



## wwPDB EM Validation Summary Report ⓘ

Apr 7, 2025 – 01:41 PM EDT

PDB ID : 8UJD / pdb\_00008ujd  
EMDB ID : EMD-42319  
Title : In situ human 60S ribosome with eIF6  
Authors : Wei, Z.; Yong, X.  
Deposited on : 2023-10-11  
Resolution : 2.96 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev117  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

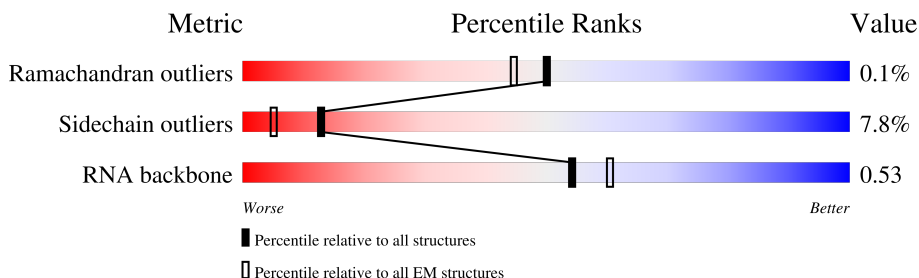
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.96 Å.

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




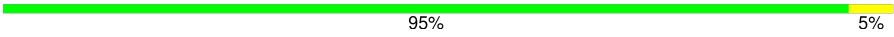
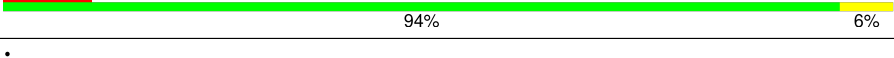
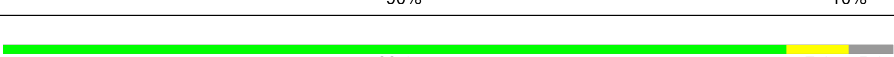
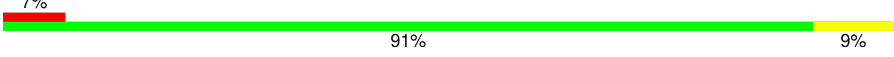
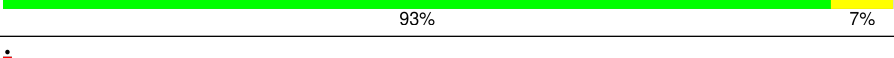
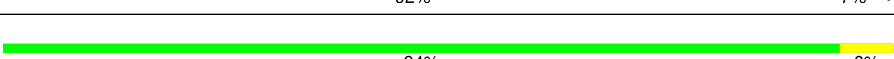
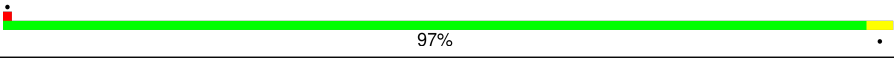
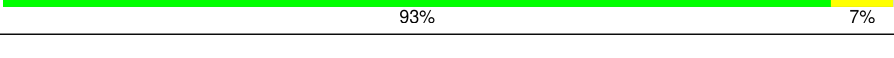
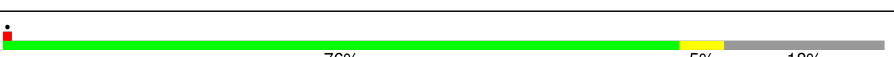
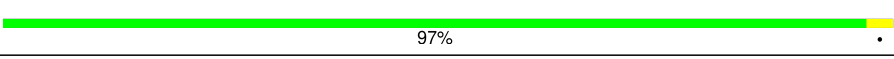
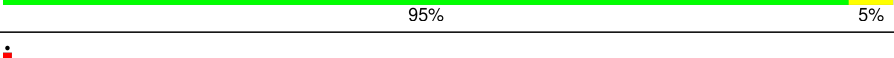
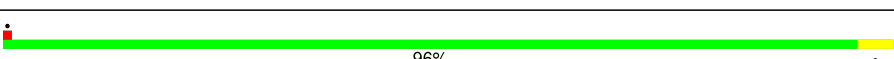
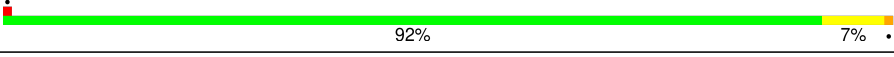
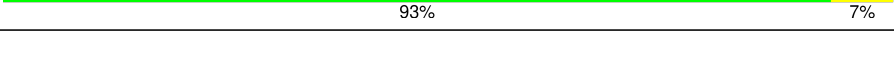
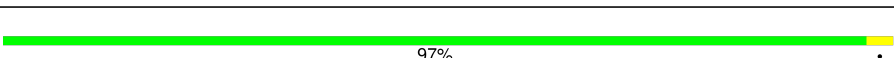
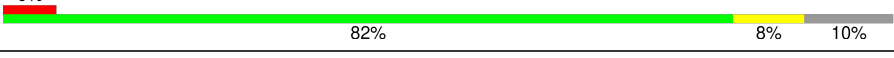
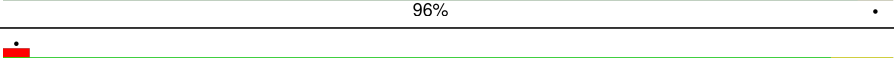
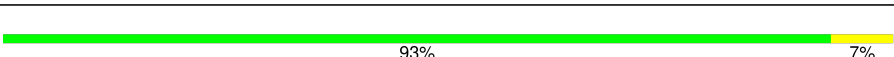



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	LW	118	<div> <div>24%</div> <div>48%</div> <div>5%</div> <div>47%</div> </div>
2	L5	5070	<div> <div>56%</div> <div>15%</div> <div>28%</div> </div>
3	L7	120	<div> <div>90%</div> <div>10%</div> </div>
4	L8	156	<div> <div>83%</div> <div>17%</div> </div>
5	LA	248	<div> <div>94%</div> <div>5%</div> </div>
6	LB	402	<div> <div>94%</div> <div>6%</div> </div>
7	LC	368	<div> <div>95%</div> <div>5%</div> </div>
8	LD	293	<div> <div>91%</div> <div>9%</div> </div>

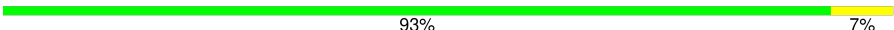

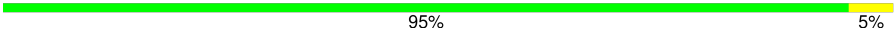





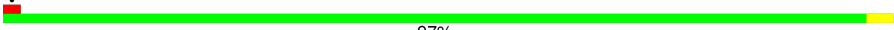


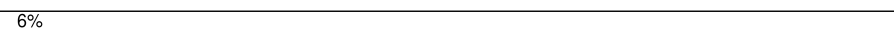

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Mol	Chain	Length	Quality of chain
9	LE	242	
10	LF	225	
11	LG	241	
12	LH	190	
13	LI	213	
14	LJ	176	
15	LL	210	
16	LM	139	
17	LN	203	
18	LO	201	
19	LP	153	
20	LQ	187	
21	LR	187	
22	LS	175	
23	LT	159	
24	LU	101	
25	LV	131	
26	LX	120	
27	LY	134	
28	LZ	135	
29	La	147	
30	Lb	121	
31	Lc	98	
32	Ld	107	
33	Le	128	

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Mol	Chain	Length	Quality of chain
34	Lf	109	 93% 7%
35	Lg	114	 89% 11%
36	Lh	122	 95% 5%
37	Li	102	 92% 8%
38	Lj	86	 93% 7%
39	Lk	69	 87% 13%
40	Ll	50	 92% 8%
41	Lm	52	 96% 4%
42	Lo	105	 97% 3%
43	Lp	91	 92% 8%
44	Lr	125	 82% 18%
45	P	225	 6% 86% 14%
46	CA	356	 43% 94% 6%

## 2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 141127 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 Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LW	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	?	-	SER	deletion	UNP A0A994J4A5
LW	?	-	GLU	deletion	UNP A0A994J4A5
LW	?	-	GLU	deletion	UNP A0A994J4A5
LW	?	-	ILE	deletion	UNP A0A994J4A5
LW	?	-	GLN	deletion	UNP A0A994J4A5
LW	?	-	LYS	deletion	UNP A0A994J4A5

- Molecule 2 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L5	3649	Total	C	N	O	P	0	0
			78229	34837	14317	25427	3648		

- Molecule 3 is a RNA chain called 5S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 4 is a RNA chain called 5.8S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 5 is a protein called 60S ribosomal protein L8.

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

- Molecule 6 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 7 is a protein called 60S ribosomal protein L4.

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

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 10 is a protein called 60S ribosomal protein L7.

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

- Molecule 11 is a protein called 60S ribosomal protein L7a.

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

- Molecule 12 is a protein called 60S ribosomal protein L9.

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

- Molecule 13 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

- Molecule 14 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 15 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 16 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 17 is a protein called 60S ribosomal protein L15.

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

- Molecule 18 is a protein called 60S ribosomal protein L13a.

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

- Molecule 19 is a protein called 60S ribosomal protein L17.

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

- Molecule 20 is a protein called 60S ribosomal protein L18.

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

- Molecule 21 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LR	153	Total	C	N	O	S	0	0
			1281	799	276	197	9		

- Molecule 22 is a protein called 60S ribosomal protein L18a.

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

- Molecule 23 is a protein called 60S ribosomal protein L21.

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

- Molecule 24 is a protein called Heparin-binding protein HBp15.

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

- Molecule 25 is a protein called 60S ribosomal protein L23.

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

- Molecule 26 is a protein called 60S ribosomal protein L23a.



Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 27 is a protein called 60S ribosomal protein L26.

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

- Molecule 28 is a protein called 60S ribosomal protein L27.

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

- Molecule 29 is a protein called 60S ribosomal protein L27a.

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

- Molecule 30 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 31 is a protein called 60S ribosomal protein L30.

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

- Molecule 32 is a protein called 60S ribosomal protein L31.

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

- Molecule 33 is a protein called 60S ribosomal protein L32.

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

- Molecule 34 is a protein called 60S ribosomal protein L35a.

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

- Molecule 35 is a protein called 60S ribosomal protein L34.

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

- Molecule 36 is a protein called 60S ribosomal protein L35.

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

- Molecule 37 is a protein called 60S ribosomal protein L36.

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

- Molecule 38 is a protein called 60S ribosomal protein L37.

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

- Molecule 39 is a protein called 60S ribosomal protein L38.

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

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 42 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 43 is a protein called 60S ribosomal protein L37a.

