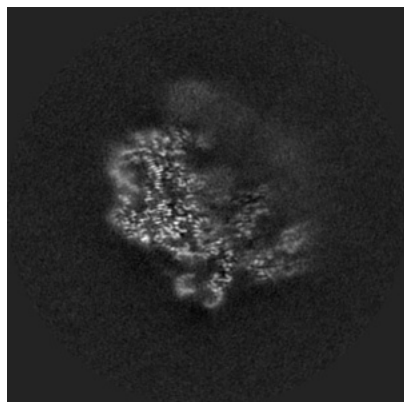


Z Index: 200

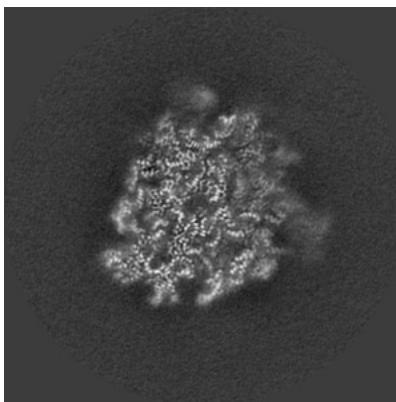
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

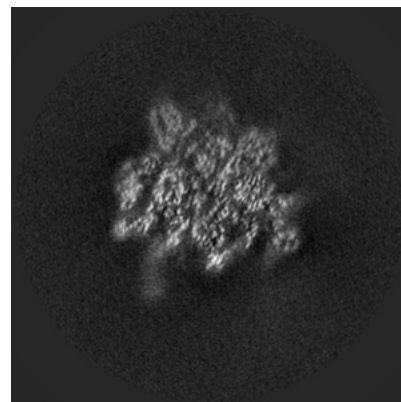
6.3.1 Primary map



X Index: 184

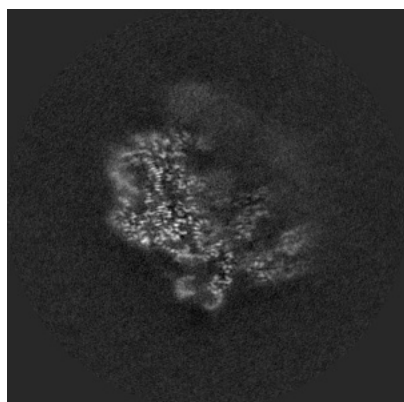


Y Index: 179

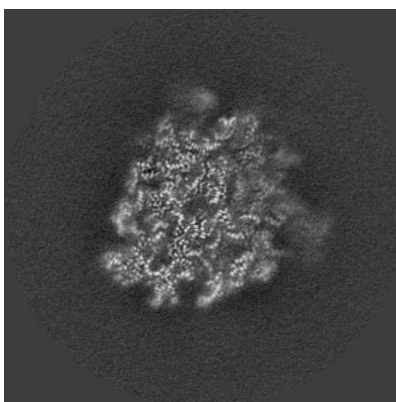


Z Index: 154

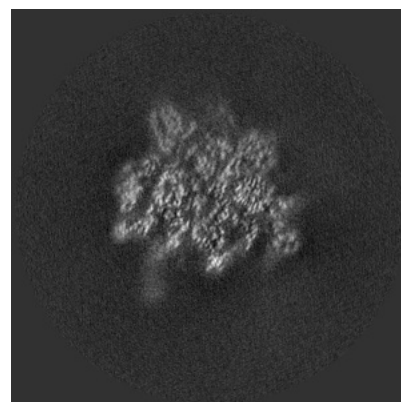
6.3.2 Raw map



X Index: 184



Y Index: 179

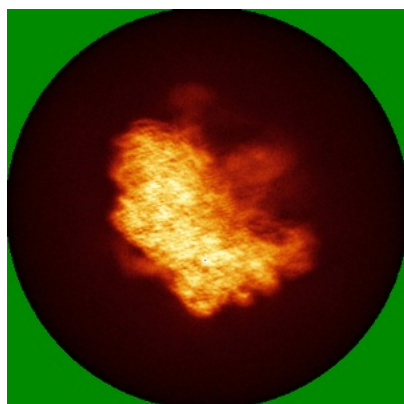


Z Index: 154

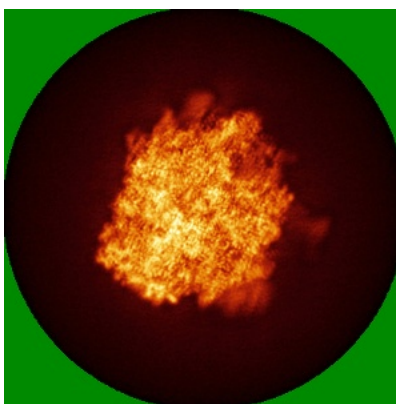
The images above show the largest variance slices of the map in three orthogonal directions.

