



wwPDB EM Validation Summary Report ⓘ

Dec 10, 2022 – 12:03 pm GMT

PDB ID : 6QT0
EMDB ID : EMD-4630
Title : Cryo-EM structures of Lsg1-TAP pre-60S ribosomal particles
Authors : Kargas, V.; Warren, A.J.
Deposited on : 2019-02-22
Resolution : 3.40 Å (reported)
Based on initial model : 4V88

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:

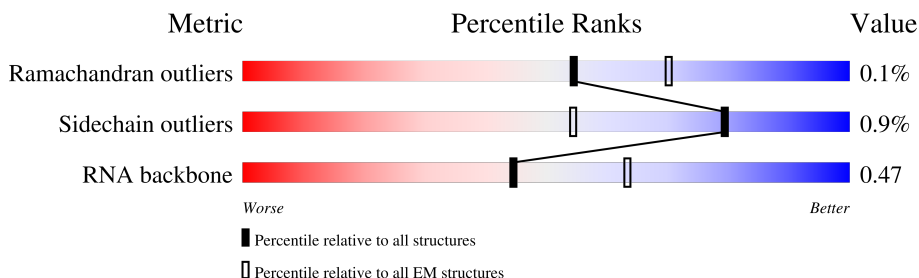
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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 3.40 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	3396	
2	B	254	
3	C	387	
4	D	362	
5	E	174	
6	F	189	
7	G	176	
8	H	256	

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Mol	Chain	Length	Quality of chain
9	q	221	34% 98%
10	J	198	5% 99%
11	K	199	9% 92% 7%
12	L	137	5% 99%
13	M	138	10% 99%
14	N	149	99%
15	O	204	99%
16	P	297	7% 95%
17	Q	186	99%
18	R	189	79% 21%
19	S	172	99%
20	T	160	7% 99%
21	U	184	83% 16%
22	V	121	7% 81% 18%
23	W	142	84% 15%
24	X	127	98%
25	Y	136	11% 99%
26	Z	120	99%
27	a	59	10% 92% 8%
28	b	244	89% 10%
29	c	105	17% 92% 8%
30	d	113	10% 92% 5%
31	e	130	93% 7%
32	f	107	97%
33	g	121	85% 15%

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Mol	Chain	Length	Quality of chain
34	h	100	 23% 98%
35	i	88	 5% 95% 5%
36	j	78	 9% 97%
37	k	51	 98%
38	l	106	 5% 89% 11%
39	m	92	 12% 99%
40	n	245	 63% 91% 9%
41	t	128	 22% 41% 59%
42	v	155	 21% 39% 61%
43	z	432	 11% 12% 88%
44	x	121	 87% 13%
45	y	158	 76% 22%

2 Entry composition [i](#)

There are 46 unique types of molecules in this entry. The entry contains 124065 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 RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	3164	67663	30231	12203	22069	3160	0	0

- Molecule 2 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	247	1878	1170	381	326	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	381	3039	1928	577	526	8	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	361	2748	1730	522	493	3	0	0

- Molecule 5 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	169	1352	847	253	248	4	0	0

- Molecule 6 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	189	1502	953	272	273	4	0	0

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	175	1399	902	251	245	1	0	0

- Molecule 8 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	223	1742	1117	309	313	3	0	0

- Molecule 9 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	q	216	1754	1111	332	304	7	0	0

- Molecule 10 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	197	1563	1005	292	265	1	0	0

- Molecule 11 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	K	186	1486	929	304	253	0	0

- Molecule 12 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	136	1002	628	189	178	7	0	0

- Molecule 13 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	137	1058	678	200	178	2	0	0

- Molecule 14 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	148	Total	C	N	O	S	0	0
			1172	749	231	189	3		

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	203	Total	C	N	O	S	0	0
			1719	1077	361	280	1		

- Molecule 16 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	286	Total	C	N	O	S	0	0
			2298	1453	400	443	2		

- Molecule 17 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	185	Total	C	N	O	S	0	0
			1440	908	290	240	2		

- Molecule 18 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	150	Total	C	N	O	S	0	0
			1209	752	257	200			

- Molecule 19 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	172	Total	C	N	O	S	0	0
			1444	930	267	243	4		

- Molecule 20 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	159	Total	C	N	O	S	0	0
			1275	805	246	220	4		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	154	Total	C	N	O	0	0
			1222	761	237	224		

- Molecule 22 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	V	99	Total	C	N	O	0	0
			786	510	129	147		

- Molecule 23 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	120	Total	C	N	O	S	0	0
			958	617	168	171	2		

- Molecule 24 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	X	125	Total	C	N	O	0	0
			984	620	191	173		

- Molecule 25 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Y	135	Total	C	N	O	0	0
			1091	710	202	179		

- Molecule 26 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	119	Total	C	N	O	S	0	0
			968	615	186	166	1		

- Molecule 27 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	a	54	Total	C	N	O	0	0
			430	268	93	69		

- Molecule 28 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	b	219	1760	1138	320	301	1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	c	97	741	479	124	137	1	0	0

- Molecule 30 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	d	107	872	553	165	153	1	0	0

- Molecule 31 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	e	121	976	618	197	160	1	0	0

- Molecule 32 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	f	106	849	540	165	143	1	0	0

- Molecule 33 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	g	103	812	504	167	137	4	0	0

- Molecule 34 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	h	98	763	477	155	129	2	0	0

- Molecule 35 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	84	Total	C	N	O	S	0	0
			665	405	145	110	5		

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	77	Total	C	N	O	S	0	0
			611	391	115	105			

- Molecule 37 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	50	Total	C	N	O	S	0	0
			435	272	97	64	2		

- Molecule 38 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	94	Total	C	N	O	S	0	0
			756	476	153	122	5		

- Molecule 39 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	91	Total	C	N	O	S	0	0
			693	429	138	120	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	224	Total	C	N	O	S	0	0
			1691	1051	293	340	7		

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	t	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 42 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	v	60	500	322	98	79	1	0	0

- Molecule 43 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	z	53	445	274	88	80	3	0	0

- Molecule 44 is a RNA chain called 5S rRNA.

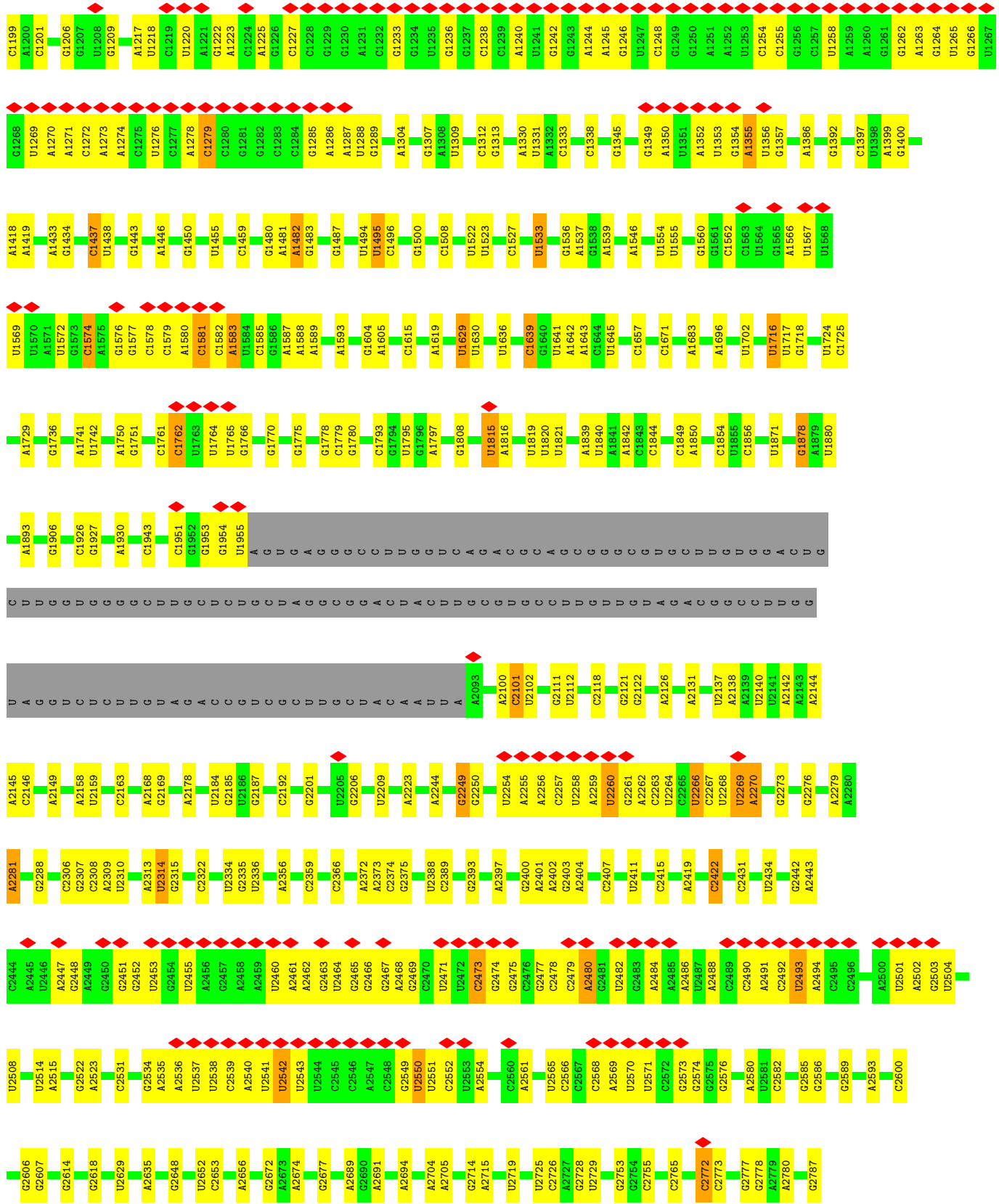
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
44	x	121	2579	1152	461	845	121	0	0

