



wwPDB EM Validation Summary Report ⓘ

Jul 8, 2026 – 04:19 PM JST

PDB ID : 9X0C / pdb_00009x0c
EMDB ID : EMD-66432
Title : Cryo-EM structure of AKT5 - D403A
Authors : Muraoka, Y.; Tanaka, Y.; Yokoyama, T.; Furuta, T.; Yamanashi, T.; Tsujii, M.; Tsubota, R.; Uozumi, N.
Deposited on : 2025-09-30
Resolution : 2.60 Å(reported)

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

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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.dev133
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) : 2.50

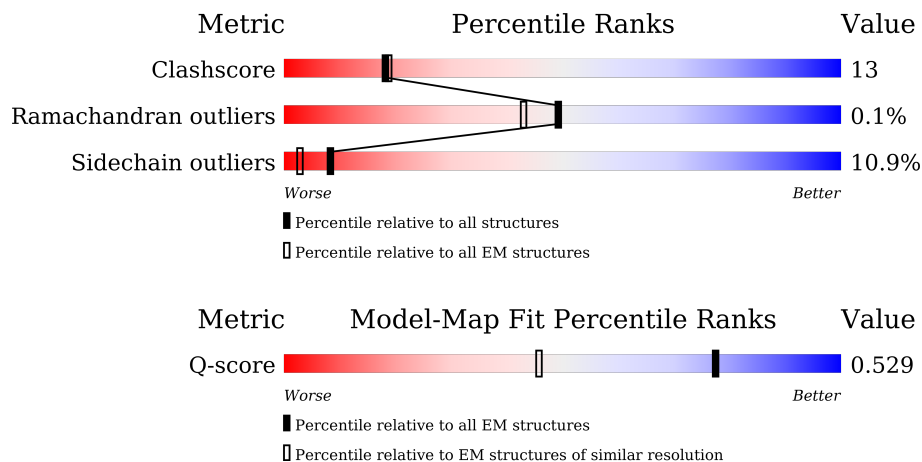
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 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	8728 (2.10 - 3.10)

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	894	9% 32% 15% • 50%
1	B	894	8% 33% 15% • 50%
1	C	894	8% 34% 14% • 50%
1	D	894	9% 34% 15% • 50%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14592 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 Probable potassium channel AKT5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	449	Total	C	N	O	S	0	0
			3648	2384	613	635	16		
1	C	449	Total	C	N	O	S	0	0
			3648	2384	613	635	16		
1	A	449	Total	C	N	O	S	0	0
			3648	2384	613	635	16		
1	D	449	Total	C	N	O	S	0	0
			3648	2384	613	635	16		

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-7	MET	-	initiating methionine	UNP Q9SCX5
B	-6	ASP	-	expression tag	UNP Q9SCX5
B	-5	TYR	-	expression tag	UNP Q9SCX5
B	-4	LYS	-	expression tag	UNP Q9SCX5
B	-3	ASP	-	expression tag	UNP Q9SCX5
B	-2	ASP	-	expression tag	UNP Q9SCX5
B	-1	ASP	-	expression tag	UNP Q9SCX5
B	0	ASP	-	expression tag	UNP Q9SCX5
B	1	LYS	-	expression tag	UNP Q9SCX5
B	403	ALA	ASP	engineered mutation	UNP Q9SCX5
B	881	HIS	-	expression tag	UNP Q9SCX5
B	882	HIS	-	expression tag	UNP Q9SCX5
B	883	HIS	-	expression tag	UNP Q9SCX5
B	884	HIS	-	expression tag	UNP Q9SCX5
B	885	HIS	-	expression tag	UNP Q9SCX5
B	886	HIS	-	expression tag	UNP Q9SCX5
C	-7	MET	-	initiating methionine	UNP Q9SCX5
C	-6	ASP	-	expression tag	UNP Q9SCX5
C	-5	TYR	-	expression tag	UNP Q9SCX5
C	-4	LYS	-	expression tag	UNP Q9SCX5
C	-3	ASP	-	expression tag	UNP Q9SCX5
C	-2	ASP	-	expression tag	UNP Q9SCX5

