



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 06:10 AM UTC

PDB ID : 7XUF / pdb_00007xuf
EMDB ID : EMD-33467
Title : Cryo-EM structure of the AKT1-AtKC1 complex from Arabidopsis thaliana
Authors : Yang, G.H.; Lu, Y.M.; Jia, Y.T.; Yang, F.; Zhang, Y.M.; Xu, X.; Li, X.M.;
Lei, J.L.
Deposited on : 2022-05-18
Resolution : 3.30 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

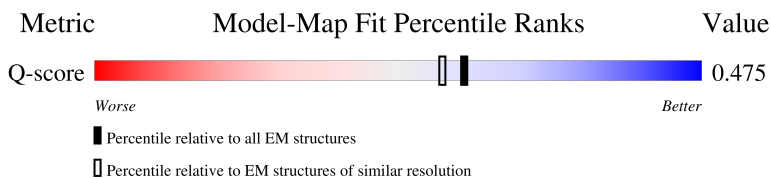
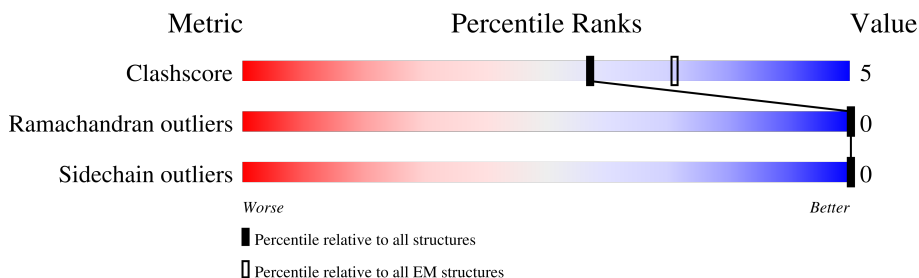
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	662	24% 63% 9% 28%
1	C	662	24% 63% 9% 28%
2	B	857	25% 46% 7% 47%
2	D	857	26% 46% 7% 47%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15041 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 Potassium channel KAT3.

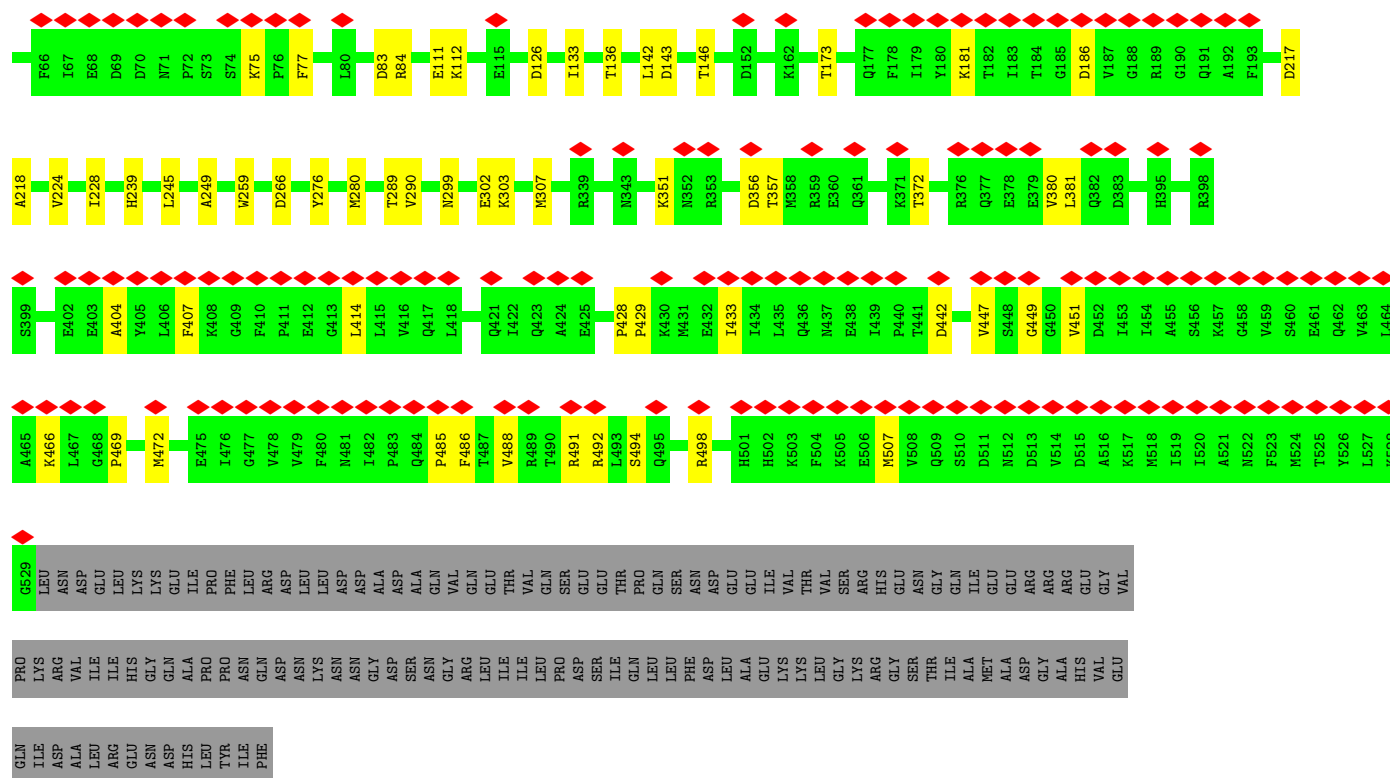
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	476	Total	C	N	O	S	0	0
			3849	2528	638	667	16		
1	C	476	Total	C	N	O	S	0	0
			3849	2528	638	667	16		

- Molecule 2 is a protein called Potassium channel AKT1.

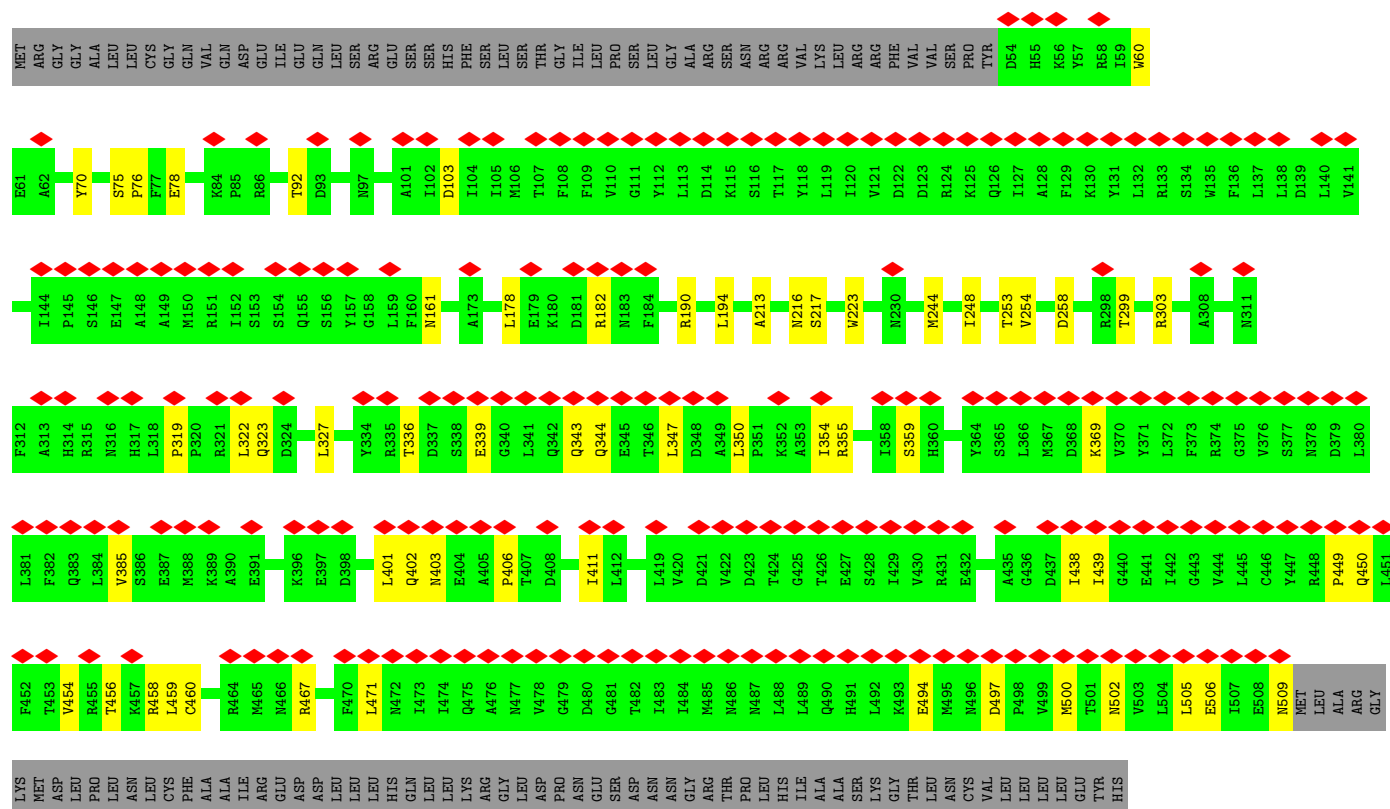
Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	456	Total	C	N	O	S	0	0
			3670	2383	624	641	22		
2	D	456	Total	C	N	O	S	0	0
			3670	2383	624	641	22		

