



wwPDB EM Validation Summary Report ⓘ

Jul 3, 2024 – 11:22 am BST

PDB ID : 7OHX
EMDB ID : EMD-12912
Title : Nog1-TAP associated immature ribosomal particles from *S. cerevisiae* after rpL34 expression shut down, population A
Authors : Milkereit, P.; Poell, G.
Deposited on : 2021-05-11
Resolution : 3.30 Å(reported)
Based on initial model : 6EM1

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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

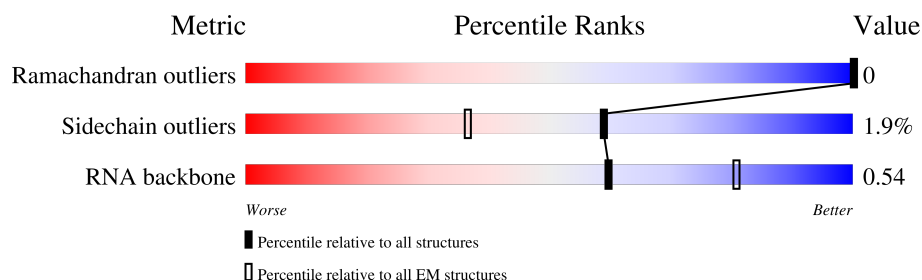
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.





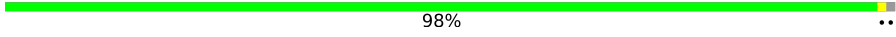


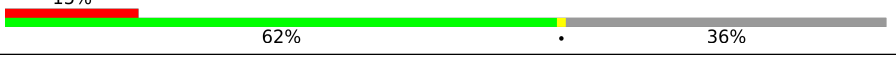

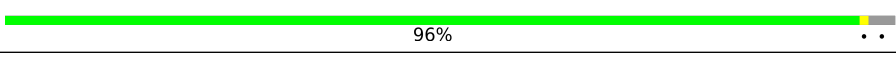
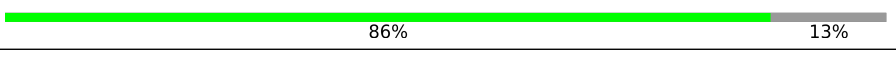
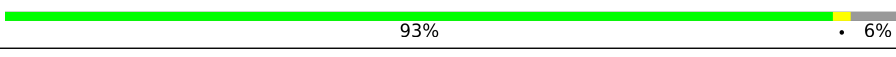

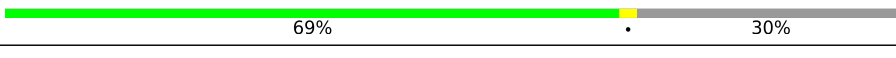
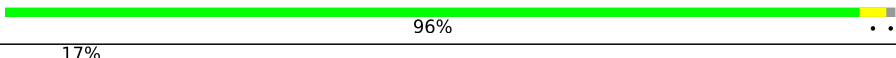
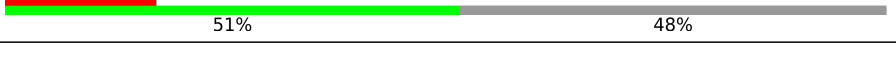
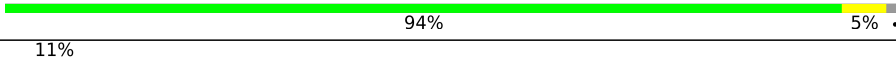

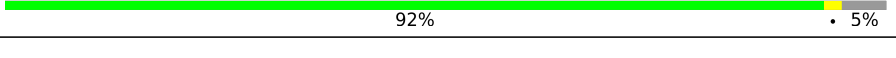
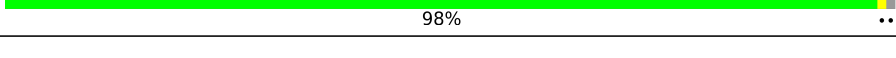
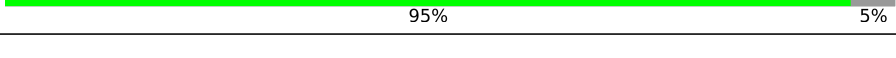

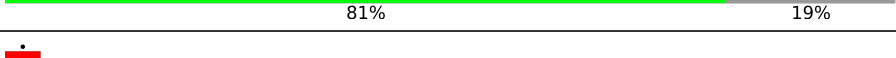


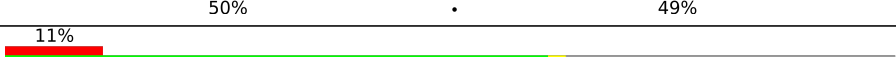

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	306	
4	4	278	
5	5	463	
6	6	232	
7	B	387	
8	C	362	




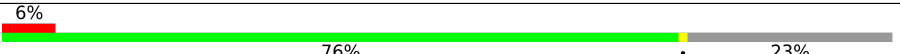
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Mol	Chain	Length	Quality of chain
9	D	505	
10	E	176	
11	F	244	
12	G	256	
13	H	191	
14	K	376	
15	L	199	
16	M	138	
17	N	204	
18	O	199	
19	P	184	
20	Q	186	
21	S	172	
22	W	236	
23	Y	127	
24	b	647	
25	e	130	
26	f	107	
27	h	120	
28	i	100	
29	j	88	
30	m	807	
31	n	605	
32	o	220	
33	t	322	

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Mol	Chain	Length	Quality of chain
34	u	199	
35	v	231	
36	x	295	
37	y	245	

2 Entry composition [i](#)

There are 38 unique types of molecules in this entry. The entry contains 157028 atoms, of which 70039 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	1561	Total	C	H	N	O	P	0	0
			50227	14926	16791	6056	10893	1561		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	2	148	Total	C	H	N	O	P	0	0
			4736	1407	1590	556	1035	148		

- Molecule 3 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	3	173	Total	C	H	N	O	S	0	0
			2908	901	1474	274	250	9		

- Molecule 4 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	4	217	Total	C	H	N	O	S	0	0
			3744	1208	1891	319	323	3		

- Molecule 5 is a protein called Ribosome biogenesis protein NSA1.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	5	385	Total	C	H	N	O	S	0	0
			6170	1957	3115	514	573	11		

- Molecule 6 is a RNA chain called ITS2.

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

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	B	315	Total	C	H	N	O	S	0	0
			5093	1593	2586	459	449	6		

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	C	343	Total	C	H	N	O	S	0	0
			5336	1643	2725	499	466	3		

- Molecule 9 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	D	424	Total	C	H	N	O	S	0	0
			6897	2179	3516	584	606	12		

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	E	151	Total	C	H	N	O	S	0	0
			2497	780	1292	215	209	1		

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	F	241	Total	C	H	N	O	S	0	0
			3969	1246	2033	351	338	1		

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	G	148	Total	C	H	N	O	S	0	0
			2345	736	1207	193	207	2		

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	H	123	Total	C	H	N	O	S	0	0
			2008	627	1026	174	178	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
14	K	239	Total	C	H	N	O	S	0	0
			3956	1250	2025	322	356	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
15	L	108	Total	C	H	N	O		0	0
			1782	541	918	180	143			

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

Mol	Chain	Residues	Atoms						AltConf	Trace
16	M	134	Total	C	H	N	O	S	0	0
			2179	668	1138	197	174	2		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
17	N	177	Total	C	H	N	O	S	0	0
			3079	948	1566	320	244	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
18	O	188	Total	C	H	N	O	S	0	0
			3080	962	1592	275	250	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
19	P	127	Total	C	H	N	O		0	0
			2014	626	1015	188	185			

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

Mol	Chain	Residues	Atoms						AltConf	Trace
20	Q	131	Total	C	H	N	O	S	0	0
			2101	645	1092	190	173	1		

- Molecule 21 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	S	170	Total	C	H	N	O	S	0	0
			2904	922	1472	265	242	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
22	W	122	Total	C	H	N	O	S	0	0
			2075	655	1050	184	184	2		

- Molecule 23 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	Y	125	Total	C	H	N	O	S	0	0
			2060	620	1076	191	173			

- Molecule 24 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	b	248	Total	C	H	N	O	S	0	0
			4030	1295	2016	333	374	12		

- Molecule 25 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	e	123	Total	C	H	N	O	S	0	0
			2057	630	1063	201	162	1		

- Molecule 26 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 27 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	h	114	Total	C	H	N	O	S	0	0
			1969	592	1038	178	160	1		

- Molecule 28 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	i	24	Total	C	H	N	O	0	0
			413	125	213	41	34		

- Molecule 29 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	j	71	Total	C	H	N	O	S	0	0
			1137	344	571	123	94	5		

- Molecule 30 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	m	106	Total	C	H	N	O	S	0	0
			1790	577	894	151	165	3		

- Molecule 31 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	n	243	Total	C	H	N	O	S	0	0
			4111	1341	2074	343	347	6		

- Molecule 32 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	o	112	Total	C	H	N	O	S	0	0
			1901	601	966	168	162	4		

- Molecule 33 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	t	202	Total	C	H	N	O	S	0	0
			3287	1018	1695	282	289	3		

- Molecule 34 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	u	100	Total	C	H	N	O	S	0	0
			1729	536	880	172	132	9		

- Molecule 35 is a protein called Nucleolar protein 16.

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

- Molecule 36 is a protein called Ribosome production factor 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	x	267	Total	C	H	N	O	S	0	0
			4573	1444	2305	413	407	4		

- Molecule 37 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	y	189	Total	C	H	N	O	S	0	0
			2854	889	1426	248	284	7		

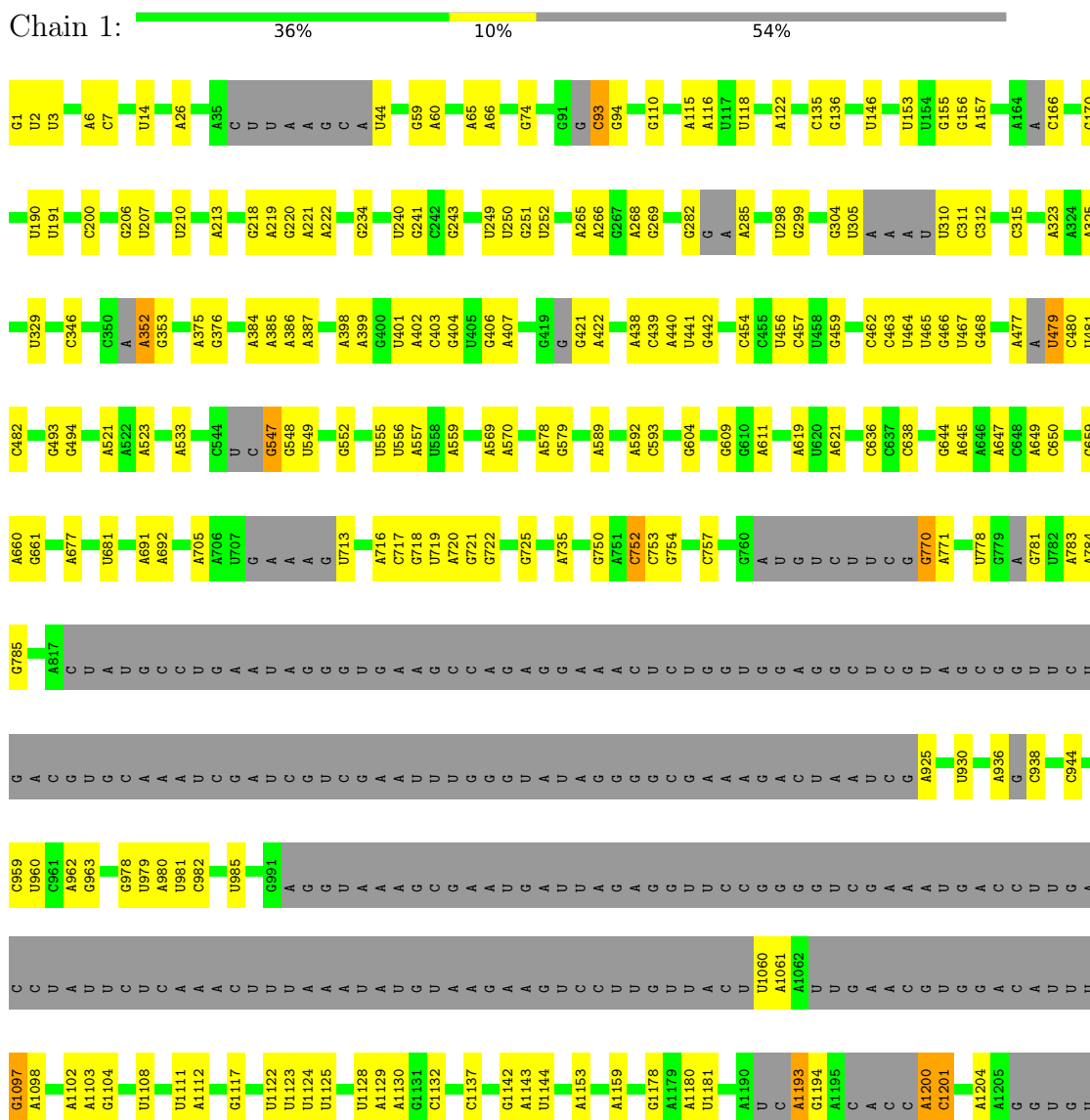
- Molecule 38 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
38	j	1	Total	Zn	0
			1	1	
38	u	1	Total	Zn	0
			1	1	