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

- Molecule 44 is a protein called 60S ribosomal protein L28.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	P	225	Total	C	N	O	S	0	0
			1712	1065	295	340	12		

- Molecule 46 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	CA	354	Total	C	N	O	S	4	0
			2764	1744	475	528	17		

- Molecule 47 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
47	L5	214	Total 214	Mg 214	0
47	L7	3	Total 3	Mg 3	0
47	L8	4	Total 4	Mg 4	0
47	LA	1	Total 1	Mg 1	0
47	LP	1	Total 1	Mg 1	0
47	LV	1	Total 1	Mg 1	0
47	Le	1	Total 1	Mg 1	0
47	Lg	1	Total 1	Mg 1	0

- Molecule 48 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

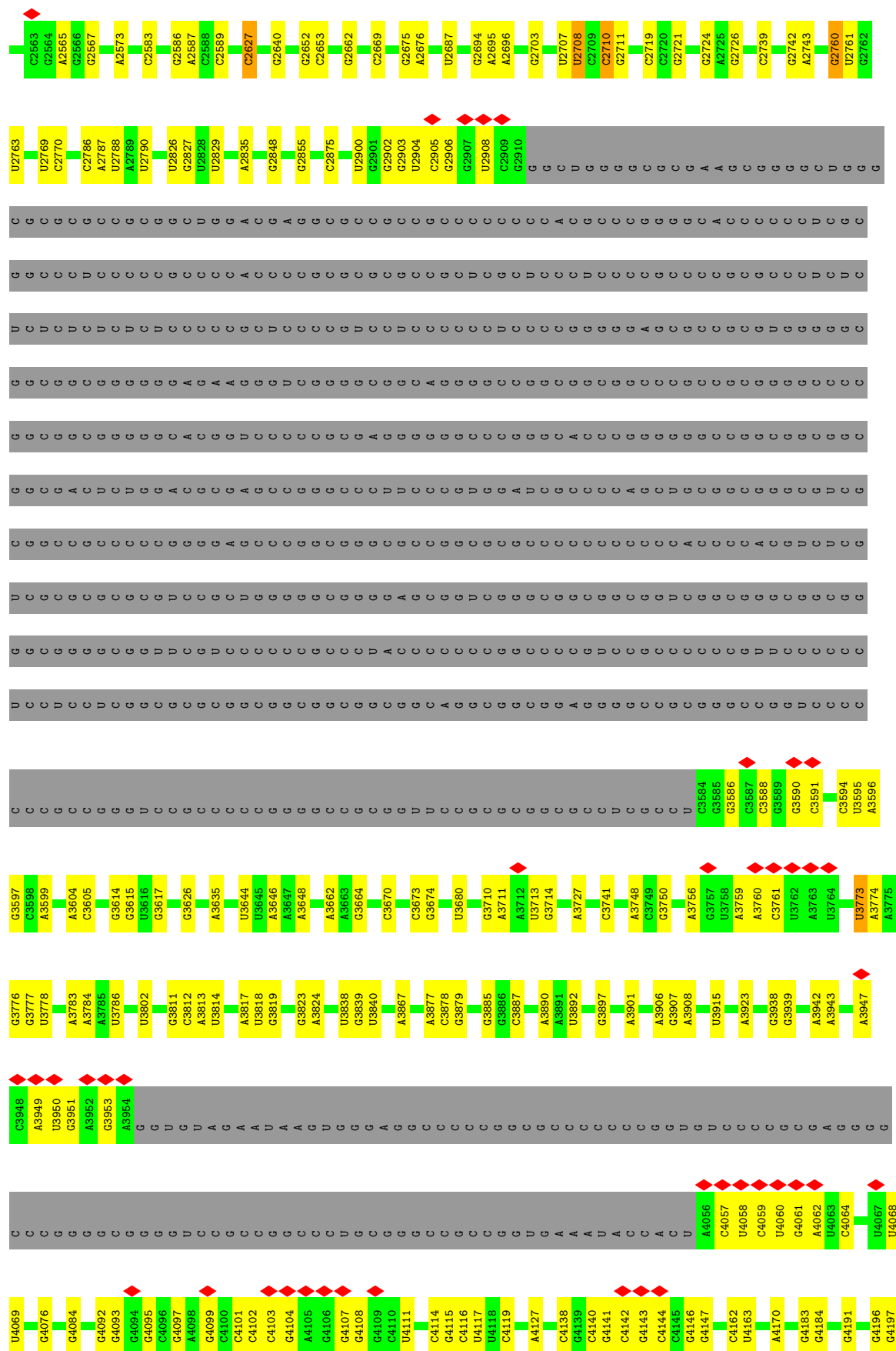
Mol	Chain	Residues	Atoms		AltConf
48	Lg	1	Total 1	Zn 1	0
48	Lj	1	Total 1	Zn 1	0
48	Lm	1	Total 1	Zn 1	0
48	Lo	1	Total 1	Zn 1	0
48	Lp	1	Total 1	Zn 1	0

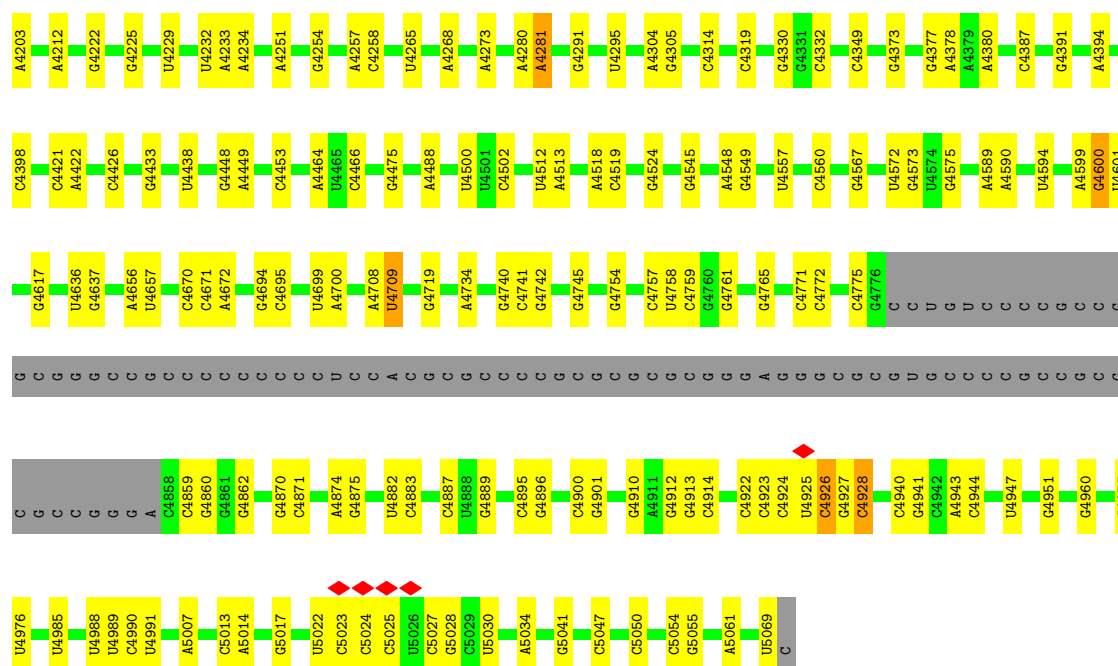
- Molecule 49 is water.

Mol	Chain	Residues	Atoms		AltConf
49	P	1	Total 1	O 1	0

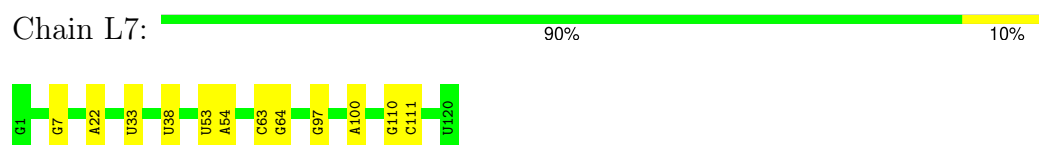




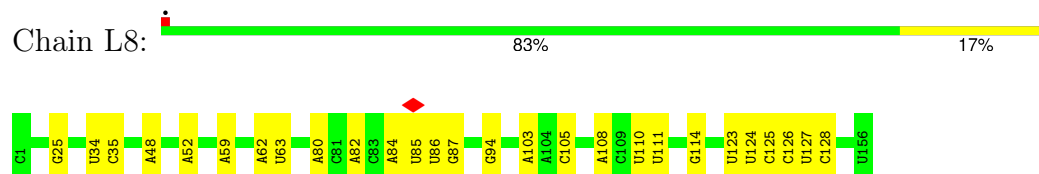




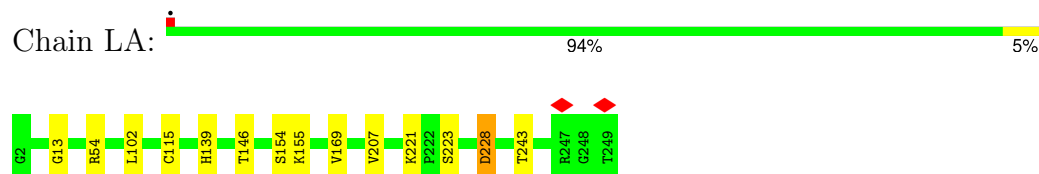
• Molecule 3: 5S rRNA [Homo sapiens]



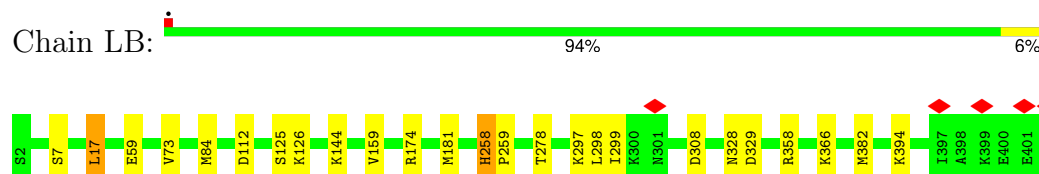
• Molecule 4: 5.8S rRNA [Homo sapiens]



• Molecule 5: 60S ribosomal protein L8



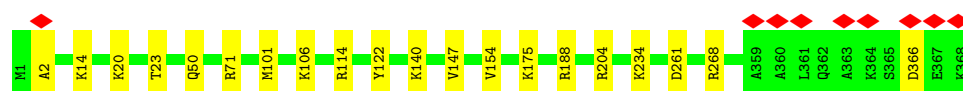
• Molecule 6: Large ribosomal subunit protein uL3



