



## wwPDB EM Validation Summary Report ⓘ

Aug 3, 2024 – 08:51 am BST

PDB ID : 8RTD  
EMDB ID : EMD-19488  
Title : Stalk-Arches-IMC structure from the fully-assembled R388 type IV secretion system determined by cryo-EM.  
Authors : Mace, K.; Waksman, G.  
Deposited on : 2024-01-25  
Resolution : 4.33 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](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:

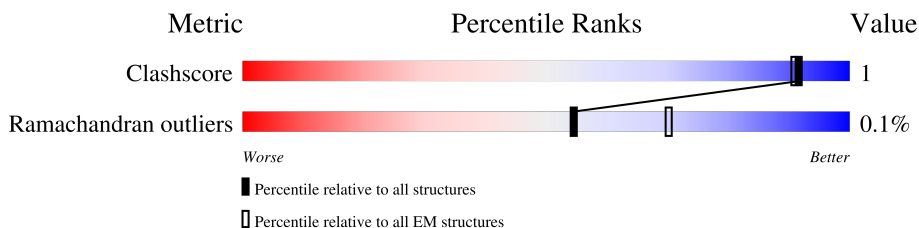
EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

# 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 4.33 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

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	229	
1	B	229	
1	C	229	
1	E	229	
1	K	229	
2	D	231	
2	F	231	
2	G	231	
2	Q	231	

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Mol	Chain	Length	Quality of chain
2	S	231	42% 95%
2	U	231	57% 83% 16%
2	X	231	13% 26% 74%
2	Y	231	55% 81% 19%
2	b	231	43% 90% 9%
2	c	231	12% 26% 74%
2	d	231	10% 16% 84%
2	i	231	12% 88%
3	Z	395	15% 84%
3	a	395	5% 12% 88%
3	e	395	10% 90%
4	H	342	11% 65% 35%
4	I	342	21% 63% 37%
4	J	342	19% 78% 20%
4	L	342	7% 77% 22%
4	M	342	7% 77% 20%
5	R	104	9% 99%
5	f	104	26% 92% 8%
5	j	104	6% 100%
6	O	823	6% 95%
6	P	823	20% 91% 8%
6	T	823	11% 95%
6	V	823	26% 85% 14%
6	g	823	28% 91% 9%
6	h	823	24% 56% 44%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 40078 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 TrwJ protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	197	969	575	197	197	0	0
1	B	197	969	575	197	197	0	0
1	C	197	969	575	197	197	0	0
1	K	197	969	575	197	197	0	0
1	E	197	969	575	197	197	0	0

- Molecule 2 is a protein called TrwG protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	D	37	183	109	37	37	0	0
2	F	28	138	82	28	28	0	0
2	G	13	64	38	13	13	0	0
2	Q	198	855	459	198	198	0	0
2	S	223	973	527	223	223	0	0
2	U	193	839	453	193	193	0	0
2	X	61	297	175	61	61	0	0
2	Y	188	814	438	188	188	0	0
2	b	210	912	492	210	210	0	0
2	c	59	287	169	59	59	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	d	38	Total	C	N	O	0	0
			184	108	38	38		
2	i	28	Total	C	N	O	0	0
			138	82	28	28		

- Molecule 3 is a protein called TrwE protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	a	49	Total	C	N	O	0	0
			242	144	49	49		
3	Z	62	Total	C	N	O	0	0
			306	182	62	62		
3	e	39	Total	C	N	O	0	0
			193	115	39	39		

- Molecule 4 is a protein called TrwI protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	L	268	Total	C	N	O	0	0
			1311	775	268	268		
4	M	272	Total	C	N	O	1	0
			1330	786	272	272		
4	H	222	Total	C	N	O	1	0
			1087	643	222	222		
4	I	217	Total	C	N	O	1	0
			1062	628	217	217		
4	J	272	Total	C	N	O	1	0
			1330	786	272	272		

- Molecule 5 is a protein called TrwM protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	j	104	Total	C	N	O	0	0
			515	307	104	104		
5	R	104	Total	C	N	O	0	0
			515	307	104	104		
5	f	96	Total	C	N	O	0	0
			475	283	96	96		

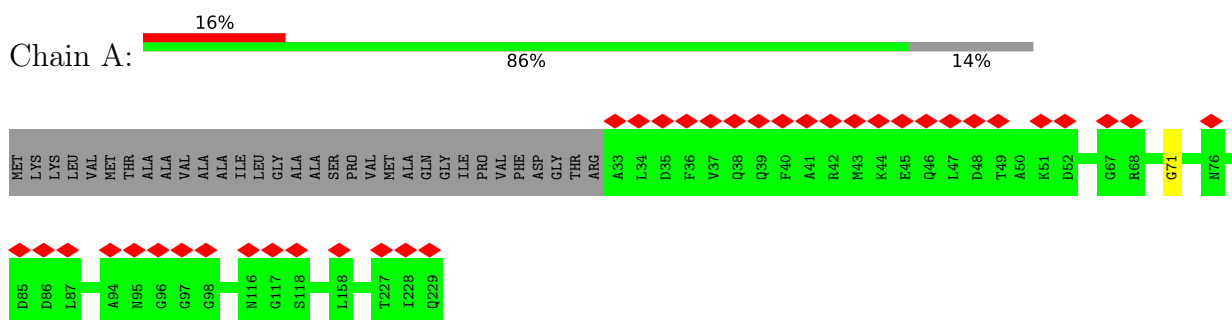
- Molecule 6 is a protein called Type IV secretion system protein virB4.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	O	799	Total 3947	C 2349	N 799	O 799	0	0
6	P	760	Total 3754	C 2234	N 760	O 760	0	0
6	T	808	Total 3992	C 2376	N 808	O 808	0	0
6	V	711	Total 3512	C 2090	N 711	O 711	0	0
6	g	753	Total 3719	C 2213	N 753	O 753	0	0
6	h	457	Total 2259	C 1345	N 457	O 457	0	0

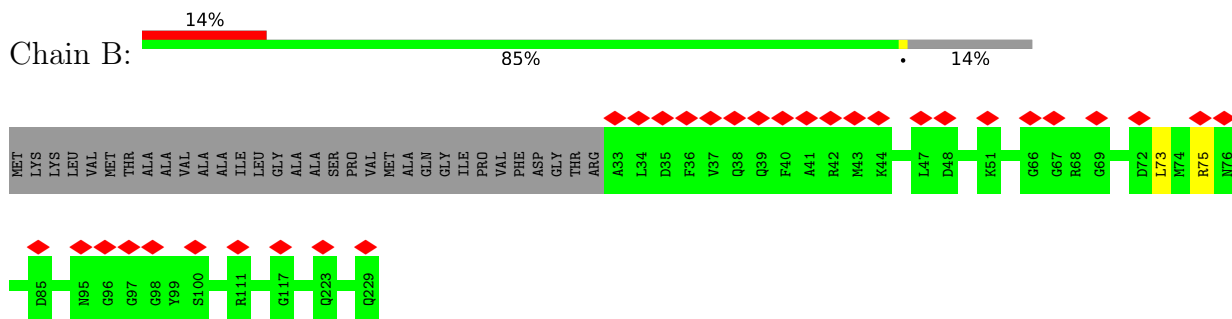
### 3 Residue-property plots [i](#)

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.