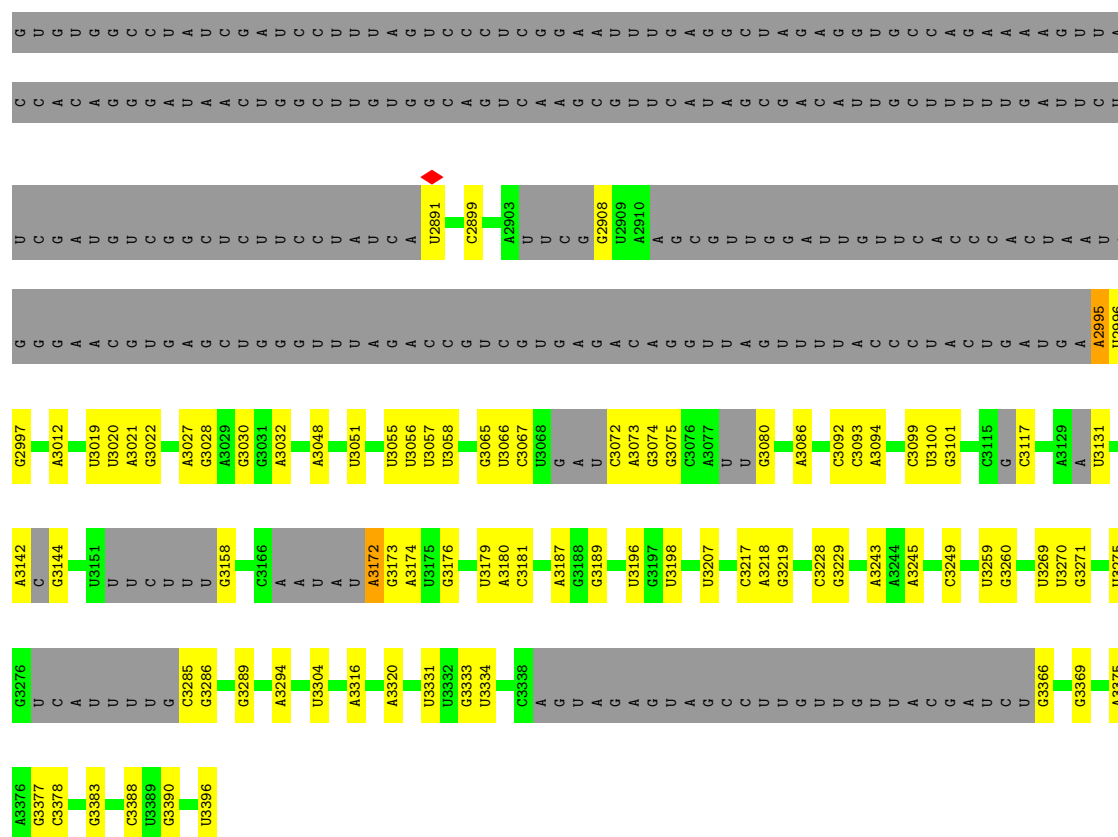
3 Residue-property plots

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

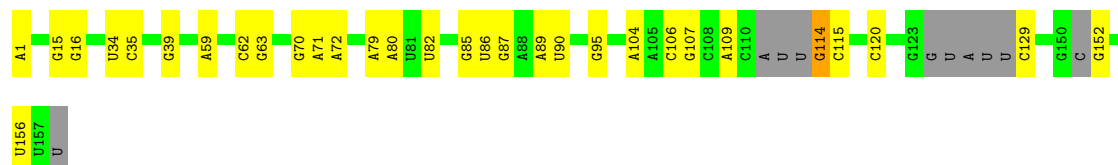






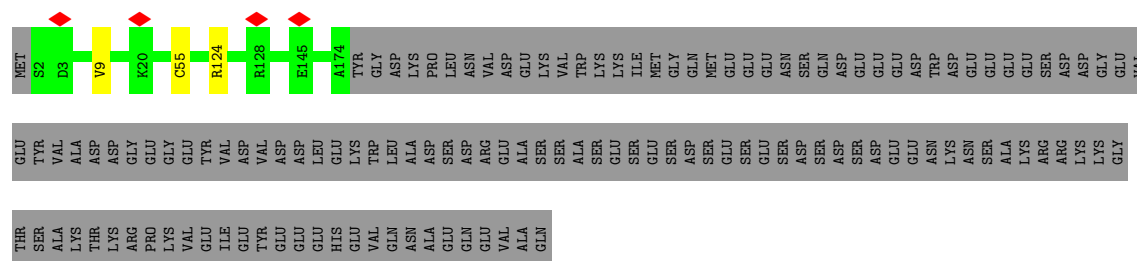
• Molecule 2: 5.8S rRNA

Chain 2: 74% 19% 6%



• Molecule 3: Protein MAK16

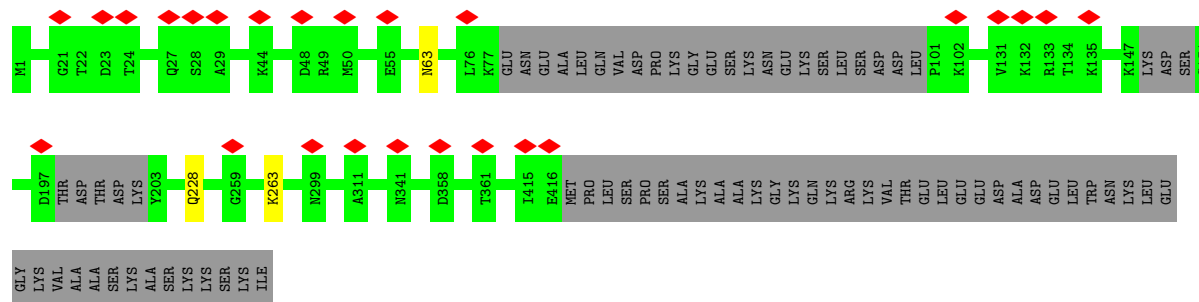
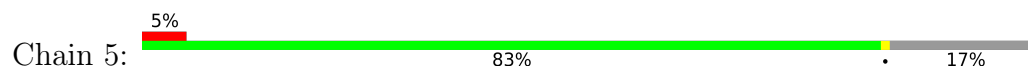
Chain 3: 56% 43% 1%



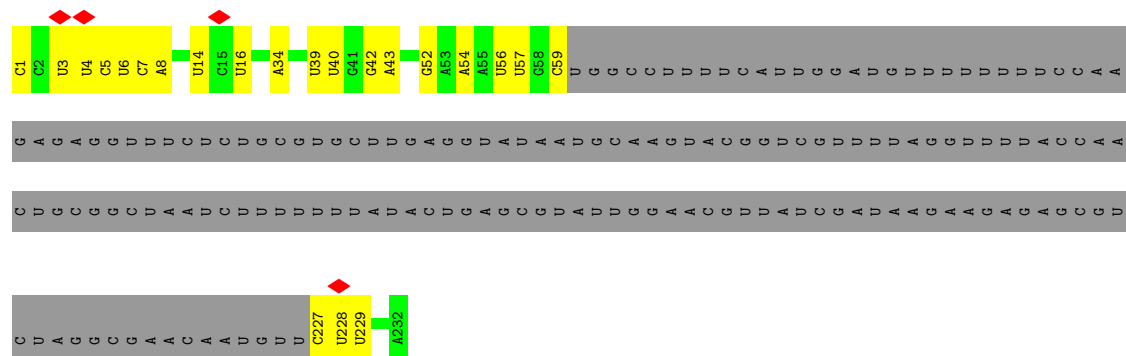
• Molecule 4: Ribosomal RNA-processing protein 1

Chain 4: 76% 22% 2%

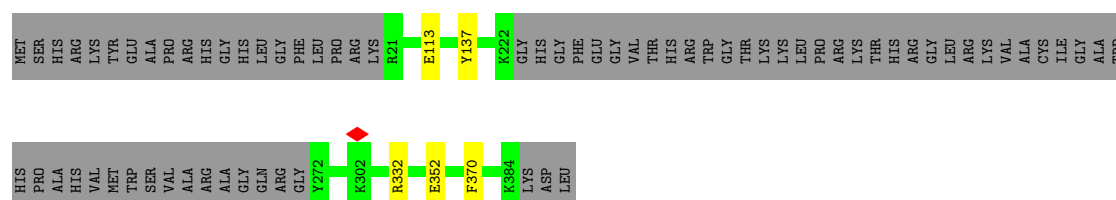
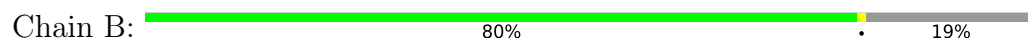
- Molecule 5: Ribosome biogenesis protein NSA1



- Molecule 6: ITS2

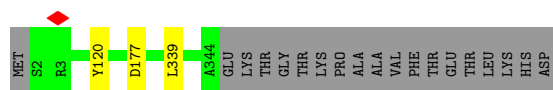


- Molecule 7: 60S ribosomal protein L3



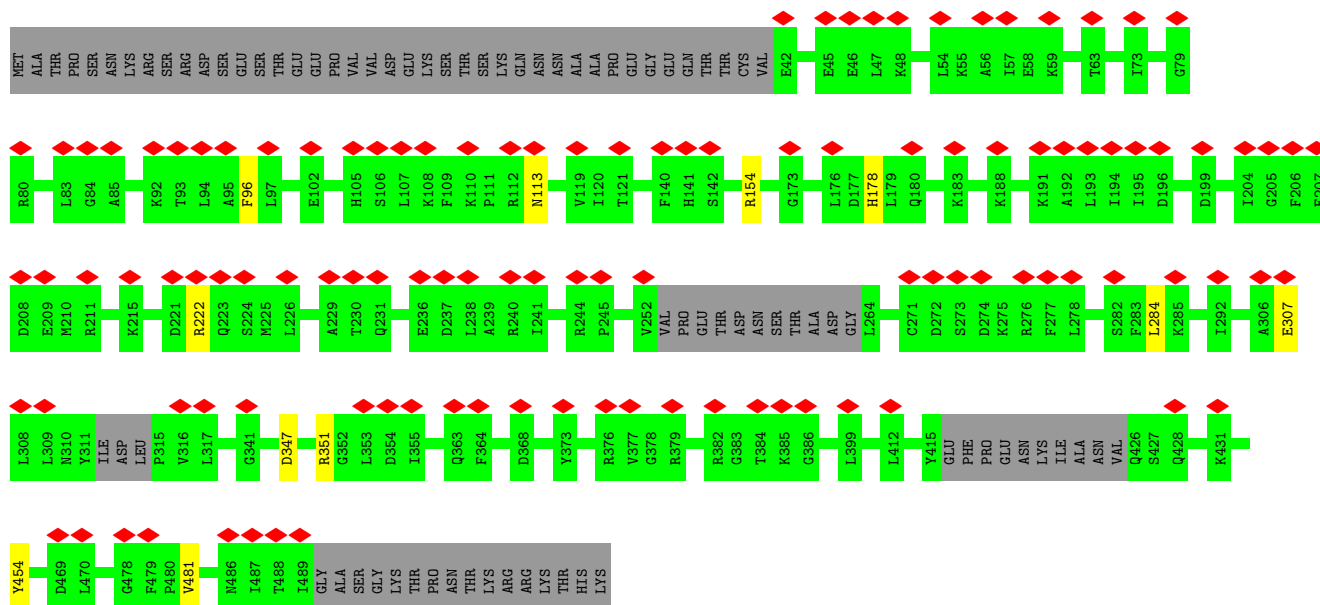
- Molecule 8: 60S ribosomal protein L4-A





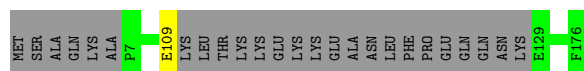
- Molecule 9: ATP-dependent RNA helicase HAS1

Chain D: 22% 82% 16%



- Molecule 10: 60S ribosomal protein L6-A

Chain E: 85% 14%



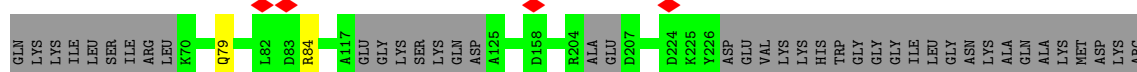
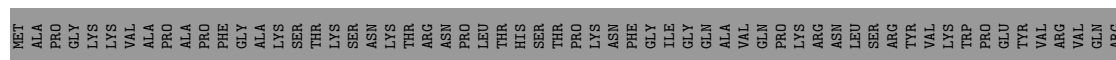
- Molecule 11: 60S ribosomal protein L7-A


Chain F: 98% ..

