



wwPDB EM Validation Summary Report ⓘ

Sep 21, 2026 – 11:10 AM EDT

PDB ID : 9YEJ / pdb_00009yej
EMDB ID : EMD-72852
Title : Structure of mink-derived HKU5 RBD in complex with ACE2 of N. viron
Authors : Li, N.; Keeler, E.; Tsybovsky, Y.; Zhou, T.
Deposited on : 2025-09-24
Resolution : 3.30 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

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:

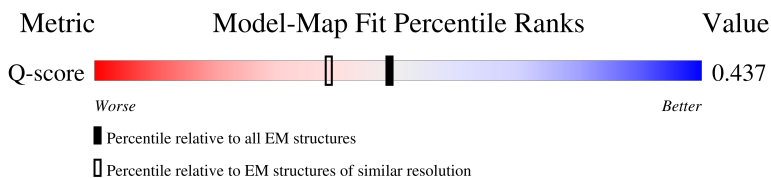
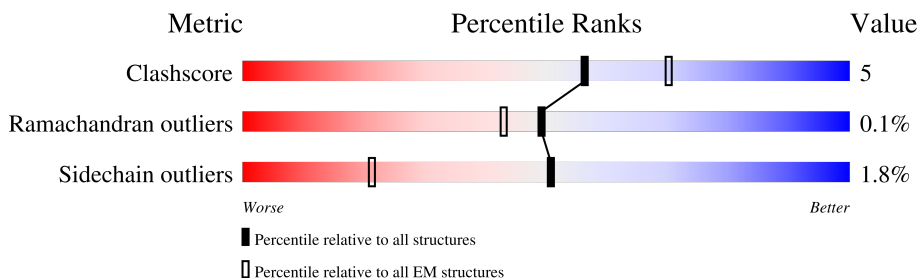
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 3.30 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	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	805	
1	C	805	
2	B	1358	
2	D	1358	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 14686 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.

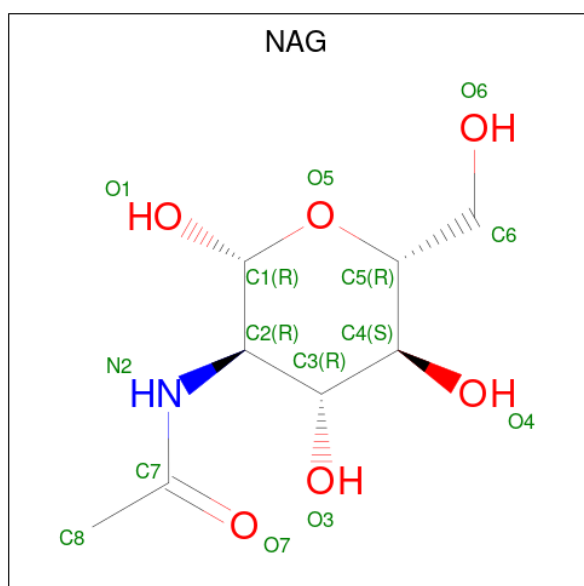
- Molecule 1 is a protein called Angiotensin-converting enzyme.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	699	Total	C	N	O	S	0	0
			5755	3674	972	1077	32		
1	C	699	Total	C	N	O	S	0	0
			5755	3674	972	1077	32		

- Molecule 2 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	199	Total	C	N	O	S	0	0
			1539	980	246	302	11		
2	D	199	Total	C	N	O	S	0	0
			1539	980	246	302	11		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

