



Full wwPDB EM Validation Report ⓘ

Jul 7, 2024 – 08:16 pm BST

PDB ID : 7PSD
EMDB ID : EMD-13612
Title : Structure of CtAtm1(E603Q) in the inward-facing open conformation
Authors : Li, P.; Wang, K.T.; Gourdon, P.E.
Deposited on : 2021-09-22
Resolution : 3.00 Å(reported)
Based on initial model : 7PQX

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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

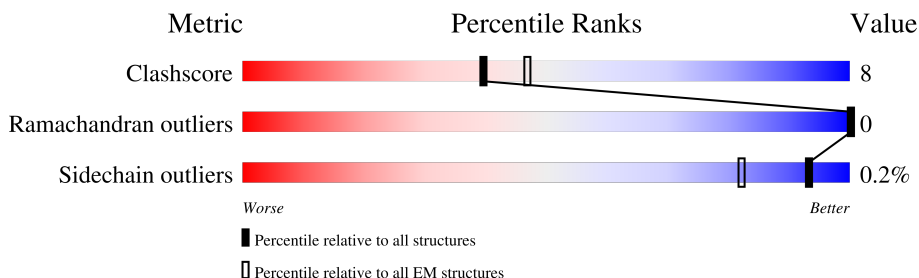
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	700	<div> <div>15%</div> <div>68%</div> <div>15%</div> <div>17%</div> </div>
1	B	700	<div> <div>14%</div> <div>68%</div> <div>15%</div> <div>17%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 9032 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 Putative iron-sulfur protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	580	Total	C	N	O	S	0	0
			4516	2892	787	825	12		
1	A	580	Total	C	N	O	S	0	0
			4516	2892	787	825	12		

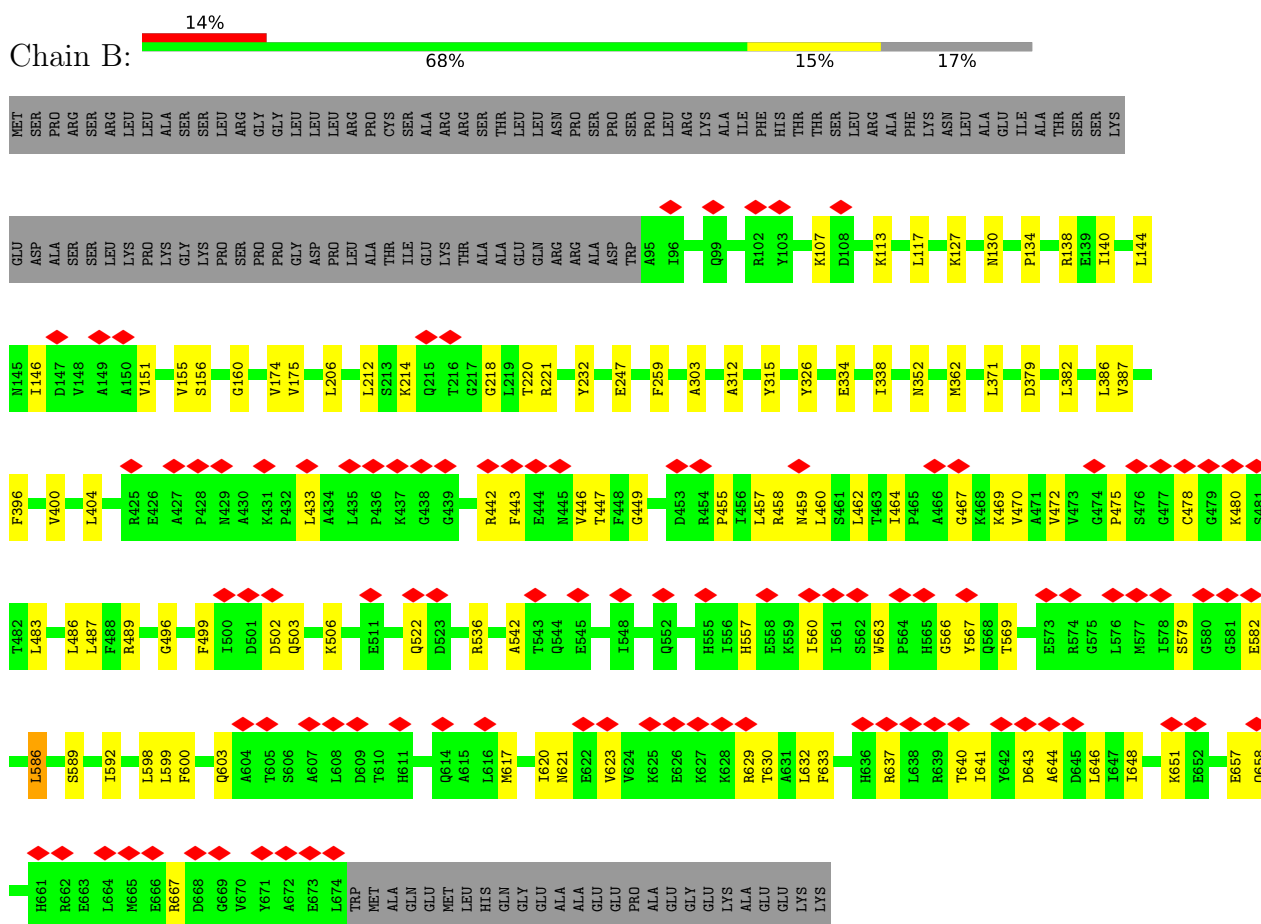
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	603	GLN	GLU	engineered mutation	UNP G0SBE6
A	603	GLN	GLU	engineered mutation	UNP G0SBE6

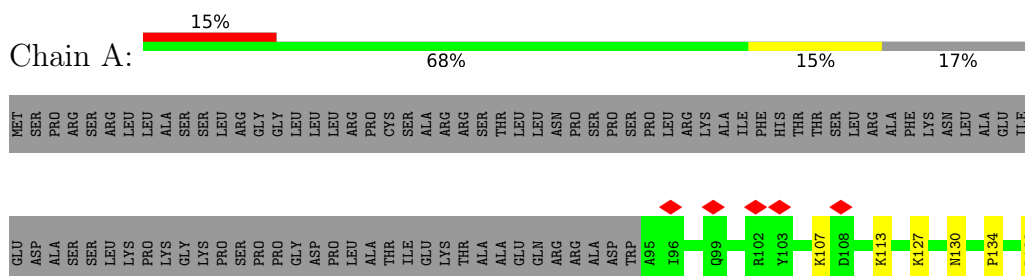
3 Residue-property plots

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: Putative iron-sulfur protein



- Molecule 1: Putative iron-sulfur protein



L593	L594	D595	L598	L599	F600	Q603	A604	T605	S606	A607	L608	D609	T610	H611	T612	E613	Q614	A615	L616	M617	I620	N621	E622	V623	V624	K625	E626	K627	K628	R629	T630	A631	L632	F633	H636	R637	L638	R639	T640	I641	Y642	D643	A644	D645	L646	T647	I648	V649	L650	K651	E652	V656	E657	Q658	
F499	I500	D501	D502	Q503	D504	I505	K506	Q522	D523	T524	P525	T530	L533	R536	A542	T543	Q544	E545	Q552	H555	I556	H557	E558	K559	I560	S561	S562	V563	P564	H565	G566	Y567	Q568	T569	E573	R574	G575	L576	M577	I578	S579	G580	G581	E582	L586	S589	T592								
P428	N429	A430	K431	P432	L433	A434	L435	P436	K437	G438	G439	R442	F443	E444	N445	V446	T447	F448	G449	D453	R454	P455	I456	L457	R458	N459	L460	S461	T462	T463	I464	P465	A466	G467	K468	K469	V470	A471	V472	V473	G474	P475	S476	G477	C478	G479	K480	S481	T482	L483	L486	L487	F488	R489	G496
A149	A150	V151	G152	S156	G160	V174	K214	Q215	T216	G217	G218	R221	Y232	E247	F259	A303	V304	Y326	E334	I338	S349	N352	M362	M363	L371	D379	L380	V381	L382	L386	V387	F396	V400	L404	R425	E426	A427																		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	108820	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	5.252	Depositor
Minimum map value	-3.032	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	0.56	Depositor
Map size (\AA)	266.24, 266.24, 266.24	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.83199996, 0.83199996, 0.83199996	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	0.67	0/4598	0.65	1/6235 (0.0%)
1	B	0.67	0/4598	0.64	1/6235 (0.0%)
All	All	0.67	0/9196	0.65	2/12470 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	586	LEU	CA-CB-CG	6.00	129.11	115.30
1	B	586	LEU	CA-CB-CG	5.99	129.08	115.30

