



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:34 PM UTC

PDB ID : 8OJ8 / pdb_00008oj8
EMDB ID : EMD-16908
Title : 60S ribosomal subunit bound to the E3-UFM1 complex - state 1 (native)
Authors : Penchev, I.; DaRosa, P.A.; Becker, T.; Beckmann, R.; Kopito, R.
Deposited on : 2023-03-24
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

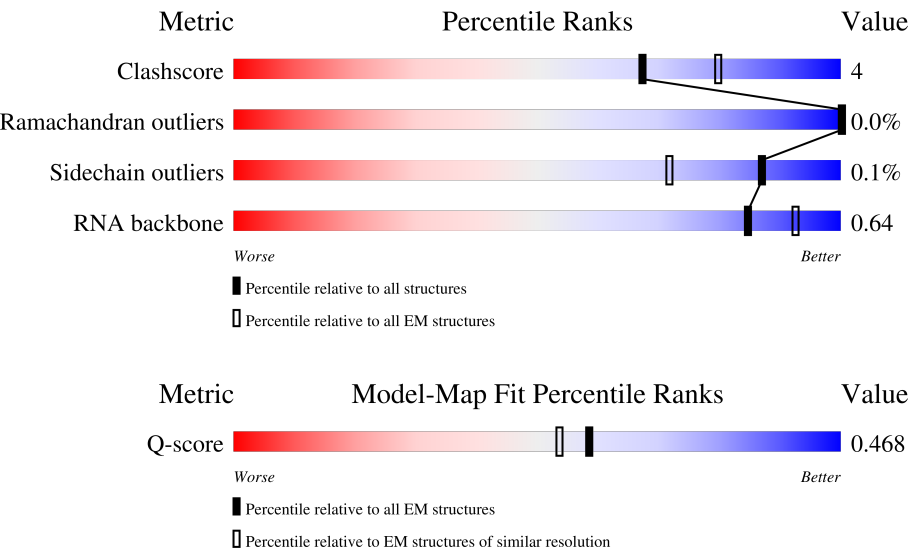
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.30 Å.

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



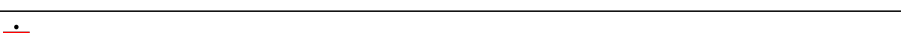
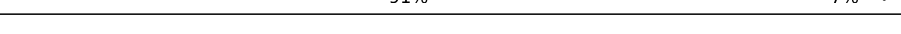
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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

Mol	Chain	Length	Quality of chain
1	1	476	58% 89% 11%
2	2	68	41% 91% 9%
3	3	96	30% 30% 70%

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Mol	Chain	Length	Quality of chain
4	5	5070	
5	7	121	
6	8	157	
7	A	794	
8	K	245	
9	LA	257	
10	LB	403	
11	LC	427	
12	LD	297	
13	LE	288	
14	LF	248	
15	LG	266	
16	LH	192	
17	LI	214	
18	LJ	178	
19	LL	211	
20	LM	215	
21	LN	204	
22	LO	203	
23	LP	184	
24	LQ	188	
25	LR	196	
26	LS	176	
27	LT	160	
28	LU	128	

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Mol	Chain	Length	Quality of chain
29	LV	140	
30	LW	157	
31	LX	156	
32	LY	145	
33	LZ	136	
34	La	148	
35	Lb	159	
36	Lc	115	
37	Ld	125	
38	Le	135	
39	Lf	110	
40	Lg	117	
41	Lh	123	
42	Li	105	
43	Lj	97	
44	Lk	70	
45	Ll	51	
46	Lm	128	
47	Lo	106	
48	Lp	92	
49	Lr	137	
50	Lz	217	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 144625 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 Protein transport protein Sec61 subunit alpha isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	426	Total	C	N	O	S	0	0
			3322	2189	535	577	21		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	145	SER	ALA	conflict	UNP P38377

- Molecule 2 is a protein called Protein transport protein Sec61 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	62	Total	C	N	O	S	0	0
			494	326	86	79	3		

- Molecule 3 is a protein called Protein transport protein Sec61 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	29	Total	C	N	O	S	0	0
			229	157	36	34	2		

- Molecule 4 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	3515	Total	C	N	O	P	0	0
			75376	33569	13808	24485	3514		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 6 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	8	148	Total	C	N	O	P	0	0
			3152	1407	563	1035	147		

- Molecule 7 is a protein called E3 UFM1-protein ligase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	474	Total	C	N	O	S	0	0
			3748	2365	643	724	16		

- Molecule 8 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	224	Total	C	N	O	S	0	0
			1704	1061	293	338	12		

- Molecule 9 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 10 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LB	402	Total	C	N	O	S	0	0
			3239	2060	608	557	14		

- Molecule 11 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 12 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 13 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LE	220	Total	C	N	O	S	0	0
			1765	1136	334	291	4		

- Molecule 14 is a protein called 60S ribosomal protein L7.

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

- Molecule 15 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 16 is a protein called 60S ribosomal protein L9.

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

- Molecule 17 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	202	Total	C	N	O	S	0	0
			1634	1038	314	269	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LI	87	ILE	MET	conflict	UNP Q96L21

- Molecule 18 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	175	Total	C	N	O	S	0	0
			1401	882	261	252	6		

- Molecule 19 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LL	201	Total	C	N	O	S	1	0
			1634	1024	342	264	4		

- Molecule 20 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LM	136	Total	C	N	O	S	0	0
			1120	719	215	179	7		

- Molecule 21 is a protein called 60S ribosomal protein L15.

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

- Molecule 22 is a protein called 60S ribosomal protein L13a.

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

- Molecule 23 is a protein called 60S ribosomal protein L17.

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

- Molecule 24 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 25 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LR	155	Total	C	N	O	S	0	0
			1294	808	278	199	9		

- Molecule 26 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 27 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 28 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 29 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 30 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LW	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 31 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LX	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 32 is a protein called 60S ribosomal protein L26.

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

- Molecule 33 is a protein called 60S ribosomal protein L27.

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

- Molecule 34 is a protein called 60S ribosomal protein L27a.

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

- Molecule 35 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 36 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 37 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 38 is a protein called 60S ribosomal protein L32.

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

- Molecule 39 is a protein called 60S ribosomal protein L35a.

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

- Molecule 40 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 41 is a protein called 60S ribosomal protein L35.

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

- Molecule 42 is a protein called 60S ribosomal protein L36.

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

- Molecule 43 is a protein called 60S ribosomal protein L37.

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

- Molecule 44 is a protein called 60S ribosomal protein L38.

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

- Molecule 45 is a protein called 60S ribosomal protein L39.

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

- Molecule 46 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 47 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lo	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 48 is a protein called 60S ribosomal protein L37a.

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

- Molecule 49 is a protein called 60S ribosomal protein L28.

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

- Molecule 50 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lz	217	Total	C	N	O	S	0	0
			1744	1114	314	307	9		

- Molecule 51 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
51	5	204	Total	Mg	0
			204	204	
51	7	2	Total	Mg	0
			2	2	
51	8	5	Total	Mg	0
			5	5	
51	LA	1	Total	Mg	0
			1	1	
51	LI	1	Total	Mg	0
			1	1	
51	LP	1	Total	Mg	0
			1	1	
51	LV	1	Total	Mg	0
			1	1	
51	Le	2	Total	Mg	0
			2	2	
51	Lf	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
51	Lj	2	Total 2	Mg 2	0

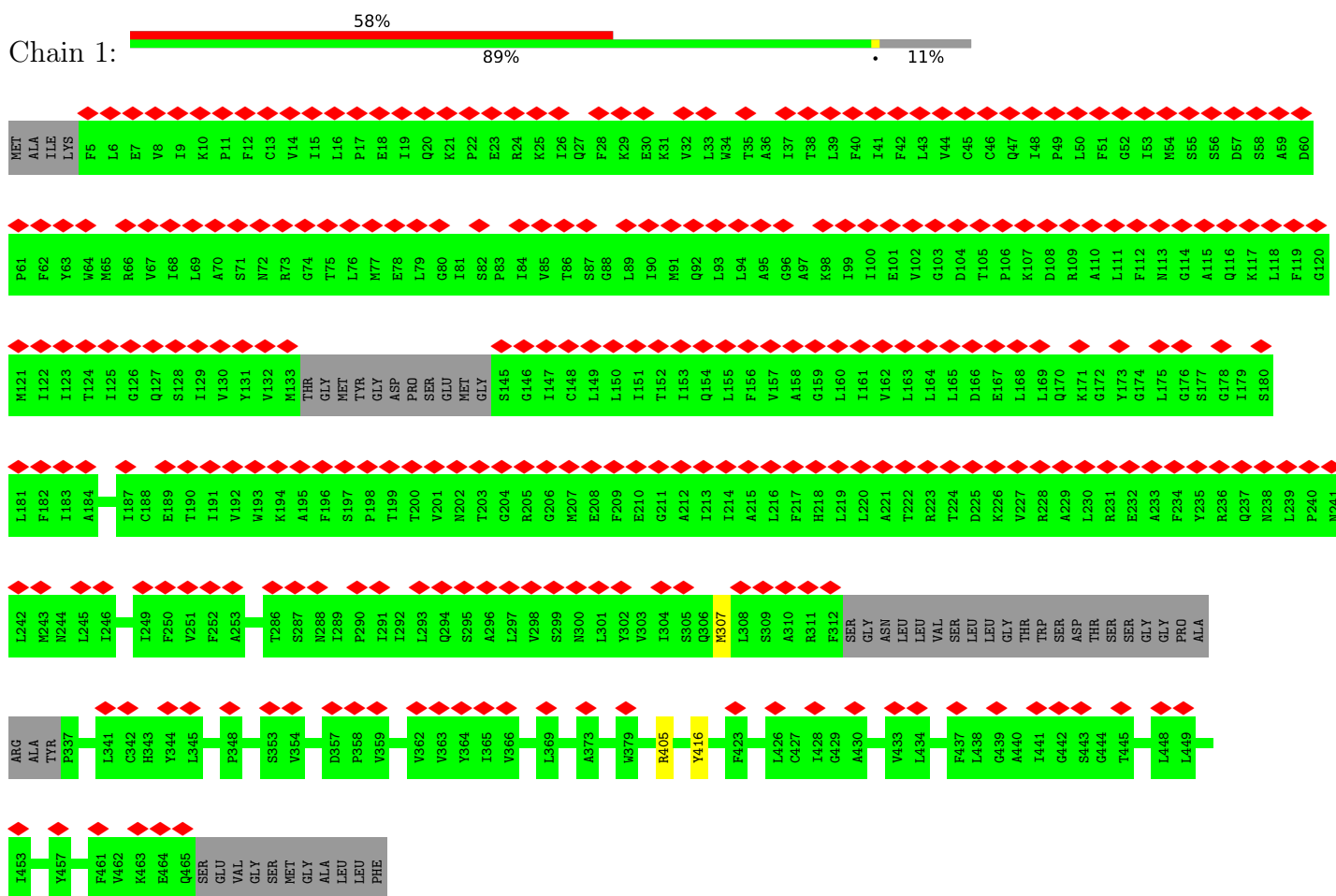
- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	Lg	1	Total 1	Zn 1	0
52	Lj	1	Total 1	Zn 1	0
52	Lm	1	Total 1	Zn 1	0
52	Lo	1	Total 1	Zn 1	0
52	Lp	1	Total 1	Zn 1	0