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

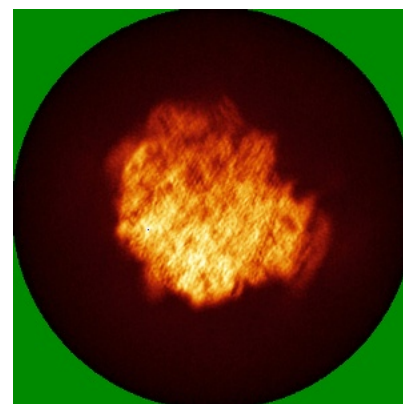
6.4.1 Primary map



X

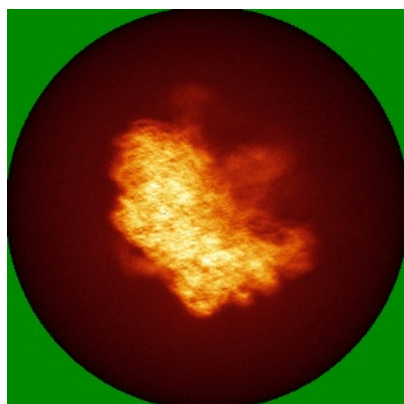


Y

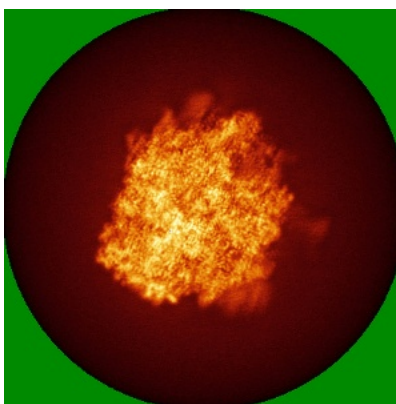


Z

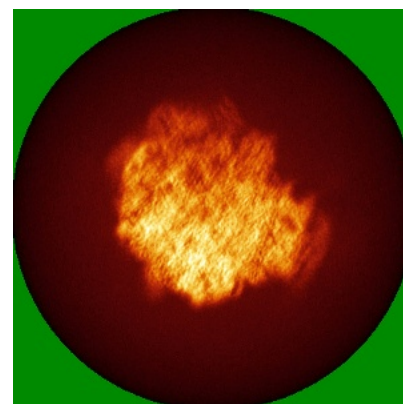
6.4.2 Raw map



X



Y

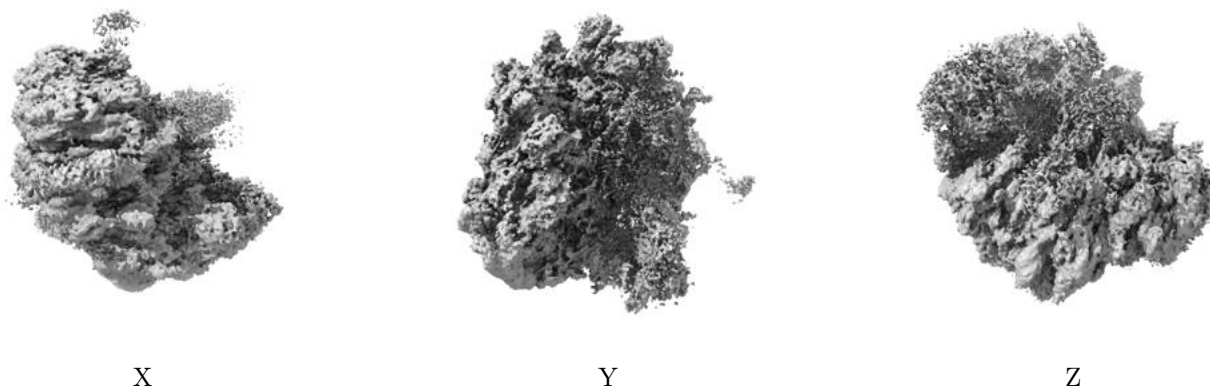


Z

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 0.016. 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.

