wwPDB EM Validation Summary Report (i)

Dec 19, 2024 – 04:08 PM EST

PDB ID	:	9DQD
EMDB ID	:	EMD-47111
Title	:	cryo-EM structure of human Cereblon/DDB1 in complex with a non-traditional CRBN binder
Authors	:	Zhu, J.; Pagarigan, B.
Deposited on	:	2024-09-23
Resolution	:	3.00 Å(reported)
Based on initial model	:	8D81

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 (i) 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 (i)) were used in the production of this report:

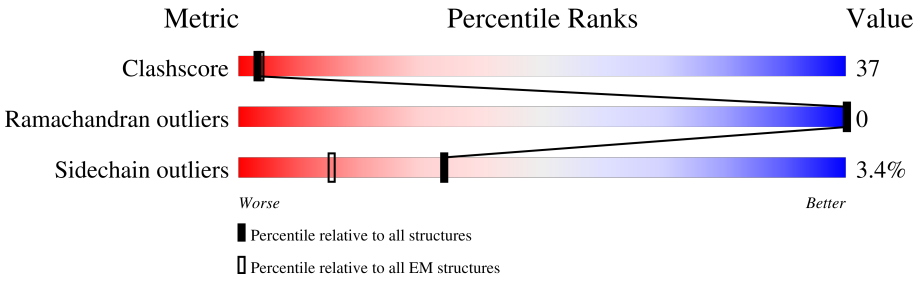
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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)
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 <=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	467	25% 52% 20%
2	B	836	57% 38%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9409 atoms, of which 24 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 Protein cereblon.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	373	3010	1922	515	550	23	0	0

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MET	-	initiating methionine	UNP Q96SW2
A	-23	SER	-	expression tag	UNP Q96SW2
A	-22	TYR	-	expression tag	UNP Q96SW2
A	-21	TYR	-	expression tag	UNP Q96SW2
A	-20	HIS	-	expression tag	UNP Q96SW2
A	-19	HIS	-	expression tag	UNP Q96SW2
A	-18	HIS	-	expression tag	UNP Q96SW2
A	-17	HIS	-	expression tag	UNP Q96SW2
A	-16	HIS	-	expression tag	UNP Q96SW2
A	-15	HIS	-	expression tag	UNP Q96SW2
A	-14	ASP	-	expression tag	UNP Q96SW2
A	-13	TYR	-	expression tag	UNP Q96SW2
A	-12	ASP	-	expression tag	UNP Q96SW2
A	-11	ILE	-	expression tag	UNP Q96SW2
A	-10	PRO	-	expression tag	UNP Q96SW2
A	-9	THR	-	expression tag	UNP Q96SW2
A	-8	THR	-	expression tag	UNP Q96SW2
A	-7	GLY	-	expression tag	UNP Q96SW2
A	-6	LEU	-	expression tag	UNP Q96SW2
A	-5	VAL	-	expression tag	UNP Q96SW2
A	-4	PRO	-	expression tag	UNP Q96SW2
A	-3	ARG	-	expression tag	UNP Q96SW2
A	-2	GLY	-	expression tag	UNP Q96SW2
A	-1	SER	-	expression tag	UNP Q96SW2
A	0	MET	-	expression tag	UNP Q96SW2

- Molecule 2 is a protein called DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	808	Total	C	N	O	S	0	0
			6349	4027	1069	1219	34		

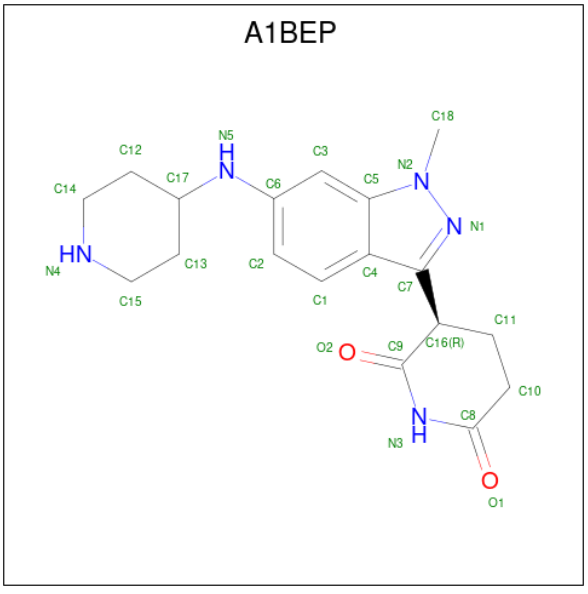
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	700	GLY	-	linker	UNP Q16531
B	701	ASN	-	linker	UNP Q16531
B	702	GLY	-	linker	UNP Q16531
B	703	ASN	-	linker	UNP Q16531
B	704	SER	-	linker	UNP Q16531
B	705	GLY	-	linker	UNP Q16531

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	

- Molecule 4 is (3R)-3-{1-methyl-6-[(piperidin-4-yl)amino]-1H-indazol-3-yl}piperidine-2,6-dione (three-letter code: A1BEP) (formula: $C_{18}H_{23}N_5O_2$) (labeled as "Ligand of Interest" by depositor).



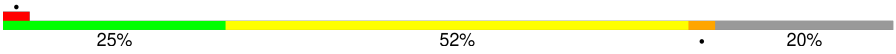
Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	H	N	O	0
			49	18	24	5	2	

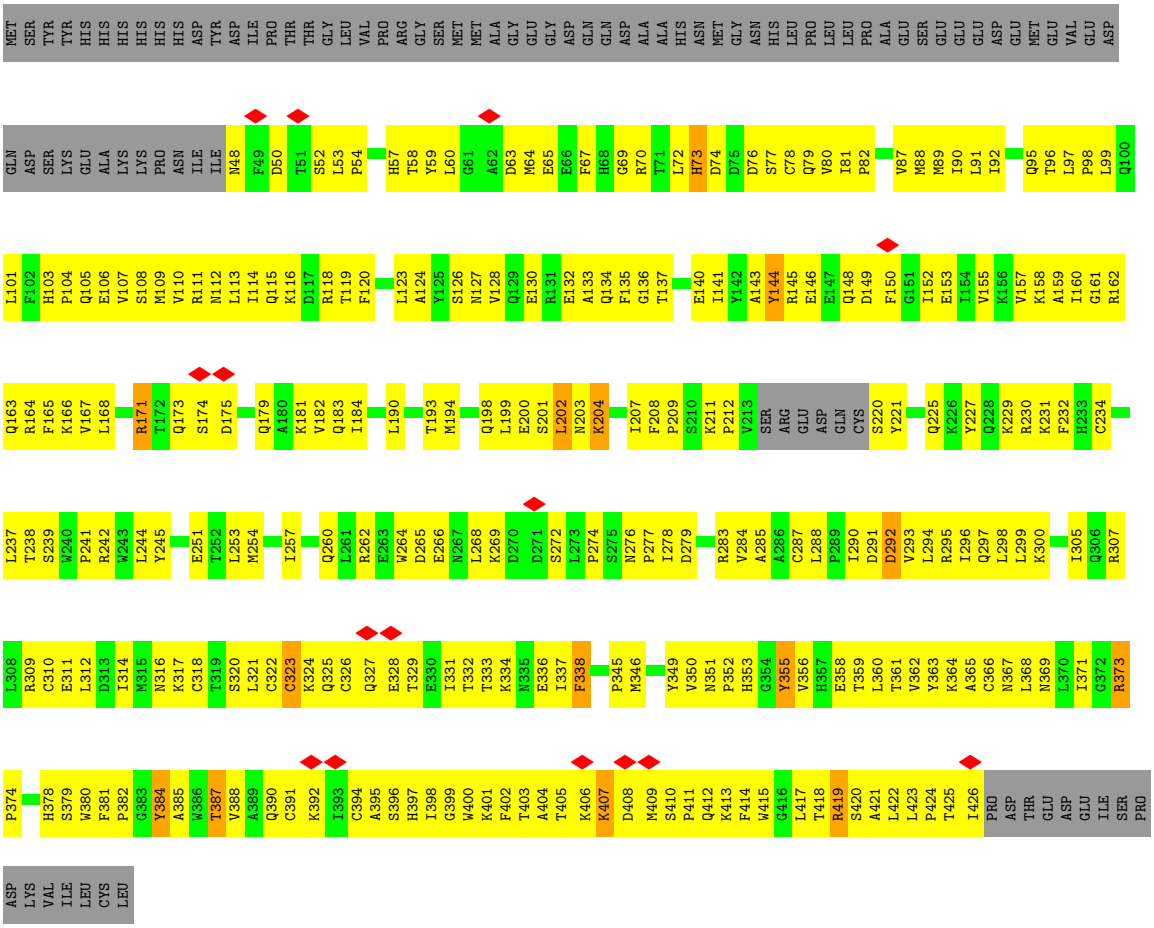
3 Residue-property plots (i)

