



wwPDB EM Validation Summary 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 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.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

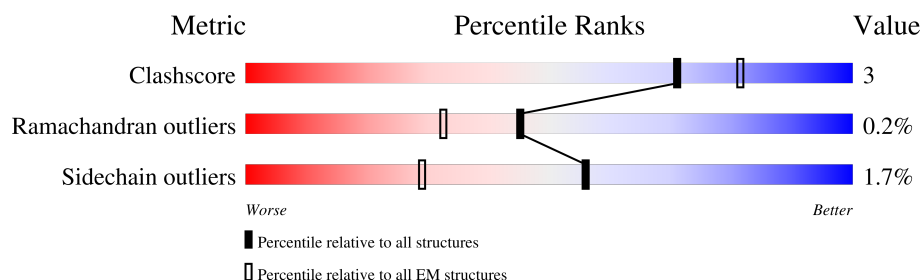
1 Overall quality at a glance

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 ≥ 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
1	A	386	Total	C	N	O	S	0	0
			2987	1856	529	579	23		

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

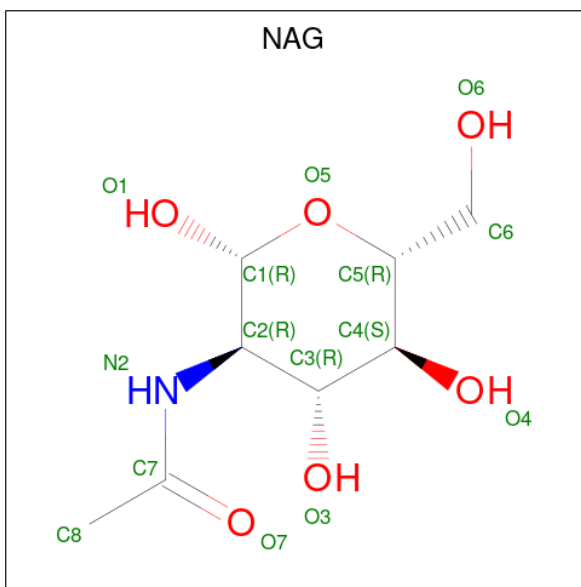
- Molecule 2 is a protein called Fab 1G01, heavy chain.

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: C₈H₁₅NO₆).

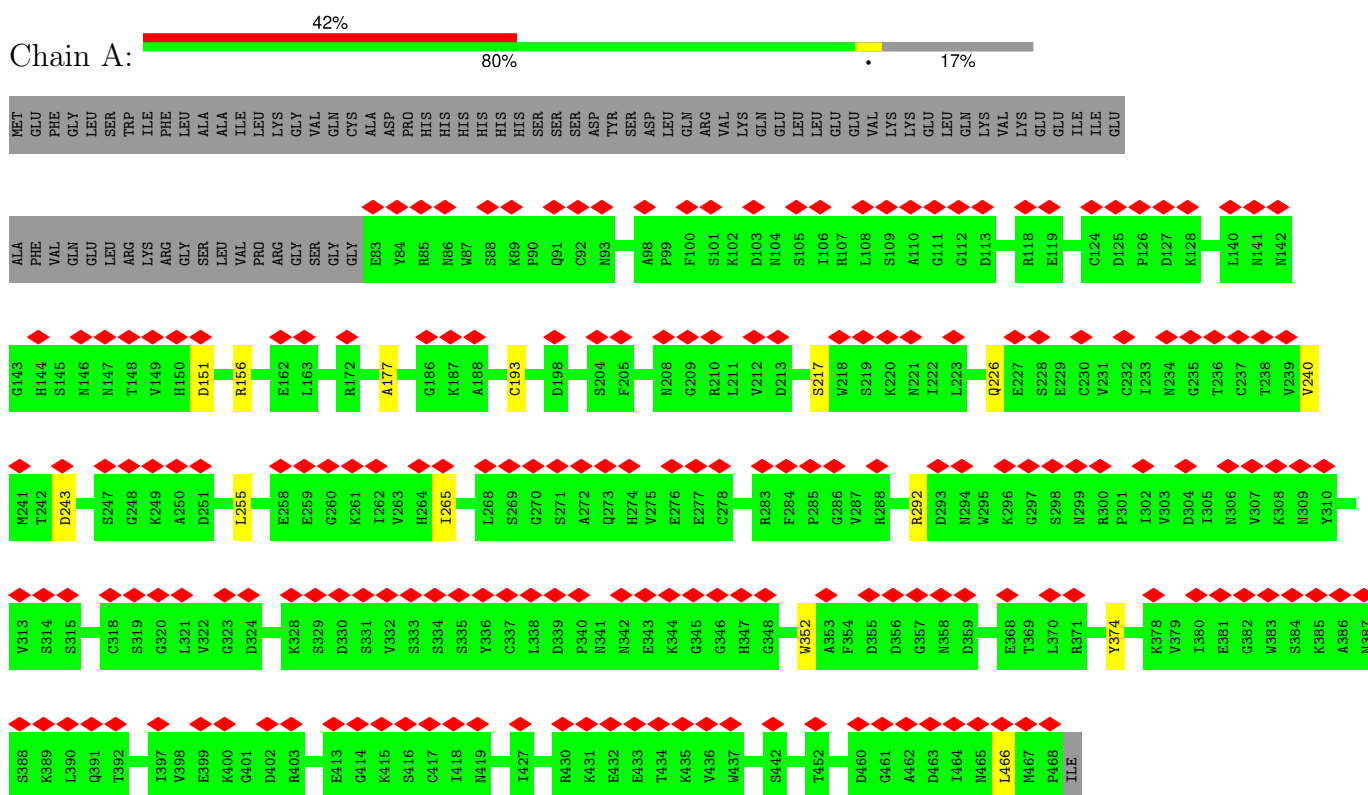


Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	A	1	Total	C	N	O	0
			14	8	1	5	

