



Full wwPDB EM Validation Report ⓘ

Oct 20, 2024 – 06:20 PM EDT

PDB ID : 7M7E
EMDB ID : EMD-23710
Title : 6-Deoxyerythronolide B synthase (DEBS) hybrid module (M3/1) in complex with antibody fragment 1B2
Authors : Cogan, D.P.; Zhang, K.; Chiu, W.; Khosla, C.
Deposited on : 2021-03-28
Resolution : 3.20 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
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) : 2.39

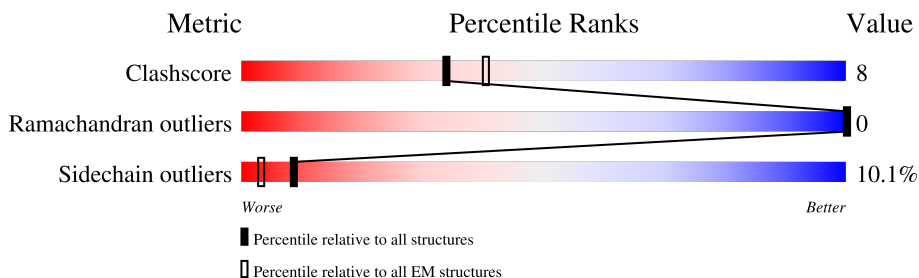
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1777	
1	B	1777	
2	C	249	
3	D	236	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16677 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 6-deoxyerythronolide-B synthase EryA2, modules 3 and 4, EryA1, 6-deoxyerythronolide-B synthase EryA3, modules 5 and 6 chimera.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	908	Total	C	N	O	S	0	0
			6771	4196	1245	1312	18		
1	A	908	Total	C	N	O	S	0	0
			6771	4196	1245	1312	18		

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	expression tag	UNP Q03132
B	2	ALA	-	expression tag	UNP Q03132
B	3	SER	-	expression tag	UNP Q03132
B	1761	SER	-	expression tag	UNP Q03133
B	1762	SER	-	expression tag	UNP Q03133
B	1763	VAL	-	expression tag	UNP Q03133
B	1764	ASP	-	expression tag	UNP Q03133
B	1765	LYS	-	expression tag	UNP Q03133
B	1766	LEU	-	expression tag	UNP Q03133
B	1767	ALA	-	expression tag	UNP Q03133
B	1768	ALA	-	expression tag	UNP Q03133
B	1769	ALA	-	expression tag	UNP Q03133
B	1770	LEU	-	expression tag	UNP Q03133
B	1771	GLU	-	expression tag	UNP Q03133
B	1772	HIS	-	expression tag	UNP Q03133
B	1773	HIS	-	expression tag	UNP Q03133
B	1774	HIS	-	expression tag	UNP Q03133
B	1775	HIS	-	expression tag	UNP Q03133
B	1776	HIS	-	expression tag	UNP Q03133
B	1777	HIS	-	expression tag	UNP Q03133
A	1	MET	-	expression tag	UNP Q03132
A	2	ALA	-	expression tag	UNP Q03132
A	3	SER	-	expression tag	UNP Q03132
A	1761	SER	-	expression tag	UNP Q03133
A	1762	SER	-	expression tag	UNP Q03133

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1763	VAL	-	expression tag	UNP Q03133
A	1764	ASP	-	expression tag	UNP Q03133
A	1765	LYS	-	expression tag	UNP Q03133
A	1766	LEU	-	expression tag	UNP Q03133
A	1767	ALA	-	expression tag	UNP Q03133
A	1768	ALA	-	expression tag	UNP Q03133
A	1769	ALA	-	expression tag	UNP Q03133
A	1770	LEU	-	expression tag	UNP Q03133
A	1771	GLU	-	expression tag	UNP Q03133
A	1772	HIS	-	expression tag	UNP Q03133
A	1773	HIS	-	expression tag	UNP Q03133
A	1774	HIS	-	expression tag	UNP Q03133
A	1775	HIS	-	expression tag	UNP Q03133
A	1776	HIS	-	expression tag	UNP Q03133
A	1777	HIS	-	expression tag	UNP Q03133

- Molecule 2 is a protein called 1B2 (heavy chain).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	205	Total	C	N	O	S	0	0
			1539	978	257	298	6		

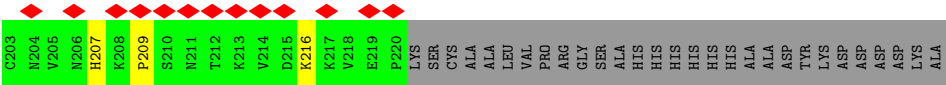
- Molecule 3 is a protein called 1B2 (light chain).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	209	Total	C	N	O	S	0	0
			1596	1001	269	320	6		

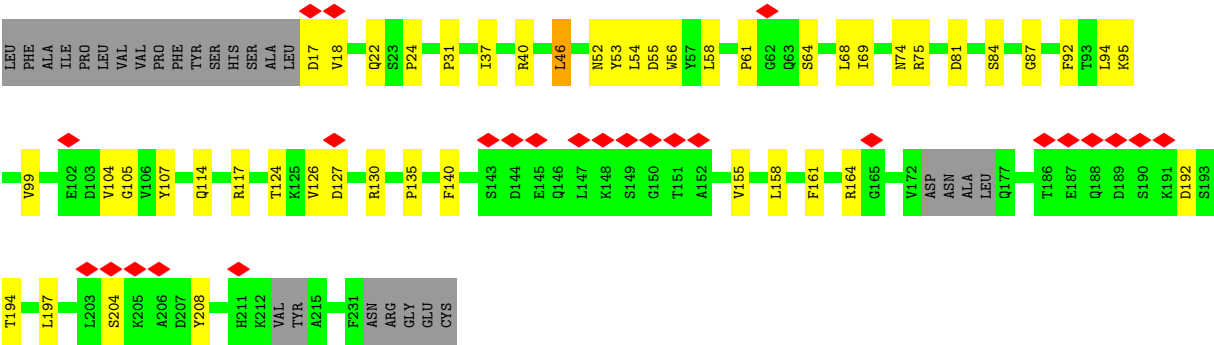


- Molecule 2: 1B2 (heavy chain)





● Molecule 3: 1B2 (light chain)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	93053	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	5.163	Depositor
Minimum map value	-3.349	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.061	Depositor
Recommended contour level	0.272	Depositor
Map size (\AA)	369.6, 369.6, 369.6	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	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	0.37	1/6900 (0.0%)	0.68	4/9386 (0.0%)
1	B	0.37	0/6900	0.66	6/9386 (0.1%)
2	C	0.27	0/1575	0.52	0/2141
3	D	0.30	0/1630	0.52	0/2212
All	All	0.36	1/17005 (0.0%)	0.64	10/23125 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	3
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	442	SER	CA-CB	-5.46	1.44	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	790	ARG	CB-CA-C	-12.13	86.14	110.40
1	A	334	ASP	CB-CA-C	-11.29	87.83	110.40
1	A	409	GLU	CA-CB-CG	7.08	128.97	113.40
1	B	409	GLU	CA-CB-CG	7.04	128.89	113.40
1	B	265	PHE	CB-CA-C	-6.73	96.94	110.40
1	A	265	PHE	CB-CA-C	-6.64	97.13	110.40
1	B	790	ARG	N-CA-CB	-6.08	99.66	110.60
1	B	529	ARG	CG-CD-NE	5.65	123.67	111.80
1	A	529	ARG	CG-CD-NE	5.63	123.63	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	452	HIS	CB-CA-C	-5.42	99.55	110.40

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	114	ARG	Sidechain
1	A	591	ARG	Sidechain
1	A	800	ARG	Sidechain
1	B	114	ARG	Sidechain
1	B	591	ARG	Sidechain
1	B	798	ASP	Mainchain

