



## wwPDB EM Validation Summary Report ⓘ

Oct 6, 2024 – 05:06 PM JST

PDB ID : 8I0N  
EMDB ID : EMD-35104  
Title : Structure of beta-arrestin1 in complex with a phosphopeptide corresponding to the human C5a anaphylatoxin chemotactic receptor 1, C5aR1 (Local refine)  
Authors : Maharana, J.; Sarma, P.; Yadav, M.K.; Banerjee, R.; Shukla, A.K.  
Deposited on : 2023-01-11  
Resolution : 3.26 Å(reported)  
Based on initial model : 8GO8

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.dev113  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
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

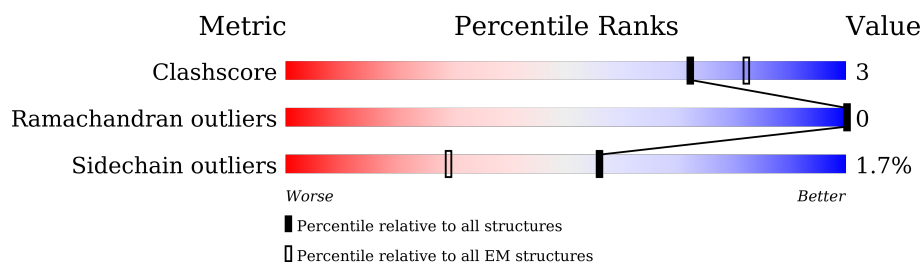
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.26 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	418	
1	B	418	
2	H	237	
2	I	237	
3	L	215	
3	M	215	
4	U	20	
4	V	20	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9141 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 Beta-arrestin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	362	Total	C	N	O	S	0	0
			2775	1775	477	513	10		
1	B	362	Total	C	N	O	S	0	0
			2767	1769	476	512	10		

- Molecule 2 is a protein called Fab30 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	117	Total	C	N	O	S	0	0
			908	578	153	174	3		
2	I	117	Total	C	N	O	S	0	0
			908	578	153	174	3		

- Molecule 3 is a protein called Fab30 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	107	Total	C	N	O	S	0	0
			804	508	132	161	3		
3	M	107	Total	C	N	O	S	0	0
			799	506	131	159	3		

- Molecule 4 is a protein called C5a anaphylatoxin chemotactic receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	U	9	Total	C	N	O	P	0	0
			90	42	12	31	5		
4	V	9	Total	C	N	O	P	0	0
			90	42	12	31	5		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	331	GLU	-	expression tag	UNP P21730

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Chain	Residue	Modelled	Actual	Comment	Reference
U	332	SEP	-	expression tag	UNP P21730
U	333	LYS	-	expression tag	UNP P21730
U	343	MET	-	expression tag	UNP P21730
U	344	ALA	-	expression tag	UNP P21730
U	345	GLN	-	expression tag	UNP P21730
U	346	LYS	-	expression tag	UNP P21730
U	347	THR	-	expression tag	UNP P21730
U	348	GLN	-	expression tag	UNP P21730
U	349	ALA	-	expression tag	UNP P21730
U	350	VAL	-	expression tag	UNP P21730
V	331	GLU	-	expression tag	UNP P21730
V	332	SEP	-	expression tag	UNP P21730
V	333	LYS	-	expression tag	UNP P21730
V	343	MET	-	expression tag	UNP P21730
V	344	ALA	-	expression tag	UNP P21730
V	345	GLN	-	expression tag	UNP P21730
V	346	LYS	-	expression tag	UNP P21730
V	347	THR	-	expression tag	UNP P21730
V	348	GLN	-	expression tag	UNP P21730
V	349	ALA	-	expression tag	UNP P21730
V	350	VAL	-	expression tag	UNP P21730



SER  
GLU  
ASN  
THR  
LYS  
VAL  
ASP  
LYS  
LYS  
VAL  
GLU  
PRO  
LYS  
SER  
CYS  
ASP  
THR  
HIS  
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HIS

- Molecule 2: Fab30 heavy chain

Chain I: 44% 5% 51%

GLU  
ILE  
SER  
GLU  
V5  
L14  
S20  
L21  
M31  
D76  
N80  
R90  
C99  
D111  
G114  
Q115  
T120  
V121  
SER  
SER  
ALA  
SER  
THR  
GLY  
LYS  
PRO  
SER  
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ALA  
PRO  
SER  
SER  
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LYS  
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ALA  
LEU  
GLY  
CYS  
LEU  
VAL  
LYS

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

- Molecule 3: Fab30 light chain

Chain L: 43% 6% 50%

S1  
D2  
L12  
D18  
R19  
R25  
Q80  
P81  
E82  
D83  
F84  
C89  
Q90  
Q91  
V97  
G100  
I107  
LYS  
ARG  
THR  
VAL  
ALA  
ALA  
PRO  
SER  
SER  
VAL  
PHE  
ILE  
PHE  
PHE  
PRO  
PRO  
ASP  
SER  
GLN  
SER  
LEU  
LYS  
SER  
GLY  
THR  
ALA  
SER  
VAL  
VAL  
CYS  
GLU  
LEU  
LEU  
ASN  
PHE  
GLY  
PRO

ARG  
GLU  
ALA  
LYS  
VAL  
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TRP  
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CYS  
GLU  
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THR  
HIS  
GLN  
LEU

SER  
SER  
PRO  
VAL  
THR  
LYS  
SER  
PHE  
ASN  
ARG  
GLY  
GLU  
CYS

- Molecule 3: Fab30 light chain

Chain M: 43% 7% 50%

S1  
Q7  
L12  
D18  
R19  
R25  
R62  
P81  
E82  
D83  
F84  
C89  
Q90  
Q91  
V97  
G100  
T103  
I107  
LYS  
ARG  
THR  
VAL  
SER  
ALA  
ALA  
PRO  
SER  
VAL  
PHE  
ILE  
PHE  
PHE  
PRO  
PRO  
SER  
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SER  
SER  
GLN  
SER  
LEU  
LYS  
VAL  
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TYR  
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THR  
THR  
LEU  
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SER  
LYS  
ALA  
ASP  
TYR  
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VAL  
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ALA  
CYS  
GLU  
VAL  
THR

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

- Molecule 4: C5a anaphylatoxin chemotactic receptor 1

Chain U: 20% 25% 55%

GLU  
SEP  
LYS  
S334  
F335  
T336  
H337  
S338  
T339  
T342  
MET  
ALA  
GLN  
LYS  
THR  
GLN  
ALA  
VAL

- Molecule 4: C5a anaphylatoxin chemotactic receptor 1

Chain V: 25% 20% 55%

GLU	SEP	LYS	S334	F335	T336	R337	S338	T339	T342	MET	ALA	GLN	LYS	THR	GLN	ALA	VAL
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	80437	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	56	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	165000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.893	Depositor
Minimum map value	-1.482	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.040	Depositor
Recommended contour level	0.25	Depositor
Map size ( $\text{\AA}$ )	393.60962, 393.60962, 393.60962	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.3667, 1.3667, 1.3667	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: SEP, TPO

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	0.27	0/2836	0.51	0/3859
1	B	0.27	0/2828	0.52	0/3850
2	H	0.28	0/932	0.49	0/1267
2	I	0.29	0/932	0.50	0/1267
3	L	0.30	0/822	0.50	0/1119
3	M	0.29	0/817	0.50	0/1113
4	U	0.25	0/35	0.63	0/42
4	V	0.23	0/35	0.56	0/42
All	All	0.28	0/9237	0.51	0/12559

There are no bond length outliers.

