



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 01:10 AM UTC

PDB ID : 9PHC / pdb_00009phc
EMDB ID : EMD-71645
Title : In vitro reconstituted complex of purified S. pombe large ribosomal subunit and SNOR
Authors : Gluc, M.; Jomaa, A.
Deposited on : 2025-07-09
Resolution : 2.80 Å(reported)

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

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

A user guide is available at
<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

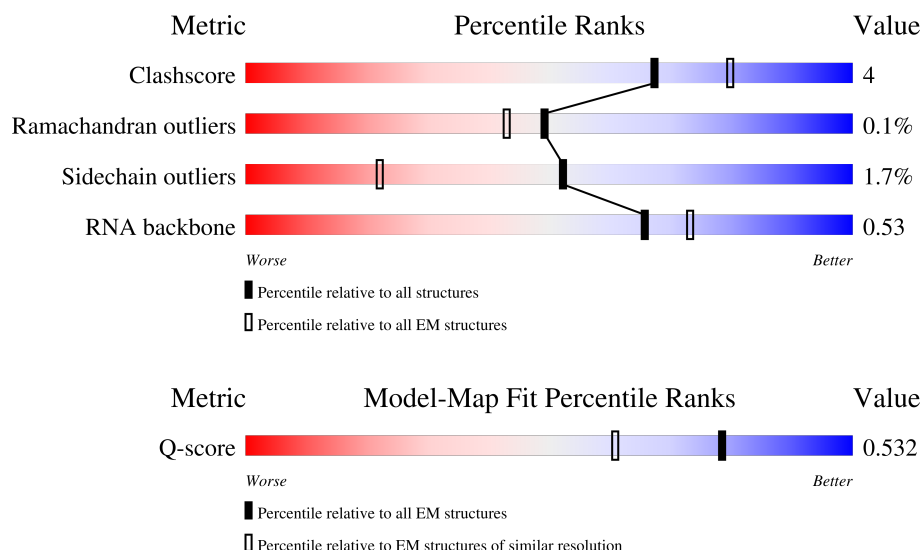
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.80 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.













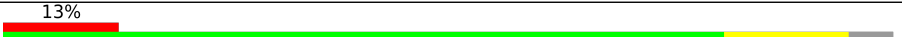


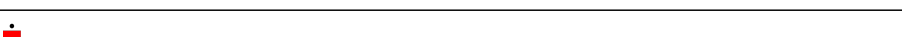
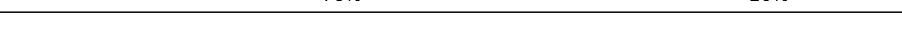
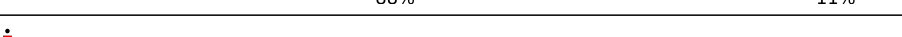



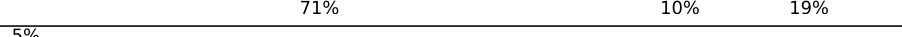





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	B0	106	
2	B1	94	
3	B2	3498	





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Mol	Chain	Length	Quality of chain
4	B3	246	
5	B4	165	
6	BN	253	
7	BO	388	
8	BP	363	
9	BQ	294	
10	BR	195	
11	BS	251	
12	BT	259	
13	BU	189	
14	BV	221	
15	BW	174	
16	BX	208	
17	BY	134	
18	BZ	201	
19	Ba	197	
20	Bb	187	
21	Bc	187	
22	Bd	193	
23	Be	176	
24	Bf	160	
25	Bg	117	
26	Bh	139	
27	Bi	149	
28	Bj	141	

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Mol	Chain	Length	Quality of chain
29	Bk	126	 79%20%..
30	Bl	136	 74%25%.
31	Bm	148	 87%12%.
32	Bn	61	 89%8%.
33	Bo	109	 6%70%17%14%
34	Bp	113	 84%7%9%.
35	Bq	127	 91%.7%
36	Br	108	 85%11%.
37	Bs	111	 79%16%5%
38	Bt	122	 89%11%.
39	Bu	99	 84%12%.
40	Bv	91	 84%7%10%.
41	Bw	74	 80%14%7%
42	Bx	51	 14%80%18%.
43	By	134	 83%16%..
44	HS	106	 21%73%19%..6%

2 Entry composition

There are 45 unique types of molecules in this entry. The entry contains 122816 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 Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B0	93	Total	C	N	O	S	0	0
			758	479	152	122	5		

- Molecule 2 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B1	93	Total	C	N	O	S	0	0
			718	442	147	123	6		

- Molecule 3 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B2	3139	Total	C	N	O	P	0	0
			67111	29989	12096	21887	3139		

- Molecule 4 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B3	119	Total	C	N	O	P	0	0
			2539	1133	454	833	119		

- Molecule 5 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B4	157	Total	C	N	O	P	0	0
			3332	1491	583	1101	157		

- Molecule 6 is a protein called Large ribosomal subunit protein uL2C.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	BN	248	Total	C	N	O	S	0	0
			1872	1166	377	324	5		

- Molecule 7 is a protein called Large ribosomal subunit protein uL3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	BO	384	Total	C	N	O	S	0	0
			3050	1929	576	535	10		

- Molecule 8 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	BP	362	Total	C	N	O	S	0	0
			2799	1768	538	490	3		

- Molecule 9 is a protein called Large ribosomal subunit protein uL18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BQ	287	Total	C	N	O	S	0	0
			2312	1461	410	437	4		

- Molecule 10 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	BR	162	Total	C	N	O	S	0	0
			1251	802	231	215	3		

- Molecule 11 is a protein called Large ribosomal subunit protein uL30C.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BS	233	Total	C	N	O	S	0	0
			1897	1211	349	334	3		

- Molecule 12 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BT	229	Total	C	N	O	S	0	0
			1772	1135	325	309	3		

- Molecule 13 is a protein called Large ribosomal subunit protein uL6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BU	168	Total	C	N	O	S	0	0
			1319	828	244	242	5		

- Molecule 14 is a protein called Large ribosomal subunit protein uL16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BV	209	Total	C	N	O	S	0	0
			1679	1060	318	293	8		

- Molecule 15 is a protein called Large ribosomal subunit protein uL5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BW	167	Total	C	N	O	S	0	0
			1346	854	252	235	5		

- Molecule 16 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BX	207	Total	C	N	O	S	0	0
			1654	1034	329	290	1		

- Molecule 17 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BY	130	Total	C	N	O	S	0	0
			1038	662	198	174	4		

- Molecule 18 is a protein called Large ribosomal subunit protein eL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BZ	200	Total	C	N	O	S	0	0
			1676	1050	348	275	3		

- Molecule 19 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Ba	196	Total	C	N	O	S	0	0
			1545	991	294	256	4		

- Molecule 20 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Bb	152	Total	C	N	O	S	0	0
			1212	770	229	210	3		

- Molecule 21 is a protein called Large ribosomal subunit protein eL18B.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Bc	186	Total	C	N	O	0	0
			1487	937	300	250		

- Molecule 22 is a protein called Large ribosomal subunit protein eL19B.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Bd	157	Total	C	N	O	S	0	0
			1301	809	275	212	5		

- Molecule 23 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Be	173	Total	C	N	O	S	0	0
			1423	916	268	234	5		

- Molecule 24 is a protein called Large ribosomal subunit protein eL21B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Bf	159	Total	C	N	O	S	0	0
			1286	810	247	226	3		

- Molecule 25 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Bg	99	Total	C	N	O	0	0
			798	518	138	142		

- Molecule 26 is a protein called Large ribosomal subunit protein uL14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Bh	134	Total	C	N	O	S	0	0
			999	630	184	177	8		

- Molecule 27 is a protein called Large ribosomal subunit protein eL24B.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Bi	63	Total	C	N	O	S	0	0
			523	336	102	82	3		

- Molecule 28 is a protein called Large ribosomal subunit protein uL23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Bj	118	Total	C	N	O	S	0	0
			947	605	175	166	1		

- Molecule 29 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Bk	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

- Molecule 30 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Bl	135	Total	C	N	O	S	0	0
			1078	698	200	178	2		

- Molecule 31 is a protein called Large ribosomal subunit protein uL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Bm	147	Total	C	N	O	S	0	0
			1171	740	235	194	2		

- Molecule 32 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	Bn	59	Total	C	N	O	0	0
			495	299	112	84		

- Molecule 33 is a protein called Large ribosomal subunit protein eL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Bo	94	Total	C	N	O	S	0	0
			705	450	121	130	4		

- Molecule 34 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Bp	103	Total	C	N	O	S	0	0
			857	538	167	149	3		

- Molecule 35 is a protein called Large ribosomal subunit protein eL32A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Bq	118	Total	C	N	O	S	0	0
			944	591	191	157	5		

- Molecule 36 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Br	104	Total	C	N	O	S	0	0
			831	531	160	137	3		

- Molecule 37 is a protein called Large ribosomal subunit protein eL34B.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Bs	106	Total	C	N	O	S	0	0
			858	538	176	142	2		

- Molecule 38 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Bt	121	Total	C	N	O		0	0
			999	629	194	176			

- Molecule 39 is a protein called Large ribosomal subunit protein eL36B.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Bu	95	Total	C	N	O	S	0	0
			759	472	159	127	1		

- Molecule 40 is a protein called Large ribosomal subunit protein eL37B.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Bv	82	Total	C	N	O	S	0	0
			652	399	140	106	7		

- Molecule 41 is a protein called Large ribosomal subunit protein eL38A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Bw	69	Total	C	N	O	S	0	0
			560	355	103	101	1		

- Molecule 42 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Bx	50	Total	C	N	O	S	0	0
			436	273	98	64	1		

- Molecule 43 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	By	133	Total	C	N	O	S	0	0
			1031	641	203	186	1		

- Molecule 44 is a protein called SDO1-like protein C21C3.19.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	HS	100	Total	C	N	O	S	0	0
			795	494	140	159	2		

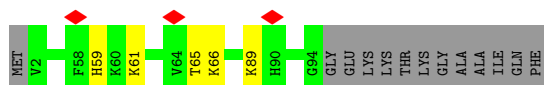
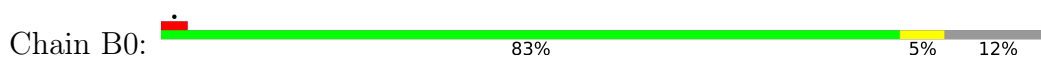
- Molecule 45 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
45	B0	1	Total	Zn	0
			1	1	
45	B1	1	Total	Zn	0
			1	1	
45	Bv	1	Total	Zn	0
			1	1	

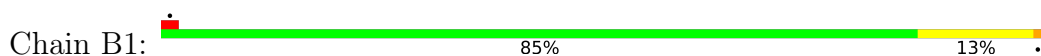
3 Residue-property plots

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.

