



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 04:21 am BST

PDB ID : 6YBW / pdb_00006ybw
EMDB ID : EMD-10775
Title : Structure of a human 48S translational initiation complex - 40S body
Authors : Brito Querido, J.; Sokabe, M.; Kraatz, S.; Gordiyenko, Y.; Skehel, M.; Fraser, C.; Ramakrishnan, V.
Deposited on : 2020-03-18
Resolution : 3.10 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:

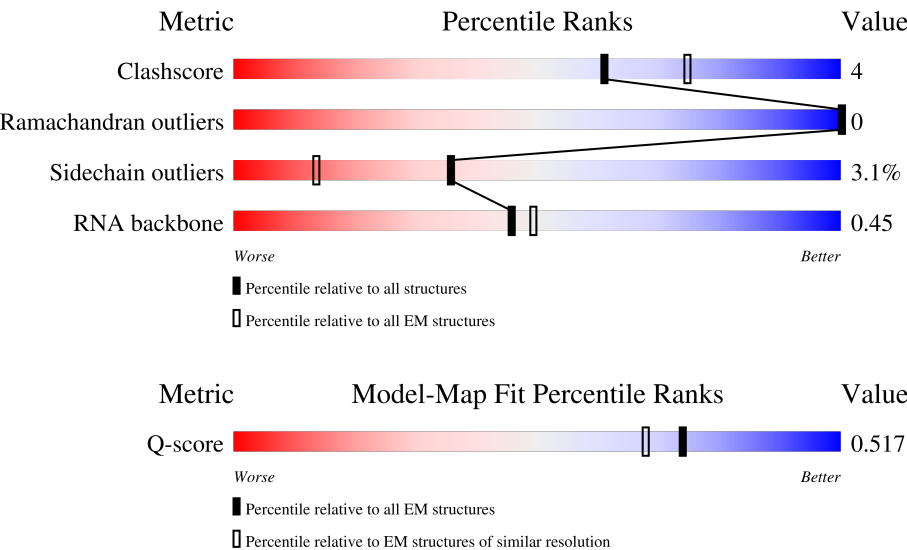
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal 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 i

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

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	14724 (2.60 - 3.60)

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	C	263	87% 10% .
2	B	157	78% 13% 10%
3	E	143	85% 13% .

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Mol	Chain	Length	Quality of chain
4	D	194	
5	G	194	
6	F	59	
7	H	84	
8	K	83	
9	J	130	
10	M	135	
11	L	293	
12	O	264	
13	N	295	
14	Q	115	
15	P	151	
16	S	249	
17	R	208	
18	T	133	
19	q	144	
20	p	113	
21	I	151	
22	z	258	
23	y	913	
24	9	25	
25	A	1869	
26	7	28	

2 Entry composition [i](#)

There are 28 unique types of molecules in this entry. The entry contains 52840 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 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	256	Total	C	N	O	S	0	0
			2035	1302	378	347	8		

- Molecule 2 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	142	Total	C	N	O	S	0	0
			1166	743	218	199	6		

- Molecule 3 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	140	Total	C	N	O	S	0	0
			1087	687	215	182	3		

- Molecule 4 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	177	Total	C	N	O	S	0	0
			1477	941	295	239	2		

- Molecule 5 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	177	Total	C	N	O	S	0	0
			1430	917	260	252	1		

- Molecule 6 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	47	Total	C	N	O	S	0	0
			378	231	85	61	1		

- Molecule 7 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	81	Total	C	N	O	S	0	0
			631	397	116	111	7		

- Molecule 8 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	81	Total	C	N	O	S	0	0
			617	380	114	118	5		

- Molecule 9 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 10 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	54	Total	C	N	O	S	0	0
			432	270	72	88	2		

- Molecule 11 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	220	Total	C	N	O	S	0	0
			1707	1104	292	301	10		

- Molecule 12 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	211	Total	C	N	O	S	0	0
			1715	1088	307	306	14		

- Molecule 13 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	207	Total	C	N	O	S	0	0
			1633	1040	288	297	8		

- Molecule 14 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	99	Total	C	N	O	S	0	0
			792	492	165	130	5		

- Molecule 15 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	131	Total	C	N	O	S	0	0
			982	600	193	183	6		

- Molecule 16 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	230	Total	C	N	O	S	0	0
			1862	1164	371	320	7		

- Molecule 17 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	198	Total	C	N	O	S	0	0
			1627	1021	322	279	5		

- Molecule 18 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 19 is a protein called Eukaryotic translation initiation factor 1A, X-chromosomal.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	q	88	Total	C	N	O	S	0	0
			714	451	129	130	4		

- Molecule 20 is a protein called Eukaryotic translation initiation factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	p	85	Total	C	N	O	S	0	0
			691	438	125	126	2		

- Molecule 21 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	I	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 22 is a protein called Eukaryotic translation initiation factor 3 subunit J.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	z	160	Total	C	N	O		0	0
			795	475	160	160			

- Molecule 23 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	y	162	Total	C	N	O	S	0	0
			1145	714	212	217	2		

- Molecule 24 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	9	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 25 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	1220	Total	C	N	O	P	0	0
			26040	11635	4689	8497	1219		

- Molecule 26 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	7	28	Total	C	O	P	0	0
			336	140	168	28		

- Molecule 27 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
27	L	1	Total	Mg	0
			1	1	
27	S	1	Total	Mg	0
			1	1	
27	A	58	Total	Mg	0
			58	58	

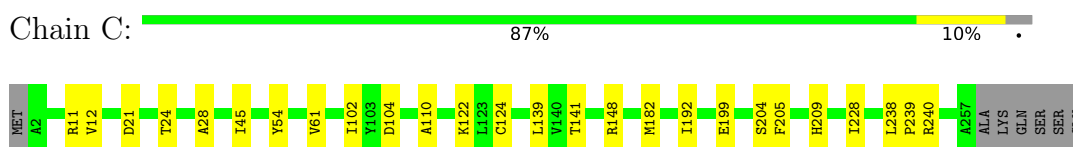
- Molecule 28 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
28	Q	1	Total 1	Zn 1	0

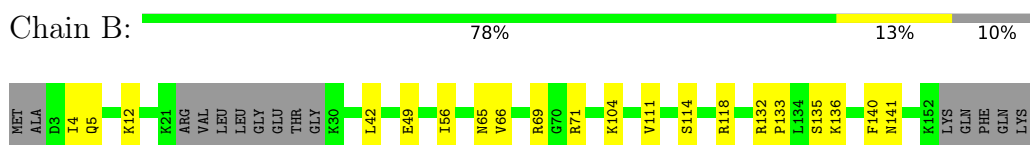
3 Residue-property plots

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.

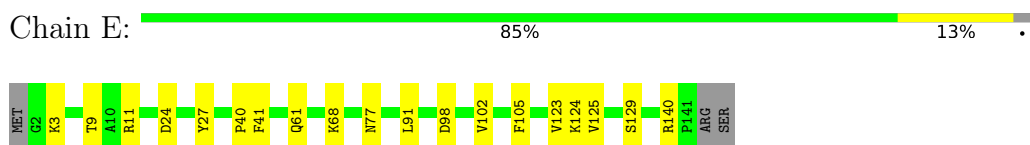
- Molecule 1: 40S ribosomal protein S4, X isoform



