Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 04:05 AM UTC

PDB ID	:	8KGL / pdb_00008kgl
EMDB ID	:	EMD-37225
Title	:	Structure of African swine fever virus topoisomerase II
Authors	:	Cong, J.; Xin, Y.; Li, X.; Chen, Y.
Deposited on	:	2023-08-19
Resolution	:	4.30 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:

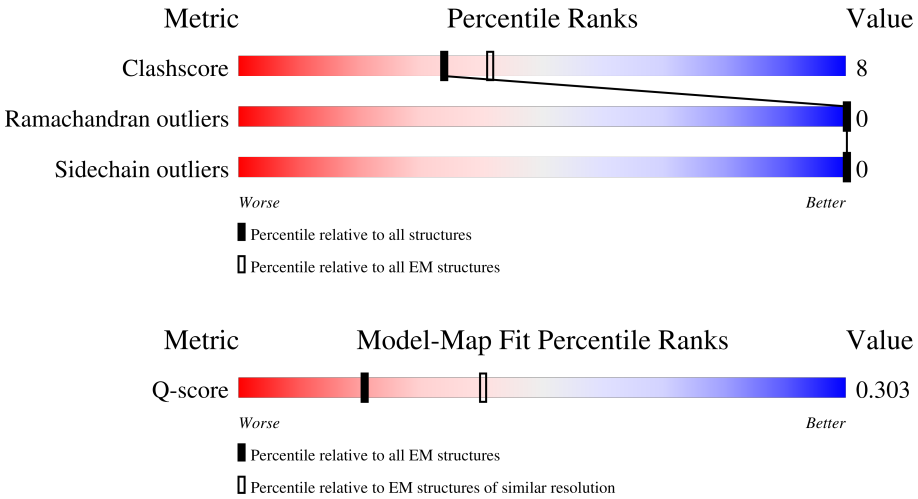
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 4.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	4585 (3.80 - 4.80)

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	1211	31% 10% 59%
1	B	1211	32% 9% 59%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 8084 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 topoisomerase 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	492	Total	C	N	O	S	0	0
			4042	2605	693	732	12		
1	B	492	Total	C	N	O	S	0	0
			4042	2605	693	732	12		

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLU	-	expression tag	UNP A0A2X0THW2
A	-2	PHE	-	expression tag	UNP A0A2X0THW2
A	-1	ALA	-	expression tag	UNP A0A2X0THW2
A	0	THR	-	expression tag	UNP A0A2X0THW2
A	1193	GLU	-	expression tag	UNP A0A2X0THW2
A	1194	ASN	-	expression tag	UNP A0A2X0THW2
A	1195	LEU	-	expression tag	UNP A0A2X0THW2
A	1196	TYR	-	expression tag	UNP A0A2X0THW2
A	1197	PHE	-	expression tag	UNP A0A2X0THW2
A	1198	GLN	-	expression tag	UNP A0A2X0THW2
A	1199	GLY	-	expression tag	UNP A0A2X0THW2
A	1200	HIS	-	expression tag	UNP A0A2X0THW2
A	1201	HIS	-	expression tag	UNP A0A2X0THW2
A	1202	HIS	-	expression tag	UNP A0A2X0THW2
A	1203	HIS	-	expression tag	UNP A0A2X0THW2
A	1204	HIS	-	expression tag	UNP A0A2X0THW2
A	1205	HIS	-	expression tag	UNP A0A2X0THW2
A	1206	HIS	-	expression tag	UNP A0A2X0THW2
A	1207	HIS	-	expression tag	UNP A0A2X0THW2
B	-3	GLU	-	expression tag	UNP A0A2X0THW2
B	-2	PHE	-	expression tag	UNP A0A2X0THW2
B	-1	ALA	-	expression tag	UNP A0A2X0THW2
B	0	THR	-	expression tag	UNP A0A2X0THW2
B	1193	GLU	-	expression tag	UNP A0A2X0THW2
B	1194	ASN	-	expression tag	UNP A0A2X0THW2
B	1195	LEU	-	expression tag	UNP A0A2X0THW2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1196	TYR	-	expression tag	UNP A0A2X0THW2
B	1197	PHE	-	expression tag	UNP A0A2X0THW2
B	1198	GLN	-	expression tag	UNP A0A2X0THW2
B	1199	GLY	-	expression tag	UNP A0A2X0THW2
B	1200	HIS	-	expression tag	UNP A0A2X0THW2
B	1201	HIS	-	expression tag	UNP A0A2X0THW2
B	1202	HIS	-	expression tag	UNP A0A2X0THW2
B	1203	HIS	-	expression tag	UNP A0A2X0THW2
B	1204	HIS	-	expression tag	UNP A0A2X0THW2
B	1205	HIS	-	expression tag	UNP A0A2X0THW2
B	1206	HIS	-	expression tag	UNP A0A2X0THW2
B	1207	HIS	-	expression tag	UNP A0A2X0THW2

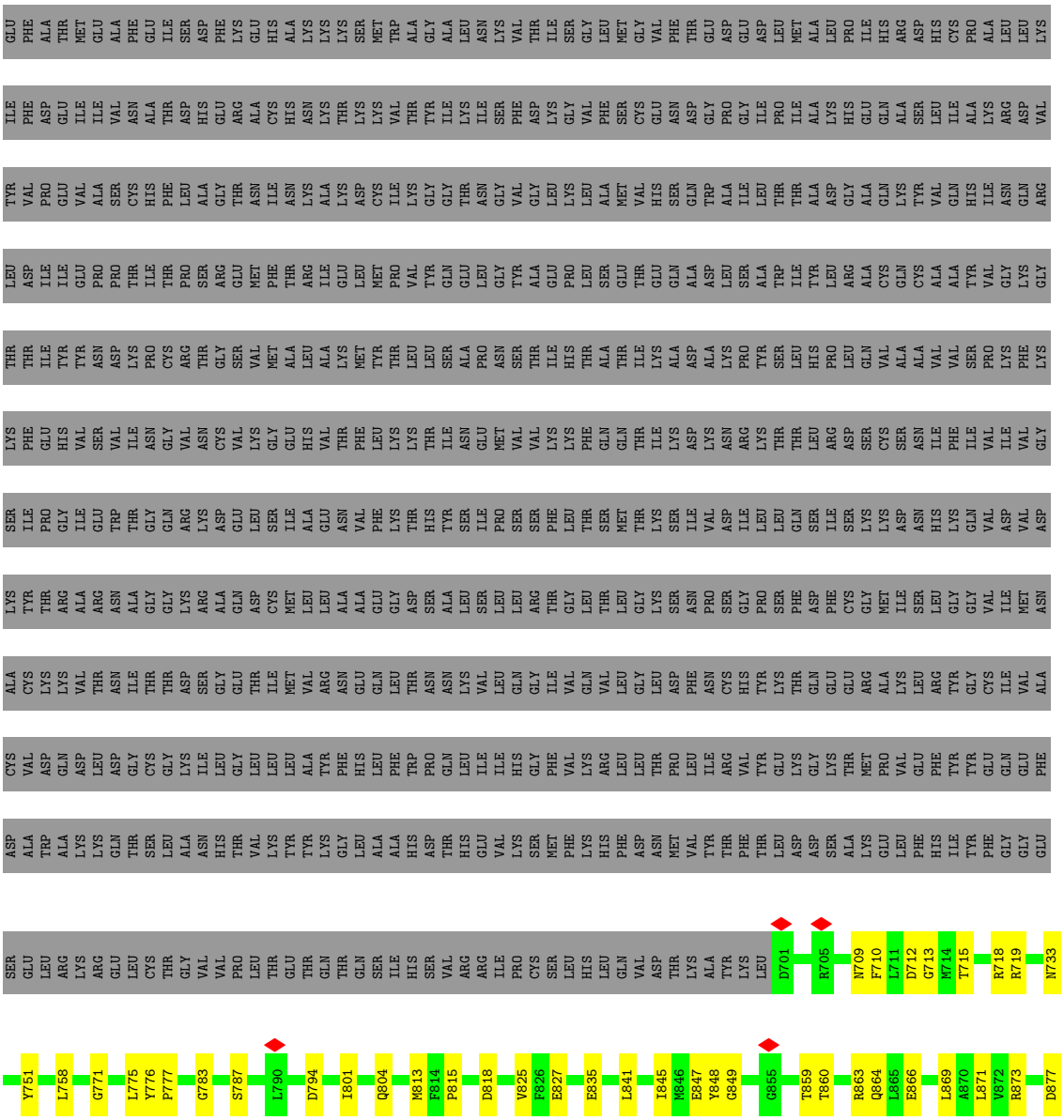
3 Residue-property plots (i)

