



## wwPDB EM Validation Summary Report ⓘ

Nov 11, 2024 – 01:48 PM JST

PDB ID : 7E33  
EMDB ID : EMD-30975  
Title : Serotonin 1E (5-HT1E) receptor-Gi protein complex  
Authors : Xu, P.; Huang, S.; Zhang, H.; Mao, C.; Zhou, X.E.; Shen, D.D.; Jiang, Y.;  
Zhang, Y.; Xu, H.E.  
Deposited on : 2021-02-07  
Resolution : 2.90 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.dev113  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
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

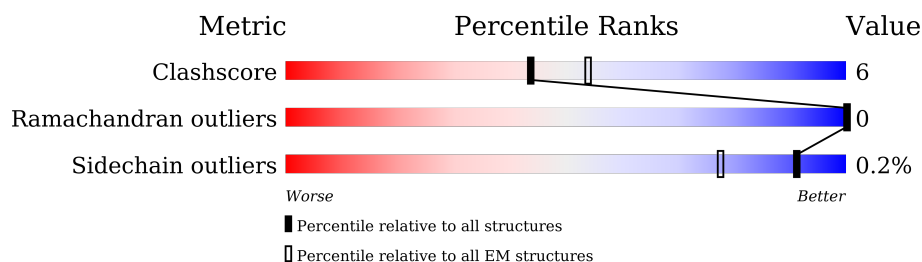
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.90 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	354	
2	B	345	
3	E	248	
4	G	71	
5	R	504	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8538 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 Guanine nucleotide-binding protein G(i) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	217	Total	C	N	O	S	0	0
			1750	1114	293	331	12		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	ASN	SER	engineered mutation	UNP P63096
A	203	ALA	GLY	engineered mutation	UNP P63096
A	245	ALA	GLU	engineered mutation	UNP P63096
A	326	SER	ALA	engineered mutation	UNP P63096

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	333	Total	C	N	O	S	0	0
			2558	1580	460	497	21		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	MET	-	initiating methionine	UNP P62873
B	-3	GLY	-	expression tag	UNP P62873
B	-2	SER	-	expression tag	UNP P62873
B	-1	LEU	-	expression tag	UNP P62873
B	0	LEU	-	expression tag	UNP P62873
B	1	GLN	-	expression tag	UNP P62873

- Molecule 3 is a protein called scFv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	229	Total	C	N	O	S	0	0
			1762	1117	292	343	10		

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	50	Total	C	N	O	S	0	0
			391	246	69	73	3		

- Molecule 5 is a protein called Soluble cytochrome b562,5-hydroxytryptamine receptor 1E.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	257	Total	C	N	O	S	0	0
			2060	1375	322	347	16		

There are 38 discrepancies between the modelled and reference sequences:

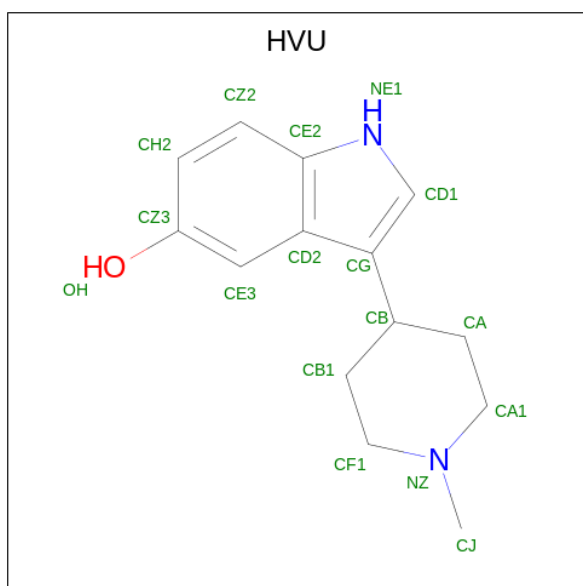
Chain	Residue	Modelled	Actual	Comment	Reference
R	-138	ASP	-	expression tag	UNP P0ABE7
R	-137	TYR	-	expression tag	UNP P0ABE7
R	-136	LYS	-	expression tag	UNP P0ABE7
R	-135	ASP	-	expression tag	UNP P0ABE7
R	-134	ASP	-	expression tag	UNP P0ABE7
R	-133	ASP	-	expression tag	UNP P0ABE7
R	-132	ASP	-	expression tag	UNP P0ABE7
R	-131	ALA	-	expression tag	UNP P0ABE7
R	-130	LYS	-	expression tag	UNP P0ABE7
R	-129	LEU	-	expression tag	UNP P0ABE7
R	-128	GLN	-	expression tag	UNP P0ABE7
R	-127	THR	-	expression tag	UNP P0ABE7
R	-126	MET	-	expression tag	UNP P0ABE7
R	-125	HIS	-	expression tag	UNP P0ABE7
R	-124	HIS	-	expression tag	UNP P0ABE7
R	-123	HIS	-	expression tag	UNP P0ABE7
R	-122	HIS	-	expression tag	UNP P0ABE7
R	-121	HIS	-	expression tag	UNP P0ABE7
R	-120	HIS	-	expression tag	UNP P0ABE7
R	-119	HIS	-	expression tag	UNP P0ABE7
R	-118	HIS	-	expression tag	UNP P0ABE7
R	-117	HIS	-	expression tag	UNP P0ABE7
R	-116	HIS	-	expression tag	UNP P0ABE7
R	-109	TRP	MET	engineered mutation	UNP P0ABE7
R	-14	ILE	HIS	engineered mutation	UNP P0ABE7
R	-10	LEU	ARG	engineered mutation	UNP P0ABE7
R	-9	ALA	-	linker	UNP P0ABE7
R	-8	SER	-	linker	UNP P0ABE7

