



## Full wwPDB EM Validation Report ⓘ

Nov 12, 2024 – 04:19 AM EST

PDB ID : 8GAT  
EMDB ID : EMD-29907  
Title : Structure of human NDS.1 Fab and 1G01 Fab in complex with influenza virus neuraminidase from A/Indiana/10/2011 (H3N2v), based on consensus cryo-EM map with only Fab 1G01 resolved  
Authors : Tsybovsky, Y.; Lederhofer, J.; Kwong, P.D.; Kanekiyo, M.  
Deposited on : 2023-02-23  
Resolution : 3.00 Å(reported)  
Based on initial model : .

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.dev113  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4.02b-467  
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) : 2.39

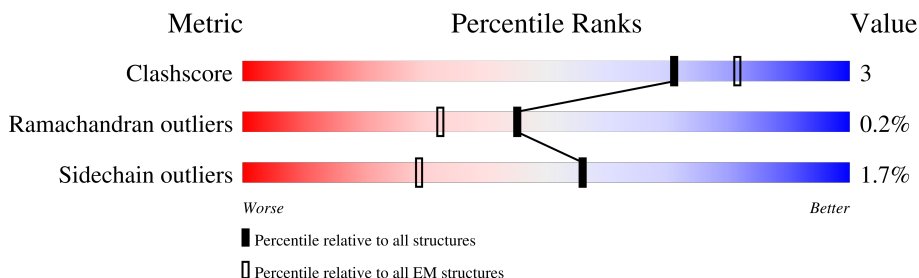
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.00 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

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	466	<div> <div>42%</div> <div>80%</div> <div>17%</div> </div>
2	M	240	<div> <div>41%</div> <div>44%</div> <div>7%</div> <div>47%</div> </div>
3	N	216	<div> <div>42%</div> <div>47%</div> <div>50%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4874 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 Vasodilator-stimulated phosphoprotein, Neuraminidase chimera.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	386	2987	1856	529	579	23	0	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	MET	-	expression tag	UNP P50552
A	5	GLU	-	expression tag	UNP P50552
A	6	PHE	-	expression tag	UNP P50552
A	7	GLY	-	expression tag	UNP P50552
A	8	LEU	-	expression tag	UNP P50552
A	9	SER	-	expression tag	UNP P50552
A	10	TRP	-	expression tag	UNP P50552
A	11	ILE	-	expression tag	UNP P50552
A	12	PHE	-	expression tag	UNP P50552
A	13	LEU	-	expression tag	UNP P50552
A	14	ALA	-	expression tag	UNP P50552
A	15	ALA	-	expression tag	UNP P50552
A	16	ILE	-	expression tag	UNP P50552
A	17	LEU	-	expression tag	UNP P50552
A	18	LYS	-	expression tag	UNP P50552
A	19	GLY	-	expression tag	UNP P50552
A	20	VAL	-	expression tag	UNP P50552
A	21	GLN	-	expression tag	UNP P50552
A	22	CYS	-	expression tag	UNP P50552
A	23	ALA	-	expression tag	UNP P50552
A	24	ASP	-	expression tag	UNP P50552
A	25	PRO	-	expression tag	UNP P50552
A	26	HIS	-	expression tag	UNP P50552
A	27	HIS	-	expression tag	UNP P50552
A	28	HIS	-	expression tag	UNP P50552
A	29	HIS	-	expression tag	UNP P50552
A	30	HIS	-	expression tag	UNP P50552

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Chain	Residue	Modelled	Actual	Comment	Reference
A	31	HIS	-	expression tag	UNP P50552
A	71	LYS	-	linker	UNP P50552
A	72	ARG	-	linker	UNP P50552
A	73	GLY	-	linker	UNP P50552
A	74	SER	-	linker	UNP P50552
A	75	LEU	-	linker	UNP P50552
A	76	VAL	-	linker	UNP P50552
A	77	PRO	-	linker	UNP P50552
A	78	ARG	-	linker	UNP P50552
A	79	GLY	-	linker	UNP P50552
A	80	SER	-	linker	UNP P50552
A	81	GLY	-	linker	UNP P50552
A	82	GLY	-	linker	UNP P50552

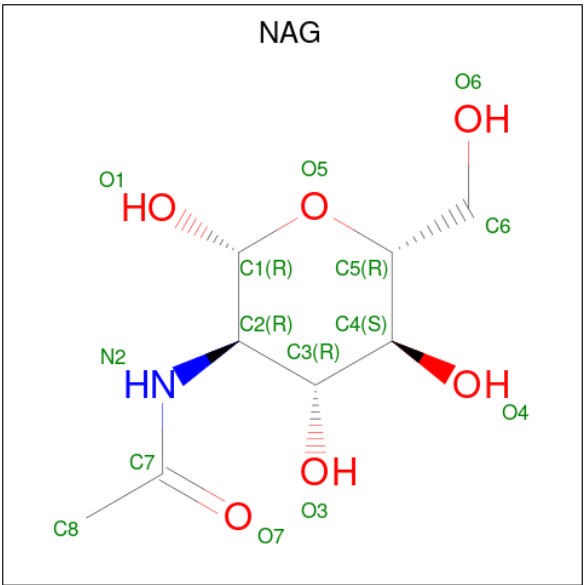
- Molecule 2 is a protein called Fab 1G01, heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	M	127	Total	C	N	O	S	0	0
			998	635	174	186	3		

- Molecule 3 is a protein called Fab 1G01, light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	108	Total	C	N	O	S	0	0
			833	534	135	162	2		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	



THR VAL PRO SER SER SER LEU GLY THR THR THR TYR TYR ILE CYS ASN VAL ASN HIS HIS LYS PRO SER SER ASN THR LYS VAL ASP LYS ARG VAL GLU PRO LYS SER CYS HIS HIS HIS HIS HIS

● Molecule 3: Fab 1G01, light chain



ASP D1 I2 Q3 L4 T5 Q6 S7 P8 S9 F10 L11 S12 A13 S14 V15 G16 D17 R18 I19 T20 T21 T22 C23 R24 A25 S26 Q27 G28 I29 D30 Q37 Q38 R39 P40 G41 K42 A43 P44 M45 L46 L47 A51 S52 L53 L54 Q55 S56 G57 V58 P59 S60 R61 F62 S63 G66 Y67

G68 T69 E70 F71 T72 L73 T74 I75 S76 S77 L78 Q79 P80 E81 D82 F83 A84 T85 Y86 Y87 C88 Q89 H90 L91 D92 S93 Y94 P95 L95A F96 F97 F98 G99 P100 G101 T102 K103 V104 D105 I106 K107 ARG THR VAL ALA ALA PRO SER VAL PHE PHE PRO PRO SER ASP GLN LEU LYS

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

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

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	62699	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	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.680	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	355.2, 355.2, 355.2	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.11, 1.11, 1.11	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: NAG

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	0.33	0/3056	0.56	0/4144
2	M	0.34	0/1026	0.68	1/1394 (0.1%)
3	N	0.30	0/855	0.55	0/1164
All	All	0.33	0/4937	0.58	1/6702 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	52	ASN	CB-CA-C	-5.42	99.57	110.40

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	A	2987	0	2841	7	0
2	M	998	0	960	22	0
3	N	833	0	808	2	0
4	A	56	0	52	0	0
All	All	4874	0	4661	31	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 3.

