



Full wwPDB EM Validation Report ⓘ

May 18, 2026 – 12:25 PM EDT

PDB ID : 10ET / pdb_000010et
EMDB ID : EMD-75118
Title : Chloroplast Glutamyl Peptidase D855N in open-closed conformation
Authors : Ehrlich, J.J.; Routray, P.; van Wijk, K.J.; Kawate, T.
Deposited on : 2026-01-15
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

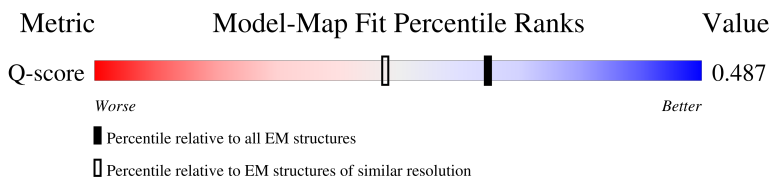
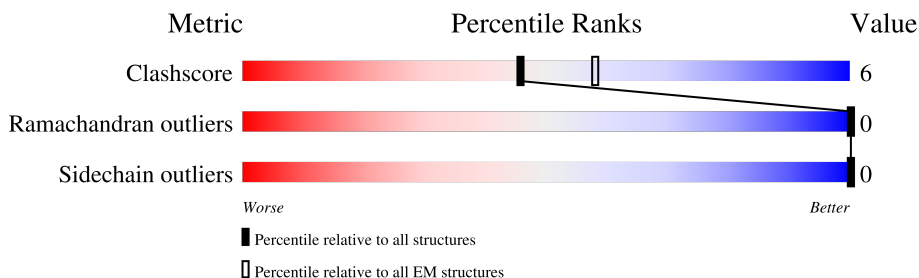
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	907	
1	B	907	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12659 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 Isoform 2 of Probable glutamyl endopeptidase, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	807	Total	C	N	O	S	0	0
			6366	4046	1092	1207	21		
1	A	797	Total	C	N	O	S	0	0
			6293	4003	1076	1193	21		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	54	HIS	-	expression tag	UNP Q8VZF3
B	55	HIS	-	expression tag	UNP Q8VZF3
B	56	HIS	-	expression tag	UNP Q8VZF3
B	57	HIS	-	expression tag	UNP Q8VZF3
B	58	HIS	-	expression tag	UNP Q8VZF3
B	59	HIS	-	expression tag	UNP Q8VZF3
B	60	GLY	-	expression tag	UNP Q8VZF3
B	61	GLY	-	expression tag	UNP Q8VZF3
B	855	ASN	ASP	engineered mutation	UNP Q8VZF3
A	55	HIS	-	expression tag	UNP Q8VZF3
A	56	HIS	-	expression tag	UNP Q8VZF3
A	57	HIS	-	expression tag	UNP Q8VZF3
A	58	HIS	-	expression tag	UNP Q8VZF3
A	59	HIS	-	expression tag	UNP Q8VZF3
A	60	HIS	-	expression tag	UNP Q8VZF3
A	61	GLY	-	expression tag	UNP Q8VZF3
A	62	GLY	-	expression tag	UNP Q8VZF3
A	855	ASN	ASP	engineered mutation	UNP Q8VZF3

GLY	G801	I638	V552	W489	L428	S354	L272
GLY	R804	T639	L553	Y490	W430	T355	T275
ASN			L554	K491	A431	D356	L276
PRO	A807	H643	N555	T492	E432	R357	P277
GLU		P644	G556	R493	T433	K358	S278
PHE	L812	Y645	S557	R494	Q434	Y359	S279
GLY		Q652	G558	T495	D435		R280
GLU	E820		A559	R496	G436	L365	G281
HIS		M655	T560	T497	G437		E282
GLU			P561	W498	D438	S370	P283
VAL	K944		Q562	V499	A439	F371	P284
HIS	K945	K661	G563	W498	K440	I372	K285
SER	P946		N564	I500	M441	V373	K286
LYS		L672	V565	S501	E442	G376	P287
LEU	H851		P566	P502	V443		L288
ARG		K680	F567	G503	W448	K380	V289
ARG	N856		L568	S504	P445	K381	P290
SER	N857	E694	D569	N505	R446	V382	S291
LEU	P853	F695	L570	D506	D447	E383	
LEU	G859	LYS	F571	V507	I449		T295
	T860	SER	D572	S508	V450	T387	T300
		LYS	I573	P509	M451	D388	K301
	Q864	ASP	N574	R510	Y450	G389	T302
	S865	ALA	E574	I511		R390	V303
		GLY	G576	L512		F391	V304
	S888	GLN	N577	F613		V392	Q305
	H889	VAL		D514		R393	V306
	I897		K578	R515		Q394	R307
	W907	G706	E579	S516		L395	T308
	L908	T717	R580	S617		C396	F309
		S718	L581	E518		D397	Q310
	N915	A719	W582	D519		L398	
THR		L720	E583	V520			D311
SER		L721	E587	Y521		E402	L312
ASP		G732		S522		D403	L313
ALA		P733	S598	S622		T404	
THR		I737	D599	P462		P405	D314
SER			Q600	P524		I406	D315
PRO			K601	G525		A407	E316
ASP		E740	E602	S526		S408	Y317
GLN		G741	G603	T527		W408	D318
LYS		D742	D604	M528		A319	A319
GLU		E743	L605	L468		S410	D320
GLY		E744	L606	D469		V411	
SER		A745	K606	L470		R412	D323
ASP		N746	M607	R531		K413	Q329
SER			E608	T532		G414	L330
ALA		E763	E609	D533		M415	V331
ASP			L610			R416	L332
LYS		R767	K611	A534		I418	L335
VAL		G768	I612				D336
SER		V769		I539		R421	K340
THR				A540		A422	E341
GLY		H780	N622	K541		D423	
THR		L791	Q628	I542		K424	A346
			L629	K543		P425	
			W630	K544		S426	L351
			P631	E545		T427	
			D632	N546			
			R633	D547			
			K634	E548			
				G549			
				T550			
				Y551			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	70609	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON I (4k x 4k)	Depositor
Maximum map value	0.666	Depositor
Minimum map value	-0.387	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	284.96, 284.96, 284.96	wwPDB
Map dimensions	208, 208, 208	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.37, 1.37, 1.37	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	0.10	0/6455	0.28	0/8781
1	B	0.11	0/6529	0.29	0/8880
All	All	0.11	0/12984	0.29	0/17661

There are no bond length outliers.

There are no bond angle outliers.

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	6293	0	6194	91	0
1	B	6366	0	6273	66	0
All	All	12659	0	12467	156	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 6.

