



# wwPDB EM Validation Summary Report ⓘ

Nov 13, 2022 – 08:46 AM EST

PDB ID : 6V0E  
EMDB ID : EMD-20995  
Title : Lipophilic Envelope-spanning Tunnel B (LetB), Model 3  
Authors : Isom, G.L.; Coudray, N.; MacRae, M.R.; McManus, C.T.; Ekiert, D.C.; Bhabha, G.  
Deposited on : 2019-11-18  
Resolution : 3.06 Å(reported)  
Based on initial model : 5UW2

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>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

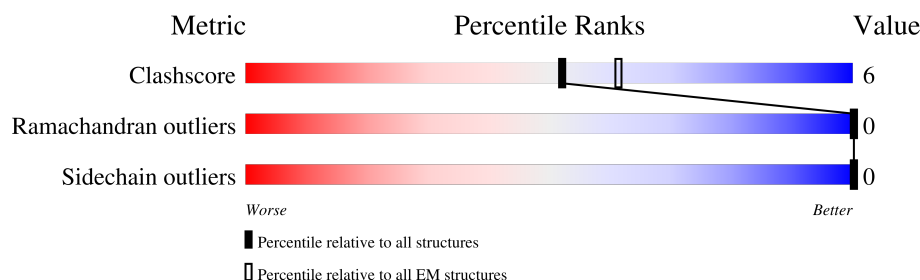
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.06 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	832	
1	B	832	
1	C	832	
1	D	832	
1	E	832	
1	F	832	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 16602 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.

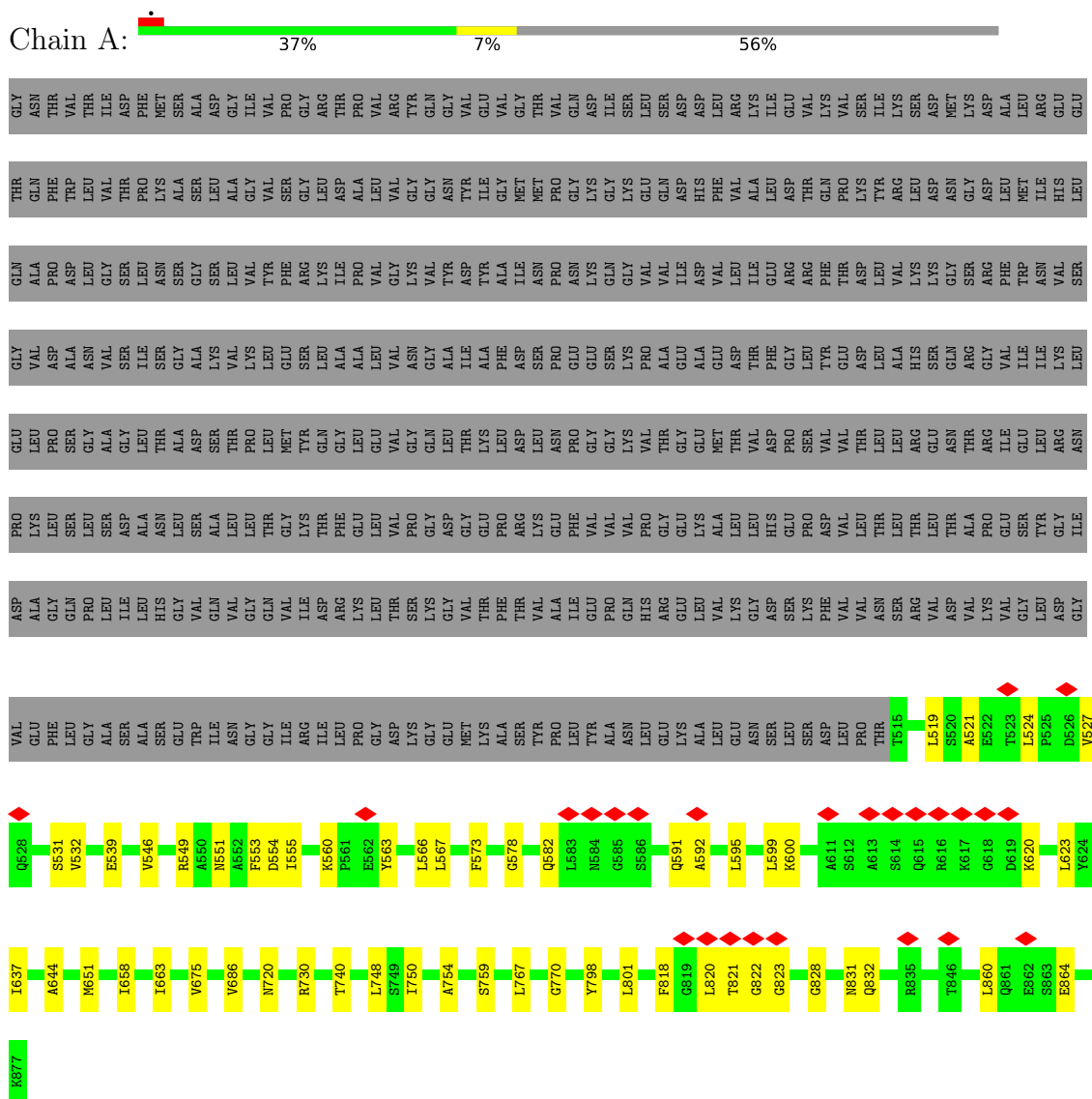
- Molecule 1 is a protein called Intermembrane transport protein YebT.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	363	Total 2767	C 1757	N 487	O 519	S 4	0	0
1	B	363	Total 2767	C 1757	N 487	O 519	S 4	0	0
1	C	363	Total 2767	C 1757	N 487	O 519	S 4	0	0
1	D	363	Total 2767	C 1757	N 487	O 519	S 4	0	0
1	E	363	Total 2767	C 1757	N 487	O 519	S 4	0	0
1	F	363	Total 2767	C 1757	N 487	O 519	S 4	0	0