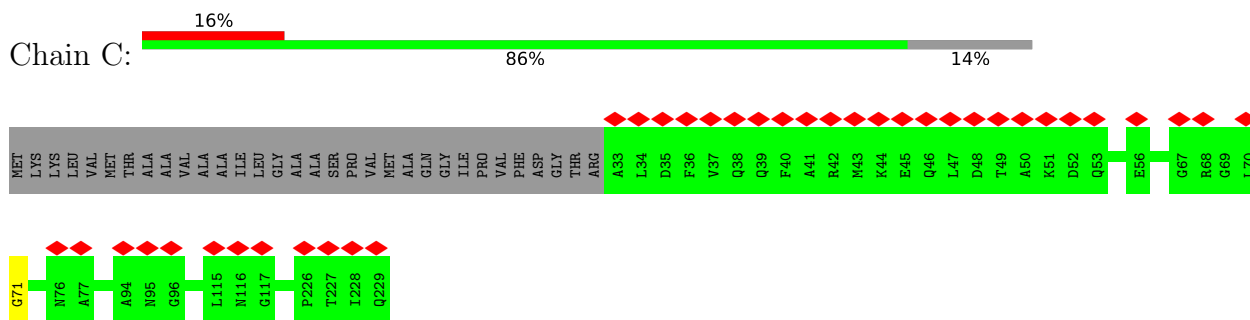
- Molecule 1: TrwJ protein



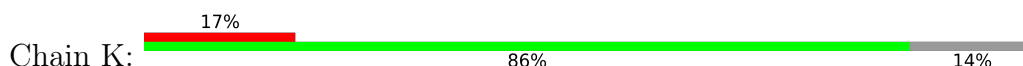
- Molecule 1: TrwJ protein



- Molecule 1: TrwJ protein



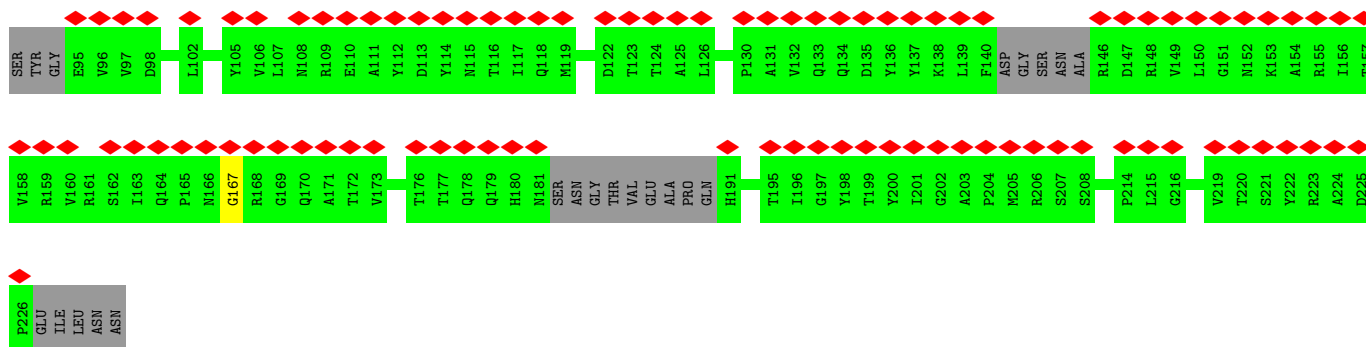
- Molecule 1: TrwJ protein



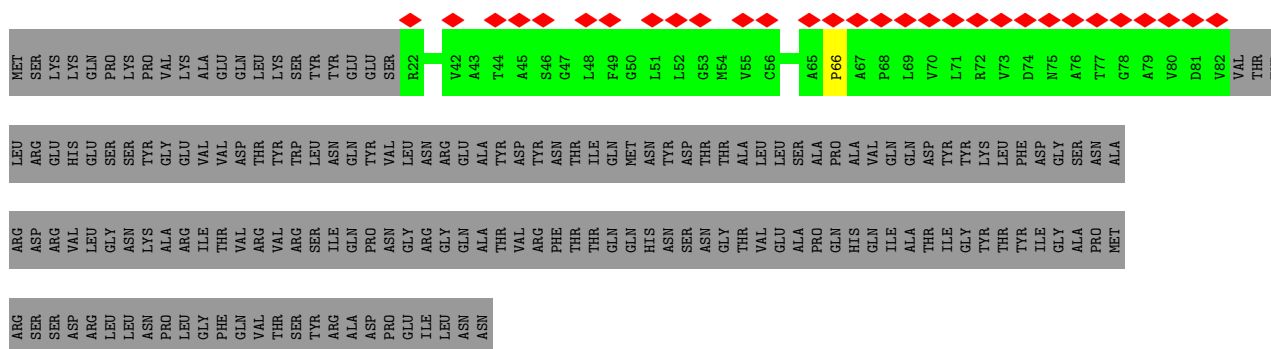




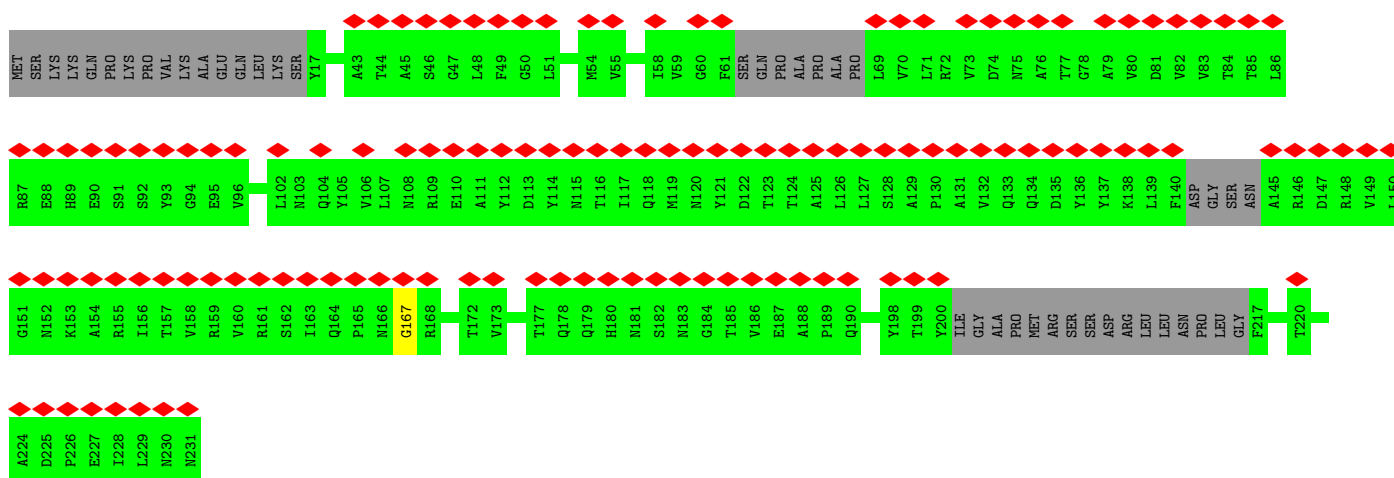
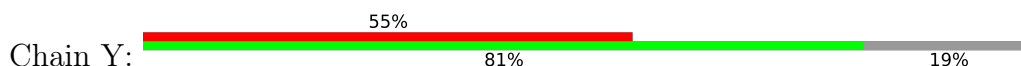




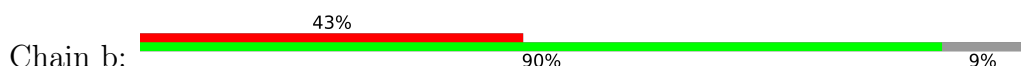
• Molecule 2: TrwG protein



• Molecule 2: TrwG protein



• Molecule 2: TrwG protein

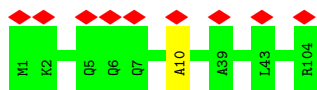




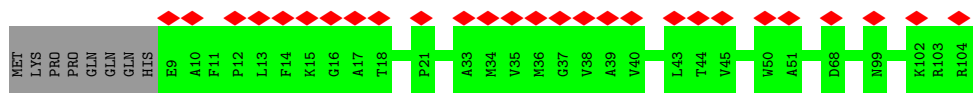
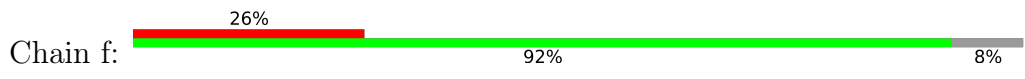




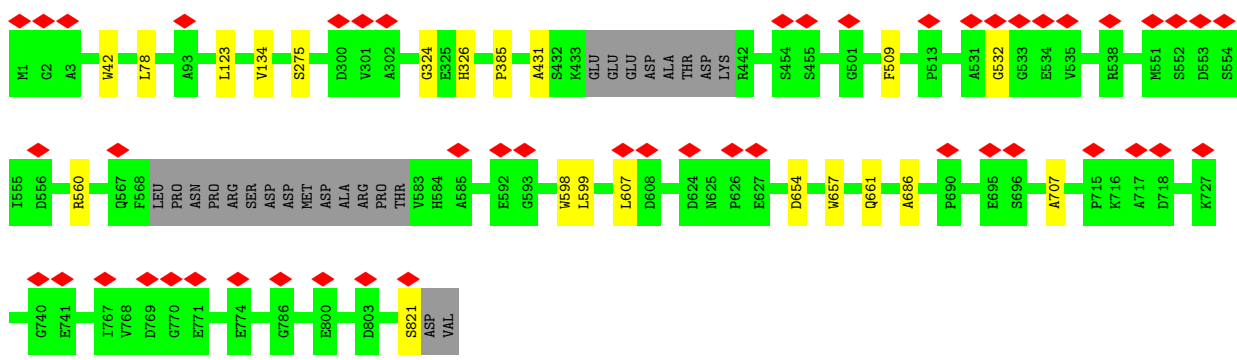
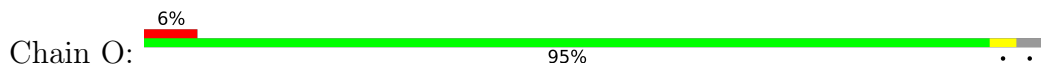