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	4516	0	4630	76	0
1	B	4516	0	4630	76	0
All	All	9032	0	9260	141	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 (141) 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:362:MET:HE3	1:B:387:VAL:HG21	1.70	0.72
1:B:467:GLY:H	1:B:630:THR:HG22	1.58	0.69
1:A:467:GLY:H	1:A:630:THR:HG22	1.58	0.69
1:A:560:ILE:HD12	1:A:567:TYR:HB3	1.75	0.68
1:B:560:ILE:HD12	1:B:567:TYR:HB3	1.75	0.67
1:B:174:VAL:HG11	1:A:352:ASN:HB3	1.78	0.65
1:A:362:MET:HE3	1:A:387:VAL:HG21	1.81	0.62
1:A:470:VAL:HG22	1:A:646:LEU:HB3	1.81	0.62
1:B:470:VAL:HG22	1:B:646:LEU:HB3	1.81	0.62
1:B:472:VAL:HA	1:B:648:ILE:O	2.00	0.61
1:A:472:VAL:HA	1:A:648:ILE:O	2.00	0.61
1:B:617:MET:O	1:B:621:ASN:ND2	2.34	0.60
1:A:617:MET:O	1:A:621:ASN:ND2	2.34	0.60
1:A:400:VAL:HG13	1:A:404:LEU:HD13	1.84	0.60
1:B:400:VAL:HG13	1:B:404:LEU:HD13	1.84	0.60
1:A:566:GLY:O	1:A:569:THR:OG1	2.15	0.59
1:A:446:VAL:HG11	1:A:486:LEU:HD21	1.85	0.59
1:B:446:VAL:HG11	1:B:486:LEU:HD21	1.85	0.59
1:B:566:GLY:O	1:B:569:THR:OG1	2.15	0.58
1:B:442:ARG:NH2	1:B:502:ASP:OD1	2.37	0.58
1:A:442:ARG:NH2	1:A:502:ASP:OD1	2.37	0.57
1:A:446:VAL:HA	1:A:496:GLY:HA3	1.86	0.57
1:B:446:VAL:HA	1:B:496:GLY:HA3	1.86	0.56
1:A:592:ILE:HG12	1:A:623:VAL:HG21	1.88	0.56
1:B:592:ILE:HG12	1:B:623:VAL:HG21	1.88	0.55
1:B:469:LYS:HE3	1:B:633:PHE:CE2	2.41	0.55
1:B:648:ILE:HG12	1:B:658:GLN:HG2	1.88	0.55
1:A:469:LYS:HE3	1:A:633:PHE:CE2	2.41	0.55
1:B:442:ARG:HB3	1:B:499:PHE:HB2	1.89	0.54
1:A:146:ILE:HD12	1:A:151:VAL:HG13	1.89	0.54
1:B:599:LEU:HD11	1:B:629:ARG:HD3	1.90	0.54
1:A:648:ILE:HG12	1:A:658:GLN:HG2	1.88	0.54
1:B:146:ILE:HD12	1:B:151:VAL:HG13	1.89	0.54
1:A:442:ARG:HB3	1:A:499:PHE:HB2	1.89	0.53
1:A:522:GLN:HB2	1:A:603:GLN:HB2	1.90	0.53
1:A:599:LEU:HD11	1:A:629:ARG:HD3	1.90	0.53
1:B:536:ARG:NH2	1:B:542:ALA:O	2.41	0.53
1:A:620:ILE:HA	1:A:623:VAL:HG12	1.90	0.53
1:B:352:ASN:HB3	1:A:174:VAL:HG11	1.91	0.53
1:B:633:PHE:HD2	1:B:641:ILE:HG12	1.73	0.53
1:A:449:GLY:HA3	1:A:455:PRO:HA	1.91	0.53
1:A:633:PHE:HD2	1:A:641:ILE:HG12	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:489:ARG:HH12	1:B:506:LYS:HE3	1.74	0.53
1:B:449:GLY:HA3	1:B:455:PRO:HA	1.91	0.53
1:A:156:SER:HA	1:A:160:GLY:HA3	1.90	0.52
1:A:259:PHE:HZ	1:A:382:LEU:HD23	1.74	0.52
1:A:536:ARG:NH2	1:A:542:ALA:O	2.41	0.52
1:B:156:SER:HA	1:B:160:GLY:HA3	1.90	0.52
1:A:232:TYR:HE2	1:A:404:LEU:HD12	1.74	0.52
1:B:232:TYR:HE2	1:B:404:LEU:HD12	1.74	0.52
1:B:259:PHE:HZ	1:B:382:LEU:HD23	1.74	0.52
1:A:396:PHE:HD1	1:A:400:VAL:HG21	1.74	0.52
1:A:433:LEU:HB3	1:A:503:GLN:HE22	1.74	0.52
1:B:620:ILE:HA	1:B:623:VAL:HG12	1.90	0.52
1:B:396:PHE:HD1	1:B:400:VAL:HG21	1.74	0.52
1:A:489:ARG:HH12	1:A:506:LYS:HE3	1.74	0.51
1:B:433:LEU:HB3	1:B:503:GLN:HE22	1.74	0.51
1:B:522:GLN:HB2	1:B:603:GLN:HB2	1.90	0.51
1:A:560:ILE:HA	1:A:563:TRP:CD1	2.46	0.51
1:B:586:LEU:O	1:B:589:SER:OG	2.29	0.50
1:B:130:ASN:ND2	1:B:247:GLU:OE2	2.45	0.50
1:B:560:ILE:HA	1:B:563:TRP:CD1	2.46	0.50
1:A:579:SER:N	1:A:582:GLU:OE1	2.41	0.50
1:B:138:ARG:NE	1:B:379:ASP:OD1	2.42	0.49
1:B:144:LEU:HD12	1:A:380:LEU:HD11	1.94	0.49
1:B:371:LEU:HD21	1:A:144:LEU:HD22	1.94	0.49
1:A:130:ASN:ND2	1:A:247:GLU:OE2	2.45	0.49
1:A:469:LYS:HE3	1:A:633:PHE:HE2	1.78	0.49
1:B:315:TYR:O	1:A:594:LYS:NZ	2.46	0.49
1:B:557:HIS:HA	1:B:560:ILE:HG12	1.95	0.49
1:A:464:ILE:HG21	1:A:632:LEU:HD11	1.94	0.49
1:B:637:ARG:HG2	1:B:640:THR:HG23	1.95	0.49
1:A:475:PRO:HG2	1:A:478:CYS:HB3	1.95	0.49
1:B:464:ILE:HG21	1:B:632:LEU:HD11	1.94	0.48
1:B:475:PRO:HG2	1:B:478:CYS:HB3	1.95	0.48
1:A:586:LEU:O	1:A:589:SER:OG	2.29	0.48
1:A:637:ARG:HG2	1:A:640:THR:HG23	1.95	0.48
1:B:469:LYS:HE3	1:B:633:PHE:HE2	1.78	0.48
1:B:138:ARG:HD2	1:B:382:LEU:HB2	1.96	0.48
1:A:557:HIS:HA	1:A:560:ILE:HG12	1.95	0.48
1:B:487:LEU:HD23	1:B:600:PHE:CZ	2.49	0.47
1:A:134:PRO:HG2	1:A:386:LEU:HD23	1.96	0.47
1:A:362:MET:CE	1:A:387:VAL:HG21	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:312:ALA:HB2	1:A:525:PRO:HG3	1.97	0.47
1:B:600:PHE:CD1	1:B:632:LEU:HB2	2.50	0.47
1:A:127:LYS:HD2	1:A:127:LYS:HA	1.73	0.47
1:A:487:LEU:HD23	1:A:600:PHE:CZ	2.49	0.47
1:A:600:PHE:CD1	1:A:632:LEU:HB2	2.50	0.47
1:B:657:GLU:OE1	1:B:667:ARG:NH1	2.44	0.46
1:A:138:ARG:HD2	1:A:382:LEU:HB2	1.96	0.46
1:B:334:GLU:O	1:B:338:ILE:HG12	2.16	0.46
1:B:475:PRO:HD3	1:B:651:LYS:NZ	2.31	0.46
1:B:107:LYS:HE3	1:B:113:LYS:HE2	1.98	0.46
1:A:362:MET:HB3	1:A:362:MET:HE2	1.66	0.46
1:B:134:PRO:HG2	1:B:386:LEU:HD23	1.96	0.46
1:B:579:SER:N	1:B:582:GLU:OE1	2.41	0.46
1:A:138:ARG:NE	1:A:379:ASP:OD1	2.42	0.46
1:B:469:LYS:HE2	1:B:644:ALA:HA	1.99	0.45
1:A:475:PRO:HD3	1:A:651:LYS:NZ	2.31	0.45
1:A:334:GLU:O	1:A:338:ILE:HG12	2.16	0.45
1:A:469:LYS:HE2	1:A:644:ALA:HA	1.99	0.45
1:B:127:LYS:HD2	1:B:127:LYS:HA	1.74	0.45
1:B:598:LEU:HD13	1:B:630:THR:OG1	2.17	0.45
1:A:107:LYS:HE3	1:A:113:LYS:HE2	1.98	0.45
1:A:443:PHE:HB2	1:A:462:LEU:HG	2.00	0.44
1:A:530:THR:OG1	1:A:533:LEU:N	2.39	0.44
1:A:598:LEU:HD13	1:A:630:THR:OG1	2.17	0.44
1:B:218:GLY:HA2	1:B:221:ARG:HH11	1.81	0.44
1:B:220:THR:HG21	1:A:304:VAL:HG23	2.00	0.43
1:B:443:PHE:HB2	1:B:462:LEU:HG	1.99	0.43
1:B:447:THR:HG22	1:B:459:ASN:H	1.83	0.43
1:A:447:THR:HG22	1:A:459:ASN:H	1.83	0.43
1:A:218:GLY:HA2	1:A:221:ARG:HH11	1.81	0.43
1:B:457:LEU:HD13	1:B:460:LEU:HD22	2.00	0.43
1:A:637:ARG:O	1:A:640:THR:OG1	2.30	0.43
1:A:259:PHE:CZ	1:A:382:LEU:HD23	2.54	0.43
1:A:457:LEU:HD13	1:A:460:LEU:HD22	2.00	0.42
1:B:303:ALA:HB2	1:B:326:TYR:CE1	2.55	0.42
1:A:480:LYS:HA	1:A:483:LEU:HD23	2.01	0.42
1:B:480:LYS:HA	1:B:483:LEU:HD23	2.01	0.42
1:B:117:LEU:HD23	1:B:117:LEU:HA	1.89	0.42
1:B:232:TYR:CE2	1:B:404:LEU:HD12	2.55	0.42
1:B:599:LEU:HD13	1:B:629:ARG:HB3	2.02	0.42
1:B:144:LEU:HD22	1:A:371:LEU:HD21	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:174:VAL:HG11	1:A:352:ASN:CB	2.47	0.41
1:A:303:ALA:HB2	1:A:326:TYR:CE1	2.55	0.41
1:B:214:LYS:HE3	1:B:214:LYS:HB3	1.72	0.41
1:A:467:GLY:N	1:A:630:THR:HG22	2.31	0.41
1:A:599:LEU:HD13	1:A:629:ARG:HB3	2.02	0.41
1:B:175:VAL:HG22	1:A:349:SER:HB2	2.03	0.41
1:B:206:LEU:HD23	1:B:206:LEU:HA	1.86	0.41
1:B:362:MET:CE	1:B:387:VAL:HG21	2.44	0.41
1:B:467:GLY:N	1:B:630:THR:HG22	2.31	0.41
1:B:212:LEU:HD23	1:B:212:LEU:HA	1.91	0.40
1:A:657:GLU:OE1	1:A:667:ARG:NH1	2.44	0.40
1:A:232:TYR:CE2	1:A:404:LEU:HD12	2.55	0.40
1:A:556:ILE:O	1:A:559:LYS:N	2.55	0.40
1:B:643:ASP:N	1:B:643:ASP:OD1	2.54	0.40
1:B:140:ILE:HD13	1:A:363:MET:SD	2.61	0.40
1:B:155:VAL:O	1:B:156:SER:HB3	2.22	0.40
1:A:214:LYS:HB3	1:A:214:LYS:HE3	1.72	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	578/700 (83%)	546 (94%)	32 (6%)	0	100	100
1	B	578/700 (83%)	546 (94%)	32 (6%)	0	100	100
All	All	1156/1400 (83%)	1092 (94%)	64 (6%)	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	481/579 (83%)	480 (100%)	1 (0%)	93	98
1	B	481/579 (83%)	480 (100%)	1 (0%)	93	98
All	All	962/1158 (83%)	960 (100%)	2 (0%)	93	98