All (31) 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:M:28:LYS:HG3	2:M:30:ASP:OD1	1.50	1.10
2:M:28:LYS:CG	2:M:30:ASP:OD1	2.14	0.95
2:M:28:LYS:HG2	2:M:31:ASP:OD2	1.76	0.85
2:M:28:LYS:CD	2:M:30:ASP:OD1	2.25	0.84
2:M:52:ASN:O	2:M:71:ARG:NH2	2.11	0.83
2:M:51:LEU:HD11	2:M:71:ARG:HB2	1.75	0.67
2:M:52:ASN:HD22	2:M:56:ILE:HB	1.61	0.64
2:M:28:LYS:HD3	2:M:30:ASP:OD1	2.04	0.58
2:M:20:LEU:HD12	2:M:80:LEU:HD23	1.90	0.53
2:M:52:ASN:HD21	2:M:56:ILE:HD12	1.75	0.52
2:M:51:LEU:HD21	2:M:71:ARG:HE	1.74	0.52
2:M:32:TYR:HE2	2:M:94:ARG:HH21	1.56	0.52
1:A:177:ALA:HB2	1:A:193:CYS:HB3	1.95	0.48
1:A:151:ASP:O	1:A:156:ARG:NH1	2.47	0.48
2:M:52:ASN:ND2	2:M:56:ILE:HB	2.27	0.47
1:A:217:SER:OG	1:A:243:ASP:OD2	2.28	0.47
2:M:52(A):TRP:CD1	2:M:52(A):TRP:C	2.88	0.46
2:M:28:LYS:HG2	2:M:31:ASP:CG	2.36	0.46
3:N:6:GLN:HG3	3:N:101:GLY:H	1.81	0.45
2:M:12:LEU:HD13	2:M:18:LEU:HD23	2.00	0.44
2:M:39:GLN:HB2	2:M:45:LEU:HD23	2.00	0.43
2:M:35:SER:HG	2:M:100(M):PHE:HE1	1.66	0.43
1:A:466:LEU:HD23	1:A:466:LEU:HA	1.79	0.43
1:A:255:LEU:HG	1:A:265:ILE:HG12	2.00	0.43
2:M:52(A):TRP:HA	2:M:71:ARG:HH12	1.84	0.42
2:M:28:LYS:HE3	2:M:28:LYS:HB2	1.61	0.42
3:N:37:GLN:HG3	3:N:86:TYR:HE1	1.84	0.42
2:M:10:ARG:NH2	2:M:11:ALA:O	2.53	0.42
2:M:78:LEU:HD23	2:M:78:LEU:HA	1.89	0.42
1:A:352:TRP:NE1	1:A:374:TYR:OH	2.51	0.41
1:A:226:GLN:HE21	1:A:240:VAL:H	1.68	0.40

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	A	384/466 (82%)	357 (93%)	27 (7%)	0	100	100
2	M	125/240 (52%)	112 (90%)	12 (10%)	1 (1%)	16	51
3	N	106/216 (49%)	98 (92%)	8 (8%)	0	100	100
All	All	615/922 (67%)	567 (92%)	47 (8%)	1 (0%)	45	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	M	56	ILE

### 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	A	334/404 (83%)	333 (100%)	1 (0%)	91	96
2	M	105/204 (52%)	99 (94%)	6 (6%)	17	49
3	N	91/188 (48%)	89 (98%)	2 (2%)	47	76
All	All	530/796 (67%)	521 (98%)	9 (2%)	56	81

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	292	ARG
2	M	28	LYS

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Mol	Chain	Res	Type
2	M	51	LEU
2	M	52	ASN
2	M	52(A)	TRP
2	M	55	ASP
2	M	78	LEU
3	N	61	ARG
3	N	89	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	294	ASN
2	M	52	ASN

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

4 ligands 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
4	NAG	A	503	1	14,14,15	0.49	0	17,19,21	0.60	0
4	NAG	A	504	1	14,14,15	0.37	0	17,19,21	0.56	0
4	NAG	A	501	1	14,14,15	0.44	0	17,19,21	0.63	0
4	NAG	A	502	1	14,14,15	0.47	0	17,19,21	0.43	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
4	NAG	A	503	1	-	2/6/23/26	0/1/1/1
4	NAG	A	504	1	-	0/6/23/26	0/1/1/1
4	NAG	A	501	1	-	0/6/23/26	0/1/1/1
4	NAG	A	502	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	503	NAG	O5-C5-C6-O6
4	A	503	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

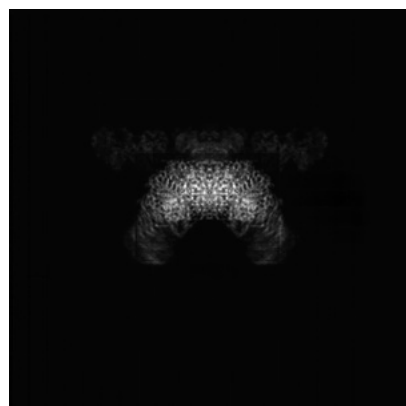
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29907. These allow visual inspection of the internal detail of the map and identification of artifacts.

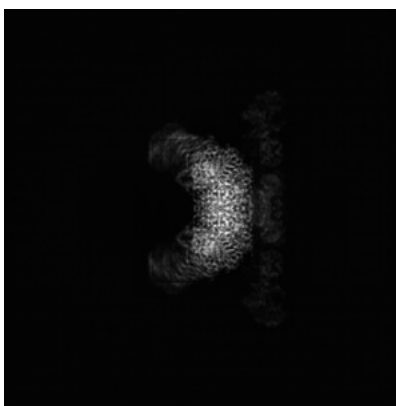
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

