



## Full wwPDB EM Validation Report ⓘ

May 20, 2025 – 04:13 PM JST

PDB ID : 8XJY / pdb\_00008xjy  
EMDB ID : EMD-38410  
Title : Cryo-EM structure of colibactin assembly line polyketide synthase ClbI KS-AT didomain crosslinked with ClbI ACP  
Authors : Kim, M.; Kim, J.; Kang, J.Y.  
Deposited on : 2023-12-22  
Resolution : 3.29 Å(reported)  
Based on initial model : .

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
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) : 2.43.1

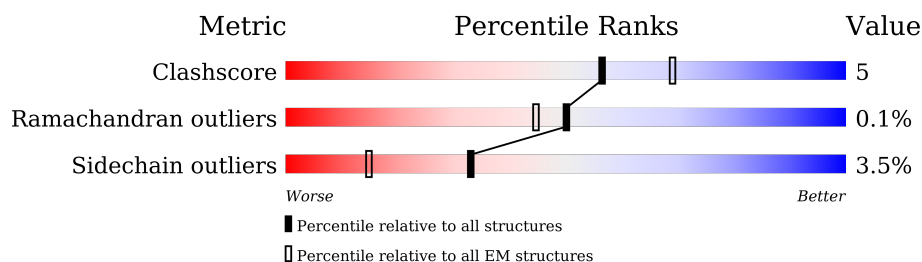
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.29 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  $\geq 3$ , 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	921	<div> <div>23%</div> <div>82%</div> <div>12%</div> <div>5%</div> </div>
1	B	921	<div> <div>14%</div> <div>81%</div> <div>14%</div> <div>5%</div> </div>
2	C	141	<div> <div>47%</div> <div>41%</div> <div>6%</div> <div>53%</div> </div>
2	D	141	<div> <div>46%</div> <div>39%</div> <div>8%</div> <div>53%</div> </div>

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 14239 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 Polyketide synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	873	Total	C	N	O	S	0	0
			6607	4178	1152	1251	26		
1	B	874	Total	C	N	O	S	0	0
			6614	4183	1153	1252	26		

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	896	LYS	-	expression tag	UNP Q0P7J9
A	897	LEU	-	expression tag	UNP Q0P7J9
A	898	SER	-	expression tag	UNP Q0P7J9
A	899	SER	-	expression tag	UNP Q0P7J9
A	900	GLY	-	expression tag	UNP Q0P7J9
A	901	LEU	-	expression tag	UNP Q0P7J9
A	902	GLU	-	expression tag	UNP Q0P7J9
A	903	VAL	-	expression tag	UNP Q0P7J9
A	904	LEU	-	expression tag	UNP Q0P7J9
A	905	PHE	-	expression tag	UNP Q0P7J9
A	906	GLN	-	expression tag	UNP Q0P7J9
A	907	GLY	-	expression tag	UNP Q0P7J9
A	908	PRO	-	expression tag	UNP Q0P7J9
A	909	SER	-	expression tag	UNP Q0P7J9
A	910	SER	-	expression tag	UNP Q0P7J9
A	911	GLY	-	expression tag	UNP Q0P7J9
A	912	HIS	-	expression tag	UNP Q0P7J9
A	913	HIS	-	expression tag	UNP Q0P7J9
A	914	HIS	-	expression tag	UNP Q0P7J9
A	915	HIS	-	expression tag	UNP Q0P7J9
A	916	HIS	-	expression tag	UNP Q0P7J9
A	917	HIS	-	expression tag	UNP Q0P7J9
A	918	HIS	-	expression tag	UNP Q0P7J9
A	919	HIS	-	expression tag	UNP Q0P7J9
A	920	HIS	-	expression tag	UNP Q0P7J9
A	921	HIS	-	expression tag	UNP Q0P7J9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	896	LYS	-	expression tag	UNP Q0P7J9
B	897	LEU	-	expression tag	UNP Q0P7J9
B	898	SER	-	expression tag	UNP Q0P7J9
B	899	SER	-	expression tag	UNP Q0P7J9
B	900	GLY	-	expression tag	UNP Q0P7J9
B	901	LEU	-	expression tag	UNP Q0P7J9
B	902	GLU	-	expression tag	UNP Q0P7J9
B	903	VAL	-	expression tag	UNP Q0P7J9
B	904	LEU	-	expression tag	UNP Q0P7J9
B	905	PHE	-	expression tag	UNP Q0P7J9
B	906	GLN	-	expression tag	UNP Q0P7J9
B	907	GLY	-	expression tag	UNP Q0P7J9
B	908	PRO	-	expression tag	UNP Q0P7J9
B	909	SER	-	expression tag	UNP Q0P7J9
B	910	SER	-	expression tag	UNP Q0P7J9
B	911	GLY	-	expression tag	UNP Q0P7J9
B	912	HIS	-	expression tag	UNP Q0P7J9
B	913	HIS	-	expression tag	UNP Q0P7J9
B	914	HIS	-	expression tag	UNP Q0P7J9
B	915	HIS	-	expression tag	UNP Q0P7J9
B	916	HIS	-	expression tag	UNP Q0P7J9
B	917	HIS	-	expression tag	UNP Q0P7J9
B	918	HIS	-	expression tag	UNP Q0P7J9
B	919	HIS	-	expression tag	UNP Q0P7J9
B	920	HIS	-	expression tag	UNP Q0P7J9
B	921	HIS	-	expression tag	UNP Q0P7J9

- Molecule 2 is a protein called Polyketide synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	66	Total	C	N	O	S	0	0
			509	320	86	99	4		
2	D	66	Total	C	N	O	S	0	0
			509	320	86	99	4		

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1011	LYS	-	expression tag	UNP Q0P7J9
C	1012	LEU	-	expression tag	UNP Q0P7J9
C	1013	SER	-	expression tag	UNP Q0P7J9
C	1014	SER	-	expression tag	UNP Q0P7J9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1015	GLY	-	expression tag	UNP Q0P7J9
C	1016	LEU	-	expression tag	UNP Q0P7J9
C	1017	GLU	-	expression tag	UNP Q0P7J9
C	1018	VAL	-	expression tag	UNP Q0P7J9
C	1019	LEU	-	expression tag	UNP Q0P7J9
C	1020	PHE	-	expression tag	UNP Q0P7J9
C	1021	GLN	-	expression tag	UNP Q0P7J9
C	1022	GLY	-	expression tag	UNP Q0P7J9
C	1023	PRO	-	expression tag	UNP Q0P7J9
C	1024	SER	-	expression tag	UNP Q0P7J9
C	1025	SER	-	expression tag	UNP Q0P7J9
C	1026	GLY	-	expression tag	UNP Q0P7J9
C	1027	HIS	-	expression tag	UNP Q0P7J9
C	1028	HIS	-	expression tag	UNP Q0P7J9
C	1029	HIS	-	expression tag	UNP Q0P7J9
C	1030	HIS	-	expression tag	UNP Q0P7J9
C	1031	HIS	-	expression tag	UNP Q0P7J9
C	1032	HIS	-	expression tag	UNP Q0P7J9
C	1033	HIS	-	expression tag	UNP Q0P7J9
C	1034	HIS	-	expression tag	UNP Q0P7J9
C	1035	HIS	-	expression tag	UNP Q0P7J9
C	1036	HIS	-	expression tag	UNP Q0P7J9
D	1011	LYS	-	expression tag	UNP Q0P7J9
D	1012	LEU	-	expression tag	UNP Q0P7J9
D	1013	SER	-	expression tag	UNP Q0P7J9
D	1014	SER	-	expression tag	UNP Q0P7J9
D	1015	GLY	-	expression tag	UNP Q0P7J9
D	1016	LEU	-	expression tag	UNP Q0P7J9
D	1017	GLU	-	expression tag	UNP Q0P7J9
D	1018	VAL	-	expression tag	UNP Q0P7J9
D	1019	LEU	-	expression tag	UNP Q0P7J9
D	1020	PHE	-	expression tag	UNP Q0P7J9
D	1021	GLN	-	expression tag	UNP Q0P7J9
D	1022	GLY	-	expression tag	UNP Q0P7J9
D	1023	PRO	-	expression tag	UNP Q0P7J9
D	1024	SER	-	expression tag	UNP Q0P7J9
D	1025	SER	-	expression tag	UNP Q0P7J9
D	1026	GLY	-	expression tag	UNP Q0P7J9
D	1027	HIS	-	expression tag	UNP Q0P7J9
D	1028	HIS	-	expression tag	UNP Q0P7J9
D	1029	HIS	-	expression tag	UNP Q0P7J9
D	1030	HIS	-	expression tag	UNP Q0P7J9

