



wwPDB EM Validation Summary Report ⓘ

Jun 24, 2026 – 02:58 AM EDT

PDB ID : 8FLF / pdb_00008ff
EMDB ID : EMD-29277
Title : Human nuclear pre-60S ribosomal subunit (State L3)
Authors : Vanden Broeck, A.; Klinge, S.
Deposited on : 2022-12-21
Resolution : 2.65 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:

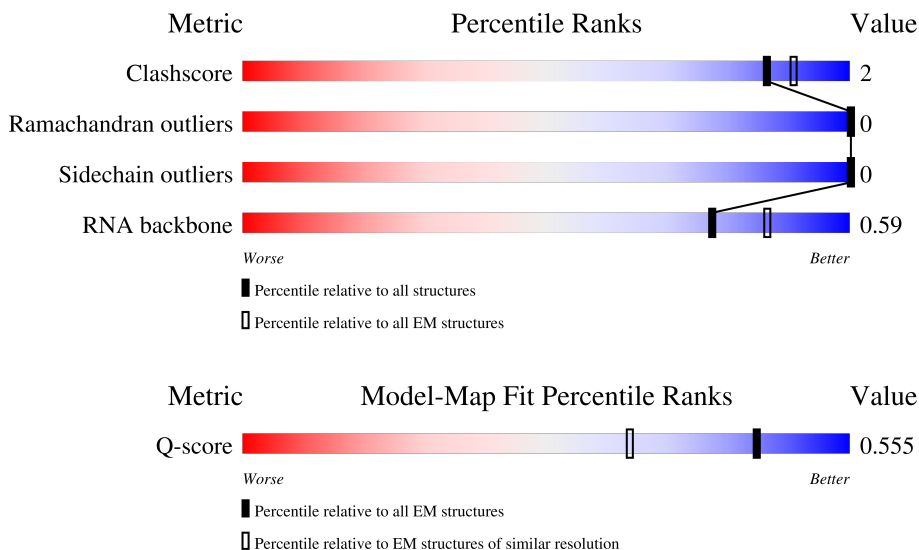
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 2.65 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.





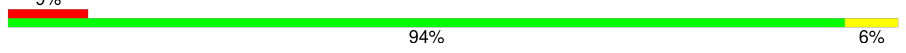
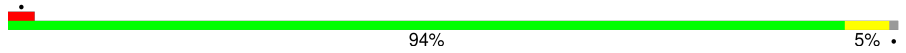



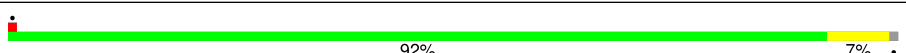
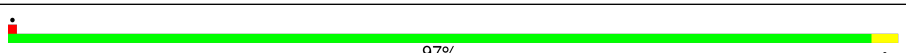
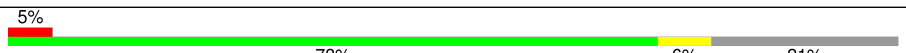
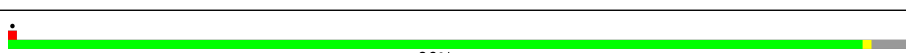
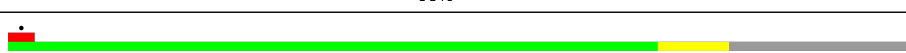

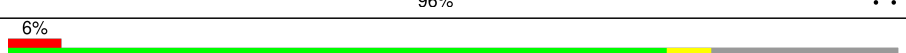
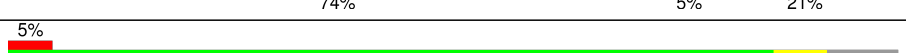

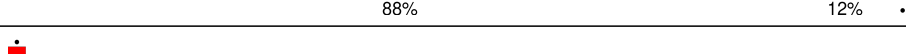
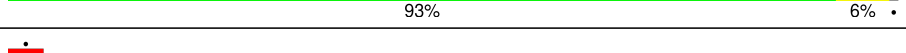

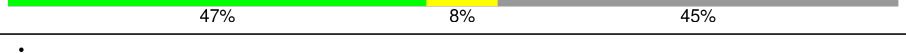
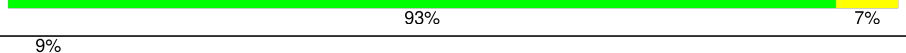


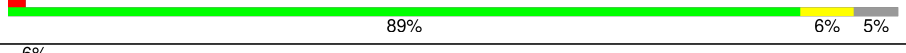
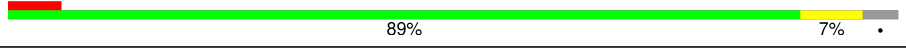
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	9050 (2.15 - 3.15)

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	BE	214	
2	L1	157	
3	L3	5070	

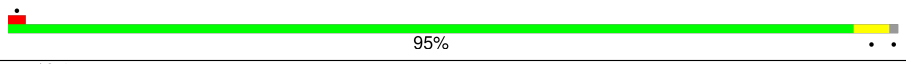
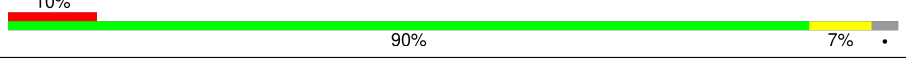
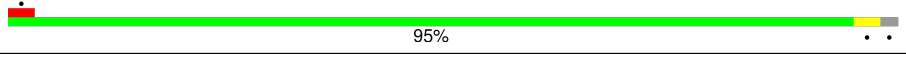
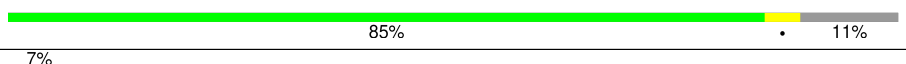

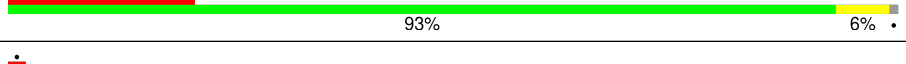

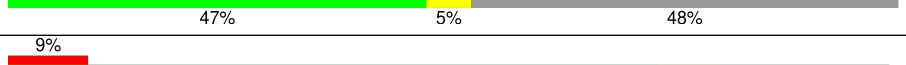
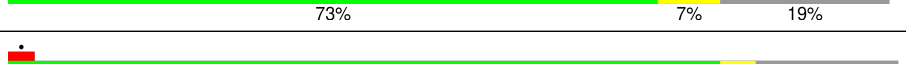
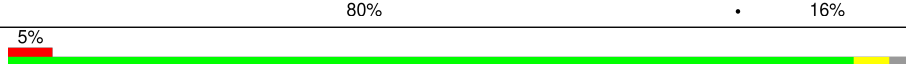
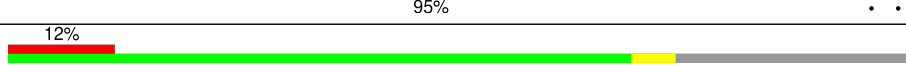
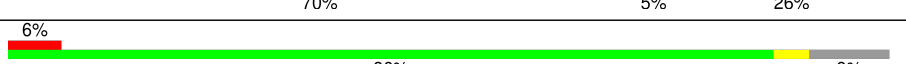

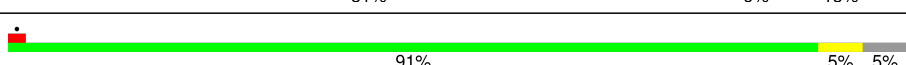
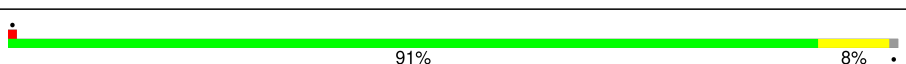
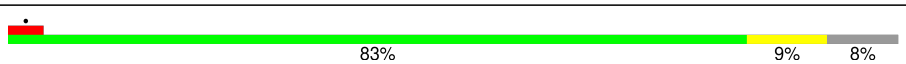
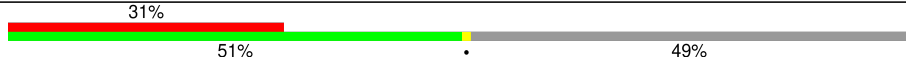



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Mol	Chain	Length	Quality of chain
4	L4	121	 81% 17%
5	L5	178	 90% 6%
6	L6	211	 94% 6%
7	L7	203	 94% 5%
8	L8	215	 59% 37%
9	L9	204	 92% 7%
10	LA	184	 80% 17%
11	LB	188	 92% 7%
12	LC	176	 97%
13	LD	196	 73% 6% 21%
14	LE	160	 96%
15	LF	128	 73% 8% 20%
16	LG	140	 96%
17	LH	156	 74% 5% 21%
18	LI	145	 86% 6% 8%
19	LJ	136	 88% 12% 7%
20	LK	148	 93% 6%
21	LL	137	 88% 9% 12%
22	LM	159	 47% 8% 45%
23	LN	403	 93% 7%
24	LO	115	 76% 7% 17%
25	LP	125	 77% 8% 15%
26	LQ	135	 89% 6% 5%
27	LR	117	 89% 7%
28	LS	123	 93% 7%

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Mol	Chain	Length	Quality of chain
29	LT	110	
30	LU	105	
31	LV	106	
32	LW	97	
33	LX	92	
34	LY	70	
35	LZ	51	
36	NK	129	
37	NP	134	
38	SA	427	
39	SB	297	
40	SC	288	
41	SD	248	
42	SE	266	
43	SF	257	
44	SG	192	
45	SK	245	
46	SQ	239	
47	SR	634	
48	SV	163	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 134730 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 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	BE	160	1295	827	242	218	8	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	L1	154	3278	1463	581	1080	154	0	0

- Molecule 3 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	L3	3325	71370	31811	13073	23161	3325	0	0

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	L4	120	2561	1141	456	844	120	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	L5	168	1349	853	251	239	6	0	0

- Molecule 6 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	L6	210	1701	1064	352	281	4	0	0

- Molecule 7 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	L7	201	1650	1063	321	261	5	0	0

- Molecule 8 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	L8	135	1111	713	213	178	7	0	0

- Molecule 9 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	L9	203	1701	1072	359	266	4	0	0

- Molecule 10 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	LA	153	1242	776	241	216	9	0	0

- Molecule 11 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	LB	187	1512	944	314	249	5	0	0

- Molecule 12 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LC	176	1461	930	284	236	11	0	0

- Molecule 13 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	LD	154	1289	805	277	198	9	0	0

- Molecule 14 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LE	154	Total	C	N	O	S	0	0
			1264	803	246	210	5		

- Molecule 15 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LF	103	Total	C	N	O	S	0	0
			842	538	148	154	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LG	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 17 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LH	124	Total	C	N	O	S	0	0
			1020	651	194	174	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LI	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 19 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LJ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 20 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LK	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 21 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	LL	125	1002	622	207	168	5	0	0

- Molecule 22 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	LM	88	723	451	157	112	3	0	0

- Molecule 23 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	LN	402	3239	2061	608	556	14	0	0

- Molecule 24 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	LO	95	738	468	131	133	6	0	0

- Molecule 25 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	LP	106	879	555	170	152	2	0	0

- Molecule 26 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	LQ	128	1053	667	216	165	5	0	0

- Molecule 27 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	LR	112	888	555	183	144	6	0	0

- Molecule 28 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	LS	122	1015	641	205	168	1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	LT	109	876	555	174	144	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	LU	102	832	521	177	129	5	0	0

- Molecule 31 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	LV	104	851	533	174	138	6	0	0

- Molecule 32 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	LW	86	705	434	155	111	5	0	0

- Molecule 33 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	LX	91	708	445	136	120	7	0	0

- Molecule 34 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	LY	69	569	366	103	99	1	0	0

- Molecule 35 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LZ	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 36 is a protein called Protein LLP homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	NK	67	Total	C	N	O	S	0	0
			581	363	128	88	2		

- Molecule 37 is a protein called Zinc finger protein 593.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	NP	108	Total	C	N	O	S	0	0
			876	537	182	153	4		

- Molecule 38 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	SA	358	Total	C	N	O	S	0	0
			2853	1797	570	473	13		

- Molecule 39 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	SB	292	Total	C	N	O	S	0	0
			2376	1499	433	430	14		

- Molecule 40 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	SC	214	Total	C	N	O	S	0	0
			1715	1103	325	283	4		

- Molecule 41 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	SD	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 42 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	SE	231	1869	1191	361	313	4	1	0

- Molecule 43 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	SF	245	1876	1177	383	310	6	0	0

- Molecule 44 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	SG	190	1518	956	284	272	6	0	0

- Molecule 45 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	SK	226	1721	1070	296	343	12	0	0

- Molecule 46 is a protein called mRNA turnover protein 4 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
46	SQ	123	610	364	123	123	0	0

- Molecule 47 is a protein called GTP-binding protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	SR	243	2002	1238	377	375	12	0	0

- Molecule 48 is a protein called Probable ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	SV	139	1184	754	229	191	10	0	0

- Molecule 49 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
49	L1	5	Total 5	Mg 5	0
49	L3	71	Total 71	Mg 71	0
49	L4	3	Total 3	Mg 3	0
49	LG	1	Total 1	Mg 1	0
49	LM	1	Total 1	Mg 1	0
49	LN	1	Total 1	Mg 1	0
49	LQ	1	Total 1	Mg 1	0
49	LT	1	Total 1	Mg 1	0
49	LW	1	Total 1	Mg 1	0
49	SA	1	Total 1	Mg 1	0
49	SF	1	Total 1	Mg 1	0

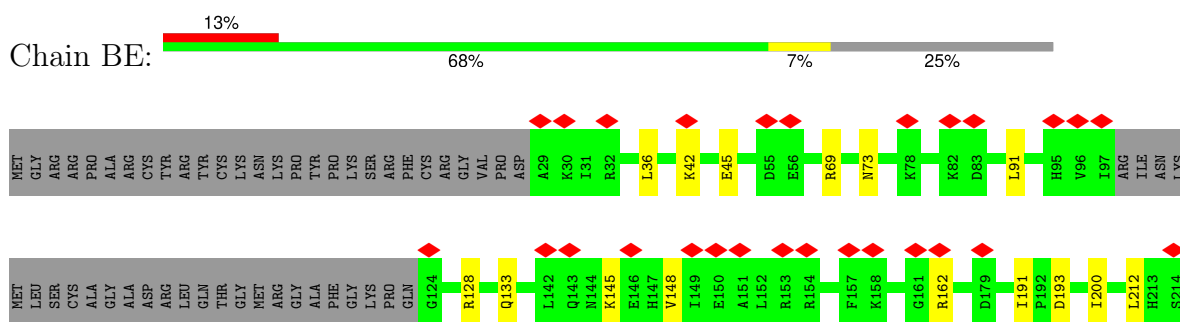
- Molecule 50 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
50	LR	1	Total 1	Zn 1	0
50	LV	1	Total 1	Zn 1	0
50	LW	1	Total 1	Zn 1	0
50	LX	1	Total 1	Zn 1	0
50	NP	1	Total 1	Zn 1	0
50	SV	1	Total 1	Zn 1	0

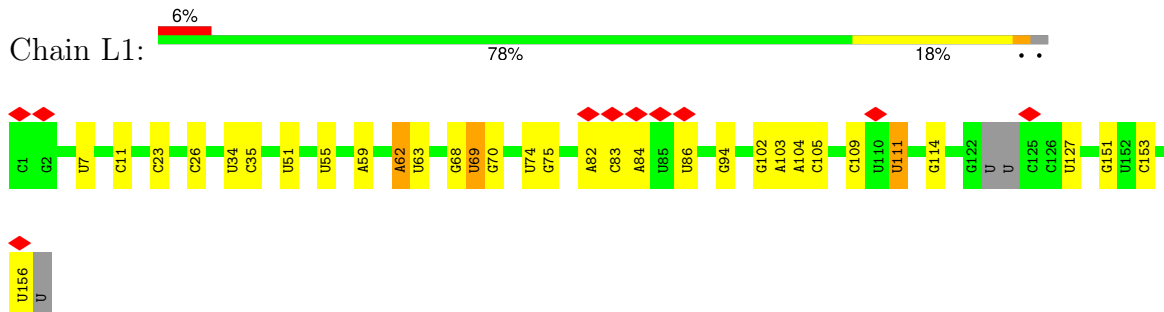
3 Residue-property plots [i](#)

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.

