



Full wwPDB EM Validation Report ⓘ

Jan 28, 2025 – 02:06 PM EST

PDB ID : 9BAP
EMDB ID : EMD-44410
Title : CryoEM structure of Apo-DIM2
Authors : Song, J.; Shao, Z.
Deposited on : 2024-04-04
Resolution : 2.88 Å(reported)

This is a Full wwPDB EM Validation 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.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

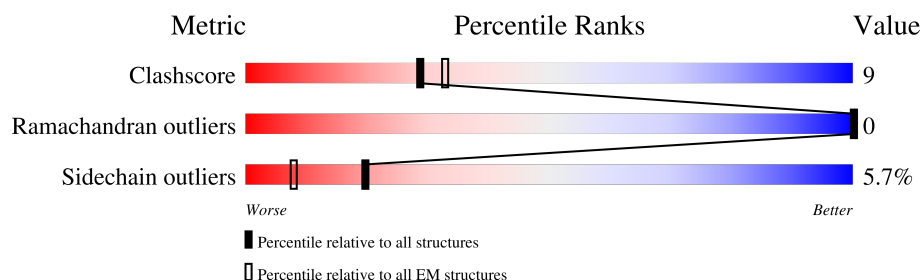
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.88 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	1456	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6535 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.

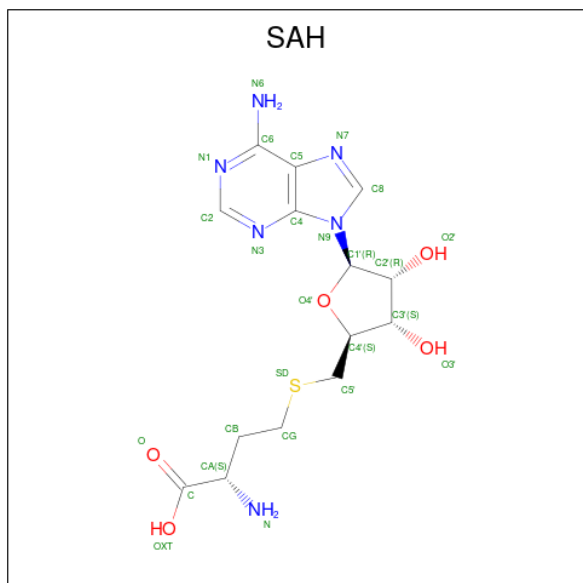
- Molecule 1 is a protein called DNA (cytosine-5-)-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	886	6508	4184	1151	1148	25	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q96W73
A	0	SER	-	expression tag	UNP Q96W73

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
2	A	1	26	14	6	5	1	0

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

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

GLY	GLY	V1216	HIS	VAL
MET	THR	G1217	THR	ASP
ASN	ALA	N1218	ALA	GLU
PHE	VAL	S1219	VAL	GLU
ILE	ASP	V1220	GLY	MET
LYS	LEU		LEU	ARG
ALA	ASP	L1226	ASP	PRO
TRP	ASP		ASP	ASP
ASN	ASP	E1234	LYS	LYS
GLY	LYS	A1235	GLY	VAL
ASN	GLY	W1236	GLN	GLY
GLY	L1237	L1237	LYS	VAL
VAL	G1238	G1238	ARG	ASP
MET	T1239	T1239	SER	VAL
SER	L1240	L1240	GLU	GLU
LYS	Y1241	Y1241	THR	VAL
SER	ASP		THR	VAL
ASP	GLU		ALA	ALA
ARG	SER		PRO	SER
LEU	ALA		ALA	PRO
PHE	VAL		VAL	GLU
PRO	VAL		LEU	ASP
SER	ALA		SER	GLN
GLU	THR		THR	ALA
GLY	ALA		SER	GLY
LYS	ALA		GLY	ARG
THR	ALA		ASP	ASN
THR	ALA		GLY	PRO
SER	ALA		SER	SER
ALA	ALA		ALA	THR
SER	VAL		ASN	ALA
VAL	GLY		ALA	SER
GLY	VAL		ALA	PRO
G1183	THR		GLY	THR
L1161	VAL		LEU	MET
R1186	PRO		GLU	THR
	VAL		ASP	VAL
	MET		ASP	LYS
	GLU		ASN	ALA
T1189	GLU		LYS	SER
V1190	PRO		ALA	GLY
Q1191	GLY		THR	THR
	ILE		THR	ILE
Q1197	GLY		HIS	LYS
G1198	THR		GLU	ALA
Y1199	THR		MET	PRO
L1200	GLU		MET	ALA
D1201	SER		ALA	ALA
	SER		PRO	PRO
L1205	ARG		THR	GLU
V1206	ARG		ARG	GLU
	PRO		LYS	LEU
T1209	SER		ARG	GLU
Q1212	ARG		SER	SER
	PRO		PRO	ASP
	VAL		ALA	ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	529317	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.022	Depositor
Minimum map value	-1.235	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.029	Depositor
Recommended contour level	0.101	Depositor
Map size (Å)	273.92, 273.92, 273.92	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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, SAH

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	0.26	0/6693	0.50	0/9158

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	6508	0	5898	114	0
2	A	26	0	19	3	0
3	A	1	0	0	0	0
All	All	6535	0	5917	114	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 9.