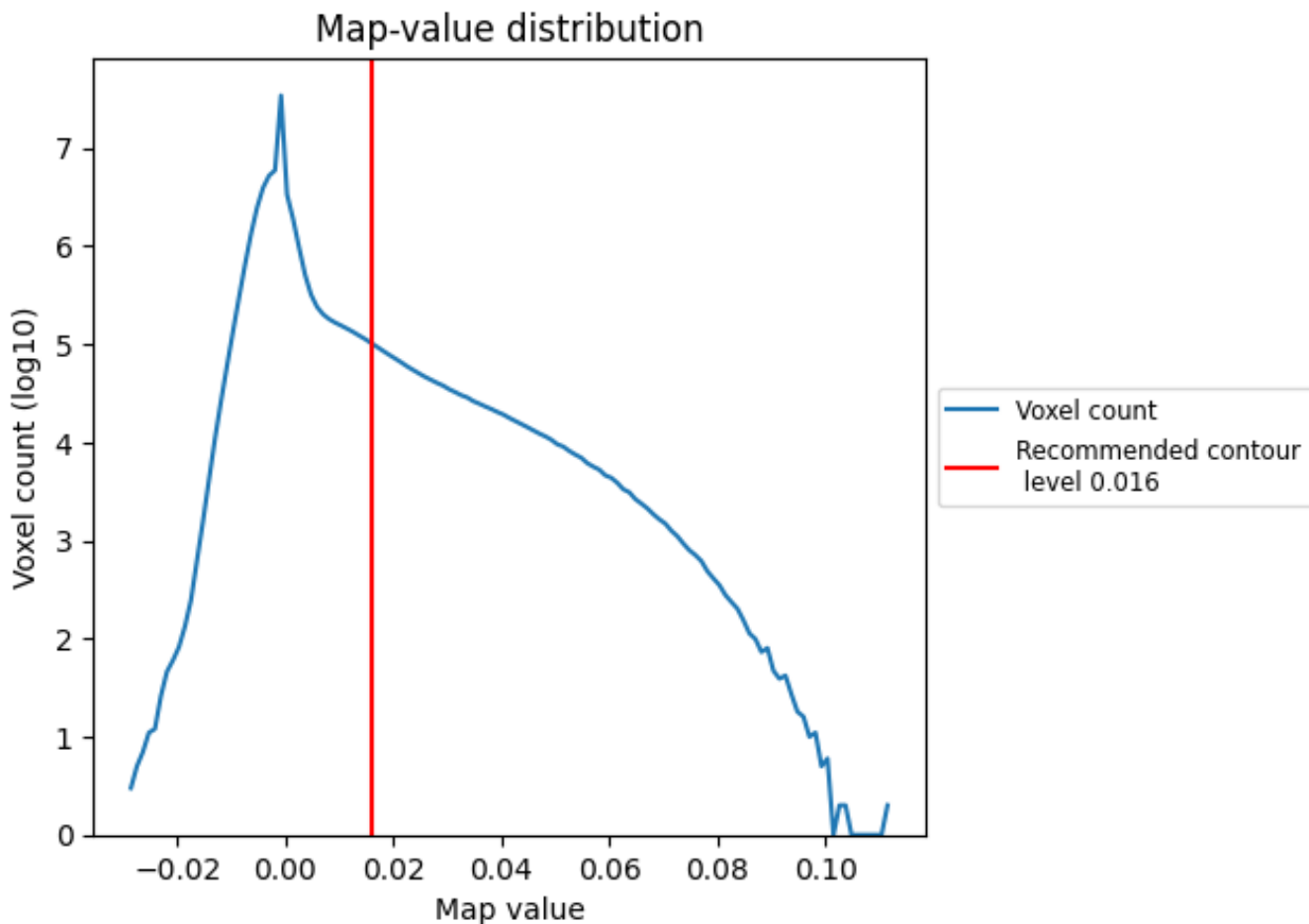
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

