



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 03:34 AM UTC

PDB ID : 7OHR / pdb_00007ohr
EMDB ID : EMD-12906
Title : Nog1-TAP associated immature ribosomal particle population E from *S. cerevisiae*
Authors : Milkereit, P.; Poell, G.
Deposited on : 2021-05-11
Resolution : 4.72 Å (reported)
Based on initial model : 6ELZ

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:

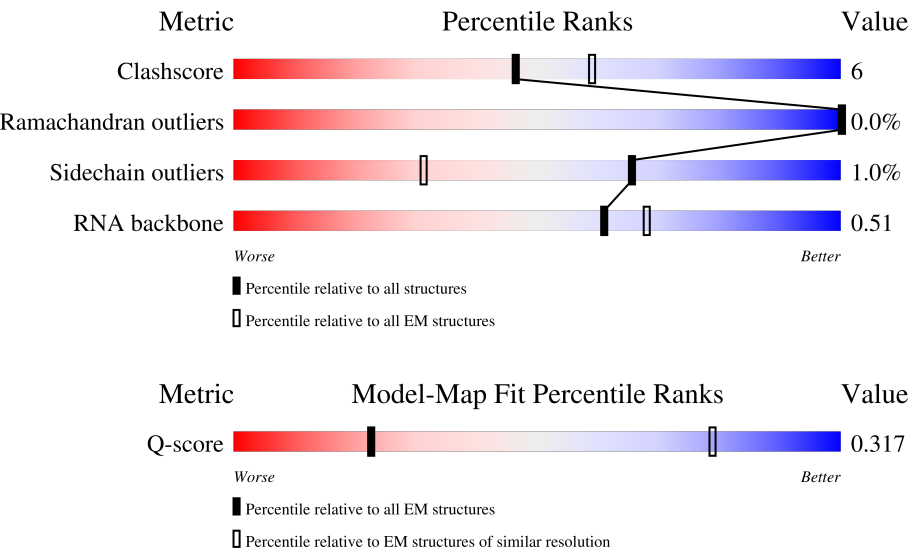
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.72 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.



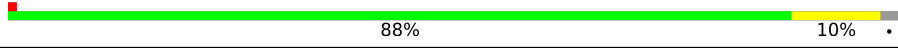
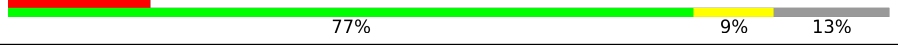
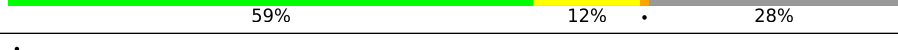
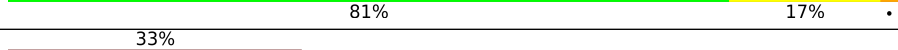
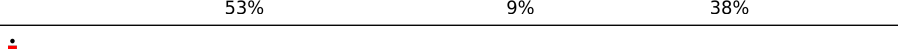
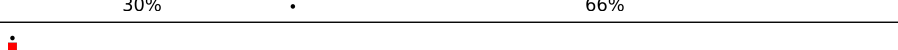
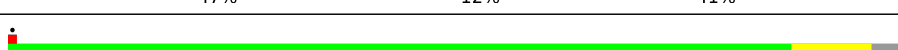
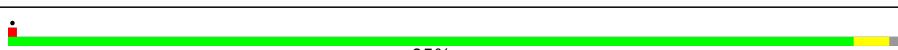
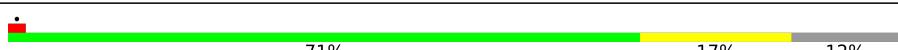
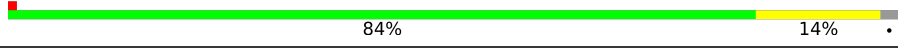
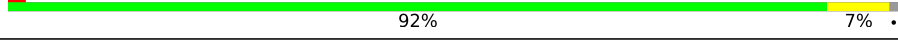
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1651 (4.22 - 5.20)

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	42%21%7%30%
2	2	158	53%34%13%
3	6	232	13%9%6%72%

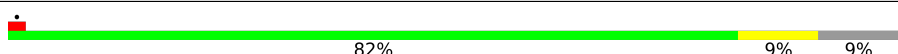
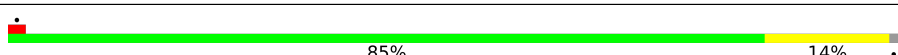
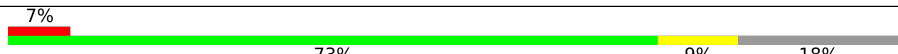
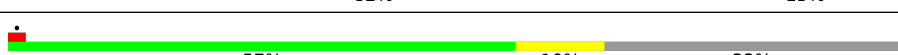
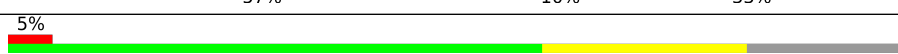
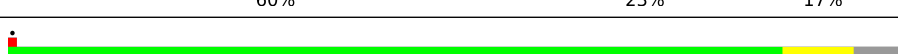
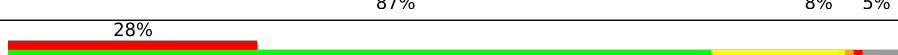
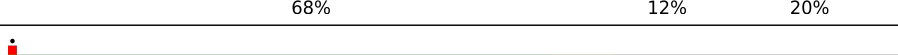
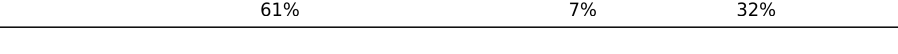
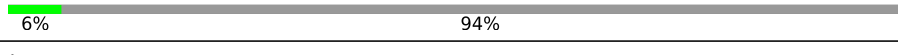
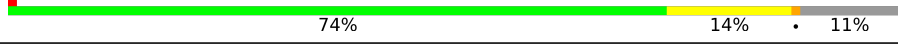
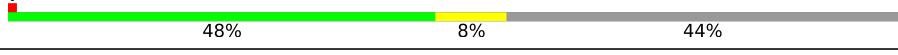
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Mol	Chain	Length	Quality of chain
4	A	291	
5	B	387	
6	C	362	
7	D	505	
8	E	176	
9	F	244	
10	G	256	
11	H	191	
12	I	663	
13	J	427	
14	K	376	
15	L	199	
16	M	138	
17	N	204	
18	O	199	
19	P	184	
20	Q	186	
21	R	189	
22	S	172	
23	U	121	
24	V	137	
25	W	236	
26	X	142	
27	Y	127	
28	Z	136	

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Mol	Chain	Length	Quality of chain
29	b	647	
30	c	105	
31	d	113	
32	e	130	
33	f	107	
34	g	121	
35	h	120	
36	i	100	
37	j	88	
38	k	78	
39	l	181	
40	m	807	
41	n	605	
42	o	220	
43	p	460	
44	q	618	
45	r	261	
46	s	520	
47	t	322	
48	u	199	
49	v	231	
50	w	841	
51	y	245	

2 Entry composition [i](#)

There are 52 unique types of molecules in this entry. The entry contains 235846 atoms, of which 105613 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	2373	Total	C	H	N	O	P	0	0
			76327	22684	25519	9188	16564	2372		

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

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

- Molecule 3 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	6	65	Total	C	H	N	O	P	0	0
			2061	614	691	228	463	65		

- Molecule 4 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	A	198	Total	C	H	N	O	S	0	0
			3250	1043	1627	284	290	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	B	335	Total	C	H	N	O	S	0	0
			5409	1694	2743	492	474	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
6	C	355	Total	C	H	N	O	S	0	0
			5556	1712	2841	514	486	3		

- Molecule 7 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	D	437	Total	C	H	N	O	S	0	0
			7106	2247	3620	600	627	12		

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	G	184	Total	C	H	N	O	S	0	0
			2960	930	1522	249	257	2		

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	H	190	Total	C	H	N	O	S	0	0
			3086	957	1576	273	276	4		

- Molecule 12 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	I	409	Total	C	H	N	O	S	0	0
			6733	2109	3445	557	606	16		

- Molecule 13 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	J	145	Total	C	H	N	O	S	0	0
			2461	759	1246	225	228	3		

- Molecule 14 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	K	257	Total	C	H	N	O	S	0	0
			4230	1337	2157	341	392	3		

- Molecule 15 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	L	118	Total	C	H	N	O		0	0
			1976	605	1010	204	157			

- Molecule 16 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	M	133	Total	C	H	N	O	S	0	0
			2168	665	1134	195	172	2		

- Molecule 17 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	N	182	Total	C	H	N	O	S	0	0
			3172	978	1613	328	252	1		

- Molecule 18 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	O	197	Total	C	H	N	O	S	0	0
			3215	1003	1660	289	262	1		

- Molecule 19 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	P	161	Total	C	H	N	O		0	0
			2591	795	1315	253	228			

- Molecule 20 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	Q	125	Total	C	H	N	O	S	0	0
			2008	617	1047	178	165	1		

- Molecule 21 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	115	Total	C	H	N	O	0	0
			1934	589	1006	187	152		

- Molecule 22 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	S	170	Total	C	H	N	O	S	0	0
			2903	922	1471	265	242	3		

- Molecule 23 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	98	Total	C	H	N	O	0	0
			1570	505	792	127	146		

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	V	134	Total	C	H	N	O	S	0	0
			2034	623	1041	187	176	7		

- Molecule 25 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	W	232	Total	C	H	N	O	S	0	0
			3773	1184	1903	321	360	5		

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	X	135	Total	C	H	N	O	S	0	0
			2182	675	1130	186	189	2		

- Molecule 27 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 28 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 29 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	b	421	Total	C	H	N	O	S	0	0
			6876	2180	3466	585	627	18		

- Molecule 30 is a protein called 60S ribosomal protein L30.

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

- Molecule 31 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	d	101	Total	C	H	N	O	S	0	0
			1700	526	875	157	141	1		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
32	e	118	Total	C	H	N	O	S	0	0
			1990	611	1029	195	154	1		

- Molecule 33 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 34 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	g	99	Total	C	H	N	O	S	0	0
			1595	477	824	154	136	4		

- Molecule 35 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	h	117	Total	C	H	N	O	S	0	0
			2031	610	1071	184	165	1		

- Molecule 36 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	i	67	Total	C	H	N	O	S	0	0
			1133	335	589	116	92	1		

- Molecule 37 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	j	73	Total	C	H	N	O	S	0	0
			1169	353	589	126	96	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	k	74	Total	C	H	N	O		0	0
			1256	380	662	111	103			

- Molecule 39 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	l	174	Total	C	H	N	O	S	0	0
			2793	887	1416	242	241	7		

- Molecule 40 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	m	645	Total	C	H	N	O	S	0	0
			10426	3322	5203	907	979	15		

- Molecule 41 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	n	411	Total	C	H	N	O	S	0	0
			6868	2179	3499	585	592	13		

- Molecule 42 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	o	133	Total	C	H	N	O	S	0	0
			2267	716	1160	198	189	4		

- Molecule 43 is a protein called Ribosome biogenesis protein YTM1.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	p	298	Total	C	H	N	O	S	0	0
			4619	1448	2298	410	457	6		

- Molecule 44 is a protein called 25S rRNA (cytosine(2870)-C(5))-methyltransferase.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	q	305	Total	C	H	N	O	S	0	0
			4819	1532	2427	413	437	10		

- Molecule 45 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	r	159	Total	C	H	N	O	S	0	0
			2682	819	1379	256	224	4		

- Molecule 46 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	s	31	Total	C	H	N	O	S	0	0
			555	156	300	57	41	1		

- Molecule 47 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	t	286	Total	C	H	N	O	S	0	0
			4752	1455	2455	426	413	3		

- Molecule 48 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	u	116	Total	C	H	N	O	S	0	0
			1987	612	1011	200	155	9		

- Molecule 49 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	v	130	Total	C	H	N	O	S	0	0
			2223	678	1136	211	195	3		

- Molecule 50 is a protein called 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	w	198	Total	C	H	N	O	S	0	0
			3373	1040	1726	304	295	8		

- Molecule 51 is a protein called Eukaryotic translation initiation factor 6.

