



wwPDB EM Validation Summary Report ⓘ

Dec 19, 2022 – 04:17 am GMT

PDB ID : 7BHP
EMDB ID : EMD-12189
Title : Cryo-EM structure of the human Ebp1 - 80S ribosome
Authors : Desogus, J.; Bhaskar, V.; Chao, J.A.
Deposited on : 2021-01-11
Resolution : 3.30 Å(reported)
Based on initial models : 2Q8K, 2V6C, 6Y0G

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

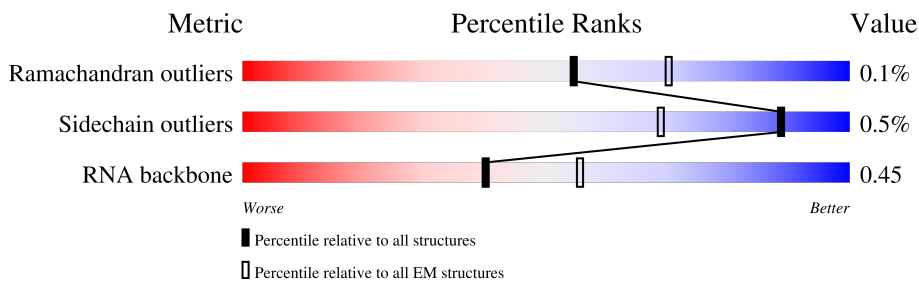
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 3.30 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	L5	5070	
2	L7	120	
3	L8	156	
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	


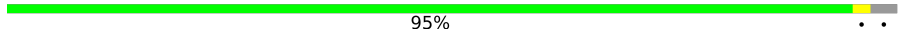


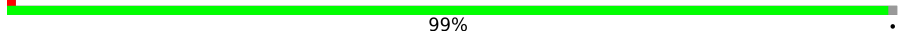
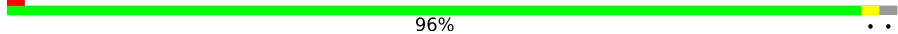

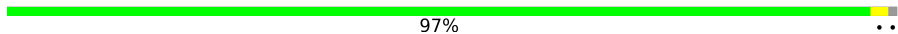




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Mol	Chain	Length	Quality of chain
9	LF	248	90% 9%
10	LG	266	82% 17%
11	LH	192	99%
12	LI	214	94% 5%
13	LJ	178	90% 10%
14	LL	211	94% 6%
15	LM	215	59% 40%
16	LN	204	100%
17	LO	203	98%
18	LP	184	83% 17%
19	LQ	188	97%
20	LR	196	76% 23%
21	LS	176	98%
22	LT	160	98%
23	LU	128	79% 21%
24	LW	157	27% 73%
25	LX	156	75% 25%
26	LY	145	91% 9%
27	LZ	136	95%
28	La	148	99%
29	Lb	159	43% 57%
30	Lc	115	82% 18%
31	Ld	125	86% 14%
32	Le	135	93% 7%
33	Lf	110	98%

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Mol	Chain	Length	Quality of chain
34	Lg	117	 87% 12%
35	Lh	123	 95%
36	Li	105	 91% 8%
37	Lj	97	 87% 11%
38	Lk	70	 99%
39	Ll	51	 96%
40	Lm	128	 40% 59%
41	Lo	106	 97%
42	Lp	92	 78% 22%
43	Lr	137	 88% 11%
44	A	394	 81% 18%
45	B	36	 53% 47%

2 Entry composition [i](#)

There are 48 unique types of molecules in this entry. The entry contains 136812 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	L5	3644	78119	34786	14297	25393	3643	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L5	2113	C	G	conflict	GB 86475748

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	L7	120	2558	1141	456	842	119	0	0

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

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

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	LA	247	1887	1183	388	310	6	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	LB	395	3183	2028	600	541	14	0	0

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	LC	359	2855	1797	571	472	15	0	0

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	LD	290	2354	1492	428	420	14	0	0

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	LE	221	1777	1142	337	294	4	0	0

- Molecule 9 is a protein called 60S ribosomal protein L7.

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

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	LG	220	1780	1135	343	298	4	0	0

- Molecule 11 is a protein called 60S ribosomal protein L9.

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

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LI	204	1643	1042	316	272	13	0	0

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	161	Total	C	N	O	S	0	0
			1294	815	244	229	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	199	Total	C	N	O	S	0	0
			1612	1011	337	260	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	129	Total	C	N	O	S	0	0
			1067	684	205	171	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

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

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	198	Total	C	N	O	S	0	0
			1625	1048	317	255	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

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

- Molecule 19 is a protein called 60S ribosomal protein L18.

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

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	LR	151	1264	787	273	195	9	0	0

- Molecule 21 is a protein called 60S ribosomal protein L18a.

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

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	LT	157	1284	815	250	214	5	0	0

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	LU	101	821	526	143	150	2	0	0

- Molecule 24 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	LW	42	350	223	69	56	2	0	0

- Molecule 25 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	LX	117	946	604	178	163	1	0	0

- Molecule 26 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	LY	132	1102	692	223	184	3	0	0

- Molecule 27 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LZ	130	Total	C	N	O	S	0	0
			1074	697	203	171	3		

- Molecule 28 is a protein called 60S ribosomal protein L27a.

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

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lb	68	Total	C	N	O	S	0	0
			559	344	122	90	3		

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lc	94	Total	C	N	O	S	0	0
			737	468	130	133	6		

- Molecule 31 is a protein called 60S ribosomal protein L31.

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

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Le	126	Total	C	N	O	S	0	0
			1043	661	214	163	5		

- Molecule 33 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lf	108	Total	C	N	O	S	0	0
			870	552	173	142	3		

- Molecule 34 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lg	103	Total	C	N	O	S	0	0
			821	513	170	132	6		

- Molecule 35 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lh	119	Total	C	N	O	S	0	0
			995	629	201	164	1		

- Molecule 36 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Li	97	Total	C	N	O	S	0	0
			803	503	171	124	5		

- Molecule 37 is a protein called 60S ribosomal protein L37.

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

- Molecule 38 is a protein called 60S ribosomal protein L38.

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

- Molecule 39 is a protein called 60S ribosomal protein L39.

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

- Molecule 40 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 41 is a protein called 60S ribosomal protein L36a.

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

- Molecule 42 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lp	72	Total	C	N	O	S	0	0
			558	353	107	91	7		

- Molecule 43 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lr	122	Total	C	N	O	S	0	0
			980	607	204	165	4		

- Molecule 44 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	A	322	Total	C	N	O	S	0	0
			2352	1514	413	412	13		

- Molecule 45 is a RNA chain called Poly GC double helix strand modeled for ES27L density next to EBP1 density.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	B	36	Total	C	N	O	P	0	0
			774	342	144	252	36		

- Molecule 46 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
46	L5	33	Total	Mg	0
			33	33	
46	L7	3	Total	Mg	0
			3	3	
46	L8	4	Total	Mg	0
			4	4	
46	L1	1	Total	Mg	0
			1	1	