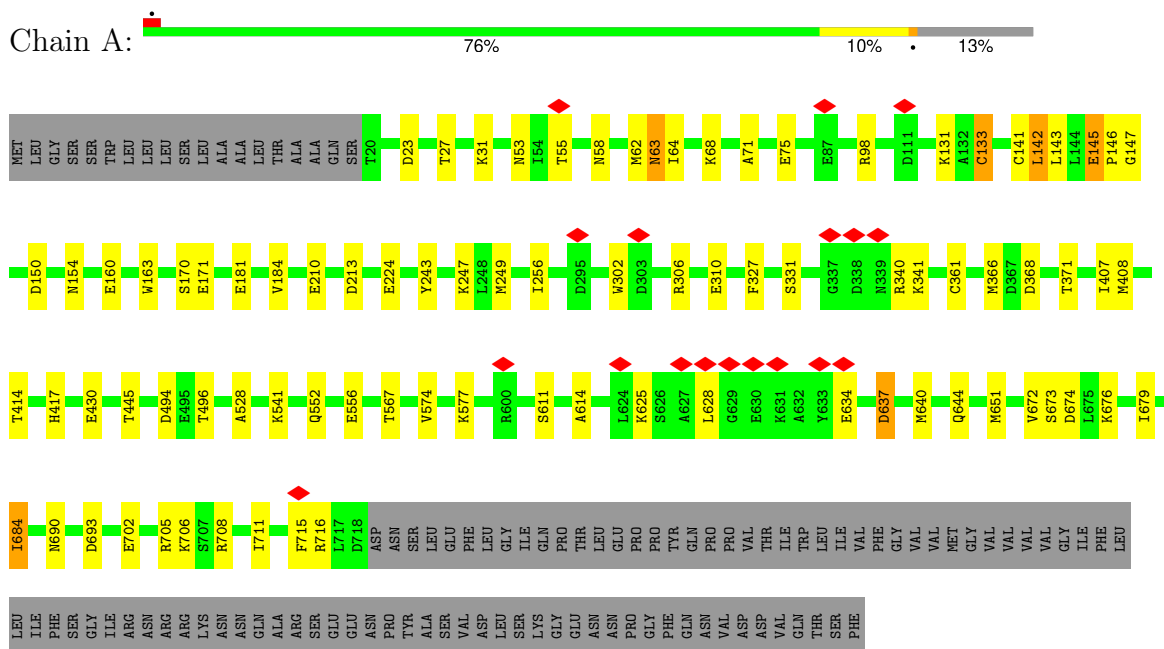


Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	

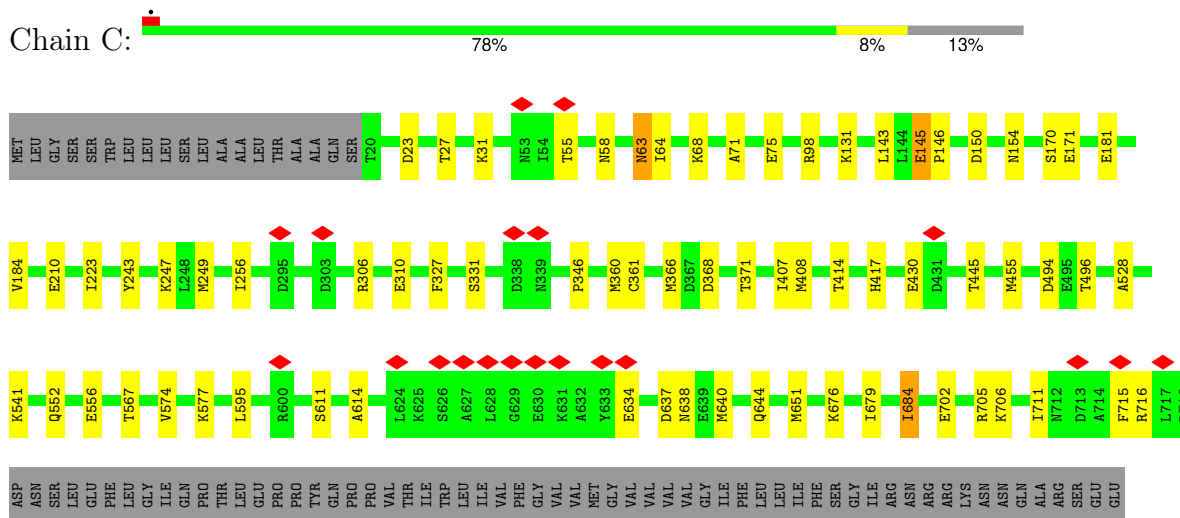
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Angiotensin-converting enzyme



• Molecule 1: Angiotensin-converting enzyme



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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	418147	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1900	Depositor
Magnification	47000	Depositor
Image detector	DIRECT ELECTRON APOLLO (4k x 4k)	Depositor
Maximum map value	1.938	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.13	Depositor
Map size (Å)	360.0, 360.0, 360.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.11	0/5915	0.31	0/8021
1	C	0.11	0/5915	0.31	0/8021
2	B	0.13	0/1581	0.32	0/2157
2	D	0.12	0/1581	0.32	0/2157
All	All	0.11	0/14992	0.31	0/20356

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	5755	0	5516	50	0
1	C	5755	0	5515	39	0
2	B	1539	0	1467	26	0
2	D	1539	0	1467	26	0
3	A	42	0	39	1	0
3	C	56	0	52	0	0
All	All	14686	0	14056	141	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 5.

The worst 5 of 141 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:133:CYS:HA	1:A:141:CYS:HB2	1.77	0.64
1:A:145:GLU:HB2	1:A:146:PRO:HD3	1.78	0.64
1:C:145:GLU:HB2	1:C:146:PRO:HD3	1.78	0.64
1:A:327:PHE:O	1:A:331:SER:OG	2.14	0.64
2:D:396:MET:SD	2:D:396:MET:N	2.67	0.64

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	697/805 (87%)	655 (94%)	41 (6%)	1 (0%)	48	75
1	C	697/805 (87%)	656 (94%)	40 (6%)	1 (0%)	48	75
2	B	197/1358 (14%)	182 (92%)	15 (8%)	0	100	100
2	D	197/1358 (14%)	182 (92%)	15 (8%)	0	100	100
All	All	1788/4326 (41%)	1675 (94%)	111 (6%)	2 (0%)	49	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	145	GLU
1	C	145	GLU

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	618/710 (87%)	609 (98%)	9 (2%)	57	72
1	C	618/710 (87%)	611 (99%)	7 (1%)	65	76
2	B	177/1181 (15%)	170 (96%)	7 (4%)	28	56
2	D	177/1181 (15%)	171 (97%)	6 (3%)	32	59
All	All	1590/3782 (42%)	1561 (98%)	29 (2%)	51	70

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	562	VAL
2	D	562	VAL
1	C	223	ILE
2	D	451	VAL
1	C	63	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	682	ASN
1	C	51	ASN
1	C	682	ASN
1	C	241	HIS
1	C	401	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

7 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	C	903	1	14,14,15	0.75	0	17,19,21	0.77	0
3	NAG	A	901	1	14,14,15	0.76	0	17,19,21	0.96	1 (5%)
3	NAG	A	902	1	14,14,15	0.42	0	17,19,21	0.91	1 (5%)
3	NAG	A	903	1	14,14,15	0.74	0	17,19,21	0.76	0
3	NAG	C	904	1	14,14,15	0.79	0	17,19,21	1.01	1 (5%)
3	NAG	C	901	1	14,14,15	0.71	0	17,19,21	0.76	0
3	NAG	C	902	1	14,14,15	0.41	0	17,19,21	0.38	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	C	903	1	-	0/6/23/26	0/1/1/1
3	NAG	A	901	1	-	0/6/23/26	0/1/1/1
3	NAG	A	902	1	-	2/6/23/26	0/1/1/1
3	NAG	A	903	1	-	0/6/23/26	0/1/1/1
3	NAG	C	904	1	-	1/6/23/26	0/1/1/1
3	NAG	C	901	1	-	0/6/23/26	0/1/1/1
3	NAG	C	902	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	902	NAG	O5-C1-C2	3.27	116.36	111.29
3	C	904	NAG	C2-N2-C7	2.22	125.87	122.90
3	A	901	NAG	C1-O5-C5	2.12	115.03	112.19

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	902	NAG	C8-C7-N2-C2
3	A	902	NAG	O7-C7-N2-C2
3	C	904	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	901	NAG	1	0

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.

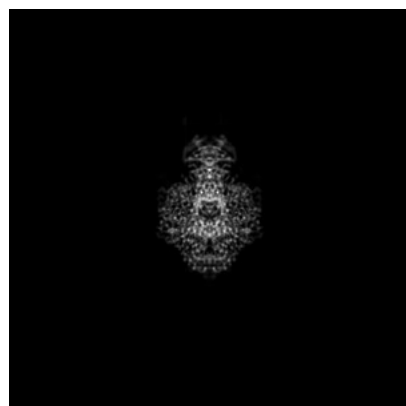
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72852. These allow visual inspection of the internal detail of the map and identification of artifacts.