All (114) 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:1234:GLU:HB3	1:A:1239:THR:HG23	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:748:ARG:NH2	1:A:1063:ALA:O	2.27	0.67
1:A:904:GLU:N	1:A:904:GLU:OE1	2.27	0.66
1:A:392:ARG:HA	1:A:892:LEU:HB3	1.77	0.65
1:A:1191:GLN:NE2	1:A:1201:ASP:OD1	2.30	0.65
1:A:385:VAL:HG23	1:A:387:PRO:HD2	1.78	0.64
1:A:1205:LEU:HD23	1:A:1212:GLN:HB3	1.78	0.64
1:A:193:PHE:HA	1:A:224:ASP:O	1.98	0.63
1:A:229:TYR:O	1:A:232:THR:OG1	2.16	0.62
1:A:294:ALA:O	1:A:298:LYS:N	2.33	0.61
1:A:611:TYR:N	1:A:630:PHE:O	2.31	0.61
1:A:656:VAL:HG22	1:A:669:PHE:HB2	1.83	0.61
1:A:854:ARG:HH21	1:A:1199:TYR:HE1	1.49	0.60
1:A:725:TYR:HB3	1:A:743:LEU:HB3	1.84	0.59
1:A:872:ASP:N	1:A:872:ASP:OD1	2.34	0.59
1:A:1000:ILE:HD12	1:A:1031:PRO:HD3	1.85	0.59
1:A:412:ILE:HD12	1:A:896:ASP:HB3	1.85	0.58
1:A:846:TYR:HB3	2:A:1501:SAH:O4'	2.03	0.58
1:A:209:ILE:HA	1:A:212:VAL:HB	1.85	0.57
1:A:266:HIS:ND1	1:A:267:ASN:OD1	2.38	0.57
1:A:248:ASN:HA	1:A:253:LEU:HD13	1.86	0.57
1:A:392:ARG:HG2	1:A:892:LEU:HG	1.87	0.56
1:A:377:GLN:HA	1:A:380:ARG:HB2	1.88	0.56
1:A:219:ASP:N	1:A:219:ASP:OD1	2.38	0.55
1:A:1209:THR:HA	1:A:1212:GLN:HG3	1.87	0.55
1:A:844:ASP:HB2	1:A:864:MET:SD	2.46	0.55
1:A:224:ASP:HB3	1:A:237:THR:HG22	1.90	0.54
1:A:414:THR:HB	1:A:417:ILE:HD13	1.89	0.54
1:A:316:LEU:HD13	1:A:382:LEU:HD21	1.89	0.54
1:A:1011:GLN:NE2	1:A:1197:GLN:OE1	2.38	0.53
1:A:878:TYR:O	1:A:882:THR:HG23	2.09	0.53
1:A:1010:PRO:HA	1:A:1161:LEU:HD12	1.89	0.53
1:A:782:MET:HG3	1:A:804:PHE:HB2	1.91	0.52
1:A:840:LEU:HB3	1:A:919:PHE:HB2	1.92	0.52
1:A:845:LEU:HD12	1:A:951:PHE:HD1	1.74	0.51
1:A:1218:ASN:O	2:A:1501:SAH:HB2	2.10	0.51
1:A:417:ILE:HG23	1:A:421:PHE:CD2	2.45	0.51
1:A:605:PHE:HB2	1:A:645:VAL:HG23	1.93	0.51
1:A:1212:GLN:O	1:A:1216:VAL:HG23	2.12	0.50
1:A:164:GLU:O	1:A:168:VAL:HG23	2.12	0.50
1:A:303:TYR:OH	1:A:322:ASP:OD2	2.23	0.50
1:A:1083:LYS:HB2	1:A:1084:PRO:HD3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:674:LEU:HD13	1:A:689:HIS:ND1	2.27	0.50
1:A:760:ASN:ND2	1:A:795:TYR:O	2.45	0.49
1:A:175:ALA:O	1:A:179:GLY:N	2.32	0.49
1:A:263:ARG:HE	1:A:273:TYR:HD2	1.59	0.49
1:A:390:TYR:H	1:A:876:HIS:HE1	1.60	0.49
1:A:412:ILE:HD11	1:A:900:ARG:HH11	1.77	0.49
1:A:263:ARG:HG2	1:A:273:TYR:HB3	1.95	0.48
1:A:261:TRP:HE1	1:A:275:LEU:HD12	1.79	0.48
1:A:421:PHE:HB3	1:A:426:LEU:HD22	1.96	0.48
1:A:300:VAL:HG21	1:A:360:ILE:HG23	1.95	0.48
1:A:1197:GLN:HG3	1:A:1216:VAL:HG12	1.97	0.47
1:A:412:ILE:HD13	1:A:900:ARG:HG2	1.95	0.47
1:A:283:TYR:CD2	1:A:287:TYR:HB2	2.50	0.47
1:A:292:TRP:HA	1:A:340:TRP:CD1	2.50	0.47
1:A:560:PRO:HG3	1:A:651:LEU:HD11	1.97	0.47
1:A:417:ILE:O	1:A:421:PHE:HB2	2.15	0.47
1:A:411:THR:HG21	1:A:946:SER:OG	2.15	0.46
1:A:186:ILE:HD12	1:A:186:ILE:HA	1.83	0.46
1:A:414:THR:HG22	1:A:416:TYR:H	1.80	0.46
1:A:171:LEU:HD23	1:A:188:PHE:CG	2.50	0.46
1:A:840:LEU:HD11	1:A:1236:TRP:NE1	2.31	0.46
1:A:214:THR:OG1	1:A:359:TYR:HA	2.16	0.46
1:A:297:GLY:HA3	1:A:359:TYR:HE2	1.81	0.46
1:A:800:THR:O	1:A:803:MET:HG3	2.15	0.46
1:A:1013:ARG:NH2	1:A:1220:VAL:HA	2.31	0.46
1:A:616:THR:HB	1:A:617:PRO:HD2	1.98	0.45
1:A:879:MET:SD	1:A:890:PRO:HG3	2.55	0.45
1:A:1000:ILE:HD13	1:A:1019:TYR:CE2	2.51	0.45
1:A:195:PHE:CD2	1:A:223:PHE:HB3	2.51	0.45
1:A:919:PHE:HE1	1:A:921:ALA:HB2	1.82	0.45
1:A:619:CYS:HB3	1:A:620:ALA:H	1.59	0.45
1:A:746:LEU:HD23	1:A:764:TYR:HA	1.98	0.45
1:A:686:GLN:HB2	1:A:689:HIS:HD2	1.81	0.44
1:A:747:LEU:HD12	1:A:765:THR:HG21	1.99	0.44
1:A:837:LYS:HE3	1:A:1237:LEU:HD11	1.99	0.44
1:A:249:TYR:HE1	1:A:298:LYS:HA	1.82	0.44
1:A:315:THR:OG1	1:A:318:CYS:SG	2.72	0.44
1:A:869:ASP:OD1	2:A:1501:SAH:H1'	2.18	0.44
1:A:674:LEU:HB2	1:A:685:LEU:HD12	2.00	0.44
1:A:963:GLY:HA3	1:A:1020:PHE:CZ	2.52	0.44
1:A:1043:ARG:HA	1:A:1059:PHE:CE1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:414:THR:N	1:A:953:SER:OG	2.50	0.44
1:A:722:SER:OG	1:A:723:ASP:N	2.50	0.43
1:A:952:ALA:HA	1:A:955:VAL:HG12	2.01	0.43
1:A:382:LEU:HA	1:A:1206:VAL:HG13	2.00	0.43
1:A:608:ILE:N	1:A:608:ILE:HD12	2.33	0.43
1:A:298:LYS:HE3	1:A:298:LYS:HB3	1.84	0.42
1:A:209:ILE:HG13	1:A:290:PHE:CE1	2.54	0.42
1:A:912:PRO:O	1:A:958:TYR:OH	2.29	0.42
1:A:658:TRP:CE3	1:A:658:TRP:HA	2.54	0.42
1:A:1081:ASP:HA	1:A:1186:ARG:HB3	2.01	0.42
1:A:611:TYR:CD2	1:A:632:SER:HB3	2.55	0.42
1:A:1093:HIS:CD2	1:A:1189:THR:HG21	2.55	0.42
1:A:393:GLN:HE22	1:A:910:ASN:HD21	1.67	0.41
1:A:782:MET:O	1:A:828:GLY:N	2.47	0.41
1:A:1043:ARG:HA	1:A:1059:PHE:HE1	1.84	0.41
1:A:1095:LEU:HD23	1:A:1189:THR:HG22	2.02	0.41
1:A:955:VAL:HG23	1:A:960:PRO:HD2	2.02	0.41
1:A:608:ILE:HD12	1:A:608:ILE:H	1.85	0.41
1:A:792:PRO:HB2	1:A:831:PRO:HG2	2.02	0.41
1:A:412:ILE:HG12	1:A:433:ALA:HB2	2.03	0.41
1:A:858:GLU:HB3	1:A:1226:LEU:HD13	2.02	0.41
1:A:278:LYS:HA	1:A:279:PRO:HD3	1.95	0.41
1:A:784:CYS:SG	1:A:827:GLN:NE2	2.75	0.41
1:A:226:VAL:HA	1:A:234:HIS:O	2.20	0.41
1:A:288:GLN:HB3	1:A:289:PRO:HD3	2.03	0.41
1:A:732:THR:HA	1:A:739:ALA:HA	2.03	0.41
1:A:971:ILE:HD13	1:A:983:LEU:HD22	2.03	0.41
1:A:1234:GLU:HA	1:A:1237:LEU:O	2.21	0.41
1:A:1013:ARG:NH2	1:A:1219:SER:O	2.52	0.40
1:A:256:VAL:HG22	1:A:298:LYS:HD3	2.02	0.40
1:A:193:PHE:CZ	1:A:276:LEU:HB3	2.57	0.40

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	874/1456 (60%)	845 (97%)	29 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	596/1248 (48%)	562 (94%)	34 (6%)	17	43

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	207	ARG
1	A	219	ASP
1	A	239	MET
1	A	264	SER
1	A	334	SER
1	A	356	ASN
1	A	391	PHE
1	A	416	TYR
1	A	580	ARG
1	A	606	ASP
1	A	637	CYS
1	A	658	TRP
1	A	680	ARG
1	A	692	CYS
1	A	716	SER
1	A	730	TYR
1	A	784	CYS
1	A	796	ASP
1	A	846	TYR
1	A	852	PHE
1	A	872	ASP

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Mol	Chain	Res	Type
1	A	896	ASP
1	A	909	ASP
1	A	917	VAL
1	A	929	PHE
1	A	954	PHE
1	A	965	LEU
1	A	987	PHE
1	A	1013	ARG
1	A	1034	SER
1	A	1050	ASN
1	A	1089	ARG
1	A	1092	ASP
1	A	1161	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	393	GLN
1	A	876	HIS

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
2	SAH	A	1501	-	23,28,28	0.98	2 (8%)	22,40,40	0.82	1 (4%)

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	SAH	A	1501	-	-	6/11/31/31	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1501	SAH	C8-N7	-2.44	1.30	1.34
2	A	1501	SAH	C1'-N9	-2.12	1.44	1.49

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1501	SAH	CB-CG-SD	-2.43	108.04	113.45

There are no chirality outliers.