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: Protein cereblon

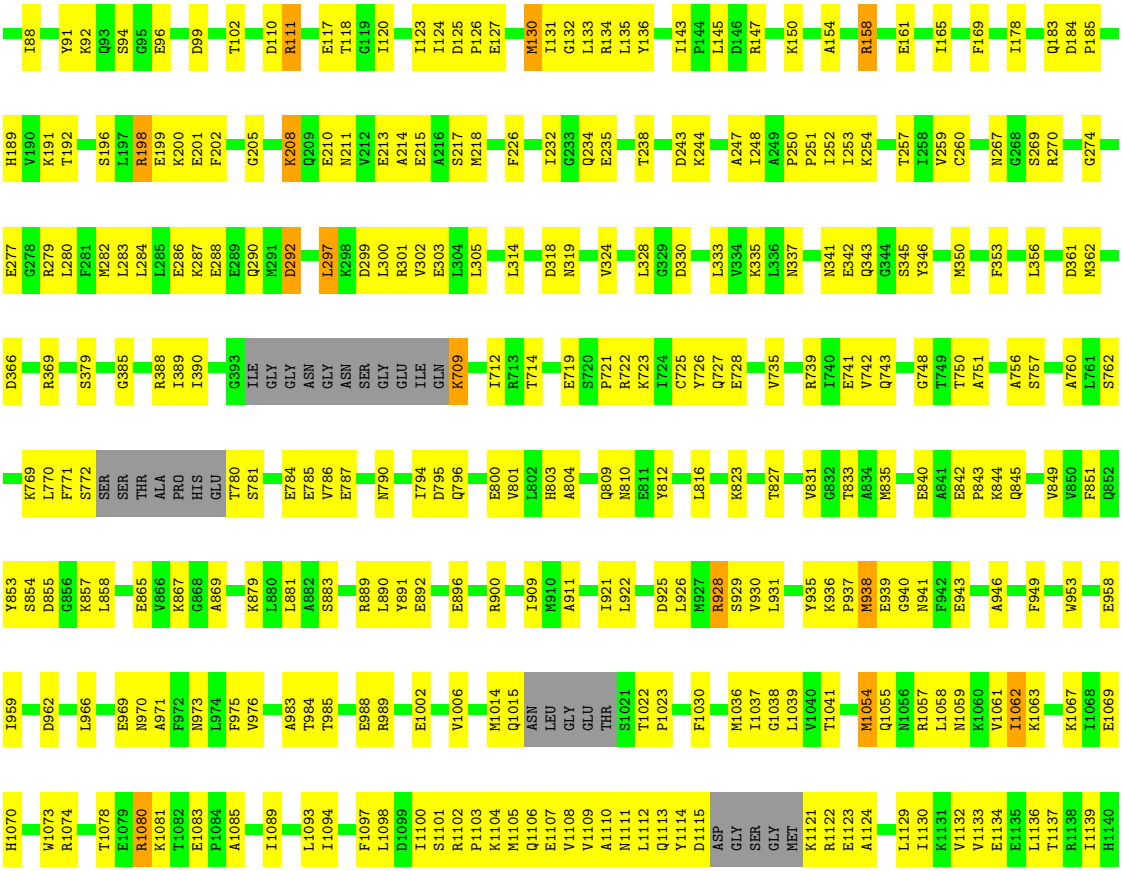
Chain A:





• Molecule 2: DNA damage-binding protein 1

Chain B:


I88 Y91 K92 Q93 S94 G95 E96 D99 T102 D110 R111 E117 T118 G119 I120 I123 I124 D125 P126 E127 M130 I131 G132 L133 R134 L135 Y136 I143 P144 L145 D146 R147 K150 A154 R158 E161 I165 F169 I178 Q183 D184 P185
H189 V190 K191 T192 S196 L197 R198 E199 K200 E201 F202 G205 K208 Q209 E210 N211 V212 E213 A214 E215 A216 S217 M218 F226 I232 G233 Q234 E235 T238 D243 K244 A247 I248 A249 P250 P251 I252 I253 K254 T257 I258 V259 C260 N267 G268 S269 R270 G274
E277 G278 R279 L280 F281 M282 L283 L284 L285 E286 K287 E288 E289 Q290 M291 D292 L297 K298 D299 L300 R301 V302 E303 L304 L305 L314 D318 N319 V324 L328 G329 D330 L333 V334 K335 L336 N337 N341 E342 Q343 G344 S345 Y346 M350 F353 L356 D361 M362
D366 R369 S379 G385 R388 I389 I390 G393 ILE GLY GLY ASN GLY ASN SER GLY GLU ILE GLN K709 I712 R713 T714 E719 S720 P721 R722 K723 I724 C725 Y726 Q727 E728 V735 R739 I740 E741 V742 Q743 G748 T749 T750 A751 A756 S757 A760 L761 S762
K769 L770 F771 S772 SER SER THR ALA PRO HIS GLU T780 S781 E784 E785 V786 E787 N790 I794 D795 Q796 E800 V801 L802 H803 A804 Q809 N810 E811 Y812 L816 K823 T827 V831 G832 T833 A834 M835 E840 A841 E842 P843 K844 Q845 V849 V850 F851 Q852
Y853 S854 D855 G856 K857 L858 E865 V866 K867 G868 A869 K879 L880 L881 A882 S883 R889 L890 Y891 E892 E896 R900 I909 M910 A911 I921 L922 D925 L926 M927 R928 S929 V930 L931 Y935 K936 P937 M938 E939 G940 N941 F942 E943 A946 F949 W953 E958
I959 D962 L966 E969 N970 A971 F972 N973 L974 F975 V976 A983 T984 T985 E988 R989 E1002 V1006 M1014 Q1015 ASN LEU GLY GLU THR S1021 T1022 P1023 F1030 M1036 I1037 G1038 L1039 V1040 T1041 M1064 Q1055 N1056 R1057 L1058 N1059 K1060 V1061 I1062 K1063 K1067 I1068 E1069
H1070 W1073 R1074 T1078 E1079 R1080 K1081 T1082 E1083 P1084 A1085 I1089 L1093 I1094 F1097 L1098 D1099 I1100 S1101 R1102 P1103 K1104 M1105 Q1106 E1107 V1108 V1109 A1110 N1111 L1112 Q1113 Y1114 D1115 ASP GLY SER GLY MET K1121 R1122 E1123 A1124 L1129 I1130 K1131 V1132 V1133 E1134 E1135 L1136 T1137 R1138 I1139 H1140

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	81146	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 ($e^-/Å^2$)	27.67, 39.28	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON IV (4k x 4k), FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.017	Depositor
Minimum map value	-0.994	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	0.064	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	229.9, 229.9, 229.9	wwPDB
Map dimensions	220, 220, 220	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	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, A1BEP

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	0.25	0/3082	0.47	0/4180
2	B	0.27	0/6461	0.49	0/8735
All	All	0.26	0/9543	0.48	0/12915

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

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	3010	0	3004	379	0
2	B	6349	0	6321	332	0
3	A	1	0	0	0	0
4	A	25	24	0	3	0
All	All	9385	24	9325	696	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 37.