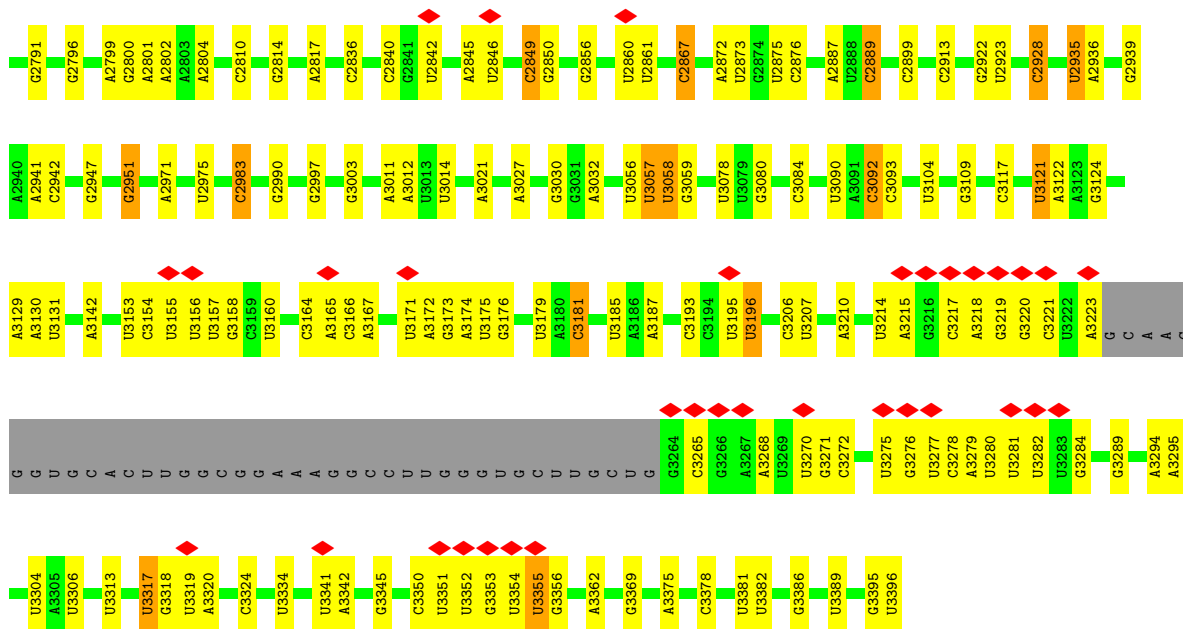
- Molecule 45 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
45	y	156	3313	1482	582	1093	156	0	0

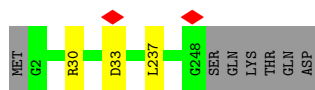
- Molecule 46 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
46	g	1	Total 1	Zn 1	0
46	i	1	Total 1	Zn 1	0
46	l	1	Total 1	Zn 1	0
46	m	1	Total 1	Zn 1	0
46	t	1	Total 1	Zn 1	0

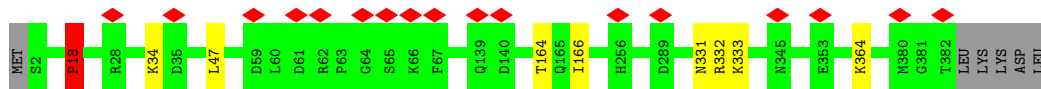




• Molecule 2: 60S ribosomal protein L2-A



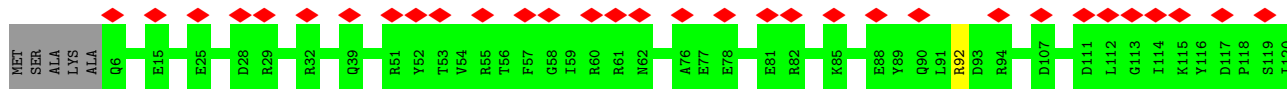
• Molecule 3: 60S ribosomal protein L3

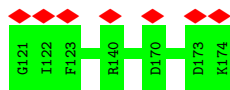


• Molecule 4: 60S ribosomal protein L4-A

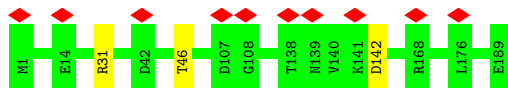


• Molecule 5: 60S ribosomal protein L11-A

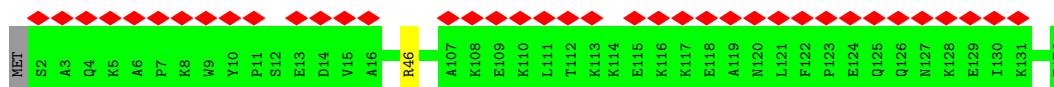




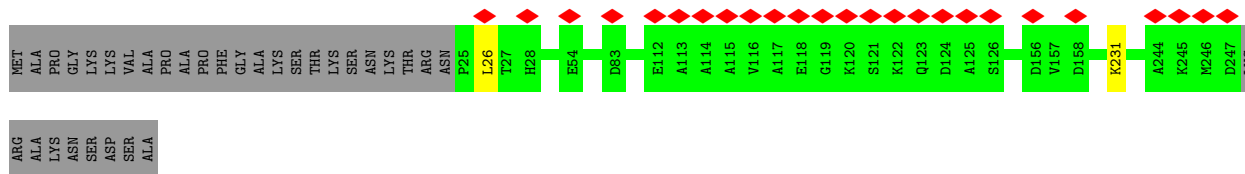
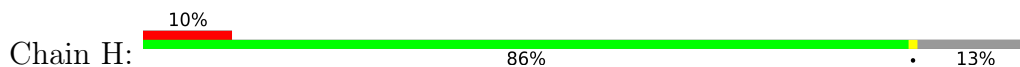
- Molecule 6: 60S ribosomal protein L9-A



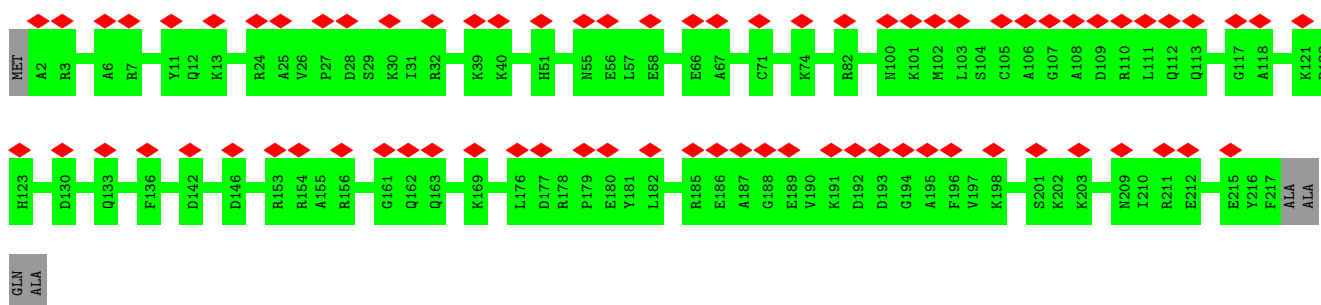
- Molecule 7: 60S ribosomal protein L6-A



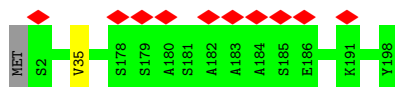
- Molecule 8: 60S ribosomal protein L8-A



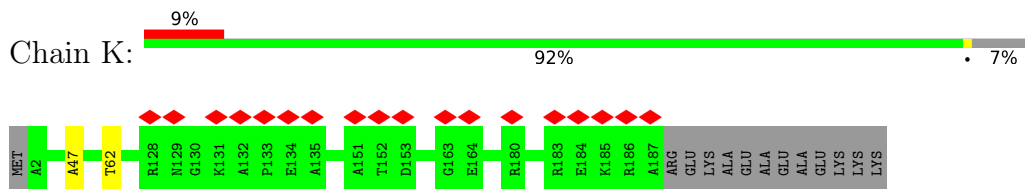
- Molecule 9: 60S ribosomal protein L10



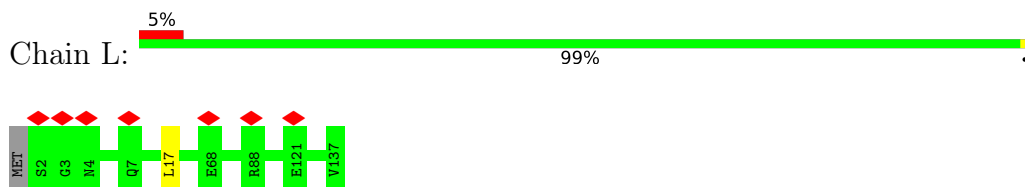
- Molecule 10: 60S ribosomal protein L16-B