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

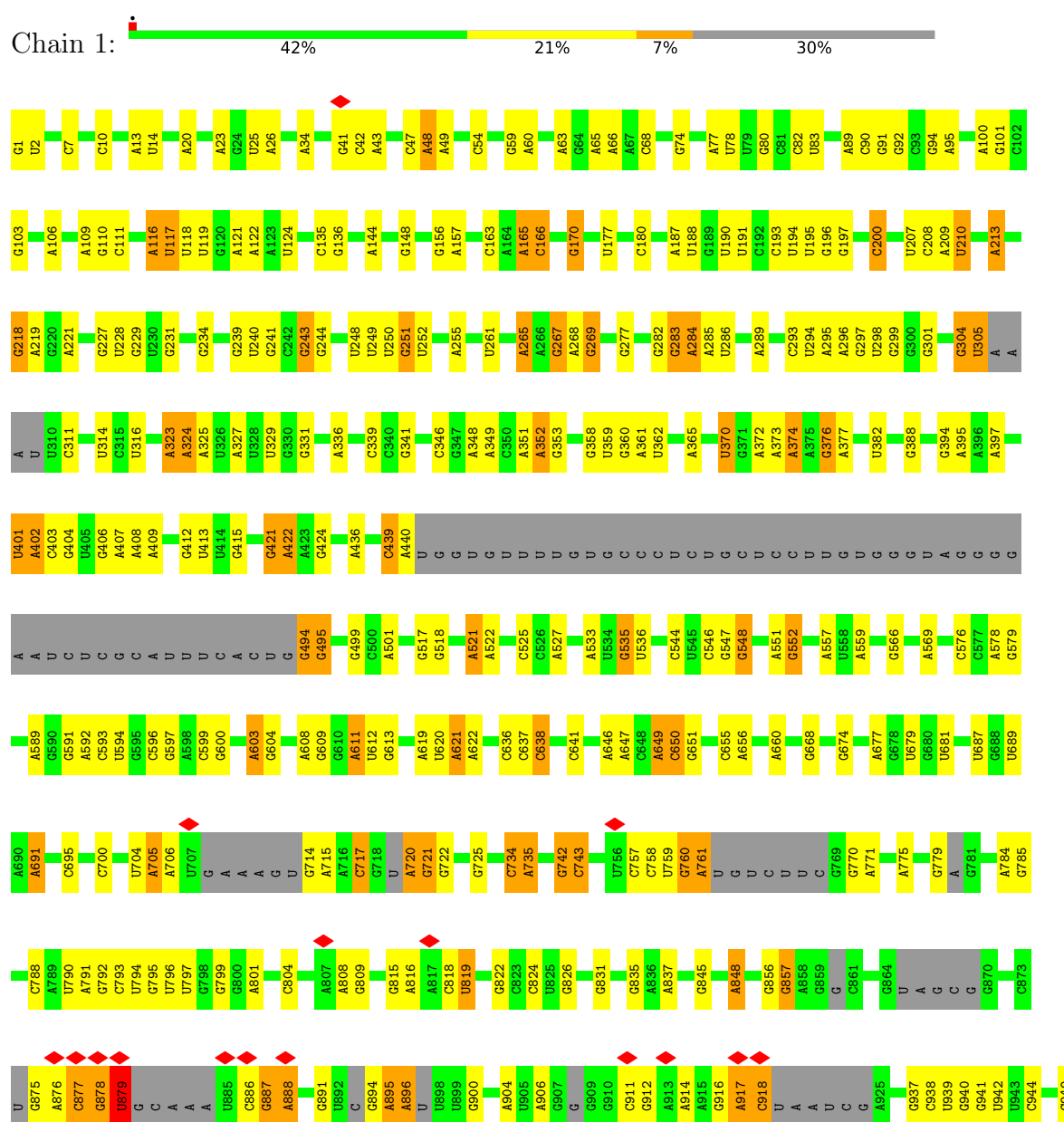
- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	j	1	Total	Zn	0
			1	1	

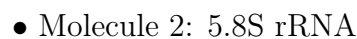
3 Residue-property plots

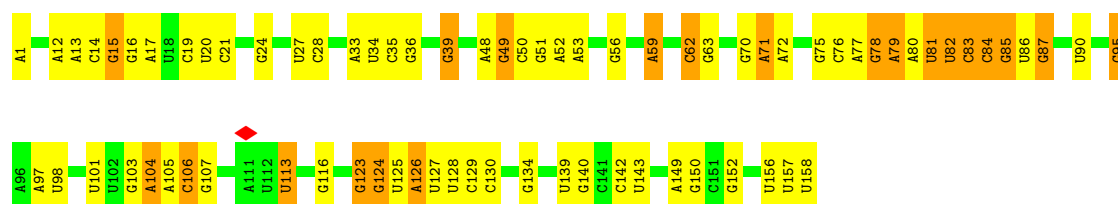
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 25S rRNA



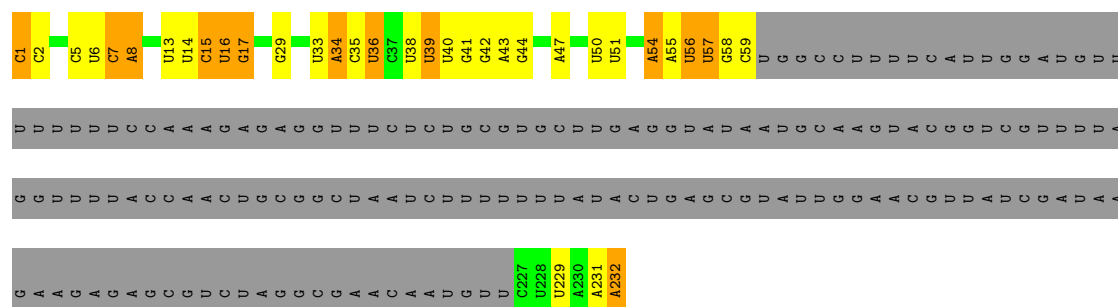






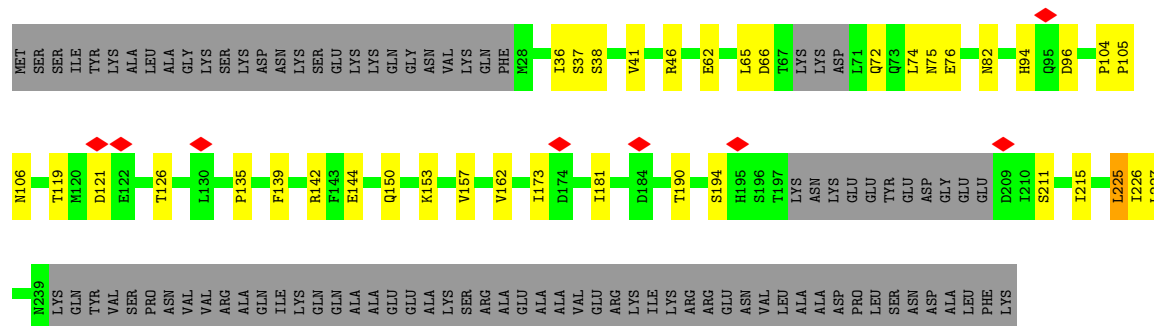
- Molecule 3: ITS2

Chain 6: 13% 9% 6% 72%



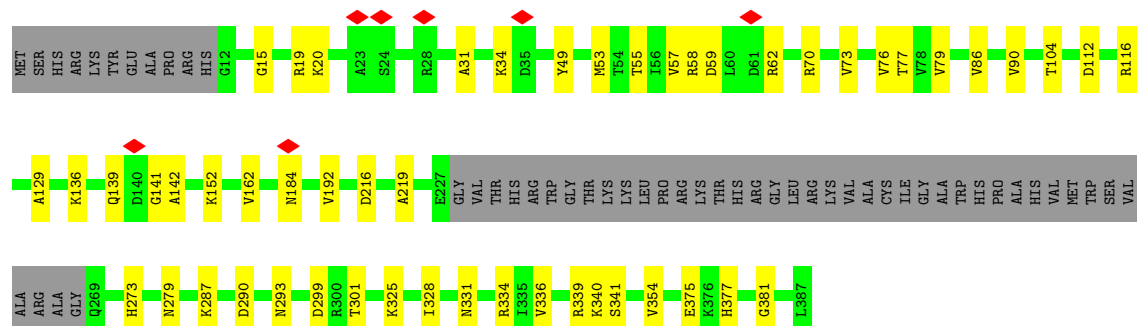
- Molecule 4: Ribosome biogenesis protein BRX1

Chain A: 55% 13% 32%

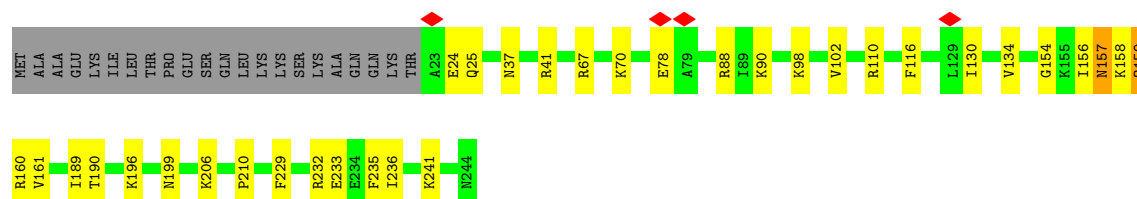


- Molecule 5: 60S ribosomal protein L3

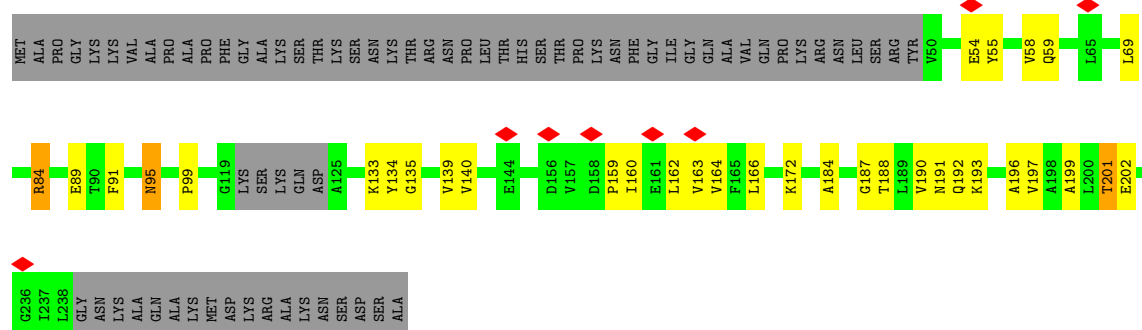
Chain B: 73% 14% 13%



- Molecule 6: 60S ribosomal protein L4-A



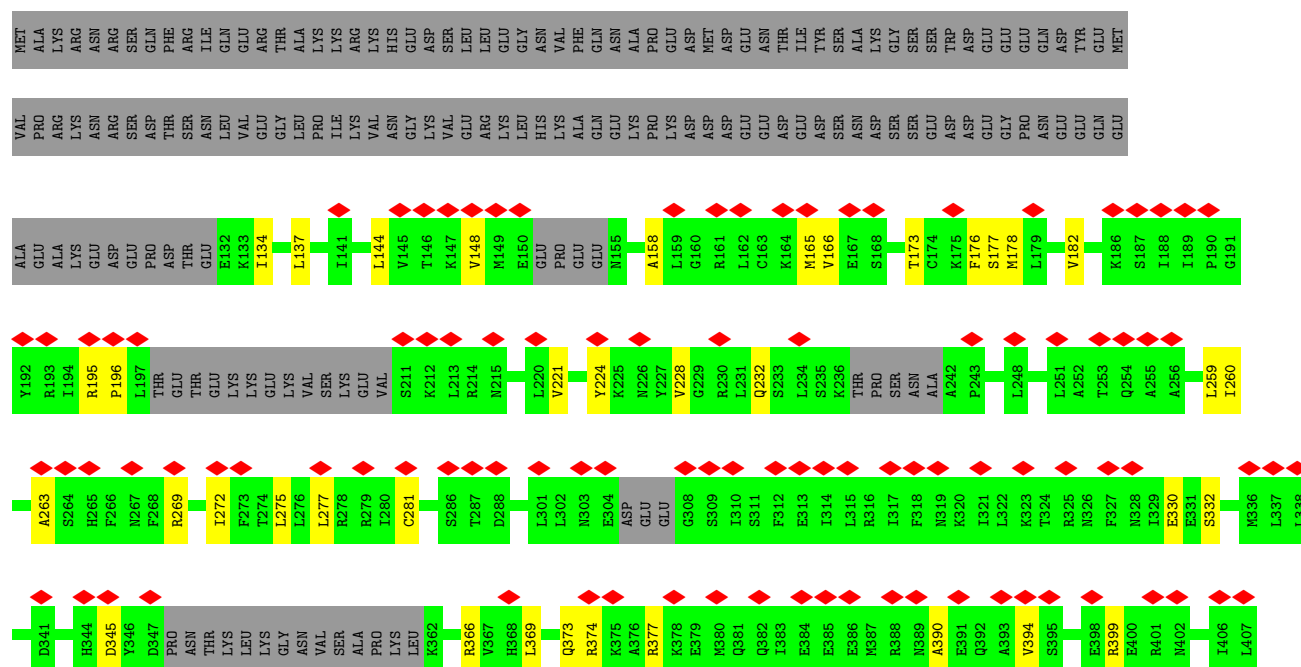
Chain G: 59% 12% 28%

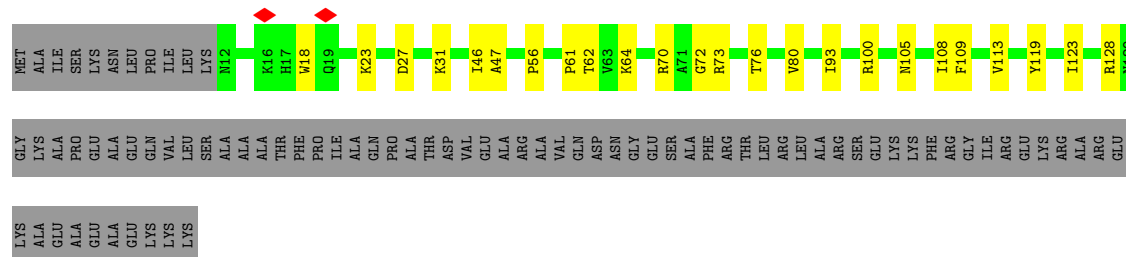


Chain H: 81% 17%

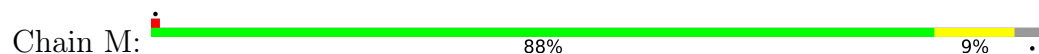


Chain I: 33% 53% 9% 38%

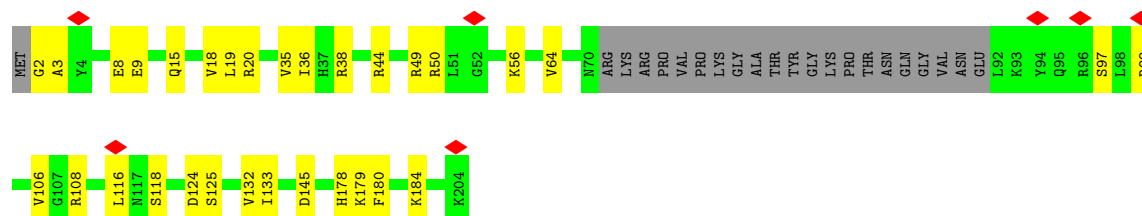
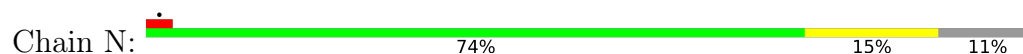




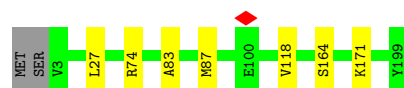
- Molecule 16: 60S ribosomal protein L14-A



