



wwPDB EM Validation Summary Report ⓘ

Jul 3, 2025 – 04:37 PM EDT

PDB ID : 9CDF / pdb_00009cdf
EMDB ID : EMD-45474
Title : Structure of MORC2 PD mutant binding to AMP-PNP
Authors : Tan, W.; Shakeel, S.
Deposited on : 2024-06-24
Resolution : 2.39 Å(reported)
Based on initial model : 5OF9

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.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
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) : 2.44

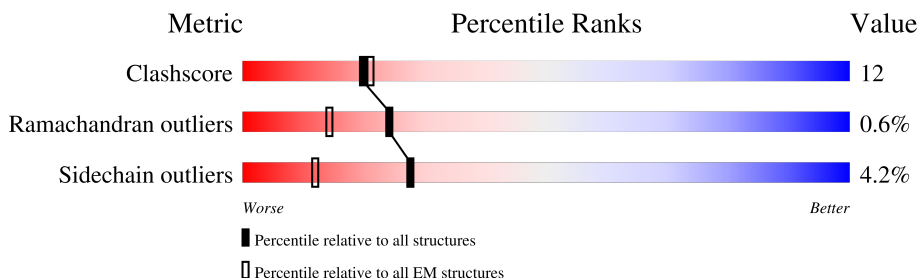
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.39 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	1032	<div> <div>8%</div> <div>34%</div> <div>14%</div> <div>•</div> <div>51%</div> </div>
1	B	1032	<div> <div>8%</div> <div>35%</div> <div>13%</div> <div>•</div> <div>51%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16433 atoms, of which 8156 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 ATPase MORC2.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	508	Total	C	H	N	O	S	1	0
			8211	2606	4085	728	766	26		
1	B	504	Total	C	H	N	O	S	0	0
			8131	2584	4046	719	755	27		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	725	ALA	SER	engineered mutation	UNP Q9Y6X9
A	730	ALA	SER	engineered mutation	UNP Q9Y6X9
A	739	ALA	SER	engineered mutation	UNP Q9Y6X9
A	743	ALA	SER	engineered mutation	UNP Q9Y6X9
A	777	ALA	SER	engineered mutation	UNP Q9Y6X9
A	779	ALA	SER	engineered mutation	UNP Q9Y6X9
B	725	ALA	SER	engineered mutation	UNP Q9Y6X9
B	730	ALA	SER	engineered mutation	UNP Q9Y6X9
B	739	ALA	SER	engineered mutation	UNP Q9Y6X9
B	743	ALA	SER	engineered mutation	UNP Q9Y6X9
B	777	ALA	SER	engineered mutation	UNP Q9Y6X9
B	779	ALA	SER	engineered mutation	UNP Q9Y6X9

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	Zn	0
			1	1	
2	B	1	Total	Zn	0
			1	1	

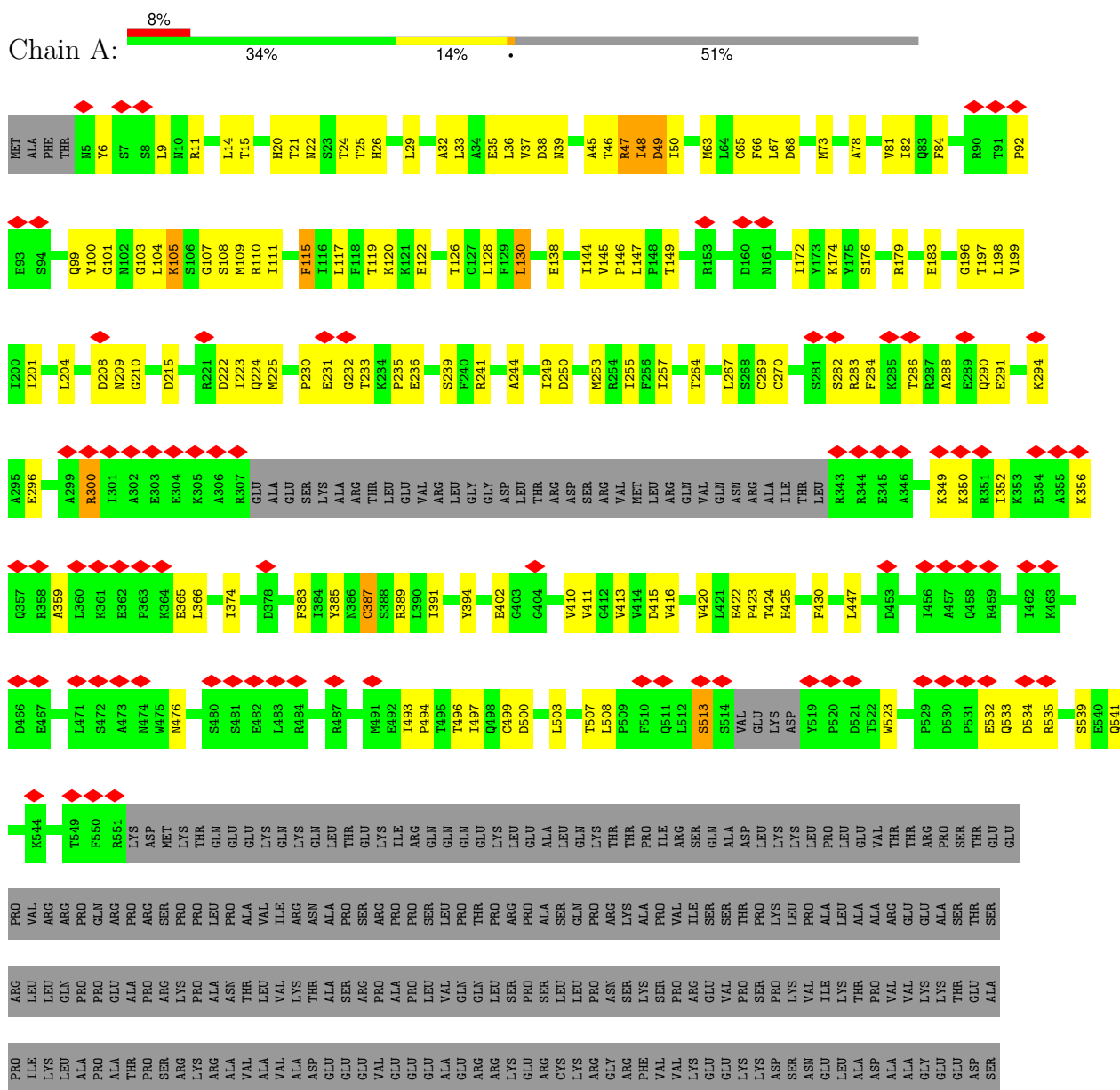
- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃) (labeled as "Ligand of Interest" by depositor).



