



wwPDB EM Validation Summary Report ⓘ

Dec 16, 2024 – 11:40 AM EST

PDB ID : 9COO
EMDB ID : EMD-45787
Title : Nanobody 4 bound to Apolipoprotein B 100
Authors : Dearborn, A.D.; Kumar, A.; Reimund, M.; Graziano, G.; Lei, H.; Neufeld, E.B.; Remaley, A.T.; Marcotrigiano, J.
Deposited on : 2024-07-17
Resolution : 3.73 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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

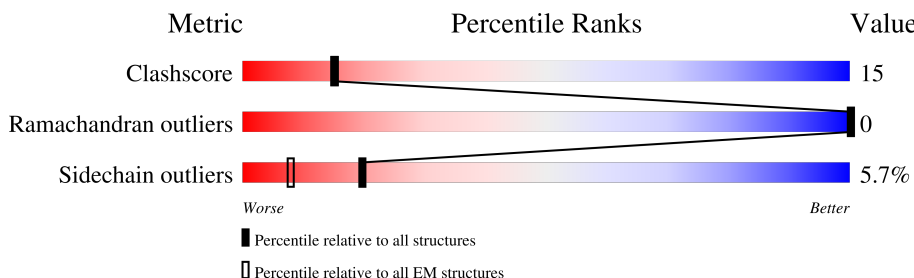
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.73 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 ≥ 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	4563	 6% 91%
2	B	545	 16% 7% 77%
3	H	234	 37% 16% 47%
4	L	219	 37% 11% 51%
5	N	131	 72% 21% 5%
6	R	795	 10% 5% 85%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7493 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 Apolipoprotein B 100.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	423	Total	C	N	O	S	0	0
			3170	1994	549	623	4		

- Molecule 2 is a protein called Maltodextrin-binding protein,Immunoglobulin G-binding protein A,Immunoglobulin G-binding protein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	128	Total	C	N	O	S	0	0
			926	575	157	193	1		

There are 47 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP C3SHQ8
B	361	ALA	GLN	conflict	UNP P99134
B	362	LEU	ASN	conflict	UNP P99134
B	365	ALA	TYR	conflict	UNP P99134
B	367	ILE	VAL	conflict	UNP P99134
B	369	ILE	ASN	conflict	UNP P99134
B	374	THR	ASN	conflict	UNP P99134
B	375	GLU	ALA	conflict	UNP P99134
B	376	GLU	ASP	conflict	UNP P99134
B	391	VAL	GLN	conflict	UNP P99134
B	393	LYS	ALA	conflict	UNP P99134
B	394	GLU	ASN	conflict	UNP P99134
B	395	ILE	VAL	conflict	UNP P99134
B	397	ALA	GLY	conflict	UNP P99134
B	400	LYS	GLN	conflict	UNP P99134
B	404	GLU	ASP	conflict	UNP P99134
B	405	HIS	SER	conflict	UNP P99134
B	?	-	ALA	deletion	UNP P99134
B	410	GLY	ASP	conflict	UNP P99134
B	411	GLY	ALA	conflict	UNP P99134

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Chain	Residue	Modelled	Actual	Comment	Reference
B	412	SER	GLN	conflict	UNP P99134
B	413	GLY	GLN	conflict	UNP P99134
B	414	GLY	ASN	conflict	UNP P99134
B	415	ALA	ASN	conflict	UNP P99134
B	416	GLY	PHE	conflict	UNP P99134
B	417	SER	ASN	conflict	UNP P99134
B	418	GLY	LYS	conflict	UNP P99134
B	468	GLY	-	linker	UNP P99134
B	469	GLY	-	linker	UNP P99134
B	470	GLY	-	linker	UNP P99134
B	471	SER	-	linker	UNP P99134
B	472	GLY	-	linker	UNP P99134
B	473	GLY	-	linker	UNP P99134
B	474	GLY	-	linker	UNP P99134
B	475	SER	-	linker	UNP P99134
B	476	GLY	-	linker	UNP P99134
B	477	GLY	-	linker	UNP P99134
B	478	SER	-	linker	UNP P99134
B	537	GLY	-	expression tag	UNP P06654
B	538	SER	-	expression tag	UNP P06654
B	539	GLY	-	expression tag	UNP P06654
B	540	HIS	-	expression tag	UNP P06654
B	541	HIS	-	expression tag	UNP P06654
B	542	HIS	-	expression tag	UNP P06654
B	543	HIS	-	expression tag	UNP P06654
B	544	HIS	-	expression tag	UNP P06654
B	545	HIS	-	expression tag	UNP P06654

- Molecule 3 is a protein called Legobody 8D3 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	125	Total	C	N	O	S	0	0
			923	587	151	179	6		

- Molecule 4 is a protein called Legobody 8D3 Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	108	Total	C	N	O	S	0	0
			769	489	121	156	3		

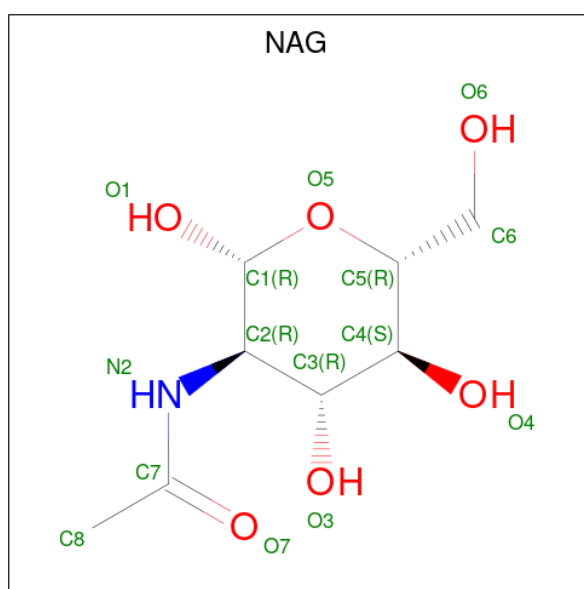
- Molecule 5 is a protein called ApoB100 nanobody 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	N	124	Total	C	N	O	S	0	0
			859	538	153	164	4		

- Molecule 6 is a protein called Low-density lipoprotein receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	R	120	Total	C	N	O	S	0	0
			801	478	132	173	18		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

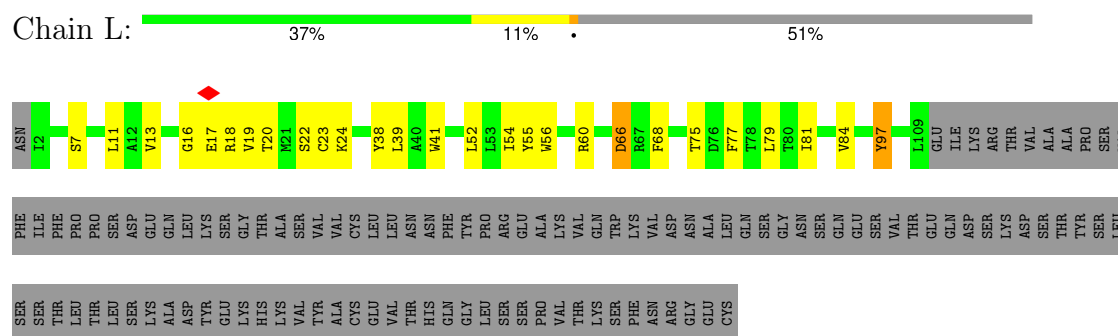
Mol	Chain	Residues	Atoms		AltConf
8	R	3	Total	Ca	0
			3	3	