The worst 5 of 696 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)
2:B:43:VAL:HG23	2:B:52:VAL:HG21	1.34	1.08
1:A:318:CYS:HA	1:A:426:ILE:HG22	1.34	1.05
1:A:168:LEU:HD11	1:A:181:LYS:HG3	1.42	1.01
2:B:143:ILE:HG12	2:B:154:ALA:HB2	1.39	1.01
1:A:321:LEU:HD11	1:A:422:LEU:HB3	1.39	1.00

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	369/467 (79%)	347 (94%)	22 (6%)	0	100	100
2	B	798/836 (96%)	752 (94%)	46 (6%)	0	100	100
All	All	1167/1303 (90%)	1099 (94%)	68 (6%)	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	337/421 (80%)	320 (95%)	17 (5%)	20	53
2	B	704/727 (97%)	686 (97%)	18 (3%)	41	72
All	All	1041/1148 (91%)	1006 (97%)	35 (3%)	34	66

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	867	LYS
2	B	928	ARG
2	B	1054	MET
1	A	381	PHE
1	A	373	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	367	ASN
2	B	183	GLN
2	B	727	GLN
2	B	337	ASN
1	A	127	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 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\#\|Z\|>2$
4	A1BEP	A	502	-	23,28,28	0.78	1 (4%)	29,40,40	0.78	2 (6%)

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
4	A1BEP	A	502	-	-	0/4/29/29	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	502	A1BEP	C7-N1	-2.82	1.30	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	502	A1BEP	C7-N1-N2	2.43	106.58	104.48
4	A	502	A1BEP	C4-C5-N2	-2.23	106.08	109.17

There are no chirality outliers.

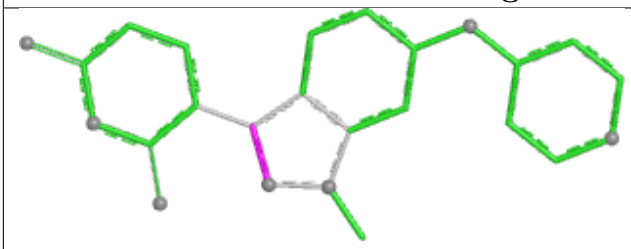
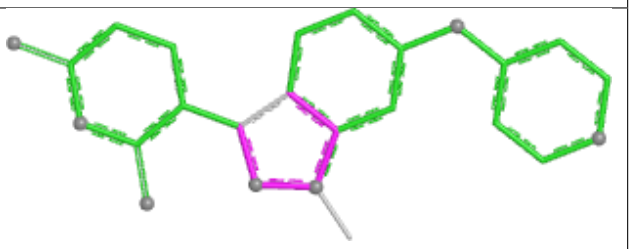
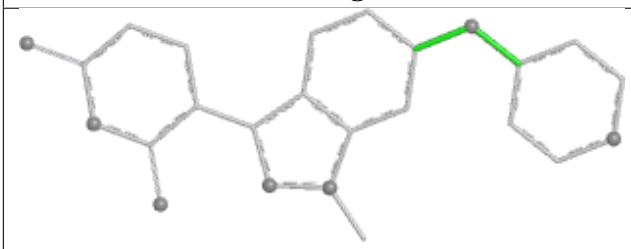
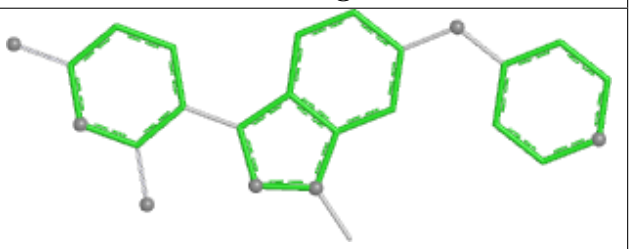
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	502	A1BEP	3	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 then 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.

Ligand A1BEP A 502	
 Bond lengths	 Bond angles
 Torsions	 Rings

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.

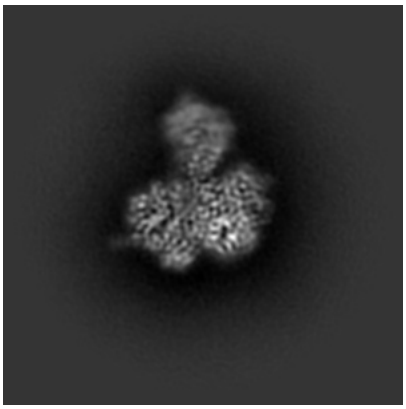
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-47111. These allow visual inspection of the internal detail of the map and identification of artifacts.

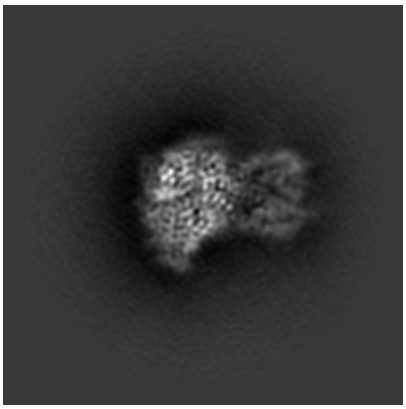
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