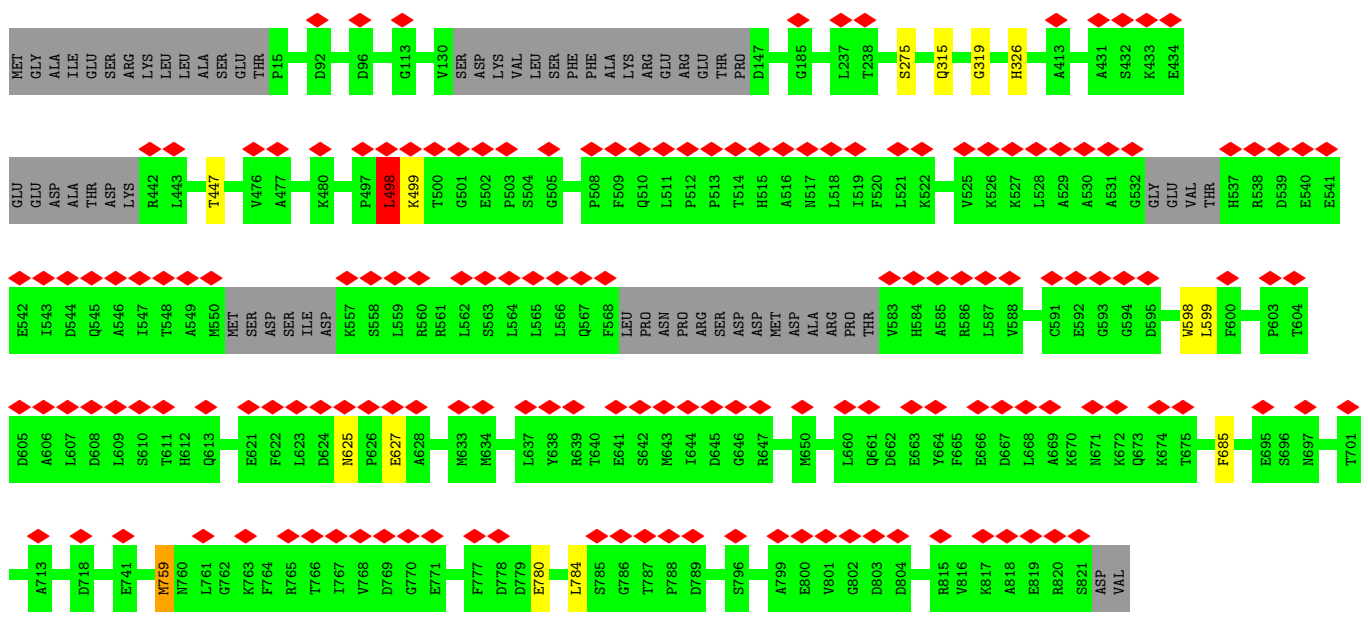
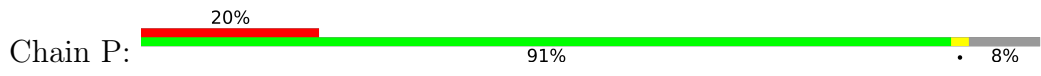
• Molecule 5: TrwM protein



• Molecule 6: Type IV secretion system protein virB4



• Molecule 6: Type IV secretion system protein virB4











## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	65173	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	57.5	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.997	Depositor
Minimum map value	-0.718	Depositor
Average map value	0.027	Depositor
Map value standard deviation	0.091	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	546.304, 546.304, 546.304	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.067, 1.067, 1.067	Depositor

## 5 Model quality

### 5.1 Standard geometry

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	0.40	0/968	0.47	0/1344
1	B	0.41	0/968	0.50	0/1344
1	C	0.41	0/968	0.47	0/1344
1	E	0.39	0/968	0.47	0/1344
1	K	0.38	0/968	0.47	0/1344
2	D	0.26	0/182	0.49	0/252
2	F	0.54	0/137	0.62	0/189
2	G	0.21	0/63	0.46	0/86
2	Q	0.44	0/852	0.79	1/1107 (0.1%)
2	S	0.45	0/972	0.75	1/1274 (0.1%)
2	U	0.52	0/835	0.78	1/1087 (0.1%)
2	X	0.51	0/296	0.56	0/408
2	Y	0.47	0/810	0.80	1/1052 (0.1%)
2	b	0.43	0/909	0.74	1/1185 (0.1%)
2	c	0.53	0/285	0.61	0/391
2	d	0.38	0/182	0.49	0/248
2	i	0.25	0/137	0.44	0/189
3	Z	0.41	0/304	0.63	0/420
3	a	0.27	0/241	0.48	0/334
3	e	0.27	0/191	0.50	0/263
4	H	0.38	0/1085	0.51	0/1502
4	I	0.37	0/1060	0.48	0/1467
4	J	0.39	0/1329	0.51	0/1841
4	L	0.36	0/1309	0.48	0/1812
4	M	0.35	0/1329	0.46	0/1841
5	R	0.29	0/514	0.49	0/715
5	f	0.29	0/474	0.49	0/659
5	j	0.29	0/514	0.49	0/715
6	O	0.35	1/3944 (0.0%)	0.52	1/5488 (0.0%)
6	P	0.40	1/3748 (0.0%)	0.81	7/5210 (0.1%)
6	T	0.35	1/3990 (0.0%)	0.52	1/5554 (0.0%)
6	V	0.38	1/3502 (0.0%)	0.82	7/4861 (0.1%)
6	g	0.36	1/3713 (0.0%)	0.52	1/5161 (0.0%)
6	h	0.29	0/2251	0.49	0/3123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
All	All	0.38	5/39998 (0.0%)	0.60	22/55154 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	E	0	1
1	K	0	1
6	P	0	2
6	V	0	2
All	All	0	8

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	V	599	LEU	C-N	6.17	1.48	1.34
6	O	599	LEU	C-N	6.14	1.48	1.34
6	g	599	LEU	C-N	6.13	1.48	1.34
6	P	599	LEU	C-N	6.13	1.48	1.34
6	T	599	LEU	C-N	6.12	1.48	1.34

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	P	759	MET	O-C-N	-31.29	72.64	122.70
6	V	759	MET	O-C-N	-31.25	72.70	122.70
6	V	759	MET	CA-C-N	19.98	161.15	117.20
6	P	759	MET	CA-C-N	19.97	161.14	117.20
6	V	498	LEU	O-C-N	-13.40	101.25	122.70

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	71	GLY	Peptide
1	C	71	GLY	Peptide
1	E	71	GLY	Peptide

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Mol	Chain	Res	Type	Group
1	K	71	GLY	Peptide
6	P	498	LEU	Mainchain

## 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	969	0	479	0	0
1	B	969	0	479	2	0
1	C	969	0	479	0	0
1	E	969	0	479	0	0
1	K	969	0	479	0	0
2	D	183	0	79	0	0
2	F	138	0	63	0	0
2	G	64	0	29	0	0
2	Q	855	0	300	1	0
2	S	973	0	349	1	0
2	U	839	0	299	0	0
2	X	297	0	147	0	0
2	Y	814	0	284	0	0
2	b	912	0	318	0	0
2	c	287	0	139	0	0
2	d	184	0	89	0	0
2	i	138	0	60	0	0
3	Z	306	0	135	6	0
3	a	242	0	113	0	0
3	e	193	0	90	0	0
4	H	1087	0	563	0	0
4	I	1062	0	544	0	0
4	J	1330	0	681	3	0
4	L	1311	0	669	8	0
4	M	1330	0	681	11	0
5	R	515	0	236	1	0
5	f	475	0	219	0	0
5	j	515	0	236	0	0
6	O	3947	0	1786	13	0
6	P	3754	0	1693	6	0
6	T	3992	0	1808	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	V	3512	0	1583	5	0
6	g	3719	0	1670	0	0
6	h	2259	0	1015	0	0
All	All	40078	0	18273	62	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 1.

The worst 5 of 62 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:O:821:SER:O	6:T:516:ALA:HB1	1.49	1.12
6:T:139:ALA:HB2	3:Z:42:PRO:O	1.49	1.12
4:M:7:THR:N	4:M:113:ALA:HB1	1.67	1.08
4:M:6:PHE:C	4:M:113:ALA:HB1	1.80	1.00
6:O:821:SER:O	6:T:516:ALA:CB	2.15	0.95

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	195/229 (85%)	194 (100%)	1 (0%)	0	100	100
1	B	195/229 (85%)	193 (99%)	2 (1%)	0	100	100
1	C	195/229 (85%)	194 (100%)	1 (0%)	0	100	100
1	E	195/229 (85%)	194 (100%)	1 (0%)	0	100	100
1	K	195/229 (85%)	193 (99%)	2 (1%)	0	100	100
2	D	35/231 (15%)	32 (91%)	3 (9%)	0	100	100
2	F	26/231 (11%)	25 (96%)	1 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	G	11/231 (5%)	8 (73%)	3 (27%)	0	100	100
2	Q	192/231 (83%)	184 (96%)	6 (3%)	2 (1%)	15	54
2	S	221/231 (96%)	209 (95%)	11 (5%)	1 (0%)	29	68
2	U	185/231 (80%)	178 (96%)	7 (4%)	0	100	100
2	X	59/231 (26%)	49 (83%)	9 (15%)	1 (2%)	9	43
2	Y	180/231 (78%)	177 (98%)	3 (2%)	0	100	100
2	b	204/231 (88%)	195 (96%)	9 (4%)	0	100	100
2	c	55/231 (24%)	54 (98%)	1 (2%)	0	100	100
2	d	34/231 (15%)	28 (82%)	6 (18%)	0	100	100
2	i	26/231 (11%)	25 (96%)	1 (4%)	0	100	100
3	Z	58/395 (15%)	54 (93%)	4 (7%)	0	100	100
3	a	47/395 (12%)	45 (96%)	2 (4%)	0	100	100
3	e	35/395 (9%)	35 (100%)	0	0	100	100
4	H	218/342 (64%)	209 (96%)	9 (4%)	0	100	100
4	I	213/342 (62%)	207 (97%)	6 (3%)	0	100	100
4	J	270/342 (79%)	258 (96%)	12 (4%)	0	100	100
4	L	264/342 (77%)	255 (97%)	9 (3%)	0	100	100
4	M	270/342 (79%)	257 (95%)	13 (5%)	0	100	100
5	R	102/104 (98%)	91 (89%)	11 (11%)	0	100	100
5	f	94/104 (90%)	84 (89%)	10 (11%)	0	100	100
5	j	102/104 (98%)	91 (89%)	11 (11%)	0	100	100
6	O	793/823 (96%)	736 (93%)	55 (7%)	2 (0%)	41	76
6	P	748/823 (91%)	705 (94%)	43 (6%)	0	100	100
6	T	804/823 (98%)	745 (93%)	59 (7%)	0	100	100
6	V	691/823 (84%)	653 (94%)	38 (6%)	0	100	100
6	g	741/823 (90%)	689 (93%)	52 (7%)	0	100	100
6	h	441/823 (54%)	415 (94%)	26 (6%)	0	100	100
All	All	8094/12062 (67%)	7661 (95%)	427 (5%)	6 (0%)	54	85

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Q	63	GLN

Continued on next page...



