



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:01 AM UTC

PDB ID : 6FIK / pdb_00006fik
EMDB ID : EMD-4266
Title : ACP2 crosslinked to the KS of the loading/condensing region of the CTB1
PKS
Authors : Herbst, D.A.; Huitt-Roehl, C.R.; Jakob, R.P.; Townsend, C.A.; Maier, T.
Deposited on : 2018-01-18
Resolution : 7.10 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

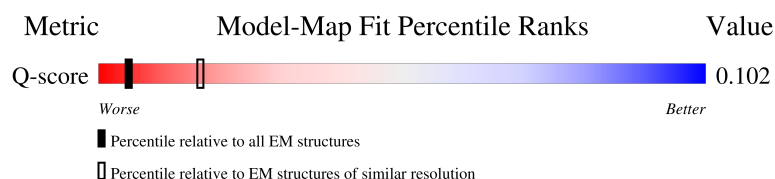
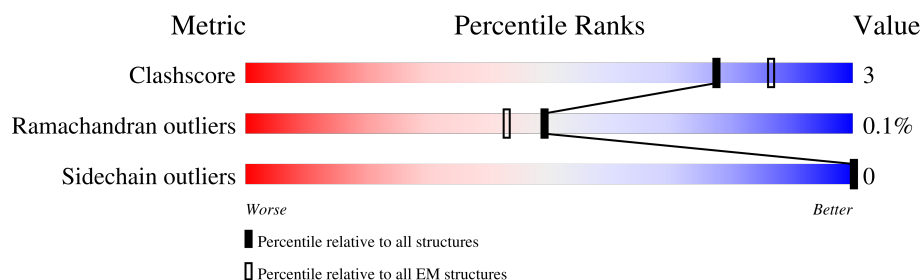
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.10 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	464 (6.60 - 7.60)

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	1304	40% 89% 8% .
1	B	1304	44% 90% 8% .
2	C	88	30% 44% . 53%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 39058 atoms, of which 19430 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 Polyketide synthase.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	1275	Total	C	H	N	O	S	0	0
			19178	6047	9536	1714	1839	42		
1	B	1275	Total	C	H	N	O	S	0	0
			19186	6049	9541	1714	1840	42		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	119	ALA	CYS	engineered mutation	UNP Q6DQW3
A	321	ALA	THR	engineered mutation	UNP Q6DQW3
A	1010	ALA	SER	engineered mutation	UNP Q6DQW3
A	1294	ALA	-	expression tag	UNP Q6DQW3
A	1295	ALA	-	expression tag	UNP Q6DQW3
A	1296	ALA	-	expression tag	UNP Q6DQW3
A	1297	LEU	-	expression tag	UNP Q6DQW3
A	1298	GLU	-	expression tag	UNP Q6DQW3
A	1299	HIS	-	expression tag	UNP Q6DQW3
A	1300	HIS	-	expression tag	UNP Q6DQW3
A	1301	HIS	-	expression tag	UNP Q6DQW3
A	1302	HIS	-	expression tag	UNP Q6DQW3
A	1303	HIS	-	expression tag	UNP Q6DQW3
A	1304	HIS	-	expression tag	UNP Q6DQW3
B	119	ALA	CYS	engineered mutation	UNP Q6DQW3
B	321	ALA	THR	engineered mutation	UNP Q6DQW3
B	1010	ALA	SER	engineered mutation	UNP Q6DQW3
B	1294	ALA	-	expression tag	UNP Q6DQW3
B	1295	ALA	-	expression tag	UNP Q6DQW3
B	1296	ALA	-	expression tag	UNP Q6DQW3
B	1297	LEU	-	expression tag	UNP Q6DQW3
B	1298	GLU	-	expression tag	UNP Q6DQW3
B	1299	HIS	-	expression tag	UNP Q6DQW3
B	1300	HIS	-	expression tag	UNP Q6DQW3
B	1301	HIS	-	expression tag	UNP Q6DQW3
B	1302	HIS	-	expression tag	UNP Q6DQW3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1303	HIS	-	expression tag	UNP Q6DQW3
B	1304	HIS	-	expression tag	UNP Q6DQW3

- Molecule 2 is a protein called Polyketide synthase.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	C	41	Total	C	H	N	O	S	0	0
			694	218	353	59	63	1		

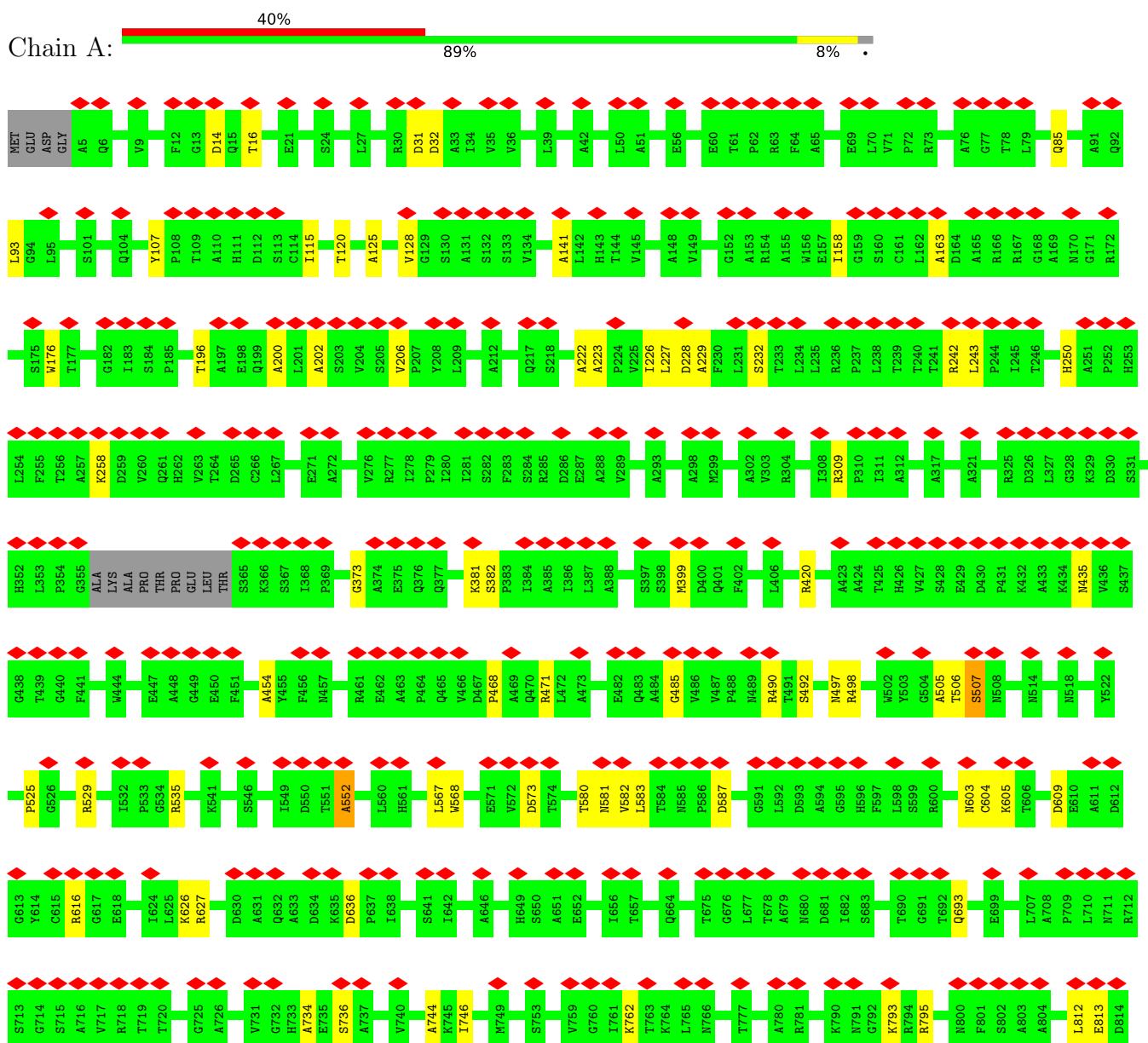
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1771	GLY	-	expression tag	UNP Q6DQW3
C	1772	SER	-	expression tag	UNP Q6DQW3
C	1773	HIS	-	expression tag	UNP Q6DQW3
C	1774	MET	-	expression tag	UNP Q6DQW3

