



Full wwPDB EM Validation Report ⓘ

Jul 27, 2026 – 01:48 PM JST

PDB ID : 9W4A / pdb_00009w4a
EMDB ID : EMD-65623
Title : cryo-EM structure of acetyl-CoA carboxyltransferase holoenzyme dimer from
Shewanella oneidensis, mutant E1238A
Authors : Wang, W.; Han, S.R.; Xu, Y.Y.; Gao, H.C.
Deposited on : 2025-07-31
Resolution : 4.25 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:

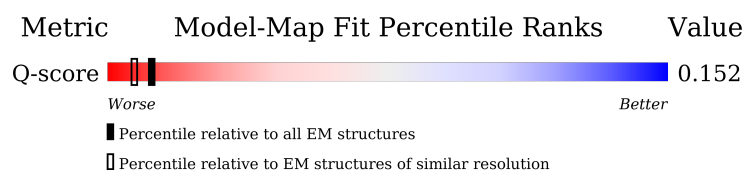
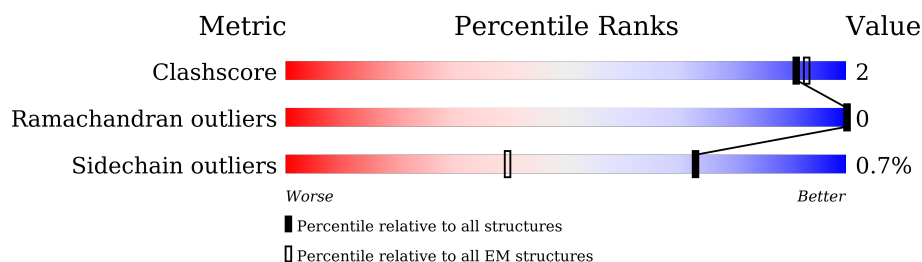
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 4.25 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	4654 (3.75 - 4.75)

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	1517	
1	B	1517	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 21198 atoms, of which 0 are hydrogens and 0 are deuteriums.

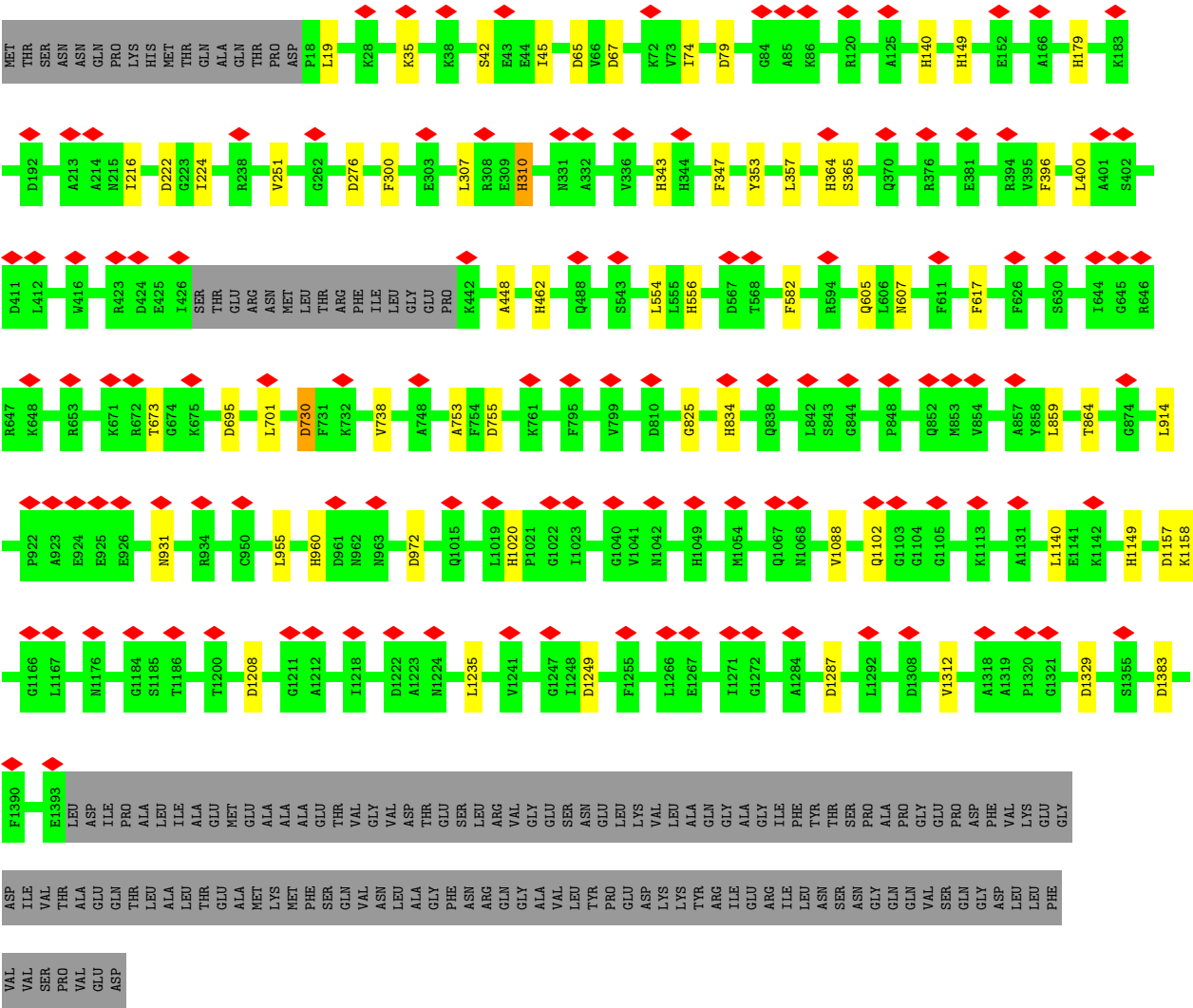
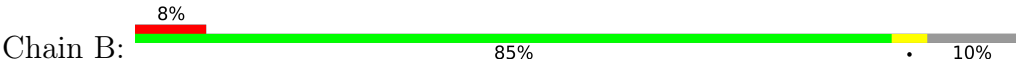
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Acetyl-CoA carboxylase multifunctional enzyme AccADCB.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1361	Total	C	N	O	S	0	0
			10599	6716	1838	2001	44		
1	B	1361	Total	C	N	O	S	0	0
			10599	6716	1838	2001	44		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1238	ALA	GLU	engineered mutation	UNP Q8EIJ9
B	1238	ALA	GLU	engineered mutation	UNP Q8EIJ9



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	95492	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	11.884	Depositor
Minimum map value	-2.073	Depositor
Average map value	-0.088	Depositor
Map value standard deviation	0.643	Depositor
Recommended contour level	2.48	Depositor
Map size ($\text{\AA}$)	238.08, 238.08, 238.08	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.93, 0.93, 0.93	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	0.89	0/10808	1.60	44/14642 (0.3%)
1	B	0.89	0/10808	1.59	50/14642 (0.3%)
All	All	0.89	0/21616	1.59	94/29284 (0.3%)

There are no bond length outliers.