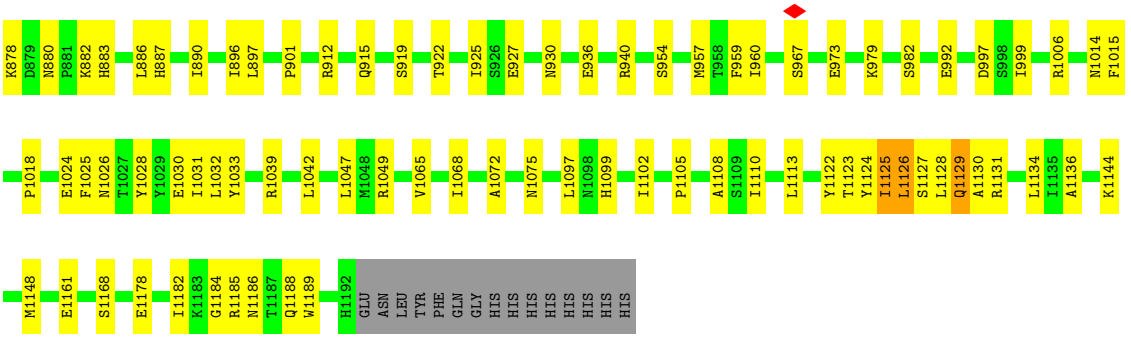
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: DNA topoisomerase 2

Chain A:



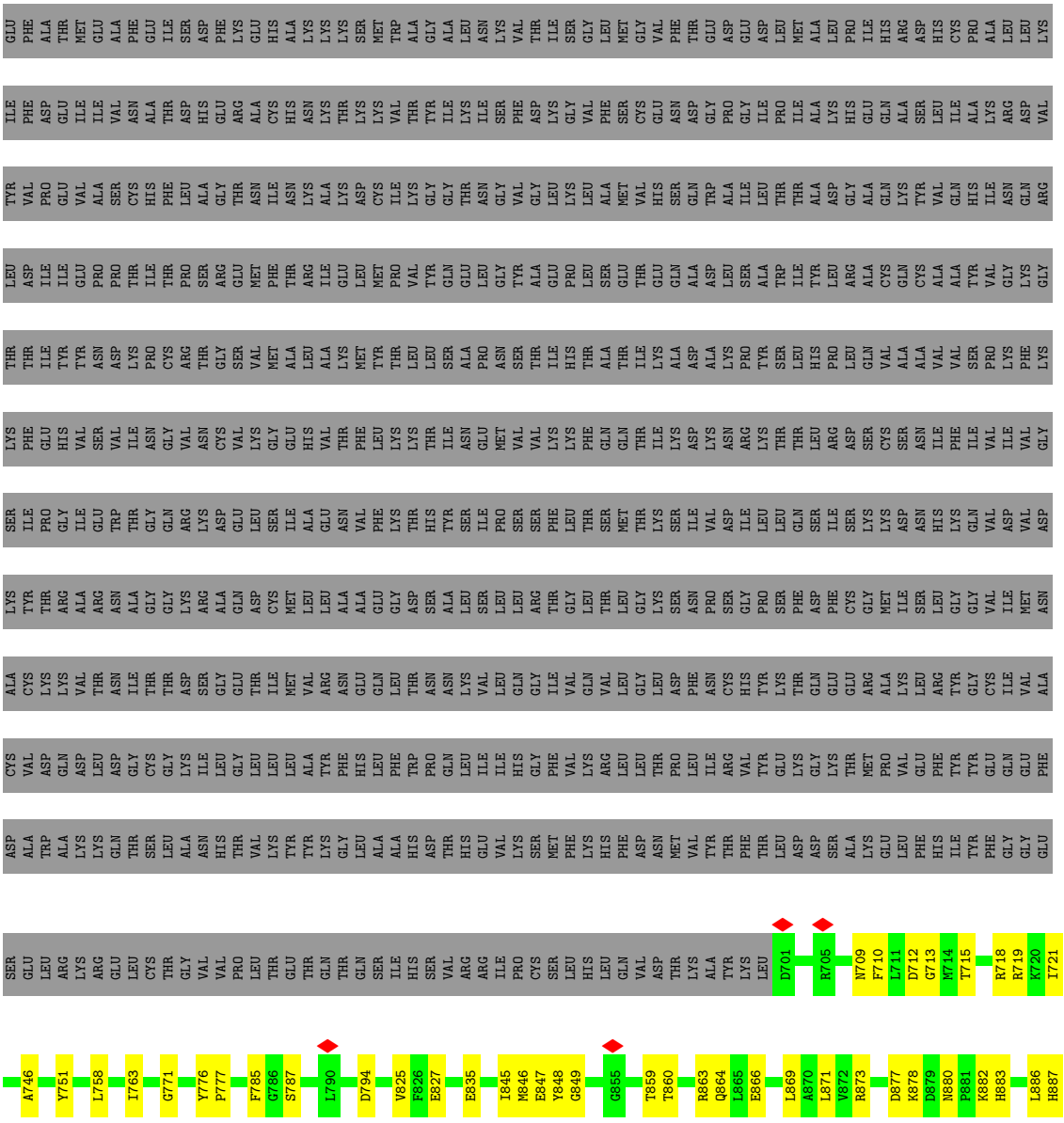


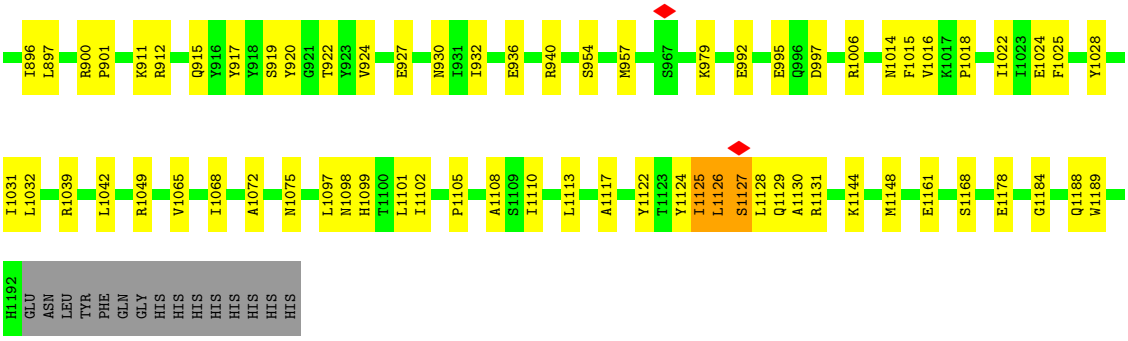


- Molecule 1: DNA topoisomerase 2

Chain B:






I896 L897 R900 P901 K911 R912 Q915 Y916 Y917 Y918 S919 Y920 G921 T922 Y923 V924 E927 N930 I931 I932 E936 R940 S954 M957 S967 K979 E992 E995 Q996 D997 R1006 N1014 F1015 V1016 K1017 P1018 I1022 I1023 E1024 F1025 Y1028
I1031 L1032 R1039 L1042 R1049 V1065 I1068 A1072 N1075 L1097 N1098 H1099 T1100 L1101 I1102 P1105 A1108 S1109 I1110 L1113 A1117 Y1122 T1123 Y1124 I1125 L1126 S1127 L1128 Q1129 A1130 R1131 K1144 M1148 E1161 S1168 E1178 G1184 Q1188 W1189
H1192 GLU ASN LEU TYR PHE GLN GLY HIS HIS HIS HIS HIS HIS HIS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	48000	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 ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.021	Depositor
Minimum map value	-0.011	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0035	Depositor
Map size (Å)	233.99998, 233.99998, 233.99998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.65, 0.65, 0.65	Depositor

5 Model quality

5.1 Standard geometry

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	0.34	0/4143	0.63	1/5602 (0.0%)
1	B	0.34	0/4143	0.63	1/5602 (0.0%)
All	All	0.34	0/8286	0.63	2/11204 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	4
All	All	0	8

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	1127	SER	N-CA-C	8.16	122.94	112.34
1	A	1127	SER	N-CA-C	5.88	123.31	110.80

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1125	ILE	Peptide
1	A	1126	LEU	Peptide
1	A	1129	GLN	Peptide
1	A	1130	ALA	Peptide
1	B	1125	ILE	Peptide
1	B	1126	LEU	Peptide
1	B	1129	GLN	Peptide

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Mol	Chain	Res	Type	Group
1	B	1130	ALA	Peptide

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	4042	0	4041	71	0
1	B	4042	0	4041	68	0
All	All	8084	0	8082	132	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 8.

