



wwPDB EM Validation Summary Report ⓘ

Mar 26, 2026 – 04:50 PM UTC

PDB ID : 7OHS / pdb_00007ohs
EMDB ID : EMD-12907
Title : Nog1-TAP associated immature ribosomal particle population F from *S. cerevisiae*
Authors : Milkereit, P.; Poell, G.
Deposited on : 2021-05-11
Resolution : 4.38 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:

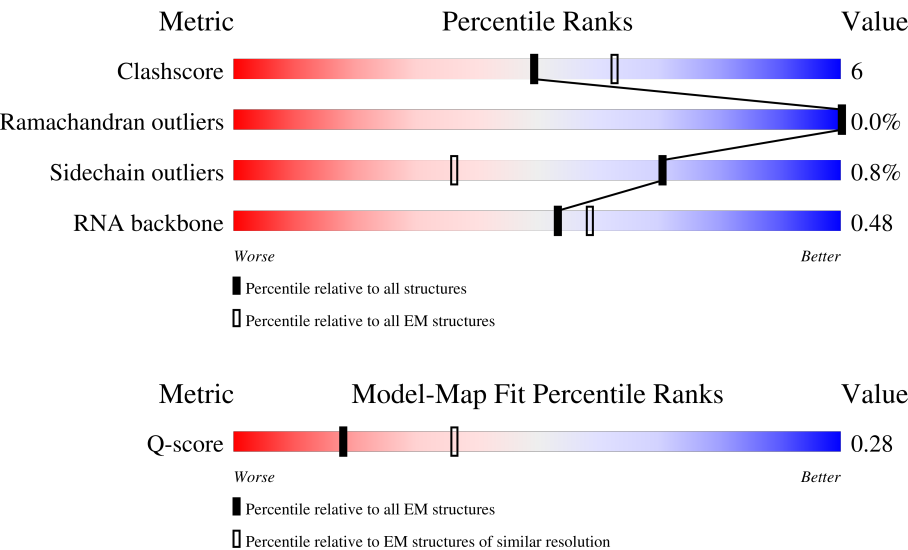
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.38 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.



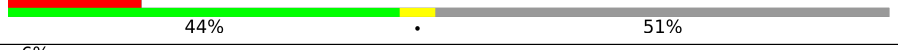
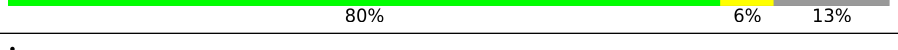
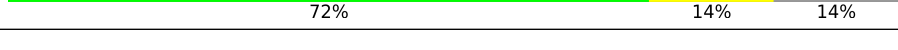
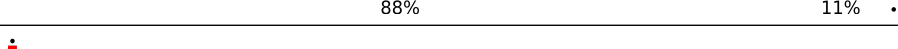
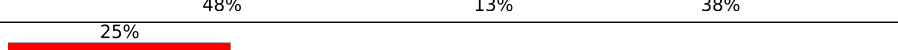
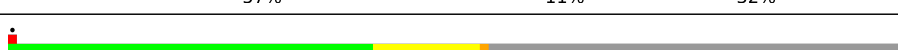
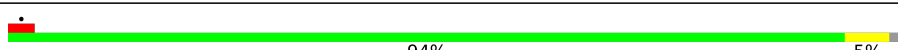
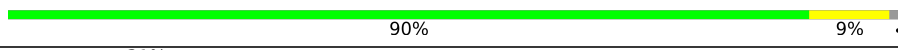
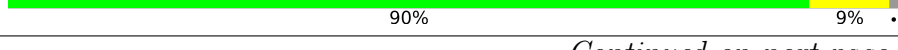
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3702 (3.88 - 4.88)

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	29%16%5%50%
2	2	158	66%18%8%7%
3	3	306	49%8%43%

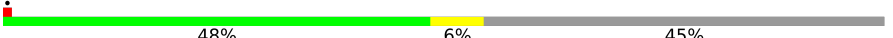
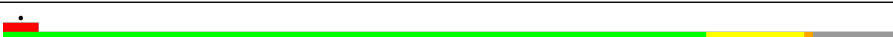
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Mol	Chain	Length	Quality of chain
4	4	278	
5	5	463	
6	6	232	
7	A	291	
8	B	387	
9	C	362	
10	D	505	
11	E	176	
12	F	244	
13	G	256	
14	H	191	
15	K	376	
16	L	199	
17	M	138	
18	N	204	
19	O	199	
20	P	184	
21	Q	186	
22	S	172	
23	V	137	
24	W	236	
25	Y	127	
26	b	647	
27	e	130	
28	f	107	

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Mol	Chain	Length	Quality of chain
29	h	120	
30	i	100	
31	j	88	
32	m	807	
33	n	605	
34	o	220	
35	r	261	
36	t	322	
37	u	199	
38	v	231	
39	x	295	
40	y	245	

2 Entry composition

There are 41 unique types of molecules in this entry. The entry contains 175937 atoms, of which 78846 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	1697	Total	C	H	N	O	P	0	0
			54624	16232	18261	6602	11832	1697		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	2	147	Total	C	H	N	O	P	0	0
			4702	1397	1579	550	1029	147		

- 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 Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	A	142	Total	C	H	N	O	S	0	0
			2379	765	1190	215	206	3		

- Molecule 8 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	B	333	Total	C	H	N	O	S	0	0
			5374	1680	2728	490	470	6		

- Molecule 9 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 10 is a protein called ATP-dependent RNA helicase HAS1.

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

- Molecule 11 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 12 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 13 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	G	158	Total	C	H	N	O	S	0	0
			2510	791	1284	208	225	2		

- Molecule 14 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	H	156	Total	C	H	N	O	S	0	0
			2560	800	1311	219	227	3		

- Molecule 15 is a protein called Proteasome-interacting protein CIC1.

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

- Molecule 16 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 17 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	M	127	Total	C	H	N	O	S	0	0
			2078	638	1086	189	163	2		

- Molecule 18 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 19 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	P	137	Total	C	H	N	O	S	0	0
			2139	666	1077	198	198			

- Molecule 21 is a protein called 60S ribosomal protein L18-A.

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

- 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	
			2904	922	1472	265	242	3	
								0	0

- Molecule 23 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	50	Total	C	H	N	O	S	
			758	241	380	69	66	2	
								0	0

- Molecule 24 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	172	Total	C	H	N	O	S	
			2834	906	1429	235	260	4	
								0	0

- Molecule 25 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 26 is a protein called Nucleolar GTP-binding protein 1.

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

- Molecule 27 is a protein called 60S ribosomal protein L32.

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

- Molecule 28 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 29 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	h	118	Total	C	H	N	O	S	0	0
			2038	612	1074	185	166	1		

- Molecule 30 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	i	70	Total	C	H	N	O	S	0	0
			1163	343	608	116	95	1		

- Molecule 31 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 32 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	m	161	Total	C	H	N	O	S	0	0
			2709	867	1347	238	253	4		

- Molecule 33 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	n	331	Total	C	H	N	O	S	0	0
			5472	1771	2764	454	475	8		

- Molecule 34 is a protein called Ribosome biogenesis protein 15.

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

- Molecule 35 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	r	68	Total	C	H	N	O	S	0	0
			1210	365	617	127	100	1		

- Molecule 36 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	t	244	Total	C	H	N	O	S	0	0
			3974	1233	2039	345	354	3		

- Molecule 37 is a protein called Ribosome biogenesis protein RLP24.

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

- Molecule 38 is a protein called Nucleolar protein 16.

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

- Molecule 39 is a protein called Ribosome production factor 1.

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

- Molecule 40 is a protein called Eukaryotic translation initiation factor 6.

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

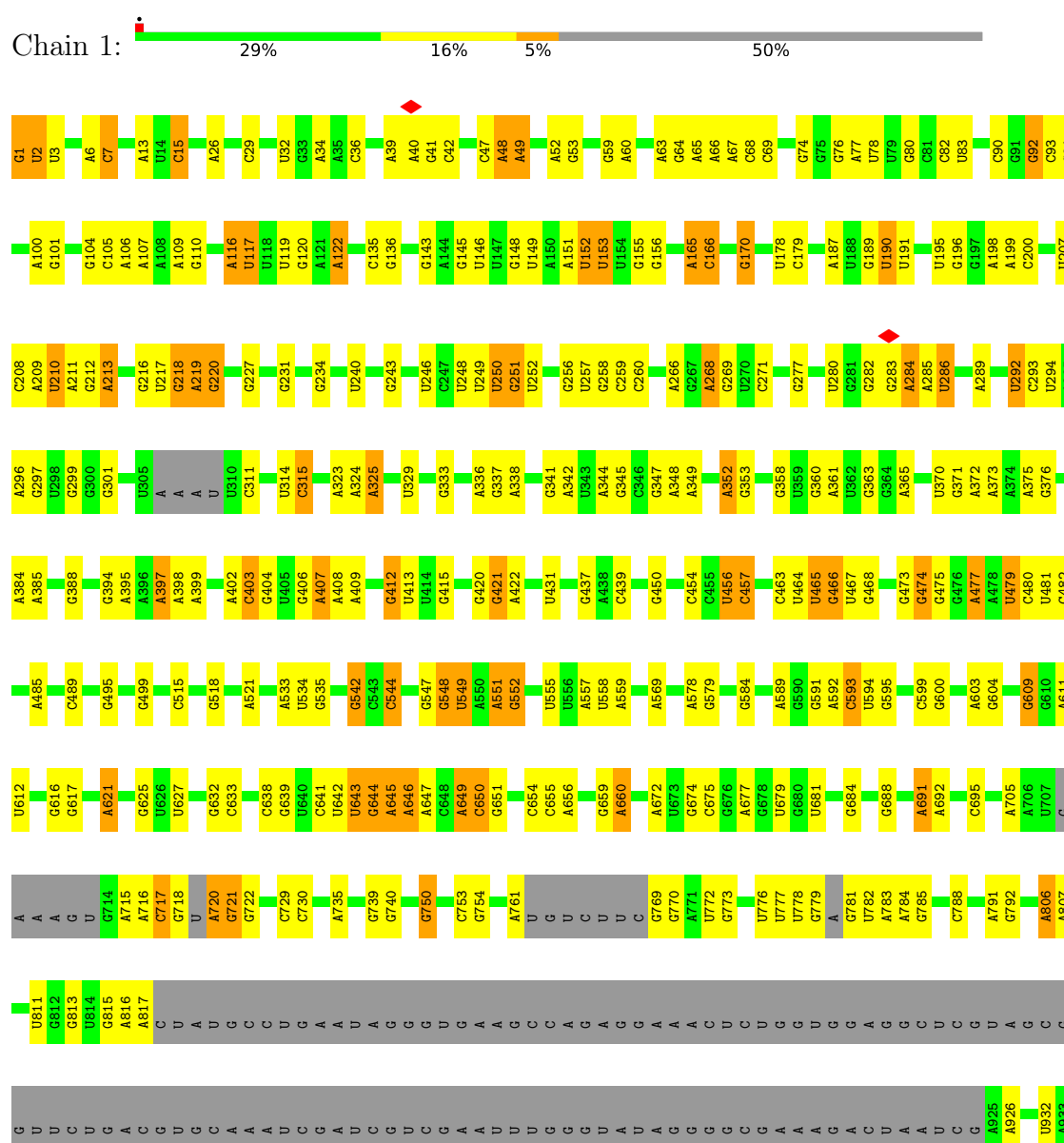
- Molecule 41 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

3 Residue-property plots

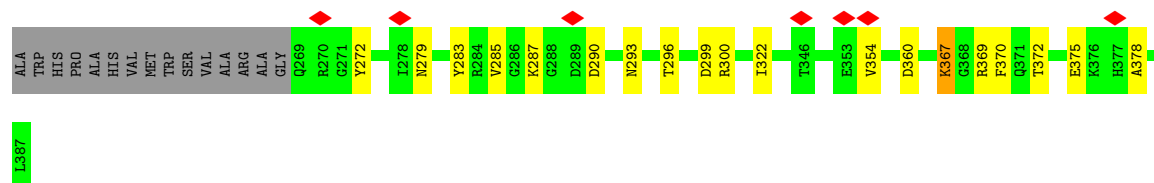
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



