



## Full wwPDB EM Validation Report ⓘ

Mar 16, 2024 – 09:37 am GMT

PDB ID : 8OHD  
EMDB ID : EMD-16880  
Title : 60S ribosomal subunit bound to the E3-UFM1 complex - state 3 (native)  
Authors : Penchev, I.; DaRosa, P.A.; Becker, T.; Beckmann, R.; Kopito, R.  
Deposited on : 2023-03-21  
Resolution : 3.10 Å (reported)

This is a Full wwPDB EM Validation 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:

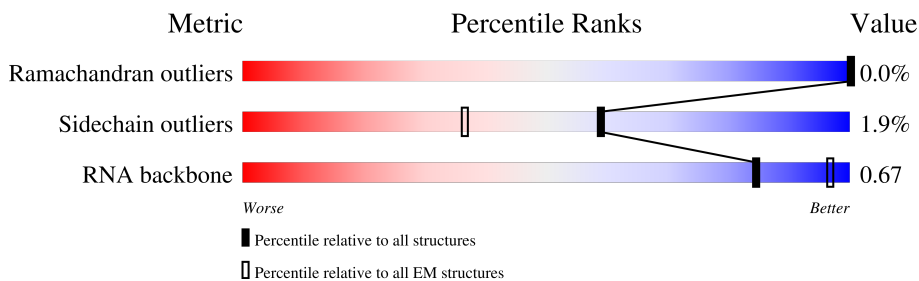
EMDB validation analysis : 0.0.1.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 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 3.10 Å.

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



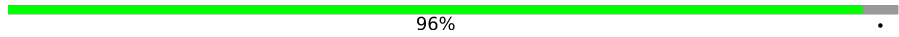
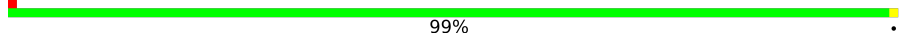

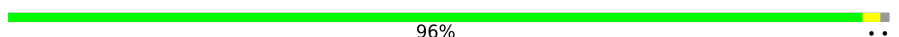






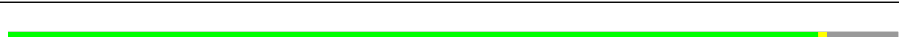


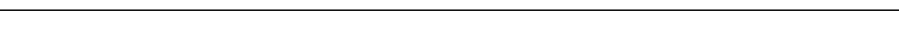
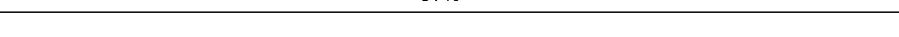
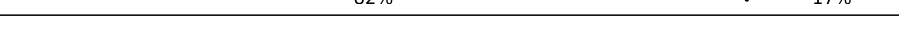
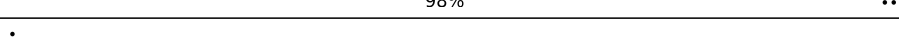

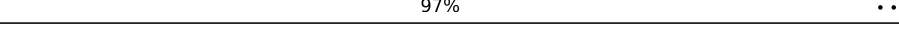
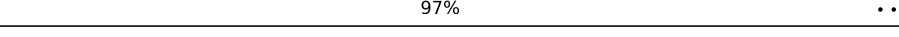

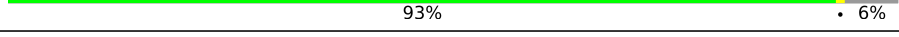



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	5	5070	
2	7	121	
3	8	157	
4	A	794	
5	B	506	
6	C	314	
7	D	85	
8	K	245	

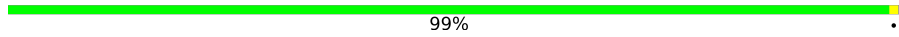




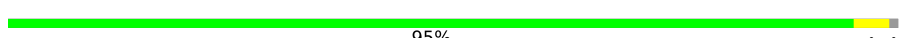




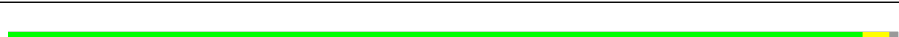


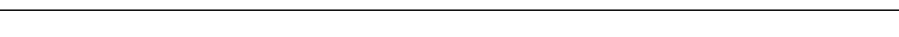
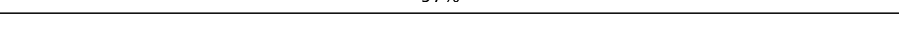
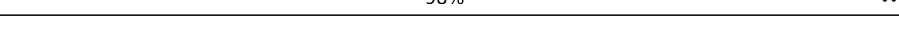

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Mol	Chain	Length	Quality of chain
9	LA	257	 96%
10	LB	403	 99%
11	LC	427	 85% 14%
12	LD	297	 96%
13	LE	288	 76% 24%
14	LF	248	 90% 9%
15	LG	266	 89% 9%
16	LH	192	 98%
17	LI	214	 92% 6%
18	LJ	178	 97%
19	LL	211	 91% 8%
20	LM	215	 62% 37%
21	LN	204	 99%
22	LO	203	 97%
23	LP	184	 82% 17%
24	LQ	188	 98%
25	LR	196	 78% 21%
26	LS	176	 97%
27	LT	160	 97%
28	LU	128	 74% 5% 21%
29	LV	140	 93% 6%
30	LW	157	 39% 61%
31	LX	156	 75% 24%
32	LY	145	 91% 8%
33	LZ	136	 99%

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Mol	Chain	Length	Quality of chain
34	La	148	 99%
35	Lb	159	 67% 31%
36	Lc	115	 82% 15%
37	Ld	125	 84% 14%
38	Le	135	 95% 5%
39	Lf	110	 95%
40	Lg	117	 97%
41	Lh	123	 98%
42	Li	105	 96%
43	Lj	97	 86% 11%
44	Lk	70	 96%
45	Ll	51	 94%
46	Lm	128	 40% 59%
47	Lo	106	 97%
48	Lp	92	 98%
49	Lr	137	 90% 9%
50	Lz	217	 98%

## 2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 146745 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	5	3474	74502	33181	13653	24195	3473	0	0

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	7	120	2561	1141	456	844	120	0	0

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	8	148	3152	1407	563	1035	147	0	0

- Molecule 4 is a protein called E3 UFM1-protein ligase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	692	5479	3453	957	1050	19	0	0

- Molecule 5 is a protein called CDK5 regulatory subunit-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	403	3234	2049	545	624	16	0	0

- Molecule 6 is a protein called DDRGK domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C	188	1547	954	279	313	1	0	0

- Molecule 7 is a protein called Ubiquitin-fold modifier 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	D	78	588	382	96	109	1	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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
			Total	C	N	O	S		
18	LJ	175	1401	882	261	252	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	LL	194	1573	987	327	255	4	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
34	La	147	1162	736	237	186	3	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
48	Lp	91	708	445	136	120	7	0	0

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

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

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

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

- Molecule 51 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
51	5	208	Total	Mg	0
			208	208	
51	7	2	Total	Mg	0
			2	2	
51	8	5	Total	Mg	0
			5	5	
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	1	Total	Mg	0
			1	1	
51	Lj	1	Total	Mg	0
			1	1	

- Molecule 52 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>AltConf</b>
52	Lm	1	Total 1	Zn 1	0
52	Lo	1	Total 1	Zn 1	0
52	Lp	1	Total 1	Zn 1	0



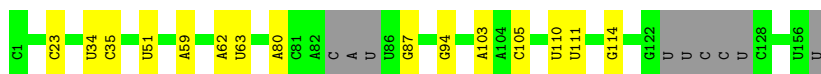
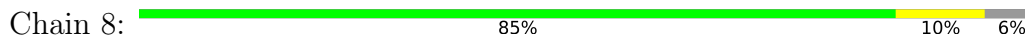




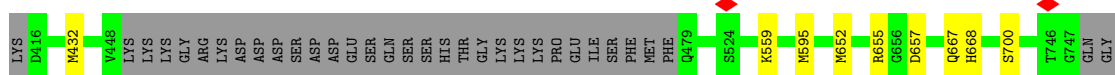
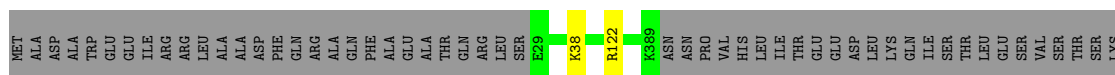
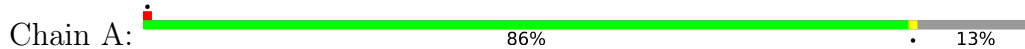
• Molecule 2: 5S rRNA



• Molecule 3: 5.8S rRNA



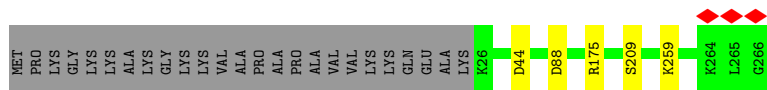
• Molecule 4: E3 UFM1-protein ligase 1







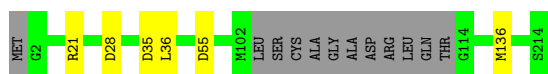
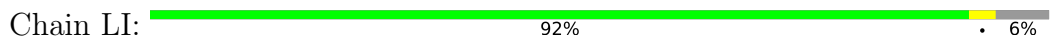




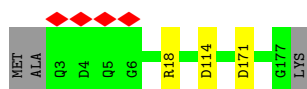
• Molecule 16: 60S ribosomal protein L9



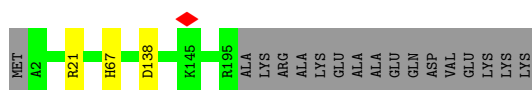
• Molecule 17: Ribosomal protein uL16-like