All (132) 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:848:TYR:HA	1:A:860:THR:O	1.84	0.78
1:B:848:TYR:HA	1:B:860:THR:O	1.86	0.74
1:A:1072:ALA:HA	1:B:1075:ASN:HD21	1.59	0.66
1:A:1075:ASN:HD21	1:B:1072:ALA:HA	1.64	0.62
1:A:1049:ARG:NH1	1:A:1108:ALA:O	2.31	0.62
1:B:1049:ARG:NH1	1:B:1108:ALA:O	2.32	0.62
1:A:1128:LEU:HD12	1:B:1128:LEU:HD12	1.81	0.62
1:B:864:GLN:NE2	1:B:901:PRO:O	2.33	0.61
1:A:864:GLN:NE2	1:A:901:PRO:O	2.34	0.61
1:A:992:GLU:HG3	1:A:997:ASP:HA	1.83	0.60
1:B:919:SER:O	1:B:1006:ARG:HA	2.02	0.59
1:B:992:GLU:HG3	1:B:997:ASP:HA	1.84	0.59
1:A:1049:ARG:HH22	1:A:1108:ALA:H	1.51	0.59
1:A:922:THR:H	1:A:936:GLU:HB3	1.67	0.58
1:A:1182:ILE:O	1:A:1186:ASN:HB2	2.04	0.58
1:A:1129:GLN:NE2	1:B:1127:SER:OG	2.37	0.58
1:A:1182:ILE:HG23	1:A:1186:ASN:HD22	1.68	0.58
1:A:880:ASN:HB3	1:A:883:HIS:HB2	1.85	0.58
1:A:1144:LYS:HG2	1:A:1148:MET:HE2	1.86	0.58
1:B:715:THR:H	1:B:718:ARG:HD3	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1049:ARG:HH22	1:B:1108:ALA:H	1.51	0.57
1:A:866:GLU:HG3	1:A:869:LEU:HD12	1.87	0.57
1:B:1144:LYS:HG2	1:B:1148:MET:HE2	1.86	0.57
1:B:880:ASN:HB3	1:B:883:HIS:HB2	1.85	0.57
1:A:1049:ARG:NH2	1:A:1105:PRO:O	2.32	0.57
1:B:912:ARG:HH21	1:B:915:GLN:HA	1.70	0.57
1:A:715:THR:H	1:A:718:ARG:HD3	1.69	0.56
1:A:882:LYS:O	1:A:886:LEU:N	2.37	0.56
1:B:771:GLY:O	1:B:940:ARG:NE	2.39	0.56
1:B:866:GLU:HG3	1:B:869:LEU:HD12	1.89	0.55
1:A:1131:ARG:N	1:B:1126:LEU:O	2.31	0.55
1:A:771:GLY:O	1:A:940:ARG:NE	2.39	0.54
1:A:919:SER:O	1:A:1006:ARG:HA	2.07	0.54
1:A:775:LEU:HB3	1:A:1185:ARG:HH22	1.72	0.54
1:A:719:ARG:NH1	1:A:835:GLU:O	2.41	0.54
1:B:777:PRO:HD2	1:B:1189:TRP:CE2	2.43	0.53
1:B:719:ARG:NH1	1:B:835:GLU:O	2.41	0.53
1:B:911:LYS:O	1:B:917:TYR:HA	2.09	0.53
1:B:776:TYR:N	1:B:847:GLU:OE2	2.38	0.53
1:B:1049:ARG:NH2	1:B:1105:PRO:O	2.32	0.52
1:B:896:ILE:HG13	1:B:897:LEU:HG	1.90	0.52
1:A:733:ASN:O	1:A:804:GLN:NE2	2.43	0.51
1:B:922:THR:H	1:B:936:GLU:HB3	1.75	0.51
1:A:896:ILE:HG13	1:A:897:LEU:HG	1.93	0.51
1:B:930:ASN:ND2	1:B:979:LYS:O	2.43	0.51
1:B:1122:TYR:HB3	1:B:1125:ILE:HD12	1.93	0.51
1:A:1122:TYR:HB3	1:A:1125:ILE:HD12	1.92	0.51
1:A:777:PRO:HD2	1:A:1189:TRP:CE2	2.46	0.51
1:A:877:ASP:O	1:A:883:HIS:ND1	2.45	0.50
1:B:883:HIS:O	1:B:887:HIS:ND1	2.45	0.50
1:A:873:ARG:NH2	1:A:1178:GLU:OE1	2.45	0.50
1:B:882:LYS:O	1:B:886:LEU:N	2.39	0.50
1:B:1110:ILE:HA	1:B:1113:LEU:HD12	1.93	0.50
1:B:877:ASP:O	1:B:883:HIS:ND1	2.44	0.50
1:B:787:SER:OG	1:B:794:ASP:OD2	2.30	0.49
1:B:873:ARG:NH2	1:B:1178:GLU:OE1	2.44	0.49
1:A:776:TYR:N	1:A:847:GLU:OE2	2.38	0.49
1:A:1126:LEU:O	1:B:1131:ARG:N	2.30	0.49
1:A:1110:ILE:HA	1:A:1113:LEU:HD12	1.93	0.49
1:B:1028:TYR:HA	1:B:1031:ILE:HD12	1.94	0.49
1:A:1028:TYR:HA	1:A:1031:ILE:HD12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:787:SER:OG	1:A:794:ASP:OD2	2.29	0.48
1:B:1101:LEU:HD23	1:B:1117:ALA:HB2	1.95	0.48
1:A:878:LYS:HA	1:A:883:HIS:CG	2.48	0.48
1:B:863:ARG:HA	1:B:901:PRO:HA	1.95	0.48
1:A:783:GLY:HA3	1:A:801:ILE:HG22	1.96	0.48
1:B:825:VAL:HG12	1:B:827:GLU:HG2	1.95	0.48
1:A:883:HIS:O	1:A:887:HIS:ND1	2.45	0.48
1:B:1014:ASN:HB3	1:B:1024:GLU:HG2	1.96	0.48
1:B:878:LYS:HA	1:B:883:HIS:CG	2.49	0.47
1:A:709:ASN:OD1	1:A:710:PHE:N	2.47	0.47
1:A:1014:ASN:HB3	1:A:1024:GLU:HG2	1.96	0.47
1:A:1039:ARG:HH11	1:A:1042:LEU:HD23	1.80	0.47
1:A:863:ARG:HA	1:A:901:PRO:HA	1.96	0.47
1:B:849:GLY:O	1:B:859:THR:HA	2.14	0.46
1:B:1039:ARG:HH11	1:B:1042:LEU:HD23	1.80	0.46
1:A:1123:THR:HA	1:A:1126:LEU:HD12	1.97	0.46
1:B:709:ASN:OD1	1:B:710:PHE:N	2.48	0.46
1:B:1161:GLU:OE2	1:B:1168:SER:N	2.49	0.46
1:A:825:VAL:HG12	1:A:827:GLU:HG2	1.97	0.46
1:B:845:ILE:HG21	1:B:1031:ILE:HD13	1.98	0.46
1:B:924:VAL:O	1:B:932:ILE:HA	2.16	0.46
1:B:954:SER:HA	1:B:957:MET:HB2	1.98	0.46
1:A:925:ILE:HD11	1:A:999:ILE:HG13	1.99	0.45
1:A:1184:GLY:O	1:A:1188:GLN:N	2.49	0.45
1:A:927:GLU:HA	1:A:930:ASN:HA	1.98	0.45
1:A:845:ILE:HG21	1:A:1031:ILE:HD13	1.98	0.45
1:B:1015:PHE:HB2	1:B:1025:PHE:HE2	1.81	0.45
1:B:1065:VAL:HA	1:B:1068:ILE:HD12	1.99	0.45
1:B:1125:ILE:HB	1:B:1126:LEU:HG	1.99	0.45
1:A:912:ARG:HH21	1:A:915:GLN:HA	1.82	0.44
1:A:1026:ASN:N	1:A:1030:GLU:OE1	2.45	0.44
1:A:1161:GLU:OE2	1:A:1168:SER:N	2.50	0.44
1:B:1099:HIS:HA	1:B:1102:ILE:HD12	2.00	0.44
1:B:846:MET:HE2	1:B:846:MET:HB3	1.91	0.44
1:A:954:SER:HA	1:A:957:MET:HB2	1.98	0.44
1:A:1015:PHE:HB2	1:A:1025:PHE:HE2	1.81	0.44
1:B:927:GLU:HA	1:B:930:ASN:HA	2.00	0.44
1:B:1184:GLY:O	1:B:1188:GLN:N	2.50	0.44
1:A:751:TYR:CE2	1:A:758:LEU:HB2	2.53	0.43
1:A:849:GLY:O	1:A:859:THR:HA	2.18	0.43
1:B:763:ILE:HG23	1:B:785:PHE:HD1	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:979:LYS:O	1:A:982:SER:OG	2.34	0.43
1:B:751:TYR:CE2	1:B:758:LEU:HB2	2.54	0.43
1:B:712:ASP:OD1	1:B:713:GLY:N	2.52	0.43
1:B:709:ASN:HD21	1:B:1018:PRO:HG3	1.84	0.43
1:A:712:ASP:OD1	1:A:713:GLY:N	2.52	0.42
1:A:1065:VAL:HA	1:A:1068:ILE:HD12	2.00	0.42
1:B:1016:VAL:HG22	1:B:1022:ILE:HG12	2.02	0.42
1:A:815:PRO:HB2	1:A:818:ASP:HB2	2.01	0.42
1:A:709:ASN:HD21	1:A:1018:PRO:HG3	1.84	0.42
1:A:967:SER:HG	1:A:973:GLU:H	1.65	0.42
1:A:1097:LEU:HD12	1:A:1124:TYR:CZ	2.55	0.42
1:A:1099:HIS:HA	1:A:1102:ILE:HD12	2.02	0.42
1:B:920:TYR:OH	1:B:995:GLU:O	2.31	0.42
1:B:1097:LEU:HD12	1:B:1124:TYR:CZ	2.54	0.42
1:A:815:PRO:HG2	1:A:1039:ARG:HH12	1.84	0.42
1:B:1098:ASN:HB3	1:B:1117:ALA:HA	2.02	0.42
1:B:897:LEU:HD23	1:B:897:LEU:HA	1.89	0.41
1:B:871:LEU:HD13	1:B:1032:LEU:HD22	2.01	0.41
1:B:864:GLN:N	1:B:900:ARG:O	2.53	0.41
1:A:1134:LEU:HD23	1:A:1136:ALA:H	1.85	0.41
1:B:746:ALA:HA	1:B:751:TYR:HB3	2.01	0.41
1:A:957:MET:HA	1:A:960:ILE:HB	2.02	0.41
1:B:718:ARG:HA	1:B:721:ILE:HD12	2.02	0.41
1:A:890:ILE:HG12	1:A:1033:TYR:CE1	2.56	0.41
1:B:1128:LEU:HD23	1:B:1128:LEU:HA	1.89	0.41
1:A:1126:LEU:HB3	1:B:1131:ARG:HG2	2.02	0.41
1:A:813:MET:HE1	1:A:841:LEU:HD12	2.04	0.40
1:A:871:LEU:HD13	1:A:1032:LEU:HD22	2.02	0.40
1:A:959:PHE:HA	1:A:979:LYS:HD2	2.04	0.40
1:A:1047:LEU:HD23	1:A:1047:LEU:HA	1.92	0.40