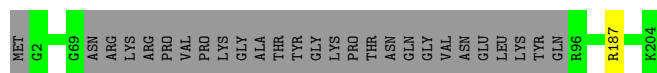


- Molecule 12: 60S ribosomal protein L8-A

Chain G: 57% 42%

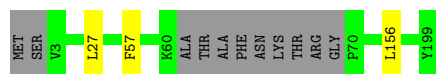


Chain N:  86% 13%



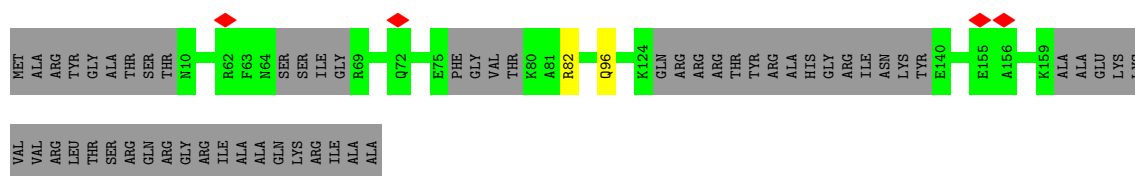
- Molecule 18: 60S ribosomal protein L16-A

Chain O:  93% 6%



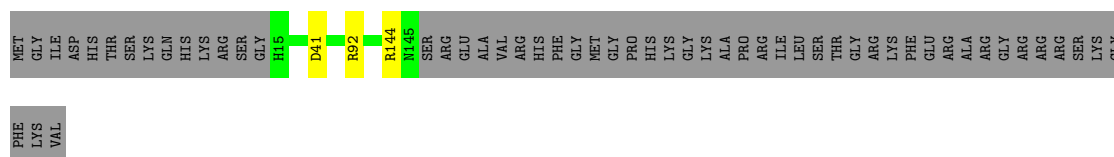
- Molecule 19: 60S ribosomal protein L17-A

Chain P:  68% 31%



- Molecule 20: 60S ribosomal protein L18-A

Chain Q:  69% 30%



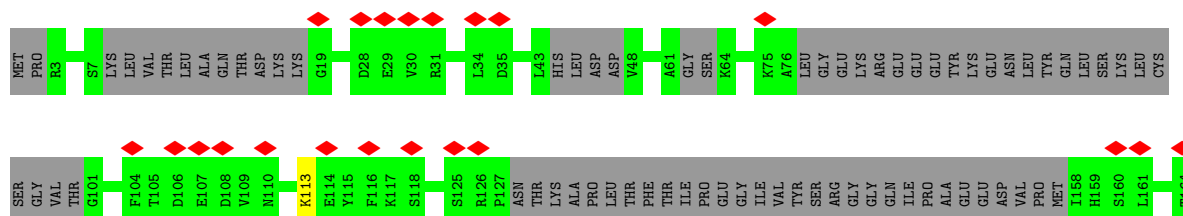
- Molecule 21: 60S ribosomal protein L20-A

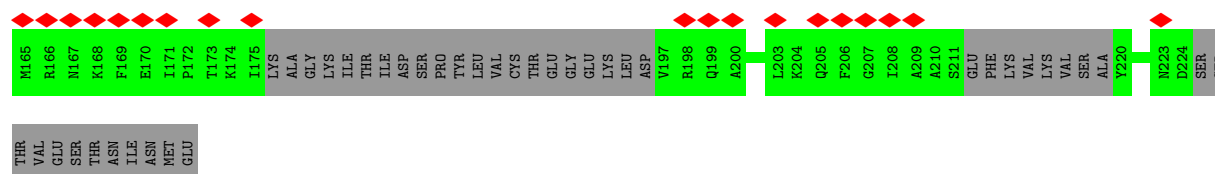
Chain S:  96%



- Molecule 22: Ribosome assembly factor MRT4

Chain W:  17% 51% 48%





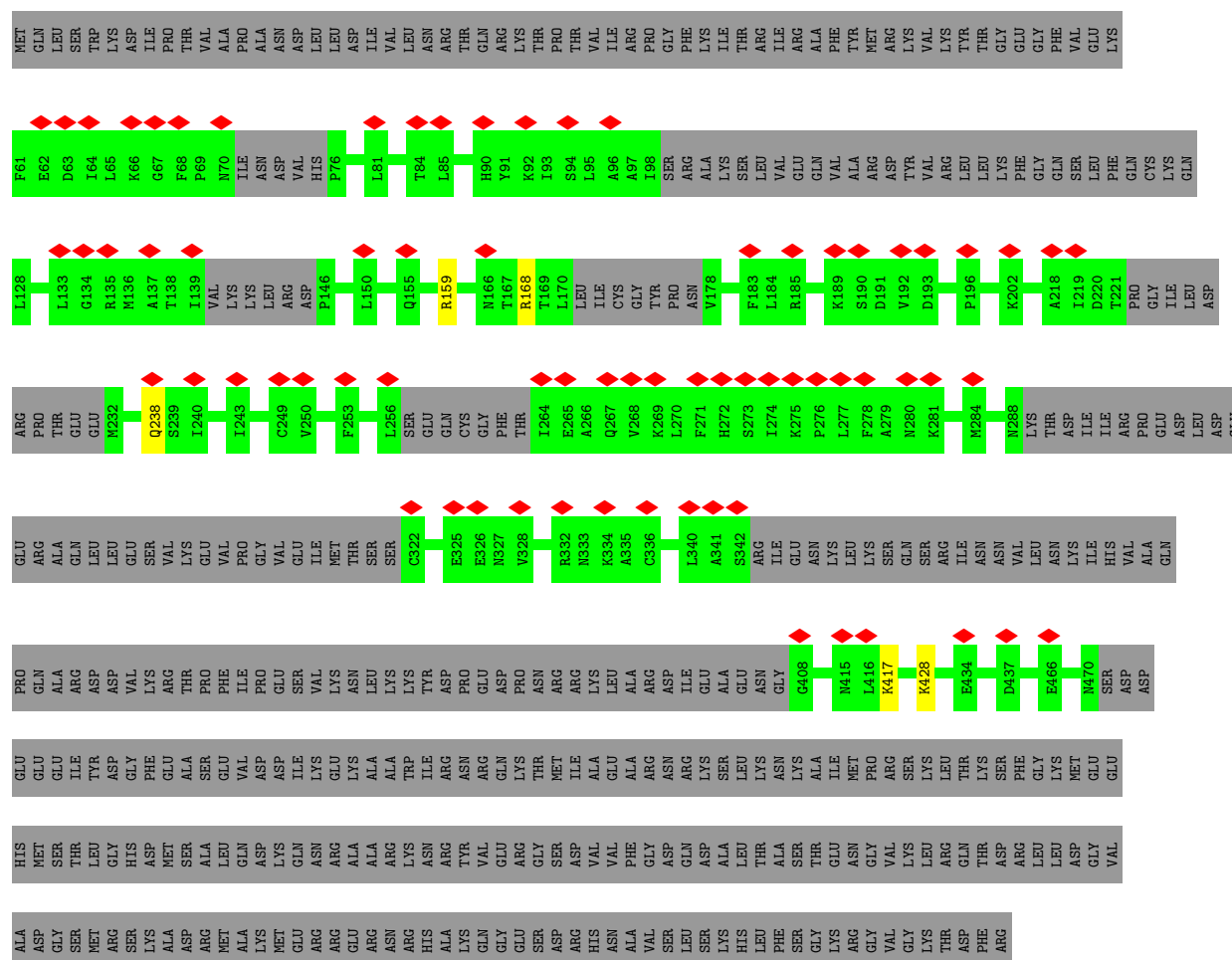
- Molecule 23: 60S ribosomal protein L26-A

Chain Y: 94% 5%



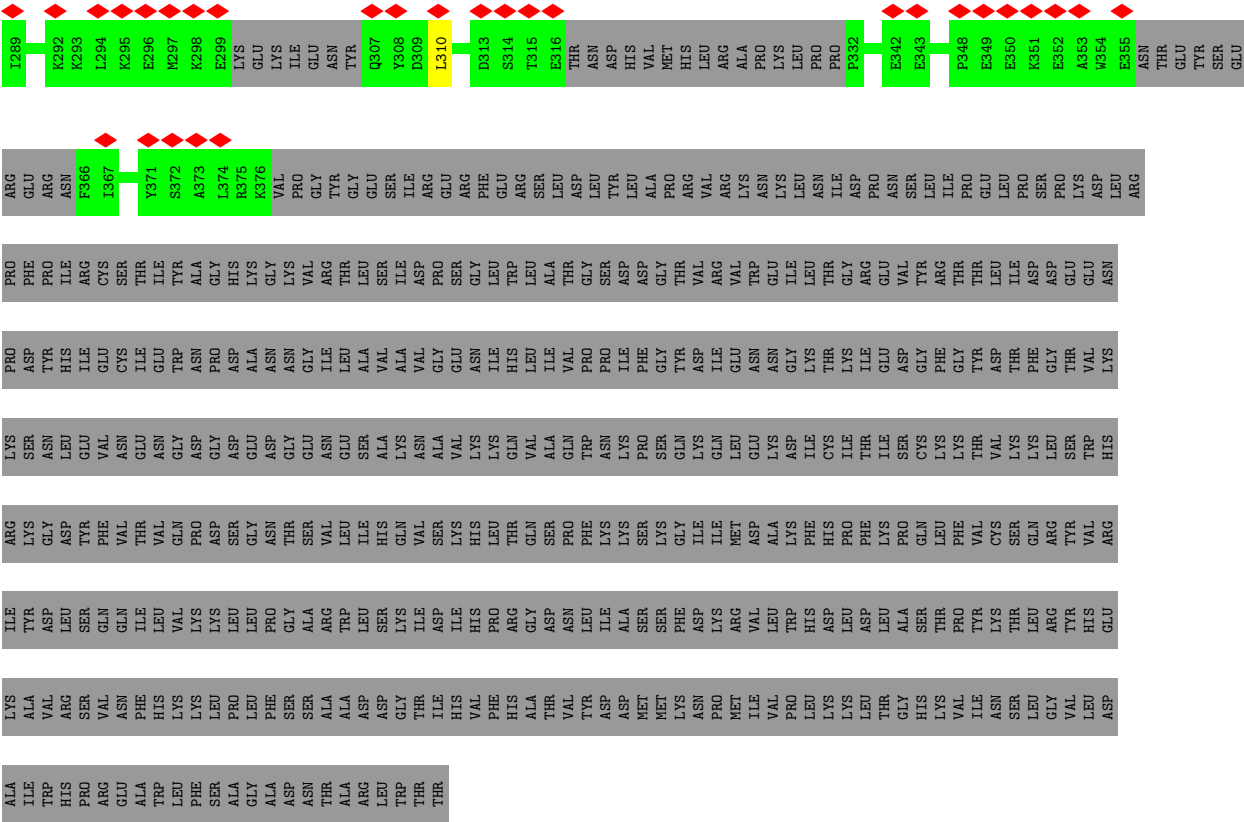
- Molecule 24: Nucleolar GTP-binding protein 1