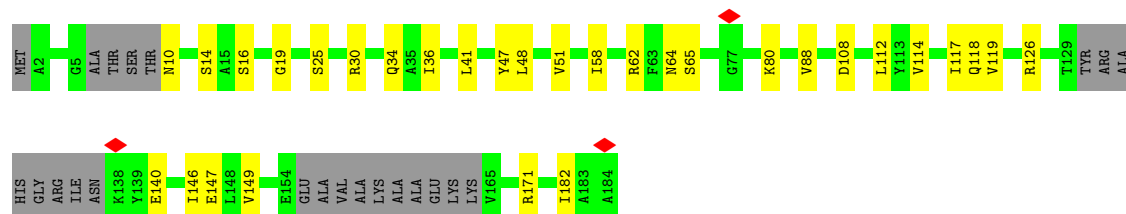
- Molecule 17: 60S ribosomal protein L15-A



- Molecule 18: 60S ribosomal protein L16-A

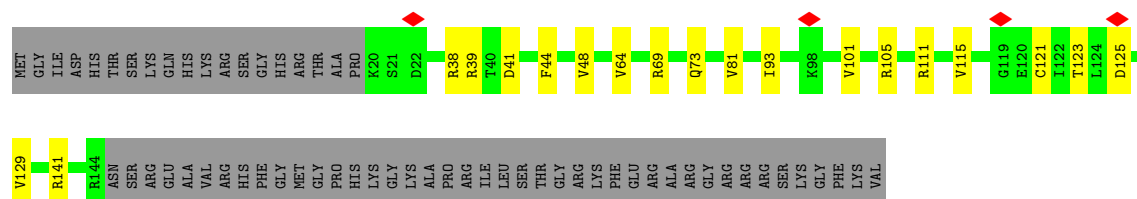


- Molecule 19: 60S ribosomal protein L17-A



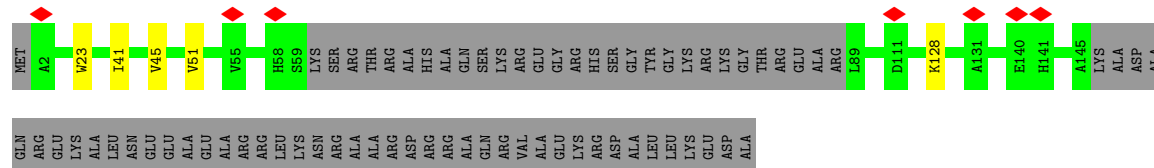
- Molecule 20: 60S ribosomal protein L18-A

Chain Q:  57% 10% 33%



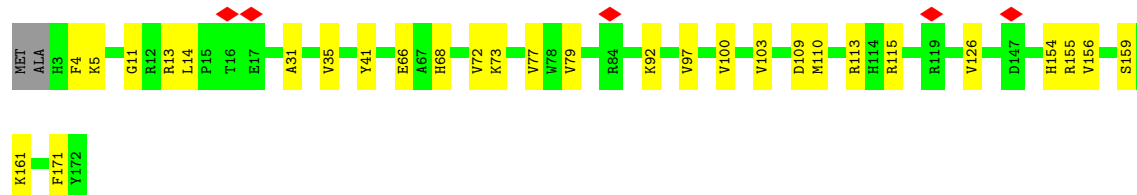
- Molecule 21: 60S ribosomal protein L19-A

Chain R:  58% 0% 39%



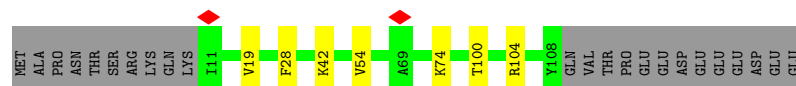
- Molecule 22: 60S ribosomal protein L20-A

Chain S:  82% 17% 0%



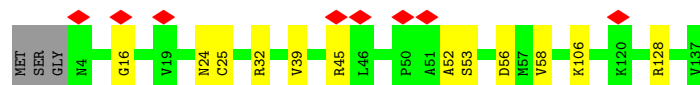
- Molecule 23: 60S ribosomal protein L22-A

Chain U:  75% 6% 19%



- Molecule 24: 60S ribosomal protein L23-A

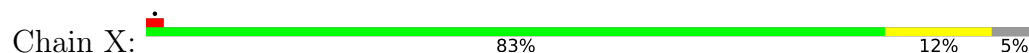
Chain V:  6% 89% 9%



- Molecule 25: Ribosome assembly factor MRT4

Chain W:  84% 14% 0%

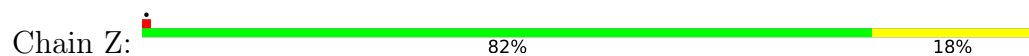
- Molecule 26: 60S ribosomal protein L25



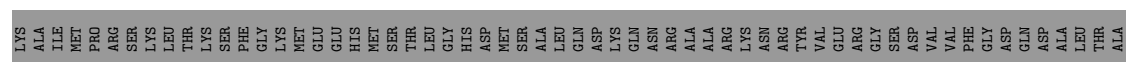
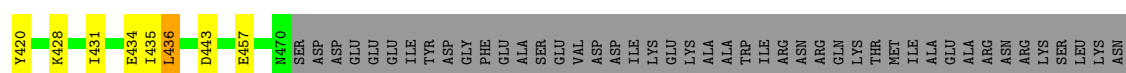
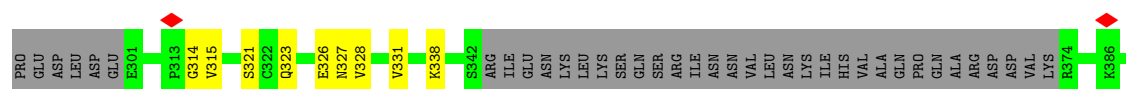
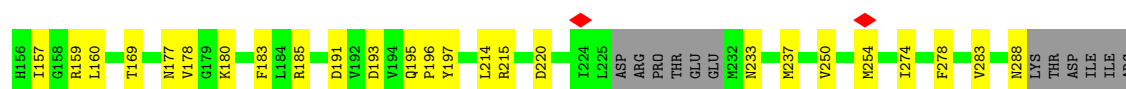
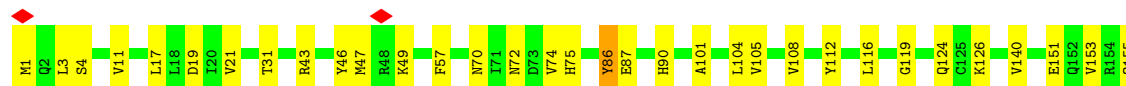
- Molecule 27: 60S ribosomal protein L26-A

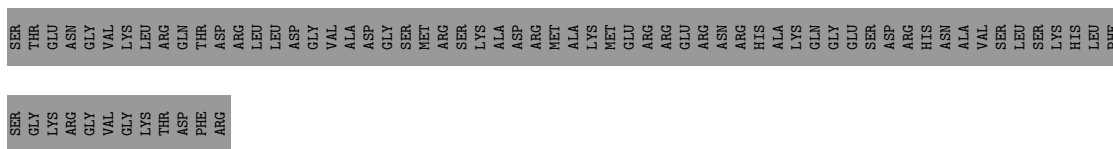


- Molecule 28: 60S ribosomal protein L27-A

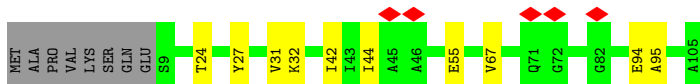
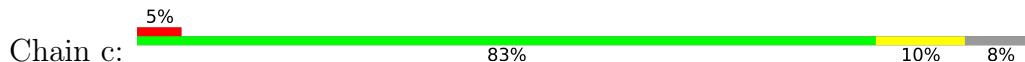


- Molecule 29: Nucleolar GTP-binding protein 1

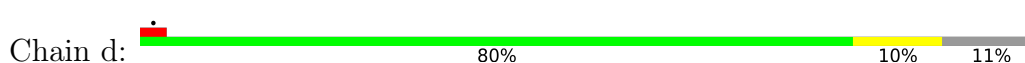




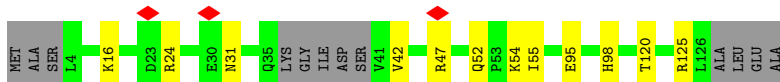
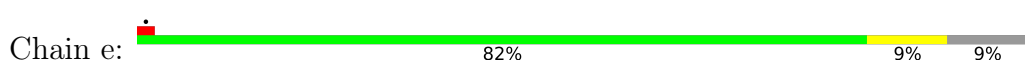
- Molecule 30: 60S ribosomal protein L30



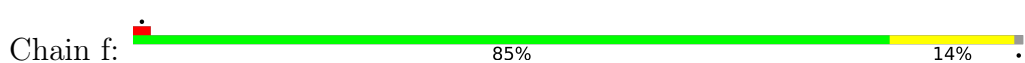
- Molecule 31: 60S ribosomal protein L31-A



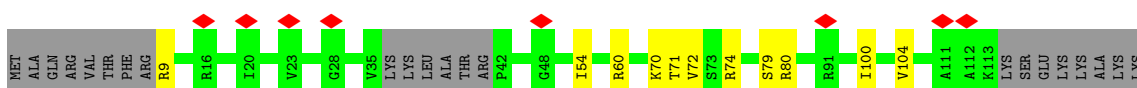
- Molecule 32: 60S ribosomal protein L32



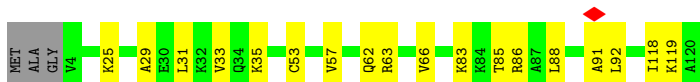
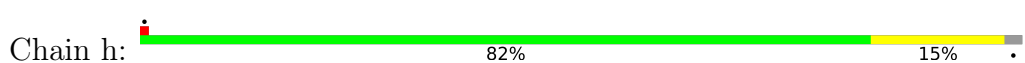
- Molecule 33: 60S ribosomal protein L33-A



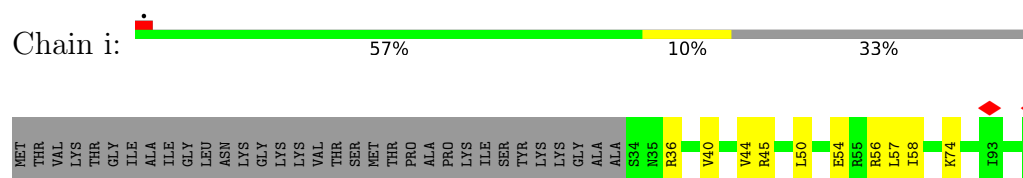
- Molecule 34: 60S ribosomal protein L34-A



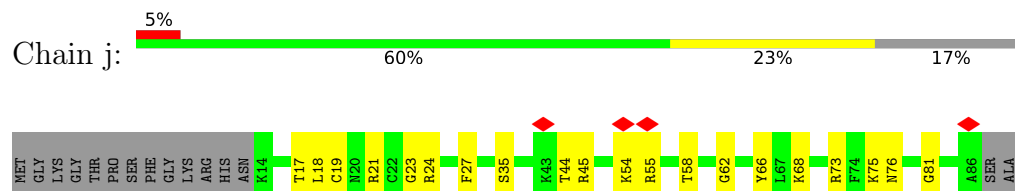
- Molecule 35: 60S ribosomal protein L35-A



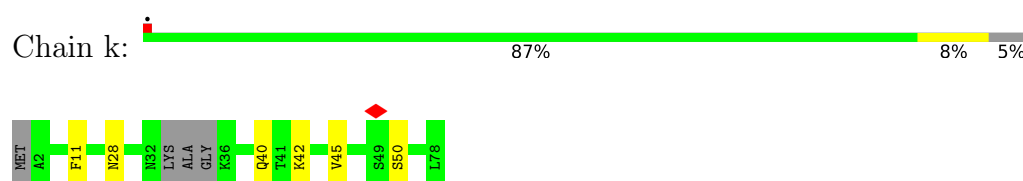
- Molecule 36: 60S ribosomal protein L36-A



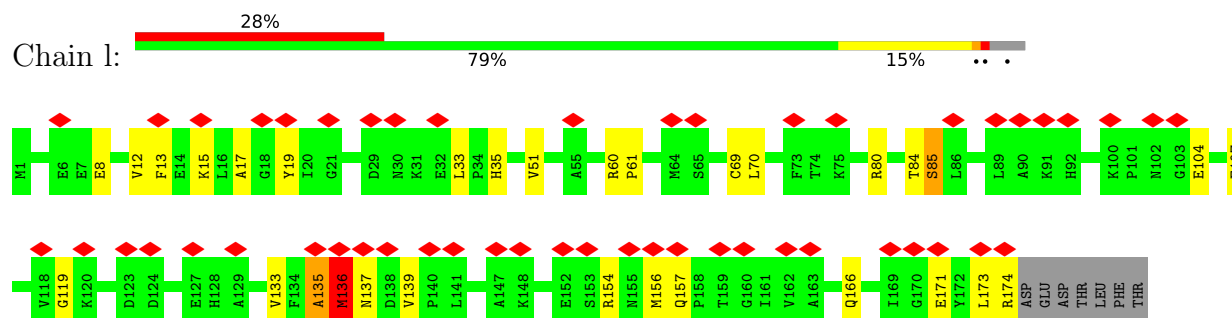
- Molecule 37: 60S ribosomal protein L37-A



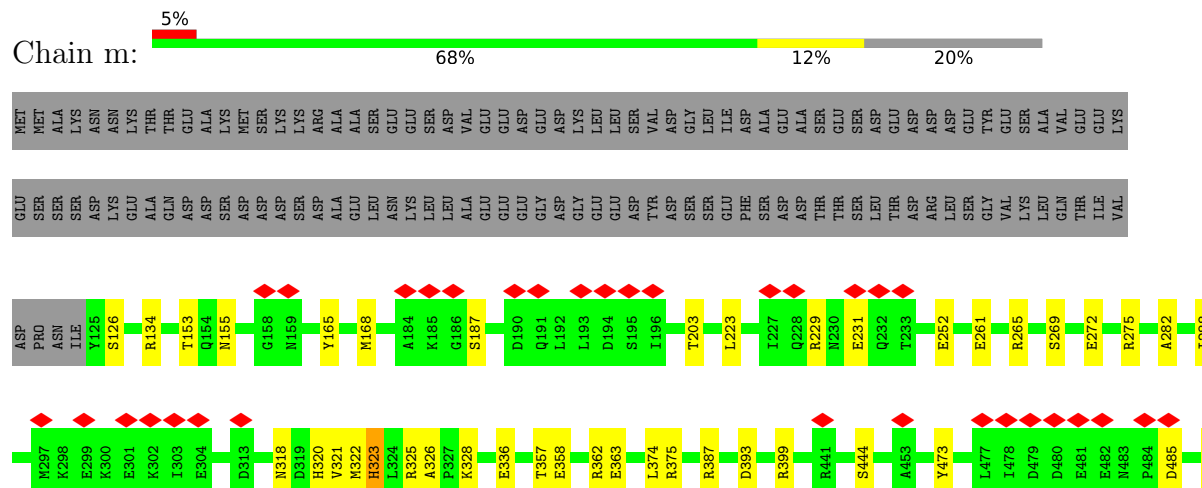
- Molecule 38: 60S ribosomal protein L38