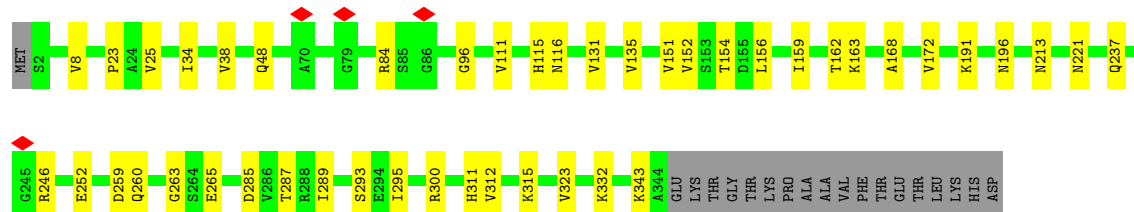






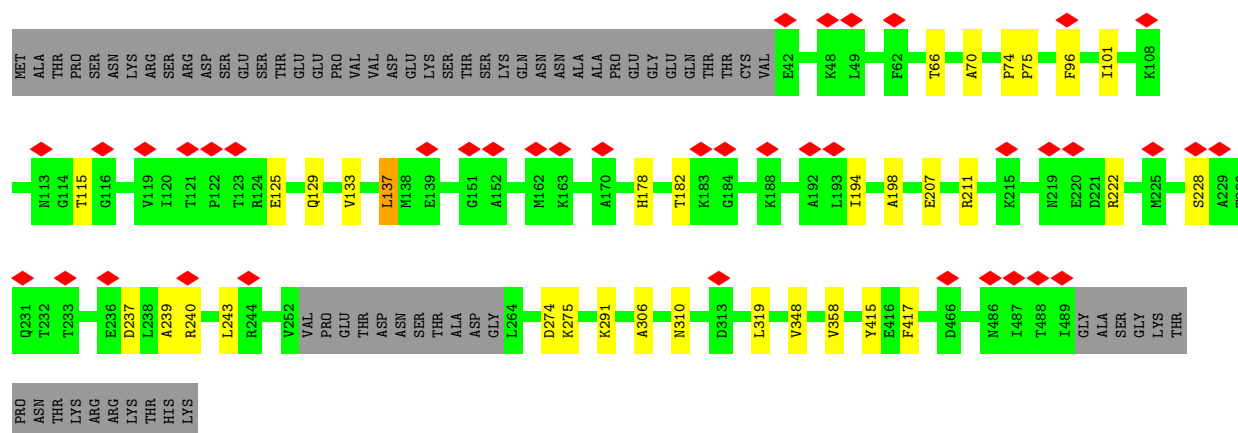
- Molecule 9: 60S ribosomal protein L4-A

Chain C: 82% 12% 5%



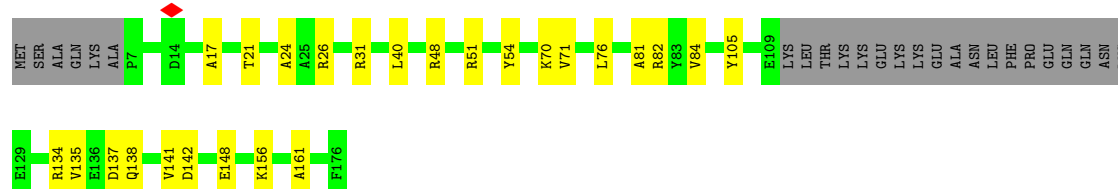
- Molecule 10: ATP-dependent RNA helicase HAS1

Chain D: 8% 80% 6% 13%



- Molecule 11: 60S ribosomal protein L6-A

Chain E: 72% 14% 14%



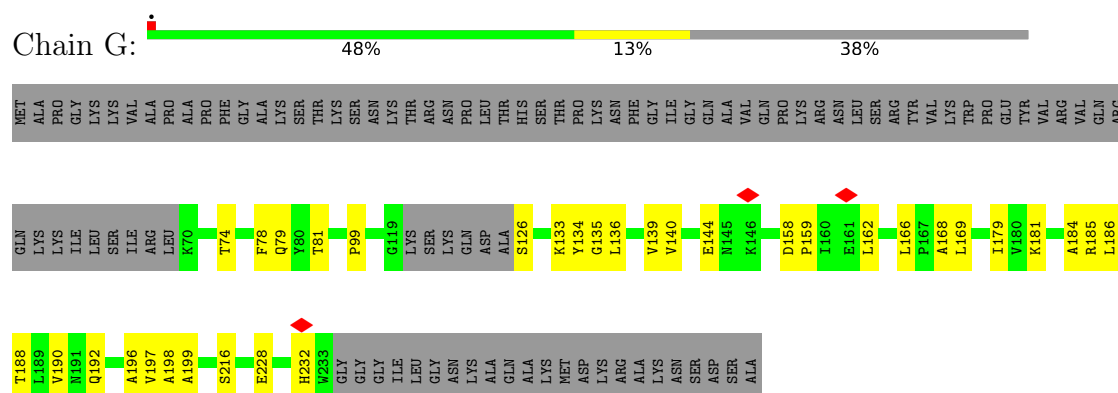
- Molecule 12: 60S ribosomal protein L7-A

Chain F: 88% 11% 1%

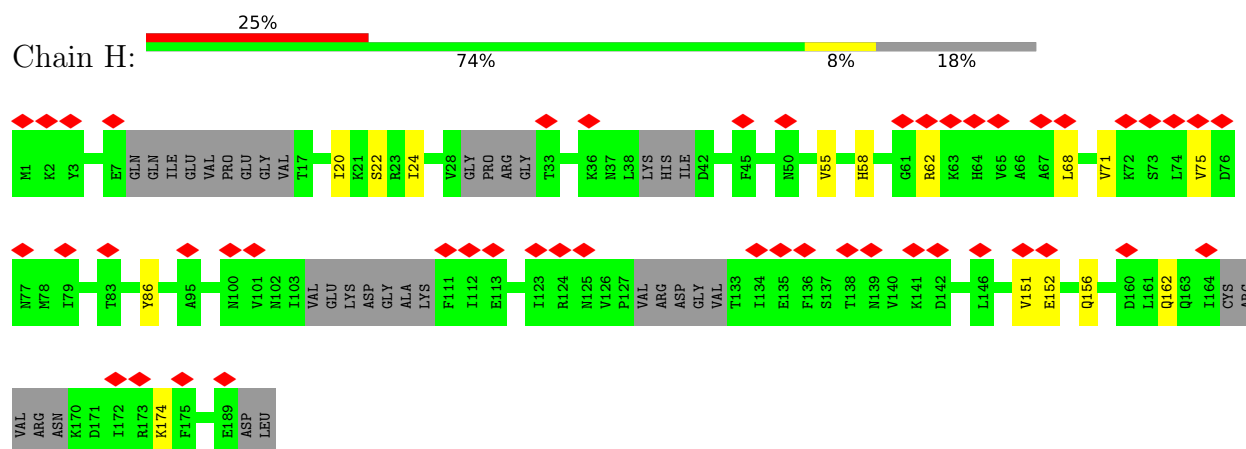




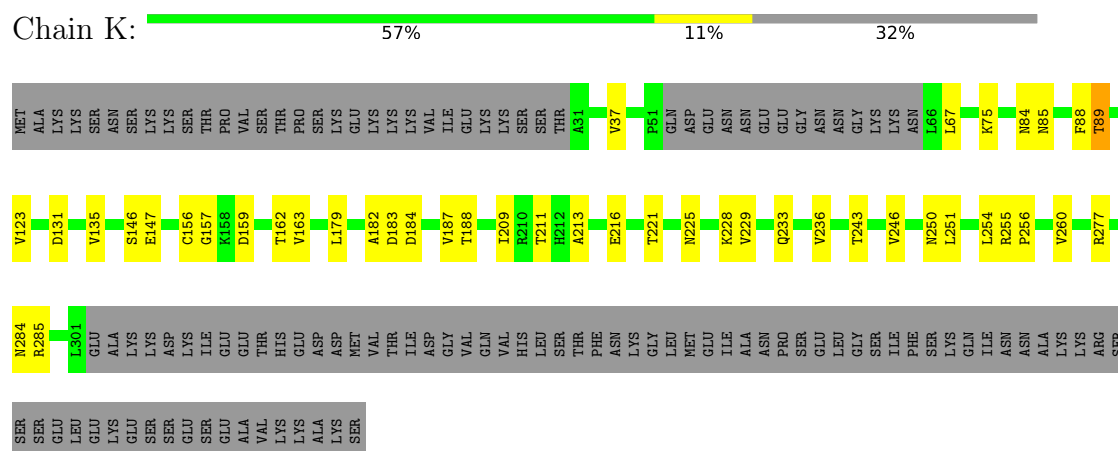
• Molecule 13: 60S ribosomal protein L8-A



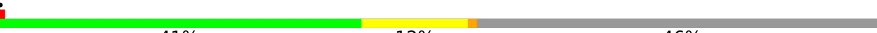
• Molecule 14: 60S ribosomal protein L9-A

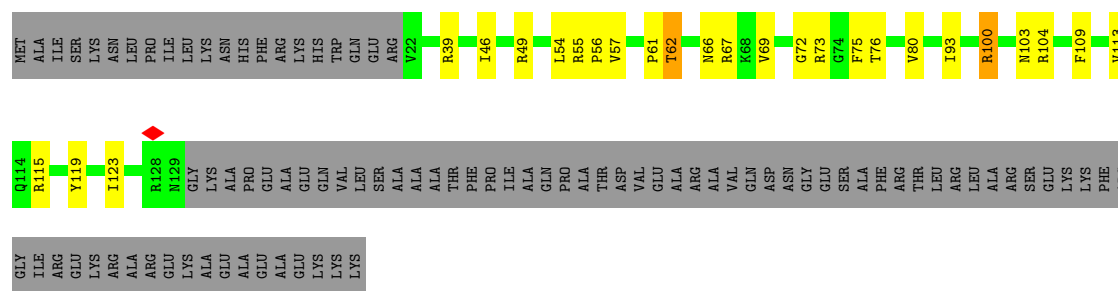


• Molecule 15: Proteasome-interacting protein CIC1



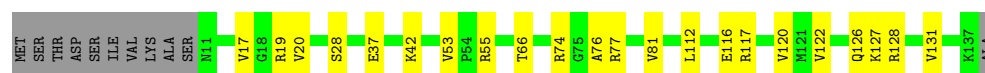
• Molecule 16: 60S ribosomal protein L13-A

Chain L: 



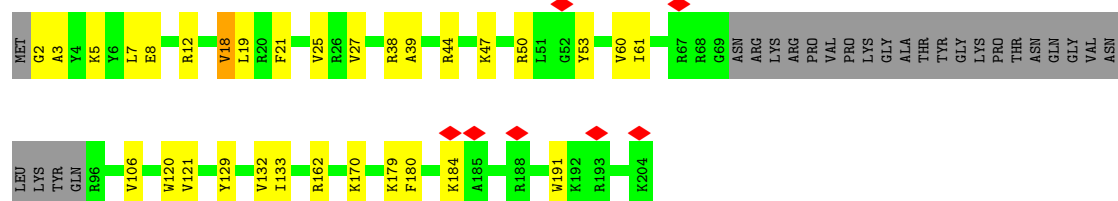
- Molecule 17: 60S ribosomal protein L14-A

Chain M: 

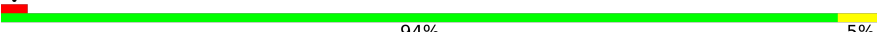


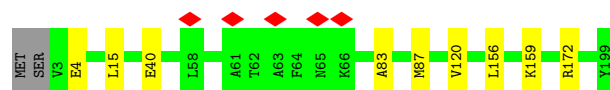
- Molecule 18: 60S ribosomal protein L15-A

Chain N: 