- Molecule 47 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

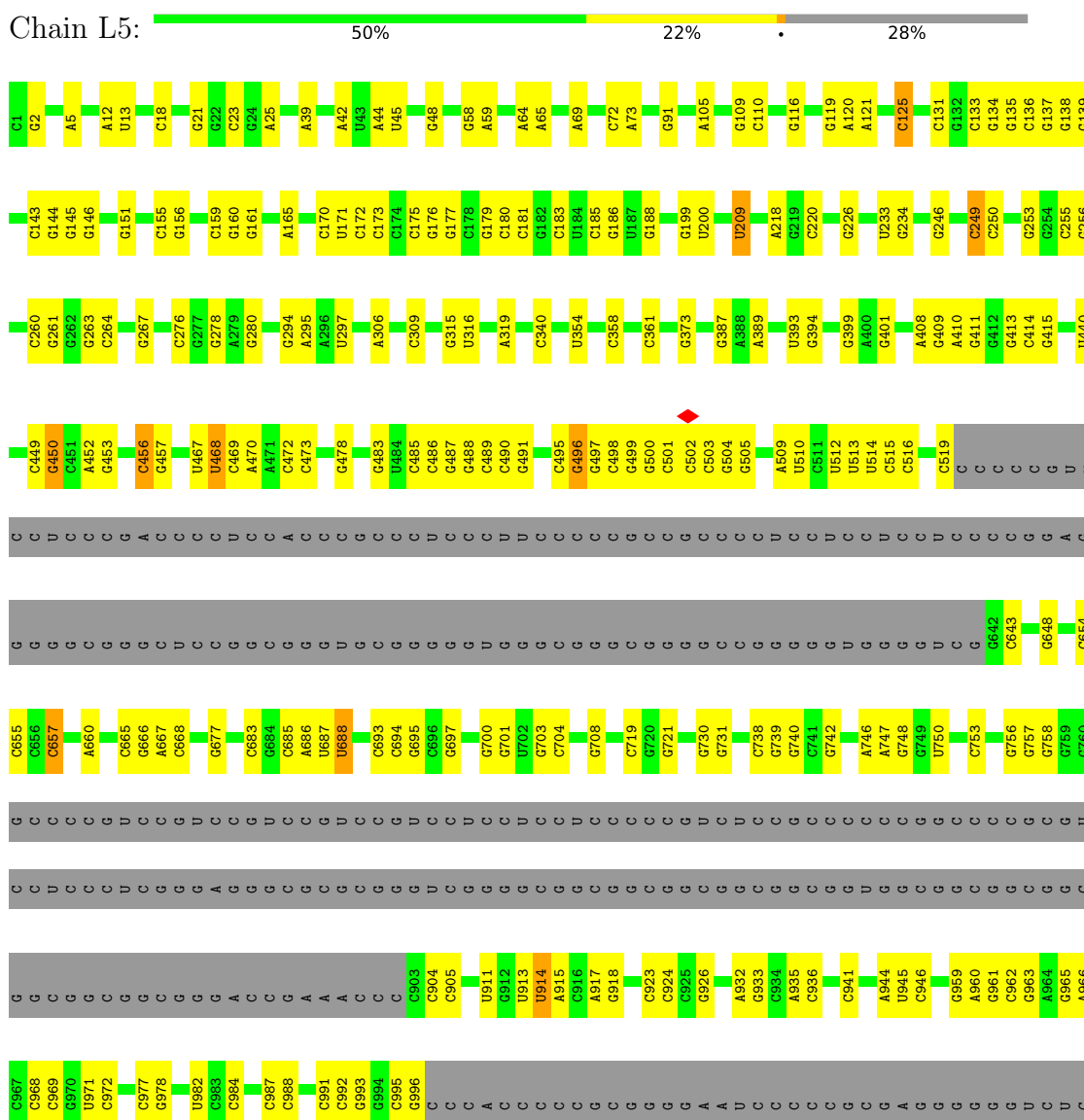
- Molecule 48 is water.

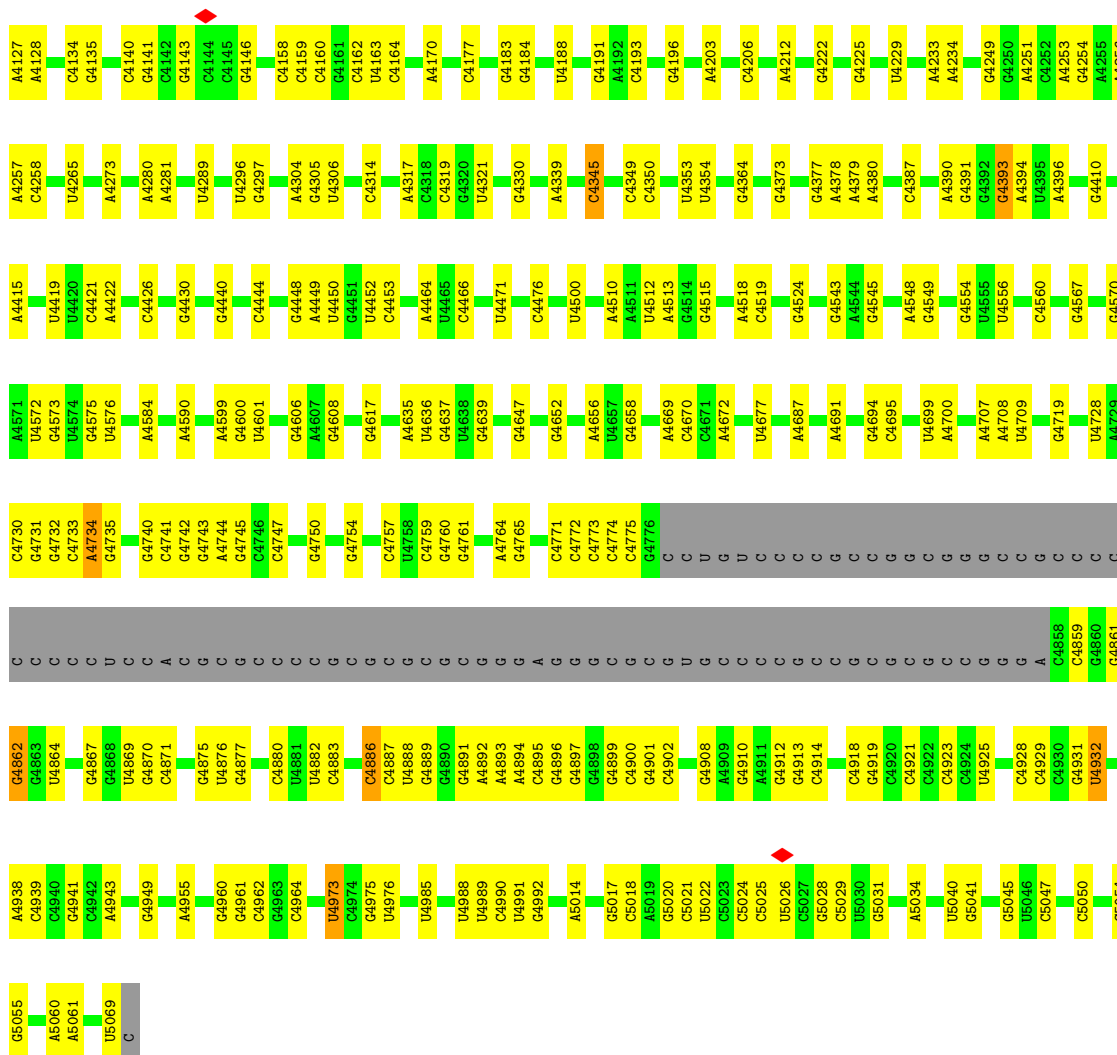
Mol	Chain	Residues	Atoms		AltConf
48	L5	5	Total 5	O 5	0
48	L7	4	Total 4	O 4	0
48	LI	1	Total 1	O 1	0

3 Residue-property plots [i](#)

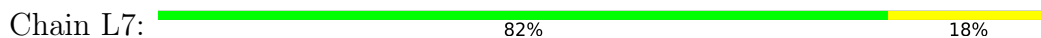
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 28S ribosomal RNA