All (156) 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:479:ASP:OD1	1:B:480:ASP:N	2.17	0.78
1:A:421:ARG:HH22	1:A:451:MET:HG2	1.47	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:690:SER:OG	1:B:786:MET:SD	2.48	0.71
1:A:780:HIS:HD2	1:A:804:ARG:HE	1.39	0.71
1:A:421:ARG:HH21	1:A:429:TYR:HB3	1.56	0.71
1:A:746:ASN:ND2	1:A:820:GLU:OE1	2.23	0.71
1:B:144:ARG:HH12	1:B:147:PRO:HG3	1.54	0.70
1:B:765:VAL:HG11	1:B:772:ARG:HH21	1.54	0.70
1:B:543:LYS:NZ	1:B:547:ASP:O	2.25	0.69
1:B:189:GLY:O	1:B:636:GLN:NE2	2.24	0.69
1:A:487:GLU:OE2	1:A:496:ARG:NH1	2.25	0.69
1:A:807:ALA:HB2	1:A:860:THR:HG22	1.76	0.68
1:A:139:LEU:HD11	1:A:180:LEU:HD23	1.77	0.66
1:A:329:GLN:NE2	1:A:341:GLU:OE1	2.29	0.65
1:B:746:ASN:ND2	1:B:820:GLU:OE1	2.28	0.64
1:A:551:TYR:HB3	1:A:570:LEU:HD12	1.80	0.64
1:B:810:ARG:HH11	1:B:817:PHE:HD1	1.46	0.64
1:B:543:LYS:NZ	1:B:544:LYS:O	2.32	0.63
1:B:557:SER:HA	1:B:566:PRO:HA	1.79	0.63
1:B:451:MET:HE3	1:B:465:LEU:HD11	1.79	0.63
1:A:489:TRP:HE1	1:A:491:LYS:HB3	1.63	0.63
1:B:205:LYS:HE3	1:B:225:ASP:OD1	1.98	0.63
1:A:530:ARG:HB2	1:A:540:ALA:HB2	1.81	0.62
1:B:694:GLU:OE1	1:B:819:ASN:ND2	2.32	0.62
1:A:496:ARG:HE	1:A:510:ARG:HH22	1.47	0.62
1:B:251:SER:OG	1:B:253:ASP:OD1	2.18	0.62
1:A:575:THR:OG1	1:A:577:ASN:ND2	2.34	0.60
1:A:542:ILE:HD11	1:A:570:LEU:HD11	1.84	0.60
1:A:471:ARG:HH22	1:A:475:ILE:HG12	1.67	0.59
1:B:366:HIS:HB3	1:B:379:PRO:HB2	1.83	0.59
1:A:520:VAL:HG22	1:A:561:PRO:HG3	1.84	0.59
1:A:496:ARG:HE	1:A:510:ARG:NH2	2.01	0.58
1:A:382:VAL:HG23	1:A:395:LEU:HB3	1.85	0.58
1:A:496:ARG:HH12	1:A:498:TRP:HE1	1.50	0.57
1:A:489:TRP:HD1	1:A:492:THR:H	1.52	0.57
1:B:248:LEU:HD11	1:B:271:LEU:HD21	1.86	0.57
1:B:470:LEU:HD22	1:B:489:TRP:HB2	1.86	0.56
1:A:449:VAL:HG23	1:A:464:VAL:HB	1.88	0.56
1:B:366:HIS:CD2	1:B:368:PRO:HD2	2.41	0.56
1:A:569:ASP:HB3	1:A:580:ARG:HA	1.89	0.55
1:B:846:PRO:HB3	1:B:878:LEU:HD22	1.88	0.55
1:B:309:PHE:HB2	1:B:312:LEU:HD11	1.88	0.55
1:B:144:ARG:HH12	1:B:147:PRO:CG	2.21	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:LEU:HD22	1:A:351:LEU:HD21	1.89	0.53
1:A:717:THR:HG23	1:A:897:ILE:HG23	1.90	0.53
1:A:161:GLY:N	1:A:311:ASP:O	2.33	0.53
1:B:183:HIS:CE1	1:B:194:GLU:HG2	2.44	0.52
1:A:283:PRO:HB2	1:A:317:TYR:HE1	1.73	0.52
1:A:393:ARG:HH22	1:A:457:LEU:HD21	1.75	0.52
1:A:117:ILE:HG23	1:A:721:LEU:HD13	1.92	0.52
1:A:812:LEU:HD12	1:A:864:GLN:HE21	1.74	0.51
1:B:511:ILE:HD11	1:B:514:ASP:HB3	1.93	0.51
1:A:791:LEU:HD11	1:A:801:GLY:HA3	1.92	0.51
1:A:612:ILE:HG12	1:A:628:GLN:HB3	1.93	0.50
1:A:564:ASN:OD1	1:A:706:GLY:N	2.44	0.50
1:A:643:HIS:HD2	1:A:645:TYR:H	1.58	0.50
1:B:307:ARG:HH12	1:B:816:GLY:HA3	1.75	0.50
1:A:455:GLU:HB3	1:A:456:PRO:HD3	1.92	0.49
1:B:435:ASP:OD2	1:B:446:ARG:NH1	2.45	0.49
1:B:784:ALA:HB1	1:B:803:ALA:HB1	1.94	0.49
1:A:422:ALA:HB3	1:A:477:TRP:HB2	1.94	0.49
1:B:267:ASP:OD1	1:B:268:ASN:N	2.42	0.49
1:B:618:SER:HB3	1:B:621:GLU:HB2	1.95	0.49
1:B:220:PHE:HE2	1:B:222:ILE:HD11	1.77	0.49
1:A:851:HIS:CG	1:A:865:SER:HG	2.27	0.48
1:B:851:HIS:CD2	1:B:852:GLY:H	2.32	0.48
1:A:418:ILE:HG12	1:A:430:TRP:HB3	1.95	0.48
1:B:580:ARG:NH1	1:B:583:GLU:OE1	2.46	0.48
1:A:496:ARG:HG2	1:A:512:LEU:HD13	1.95	0.47
1:A:568:LEU:HB3	1:A:582:TRP:HB3	1.95	0.47
1:B:205:LYS:CE	1:B:225:ASP:OD1	2.60	0.47
1:A:465:LEU:HD22	1:A:500:ILE:HG21	1.97	0.47
1:A:780:HIS:CD2	1:A:804:ARG:HH21	2.33	0.47
1:B:834:MET:HE2	1:B:834:MET:HB3	1.82	0.47
1:A:557:SER:HA	1:A:566:PRO:HA	1.97	0.46
1:B:812:LEU:HD12	1:B:864:GLN:NE2	2.30	0.46
1:B:276:ILE:HG21	1:B:280:ARG:HH21	1.80	0.46
1:A:276:ILE:HD13	1:A:280:ARG:NH1	2.31	0.46
1:A:438:ASP:HB3	1:A:441:MET:HE1	1.98	0.46
1:A:718:SER:OG	1:A:719:ALA:N	2.49	0.46
1:B:611:LYS:HE2	1:B:629:LEU:HD21	1.97	0.46
1:A:421:ARG:NH2	1:A:429:TYR:HB3	2.28	0.46
1:A:471:ARG:HH12	1:A:475:ILE:HD11	1.81	0.46
1:B:205:LYS:NZ	1:B:225:ASP:OD1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:880:ARG:HH21	1:A:295:THR:HG21	1.79	0.46
