



## Full wwPDB EM Validation Report ⓘ

Oct 11, 2025 – 07:41 am BST

PDB ID : 9Q9L / pdb\_00009q9l  
EMDB ID : EMD-52963  
Title : HSV-1 prefusion glycoprotein B  
Authors : Vollmer, B.; Mulvaney, T.; Ebel, H.; Nentwig, J.; Gruenewald, K.  
Deposited on : 2025-02-26  
Resolution : 2.64 Å(reported)  
Based on initial model : .

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev129  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.46

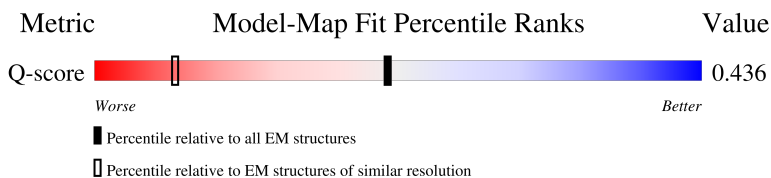
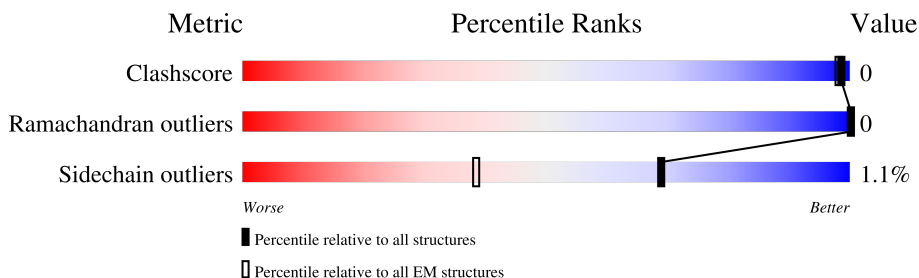
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*



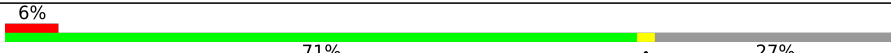
The reported resolution of this entry is 2.64 Å.

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	8968 ( 2.14 - 3.14 )

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	954	
1	B	954	
1	C	954	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 32571 atoms, of which 16035 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 Glycoprotein B.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	693	Total	C	H	N	O	S	0	0
			10857	3488	5345	971	1023	30		
1	B	693	Total	C	H	N	O	S	0	0
			10857	3488	5345	971	1023	30		
1	C	693	Total	C	H	N	O	S	0	0
			10857	3488	5345	971	1023	30		

There are 165 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	392	CYS	SER	engineered mutation	UNP A1Z0P7
A	516	PRO	HIS	engineered mutation	UNP A1Z0P7
A	532	CYS	GLN	engineered mutation	UNP A1Z0P7
A	709	VAL	ASN	engineered mutation	UNP A1Z0P7
A	889	ALA	TYR	engineered mutation	UNP A1Z0P7
A	905	GLN	-	expression tag	UNP A1Z0P7
A	906	LEU	-	expression tag	UNP A1Z0P7
A	907	GLY	-	expression tag	UNP A1Z0P7
A	908	SER	-	expression tag	UNP A1Z0P7
A	909	GLY	-	expression tag	UNP A1Z0P7
A	910	SER	-	expression tag	UNP A1Z0P7
A	911	GLY	-	expression tag	UNP A1Z0P7
A	912	THR	-	expression tag	UNP A1Z0P7
A	913	LEU	-	expression tag	UNP A1Z0P7
A	914	GLU	-	expression tag	UNP A1Z0P7
A	915	VAL	-	expression tag	UNP A1Z0P7
A	916	LEU	-	expression tag	UNP A1Z0P7
A	917	PHE	-	expression tag	UNP A1Z0P7
A	918	GLN	-	expression tag	UNP A1Z0P7
A	919	GLY	-	expression tag	UNP A1Z0P7
A	920	PRO	-	expression tag	UNP A1Z0P7
A	921	GLY	-	expression tag	UNP A1Z0P7
A	922	GLY	-	expression tag	UNP A1Z0P7
A	923	SER	-	expression tag	UNP A1Z0P7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	924	GLY	-	expression tag	UNP A1Z0P7
A	925	SER	-	expression tag	UNP A1Z0P7
A	926	ALA	-	expression tag	UNP A1Z0P7
A	927	TRP	-	expression tag	UNP A1Z0P7
A	928	SER	-	expression tag	UNP A1Z0P7
A	929	HIS	-	expression tag	UNP A1Z0P7
A	930	PRO	-	expression tag	UNP A1Z0P7
A	931	GLN	-	expression tag	UNP A1Z0P7
A	932	PHE	-	expression tag	UNP A1Z0P7
A	933	GLU	-	expression tag	UNP A1Z0P7
A	934	LYS	-	expression tag	UNP A1Z0P7
A	935	GLY	-	expression tag	UNP A1Z0P7
A	936	GLY	-	expression tag	UNP A1Z0P7
A	937	GLY	-	expression tag	UNP A1Z0P7
A	938	SER	-	expression tag	UNP A1Z0P7
A	939	GLY	-	expression tag	UNP A1Z0P7
A	940	GLY	-	expression tag	UNP A1Z0P7
A	941	GLY	-	expression tag	UNP A1Z0P7
A	942	SER	-	expression tag	UNP A1Z0P7
A	943	GLY	-	expression tag	UNP A1Z0P7
A	944	GLY	-	expression tag	UNP A1Z0P7
A	945	SER	-	expression tag	UNP A1Z0P7
A	946	ALA	-	expression tag	UNP A1Z0P7
A	947	TRP	-	expression tag	UNP A1Z0P7
A	948	SER	-	expression tag	UNP A1Z0P7
A	949	HIS	-	expression tag	UNP A1Z0P7
A	950	PRO	-	expression tag	UNP A1Z0P7
A	951	GLN	-	expression tag	UNP A1Z0P7
A	952	PHE	-	expression tag	UNP A1Z0P7
A	953	GLU	-	expression tag	UNP A1Z0P7
A	954	LYS	-	expression tag	UNP A1Z0P7
B	392	CYS	SER	engineered mutation	UNP A1Z0P7
B	516	PRO	HIS	engineered mutation	UNP A1Z0P7
B	532	CYS	GLN	engineered mutation	UNP A1Z0P7
B	709	VAL	ASN	engineered mutation	UNP A1Z0P7
B	889	ALA	TYR	engineered mutation	UNP A1Z0P7
B	905	GLN	-	expression tag	UNP A1Z0P7
B	906	LEU	-	expression tag	UNP A1Z0P7
B	907	GLY	-	expression tag	UNP A1Z0P7
B	908	SER	-	expression tag	UNP A1Z0P7
B	909	GLY	-	expression tag	UNP A1Z0P7
B	910	SER	-	expression tag	UNP A1Z0P7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	911	GLY	-	expression tag	UNP A1Z0P7
B	912	THR	-	expression tag	UNP A1Z0P7
B	913	LEU	-	expression tag	UNP A1Z0P7
B	914	GLU	-	expression tag	UNP A1Z0P7
B	915	VAL	-	expression tag	UNP A1Z0P7
B	916	LEU	-	expression tag	UNP A1Z0P7
B	917	PHE	-	expression tag	UNP A1Z0P7
B	918	GLN	-	expression tag	UNP A1Z0P7
B	919	GLY	-	expression tag	UNP A1Z0P7
B	920	PRO	-	expression tag	UNP A1Z0P7
B	921	GLY	-	expression tag	UNP A1Z0P7
B	922	GLY	-	expression tag	UNP A1Z0P7
B	923	SER	-	expression tag	UNP A1Z0P7
B	924	GLY	-	expression tag	UNP A1Z0P7
B	925	SER	-	expression tag	UNP A1Z0P7
B	926	ALA	-	expression tag	UNP A1Z0P7
B	927	TRP	-	expression tag	UNP A1Z0P7
B	928	SER	-	expression tag	UNP A1Z0P7
B	929	HIS	-	expression tag	UNP A1Z0P7
B	930	PRO	-	expression tag	UNP A1Z0P7
B	931	GLN	-	expression tag	UNP A1Z0P7
B	932	PHE	-	expression tag	UNP A1Z0P7
B	933	GLU	-	expression tag	UNP A1Z0P7
B	934	LYS	-	expression tag	UNP A1Z0P7
B	935	GLY	-	expression tag	UNP A1Z0P7
B	936	GLY	-	expression tag	UNP A1Z0P7
B	937	GLY	-	expression tag	UNP A1Z0P7
B	938	SER	-	expression tag	UNP A1Z0P7
B	939	GLY	-	expression tag	UNP A1Z0P7
B	940	GLY	-	expression tag	UNP A1Z0P7
B	941	GLY	-	expression tag	UNP A1Z0P7
B	942	SER	-	expression tag	UNP A1Z0P7
B	943	GLY	-	expression tag	UNP A1Z0P7
B	944	GLY	-	expression tag	UNP A1Z0P7
B	945	SER	-	expression tag	UNP A1Z0P7
B	946	ALA	-	expression tag	UNP A1Z0P7
B	947	TRP	-	expression tag	UNP A1Z0P7
B	948	SER	-	expression tag	UNP A1Z0P7
B	949	HIS	-	expression tag	UNP A1Z0P7
B	950	PRO	-	expression tag	UNP A1Z0P7
B	951	GLN	-	expression tag	UNP A1Z0P7
B	952	PHE	-	expression tag	UNP A1Z0P7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	953	GLU	-	expression tag	UNP A1Z0P7
B	954	LYS	-	expression tag	UNP A1Z0P7
C	392	CYS	SER	engineered mutation	UNP A1Z0P7
C	516	PRO	HIS	engineered mutation	UNP A1Z0P7
C	532	CYS	GLN	engineered mutation	UNP A1Z0P7
C	709	VAL	ASN	engineered mutation	UNP A1Z0P7
C	889	ALA	TYR	engineered mutation	UNP A1Z0P7
C	905	GLN	-	expression tag	UNP A1Z0P7
C	906	LEU	-	expression tag	UNP A1Z0P7
C	907	GLY	-	expression tag	UNP A1Z0P7
C	908	SER	-	expression tag	UNP A1Z0P7
C	909	GLY	-	expression tag	UNP A1Z0P7
C	910	SER	-	expression tag	UNP A1Z0P7
C	911	GLY	-	expression tag	UNP A1Z0P7
C	912	THR	-	expression tag	UNP A1Z0P7
C	913	LEU	-	expression tag	UNP A1Z0P7
C	914	GLU	-	expression tag	UNP A1Z0P7
C	915	VAL	-	expression tag	UNP A1Z0P7
C	916	LEU	-	expression tag	UNP A1Z0P7
C	917	PHE	-	expression tag	UNP A1Z0P7
C	918	GLN	-	expression tag	UNP A1Z0P7
C	919	GLY	-	expression tag	UNP A1Z0P7
C	920	PRO	-	expression tag	UNP A1Z0P7
C	921	GLY	-	expression tag	UNP A1Z0P7
C	922	GLY	-	expression tag	UNP A1Z0P7
C	923	SER	-	expression tag	UNP A1Z0P7
C	924	GLY	-	expression tag	UNP A1Z0P7
C	925	SER	-	expression tag	UNP A1Z0P7
C	926	ALA	-	expression tag	UNP A1Z0P7
C	927	TRP	-	expression tag	UNP A1Z0P7
C	928	SER	-	expression tag	UNP A1Z0P7
C	929	HIS	-	expression tag	UNP A1Z0P7
C	930	PRO	-	expression tag	UNP A1Z0P7
C	931	GLN	-	expression tag	UNP A1Z0P7
C	932	PHE	-	expression tag	UNP A1Z0P7
C	933	GLU	-	expression tag	UNP A1Z0P7
C	934	LYS	-	expression tag	UNP A1Z0P7
C	935	GLY	-	expression tag	UNP A1Z0P7
C	936	GLY	-	expression tag	UNP A1Z0P7
C	937	GLY	-	expression tag	UNP A1Z0P7
C	938	SER	-	expression tag	UNP A1Z0P7
C	939	GLY	-	expression tag	UNP A1Z0P7