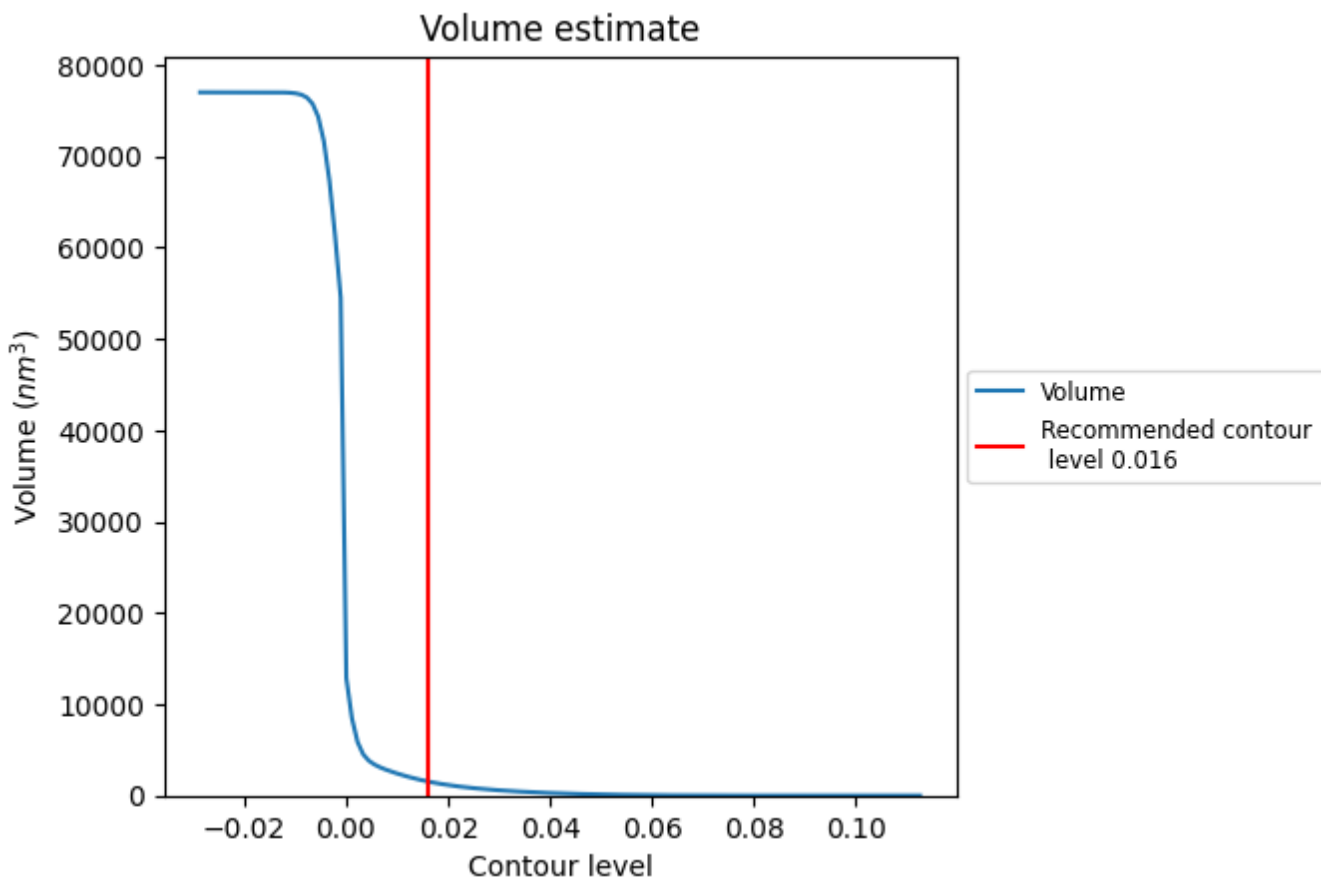
This section contains the results of statistical analysis of the map.

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.