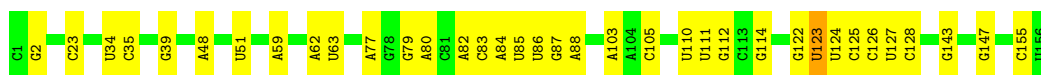
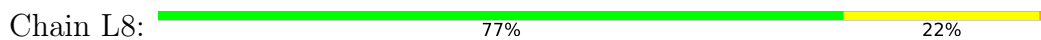




• Molecule 2: 5S ribosomal RNA

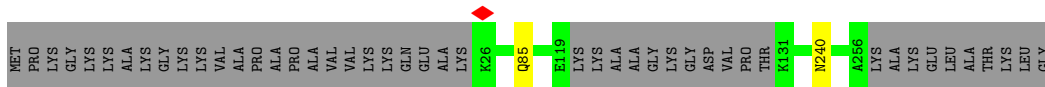


• Molecule 3: 5.8S ribosomal RNA

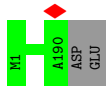


• Molecule 4: 60S ribosomal protein L8

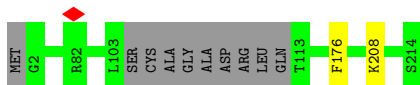




• Molecule 11: 60S ribosomal protein L9



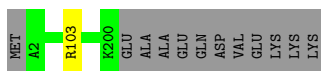
• Molecule 12: 60S ribosomal protein L10-like



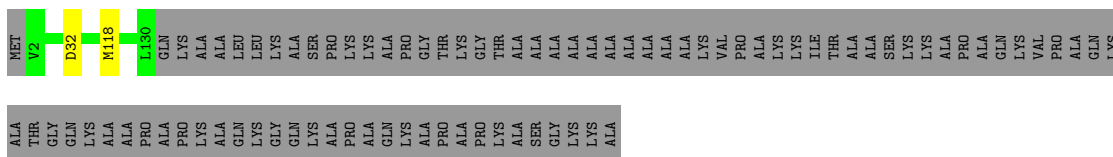
• Molecule 13: 60S ribosomal protein L11



• Molecule 14: 60S ribosomal protein L13



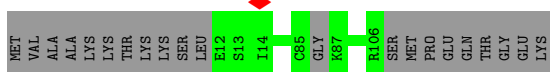
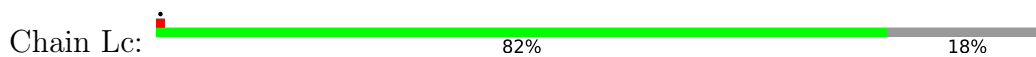
• Molecule 15: 60S ribosomal protein L14



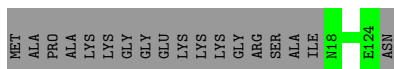
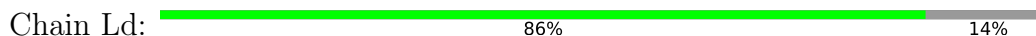
• Molecule 16: 60S ribosomal protein L15



• Molecule 17: 60S ribosomal protein L13a



- Molecule 31: 60S ribosomal protein L31



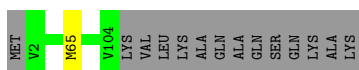
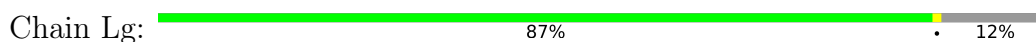
- Molecule 32: 60S ribosomal protein L32



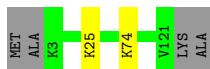
- Molecule 33: 60S ribosomal protein L35a



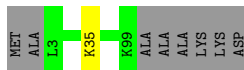
- Molecule 34: 60S ribosomal protein L34




- Molecule 35: 60S ribosomal protein L35

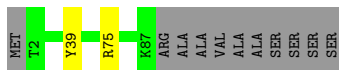


- Molecule 36: 60S ribosomal protein L36



- Molecule 37: 60S ribosomal protein L37

Chain Lj:  87% 11%



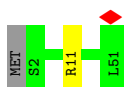
- Molecule 38: 60S ribosomal protein L38

Chain Lk:  99%



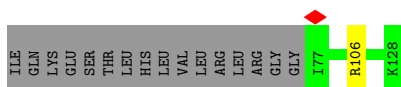
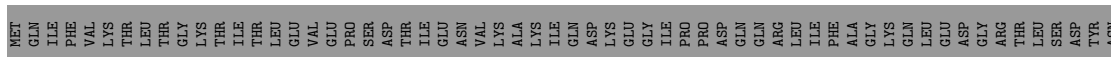
- Molecule 39: 60S ribosomal protein L39

Chain Ll:  96%



- Molecule 40: Ubiquitin-60S ribosomal protein L40

Chain Lm:  40% 59%




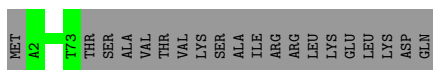
- Molecule 41: 60S ribosomal protein L36a

Chain Lo:  97%




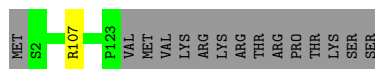
- Molecule 42: 60S ribosomal protein L37a

Chain Lp:  78% 22%



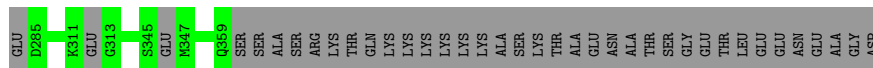
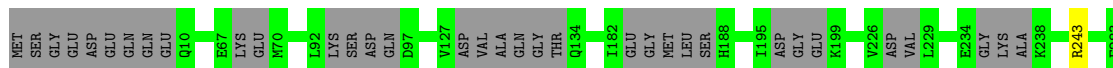
- Molecule 43: 60S ribosomal protein L28

Chain Lr:  88% 11%



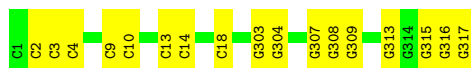
- Molecule 44: Proliferation-associated protein 2G4

Chain A: 81% 18%



- Molecule 45: Poly GC double helix strand modeled for ES27L density next to EBP1 density

Chain B: 53% 47%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44556	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.029	Depositor
Minimum map value	-0.008	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	516.0, 516.0, 516.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	L5	0.74	1/87379 (0.0%)	0.92	93/136294 (0.1%)
2	L7	0.72	0/2858	0.87	0/4455
3	L8	0.77	1/3701 (0.0%)	0.92	7/5766 (0.1%)
4	LA	0.42	0/1925	0.60	1/2581 (0.0%)
5	LB	0.40	0/3251	0.55	1/4351 (0.0%)
6	LC	0.39	0/2909	0.52	0/3907
7	LD	0.38	0/2400	0.50	0/3215
8	LE	0.36	0/1811	0.51	0/2428
9	LF	0.43	0/1905	0.54	1/2539 (0.0%)
10	LG	0.37	0/1811	0.50	0/2441
11	LH	0.38	0/1537	0.53	0/2066
12	LI	0.41	0/1682	0.52	0/2247
13	LJ	0.34	0/1314	0.53	0/1754
14	LL	0.38	0/1643	0.53	0/2199
15	LM	0.42	0/1089	0.58	2/1457 (0.1%)
16	LN	0.45	0/1746	0.49	0/2338
17	LO	0.41	0/1657	0.52	0/2216
18	LP	0.43	0/1268	0.54	0/1701
19	LQ	0.41	0/1537	0.55	1/2052 (0.0%)
20	LR	0.35	0/1280	0.51	1/1694 (0.1%)
21	LS	0.41	0/1493	0.53	0/2003
22	LT	0.40	0/1312	0.49	0/1753
23	LU	0.34	0/835	0.52	0/1122
24	LW	0.38	0/359	0.49	0/477
25	LX	0.39	0/963	0.55	0/1299
26	LY	0.38	0/1119	0.51	0/1488
27	LZ	0.40	0/1096	0.54	0/1459
28	La	0.41	0/1191	0.52	0/1591
29	Lb	0.39	0/569	0.53	0/750
30	Lc	0.38	0/746	0.53	0/1000
31	Ld	0.39	0/903	0.51	0/1216
32	Le	0.41	0/1061	0.52	0/1415

