



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:17 PM UTC

PDB ID : 5X8T / pdb_00005x8t
EMDB ID : EMD-6711
Title : Structure of the 50S large subunit of chloroplast ribosome from spinach
Authors : Ahmed, T.; Shi, J.; Bhushan, S.
Deposited on : 2017-03-03
Resolution : 3.30 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

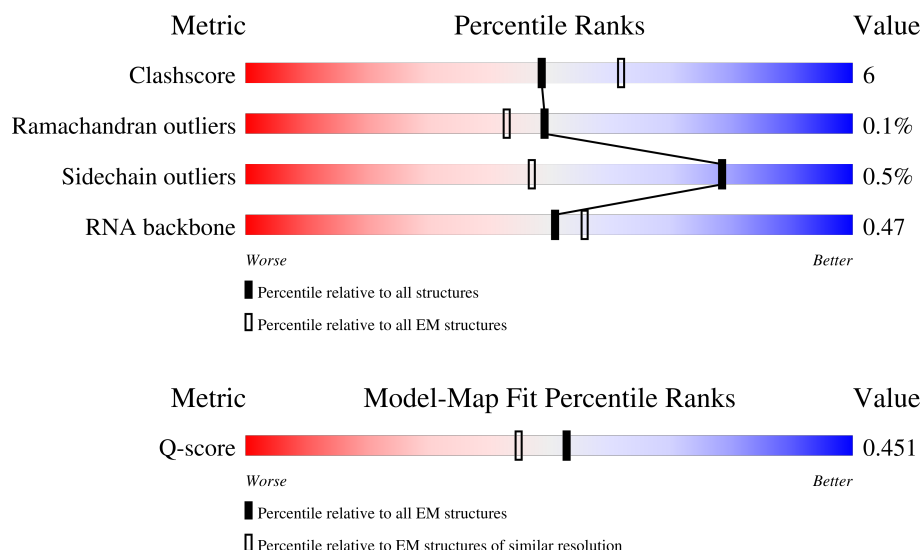
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



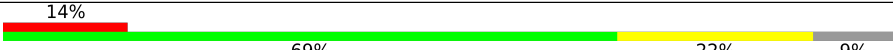
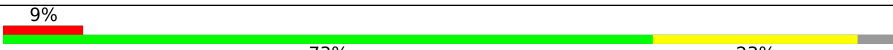
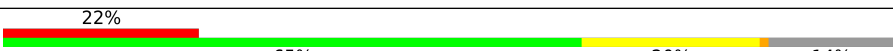
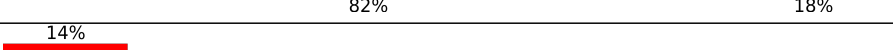
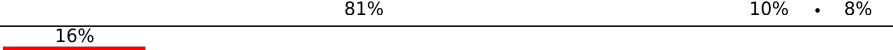
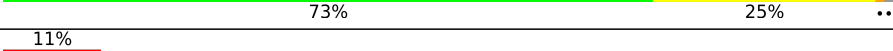
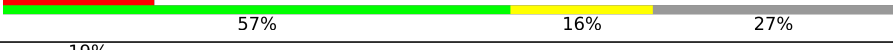
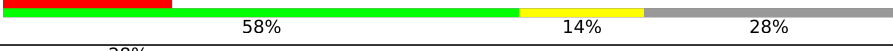
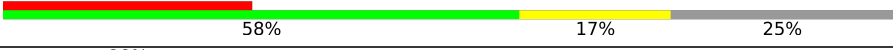
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	56	
2	2	65	
3	3	61	

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Mol	Chain	Length	Quality of chain
4	4	73	
5	5	37	
6	6	142	
7	7	116	
8	B	121	
9	C	271	
10	D	221	
11	E	243	
12	F	220	
13	G	182	
14	H	155	
15	K	197	
16	L	121	
17	M	192	
18	N	135	
19	O	116	
20	P	123	
21	Q	156	
22	R	127	
23	S	201	
24	T	199	
25	U	122	
26	V	145	
27	W	106	
28	X	137	

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Mol	Chain	Length	Quality of chain
29	Y	77	12% 66% 29%
30	Z	109	37% 63% 19% 17%
31	A	2810	12% 64% 32% 5%
32	0	94	65% 60% 6% 32%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 91714 atoms, of which 0 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 protein called 50S ribosomal protein L32, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	1	46	Total	C	N	O	0	0
			378	250	70	58		

- Molecule 2 is a protein called 50S ribosomal protein L33, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	51	Total	C	N	O	S	0	0
			415	258	83	70	4		

- Molecule 3 is a protein called 50S ribosomal protein L34, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	57	Total	C	N	O	S	0	0
			445	268	103	71	3		

- Molecule 4 is a protein called 50S ribosomal protein L35, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	69	Total	C	N	O	S	0	0
			563	353	119	90	1		

- Molecule 5 is a protein called 50S ribosomal protein L36, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	37	Total	C	N	O	S	0	0
			304	186	70	44	4		

- Molecule 6 is a protein called protein cL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	49	Total	C	N	O	S	0	0
			422	268	92	57	5		

- Molecule 7 is a protein called protein cL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	46	Total	C	N	O	S	0	0
			368	237	71	59	1		

- Molecule 8 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	117	Total	C	N	O	P	0	0
			2500	1116	452	815	117		

- Molecule 9 is a protein called 50S ribosomal protein L2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	247	Total	C	N	O	S	0	0
			1904	1181	390	327	6		

- Molecule 10 is a protein called protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	212	Total	C	N	O	S	0	0
			1620	1025	295	289	11		

- Molecule 11 is a protein called 50S ribosomal protein L4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	210	Total	C	N	O	S	0	0
			1655	1052	308	292	3		

- Molecule 12 is a protein called 50S ribosomal protein L5, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	175	Total	C	N	O	S	0	0
			1351	862	233	248	8		

- Molecule 13 is a protein called protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	173	Total	C	N	O	S	0	0
			1353	855	249	245	4		

- Molecule 14 is a protein called protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	53	Total	C	N	O	S	0	0
			423	280	74	68	1		

- Molecule 15 is a protein called 50S ribosomal protein L13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	193	Total	C	N	O	S	0	0
			1568	1000	289	274	5		

- Molecule 16 is a protein called 50S ribosomal protein L14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	121	Total	C	N	O	S	0	0
			942	588	179	170	5		

- Molecule 17 is a protein called protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	177	Total	C	N	O	S	0	0
			1342	836	264	236	6		

- Molecule 18 is a protein called 50S ribosomal protein L16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	134	Total	C	N	O	S	0	0
			1067	672	217	173	5		

- Molecule 19 is a protein called protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	116	Total	C	N	O	S	0	0
			944	592	193	155	4		

- Molecule 20 is a protein called protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	120	Total	C	N	O	S	0	0
			947	589	183	170	5		

- Molecule 21 is a protein called 50S ribosomal protein L19, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	118	Total	C	N	O	S	0	0
			953	610	186	156	1		

- Molecule 22 is a protein called 50S ribosomal protein L20, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	115	Total	C	N	O	S	0	0
			996	633	208	153	2		

- Molecule 23 is a protein called 50S ribosomal protein L21, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	147	Total	C	N	O		0	0
			1171	759	202	210			

- Molecule 24 is a protein called 50S ribosomal protein L22, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	144	Total	C	N	O	S	0	0
			1149	731	210	200	8		

- Molecule 25 is a protein called 50S ribosomal protein L23, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	92	Total	C	N	O	S	0	0
			740	477	129	132	2		

- Molecule 26 is a protein called 50S ribosomal protein L24, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	124	Total	C	N	O	S	0	0
			993	624	187	180	2		

- Molecule 27 is a RNA chain called 4.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	102	Total	C	N	O	P	0	0
			2187	977	403	705	102		

- Molecule 28 is a protein called protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	X	100	Total	C	N	O	0	0
			810	511	159	140		

- Molecule 29 is a protein called protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	74	Total	C	N	O	S	0	0
			605	385	121	98	1		

- Molecule 30 is a protein called protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	90	Total	C	N	O	S	0	0
			754	470	150	131	3		

- Molecule 31 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	A	2809	Total	C	N	O	P	0	0
			60324	26912	11166	19437	2809		

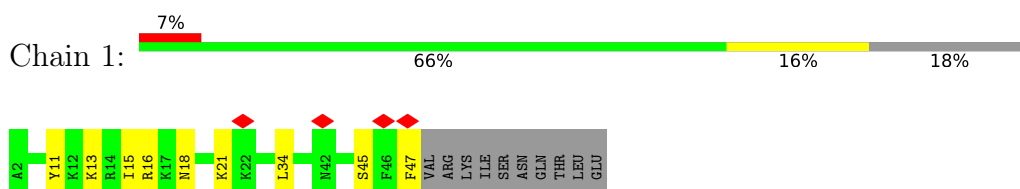
- Molecule 32 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	0	64	Total	C	N	O	S	0	0
			521	330	89	100	2		

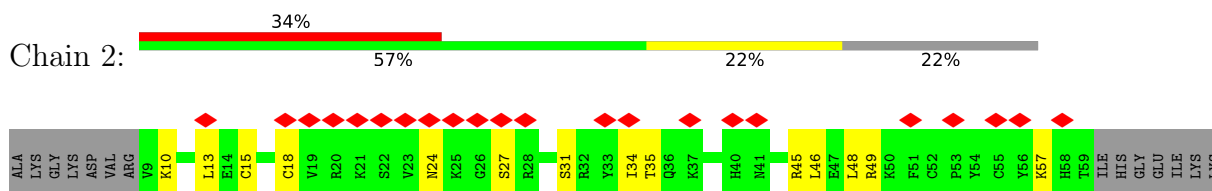
3 Residue-property plots [i](#)

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.