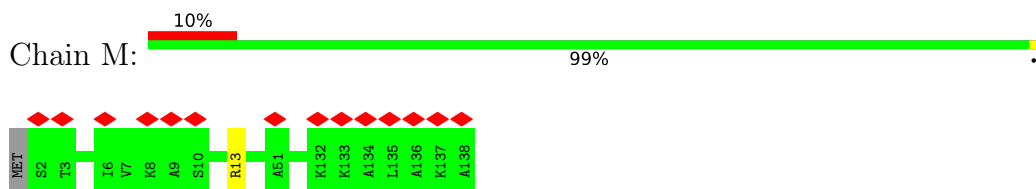
- Molecule 11: 60S ribosomal protein L13-A



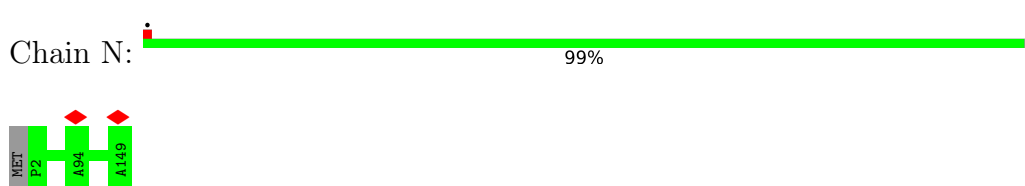
- Molecule 12: 60S ribosomal protein L23-A



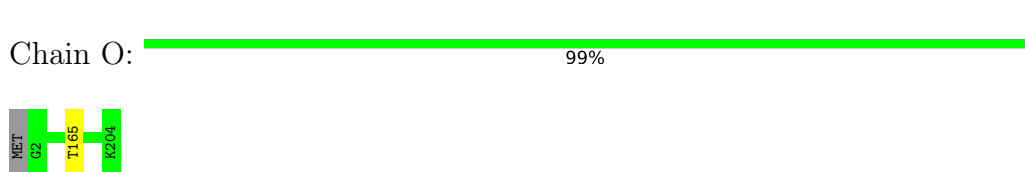
- Molecule 13: 60S ribosomal protein L14-A



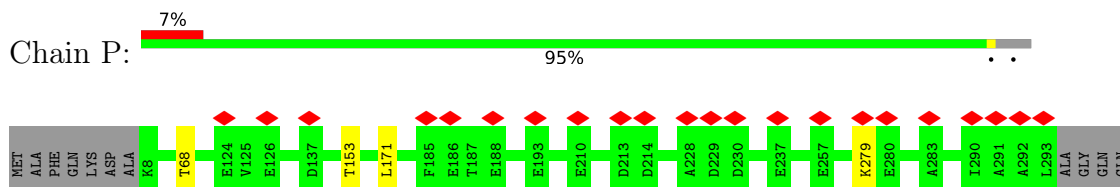
- Molecule 14: 60S ribosomal protein L28



- Molecule 15: 60S ribosomal protein L15-A

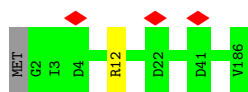


- Molecule 16: 60S ribosomal protein L5

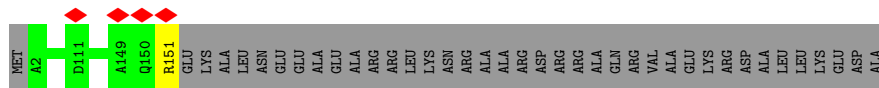
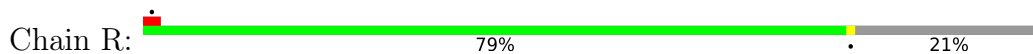


- Molecule 17: 60S ribosomal protein L18-A





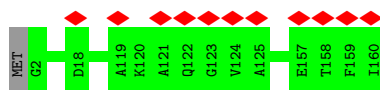
- Molecule 18: 60S ribosomal protein L19-A



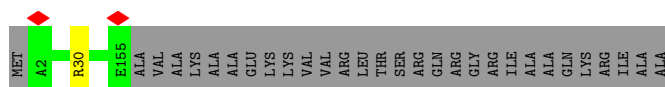
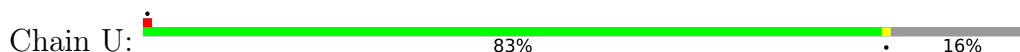
- Molecule 19: 60S ribosomal protein L20-A



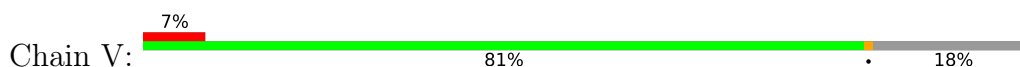
- Molecule 20: 60S ribosomal protein L21-A



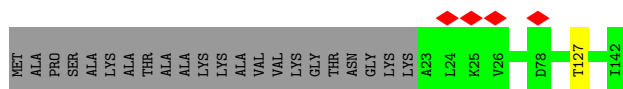
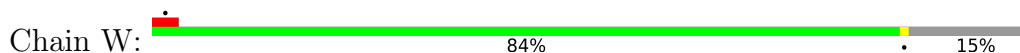
- Molecule 21: 60S ribosomal protein L17-A



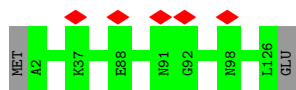
- Molecule 22: 60S ribosomal protein L22-A



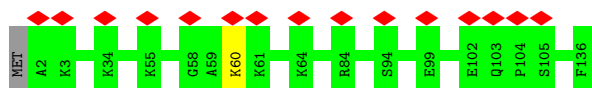
- Molecule 23: 60S ribosomal protein L25



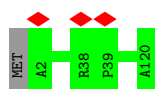
- Molecule 24: 60S ribosomal protein L26-A



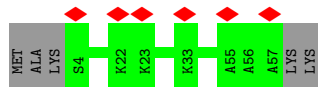
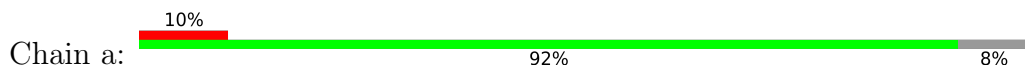
- Molecule 25: 60S ribosomal protein L27-A



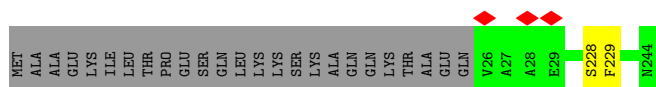
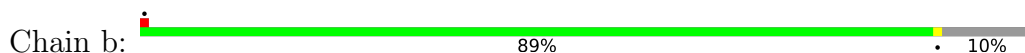
- Molecule 26: 60S ribosomal protein L35-A



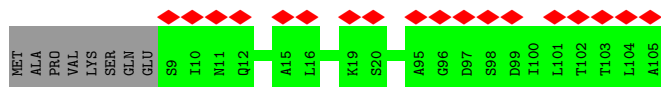
- Molecule 27: 60S ribosomal protein L29



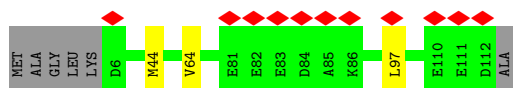
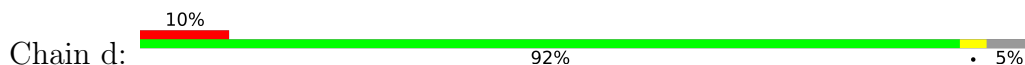
- Molecule 28: 60S ribosomal protein L7-A



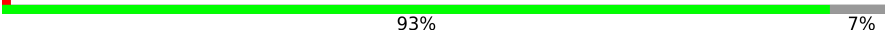
- Molecule 29: 60S ribosomal protein L30

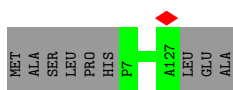


- Molecule 30: 60S ribosomal protein L31-A



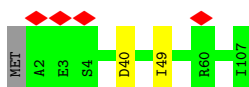
- Molecule 31: 60S ribosomal protein L32

Chain e:  93% 7%




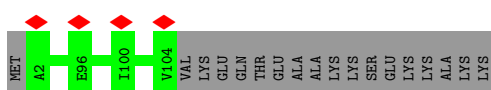
- Molecule 32: 60S ribosomal protein L33-A

Chain f:  97%



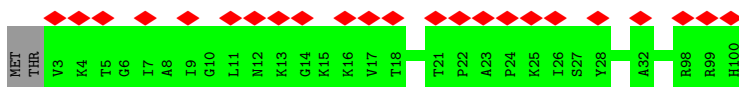
- Molecule 33: 60S ribosomal protein L34-A

Chain g:  85% 15%

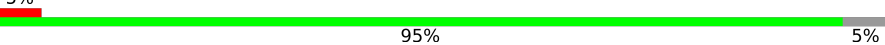


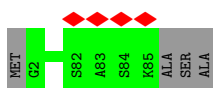
- Molecule 34: 60S ribosomal protein L36-A

Chain h:  23% 98%



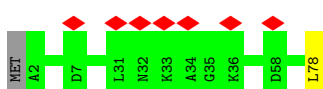
- Molecule 35: 60S ribosomal protein L37-A

Chain i:  5% 95% 5%



- Molecule 36: 60S ribosomal protein L38

Chain j:  9% 97%

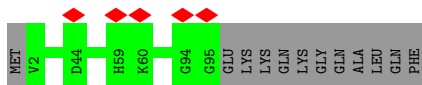
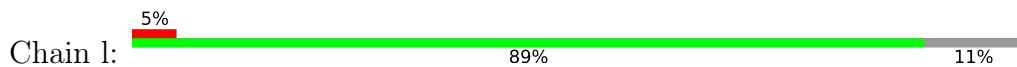


