



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2025 – 10:58 AM EDT

PDB ID : 9BCV
EMDB ID : EMD-44440
Title : Cyclase domain of GC-A bound to ANP
Authors : Liu, S.; Huang, X.
Deposited on : 2024-04-09
Resolution : 3.20 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.dev117
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
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)	:	2.41.4

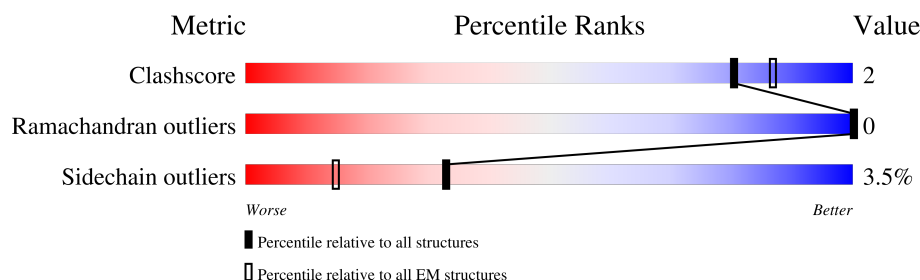
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	1029	
1	B	1029	
2	C	120	
2	D	120	
2	E	120	
2	F	120	
2	G	120	
2	H	120	

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Mol	Chain	Length	Quality of chain
2	I	120	<div><div></div><div>93%</div><div>7%</div></div>
2	J	120	<div><div></div><div>97%</div><div>..</div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7729 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.

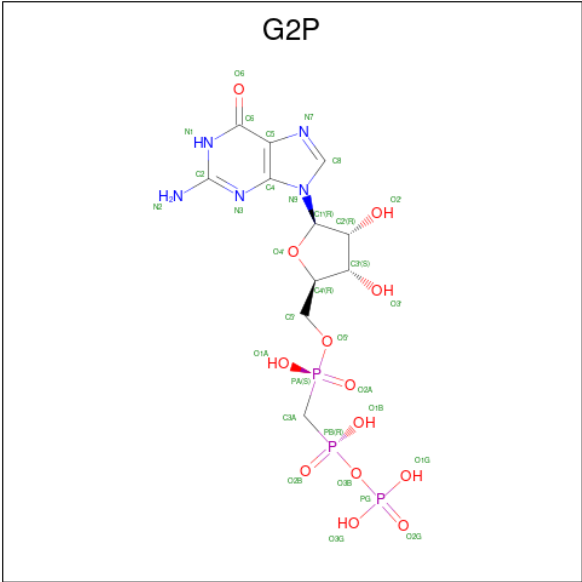
- Molecule 1 is a protein called Atrial natriuretic peptide receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	211	Total	C	N	O	S	0	0
			1568	1001	278	280	9		
1	B	211	Total	C	N	O	S	0	0
			1580	1004	278	290	8		

- Molecule 2 is a protein called Fab fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	G	119	Total	C	N	O	0	0
			595	357	119	119		
2	H	112	Total	C	N	O	0	0
			560	336	112	112		
2	J	117	Total	C	N	O	0	0
			585	351	117	117		
2	I	112	Total	C	N	O	0	0
			560	336	112	112		
2	C	115	Total	C	N	O	0	0
			575	345	115	115		
2	D	106	Total	C	N	O	0	0
			530	318	106	106		
2	E	116	Total	C	N	O	0	0
			580	348	116	116		
2	F	106	Total	C	N	O	0	0
			530	318	106	106		

- Molecule 3 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: G2P) (formula: C₁₁H₁₈N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			32	11	5	13	3	
3	A	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	Mg	0
			1	1	
4	B	1	Total	Mg	0
			1	1	

LEU	ASP	ASN	LEU	LEU	SER	ARG	MET	GLU	GLN	TYR	ALA	ASN	ASN	LEU	GLU	GLU	THR	GLN	ALA	TYR	ALA	ARG	LYS	ARG	LYS	A845
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P934	Y935	R936	Y948	L953	Y956	Y961	R962	L971	R972	L987	M1000	R1004	M1008	L1034	R1035	G1036	D1037	V1038	E1039	M1040	K1041	K1043	G1044	K1045	R1055	GLY	SER	SER	THR	ARG	GLY
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● Molecule 1: Atrial natriuretic peptide receptor 1



GLY	ASN	LEU	THR	ALA	VAL	VAL	VAL	VAL	PRO	ASP	ALA	ASN	THR	THR	ASP	GLN	VAL	GLY	ALA	LEU	ALA	PRO	ASP	GLY	GLY	SER	SER	THR	ARG	GLY	CYS
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SER	ASP	THR	ALA	ALA	PRO	LEU	ALA	VAL	GLY	ASP	GLY	LEU	LYS	THR	GLY	VAL	THR	GLY	GLY	ALA	ALA	PRO	ALA	ALA	HIS	LEU	LEU	LEU	THR	THR	VAL	TYR
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ALA	LEU	THR	THR	ARG	GLY	PRO	ALA	GLY	ASP	GLY	LEU	GLY	LEU	THR	GLY	ASP	GLY	THR	THR	VAL	ALA	LEU	ALA	TRP	GLY	LEU	LEU	LEU	THR	VAL	ASN
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ILE	THR	VAL	ASP	HIS	LEU	GLY	PHE	GLY	ASP	GLY	LEU	SER	HIS	THR	THR	ARG	THR	THR	THR	VAL	ALA	LEU	LEU	LYS	ARG	GLY	LEU	LEU	THR	PHE	HIS
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LEU	ASP	ILE	PHE	GLY	GLN	SER	GLY	GLN	ASP	GLY	GLY	PRO	ALA	HIS	PRO	ARG	ARG	THR	THR	VAL	ALA	LEU	GLN	ILE	GLY	GLN	LEU	GLY	GLY	GLY	LEU
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ALA	TYR	GLU	GLY	PHE	ASN	PHE	THR	MET	ASP	GLY	GLY	VAL	VAL	ASN	SER	PHE	HIS	ASP	THR	THR	ILE	PRO	ALA	LEU	GLY	LEU	LEU	LEU	THR	GLN	VAL
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THR	GLY	TYR	LEU	LYS	ILE	ASP	SER	SER	GLY	ARG	GLY	THR	THR	THR	ASP	MET	GLY	PRO	ASP	THR	VAL	GLY	ASN	GLY	LEU	LEU	LEU	LEU	THR	GLY	ILE
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PRO	LYS	CYS	GLY	PHE	ASN	GLY	SER	GLY	ASP	PRO	CYS	GLN	ASP	GLY	VAL	GLY	GLY	VAL	GLY	ASP	GLY	LEU	VAL	LEU	LEU	LEU	LEU	THR	GLY	THR	LYS
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GLY	ASP	VAL	GLY	TYR	SER	SER	LEU	GLY	ARG	GLY	LEU	SER	GLY	ALA	THR	THR	GLY	ASN	VAL	GLY	GLY	LEU	GLY	GLY	GLY	LEU	VAL	THR	GLY	VAL	LYS
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ARG	ILE	GLY	LEU	THR	LYS	VAL	LEU	PHE	GLY	THR	LEU	HIS	THR	VAL	GLN	ASN	GLY	THR	THR	ARG	PHE	VAL	GLY	ASN	GLY	LEU	THR	THR	THR	THR	ASP
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TRP	MET	PHE	ARG	SER	SER	LEU	THR	LEU	VAL	ASP	VAL	LYS	GLY	MET	PHE	HIS	GLY	THR	THR	GLY	GLY	LEU	GLY	GLY	GLY	LEU	THR	THR	THR	GLN	GLY
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HIS	THR	VAL	TYR	ALA	LYS	LYS	LEU	THR	THR	THR	PRO	GLY	LEU	LEU	ARG	ALA	THR	THR	THR	THR	THR	GLY	GLY	GLY	GLY	LEU	LEU	THR	THR	THR	ILE
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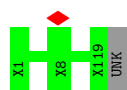
GLY	ARG	VAL	GLY	ARG	GLY	GLY	GLN	PRO	PRO	THR	PRO	PRO	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ILE
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LEU	ASP	ASN	LEU	LEU	SER	ARG	MET	GLY	GLN	PRO	GLY	GLY	ASN	ASN	LEU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LYS
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C939	R987	E1022	F1023	D1033	V1034	E1035	M1036	K1037	G1038	K1039	G1040	K1041	G1042	SER	THR	THR	ARG	GLY
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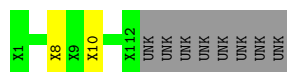
- Molecule 2: Fab fragment

