



wwPDB EM Validation Summary Report ⓘ

Jun 29, 2025 – 05:56 am BST

PDB ID : 8Q91 / pdb_00008q91
EMDB ID : EMD-18267
Title : Structure of the human 20S U5 snRNP core
Authors : Schneider, S.; Galej, W.P.
Deposited on : 2023-08-19
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.dev118
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

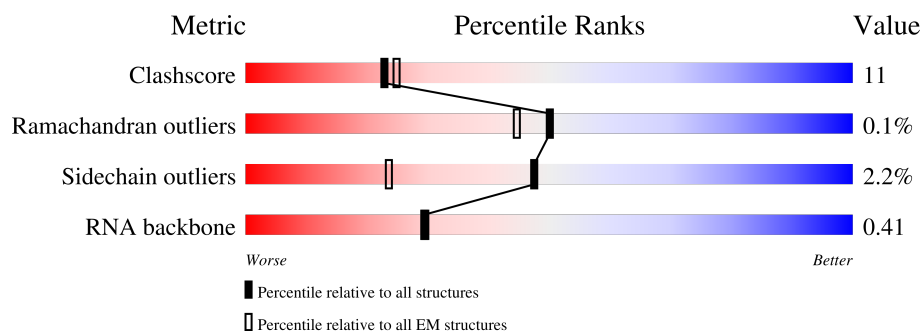
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	F	341	
2	A	2335	
3	5	117	
4	E	941	
5	D	820	
6	C	972	
7	B	2136	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	m	86	<div><div></div><div>10%</div><div>76%</div><div>9%</div><div>15%</div></div>
9	n	76	<div><div></div><div>22%</div><div>86%</div><div>12%</div><div></div></div>
10	i	119	<div><div></div><div></div><div>65%</div><div></div><div>32%</div></div>
11	j	118	<div><div></div><div>16%</div><div>80%</div><div></div><div>17%</div></div>
12	k	126	<div><div></div><div></div><div>60%</div><div>7%</div><div>33%</div></div>
13	h	240	<div><div></div><div></div><div>28%</div><div></div><div>70%</div></div>
14	l	92	<div><div></div><div>5%</div><div>75%</div><div>8%</div><div>16%</div></div>

2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 26706 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 CD2 antigen cytoplasmic tail-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	F	140	Total	C	N	O	S	0	0
			887	552	165	169	1		

- Molecule 2 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	1627	Total	C	N	O	S	0	0
			13247	8535	2321	2333	58		

- Molecule 3 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5	104	Total	C	N	O	P	0	0
			2192	983	372	734	103		

- Molecule 4 is a protein called Pre-mRNA-processing factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	E	60	Total	C	N	O	0	0
			300	180	60	60		

- Molecule 5 is a protein called Probable ATP-dependent RNA helicase DDX23.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	D	54	Total	C	N	O	0	0
			455	294	78	83		

- Molecule 6 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	847	Total	C	N	O	S	0	0
			6629	4238	1108	1250	33		

- Molecule 7 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	27	Total	C	N	O	S	0	0
			201	123	38	39	1		

- Molecule 8 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	m	73	Total	C	N	O	0	0
			356	210	73	73		

- Molecule 9 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	n	74	Total	C	N	O	0	0
			364	215	74	75		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	i	81	Total	C	N	O	0	0
			401	239	81	81		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	j	98	Total	C	N	O	0	0
			487	291	98	98		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	k	84	Total	C	N	O	0	0
			414	246	84	84		

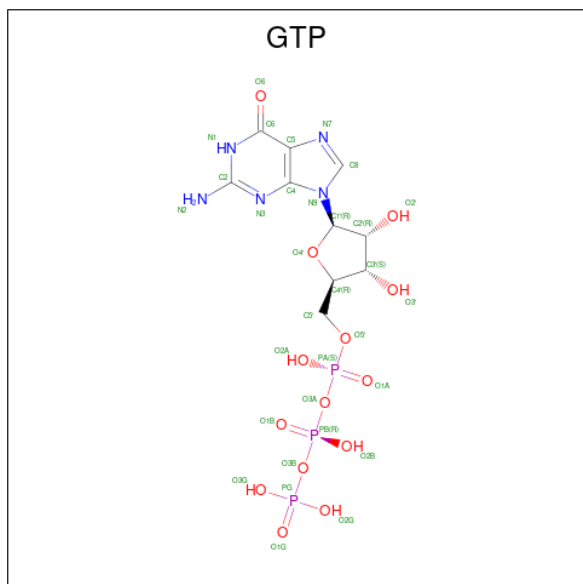
- Molecule 13 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	h	73	Total	C	N	O	0	0
			360	214	73	73		

- Molecule 14 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	1	77	Total	C	N	O	0	0
			381	227	77	77		

- Molecule 15 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).

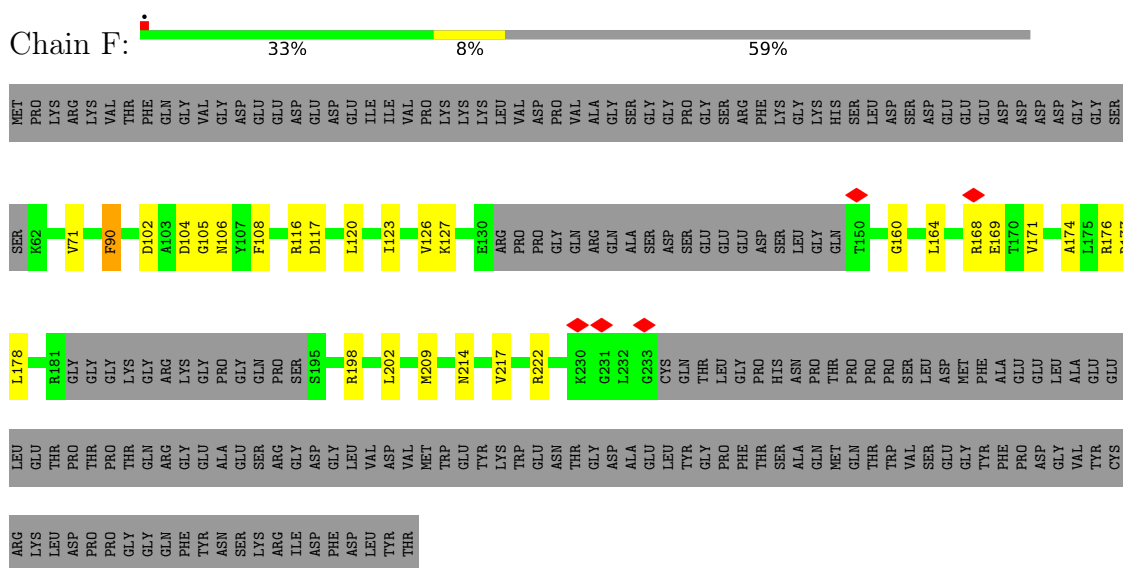


Mol	Chain	Residues	Atoms					AltConf
15	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

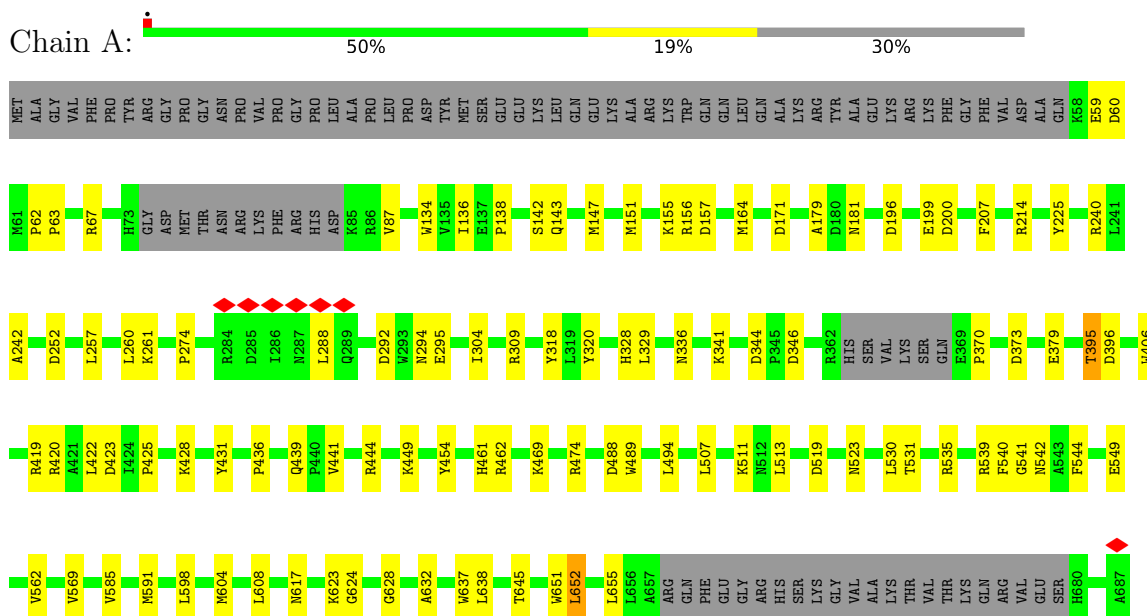
3 Residue-property plots

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: CD2 antigen cytoplasmic tail-binding protein 2