1:B:685:PRO:HB2	1:B:727:PHE:CD1	2.52	0.45
1:B:660:ARG:NH1	1:B:756:SER:OG	2.45	0.45
1:B:732:GLY:N	1:B:733:PRO:HD3	2.32	0.45
1:A:421:ARG:HG3	1:A:424:LYS:HB2	1.97	0.45
1:B:276:ILE:HD13	1:B:280:ARG:HH21	1.81	0.45
1:A:506:ASP:OD1	1:A:507:VAL:N	2.42	0.45
1:A:431:ALA:HB2	1:A:449:VAL:HG12	1.99	0.45
1:B:591:GLU:HG2	1:B:616:LYS:HG2	1.98	0.45
1:A:530:ARG:HH22	1:A:603:GLY:H	1.65	0.45
1:B:779:GLY:HA3	1:B:783:GLY:C	2.42	0.44
1:A:393:ARG:NH2	1:A:457:LEU:HD21	2.31	0.44
1:B:748:ARG:NH1	1:B:752:GLN:HE21	2.15	0.44
1:A:160:ALA:HB2	1:A:313:LEU:HD11	1.99	0.44
1:A:475:ILE:HD12	1:A:485:VAL:HG22	2.00	0.44
1:A:510:ARG:NH2	1:A:512:LEU:HD22	2.31	0.44
1:B:740:GLU:N	1:B:743:GLU:OE1	2.47	0.44
1:A:510:ARG:CZ	1:A:512:LEU:HB2	2.47	0.44
1:A:732:GLY:N	1:A:733:PRO:HD3	2.33	0.44
1:A:737:ILE:HG22	1:A:745:ALA:HB1	1.98	0.44
1:A:851:HIS:ND1	1:A:865:SER:OG	2.34	0.44
1:A:237:VAL:HG21	1:A:248:LEU:HD13	1.99	0.44
1:A:610:LEU:HB3	1:A:630:TRP:CD1	2.53	0.44
1:B:113:PRO:HD3	1:B:898:MET:HG3	1.99	0.44
1:B:471:ARG:HD3	1:B:471:ARG:HA	1.72	0.43
1:A:497:THR:HB	1:A:511:ILE:HB	1.99	0.43
1:A:629:LEU:HG	1:A:631:PRO:HD2	2.00	0.43
1:B:748:ARG:HH12	1:B:752:GLN:HE21	1.65	0.43
1:A:622:ASN:HD22	1:A:644:PRO:HD3	1.82	0.43
1:A:844:LYS:HD3	1:A:844:LYS:HA	1.67	0.43
1:B:812:LEU:HD12	1:B:864:GLN:HE22	1.84	0.43
1:A:652:GLN:HB2	1:A:672:LEU:HB2	2.00	0.43
1:A:421:ARG:HG2	1:A:427:THR:O	2.19	0.43
1:B:804:ARG:O	1:B:805:SER:OG	2.28	0.43
1:B:226:GLU:HG3	1:B:231:SER:HB2	2.01	0.43
1:B:551:TYR:HB3	1:B:570:LEU:HD22	2.01	0.43
1:A:222:ILE:O	1:A:233:PRO:HA	2.19	0.43
1:B:478:CYS:HB2	1:B:539:ILE:HB	2.00	0.42
1:A:555:ASN:HB3	1:A:568:LEU:HD13	2.01	0.42
1:A:569:ASP:OD1	1:A:569:ASP:N	2.52	0.42
1:A:763:GLU:OE2	1:A:767:ARG:NE	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:ASN:O	1:A:231:SER:OG	2.35	0.42
1:B:813:THR:O	1:B:813:THR:OG1	2.32	0.42
1:A:272:LEU:HD21	1:A:330:LEU:HD13	2.01	0.42
1:A:846:PRO:HB2	1:A:907:TRP:HZ2	1.84	0.42
1:A:158:LYS:HD3	1:A:311:ASP:OD1	2.19	0.42
1:B:608:GLU:HG3	1:B:609:GLU:HG3	2.02	0.42
1:A:276:ILE:HD13	1:A:280:ARG:HH12	1.85	0.42
1:B:902:TRP:CZ2	1:B:906:ARG:HD2	2.55	0.42
1:B:152:LEU:HD22	1:B:893:ALA:HB2	2.02	0.42
1:B:169:ASN:HD21	1:B:280:ARG:HH22	1.67	0.41
1:A:672:LEU:HD21	1:A:769:VAL:HG11	2.02	0.41
1:A:139:LEU:HD12	1:A:181:GLY:O	2.20	0.41
1:B:777:VAL:O	1:B:801:GLY:HA2	2.20	0.41
1:A:356:ASP:OD1	1:A:356:ASP:N	2.54	0.41
1:A:370:SER:HB3	1:A:373:VAL:HB	2.01	0.41
1:A:354:SER:OG	1:A:356:ASP:OD1	2.36	0.41
1:A:421:ARG:HD3	1:A:421:ARG:HA	1.73	0.41
1:A:472:TYR:H	1:A:487:GLU:HA	1.85	0.41
1:B:280:ARG:HD2	1:B:324:TYR:CE1	2.56	0.41
1:B:629:LEU:HD23	1:B:629:LEU:HA	1.88	0.41
1:A:171:ARG:H	1:A:171:ARG:HG2	1.67	0.41
1:A:390:ARG:NH1	1:A:392:VAL:HG22	2.36	0.41
1:A:638:ILE:HG13	1:A:639:THR:HG23	2.03	0.41
1:B:515:ARG:HG3	1:B:515:ARG:HH11	1.86	0.41
1:A:655:MET:HE2	1:A:655:MET:HB3	1.79	0.41
1:A:888:SER:OG	1:A:889:HIS:N	2.54	0.41
1:B:723:LEU:HD12	1:B:723:LEU:HA	1.92	0.40
1:A:489:TRP:CD1	1:A:492:THR:H	2.34	0.40
1:B:778:GLY:HA2	1:B:802:ILE:O	2.22	0.40
1:B:780:HIS:HD2	1:B:804:ARG:HH21	1.69	0.40
1:A:908:LEU:HD23	1:A:908:LEU:HA	1.93	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	793/907 (87%)	769 (97%)	24 (3%)	0	100	100
1	B	805/907 (89%)	778 (97%)	27 (3%)	0	100	100
All	All	1598/1814 (88%)	1547 (97%)	51 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	691/772 (90%)	691 (100%)	0	100	100
1	B	698/772 (90%)	698 (100%)	0	100	100
All	All	1389/1544 (90%)	1389 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	183	HIS
1	B	257	ASN
1	B	305	GLN
1	B	366	HIS
1	B	643	HIS
1	B	780	HIS
1	B	789	ASN
1	B	796	HIS
1	B	818	GLN
1	B	864	GLN
1	B	889	HIS
1	B	899	HIS
1	A	217	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	298	ASN
1	A	329	GLN
1	A	452	GLN
1	A	577	ASN
1	A	643	HIS
1	A	659	GLN
1	A	780	HIS
1	A	841	ASN
1	A	864	GLN
1	A	875	HIS
1	A	909	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.