Chain G:  99%



- Molecule 2: Fab fragment

Chain H:  92% 7%




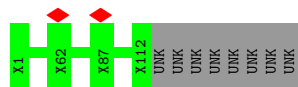
- Molecule 2: Fab fragment

Chain J:  97%



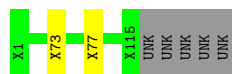
- Molecule 2: Fab fragment

Chain I:  93% 7%




- Molecule 2: Fab fragment

Chain C:  94%



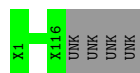
- Molecule 2: Fab fragment

Chain D:  87% 12%




- Molecule 2: Fab fragment

Chain E:  97%



- Molecule 2: Fab fragment

Chain F:  87% 12%

X1	X29	X30	X31	X106	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	112661	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	4.509	Depositor
Minimum map value	-3.251	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.127	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	304.64, 304.64, 304.64	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	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: G2P, MG

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	0.28	0/1596	0.51	0/2168
1	B	0.28	0/1608	0.51	0/2184
All	All	0.28	0/3204	0.51	0/4352

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1568	0	1527	16	0
1	B	1580	0	1537	8	0
2	C	575	0	131	1	0
2	D	530	0	118	1	0
2	E	580	0	132	0	0
2	F	530	0	116	1	0
2	G	595	0	133	0	0
2	H	560	0	123	1	0
2	I	560	0	121	0	0
2	J	585	0	126	1	0
3	A	64	0	27	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	1	0	0	0	0
4	B	1	0	0	0	0
All	All	7729	0	4091	29	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 2.

The worst 5 of 29 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:896:GLN:NE2	2:J:103:UNK:O	2.25	0.70
1:A:1034:LEU:HG	1:A:1036:GLY:H	1.69	0.57
1:B:935:ARG:NH1	1:B:1022:GLU:OE2	2.39	0.55
1:A:933:LEU:HB3	1:A:934:PRO:HD3	1.89	0.55
1:B:921:ASP:OD1	1:B:921:ASP:N	2.37	0.55

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	209/1029 (20%)	206 (99%)	3 (1%)	0	100	100
1	B	209/1029 (20%)	204 (98%)	5 (2%)	0	100	100
All	All	418/2058 (20%)	410 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	153/871 (18%)	148 (97%)	5 (3%)	33	64
1	B	158/871 (18%)	152 (96%)	6 (4%)	28	60
All	All	311/1742 (18%)	300 (96%)	11 (4%)	33	63

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	923	TYR
1	B	939	CYS
1	B	1023	PHE
1	B	987	ARG
1	A	987	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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, 2 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	G2P	A	1102	4	25,34,34	1.49	5 (20%)	32,54,54	2.60	9 (28%)
3	G2P	A	1101	4	25,34,34	1.52	5 (20%)	32,54,54	2.49	8 (25%)

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	G2P	A	1102	4	-	4/15/38/38	0/3/3/3
3	G2P	A	1101	4	-	4/15/38/38	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1102	G2P	C6-N1	4.41	1.40	1.33
3	A	1101	G2P	C6-N1	4.32	1.40	1.33
3	A	1101	G2P	PB-O3B	2.86	1.61	1.58
3	A	1102	G2P	PB-O3B	2.81	1.61	1.58
3	A	1101	G2P	C8-N7	-2.59	1.30	1.34

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1102	G2P	C5-C6-N1	-9.54	110.66	123.42
3	A	1101	G2P	C5-C6-N1	-9.49	110.74	123.42
3	A	1102	G2P	C2-N1-C6	7.18	125.95	115.96
3	A	1101	G2P	C2-N1-C6	7.16	125.92	115.96
3	A	1102	G2P	N3-C2-N1	-3.16	123.20	127.21

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

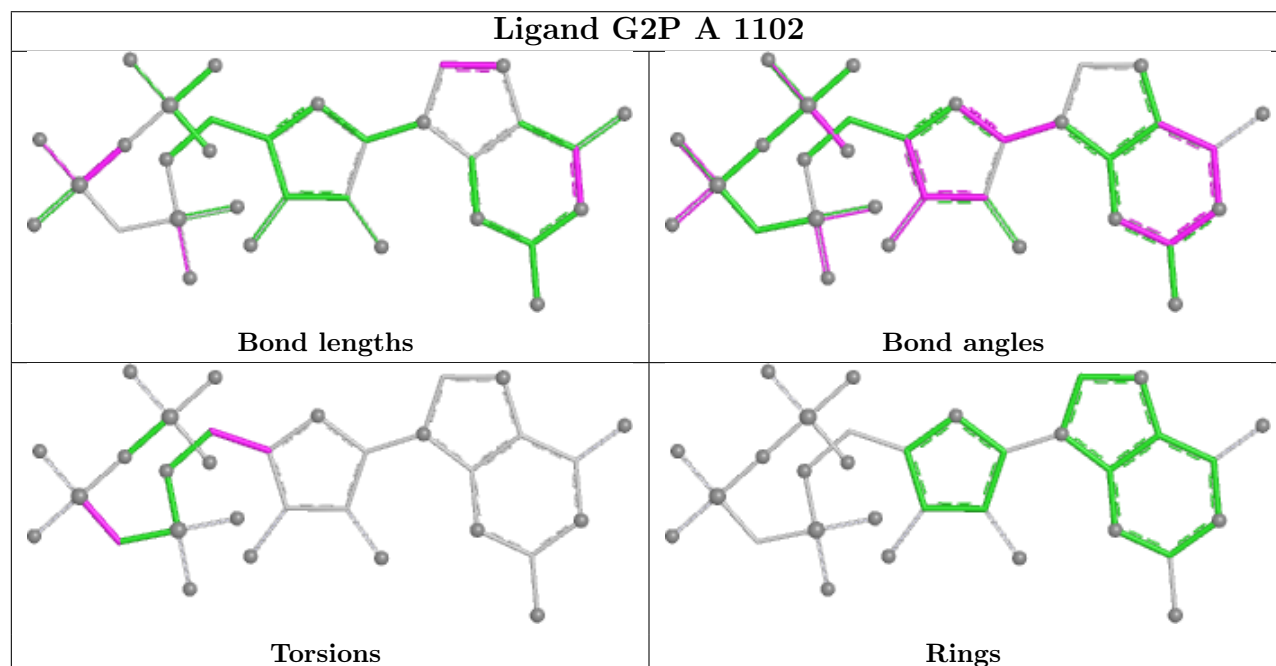
Mol	Chain	Res	Type	Atoms
3	A	1101	G2P	C5'-O5'-PA-O2A
3	A	1102	G2P	PA-C3A-PB-O3B
3	A	1102	G2P	C3'-C4'-C5'-O5'
3	A	1102	G2P	O4'-C4'-C5'-O5'
3	A	1101	G2P	C3'-C4'-C5'-O5'