3 Residue-property plots

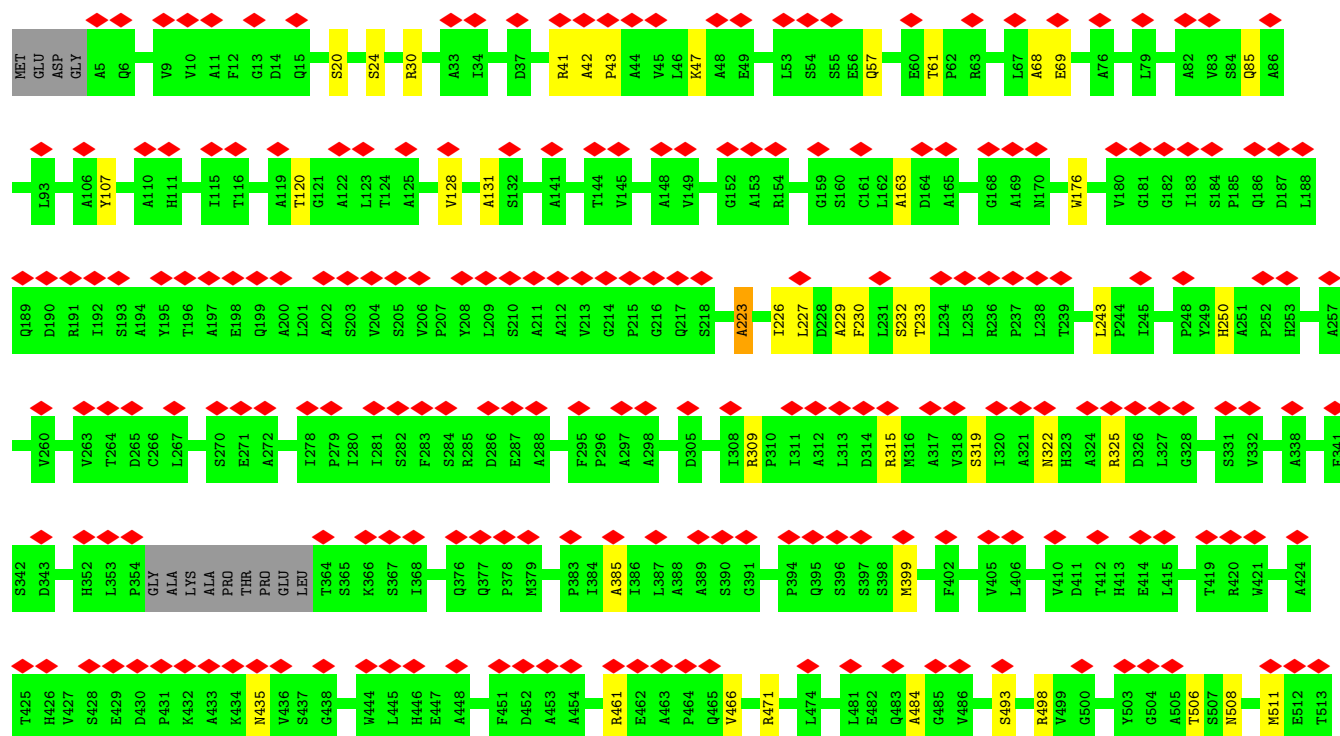
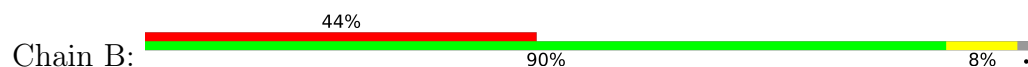
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

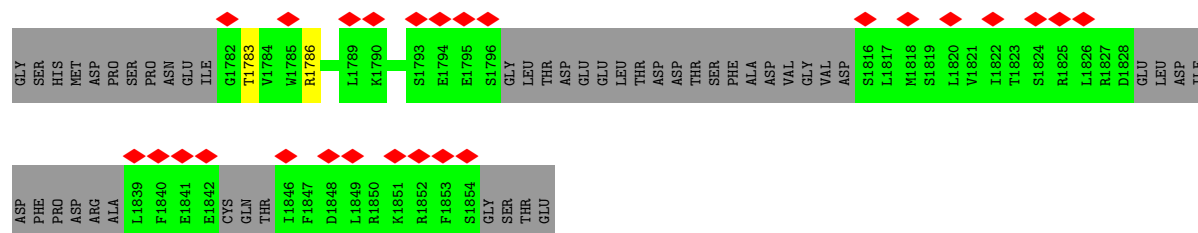
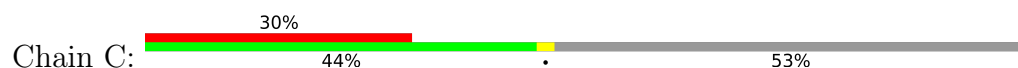




• Molecule 1: Polyketide synthase



- Molecule 2: Polyketide synthase



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	25107	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 ($e^-/\text{\AA}^2$)	41	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	27707	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.126	Depositor
Minimum map value	-0.066	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.031	Depositor
Map size (Å)	278.46, 278.46, 278.46	wwPDB
Map dimensions	210, 210, 210	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.326, 1.326, 1.326	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.47	3/9854 (0.0%)	0.77	4/13426 (0.0%)
1	B	0.43	2/9857 (0.0%)	0.72	1/13431 (0.0%)
2	C	0.37	0/342	0.64	0/452
All	All	0.45	5/20053 (0.0%)	0.74	5/27309 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1198	GLY	C-N	8.04	1.52	1.33
1	A	1198	GLY	C-N	7.62	1.51	1.33
1	A	420	ARG	CZ-NH2	7.44	1.43	1.33
1	B	243	LEU	C-N	7.31	1.50	1.33
1	A	243	LEU	C-N	6.61	1.49	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	507	SER	CA-CB-OG	-7.64	95.82	111.10
1	A	381	LYS	CB-CG-CD	7.38	128.27	111.30
1	A	871	THR	CB-CA-C	-5.87	101.04	110.79
1	B	223	ALA	N-CA-C	5.55	116.81	109.93
1	A	471	ARG	NE-CZ-NH2	5.11	123.80	119.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9642	9536	9537	58	0
1	B	9645	9541	9541	58	0
2	C	341	353	349	1	0
All	All	19628	19430	19427	112	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 3.

