



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 09:40 PM UTC

PDB ID : 8KAB / pdb_00008kab
EMDB ID : EMD-37007
Title : Mycobacterium smegmatis 50S ribosomal subunit-HflX complex
Authors : Srinivasan, K.; Banerjee, A.; Sengupta, J.
Deposited on : 2023-08-02
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

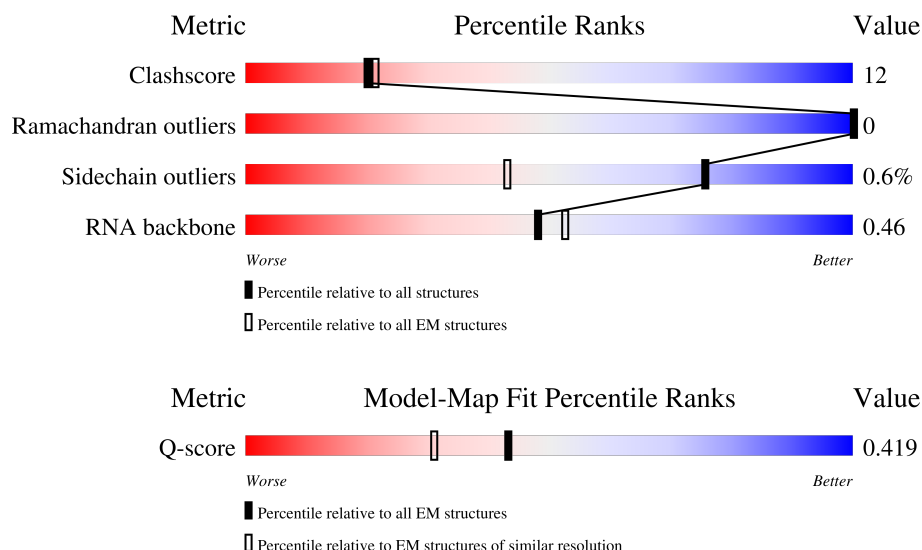
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.30 Å.

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



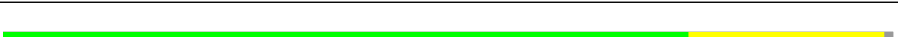
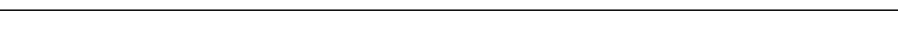
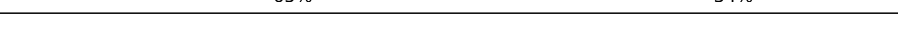
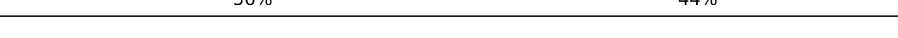
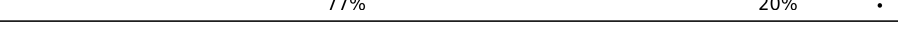
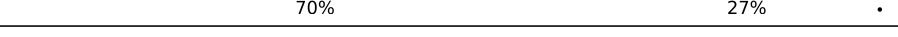
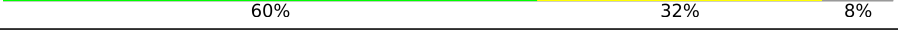
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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

Mol	Chain	Length	Quality of chain
1	3	24	
2	A	3120	
3	B	118	

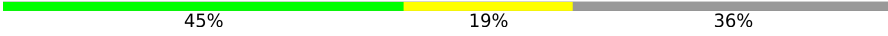
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Mol	Chain	Length	Quality of chain
4	C	278	
5	D	217	
6	E	215	
7	F	187	
8	G	179	
9	H	151	
10	I	175	
11	J	142	
12	K	147	
13	L	122	
14	M	147	
15	N	138	
16	O	199	
17	P	127	
18	Q	113	
19	R	129	
20	S	103	
21	T	153	
22	U	100	
23	V	105	
24	W	215	
25	X	88	
26	Y	64	
27	Z	77	
28	a	61	

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Mol	Chain	Length	Quality of chain
29	b	57	
30	c	55	
31	d	47	
32	e	64	
33	f	37	
34	g	75	
35	h	483	

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 100780 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 2 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	3111	Total	C	N	O	P	0	0
			66813	29778	12283	21641	3111		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 10 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 11 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 15 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	126	Total	C	N	O		0	0
			956	586	199	171			

- Molecule 18 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 19 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 20 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	100	Total	C	N	O		0	0
			754	478	137	139			

- Molecule 21 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 24 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	a	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 30 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	48	Total	C	N	O	S	0	0
			397	244	81	68	4		

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	e	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 34 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

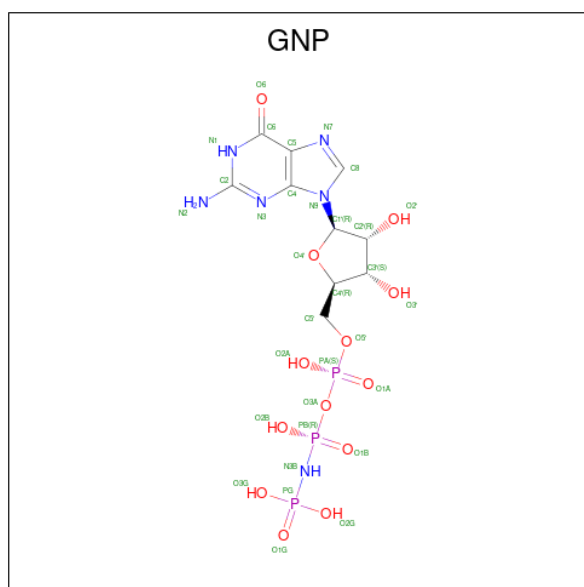
- Molecule 35 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	430	Total	C	N	O	S	0	0
			3256	2016	603	630	7		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	471	LYS	-	expression tag	UNP A0QVY1
h	472	LEU	-	expression tag	UNP A0QVY1
h	473	ALA	-	expression tag	UNP A0QVY1
h	474	ALA	-	expression tag	UNP A0QVY1
h	475	ALA	-	expression tag	UNP A0QVY1
h	476	LEU	-	expression tag	UNP A0QVY1
h	477	GLU	-	expression tag	UNP A0QVY1
h	478	HIS	-	expression tag	UNP A0QVY1
h	479	HIS	-	expression tag	UNP A0QVY1
h	480	HIS	-	expression tag	UNP A0QVY1
h	481	HIS	-	expression tag	UNP A0QVY1
h	482	HIS	-	expression tag	UNP A0QVY1
h	483	HIS	-	expression tag	UNP A0QVY1

- Molecule 36 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
36	h	1	Total	C	N	O	P	0
			32	10	6	13	3	

3 Residue-property plots

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

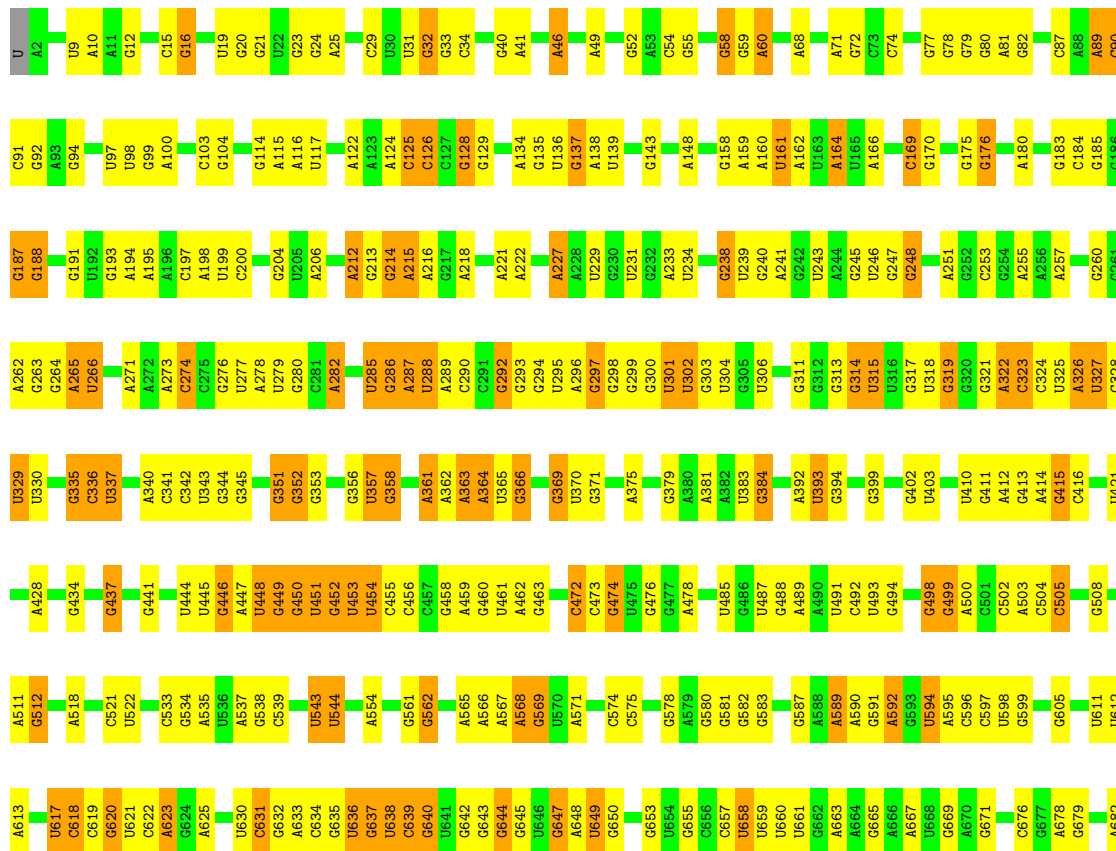
- Molecule 1: 50S ribosomal protein bL37

Chain 3: 