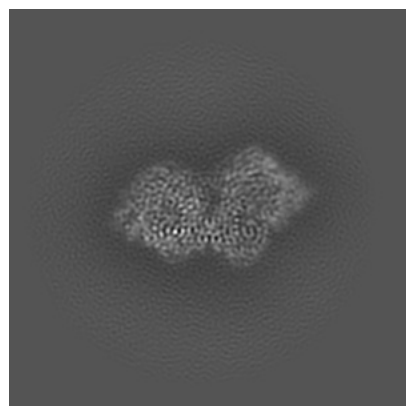
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75118. These allow visual inspection of the internal detail of the map and identification of artifacts.

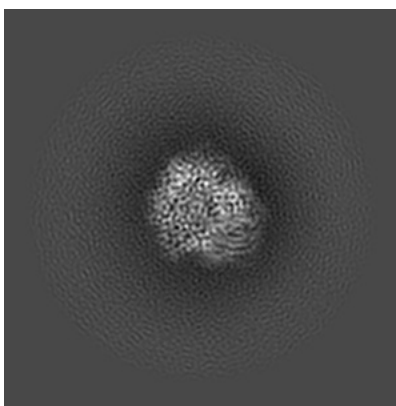
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

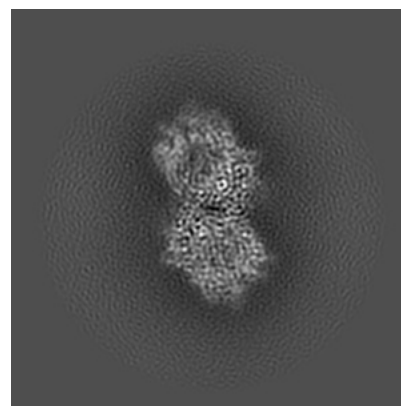
6.1.1 Primary map



X

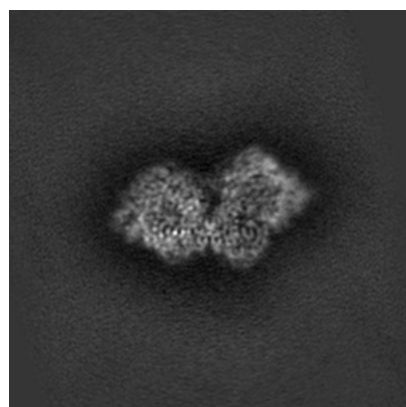


Y

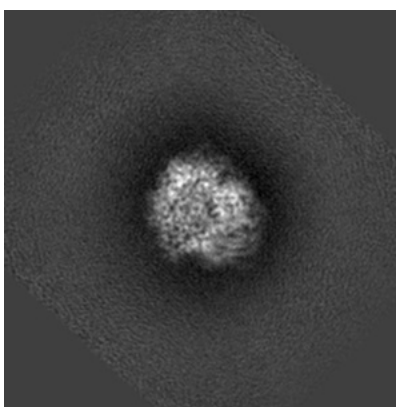


Z

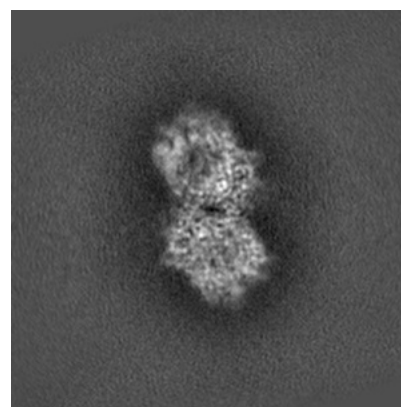
6.1.2 Raw map



X



Y

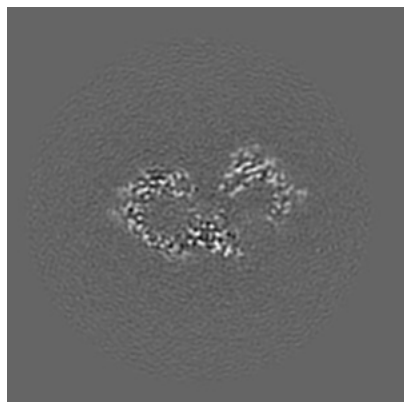


Z

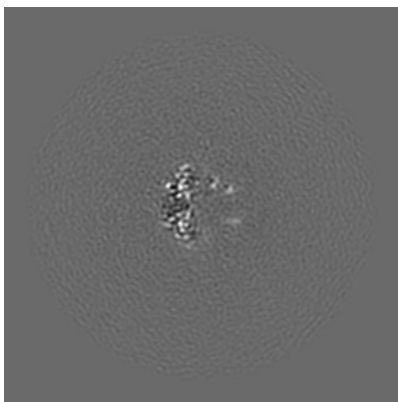
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

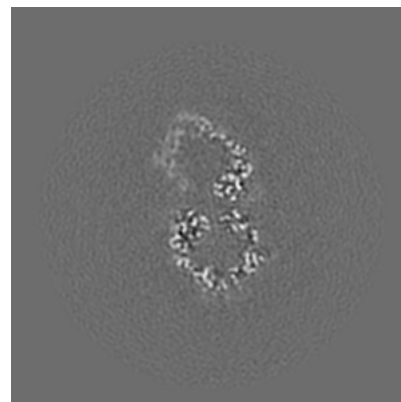
6.2.1 Primary map



X Index: 104



Y Index: 104

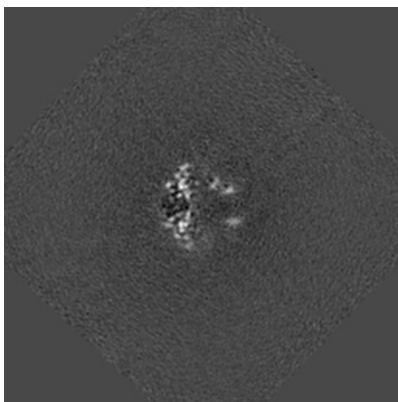


Z Index: 104

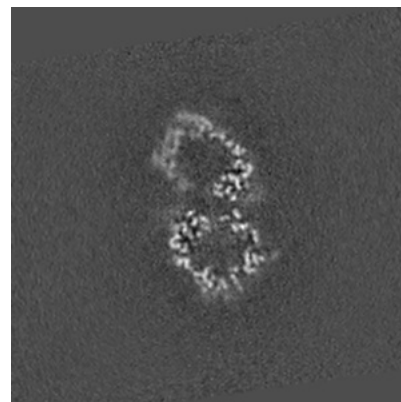
6.2.2 Raw map



X Index: 104



Y Index: 104

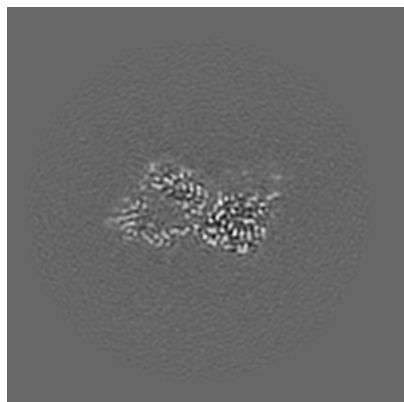


Z Index: 104

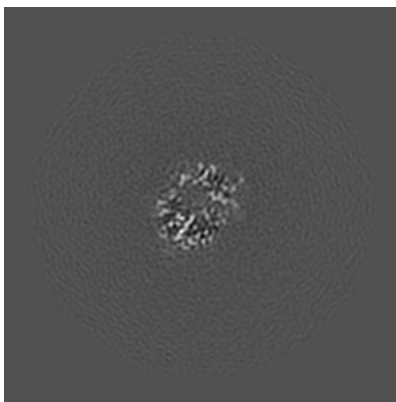
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

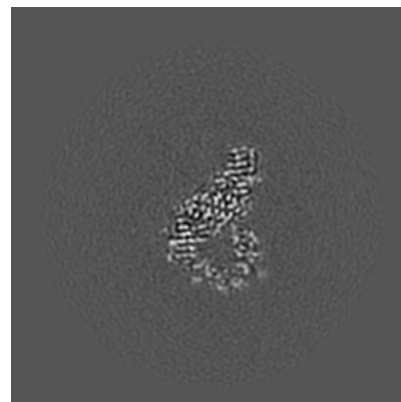
6.3.1 Primary map



X Index: 116

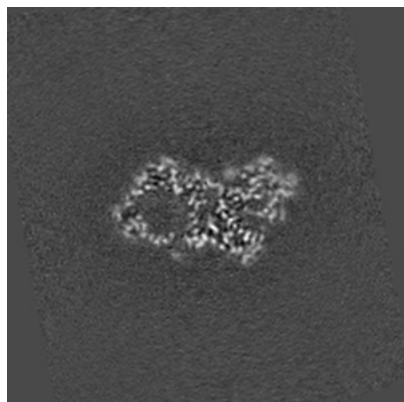


Y Index: 93

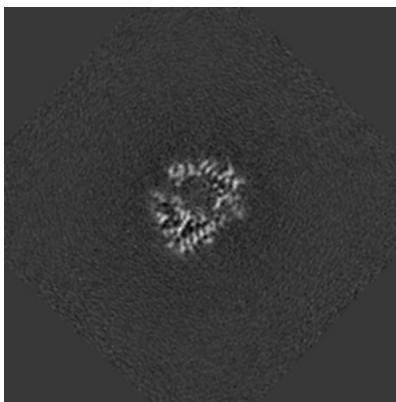


Z Index: 91

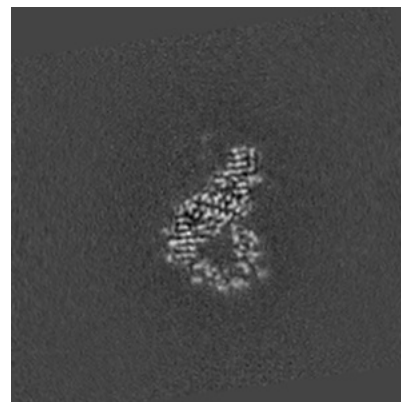
6.3.2 Raw map



X Index: 112



Y Index: 90

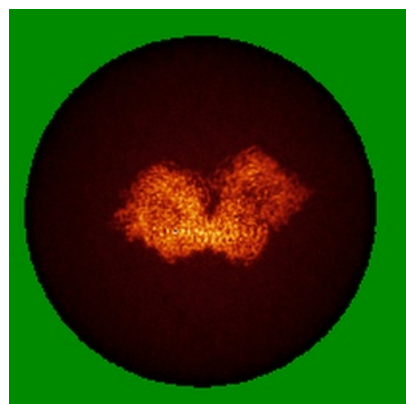


Z Index: 91

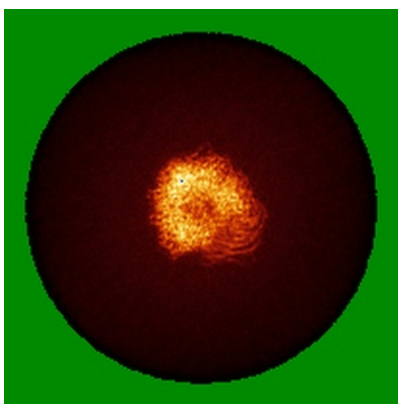
The images above show the largest variance slices of the map in three orthogonal directions.