There are no bond angle outliers.

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	2775	0	2779	16	0
1	B	2767	0	2765	17	0
2	H	908	0	860	7	0
2	I	908	0	860	8	0
3	L	804	0	776	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	M	799	0	767	7	0
4	U	90	0	59	0	0
4	V	90	0	59	0	0
All	All	9141	0	8925	58	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 58 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:B:76:ARG:NH1	1:B:78:ASP:OD1	2.27	0.68
3:L:82:GLU:N	3:L:82:GLU:OE2	2.28	0.66
1:A:26:ASP:OD2	1:A:363:ARG:NH2	2.35	0.58
1:B:232:LYS:NZ	1:B:257:GLU:OE2	2.38	0.57
2:H:31:ASN:HA	2:H:80:ASN:ND2	2.20	0.56

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	360/418 (86%)	340 (94%)	20 (6%)	0	100	100
1	B	360/418 (86%)	342 (95%)	18 (5%)	0	100	100
2	H	115/237 (48%)	111 (96%)	4 (4%)	0	100	100
2	I	115/237 (48%)	110 (96%)	5 (4%)	0	100	100
3	L	105/215 (49%)	102 (97%)	3 (3%)	0	100	100
3	M	105/215 (49%)	102 (97%)	3 (3%)	0	100	100
4	U	4/20 (20%)	3 (75%)	1 (25%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	V	4/20 (20%)	3 (75%)	1 (25%)	0	100	100
All	All	1168/1780 (66%)	1113 (95%)	55 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 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	301/372 (81%)	297 (99%)	4 (1%)	65	78
1	B	300/372 (81%)	295 (98%)	5 (2%)	56	73
2	H	94/200 (47%)	92 (98%)	2 (2%)	48	69
2	I	94/200 (47%)	93 (99%)	1 (1%)	70	81
3	L	89/190 (47%)	86 (97%)	3 (3%)	32	57
3	M	87/190 (46%)	86 (99%)	1 (1%)	70	81
4	U	4/12 (33%)	3 (75%)	1 (25%)	0	2
4	V	4/12 (33%)	4 (100%)	0	100	100
All	All	973/1548 (63%)	956 (98%)	17 (2%)	56	73

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	L	89	CYS
4	U	335	PHE
1	B	160	LYS
1	B	297	ASP
2	H	65	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

10 non-standard protein/DNA/RNA residues 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	SEP	U	334	4	8,9,10	0.58	0	8,12,14	0.62	0
4	TPO	V	336	4	8,10,11	1.06	0	10,14,16	1.85	1 (10%)
4	TPO	U	336	4	8,10,11	1.05	0	10,14,16	1.84	1 (10%)
4	SEP	V	334	4	8,9,10	0.58	0	8,12,14	0.61	0
4	SEP	V	338	4	8,9,10	1.53	1 (12%)	8,12,14	1.30	1 (12%)
4	SEP	U	338	4	8,9,10	1.54	1 (12%)	8,12,14	1.25	1 (12%)
4	TPO	V	339	4	8,10,11	1.57	1 (12%)	10,14,16	1.93	1 (10%)
4	TPO	U	342	4	8,10,11	1.65	1 (12%)	10,14,16	1.24	2 (20%)
4	TPO	U	339	4	8,10,11	1.07	0	10,14,16	1.89	1 (10%)
4	TPO	V	342	4	8,10,11	1.63	1 (12%)	10,14,16	1.57	2 (20%)

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	SEP	U	334	4	-	4/5/8/10	-
4	TPO	V	336	4	-	0/9/11/13	-
4	TPO	U	336	4	-	0/9/11/13	-
4	SEP	V	334	4	-	5/5/8/10	-
4	SEP	V	338	4	-	0/5/8/10	-
4	SEP	U	338	4	-	0/5/8/10	-
4	TPO	V	339	4	-	2/9/11/13	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	TPO	U	342	4	-	4/9/11/13	-
4	TPO	U	339	4	-	3/9/11/13	-
4	TPO	V	342	4	-	2/9/11/13	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	V	342	TPO	P-O1P	3.43	1.61	1.50
4	U	342	TPO	P-O1P	3.40	1.61	1.50
4	V	339	TPO	P-O1P	3.38	1.61	1.50
4	U	338	SEP	P-O1P	3.38	1.61	1.50
4	V	338	SEP	P-O1P	3.35	1.61	1.50

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	V	339	TPO	P-OG1-CB	-5.46	106.72	123.21
4	U	339	TPO	P-OG1-CB	-5.32	107.13	123.21
4	V	336	TPO	P-OG1-CB	-5.24	107.38	123.21
4	U	336	TPO	P-OG1-CB	-5.18	107.56	123.21
4	V	342	TPO	P-OG1-CB	-3.86	111.56	123.21

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	U	334	SEP	N-CA-CB-OG
4	U	334	SEP	CB-OG-P-O2P
4	U	339	TPO	N-CA-CB-OG1
4	U	342	TPO	CG2-CB-OG1-P
4	U	342	TPO	CB-OG1-P-O3P

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides 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.

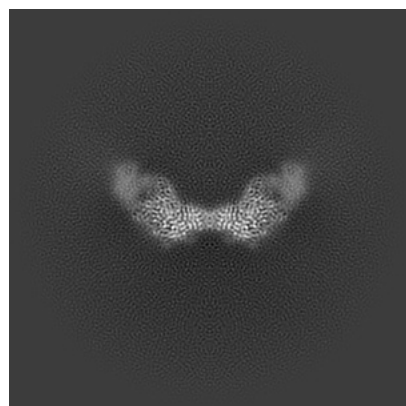
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35104. These allow visual inspection of the internal detail of the map and identification of artifacts.