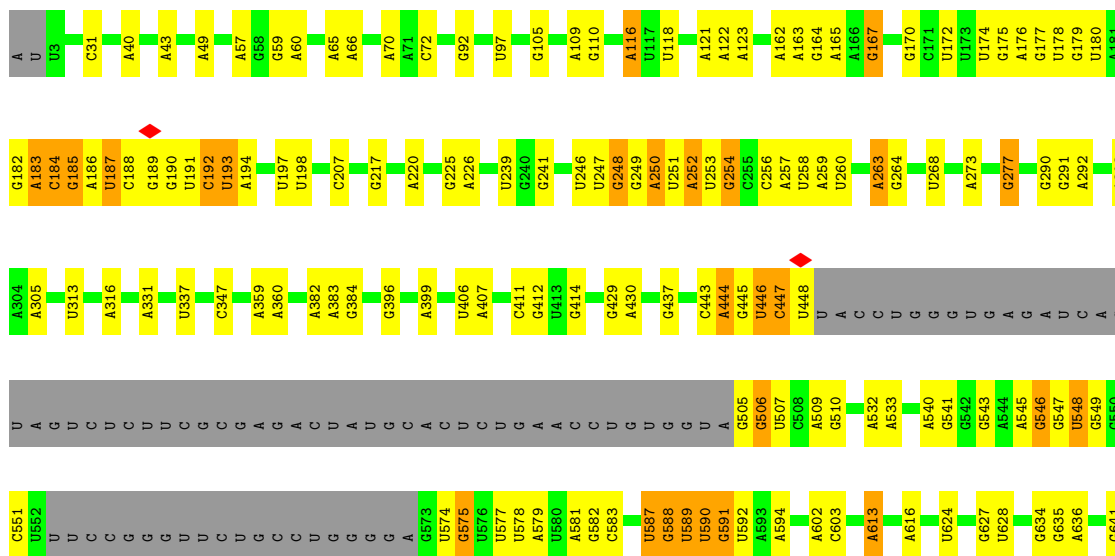
- Molecule 1: Large ribosomal subunit protein eL42



- Molecule 2: Large ribosomal subunit protein eL43A




- Molecule 3: 28S ribosomal RNA







- Chain BN:  83% 15%




- Chain BO:  87% 11%



- Chain BP:  91% 9%

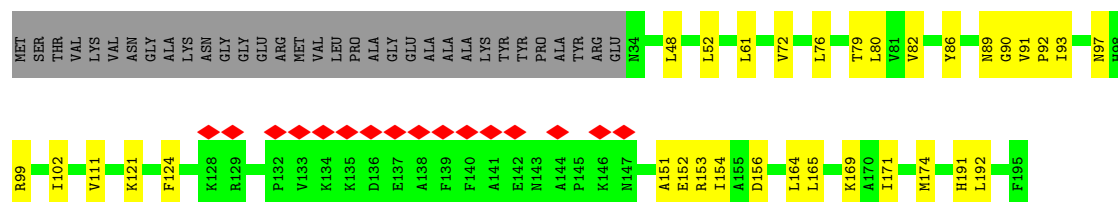


- Chain BQ: 




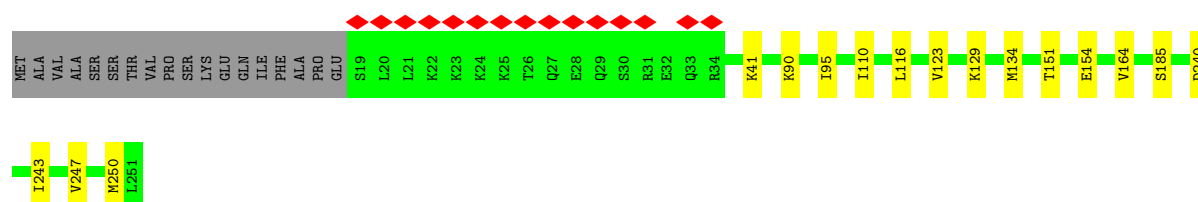
- Molecule 10: Large ribosomal subunit protein eL6

Chain BR: 




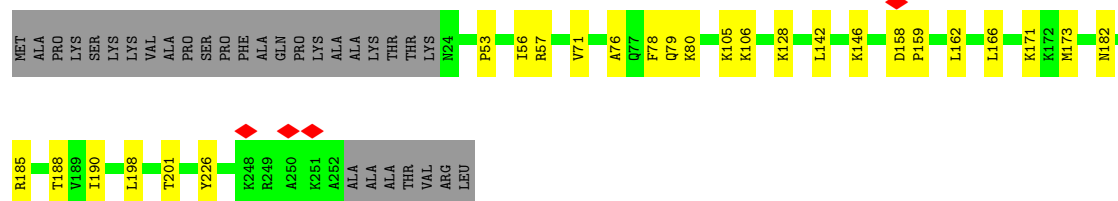
- Molecule 11: Large ribosomal subunit protein uL30C

Chain BS: 



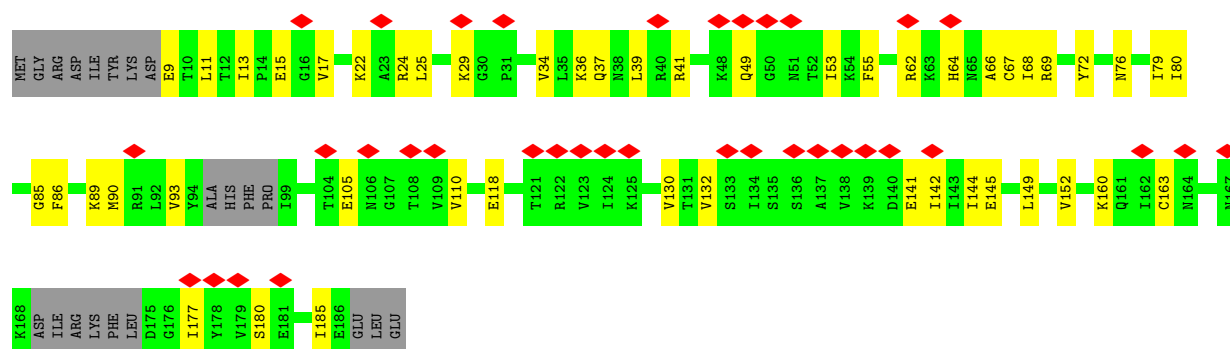
- Molecule 12: Large ribosomal subunit protein eL8

Chain BT: 




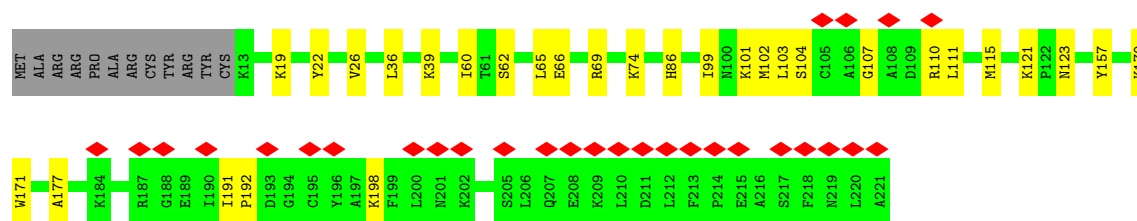
- Molecule 13: Large ribosomal subunit protein uL6B

Chain BU: 

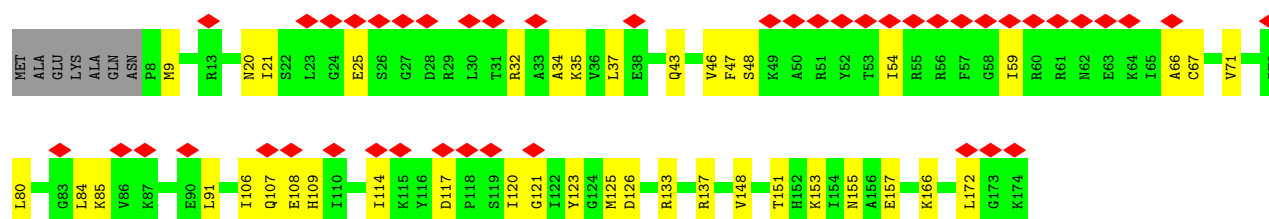
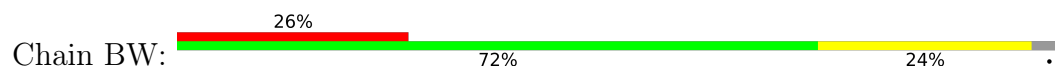


- Molecule 14: Large ribosomal subunit protein uL16A

Chain BV: 



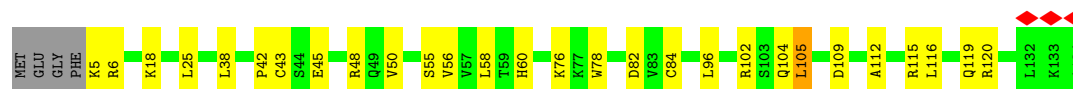
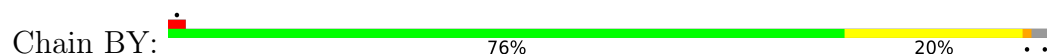
- Molecule 15: Large ribosomal subunit protein uL5A



- Molecule 16: Large ribosomal subunit protein eL13



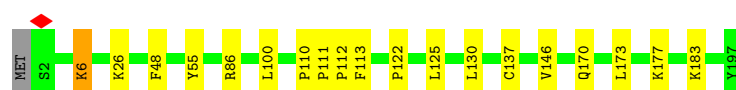
- Molecule 17: Large ribosomal subunit protein eL14




- Molecule 18: Large ribosomal subunit protein eL15B

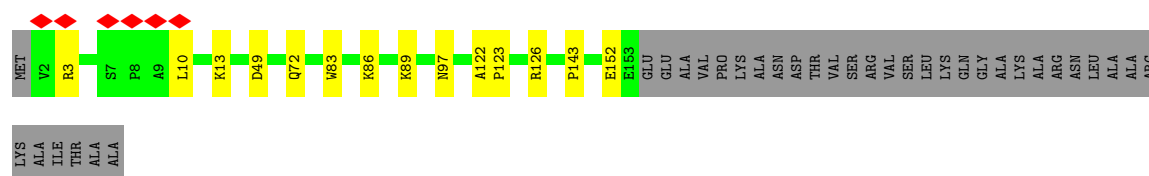


- Molecule 19: Large ribosomal subunit protein uL13A



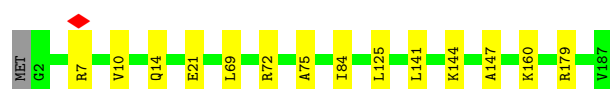
- Molecule 20: Large ribosomal subunit protein uL22A

