



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:19 PM UTC

PDB ID : 6OR5 / pdb_00006or5
EMDB ID : EMD-9032
Title : Full-length S. pombe Mdn1 in the presence of AMPPNP (ring region)
Authors : Chen, Z.; Suzuki, H.; Wang, A.C.; DiMaio, F.; Walz, T.; Kapoor, T.M.
Deposited on : 2019-04-29
Resolution : 4.00 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

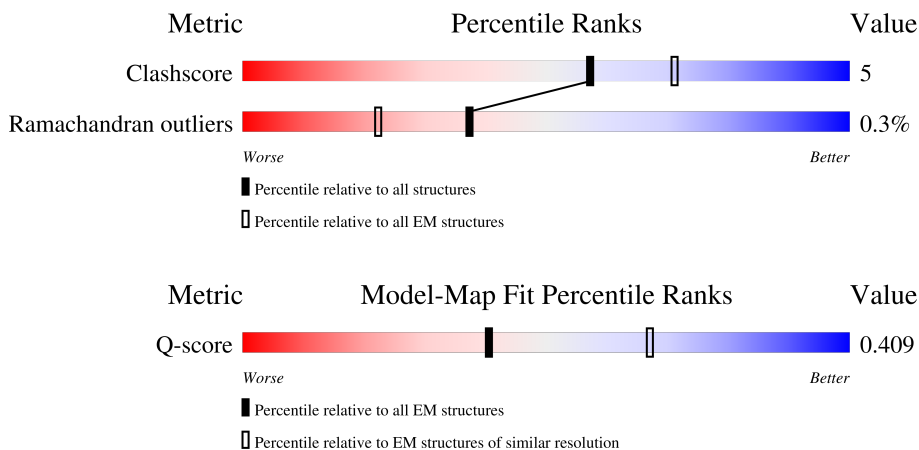
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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	-
Q-score	-	25397	7587 (3.50 - 4.50)

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	4717	

2 Entry composition [i](#)

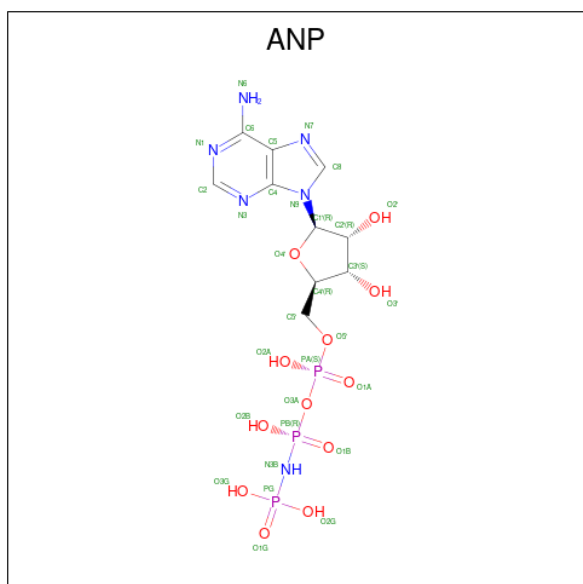
There are 2 unique types of molecules in this entry. The entry contains 10364 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Midasin.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	2058	10209	6093	2058	2058	0	0

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).

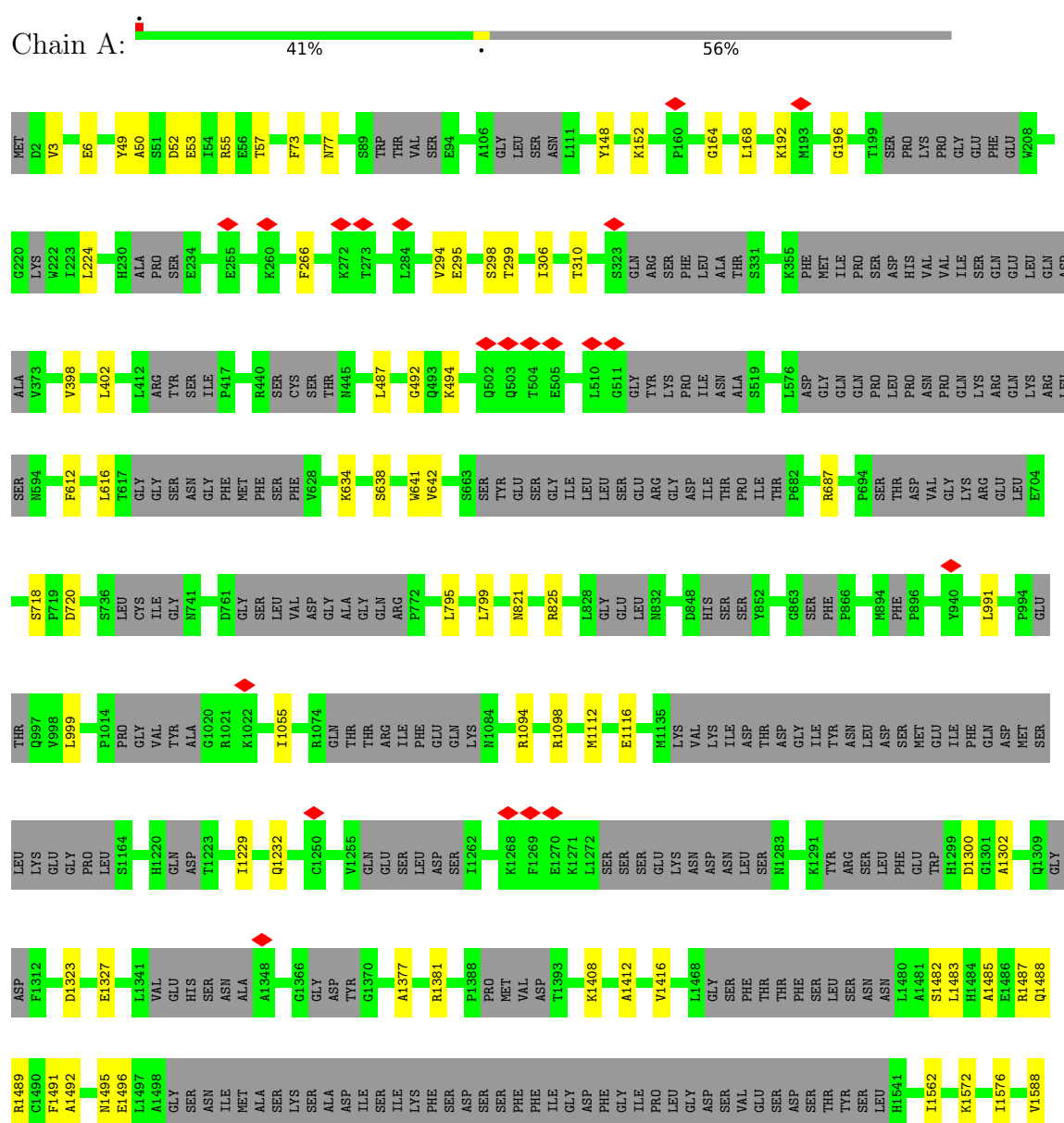


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
2	A	1	31	10	6	12	3	0
2	A	1	31	10	6	12	3	0
2	A	1	31	10	6	12	3	0
2	A	1	31	10	6	12	3	0
2	A	1	31	10	6	12	3	0