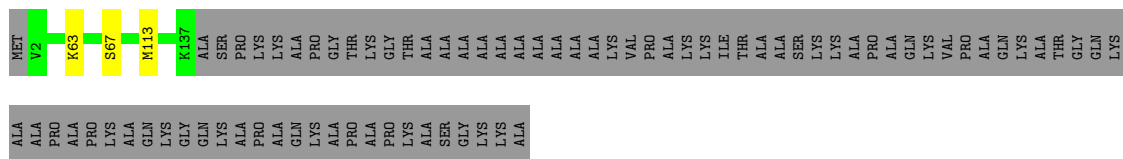
• Molecule 18: 60S ribosomal protein L11



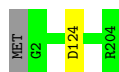
• Molecule 19: 60S ribosomal protein L13



• Molecule 20: 60S ribosomal protein L14



• Molecule 21: 60S ribosomal protein L15




• Molecule 22: 60S ribosomal protein L13a






THR  
LYS  
ALA  
SER  
GLU

- Molecule 36: 60S ribosomal protein L30

Chain Lc:  82% 15%

MET VAL ALA ALA LYS LYS THR LYS K9 S75 C92 S102 R106 SER MET PRO GLU GLN THR GLY GLU LYS

- Molecule 37: 60S ribosomal protein L31

Chain Ld:  84% 14%

MET ALA PRO ALA LYS LYS GLY GLY MET M54 R56 E56 F124 ASN

- Molecule 38: 60S ribosomal protein L32

Chain Le:  95% 5%

MET K2 L129 ARG SER GLU GLU ASN GLU

- Molecule 39: 60S ribosomal protein L35a

Chain Lf:  95%

MET S2 D37 K63 R69 S90 I110

- Molecule 40: 60S ribosomal protein L34

Chain Lg:  97%

MET V2 H73 K115 ALA LYS

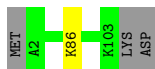
- Molecule 41: 60S ribosomal protein L35

Chain Lh:  98%

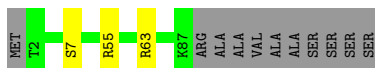
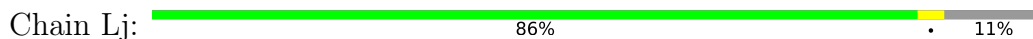
MET K2 K87 A123

- Molecule 42: 60S ribosomal protein L36

Chain Li:  96%



- Molecule 43: 60S ribosomal protein L37



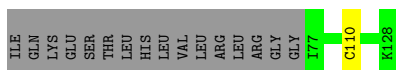
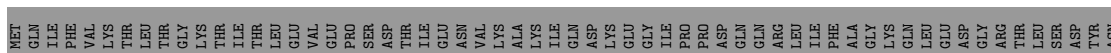
- Molecule 44: 60S ribosomal protein L38



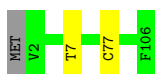
- Molecule 45: 60S ribosomal protein L39



- Molecule 46: Ubiquitin-60S ribosomal protein L40



- Molecule 47: 60S ribosomal protein L36a

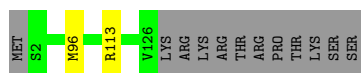


- Molecule 48: 60S ribosomal protein L37a



- Molecule 49: 60S ribosomal protein L28

Chain Lr:  90% . 9%



- Molecule 50: 60S ribosomal protein L10a

Chain Lz:  98% .





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	123096	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	0.052	Depositor
Minimum map value	-0.015	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0055	Depositor
Map size (Å)	392.58, 392.58, 392.58	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: ZN, MG

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	5	0.15	0/83342	0.65	0/129985
2	7	0.15	0/2861	0.65	0/4459
3	8	0.15	0/3520	0.66	1/5481 (0.0%)
4	A	0.23	0/5549	0.45	0/7469
5	B	0.24	0/3280	0.43	0/4426
6	C	0.23	0/1560	0.47	0/2085
7	D	0.25	0/601	0.45	0/818
8	K	0.23	0/1728	0.48	0/2351
9	LA	0.25	0/1936	0.56	0/2596
10	LB	0.24	0/3307	0.50	0/4424
11	LC	0.23	0/2981	0.52	0/4002
12	LD	0.24	0/2428	0.49	0/3252
13	LE	0.24	0/1799	0.51	0/2414
14	LF	0.24	0/1905	0.51	0/2539
15	LG	0.24	0/1960	0.50	0/2637
16	LH	0.24	0/1537	0.51	0/2066
17	LI	0.25	0/1673	0.51	0/2234
18	LJ	0.24	0/1424	0.51	0/1904
19	LL	0.24	0/1604	0.56	0/2149
20	LM	0.25	0/1142	0.51	0/1527
21	LN	0.24	0/1746	0.57	0/2338
22	LO	0.24	0/1682	0.51	0/2250
23	LP	0.24	0/1268	0.50	0/1701
24	LQ	0.25	0/1537	0.59	0/2052
25	LR	0.24	0/1310	0.56	0/1734
26	LS	0.25	0/1493	0.53	0/2003
27	LT	0.25	0/1326	0.51	0/1770
28	LU	0.27	0/839	0.48	0/1126
29	LV	0.26	0/993	0.52	0/1332
30	LW	0.26	0/532	0.50	0/708
31	LX	0.25	0/984	0.51	0/1323
32	LY	0.25	0/1132	0.54	0/1504

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	LZ	0.26	0/1130	0.52	0/1507
34	La	0.23	0/1191	0.50	0/1591
35	Lb	0.25	0/889	0.53	0/1175
36	Lc	0.25	0/774	0.49	0/1038
37	Ld	0.24	0/903	0.54	0/1216
38	Le	0.24	0/1071	0.53	0/1429
39	Lf	0.26	0/895	0.57	0/1198
40	Lg	0.24	0/916	0.56	0/1220
41	Lh	0.24	0/1023	0.52	0/1351
42	Li	0.24	0/843	0.56	0/1115
43	Lj	0.24	0/720	0.58	0/952
44	Lk	0.26	0/575	0.52	0/761
45	Ll	0.24	0/454	0.56	0/599
46	Lm	0.24	0/435	0.51	0/575
47	Lo	0.25	0/877	0.53	0/1156
48	Lp	0.25	0/718	0.53	0/953
49	Lr	0.23	0/1017	0.55	0/1364
50	Lz	0.24	0/1772	0.46	0/2375
All	All	0.19	0/157182	0.60	1/230234 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	8	111	U	C2-N1-C1'	5.28	124.04	117.70

There are no chirality outliers.

There are no planarity outliers.

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

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

## 5.3 Torsion angles [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	
4	A	684/794 (86%)	675 (99%)	9 (1%)	0	100	100
5	B	397/506 (78%)	389 (98%)	8 (2%)	0	100	100
6	C	186/314 (59%)	186 (100%)	0	0	100	100
7	D	76/85 (89%)	76 (100%)	0	0	100	100
8	K	222/245 (91%)	216 (97%)	6 (3%)	0	100	100
9	LA	246/257 (96%)	241 (98%)	5 (2%)	0	100	100
10	LB	400/403 (99%)	395 (99%)	5 (1%)	0	100	100
11	LC	366/427 (86%)	357 (98%)	9 (2%)	0	100	100
12	LD	291/297 (98%)	287 (99%)	3 (1%)	1 (0%)	41	73
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%)	236 (99%)	3 (1%)	0	100	100
16	LH	188/192 (98%)	186 (99%)	2 (1%)	0	100	100
17	LI	198/214 (92%)	196 (99%)	2 (1%)	0	100	100
18	LJ	173/178 (97%)	171 (99%)	2 (1%)	0	100	100
19	LL	192/211 (91%)	187 (97%)	5 (3%)	0	100	100
20	LM	134/215 (62%)	132 (98%)	2 (2%)	0	100	100
21	LN	201/204 (98%)	195 (97%)	6 (3%)	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%)	152 (99%)	1 (1%)	0	100	100
26	LS	173/176 (98%)	168 (97%)	5 (3%)	0	100	100
27	LT	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
28	LU	99/128 (77%)	95 (96%)	3 (3%)	1 (1%)	15	49
29	LV	129/140 (92%)	127 (98%)	2 (2%)	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%)	131 (99%)	1 (1%)	0	100	100
33	LZ	133/136 (98%)	131 (98%)	2 (2%)	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%)	105 (100%)	0	0	100	100
36	Lc	96/115 (84%)	96 (100%)	0	0	100	100
37	Ld	105/125 (84%)	103 (98%)	2 (2%)	0	100	100
38	Le	126/135 (93%)	125 (99%)	1 (1%)	0	100	100
39	Lf	107/110 (97%)	107 (100%)	0	0	100	100
40	Lg	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
41	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
42	Li	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
43	Lj	84/97 (87%)	83 (99%)	1 (1%)	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%)	50 (100%)	0	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%)	123 (100%)	0	0	100	100
50	Lz	215/217 (99%)	208 (97%)	7 (3%)	0	100	100
All	All	8112/9348 (87%)	7976 (98%)	134 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	LD	4	VAL
28	LU	67	LYS