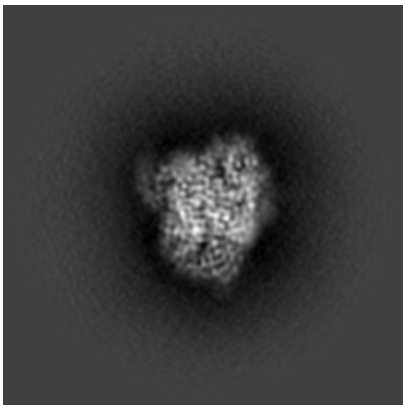
6.1.1 Primary map



X

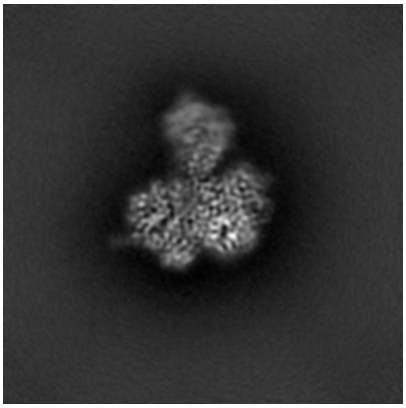


Y

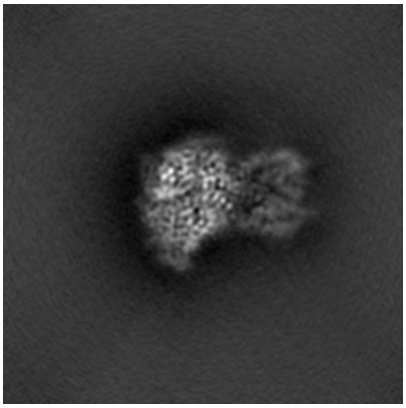


Z

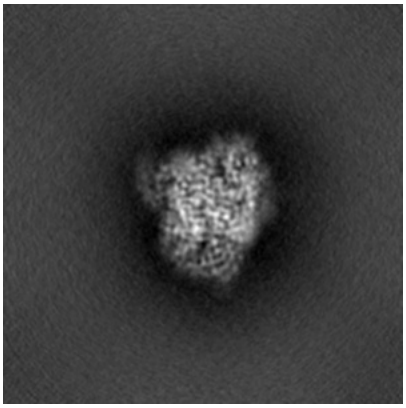
6.1.2 Raw map



X



Y

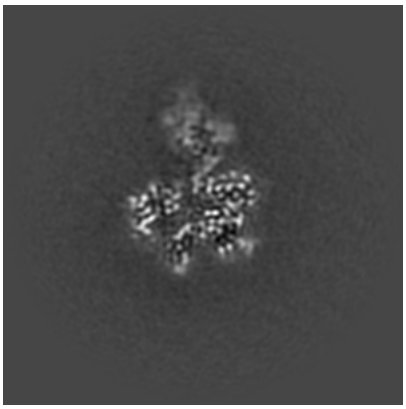


Z

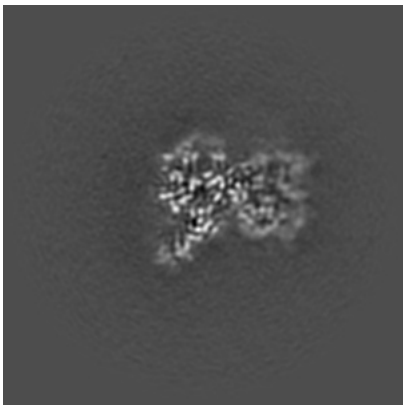
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

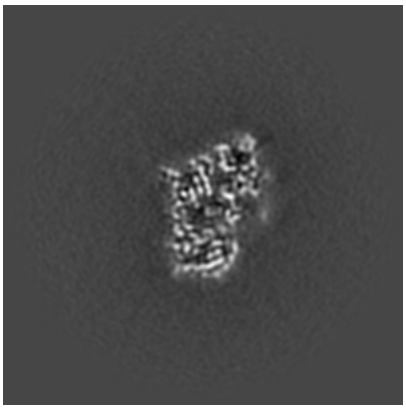
6.2.1 Primary map



X Index: 110

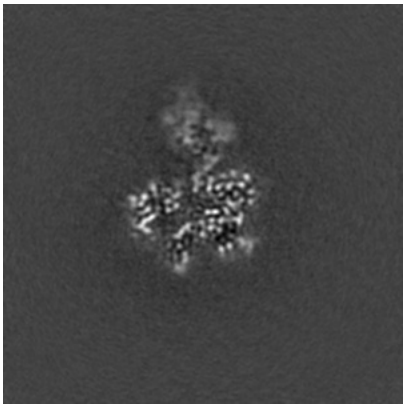


Y Index: 110

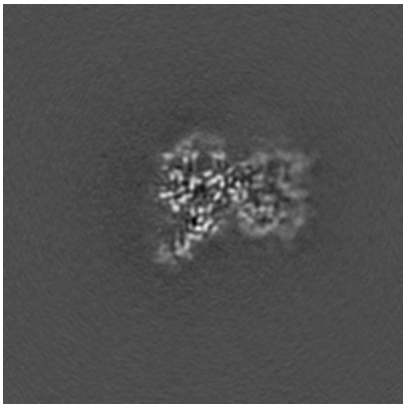


Z Index: 110

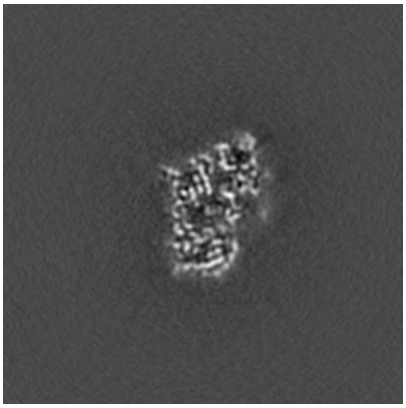
6.2.2 Raw map



X Index: 110



Y Index: 110

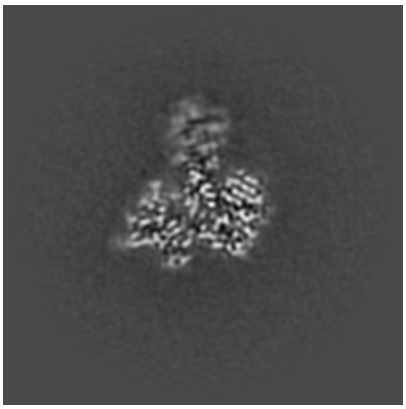


Z Index: 110

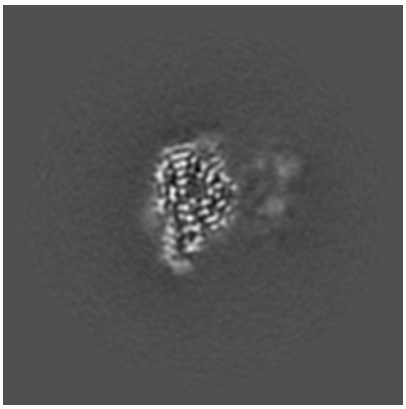
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

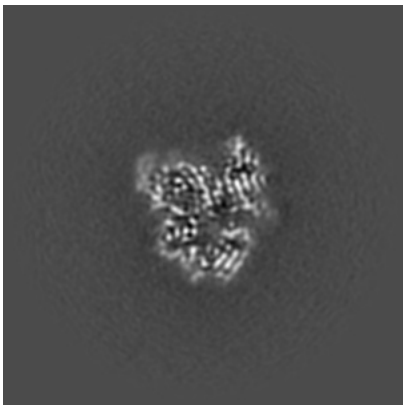
6.3.1 Primary map



X Index: 124

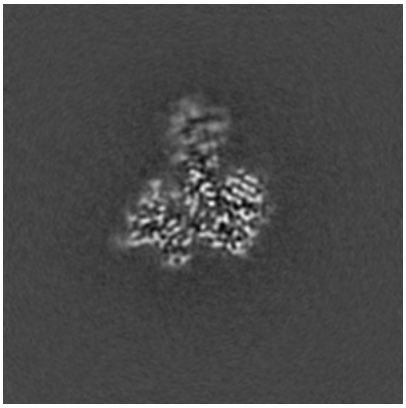


Y Index: 124

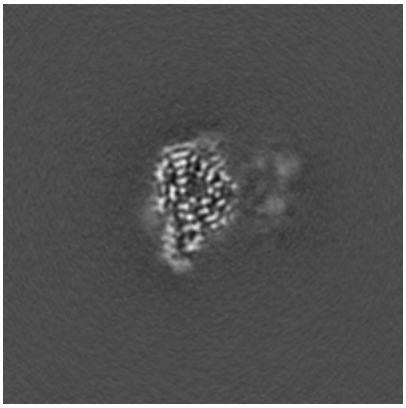


Z Index: 100

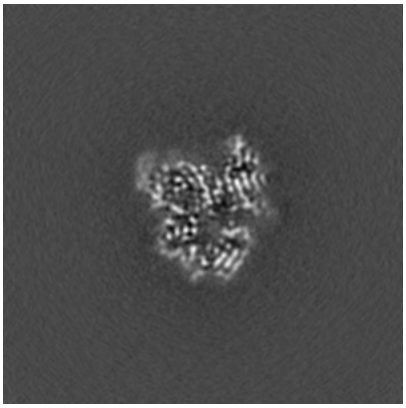
6.3.2 Raw map



X Index: 124



Y Index: 124

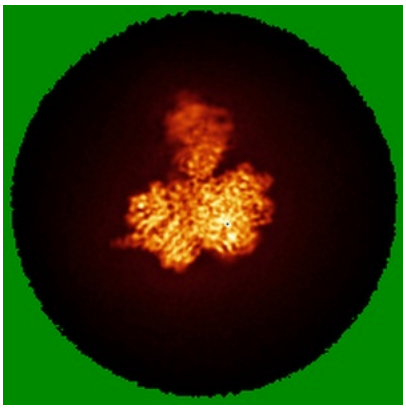


Z Index: 100

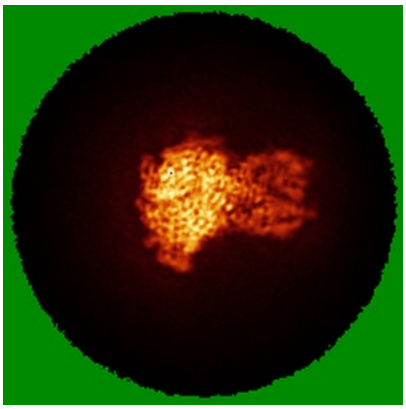
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