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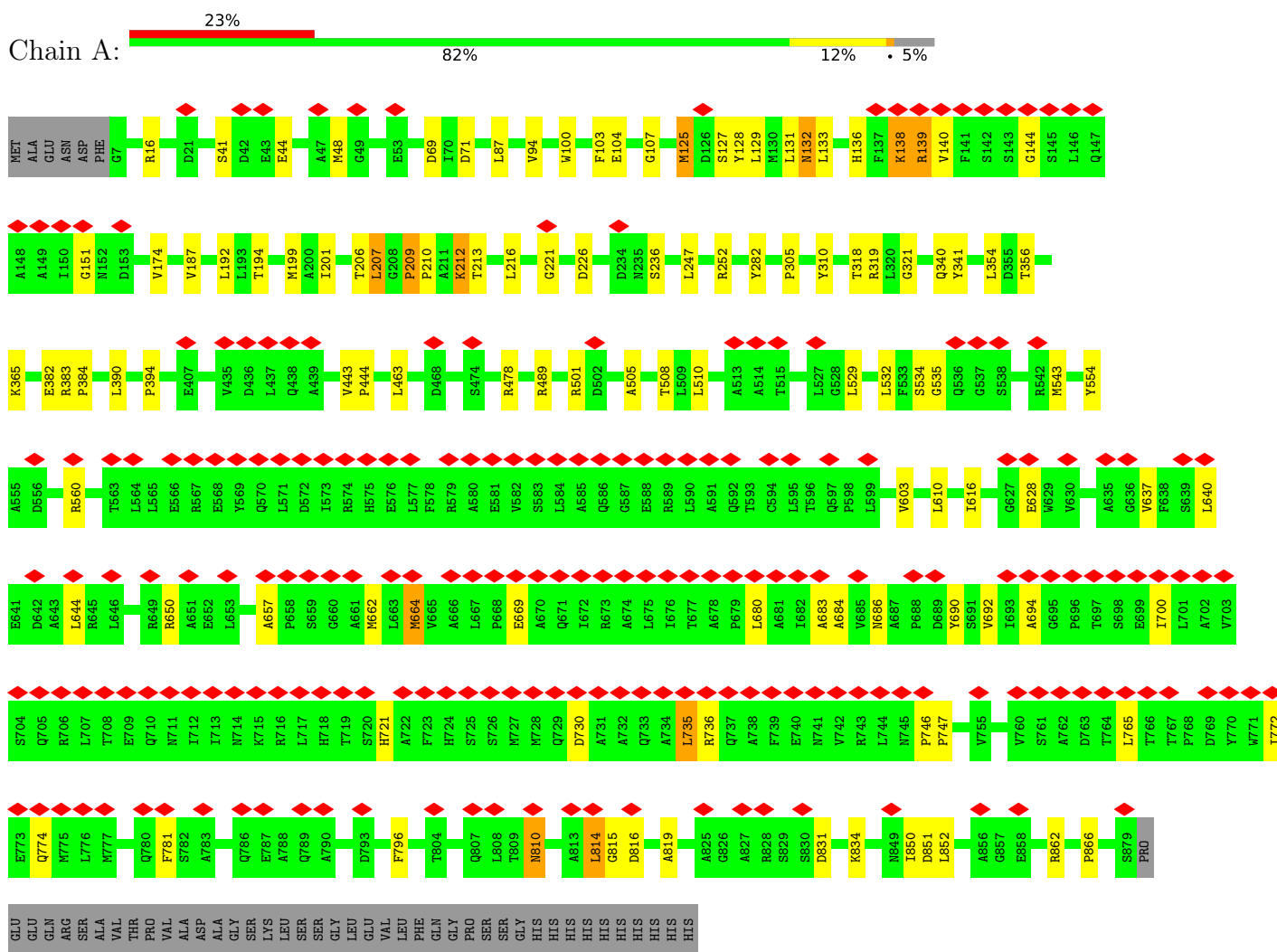
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Chain	Residue	Modelled	Actual	Comment	Reference
D	1031	HIS	-	expression tag	UNP Q0P7J9
D	1032	HIS	-	expression tag	UNP Q0P7J9
D	1033	HIS	-	expression tag	UNP Q0P7J9
D	1034	HIS	-	expression tag	UNP Q0P7J9
D	1035	HIS	-	expression tag	UNP Q0P7J9
D	1036	HIS	-	expression tag	UNP Q0P7J9

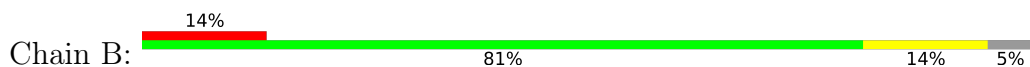
### 3 Residue-property plots

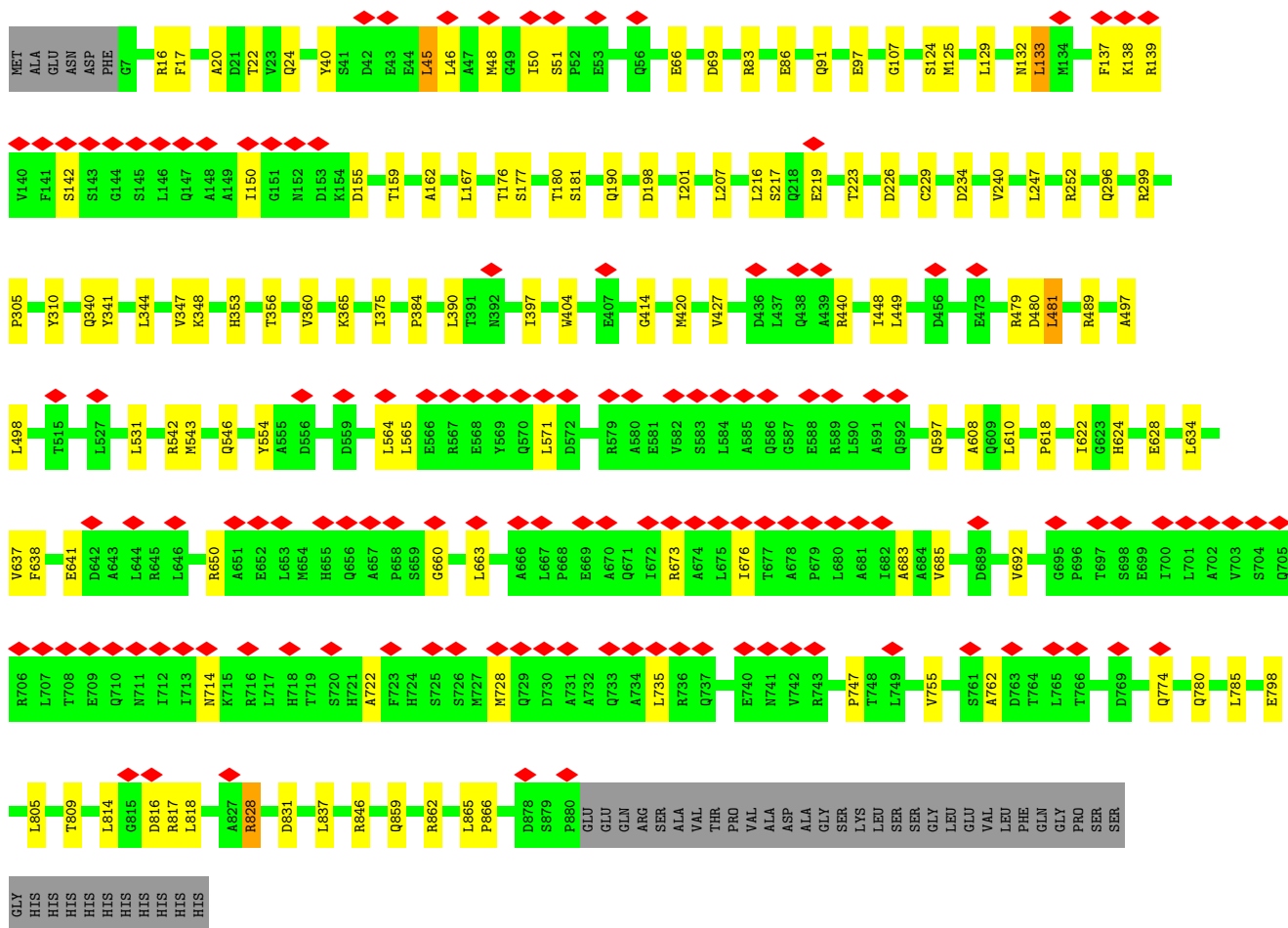
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

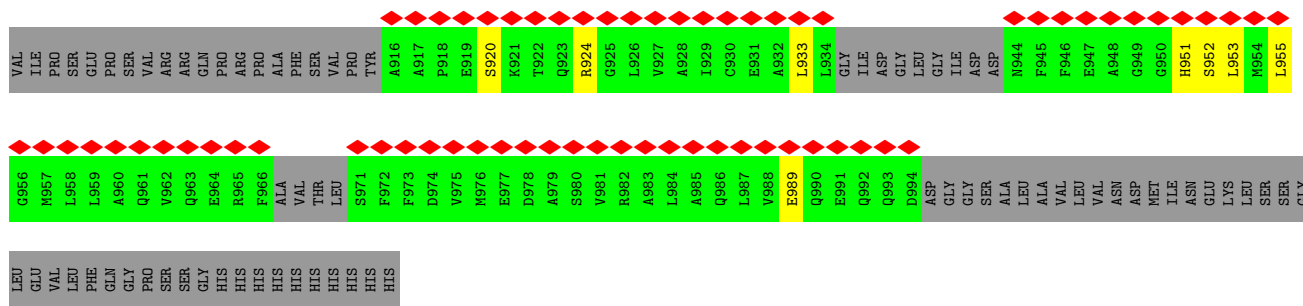
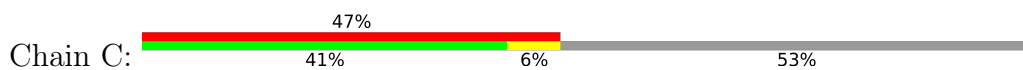


#### • Molecule 1: Polyketide synthase

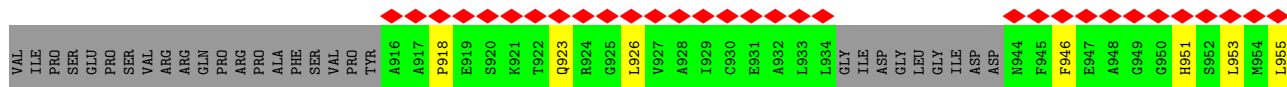
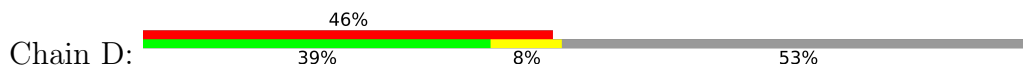