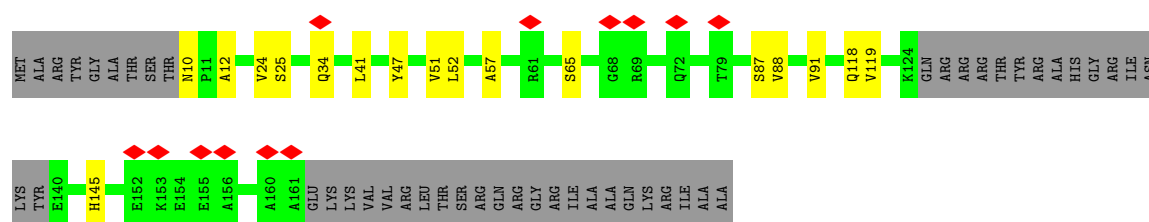
- Molecule 19: 60S ribosomal protein L16-A

Chain O: 

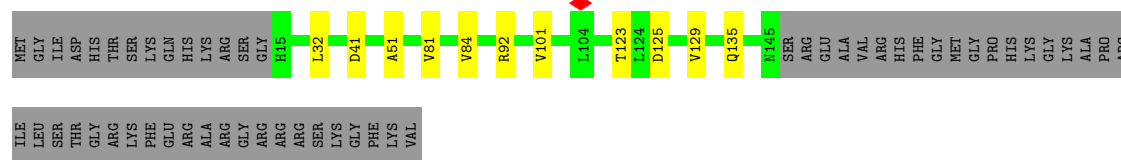


- Molecule 20: 60S ribosomal protein L17-A

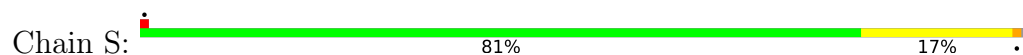
Chain P: 



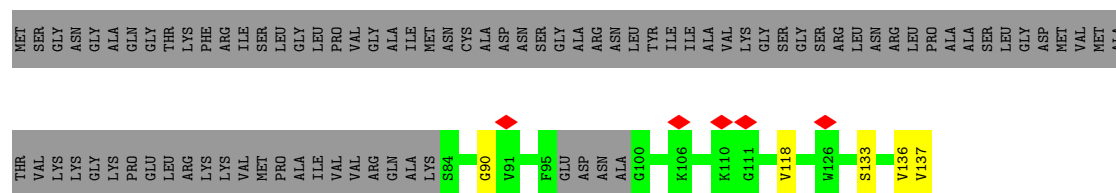
- Molecule 21: 60S ribosomal protein L18-A



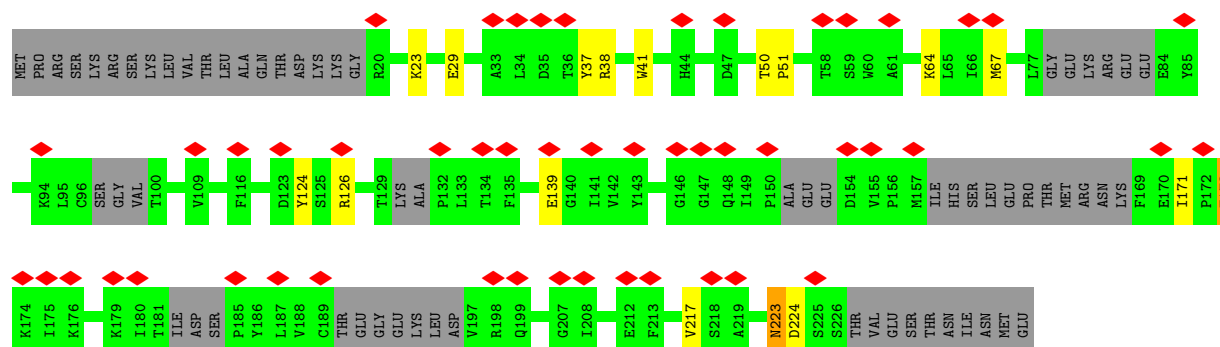
- Molecule 22: 60S ribosomal protein L20-A



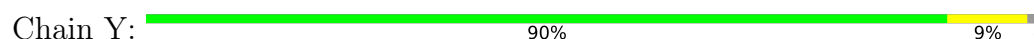
- Molecule 23: 60S ribosomal protein L23-A



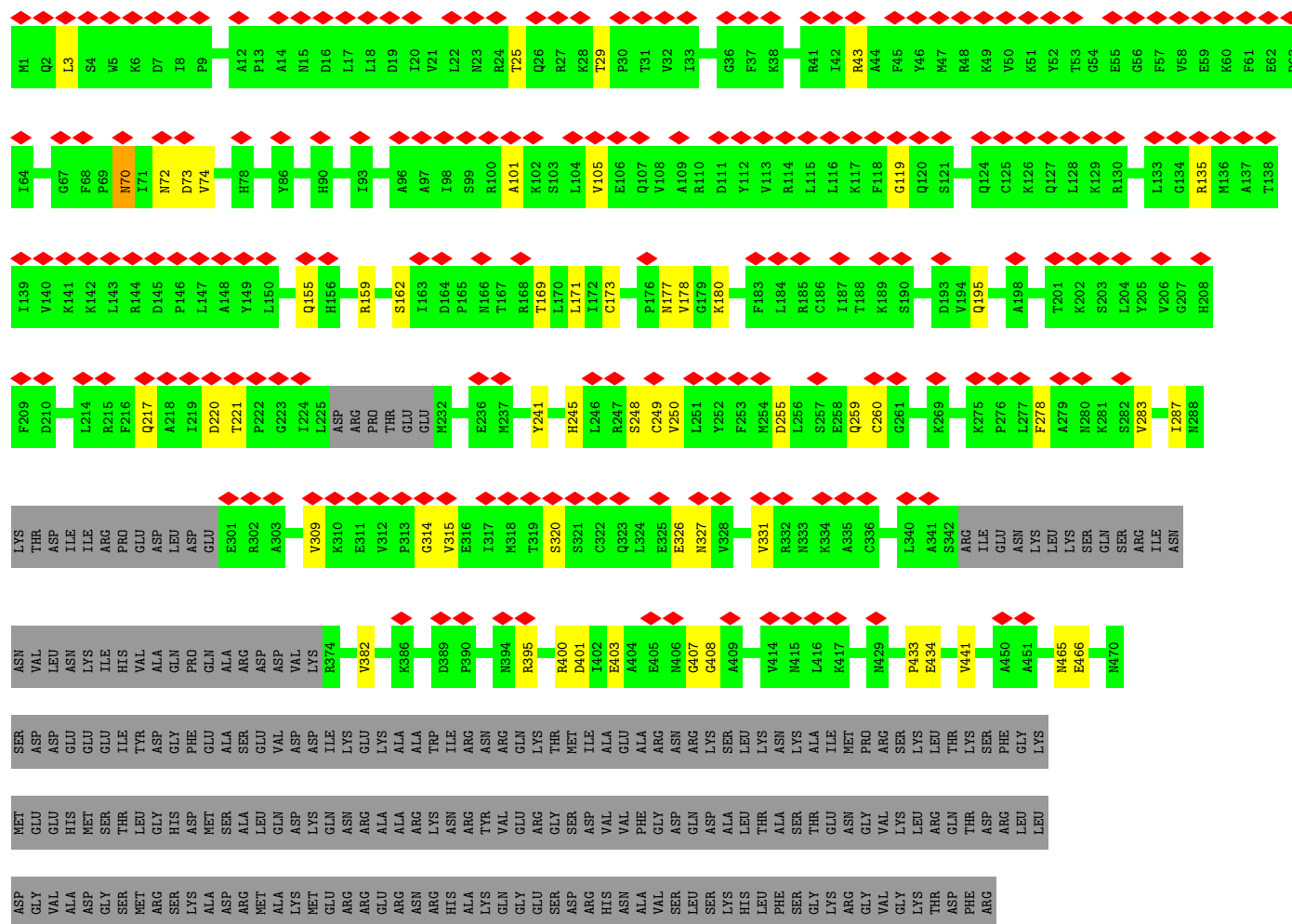
- Molecule 24: Ribosome assembly factor MRT4



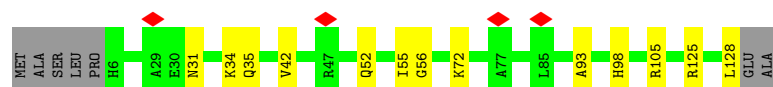
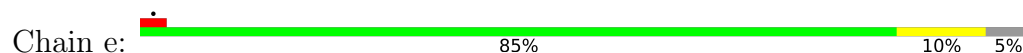
- Molecule 25: 60S ribosomal protein L26-A



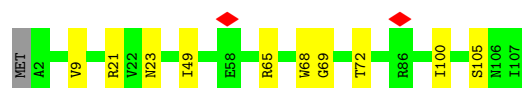
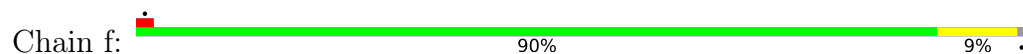
- Molecule 26: Nucleolar GTP-binding protein 1



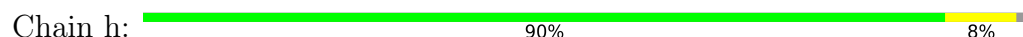
- Molecule 27: 60S ribosomal protein L32



- Molecule 28: 60S ribosomal protein L33-A

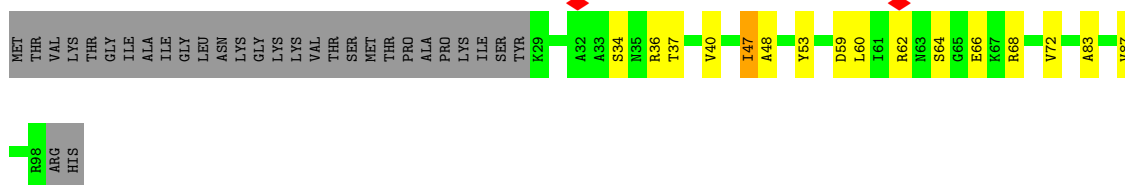


- Molecule 29: 60S ribosomal protein L35-A

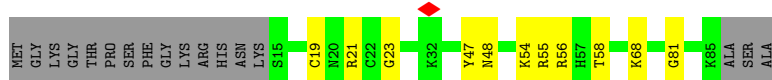




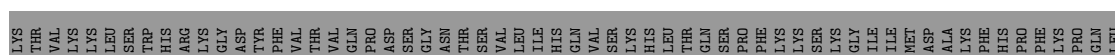
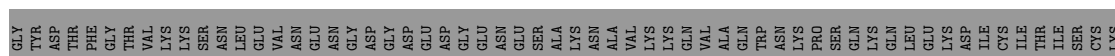
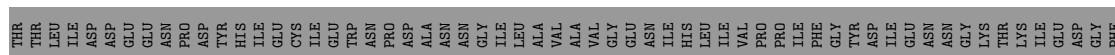
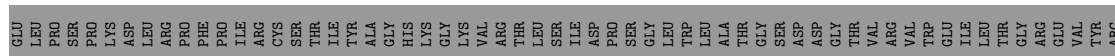
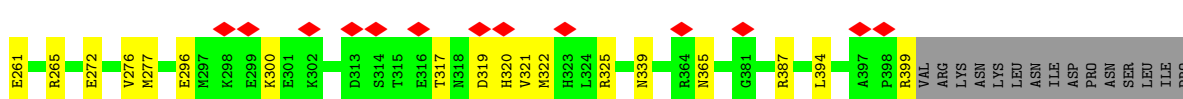
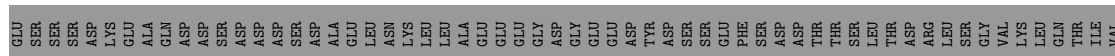
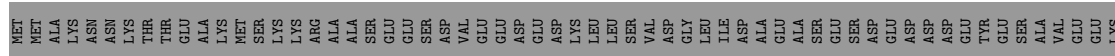
- Molecule 30: 60S ribosomal protein L36-A