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	490/1211 (40%)	450 (92%)	40 (8%)	0	100	100
1	B	490/1211 (40%)	453 (92%)	37 (8%)	0	100	100
All	All	980/2422 (40%)	903 (92%)	77 (8%)	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	435/1059 (41%)	435 (100%)	0	100	100
1	B	435/1059 (41%)	435 (100%)	0	100	100
All	All	870/2118 (41%)	870 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	789	HIS
1	A	1012	HIS
1	A	1075	ASN
1	A	1099	HIS
1	A	1149	GLN
1	A	1186	ASN
1	B	753	HIS
1	B	789	HIS
1	B	804	GLN
1	B	1012	HIS
1	B	1014	ASN
1	B	1075	ASN
1	B	1099	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	1149	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

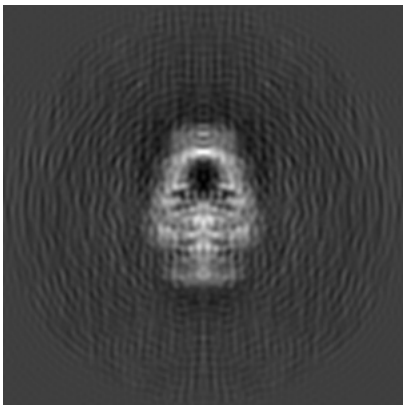
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-37225. These allow visual inspection of the internal detail of the map and identification of artifacts.

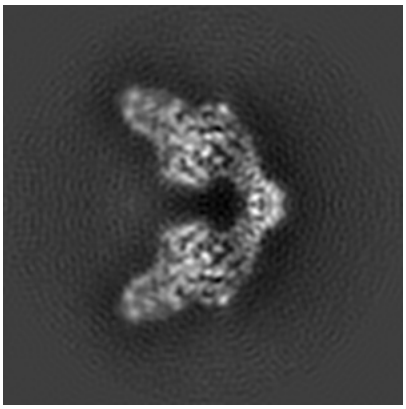
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

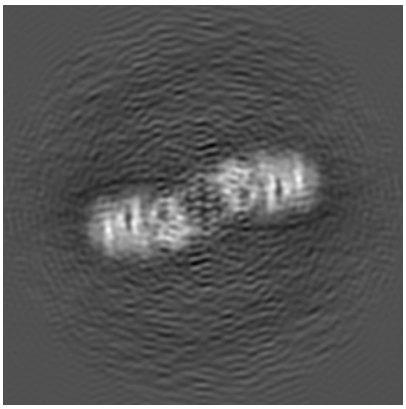
6.1.1 Primary map



X

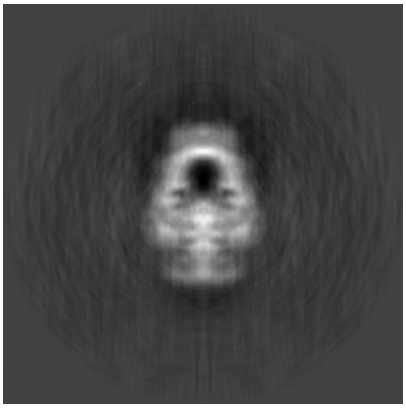


Y

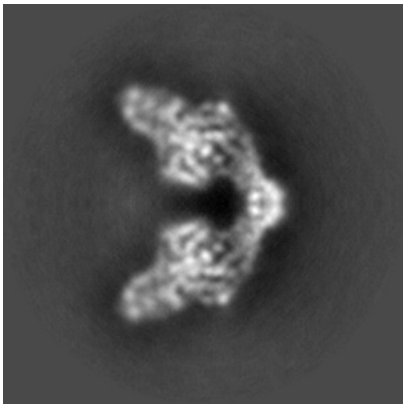


Z

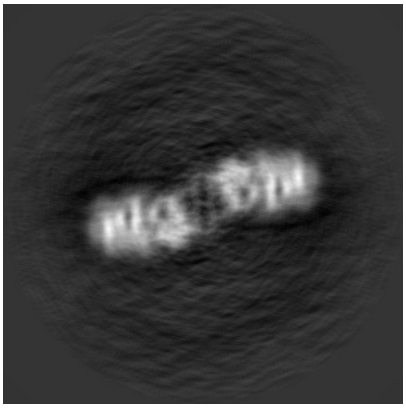
6.1.2 Raw map



X



Y

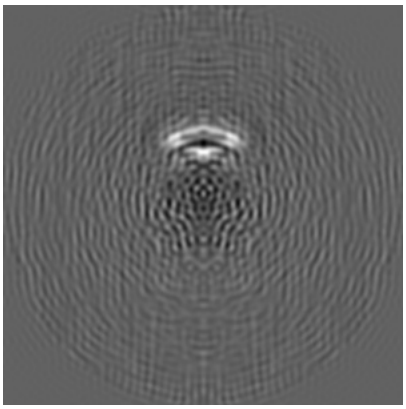


Z

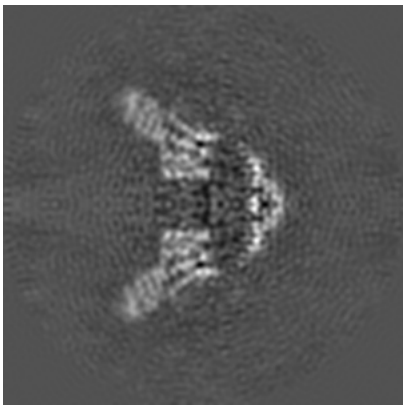
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