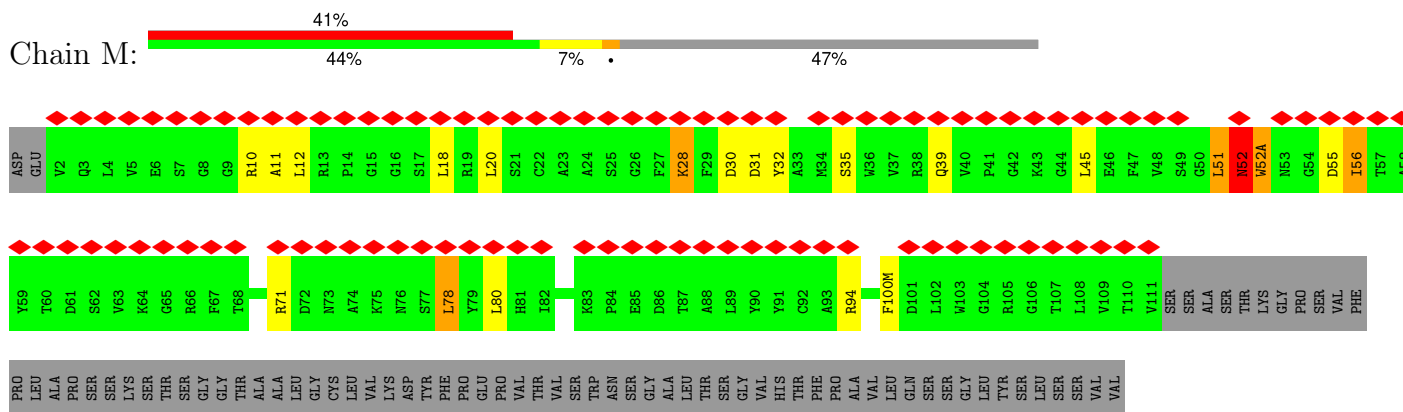
3 Residue-property plots

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: Vasodilator-stimulated phosphoprotein, Neuraminidase chimera



- Molecule 2: Fab 1G01, heavy chain



THR
VAL
PRO
SER
SER
SER
LEU
GLY
THR
THR
GLN
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TYR
TYR
ILE
CYS
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VAL
ASN
HIS
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LYS
PRO
SER
SER
ASN
THR
LYS
VAL
ASP
LYS
ARG
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GLU
PRO
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SER
CYS
HIS
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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
I21
T22
C23
R24
A25
S26
Q27
G28
I29
D30
Q37
Q38
R39
P40
G41
K42
A43
P44
N45
L46
L47
A51
S52
L53
L54
Q55
S56
G57
V58
P59
S60
R61
F62
S63
G66
Y67

G68
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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
T97
F98
G99
P100
G101
T102
K103
V104
D105
I106
K107
ARG
THR
VAL
ALA
ALA
PRO
SER
VAL
PHE
ILE
PHE
PRO
PRO
SER
ASP
GLU
GLN
LEU
LYS

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ALA
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SER
SER
PRO
VAL
THR
LYS
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.

The worst 5 of 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

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	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 [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	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

5 of 9 residues with a non-rotameric sidechain are listed below:

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

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

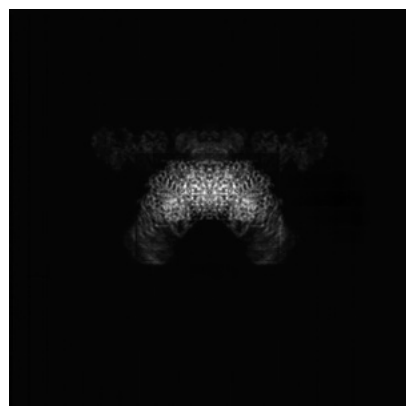
6 Map visualisation [i](#)

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

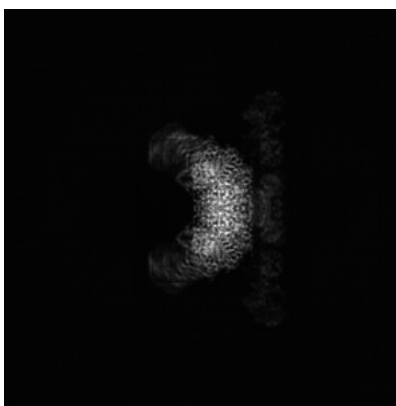
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