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	K	0
			2	2	
3	B	1	Total	K	0
			1	1	



• Molecule 2: Potassium channel AKT1



- Molecule 2: Potassium channel AKT1



ASN	PHE	ALA	GLY	ASN	LEU	T453	M368	L318	E147	Y70	MET
ASP	PHE	LEU	ASP	CYS	PRO	V454	K389	P319	A148	S75	ARG
ASN	ARG	VAL	VAL	ASP	LEU	R455	A390	P320	A149	P76	GLY
ASN	GLU	GLU	THR	ALA	LEU	T456	E391	R321	M150	F77	ALA
LEU	LEU	LYS	ARG	GLU	CYS	K457	Y392	L322	R151	E78	LEU
PHE	PHE	LEU	PRO	GLY	PHE	R458		Q323	I152		LEU
GLY	HIS	HIS	ARG	SER	ALA		K396	D324	I152	I91	CYS
ILE	GLU	GLU	ALA	VAL	ALA	M465	E397	K333	S153	T92	GLY
THR	THR	THR	ALA	PRO	ILE	M466	D398		S154	N93	VAL
GLY	GLY	GLY	GLY	LEU	ARG	R467		Y394	Q155	N94	GLN
THR	THR	THR	THR	TRP	GLU	T468		R335	Q156		ASP
HIS	HIS	HIS	SER	GLU	ASP	T469	L401	T336	S156	N97	GLU
THR	THR	ALA	ALA	ALA	ASP		Q402	D337	Y157		ILE
VAL	VAL	LEU	LEU	MET	LEU	F470	M403	D337	R167	A98	GLU
GLU	GLU	HIS	HIS	VAL	LEU	L471	E404	S338	L168	F100	GLN
SER	SER	ALA	GLY	GLY	GLN	N472	A405	E339	R169		SER
SER	SER	SER	VAL	HIS	LEU	I473	P406	C340		A101	ARG
VAL	VAL	VAL	CYS	GLU	LEU	I474	T407	L341	I102	I102	GLU
PRO	PRO	PRO	GLU	LYS	LYS	Q475	D408	Q342	R177	I103	GLU
LEU	VAL	LEU	VAL	VAL	ARG	A476	F409	Q343	E179	I104	SER
ASP	ASP	LYS	ILE	LYS	GLY	N477		Q344	K180	I105	SER
GLU	GLU	GLU	GLU	VAL	LEU	V478	L412	Q444	D151	M106	PHE
GLY	GLY	MET	MET	LEU	ASP		V413	T346	R182	T107	SER
ARG	ILE	VAL	VAL	LEU	PRO	G479		D348	M183	F108	LEU
THR	ARG	LYS	LYS	GLU	ASN	T416	T416	L347	E184	F109	THR
PHE	PHE	TYR	TYR	HIS	GLU	D480	A417	D348	N185	V110	GLY
LEU	LEU	LEU	LEU	GLY	ASP	T481	A417		Y186	G111	ILE
GLY	GLY	LEU	LEU	SER	ASP	T482	L419	K352	F187	Y112	LEU
ARG	ARG	GLU	GLU	THR	ASN	I483		A353			LEU
PHE	PHE	GLM	GLM	ILE	ASN	I484	V420	A354	A213	L113	PRO
THR	THR	ALA	ALA	ASP	GLY	M485	D421	I354	N216	D114	SER
ASP	VAL	VAL	VAL	ASP	PRO	N486	V422	R355	S217	K115	LEU
ASN	ASN	ASN	ASN	VAL	LEU	N487	D423	I358		S116	ALA
CYS	CYS	LYS	LYS	GLY	LEU	L488	T424	S359	W223	T117	ARG
ALA	ILE	ARG	GLN	HIS	HIS	L488	Q425	H360	Y118	L119	SER
GLU	ARG	GLN	ASP	PHE	ILE	L489	C425	F361	A229		ASN
LYS	PRO	ASP	MET	GLY	ALA	Q490	T426	L362	N230	I120	ARG
ASP	ASP	MET	MET	CYS	ALA	H491	E427	F363		V121	VAL
SER	SER	SER	GLY	CYS	SER	L492	S428		T253	D122	LYS
ILE	ARG	ARG	GLY	THR	LYS	L492	I429	Y364	V254	D123	LEU
ALA	GLU	GLU	TRP	ALA	GLY	K493		S365		R124	ARG
VAL	VAL	VAL	THR	ALA	THR	E494	V430	S365	I271	K124	PHE
SER	SER	SER	PRO	GLU	LEU	M495	R431	L366	L291	Q125	VAL
LEU	LEU	LEU	ARG	GLN	ASN			M367		I126	VAL
VAL	ARG	ASP	ASP	GLY	CYS	N496	E432	L291	T296	Q126	VAL
LEU	ILE	LEU	LEU	ASN	VAL	D497	V433	D368	S297	A128	SER
LEU	ARG	ALA	ALA	LEU	LEU	P498	K434	K369		F129	PRO
PRO	THR	GLU	GLU	LYS	LEU	V499	A435	V370	R298	K130	ASN
GLY	THR	GLM	GLM	LEU	LEU	M500	G436	Y371	R300	Y131	ARG
SER	ARG	GLY	GLY	LYS	GLU	T501	D437	F372	R303	L132	PHE
PHE	ALA	GLY	GLY	LYS	TYR	L501	I438	F373			VAL
LYS	ARG	HIS	HIS	GLU	HIS	M502	D437	R374	A308	R133	VAL
GLU	ARG	GLY	ASP	ILE	ALA	V503	I439	G375	N311	F136	SER
LEU	LEU	GLU	VAL	VAL	LEU	L504	Q440	V376		L137	PRO
LEU	LEU	ILE	LEU	LEU	ASP	L504	E441	G375	A308	D139	ASN
GLU	GLU	LYS	HIS	HIS	PRO	L505	E441	V376		I140	
						E506	I442	S377			
						E507	G443	N378		W136	
						E508	V444	D379	H314	F136	
						N509	L445	L380	H317	L138	
							C446	L381			
							Y447	F382		I144	
							R448	Q383		P146	
							P449	L384			
							Q450	V385		S146	
							L451	S386			
							F452	E387			

LEU
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	104142	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5959	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	8.803	Depositor
Minimum map value	-5.899	Depositor
Average map value	0.012	Depositor
Map value standard deviation	0.183	Depositor
Recommended contour level	0.823	Depositor
Map size ($\text{\AA}$)	240.8, 240.8, 240.8	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.86, 0.86, 0.86	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: K

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	0.15	0/3946	0.37	0/5351
1	C	0.14	0/3946	0.34	0/5351
2	B	0.13	0/3757	0.33	0/5103
2	D	0.13	0/3757	0.31	0/5103
All	All	0.14	0/15406	0.34	0/20908