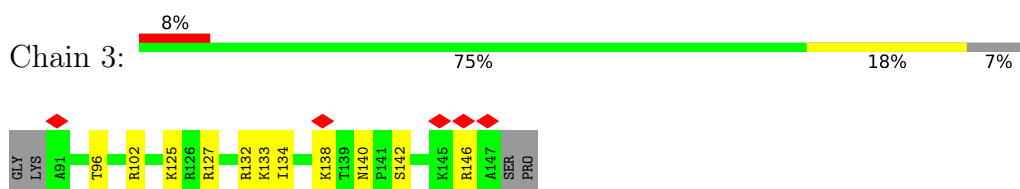
- Molecule 1: 50S ribosomal protein L32, chloroplastic



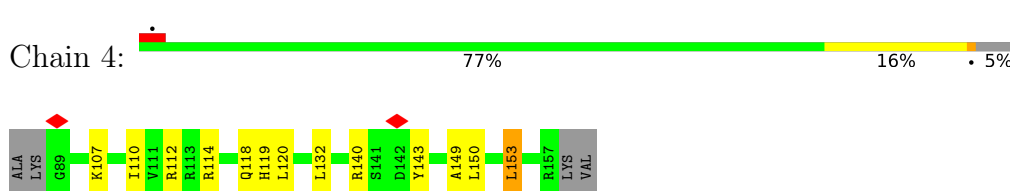
- Molecule 2: 50S ribosomal protein L33, chloroplastic



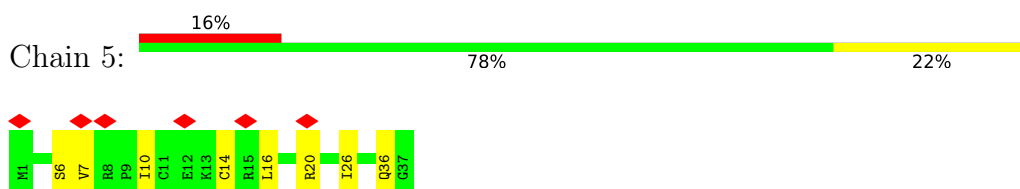
- Molecule 3: 50S ribosomal protein L34, chloroplastic



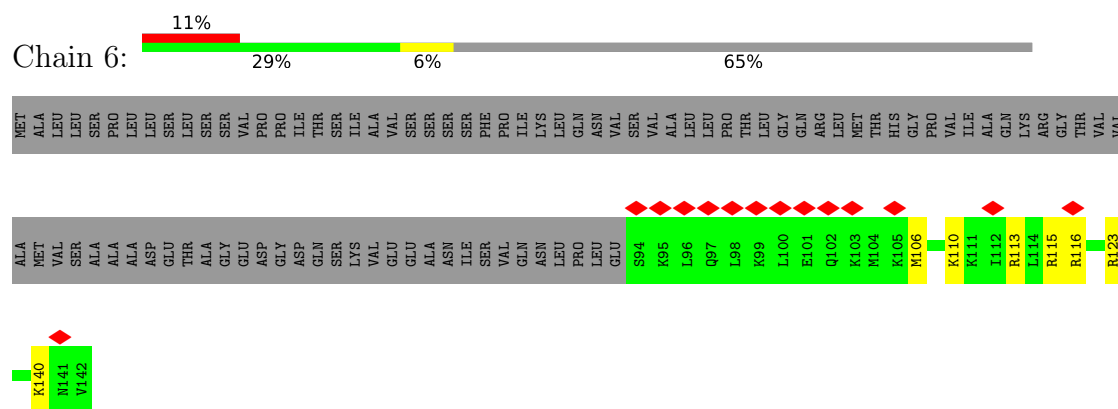
- Molecule 4: 50S ribosomal protein L35, chloroplastic



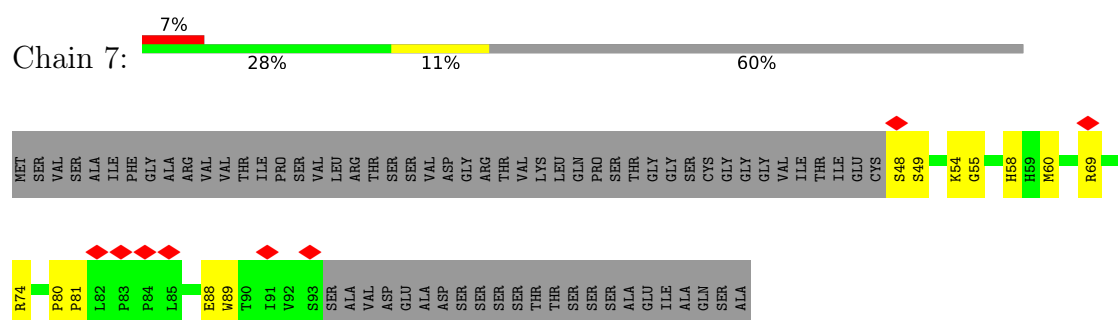
- Molecule 5: 50S ribosomal protein L36, chloroplastic



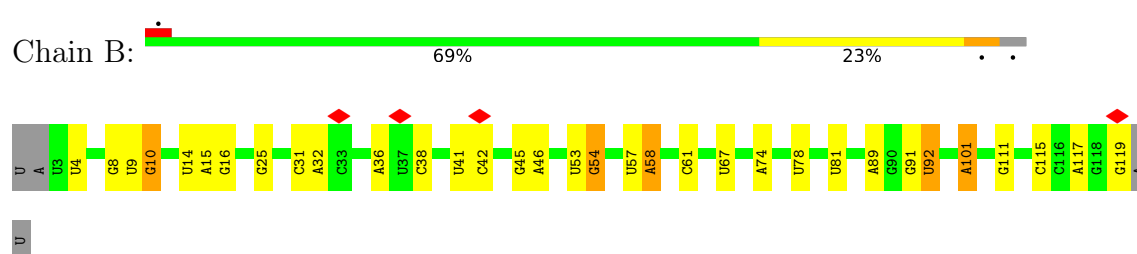
- Molecule 6: protein cL37



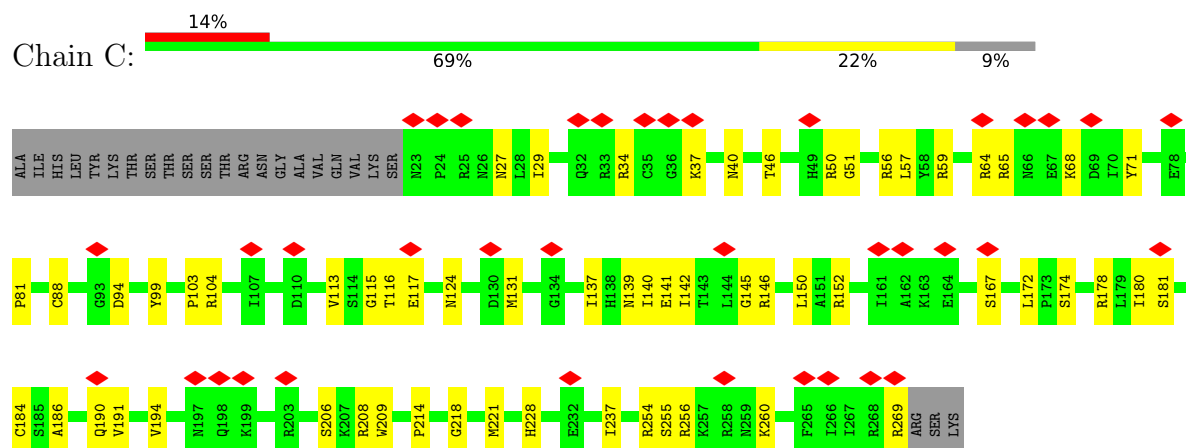
- Molecule 7: protein cL38



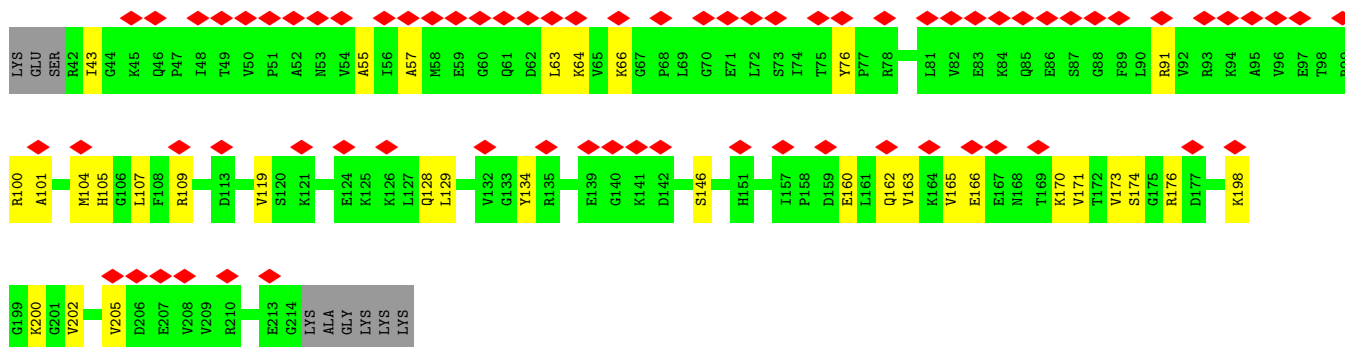
- Molecule 8: 5S rRNA



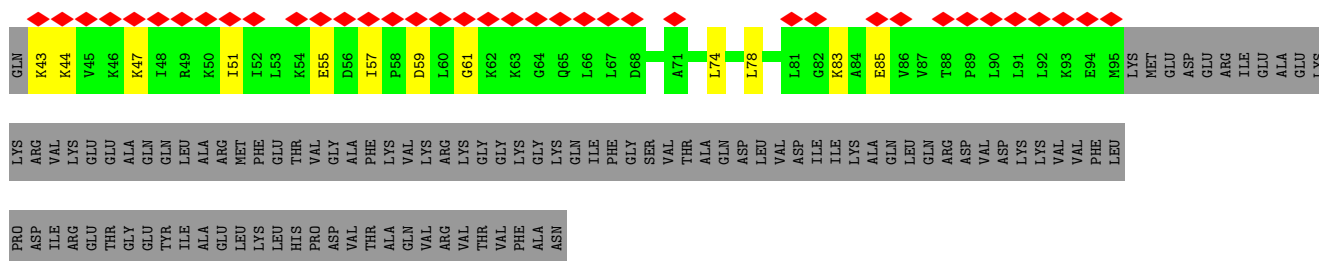
- Molecule 9: 50S ribosomal protein L2, chloroplastic