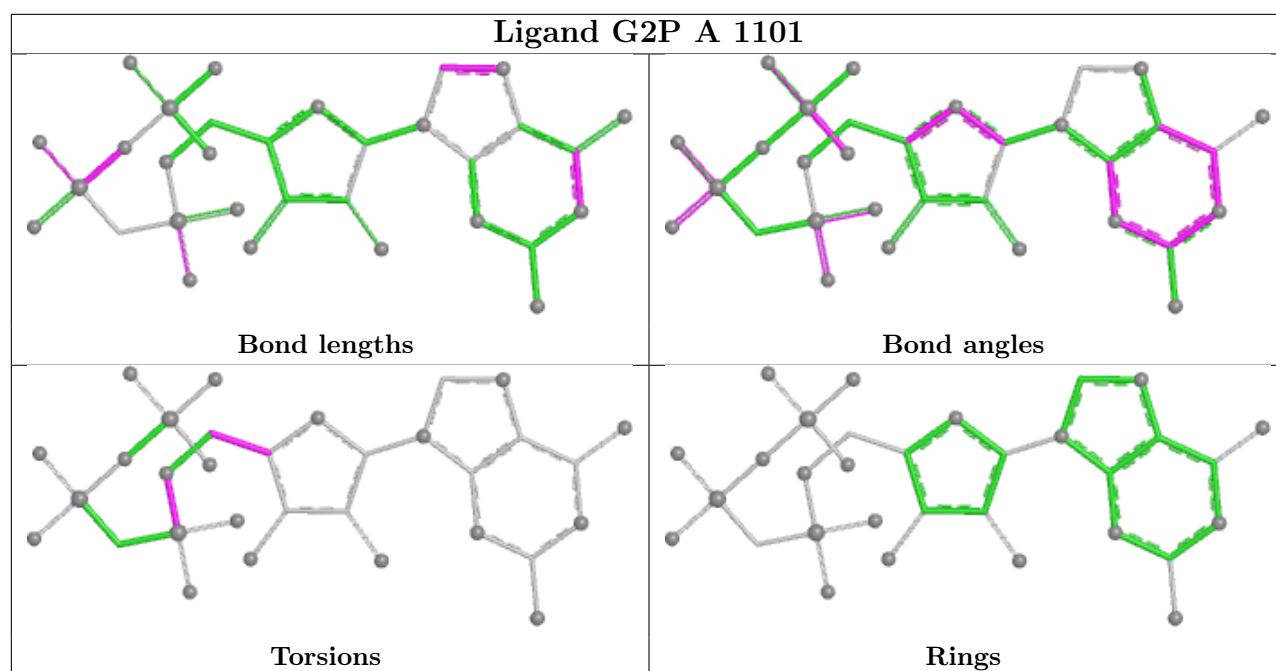
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1102	G2P	4	0
3	A	1101	G2P	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.

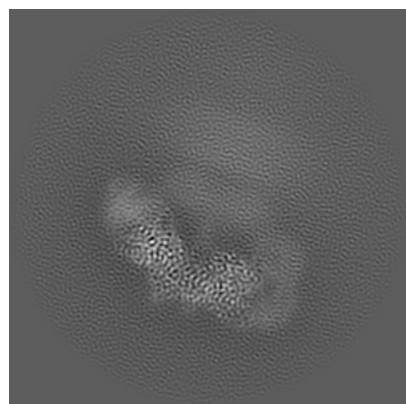
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44440. These allow visual inspection of the internal detail of the map and identification of artifacts.

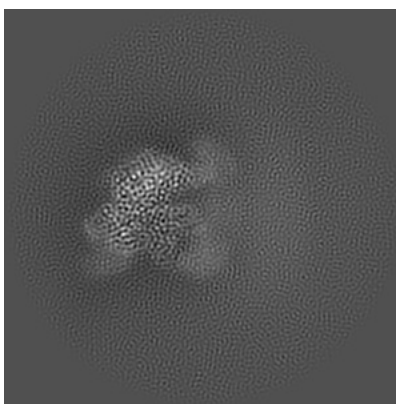
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

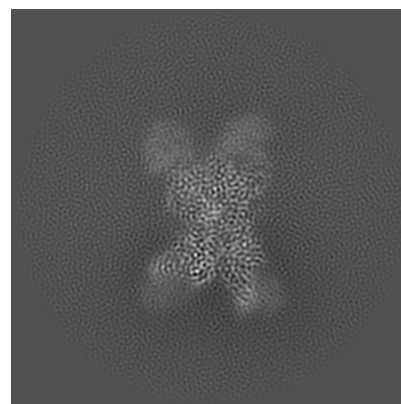
6.1.1 Primary map



X

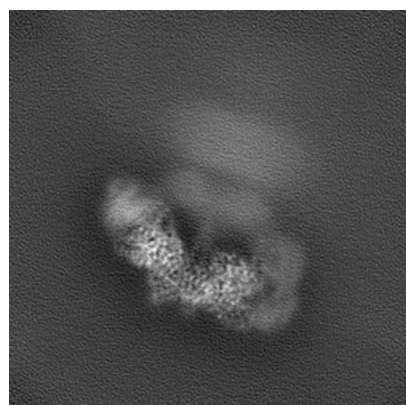


Y

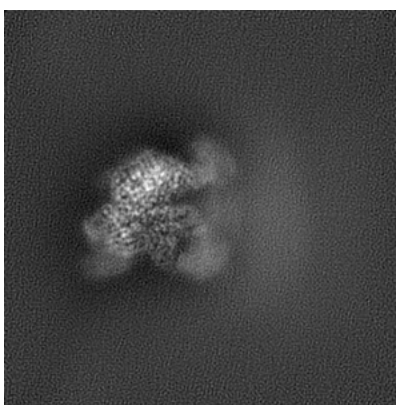


Z

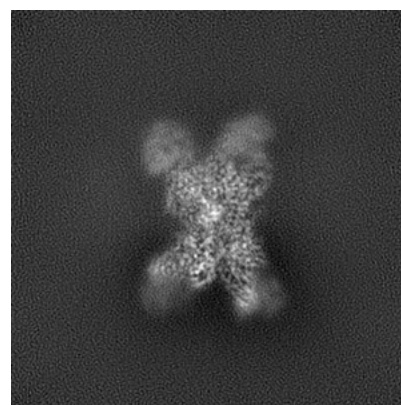
6.1.2 Raw map



X



Y

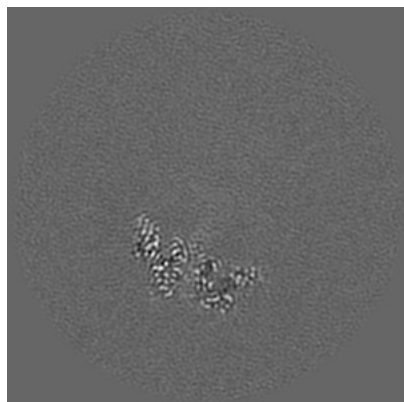


Z

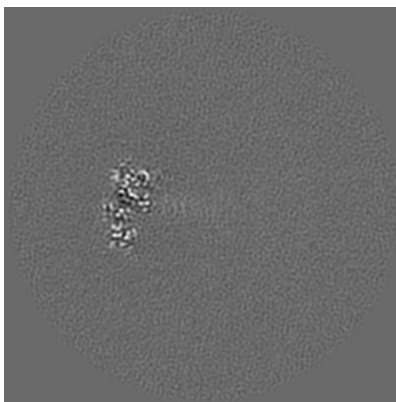
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