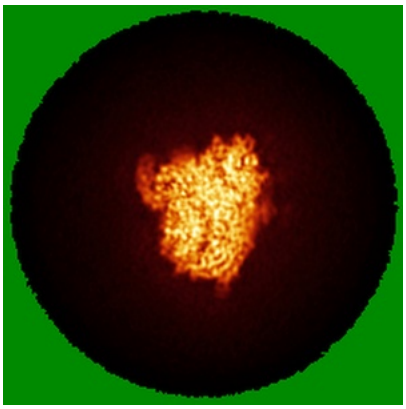
6.4.1 Primary map



X

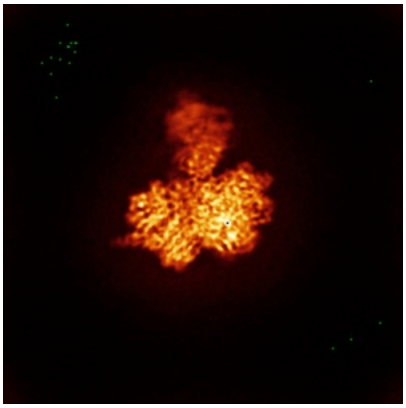


Y

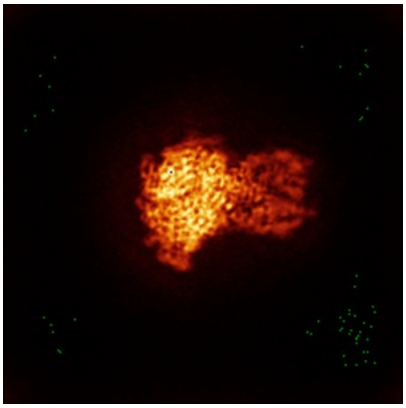


Z

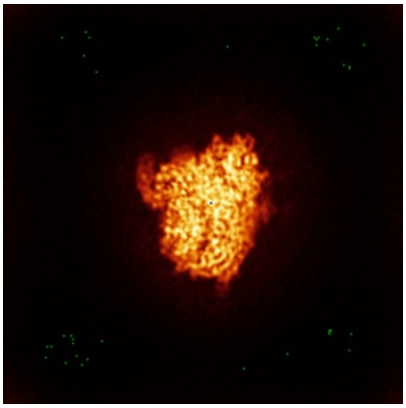
6.4.2 Raw map



X



Y

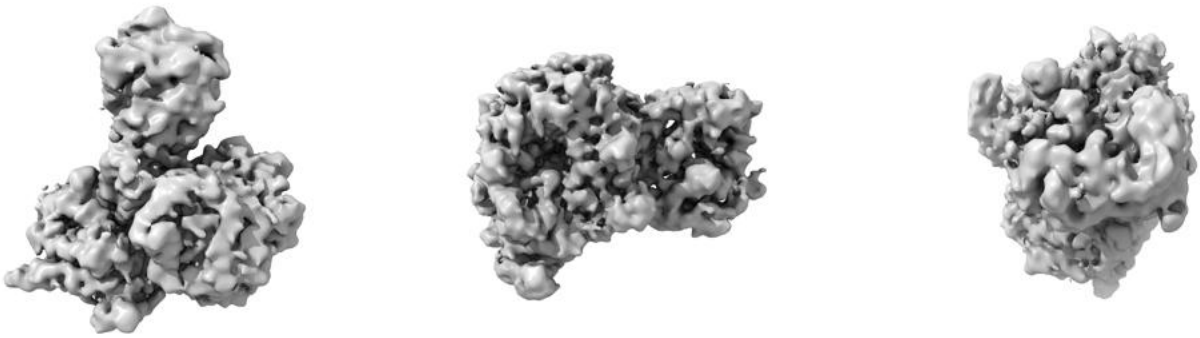


Z

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)

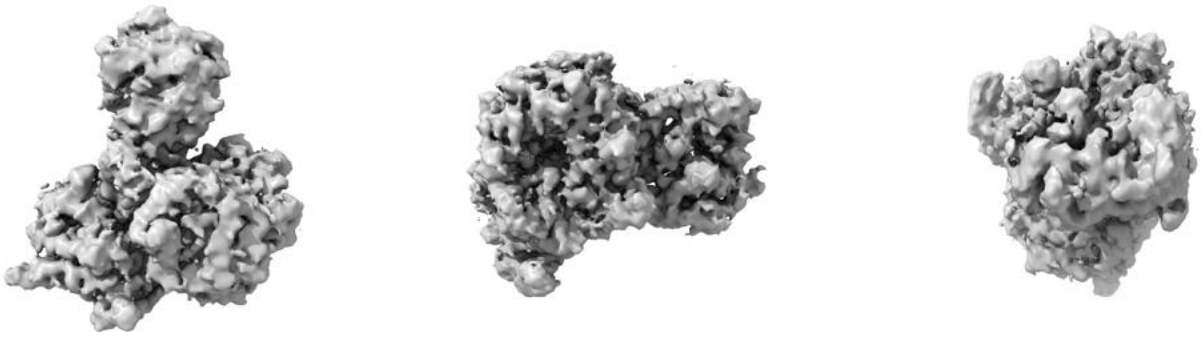
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. 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



X Y Z

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.