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

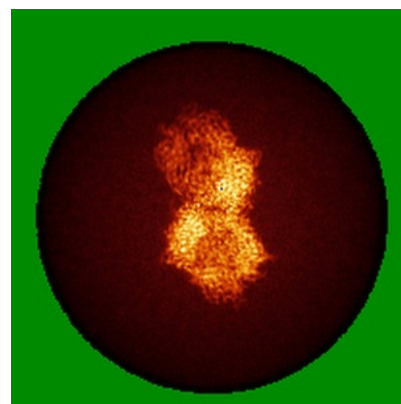
6.4.1 Primary map



X

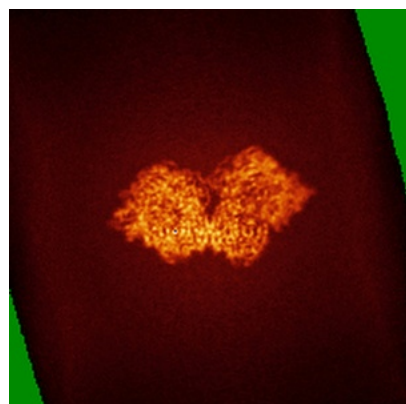


Y

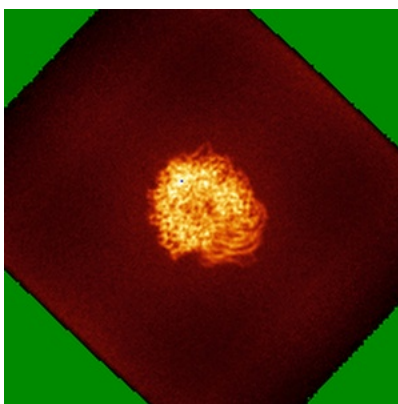


Z

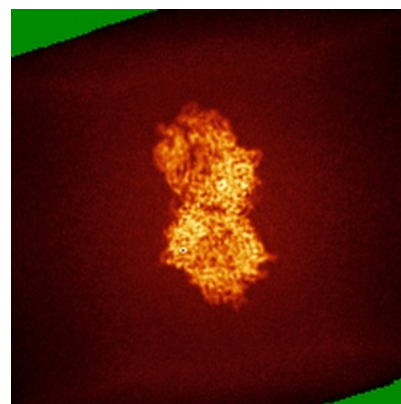
6.4.2 Raw map



X



Y

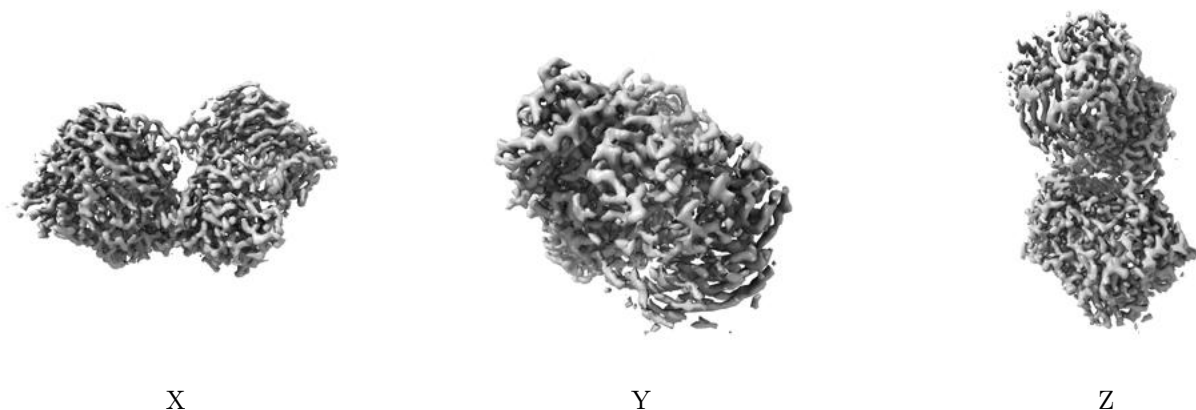


Z

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.

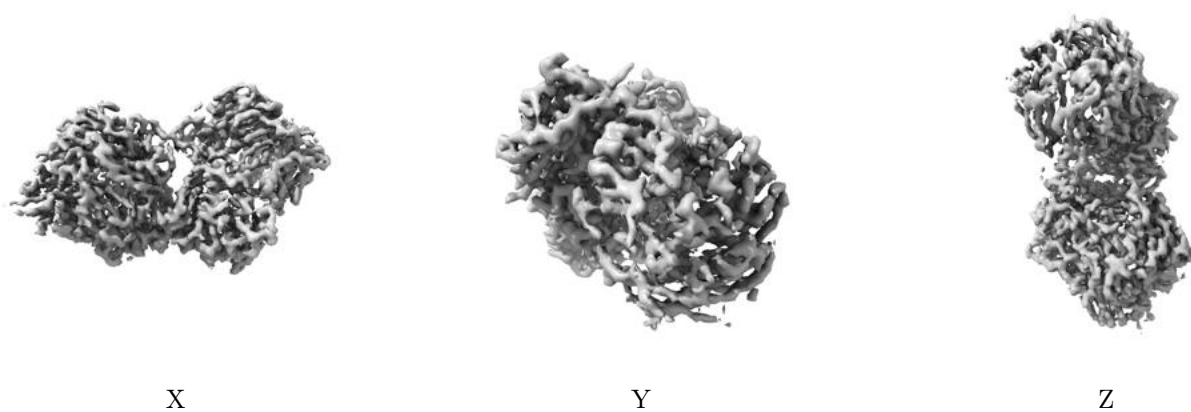
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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.

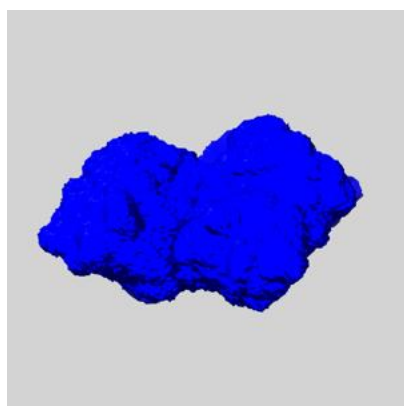
6.6 Mask visualisation [i](#)

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

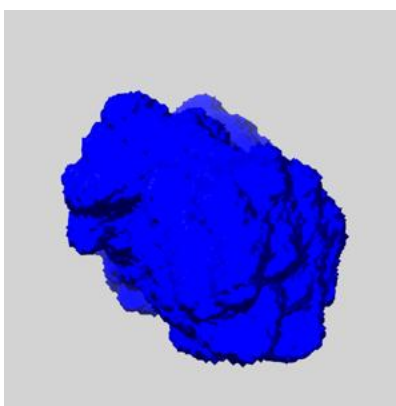
A mask typically either:

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

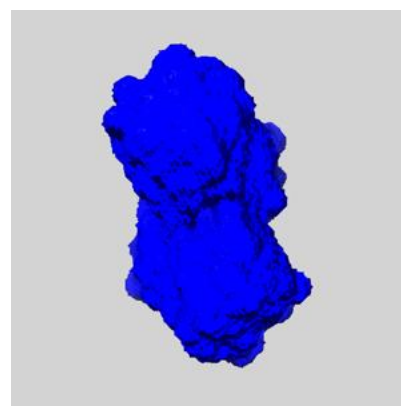
6.6.1 emd_75118_msk_1.map [i](#)



X



Y

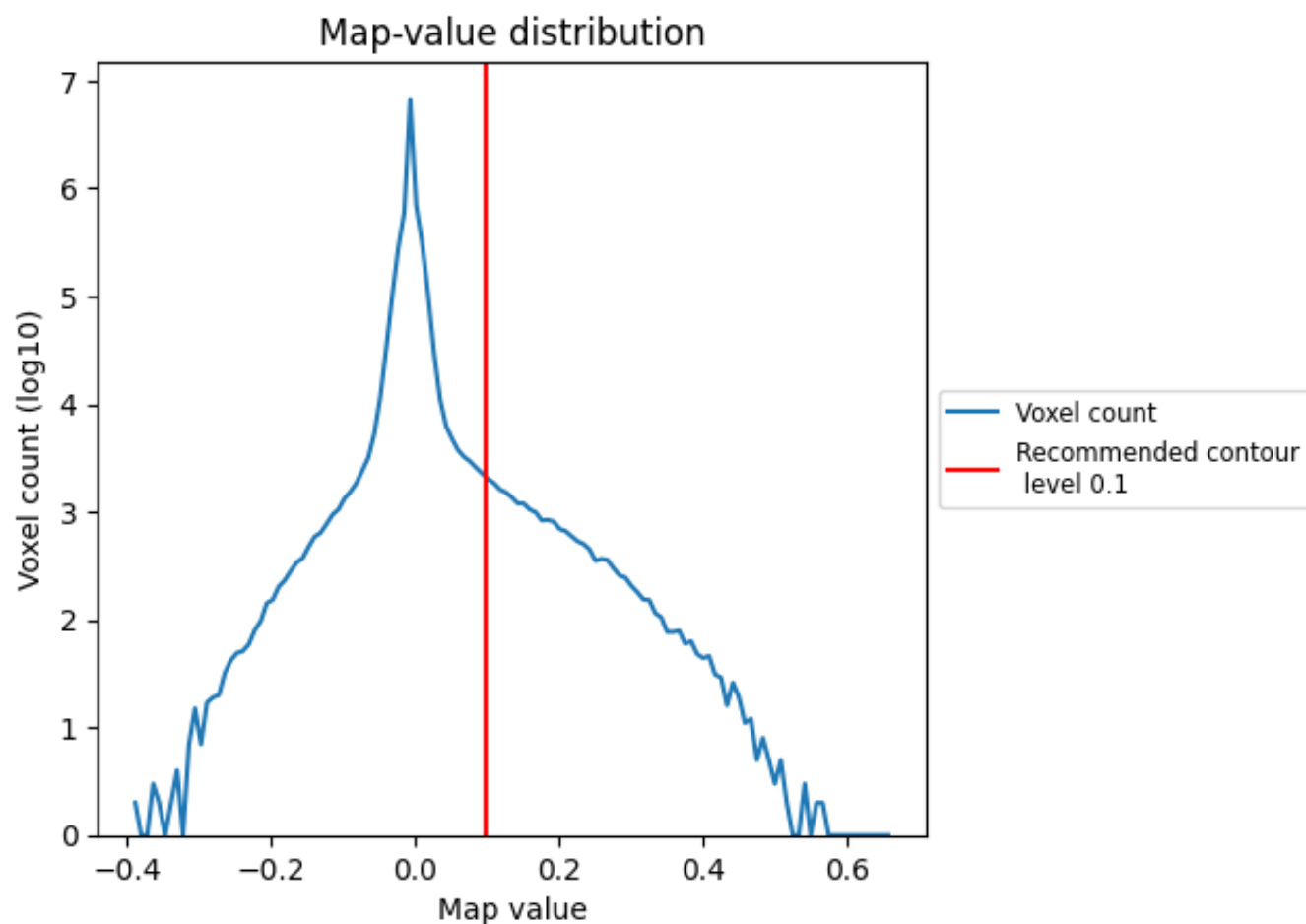


Z

7 Map analysis [i](#)

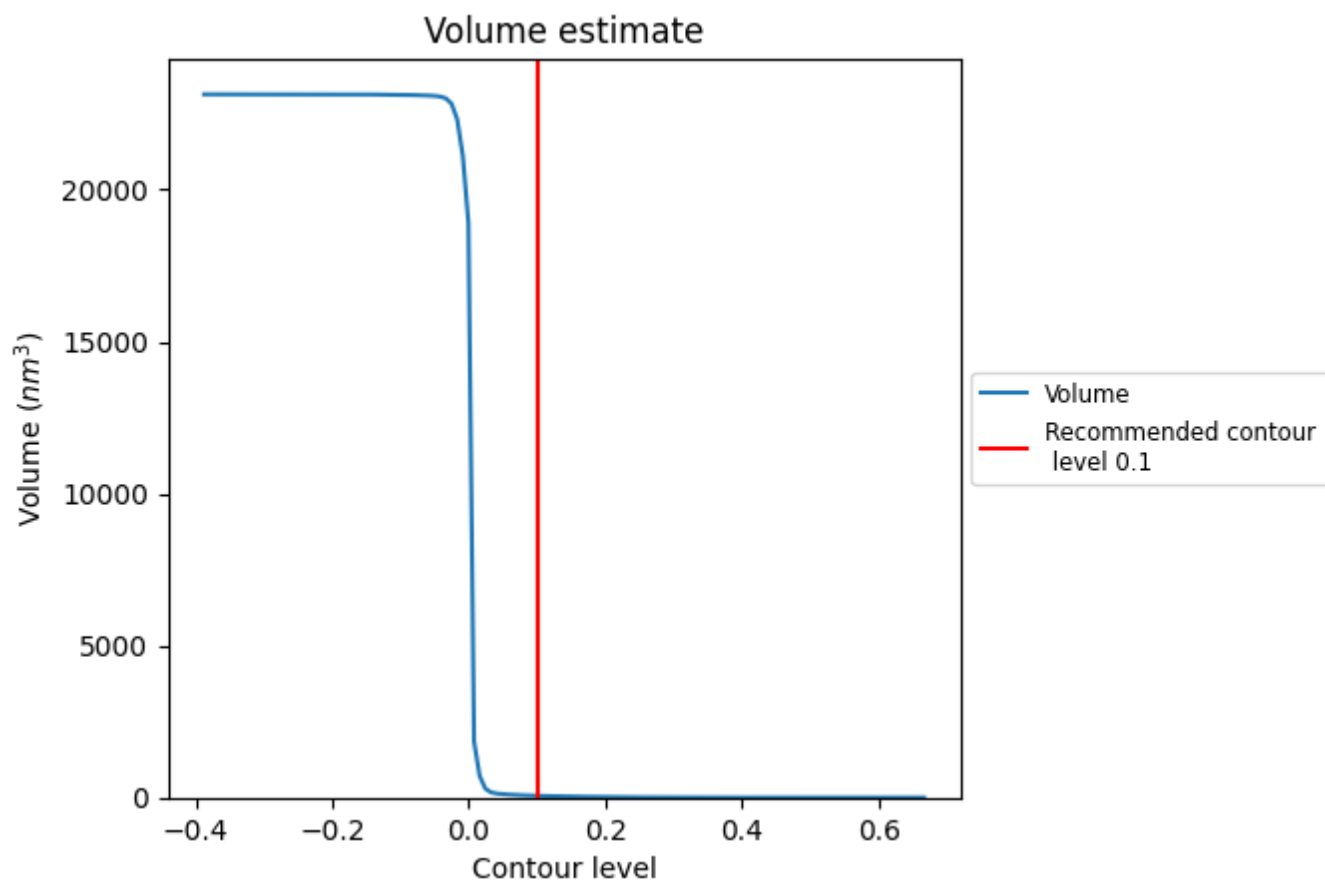
This section contains the results of statistical analysis of the map.