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	458	ARG
1	A	458	ARG

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

Mol	Chain	Res	Type
1	B	503	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 monosaccharides 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.

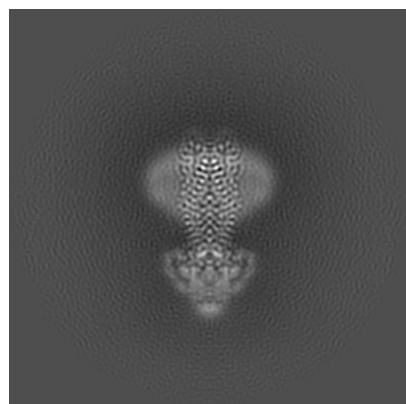
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13612. These allow visual inspection of the internal detail of the map and identification of artifacts.

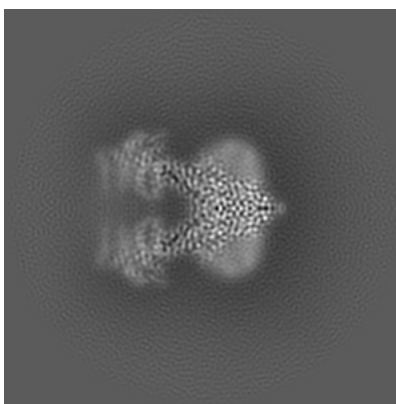
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