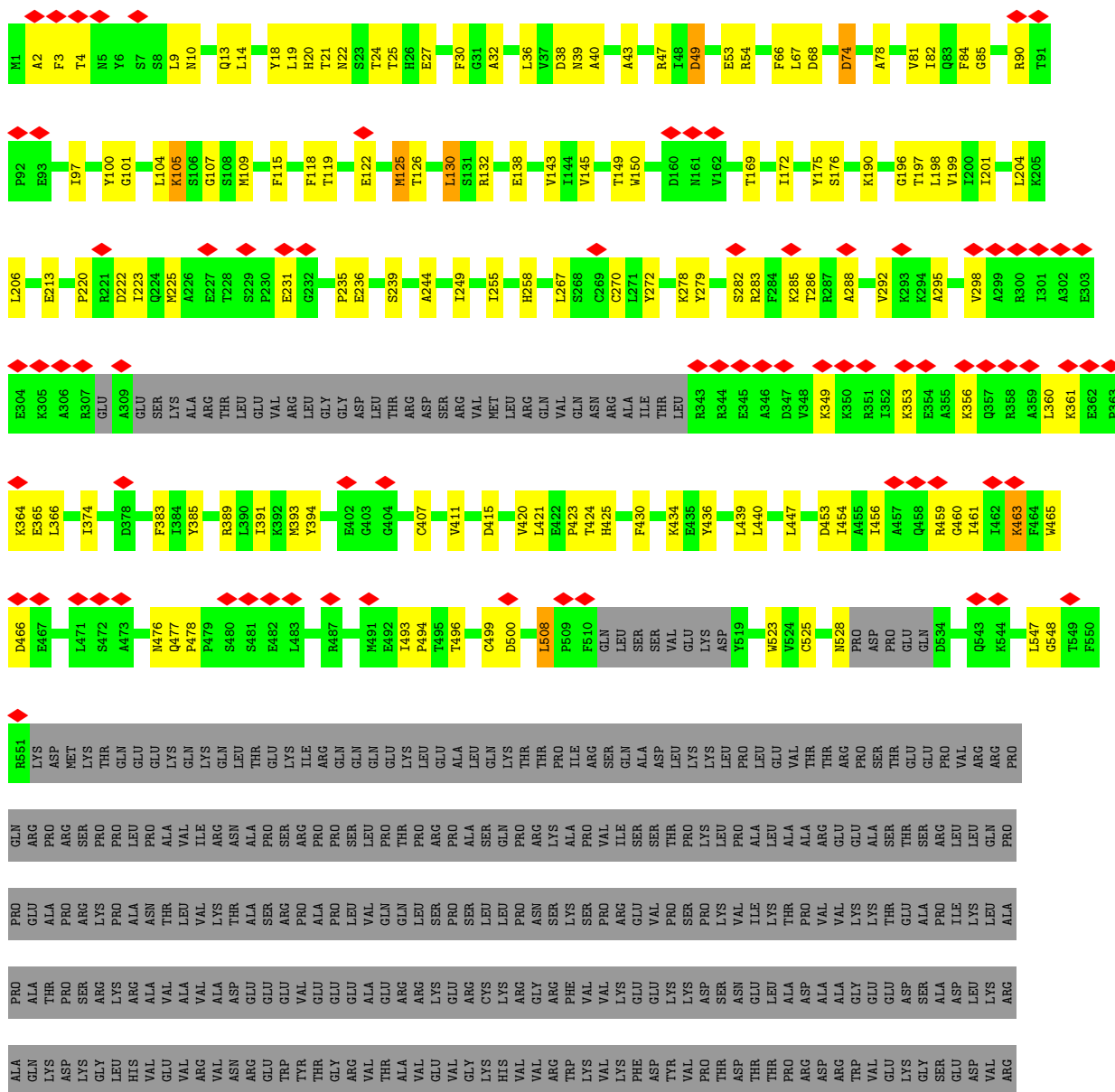
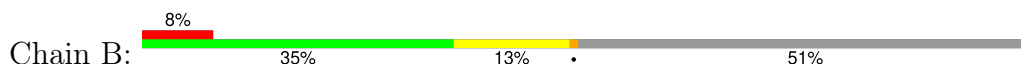
3 Residue-property plots

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: ATPase MORC2



- Molecule 1: ATPase MORC2



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

GLY

ASP

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	201271	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	1100	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.582	Depositor
Minimum map value	-1.103	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.111	Depositor
Map size (Å)	209.92, 209.92, 209.92	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	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: MG, ANP, 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	0.29	0/4217	0.61	0/5680
1	B	0.28	0/4170	0.59	2/5612 (0.0%)
All	All	0.29	0/8387	0.60	2/11292 (0.0%)

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	B	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	459	ARG	CA-C-N	9.34	139.72	121.41
1	B	459	ARG	C-N-CA	9.34	139.72	121.41

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	132	ARG	Sidechain

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	4126	4085	4086	109	0
1	B	4085	4046	4048	102	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	31	13	13	4	0
3	B	31	12	13	5	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
All	All	8277	8156	8160	200	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 12.

The worst 5 of 200 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:B:454:ILE:HD12	1:B:456:ILE:HD12	1.47	0.94
1:B:421:LEU:HD12	1:B:439:LEU:HD13	1.58	0.85
1:B:231:GLU:O	1:B:476:ASN:ND2	2.14	0.80
1:A:244:ALA:HB1	1:A:255:ILE:HD13	1.65	0.78
1:B:244:ALA:HB1	1:B:255:ILE:HD13	1.63	0.78

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	503/1032 (49%)	448 (89%)	52 (10%)	3 (1%)	22	33
1	B	495/1032 (48%)	456 (92%)	36 (7%)	3 (1%)	22	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	998/2064 (48%)	904 (91%)	88 (9%)	6 (1%)	24	33

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	231	GLU
1	B	3	PHE
1	A	282	SER
1	B	206	LEU
1	A	122	GLU

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	445/913 (49%)	427 (96%)	18 (4%)	27	45
1	B	438/913 (48%)	419 (96%)	19 (4%)	25	42
All	All	883/1826 (48%)	846 (96%)	37 (4%)	27	43

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	213	GLU
1	B	466	ASP
1	B	349	LYS
1	B	365	GLU
1	A	300	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	99	GLN
1	B	263	GLN
1	B	438	HIS

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Mol	Chain	Res	Type
1	A	376	HIS
1	A	83	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, 4 are monoatomic - leaving 2 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	$\# Z > 2$
3	ANP	A	1102	4	29,33,33	2.39	6 (20%)	31,52,52	2.01	7 (22%)
3	ANP	B	1102	4	29,33,33	2.45	7 (24%)	31,52,52	1.69	4 (12%)

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	ANP	A	1102	4	-	3/14/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ANP	B	1102	4	-	4/14/38/38	0/3/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1102	ANP	PB-O3A	8.68	1.69	1.59
3	B	1102	ANP	PB-O3A	8.68	1.69	1.59
3	B	1102	ANP	PG-N3B	6.09	1.79	1.63
3	A	1102	ANP	PG-N3B	5.92	1.78	1.63
3	B	1102	ANP	PG-O1G	4.43	1.52	1.46

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1102	ANP	O1G-PG-N3B	-5.83	103.19	111.77
3	A	1102	ANP	O2B-PB-O1B	5.37	121.39	109.87
3	B	1102	ANP	O2B-PB-O1B	5.12	120.86	109.87
3	B	1102	ANP	O1G-PG-N3B	-4.99	104.42	111.77
3	A	1102	ANP	C4'-O4'-C1'	3.32	112.97	109.92

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1102	ANP	PB-N3B-PG-O1G
3	A	1102	ANP	PA-O3A-PB-O2B
3	B	1102	ANP	PB-N3B-PG-O1G
3	B	1102	ANP	PA-O3A-PB-O2B
3	B	1102	ANP	PB-O3A-PA-O5'