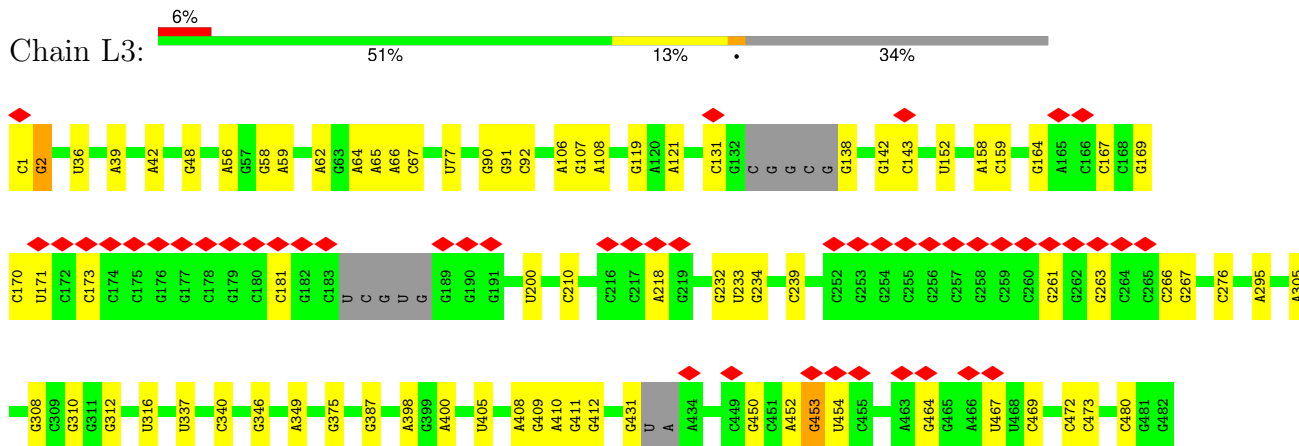
- Molecule 1: 60S ribosomal protein L10

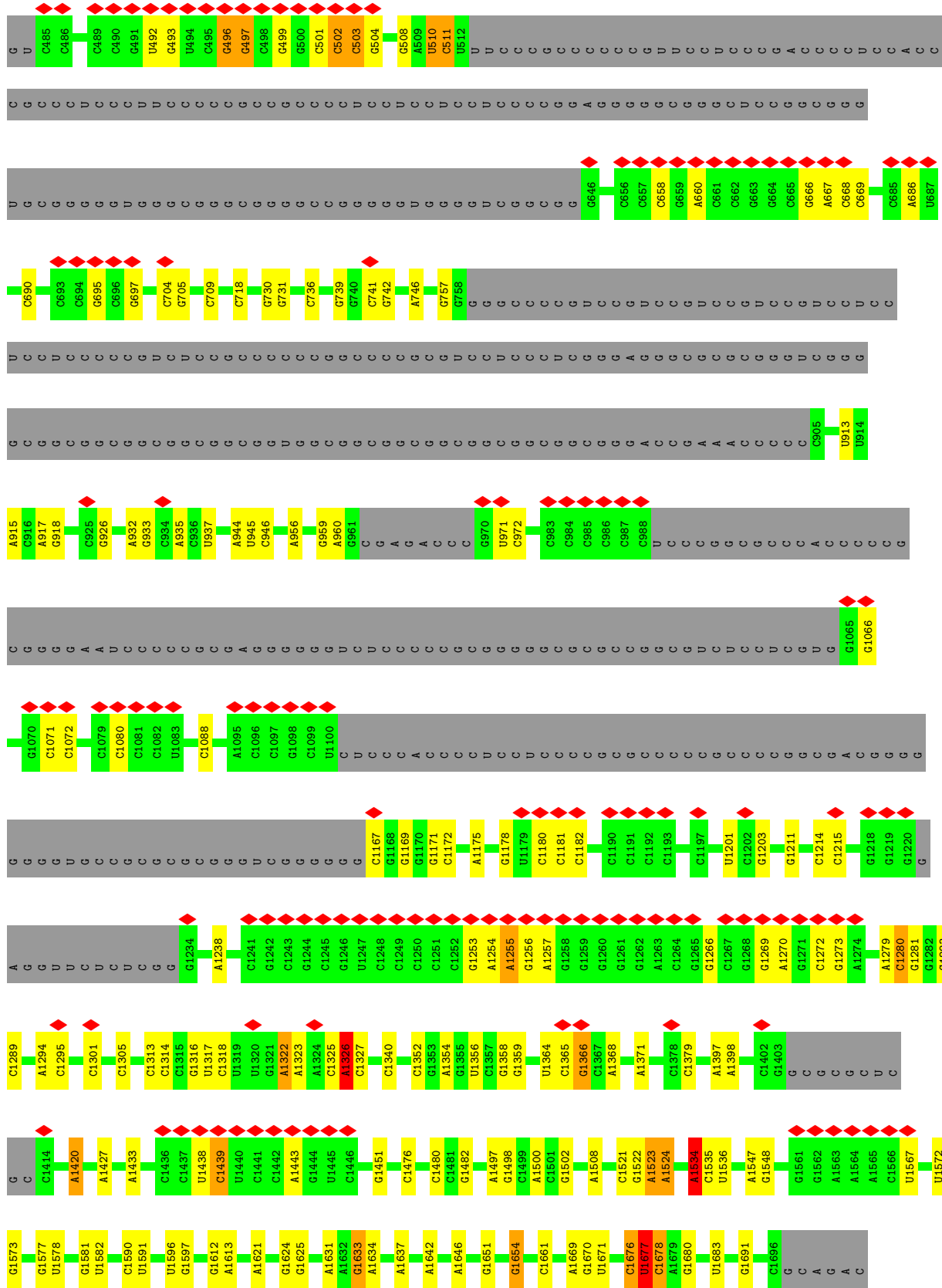


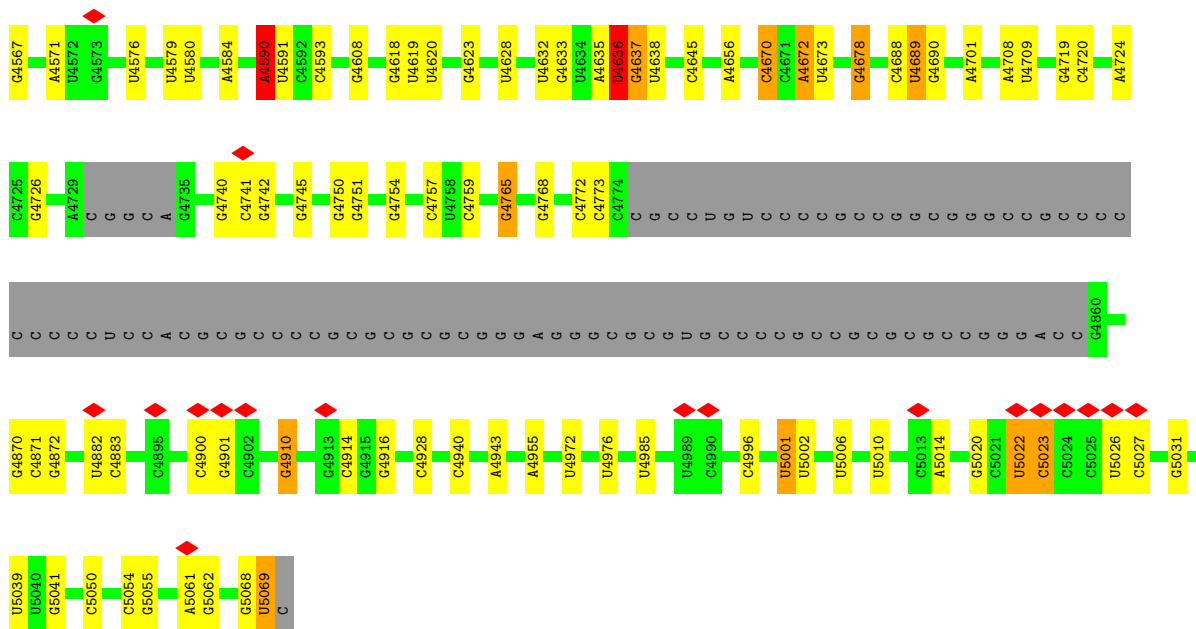
- Molecule 2: 5.8S rRNA



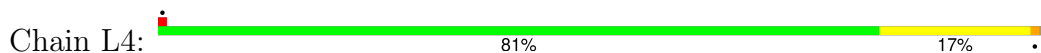
- Molecule 3: 28S rRNA



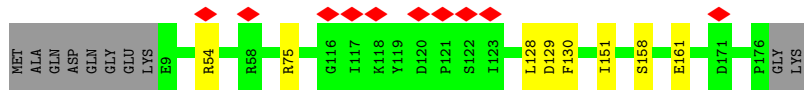
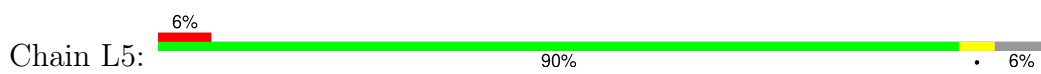




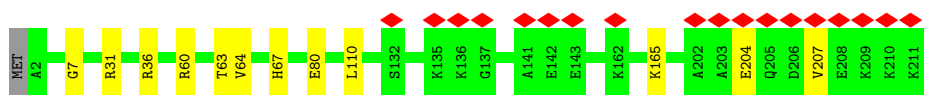
• Molecule 4: 5S rRNA



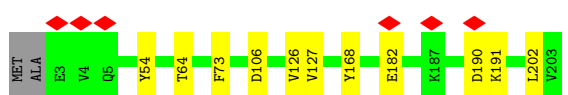
• Molecule 5: 60S ribosomal protein L11



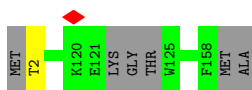
• Molecule 6: 60S ribosomal protein L13



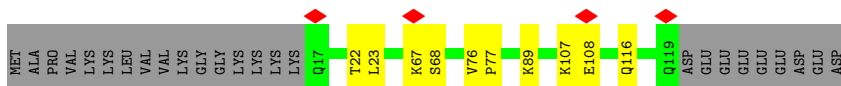
• Molecule 7: 60S ribosomal protein L13a



• Molecule 8: 60S ribosomal protein L14



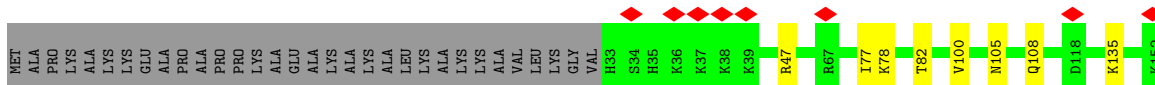
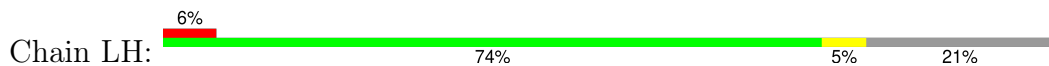
- Molecule 15: 60S ribosomal protein L22



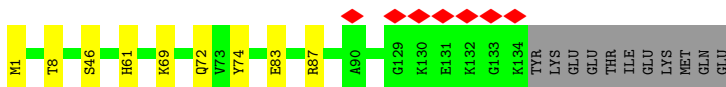
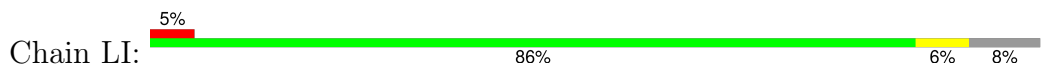
- Molecule 16: 60S ribosomal protein L23



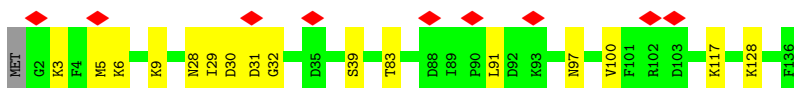
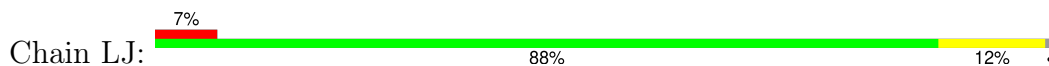
- Molecule 17: 60S ribosomal protein L23a