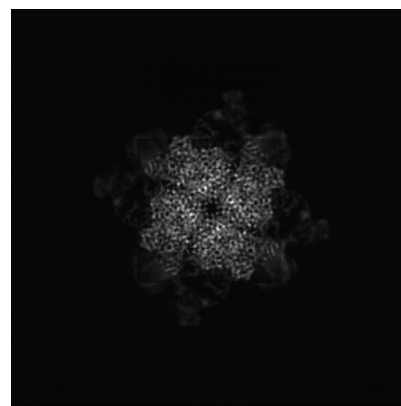
6.1.1 Primary map



X

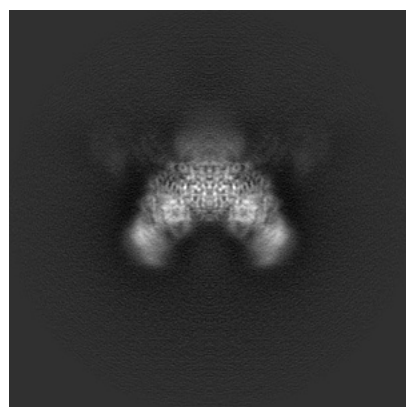


Y

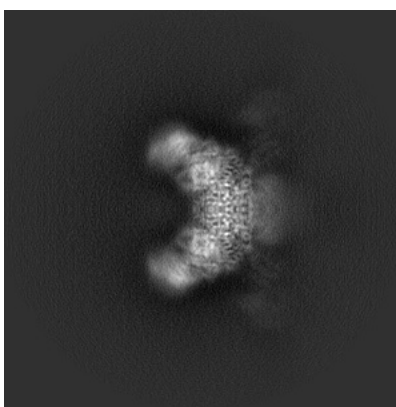


Z

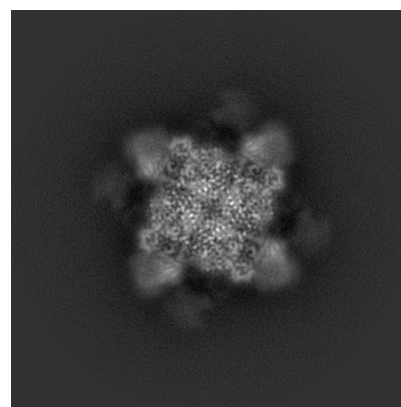
6.1.2 Raw map



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

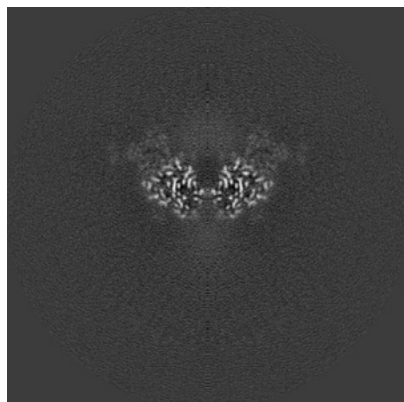


Y Index: 160

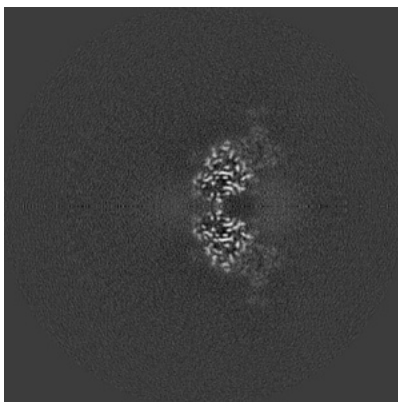


Z Index: 160

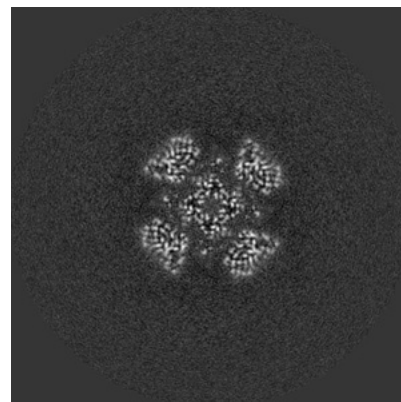
6.2.2 Raw map



X Index: 160



Y Index: 160

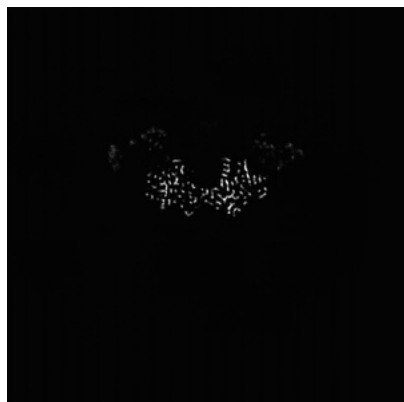


Z Index: 160

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

6.3 Largest variance slices [i](#)

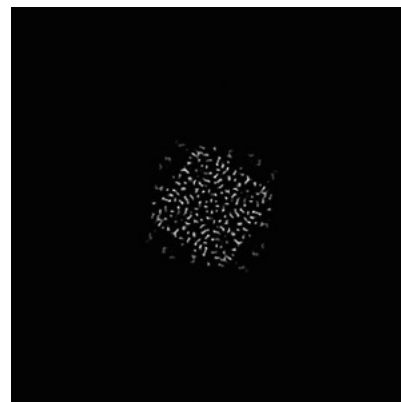
6.3.1 Primary map



X Index: 155

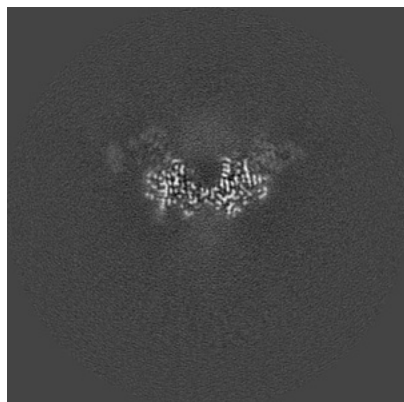


Y Index: 155

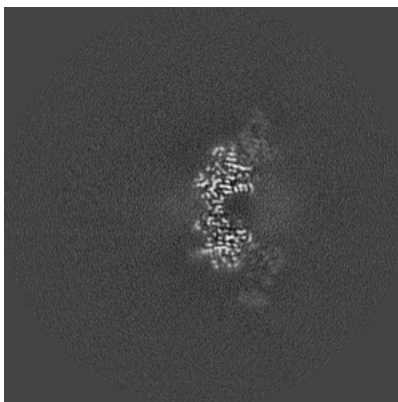


Z Index: 172

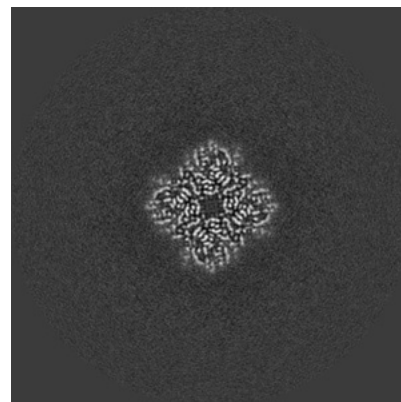
6.3.2 Raw map



X Index: 155



Y Index: 165

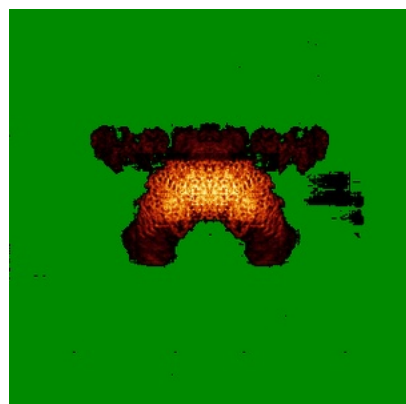


Z Index: 178

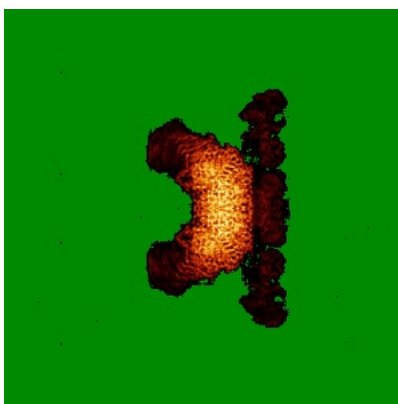
The images above show the largest variance slices of the map in three orthogonal directions.