3 Residue-property plots [i](#)

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: Midasin







	Glu	Phe	Ser	Glu
	Glu	Gly	Gln	Gly
	Lys	Gln	Ser	Thr
	Pro	Ser	Gly	Ala
	Met	Asn	Ser	Thr
	Ile	Thr	Val	Lys
	Val	Asn	Leu	Met
	Phe	Val	Leu	Gln
	Val	Ala	Leu	Gly
	Ile	Ala	Leu	Gly
	Leu	Leu	Glu	Arg
	Leu	Ala	Thr	Phe
	Asp	Ala	Leu	Arg
	Asn	Asp	Leu	Thr
	Val	Ala	Ala	Thr
	Asn	Ser	Leu	Thr
	Thr	Met	Val	Lys
	Gln	Lys	Thr	Arg
	Lys	Cys	Lys	Leu
	Lys	Phe	Ala	Asn
	Ser	Asn	Leu	Met
	Ser	Tyr	Ser	Lys
	Ile	Ala	Leu	Arg
	Leu	Asn	Leu	Ile
	Asp	Thr	Glu	Ile
	Ile	Ala	Val	Pro
	Lys	Ser	Gly	Tyr
	Lys	His	Gln	Ile
	Val	His	Ile	Ala
	Tyr	Arg	Val	Ser
	Tyr	Ser	Val	Gln
	Asp	Asn	Met	Phe
	Thr	Ser	Lys	Lys
	Lys	Asp	Phe	Asp
	Glu	Ile	Gly	Asp
	Asp	Arg	Glu	Lys
	Gly	Gln	Gln	Ile
	Thr	Leu	Pro	Trp
	Met	Glu	Glu	Arg
	Asp	Ile	Leu	Arg
	Leu	Ile	Leu	Arg
	Lys	Ile	His	Val
	Ile	Ser	Pro	Lys
	Gln	Asp	Phe	Pro
	Pro	Gly	Asp	Ser
	Tyr	Ile	Lys	Lys
	Ile	Cys	Gln	Arg
	Asp	Glu	Phe	Thr
	Glu	Asp	Ser	Tyr
	Phe	His	Ser	Gln
	Ala	Asp	Glu	Val
	Phe	Ser	Ser	Met
	Asp	Ile	Gly	Ile
	Tyr	Arg	Val	Lys
	Lys	Lys	Gln	Ile
	Leu	Leu	Met	Asp
	Val	Leu	Phe	Asp
	Val	Arg	Ser	Lys
	Arg	Arg	His	Lys
	Ala	Gln	Phe	Ser
	Thr	Lys	Thr	Met

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	313336	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 ($e^-/\text{\AA}^2$)	88.8	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	22.052	Depositor
Minimum map value	-9.278	Depositor
Average map value	-0.030	Depositor
Map value standard deviation	0.761	Depositor
Recommended contour level	6	Depositor
Map size (Å)	390.0, 390.0, 390.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	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: ANP

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	0.38	0/10153	0.64	2/14076 (0.0%)

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	A	1055	ILE	N-CA-C	7.74	119.01	108.17
1	A	2786	VAL	N-CA-C	5.23	111.81	106.21

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	10209	0	4438	65	0
2	A	155	0	65	8	0
All	All	10364	0	4503	72	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 72 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:2059:VAL:O	1:A:2071:THR:HA	1.75	0.87
1:A:50:ALA:O	1:A:55:ARG:CB	2.26	0.83
1:A:1659:ALA:HA	1:A:1666:LYS:CB	2.10	0.82
1:A:2222:PHE:O	1:A:2226:TYR:CB	2.28	0.81
1:A:821:ASN:O	1:A:825:ARG:CB	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	1946/4717 (41%)	1604 (82%)	337 (17%)	5 (0%)	36	70

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2073	LYS
1	A	2232	LEU
1	A	1408	LYS
1	A	1672	PRO
1	A	2075	HIS

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

5 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
2	ANP	A	7203	-	33,33,33	2.18	7 (21%)	45,52,52	0.62	1 (2%)
2	ANP	A	7202	-	33,33,33	1.65	4 (12%)	45,52,52	0.65	0
2	ANP	A	7205	-	33,33,33	1.72	4 (12%)	45,52,52	1.09	5 (11%)
2	ANP	A	7201	-	33,33,33	2.14	6 (18%)	45,52,52	0.87	2 (4%)
2	ANP	A	7204	-	33,33,33	1.86	4 (12%)	45,52,52	0.65	1 (2%)

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
2	ANP	A	7203	-	-	4/18/38/38	0/3/3/3
2	ANP	A	7202	-	-	5/18/38/38	0/3/3/3
2	ANP	A	7205	-	-	7/18/38/38	0/3/3/3
2	ANP	A	7201	-	-	7/18/38/38	0/3/3/3
2	ANP	A	7204	-	-	4/18/38/38	0/3/3/3

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	7203	ANP	PG-O1G	8.19	1.58	1.46
2	A	7201	ANP	PG-O1G	8.06	1.58	1.46
2	A	7204	ANP	PG-O1G	7.89	1.58	1.46
2	A	7202	ANP	PG-O1G	7.83	1.58	1.46
2	A	7205	ANP	PG-O1G	7.66	1.57	1.46

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	7205	ANP	C4-N9-C1'	3.13	133.95	126.63
2	A	7205	ANP	O3A-PB-N3B	2.92	114.68	106.59
2	A	7205	ANP	C1'-N9-C8	-2.89	120.68	127.09
2	A	7201	ANP	O1B-PB-N3B	-2.86	107.55	111.77
2	A	7201	ANP	O1G-PG-N3B	-2.70	107.79	111.77

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	7201	ANP	PB-N3B-PG-O1G
2	A	7201	ANP	PG-N3B-PB-O1B
2	A	7201	ANP	C5'-O5'-PA-O1A
2	A	7201	ANP	C5'-O5'-PA-O2A
2	A	7201	ANP	C5'-O5'-PA-O3A

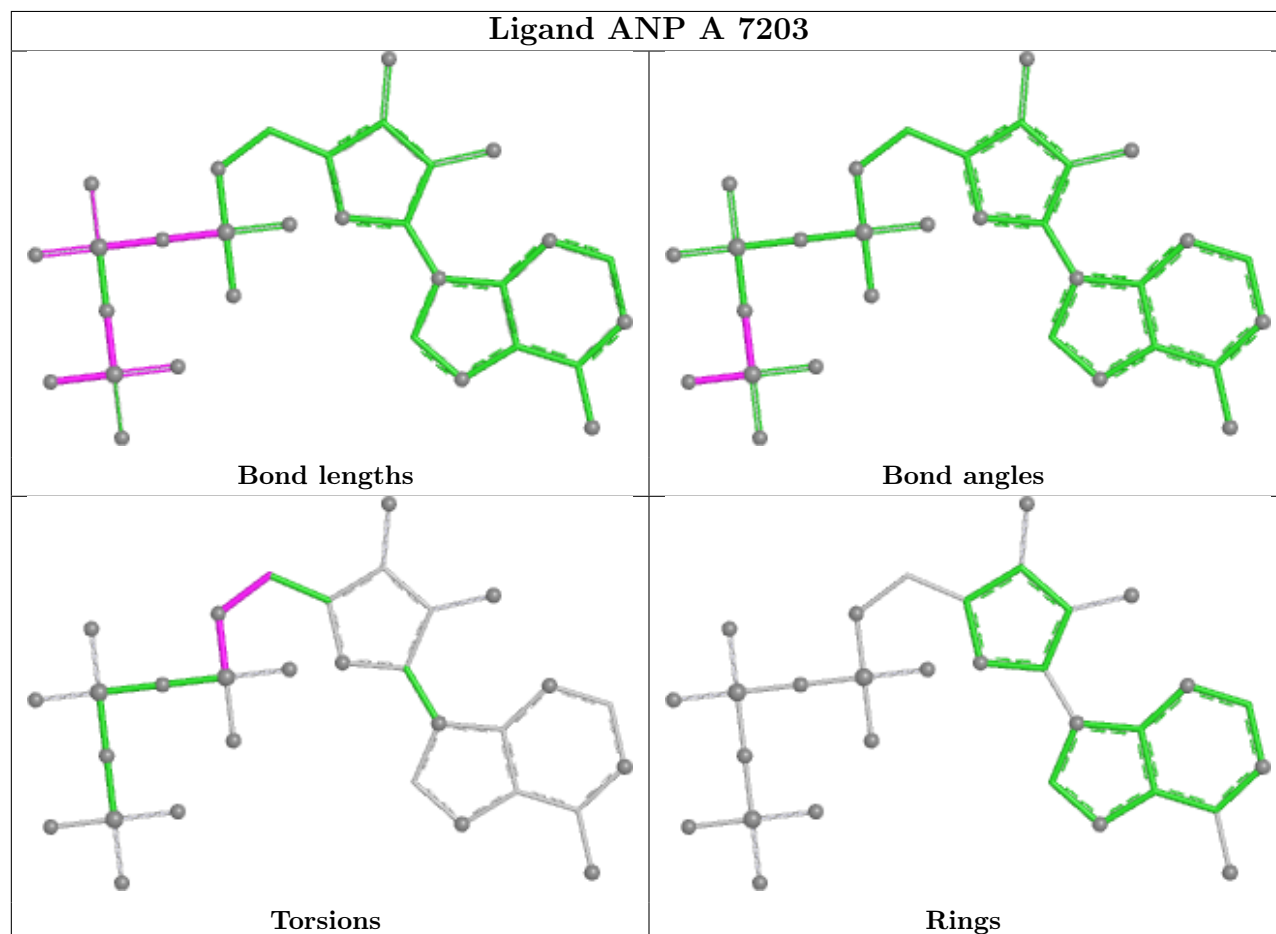
There are no ring outliers.