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	6771	0	6634	104	0
1	B	6771	0	6634	103	0
2	C	1539	0	1513	32	0
3	D	1596	0	1561	27	0
All	All	16677	0	16342	263	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (263) 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:440:ARG:HG3	1:B:454:ILE:HA	1.62	0.82
1:A:800:ARG:HB3	1:A:800:ARG:CZ	2.21	0.69
1:B:333:VAL:HG11	1:B:440:ARG:HH21	1.58	0.69
2:C:19:SER:HA	2:C:87:MET:O	1.92	0.69
1:A:764:ARG:HG2	1:A:765:GLU:N	2.07	0.69
1:A:645:GLU:HA	1:A:645:GLU:OE1	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:620:ARG:HD2	1:A:683:ARG:HH12	1.60	0.67
1:B:645:GLU:OE1	1:B:645:GLU:HA	1.93	0.67
1:A:711:ARG:NH2	1:A:724:VAL:O	2.27	0.67
1:B:711:ARG:NH2	1:B:724:VAL:O	2.27	0.67
3:D:158:LEU:HB2	3:D:197:LEU:HB3	1.76	0.66
2:C:11:GLY:HA2	2:C:116:VAL:HB	1.78	0.66
1:A:63:GLU:HA	1:A:63:GLU:OE1	1.96	0.66
1:A:438:ARG:HG2	1:A:456:GLU:HG3	1.78	0.66
1:B:701:VAL:HG21	1:B:723:VAL:HG11	1.78	0.66
1:A:841:GLU:OE1	1:A:841:GLU:HA	1.95	0.66
1:B:841:GLU:HA	1:B:841:GLU:OE1	1.95	0.65
1:B:620:ARG:HD2	1:B:683:ARG:HH12	1.60	0.65
1:B:499:ARG:O	1:B:529:ARG:NH2	2.30	0.65
1:B:665:ALA:HB2	1:B:779:ALA:HB2	1.79	0.65
1:B:63:GLU:OE1	1:B:63:GLU:HA	1.96	0.65
1:A:499:ARG:O	1:A:529:ARG:NH2	2.30	0.65
1:B:487:ARG:N	1:B:487:ARG:HD3	2.13	0.64
1:A:665:ALA:HB2	1:A:779:ALA:HB2	1.79	0.64
1:A:487:ARG:HD3	1:A:487:ARG:N	2.13	0.64
3:D:22:GLN:HE21	3:D:40:ARG:HB2	1.61	0.63
3:D:17:ASP:O	3:D:114:GLN:NE2	2.32	0.63
1:A:771:THR:O	1:A:771:THR:OG1	2.15	0.62
2:C:177:LEU:HD13	2:C:183:TYR:HE1	1.63	0.62
1:A:715:ALA:HB3	1:A:724:VAL:HG23	1.82	0.62
1:B:669:GLU:OE1	1:B:669:GLU:HA	2.00	0.61
1:A:762:ARG:HH11	1:A:762:ARG:CG	2.14	0.61
1:B:715:ALA:HB3	1:B:724:VAL:HG23	1.82	0.61
1:A:194:GLU:OE1	1:A:194:GLU:HA	2.01	0.61
1:A:669:GLU:OE1	1:A:669:GLU:HA	2.00	0.61
1:A:766:GLU:O	1:A:770:THR:HG23	2.01	0.60
1:B:194:GLU:HA	1:B:194:GLU:OE1	2.01	0.60
1:B:300:GLN:HG3	1:B:302:GLY:H	1.67	0.60
1:B:466:THR:HA	1:B:893:ALA:HB3	1.83	0.59
1:A:803:TYR:HE1	1:A:807:ARG:HB2	1.67	0.59
1:A:300:GLN:HG3	1:A:302:GLY:H	1.67	0.59
1:A:466:THR:HA	1:A:893:ALA:HB3	1.83	0.59
1:B:803:TYR:HE1	1:B:807:ARG:HB2	1.67	0.58
1:A:229:GLY:HA3	1:A:273:LEU:HD23	1.84	0.58
1:A:803:TYR:CE1	1:A:807:ARG:HB2	2.38	0.58
1:B:694:VAL:HG12	1:B:723:VAL:HG12	1.85	0.58
1:A:762:ARG:HH11	1:A:762:ARG:HG2	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:ASP:OD1	1:B:169:ASP:N	2.36	0.57
1:B:229:GLY:HA3	1:B:273:LEU:HD23	1.84	0.57
2:C:77:ASP:O	2:C:81:SER:N	2.36	0.57
2:C:105:THR:HG23	3:D:117:ARG:HH22	1.69	0.57
1:B:803:TYR:CE1	1:B:807:ARG:HB2	2.38	0.57
1:A:587:ALA:O	1:A:591:ARG:HB2	2.05	0.57
1:A:169:ASP:OD1	1:A:169:ASP:N	2.36	0.57
2:C:155:GLU:HG2	2:C:183:TYR:CE2	2.39	0.57
1:B:524:VAL:HG22	1:B:549:VAL:HG22	1.86	0.57
1:B:232:ALA:HB2	1:B:382:ALA:HB3	1.86	0.56
1:B:587:ALA:O	1:B:591:ARG:HB2	2.05	0.56
1:A:232:ALA:HB2	1:A:382:ALA:HB3	1.86	0.56
1:A:524:VAL:HG22	1:A:549:VAL:HG22	1.85	0.56
3:D:61:PRO:HD3	3:D:105:GLY:HA2	1.86	0.56
1:A:764:ARG:HB2	1:A:803:TYR:HE2	1.71	0.56
1:A:764:ARG:HB2	1:A:803:TYR:CE2	2.41	0.56
3:D:75:ARG:NH1	3:D:81:ASP:HA	2.21	0.56
2:C:111:GLY:O	3:D:64:SER:OG	2.21	0.55
2:C:14:VAL:HG11	2:C:90:LEU:HD12	1.88	0.55
1:B:456:GLU:HG2	1:B:457:GLU:H	1.72	0.54
1:B:495:GLU:HA	1:B:498:GLU:HG3	1.89	0.54
2:C:207:HIS:CE1	2:C:209:PRO:HG2	2.43	0.54
1:B:877:HIS:HB2	1:B:883:ILE:HG13	1.90	0.54
1:A:125:LEU:HD12	1:A:233:VAL:HG21	1.90	0.54
1:A:495:GLU:HA	1:A:498:GLU:HG3	1.89	0.54
1:A:877:HIS:HB2	1:A:883:ILE:HG13	1.90	0.54
1:B:434:GLU:OE1	1:B:434:GLU:N	2.41	0.54
1:B:125:LEU:HD12	1:B:233:VAL:HG21	1.90	0.53
1:A:434:GLU:N	1:A:434:GLU:OE1	2.41	0.53
2:C:7:VAL:HB	2:C:25:THR:HG22	1.89	0.53
1:A:856:VAL:HG21	1:A:876:ALA:HB2	1.90	0.53
1:B:856:VAL:HG21	1:B:876:ALA:HB2	1.90	0.53
2:C:53:ILE:HD12	2:C:76:ARG:HD2	1.91	0.52
2:C:8:GLN:H	2:C:112:GLN:HE22	1.56	0.52
1:B:734:ALA:O	1:B:738:ASP:HB2	2.09	0.52
2:C:177:LEU:HD13	2:C:183:TYR:CE1	2.42	0.52
1:B:440:ARG:HD2	1:B:454:ILE:HD13	1.92	0.52
1:B:683:ARG:O	1:B:686:SER:OG	2.27	0.52
1:B:771:THR:O	1:B:771:THR:OG1	2.15	0.52
1:A:681:LEU:HD21	1:A:766:GLU:HB2	1.91	0.52
1:A:734:ALA:O	1:A:738:ASP:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:175:ALA:HB2	2:C:185:LEU:HD23	1.93	0.51
2:C:95:THR:HG22	2:C:118:VAL:H	1.76	0.51
2:C:14:VAL:HA	2:C:18:ARG:HH21	1.75	0.50
1:A:474:VAL:HG13	1:A:889:LEU:HD21	1.94	0.50
1:B:332:ASP:HA	1:B:435:ARG:HH21	1.75	0.50
1:B:529:ARG:HH11	1:B:529:ARG:CG	2.25	0.50
1:A:141:PRO:HD2	1:A:516:ALA:HB2	1.94	0.50
2:C:8:GLN:HG2	2:C:114:THR:HG23	1.93	0.50
1:A:380:THR:O	1:A:381:GLN:HG2	2.12	0.50
2:C:128:VAL:HG22	2:C:149:VAL:HG22	1.94	0.50
1:A:529:ARG:CG	1:A:529:ARG:HH11	2.25	0.50
1:B:380:THR:O	1:B:381:GLN:HG2	2.12	0.49
1:A:608:VAL:HG11	1:A:627:VAL:HG21	1.94	0.49
1:B:141:PRO:HD2	1:B:516:ALA:HB2	1.94	0.49
2:C:155:GLU:HG2	2:C:183:TYR:HE2	1.74	0.49
1:A:202:THR:HG22	1:A:205:SER:HB3	1.95	0.49
2:C:77:ASP:O	2:C:81:SER:HA	2.12	0.49
3:D:58:LEU:HB2	3:D:68:LEU:HD11	1.93	0.49
1:B:474:VAL:HG13	1:B:889:LEU:HD21	1.94	0.49
3:D:69:ILE:HG23	3:D:74:ASN:O	2.13	0.49
1:B:788:GLU:O	1:B:790:ARG:HB2	2.13	0.49
1:B:608:VAL:HG11	1:B:627:VAL:HG21	1.94	0.49
2:C:8:GLN:NE2	2:C:98:TYR:O	2.44	0.49
1:B:803:TYR:O	1:B:806:LEU:N	2.47	0.48
1:B:649:VAL:HG23	1:B:783:PHE:HD1	1.79	0.48
1:A:766:GLU:OE1	1:A:766:GLU:N	2.31	0.48
1:B:711:ARG:CZ	1:B:714:VAL:HA	2.43	0.48
1:A:711:ARG:CZ	1:A:714:VAL:HA	2.43	0.48
1:A:161:GLY:H	1:A:911:PRO:HA	1.79	0.48
1:A:202:THR:HG22	1:A:202:THR:O	2.13	0.48
1:A:483:THR:HB	1:A:487:ARG:NH2	2.28	0.48
3:D:135:PRO:HB3	3:D:161:PHE:HB3	1.95	0.48
1:B:714:VAL:O	1:B:809:THR:HG22	2.14	0.48
2:C:77:ASP:O	2:C:81:SER:CA	2.61	0.48
1:B:202:THR:HG22	1:B:202:THR:O	2.13	0.48
1:A:649:VAL:HG23	1:A:783:PHE:HD1	1.79	0.48
1:B:202:THR:HG22	1:B:205:SER:HB3	1.95	0.47
2:C:77:ASP:OD1	2:C:77:ASP:N	2.47	0.47
1:A:674:LEU:HD21	1:A:774:ILE:HD11	1.96	0.47
1:A:803:TYR:O	1:A:806:LEU:N	2.47	0.47
1:B:483:THR:HB	1:B:487:ARG:NH2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:37:SER:HB2	2:C:101:THR:OG1	2.14	0.47
1:B:331:GLY:O	1:B:435:ARG:NH2	2.47	0.47
1:B:682:MET:HG2	1:B:753:TYR:CD2	2.49	0.47
1:A:336:VAL:HG12	1:A:368:LEU:HD21	1.96	0.47
1:A:714:VAL:O	1:A:809:THR:HG22	2.14	0.46