• Molecule 7: 60S ribosomal protein L4



Chain LC:  95% 5%




- Molecule 8: Large ribosomal subunit protein uL18

Chain LD:  91% 9%



- Molecule 9: 60S ribosomal protein L6

Chain LE:  6% 90% 7%



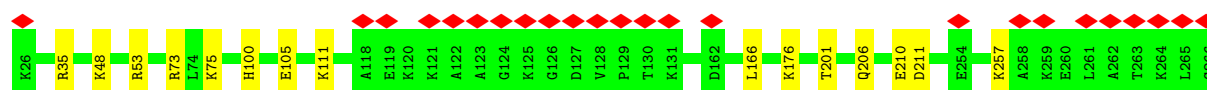
- Molecule 10: 60S ribosomal protein L7

Chain LF:  95% 5%



- Molecule 11: 60S ribosomal protein L7a

Chain LG:  10% 94% 6%



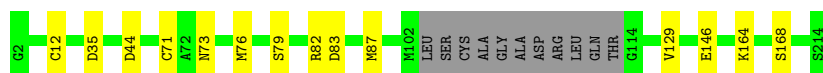
- Molecule 12: 60S ribosomal protein L9

Chain LH:  90% 10%

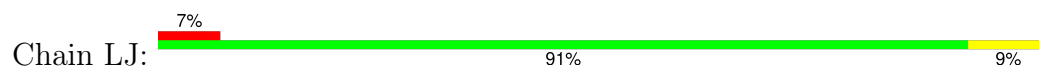


- Molecule 13: Ribosomal protein uL16-like

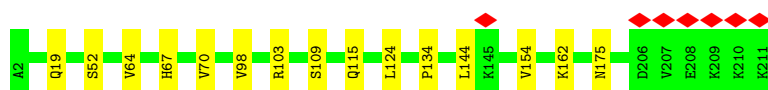
Chain LI:  88% 7% 5%



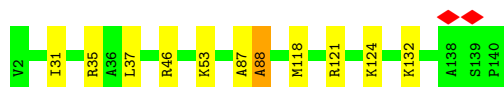
- Molecule 14: 60S ribosomal protein L11



- Molecule 15: Large ribosomal subunit protein eL13



- Molecule 16: 60S ribosomal protein L14



- Molecule 17: 60S ribosomal protein L15



- Molecule 18: 60S ribosomal protein L13a



- Molecule 19: 60S ribosomal protein L17




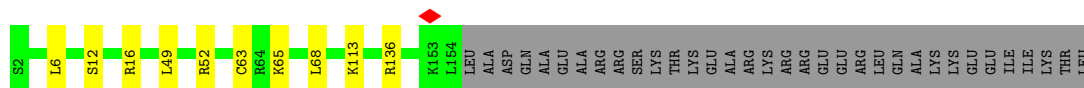
- Molecule 20: 60S ribosomal protein L18

Chain LQ:  95% 5% •



- Molecule 21: 60S ribosomal protein L19

Chain LR:  76% 5% 18%



- Molecule 22: 60S ribosomal protein L18a

Chain LS:  97% •




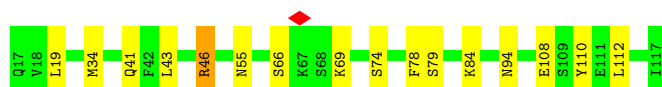
- Molecule 23: 60S ribosomal protein L21

Chain LT:  95% 5%



- Molecule 24: Heparin-binding protein HBp15

Chain LU:  84% 15% •



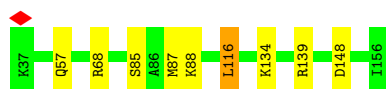
- Molecule 25: 60S ribosomal protein L23

Chain LV:  96% •



- Molecule 26: 60S ribosomal protein L23a

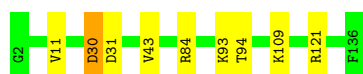
Chain LX:  92% 7% •



## • Molecule 27: 60S ribosomal protein L26

Chain LY:  93% 7%


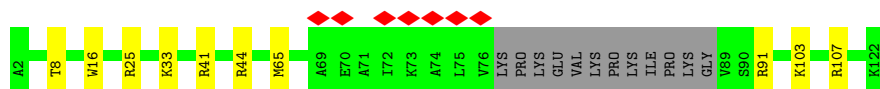
## • Molecule 28: 60S ribosomal protein L27

Chain LZ:  93% 6%

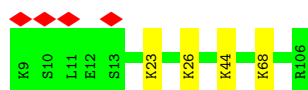
## • Molecule 29: 60S ribosomal protein L27a

Chain La:  97%

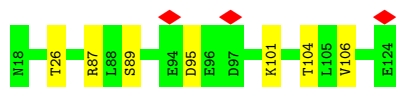
## • Molecule 30: Large ribosomal subunit protein eL29

Chain Lb:  6% 82% 8% 10%

## • Molecule 31: 60S ribosomal protein L30

Chain Lc:  96%

## • Molecule 32: 60S ribosomal protein L31

Chain Ld:  93% 7%

## • Molecule 33: 60S ribosomal protein L32

Chain Le:  93% 7%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf: 93% 7%



- Molecule 35: 60S ribosomal protein L34

Chain Lg: 89% 11%



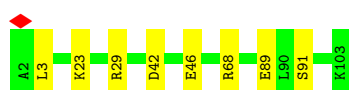
- Molecule 36: 60S ribosomal protein L35

Chain Lh: 95% 5%



- Molecule 37: 60S ribosomal protein L36

Chain Li: 92% 8%



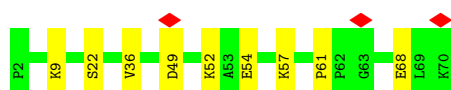
- Molecule 38: 60S ribosomal protein L37

Chain Lj: 93% 7%



- Molecule 39: 60S ribosomal protein L38

Chain Lk: 87% 13%



- Molecule 40: 60S ribosomal protein L39

Chain Ll: 92% 8%



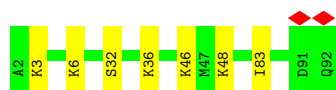
- Molecule 41: Large ribosomal subunit protein eL40



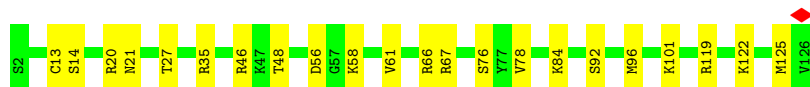
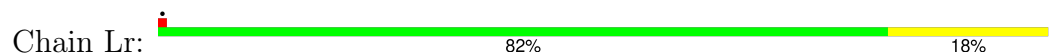
- Molecule 42: 60S ribosomal protein L36a



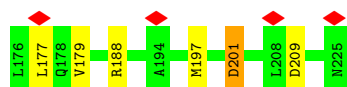
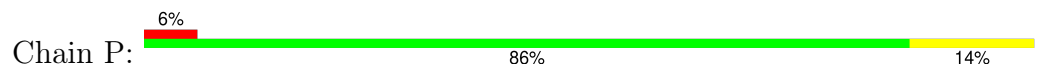
- Molecule 43: 60S ribosomal protein L37a



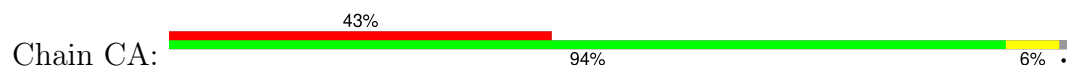
- Molecule 44: 60S ribosomal protein L28

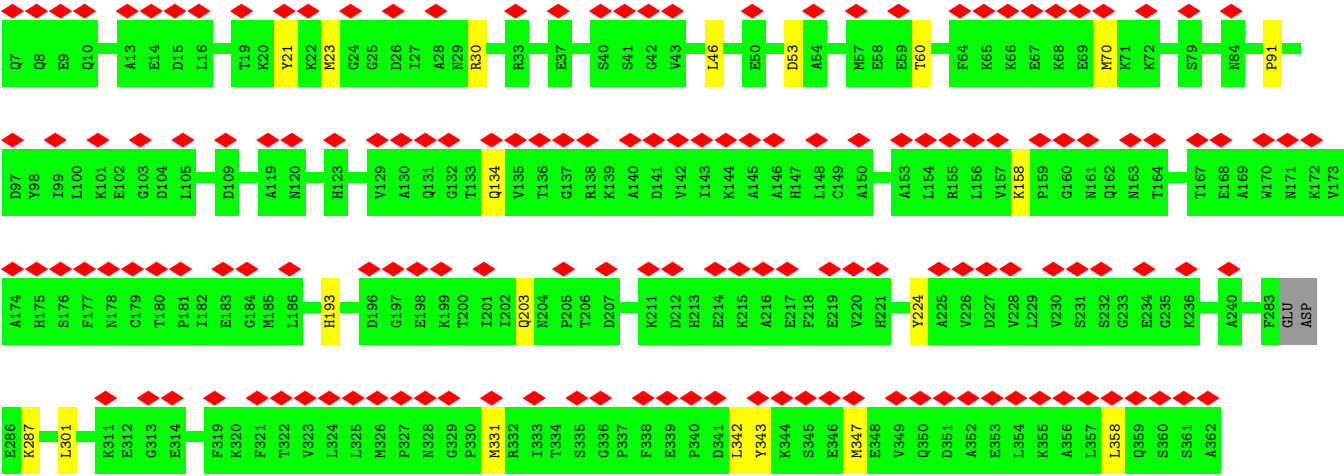


- Molecule 45: Eukaryotic translation initiation factor 6



- Molecule 46: Proliferation-associated protein 2G4





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	132478	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.629	Depositor
Minimum map value	-0.281	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.065	Depositor
Map size ( $\text{\AA}$ )	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.068, 1.068, 1.068	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	LW	0.32	0/541	0.60	0/720
2	L5	0.50	0/87512	0.87	104/136518 (0.1%)
3	L7	0.48	0/2861	0.81	0/4459
4	L8	0.50	0/3701	0.81	2/5766 (0.0%)
5	LA	0.35	0/1936	0.63	1/2596 (0.0%)
6	LB	0.34	0/3306	0.60	2/4424 (0.0%)
7	LC	0.33	0/2981	0.59	1/4002 (0.0%)
8	LD	0.32	0/2428	0.56	1/3252 (0.0%)
9	LE	0.31	0/1942	0.60	0/2606
10	LF	0.35	0/1905	0.58	0/2539
11	LG	0.32	0/1960	0.56	0/2637
12	LH	0.33	0/1537	0.61	1/2066 (0.0%)
13	LI	0.33	0/1673	0.59	0/2233
14	LJ	0.31	0/1433	0.65	0/1915
15	LL	0.34	0/1732	0.65	2/2315 (0.1%)
16	LM	0.33	0/1161	0.57	0/1554
17	LN	0.35	0/1746	0.60	0/2338
18	LO	0.34	0/1682	0.57	0/2250
19	LP	0.33	0/1268	0.54	0/1701
20	LQ	0.35	0/1537	0.63	1/2052 (0.0%)
21	LR	0.30	0/1296	0.62	1/1713 (0.1%)
22	LS	0.36	0/1493	0.61	1/2003 (0.0%)
23	LT	0.36	0/1326	0.61	0/1770
24	LU	0.38	0/839	0.72	1/1126 (0.1%)
25	LV	0.34	0/993	0.59	0/1332
26	LX	0.32	0/1002	0.59	1/1345 (0.1%)
27	LY	0.34	0/1132	0.59	0/1504
28	LZ	0.33	0/1130	0.59	1/1507 (0.1%)
29	La	0.34	0/1191	0.54	0/1591
30	Lb	0.27	0/889	0.58	0/1175
31	Lc	0.36	0/774	0.62	0/1038
32	Ld	0.33	0/903	0.59	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Le	0.36	0/1071	0.61	0/1429
34	Lf	0.37	0/895	0.62	0/1198
35	Lg	0.34	0/916	0.63	0/1220
36	Lh	0.30	0/1023	0.59	0/1351
37	Li	0.29	0/843	0.62	0/1115
38	Lj	0.35	0/720	0.62	0/952
39	Lk	0.34	0/575	0.71	1/761 (0.1%)
40	Ll	0.30	0/454	0.61	0/599
41	Lm	0.30	0/435	0.54	0/575
42	Lo	0.32	0/876	0.59	0/1156
43	Lp	0.33	0/718	0.57	0/953
44	Lr	0.32	0/1017	0.59	0/1364
45	P	0.32	0/1736	0.68	1/2362 (0.0%)
46	CA	0.29	0/2810	0.64	3/3780 (0.1%)
All	All	0.44	0/151899	0.78	125/224078 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	LA	0	1
6	LB	0	2
15	LL	0	1
16	LM	0	2
18	LO	0	1
24	LU	0	1
34	Lf	0	3
38	Lj	0	1
All	All	0	12

There are no bond length outliers.