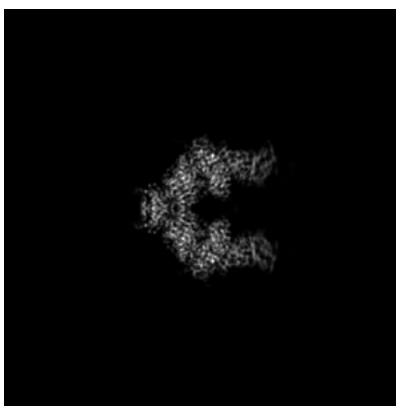
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

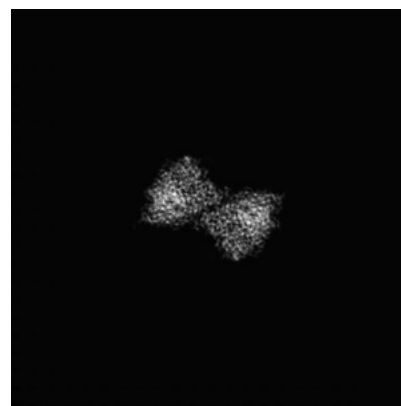
6.1.1 Primary map



X

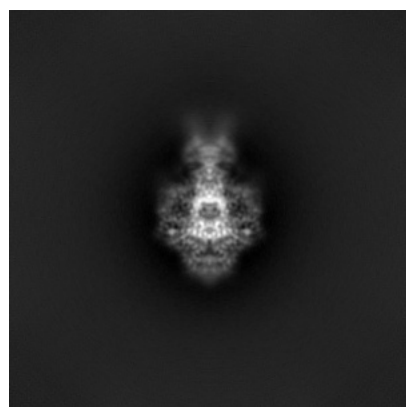


Y

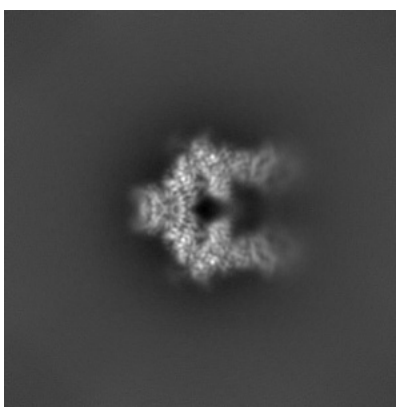


Z

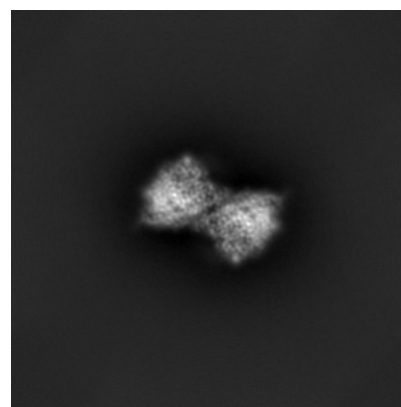
6.1.2 Raw map



X



Y

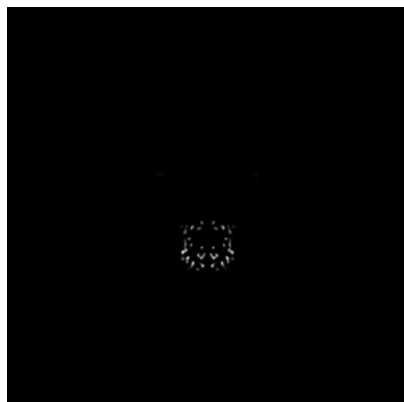


Z

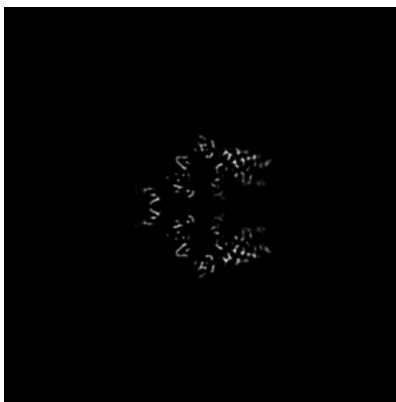
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 180