• Molecule 2: Pre-mRNA-processing-splicing factor 8







ILE	ARG	GLU	TRP	TRP	TRP	ALA	ALA
GLY	THR	CYS	LEU	LEU	VAL	ALA	ALA
ASP	VAL	PRO	LEU	LEU	GLN	ARG	GLN
ILE	LYS	ASN	LEU	SER	ASP	SER	VAL
LEU	ILE	SER	SER	ASN	ILE	LEU	PRO
ARG	ASP	GLY	ARG	LEU	ARG	ALA	SER
LEU	SER	ILE	LEU	LEU	ARG	ALA	SER
VAL	ASP	LEU	GLU	GLU	ALA	LEU	LYS
ALA	LEU	TRP	GLU	GLU	GLN	ALA	LYS
ALA	GLY	SER	LYS	LYS	GLN	PHE	SER
ARG	ASP	GLU	ILE	GLN	CYS	ASN	TRP
ARG	THR	ILE	PHE	GLU	GLU	ASN	LEU
VAL	PHE	ALA	ALA	ARG	GLU	PRO	ARG
THR	THR	LEU	LEU	THR	GLU	ASN	ARG
ASN	ALA	PHE	GLU	GLU	GLU	ALA	VAL
PHE	THR	GLY	GLU	GLU	GLU	SER	VAL
	TYR	ALA	ALA	ALA	LEU	GLU	TYR
	LYS	ARG	ARG	ARG	ALA	GLU	PHE
	PHE	PRO	ALA	ALA	HIS	ILE	GLY
	GLU	GLN	ILE	ILE	TYR	TRP	LYS
	GLU	ARG	LEU	LEU	GLU	LEU	GLU
	GLN	ARG	GLU	GLU	ASP	ALA	ASN
	HIS	THR	LYS	SER	PRO	VAL	THR
	GLY	THR	LYS	ARG	LYS	LYS	ARG
	THR	SER	SER	ARG	LYS	ASN	ALA
	GLU	VAL	ASP	LYS	LEU	GLY	LEU
	GLN	ALA	ALA	ASN	MET	SER	GLU
	GLN	LEU	PRO	PRO	MET	GLU	GLU
	GLU	LYS	LYS	LYS	LYS	ASN	ALA
	GLU	LYS	ASN	GLY	GLY	ASP	LEU
	VAL	CYS	PRO	PRO	ILE	TYR	LEU
	ARG	GLU	GLY	GLY	GLU	GLU	GLN
	LYS	HIS	LEU	LEU	GLU	ARG	ALA
	ARG	ASP	TRP	TRP	GLN	ALA	VAL
	CYS	PRO	LEU	LEU	GLN	ALA	VAL
	GLU	HIS	GLU	GLU	LYS	ARG	ALA
	SER	VAL	SER	SER	GLU	ARG	HIS
	ALA	LEU	VAL	VAL	MET	LEU	CYS
	GLU	LEU	LEU	ARG	MET	LEU	PRO
	PRO	ALA	LEU	LEU	GLU	ALA	LYS
	ARG	VAL	GLU	GLU	LYS	LYS	ALA
	HIS	ALA	TYR	TYR	ALA	ALA	GLU
	GLY	LYS	ARG	ARG	ARG	VAL	VAL
	LEU	LEU	GLU	GLU	SER	SER	LEU
	TRP	TRP	LEU	LEU	ALA	ALA	TRP
	CYS	SER	LYS	LYS	ASN	PRO	MET
	ALA	GLN	ASN	ASN	GLN	THR	GLY
	VAL	ARG	ILE	ILE	GLY	ALA	ALA
	SER	LYS	LYS	ASN	LYS	VAL	LYS
	LYS	ILE	THR	THR	LYS	PHE	LYS
	ALA	ALA	LEU	LEU	CYS	MET	TRP
	ASN	ARG	MET	MET	PRO	LYS	LEU
	THR	TRP	ALA	ALA	PRO	SER	ALA
	TRP	GLN	LYS	LYS	GLY	VAL	GLY
	GLN	TRP	ALA	ALA	THR	LYS	ASP
	LYS	PHE	GLN	GLN	PRO	LEU	PRO
	THR	THR	THR	THR	THR	THR	THR

- Molecule 5: Probable ATP-dependent RNA helicase DDX23

Chain D: 5% • 93%

[illegible]





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	76918	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.5	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.051	Depositor
Minimum map value	-0.392	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	526.6296, 526.6296, 526.6296	wwPDB
Map dimensions	504, 504, 504	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0449, 1.0449, 1.0449	Depositor

5 Model quality

5.1 Standard geometry

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

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	F	0.21	0/896	0.44	0/1224
2	A	0.17	0/13608	0.38	1/18483 (0.0%)
3	5	0.12	0/2444	0.30	0/3798
4	E	0.10	0/298	0.27	0/414
5	D	0.17	0/464	0.44	0/620
6	C	0.18	0/6777	0.39	4/9214 (0.0%)
7	B	0.19	0/202	0.50	0/268
8	m	0.30	0/355	0.63	0/490
9	n	0.19	0/363	0.54	0/501
10	i	0.35	0/400	0.60	0/556
11	j	0.17	0/485	0.47	0/674
12	k	0.23	0/413	0.45	0/573
13	h	0.21	0/358	0.57	1/495 (0.2%)
14	l	0.22	0/380	0.82	2/528 (0.4%)
All	All	0.18	0/27443	0.40	8/37838 (0.0%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	l	15	VAL	CA-C-N	7.75	135.25	121.76
14	l	15	VAL	C-N-CA	7.75	135.25	121.76
6	C	144	CYS	N-CA-CB	7.07	120.47	109.94
13	h	10	LEU	N-CA-C	-5.82	105.44	112.54
2	A	867	ILE	CA-CB-CG1	5.49	119.73	110.40

There are no chirality outliers.

There are no planarity outliers.

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	F	887	0	714	30	0
2	A	13247	0	12877	344	0
3	5	2192	0	1111	42	0
4	E	300	0	132	0	0
5	D	455	0	450	13	0
6	C	6629	0	6607	124	0
7	B	201	0	214	10	0
8	m	356	0	156	5	0
9	n	364	0	160	6	0
10	i	401	0	165	2	0
11	j	487	0	199	2	0
12	k	414	0	185	6	0
13	h	360	0	149	4	0
14	l	381	0	159	5	0
15	C	32	0	12	1	0
All	All	26706	0	23290	552	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 11.