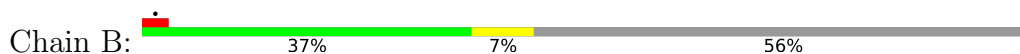
### 3 Residue-property plots

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: Intermembrane transport protein YebT



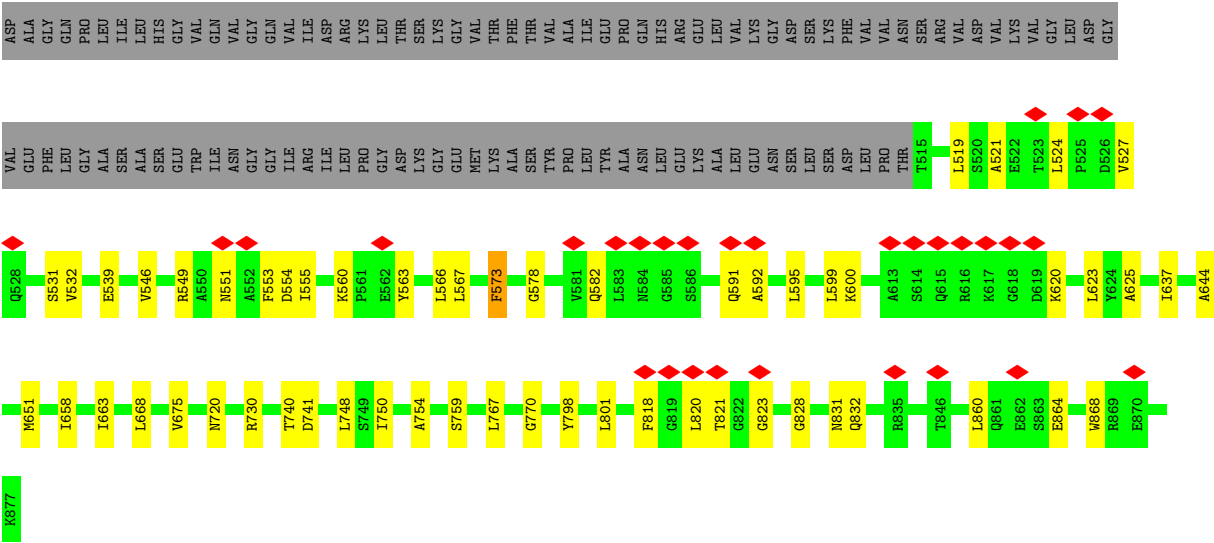
- Molecule 1: Intermembrane transport protein YebT



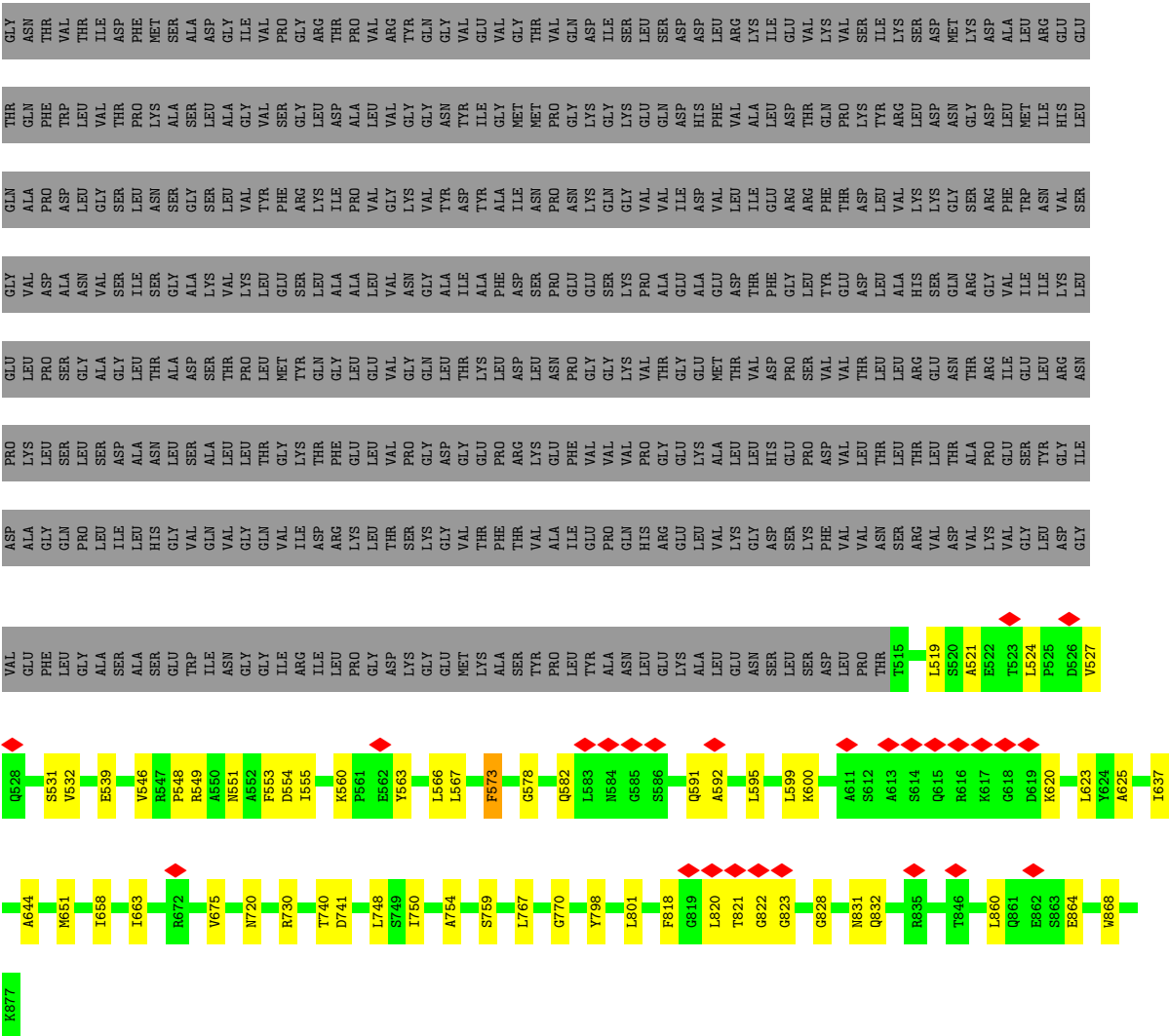
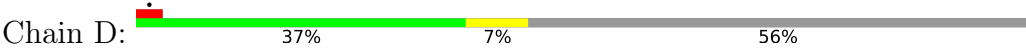