3:D:140:PHE:HB2	3:D:155:VAL:CG1	2.45	0.46
1:B:674:LEU:HD21	1:B:774:ILE:HD11	1.96	0.46
1:A:572:TRP:HB3	1:A:861:ARG:NH1	2.31	0.46
3:D:31:PRO:HA	3:D:99:VAL:HB	1.97	0.46
1:A:300:GLN:NE2	1:A:448:GLY:HA3	2.30	0.46
1:B:161:GLY:H	1:B:911:PRO:HA	1.79	0.46
1:B:680:ARG:O	1:B:680:ARG:HG2	2.15	0.46
1:B:798:ASP:C	1:B:800:ARG:N	2.68	0.46
1:A:620:ARG:HB3	1:A:683:ARG:HH12	1.81	0.46
3:D:46:LEU:HA	3:D:52:ASN:HA	1.97	0.46
1:A:337:GLU:HG3	1:A:392:VAL:CG2	2.46	0.46
1:A:592:ALA:O	1:A:595:GLU:HG3	2.16	0.46
1:A:698:GLU:HA	1:A:698:GLU:OE1	2.15	0.46
1:B:620:ARG:HB3	1:B:683:ARG:HH12	1.81	0.46
1:A:622:ASP:OD1	1:A:622:ASP:N	2.49	0.46
1:A:680:ARG:O	1:A:680:ARG:HG2	2.15	0.46
1:B:592:ALA:O	1:B:595:GLU:HG3	2.16	0.46
1:A:580:LEU:HD23	1:A:587:ALA:HA	1.98	0.46
1:B:564:LEU:HD23	1:B:650:VAL:HB	1.98	0.45
1:B:470:ASP:OD1	1:B:470:ASP:N	2.49	0.45
1:B:300:GLN:NE2	1:B:448:GLY:HA3	2.30	0.45
1:A:683:ARG:O	1:A:686:SER:OG	2.27	0.45
1:B:803:TYR:O	1:B:804:ARG:C	2.55	0.45
1:A:603:TRP:CZ2	1:A:623:VAL:HG23	2.52	0.45
1:A:759:GLN:OE1	1:A:762:ARG:NH2	2.50	0.45
1:A:766:GLU:H	1:A:766:GLU:CD	2.19	0.45
3:D:104:VAL:HG12	3:D:127:ASP:HA	1.99	0.45
1:B:71:ASP:O	1:B:906:ARG:NH2	2.49	0.45
1:B:580:LEU:HD23	1:B:587:ALA:HA	1.98	0.45
1:A:564:LEU:HD23	1:A:650:VAL:HB	1.98	0.45
1:A:71:ASP:O	1:A:906:ARG:NH2	2.49	0.45
2:C:41:GLN:HB3	2:C:97:VAL:HG13	1.99	0.45
1:B:572:TRP:HB3	1:B:861:ARG:NH1	2.31	0.45
3:D:140:PHE:HB2	3:D:155:VAL:HG12	1.99	0.45
1:B:603:TRP:CZ2	1:B:623:VAL:HG23	2.52	0.44
1:B:749:ILE:HB	1:B:751:VAL:HG23	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:767:LEU:O	1:B:771:THR:HG23	2.17	0.44
1:A:867:SER:O	1:A:871:ARG:HG3	2.17	0.44
2:C:15:GLN:H	2:C:18:ARG:NE	2.15	0.44
1:A:621:VAL:HG21	1:A:753:TYR:HE2	1.82	0.44
1:B:803:TYR:CD1	1:B:803:TYR:C	2.91	0.44
1:A:15:ARG:HD2	1:A:15:ARG:HA	1.80	0.44
1:A:260:ALA:HB2	1:A:411:THR:HA	2.00	0.44
1:B:681:LEU:HD21	1:B:766:GLU:CB	2.47	0.44
1:B:18:LEU:HD12	1:B:18:LEU:HA	1.76	0.44
3:D:130:ARG:HH11	3:D:192:ASP:HB2	1.83	0.44
1:B:440:ARG:HD3	1:B:454:ILE:HG23	1.99	0.44
1:A:489:GLN:O	1:A:493:ILE:HG12	2.18	0.44
1:A:104:PHE:CD1	1:A:124:ARG:HB3	2.53	0.44
2:C:110:TRP:HB2	3:D:64:SER:HB3	2.00	0.44
1:B:127:LEU:HD23	1:B:187:ILE:HG12	2.01	0.43
1:B:438:ARG:HG2	1:B:456:GLU:HG3	2.00	0.43
1:A:593:CYS:SG	1:A:668:LEU:HD11	2.58	0.43
1:A:803:TYR:CD1	1:A:803:TYR:C	2.91	0.43
3:D:56:TRP:HB2	3:D:69:ILE:HB	1.99	0.43
1:B:489:GLN:O	1:B:493:ILE:HG12	2.18	0.43
2:C:130:PRO:HD3	2:C:216:LYS:HE2	2.00	0.43
1:B:640:ARG:HH12	1:B:780:ARG:HH22	1.66	0.43
2:C:64:TYR:HE1	2:C:74:ILE:HG13	1.82	0.43
1:B:366:ARG:HH22	1:B:435:ARG:HD3	1.83	0.43
1:B:694:VAL:CG1	1:B:723:VAL:HG12	2.48	0.43
1:A:127:LEU:HD23	1:A:187:ILE:HG12	2.00	0.43
3:D:127:ASP:N	3:D:127:ASP:OD1	2.52	0.43
1:B:104:PHE:CD1	1:B:124:ARG:HB3	2.53	0.43
1:B:867:SER:O	1:B:871:ARG:HG3	2.17	0.43
1:A:366:ARG:HH22	1:A:435:ARG:HD3	1.83	0.43
1:A:603:TRP:HZ3	1:A:605:VAL:HA	1.84	0.43
1:A:263:ASP:OD1	1:A:263:ASP:N	2.52	0.43
1:A:640:ARG:HH12	1:A:780:ARG:HH22	1.66	0.43
2:C:15:GLN:H	2:C:18:ARG:HE	1.66	0.43
1:B:410:PRO:HB2	1:B:416:TRP:NE1	2.34	0.43
1:B:603:TRP:HZ3	1:B:605:VAL:HA	1.84	0.43
1:B:622:ASP:OD1	1:B:622:ASP:N	2.49	0.43
1:A:487:ARG:HD3	1:A:487:ARG:H	1.83	0.43
1:A:760:ILE:O	1:A:763:VAL:HG12	2.19	0.43
3:D:204:SER:O	3:D:208:TYR:N	2.45	0.43
1:A:410:PRO:HB2	1:A:416:TRP:NE1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:263:ASP:OD1	1:B:263:ASP:N	2.52	0.42
1:B:593:CYS:SG	1:B:668:LEU:HD11	2.58	0.42
1:A:60:GLU:OE1	1:A:60:GLU:N	2.52	0.42
1:A:803:TYR:O	1:A:804:ARG:C	2.58	0.42
1:B:260:ALA:HB2	1:B:411:THR:HA	2.00	0.42
3:D:84:SER:HB3	3:D:95:LYS:HG3	2.01	0.42
1:B:681:LEU:HD21	1:B:766:GLU:HB3	2.01	0.42
1:A:711:ARG:NH2	1:A:715:ALA:H	2.17	0.42
1:A:852:ASP:OD1	1:A:852:ASP:N	2.50	0.42
3:D:24:PRO:O	3:D:124:THR:OG1	2.29	0.42
1:B:347:ASP:HB2	1:B:348:PRO:HD3	2.02	0.42
1:B:674:LEU:HD11	1:B:802:TRP:CD1	2.54	0.42
1:A:121:PRO:HB3	1:A:124:ARG:HH21	1.85	0.42
2:C:14:VAL:HB	2:C:118:VAL:HA	2.01	0.42
3:D:107:TYR:HE1	3:D:126:VAL:HG11	1.84	0.42
1:B:60:GLU:N	1:B:60:GLU:OE1	2.52	0.42
1:B:711:ARG:NH2	1:B:715:ALA:H	2.17	0.42
1:A:825:ASP:N	1:A:825:ASP:OD1	2.52	0.42
1:A:827:PHE:HB2	1:A:855:VAL:HG22	2.01	0.42
1:A:45:PRO:HD3	1:A:269:GLU:O	2.20	0.42
1:A:803:TYR:C	1:A:803:TYR:HD1	2.23	0.42
1:B:703:GLU:HG2	1:B:706:ARG:HH12	1.84	0.41
3:D:130:ARG:NH1	3:D:194:THR:OG1	2.42	0.41
1:B:803:TYR:C	1:B:803:TYR:HD1	2.23	0.41
1:A:347:ASP:HB2	1:A:348:PRO:HD3	2.02	0.41
3:D:37:ILE:HD12	3:D:94:LEU:HD23	2.01	0.41
1:B:45:PRO:HD3	1:B:269:GLU:O	2.20	0.41
1:A:203:ALA:HB1	1:A:446:ILE:HG22	2.03	0.41
1:A:220:LYS:HB2	1:A:220:LYS:HE3	1.76	0.41
1:A:537:ARG:HA	1:A:537:ARG:HD3	1.71	0.41
1:B:827:PHE:HB2	1:B:855:VAL:HG22	2.01	0.41
1:B:121:PRO:HB3	1:B:124:ARG:HH21	1.84	0.41
1:B:797:LEU:HD22	1:B:801:TYR:CD2	2.56	0.41
1:B:803:TYR:O	1:B:803:TYR:HD1	2.03	0.41
1:A:212:HIS:ND1	1:A:296:SER:OG	2.40	0.41
1:A:803:TYR:O	1:A:803:TYR:HD1	2.03	0.41
1:B:711:ARG:NH2	1:B:725:VAL:HA	2.36	0.41
1:A:766:GLU:O	1:A:769:GLU:HG3	2.21	0.41
2:C:50:VAL:HG22	2:C:68:VAL:HG21	2.03	0.41
3:D:17:ASP:CG	3:D:18:VAL:H	2.24	0.41
1:A:674:LEU:HD11	1:A:802:TRP:CD1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:825:ASP:N	1:B:825:ASP:OD1	2.52	0.41
1:A:534:ARG:HA	1:A:537:ARG:HB2	2.02	0.41
1:A:711:ARG:NH2	1:A:725:VAL:HA	2.36	0.41
1:A:607:ASP:OD1	1:A:612:ALA:HB3	2.21	0.40
1:B:203:ALA:HB1	1:B:446:ILE:HG22	2.02	0.40
1:B:323:LEU:HD11	1:B:358:TYR:CE1	2.56	0.40
1:B:534:ARG:HA	1:B:537:ARG:HB2	2.02	0.40
1:B:607:ASP:OD1	1:B:612:ALA:HB3	2.21	0.40
1:B:764:ARG:HH21	1:B:800:ARG:HH12	1.69	0.40
1:A:317:ARG:O	1:A:321:GLN:HG3	2.21	0.40
3:D:87:GLY:HA3	3:D:92:PHE:HA	2.04	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	906/1777 (51%)	869 (96%)	37 (4%)	0	100	100
1	B	906/1777 (51%)	871 (96%)	35 (4%)	0	100	100
2	C	199/249 (80%)	192 (96%)	7 (4%)	0	100	100
3	D	203/236 (86%)	195 (96%)	8 (4%)	0	100	100
All	All	2214/4039 (55%)	2127 (96%)	87 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	686/1322 (52%)	608 (89%)	78 (11%)	4	21
1	B	686/1322 (52%)	599 (87%)	87 (13%)	3	17
2	C	170/203 (84%)	166 (98%)	4 (2%)	44	71
3	D	185/208 (89%)	180 (97%)	5 (3%)	40	69
All	All	1727/3055 (56%)	1553 (90%)	174 (10%)	9	26

