



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:31 AM UTC

PDB ID : 9DXH / pdb_00009dxh
EMDB ID : EMD-47288
Title : attPmm and attBmm bound serine integrase complex in the pre-rotation state
Authors : Shin, H.; Rice, P.A.; Olorunniji, F.J.
Deposited on : 2024-10-11
Resolution : 4.69 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.dev132
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) : 2.49

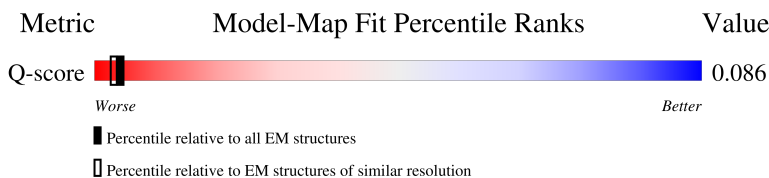
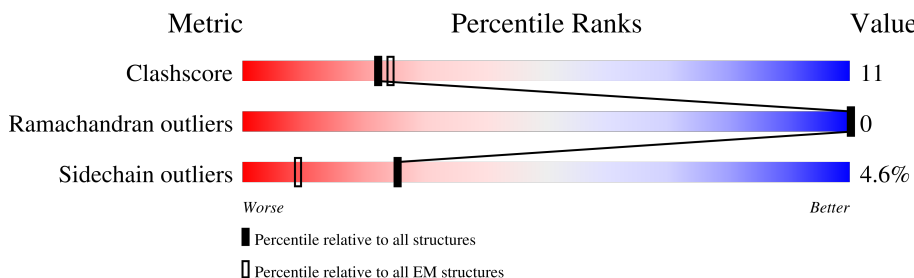
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.69 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	1970 (4.19 - 5.19)

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	545	
1	C	545	
1	I	545	
1	K	545	

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Mol	Chain	Length	Quality of chain
2	E	34	
2	M	34	
3	F	33	
3	N	33	
4	G	25	
4	O	25	
5	H	24	
5	P	24	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 42532 atoms, of which 20350 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 Resolvase homolog YokA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	535	Total	C	H	N	O	S	0	0
			8781	2744	4425	753	841	18		
1	C	535	Total	C	H	N	O	S	0	0
			8781	2744	4425	753	841	18		
1	I	535	Total	C	H	N	O	S	0	0
			8781	2744	4425	753	841	18		
1	K	535	Total	C	H	N	O	S	0	0
			8781	2744	4425	753	841	18		

- Molecule 2 is a DNA chain called DNA (34-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
2	E	34	Total	C	H	N	O	P	0	0
			1087	337	393	110	213	34		
2	M	34	Total	C	H	N	O	P	0	0
			1087	337	393	110	213	34		

- Molecule 3 is a DNA chain called DNA (33-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
3	F	33	Total	C	H	N	O	P	0	0
			1052	326	373	130	190	33		
3	N	33	Total	C	H	N	O	P	0	0
			1052	326	373	130	190	33		

- Molecule 4 is a DNA chain called DNA (25-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
4	G	25	Total	C	H	N	O	P	0	0
			796	246	285	90	150	25		
4	O	25	Total	C	H	N	O	P	0	0
			796	246	285	90	150	25		

- Molecule 5 is a DNA chain called DNA (24-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
5	H	24	Total	C	H	N	O	P	0	0
			767	237	274	87	145	24		
5	P	24	Total	C	H	N	O	P	0	0
			767	237	274	87	145	24		

- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
6	A	1	Total	Zn	0
			1	1	
6	C	1	Total	Zn	0
			1	1	
6	I	1	Total	Zn	0
			1	1	
6	K	1	Total	Zn	0
			1	1	

3 Residue-property plots

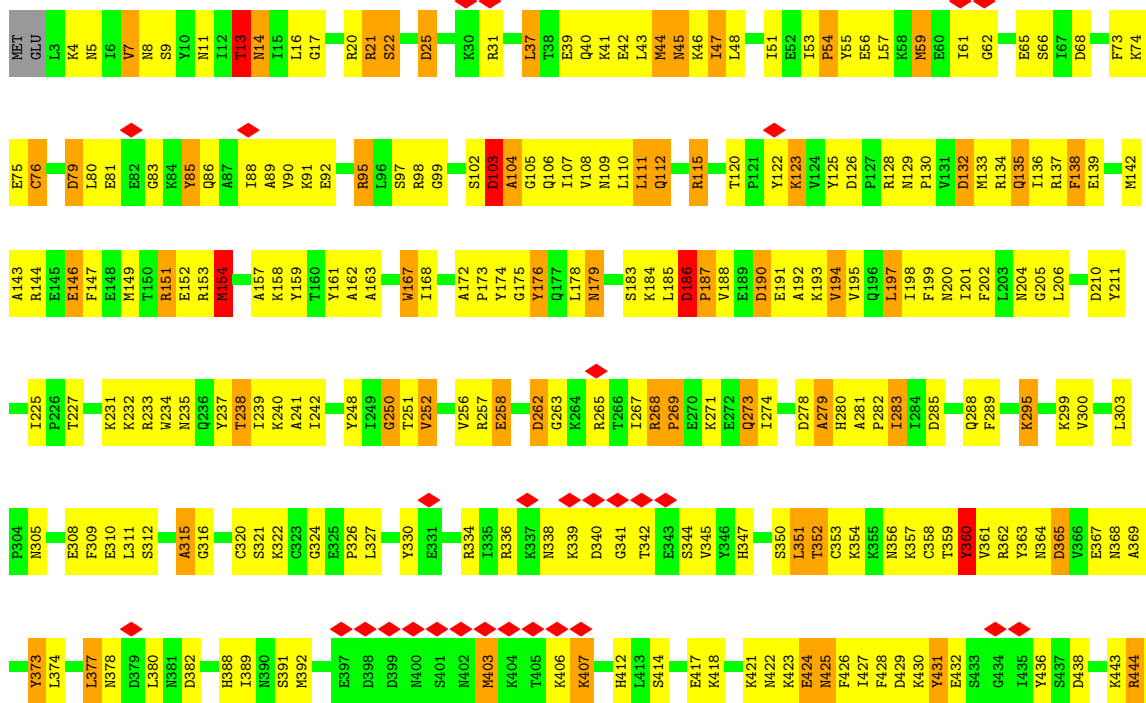
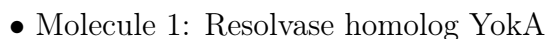
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Resolvase homolog Yoka