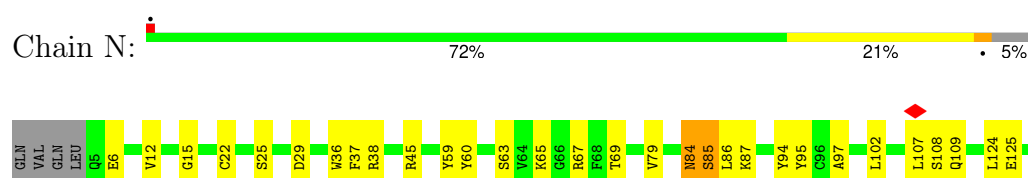




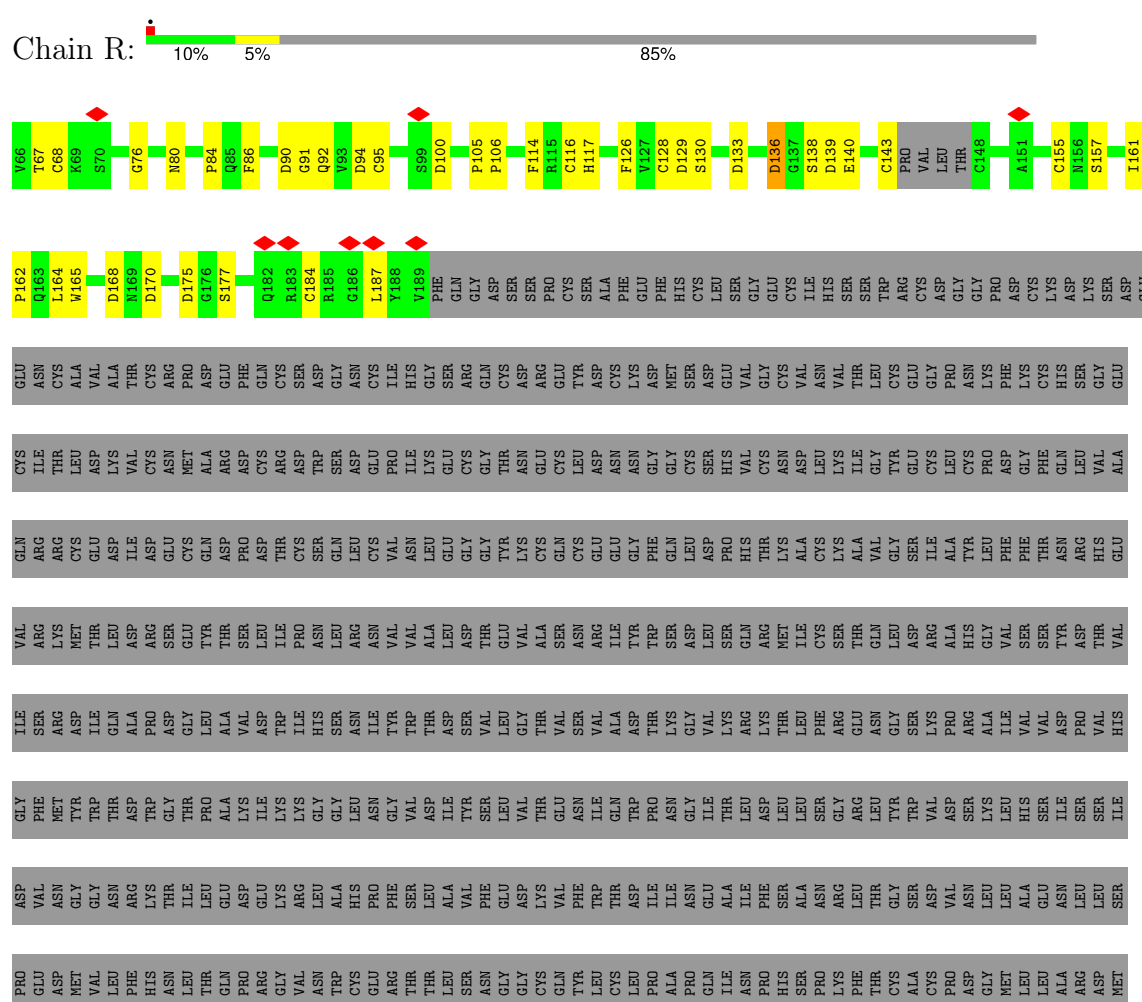
• Molecule 4: Legobody 8D3 Fab Light Chain



• Molecule 5: ApoB100 nanobody 4



• Molecule 6: Low-density lipoprotein receptor



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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	527598	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 ($e^-/\text{\AA}^2$)	51.38	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	0.714	Depositor
Minimum map value	-0.368	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	557.76, 557.76, 557.76	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.6600001, 1.6600001, 1.6600001	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CA, 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	0.26	0/3225	0.55	0/4374
2	B	0.28	0/940	0.47	0/1284
3	H	0.32	0/948	0.53	0/1293
4	L	0.30	0/789	0.55	1/1087 (0.1%)
5	N	0.31	0/877	0.52	0/1196
6	R	0.26	0/817	0.44	0/1117
All	All	0.28	0/7596	0.52	1/10351 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	66	ASP	CB-CG-OD1	5.48	123.23	118.30

There are no chirality outliers.

There are no planarity outliers.

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	3170	0	3049	104	0
2	B	926	0	834	28	0
3	H	923	0	838	28	0
4	L	769	0	685	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	N	859	0	767	19	0
6	R	801	0	604	33	0
7	A	42	0	39	2	0
8	R	3	0	0	0	0
All	All	7493	0	6816	210	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 15.

The worst 5 of 210 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)
4:L:18:ARG:HA	4:L:81:ILE:O	1.59	1.01
1:A:3347:VAL:HG23	1:A:3348:ILE:HG13	1.65	0.78
2:B:448:ASP:OD2	2:B:454:ASN:ND2	2.18	0.76
6:R:161:ILE:HG13	6:R:162:PRO:HD2	1.68	0.75
1:A:3093:PHE:HB3	1:A:3096:TYR:HB2	1.71	0.73

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	417/4563 (9%)	383 (92%)	34 (8%)	0	100	100
2	B	124/545 (23%)	119 (96%)	5 (4%)	0	100	100
3	H	121/234 (52%)	116 (96%)	5 (4%)	0	100	100
4	L	106/219 (48%)	97 (92%)	9 (8%)	0	100	100
5	N	122/131 (93%)	113 (93%)	9 (7%)	0	100	100
6	R	116/795 (15%)	110 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1006/6487 (16%)	938 (93%)	68 (7%)	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	339/4080 (8%)	316 (93%)	23 (7%)	13	39
2	B	91/433 (21%)	88 (97%)	3 (3%)	33	57
3	H	93/199 (47%)	87 (94%)	6 (6%)	14	41
4	L	77/192 (40%)	74 (96%)	3 (4%)	27	53
5	N	75/103 (73%)	70 (93%)	5 (7%)	13	40
6	R	82/703 (12%)	79 (96%)	3 (4%)	29	54
All	All	757/5710 (13%)	714 (94%)	43 (6%)	20	45

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	69	THR
5	N	25	SER
3	H	71	SER
4	L	23	CYS
5	N	84	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	420	GLN
2	B	421	GLN

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 ⓘ

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 for Mogul analysis.