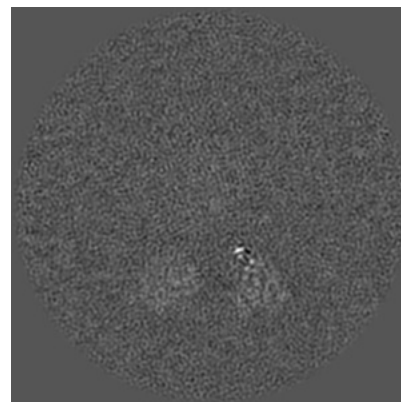
6.2.1 Primary map



X Index: 128

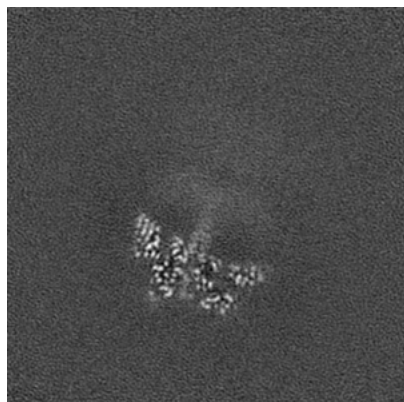


Y Index: 128

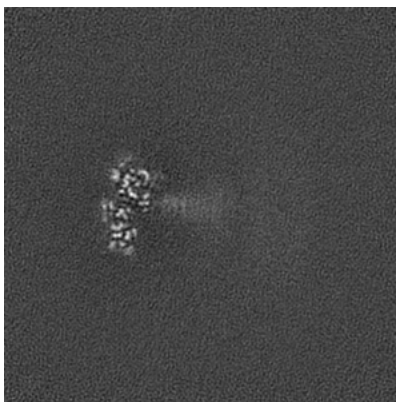


Z Index: 128

6.2.2 Raw map



X Index: 128



Y Index: 128

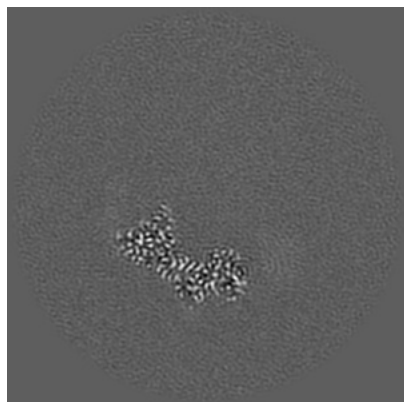


Z Index: 128

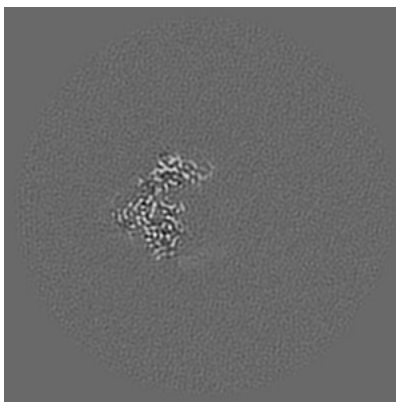
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

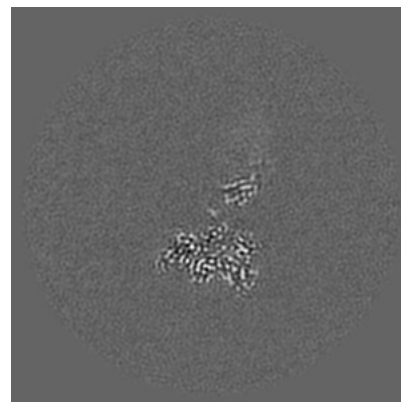
6.3.1 Primary map



X Index: 144

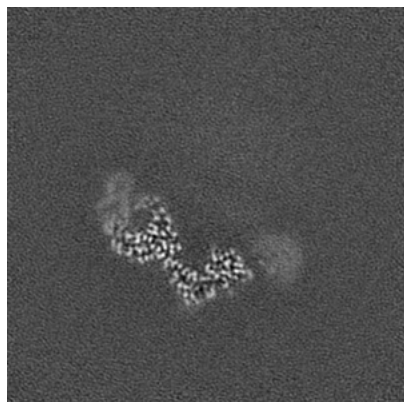


Y Index: 96

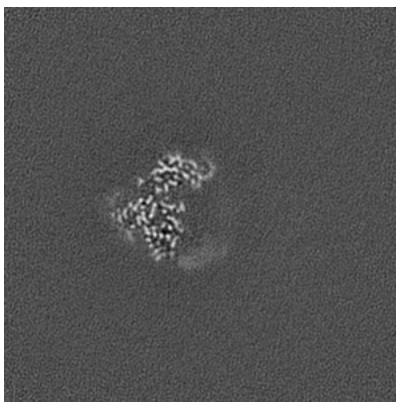


Z Index: 97

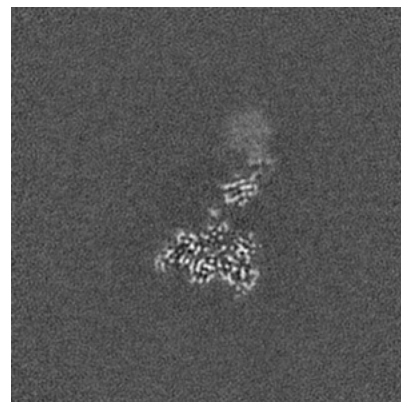
6.3.2 Raw map



X Index: 150



Y Index: 96

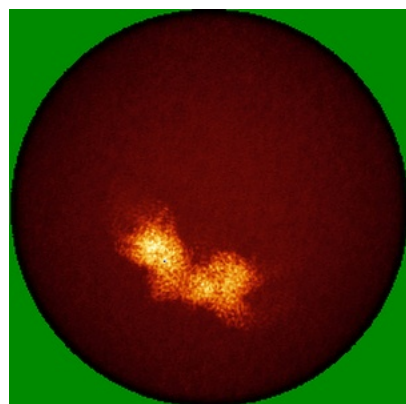


Z Index: 97

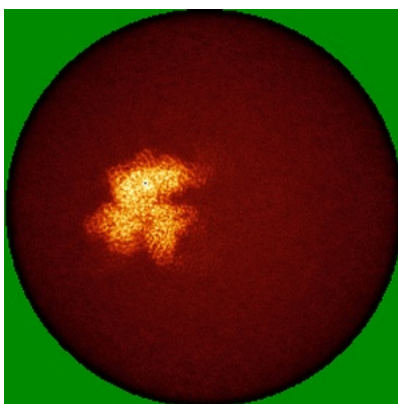
The images above show the largest variance slices of the map in three orthogonal directions.