Chain b: 11% 38% 62%

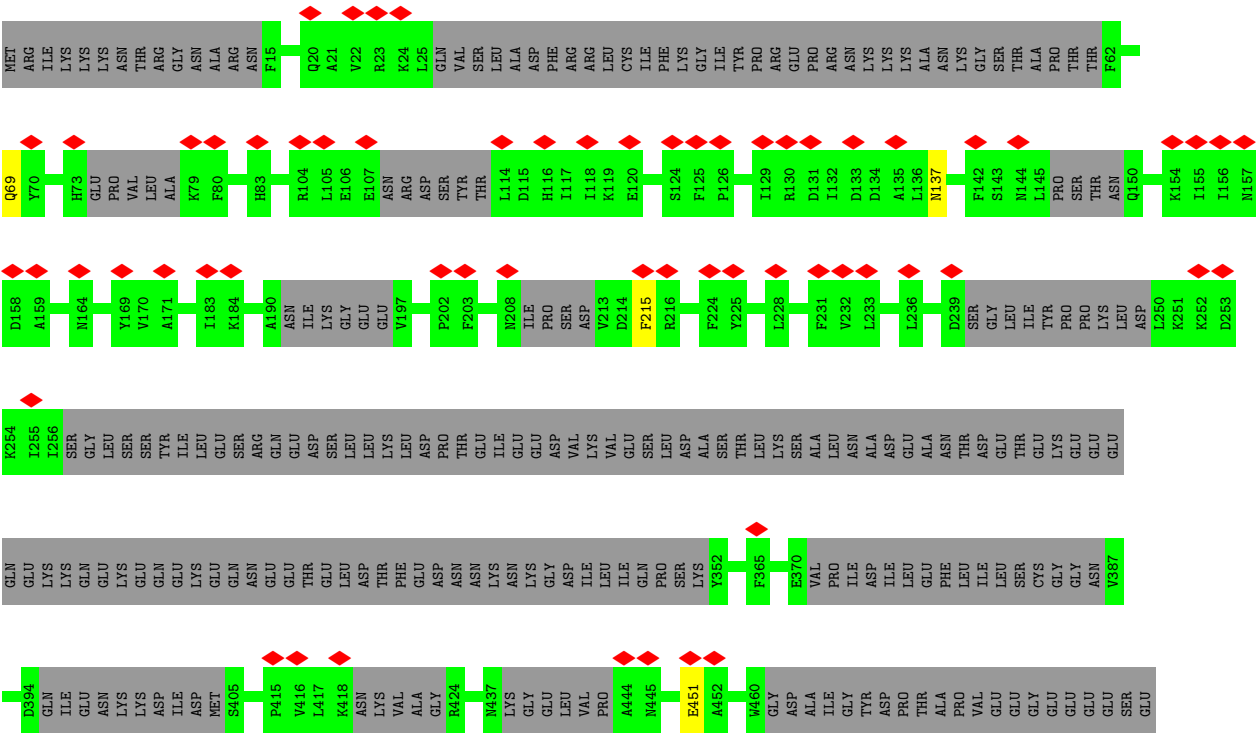


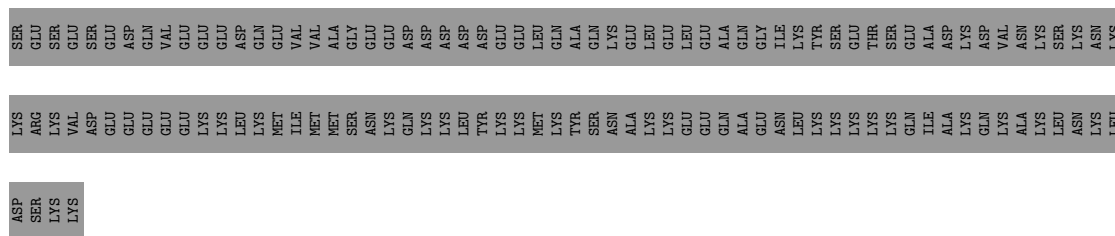
- Molecule 25: 60S ribosomal protein L32

Chain e: 92% 5%

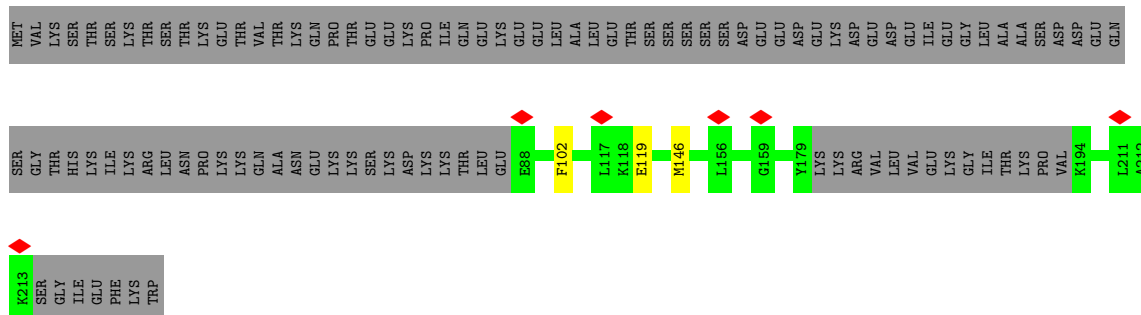


• Molecule 31: Pescadillo homolog

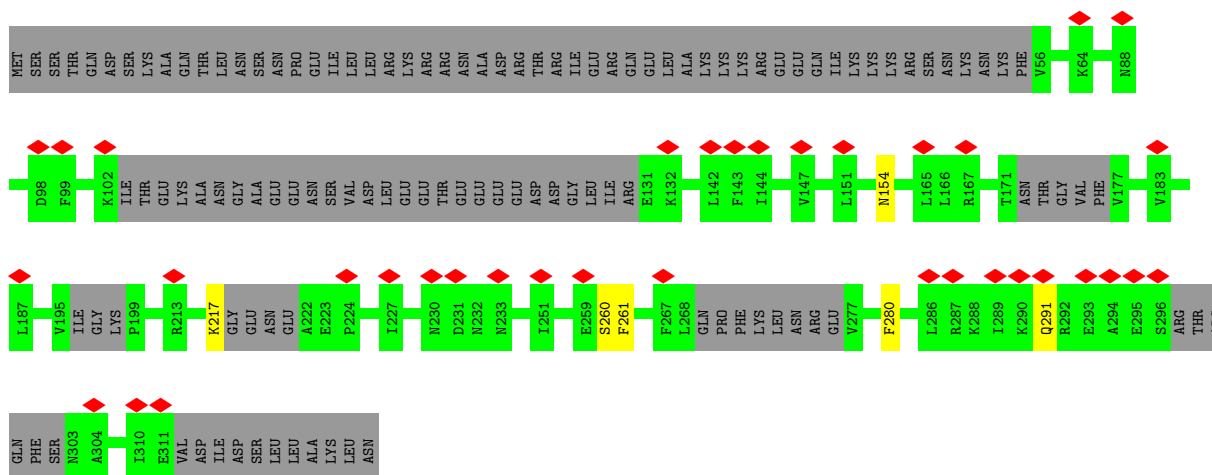




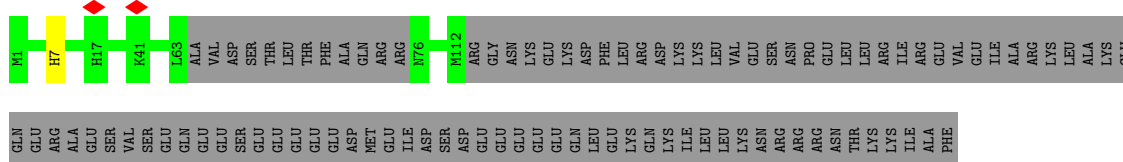
- Molecule 32: Ribosome biogenesis protein 15



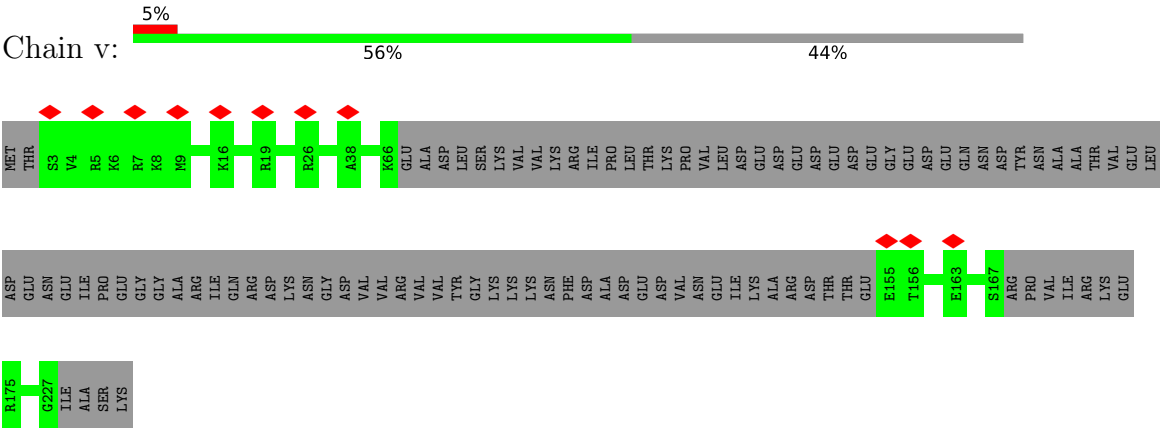
- Molecule 33: Ribosome biogenesis protein RLP7



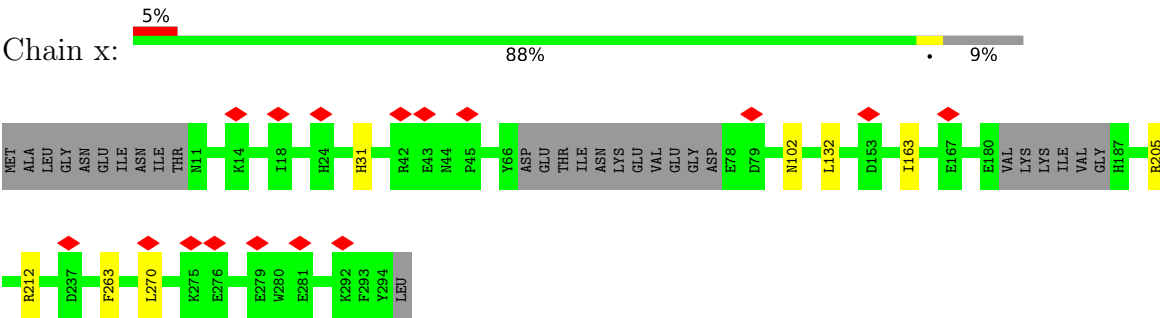
- Molecule 34: Ribosome biogenesis protein RLP24