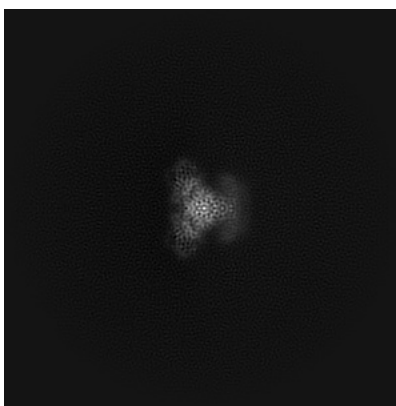
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

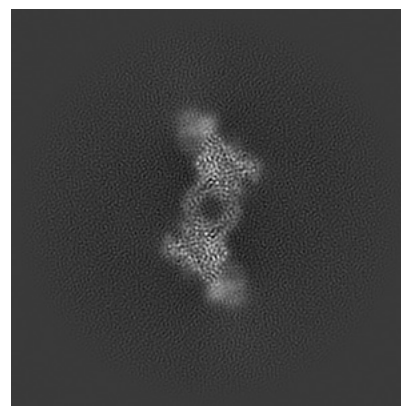
#### 6.1.1 Primary map



X

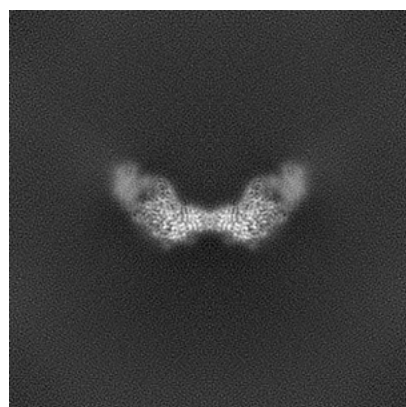


Y

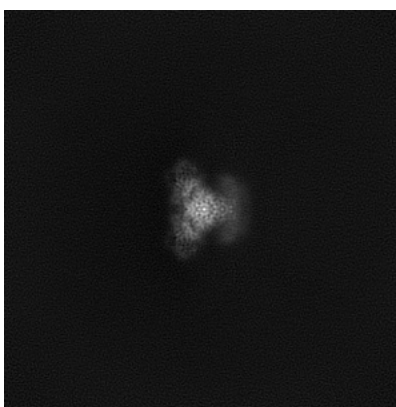


Z

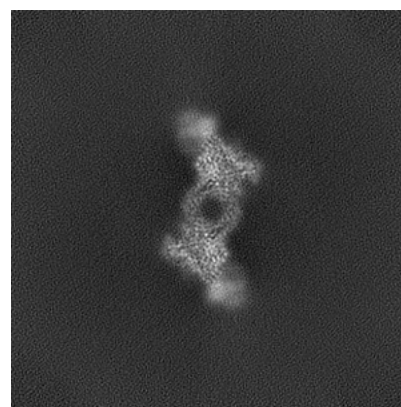
#### 6.1.2 Raw map



X



Y



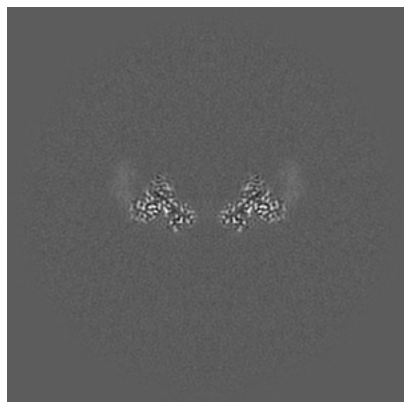
Z

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

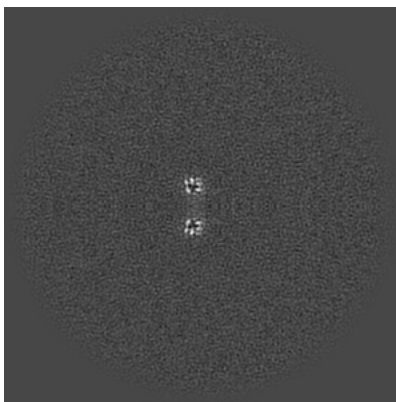


## 6.2 Central slices [i](#)

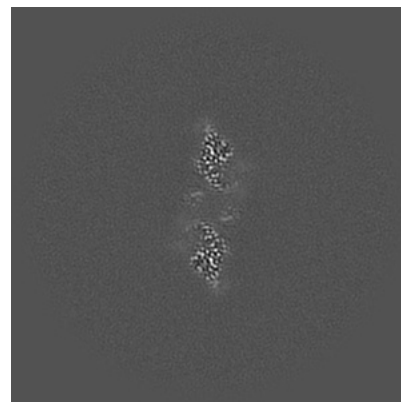
### 6.2.1 Primary map



X Index: 144

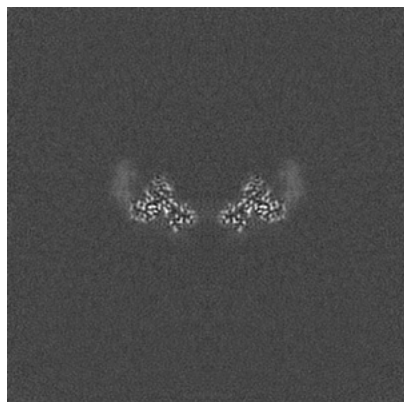


Y Index: 144

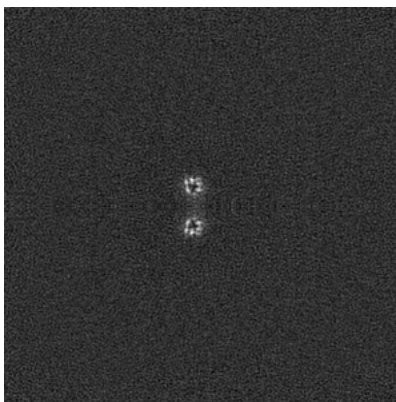


Z Index: 144

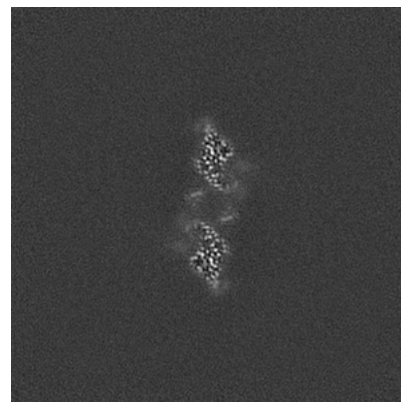
### 6.2.2 Raw map



X Index: 144



Y Index: 144



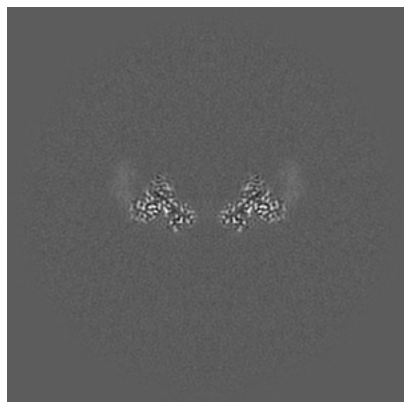
Z Index: 144

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

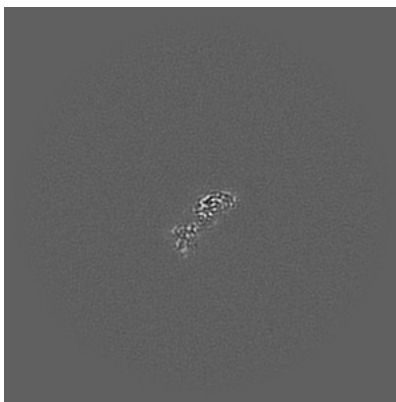