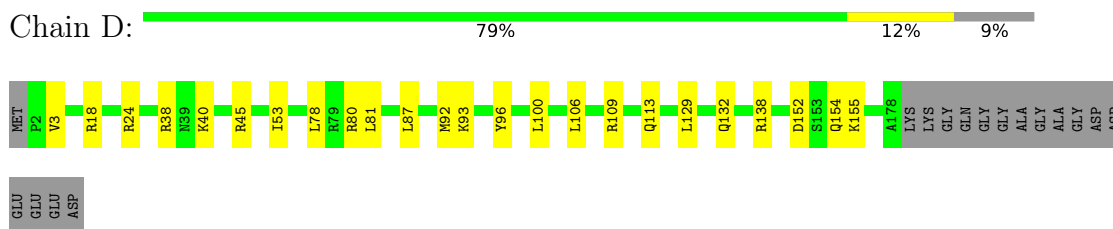
- Molecule 2: 40S ribosomal protein S11



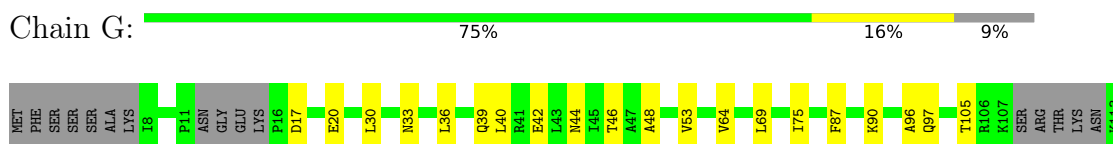
- Molecule 3: 40S ribosomal protein S23

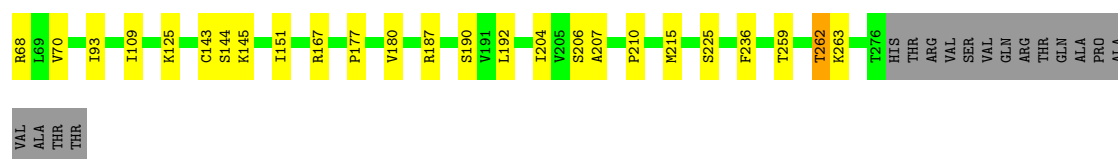


- Molecule 4: 40S ribosomal protein S9

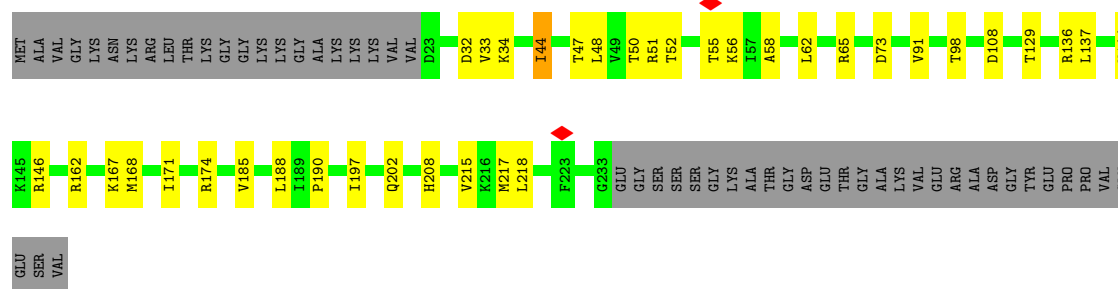


- Molecule 5: 40S ribosomal protein S7

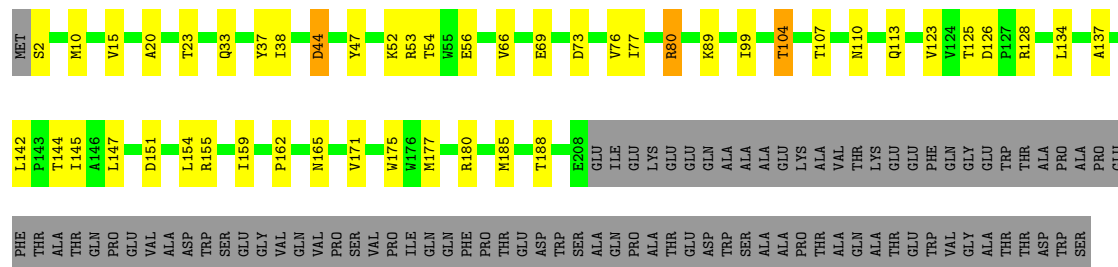




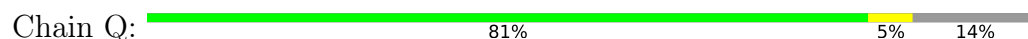
- Molecule 12: 40S ribosomal protein S3a



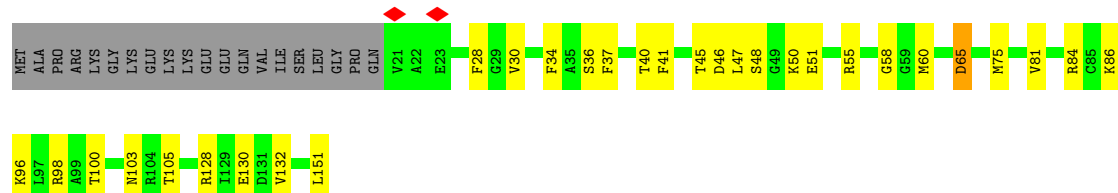
- Molecule 13: 40S ribosomal protein SA



- Molecule 14: 40S ribosomal protein S26

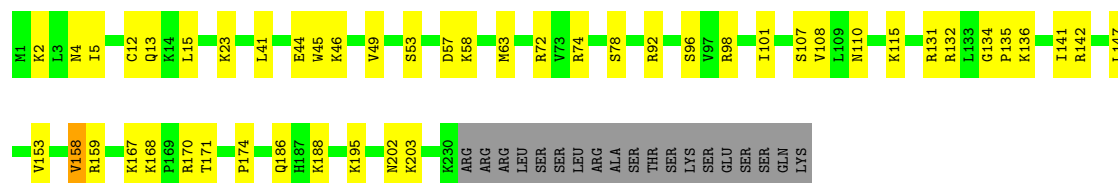


- Molecule 15: 40S ribosomal protein S14



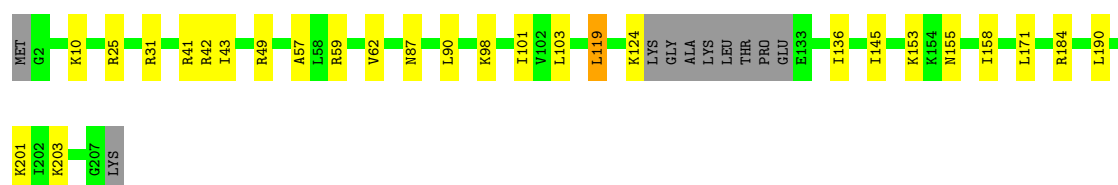
- Molecule 16: 40S ribosomal protein S6

Chain S:  73% 19% 8%



- Molecule 17: 40S ribosomal protein S8

Chain R:  82% 12% 5%

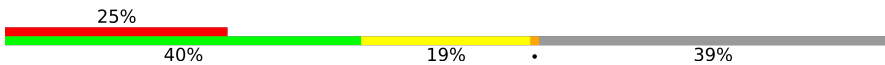


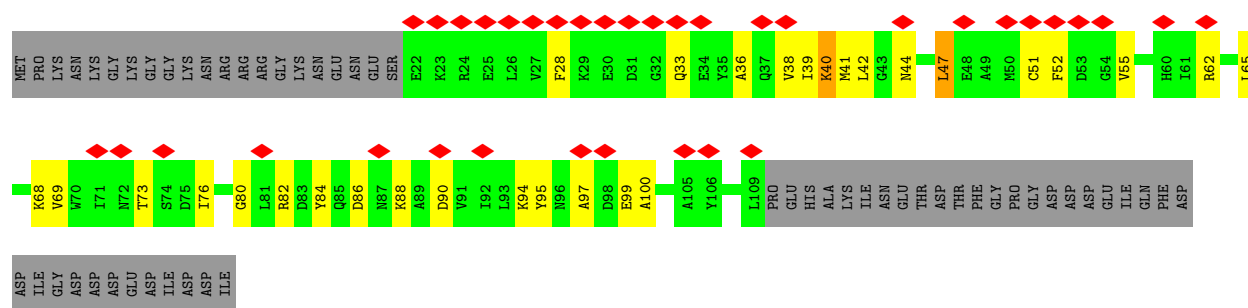
- Molecule 18: 40S ribosomal protein S24

Chain T:  81% 12% 6%



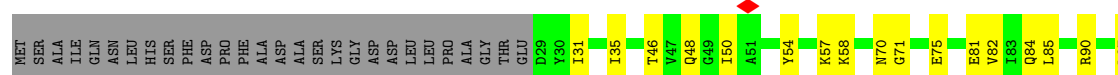
- Molecule 19: Eukaryotic translation initiation factor 1A, X-chromosomal

Chain q:  25% 40% 19% 39%



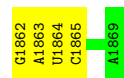
- Molecule 20: Eukaryotic translation initiation factor 1

Chain p:  55% 19% 25%









- Molecule 26: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	144882	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 ($e^-/\text{\AA}^2$)	107	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.410	Depositor
Minimum map value	-0.228	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	537.0, 537.0, 537.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.074, 1.074, 1.074	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MA6, ZN, UR3, OMC, A2M, MG, OMG, 5MU, OMU, 6MZ, PSU

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	C	0.23	0/2077	0.52	0/2796
2	B	0.24	0/1186	0.48	0/1585
3	E	0.25	0/1105	0.55	0/1476
4	D	0.23	0/1502	0.53	0/2008
5	G	0.27	0/1451	0.61	0/1942
6	F	0.18	0/380	0.42	0/496
7	H	0.22	0/644	0.49	0/864
8	K	0.22	0/623	0.44	0/833
9	J	0.27	0/1051	0.55	0/1406
10	M	0.25	0/438	0.61	0/593
11	L	0.24	0/1743	0.52	0/2354
12	O	0.24	0/1742	0.59	2/2330 (0.1%)
13	N	0.24	0/1670	0.51	0/2271
14	Q	0.27	0/805	0.57	0/1079
15	P	0.24	0/994	0.60	0/1332
16	S	0.24	0/1885	0.60	0/2510
17	R	0.25	0/1654	0.59	0/2203
18	T	0.22	0/1032	0.50	0/1371
19	q	0.26	0/722	0.72	0/963
20	p	0.24	0/701	0.66	0/936
21	I	0.25	0/1232	0.62	0/1656
22	z	0.24	0/792	0.79	2/1101 (0.2%)
23	y	0.30	0/1156	0.72	0/1561
24	9	0.25	0/231	0.61	0/294
25	A	0.27	1/28528 (0.0%)	0.46	1/44454 (0.0%)
26	7	0.29	0/363	0.77	0/556
All	All	0.26	1/55707 (0.0%)	0.52	5/80970 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	116	OMU	O3'-P	5.06	1.61	1.56