All (174) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	5	ASP
1	B	6	SER
1	B	8	LYS
1	B	9	VAL
1	B	11	GLU
1	B	13	LEU
1	B	18	LEU
1	B	21	ARG
1	B	59	ARG
1	B	60	GLU
1	B	63	GLU
1	B	78	ARG
1	B	79	LEU
1	B	114	ARG
1	B	162	GLU
1	B	169	ASP
1	B	175	VAL
1	B	194	GLU
1	B	201	ASP
1	B	220	LYS
1	B	265	PHE
1	B	325	SER
1	B	343	THR
1	B	357	THR
1	B	367	PRO
1	B	389	LEU
1	B	409	GLU
1	B	415	ASP
1	B	432	ARG
1	B	434	GLU

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Mol	Chain	Res	Type
1	B	435	ARG
1	B	436	THR
1	B	440	ARG
1	B	461	ARG
1	B	462	GLU
1	B	464	ARG
1	B	465	GLU
1	B	466	THR
1	B	467	THR
1	B	487	ARG
1	B	517	ARG
1	B	527	SER
1	B	529	ARG
1	B	537	ARG
1	B	557	ASP
1	B	580	LEU
1	B	591	ARG
1	B	595	GLU
1	B	596	SER
1	B	600	MET
1	B	610	ARG
1	B	618	LEU
1	B	645	GLU
1	B	668	LEU
1	B	669	GLU
1	B	673	LYS
1	B	674	LEU
1	B	681	LEU
1	B	682	MET
1	B	688	GLU
1	B	696	LEU
1	B	698	GLU
1	B	704	ARG
1	B	705	LEU
1	B	706	ARG
1	B	717	VAL
1	B	723	VAL
1	B	745	ARG
1	B	746	VAL
1	B	747	ARG
1	B	749	ILE
1	B	750	ASP