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

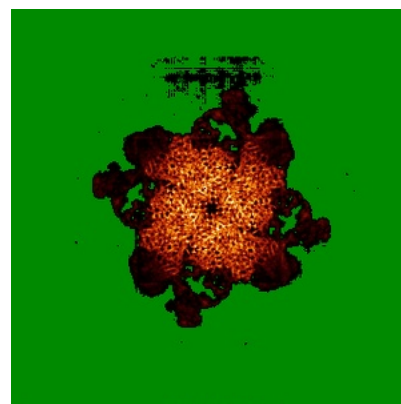
6.4.1 Primary map



X

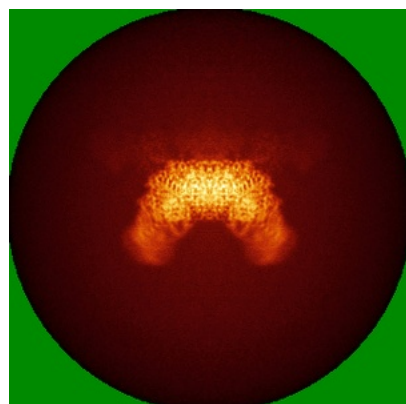


Y

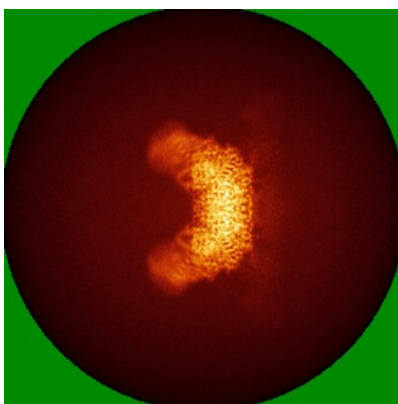


Z

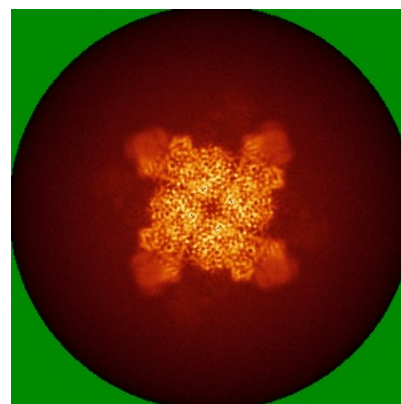
6.4.2 Raw map



X



Y

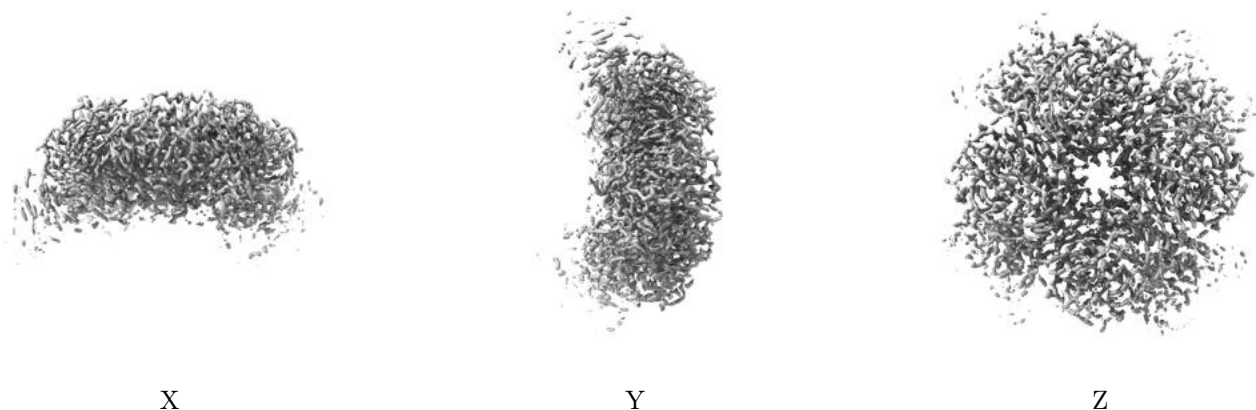


Z

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.

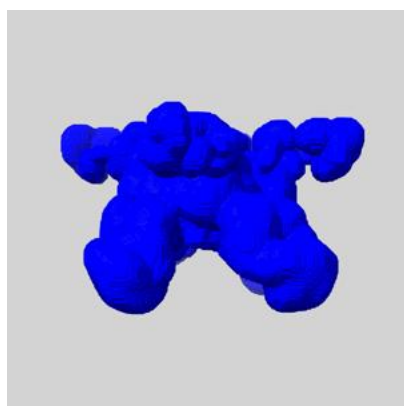
6.6 Mask visualisation [i](#)

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

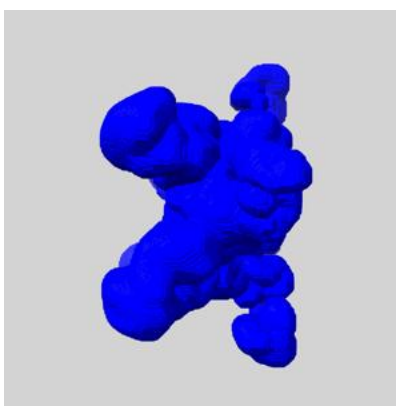
A mask typically either:

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

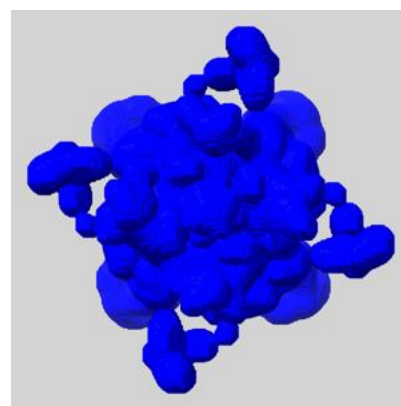
6.6.1 emd_29907_msk_1.map [i](#)