The worst 5 of 552 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)
2:A:1474:MET:HE3	2:A:1474:MET:HA	1.51	0.91
2:A:885:LEU:HD21	2:A:922:LEU:HD21	1.53	0.89
2:A:1365:ILE:HG13	2:A:1474:MET:HE1	1.55	0.86
2:A:1307:MET:HE3	2:A:1307:MET:H	1.39	0.86
2:A:813:THR:HG21	2:A:996:LEU:HD11	1.59	0.84

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	F	134/341 (39%)	123 (92%)	10 (8%)	1 (1%)	19	51
2	A	1615/2335 (69%)	1558 (96%)	56 (4%)	1 (0%)	48	79
4	E	56/941 (6%)	56 (100%)	0	0	100	100
5	D	50/820 (6%)	49 (98%)	1 (2%)	0	100	100
6	C	845/972 (87%)	813 (96%)	31 (4%)	1 (0%)	48	79
7	B	25/2136 (1%)	25 (100%)	0	0	100	100
8	m	71/86 (83%)	68 (96%)	3 (4%)	0	100	100
9	n	72/76 (95%)	64 (89%)	8 (11%)	0	100	100
10	i	79/119 (66%)	73 (92%)	6 (8%)	0	100	100
11	j	94/118 (80%)	84 (89%)	10 (11%)	0	100	100
12	k	82/126 (65%)	78 (95%)	4 (5%)	0	100	100
13	h	69/240 (29%)	67 (97%)	2 (3%)	0	100	100
14	l	75/92 (82%)	72 (96%)	3 (4%)	0	100	100
All	All	3267/8402 (39%)	3130 (96%)	134 (4%)	3 (0%)	50	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	1020	LYS
6	C	148	CYS
1	F	126	VAL

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	F	58/281 (21%)	57 (98%)	1 (2%)	56	78
2	A	1384/2108 (66%)	1357 (98%)	27 (2%)	50	74
5	D	48/721 (7%)	44 (92%)	4 (8%)	9	33
6	C	737/866 (85%)	721 (98%)	16 (2%)	47	71
7	B	22/1908 (1%)	21 (96%)	1 (4%)	23	53
All	All	2249/5884 (38%)	2200 (98%)	49 (2%)	47	71

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	D	244	SER
6	C	162	ASP
5	D	246	GLU
6	C	109	LEU
6	C	357	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
6	C	139	HIS
6	C	337	GLN
6	C	571	ASN
6	C	451	HIS
2	A	542	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	5	101/117 (86%)	34 (33%)	4 (3%)

5 of 34 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	5	4	C
3	5	5	U
3	5	6	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	5	9	G
3	5	20	G

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	5	57	G
3	5	58	U
3	5	96	A
3	5	105	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](#)

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	$\# Z > 2$
15	GTP	C	1001	-	26,34,34	1.06	3 (11%)	32,54,54	0.75	0

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
15	GTP	C	1001	-	-	2/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	C	1001	GTP	C5-C6	-2.73	1.41	1.47
15	C	1001	GTP	C8-N7	-2.18	1.31	1.35
15	C	1001	GTP	C5-C4	-2.03	1.37	1.43

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

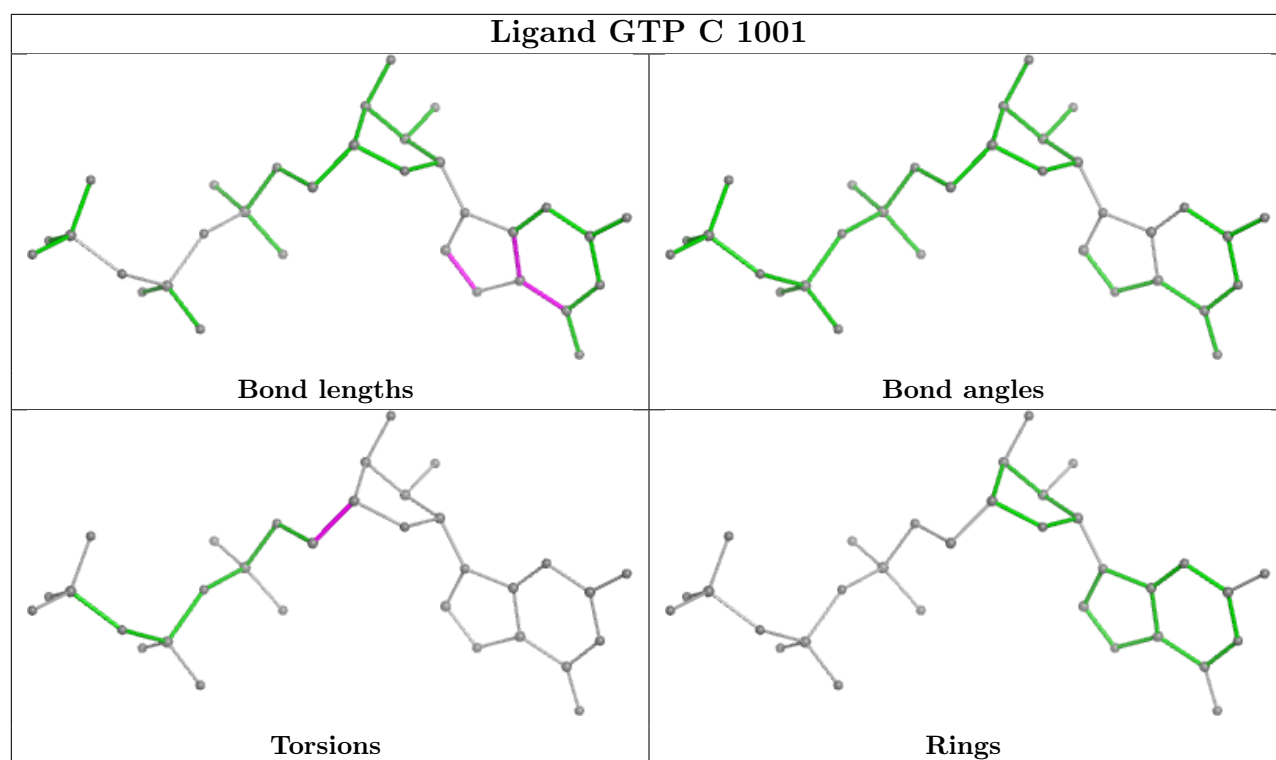
Mol	Chain	Res	Type	Atoms
15	C	1001	GTP	O4'-C4'-C5'-O5'
15	C	1001	GTP	C3'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	C	1001	GTP	1	0

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.

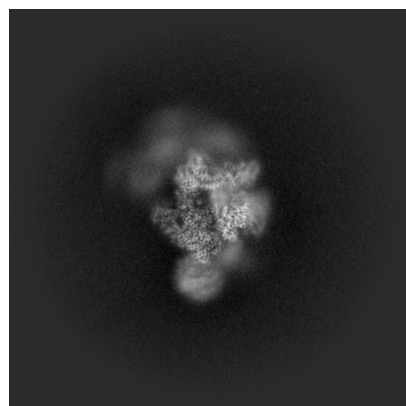
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18267. These allow visual inspection of the internal detail of the map and identification of artifacts.

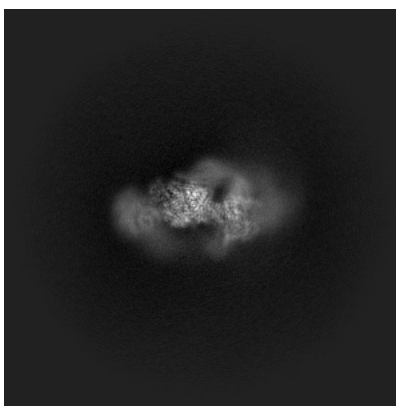
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