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Chain	Residue	Modelled	Actual	Comment	Reference
R	-7	GLU	-	linker	UNP P0ABE7
R	-6	ASN	-	linker	UNP P0ABE7
R	-5	LEU	-	linker	UNP P0ABE7
R	-4	TYR	-	linker	UNP P0ABE7
R	-3	PHE	-	linker	UNP P0ABE7
R	-2	GLN	-	linker	UNP P0ABE7
R	-1	GLY	-	linker	UNP P0ABE7
R	0	GLY	-	linker	UNP P0ABE7
R	1	THR	-	linker	UNP P0ABE7
R	111	TRP	LEU	engineered mutation	UNP P28566

- Molecule 6 is 3-(1-methylpiperidin-4-yl)-1H-indol-5-ol (three-letter code: HVU) (formula:  $C_{14}H_{18}N_2O$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
6	R	1	Total	C	N	O	0
			17	14	2	1	





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	163354	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 ( $e^-/\text{\AA}^2$ )	62	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	49310	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.540	Depositor
Minimum map value	-0.350	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.06	Depositor
Map size ( $\text{\AA}$ )	200.63998, 200.63998, 200.63998	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.045, 1.045, 1.045	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: HVU

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	0.24	0/1779	0.39	0/2385
2	B	0.24	0/2605	0.45	0/3532
3	E	0.25	0/1806	0.43	0/2448
4	G	0.25	0/397	0.36	0/535
5	R	0.24	0/2107	0.38	0/2872
All	All	0.24	0/8694	0.41	0/11772

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	1750	0	1746	33	0
2	B	2558	0	2468	28	0
3	E	1762	0	1692	12	0
4	G	391	0	402	5	0
5	R	2060	0	2176	35	0
6	R	17	0	0	2	0
All	All	8538	0	8484	108	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 6.

The worst 5 of 108 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:B:331:SER:OG	2:B:333:ASP:OD1	1.92	0.87
1:A:203:ALA:O	1:A:205:ARG:NH1	2.13	0.82
2:B:145:TYR:OH	2:B:188:MET:SD	2.38	0.81
2:B:245:SER:OG	2:B:247:ASP:OD2	2.03	0.76
5:R:73:VAL:HG23	5:R:74:LEU:HD12	1.67	0.76

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	211/354 (60%)	211 (100%)	0	0	100	100
2	B	331/345 (96%)	322 (97%)	9 (3%)	0	100	100
3	E	225/248 (91%)	224 (100%)	1 (0%)	0	100	100
4	G	48/71 (68%)	47 (98%)	1 (2%)	0	100	100
5	R	251/504 (50%)	249 (99%)	2 (1%)	0	100	100
All	All	1066/1522 (70%)	1053 (99%)	13 (1%)	0	100	100

There are no Ramachandran outliers to report.

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

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	193/305 (63%)	193 (100%)	0	100	100
2	B	276/287 (96%)	276 (100%)	0	100	100
3	E	194/201 (96%)	194 (100%)	0	100	100
4	G	42/58 (72%)	42 (100%)	0	100	100
5	R	230/447 (52%)	228 (99%)	2 (1%)	75	92
All	All	935/1298 (72%)	933 (100%)	2 (0%)	91	98

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	R	210	LYS
5	R	310	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
5	R	112	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

1 ligand is 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
6	HVU	R	501	-	19,19,19	3.73	9 (47%)	22,27,27	1.85	7 (31%)

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
6	HVU	R	501	-	-	2/2/14/14	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	R	501	HVU	CG-CD2	9.49	1.51	1.40
6	R	501	HVU	CJ-NZ	-6.63	1.31	1.46
6	R	501	HVU	CA1-NZ	-6.60	1.32	1.46
6	R	501	HVU	CF1-NZ	-5.50	1.34	1.46
6	R	501	HVU	CD1-NE1	-3.91	1.28	1.36

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	R	501	HVU	CG-CD2-CE2	-4.86	101.77	106.83
6	R	501	HVU	CZ3-CE3-CD2	-2.92	118.60	120.64
6	R	501	HVU	CD2-CE2-NE1	-2.76	101.78	107.92
6	R	501	HVU	CF1-CB1-CB	-2.64	107.92	111.04
6	R	501	HVU	CG-CD1-NE1	-2.38	104.25	108.79

There are no chirality outliers.

All (2) torsion outliers are listed below:

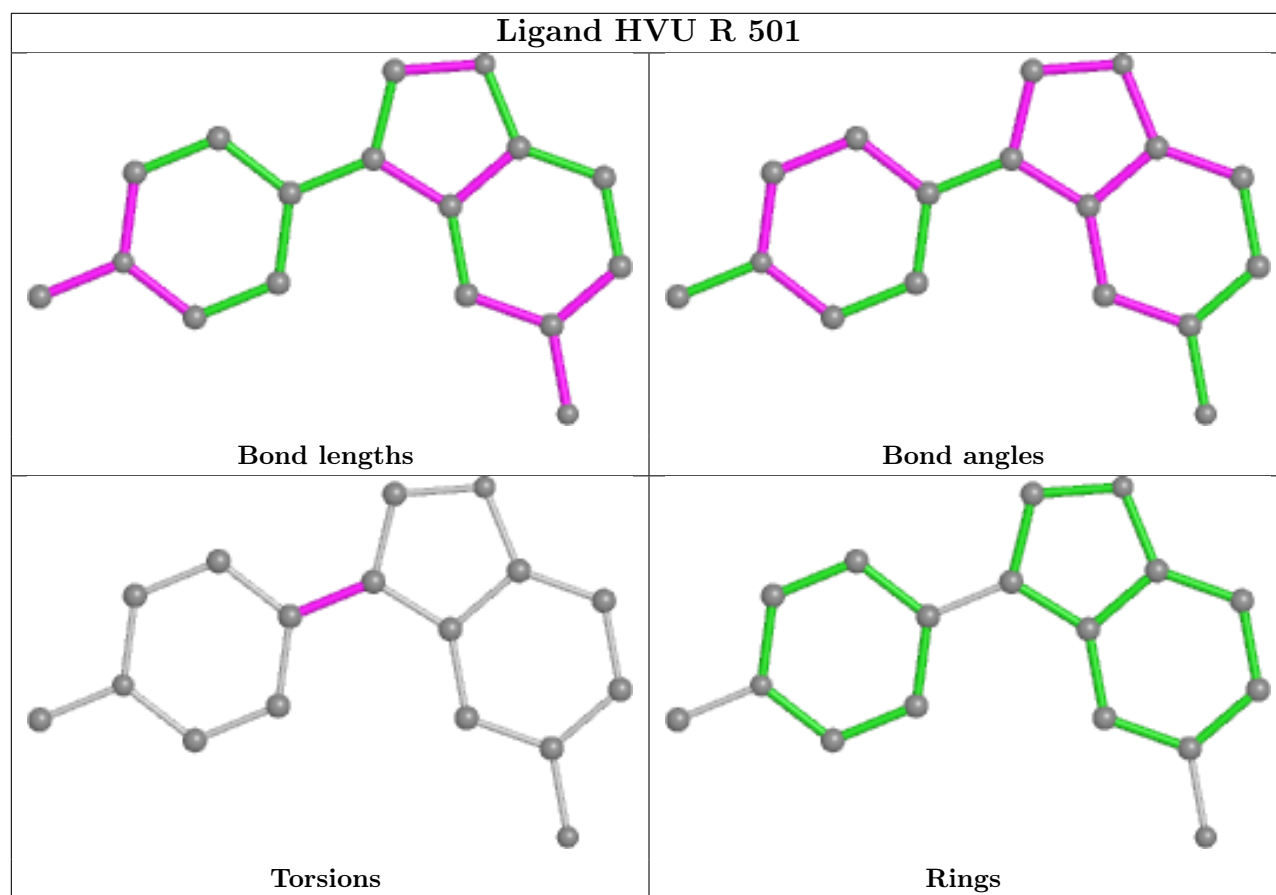
Mol	Chain	Res	Type	Atoms
6	R	501	HVU	CA-CB-CG-CD1
6	R	501	HVU	CB1-CB-CG-CD1

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	R	501	HVU	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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.

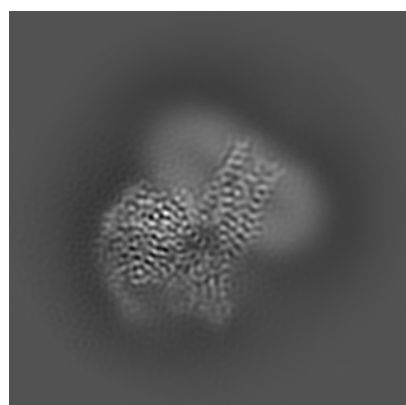
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30975. These allow visual inspection of the internal detail of the map and identification of artifacts.

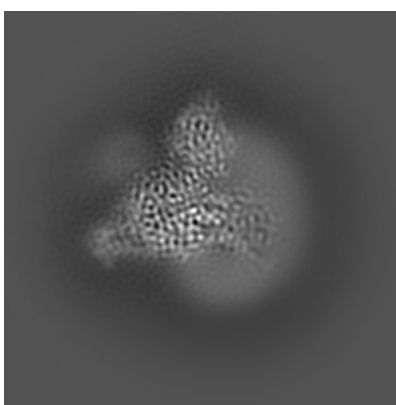
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

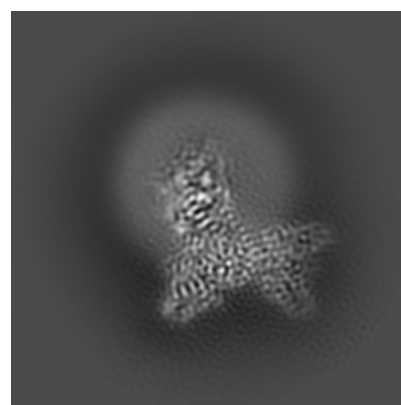
#### 6.1.1 Primary map



X



Y

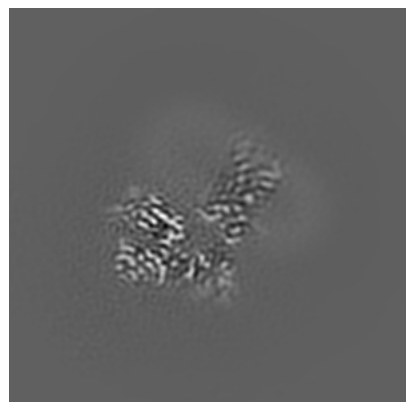


Z

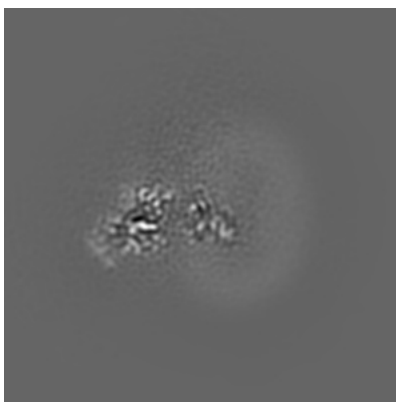
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