All (94) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	972	ASP	CA-CB-CG	9.14	121.74	112.60
1	A	1287	ASP	CA-CB-CG	7.82	120.42	112.60
1	A	607	ASN	CA-CB-CG	7.77	120.37	112.60
1	B	730	ASP	CA-CB-CG	7.66	120.26	112.60
1	B	607	ASN	CA-CB-CG	7.65	120.25	112.60
1	A	1329	ASP	CA-CB-CG	7.05	119.65	112.60
1	B	1287	ASP	CA-CB-CG	7.04	119.64	112.60
1	B	825	GLY	CA-C-N	6.97	127.83	120.03
1	B	825	GLY	C-N-CA	6.97	127.83	120.03
1	B	1329	ASP	CA-CB-CG	6.91	119.51	112.60
1	B	65	ASP	CA-CB-CG	6.71	119.31	112.60
1	B	695	ASP	CA-CB-CG	6.71	119.31	112.60
1	A	695	ASP	CA-CB-CG	6.69	119.29	112.60
1	A	105	PHE	CA-CB-CG	6.61	120.41	113.80
1	A	505	ASN	CA-C-N	6.16	128.82	120.38
1	A	505	ASN	C-N-CA	6.16	128.82	120.38
1	A	1249	ASP	CA-CB-CG	6.14	118.74	112.60
1	A	1232	ASN	CA-CB-CG	6.13	118.73	112.60
1	A	241	ASN	CB-CA-C	6.02	119.82	111.63
1	A	590	ASP	CA-CB-CG	6.01	118.61	112.60
1	A	65	ASP	CA-CB-CG	5.91	118.50	112.60
1	B	582	PHE	CA-CB-CG	5.91	119.70	113.80
1	A	79	ASP	CA-CB-CG	5.90	118.50	112.60
1	B	1157	ASP	CA-CB-CG	5.89	118.49	112.60
1	B	364	HIS	CA-CB-CG	5.79	119.59	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	755	ASP	CA-CB-CG	5.74	118.33	112.60
1	B	222	ASP	CA-CB-CG	5.73	118.33	112.60
1	A	347	PHE	CA-C-N	5.72	126.29	119.94
1	A	347	PHE	C-N-CA	5.72	126.29	119.94
1	B	79	ASP	CA-CB-CG	5.68	118.28	112.60
1	B	1102	GLN	CA-C-N	5.65	125.71	120.34
1	B	1102	GLN	C-N-CA	5.65	125.71	120.34
1	A	179	HIS	CE1-NE2-CD2	-5.61	103.39	109.00
1	A	1208	ASP	CA-CB-CG	5.59	118.19	112.60
1	A	382	GLY	CA-C-N	5.55	127.98	120.38
1	A	382	GLY	C-N-CA	5.55	127.98	120.38
1	B	276	ASP	CA-CB-CG	5.51	118.11	112.60
1	B	347	PHE	CA-C-N	5.51	126.09	119.98
1	B	347	PHE	C-N-CA	5.51	126.09	119.98
1	A	831	PHE	N-CA-C	5.50	118.79	111.75
1	A	179	HIS	ND1-CE1-NE2	5.49	113.89	108.40
1	A	222	ASP	CA-CB-CG	5.48	118.08	112.60
1	B	35	LYS	N-CA-C	5.46	116.92	111.07
1	B	1249	ASP	CA-CB-CG	5.45	118.05	112.60
1	B	67	ASP	CA-CB-CG	5.44	118.04	112.60
1	B	755	ASP	CA-CB-CG	5.41	118.01	112.60
1	B	462	HIS	ND1-CE1-NE2	5.41	113.81	108.40
1	A	946	HIS	CE1-NE2-CD2	-5.37	103.63	109.00
1	B	1208	ASP	CA-CB-CG	5.37	117.97	112.60
1	B	1149	HIS	ND1-CE1-NE2	5.35	113.75	108.40
1	A	822	ASP	CA-CB-CG	5.31	117.91	112.60
1	B	310	HIS	ND1-CE1-NE2	5.31	113.71	108.40
1	A	996	THR	CA-C-N	5.30	127.64	120.38
1	A	996	THR	C-N-CA	5.30	127.64	120.38
1	B	960	HIS	ND1-CE1-NE2	5.29	113.69	108.40
1	B	1383	ASP	CA-CB-CG	5.27	117.87	112.60
1	B	931	ASN	CA-C-N	5.25	128.56	121.20
1	B	931	ASN	C-N-CA	5.25	128.56	121.20
1	A	946	HIS	ND1-CE1-NE2	5.24	113.64	108.40
1	A	176	ASN	CA-C-N	5.20	127.56	120.54
1	A	176	ASN	C-N-CA	5.20	127.56	120.54
1	A	981	ASP	CA-CB-CG	5.18	117.78	112.60
1	A	140	HIS	CE1-NE2-CD2	-5.14	103.86	109.00
1	B	673	THR	CA-C-N	5.12	127.84	120.11
1	B	673	THR	C-N-CA	5.12	127.84	120.11
1	B	343	HIS	CE1-NE2-CD2	-5.11	103.89	109.00
1	A	139	HIS	CE1-NE2-CD2	-5.10	103.90	109.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1020	HIS	CE1-NE2-CD2	-5.10	103.90	109.00
1	B	310	HIS	CE1-NE2-CD2	-5.09	103.91	109.00
1	B	364	HIS	CE1-NE2-CD2	-5.08	103.92	109.00
1	A	462	HIS	CE1-NE2-CD2	-5.08	103.92	109.00
1	B	753	ALA	CA-C-N	5.07	127.97	120.82
1	B	753	ALA	C-N-CA	5.07	127.97	120.82
1	A	631	ASP	CA-CB-CG	5.07	117.67	112.60
1	A	478	HIS	ND1-CE1-NE2	5.07	113.47	108.40
1	B	556	HIS	CE1-NE2-CD2	-5.07	103.94	109.00
1	A	462	HIS	ND1-CE1-NE2	5.06	113.46	108.40
1	A	409	ASP	CA-CB-CG	5.06	117.66	112.60
1	B	834	HIS	ND1-CE1-NE2	5.06	113.46	108.40
1	B	834	HIS	CE1-NE2-CD2	-5.05	103.94	109.00
1	B	448	ALA	CA-C-N	5.05	127.01	120.44
1	B	448	ALA	C-N-CA	5.05	127.01	120.44
1	B	149	HIS	ND1-CE1-NE2	5.05	113.45	108.40
1	A	280	HIS	CE1-NE2-CD2	-5.05	103.95	109.00
1	B	556	HIS	ND1-CE1-NE2	5.04	113.44	108.40
1	A	343	HIS	CE1-NE2-CD2	-5.03	103.97	109.00
1	B	140	HIS	ND1-CE1-NE2	5.03	113.43	108.40
1	A	101	HIS	ND1-CE1-NE2	5.02	113.42	108.40
1	B	179	HIS	CE1-NE2-CD2	-5.02	103.98	109.00
1	A	36	HIS	CE1-NE2-CD2	-5.01	103.99	109.00
1	A	344	HIS	CE1-NE2-CD2	-5.01	103.99	109.00
1	B	140	HIS	CE1-NE2-CD2	-5.01	103.99	109.00
1	A	1265	HIS	ND1-CE1-NE2	5.00	113.41	108.40
1	B	149	HIS	CE1-NE2-CD2	-5.00	104.00	109.00

