



## Full wwPDB EM Validation Report ⓘ

Jul 10, 2023 – 05:04 pm BST

PDB ID : 8CLK  
EMDB ID : EMD-16715  
Title : TFIIC TauA complex  
Authors : Seifert-Davila, W.; Girbig, M.; Hauptmann, L.; Hoffmann, T.; Eustermann, S.; Mueller, C.W.  
Deposited on : 2023-02-16  
Resolution : 3.50 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev50  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.34

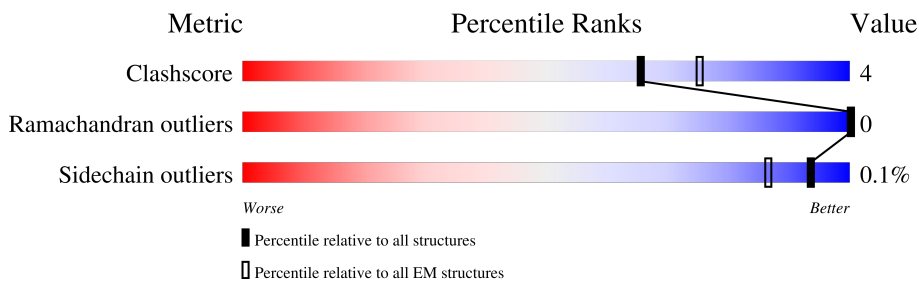
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	A	2158	
2	D	886	
3	E	533	
4	F	213	

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 10799 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 General transcription factor 3C polypeptide 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	611	4899	3112	852	902	33	0	0

There are 49 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2110	GLY	-	expression tag	UNP Q12789
A	2111	GLY	-	expression tag	UNP Q12789
A	2112	GLY	-	expression tag	UNP Q12789
A	2113	SER	-	expression tag	UNP Q12789
A	2114	GLY	-	expression tag	UNP Q12789
A	2115	GLY	-	expression tag	UNP Q12789
A	2116	GLY	-	expression tag	UNP Q12789
A	2117	SER	-	expression tag	UNP Q12789
A	2118	GLY	-	expression tag	UNP Q12789
A	2119	GLY	-	expression tag	UNP Q12789
A	2120	SER	-	expression tag	UNP Q12789
A	2121	LEU	-	expression tag	UNP Q12789
A	2122	GLU	-	expression tag	UNP Q12789
A	2123	VAL	-	expression tag	UNP Q12789
A	2124	LEU	-	expression tag	UNP Q12789
A	2125	PHE	-	expression tag	UNP Q12789
A	2126	GLN	-	expression tag	UNP Q12789
A	2127	GLY	-	expression tag	UNP Q12789
A	2128	PRO	-	expression tag	UNP Q12789
A	2129	GLY	-	expression tag	UNP Q12789
A	2130	SER	-	expression tag	UNP Q12789
A	2131	GLY	-	expression tag	UNP Q12789
A	2132	SER	-	expression tag	UNP Q12789
A	2133	ASP	-	expression tag	UNP Q12789
A	2134	TYR	-	expression tag	UNP Q12789
A	2135	LYS	-	expression tag	UNP Q12789
A	2136	ASP	-	expression tag	UNP Q12789
A	2137	ASP	-	expression tag	UNP Q12789

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Chain	Residue	Modelled	Actual	Comment	Reference
A	2138	ASP	-	expression tag	UNP Q12789
A	2139	ASP	-	expression tag	UNP Q12789
A	2140	LYS	-	expression tag	UNP Q12789
A	2141	GLY	-	expression tag	UNP Q12789
A	2142	ASP	-	expression tag	UNP Q12789
A	2143	TYR	-	expression tag	UNP Q12789
A	2144	LYS	-	expression tag	UNP Q12789
A	2145	ASP	-	expression tag	UNP Q12789
A	2146	ASP	-	expression tag	UNP Q12789
A	2147	ASP	-	expression tag	UNP Q12789
A	2148	ASP	-	expression tag	UNP Q12789
A	2149	LYS	-	expression tag	UNP Q12789
A	2150	GLY	-	expression tag	UNP Q12789
A	2151	ASP	-	expression tag	UNP Q12789
A	2152	TYR	-	expression tag	UNP Q12789
A	2153	LYS	-	expression tag	UNP Q12789
A	2154	ASP	-	expression tag	UNP Q12789
A	2155	ASP	-	expression tag	UNP Q12789
A	2156	ASP	-	expression tag	UNP Q12789
A	2157	ASP	-	expression tag	UNP Q12789
A	2158	LYS	-	expression tag	UNP Q12789

- Molecule 2 is a protein called General transcription factor 3C polypeptide 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	D	457	3667	2351	626	667	23	0	0

- Molecule 3 is a protein called General transcription factor 3C polypeptide 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	E	174	1421	912	250	250	9	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-13	MET	-	initiating methionine	UNP Q9Y5Q8
E	-12	HIS	-	expression tag	UNP Q9Y5Q8
E	-11	HIS	-	expression tag	UNP Q9Y5Q8
E	-10	HIS	-	expression tag	UNP Q9Y5Q8
E	-9	HIS	-	expression tag	UNP Q9Y5Q8

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-8	HIS	-	expression tag	UNP Q9Y5Q8
E	-7	HIS	-	expression tag	UNP Q9Y5Q8
E	-6	GLU	-	expression tag	UNP Q9Y5Q8
E	-5	ASN	-	expression tag	UNP Q9Y5Q8
E	-4	LEU	-	expression tag	UNP Q9Y5Q8
E	-3	TYR	-	expression tag	UNP Q9Y5Q8
E	-2	PHE	-	expression tag	UNP Q9Y5Q8
E	-1	GLN	-	expression tag	UNP Q9Y5Q8
E	0	GLY	-	expression tag	UNP Q9Y5Q8

- Molecule 4 is a protein called General transcription factor 3C polypeptide 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	F	102	812	510	128	167	7	0	0











## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55079	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 ( $e^-/\text{\AA}^2$ )	42.8	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.181	Depositor
Minimum map value	-3.635	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.082	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	289.344, 289.344, 289.344	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82199997, 0.82199997, 0.82199997	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	A	0.30	0/5001	0.55	0/6771
2	D	0.32	0/3743	0.53	0/5062
3	E	0.38	0/1457	0.60	0/1968
4	F	0.30	0/819	0.51	0/1099
All	All	0.32	0/11020	0.55	0/14900

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
3	E	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	E	22	ARG	Sidechain

### 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	A	4899	0	4900	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	3667	0	3670	28	0
3	E	1421	0	1431	26	0
4	F	812	0	804	5	0
All	All	10799	0	10805	88	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.