Frequency	Percentage
Daily	37%
Weekly	7%
Monthly	56%





● Molecule 1: Intermembrane transport protein YebT



Chain E:



8377	A644	Q528	VAL	GLU	ASP	PRO	GLU	GLY	THR	GLN	THR	GLY
	M651	S531 V532	LEU	PHE	GLY	LYS	LEU	LEU	PRO	PRO	GLN	ASN
	I663	E539	ALA	SER	LEU	LEU	LEU	GLY	GLY	GLY	VAL	ILE
	I668	V546	ALA	SER	ILE	ASP	ASP	GLY	THR	THR	ASP	GLY
	R672	R549 A550	GLU	GLY	HIS	LEU	ALA	ALA	THR	LEU	PRO	PHE
	V675	N551 A552	ILE	ASN	GLN	SER	SER	ASP	ASP	GLY	SER	ALA
	N720	F553 D554	GLY	GLN	GLY	GLY	LEU	LEU	THR	VAL	GLY	ILE
	R730	I555	ILE	ASP	ILE	THR	THR	GLN	SER	ARG	GLY	GLY
	T740	K560	ILE	LEU	ASP	ARG	PHE	THR	GLN	LYS	LEU	ARG
	D741	P561 E562	PRO	GLY	LYS	LEU	LEU	LEU	GLY	ALA	ILE	ASP
L748	S749 I760	ASP	GLY	THR	THR	VAL	VAL	VAL	GLY	VAL	LEU	
A754	L566 L567	LYS	GLY	LYS	SER	PRO	GLY	GLN	ASN	GLY	GLN	
S759	F573	MET	GLY	VAL	THR	GLY	GLY	THR	ASN	TYR	ASN	
L767	G578	ALA	SER	PHE	THR	ARG	ASP	LEU	ILE	MET	GLY	
G770	V581 Q582	PRO	LEU	VAL	GLY	GLY	ASN	ASN	PRO	MET	THR	
F818	L583 N584	TYR	ALA	GLY	PHE	GLY	GLY	GLY	ASN	PRO	VAL	
G819	G885	ASN	ASN	GLN	PRO	VAL	VAL	GLY	GLY	LYS	ILE	
L820	T821	LEU	LEU	HIS	ARG	PRO	VAL	LYS	GLY	LYS	LEU	
G822	S586	GLY	GLY	GLY	GLY	GLY	THR	VAL	VAL	GLY	LEU	
G823	Q591	LYS	ALA	LEU	GLY	GLY	GLY	GLY	ILE	ASP	ASP	
V824	A592	LEU	LEU	VAL	ALA	ALA	MET	GLY	VAL	PHE	LEU	
V825	L595	ASN	ASN	LYS	GLY	LEU	VAL	THR	ASP	ALA	ARG	
G828	L599 K600	SER	SER	ASP	ASP	HIS	ASP	THR	PHE	ILE	LYS	
N831	Q832	ASP	ASP	PHE	LYS	PRO	SER	VAL	TYR	ARG	VAL	
R835	A611 S612	PRO	LEU	VAL	VAL	LEU	THR	THR	GLY	PRO	VAL	
T846	A613 S614	THR	THR	ASN	SER	THR	LEU	LEU	LEU	LYS	SER	
E854	Q615 R616	VAL	ARG	VAL	VAL	THR	GLU	GLY	VAL	ARG	ASN	
L860	K617 G618	LYS	THR	VAL	VAL	ALA	PRO	GLY	ARG	SER	LYS	
E864	D619 K620	GLY	TYR	GLY	LEU	SER	GLY	ILE	GLY	TRP	ALA	
-	-	-	D526	GLY	ASP	GLY	ASN	LEU	LEU	ILE	ARG	

Chain F:

[illegible]





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	101464	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 ( $e^-/\text{\AA}^2$ )	80	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.385	Depositor
Minimum map value	-0.184	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	366.8, 366.8, 366.8	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.31, 1.31, 1.31	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.41	0/2822	0.62	1/3831 (0.0%)
1	B	0.41	0/2822	0.62	2/3831 (0.1%)
1	C	0.41	0/2822	0.62	2/3831 (0.1%)
1	D	0.41	0/2822	0.62	2/3831 (0.1%)
1	E	0.41	0/2822	0.62	1/3831 (0.0%)
1	F	0.41	0/2822	0.62	2/3831 (0.1%)
All	All	0.41	0/16932	0.62	10/22986 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	567	LEU	CA-CB-CG	5.89	128.86	115.30
1	B	567	LEU	CA-CB-CG	5.89	128.85	115.30
1	D	567	LEU	CA-CB-CG	5.89	128.84	115.30
1	C	567	LEU	CA-CB-CG	5.88	128.82	115.30
1	A	567	LEU	CA-CB-CG	5.88	128.81	115.30