All (6) torsion outliers are listed below:

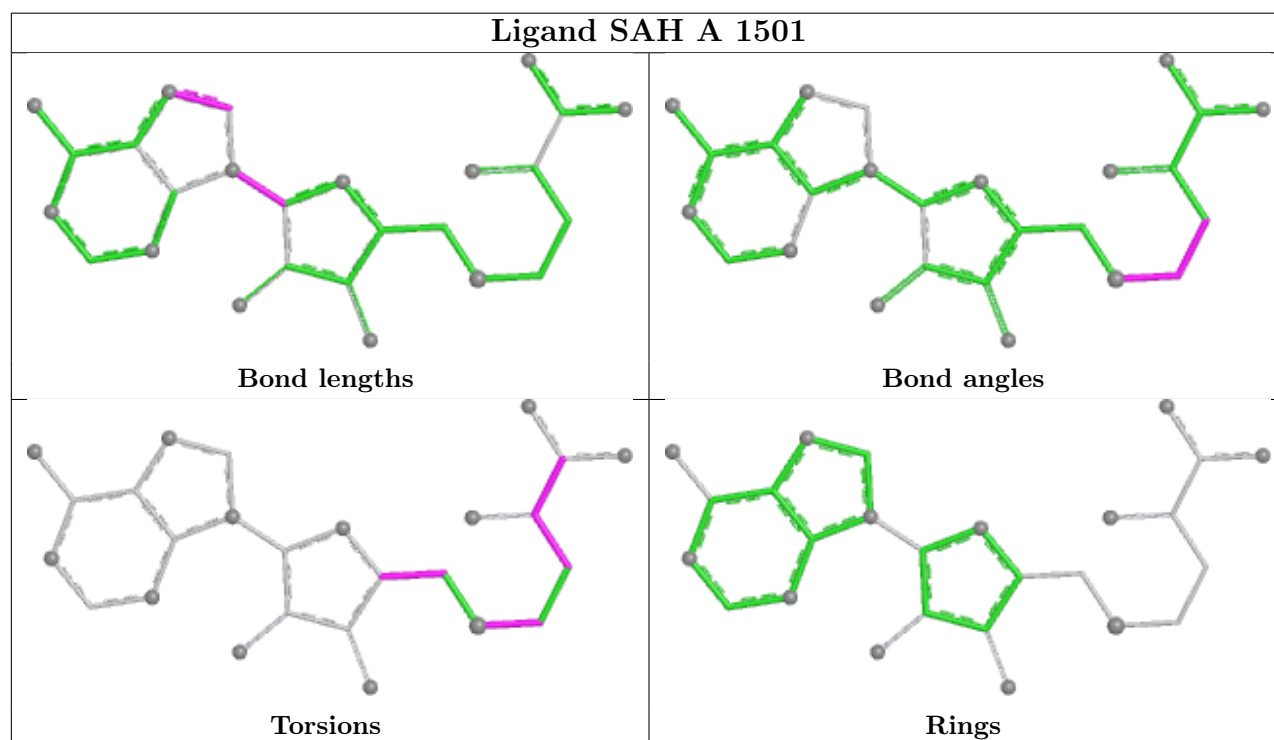
Mol	Chain	Res	Type	Atoms
2	A	1501	SAH	N-CA-CB-CG
2	A	1501	SAH	O-C-CA-CB
2	A	1501	SAH	OXT-C-CA-CB
2	A	1501	SAH	C3'-C4'-C5'-SD
2	A	1501	SAH	O4'-C4'-C5'-SD
2	A	1501	SAH	CB-CG-SD-C5'

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1501	SAH	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 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.

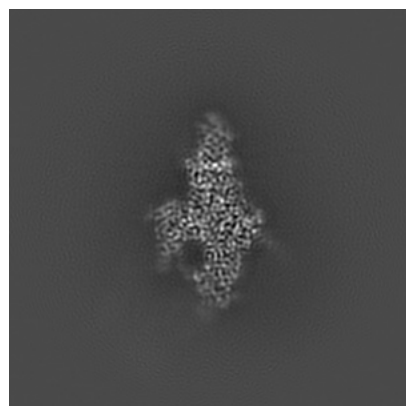
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44410. These allow visual inspection of the internal detail of the map and identification of artifacts.

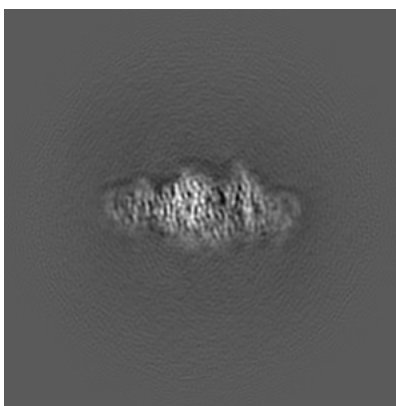
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