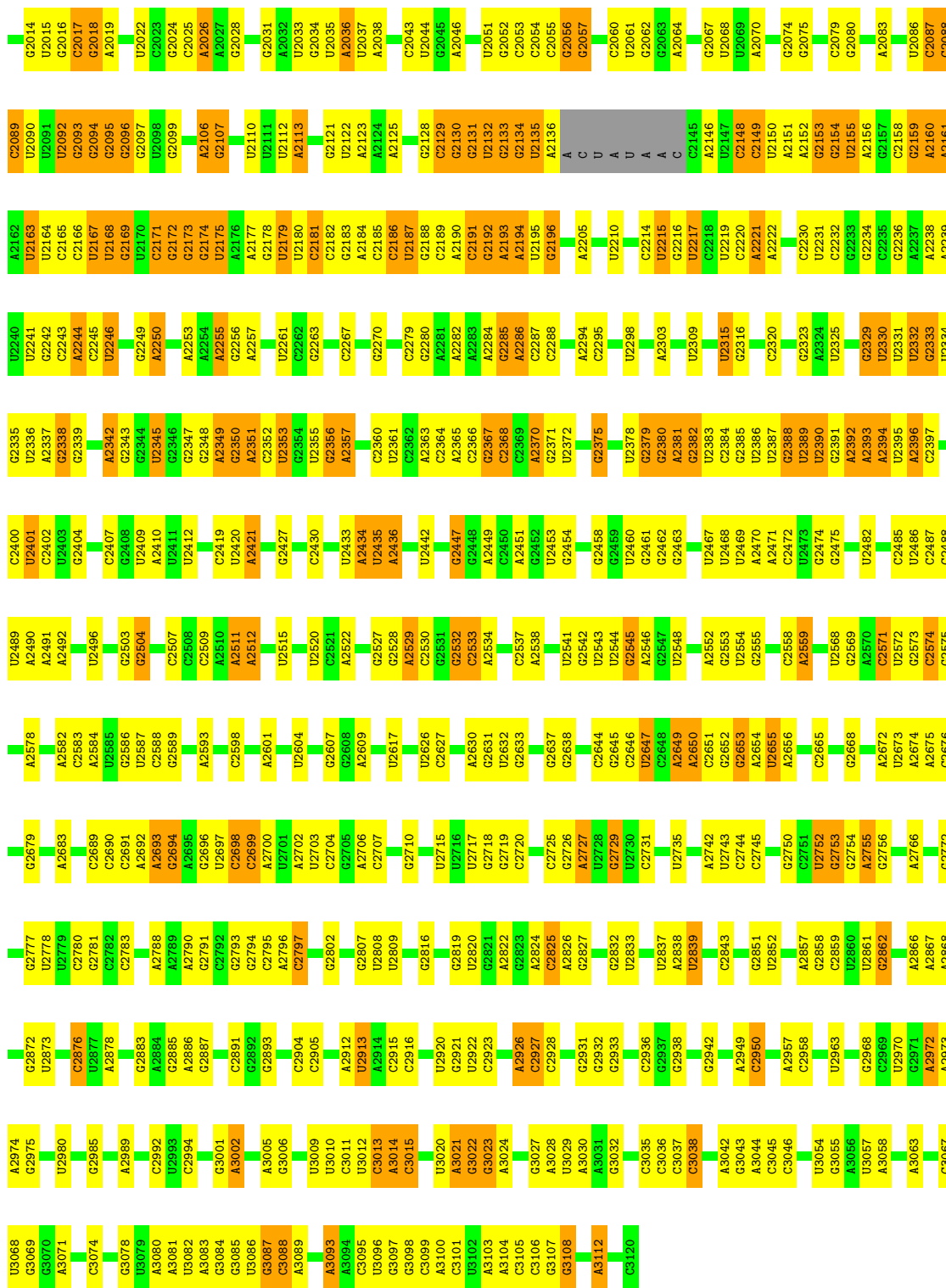


- Molecule 2: 23S rRNA

Chain A: 







• Molecule 3: 5S rRNA

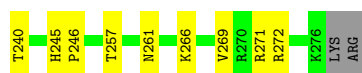
Chain B: 57% 37% 6%





• Molecule 4: 50S ribosomal protein L2

Chain C: 71% 28% .



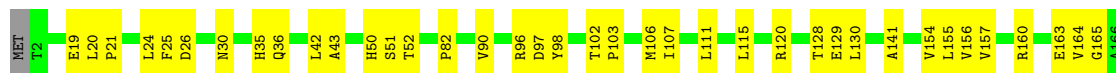
• Molecule 5: 50S ribosomal protein L3

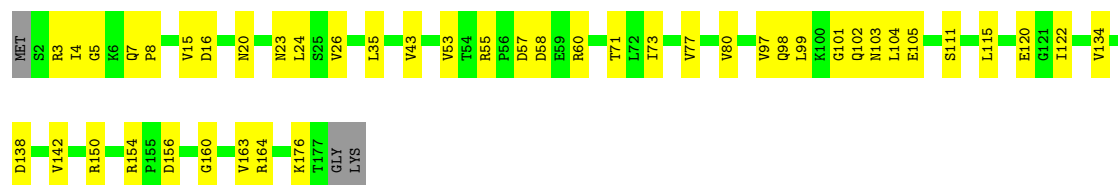
Chain D: 72% 26% .



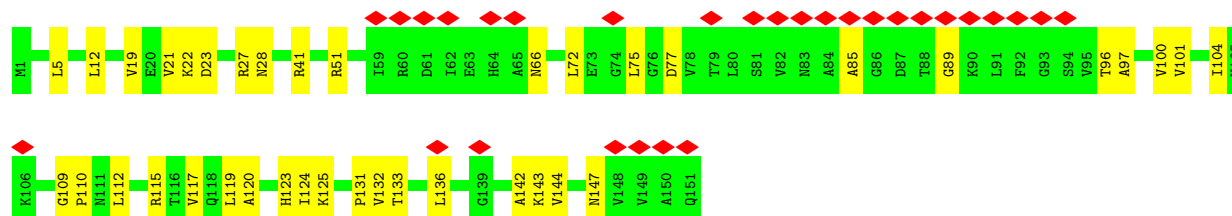
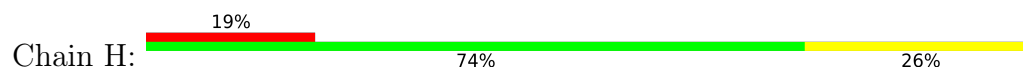
• Molecule 6: 50S ribosomal protein L4

Chain E: 72% 26% .

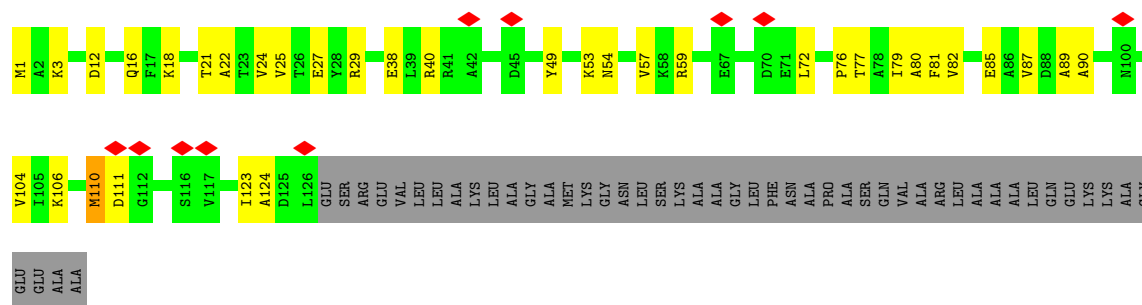




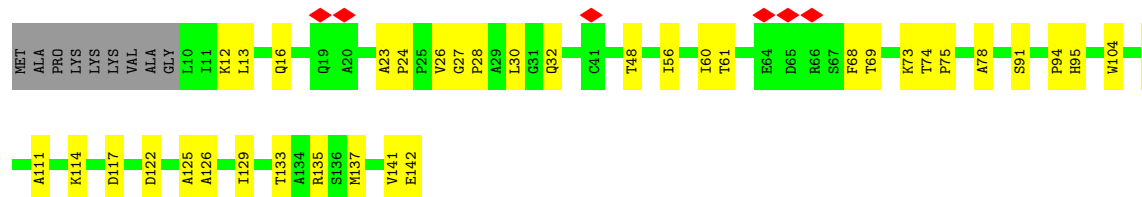
• Molecule 9: 50S ribosomal protein L9



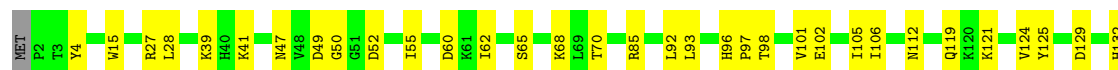
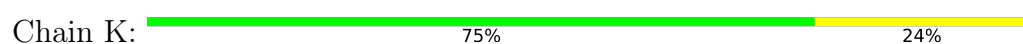
• Molecule 10: 50S ribosomal protein L10



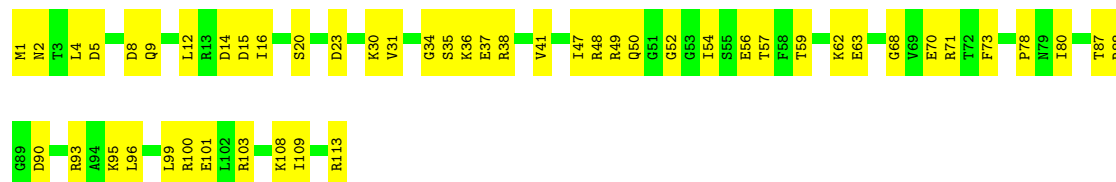
• Molecule 11: 50S ribosomal protein L11



• Molecule 12: 50S ribosomal protein L13



Chain Q:  56% 44%



- Molecule 19: 50S ribosomal protein L20

Chain R:  76% 20% .