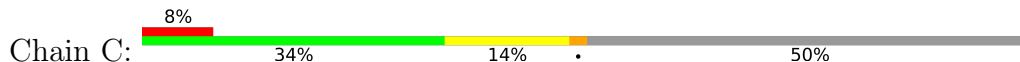
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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	ASP	-	expression tag	UNP Q9SCX5
C	0	ASP	-	expression tag	UNP Q9SCX5
C	1	LYS	-	expression tag	UNP Q9SCX5
C	403	ALA	ASP	engineered mutation	UNP Q9SCX5
C	881	HIS	-	expression tag	UNP Q9SCX5
C	882	HIS	-	expression tag	UNP Q9SCX5
C	883	HIS	-	expression tag	UNP Q9SCX5
C	884	HIS	-	expression tag	UNP Q9SCX5
C	885	HIS	-	expression tag	UNP Q9SCX5
C	886	HIS	-	expression tag	UNP Q9SCX5
A	-7	MET	-	initiating methionine	UNP Q9SCX5
A	-6	ASP	-	expression tag	UNP Q9SCX5
A	-5	TYR	-	expression tag	UNP Q9SCX5
A	-4	LYS	-	expression tag	UNP Q9SCX5
A	-3	ASP	-	expression tag	UNP Q9SCX5
A	-2	ASP	-	expression tag	UNP Q9SCX5
A	-1	ASP	-	expression tag	UNP Q9SCX5
A	0	ASP	-	expression tag	UNP Q9SCX5
A	1	LYS	-	expression tag	UNP Q9SCX5
A	403	ALA	ASP	engineered mutation	UNP Q9SCX5
A	881	HIS	-	expression tag	UNP Q9SCX5
A	882	HIS	-	expression tag	UNP Q9SCX5
A	883	HIS	-	expression tag	UNP Q9SCX5
A	884	HIS	-	expression tag	UNP Q9SCX5
A	885	HIS	-	expression tag	UNP Q9SCX5
A	886	HIS	-	expression tag	UNP Q9SCX5
D	-7	MET	-	initiating methionine	UNP Q9SCX5
D	-6	ASP	-	expression tag	UNP Q9SCX5
D	-5	TYR	-	expression tag	UNP Q9SCX5
D	-4	LYS	-	expression tag	UNP Q9SCX5
D	-3	ASP	-	expression tag	UNP Q9SCX5
D	-2	ASP	-	expression tag	UNP Q9SCX5
D	-1	ASP	-	expression tag	UNP Q9SCX5
D	0	ASP	-	expression tag	UNP Q9SCX5
D	1	LYS	-	expression tag	UNP Q9SCX5
D	403	ALA	ASP	engineered mutation	UNP Q9SCX5
D	881	HIS	-	expression tag	UNP Q9SCX5
D	882	HIS	-	expression tag	UNP Q9SCX5
D	883	HIS	-	expression tag	UNP Q9SCX5
D	884	HIS	-	expression tag	UNP Q9SCX5
D	885	HIS	-	expression tag	UNP Q9SCX5
D	886	HIS	-	expression tag	UNP Q9SCX5

[illegible]

- Molecule 1: Probable potassium channel AKT5



MET	ASP	TYR	LYS	ASP	ASP	ASP	ASP	LYS	GLY	ILE	GLU	GLY	LYS	ARG	LYS	LYS	LYS	MET	VAL	TRP	PHE	PRO	PRO	GLU	GLY	VAL	ILE	LYS	GLU	ALA	ALA	GLU	GLY	THR	MET	SER	SER	HIS	TYR	SER	PHE	SER	SER	LYS	GLY	LEU	LEU	PRO	PRO	PRO	LEU
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D135	K136	A137	T138	Y139	L140	L141	V142	D143	D144	P145	K146	R147	W150	R151	Y152	T153	S154	T155	W156	I157	I158	F159	D160	V161	V162	V165	E168	L169	F170	G171	S172	L103	Q104	T105	P106	R107	A108	P109	L113	D114	N115	N118	A122	I125	T128	L134			
Y208	L219	S222	W245	F247	E252	Q257	L260	I272	S276	T277	T278	G279	N286	E289	E290	I294	W298	L305	N311	V316	V317	H318	D392	K393	T394	Y395	S321	R322	T323	R324	N325	F326	R327	D328	Q331	A332	F336	A337	Q338	R339	N340	N341	E203	K204	D205	R206	R207		
L344	G345	L346	Q347	E348	H353	L354	S355	L356	R357	Y358	R359	T360	D361	S362	E363	G364	L365	Q366	Q367	Q368	E369	I370	I371	P375	I378	I382	E389	V390	S391	D392	K393	T394	Y395	L396	F397	H398	G399	I400	L405	V409	S410	E411	Y416	E421	L425	R426	N427	E428	
D432	F433	Y434	I435	M436	A440	V441	D442	R446	V447	M448	G449	V450	V453	Q458	E465	V466	Q467	V468	V478	K481	R482	L483	S484	L487	R488	L489	M490	R491	L497	V498	Q499	D504	G505	A506	I507	N510	D518	SER	THR	ASP	PRO	VAL	MET	LYS	GLY	ILE			
GLY	VAL	GLY	ALA	THR	ALA	ARG	SER	SER	ARG	HIS	ILE	LYS	LEU	ARG	CYS	PHE	I70	V71	S72	P73	F74	R77	Y78	R79	A80	W81	D82	W83	F84	L85	L88	S96	P97	F102	L103	Q104	T105	P106	R107	A108	P109	L113	D114	N115	N118	A122	I125	T128	L134

LEU ALA GLU GLU THR GLU LEU LEU MET LEU LEU ALA ALA GLN GLY LYS MET ASP ASP LEU LEU PRO PRO SER SER LEU LEU CYS CYS PHE ALA ALA ALA ALA ARG GLY GLY ASP ASP ASP LEU LEU LEU LEU HIS HIS GLN GLN LEU LEU LEU LEU LYS ARG ARG GLY GLY THR THR ASP ASP LYS LYS ASN ASN ASN ASN GLY ARG ARG THR THR ALA ALA ALA ALA HIS HIS LLE LLE ALA ALA SER SER LYS LYS GLY GLY