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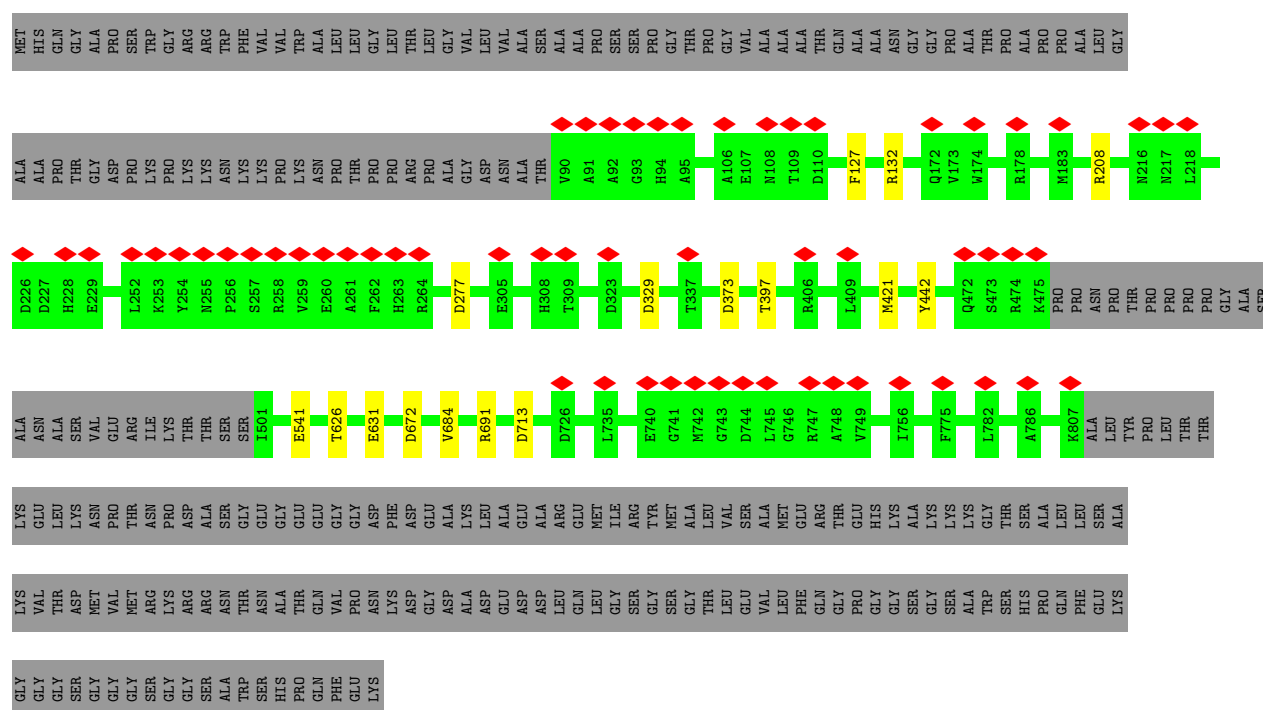
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Chain	Residue	Modelled	Actual	Comment	Reference
C	940	GLY	-	expression tag	UNP A1Z0P7
C	941	GLY	-	expression tag	UNP A1Z0P7
C	942	SER	-	expression tag	UNP A1Z0P7
C	943	GLY	-	expression tag	UNP A1Z0P7
C	944	GLY	-	expression tag	UNP A1Z0P7
C	945	SER	-	expression tag	UNP A1Z0P7
C	946	ALA	-	expression tag	UNP A1Z0P7
C	947	TRP	-	expression tag	UNP A1Z0P7
C	948	SER	-	expression tag	UNP A1Z0P7
C	949	HIS	-	expression tag	UNP A1Z0P7
C	950	PRO	-	expression tag	UNP A1Z0P7
C	951	GLN	-	expression tag	UNP A1Z0P7
C	952	PHE	-	expression tag	UNP A1Z0P7
C	953	GLU	-	expression tag	UNP A1Z0P7
C	954	LYS	-	expression tag	UNP A1Z0P7