• Molecule 2: Polyketide synthase



• 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	362401	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)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.206	Depositor
Minimum map value	-0.116	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.023	Depositor
Map size (Å)	273.152, 273.152, 273.152	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.067, 1.067, 1.067	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	0.40	0/6753	0.67	3/9201 (0.0%)
1	B	0.40	0/6761	0.67	4/9213 (0.0%)
2	C	0.26	0/513	0.75	1/686 (0.1%)
2	D	0.27	0/513	0.81	2/686 (0.3%)
All	All	0.39	0/14540	0.67	10/19786 (0.1%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	132	ASN	N-CA-C	-6.83	105.50	114.31
2	D	963	GLN	CA-C-N	-6.13	112.47	122.65
2	D	963	GLN	C-N-CA	-6.13	112.47	122.65
1	A	209	PRO	N-CA-C	5.72	117.68	110.70
1	B	480	ASP	N-CA-C	-5.55	104.74	112.45
1	B	481	LEU	CA-C-O	-5.21	115.94	121.94
1	B	481	LEU	N-CA-C	-5.18	103.85	110.53
1	A	815	GLY	CA-C-O	-5.17	116.57	120.76
1	B	479	ARG	N-CA-C	-5.09	107.11	113.72
2	C	989	GLU	N-CA-CB	5.02	118.58	110.40

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	6607	0	6506	64	0
1	B	6614	0	6513	65	0
2	C	509	0	495	4	0
2	D	509	0	495	7	0
All	All	14239	0	14009	133	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 5.

All (133) 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:B:347:VAL:HG22	1:B:365:LYS:HD3	1.69	0.73
1:B:531:LEU:HD13	1:B:618:PRO:HB3	1.79	0.64
1:A:444:PRO:O	1:A:478:ARG:NH1	2.31	0.63
1:B:310:TYR:OH	1:B:365:LYS:NZ	2.33	0.62
1:A:478:ARG:NH2	1:A:501:ARG:O	2.34	0.61
1:A:310:TYR:OH	1:A:365:LYS:NZ	2.35	0.60
1:A:489:ARG:NH2	1:A:866:PRO:O	2.34	0.59
1:A:94:VAL:HG11	1:A:207:LEU:HD21	1.85	0.59
1:B:107:GLY:O	1:B:862:ARG:NH2	2.36	0.59
1:A:640:LEU:O	1:A:644:LEU:HB2	2.03	0.58
1:A:340:GLN:H	1:A:394:PRO:HA	1.67	0.58
1:A:810:ASN:HA	1:A:814:LEU:HD12	1.85	0.58
2:C:951:HIS:HA	2:C:955:LEU:HD21	1.85	0.58
1:B:83:ARG:NH2	1:B:86:GLU:OE1	2.37	0.58
1:A:683:ALA:HB2	1:A:694:ALA:HB2	1.85	0.57
1:A:796:PHE:HE2	1:A:814:LEU:HD21	1.69	0.57
1:B:564:LEU:HD11	1:B:641:GLU:HG3	1.86	0.57
1:A:221:GLY:O	1:A:319:ARG:NH1	2.38	0.56
1:A:192:LEU:O	1:A:252:ARG:NH1	2.38	0.56
1:B:554:TYR:HB2	1:B:610:LEU:HD13	1.86	0.56
1:B:448:ILE:HD11	1:B:837:LEU:HD22	1.88	0.56
2:C:933:LEU:HD21	2:C:955:LEU:HD13	1.87	0.56
1:A:144:GLY:HA2	2:D:953:LEU:HD21	1.88	0.55
1:A:554:TYR:HB2	1:A:610:LEU:HD12	1.89	0.55
1:B:608:ALA:HB1	1:B:634:LEU:HD21	1.89	0.55
1:B:16:ARG:NH1	1:B:69:ASP:O	2.40	0.54
1:B:340:GLN:NE2	1:B:390:LEU:O	2.41	0.54
1:B:305:PRO:O	1:B:341:TYR:OH	2.25	0.54
1:A:650:ARG:HA	1:A:735:LEU:HD11	1.88	0.54
1:B:16:ARG:NH2	1:B:97:GLU:OE1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:CYS:HB2	1:B:240:VAL:HG12	1.89	0.54
1:B:597:GLN:OE1	1:B:650:ARG:NH1	2.42	0.53
1:B:22:THR:HG22	1:B:24:GLN:H	1.71	0.53
2:D:918:PRO:HB2	2:D:923:GLN:HB2	1.91	0.53
1:B:176:THR:O	1:B:180:THR:OG1	2.26	0.53
1:B:17:PHE:HB2	1:B:20:ALA:HB3	1.89	0.53
1:B:344:LEU:HB3	1:B:397:ILE:HG12	1.90	0.53
1:B:785:LEU:HD21	1:B:809:THR:HG23	1.91	0.53
2:D:918:PRO:HB3	2:D:926:LEU:HD21	1.90	0.52
1:B:177:SER:HB3	1:B:420:MET:H	1.73	0.52
2:C:952:SER:OG	2:C:953:LEU:N	2.41	0.52
1:A:543:MET:HE3	1:A:603:VAL:HG21	1.90	0.52
1:B:375:ILE:HG13	1:B:404:TRP:HB2	1.91	0.52
1:B:440:ARG:NH1	1:B:859:GLN:O	2.43	0.52
1:B:181:SER:HB3	1:B:360:VAL:HB	1.92	0.52
1:B:384:PRO:HB3	1:B:390:LEU:HD23	1.91	0.51
1:B:234:ASP:OD1	1:B:234:ASP:N	2.43	0.51
1:B:747:PRO:HG2	1:B:762:ALA:HA	1.91	0.51
1:B:728:MET:SD	1:B:728:MET:N	2.83	0.51
1:B:124:SER:OG	1:B:125:MET:N	2.42	0.51
2:C:920:SER:O	2:C:924:ARG:NH1	2.43	0.51
1:A:684:ALA:HB3	1:A:692:VAL:HB	1.93	0.50
1:A:282:TYR:OH	1:B:159:THR:OG1	2.29	0.50
1:A:560:ARG:HE	1:A:640:LEU:HD23	1.78	0.49
1:A:384:PRO:HG3	1:A:390:LEU:HD12	1.94	0.49
1:A:683:ALA:HB3	1:A:692:VAL:HG12	1.93	0.49
1:A:730:ASP:N	1:A:730:ASP:OD1	2.46	0.49
1:A:534:SER:OG	1:A:535:GLY:N	2.46	0.49
1:B:685:VAL:HB	1:B:780:GLN:HG2	1.94	0.49
1:B:489:ARG:NH2	1:B:866:PRO:O	2.43	0.49
1:B:565:LEU:HD21	1:B:571:LEU:HD12	1.93	0.49
1:B:296:GLN:HG3	1:B:299:ARG:HH11	1.77	0.48
1:A:16:ARG:NH1	1:A:69:ASP:O	2.45	0.48
1:A:138:LYS:H	1:A:138:LYS:HG2	1.47	0.48
1:A:637:VAL:HG21	1:A:765:LEU:HD23	1.95	0.48
1:A:532:LEU:HD13	1:A:796:PHE:HB3	1.94	0.48
1:B:201:ILE:HD11	1:B:247:LEU:HD13	1.95	0.48
1:A:128:TYR:HA	1:A:209:PRO:HG2	1.97	0.47
1:A:664:MET:HB3	1:A:664:MET:HE3	1.69	0.47
1:A:796:PHE:CE2	1:A:814:LEU:HD21	2.49	0.47
1:A:194:THR:OG1	1:B:190:GLN:OE1	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:ALA:HA	1:A:508:THR:HG22	1.96	0.47
1:A:657:ALA:HB3	1:A:721:HIS:HD2	1.79	0.47
2:D:951:HIS:HA	2:D:955:LEU:HD12	1.96	0.47
1:A:680:LEU:HD22	1:A:700:ILE:HG13	1.97	0.47
1:A:87:LEU:HD21	2:D:958:LEU:HD11	1.96	0.46
1:A:174:VAL:HG11	1:A:187:VAL:HG21	1.97	0.46
1:A:318:THR:HG23	1:A:321:GLY:H	1.81	0.46
1:B:828:ARG:HB2	1:B:831:ASP:HB2	1.96	0.46
1:A:127:SER:HB3	1:A:209:PRO:HD2	1.97	0.46
1:B:40:TYR:OH	1:B:66:GLU:OE2	2.29	0.46
1:B:219:GLU:HB2	2:D:946:PHE:HB3	1.98	0.46
1:B:45:LEU:HD23	1:B:45:LEU:HA	1.75	0.45
1:B:162:ALA:HA	1:B:167:LEU:HD12	1.97	0.45
1:A:305:PRO:O	1:A:341:TYR:OH	2.35	0.45
1:A:443:VAL:HG12	1:A:478:ARG:HH11	1.80	0.45
1:A:814:LEU:HD23	1:A:814:LEU:HA	1.63	0.45
1:B:564:LEU:HD21	1:B:641:GLU:HA	1.98	0.45
1:A:71:ASP:N	1:A:71:ASP:OD1	2.41	0.44
1:A:686:ASN:HA	1:A:781:PHE:HB3	1.99	0.44
1:B:91:GLN:HG2	1:B:207:LEU:HB2	1.99	0.44
1:B:348:LYS:HG2	1:B:353:HIS:HA	1.99	0.44
1:B:755:VAL:HG11	1:B:774:GLN:HG2	1.98	0.44
1:A:201:ILE:HG12	1:A:247:LEU:HD22	1.99	0.44
1:B:201:ILE:HG12	1:B:247:LEU:HD22	1.99	0.44
1:B:814:LEU:HB3	1:B:817:ARG:HB2	1.98	0.44
1:A:686:ASN:HB2	1:A:690:TYR:HD1	1.83	0.44
1:B:663:LEU:HD11	1:B:714:ASN:HB2	1.99	0.43
1:A:796:PHE:O	1:A:819:ALA:HA	2.18	0.43
1:B:798:GLU:HG3	1:B:805:LEU:HB2	1.99	0.43
1:A:133:LEU:HD23	1:A:133:LEU:HA	1.86	0.43
1:B:489:ARG:HH22	1:B:865:LEU:HB2	1.84	0.43
1:B:683:ALA:HB3	1:B:692:VAL:HG12	2.01	0.42
1:A:129:LEU:HA	1:A:132:ASN:HB2	2.00	0.42
1:A:628:GLU:HB3	1:A:774:GLN:HE22	1.84	0.42
1:A:226:ASP:OD1	1:A:226:ASP:N	2.45	0.42
1:B:846:ARG:H	1:B:846:ARG:HG2	1.67	0.42
2:D:973:PHE:HA	2:D:976:MET:HE2	2.01	0.42
1:A:139:ARG:HE	1:A:139:ARG:HB3	1.63	0.42
1:B:414:GLY:HA2	1:B:427:VAL:O	2.20	0.42
1:B:448:ILE:HA	1:B:498:LEU:O	2.20	0.42
1:B:637:VAL:HG23	1:B:638:PHE:CD1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:463:LEU:HD22	1:A:510:LEU:HD22	2.02	0.41
1:A:151:GLY:HA2	1:B:420:MET:HE1	2.01	0.41
1:A:212:LYS:HB2	1:A:212:LYS:HE2	1.38	0.41
1:A:736:ARG:HE	1:A:772:ILE:HG21	1.85	0.41
1:B:133:LEU:HD13	1:B:133:LEU:HA	1.71	0.41
1:B:181:SER:OG	1:B:356:THR:O	2.33	0.41
1:B:673:ARG:HA	1:B:676:ILE:HG22	2.03	0.41
1:A:529:LEU:HD22	1:A:616:ILE:HG12	2.02	0.41
1:B:198:ASP:OD1	1:B:252:ARG:NH2	2.42	0.41
1:A:41:SER:N	1:A:44:GLU:OE2	2.52	0.41
1:A:125:MET:HB2	1:B:150:ILE:HG12	2.02	0.41
1:B:129:LEU:HA	1:B:132:ASN:HB2	2.02	0.41
1:B:660:GLY:HA3	1:B:722:ALA:HB2	2.03	0.41
1:B:449:LEU:O	1:B:497:ALA:HA	2.21	0.41
1:B:155:ASP:OD1	1:B:155:ASP:N	2.45	0.40
1:A:100:TRP:NE1	1:A:104:GLU:OE1	2.54	0.40
1:A:103:PHE:HE1	1:A:199:MET:HE3	1.85	0.40
1:A:382:GLU:OE1	1:A:383:ARG:NH2	2.54	0.40
1:A:48:MET:HE2	1:A:48:MET:HB3	1.99	0.40
1:A:107:GLY:O	1:A:862:ARG:NE	2.42	0.40
1:A:746:PRO:HA	1:A:747:PRO:HD3	1.91	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	871/921 (95%)	812 (93%)	58 (7%)	1 (0%)	48	76
1	B	872/921 (95%)	816 (94%)	56 (6%)	0	100	100
2	C	60/141 (43%)	56 (93%)	4 (7%)	0	100	100
2	D	60/141 (43%)	56 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1863/2124 (88%)	1740 (93%)	122 (6%)	1 (0%)	50 76