*Continued from previous page...*

Mol	Chain	Res	Type
2	S	64	PRO
6	O	607	LEU
2	Q	66	PRO
2	X	66	PRO

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

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 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-19488. These allow visual inspection of the internal detail of the map and identification of artifacts.

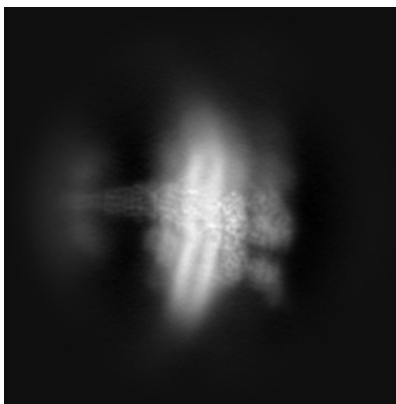
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

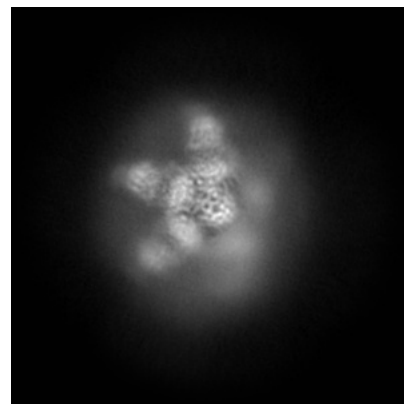
#### 6.1.1 Primary map



X

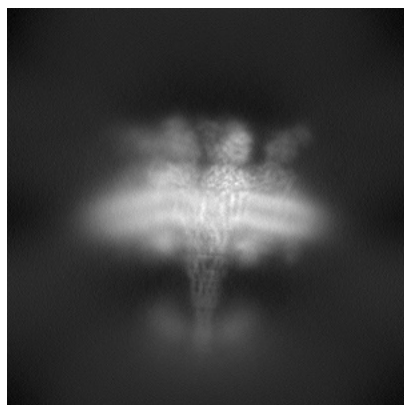


Y

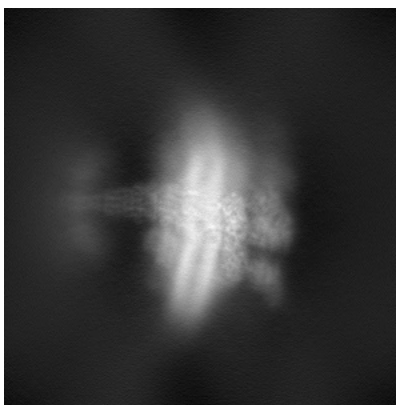


Z

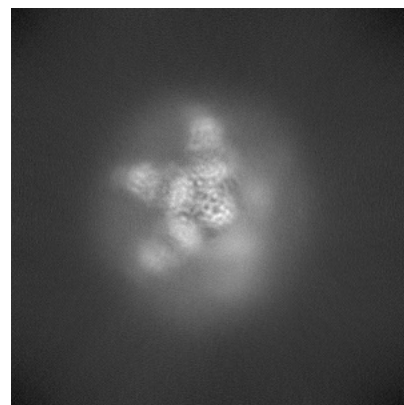
#### 6.1.2 Raw map



X



Y

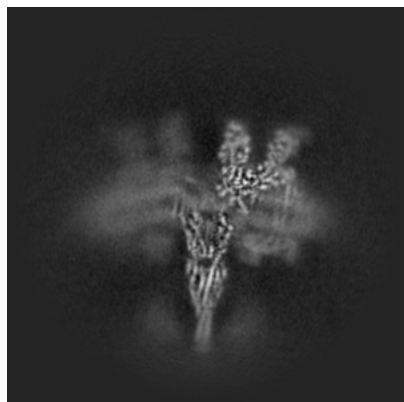


Z

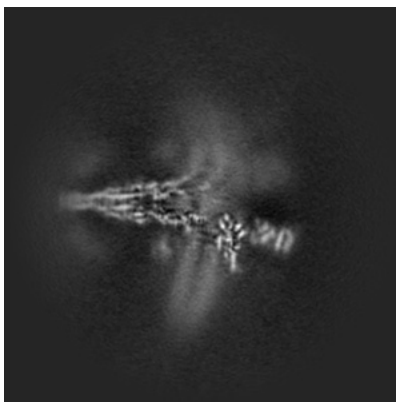
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

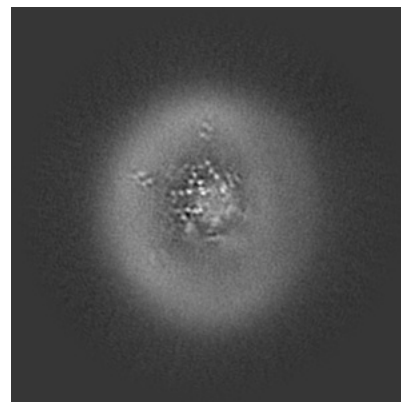
### 6.2.1 Primary map



X Index: 256

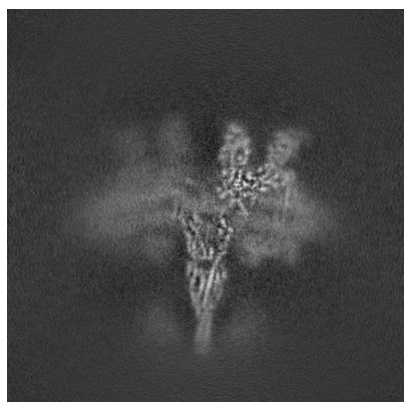


Y Index: 256

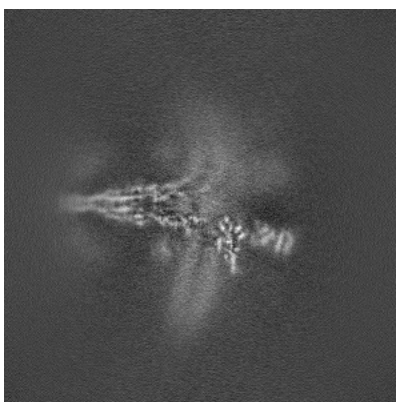


Z Index: 256

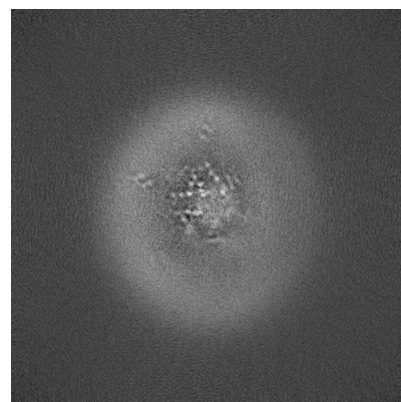
### 6.2.2 Raw map



X Index: 256



Y Index: 256

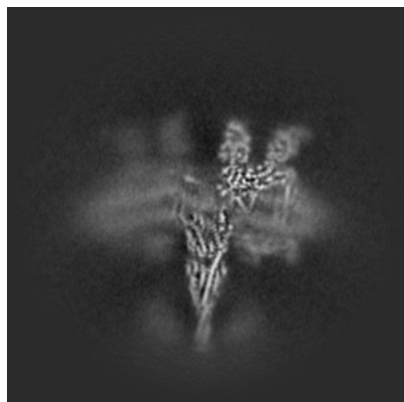


Z Index: 256

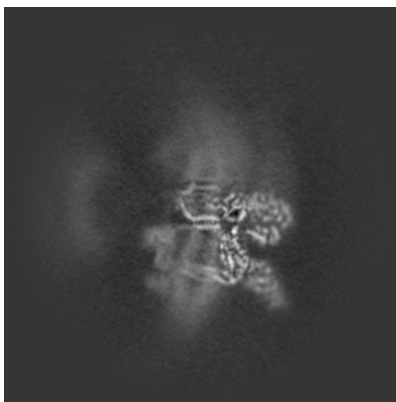
The images above show central slices of the map in three orthogonal directions.