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Mol	Chain	Res	Type
1	B	753	TYR
1	B	762	ARG
1	B	763	VAL
1	B	764	ARG
1	B	767	LEU
1	B	771	THR
1	B	800	ARG
1	B	803	TYR
1	B	808	GLU
1	B	841	GLU
1	B	845	GLU
1	B	846	GLU
1	B	851	GLU
1	B	865	ASP
1	B	886	ASP
1	A	5	ASP
1	A	8	LYS
1	A	9	VAL
1	A	11	GLU
1	A	18	LEU
1	A	21	ARG
1	A	59	ARG
1	A	60	GLU
1	A	63	GLU
1	A	78	ARG
1	A	79	LEU
1	A	114	ARG
1	A	162	GLU
1	A	169	ASP
1	A	175	VAL
1	A	194	GLU
1	A	201	ASP
1	A	220	LYS
1	A	325	SER
1	A	329	GLU
1	A	343	THR
1	A	355	LEU
1	A	362	ARG
1	A	367	PRO
1	A	389	LEU
1	A	409	GLU
1	A	415	ASP

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Mol	Chain	Res	Type
1	A	432	ARG
1	A	434	GLU
1	A	435	ARG
1	A	461	ARG
1	A	464	ARG
1	A	465	GLU
1	A	466	THR
1	A	467	THR
1	A	487	ARG
1	A	517	ARG
1	A	527	SER
1	A	529	ARG
1	A	537	ARG
1	A	557	ASP
1	A	580	LEU
1	A	591	ARG
1	A	595	GLU
1	A	596	SER
1	A	600	MET
1	A	610	ARG
1	A	618	LEU
1	A	645	GLU
1	A	668	LEU
1	A	669	GLU
1	A	673	LYS
1	A	674	LEU
1	A	681	LEU
1	A	682	MET
1	A	688	GLU
1	A	698	GLU
1	A	705	LEU
1	A	706	ARG
1	A	717	VAL
1	A	723	VAL
1	A	745	ARG
1	A	746	VAL
1	A	747	ARG
1	A	749	ILE
1	A	750	ASP
1	A	762	ARG
1	A	764	ARG
1	A	771	THR

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Mol	Chain	Res	Type
1	A	800	ARG
1	A	803	TYR
1	A	808	GLU
1	A	841	GLU
1	A	845	GLU
1	A	846	GLU
1	A	851	GLU
1	A	865	ASP
1	A	886	ASP
2	C	116	VAL
2	C	117	THR
2	C	118	VAL
2	C	119	SER
3	D	46	LEU
3	D	53	TYR
3	D	54	LEU
3	D	55	ASP
3	D	164	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	D	22	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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

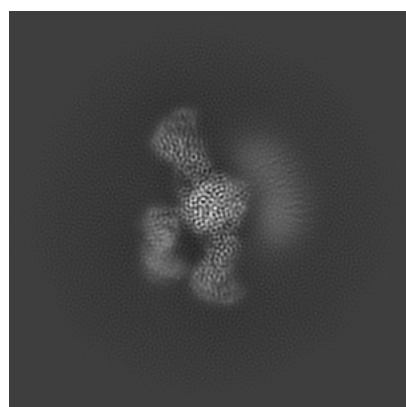
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23710. These allow visual inspection of the internal detail of the map and identification of artifacts.

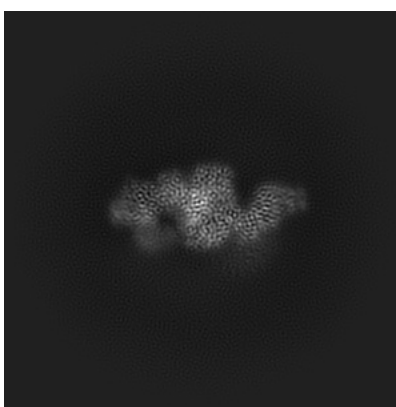
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

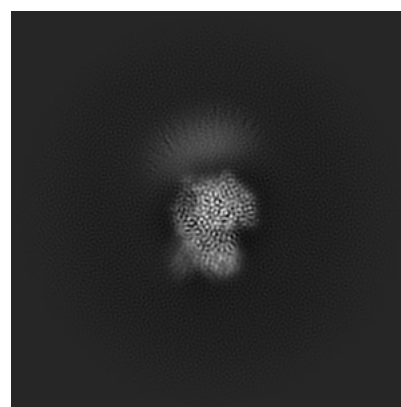
6.1.1 Primary map



X



Y

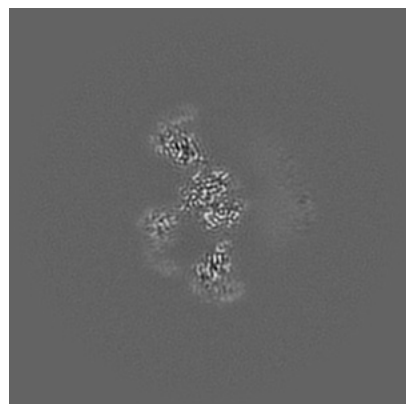


Z

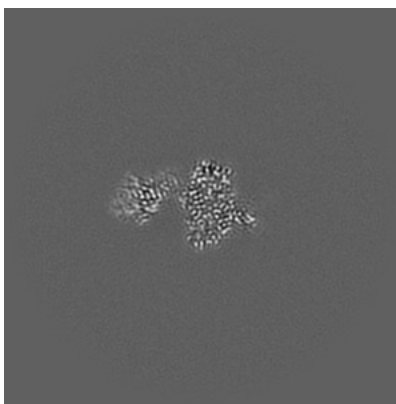
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

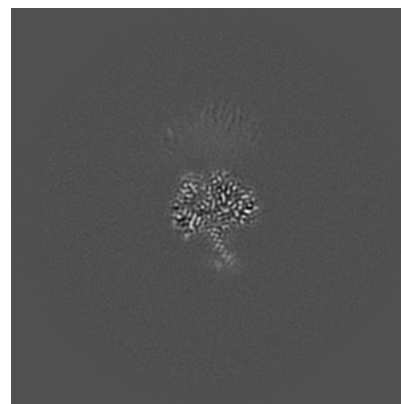
6.2.1 Primary map



X Index: 168



Y Index: 168

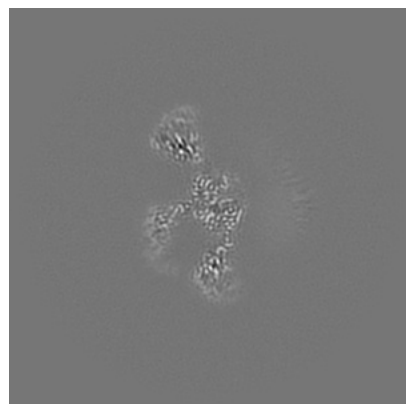


Z Index: 168

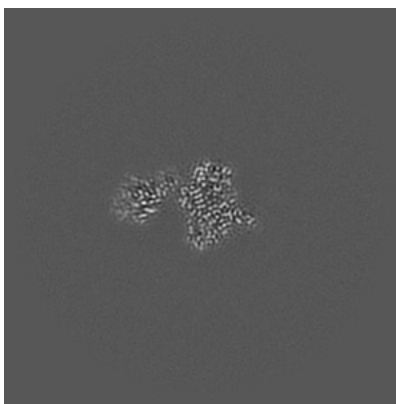
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

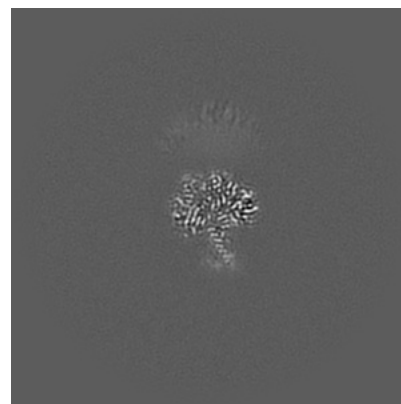
6.3.1 Primary map



X Index: 172



Y Index: 169

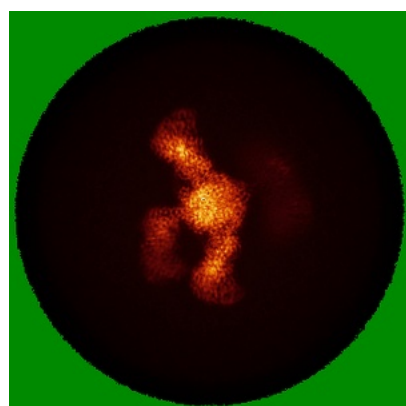


Z Index: 167

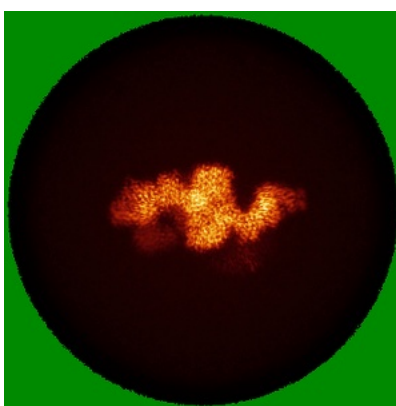
The images above show the largest variance slices of the map in three orthogonal directions.