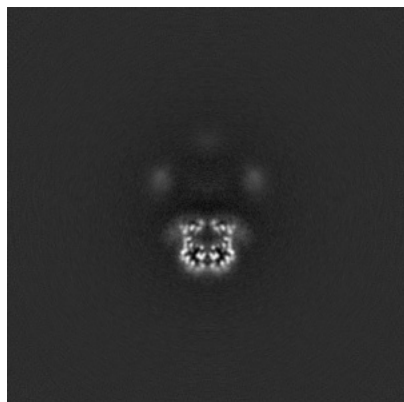


Y Index: 180

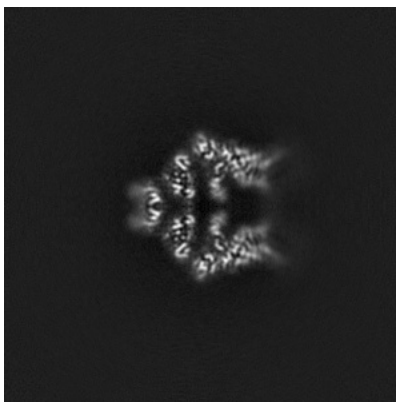


Z Index: 180

6.2.2 Raw map



X Index: 180



Y Index: 180

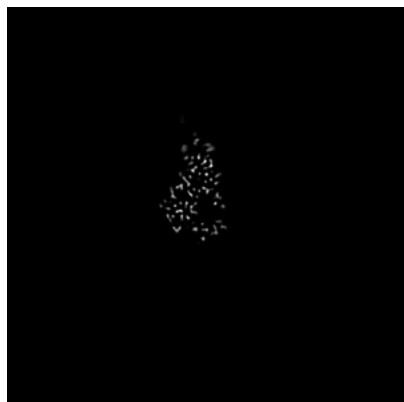


Z Index: 180

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

6.3 Largest variance slices [i](#)

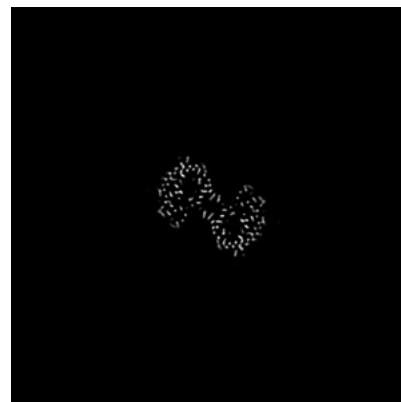
6.3.1 Primary map



X Index: 217

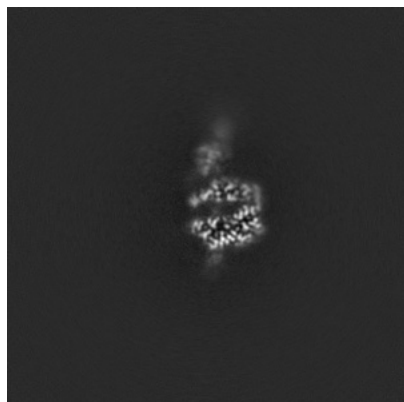


Y Index: 172

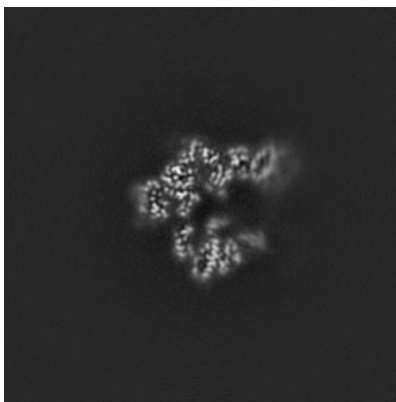


Z Index: 160

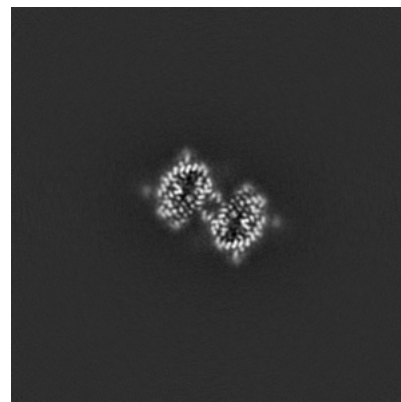
6.3.2 Raw map



X Index: 156



Y Index: 172

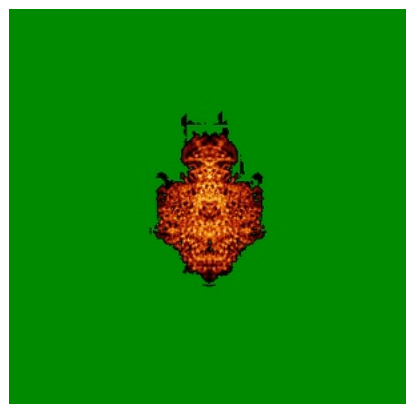


Z Index: 159

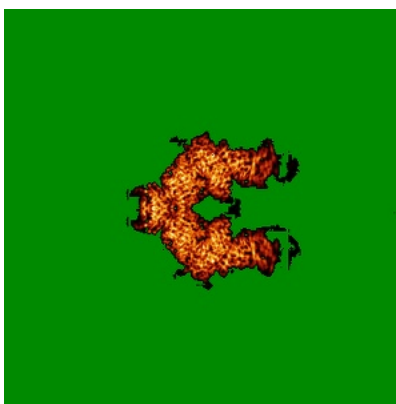
The images above show the largest variance slices of the map in three orthogonal directions.

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

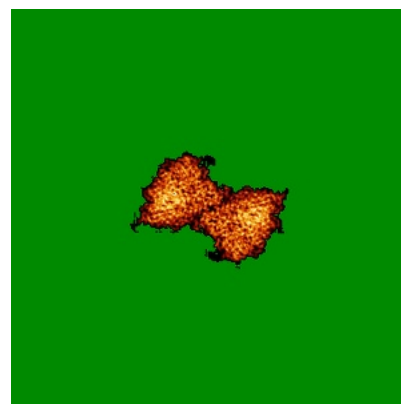
6.4.1 Primary map



X

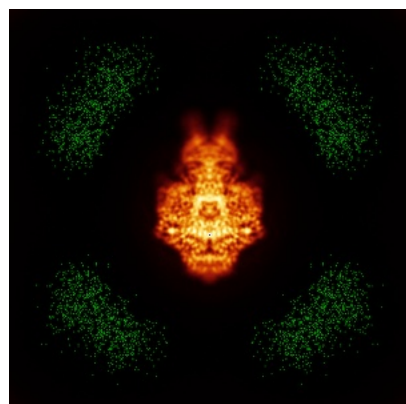


Y

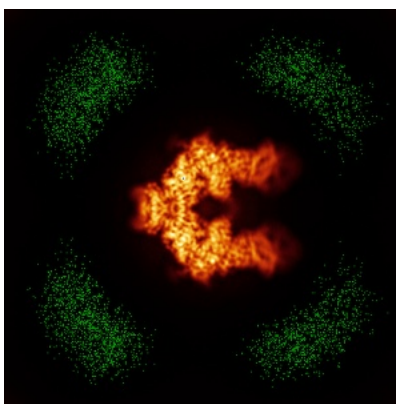


Z

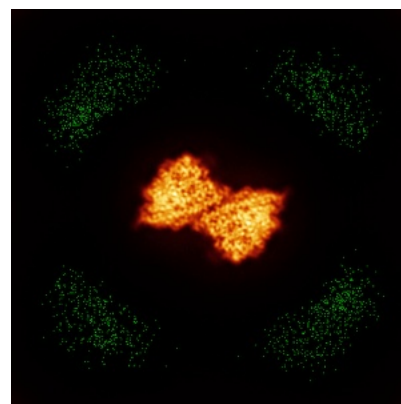
6.4.2 Raw map



X



Y

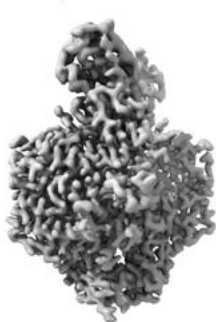


Z

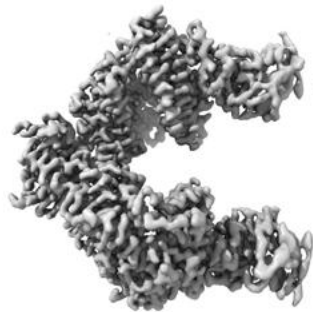
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

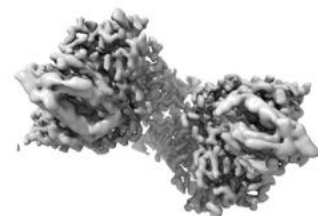
6.5.1 Primary map



X



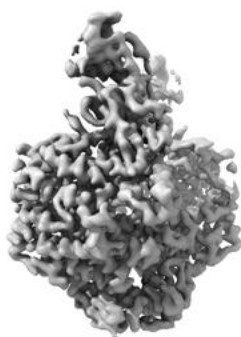
Y



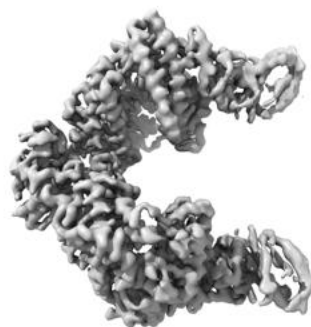
Z

The images above show the 3D surface view of the map at the recommended contour level 0.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

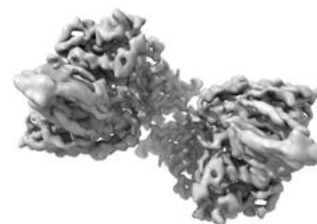
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