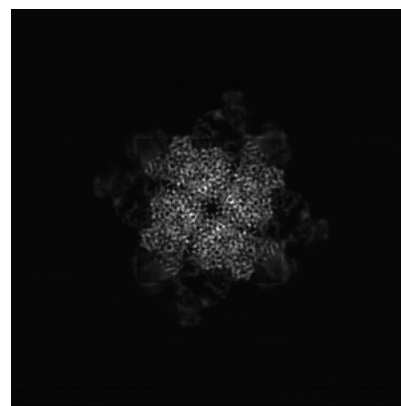
#### 6.1.1 Primary map



X

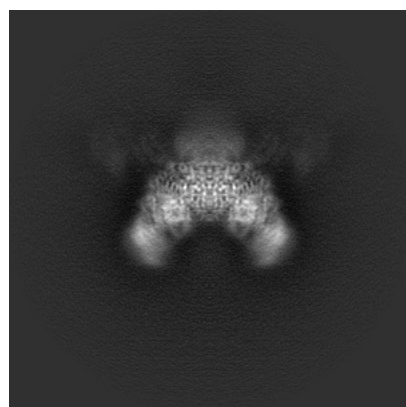


Y

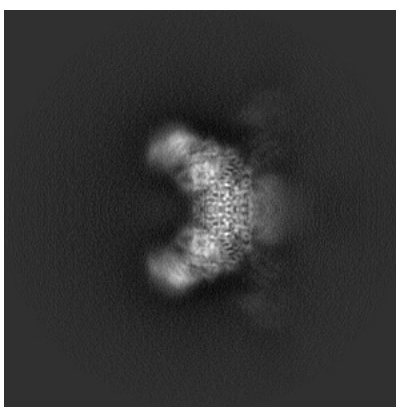


Z

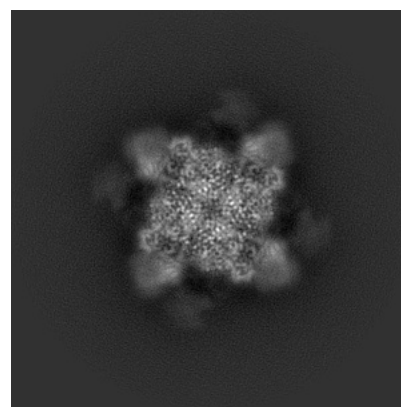
#### 6.1.2 Raw map



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: 160

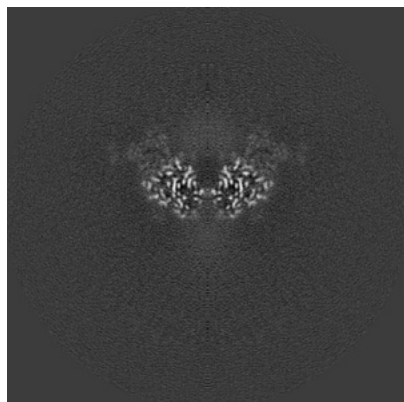


Y Index: 160

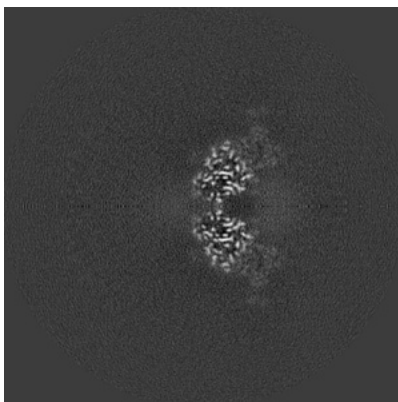


Z Index: 160

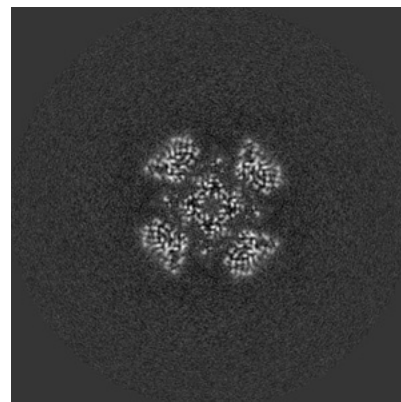
### 6.2.2 Raw map



X Index: 160



Y Index: 160

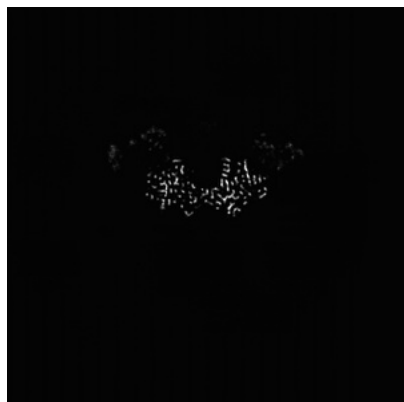


Z Index: 160

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

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

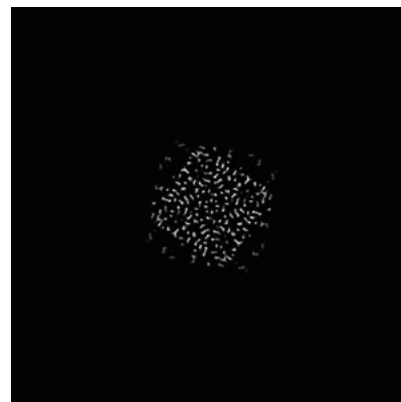
### 6.3.1 Primary map



X Index: 155

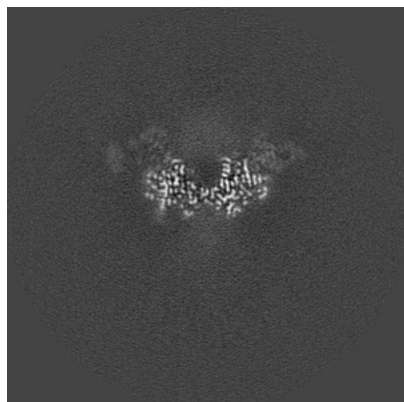


Y Index: 155

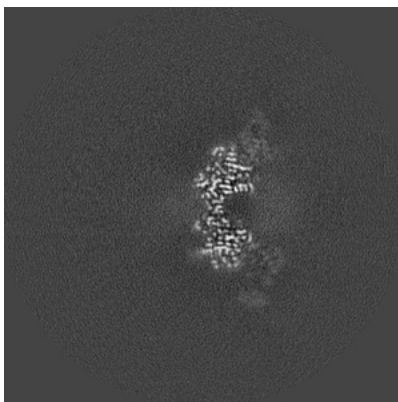


Z Index: 172

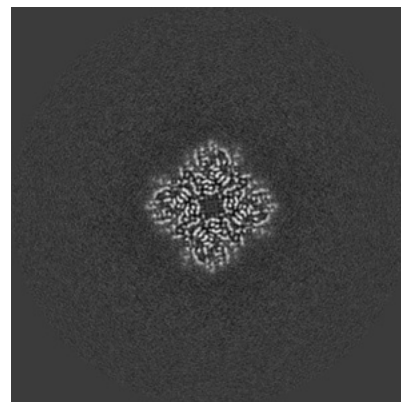
### 6.3.2 Raw map



X Index: 155



Y Index: 165

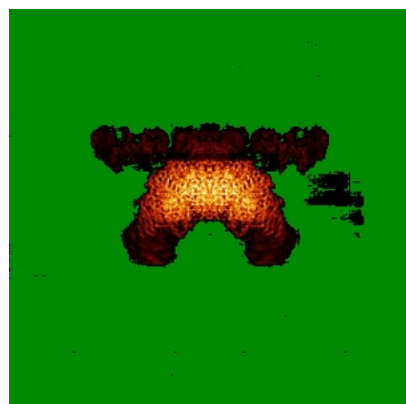


Z Index: 178

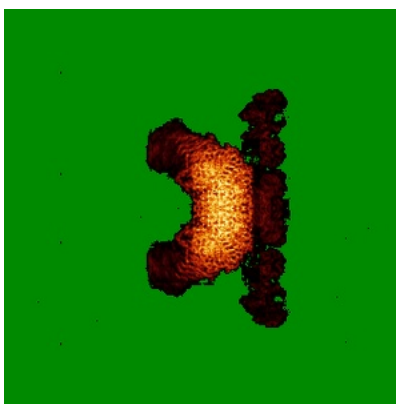
The images above show the largest variance slices of the map in three orthogonal directions.