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

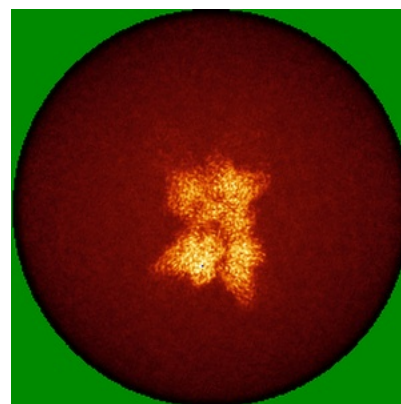
6.4.1 Primary map



X

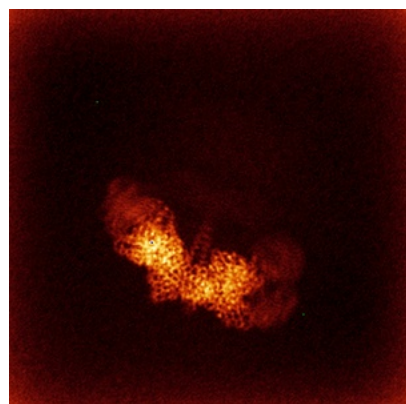


Y

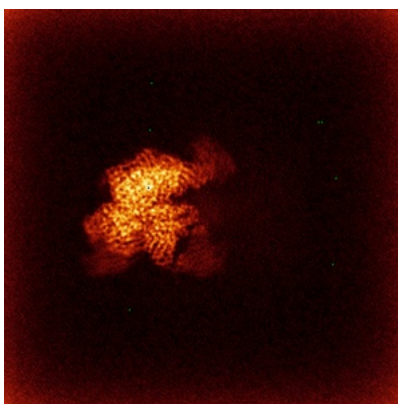


Z

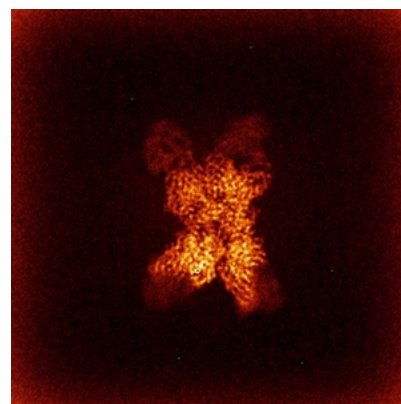
6.4.2 Raw map



X



Y

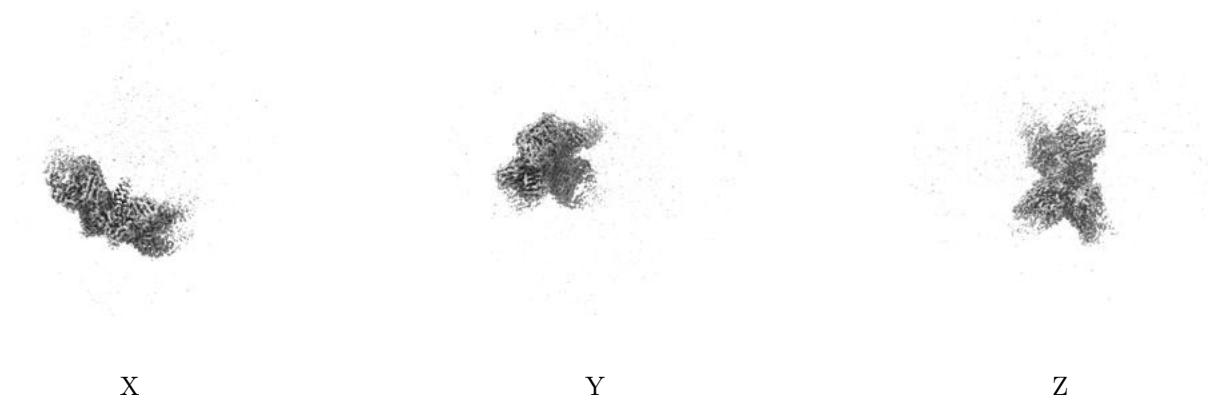


Z

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.

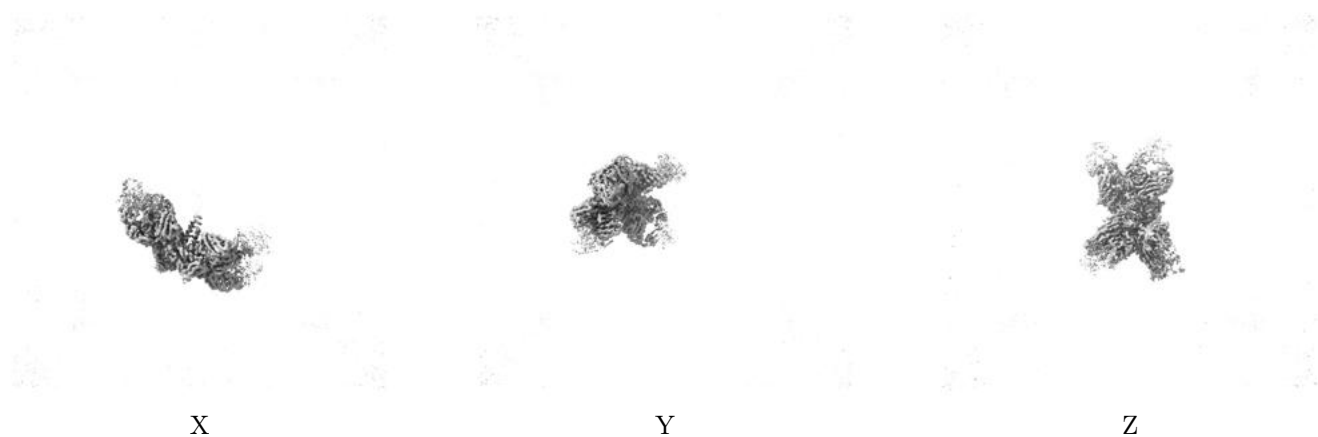
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. 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.

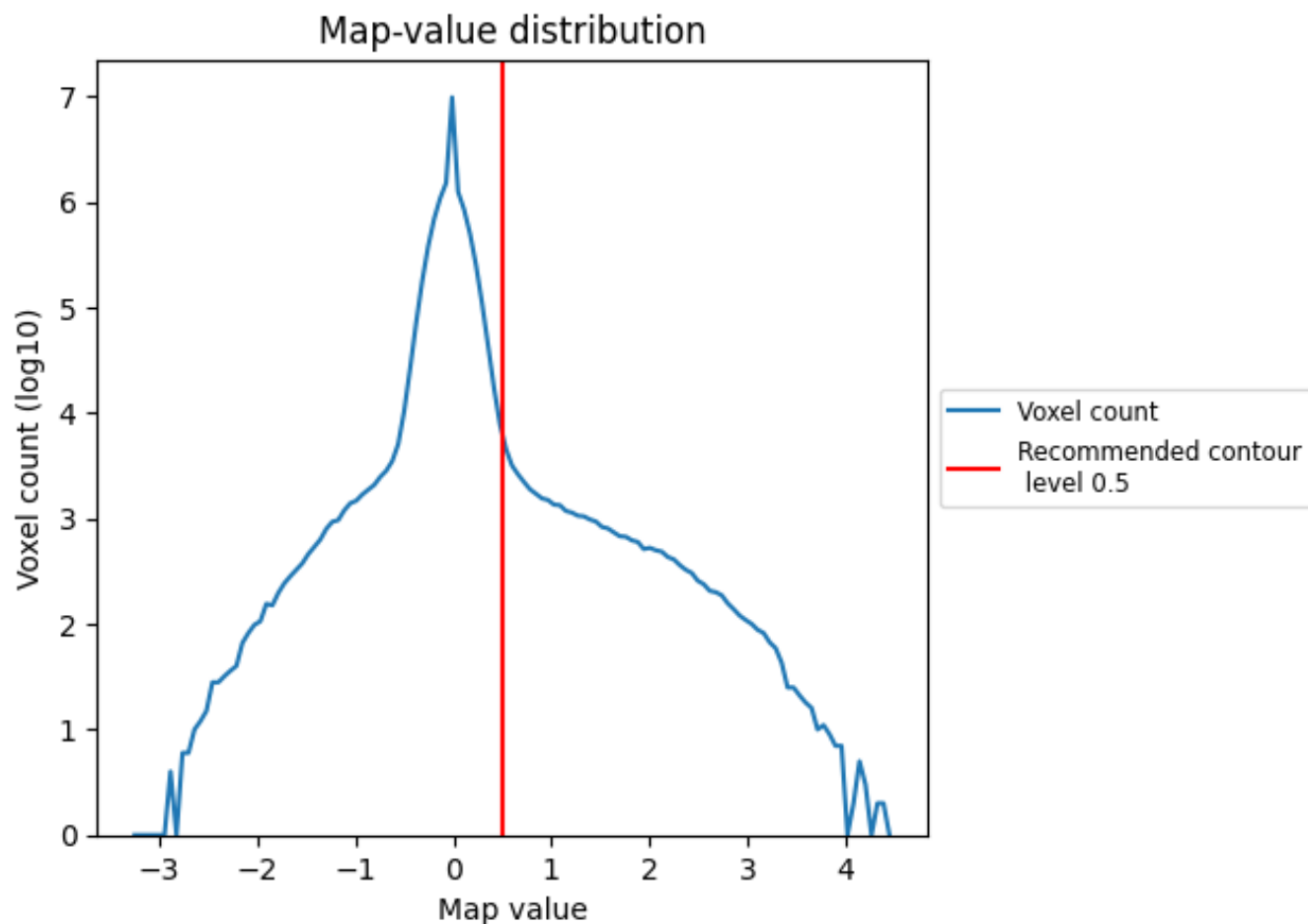
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

