wwPDB EM Validation Summary Report

Mar 12, 2026 – 06:25 AM UTC

PDB ID	:	7OHY / pdb_00007ohy
EMDB ID	:	EMD-12913
Title	:	Nog1-TAP associated immature ribosomal particles from S. cerevisiae after rpL34 expression shut down, population B
Authors	:	Milkereit, P.; Poell, G.
Deposited on	:	2021-05-11
Resolution	:	3.90 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 (i) 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 (i)) were used in the production of this report:

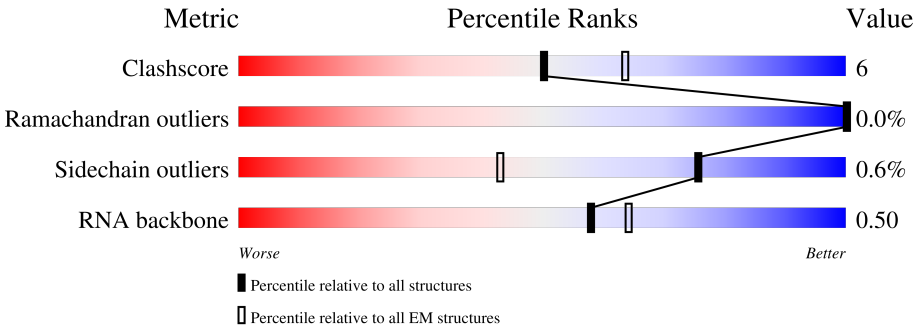
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

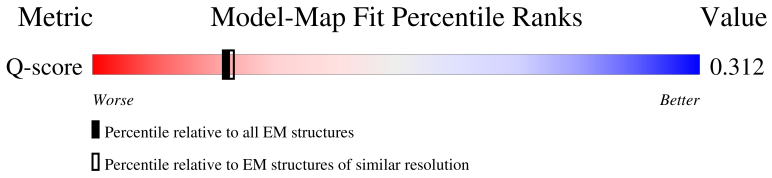
1 Overall quality at a glance

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

The reported resolution of this entry is 3.90 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	8855 (3.40 - 4.40)

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 <=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	30% 15% 5% 50%
2	2	158	50% 33% 11% 6%
3	B	387	73% 13% 14%

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Mol	Chain	Length	Quality of chain
4	C	362	84% 10% 5%
5	E	176	78% 7% 14%
6	F	244	84% 9% 7%
7	G	256	11% 34% 8% 58%
8	H	191	5% 86% 12%
9	L	199	45% 8% 46%
10	M	138	86% 11%
11	N	204	77% 9% 13%
12	O	199	93% 6%
13	P	184	5% 62% 7% 32%
14	Q	186	62% 8% 30%
15	S	172	85% 14%
16	V	137	34% 69% 12% 19%
17	W	236	22% 81% 15%
18	Y	127	88% 10%
19	b	647	19% 52% 6% 42%
20	e	130	90% 6%
21	f	107	84% 15%
22	h	120	7% 88% 12%
23	j	88	64% 17% 19%
24	r	261	10% 25% 73%
25	u	199	5% 51% 7% 42%
26	y	245	8% 79% 13% 8%

2 Entry composition (i)

There are 27 unique types of molecules in this entry. The entry contains 125318 atoms, of which 53608 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	1	1689	54311	16140	18161	6526	11795	1689	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
2	2	148	4733	1406	1590	554	1035	148	0	0

- Molecule 3 is a protein called 60S ribosomal protein L3.

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

- Molecule 4 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 5 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 6 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	F	228	3749	1180	1917	334	317	1	0	0

- Molecule 7 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	108	Total	C	H	N	O	S	0	0
			1751	544	911	147	147	2		

- Molecule 8 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 11 is a protein called 60S ribosomal protein L15-A.

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

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

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

- Molecule 13 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	126	Total	C	H	N	O	0	0
			1998	624	1005	186	183		

- Molecule 14 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 15 is a protein called 60S ribosomal protein L20-A.

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
16	V	111	Total	C	H	N	O	S	0	0
			1693	522	867	151	146	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
17	W	227	Total	C	H	N	O	S	0	0
			3683	1157	1852	315	354	5		

- Molecule 18 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 19 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	b	375	Total	C	H	N	O	S	0	0
			6144	1950	3104	515	557	18		

- Molecule 20 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	e	125	Total	C	H	N	O	S	0	0
			2090	641	1081	203	164	1		

- Molecule 21 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 24 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	r	71	Total	C	H	N	O	S	0	0
			1250	377	638	130	104	1		

- Molecule 25 is a protein called Ribosome biogenesis protein RLP24.

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

- Molecule 26 is a protein called Eukaryotic translation initiation factor 6.

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

- Molecule 27 is ZINC ION (CCD ID: ZN) (formula: Zn).

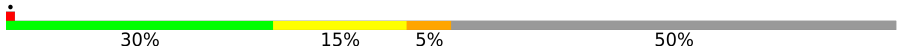
Mol	Chain	Residues	Atoms		AltConf
27	j	1	Total	Zn	0
			1	1	
27	u	1	Total	Zn	0
			1	1	

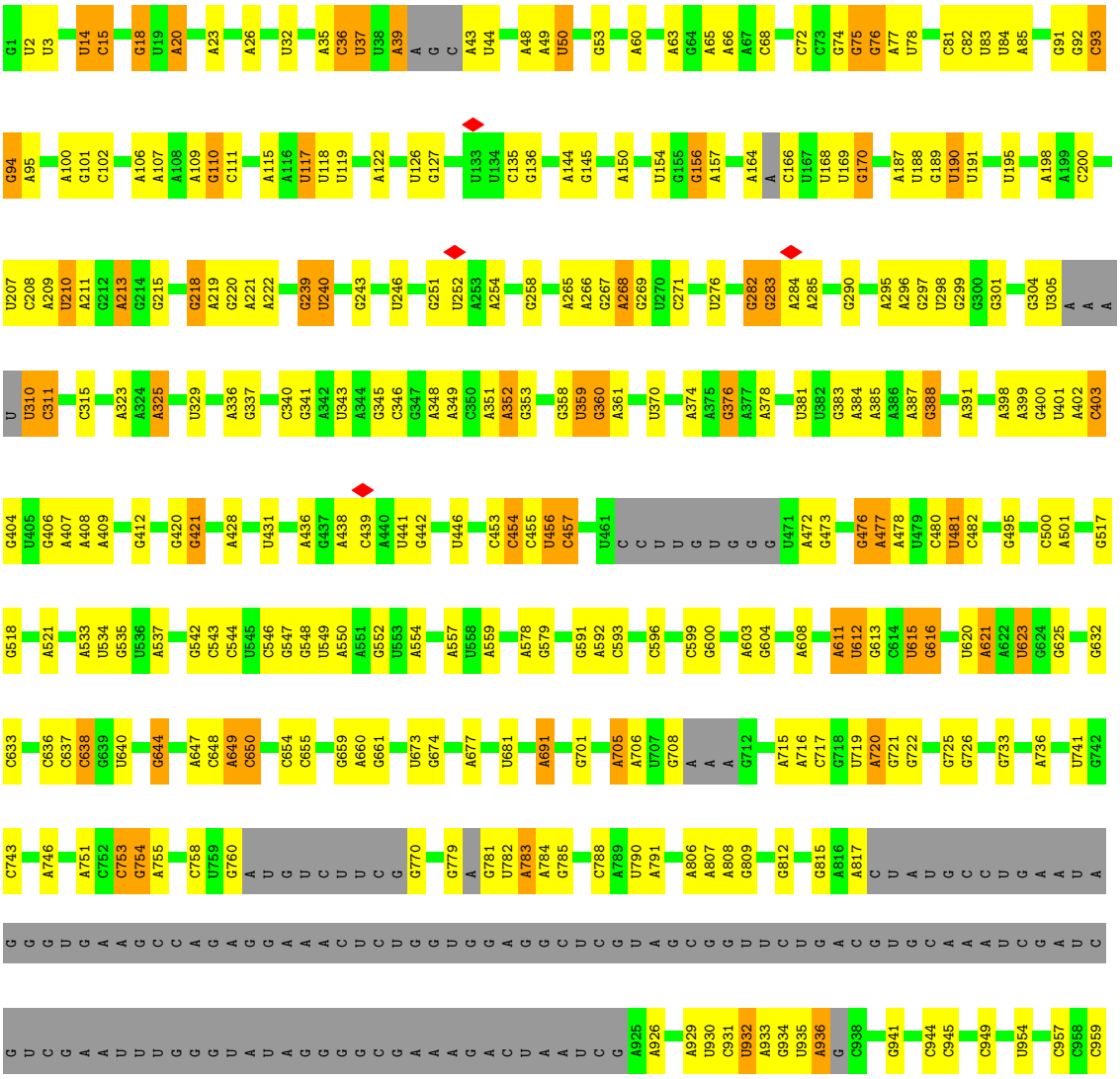
3 Residue-property plots (i)

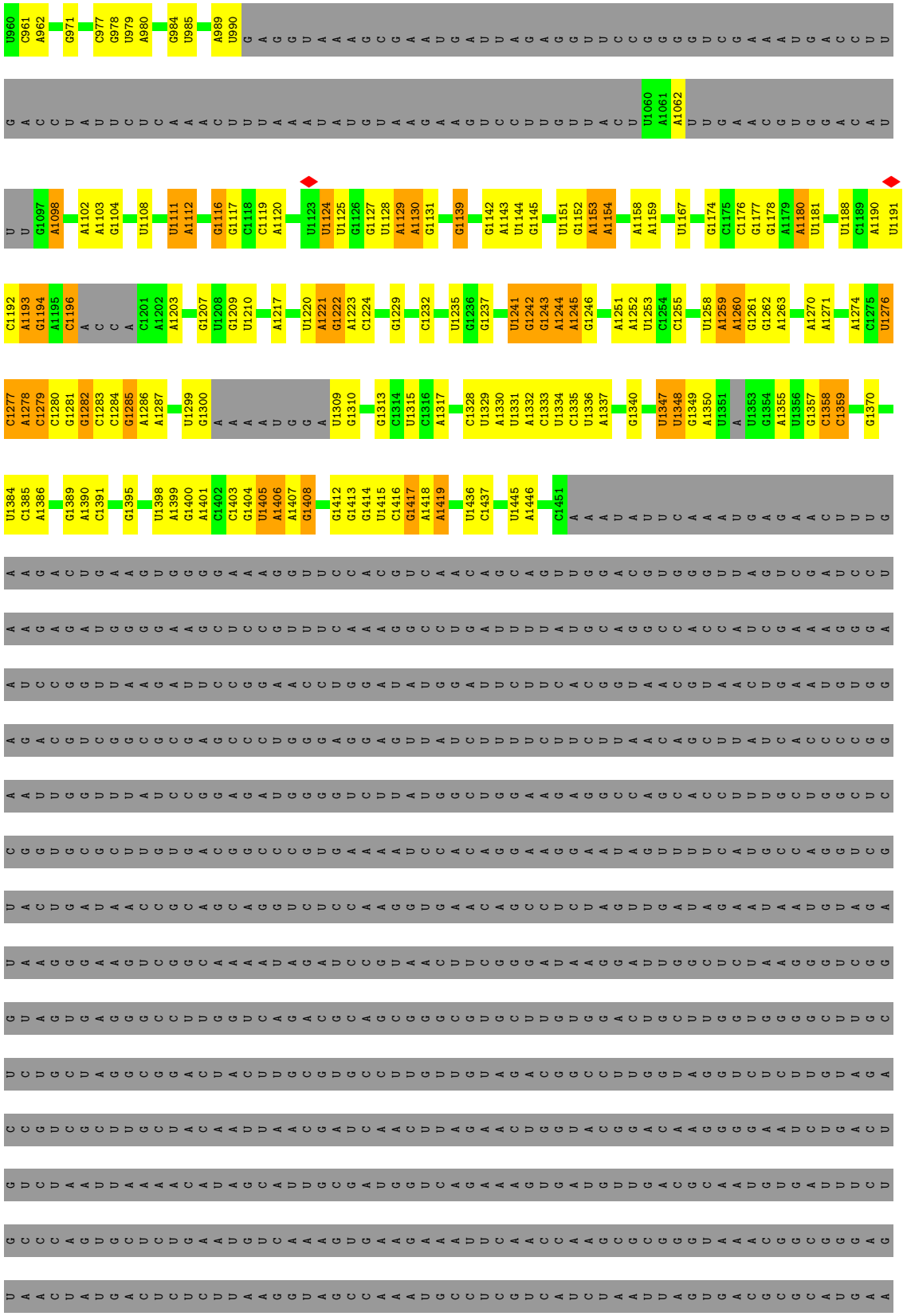
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