X



Y

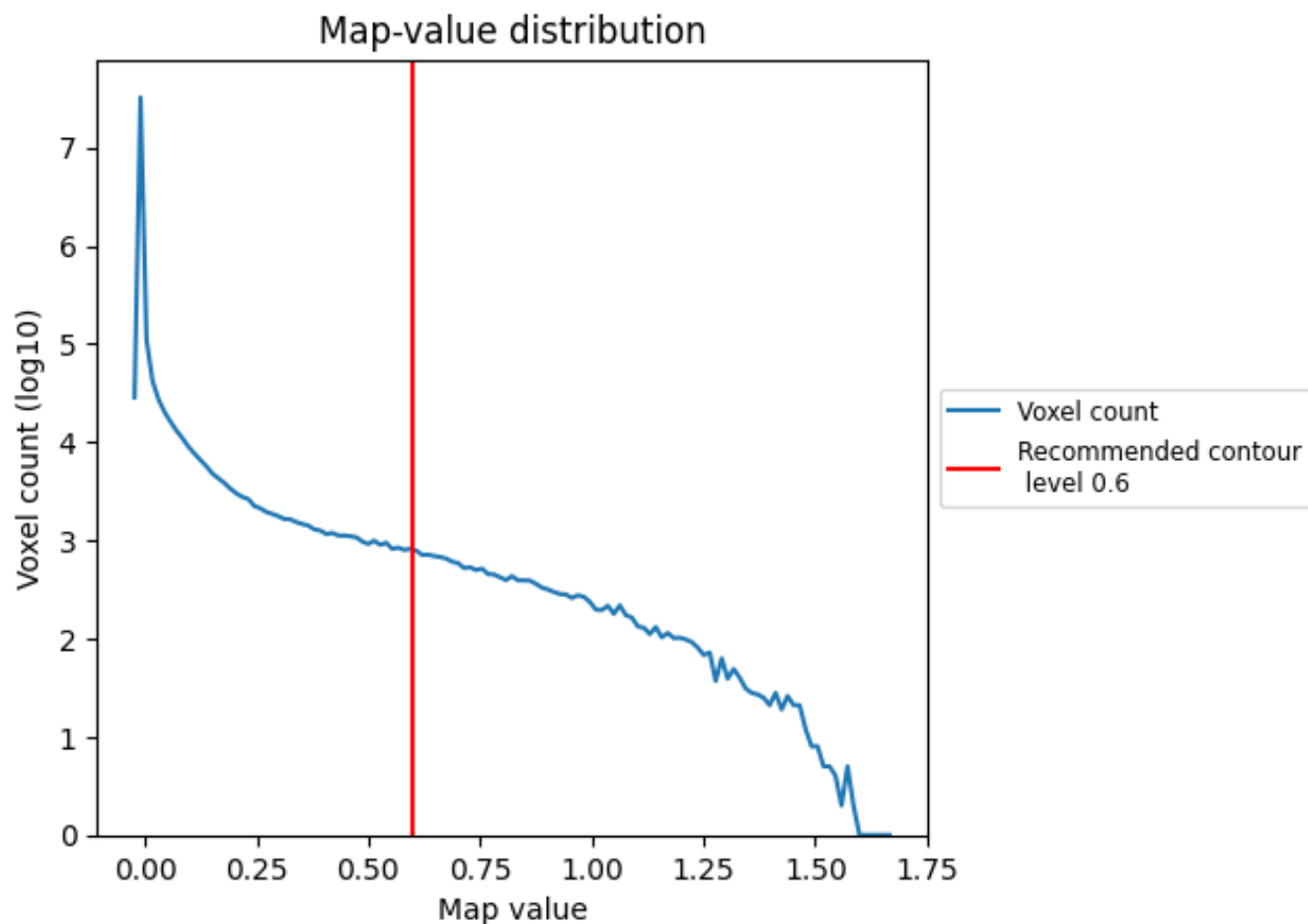


Z

7 Map analysis [i](#)

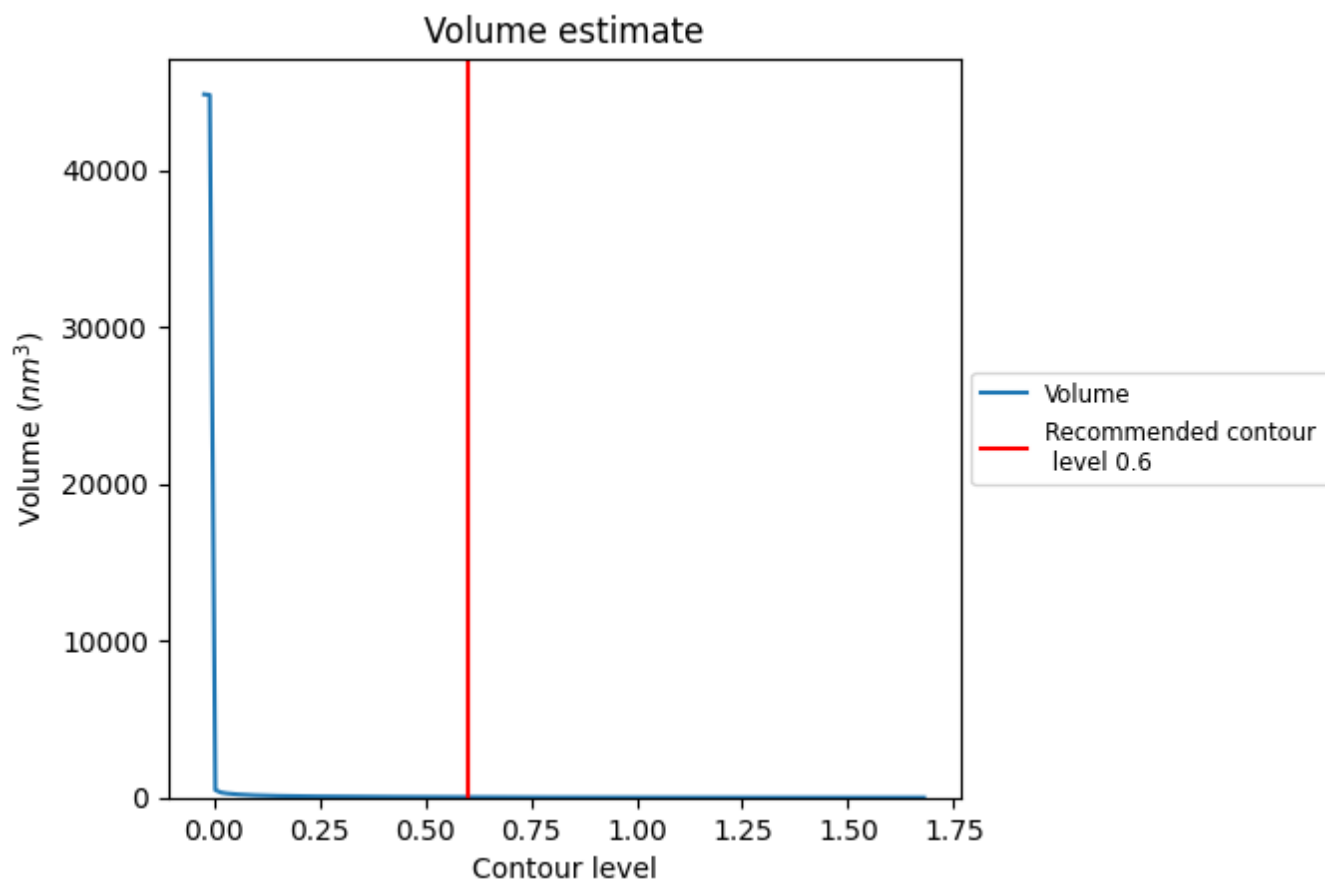
This section contains the results of statistical analysis of the map.