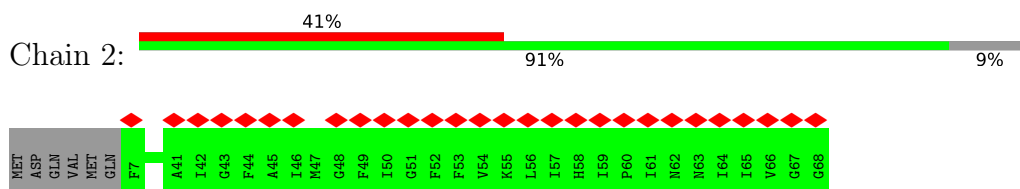
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Protein transport protein Sec61 subunit alpha isoform 1



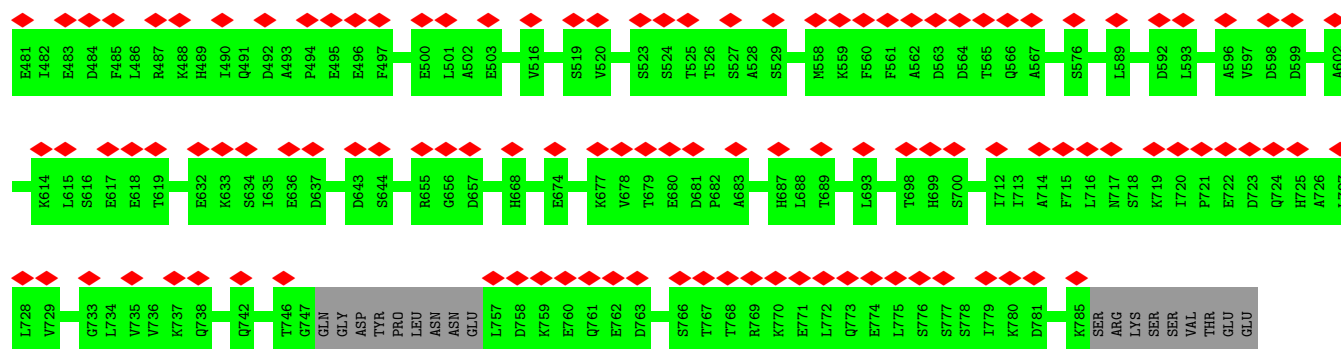
- Molecule 2: Protein transport protein Sec61 subunit gamma



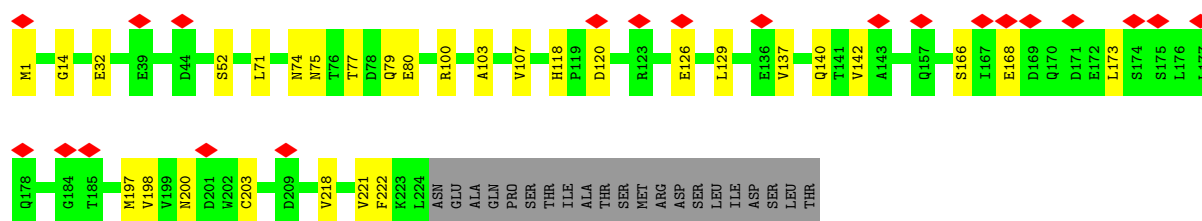
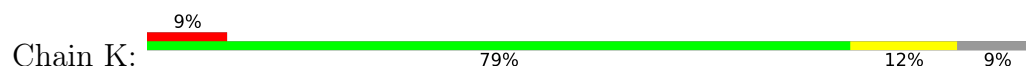
- Molecule 3: Protein transport protein Sec61 subunit beta



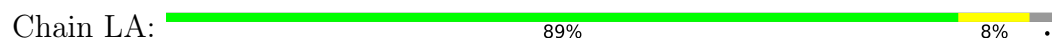




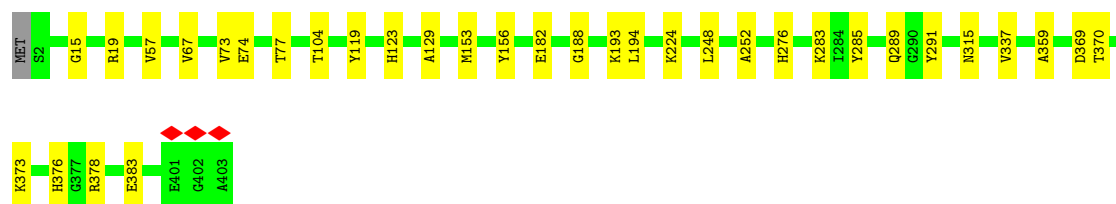
• Molecule 8: Eukaryotic translation initiation factor 6



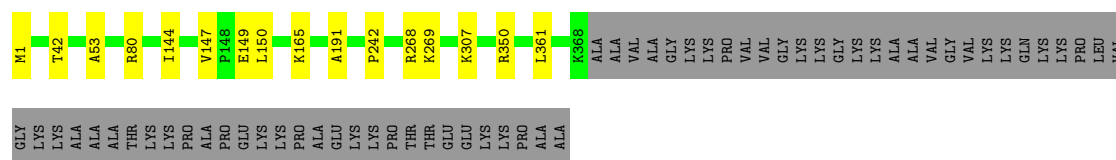
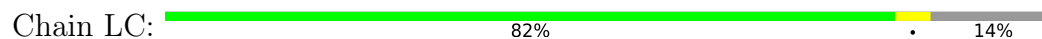
• Molecule 9: 60S ribosomal protein L8



• Molecule 10: 60S ribosomal protein L3



• Molecule 11: 60S ribosomal protein L4



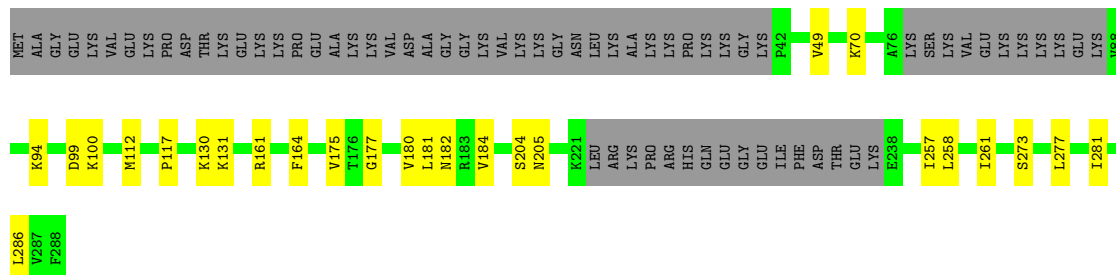
- Molecule 12: 60S ribosomal protein L5

Chain LD:  89% 9%



- Molecule 13: 60S ribosomal protein L6

Chain LE:  67% 9% 24%



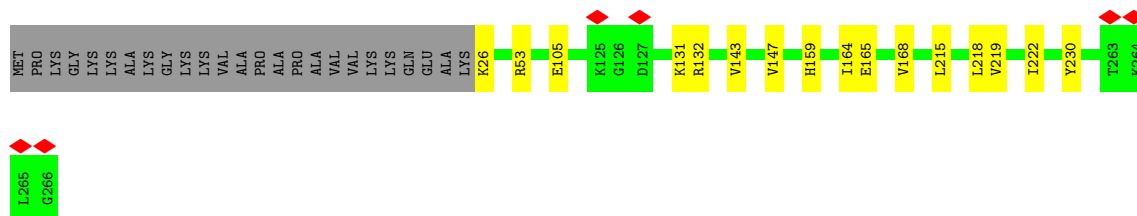
- Molecule 14: 60S ribosomal protein L7

Chain LF:  84% 7% 9%



- Molecule 15: 60S ribosomal protein L7a

Chain LG:  85% 6% 9%



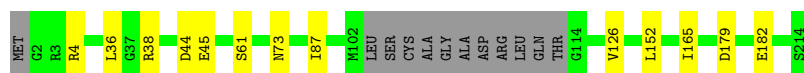
- Molecule 16: 60S ribosomal protein L9

Chain LH:  89% 10%



- Molecule 17: Ribosomal protein uL16-like

Chain LI:  88% 6% 6%



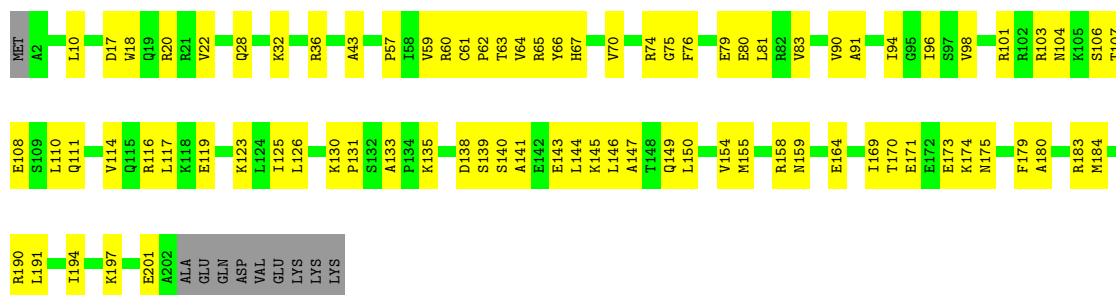
- Molecule 18: 60S ribosomal protein L11

Chain LJ: 91% 7%



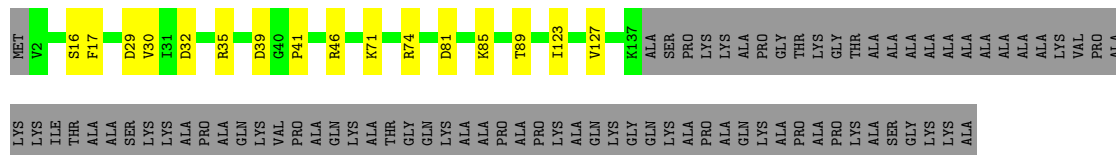
- Molecule 19: 60S ribosomal protein L13

Chain LL: 56% 39% 5%



- Molecule 20: 60S ribosomal protein L14

Chain LM: 56% 7% 37%



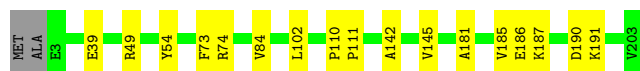
- Molecule 21: 60S ribosomal protein L15

Chain LN: 91% 8%



- Molecule 22: 60S ribosomal protein L13a

Chain LO: 91% 8%



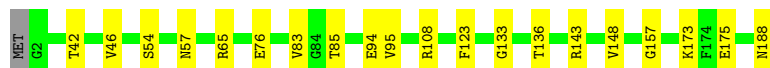
- Molecule 23: 60S ribosomal protein L17