All (112) 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:223:ALA:O	1:A:227:LEU:N	2.14	0.80
1:B:223:ALA:O	1:B:227:LEU:N	2.13	0.80
1:A:485:GLY:O	1:A:490:ARG:NH2	2.15	0.79
1:B:30:ARG:NH1	1:B:643:LEU:O	2.15	0.79
1:A:497:ASN:ND2	1:B:69:GLU:OE1	2.16	0.78
1:B:322:ASN:OD1	1:B:325:ARG:NH2	2.18	0.76
1:B:786:TRP:O	1:B:794:ARG:NH1	2.18	0.75
1:B:85:GLN:OE1	1:B:120:THR:OG1	2.03	0.74
1:A:93:LEU:HD23	1:A:141:ALA:HB1	1.71	0.72
1:B:57:GLN:O	1:B:61:THR:OG1	2.08	0.71
1:A:924:THR:OG1	1:A:1194:GLU:OE2	2.09	0.71
1:B:924:THR:OG1	1:B:1194:GLU:OE2	2.08	0.71
1:B:484:ALA:O	1:B:874:ARG:NH2	2.23	0.71
1:B:506:THR:O	1:B:529:ARG:NH2	2.26	0.69
1:B:508:ASN:ND2	1:B:511:MET:SD	2.66	0.69
1:A:525:PRO:O	1:A:535:ARG:NH2	2.25	0.69
1:B:952:ASP:OD1	1:B:962:SER:OG	2.07	0.68
1:A:587:ASP:OD2	1:A:1283:LYS:NZ	2.27	0.68
1:A:995:LEU:O	1:A:998:SER:OG	2.08	0.67
1:B:603:ASN:OD1	1:B:604:CYS:N	2.29	0.66
1:B:461:ARG:NH2	1:B:520:ASP:OD2	2.29	0.66
1:B:587:ASP:OD2	1:B:1283:LYS:NZ	2.30	0.65
1:A:196:THR:O	1:A:200:ALA:N	2.29	0.65
1:B:1055:ALA:N	1:B:1081:GLN:O	2.30	0.65
1:A:1055:ALA:N	1:A:1081:GLN:O	2.29	0.64
1:B:626:LYS:NZ	1:B:636:ASP:OD2	2.27	0.64
1:A:603:ASN:OD1	1:A:604:CYS:N	2.30	0.64
1:A:85:GLN:NE2	1:A:120:THR:OG1	2.33	0.62
1:A:399:MET:HE1	1:A:744:ALA:HB1	1.82	0.61
1:B:493:SER:OG	1:B:634:ASP:OD2	2.19	0.60
1:A:382:SER:OG	1:A:568:TRP:NE1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:580:THR:O	1:A:736:SER:OG	2.21	0.58
1:A:795:ARG:NH2	1:A:813:GLU:OE2	2.37	0.58
1:A:793:LYS:NZ	1:A:815:ALA:O	2.37	0.57
1:B:788:ARG:NH2	1:B:817:GLU:OE2	2.38	0.57
1:A:878:HIS:O	1:A:881:ARG:NE	2.36	0.56
1:B:399:MET:HE1	1:B:744:ALA:HB1	1.86	0.56
1:B:572:VAL:O	1:B:627:ARG:NH1	2.38	0.56
1:B:795:ARG:NH2	1:B:813:GLU:OE2	2.38	0.55
1:A:976:ALA:HB1	1:A:980:LEU:HD23	1.88	0.55
1:A:158:ILE:HD11	1:B:950:ARG:HE	1.72	0.55
1:A:1220:ASN:OD1	1:A:1221:LYS:N	2.39	0.55
1:A:454:ALA:HB1	1:A:837:LYS:HB3	1.88	0.54
1:A:14:ASP:OD1	1:A:16:THR:OG1	2.14	0.54
1:A:976:ALA:HB3	1:A:981:GLN:NE2	2.22	0.53
1:A:507:SER:O	1:A:507:SER:OG	2.26	0.53
1:A:626:LYS:NZ	1:A:636:ASP:OD2	2.41	0.53
1:B:163:ALA:HB3	1:B:176:TRP:HH2	1.74	0.53
1:B:995:LEU:O	1:B:998:SER:OG	2.24	0.52
1:B:20:SER:O	1:B:24:SER:OG	2.24	0.51
1:B:609:ASP:O	1:B:693:GLN:NE2	2.40	0.51
1:B:854:ASP:OD1	1:B:893:ARG:NE	2.44	0.51
1:A:492:SER:O	1:B:47:LYS:NZ	2.44	0.50
1:A:505:ALA:O	1:A:529:ARG:NH1	2.44	0.50
1:B:1180:ALA:HB1	1:B:1186:LEU:HD13	1.93	0.50
1:A:31:ASP:OD1	1:A:32:ASP:N	2.45	0.49
1:A:605:LYS:HD3	1:A:762:LYS:HD2	1.93	0.49
1:B:899:GLN:HB3	1:B:903:ARG:HH12	1.76	0.49
1:A:1280:SER:HA	1:A:1283:LYS:HE3	1.94	0.49
1:B:868:SER:O	1:B:872:THR:OG1	2.29	0.49
1:A:954:ILE:HG22	1:A:958:MET:HE2	1.95	0.48
1:A:250:HIS:ND1	1:A:309:ARG:O	2.41	0.48
1:A:583:LEU:HD22	1:A:616:ARG:NH1	2.29	0.48
1:B:825:ASP:OD2	1:B:830:HIS:NE2	2.31	0.48
1:B:315:ARG:O	1:B:319:SER:OG	2.31	0.47
1:A:163:ALA:HB3	1:A:176:TRP:HH2	1.79	0.47
1:A:107:TYR:OH	1:A:128:VAL:O	2.31	0.47
1:B:230:PHE:O	1:B:233:THR:OG1	2.31	0.47
1:A:1180:ALA:HB1	1:A:1186:LEU:HD13	1.96	0.47
1:B:609:ASP:OD1	1:B:767:HIS:ND1	2.44	0.46
2:C:1783:THR:HA	2:C:1786:ARG:HE	1.80	0.46
1:B:107:TYR:OH	1:B:128:VAL:O	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:373:GLY:O	1:B:41:ARG:NH2	2.49	0.46
1:B:385:ALA:HB1	1:B:638:ILE:HG23	1.98	0.46
1:A:258:LYS:NZ	1:B:952:ASP:OD2	2.49	0.46
1:B:580:THR:O	1:B:736:SER:OG	2.34	0.45
1:A:567:LEU:O	1:A:627:ARG:NH1	2.45	0.45
1:B:581:ASN:ND2	1:B:617:GLY:O	2.50	0.45
1:B:498:ARG:HE	1:B:573:ASP:CG	2.24	0.44
1:B:107:TYR:OH	1:B:131:ALA:O	2.35	0.44
1:A:498:ARG:NH2	1:A:573:ASP:OD2	2.50	0.44
1:B:793:LYS:NZ	1:B:815:ALA:O	2.50	0.43
1:B:42:ALA:HB3	1:B:43:PRO:HD3	2.00	0.43
1:B:1280:SER:HA	1:B:1283:LYS:HE3	2.00	0.43
1:A:202:ALA:O	1:A:206:VAL:N	2.52	0.43
1:A:468:PRO:HB2	1:A:582:VAL:HG11	2.00	0.42
1:A:903:ARG:HH21	1:A:1238:LEU:HD22	1.84	0.42
1:A:746:ILE:HG21	1:A:812:LEU:HD23	2.02	0.42
1:B:711:ASN:OD1	1:B:714:GLY:N	2.50	0.42
1:A:581:ASN:ND2	1:A:734:ALA:O	2.52	0.42
1:A:1116:HIS:ND1	1:A:1169:SER:O	2.53	0.42
1:B:899:GLN:HB3	1:B:903:ARG:NH1	2.34	0.42
1:A:115:ILE:HG22	1:A:125:ALA:HB1	2.02	0.42
1:A:228:ASP:OD1	1:A:242:ARG:NH1	2.53	0.42
1:B:950:ARG:O	1:B:954:ILE:HG12	2.20	0.42
1:A:435:ASN:ND2	1:A:1280:SER:O	2.48	0.41
1:B:68:ALA:HB3	1:B:670:GLN:HG3	2.02	0.41
1:B:223:ALA:HB3	1:B:226:ILE:HB	2.01	0.41
1:A:229:ALA:O	1:A:232:SER:OG	2.27	0.41
1:A:609:ASP:O	1:A:693:GLN:NE2	2.52	0.41
1:A:881:ARG:HB2	1:A:1237:TYR:HB3	2.03	0.41
1:A:506:THR:OG1	1:A:552:ALA:O	2.39	0.41
1:A:870:THR:O	1:A:874:ARG:N	2.53	0.41
1:A:1209:VAL:HG21	1:A:1213:MET:SD	2.60	0.41
1:B:466:VAL:HG12	1:B:471:ARG:HG3	2.03	0.40
1:B:557:LEU:CD1	1:B:800:ASN:HB3	2.51	0.40
1:B:435:ASN:ND2	1:B:1280:SER:O	2.53	0.40
1:B:556:SER:HB2	1:B:740:VAL:HG13	2.04	0.40
1:A:223:ALA:HB3	1:A:226:ILE:HB	2.03	0.40
1:B:229:ALA:O	1:B:232:SER:OG	2.39	0.40
1:B:250:HIS:ND1	1:B:309:ARG:O	2.46	0.40
1:A:176:TRP:CZ3	1:A:223:ALA:HA	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	1271/1304 (98%)	1216 (96%)	52 (4%)	3 (0%)	43	78
1	B	1271/1304 (98%)	1237 (97%)	34 (3%)	0	100	100
2	C	33/88 (38%)	31 (94%)	2 (6%)	0	100	100
All	All	2575/2696 (96%)	2484 (96%)	88 (3%)	3 (0%)	49	83