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lf	0.43	0/889	0.54	0/1190
34	Lg	0.41	0/831	0.58	1/1108 (0.1%)
35	Lh	0.35	0/1003	0.55	1/1326 (0.1%)
36	Li	0.36	0/814	0.51	0/1076
37	Lj	0.45	0/720	0.59	0/952
38	Lk	0.36	0/575	0.57	0/761
39	Ll	0.37	0/454	0.60	1/599 (0.2%)
40	Lm	0.34	0/435	0.51	0/575
41	Lo	0.40	0/876	0.58	1/1156 (0.1%)
42	Lp	0.44	0/568	0.53	0/754
43	Lr	0.39	0/995	0.51	0/1334
44	A	0.32	0/2387	0.49	0/3218
45	B	0.45	0/861	1.16	4/1338 (0.3%)
All	All	0.63	2/147758 (0.0%)	0.81	115/218661 (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	LB	0	1
8	LE	0	1
9	LF	0	1
12	LI	0	1
19	LQ	0	1
37	Lj	0	1
All	All	0	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L8	62	A	N9-C4	-6.35	1.34	1.37
1	L5	1296	G	N9-C4	-5.16	1.33	1.38

The worst 5 of 115 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	1296	G	N3-C4-N9	-9.46	120.32	126.00
1	L5	1296	G	C4-N9-C1'	-8.94	114.87	126.50
1	L5	1996	C	N1-C2-O2	8.34	123.91	118.90
1	L5	468	U	C5-C6-N1	8.30	126.85	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	468	U	C2-N1-C1'	8.27	127.62	117.70

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	LB	390	GLY	Peptide
8	LE	130	LYS	Peptide
9	LF	162	ILE	Peptide
12	LI	176	PHE	Peptide
19	LQ	161	SER	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	
4	LA	245/257 (95%)	205 (84%)	39 (16%)	1 (0%)	34	66
5	LB	393/403 (98%)	339 (86%)	54 (14%)	0	100	100
6	LC	357/427 (84%)	316 (88%)	41 (12%)	0	100	100
7	LD	288/297 (97%)	262 (91%)	26 (9%)	0	100	100
8	LE	215/288 (75%)	183 (85%)	32 (15%)	0	100	100
9	LF	223/248 (90%)	210 (94%)	13 (6%)	0	100	100
10	LG	216/266 (81%)	191 (88%)	25 (12%)	0	100	100
11	LH	188/192 (98%)	168 (89%)	20 (11%)	0	100	100
12	LI	200/214 (94%)	165 (82%)	35 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	LJ	157/178 (88%)	138 (88%)	19 (12%)	0	100	100
14	LL	197/211 (93%)	178 (90%)	19 (10%)	0	100	100
15	LM	127/215 (59%)	115 (91%)	12 (9%)	0	100	100
16	LN	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
17	LO	196/203 (97%)	180 (92%)	16 (8%)	0	100	100
18	LP	151/184 (82%)	140 (93%)	11 (7%)	0	100	100
19	LQ	185/188 (98%)	172 (93%)	11 (6%)	2 (1%)	14	45
20	LR	149/196 (76%)	140 (94%)	9 (6%)	0	100	100
21	LS	173/176 (98%)	147 (85%)	26 (15%)	0	100	100
22	LT	155/160 (97%)	137 (88%)	18 (12%)	0	100	100
23	LU	99/128 (77%)	89 (90%)	10 (10%)	0	100	100
24	LW	38/157 (24%)	33 (87%)	5 (13%)	0	100	100
25	LX	115/156 (74%)	99 (86%)	16 (14%)	0	100	100
26	LY	130/145 (90%)	117 (90%)	13 (10%)	0	100	100
27	LZ	126/136 (93%)	114 (90%)	12 (10%)	0	100	100
28	La	145/148 (98%)	129 (89%)	16 (11%)	0	100	100
29	Lb	66/159 (42%)	56 (85%)	10 (15%)	0	100	100
30	Lc	90/115 (78%)	83 (92%)	7 (8%)	0	100	100
31	Ld	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
32	Le	124/135 (92%)	114 (92%)	10 (8%)	0	100	100
33	Lf	106/110 (96%)	93 (88%)	13 (12%)	0	100	100
34	Lg	101/117 (86%)	87 (86%)	14 (14%)	0	100	100
35	Lh	117/123 (95%)	108 (92%)	9 (8%)	0	100	100
36	Li	95/105 (90%)	90 (95%)	5 (5%)	0	100	100
37	Lj	84/97 (87%)	71 (84%)	13 (16%)	0	100	100
38	Lk	67/70 (96%)	60 (90%)	7 (10%)	0	100	100
39	Ll	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
40	Lm	50/128 (39%)	46 (92%)	4 (8%)	0	100	100
41	Lo	103/106 (97%)	87 (84%)	15 (15%)	1 (1%)	15	46
42	Lp	70/92 (76%)	61 (87%)	9 (13%)	0	100	100
43	Lr	120/137 (88%)	104 (87%)	16 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	A	300/394 (76%)	265 (88%)	35 (12%)	0	100	100
All	All	6315/7441 (85%)	5623 (89%)	688 (11%)	4 (0%)	54	81

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	LA	247	ARG
19	LQ	160	HIS
41	Lo	103	VAL
19	LQ	159	PRO

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	LA	188/199 (94%)	185 (98%)	3 (2%)	62	79
5	LB	342/349 (98%)	339 (99%)	3 (1%)	78	87
6	LC	298/348 (86%)	296 (99%)	2 (1%)	84	90
7	LD	243/250 (97%)	243 (100%)	0	100	100
8	LE	195/252 (77%)	193 (99%)	2 (1%)	76	86
9	LF	194/215 (90%)	194 (100%)	0	100	100
10	LG	190/223 (85%)	188 (99%)	2 (1%)	73	85
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	172/181 (95%)	171 (99%)	1 (1%)	86	91
13	LJ	136/149 (91%)	135 (99%)	1 (1%)	84	90
14	LL	167/177 (94%)	166 (99%)	1 (1%)	86	91
15	LM	111/161 (69%)	111 (100%)	0	100	100
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	170/174 (98%)	170 (100%)	0	100	100
18	LP	134/163 (82%)	134 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	LQ	164/165 (99%)	163 (99%)	1 (1%)	86	91
20	LR	135/175 (77%)	134 (99%)	1 (1%)	84	90
21	LS	156/157 (99%)	154 (99%)	2 (1%)	69	82
22	LT	138/140 (99%)	138 (100%)	0	100	100
23	LU	90/115 (78%)	90 (100%)	0	100	100
24	LW	37/126 (29%)	37 (100%)	0	100	100
25	LX	102/133 (77%)	102 (100%)	0	100	100
26	LY	123/135 (91%)	123 (100%)	0	100	100
27	LZ	113/118 (96%)	112 (99%)	1 (1%)	78	87
28	La	120/121 (99%)	119 (99%)	1 (1%)	81	89
29	Lb	58/126 (46%)	58 (100%)	0	100	100
30	Lc	80/97 (82%)	80 (100%)	0	100	100
31	Ld	98/110 (89%)	98 (100%)	0	100	100
32	Le	114/121 (94%)	114 (100%)	0	100	100
33	Lf	87/89 (98%)	87 (100%)	0	100	100
34	Lg	89/100 (89%)	89 (100%)	0	100	100
35	Lh	108/110 (98%)	107 (99%)	1 (1%)	78	87
36	Li	85/89 (96%)	84 (99%)	1 (1%)	71	83
37	Lj	73/80 (91%)	72 (99%)	1 (1%)	67	82
38	Lk	64/65 (98%)	64 (100%)	0	100	100
39	Ll	47/48 (98%)	47 (100%)	0	100	100
40	Lm	48/116 (41%)	47 (98%)	1 (2%)	53	75
41	Lo	93/94 (99%)	93 (100%)	0	100	100
42	Lp	57/75 (76%)	57 (100%)	0	100	100
43	Lr	106/121 (88%)	105 (99%)	1 (1%)	78	87
44	A	223/336 (66%)	222 (100%)	1 (0%)	91	95
All	All	5488/6346 (86%)	5461 (100%)	27 (0%)	89	93