- Molecule 37: 60S ribosomal protein L39

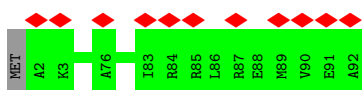
Chain k:  98%



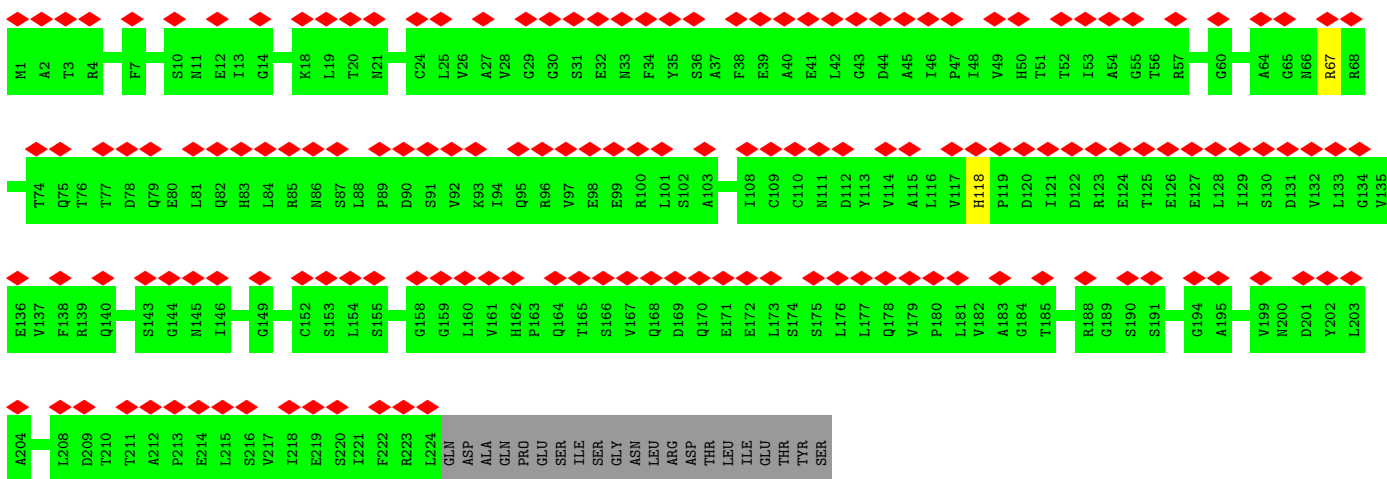
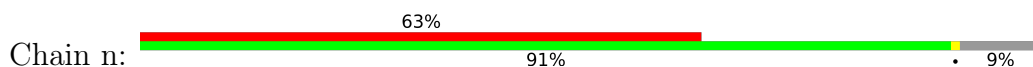
- Molecule 38: 60S ribosomal protein L42-A



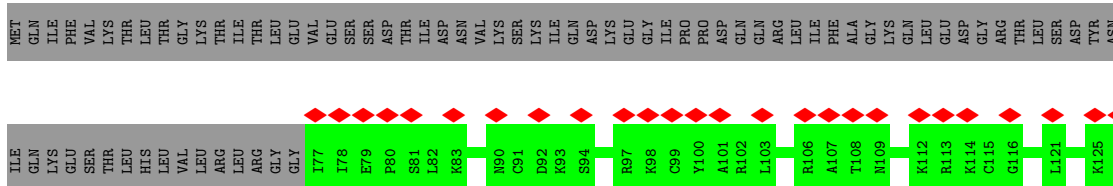
- Molecule 39: 60S ribosomal protein L43-A



- Molecule 40: Eukaryotic translation initiation factor 6

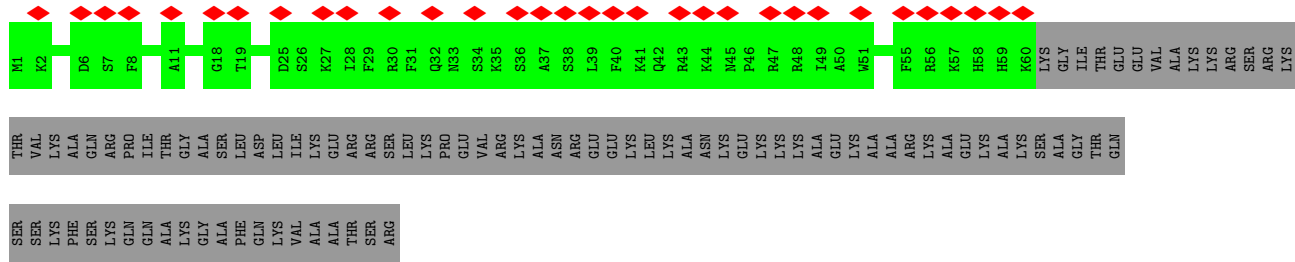


- Molecule 41: Ubiquitin-60S ribosomal protein L40

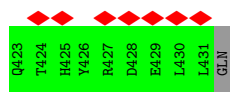
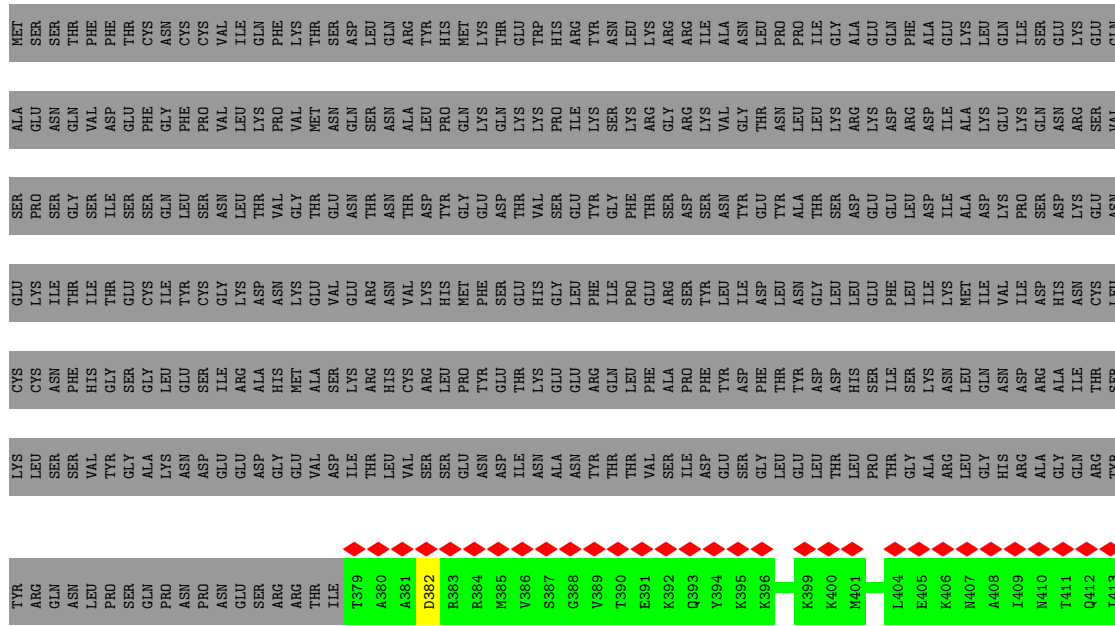


- Molecule 42: 60S ribosomal protein L24-A

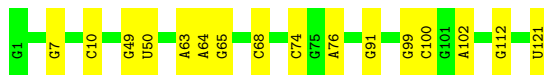
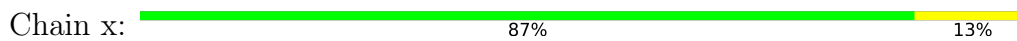




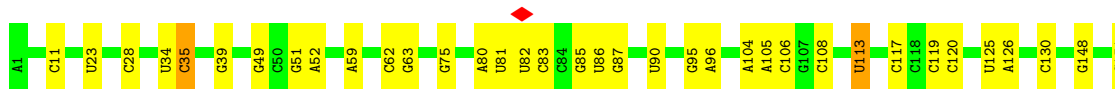
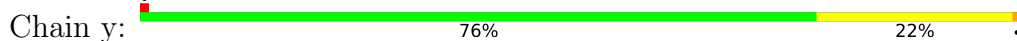
● Molecule 43: Cytoplasmic 60S subunit biogenesis factor REH1