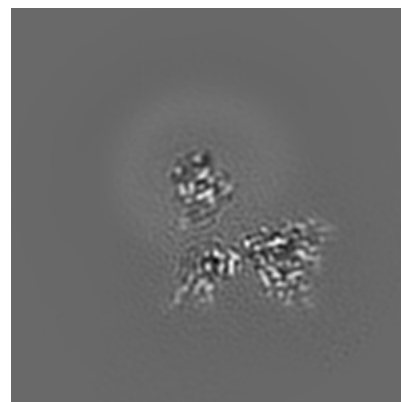
#### 6.2.1 Primary map



X Index: 96



Y Index: 96

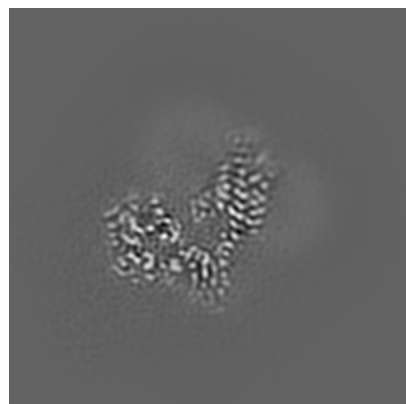


Z Index: 96

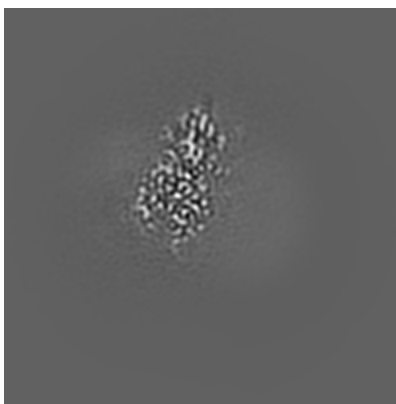
The images above show central slices of the map in three orthogonal directions.

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

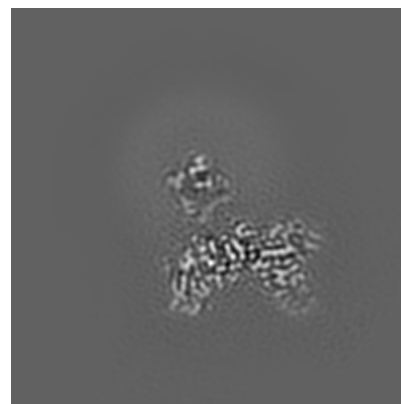
### 6.3.1 Primary map



X Index: 91



Y Index: 74

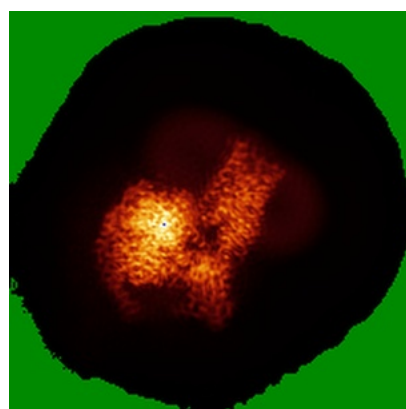


Z Index: 89

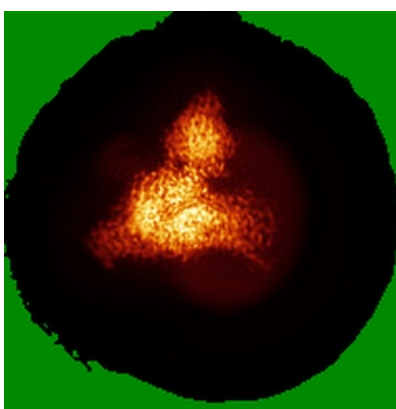
The images above show the largest variance slices of the map in three orthogonal directions.

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

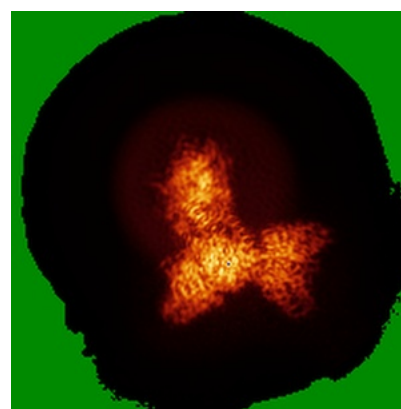
### 6.4.1 Primary map



X



Y



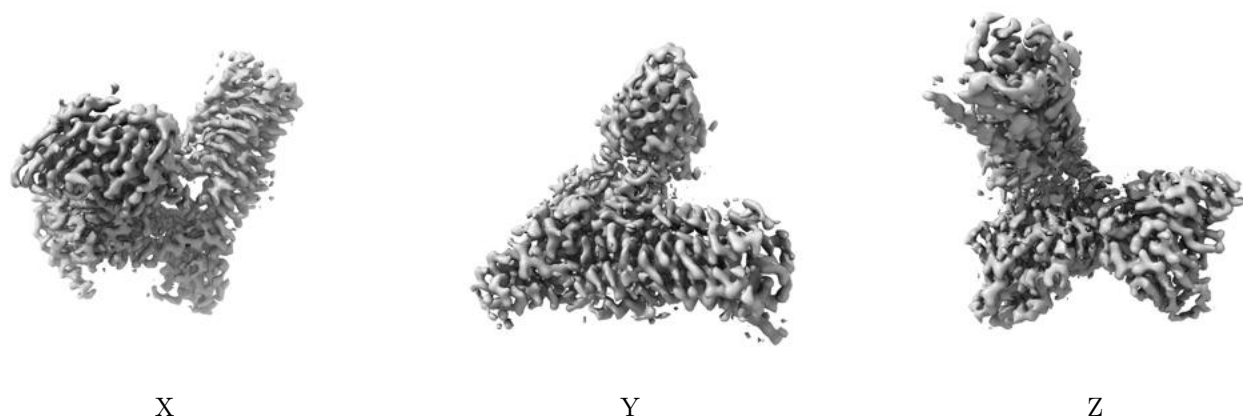
Z

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 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