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

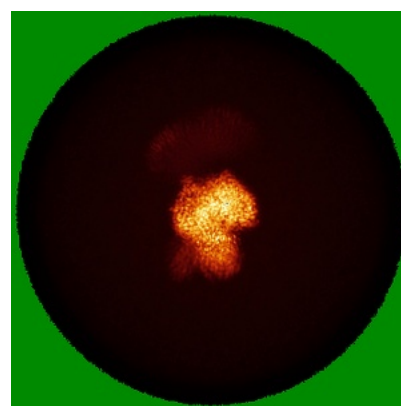
6.4.1 Primary map



X



Y

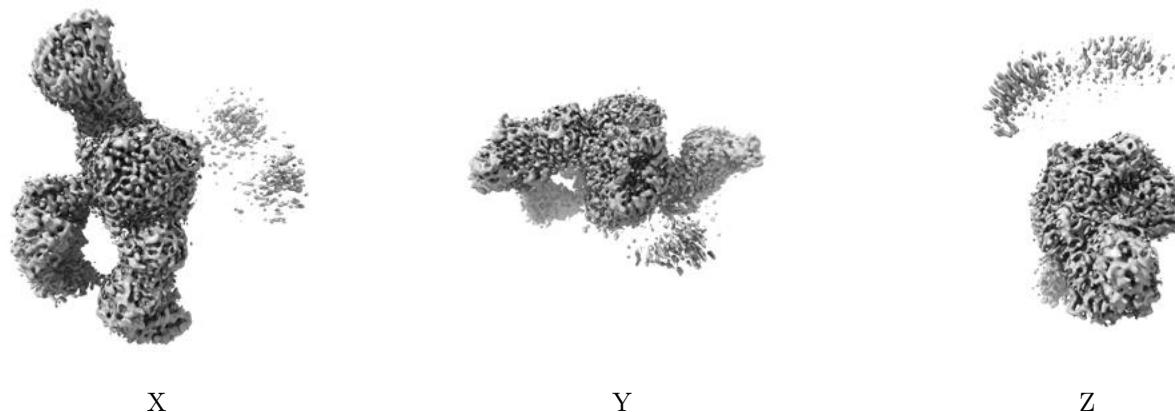


Z

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

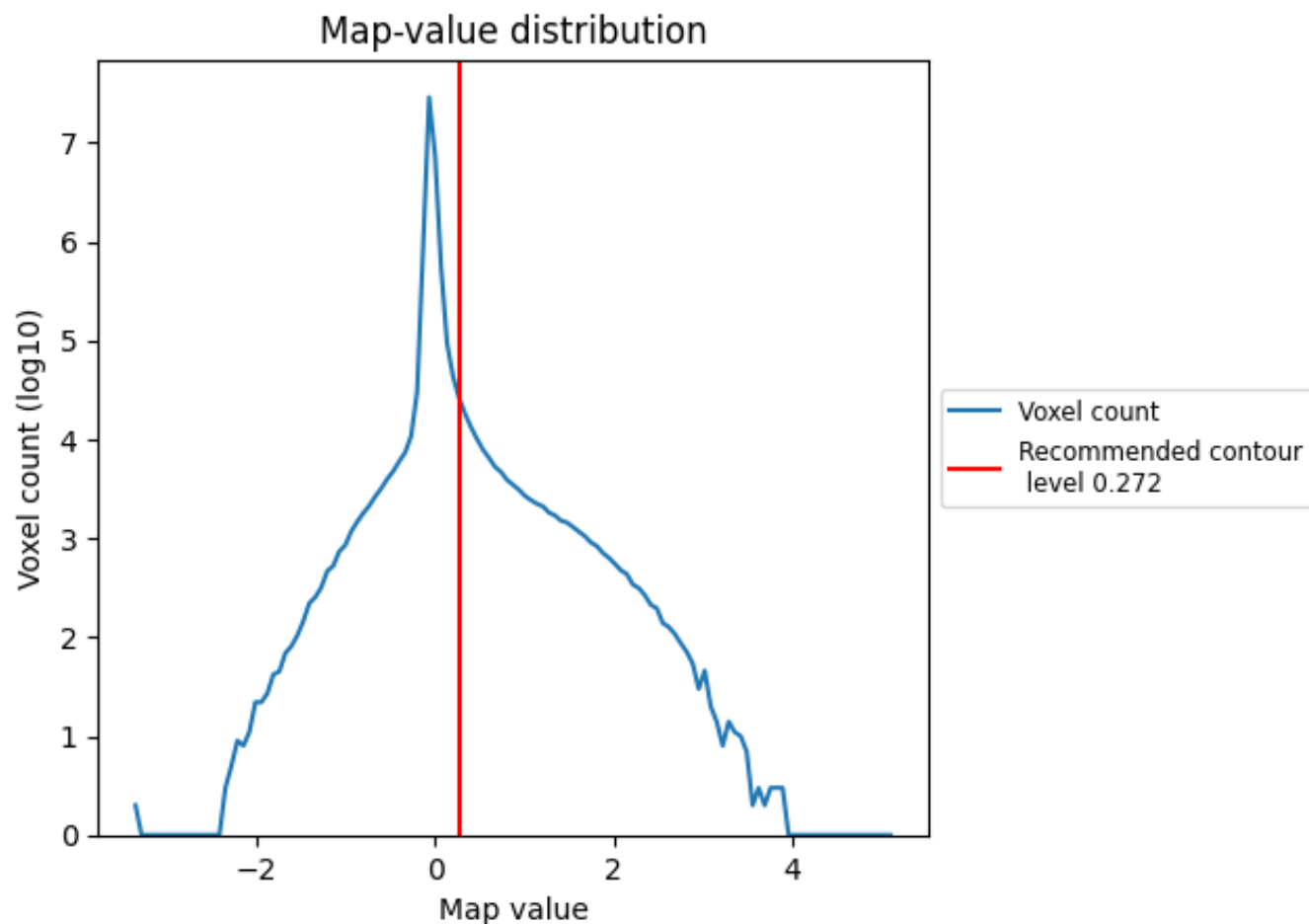
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