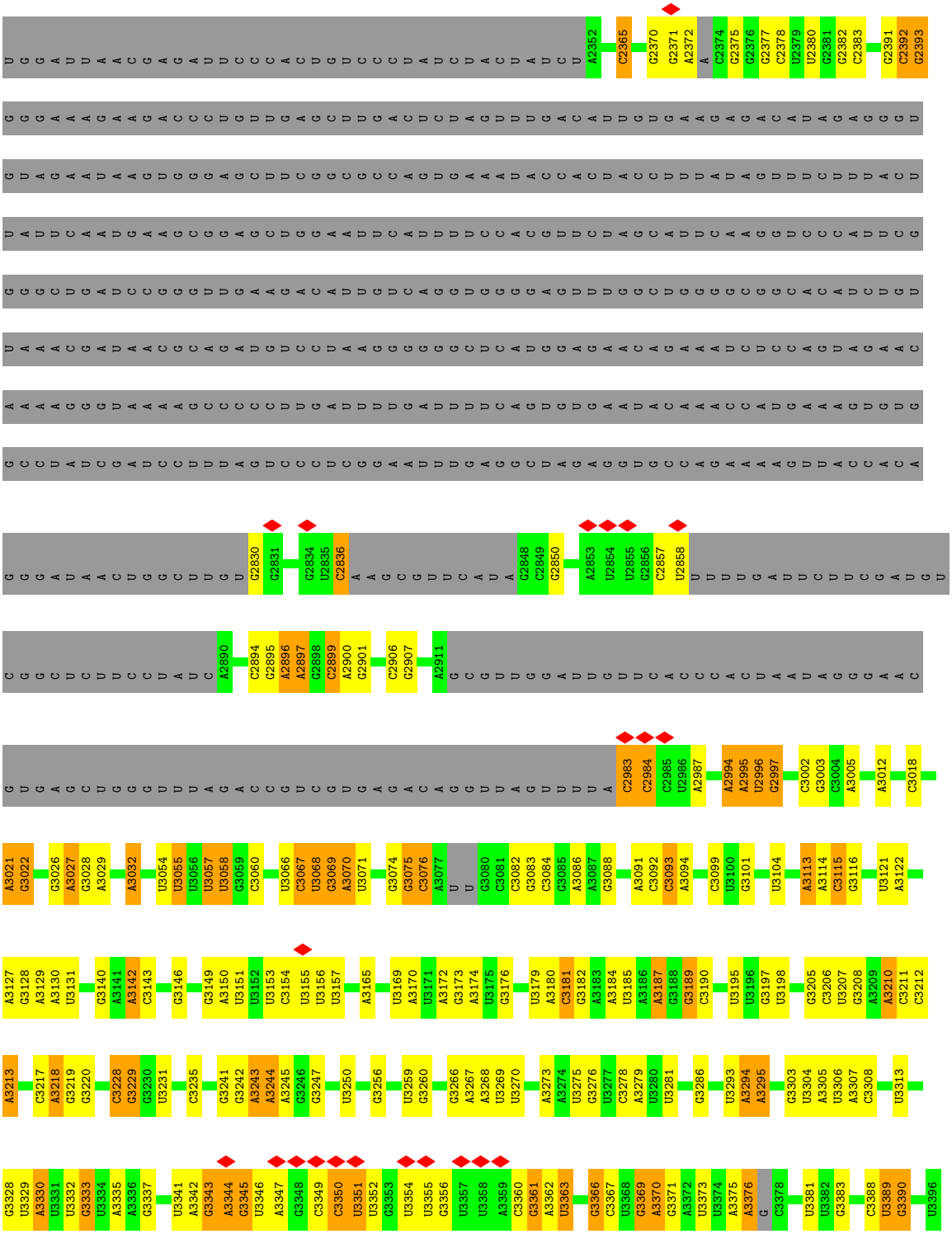
- Molecule 1: 25S rRNA

Chain 1:



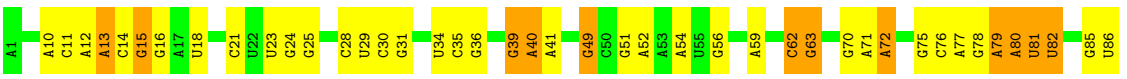


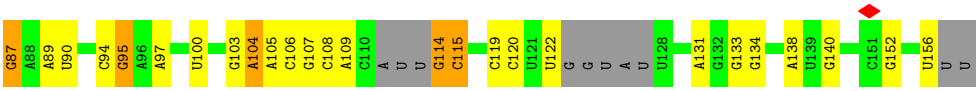

U960 C961 A962 G971 C977 G978 U979 A980 G984 U985 A989 U990
U1060 A1061 A1062
U G1097 A1098 A1102 A1103 G1104 U1108 U1111 A1112 G1116 G1117 C1118 C1119 A1120 U1123 U1124 U1125 G1126 G1127 U1128 A1129 A1130 G1131 G1139 G1142 A1143 U1144 G1145 U1151 G1152 A1153 A1154 A1158 A1159 U1167 G1174 C1175 C1176 G1177 G1178 A1179 A1180 U1181 U1188 C1189 A1190 U1191
C1192 A1193 G1194 A1195 C1196 C1201 A1202 A1203 G1207 U1208 G1209 U1210 A1217 U1220 A1221 G1222 A1223 C1224 G1229 C1232 U1235 G1236 G1237 U1241 G1242 G1243 A1244 A1245 G1246 A1251 A1252 U1253 C1254 C1255 U1258 A1259 A1260 G1261 G1262 A1263 A1270 A1271 A1274 C1275 U1276
C1277 A1278 C1279 C1280 G1281 G1282 C1283 C1284 G1285 A1286 A1287 U1299 G1300 U1309 G1310 G1313 C1314 U1315 C1316 A1317 C1328 U1329 A1330 U1331 A1332 C1333 U1334 C1335 U1336 A1337 G1340 U1347 U1348 G1349 A1350 U1351 U1353 G1354 A1355 U1356 G1357 C1358 C1359 G1370
U1384 C1385 A1386 G1389 A1390 C1391 G1395 U1398 A1399 G1400 A1401 C1402 C1403 G1404 U1405 A1406 A1407 G1408 G1412 G1413 G1414 U1415 C1416 G1417 A1418 A1419 U1436 C1437 U1445 A1446 C1451



• Molecule 2: 5.8S rRNA

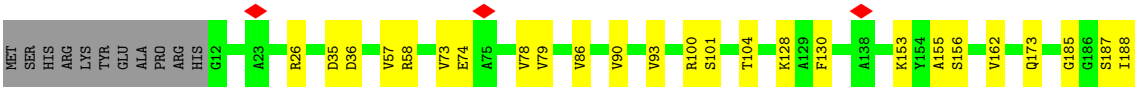
Chain 2:





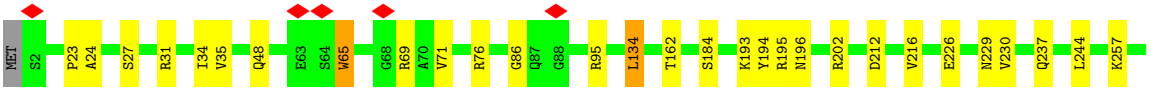
• Molecule 3: 60S ribosomal protein L3

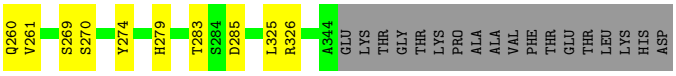
Chain B:



• Molecule 4: 60S ribosomal protein L4-A

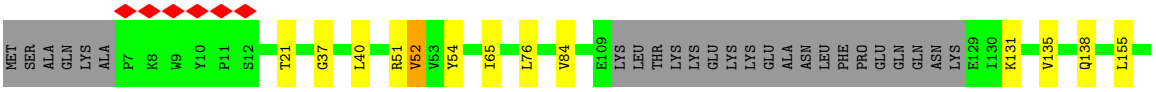
Chain C:





• Molecule 5: 60S ribosomal protein L6-A

Chain E:

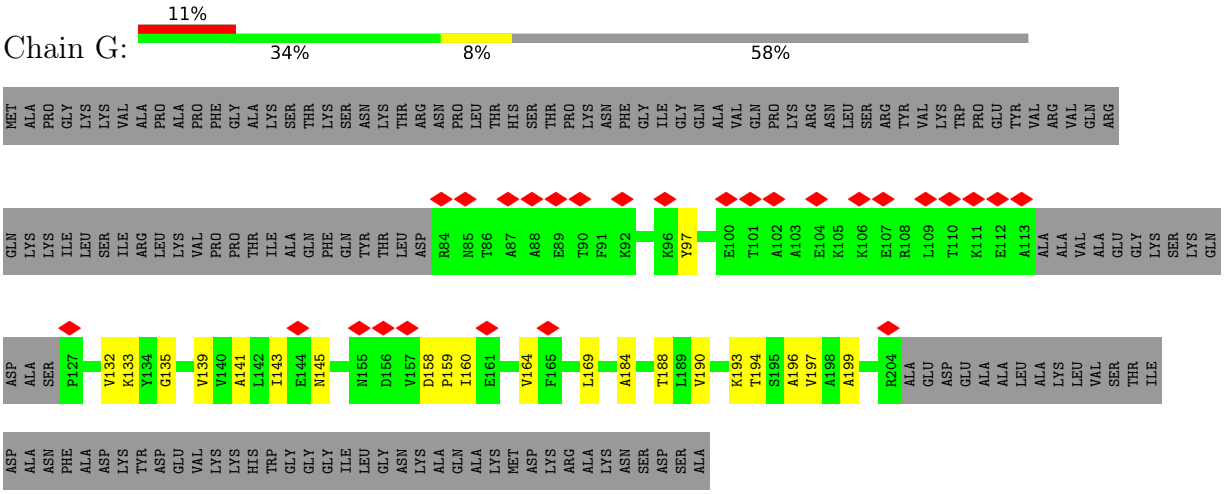


• Molecule 6: 60S ribosomal protein L7-A

Chain F:

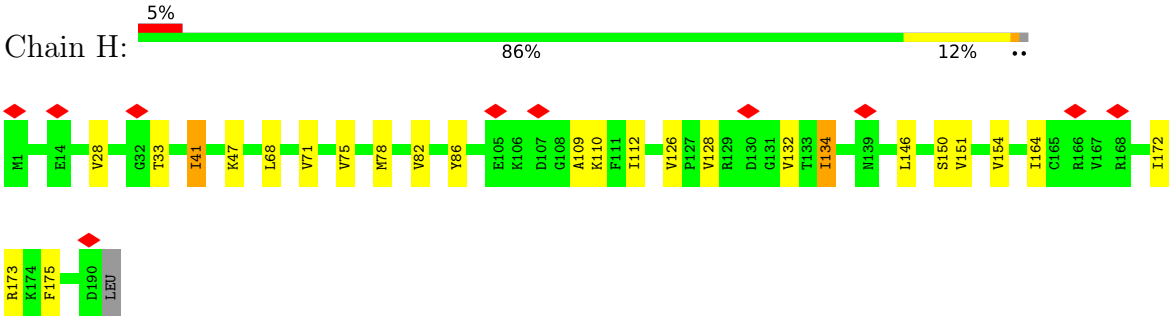
• Molecule 7: 60S ribosomal protein L8-A

Chain G:



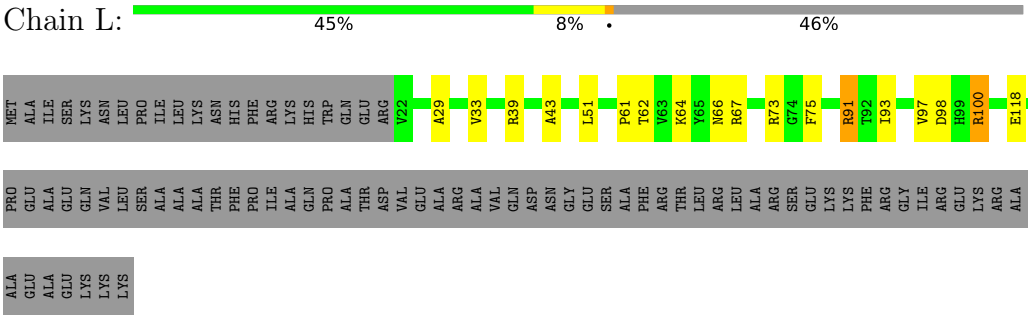
• Molecule 8: 60S ribosomal protein L9-A

Chain H:



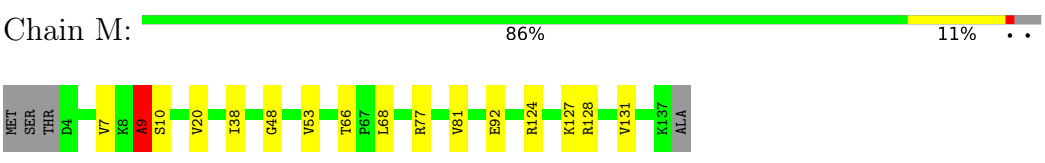
• Molecule 9: 60S ribosomal protein L13-A

Chain L:



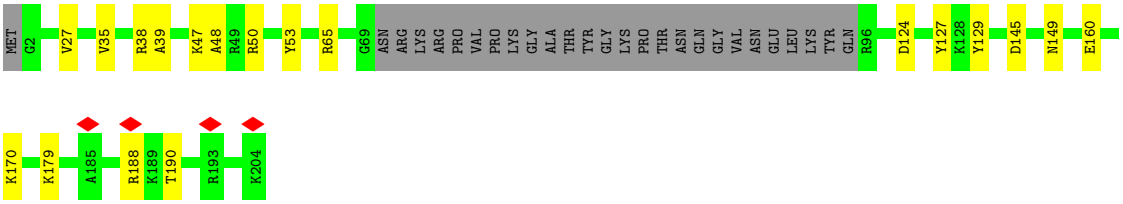
• Molecule 10: 60S ribosomal protein L14-A

Chain M:

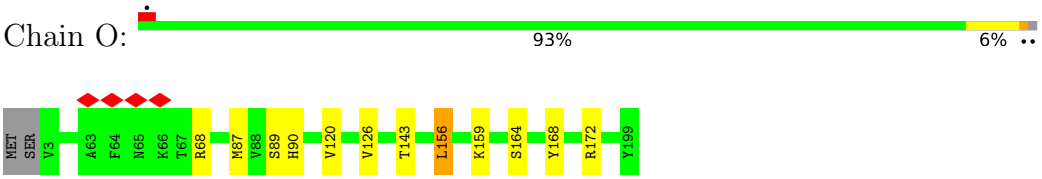


• Molecule 11: 60S ribosomal protein L15-A

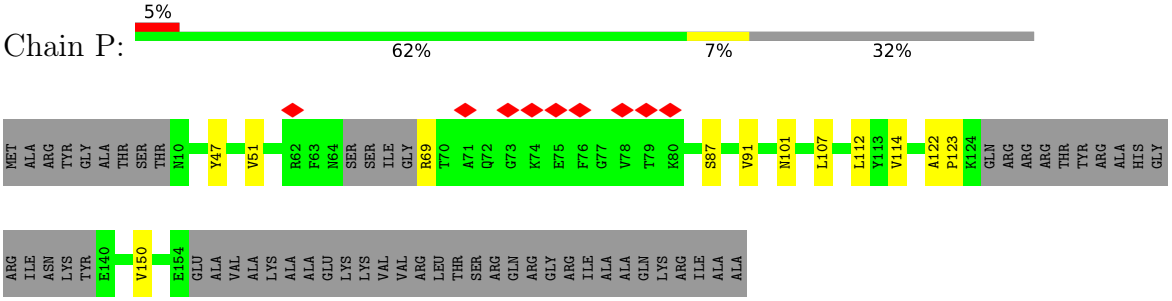
Chain N:



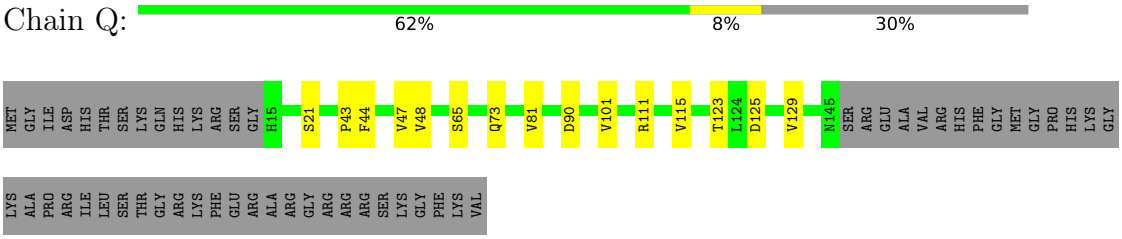
• Molecule 12: 60S ribosomal protein L16-A



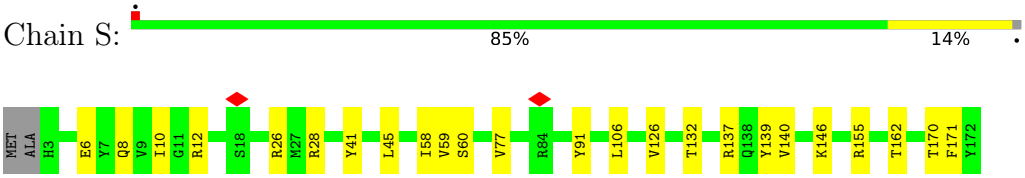
• Molecule 13: 60S ribosomal protein L17-A



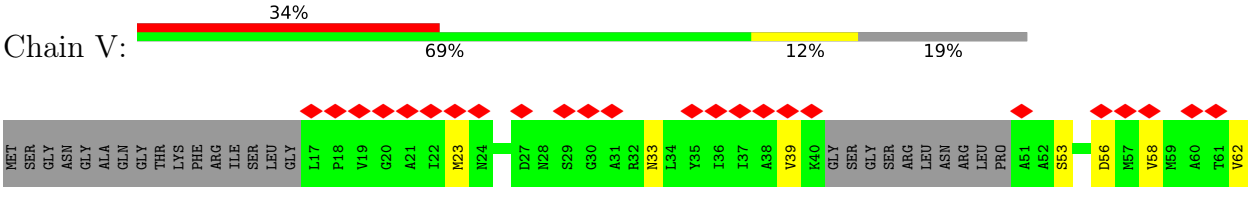
• Molecule 14: 60S ribosomal protein L18-A

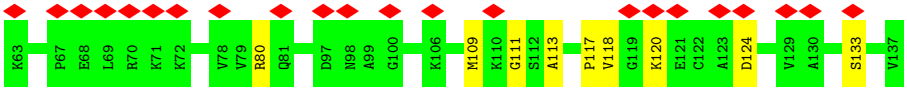


• Molecule 15: 60S ribosomal protein L20-A



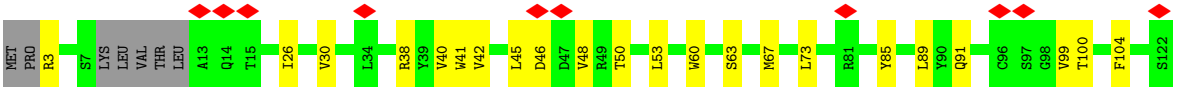
• Molecule 16: 60S ribosomal protein L23-A

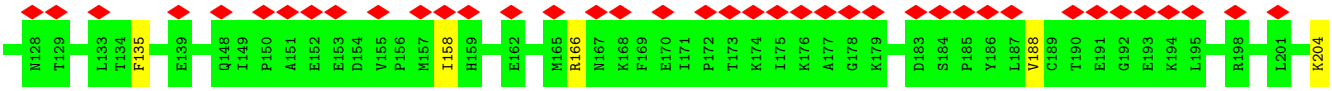


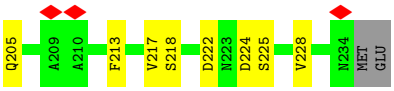


• Molecule 17: Ribosome assembly factor MRT4

Chain W:





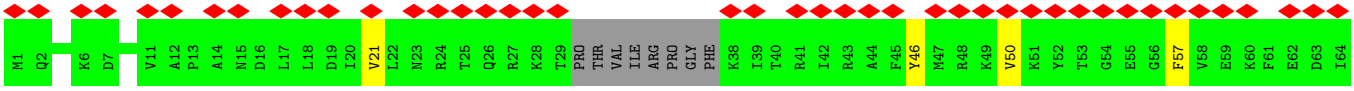


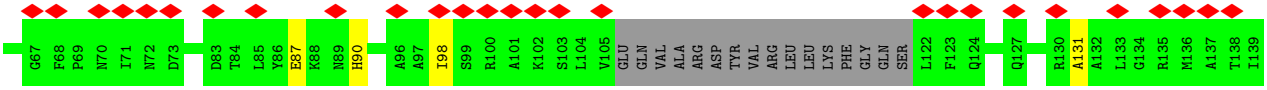
• Molecule 18: 60S ribosomal protein L26-A

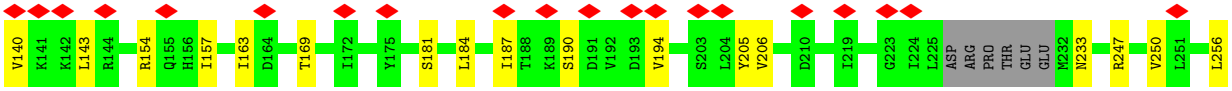
Chain Y:

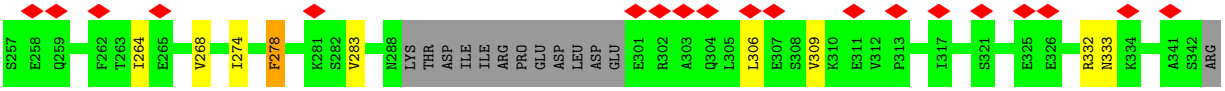
• Molecule 19: Nucleolar GTP-binding protein 1

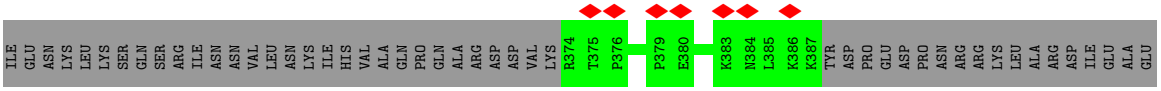
Chain b:

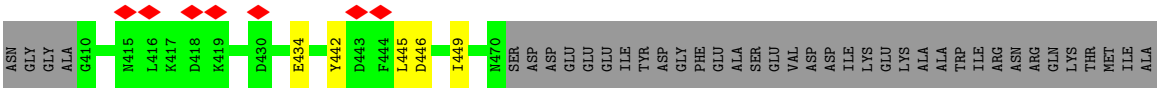


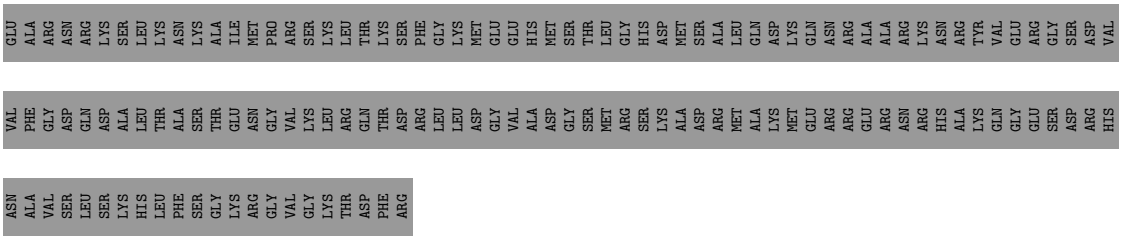






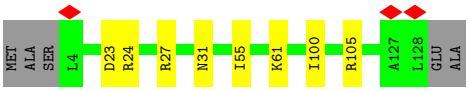






• Molecule 20: 60S ribosomal protein L32

Chain e:

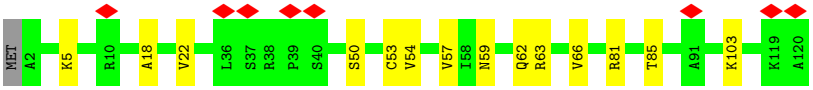


• Molecule 21: 60S ribosomal protein L33-A

Chain f:

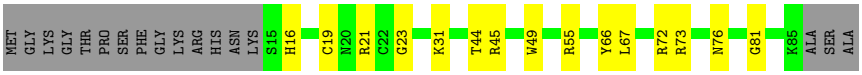
• Molecule 22: 60S ribosomal protein L35-A

Chain h:



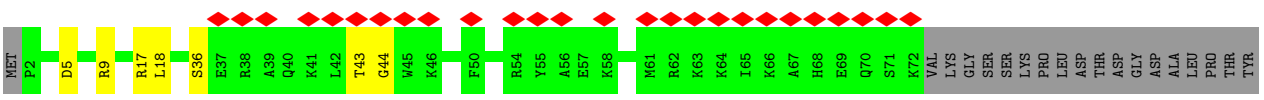
• Molecule 23: 60S ribosomal protein L37-A

Chain j:



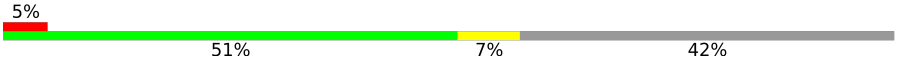
• Molecule 24: Ribosome biogenesis protein NSA2

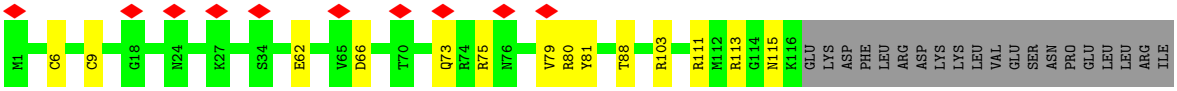
Chain r:



• Molecule 25: Ribosome biogenesis protein RLP24

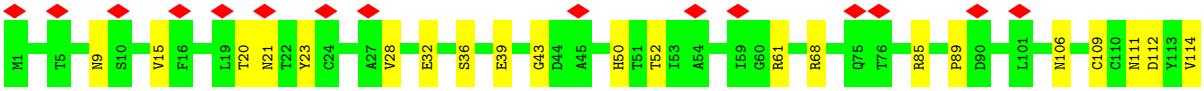
Chain u:





• Molecule 26: Eukaryotic translation initiation factor 6

Chain y:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	18398	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 ($e^-/Å^2$)	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	0.128	Depositor
Minimum map value	-0.043	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.006	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	0.07	0/40444	0.22	0/63013
2	2	0.09	0/3510	0.25	0/5460
3	B	0.11	0/2699	0.27	0/3626
4	C	0.10	0/2660	0.25	0/3601
5	E	0.10	0/1226	0.23	0/1648
6	F	0.10	0/1869	0.24	0/2514
7	G	0.12	0/852	0.27	0/1148
8	H	0.09	0/1531	0.27	0/2062
9	L	0.12	0/877	0.28	0/1179
10	M	0.11	0/1056	0.24	0/1421
11	N	0.12	0/1544	0.24	0/2065
12	O	0.10	0/1585	0.23	0/2128
13	P	0.10	0/1010	0.22	0/1359
14	Q	0.10	0/1024	0.22	0/1385
15	S	0.10	0/1468	0.26	0/1973
16	V	0.10	0/838	0.24	0/1128
17	W	0.10	0/1862	0.26	0/2508
18	Y	0.11	0/995	0.25	0/1329
19	b	0.09	0/3093	0.26	0/4163
20	e	0.10	0/1030	0.22	0/1379
21	f	0.12	0/868	0.27	0/1168
22	h	0.11	0/978	0.28	0/1301
23	j	0.12	0/578	0.25	0/767
24	r	0.10	0/622	0.23	0/816
25	u	0.11	0/996	0.31	0/1324
26	y	0.08	0/1722	0.24	0/2343
All	All	0.09	0/76937	0.23	0/112808

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a

sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
10	M	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	M	9	ALA	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	36150	18161	18183	386	0
2	2	3143	1590	1593	47	0
3	B	2646	2728	2726	36	0
4	C	2611	2725	2724	28	0
5	E	1205	1292	1291	8	0
6	F	1832	1917	1916	18	0
7	G	840	911	910	14	0
8	H	1510	1576	1576	19	0
9	L	864	918	917	14	0
10	M	1041	1138	1137	11	0
11	N	1513	1566	1564	13	0
12	O	1555	1660	1659	10	0
13	P	993	1005	1002	8	0
14	Q	1009	1092	1091	9	0
15	S	1432	1472	1470	17	0
16	V	826	867	865	9	0
17	W	1831	1852	1850	26	0
18	Y	984	1076	1075	10	0
19	b	3040	3104	3098	27	0
20	e	1009	1081	1080	6	0
21	f	850	881	880	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	h	969	1079	1078	10	0
23	j	566	571	566	14	0
24	r	612	638	638	8	0
25	u	976	1011	1007	13	0
26	y	1701	1697	1697	18	0
27	j	1	0	0	0	0
27	u	1	0	0	0	0
All	All	71710	53608	53593	668	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 668 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)
1:1:1259:A:O2'	1:1:1260:A:O5'	1.78	1.00
2:2:114:G:O2'	2:2:115:C:OP1	1.88	0.92
1:1:3084:C:O2'	1:1:3332:U:OP1	1.88	0.91
1:1:408:A:N3	1:1:655:C:O2'	2.08	0.87
1:1:1310:G:O2'	1:1:2380:U:O2'	1.92	0.87

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	B	329/387 (85%)	309 (94%)	20 (6%)	0	100	100
4	C	341/362 (94%)	325 (95%)	16 (5%)	0	100	100
5	E	147/176 (84%)	143 (97%)	4 (3%)	0	100	100
6	F	226/244 (93%)	217 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	104/256 (41%)	98 (94%)	6 (6%)	0	100	100
8	H	188/191 (98%)	176 (94%)	12 (6%)	0	100	100
9	L	106/199 (53%)	98 (92%)	8 (8%)	0	100	100
10	M	132/138 (96%)	126 (96%)	5 (4%)	1 (1%)	16	50
11	N	173/204 (85%)	171 (99%)	2 (1%)	0	100	100
12	O	195/199 (98%)	190 (97%)	5 (3%)	0	100	100
13	P	120/184 (65%)	119 (99%)	1 (1%)	0	100	100
14	Q	129/186 (69%)	128 (99%)	1 (1%)	0	100	100
15	S	168/172 (98%)	155 (92%)	13 (8%)	0	100	100
16	V	107/137 (78%)	105 (98%)	2 (2%)	0	100	100
17	W	223/236 (94%)	218 (98%)	5 (2%)	0	100	100
18	Y	123/127 (97%)	120 (98%)	3 (2%)	0	100	100
19	b	361/647 (56%)	347 (96%)	14 (4%)	0	100	100
20	e	123/130 (95%)	120 (98%)	3 (2%)	0	100	100
21	f	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
22	h	117/120 (98%)	107 (92%)	10 (8%)	0	100	100
23	j	69/88 (78%)	67 (97%)	2 (3%)	0	100	100
24	r	69/261 (26%)	63 (91%)	6 (9%)	0	100	100
25	u	114/199 (57%)	108 (95%)	6 (5%)	0	100	100
26	y	223/245 (91%)	214 (96%)	9 (4%)	0	100	100
All	All	3991/5195 (77%)	3824 (96%)	166 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	M	9	ALA