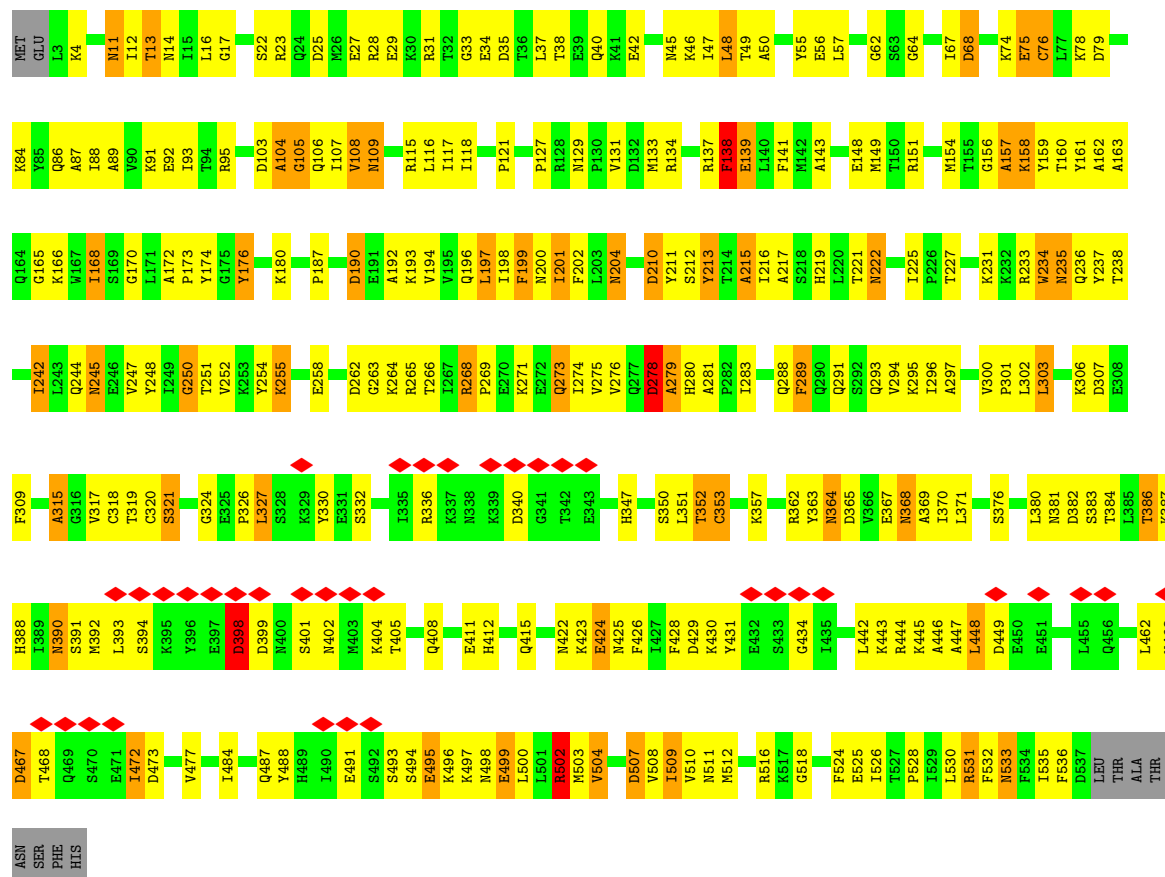


• Molecule 1: Resolvase homolog Yoka





- Molecule 1: Resolvase homolog YokA

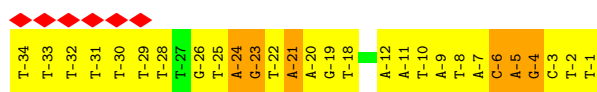


- Molecule 2: DNA (34-MER)