- Molecule 18: 60S ribosomal protein L26



- Molecule 19: 60S ribosomal protein L27

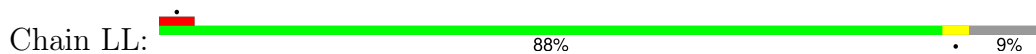


- Molecule 20: 60S ribosomal protein L27a

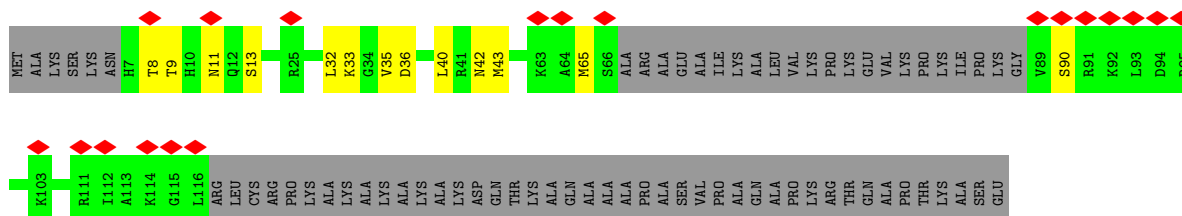




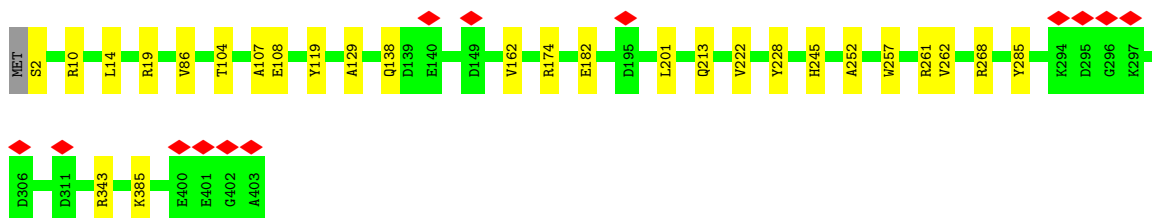
- Molecule 21: 60S ribosomal protein L28



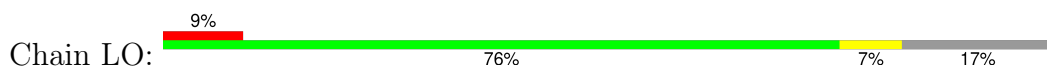
- Molecule 22: 60S ribosomal protein L29



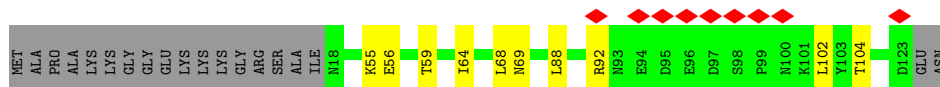
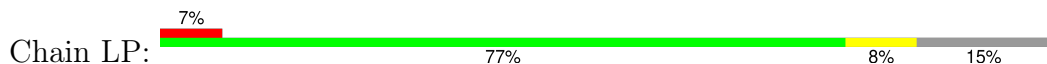
- Molecule 23: 60S ribosomal protein L3



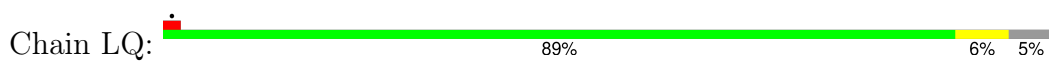
- Molecule 24: 60S ribosomal protein L30



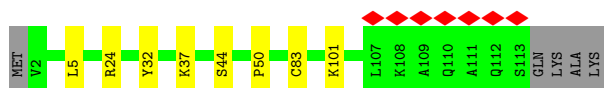
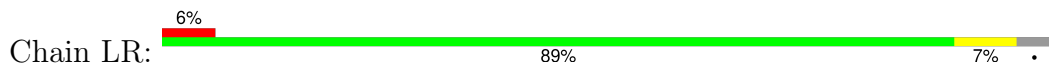
- Molecule 25: 60S ribosomal protein L31



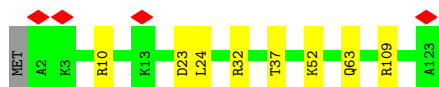
- Molecule 26: 60S ribosomal protein L32



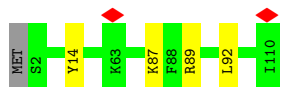
• Molecule 27: 60S ribosomal protein L34



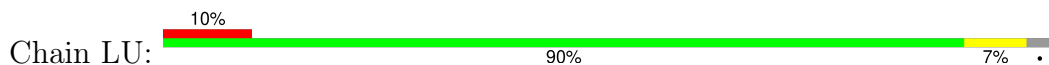
• Molecule 28: 60S ribosomal protein L35



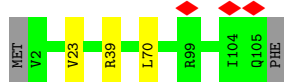
• Molecule 29: 60S ribosomal protein L35a



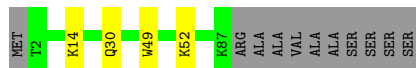
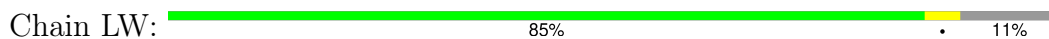
• Molecule 30: 60S ribosomal protein L36

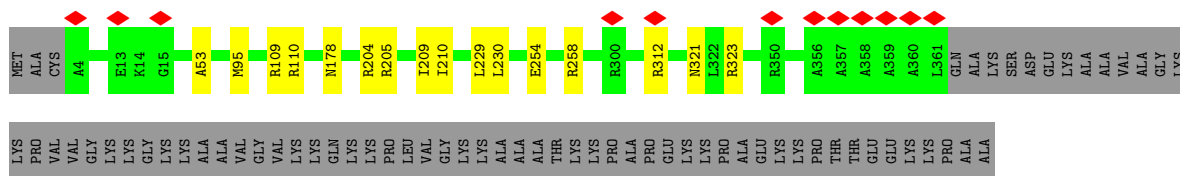


• Molecule 31: 60S ribosomal protein L36a



• Molecule 32: 60S ribosomal protein L37

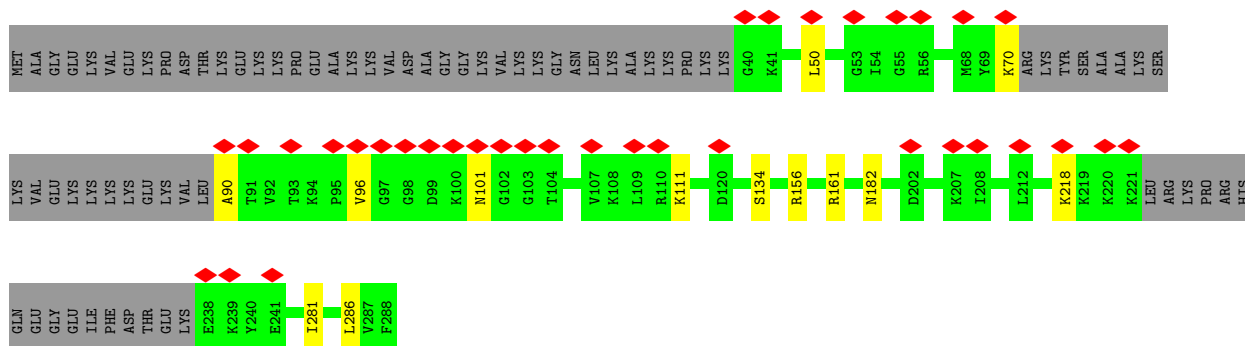




• Molecule 39: 60S ribosomal protein L5



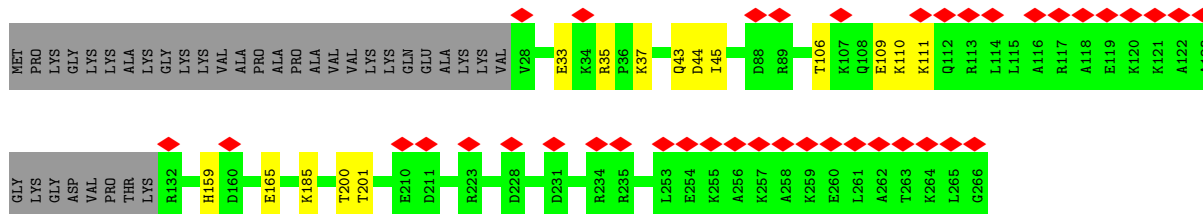
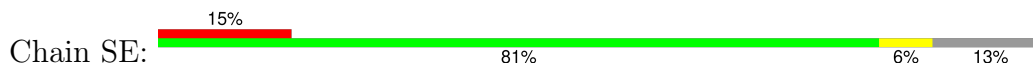
• Molecule 40: 60S ribosomal protein L6



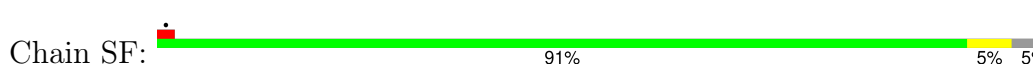
• Molecule 41: 60S ribosomal protein L7



• Molecule 42: 60S ribosomal protein L7a



• Molecule 43: 60S ribosomal protein L8



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	33770	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	10.729	Depositor
Minimum map value	-1.531	Depositor
Average map value	0.052	Depositor
Map value standard deviation	0.180	Depositor
Recommended contour level	0.95	Depositor
Map size (\AA)	514.56, 514.56, 514.56	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.072, 1.072, 1.072	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, 6MZ, HIC, OMU, UR3, OMG, 1MA, MG, PSU, OMC, A2M

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	BE	0.12	0/1323	0.30	0/1767
2	L1	0.15	0/3589	0.24	0/5589
3	L3	0.18	0/77299	0.27	0/120555
4	L4	0.23	0/2861	0.28	0/4459
5	L5	0.14	0/1372	0.30	0/1836
6	L6	0.14	0/1732	0.29	0/2315
7	L7	0.16	0/1682	0.29	0/2250
8	L8	0.15	0/1133	0.27	0/1516
9	L9	0.14	0/1746	0.27	0/2338
10	LA	0.14	0/1268	0.30	0/1701
11	LB	0.15	0/1536	0.31	0/2052
12	LC	0.18	0/1501	0.30	0/2013
13	LD	0.12	0/1305	0.25	0/1727
14	LE	0.18	0/1291	0.34	0/1724
15	LF	0.12	0/856	0.31	0/1149
16	LG	0.14	0/1048	0.32	0/1402
17	LH	0.11	0/1039	0.28	0/1394
18	LI	0.13	0/1132	0.28	0/1504
19	LJ	0.13	0/1130	0.27	0/1507
20	LK	0.15	0/1191	0.28	0/1591
21	LL	0.12	0/1017	0.26	0/1364
22	LM	0.14	0/735	0.31	0/970
23	LN	0.14	0/3294	0.30	0/4406
24	LO	0.11	0/748	0.24	0/1004
25	LP	0.14	0/894	0.28	0/1204
26	LQ	0.14	0/1071	0.28	0/1429
27	LR	0.14	0/898	0.33	0/1197
28	LS	0.11	0/1023	0.24	0/1351
29	LT	0.14	0/895	0.30	0/1198
30	LU	0.12	0/843	0.27	0/1115
31	LV	0.17	0/864	0.31	0/1140
32	LW	0.15	0/720	0.32	0/952

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LX	0.14	0/718	0.34	0/953
34	LY	0.11	0/575	0.27	0/761
35	LZ	0.14	0/454	0.27	0/599
36	NK	0.12	0/587	0.25	0/767
37	NP	0.12	0/893	0.27	0/1194
38	SA	0.14	0/2907	0.28	0/3905
39	SB	0.17	0/2421	0.30	0/3241
40	SC	0.12	0/1748	0.29	0/2345
41	SD	0.14	0/1905	0.28	0/2539
42	SE	0.13	0/1903	0.30	0/2559
43	SF	0.14	0/1914	0.32	0/2567
44	SG	0.15	0/1537	0.27	0/2066
45	SK	0.14	0/1745	0.31	0/2374
46	SQ	0.07	0/608	0.24	0/845
47	SR	0.11	0/2026	0.28	0/2690
48	SV	0.17	0/1207	0.31	0/1600
All	All	0.16	0/142184	0.28	0/208724

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	BE	1295	0	1331	10	0
2	L1	3278	0	1665	11	0
3	L3	71370	0	36162	287	0
4	L4	2561	0	1295	9	0
5	L5	1349	0	1383	6	0
6	L6	1701	0	1818	8	0
7	L7	1650	0	1794	8	0
8	L8	1111	0	1174	8	0
9	L9	1701	0	1749	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	LA	1242	0	1269	4	0
11	LB	1512	0	1628	10	0
12	LC	1461	0	1502	4	0
13	LD	1289	0	1429	10	0
14	LE	1264	0	1328	1	0
15	LF	842	0	864	7	0
16	LG	1034	0	1097	6	0
17	LH	1020	0	1098	6	0
18	LI	1115	0	1205	8	0
19	LJ	1107	0	1182	9	0
20	LK	1162	0	1213	7	0
21	LL	1002	0	1068	4	0
22	LM	723	0	779	11	0
23	LN	3239	0	3377	20	0
24	LO	738	0	774	4	0
25	LP	879	0	924	6	0
26	LQ	1053	0	1147	6	0
27	LR	888	0	977	7	0
28	LS	1015	0	1148	6	0
29	LT	876	0	912	3	0
30	LU	832	0	917	5	0
31	LV	851	0	920	3	0
32	LW	705	0	737	4	0
33	LX	708	0	756	10	0
34	LY	569	0	637	5	0
35	LZ	444	0	483	6	0
36	NK	581	0	656	5	0
37	NP	876	0	881	7	0
38	SA	2853	0	3028	12	0
39	SB	2376	0	2403	7	0
40	SC	1715	0	1862	10	0
41	SD	1870	0	1996	10	0
42	SE	1869	0	2014	12	0
43	SF	1876	0	1970	12	0
44	SG	1518	0	1601	10	0
45	SK	1721	0	1695	14	0
46	SQ	610	0	257	1	0
47	SR	2002	0	2072	9	0
48	SV	1184	0	1248	14	0
49	L1	5	0	0	0	0
49	L3	71	0	0	0	0
49	L4	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	LG	1	0	0	0	0
49	LM	1	0	0	0	0
49	LN	1	0	0	0	0
49	LQ	1	0	0	0	0
49	LT	1	0	0	0	0
49	LW	1	0	0	0	0
49	SA	1	0	0	0	0
49	SF	1	0	0	0	0
50	LR	1	0	0	0	0
50	LV	1	0	0	0	0
50	LW	1	0	0	0	0
50	LX	1	0	0	0	0
50	NP	1	0	0	0	0
50	SV	1	0	0	0	0
All	All	134730	0	99425	482	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 2.