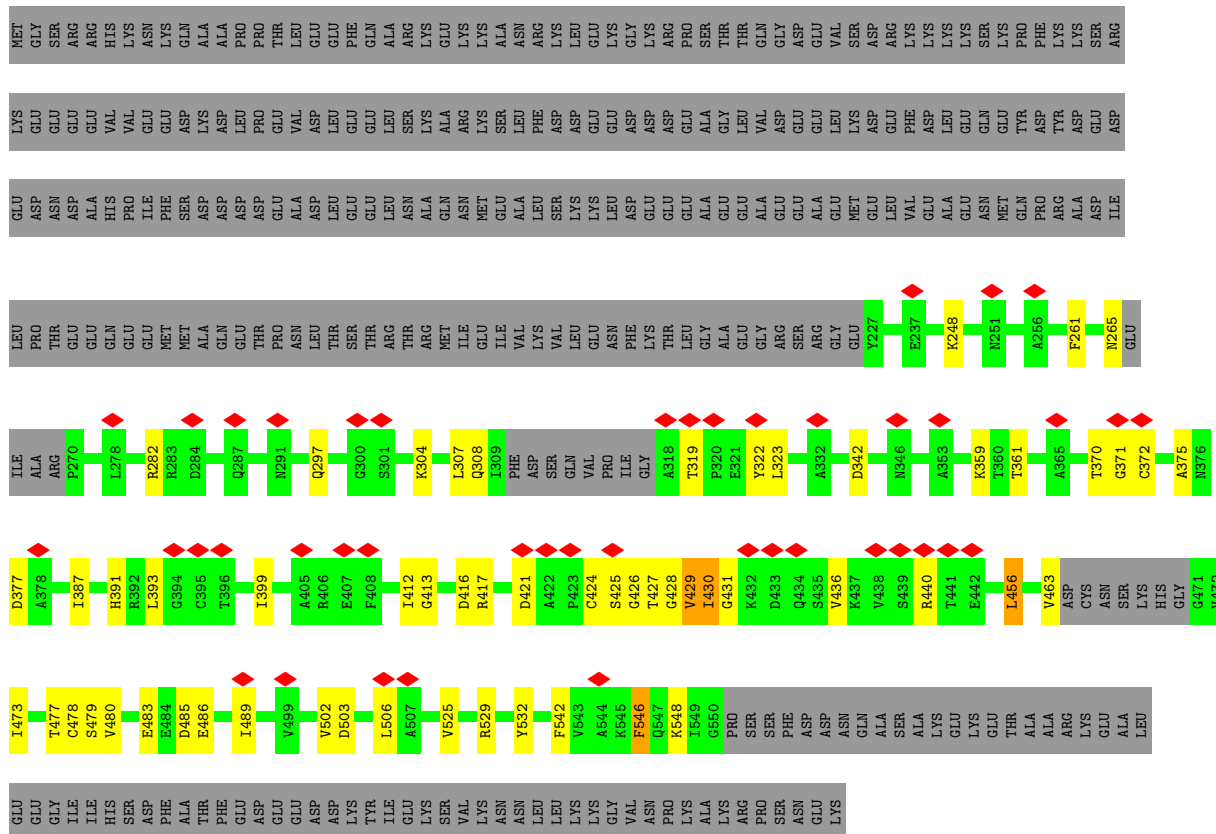
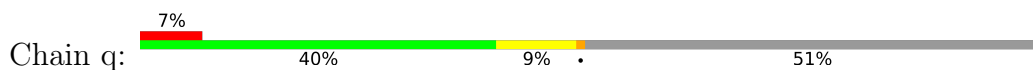
- Molecule 39: 60S ribosome subunit biogenesis protein NIP7



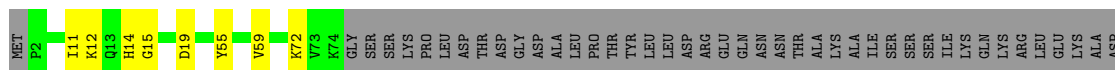
- Molecule 40: Ribosome biogenesis protein ERB1

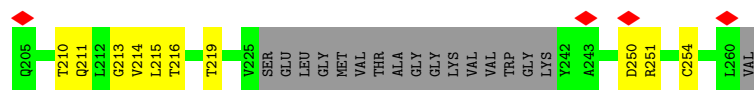


- Molecule 44: 25S rRNA (cytosine(2870)-C(5))-methyltransferase

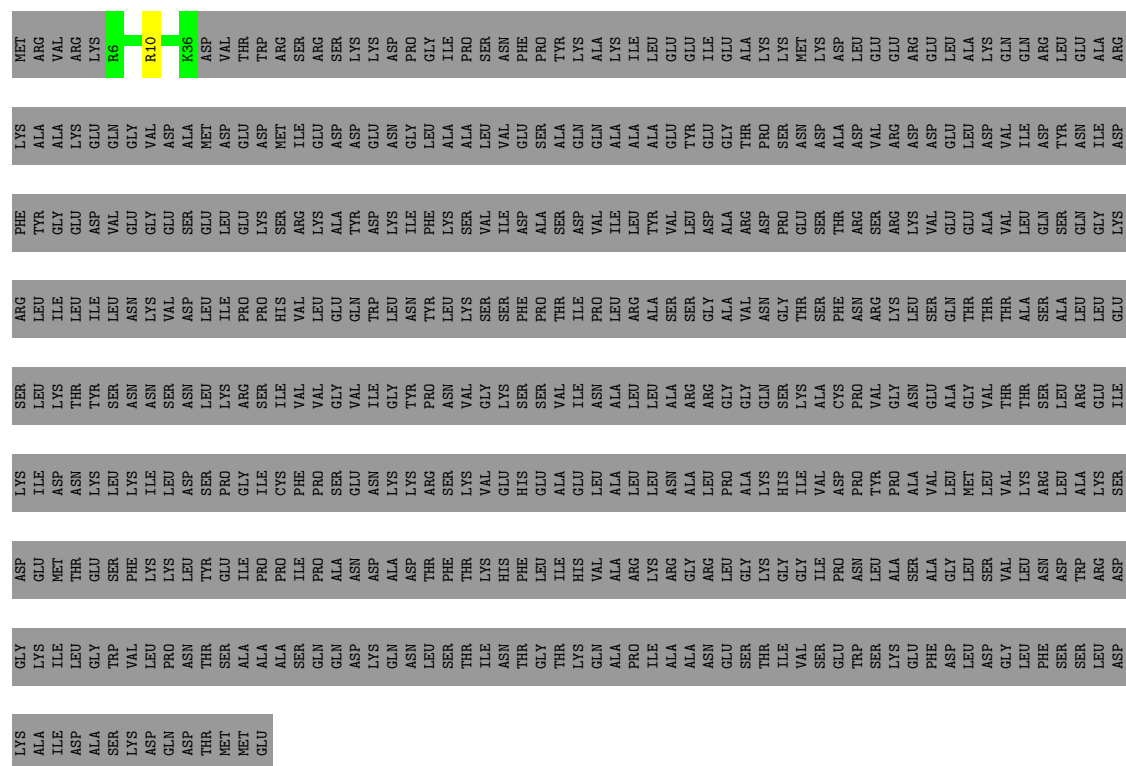


- Molecule 45: Ribosome biogenesis protein NSA2

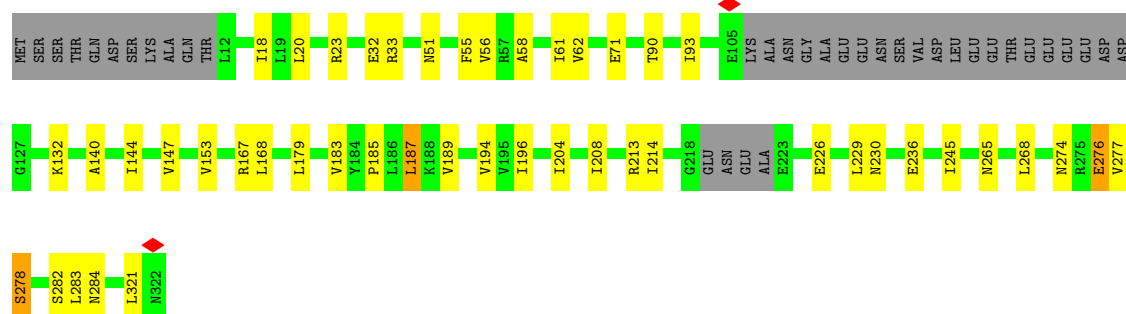




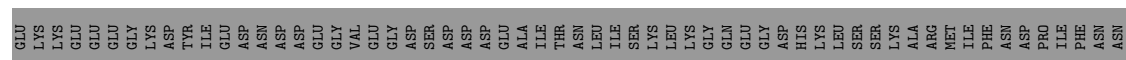
- Molecule 46: Nuclear GTP-binding protein NUG1