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	B	280/323 (87%)	280 (100%)	0	100	100
4	C	273/289 (94%)	270 (99%)	3 (1%)	65	74
5	E	131/153 (86%)	129 (98%)	2 (2%)	57	70
6	F	191/205 (93%)	189 (99%)	2 (1%)	68	75
7	G	89/208 (43%)	89 (100%)	0	100	100
8	H	170/171 (99%)	168 (99%)	2 (1%)	63	72
9	L	87/159 (55%)	84 (97%)	3 (3%)	32	55
10	M	106/109 (97%)	106 (100%)	0	100	100
11	N	153/176 (87%)	152 (99%)	1 (1%)	76	78
12	O	160/162 (99%)	157 (98%)	3 (2%)	50	66
13	P	103/146 (70%)	103 (100%)	0	100	100
14	Q	107/151 (71%)	107 (100%)	0	100	100
15	S	155/156 (99%)	155 (100%)	0	100	100
16	V	86/105 (82%)	86 (100%)	0	100	100
17	W	204/213 (96%)	204 (100%)	0	100	100
18	Y	108/110 (98%)	107 (99%)	1 (1%)	70	75
19	b	339/573 (59%)	337 (99%)	2 (1%)	78	80
20	e	108/111 (97%)	108 (100%)	0	100	100
21	f	90/91 (99%)	90 (100%)	0	100	100
22	h	104/105 (99%)	103 (99%)	1 (1%)	68	75
23	j	59/71 (83%)	59 (100%)	0	100	100
24	r	63/229 (28%)	63 (100%)	0	100	100
25	u	101/180 (56%)	101 (100%)	0	100	100
26	y	193/211 (92%)	192 (100%)	1 (0%)	81	82
All	All	3460/4407 (78%)	3439 (99%)	21 (1%)	76	80

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	O	156	LEU
19	b	278	PHE
26	y	173	LEU
19	b	434	GLU
18	Y	37	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
22	h	59	ASN
22	h	104	GLN
26	y	82	GLN
11	N	117	ASN
9	L	103	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1668/3396 (49%)	343 (20%)	43 (2%)
2	2	146/158 (92%)	34 (23%)	2 (1%)
All	All	1814/3554 (51%)	377 (20%)	45 (2%)

5 of 377 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	3	U
1	1	15	C
1	1	18	G
1	1	20	A

5 of 45 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1385	C
1	1	2995	A
1	1	1405	U
1	1	2896	A
1	1	3228	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 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 (i)

There are no chain breaks in this entry.

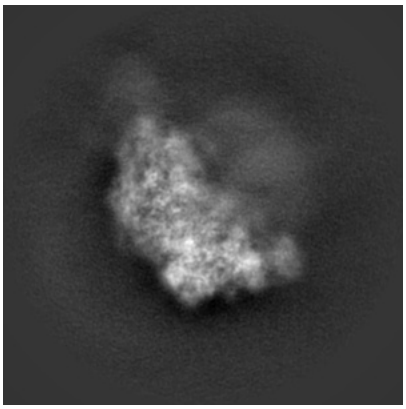
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-12913. These allow visual inspection of the internal detail of the map and identification of artifacts.

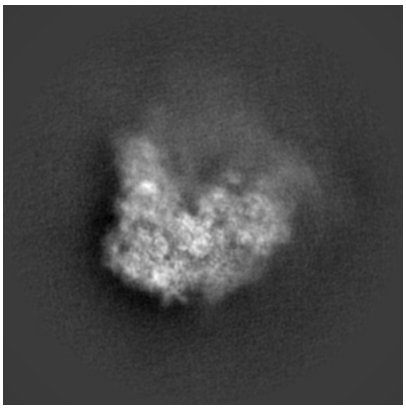
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

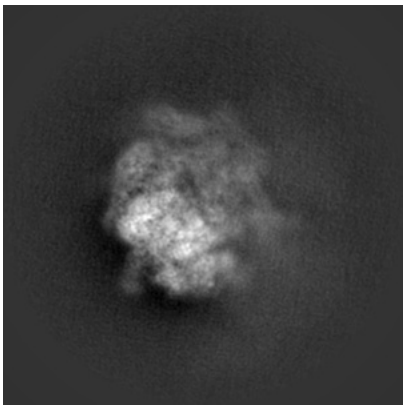
6.1.1 Primary map



X

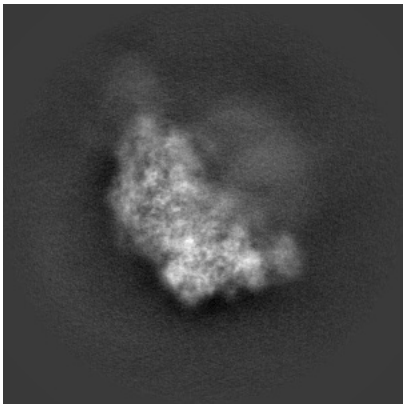


Y

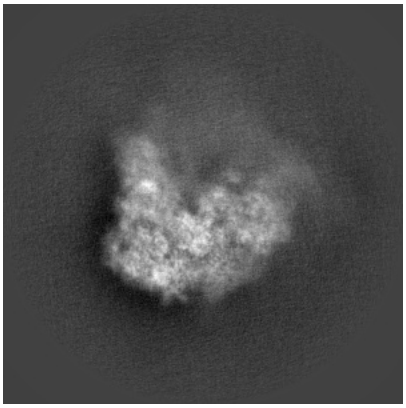


Z

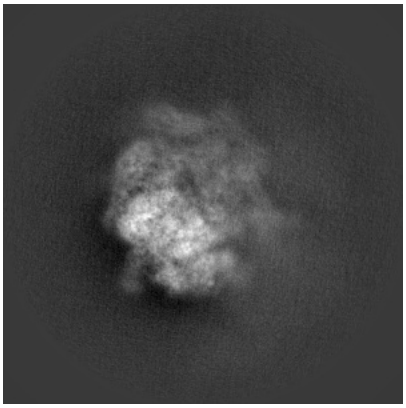
6.1.2 Raw map



X



Y

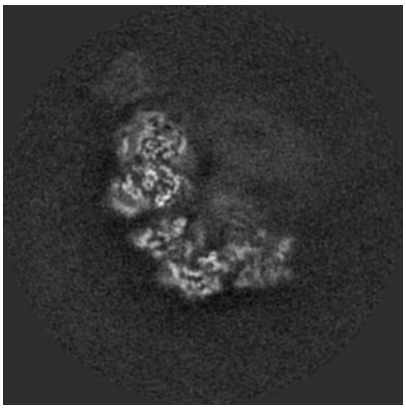


Z

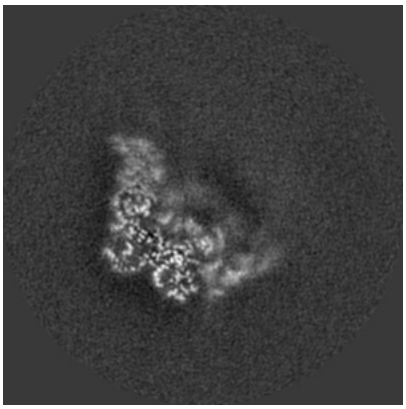
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

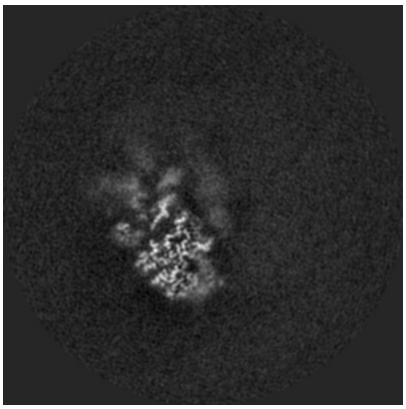
6.2.1 Primary map



X Index: 200

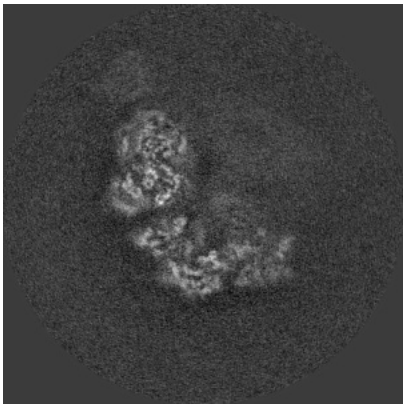


Y Index: 200

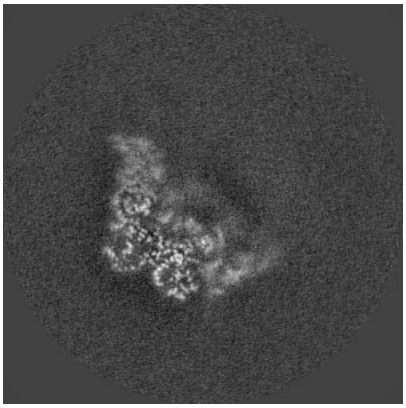


Z Index: 200

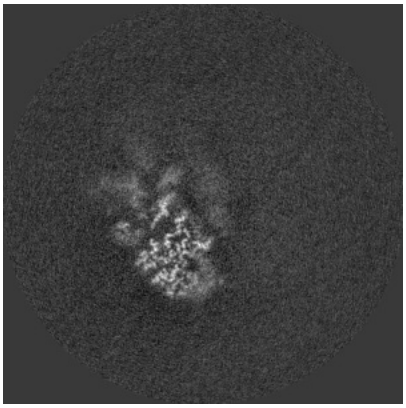
6.2.2 Raw map



X Index: 200



Y Index: 200

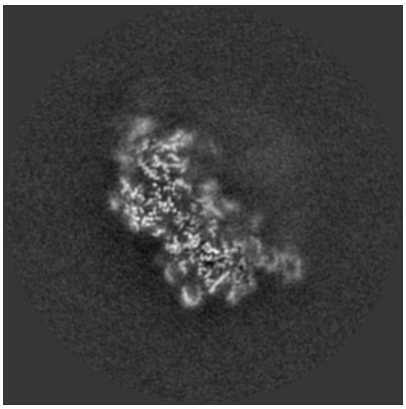


Z Index: 200

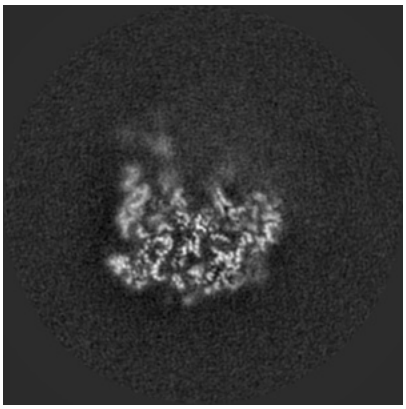
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