All (88) 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)
1:A:1704:CYS:SG	1:A:2095:ARG:NH2	2.52	0.79
3:E:65:ARG:NH2	3:E:68:ASP:OD2	2.22	0.72
2:D:819:ARG:NH1	3:E:126:MET:SD	2.64	0.70
1:A:1544:PHE:O	1:A:1585:ARG:NH1	2.28	0.64
1:A:1353:ARG:NH1	1:A:1356:ASP:OD2	2.33	0.62
1:A:1516:PRO:HD2	1:A:1519:ILE:HD11	1.81	0.61
1:A:1756:GLY:O	1:A:1802:ARG:NH2	2.30	0.61
1:A:1779:THR:HG23	1:A:1782:ASP:H	1.64	0.61
3:E:96:LYS:HA	3:E:103:ALA:HA	1.82	0.60
3:E:20:ARG:NH1	4:F:37:SER:O	2.34	0.59
2:D:608:ASP:OD1	2:D:609:ALA:N	2.36	0.57
2:D:843:LEU:HD21	3:E:134:VAL:HG21	1.88	0.55
2:D:851:ASP:O	2:D:857:ARG:NH2	2.40	0.55
2:D:655:TYR:CE2	2:D:657:SER:HB3	2.43	0.54
2:D:789:ARG:NH2	3:E:185:ARG:O	2.33	0.54
2:D:815:TYR:CD1	2:D:859:ILE:HG22	2.42	0.53
1:A:1535:LYS:NZ	1:A:1680:ARG:O	2.26	0.53
1:A:1987:TRP:CD1	1:A:2000:LYS:HE2	2.44	0.53
1:A:1479:ARG:NH1	1:A:1480:ARG:O	2.41	0.53
2:D:756:TYR:CE2	2:D:772:CYS:HB3	2.44	0.52
2:D:462:HIS:CE1	2:D:466:LEU:HD11	2.45	0.51
3:E:94:ARG:HA	3:E:105:SER:HA	1.91	0.51
1:A:1464:LEU:HD21	1:A:1496:PHE:H	1.76	0.51
1:A:1434:GLN:NE2	1:A:2028:VAL:O	2.43	0.51
3:E:59:ARG:NH2	3:E:77:ASN:OD1	2.42	0.51
1:A:1989:VAL:HG12	1:A:1991:ASP:H	1.76	0.50
3:E:182:TYR:CZ	3:E:184:TYR:HA	2.46	0.50
2:D:701:GLN:HB3	3:E:160:PHE:O	2.12	0.50
1:A:1535:LYS:HE3	1:A:1681:CYS:HA	1.91	0.49
1:A:2085:PRO:O	2:D:832:HIS:NE2	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1505:GLN:O	1:A:1509:ARG:HG3	2.12	0.49
1:A:1432:LEU:HD13	1:A:1814:LEU:HD13	1.95	0.48
3:E:30:PRO:HD3	3:E:123:PHE:CD2	2.49	0.47
1:A:1508:TYR:O	1:A:1512:THR:N	2.46	0.47
2:D:753:LEU:HD11	2:D:777:PHE:CZ	2.49	0.47
3:E:133:ALA:HA	3:E:167:TYR:CZ	2.49	0.47
1:A:1503:LEU:HD22	1:A:1507:TYR:CE1	2.49	0.47
1:A:1514:ARG:O	3:E:185:ARG:NH2	2.46	0.47
2:D:428:ALA:HA	2:D:431:PHE:CD2	2.50	0.47
1:A:1326:ASN:HB2	3:E:79:PHE:CD1	2.50	0.47
2:D:569:ASN:OD1	2:D:570:ARG:N	2.49	0.46
2:D:461:ARG:NH2	2:D:464:GLU:HG3	2.30	0.46
3:E:129:PHE:HB2	3:E:173:PHE:CB	2.46	0.46
3:E:21:GLU:OE2	3:E:22:ARG:NH1	2.44	0.46
1:A:1349:ASP:N	1:A:1349:ASP:OD1	2.49	0.45
1:A:1722:LEU:HG	1:A:1726:VAL:HG23	1.98	0.45
1:A:2088:ASP:OD2	1:A:2092:ARG:NE	2.43	0.45
2:D:478:SER:O	2:D:482:VAL:HG23	2.17	0.45
1:A:1390:PRO:HG2	1:A:1396:LEU:HA	1.99	0.45
1:A:1516:PRO:CD	1:A:1519:ILE:HD11	2.45	0.45
1:A:1587:PRO:HD2	1:A:1673:CYS:SG	2.57	0.45
2:D:686:TYR:HA	2:D:689:ILE:HG22	1.99	0.45
1:A:1388:GLU:O	1:A:1400:TYR:OH	2.30	0.45
3:E:133:ALA:HB3	3:E:146:TYR:CZ	2.51	0.45
1:A:1738:ASP:CG	1:A:1777:THR:H	2.20	0.45
1:A:2088:ASP:CG	1:A:2092:ARG:HE	2.19	0.45
2:D:641:ARG:NE	2:D:644:GLU:OE2	2.40	0.44
2:D:438:ASN:OD1	2:D:439:SER:N	2.50	0.44
3:E:60:LEU:HB3	3:E:76:ALA:HB3	1.99	0.44
4:F:30:ILE:HG13	4:F:33:SER:HB2	2.00	0.44
1:A:1278:ILE:HG23	1:A:1337:LEU:HD13	1.99	0.44
1:A:1759:LYS:HE2	1:A:1759:LYS:HB3	1.86	0.43
1:A:2007:LEU:HG	1:A:2011:MET:SD	2.58	0.43
2:D:719:HIS:ND1	2:D:742:ASN:HB3	2.32	0.43
3:E:92:THR:N	4:F:17:GLU:O	2.47	0.43
2:D:635:SER:HA	2:D:638:ASP:OD2	2.18	0.43
2:D:722:CYS:SG	2:D:742:ASN:ND2	2.89	0.43
1:A:1401:ARG:N	4:F:111:THR:O	2.52	0.42
1:A:1702:THR:HA	1:A:2096:VAL:HG13	2.01	0.42
1:A:1698:LEU:HD21	1:A:2092:ARG:NH1	2.33	0.42
2:D:738:LEU:HA	2:D:741:HIS:ND1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:84:LEU:HD23	3:E:116:ILE:HA	2.00	0.42
2:D:753:LEU:HD11	2:D:777:PHE:CE2	2.54	0.42
2:D:828:HIS:CD2	2:D:829:LEU:HG	2.55	0.42
2:D:750:LYS:HE3	2:D:750:LYS:HB2	1.89	0.42
1:A:1346:LEU:HD21	1:A:1374:LEU:HD23	2.02	0.42
3:E:13:ALA:HB2	4:F:46:LEU:HB3	2.02	0.42
3:E:148:LYS:HD3	3:E:164:LEU:HD13	2.02	0.42
1:A:1326:ASN:HB2	3:E:79:PHE:CG	2.55	0.41
1:A:1392:THR:HG22	1:A:1395:GLU:HG2	2.03	0.41
2:D:744:PHE:CZ	2:D:779:HIS:CE1	3.08	0.41
1:A:1293:THR:HG22	1:A:1294:TRP:H	1.85	0.41
1:A:1294:TRP:HB2	1:A:1313:SER:HB3	2.03	0.41
1:A:1412:THR:HG22	1:A:1413:ARG:N	2.36	0.41
1:A:1519:ILE:CD1	3:E:184:TYR:HB2	2.51	0.40
1:A:1738:ASP:HA	1:A:1776:ARG:HH11	1.85	0.40
2:D:789:ARG:CZ	3:E:182:TYR:HD1	2.33	0.40
3:E:182:TYR:OH	3:E:184:TYR:HA	2.22	0.40

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	A	603/2158 (28%)	591 (98%)	12 (2%)	0	100	100
2	D	451/886 (51%)	441 (98%)	10 (2%)	0	100	100
3	E	170/533 (32%)	162 (95%)	8 (5%)	0	100	100
4	F	96/213 (45%)	92 (96%)	4 (4%)	0	100	100
All	All	1320/3790 (35%)	1286 (97%)	34 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	548/1898 (29%)	547 (100%)	1 (0%)	93	98
2	D	397/782 (51%)	397 (100%)	0	100	100
3	E	155/470 (33%)	155 (100%)	0	100	100
4	F	95/194 (49%)	95 (100%)	0	100	100
All	All	1195/3344 (36%)	1194 (100%)	1 (0%)	93	98

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2103	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1328	GLN
1	A	1431	ASN
1	A	1478	ASN
2	D	823	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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.