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	10599	0	10598	53	0
1	B	10599	0	10598	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	21198	0	21196	66	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (66) 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:762:PHE:HZ	1:A:804:ILE:CG1	1.52	1.23
1:A:762:PHE:CE1	1:A:766:LEU:HD11	1.79	1.17
1:A:762:PHE:CZ	1:A:804:ILE:HD11	1.81	1.15
1:A:762:PHE:CZ	1:A:804:ILE:CD1	2.32	1.12
1:A:762:PHE:CE1	1:A:766:LEU:CD1	2.31	1.11
1:A:762:PHE:HZ	1:A:804:ILE:CD1	1.63	1.07
1:A:762:PHE:CE2	1:A:804:ILE:HD11	1.89	1.06
1:A:762:PHE:CZ	1:A:804:ILE:HG13	1.91	1.06
1:A:762:PHE:CZ	1:A:804:ILE:CG1	2.42	1.02
1:A:762:PHE:HE1	1:A:766:LEU:CD1	1.71	1.02
1:A:762:PHE:HZ	1:A:804:ILE:HG13	1.21	0.96
1:A:762:PHE:CE1	1:A:766:LEU:HD12	2.07	0.87
1:A:762:PHE:HE1	1:A:766:LEU:HD12	1.45	0.78
1:A:1189:PRO:HD3	1:A:1219:TYR:OH	1.84	0.77
1:A:762:PHE:CZ	1:A:766:LEU:HD11	2.25	0.69
1:A:593:VAL:HA	1:A:596:GLU:HG3	1.74	0.68
1:A:762:PHE:HE2	1:A:804:ILE:HD11	1.56	0.67
1:A:593:VAL:HA	1:A:596:GLU:CG	2.25	0.66
1:A:593:VAL:O	1:A:596:GLU:HG3	1.98	0.63
1:A:702:LEU:HD23	1:A:702:LEU:H	1.65	0.62
1:A:762:PHE:CG	1:A:800:VAL:HG13	2.35	0.61
1:A:241:ASN:HD21	1:A:391:GLU:HB2	1.65	0.61
1:A:1079:LEU:HD11	1:A:1140:LEU:HB2	1.83	0.60
1:A:762:PHE:CE1	1:A:804:ILE:HG13	2.36	0.60
1:A:596:GLU:OE2	1:A:597:GLN:HG3	2.01	0.60
1:A:762:PHE:CD2	1:A:800:VAL:HG13	2.37	0.60
1:A:1188:LEU:HA	1:A:1219:TYR:CZ	2.38	0.58
1:A:1354:ASP:OD2	1:A:1369:LYS:HE3	2.04	0.56
1:A:371:TYR:OH	1:A:708:ARG:CG	2.52	0.56
1:A:762:PHE:C	1:A:762:PHE:CD1	2.84	0.55
1:A:406:LEU:C	1:A:406:LEU:HD23	2.33	0.54
1:A:241:ASN:ND2	1:A:391:GLU:HB2	2.22	0.54
1:A:371:TYR:OH	1:A:708:ARG:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1189:PRO:CD	1:A:1219:TYR:OH	2.55	0.52
1:A:453:LEU:HD22	1:A:512:PHE:HB2	1.91	0.52
1:A:593:VAL:CA	1:A:596:GLU:HG3	2.39	0.51
1:B:738:VAL:HG11	1:B:914:LEU:HD22	1.92	0.51
1:A:307:LEU:HD21	1:A:350:ALA:HB2	1.91	0.50
1:A:593:VAL:C	1:A:596:GLU:HG3	2.36	0.50
1:A:1155:LEU:HD11	1:A:1165:LEU:HD11	1.94	0.50
1:B:74:ILE:HA	1:B:224:ILE:HD11	1.94	0.50
1:A:453:LEU:HD21	1:A:508:LEU:HB3	1.95	0.48
1:A:19:LEU:HD11	1:A:353:TYR:CE2	2.48	0.47
1:A:1188:LEU:HA	1:A:1219:TYR:OH	2.14	0.47
1:B:42:SER:HA	1:B:45:ILE:HD12	1.96	0.47
1:A:240:TYR:O	1:A:241:ASN:OD1	2.33	0.47
1:A:593:VAL:O	1:A:596:GLU:OE2	2.32	0.47
1:A:1277:VAL:HG13	1:A:1349:LEU:HD21	1.97	0.46
1:A:406:LEU:HD11	1:A:416:TRP:HB2	1.97	0.46
1:A:406:LEU:HD23	1:A:406:LEU:O	2.15	0.46
1:A:762:PHE:CD1	1:A:800:VAL:HG13	2.50	0.45
1:B:1088:VAL:HG12	1:B:1140:LEU:HD22	1.99	0.45
1:B:300:PHE:CE2	1:B:307:LEU:HD22	2.51	0.45
1:B:353:TYR:CE1	1:B:357:LEU:HD11	2.52	0.44
1:B:859:LEU:HB3	1:B:864:THR:HG21	1.99	0.44
1:B:396:PHE:CE2	1:B:400:LEU:HD11	2.53	0.44
1:A:762:PHE:CD2	1:A:800:VAL:CG1	3.00	0.44
1:B:955:LEU:HD21	1:B:1235:LEU:HD22	1.98	0.43
1:A:702:LEU:H	1:A:702:LEU:CD2	2.29	0.43
1:A:251:VAL:HA	1:A:702:LEU:HD12	2.00	0.43
1:A:593:VAL:HA	1:A:596:GLU:HG2	2.01	0.43
1:A:738:VAL:HG11	1:A:914:LEU:HD22	1.99	0.43
1:B:19:LEU:HD22	1:B:310:HIS:CD2	2.54	0.43
1:B:19:LEU:HD22	1:B:310:HIS:CG	2.55	0.41
1:B:45:ILE:HD11	1:B:216:ILE:HD13	2.02	0.40
1:B:554:LEU:HD23	1:B:617:PHE:CE1	2.56	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	1357/1517 (90%)	1306 (96%)	51 (4%)	0	100	100
1	B	1357/1517 (90%)	1310 (96%)	47 (4%)	0	100	100
All	All	2714/3034 (90%)	2616 (96%)	98 (4%)	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	1146/1277 (90%)	1138 (99%)	8 (1%)	76	78
1	B	1146/1277 (90%)	1139 (99%)	7 (1%)	78	80
All	All	2292/2554 (90%)	2277 (99%)	15 (1%)	73	78

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	117	ARG
1	A	227	THR
1	A	546	LEU
1	A	733	GLU
1	A	755	ASP
1	A	1049	HIS
1	A	1147	LEU
1	A	1358	LEU

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Mol	Chain	Res	Type
1	B	251	VAL
1	B	365	SER
1	B	605	GLN
1	B	701	LEU
1	B	730	ASP
1	B	1158	LYS
1	B	1312	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (52) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	78	GLN
1	A	175	GLN
1	A	241	ASN
1	A	279	GLN
1	A	320	ASN
1	A	413	ASN
1	A	418	ASN
1	A	462	HIS
1	A	467	ASN
1	A	470	ASN
1	A	496	GLN
1	A	505	ASN
1	A	528	ASN
1	A	561	HIS
1	A	570	ASN
1	A	640	ASN
1	A	750	GLN
1	A	846	ASN
1	A	891	GLN
1	A	931	ASN
1	A	962	ASN
1	A	995	ASN
1	A	1067	GLN
1	A	1081	ASN
1	A	1102	GLN
1	A	1135	ASN
1	A	1149	HIS
1	A	1220	ASN
1	A	1341	ASN
1	A	1350	HIS

Continued on next page...

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Mol	Chain	Res	Type
1	B	22	GLN
1	B	25	HIS
1	B	78	GLN
1	B	279	GLN
1	B	368	GLN
1	B	478	HIS
1	B	505	ASN
1	B	552	ASN
1	B	553	ASN
1	B	566	GLN
1	B	640	ASN
1	B	684	GLN
1	B	887	ASN
1	B	960	HIS
1	B	963	ASN
1	B	1003	ASN
1	B	1056	ASN
1	B	1065	GLN
1	B	1224	ASN
1	B	1236	GLN
1	B	1309	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](#)

There are no ligands in this entry.

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.

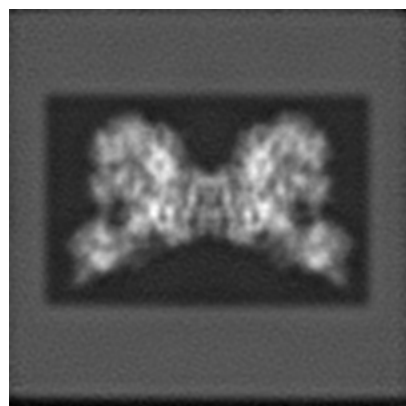
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65623. These allow visual inspection of the internal detail of the map and identification of artifacts.