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	688	U	P-O3'-C3'	5.23	128.04	120.20
12	O	190	PRO	CA-C-N	5.17	130.16	122.82
12	O	190	PRO	C-N-CA	5.17	130.16	122.82
22	z	193	ILE	CA-C-N	5.03	131.14	121.54
22	z	193	ILE	C-N-CA	5.03	131.14	121.54

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	C	2035	0	2138	15	0
2	B	1166	0	1233	12	0
3	E	1087	0	1154	10	0
4	D	1477	0	1589	15	0
5	G	1430	0	1520	15	0
6	F	378	0	417	1	0
7	H	631	0	657	5	0
8	K	617	0	622	1	0
9	J	1034	0	1080	11	0
10	M	432	0	429	6	0
11	L	1707	0	1794	13	0
12	O	1715	0	1785	25	0
13	N	1633	0	1640	27	0
14	Q	792	0	843	3	0
15	P	982	0	1005	21	0
16	S	1862	0	2018	36	0
17	R	1627	0	1706	17	0
18	T	1015	0	1086	12	0
19	q	714	0	735	15	0
20	p	691	0	706	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	I	1208	0	1294	10	0
22	z	795	0	341	0	0
23	y	1145	0	1000	13	0
24	9	230	0	276	1	0
25	A	26040	0	13175	166	0
26	7	336	0	169	2	0
27	A	58	0	0	0	0
27	L	1	0	0	0	0
27	S	1	0	0	0	0
28	Q	1	0	0	0	0
All	All	52840	0	40412	389	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 389 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)
25:A:885:U:H3	25:A:901:G:H1	1.07	0.97
25:A:1722:G:H1	25:A:1812:U:H3	1.07	0.93
25:A:1033:G:H1	25:A:1080:A:HO2'	1.28	0.81
12:O:52:THR:HG22	12:O:58:ALA:H	1.55	0.71
2:B:4:ILE:HG13	2:B:5:GLN:HE21	1.57	0.69

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	C	254/263 (97%)	251 (99%)	3 (1%)	0	100	100
2	B	138/157 (88%)	136 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	E	138/143 (96%)	133 (96%)	5 (4%)	0	100	100
4	D	175/194 (90%)	173 (99%)	2 (1%)	0	100	100
5	G	171/194 (88%)	165 (96%)	6 (4%)	0	100	100
6	F	43/59 (73%)	43 (100%)	0	0	100	100
7	H	79/84 (94%)	77 (98%)	2 (2%)	0	100	100
8	K	79/83 (95%)	75 (95%)	4 (5%)	0	100	100
9	J	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
10	M	52/135 (38%)	51 (98%)	1 (2%)	0	100	100
11	L	218/293 (74%)	211 (97%)	7 (3%)	0	100	100
12	O	209/264 (79%)	200 (96%)	9 (4%)	0	100	100
13	N	205/295 (70%)	195 (95%)	10 (5%)	0	100	100
14	Q	97/115 (84%)	93 (96%)	4 (4%)	0	100	100
15	P	129/151 (85%)	125 (97%)	4 (3%)	0	100	100
16	S	228/249 (92%)	222 (97%)	6 (3%)	0	100	100
17	R	194/208 (93%)	186 (96%)	8 (4%)	0	100	100
18	T	123/133 (92%)	122 (99%)	1 (1%)	0	100	100
19	q	86/144 (60%)	75 (87%)	11 (13%)	0	100	100
20	p	83/113 (74%)	80 (96%)	3 (4%)	0	100	100
21	I	148/151 (98%)	135 (91%)	13 (9%)	0	100	100
22	z	154/258 (60%)	139 (90%)	15 (10%)	0	100	100
23	y	158/913 (17%)	152 (96%)	6 (4%)	0	100	100
24	9	22/25 (88%)	22 (100%)	0	0	100	100
All	All	3310/4754 (70%)	3186 (96%)	124 (4%)	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	C	220/225 (98%)	218 (99%)	2 (1%)	70	80
2	B	129/141 (92%)	128 (99%)	1 (1%)	73	81
3	E	112/115 (97%)	109 (97%)	3 (3%)	39	67
4	D	158/168 (94%)	156 (99%)	2 (1%)	61	77
5	G	159/174 (91%)	150 (94%)	9 (6%)	18	49
6	F	38/48 (79%)	37 (97%)	1 (3%)	40	68
7	H	73/76 (96%)	72 (99%)	1 (1%)	59	76
8	K	65/67 (97%)	62 (95%)	3 (5%)	24	55
9	J	112/113 (99%)	110 (98%)	2 (2%)	51	73
10	M	51/122 (42%)	48 (94%)	3 (6%)	18	48
11	L	186/225 (83%)	179 (96%)	7 (4%)	29	60
12	O	192/231 (83%)	188 (98%)	4 (2%)	47	71
13	N	173/243 (71%)	165 (95%)	8 (5%)	24	55
14	Q	86/98 (88%)	84 (98%)	2 (2%)	44	70
15	P	102/119 (86%)	98 (96%)	4 (4%)	28	60
16	S	200/218 (92%)	198 (99%)	2 (1%)	68	79
17	R	172/180 (96%)	167 (97%)	5 (3%)	37	66
18	T	107/115 (93%)	104 (97%)	3 (3%)	38	66
19	q	75/123 (61%)	66 (88%)	9 (12%)	5	21
20	p	74/96 (77%)	69 (93%)	5 (7%)	14	42
21	I	130/131 (99%)	126 (97%)	4 (3%)	35	64
23	y	91/811 (11%)	87 (96%)	4 (4%)	25	56
24	9	23/24 (96%)	23 (100%)	0	100	100
All	All	2728/3863 (71%)	2644 (97%)	84 (3%)	36	64

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	R	145	ILE
20	p	46	THR
18	T	27	VAL
19	q	47	LEU
20	p	108	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52

such sidechains are listed below:

Mol	Chain	Res	Type
12	O	159	GLN
16	S	110	ASN
20	p	107	GLN
12	O	186	ASN
13	N	29	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	A	1210/1869 (64%)	302 (24%)	13 (1%)
26	7	27/28 (96%)	20 (74%)	0
All	All	1237/1897 (65%)	322 (26%)	13 (1%)

5 of 322 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
25	A	2	A
25	A	4	C
25	A	17	C
25	A	23	G
25	A	33	G

5 of 13 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	A	1753	C
25	A	1757	G
25	A	1834	A
25	A	1775	U
25	A	1781	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

24 non-standard protein/DNA/RNA residues are 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	$\# Z > 2$
25	UR3	A	1830	25	19,22,23	0.38	0	26,32,35	1.03	2 (7%)
25	A2M	A	1031	25	22,25,26	0.16	0	31,36,39	0.46	0
25	A2M	A	27	25,27	22,25,26	0.17	0	31,36,39	0.40	0
25	OMC	A	174	25,27	19,22,23	0.37	0	26,31,34	0.43	0
25	A2M	A	484	25	22,25,26	0.19	0	31,36,39	0.37	0
25	A2M	A	159	25	22,25,26	0.17	0	31,36,39	0.35	0
25	A2M	A	166	25	22,25,26	0.15	0	31,36,39	0.61	0
25	PSU	A	823	25	18,21,22	1.01	1 (5%)	22,30,33	0.68	0
25	PSU	A	612	25	18,21,22	1.04	2 (11%)	22,30,33	0.80	1 (4%)
25	MA6	A	1850	25	23,26,27	0.40	0	34,38,41	0.70	1 (2%)
25	MA6	A	1851	25	23,26,27	0.39	0	34,38,41	0.78	1 (2%)
25	OMG	A	644	25	23,26,27	0.37	0	33,38,41	0.43	0
25	PSU	A	119	25	18,21,22	0.94	1 (5%)	22,30,33	0.67	0
25	OMG	A	509	25,27	23,26,27	0.37	0	33,38,41	0.48	0
25	OMC	A	1703	25	19,22,23	0.37	0	26,31,34	0.38	0
25	OMC	A	517	25	19,22,23	0.42	0	26,31,34	0.39	0
25	5MU	A	814	25	19,22,23	0.39	0	28,32,35	0.56	0
25	OMU	A	121	25	19,22,23	0.37	0	26,31,34	0.47	0
25	OMG	A	683	25	23,26,27	0.38	0	33,38,41	0.57	0
25	6MZ	A	1832	25,27	22,25,26	0.44	0	30,36,39	0.62	1 (3%)
25	A2M	A	668	25,27	22,25,26	0.25	0	31,36,39	0.50	0
25	OMU	A	116	25	19,22,23	0.33	0	26,31,34	0.48	0
25	PSU	A	1081	25	18,21,22	1.02	2 (11%)	22,30,33	0.79	0
25	PSU	A	822	25	18,21,22	1.00	1 (5%)	22,30,33	0.80	1 (4%)

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
25	UR3	A	1830	25	-	2/7/25/26	0/2/2/2
25	A2M	A	1031	25	-	0/9/27/28	0/3/3/3
25	A2M	A	27	25,27	-	0/9/27/28	0/3/3/3
25	OMC	A	174	25,27	-	0/9/27/28	0/2/2/2
25	A2M	A	484	25	-	0/9/27/28	0/3/3/3
25	A2M	A	159	25	-	2/9/27/28	0/3/3/3

Continued on next page...