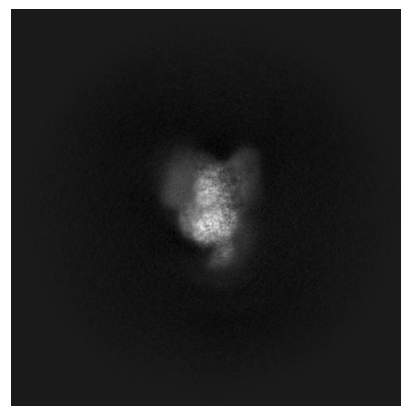
6.1.1 Primary map



X

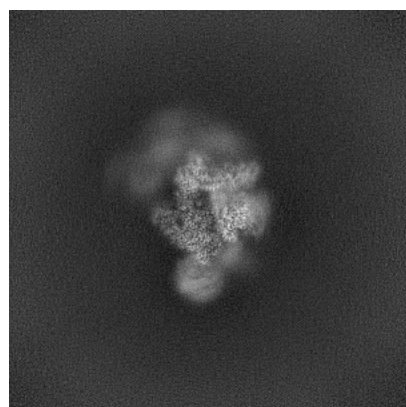


Y

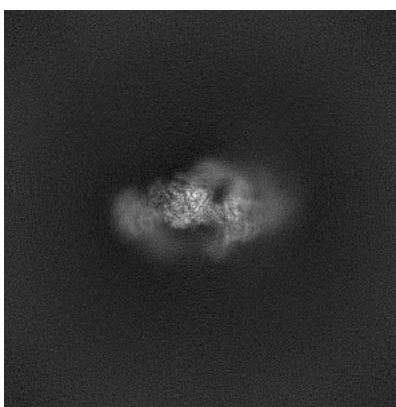


Z

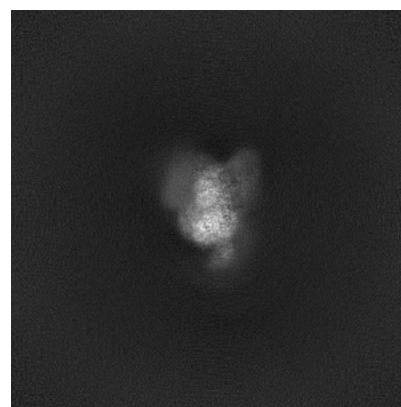
6.1.2 Raw map



X



Y

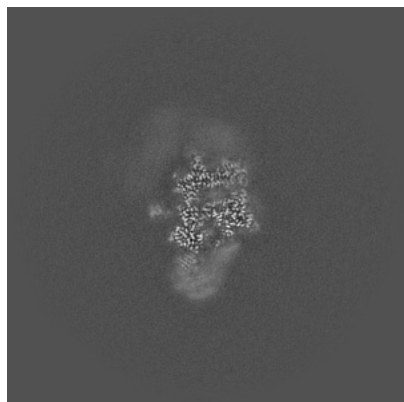


Z

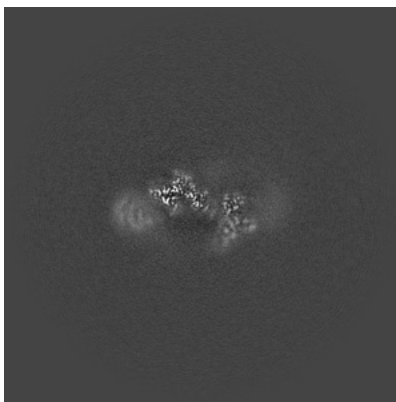
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

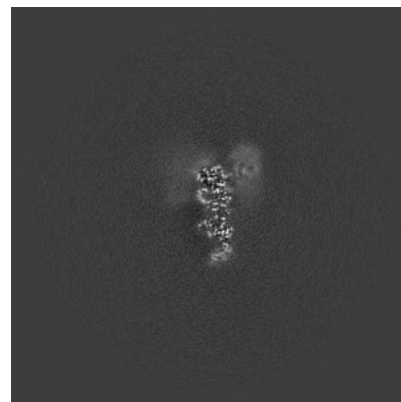
6.2.1 Primary map



X Index: 252

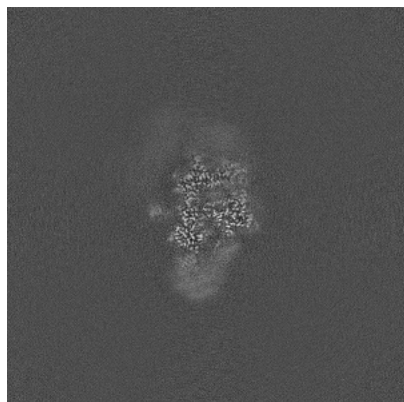


Y Index: 252

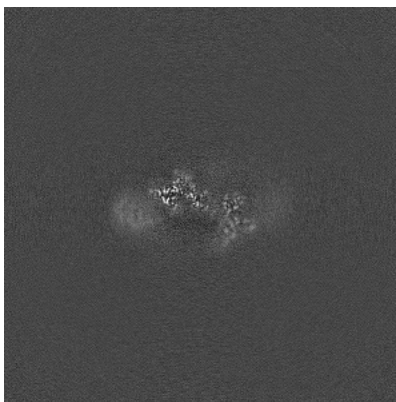


Z Index: 252

6.2.2 Raw map



X Index: 252



Y Index: 252

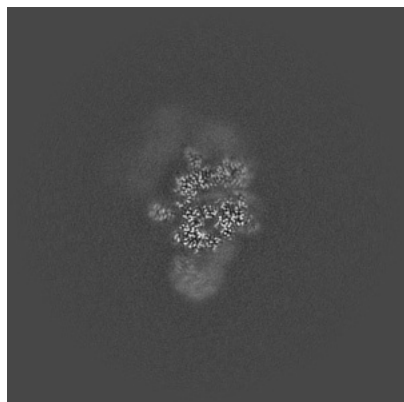


Z Index: 252

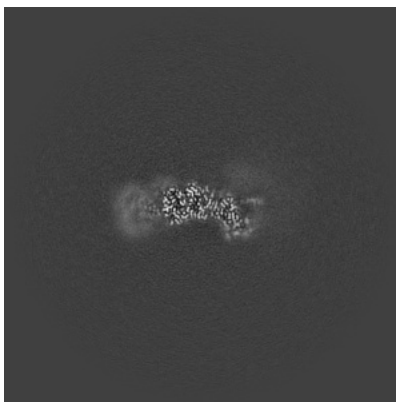
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

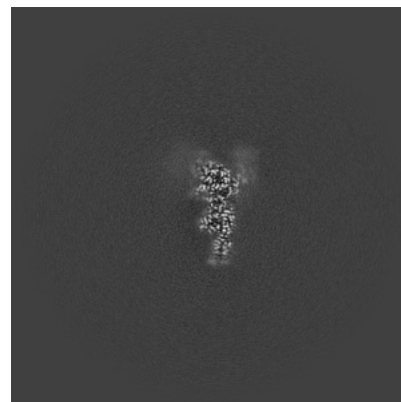
6.3.1 Primary map



X Index: 256

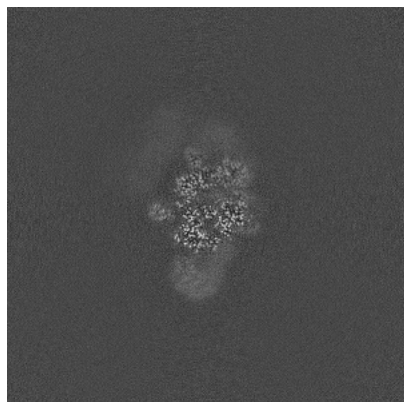


Y Index: 228

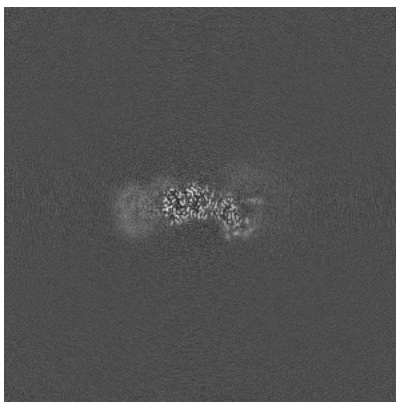


Z Index: 241

6.3.2 Raw map



X Index: 256



Y Index: 228

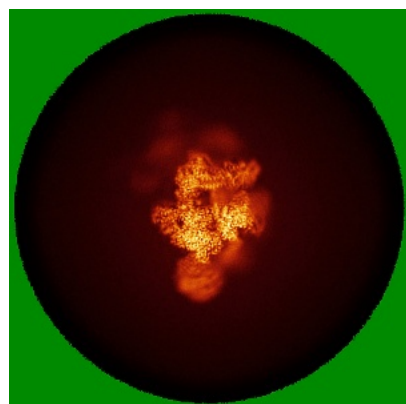


Z Index: 241

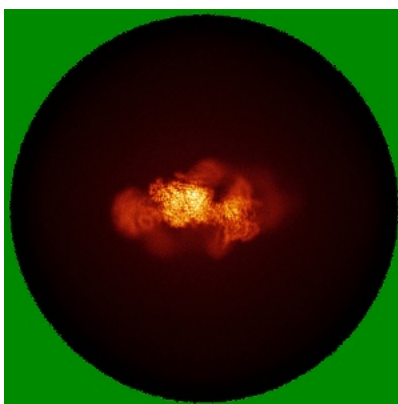
The images above show the largest variance slices of the map in three orthogonal directions.