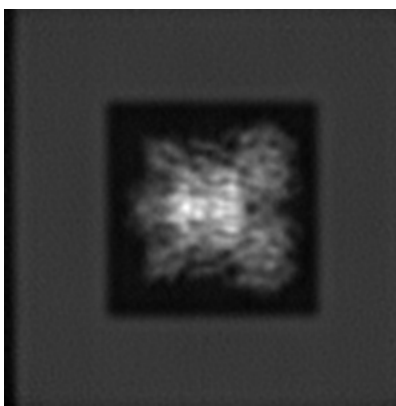
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

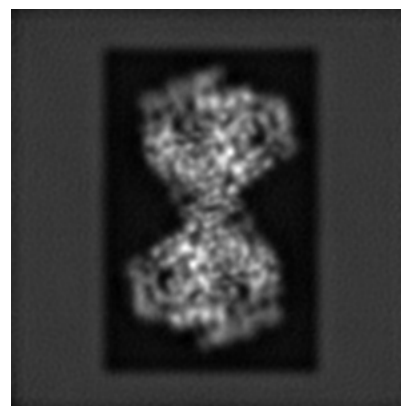
6.1.1 Primary map



X

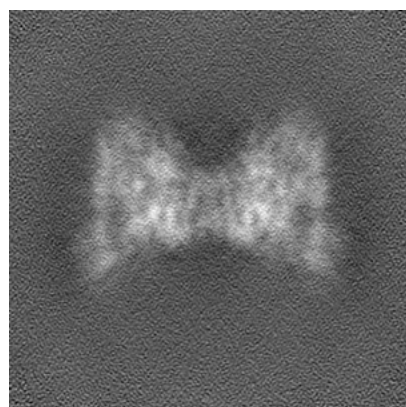


Y

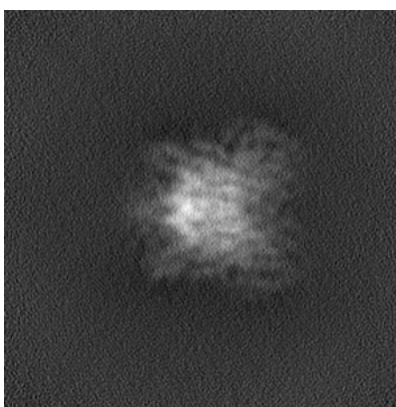


Z

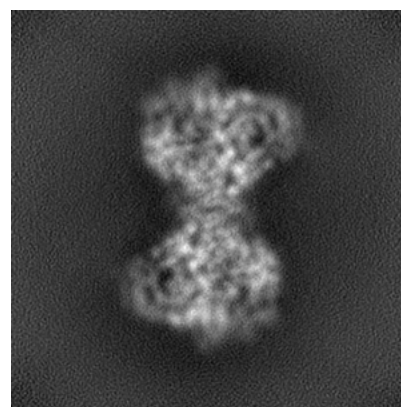
6.1.2 Raw map



X



Y



Z

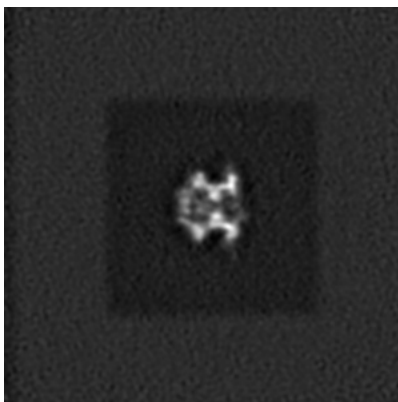
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

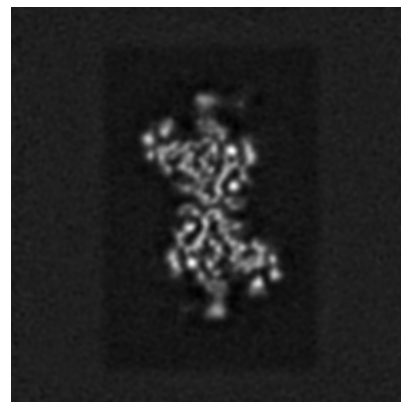
6.2.1 Primary map



X Index: 128

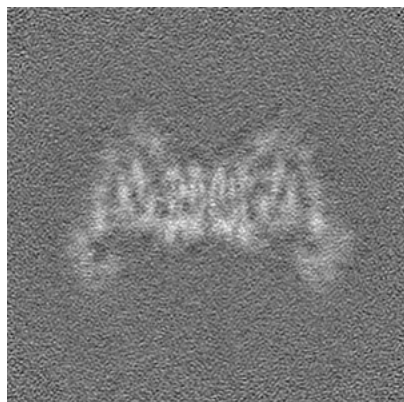


Y Index: 128

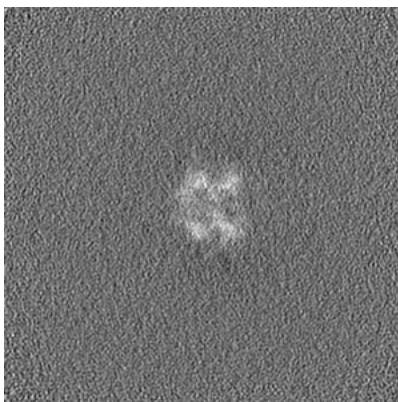


Z Index: 128

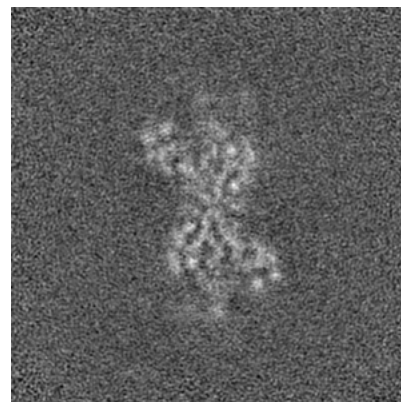
6.2.2 Raw map



X Index: 128



Y Index: 128

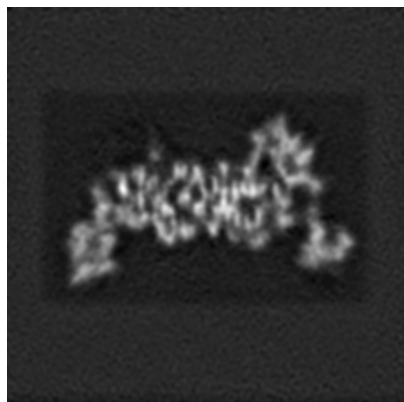


Z Index: 128

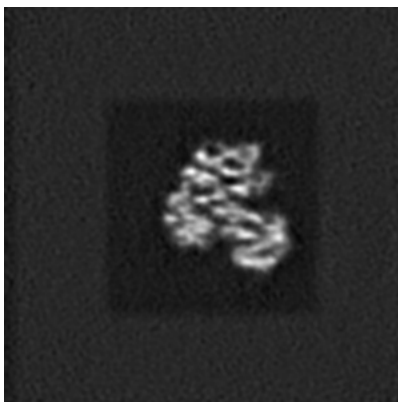
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