Chain LP:  71% 12% 17%



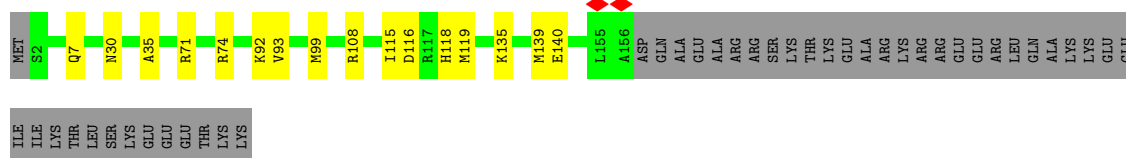
- Molecule 24: 60S ribosomal protein L18

Chain LQ:  89% 11%



- Molecule 25: 60S ribosomal protein L19

Chain LR:  71% 8% 21%



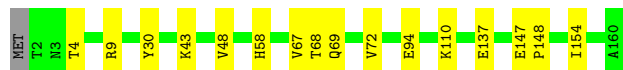
- Molecule 26: 60S ribosomal protein L18a

Chain LS:  90% 9%



- Molecule 27: 60S ribosomal protein L21

Chain LT:  89% 10%



- Molecule 28: 60S ribosomal protein L22

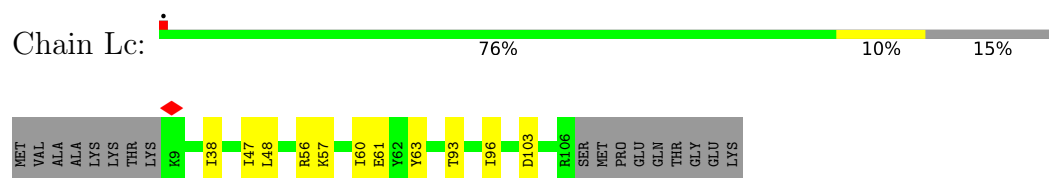
Chain LU:  70% 9% 21%



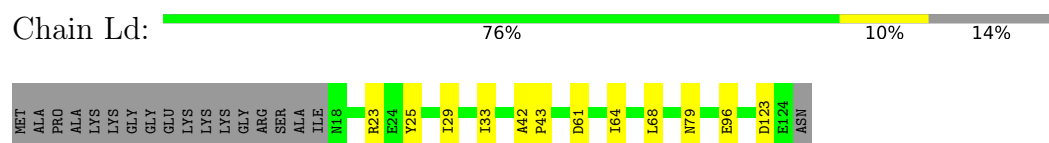
- Molecule 29: 60S ribosomal protein L23

Chain LV:  85% 9% 6%

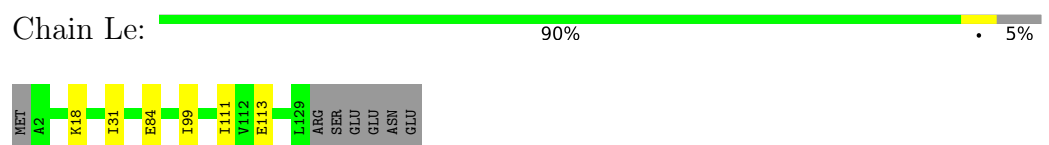
- Molecule 36: 60S ribosomal protein L30



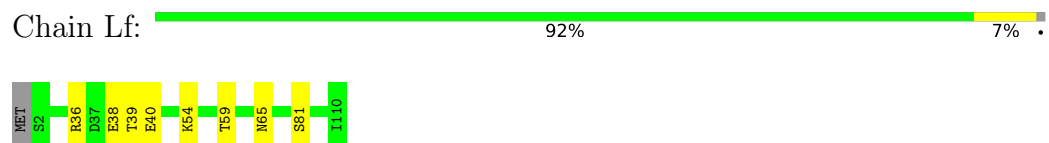
- Molecule 37: 60S ribosomal protein L31



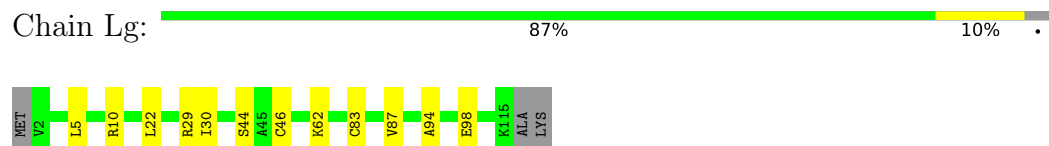
- Molecule 38: 60S ribosomal protein L32



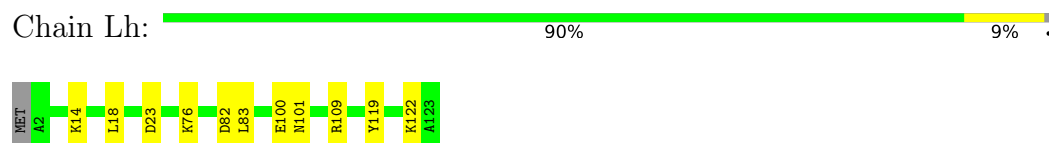
- Molecule 39: 60S ribosomal protein L35a



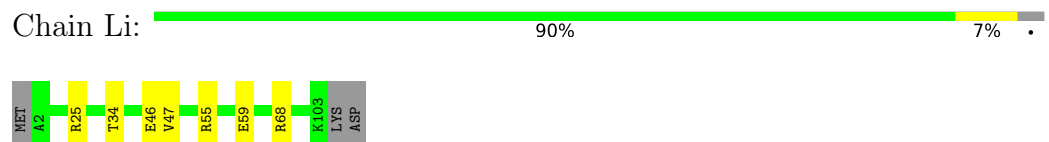
- Molecule 40: 60S ribosomal protein L34



- Molecule 41: 60S ribosomal protein L35

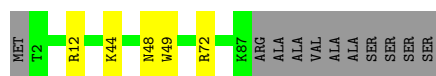


- Molecule 42: 60S ribosomal protein L36



- Molecule 43: 60S ribosomal protein L37

Chain Lj:  84% 5% 11%



- Molecule 44: 60S ribosomal protein L38

Chain Lk:  79% 20% .



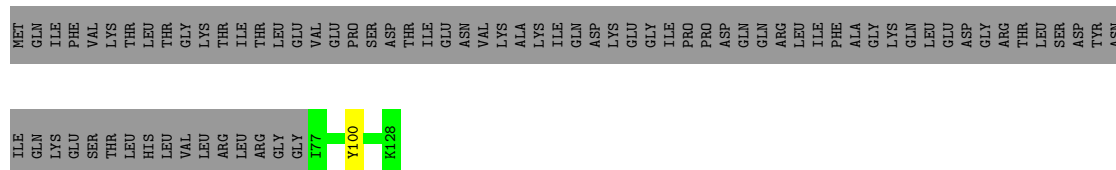
- Molecule 45: 60S ribosomal protein L39

Chain Ll:  88% 10% .

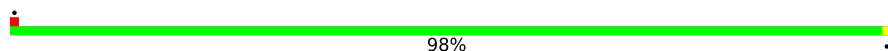


- Molecule 46: Ubiquitin-60S ribosomal protein L40

Chain Lm:  40% 59%



- Molecule 47: 60S ribosomal protein L36a

Chain Lo:  98% ..



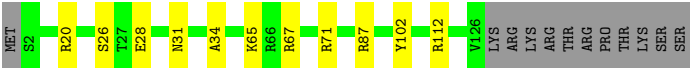
- Molecule 48: 60S ribosomal protein L37a

Chain Lp:  85% 14% .

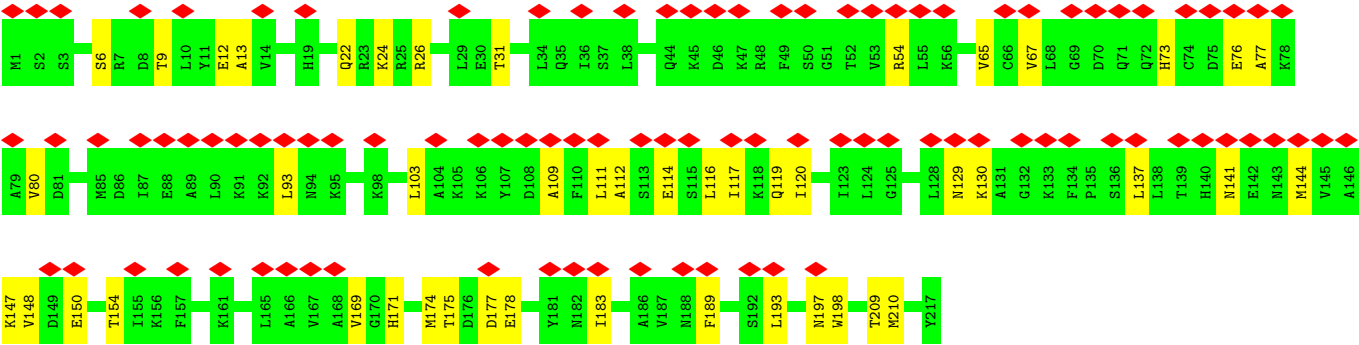
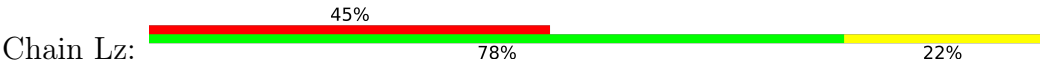


- Molecule 49: 60S ribosomal protein L28

Chain Lr:  83% 8% 9%



• Molecule 50: 60S ribosomal protein L10a



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	20750	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)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.044	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0055	Depositor
Map size ($\text{\AA}$)	392.58, 392.58, 392.58	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.727, 0.727, 0.727	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.12	0/3393	0.30	0/4597
2	2	0.16	0/504	0.32	0/673
3	3	0.13	0/236	0.31	0/321
4	5	0.08	0/84316	0.20	0/131502
5	7	0.07	0/2861	0.19	0/4459
6	8	0.08	0/3520	0.21	0/5481
7	A	0.21	0/3797	0.34	0/5103
8	K	0.08	0/1728	0.22	0/2351
9	LA	0.10	0/1936	0.22	0/2596
10	LB	0.08	0/3307	0.21	0/4424
11	LC	0.08	0/2981	0.20	0/4002
12	LD	0.09	0/2428	0.20	0/3252
13	LE	0.07	0/1799	0.20	0/2414
14	LF	0.10	0/1905	0.22	0/2539
15	LG	0.09	0/1960	0.21	0/2637
16	LH	0.10	0/1537	0.21	0/2066
17	LI	0.10	0/1673	0.21	0/2234
18	LJ	0.09	0/1424	0.22	0/1904
19	LL	0.09	0/1668	0.19	0/2232
20	LM	0.10	0/1142	0.21	0/1527
21	LN	0.10	0/1746	0.20	0/2338
22	LO	0.10	0/1682	0.22	0/2250
23	LP	0.09	0/1268	0.22	0/1701
24	LQ	0.10	0/1537	0.21	0/2052
25	LR	0.09	0/1310	0.21	0/1734
26	LS	0.09	0/1493	0.22	0/2003
27	LT	0.09	0/1326	0.22	0/1770
28	LU	0.10	0/839	0.24	0/1126
29	LV	0.09	0/993	0.20	0/1332
30	LW	0.11	0/532	0.23	0/708
31	LX	0.08	0/984	0.20	0/1323
32	LY	0.09	0/1132	0.20	0/1504