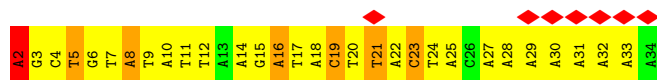
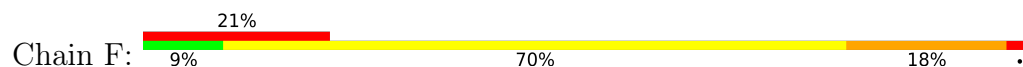


- Molecule 2: DNA (34-MER)

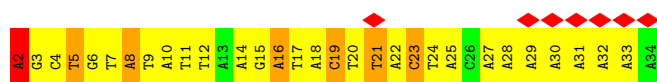
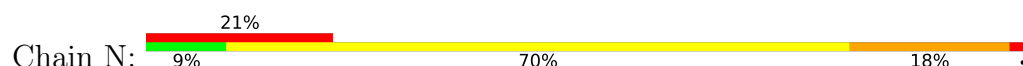




- Molecule 3: DNA (33-MER)



- Molecule 3: DNA (33-MER)



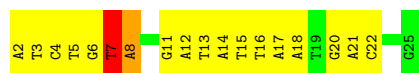
- Molecule 4: DNA (25-MER)



- Molecule 4: DNA (25-MER)



- Molecule 5: DNA (24-MER)



- Molecule 5: DNA (24-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44115	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	65	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.642	Depositor
Minimum map value	-0.001	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.01	Depositor
Map size (\AA)	463.27502, 482.44504, 412.15503	wwPDB
Map dimensions	435, 453, 387	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.065, 1.065, 1.065	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	2.39	88/4423 (2.0%)	2.44	376/5942 (6.3%)
1	C	2.39	80/4423 (1.8%)	2.43	364/5942 (6.1%)
1	I	2.42	91/4423 (2.1%)	2.45	386/5942 (6.5%)
1	K	2.43	83/4423 (1.9%)	2.47	383/5942 (6.4%)
2	E	1.40	7/774 (0.9%)	1.45	2/1193 (0.2%)
2	M	1.43	7/774 (0.9%)	1.46	2/1193 (0.2%)
3	F	1.49	5/764 (0.7%)	1.50	5/1176 (0.4%)
3	N	1.45	5/764 (0.7%)	1.47	6/1176 (0.5%)
4	G	1.75	9/572 (1.6%)	1.83	5/880 (0.6%)
4	O	1.76	10/572 (1.7%)	1.83	4/880 (0.5%)
5	H	1.70	9/552 (1.6%)	1.75	3/850 (0.4%)
5	P	1.70	10/552 (1.8%)	1.75	3/850 (0.4%)
All	All	2.24	404/23016 (1.8%)	2.26	1539/31966 (4.8%)

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	A	0	2
1	I	0	2
1	K	0	1
2	E	0	1
2	M	0	1
3	F	0	1
3	N	0	1
4	G	0	2
4	O	0	2
5	H	0	1
5	P	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	15

The worst 5 of 404 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	412	HIS	CE1-NE2	-8.98	1.23	1.32
1	A	412	HIS	CE1-NE2	-8.94	1.23	1.32
1	I	489	HIS	ND1-CE1	-8.88	1.23	1.32
1	K	412	HIS	CE1-NE2	-8.87	1.23	1.32
1	I	489	HIS	CE1-NE2	-8.86	1.23	1.32

The worst 5 of 1539 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	231	LYS	CA-C-N	9.10	133.01	120.63
1	I	231	LYS	C-N-CA	9.10	133.01	120.63
1	C	199	PHE	CA-CB-CG	8.66	122.46	113.80
1	K	199	PHE	CA-CB-CG	8.61	122.41	113.80
1	A	167	TRP	CA-C-N	8.55	132.22	123.16

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	137	ARG	Sidechain
1	A	248	TYR	Sidechain
2	E	-1	DT	Sidechain
3	F	2	DA	Sidechain
4	G	-12	DT	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	4356	4425	4420	96	0
1	C	4356	4425	4420	70	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	4356	4425	4420	103	0
1	K	4356	4425	4420	74	0
2	E	694	393	361	35	0
2	M	694	393	360	36	0
3	F	679	373	339	36	0
3	N	679	373	340	32	0
4	G	511	285	247	16	0
4	O	511	285	247	16	0
5	H	493	274	242	9	0
5	P	493	274	242	6	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
6	I	1	0	0	0	0
6	K	1	0	0	0	0
All	All	22182	20350	20058	470	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 11.

The worst 5 of 470 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:404:LYS:O	1:C:405:THR:OG1	1.98	0.82
1:K:404:LYS:O	1:K:405:THR:OG1	1.98	0.81
1:I:403:MET:HE2	1:I:403:MET:O	1.82	0.80
4:O:-25:DC:N3	4:O:-24:DA:N6	2.30	0.80
4:G:-25:DC:N3	4:G:-24:DA:N6	2.30	0.79

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	533/545 (98%)	494 (93%)	39 (7%)	0	100	100
1	C	533/545 (98%)	495 (93%)	38 (7%)	0	100	100
1	I	533/545 (98%)	493 (92%)	40 (8%)	0	100	100
1	K	533/545 (98%)	498 (93%)	35 (7%)	0	100	100
All	All	2132/2180 (98%)	1980 (93%)	152 (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	490/499 (98%)	465 (95%)	25 (5%)	21	43
1	C	490/499 (98%)	469 (96%)	21 (4%)	26	48
1	I	490/499 (98%)	465 (95%)	25 (5%)	21	43
1	K	490/499 (98%)	470 (96%)	20 (4%)	27	49
All	All	1960/1996 (98%)	1869 (95%)	91 (5%)	25	46