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	A2M	A	166	25	-	0/9/27/28	0/3/3/3
25	PSU	A	823	25	-	0/7/25/26	0/2/2/2
25	PSU	A	612	25	-	0/7/25/26	0/2/2/2
25	MA6	A	1850	25	-	3/11/29/30	0/3/3/3
25	MA6	A	1851	25	-	5/11/29/30	0/3/3/3
25	OMG	A	644	25	-	1/9/27/28	0/3/3/3
25	PSU	A	119	25	-	0/7/25/26	0/2/2/2
25	OMG	A	509	25,27	-	0/9/27/28	0/3/3/3
25	OMC	A	1703	25	-	0/9/27/28	0/2/2/2
25	OMC	A	517	25	-	0/9/27/28	0/2/2/2
25	5MU	A	814	25	-	0/7/25/26	0/2/2/2
25	OMU	A	121	25	-	0/9/27/28	0/2/2/2
25	OMG	A	683	25	-	0/9/27/28	0/3/3/3
25	6MZ	A	1832	25,27	-	2/9/27/28	0/3/3/3
25	A2M	A	668	25,27	-	2/9/27/28	0/3/3/3
25	OMU	A	116	25	-	0/9/27/28	0/2/2/2
25	PSU	A	1081	25	-	1/7/25/26	0/2/2/2
25	PSU	A	822	25	-	0/7/25/26	0/2/2/2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	823	PSU	C6-C5	3.48	1.39	1.35
25	A	1081	PSU	C6-C5	3.38	1.39	1.35
25	A	119	PSU	C6-C5	3.35	1.39	1.35
25	A	822	PSU	C6-C5	3.32	1.39	1.35
25	A	612	PSU	C6-C5	3.31	1.39	1.35

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	1851	MA6	C2-N1-C6	2.92	118.65	111.75
25	A	1850	MA6	C2-N1-C6	2.91	118.62	111.75
25	A	1830	UR3	C6-N1-C2	-2.42	119.62	121.79
25	A	612	PSU	O4'-C1'-C2'	2.35	108.46	105.14
25	A	1830	UR3	C1'-N1-C2	2.26	120.81	116.99

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	A	1832	6MZ	N1-C6-N6-C9
25	A	1850	MA6	C5-C6-N6-C10
25	A	1851	MA6	O4'-C4'-C5'-O5'
25	A	1851	MA6	C5-C6-N6-C10
25	A	668	A2M	O4'-C4'-C5'-O5'

There are no ring outliers.

7 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	A	174	OMC	1	0
25	A	1850	MA6	2	0
25	A	1703	OMC	1	0
25	A	121	OMU	1	0
25	A	683	OMG	1	0
25	A	1832	6MZ	1	0
25	A	116	OMU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 61 ligands modelled in this entry, 61 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 ⓘ

There are no chain breaks in this entry.

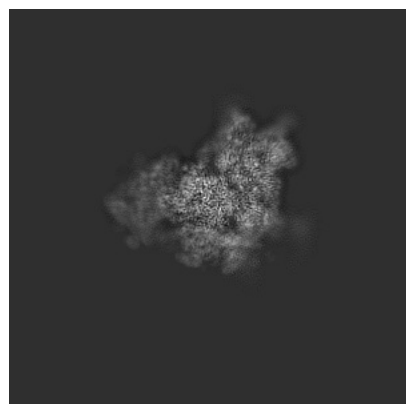
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10775. These allow visual inspection of the internal detail of the map and identification of artifacts.

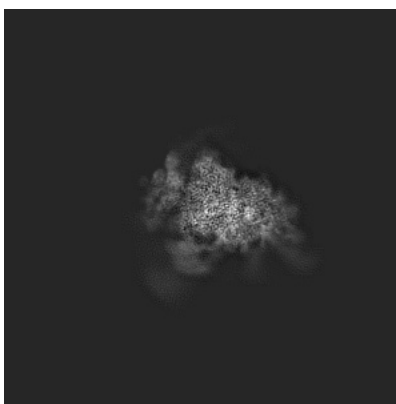
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

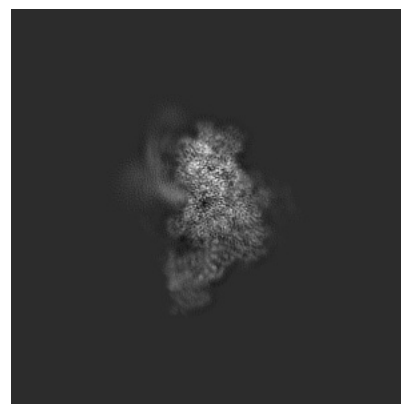
6.1.1 Primary map



X

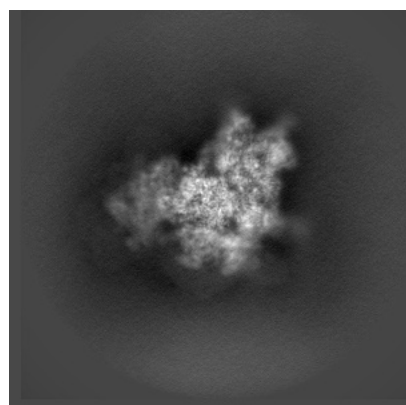


Y

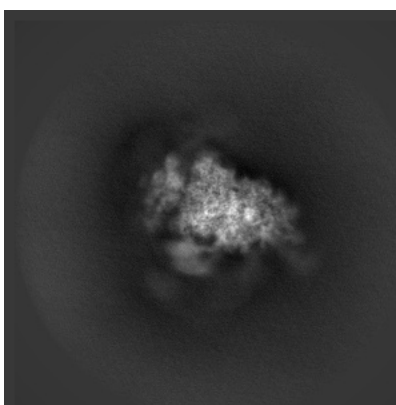


Z

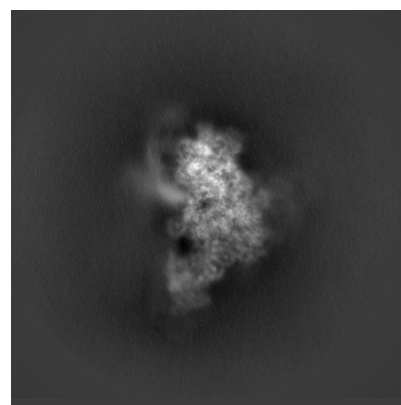
6.1.2 Raw map



X



Y

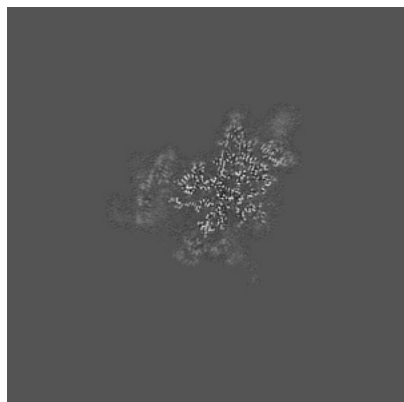


Z

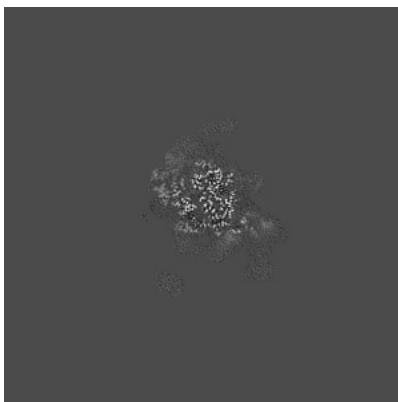
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