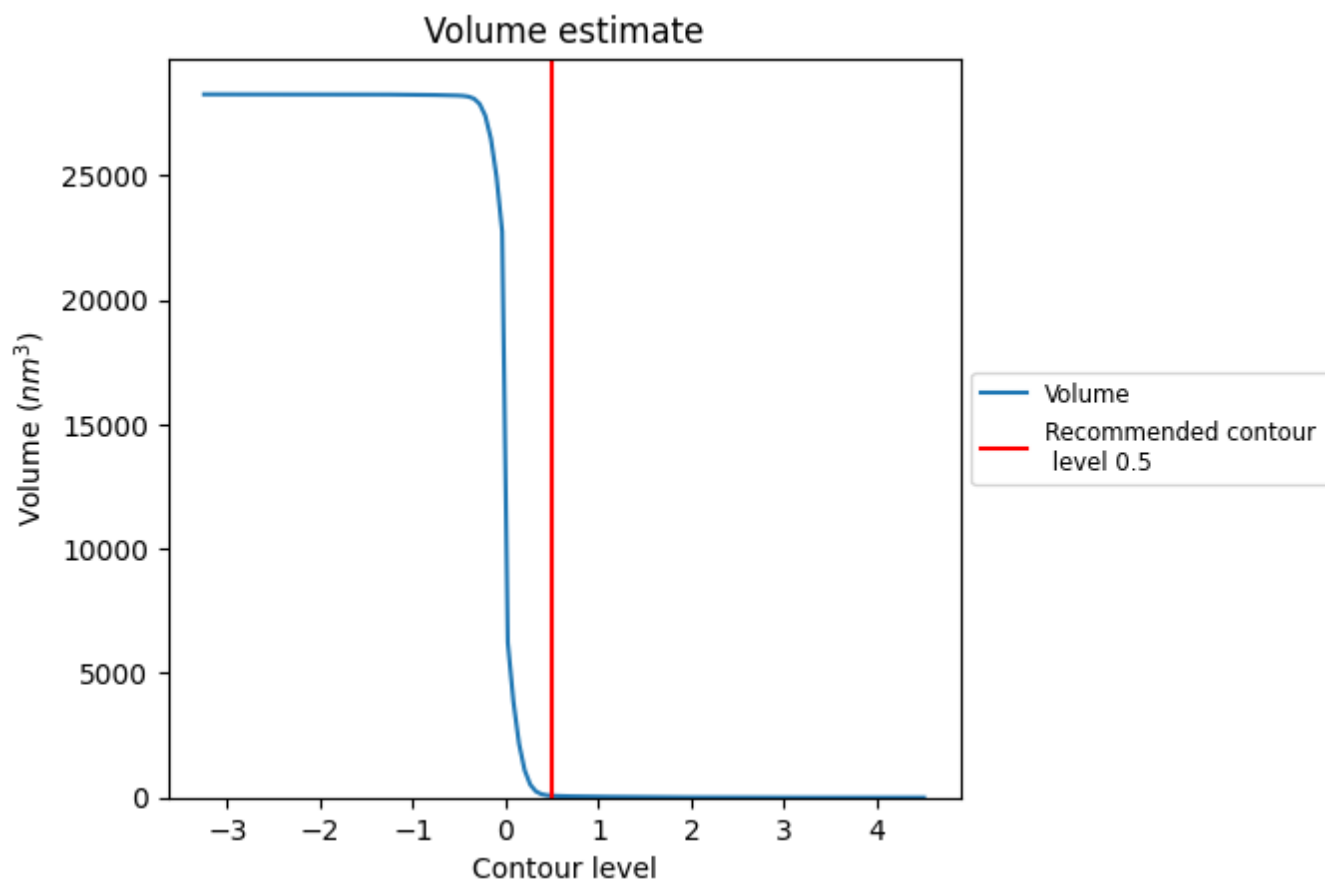
This section contains the results of statistical analysis of the map.

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.

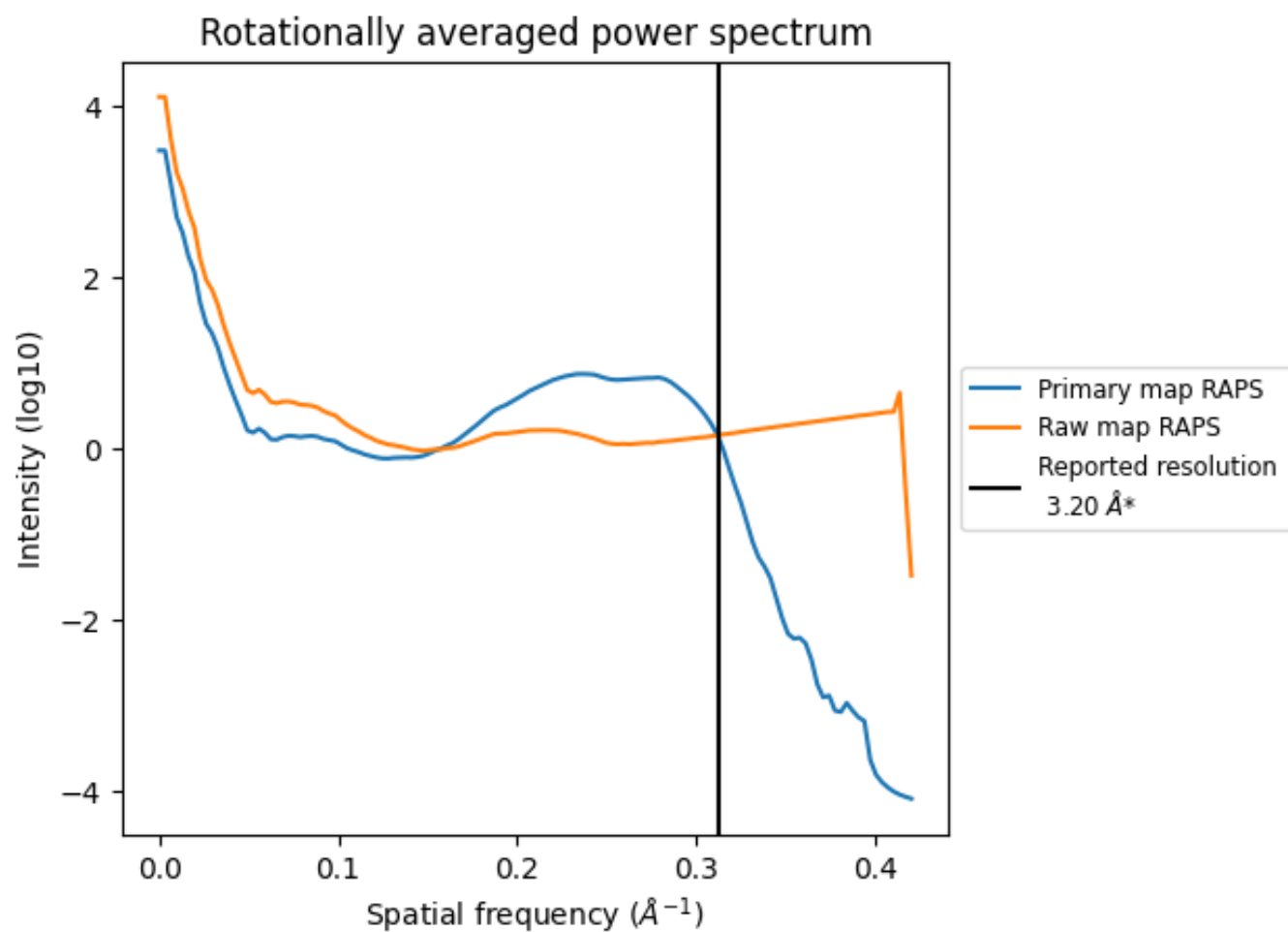
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 74 nm³; this corresponds to an approximate mass of 67 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](#)