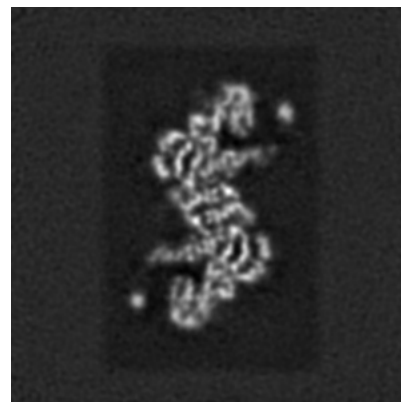
6.3.1 Primary map



X Index: 132

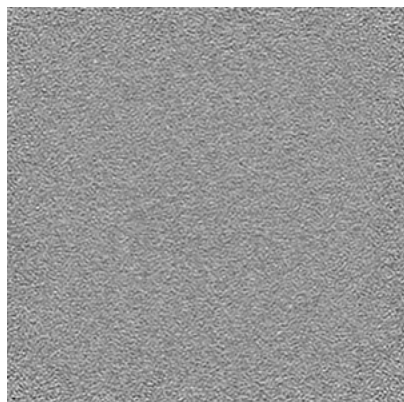


Y Index: 101

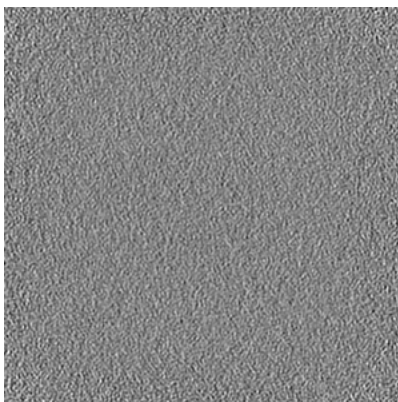


Z Index: 146

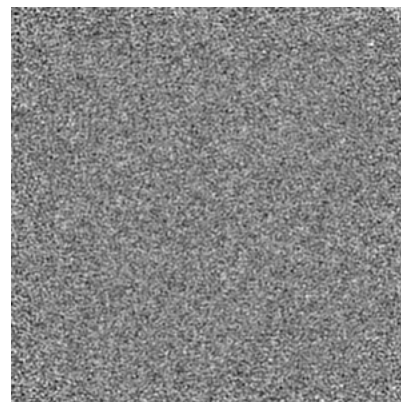
6.3.2 Raw map



X Index: 0



Y Index: 0

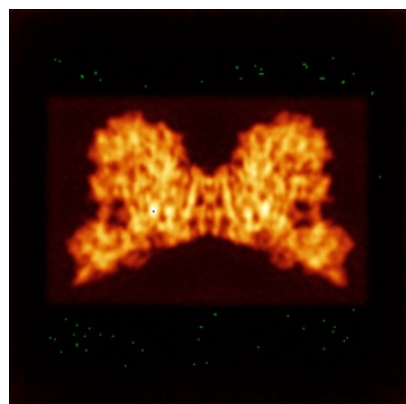


Z Index: 0

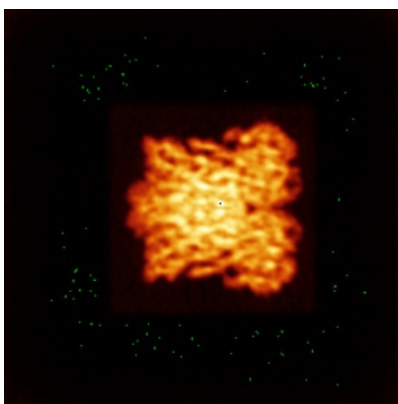
The images above show the largest variance slices of the map in three orthogonal directions.

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

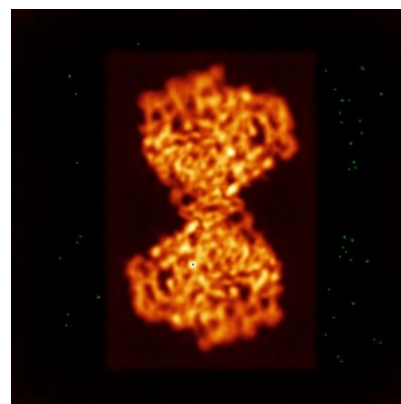
6.4.1 Primary map



X

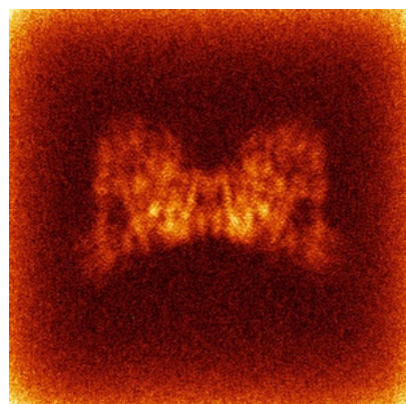


Y

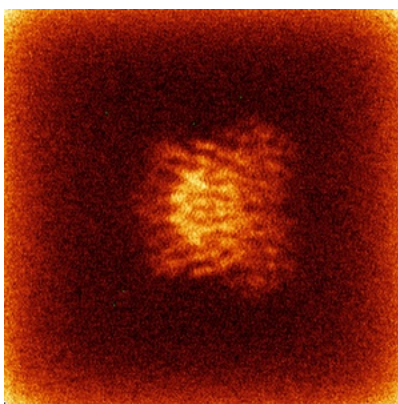


Z

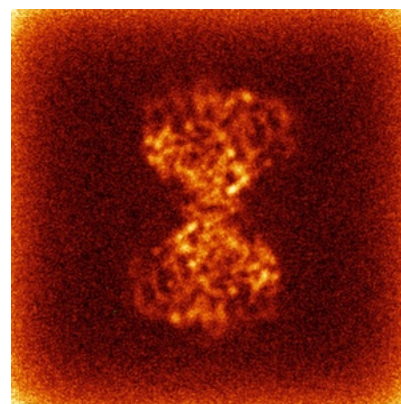
6.4.2 Raw map



X



Y

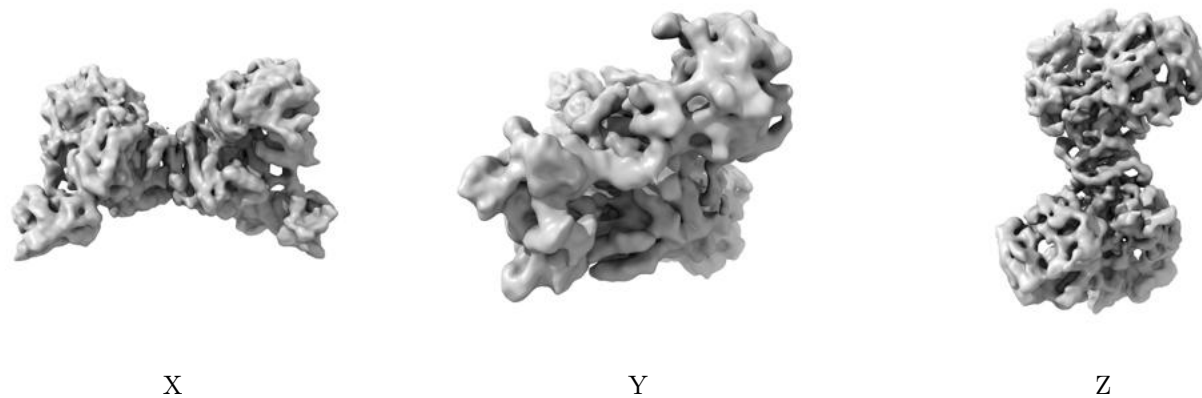


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

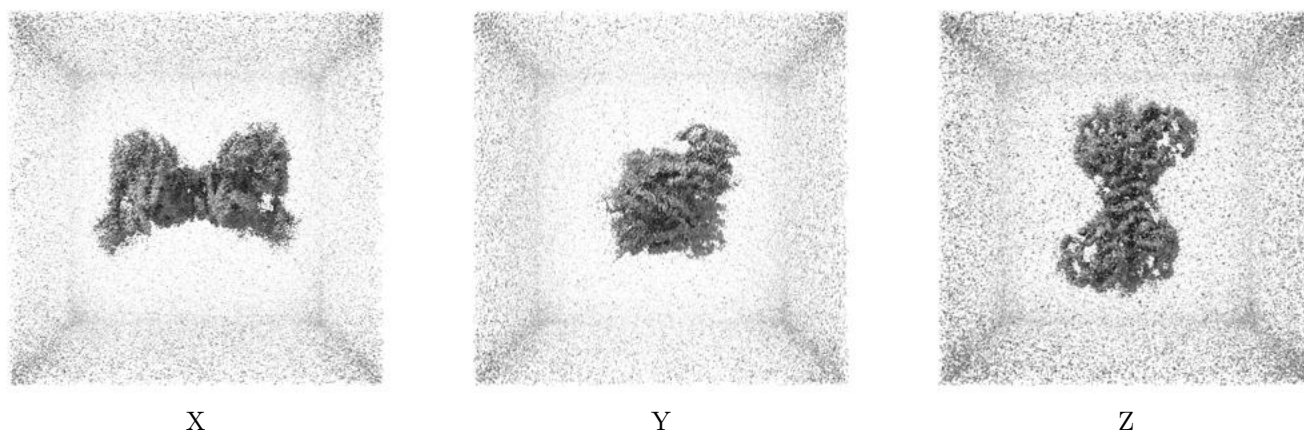
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.48. 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.