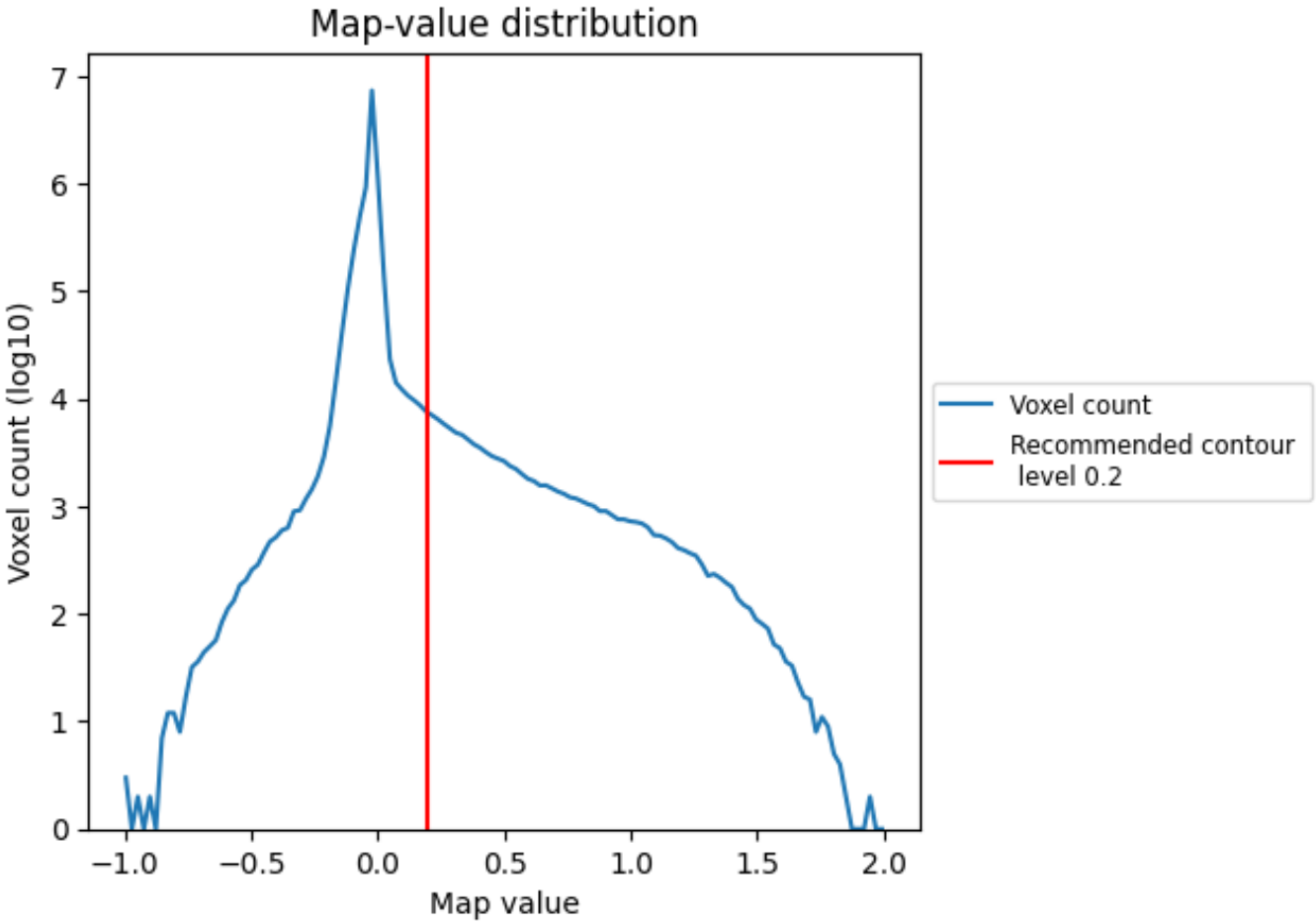
6.6 Mask visualisation (i)

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

7 Map analysis

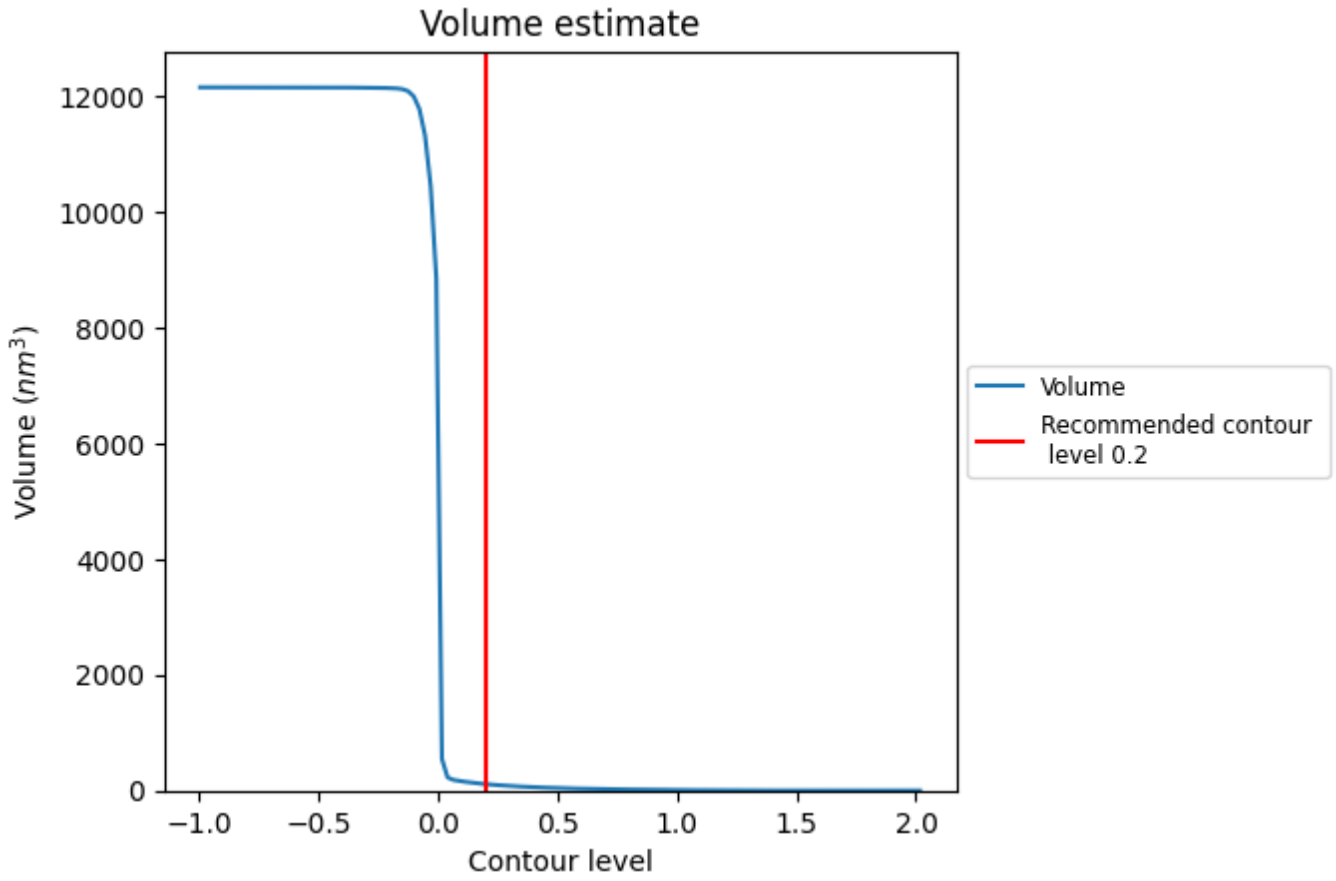
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