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.

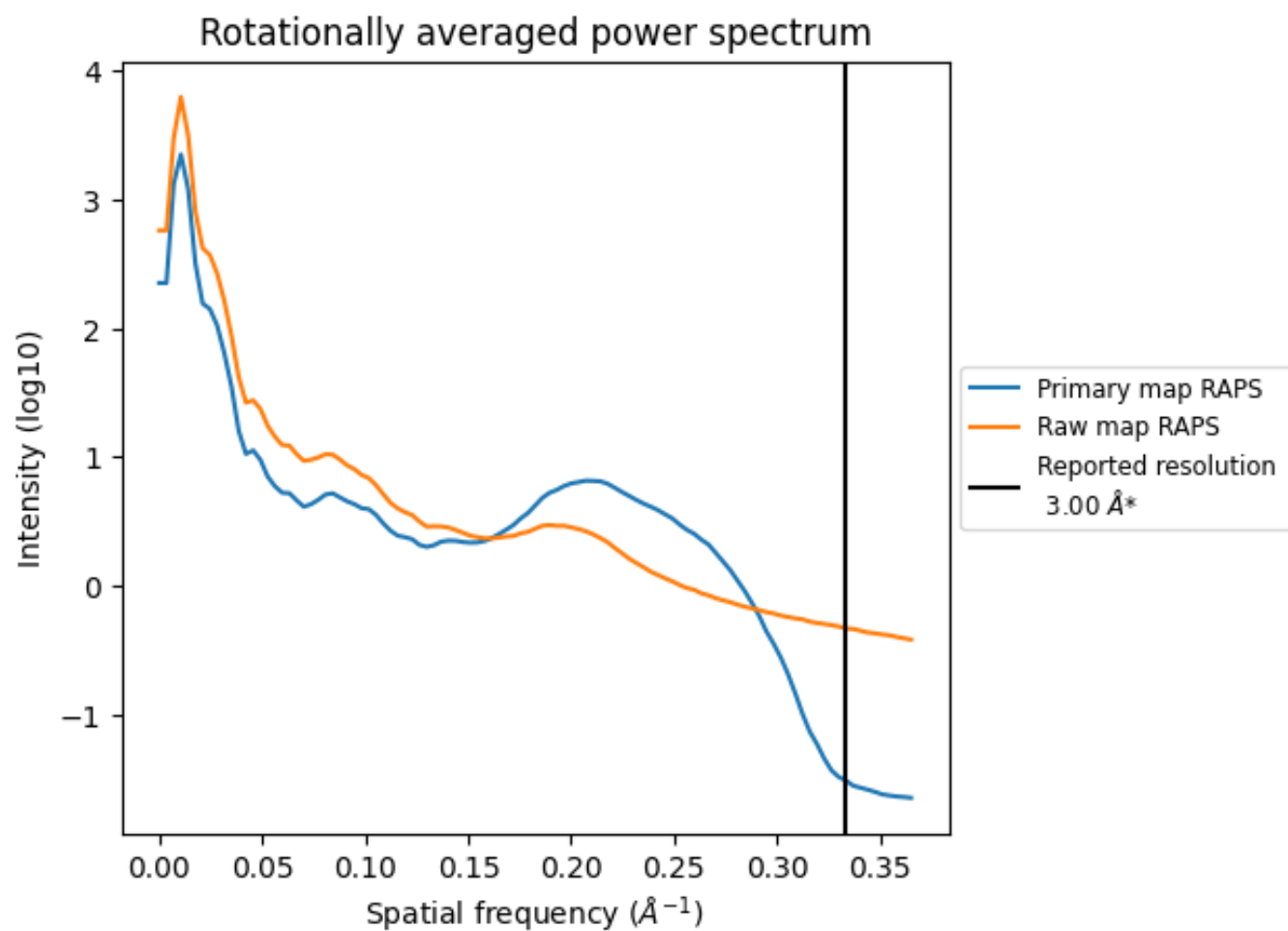
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 58 nm^3 ; this corresponds to an approximate mass of 53 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 ⓘ

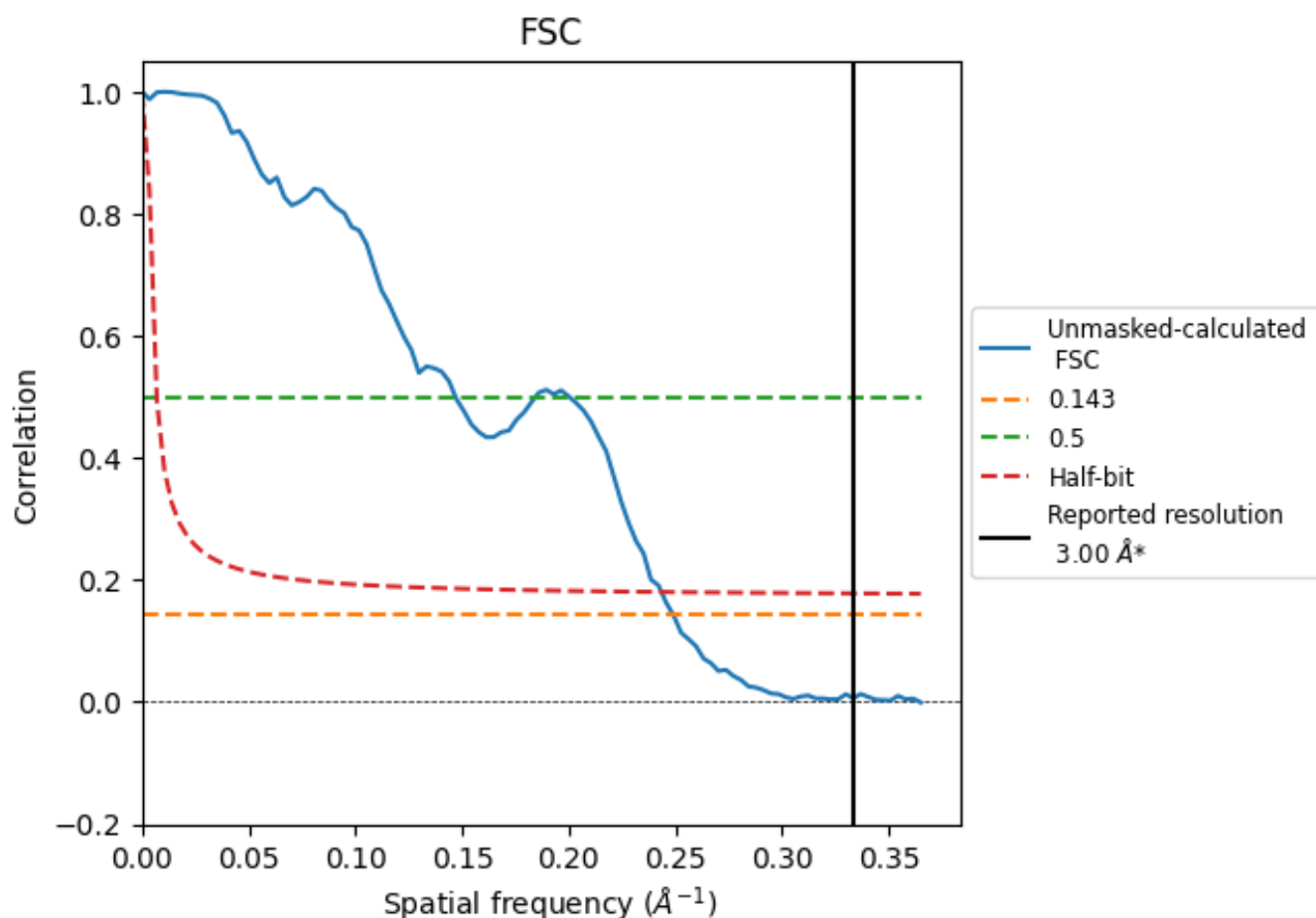


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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](#)