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	612/704 (87%)	601 (98%)	11 (2%)	59	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	B	360/438 (82%)	348 (97%)	12 (3%)	38	69
6	C	162/254 (64%)	160 (99%)	2 (1%)	71	88
7	D	66/72 (92%)	64 (97%)	2 (3%)	41	71
8	K	194/213 (91%)	188 (97%)	6 (3%)	40	70
9	LA	190/199 (96%)	190 (100%)	0	100	100
10	LB	348/349 (100%)	345 (99%)	3 (1%)	78	91
11	LC	306/348 (88%)	303 (99%)	3 (1%)	76	90
12	LD	246/250 (98%)	240 (98%)	6 (2%)	49	76
13	LE	194/252 (77%)	192 (99%)	2 (1%)	76	90
14	LF	194/215 (90%)	191 (98%)	3 (2%)	65	85
15	LG	203/223 (91%)	198 (98%)	5 (2%)	47	75
16	LH	169/171 (99%)	167 (99%)	2 (1%)	71	88
17	LI	172/181 (95%)	166 (96%)	6 (4%)	36	68
18	LJ	147/149 (99%)	144 (98%)	3 (2%)	55	80
19	LL	164/177 (93%)	161 (98%)	3 (2%)	59	82
20	LM	116/161 (72%)	113 (97%)	3 (3%)	46	74
21	LN	171/172 (99%)	170 (99%)	1 (1%)	86	94
22	LO	173/174 (99%)	169 (98%)	4 (2%)	50	77
23	LP	134/163 (82%)	131 (98%)	3 (2%)	52	78
24	LQ	164/165 (99%)	162 (99%)	2 (1%)	71	88
25	LR	138/175 (79%)	135 (98%)	3 (2%)	52	78
26	LS	156/157 (99%)	152 (97%)	4 (3%)	46	74
27	LT	139/140 (99%)	135 (97%)	4 (3%)	42	72
28	LU	91/115 (79%)	86 (94%)	5 (6%)	21	53
29	LV	101/107 (94%)	100 (99%)	1 (1%)	76	90
30	LW	54/126 (43%)	54 (100%)	0	100	100
31	LX	106/133 (80%)	105 (99%)	1 (1%)	78	91
32	LY	124/135 (92%)	122 (98%)	2 (2%)	62	84
33	LZ	117/118 (99%)	117 (100%)	0	100	100
34	La	120/121 (99%)	119 (99%)	1 (1%)	81	92
35	Lb	88/126 (70%)	85 (97%)	3 (3%)	37	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	Lc	83/97 (86%)	79 (95%)	4 (5%)	25	58
37	Ld	98/110 (89%)	96 (98%)	2 (2%)	55	80
38	Le	114/121 (94%)	114 (100%)	0	100	100
39	Lf	88/89 (99%)	84 (96%)	4 (4%)	27	60
40	Lg	98/100 (98%)	97 (99%)	1 (1%)	76	90
41	Lh	109/110 (99%)	108 (99%)	1 (1%)	78	91
42	Li	86/89 (97%)	85 (99%)	1 (1%)	71	88
43	Lj	73/80 (91%)	70 (96%)	3 (4%)	30	64
44	Lk	64/65 (98%)	62 (97%)	2 (3%)	40	70
45	Ll	47/48 (98%)	45 (96%)	2 (4%)	29	62
46	Lm	48/116 (41%)	47 (98%)	1 (2%)	53	79
47	Lo	93/94 (99%)	91 (98%)	2 (2%)	52	78
48	Lp	74/75 (99%)	73 (99%)	1 (1%)	67	86
49	Lr	109/121 (90%)	107 (98%)	2 (2%)	59	82
50	Lz	196/196 (100%)	192 (98%)	4 (2%)	55	80
All	All	7099/7994 (89%)	6963 (98%)	136 (2%)	59	81

All (136) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	38	LYS
4	A	122	ARG
4	A	432	MET
4	A	559	LYS
4	A	595	MET
4	A	652	MET
4	A	655	ARG
4	A	657	ASP
4	A	667	GLN
4	A	668	HIS
4	A	700	SER
5	B	1	MET
5	B	26	CYS
5	B	28	LEU
5	B	67	HIS
5	B	95	LYS
5	B	120	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
5	B	131	LYS
5	B	339	ASP
5	B	341	LEU
5	B	422	MET
5	B	456	GLN
5	B	502	MET
6	C	207	MET
6	C	236	SER
7	D	53	ASP
7	D	75	ARG
8	K	1	MET
8	K	67	ARG
8	K	109	THR
8	K	166	SER
8	K	185	THR
8	K	197	MET
10	LB	134	CYS
10	LB	200	ARG
10	LB	396	ARG
11	LC	122	TYR
11	LC	348	LYS
11	LC	368	LYS
12	LD	197	LYS
12	LD	224	SER
12	LD	235	MET
12	LD	239	MET
12	LD	259	LYS
12	LD	262	LYS
13	LE	56	ARG
13	LE	120	ASP
14	LF	31	LYS
14	LF	134	ARG
14	LF	189	ASP
15	LG	44	ASP
15	LG	88	ASP
15	LG	175	ARG
15	LG	209	SER
15	LG	259	LYS
16	LH	110	SER
16	LH	115	ARG
17	LI	21	ARG
17	LI	28	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
17	LI	35	ASP
17	LI	36	LEU
17	LI	55	ASP
17	LI	136	MET
18	LJ	18	ARG
18	LJ	114	ASP
18	LJ	171	ASP
19	LL	21	ARG
19	LL	67	HIS
19	LL	138	ASP
20	LM	63	LYS
20	LM	67	SER
20	LM	113	MET
21	LN	124	ASP
22	LO	53	LYS
22	LO	118	MET
22	LO	173	GLN
22	LO	175	MET
23	LP	9	GLU
23	LP	57	CYS
23	LP	153	LYS
24	LQ	66	MET
24	LQ	94	GLU
25	LR	114	LYS
25	LR	149	LYS
25	LR	153	LYS
26	LS	31	ARG
26	LS	85	ASP
26	LS	86	SER
26	LS	169	THR
27	LT	17	ARG
27	LT	52	MET
27	LT	68	THR
27	LT	114	GLN
28	LU	25	CYS
28	LU	30	GLU
28	LU	97	ARG
28	LU	106	SER
28	LU	108	GLU
29	LV	60	MET
31	LX	120	ASP
32	LY	74	TYR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
32	LY	120	GLU
34	La	92	LYS
35	Lb	63	LYS
35	Lb	70	GLU
35	Lb	94	ASP
36	Lc	75	SER
36	Lc	92	CYS
36	Lc	102	SER
36	Lc	106	ARG
37	Ld	54	MET
37	Ld	56	GLU
39	Lf	37	ASP
39	Lf	63	LYS
39	Lf	89	ARG
39	Lf	90	SER
40	Lg	73	HIS
41	Lh	87	LYS
42	Li	86	LYS
43	Lj	7	SER
43	Lj	55	ARG
43	Lj	63	ARG
44	Lk	21	LYS
44	Lk	68	GLU
45	Ll	37	TYR
45	Ll	47	THR
46	Lm	110	CYS
47	Lo	7	THR
47	Lo	77	CYS
48	Lp	91	ASP
49	Lr	96	MET
49	Lr	113	ARG
50	Lz	4	LYS
50	Lz	41	TYR
50	Lz	56	LYS
50	Lz	72	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
27	LT	54	HIS
39	Lf	65	ASN

5.3.3 RNA 

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3451/5070 (68%)	371 (10%)	4 (0%)
2	7	119/121 (98%)	5 (4%)	0
3	8	145/157 (92%)	14 (9%)	0
All	All	3715/5348 (69%)	390 (10%)	4 (0%)