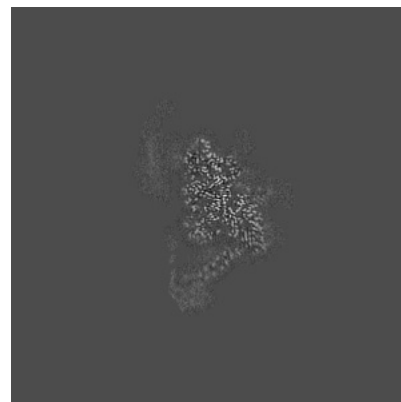
6.2.1 Primary map



X Index: 250

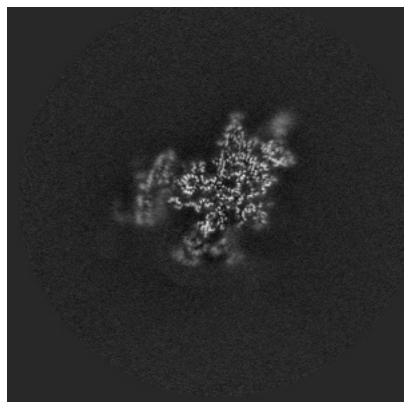


Y Index: 250

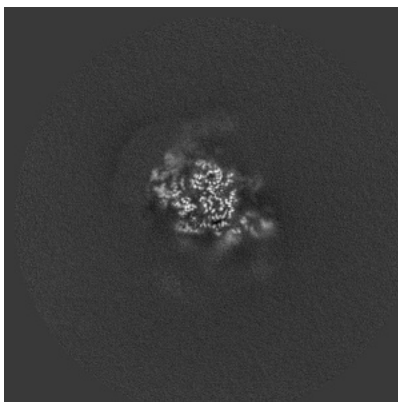


Z Index: 250

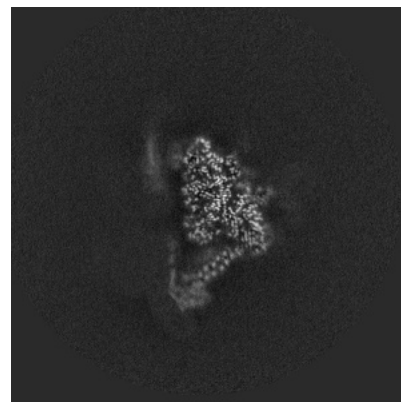
6.2.2 Raw map



X Index: 250



Y Index: 250

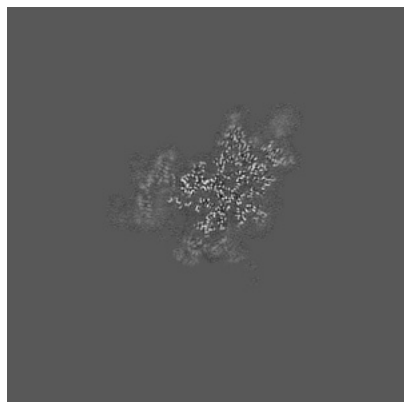


Z Index: 250

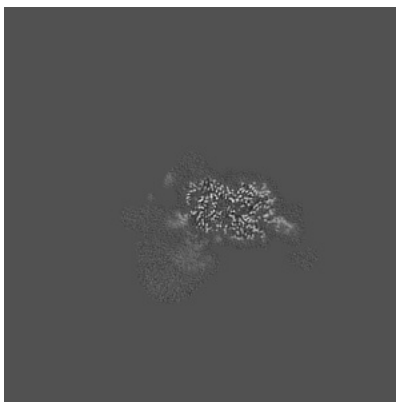
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

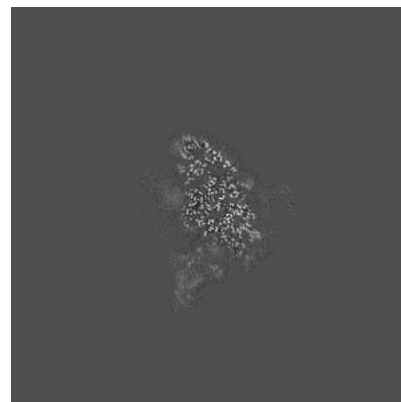
6.3.1 Primary map



X Index: 251

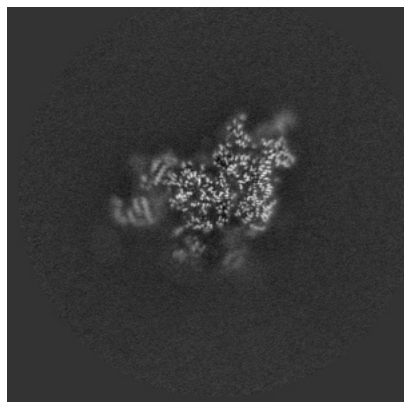


Y Index: 302

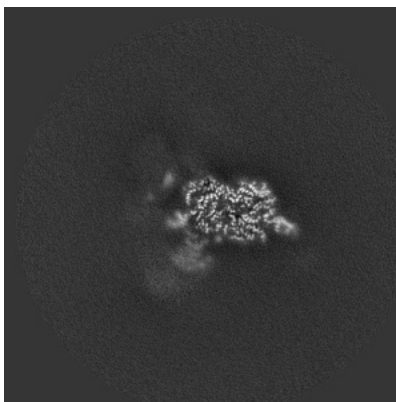


Z Index: 270

6.3.2 Raw map



X Index: 244



Y Index: 302

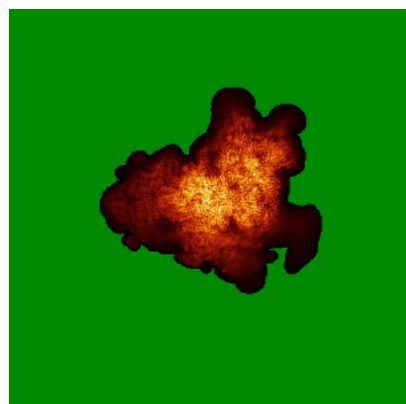


Z Index: 271

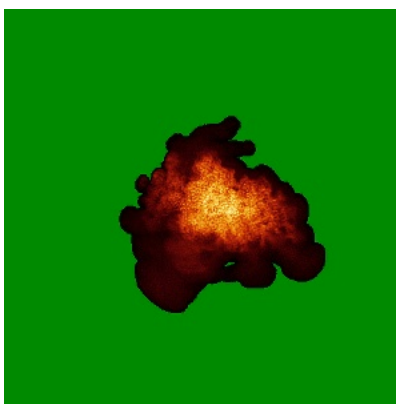
The images above show the largest variance slices of the map in three orthogonal directions.

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

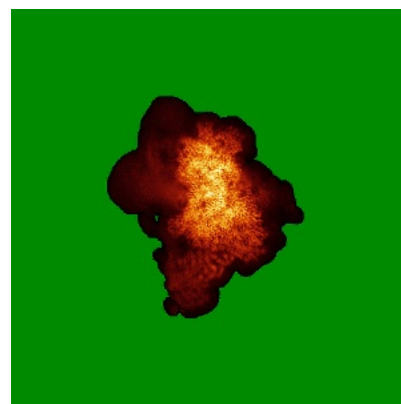
6.4.1 Primary map



X

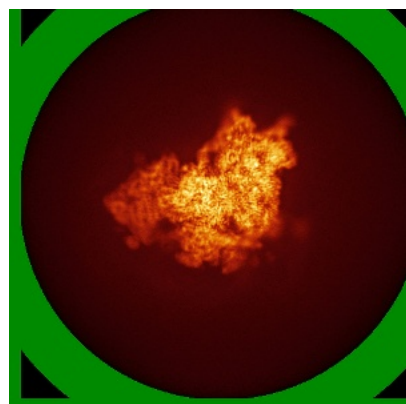


Y

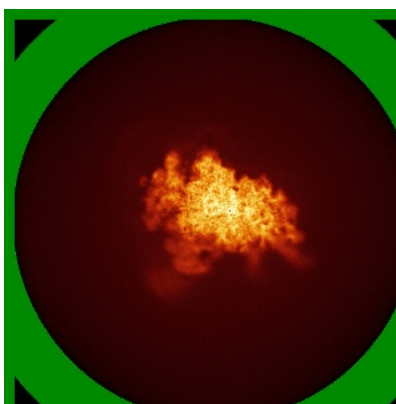


Z

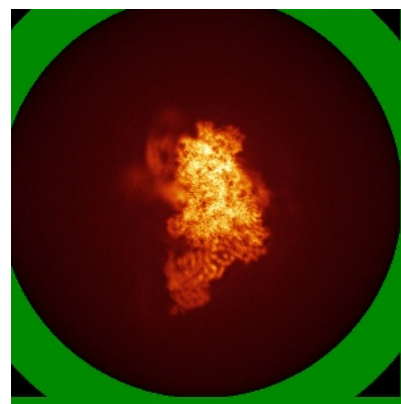
6.4.2 Raw map



X



Y

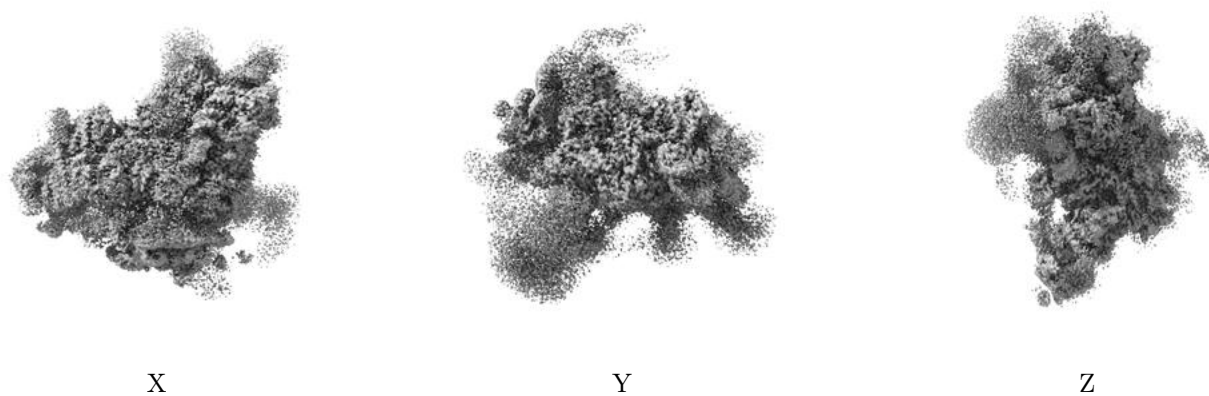


Z

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.