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	LL	103	ARG
21	LS	120	ARG

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Mol	Chain	Res	Type
40	Lm	106	ARG
20	LR	107	ARG
21	LS	160	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
12	LI	144	ASN
36	Li	26	HIS
14	LL	115	GLN
28	La	120	GLN
14	LL	111	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3627/5070 (71%)	1096 (30%)	32 (0%)
2	L7	119/120 (99%)	22 (18%)	0
3	L8	155/156 (99%)	33 (21%)	2 (1%)
45	B	33/36 (91%)	14 (42%)	0
All	All	3934/5382 (73%)	1165 (29%)	34 (0%)

5 of 1165 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	5	A
1	L5	13	U
1	L5	18	C
1	L5	21	G

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	4699	U
1	L5	4731	G
3	L8	86	U
1	L5	2108	G
1	L5	2084	C

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 45 ligands modelled in this entry, 45 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
45	B	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	18:C	O3'	300:G	P	15.70
1	B	313:G	O3'	314:G	P	4.54

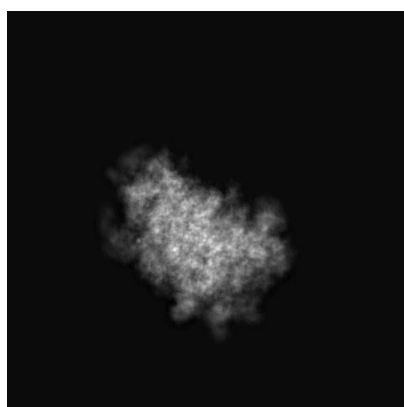
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12189. These allow visual inspection of the internal detail of the map and identification of artifacts.

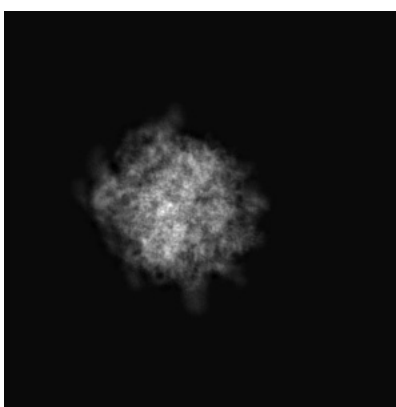
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

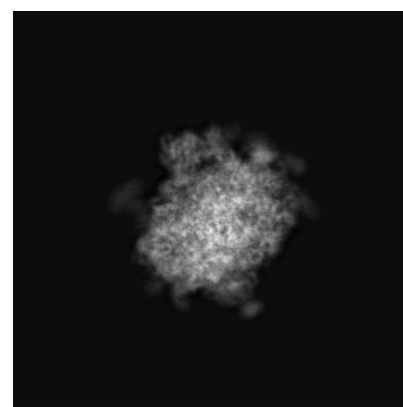
6.1.1 Primary map



X



Y

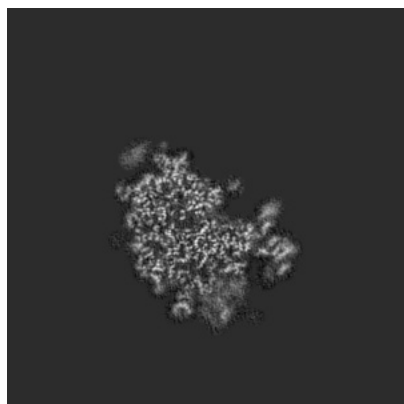


Z

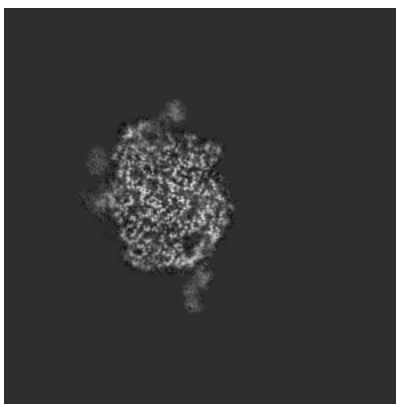
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

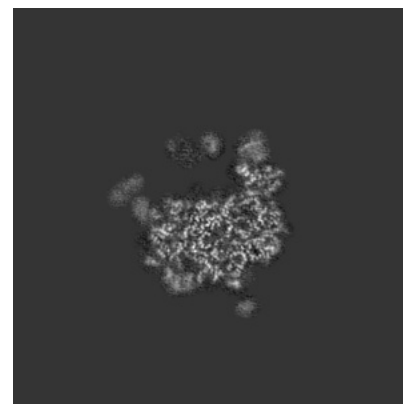
6.2.1 Primary map



X Index: 300



Y Index: 300

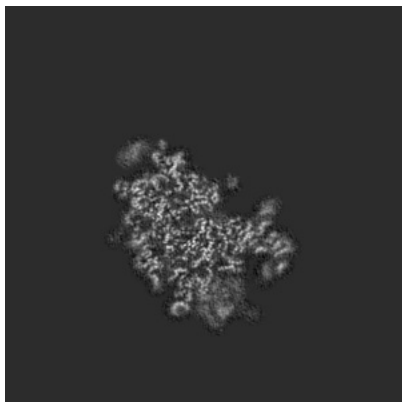


Z Index: 300

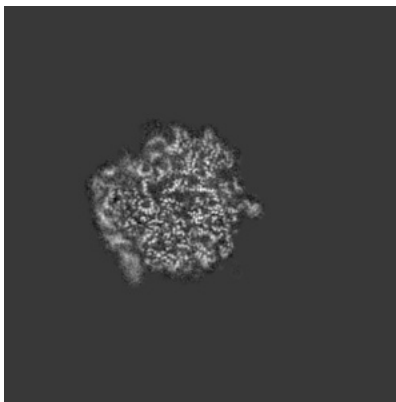
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

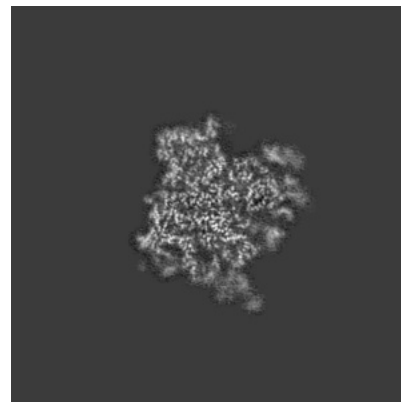
6.3.1 Primary map



X Index: 303



Y Index: 267



Z Index: 241

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

6.4 Orthogonal surface views [i](#)

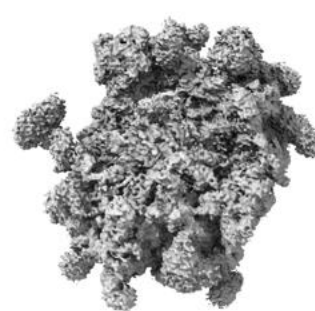
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.004. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