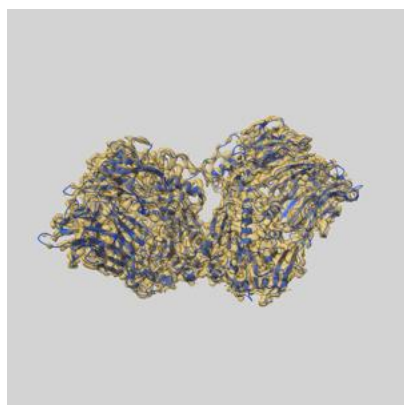
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.02	6.81	4.11

*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 4.02 differs from the reported value 3.0 by more than 10 %

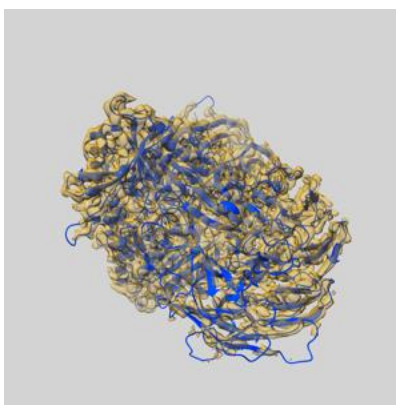
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-75118 and PDB model 10ET. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

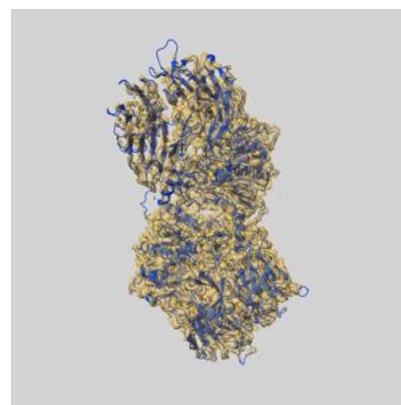
9.1 Map-model overlay [i](#)



X



Y



Z

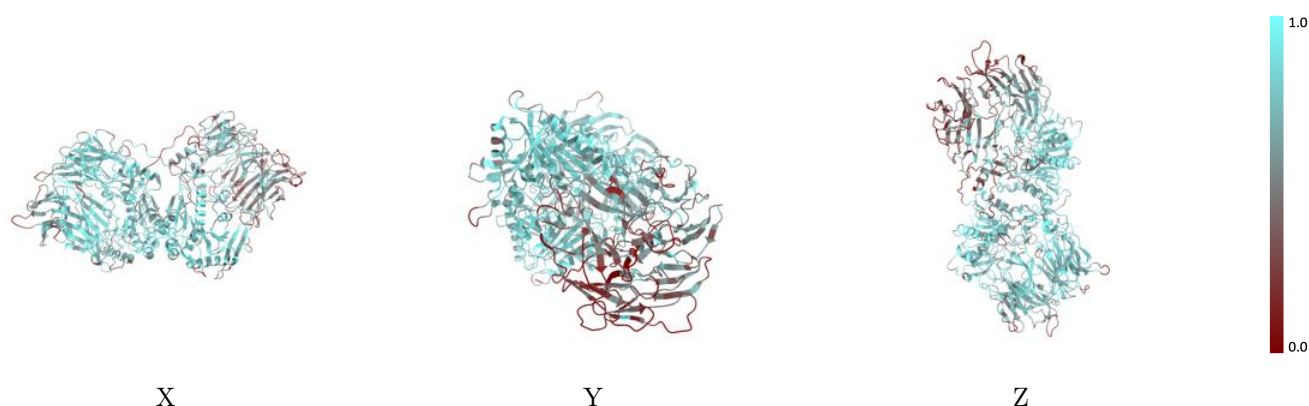
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



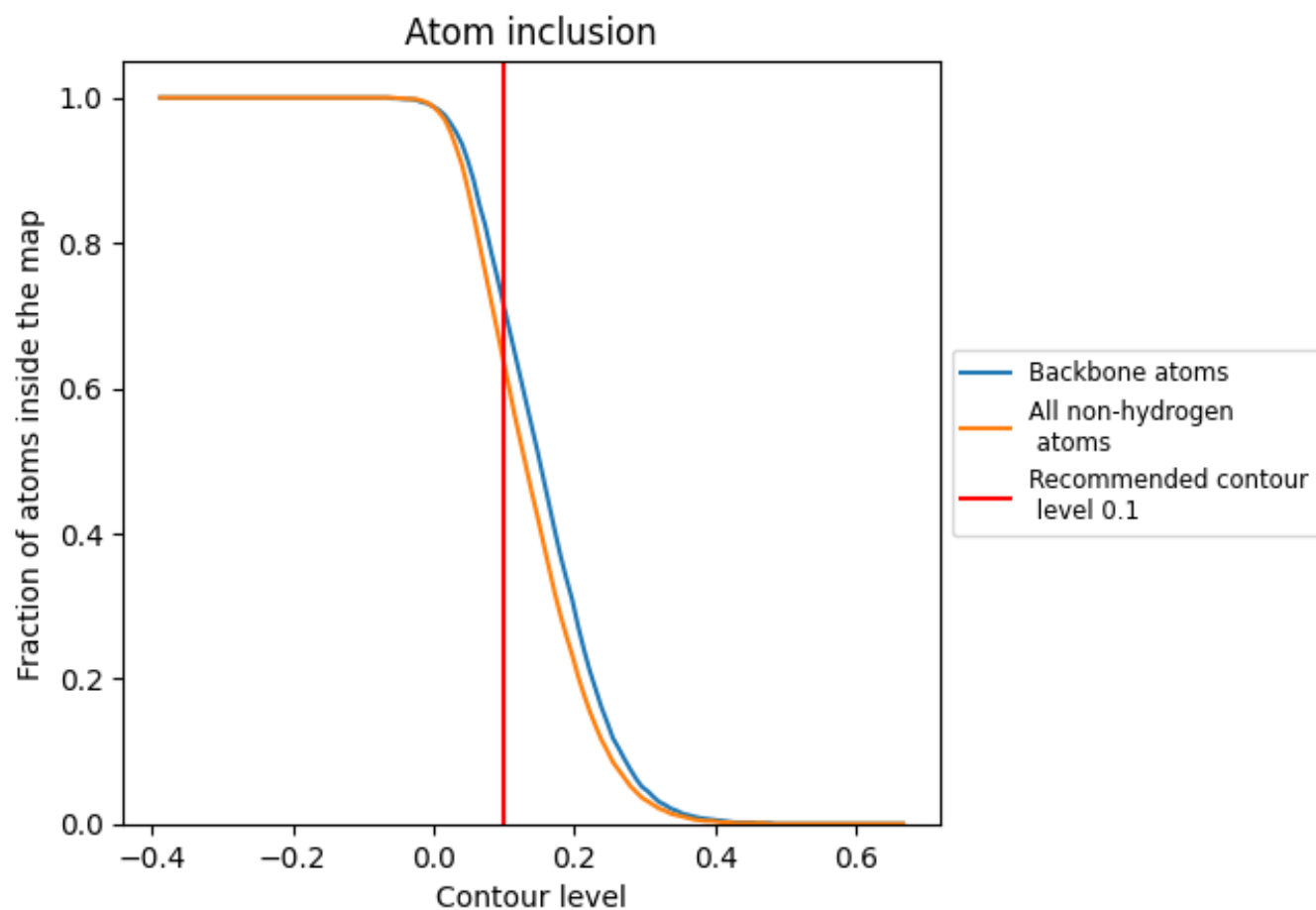
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 63% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6340	<div></div> 0.4870
A	<div></div> 0.5480	<div></div> 0.4590
B	<div></div> 0.7200	<div></div> 0.5140