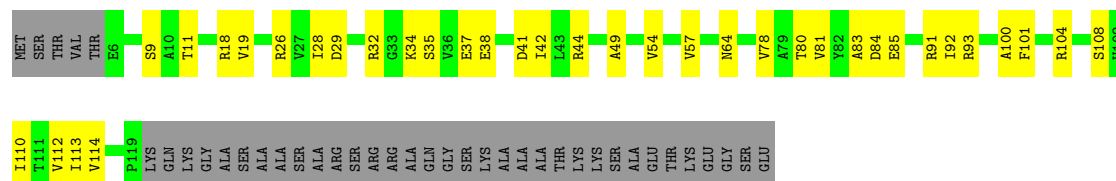
- Molecule 20: 50S ribosomal protein L21

Chain S:  77% 20% .



- Molecule 21: 50S ribosomal protein L22

Chain T:  51% 24% 25%



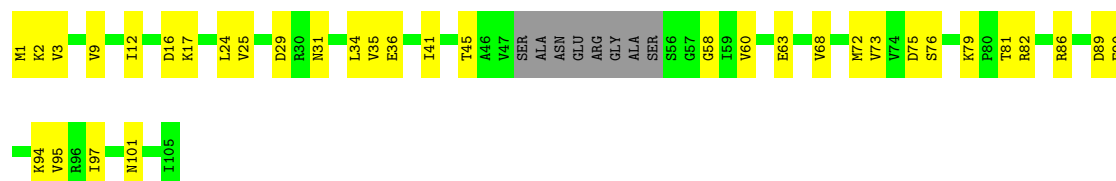
- Molecule 22: 50S ribosomal protein L23

Chain U:  70% 27% .



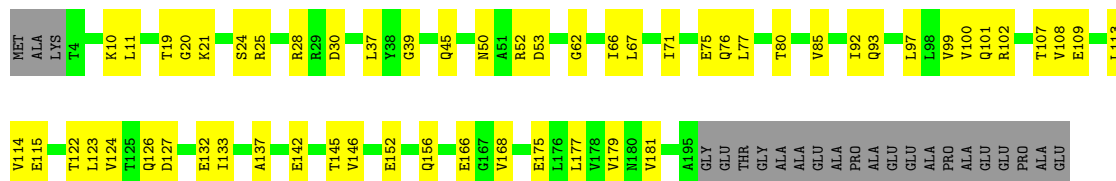
- Molecule 23: 50S ribosomal protein L24

Chain V:  60% 32% 8%



- Molecule 24: 50S ribosomal protein L25

Chain W:  63% 26% 11%



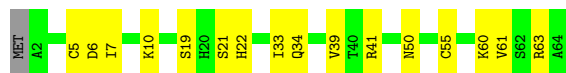
- Molecule 25: 50S ribosomal protein L27

Chain X:  76% 14% 10%



- Molecule 26: 50S ribosomal protein L28

Chain Y:  73% 25% .



- Molecule 27: 50S ribosomal protein L29

Chain Z:  49% 34% 17%



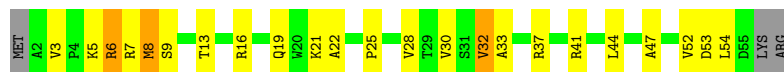
- Molecule 28: 50S ribosomal protein L30

Chain a:  70% 26% .



- Molecule 29: 50S ribosomal protein L32

Chain b:  54% 35% 5% 5%



- Molecule 30: 50S ribosomal protein L33 1

Chain c:  69% 18% 13%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	121211	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 ($e^-/\text{\AA}^2$)	28.26	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.086	Depositor
Minimum map value	-0.017	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	449.40002, 449.40002, 449.40002	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	3	0.23	0/191	0.44	0/247
2	A	0.26	0/74812	0.32	0/116731
3	B	0.20	0/2821	0.27	0/4396
4	C	0.24	0/2153	0.36	0/2895
5	D	0.25	0/1609	0.40	0/2165
6	E	0.24	0/1592	0.36	0/2153
7	F	0.15	0/1467	0.37	0/1973
8	G	0.16	0/1369	0.30	0/1848
9	H	0.14	0/1027	0.34	0/1398
10	I	0.14	0/925	0.31	0/1246
11	J	0.13	0/1006	0.32	0/1364
12	K	0.25	0/1157	0.36	0/1567
13	L	0.21	0/946	0.32	0/1268
14	M	0.24	0/1091	0.38	0/1457
15	N	0.21	0/1118	0.37	0/1506
16	O	0.25	0/945	0.42	0/1267
17	P	0.19	0/966	0.34	0/1298
18	Q	0.21	0/921	0.34	0/1236
19	R	0.30	0/1000	0.34	0/1341
20	S	0.22	0/764	0.29	0/1030
21	T	0.25	0/887	0.36	0/1204
22	U	0.21	0/766	0.32	0/1030
23	V	0.18	0/738	0.33	0/987
24	W	0.16	0/1443	0.33	0/1970
25	X	0.24	0/595	0.34	0/798
26	Y	0.24	0/478	0.38	0/641
27	Z	0.23	0/534	0.36	0/713
28	a	0.23	0/477	0.31	0/640
29	b	0.35	0/427	0.58	0/572
30	c	0.15	0/405	0.34	0/542
31	d	0.28	0/380	0.34	0/500
32	e	0.14	0/507	0.31	0/672

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.26	0/303	0.36	0/401
34	g	0.14	0/372	0.26	0/503
35	h	0.27	0/3297	0.50	2/4468 (0.0%)
All	All	0.25	0/109489	0.33	2/164027 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	h	198	VAL	N-CA-C	8.88	118.88	110.53
35	h	49	VAL	N-CA-C	5.92	118.15	108.97

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3	189	0	205	6	0
2	A	66813	0	33615	1159	0
3	B	2522	0	1285	41	0
4	C	2110	0	2165	65	0
5	D	1587	0	1630	45	0
6	E	1569	0	1607	46	0
7	F	1445	0	1476	66	0
8	G	1348	0	1399	35	0
9	H	1018	0	988	35	0
10	I	918	0	959	31	0
11	J	990	0	1021	42	0
12	K	1130	0	1167	33	0
13	L	938	0	1000	36	0
14	M	1078	0	1151	32	0
15	N	1092	0	1128	23	0
16	O	928	0	972	23	0
17	P	956	0	991	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	Q	907	0	938	40	0
19	R	988	0	1038	21	0
20	S	754	0	802	17	0
21	T	873	0	909	34	0
22	U	756	0	802	23	0
23	V	732	0	782	29	0
24	W	1428	0	1443	46	0
25	X	586	0	601	13	0
26	Y	470	0	484	11	0
27	Z	531	0	541	27	0
28	a	474	0	500	17	0
29	b	423	0	463	26	0
30	c	397	0	407	9	0
31	d	377	0	411	17	0
32	e	502	0	541	17	0
33	f	299	0	324	6	0
34	g	364	0	352	11	0
35	h	3256	0	3311	166	0
36	h	32	0	13	0	0
All	All	100780	0	67421	2007	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 2007 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:102:THR:HG23	6:E:107:ILE:HD11	1.27	1.16
35:h:73:LEU:O	35:h:76:THR:HG22	1.46	1.14
21:T:92:ILE:HD11	21:T:100:ALA:HB1	1.39	1.01
12:K:125:TYR:HH	12:K:132:HIS:HE2	1.06	1.00
2:A:329:U:O2	2:A:446:G:O6	1.81	0.98

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3	21/24 (88%)	18 (86%)	3 (14%)	0	100	100
4	C	273/278 (98%)	244 (89%)	29 (11%)	0	100	100
5	D	212/217 (98%)	188 (89%)	24 (11%)	0	100	100
6	E	207/215 (96%)	195 (94%)	12 (6%)	0	100	100
7	F	180/187 (96%)	172 (96%)	8 (4%)	0	100	100
8	G	174/179 (97%)	170 (98%)	4 (2%)	0	100	100
9	H	149/151 (99%)	137 (92%)	12 (8%)	0	100	100
10	I	124/175 (71%)	122 (98%)	2 (2%)	0	100	100
11	J	131/142 (92%)	122 (93%)	9 (7%)	0	100	100
12	K	144/147 (98%)	135 (94%)	9 (6%)	0	100	100
13	L	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
14	M	143/147 (97%)	134 (94%)	9 (6%)	0	100	100
15	N	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
16	O	116/199 (58%)	108 (93%)	8 (7%)	0	100	100
17	P	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
18	Q	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
19	R	122/129 (95%)	116 (95%)	6 (5%)	0	100	100
20	S	98/103 (95%)	93 (95%)	5 (5%)	0	100	100
21	T	112/153 (73%)	105 (94%)	7 (6%)	0	100	100
22	U	95/100 (95%)	91 (96%)	4 (4%)	0	100	100
23	V	93/105 (89%)	92 (99%)	1 (1%)	0	100	100
24	W	190/215 (88%)	185 (97%)	5 (3%)	0	100	100
25	X	77/88 (88%)	70 (91%)	7 (9%)	0	100	100
26	Y	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
27	Z	62/77 (80%)	62 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	a	57/61 (93%)	56 (98%)	1 (2%)	0	100	100
29	b	52/57 (91%)	49 (94%)	3 (6%)	0	100	100
30	c	46/55 (84%)	44 (96%)	2 (4%)	0	100	100
31	d	44/47 (94%)	39 (89%)	5 (11%)	0	100	100
32	e	61/64 (95%)	61 (100%)	0	0	100	100
33	f	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
34	g	46/75 (61%)	45 (98%)	1 (2%)	0	100	100
35	h	428/483 (89%)	388 (91%)	40 (9%)	0	100	100
All	All	4042/4474 (90%)	3786 (94%)	256 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	3	18/19 (95%)	18 (100%)	0	100	100
4	C	215/218 (99%)	215 (100%)	0	100	100
5	D	160/163 (98%)	160 (100%)	0	100	100
6	E	169/173 (98%)	169 (100%)	0	100	100
7	F	151/156 (97%)	151 (100%)	0	100	100
8	G	148/150 (99%)	147 (99%)	1 (1%)	76	80
9	H	90/116 (78%)	90 (100%)	0	100	100
10	I	89/120 (74%)	88 (99%)	1 (1%)	65	76
11	J	102/108 (94%)	102 (100%)	0	100	100
12	K	119/120 (99%)	119 (100%)	0	100	100
13	L	100/100 (100%)	100 (100%)	0	100	100
14	M	112/114 (98%)	111 (99%)	1 (1%)	70	78
15	N	114/116 (98%)	114 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	O	97/158 (61%)	97 (100%)	0	100	100
17	P	93/94 (99%)	93 (100%)	0	100	100
18	Q	100/100 (100%)	100 (100%)	0	100	100
19	R	97/99 (98%)	97 (100%)	0	100	100
20	S	81/83 (98%)	81 (100%)	0	100	100
21	T	90/117 (77%)	90 (100%)	0	100	100
22	U	83/85 (98%)	83 (100%)	0	100	100
23	V	81/86 (94%)	81 (100%)	0	100	100
24	W	155/168 (92%)	155 (100%)	0	100	100
25	X	58/63 (92%)	58 (100%)	0	100	100
26	Y	50/51 (98%)	50 (100%)	0	100	100
27	Z	58/66 (88%)	58 (100%)	0	100	100
28	a	52/54 (96%)	52 (100%)	0	100	100
29	b	43/46 (94%)	39 (91%)	4 (9%)	8	30
30	c	46/52 (88%)	46 (100%)	0	100	100
31	d	35/36 (97%)	35 (100%)	0	100	100
32	e	53/54 (98%)	53 (100%)	0	100	100
33	f	35/35 (100%)	35 (100%)	0	100	100
34	g	43/63 (68%)	43 (100%)	0	100	100
35	h	339/382 (89%)	326 (96%)	13 (4%)	29	57
All	All	3276/3565 (92%)	3256 (99%)	20 (1%)	76	81