Chain Bb:  74% 7% 19%




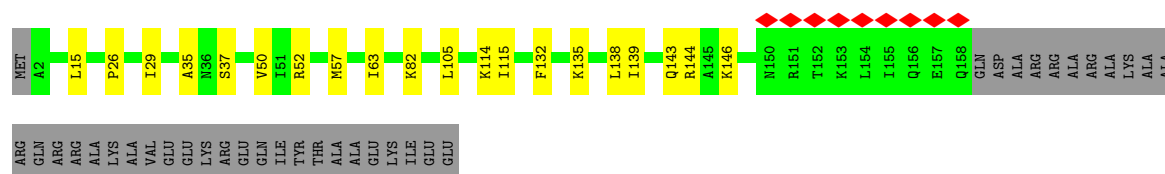
- Molecule 21: Large ribosomal subunit protein eL18B

Chain Bc:  92% 7%




- Molecule 22: Large ribosomal subunit protein eL19B

Chain Bd:  5% 71% 10% 19%




- Molecule 23: Large ribosomal subunit protein eL20A

Chain Be:  5% 74% 24%




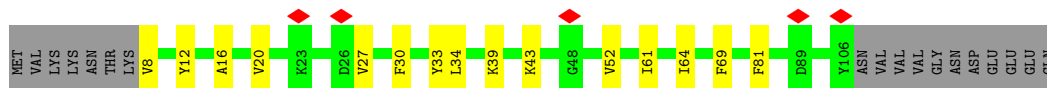
- Molecule 24: Large ribosomal subunit protein eL21B

Chain Bf:  6% 85% 14%

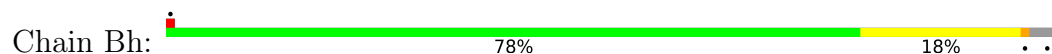


- Molecule 25: Large ribosomal subunit protein eL22

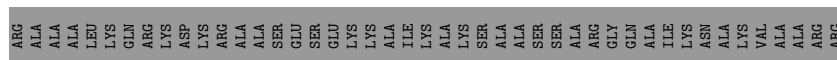
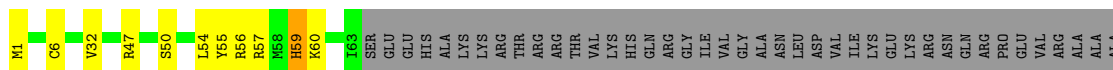
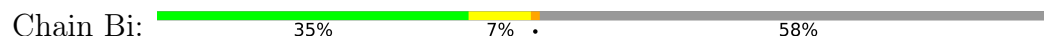
Chain Bg:  72% 13% 15%



- Molecule 26: Large ribosomal subunit protein uL14B



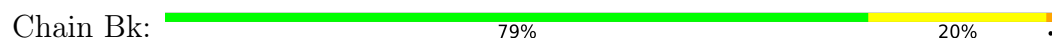
- Molecule 27: Large ribosomal subunit protein eL24B



- Molecule 28: Large ribosomal subunit protein uL23A



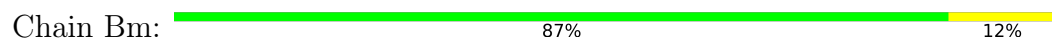
- Molecule 29: Large ribosomal subunit protein uL24



- Molecule 30: Large ribosomal subunit protein eL27A



- Molecule 31: Large ribosomal subunit protein uL15B





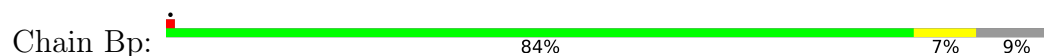
- Molecule 32: Large ribosomal subunit protein eL29



- Molecule 33: Large ribosomal subunit protein eL30A



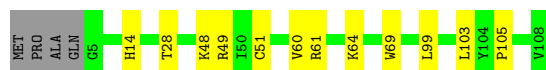
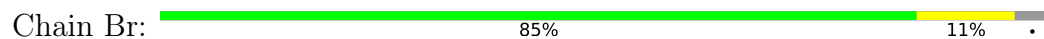
- Molecule 34: Large ribosomal subunit protein eL31



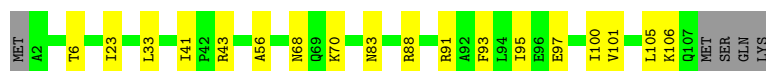
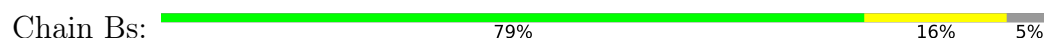
- Molecule 35: Large ribosomal subunit protein eL32A



- Molecule 36: Large ribosomal subunit protein eL33A



- Molecule 37: Large ribosomal subunit protein eL34B

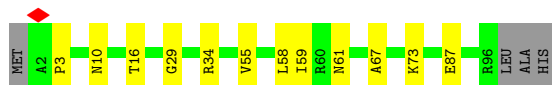
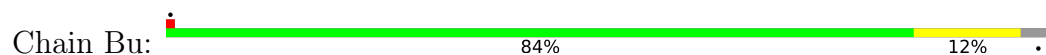


- Molecule 38: Large ribosomal subunit protein uL29

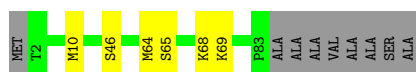
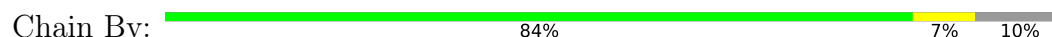




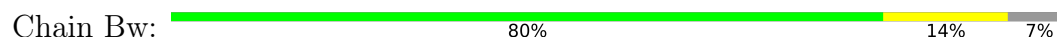
- Molecule 39: Large ribosomal subunit protein eL36B



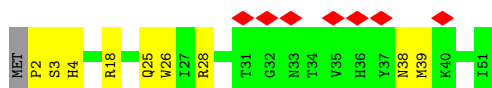
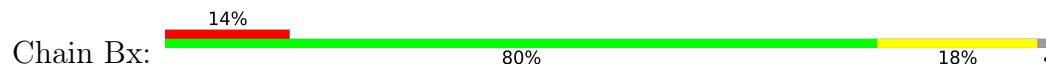
- Molecule 40: Large ribosomal subunit protein eL37B



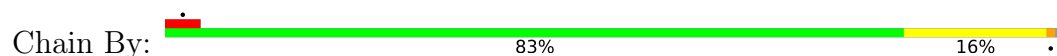
- Molecule 41: Large ribosomal subunit protein eL38A



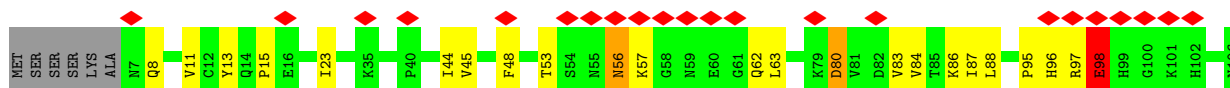
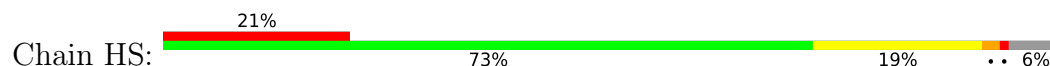
- Molecule 42: Large ribosomal subunit protein eL39



- Molecule 43: Large ribosomal subunit protein eL28



- Molecule 44: SDO1-like protein C21C3.19



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	110548	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.030	Depositor
Minimum map value	-0.011	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.002	Depositor
Map size (Å)	430.08, 430.08, 430.08	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84, 0.84, 0.84	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

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	B0	0.10	0/772	0.28	0/1025
2	B1	0.11	0/727	0.37	0/973
3	B2	0.08	0/75119	0.18	0/117094
4	B3	0.07	0/2838	0.15	0/4422
5	B4	0.08	0/3723	0.16	0/5796
6	BN	0.13	0/1910	0.31	0/2575
7	BO	0.11	0/3116	0.29	0/4190
8	BP	0.11	0/2852	0.29	0/3850
9	BQ	0.14	0/2361	0.40	0/3173
10	BR	0.12	0/1275	0.33	0/1719
11	BS	0.11	0/1929	0.33	1/2583 (0.0%)
12	BT	0.13	0/1801	0.36	0/2430
13	BU	0.23	0/1330	0.53	0/1789
14	BV	0.11	0/1712	0.31	0/2294
15	BW	0.15	0/1369	0.41	0/1830
16	BX	0.12	0/1686	0.28	0/2267
17	BY	0.11	0/1054	0.29	0/1413
18	BZ	0.11	0/1717	0.31	1/2306 (0.0%)
19	Ba	0.11	0/1575	0.28	0/2109
20	Bb	0.10	0/1237	0.31	0/1661
21	Bc	0.11	0/1511	0.28	0/2021
22	Bd	0.11	0/1320	0.31	0/1757
23	Be	0.12	0/1458	0.31	0/1961
24	Bf	0.11	0/1314	0.29	0/1771
25	Bg	0.14	0/812	0.40	0/1090
26	Bh	0.13	0/1015	0.36	0/1369
27	Bi	0.13	0/534	0.39	0/709
28	Bj	0.12	0/963	0.33	0/1296
29	Bk	0.12	0/1008	0.32	0/1341
30	Bl	0.17	0/1101	0.40	0/1477
31	Bm	0.13	0/1200	0.33	0/1611
32	Bn	0.11	0/503	0.28	0/664

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Bo	0.13	0/714	0.33	0/961
34	Bp	0.11	0/872	0.31	0/1172
35	Bq	0.11	0/958	0.30	0/1278
36	Br	0.11	0/853	0.31	0/1146
37	Bs	0.13	0/870	0.31	0/1165
38	Bt	0.11	0/1008	0.31	0/1340
39	Bu	0.09	0/766	0.23	0/1017
40	Bv	0.09	0/666	0.26	0/881
41	Bw	0.20	0/566	0.56	0/757
42	Bx	0.13	0/447	0.44	0/597
43	By	0.11	0/1045	0.31	0/1404
44	HS	0.13	0/808	0.36	0/1092
All	All	0.10	0/132415	0.24	2/195376 (0.0%)

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
18	BZ	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	BS	240	ASP	CB-CA-C	-5.62	110.08	116.54
18	BZ	148	ILE	N-CA-C	-5.10	107.74	112.43