## 6.3 Largest variance slices [i](#)

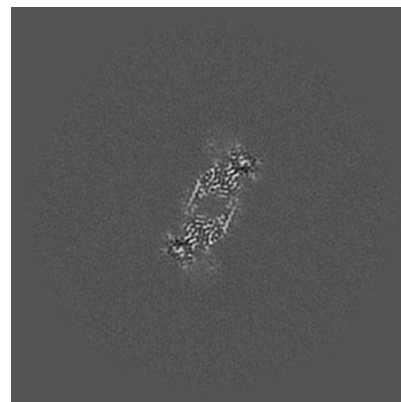
### 6.3.1 Primary map



X Index: 144

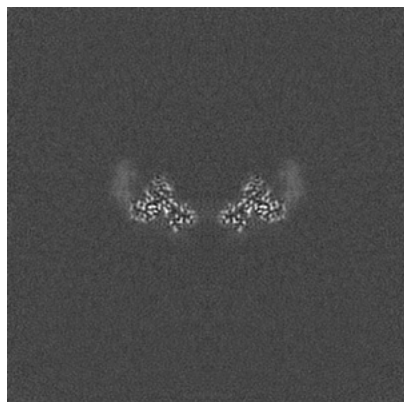


Y Index: 109

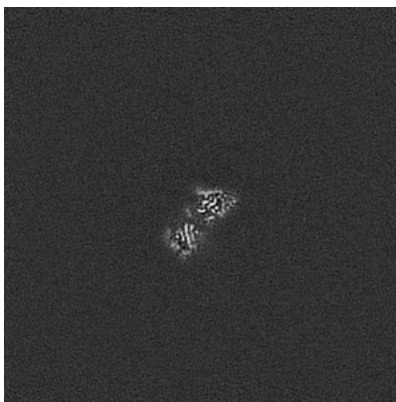


Z Index: 132

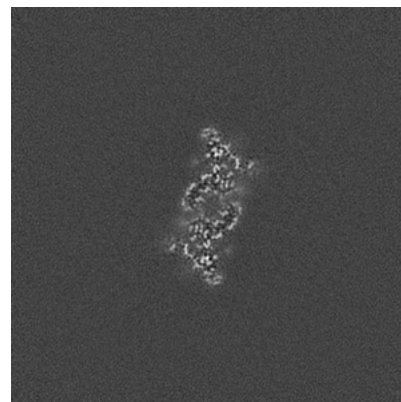
### 6.3.2 Raw map



X Index: 144



Y Index: 112

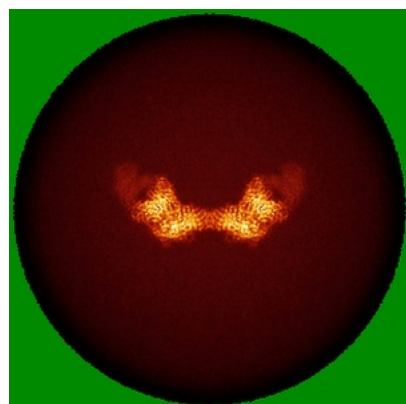


Z Index: 138

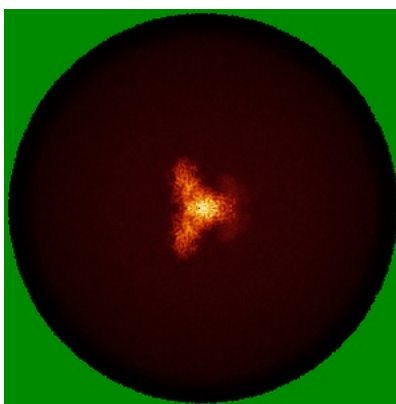
The images above show the largest variance slices of the map in three orthogonal directions.

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

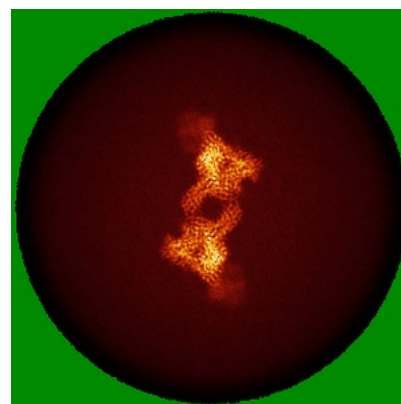
### 6.4.1 Primary map



X

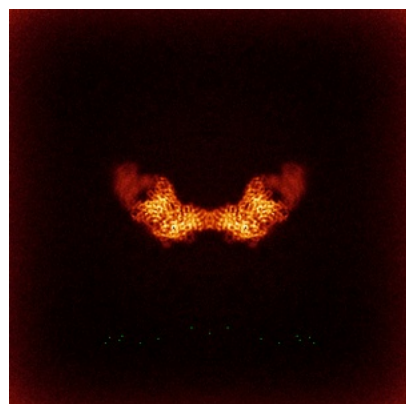


Y

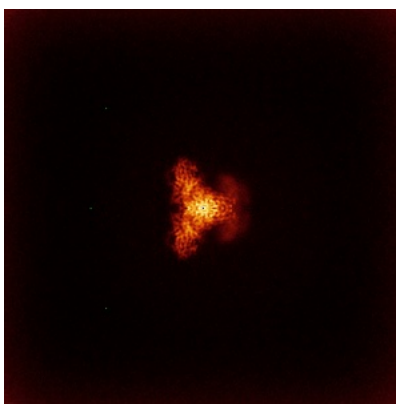


Z

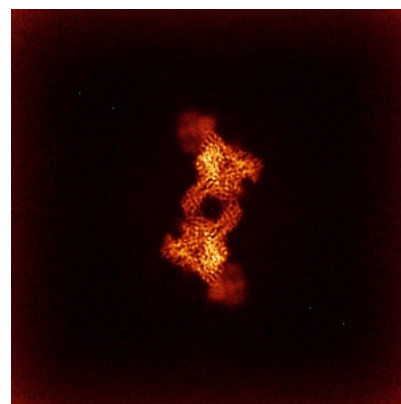
### 6.4.2 Raw map



X



Y

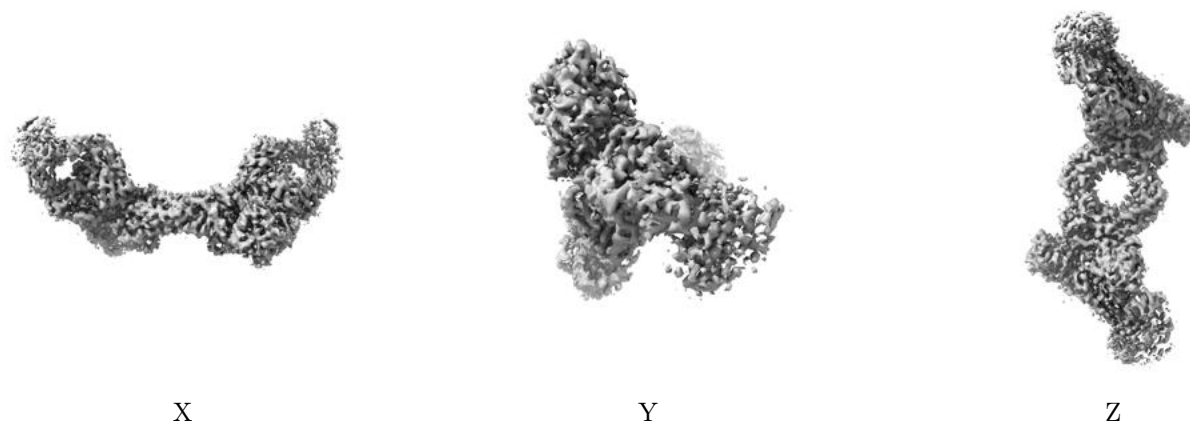


Z

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.