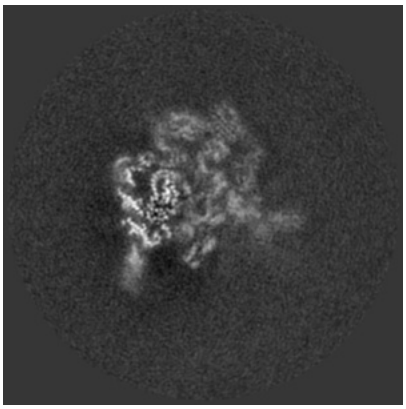
6.3.1 Primary map



X Index: 165

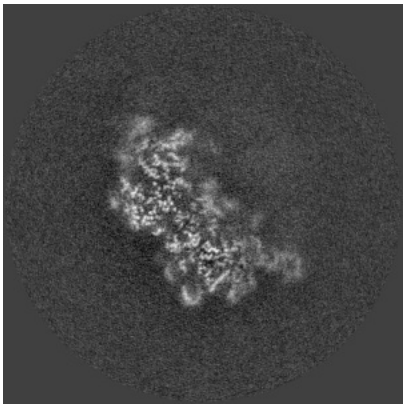


Y Index: 172

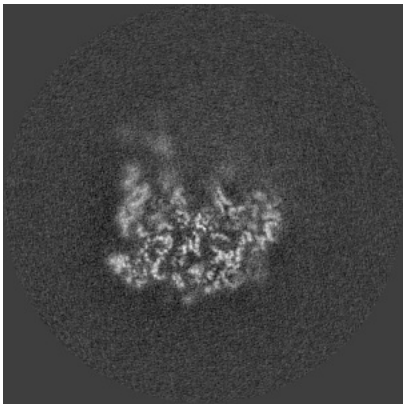


Z Index: 153

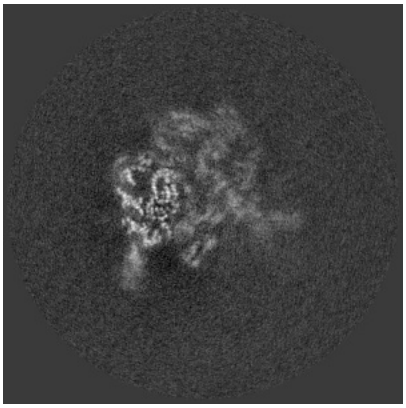
6.3.2 Raw map



X Index: 165



Y Index: 172

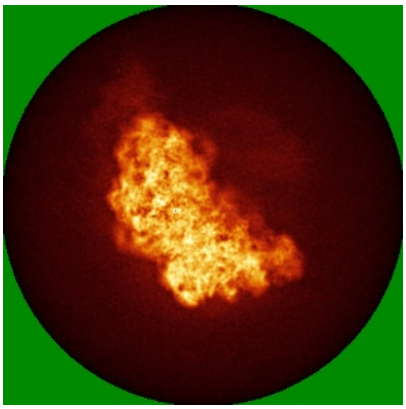


Z Index: 154

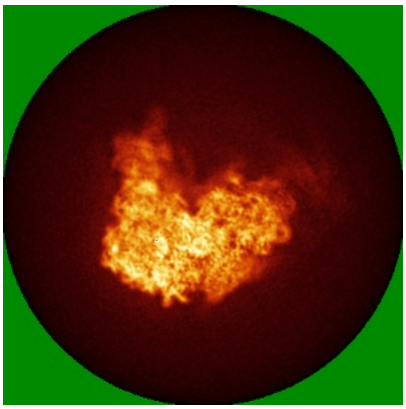
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

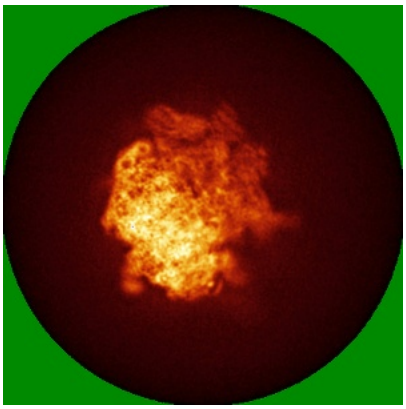
6.4.1 Primary map



X

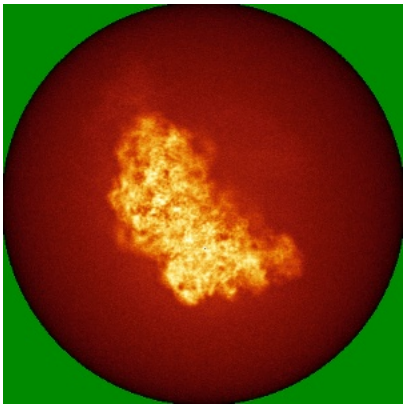


Y

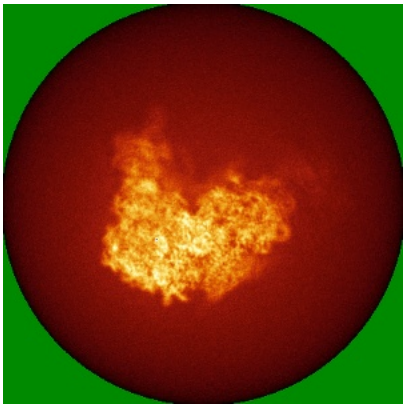


Z

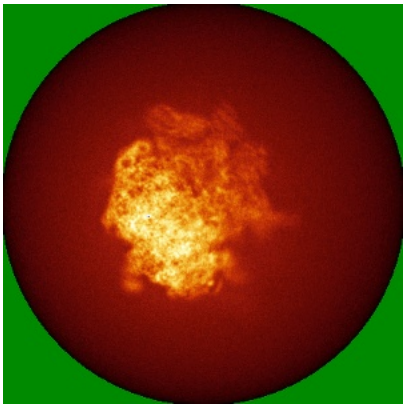
6.4.2 Raw map



X



Y



Z

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

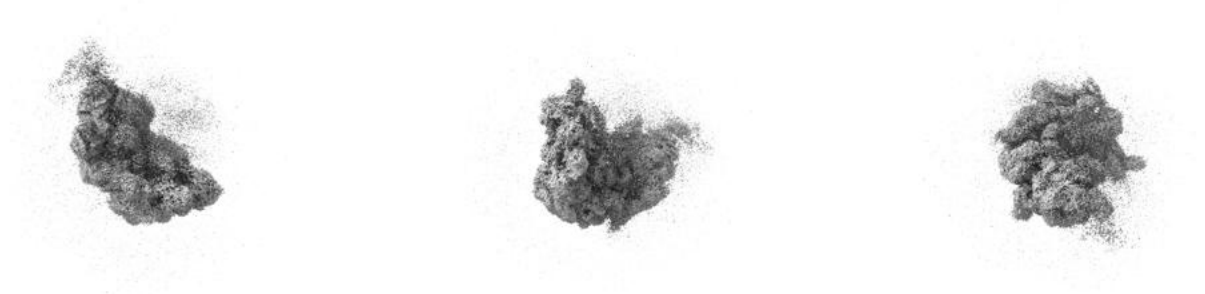
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

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



X Y Z

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.

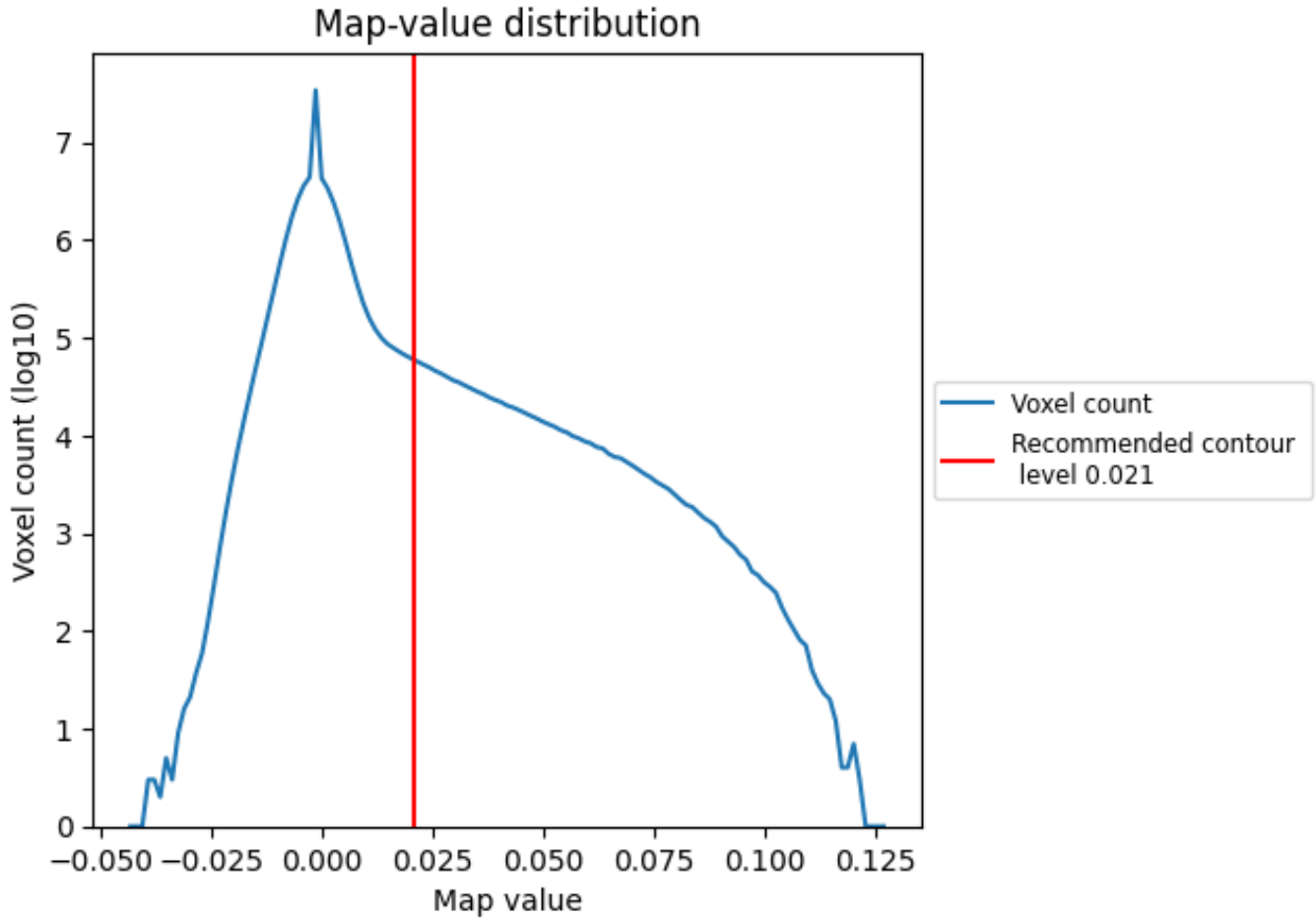
6.6 Mask visualisation (i)