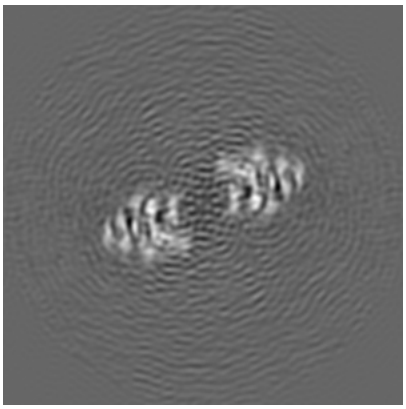
6.2.1 Primary map



X Index: 180

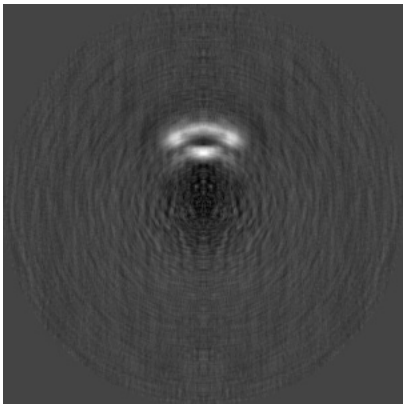


Y Index: 180

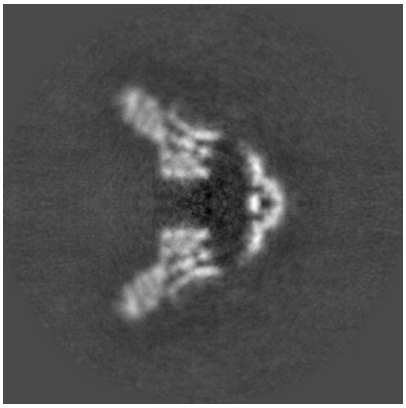


Z Index: 180

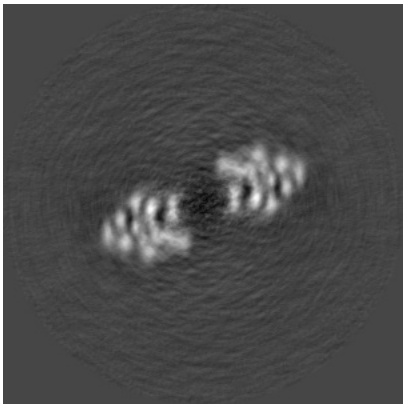
6.2.2 Raw map



X Index: 180



Y Index: 180

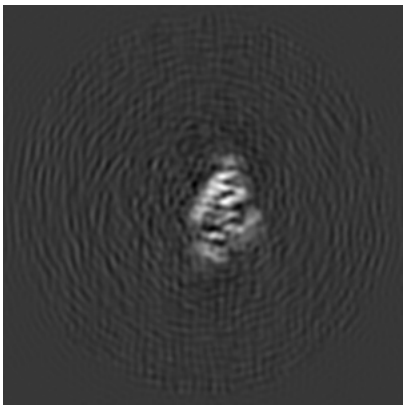


Z Index: 180

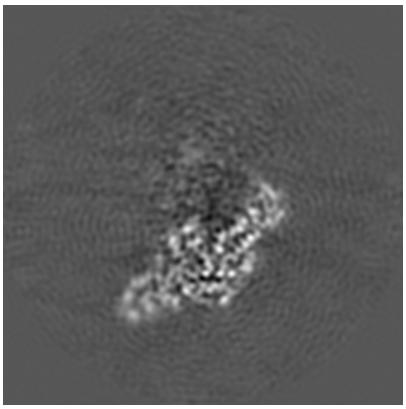
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

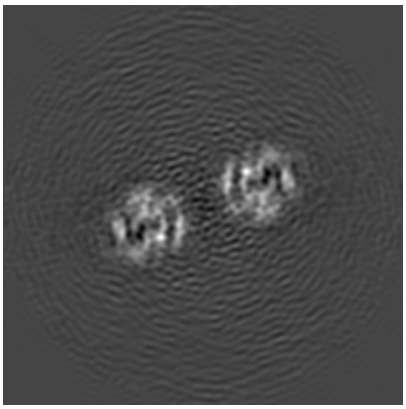
6.3.1 Primary map



X Index: 242

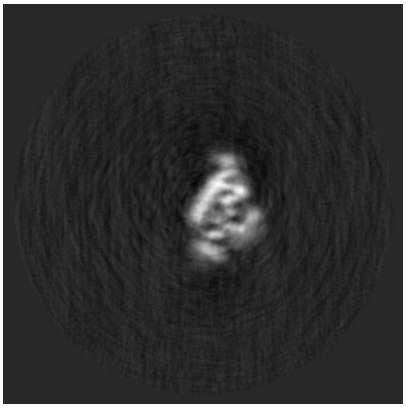


Y Index: 162

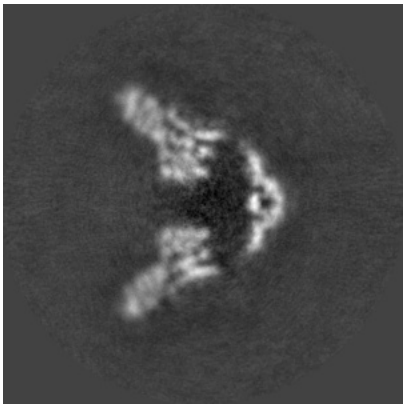


Z Index: 167

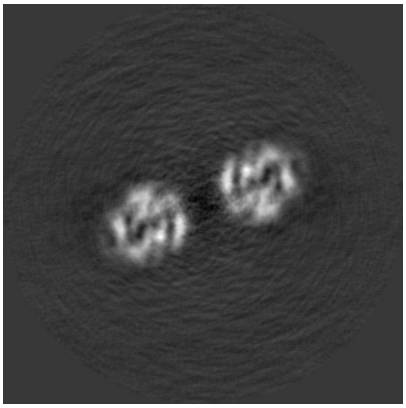
6.3.2 Raw map



X Index: 241



Y Index: 182

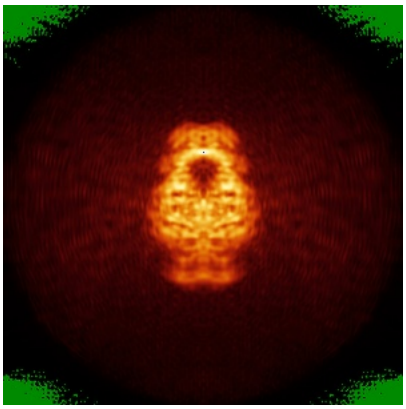


Z Index: 167

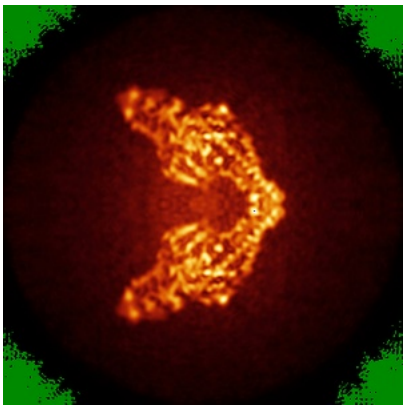
The images above show the largest variance slices of the map in three orthogonal directions.

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

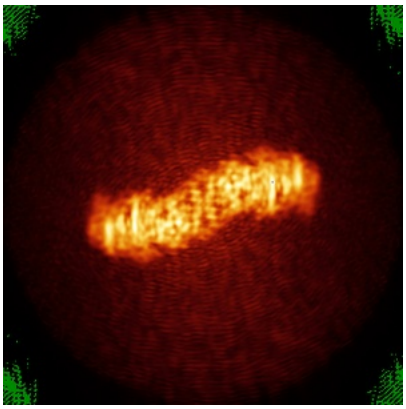
6.4.1 Primary map



X

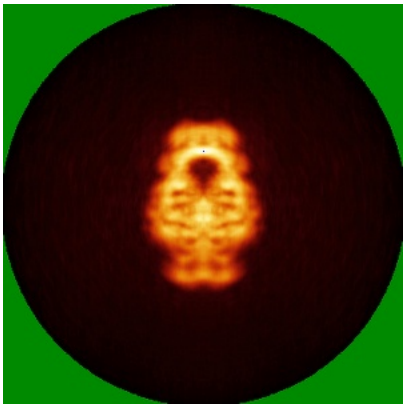


Y



Z

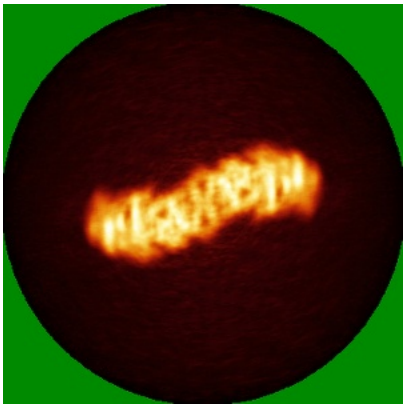
6.4.2 Raw map



X



Y

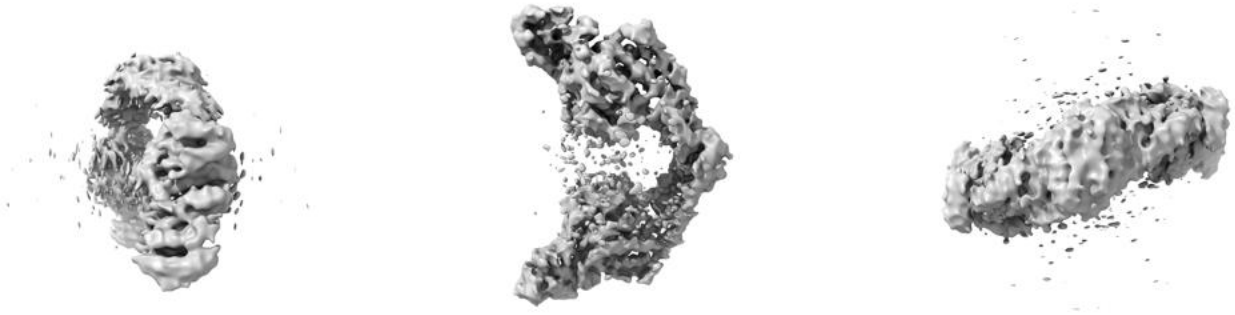


Z

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 0.0035. 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.