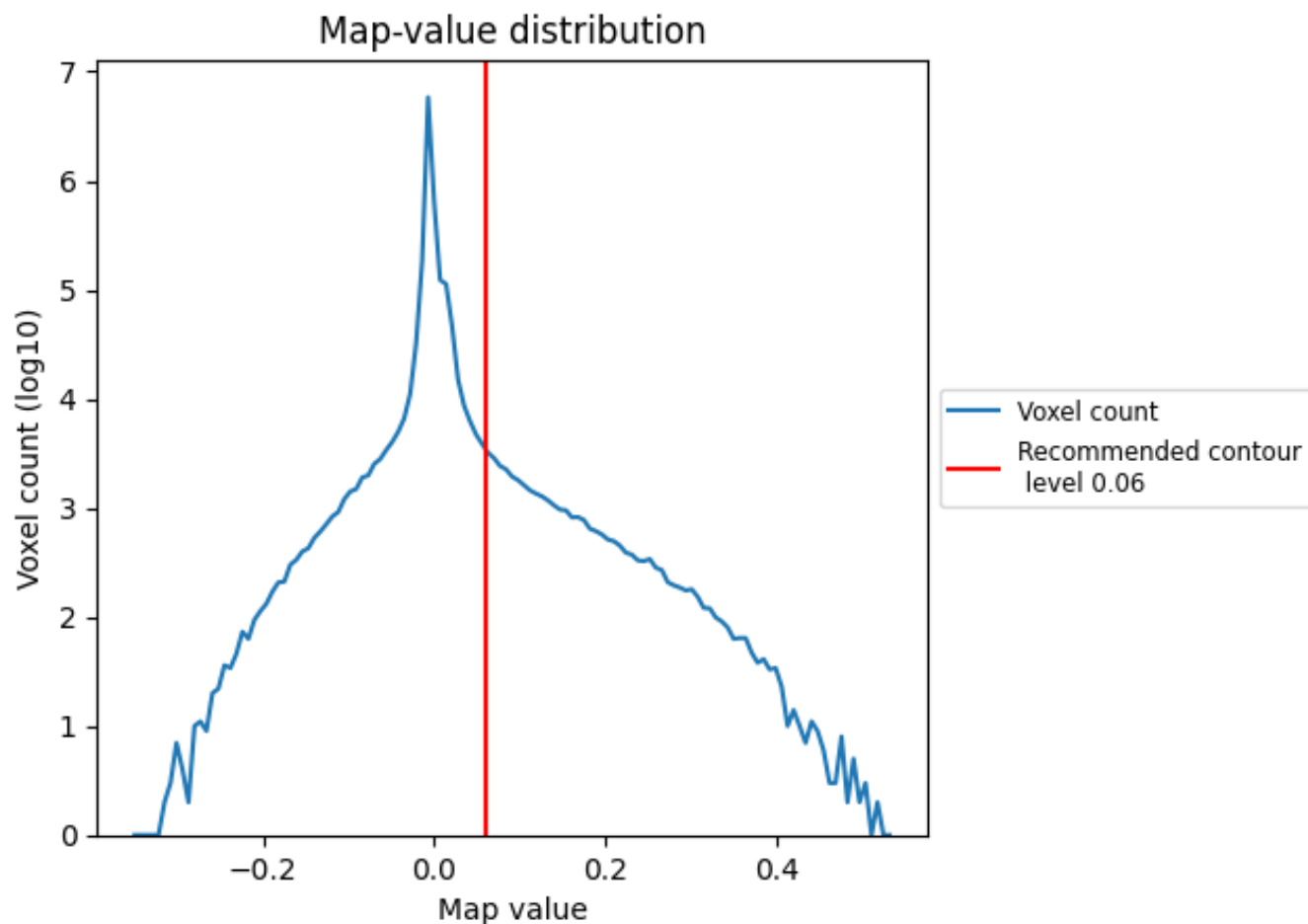
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