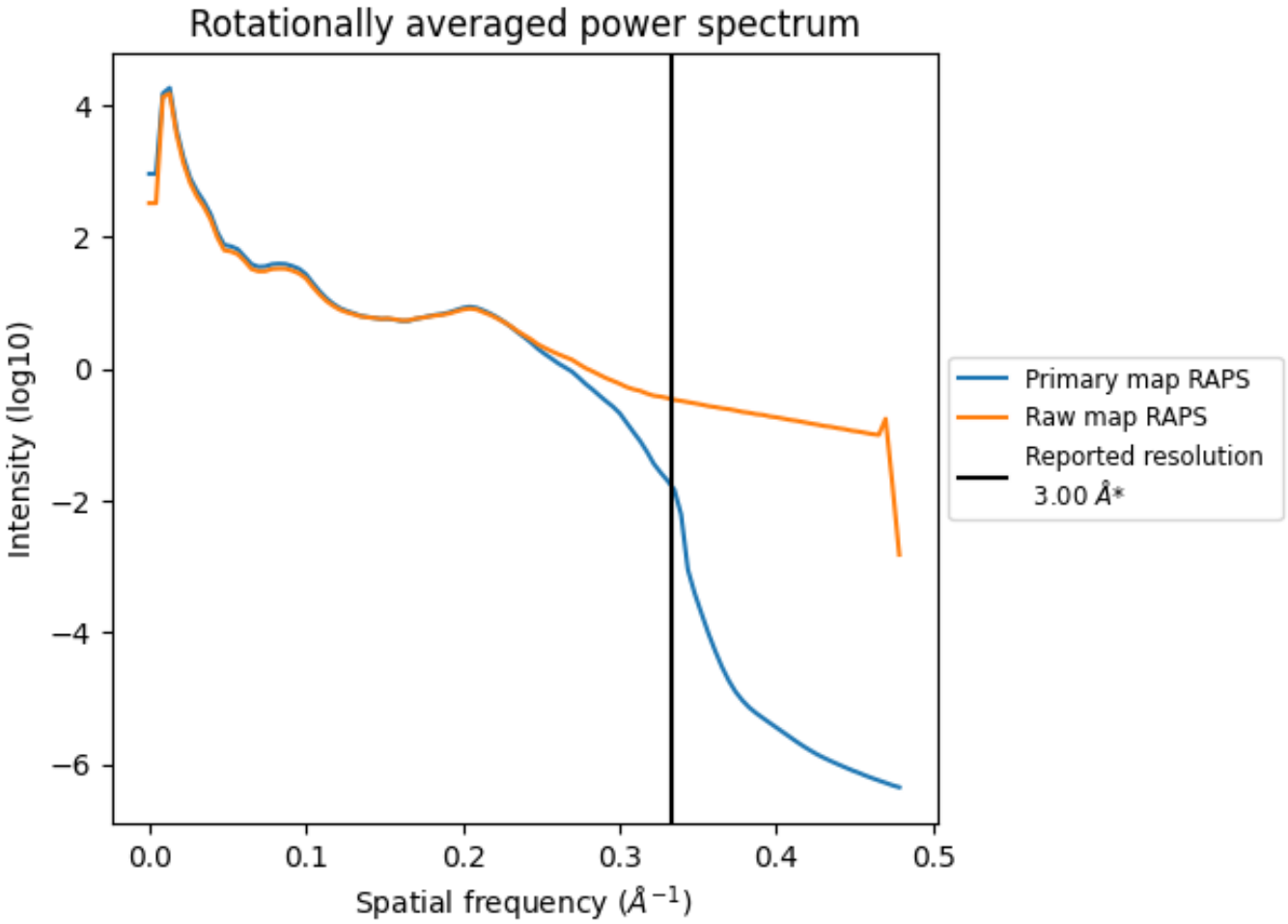
7.2 Volume estimate (i)



The volume at the recommended contour level is 112 nm^3; this corresponds to an approximate mass of 101 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)

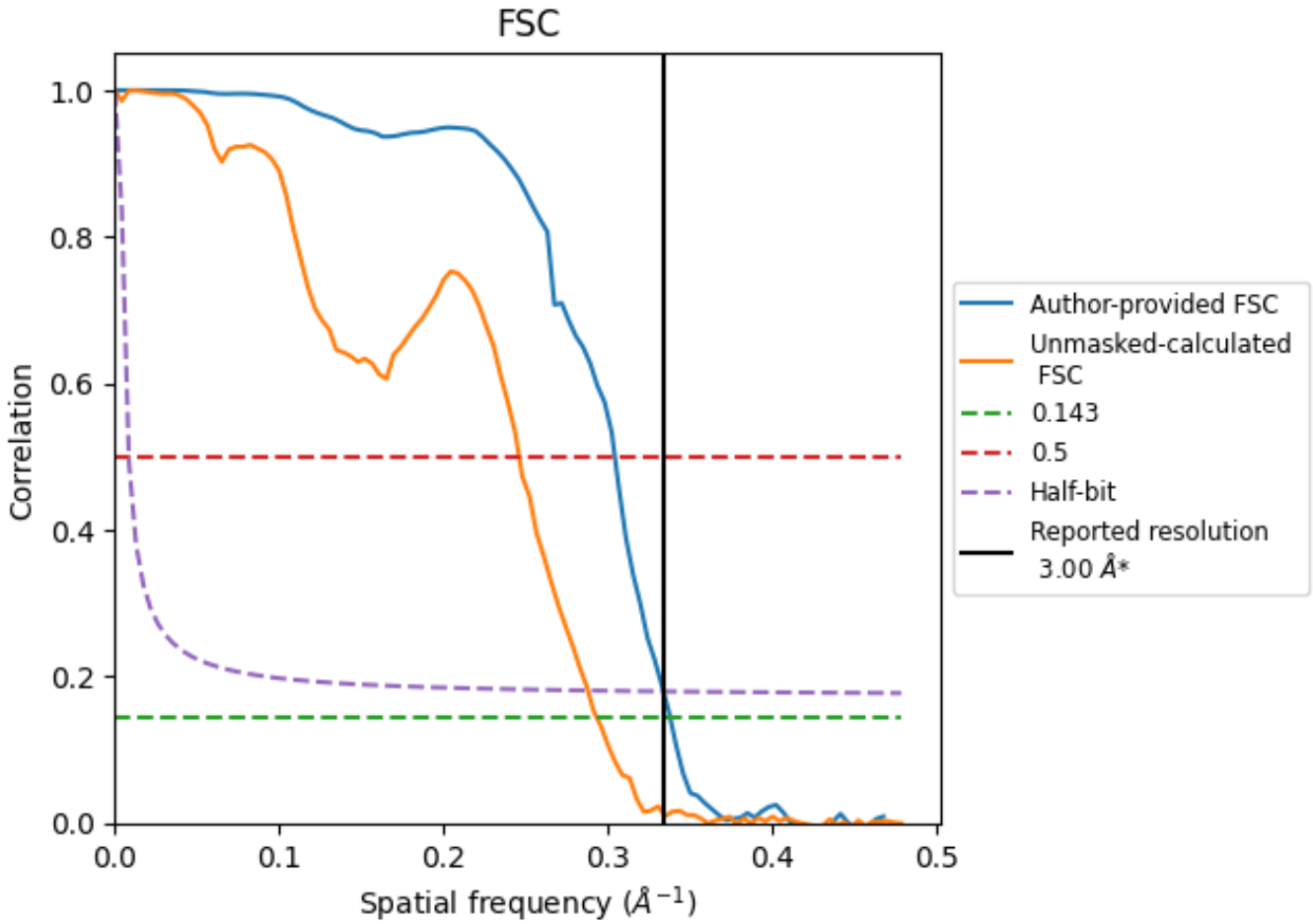


*Reported resolution corresponds to spatial frequency of 0.333 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.333 $Å^{-1}$

8.2 Resolution estimates (i)

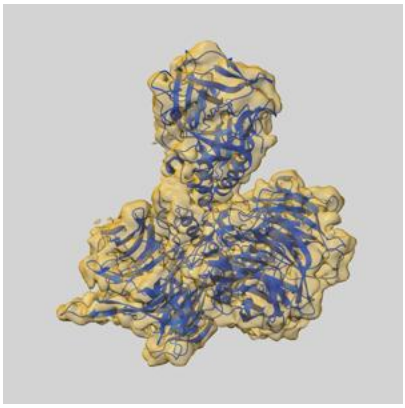
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.96	3.29	3.00
Unmasked-calculated*	3.41	4.07	3.47

*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 3.41 differs from the reported value 3.0 by more than 10 %

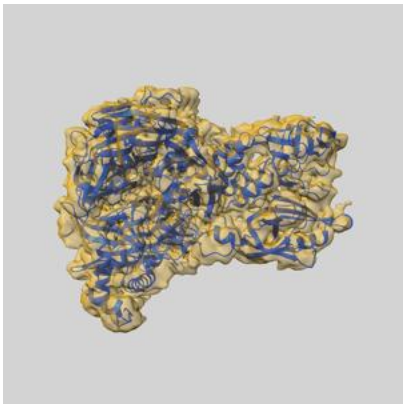
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-47111 and PDB model 9DQD. Per-residue inclusion information can be found in section 3 on page 5.