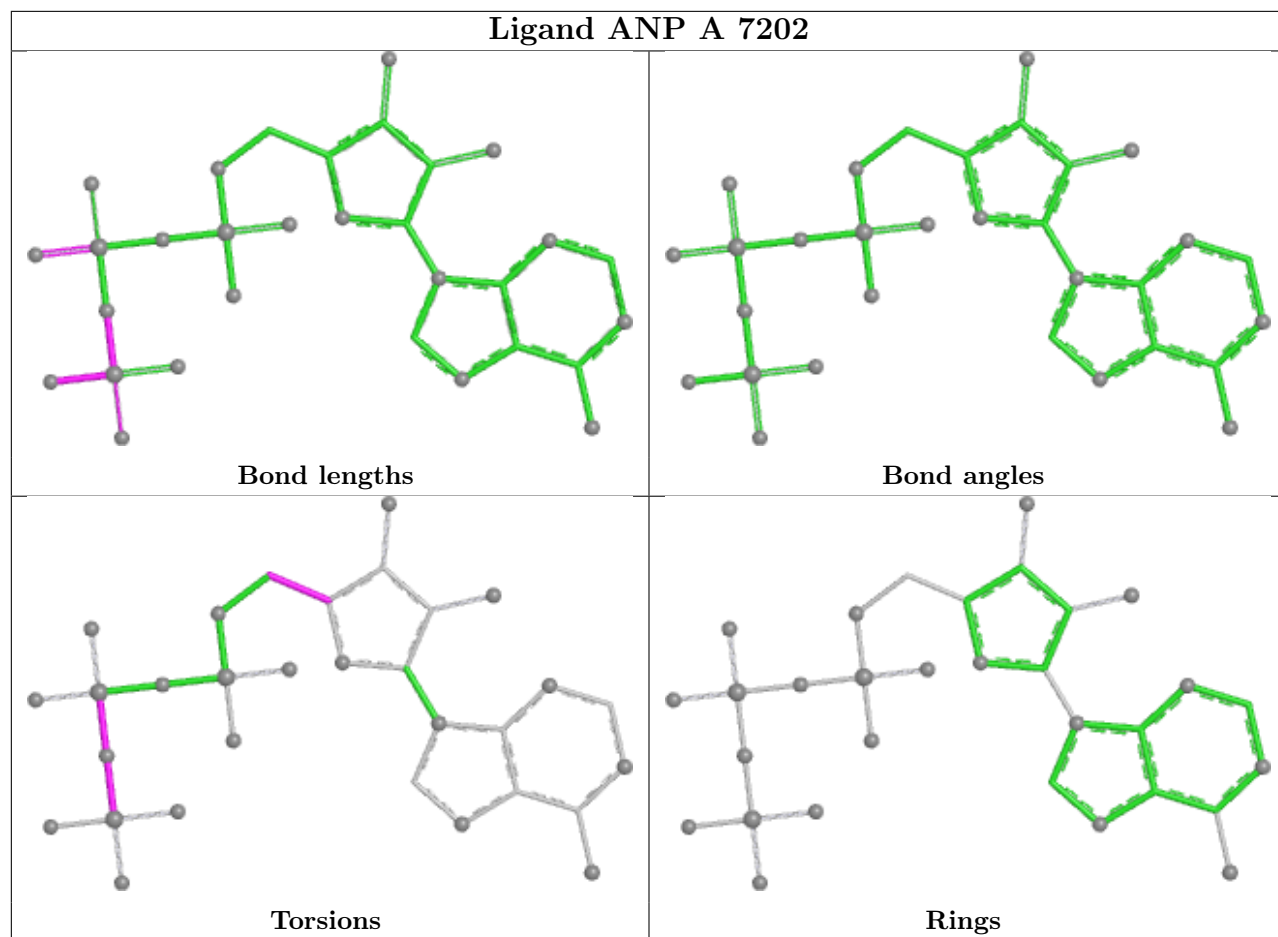
5 monomers are involved in 8 short contacts:

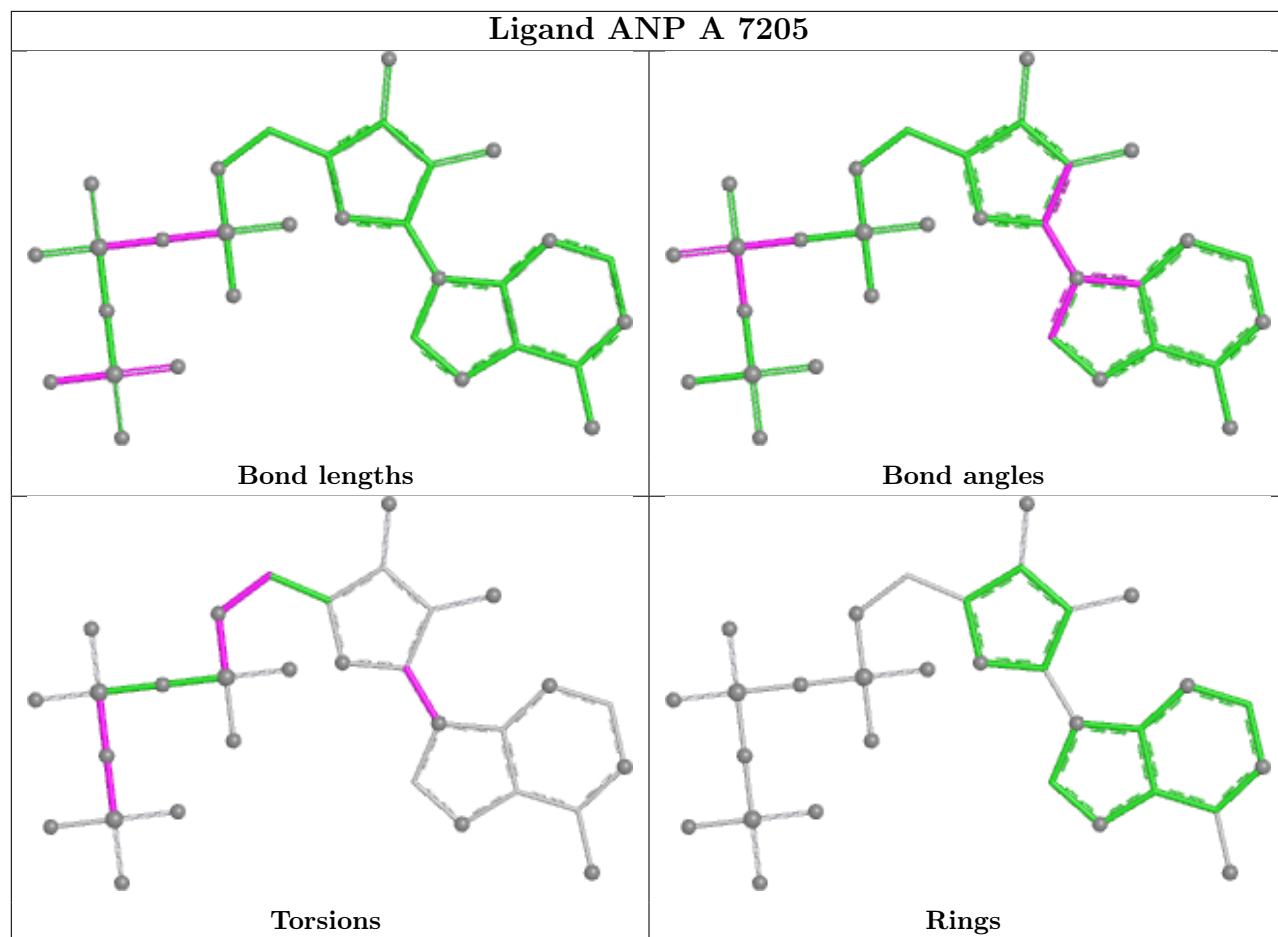
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	7203	ANP	1	0
2	A	7202	ANP	2	0
2	A	7205	ANP	3	0
2	A	7201	ANP	1	0
2	A	7204	ANP	1	0