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	222	ALA
1	A	552	ALA
1	A	1234	ALA

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	1025/1046 (98%)	1025 (100%)	0	100	100
1	B	1026/1046 (98%)	1026 (100%)	0	100	100
2	C	39/80 (49%)	39 (100%)	0	100	100
All	All	2090/2172 (96%)	2090 (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 (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	GLN
1	A	104	GLN
1	A	352	HIS
1	A	791	ASN
1	A	800	ASN
1	A	807	ASN
1	A	856	HIS
1	A	915	ASN
1	A	981	GLN
1	A	1203	GLN
1	B	262	HIS
1	B	352	HIS
1	B	376	GLN
1	B	408	ASN
1	B	483	GLN
1	B	537	ASN
1	B	670	GLN
1	B	733	HIS
1	B	791	ASN
1	B	807	ASN
1	B	856	HIS
1	B	878	HIS
1	B	1203	GLN

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.

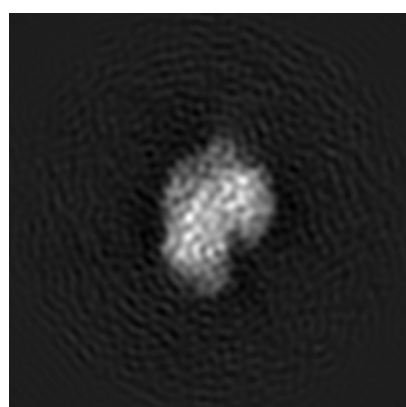
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4266. These allow visual inspection of the internal detail of the map and identification of artifacts.

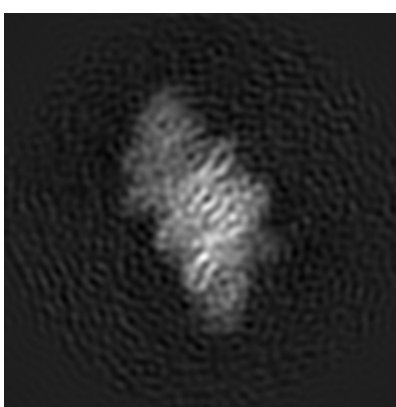
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

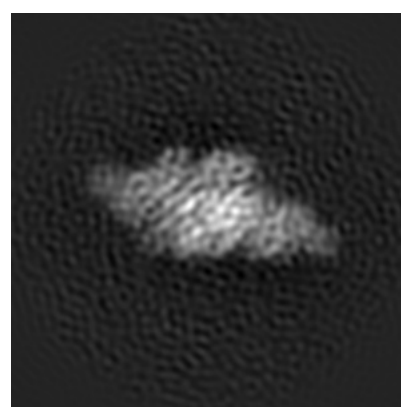
6.1.1 Primary map



X



Y

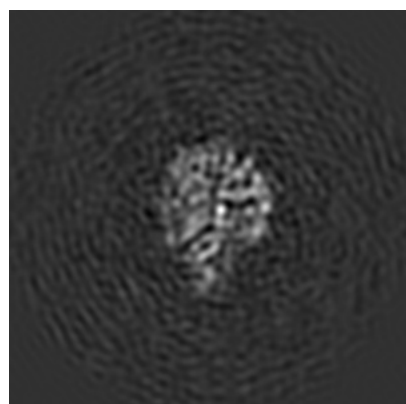


Z

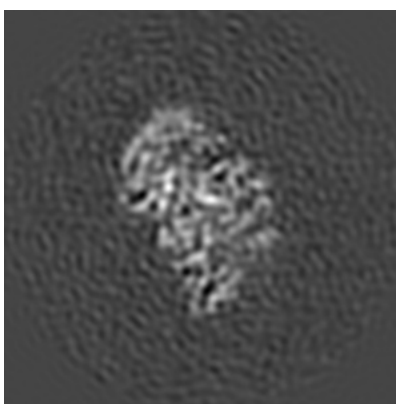
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