The worst 5 of 482 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)
6:L6:60:ARG:NH2	6:L6:67:HIS:O	2.05	0.89
42:SE:106:THR:OG1	42:SE:109:GLU:OE1	1.92	0.86
4:L4:40:U:O2	5:L5:75:ARG:NH1	2.09	0.86
3:L3:2520:C:O2	3:L3:2640:G:N2	2.09	0.85
2:L1:51:U:OP2	35:LZ:21:ARG:NH2	2.09	0.85

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	
1	BE	156/214 (73%)	152 (97%)	4 (3%)	0	100	100
5	L5	166/178 (93%)	164 (99%)	2 (1%)	0	100	100
6	L6	208/211 (99%)	203 (98%)	5 (2%)	0	100	100
7	L7	199/203 (98%)	199 (100%)	0	0	100	100
8	L8	133/215 (62%)	132 (99%)	1 (1%)	0	100	100
9	L9	201/204 (98%)	199 (99%)	2 (1%)	0	100	100
10	LA	151/184 (82%)	148 (98%)	3 (2%)	0	100	100
11	LB	185/188 (98%)	182 (98%)	3 (2%)	0	100	100
12	LC	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
13	LD	152/196 (78%)	150 (99%)	2 (1%)	0	100	100
14	LE	150/160 (94%)	143 (95%)	7 (5%)	0	100	100
15	LF	101/128 (79%)	100 (99%)	1 (1%)	0	100	100
16	LG	137/140 (98%)	135 (98%)	2 (2%)	0	100	100
17	LH	122/156 (78%)	121 (99%)	1 (1%)	0	100	100
18	LI	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
19	LJ	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
20	LK	145/148 (98%)	143 (99%)	2 (1%)	0	100	100
21	LL	123/137 (90%)	121 (98%)	2 (2%)	0	100	100
22	LM	84/159 (53%)	82 (98%)	2 (2%)	0	100	100
23	LN	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
24	LO	93/115 (81%)	93 (100%)	0	0	100	100
25	LP	104/125 (83%)	104 (100%)	0	0	100	100
26	LQ	126/135 (93%)	126 (100%)	0	0	100	100
27	LR	110/117 (94%)	108 (98%)	2 (2%)	0	100	100
28	LS	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
29	LT	107/110 (97%)	107 (100%)	0	0	100	100
30	LU	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
31	LV	102/106 (96%)	98 (96%)	4 (4%)	0	100	100
32	LW	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
33	LX	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
34	LY	67/70 (96%)	67 (100%)	0	0	100	100
35	LZ	48/51 (94%)	46 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	NK	63/129 (49%)	63 (100%)	0	0	100	100
37	NP	104/134 (78%)	104 (100%)	0	0	100	100
38	SA	356/427 (83%)	349 (98%)	7 (2%)	0	100	100
39	SB	290/297 (98%)	286 (99%)	4 (1%)	0	100	100
40	SC	208/288 (72%)	199 (96%)	9 (4%)	0	100	100
41	SD	223/248 (90%)	219 (98%)	4 (2%)	0	100	100
42	SE	228/266 (86%)	226 (99%)	2 (1%)	0	100	100
43	SF	243/257 (95%)	237 (98%)	6 (2%)	0	100	100
44	SG	188/192 (98%)	188 (100%)	0	0	100	100
45	SK	224/245 (91%)	218 (97%)	6 (3%)	0	100	100
46	SQ	119/239 (50%)	118 (99%)	1 (1%)	0	100	100
47	SR	237/634 (37%)	237 (100%)	0	0	100	100
48	SV	137/163 (84%)	135 (98%)	2 (2%)	0	100	100
All	All	7021/8446 (83%)	6910 (98%)	111 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	BE	137/181 (76%)	137 (100%)	0	100	100
5	L5	142/149 (95%)	142 (100%)	0	100	100
6	L6	176/177 (99%)	176 (100%)	0	100	100
7	L7	173/174 (99%)	173 (100%)	0	100	100
8	L8	115/161 (71%)	115 (100%)	0	100	100
9	L9	171/172 (99%)	171 (100%)	0	100	100
10	LA	134/163 (82%)	134 (100%)	0	100	100
11	LB	164/165 (99%)	164 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	LC	157/157 (100%)	157 (100%)	0	100	100
13	LD	138/175 (79%)	138 (100%)	0	100	100
14	LE	136/140 (97%)	136 (100%)	0	100	100
15	LF	93/115 (81%)	93 (100%)	0	100	100
16	LG	106/107 (99%)	106 (100%)	0	100	100
17	LH	112/133 (84%)	112 (100%)	0	100	100
18	LI	124/135 (92%)	124 (100%)	0	100	100
19	LJ	117/118 (99%)	117 (100%)	0	100	100
20	LK	120/121 (99%)	120 (100%)	0	100	100
21	LL	109/121 (90%)	109 (100%)	0	100	100
22	LM	74/126 (59%)	74 (100%)	0	100	100
23	LN	347/348 (100%)	347 (100%)	0	100	100
24	LO	80/97 (82%)	80 (100%)	0	100	100
25	LP	97/110 (88%)	97 (100%)	0	100	100
26	LQ	114/121 (94%)	114 (100%)	0	100	100
27	LR	96/100 (96%)	96 (100%)	0	100	100
28	LS	109/110 (99%)	109 (100%)	0	100	100
29	LT	88/89 (99%)	88 (100%)	0	100	100
30	LU	86/89 (97%)	86 (100%)	0	100	100
31	LV	92/94 (98%)	92 (100%)	0	100	100
32	LW	73/80 (91%)	73 (100%)	0	100	100
33	LX	74/75 (99%)	74 (100%)	0	100	100
34	LY	64/65 (98%)	64 (100%)	0	100	100
35	LZ	47/48 (98%)	47 (100%)	0	100	100
36	NK	61/115 (53%)	61 (100%)	0	100	100
37	NP	92/114 (81%)	92 (100%)	0	100	100
38	SA	298/348 (86%)	298 (100%)	0	100	100
39	SB	246/250 (98%)	246 (100%)	0	100	100
40	SC	189/252 (75%)	189 (100%)	0	100	100
41	SD	194/215 (90%)	194 (100%)	0	100	100
42	SE	198/223 (89%)	198 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	SF	188/199 (94%)	188 (100%)	0	100	100
44	SG	169/171 (99%)	169 (100%)	0	100	100
45	SK	196/213 (92%)	196 (100%)	0	100	100
47	SR	218/574 (38%)	218 (100%)	0	100	100
48	SV	128/149 (86%)	128 (100%)	0	100	100
All	All	6042/7039 (86%)	6042 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
28	LS	98	HIS
45	SK	156	ASN
37	NP	13	HIS
45	SK	75	ASN
42	SE	82	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	L1	152/157 (96%)	19 (12%)	0
3	L3	3295/5070 (64%)	408 (12%)	5 (0%)
4	L4	119/121 (98%)	11 (9%)	0
All	All	3566/5348 (66%)	438 (12%)	5 (0%)

5 of 438 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	L1	23	C
2	L1	34	U
2	L1	35	C
2	L1	59	A
2	L1	62	A

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	L3	496	G
3	L3	502	C
3	L3	503	C
3	L3	2095	A
3	L3	2469	C