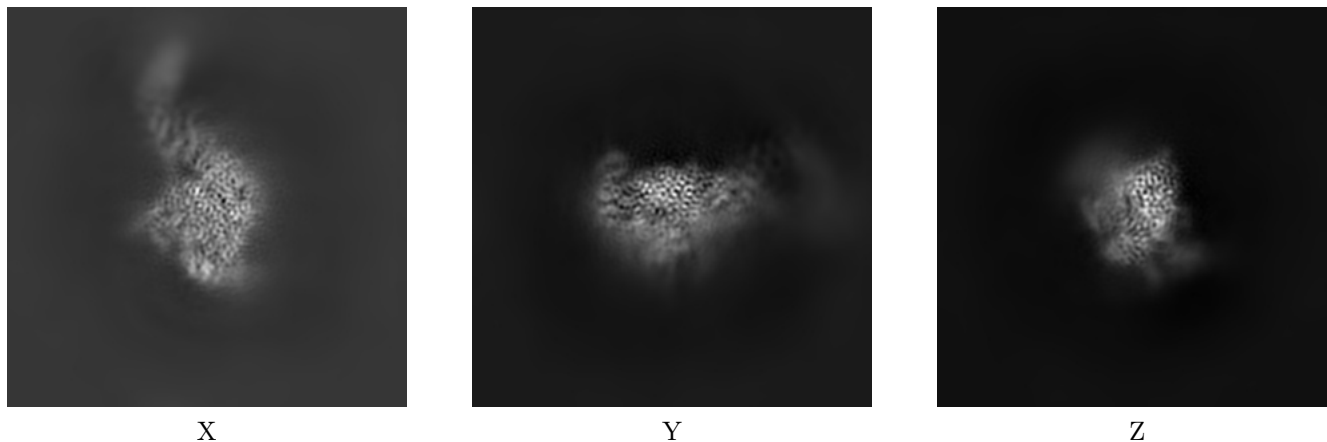
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16715. These allow visual inspection of the internal detail of the map and identification of artifacts.

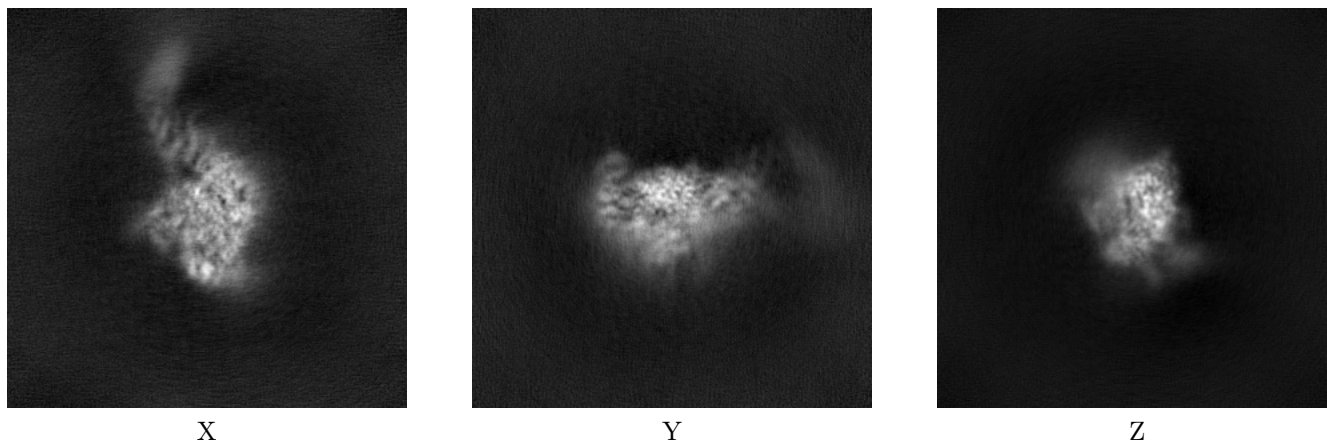
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

#### 6.1.1 Primary map



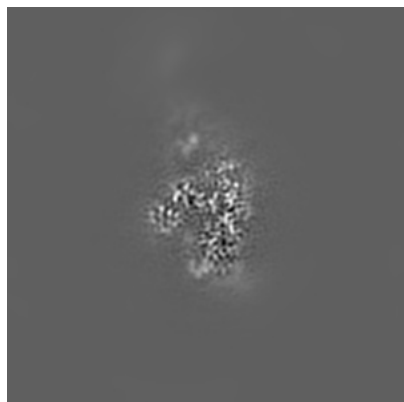
#### 6.1.2 Raw map



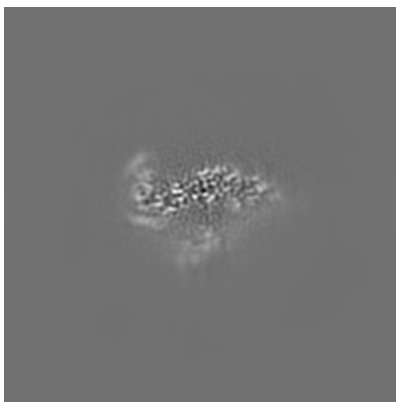
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

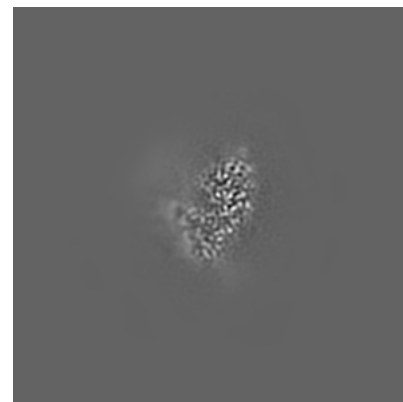
### 6.2.1 Primary map



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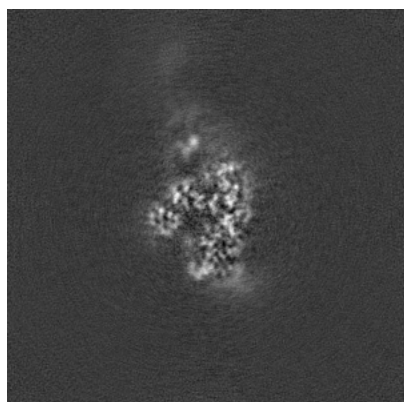