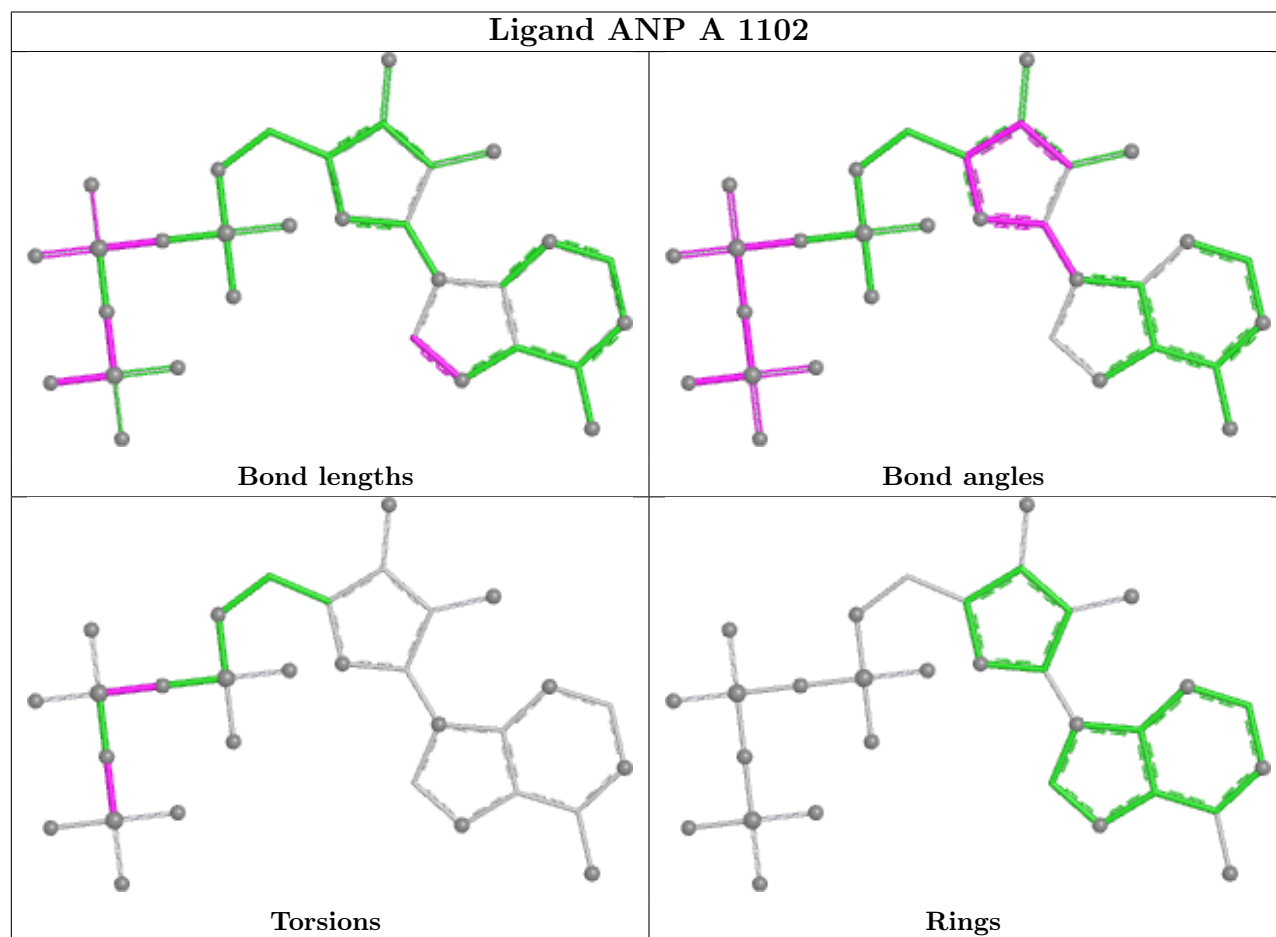
There are no ring outliers.

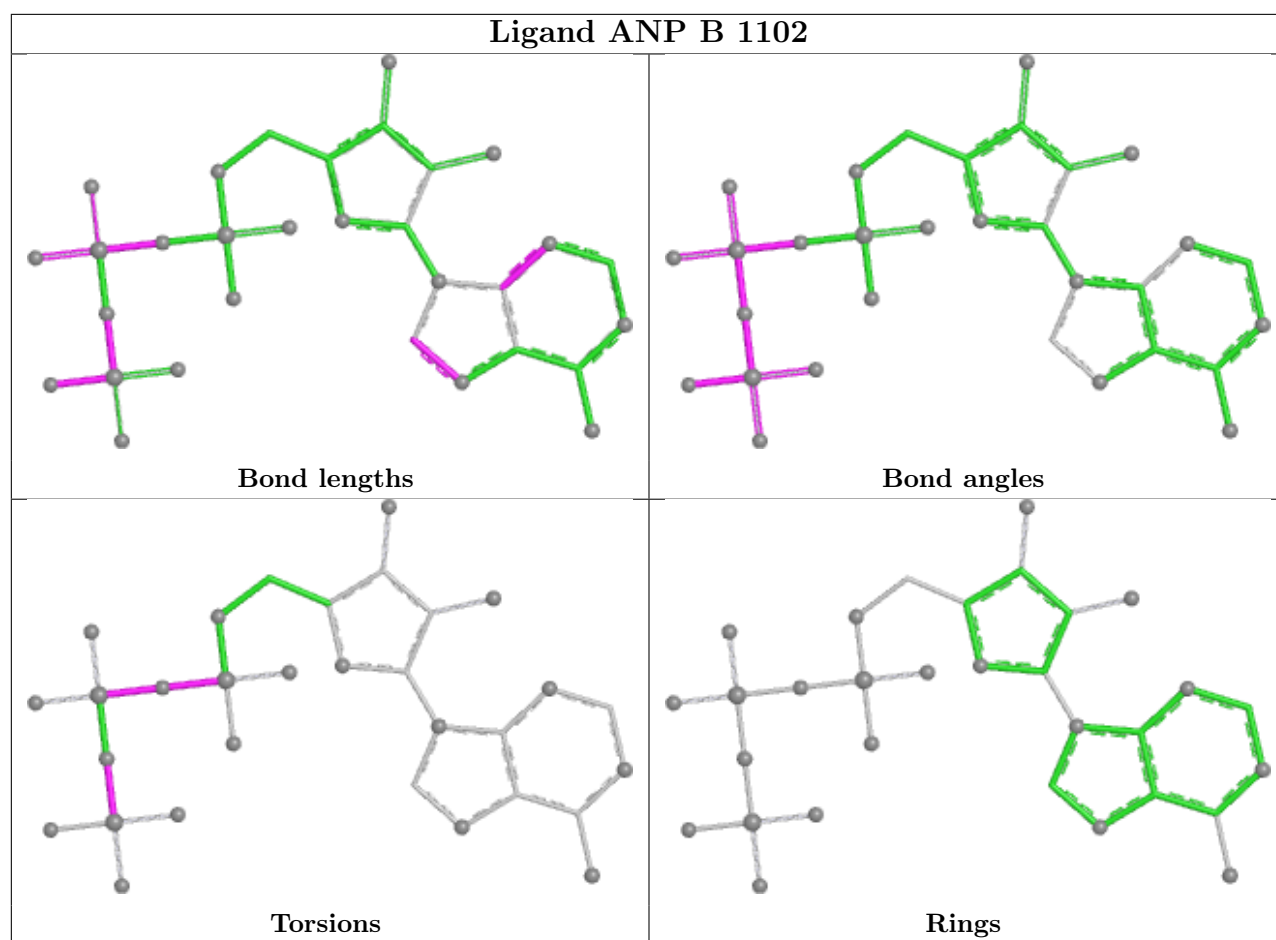
2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1102	ANP	4	0
3	B	1102	ANP	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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.

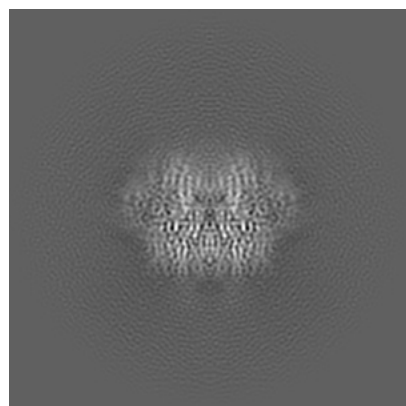
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45474. These allow visual inspection of the internal detail of the map and identification of artifacts.

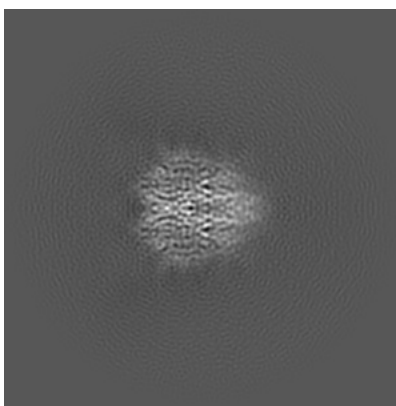
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