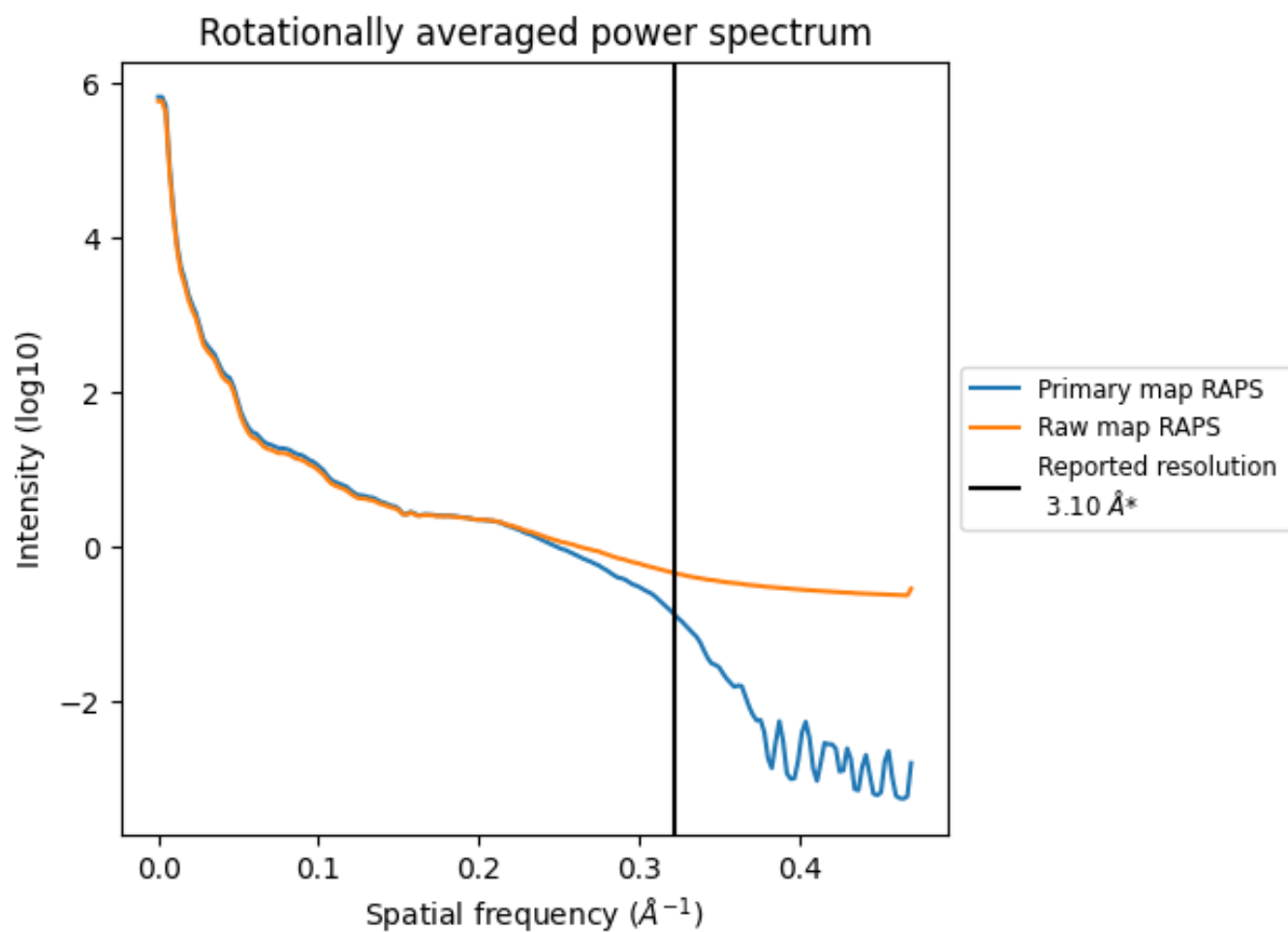
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1549 nm³; this corresponds to an approximate mass of 1400 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