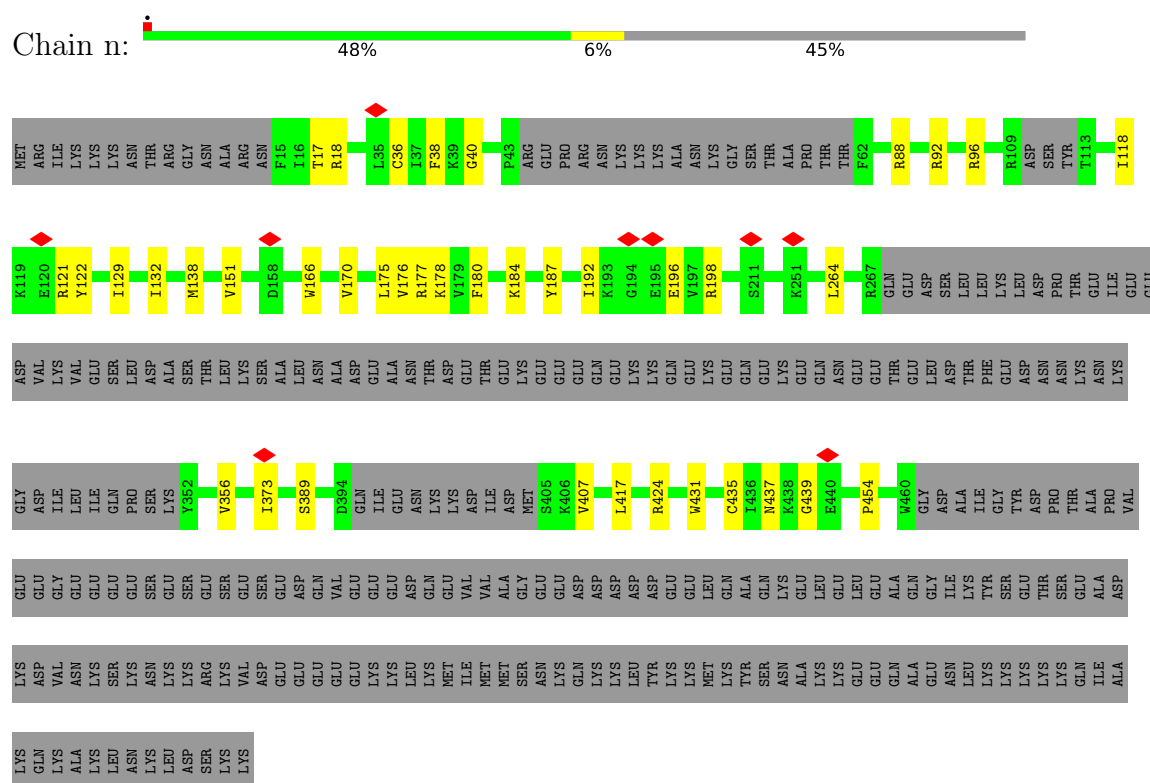
- Molecule 31: 60S ribosomal protein L37-A



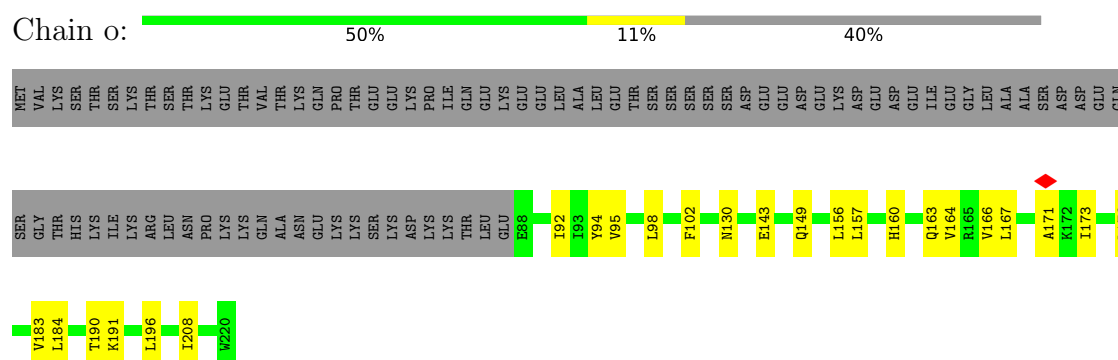
- Molecule 32: Ribosome biogenesis protein ERB1



- Molecule 33: Pescadillo homolog

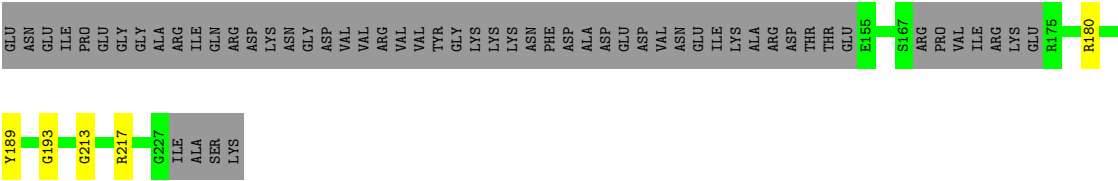


- Molecule 34: Ribosome biogenesis protein 15

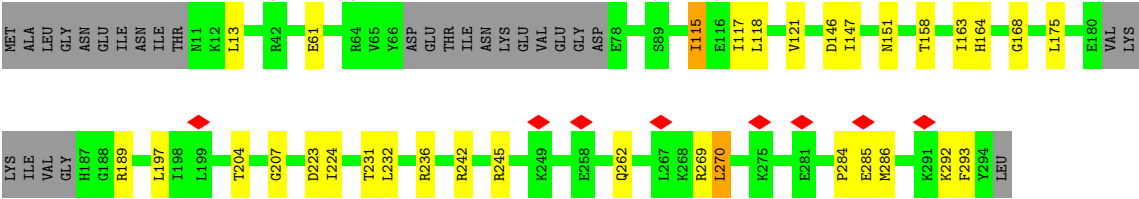
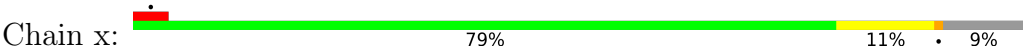


- Molecule 35: Ribosome biogenesis protein NSA2

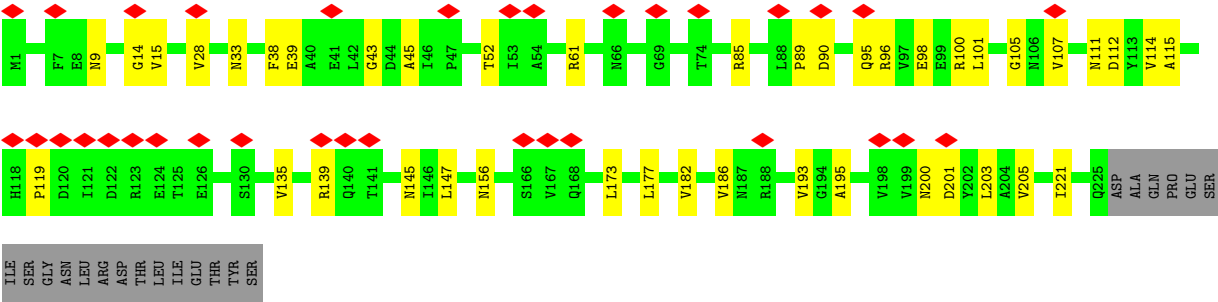




• Molecule 39: Ribosome production factor 1



• Molecule 40: 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	9258	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	0.100	Depositor
Minimum map value	-0.032	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.022	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	0.07	0/40695	0.22	0/63419
2	2	0.08	0/3488	0.22	0/5426
3	3	0.11	0/1461	0.27	0/1958
4	4	0.11	0/1895	0.27	0/2549
5	5	0.07	0/3109	0.20	0/4187
6	6	0.09	0/1527	0.29	0/2371
7	A	0.10	0/1220	0.25	0/1646
8	B	0.10	0/2699	0.24	0/3626
9	C	0.10	0/2660	0.25	0/3601
10	D	0.10	0/3552	0.23	0/4789
11	E	0.09	0/1226	0.21	0/1648
12	F	0.10	0/1974	0.23	0/2654
13	G	0.09	0/1247	0.24	0/1688
14	H	0.07	0/1261	0.22	0/1690
15	K	0.09	0/2107	0.23	0/2845
16	L	0.12	0/877	0.26	0/1179
17	M	0.11	0/1007	0.21	0/1355
18	N	0.12	0/1544	0.23	0/2065
19	O	0.10	0/1585	0.23	0/2128
20	P	0.09	0/1080	0.21	0/1455
21	Q	0.10	0/1024	0.22	0/1385
22	S	0.10	0/1468	0.24	0/1973
23	V	0.12	0/386	0.21	0/520
24	W	0.09	0/1428	0.22	0/1918
25	Y	0.10	0/995	0.25	0/1329
26	b	0.09	0/3474	0.24	0/4683
27	e	0.10	0/1014	0.22	0/1356
28	f	0.11	0/868	0.25	0/1168
29	h	0.12	0/973	0.24	0/1294
30	i	0.13	0/558	0.26	0/738
31	j	0.12	0/578	0.25	0/767
32	m	0.09	0/1401	0.25	0/1895

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	n	0.10	0/2774	0.23	0/3751
34	o	0.10	0/1129	0.24	0/1502
35	r	0.10	0/602	0.24	0/787
36	t	0.11	0/1961	0.27	0/2639
37	u	0.09	0/996	0.28	0/1324
38	v	0.10	0/1100	0.19	0/1456
39	x	0.11	0/2313	0.34	0/3100
40	y	0.08	0/1722	0.24	0/2343
All	All	0.09	0/102978	0.23	0/148207

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
39	x	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
39	x	168	GLY	Peptide
39	x	285	GLU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	36363	18261	18281	462	0
2	2	3123	1579	1581	32	0
3	3	1434	1474	1473	15	0
4	4	1853	1891	1887	20	0
5	5	3055	3115	3113	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	6	1370	691	692	33	0
7	A	1189	1190	1186	9	0
8	B	2646	2728	2726	35	0
9	C	2611	2725	2724	41	0
10	D	3486	3620	3618	18	0
11	E	1205	1292	1291	17	0
12	F	1936	2033	2032	20	0
13	G	1226	1284	1282	28	0
14	H	1249	1311	1305	12	0
15	K	2073	2157	2155	32	0
16	L	864	918	917	18	0
17	M	992	1086	1085	13	0
18	N	1513	1566	1564	23	0
19	O	1555	1660	1659	6	0
20	P	1062	1077	1075	11	0
21	Q	1009	1092	1091	11	0
22	S	1432	1472	1470	22	0
23	V	378	380	378	3	0
24	W	1405	1429	1423	12	0
25	Y	984	1076	1075	8	0
26	b	3410	3466	3463	35	0
27	e	994	1063	1062	12	0
28	f	850	881	880	8	0
29	h	964	1074	1073	6	0
30	i	555	608	607	11	0
31	j	566	571	566	11	0
32	m	1362	1347	1347	13	0
33	n	2708	2764	2759	25	0
34	o	1107	1160	1159	19	0
35	r	593	617	616	10	0
36	t	1935	2039	2037	27	0
37	u	976	1011	1009	15	0
38	v	1087	1136	1133	7	0
39	x	2268	2305	2302	20	0
40	y	1701	1697	1697	27	0
41	j	1	0	0	0	0
41	u	1	0	0	0	0
All	All	97091	78846	78793	981	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 981 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)
1:1:3019:U:O2'	1:1:3020:U:O5'	1.86	0.94
6:6:15:C:O2'	6:6:16:U:OP2	1.88	0.91
1:1:3061:G:O2'	1:1:3334:U:OP1	1.91	0.88
1:1:1347:U:O2'	1:1:1348:U:OP1	1.92	0.87
1:1:1:G:O2'	1:1:2:U:OP2	1.93	0.86