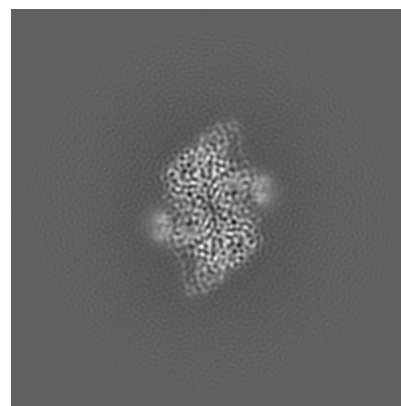
6.1.1 Primary map



X

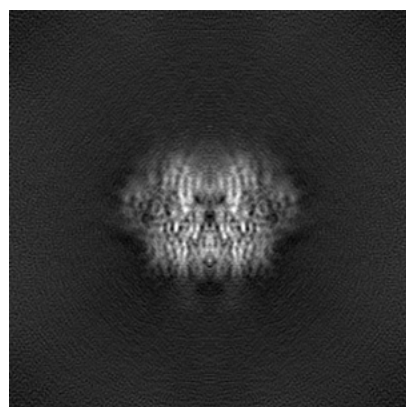


Y

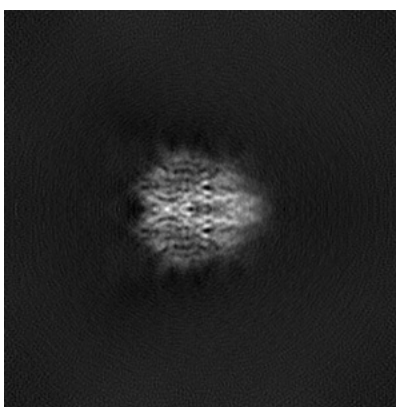


Z

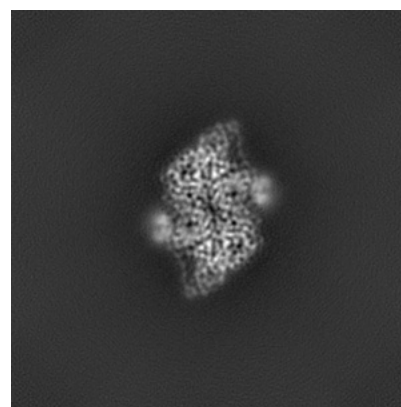
6.1.2 Raw map



X



Y

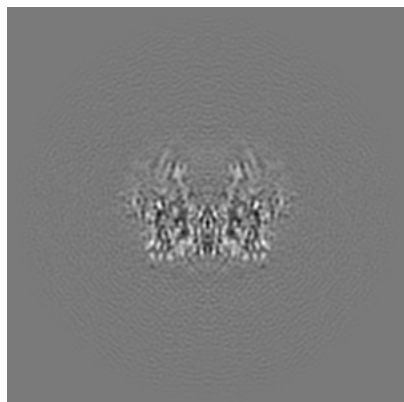


Z

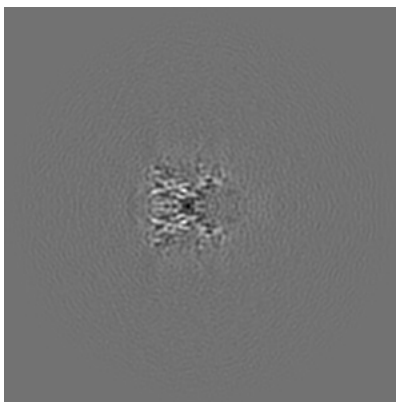
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

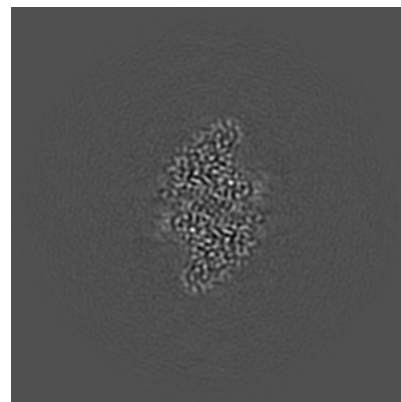
6.2.1 Primary map



X Index: 128

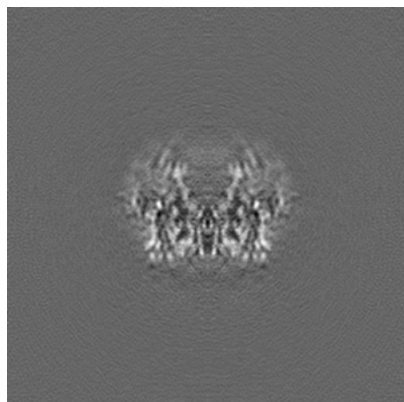


Y Index: 128

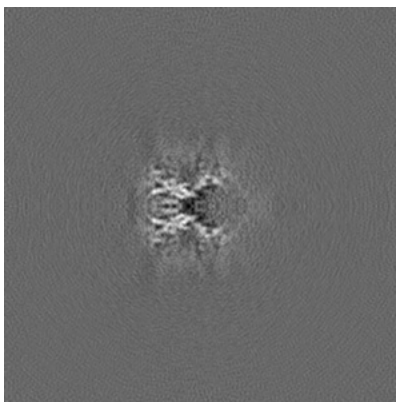


Z Index: 128

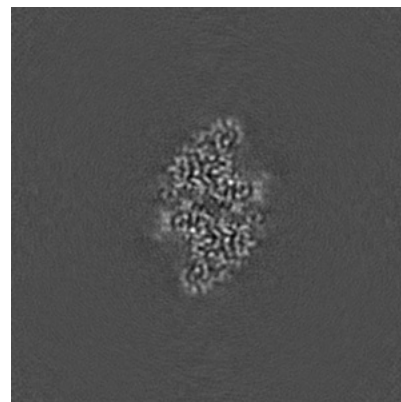
6.2.2 Raw map



X Index: 128



Y Index: 128

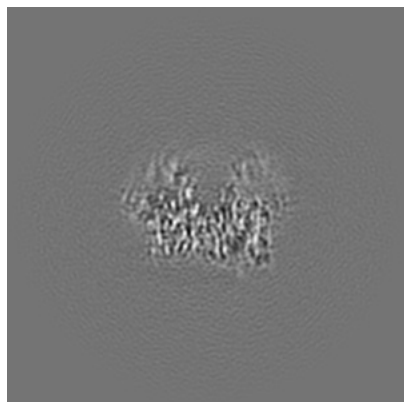


Z Index: 128

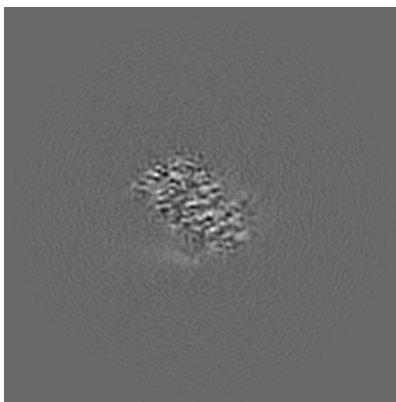
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