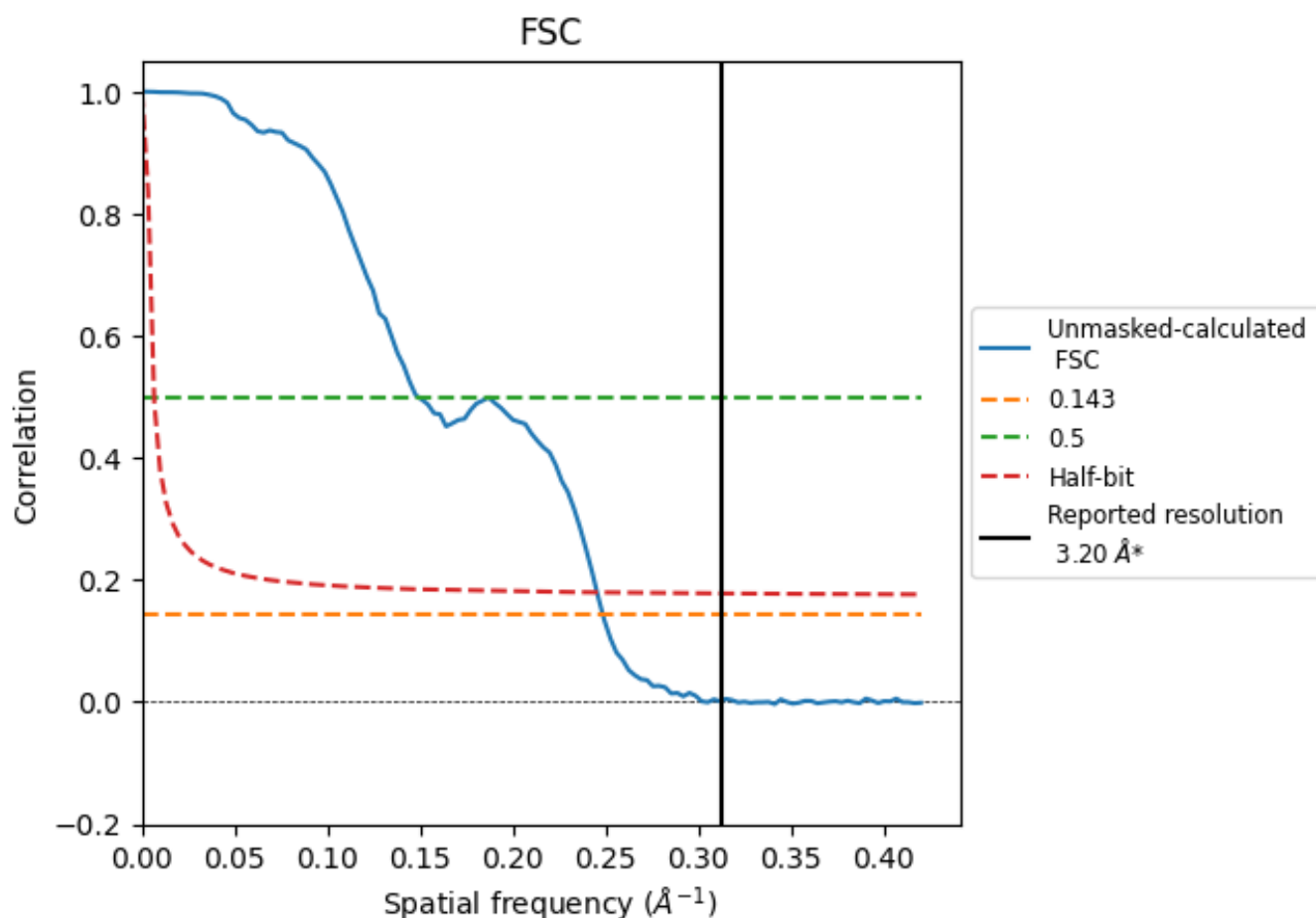


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

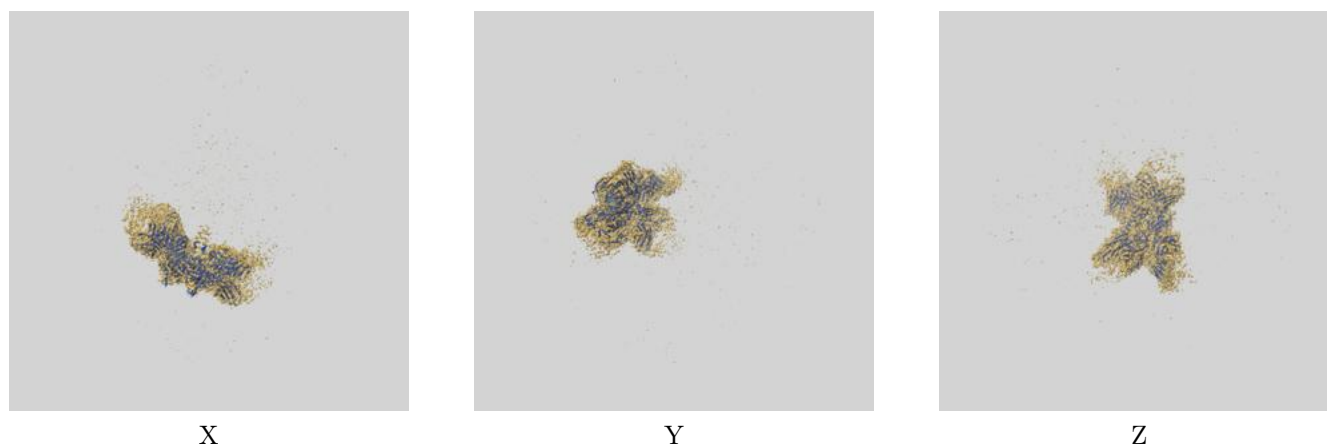
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.02	6.72	4.07

*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 4.02 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