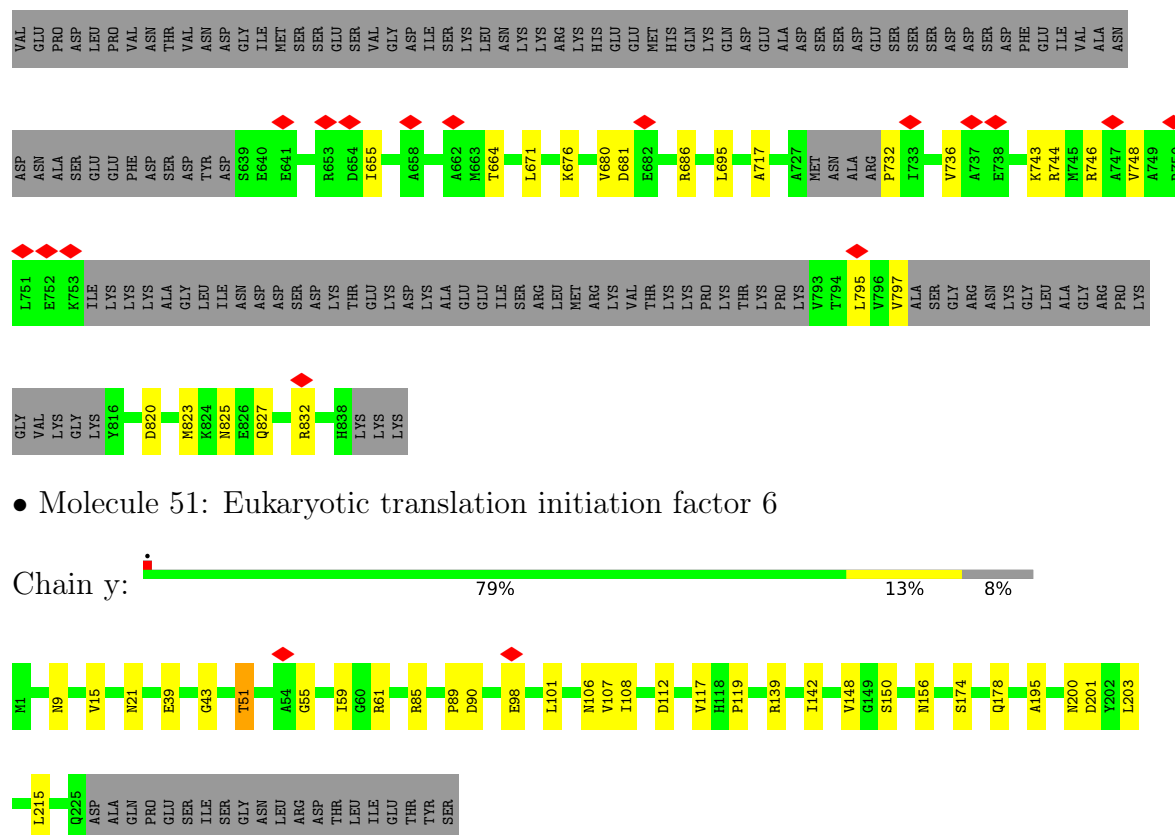


- Molecule 47: Ribosome biogenesis protein RLP7

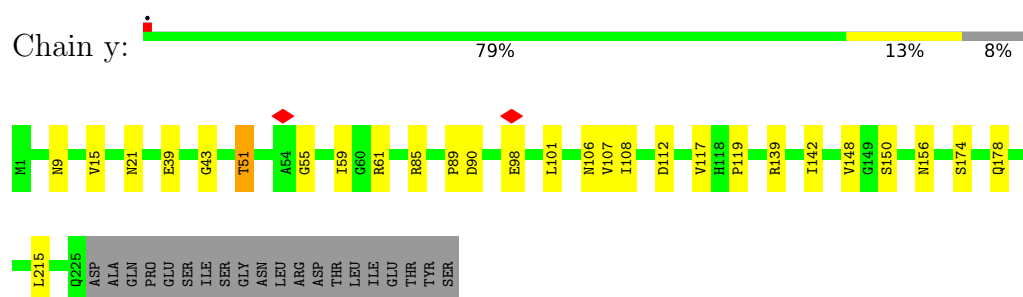


- Molecule 48: Ribosome biogenesis protein RLP24





- Molecule 51: 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	8455	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	0.098	Depositor
Minimum map value	-0.032	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.021	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:
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	0.21	6/56847 (0.0%)	0.22	0/88571
2	2	0.08	0/3746	0.23	0/5832
3	6	0.08	0/1527	0.26	0/2371
4	A	0.10	0/1663	0.24	0/2248
5	B	0.10	0/2720	0.24	0/3654
6	C	0.09	0/2765	0.24	0/3743
7	D	0.09	0/3552	0.23	0/4789
8	E	0.11	0/1137	0.22	0/1525
9	F	0.11	0/1821	0.29	0/2451
10	G	0.10	0/1463	0.25	0/1978
11	H	0.08	0/1531	0.25	0/2062
12	I	0.10	0/3327	0.23	0/4464
13	J	0.10	0/1232	0.24	0/1642
14	K	0.09	0/2107	0.23	0/2845
15	L	0.12	0/984	0.27	0/1322
16	M	0.10	0/1048	0.21	0/1410
17	N	0.12	0/1591	0.22	0/2128
18	O	0.10	0/1585	0.22	0/2128
19	P	0.11	0/1294	0.24	0/1734
20	Q	0.10	0/974	0.21	0/1316
21	R	0.10	0/941	0.23	0/1262
22	S	0.11	0/1468	0.27	0/1973
23	U	0.09	0/794	0.20	0/1076
24	V	0.10	0/1008	0.23	0/1356
25	W	0.09	0/1902	0.23	0/2564
26	X	0.09	0/1067	0.21	0/1436
27	Y	0.11	0/1004	0.23	0/1341
28	Z	0.11	0/1118	0.24	0/1497
29	b	0.09	0/3474	0.25	0/4683
30	c	0.09	0/751	0.19	0/1008
31	d	0.11	0/838	0.25	0/1123
32	e	0.10	0/981	0.22	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.11	0/868	0.26	0/1168
34	g	0.11	0/779	0.23	0/1040
35	h	0.11	0/969	0.25	0/1289
36	i	0.13	0/548	0.25	0/726
37	j	0.12	0/592	0.26	0/785
38	k	0.11	0/599	0.20	0/800
39	l	0.83	3/1408 (0.2%)	0.71	4/1899 (0.2%)
40	m	0.09	0/5356	0.23	0/7264
41	n	0.08	0/3441	0.22	0/4625
42	o	0.10	0/1129	0.25	0/1502
43	p	0.09	0/2362	0.24	0/3200
44	q	0.09	0/2439	0.26	0/3297
45	r	0.10	0/1323	0.25	0/1765
46	s	0.14	0/255	0.21	0/327
47	t	0.11	0/2323	0.27	0/3113
48	u	0.10	0/996	0.28	0/1324
49	v	0.10	0/1100	0.21	0/1456
50	w	0.09	0/1663	0.19	0/2206
51	y	0.08	0/1722	0.22	0/2343
All	All	0.18	9/138132 (0.0%)	0.24	4/198973 (0.0%)

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	F	0	1
11	H	0	1
All	All	0	2

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	l	135	ALA	C-N	26.66	1.70	1.33
1	1	879	U	N3-C4	22.89	1.84	1.38
1	1	879	U	C2-N3	22.60	1.82	1.37
1	1	879	U	N1-C2	19.49	1.77	1.38
1	1	879	U	N1-C6	18.30	1.74	1.38

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	1	135	ALA	CA-C-N	18.73	155.41	121.70
39	1	135	ALA	C-N-CA	18.73	155.41	121.70
39	1	135	ALA	CA-C-O	-7.46	111.54	120.56
39	1	136	MET	N-CA-C	7.07	130.79	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	F	157	ASN	Peptide
11	H	22	SER	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	50808	25519	25553	641	0
2	2	3353	1695	1695	64	0
3	6	1370	691	692	21	0
4	A	1623	1627	1624	28	0
5	B	2666	2743	2741	37	0
6	C	2715	2841	2839	26	0
7	D	3486	3620	3618	31	0
8	E	1121	1217	1215	15	0
9	F	1784	1863	1862	33	0
10	G	1438	1522	1520	25	0
11	H	1510	1576	1576	29	0
12	I	3288	3445	3435	33	0
13	J	1215	1246	1245	15	0
14	K	2073	2157	2155	30	0
15	L	966	1010	1009	20	0
16	M	1034	1134	1132	11	0
17	N	1559	1613	1611	24	0
18	O	1555	1660	1659	5	0
19	P	1276	1315	1311	21	0
20	Q	961	1047	1046	15	0
21	R	928	1006	1004	3	0
22	S	1432	1471	1470	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	U	778	792	791	6	0
24	V	993	1041	1040	7	0
25	W	1870	1903	1902	24	0
26	X	1052	1130	1128	13	0
27	Y	993	1082	1081	7	0
28	Z	1092	1156	1155	15	0
29	b	3410	3466	3463	53	0
30	c	743	798	797	7	0
31	d	825	875	874	7	0
32	e	961	1029	1027	12	0
33	f	850	881	880	12	0
34	g	771	824	823	9	0
35	h	960	1071	1070	17	0
36	i	544	589	588	7	0
37	j	580	589	584	16	0
38	k	594	662	660	4	0
39	l	1377	1416	1415	63	0
40	m	5223	5203	5201	69	0
41	n	3369	3499	3496	33	0
42	o	1107	1160	1159	20	0
43	p	2321	2298	2294	21	0
44	q	2392	2427	2424	40	0
45	r	1303	1379	1376	21	0
46	s	255	300	299	1	0
47	t	2297	2455	2452	32	0
48	u	976	1011	1011	15	0
49	v	1087	1136	1133	15	0
50	w	1647	1726	1718	19	0
51	y	1701	1697	1697	20	0
52	j	1	0	0	0	0
All	All	130233	105613	105550	1414	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 6.

The worst 5 of 1414 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:879:U:C5	1:1:879:U:C4	1.76	1.69
1:1:879:U:C2	39:1:136:MET:N	1.73	1.53
1:1:879:U:C6	1:1:879:U:N1	1.74	1.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:l:136:MET:N	39:l:136:MET:CA	1.72	1.52
1:l:879:U:C2	1:l:879:U:N1	1.77	1.52

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	192/291 (66%)	185 (96%)	7 (4%)	0	100	100
5	B	331/387 (86%)	318 (96%)	13 (4%)	0	100	100
6	C	351/362 (97%)	337 (96%)	14 (4%)	0	100	100
7	D	433/505 (86%)	423 (98%)	10 (2%)	0	100	100
8	E	137/176 (78%)	136 (99%)	1 (1%)	0	100	100
9	F	220/244 (90%)	209 (95%)	10 (4%)	1 (0%)	24	63
10	G	180/256 (70%)	173 (96%)	7 (4%)	0	100	100
11	H	188/191 (98%)	179 (95%)	9 (5%)	0	100	100
12	I	389/663 (59%)	371 (95%)	18 (5%)	0	100	100
13	J	143/427 (34%)	141 (99%)	2 (1%)	0	100	100
14	K	253/376 (67%)	240 (95%)	13 (5%)	0	100	100
15	L	116/199 (58%)	110 (95%)	6 (5%)	0	100	100
16	M	129/138 (94%)	128 (99%)	1 (1%)	0	100	100
17	N	178/204 (87%)	177 (99%)	1 (1%)	0	100	100
18	O	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
19	P	153/184 (83%)	149 (97%)	4 (3%)	0	100	100
20	Q	123/186 (66%)	122 (99%)	1 (1%)	0	100	100
21	R	111/189 (59%)	108 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	S	168/172 (98%)	155 (92%)	13 (8%)	0	100	100
23	U	96/121 (79%)	94 (98%)	2 (2%)	0	100	100
24	V	132/137 (96%)	130 (98%)	2 (2%)	0	100	100
25	W	230/236 (98%)	228 (99%)	2 (1%)	0	100	100
26	X	131/142 (92%)	124 (95%)	7 (5%)	0	100	100
27	Y	124/127 (98%)	124 (100%)	0	0	100	100
28	Z	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
29	b	413/647 (64%)	399 (97%)	14 (3%)	0	100	100
30	c	95/105 (90%)	95 (100%)	0	0	100	100
31	d	97/113 (86%)	94 (97%)	3 (3%)	0	100	100
32	e	114/130 (88%)	111 (97%)	3 (3%)	0	100	100
33	f	104/107 (97%)	102 (98%)	2 (2%)	0	100	100
34	g	95/121 (78%)	94 (99%)	1 (1%)	0	100	100
35	h	115/120 (96%)	107 (93%)	8 (7%)	0	100	100
36	i	65/100 (65%)	65 (100%)	0	0	100	100
37	j	71/88 (81%)	70 (99%)	1 (1%)	0	100	100
38	k	70/78 (90%)	70 (100%)	0	0	100	100
39	l	172/181 (95%)	165 (96%)	6 (4%)	1 (1%)	21	59
40	m	641/807 (79%)	625 (98%)	16 (2%)	0	100	100
41	n	403/605 (67%)	393 (98%)	10 (2%)	0	100	100
42	o	131/220 (60%)	124 (95%)	7 (5%)	0	100	100
43	p	288/460 (63%)	280 (97%)	8 (3%)	0	100	100
44	q	297/618 (48%)	281 (95%)	14 (5%)	2 (1%)	18	55
45	r	151/261 (58%)	143 (95%)	8 (5%)	0	100	100
46	s	29/520 (6%)	29 (100%)	0	0	100	100
47	t	280/322 (87%)	263 (94%)	17 (6%)	0	100	100
48	u	114/199 (57%)	113 (99%)	1 (1%)	0	100	100
49	v	124/231 (54%)	123 (99%)	1 (1%)	0	100	100
50	w	180/841 (21%)	177 (98%)	3 (2%)	0	100	100
51	y	223/245 (91%)	220 (99%)	3 (1%)	0	100	100
All	All	9108/13367 (68%)	8827 (97%)	277 (3%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
39	l	136	MET
44	q	429	VAL
9	F	159	GLN
44	q	430	ILE

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	A	185/263 (70%)	181 (98%)	4 (2%)	45	64
5	B	282/323 (87%)	281 (100%)	1 (0%)	84	83
6	C	286/289 (99%)	283 (99%)	3 (1%)	68	76
7	D	381/440 (87%)	377 (99%)	4 (1%)	68	76
8	E	122/153 (80%)	120 (98%)	2 (2%)	55	69
9	F	186/205 (91%)	186 (100%)	0	100	100
10	G	150/208 (72%)	146 (97%)	4 (3%)	39	60
11	H	170/171 (99%)	168 (99%)	2 (1%)	63	73
12	I	373/602 (62%)	369 (99%)	4 (1%)	65	74
13	J	133/383 (35%)	133 (100%)	0	100	100
14	K	238/346 (69%)	234 (98%)	4 (2%)	53	68
15	L	97/159 (61%)	96 (99%)	1 (1%)	68	76
16	M	105/109 (96%)	105 (100%)	0	100	100
17	N	158/176 (90%)	157 (99%)	1 (1%)	78	81
18	O	160/162 (99%)	158 (99%)	2 (1%)	61	72
19	P	130/146 (89%)	129 (99%)	1 (1%)	73	78
20	Q	102/151 (68%)	102 (100%)	0	100	100
21	R	98/154 (64%)	98 (100%)	0	100	100
22	S	155/156 (99%)	154 (99%)	1 (1%)	78	81
23	U	85/107 (79%)	84 (99%)	1 (1%)	63	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	V	103/105 (98%)	102 (99%)	1 (1%)	68	76
25	W	209/213 (98%)	208 (100%)	1 (0%)	81	82
26	X	111/118 (94%)	111 (100%)	0	100	100
27	Y	109/110 (99%)	109 (100%)	0	100	100
28	Z	115/116 (99%)	115 (100%)	0	100	100
29	b	377/573 (66%)	370 (98%)	7 (2%)	50	66
30	c	81/88 (92%)	80 (99%)	1 (1%)	63	73
31	d	89/97 (92%)	89 (100%)	0	100	100
32	e	103/111 (93%)	103 (100%)	0	100	100
33	f	90/91 (99%)	90 (100%)	0	100	100
34	g	84/103 (82%)	84 (100%)	0	100	100
35	h	104/105 (99%)	104 (100%)	0	100	100
36	i	57/82 (70%)	55 (96%)	2 (4%)	32	53
37	j	60/71 (84%)	59 (98%)	1 (2%)	53	68
38	k	67/69 (97%)	67 (100%)	0	100	100
39	l	149/156 (96%)	148 (99%)	1 (1%)	76	79
40	m	582/723 (80%)	574 (99%)	8 (1%)	59	71
41	n	371/548 (68%)	370 (100%)	1 (0%)	86	84
42	o	118/199 (59%)	116 (98%)	2 (2%)	53	68
43	p	265/413 (64%)	261 (98%)	4 (2%)	57	71
44	q	258/535 (48%)	255 (99%)	3 (1%)	63	73
45	r	142/229 (62%)	138 (97%)	4 (3%)	38	59
46	s	27/445 (6%)	27 (100%)	0	100	100
47	t	256/287 (89%)	251 (98%)	5 (2%)	48	66
48	u	101/180 (56%)	101 (100%)	0	100	100
49	v	116/205 (57%)	115 (99%)	1 (1%)	70	77
50	w	179/745 (24%)	178 (99%)	1 (1%)	78	81
51	y	193/211 (92%)	191 (99%)	2 (1%)	68	76
All	All	8112/11631 (70%)	8032 (99%)	80 (1%)	65	76

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	n	566	LEU
47	t	32	GLU
42	o	137	LEU
44	q	542	PHE
47	t	278	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
47	t	238	GLN
47	t	303	ASN
51	y	145	ASN
19	P	45	GLN
18	O	55	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2345/3396 (69%)	454 (19%)	50 (2%)
2	2	157/158 (99%)	34 (21%)	3 (1%)
3	6	64/232 (27%)	22 (34%)	3 (4%)
All	All	2566/3786 (67%)	510 (19%)	56 (2%)

5 of 510 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	7	C
1	1	14	U
1	1	26	A
1	1	41	G

5 of 56 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1582	C
3	6	56	U
1	1	1861	G
3	6	16	U
1	1	3350	C

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 1 ligands modelled in this entry, 1 is 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
39	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	135:ALA	C	136:MET	N	1.70

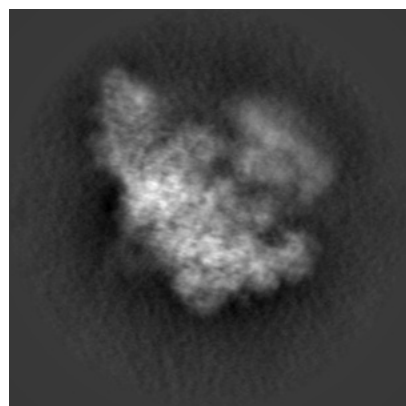
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12906. These allow visual inspection of the internal detail of the map and identification of artifacts.