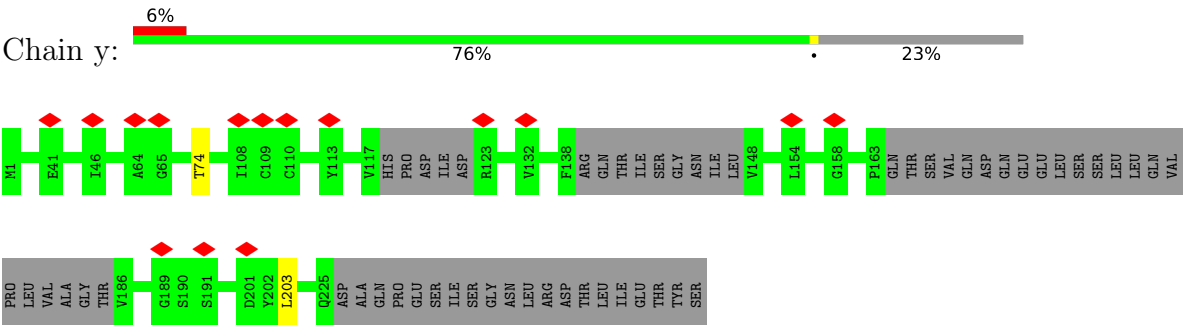
- Molecule 35: Nucleolar protein 16



• Molecule 36: Ribosome production factor 1



• Molecule 37: 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	76751	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 ($e^-/\text{\AA}^2$)	88	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	0.115	Depositor
Minimum map value	-0.045	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.014	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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.15	0/37394	0.74	44/58219 (0.1%)
2	2	0.16	0/3513	0.76	5/5463 (0.1%)
3	3	0.23	0/1461	0.38	0/1958
4	4	0.24	0/1895	0.37	0/2549
5	5	0.24	0/3109	0.42	0/4187
6	6	0.16	0/1527	0.76	2/2371 (0.1%)
7	B	0.24	0/2556	0.43	0/3437
8	C	0.24	0/2660	0.41	0/3601
9	D	0.24	0/3443	0.40	0/4636
10	E	0.24	0/1226	0.40	0/1648
11	F	0.25	0/1974	0.38	0/2654
12	G	0.25	0/1155	0.41	0/1563
13	H	0.23	0/992	0.40	0/1328
14	K	0.24	0/1963	0.40	0/2647
15	L	0.24	0/877	0.40	0/1179
16	M	0.24	0/1056	0.39	0/1421
17	N	0.23	0/1544	0.40	0/2065
18	O	0.24	0/1516	0.40	0/2033
19	P	0.24	0/1014	0.38	0/1362
20	Q	0.24	0/1024	0.42	0/1385
21	S	0.24	0/1468	0.41	0/1973
22	W	0.23	0/1038	0.39	0/1385
23	Y	0.24	0/995	0.41	0/1329
24	b	0.24	0/2047	0.38	0/2749
25	e	0.23	0/1014	0.41	0/1356
26	f	0.25	0/868	0.41	0/1168
27	h	0.24	0/938	0.38	0/1245
28	i	0.26	0/202	0.39	0/269
29	j	0.24	0/578	0.41	0/767
30	m	0.23	0/920	0.37	0/1239
31	n	0.24	0/2081	0.36	0/2796
32	o	0.24	0/952	0.39	0/1264

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	t	0.24	0/1608	0.39	0/2157
34	u	0.25	0/867	0.39	0/1150
35	v	0.23	0/1100	0.37	0/1456
36	x	0.24	0/2313	0.41	0/3100
37	y	0.23	0/1443	0.44	0/1956
All	All	0.20	0/92331	0.60	51/133065 (0.0%)

There are no bond length outliers.

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	3285	C	OP1-P-OP2	-6.90	109.25	119.60
1	1	1280	C	OP1-P-OP2	-6.82	109.37	119.60
1	1	2378	C	OP1-P-OP2	-6.82	109.37	119.60
1	1	1234	G	OP1-P-OP2	-6.82	109.38	119.60
1	1	1060	U	OP1-P-OP2	-6.81	109.38	119.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
3	3	171/306 (56%)	160 (94%)	11 (6%)	0	100	100
4	4	209/278 (75%)	185 (88%)	24 (12%)	0	100	100
5	5	377/463 (81%)	363 (96%)	14 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	B	311/387 (80%)	296 (95%)	15 (5%)	0	100	100
8	C	341/362 (94%)	327 (96%)	14 (4%)	0	100	100
9	D	416/505 (82%)	405 (97%)	11 (3%)	0	100	100
10	E	147/176 (84%)	143 (97%)	4 (3%)	0	100	100
11	F	239/244 (98%)	234 (98%)	5 (2%)	0	100	100
12	G	142/256 (56%)	137 (96%)	5 (4%)	0	100	100
13	H	113/191 (59%)	105 (93%)	8 (7%)	0	100	100
14	K	233/376 (62%)	226 (97%)	7 (3%)	0	100	100
15	L	106/199 (53%)	101 (95%)	5 (5%)	0	100	100
16	M	132/138 (96%)	129 (98%)	3 (2%)	0	100	100
17	N	173/204 (85%)	169 (98%)	4 (2%)	0	100	100
18	O	184/199 (92%)	180 (98%)	4 (2%)	0	100	100
19	P	119/184 (65%)	116 (98%)	3 (2%)	0	100	100
20	Q	129/186 (69%)	129 (100%)	0	0	100	100
21	S	168/172 (98%)	159 (95%)	9 (5%)	0	100	100
22	W	106/236 (45%)	106 (100%)	0	0	100	100
23	Y	123/127 (97%)	121 (98%)	2 (2%)	0	100	100
24	b	230/647 (36%)	222 (96%)	8 (4%)	0	100	100
25	e	121/130 (93%)	121 (100%)	0	0	100	100
26	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
27	h	110/120 (92%)	101 (92%)	9 (8%)	0	100	100
28	i	22/100 (22%)	22 (100%)	0	0	100	100
29	j	69/88 (78%)	68 (99%)	1 (1%)	0	100	100
30	m	98/807 (12%)	95 (97%)	3 (3%)	0	100	100
31	n	217/605 (36%)	215 (99%)	2 (1%)	0	100	100
32	o	108/220 (49%)	107 (99%)	1 (1%)	0	100	100
33	t	188/322 (58%)	178 (95%)	10 (5%)	0	100	100
34	u	96/199 (48%)	91 (95%)	5 (5%)	0	100	100
35	v	124/231 (54%)	121 (98%)	3 (2%)	0	100	100
36	x	261/295 (88%)	244 (94%)	17 (6%)	0	100	100
37	y	181/245 (74%)	179 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	5868/9305 (63%)	5653 (96%)	215 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	
3	3	155/274 (57%)	152 (98%)	3 (2%)	57	77
4	4	203/257 (79%)	198 (98%)	5 (2%)	47	72
5	5	343/410 (84%)	340 (99%)	3 (1%)	78	87
7	B	267/323 (83%)	262 (98%)	5 (2%)	57	77
8	C	273/289 (94%)	270 (99%)	3 (1%)	73	85
9	D	369/440 (84%)	358 (97%)	11 (3%)	41	68
10	E	131/153 (86%)	130 (99%)	1 (1%)	81	89
11	F	204/205 (100%)	202 (99%)	2 (1%)	76	86
12	G	119/208 (57%)	117 (98%)	2 (2%)	60	78
13	H	110/171 (64%)	108 (98%)	2 (2%)	59	78
14	K	220/346 (64%)	215 (98%)	5 (2%)	50	73
15	L	87/159 (55%)	87 (100%)	0	100	100
16	M	106/109 (97%)	105 (99%)	1 (1%)	78	87
17	N	153/176 (87%)	152 (99%)	1 (1%)	84	90
18	O	154/162 (95%)	151 (98%)	3 (2%)	57	77
19	P	103/146 (70%)	101 (98%)	2 (2%)	57	77
20	Q	107/151 (71%)	104 (97%)	3 (3%)	43	70
21	S	155/156 (99%)	150 (97%)	5 (3%)	39	67
22	W	112/213 (53%)	111 (99%)	1 (1%)	78	87
23	Y	108/110 (98%)	102 (94%)	6 (6%)	21	52
24	b	221/573 (39%)	216 (98%)	5 (2%)	50	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	e	106/111 (96%)	103 (97%)	3 (3%)	43	70
26	f	90/91 (99%)	89 (99%)	1 (1%)	73	85
27	h	99/105 (94%)	99 (100%)	0	100	100
28	i	22/82 (27%)	22 (100%)	0	100	100
29	j	59/71 (83%)	59 (100%)	0	100	100
30	m	99/723 (14%)	98 (99%)	1 (1%)	76	86
31	n	222/548 (40%)	218 (98%)	4 (2%)	59	78
32	o	99/199 (50%)	96 (97%)	3 (3%)	41	68
33	t	178/287 (62%)	172 (97%)	6 (3%)	37	65
34	u	88/180 (49%)	87 (99%)	1 (1%)	73	85
35	v	116/205 (57%)	116 (100%)	0	100	100
36	x	252/276 (91%)	244 (97%)	8 (3%)	39	67
37	y	160/211 (76%)	158 (99%)	2 (1%)	69	82
All	All	5290/8120 (65%)	5192 (98%)	98 (2%)	59	77

5 of 98 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	W	113	LYS
25	e	98	HIS
23	Y	51	ARG
24	b	168	ARG
31	n	137	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
13	H	163	GLN
33	t	154	ASN
20	Q	45	ASN
37	y	9	ASN
30	m	369	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1530/3396 (45%)	291 (19%)	37 (2%)
2	2	145/158 (91%)	26 (17%)	1 (0%)
6	6	63/232 (27%)	20 (31%)	1 (1%)
All	All	1738/3786 (45%)	337 (19%)	39 (2%)

5 of 337 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	3	U
1	1	6	A
1	1	7	C
1	1	14	U

5 of 39 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1405	U
1	1	3228	C
1	1	2995	A
1	1	3074	G
2	2	114	G

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

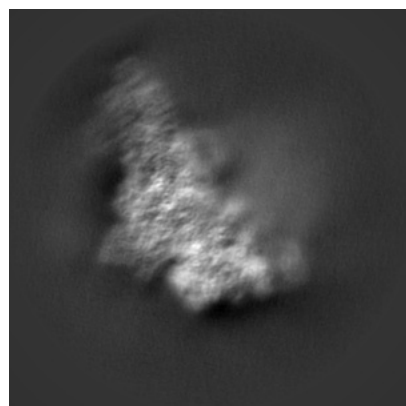
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12912. These allow visual inspection of the internal detail of the map and identification of artifacts.

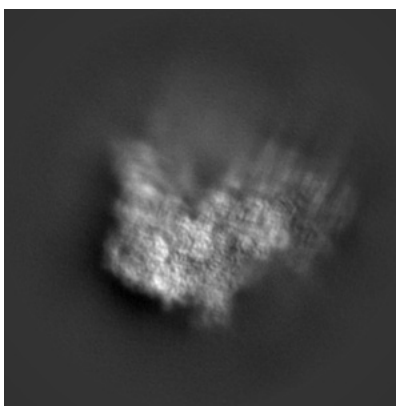
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

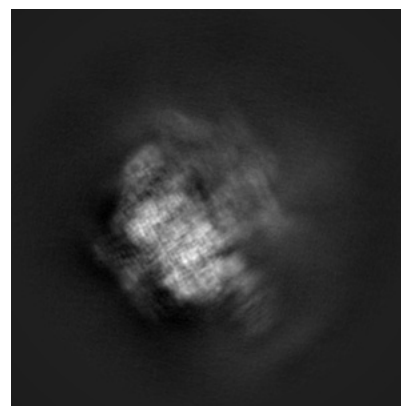
6.1.1 Primary map



X

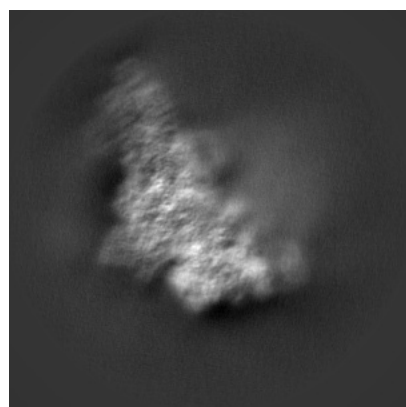


Y

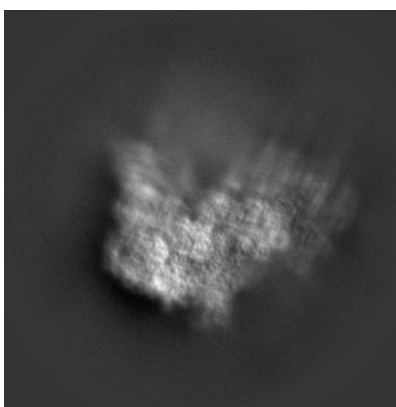


Z

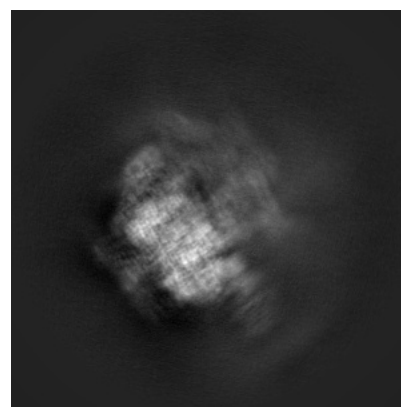
6.1.2 Raw map



X



Y

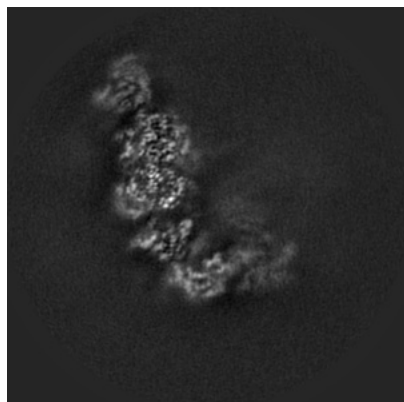


Z

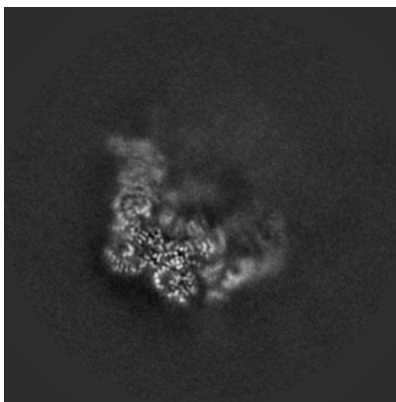
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