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	2767	0	2795	37	0
1	B	2767	0	2795	36	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2767	0	2795	37	0
1	D	2767	0	2795	38	0
1	E	2767	0	2795	36	0
1	F	2767	0	2795	38	0
All	All	16602	0	16770	190	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 190 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:C:818:PHE:HB3	1:D:823:GLY:H	1.55	0.71
1:A:823:GLY:H	1:F:818:PHE:HB3	1.57	0.69
1:A:818:PHE:HB3	1:B:823:GLY:H	1.58	0.68
1:D:818:PHE:HB3	1:E:823:GLY:H	1.60	0.66
1:C:546:VAL:HG23	1:C:555:ILE:HG12	1.80	0.63

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	361/832 (43%)	341 (94%)	20 (6%)	0	100	100
1	B	361/832 (43%)	342 (95%)	19 (5%)	0	100	100
1	C	361/832 (43%)	342 (95%)	19 (5%)	0	100	100
1	D	361/832 (43%)	342 (95%)	19 (5%)	0	100	100
1	E	361/832 (43%)	342 (95%)	19 (5%)	0	100	100
1	F	361/832 (43%)	342 (95%)	19 (5%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2166/4992 (43%)	2051 (95%)	115 (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	291/683 (43%)	291 (100%)	0	100	100
1	B	291/683 (43%)	291 (100%)	0	100	100
1	C	291/683 (43%)	291 (100%)	0	100	100
1	D	291/683 (43%)	291 (100%)	0	100	100
1	E	291/683 (43%)	291 (100%)	0	100	100
1	F	291/683 (43%)	291 (100%)	0	100	100
All	All	1746/4098 (43%)	1746 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	832	GLN
1	F	832	GLN
1	F	591	GLN
1	C	832	GLN
1	E	591	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

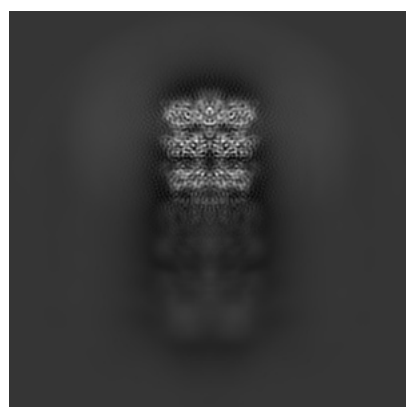
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20995. These allow visual inspection of the internal detail of the map and identification of artifacts.

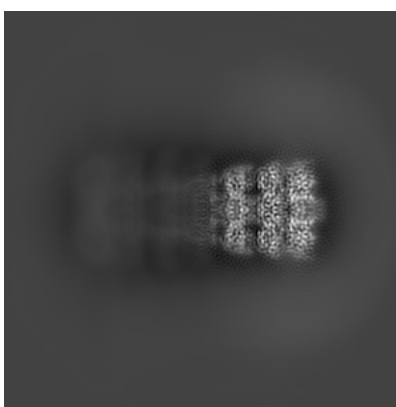
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

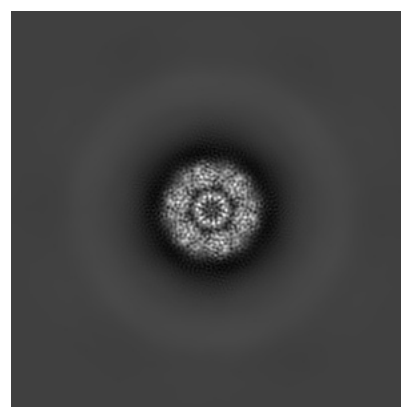
#### 6.1.1 Primary map



X



Y



Z

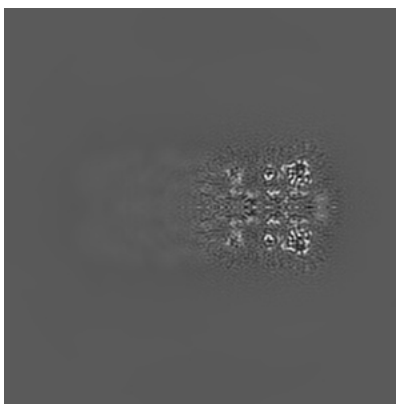
The images above show the map projected in three orthogonal directions.