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	h	213	ARG
35	h	258	LYS
35	h	307	LEU
35	h	270	VAL
29	b	32	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
20	S	85	HIS
24	W	129	ASN
34	g	6	HIS
24	W	61	HIS
25	X	44	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	A	3109/3120 (99%)	669 (21%)	54 (1%)
3	B	117/118 (99%)	14 (11%)	1 (0%)
All	All	3226/3238 (99%)	683 (21%)	55 (1%)

5 of 683 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	A	9	U
2	A	12	G
2	A	16	G
2	A	19	U
2	A	20	G

5 of 55 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A	1533	U
2	A	1578	G
3	B	10	G
2	A	2350	G
2	A	1537	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 oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
36	GNP	h	501	-	34,34,34	1.35	5 (14%)	47,54,54	0.94	1 (2%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	GNP	h	501	-	-	9/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	h	501	GNP	PB-O3A	4.82	1.65	1.59
36	h	501	GNP	PB-O1B	3.24	1.51	1.46
36	h	501	GNP	PG-N3B	3.02	1.71	1.63
36	h	501	GNP	PG-O1G	2.79	1.50	1.46
36	h	501	GNP	PB-O2B	-2.19	1.51	1.56

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	h	501	GNP	O4'-C4'-C3'	-2.00	101.18	105.15

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
36	h	501	GNP	PB-N3B-PG-O1G
36	h	501	GNP	PG-N3B-PB-O1B

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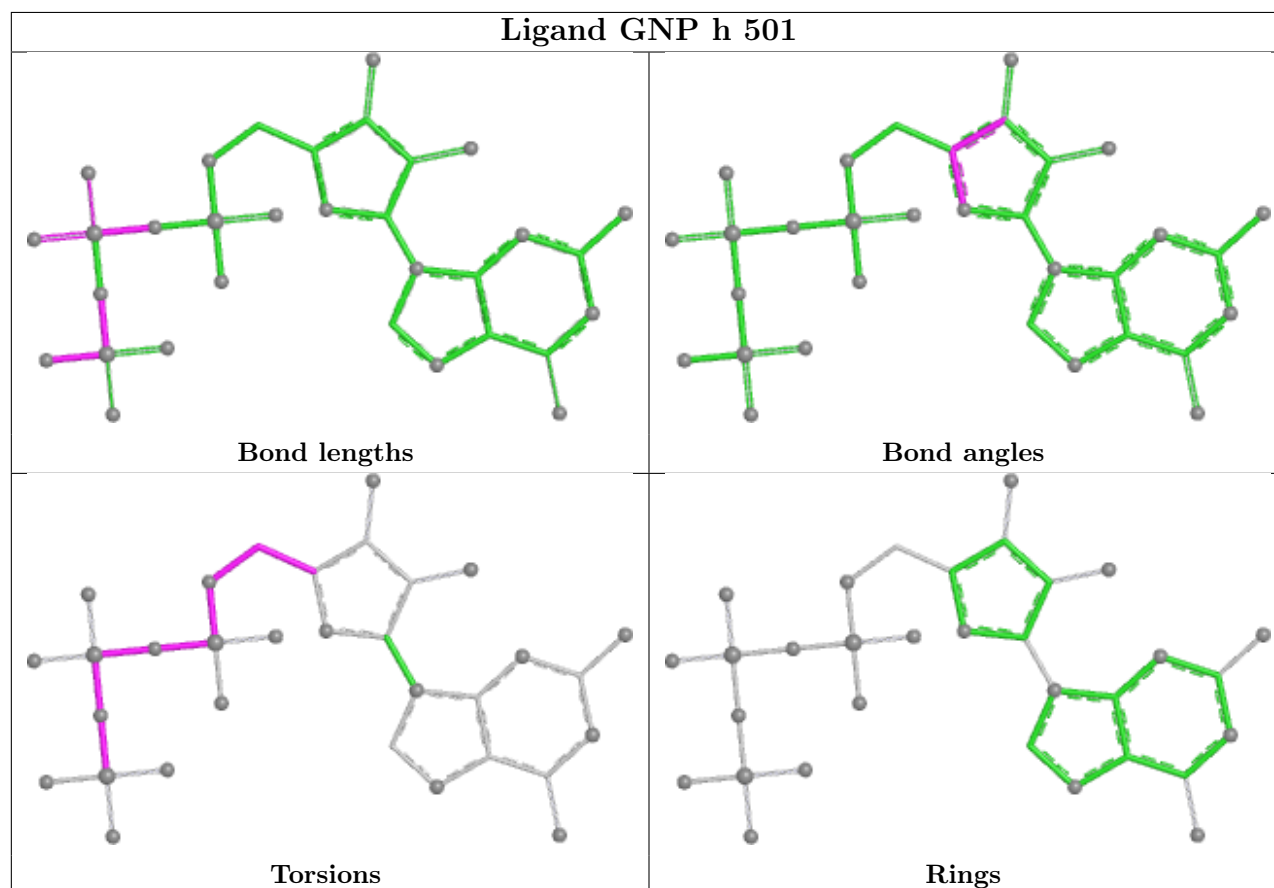
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Mol	Chain	Res	Type	Atoms
36	h	501	GNP	C5'-O5'-PA-O3A
36	h	501	GNP	C5'-O5'-PA-O2A
36	h	501	GNP	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

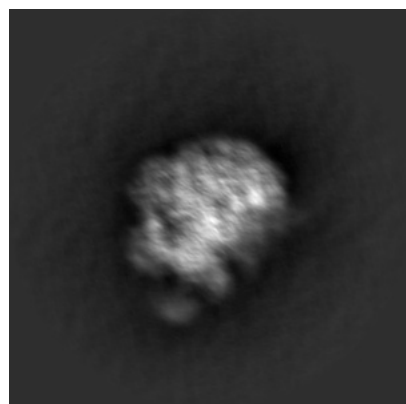
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37007. These allow visual inspection of the internal detail of the map and identification of artifacts.

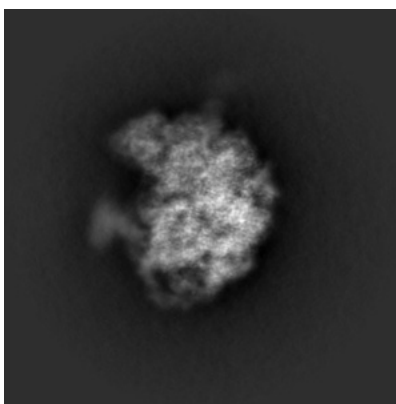
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

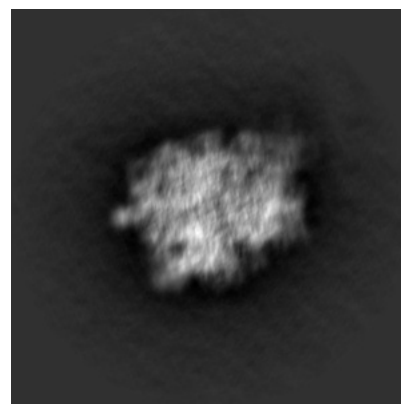
6.1.1 Primary map



X

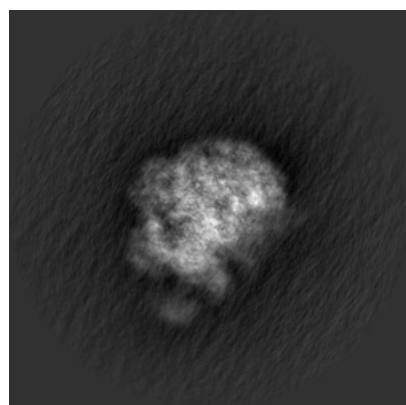


Y

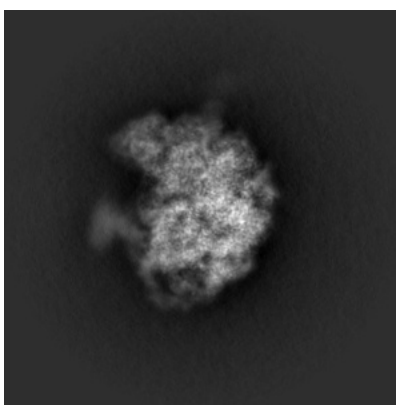


Z

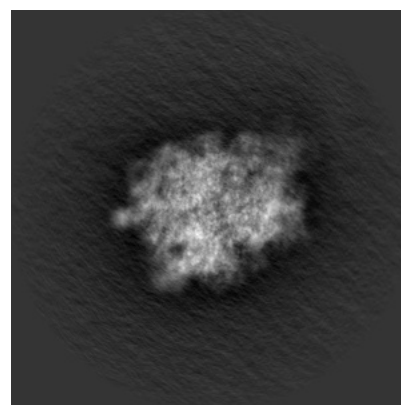
6.1.2 Raw map



X



Y

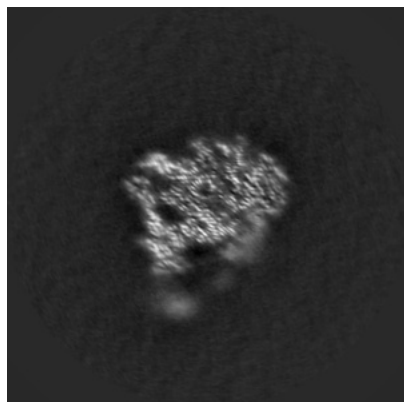


Z

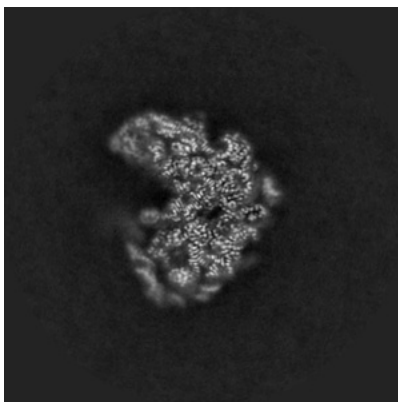
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