Y Index: 176

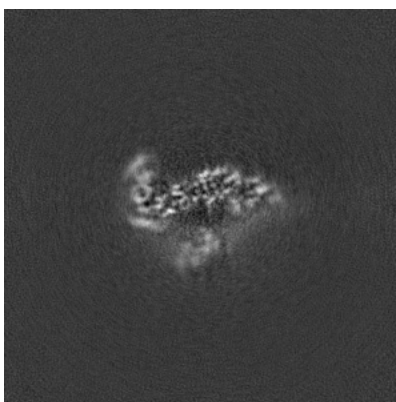


Z Index: 176

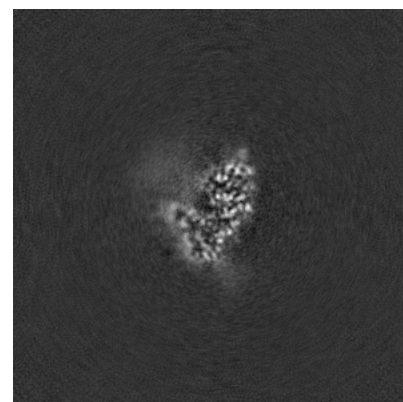
### 6.2.2 Raw map



X Index: 176



Y Index: 176

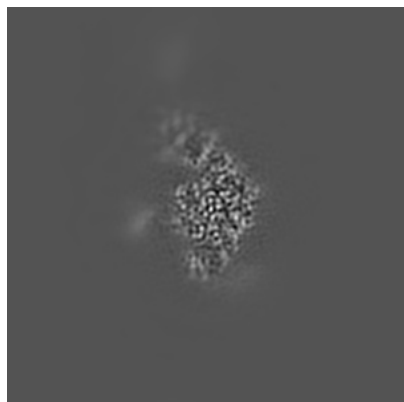


Z Index: 176

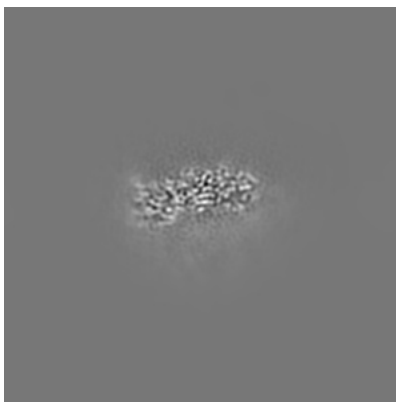
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

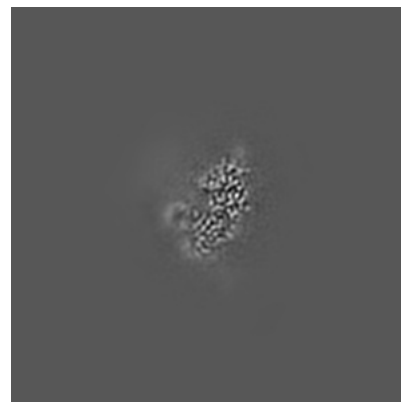
### 6.3.1 Primary map



X Index: 191

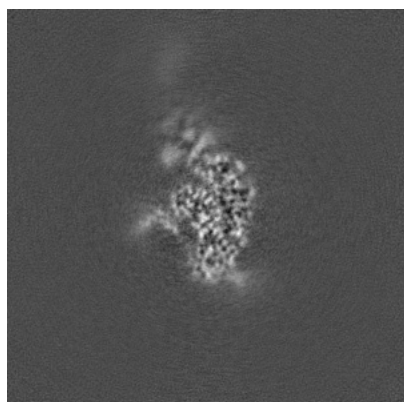


Y Index: 187

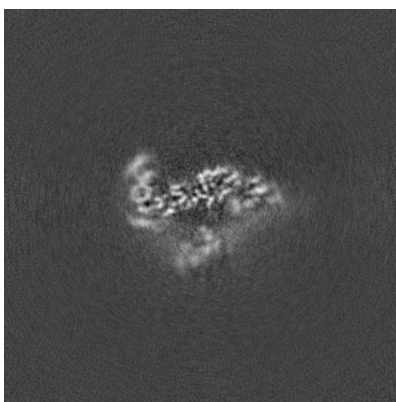


Z Index: 180

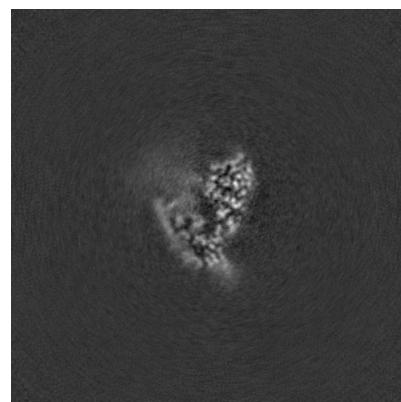
### 6.3.2 Raw map



X Index: 184



Y Index: 175

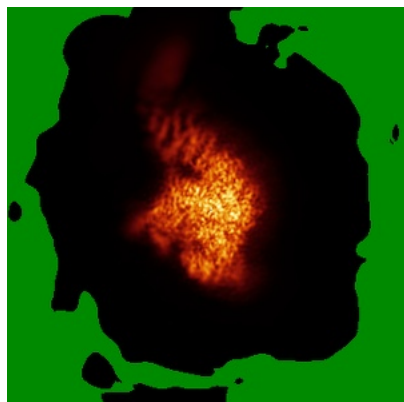


Z Index: 170

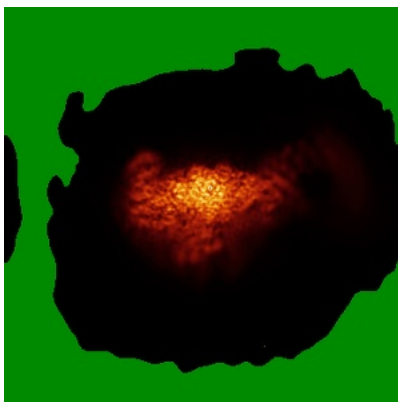
The images above show the largest variance slices of the map in three orthogonal directions.