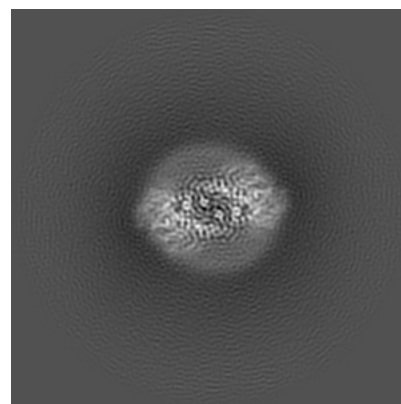
6.1.1 Primary map



X

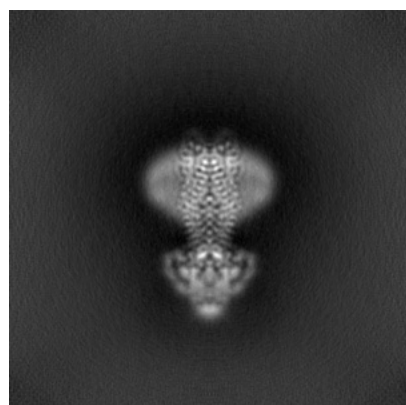


Y

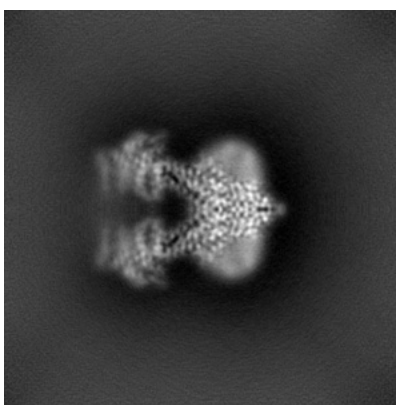


Z

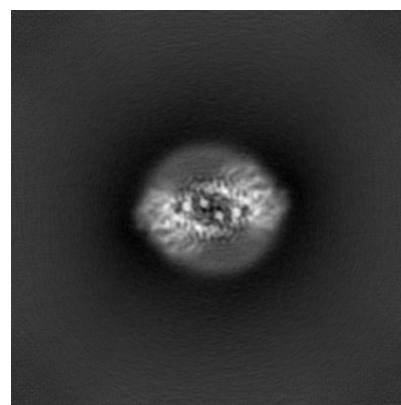
6.1.2 Raw map



X



Y

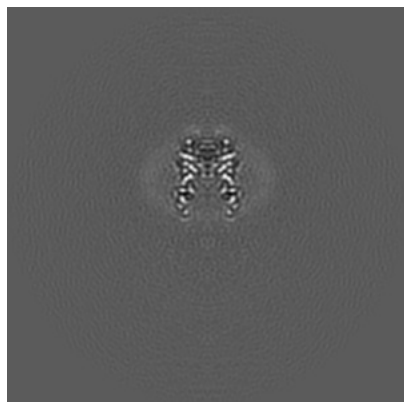


Z

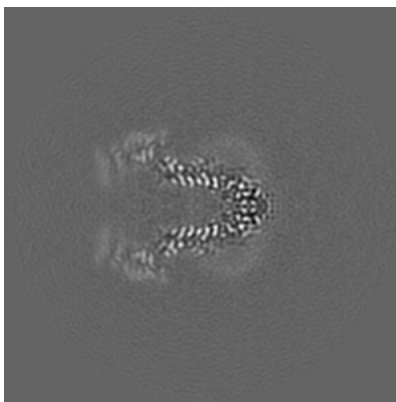
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

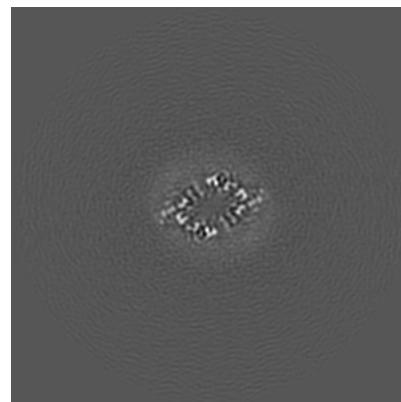
6.2.1 Primary map



X Index: 160

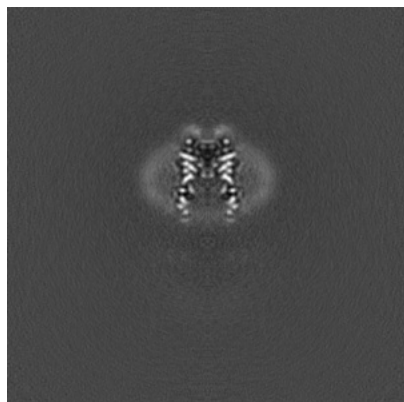


Y Index: 160

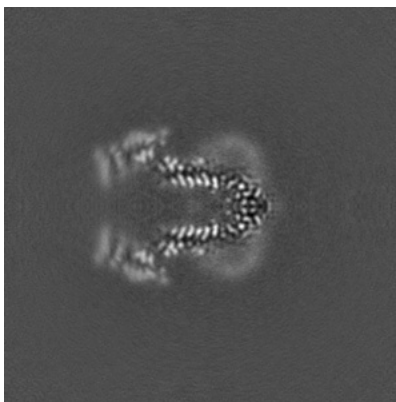


Z Index: 160

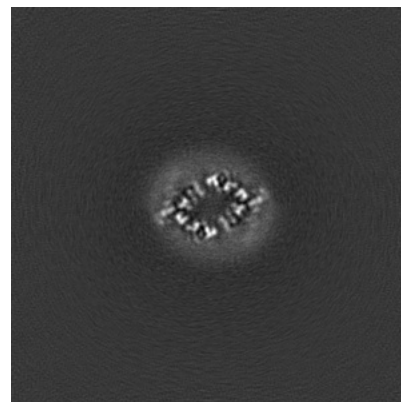
6.2.2 Raw map



X Index: 160



Y Index: 160

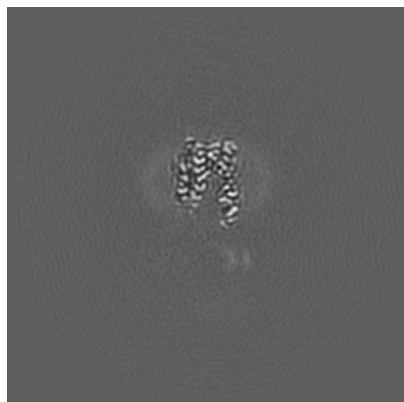


Z Index: 160

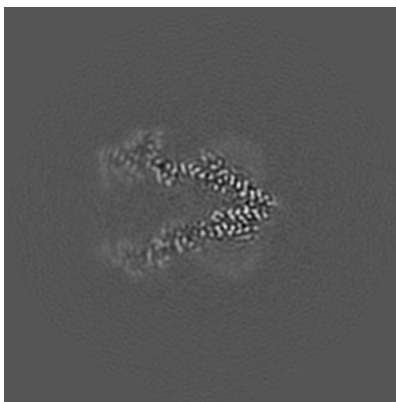
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