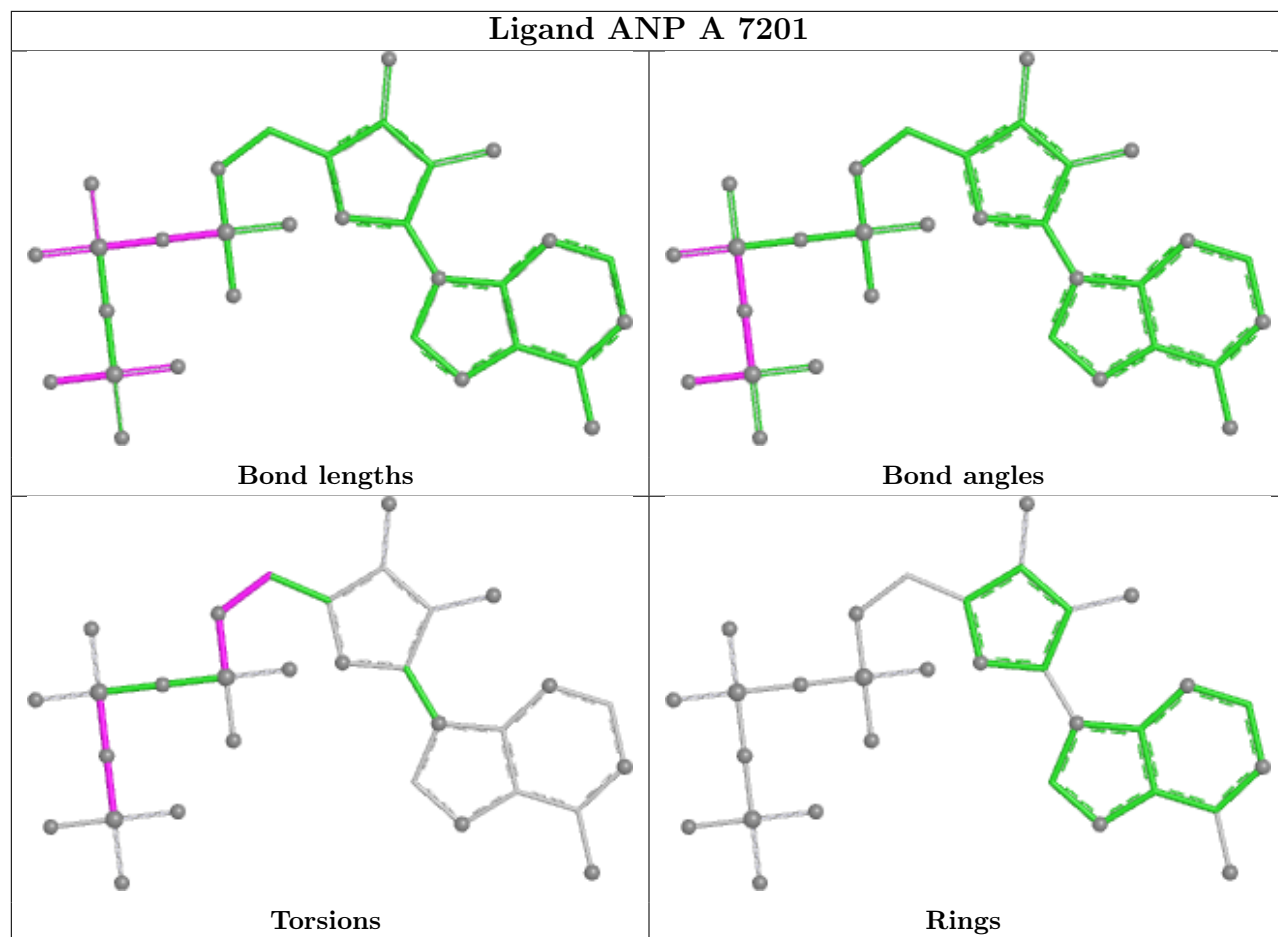
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

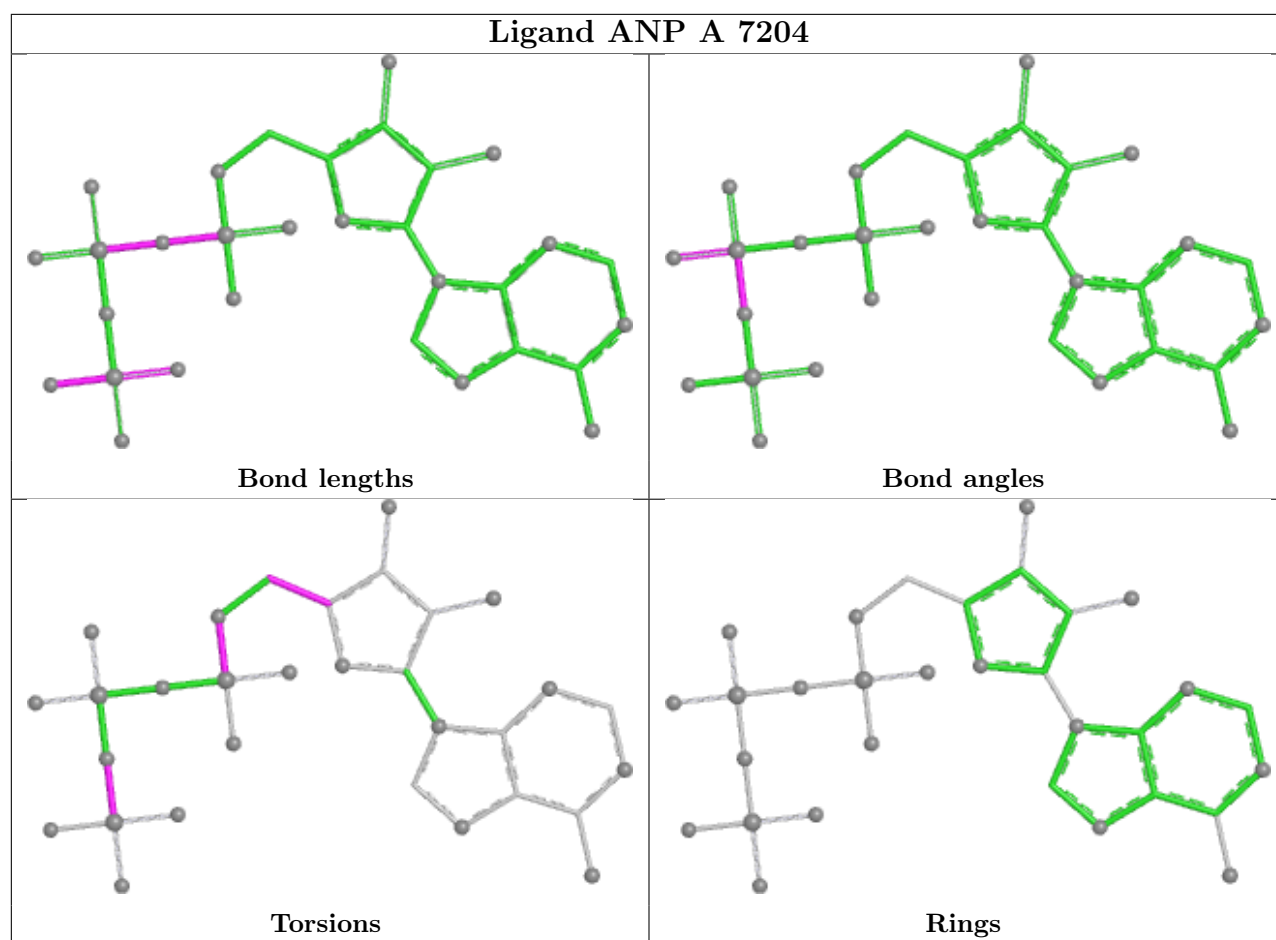
in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers 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.