5 of 91 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	154	MET
1	K	11	ASN
1	I	262	ASP
1	I	425	ASN
1	K	75	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	408	GLN
1	K	293	GLN
1	I	204	ASN

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Mol	Chain	Res	Type
1	K	109	ASN
1	I	109	ASN

5.3.3 RNA [i](#)

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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

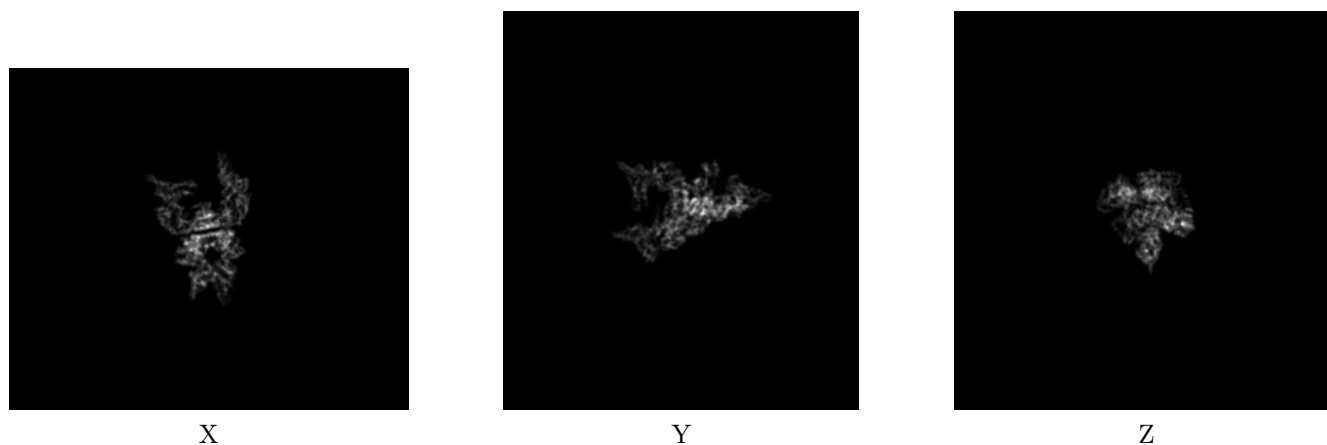
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47288. 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](#)