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	210	PRO

### 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	681/721 (94%)	655 (96%)	26 (4%)	28 56
1	B	682/721 (95%)	657 (96%)	25 (4%)	29 56
2	C	53/116 (46%)	53 (100%)	0	100 100
2	D	53/116 (46%)	53 (100%)	0	100 100
All	All	1469/1674 (88%)	1418 (96%)	51 (4%)	33 58

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	125	MET
1	A	131	LEU
1	A	136	HIS
1	A	138	LYS
1	A	139	ARG
1	A	140	VAL
1	A	206	THR
1	A	207	LEU
1	A	212	LYS
1	A	213	THR
1	A	216	LEU
1	A	236	SER
1	A	354	LEU
1	A	356	THR

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Mol	Chain	Res	Type
1	A	662	MET
1	A	664	MET
1	A	669	GLU
1	A	735	LEU
1	A	810	ASN
1	A	814	LEU
1	A	816	ASP
1	A	831	ASP
1	A	834	LYS
1	A	850	ILE
1	A	851	ASP
1	A	852	LEU
1	B	45	LEU
1	B	46	LEU
1	B	48	MET
1	B	50	ILE
1	B	51	SER
1	B	133	LEU
1	B	137	PHE
1	B	138	LYS
1	B	139	ARG
1	B	142	SER
1	B	216	LEU
1	B	217	SER
1	B	223	THR
1	B	226	ASP
1	B	481	LEU
1	B	542	ARG
1	B	543	MET
1	B	546	GLN
1	B	622	ILE
1	B	624	HIS
1	B	628	GLU
1	B	735	LEU
1	B	816	ASP
1	B	818	LEU
1	B	828	ARG

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	132	ASN

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Mol	Chain	Res	Type
1	A	166	ASN
1	A	218	GLN
1	A	609	GLN
1	A	624	HIS
1	A	737	GLN
1	A	774	GLN
1	A	780	GLN
1	A	807	GLN
1	B	152	ASN
1	B	218	GLN
1	B	228	HIS
1	B	392	ASN
1	B	424	ASN
1	B	512	GLN
1	B	526	GLN
1	B	536	GLN
1	B	586	GLN
1	B	624	HIS
1	B	686	ASN
1	B	711	ASN
2	C	944	ASN
2	C	993	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.

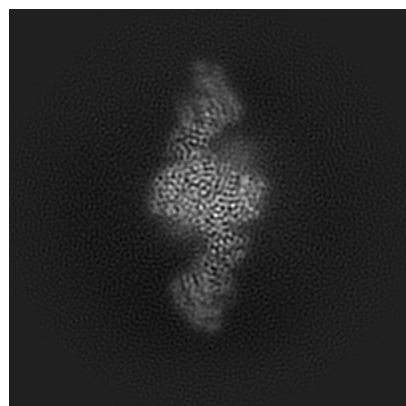
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38410. These allow visual inspection of the internal detail of the map and identification of artifacts.

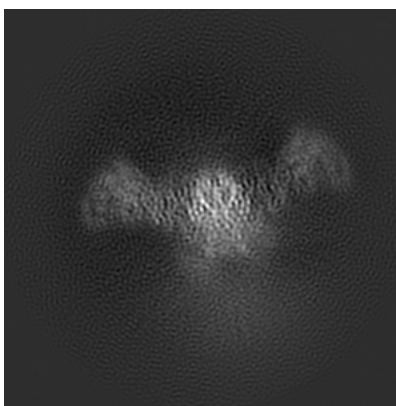
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

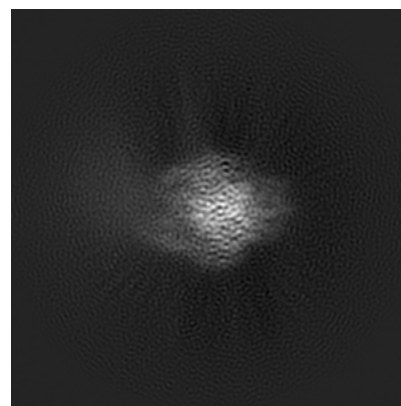
#### 6.1.1 Primary map



X

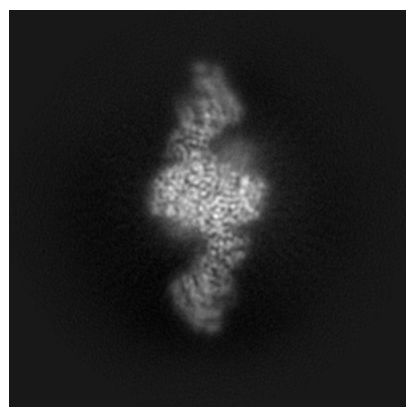


Y

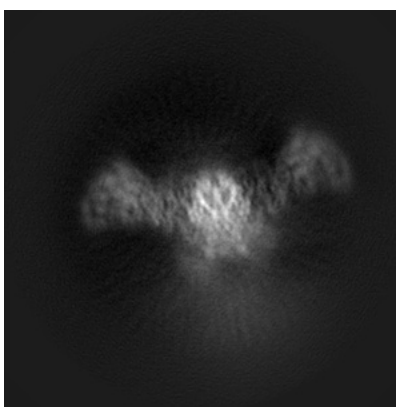


Z

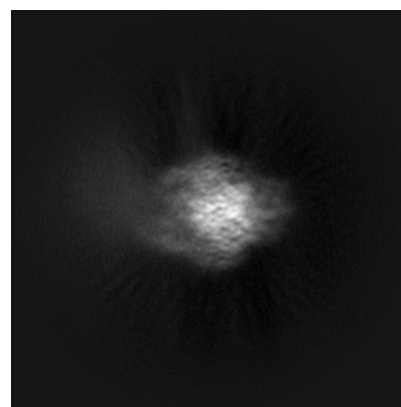
#### 6.1.2 Raw map



X



Y

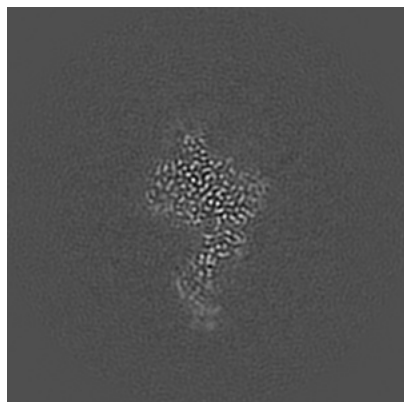


Z

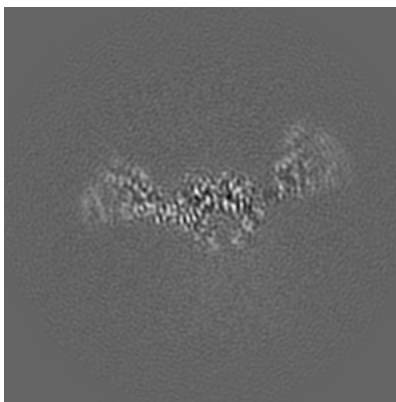
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