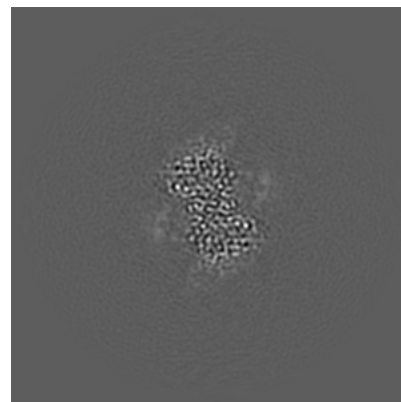
6.3.1 Primary map



X Index: 125

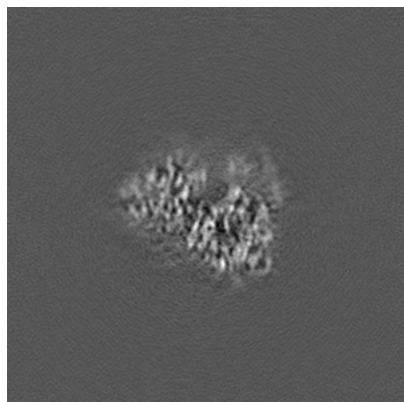


Y Index: 111

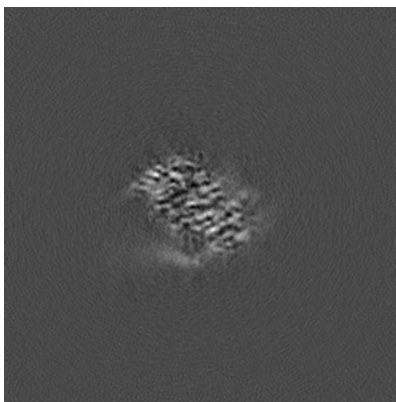


Z Index: 115

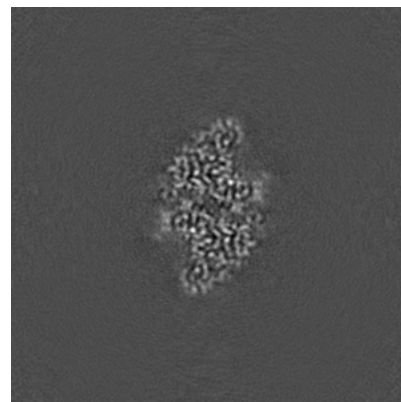
6.3.2 Raw map



X Index: 120



Y Index: 111

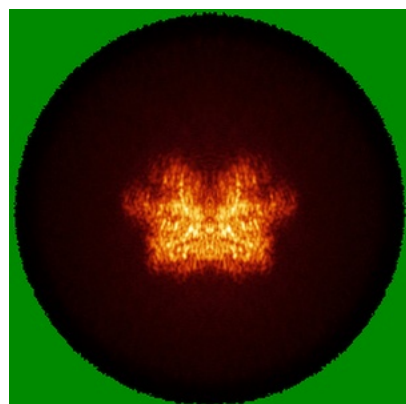


Z Index: 128

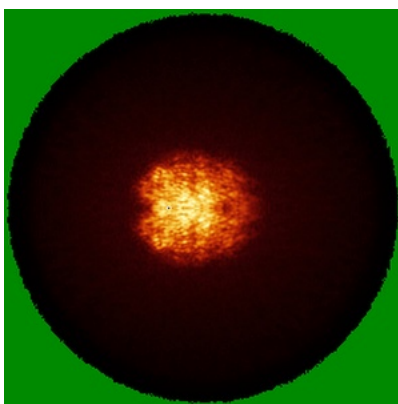
The images above show the largest variance slices of the map in three orthogonal directions.

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

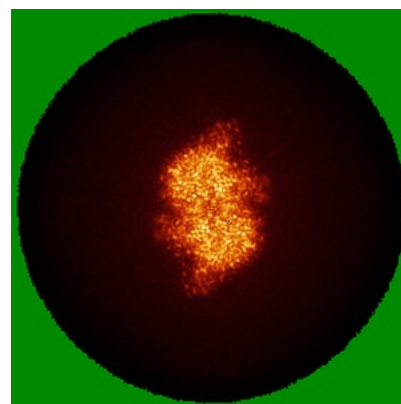
6.4.1 Primary map



X

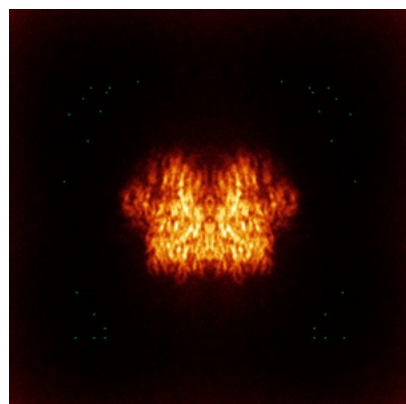


Y

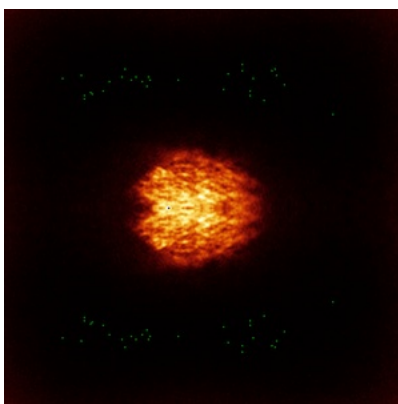


Z

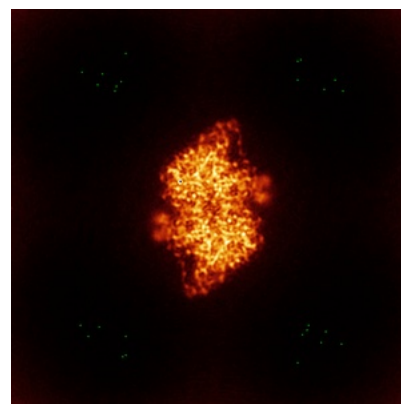
6.4.2 Raw map



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.

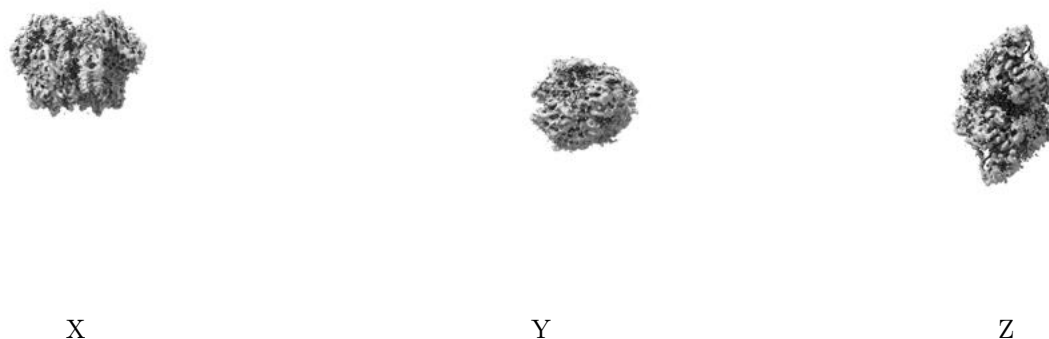
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.111. 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.

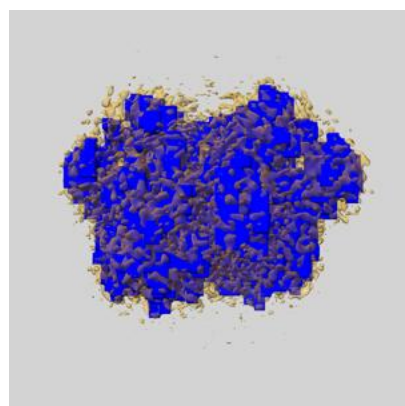
6.6 Mask visualisation [i](#)

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

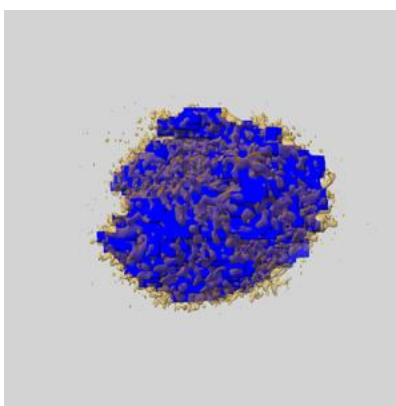
A mask typically either:

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

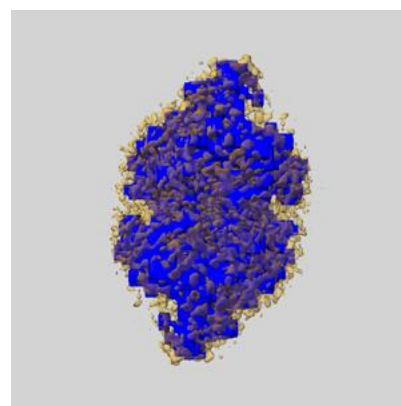
6.6.1 emd_45474_msk_1.map [i](#)