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	
3	3	171/306 (56%)	157 (92%)	13 (8%)	1 (1%)	21	58
4	4	209/278 (75%)	192 (92%)	17 (8%)	0	100	100
5	5	377/463 (81%)	370 (98%)	7 (2%)	0	100	100
7	A	134/291 (46%)	123 (92%)	11 (8%)	0	100	100
8	B	329/387 (85%)	313 (95%)	16 (5%)	0	100	100
9	C	341/362 (94%)	327 (96%)	14 (4%)	0	100	100
10	D	433/505 (86%)	415 (96%)	18 (4%)	0	100	100
11	E	147/176 (84%)	142 (97%)	5 (3%)	0	100	100
12	F	239/244 (98%)	233 (98%)	6 (2%)	0	100	100
13	G	154/256 (60%)	149 (97%)	5 (3%)	0	100	100
14	H	142/191 (74%)	138 (97%)	4 (3%)	0	100	100
15	K	253/376 (67%)	244 (96%)	9 (4%)	0	100	100
16	L	106/199 (53%)	103 (97%)	3 (3%)	0	100	100
17	M	125/138 (91%)	124 (99%)	1 (1%)	0	100	100
18	N	173/204 (85%)	172 (99%)	1 (1%)	0	100	100
19	O	195/199 (98%)	190 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	P	133/184 (72%)	130 (98%)	3 (2%)	0	100	100
21	Q	129/186 (69%)	127 (98%)	2 (2%)	0	100	100
22	S	168/172 (98%)	158 (94%)	10 (6%)	0	100	100
23	V	46/137 (34%)	46 (100%)	0	0	100	100
24	W	156/236 (66%)	152 (97%)	4 (3%)	0	100	100
25	Y	123/127 (97%)	121 (98%)	2 (2%)	0	100	100
26	b	413/647 (64%)	391 (95%)	22 (5%)	0	100	100
27	e	121/130 (93%)	118 (98%)	3 (2%)	0	100	100
28	f	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
29	h	116/120 (97%)	108 (93%)	8 (7%)	0	100	100
30	i	68/100 (68%)	65 (96%)	3 (4%)	0	100	100
31	j	69/88 (78%)	68 (99%)	1 (1%)	0	100	100
32	m	159/807 (20%)	154 (97%)	5 (3%)	0	100	100
33	n	321/605 (53%)	311 (97%)	10 (3%)	0	100	100
34	o	131/220 (60%)	123 (94%)	8 (6%)	0	100	100
35	r	64/261 (24%)	64 (100%)	0	0	100	100
36	t	240/322 (74%)	222 (92%)	18 (8%)	0	100	100
37	u	114/199 (57%)	113 (99%)	1 (1%)	0	100	100
38	v	124/231 (54%)	121 (98%)	3 (2%)	0	100	100
39	x	261/295 (88%)	236 (90%)	25 (10%)	0	100	100
40	y	223/245 (91%)	217 (97%)	6 (3%)	0	100	100
All	All	6811/9994 (68%)	6538 (96%)	272 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	3	40	ARG

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%)	154 (99%)	1 (1%)	78	80
4	4	203/257 (79%)	200 (98%)	3 (2%)	57	70
5	5	343/410 (84%)	341 (99%)	2 (1%)	78	80
7	A	134/263 (51%)	133 (99%)	1 (1%)	76	79
8	B	280/323 (87%)	278 (99%)	2 (1%)	76	79
9	C	273/289 (94%)	273 (100%)	0	100	100
10	D	381/440 (87%)	377 (99%)	4 (1%)	68	76
11	E	131/153 (86%)	130 (99%)	1 (1%)	73	77
12	F	204/205 (100%)	203 (100%)	1 (0%)	81	81
13	G	128/208 (62%)	125 (98%)	3 (2%)	44	63
14	H	142/171 (83%)	142 (100%)	0	100	100
15	K	238/346 (69%)	237 (100%)	1 (0%)	84	82
16	L	87/159 (55%)	85 (98%)	2 (2%)	44	63
17	M	100/109 (92%)	100 (100%)	0	100	100
18	N	153/176 (87%)	151 (99%)	2 (1%)	61	72
19	O	160/162 (99%)	157 (98%)	3 (2%)	50	66
20	P	109/146 (75%)	107 (98%)	2 (2%)	51	66
21	Q	107/151 (71%)	107 (100%)	0	100	100
22	S	155/156 (99%)	154 (99%)	1 (1%)	78	80
23	V	39/105 (37%)	39 (100%)	0	100	100
24	W	156/213 (73%)	154 (99%)	2 (1%)	61	72
25	Y	108/110 (98%)	108 (100%)	0	100	100
26	b	377/573 (66%)	375 (100%)	2 (0%)	81	81
27	e	106/111 (96%)	106 (100%)	0	100	100
28	f	90/91 (99%)	90 (100%)	0	100	100
29	h	104/105 (99%)	104 (100%)	0	100	100
30	i	57/82 (70%)	55 (96%)	2 (4%)	32	53
31	j	59/71 (83%)	59 (100%)	0	100	100
32	m	150/723 (21%)	150 (100%)	0	100	100
33	n	299/548 (55%)	297 (99%)	2 (1%)	76	79
34	o	118/199 (59%)	116 (98%)	2 (2%)	53	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	r	61/229 (27%)	60 (98%)	1 (2%)	55	69
36	t	216/287 (75%)	214 (99%)	2 (1%)	70	76
37	u	101/180 (56%)	100 (99%)	1 (1%)	68	76
38	v	116/205 (57%)	116 (100%)	0	100	100
39	x	252/276 (91%)	250 (99%)	2 (1%)	73	77
40	y	193/211 (92%)	192 (100%)	1 (0%)	81	81
All	All	6085/8717 (70%)	6039 (99%)	46 (1%)	70	77

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	S	12	ARG
33	n	417	LEU
24	W	173	THR
26	b	171	LEU
34	o	102	PHE

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

Mol	Chain	Res	Type
22	S	62	ASN
37	u	5	GLN
26	b	156	HIS
36	t	154	ASN
34	o	130	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1683/3396 (49%)	361 (21%)	44 (2%)
2	2	144/158 (91%)	24 (16%)	1 (0%)
6	6	65/232 (28%)	24 (36%)	5 (7%)
All	All	1892/3786 (49%)	409 (21%)	50 (2%)

5 of 409 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U

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Mol	Chain	Res	Type
1	1	3	U
1	1	6	A
1	1	7	C
1	1	15	C

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2393	G
1	1	3019	U
6	6	229	U
1	1	2852	C
1	1	2887	A

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 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

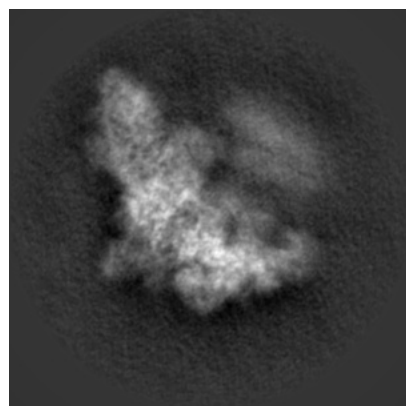
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12907. These allow visual inspection of the internal detail of the map and identification of artifacts.

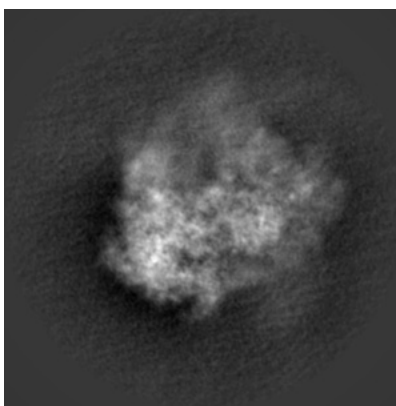
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

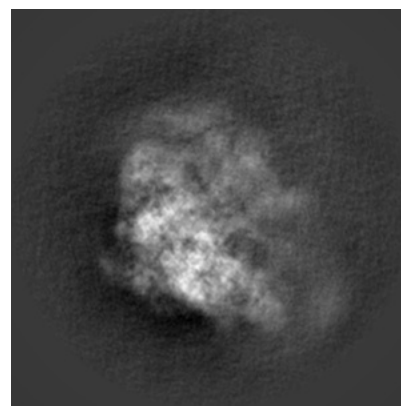
6.1.1 Primary map



X

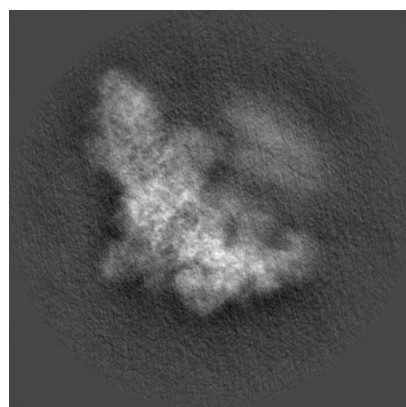


Y

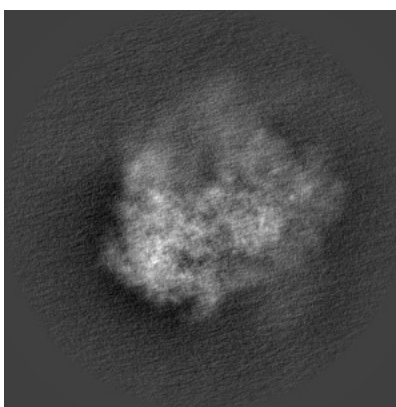


Z

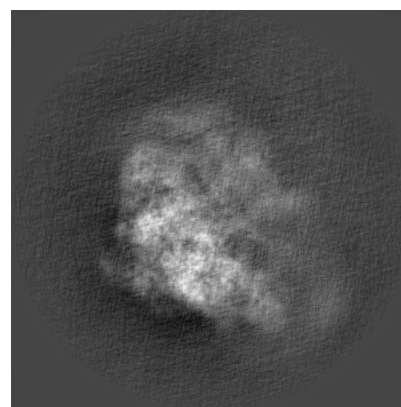
6.1.2 Raw map



X



Y

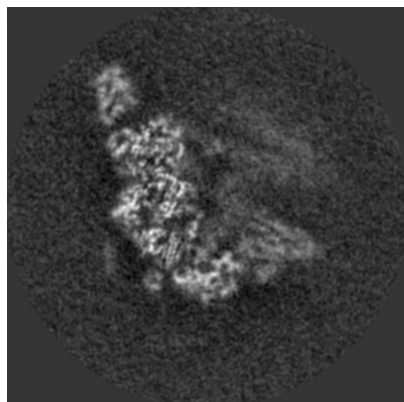


Z

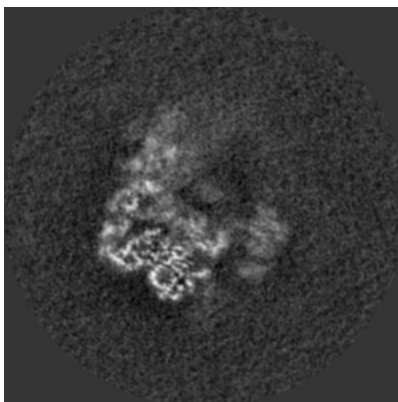
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