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

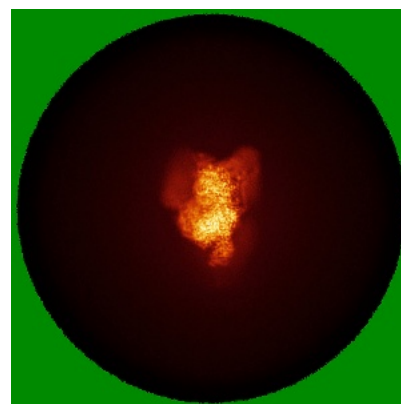
6.4.1 Primary map



X

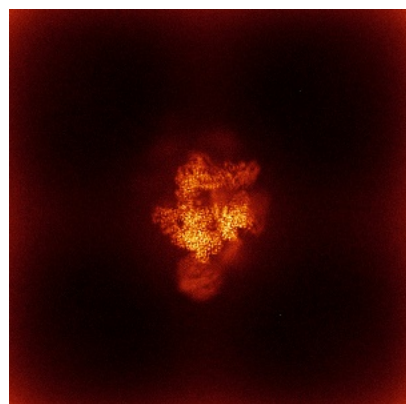


Y

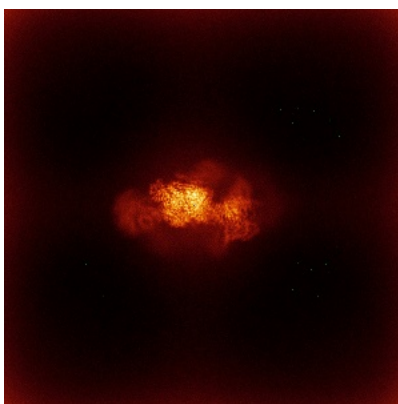


Z

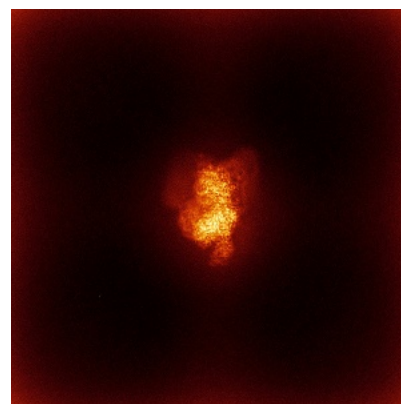
6.4.2 Raw map



X



Y

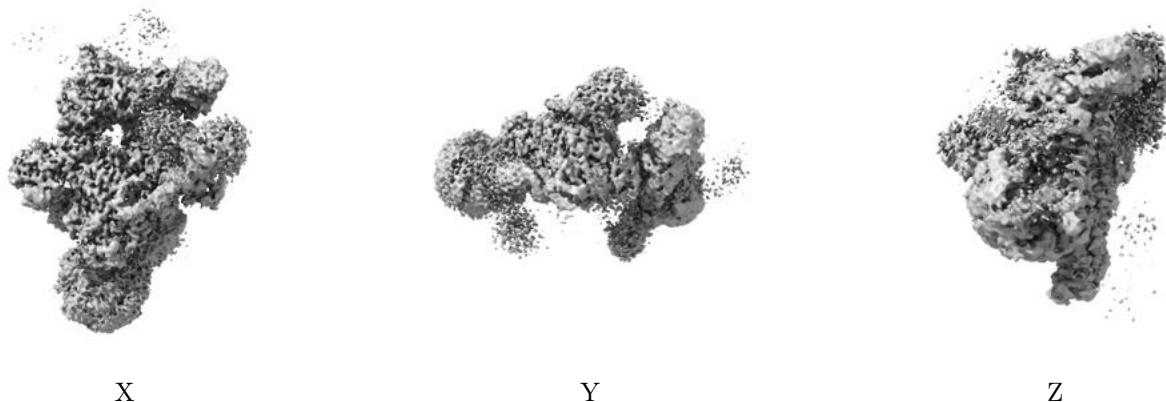


Z

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.

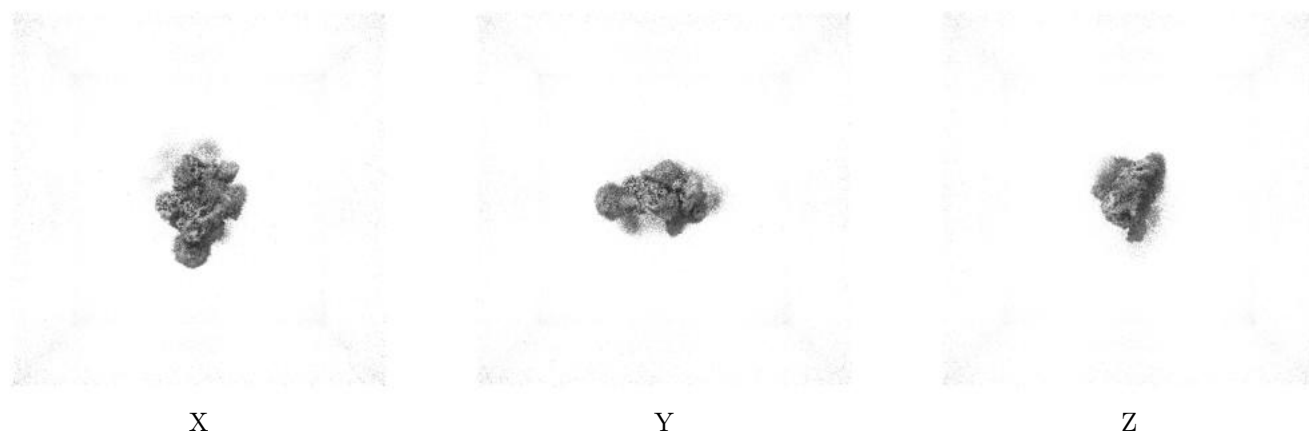
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. 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.

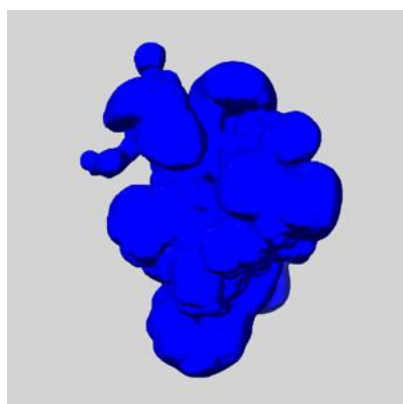
6.6 Mask visualisation [i](#)

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

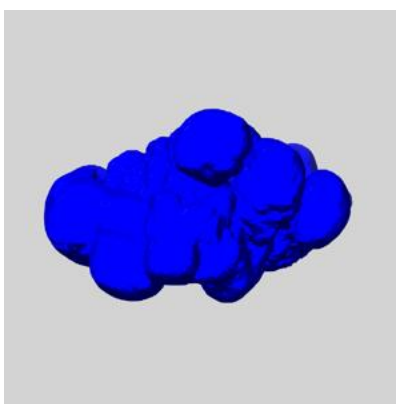
A mask typically either:

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

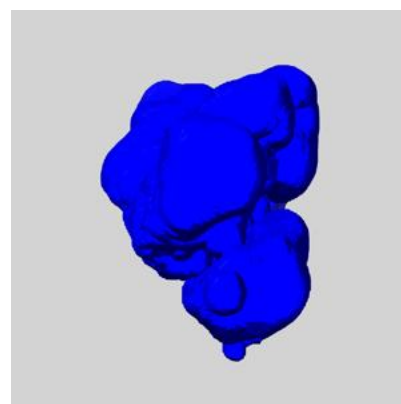
6.6.1 emd_18267_msk_1.map [i](#)