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

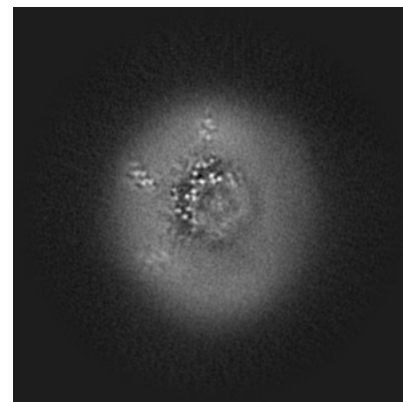
### 6.3.1 Primary map



X Index: 254

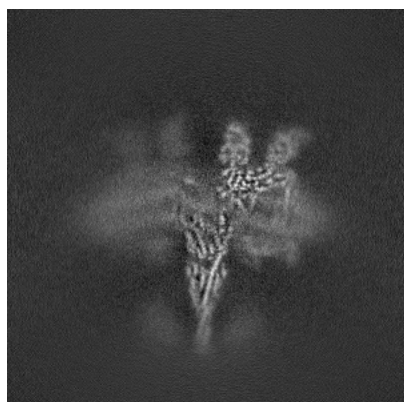


Y Index: 288

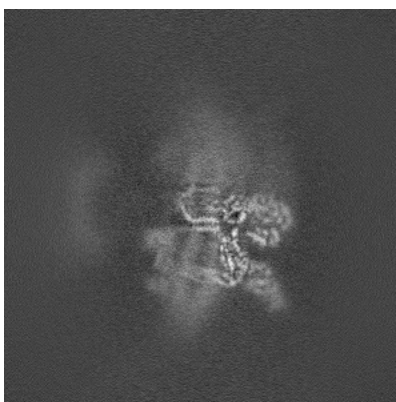


Z Index: 266

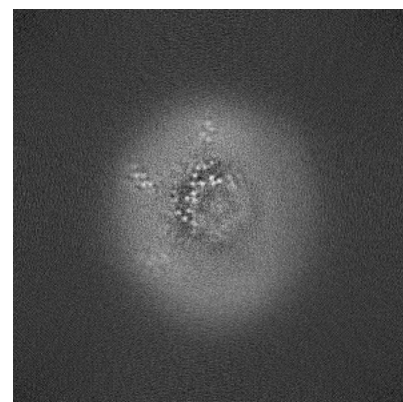
### 6.3.2 Raw map



X Index: 254



Y Index: 288

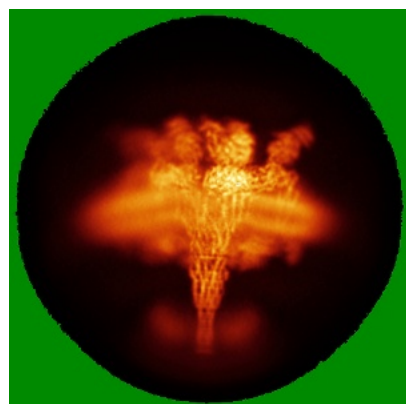


Z Index: 266

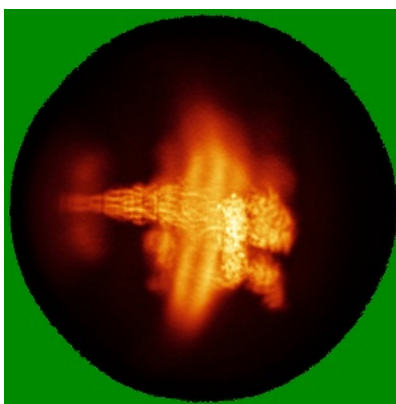
The images above show the largest variance slices of the map in three orthogonal directions.

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

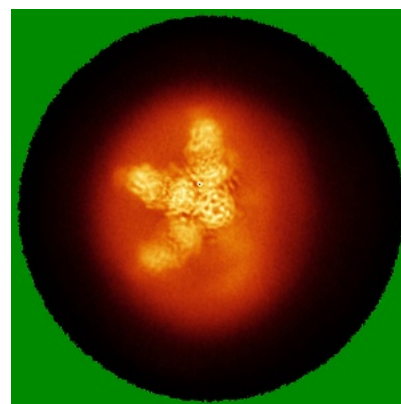
### 6.4.1 Primary map



X



Y

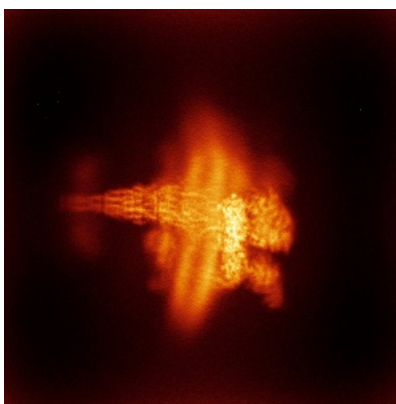


Z

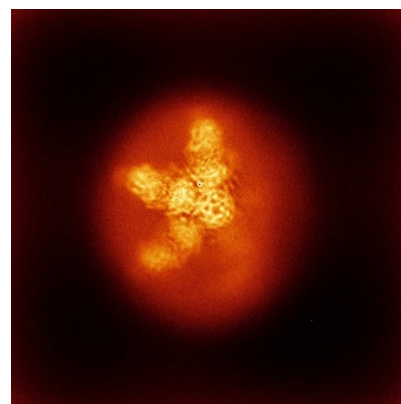
### 6.4.2 Raw map



X



Y

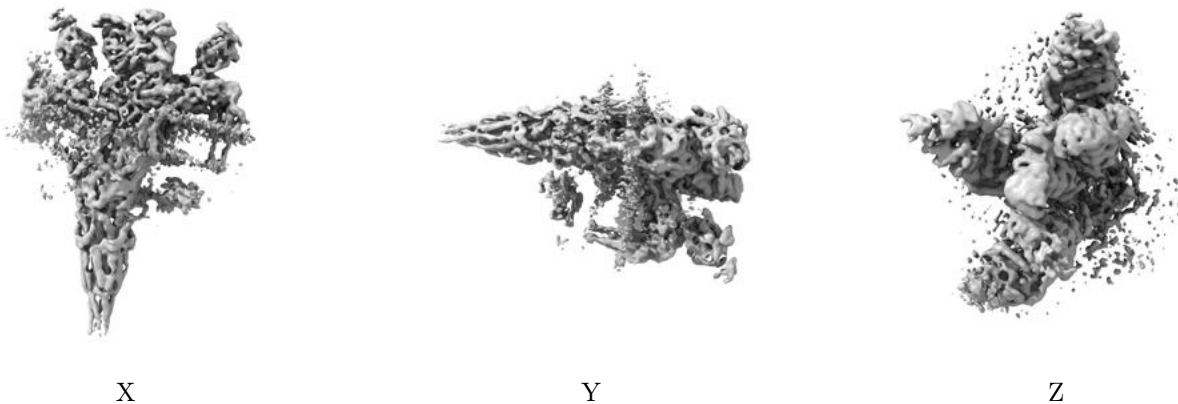


Z

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.

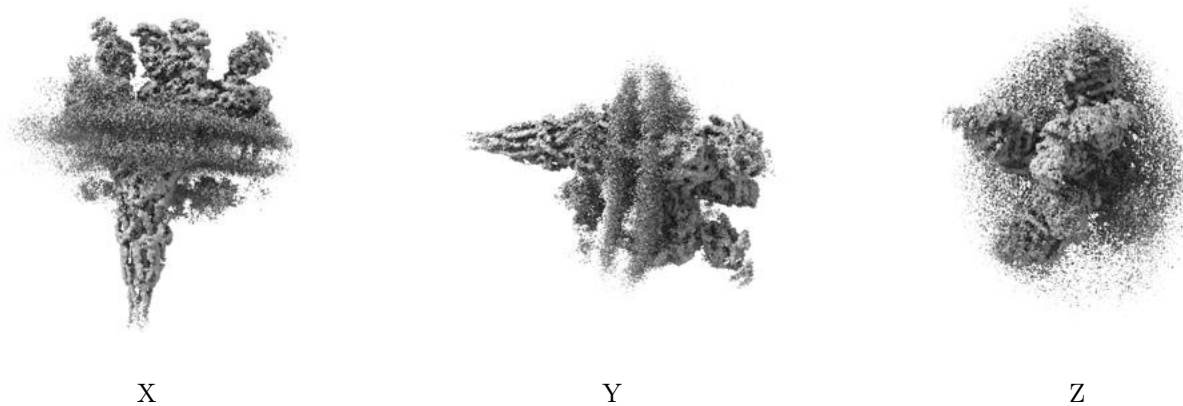
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.6. 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.