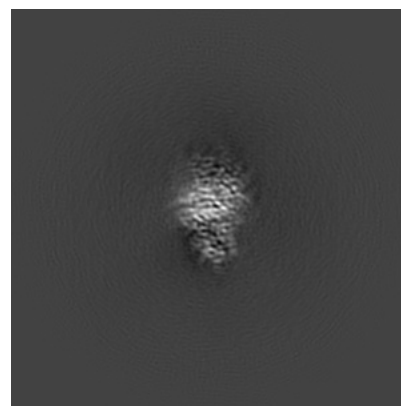
6.1.1 Primary map



X

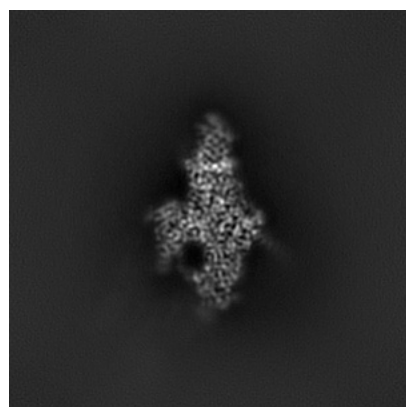


Y

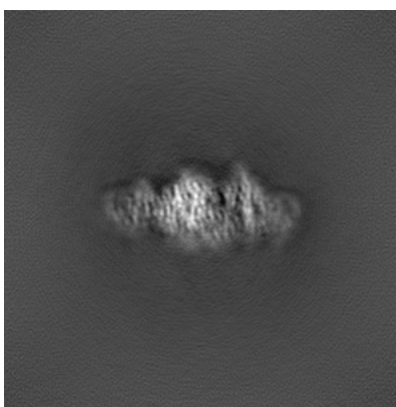


Z

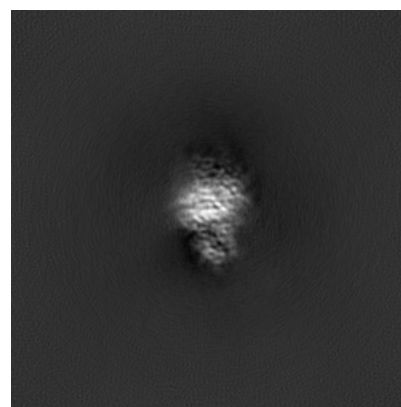
6.1.2 Raw map



X



Y

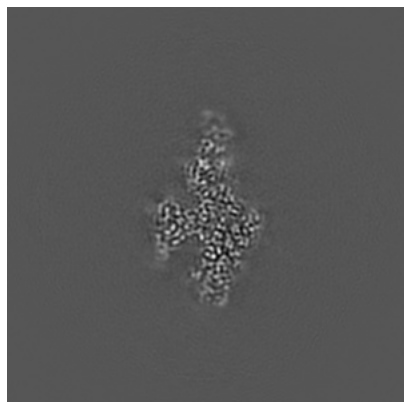


Z

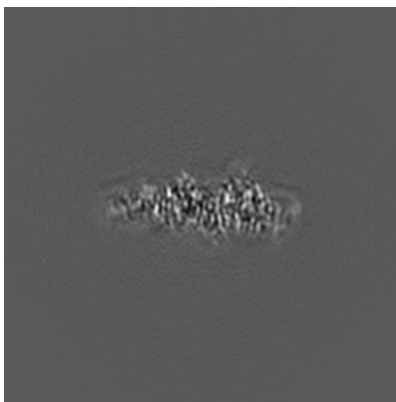
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

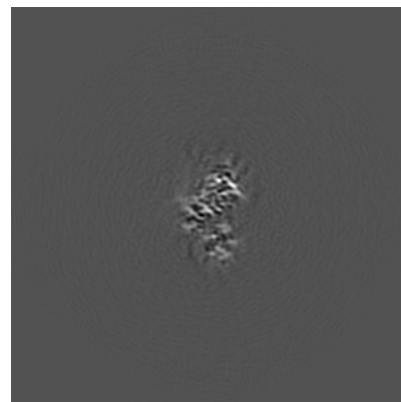
6.2.1 Primary map



X Index: 128

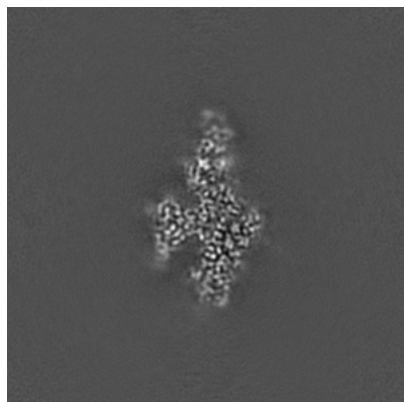


Y Index: 128

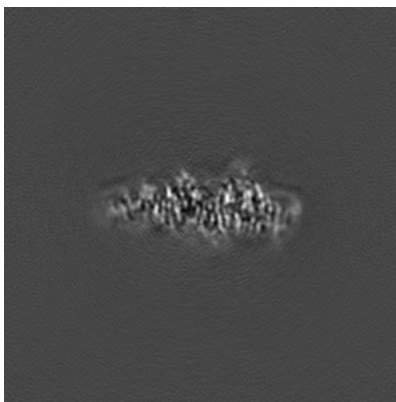


Z Index: 128

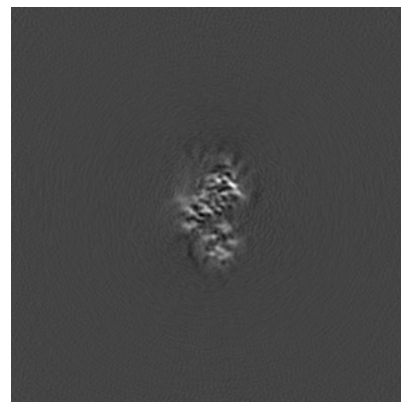
6.2.2 Raw map



X Index: 128



Y Index: 128

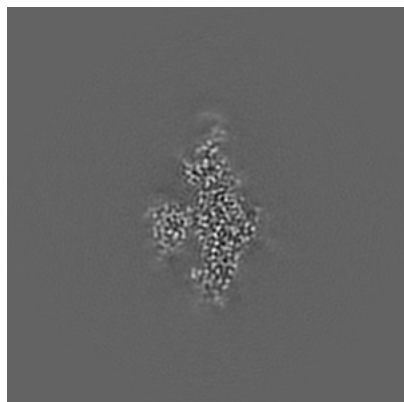


Z Index: 128

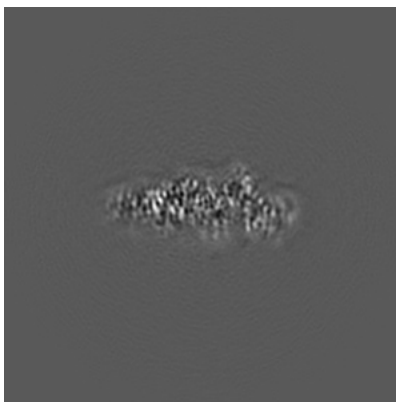
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

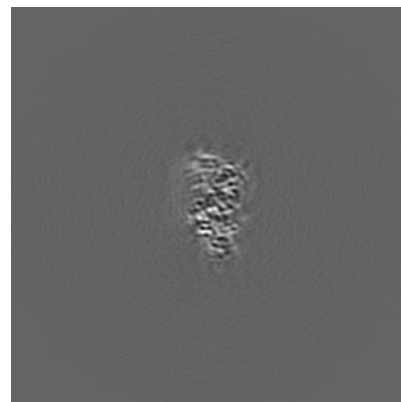
6.3.1 Primary map



X Index: 131

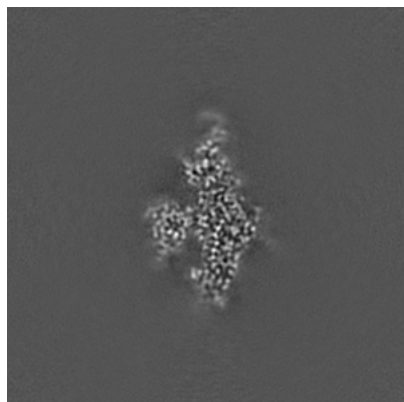


Y Index: 132

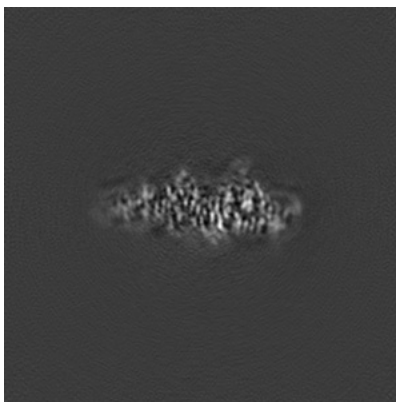


Z Index: 120

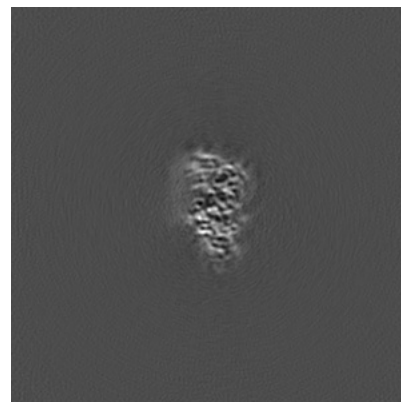
6.3.2 Raw map



X Index: 131



Y Index: 127

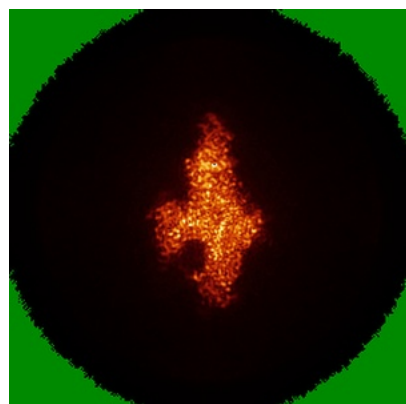


Z Index: 120

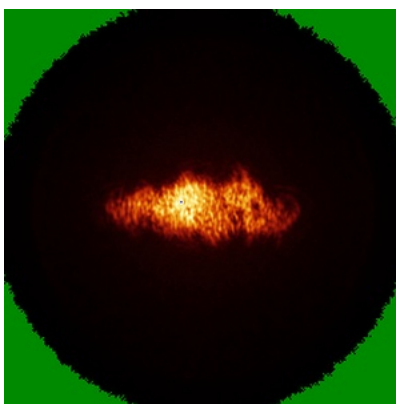
The images above show the largest variance slices of the map in three orthogonal directions.