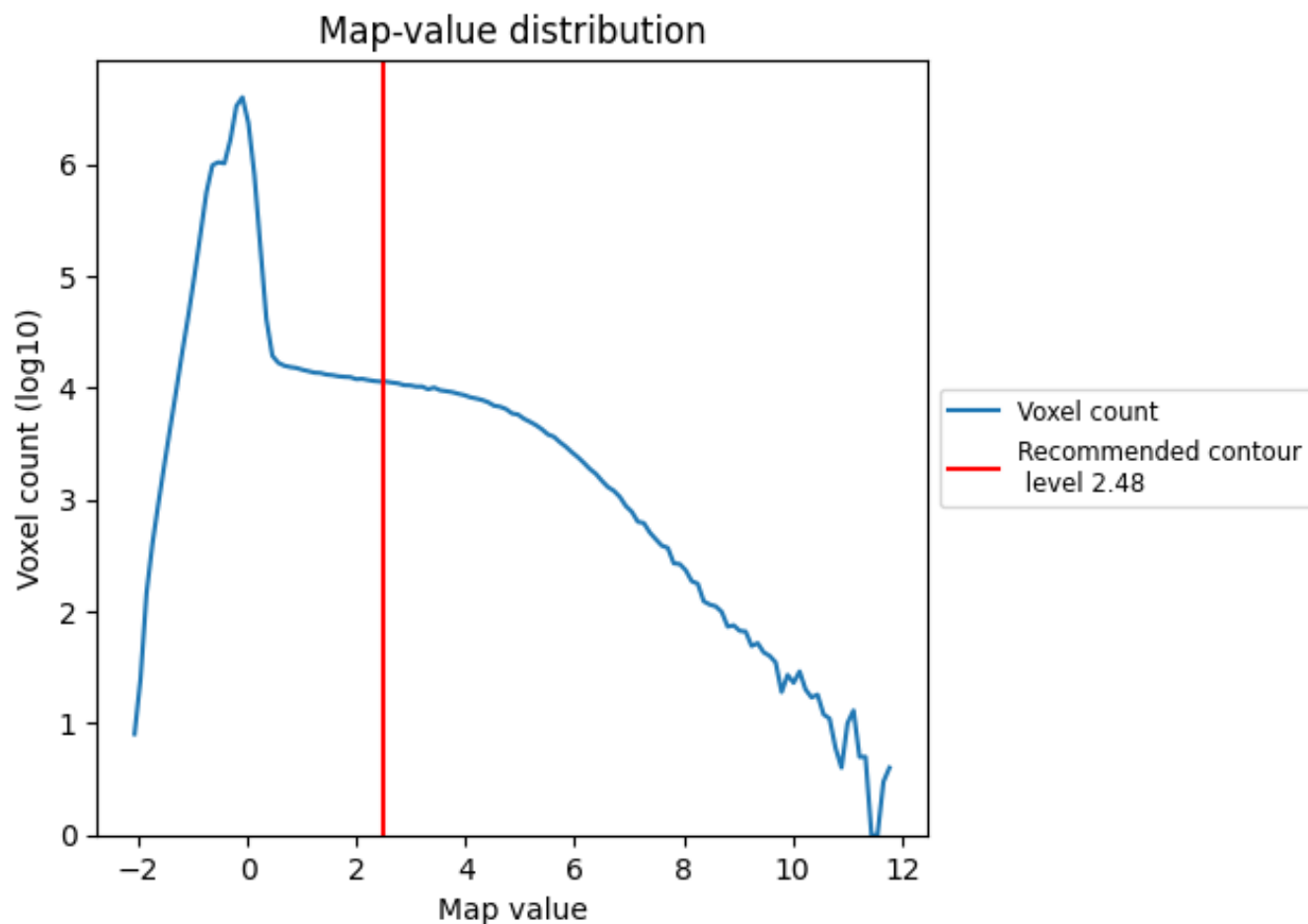
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

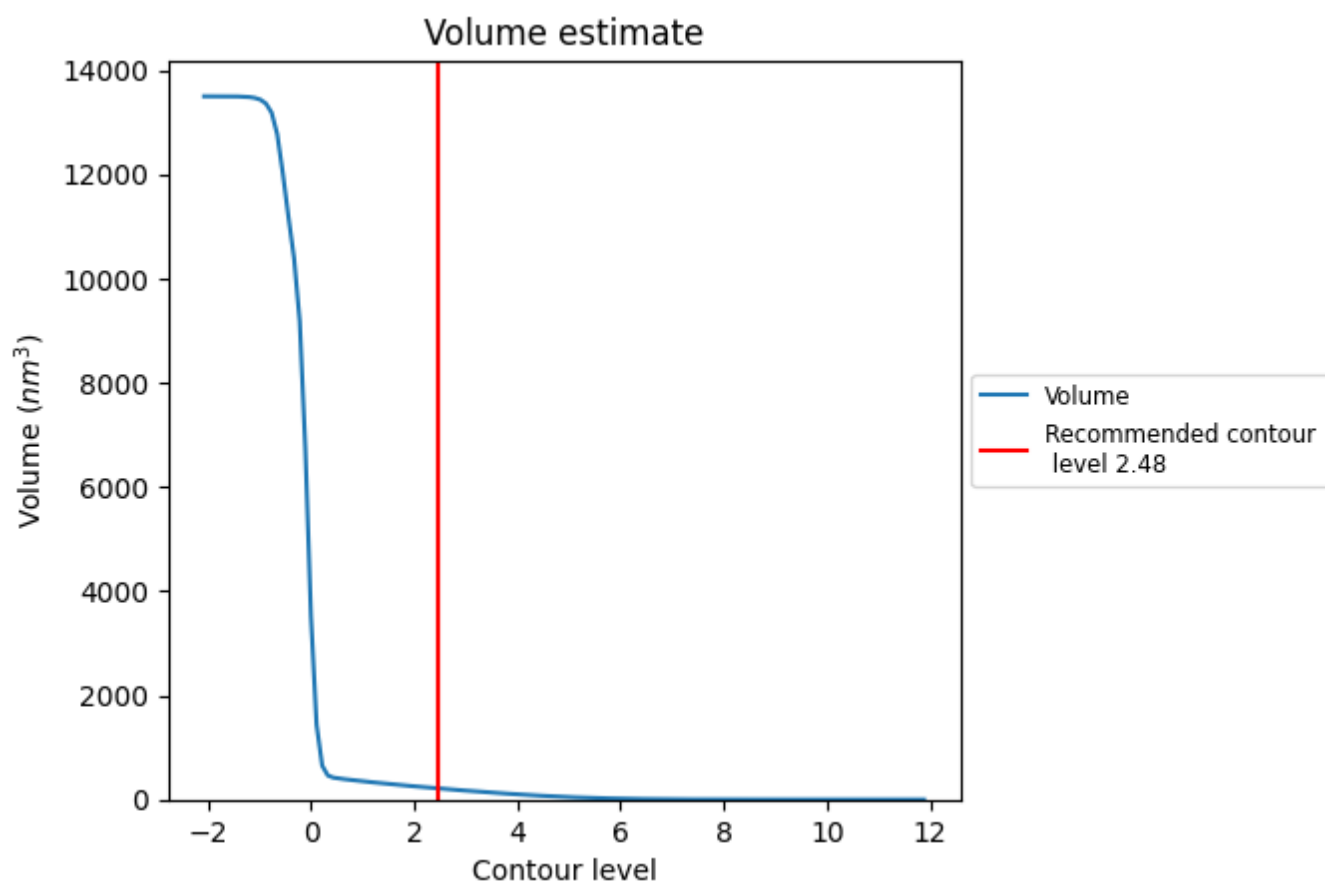
This section contains the results of statistical analysis of the map.

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.