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 [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	3849	0	3868	33	0
1	C	3849	0	3868	40	0
2	B	3670	0	3663	41	0
2	D	3670	0	3663	38	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
All	All	15041	0	15062	145	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (145) 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)
2:B:467:ARG:HH21	2:B:471:LEU:HD11	1.46	0.79
2:B:502:ASN:HB3	2:B:506:GLU:HG2	1.71	0.71
1:C:75:LYS:HG2	1:C:77:PHE:H	1.56	0.71
2:D:376:VAL:HG11	2:D:380:LEU:HB3	1.75	0.69
2:B:213:ALA:HB2	2:B:223:TRP:HE1	1.58	0.69
1:A:111:GLU:O	1:A:112:LYS:HG2	1.94	0.68
1:C:442:ASP:OD2	1:C:498:ARG:NH2	2.27	0.68
2:B:182:ARG:HA	2:B:182:ARG:HH11	1.59	0.68
2:B:502:ASN:HA	2:B:505:LEU:HB2	1.76	0.67
2:B:344:GLN:HA	2:B:347:LEU:HB3	1.77	0.66
2:D:401:LEU:HB2	2:D:404:GLU:HG3	1.77	0.66
1:A:398:ARG:NH2	1:A:412:GLU:OE2	2.29	0.65
1:C:449:GLY:HA3	1:C:494:SER:HB3	1.79	0.65
2:D:78:GLU:OE2	2:D:157:TYR:OH	2.14	0.64
2:B:411:ILE:HG12	2:B:438:ILE:HG12	1.79	0.64
2:D:333:LYS:HE3	2:D:341:LEU:HD13	1.79	0.63
2:B:406:PRO:HG3	2:B:450:GLN:HG2	1.81	0.63
2:B:497:ASP:HA	2:B:500:MET:HE2	1.82	0.62
1:C:404:ALA:HB1	1:C:472:MET:HE2	1.82	0.61
2:D:213:ALA:HB2	2:D:223:TRP:HE1	1.65	0.61
1:A:176:ILE:HD12	1:A:196:LEU:HD21	1.81	0.61
1:A:257:ASP:O	1:A:299:ASN:ND2	2.35	0.59
2:B:60:TRP:HH2	2:B:103:ASP:HA	1.68	0.59
1:C:239:HIS:HA	1:C:280:MET:HE1	1.83	0.59
2:D:296:THR:HG23	2:D:300:ARG:HH21	1.68	0.59
2:D:379:ASP:OD1	2:D:380:LEU:N	2.35	0.59
2:B:456:THR:OG1	2:B:460:CYS:SG	2.60	0.58
2:B:70:TYR:OH	2:B:92:THR:OG1	2.21	0.58
1:A:390:SER:O	1:A:394:GLN:HG2	2.03	0.58
2:D:341:LEU:HD11	2:D:392:TYR:HB2	1.85	0.58
2:B:70:TYR:HH	2:B:92:THR:HG1	1.53	0.57
1:C:181:LYS:HB2	1:C:186:ASP:HA	1.86	0.56
2:D:213:ALA:HB2	2:D:223:TRP:NE1	2.21	0.56
2:D:419:LEU:HB3	2:D:431:ARG:HB2	1.87	0.56
2:B:323:GLN:HG2	2:B:327:LEU:HD13	1.89	0.55
1:C:414:LEU:HD21	1:C:507:MET:HG2	1.89	0.55
1:C:75:LYS:HD3	1:C:77:PHE:HB2	1.89	0.55
1:C:356:ASP:OD1	1:C:357:THR:N	2.40	0.55
2:D:427:GLU:OE2	2:D:455:ARG:NH1	2.39	0.54
2:B:339:GLU:HB2	1:C:351:LYS:HD3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:439:ILE:HD12	2:B:454:VAL:HG21	1.90	0.53
2:B:350:LEU:O	2:B:355:ARG:NH2	2.41	0.53
2:B:505:LEU:O	2:B:509:ASN:N	2.42	0.53
1:A:449:GLY:HA3	1:A:494:SER:HB3	1.90	0.53
1:C:372:THR:HG21	1:C:428:PRO:HG3	1.90	0.53
1:A:429:PRO:HB3	1:A:492:ARG:HA	1.91	0.53
1:C:83:ASP:OD1	1:C:84:ARG:N	2.41	0.53
2:D:344:GLN:O	2:D:348:ASP:N	2.43	0.51
1:C:433:ILE:HG13	1:C:488:VAL:HG13	1.92	0.51
1:A:453:ILE:H	1:A:465:ALA:HB1	1.76	0.51
2:D:181:ASP:OD1	2:D:182:ARG:N	2.43	0.50
2:B:213:ALA:HB2	2:B:223:TRP:NE1	2.24	0.50
1:A:430:LYS:O	1:A:431:MET:HE2	2.12	0.50
1:C:111:GLU:HG2	1:C:112:LYS:N	2.26	0.50
2:D:75:SER:OG	2:D:76:PRO:HD3	2.11	0.50
1:C:451:VAL:O	1:C:491:ARG:NH2	2.45	0.49
2:D:185:ASN:OD1	2:D:186:TYR:N	2.46	0.49
2:D:299:THR:O	2:D:303:ARG:HG3	2.13	0.49
1:A:289:THR:HA	2:B:254:VAL:HG22	1.94	0.48
1:A:345:ILE:HD11	1:A:366:MET:HE3	1.94	0.48
1:C:249:ALA:HB2	1:C:259:TRP:HE1	1.78	0.48
2:B:75:SER:OG	2:B:76:PRO:HD3	2.14	0.48
2:B:182:ARG:HA	2:B:182:ARG:NH1	2.26	0.48
1:C:266:ASP:N	1:C:266:ASP:OD1	2.45	0.48
2:D:100:PHE:O	2:D:104:ILE:HG13	2.14	0.47
2:D:139:ASP:OD2	2:D:169:ARG:NH2	2.47	0.47
1:A:290:VAL:HG22	2:D:253:THR:HA	1.95	0.47
2:B:216:ASN:OD1	2:B:217:SER:N	2.48	0.47
2:B:359:SER:HB3	2:B:385:VAL:HG12	1.96	0.47
1:C:126:ASP:OD1	1:C:173:THR:OG1	2.33	0.47
2:B:319:PRO:HB2	2:B:322:LEU:HD13	1.96	0.47
2:B:401:LEU:HG	2:B:402:GLN:H	1.79	0.46
1:A:349:THR:HG21	1:A:359:ARG:HG3	1.97	0.46
2:D:216:ASN:OD1	2:D:217:SER:N	2.49	0.46
1:A:224:VAL:O	1:A:228:ILE:HG13	2.16	0.46
1:A:432:GLU:HG3	1:A:489:ARG:HG2	1.98	0.46
1:C:217:ASP:OD1	1:C:218:ALA:N	2.49	0.46
2:D:319:PRO:HD2	2:D:322:LEU:HD12	1.98	0.46
2:B:78:GLU:OE1	2:B:161:ASN:ND2	2.49	0.45
2:B:253:THR:HA	1:C:290:VAL:HG22	1.98	0.45
2:D:354:ILE:O	2:D:358:ILE:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:458:ARG:HG2	2:B:459:LEU:H	1.80	0.45
1:A:284:ILE:HD12	2:D:271:ILE:HG23	1.98	0.45
1:A:461:GLU:HG2	1:A:463:VAL:HG13	1.98	0.45
2:D:496:ASN:CG	2:D:498:PRO:HD2	2.42	0.45
1:A:214:LEU:HB3	1:A:225:ILE:HD13	1.98	0.44
1:C:224:VAL:O	1:C:228:ILE:HG13	2.17	0.44
1:A:521:ALA:O	1:A:524:MET:HG3	2.17	0.44
2:B:403:ASN:OD1	2:B:449:PRO:HB2	2.17	0.44
2:D:187:PHE:CD1	2:D:291:LEU:HD11	2.52	0.44
2:D:439:ILE:HG21	2:D:454:VAL:HG21	1.98	0.44
2:B:244:MET:O	2:B:248:ILE:HG13	2.18	0.44
1:A:137:PHE:HE1	1:A:160:TYR:HD2	1.64	0.44
1:A:249:ALA:HB2	1:A:259:TRP:HE1	1.83	0.44
1:A:453:ILE:H	1:A:465:ALA:CB	2.30	0.44
1:C:442:ASP:OD1	1:C:442:ASP:N	2.49	0.43
1:A:93:LEU:O	1:A:97:VAL:HG23	2.18	0.43
1:C:289:THR:HA	2:D:254:VAL:HG22	1.99	0.43
2:D:100:PHE:CE2	2:D:167:ARG:HD3	2.53	0.43
2:D:70:TYR:OH	2:D:92:THR:OG1	2.25	0.43
1:C:429:PRO:HB3	1:C:492:ARG:HA	2.00	0.43
1:C:146:THR:HG23	2:D:458:ARG:HG3	2.01	0.43
1:C:380:VAL:HG23	1:C:381:LEU:HD12	2.01	0.43
1:A:83:ASP:OD1	1:A:84:ARG:N	2.47	0.43
1:C:111:GLU:O	1:C:112:LYS:HG2	2.17	0.43
2:B:258:ASP:OD1	2:B:258:ASP:N	2.49	0.43
1:C:142:LEU:HD23	1:C:143:ASP:O	2.19	0.43
1:C:414:LEU:HD11	1:C:507:MET:HG3	2.00	0.43
1:C:133:ILE:O	1:C:136:THR:HG22	2.19	0.42
1:A:143:ASP:OD1	1:A:144:ASN:N	2.46	0.42
1:C:303:LYS:O	1:C:307:MET:HG3	2.18	0.42
1:C:404:ALA:HB3	1:C:407:PHE:HB2	2.01	0.42
1:A:451:VAL:HG12	1:A:490:THR:HG22	2.00	0.42
2:B:350:LEU:HD23	2:B:354:ILE:HG21	2.00	0.42
2:B:494:GLU:OE2	2:B:497:ASP:HB2	2.20	0.42
1:C:491:ARG:HG2	1:C:492:ARG:HG3	2.00	0.42
2:B:369:LYS:HE2	2:B:369:LYS:HB2	1.86	0.42
1:A:141:TYR:HE1	1:A:156:ILE:HG22	1.84	0.42
1:C:276:TYR:HE1	1:C:280:MET:HE3	1.84	0.42
2:B:299:THR:O	2:B:303:ARG:HG3	2.20	0.41
1:A:181:LYS:HE2	1:A:188:GLY:HA2	2.02	0.41
1:A:154:LYS:HB2	1:A:154:LYS:HE2	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:GLU:N	1:A:461:GLU:OE1	2.54	0.41
2:B:336:THR:HG22	2:B:336:THR:O	2.21	0.41
1:A:426:TYR:CE1	1:A:495:GLN:HB2	2.56	0.41
1:C:245:LEU:HD12	1:C:245:LEU:HA	1.88	0.41
1:A:338:MET:O	1:A:342:ILE:HG12	2.21	0.41
2:D:59:ILE:HD13	2:D:59:ILE:HA	1.94	0.41
2:D:343:GLN:O	2:D:346:THR:OG1	2.27	0.41
2:B:178:LEU:HD12	2:B:178:LEU:O	2.21	0.41
2:B:347:LEU:HD12	2:B:350:LEU:HD13	2.03	0.41
2:D:428:SER:HB2	2:D:430:VAL:HG13	2.03	0.41
1:A:288:THR:O	1:A:289:THR:OG1	2.35	0.41
2:B:190:ARG:O	2:B:194:LEU:HG	2.21	0.41
1:C:276:TYR:CE1	1:C:280:MET:HE3	2.56	0.41
1:C:299:ASN:HB2	1:C:302:GLU:HG2	2.03	0.41
1:C:485:PRO:HG2	1:C:486:PHE:CD2	2.56	0.40
2:D:384:LEU:HD21	2:D:470:PHE:HE1	1.86	0.40
2:D:371:TYR:OH	2:D:491:HIS:HB3	2.21	0.40
1:C:447:VAL:O	1:C:469:PRO:HB3	2.22	0.40
2:D:230:ASN:OD1	2:D:230:ASN:N	2.54	0.40
2:D:438:ILE:O	2:D:439:ILE:HD13	2.21	0.40
2:B:343:GLN:O	2:B:347:LEU:N	2.54	0.40
1:C:466:LYS:HG2	1:C:491:ARG:NH1	2.36	0.40
2:D:363:PHE:HE1	2:D:413:VAL:HG21	1.87	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	474/662 (72%)	445 (94%)	29 (6%)	0	100	100
1	C	474/662 (72%)	452 (95%)	22 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	454/857 (53%)	435 (96%)	19 (4%)	0	100	100
2	D	454/857 (53%)	428 (94%)	26 (6%)	0	100	100
All	All	1856/3038 (61%)	1760 (95%)	96 (5%)	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	409/584 (70%)	409 (100%)	0	100	100
1	C	409/584 (70%)	409 (100%)	0	100	100
2	B	393/747 (53%)	393 (100%)	0	100	100
2	D	393/747 (53%)	393 (100%)	0	100	100
All	All	1604/2662 (60%)	1604 (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 (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	299	ASN
2	B	94	ASN
2	B	311	ASN
2	B	325	GLN
2	B	502	ASN
2	D	161	ASN
2	D	227	ASN
2	D	343	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](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