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.

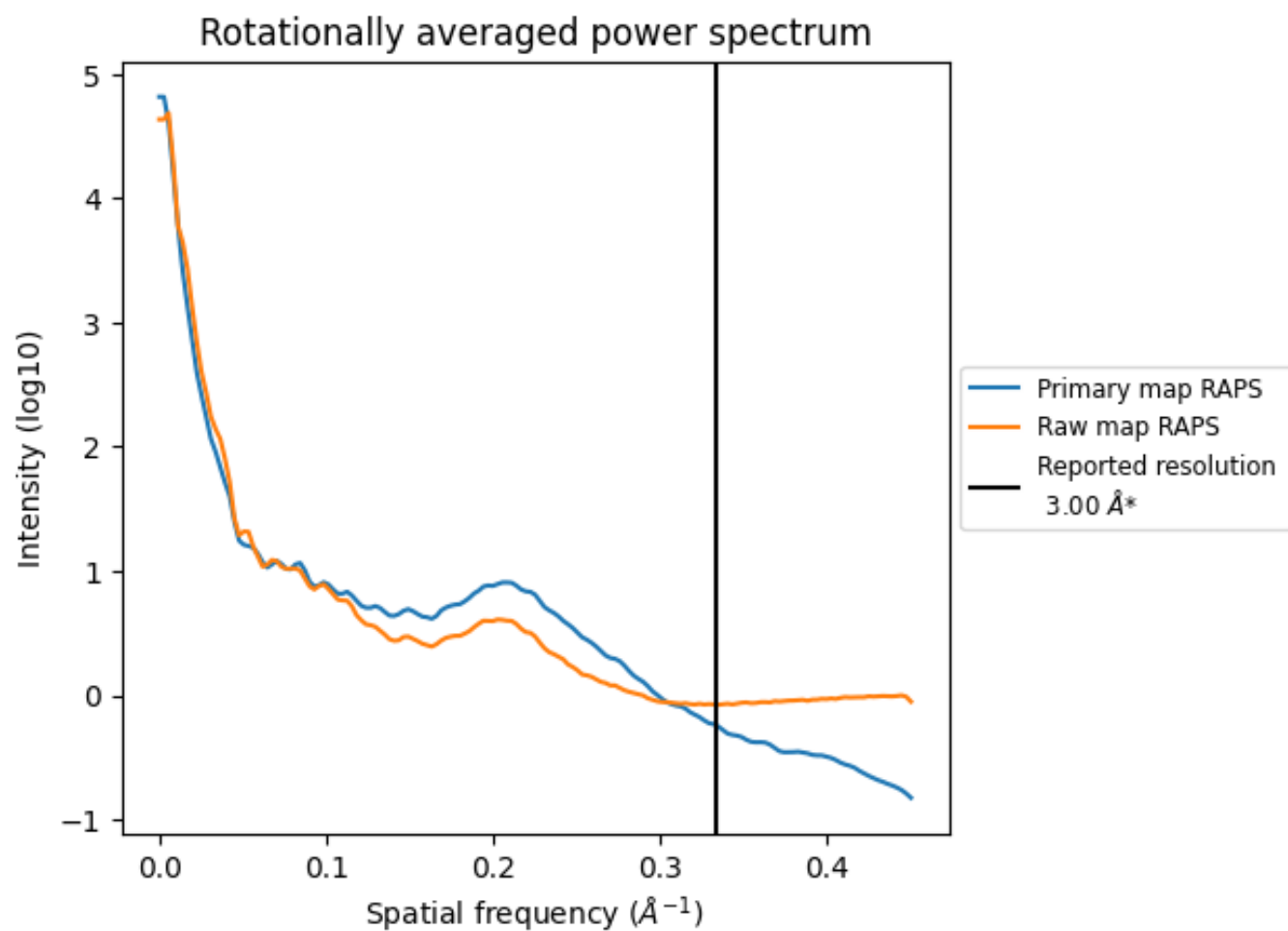
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 24 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 ⓘ