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	$\# Z > 2$
7	NAG	A	4601	1	14,14,15	0.72	0	17,19,21	0.87	1 (5%)
7	NAG	A	4603	-	14,14,15	0.71	0	17,19,21	0.76	0
7	NAG	A	4602	1	14,14,15	0.79	0	17,19,21	2.25	3 (17%)

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
7	NAG	A	4601	1	-	0/6/23/26	0/1/1/1
7	NAG	A	4603	-	-	2/6/23/26	0/1/1/1
7	NAG	A	4602	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	4602	NAG	C2-N2-C7	7.96	133.57	122.90
7	A	4602	NAG	C8-C7-N2	2.83	120.82	116.12
7	A	4601	NAG	O5-C1-C2	-2.25	107.81	111.29
7	A	4602	NAG	O7-C7-C8	-2.03	118.44	122.05

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	4602	NAG	C8-C7-N2-C2
7	A	4602	NAG	O7-C7-N2-C2
7	A	4603	NAG	C8-C7-N2-C2
7	A	4603	NAG	O7-C7-N2-C2
7	A	4602	NAG	C1-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	4601	NAG	1	0
7	A	4602	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.

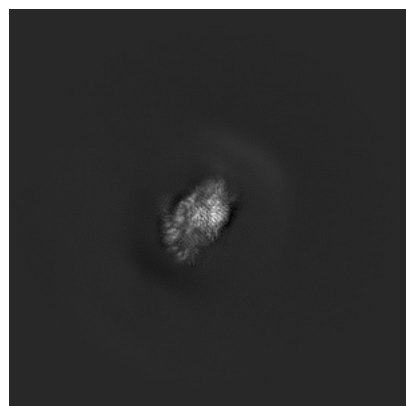
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45787. These allow visual inspection of the internal detail of the map and identification of artifacts.

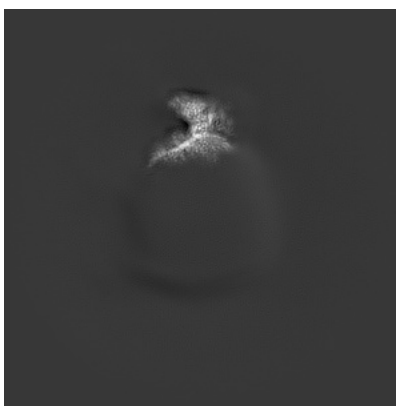
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

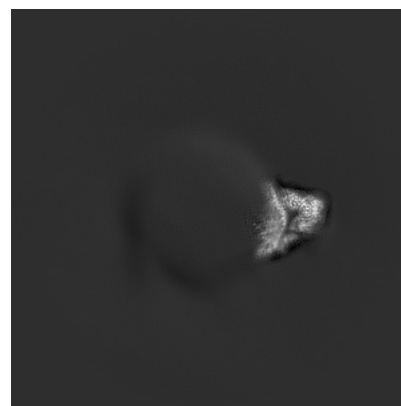
6.1.1 Primary map



X

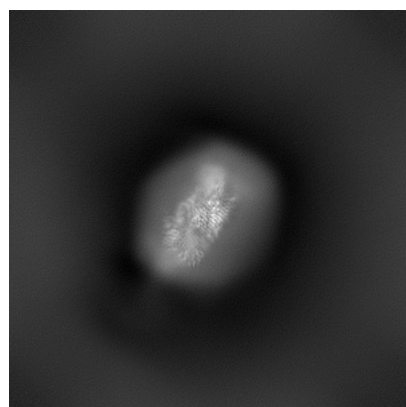


Y

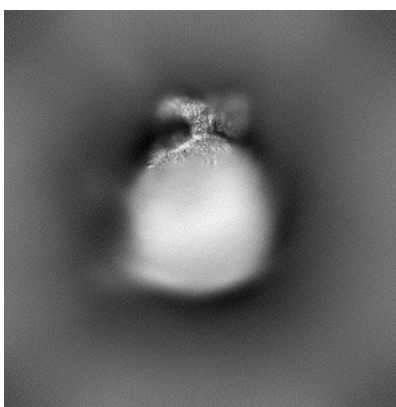


Z

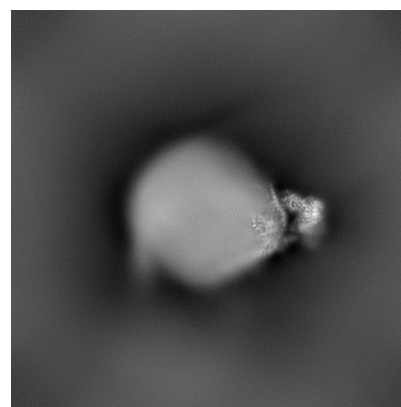
6.1.2 Raw map



X



Y

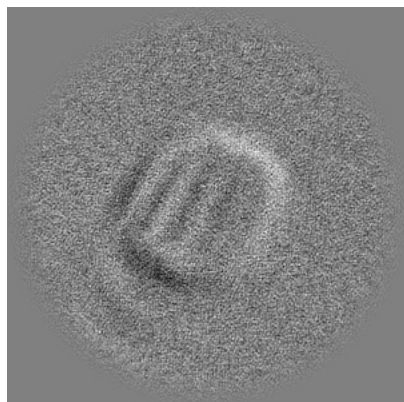


Z

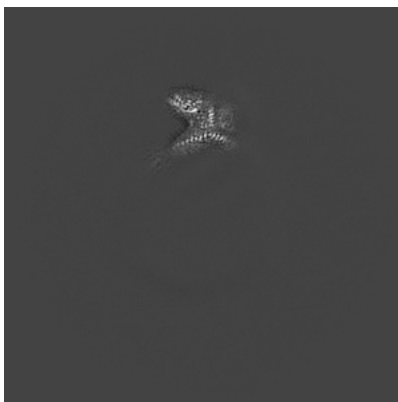
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