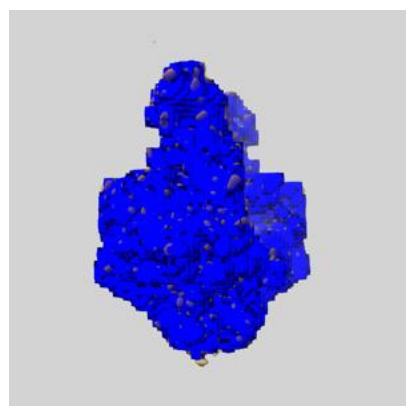
6.6 Mask visualisation [i](#)

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

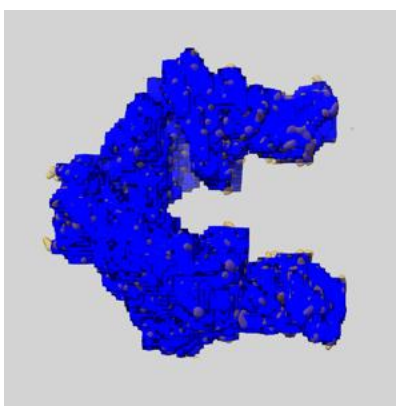
A mask typically either:

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

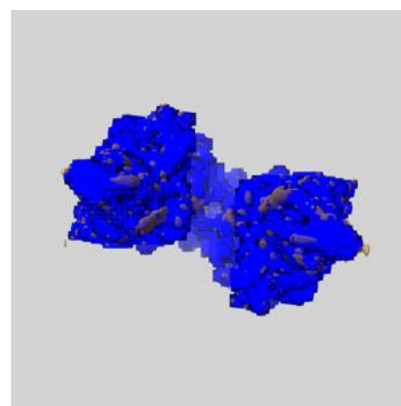
6.6.1 emd_72852_msk_1.map [i](#)