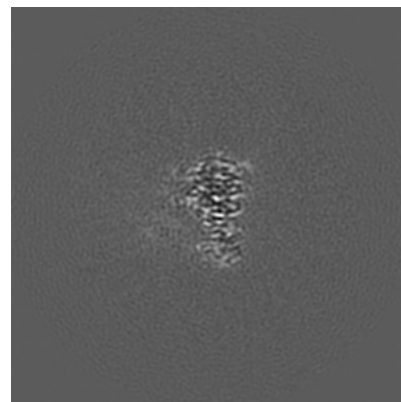
### 6.2.1 Primary map



X Index: 128

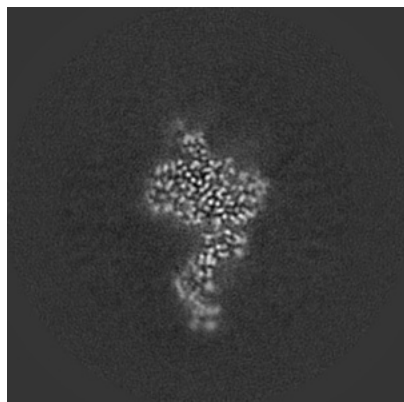


Y Index: 128

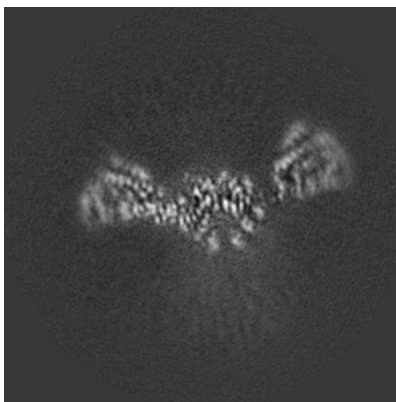


Z Index: 128

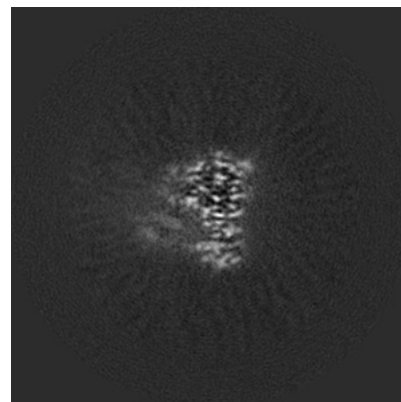
### 6.2.2 Raw map



X Index: 128



Y Index: 128

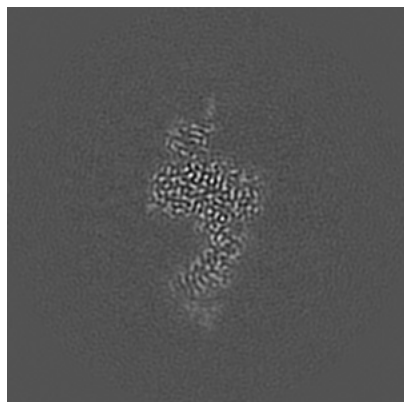


Z Index: 128

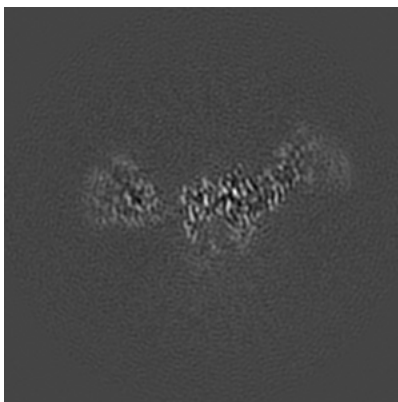
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

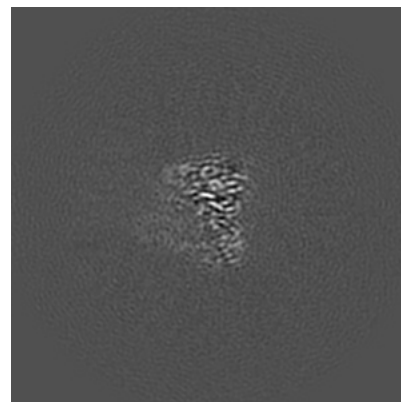
### 6.3.1 Primary map



X Index: 135

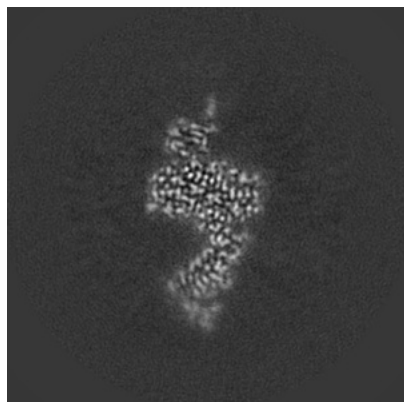


Y Index: 123

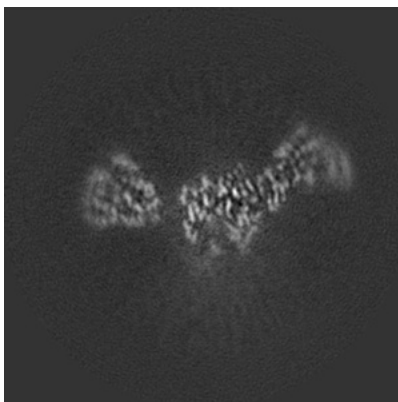


Z Index: 130

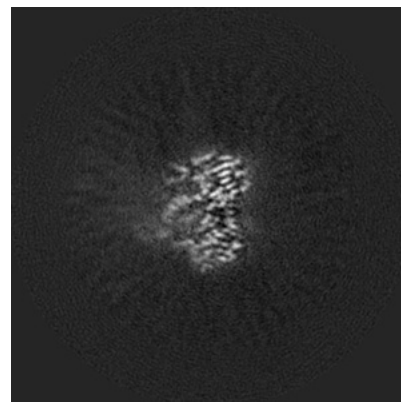
### 6.3.2 Raw map



X Index: 135



Y Index: 123

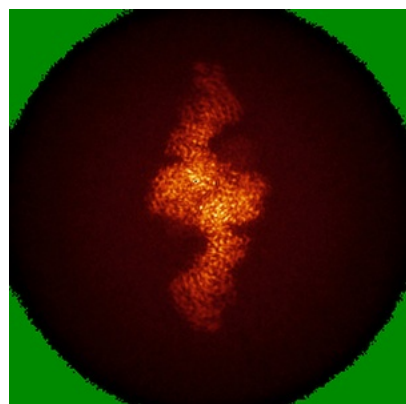


Z Index: 135

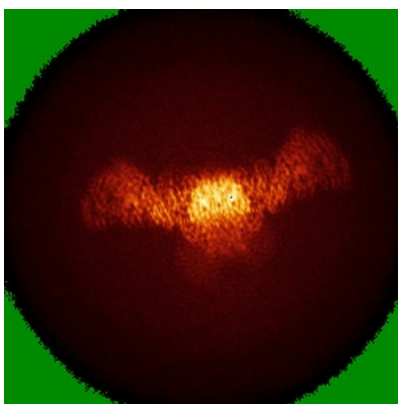
The images above show the largest variance slices of the map in three orthogonal directions.