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

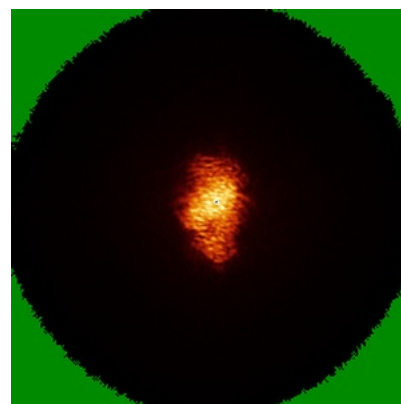
6.4.1 Primary map



X

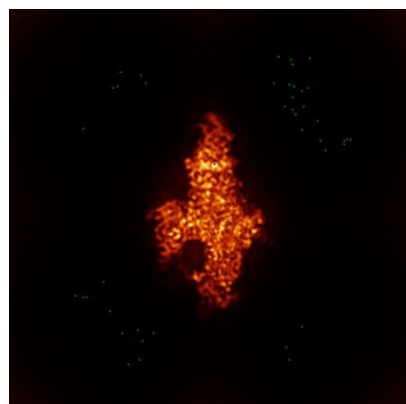


Y

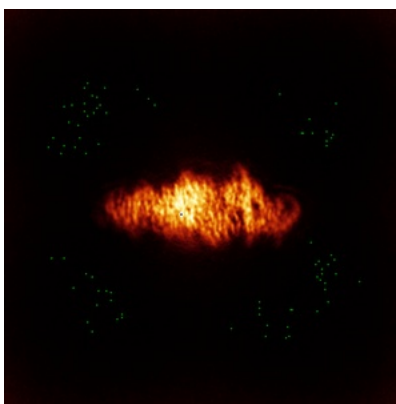


Z

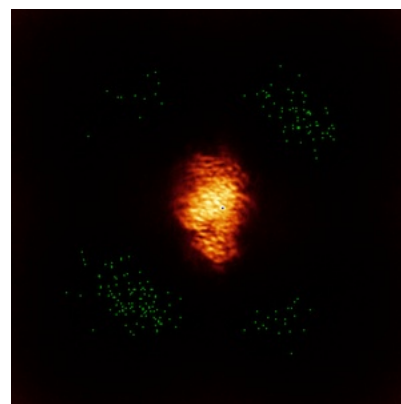
6.4.2 Raw map



X



Y

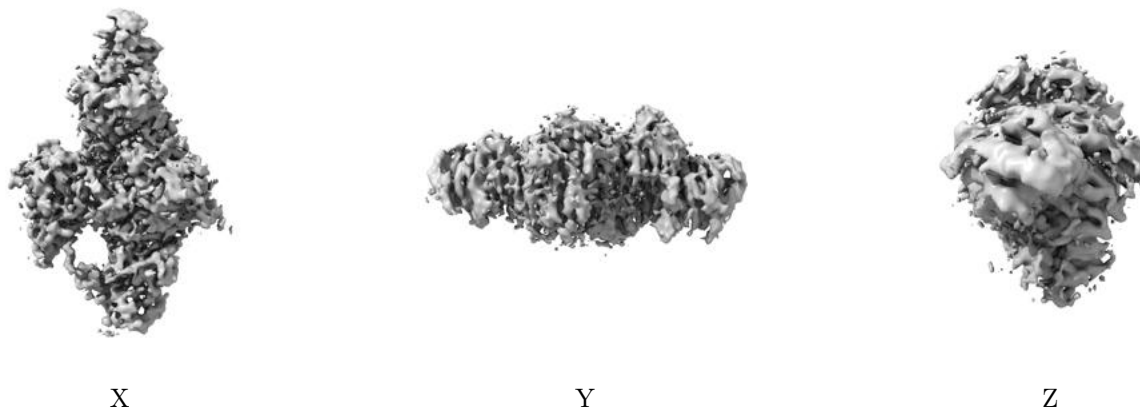


Z

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.

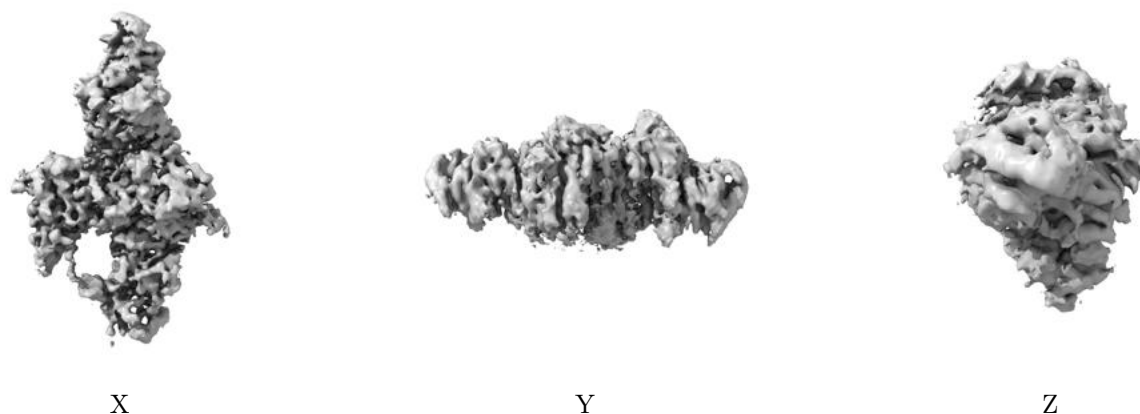
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.101. 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.