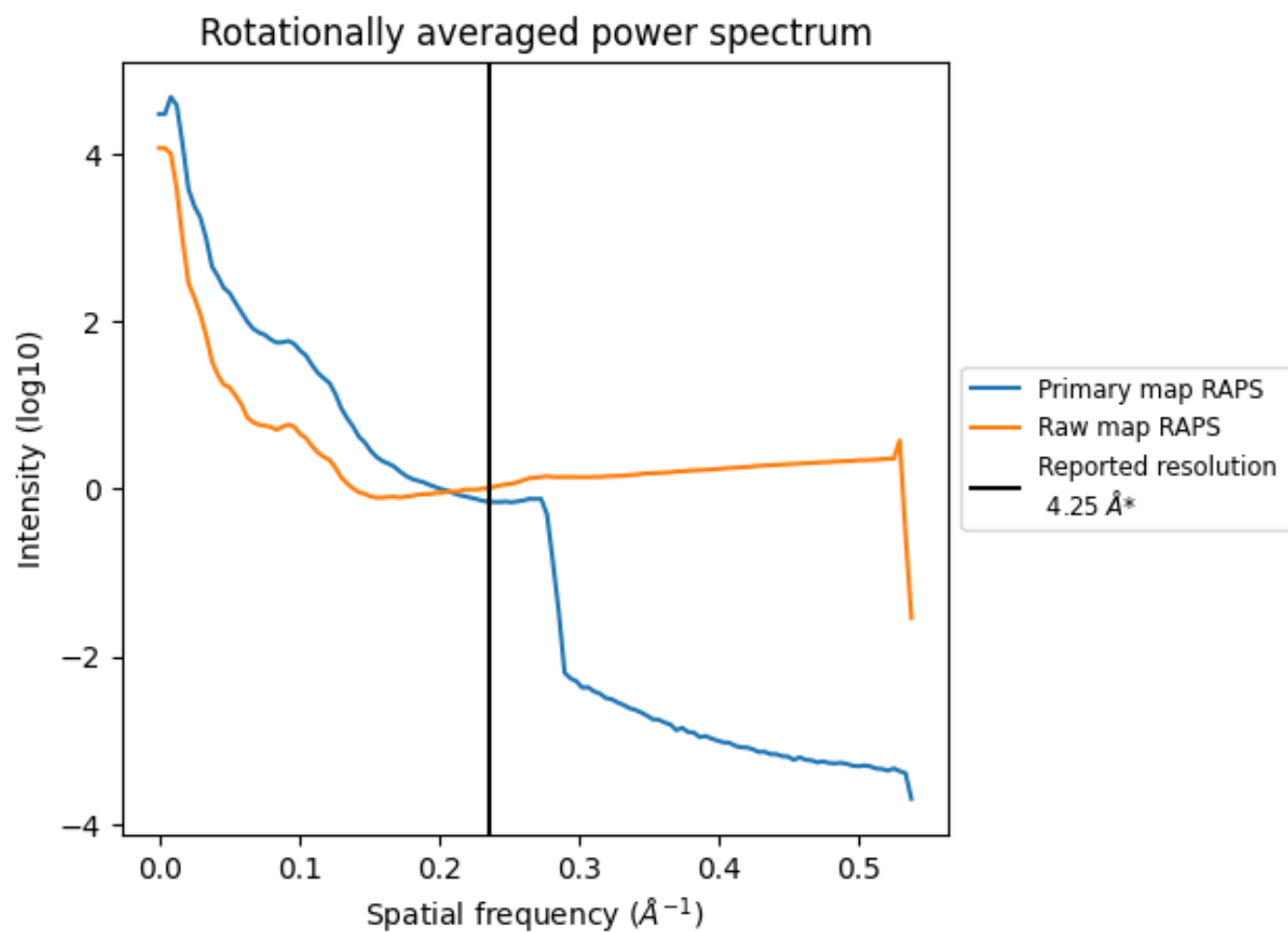
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 213 nm^3 ; this corresponds to an approximate mass of 193 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 ⓘ

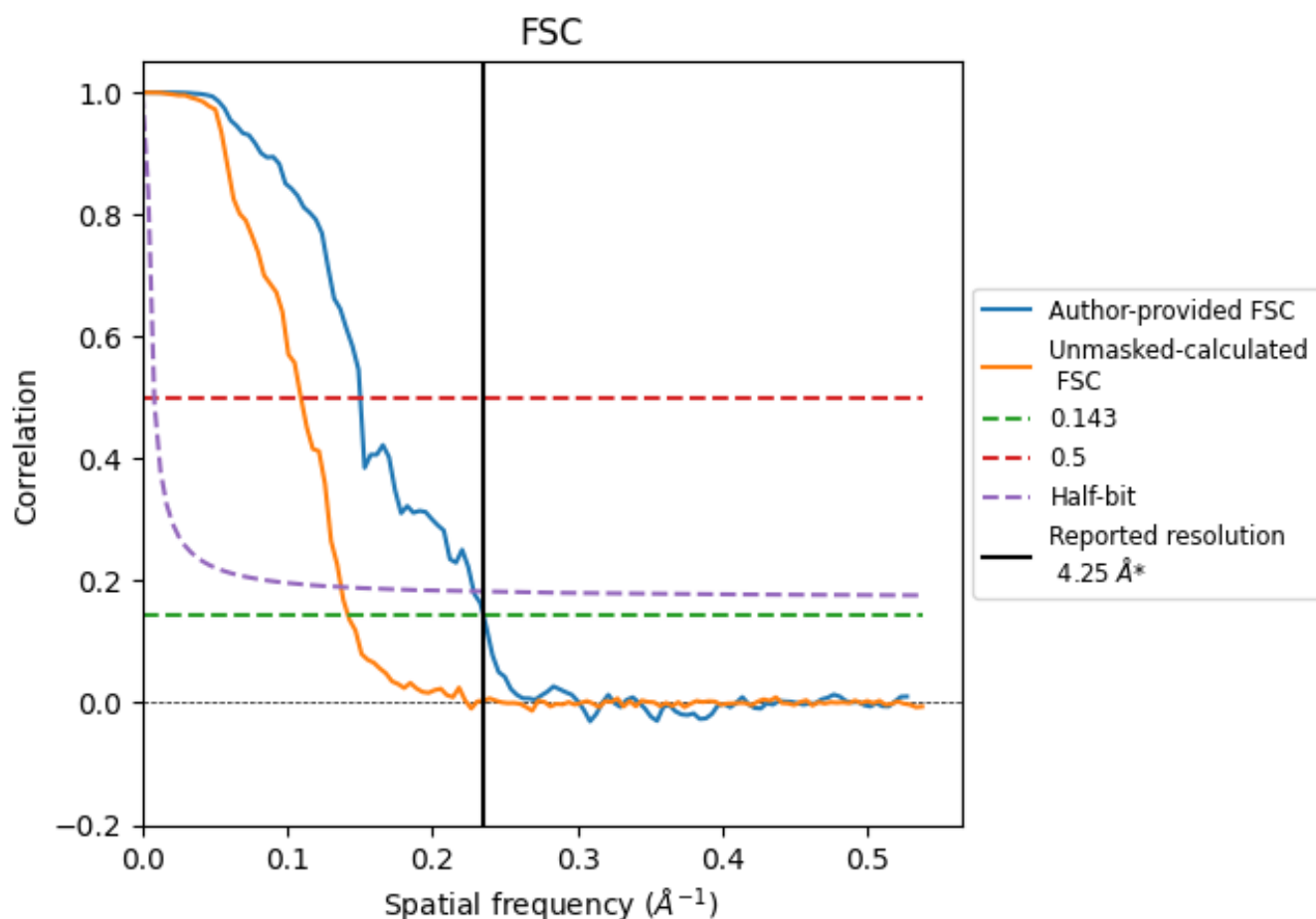


*Reported resolution corresponds to spatial frequency of 0.235 Å⁻¹

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 0.235 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

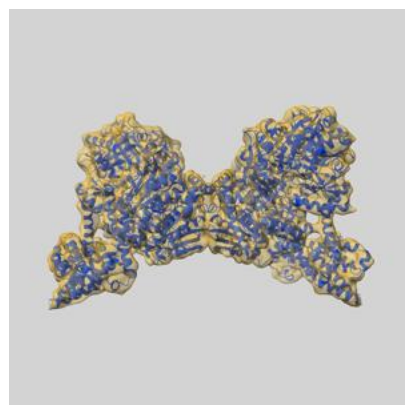
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.25	-	-
Author-provided FSC curve	4.25	6.65	4.37
Unmasked-calculated*	7.04	9.14	7.29

*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 7.04 differs from the reported value 4.25 by more than 10 %

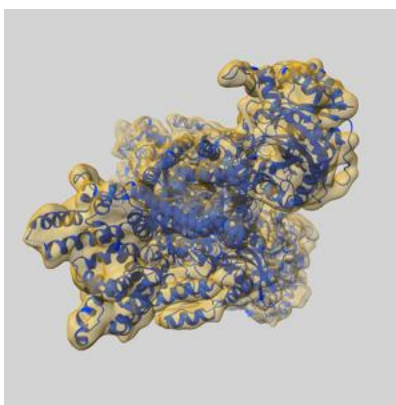
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-65623 and PDB model 9W4A. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