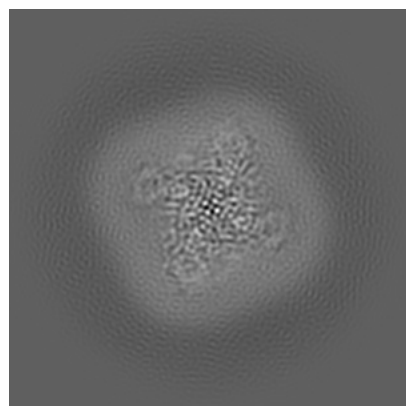
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33467. These allow visual inspection of the internal detail of the map and identification of artifacts.

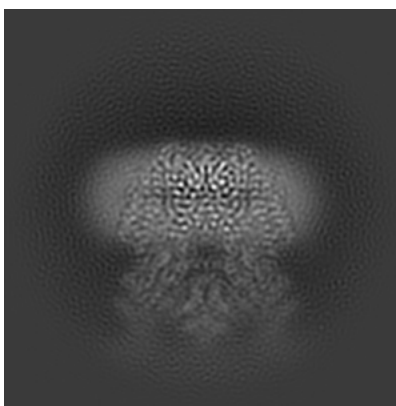
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

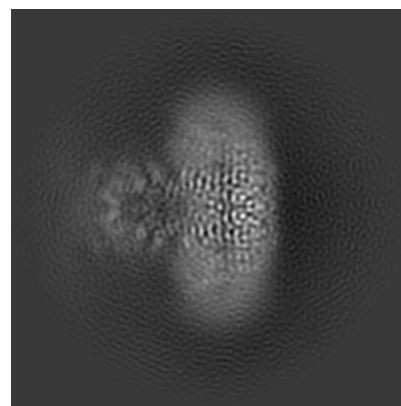
6.1.1 Primary map



X

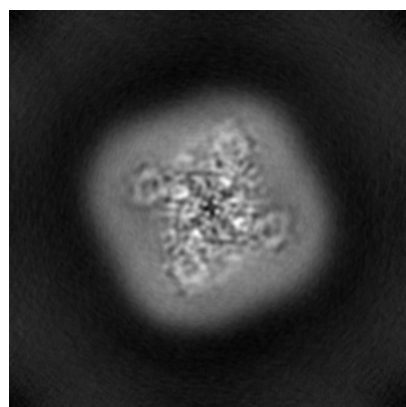


Y

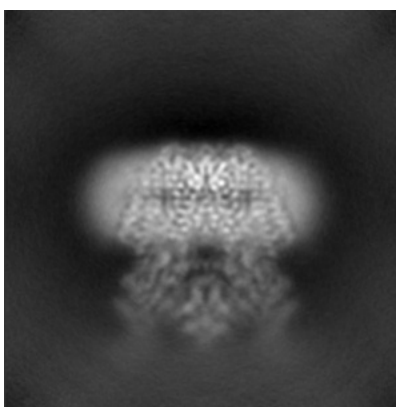


Z

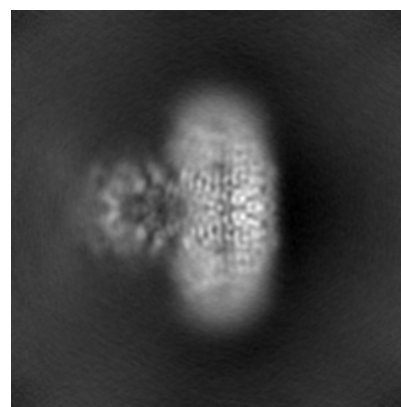
6.1.2 Raw map



X



Y

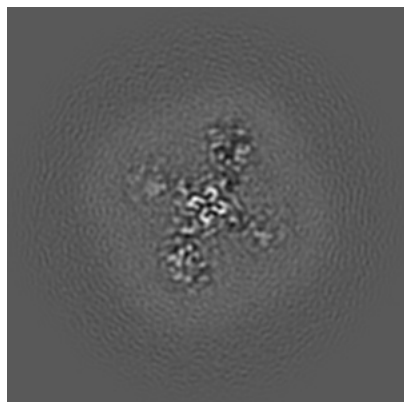


Z

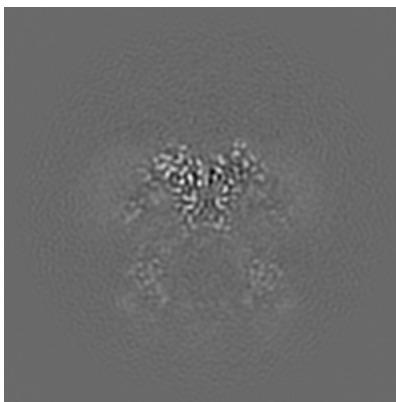
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