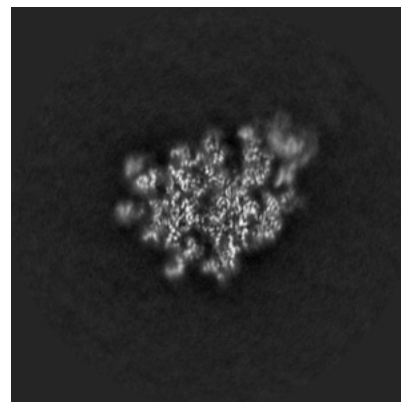
6.2.1 Primary map



X Index: 210

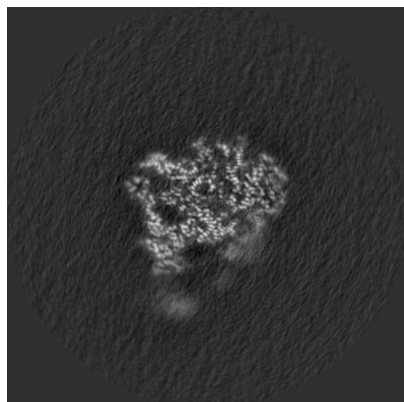


Y Index: 210

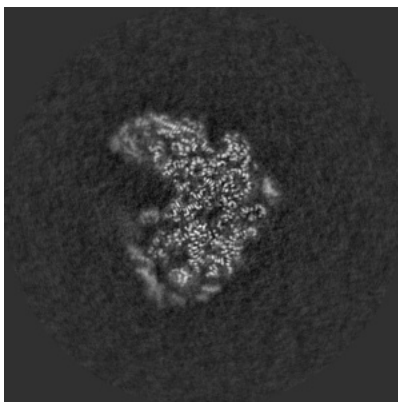


Z Index: 210

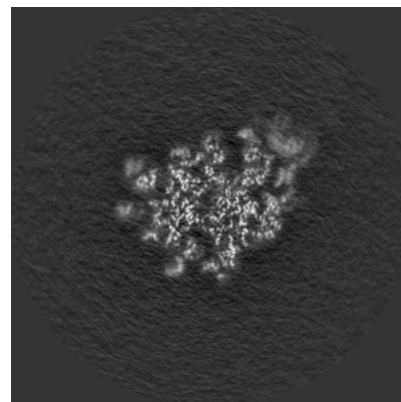
6.2.2 Raw map



X Index: 210



Y Index: 210

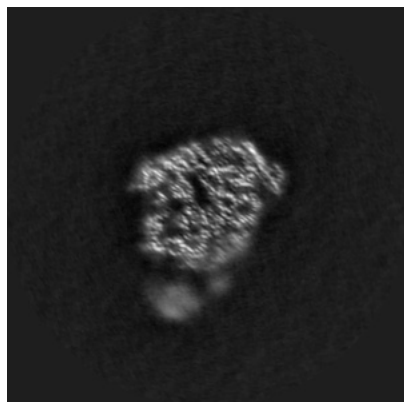


Z Index: 210

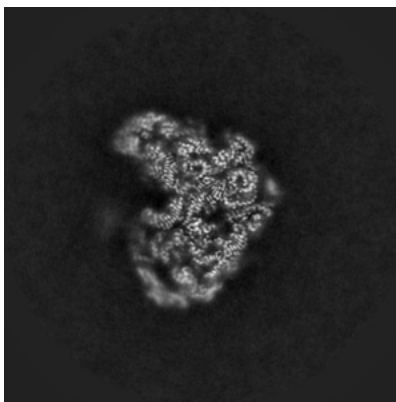
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

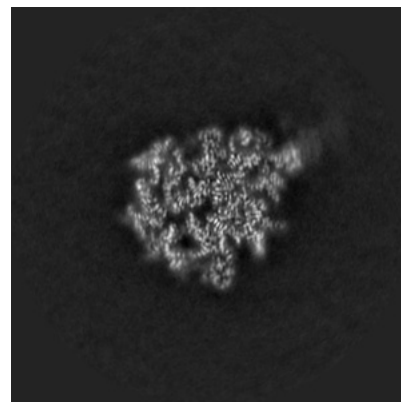
6.3.1 Primary map



X Index: 197

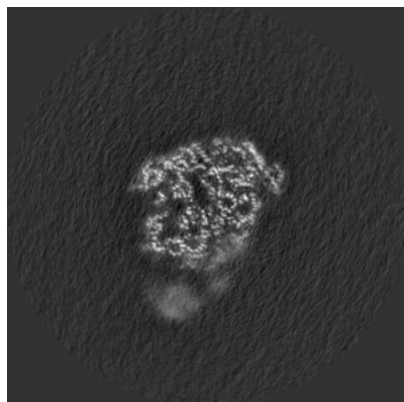


Y Index: 205

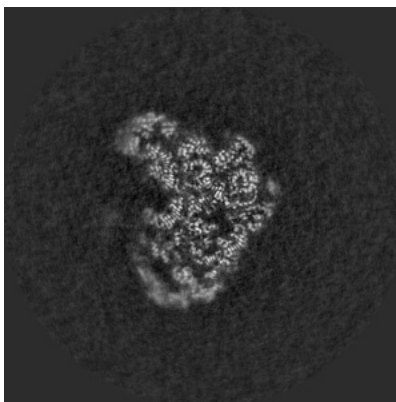


Z Index: 224

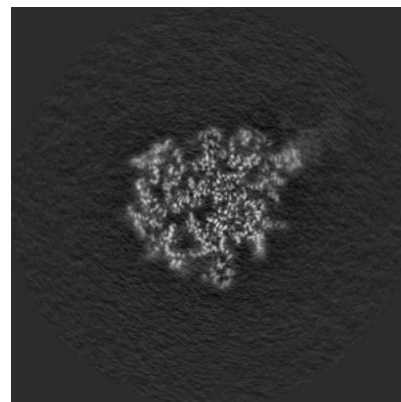
6.3.2 Raw map



X Index: 197



Y Index: 204

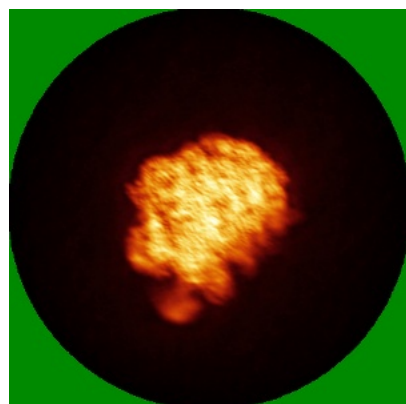


Z Index: 224

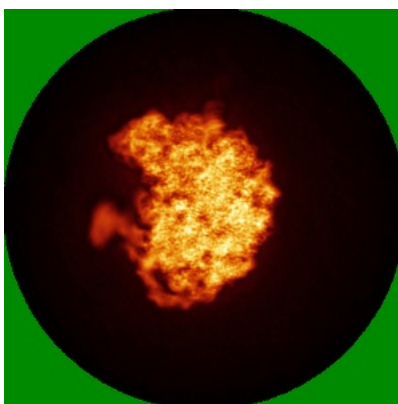
The images above show the largest variance slices of the map in three orthogonal directions.