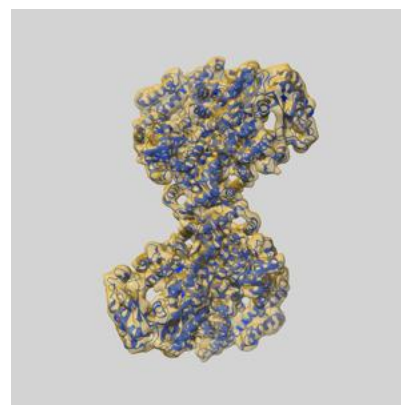
9.1 Map-model overlay [i](#)



X



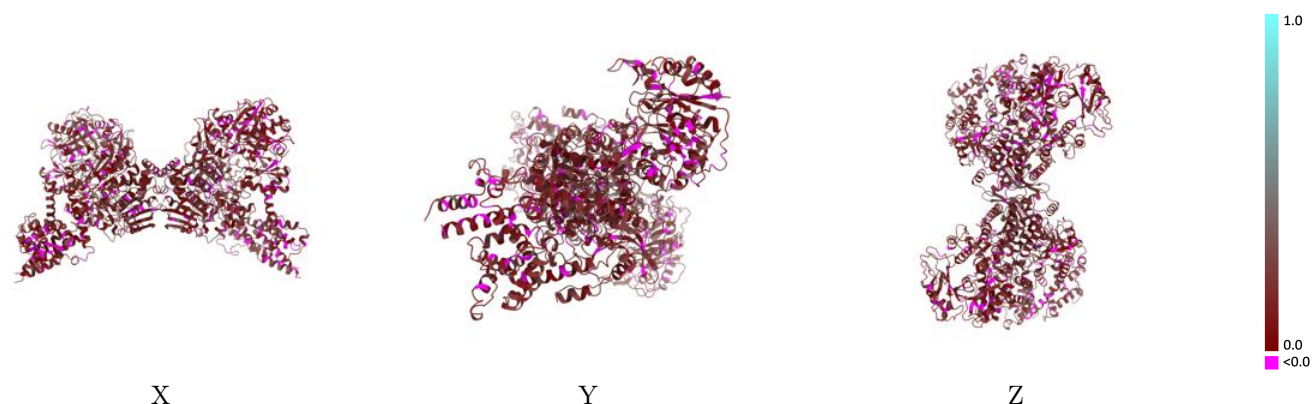
Y



Z

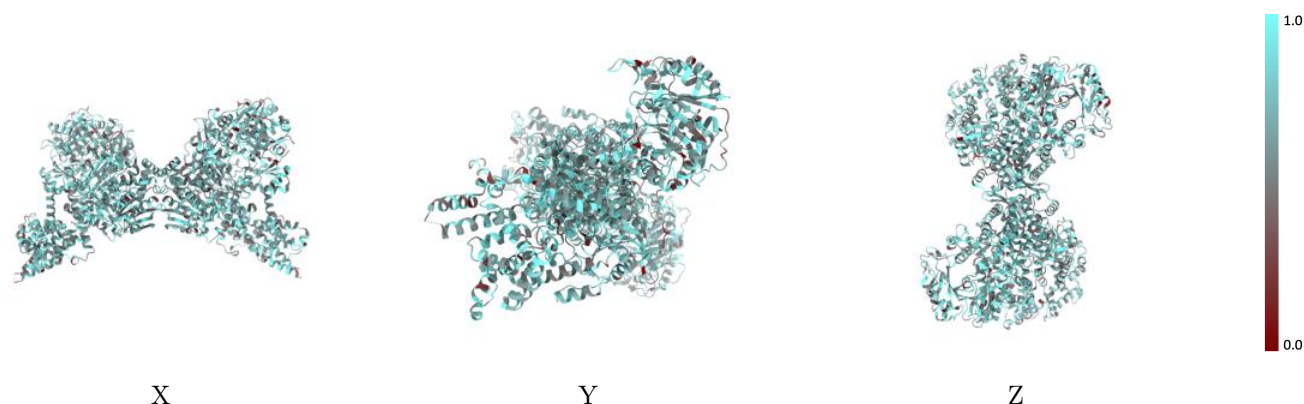
The images above show the 3D surface view of the map at the recommended contour level 2.48 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



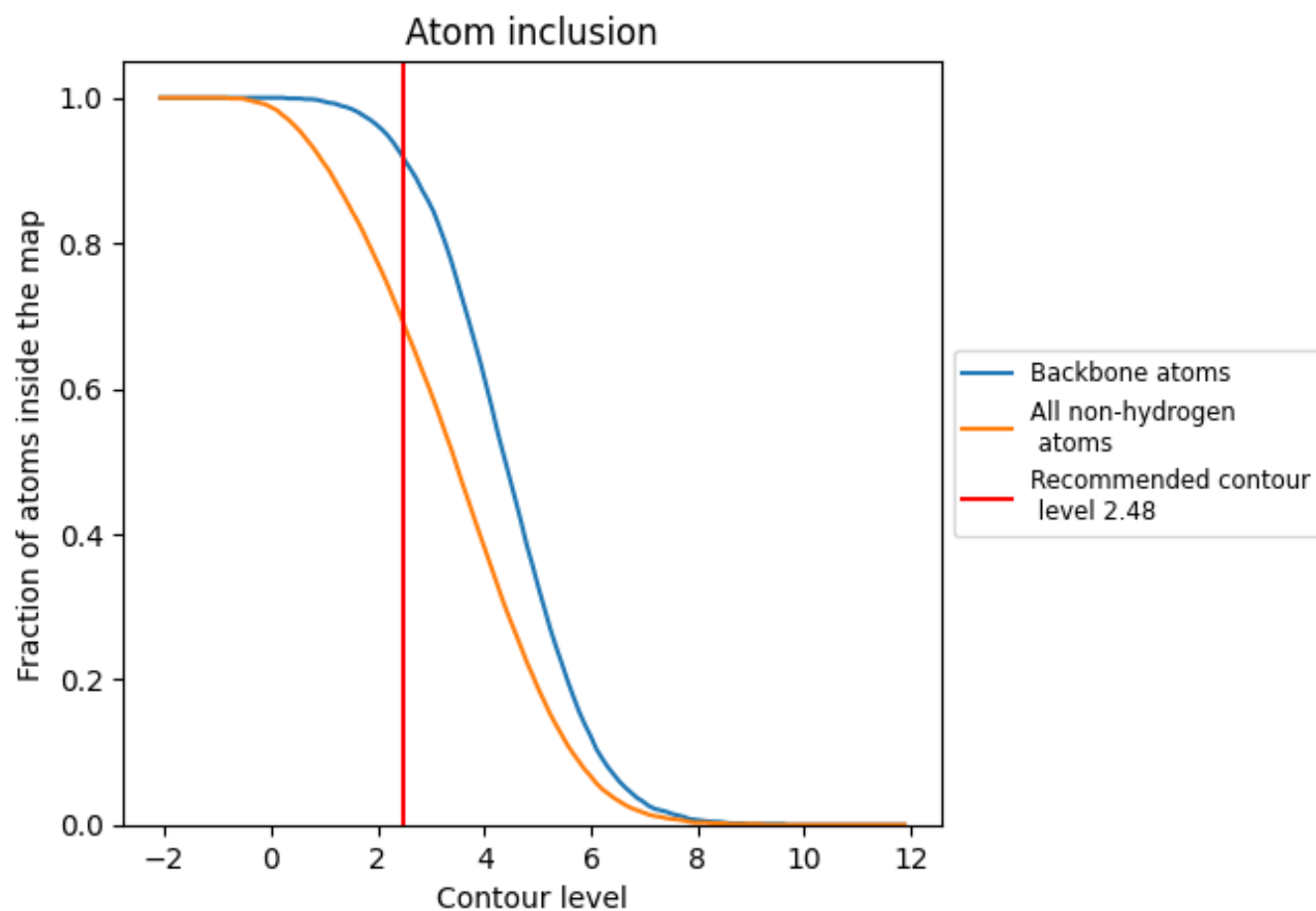
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.48).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 69% 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 (2.48) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6910	0.1520
A	0.6940	0.1550
B	0.6870	0.1500