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LZ	0.11	0/1130	0.21	0/1507
34	La	0.07	0/1191	0.19	0/1591
35	Lb	0.11	0/889	0.24	0/1175
36	Lc	0.12	0/774	0.26	0/1038
37	Ld	0.10	0/903	0.24	0/1216
38	Le	0.08	0/1071	0.19	0/1429
39	Lf	0.10	0/895	0.23	0/1198
40	Lg	0.09	0/916	0.21	0/1220
41	Lh	0.10	0/1023	0.20	0/1351
42	Li	0.10	0/843	0.20	0/1115
43	Lj	0.09	0/720	0.19	0/952
44	Lk	0.10	0/575	0.25	0/761
45	Ll	0.13	0/454	0.26	0/599
46	Lm	0.11	0/435	0.21	0/575
47	Lo	0.09	0/877	0.19	0/1156
48	Lp	0.11	0/718	0.23	0/953
49	Lr	0.09	0/1017	0.20	0/1364
50	Lz	0.17	0/1772	0.28	0/2375
All	All	0.09	0/155160	0.21	0/227730

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	1	3322	0	3449	2	0
2	2	494	0	527	0	0
3	3	229	0	245	0	0
4	5	75376	0	38082	443	0
5	7	2561	0	1295	17	0
6	8	3152	0	1601	17	0
7	A	3748	0	3828	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	K	1704	0	1683	18	0
9	LA	1898	0	1993	17	0
10	LB	3239	0	3376	27	0
11	LC	2927	0	3104	17	0
12	LD	2382	0	2410	22	0
13	LE	1765	0	1917	19	0
14	LF	1870	0	1996	12	0
15	LG	1927	0	2074	12	0
16	LH	1518	0	1601	17	0
17	LI	1634	0	1673	11	0
18	LJ	1401	0	1428	9	0
19	LL	1634	0	1754	86	0
20	LM	1120	0	1187	11	0
21	LN	1701	0	1749	13	0
22	LO	1650	0	1794	12	0
23	LP	1242	0	1269	16	0
24	LQ	1513	0	1628	16	0
25	LR	1294	0	1434	14	0
26	LS	1453	0	1490	12	0
27	LT	1298	0	1366	15	0
28	LU	825	0	850	8	0
29	LV	979	0	1039	8	0
30	LW	519	0	533	6	0
31	LX	967	0	1040	7	0
32	LY	1115	0	1205	7	0
33	LZ	1107	0	1182	14	0
34	La	1162	0	1213	14	0
35	Lb	876	0	948	11	0
36	Lc	764	0	804	7	0
37	Ld	888	0	930	8	0
38	Le	1053	0	1147	5	0
39	Lf	876	0	912	7	0
40	Lg	906	0	998	9	0
41	Lh	1015	0	1148	9	0
42	Li	832	0	917	9	0
43	Lj	705	0	737	5	0
44	Lk	569	0	637	10	0
45	Ll	444	0	483	3	0
46	Lm	429	0	465	1	0
47	Lo	863	0	929	1	0
48	Lp	708	0	756	10	0
49	Lr	1002	0	1068	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	Lz	1744	0	1859	32	0
51	5	204	0	0	0	0
51	7	2	0	0	0	0
51	8	5	0	0	0	0
51	LA	1	0	0	0	0
51	LI	1	0	0	0	0
51	LP	1	0	0	0	0
51	LV	1	0	0	0	0
51	Le	2	0	0	0	0
51	Lf	1	0	0	0	0
51	Lj	2	0	0	0	0
52	Lg	1	0	0	0	0
52	Lj	1	0	0	0	0
52	Lm	1	0	0	0	0
52	Lo	1	0	0	0	0
52	Lp	1	0	0	0	0
All	All	144625	0	107753	863	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 4.

The worst 5 of 863 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)
4:5:326:C:P	19:LL:103:ARG:NH2	2.27	1.08
4:5:326:C:OP1	19:LL:103:ARG:NH2	1.95	1.00
4:5:664:G:H21	4:5:667:A:N6	1.64	0.94
4:5:326:C:OP2	19:LL:103:ARG:NH2	2.01	0.92
4:5:2693:G:OP1	44:Lk:35:LYS:NZ	2.02	0.91

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	1	420/476 (88%)	403 (96%)	17 (4%)	0	100	100
2	2	60/68 (88%)	59 (98%)	1 (2%)	0	100	100
3	3	27/96 (28%)	27 (100%)	0	0	100	100
7	A	466/794 (59%)	448 (96%)	18 (4%)	0	100	100
8	K	222/245 (91%)	216 (97%)	6 (3%)	0	100	100
9	LA	246/257 (96%)	236 (96%)	10 (4%)	0	100	100
10	LB	400/403 (99%)	396 (99%)	4 (1%)	0	100	100
11	LC	366/427 (86%)	359 (98%)	7 (2%)	0	100	100
12	LD	291/297 (98%)	284 (98%)	6 (2%)	1 (0%)	36	65
13	LE	214/288 (74%)	205 (96%)	9 (4%)	0	100	100
14	LF	223/248 (90%)	219 (98%)	4 (2%)	0	100	100
15	LG	239/266 (90%)	231 (97%)	8 (3%)	0	100	100
16	LH	188/192 (98%)	186 (99%)	2 (1%)	0	100	100
17	LI	198/214 (92%)	194 (98%)	4 (2%)	0	100	100
18	LJ	173/178 (97%)	170 (98%)	3 (2%)	0	100	100
19	LL	200/211 (95%)	197 (98%)	3 (2%)	0	100	100
20	LM	134/215 (62%)	131 (98%)	3 (2%)	0	100	100
21	LN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
22	LO	199/203 (98%)	198 (100%)	1 (0%)	0	100	100
23	LP	151/184 (82%)	149 (99%)	2 (1%)	0	100	100
24	LQ	185/188 (98%)	182 (98%)	3 (2%)	0	100	100
25	LR	153/196 (78%)	149 (97%)	4 (3%)	0	100	100
26	LS	173/176 (98%)	166 (96%)	7 (4%)	0	100	100
27	LT	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
28	LU	99/128 (77%)	96 (97%)	2 (2%)	1 (1%)	12	40
29	LV	129/140 (92%)	125 (97%)	4 (3%)	0	100	100
30	LW	60/157 (38%)	59 (98%)	1 (2%)	0	100	100
31	LX	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
32	LY	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
33	LZ	133/136 (98%)	129 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	La	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
35	Lb	105/159 (66%)	103 (98%)	2 (2%)	0	100	100
36	Lc	96/115 (84%)	96 (100%)	0	0	100	100
37	Ld	105/125 (84%)	101 (96%)	4 (4%)	0	100	100
38	Le	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
39	Lf	107/110 (97%)	107 (100%)	0	0	100	100
40	Lg	112/117 (96%)	112 (100%)	0	0	100	100
41	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
42	Li	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
43	Lj	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
44	Lk	67/70 (96%)	67 (100%)	0	0	100	100
45	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
46	Lm	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
47	Lo	103/106 (97%)	101 (98%)	2 (2%)	0	100	100
48	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
49	Lr	123/137 (90%)	122 (99%)	1 (1%)	0	100	100
50	Lz	215/217 (99%)	209 (97%)	6 (3%)	0	100	100
All	All	7750/9083 (85%)	7566 (98%)	182 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	LD	4	VAL
28	LU	19	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	361/399 (90%)	360 (100%)	1 (0%)	86	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	2	53/59 (90%)	53 (100%)	0	100	100
3	3	26/74 (35%)	26 (100%)	0	100	100
7	A	420/704 (60%)	418 (100%)	2 (0%)	81	83
8	K	194/213 (91%)	194 (100%)	0	100	100
9	LA	190/199 (96%)	190 (100%)	0	100	100
10	LB	348/349 (100%)	348 (100%)	0	100	100
11	LC	306/348 (88%)	306 (100%)	0	100	100
12	LD	246/250 (98%)	246 (100%)	0	100	100
13	LE	194/252 (77%)	194 (100%)	0	100	100
14	LF	194/215 (90%)	194 (100%)	0	100	100
15	LG	203/223 (91%)	203 (100%)	0	100	100
16	LH	169/171 (99%)	169 (100%)	0	100	100
17	LI	172/181 (95%)	172 (100%)	0	100	100
18	LJ	147/149 (99%)	147 (100%)	0	100	100
19	LL	169/177 (96%)	169 (100%)	0	100	100
20	LM	116/161 (72%)	116 (100%)	0	100	100
21	LN	171/172 (99%)	170 (99%)	1 (1%)	78	81
22	LO	173/174 (99%)	173 (100%)	0	100	100
23	LP	134/163 (82%)	134 (100%)	0	100	100
24	LQ	164/165 (99%)	164 (100%)	0	100	100
25	LR	138/175 (79%)	138 (100%)	0	100	100
26	LS	156/157 (99%)	156 (100%)	0	100	100
27	LT	139/140 (99%)	139 (100%)	0	100	100
28	LU	91/115 (79%)	91 (100%)	0	100	100
29	LV	101/107 (94%)	101 (100%)	0	100	100
30	LW	54/126 (43%)	54 (100%)	0	100	100
31	LX	106/133 (80%)	106 (100%)	0	100	100
32	LY	124/135 (92%)	124 (100%)	0	100	100
33	LZ	117/118 (99%)	117 (100%)	0	100	100
34	La	120/121 (99%)	120 (100%)	0	100	100
35	Lb	88/126 (70%)	88 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	Lc	83/97 (86%)	83 (100%)	0	100	100
37	Ld	98/110 (89%)	98 (100%)	0	100	100
38	Le	114/121 (94%)	114 (100%)	0	100	100
39	Lf	88/89 (99%)	88 (100%)	0	100	100
40	Lg	98/100 (98%)	98 (100%)	0	100	100
41	Lh	109/110 (99%)	109 (100%)	0	100	100
42	Li	86/89 (97%)	86 (100%)	0	100	100
43	Lj	73/80 (91%)	73 (100%)	0	100	100
44	Lk	64/65 (98%)	64 (100%)	0	100	100
45	Ll	47/48 (98%)	47 (100%)	0	100	100
46	Lm	48/116 (41%)	48 (100%)	0	100	100
47	Lo	93/94 (99%)	93 (100%)	0	100	100
48	Lp	74/75 (99%)	74 (100%)	0	100	100
49	Lr	109/121 (90%)	109 (100%)	0	100	100
50	Lz	196/196 (100%)	196 (100%)	0	100	100
All	All	6764/7762 (87%)	6760 (100%)	4 (0%)	87	90

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	307	MET
7	A	267	LEU
7	A	329	LEU
21	LN	124	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
30	LW	48	GLN
36	Lc	72	HIS
30	LW	50	ASN
31	LX	107	HIS
39	Lf	99	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	5	3491/5070 (68%)	378 (10%)	4 (0%)
5	7	119/121 (98%)	5 (4%)	0
6	8	145/157 (92%)	14 (9%)	0
All	All	3755/5348 (70%)	397 (10%)	4 (0%)

5 of 397 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	5	2	G
4	5	13	U
4	5	39	A
4	5	42	A
4	5	48	G

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	5	739	G
4	5	1633	G
4	5	3964	U
4	5	4699	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 225 ligands modelled in this entry, 225 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.