- Molecule 1: Glycoprotein B



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	275470	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	47.38	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.331	Depositor
Minimum map value	-1.051	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.0769	Depositor
Map size (Å)	343.2, 343.2, 343.2	wwPDB
Map dimensions	520, 520, 520	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.66, 0.66, 0.66	Depositor

## 5 Model quality

### 5.1 Standard geometry

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	0.54	0/5645	1.41	6/7662 (0.1%)
1	B	0.54	0/5645	1.41	7/7662 (0.1%)
1	C	0.54	0/5645	1.41	7/7662 (0.1%)
All	All	0.54	0/16935	1.41	20/22986 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	672	ASP	CA-CB-CG	7.55	120.15	112.60
1	C	672	ASP	CA-CB-CG	7.41	120.01	112.60
1	A	713	ASP	CA-CB-CG	6.85	119.45	112.60
1	B	672	ASP	CA-CB-CG	6.78	119.38	112.60
1	C	713	ASP	CA-CB-CG	6.76	119.36	112.60
1	B	713	ASP	CA-CB-CG	6.51	119.11	112.60
1	A	208	ARG	N-CA-C	6.18	120.55	113.19
1	C	208	ARG	N-CA-C	6.12	120.47	113.19
1	A	684	VAL	N-CA-C	5.98	115.48	108.96
1	A	373	ASP	CA-CB-CG	5.89	118.49	112.60
1	B	208	ARG	N-CA-C	5.83	120.13	113.19
1	C	684	VAL	N-CA-C	5.75	115.23	108.96
1	B	684	VAL	N-CA-C	5.44	114.89	108.96
1	A	626	THR	N-CA-C	5.35	119.91	112.90
1	C	373	ASP	CA-CB-CG	5.34	117.94	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	626	THR	N-CA-C	5.30	119.85	112.90
1	C	277	ASP	CA-CB-CG	5.22	117.82	112.60
1	C	626	THR	N-CA-C	5.09	119.57	112.90
1	B	592	ARG	CA-C-N	5.04	125.32	119.47
1	B	592	ARG	C-N-CA	5.04	125.32	119.47

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	691	ARG	Sidechain

## 5.2 Too-close contacts

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	5512	5345	5343	1	0
1	B	5512	5345	5343	1	0
1	C	5512	5345	5343	1	0
All	All	16536	16035	16029	3	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 0.

All (3) 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:A:397:THR:HG21	1:A:442:TYR:HB3	1.96	0.48
1:C:397:THR:HG21	1:C:442:TYR:HB3	1.95	0.48
1:B:397:THR:HG21	1:B:442:TYR:HB3	1.95	0.47

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	689/954 (72%)	675 (98%)	14 (2%)	0	100	100
1	B	689/954 (72%)	675 (98%)	14 (2%)	0	100	100
1	C	689/954 (72%)	674 (98%)	15 (2%)	0	100	100
All	All	2067/2862 (72%)	2024 (98%)	43 (2%)	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	584/778 (75%)	578 (99%)	6 (1%)	73	85
1	B	584/778 (75%)	576 (99%)	8 (1%)	62	78
1	C	584/778 (75%)	578 (99%)	6 (1%)	73	85
All	All	1752/2334 (75%)	1732 (99%)	20 (1%)	69	83

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	127	PHE
1	A	136	ARG
1	A	187	GLU
1	A	309	THR
1	A	541	GLU

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Mol	Chain	Res	Type
1	A	710	GLN
1	B	127	PHE
1	B	128	GLU
1	B	169	THR
1	B	267	THR
1	B	309	THR
1	B	541	GLU
1	B	631	GLU
1	B	658	GLN
1	C	127	PHE
1	C	132	ARG
1	C	329	ASP
1	C	421	MET
1	C	541	GLU
1	C	631	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	126	GLN
1	A	141	ASN
1	A	238	ASN
1	A	430	ASN
1	A	438	GLN
1	A	507	GLN
1	A	511	ASN
1	A	728	ASN
1	B	126	GLN
1	B	507	GLN
1	B	511	ASN
1	C	126	GLN
1	C	141	ASN
1	C	238	ASN
1	C	430	ASN
1	C	438	GLN
1	C	468	HIS
1	C	728	ASN

### 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 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.

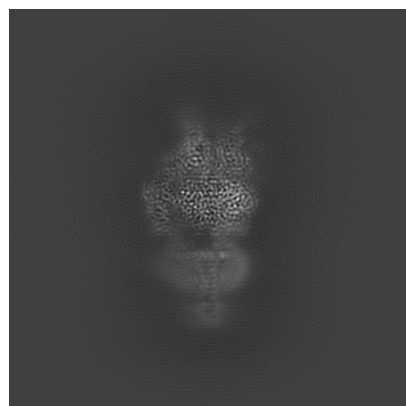
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52963. These allow visual inspection of the internal detail of the map and identification of artifacts.

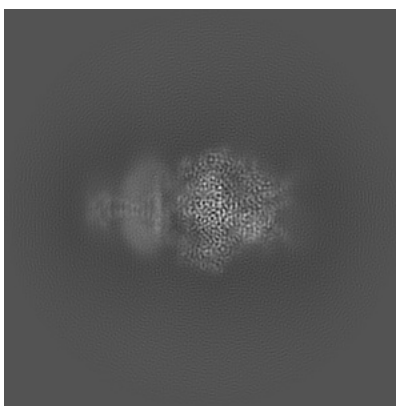
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