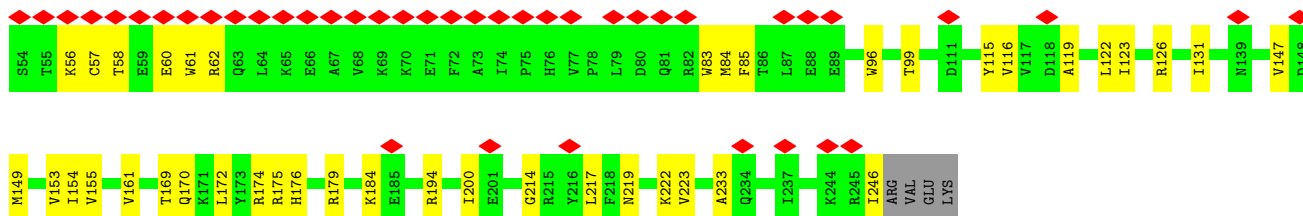
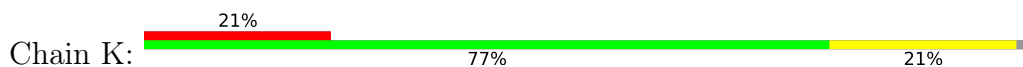
- Molecule 10: protein L3



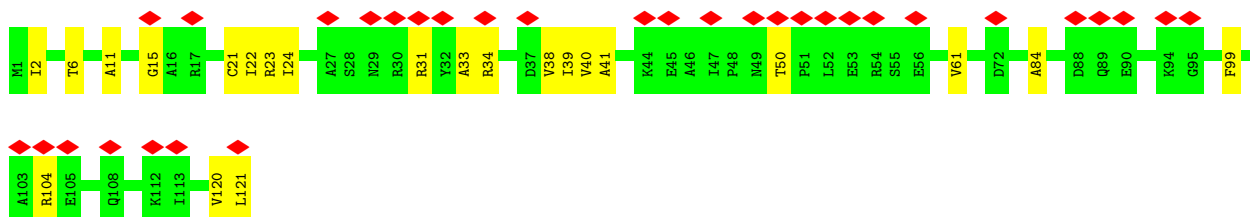
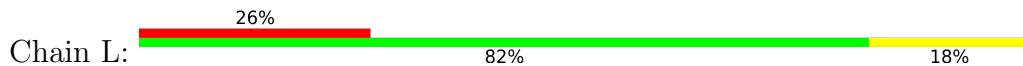
• Molecule 14: protein L9



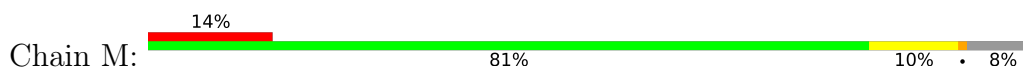
• Molecule 15: 50S ribosomal protein L13, chloroplastic

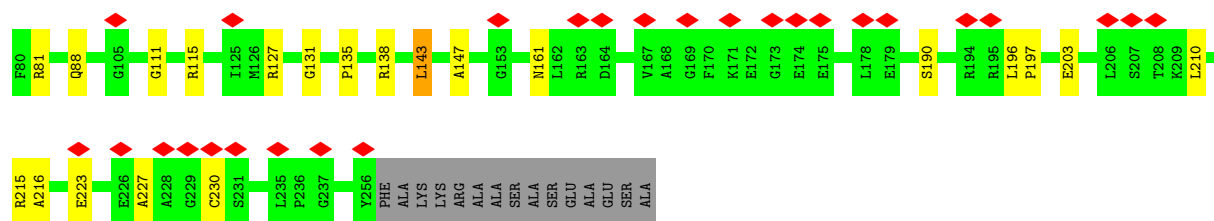


• Molecule 16: 50S ribosomal protein L14, chloroplastic

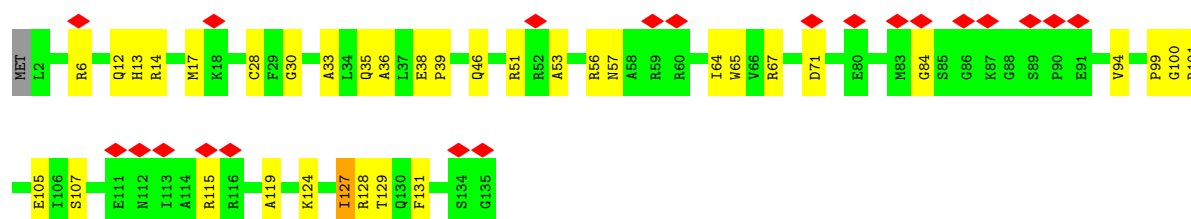
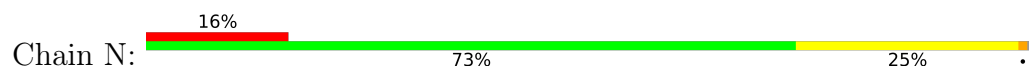


• Molecule 17: protein L15

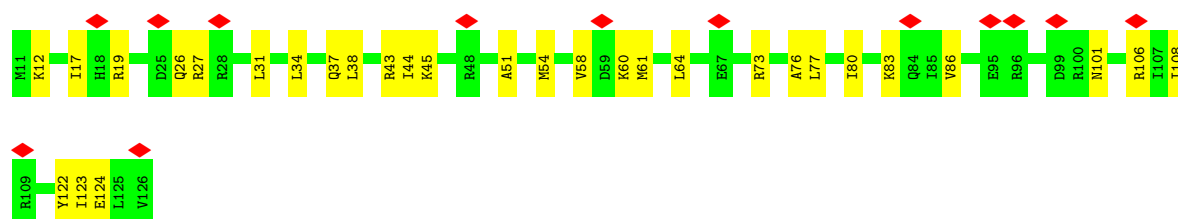
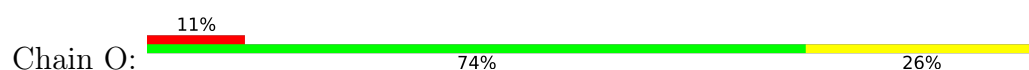




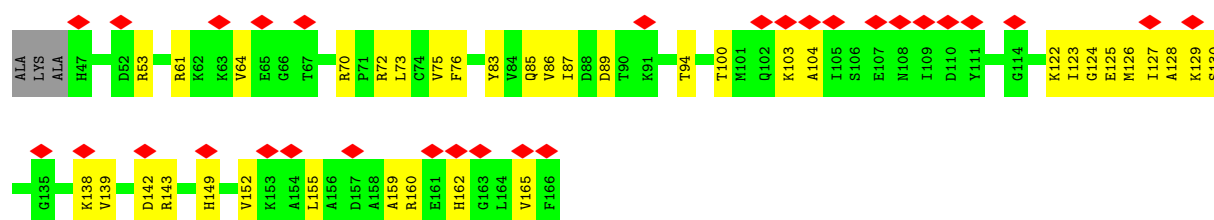
- Molecule 18: 50S ribosomal protein L16, chloroplastic



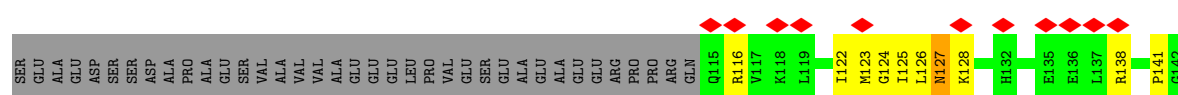
- Molecule 19: protein L17

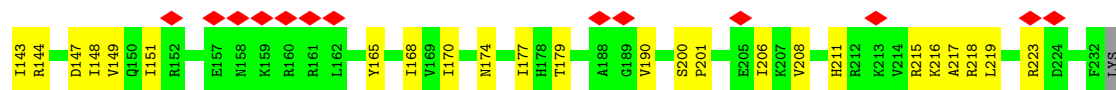


- Molecule 20: protein L18



- Molecule 21: 50S ribosomal protein L19, chloroplastic

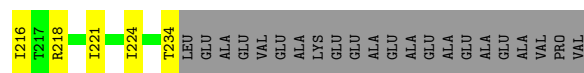
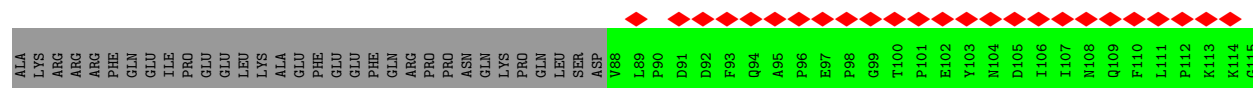




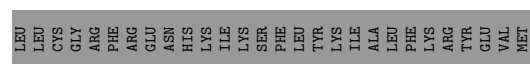
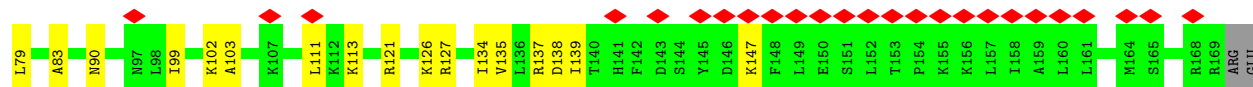
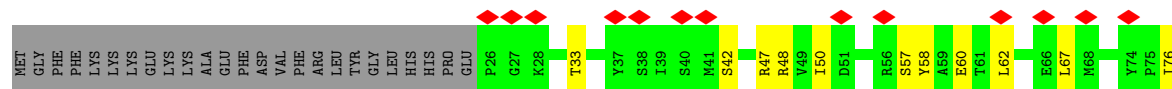
- Molecule 22: 50S ribosomal protein L20, chloroplastic