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

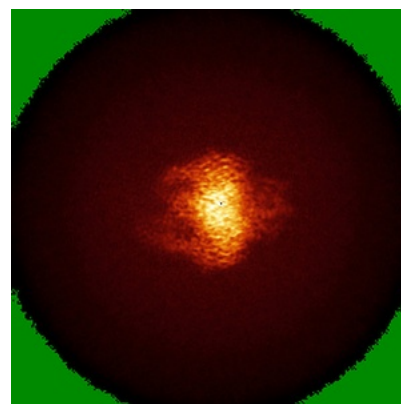
### 6.4.1 Primary map



X

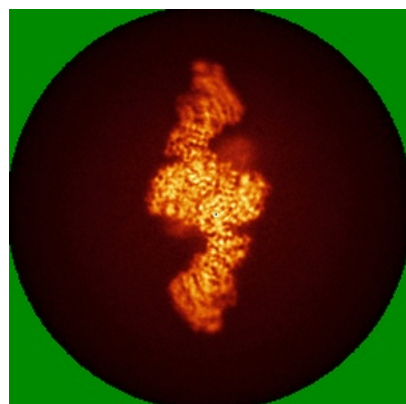


Y

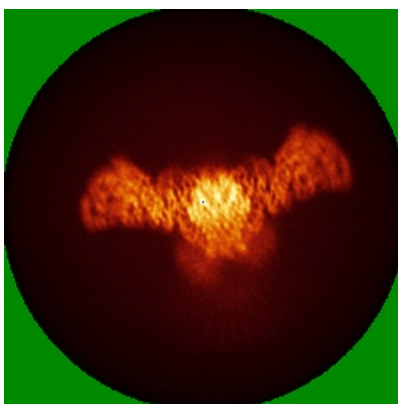


Z

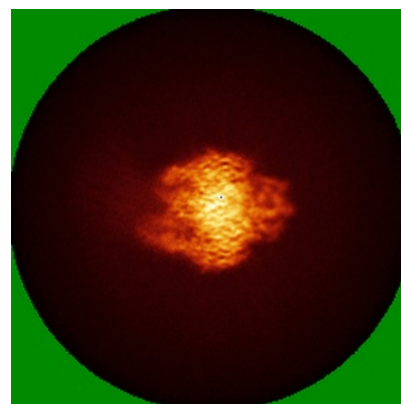
### 6.4.2 Raw map



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

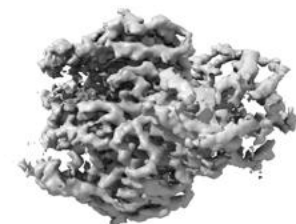
### 6.5.2 Raw map



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.



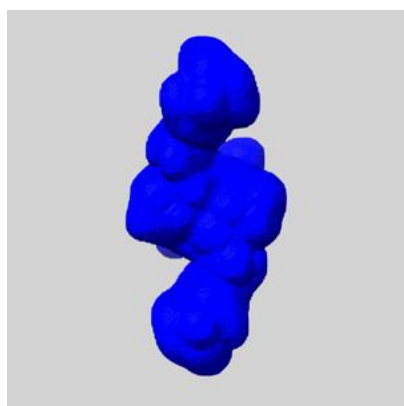
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

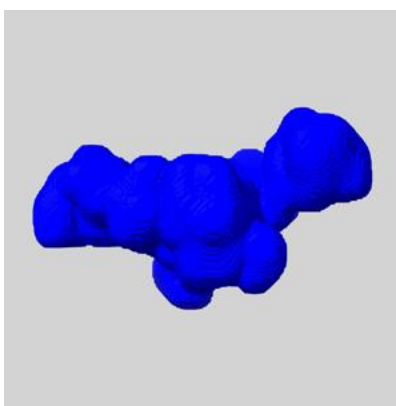
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

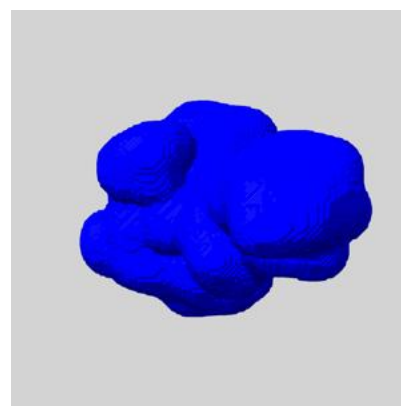
### 6.6.1 emd\_38410\_msk\_1.map [i](#)



X



Y

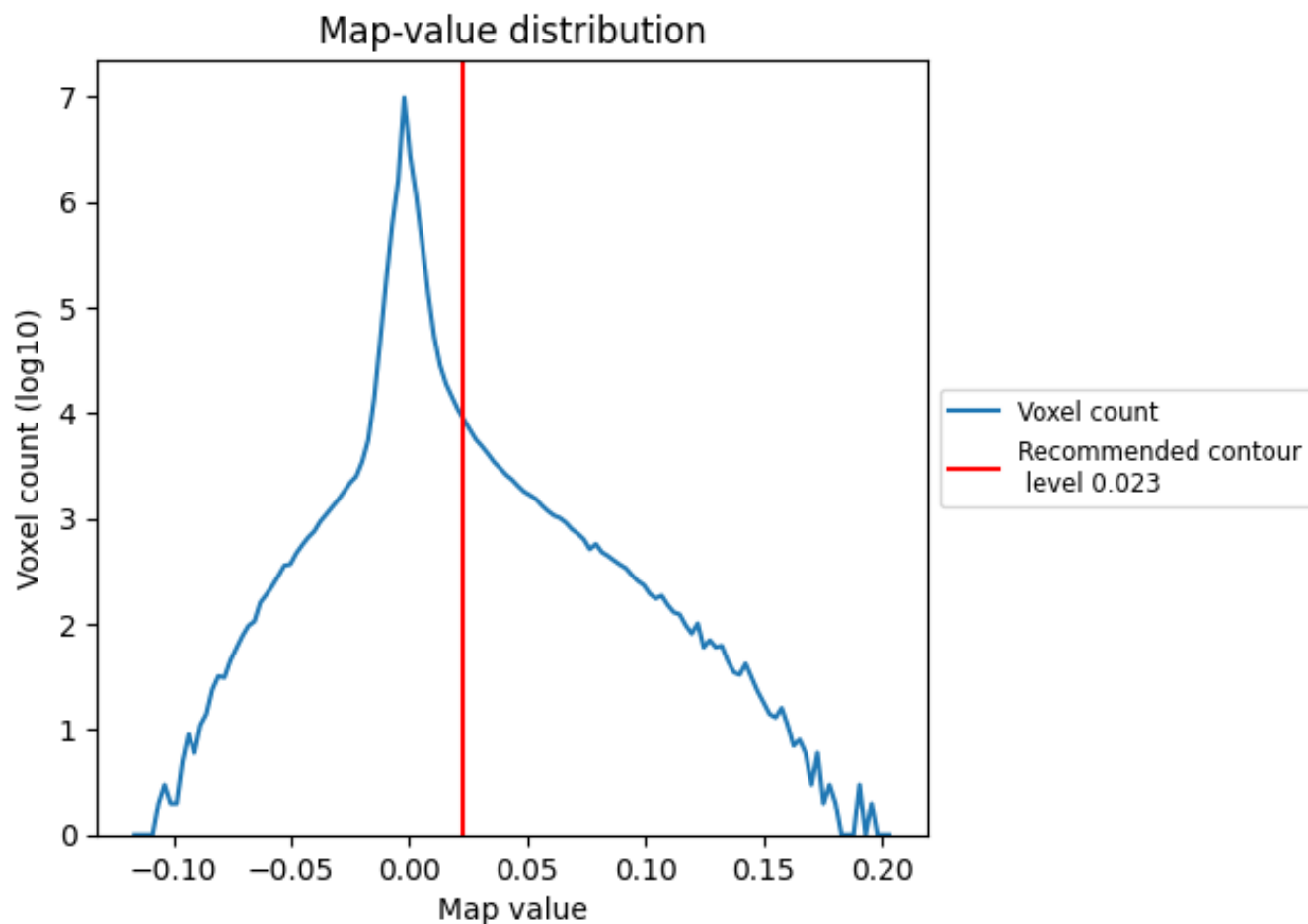


Z

## 7 Map analysis [i](#)

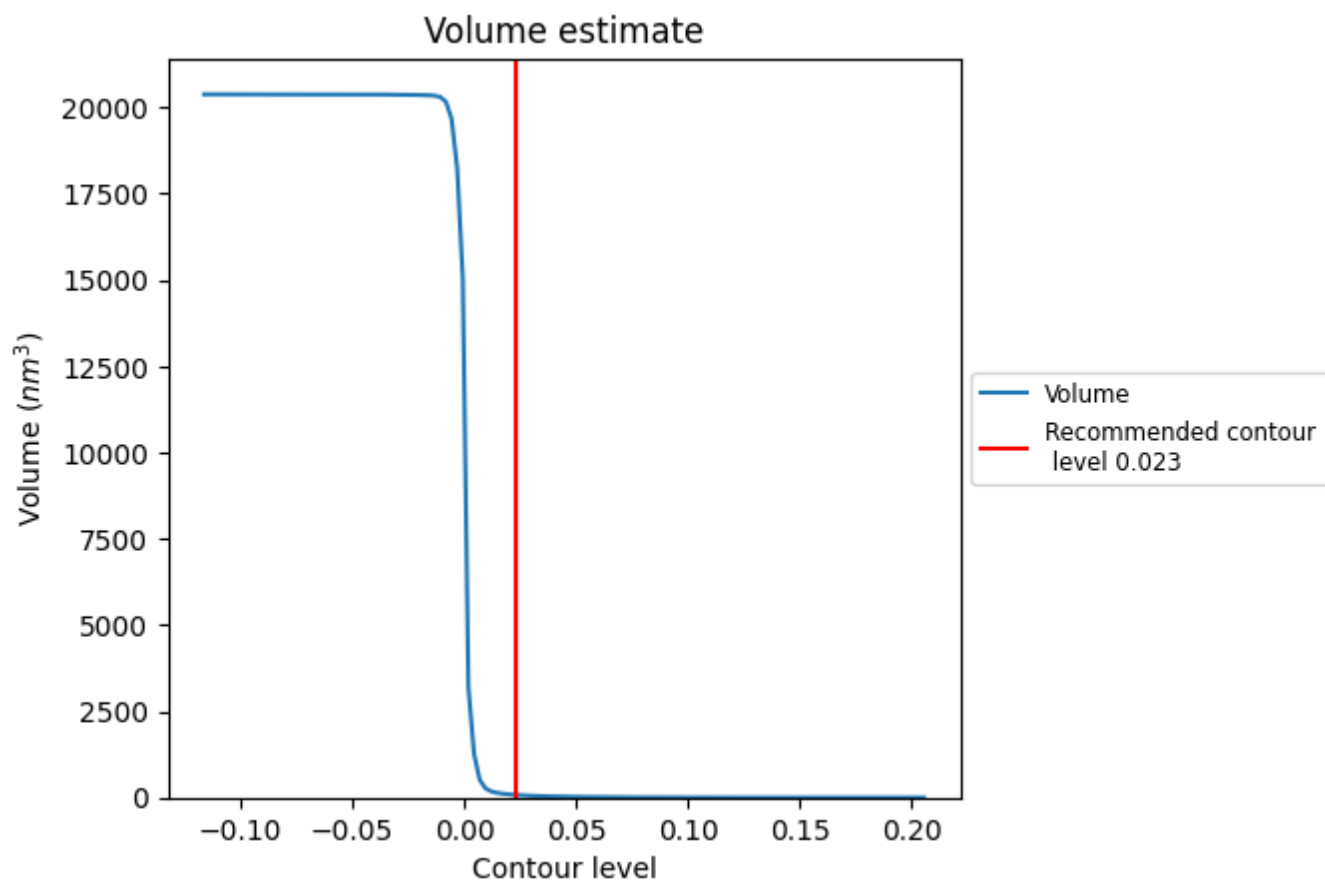
This section contains the results of statistical analysis of the map.