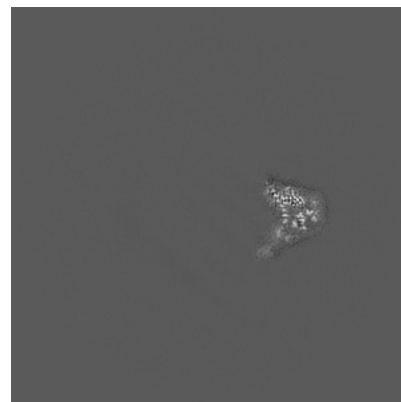
6.2.1 Primary map



X Index: 168

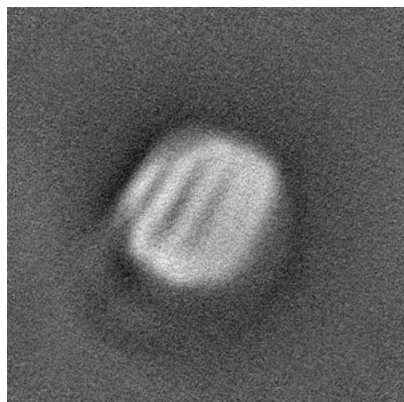


Y Index: 168

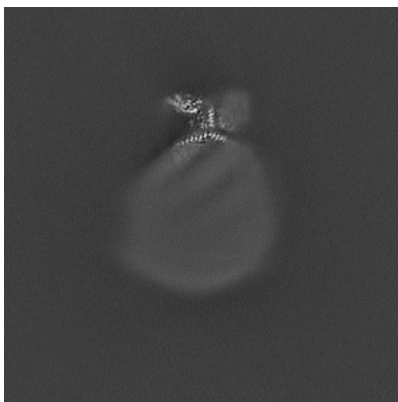


Z Index: 168

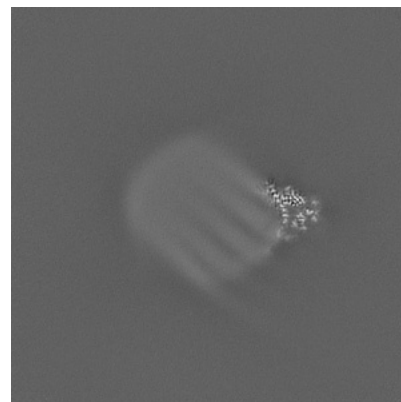
6.2.2 Raw map



X Index: 168



Y Index: 168

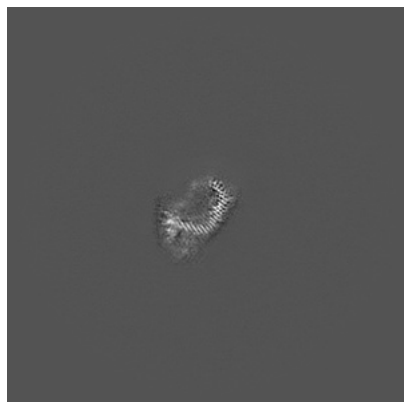


Z Index: 168

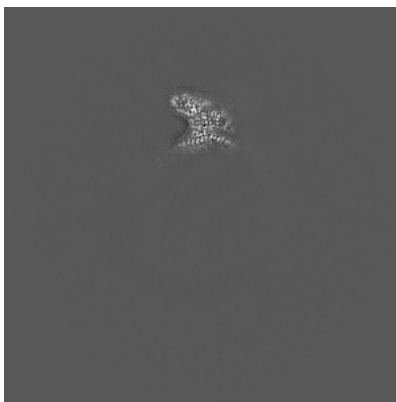
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 221

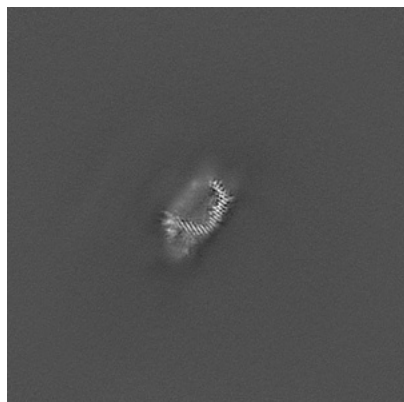


Y Index: 171

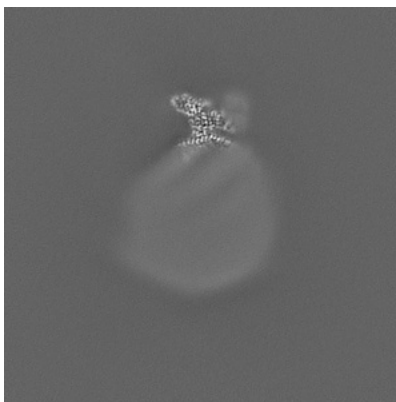


Z Index: 159

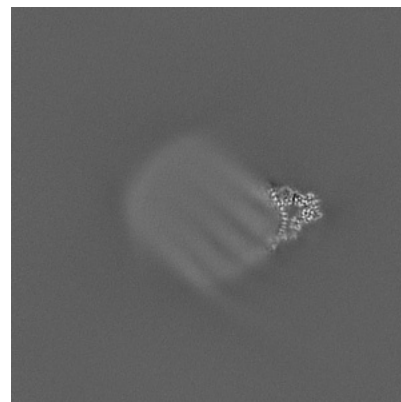
6.3.2 Raw map



X Index: 221



Y Index: 171

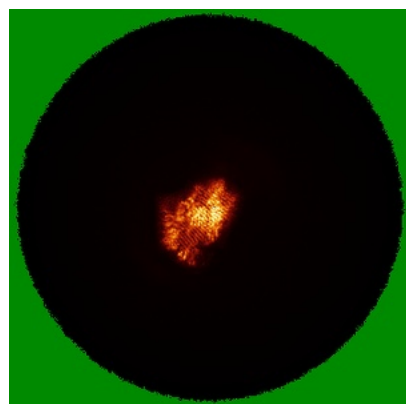


Z Index: 163

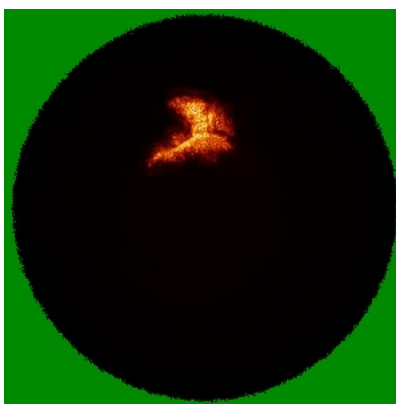
The images above show the largest variance slices of the map in three orthogonal directions.