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

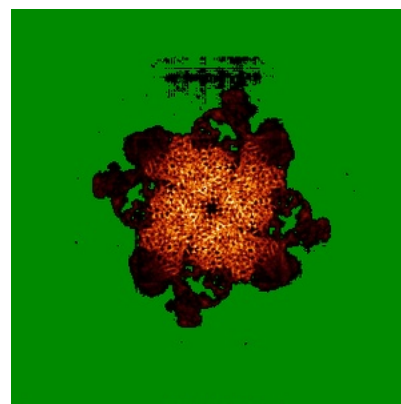
### 6.4.1 Primary map



X

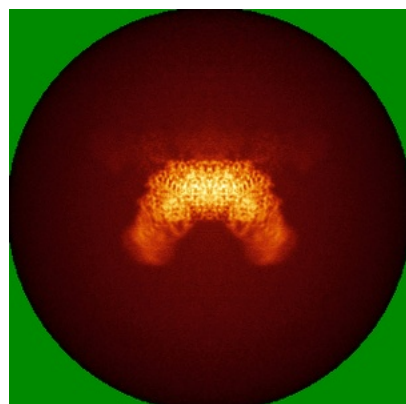


Y

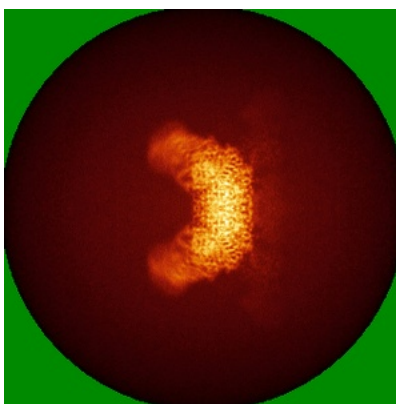


Z

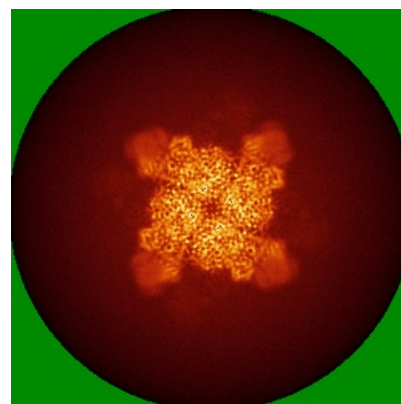
### 6.4.2 Raw map



X



Y

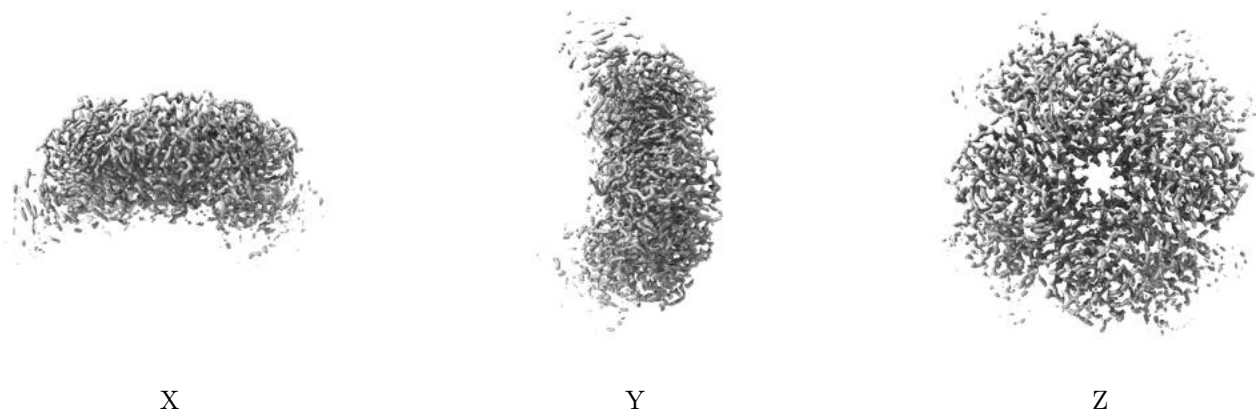


Z

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.

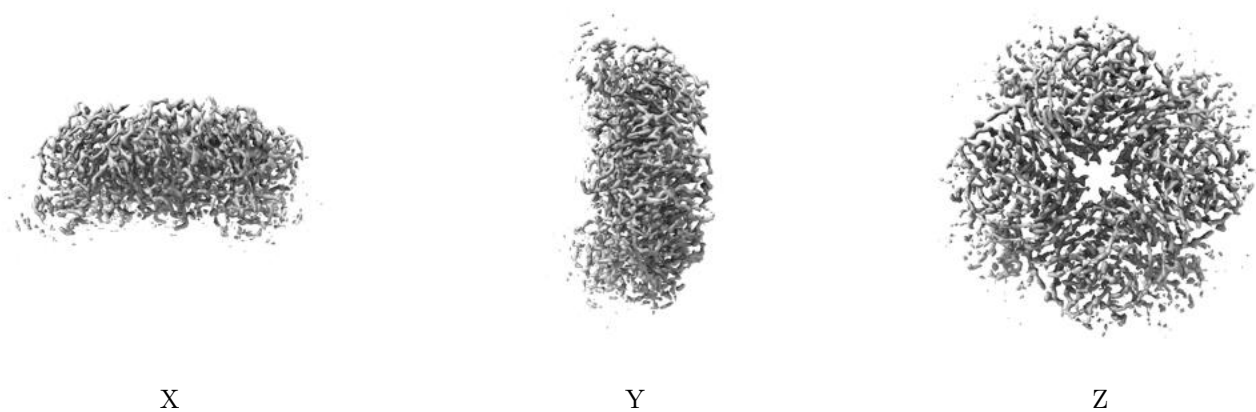
## 6.5 Orthogonal surface views [i](#)

### 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.

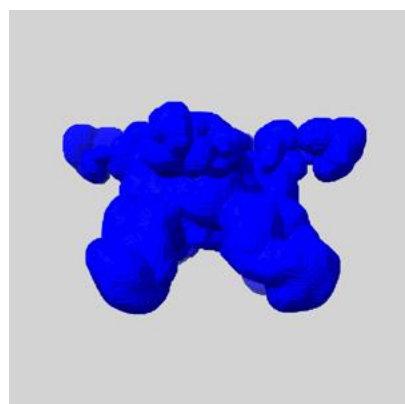
## 6.6 Mask visualisation [i](#)

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

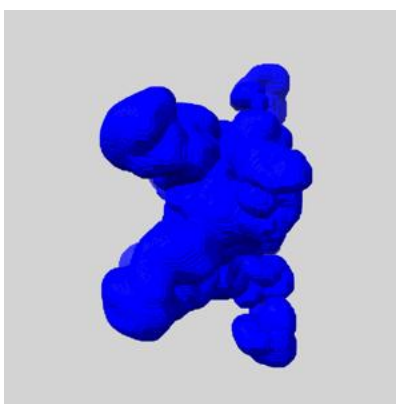
A mask typically either:

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

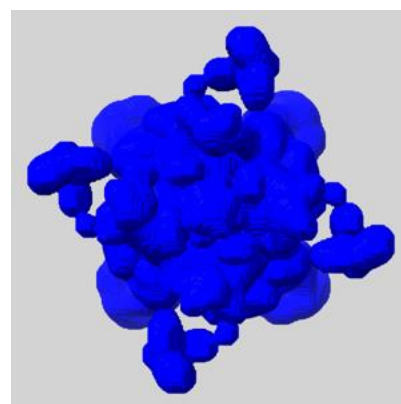
### 6.6.1 emd\_29907\_msk\_1.map [i](#)



X



Y

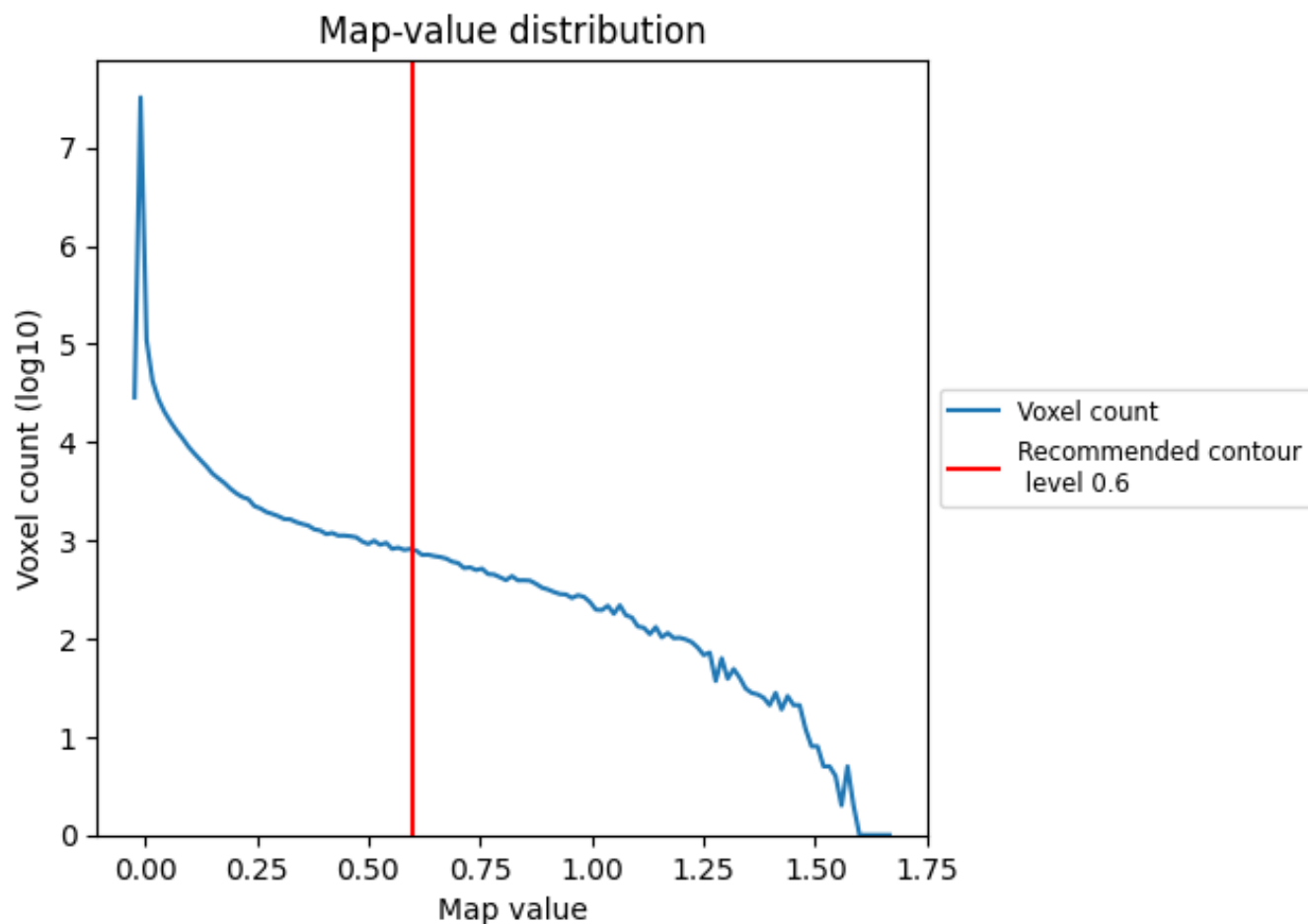


Z

## 7 Map analysis [i](#)

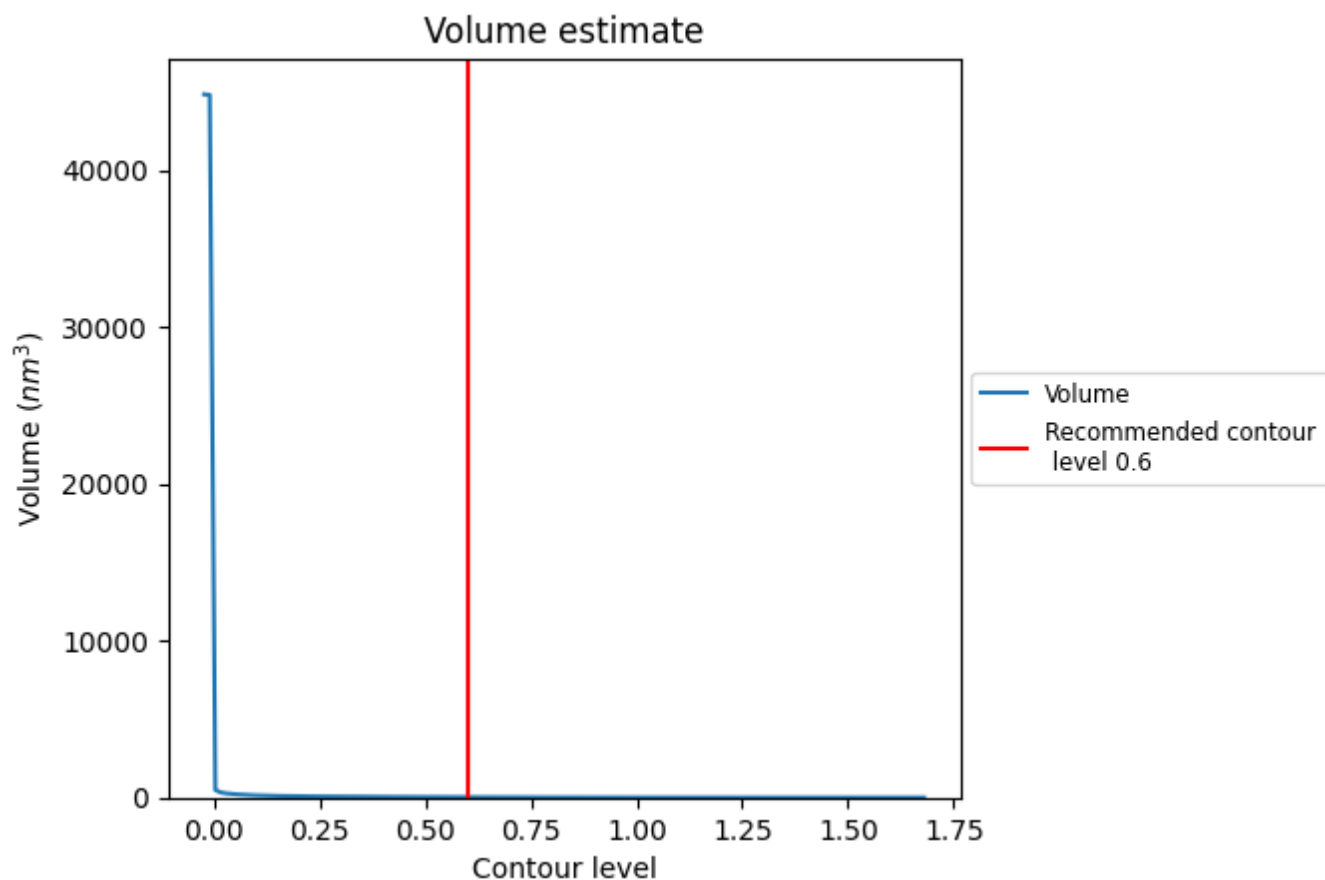
This section contains the results of statistical analysis of the map.