All (390) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	13	U
1	5	39	A
1	5	42	A
1	5	48	G
1	5	59	A
1	5	64	A
1	5	65	A
1	5	73	A
1	5	91	G
1	5	98	A
1	5	110	C
1	5	119	G
1	5	120	A
1	5	133	C
1	5	134	G
1	5	135	G
1	5	136	C
1	5	141	C
1	5	142	G
1	5	143	C
1	5	159	C
1	5	172	C
1	5	178	C
1	5	179	G
1	5	200	U
1	5	209	U
1	5	218	A
1	5	219	G
1	5	233	U
1	5	234	G
1	5	253	G
1	5	266	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	5	280	G
1	5	297	U
1	5	316	U
1	5	340	C
1	5	387	G
1	5	409	G
1	5	410	A
1	5	412	G
1	5	413	G
1	5	449	C
1	5	450	G
1	5	453	G
1	5	454	U
1	5	467	U
1	5	485	C
1	5	662	C
1	5	666	G
1	5	669	C
1	5	686	A
1	5	687	U
1	5	697	G
1	5	704	C
1	5	705	G
1	5	731	G
1	5	738	C
1	5	739	G
1	5	740	G
1	5	760	G
1	5	915	A
1	5	917	A
1	5	925	C
1	5	926	G
1	5	933	G
1	5	936	C
1	5	943	A
1	5	944	A
1	5	945	U
1	5	956	A
1	5	960	A
1	5	961	G
1	5	962	C
1	5	965	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	5	967	C
1	5	968	C
1	5	969	C
1	5	982	U
1	5	1072	C
1	5	1078	A
1	5	1101	C
1	5	1170	G
1	5	1182	C
1	5	1183	C
1	5	1199	G
1	5	1211	G
1	5	1215	C
1	5	1241	C
1	5	1266	G
1	5	1269	G
1	5	1270	A
1	5	1272	C
1	5	1273	G
1	5	1284	G
1	5	1287	G
1	5	1293	G
1	5	1302	U
1	5	1303	A
1	5	1304	C
1	5	1326	A
1	5	1339	U
1	5	1354	A
1	5	1359	G
1	5	1366	G
1	5	1387	A
1	5	1397	A
1	5	1399	G
1	5	1403	G
1	5	1413	C
1	5	1415	G
1	5	1438	U
1	5	1439	C
1	5	1443	A
1	5	1445	U
1	5	1498	G
1	5	1502	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	5	1516	G
1	5	1534	A
1	5	1547	A
1	5	1578	U
1	5	1591	U
1	5	1596	U
1	5	1624	G
1	5	1625	G
1	5	1631	A
1	5	1633	G
1	5	1634	A
1	5	1638	A
1	5	1654	G
1	5	1661	C
1	5	1676	C
1	5	1677	U
1	5	1697	G
1	5	1699	A
1	5	1701	A
1	5	1742	A
1	5	1755	C
1	5	1758	G
1	5	1761	G
1	5	1765	A
1	5	1766	A
1	5	1767	A
1	5	1768	C
1	5	1787	A
1	5	1804	A
1	5	1836	G
1	5	1837	A
1	5	1842	G
1	5	1855	G
1	5	1869	G
1	5	1897	A
1	5	1918	U
1	5	1921	C
1	5	1922	G
1	5	1931	C
1	5	1932	A
1	5	1940	G
1	5	1941	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	5	1948	G
1	5	1961	G
1	5	2024	G
1	5	2026	A
1	5	2043	A
1	5	2046	G
1	5	2048	U
1	5	2055	G
1	5	2056	G
1	5	2069	A
1	5	2084	C
1	5	2092	G
1	5	2093	A
1	5	2096	G
1	5	2098	G
1	5	2102	G
1	5	2103	G
1	5	2107	C
1	5	2261	G
1	5	2300	A
1	5	2301	G
1	5	2313	A
1	5	2314	G
1	5	2331	G
1	5	2348	G
1	5	2351	C
1	5	2360	A
1	5	2395	A
1	5	2397	G
1	5	2417	A
1	5	2421	G
1	5	2470	C
1	5	2471	G
1	5	2474	G
1	5	2475	G
1	5	2478	C
1	5	2504	C
1	5	2505	C
1	5	2506	G
1	5	2513	A
1	5	2554	U
1	5	2583	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	5	2587	A
1	5	2589	C
1	5	2601	A
1	5	2627	C
1	5	2653	C
1	5	2660	A
1	5	2669	C
1	5	2687	U
1	5	2694	G
1	5	2695	A
1	5	2696	A
1	5	2708	U
1	5	2711	G
1	5	2743	A
1	5	2761	U
1	5	2764	A
1	5	2769	U
1	5	2788	U
1	5	2790	U
1	5	2814	C
1	5	2826	U
1	5	2827	G
1	5	2855	G
1	5	3597	G
1	5	3605	C
1	5	3615	G
1	5	3618	C
1	5	3626	G
1	5	3635	A
1	5	3653	A
1	5	3662	A
1	5	3673	C
1	5	3709	U
1	5	3710	G
1	5	3712	A
1	5	3713	U
1	5	3753	G
1	5	3774	A
1	5	3776	G
1	5	3777	G
1	5	3784	A
1	5	3811	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	5	3814	U
1	5	3817	A
1	5	3819	G
1	5	3838	U
1	5	3839	G
1	5	3840	U
1	5	3877	A
1	5	3878	C
1	5	3879	G
1	5	3897	G
1	5	3898	G
1	5	3901	A
1	5	3906	A
1	5	3907	G
1	5	3908	A
1	5	3915	U
1	5	3939	G
1	5	3951	G
1	5	3956	G
1	5	3958	G
1	5	3961	G
1	5	3962	A
1	5	3963	A
1	5	3965	A
1	5	3966	A
1	5	3967	G
1	5	3968	U
1	5	3969	G
1	5	3974	G
1	5	3975	C
1	5	4040	C
1	5	4045	G
1	5	4046	A
1	5	4048	A
1	5	4049	U
1	5	4050	A
1	5	4051	C
1	5	4061	G
1	5	4076	G
1	5	4098	A
1	5	4119	C
1	5	4122	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	5	4163	U
1	5	4170	A
1	5	4183	G
1	5	4184	G
1	5	4191	G
1	5	4203	A
1	5	4229	U
1	5	4233	A
1	5	4234	A
1	5	4251	A
1	5	4254	G
1	5	4266	G
1	5	4268	A
1	5	4273	A
1	5	4281	A
1	5	4291	G
1	5	4305	G
1	5	4330	G
1	5	4332	C
1	5	4339	A
1	5	4373	G
1	5	4377	G
1	5	4378	A
1	5	4387	C
1	5	4394	A
1	5	4421	C
1	5	4422	A
1	5	4437	U
1	5	4448	G
1	5	4464	A
1	5	4465	U
1	5	4466	C
1	5	4500	U
1	5	4512	U
1	5	4513	A
1	5	4524	G
1	5	4548	A
1	5	4549	G
1	5	4567	G
1	5	4584	A
1	5	4590	A
1	5	4636	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	5	4637	G
1	5	4656	A
1	5	4670	C
1	5	4671	C
1	5	4672	A
1	5	4708	A
1	5	4709	U
1	5	4720	C
1	5	4730	C
1	5	4731	G
1	5	4732	G
1	5	4734	A
1	5	4741	C
1	5	4742	G
1	5	4743	G
1	5	4745	G
1	5	4750	G
1	5	4754	G
1	5	4757	C
1	5	4759	C
1	5	4761	G
1	5	4765	G
1	5	4771	C
1	5	4870	G
1	5	4871	C
1	5	4882	U
1	5	4883	C
1	5	4895	C
1	5	4900	C
1	5	4901	G
1	5	4910	A
1	5	4912	G
1	5	4943	A
1	5	4976	U
1	5	4988	U
1	5	4990	C
1	5	4991	U
1	5	4994	G
1	5	5017	G
1	5	5034	A
1	5	5041	G
1	5	5050	C

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Mol	Chain	Res	Type
1	5	5062	G
1	5	5069	U
2	7	7	G
2	7	53	U
2	7	54	A
2	7	64	G
2	7	110	G
3	8	23	C
3	8	34	U
3	8	35	C
3	8	51	U
3	8	59	A
3	8	62	A
3	8	63	U
3	8	80	A
3	8	87	G
3	8	94	G
3	8	103	A
3	8	105	C
3	8	110	U
3	8	114	G

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	739	G
1	5	1590	C
1	5	1633	G
1	5	3964	U

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

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

#### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

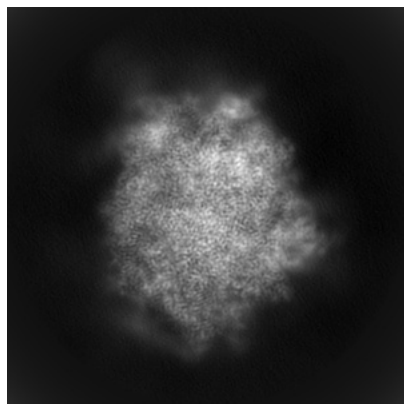
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16880. These allow visual inspection of the internal detail of the map and identification of artifacts.

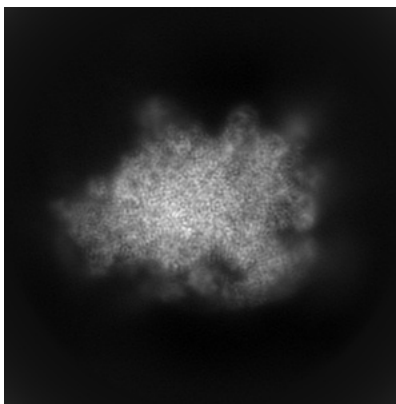
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

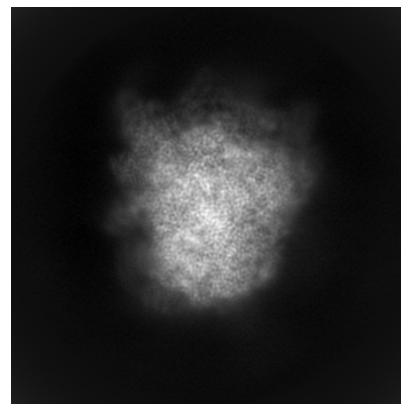
#### 6.1.1 Primary map



X

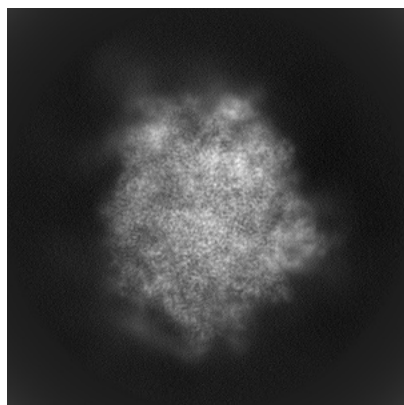


Y

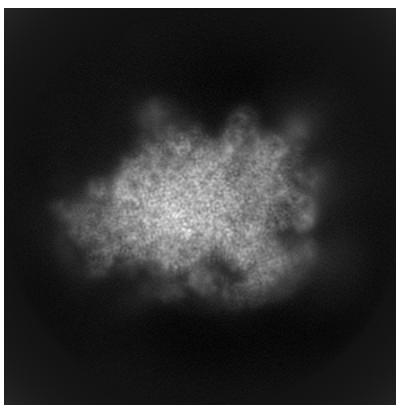


Z

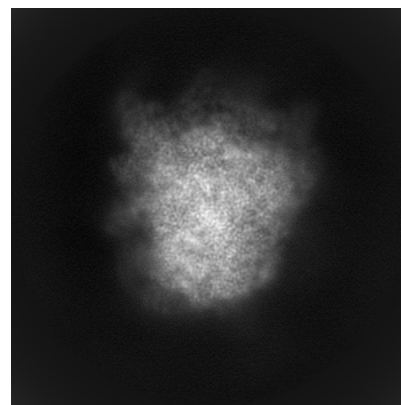
#### 6.1.2 Raw map



X



Y

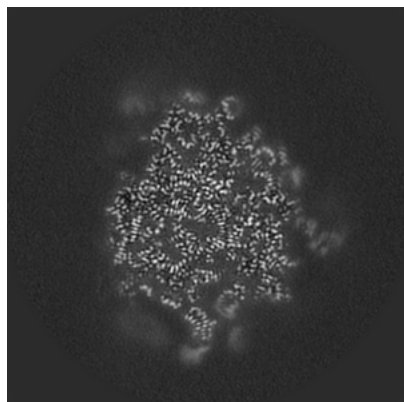


Z

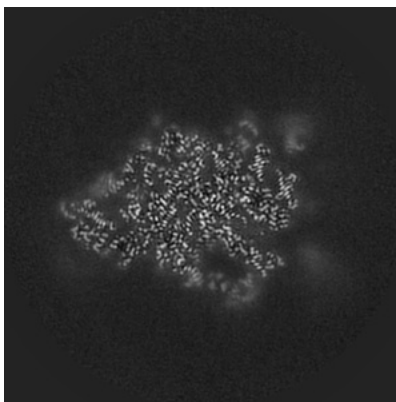
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