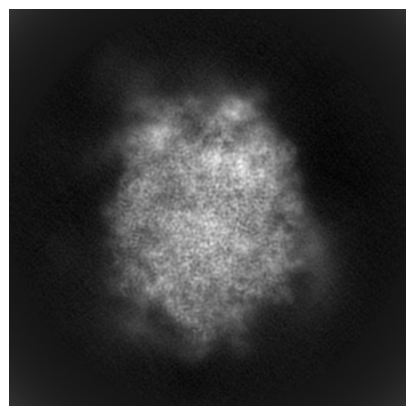
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16908. These allow visual inspection of the internal detail of the map and identification of artifacts.

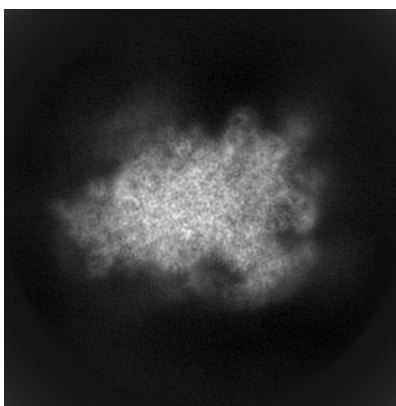
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

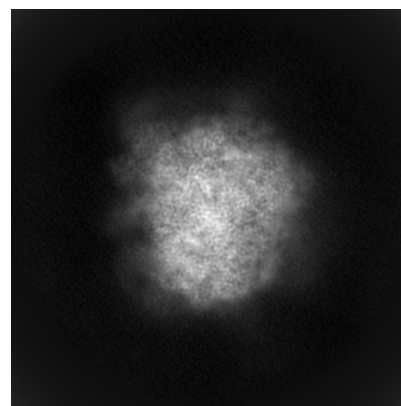
6.1.1 Primary map



X

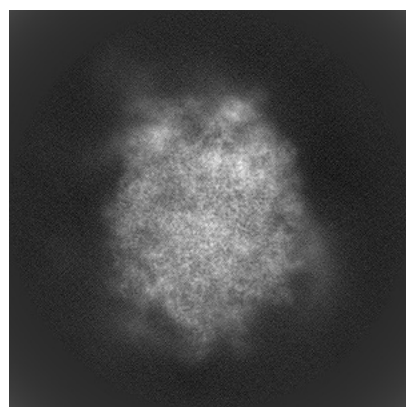


Y

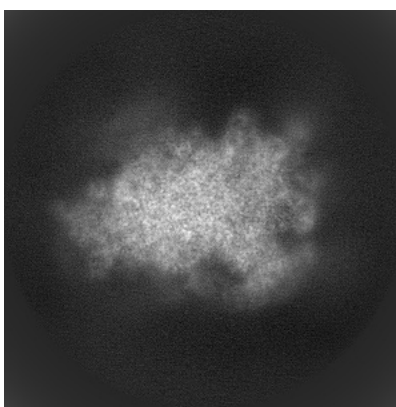


Z

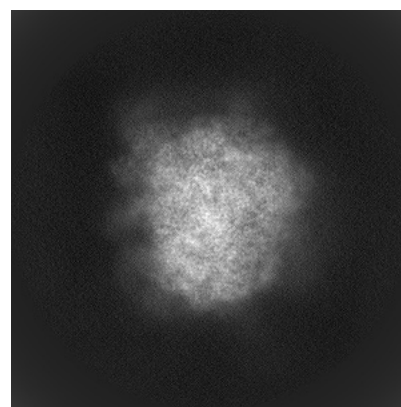
6.1.2 Raw map



X



Y

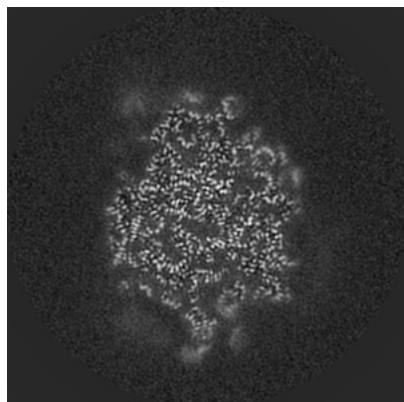


Z

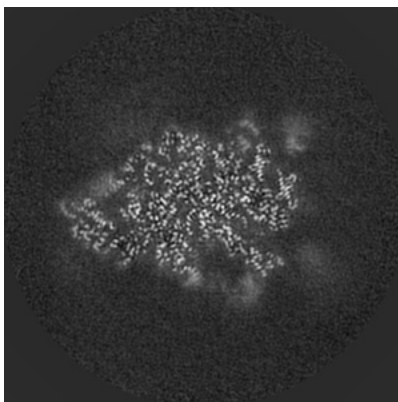
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

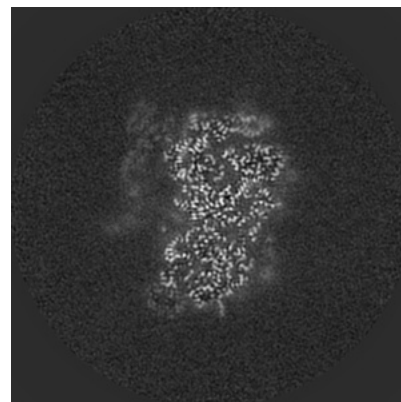
6.2.1 Primary map



X Index: 270

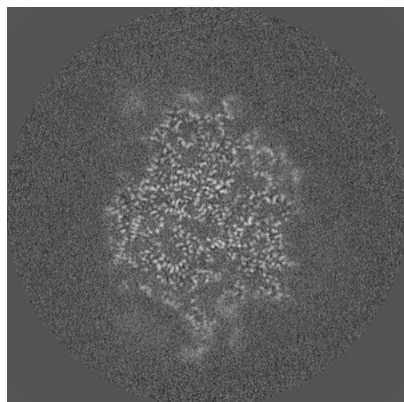


Y Index: 270

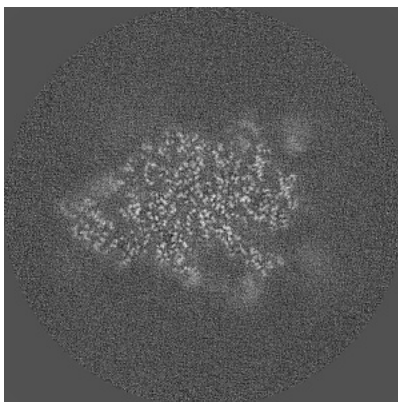


Z Index: 270

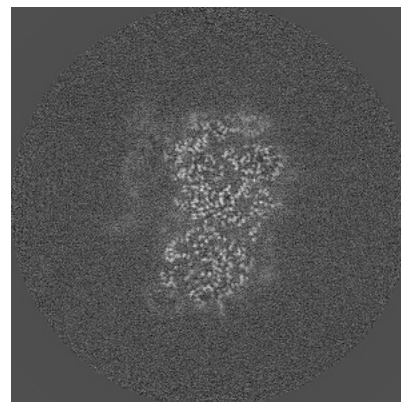
6.2.2 Raw map



X Index: 270



Y Index: 270

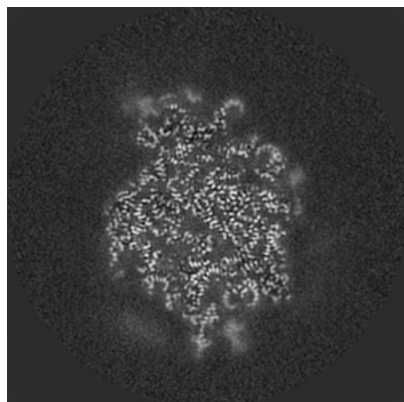


Z Index: 270

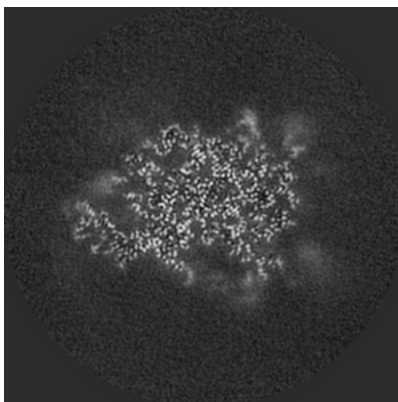
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

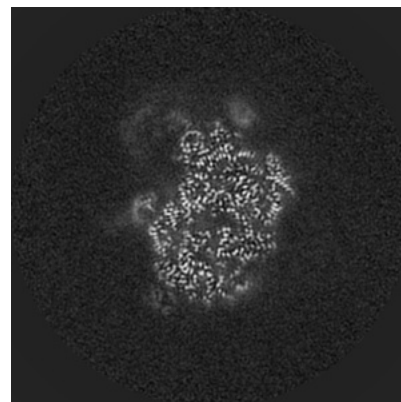
6.3.1 Primary map



X Index: 261

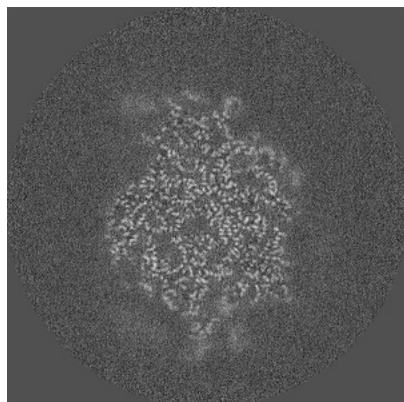


Y Index: 276

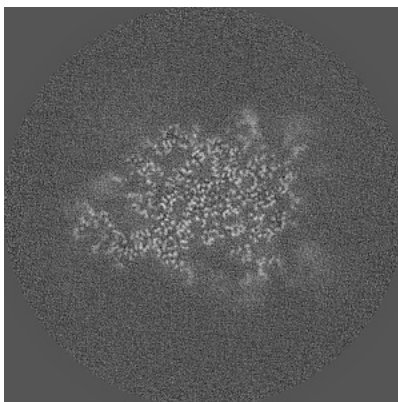


Z Index: 249

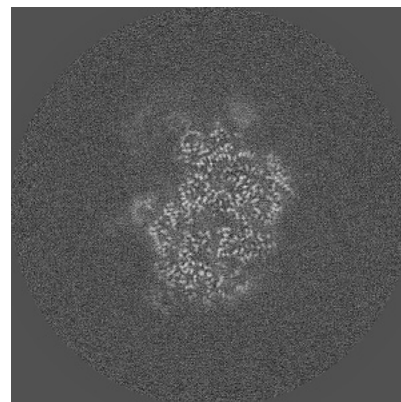
6.3.2 Raw map



X Index: 266



Y Index: 277

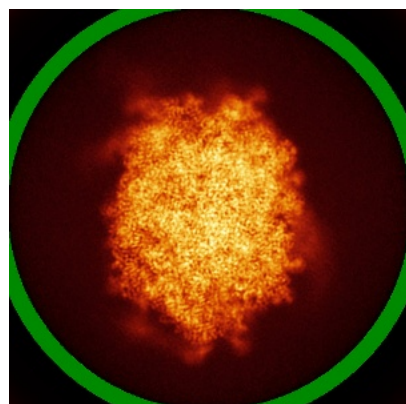


Z Index: 249

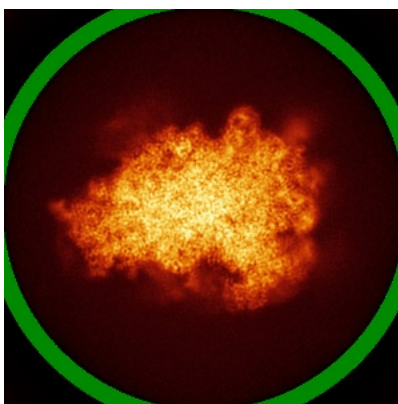
The images above show the largest variance slices of the map in three orthogonal directions.