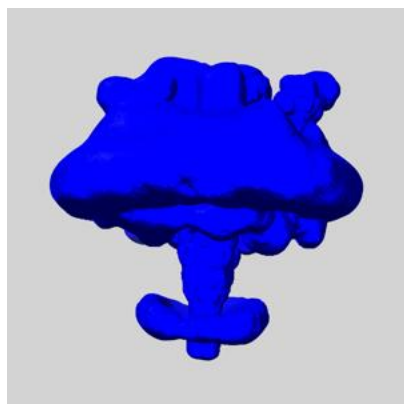
## 6.6 Mask visualisation [i](#)

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

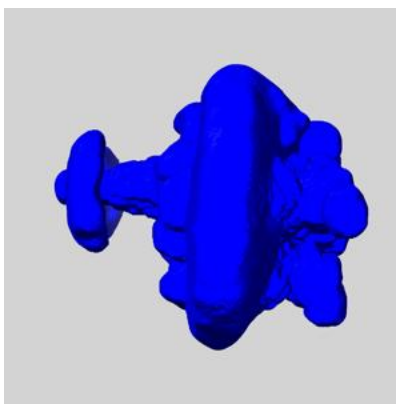
A mask typically either:

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

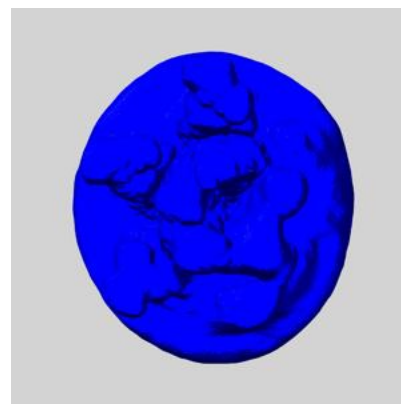
### 6.6.1 emd\_19488\_msk\_1.map [i](#)



X



Y

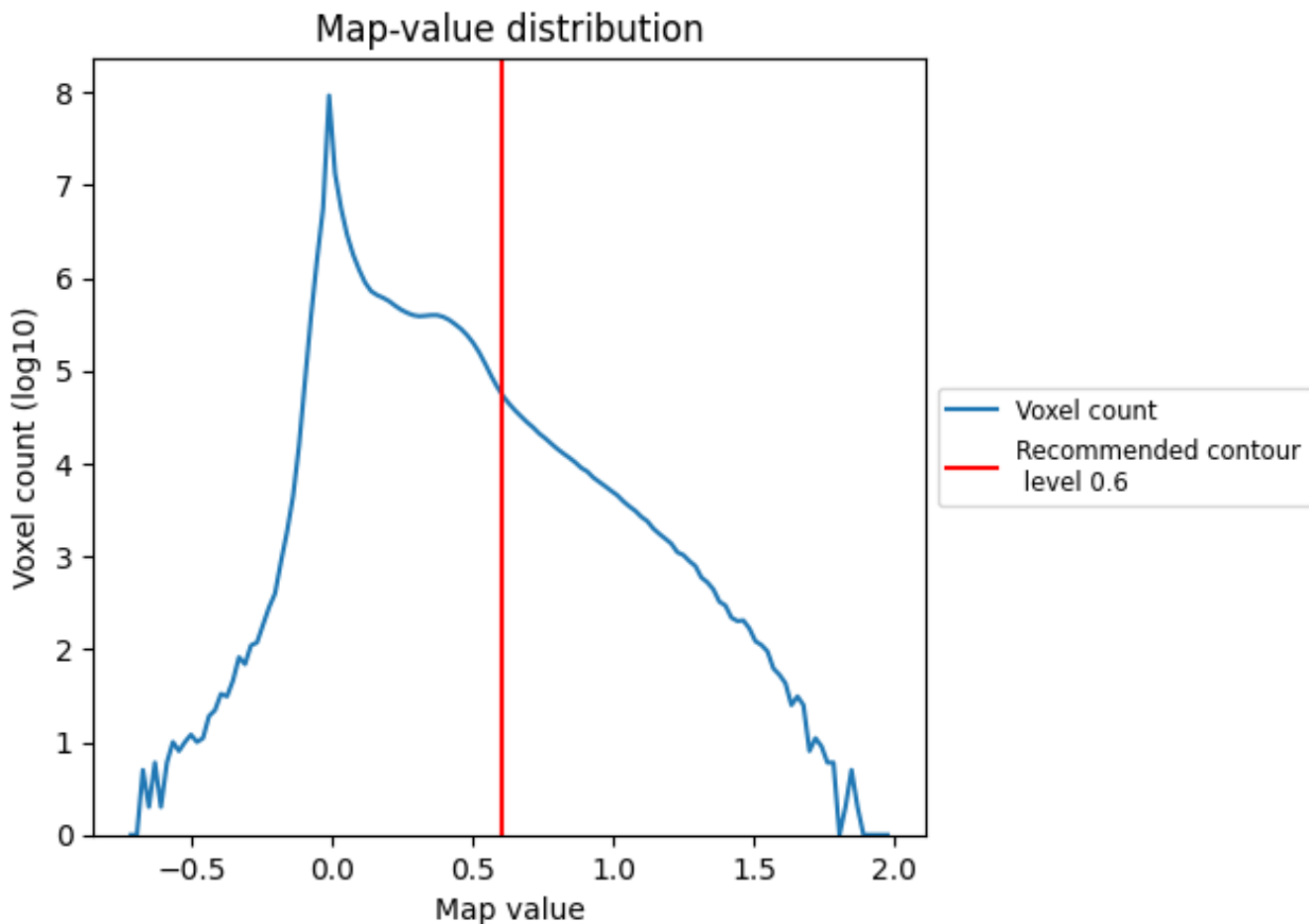


Z

## 7 Map analysis [i](#)

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

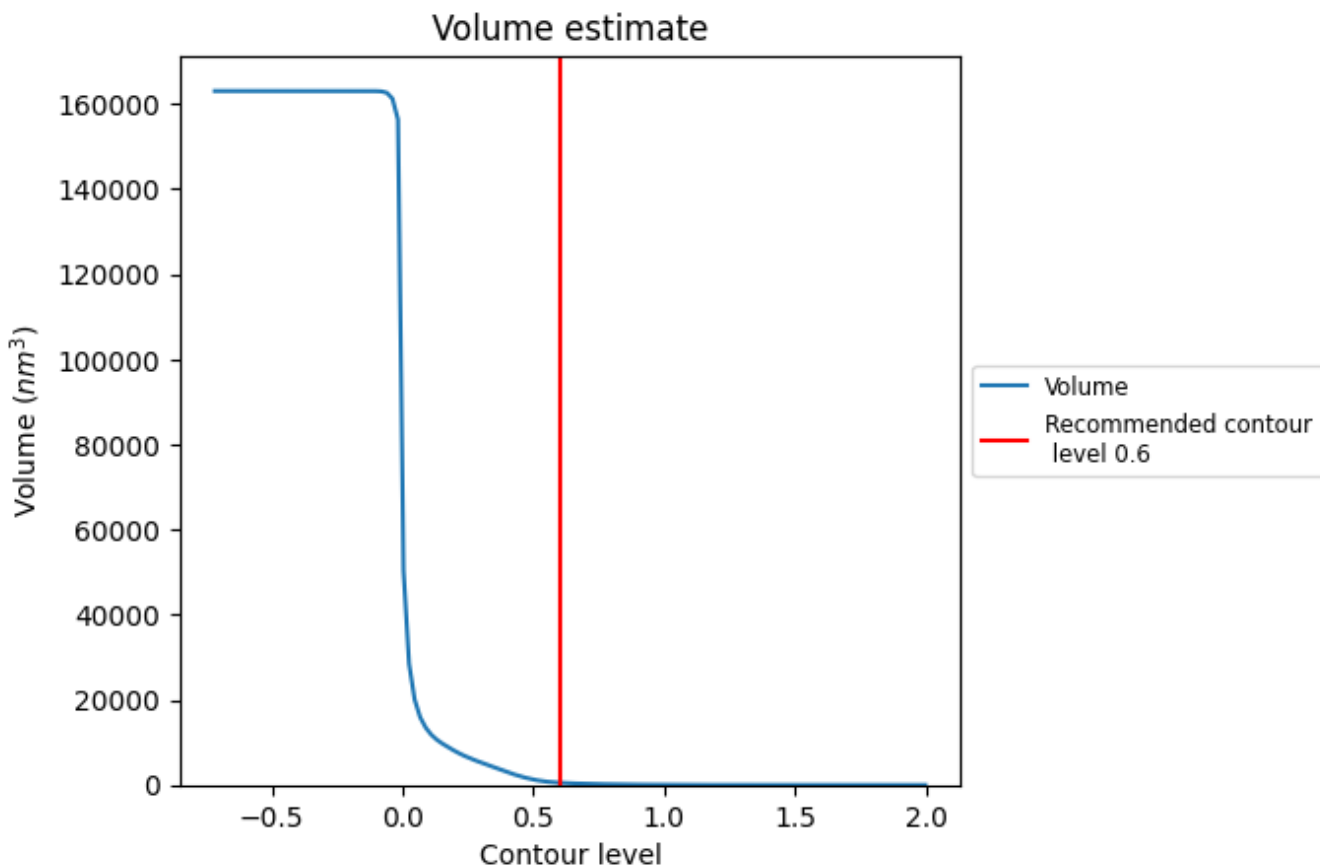
### 7.1 Map-value distribution [i](#)



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.