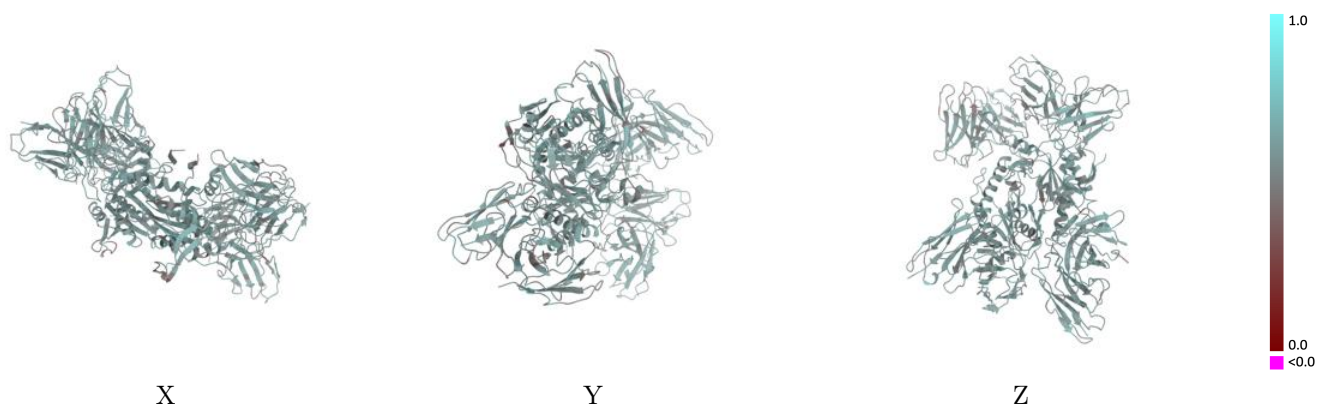
This section contains information regarding the fit between EMDB map EMD-44440 and PDB model 9BCV. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



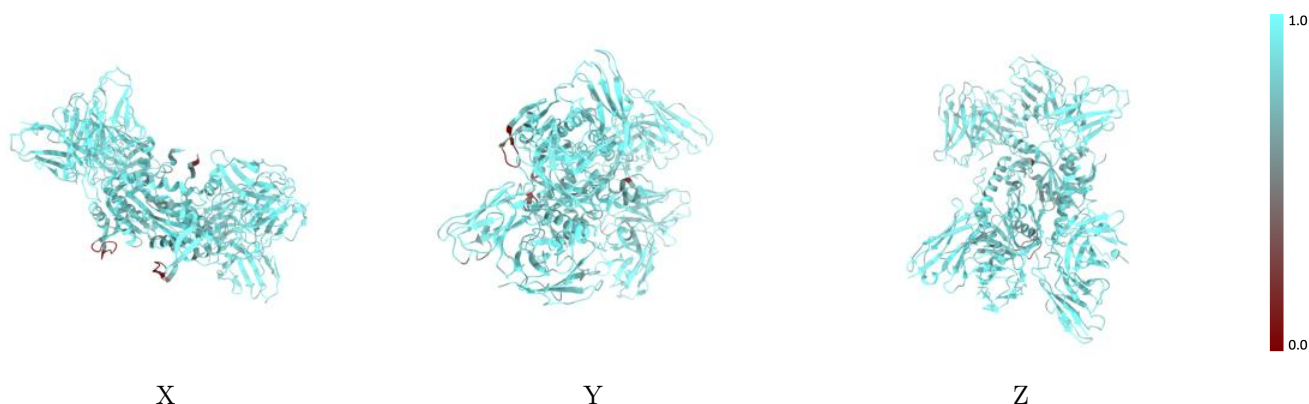
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



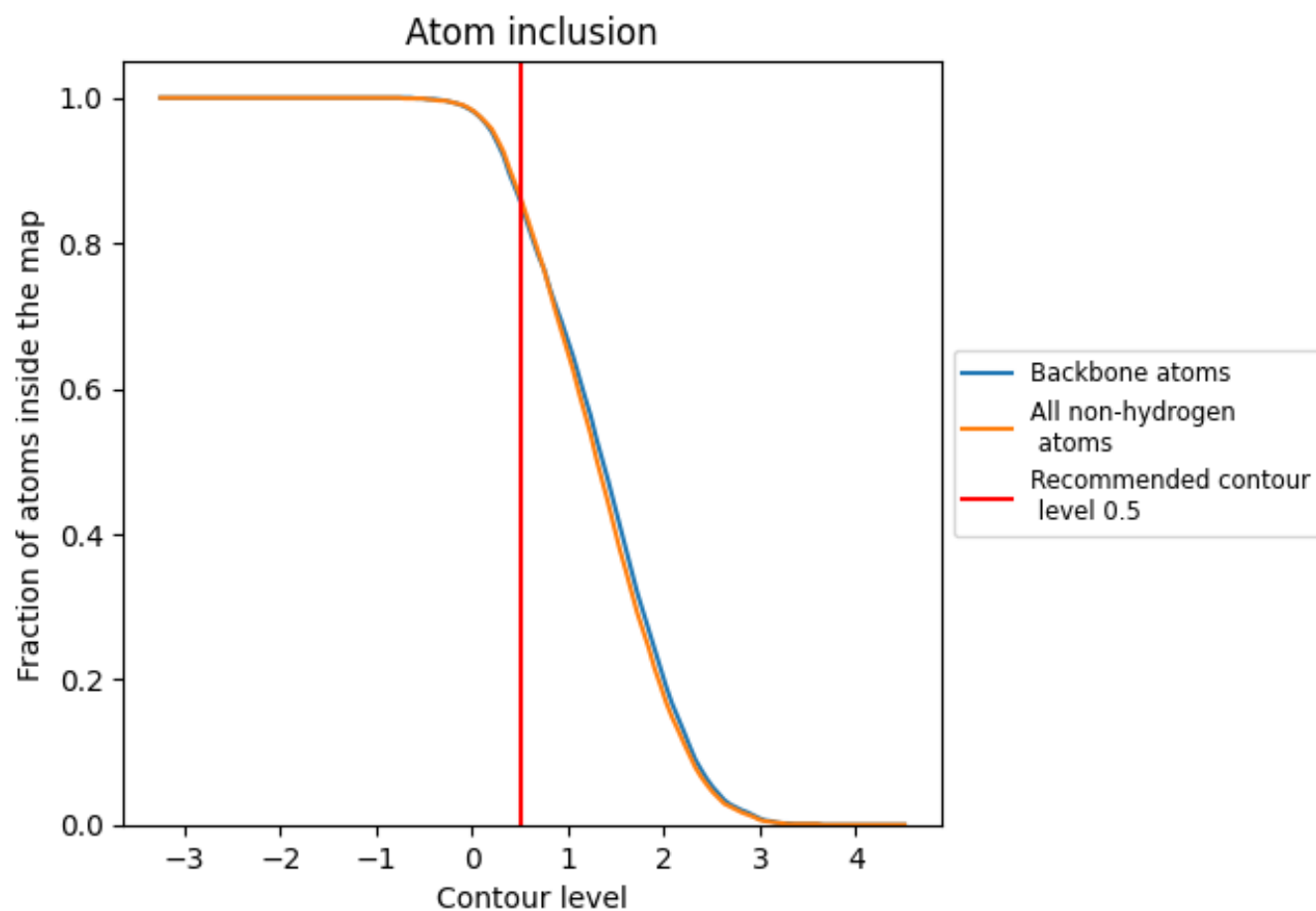
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8630	<div><div></div></div> 0.5640
A	<div><div></div></div> 0.8450	<div><div></div></div> 0.5730
B	<div><div></div></div> 0.8430	<div><div></div></div> 0.5730
C	<div><div></div></div> 0.8800	<div><div></div></div> 0.5540
D	<div><div></div></div> 0.8750	<div><div></div></div> 0.5570
E	<div><div></div></div> 0.8840	<div><div></div></div> 0.5670
F	<div><div></div></div> 0.8980	<div><div></div></div> 0.5600
G	<div><div></div></div> 0.8890	<div><div></div></div> 0.5590
H	<div><div></div></div> 0.8860	<div><div></div></div> 0.5670
I	<div><div></div></div> 0.8520	<div><div></div></div> 0.5520
J	<div><div></div></div> 0.8500	<div><div></div></div> 0.5410

1.0

0.0

<0.0