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

110 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PSU	L3	3734	3	18,21,22	1.14	1 (5%)	21,30,33	1.98	5 (23%)
3	PSU	L3	1781	3	18,21,22	1.12	1 (5%)	21,30,33	1.93	5 (23%)
3	OMC	L3	3887	3	19,22,23	0.52	0	25,31,34	0.66	0
3	A2M	L3	3718	3	22,25,26	0.91	1 (4%)	30,36,39	2.02	7 (23%)
3	UR3	L3	4530	3	19,22,23	1.09	3 (15%)	26,32,35	1.49	2 (7%)
3	PSU	L3	4361	3	18,21,22	1.10	1 (5%)	21,30,33	2.00	5 (23%)
3	A2M	L3	2815	3	22,25,26	0.87	0	30,36,39	2.09	8 (26%)
3	A2M	L3	3724	3	22,25,26	0.87	0	30,36,39	2.05	7 (23%)
3	OMG	L3	4618	3	23,26,27	0.49	0	32,38,41	0.55	0
3	PSU	L3	4353	3	18,21,22	1.07	1 (5%)	21,30,33	1.98	5 (23%)
3	PSU	L3	4576	3	18,21,22	1.10	1 (5%)	21,30,33	1.95	5 (23%)
3	PSU	L3	4500	3	18,21,22	1.12	1 (5%)	21,30,33	1.94	5 (23%)
3	PSU	L3	3695	3	18,21,22	1.10	1 (5%)	21,30,33	1.97	5 (23%)
3	OMG	L3	2424	3	23,26,27	0.48	0	32,38,41	0.45	0
3	PSU	L3	4636	3	18,21,22	1.10	1 (5%)	21,30,33	2.00	5 (23%)
3	PSU	L3	4628	3	18,21,22	1.06	1 (5%)	21,30,33	1.90	5 (23%)
3	PSU	L3	4457	3	18,21,22	1.10	1 (5%)	21,30,33	1.98	6 (28%)
3	PSU	L3	4299	3	18,21,22	1.00	1 (5%)	21,30,33	1.97	5 (23%)
3	PSU	L3	1862	3	18,21,22	1.10	1 (5%)	21,30,33	1.92	6 (28%)
3	OMC	L3	2365	3	19,22,23	0.54	0	25,31,34	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	A2M	L3	1326	3	22,25,26	0.89	0	30,36,39	2.12	8 (26%)
3	PSU	L3	4972	3	18,21,22	1.09	1 (5%)	21,30,33	1.93	5 (23%)
3	OMU	L3	4620	3	19,22,23	2.01	6 (31%)	25,31,34	1.72	4 (16%)
3	PSU	L3	3822	3	18,21,22	1.17	1 (5%)	21,30,33	1.98	5 (23%)
3	OMG	L3	4499	3	23,26,27	0.43	0	32,38,41	0.47	0
3	PSU	L3	1744	3	18,21,22	1.11	1 (5%)	21,30,33	1.97	5 (23%)
3	PSU	L3	3730	3	18,21,22	1.08	1 (5%)	21,30,33	1.95	5 (23%)
3	PSU	L3	4579	3	18,21,22	1.05	2 (11%)	21,30,33	1.90	4 (19%)
3	PSU	L3	3715	3	18,21,22	1.13	1 (5%)	21,30,33	1.94	6 (28%)
23	HIC	LN	245	23	10,11,12	1.51	1 (10%)	9,14,16	1.22	1 (11%)
3	PSU	L3	2632	3	18,21,22	1.09	1 (5%)	21,30,33	1.86	4 (19%)
3	OMC	L3	2824	3	19,22,23	0.52	0	25,31,34	0.64	0
3	PSU	L3	3853	3	18,21,22	1.09	1 (5%)	21,30,33	1.83	4 (19%)
3	OMC	L3	2351	49,3	19,22,23	0.57	0	25,31,34	0.81	1 (4%)
3	OMC	L3	4536	3	19,22,23	0.53	0	25,31,34	0.64	0
3	OMU	L3	4306	3	19,22,23	2.02	6 (31%)	25,31,34	1.88	4 (16%)
3	PSU	L3	4532	3	18,21,22	1.08	1 (5%)	21,30,33	1.97	5 (23%)
3	OMG	L3	4370	3	23,26,27	0.53	0	32,38,41	0.59	0
3	PSU	L3	1677	3	18,21,22	1.04	1 (5%)	21,30,33	1.89	5 (23%)
3	A2M	L3	1524	3	22,25,26	0.87	0	30,36,39	2.12	8 (26%)
3	PSU	L3	3851	3	18,21,22	1.10	1 (5%)	21,30,33	1.91	5 (23%)
3	A2M	L3	2363	49,3	22,25,26	0.87	1 (4%)	30,36,39	2.01	7 (23%)
3	A2M	L3	3825	3	22,25,26	0.85	0	30,36,39	2.09	7 (23%)
3	OMG	L3	3899	3	23,26,27	0.49	0	32,38,41	0.55	0
3	PSU	L3	5010	3	18,21,22	1.10	1 (5%)	21,30,33	1.90	5 (23%)
3	OMG	L3	4392	3	23,26,27	0.48	0	32,38,41	0.48	0
3	PSU	L3	4296	3	18,21,22	1.10	2 (11%)	21,30,33	2.01	5 (23%)
3	1MA	L3	1322	3	21,25,26	0.41	0	30,37,40	0.76	1 (3%)
3	PSU	L3	3639	3	18,21,22	1.10	1 (5%)	21,30,33	1.93	6 (28%)
3	OMG	L3	3744	3	23,26,27	0.46	0	32,38,41	0.47	0
3	PSU	L3	1683	3	18,21,22	1.11	2 (11%)	21,30,33	2.06	5 (23%)
3	PSU	L3	4689	3	18,21,22	1.06	1 (5%)	21,30,33	2.06	5 (23%)
2	PSU	L1	55	2	18,21,22	1.11	1 (5%)	21,30,33	2.00	5 (23%)
3	OMG	L3	4228	3	23,26,27	0.53	0	32,38,41	0.57	0
2	OMG	L1	75	2	23,26,27	0.48	0	32,38,41	0.47	0
3	PSU	L3	4312	3	18,21,22	1.08	1 (5%)	21,30,33	2.00	5 (23%)
3	OMG	L3	1316	3	23,26,27	0.49	0	32,38,41	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	A2M	L3	1871	3	22,25,26	0.85	0	30,36,39	2.14	8 (26%)
3	OMC	L3	3701	3	19,22,23	0.49	0	25,31,34	0.59	0
3	PSU	L3	3884	3	18,21,22	1.10	1 (5%)	21,30,33	1.93	4 (19%)
3	PSU	L3	1860	3	18,21,22	1.04	2 (11%)	21,30,33	1.87	5 (23%)
3	A2M	L3	4590	3	22,25,26	0.90	1 (4%)	30,36,39	2.04	7 (23%)
3	PSU	L3	3844	3	18,21,22	1.11	1 (5%)	21,30,33	1.97	5 (23%)
2	PSU	L1	69	2	18,21,22	1.11	1 (5%)	21,30,33	1.94	5 (23%)
3	OMG	L3	4623	3	23,26,27	0.49	0	32,38,41	0.54	0
3	PSU	L3	1792	3	18,21,22	1.06	1 (5%)	21,30,33	1.93	5 (23%)
3	PSU	L3	1779	3	18,21,22	1.11	1 (5%)	21,30,33	1.93	5 (23%)
3	OMC	L3	1340	3	19,22,23	0.57	0	25,31,34	0.72	0
3	PSU	L3	4471	3	18,21,22	1.11	1 (5%)	21,30,33	1.95	5 (23%)
3	A2M	L3	398	3	22,25,26	0.86	0	30,36,39	2.12	8 (26%)
3	A2M	L3	4523	3	22,25,26	0.85	0	30,36,39	2.11	8 (26%)
3	OMC	L3	2861	3	19,22,23	0.52	0	25,31,34	0.63	0
3	PSU	L3	4521	3	18,21,22	1.07	1 (5%)	21,30,33	1.92	5 (23%)
3	OMC	L3	2804	3	19,22,23	0.52	0	25,31,34	0.64	0
3	PSU	L3	4493	3	18,21,22	1.11	1 (5%)	21,30,33	1.94	4 (19%)
3	PSU	L3	4293	3	18,21,22	1.03	1 (5%)	21,30,33	1.88	4 (19%)
3	PSU	L3	5001	3	18,21,22	1.11	1 (5%)	21,30,33	1.96	5 (23%)
3	OMC	L3	4456	3	19,22,23	0.54	0	25,31,34	0.66	0
3	OMG	L3	2876	3	23,26,27	0.48	0	32,38,41	0.46	0
3	A2M	L3	3830	3	22,25,26	0.85	0	30,36,39	2.08	8 (26%)
3	A2M	L3	400	3	22,25,26	0.86	0	30,36,39	2.11	8 (26%)
3	PSU	L3	4552	3	18,21,22	1.06	1 (5%)	21,30,33	1.94	5 (23%)
3	OMU	L3	4498	3	19,22,23	2.11	7 (36%)	25,31,34	1.80	5 (20%)
3	6MZ	L3	4220	3	22,25,26	1.13	1 (4%)	29,36,39	2.16	9 (31%)
3	OMG	L3	1522	3	23,26,27	0.51	0	32,38,41	0.53	0
3	OMU	L3	3925	3	19,22,23	1.99	6 (31%)	25,31,34	1.88	5 (20%)
3	OMC	L3	3841	3	19,22,23	0.52	0	25,31,34	0.66	0
3	A2M	L3	2787	3	22,25,26	0.87	1 (4%)	30,36,39	2.10	7 (23%)
3	OMG	L3	3627	3	23,26,27	0.49	0	32,38,41	0.55	0
3	PSU	L3	1782	3	18,21,22	1.11	1 (5%)	21,30,33	1.94	5 (23%)
3	PSU	L3	2508	3	18,21,22	1.06	1 (5%)	21,30,33	1.92	5 (23%)
3	PSU	L3	1536	3	18,21,22	1.09	1 (5%)	21,30,33	1.93	5 (23%)
3	A2M	L3	2401	3	22,25,26	0.87	0	30,36,39	2.13	8 (26%)
3	A2M	L3	4571	3	22,25,26	0.86	0	30,36,39	2.02	7 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PSU	L3	4673	3	18,21,22	1.10	2 (11%)	21,30,33	1.95	5 (23%)
3	OMG	L3	4637	3	23,26,27	0.49	0	32,38,41	0.49	0
3	PSU	L3	1582	3	18,21,22	1.06	1 (5%)	21,30,33	1.92	5 (23%)
3	PSU	L3	3637	3	18,21,22	1.09	1 (5%)	21,30,33	2.01	5 (23%)
3	PSU	L3	2839	3	18,21,22	1.09	1 (5%)	21,30,33	1.95	5 (23%)
3	OMC	L3	2422	49,3	19,22,23	0.52	0	25,31,34	0.71	0
3	OMU	L3	4227	3	19,22,23	2.02	6 (31%)	25,31,34	1.82	5 (20%)
3	OMG	L3	4494	3	23,26,27	0.52	0	32,38,41	0.48	0
3	A2M	L3	1534	49,3	22,25,26	0.88	1 (4%)	30,36,39	2.10	8 (26%)
3	OMG	L3	2364	3	23,26,27	0.48	0	32,38,41	0.50	0
3	PSU	L3	3920	49,3	18,21,22	1.08	1 (5%)	21,30,33	1.89	4 (19%)
3	A2M	L3	3867	3	22,25,26	0.88	0	30,36,39	2.11	7 (23%)
3	OMU	L3	2837	3	19,22,23	2.04	7 (36%)	25,31,34	1.84	5 (20%)
3	OMG	L3	1625	3	23,26,27	0.48	0	32,38,41	0.46	0
3	OMU	L3	2415	3	19,22,23	2.03	6 (31%)	25,31,34	1.84	5 (20%)
3	OMC	L3	3869	3	19,22,23	0.55	0	25,31,34	0.68	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PSU	L3	3734	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	1781	3	-	0/7/25/26	0/2/2/2
3	OMC	L3	3887	3	-	2/9/27/28	0/2/2/2
3	A2M	L3	3718	3	-	1/9/27/28	0/3/3/3
3	UR3	L3	4530	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	4361	3	-	0/7/25/26	0/2/2/2
3	A2M	L3	2815	3	-	0/9/27/28	0/3/3/3
3	A2M	L3	3724	3	-	1/9/27/28	0/3/3/3
3	OMG	L3	4618	3	-	1/9/27/28	0/3/3/3
3	PSU	L3	4353	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	4576	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	4500	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	3695	3	-	0/7/25/26	0/2/2/2
3	OMG	L3	2424	3	-	1/9/27/28	0/3/3/3
3	PSU	L3	4636	3	-	3/7/25/26	0/2/2/2
3	PSU	L3	4628	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	4457	3	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PSU	L3	4299	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	1862	3	-	2/7/25/26	0/2/2/2
3	OMC	L3	2365	3	-	0/9/27/28	0/2/2/2
3	A2M	L3	1326	3	-	3/9/27/28	0/3/3/3
3	PSU	L3	4972	3	-	0/7/25/26	0/2/2/2
3	OMU	L3	4620	3	-	0/9/27/28	0/2/2/2
3	PSU	L3	3822	3	-	0/7/25/26	0/2/2/2
3	OMG	L3	4499	3	-	1/9/27/28	0/3/3/3
3	PSU	L3	1744	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	3730	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	4579	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	3715	3	-	0/7/25/26	0/2/2/2
23	HIC	LN	245	23	-	0/5/6/8	0/1/1/1
3	PSU	L3	2632	3	-	0/7/25/26	0/2/2/2
3	OMC	L3	2824	3	-	1/9/27/28	0/2/2/2
3	PSU	L3	3853	3	-	0/7/25/26	0/2/2/2
3	OMC	L3	2351	49,3	-	2/9/27/28	0/2/2/2
3	OMC	L3	4536	3	-	1/9/27/28	0/2/2/2
3	OMU	L3	4306	3	-	4/9/27/28	0/2/2/2
3	PSU	L3	4532	3	-	0/7/25/26	0/2/2/2
3	OMG	L3	4370	3	-	0/9/27/28	0/3/3/3
3	PSU	L3	1677	3	-	3/7/25/26	0/2/2/2
3	A2M	L3	1524	3	-	2/9/27/28	0/3/3/3
3	PSU	L3	3851	3	-	0/7/25/26	0/2/2/2
3	A2M	L3	2363	49,3	-	0/9/27/28	0/3/3/3
3	A2M	L3	3825	3	-	0/9/27/28	0/3/3/3
3	OMG	L3	3899	3	-	1/9/27/28	0/3/3/3
3	PSU	L3	5010	3	-	0/7/25/26	0/2/2/2
3	OMG	L3	4392	3	-	1/9/27/28	0/3/3/3
3	PSU	L3	4296	3	-	0/7/25/26	0/2/2/2
3	1MA	L3	1322	3	-	2/7/25/26	0/3/3/3
3	PSU	L3	3639	3	-	0/7/25/26	0/2/2/2
3	OMG	L3	3744	3	-	1/9/27/28	0/3/3/3
3	PSU	L3	1683	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	4689	3	-	0/7/25/26	0/2/2/2
2	PSU	L1	55	2	-	0/7/25/26	0/2/2/2
3	OMG	L3	4228	3	-	0/9/27/28	0/3/3/3
2	OMG	L1	75	2	-	1/9/27/28	0/3/3/3
3	PSU	L3	4312	3	-	0/7/25/26	0/2/2/2
3	OMG	L3	1316	3	-	1/9/27/28	0/3/3/3
3	A2M	L3	1871	3	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OMC	L3	3701	3	-	7/9/27/28	0/2/2/2
3	PSU	L3	3884	3	-	2/7/25/26	0/2/2/2
3	PSU	L3	1860	3	-	0/7/25/26	0/2/2/2
3	A2M	L3	4590	3	-	1/9/27/28	0/3/3/3
3	PSU	L3	3844	3	-	1/7/25/26	0/2/2/2
2	PSU	L1	69	2	-	0/7/25/26	0/2/2/2
3	OMG	L3	4623	3	-	0/9/27/28	0/3/3/3
3	PSU	L3	1792	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	1779	3	-	0/7/25/26	0/2/2/2
3	OMC	L3	1340	3	-	1/9/27/28	0/2/2/2
3	PSU	L3	4471	3	-	0/7/25/26	0/2/2/2
3	A2M	L3	398	3	-	0/9/27/28	0/3/3/3
3	A2M	L3	4523	3	-	2/9/27/28	0/3/3/3
3	OMC	L3	2861	3	-	1/9/27/28	0/2/2/2
3	PSU	L3	4521	3	-	0/7/25/26	0/2/2/2
3	OMC	L3	2804	3	-	1/9/27/28	0/2/2/2
3	PSU	L3	4493	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	4293	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	5001	3	-	0/7/25/26	0/2/2/2
3	OMC	L3	4456	3	-	0/9/27/28	0/2/2/2
3	OMG	L3	2876	3	-	0/9/27/28	0/3/3/3
3	A2M	L3	3830	3	-	1/9/27/28	0/3/3/3
3	A2M	L3	400	3	-	0/9/27/28	0/3/3/3
3	PSU	L3	4552	3	-	0/7/25/26	0/2/2/2
3	OMU	L3	4498	3	-	0/9/27/28	0/2/2/2
3	6MZ	L3	4220	3	-	0/9/27/28	0/3/3/3
3	OMG	L3	1522	3	-	0/9/27/28	0/3/3/3
3	OMU	L3	3925	3	-	1/9/27/28	0/2/2/2
3	OMC	L3	3841	3	-	1/9/27/28	0/2/2/2
3	A2M	L3	2787	3	-	5/9/27/28	0/3/3/3
3	OMG	L3	3627	3	-	1/9/27/28	0/3/3/3
3	PSU	L3	1782	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	2508	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	1536	3	-	0/7/25/26	0/2/2/2
3	A2M	L3	2401	3	-	2/9/27/28	0/3/3/3
3	A2M	L3	4571	3	-	2/9/27/28	0/3/3/3
3	PSU	L3	4673	3	-	0/7/25/26	0/2/2/2
3	OMG	L3	4637	3	-	3/9/27/28	0/3/3/3
3	PSU	L3	1582	3	-	0/7/25/26	0/2/2/2
3	PSU	L3	3637	3	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PSU	L3	2839	3	-	2/7/25/26	0/2/2/2
3	OMC	L3	2422	49,3	-	1/9/27/28	0/2/2/2
3	OMU	L3	4227	3	-	1/9/27/28	0/2/2/2
3	OMG	L3	4494	3	-	0/9/27/28	0/3/3/3
3	A2M	L3	1534	49,3	-	0/9/27/28	0/3/3/3
3	OMG	L3	2364	3	-	1/9/27/28	0/3/3/3
3	PSU	L3	3920	49,3	-	0/7/25/26	0/2/2/2
3	A2M	L3	3867	3	-	2/9/27/28	0/3/3/3
3	OMU	L3	2837	3	-	1/9/27/28	0/2/2/2
3	OMG	L3	1625	3	-	2/9/27/28	0/3/3/3
3	OMU	L3	2415	3	-	0/9/27/28	0/2/2/2
3	OMC	L3	3869	3	-	1/9/27/28	0/2/2/2

The worst 5 of 109 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L3	4498	OMU	C6-N1	4.87	1.49	1.38
3	L3	4620	OMU	C6-N1	4.71	1.49	1.38
3	L3	2415	OMU	C6-N1	4.69	1.49	1.38
3	L3	4227	OMU	C6-N1	4.65	1.49	1.38
3	L3	2837	OMU	C6-N1	4.64	1.49	1.38

The worst 5 of 430 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L3	1326	A2M	C5-C4-N3	-5.74	118.82	126.72
3	L3	3825	A2M	C5-C4-N3	-5.68	118.89	126.72
3	L3	3925	OMU	C4-N3-C2	-5.67	119.58	126.61
3	L3	2815	A2M	C5-C4-N3	-5.65	118.94	126.72
3	L3	3718	A2M	C5-C4-N3	-5.61	118.99	126.72

There are no chirality outliers.

5 of 79 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	L1	75	OMG	C1'-C2'-O2'-CM2
3	L3	1316	OMG	C1'-C2'-O2'-CM2
3	L3	1326	A2M	C1'-C2'-O2'-CM'
3	L3	1340	OMC	C1'-C2'-O2'-CM2
3	L3	1871	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

57 monomers are involved in 89 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L3	3734	PSU	1	0
3	L3	3718	A2M	4	0
3	L3	4530	UR3	1	0
3	L3	2815	A2M	1	0
3	L3	3724	A2M	3	0
3	L3	4618	OMG	2	0
3	L3	4500	PSU	2	0
3	L3	3695	PSU	1	0
3	L3	2424	OMG	1	0
3	L3	4636	PSU	1	0
3	L3	4457	PSU	1	0
3	L3	4299	PSU	1	0
3	L3	1326	A2M	5	0
3	L3	4499	OMG	1	0
3	L3	1744	PSU	3	0
3	L3	3715	PSU	1	0
3	L3	2824	OMC	2	0
3	L3	2351	OMC	2	0
3	L3	4306	OMU	3	0
3	L3	1677	PSU	3	0
3	L3	1524	A2M	1	0
3	L3	3851	PSU	1	0
3	L3	2363	A2M	2	0
3	L3	3899	OMG	1	0
3	L3	4392	OMG	1	0
3	L3	4296	PSU	1	0
3	L3	3744	OMG	3	0
3	L3	4689	PSU	1	0
2	L1	75	OMG	1	0
3	L3	1316	OMG	1	0
3	L3	1860	PSU	2	0
3	L3	4590	A2M	1	0
2	L1	69	PSU	2	0
3	L3	4623	OMG	1	0
3	L3	1779	PSU	2	0
3	L3	1340	OMC	1	0
3	L3	4523	A2M	1	0
3	L3	2861	OMC	1	0
3	L3	2804	OMC	1	0
3	L3	5001	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L3	2876	OMG	1	0
3	L3	3830	A2M	1	0
3	L3	4220	6MZ	1	0
3	L3	1522	OMG	1	0
3	L3	3925	OMU	1	0
3	L3	3841	OMC	1	0
3	L3	3627	OMG	1	0
3	L3	4637	OMG	2	0
3	L3	2839	PSU	1	0
3	L3	2422	OMC	2	0
3	L3	4227	OMU	2	0
3	L3	1534	A2M	3	0
3	L3	2364	OMG	2	0
3	L3	3867	A2M	1	0
3	L3	2837	OMU	1	0
3	L3	2415	OMU	2	0
3	L3	3869	OMC	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 93 ligands modelled in this entry, 93 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

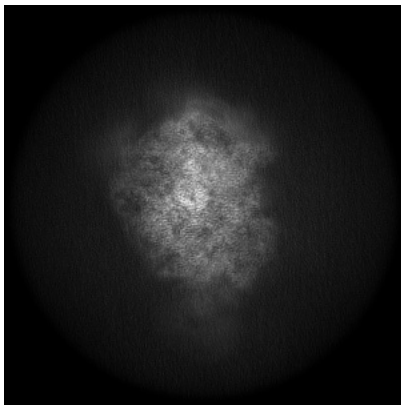
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29277. These allow visual inspection of the internal detail of the map and identification of artifacts.