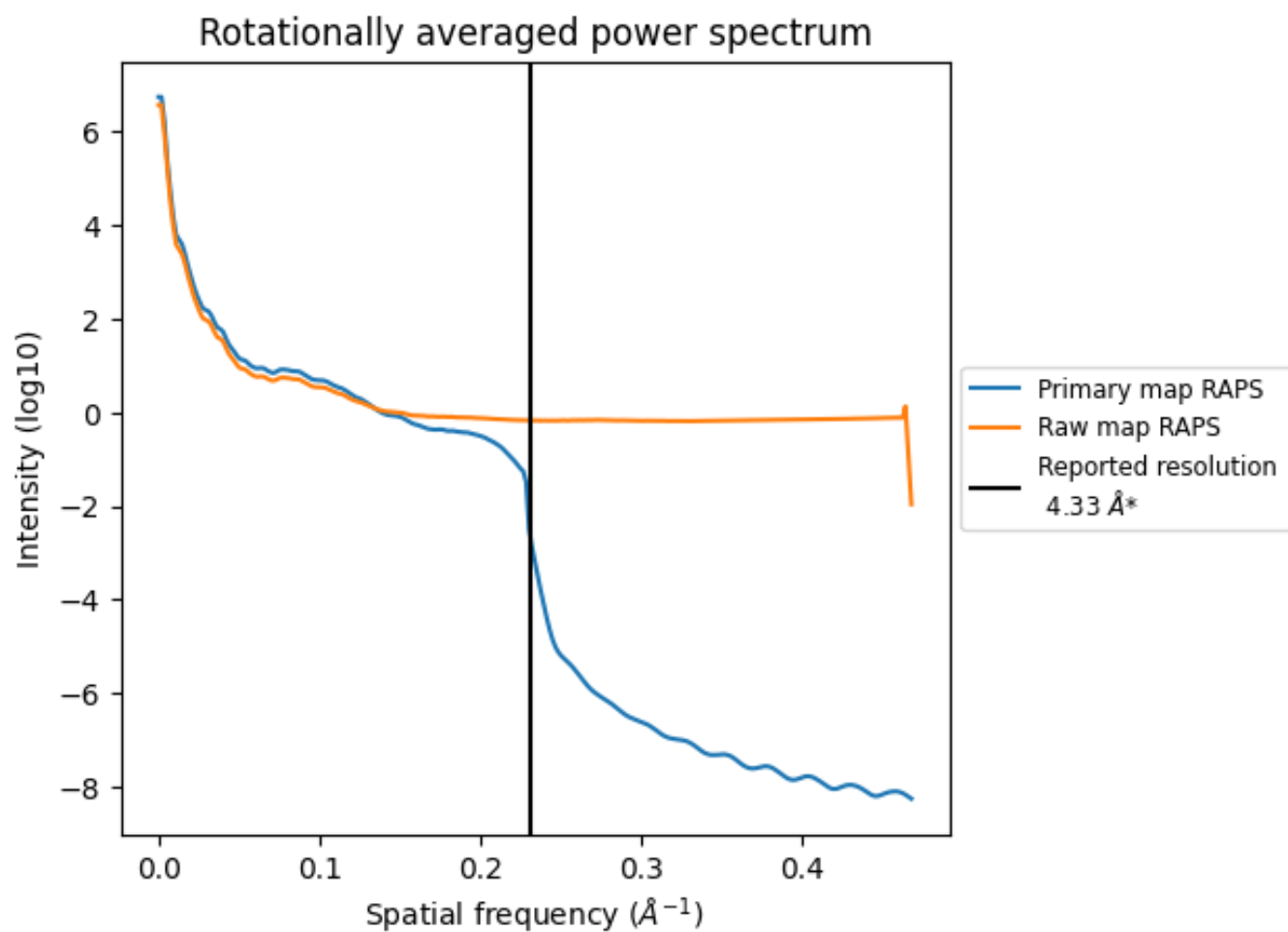
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 513  $\text{nm}^3$ ; this corresponds to an approximate mass of 464 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

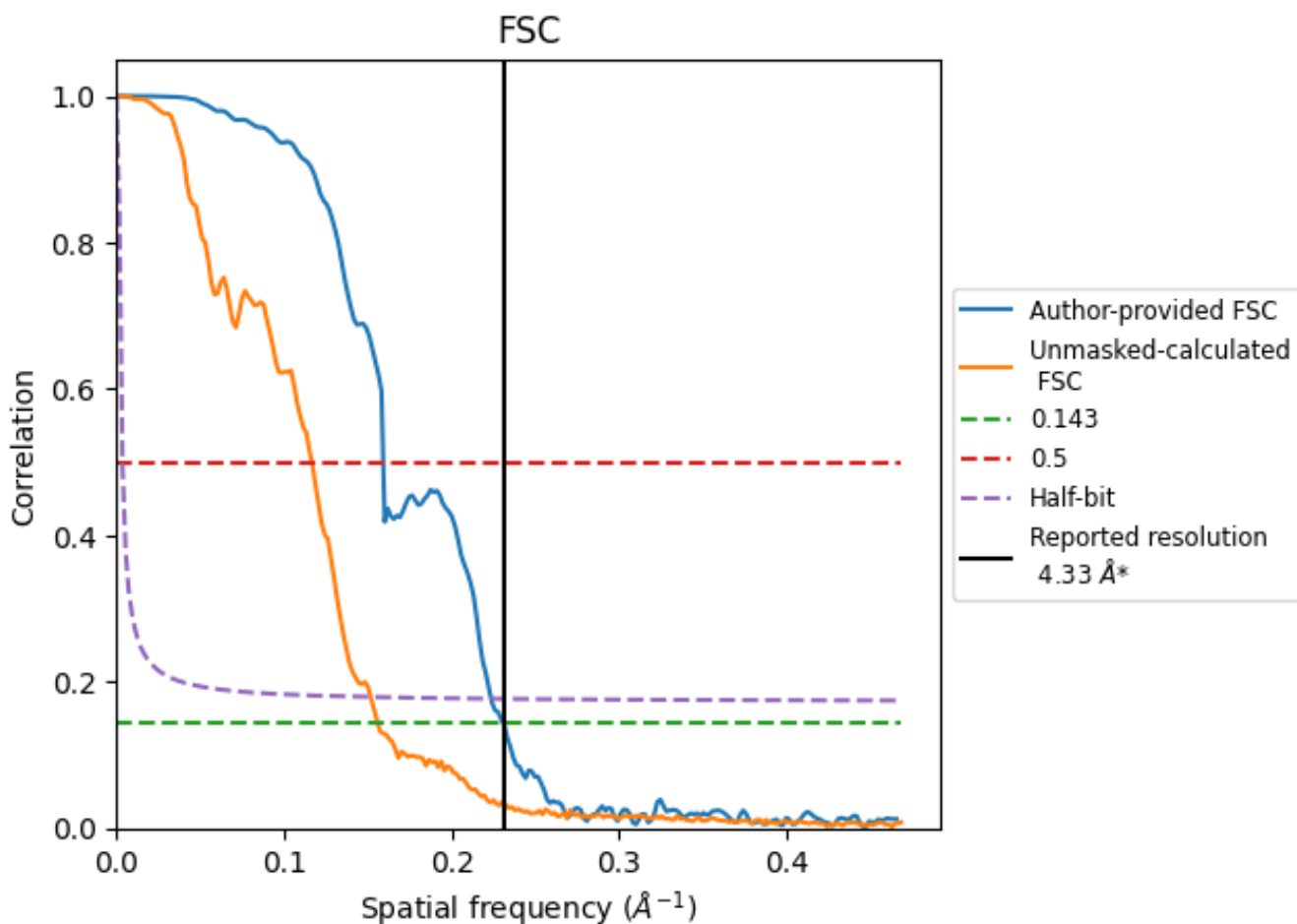


\*Reported resolution corresponds to spatial frequency of 0.231 Å<sup>-1</sup>

## 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 0.231 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

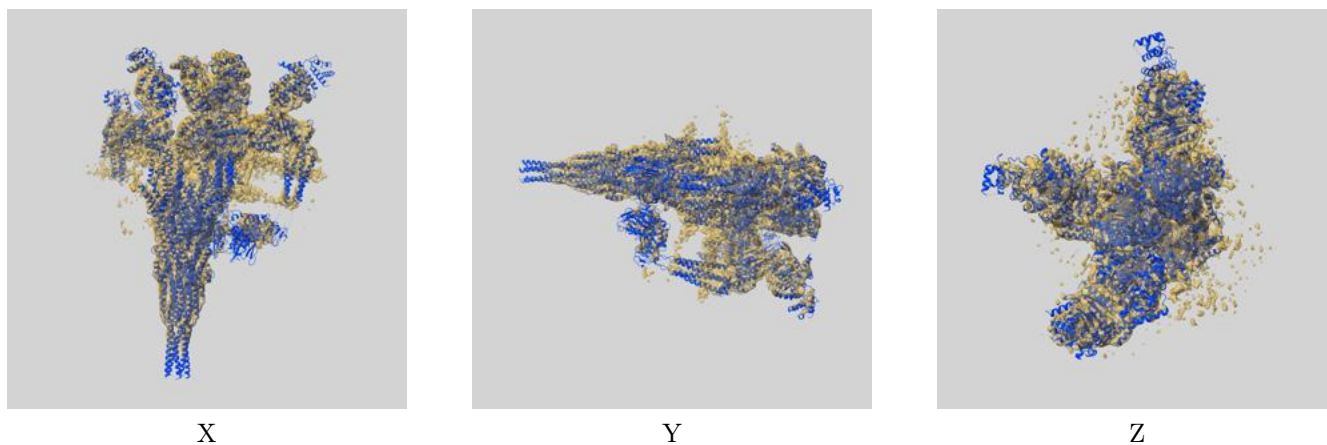
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.33	-	-
Author-provided FSC curve	4.33	6.28	4.47
Unmasked-calculated*	6.41	8.58	6.58