### 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.

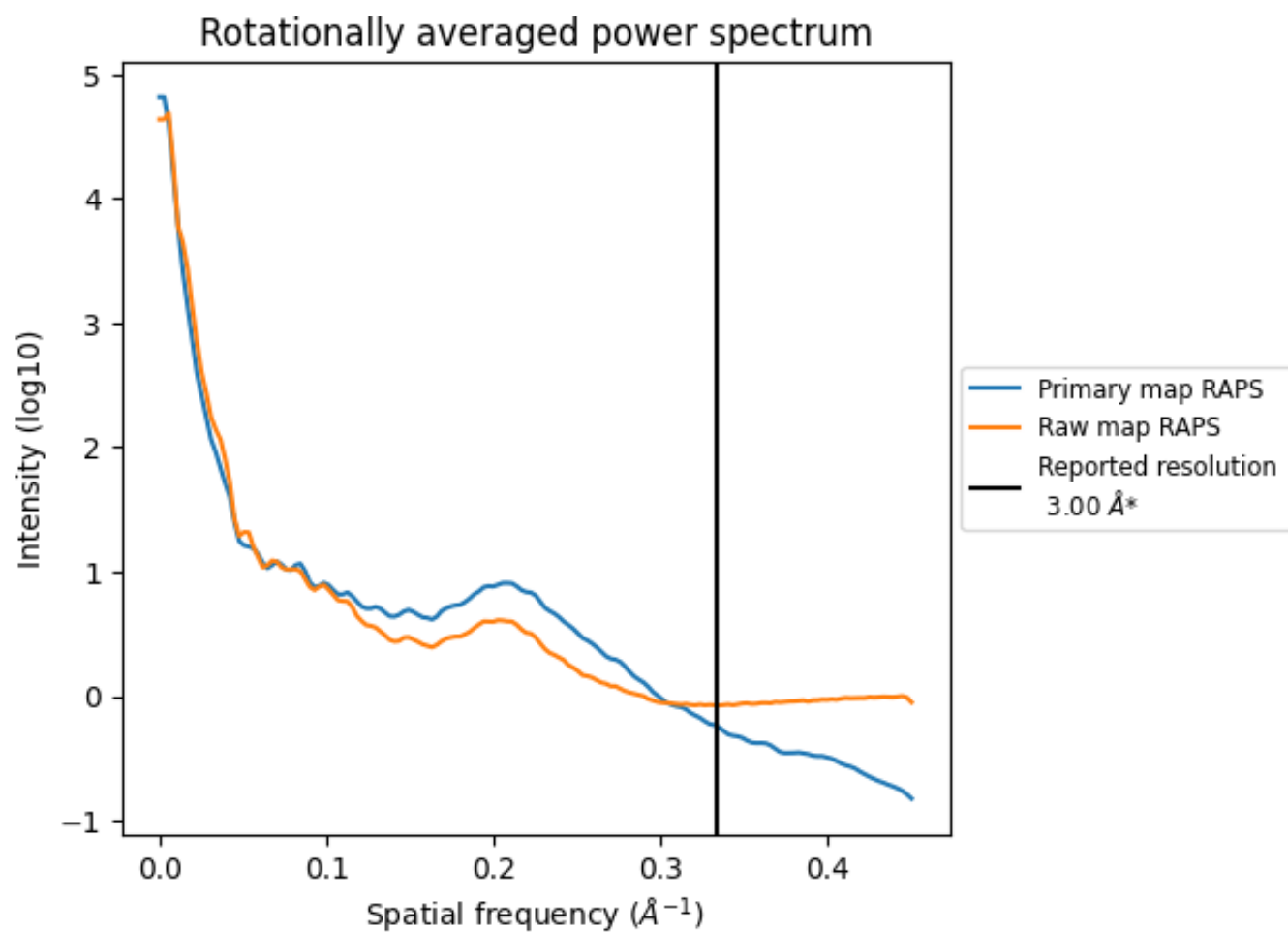
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 24  $\text{nm}^3$ ; this corresponds to an approximate mass of 21 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 ⓘ