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

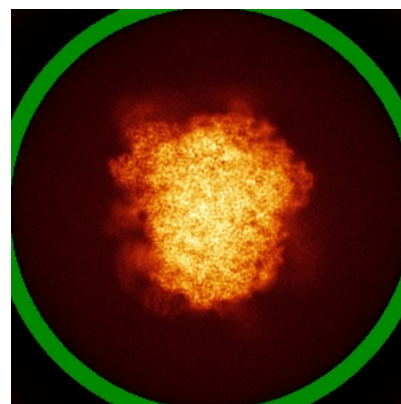
6.4.1 Primary map



X

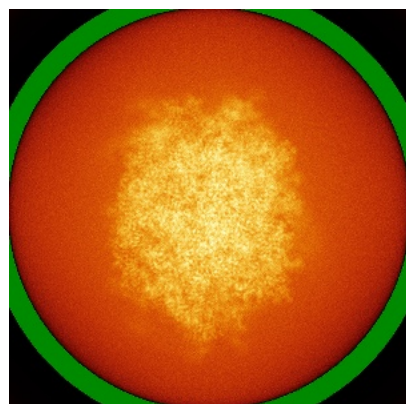


Y

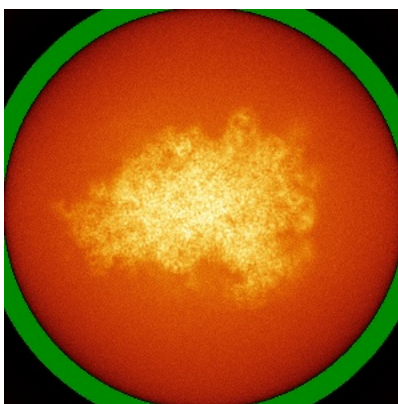


Z

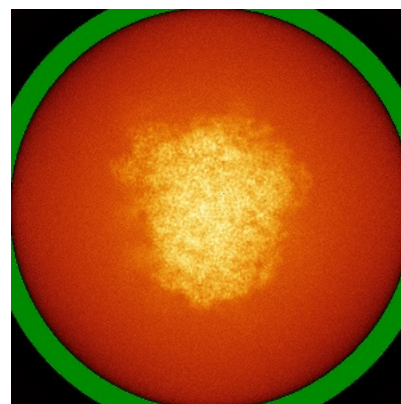
6.4.2 Raw map



X



Y

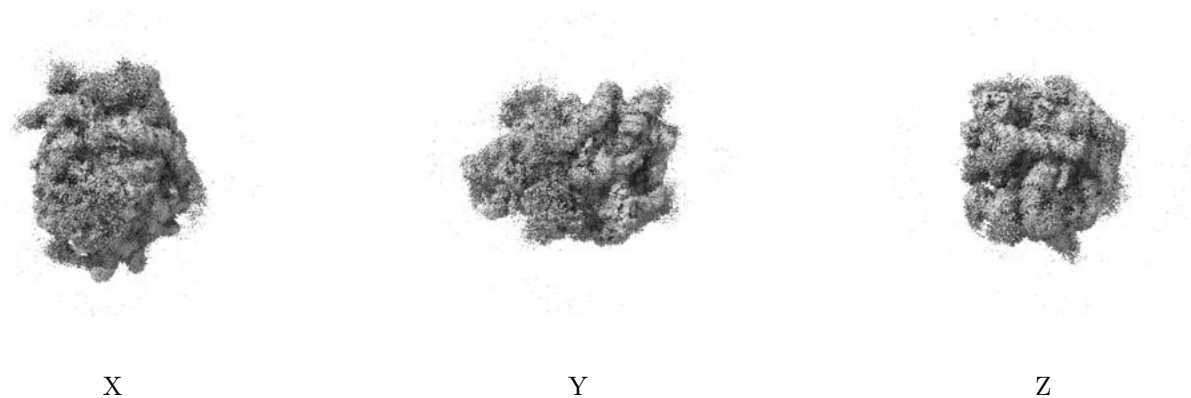


Z

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

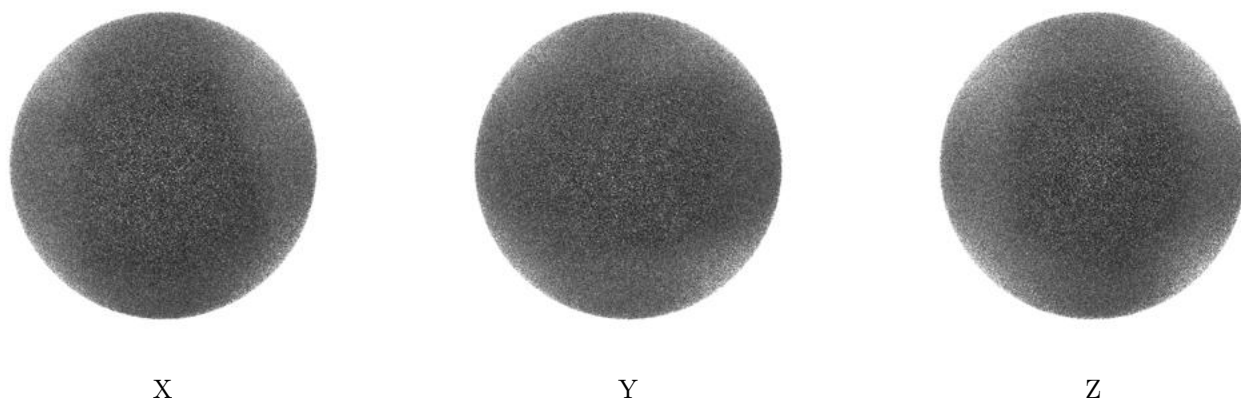
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0055. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

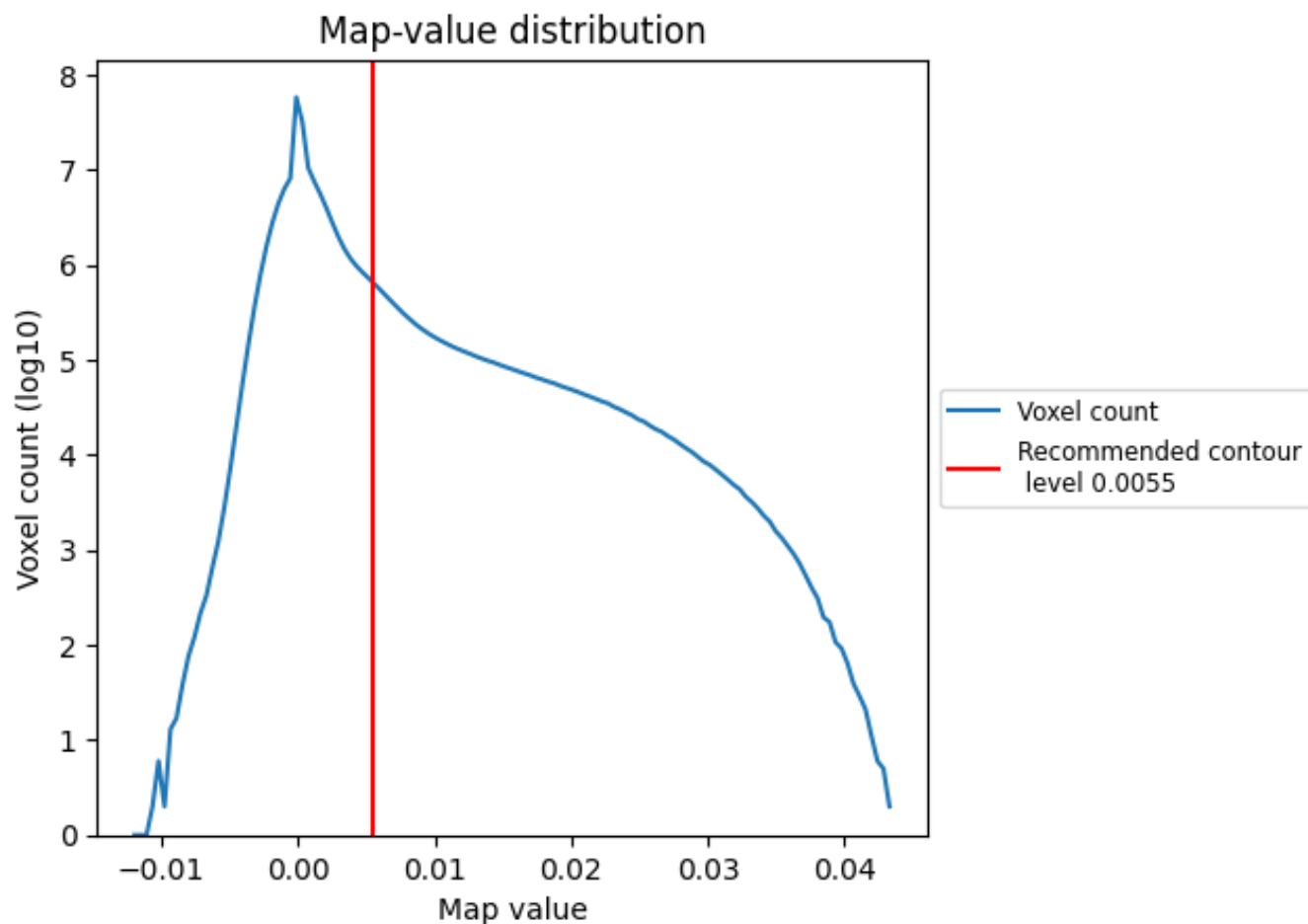
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