X



Y

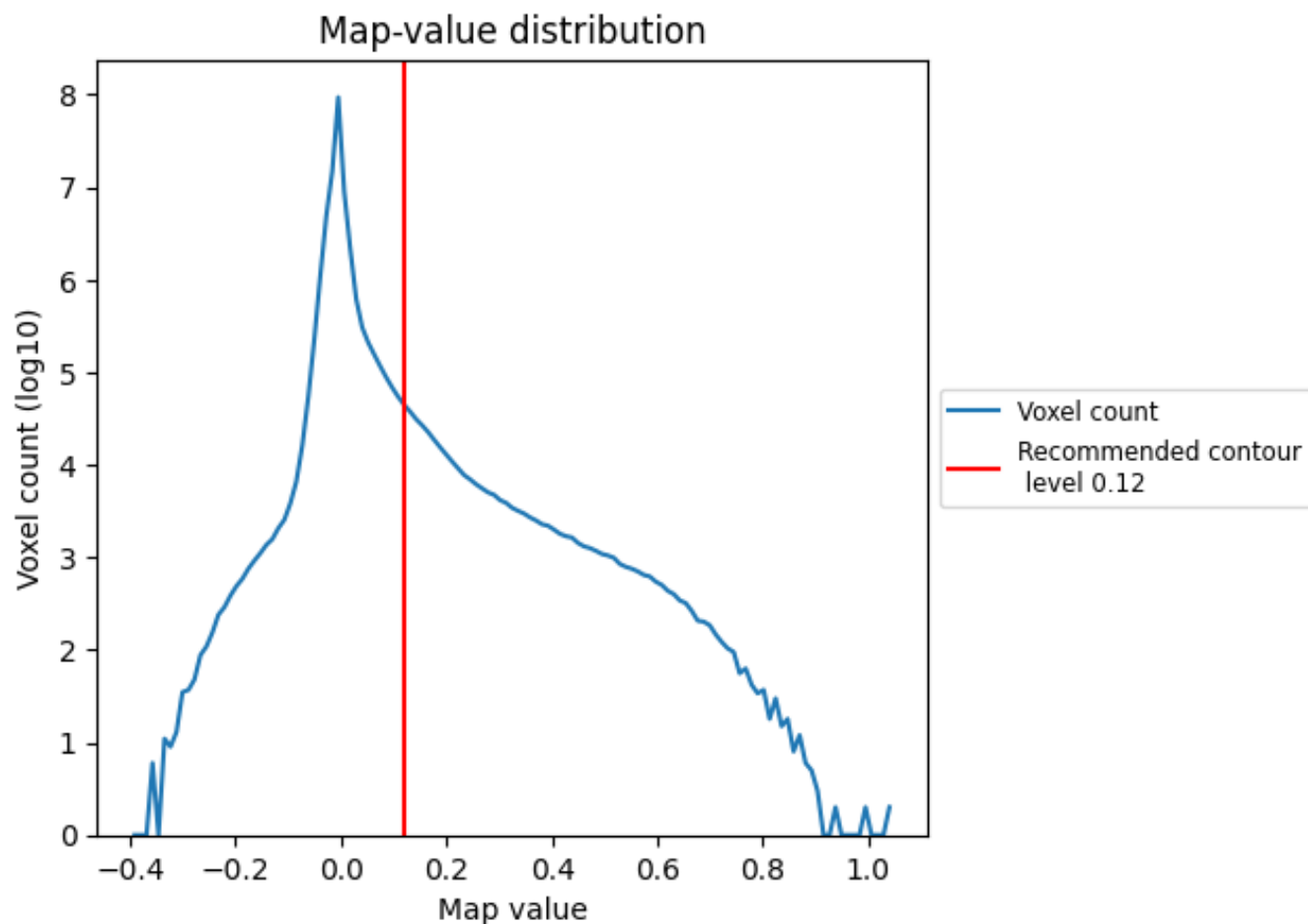


Z

7 Map analysis [i](#)

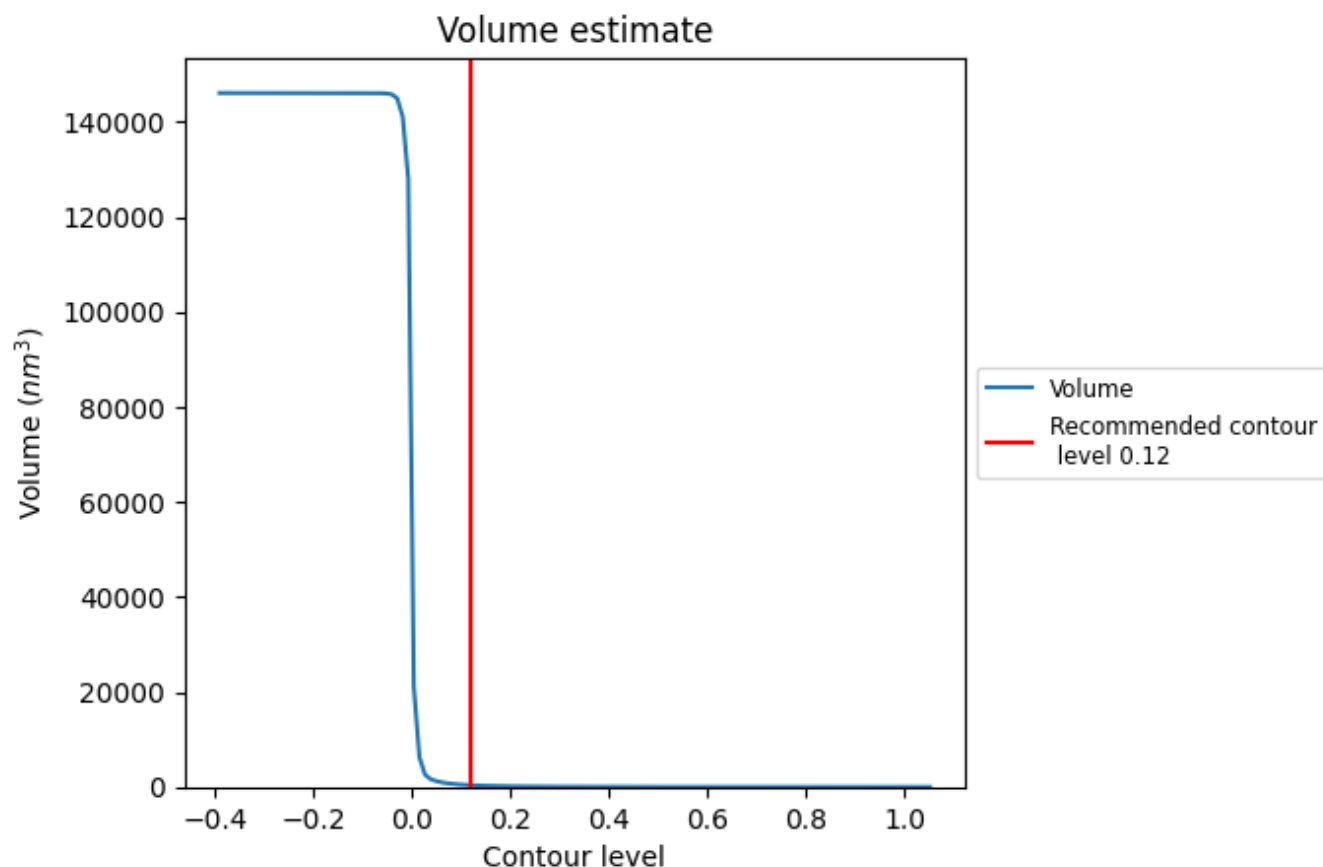
This section contains the results of statistical analysis of the map.

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.