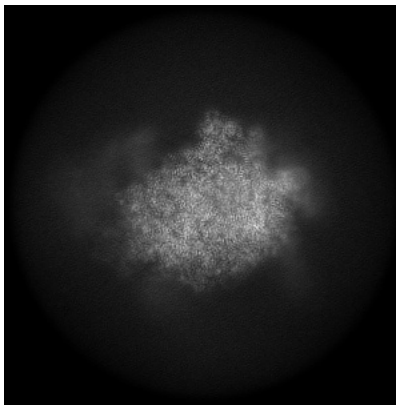
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

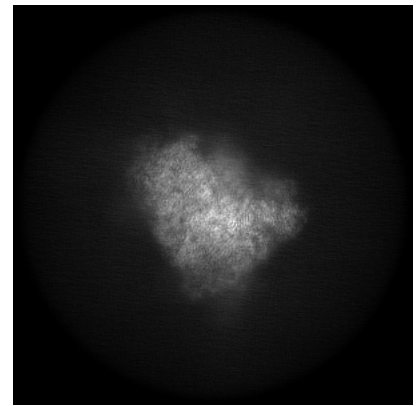
6.1.1 Primary map



X

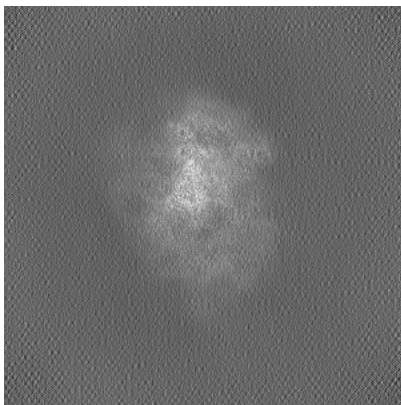


Y

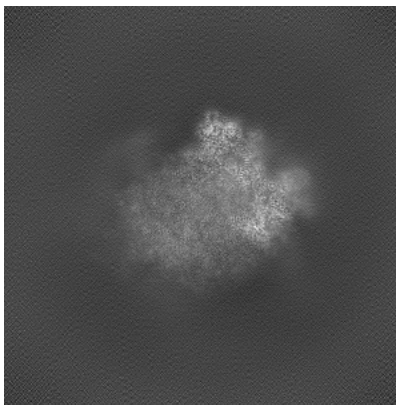


Z

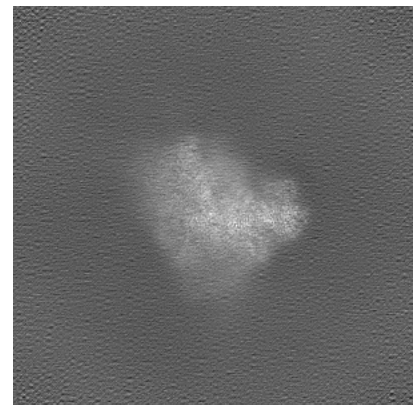
6.1.2 Raw map



X



Y

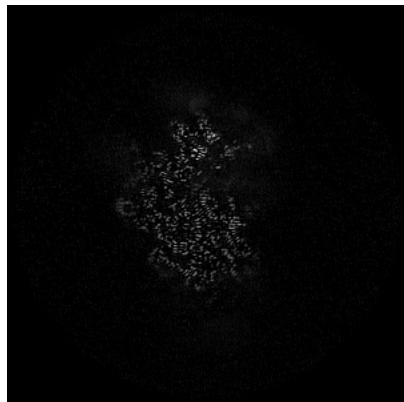


Z

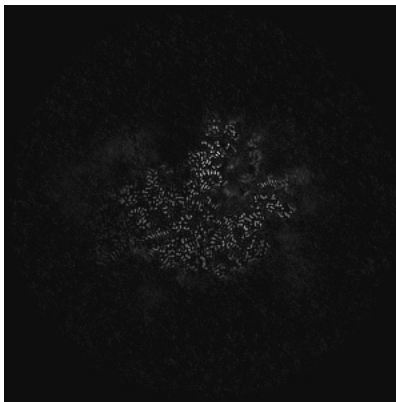
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

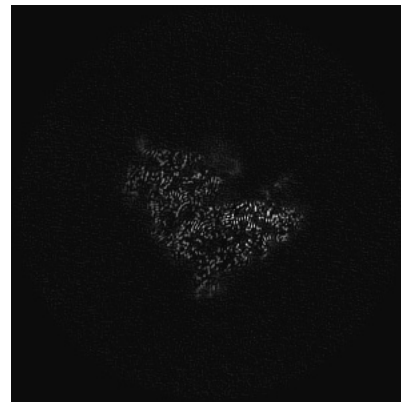
6.2.1 Primary map



X Index: 240

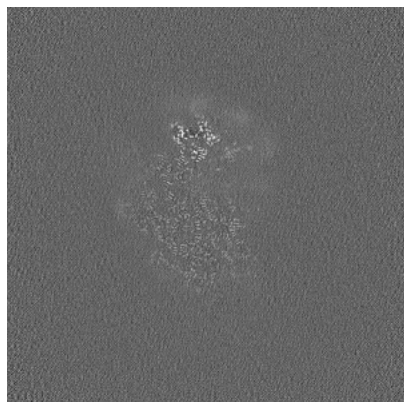


Y Index: 240

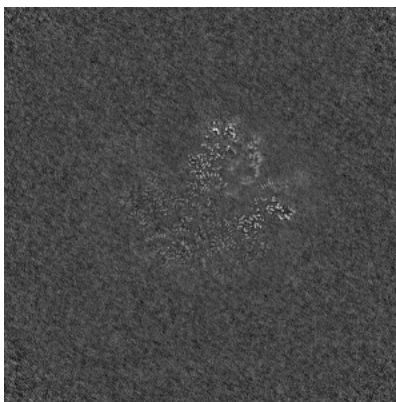


Z Index: 240

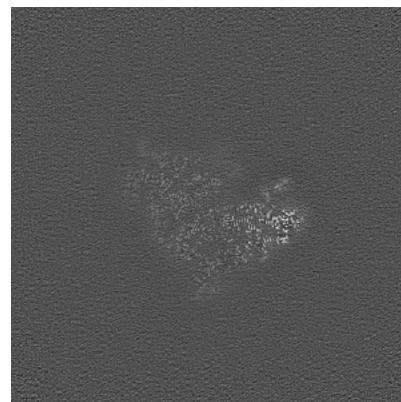
6.2.2 Raw map



X Index: 240



Y Index: 240

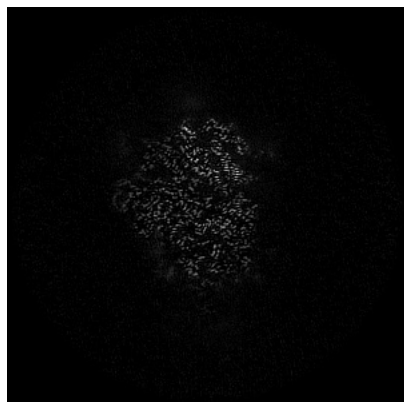


Z Index: 240

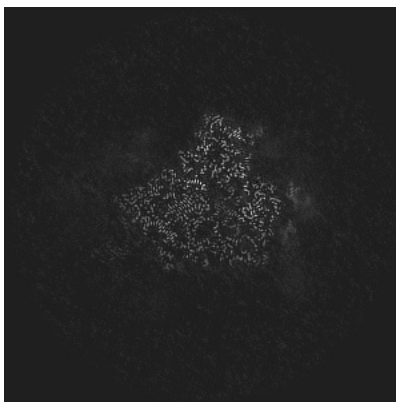
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

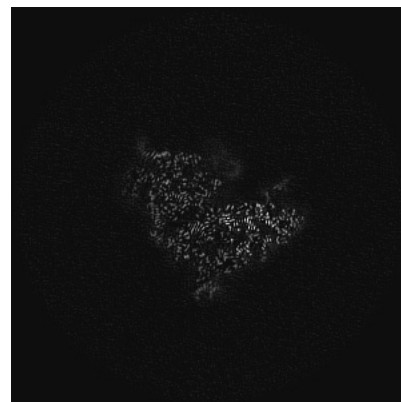
6.3.1 Primary map



X Index: 226

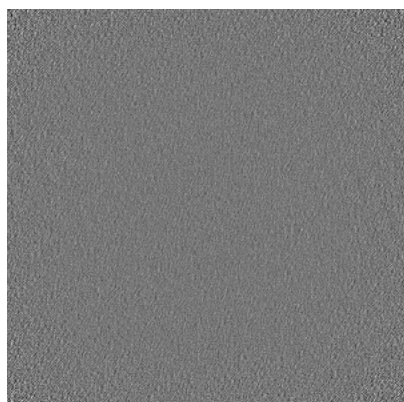


Y Index: 227

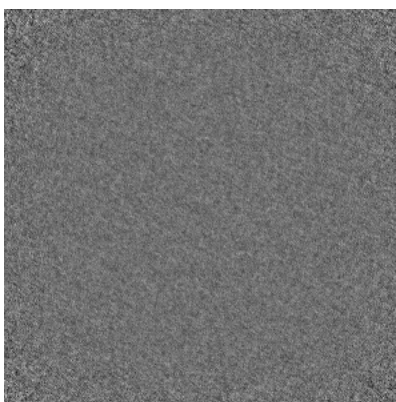


Z Index: 241

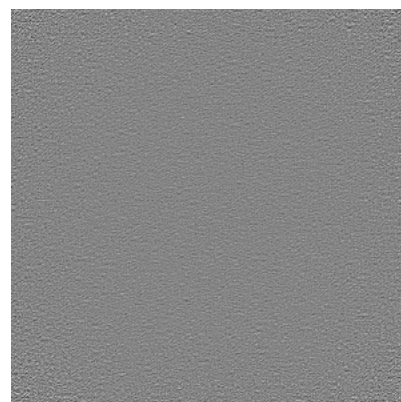
6.3.2 Raw map



X Index: 0



Y Index: 0

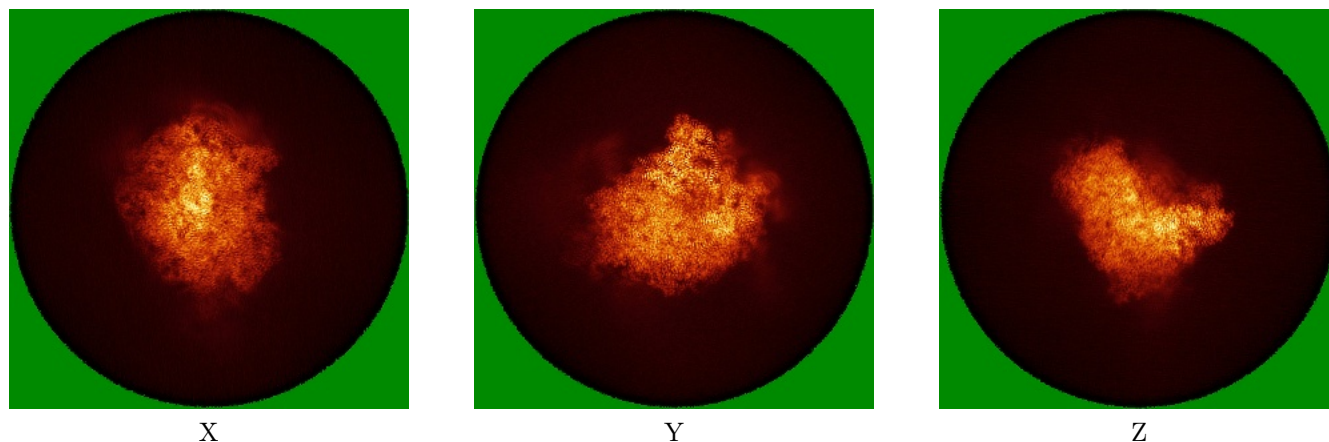


Z Index: 0

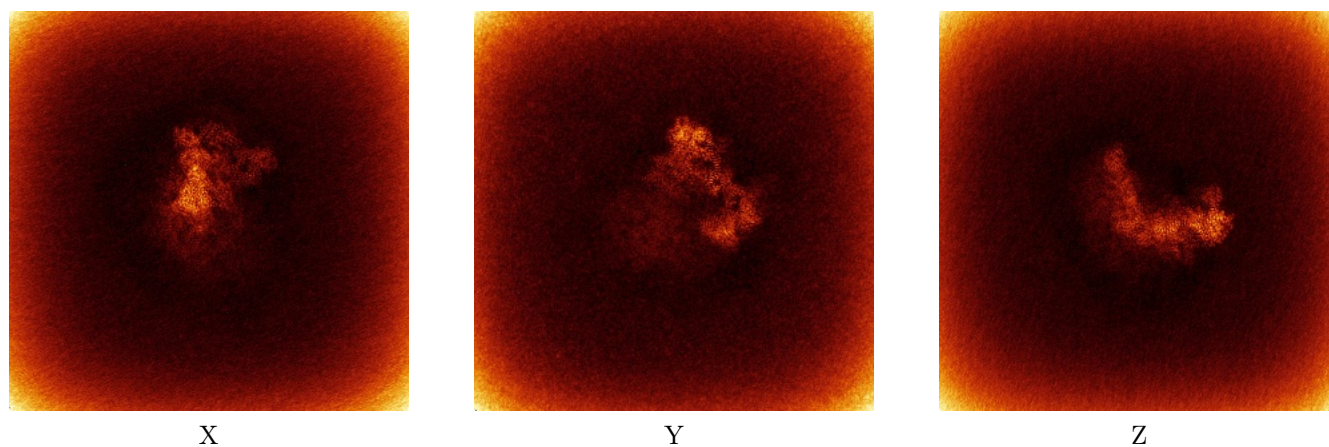
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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.