The worst 5 of 125 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	CA	91	PRO	CA-N-CD	-12.06	94.61	111.50
2	L5	485	C	C2-N1-C1'	11.09	131.00	118.80
15	LL	134	PRO	CA-N-CD	-10.56	96.71	111.50
2	L5	2710	C	N1-C2-O2	10.32	125.09	118.90
2	L5	2710	C	C2-N1-C1'	9.21	128.93	118.80

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	LA	13	GLY	Peptide
6	LB	17	LEU	Peptide
6	LB	258	HIS	Peptide
15	LL	154	VAL	Peptide
16	LM	87	ALA	Peptide

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [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	LW	61/118 (52%)	55 (90%)	6 (10%)	0	100	100
5	LA	246/248 (99%)	220 (89%)	26 (11%)	0	100	100
6	LB	400/402 (100%)	371 (93%)	29 (7%)	0	100	100
7	LC	366/368 (100%)	340 (93%)	26 (7%)	0	100	100
8	LD	291/293 (99%)	274 (94%)	17 (6%)	0	100	100
9	LE	232/242 (96%)	209 (90%)	23 (10%)	0	100	100
10	LF	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
11	LG	239/241 (99%)	223 (93%)	16 (7%)	0	100	100
12	LH	188/190 (99%)	174 (93%)	14 (7%)	0	100	100
13	LI	198/213 (93%)	187 (94%)	11 (6%)	0	100	100
14	LJ	174/176 (99%)	159 (91%)	15 (9%)	0	100	100
15	LL	208/210 (99%)	193 (93%)	15 (7%)	0	100	100
16	LM	137/139 (99%)	126 (92%)	10 (7%)	1 (1%)	19	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	LN	201/203 (99%)	189 (94%)	11 (6%)	1 (0%)	25	50
18	LO	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
19	LP	151/153 (99%)	143 (95%)	8 (5%)	0	100	100
20	LQ	185/187 (99%)	178 (96%)	7 (4%)	0	100	100
21	LR	149/187 (80%)	144 (97%)	5 (3%)	0	100	100
22	LS	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
23	LT	157/159 (99%)	144 (92%)	13 (8%)	0	100	100
24	LU	99/101 (98%)	80 (81%)	19 (19%)	0	100	100
25	LV	129/131 (98%)	122 (95%)	7 (5%)	0	100	100
26	LX	118/120 (98%)	117 (99%)	1 (1%)	0	100	100
27	LY	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
28	LZ	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
29	La	145/147 (99%)	136 (94%)	9 (6%)	0	100	100
30	Lb	105/121 (87%)	99 (94%)	6 (6%)	0	100	100
31	Lc	96/98 (98%)	89 (93%)	7 (7%)	0	100	100
32	Ld	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
33	Le	126/128 (98%)	118 (94%)	8 (6%)	0	100	100
34	Lf	107/109 (98%)	97 (91%)	9 (8%)	1 (1%)	14	35
35	Lg	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
36	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
37	Li	100/102 (98%)	94 (94%)	6 (6%)	0	100	100
38	Lj	84/86 (98%)	78 (93%)	6 (7%)	0	100	100
39	Lk	67/69 (97%)	62 (92%)	5 (8%)	0	100	100
40	Ll	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
41	Lm	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
42	Lo	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
43	Lp	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
44	Lr	123/125 (98%)	115 (94%)	8 (6%)	0	100	100
45	P	223/225 (99%)	209 (94%)	12 (5%)	2 (1%)	14	35
46	CA	350/356 (98%)	330 (94%)	20 (6%)	0	100	100
All	All	6942/7158 (97%)	6499 (94%)	438 (6%)	5 (0%)	50	72

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
45	P	201	ASP
17	LN	124	ASP
16	LM	88	ALA
45	P	32	GLU
34	Lf	107	PRO

### 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	LW	55/97 (57%)	49 (89%)	6 (11%)	5	15
5	LA	190/190 (100%)	177 (93%)	13 (7%)	13	32
6	LB	348/348 (100%)	325 (93%)	23 (7%)	14	33
7	LC	306/306 (100%)	287 (94%)	19 (6%)	15	36
8	LD	246/247 (100%)	220 (89%)	26 (11%)	5	16
9	LE	209/215 (97%)	191 (91%)	18 (9%)	8	23
10	LF	194/194 (100%)	183 (94%)	11 (6%)	17	39
11	LG	203/205 (99%)	188 (93%)	15 (7%)	11	28
12	LH	169/169 (100%)	151 (89%)	18 (11%)	5	15
13	LI	172/180 (96%)	158 (92%)	14 (8%)	9	24
14	LJ	148/148 (100%)	133 (90%)	15 (10%)	6	18
15	LL	176/176 (100%)	163 (93%)	13 (7%)	11	28
16	LM	118/118 (100%)	109 (92%)	9 (8%)	11	27
17	LN	171/171 (100%)	159 (93%)	12 (7%)	12	31
18	LO	173/173 (100%)	167 (96%)	6 (4%)	31	56
19	LP	134/134 (100%)	123 (92%)	11 (8%)	9	24
20	LQ	164/164 (100%)	154 (94%)	10 (6%)	15	36
21	LR	137/166 (82%)	128 (93%)	9 (7%)	14	33
22	LS	156/156 (100%)	152 (97%)	4 (3%)	41	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	LT	139/139 (100%)	131 (94%)	8 (6%)	17	38
24	LU	91/91 (100%)	76 (84%)	15 (16%)	2	4
25	LV	101/101 (100%)	96 (95%)	5 (5%)	20	44
26	LX	108/108 (100%)	99 (92%)	9 (8%)	9	24
27	LY	124/124 (100%)	115 (93%)	9 (7%)	11	29
28	LZ	117/117 (100%)	108 (92%)	9 (8%)	10	27
29	La	120/120 (100%)	116 (97%)	4 (3%)	33	58
30	Lb	88/101 (87%)	78 (89%)	10 (11%)	4	14
31	Lc	83/83 (100%)	79 (95%)	4 (5%)	21	46
32	Ld	98/98 (100%)	91 (93%)	7 (7%)	12	31
33	Le	114/114 (100%)	105 (92%)	9 (8%)	10	25
34	Lf	88/88 (100%)	84 (96%)	4 (4%)	23	48
35	Lg	98/98 (100%)	86 (88%)	12 (12%)	4	12
36	Lh	109/109 (100%)	103 (94%)	6 (6%)	18	41
37	Li	86/86 (100%)	78 (91%)	8 (9%)	7	20
38	Lj	73/73 (100%)	68 (93%)	5 (7%)	13	32
39	Lk	64/64 (100%)	56 (88%)	8 (12%)	3	11
40	Ll	47/47 (100%)	43 (92%)	4 (8%)	8	23
41	Lm	48/48 (100%)	46 (96%)	2 (4%)	25	50
42	Lo	93/93 (100%)	90 (97%)	3 (3%)	34	59
43	Lp	74/74 (100%)	67 (90%)	7 (10%)	7	19
44	Lr	109/109 (100%)	87 (80%)	22 (20%)	1	2
45	P	195/195 (100%)	165 (85%)	30 (15%)	2	6
46	CA	303/305 (99%)	286 (94%)	17 (6%)	17	40
All	All	6039/6142 (98%)	5570 (92%)	469 (8%)	13	26

5 of 469 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	LQ	28	LEU
45	P	162	HIS
26	LX	134	LYS
45	P	116	LEU
43	Lp	83	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
17	LN	8	GLN
21	LR	134	ASN
45	P	145	GLN
45	P	68	HIS
11	LG	46	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	L5	3638/5070 (71%)	768 (21%)	18 (0%)
3	L7	119/120 (99%)	12 (10%)	0
4	L8	155/156 (99%)	26 (16%)	0
All	All	3912/5346 (73%)	806 (20%)	18 (0%)

5 of 806 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	L5	2	G
2	L5	17	A
2	L5	25	A
2	L5	26	C
2	L5	30	C

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L5	3673	C
2	L5	4913	G
2	L5	4699	U
2	L5	2416	G
2	L5	3614	G

## 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 [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 231 ligands modelled in this entry, 231 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
21	LR	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	LR	134:ASN	C	135:LYS	N	2.96



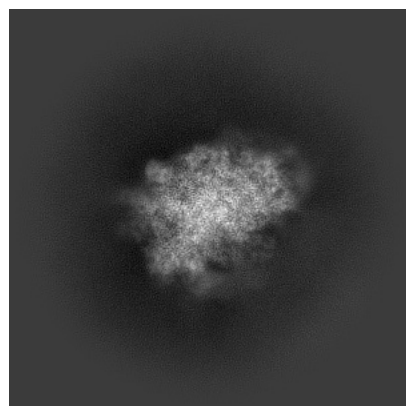
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42319. These allow visual inspection of the internal detail of the map and identification of artifacts.