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

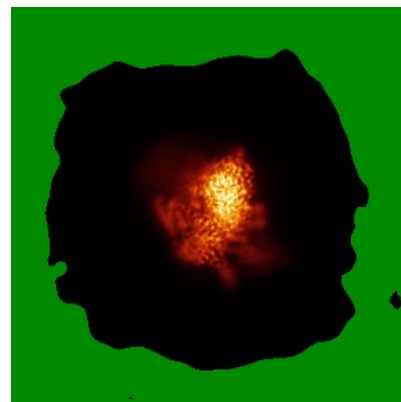
### 6.4.1 Primary map



X

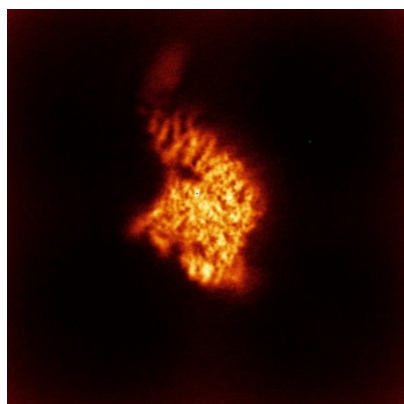


Y

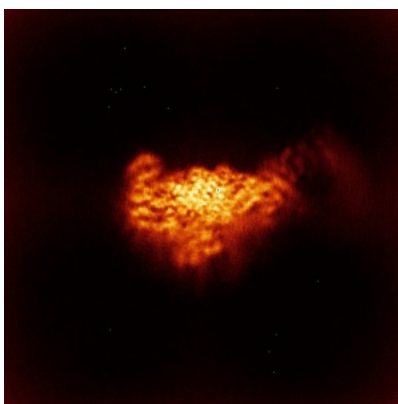


Z

### 6.4.2 Raw map



X



Y

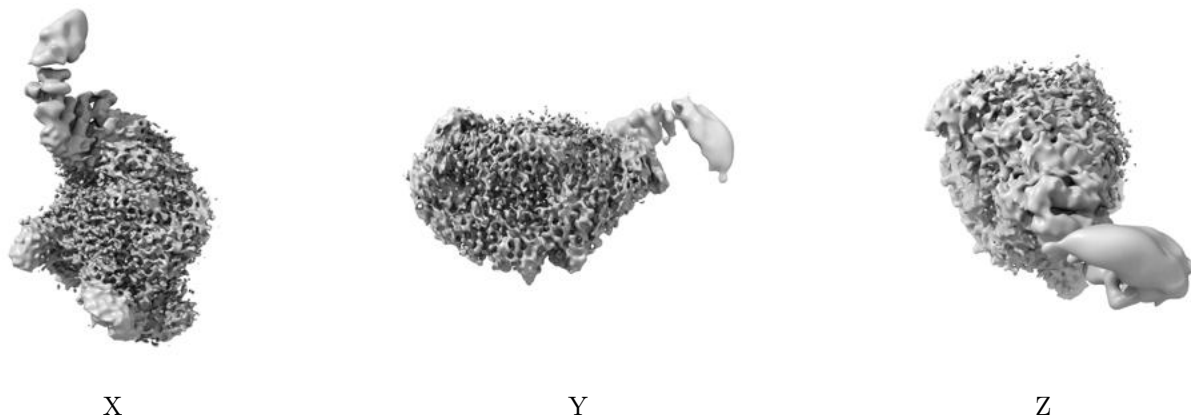


Z

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.

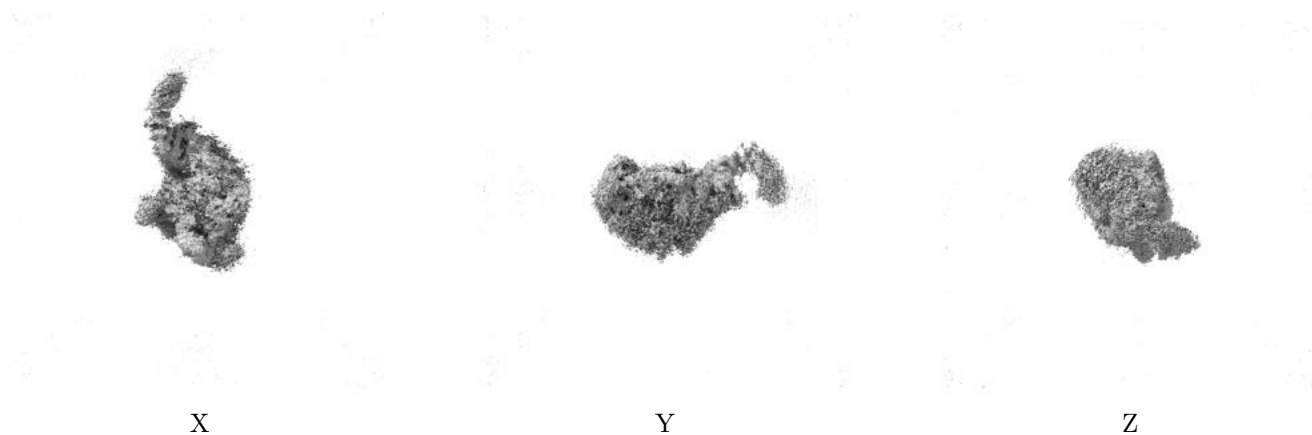
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. 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.

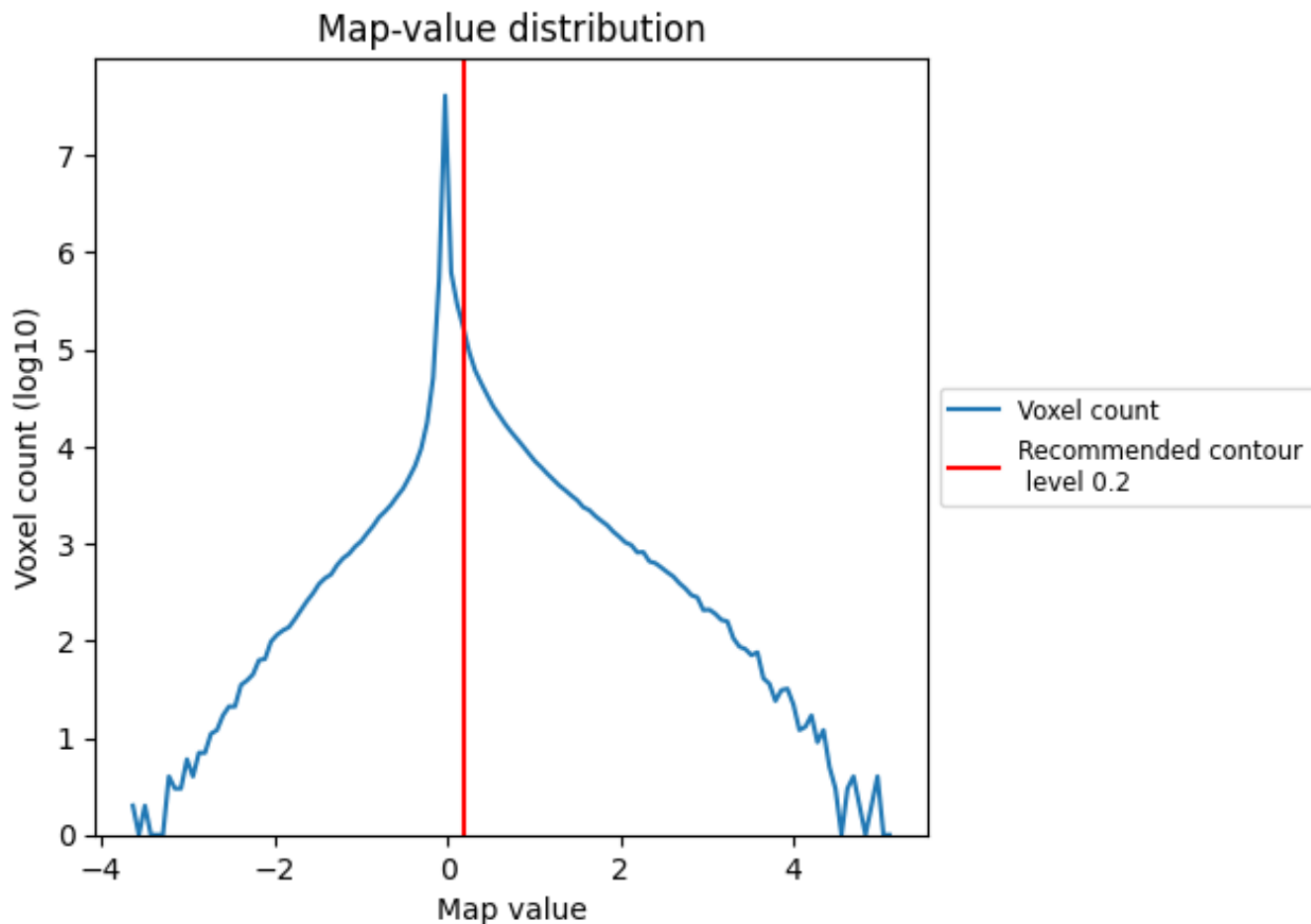
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