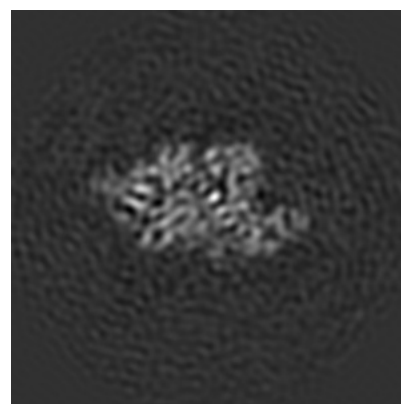
6.2.1 Primary map



X Index: 105



Y Index: 105

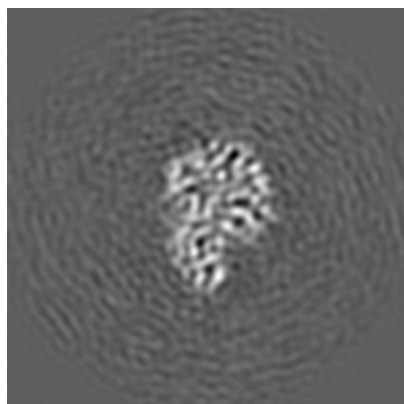


Z Index: 105

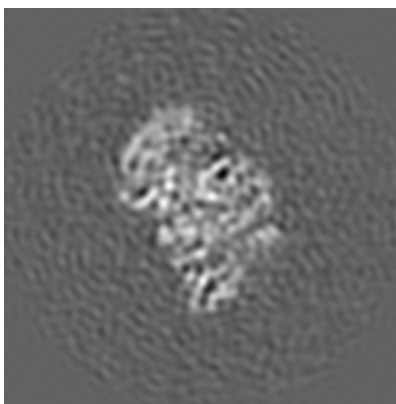
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

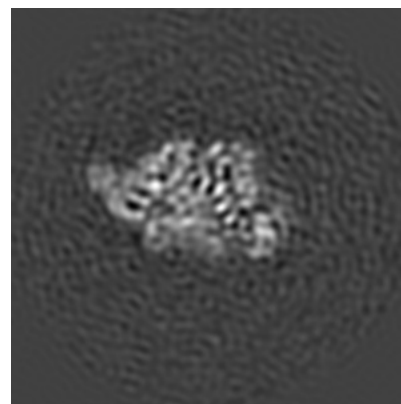
6.3.1 Primary map



X Index: 113



Y Index: 106

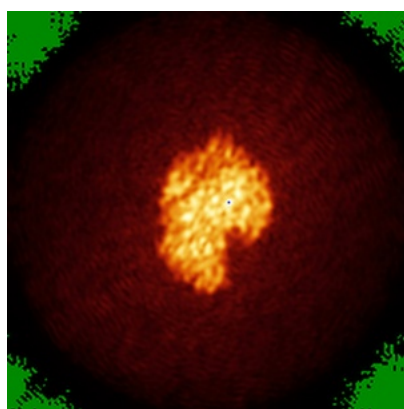


Z Index: 108

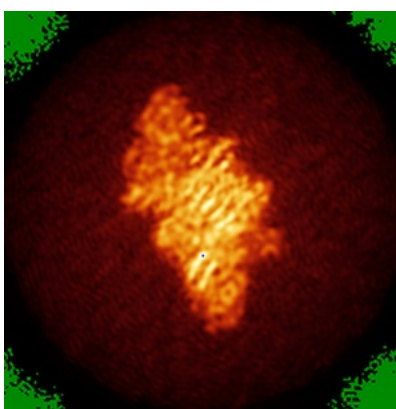
The images above show the largest variance slices of the map in three orthogonal directions.

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

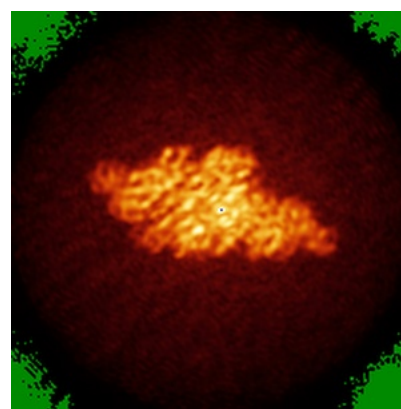
6.4.1 Primary map



X



Y

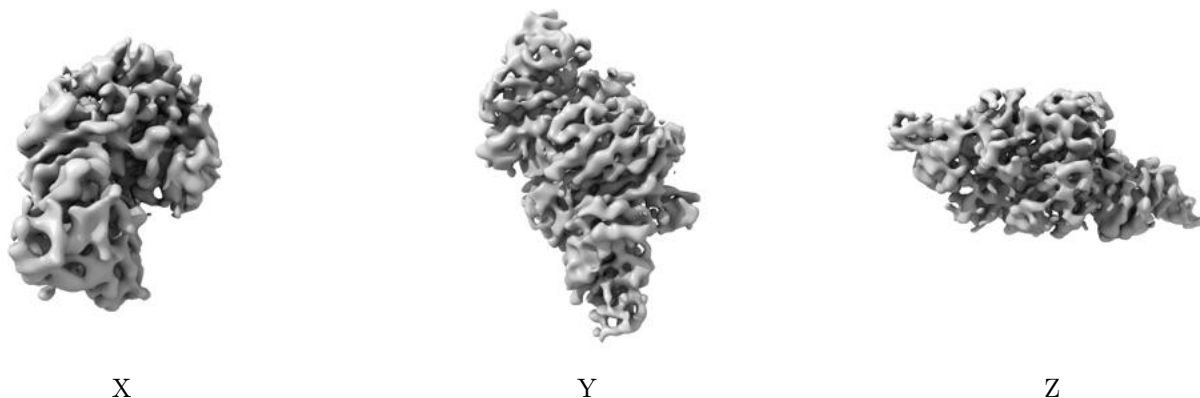


Z

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 0.031. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