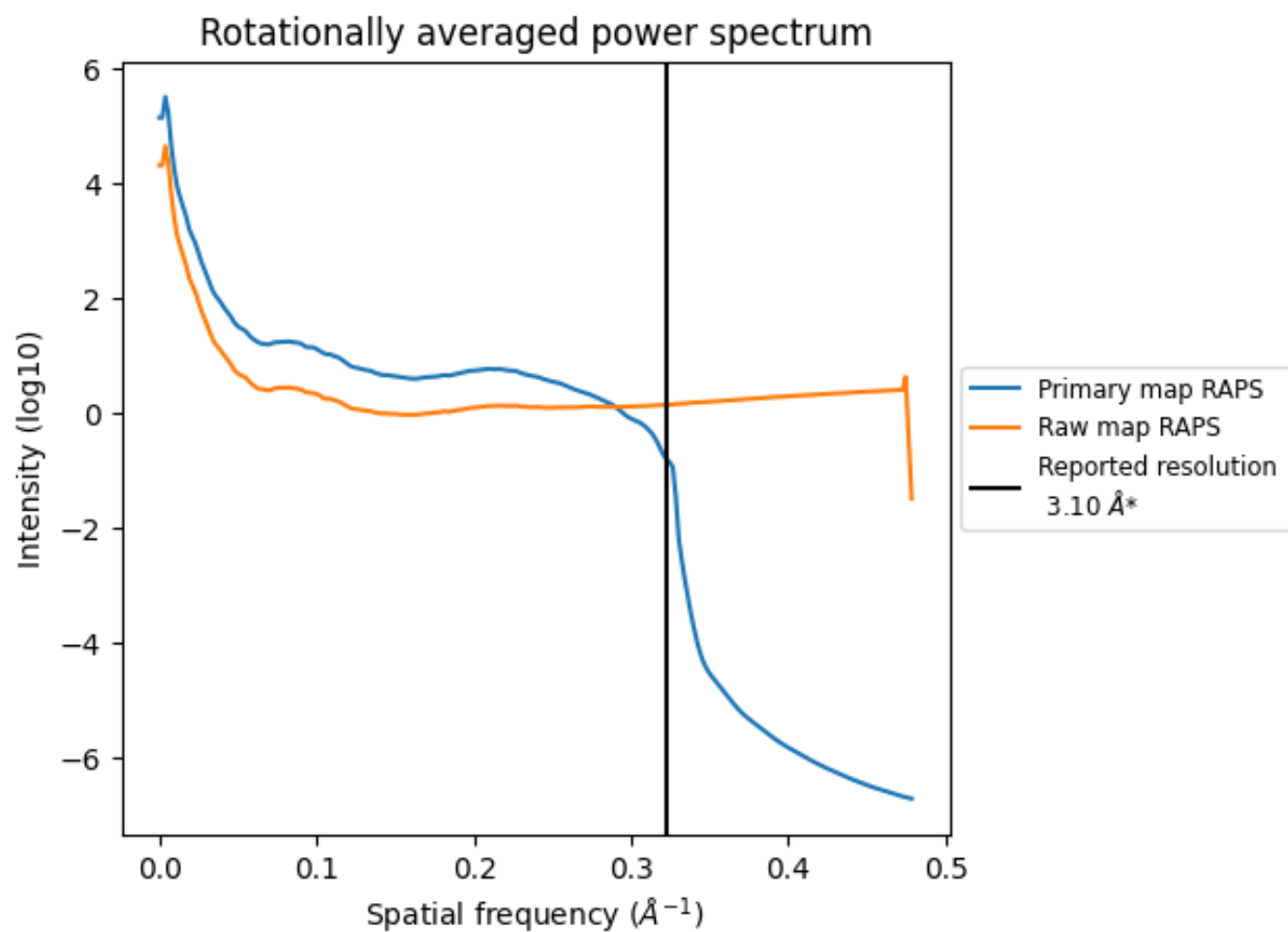
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 362 nm³; this corresponds to an approximate mass of 327 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 ⓘ

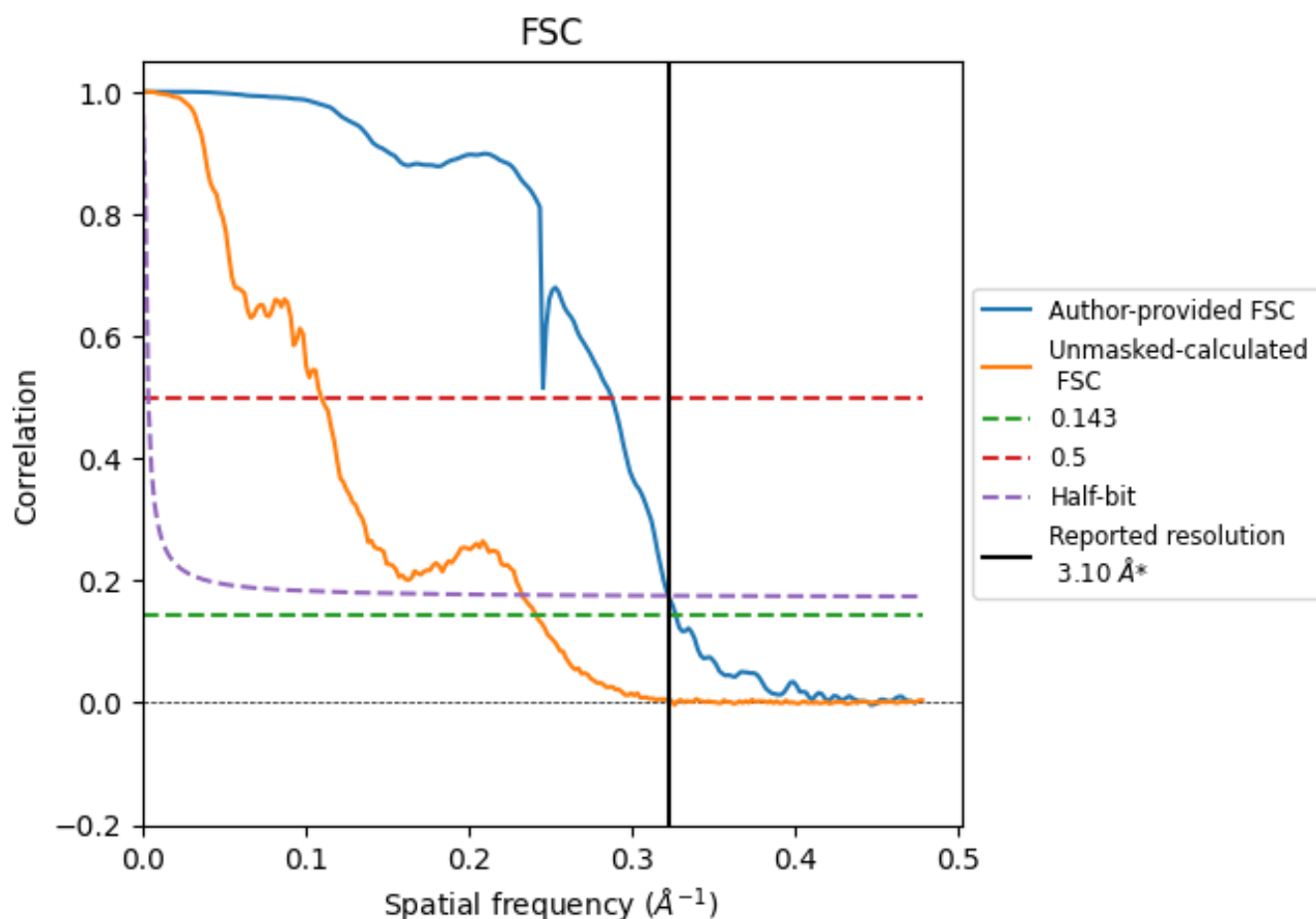


*Reported resolution corresponds to spatial frequency of 0.323 \AA^{-1}

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 0.323 \AA^{-1}

8.2 Resolution estimates [i](#)

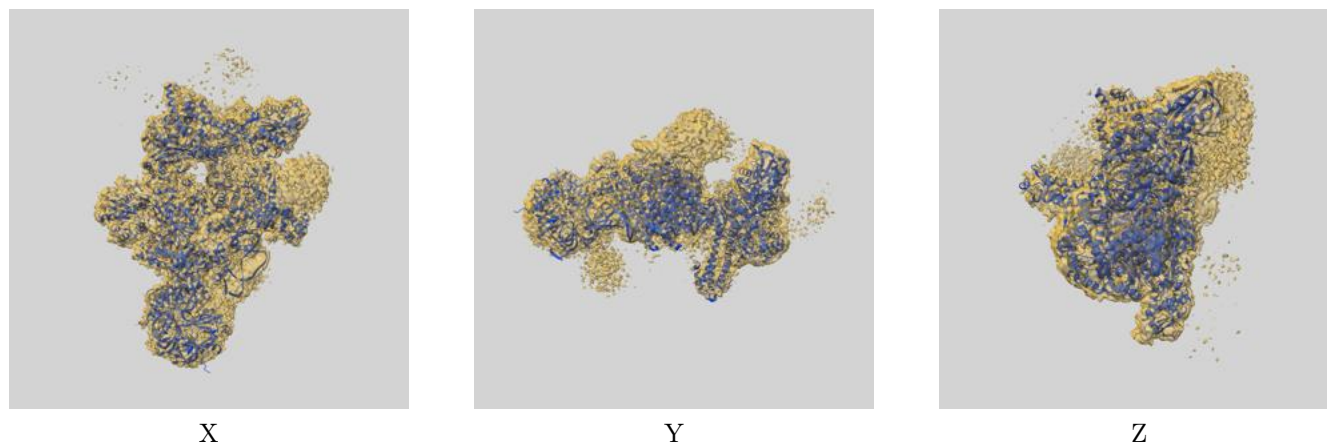
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.06	3.47	3.10
Unmasked-calculated*	4.14	9.11	4.29