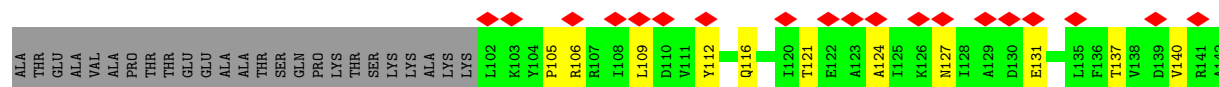
- Molecule 23: 50S ribosomal protein L21, chloroplastic

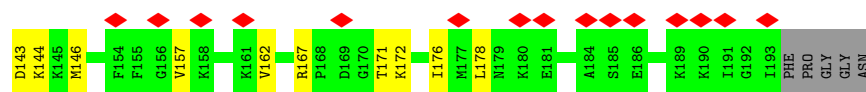


- Molecule 24: 50S ribosomal protein L22, chloroplastic

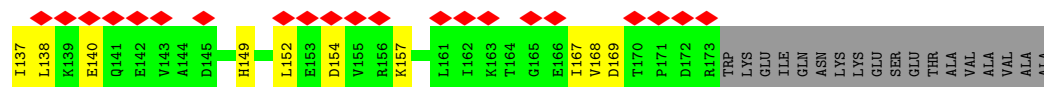
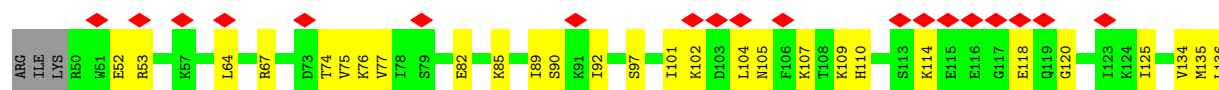


- Molecule 25: 50S ribosomal protein L23, chloroplastic

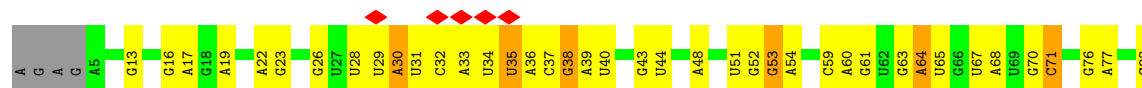




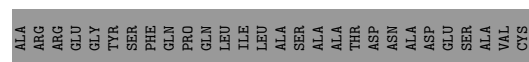
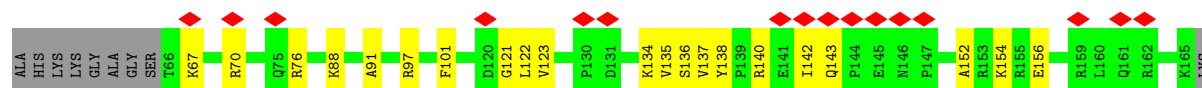
- Molecule 26: 50S ribosomal protein L24, chloroplastic



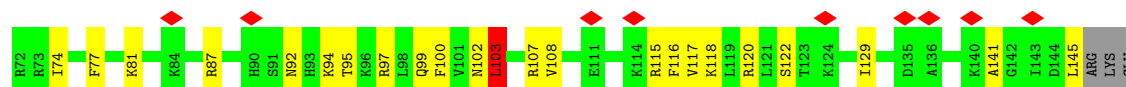
- Molecule 27: 4.8S rRNA



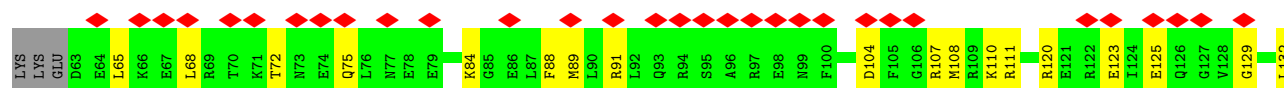
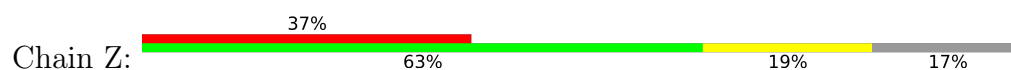
- Molecule 28: protein L27

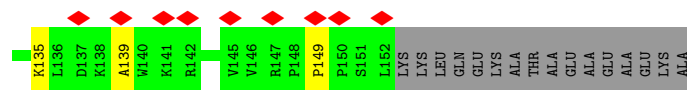


- Molecule 29: protein L28

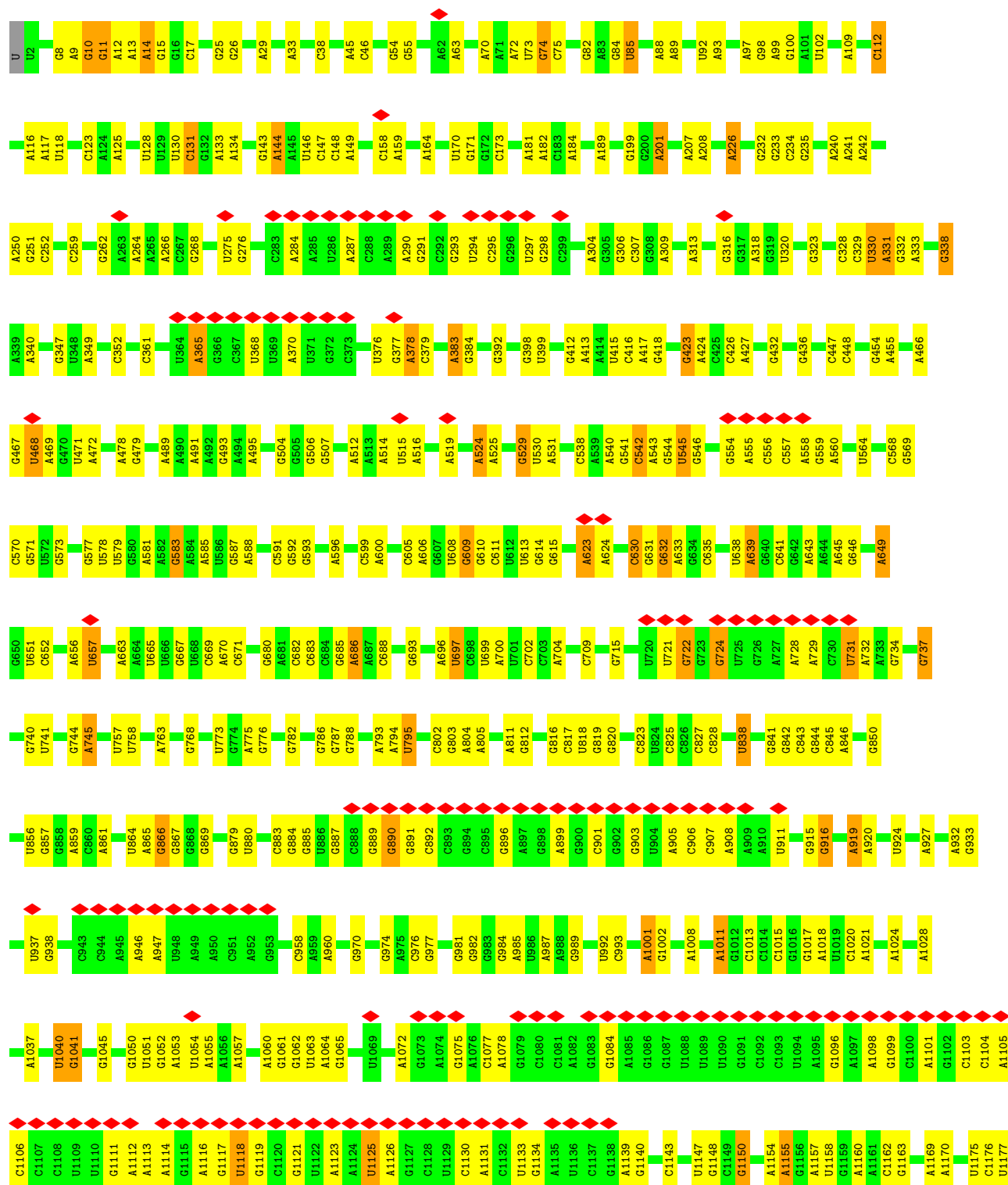


- Molecule 30: protein L29

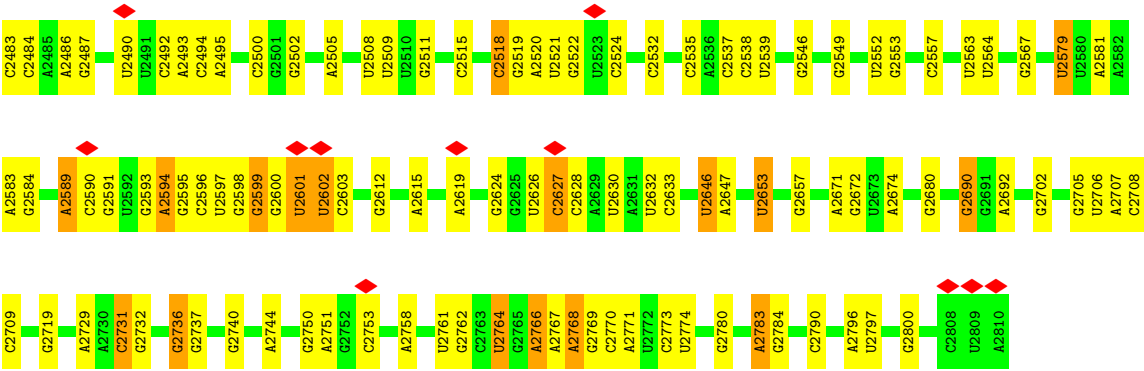




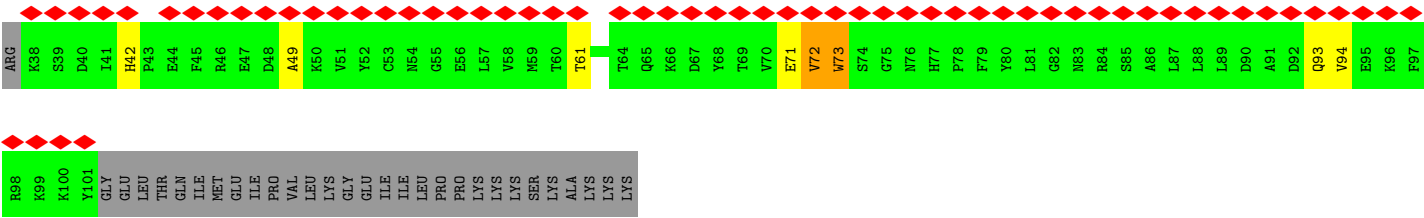
• Molecule 31: 23S rRNA







● Molecule 32: 50S ribosomal protein L31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	81305	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3700	Depositor
Magnification	133333	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.644	Depositor
Minimum map value	-0.445	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.09	Depositor
Map size ($\text{\AA}$)	403.19998, 403.19998, 403.19998	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