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

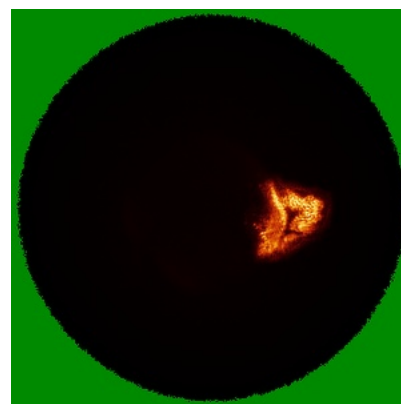
6.4.1 Primary map



X

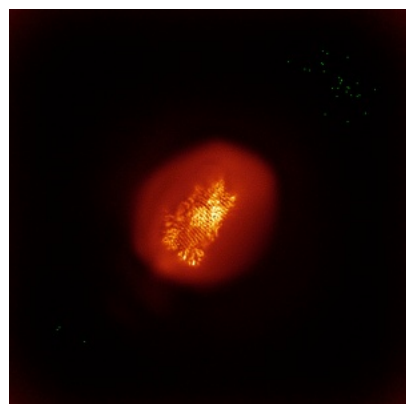


Y

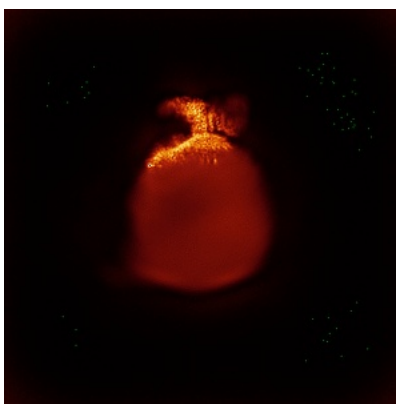


Z

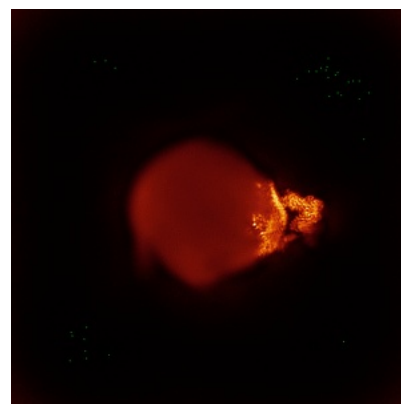
6.4.2 Raw map



X



Y

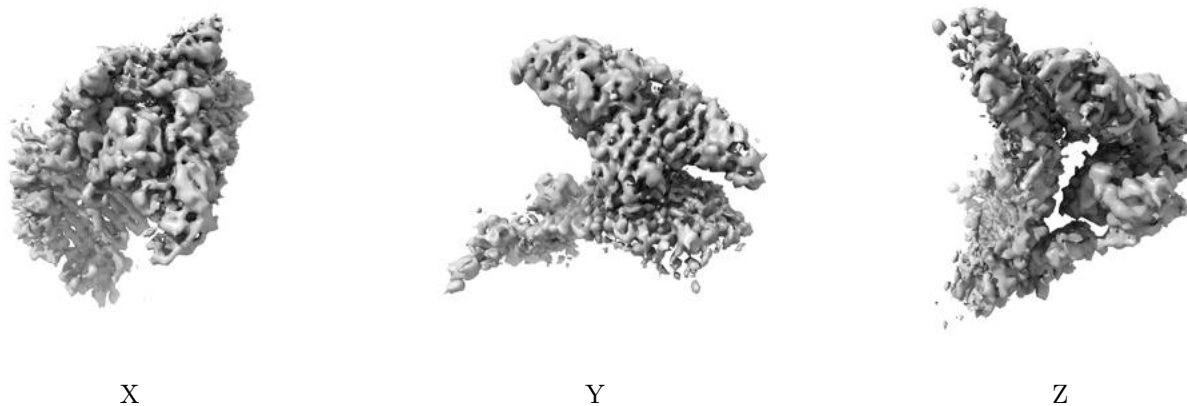


Z

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 0.11. 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.

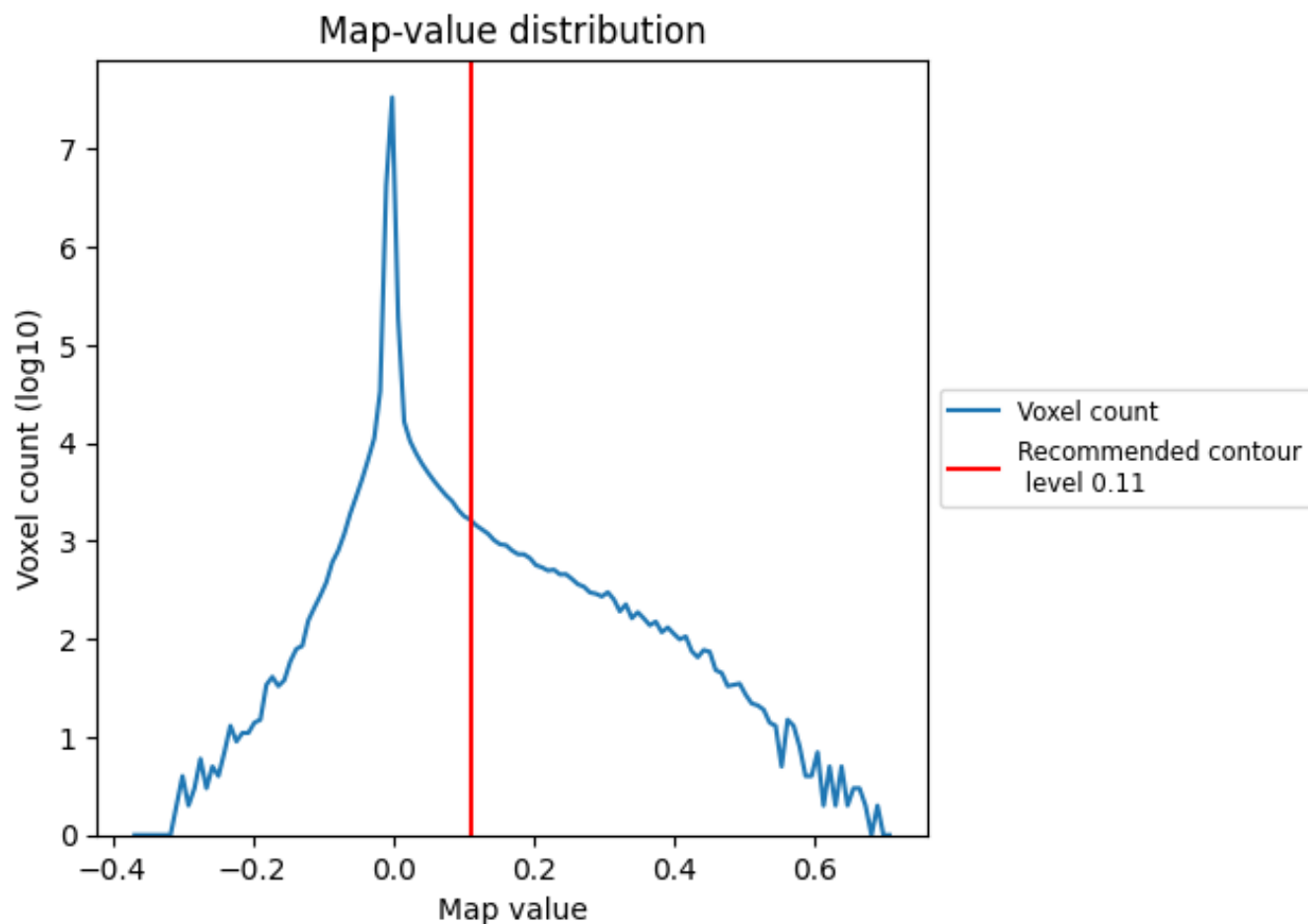
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