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

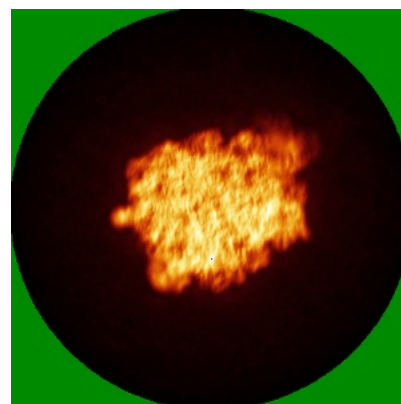
6.4.1 Primary map



X

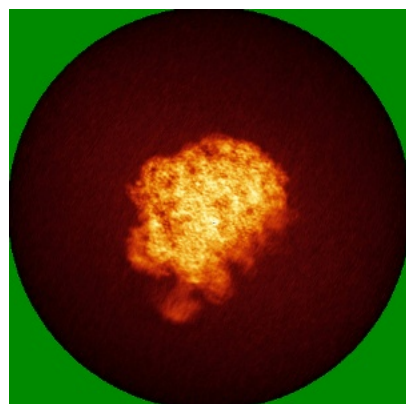


Y

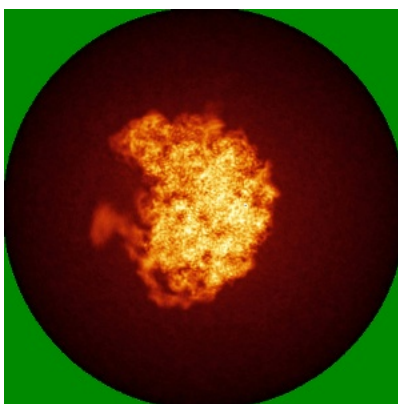


Z

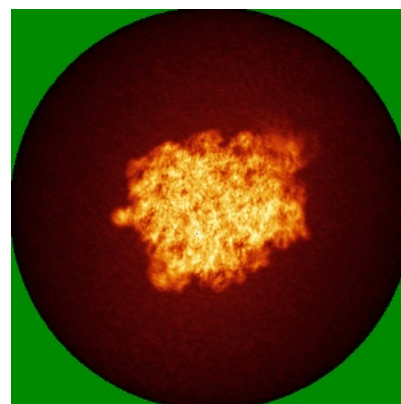
6.4.2 Raw map



X



Y

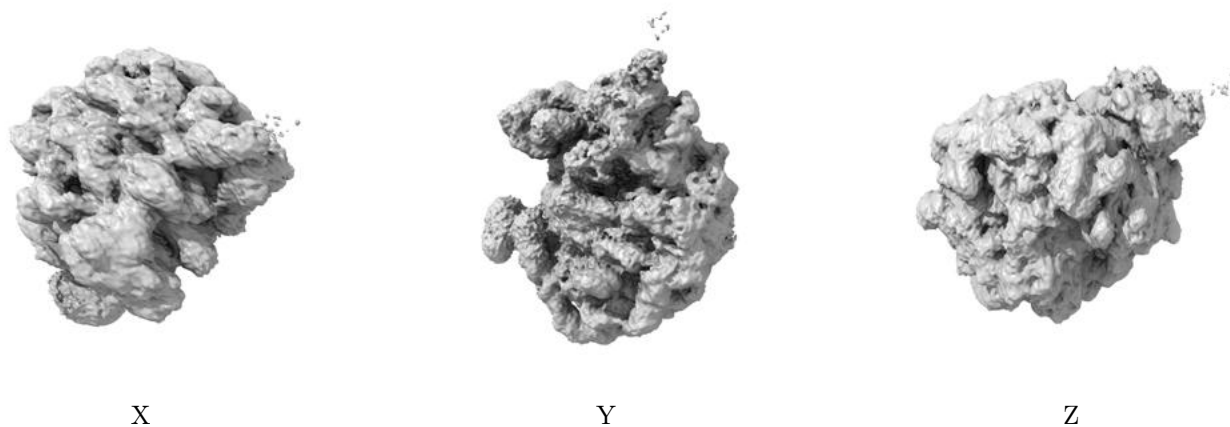


Z

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

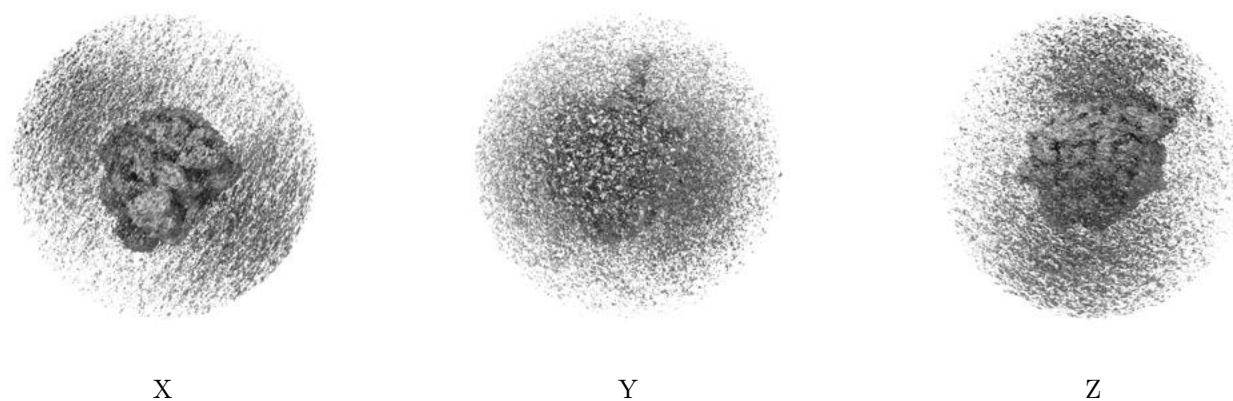
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

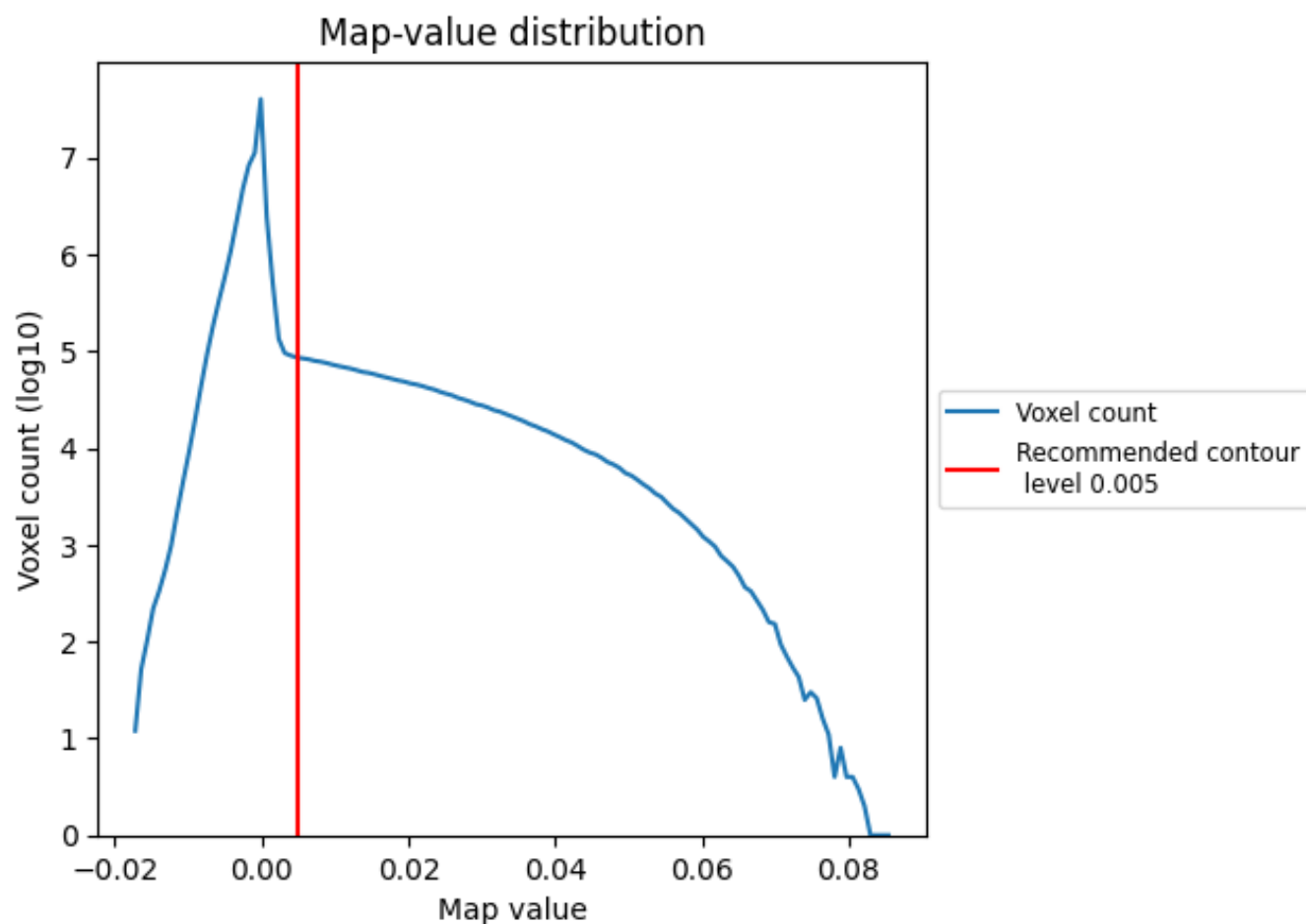
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

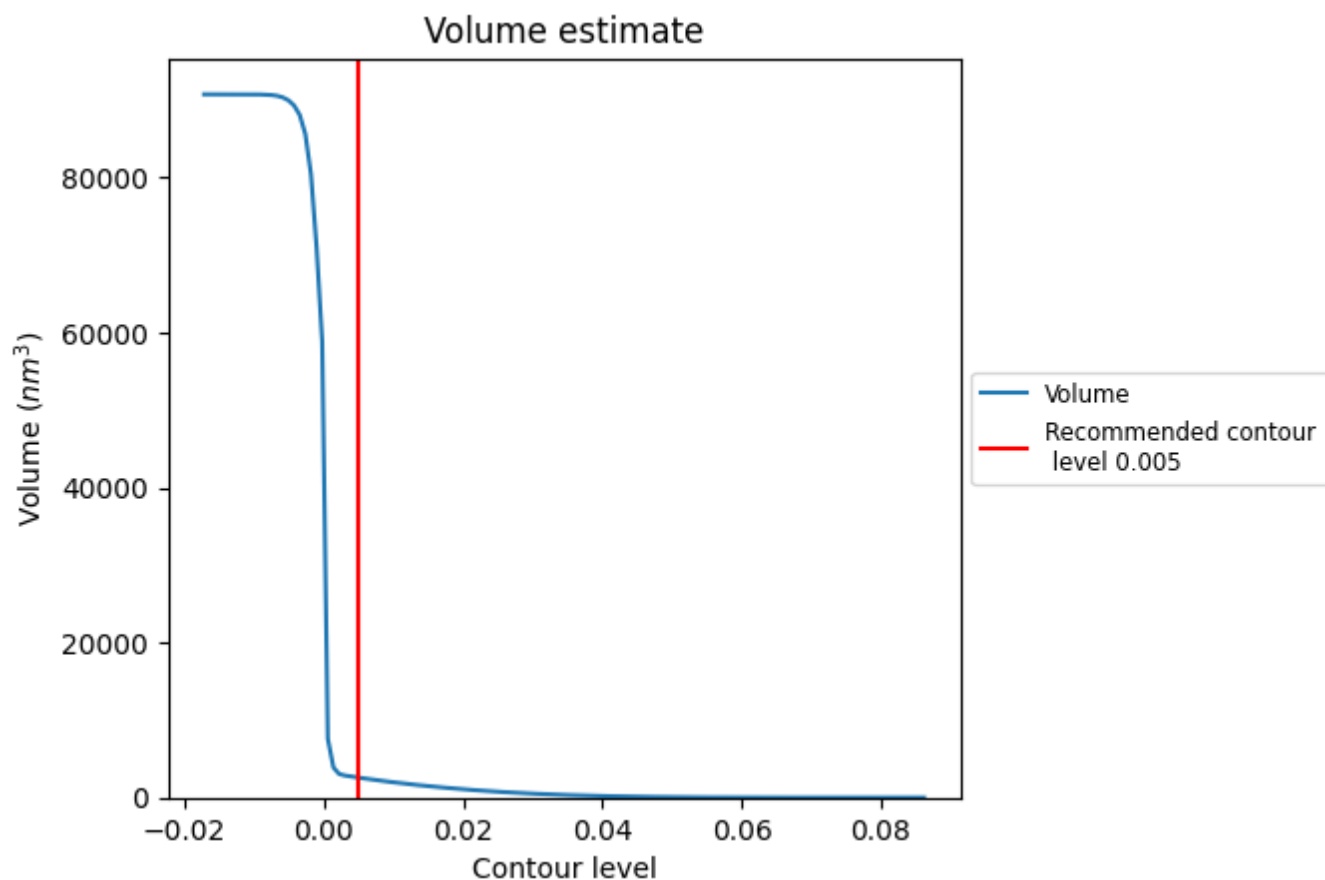
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