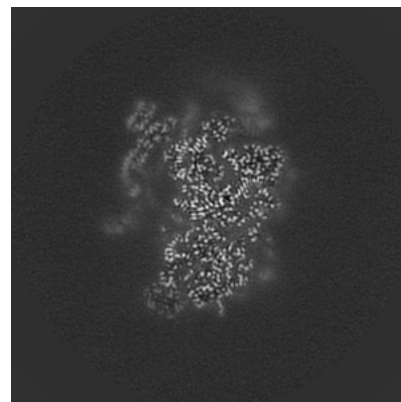
### 6.2.1 Primary map



X Index: 270

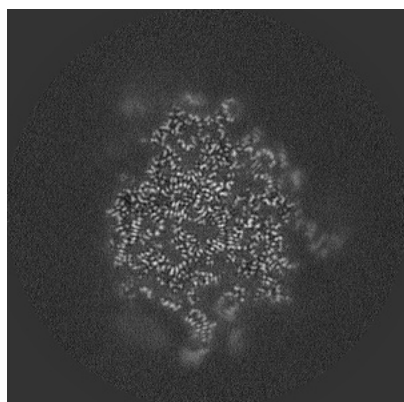


Y Index: 270

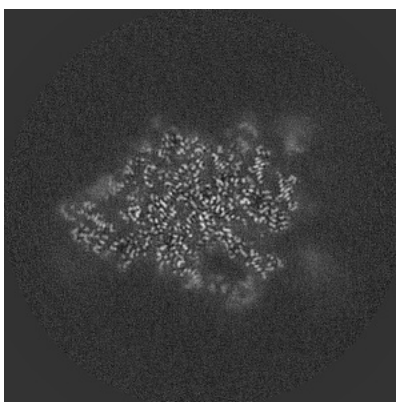


Z Index: 270

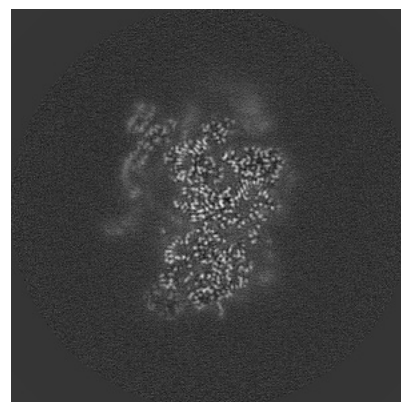
### 6.2.2 Raw map



X Index: 270



Y Index: 270

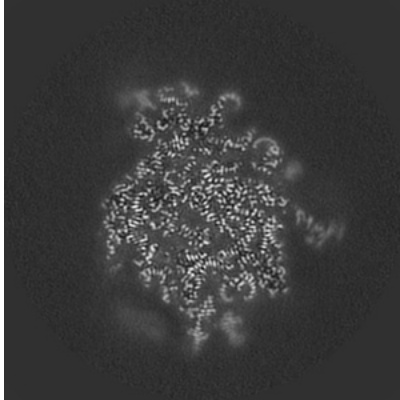


Z Index: 270

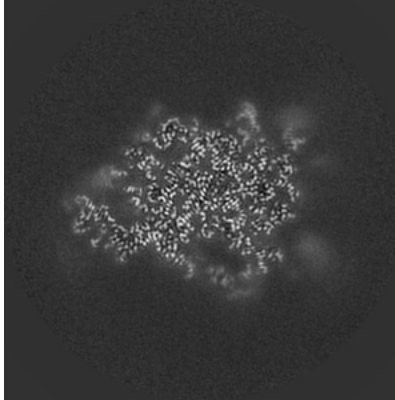
The images above show central slices of the map in three orthogonal directions.