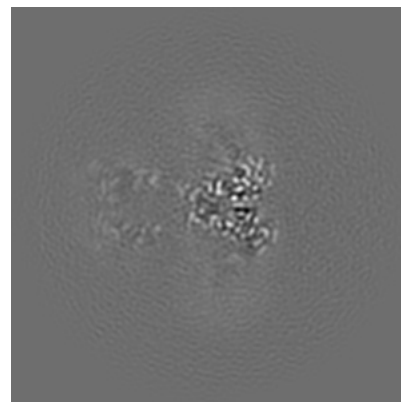
6.2.1 Primary map



X Index: 140

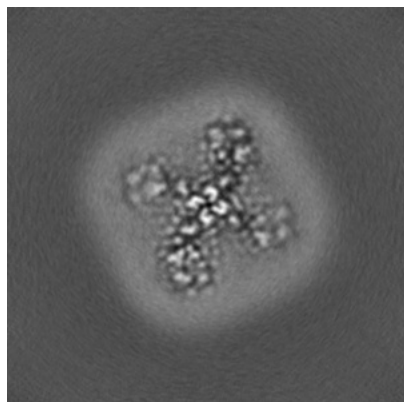


Y Index: 140

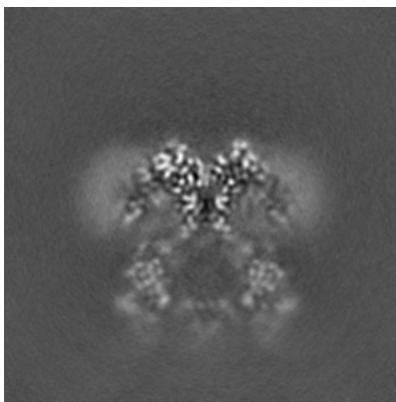


Z Index: 140

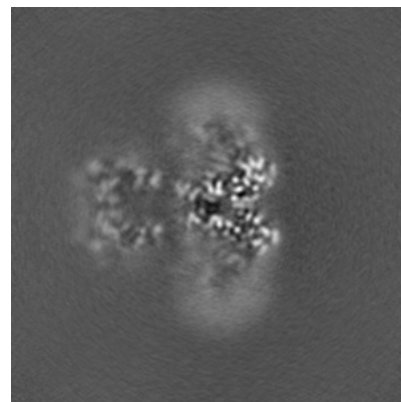
6.2.2 Raw map



X Index: 140



Y Index: 140

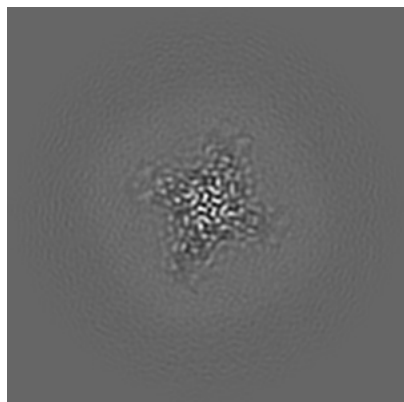


Z Index: 140

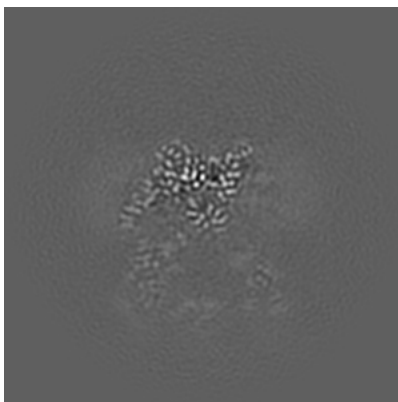
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

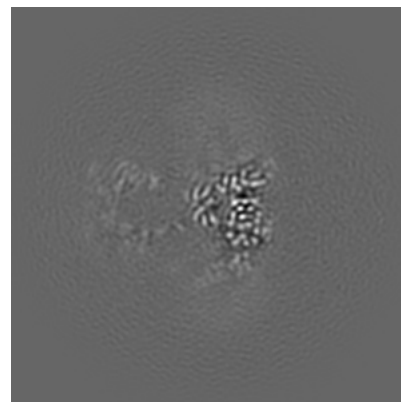
6.3.1 Primary map



X Index: 160

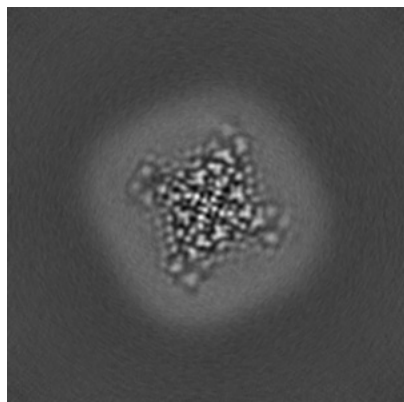


Y Index: 135

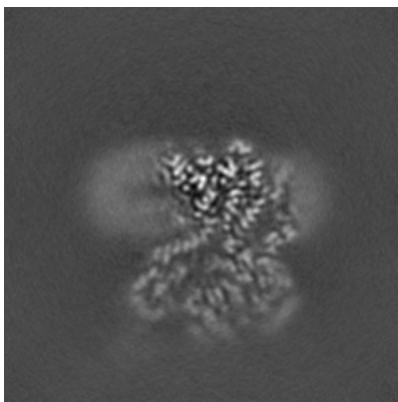


Z Index: 146

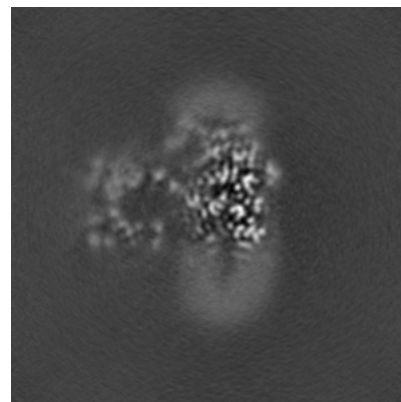
6.3.2 Raw map



X Index: 162



Y Index: 152

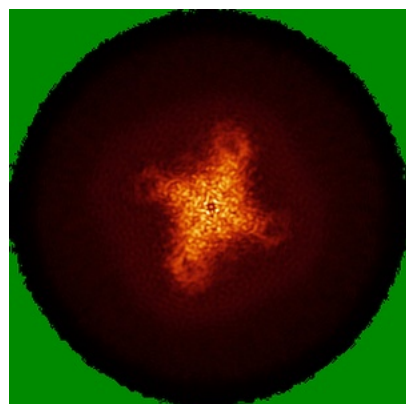


Z Index: 131

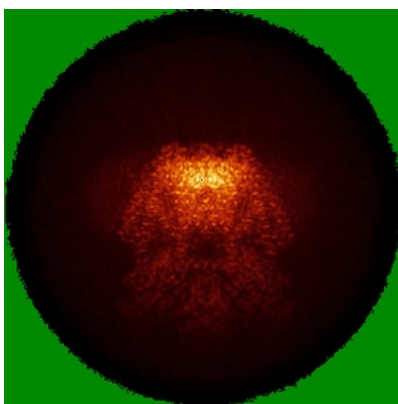
The images above show the largest variance slices of the map in three orthogonal directions.