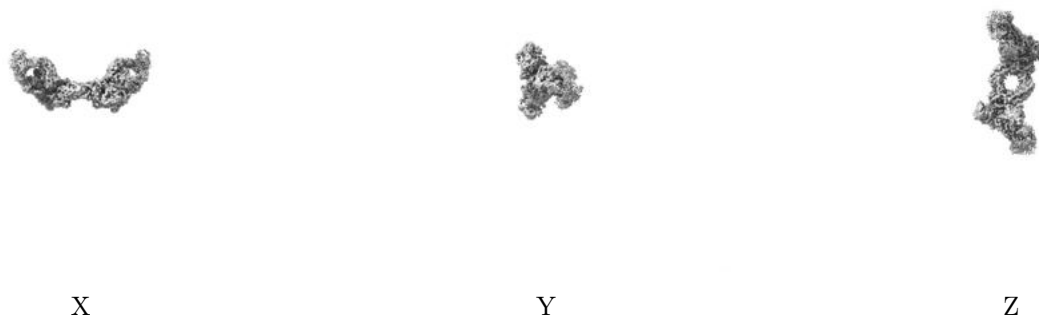
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. 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.

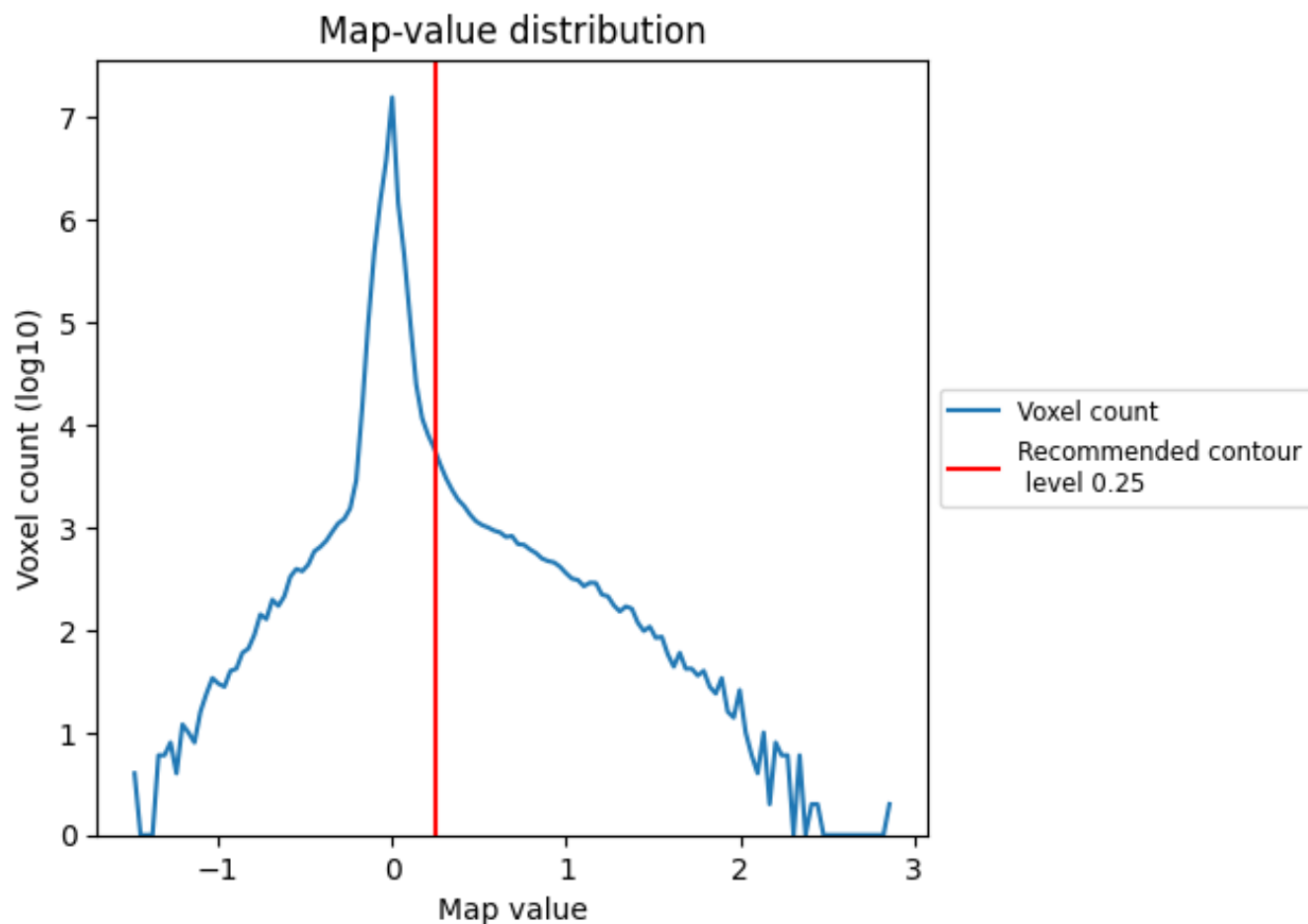
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