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

7 Map analysis

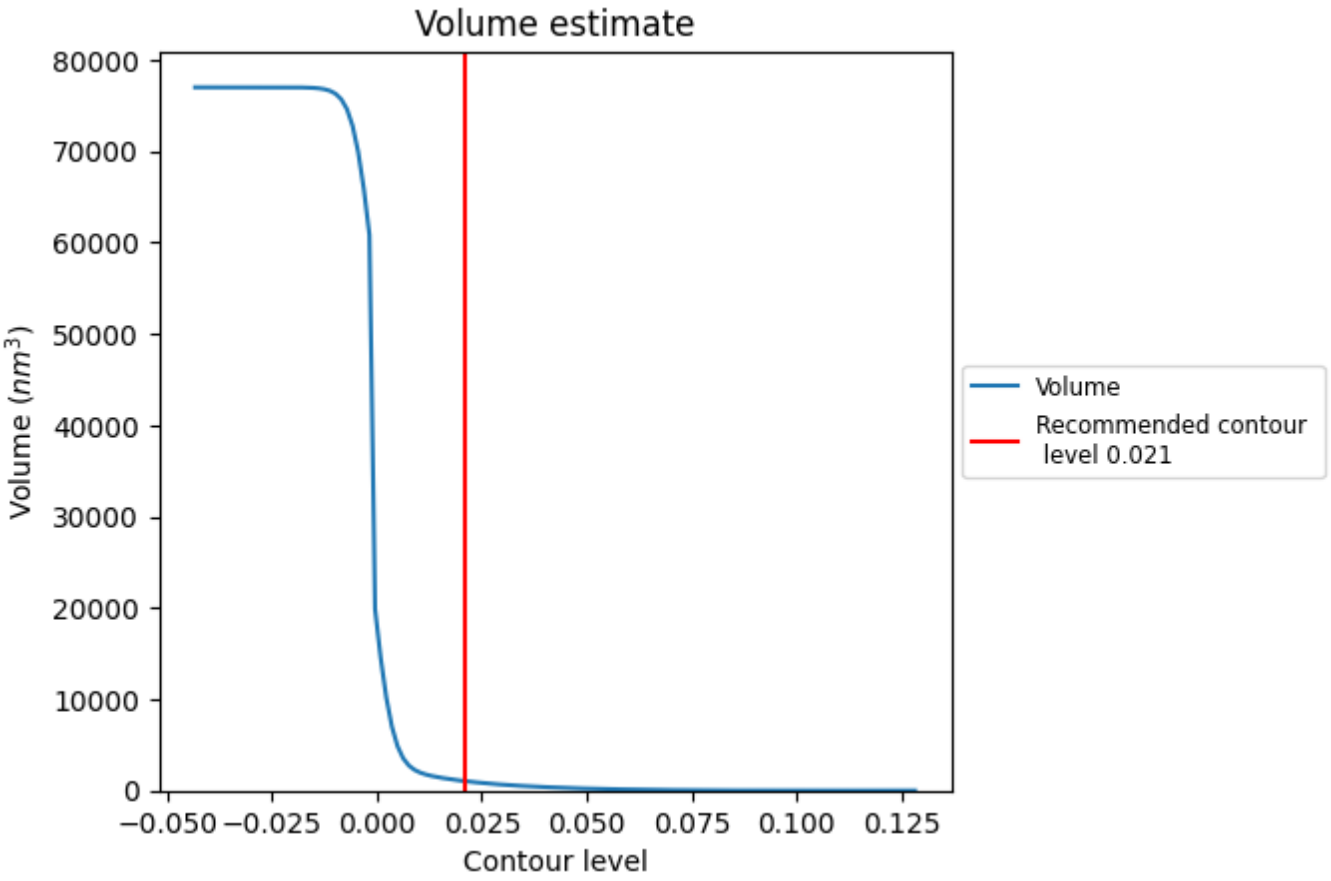
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

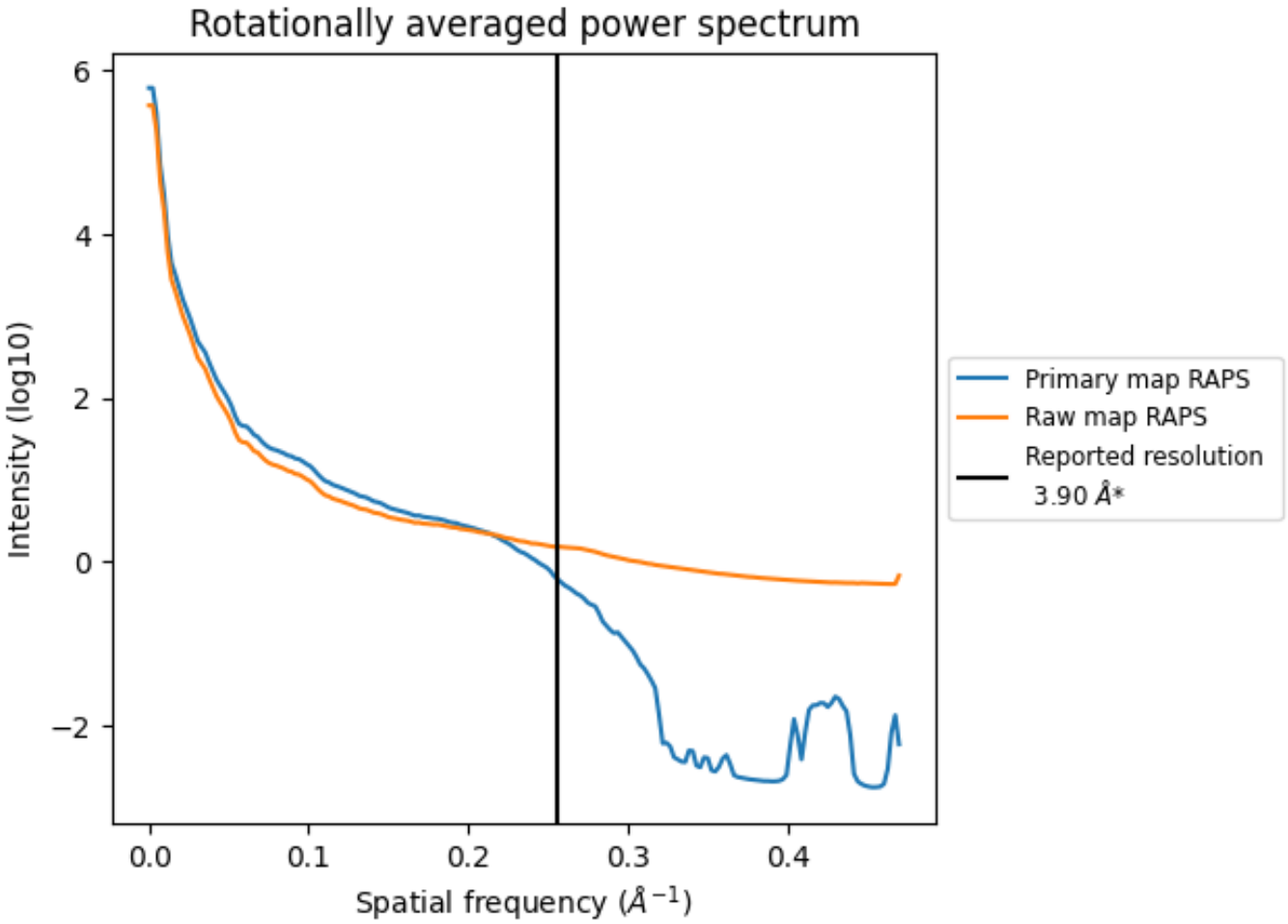
7.2 Volume estimate (i)



The volume at the recommended contour level is 1034 nm^3; this corresponds to an approximate mass of 934 kDa.

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

7.3 Rotationally averaged power spectrum (i)

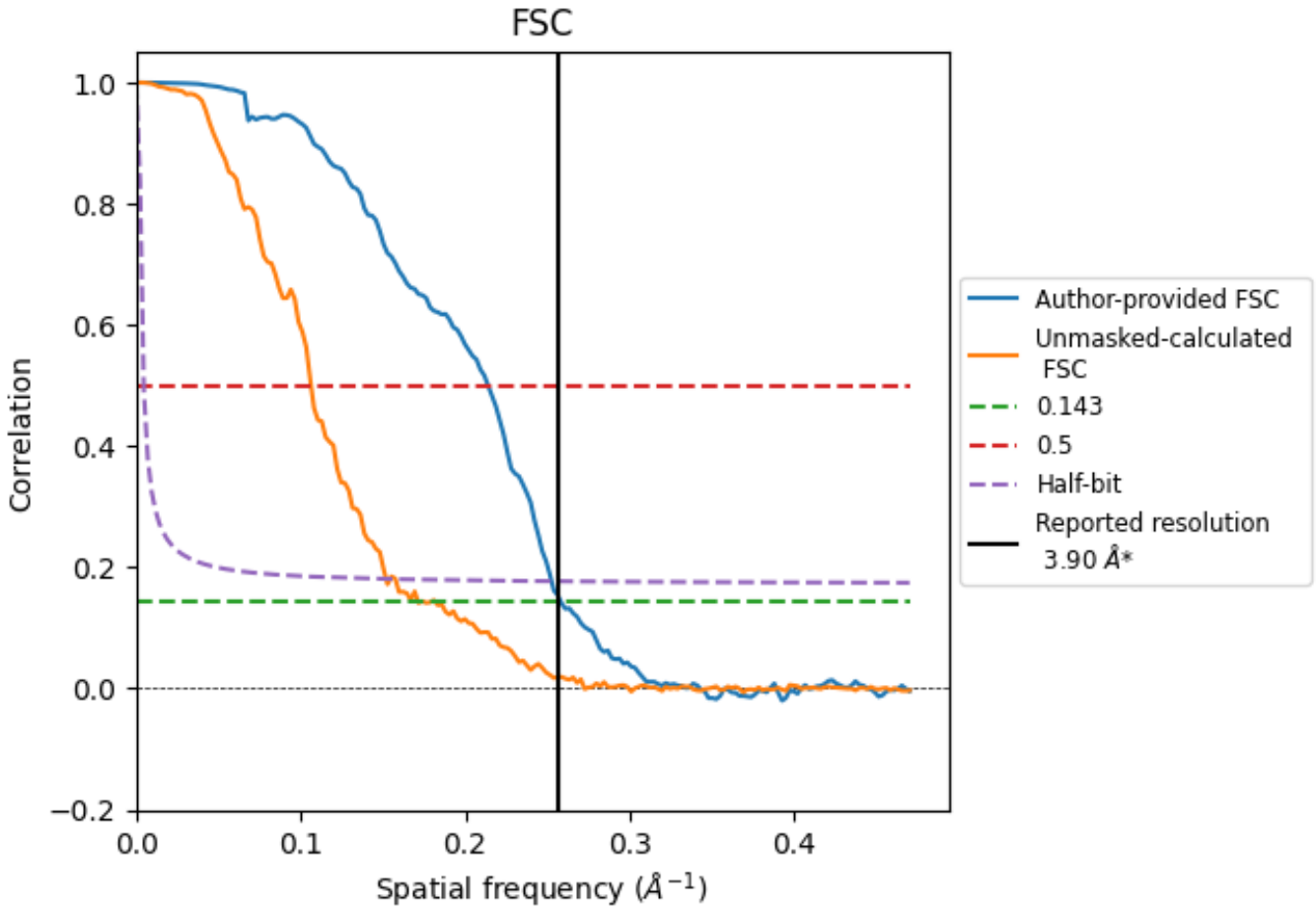


*Reported resolution corresponds to spatial frequency of 0.256 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.256 Å^{-1}