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

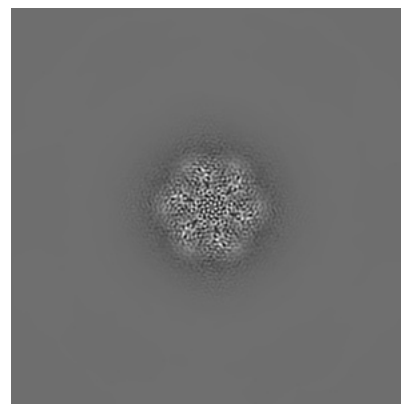
#### 6.2.1 Primary map



X Index: 140



Y Index: 140

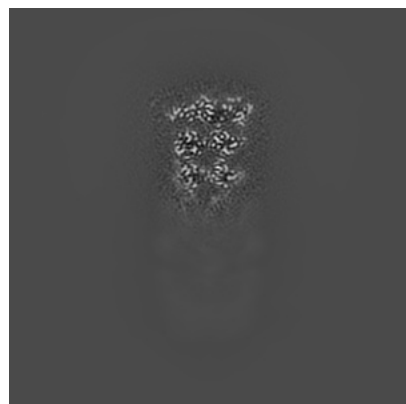


Z Index: 140

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

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

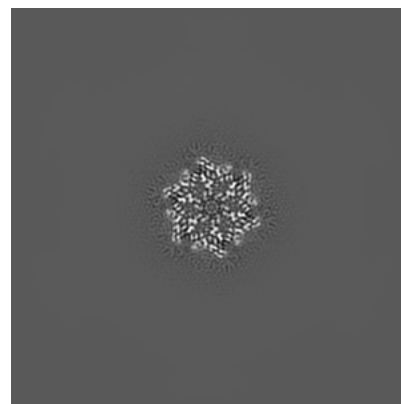
### 6.3.1 Primary map



X Index: 121



Y Index: 134

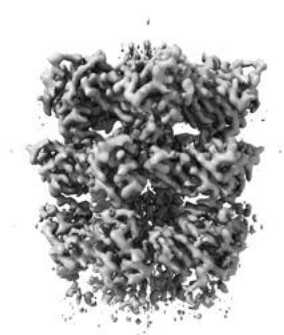


Z Index: 188

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

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

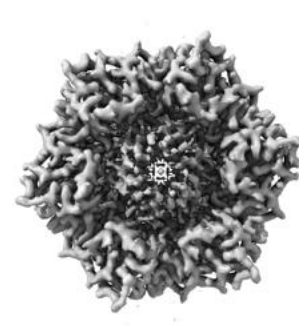
### 6.4.1 Primary map



X



Y



Z

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.

## 6.5 Mask visualisation

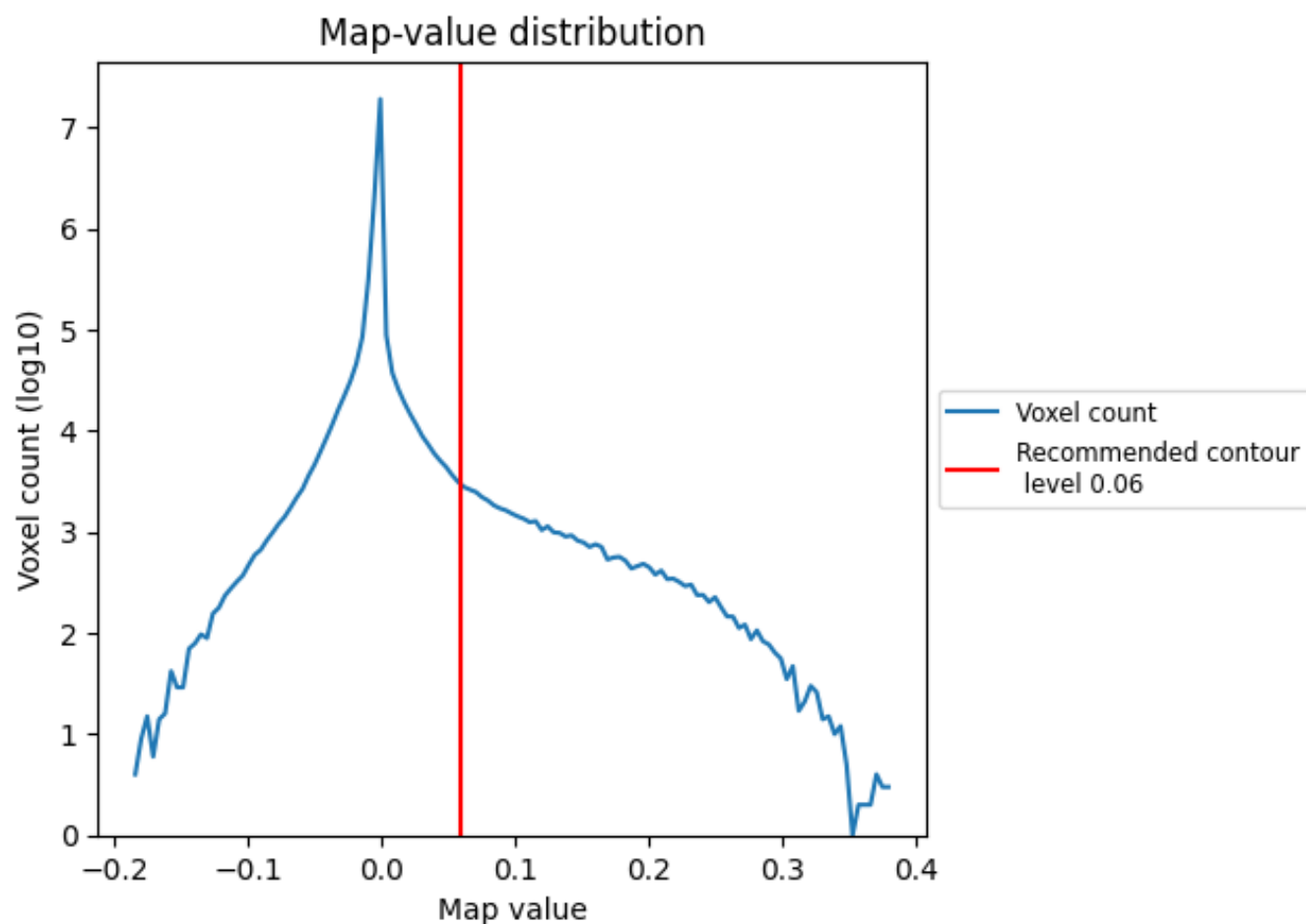
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