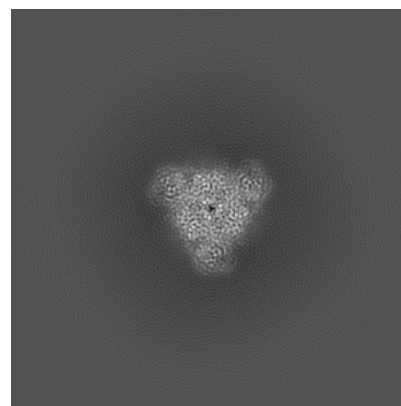
#### 6.1.1 Primary map



X

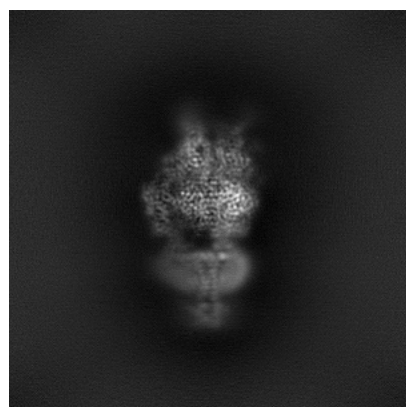


Y

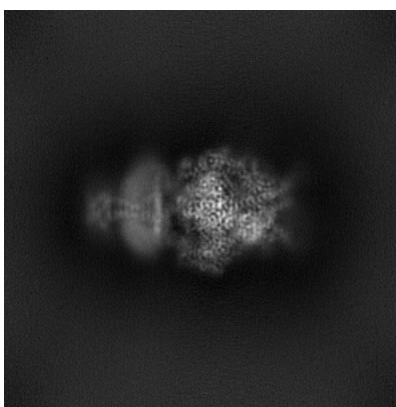


Z

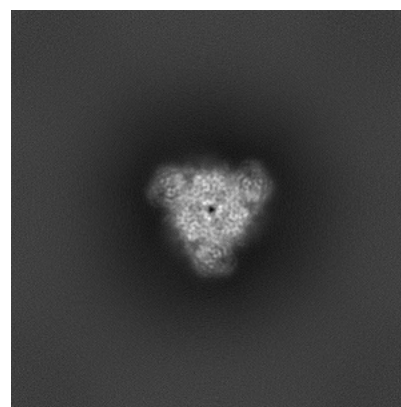
#### 6.1.2 Raw map



X



Y



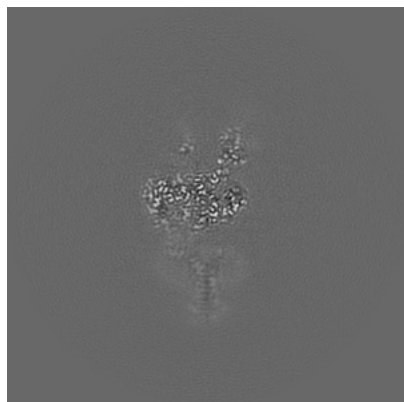
Z

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

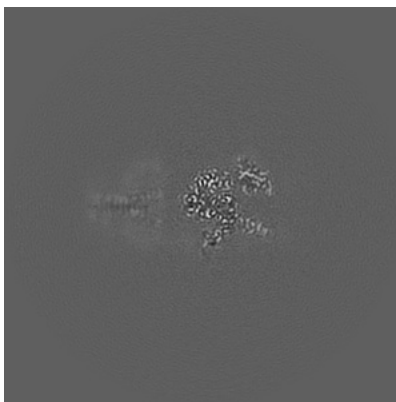


## 6.2 Central slices [i](#)

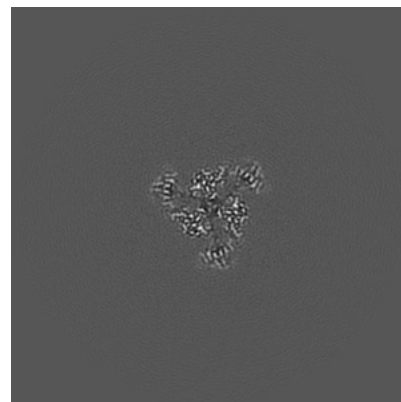
### 6.2.1 Primary map



X Index: 260

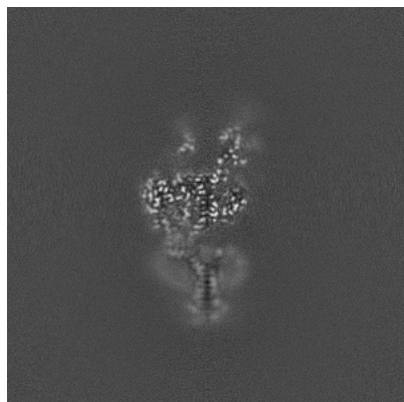


Y Index: 260

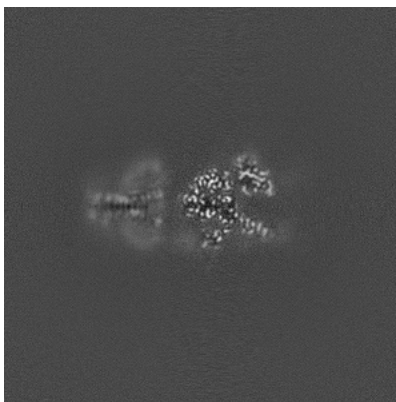


Z Index: 260

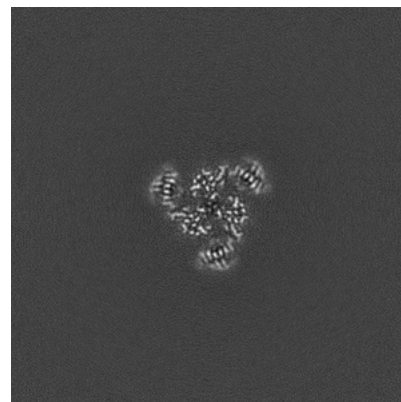
### 6.2.2 Raw map



X Index: 260



Y Index: 260

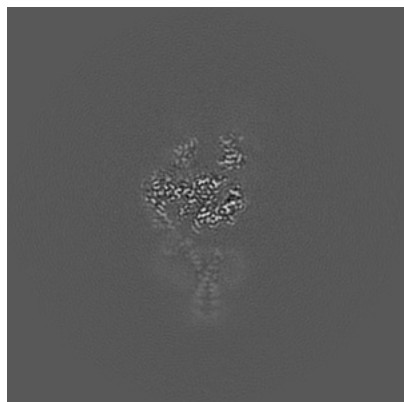


Z Index: 260

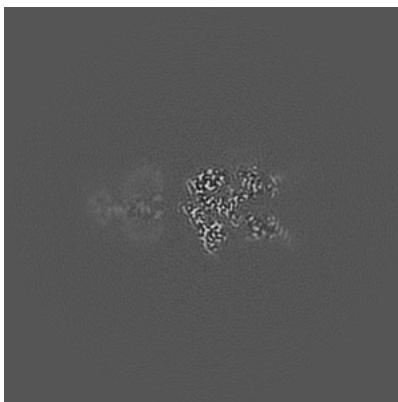
The images above show central slices of the map in three orthogonal directions.

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

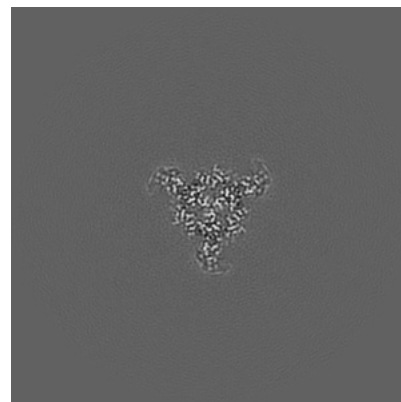
### 6.3.1 Primary map



X Index: 255

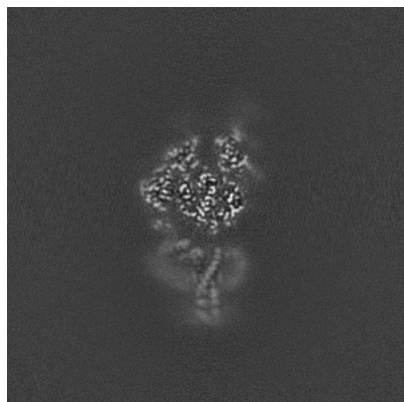


Y Index: 249

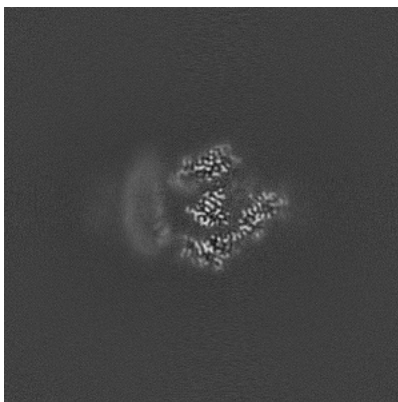


Z Index: 279

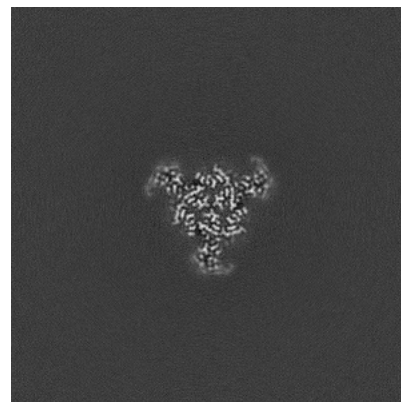
### 6.3.2 Raw map



X Index: 251



Y Index: 293

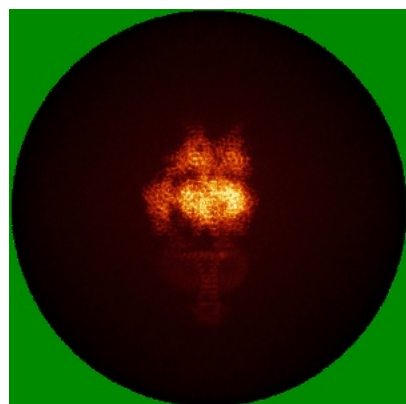


Z Index: 280

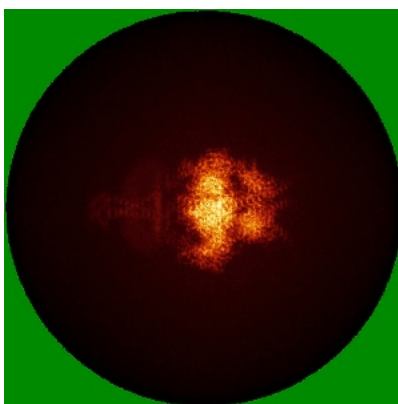
The images above show the largest variance slices of the map in three orthogonal directions.