● Molecule 44: 5S rRNA



● Molecule 45: 5.8S rRNA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	46734	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	63	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	0.468	Depositor
Minimum map value	-0.255	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.07	Depositor
Map size (\AA)	383.40002, 383.40002, 383.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.065, 1.065, 1.065	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	A	1.04	2/75742 (0.0%)	1.07	295/118089 (0.2%)
2	B	0.55	0/1912	0.64	0/2569
3	C	0.54	0/3110	0.63	3/4184 (0.1%)
4	D	0.56	0/2800	0.60	0/3791
5	E	0.33	0/1373	0.56	0/1841
6	F	0.38	0/1523	0.54	0/2051
7	G	0.39	0/1423	0.59	0/1911
8	H	0.46	0/1774	0.57	1/2395 (0.0%)
9	q	0.39	0/1791	0.55	0/2402
10	J	0.52	0/1593	0.54	0/2137
11	K	0.53	0/1511	0.56	0/2031
12	L	0.49	0/1017	0.61	1/1368 (0.1%)
13	M	0.42	0/1073	0.59	0/1445
14	N	0.59	0/1203	0.59	0/1611
15	O	0.65	0/1756	0.60	0/2353
16	P	0.41	0/2347	0.55	1/3167 (0.0%)
17	Q	0.53	0/1464	0.59	0/1964
18	R	0.48	0/1226	0.50	0/1637
19	S	0.50	0/1480	0.55	0/1989
20	T	0.52	0/1299	0.57	0/1742
21	U	0.57	0/1245	0.57	0/1676
22	V	0.41	0/802	0.61	0/1087
23	W	0.53	0/973	0.58	0/1313
24	X	0.48	0/995	0.58	0/1329
25	Y	0.40	0/1117	0.56	0/1496
26	Z	0.46	0/977	0.55	0/1300
27	a	0.43	0/441	0.57	0/589
28	b	0.54	0/1797	0.58	0/2419
29	c	0.43	0/749	0.55	0/1007
30	d	0.49	0/886	0.62	2/1190 (0.2%)
31	e	0.54	0/995	0.57	0/1329
32	f	0.60	0/867	0.70	1/1167 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.54	0/822	0.62	0/1099
34	h	0.37	0/770	0.51	0/1023
35	i	0.68	0/680	0.60	0/901
36	j	0.42	0/617	0.56	0/825
37	k	0.52	0/442	0.55	0/587
38	l	0.47	0/768	0.55	0/1016
39	m	0.52	0/700	0.58	0/933
40	n	0.36	0/1712	0.66	0/2330
41	t	0.32	0/423	0.52	0/562
42	v	0.36	0/512	0.51	0/680
43	z	0.34	0/448	0.59	1/593 (0.2%)
44	x	0.81	0/2883	0.97	1/4491 (0.0%)
45	y	1.15	0/3702	1.08	13/5764 (0.2%)
All	All	0.87	2/133740 (0.0%)	0.92	319/197383 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	35	A	N9-C4	-5.66	1.34	1.37
1	A	2168	A	N9-C4	-5.19	1.34	1.37

The worst 5 of 319 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1196	C	C2-N1-C1'	10.79	130.66	118.80
1	A	922	U	C2-N1-C1'	9.85	129.52	117.70
1	A	3317	U	N3-C2-O2	-9.78	115.36	122.20
1	A	1196	C	N1-C2-O2	9.47	124.58	118.90
1	A	1196	C	C6-N1-C2	-9.35	116.56	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	245/254 (96%)	220 (90%)	25 (10%)	0	100	100
3	C	379/387 (98%)	353 (93%)	24 (6%)	2 (0%)	29	61
4	D	359/362 (99%)	332 (92%)	27 (8%)	0	100	100
5	E	167/174 (96%)	155 (93%)	12 (7%)	0	100	100
6	F	187/189 (99%)	176 (94%)	11 (6%)	0	100	100
7	G	173/176 (98%)	151 (87%)	22 (13%)	0	100	100
8	H	221/256 (86%)	207 (94%)	14 (6%)	0	100	100
9	q	214/221 (97%)	193 (90%)	21 (10%)	0	100	100
10	J	195/198 (98%)	189 (97%)	6 (3%)	0	100	100
11	K	184/199 (92%)	168 (91%)	15 (8%)	1 (0%)	29	61
12	L	134/137 (98%)	125 (93%)	9 (7%)	0	100	100
13	M	135/138 (98%)	126 (93%)	9 (7%)	0	100	100
14	N	146/149 (98%)	136 (93%)	10 (7%)	0	100	100
15	O	201/204 (98%)	186 (92%)	15 (8%)	0	100	100
16	P	284/297 (96%)	264 (93%)	20 (7%)	0	100	100
17	Q	183/186 (98%)	177 (97%)	6 (3%)	0	100	100
18	R	148/189 (78%)	145 (98%)	3 (2%)	0	100	100
19	S	170/172 (99%)	160 (94%)	10 (6%)	0	100	100
20	T	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
21	U	152/184 (83%)	146 (96%)	6 (4%)	0	100	100
22	V	97/121 (80%)	88 (91%)	8 (8%)	1 (1%)	15	46
23	W	118/142 (83%)	105 (89%)	13 (11%)	0	100	100
24	X	123/127 (97%)	112 (91%)	11 (9%)	0	100	100
25	Y	133/136 (98%)	119 (90%)	14 (10%)	0	100	100
26	Z	117/120 (98%)	113 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	a	52/59 (88%)	49 (94%)	3 (6%)	0	100	100
28	b	217/244 (89%)	205 (94%)	12 (6%)	0	100	100
29	c	95/105 (90%)	93 (98%)	2 (2%)	0	100	100
30	d	105/113 (93%)	91 (87%)	14 (13%)	0	100	100
31	e	119/130 (92%)	113 (95%)	6 (5%)	0	100	100
32	f	104/107 (97%)	93 (89%)	11 (11%)	0	100	100
33	g	101/121 (84%)	94 (93%)	7 (7%)	0	100	100
34	h	96/100 (96%)	94 (98%)	2 (2%)	0	100	100
35	i	82/88 (93%)	74 (90%)	8 (10%)	0	100	100
36	j	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
37	k	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
38	l	92/106 (87%)	86 (94%)	6 (6%)	0	100	100
39	m	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
40	n	222/245 (91%)	195 (88%)	27 (12%)	0	100	100
41	t	50/128 (39%)	45 (90%)	5 (10%)	0	100	100
42	v	58/155 (37%)	56 (97%)	2 (3%)	0	100	100
43	z	51/432 (12%)	45 (88%)	6 (12%)	0	100	100
All	All	6278/7232 (87%)	5828 (93%)	446 (7%)	4 (0%)	54	82

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	18	PRO
11	K	47	ALA
22	V	52	ASN
3	C	364	LYS

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	
2	B	189/196 (96%)	186 (98%)	3 (2%)	62	81
3	C	317/323 (98%)	310 (98%)	7 (2%)	52	75
4	D	288/289 (100%)	280 (97%)	8 (3%)	43	70
5	E	147/150 (98%)	146 (99%)	1 (1%)	84	92
6	F	169/169 (100%)	166 (98%)	3 (2%)	59	79
7	G	152/153 (99%)	151 (99%)	1 (1%)	84	92
8	H	183/208 (88%)	182 (100%)	1 (0%)	88	94
9	q	185/187 (99%)	185 (100%)	0	100	100
10	J	163/164 (99%)	162 (99%)	1 (1%)	86	94
11	K	149/159 (94%)	148 (99%)	1 (1%)	84	92
12	L	104/105 (99%)	104 (100%)	0	100	100
13	M	108/109 (99%)	107 (99%)	1 (1%)	78	90
14	N	118/119 (99%)	118 (100%)	0	100	100
15	O	175/176 (99%)	174 (99%)	1 (1%)	86	94
16	P	237/245 (97%)	234 (99%)	3 (1%)	69	84
17	Q	150/151 (99%)	149 (99%)	1 (1%)	84	92
18	R	124/154 (80%)	123 (99%)	1 (1%)	81	91
19	S	156/156 (100%)	154 (99%)	2 (1%)	69	84
20	T	136/137 (99%)	136 (100%)	0	100	100
21	U	125/146 (86%)	124 (99%)	1 (1%)	81	91
22	V	86/107 (80%)	85 (99%)	1 (1%)	71	85
23	W	104/118 (88%)	103 (99%)	1 (1%)	76	88
24	X	108/110 (98%)	108 (100%)	0	100	100
25	Y	115/116 (99%)	114 (99%)	1 (1%)	78	90
26	Z	104/105 (99%)	104 (100%)	0	100	100
27	a	43/47 (92%)	43 (100%)	0	100	100
28	b	184/205 (90%)	182 (99%)	2 (1%)	73	86
29	c	81/88 (92%)	81 (100%)	0	100	100
30	d	94/97 (97%)	93 (99%)	1 (1%)	73	86
31	e	104/111 (94%)	104 (100%)	0	100	100
32	f	90/91 (99%)	89 (99%)	1 (1%)	73	86
33	g	88/103 (85%)	88 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	h	80/82 (98%)	80 (100%)	0	100	100
35	i	69/71 (97%)	69 (100%)	0	100	100
36	j	68/69 (99%)	67 (98%)	1 (2%)	65	82
37	k	45/46 (98%)	45 (100%)	0	100	100
38	l	81/91 (89%)	81 (100%)	0	100	100
39	m	71/72 (99%)	71 (100%)	0	100	100
40	n	192/211 (91%)	190 (99%)	2 (1%)	76	88
41	t	47/116 (40%)	47 (100%)	0	100	100
42	v	53/129 (41%)	53 (100%)	0	100	100
43	z	48/392 (12%)	48 (100%)	0	100	100
All	All	5330/6073 (88%)	5284 (99%)	46 (1%)	79	90

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

Mol	Chain	Res	Type
16	P	68	THR
21	U	30	ARG
16	P	153	THR
18	R	151	ARG
23	W	127	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
33	g	11	ASN
35	i	28	HIS
35	i	13	ASN
37	k	25	GLN
10	J	25	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3160/3396 (93%)	710 (22%)	19 (0%)
44	x	120/121 (99%)	15 (12%)	0
45	y	155/158 (98%)	29 (18%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	3435/3675 (93%)	754 (21%)	19 (0%)

5 of 754 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	18	G
1	A	22	G
1	A	26	A
1	A	40	A
1	A	43	A

5 of 19 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2266	U
1	A	2493	U
1	A	3121	U
1	A	2462	A
1	A	1716	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 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.