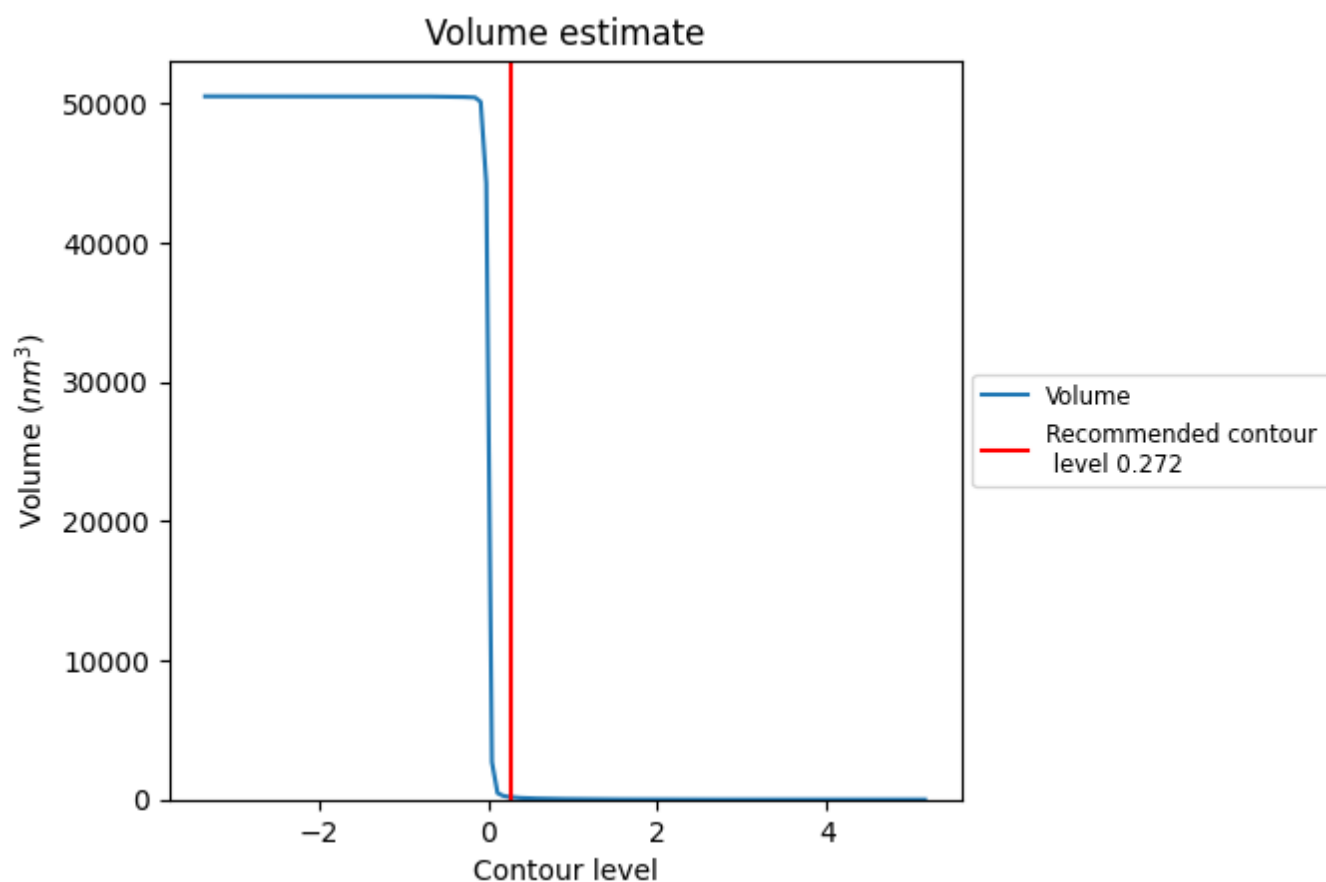
This section contains the results of statistical analysis of the map.

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.

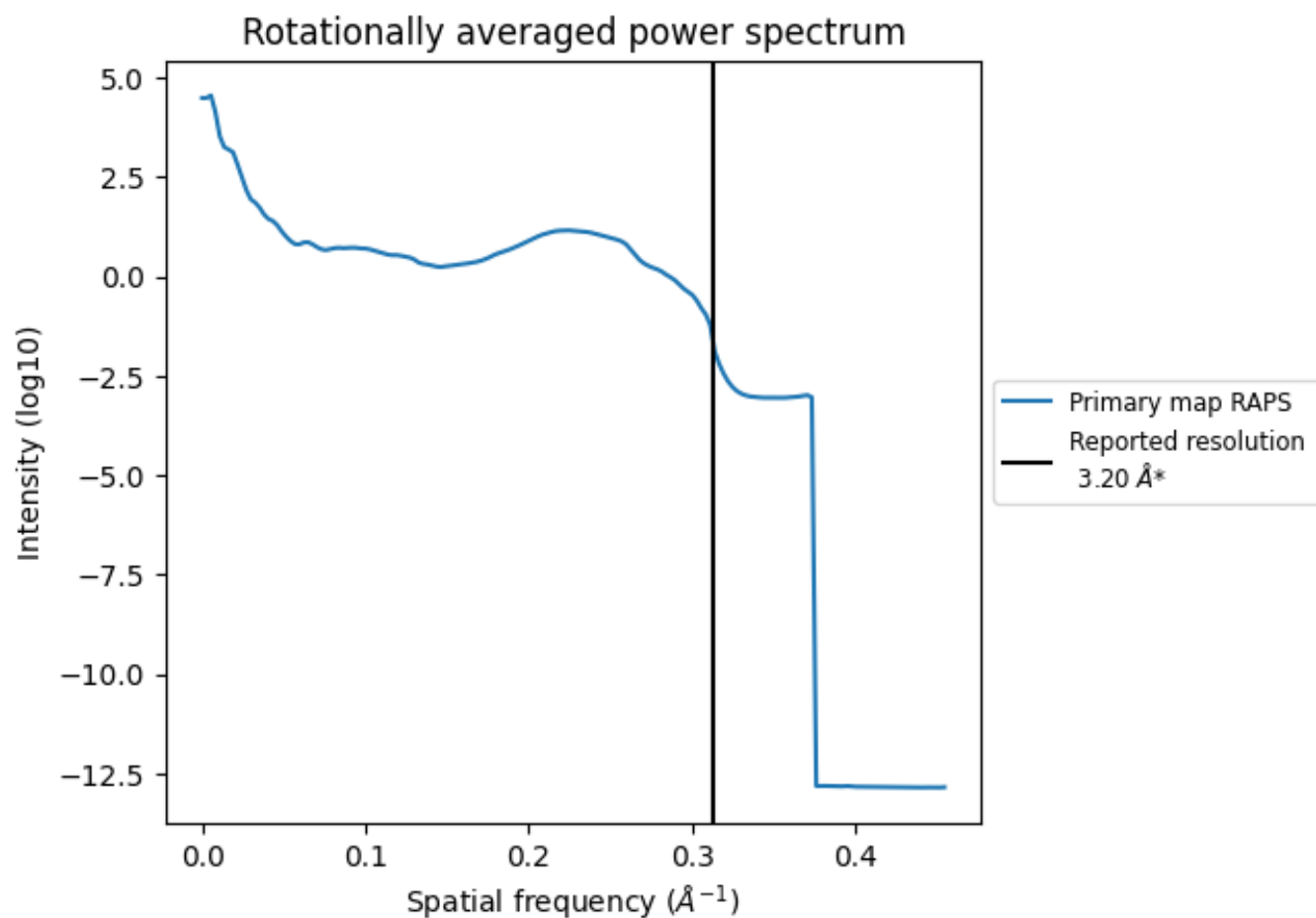
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 173 nm^3 ; this corresponds to an approximate mass of 156 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 0.312 \AA^{-1}

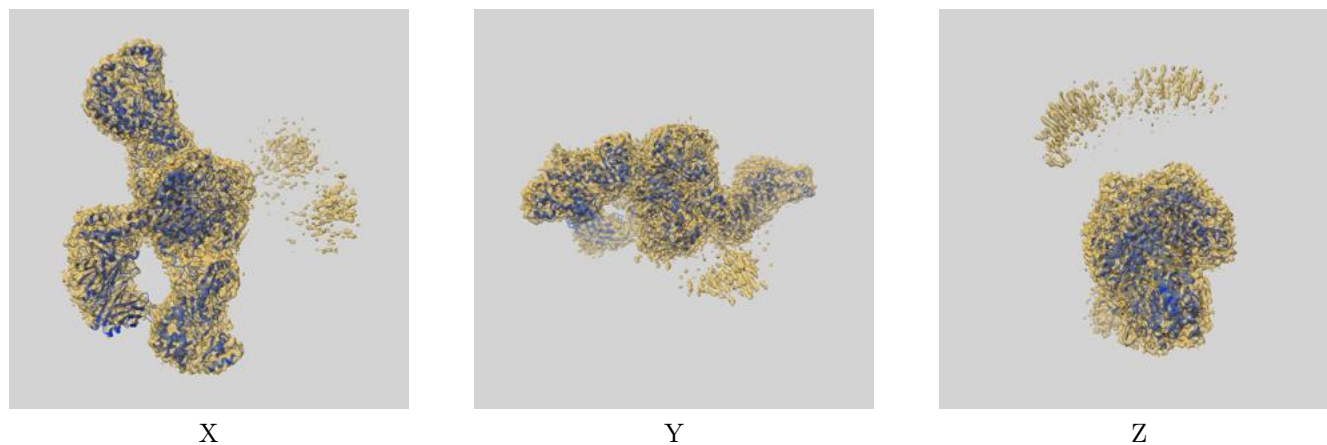
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