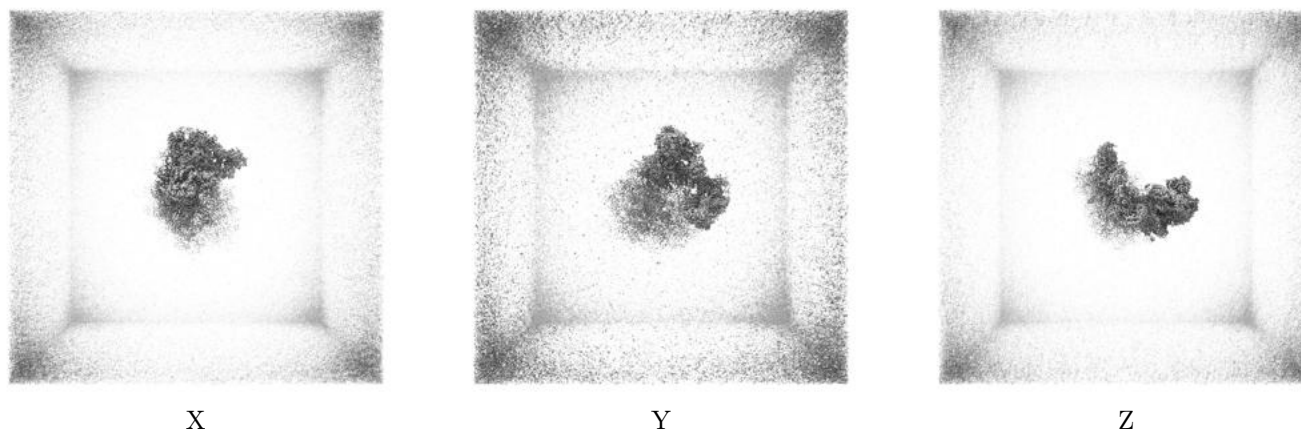
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.95. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

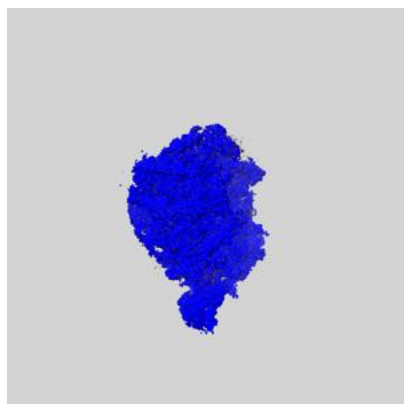
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

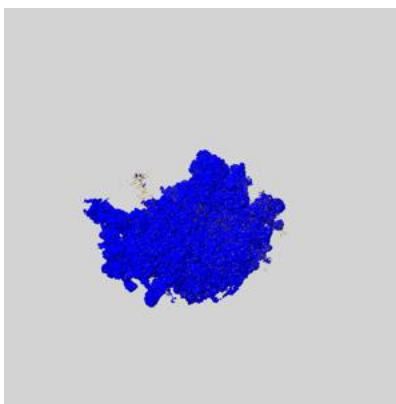
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

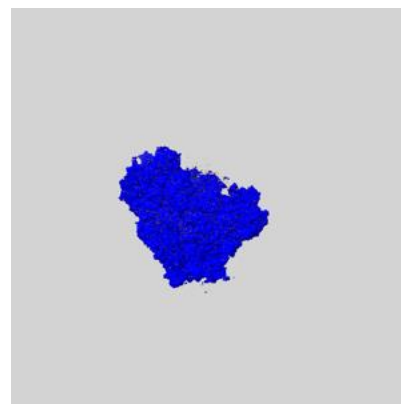
6.6.1 emd_29277_msk_1.map [i](#)



X



Y

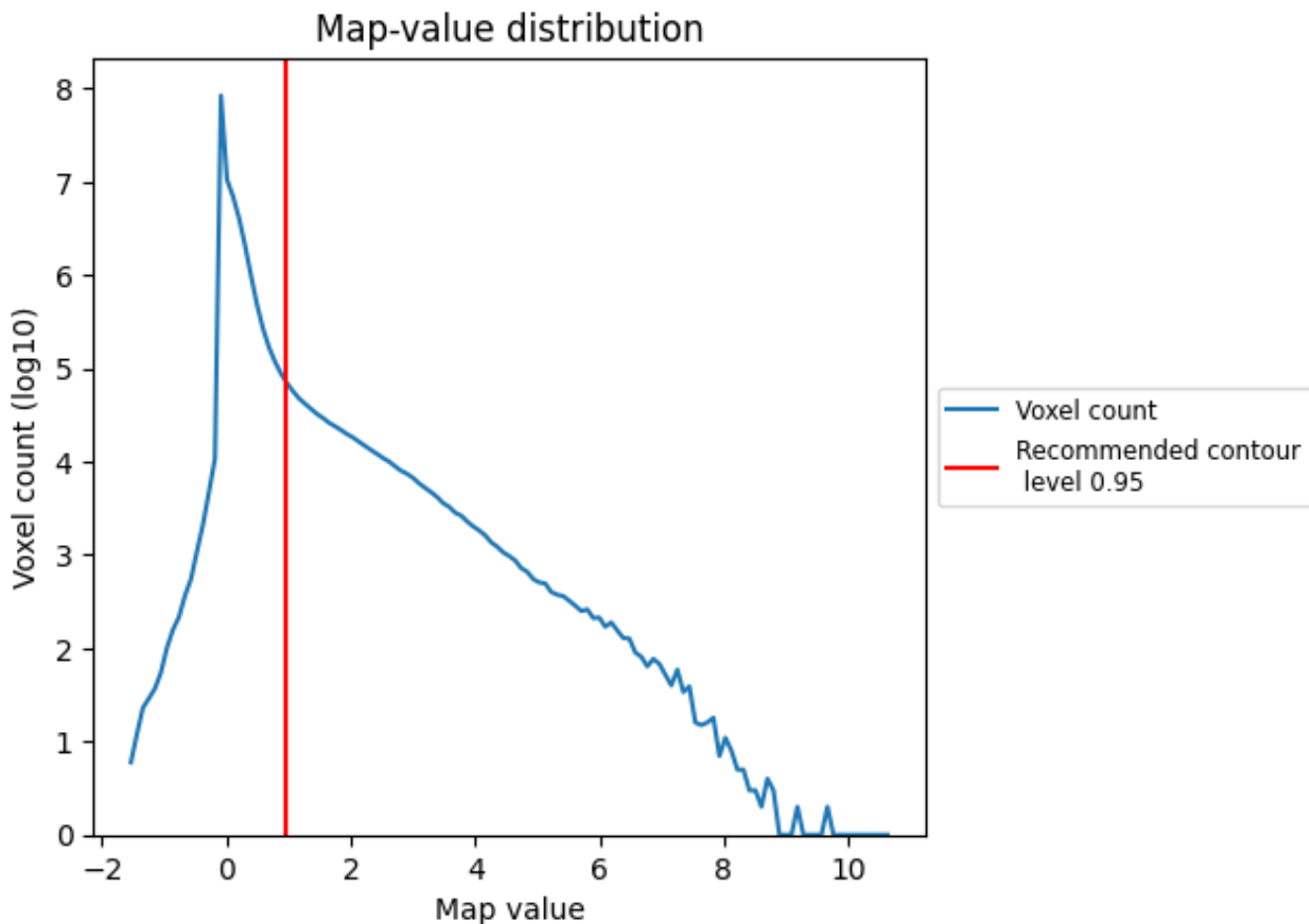


Z

7 Map analysis [i](#)

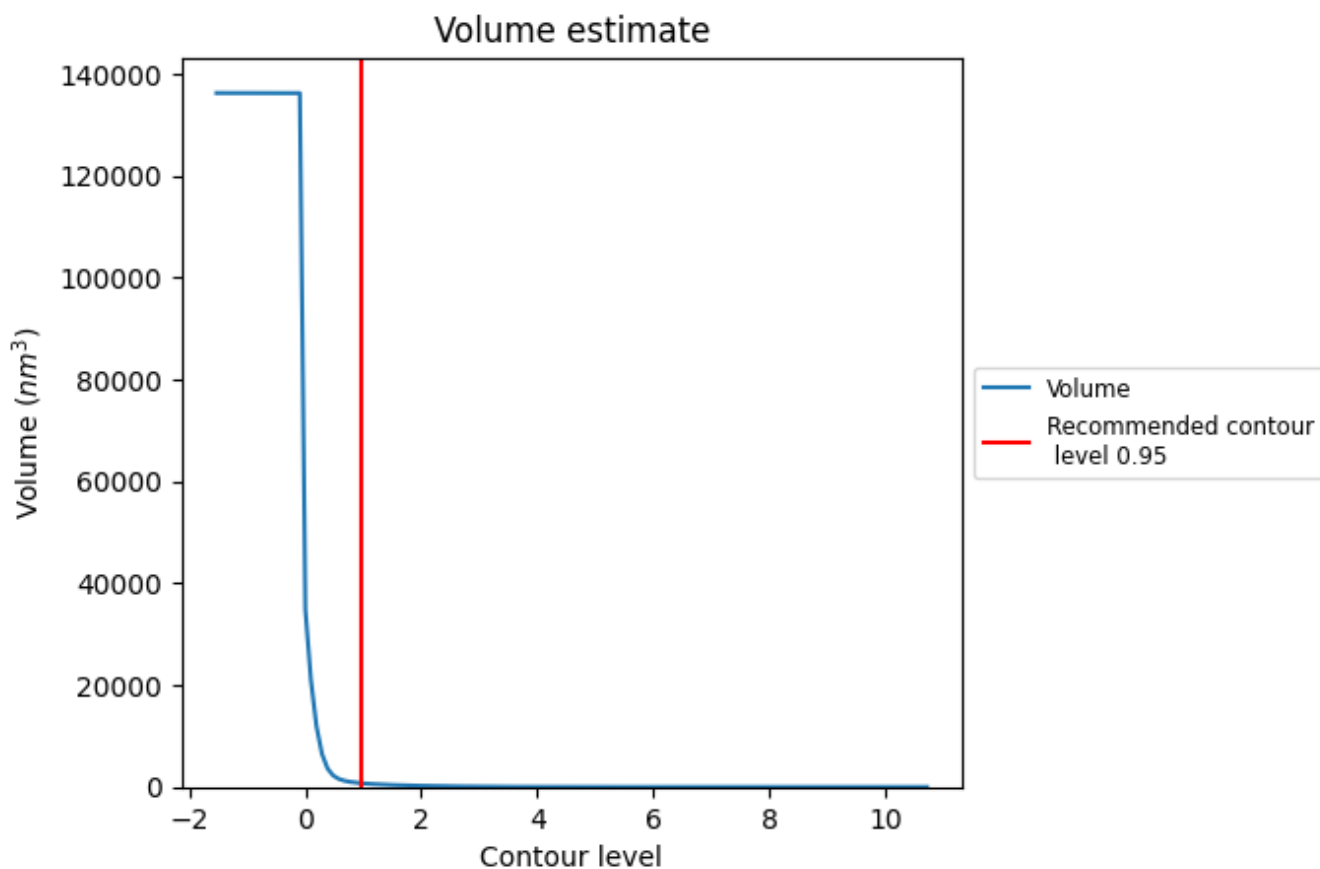
This section contains the results of statistical analysis of the map.

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.

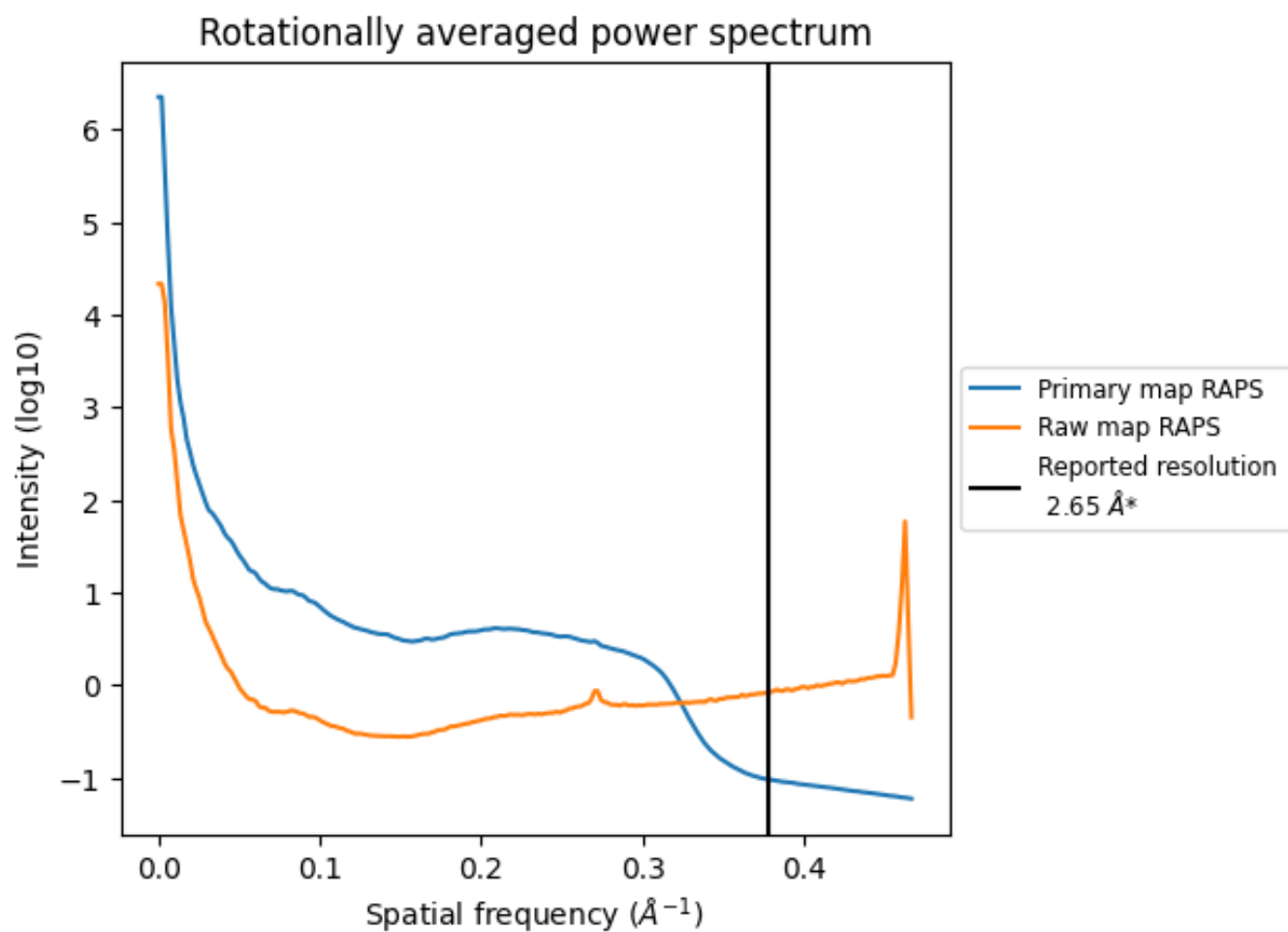
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 751 nm³; this corresponds to an approximate mass of 678 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