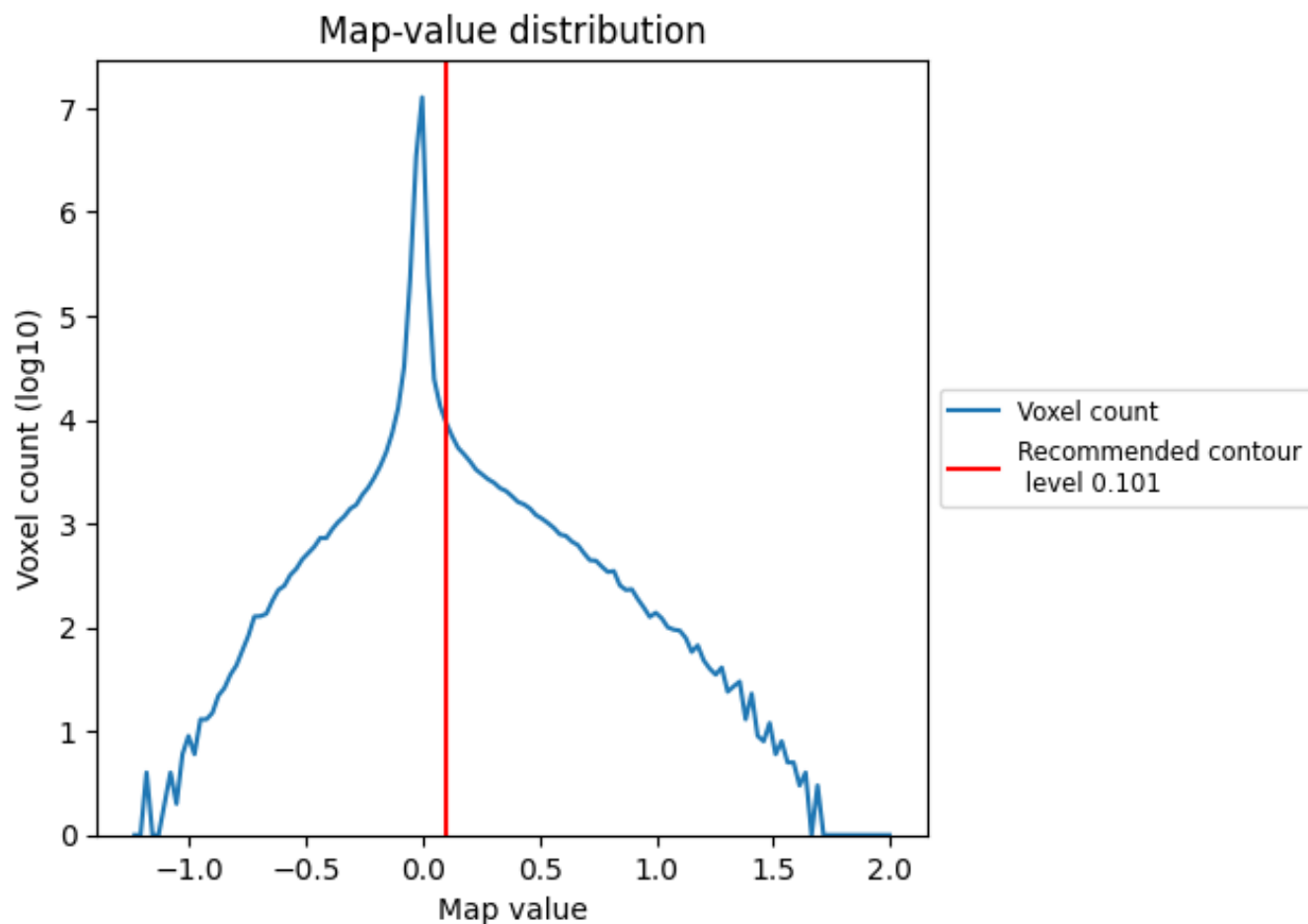
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

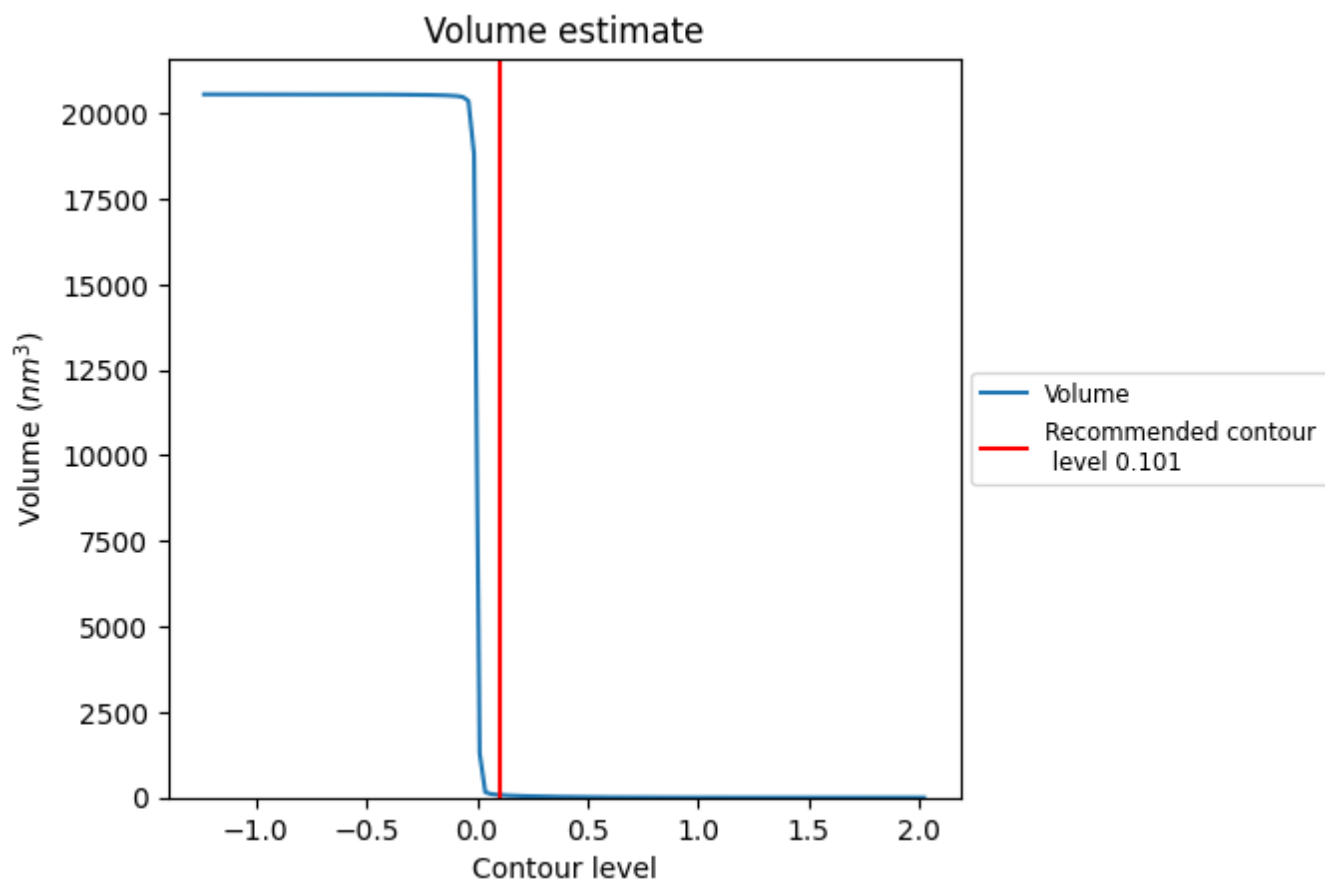
This section contains the results of statistical analysis of the map.

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.