GLN	CYS	TYR	VAL	LEU	LEU	HIS	GLY	ALA	ASP	PRO	ASN	ILE	ARG	ASP	SER	GLU	GLY	SER	PRO	TRP	GLU	ALA	ILE	ILE	GLY	ARG	HIS	GLU	GLU	ASN	ALA	LYS	LEU	LEU	LEU	SER	LEU	SER	GLU	ASN	GLY	GLY	ALA	THR	VAL	THR	ASP	PHE	THR	TYR	GLY	SER	CYS	LEU	ALA	VAL	ASP	GLN
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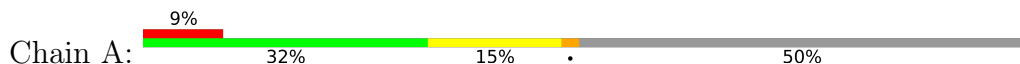
GLY GLN ASN ASP LEU ALA LEU LYS ASP ILE VAL LYS TYR GLY SER ILE LEU THR HIS ARG ALA VAL SER GLY ASN THR THR LEU ASP VAL ASP LEU LEU LEU ILE VAL GLN PHE LEU LEU LEU LYS GLY ALA ASP MET ASP LYS PRO ASP VAL TYR GLY TRP TRP

[illegible]

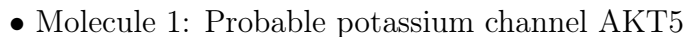
ALA ARG ALA VAL GLN ARG ARG LYS LEU SER ASN PHE LYS ASN SER LEU PHE GLY ILE MET NET ASP GLY GLY ALA THR LYS THR THR THR GLY ILE SER GLY VAL VAL GLY VAL TYR PRO ALA ARG VAL THR ILE SER GLY GLU ALA SER SER SER

[illegible]

- Molecule 1: Probable potassium channel AKT5



MET	ASP	TYR	LYS	ASP	ASP	ASP	ASP	LYS	GLY	ILE	GLU	LYS	ARG	LYS	LYS	LYS	MET	VAL	TRP	TRP	PRO	GLU	LYS	HIS	GLY	GLU	ALA	GLU	ILE	LYS	GLU	GLU	ALA	ASP	ASP	ALA	ALA	GLU	GLY	THR	GLY	ARG	SER	ILE	HIS	SER	MET	SER	LYS	GLY	LEU	PRO	PRO	LEU
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HIS	SER	MET	TYR	CYS	SER	MET	G439	Y358	T246
	HIS	PRO	GLY	LEU	LYS	GLY	A440	R359	F247
HIS	SER	PRO	TRP	ALA	GLY	GLY	V441	T360	M248
	HIS	LEU	THR	VAL	SER	ILE	D442	D361	E252
HIS	VAL	ALA	ALA	GLY	GLN	LEU	I443	S362	E257
	VAL	ALA	ARG	GLY	TYR	ALA	R446	E363	L260
HIS	VAL	ALA	ALA	ASN	CYS	THR	V447	G364	T272
	VAL	VAL	LEU	ASN	VAL	THR	N448	L365	L260
HIS	PRO	GLN	GLU	ASN	LEU	LEU	G449	Q366	T272
	ASP	ARG	HIS	ALA	LEU	MET	G449	Q366	T272
HIS	SER	ARG	GLN	LEU	LEU	LEU	V450	Q367	S276
	SER	LYS	GLY	LYS	GLU	ALA	V450	Q367	S276
HIS	GLU	HIS	HIS	ASP	HIS	GLN	D451	Q368	T277
	GLU	LEU	HIS	ASP	GLY	GLY	D452	E369	T278
HIS	SER	SER	GLU	ILE	GLY	GLY	V453	T370	T278
	LEU	ASN	ASP	VAL	ALA	LYS	V453	T370	T278
HIS	ILE	PHE	ILE	LYS	ALA	LYS	Q458	D372	N286
	ILE	GLU	LYS	TYR	PRO	ASP	Q458	D372	N286
HIS	GLY	ILE	ASN	GLY	ASN	LEU	F463	P375	E289
	GLY	GLY	SER	GLY	ILE	PRO	F463	P375	E289
HIS	GLY	LEU	PHE	ASP	ARG	LEU	V466	K376	T294
	LYS	PHE	TYR	ILE	ASP	SER	V466	K376	T294
HIS	LYS	GLY	ASN	SER	ASP	LEU	D467	A377	T294
	LYS	GLY	ASN	SER	ASP	LEU	D467	A377	T294
HIS	ILE	ILE	GLN	LEU	GLY	CYS	V468	T378	M298
	GLY	MET	ARG	SER	GLY	PHE	V468	T378	M298
HIS	PHE	SER	PRO	ASP	SER	ALA	R472	I382	L305
	VAL	ALA	VAL	VAL	SER	ALA	R472	I382	L305
HIS	ALA	ALA	GLU	ASN	VAL	ALA	Q473	F387	N311
	THR	ALA	ARG	GLY	PRO	ALA	Q473	F387	N311
HIS	LYS	LYS	LYS	THR	LEU	ARG	L475	V390	V316
	LYS	THR	LYS	THR	TRP	GLY	L475	V390	V316
HIS	ILE	GLY	THR	THR	GLU	ASP	V478	V391	V317
	GLY	GLY	THR	THR	ALA	ASP	V478	V391	V317
HIS	ASP	ASP	ILE	ALA	ALA	ASP	D392	H319	H319
	GLU	GLU	LEU	LEU	ILE	LEU	D392	H319	H319
HIS	SER	GLY	VAL	HIS	ILE	LEU	R482	K393	V318
	GLY	GLY	VAL	HIS	ILE	LEU	R482	K393	V318
HIS	ARG	GLY	SER	ARG	GLY	LEU	L483	T320	H319
	ALA	ALA	GLY	ALA	GLY	LEU	L483	T320	H319
HIS	ALA	ALA	GLY	ALA	ARG	HIS	S484	Y395	S321
	ALA	SER	THR	VAL	HIS	GLN	Q485	L396	S321
HIS	GLY	SER	THR	VAL	HIS	GLN	L486	F397	R322
	GLY	SER	THR	VAL	HIS	GLN	L486	F397	R322
HIS	THR	THR	PRO	SER	GLY	LEU	L487	H398	T323
	ARG	THR	PRO	SER	GLY	LEU	L487	H398	T323
HIS	ILE	ARG	GLU	GLY	GLU	LEU	R488	G398	R324
	THR	THR	ILE	ASN	LYS	LYS	R488	G398	R324
HIS	GLY	GLY	LYS	ASN	ALA	ARG	N490	F326	N325
	ILE	ILE	PRO	LEU	LYS	GLY	N490	F326	N325
HIS	ARG	SER	LEU	GLY	LEU	SER	R491	L405	F326
	ARG	SER	LEU	GLY	LEU	SER	R491	L405	F326
HIS	GLU	GLU	MET	ILE	LEU	ASN	L495	L408	R327
	ILE	GLY	LYS	VAL	SER	PRO	L495	L408	R327
HIS	VAL	VAL	HIS	GLN	SER	PRO	N496	V409	D328
	ASP	GLY	SER	PHE	ASN	ASN	N496	V409	D328
HIS	GLY	GLY	SER	ASN	GLY	THR	L497	E411	Q331
	GLY	GLY	SER	ASN	GLY	THR	L497	E411	Q331
HIS	ASP	VAL	GLU	LEU	ALA	ASP	Q499	A414	A332
	ASP	VAL	GLU	LEU	ALA	ASP	Q499	A414	A332
HIS	PHE	TYR	PRO	GLY	THR	LYS	D504	V423	A337
	LEU	PRO	VAL	LYS	LEU	ASN	D504	V423	A337
HIS	LEU	ALA	MET	GLY	SER	GLY	G505	T424	Q338
	LEU	ALA	MET	GLY	SER	GLY	G505	T424	Q338
HIS	LEU	ARG	THR	ALA	PHE	ARG	A506	L425	N340
	LEU	ARG	THR	ALA	PHE	ARG	A506	L425	N340
HIS	VAL	VAL	HIS	ASP	ASP	THR	I507	R426	N341
	VAL	VAL	HIS	ASP	ASP	THR	I507	R426	N341
HIS	LYS	THR	HIS	MET	THR	ALA	N510	N427	L344
	VAL	THR	HIS	MET	THR	ALA	N510	N427	L344
HIS	ILE	ILE	HIS	ASP	VAL	LEU	G516	E428	G345
	SER	SER	HIS	ASP	GLY	HIS	G516	E428	G345
HIS	HIS	GLY	SER	LYS	THR	ILE	F433	T436	Q347
	HIS	GLY	SER	LYS	THR	ILE	F433	T436	Q347
HIS	GLY	ARG	GLY	PRO	PHE	ALA	THR	T435	E348
	GLY	ARG	GLY	PRO	PHE	ALA	THR	T435	E348
HIS	THR	GLU	GLU	ASP	ASP	PRO	ASP	M436	Q347
	THR	GLU	GLU	ASP	ASP	PRO	ASP	M436	Q347
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
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	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
	THR	GLU	GLU	VAL	THR	ALA	PRO	V437	E348
HIS	THR	GLU	GLU	VAL	THR	ALA	PRO</		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	186912	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.762	Depositor
Minimum map value	-1.507	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.184	Depositor
Map size (Å)	369.6, 369.6, 369.6	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	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	0.96	0/3745	1.20	0/5094
1	B	0.96	0/3745	1.21	0/5094
1	C	0.96	0/3745	1.21	0/5094
1	D	0.96	0/3745	1.21	0/5094
All	All	0.96	0/14980	1.21	0/20376