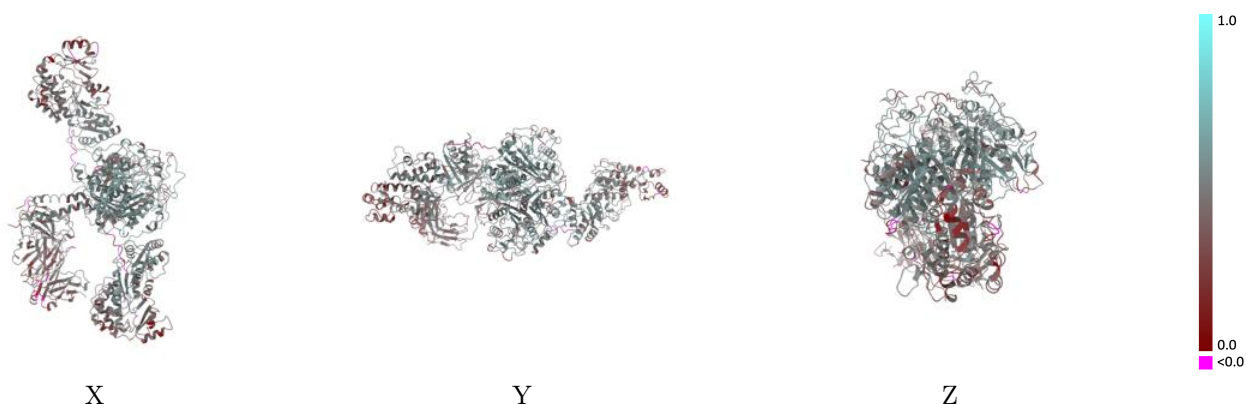
This section contains information regarding the fit between EMDB map EMD-23710 and PDB model 7M7E. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



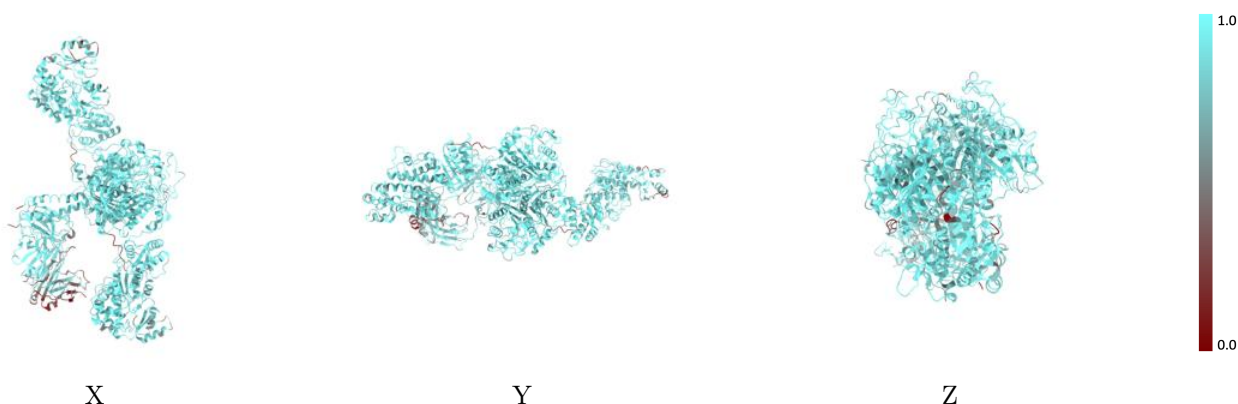
The images above show the 3D surface view of the map at the recommended contour level 0.272 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



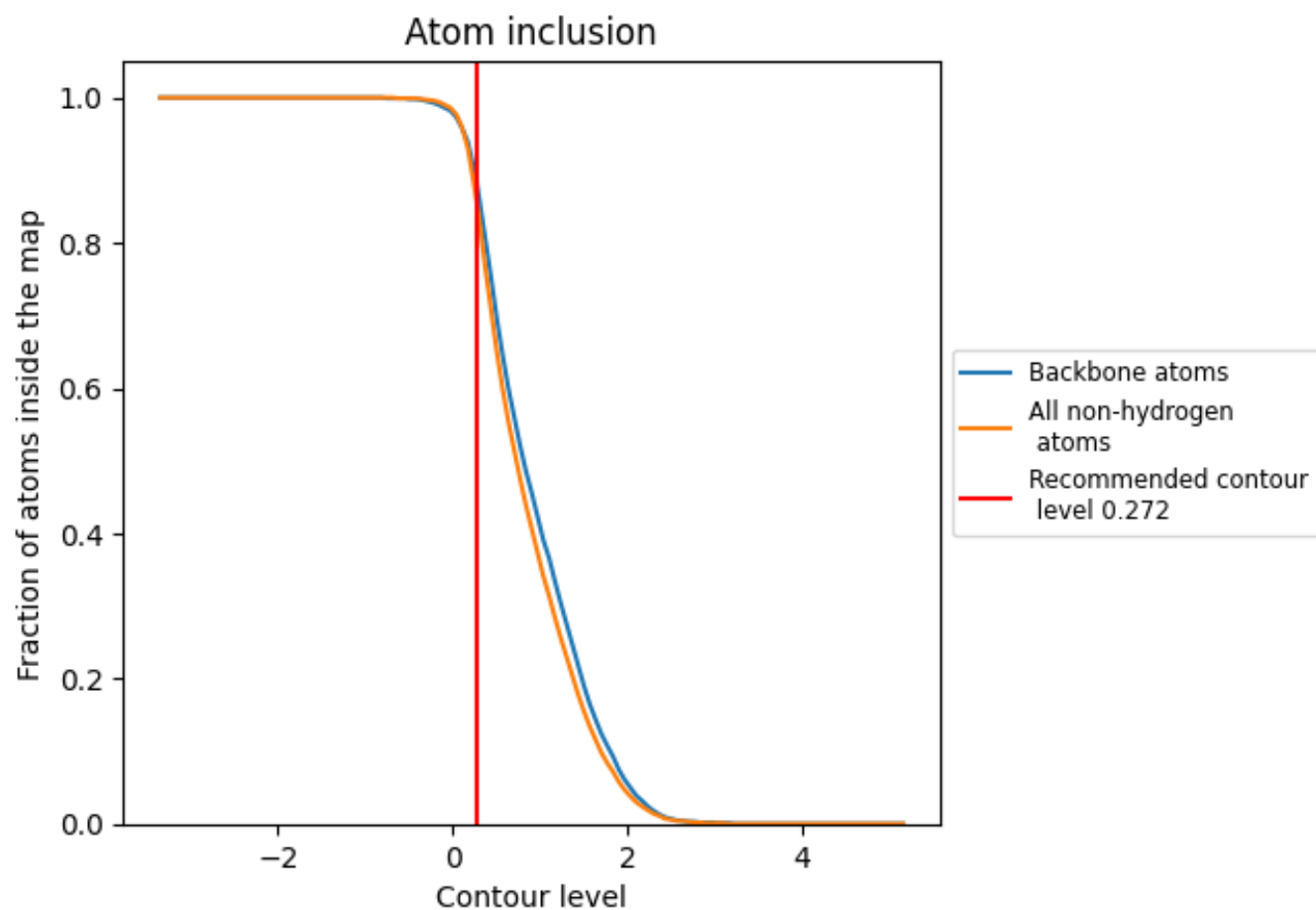
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.272).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 86% 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 (0.272) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8610	<div></div> 0.4490
A	<div></div> 0.8980	<div></div> 0.4790
B	<div></div> 0.8820	<div></div> 0.4550
C	<div></div> 0.7080	<div></div> 0.3920
D	<div></div> 0.7610	<div></div> 0.3520