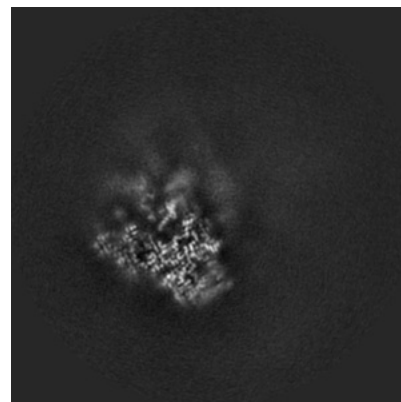
6.2.1 Primary map



X Index: 200

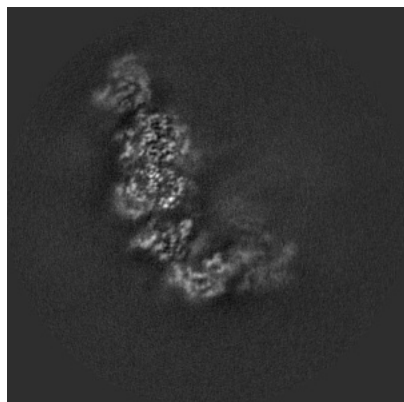


Y Index: 200

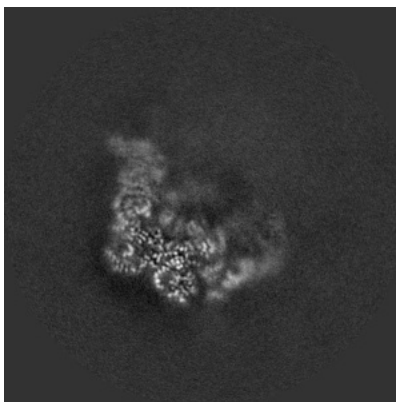


Z Index: 200

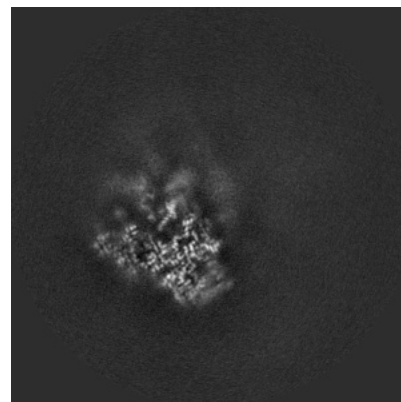
6.2.2 Raw map



X Index: 200



Y Index: 200

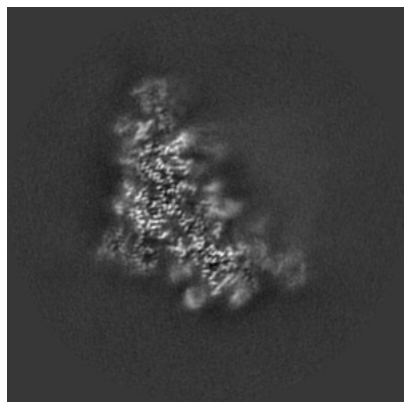


Z Index: 200

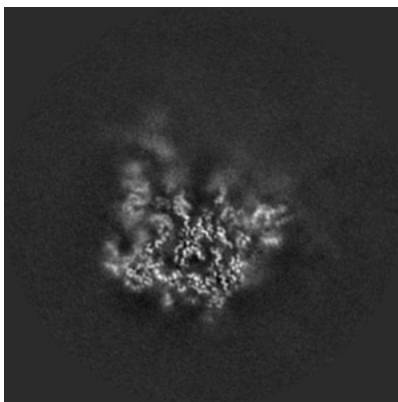
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

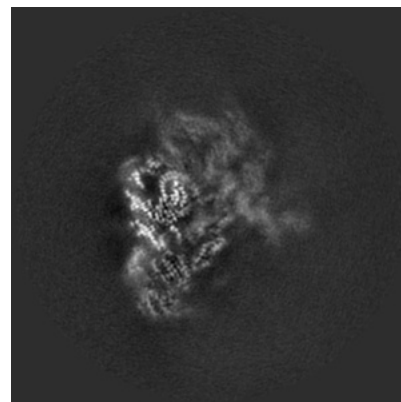
6.3.1 Primary map



X Index: 165

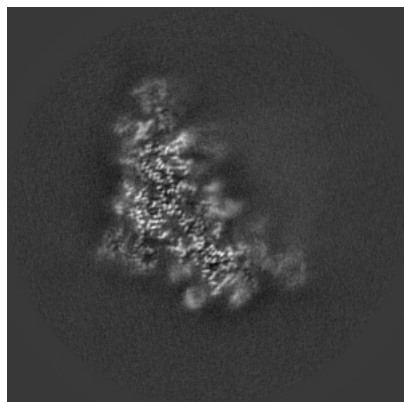


Y Index: 177

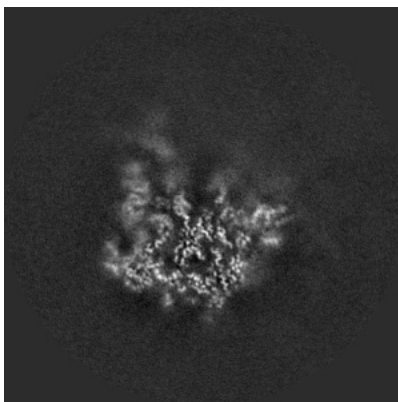


Z Index: 153

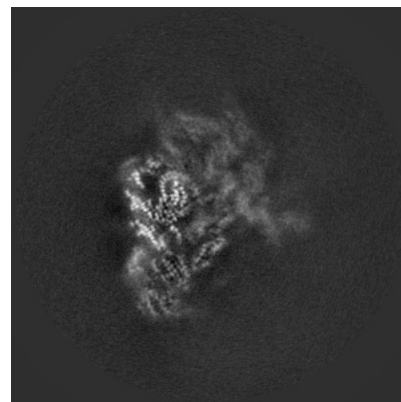
6.3.2 Raw map



X Index: 165



Y Index: 177

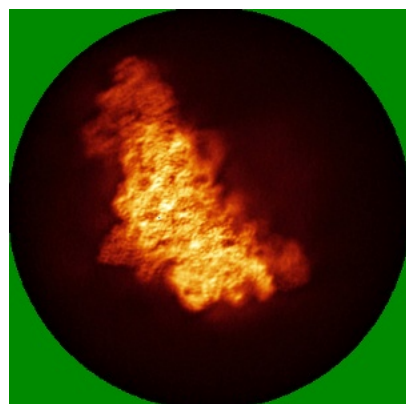


Z Index: 153

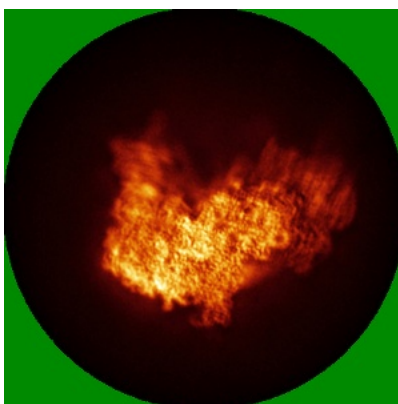
The images above show the largest variance slices of the map in three orthogonal directions.

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

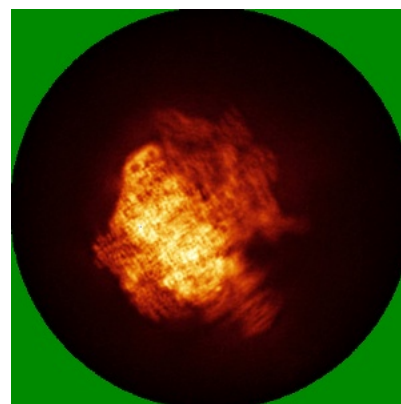
6.4.1 Primary map



X

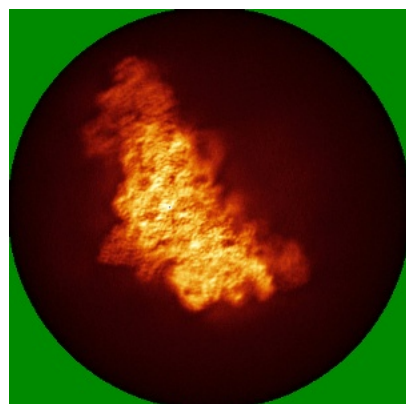


Y

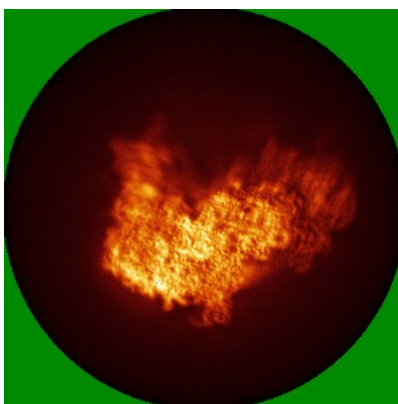


Z

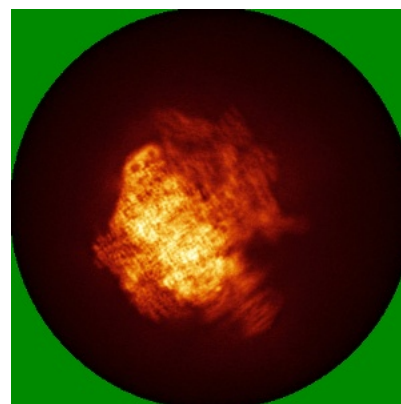
6.4.2 Raw map



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 0.014. 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.