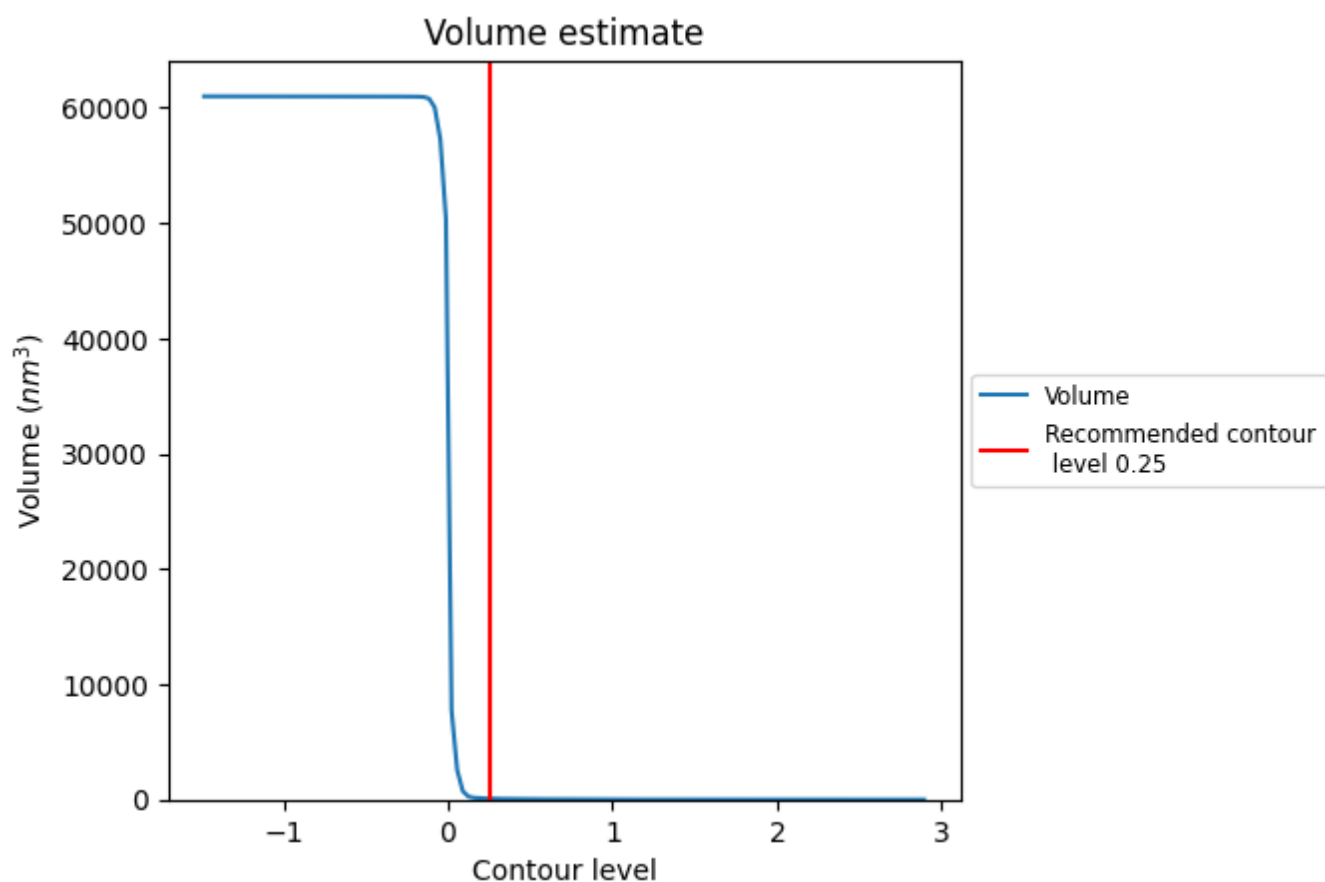
This section contains the results of statistical analysis of the map.

### 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.

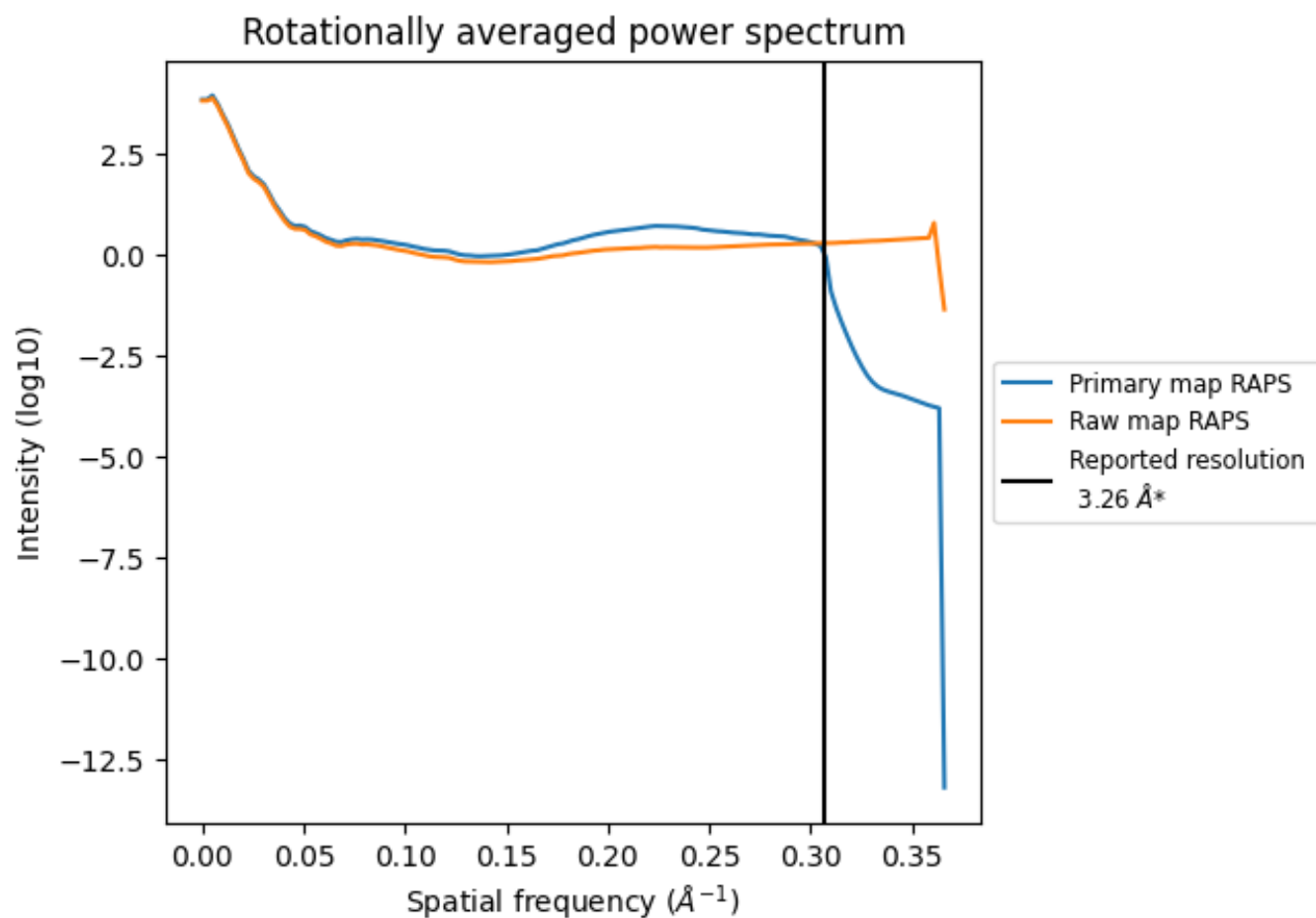
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 86 nm<sup>3</sup>; this corresponds to an approximate mass of 78 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 ⓘ