X



Y

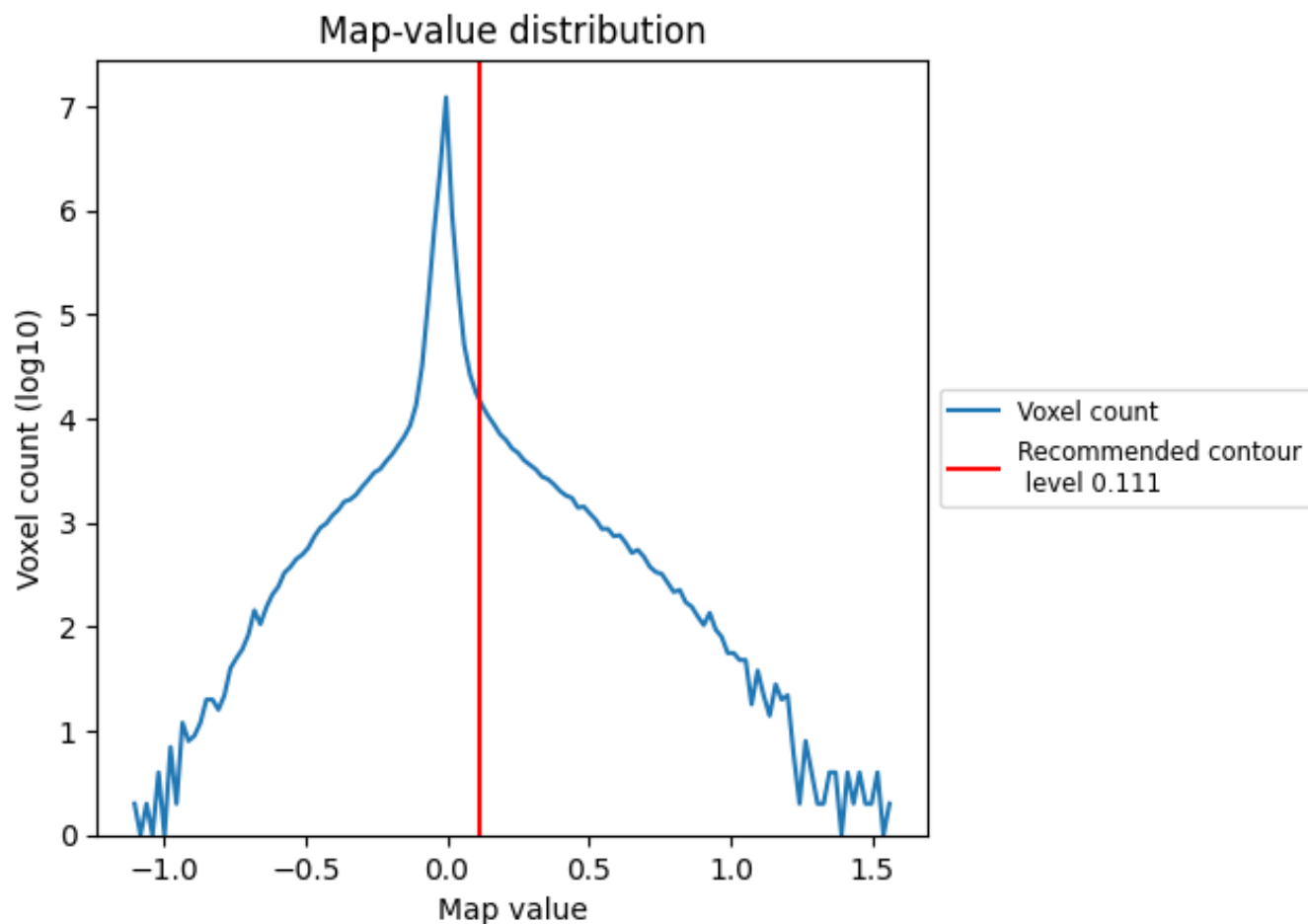


Z

7 Map analysis [i](#)

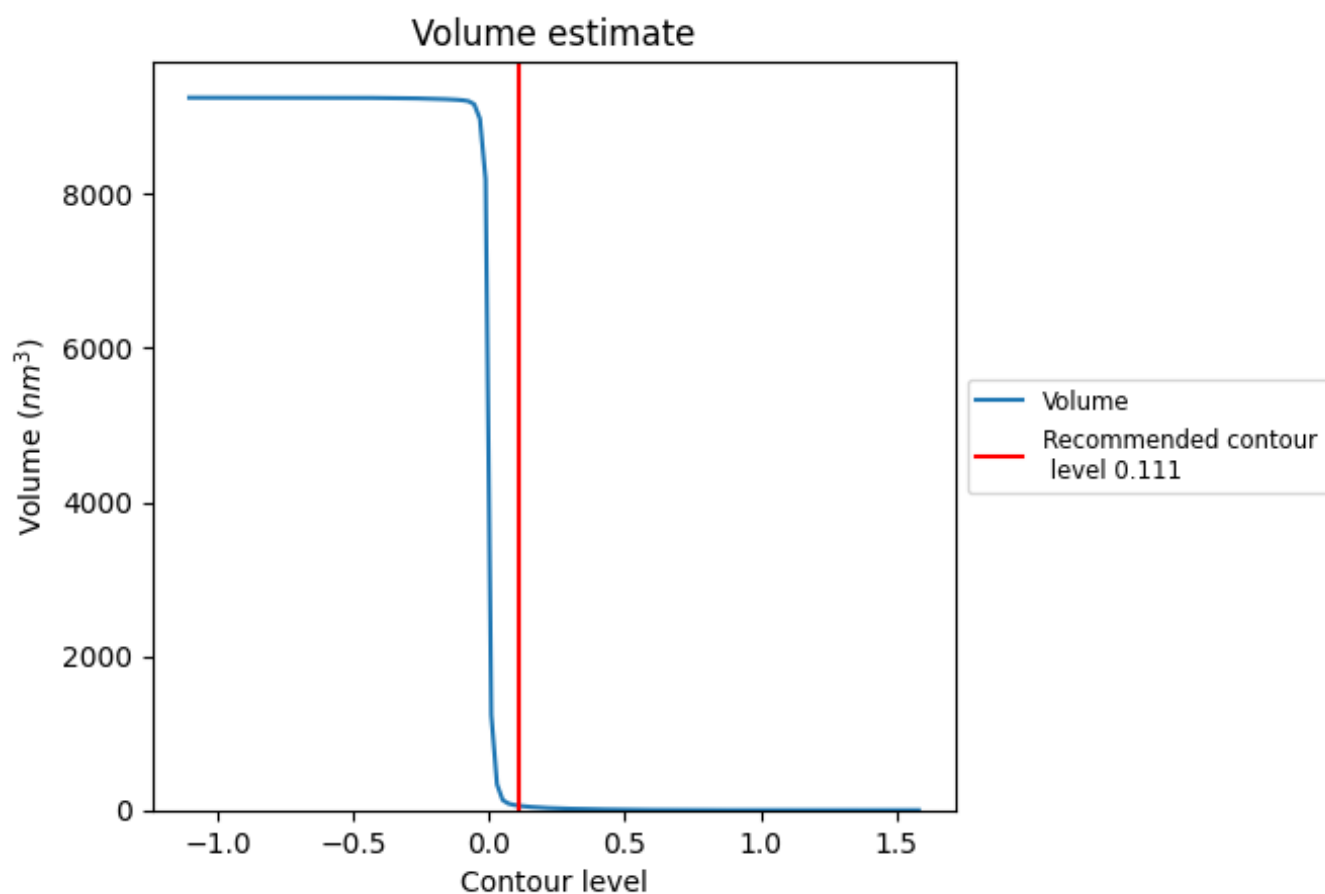
This section contains the results of statistical analysis of the map.

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.