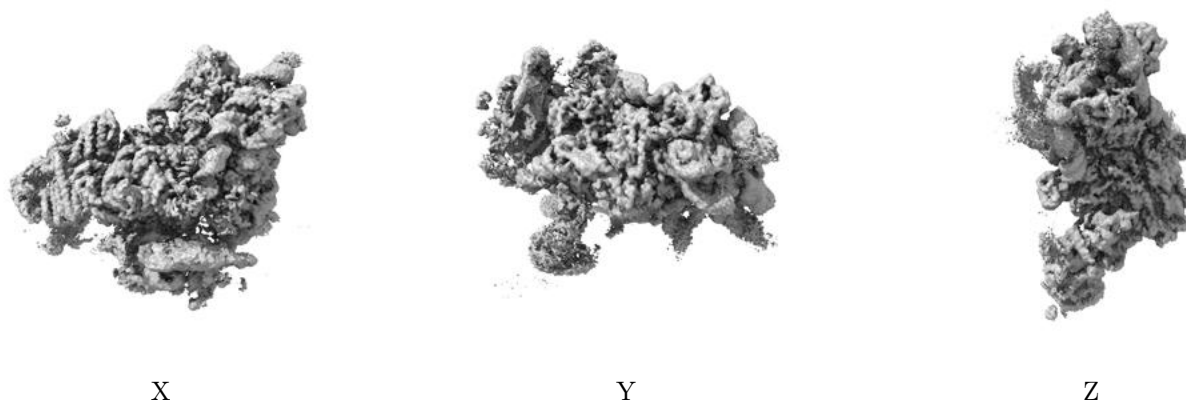
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. 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.

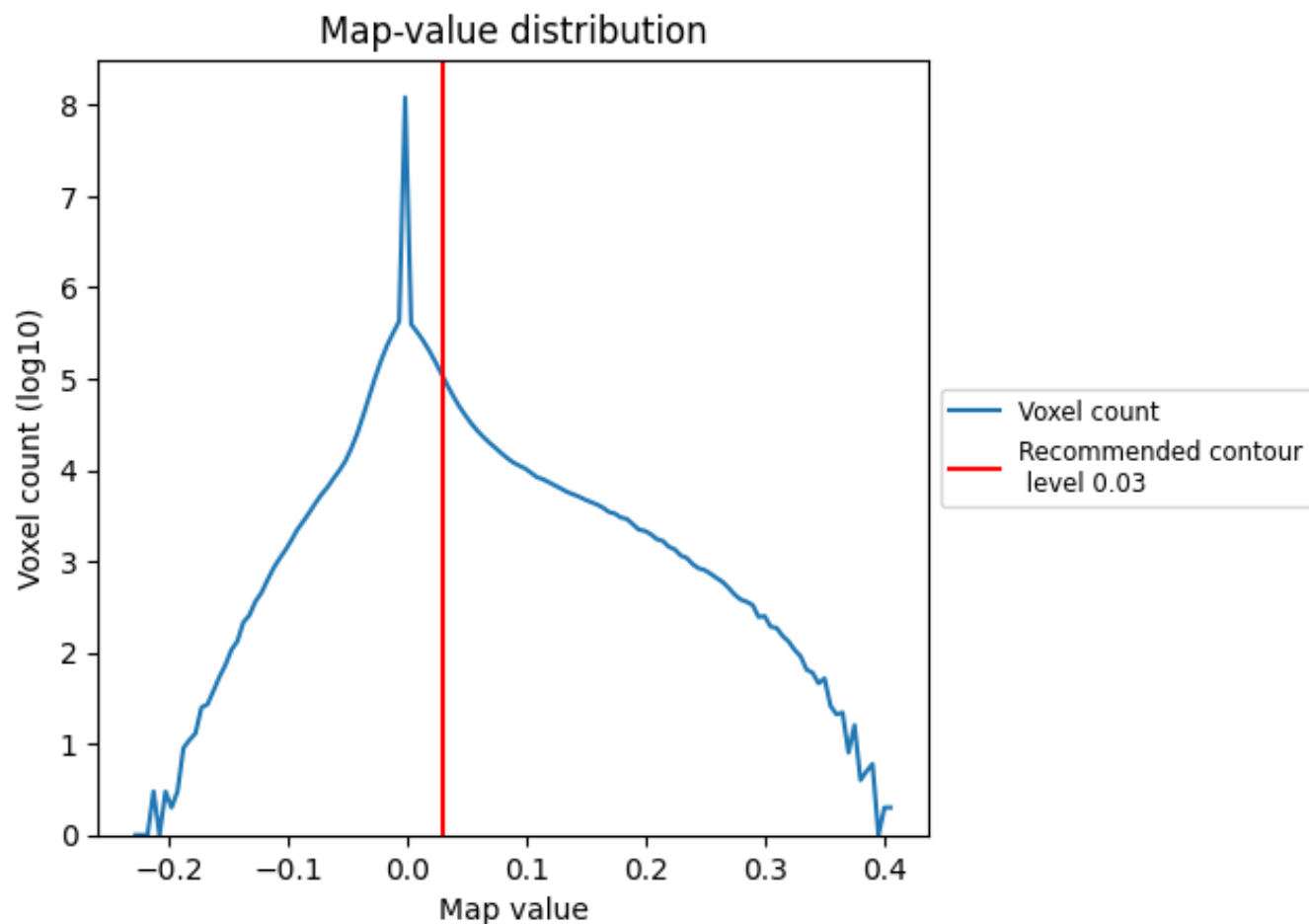
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

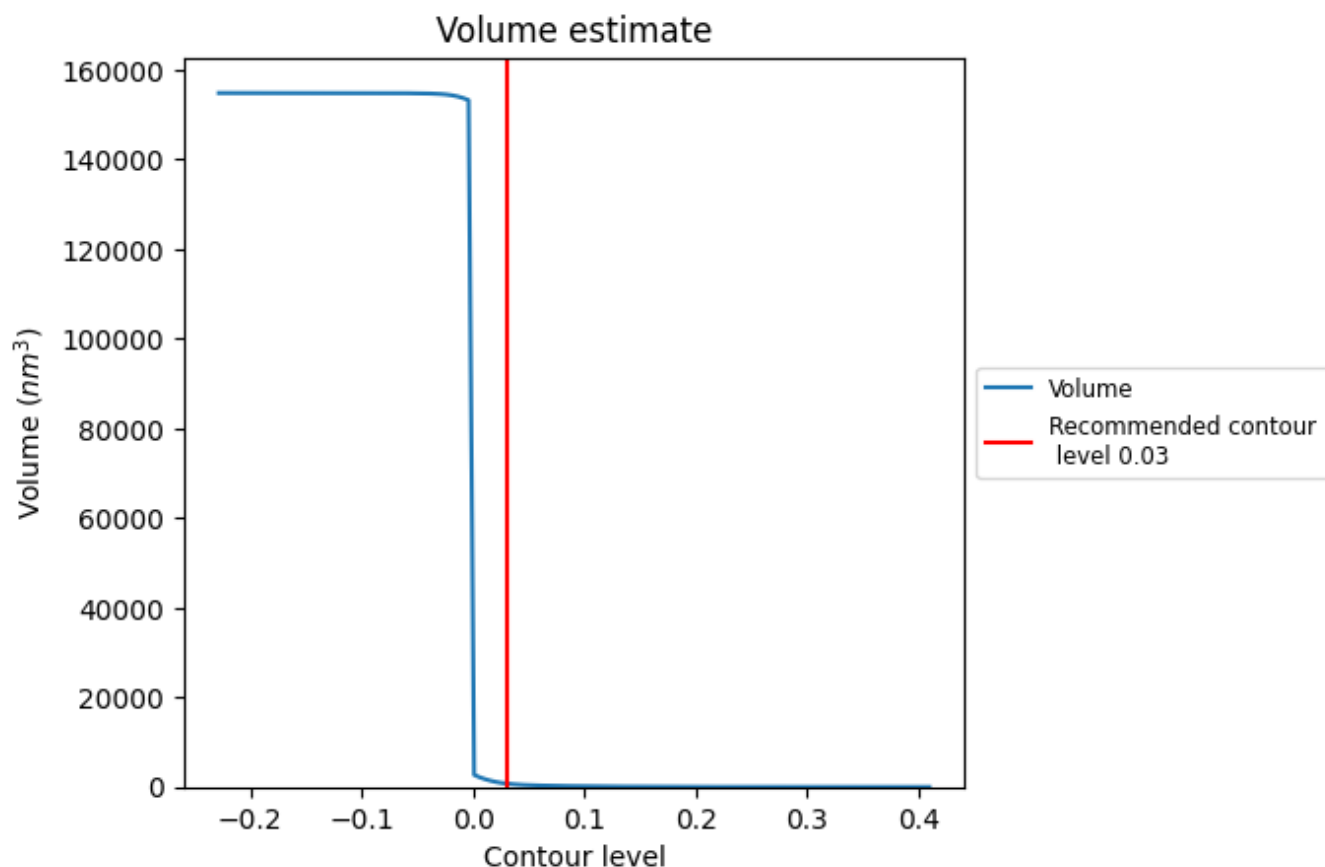
This section contains the results of statistical analysis of the map.