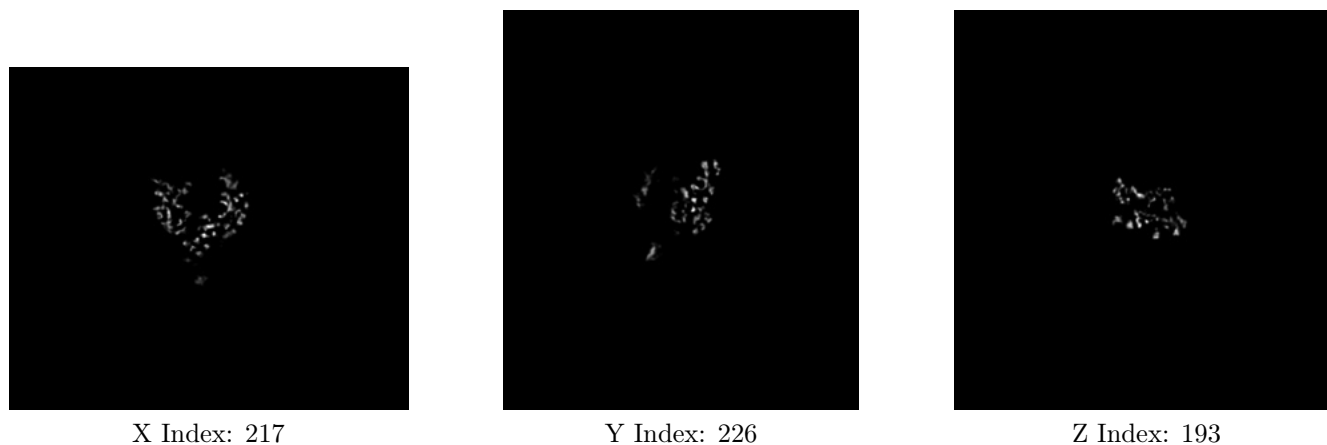
6.1.1 Primary map



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

6.2 Central slices [i](#)

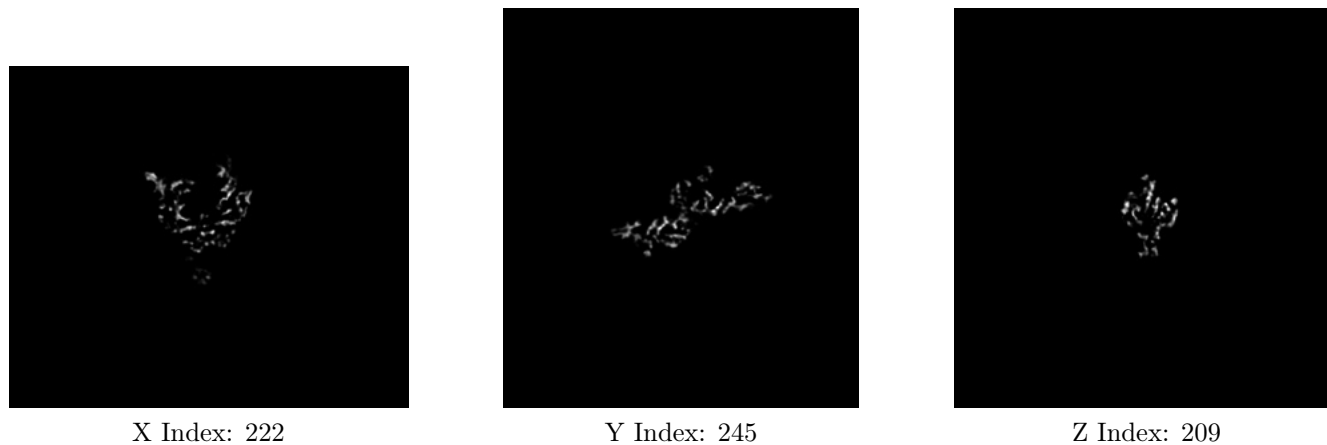
6.2.1 Primary map



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

6.3 Largest variance slices [i](#)

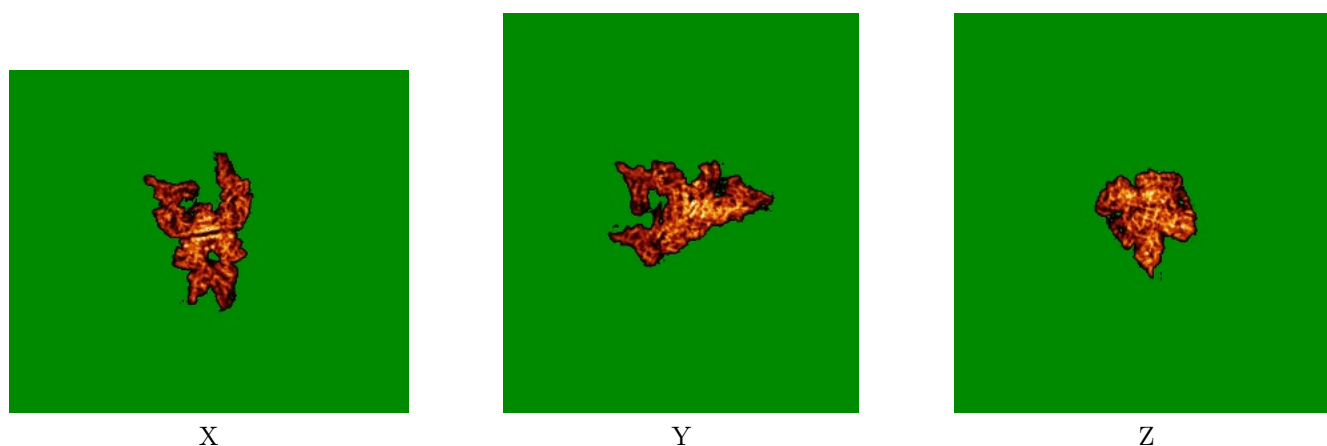