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

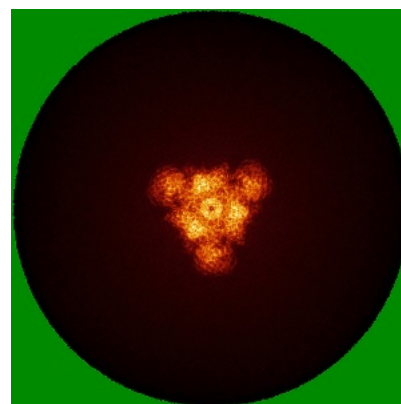
### 6.4.1 Primary map



X

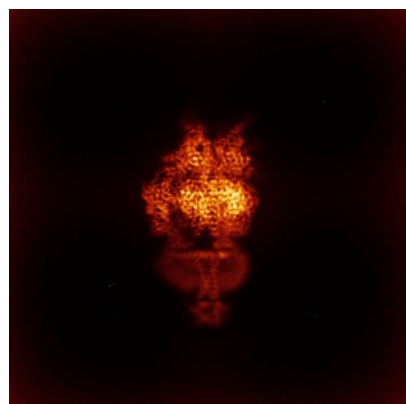


Y

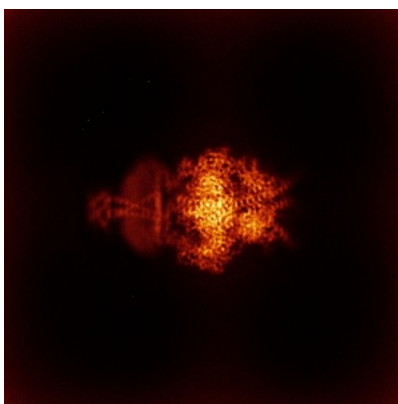


Z

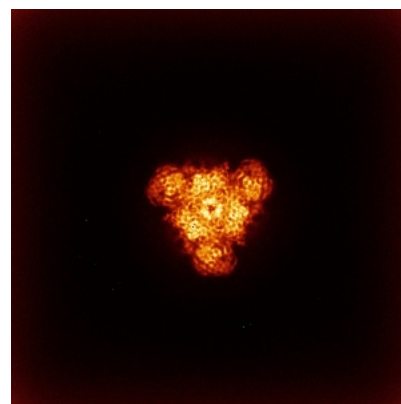
### 6.4.2 Raw map



X



Y

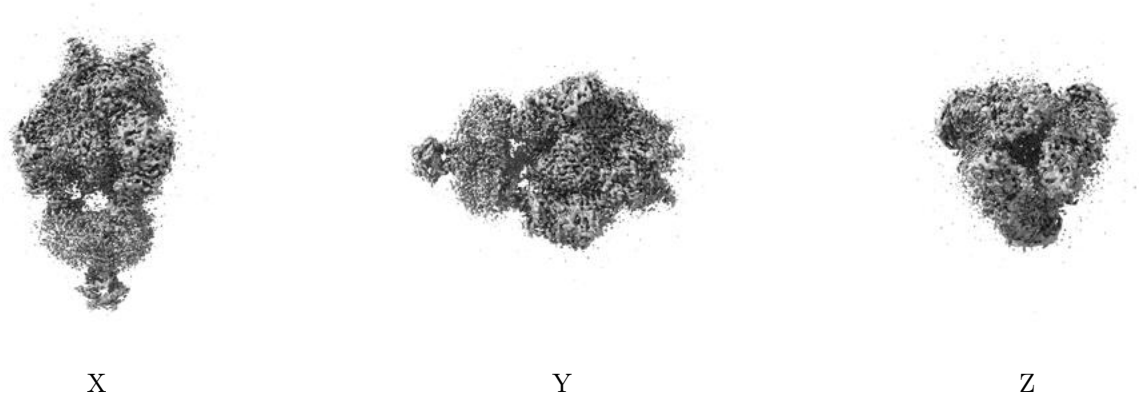


Z

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.

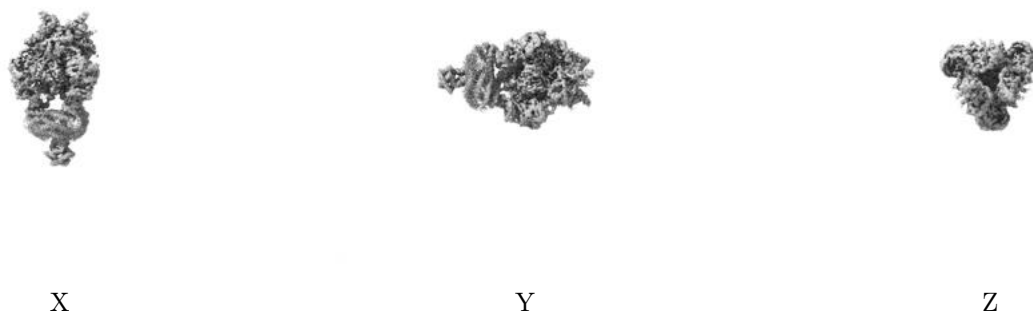
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0769. 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.