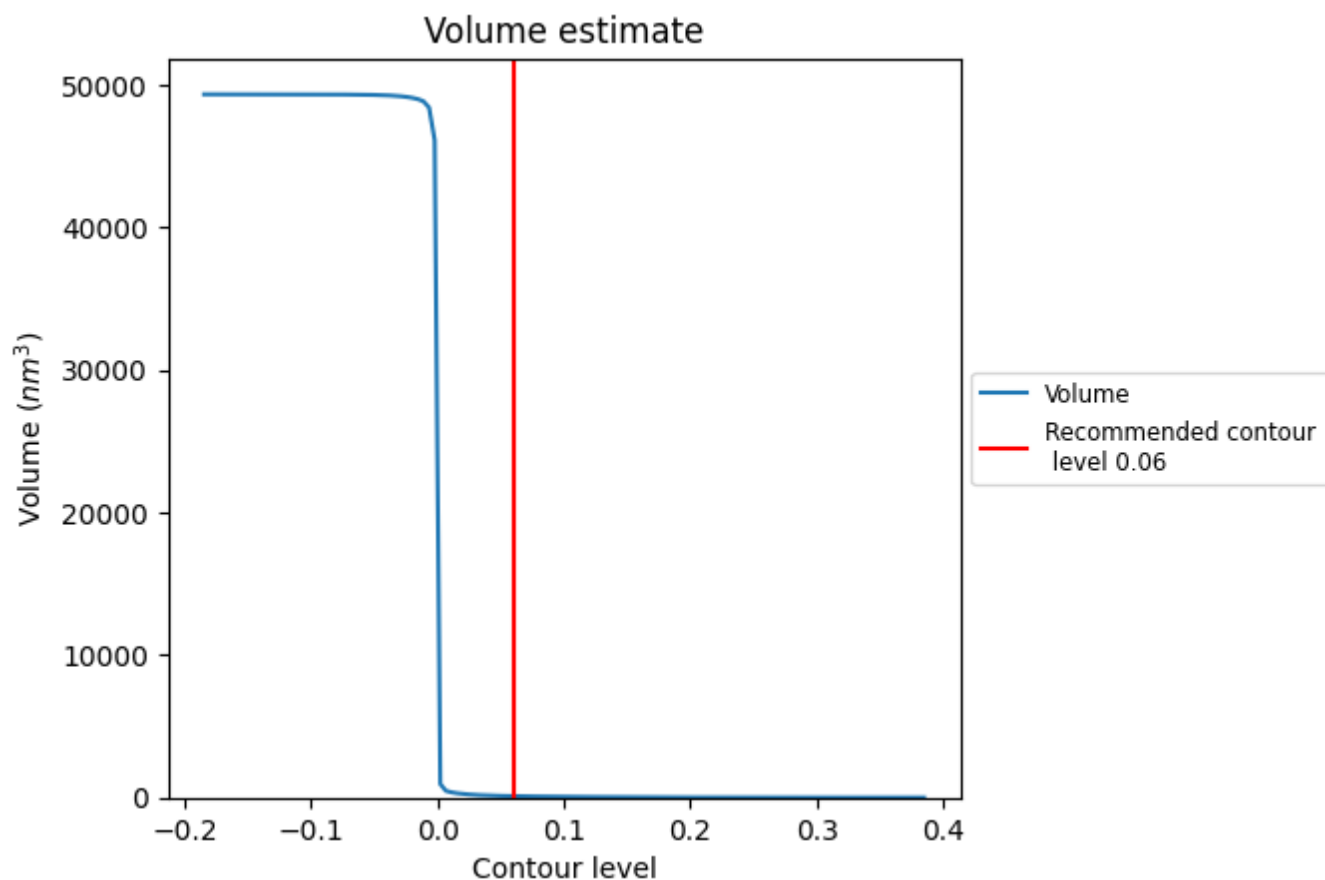
This section contains the results of statistical analysis of the map.

### 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.

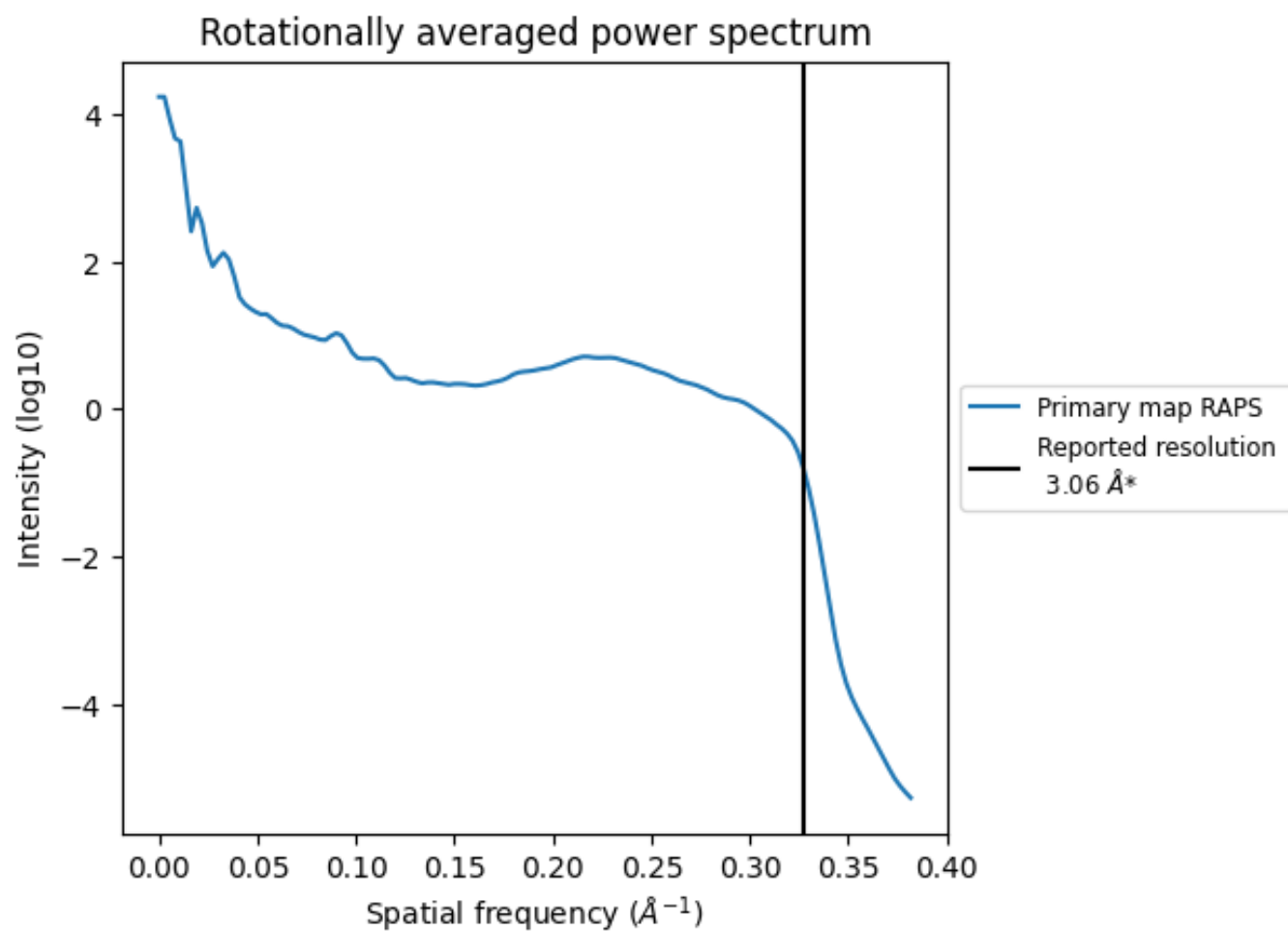
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 99  $\text{nm}^3$ ; this corresponds to an approximate mass of 89 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 0.327 Å<sup>-1</sup>