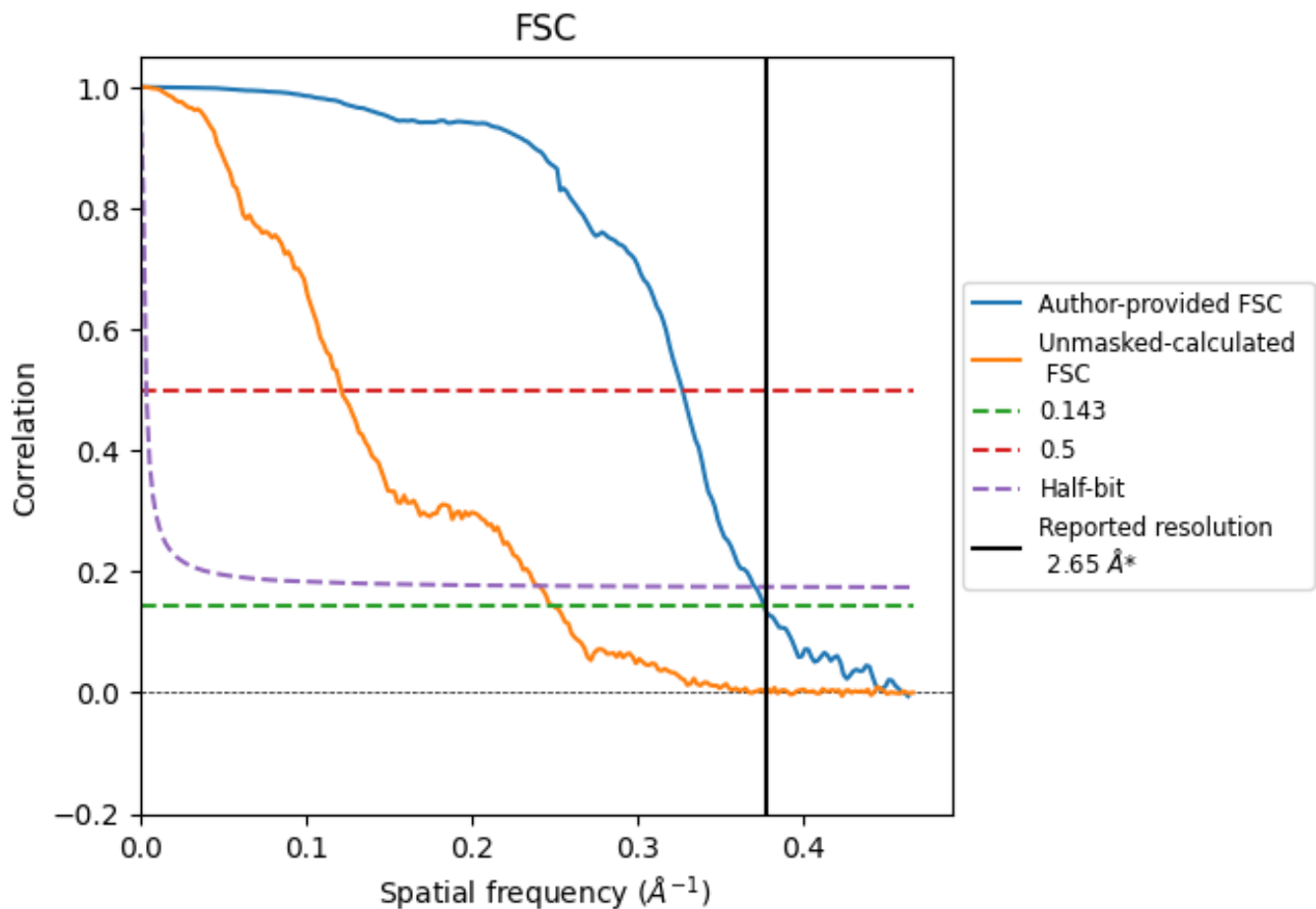


*Reported resolution corresponds to spatial frequency of 0.377 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.377 Å⁻¹

8.2 Resolution estimates [i](#)

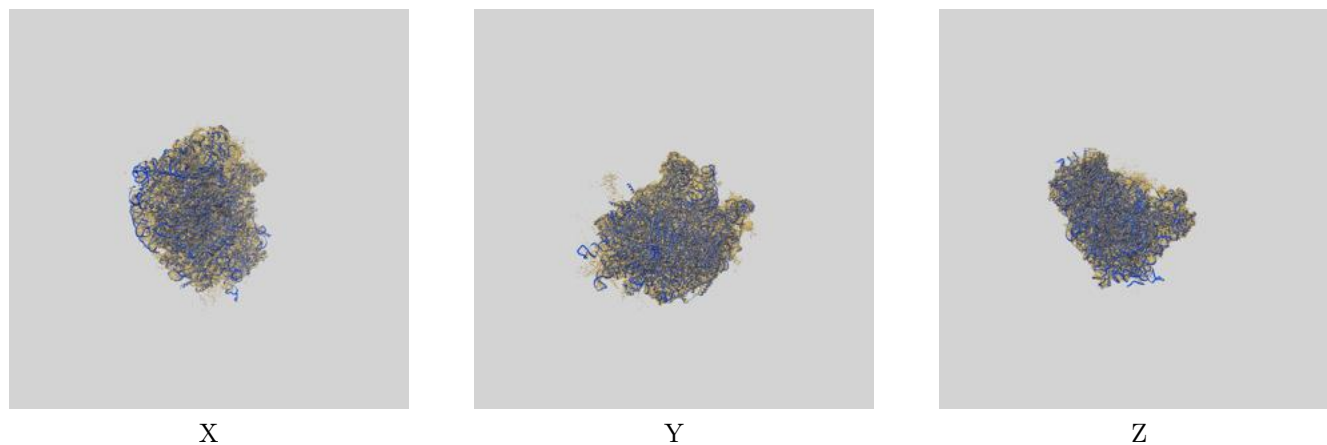
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.65	-	-
Author-provided FSC curve	2.65	3.06	2.69
Unmasked-calculated*	4.01	8.23	4.15

*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 4.01 differs from the reported value 2.65 by more than 10 %

9 Map-model fit [i](#)

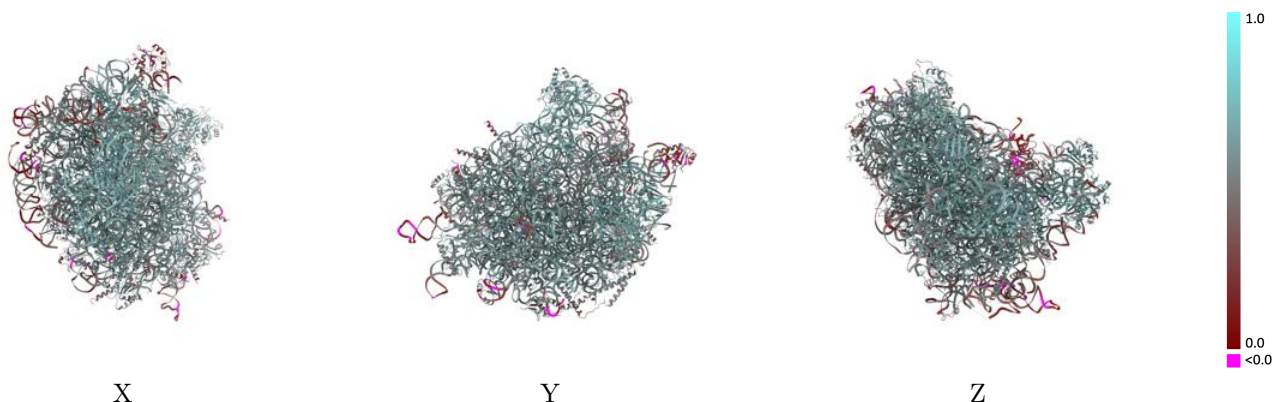
This section contains information regarding the fit between EMDB map EMD-29277 and PDB model 8FLF. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



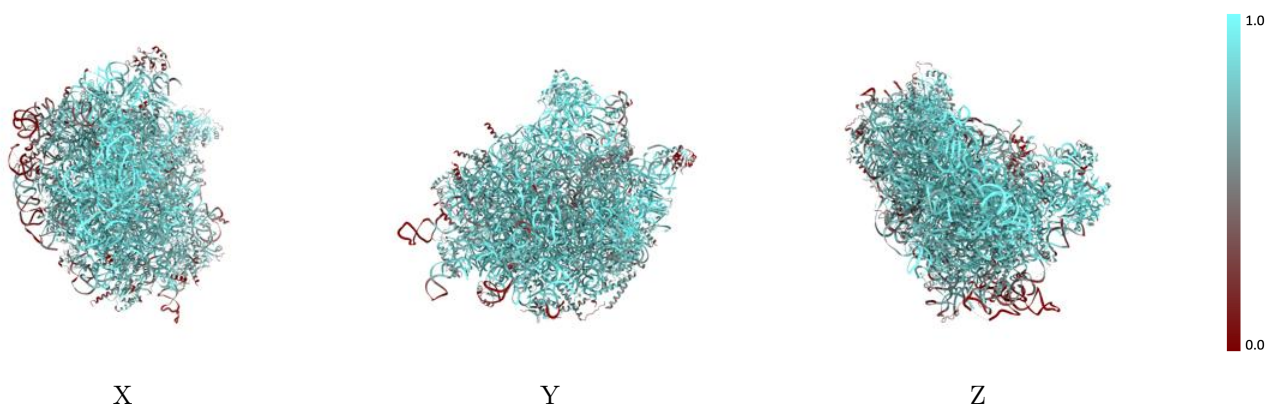
The images above show the 3D surface view of the map at the recommended contour level 0.95 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



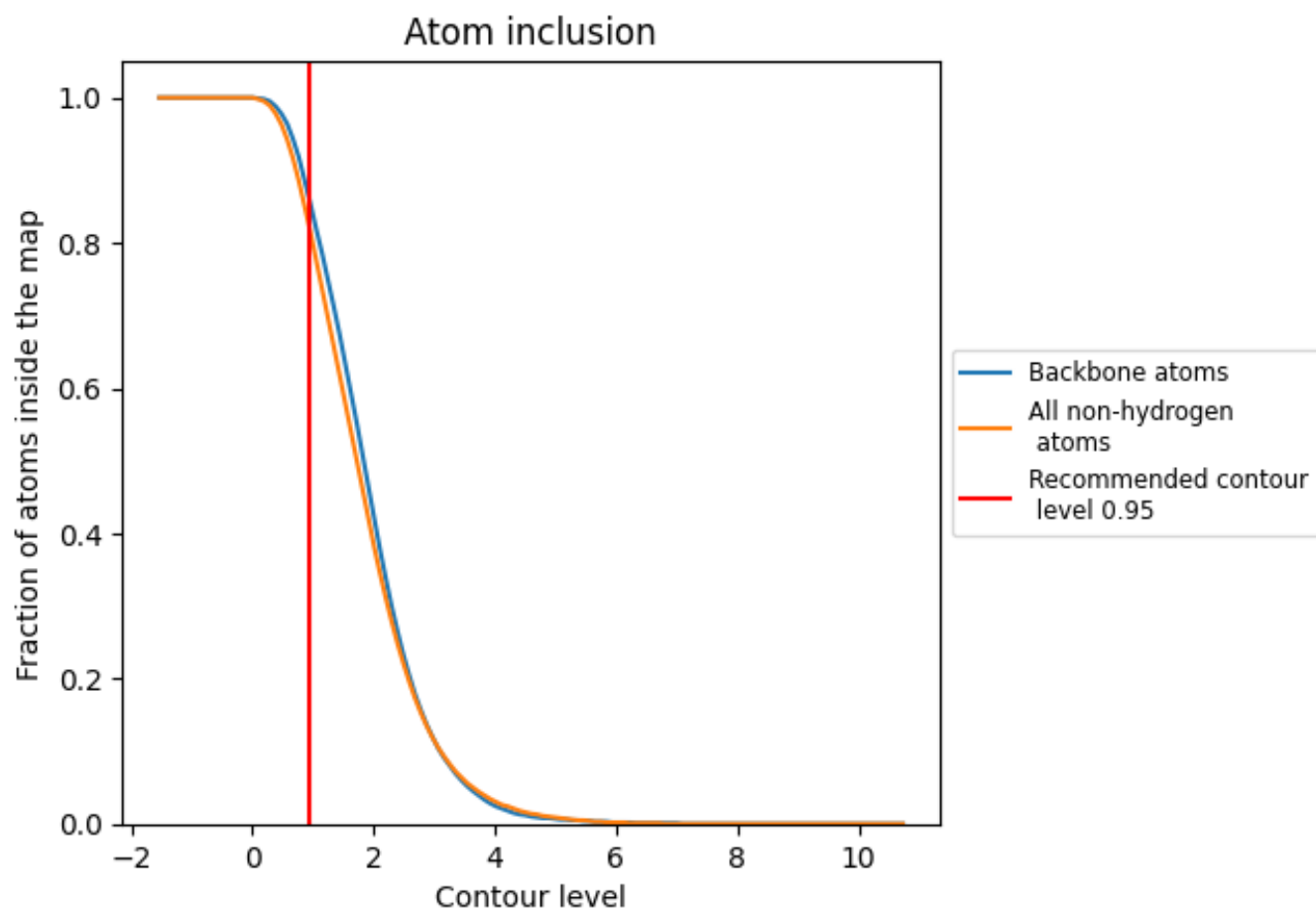
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.95).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





























The table lists the average atom inclusion at the recommended contour level (0.95) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8180	 0.5550
BE	 0.6160	 0.4590
L1	 0.8800	 0.5740
L3	 0.8370	 0.5410
L4	 0.9890	 0.6320
L5	 0.7940	 0.5730
L6	 0.7470	 0.5480
L7	 0.8770	 0.6090
L8	 0.8820	 0.6090
L9	 0.8800	 0.6060
LA	 0.8120	 0.5840
LB	 0.8490	 0.6010
LC	 0.9590	 0.6490
LD	 0.7670	 0.5600
LE	 0.8970	 0.6110
LF	 0.6980	 0.5260
LG	 0.8580	 0.6070
LH	 0.7420	 0.5730
LI	 0.7620	 0.5620
LJ	 0.7200	 0.5380
LK	 0.8740	 0.6060
LL	 0.7900	 0.5670
LM	 0.6720	 0.5390
LN	 0.8240	 0.5880
LO	 0.6800	 0.5250
LP	 0.7520	 0.5550
LQ	 0.8080	 0.5880
LR	 0.7750	 0.5630
LS	 0.7260	 0.5450
LT	 0.8520	 0.5980
LU	 0.7080	 0.5360
LV	 0.8780	 0.6220
LW	 0.8690	 0.6010
LX	 0.7200	 0.5440
LY	 0.6160	 0.5090



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Chain	Atom inclusion	Q-score
LZ	 0.8700	 0.6020
NK	 0.5110	 0.4630
NP	 0.6930	 0.5560
SA	 0.8100	 0.5820
SB	 0.8750	 0.6080
SC	 0.6380	 0.5180
SD	 0.8260	 0.5850
SE	 0.6550	 0.5060
SF	 0.8210	 0.5930
SG	 0.8950	 0.6110
SK	 0.8200	 0.5820
SQ	 0.3750	 0.2460
SR	 0.6360	 0.5100
SV	 0.7500	 0.5490