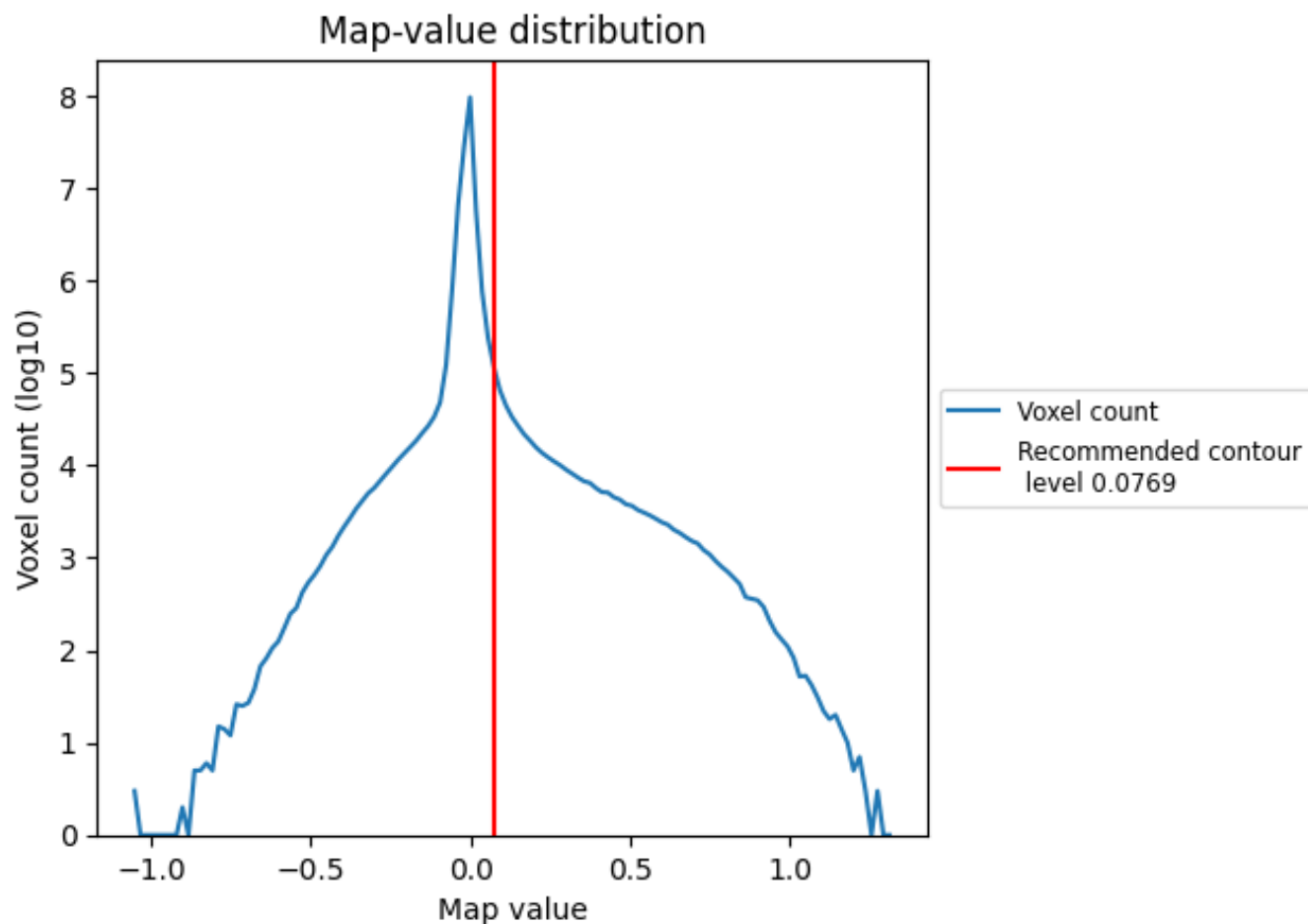
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

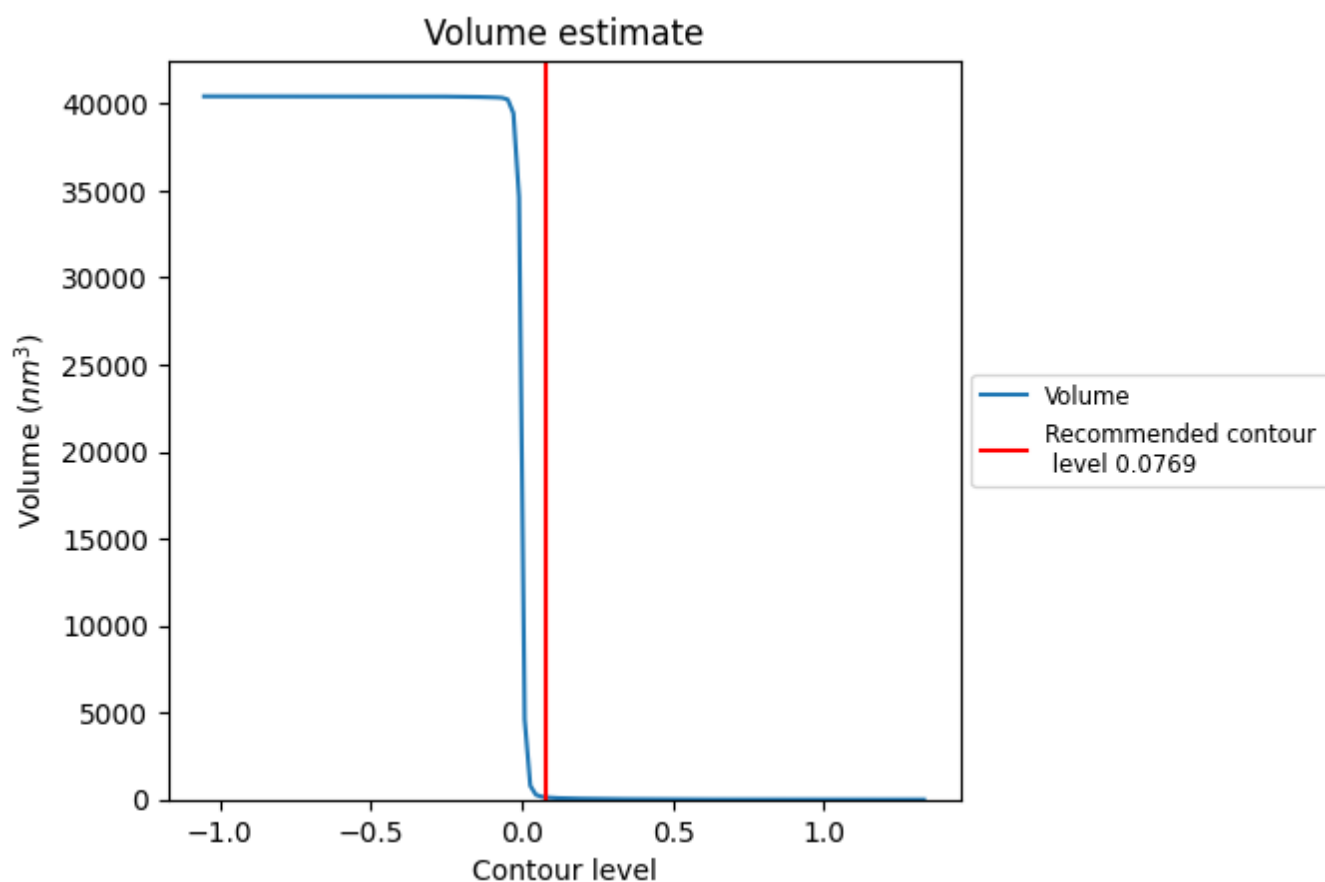
This section contains the results of statistical analysis of the map.

### 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.

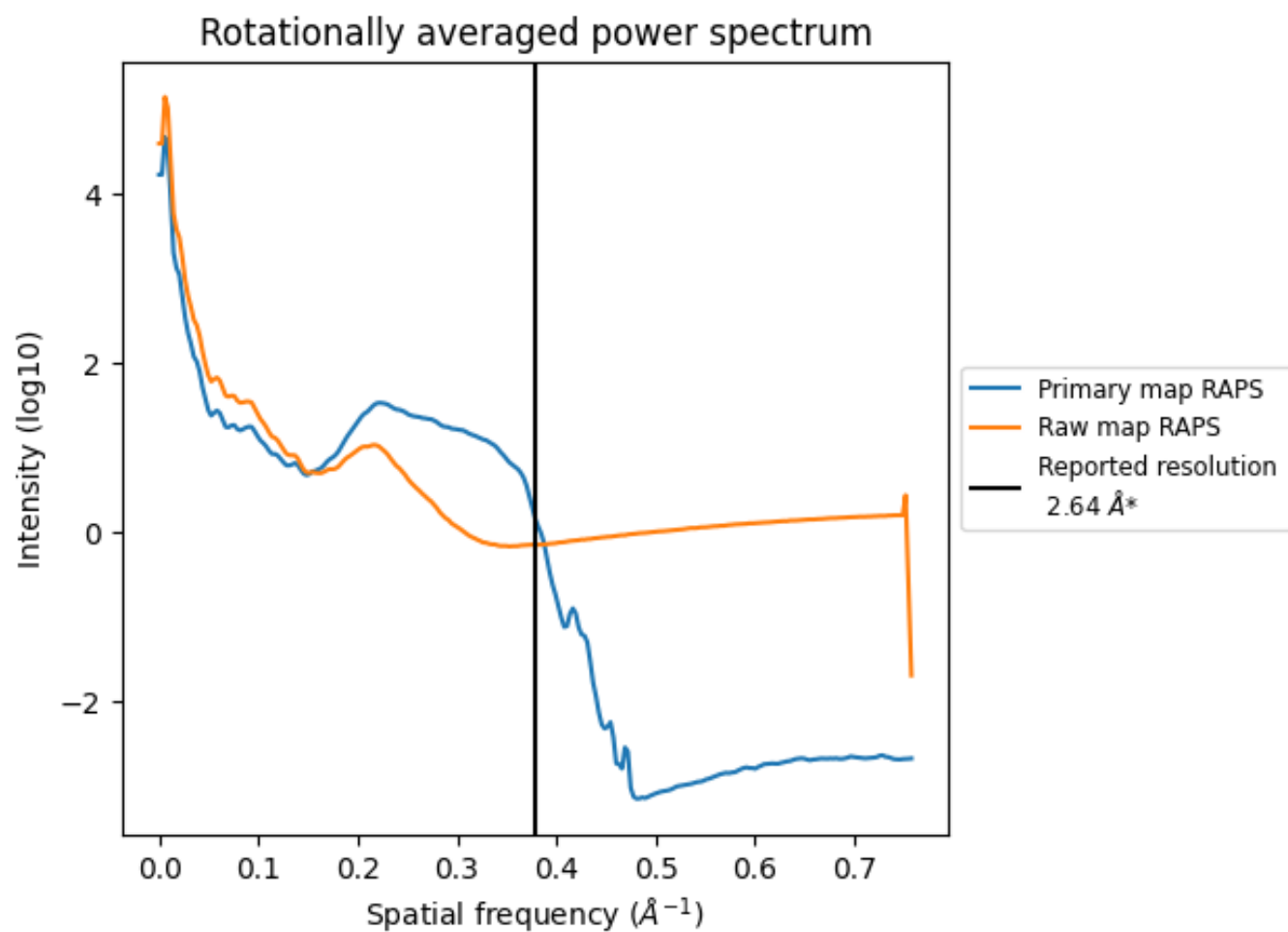
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 139 nm<sup>3</sup>; this corresponds to an approximate mass of 125 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 ⓘ