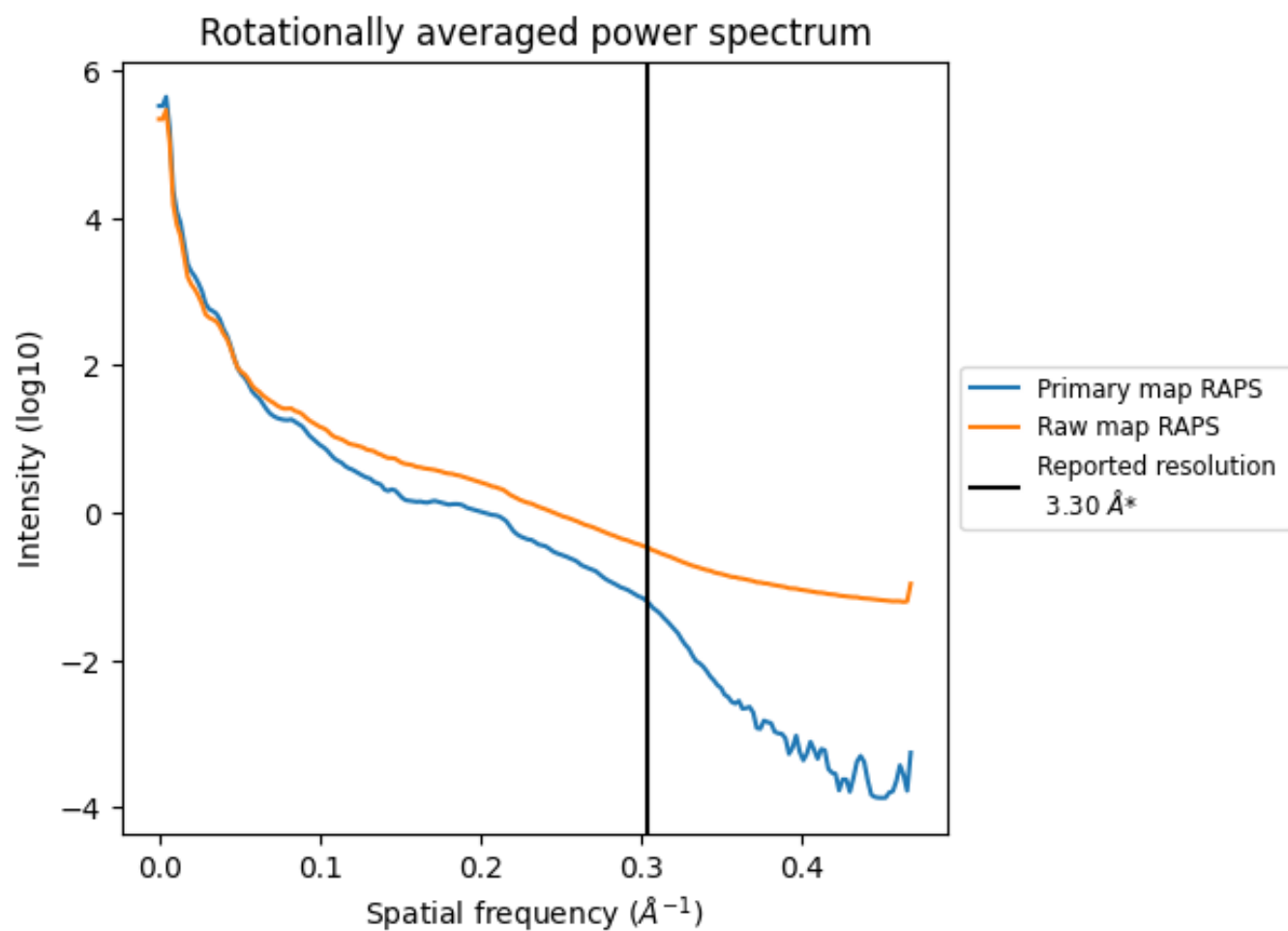
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2573 nm³; this corresponds to an approximate mass of 2324 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

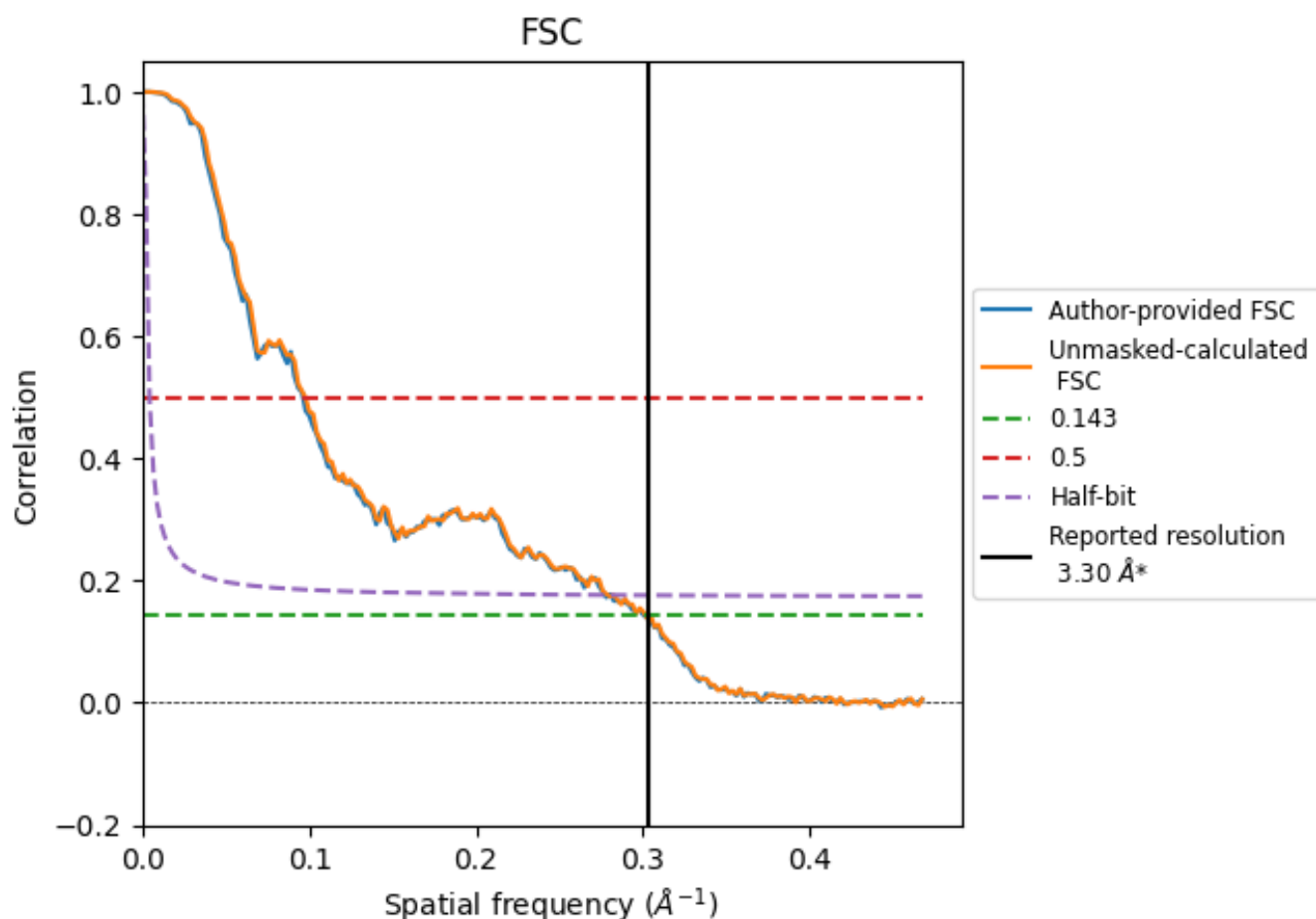


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

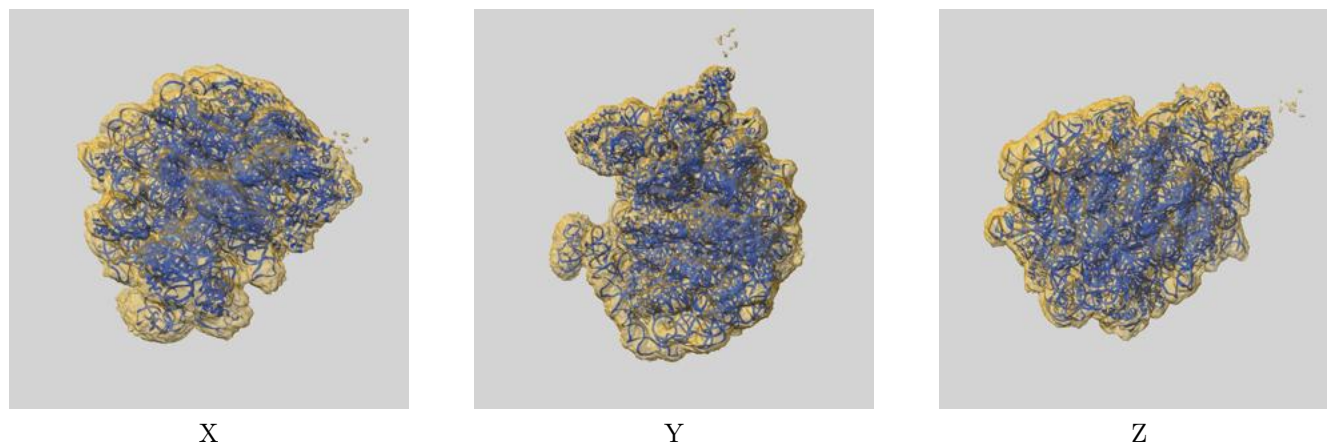
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.33	10.38	3.61
Unmasked-calculated*	3.32	10.24	3.58