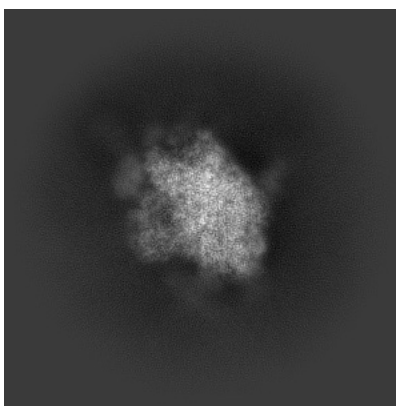
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

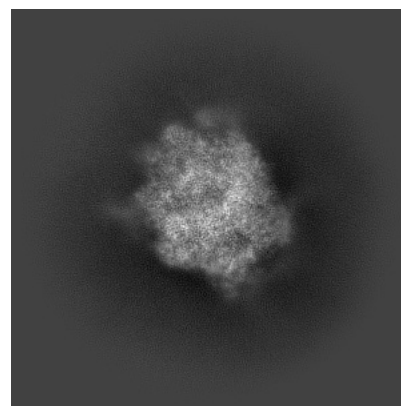
#### 6.1.1 Primary map



X

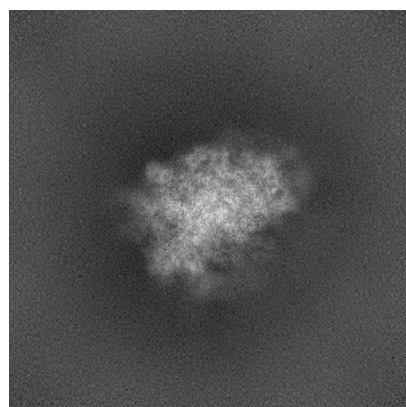


Y

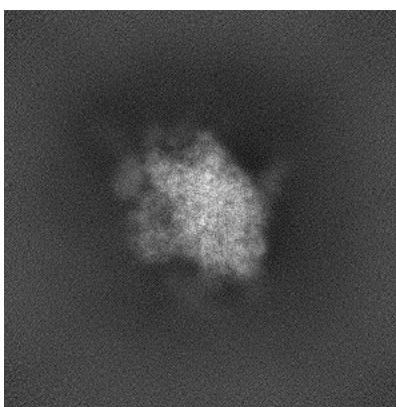


Z

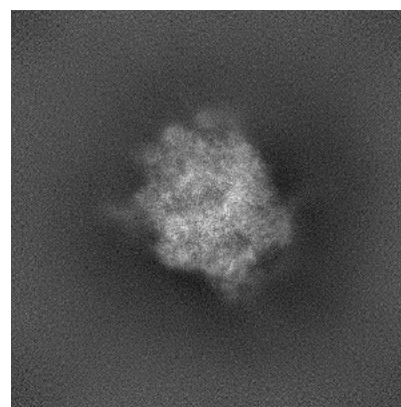
#### 6.1.2 Raw map



X



Y

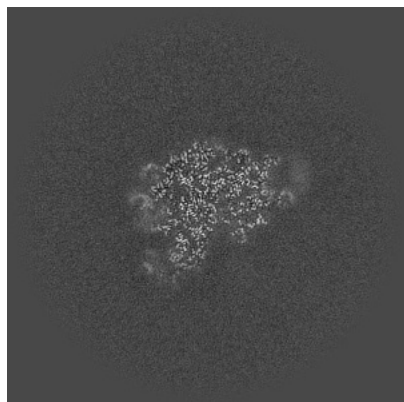


Z

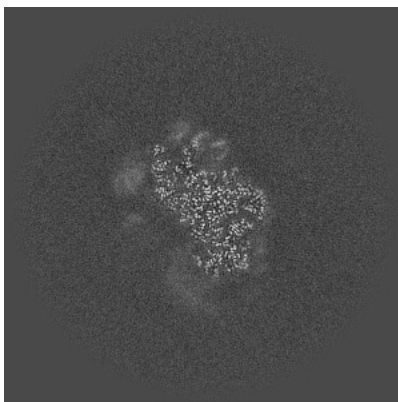
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

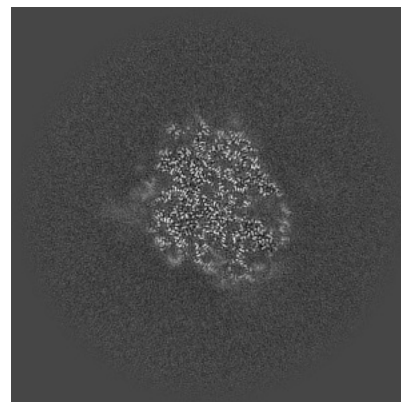
### 6.2.1 Primary map



X Index: 256

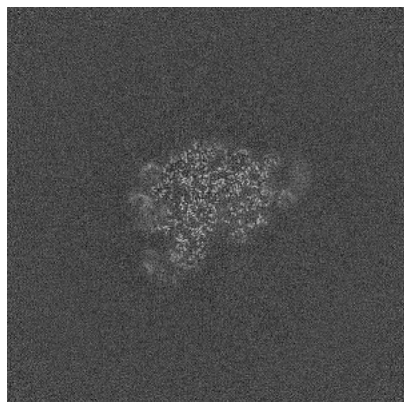


Y Index: 256

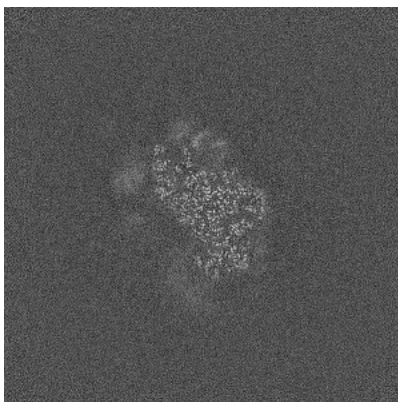


Z Index: 256

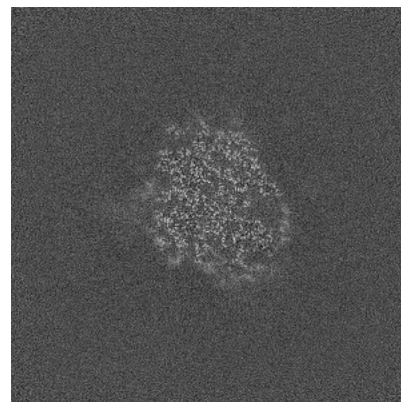
### 6.2.2 Raw map



X Index: 256



Y Index: 256

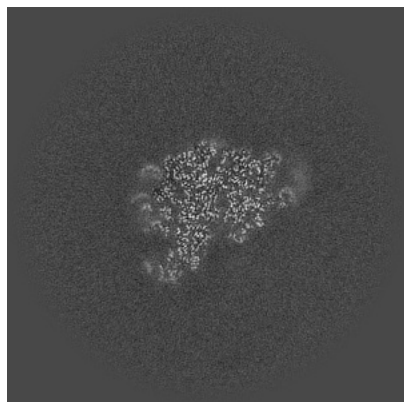


Z Index: 256

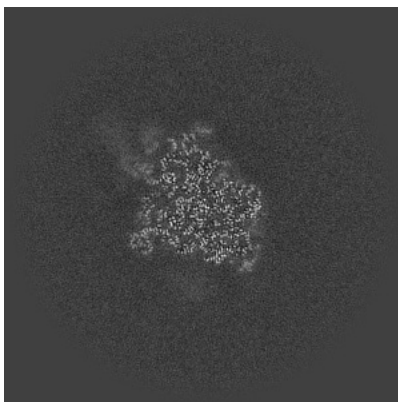
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