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	3648	0	3646	118	0
1	B	3648	0	3646	114	0
1	C	3648	0	3646	99	0
1	D	3648	0	3646	105	0
All	All	14592	0	14584	385	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 13.

The worst 5 of 385 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:C:442:ASP:OD2	1:C:481:LYS:HD2	1.53	1.09
1:A:356:LEU:HD11	1:A:483:LEU:CD1	1.90	1.01
1:A:443:ILE:HG12	1:A:463:PHE:HZ	1.28	0.97
1:D:294:ILE:HG22	1:D:298:MET:HE2	1.51	0.92
1:B:294:ILE:HG22	1:B:298:MET:HE2	1.52	0.91

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	447/894 (50%)	416 (93%)	31 (7%)	0	100	100
1	B	447/894 (50%)	417 (93%)	30 (7%)	0	100	100
1	C	447/894 (50%)	418 (94%)	28 (6%)	1 (0%)	43	66
1	D	447/894 (50%)	415 (93%)	32 (7%)	0	100	100
All	All	1788/3576 (50%)	1666 (93%)	121 (7%)	1 (0%)	49	70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	279	GLY

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	393/761 (52%)	347 (88%)	46 (12%)	5	11
1	B	393/761 (52%)	347 (88%)	46 (12%)	5	11
1	C	393/761 (52%)	351 (89%)	42 (11%)	6	14
1	D	393/761 (52%)	355 (90%)	38 (10%)	8	17
All	All	1572/3044 (52%)	1400 (89%)	172 (11%)	8	13

5 of 172 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	305	LEU
1	D	143	ASP
1	A	391	VAL
1	A	489	LEU
1	D	175	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	175	HIS
1	D	496	ASN
1	A	452	GLN
1	D	485	GLN
1	D	515	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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.