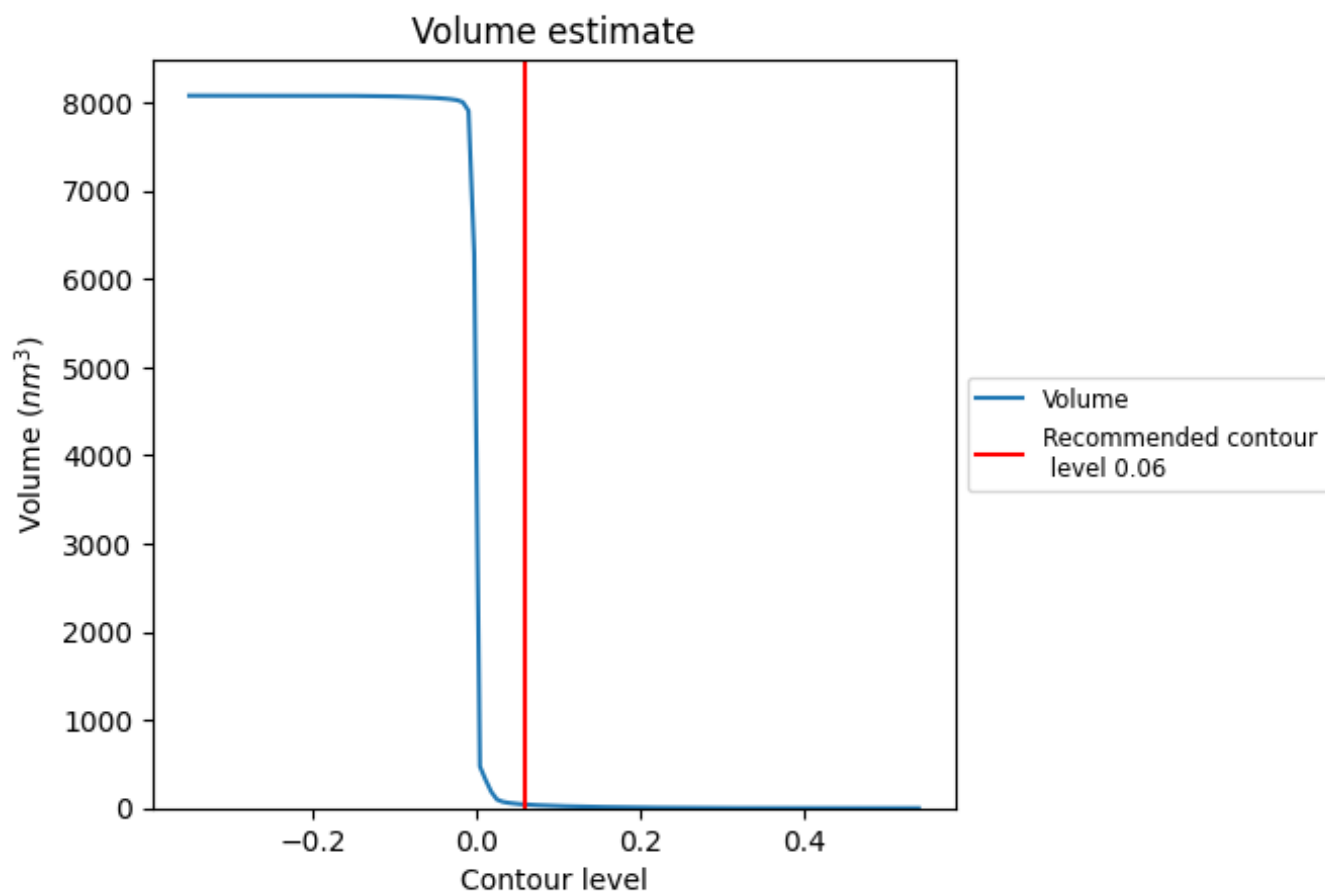
This section contains the results of statistical analysis of the map.

### 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.

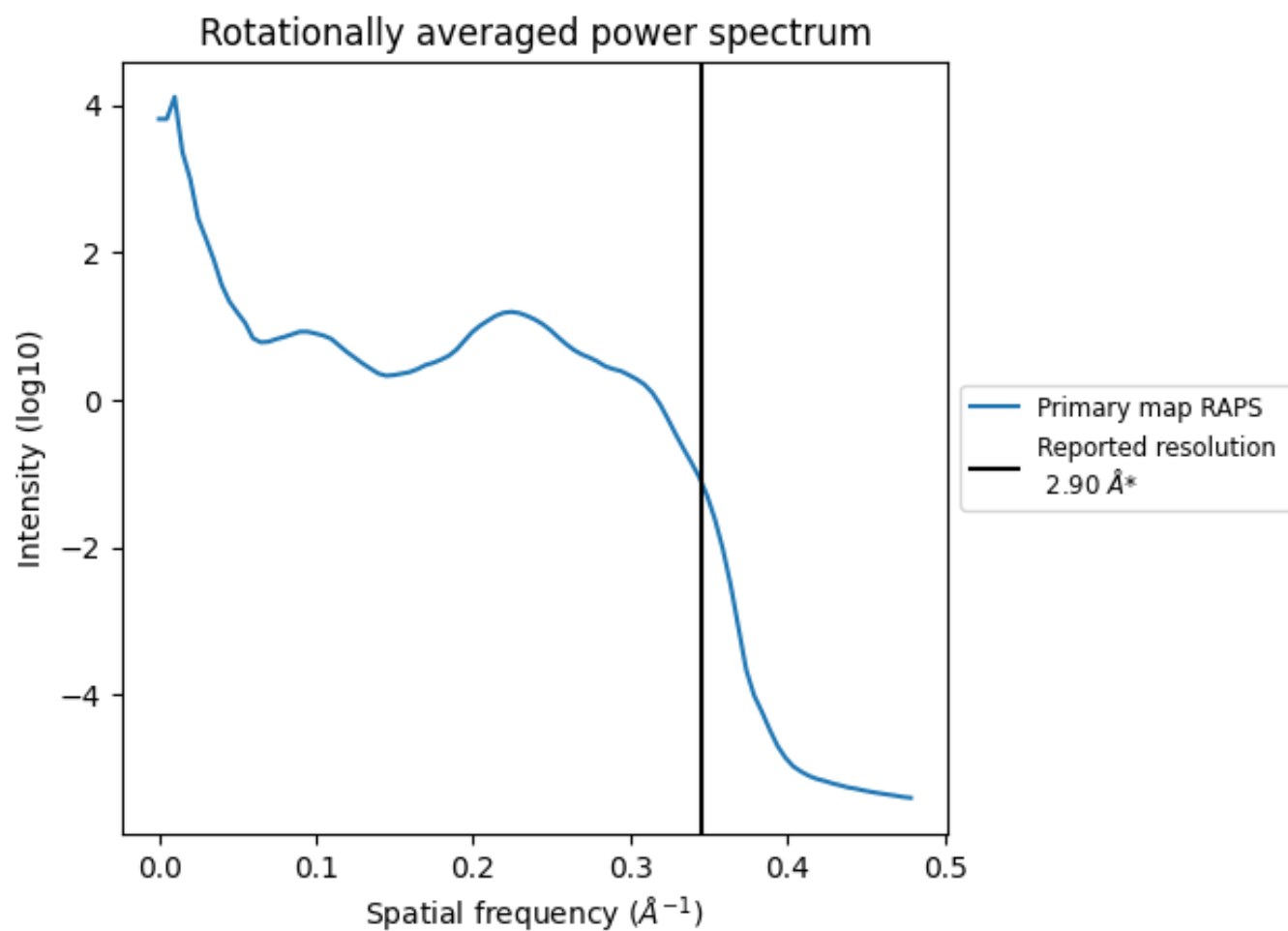
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 41 nm<sup>3</sup>; this corresponds to an approximate mass of 37 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 0.345 Å<sup>-1</sup>