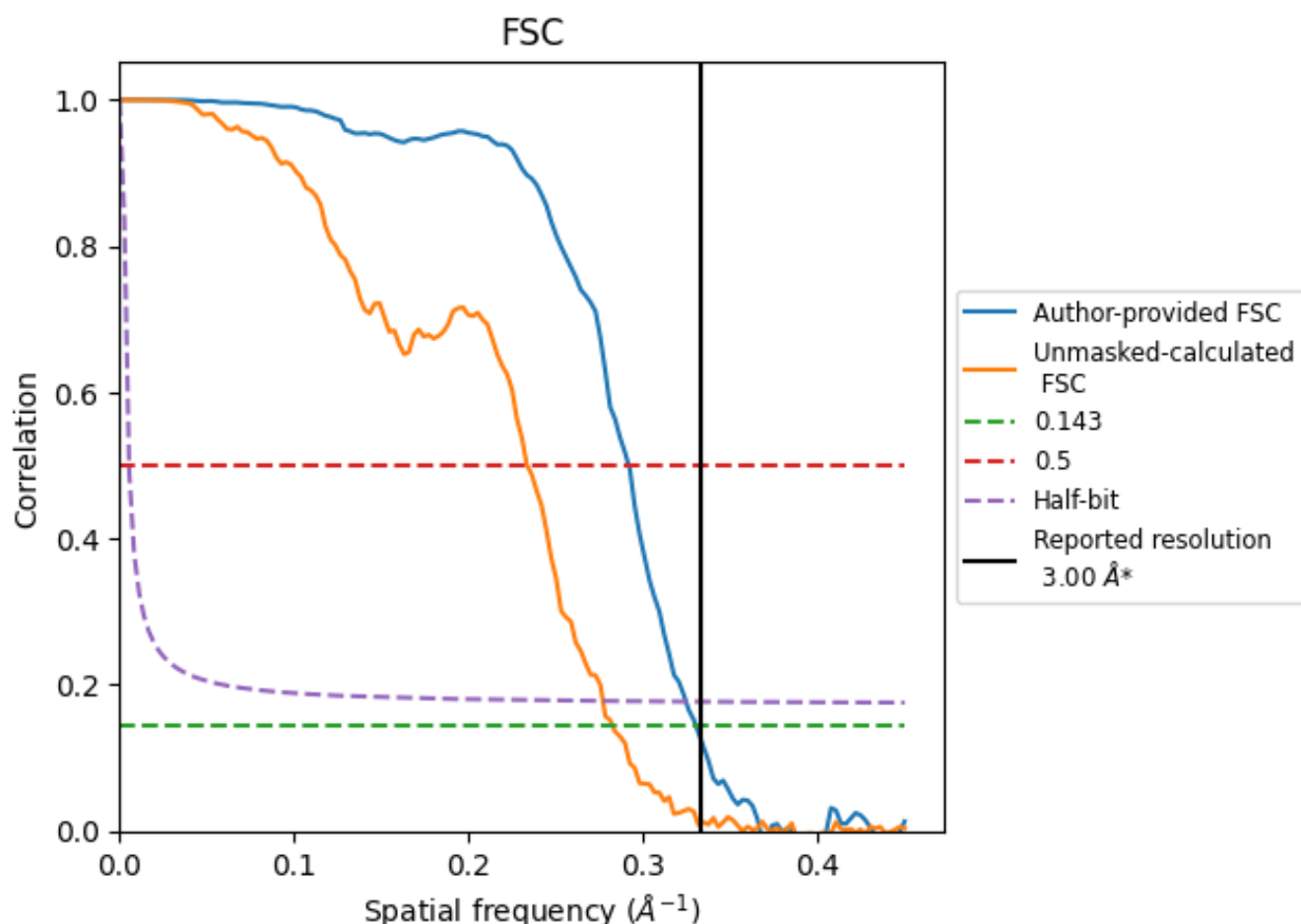


\*Reported resolution corresponds to spatial frequency of 0.333 Å<sup>-1</sup>

## 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 0.333  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.02	3.42	3.08
Unmasked-calculated*	3.53	4.28	3.61

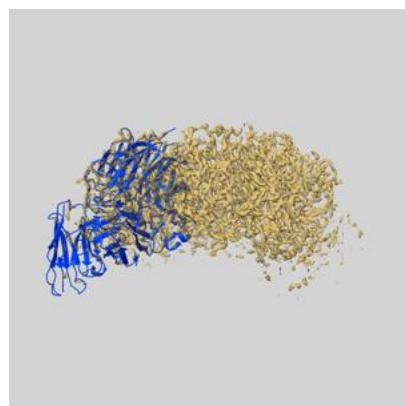
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.53 differs from the reported value 3.0 by more than 10 %

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

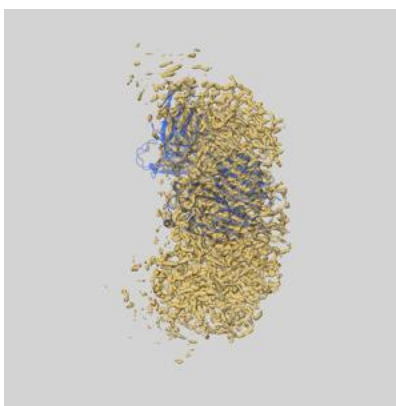
This section contains information regarding the fit between EMDB map EMD-29907 and PDB model 8GAT. Per-residue inclusion information can be found in section 3 on page 6.

### 9.1 Map-model overlays

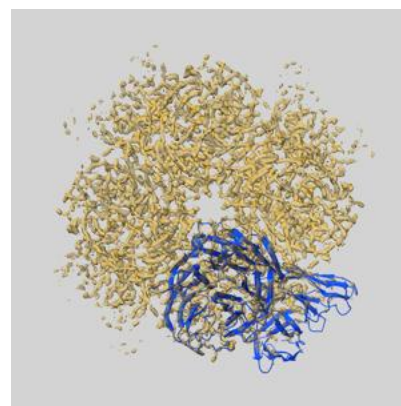
#### 9.1.1 Map-model overlay [i](#)



X

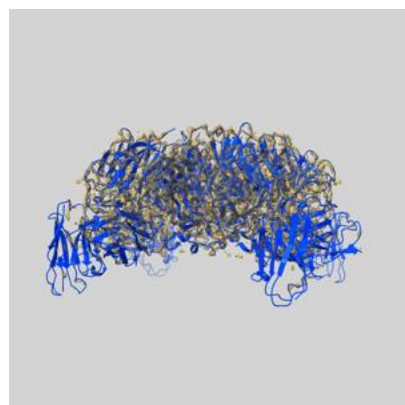


Y

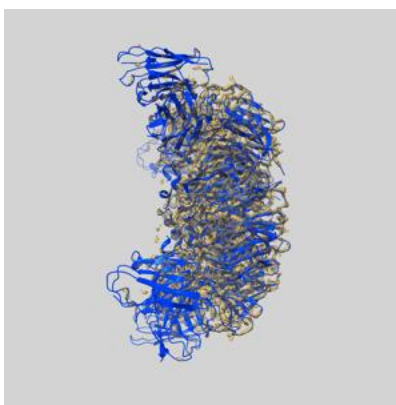


Z

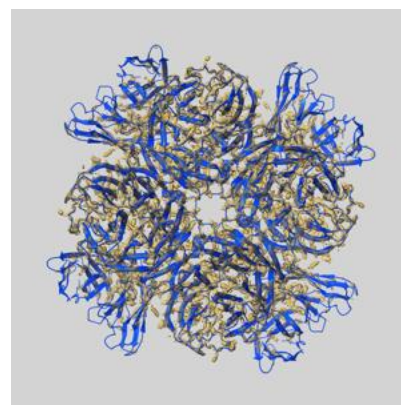
#### 9.1.2 Map-model assembly overlay [i](#)