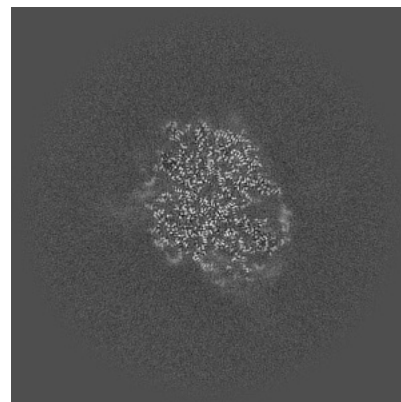
### 6.3.1 Primary map



X Index: 253

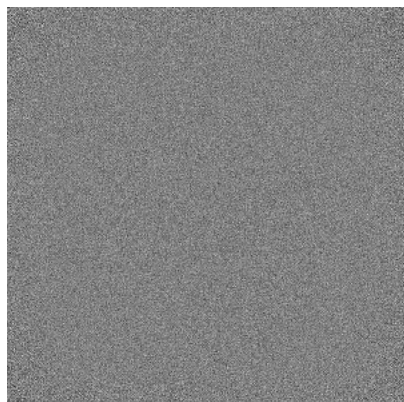


Y Index: 233

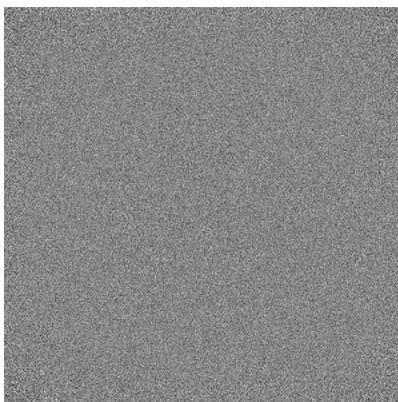


Z Index: 258

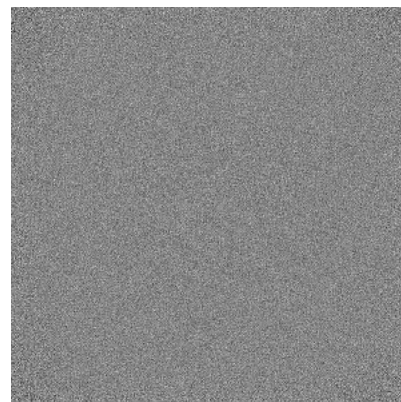
### 6.3.2 Raw map



X Index: 0



Y Index: 0



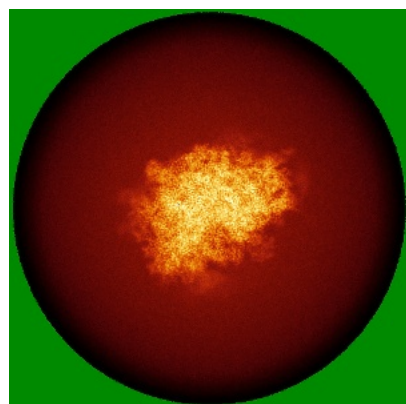
Z Index: 0

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

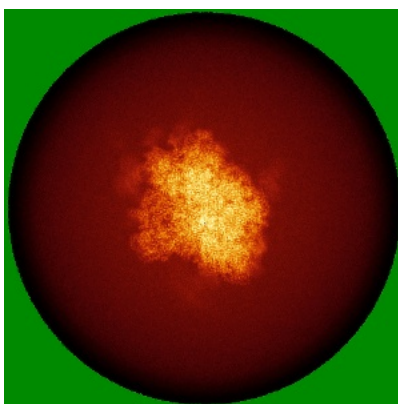


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

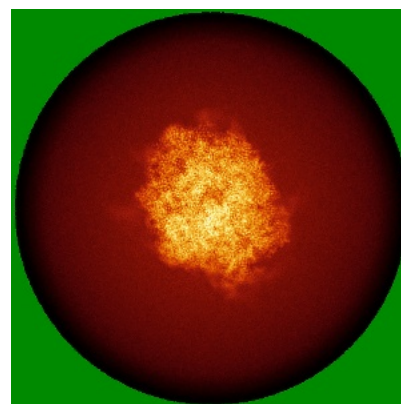
### 6.4.1 Primary map



X

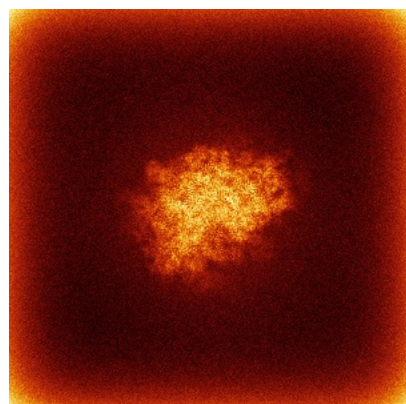


Y

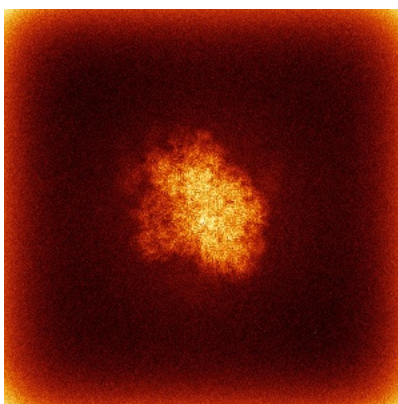


Z

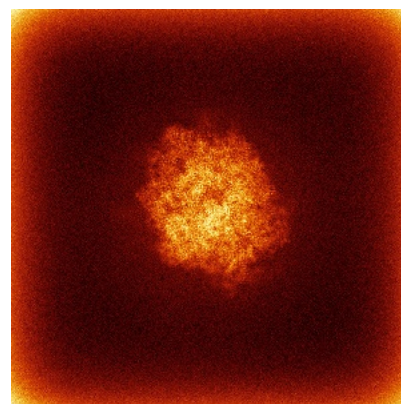
### 6.4.2 Raw map



X



Y

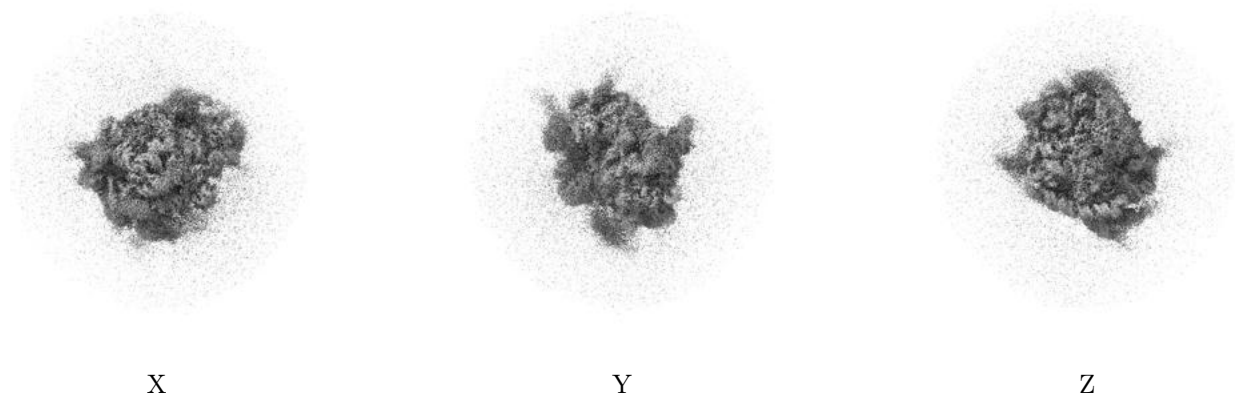


Z

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.

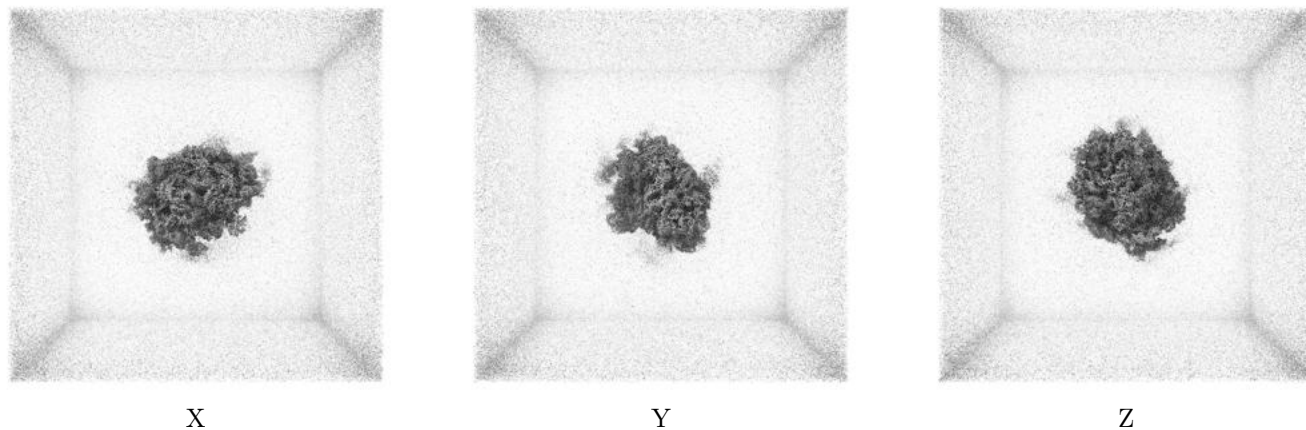
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.065. 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.

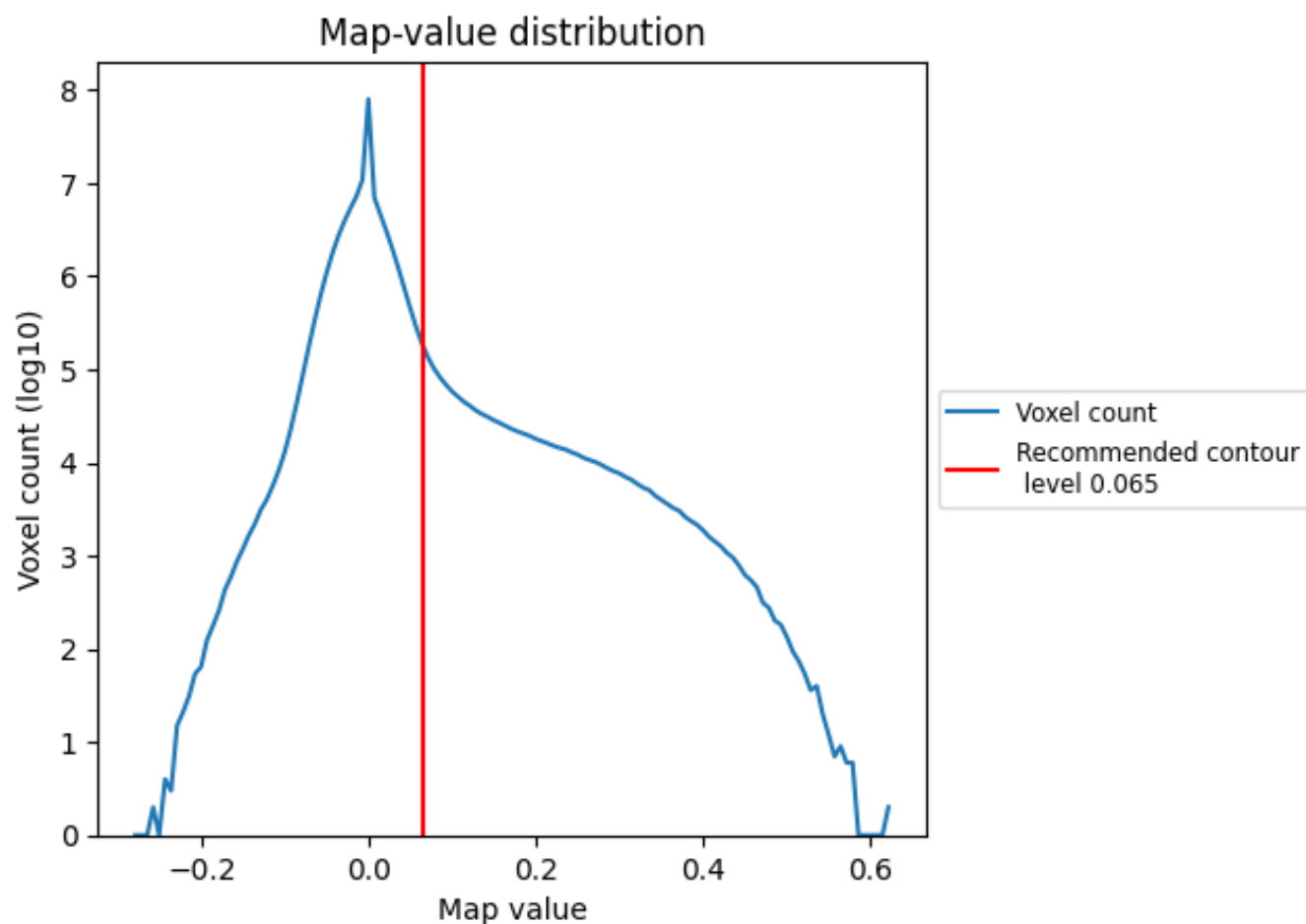
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