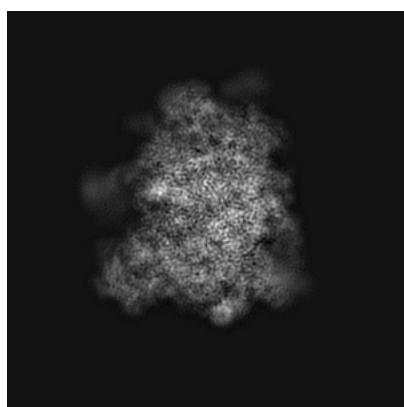
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4630. These allow visual inspection of the internal detail of the map and identification of artifacts.

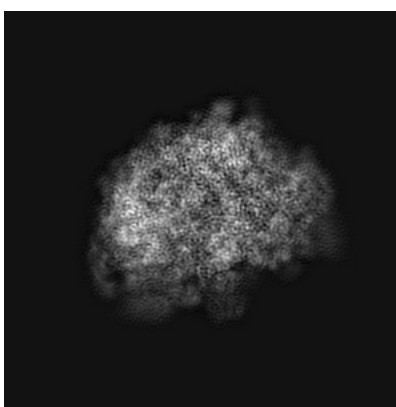
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

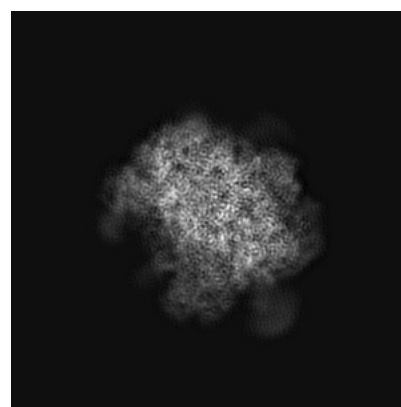
6.1.1 Primary map



X



Y

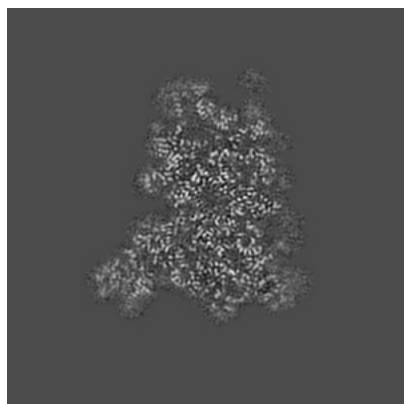


Z

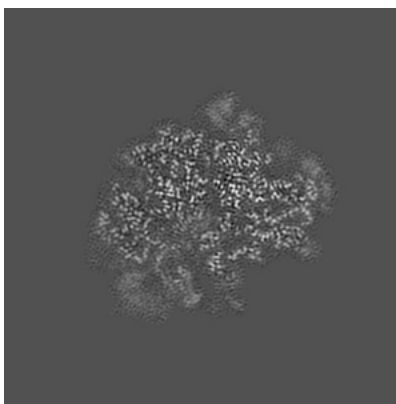
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

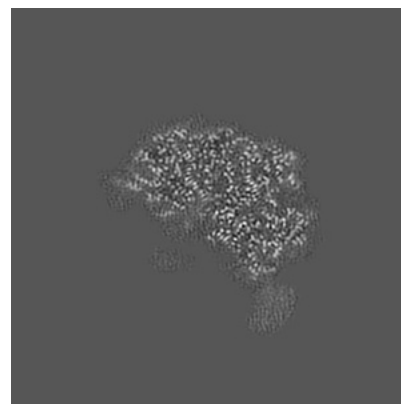
6.2.1 Primary map



X Index: 180



Y Index: 180

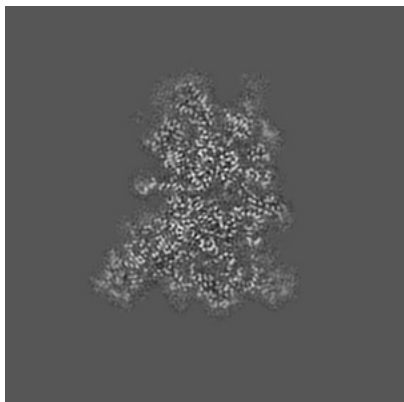


Z Index: 180

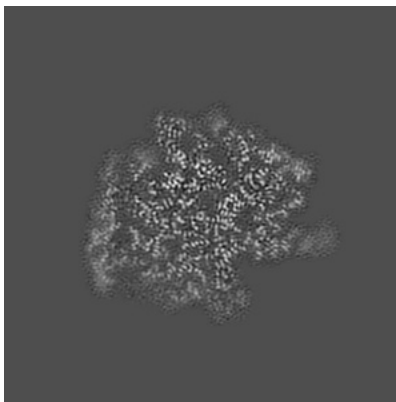
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