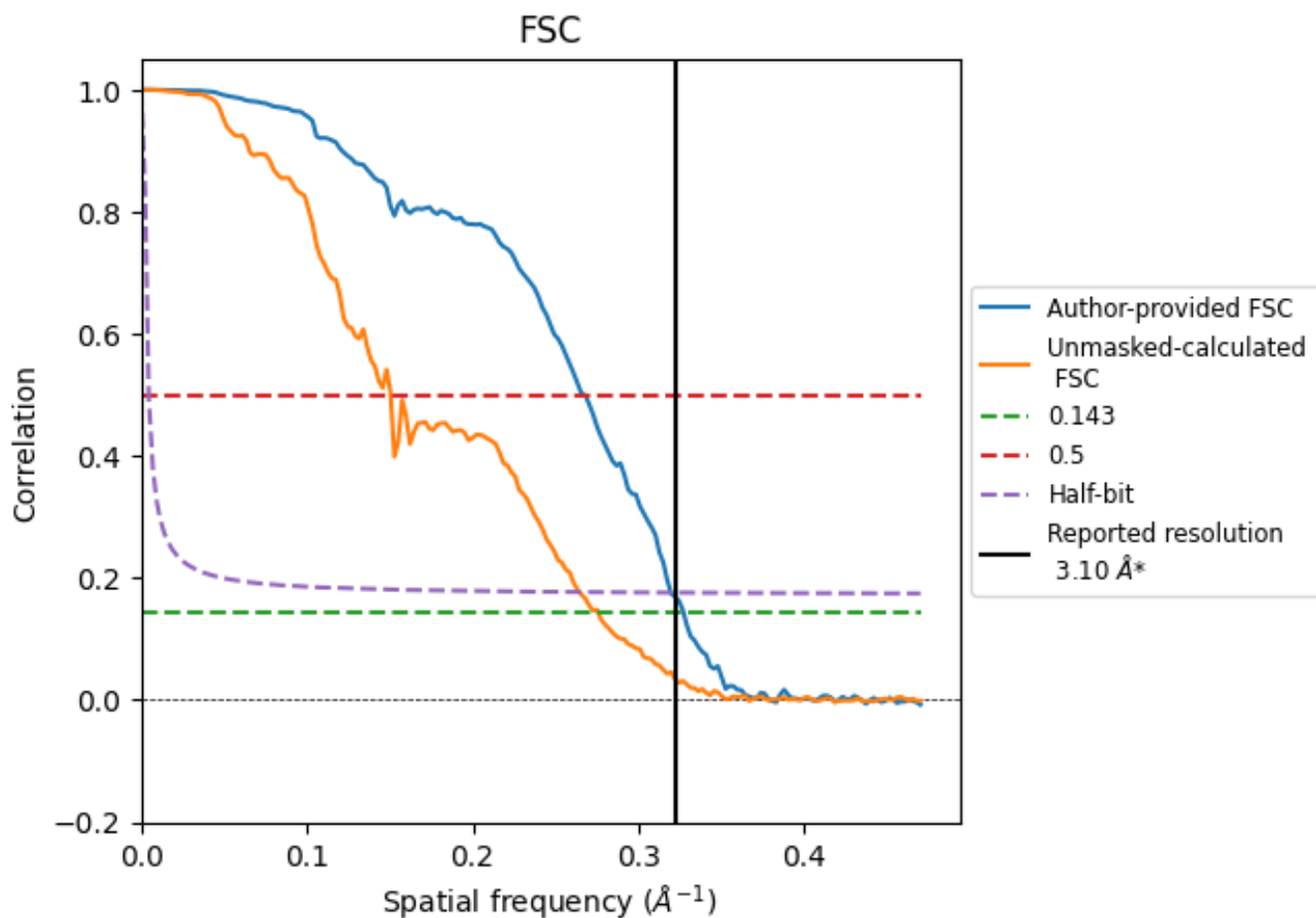


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.06	3.74	3.13
Unmasked-calculated*	3.63	6.64	3.78

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.63 differs from the reported value 3.1 by more than 10 %