X



Y

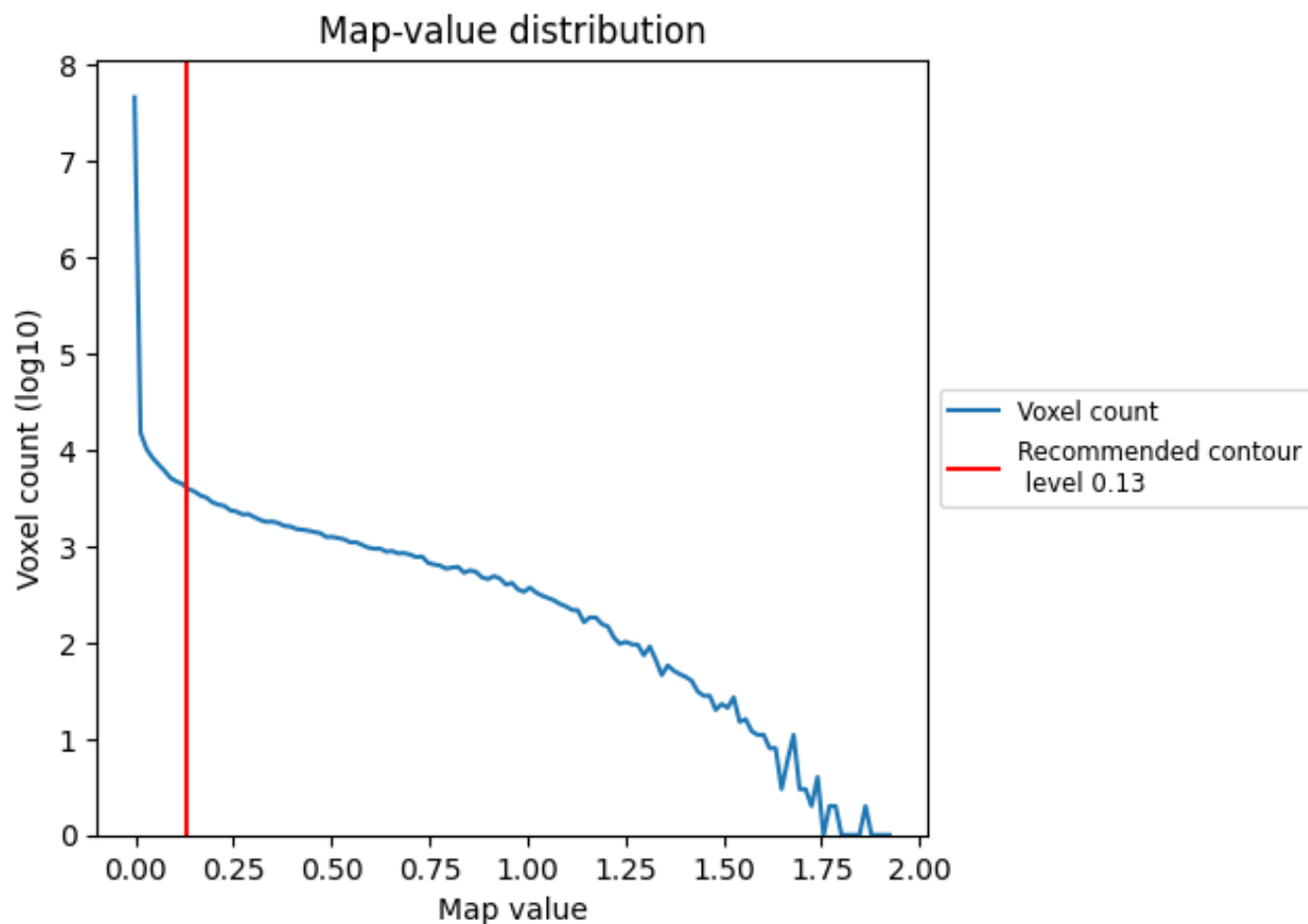


Z

7 Map analysis [i](#)

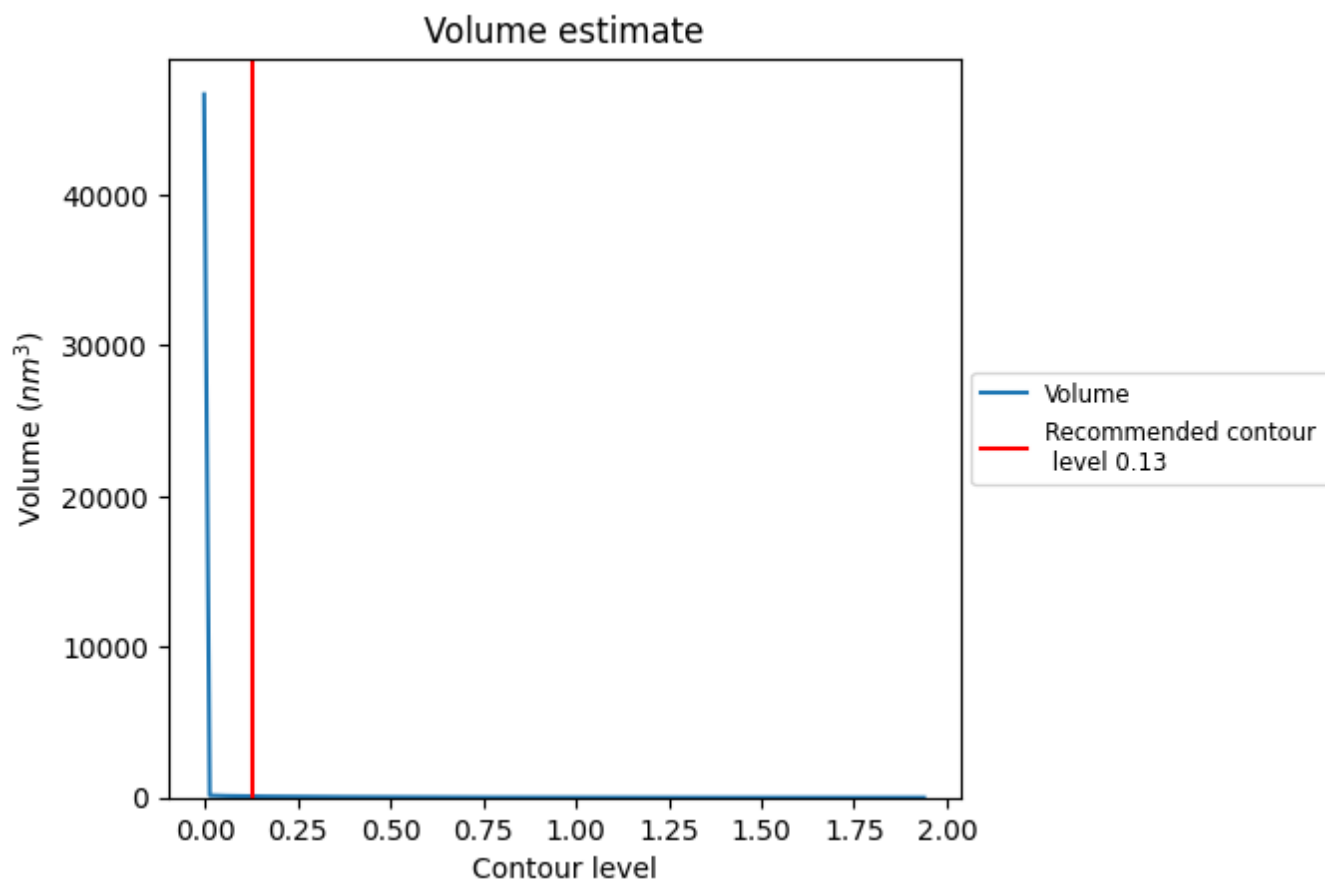
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

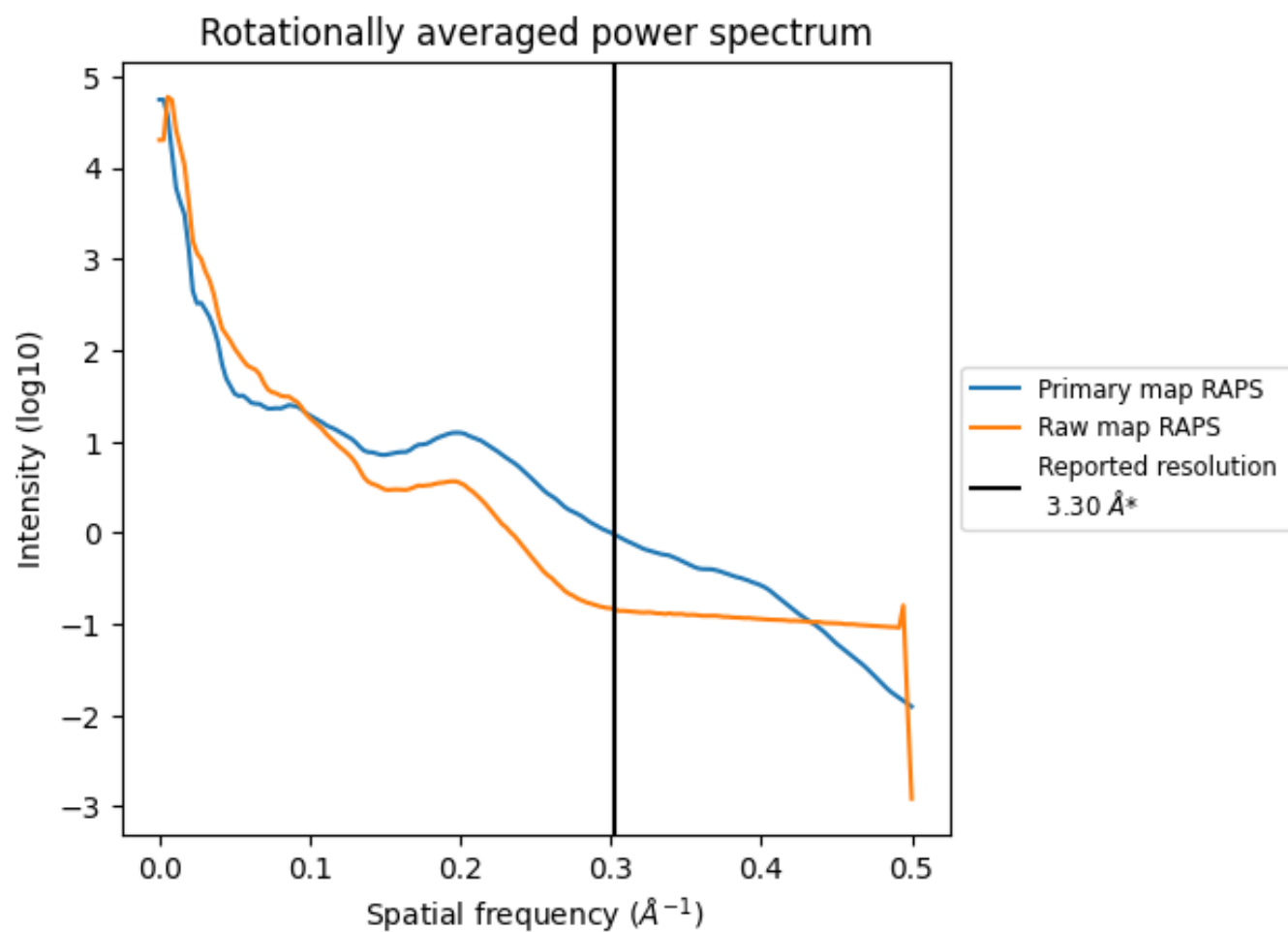
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 83 nm^3 ; this corresponds to an approximate mass of 75 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 ⓘ