### 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.

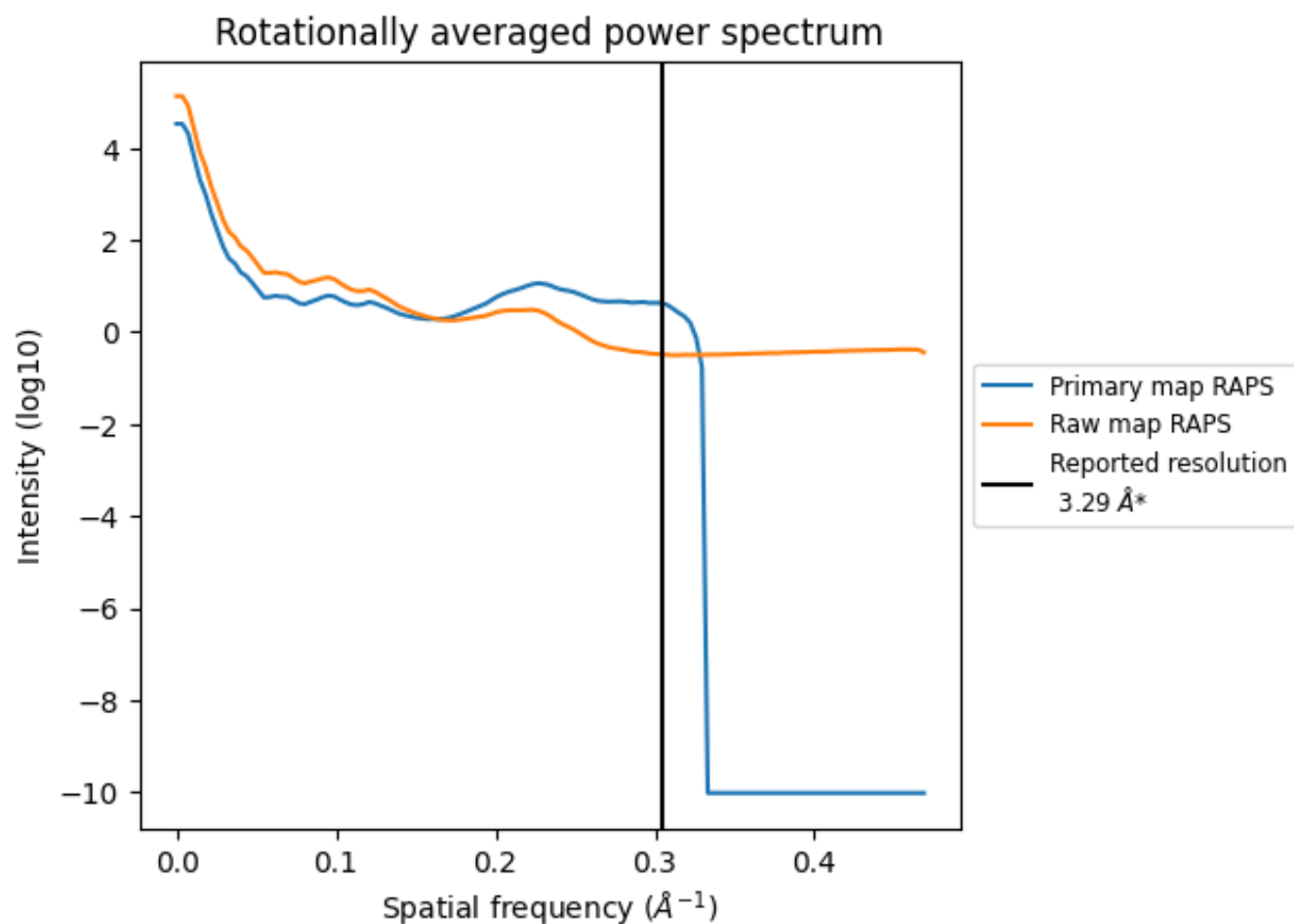
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 76  $\text{nm}^3$ ; this corresponds to an approximate mass of 68 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 ⓘ

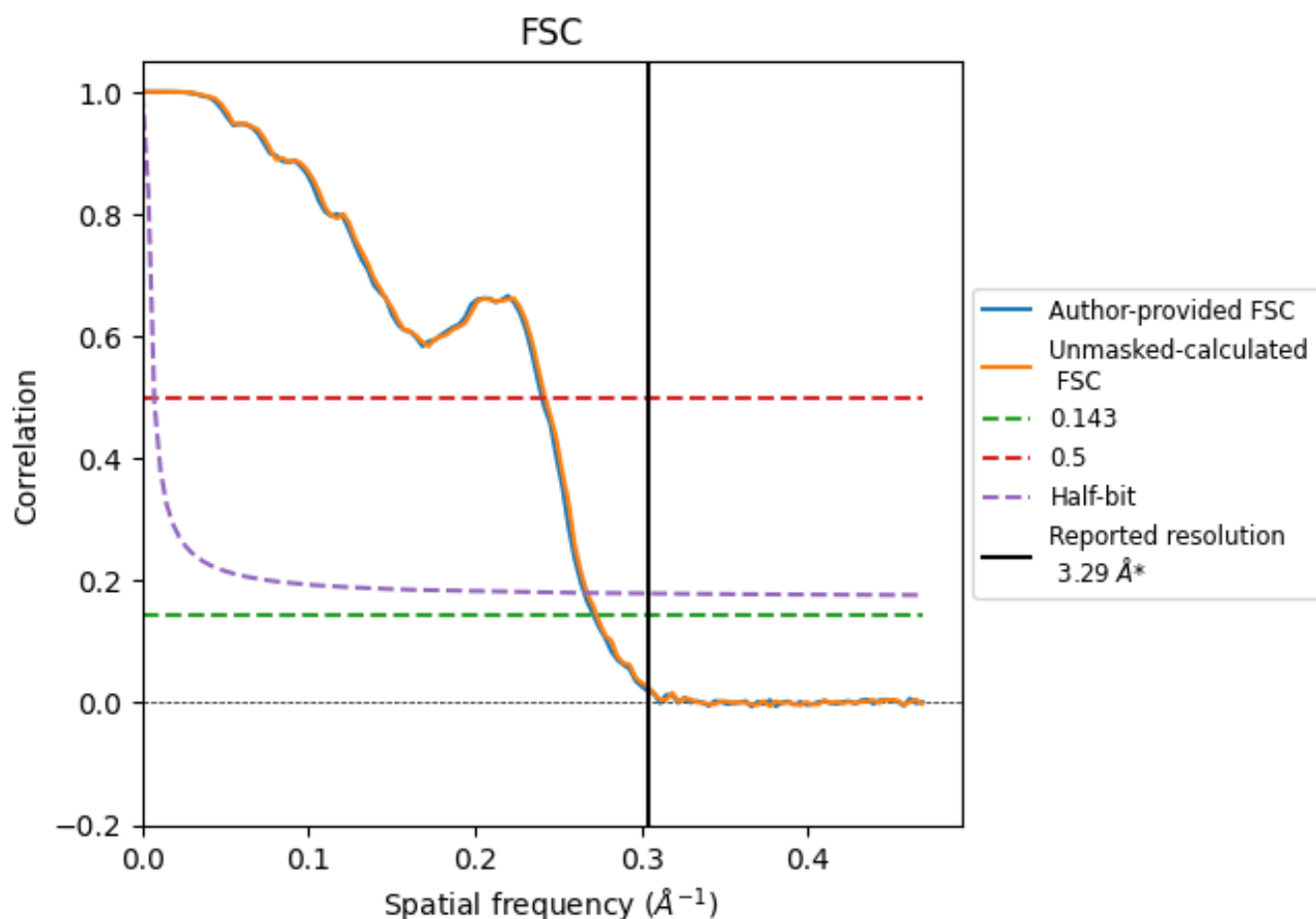


\*Reported resolution corresponds to spatial frequency of 0.304 Å<sup>-1</sup>

## 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  $0.304 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.29	-	-
Author-provided FSC curve	3.69	4.16	3.77
Unmasked-calculated*	3.66	4.13	3.74