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.

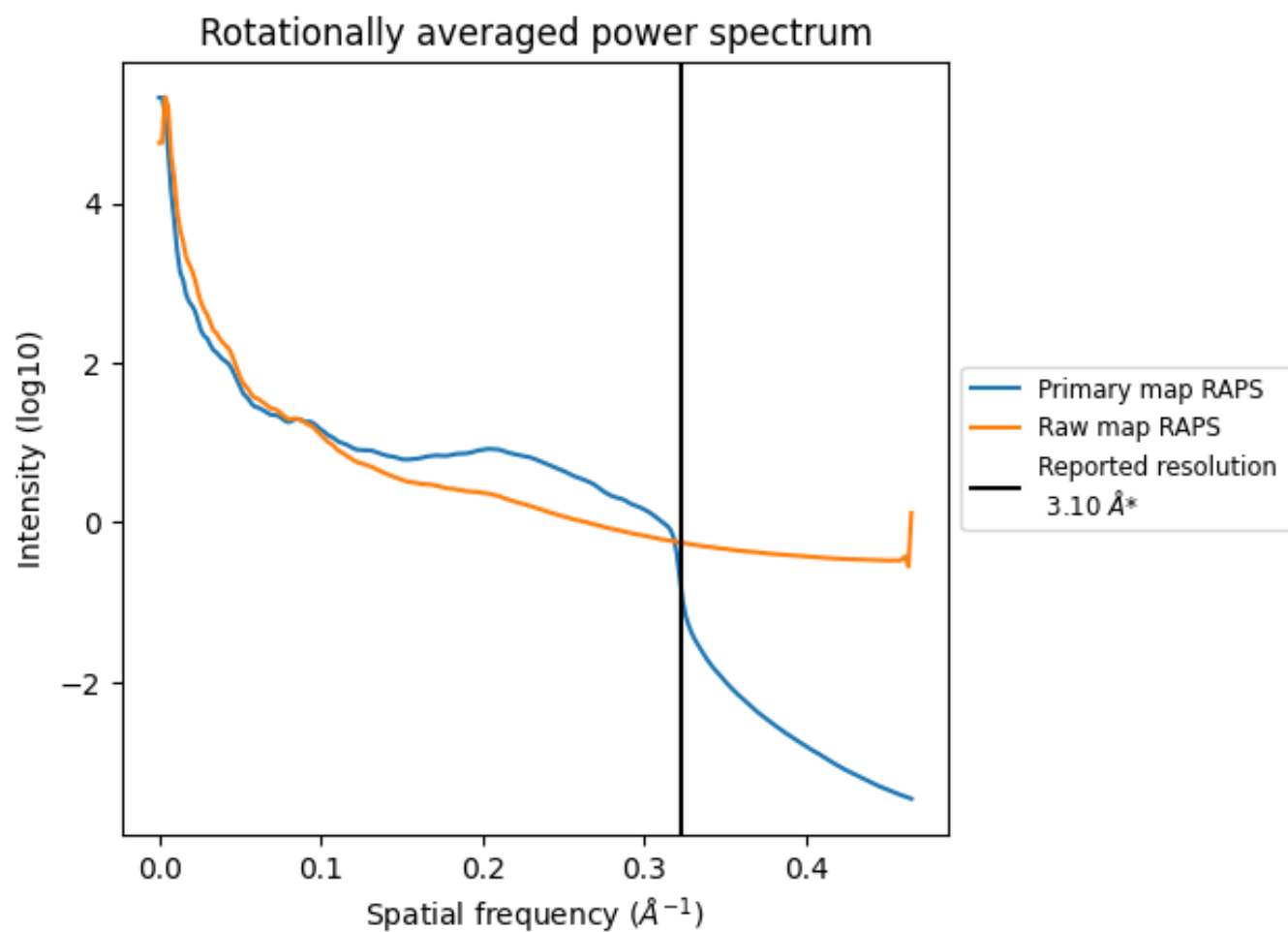
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 758 nm^3 ; this corresponds to an approximate mass of 685 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 ⓘ

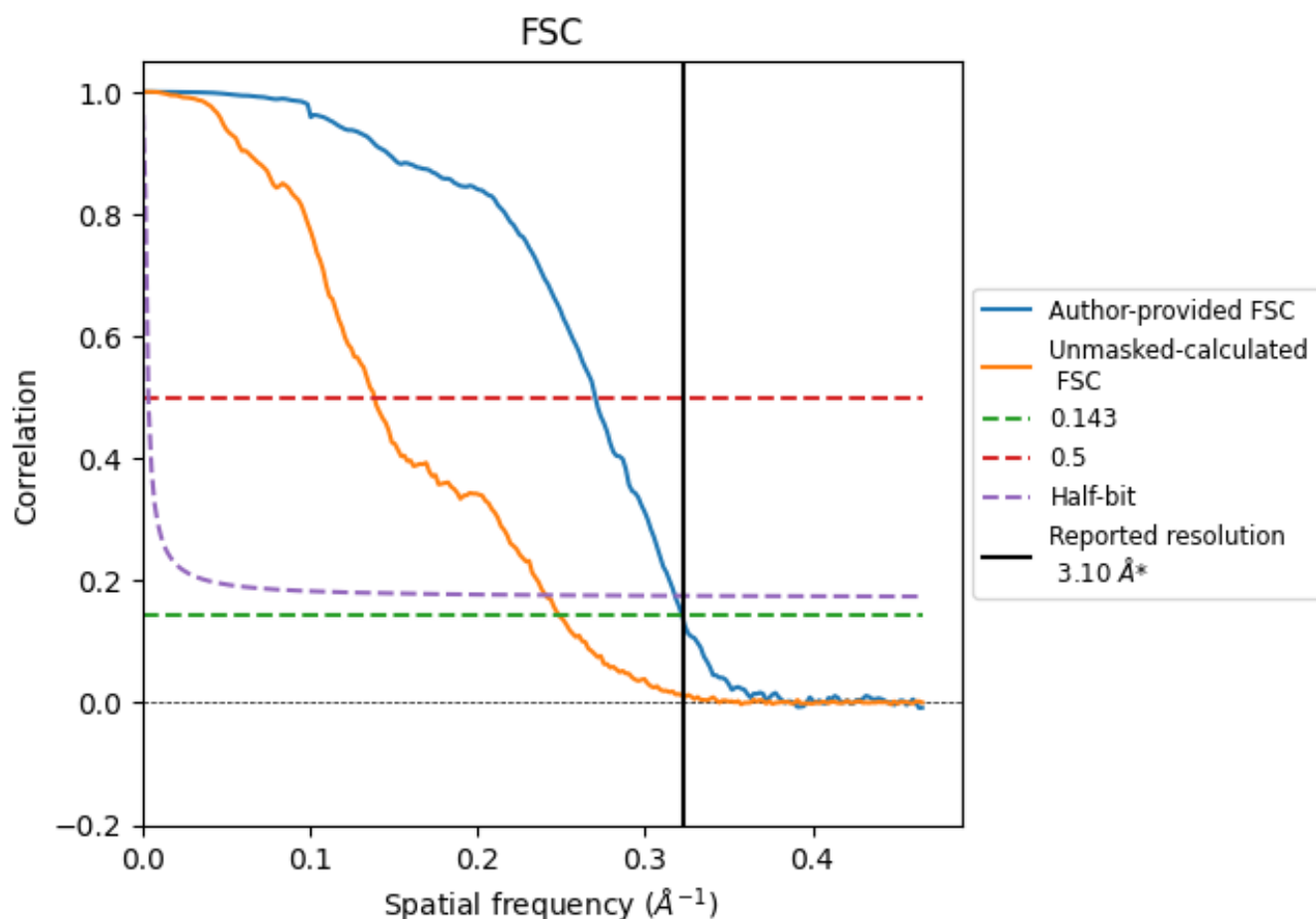


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 $0.323 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

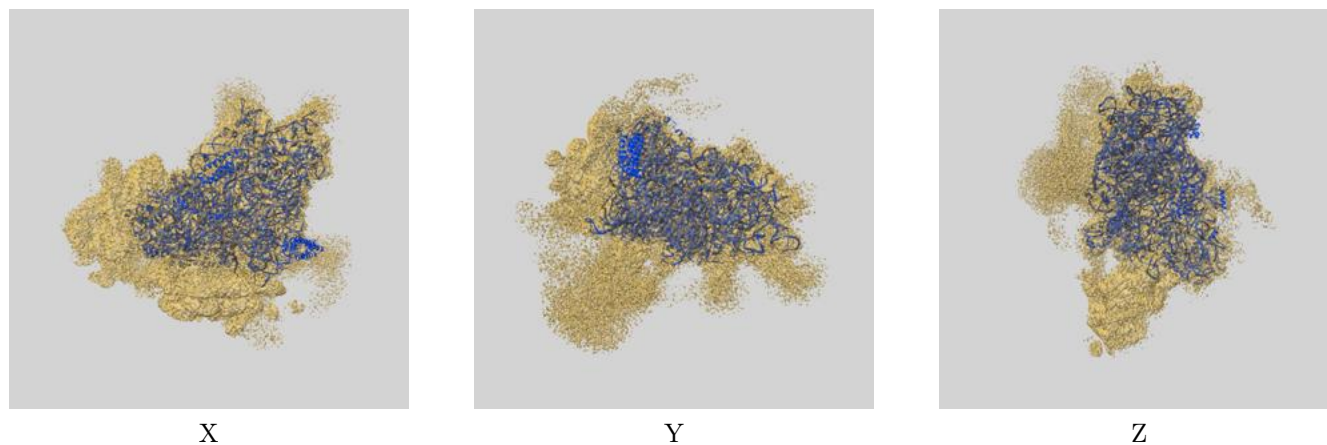
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.10	3.70	3.14
Unmasked-calculated*	4.02	7.22	4.15