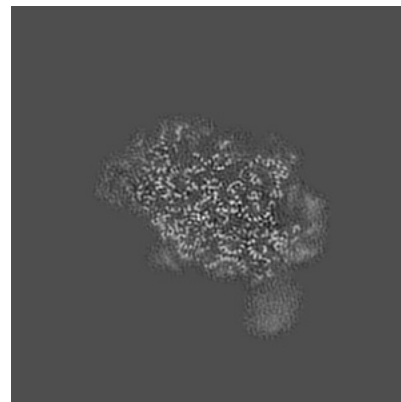
6.3.1 Primary map



X Index: 189



Y Index: 196

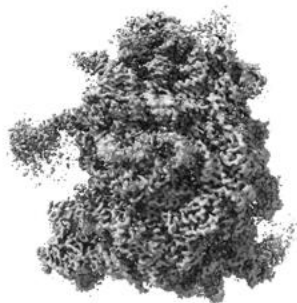


Z Index: 199

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

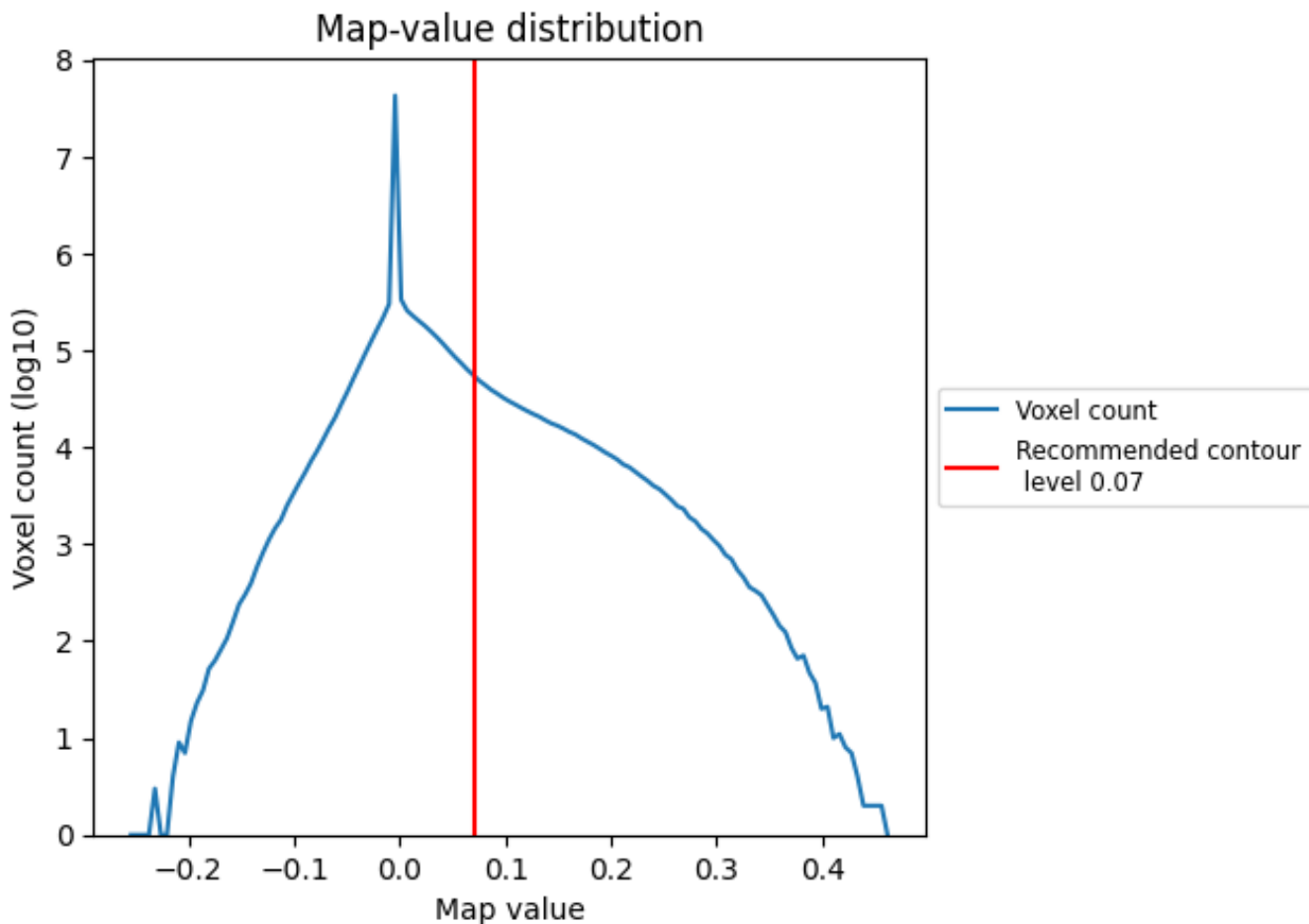
6.5 Mask visualisation

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

7 Map analysis [i](#)

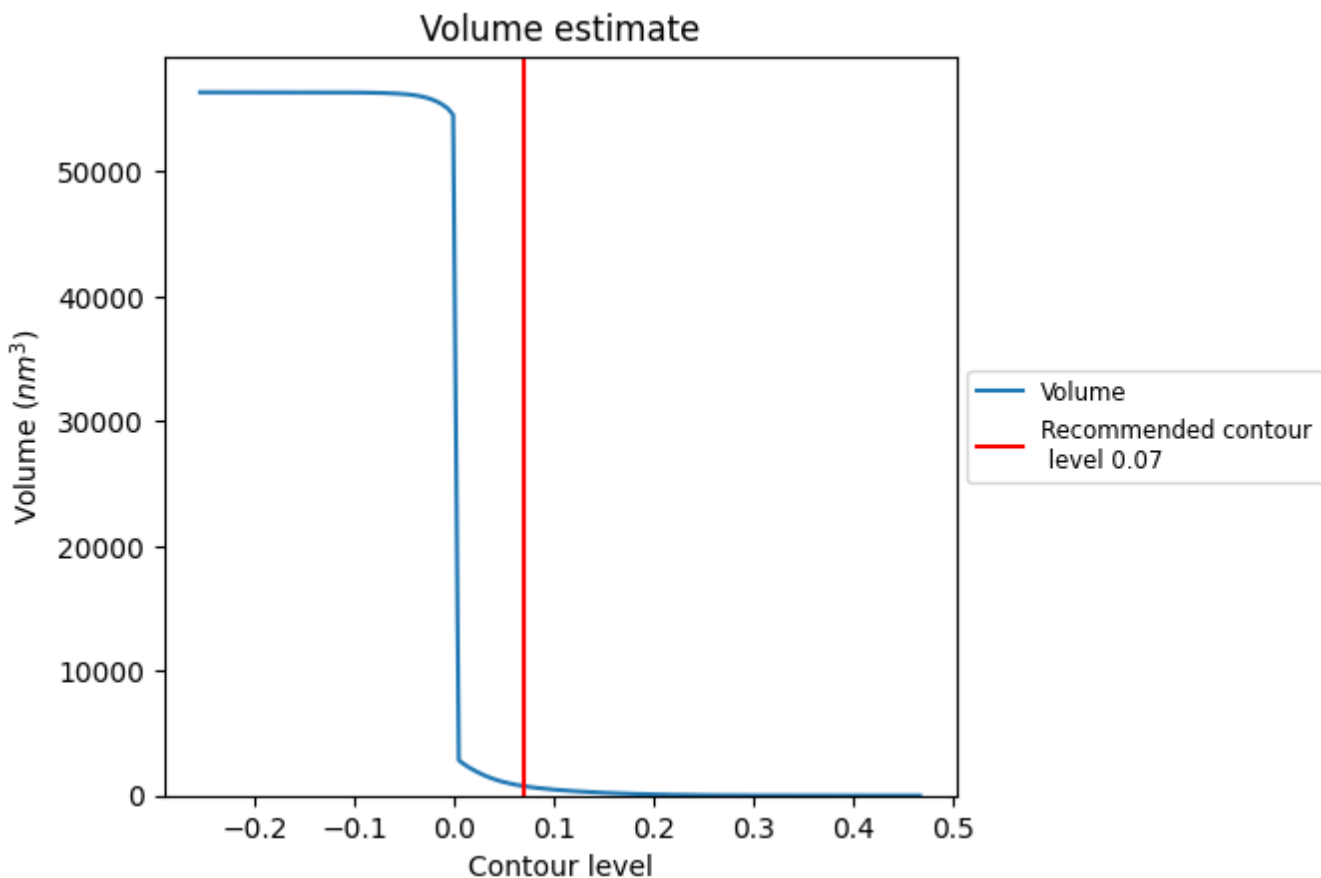
This section contains the results of statistical analysis of the map.

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.

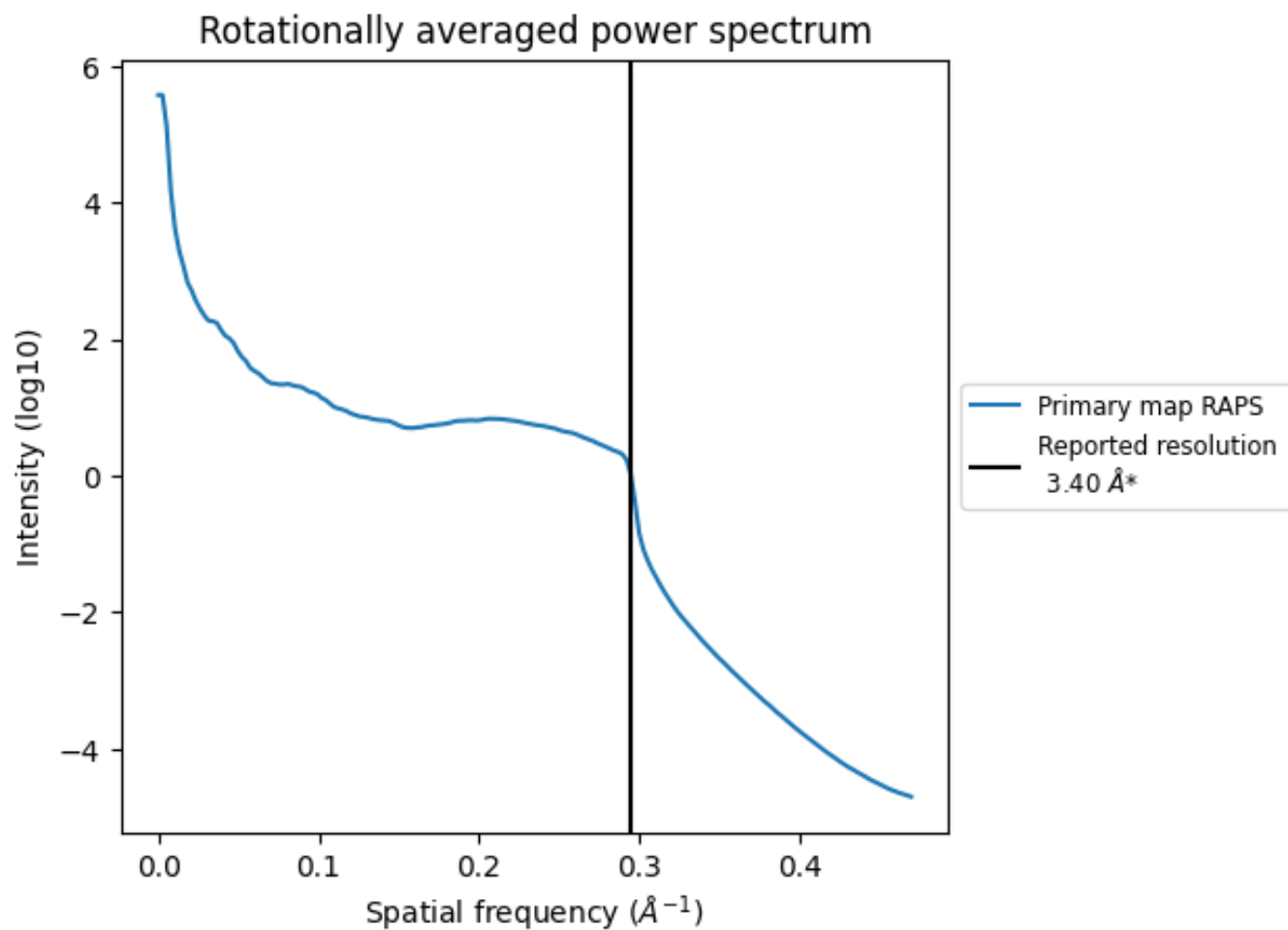
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 759 nm³; this corresponds to an approximate mass of 685 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 0.294\AA^{-1}

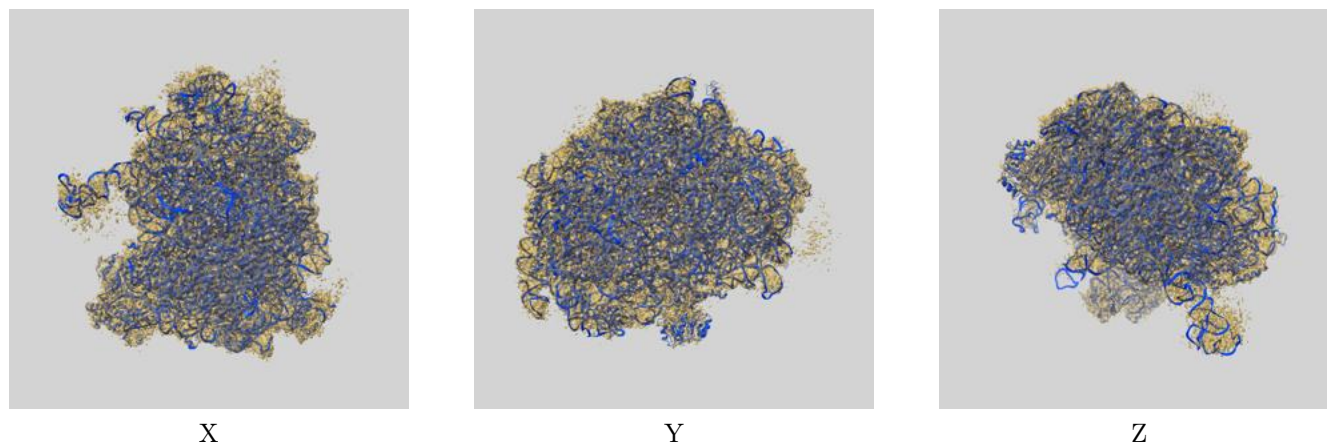
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