\*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 6.41 differs from the reported value 4.33 by more than 10 %

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

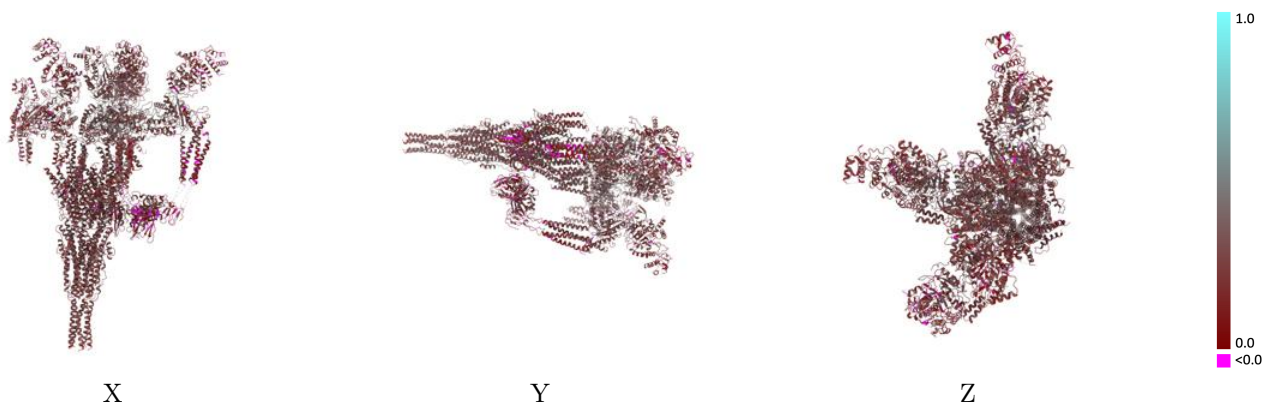
This section contains information regarding the fit between EMDB map EMD-19488 and PDB model 8RTD. Per-residue inclusion information can be found in section 3 on page 7.

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



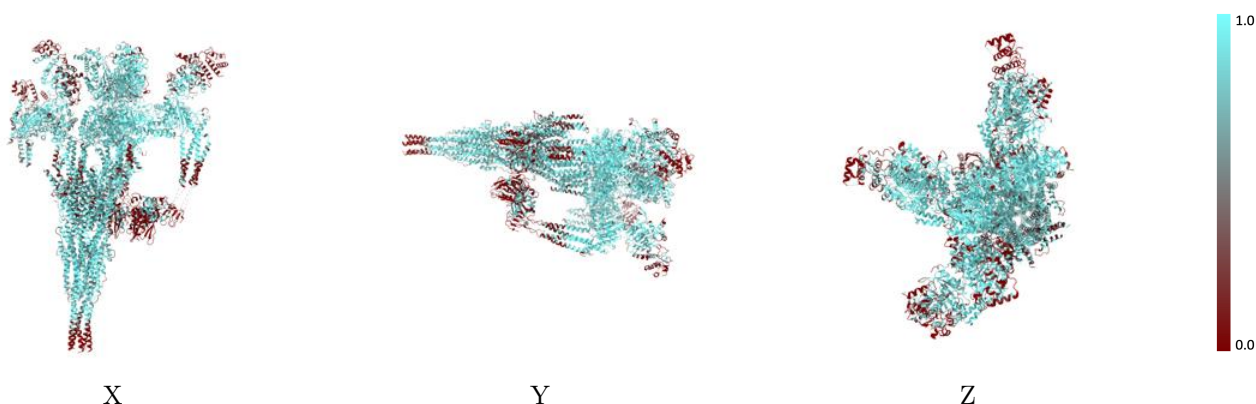
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



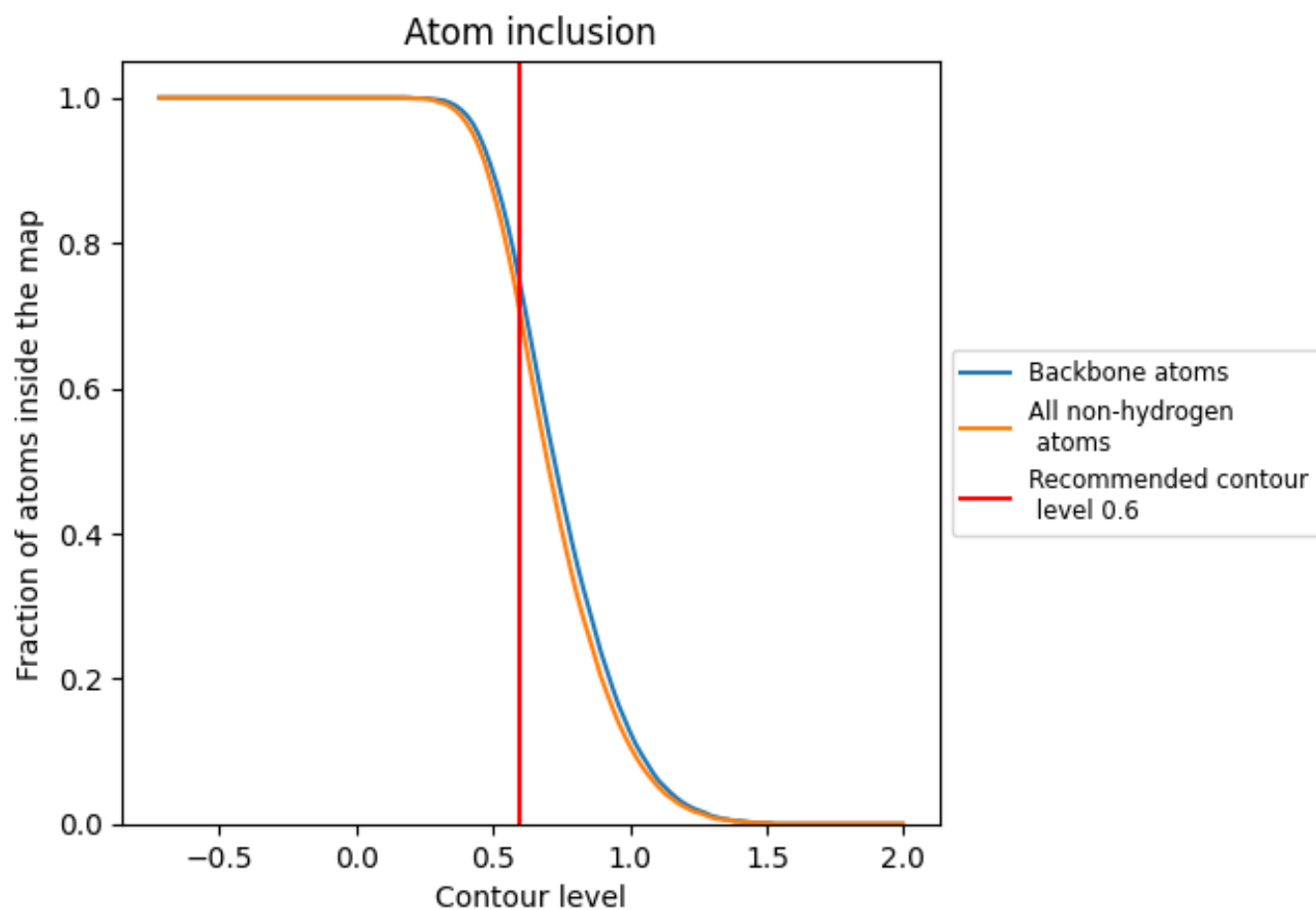
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 70% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7020	 0.2670
A	 0.7390	 0.2840
B	 0.7550	 0.2990
C	 0.7060	 0.2950
D	 0.6180	 0.1890
E	 0.7220	 0.2770
F	 0.7460	 0.2080
G	 0.7030	 0.2230
H	 0.7280	 0.2590
I	 0.6360	 0.2490
J	 0.7100	 0.2510
K	 0.7350	 0.2820
L	 0.8560	 0.2990
M	 0.8330	 0.3000
O	 0.8940	 0.3280
P	 0.7600	 0.2720
Q	 0.4100	 0.2250
R	 0.8520	 0.3080
S	 0.5180	 0.2200
T	 0.8420	 0.3070
U	 0.3150	 0.1880
V	 0.6630	 0.2660
X	 0.4440	 0.1730
Y	 0.3210	 0.1700
Z	 0.7060	 0.2860
a	 0.5700	 0.2590
b	 0.4710	 0.2070
c	 0.5050	 0.1330
d	 0.3640	 0.1210
e	 0.5860	 0.2780
f	 0.6950	 0.2640
g	 0.6510	 0.2500
h	 0.5530	 0.2110
i	 0.6740	 0.1940
j	 0.8760	 0.3330