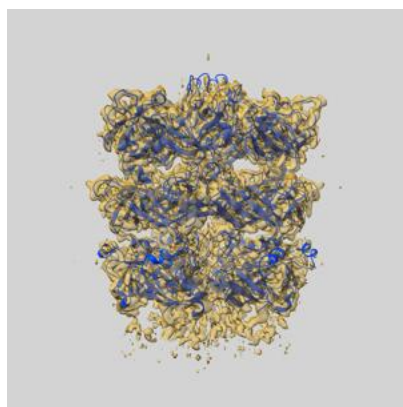
## 8 Fourier-Shell correlation ⓘ

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

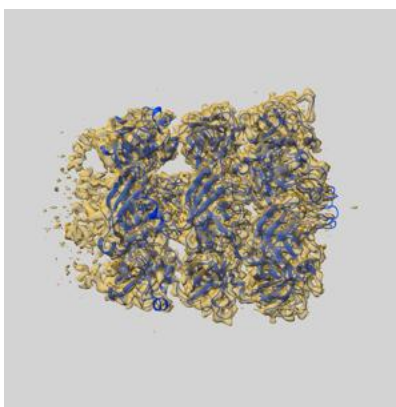
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20995 and PDB model 6V0E. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

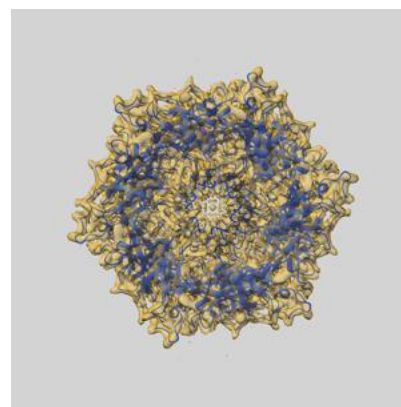
### 9.1 Map-model overlay [i](#)