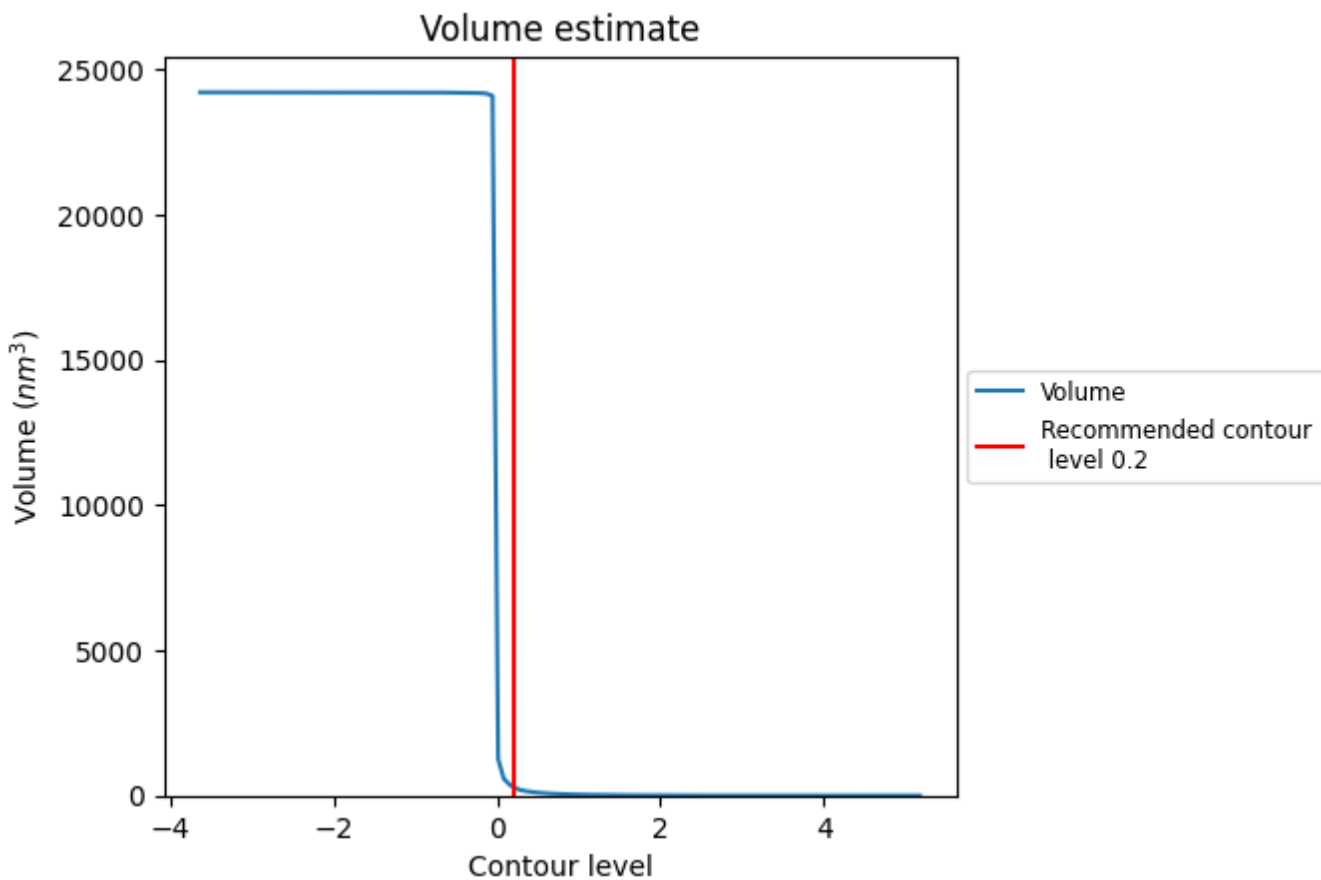
This section contains the results of statistical analysis of the map.

### 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.

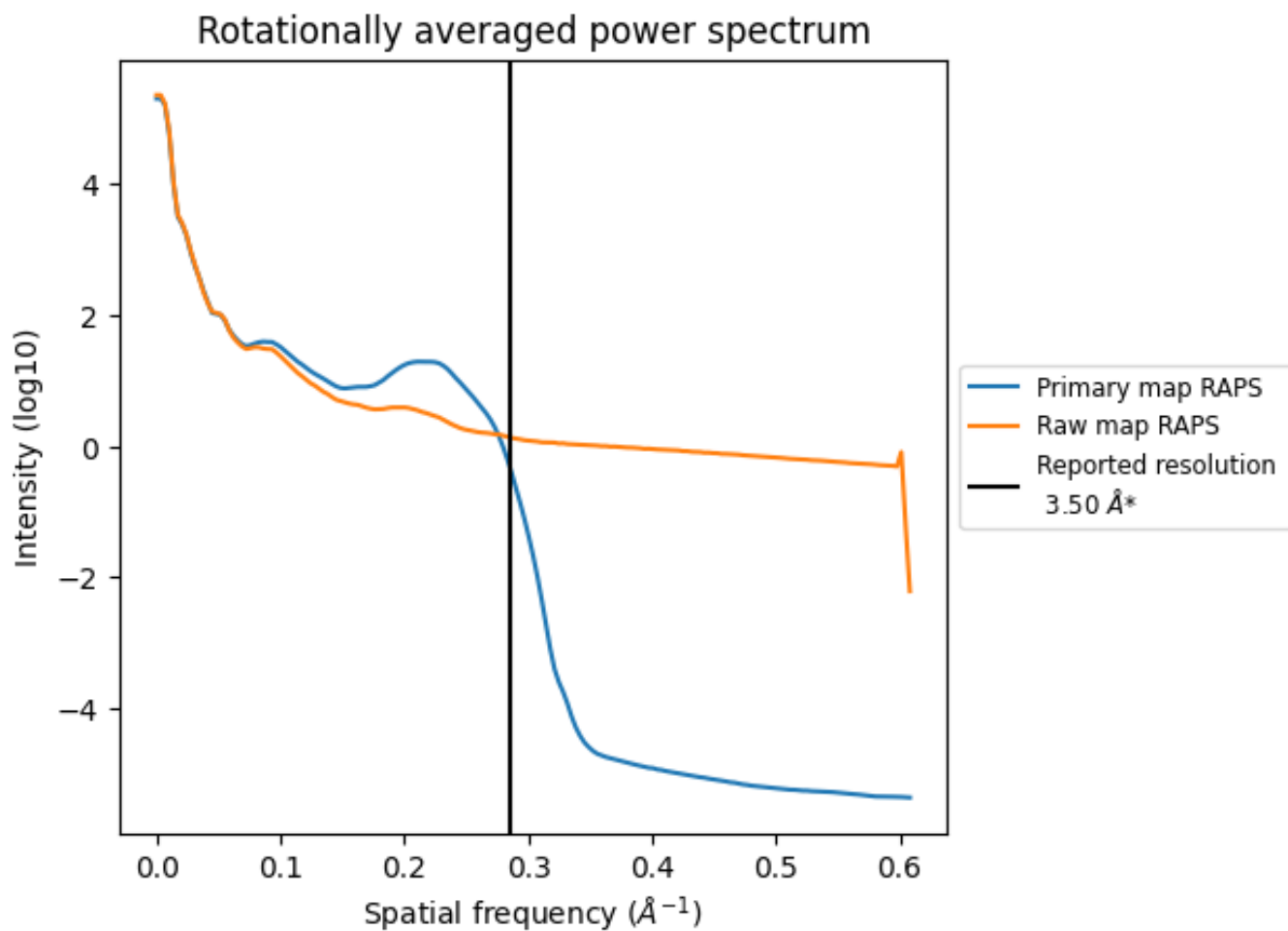
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 297 nm<sup>3</sup>; this corresponds to an approximate mass of 268 kDa.