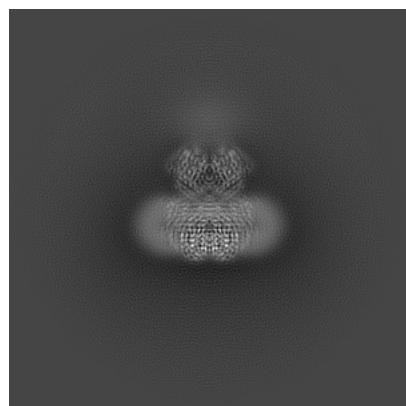
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66432. These allow visual inspection of the internal detail of the map and identification of artifacts.

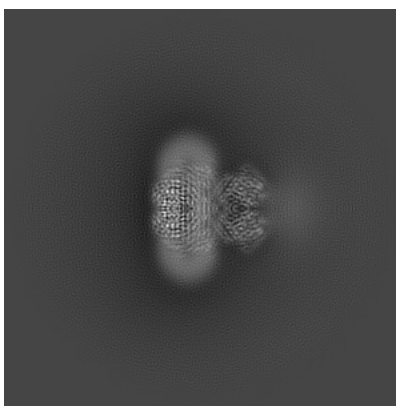
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

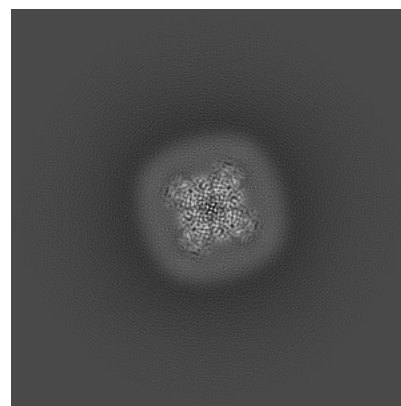
6.1.1 Primary map



X

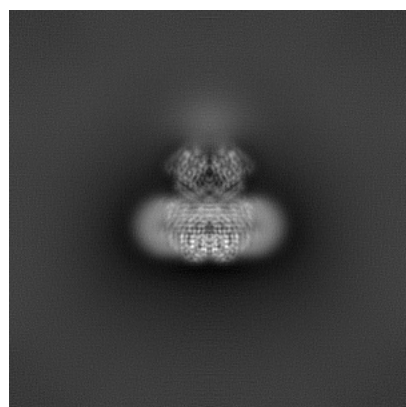


Y

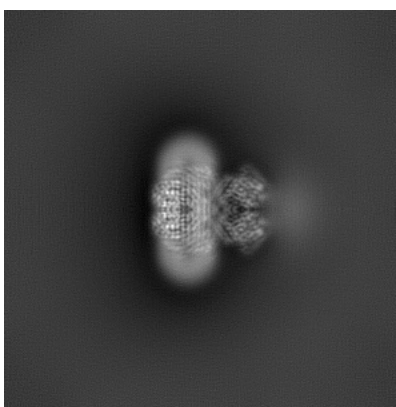


Z

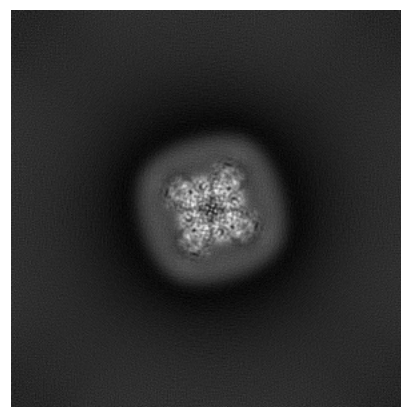
6.1.2 Raw map



X



Y

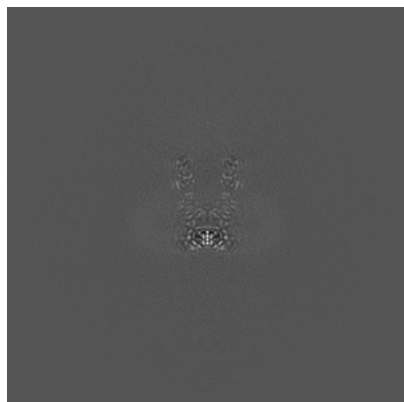


Z

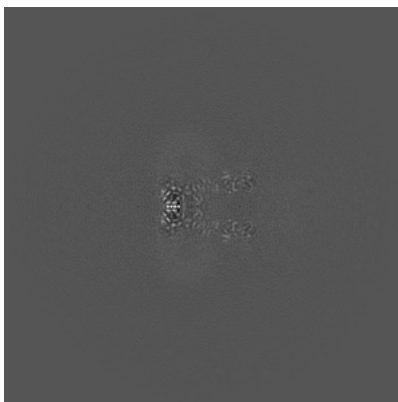
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