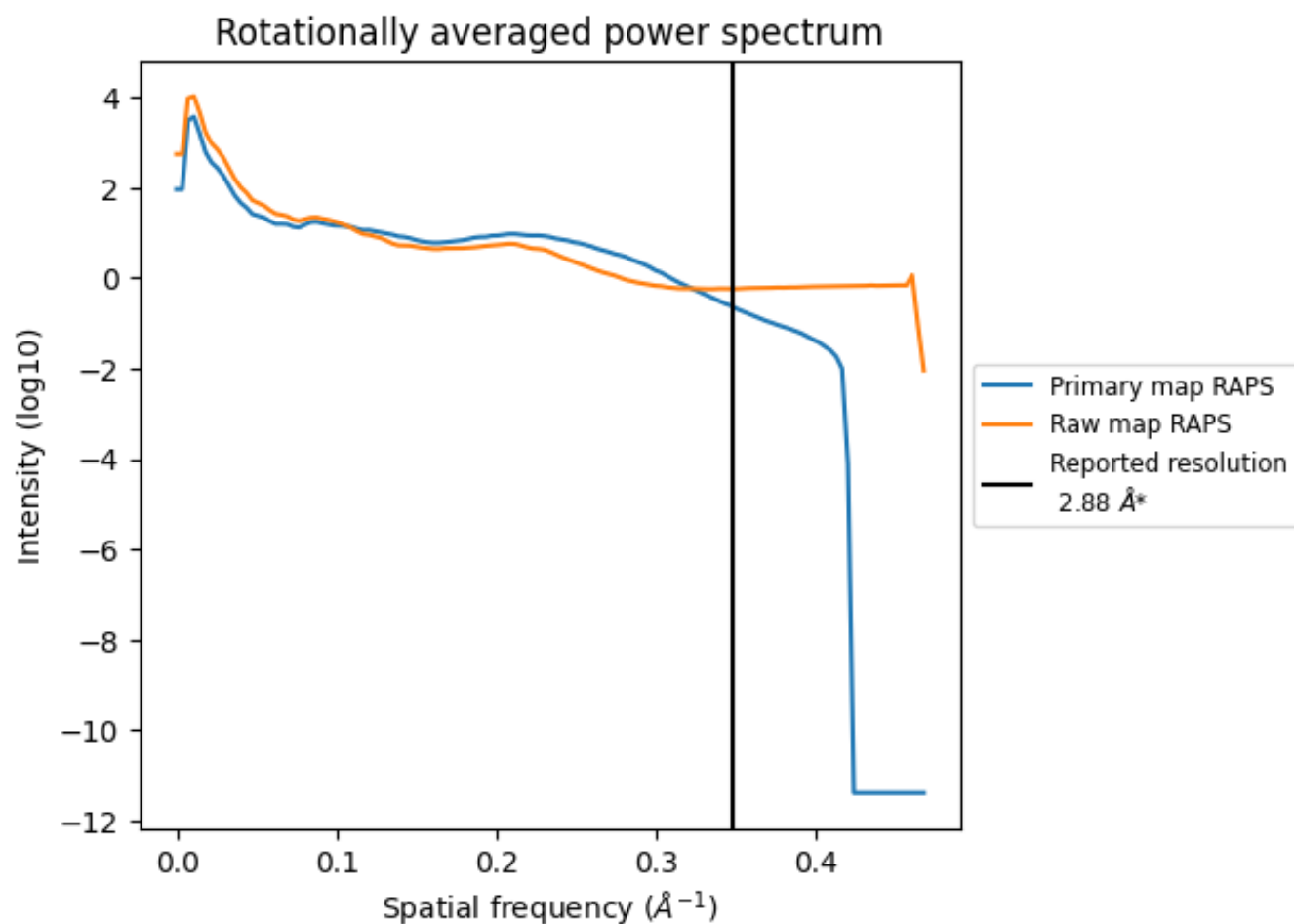
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 78 nm^3 ; this corresponds to an approximate mass of 70 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 ⓘ

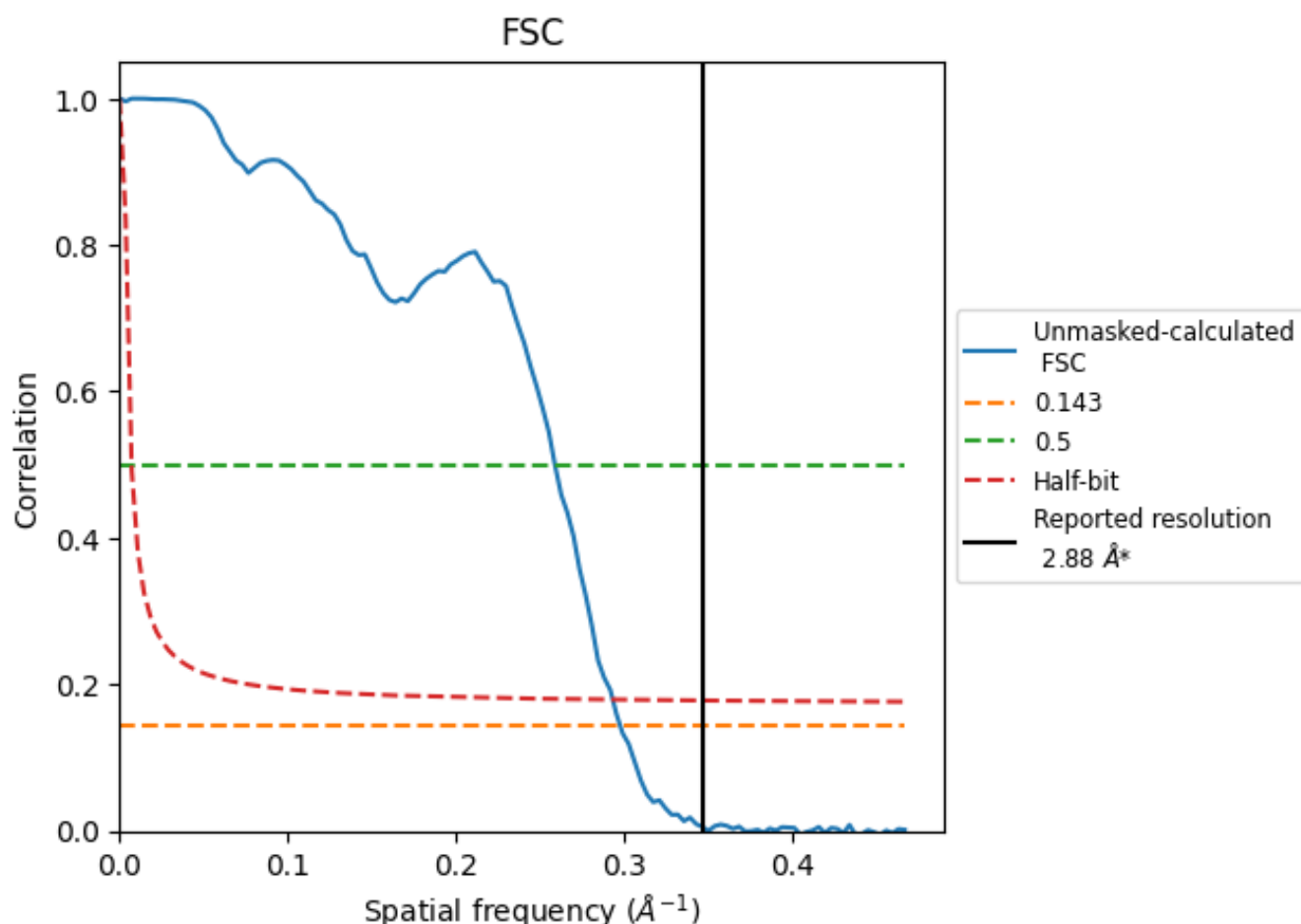


*Reported resolution corresponds to spatial frequency of 0.347 Å⁻¹

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 0.347 \AA^{-1}

8.2 Resolution estimates [i](#)

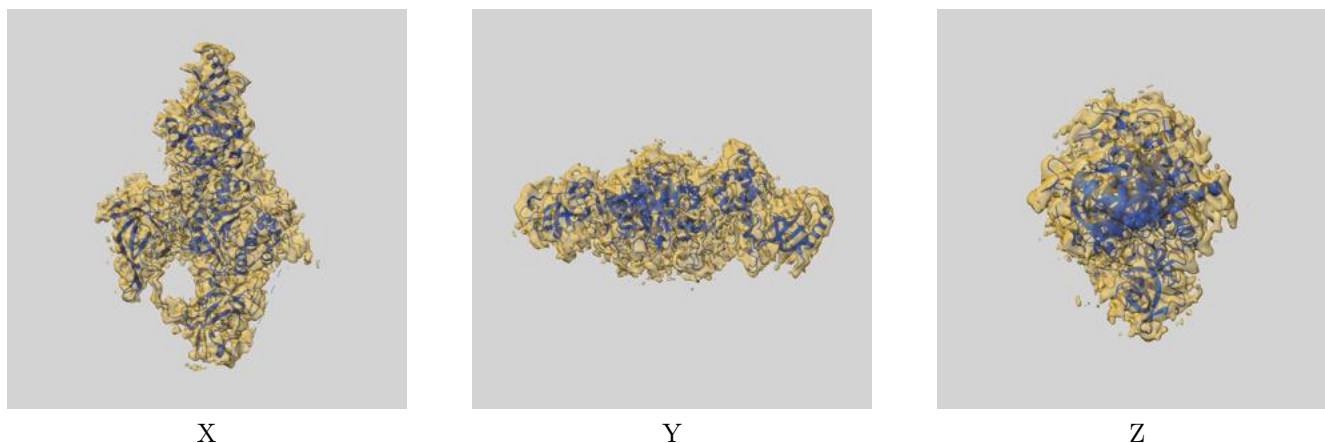
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.88	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.36	3.86	3.41