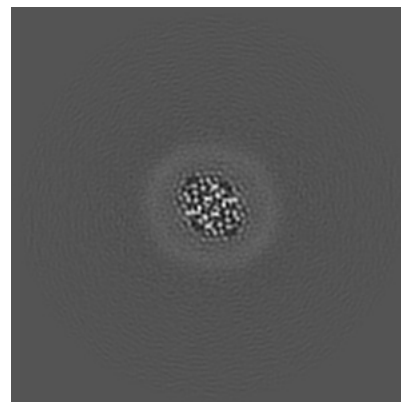
6.3.1 Primary map



X Index: 168

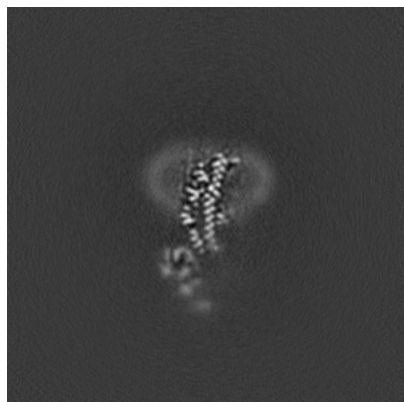


Y Index: 166

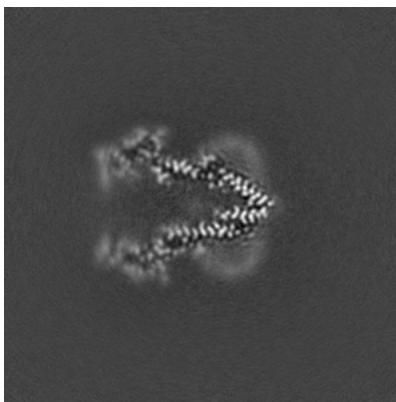


Z Index: 193

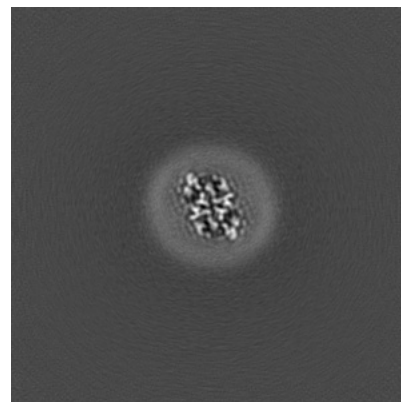
6.3.2 Raw map



X Index: 141



Y Index: 164

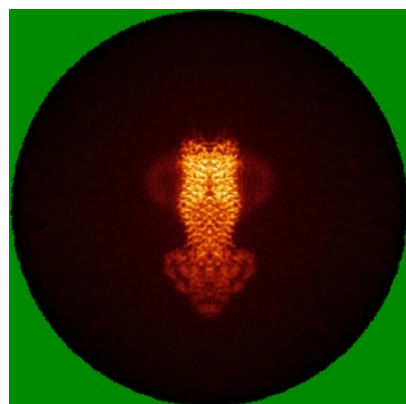


Z Index: 197

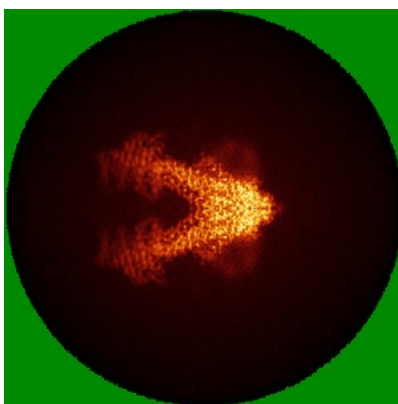
The images above show the largest variance slices of the map in three orthogonal directions.

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

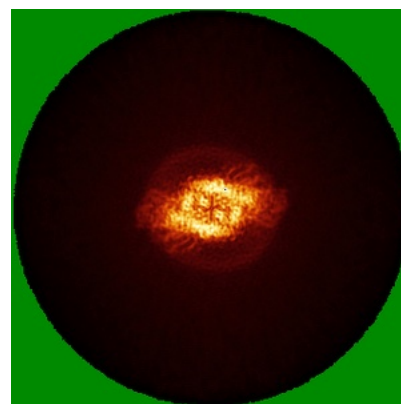
6.4.1 Primary map



X

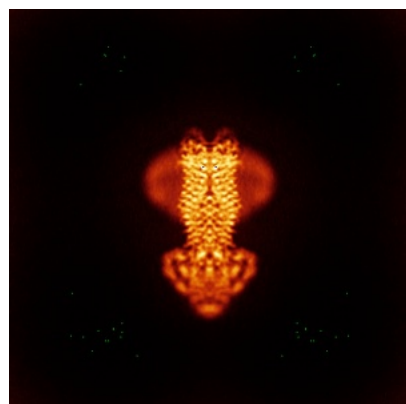


Y

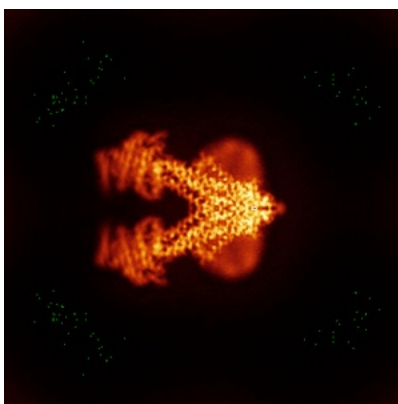


Z

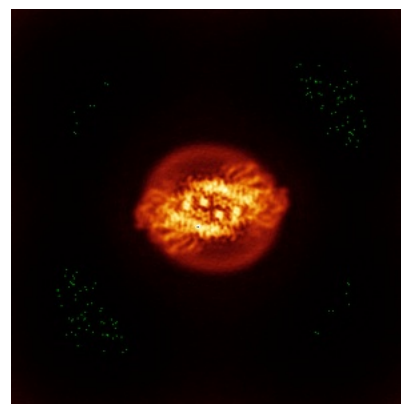
6.4.2 Raw map



X



Y

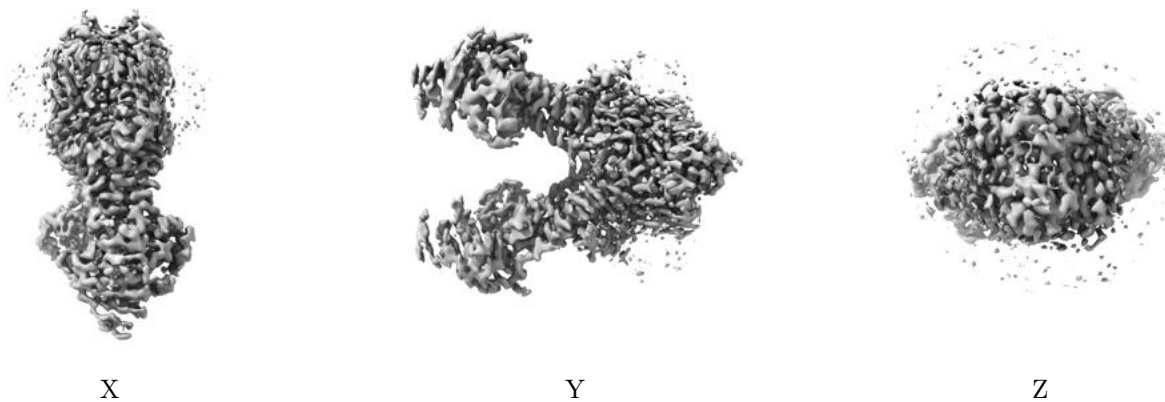


Z

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

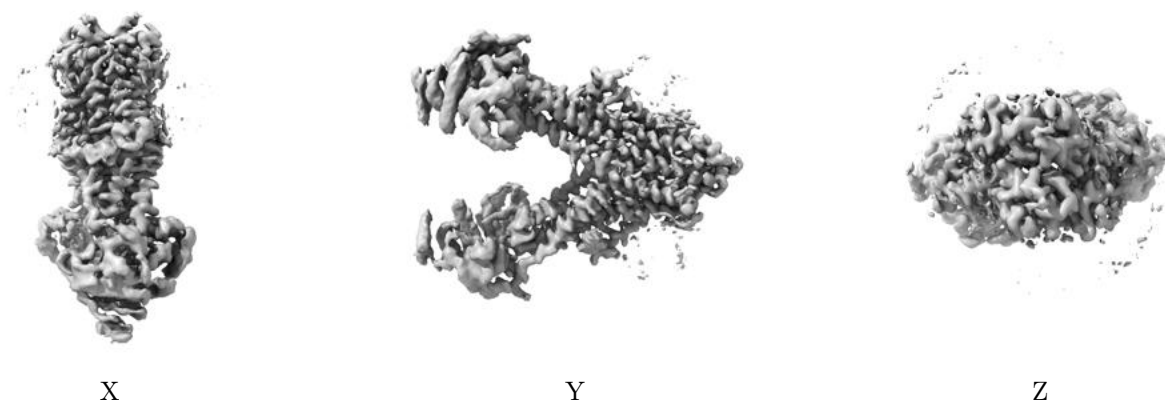
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.56. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