8.2 Resolution estimates (i)

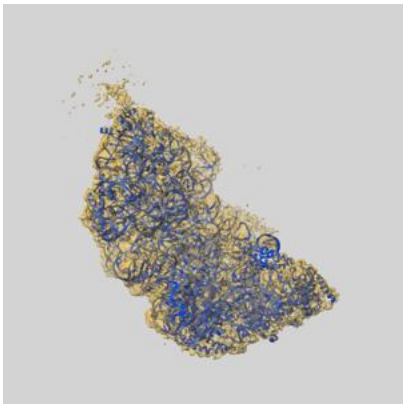
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.87	4.68	3.96
Unmasked-calculated*	5.83	9.41	6.58

*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 5.83 differs from the reported value 3.9 by more than 10 %

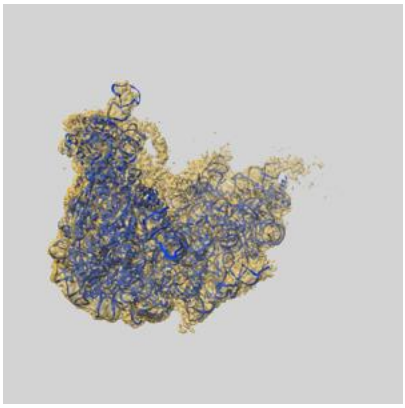
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-12913 and PDB model 7OHY. Per-residue inclusion information can be found in section 3 on page 8.

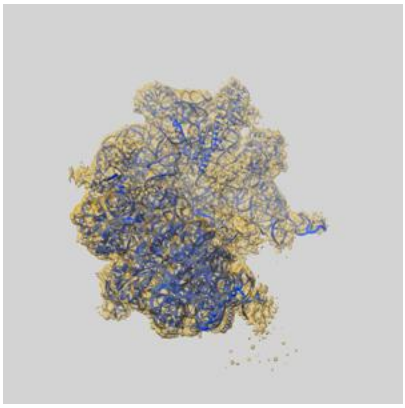
9.1 Map-model overlay



X



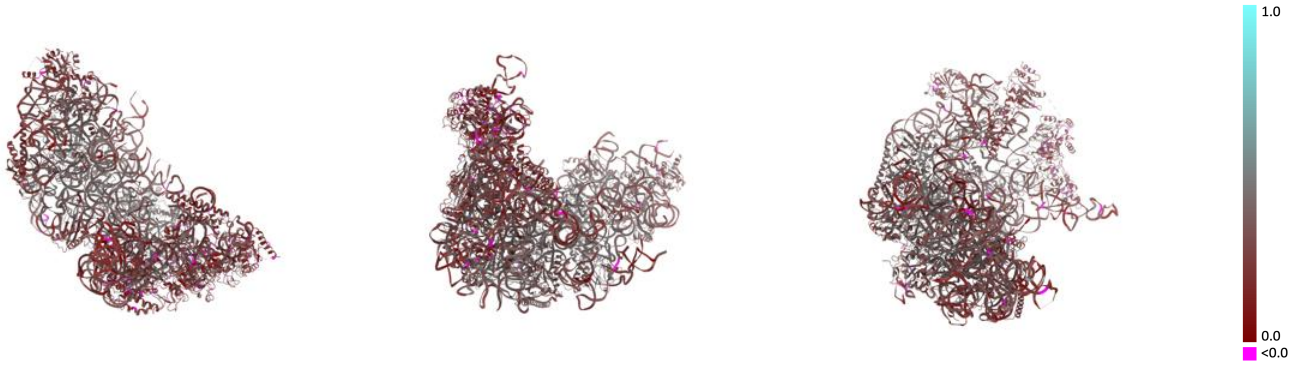
Y



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.

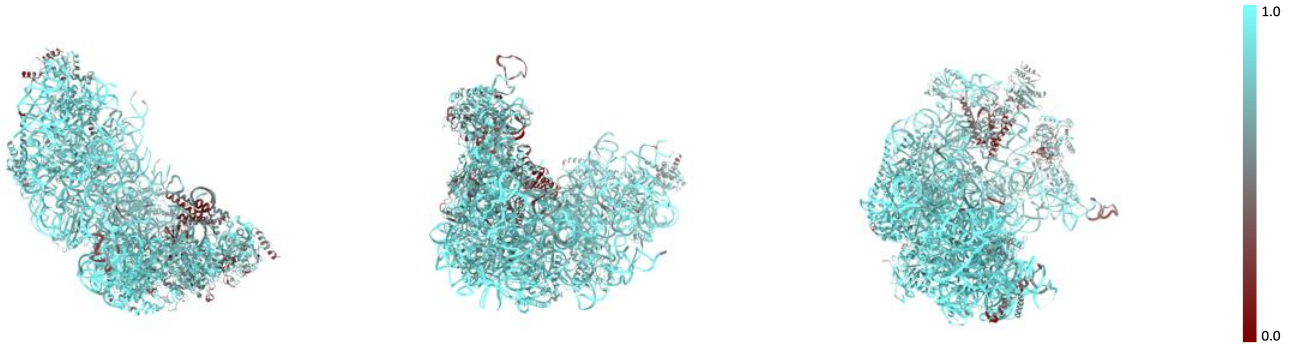
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

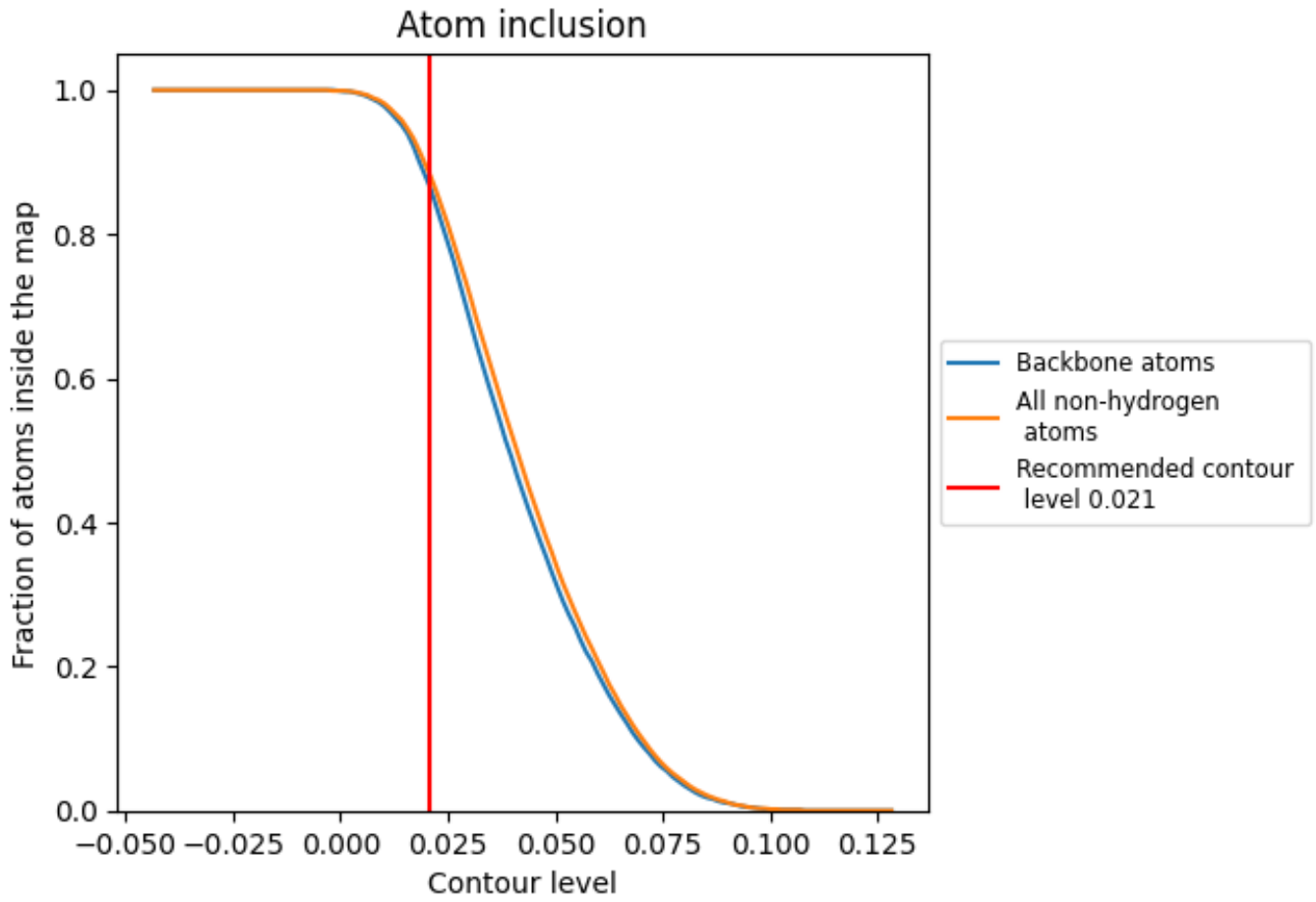
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.021).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.021) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8810	0.3120
1	0.9440	0.3060
2	0.9450	0.3010
B	0.8980	0.3040
C	0.8880	0.4000
E	0.8870	0.3850
F	0.8780	0.3780
G	0.5970	0.2570
H	0.7480	0.3300
L	0.9180	0.3530
M	0.9120	0.3870
N	0.8340	0.3200
O	0.8640	0.3820
P	0.7850	0.3190
Q	0.8950	0.3720
S	0.8900	0.3650
V	0.4940	0.2360
W	0.6400	0.2340
Y	0.9130	0.3660
b	0.5330	0.2190
e	0.8580	0.4180
f	0.8920	0.4390
h	0.7590	0.2770
j	0.8580	0.3820
r	0.5230	0.2860
u	0.8000	0.1770
y	0.7000	0.2270