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	0.20	0/387	0.53	0/513
2	2	0.30	0/422	0.81	0/564
3	3	0.22	0/447	0.58	0/588
4	4	0.24	0/569	0.64	0/752
5	5	0.26	0/306	0.69	0/403
6	6	0.19	0/425	0.50	0/551
7	7	0.23	0/382	0.65	2/520 (0.4%)
8	B	0.16	0/2796	0.36	0/4357
9	C	0.24	0/1938	0.64	0/2603
10	D	0.26	0/1646	0.63	0/2201
11	E	0.25	0/1687	0.67	0/2271
12	F	0.21	0/1372	0.55	0/1848
13	G	0.19	0/1374	0.55	2/1849 (0.1%)
14	H	0.20	0/427	0.60	0/568
15	K	0.20	0/1608	0.50	0/2174
16	L	0.23	0/951	0.55	0/1282
17	M	0.21	0/1361	0.53	0/1806
18	N	0.27	0/1089	0.68	0/1461
19	O	0.23	0/959	0.61	0/1280
20	P	0.21	0/963	0.54	0/1293
21	Q	0.29	0/967	0.74	2/1300 (0.2%)
22	R	0.31	0/1013	0.69	0/1351
23	S	0.25	0/1199	0.65	0/1633
24	T	0.21	0/1168	0.55	0/1566
25	U	0.19	0/749	0.53	0/1006
26	V	0.21	0/1006	0.66	0/1343
27	W	0.18	0/2449	0.43	0/3817
28	X	0.24	0/825	0.60	1/1099 (0.1%)
29	Y	0.22	0/615	0.60	1/819 (0.1%)
30	Z	0.20	0/762	0.56	0/1012
31	A	0.17	0/67572	0.35	0/105421
32	0	0.26	0/533	0.75	0/718
All	All	0.19	0/99967	0.43	8/149969 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
17	M	0	1
21	Q	0	1
23	S	0	1
32	0	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	Q	223	ARG	CA-C-N	5.67	134.91	124.82
21	Q	223	ARG	C-N-CA	5.67	134.91	124.82
7	7	55	GLY	CA-C-N	5.57	132.18	121.54
7	7	55	GLY	C-N-CA	5.57	132.18	121.54
28	X	134	LYS	N-CA-C	5.56	117.42	110.91

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
32	0	73	TRP	Peptide
17	M	143	LEU	Peptide
21	Q	190	VAL	Peptide
23	S	174	THR	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	378	0	415	8	0
2	2	415	0	434	8	0
3	3	445	0	501	11	0
4	4	563	0	623	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	5	304	0	345	7	0
6	6	422	0	508	9	0
7	7	368	0	386	7	0
8	B	2500	0	1263	13	0
9	C	1904	0	1985	43	0
10	D	1620	0	1699	36	0
11	E	1655	0	1725	39	0
12	F	1351	0	1407	28	0
13	G	1353	0	1416	19	0
14	H	423	0	490	7	0
15	K	1568	0	1595	27	0
16	L	942	0	996	15	0
17	M	1342	0	1417	17	0
18	N	1067	0	1122	28	0
19	O	944	0	1004	27	0
20	P	947	0	966	30	0
21	Q	953	0	1045	25	0
22	R	996	0	1062	37	0
23	S	1171	0	1216	25	0
24	T	1149	0	1220	22	0
25	U	740	0	795	15	0
26	V	993	0	1055	25	0
27	W	2187	0	1102	19	0
28	X	810	0	847	14	0
29	Y	605	0	652	17	0
30	Z	754	0	808	13	0
31	A	60324	0	30377	443	0
32	0	521	0	499	4	0
All	All	91714	0	60975	850	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 850 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)
31:A:63:A:H61	31:A:89:A:N6	1.59	1.01
31:A:2118:U:H3	31:A:2199:G:H1	1.08	0.99
31:A:293:G:H21	31:A:365:A:N6	1.61	0.98
31:A:293:G:N2	31:A:365:A:H62	1.61	0.98
31:A:1505:C:H42	31:A:1515:G:H1	1.09	0.98

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	44/56 (79%)	39 (89%)	5 (11%)	0	100	100
2	2	49/65 (75%)	39 (80%)	10 (20%)	0	100	100
3	3	55/61 (90%)	49 (89%)	6 (11%)	0	100	100
4	4	67/73 (92%)	59 (88%)	8 (12%)	0	100	100
5	5	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
6	6	47/142 (33%)	46 (98%)	1 (2%)	0	100	100
7	7	44/116 (38%)	41 (93%)	3 (7%)	0	100	100
9	C	245/271 (90%)	213 (87%)	32 (13%)	0	100	100
10	D	210/221 (95%)	188 (90%)	22 (10%)	0	100	100
11	E	208/243 (86%)	180 (86%)	28 (14%)	0	100	100
12	F	173/220 (79%)	161 (93%)	12 (7%)	0	100	100
13	G	171/182 (94%)	161 (94%)	10 (6%)	0	100	100
14	H	51/155 (33%)	47 (92%)	4 (8%)	0	100	100
15	K	191/197 (97%)	178 (93%)	13 (7%)	0	100	100
16	L	119/121 (98%)	103 (87%)	16 (13%)	0	100	100
17	M	175/192 (91%)	163 (93%)	11 (6%)	1 (1%)	21	52
18	N	132/135 (98%)	111 (84%)	21 (16%)	0	100	100
19	O	114/116 (98%)	104 (91%)	10 (9%)	0	100	100
20	P	118/123 (96%)	116 (98%)	2 (2%)	0	100	100
21	Q	116/156 (74%)	100 (86%)	16 (14%)	0	100	100
22	R	113/127 (89%)	105 (93%)	8 (7%)	0	100	100
23	S	145/201 (72%)	118 (81%)	27 (19%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	T	142/199 (71%)	126 (89%)	16 (11%)	0	100	100
25	U	90/122 (74%)	86 (96%)	4 (4%)	0	100	100
26	V	122/145 (84%)	109 (89%)	13 (11%)	0	100	100
28	X	98/137 (72%)	87 (89%)	11 (11%)	0	100	100
29	Y	72/77 (94%)	66 (92%)	6 (8%)	0	100	100
30	Z	88/109 (81%)	87 (99%)	1 (1%)	0	100	100
32	0	62/94 (66%)	54 (87%)	6 (10%)	2 (3%)	3	19
All	All	3296/4093 (80%)	2967 (90%)	326 (10%)	3 (0%)	49	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	0	72	VAL
17	M	197	PRO
32	0	73	TRP

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	
1	1	39/49 (80%)	39 (100%)	0	100	100
2	2	48/59 (81%)	46 (96%)	2 (4%)	26	55
3	3	47/50 (94%)	47 (100%)	0	100	100
4	4	59/62 (95%)	58 (98%)	1 (2%)	53	71
5	5	34/34 (100%)	34 (100%)	0	100	100
6	6	46/124 (37%)	46 (100%)	0	100	100
7	7	40/96 (42%)	40 (100%)	0	100	100
9	C	195/216 (90%)	194 (100%)	1 (0%)	81	83
10	D	174/182 (96%)	174 (100%)	0	100	100
11	E	176/205 (86%)	174 (99%)	2 (1%)	65	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	F	148/183 (81%)	148 (100%)	0	100	100
13	G	147/154 (96%)	147 (100%)	0	100	100
14	H	47/134 (35%)	47 (100%)	0	100	100
15	K	167/171 (98%)	167 (100%)	0	100	100
16	L	101/101 (100%)	100 (99%)	1 (1%)	68	76
17	M	135/144 (94%)	134 (99%)	1 (1%)	76	80
18	N	107/108 (99%)	105 (98%)	2 (2%)	50	68
19	O	96/96 (100%)	96 (100%)	0	100	100
20	P	99/100 (99%)	99 (100%)	0	100	100
21	Q	104/135 (77%)	103 (99%)	1 (1%)	68	76
22	R	102/114 (90%)	102 (100%)	0	100	100
23	S	129/174 (74%)	128 (99%)	1 (1%)	73	79
24	T	126/176 (72%)	126 (100%)	0	100	100
25	U	81/103 (79%)	81 (100%)	0	100	100
26	V	112/129 (87%)	111 (99%)	1 (1%)	70	78
28	X	85/111 (77%)	85 (100%)	0	100	100
29	Y	64/67 (96%)	63 (98%)	1 (2%)	55	72
30	Z	83/97 (86%)	82 (99%)	1 (1%)	63	75
32	O	56/83 (68%)	56 (100%)	0	100	100
All	All	2847/3457 (82%)	2832 (100%)	15 (0%)	78	83

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	M	196	LEU
29	Y	103	LEU
18	N	94	VAL
30	Z	125	GLU
23	S	163	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
20	P	81	HIS

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Mol	Chain	Res	Type
23	S	212	HIS
20	P	93	HIS
22	R	99	GLN
24	T	52	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	W	101/106 (95%)	30 (29%)	4 (3%)
31	A	2808/2810 (99%)	592 (21%)	3 (0%)
8	B	116/121 (95%)	21 (18%)	1 (0%)
All	All	3025/3037 (99%)	643 (21%)	8 (0%)

5 of 643 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	B	4	U
8	B	10	G
8	B	14	U
8	B	15	A
8	B	16	G

5 of 8 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
31	A	556	C
31	A	514	A
27	W	97	A
27	W	33	A
31	A	97	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](#)

There are no ligands in this entry.