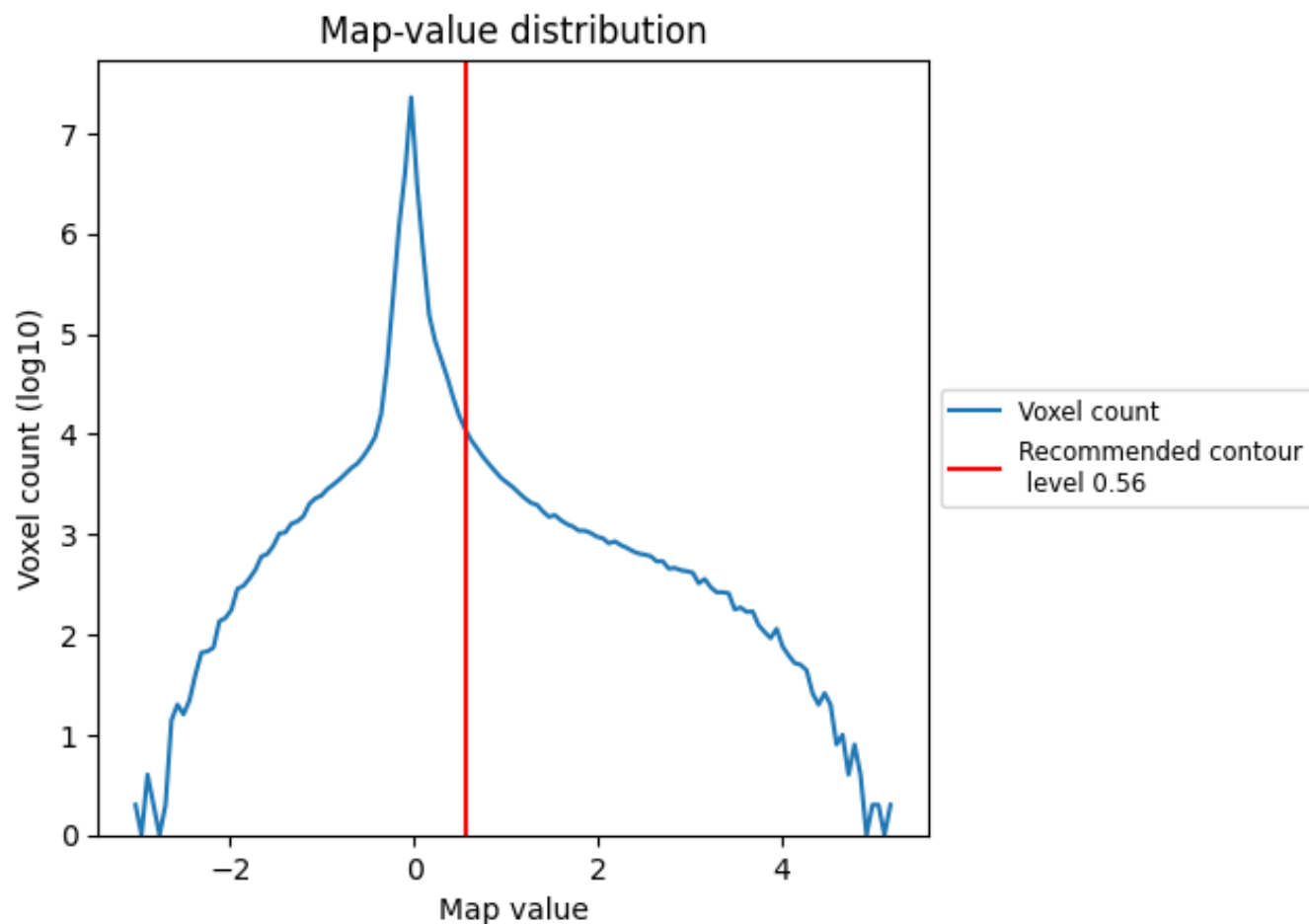
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

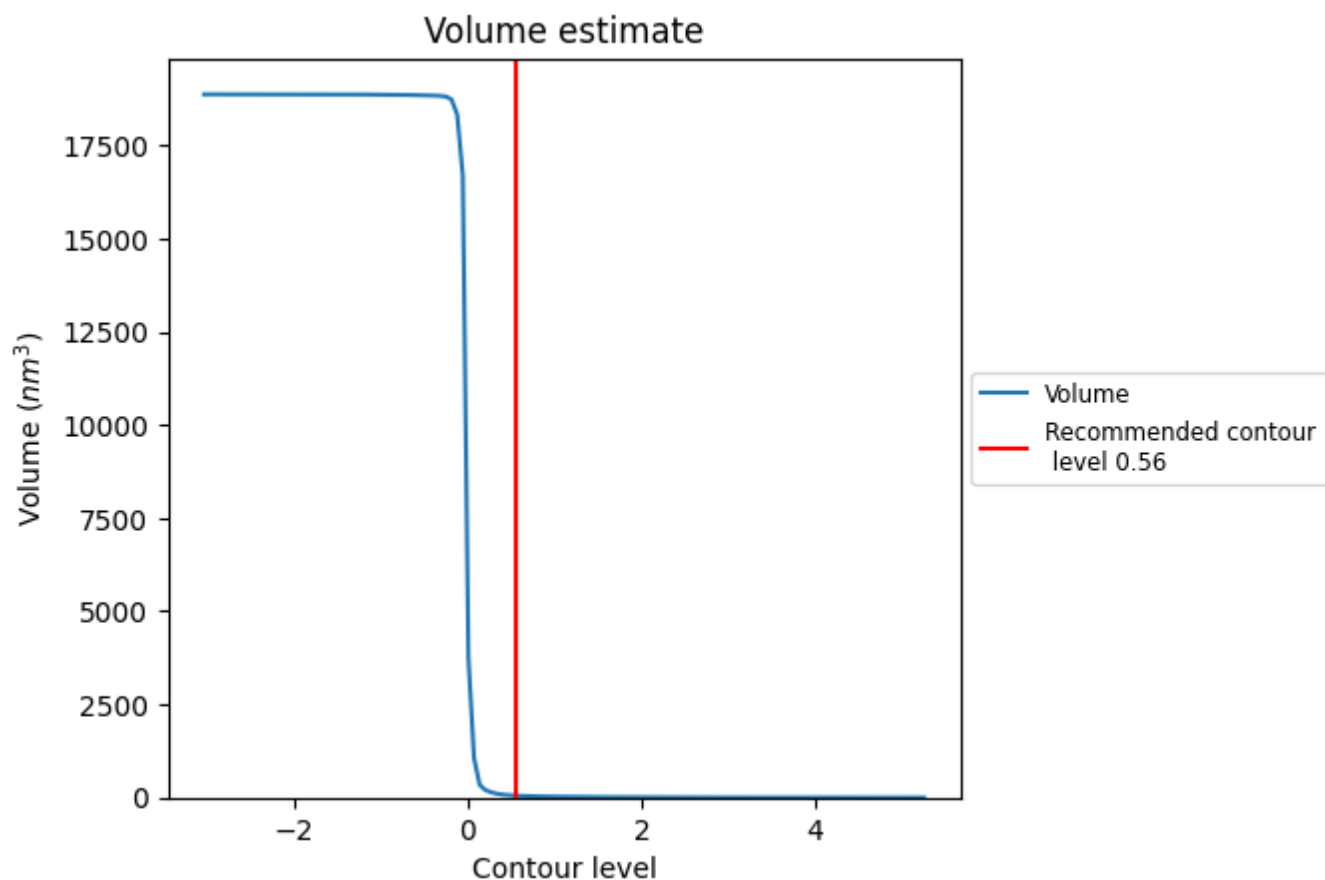
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