*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 3.36 differs from the reported value 2.88 by more than 10 %

9 Map-model fit [i](#)

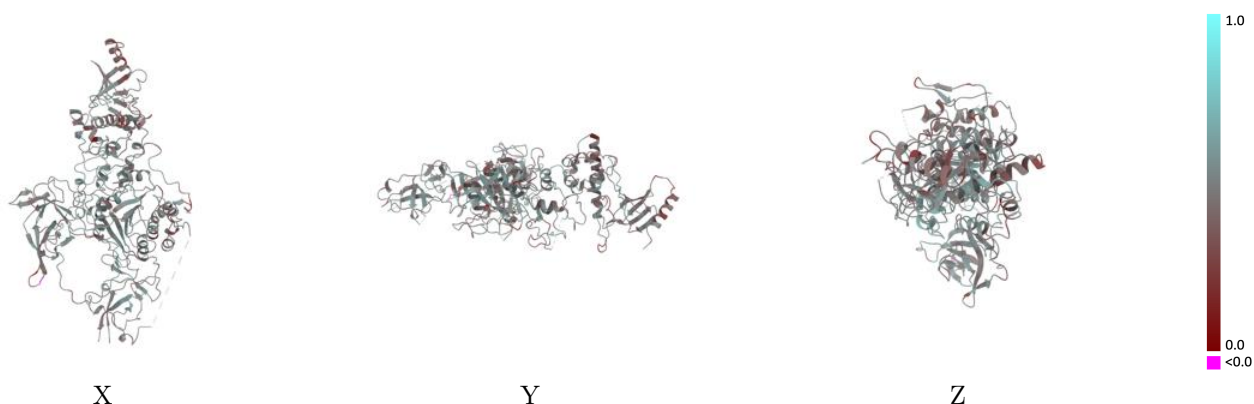
This section contains information regarding the fit between EMDB map EMD-44410 and PDB model 9BAP. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



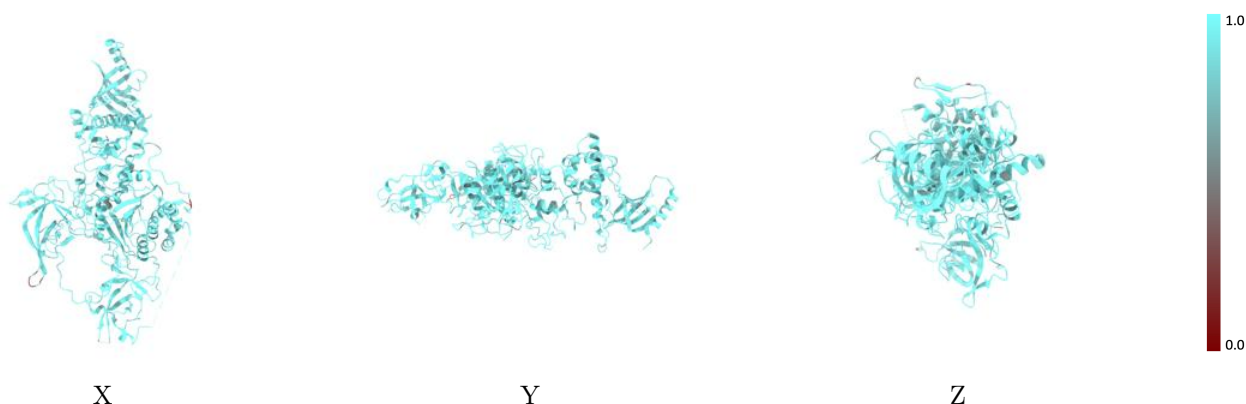
The images above show the 3D surface view of the map at the recommended contour level 0.101 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



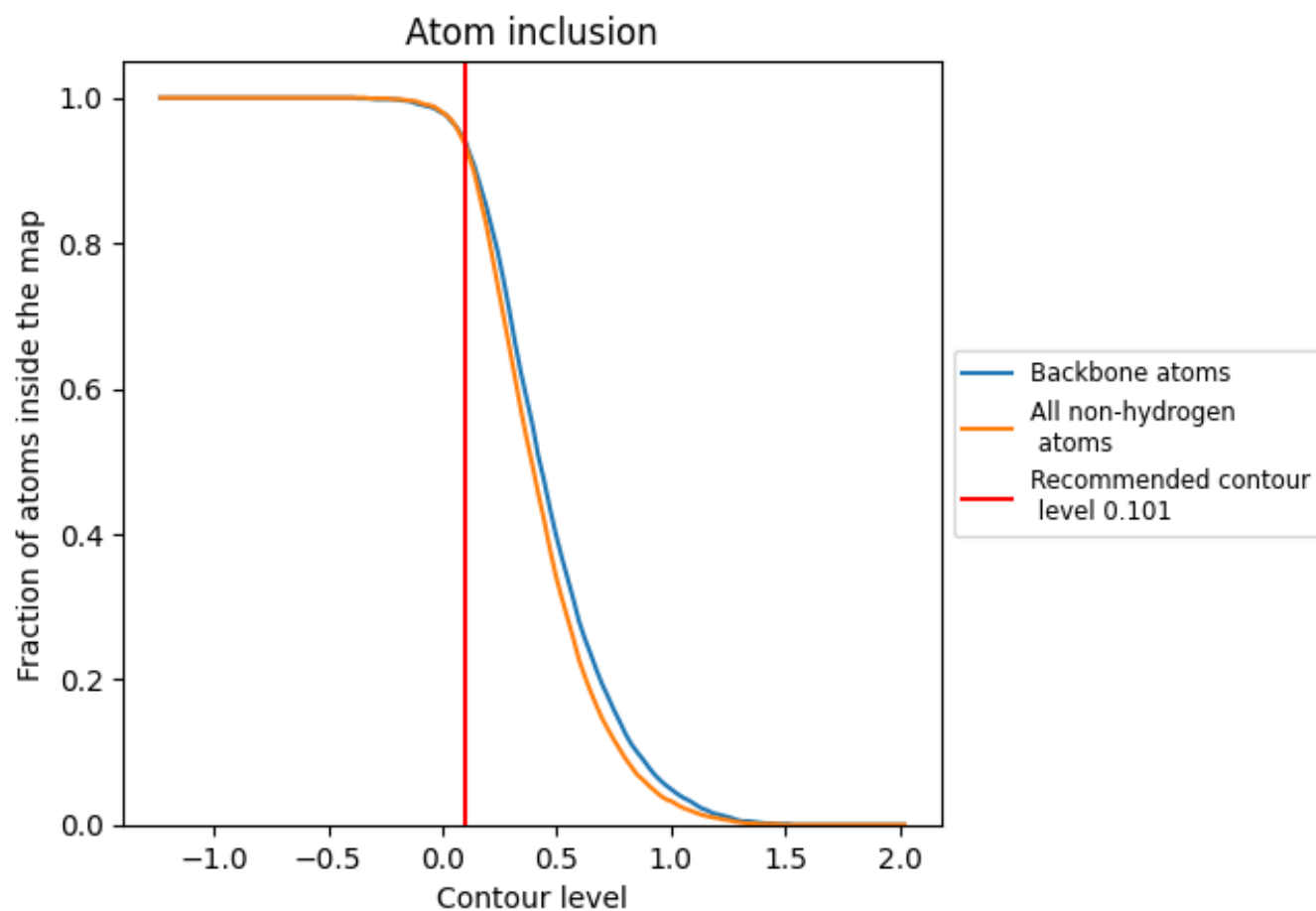
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.101).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.101) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.9340	<div><div></div></div> 0.4810
A	<div><div></div></div> 0.9340	<div><div></div></div> 0.4810