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.

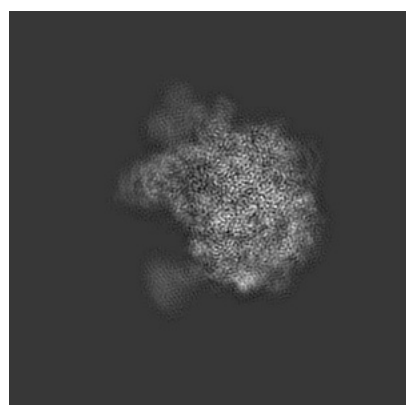
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6711. These allow visual inspection of the internal detail of the map and identification of artifacts.

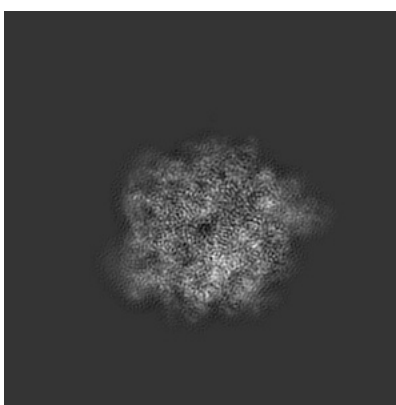
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

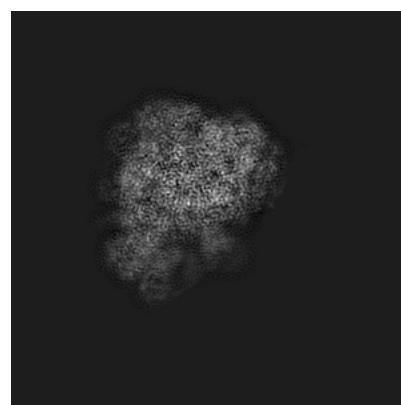
6.1.1 Primary map



X



Y

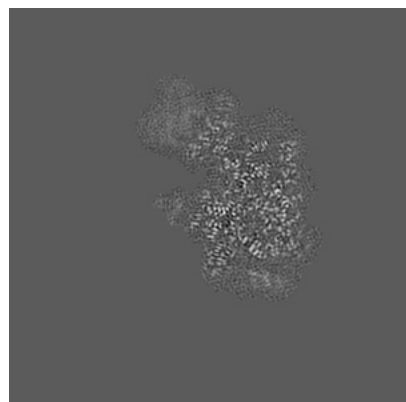


Z

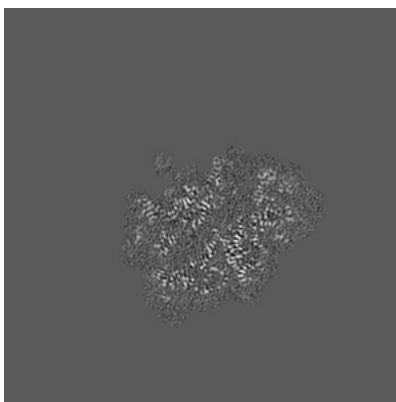
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

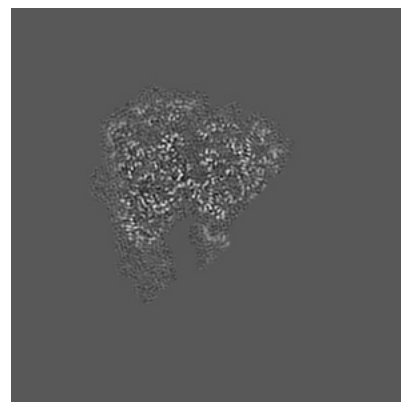
6.2.1 Primary map



X Index: 192



Y Index: 192

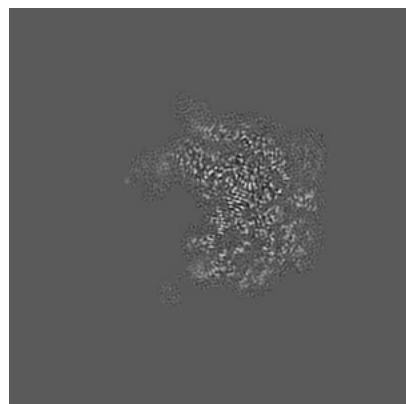


Z Index: 192

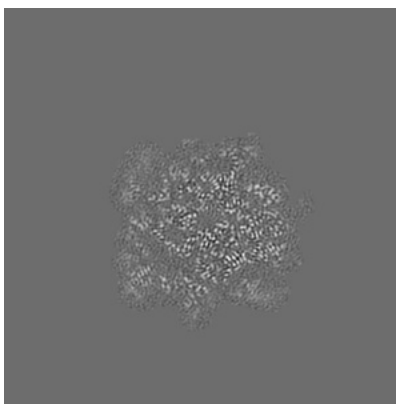
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

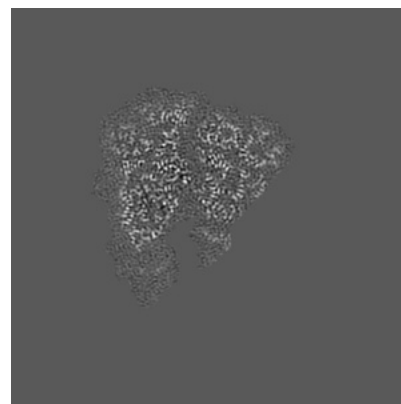
6.3.1 Primary map



X Index: 163



Y Index: 221

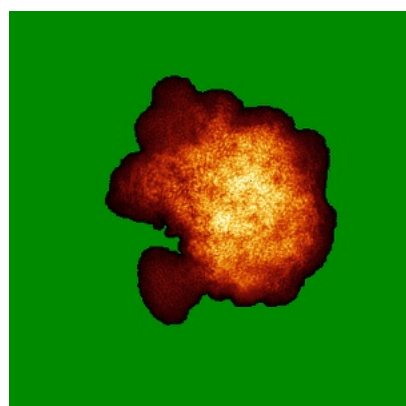


Z Index: 195

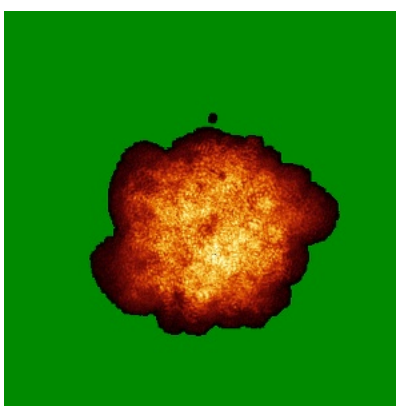
The images above show the largest variance slices of the map in three orthogonal directions.

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

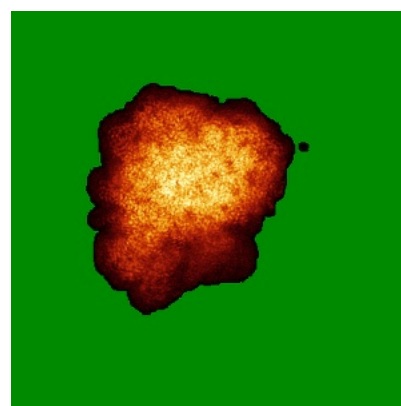
6.4.1 Primary map



X



Y

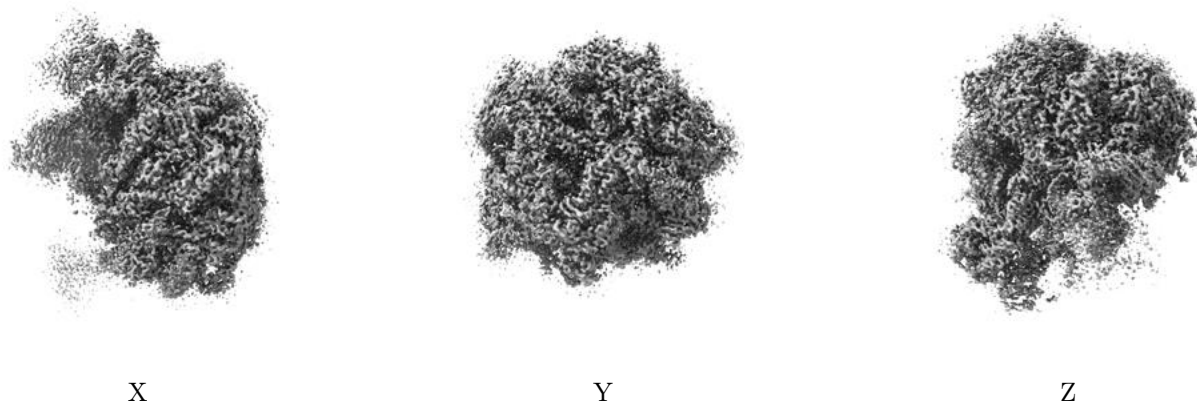


Z

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 0.09. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