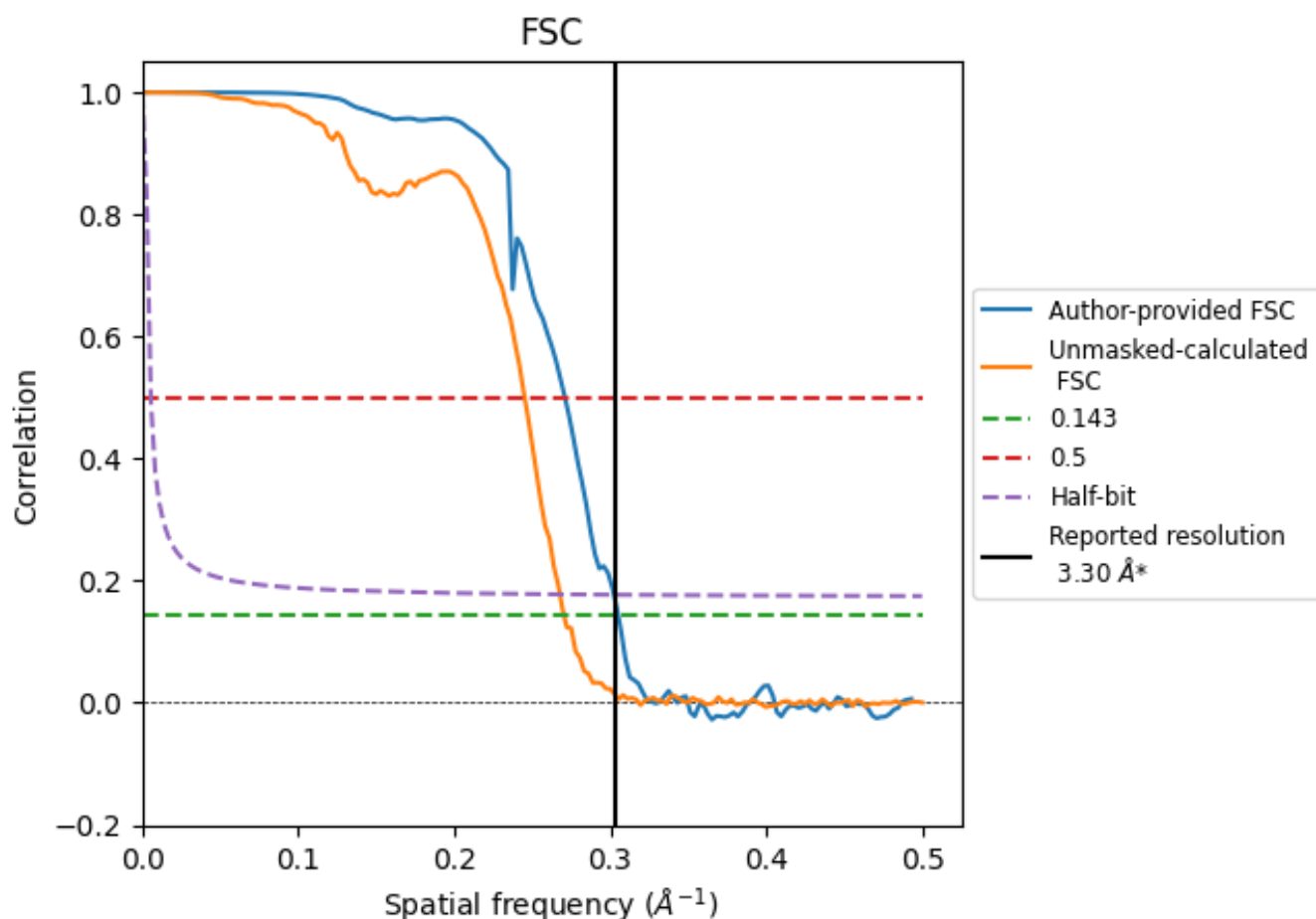


*Reported resolution corresponds to spatial frequency of $0.303 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

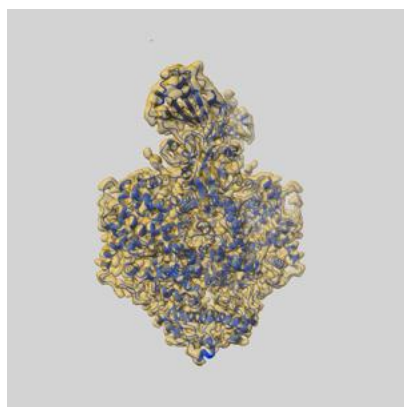
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.28	3.69	3.31
Unmasked-calculated*	3.70	4.08	3.73

*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 3.70 differs from the reported value 3.3 by more than 10 %

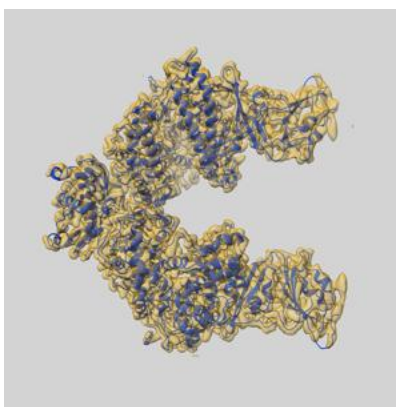
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-72852 and PDB model 9YEJ. Per-residue inclusion information can be found in section [3](#) on page [5](#).

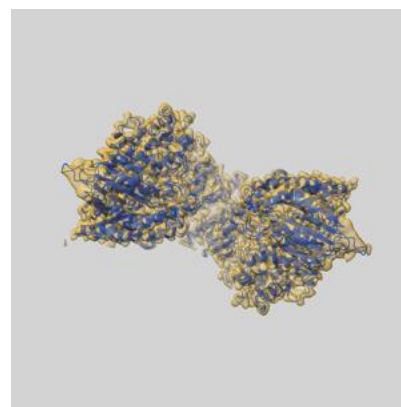
9.1 Map-model overlay [i](#)