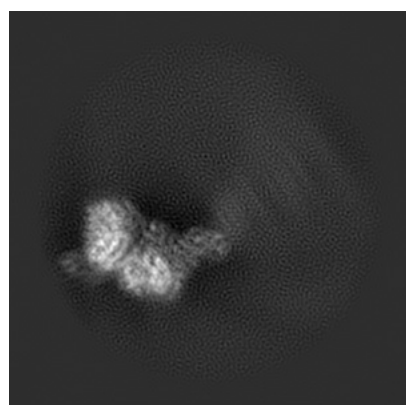
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9032. These allow visual inspection of the internal detail of the map and identification of artifacts.

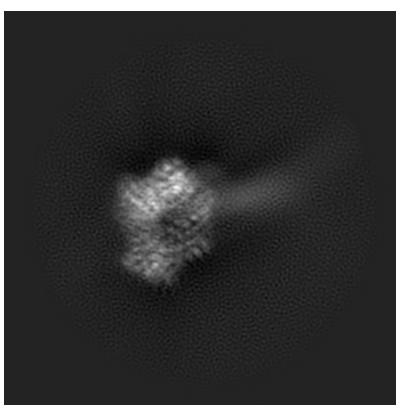
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

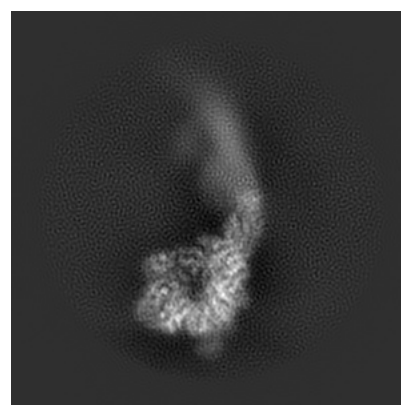
6.1.1 Primary map



X



Y

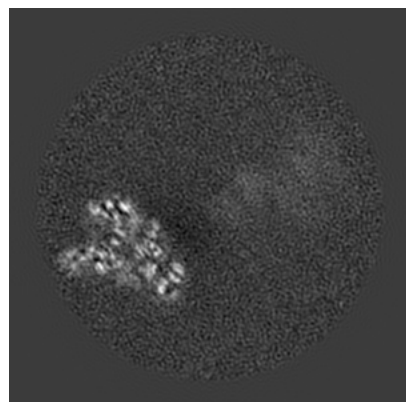


Z

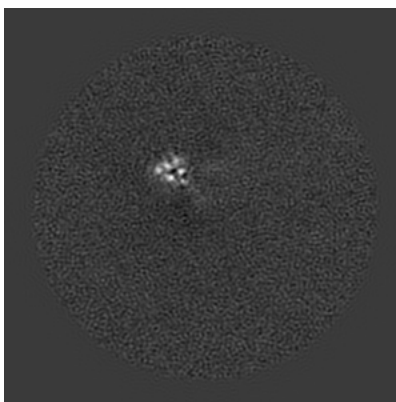
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

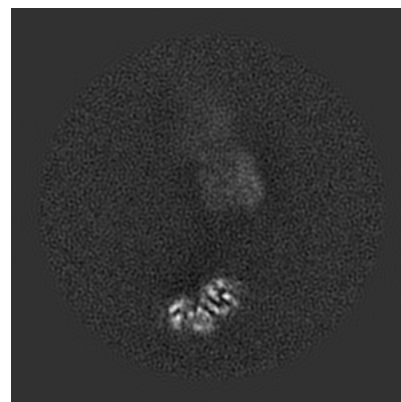
6.2.1 Primary map



X Index: 150



Y Index: 150

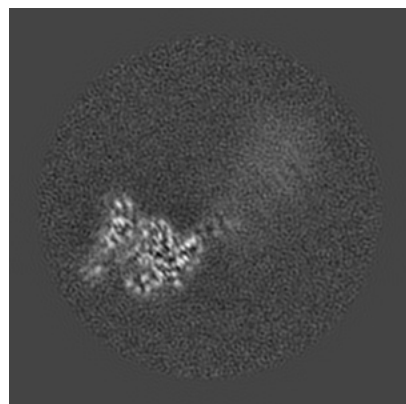


Z Index: 150

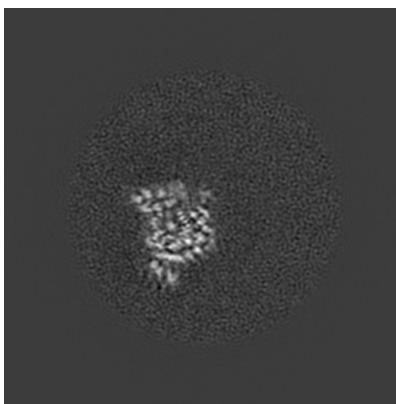
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

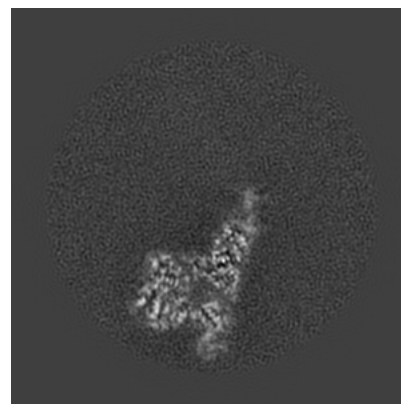
6.3.1 Primary map



X Index: 164



Y Index: 70

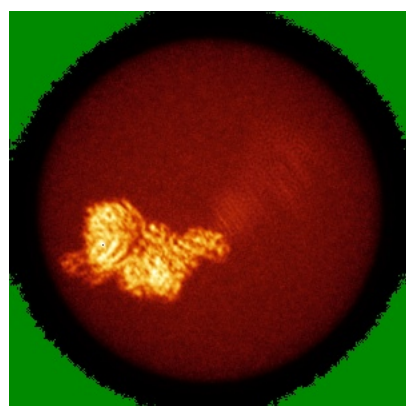


Z Index: 113

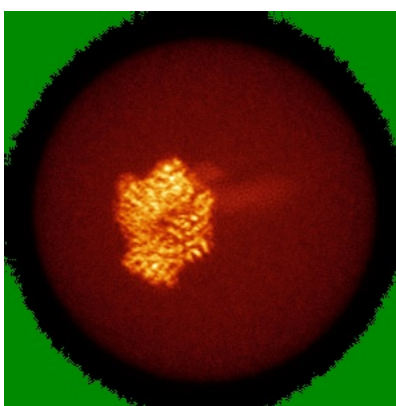
The images above show the largest variance slices of the map in three orthogonal directions.