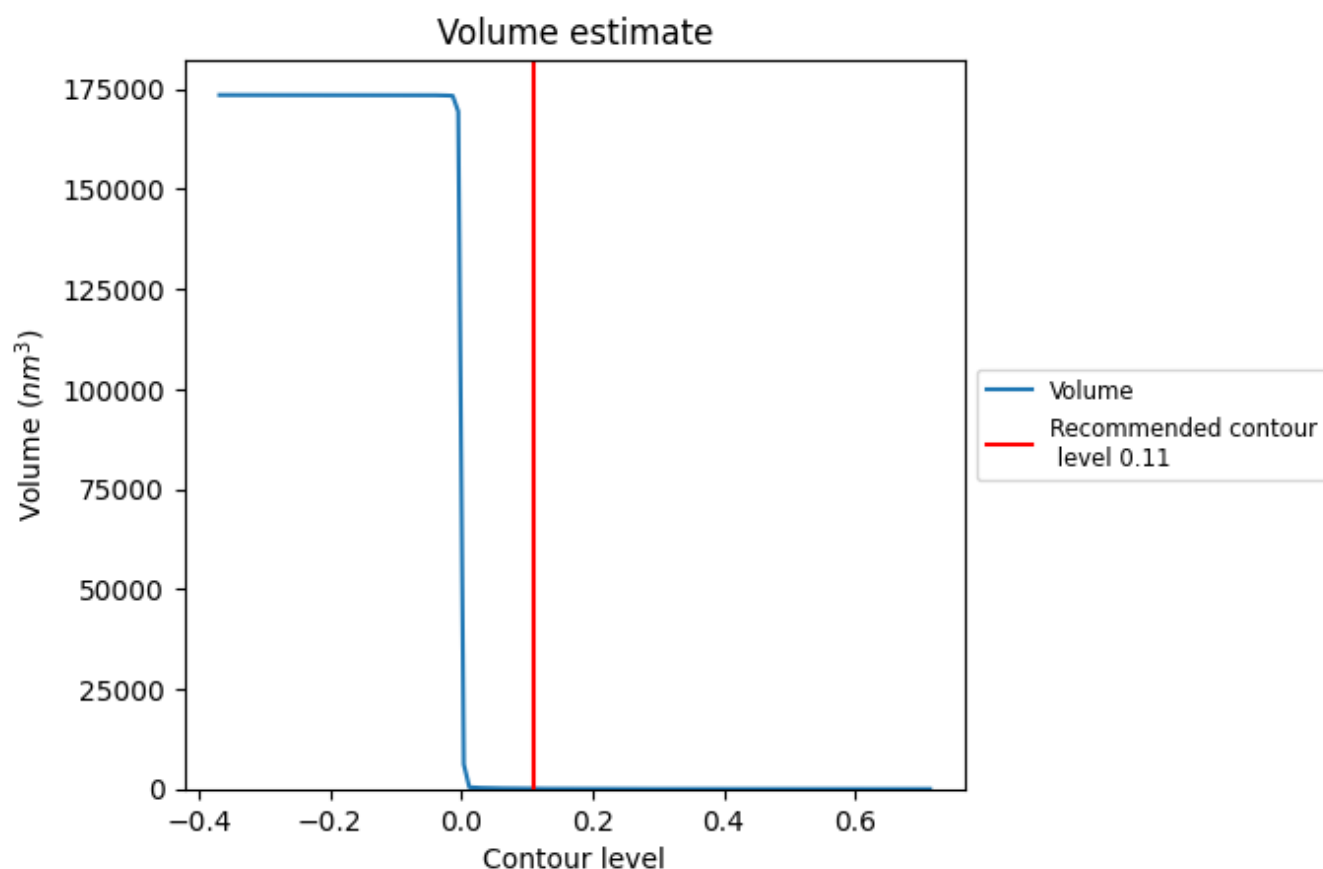
This section contains the results of statistical analysis of the map.

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.

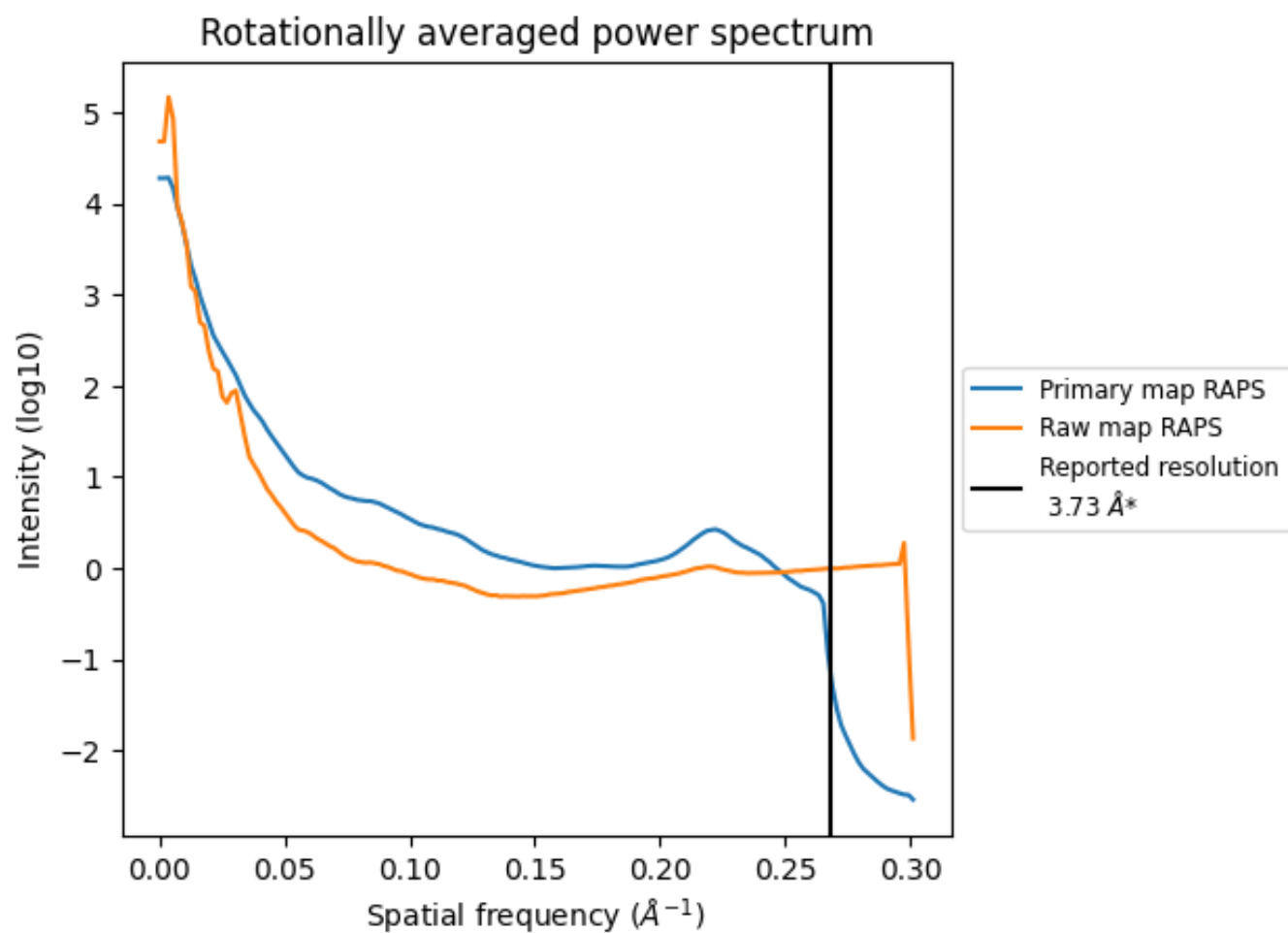
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 88 nm^3 ; this corresponds to an approximate mass of 79 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 ⓘ