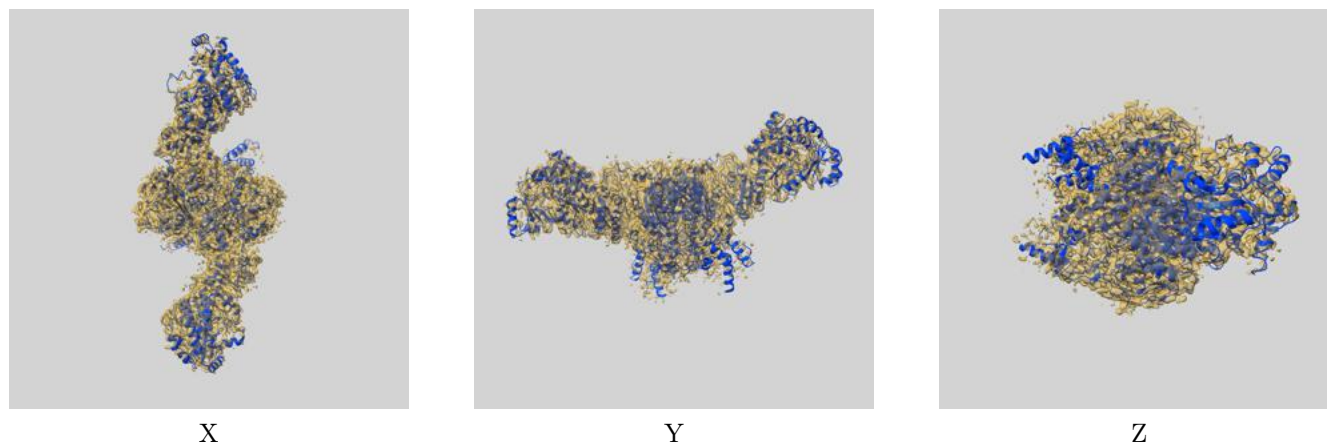
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.69 differs from the reported value 3.29 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.66 differs from the reported value 3.29 by more than 10 %

## 9 Map-model fit [i](#)

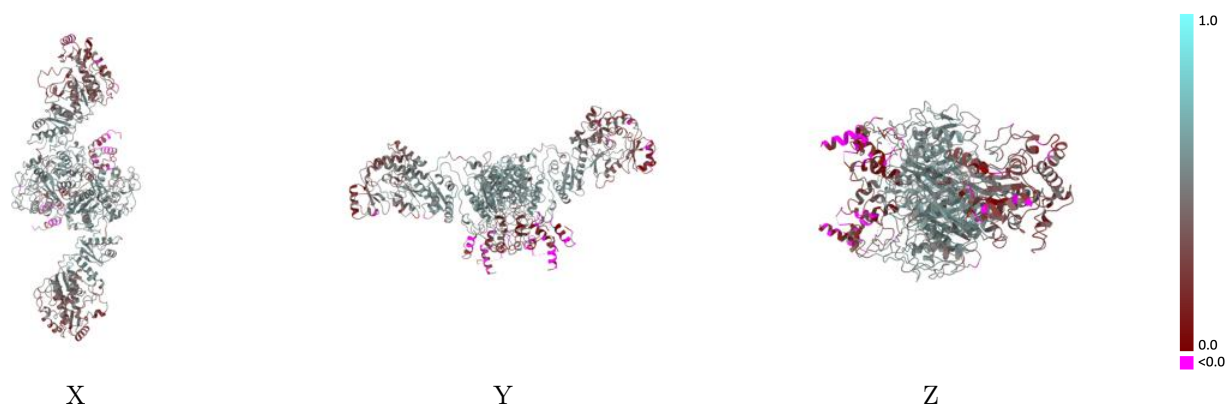
This section contains information regarding the fit between EMDB map EMD-38410 and PDB model 8XJY. Per-residue inclusion information can be found in section [3](#) on page [7](#).

### 9.1 Map-model overlay [i](#)



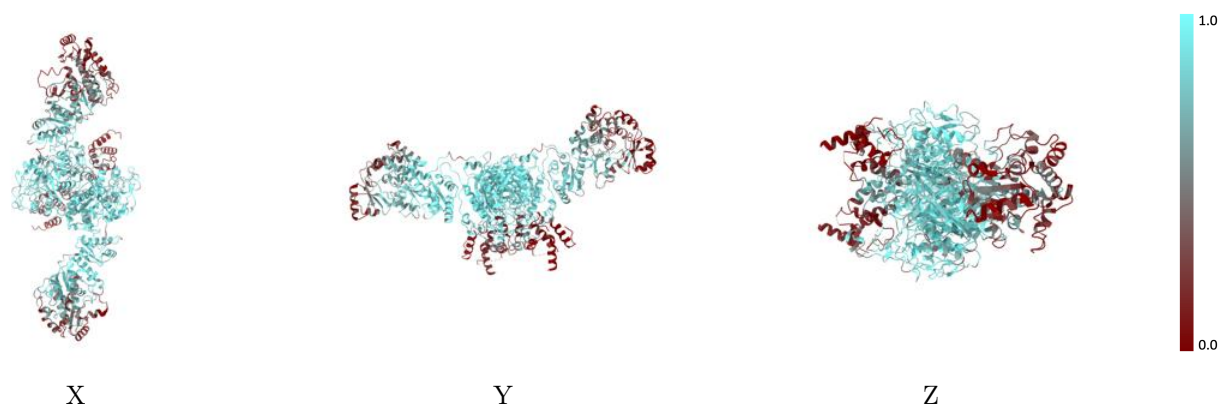
The images above show the 3D surface view of the map at the recommended contour level 0.023 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

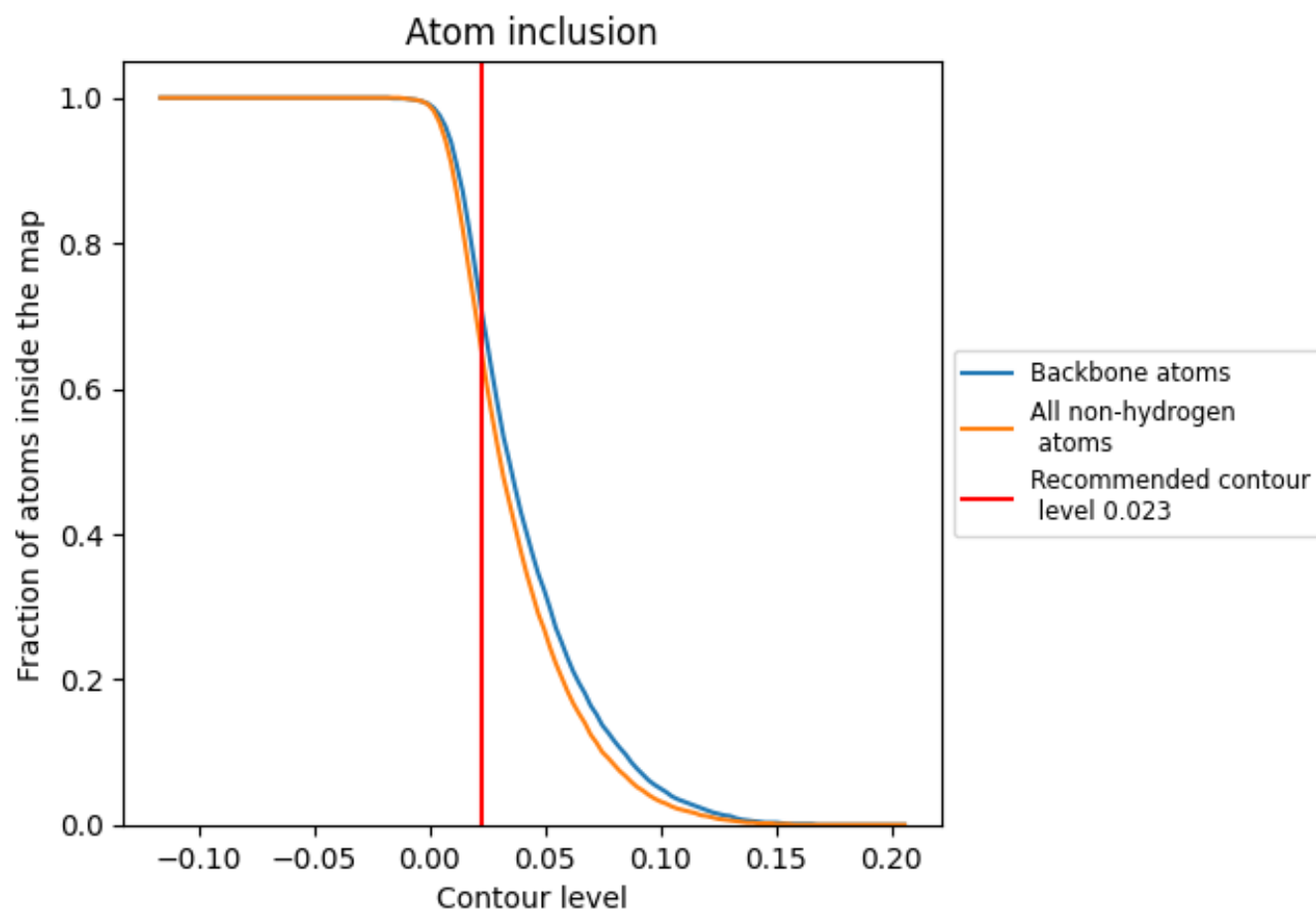
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.023).



## 9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 64% 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 (0.023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6430	<div></div> 0.4290
A	<div></div> 0.6480	<div></div> 0.4430
B	<div></div> 0.7280	<div></div> 0.4680
C	<div></div> 0.0660	<div></div> 0.1060
D	<div></div> 0.0520	<div></div> 0.0780