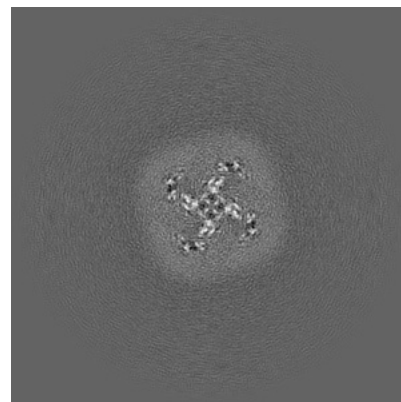
6.2.1 Primary map



X Index: 224

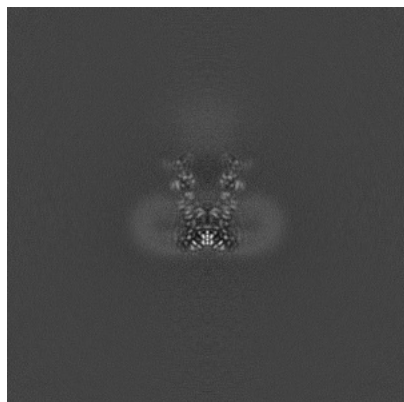


Y Index: 224

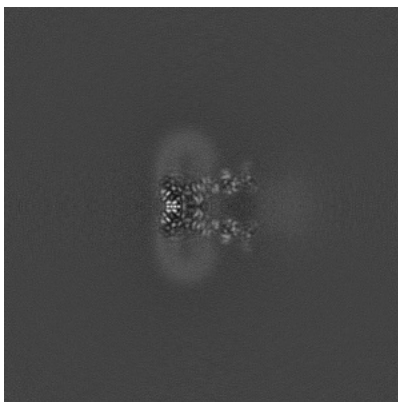


Z Index: 224

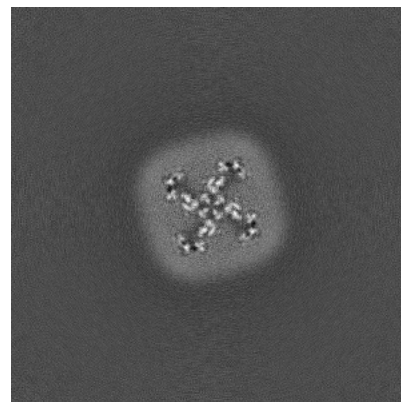
6.2.2 Raw map



X Index: 224



Y Index: 224

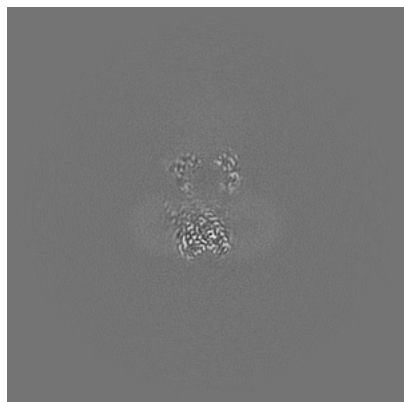


Z Index: 224

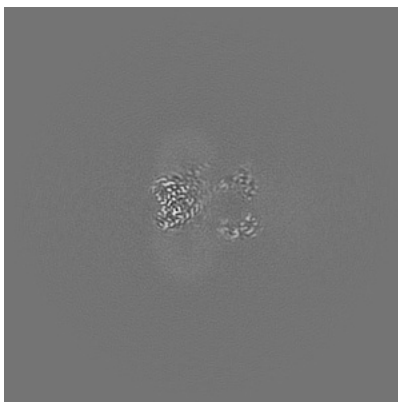
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