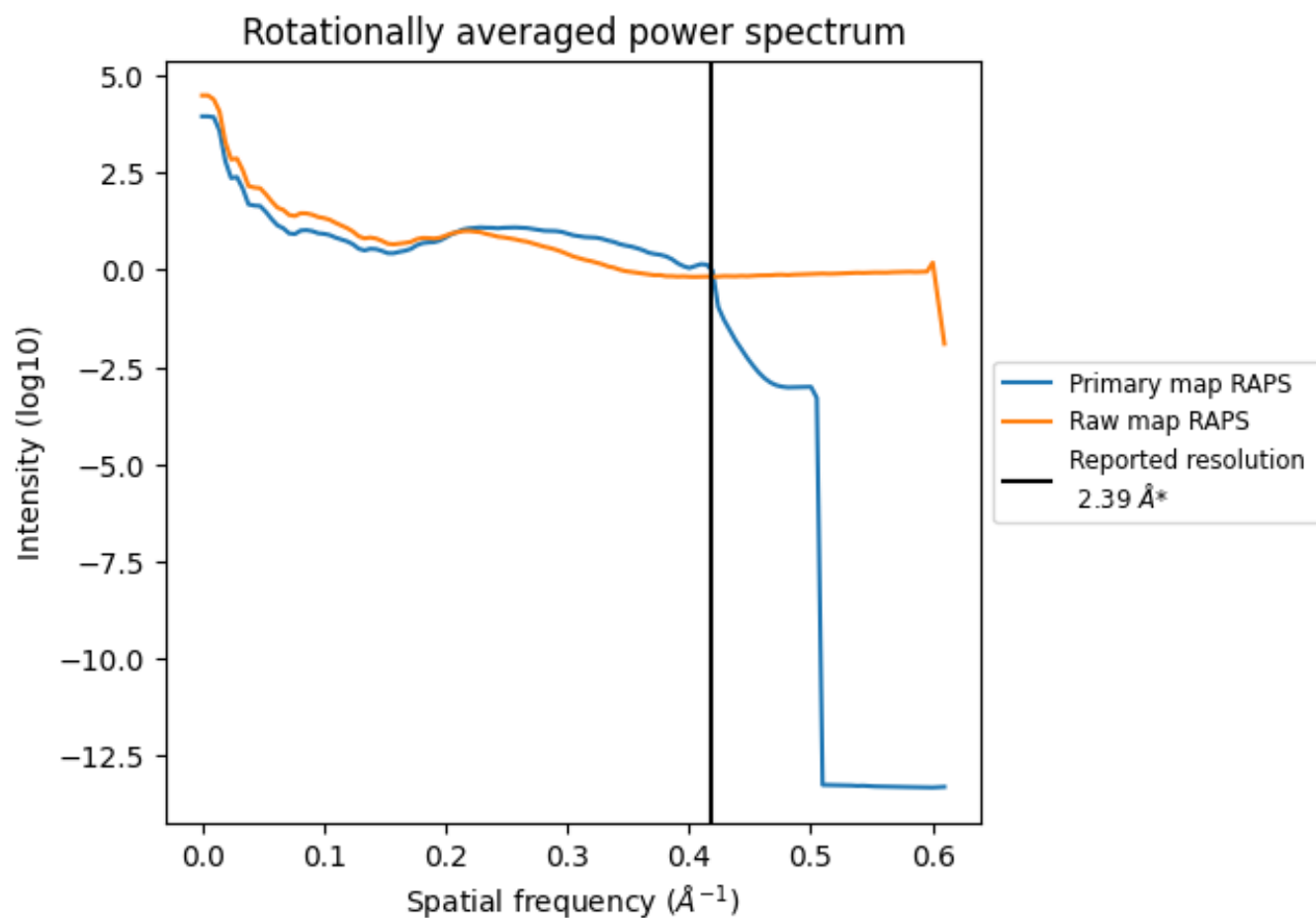
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 57 nm³; this corresponds to an approximate mass of 52 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 ⓘ

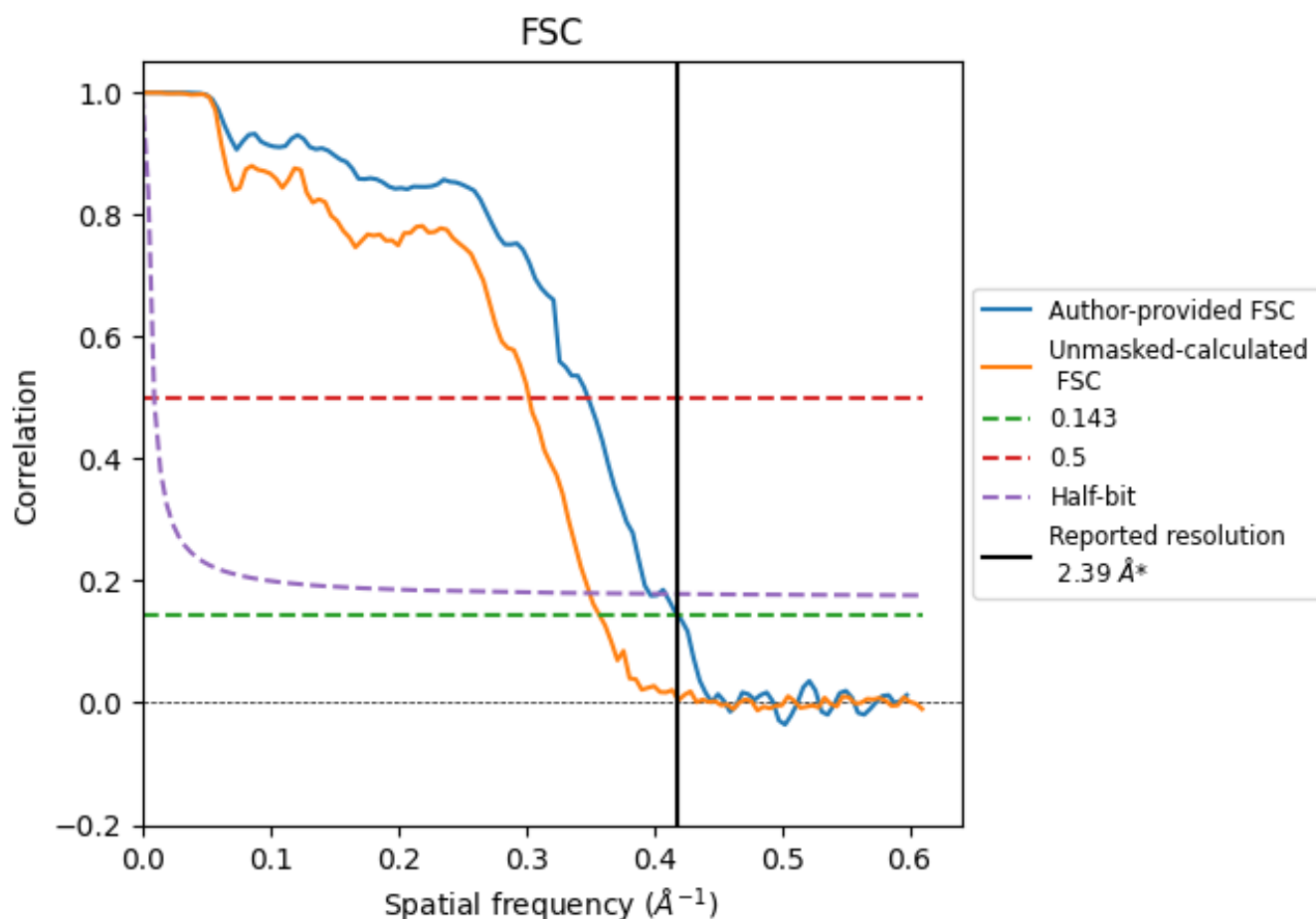


*Reported resolution corresponds to spatial frequency of 0.418 \AA^{-1}

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 0.418 \AA^{-1}

8.2 Resolution estimates [i](#)

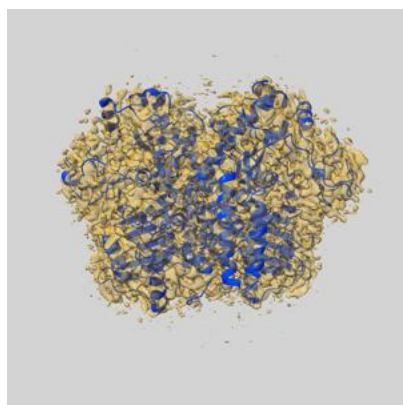
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.39	-	-
Author-provided FSC curve	2.39	2.87	2.52
Unmasked-calculated*	2.80	3.31	2.86

*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 2.80 differs from the reported value 2.39 by more than 10 %

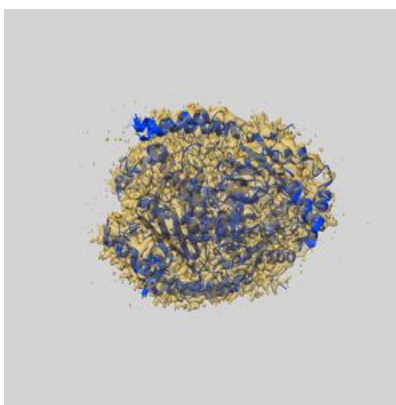
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-45474 and PDB model 9CDF. Per-residue inclusion information can be found in section [3](#) on page [5](#).