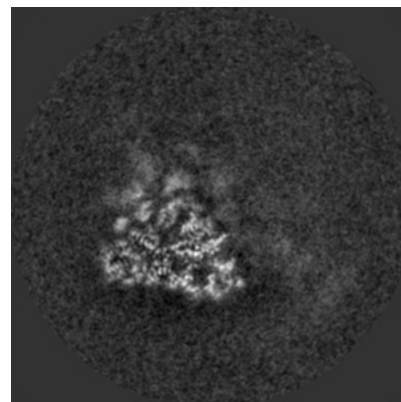
6.2.1 Primary map



X Index: 200

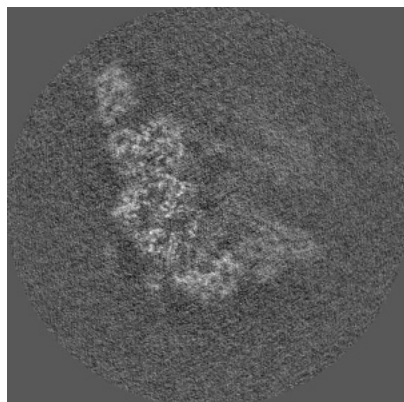


Y Index: 200

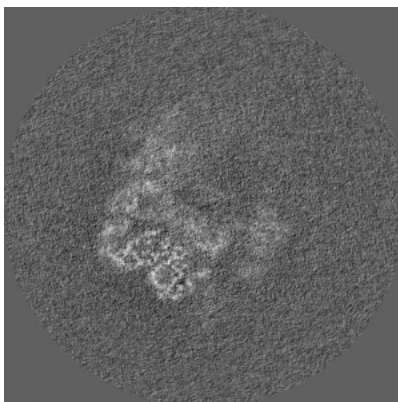


Z Index: 200

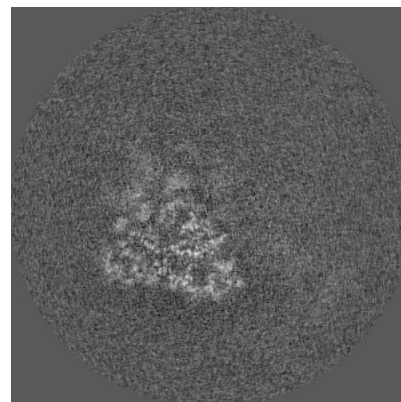
6.2.2 Raw map



X Index: 200



Y Index: 200

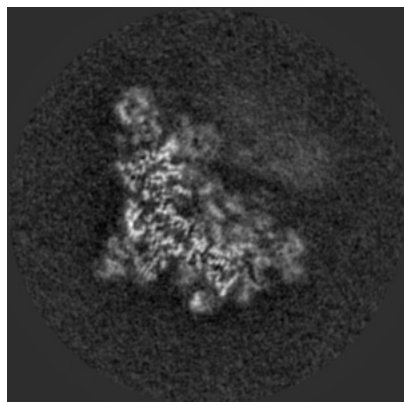


Z Index: 200

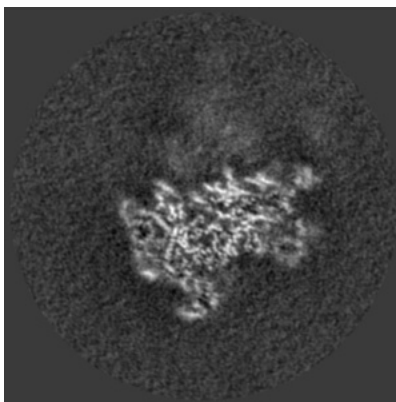
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

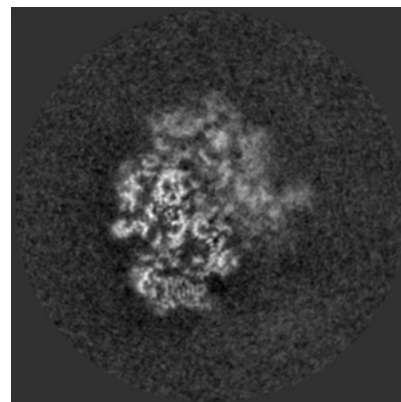
6.3.1 Primary map



X Index: 167

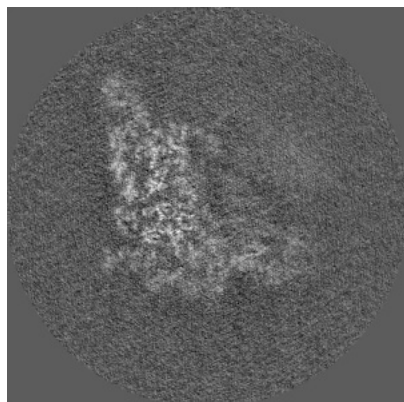


Y Index: 146

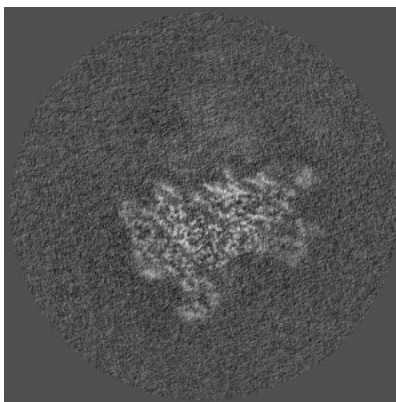


Z Index: 155

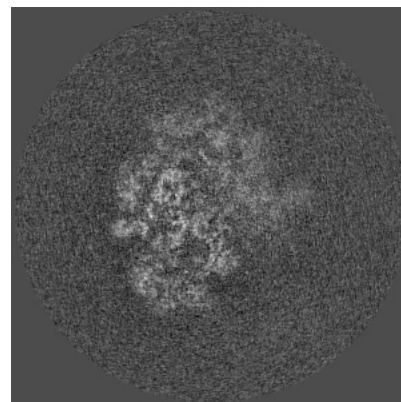
6.3.2 Raw map



X Index: 190



Y Index: 147

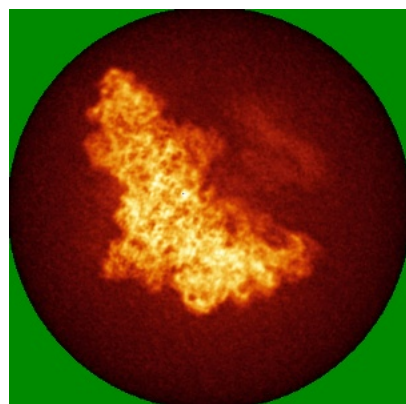


Z Index: 155

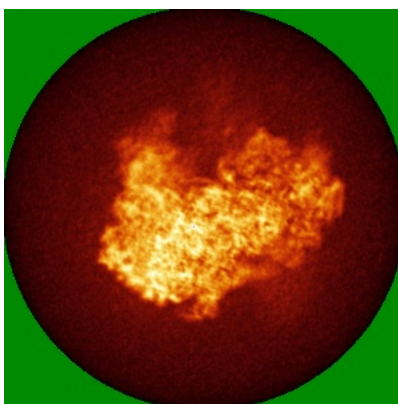
The images above show the largest variance slices of the map in three orthogonal directions.

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

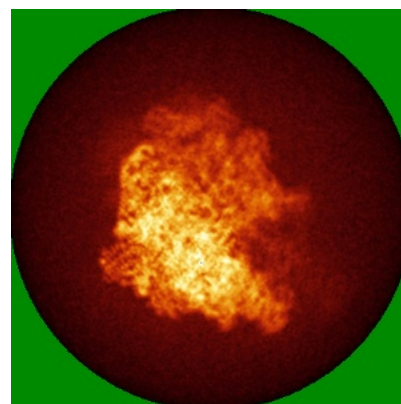
6.4.1 Primary map



X

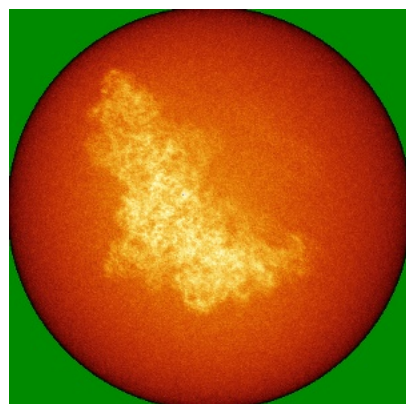


Y

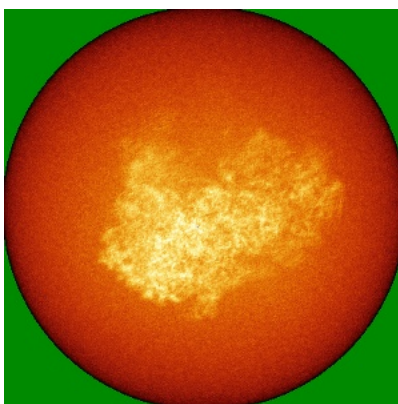


Z

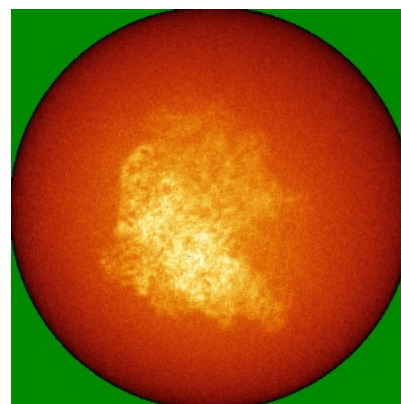
6.4.2 Raw map



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.

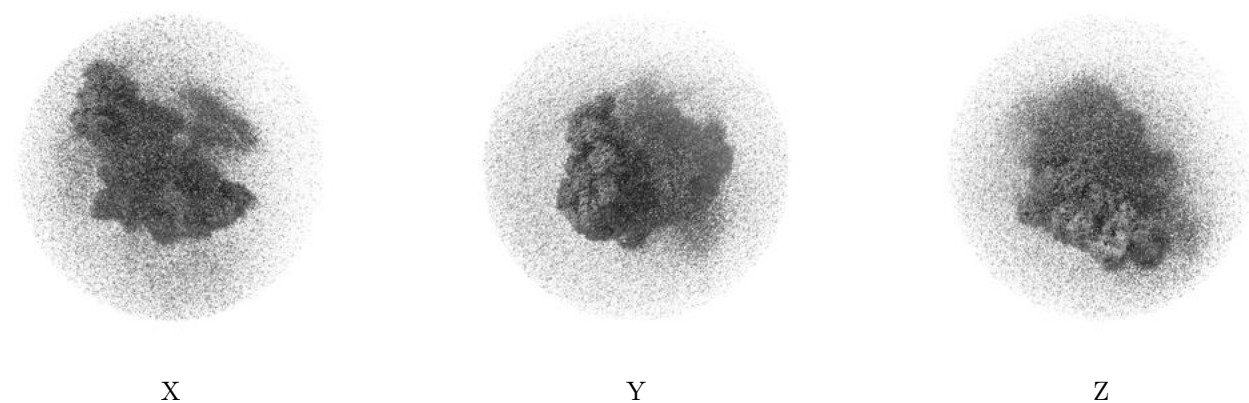
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.022. 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.

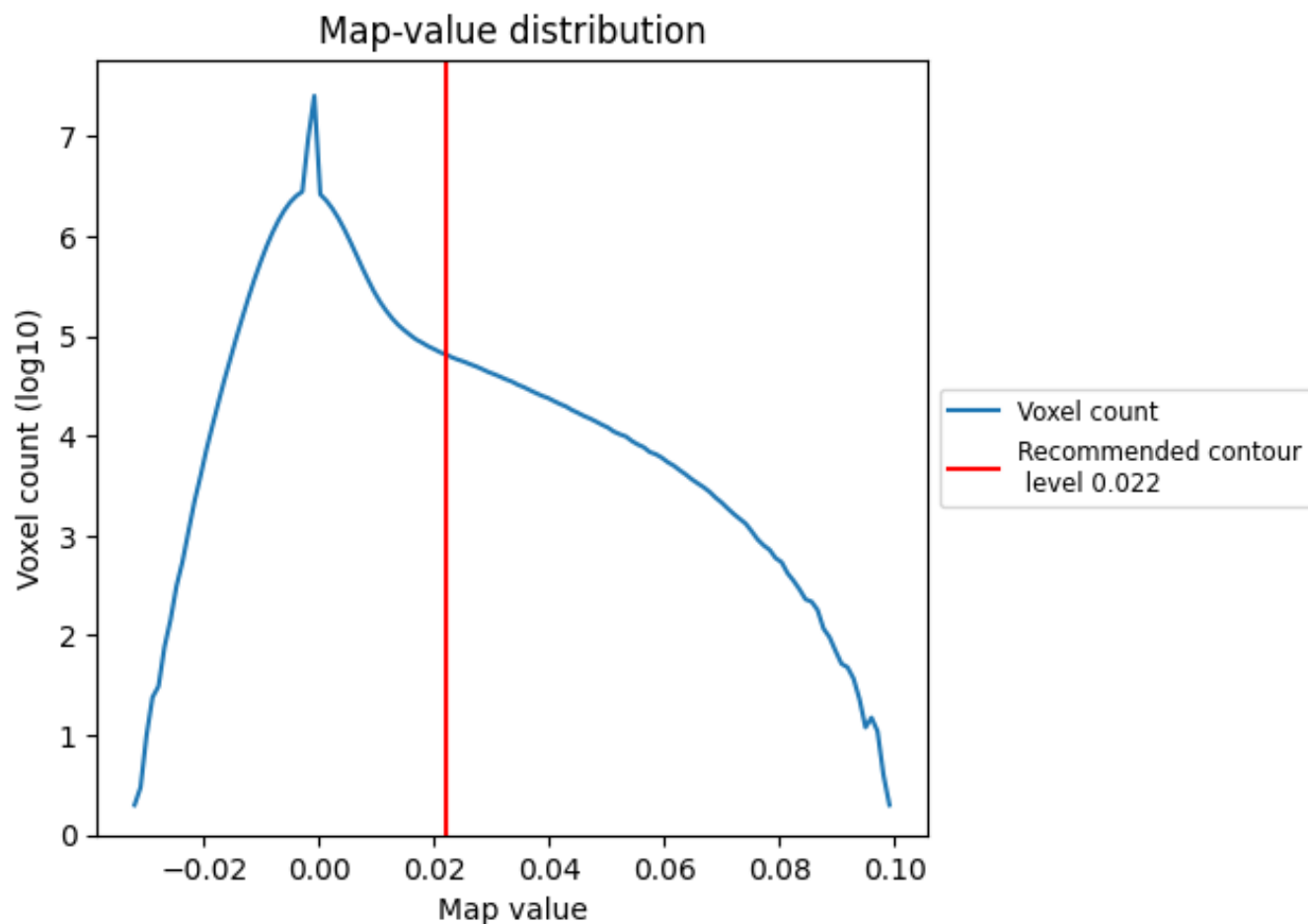
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