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

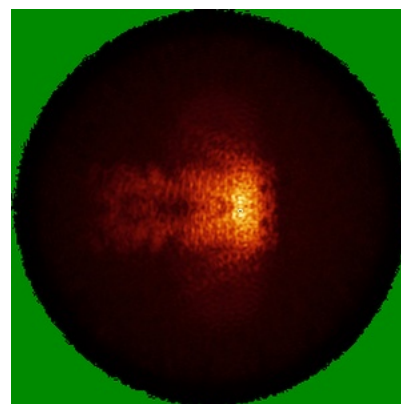
6.4.1 Primary map



X

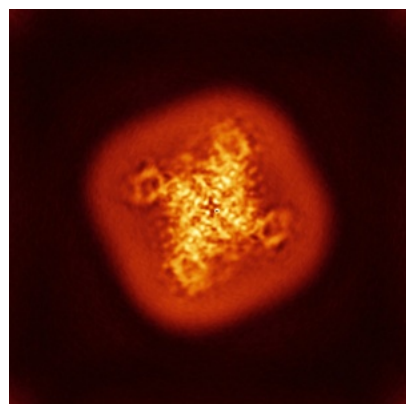


Y

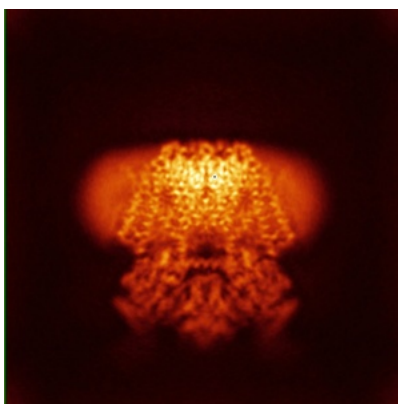


Z

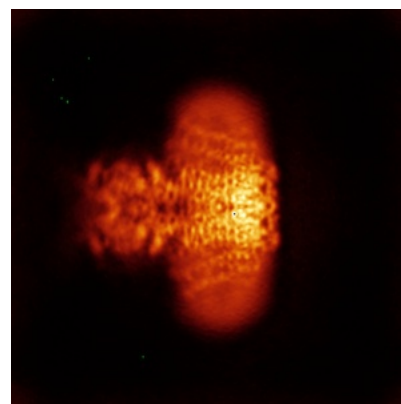
6.4.2 Raw map



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

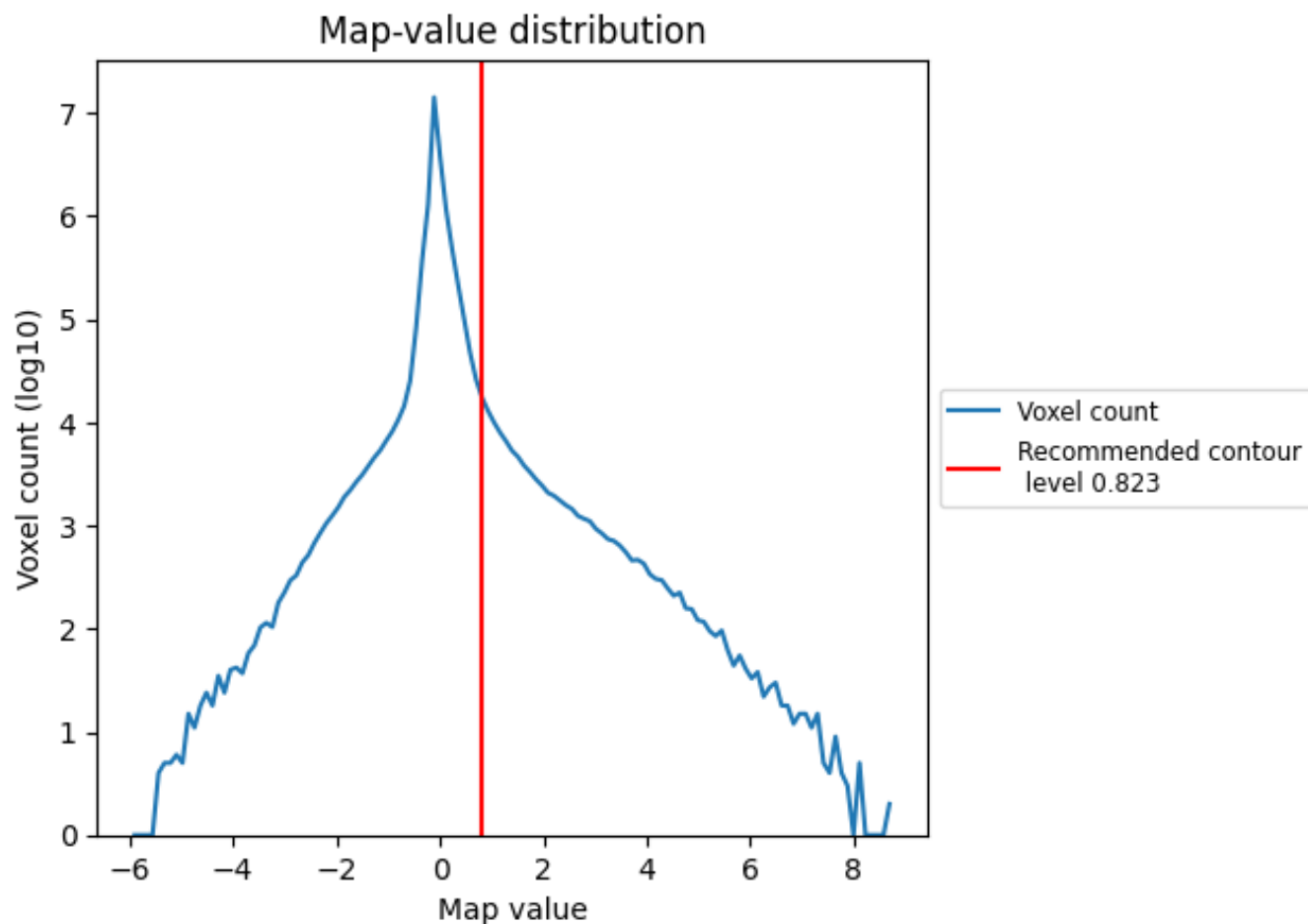
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

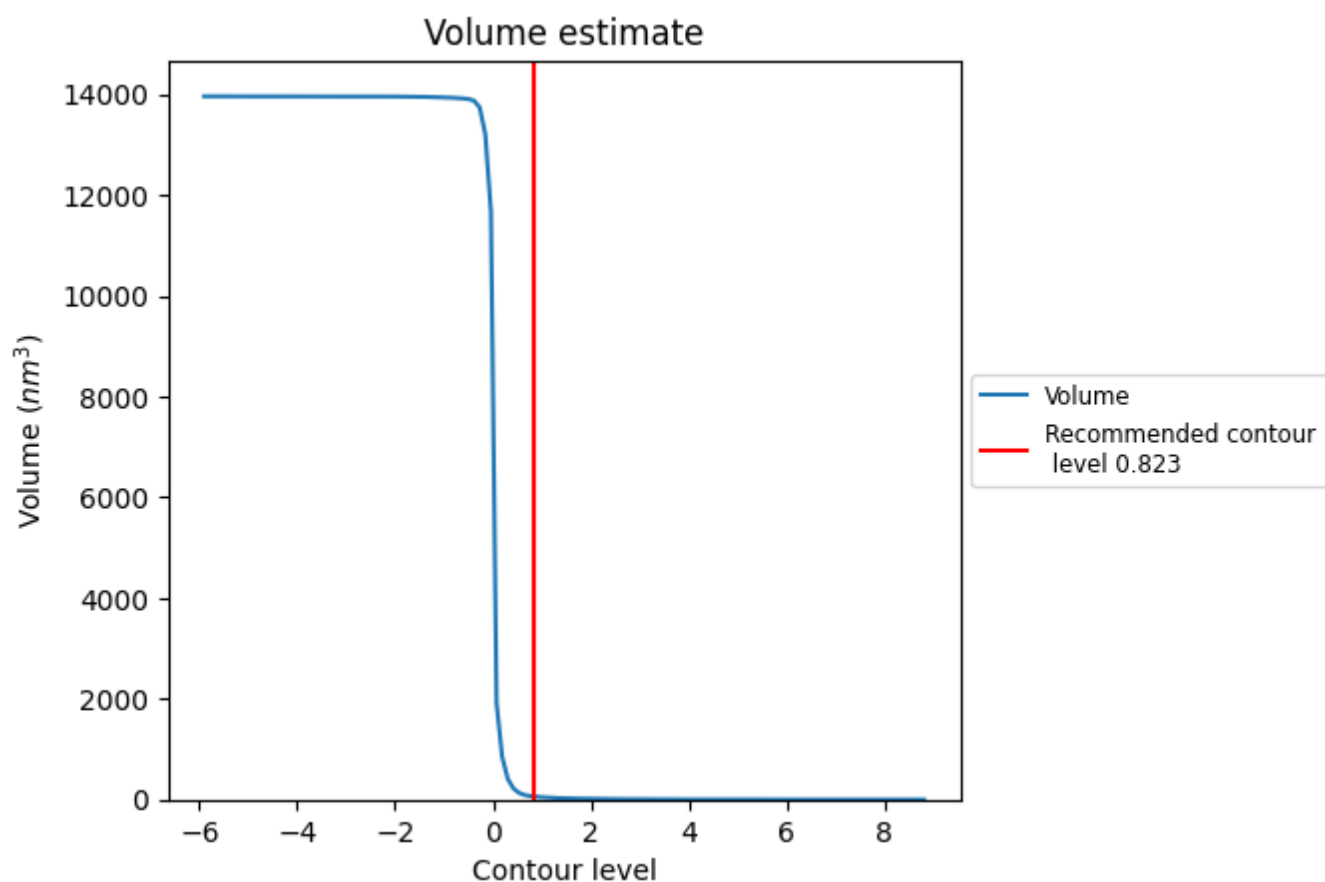
This section contains the results of statistical analysis of the map.