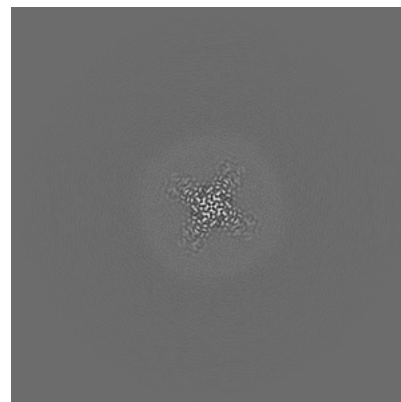
6.3.1 Primary map



X Index: 216

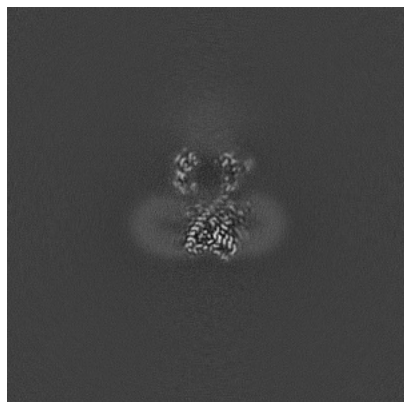


Y Index: 216

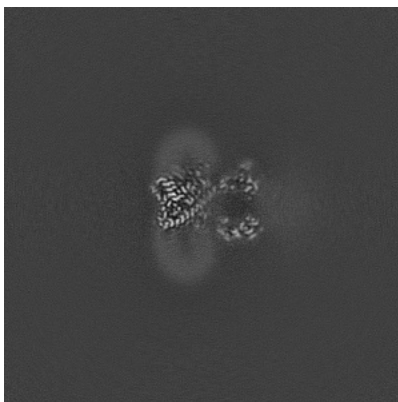


Z Index: 190

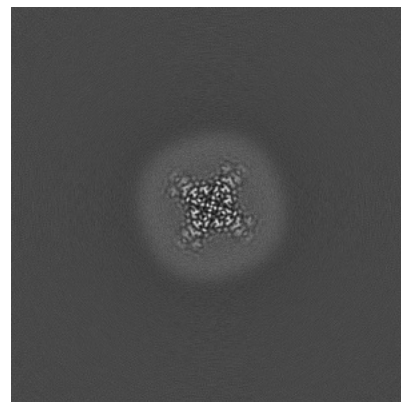
6.3.2 Raw map



X Index: 231



Y Index: 217

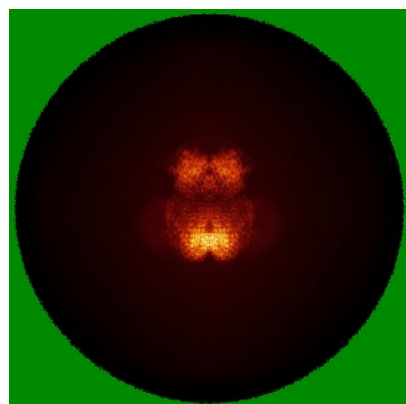


Z Index: 188

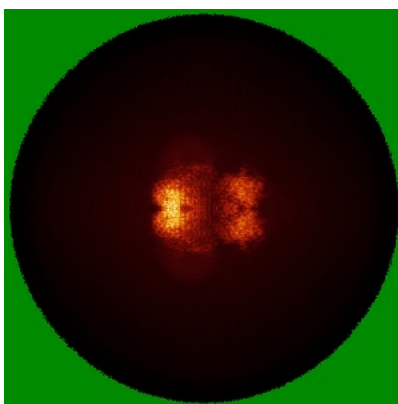
The images above show the largest variance slices of the map in three orthogonal directions.

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

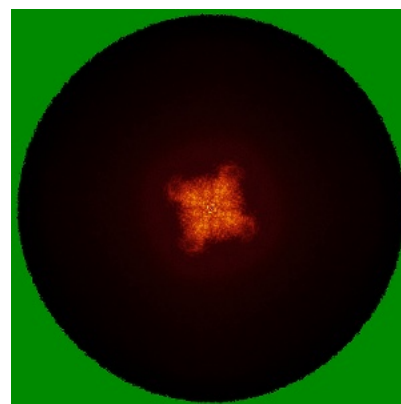
6.4.1 Primary map



X

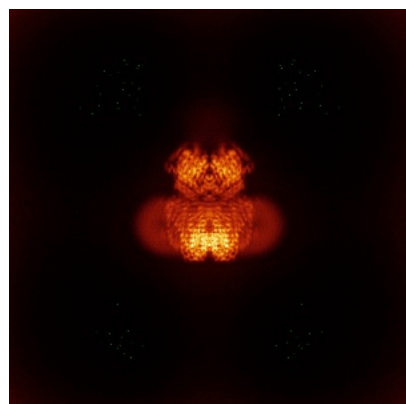


Y

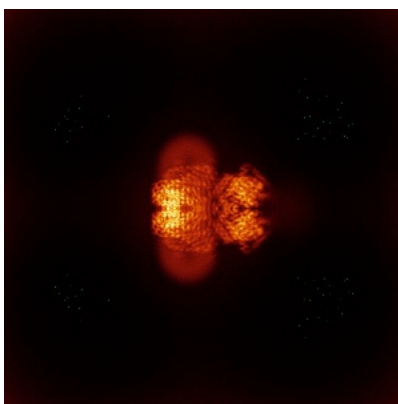


Z

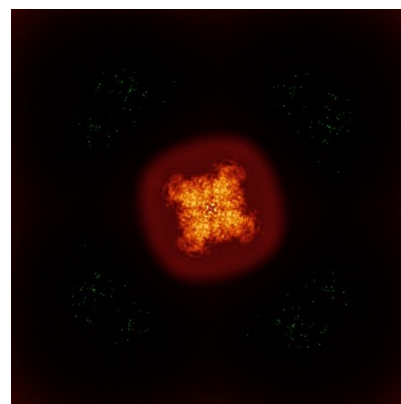
6.4.2 Raw map



X



Y

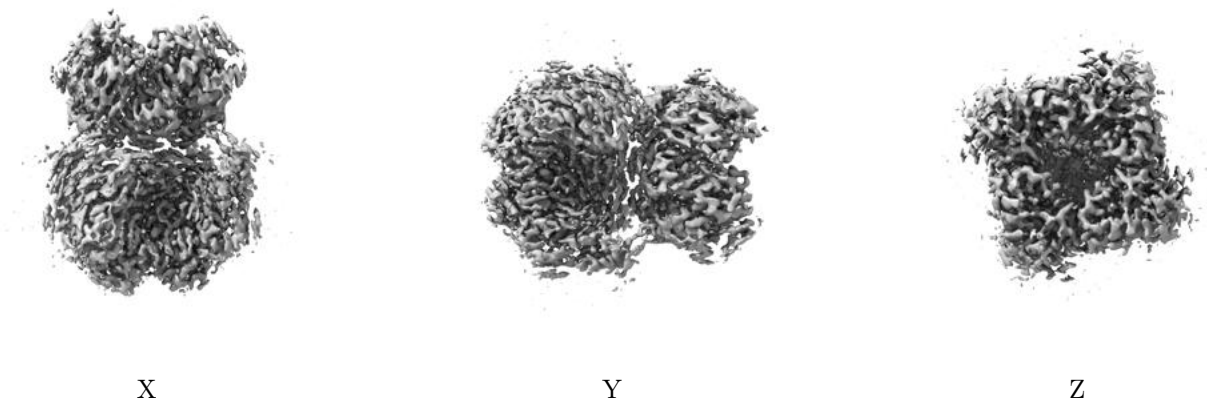


Z

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.