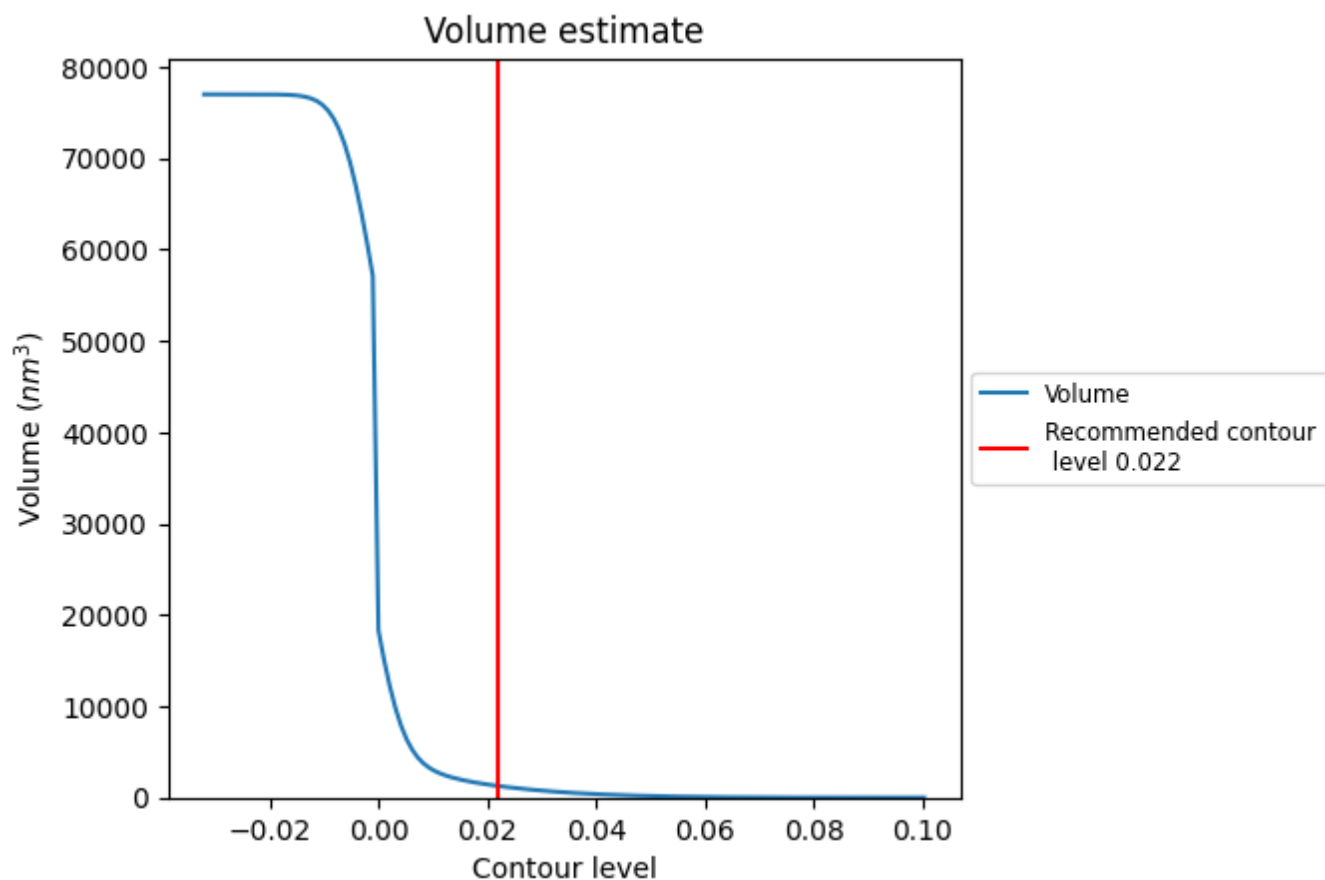
This section contains the results of statistical analysis of the map.

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.

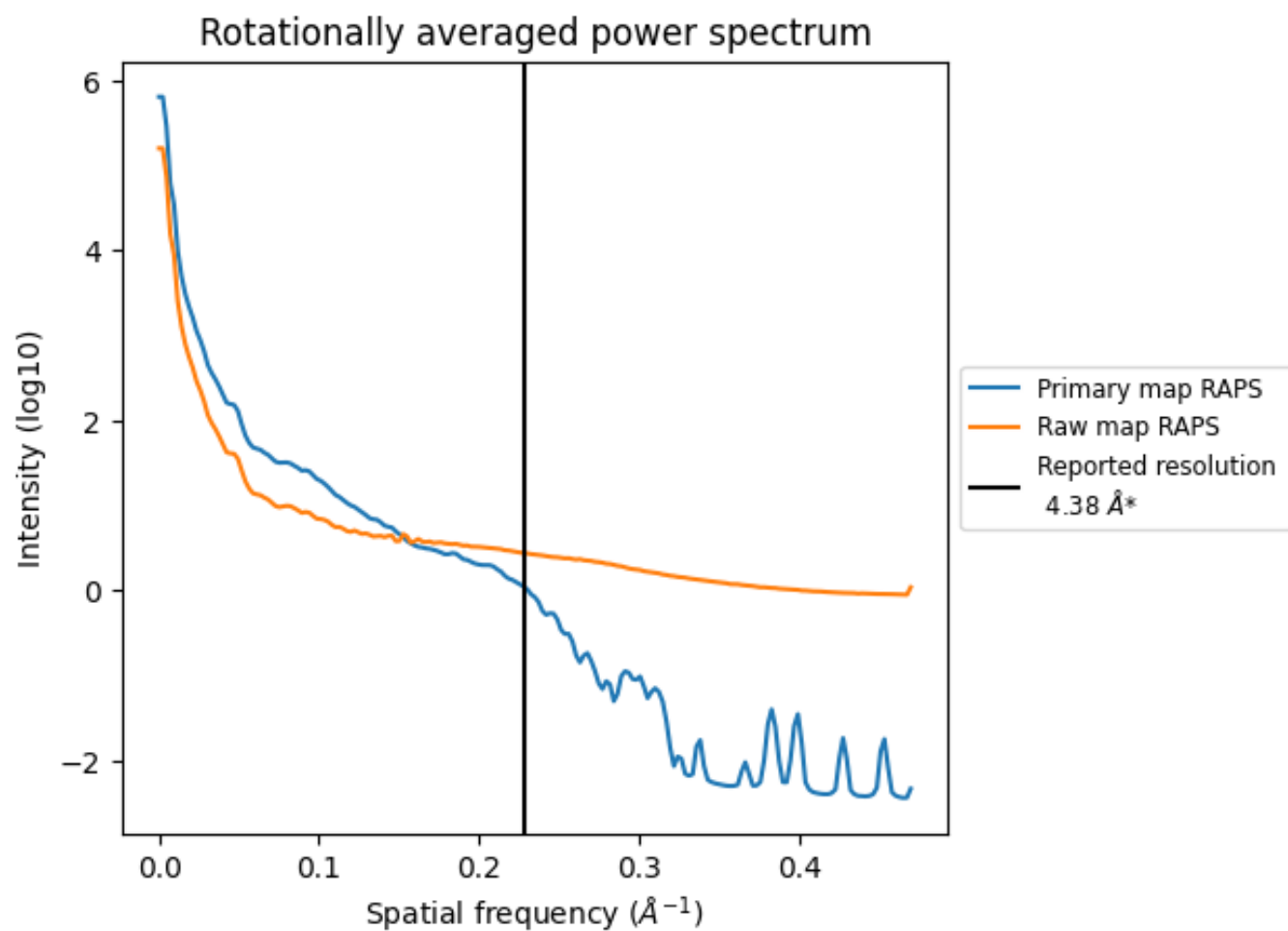
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1266 nm³; this corresponds to an approximate mass of 1144 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 ⓘ

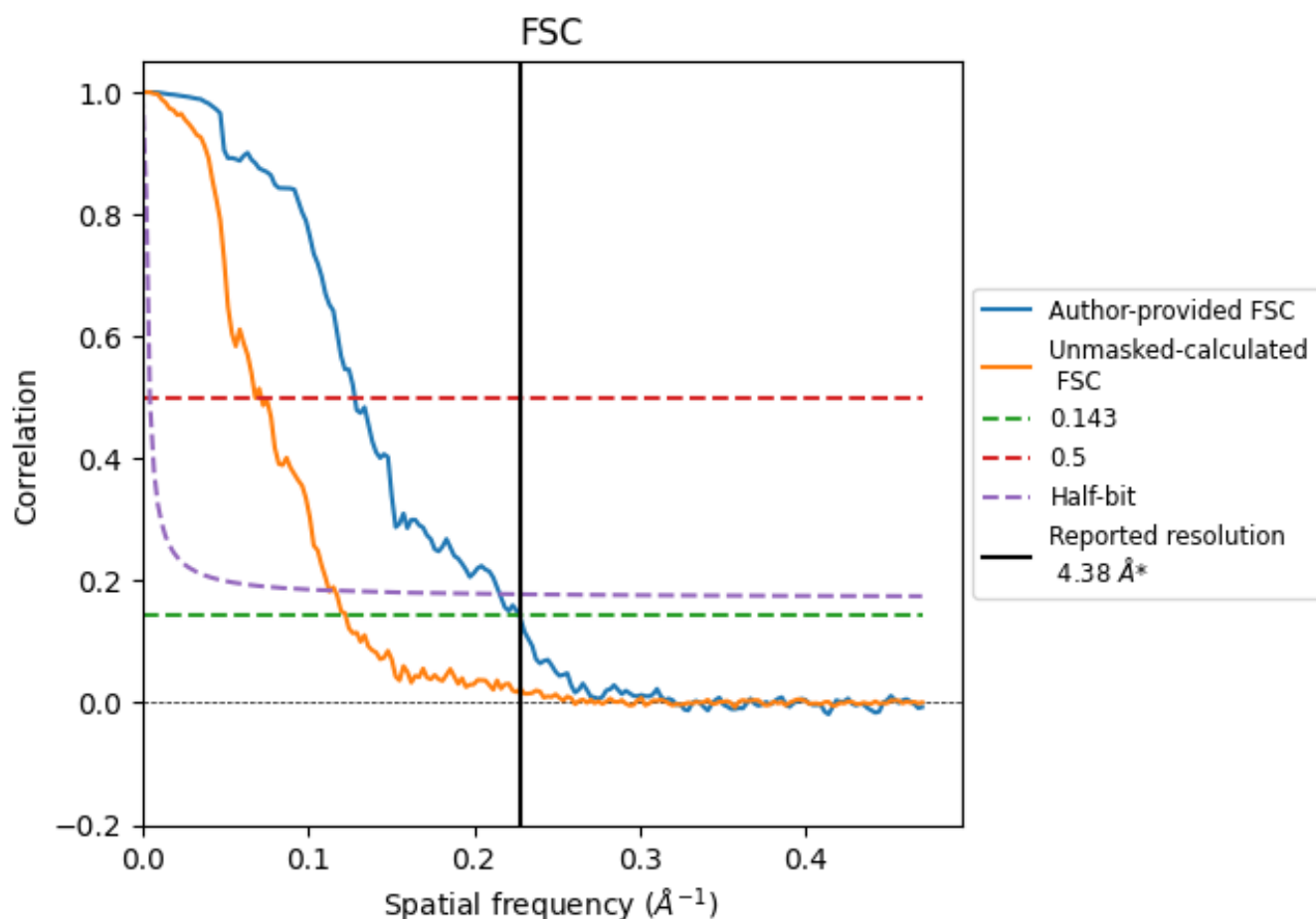


*Reported resolution corresponds to spatial frequency of 0.228 Å⁻¹

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 0.228 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