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

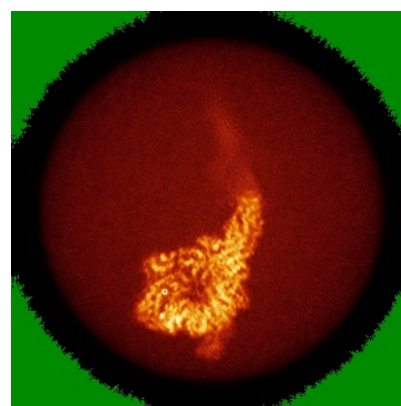
6.4.1 Primary map



X



Y

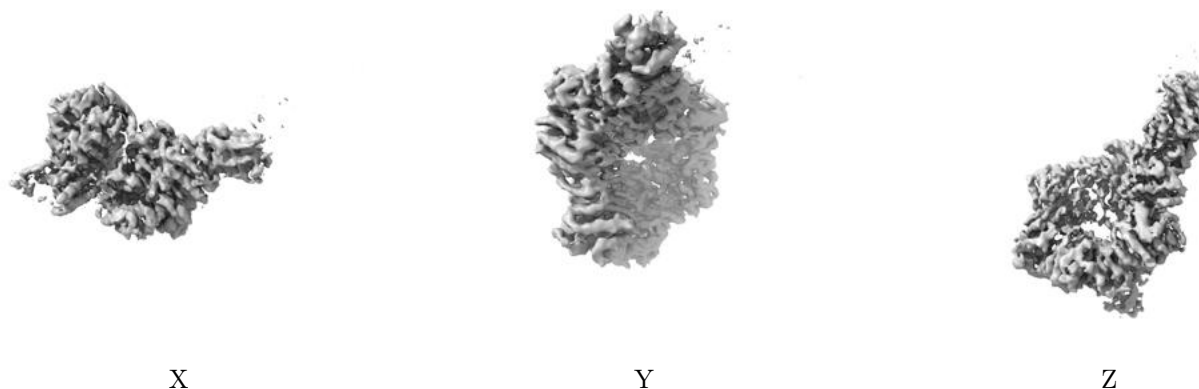


Z

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

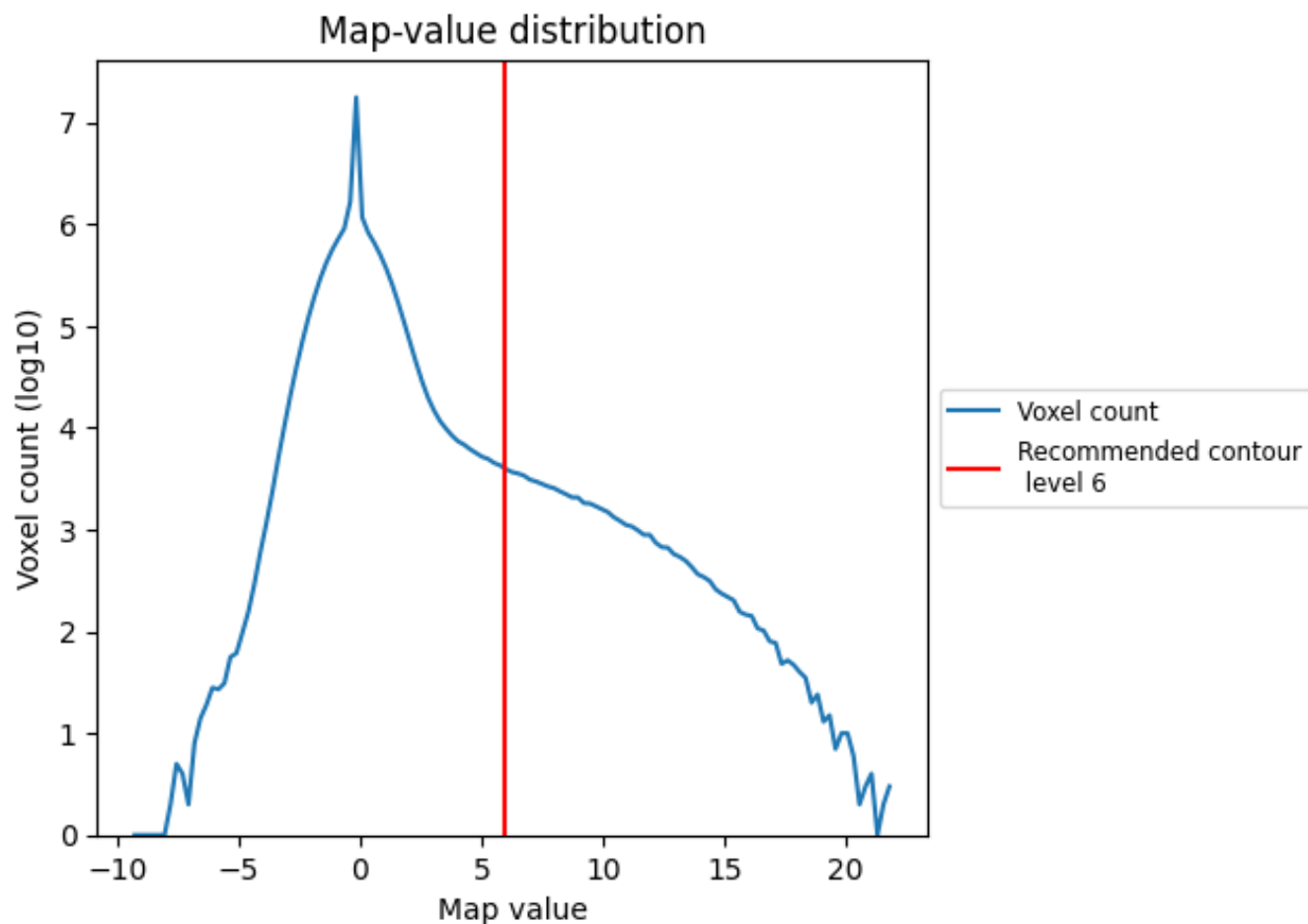
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