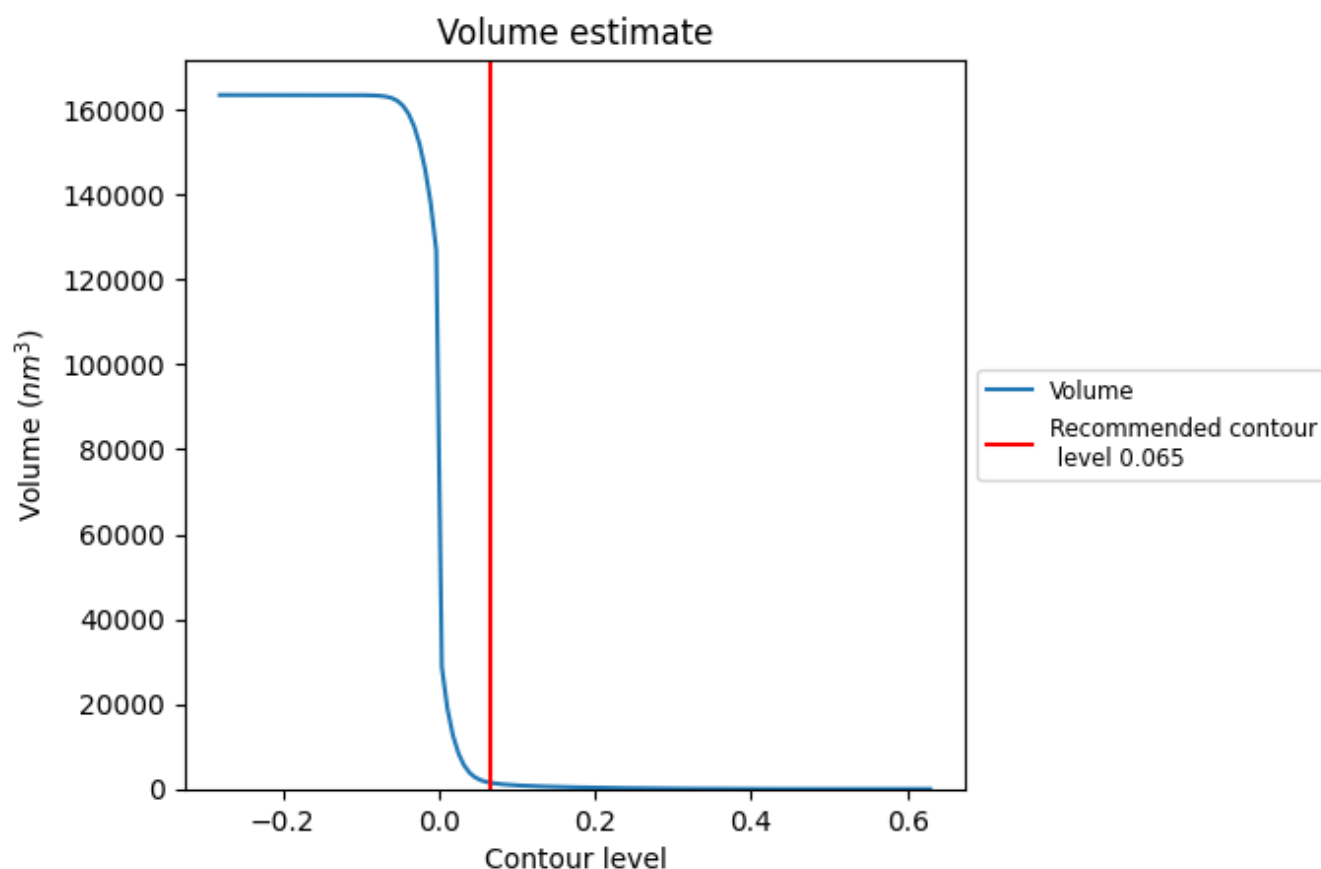
This section contains the results of statistical analysis of the map.

### 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.

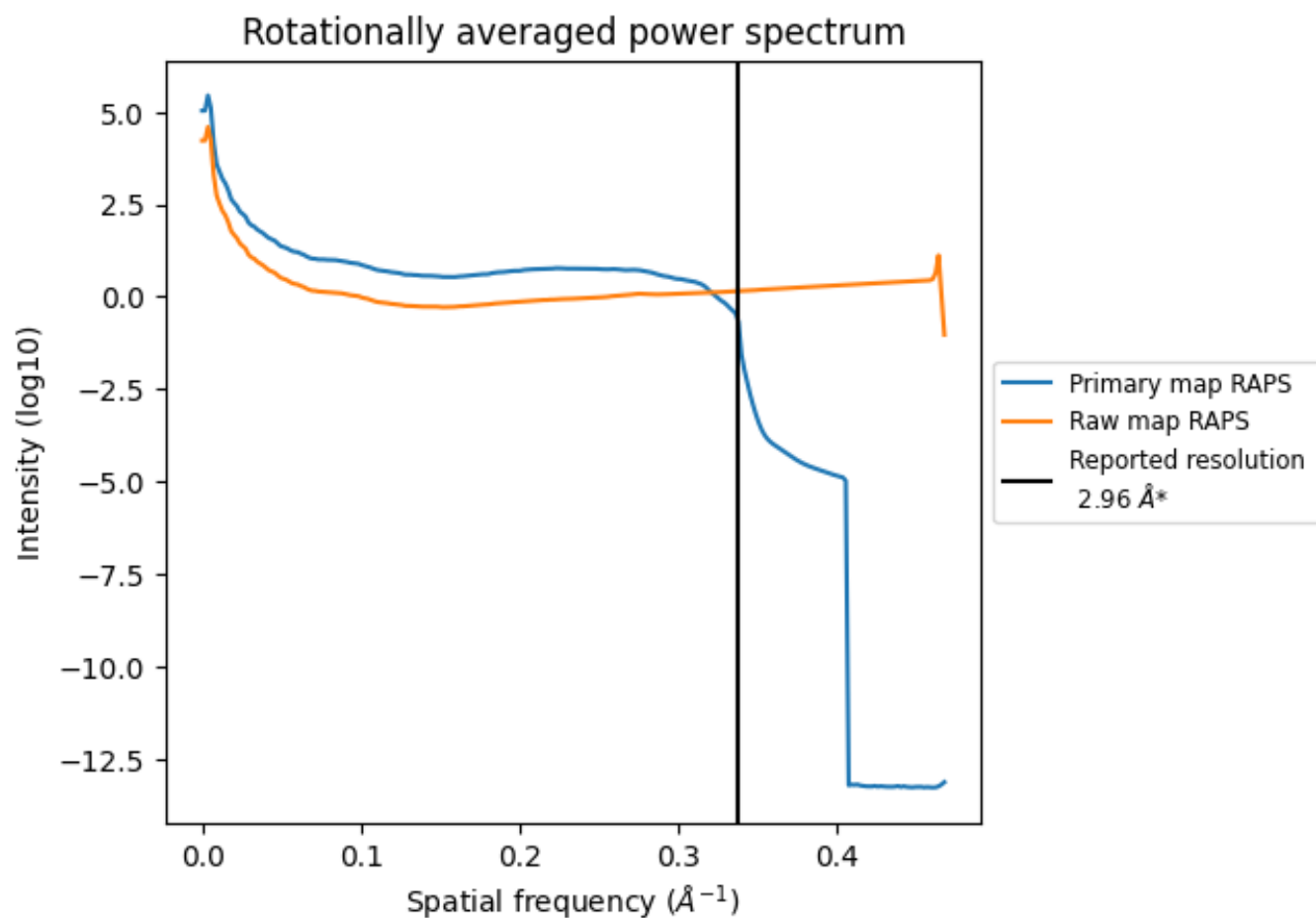
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1513  $\text{nm}^3$ ; this corresponds to an approximate mass of 1366 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 ⓘ



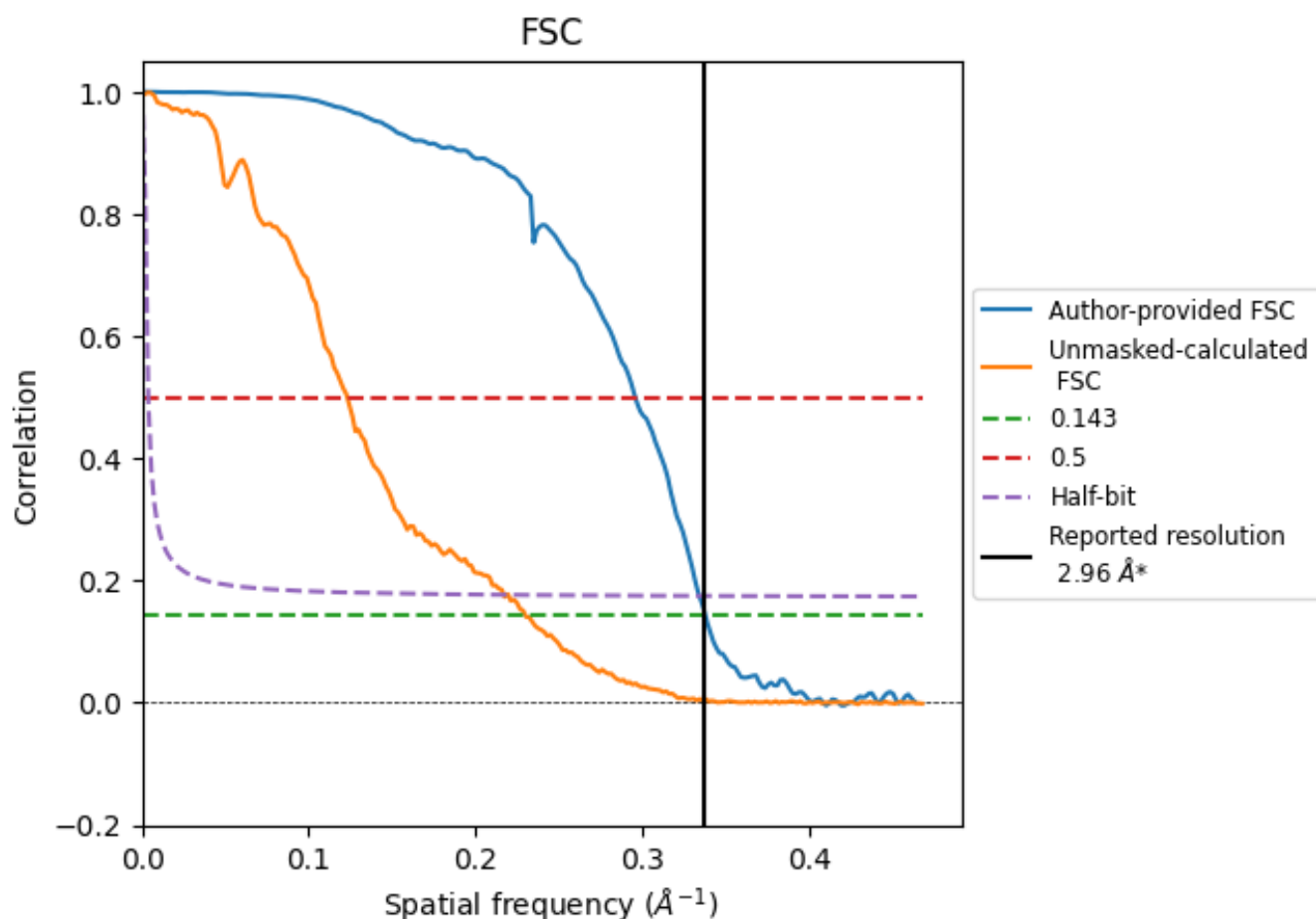
\*Reported resolution corresponds to spatial frequency of 0.338 Å<sup>-1</sup>