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

### 7.3 Rotationally averaged power spectrum [i](#)



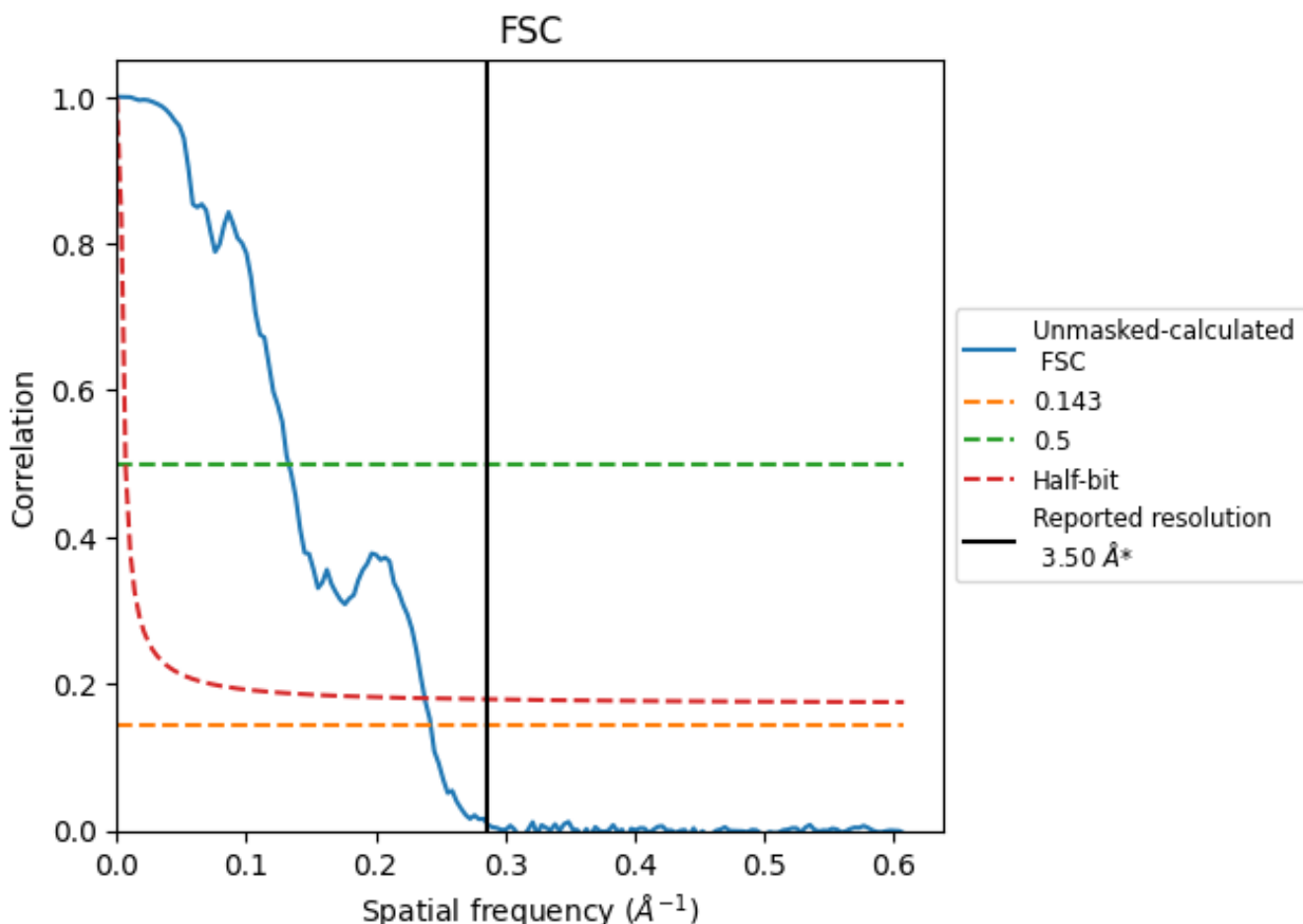
\*Reported resolution corresponds to spatial frequency of 0.286 Å<sup>-1</sup>



## 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 0.286 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

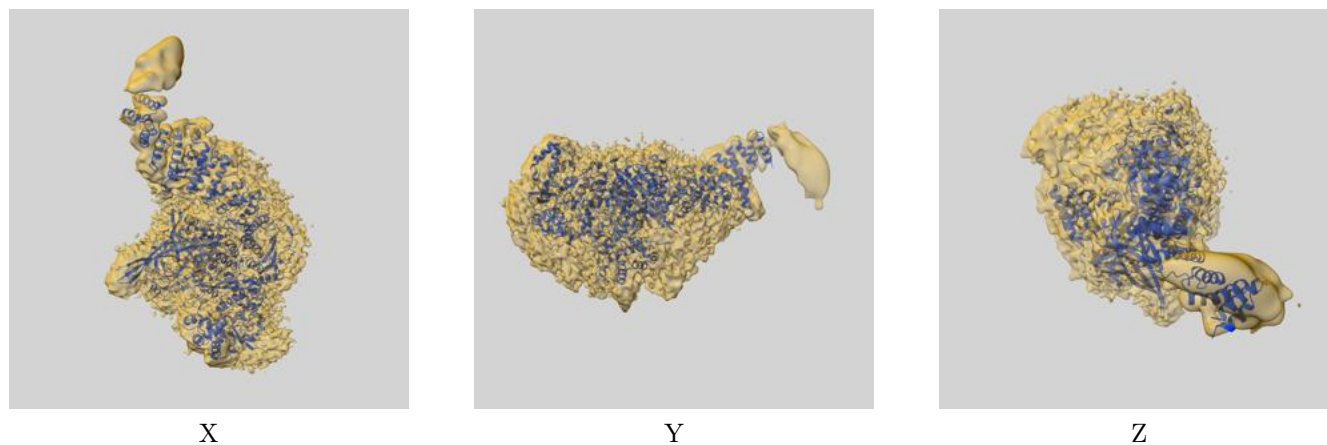
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.12	7.53	4.20

\*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 4.12 differs from the reported value 3.5 by more than 10 %