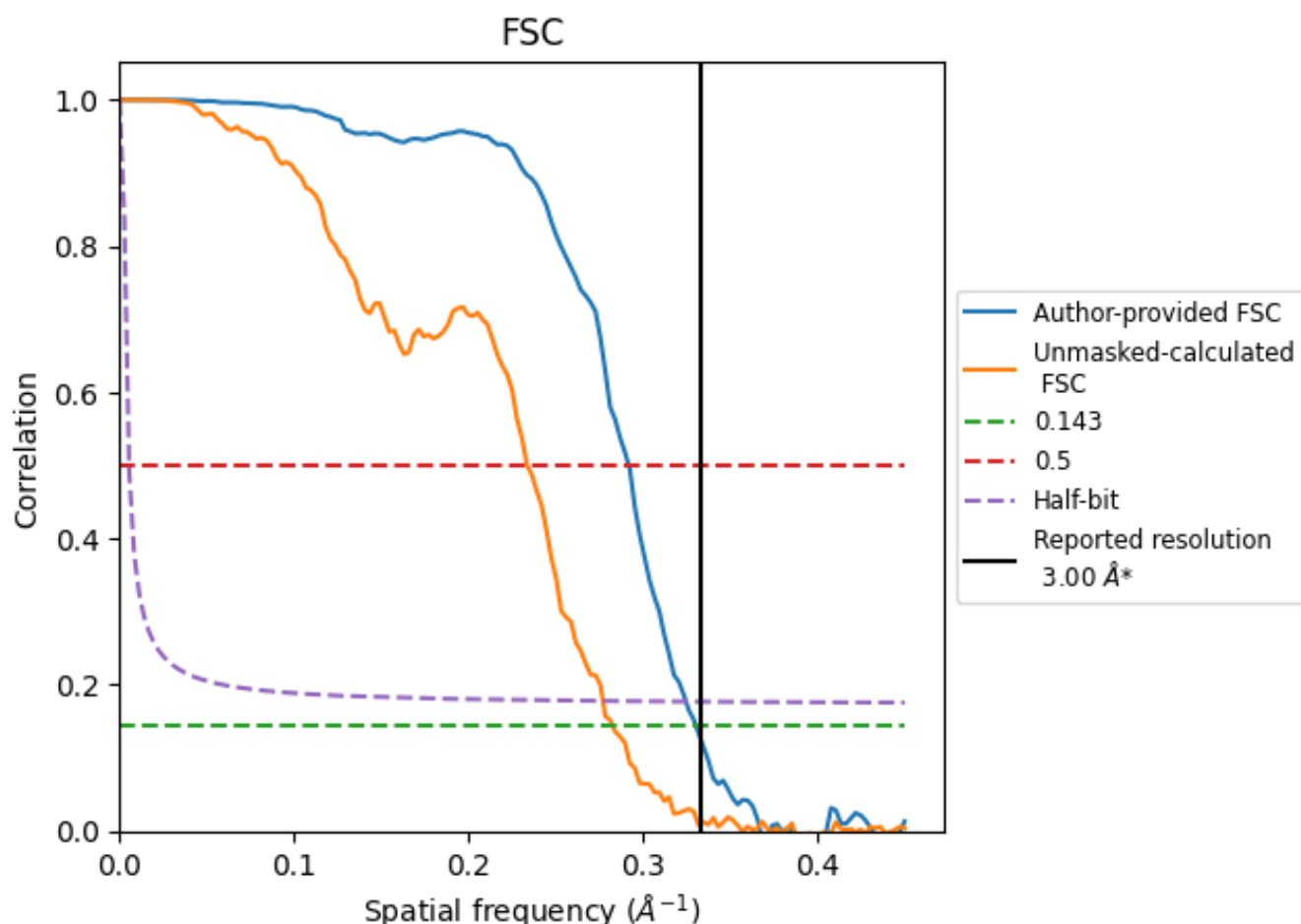


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻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

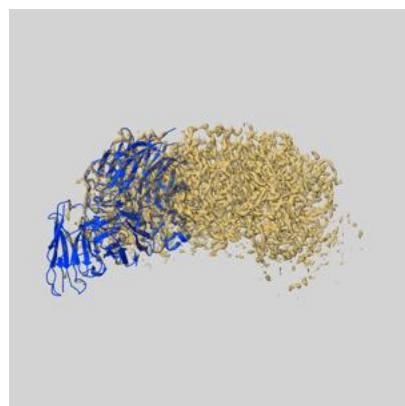
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.53 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

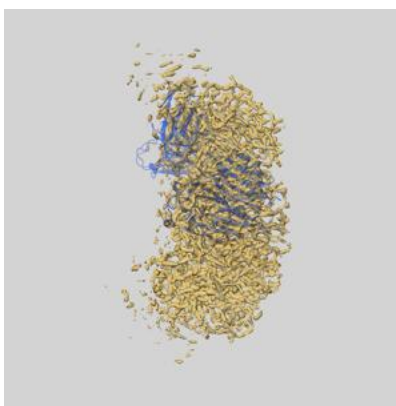
This section contains information regarding the fit between EMDB map EMD-29907 and PDB model 8GAT. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

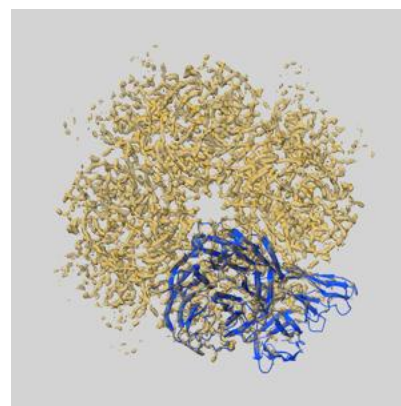
9.1.1 Map-model overlay [i](#)



X

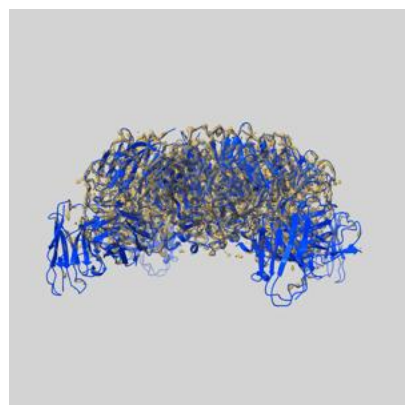


Y

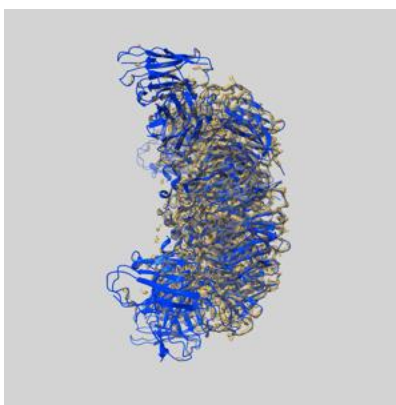


Z

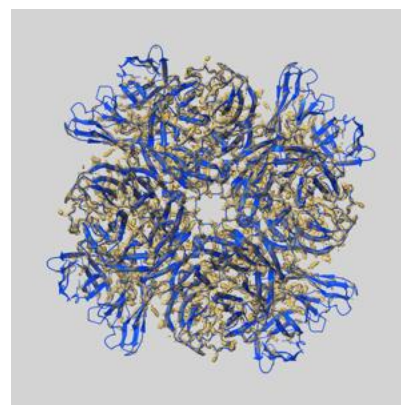
9.1.2 Map-model assembly overlay [i](#)