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
18	BZ	183	SER	Peptide

5.2 Too-close contacts

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	B0	758	0	815	3	0
2	B1	718	0	751	8	0
3	B2	67111	0	33740	265	0
4	B3	2539	0	1283	16	0
5	B4	3332	0	1684	14	0
6	BN	1872	0	1917	25	0
7	BO	3050	0	3125	33	0
8	BP	2799	0	2925	16	0
9	BQ	2312	0	2272	41	0
10	BR	1251	0	1337	18	0
11	BS	1897	0	1984	9	0
12	BT	1772	0	1866	17	0
13	BU	1319	0	1389	44	0
14	BV	1679	0	1718	26	0
15	BW	1346	0	1397	27	0
16	BX	1654	0	1705	12	0
17	BY	1038	0	1115	18	0
18	BZ	1676	0	1712	16	0
19	Ba	1545	0	1641	16	0
20	Bb	1212	0	1239	10	0
21	Bc	1487	0	1597	10	0
22	Bd	1301	0	1393	14	0
23	Be	1423	0	1488	28	0
24	Bf	1286	0	1310	15	0
25	Bg	798	0	834	10	0
26	Bh	999	0	1047	15	0
27	Bi	523	0	555	9	0
28	Bj	947	0	1012	11	0
29	Bk	998	0	1090	16	0
30	Bl	1078	0	1154	22	0
31	Bm	1171	0	1215	11	0
32	Bn	495	0	504	4	0
33	Bo	705	0	746	12	0
34	Bp	857	0	891	4	0
35	Bq	944	0	1005	3	0
36	Br	831	0	858	5	0
37	Bs	858	0	925	13	0
38	Bt	999	0	1092	8	0
39	Bu	759	0	840	6	0
40	Bv	652	0	663	3	0
41	Bw	560	0	608	9	0
42	Bx	436	0	463	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	By	1031	0	1080	16	0
44	HS	795	0	788	15	0
45	B0	1	0	0	0	0
45	B1	1	0	0	0	0
45	Bv	1	0	0	0	0
All	All	122816	0	88773	809	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 809 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)
3:B2:2356:U:H3	3:B2:2360:G:H22	1.25	0.82
7:BO:76:VAL:HG21	7:BO:323:MET:HE3	1.60	0.82
11:BS:41:LYS:HE3	11:BS:41:LYS:HA	1.62	0.81
15:BW:48:SER:HB2	15:BW:66:ALA:HB3	1.65	0.78
23:Be:97:THR:HG23	23:Be:100:GLY:H	1.47	0.78

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B0	91/106 (86%)	86 (94%)	5 (6%)	0	100	100
2	B1	91/94 (97%)	87 (96%)	4 (4%)	0	100	100
6	BN	246/253 (97%)	238 (97%)	8 (3%)	0	100	100
7	BO	382/388 (98%)	367 (96%)	14 (4%)	1 (0%)	36	66
8	BP	360/363 (99%)	350 (97%)	10 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	BQ	285/294 (97%)	259 (91%)	25 (9%)	1 (0%)	30	60
10	BR	160/195 (82%)	145 (91%)	15 (9%)	0	100	100
11	BS	231/251 (92%)	223 (96%)	8 (4%)	0	100	100
12	BT	227/259 (88%)	218 (96%)	9 (4%)	0	100	100
13	BU	162/189 (86%)	153 (94%)	9 (6%)	0	100	100
14	BV	207/221 (94%)	201 (97%)	6 (3%)	0	100	100
15	BW	165/174 (95%)	150 (91%)	13 (8%)	2 (1%)	10	34
16	BX	205/208 (99%)	201 (98%)	4 (2%)	0	100	100
17	BY	128/134 (96%)	127 (99%)	1 (1%)	0	100	100
18	BZ	198/201 (98%)	187 (94%)	11 (6%)	0	100	100
19	Ba	194/197 (98%)	191 (98%)	3 (2%)	0	100	100
20	Bb	150/187 (80%)	144 (96%)	6 (4%)	0	100	100
21	Bc	184/187 (98%)	181 (98%)	3 (2%)	0	100	100
22	Bd	155/193 (80%)	151 (97%)	3 (2%)	1 (1%)	21	51
23	Be	171/176 (97%)	166 (97%)	4 (2%)	1 (1%)	21	51
24	Bf	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
25	Bg	97/117 (83%)	89 (92%)	8 (8%)	0	100	100
26	Bh	132/139 (95%)	127 (96%)	5 (4%)	0	100	100
27	Bi	61/149 (41%)	59 (97%)	2 (3%)	0	100	100
28	Bj	116/141 (82%)	111 (96%)	5 (4%)	0	100	100
29	Bk	123/126 (98%)	122 (99%)	1 (1%)	0	100	100
30	Bl	133/136 (98%)	125 (94%)	8 (6%)	0	100	100
31	Bm	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
32	Bn	57/61 (93%)	54 (95%)	3 (5%)	0	100	100
33	Bo	92/109 (84%)	90 (98%)	2 (2%)	0	100	100
34	Bp	101/113 (89%)	99 (98%)	2 (2%)	0	100	100
35	Bq	116/127 (91%)	113 (97%)	3 (3%)	0	100	100
36	Br	102/108 (94%)	100 (98%)	2 (2%)	0	100	100
37	Bs	104/111 (94%)	102 (98%)	2 (2%)	0	100	100
38	Bt	119/122 (98%)	114 (96%)	5 (4%)	0	100	100
39	Bu	93/99 (94%)	91 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	Bv	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
41	Bw	67/74 (90%)	66 (98%)	1 (2%)	0	100	100
42	Bx	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
43	By	131/134 (98%)	126 (96%)	5 (4%)	0	100	100
44	HS	98/106 (92%)	83 (85%)	12 (12%)	3 (3%)	3	12
All	All	6164/6692 (92%)	5908 (96%)	247 (4%)	9 (0%)	49	77

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	BW	46	VAL
15	BW	133	ARG
22	Bd	35	ALA
44	HS	56	ASN
44	HS	80	ASP

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	B0	84/93 (90%)	83 (99%)	1 (1%)	63	87
2	B1	74/75 (99%)	72 (97%)	2 (3%)	39	74
6	BN	188/192 (98%)	186 (99%)	2 (1%)	65	87
7	BO	318/326 (98%)	314 (99%)	4 (1%)	61	86
8	BP	293/294 (100%)	289 (99%)	4 (1%)	59	85
9	BQ	235/241 (98%)	233 (99%)	2 (1%)	70	89
10	BR	132/155 (85%)	130 (98%)	2 (2%)	57	84
11	BS	198/213 (93%)	195 (98%)	3 (2%)	57	84
12	BT	182/212 (86%)	180 (99%)	2 (1%)	65	87
13	BU	149/168 (89%)	148 (99%)	1 (1%)	76	91
14	BV	177/187 (95%)	177 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	BW	141/146 (97%)	138 (98%)	3 (2%)	47	79
16	BX	166/167 (99%)	160 (96%)	6 (4%)	31	66
17	BY	110/113 (97%)	105 (96%)	5 (4%)	24	58
18	BZ	175/176 (99%)	173 (99%)	2 (1%)	65	87
19	Ba	159/160 (99%)	158 (99%)	1 (1%)	78	92
20	Bb	124/149 (83%)	123 (99%)	1 (1%)	73	90
21	Bc	157/158 (99%)	156 (99%)	1 (1%)	78	92
22	Bd	136/163 (83%)	134 (98%)	2 (2%)	57	84
23	Be	151/154 (98%)	146 (97%)	5 (3%)	33	69
24	Bf	138/139 (99%)	131 (95%)	7 (5%)	21	54
25	Bg	86/103 (84%)	86 (100%)	0	100	100
26	Bh	103/107 (96%)	100 (97%)	3 (3%)	37	73
27	Bi	57/121 (47%)	55 (96%)	2 (4%)	32	67
28	Bj	105/122 (86%)	102 (97%)	3 (3%)	37	73
29	Bk	110/111 (99%)	107 (97%)	3 (3%)	39	74
30	Bl	114/115 (99%)	110 (96%)	4 (4%)	32	67
31	Bm	122/123 (99%)	120 (98%)	2 (2%)	55	83
32	Bn	50/51 (98%)	49 (98%)	1 (2%)	48	80
33	Bo	75/87 (86%)	75 (100%)	0	100	100
34	Bp	94/102 (92%)	93 (99%)	1 (1%)	65	87
35	Bq	100/107 (94%)	100 (100%)	0	100	100
36	Br	91/94 (97%)	88 (97%)	3 (3%)	33	69
37	Bs	91/96 (95%)	90 (99%)	1 (1%)	65	87
38	Bt	106/107 (99%)	104 (98%)	2 (2%)	50	81
39	Bu	81/84 (96%)	78 (96%)	3 (4%)	30	65
40	Bv	68/71 (96%)	66 (97%)	2 (3%)	37	73
41	Bw	63/66 (96%)	63 (100%)	0	100	100
42	Bx	46/47 (98%)	45 (98%)	1 (2%)	45	78
43	By	112/113 (99%)	110 (98%)	2 (2%)	51	82
44	HS	92/97 (95%)	90 (98%)	2 (2%)	45	78
All	All	5253/5605 (94%)	5162 (98%)	91 (2%)	52	83

5 of 91 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	Bh	79	ILE
31	Bm	86	THR
27	Bi	1	MET
29	Bk	56	THR
36	Br	28	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
32	Bn	19	ASN
40	Bv	76	ASN
34	Bp	50	GLN
38	Bt	15	ASN
14	BV	14	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	B2	3132/3498 (89%)	618 (19%)	20 (0%)
4	B3	118/246 (47%)	16 (13%)	1 (0%)
5	B4	156/165 (94%)	30 (19%)	1 (0%)
All	All	3406/3909 (87%)	664 (19%)	22 (0%)

5 of 664 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	B2	40	A
3	B2	43	A
3	B2	49	A
3	B2	59	G
3	B2	60	A

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	B2	3260	A
3	B2	3328	U
3	B2	3298	C
3	B2	3373	C

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Mol	Chain	Res	Type
3	B2	1272	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 [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

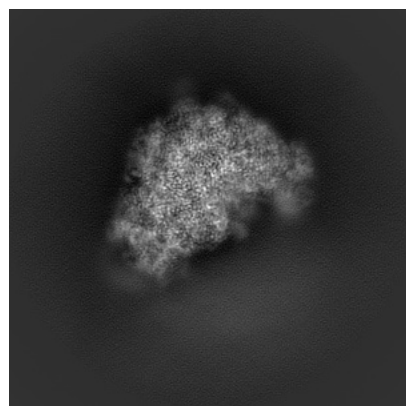
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71645. These allow visual inspection of the internal detail of the map and identification of artifacts.