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

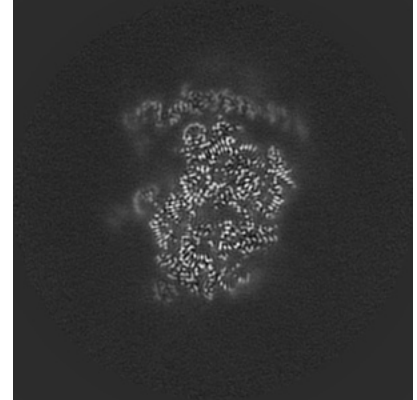
### 6.3.1 Primary map



X Index: 260

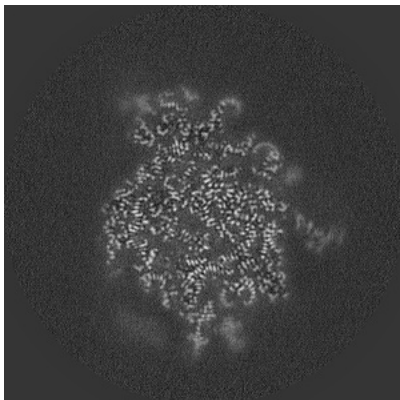


Y Index: 276

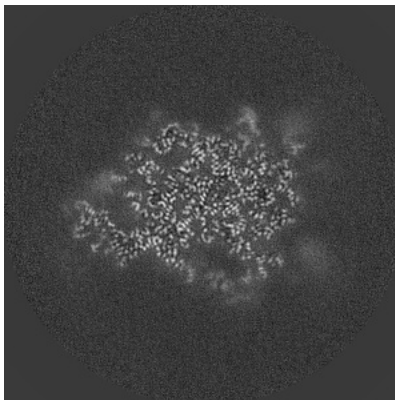


Z Index: 248

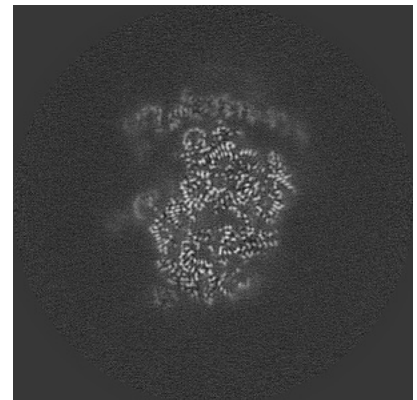
### 6.3.2 Raw map



X Index: 260



Y Index: 276



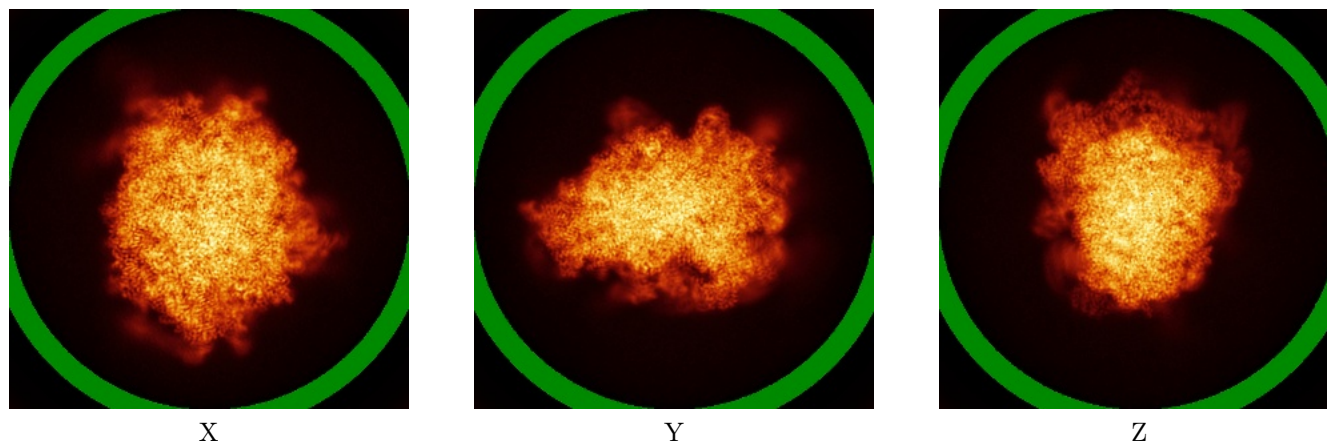
Z Index: 248

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

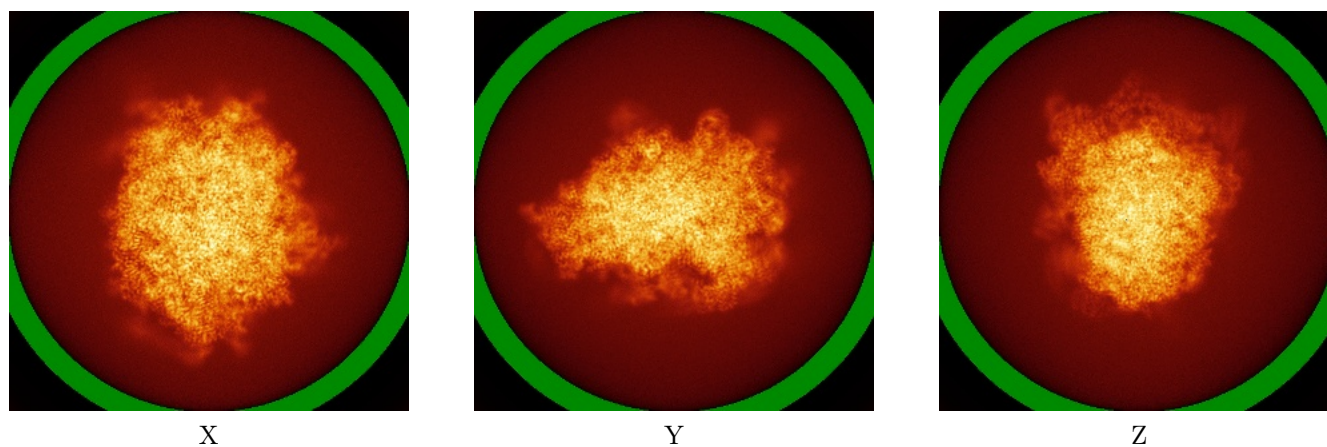


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

### 6.4.1 Primary map



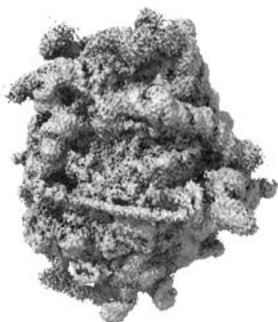
### 6.4.2 Raw map



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

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

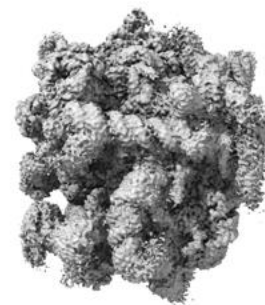
### 6.5.1 Primary map



X



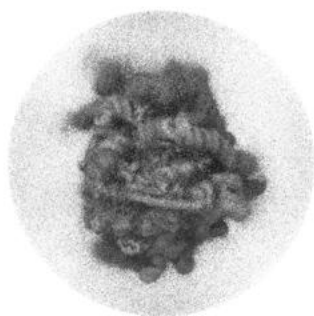
Y



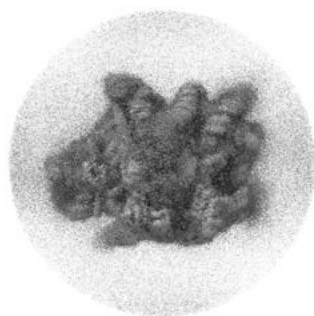
Z

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.

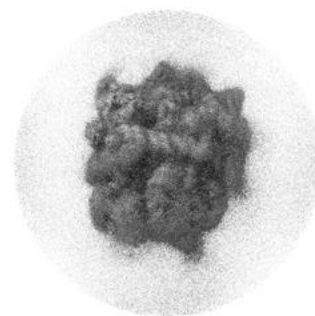
### 6.5.2 Raw map



X



Y



Z

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.

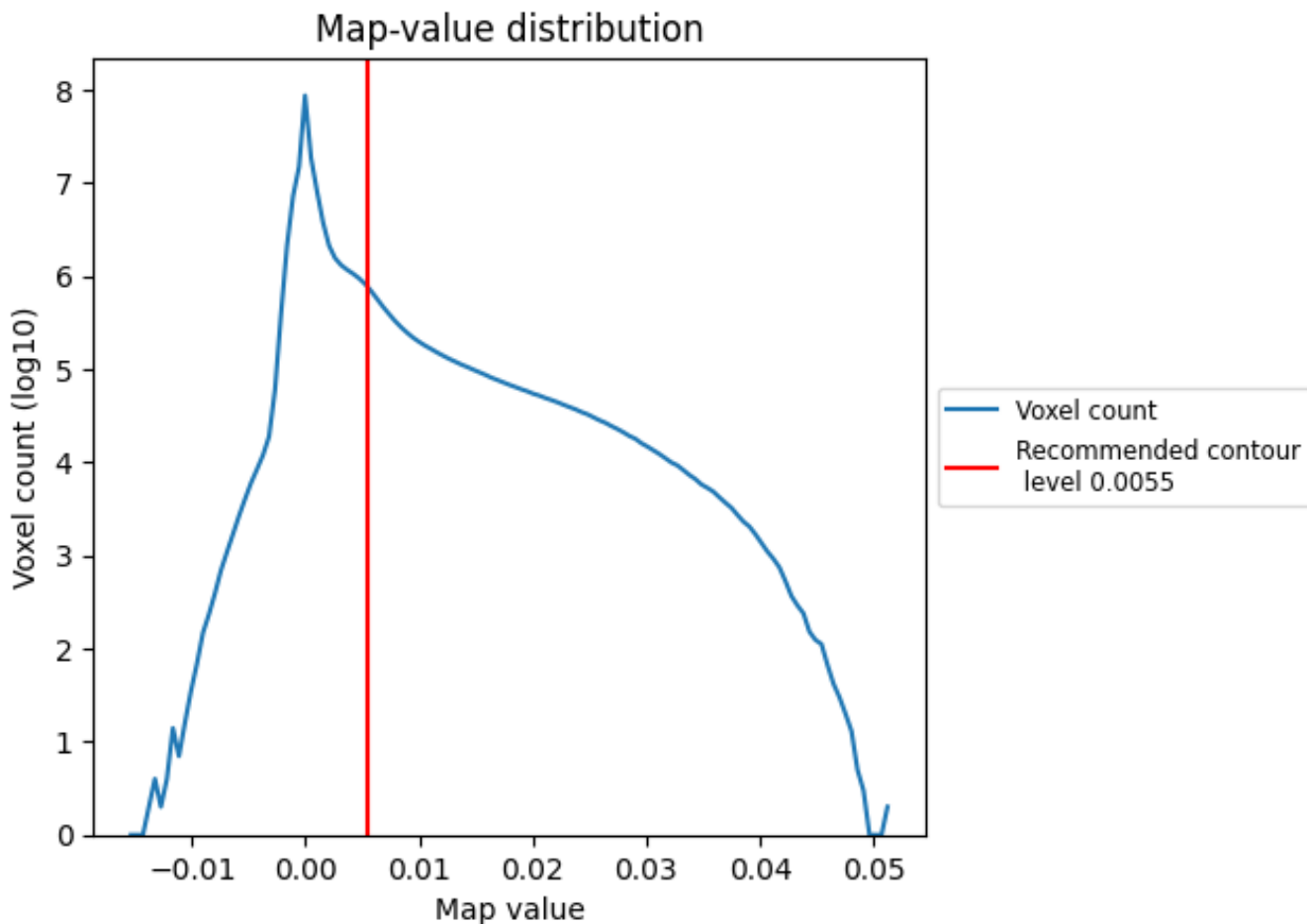
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

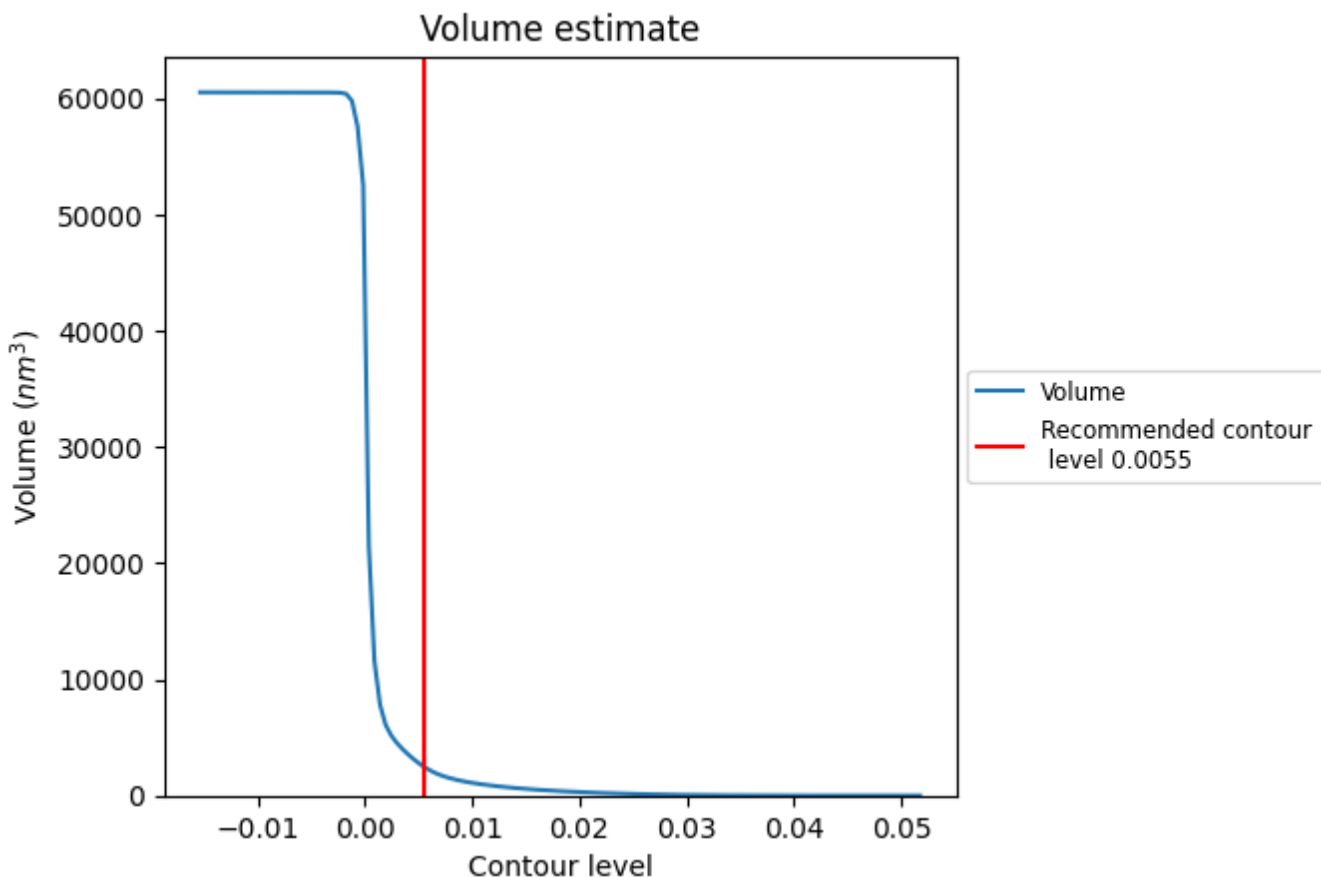
This section contains the results of statistical analysis of the map.