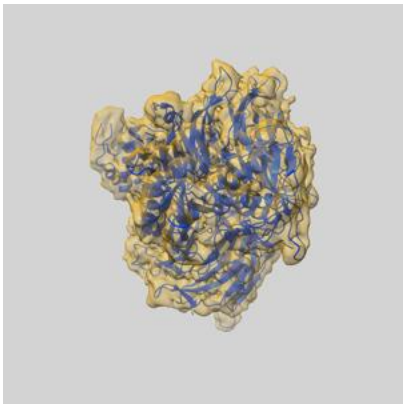
9.1 Map-model overlay



X



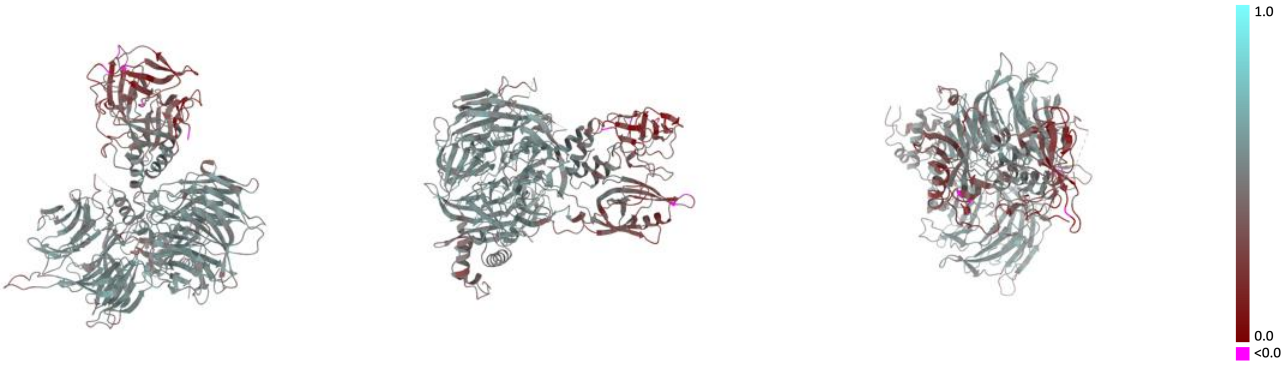
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2 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.

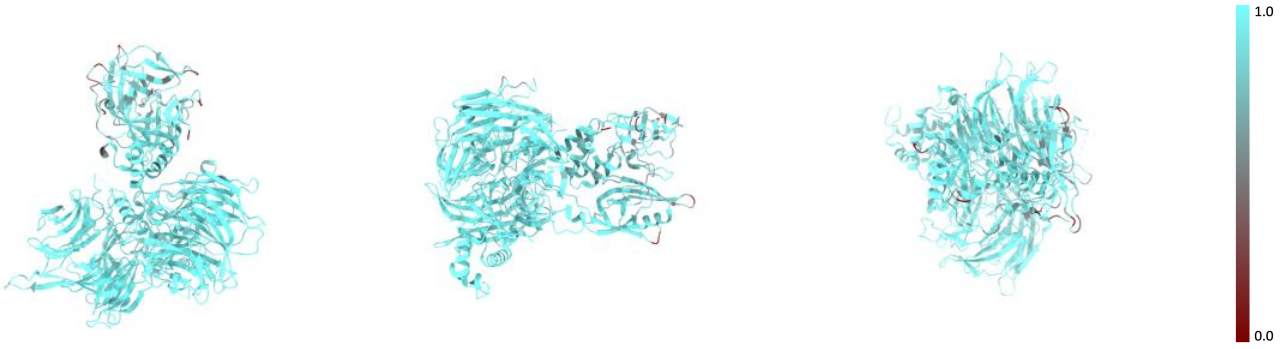
9.2 Q-score mapped to coordinate model



X Y Z

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.

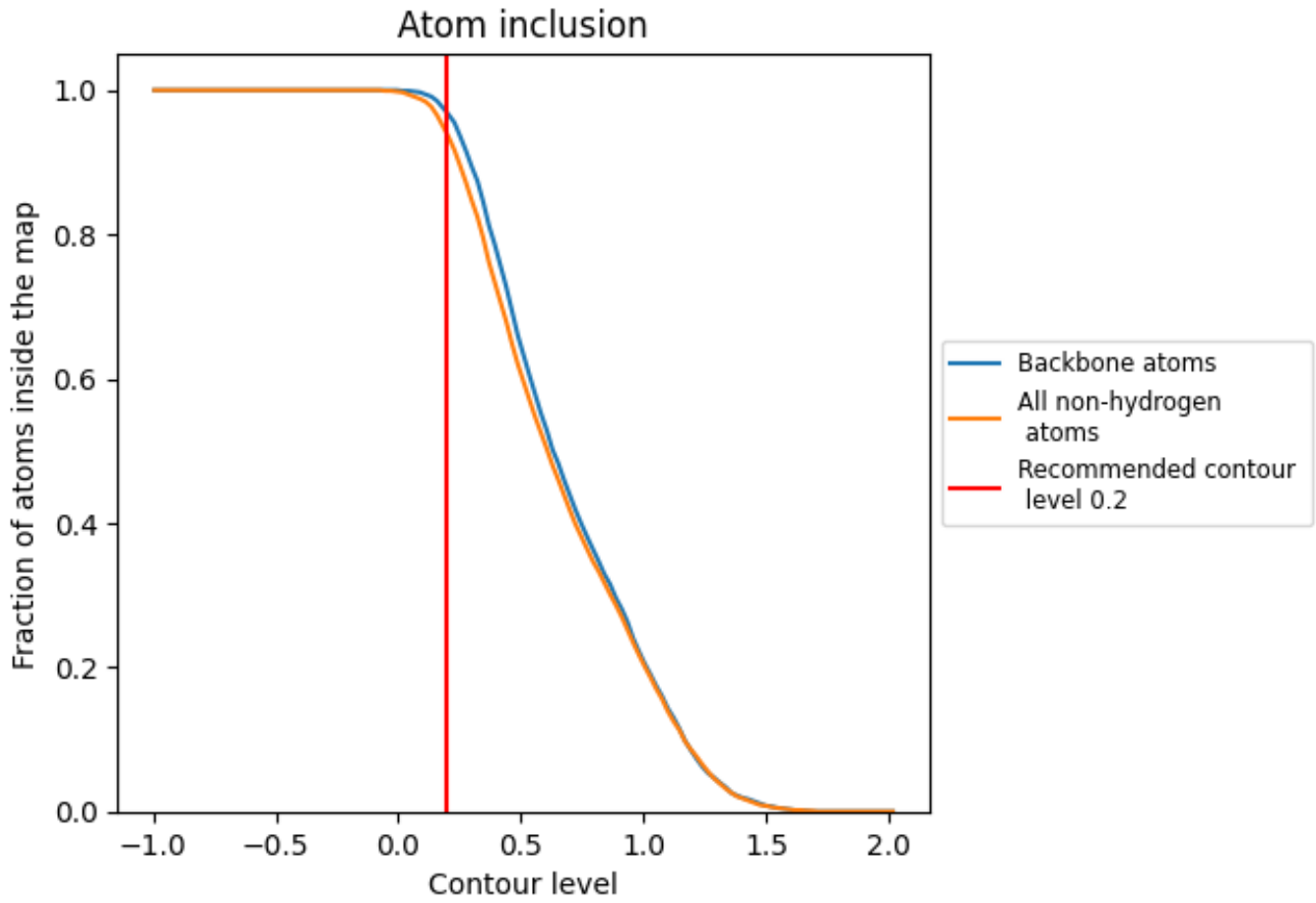
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.2).

9.4 Atom inclusion (i)



At the recommended contour level, 97% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9380	0.4670
A	0.8580	0.3600
B	0.9770	0.5180