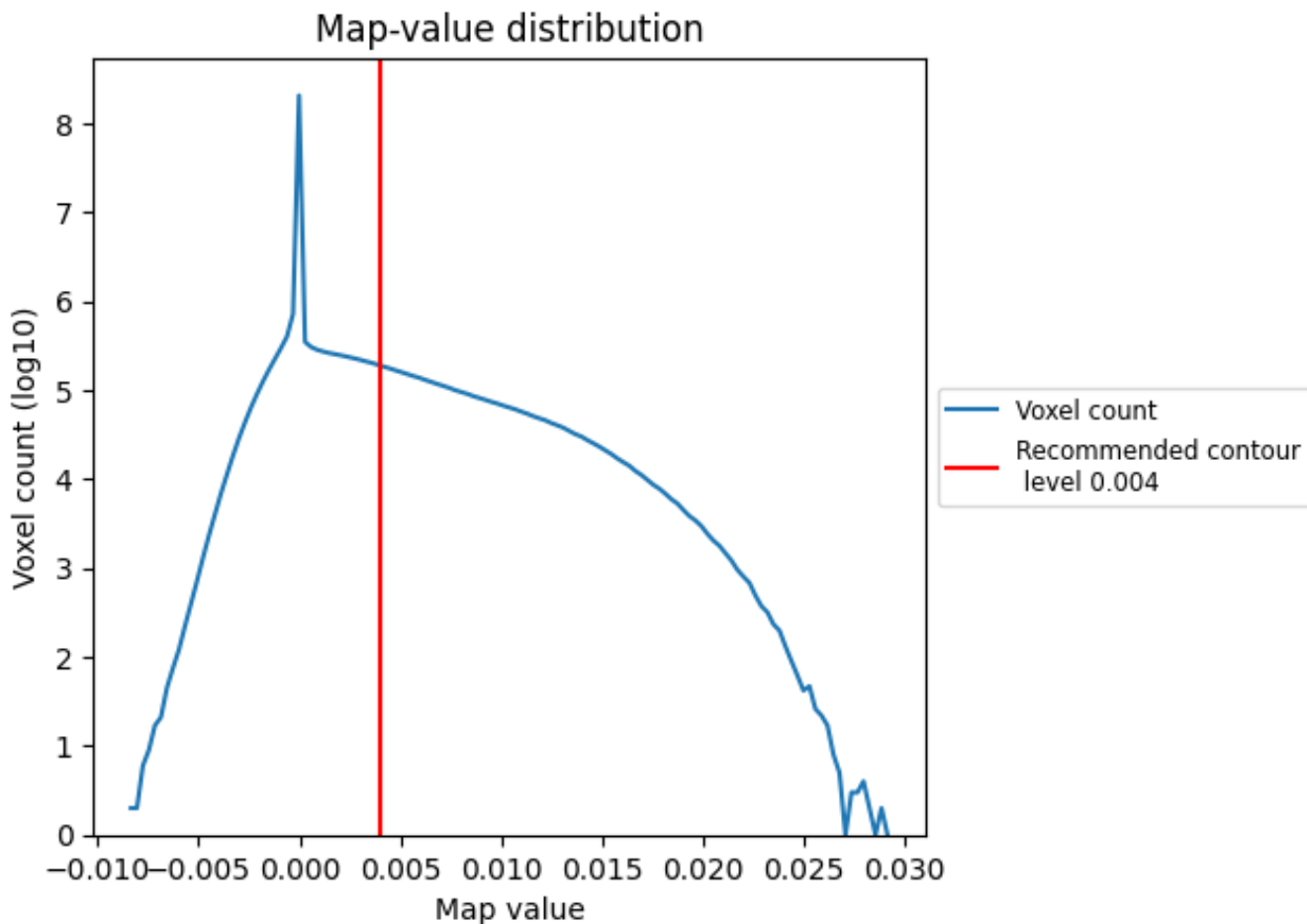
6.5 Mask visualisation

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

7 Map analysis [i](#)

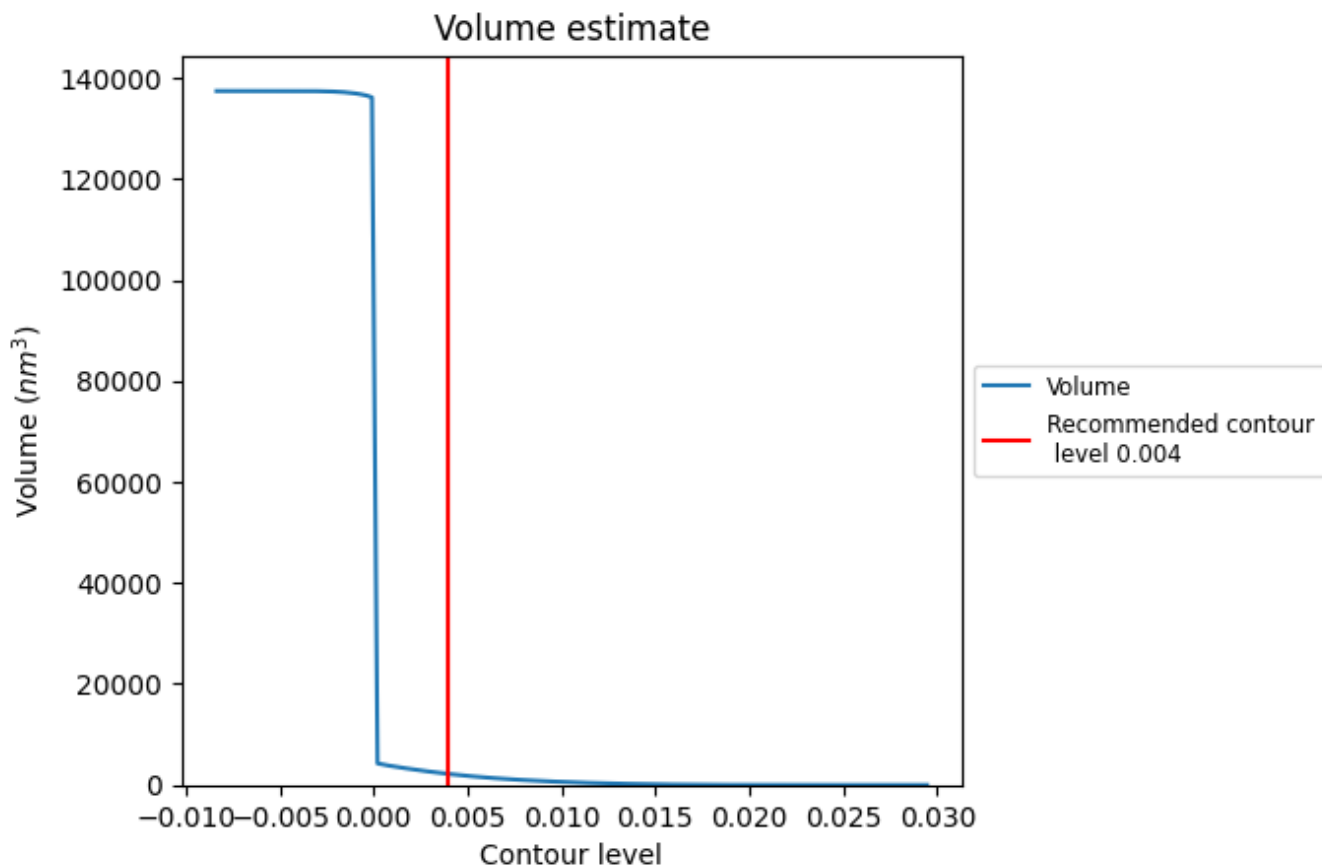
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