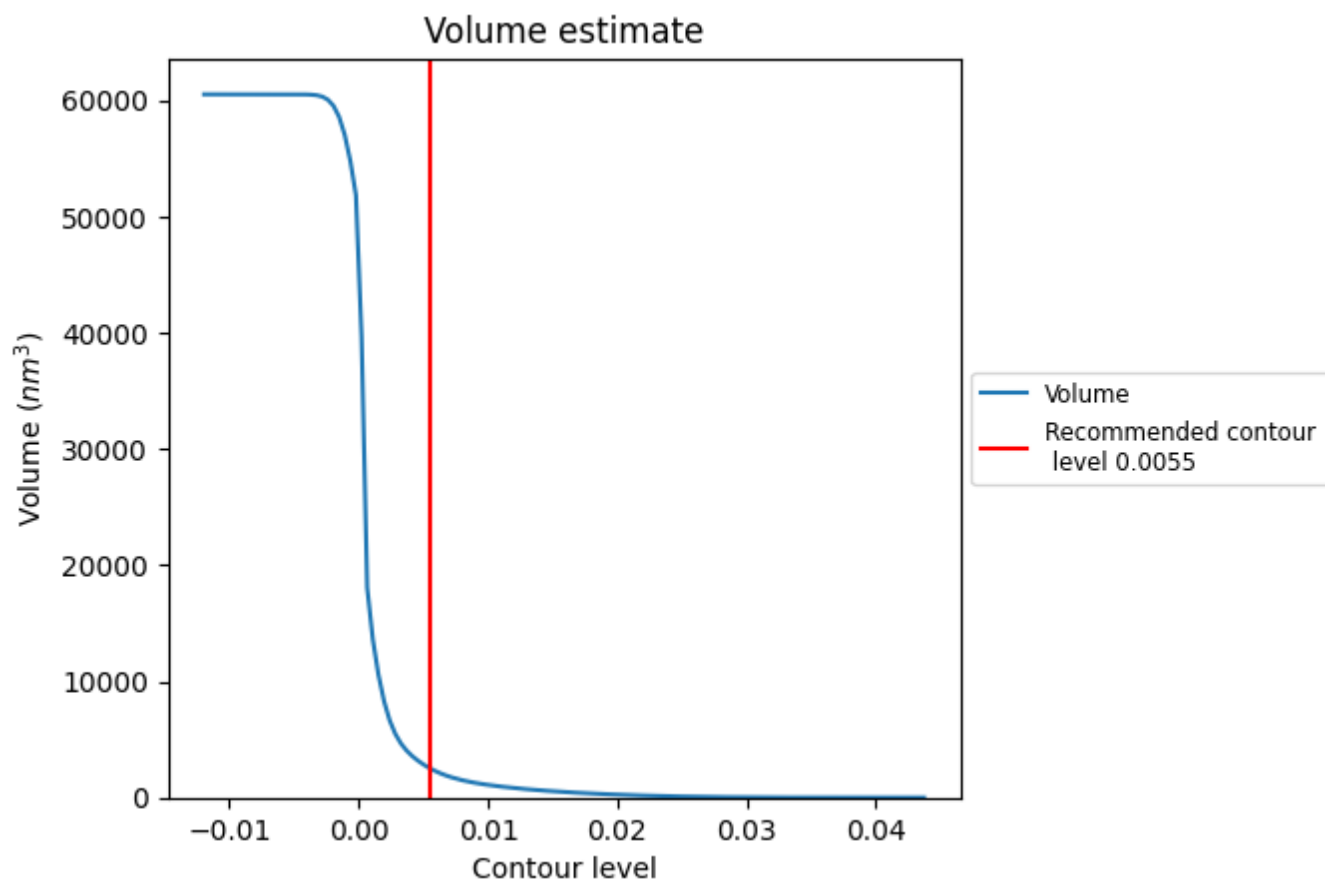
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

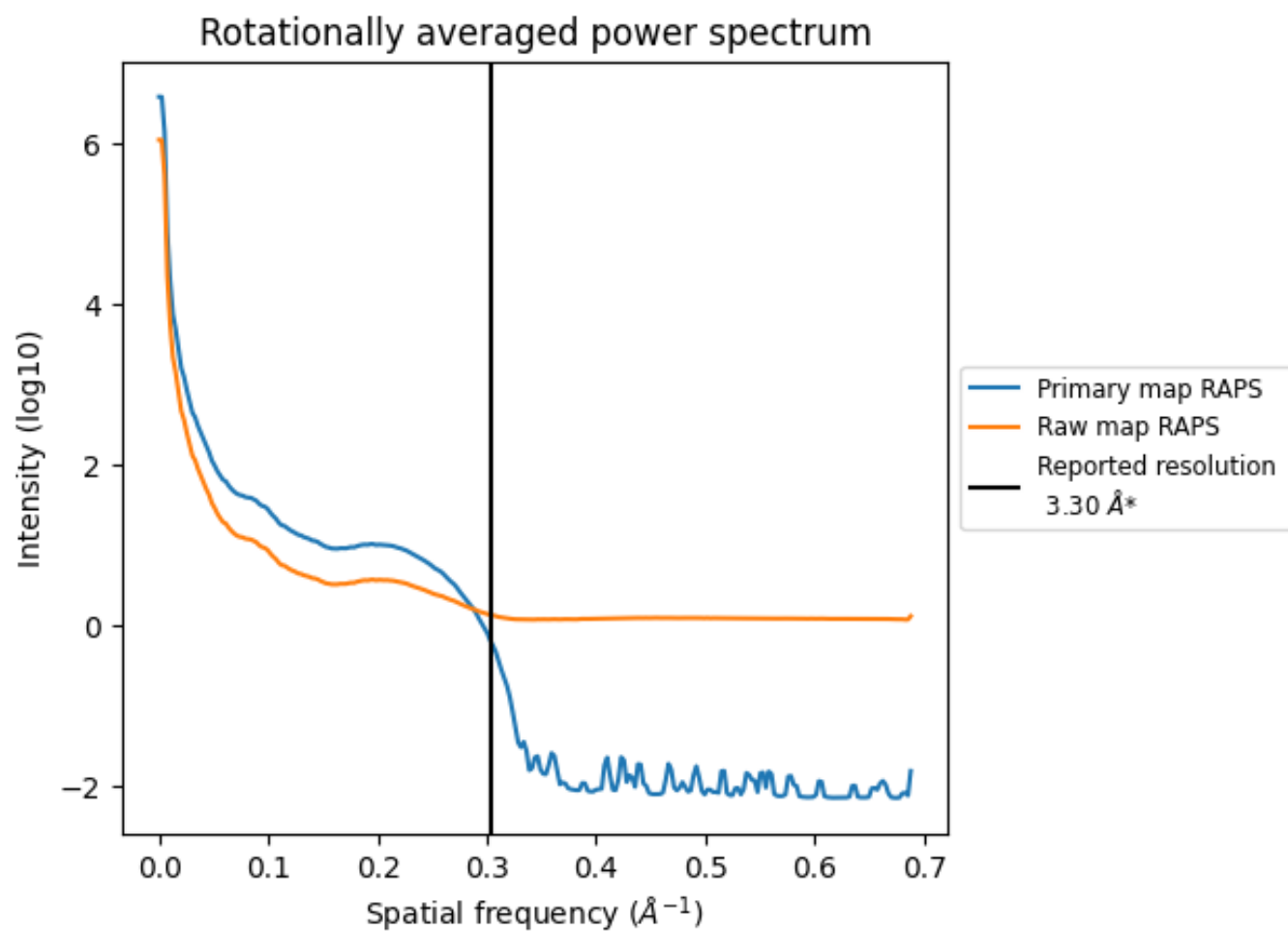
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2529 nm³; this corresponds to an approximate mass of 2284 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