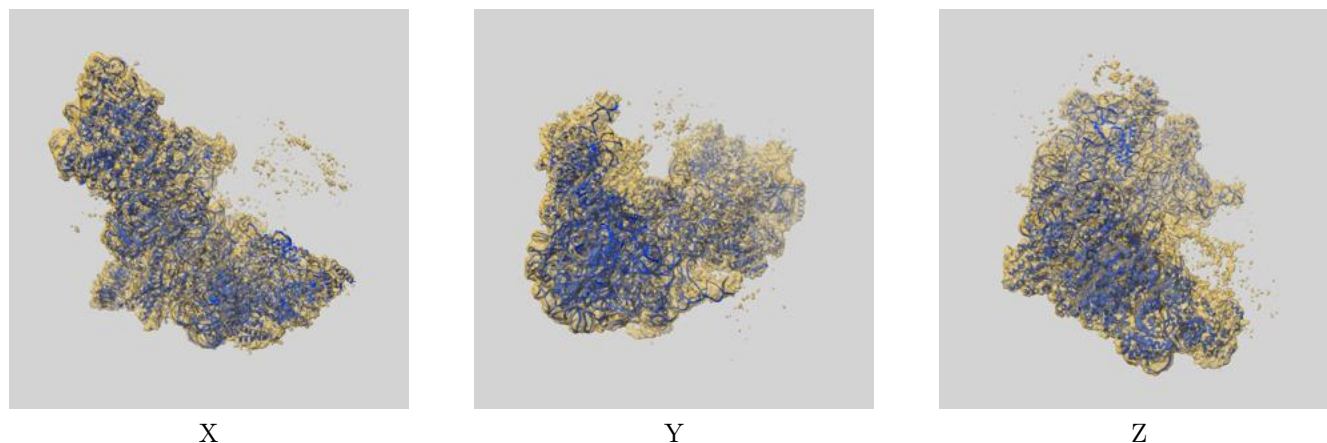
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.38	-	-
Author-provided FSC curve	4.40	7.81	4.64
Unmasked-calculated*	8.16	14.68	8.87

*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 8.16 differs from the reported value 4.38 by more than 10 %

9 Map-model fit [i](#)

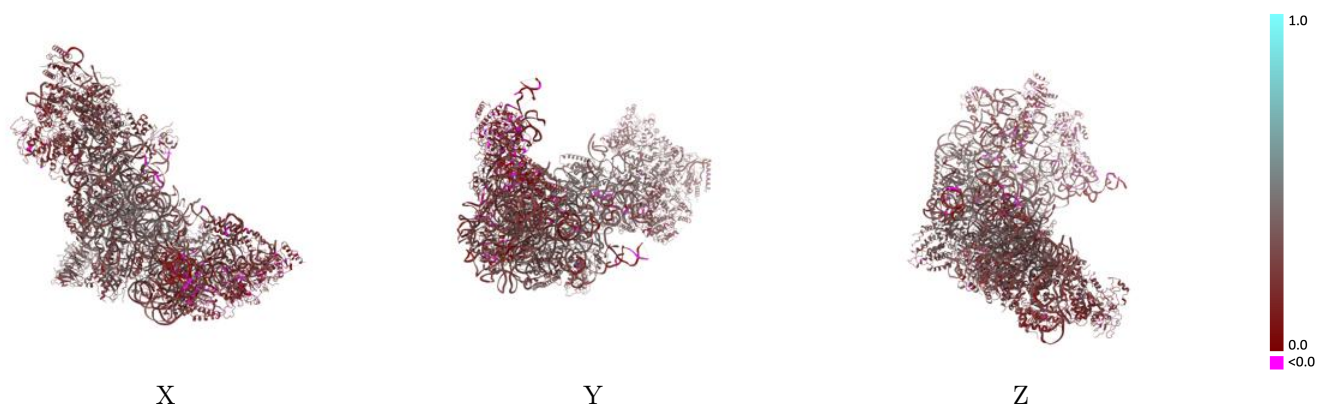
This section contains information regarding the fit between EMDB map EMD-12907 and PDB model 7OHS. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



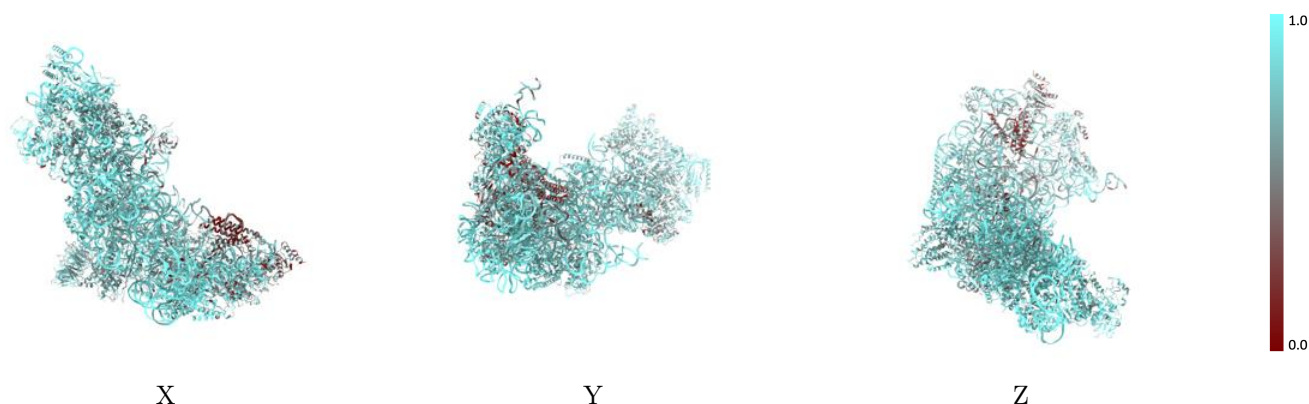
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



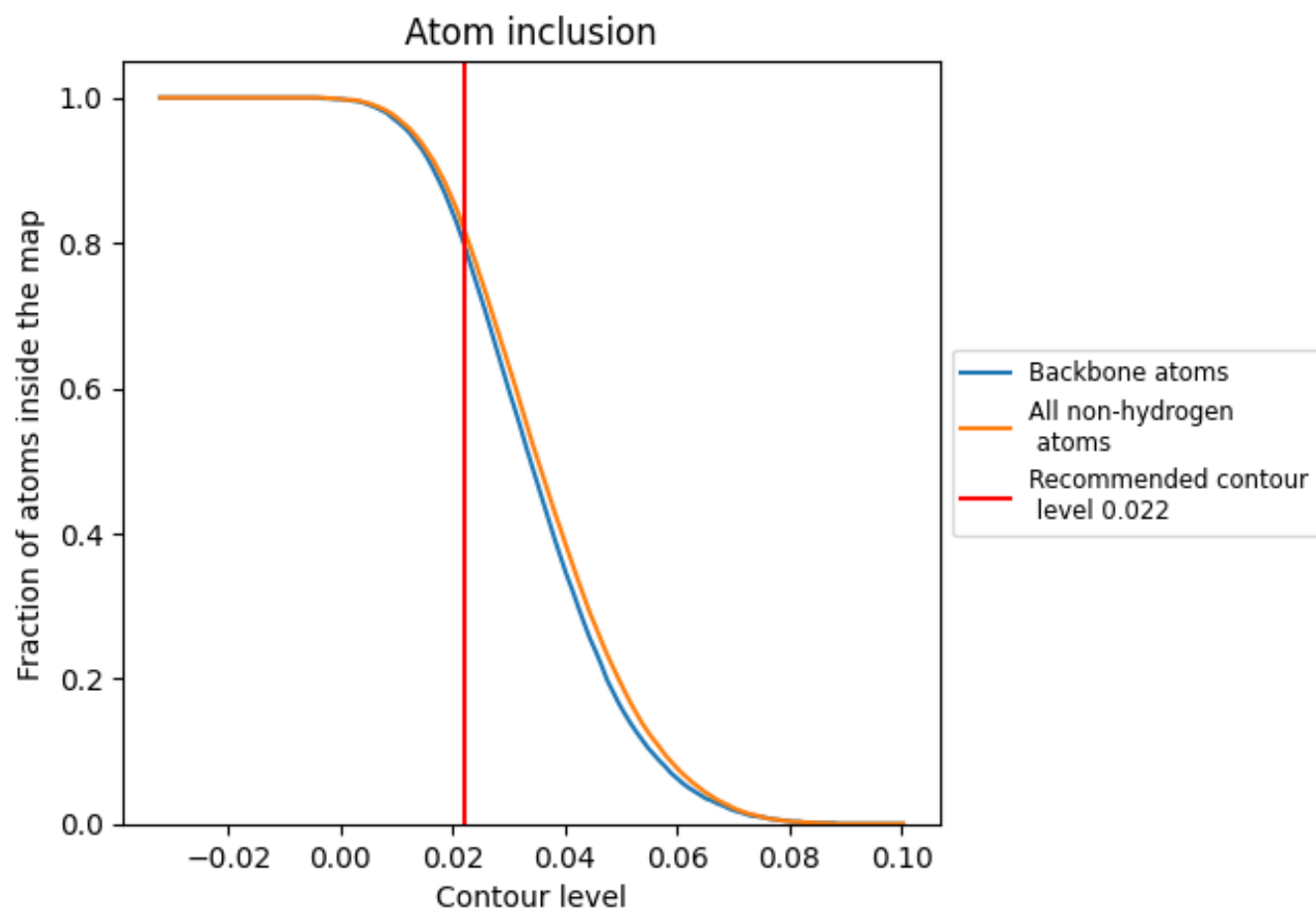
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.022).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 82% 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 (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8190	 0.2800
1	 0.9080	 0.2800
2	 0.9600	 0.3070
3	 0.7410	 0.3080
4	 0.7770	 0.2830
5	 0.7480	 0.3230
6	 0.9500	 0.2650
A	 0.5870	 0.2290
B	 0.8180	 0.2240
C	 0.8020	 0.3580
D	 0.6940	 0.2680
E	 0.8740	 0.3480
F	 0.8160	 0.3400
G	 0.7570	 0.3140
H	 0.5210	 0.2530
K	 0.8310	 0.2400
L	 0.8280	 0.3380
M	 0.8810	 0.3310
N	 0.7510	 0.3200
O	 0.8020	 0.3210
P	 0.6940	 0.3010
Q	 0.7810	 0.3540
S	 0.8230	 0.3070
V	 0.7870	 0.2190
W	 0.5690	 0.2040
Y	 0.8460	 0.3530
b	 0.4560	 0.1990
e	 0.7410	 0.3650
f	 0.8310	 0.3780
h	 0.8020	 0.3050
i	 0.7630	 0.2700
j	 0.8360	 0.3470
m	 0.7610	 0.2500
n	 0.7890	 0.2350
o	 0.8680	 0.2520



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Chain	Atom inclusion	Q-score
r	 0.4950	 0.2470
t	 0.7790	 0.2380
u	 0.7790	 0.1610
v	 0.7920	 0.3100
x	 0.7050	 0.2990
y	 0.7020	 0.1560