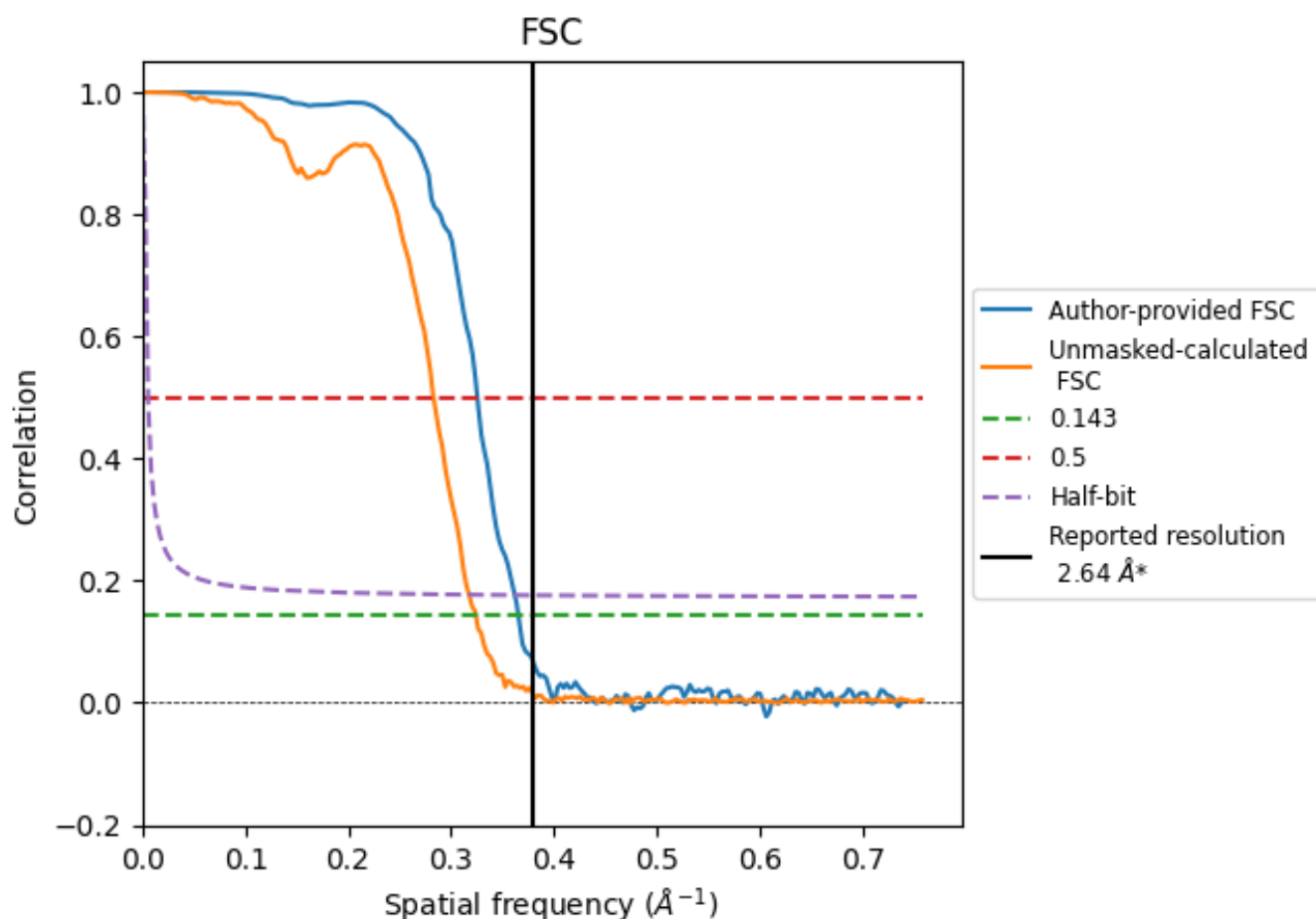


\*Reported resolution corresponds to spatial frequency of 0.379 Å<sup>-1</sup>

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



## 8.2 Resolution estimates [i](#)

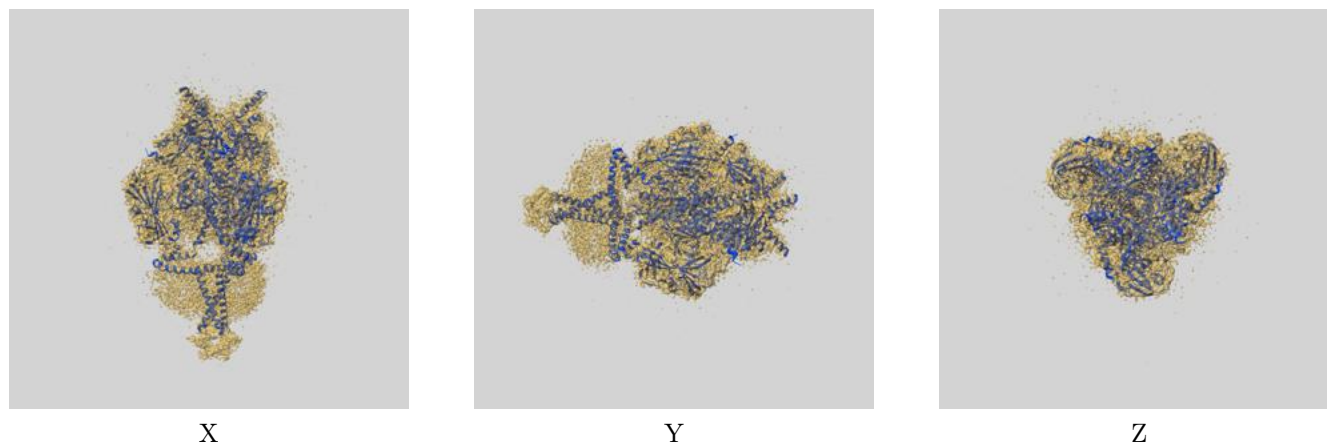
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.64	-	-
Author-provided FSC curve	2.74	3.07	2.76
Unmasked-calculated*	3.09	3.53	3.15