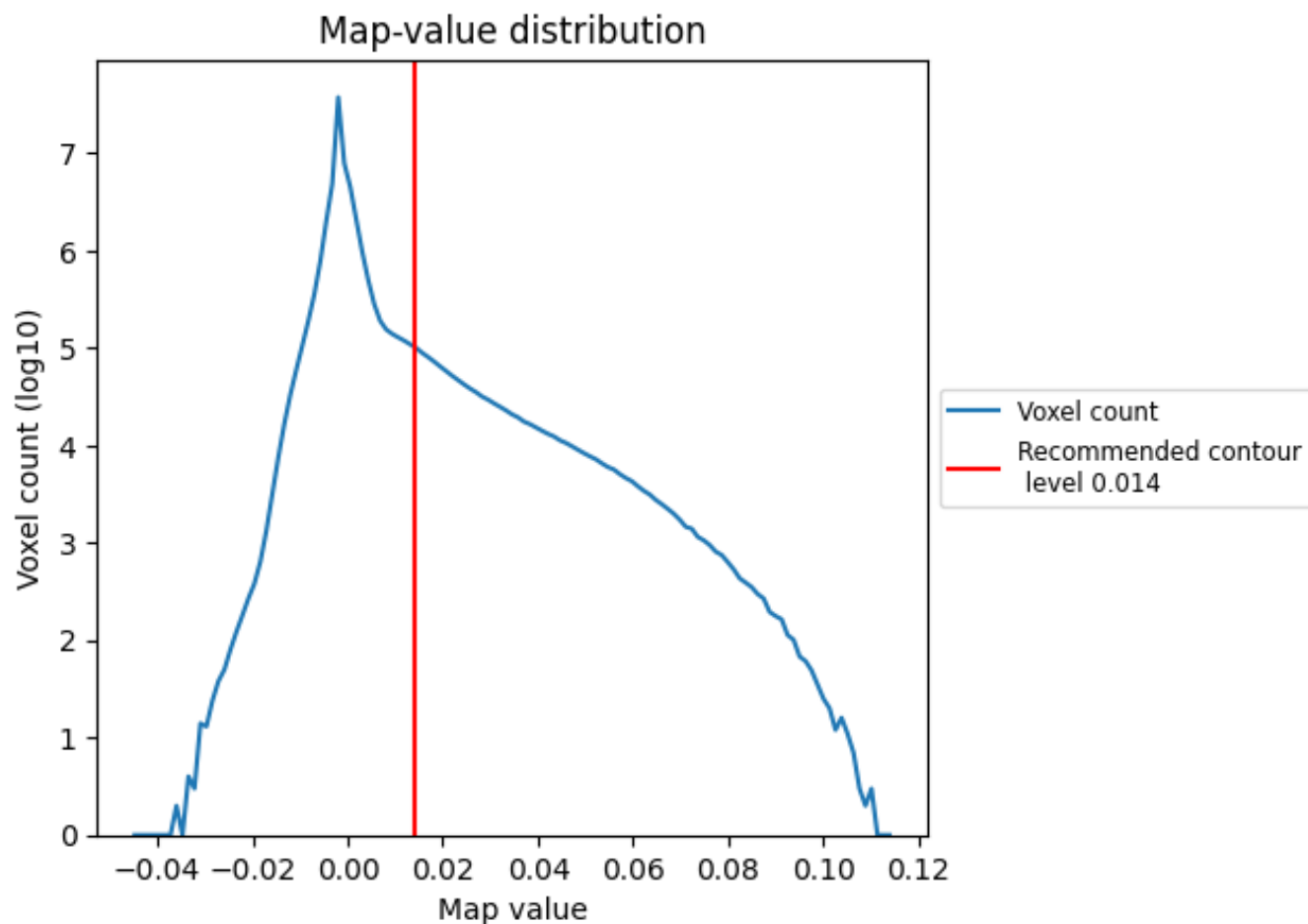
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

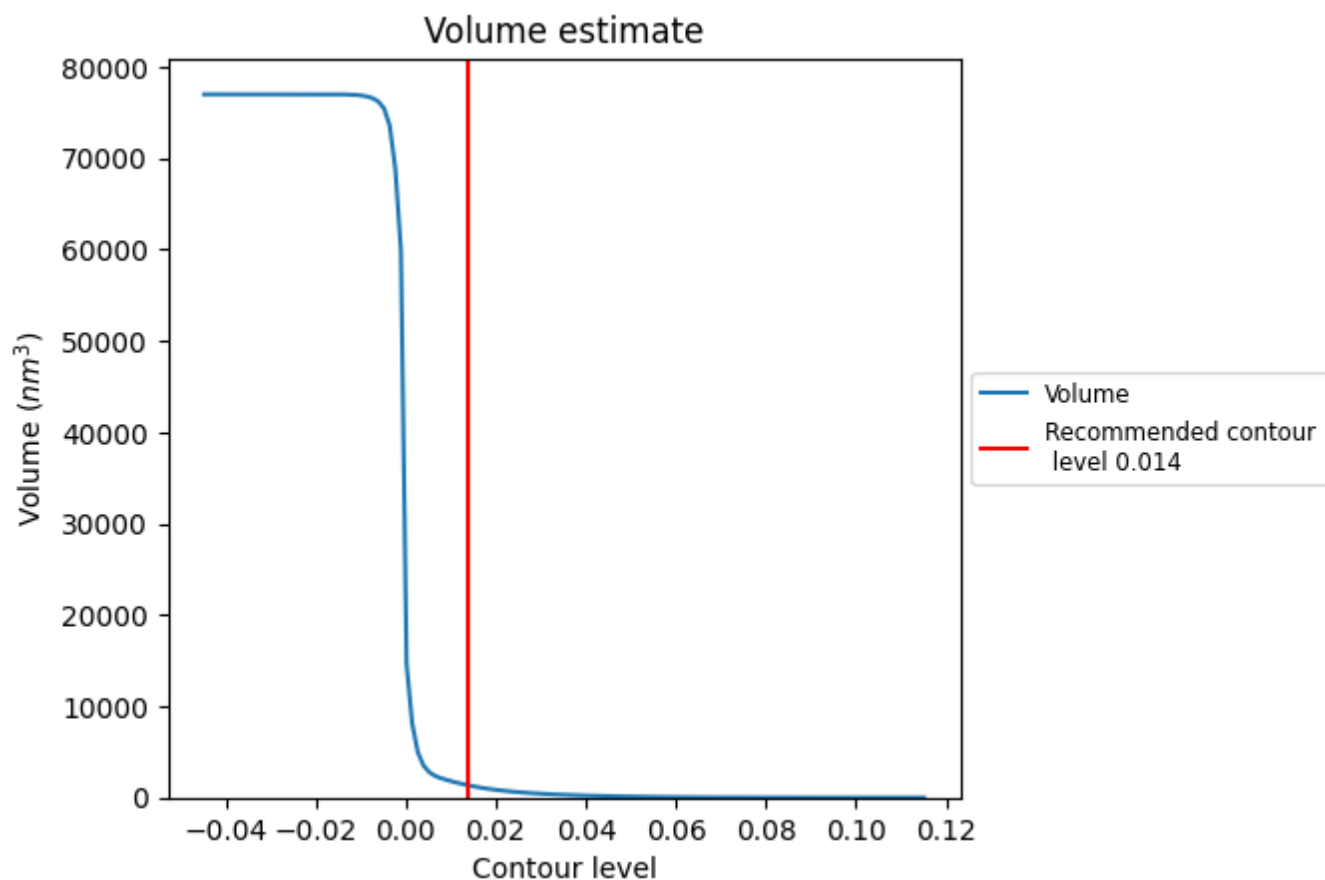
This section contains the results of statistical analysis of the map.

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.

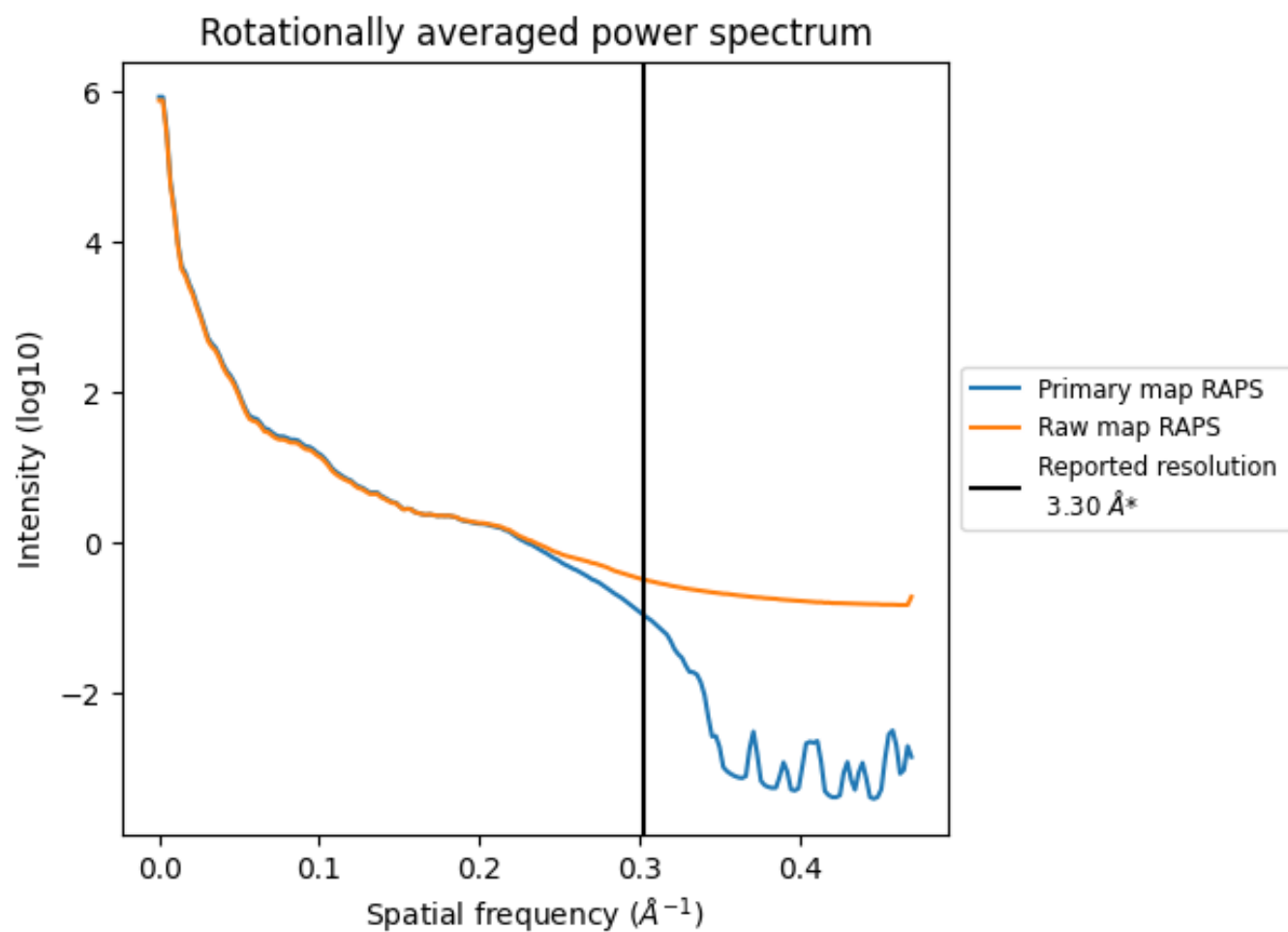
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1331 nm³; this corresponds to an approximate mass of 1202 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 ⓘ