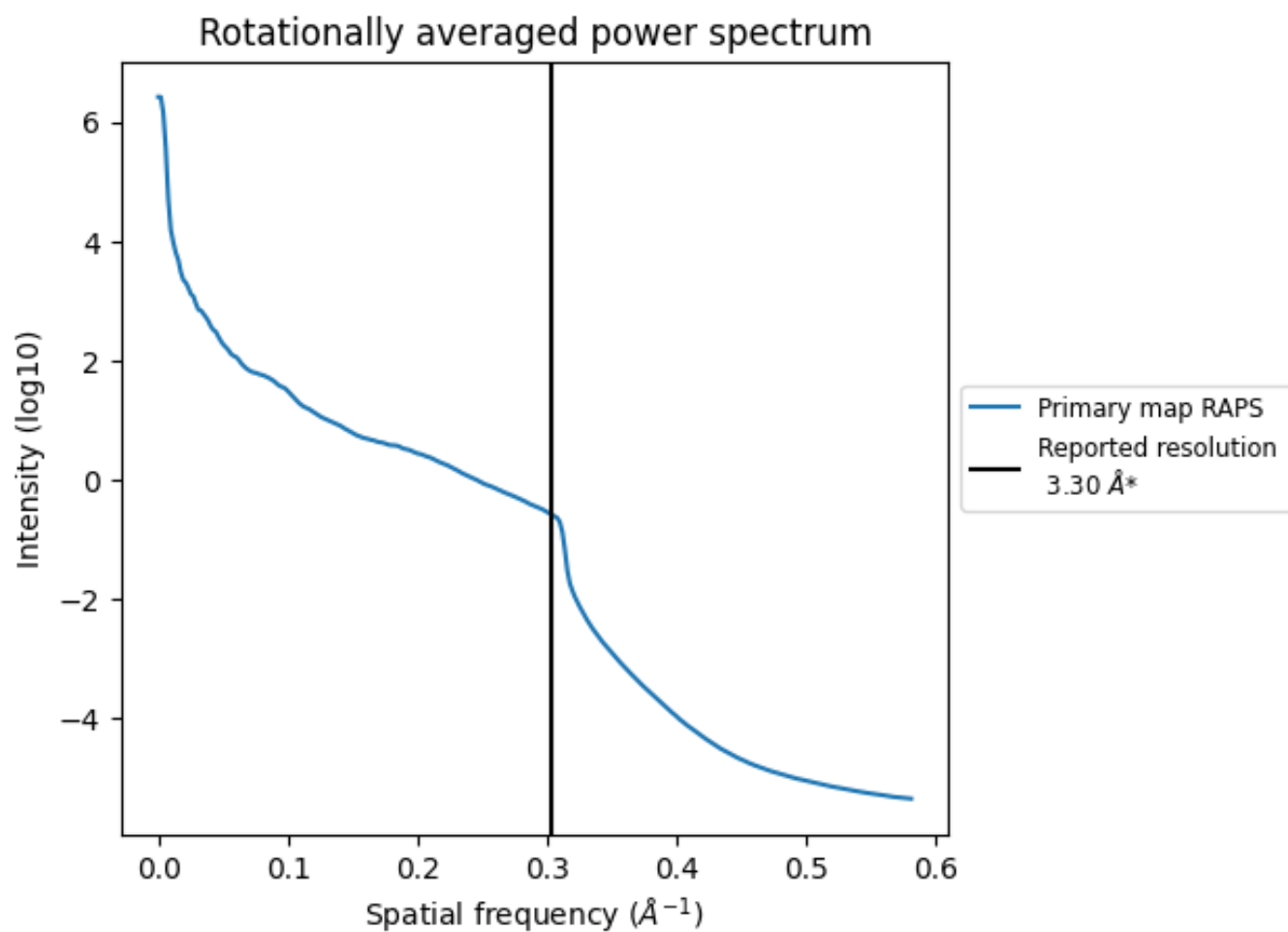
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2181 nm³; this corresponds to an approximate mass of 1970 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 0.303\AA^{-1}

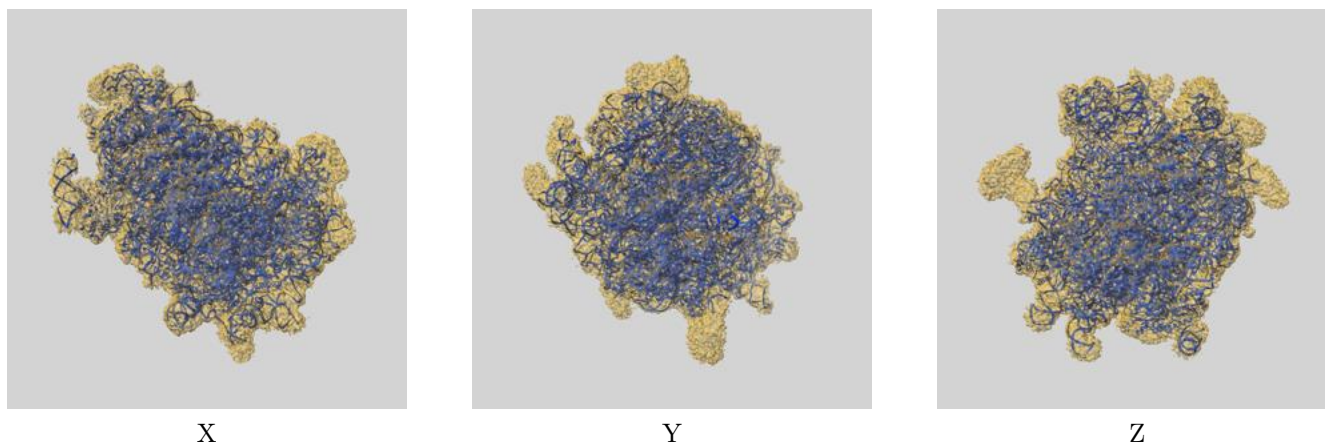
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

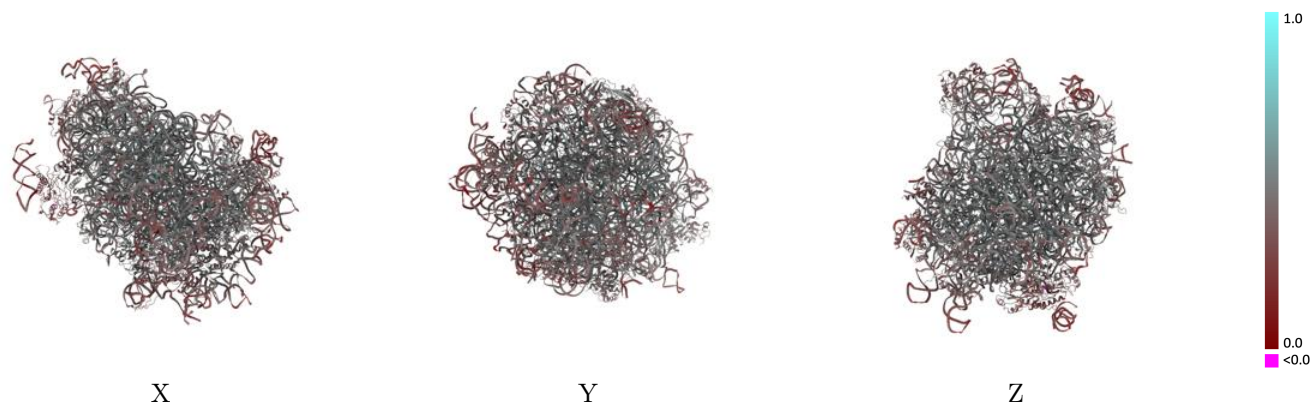
This section contains information regarding the fit between EMDB map EMD-12189 and PDB model 7BHP. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