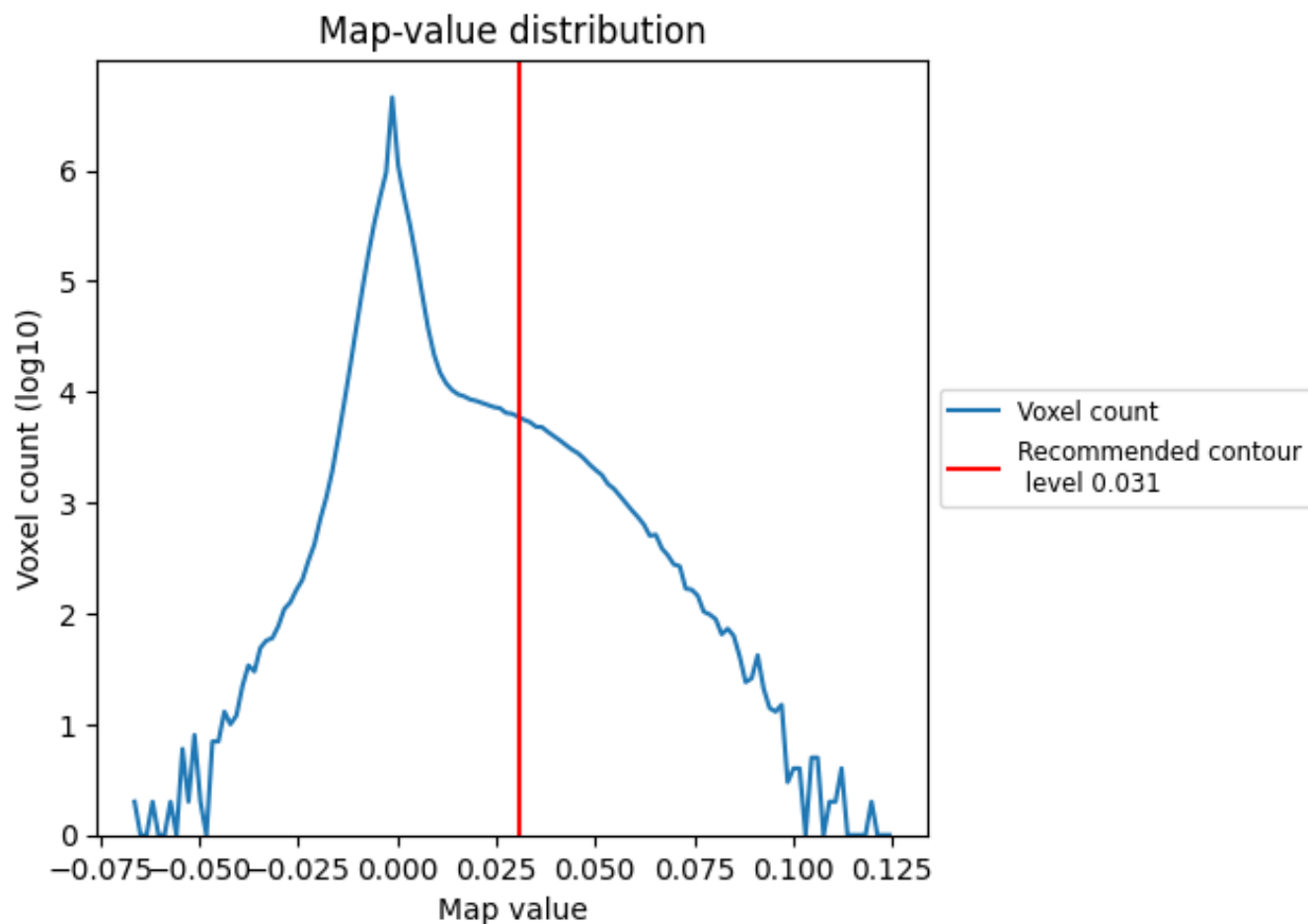
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

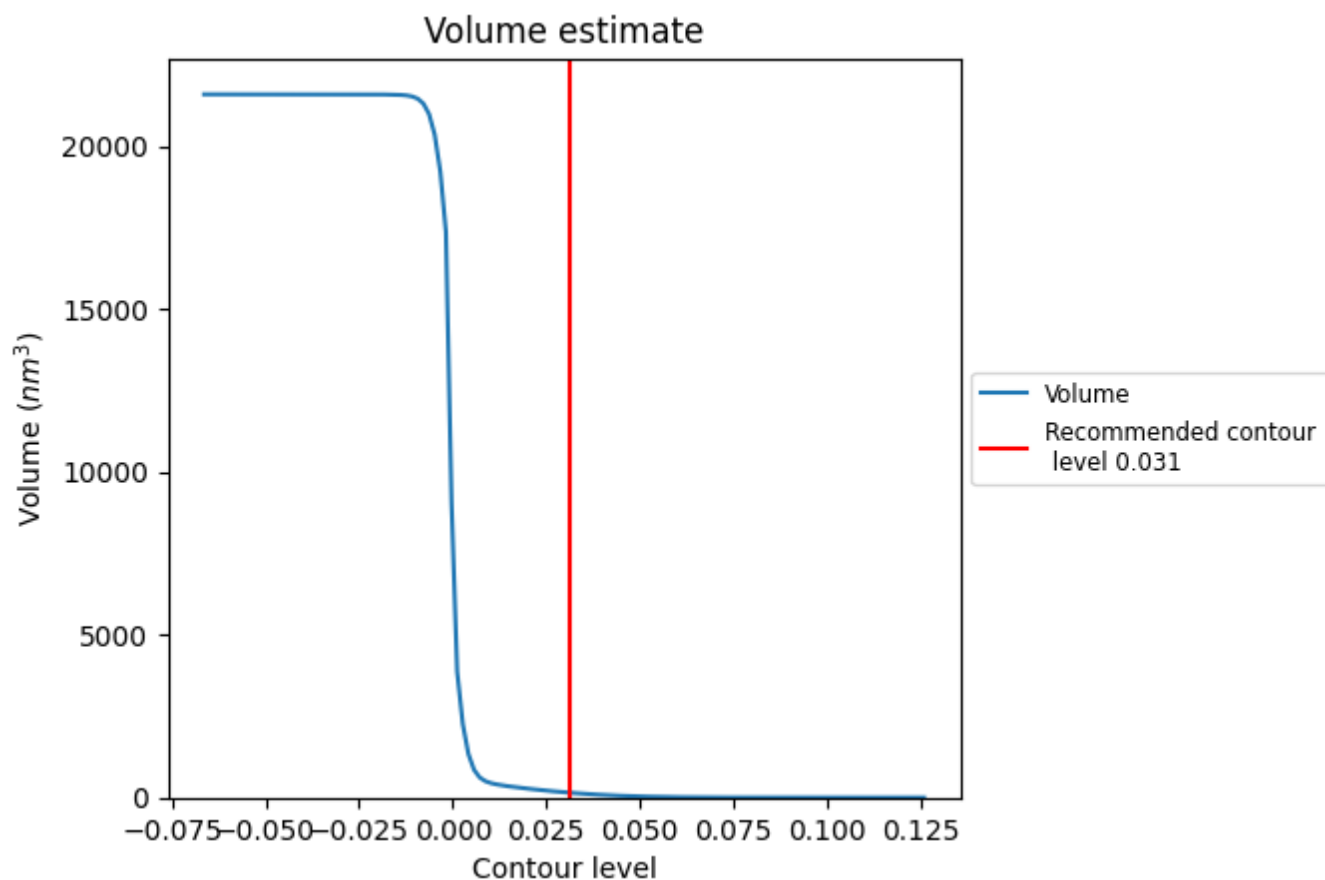
This section contains the results of statistical analysis of the map.

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.