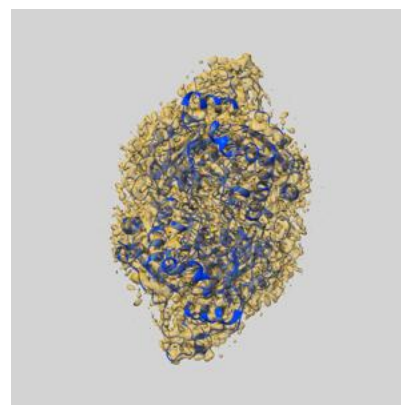
9.1 Map-model overlay [i](#)



X



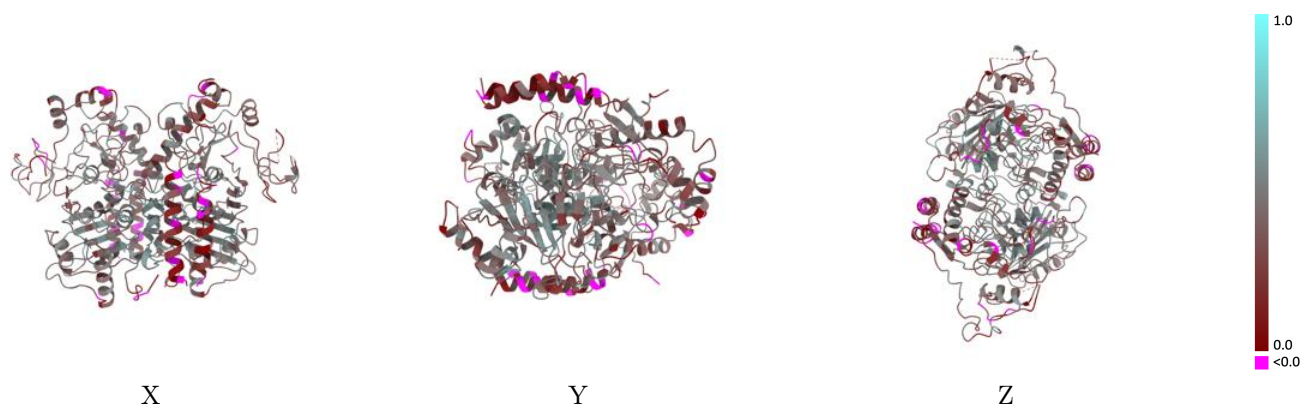
Y



Z

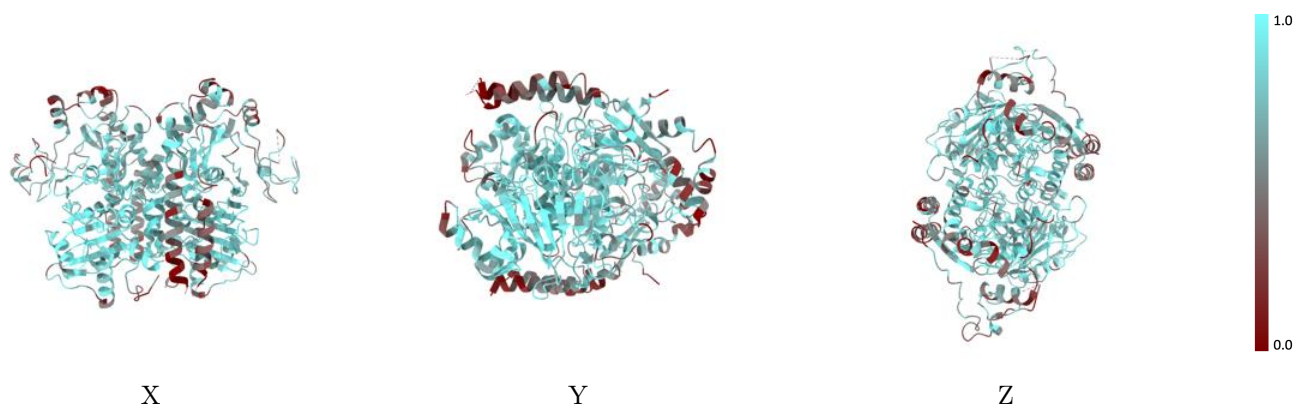
The images above show the 3D surface view of the map at the recommended contour level 0.111 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



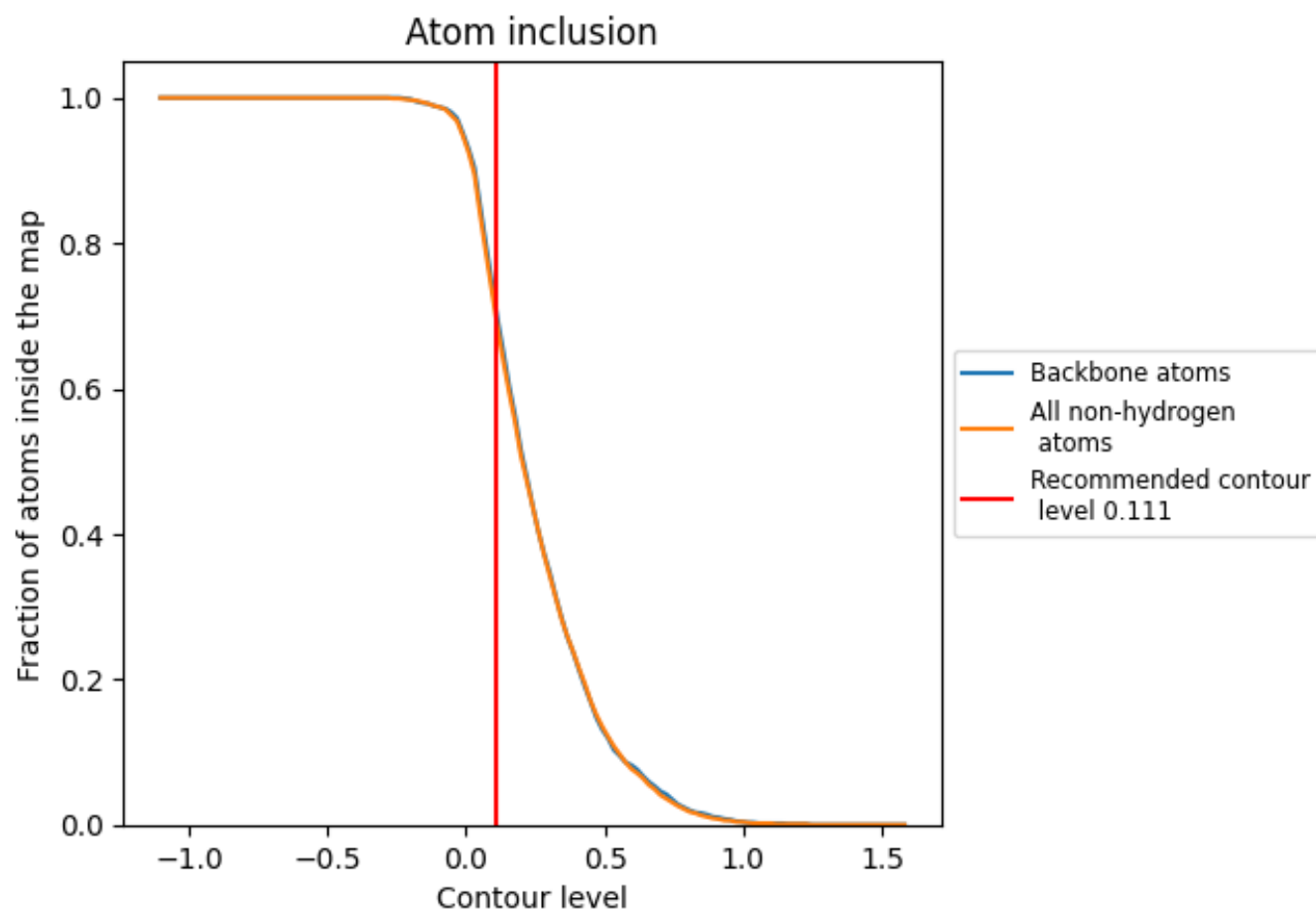
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.111).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 69% 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 (0.111) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6890	<div></div> 0.3600
A	<div></div> 0.6950	<div></div> 0.3580
B	<div></div> 0.6950	<div></div> 0.3610