6.3.1 Primary map



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

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

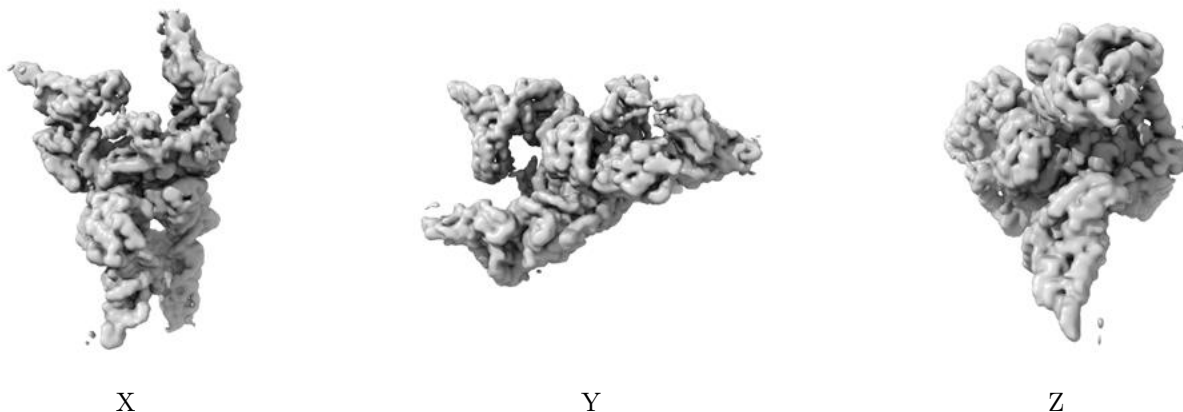
6.4.1 Primary map



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

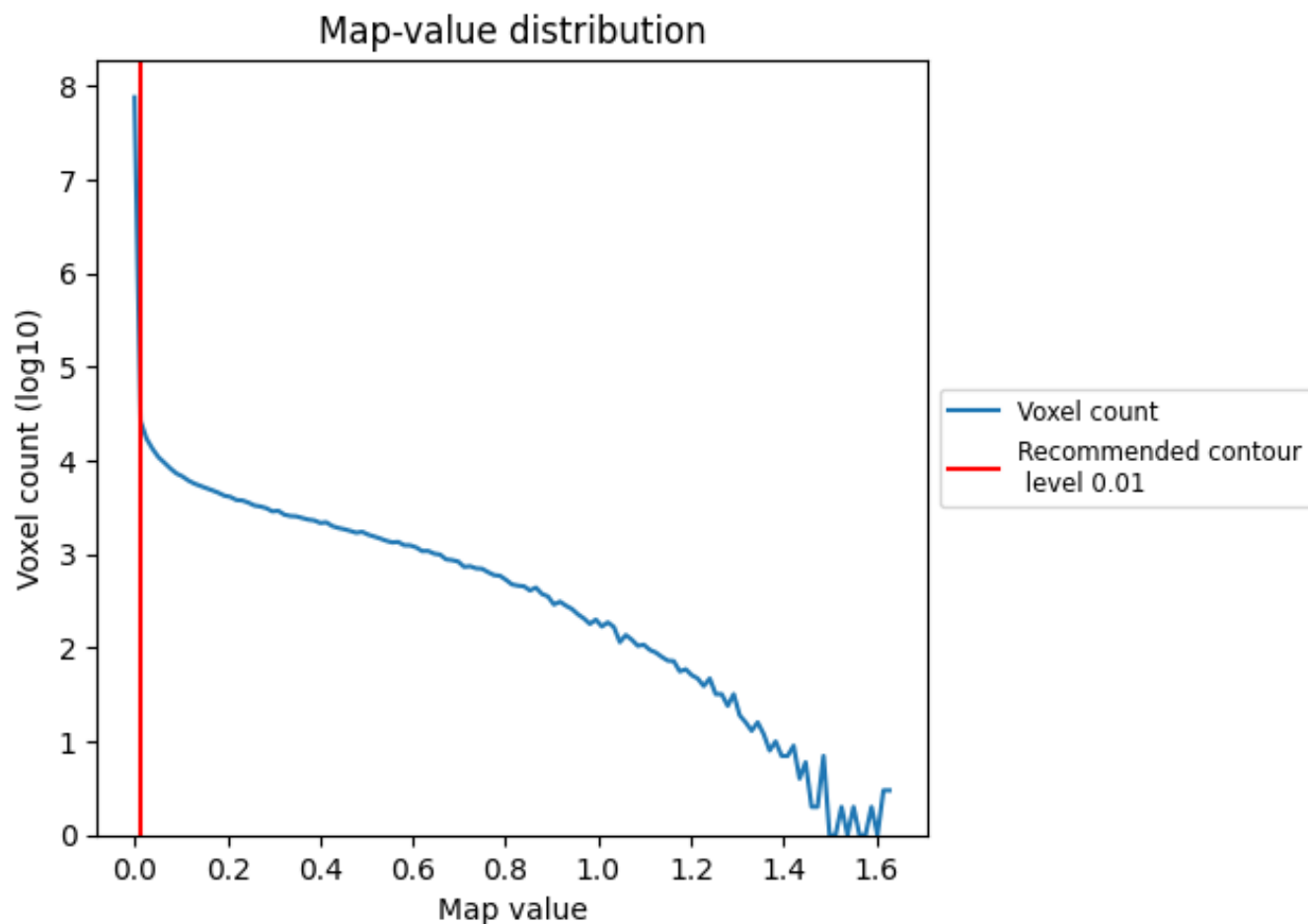
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