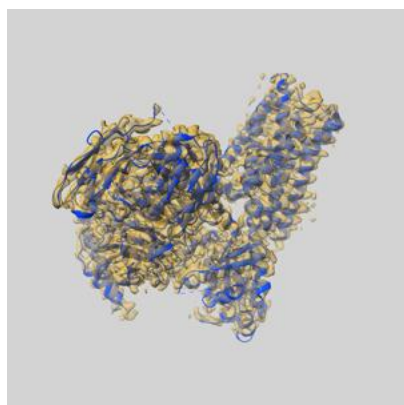
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

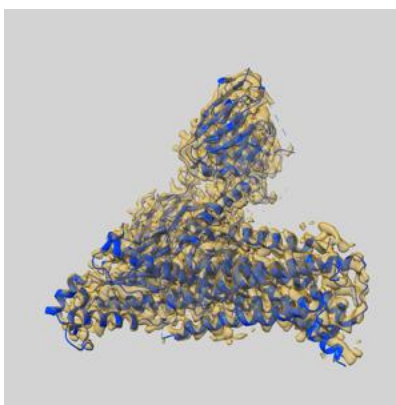
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30975 and PDB model 7E33. Per-residue inclusion information can be found in section [3](#) on page [6](#).

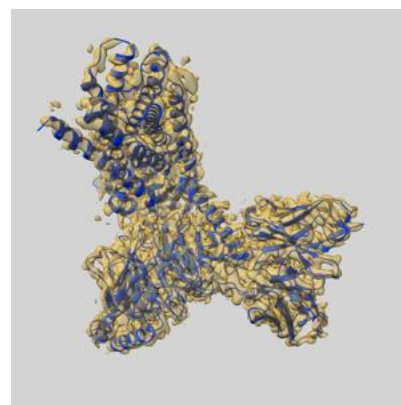
### 9.1 Map-model overlay [i](#)