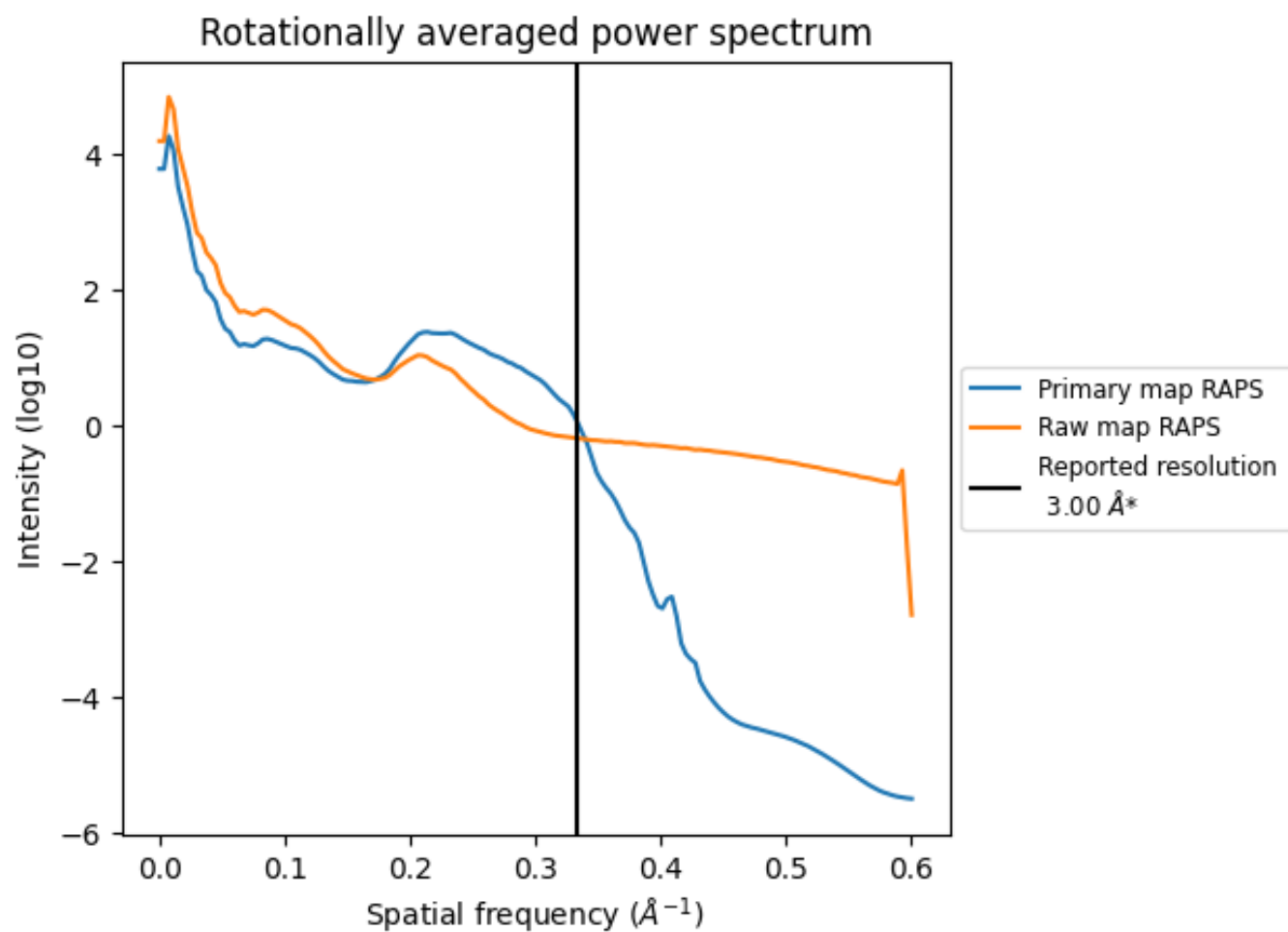
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 50 nm³; this corresponds to an approximate mass of 45 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 ⓘ

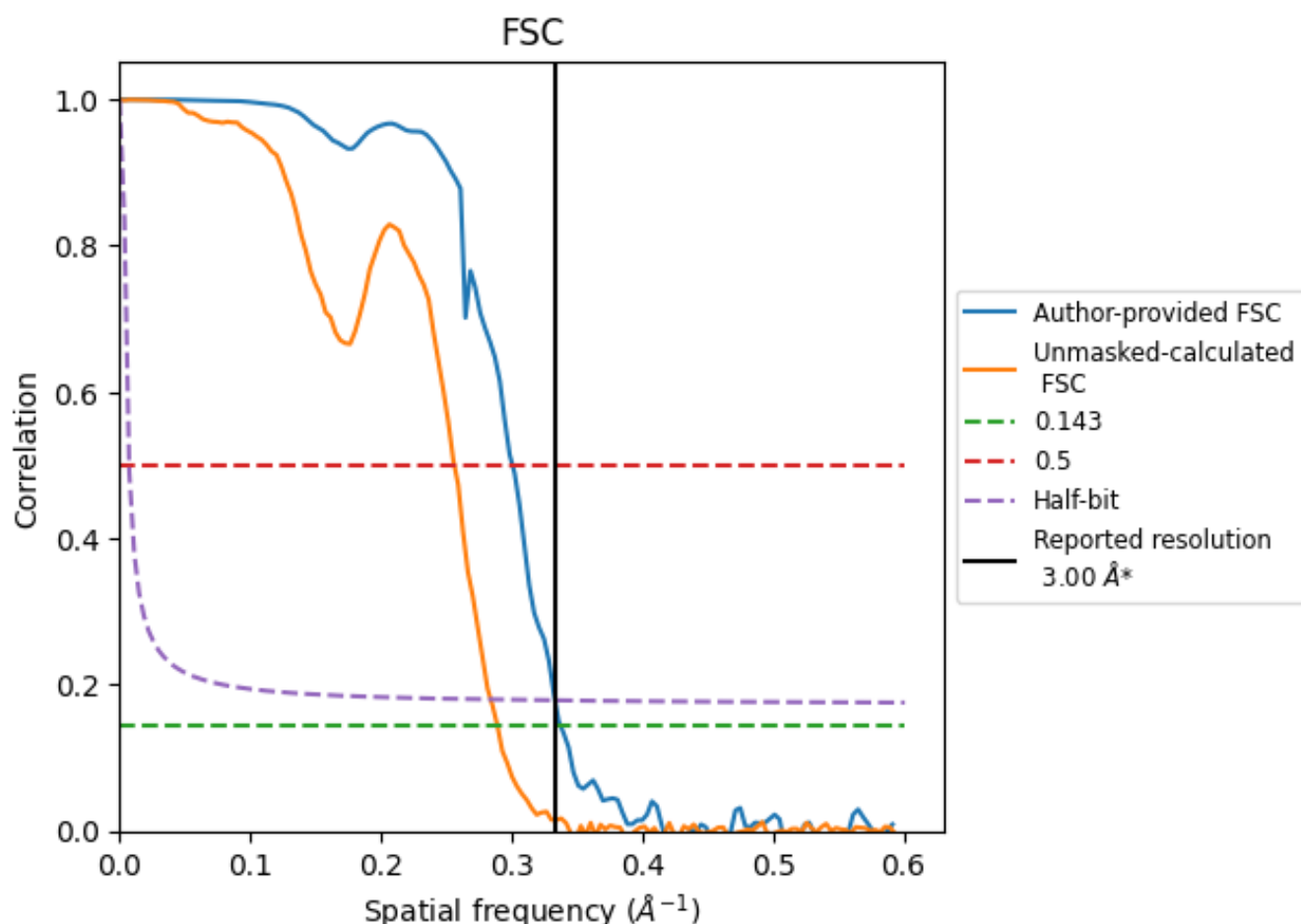


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 \AA^{-1}

8.2 Resolution estimates [i](#)

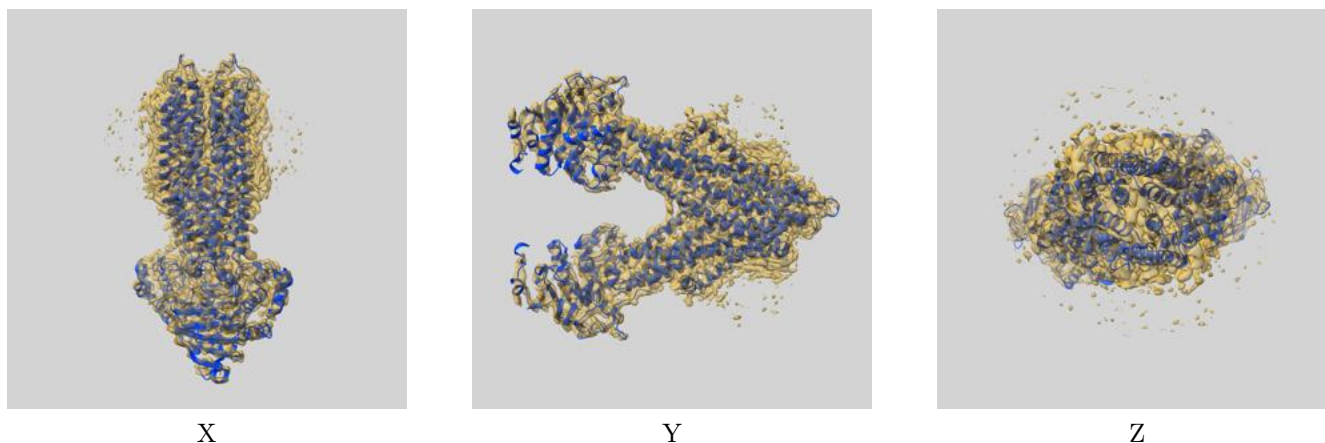
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.96	3.33	3.00
Unmasked-calculated*	3.46	3.90	3.52