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

9 Map-model fit [i](#)

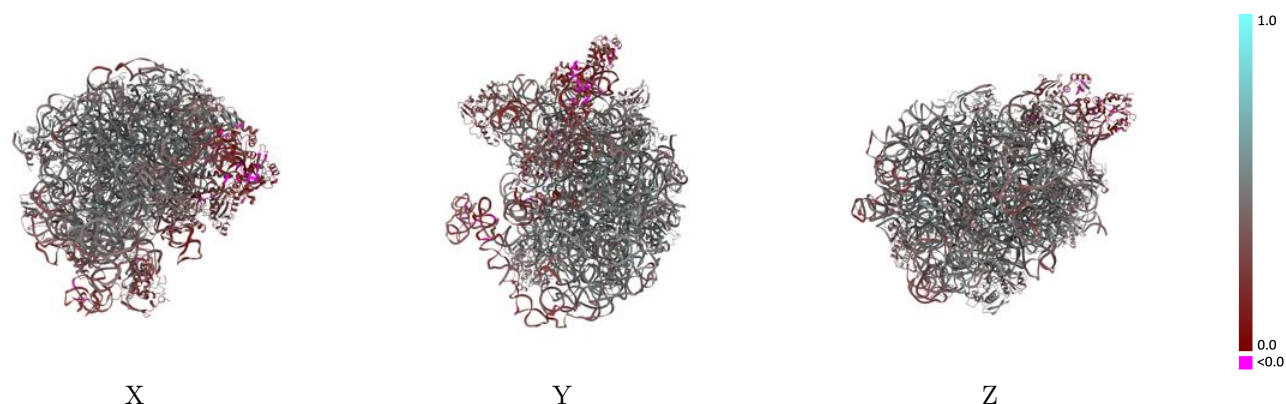
This section contains information regarding the fit between EMDB map EMD-37007 and PDB model 8KAB. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



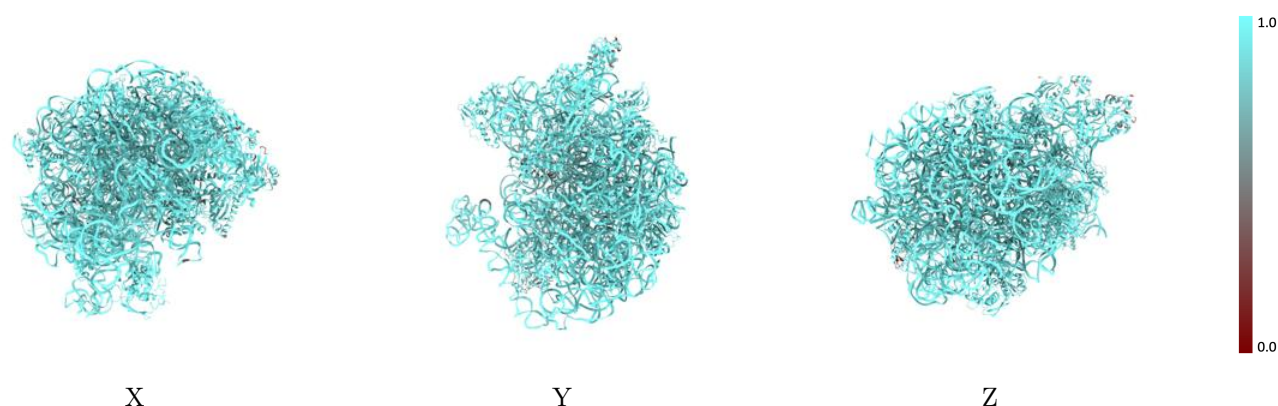
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



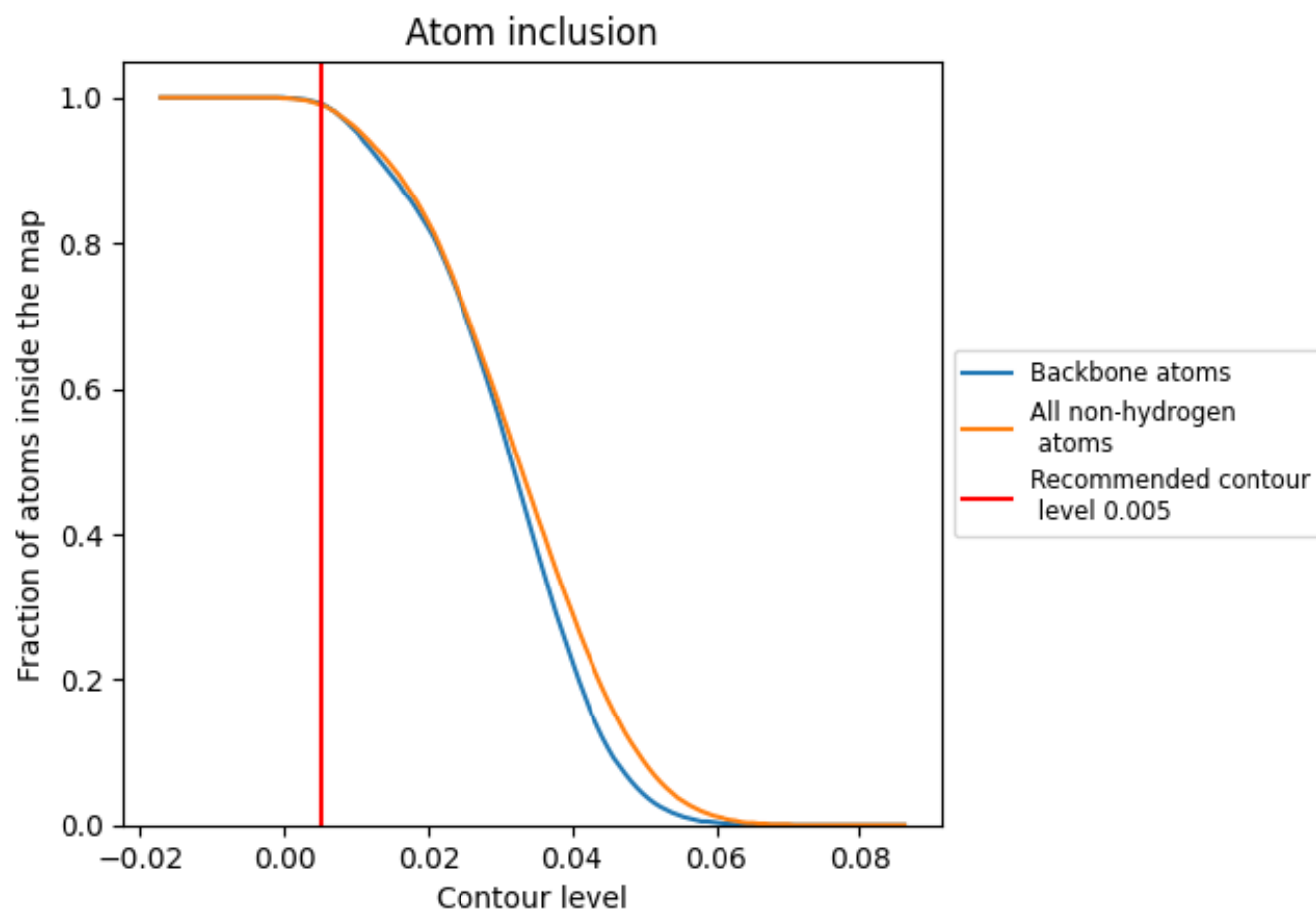
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9900	 0.4190
3	 1.0000	 0.4790
A	 0.9990	 0.4260
B	 1.0000	 0.4180
C	 1.0000	 0.4780
D	 1.0000	 0.4760
E	 0.9990	 0.4580
F	 0.9980	 0.3130
G	 1.0000	 0.3980
H	 0.7220	 0.3200
I	 0.8850	 0.1820
J	 0.9370	 0.1360
K	 0.9980	 0.4870
L	 0.9990	 0.4590
M	 0.9990	 0.4500
N	 0.9950	 0.4680
O	 1.0000	 0.4900
P	 1.0000	 0.3950
Q	 0.9990	 0.4340
R	 1.0000	 0.4790
S	 0.9990	 0.4820
T	 0.9990	 0.4710
U	 1.0000	 0.4510
V	 1.0000	 0.4150
W	 0.9960	 0.4070
X	 1.0000	 0.4940
Y	 1.0000	 0.4760
Z	 1.0000	 0.4120
a	 0.9940	 0.4870
b	 1.0000	 0.4460
c	 0.9720	 0.4180
d	 1.0000	 0.5050
e	 0.8520	 0.3900
f	 1.0000	 0.4680
g	 0.9970	 0.2610
h	 0.8900	 0.2670