X



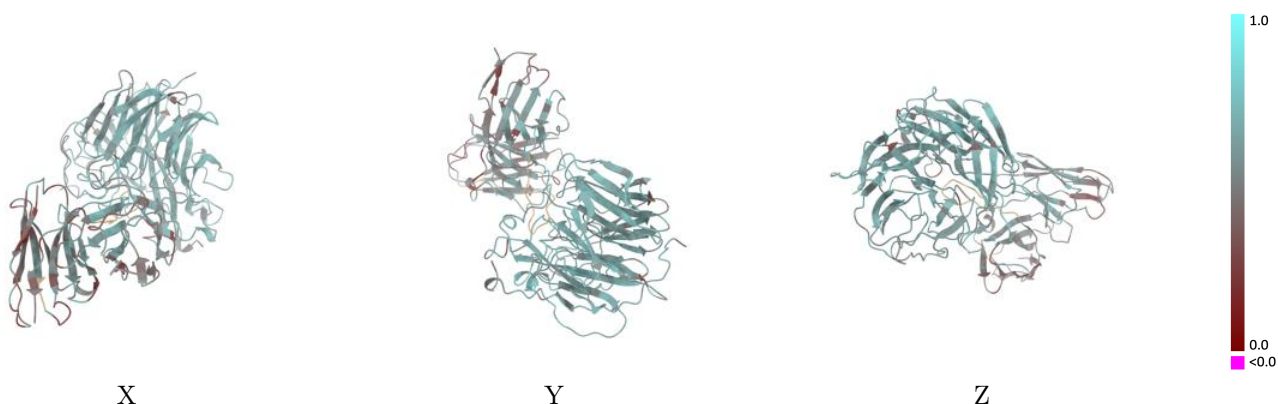
Y



Z

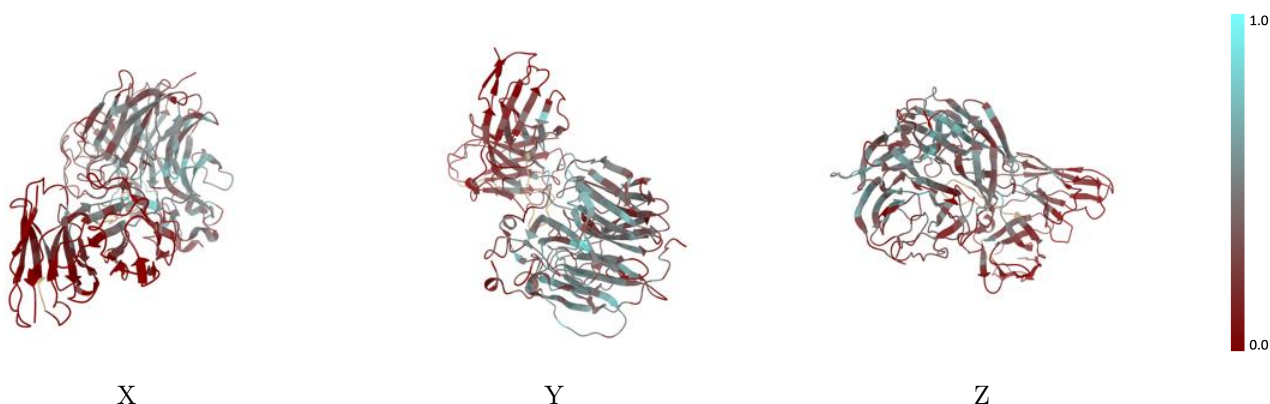
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



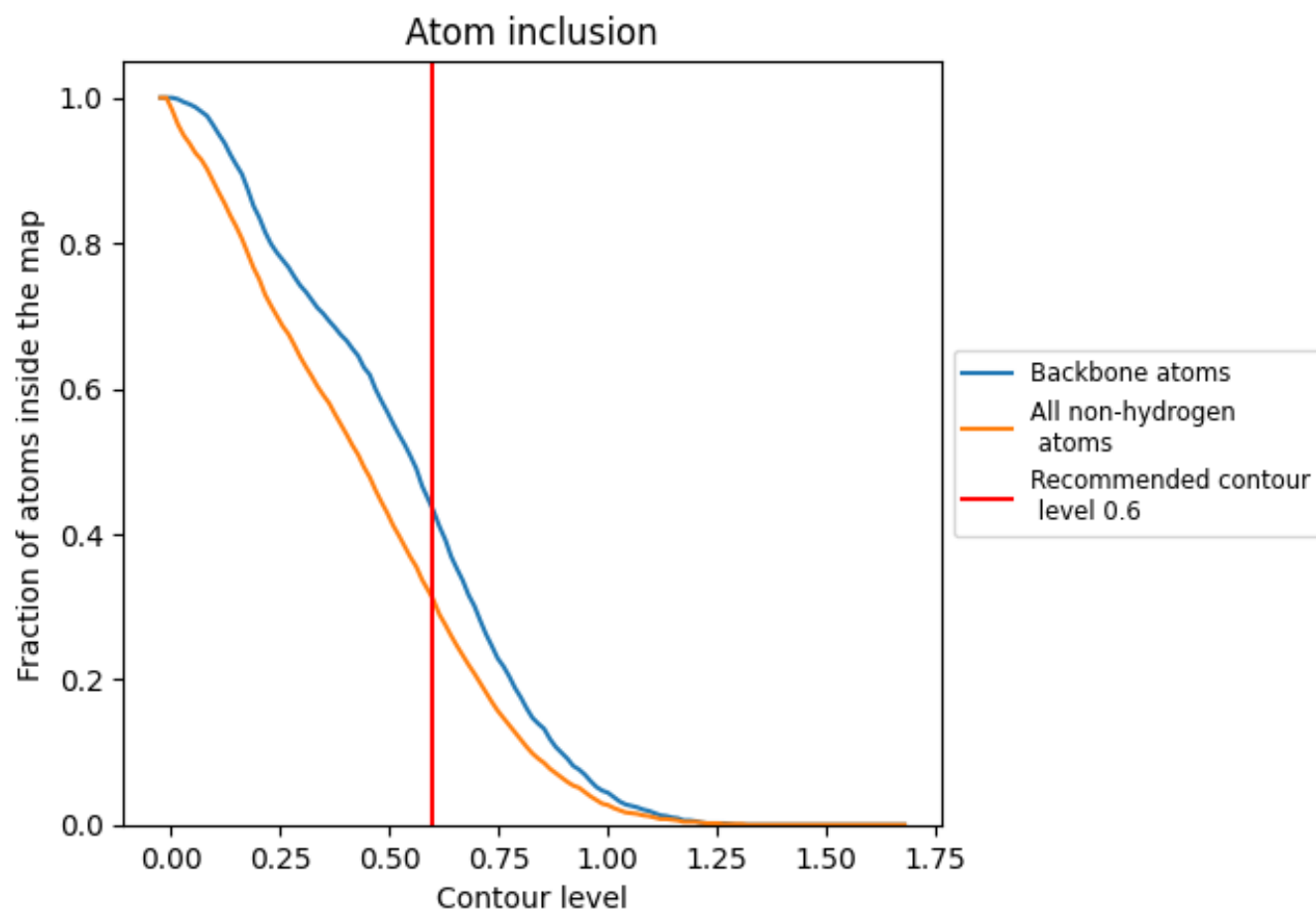
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 43% of all backbone atoms, 31% 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	<div></div> 0.3110	<div></div> 0.5620
A	<div></div> 0.3960	<div></div> 0.5990
M	<div></div> 0.1560	<div></div> 0.4850
N	<div></div> 0.1810	<div></div> 0.5190