*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 4.14 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

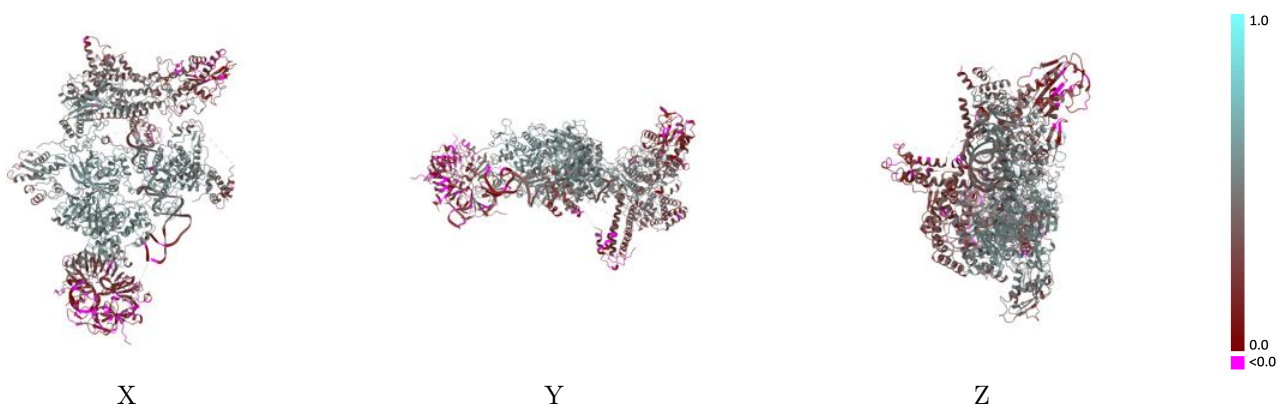
This section contains information regarding the fit between EMDB map EMD-18267 and PDB model 8Q91. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



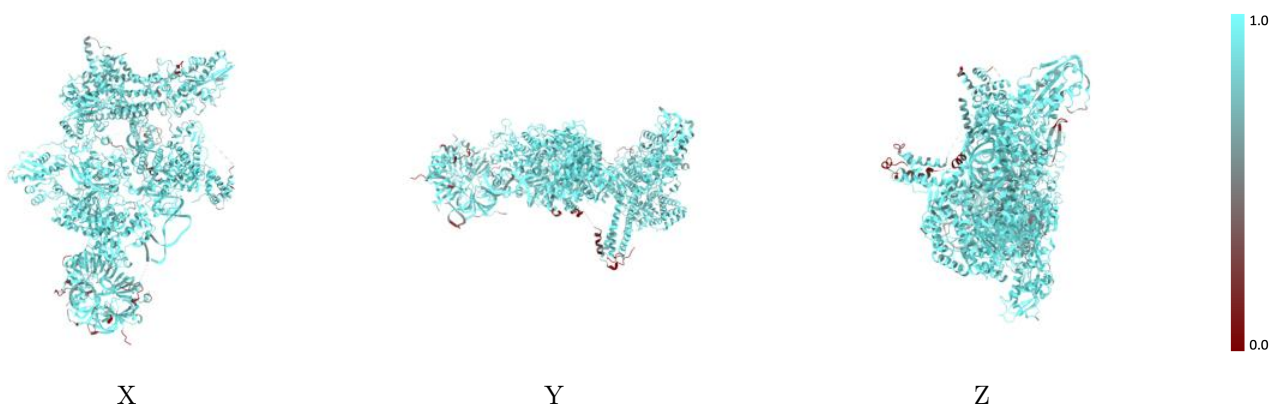
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



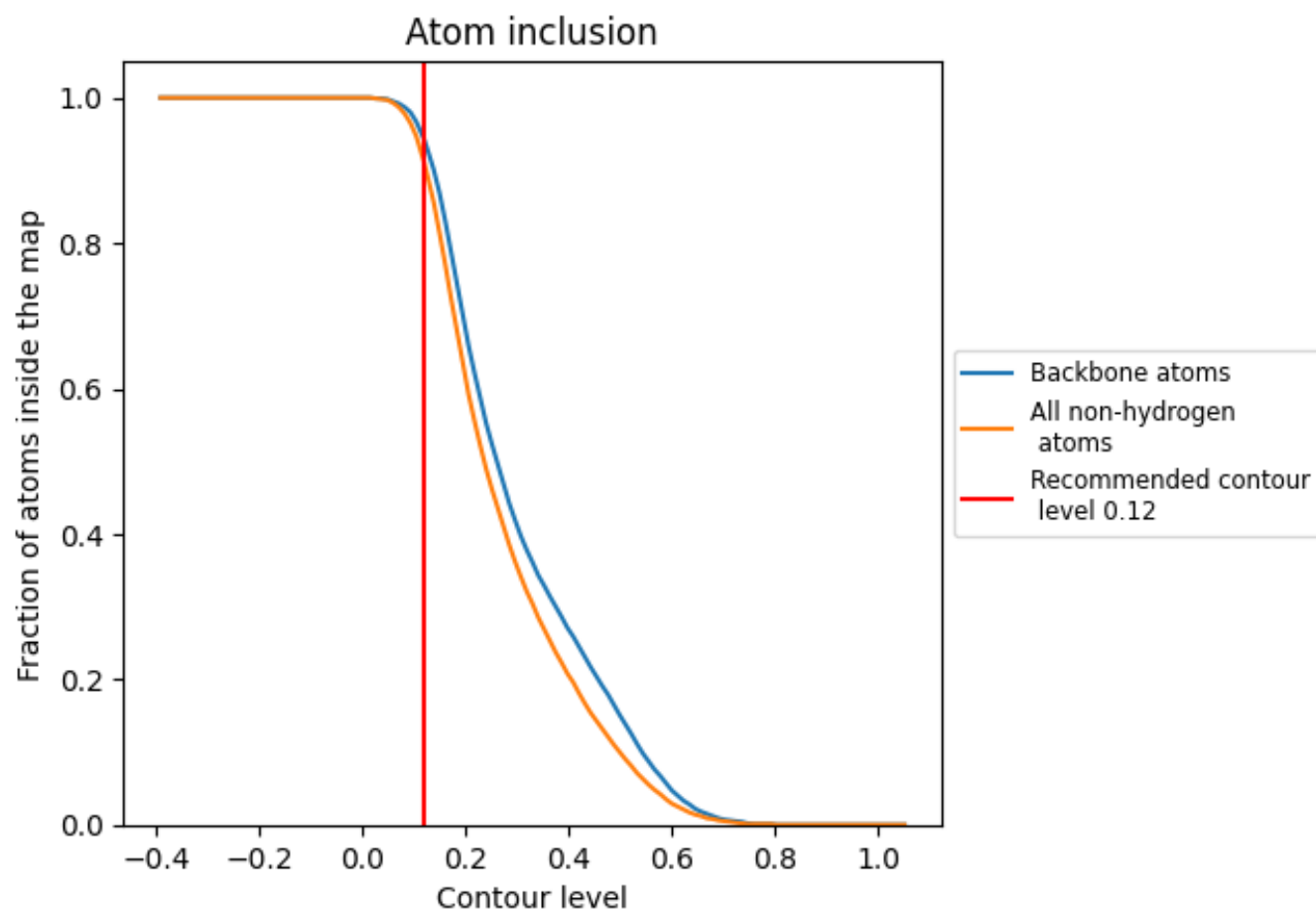
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).































9.4 Atom inclusion ⓘ



At the recommended contour level, 94% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9100	 0.4170
5	 0.8850	 0.2720
A	 0.9190	 0.4350
B	 0.7870	 0.4280
C	 0.9590	 0.5270
D	 0.8880	 0.5120
E	 0.4570	 0.2020
F	 0.8490	 0.3660
h	 0.8940	 0.2550
i	 0.9250	 0.1800
j	 0.7700	 0.0980
k	 0.9350	 0.3980
l	 0.8920	 0.1310
m	 0.8480	 0.0930
n	 0.7450	 0.2620