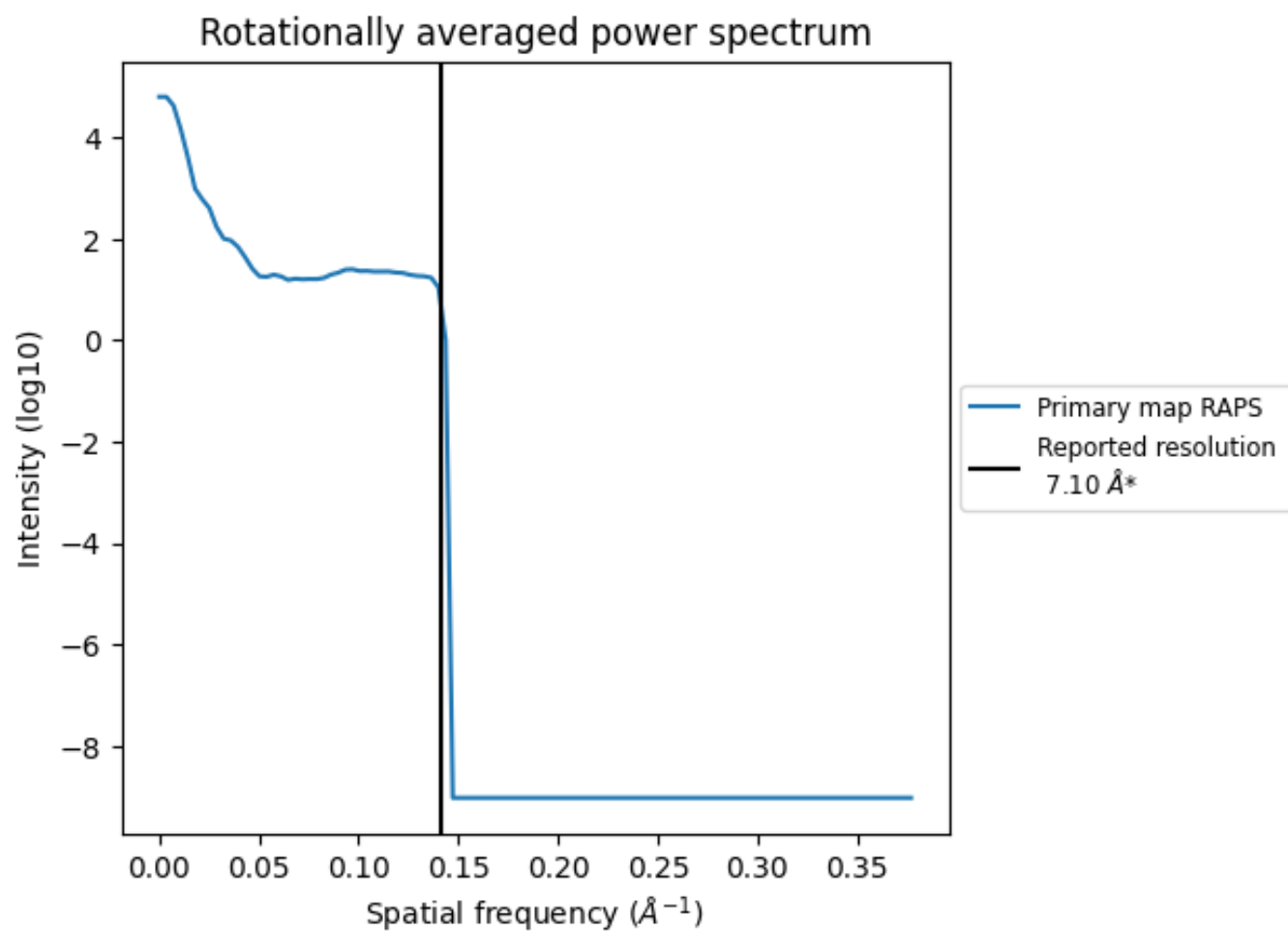
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 151 nm³; this corresponds to an approximate mass of 137 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 ⓘ

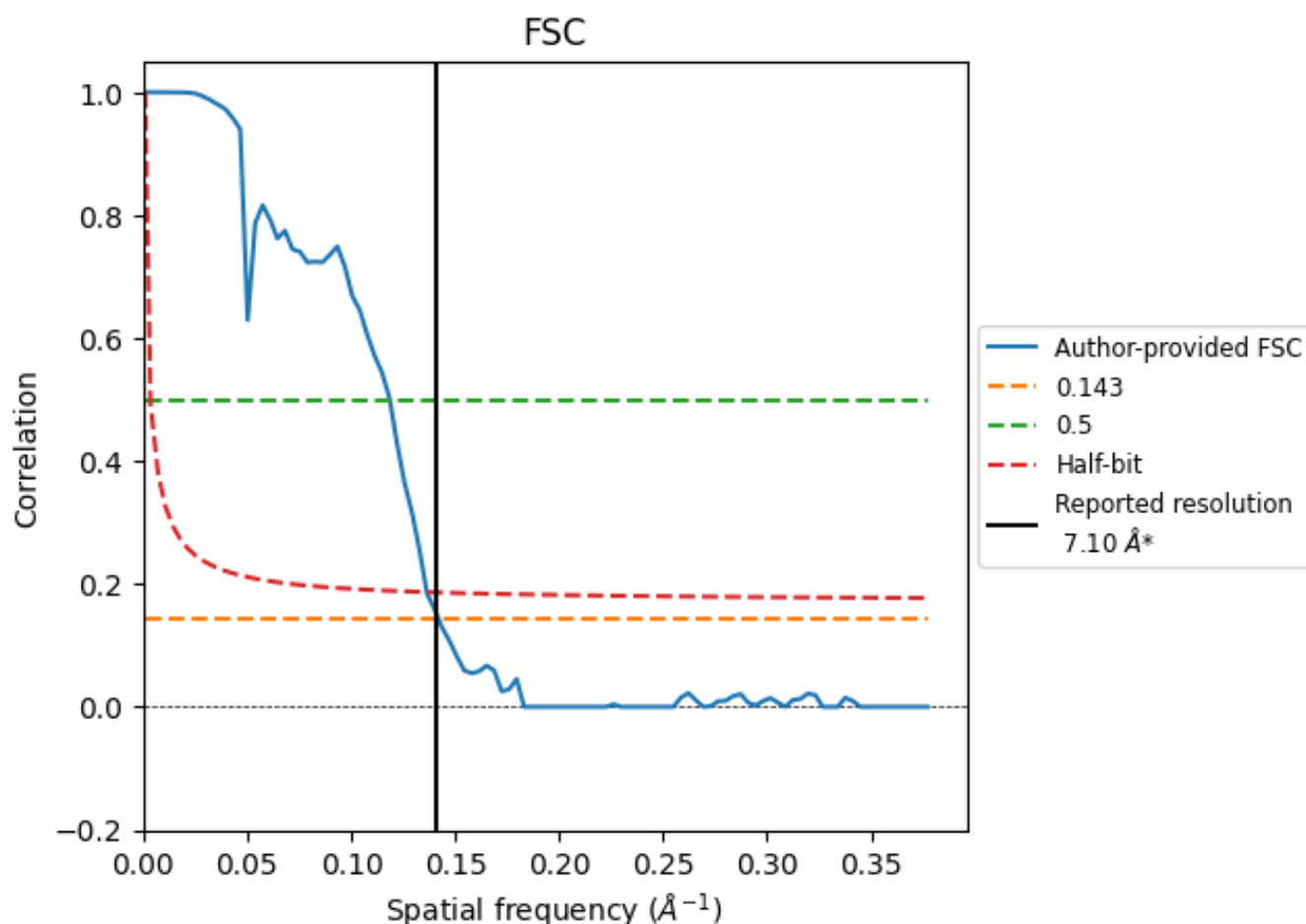


*Reported resolution corresponds to spatial frequency of 0.141 Å⁻¹

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 0.141 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

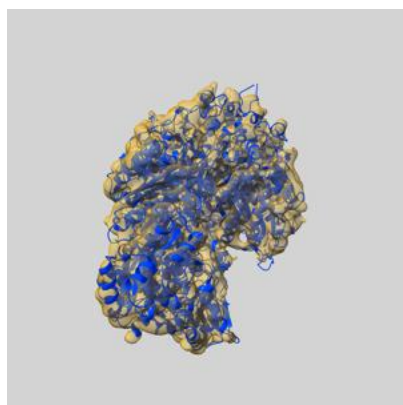
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.10	-	-
Author-provided FSC curve	7.04	8.43	7.34
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