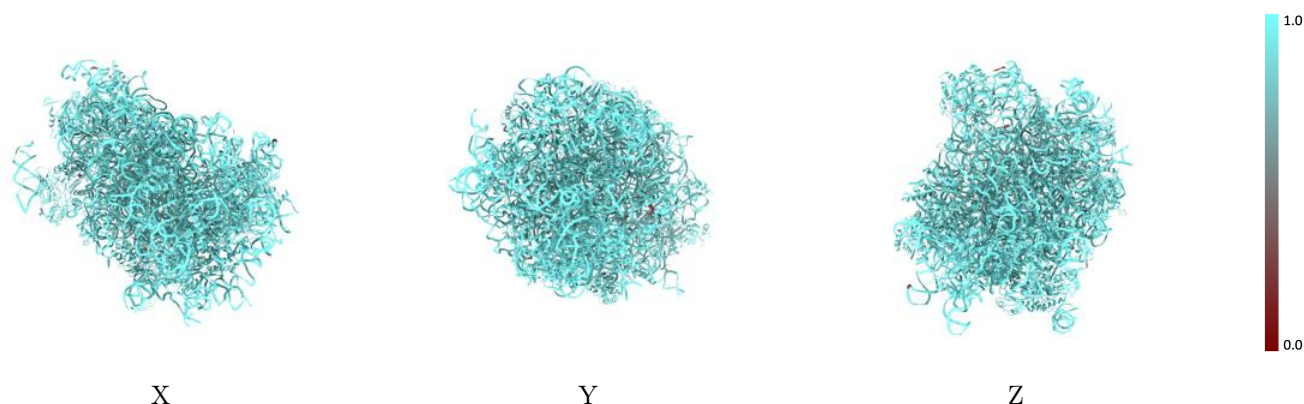
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



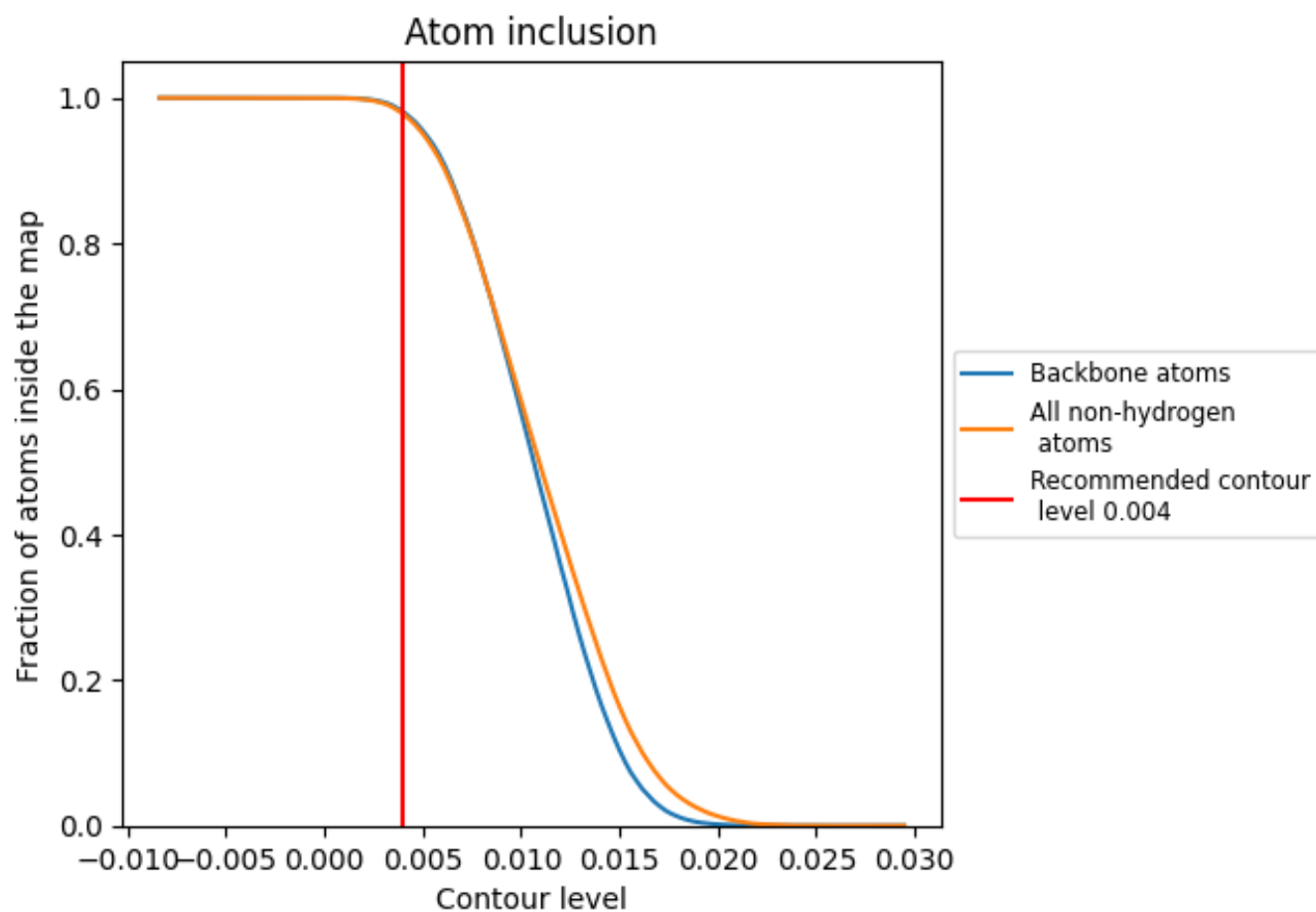
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.004).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% 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 (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9783	 0.4390
A	 0.9526	 0.3530
B	 0.9264	 0.2410
L5	 0.9925	 0.4370
L7	 0.9992	 0.4440
L8	 0.9931	 0.4510
LA	 0.9337	 0.4700
LB	 0.9491	 0.4600
LC	 0.9576	 0.4730
LD	 0.9759	 0.4060
LE	 0.9572	 0.4200
LF	 0.9507	 0.4530
LG	 0.9467	 0.4110
LH	 0.9642	 0.4410
LI	 0.9649	 0.4400
LJ	 0.9665	 0.3810
LL	 0.9586	 0.4390
LM	 0.9672	 0.4410
LN	 0.9599	 0.4870
LO	 0.9529	 0.4540
LP	 0.9569	 0.4650
LQ	 0.9475	 0.4740
LR	 0.9677	 0.4520
LS	 0.9586	 0.4650
LT	 0.9592	 0.4600
LU	 0.9714	 0.3950
LW	 0.9320	 0.4300
LX	 0.9554	 0.4550
LY	 0.9850	 0.4530
LZ	 0.9615	 0.4250
La	 0.9584	 0.4760
Lb	 0.9595	 0.4330
Lc	 0.9292	 0.4070
Ld	 0.9627	 0.4640
Le	 0.9543	 0.4920



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Chain	Atom inclusion	Q-score
Lf	 0.9713	 0.4890
Lg	 0.9605	 0.4730
Lh	 0.9417	 0.4360
Li	 0.9597	 0.4340
Lj	 0.9866	 0.4900
Lk	 0.9048	 0.3940
Ll	 0.9670	 0.4550
Lm	 0.9591	 0.4470
Lo	 0.9618	 0.4360
Lp	 0.9503	 0.4780
Lr	 0.9681	 0.4680