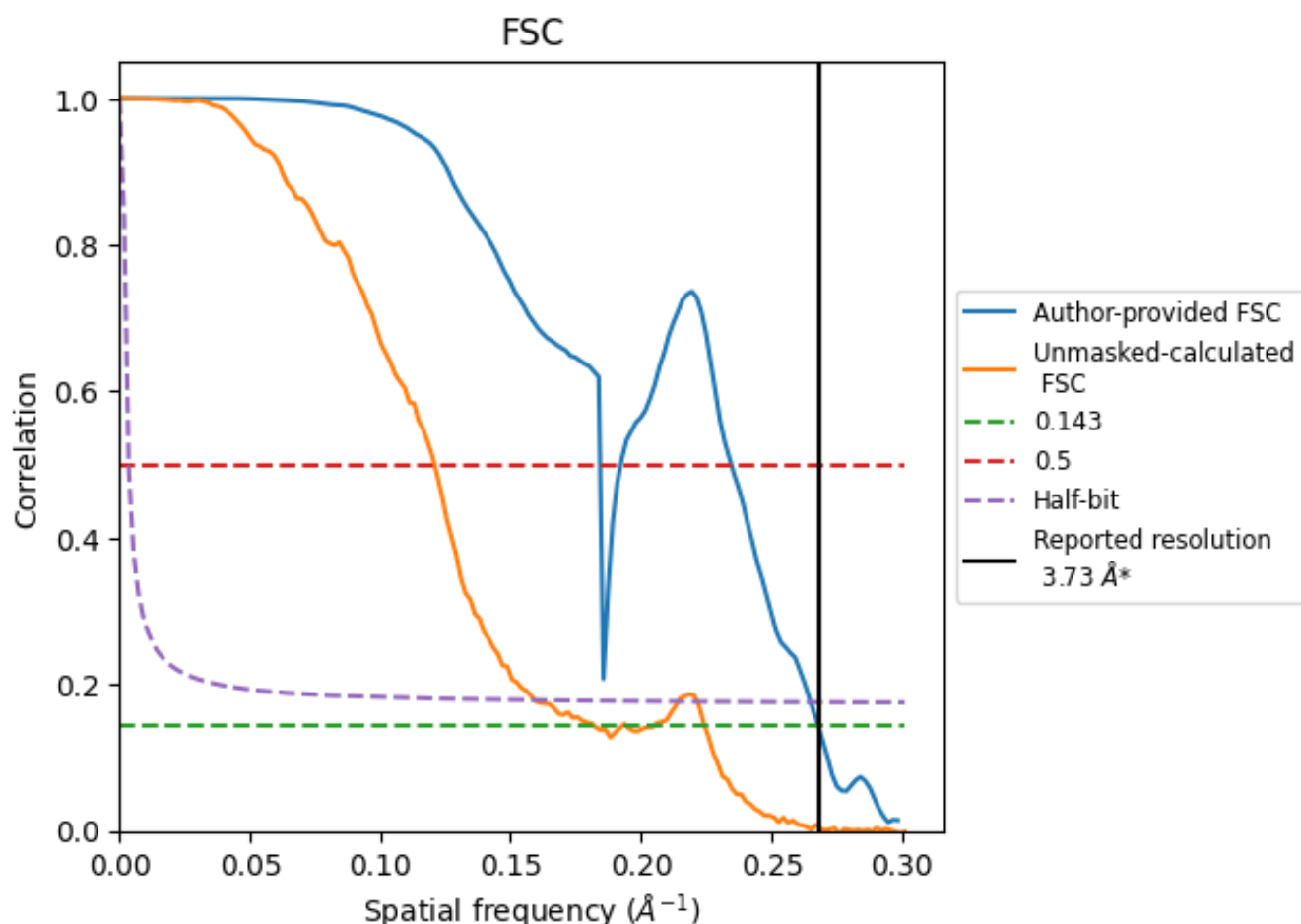


*Reported resolution corresponds to spatial frequency of 0.268 Å⁻¹

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 0.268 Å⁻¹

8.2 Resolution estimates [i](#)

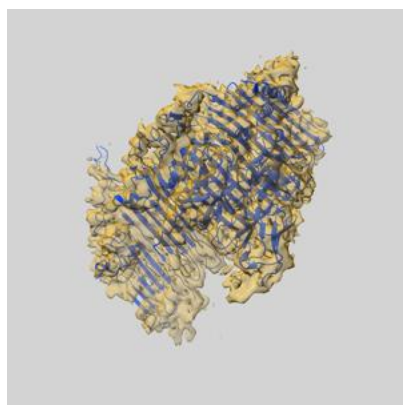
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.73	-	-
Author-provided FSC curve	3.73	5.43	3.77
Unmasked-calculated*	5.49	8.28	6.28

*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 5.49 differs from the reported value 3.73 by more than 10 %

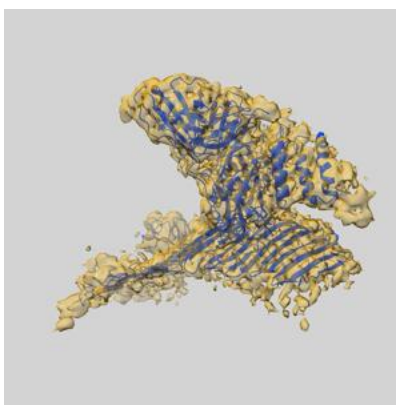
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-45787 and PDB model 9COO. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

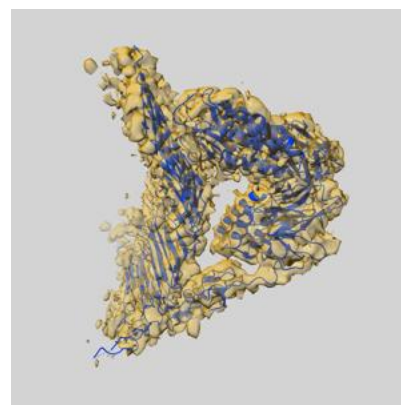
9.1 Map-model overlay [i](#)