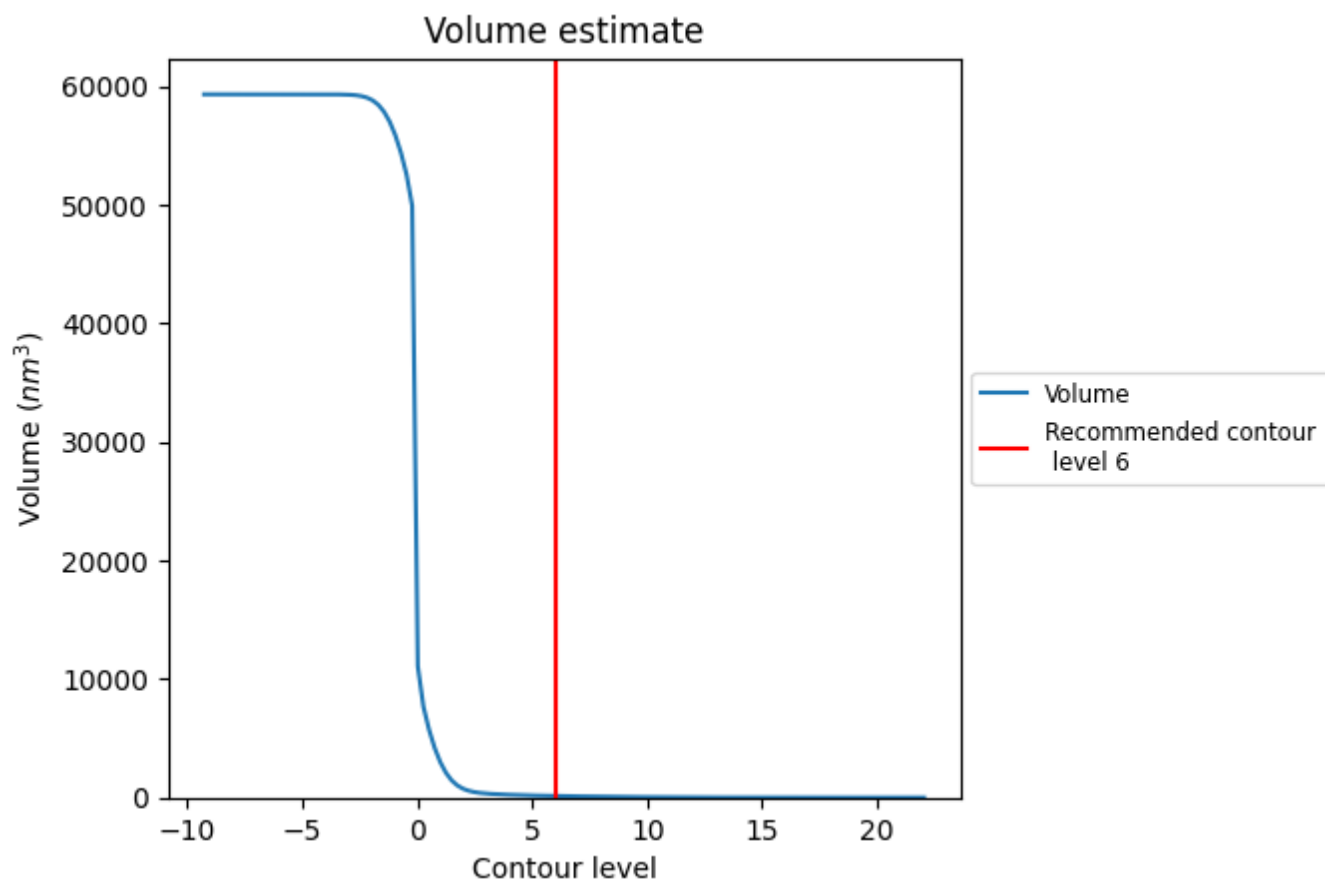
This section contains the results of statistical analysis of the map.

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.

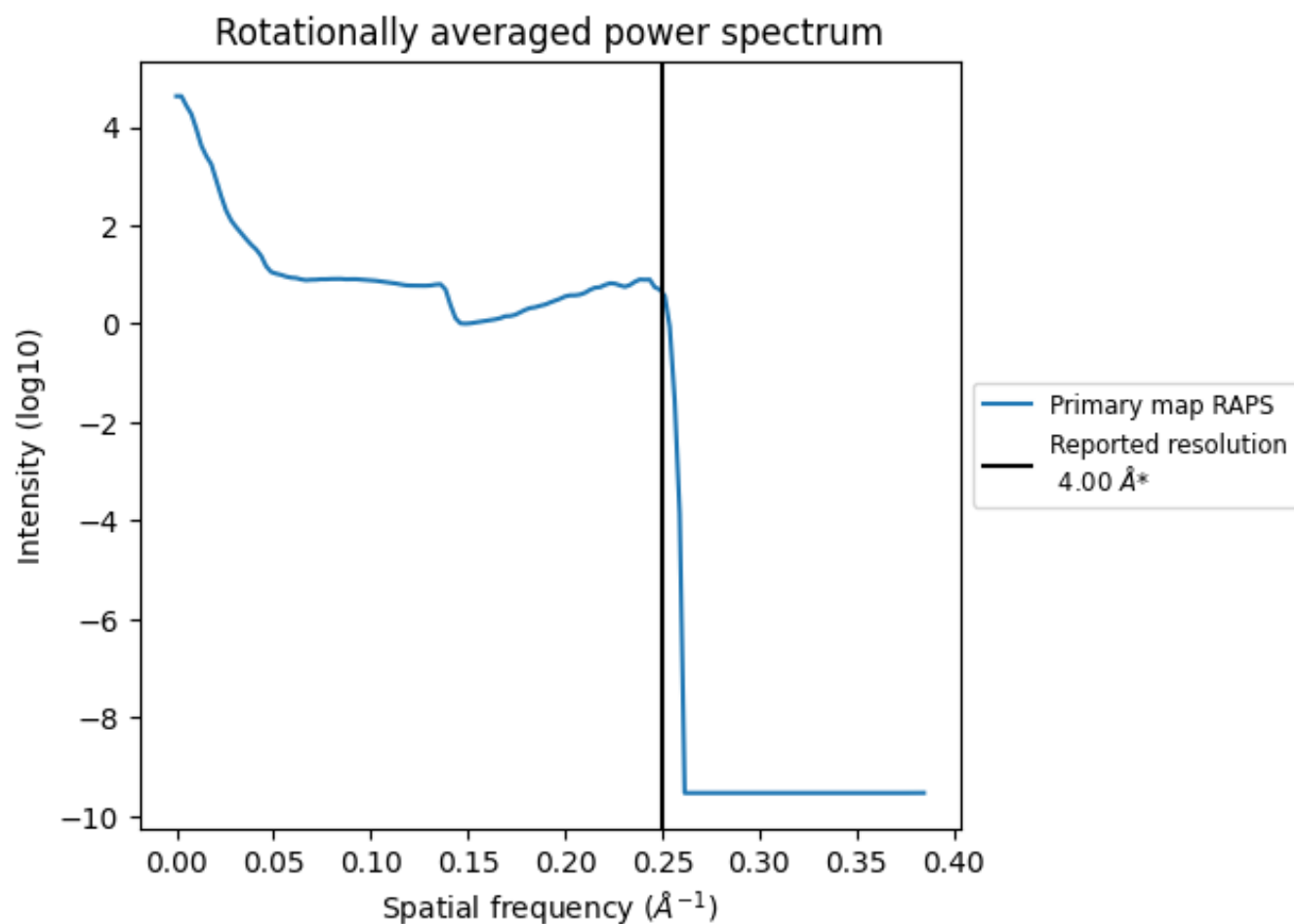
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 134 nm³; this corresponds to an approximate mass of 121 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 ⓘ