X



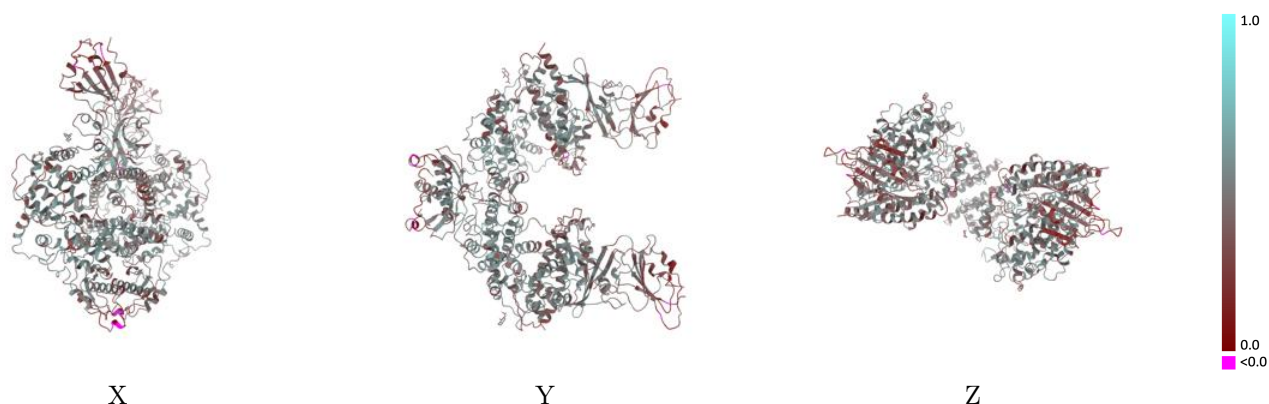
Y



Z

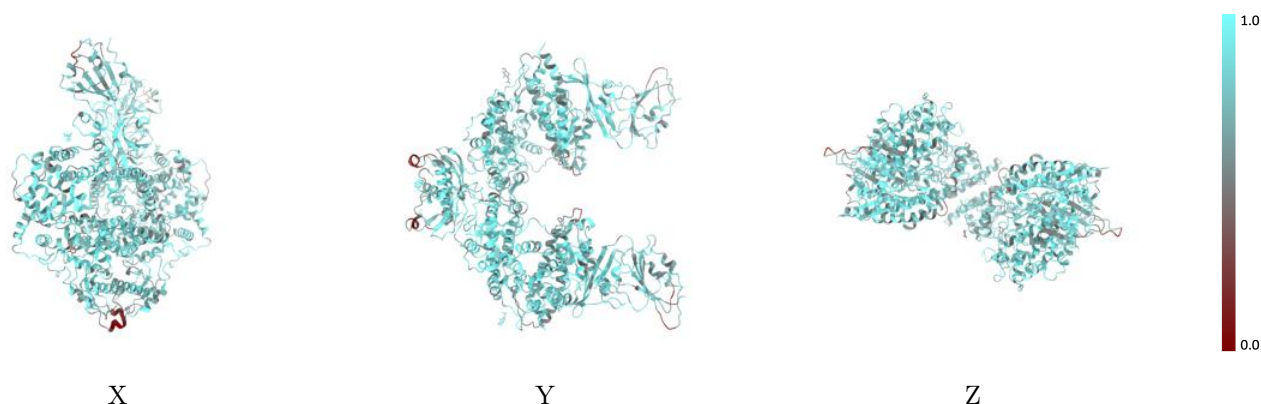
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



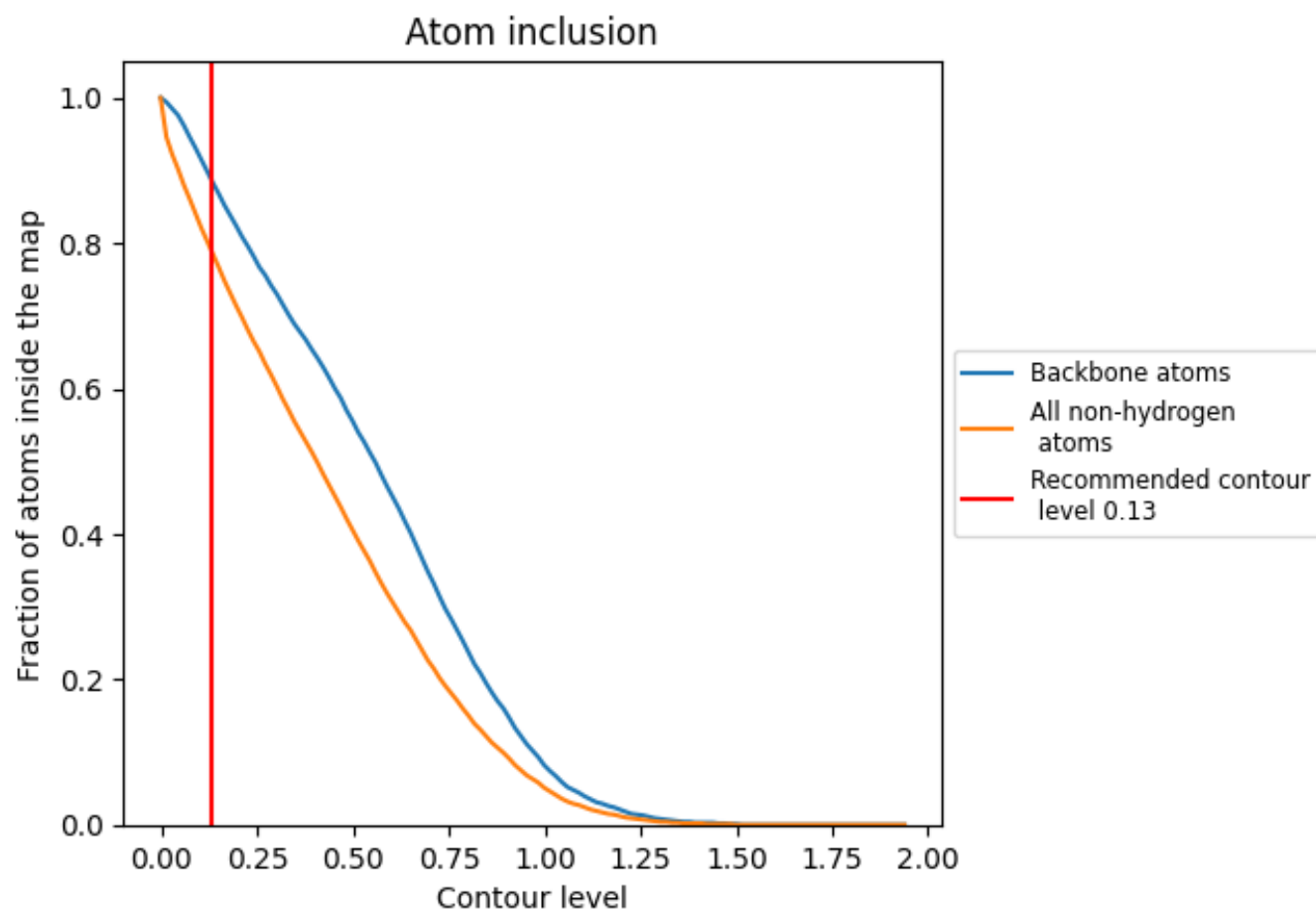
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 79% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7900	0.4370
A	0.7980	0.4570
B	0.7580	0.3650
C	0.7980	0.4560
D	0.7600	0.3640