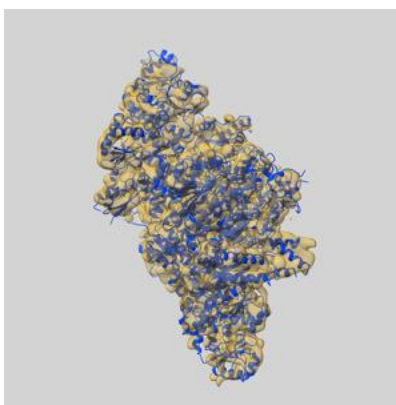
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4266 and PDB model 6FIK. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

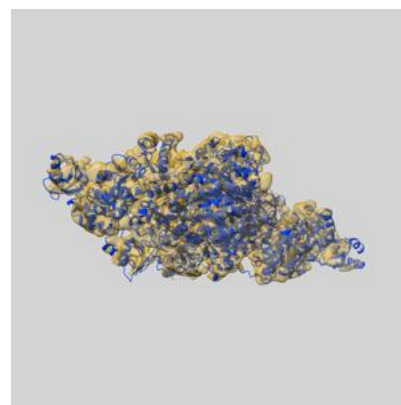
9.1 Map-model overlay [i](#)



X



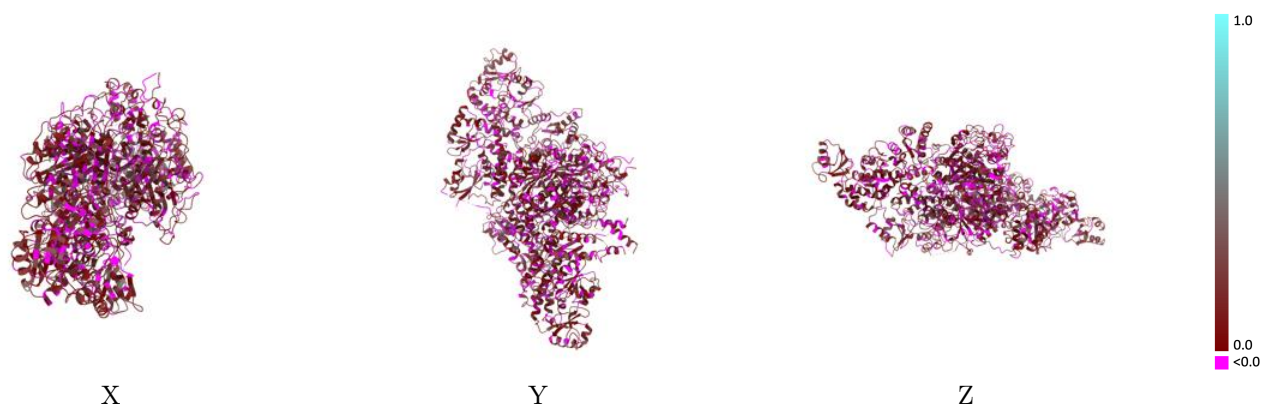
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.031 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](#)

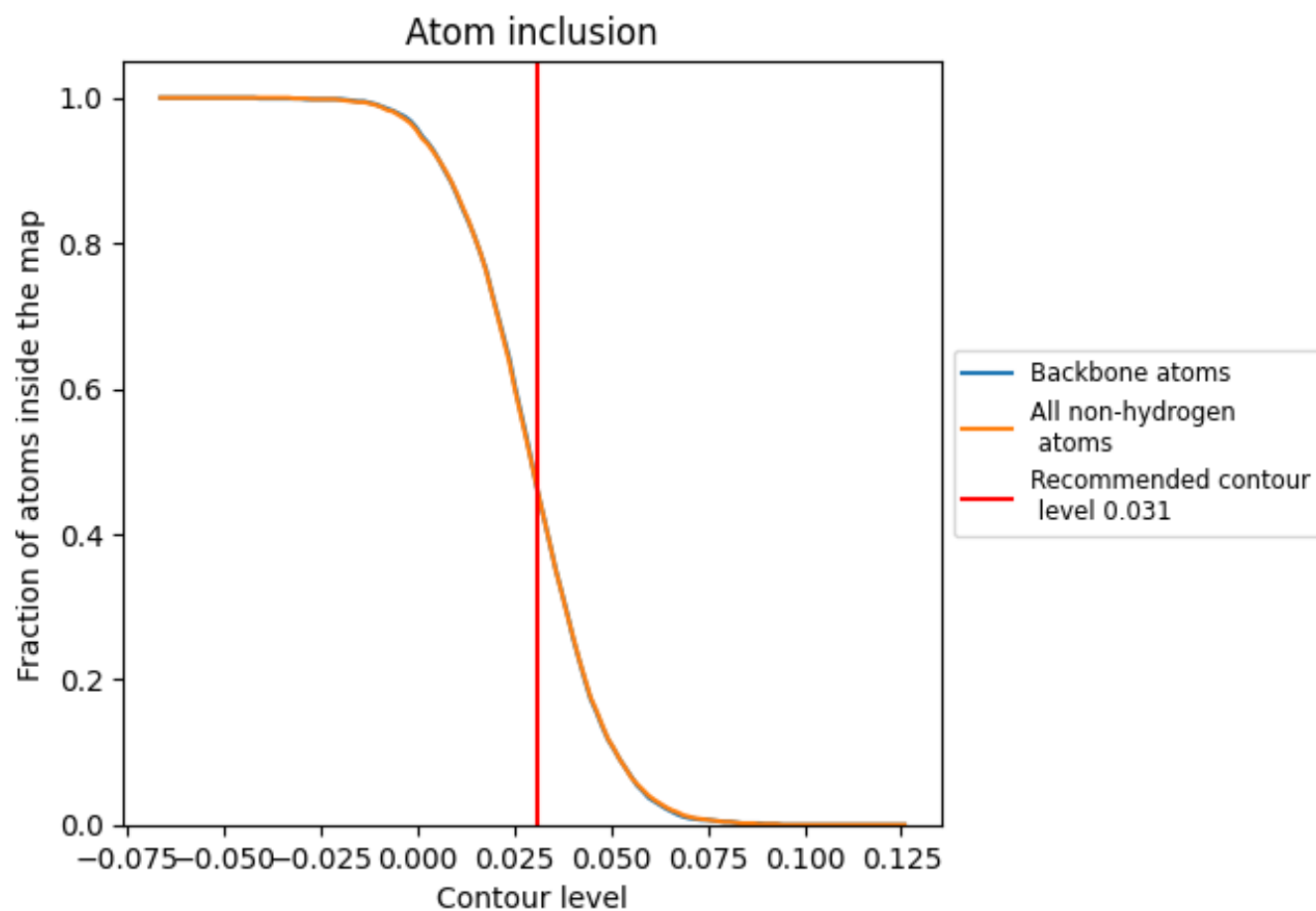


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 46% of all backbone atoms, 46% 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 (0.031) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4610	0.1020
A	0.4780	0.1010
B	0.4590	0.1040
C	0.3670	0.0820