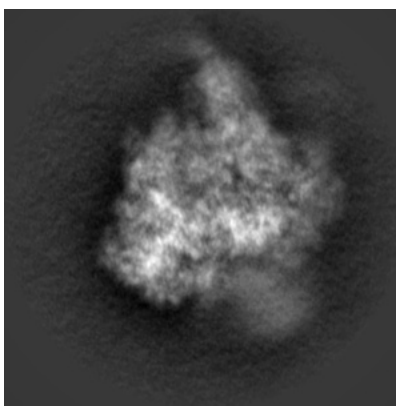
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

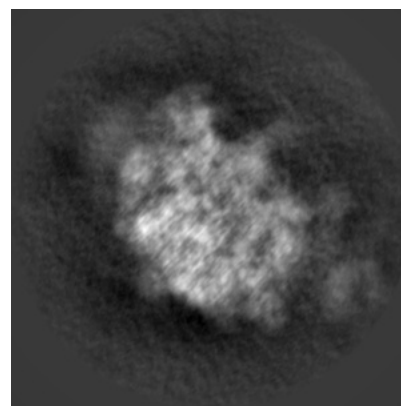
6.1.1 Primary map



X

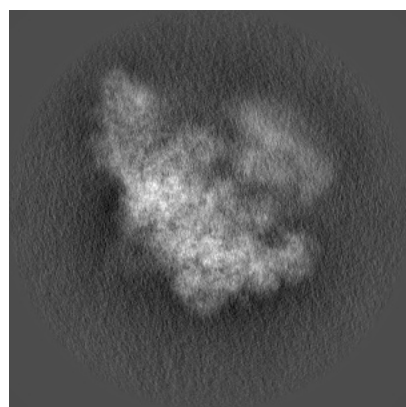


Y

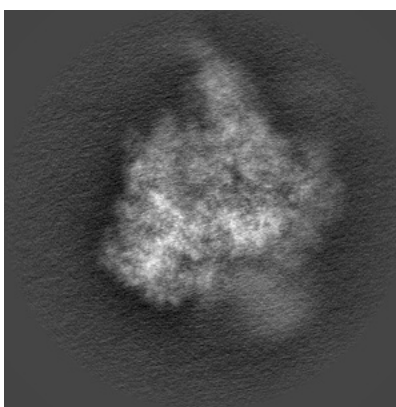


Z

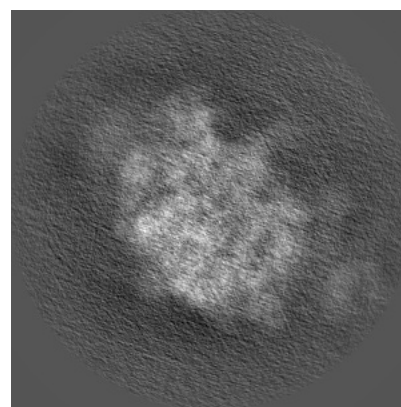
6.1.2 Raw map



X



Y

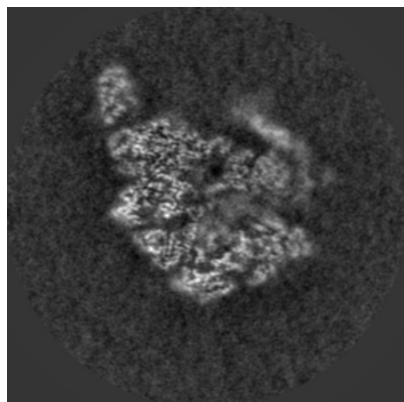


Z

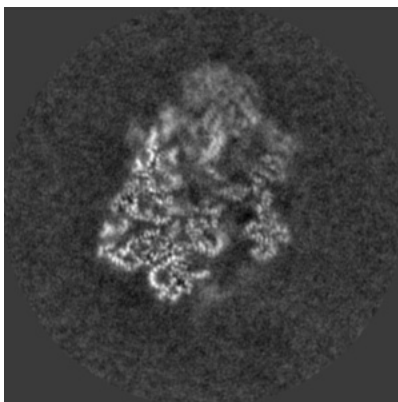
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

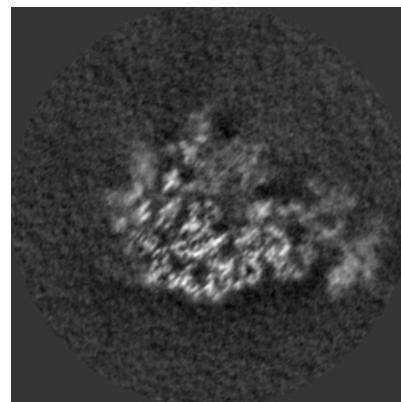
6.2.1 Primary map



X Index: 200

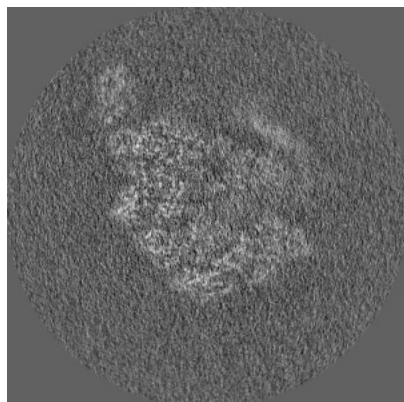


Y Index: 200

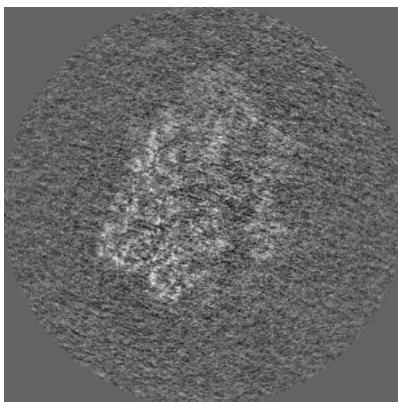


Z Index: 200

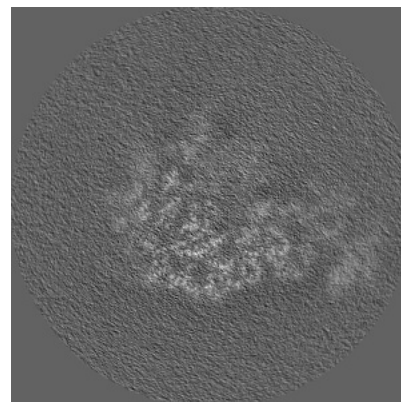
6.2.2 Raw map



X Index: 200



Y Index: 200

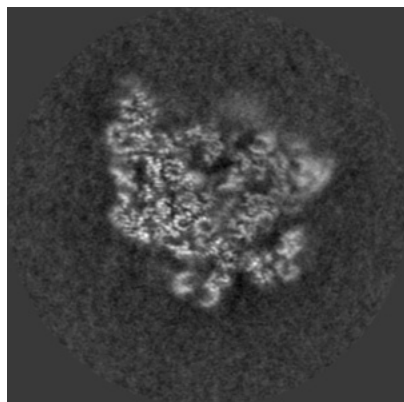


Z Index: 200

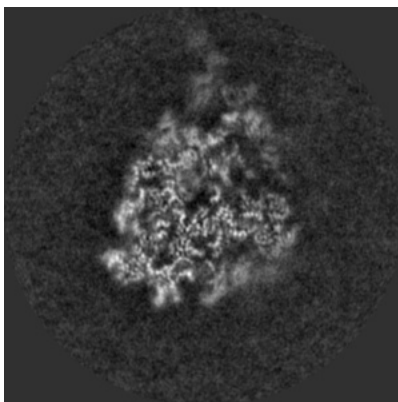
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

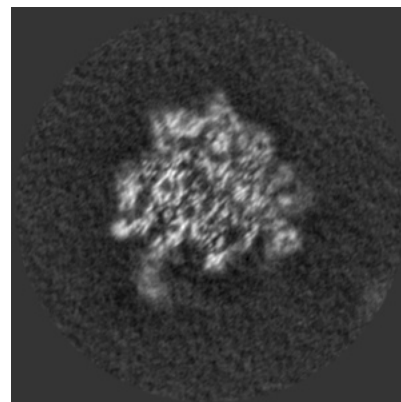
6.3.1 Primary map



X Index: 183

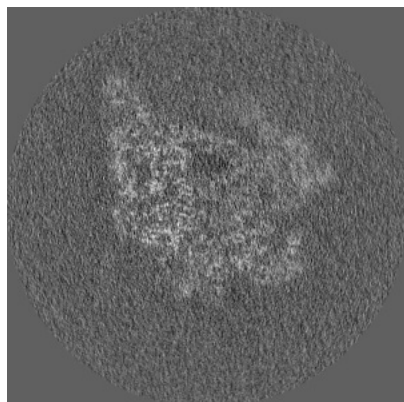


Y Index: 178

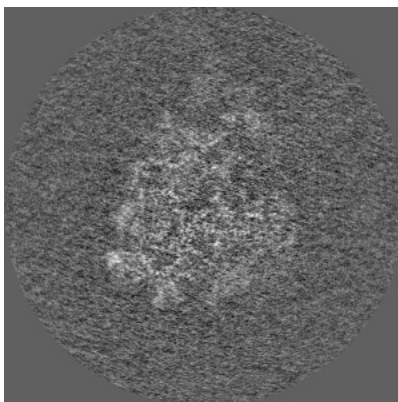


Z Index: 155

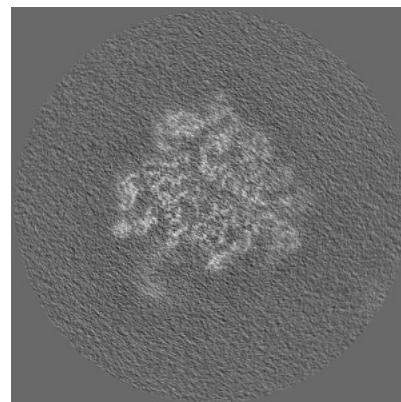
6.3.2 Raw map



X Index: 190



Y Index: 177

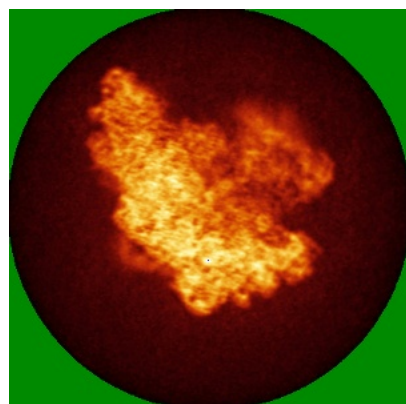


Z Index: 157

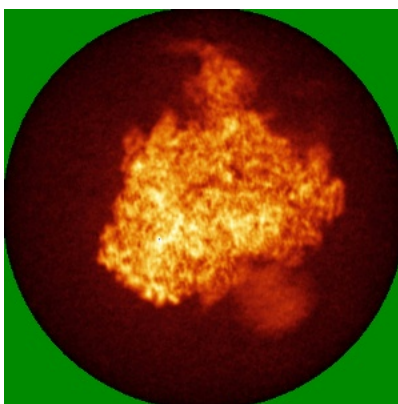
The images above show the largest variance slices of the map in three orthogonal directions.

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

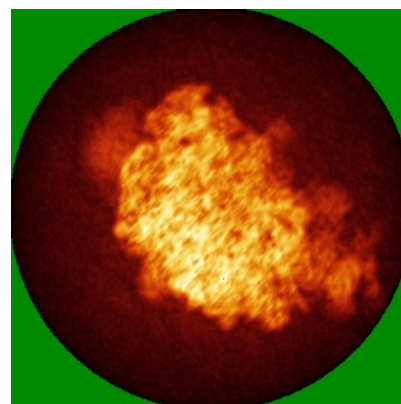
6.4.1 Primary map



X

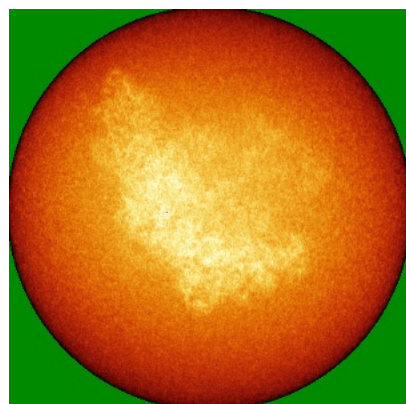


Y

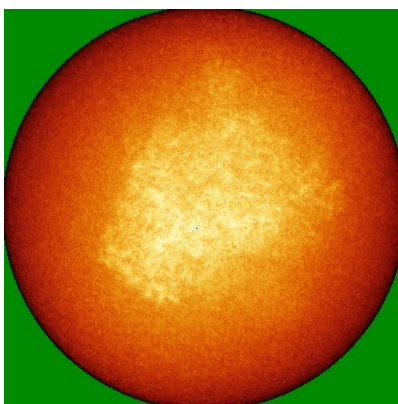


Z

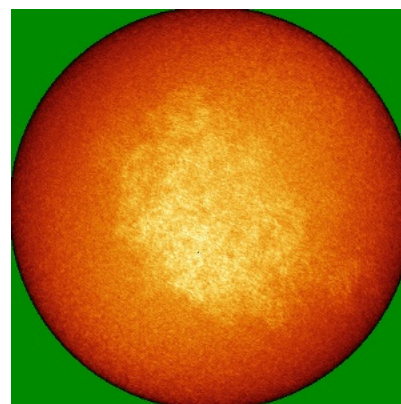
6.4.2 Raw map



X



Y

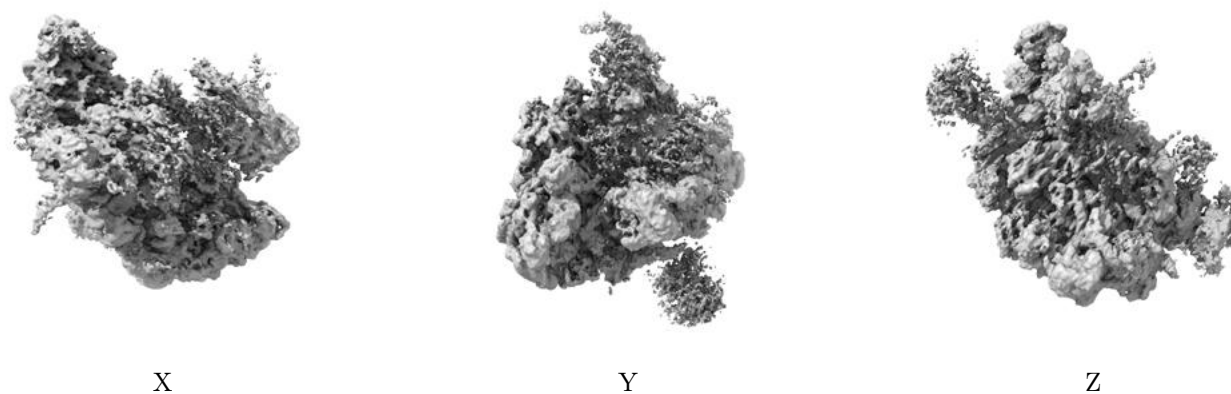


Z

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.