X



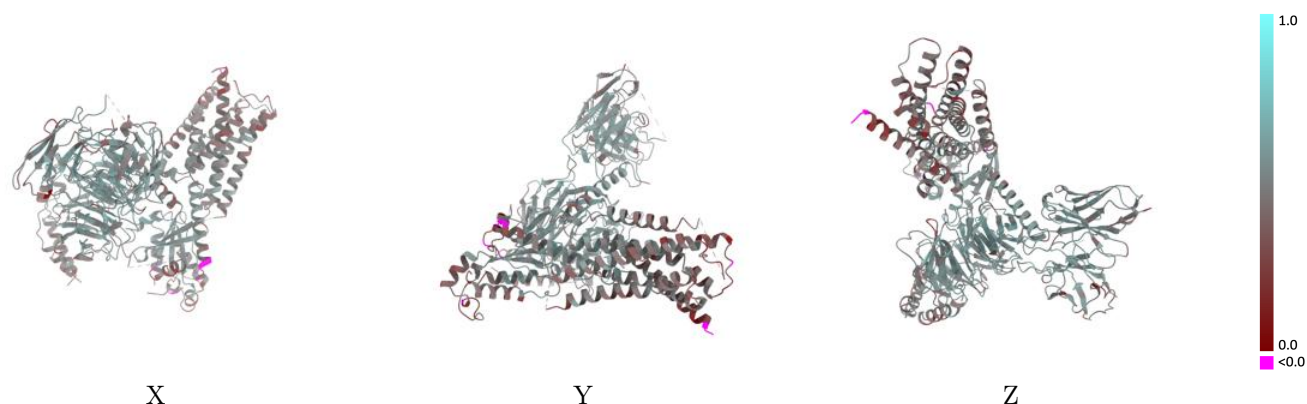
Y



Z

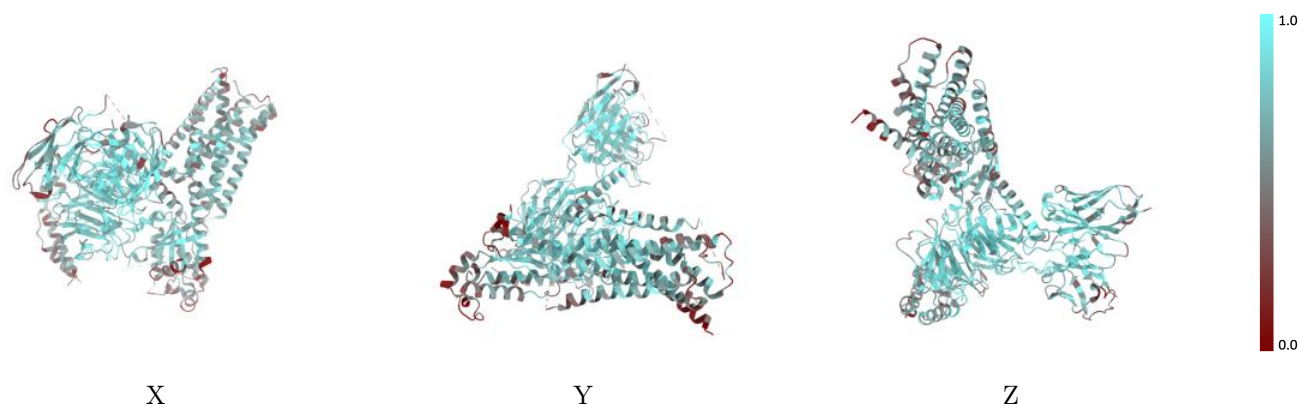
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



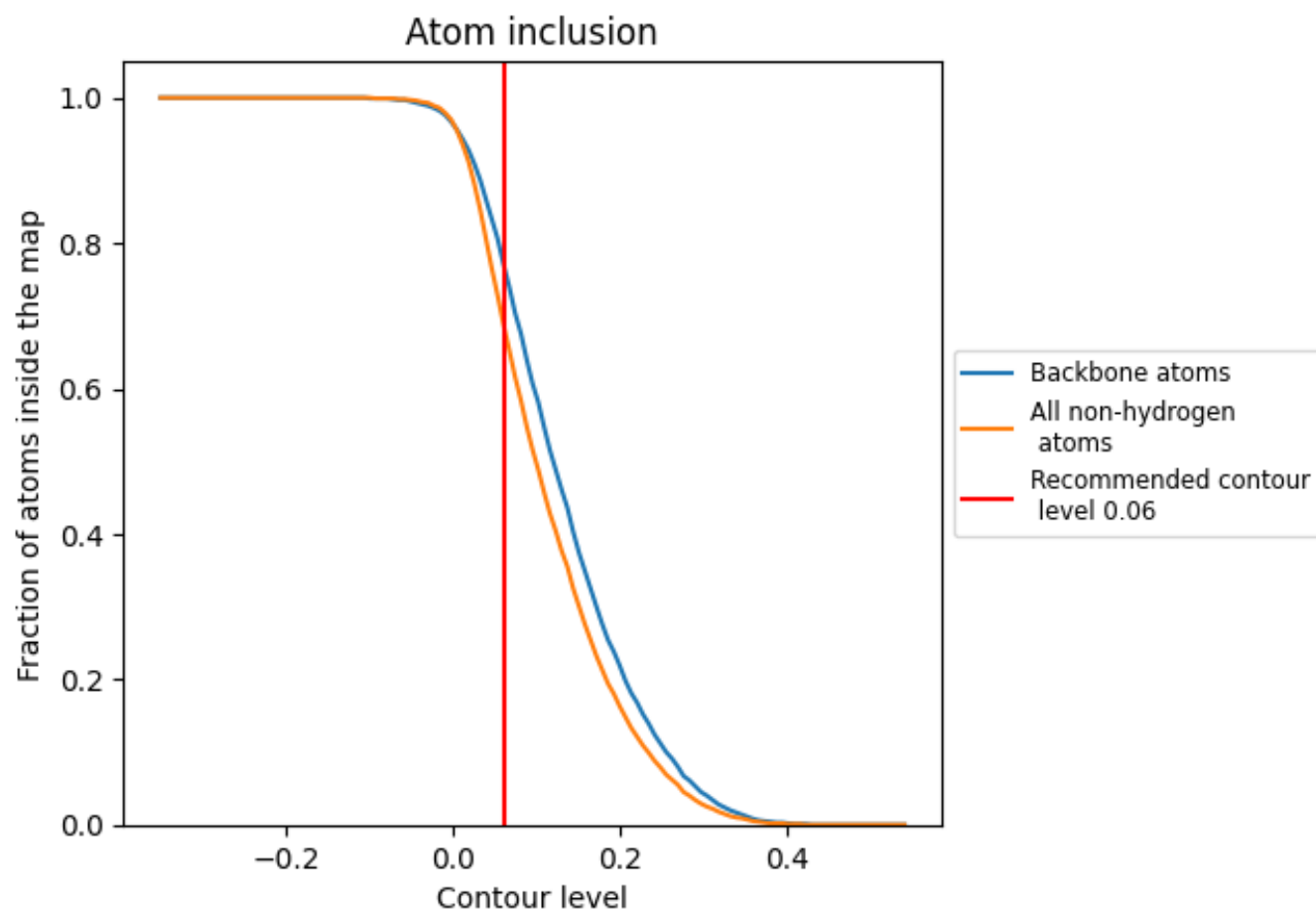
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 69% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6880	<div></div> 0.4810
A	<div></div> 0.6170	<div></div> 0.4650
B	<div></div> 0.7770	<div></div> 0.5210
E	<div></div> 0.7340	<div></div> 0.5200
G	<div></div> 0.5940	<div></div> 0.4450
R	<div></div> 0.6170	<div></div> 0.4160