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.

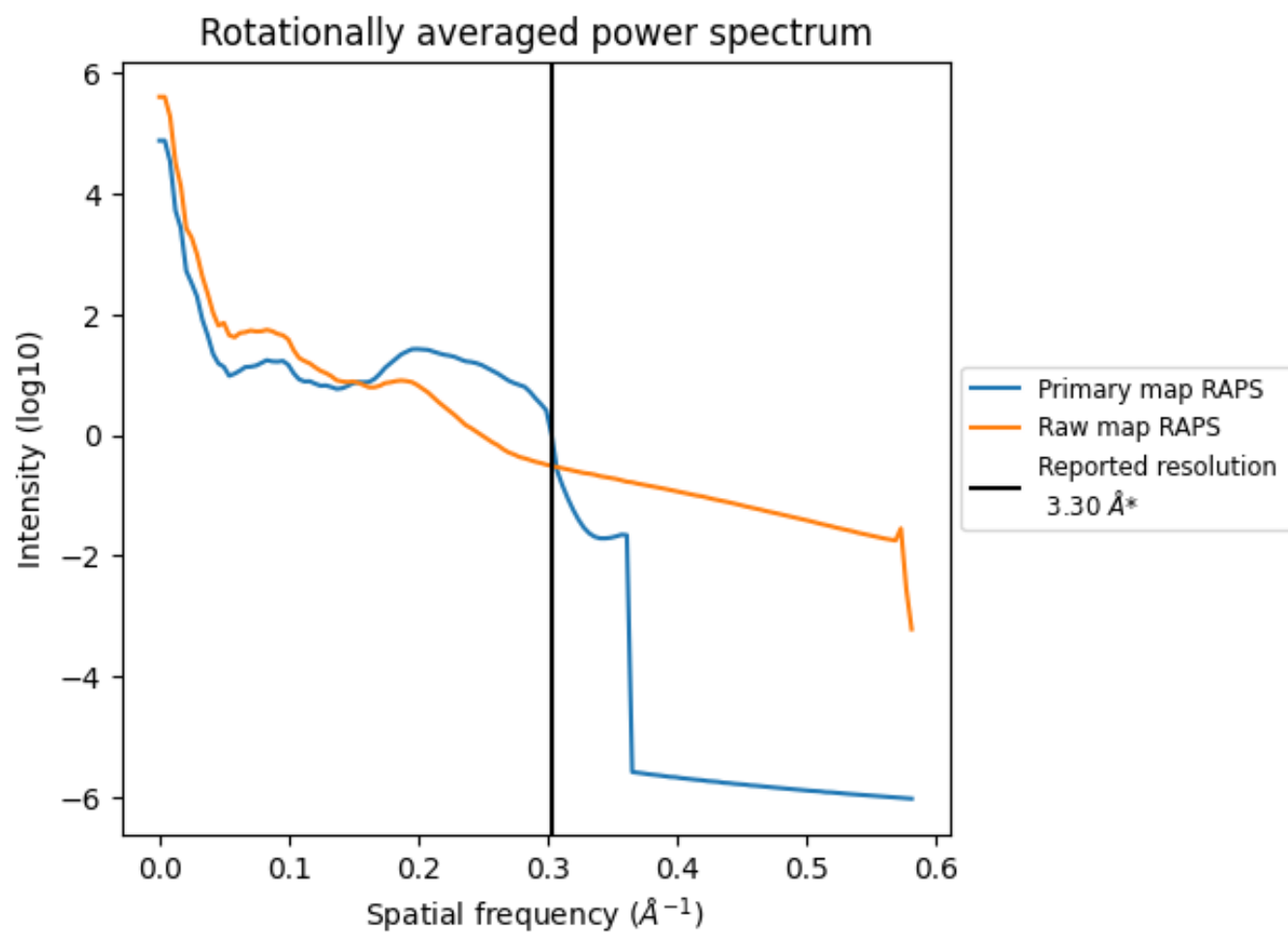
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 62 nm³; this corresponds to an approximate mass of 56 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 ⓘ

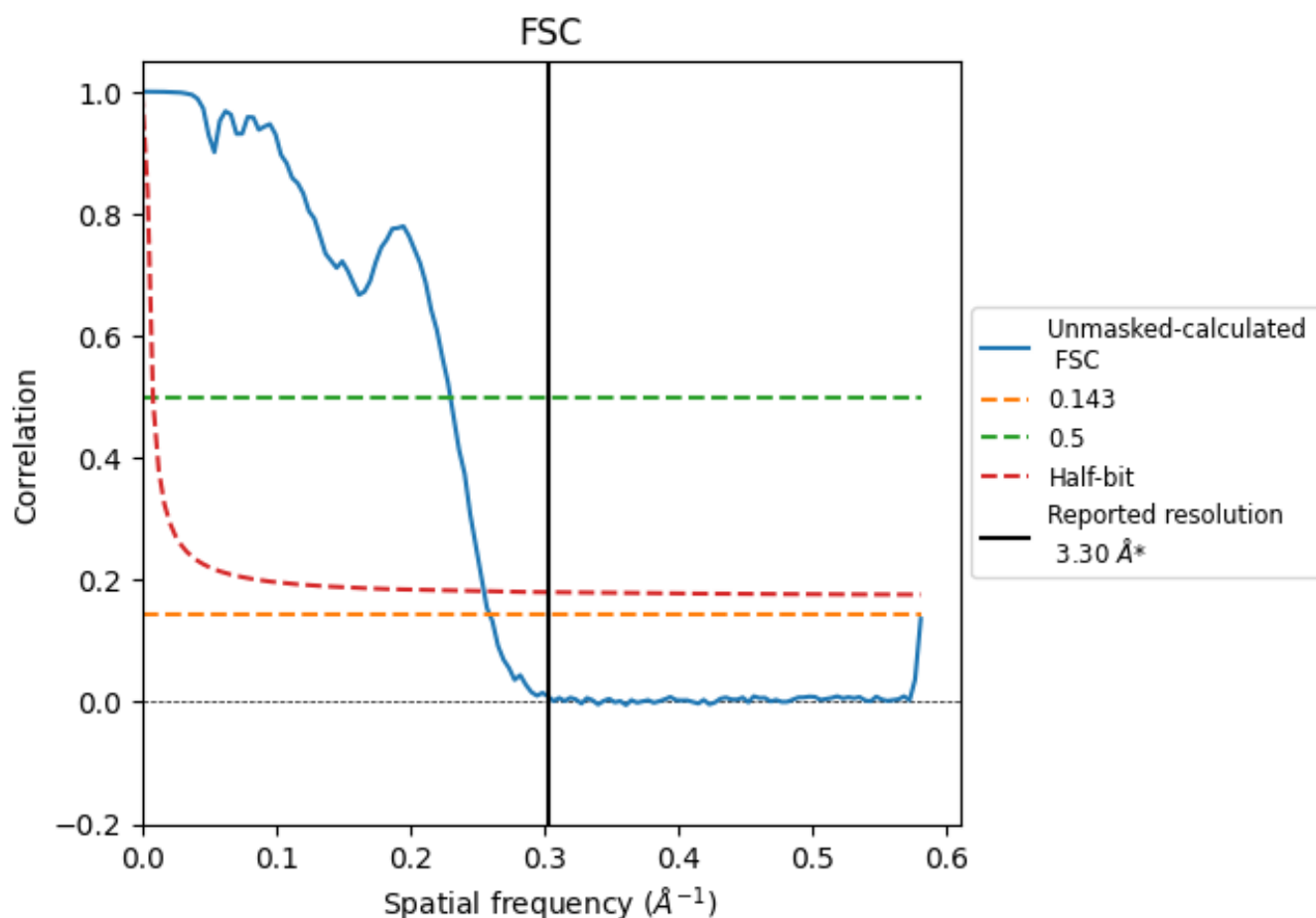


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.85	4.34	3.92

*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 3.85 differs from the reported value 3.3 by more than 10 %