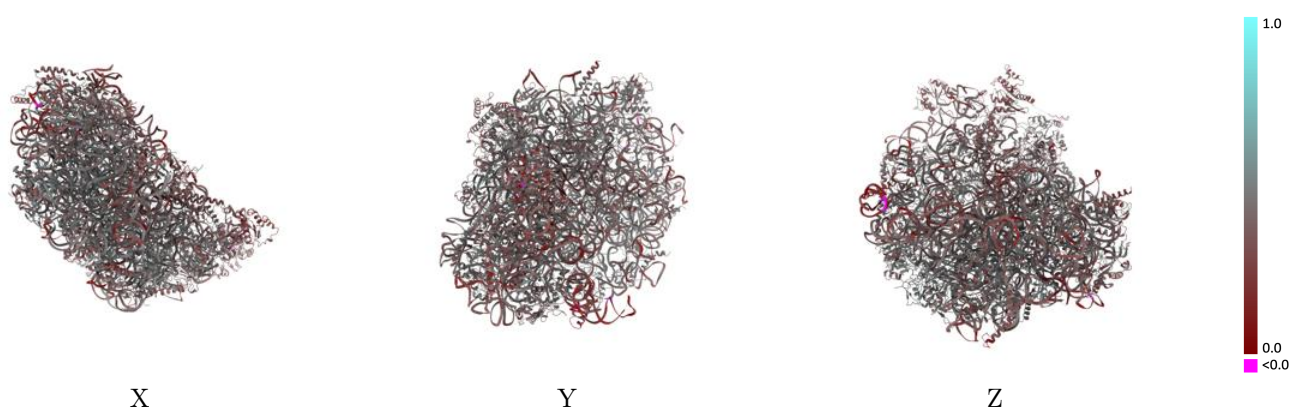
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12866 and PDB model 7OF1. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)

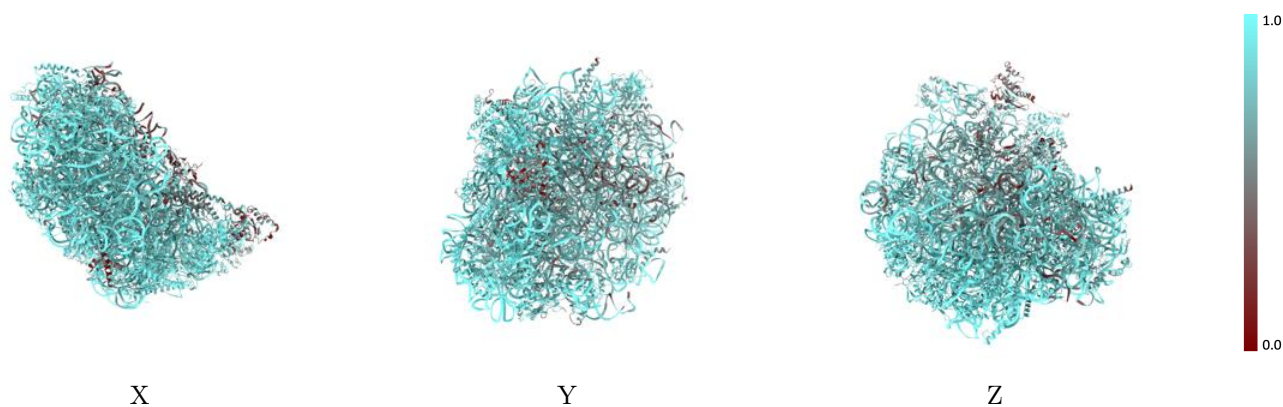
This section was not generated.