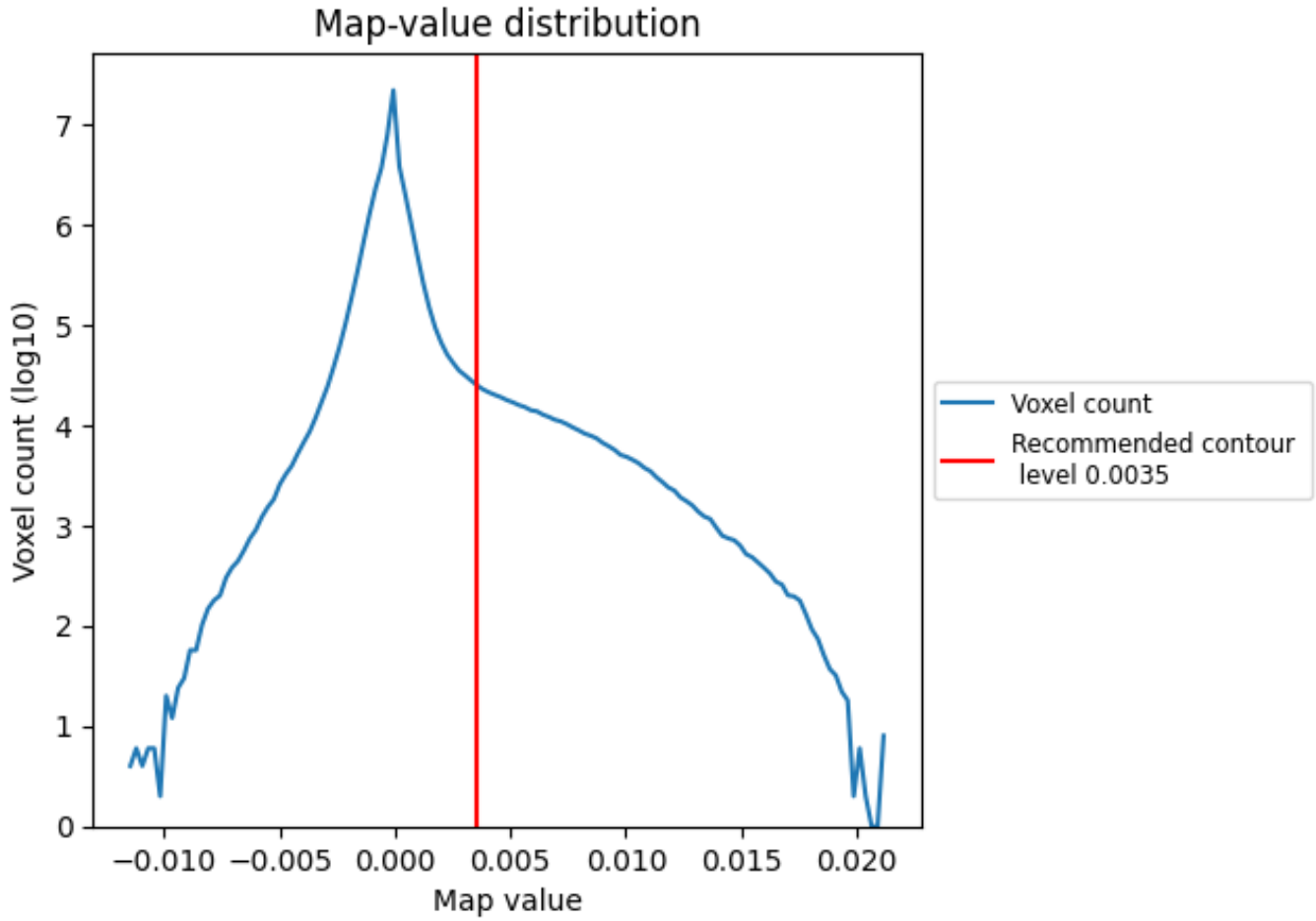
6.6 Mask visualisation (i)

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

7 Map analysis

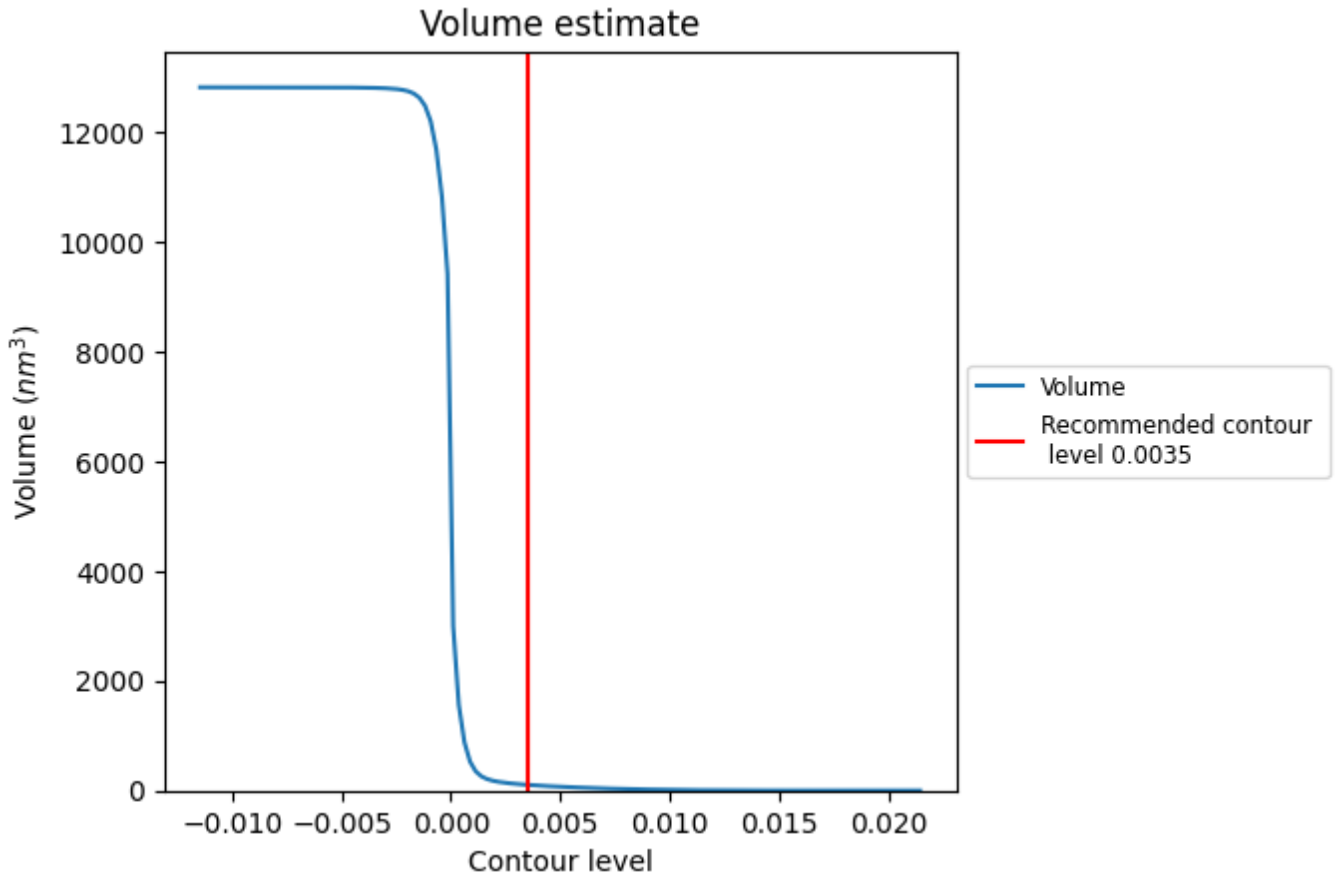
This section contains the results of statistical analysis of the map.