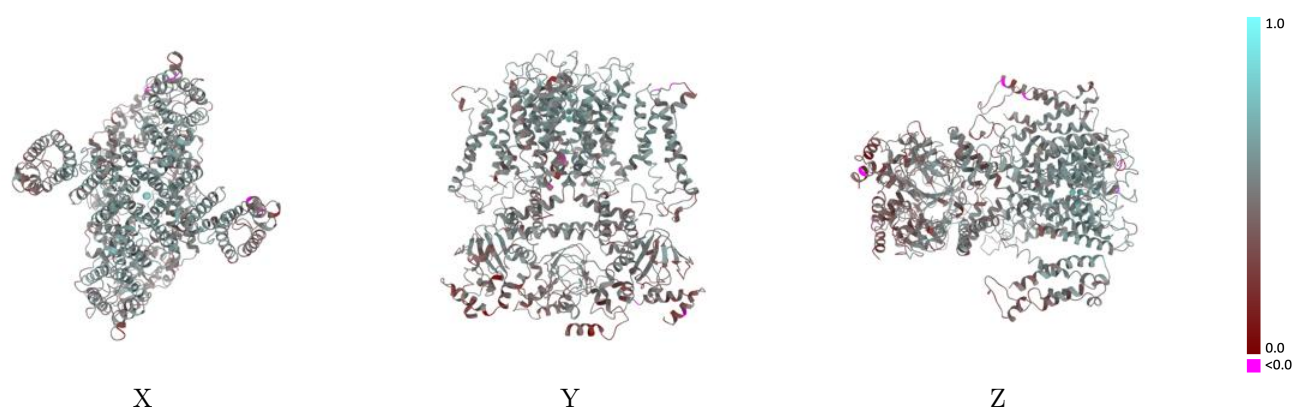
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-33467 and PDB model 7XUF. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

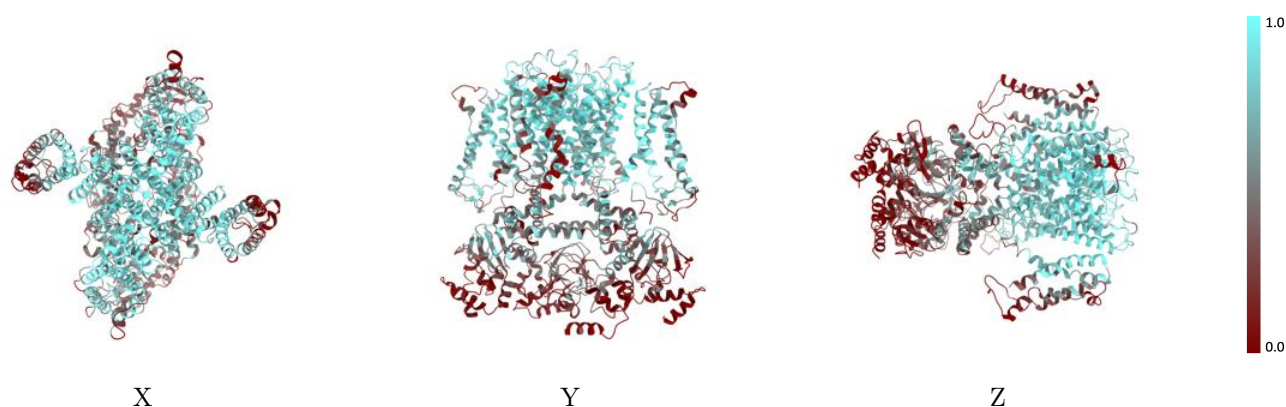
This section was not generated.

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



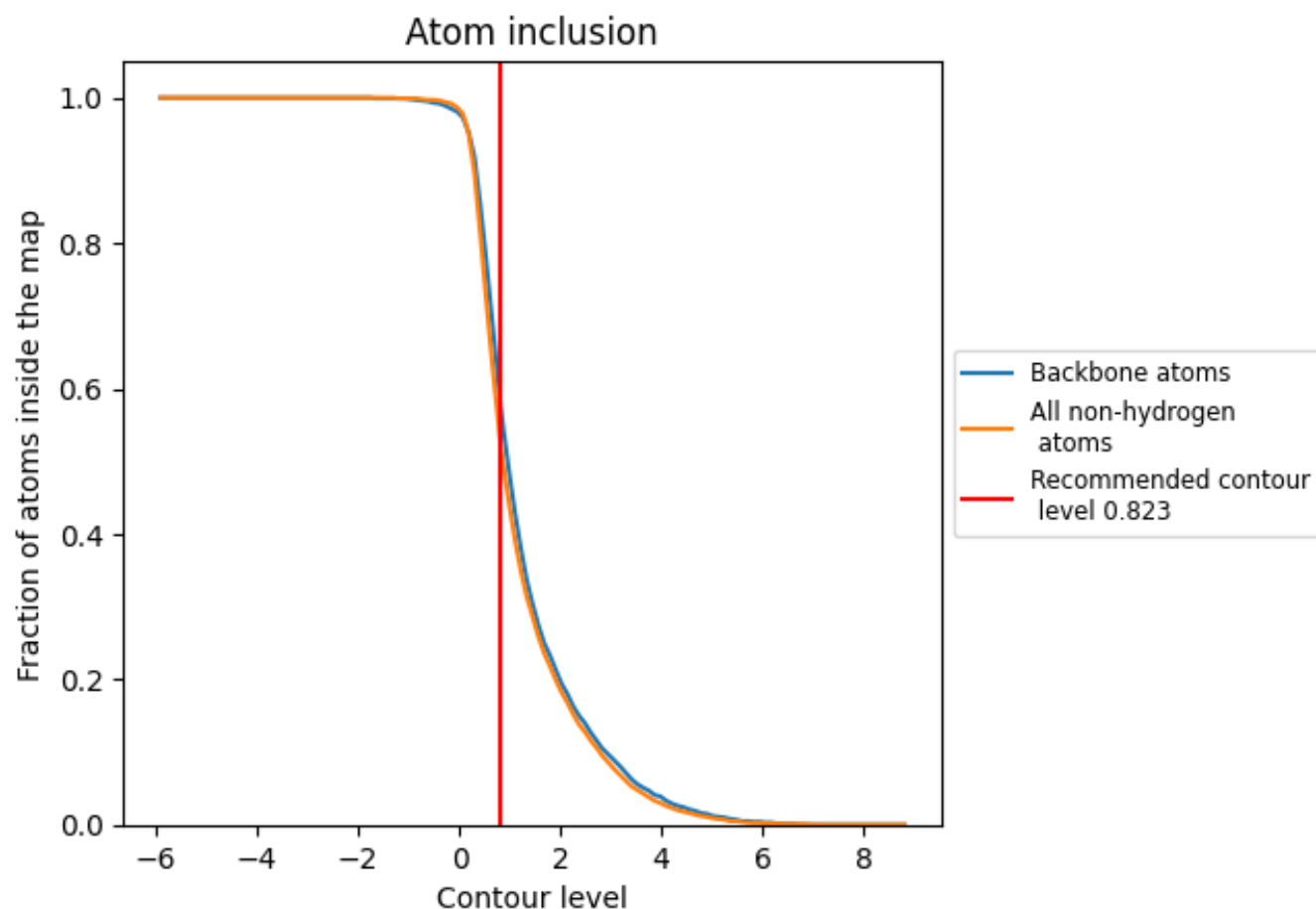
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.823).

9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 52% 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 (0.823) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5220	0.4750
A	0.5760	0.4900
B	0.4720	0.4560
C	0.5680	0.4920
D	0.4680	0.4620