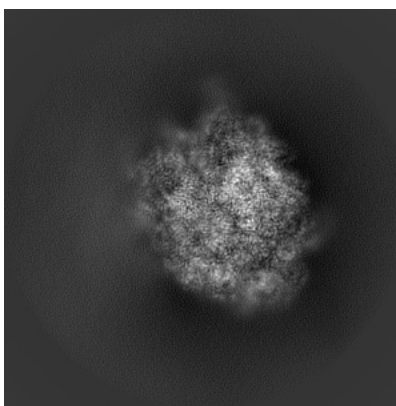
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

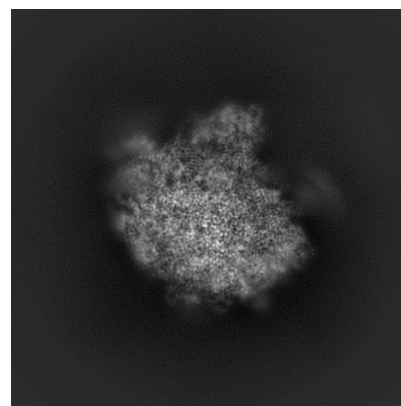
6.1.1 Primary map



X

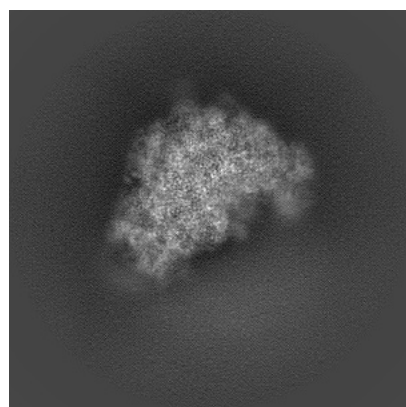


Y

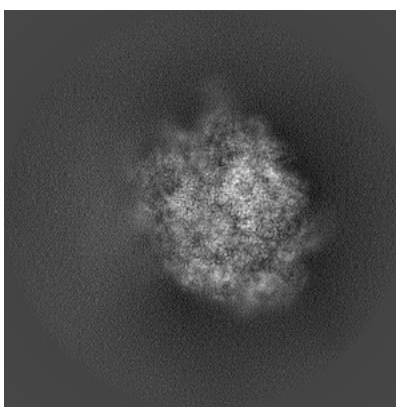


Z

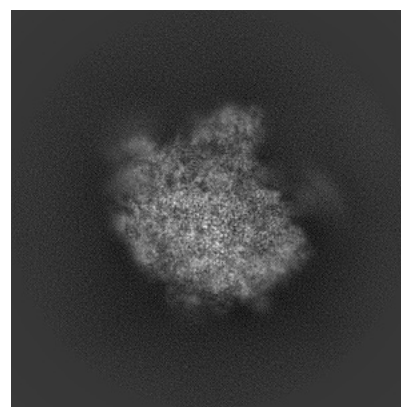
6.1.2 Raw map



X



Y

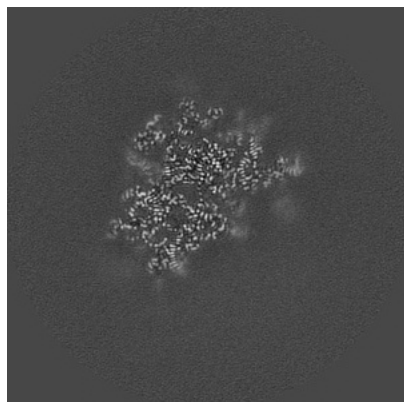


Z

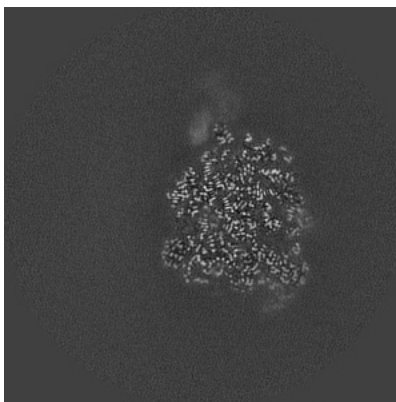
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

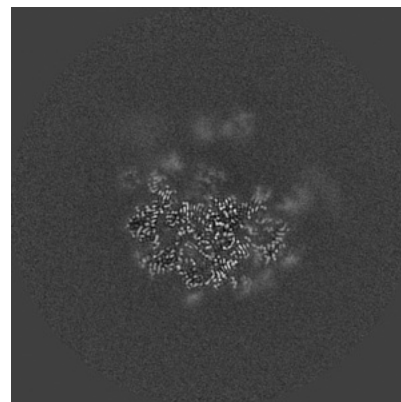
6.2.1 Primary map



X Index: 256

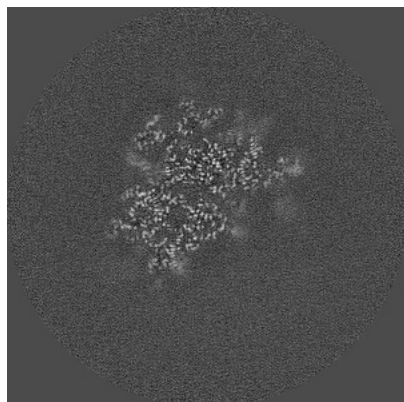


Y Index: 256

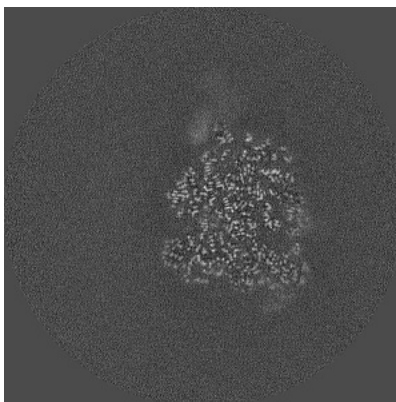


Z Index: 256

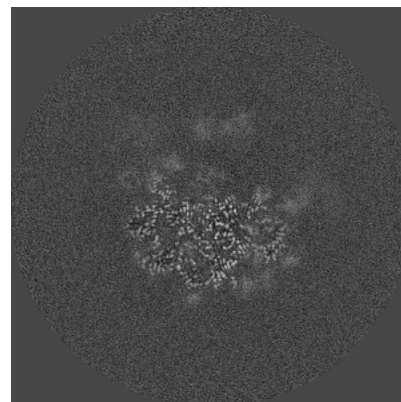
6.2.2 Raw map



X Index: 256



Y Index: 256

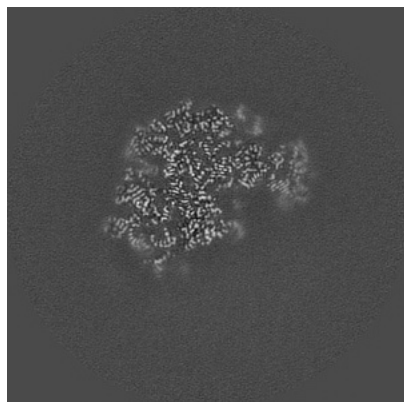


Z Index: 256

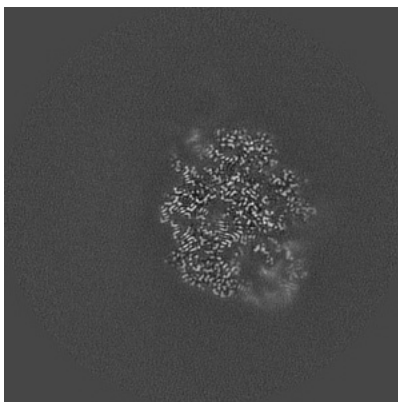
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

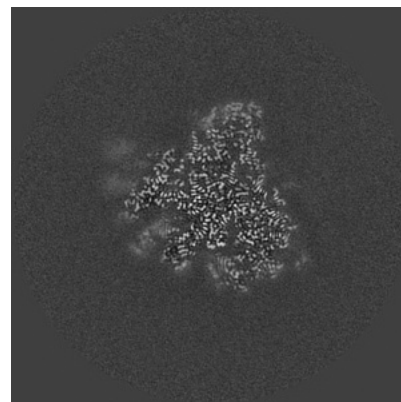
6.3.1 Primary map



X Index: 271

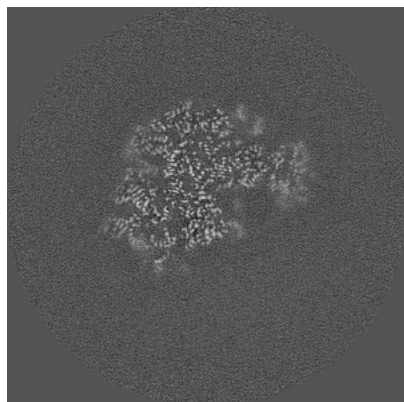


Y Index: 241

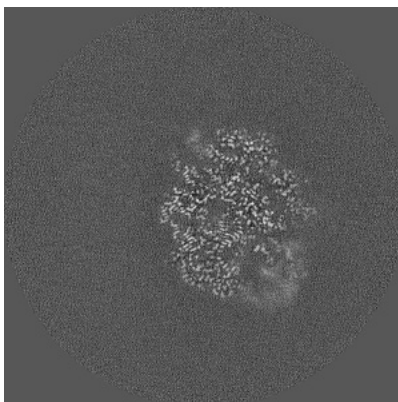


Z Index: 306

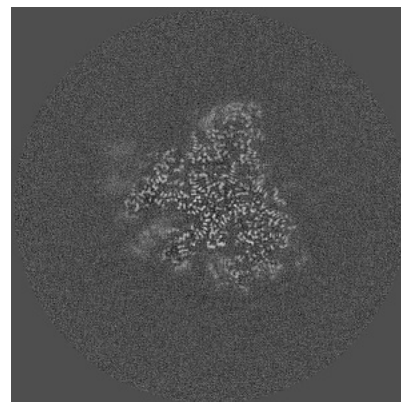
6.3.2 Raw map



X Index: 271



Y Index: 241

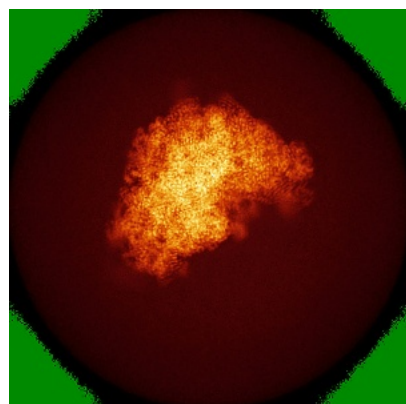


Z Index: 306

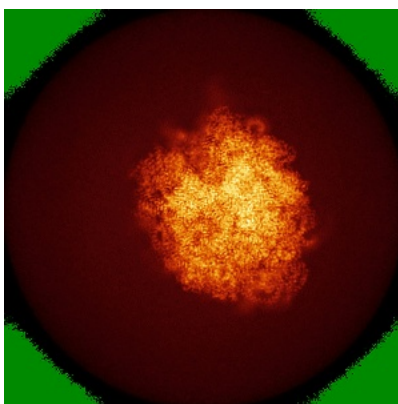
The images above show the largest variance slices of the map in three orthogonal directions.