X



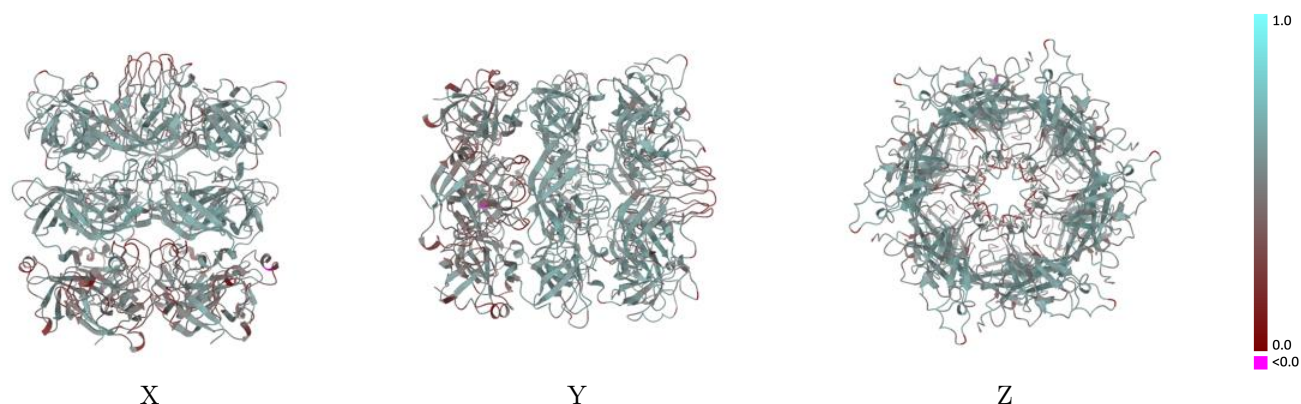
Y



Z

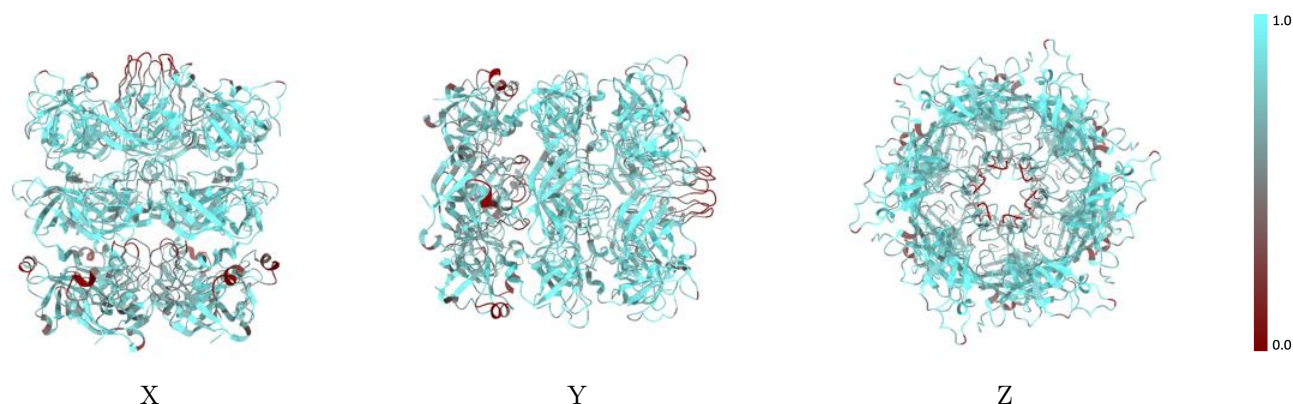
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



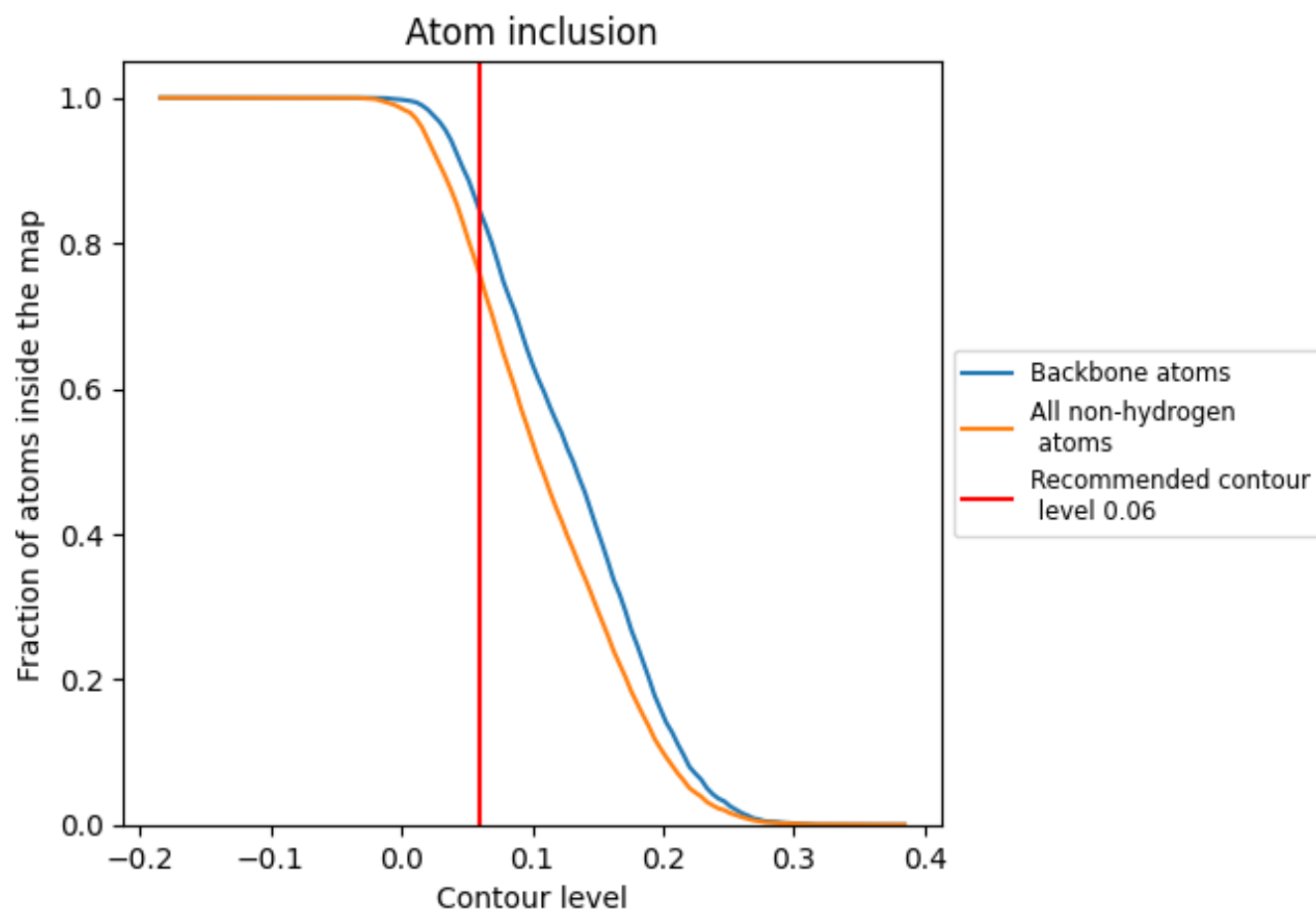
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 84% of all backbone atoms, 76% 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></div></div> 0.7559	<div><div></div></div> 0.5010
A	<div><div></div></div> 0.7569	<div><div></div></div> 0.5040
B	<div><div></div></div> 0.7558	<div><div></div></div> 0.5010
C	<div><div></div></div> 0.7551	<div><div></div></div> 0.5000
D	<div><div></div></div> 0.7580	<div><div></div></div> 0.5040
E	<div><div></div></div> 0.7551	<div><div></div></div> 0.4990
F	<div><div></div></div> 0.7547	<div><div></div></div> 0.5000

1.0

0.0

<0.0