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.02 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

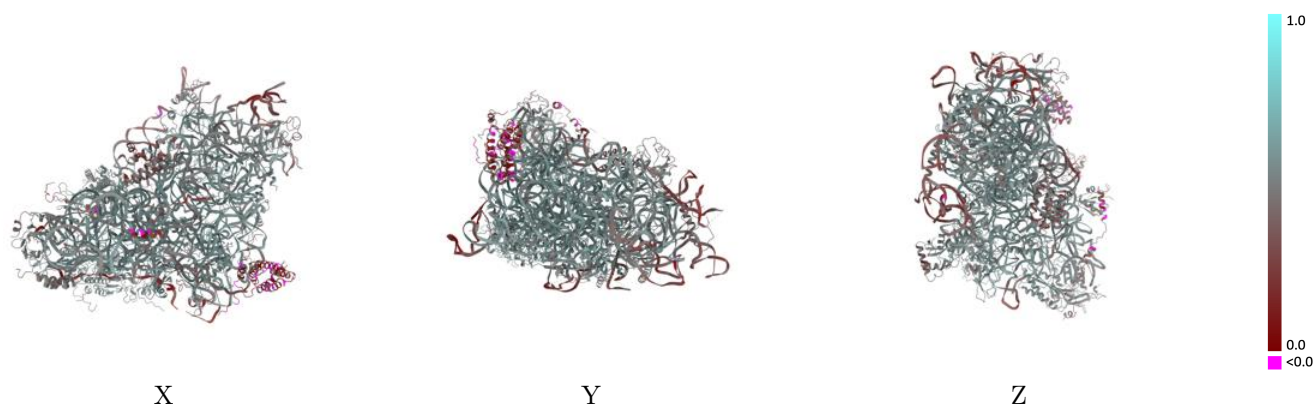
This section contains information regarding the fit between EMDB map EMD-10775 and PDB model 6YBW. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

9.1 Map-model overlay [i](#)



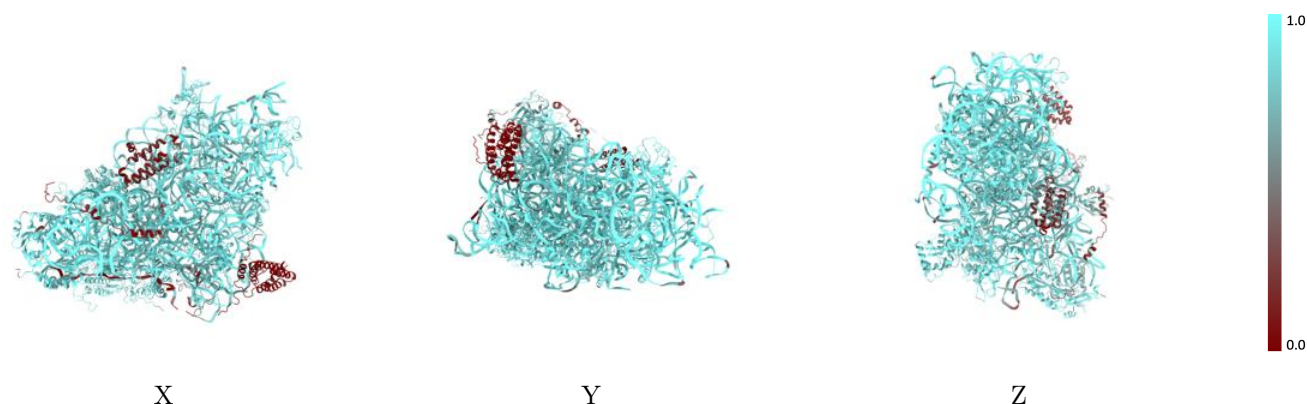
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



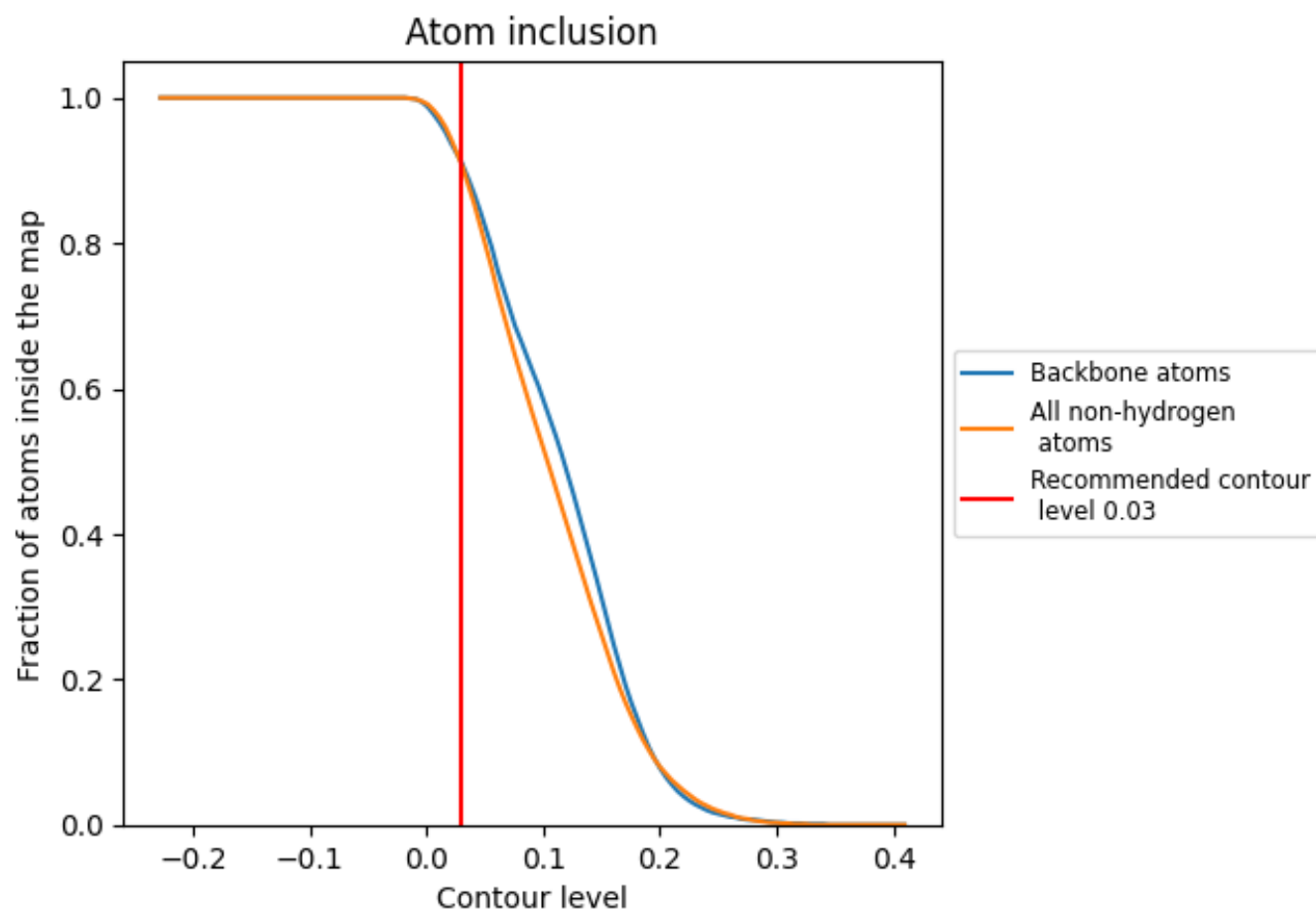
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 91% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9080	 0.5170
7	 0.1250	 0.2210
9	 0.7940	 0.5160
A	 0.9690	 0.5160
B	 0.9440	 0.5720
C	 0.9530	 0.5760
D	 0.9330	 0.5650
E	 0.9600	 0.5810
F	 0.9480	 0.5630
G	 0.9020	 0.5070
H	 0.9370	 0.5590
I	 0.9230	 0.5470
J	 0.9510	 0.5840
K	 0.9540	 0.5660
L	 0.9310	 0.5690
M	 0.8660	 0.5050
N	 0.9400	 0.5570
O	 0.9280	 0.5300
P	 0.9060	 0.5240
Q	 0.9330	 0.5590
R	 0.9420	 0.5270
S	 0.9330	 0.4950
T	 0.9500	 0.5460
p	 0.7620	 0.4760
q	 0.4590	 0.3740
y	 0.2240	 0.3430
z	 0.0190	 0.1780