X



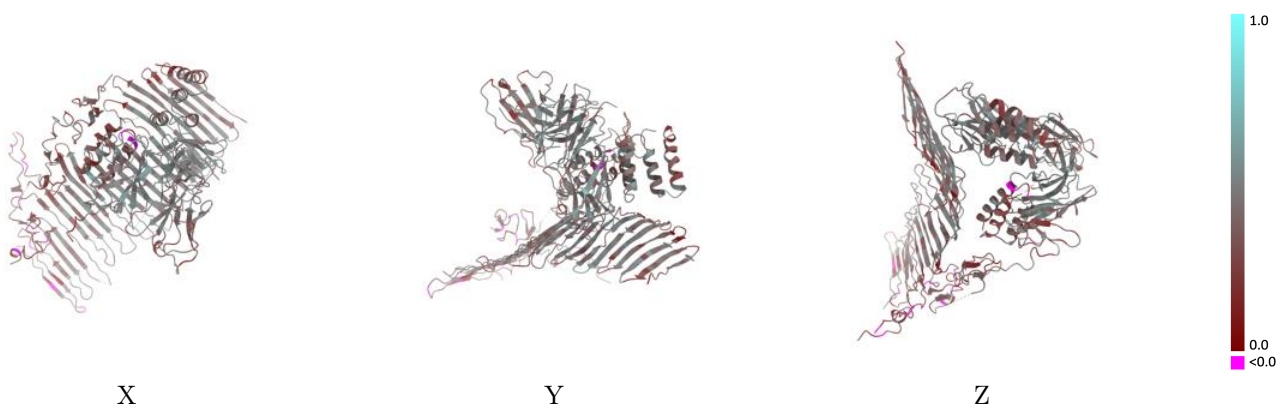
Y



Z

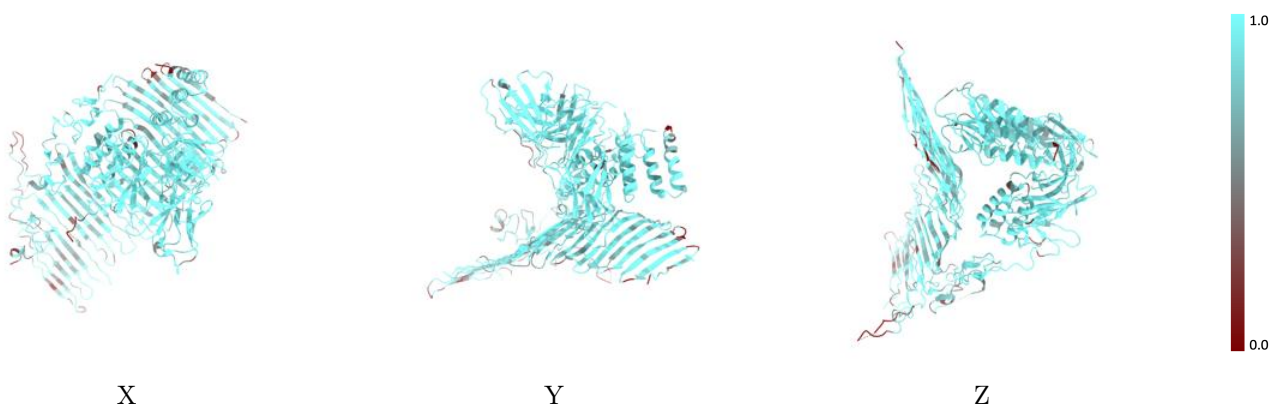
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



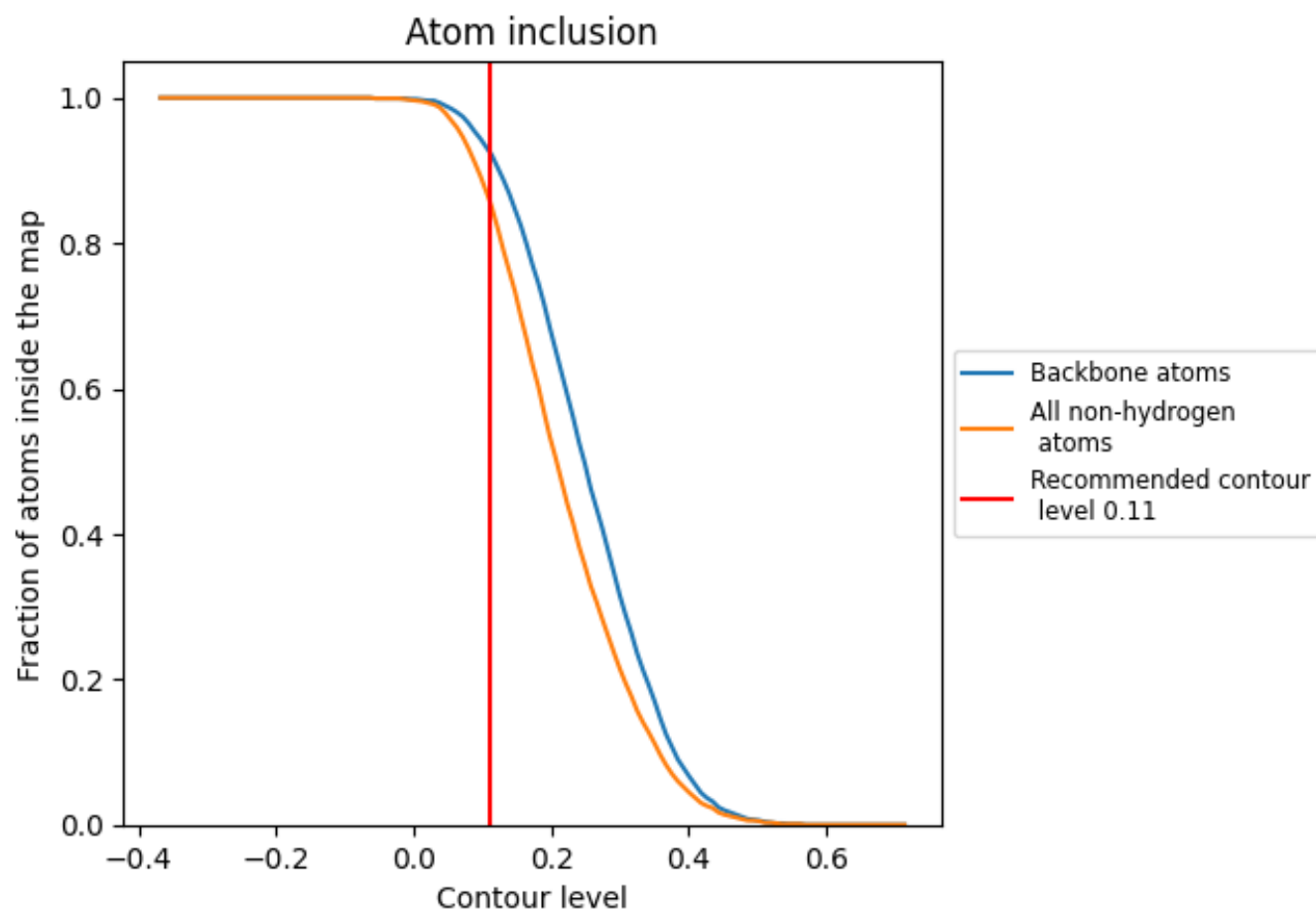
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 86% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8600	<div><div></div></div> 0.3960
A	<div><div></div></div> 0.7960	<div><div></div></div> 0.3820
B	<div><div></div></div> 0.8820	<div><div></div></div> 0.3700
H	<div><div></div></div> 0.9210	<div><div></div></div> 0.4660
L	<div><div></div></div> 0.9290	<div><div></div></div> 0.4320
N	<div><div></div></div> 0.9630	<div><div></div></div> 0.4620
R	<div><div></div></div> 0.8450	<div><div></div></div> 0.2970

1.0

0.0

<0.0