X



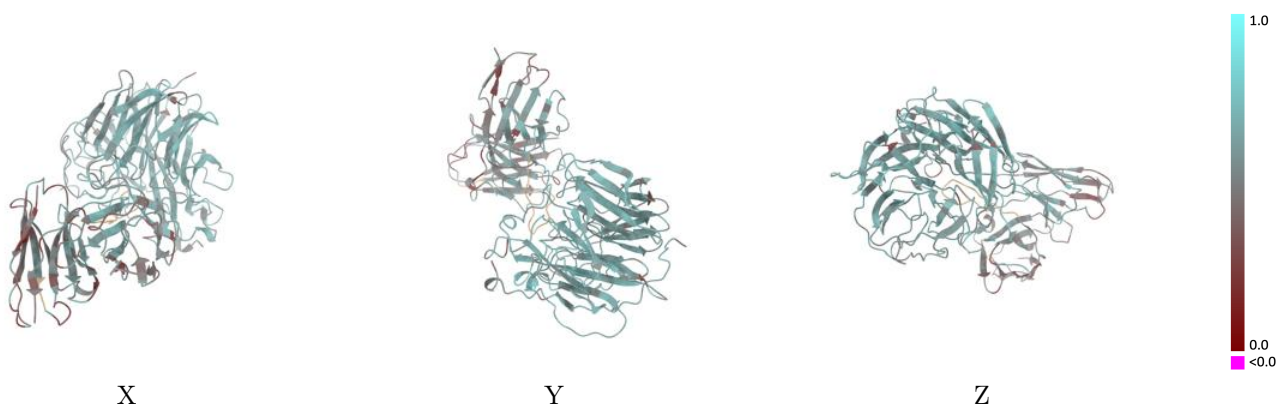
Y



Z

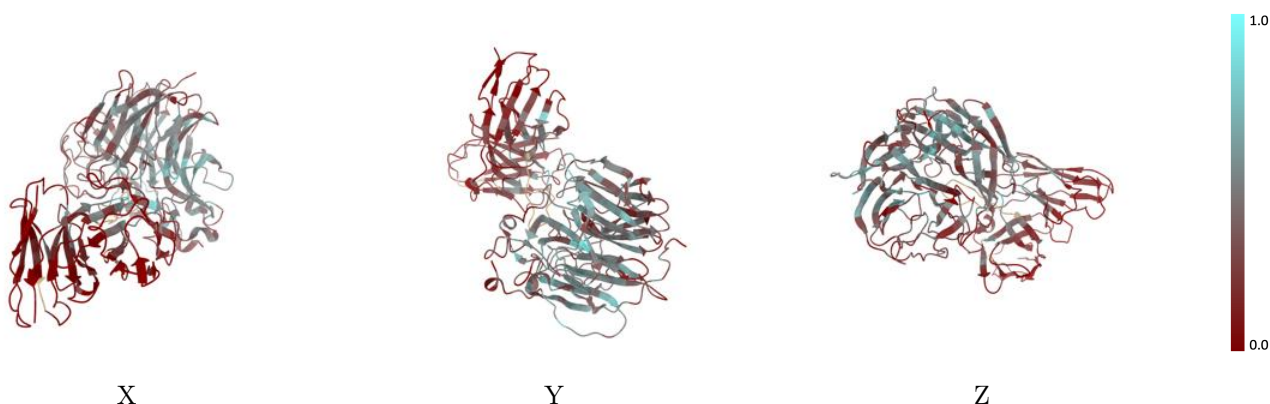
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



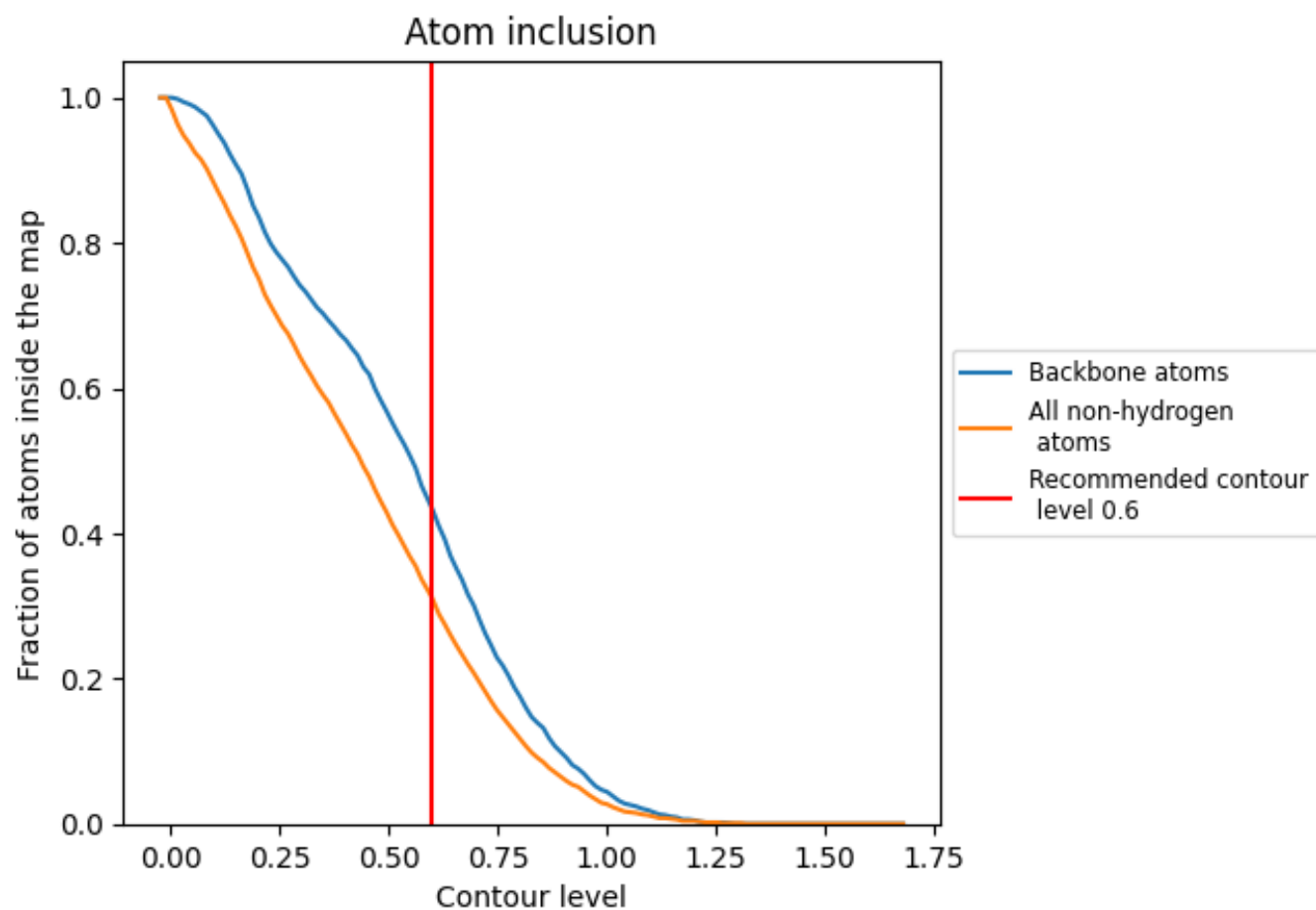
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