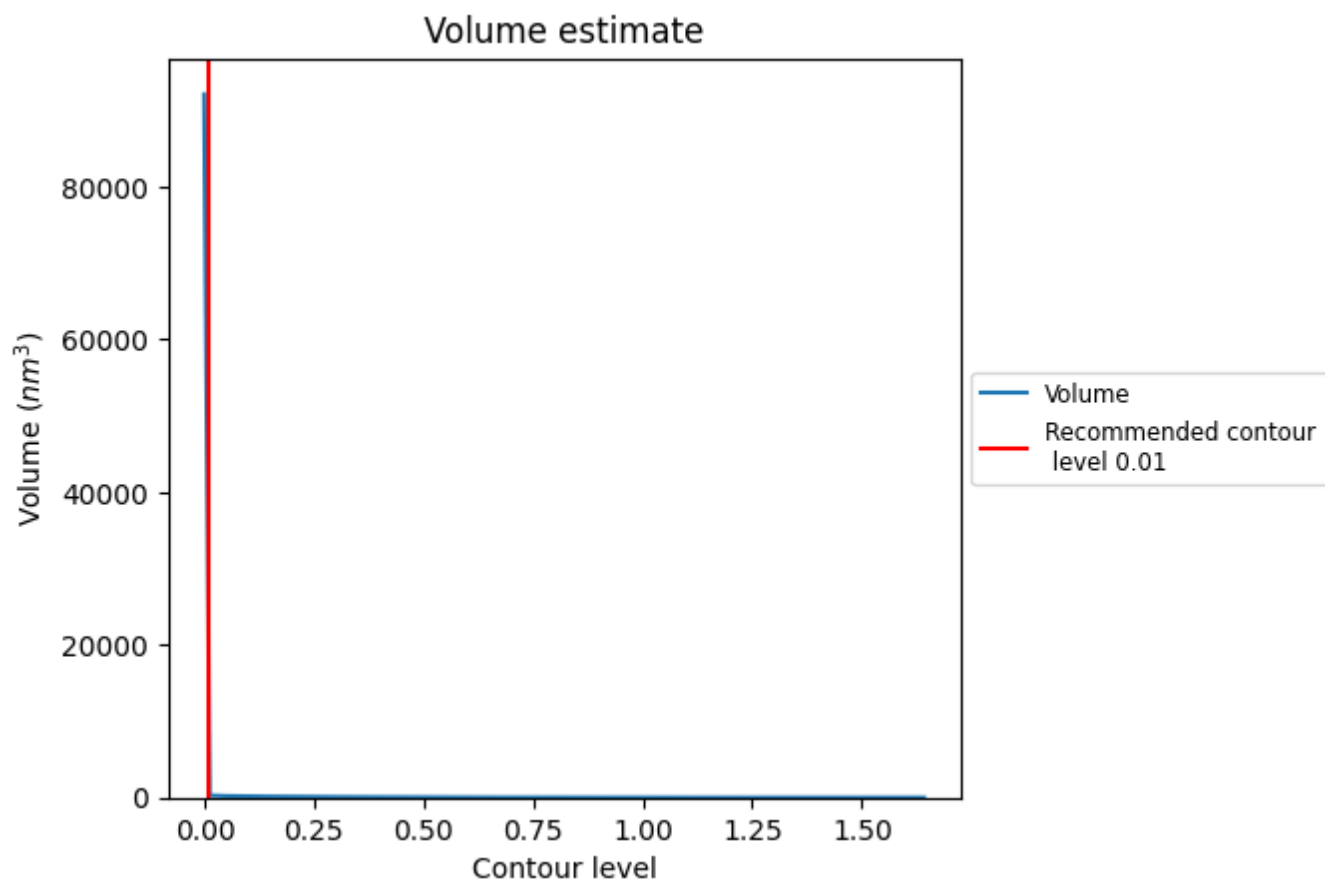
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 15136 nm³; this corresponds to an approximate mass of 13673 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 [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation

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

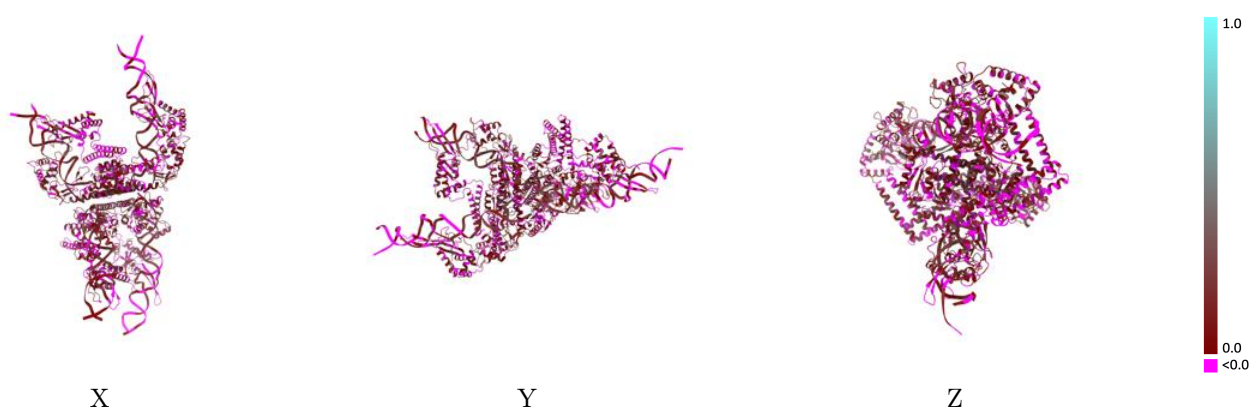
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-47288 and PDB model 9DXH. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

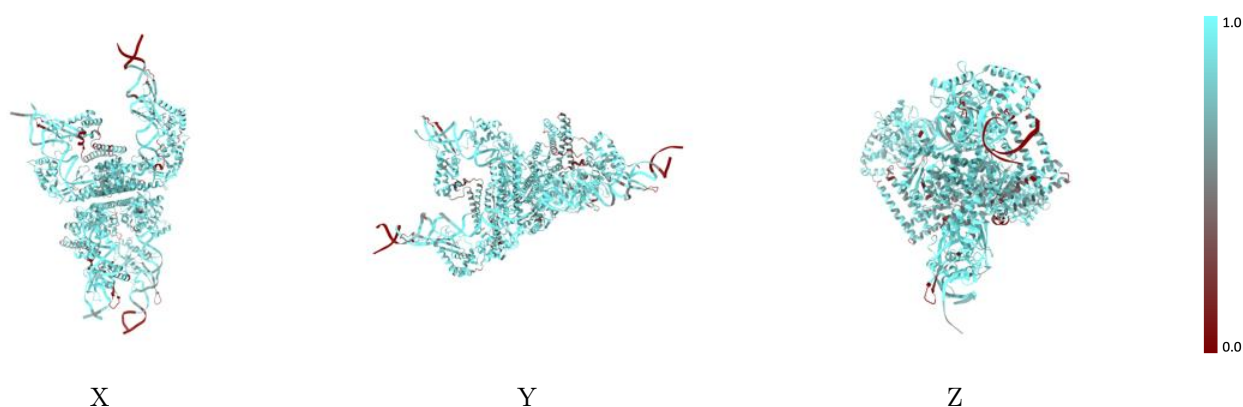
This section was not generated.