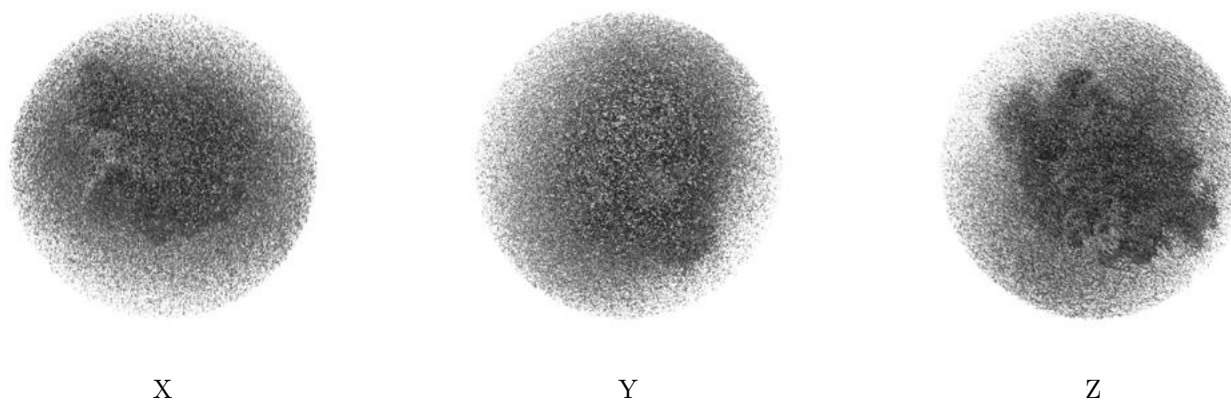
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.021. 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.

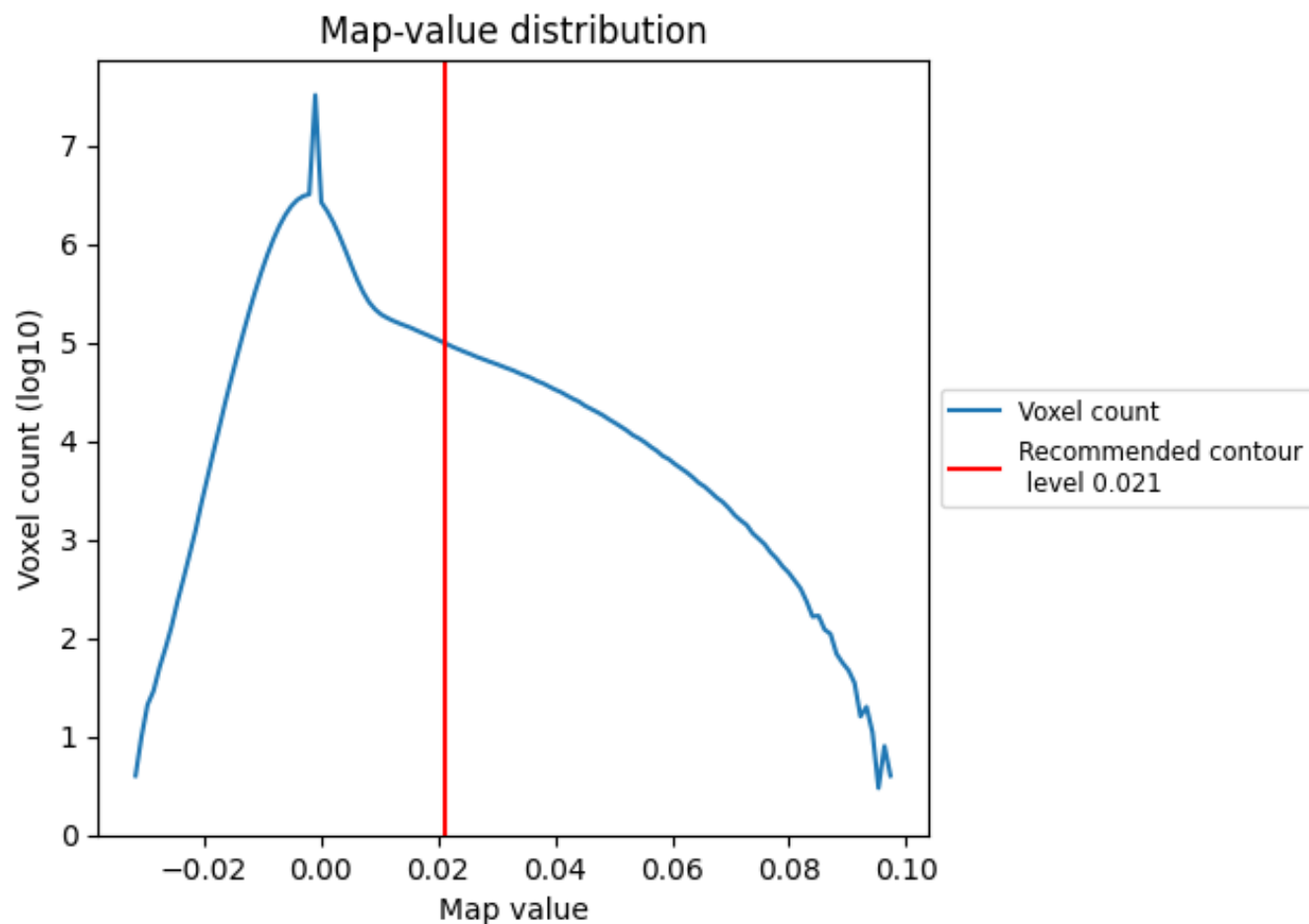
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

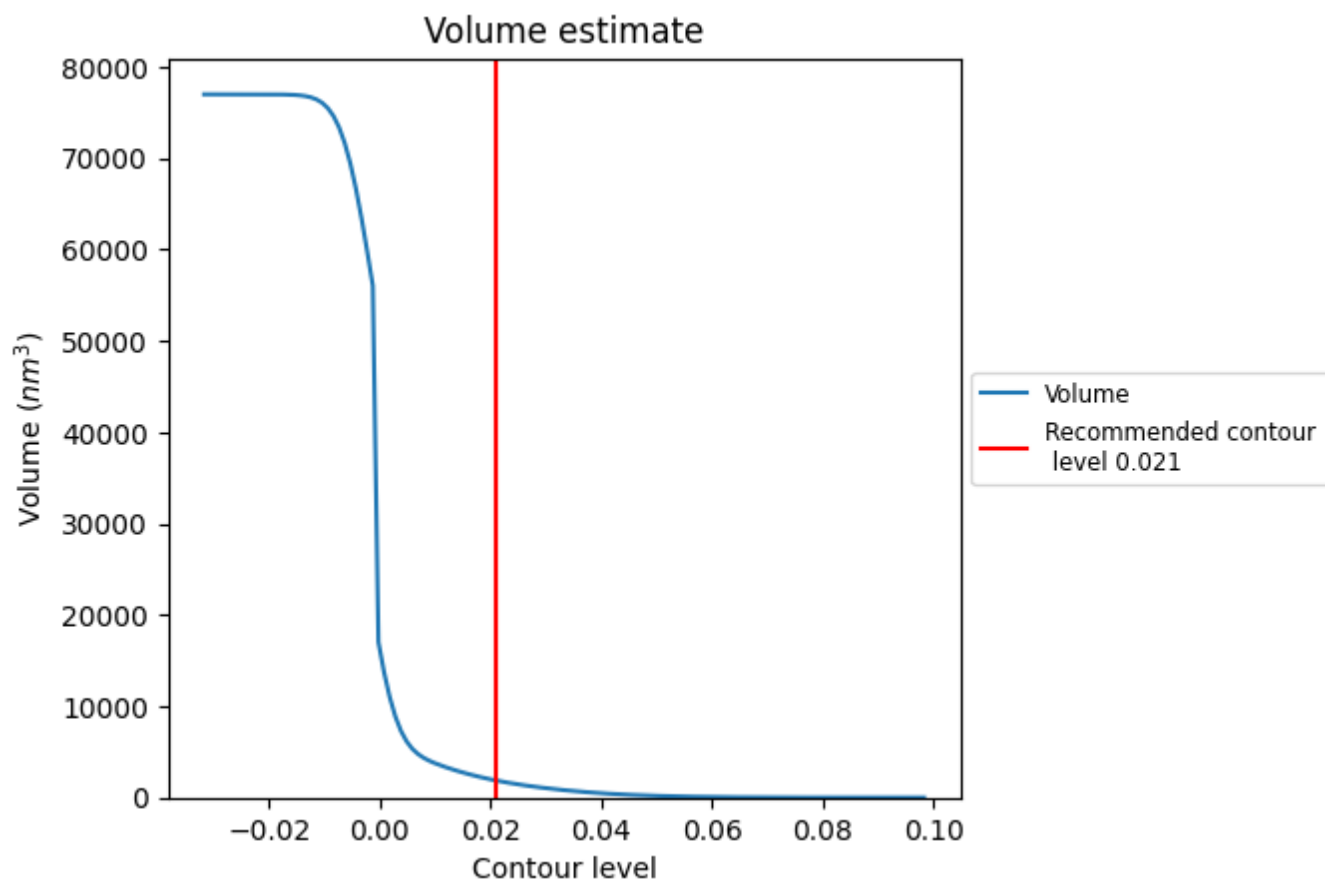
This section contains the results of statistical analysis of the map.

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.

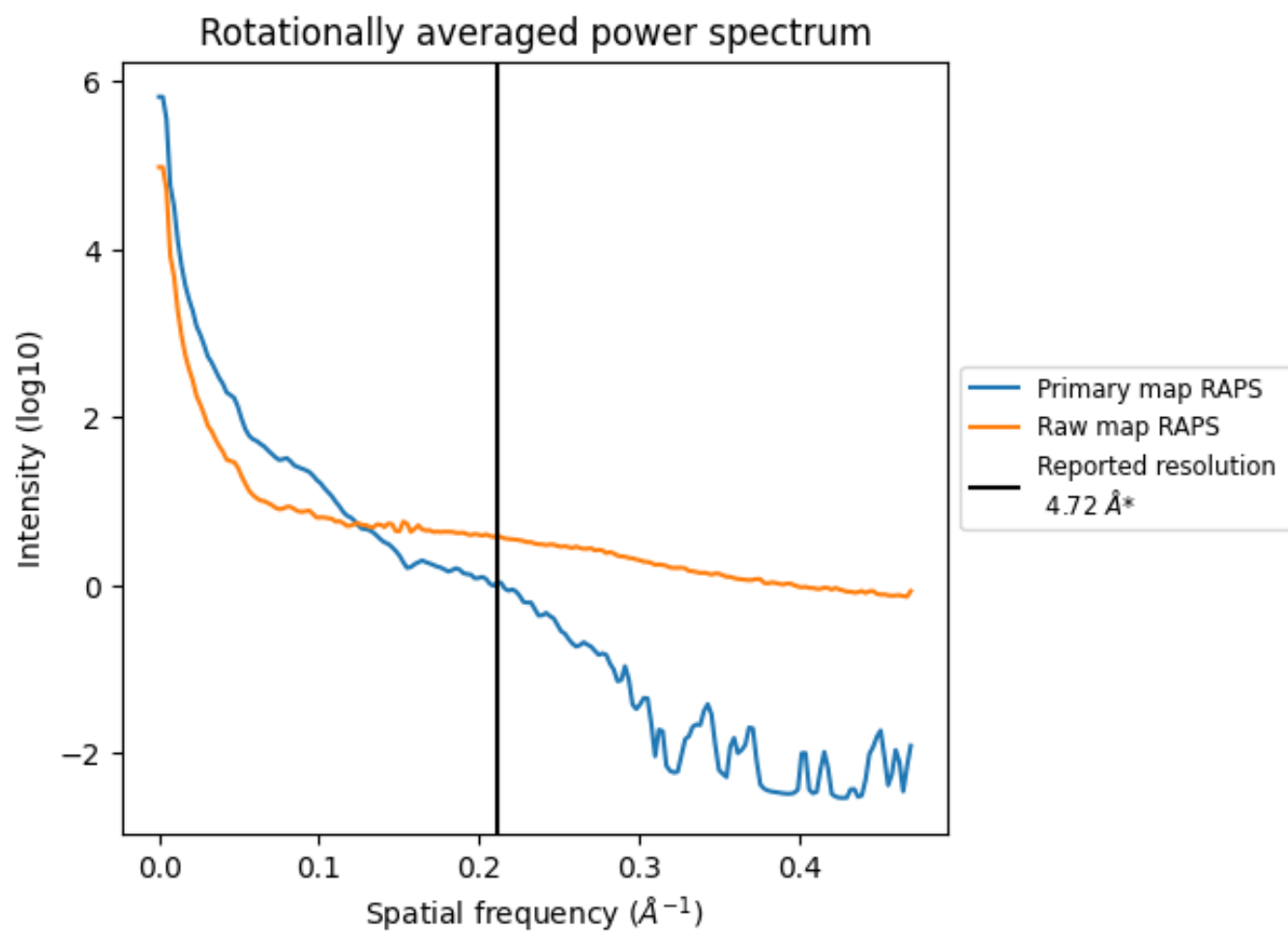
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1876 nm³; this corresponds to an approximate mass of 1695 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 ⓘ