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

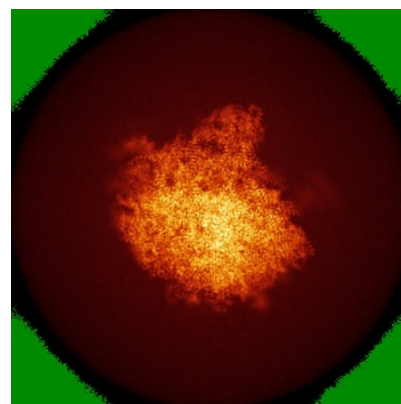
6.4.1 Primary map



X

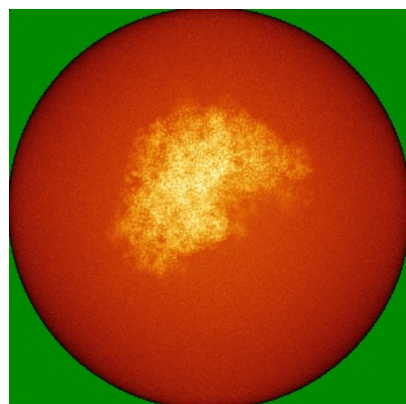


Y

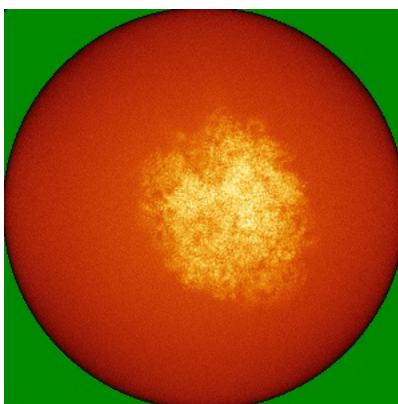


Z

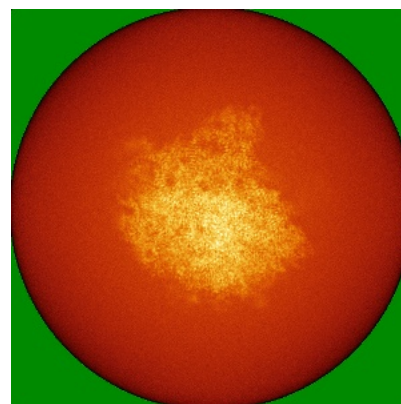
6.4.2 Raw map



X



Y

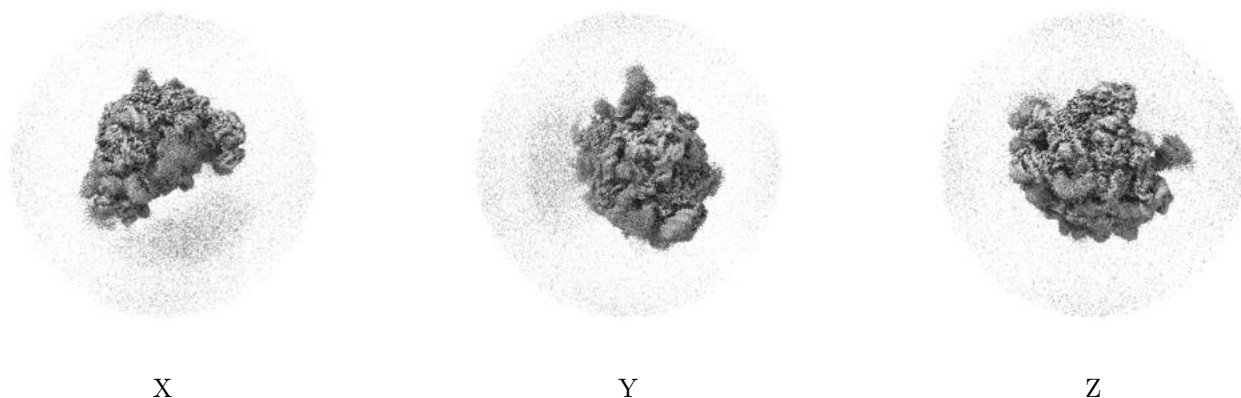


Z

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.

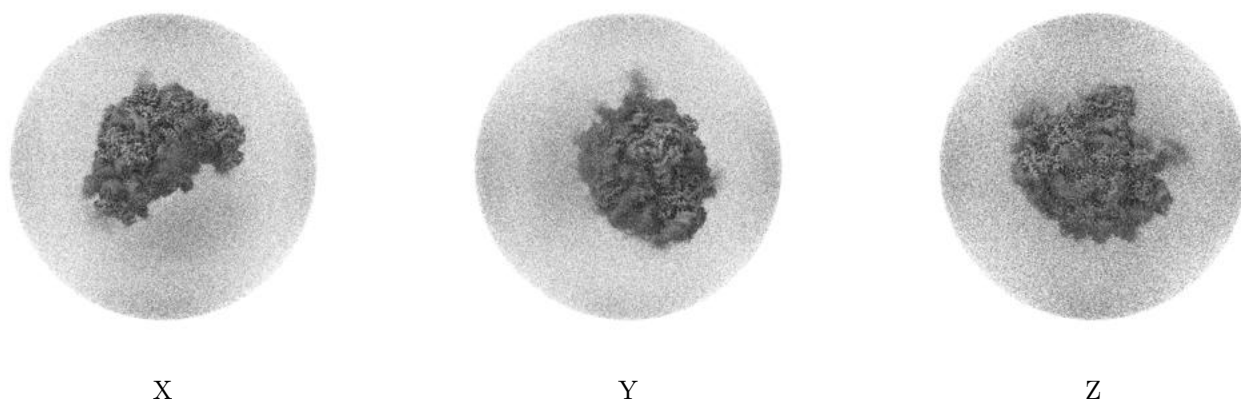
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.002. 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.

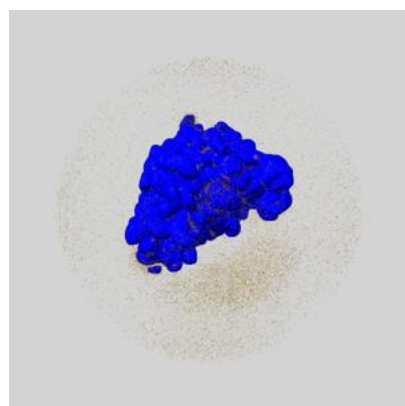
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

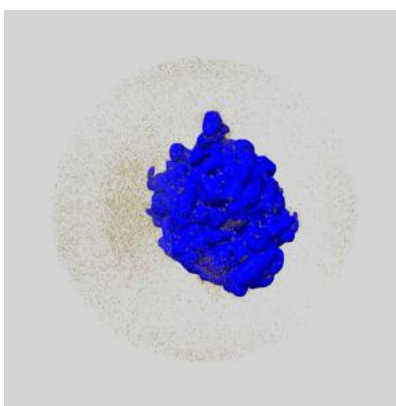
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

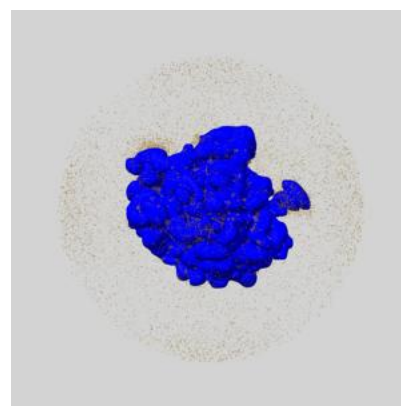
6.6.1 emd_71645_msk_1.map [i](#)