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



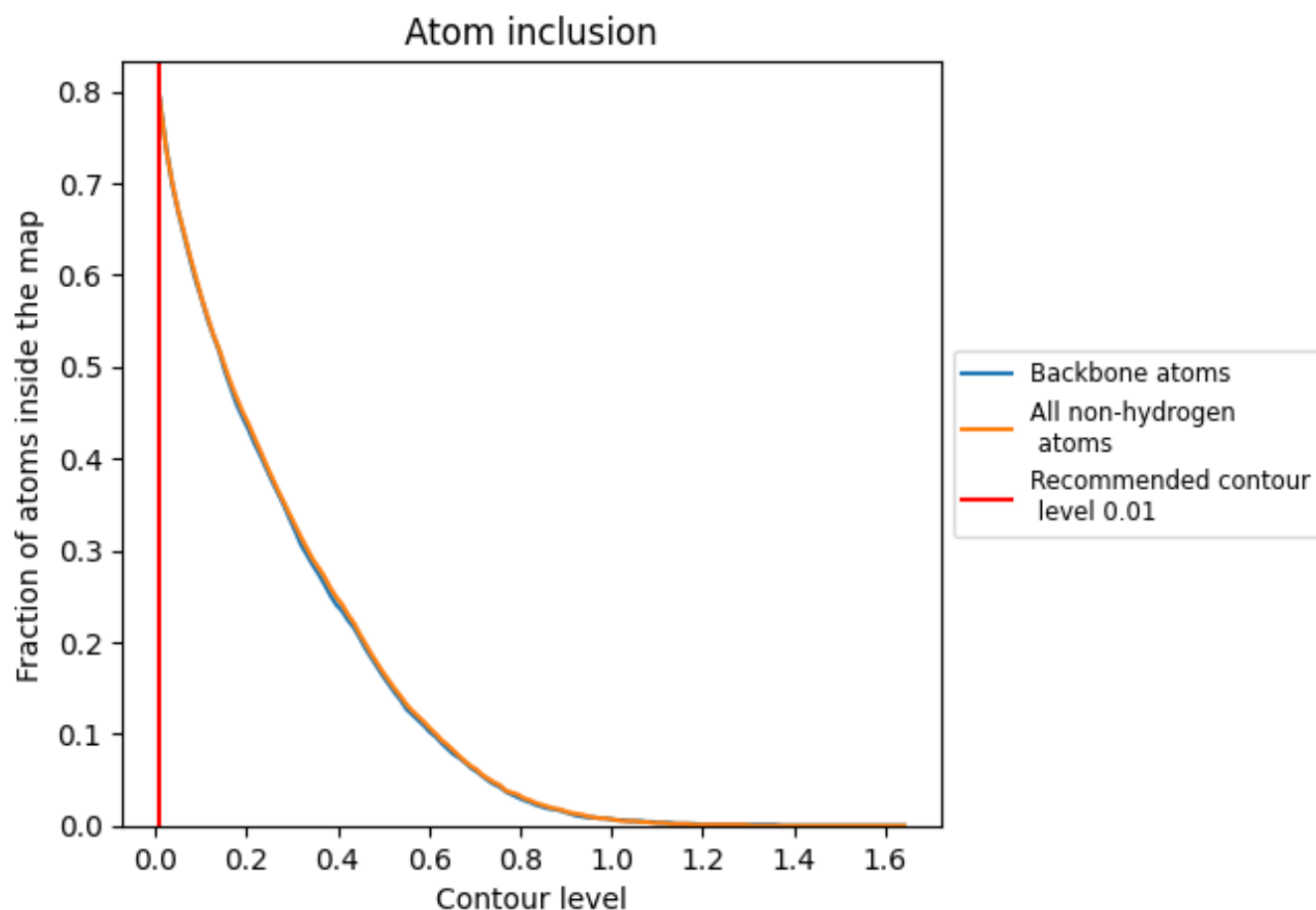
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7920	<div></div> 0.0860
A	<div></div> 0.7970	<div></div> 0.0720
C	<div></div> 0.7820	<div></div> 0.0710
E	<div></div> 0.7390	<div></div> 0.1040
F	<div></div> 0.7050	<div></div> 0.1110
G	<div></div> 0.9280	<div></div> 0.1660
H	<div></div> 0.8970	<div></div> 0.1690
I	<div></div> 0.8260	<div></div> 0.0770
K	<div></div> 0.8050	<div></div> 0.0760
M	<div></div> 0.7520	<div></div> 0.0960
N	<div></div> 0.7160	<div></div> 0.1130
O	<div></div> 0.9370	<div></div> 0.1730
P	<div></div> 0.9210	<div></div> 0.1720

1.0

0.0

<0.0