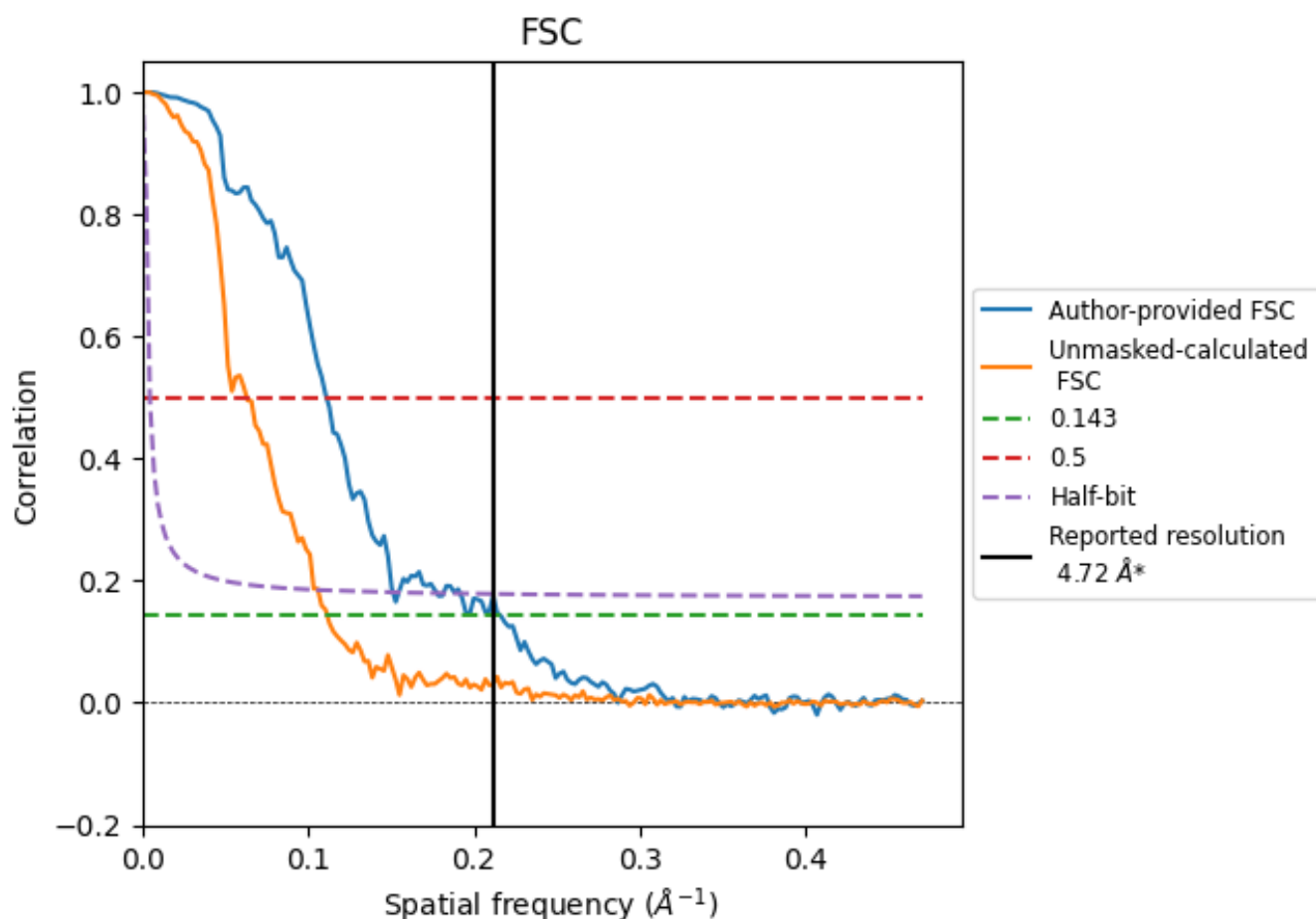


*Reported resolution corresponds to spatial frequency of 0.212 Å⁻¹

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 0.212 Å⁻¹

8.2 Resolution estimates [i](#)

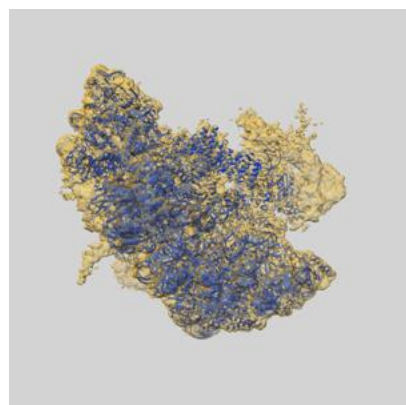
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.72	-	-
Author-provided FSC curve	4.64	9.00	6.61
Unmasked-calculated*	8.97	15.87	9.44

*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 8.97 differs from the reported value 4.72 by more than 10 %

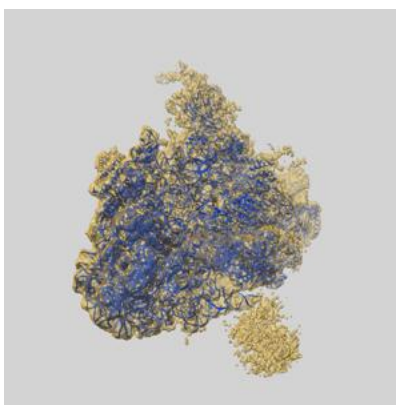
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12906 and PDB model 7OHR. Per-residue inclusion information can be found in section [3](#) on page [13](#).

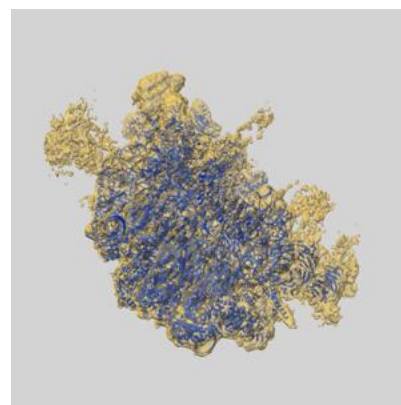
9.1 Map-model overlay [i](#)



X



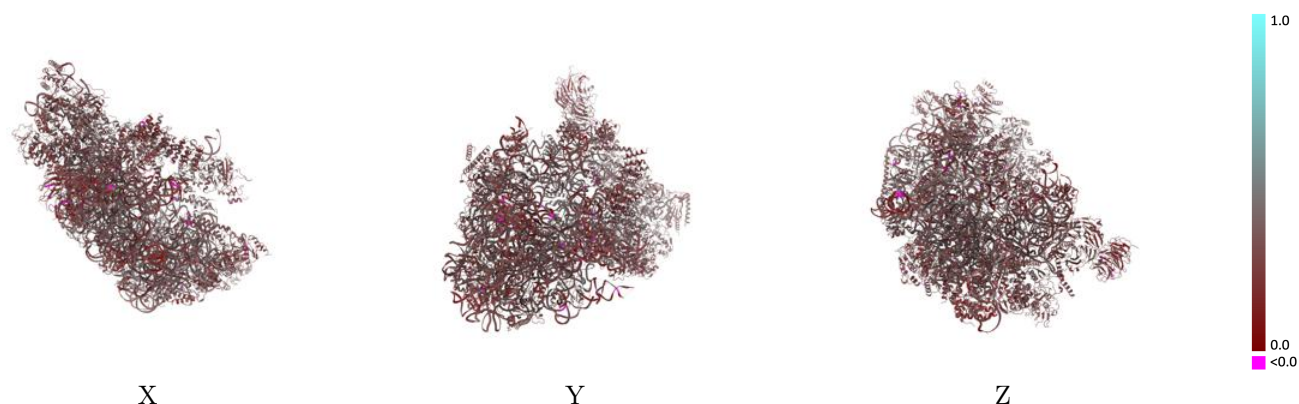
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.021 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](#)

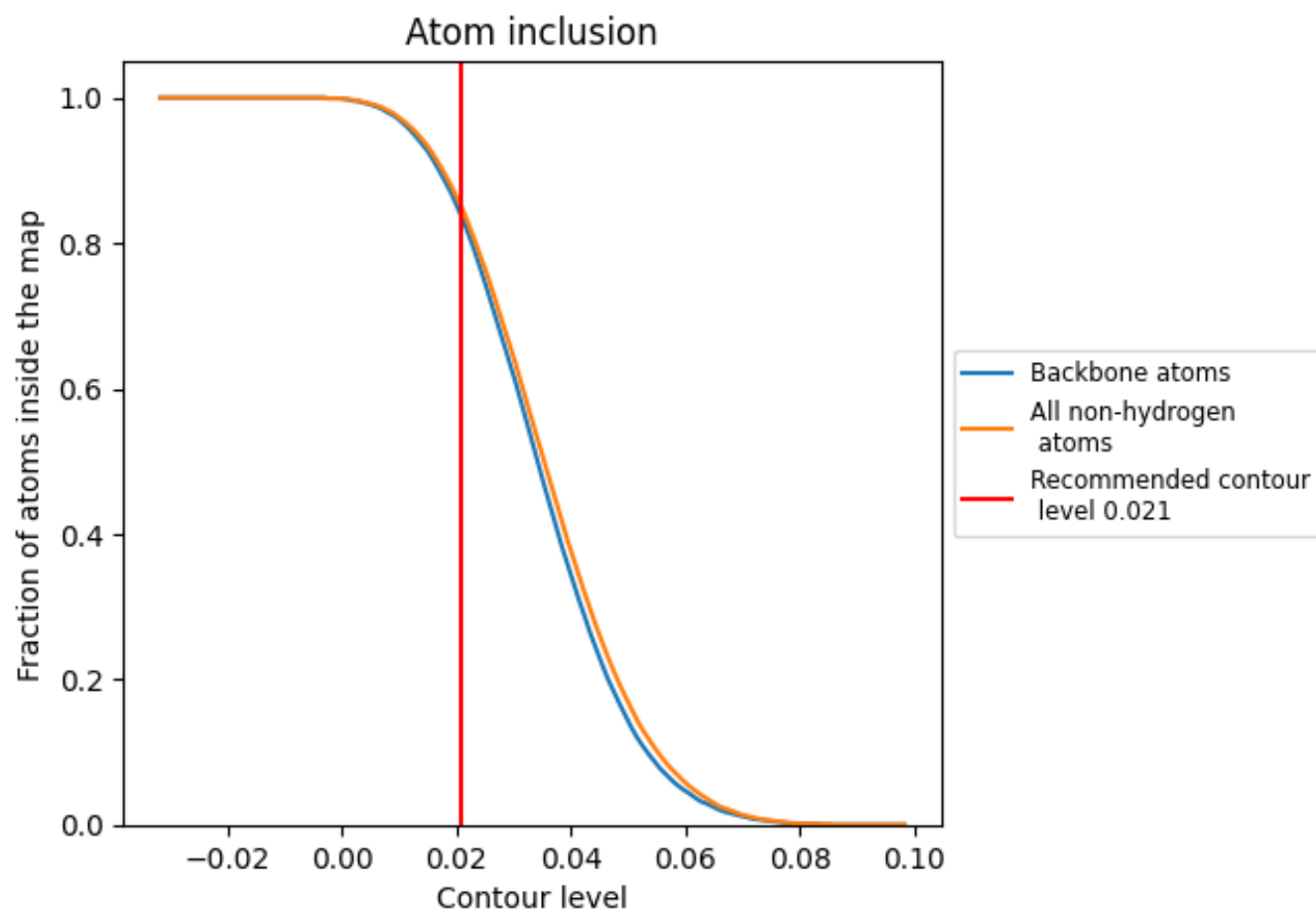


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 85% 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 (0.021) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8480	 0.3170
1	 0.9360	 0.3180
2	 0.9480	 0.3400
6	 0.9560	 0.3060
A	 0.7890	 0.3360
B	 0.8610	 0.3530
C	 0.8260	 0.3580
D	 0.6810	 0.2970
E	 0.8990	 0.3540
F	 0.8250	 0.3280
G	 0.7690	 0.3240
H	 0.8230	 0.3340
I	 0.3910	 0.2770
J	 0.7070	 0.2970
K	 0.8460	 0.2930
L	 0.7960	 0.3420
M	 0.8690	 0.3460
N	 0.7670	 0.3780
O	 0.8260	 0.3650
P	 0.7960	 0.3550
Q	 0.7990	 0.3460
R	 0.7430	 0.3200
S	 0.8190	 0.3260
U	 0.8480	 0.2680
V	 0.7710	 0.3330
W	 0.8810	 0.2720
X	 0.8120	 0.3570
Y	 0.8610	 0.3560
Z	 0.8530	 0.3000
b	 0.8010	 0.2710
c	 0.8180	 0.2790
d	 0.8120	 0.3470
e	 0.7790	 0.3730
f	 0.8470	 0.3800
g	 0.7430	 0.3140



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Chain	Atom inclusion	Q-score
h	 0.8190	 0.3520
i	 0.7750	 0.3550
j	 0.8010	 0.3740
k	 0.7250	 0.3070
l	 0.5750	 0.3030
m	 0.7940	 0.3030
n	 0.8480	 0.3270
o	 0.8710	 0.2930
p	 0.9240	 0.2240
q	 0.7000	 0.2640
r	 0.7150	 0.3110
s	 0.7290	 0.3340
t	 0.8410	 0.3010
u	 0.8870	 0.3110
v	 0.8100	 0.3250
w	 0.6230	 0.3050
y	 0.8600	 0.3110