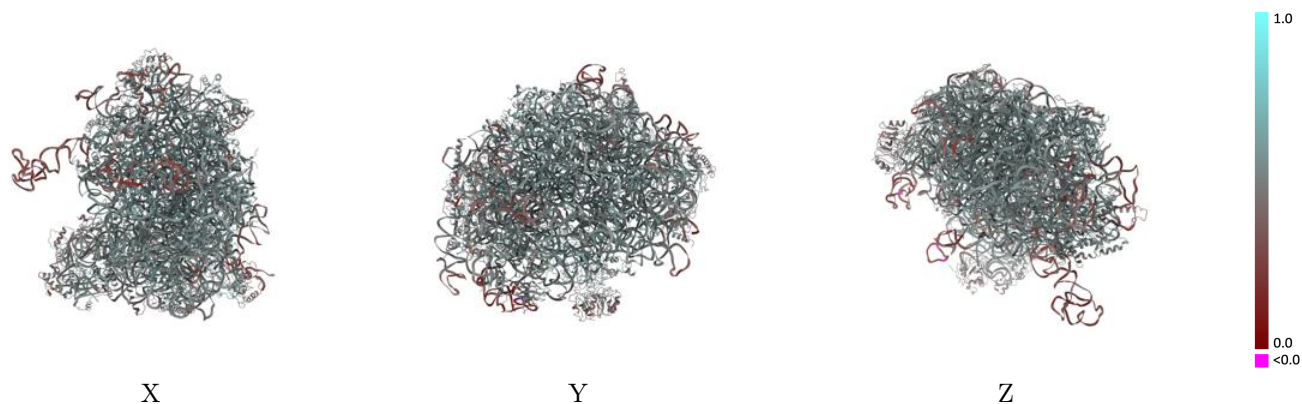
This section contains information regarding the fit between EMDB map EMD-4630 and PDB model 6QT0. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



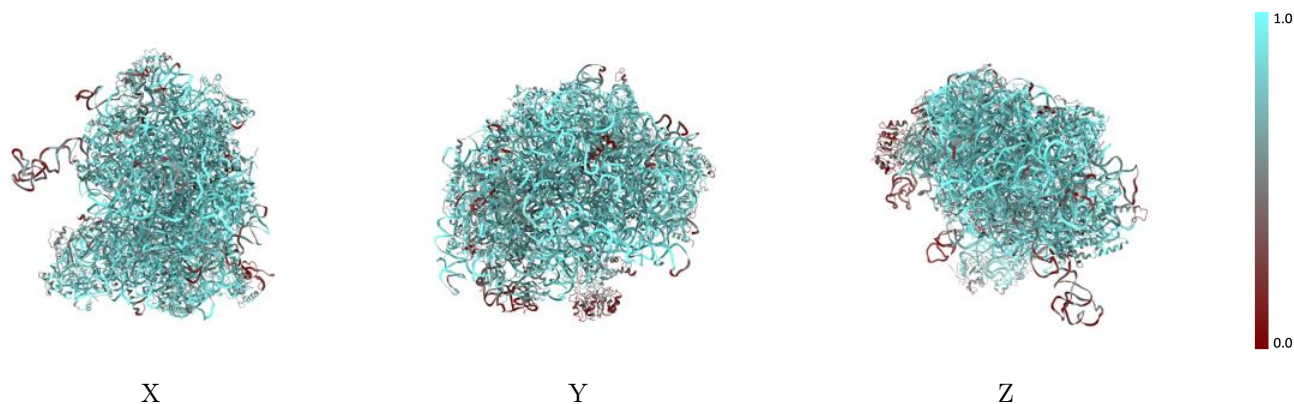
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



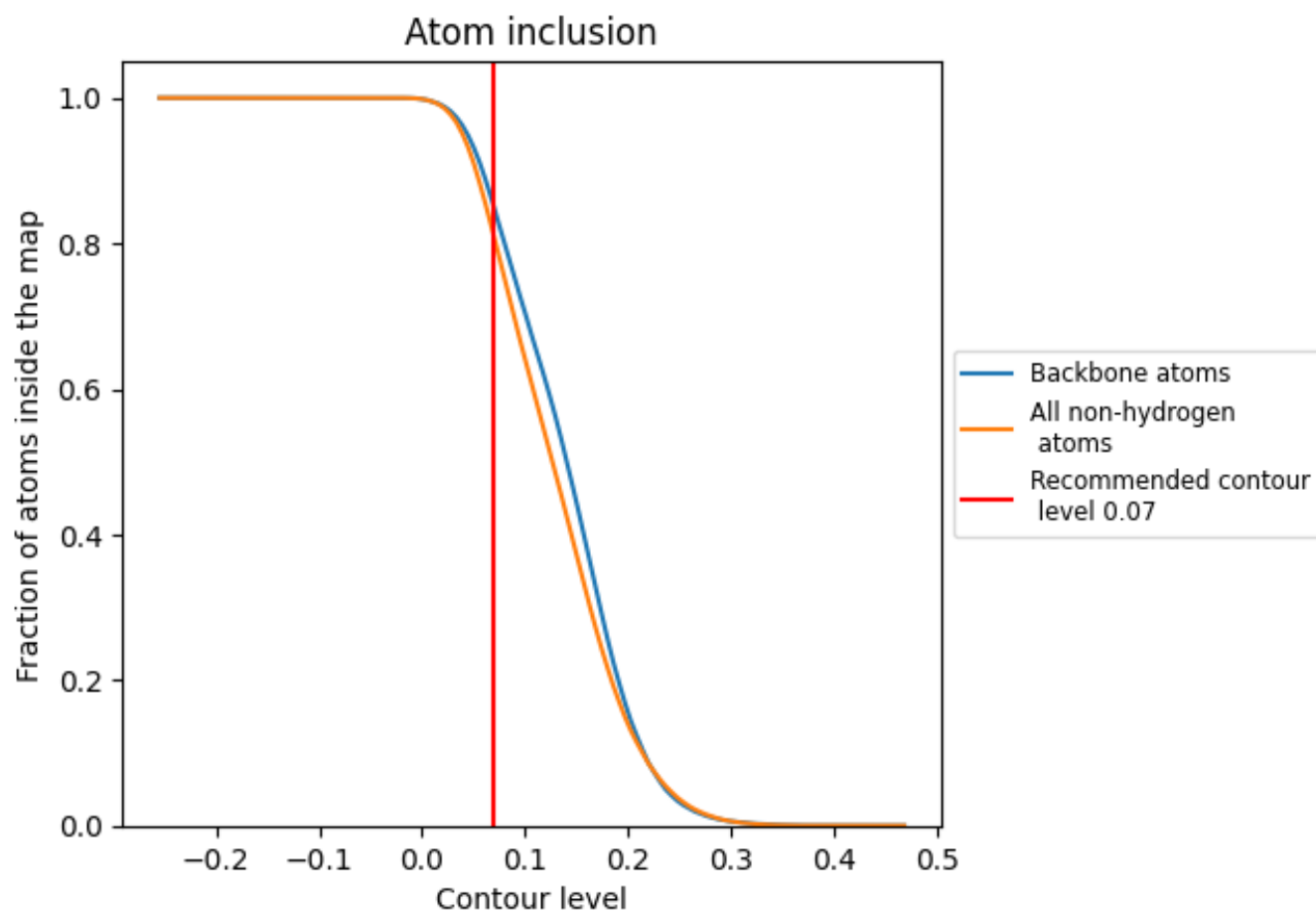
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 81% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8081	 0.5130
A	 0.8537	 0.5010
B	 0.8179	 0.5630
C	 0.8047	 0.5470
D	 0.8071	 0.5510
E	 0.5814	 0.4370
F	 0.7001	 0.5080
G	 0.6264	 0.4690
H	 0.7138	 0.5050
J	 0.7711	 0.5410
K	 0.7626	 0.5400
L	 0.7331	 0.5430
M	 0.7274	 0.5050
N	 0.8571	 0.5620
O	 0.8527	 0.5720
P	 0.7548	 0.4950
Q	 0.8494	 0.5650
R	 0.8040	 0.5470
S	 0.7787	 0.5400
T	 0.7619	 0.5410
U	 0.8229	 0.5640
V	 0.6801	 0.4940
W	 0.7959	 0.5500
X	 0.8140	 0.5530
Y	 0.7131	 0.4900
Z	 0.8047	 0.5440
a	 0.7262	 0.5330
b	 0.8056	 0.5470
c	 0.6722	 0.4720
d	 0.7435	 0.5350
e	 0.8126	 0.5670
f	 0.8098	 0.5600
g	 0.7985	 0.5520
h	 0.5943	 0.5050
i	 0.8500	 0.5710



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Chain	Atom inclusion	Q-score
j	 0.7191	 0.5170
k	 0.8237	 0.5720
l	 0.7859	 0.5570
m	 0.6996	 0.5260
n	 0.3045	 0.4410
q	 0.4932	 0.5000
t	 0.4109	 0.5040
v	 0.4360	 0.5080
x	 0.9321	 0.5020
y	 0.9342	 0.5350
z	 0.1531	 0.4430