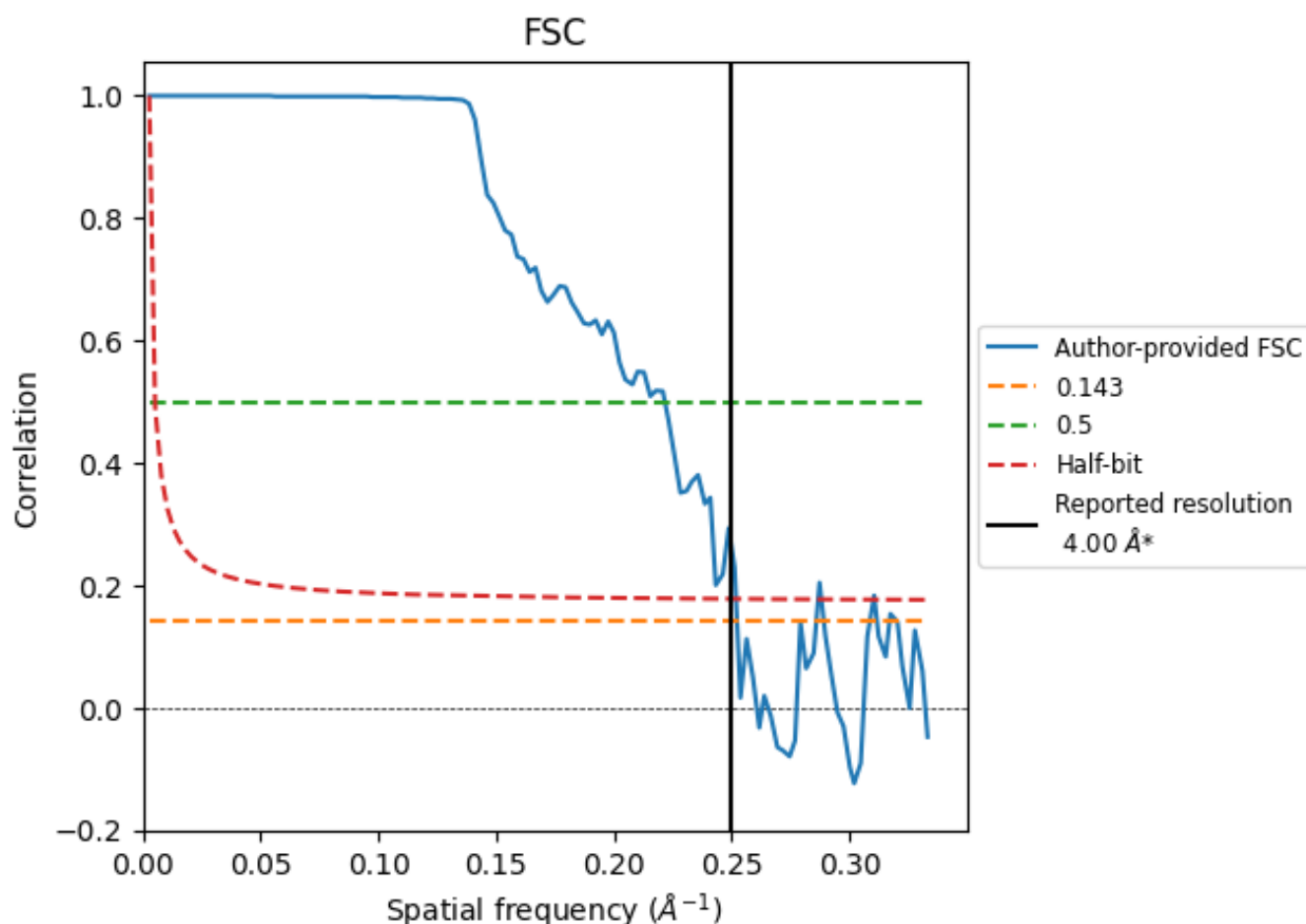


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

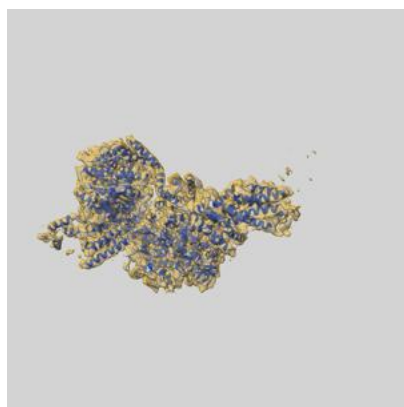
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	3.96	4.51	3.97
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

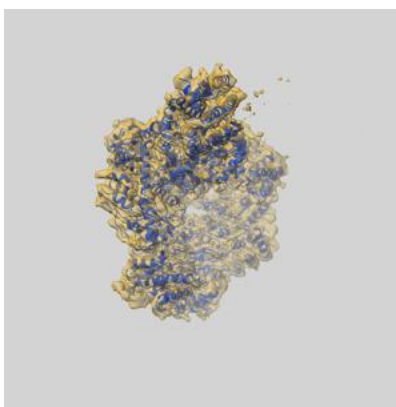
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9032 and PDB model 6OR5. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

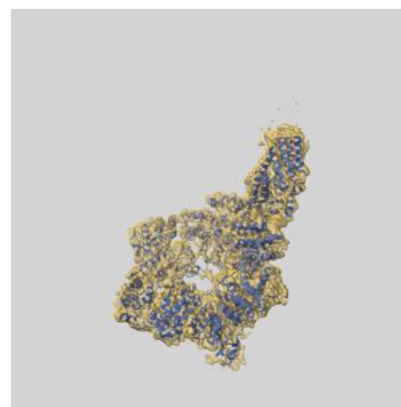
9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 6.0 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](#)



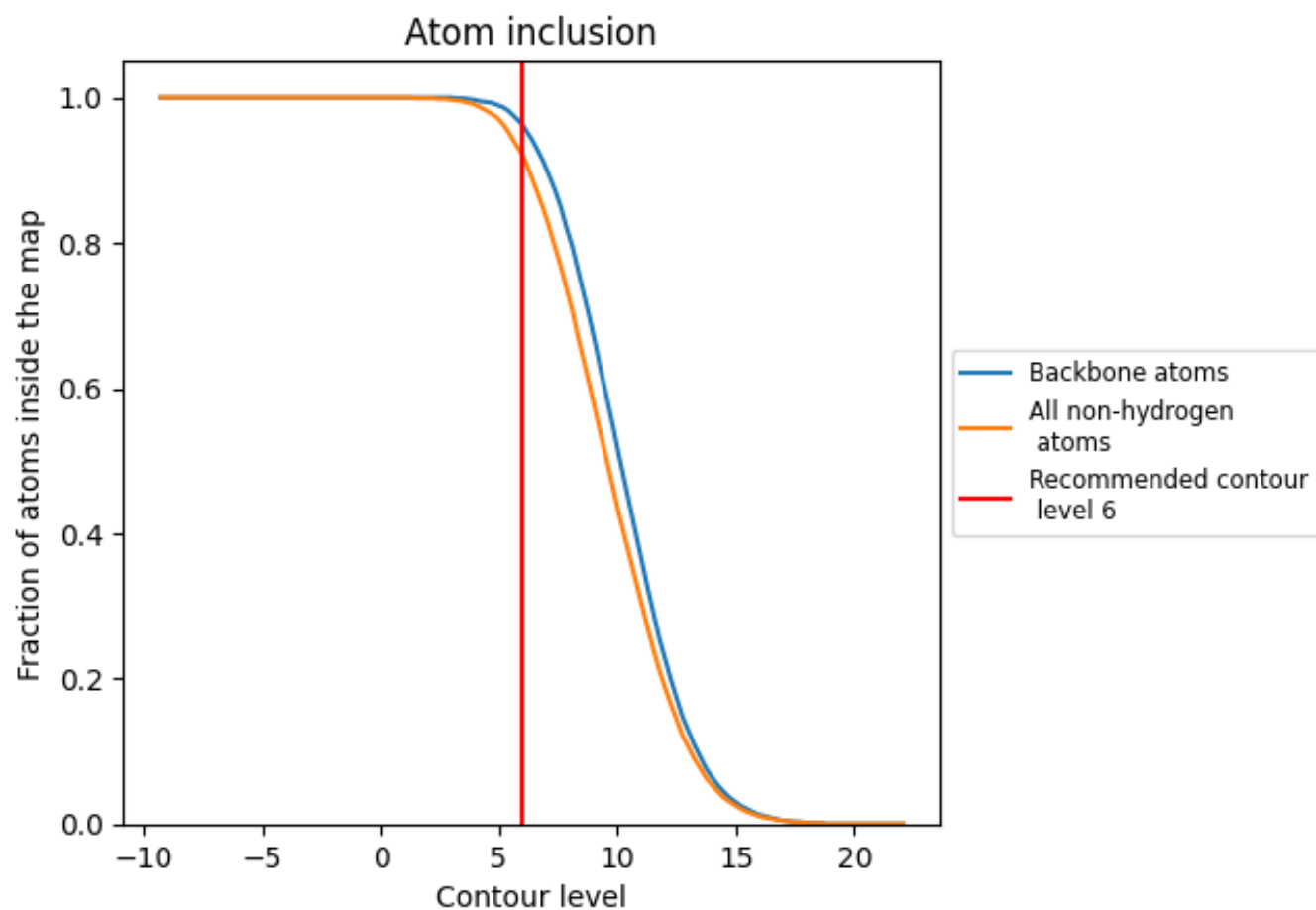
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 92% 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 (6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9210	0.4090
A	0.9210	0.4090