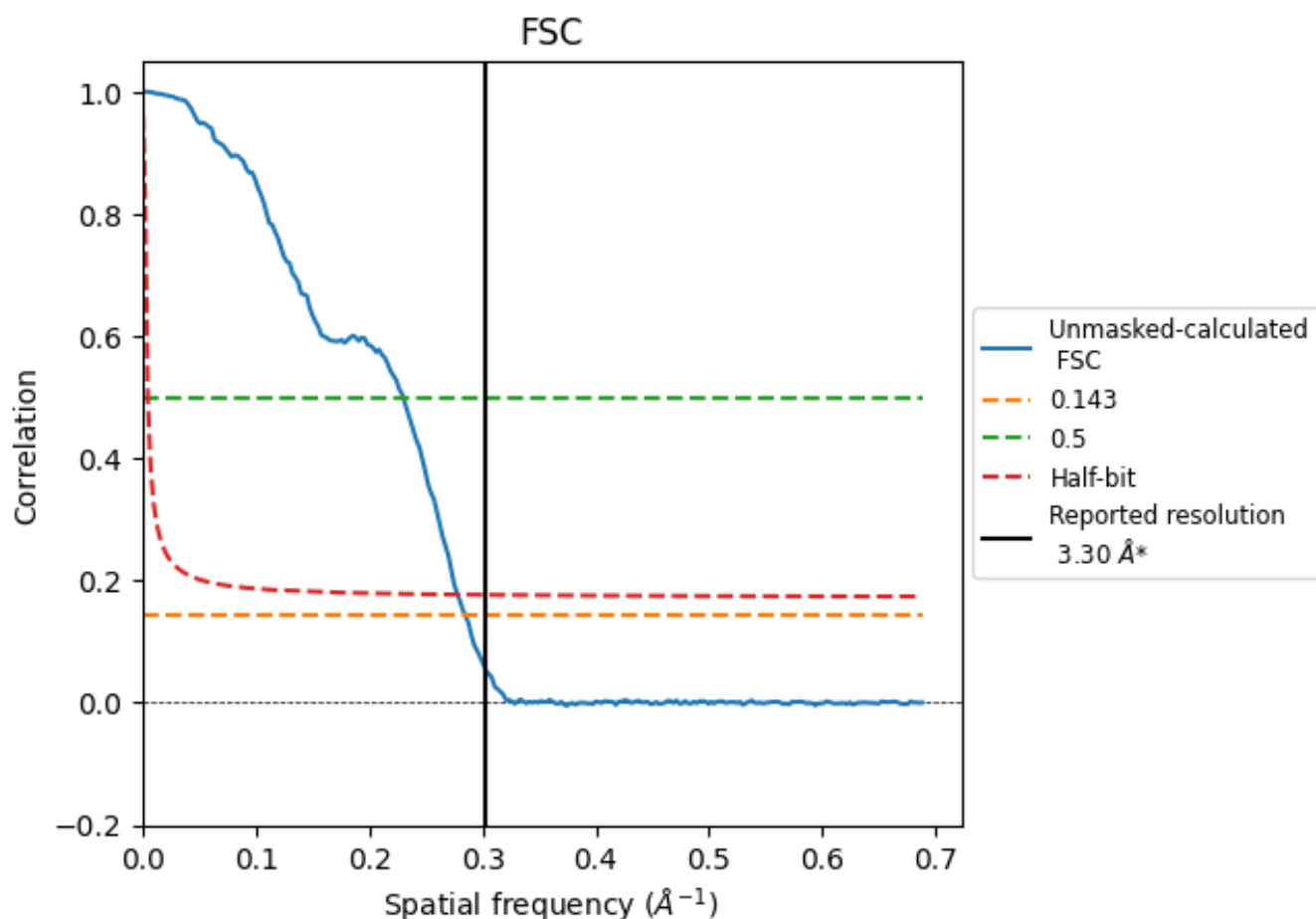


*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

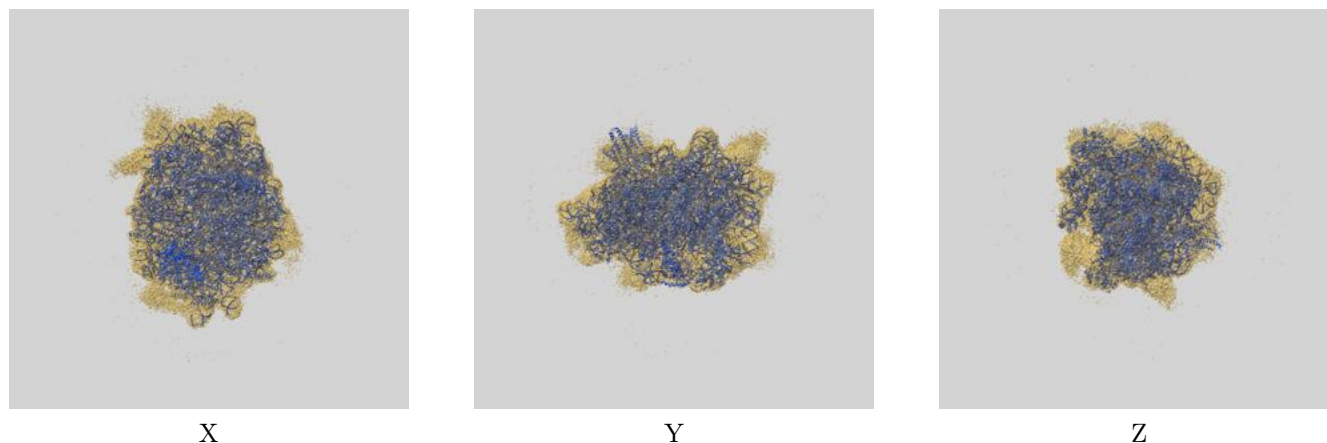
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.51	4.35	3.60

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

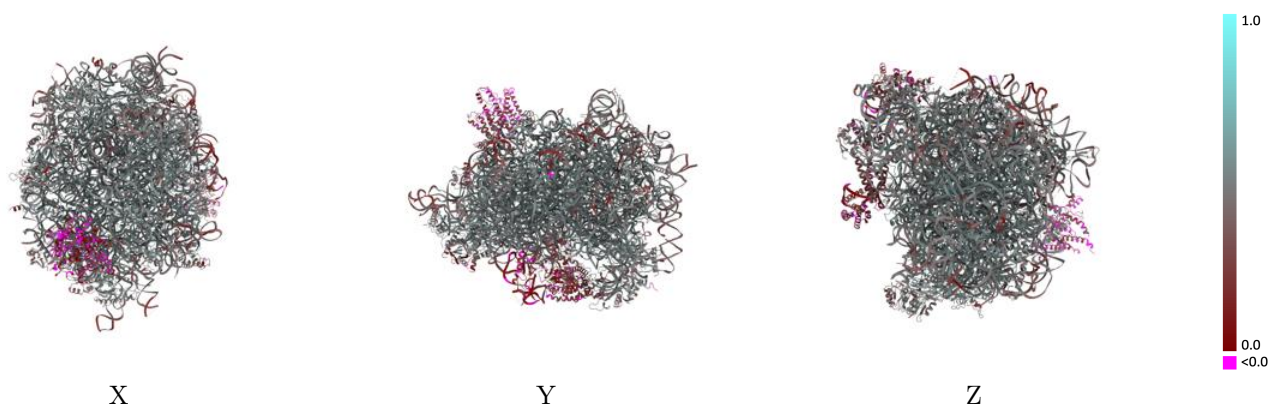
This section contains information regarding the fit between EMDB map EMD-16908 and PDB model 8OJ8. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



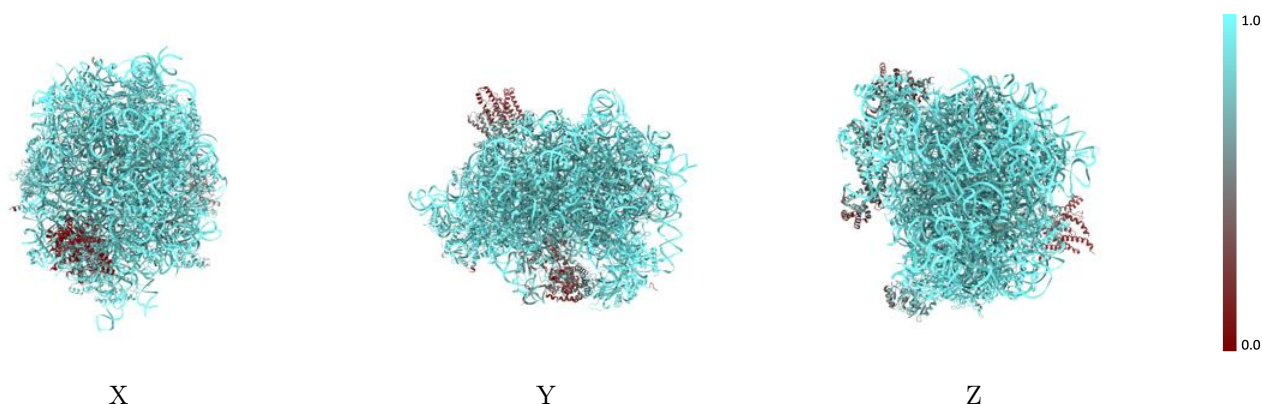
The images above show the 3D surface view of the map at the recommended contour level 0.0055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



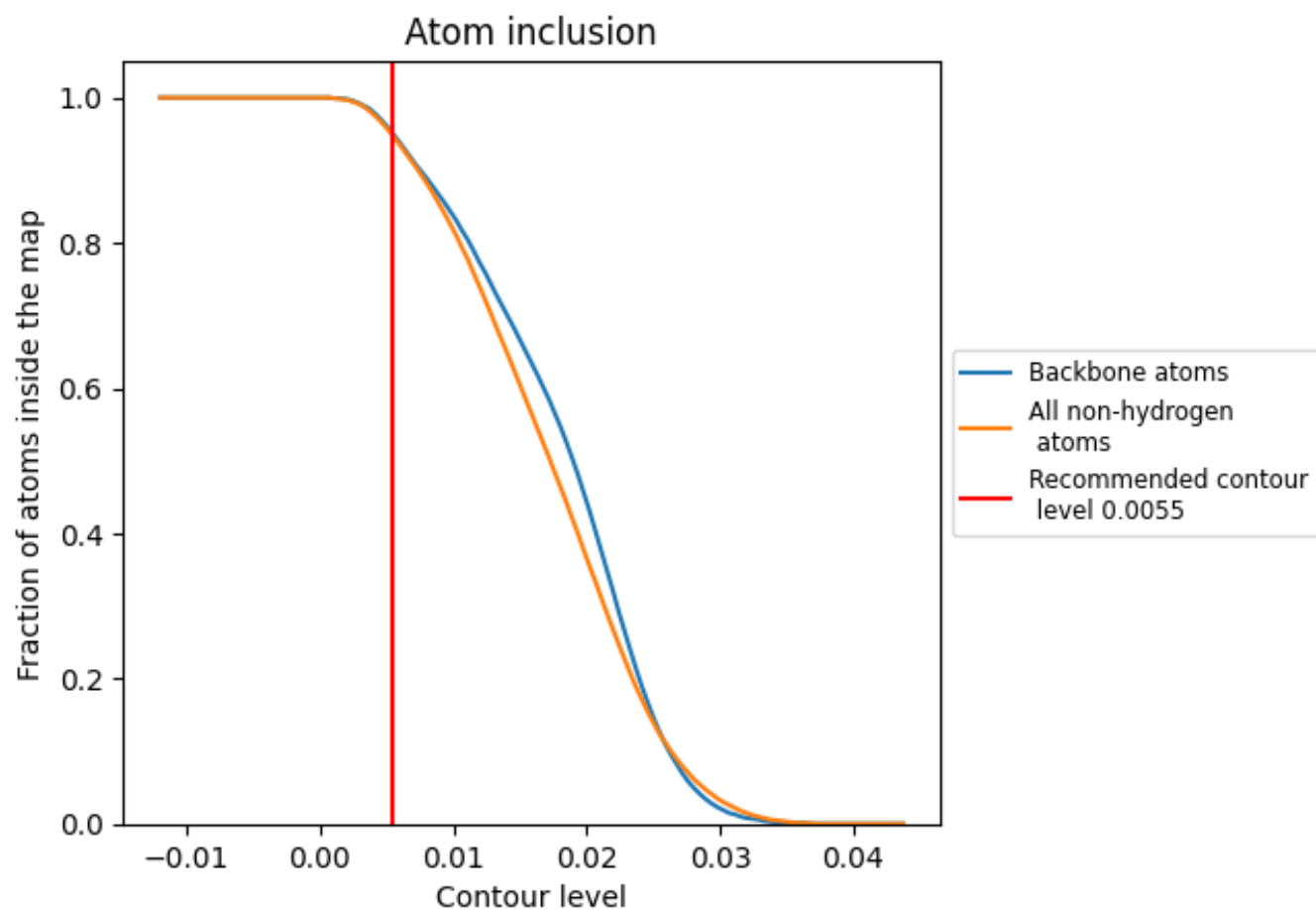
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0055).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 95% 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 (0.0055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9470	 0.4680
1	 0.3330	 0.1240
2	 0.4320	 0.1650
3	 0.0130	 0.0300
5	 0.9930	 0.4760
7	 0.9980	 0.4980
8	 0.9920	 0.4990
A	 0.4900	 0.2220
K	 0.6820	 0.4190
LA	 0.9890	 0.5340
LB	 0.9770	 0.5140
LC	 0.9850	 0.5220
LD	 0.9760	 0.4900
LE	 0.9880	 0.5050
LF	 0.9930	 0.5190
LG	 0.9450	 0.4640
LH	 0.9800	 0.4980
LI	 0.9840	 0.5150
LJ	 0.9420	 0.4440
LL	 0.9850	 0.5210
LM	 0.9850	 0.5150
LN	 0.9980	 0.5490
LO	 0.9820	 0.5130
LP	 0.9910	 0.5300
LQ	 0.9960	 0.5350
LR	 0.9640	 0.4940
LS	 0.9880	 0.5270
LT	 0.9870	 0.5110
LU	 0.9590	 0.4120
LV	 0.9770	 0.5060
LW	 0.9940	 0.5170
LX	 0.9850	 0.5190
LY	 0.9930	 0.5190
LZ	 0.9760	 0.4900
La	 0.9890	 0.5380



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Chain	Atom inclusion	Q-score
Lb	 0.9620	 0.4630
Lc	 0.9590	 0.4740
Ld	 0.9650	 0.4950
Le	 0.9970	 0.5350
Lf	 0.9950	 0.5430
Lg	 0.9710	 0.5060
Lh	 0.9820	 0.4990
Li	 0.9750	 0.4980
Lj	 0.9960	 0.5450
Lk	 0.9120	 0.4460
Ll	 0.9880	 0.5300
Lm	 0.9760	 0.5010
Lo	 0.9690	 0.5240
Lp	 0.9800	 0.4950
Lr	 0.9930	 0.5280
Lz	 0.4790	 0.1970