### 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.

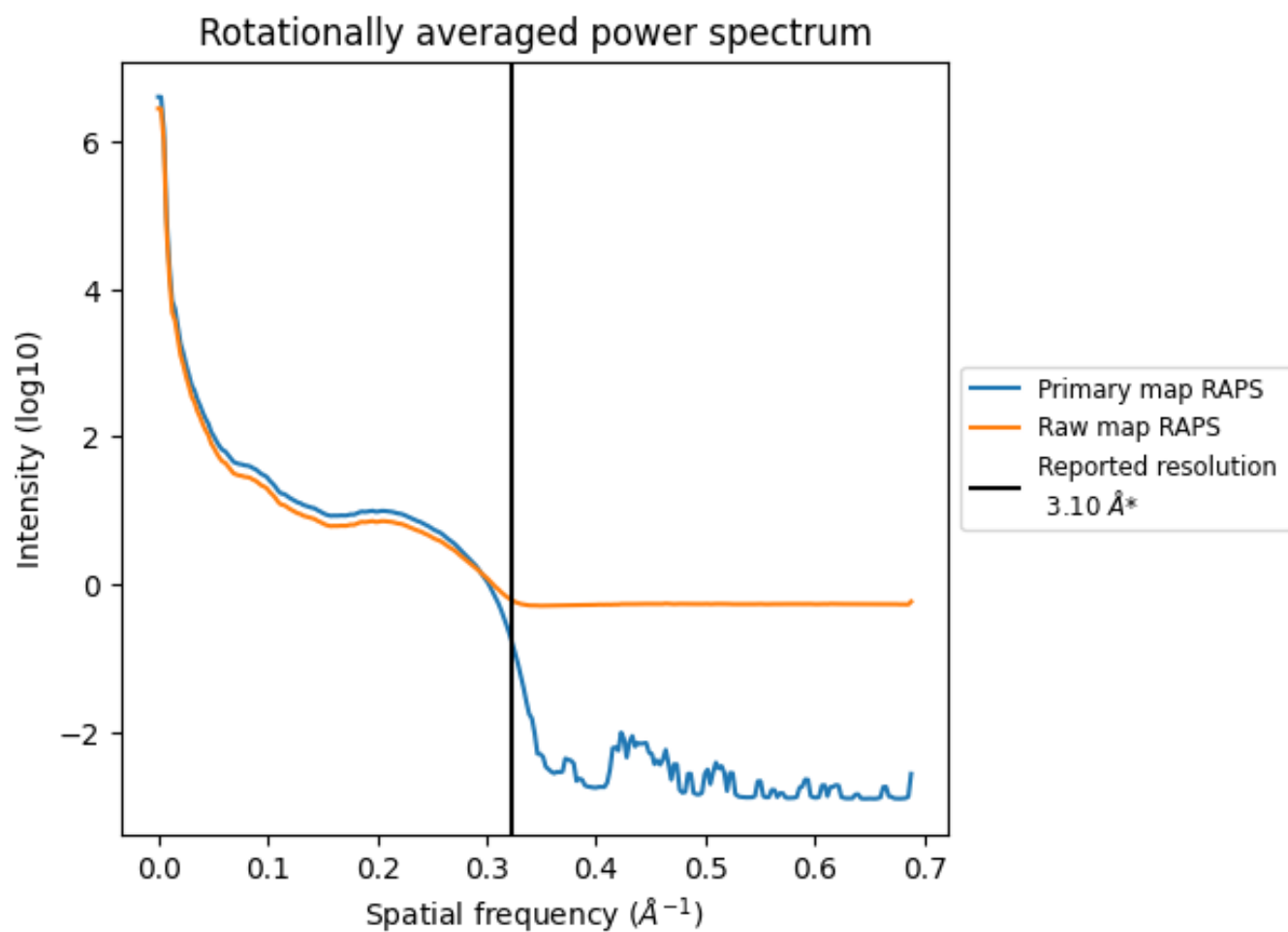
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2480 nm<sup>3</sup>; this corresponds to an approximate mass of 2240 kDa.

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

### 7.3 Rotationally averaged power spectrum [i](#)

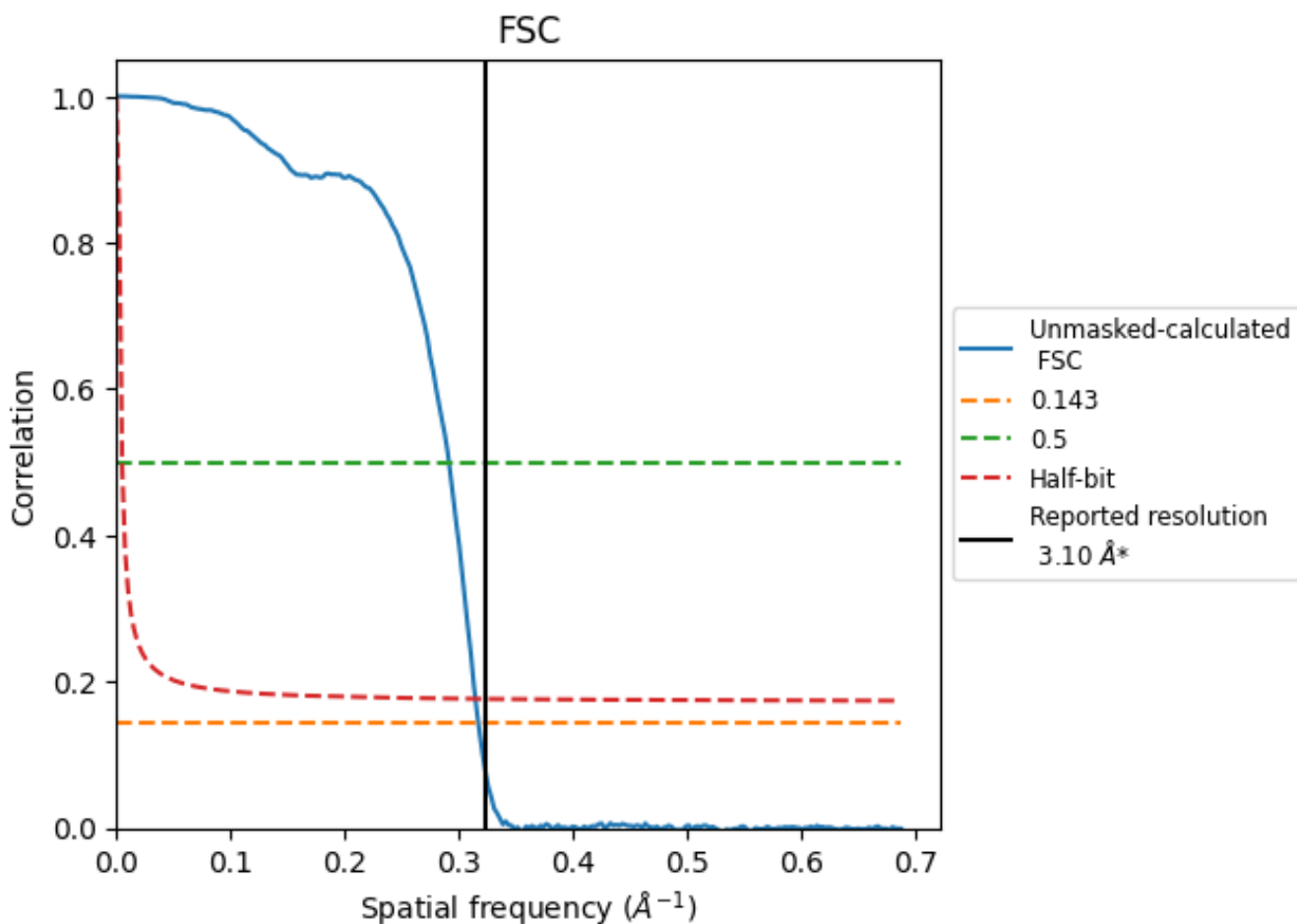


\*Reported resolution corresponds to spatial frequency of 0.323 Å<sup>-1</sup>

## 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 0.323 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

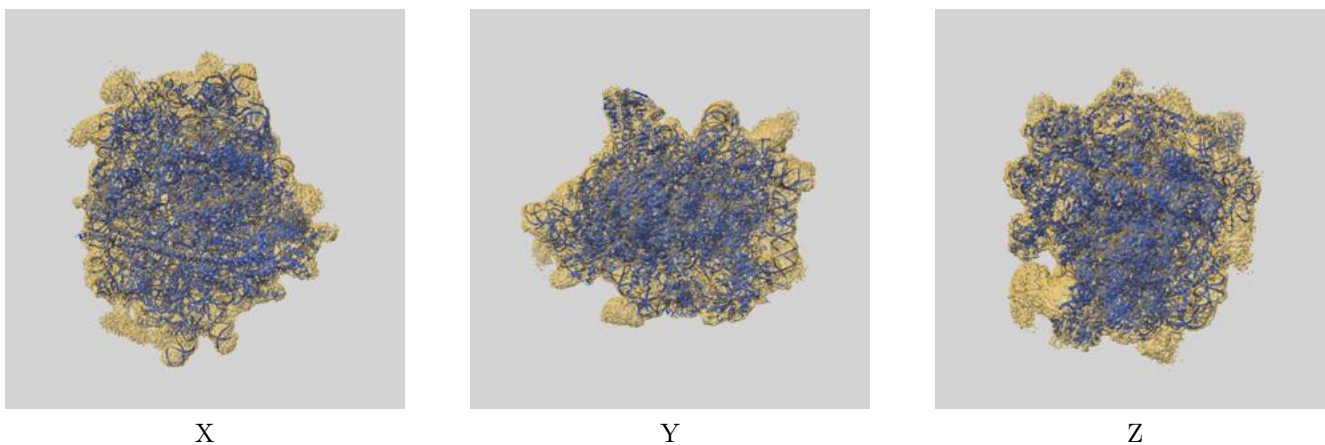
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.15	3.43	3.18

\*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-16880 and PDB model 8OHD. Per-residue inclusion information can be found in section [3](#) on page [14](#).