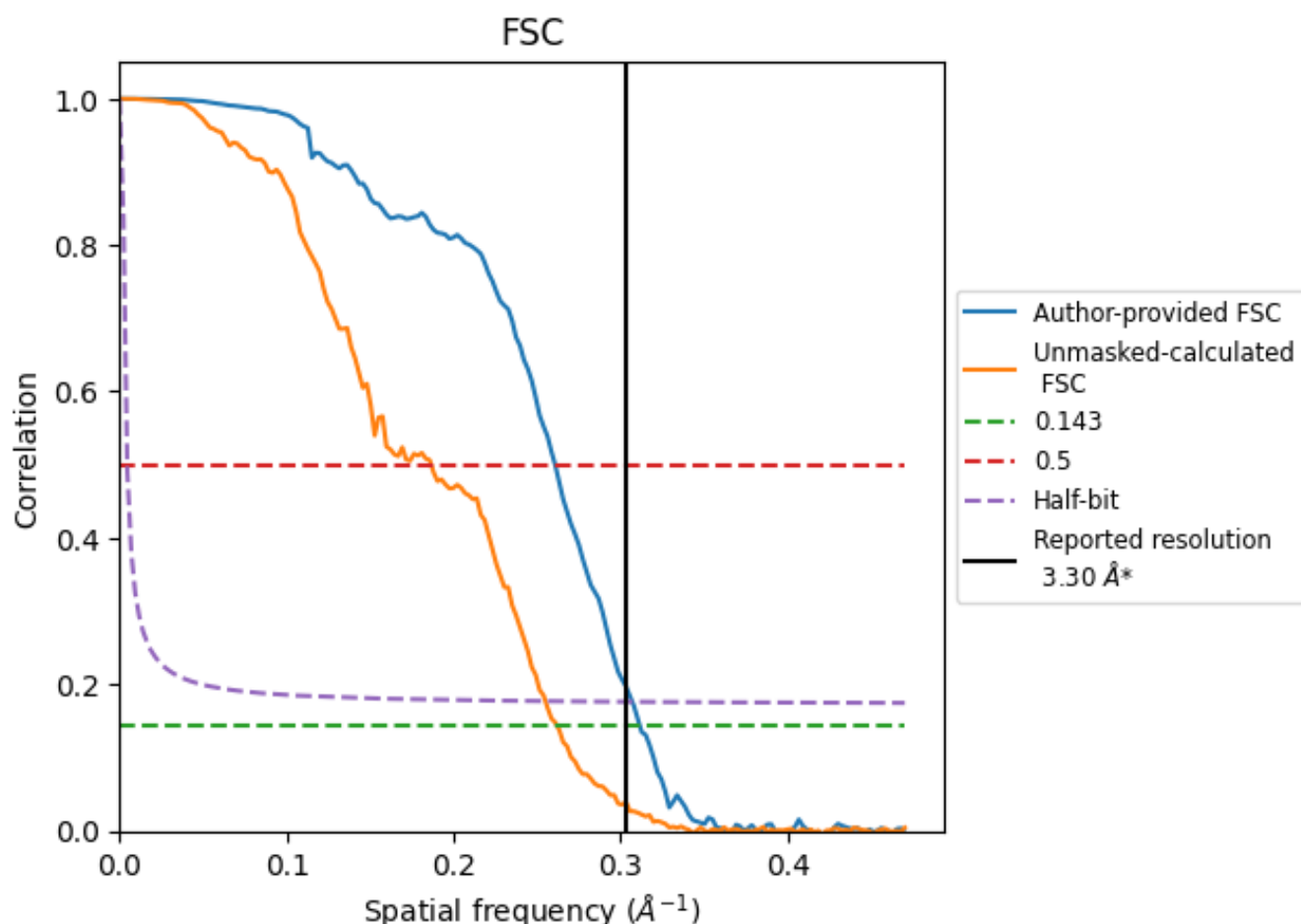


*Reported resolution corresponds to spatial frequency of 0.303 \AA^{-1}

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 0.303 \AA^{-1}

8.2 Resolution estimates [i](#)

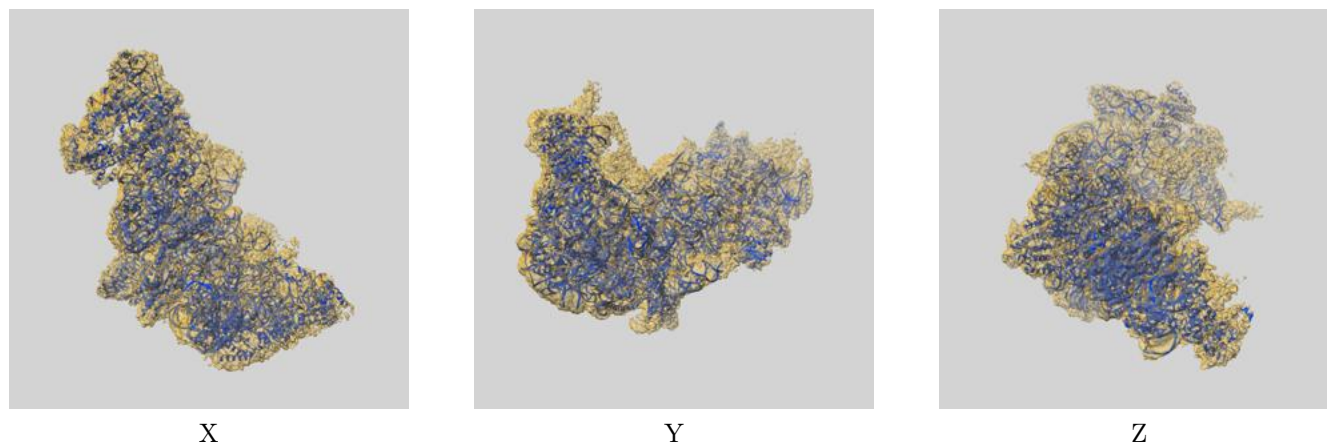
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.21	3.83	3.26
Unmasked-calculated*	3.82	5.36	3.92

*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 3.82 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

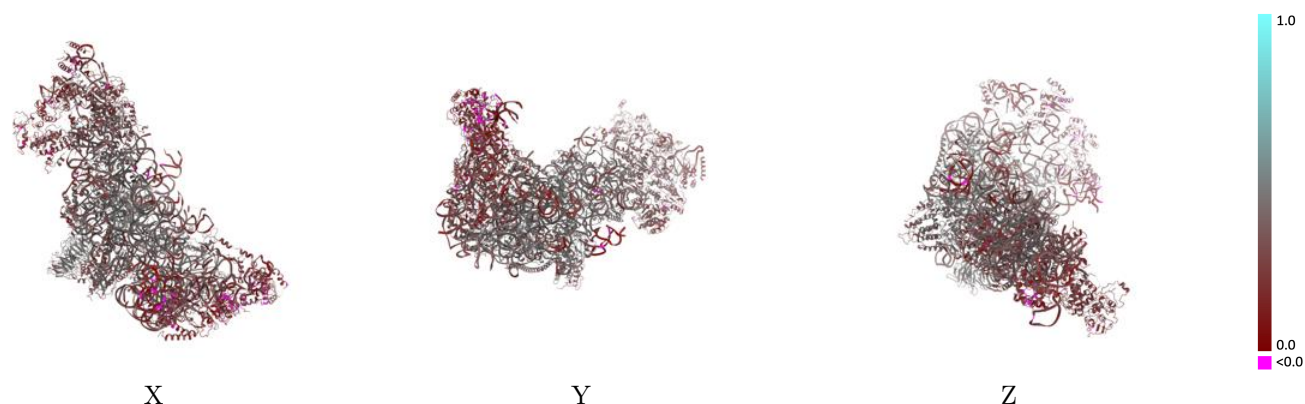
This section contains information regarding the fit between EMDB map EMD-12912 and PDB model 7OHX. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



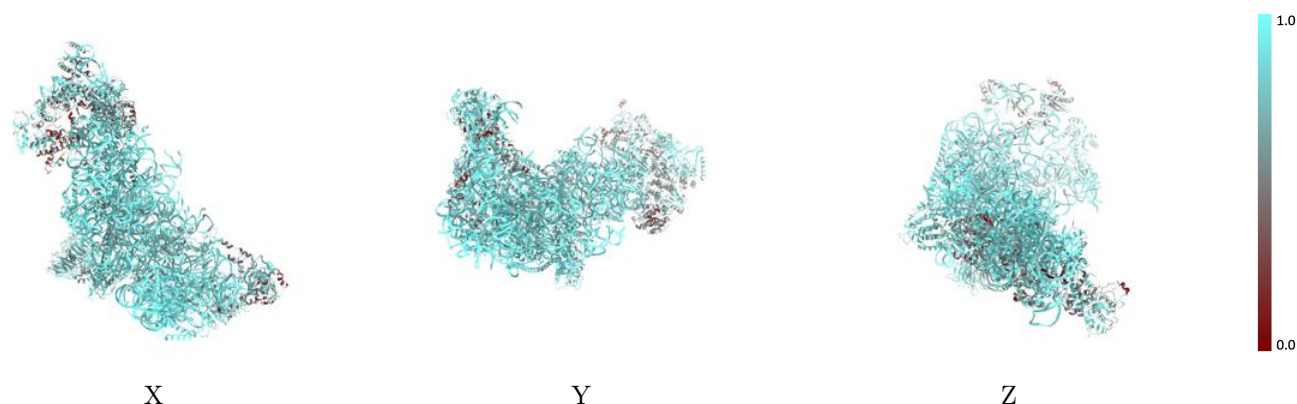
The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



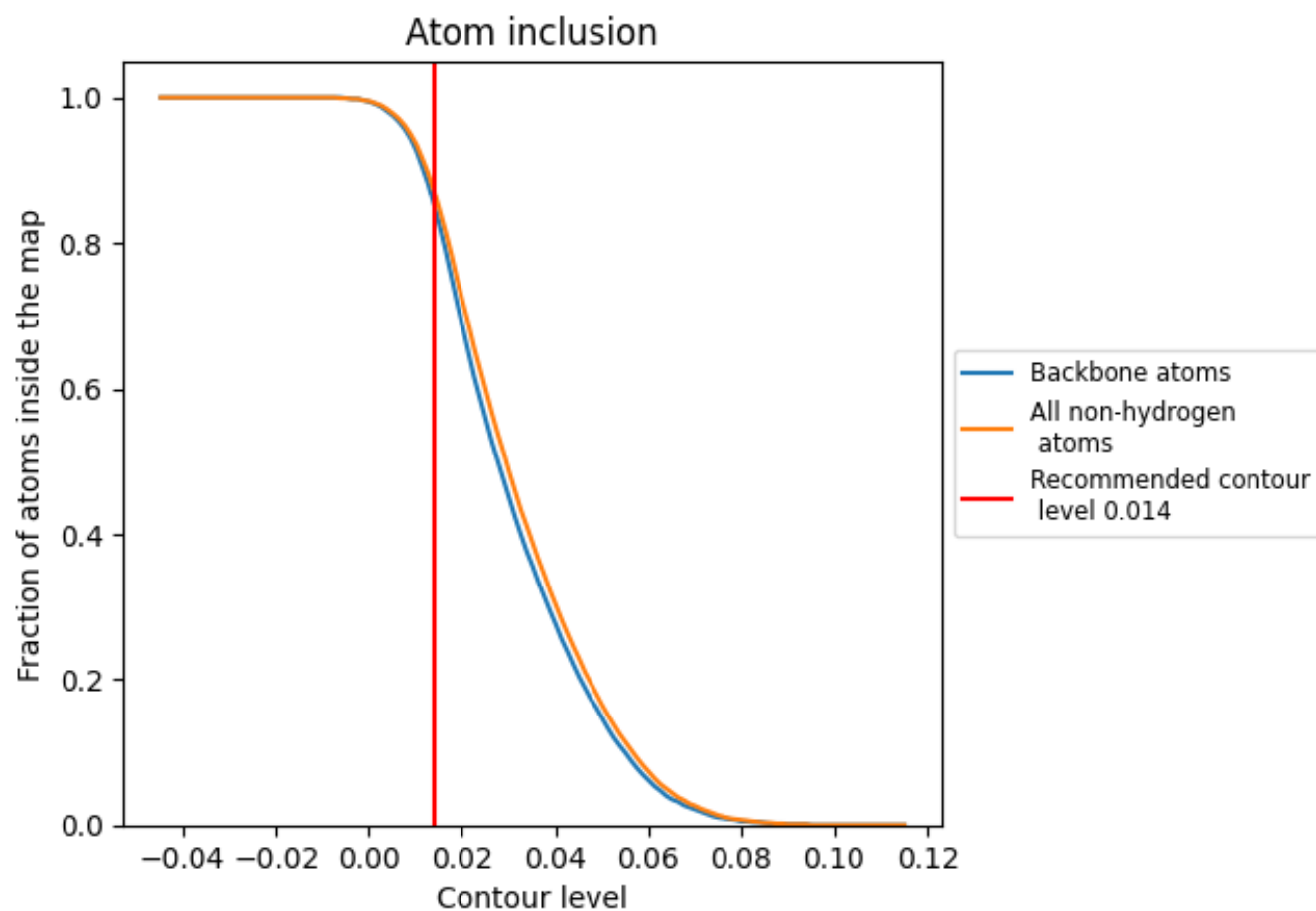
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.014).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 85% of all backbone atoms, 87% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8710	 0.3450
1	 0.9650	 0.3410
2	 0.9730	 0.3560
3	 0.8100	 0.4070
4	 0.8590	 0.3730
5	 0.7900	 0.4190
6	 0.8430	 0.2720
B	 0.9460	 0.2960
C	 0.9210	 0.4480
D	 0.5740	 0.2970
E	 0.9530	 0.4260
F	 0.9050	 0.4270
G	 0.7980	 0.3530
H	 0.6470	 0.3110
K	 0.6070	 0.2440
L	 0.9400	 0.4250
M	 0.9310	 0.4040
N	 0.9110	 0.4050
O	 0.9200	 0.4060
P	 0.8050	 0.3860
Q	 0.9230	 0.4400
S	 0.9110	 0.3880
W	 0.5440	 0.2360
Y	 0.9560	 0.4300
b	 0.6100	 0.2080
e	 0.8650	 0.4620
f	 0.9480	 0.4650
h	 0.8740	 0.3780
i	 0.8520	 0.3220
j	 0.9390	 0.4610
m	 0.6000	 0.3000
n	 0.5900	 0.2620
o	 0.7750	 0.2760
t	 0.6500	 0.2570
u	 0.8940	 0.1950



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Chain	Atom inclusion	Q-score
v	 0.7320	 0.3710
x	 0.7460	 0.3680
y	 0.7870	 0.1900