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.46 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

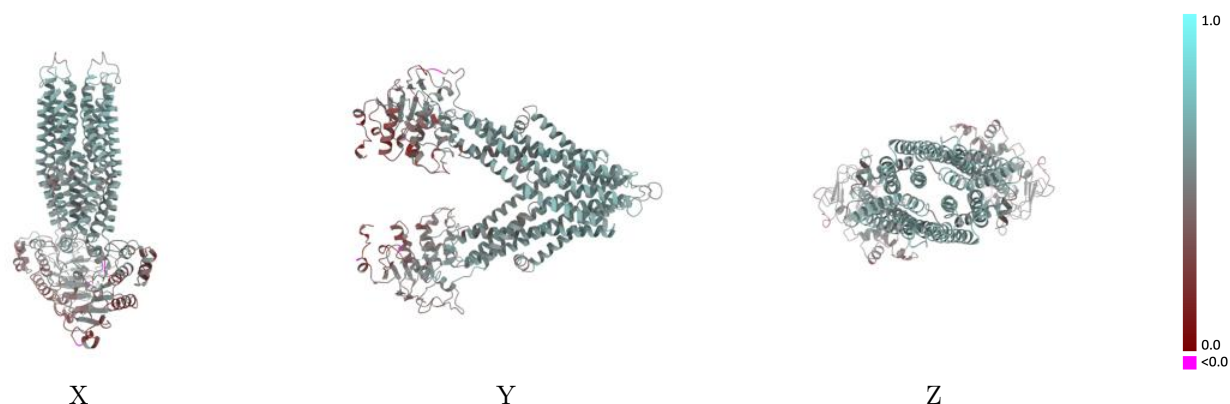
This section contains information regarding the fit between EMDB map EMD-13612 and PDB model 7PSD. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



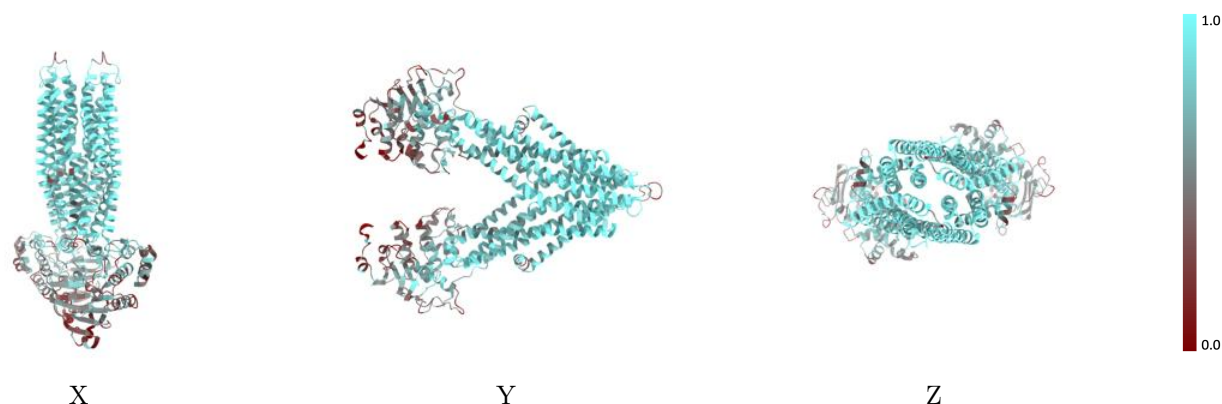
The images above show the 3D surface view of the map at the recommended contour level 0.56 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



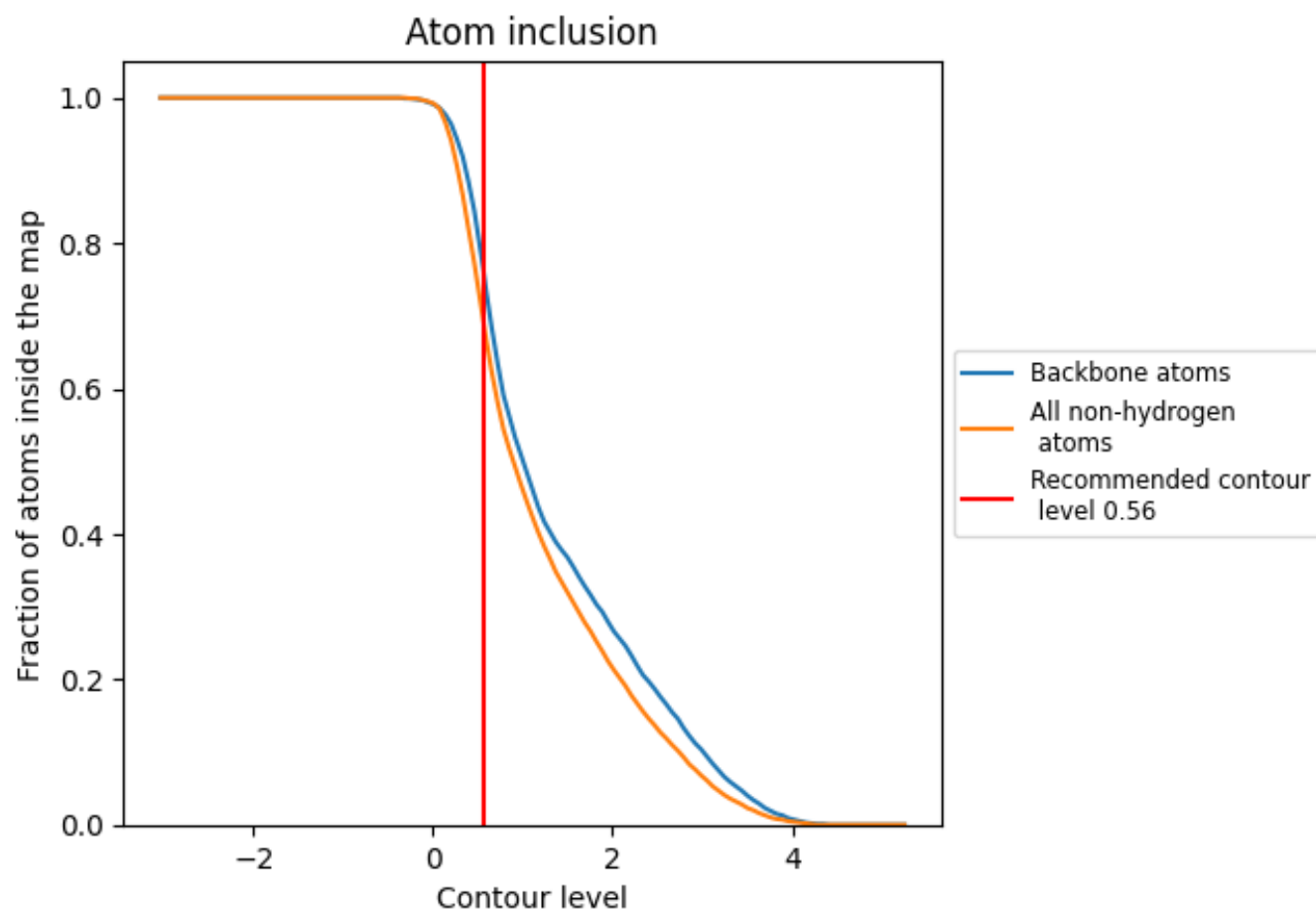
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.56).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 70% 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 (0.56) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6960	<div></div> 0.4990
A	<div></div> 0.6950	<div></div> 0.4980
B	<div></div> 0.6970	<div></div> 0.4990