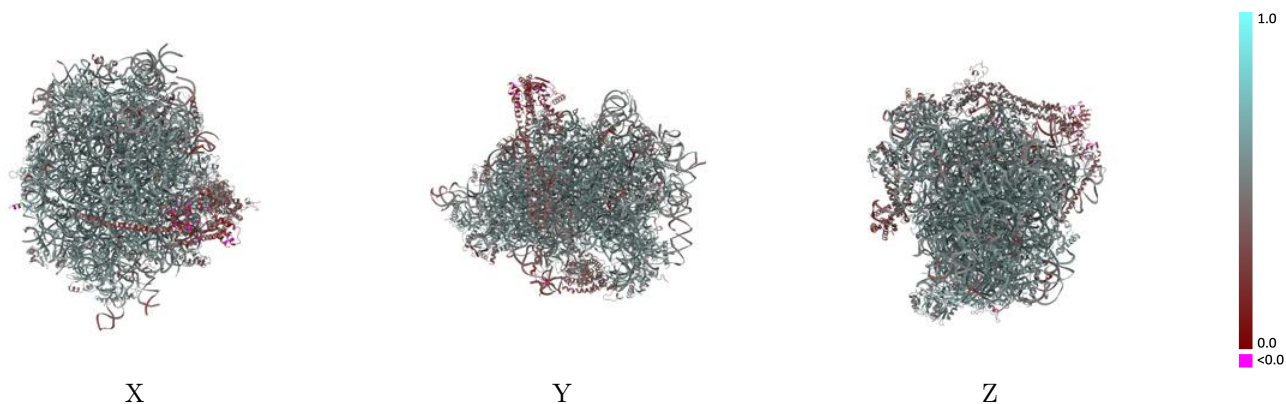
### 9.1 Map-model overlay [i](#)



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.

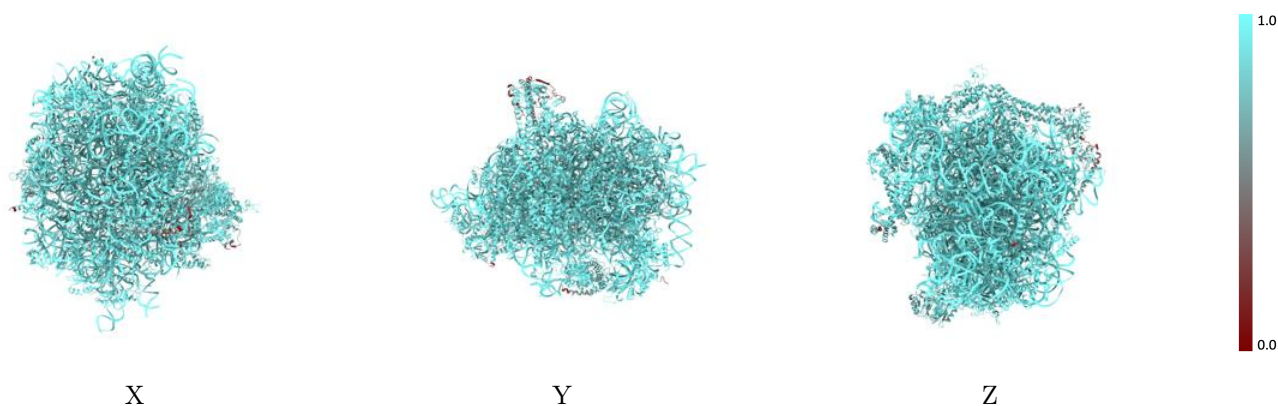


## 9.2 Q-score mapped to coordinate model [i](#)



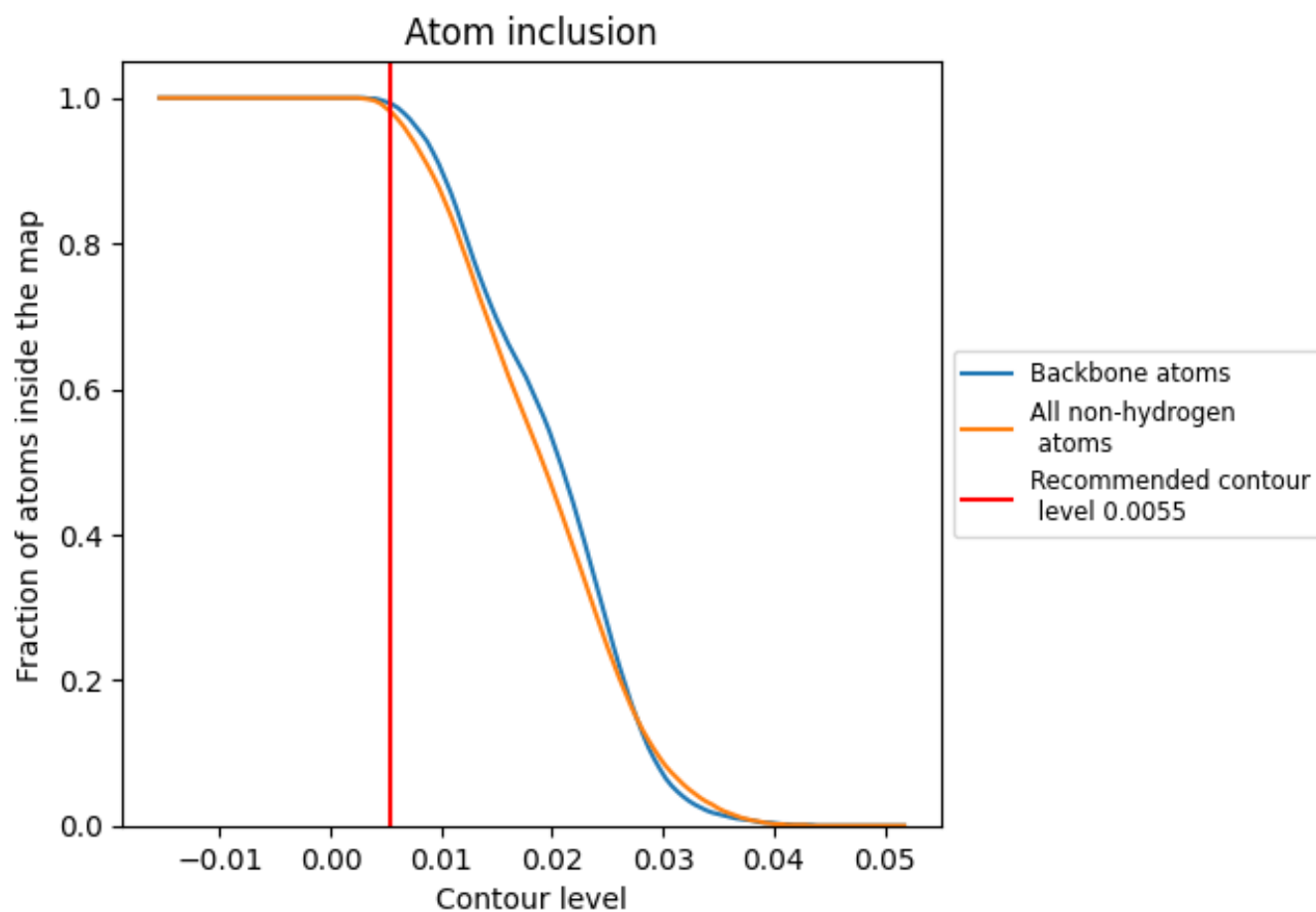
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 99% of all backbone atoms, 98% 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	 0.9800	 0.5310
5	 0.9990	 0.5420
7	 0.9990	 0.5580
8	 1.0000	 0.5580
A	 0.9010	 0.3960
B	 0.8540	 0.3040
C	 0.7120	 0.2650
D	 0.6670	 0.1940
K	 0.7950	 0.5090
LA	 0.9970	 0.5820
LB	 0.9830	 0.5670
LC	 0.9850	 0.5610
LD	 0.9790	 0.5360
LE	 0.9940	 0.5470
LF	 0.9960	 0.5640
LG	 0.9640	 0.5160
LH	 0.9920	 0.5580
LI	 0.9920	 0.5650
LJ	 0.9470	 0.5100
LL	 0.9830	 0.5470
LM	 0.9950	 0.5570
LN	 0.9990	 0.5860
LO	 0.9910	 0.5670
LP	 0.9940	 0.5750
LQ	 0.9970	 0.5750
LR	 0.9770	 0.5550
LS	 0.9960	 0.5770
LT	 0.9940	 0.5500
LU	 0.9770	 0.4900
LV	 0.9970	 0.5660
LW	 1.0000	 0.5740
LX	 0.9930	 0.5560
LY	 0.9870	 0.5590
LZ	 0.9940	 0.5500
La	 0.9910	 0.5790



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Chain	Atom inclusion	Q-score
Lb	 0.9620	 0.5180
Lc	 0.9710	 0.5360
Ld	 0.9850	 0.5500
Le	 0.9980	 0.5770
Lf	 0.9960	 0.5840
Lg	 0.9920	 0.5590
Lh	 0.9870	 0.5500
Li	 0.9810	 0.5420
Lj	 0.9990	 0.5850
Lk	 0.9610	 0.5190
Ll	 1.0000	 0.5680
Lm	 0.9930	 0.5630
Lo	 0.9810	 0.5620
Lp	 0.9900	 0.5560
Lr	 0.9990	 0.5680
Lz	 0.9310	 0.4320