## 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 0.338 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

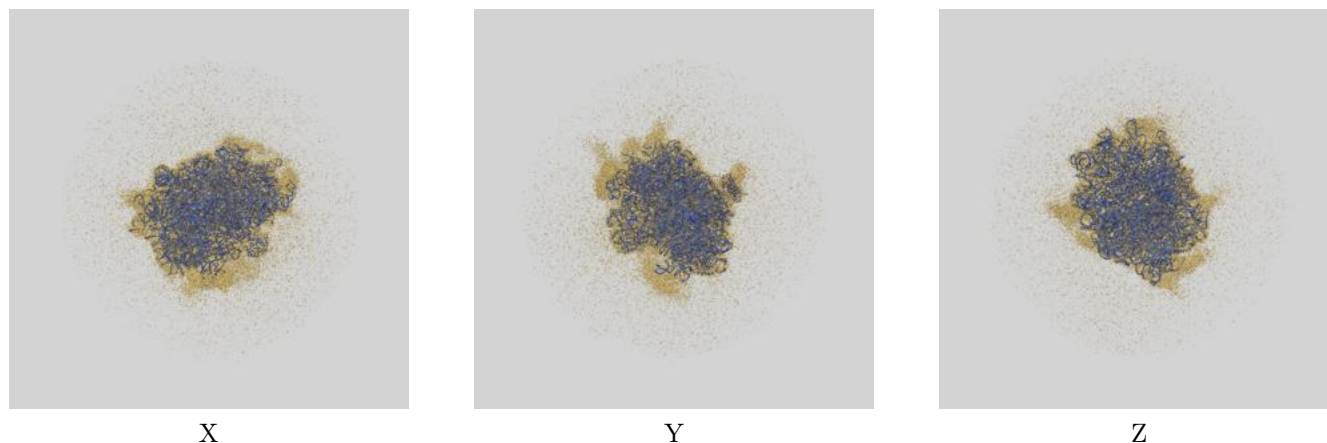
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.96	-	-
Author-provided FSC curve	2.96	3.38	2.99
Unmasked-calculated*	4.35	8.13	4.61

\*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 4.35 differs from the reported value 2.96 by more than 10 %

## 9 Map-model fit [i](#)

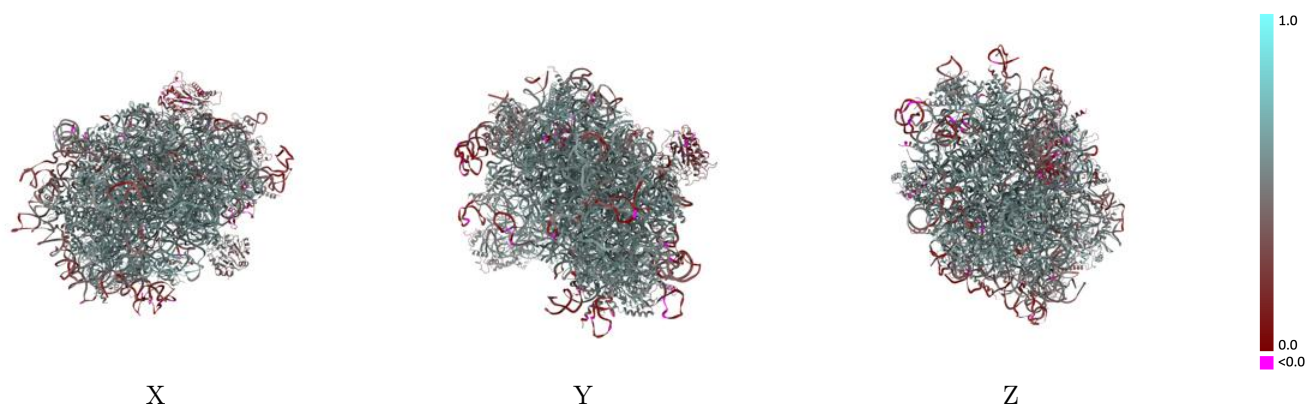
This section contains information regarding the fit between EMDB map EMD-42319 and PDB model 8UJD. Per-residue inclusion information can be found in section [3](#) on page [13](#).

### 9.1 Map-model overlay [i](#)



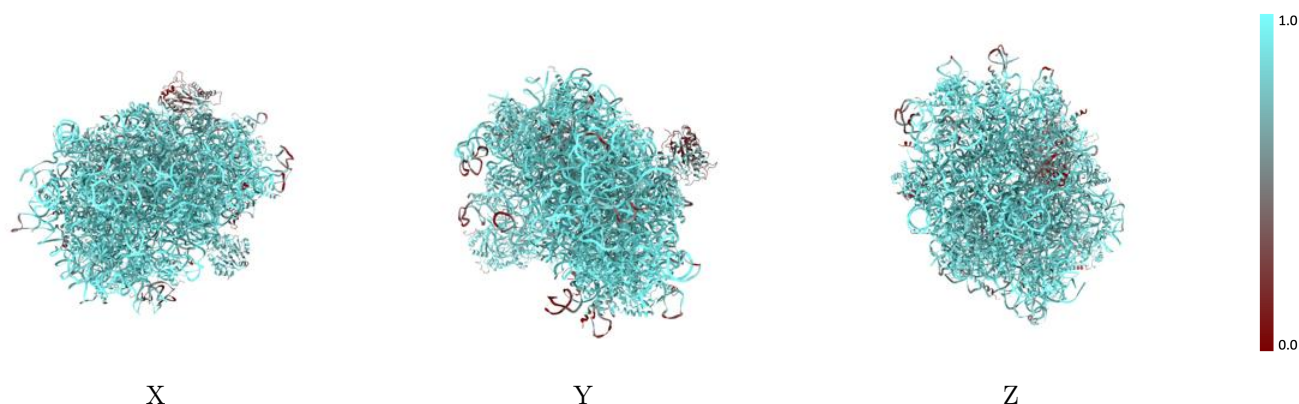
The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



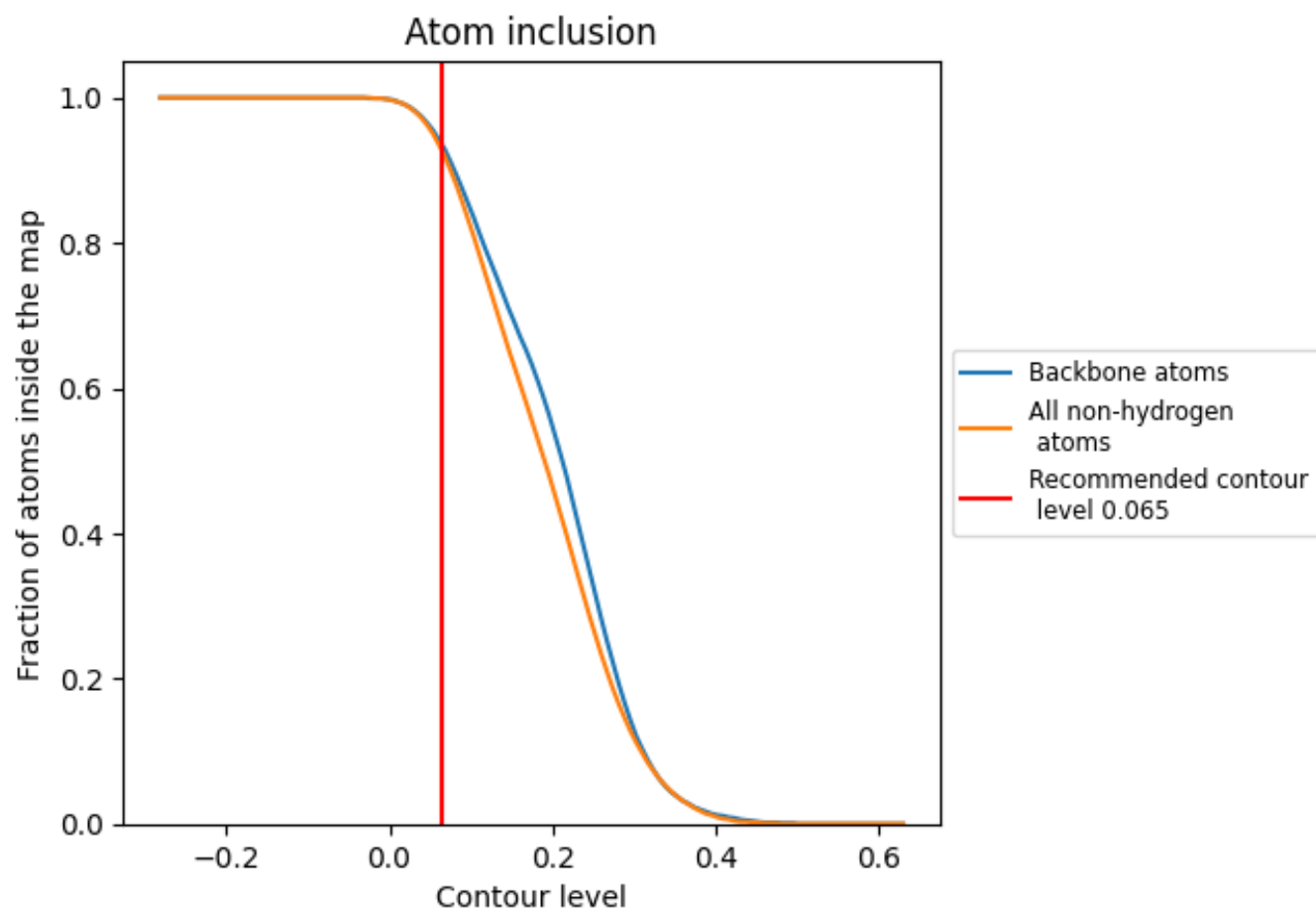
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.065).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% 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 (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9260	 0.5160
CA	 0.4860	 0.2980
L5	 0.9400	 0.5010
L7	 0.9910	 0.5520
L8	 0.9650	 0.5360
LA	 0.9620	 0.5800
LB	 0.9380	 0.5690
LC	 0.9400	 0.5670
LD	 0.9220	 0.5260
LE	 0.8790	 0.5140
LF	 0.9650	 0.5720
LG	 0.8640	 0.5080
LH	 0.9230	 0.5520
LI	 0.9230	 0.5640
LJ	 0.8280	 0.4470
LL	 0.9090	 0.5420
LM	 0.9400	 0.5540
LN	 0.9820	 0.5930
LO	 0.9530	 0.5700
LP	 0.9580	 0.5880
LQ	 0.9660	 0.5880
LR	 0.9430	 0.5530
LS	 0.9670	 0.5850
LT	 0.9360	 0.5520
LU	 0.8600	 0.4300
LV	 0.9410	 0.5640
LW	 0.4640	 0.1810
LX	 0.9290	 0.5620
LY	 0.9470	 0.5700
LZ	 0.9440	 0.5490
La	 0.9680	 0.5900
Lb	 0.8940	 0.5210
Lc	 0.9120	 0.5260
Ld	 0.9370	 0.5460
Le	 0.9770	 0.5910



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Chain	Atom inclusion	Q-score
Lf	 0.9660	 0.5890
Lg	 0.9320	 0.5570
Lh	 0.9350	 0.5550
Li	 0.9260	 0.5470
Lj	 0.9730	 0.5790
Lk	 0.8580	 0.5030
Ll	 0.9570	 0.5770
Lm	 0.9350	 0.5730
Lo	 0.9310	 0.5640
Lp	 0.9420	 0.5610
Lr	 0.9550	 0.5760
P	 0.7620	 0.4140