X



Y

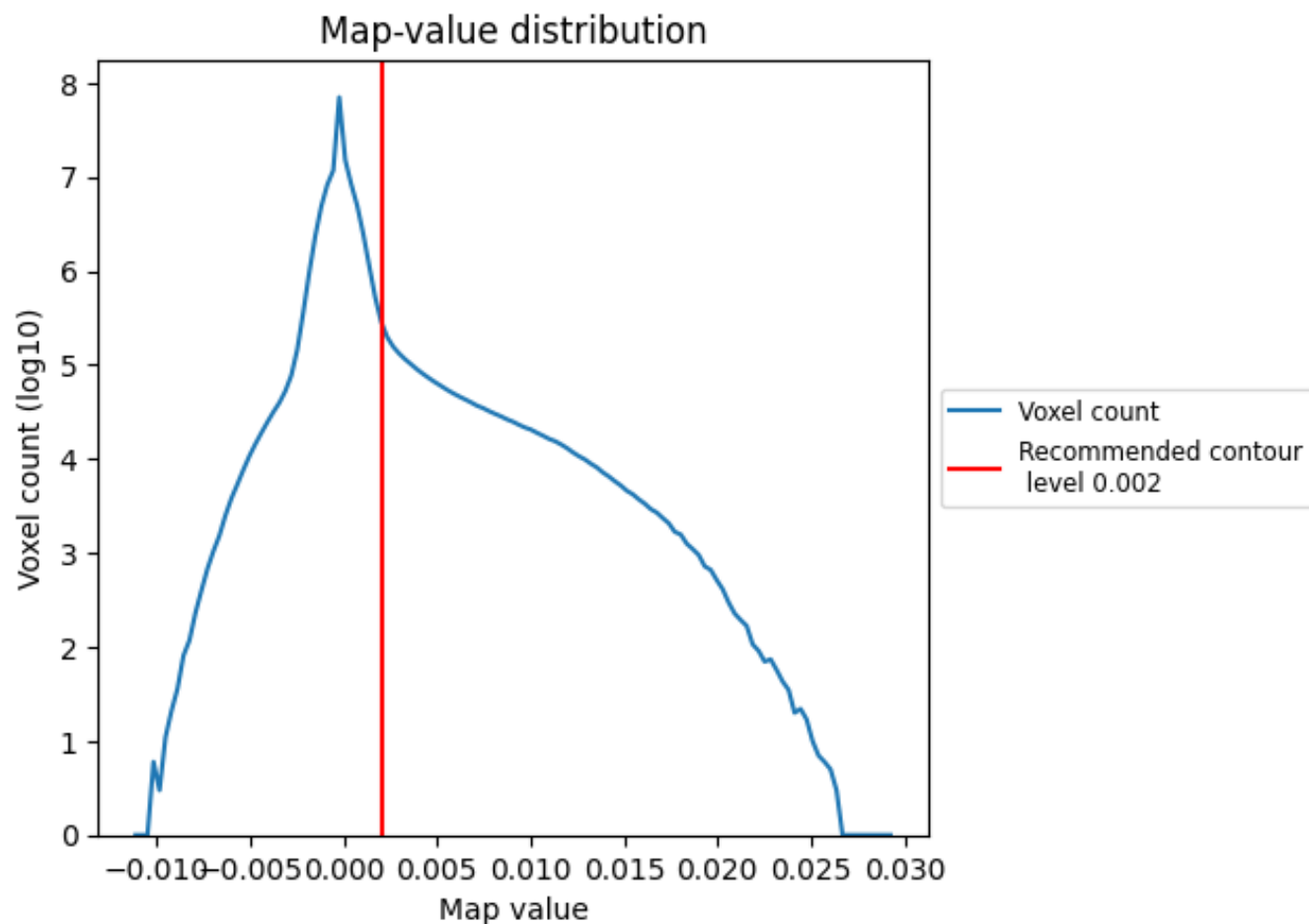


Z

7 Map analysis [i](#)

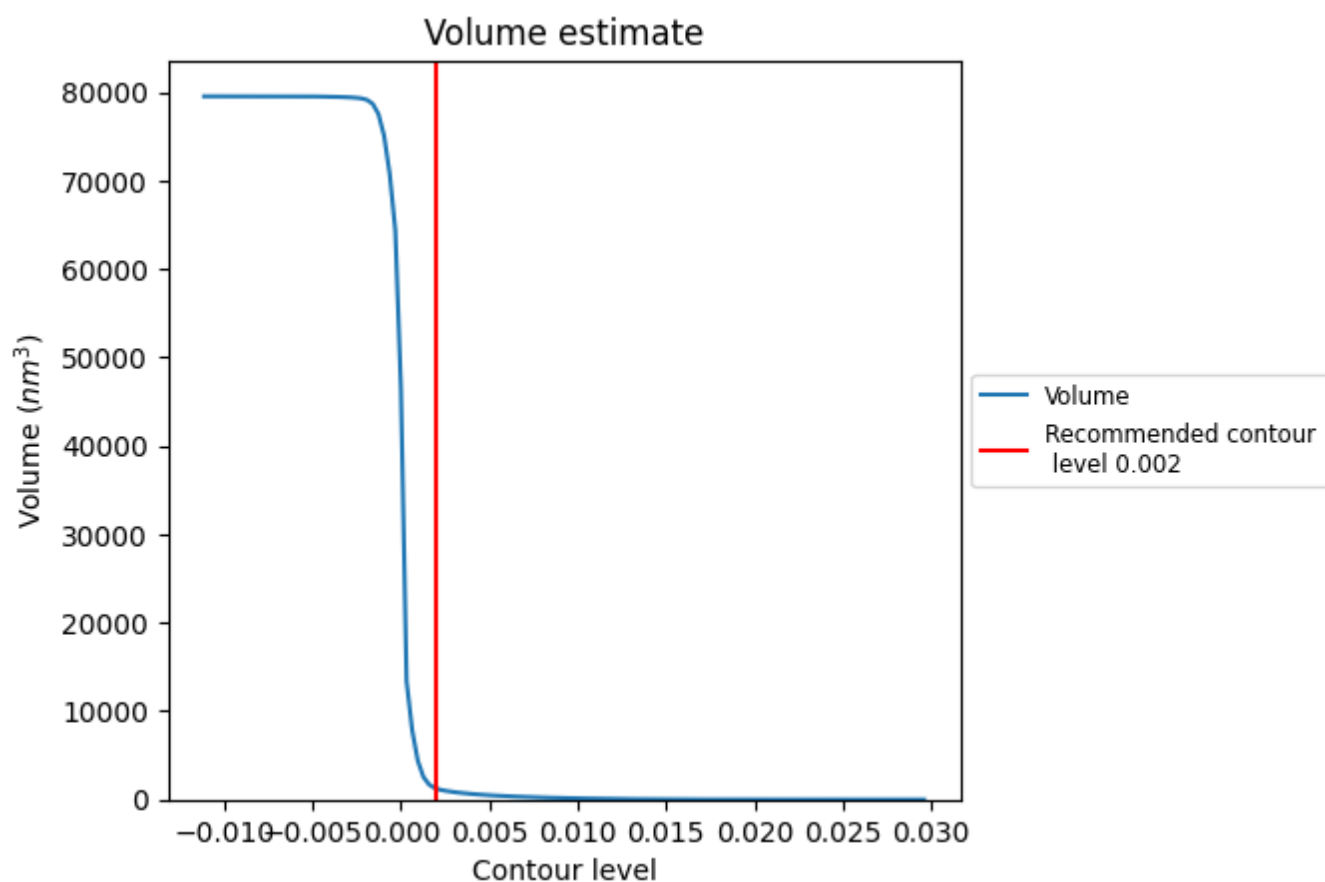
This section contains the results of statistical analysis of the map.

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.

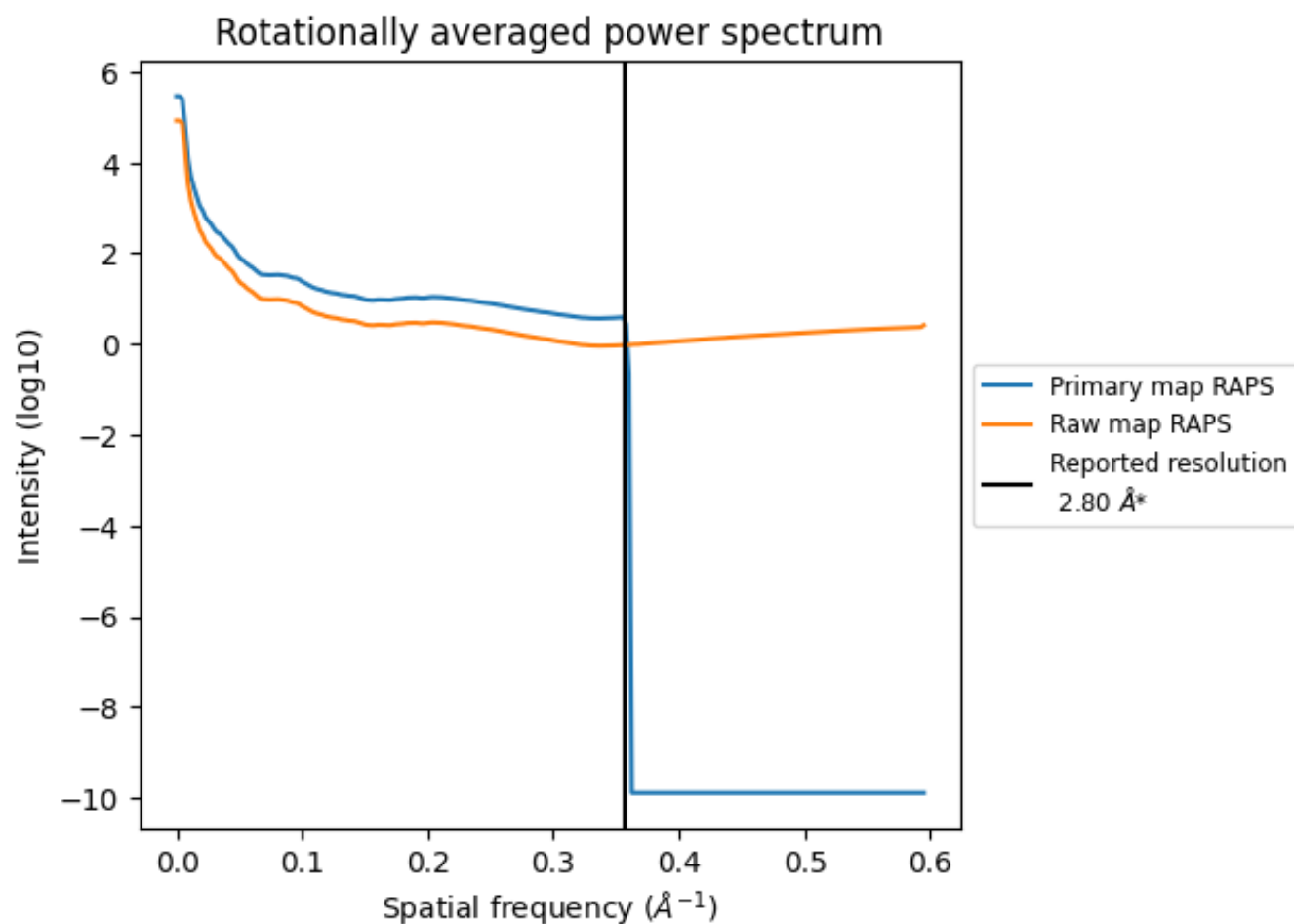
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1250 nm³; this corresponds to an approximate mass of 1129 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 ⓘ

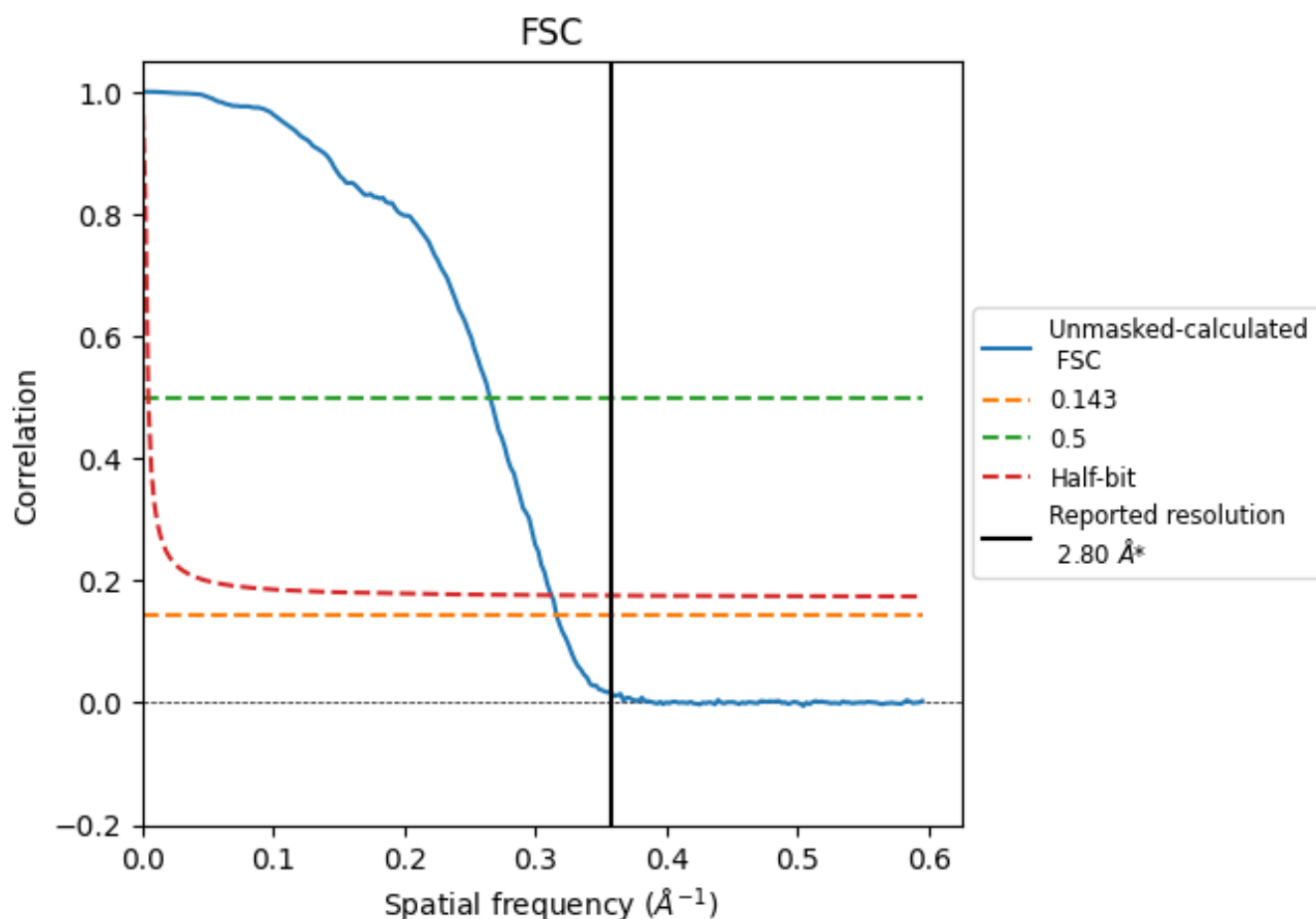


*Reported resolution corresponds to spatial frequency of 0.357 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