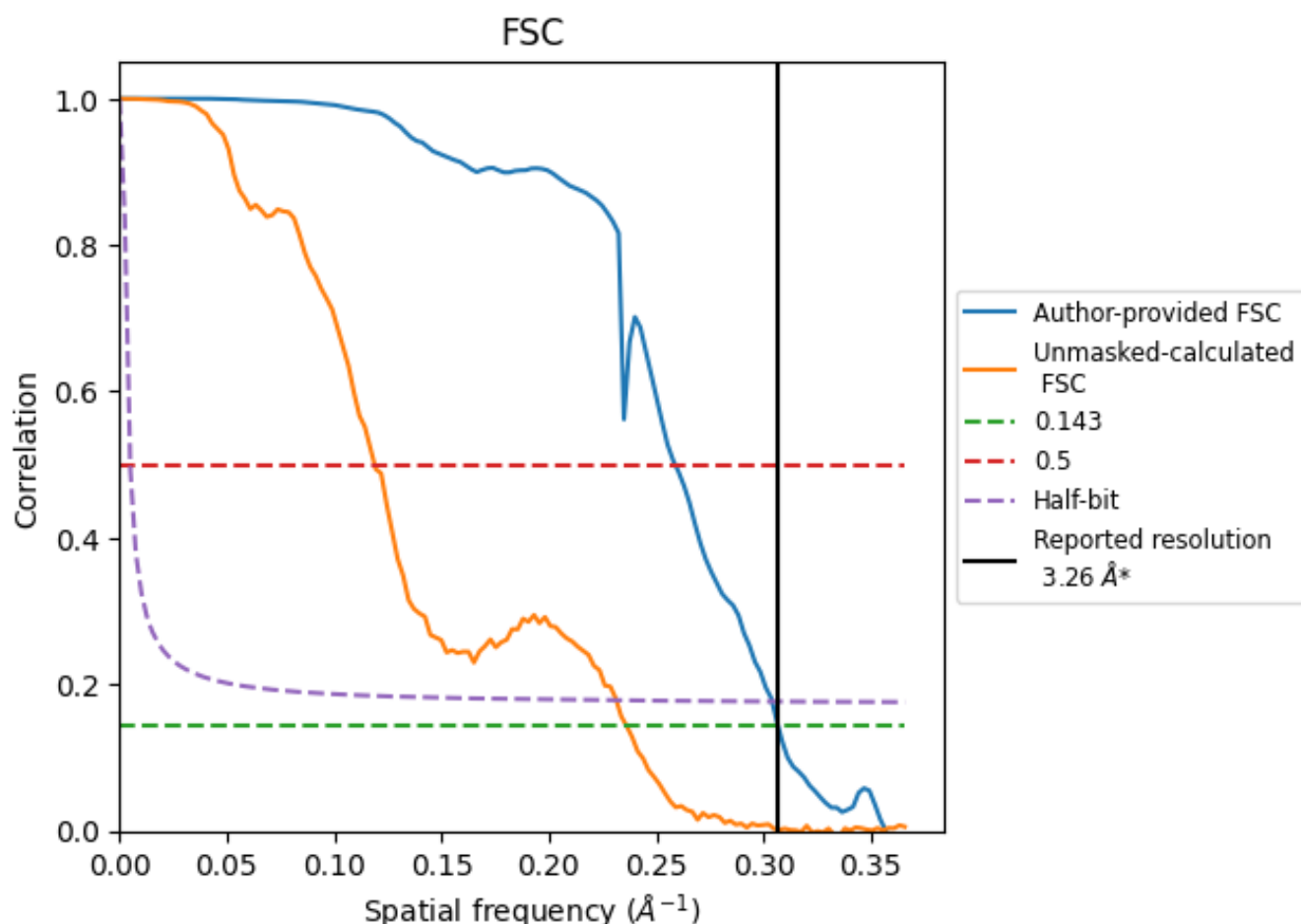


\*Reported resolution corresponds to spatial frequency of 0.307 Å<sup>-1</sup>

## 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 0.307 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	3.26	-	-
Author-provided FSC curve	3.26	3.86	3.29
Unmasked-calculated*	4.23	8.42	4.32

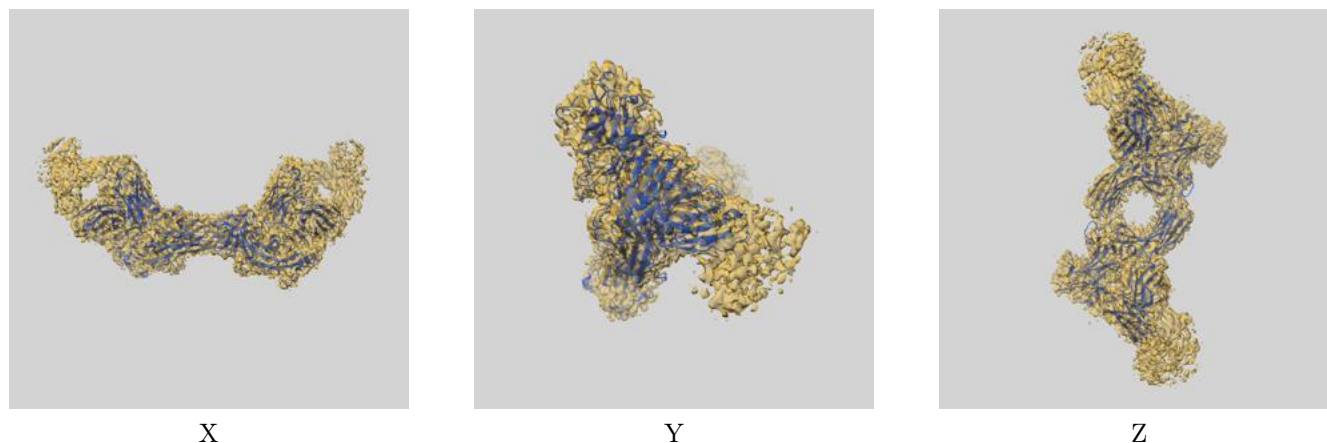
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.23 differs from the reported value 3.26 by more than 10 %



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

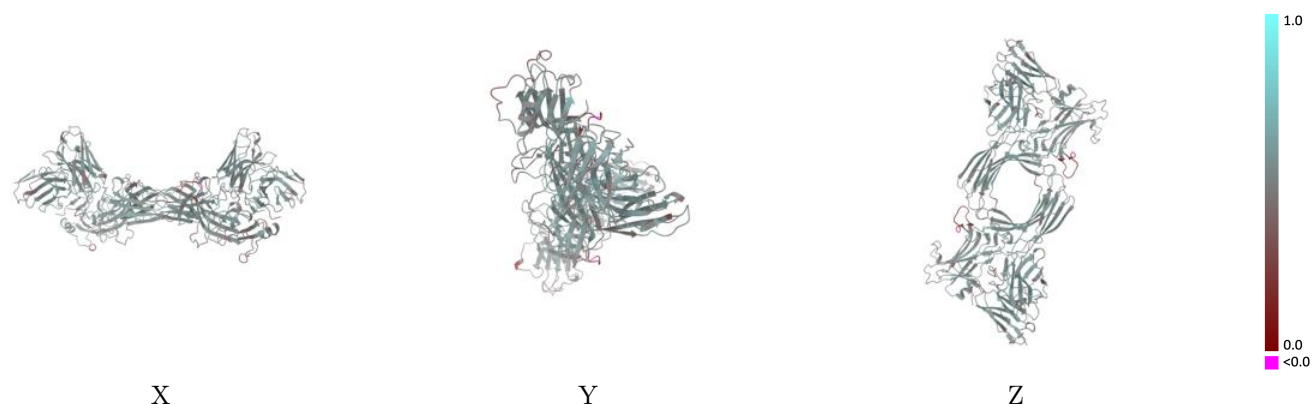
This section contains information regarding the fit between EMDB map EMD-35104 and PDB model 8I0N. Per-residue inclusion information can be found in section 3 on page 5.