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.

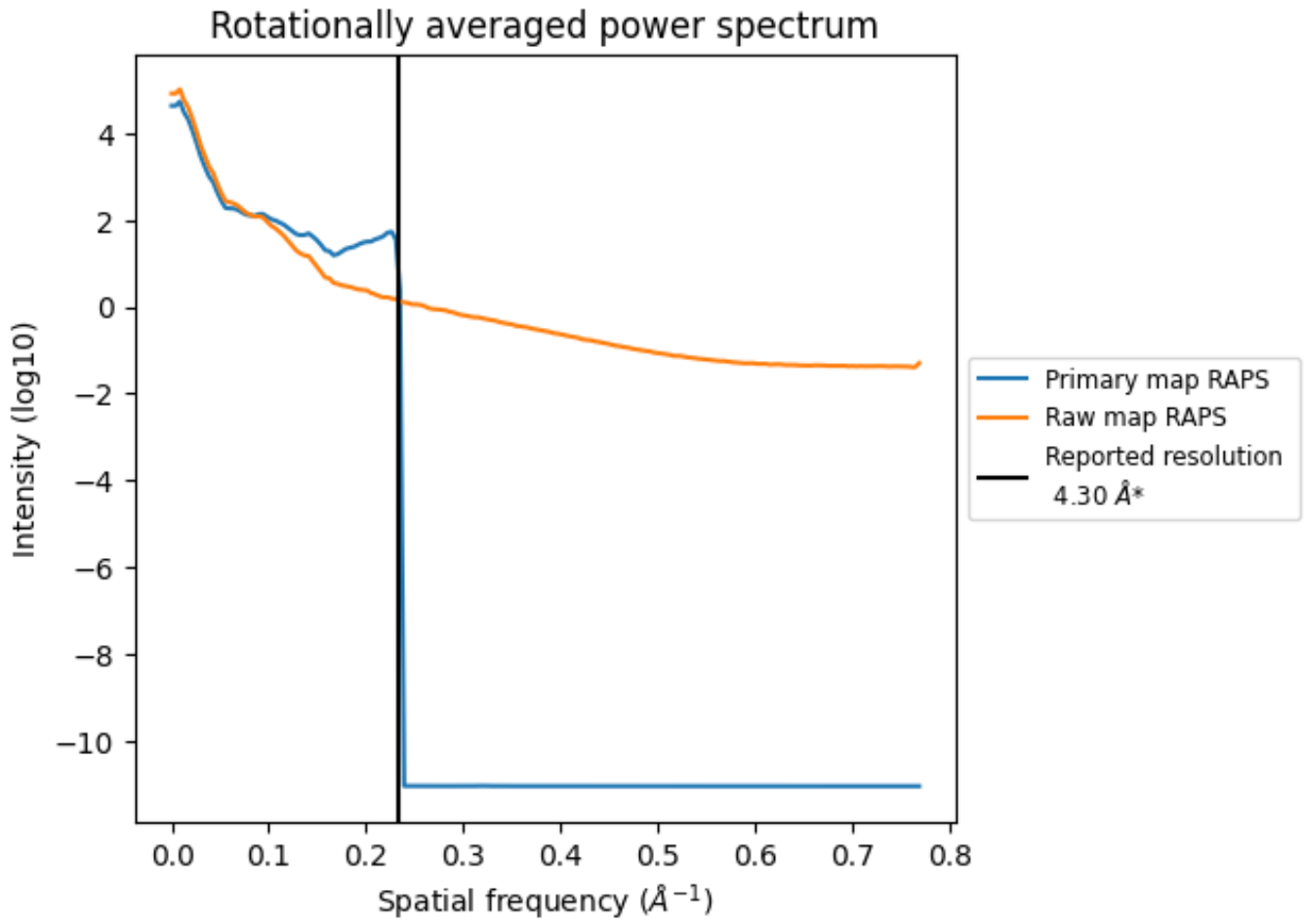
7.2 Volume estimate



The volume at the recommended contour level is 104 nm^3; this corresponds to an approximate mass of 94 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)

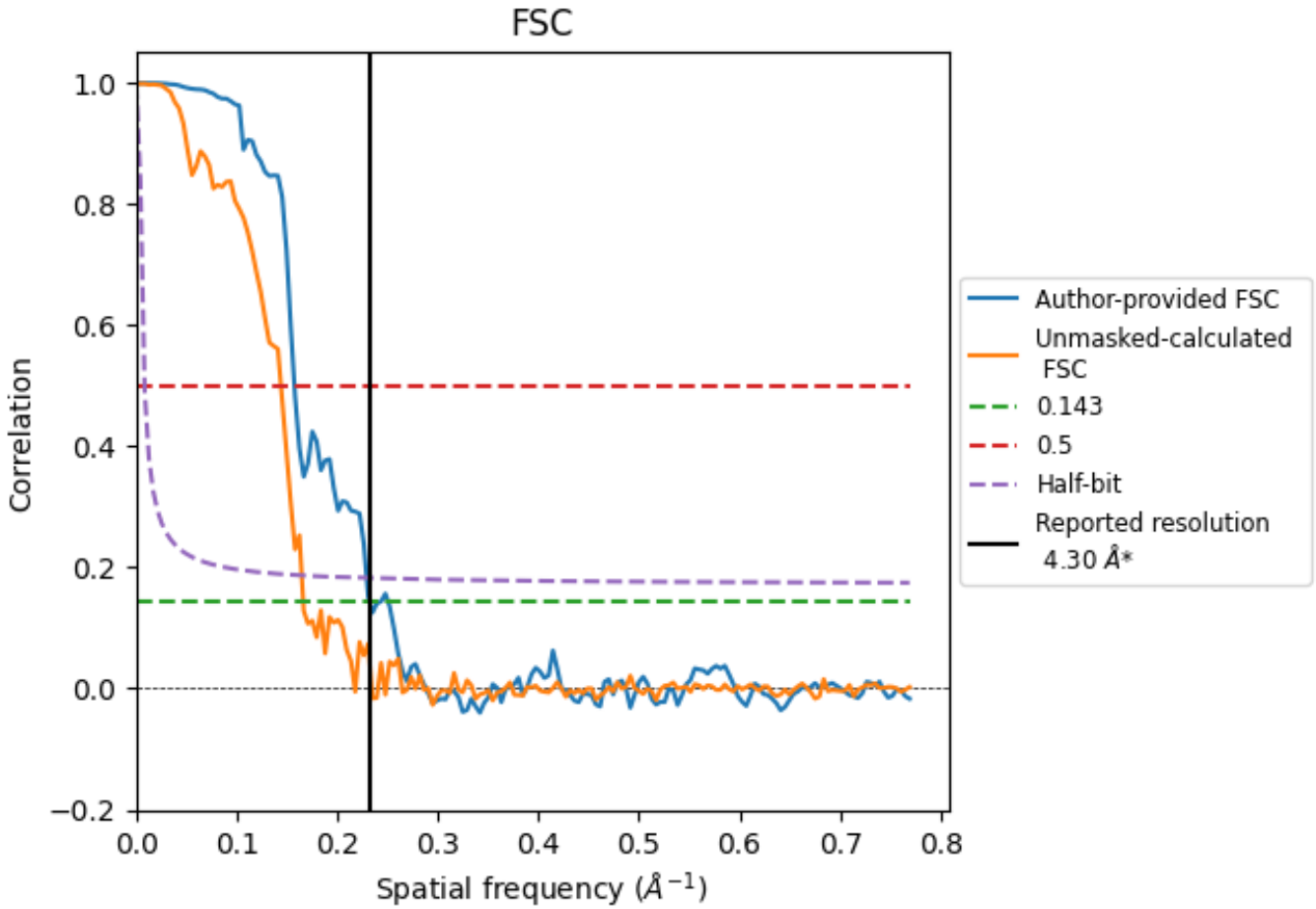


*Reported resolution corresponds to spatial frequency of 0.233 Å^{-1}

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 0.233 Å^{-1}

8.2 Resolution estimates (i)

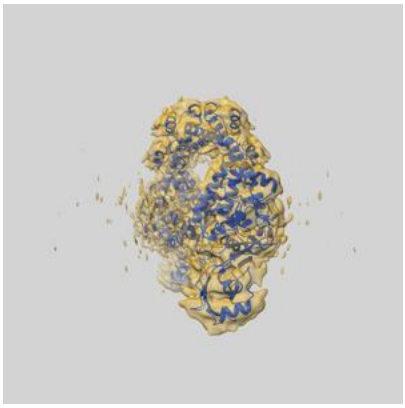
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.31	6.35	4.36
Unmasked-calculated*	6.02	6.94	6.07

*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 6.02 differs from the reported value 4.3 by more than 10 %

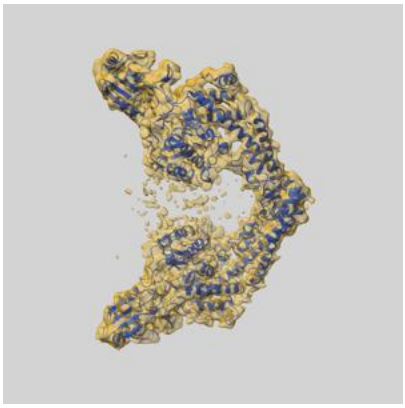
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-37225 and PDB model 8KGL. Per-residue inclusion information can be found in section 3 on page 5.