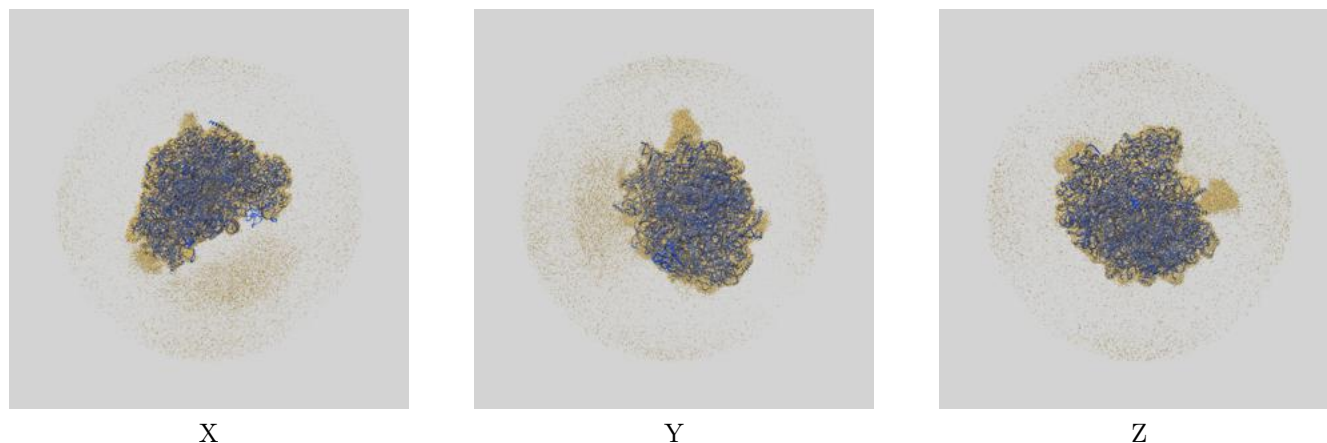
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.16	3.77	3.20

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.16 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

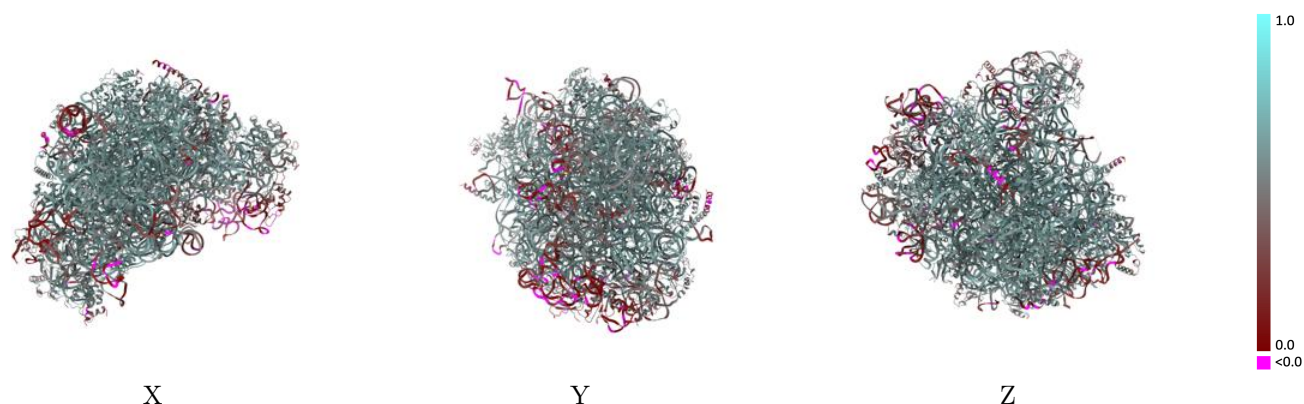
This section contains information regarding the fit between EMDB map EMD-71645 and PDB model 9PHC. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.002 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](#)



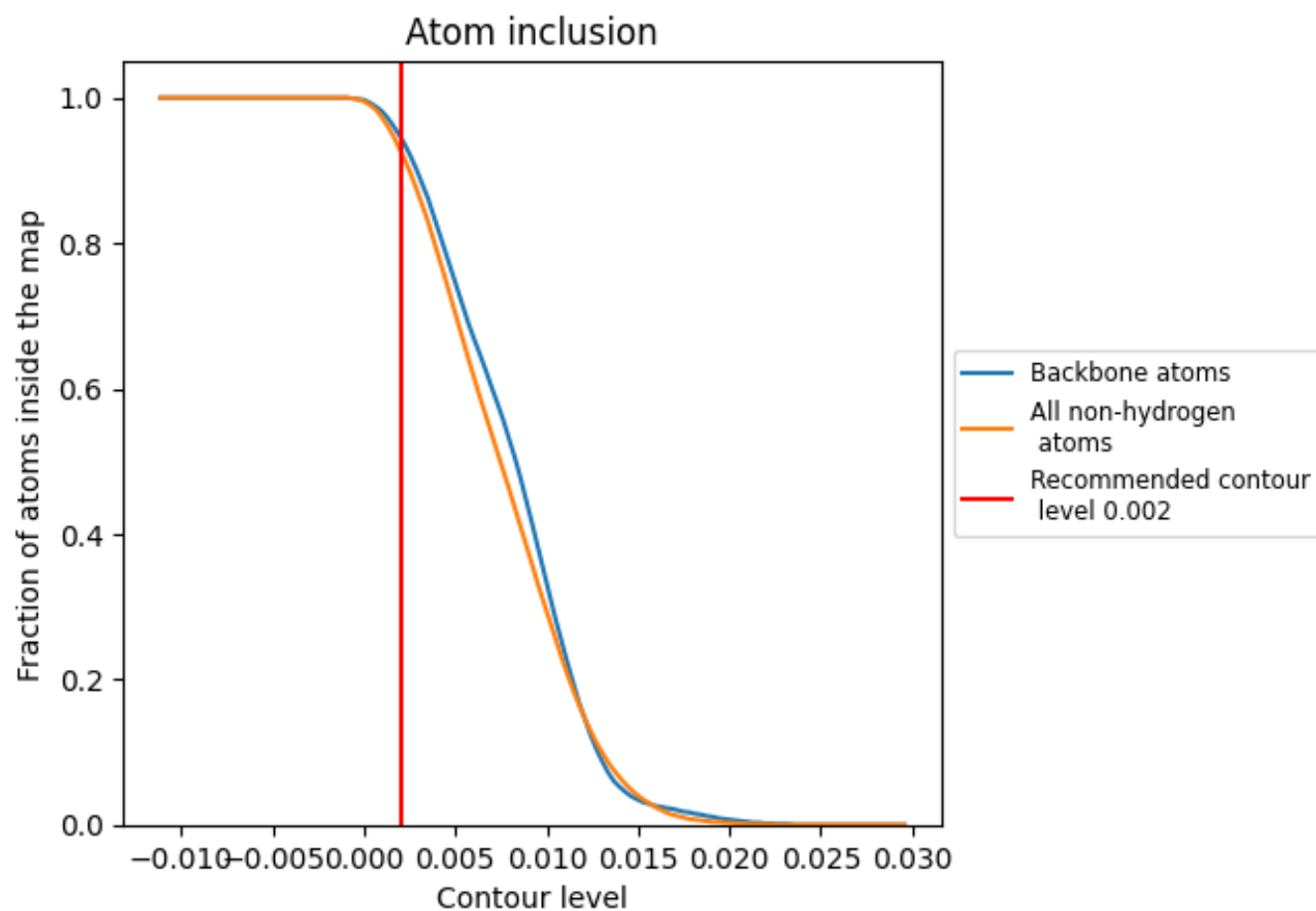
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.002).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















The table lists the average atom inclusion at the recommended contour level (0.002) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9270	 0.5320
B0	 0.8650	 0.5290
B1	 0.9460	 0.5710
B2	 0.9380	 0.5230
B3	 0.9840	 0.5530
B4	 0.9660	 0.5520
BN	 0.9720	 0.6110
BO	 0.9710	 0.5980
BP	 0.9730	 0.6020
BQ	 0.8890	 0.4920
BR	 0.8570	 0.4950
BS	 0.8920	 0.5600
BT	 0.9250	 0.5450
BU	 0.6160	 0.2690
BV	 0.7830	 0.4690
BW	 0.6460	 0.2700
BX	 0.9280	 0.5720
BY	 0.9360	 0.5280
BZ	 0.9880	 0.6230
Ba	 0.9710	 0.5890
Bb	 0.9290	 0.5800
Bc	 0.9620	 0.6010
Bd	 0.9060	 0.5470
Be	 0.9320	 0.5720
Bf	 0.8920	 0.5360
Bg	 0.7650	 0.3960
Bh	 0.9590	 0.5820
Bi	 0.9190	 0.5460
Bj	 0.9630	 0.5770
Bk	 0.9640	 0.5760
Bl	 0.9240	 0.5140
Bm	 0.9740	 0.6120
Bn	 0.9310	 0.5720
Bo	 0.8570	 0.4890
Bp	 0.9440	 0.5700



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Chain	Atom inclusion	Q-score
Bq	 0.9700	 0.6060
Br	 0.9730	 0.6040
Bs	 0.9660	 0.5990
Bt	 0.9530	 0.5720
Bu	 0.9450	 0.5670
Bv	 0.9840	 0.6180
Bw	 0.9010	 0.4840
Bx	 0.8100	 0.4910
By	 0.9060	 0.5460
HS	 0.5540	 0.3290