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



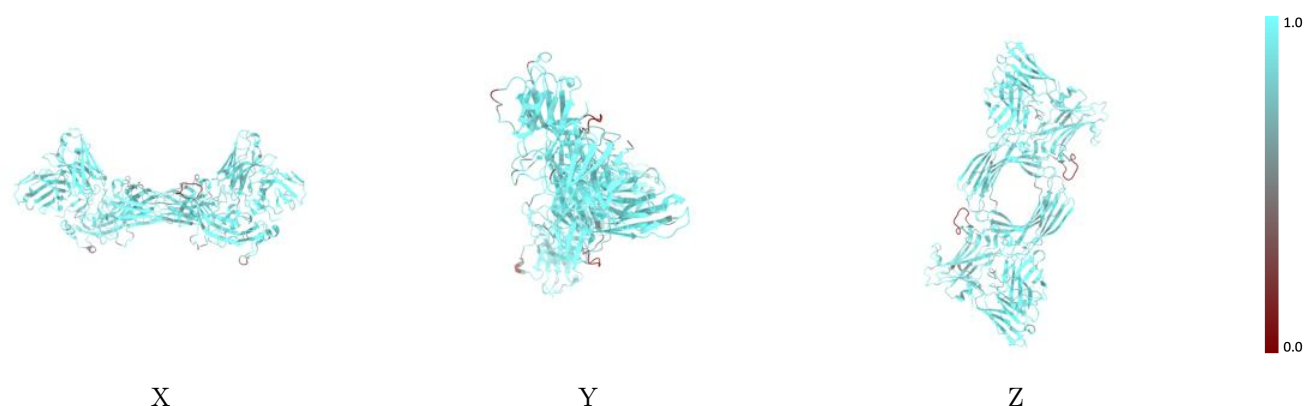
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



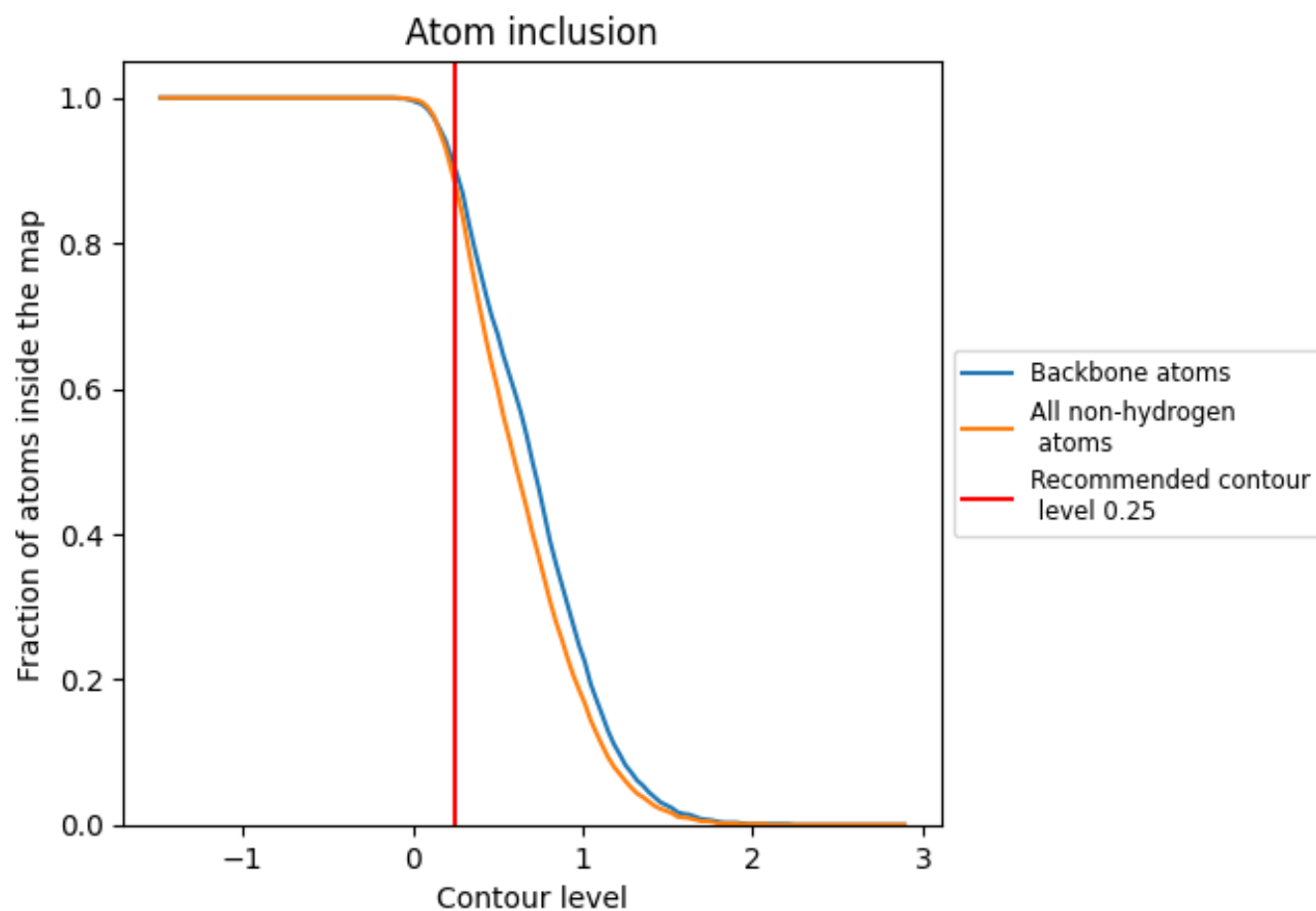
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 88% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8810	<div><div></div></div> 0.5130
A	<div><div></div></div> 0.8550	<div><div></div></div> 0.5020
B	<div><div></div></div> 0.8510	<div><div></div></div> 0.5020
H	<div><div></div></div> 0.9300	<div><div></div></div> 0.5360
I	<div><div></div></div> 0.9300	<div><div></div></div> 0.5350
L	<div><div></div></div> 0.9150	<div><div></div></div> 0.5260
M	<div><div></div></div> 0.9230	<div><div></div></div> 0.5270
U	<div><div></div></div> 0.9430	<div><div></div></div> 0.5020
V	<div><div></div></div> 0.9200	<div><div></div></div> 0.5000

1.0

0.0

<0.0