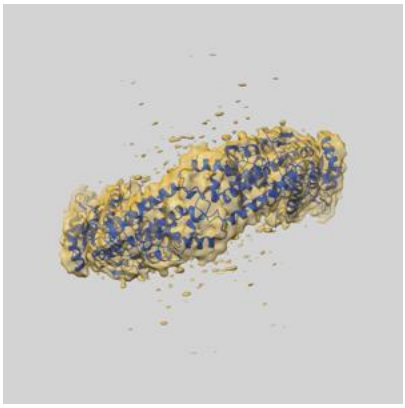
9.1 Map-model overlay



X



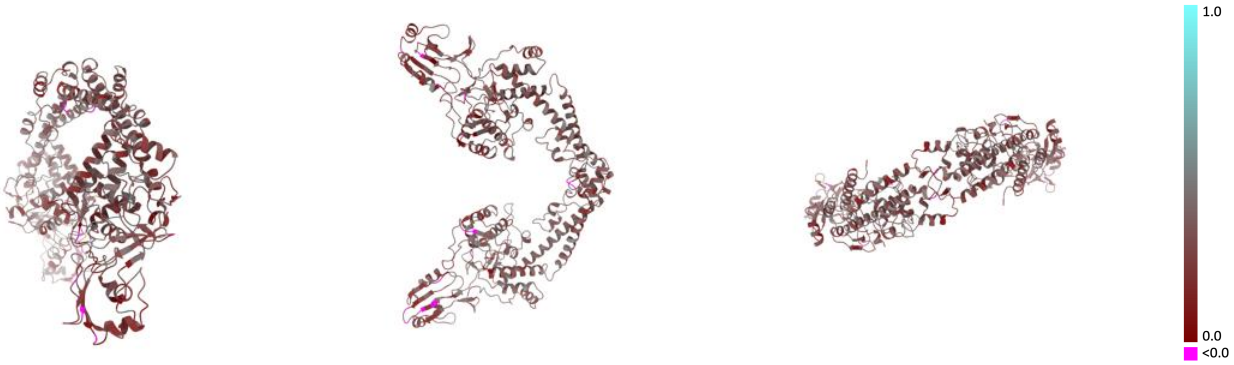
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0035 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.

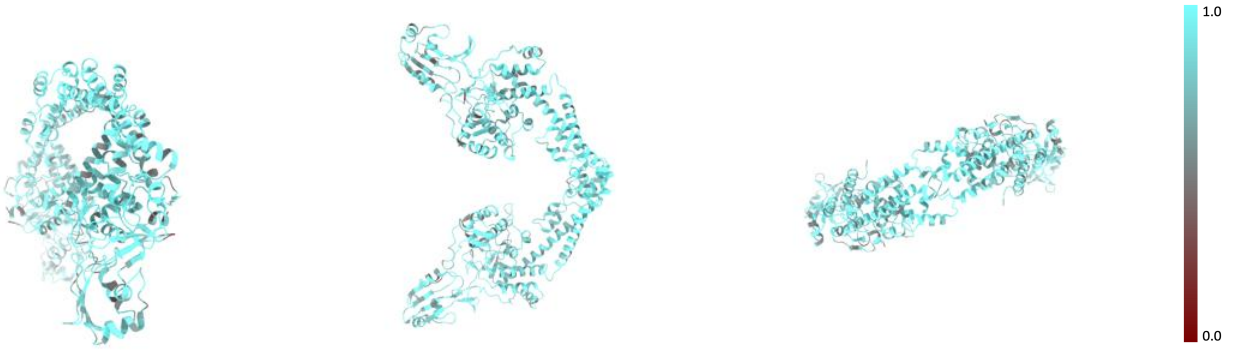
9.2 Q-score mapped to coordinate model (i)



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.

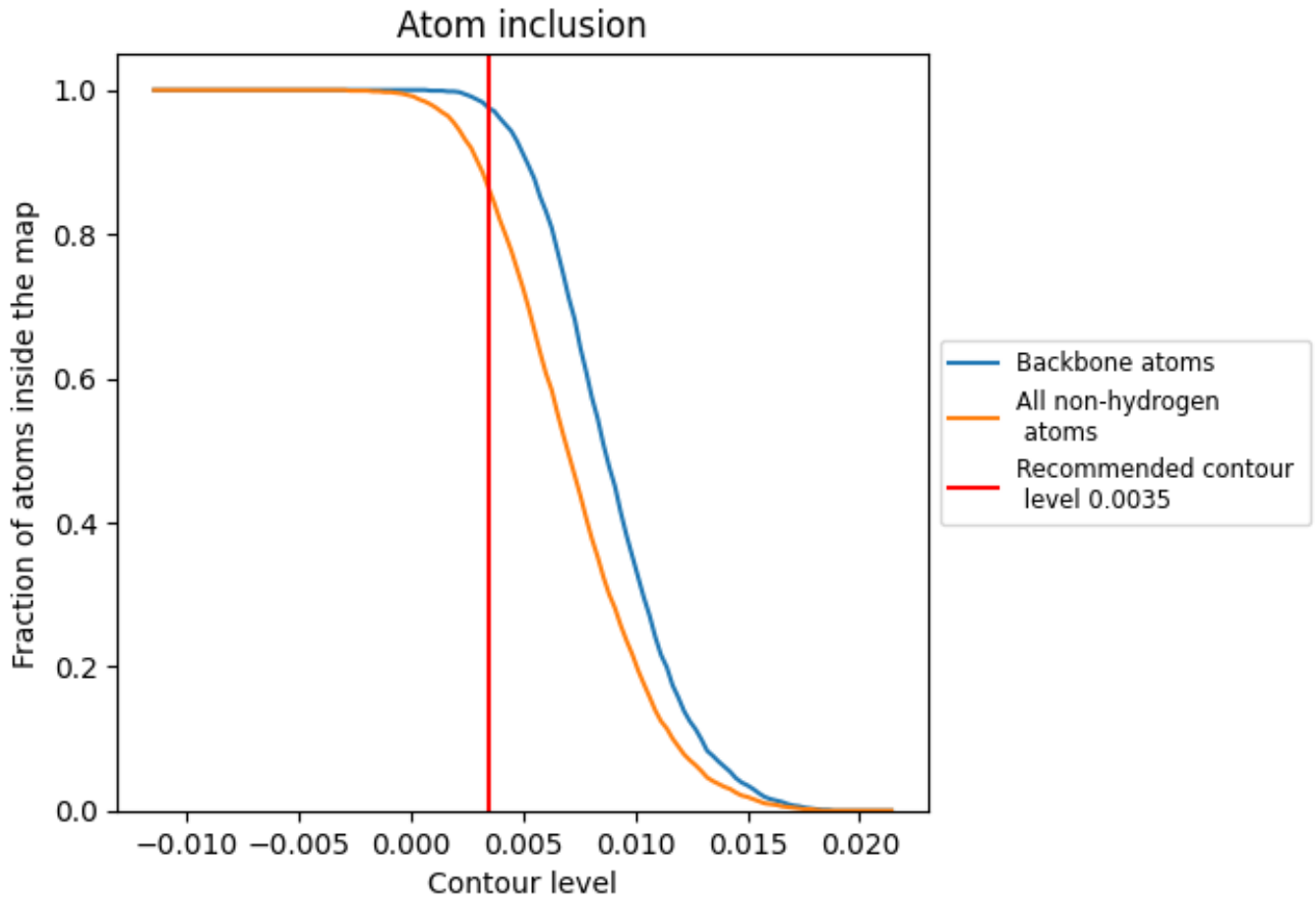
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.0035).

9.4 Atom inclusion (i)



At the recommended contour level, 97% of all backbone atoms, 86% 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 (0.0035) and Q-score for the entire model and for each chain.



Chain	Atom inclusion	Q-score
All	0.8600	0.3030
A	0.8590	0.3020
B	0.8610	0.3030