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



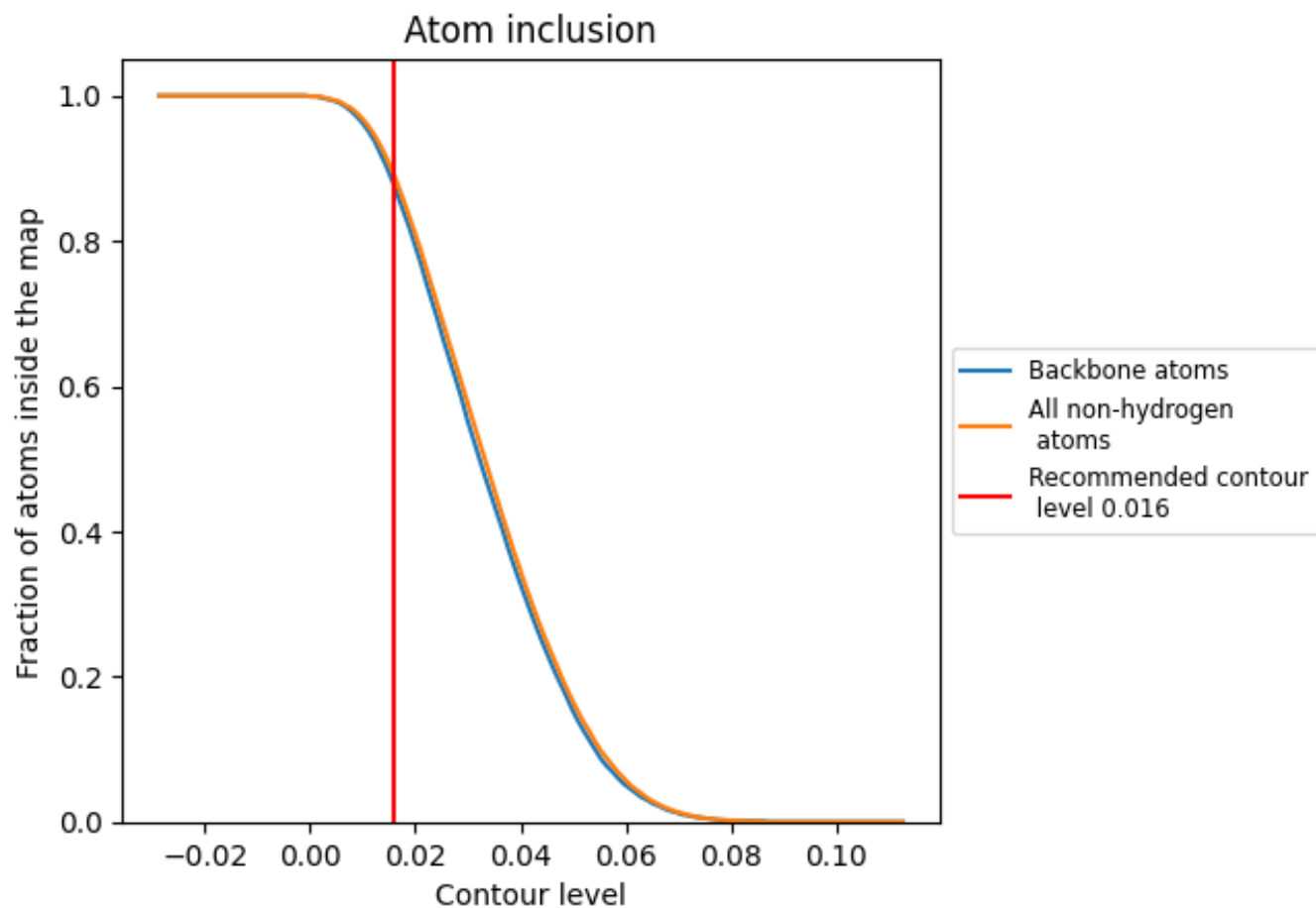
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.016).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 89% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8900	 0.4110
1	 0.9300	 0.4010
2	 0.9850	 0.4390
3	 0.7890	 0.3380
A	 0.7200	 0.4180
B	 0.8970	 0.4460
C	 0.9280	 0.4700
E	 0.9260	 0.4410
F	 0.9090	 0.4350
G	 0.8460	 0.3860
H	 0.8520	 0.4350
L	 0.9190	 0.4510
M	 0.9180	 0.4410
N	 0.8570	 0.4500
O	 0.9080	 0.4660
P	 0.9180	 0.4680
Q	 0.8880	 0.4520
R	 0.8180	 0.4380
S	 0.8810	 0.4310
T	 0.7150	 0.2920
U	 0.8300	 0.3900
V	 0.8850	 0.4450
W	 0.7250	 0.3180
X	 0.8970	 0.4650
Y	 0.9660	 0.4760
Z	 0.8500	 0.4010
a	 0.8780	 0.4380
b	 0.5550	 0.3360
c	 0.8660	 0.3970
d	 0.8500	 0.4590
e	 0.9160	 0.4870
f	 0.9370	 0.5000
g	 0.8680	 0.4510
h	 0.9500	 0.4470
i	 0.8400	 0.4170



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
j	 0.9270	 0.4840
k	 0.7100	 0.4140
l	 0.8890	 0.4770
m	 0.4730	 0.3410
p	 0.6710	 0.4230
r	 0.7490	 0.3820
u	 0.8290	 0.4120
y	 0.9420	 0.4170