\*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 3.09 differs from the reported value 2.64 by more than 10 %

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

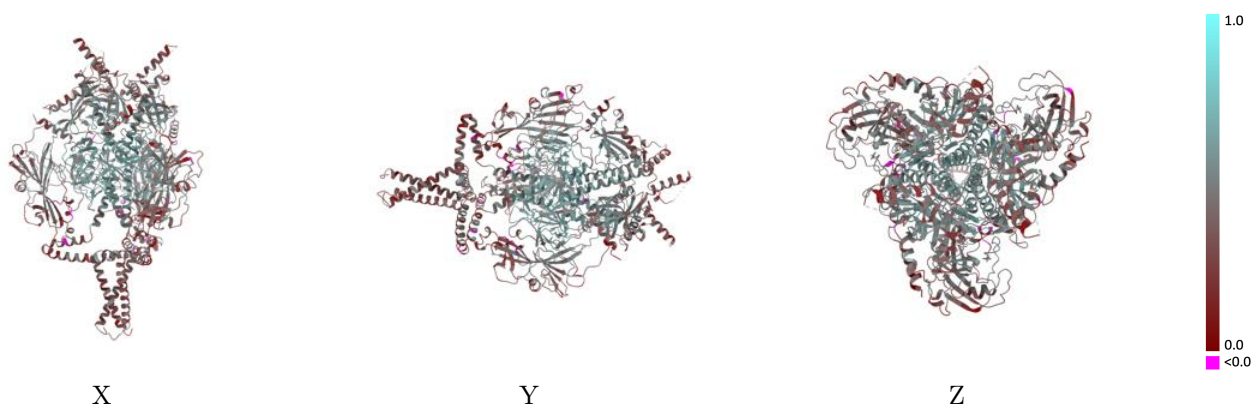
This section contains information regarding the fit between EMDB map EMD-52963 and PDB model 9Q9L. Per-residue inclusion information can be found in section [3](#) on page [8](#).

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



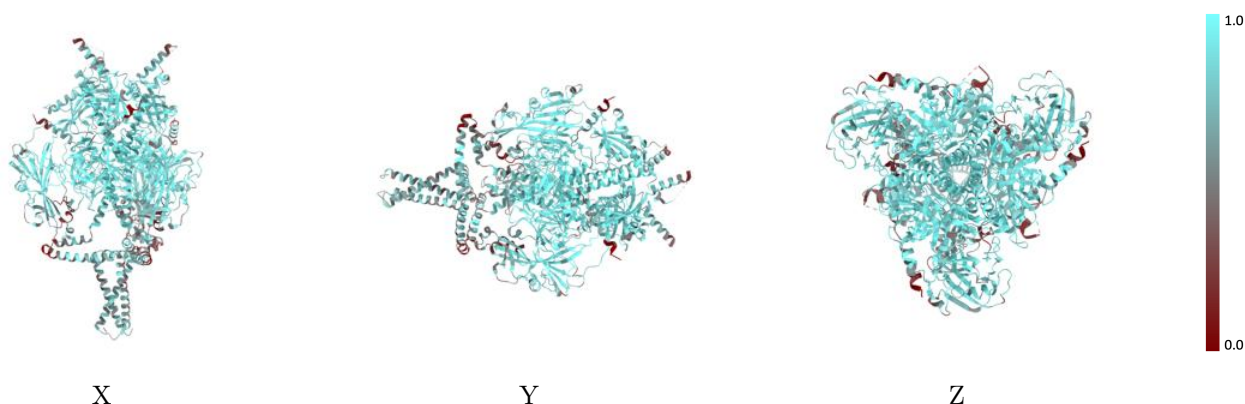
The images above show the 3D surface view of the map at the recommended contour level 0.0769 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



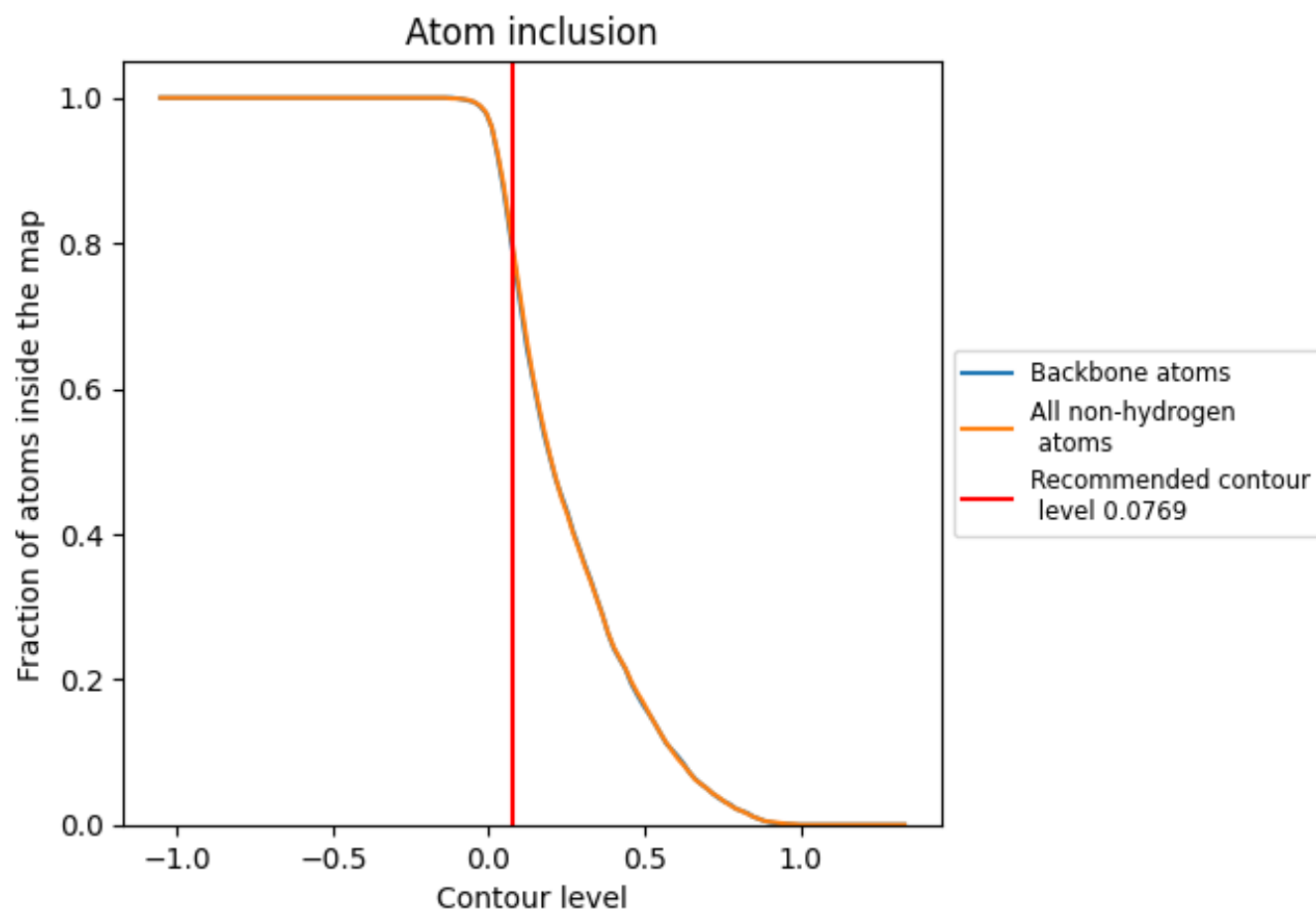
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0769).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 80% 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 (0.0769) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7960	<div></div> 0.4360
A	<div></div> 0.7990	<div></div> 0.4340
B	<div></div> 0.7990	<div></div> 0.4370
C	<div></div> 0.8000	<div></div> 0.4380