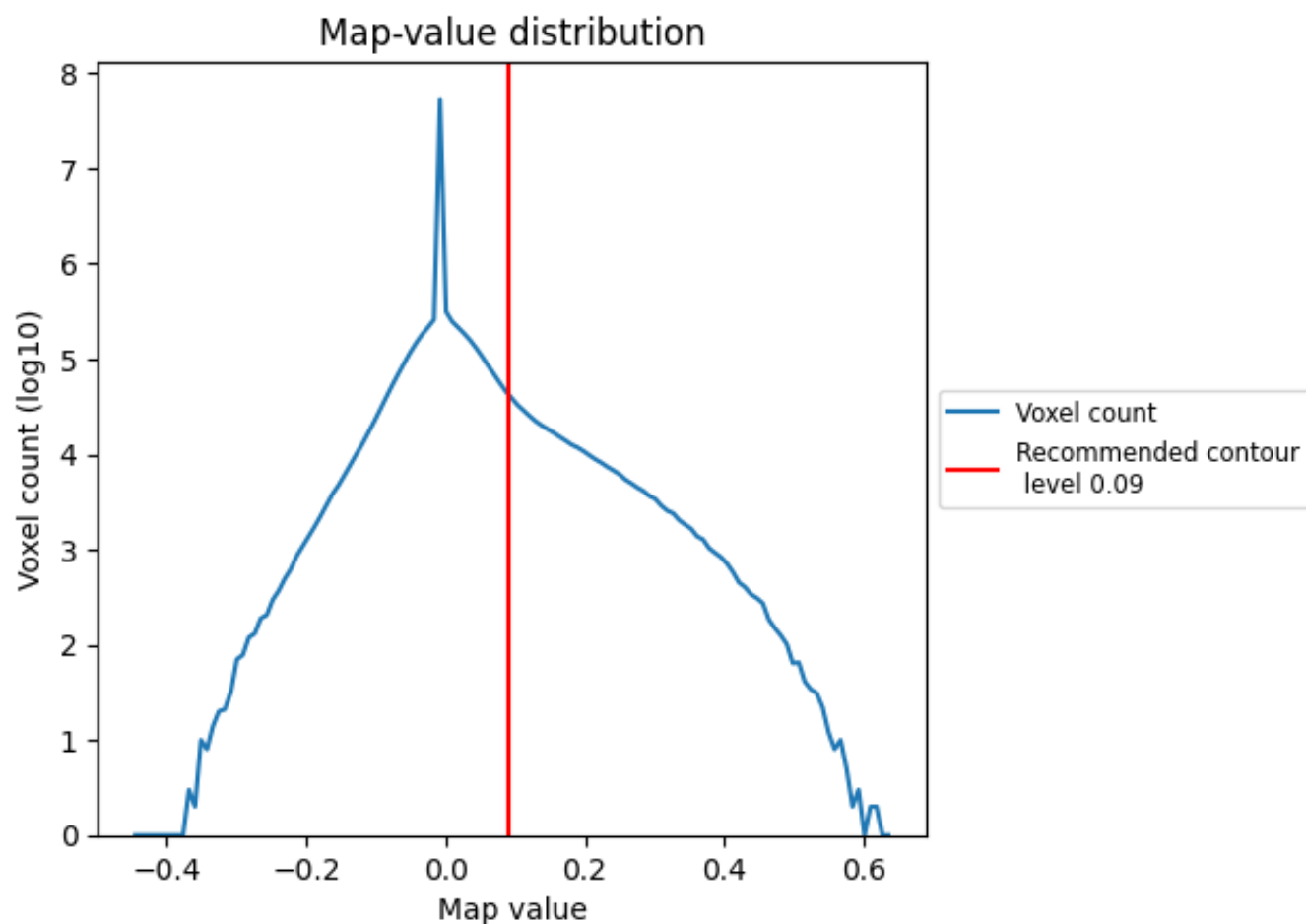
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

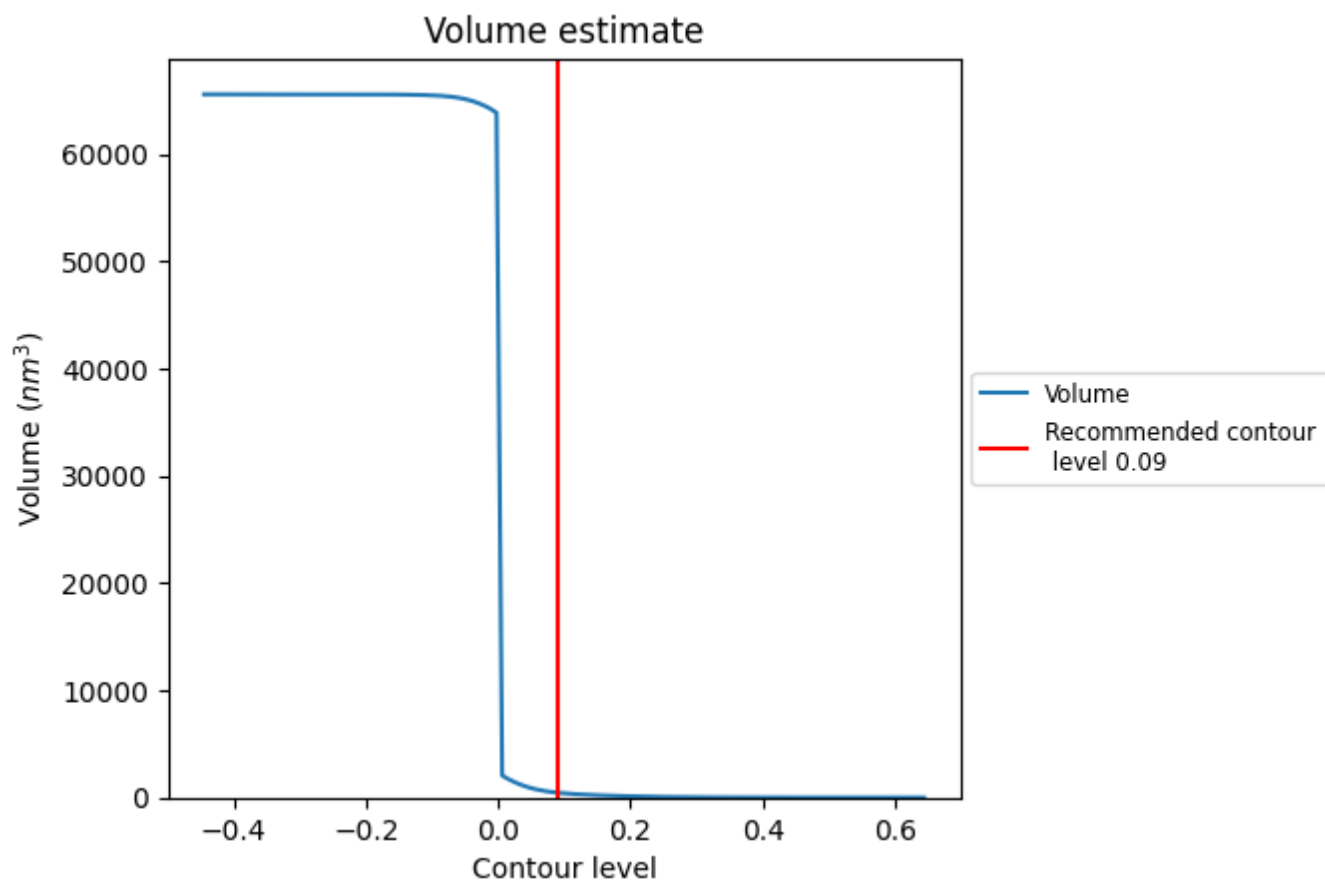
This section contains the results of statistical analysis of the map.

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.

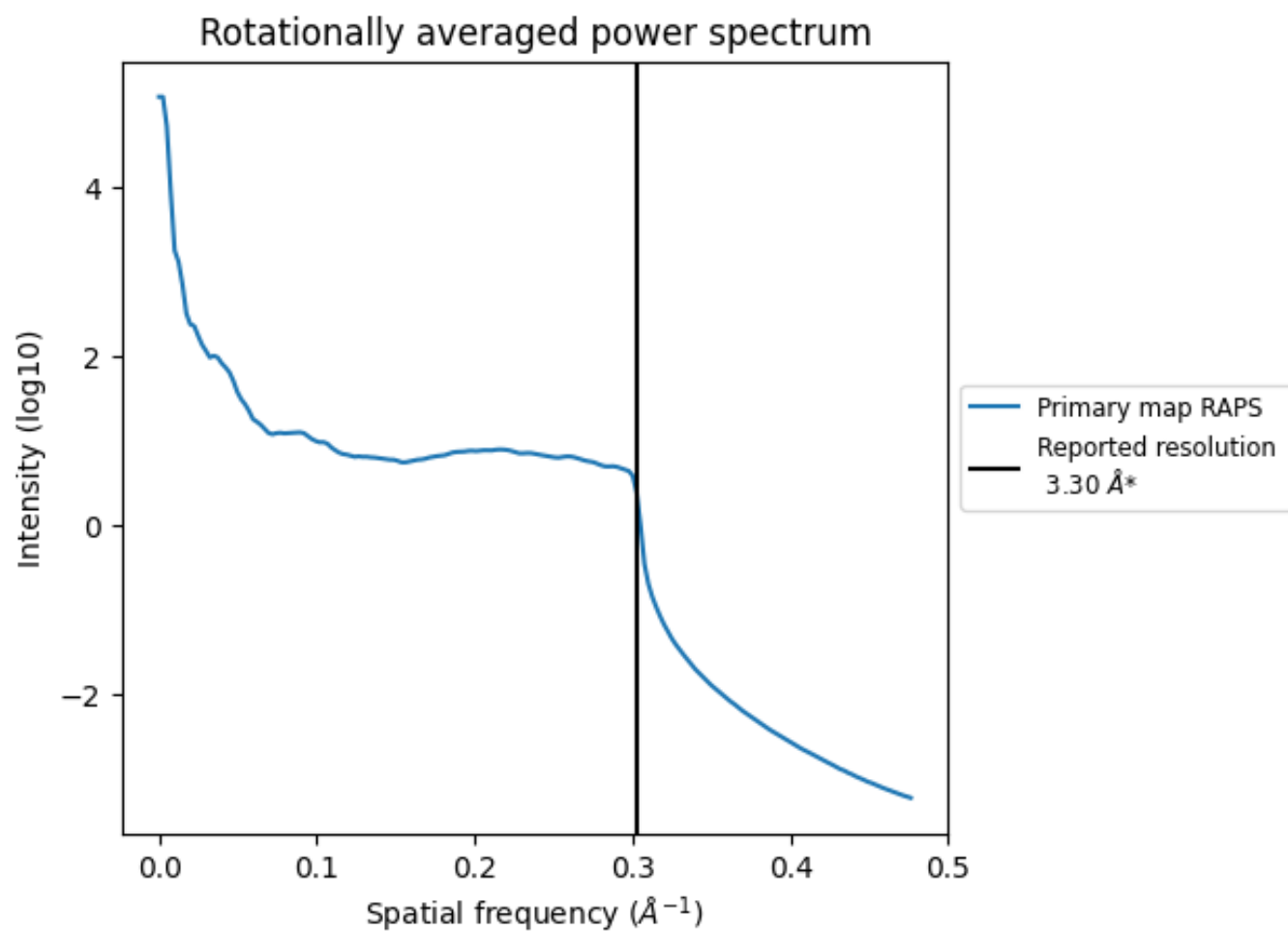
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 450 nm³; this corresponds to an approximate mass of 407 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