## 9 Map-model fit [i](#)

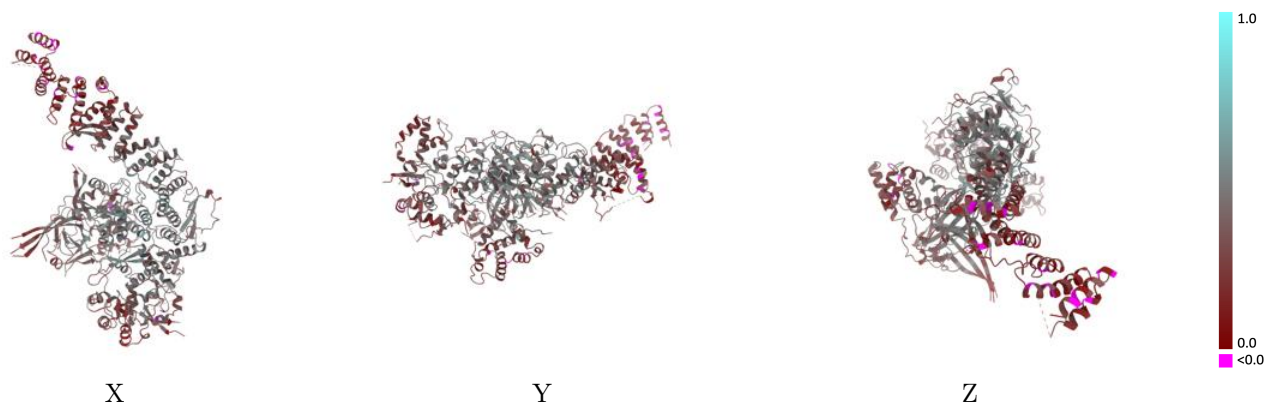
This section contains information regarding the fit between EMDB map EMD-16715 and PDB model 8CLK. Per-residue inclusion information can be found in section 3 on page 6.

### 9.1 Map-model overlay [i](#)



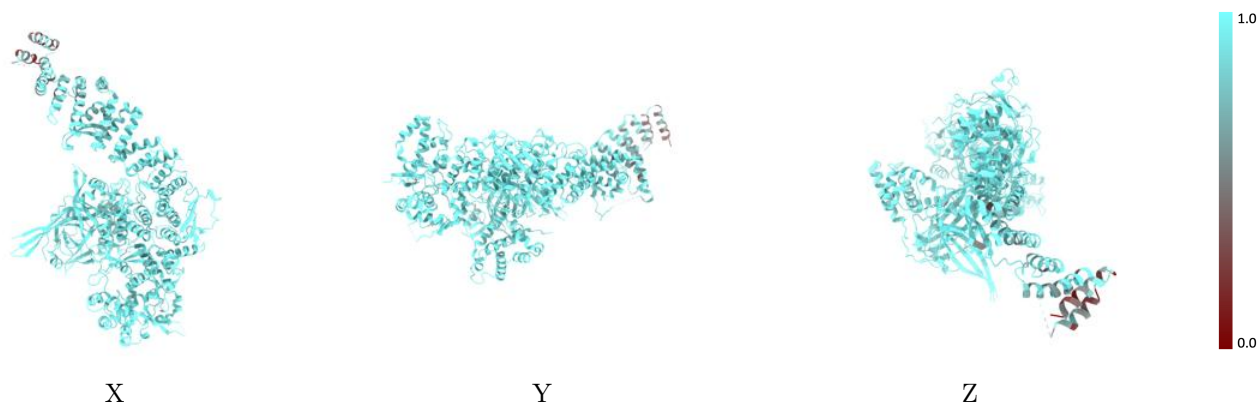
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



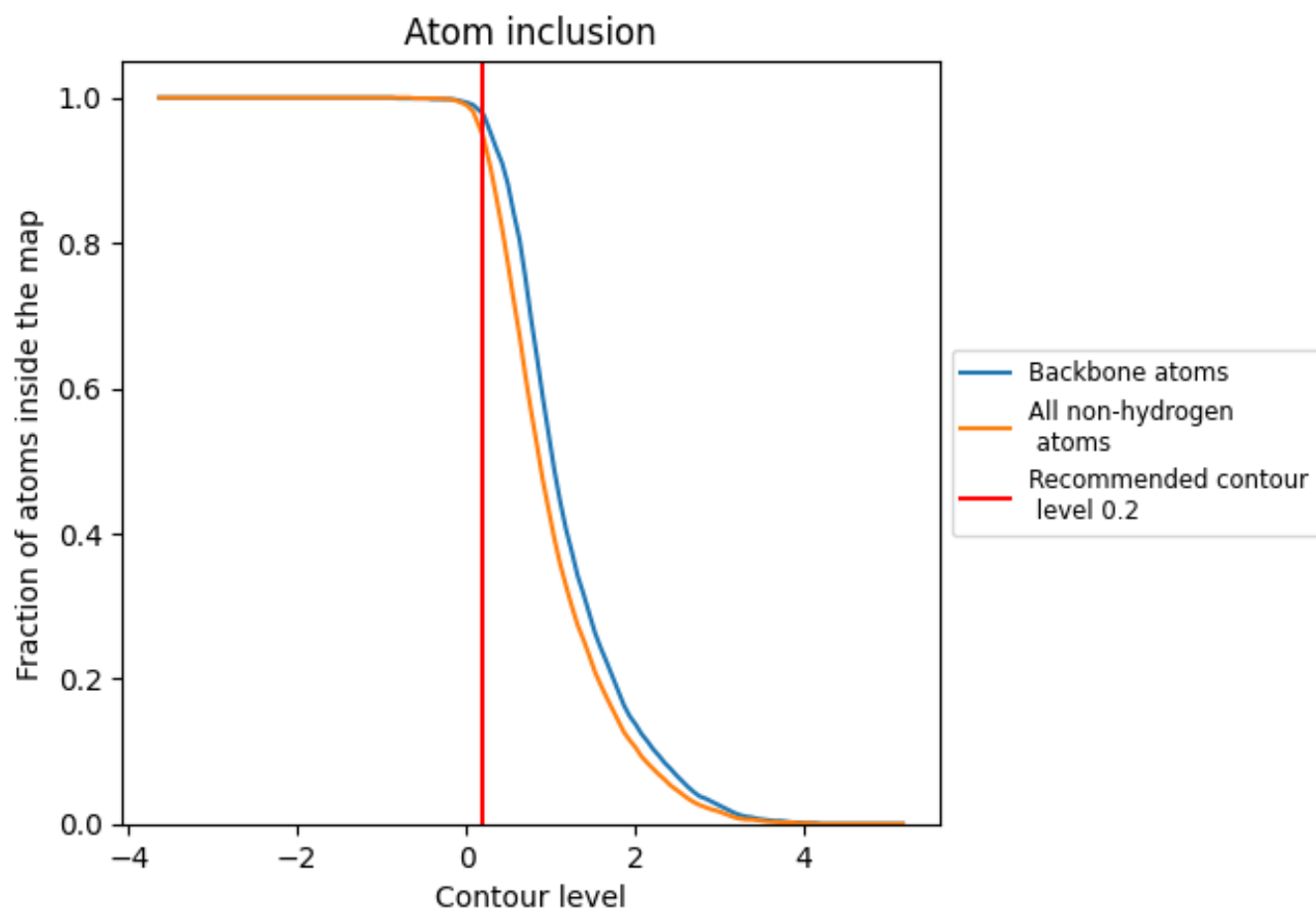
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).







## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9480	 0.3580
A	 0.9660	 0.3510
D	 0.9090	 0.3350
E	 0.9730	 0.4310
F	 0.9730	 0.3740