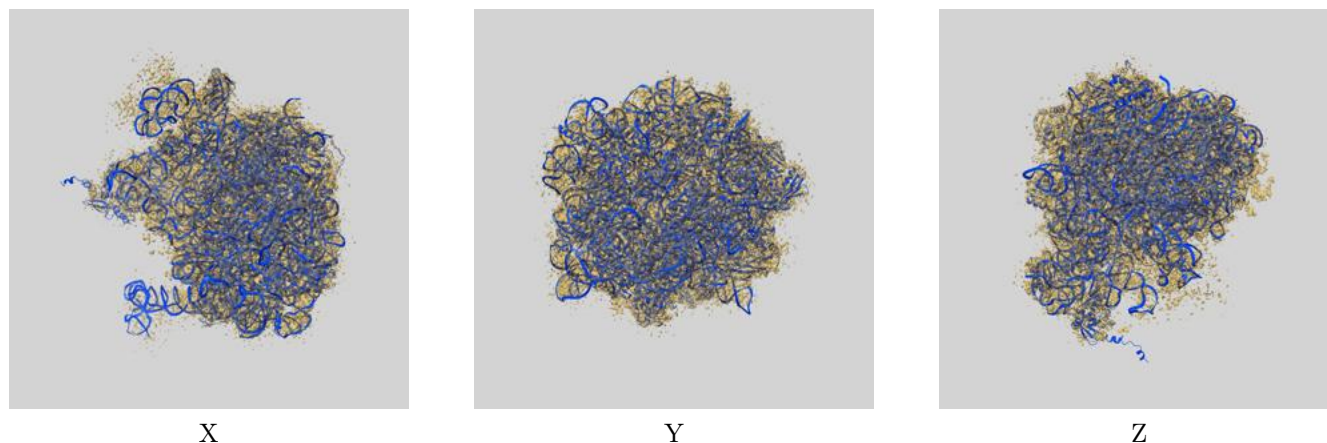
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

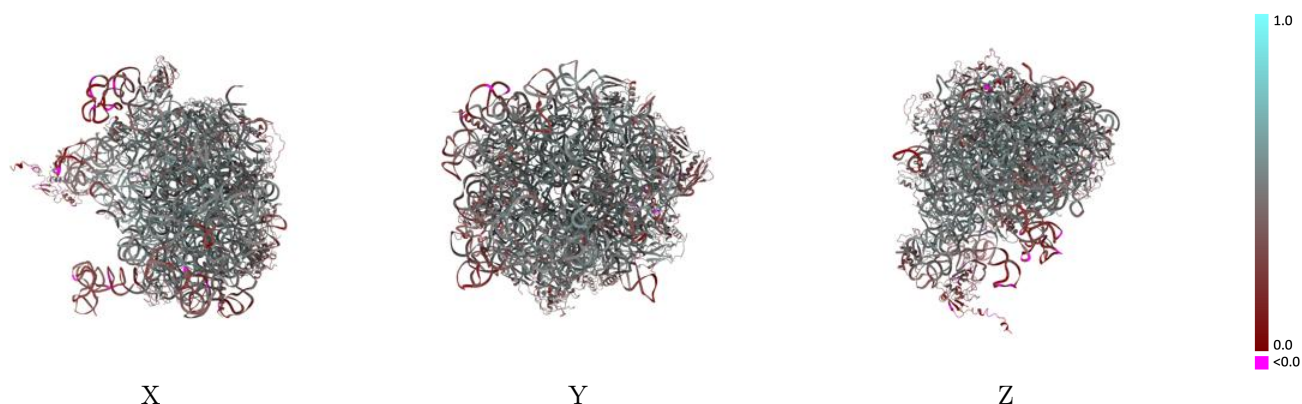
This section contains information regarding the fit between EMDB map EMD-6711 and PDB model 5X8T. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

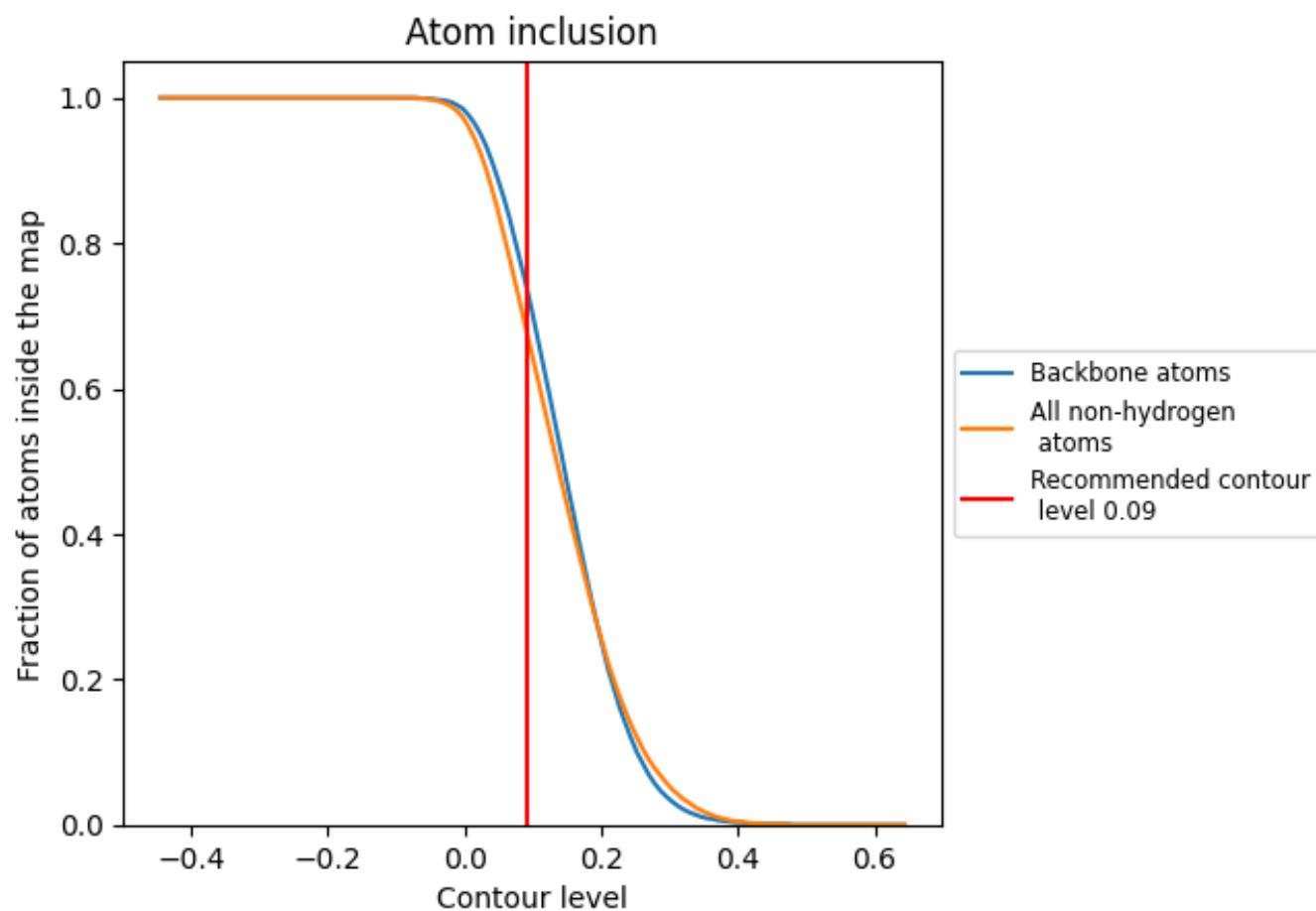


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 68% 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 (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6830	 0.4510
0	 0.0780	 0.1380
1	 0.6110	 0.4100
2	 0.5320	 0.3480
3	 0.6790	 0.4750
4	 0.7030	 0.4840
5	 0.6600	 0.4090
6	 0.4890	 0.3800
7	 0.6250	 0.4670
A	 0.7350	 0.4700
B	 0.7310	 0.4450
C	 0.6160	 0.4290
D	 0.6530	 0.4620
E	 0.5760	 0.4120
F	 0.2800	 0.2780
G	 0.4480	 0.3690
H	 0.2370	 0.3220
K	 0.5880	 0.4420
L	 0.5430	 0.4270
M	 0.6450	 0.4440
N	 0.6290	 0.4170
O	 0.6450	 0.4360
P	 0.5470	 0.3950
Q	 0.5600	 0.4240
R	 0.6570	 0.4170
S	 0.5420	 0.4110
T	 0.5260	 0.4070
U	 0.4890	 0.4060
V	 0.4980	 0.3810
W	 0.7640	 0.4760
X	 0.6030	 0.4270
Y	 0.6280	 0.4550
Z	 0.4720	 0.3770