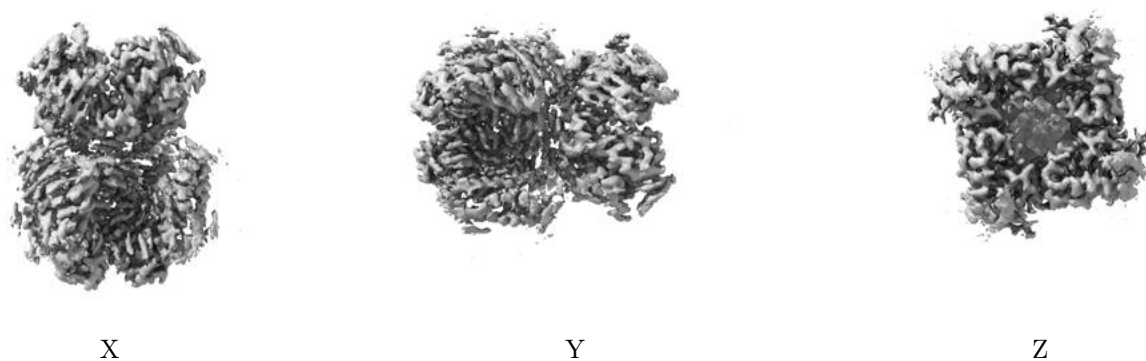
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.184. 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.

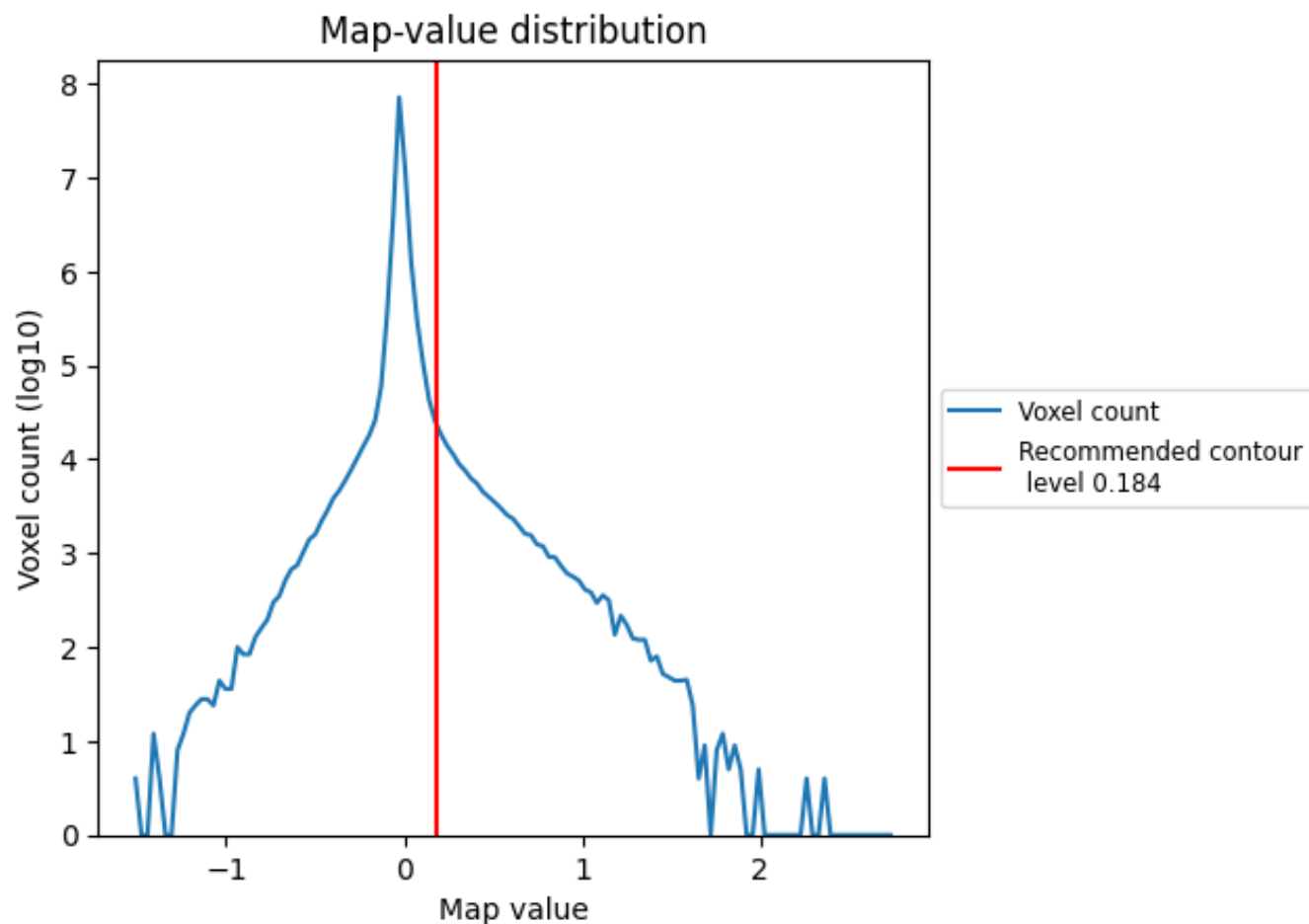
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

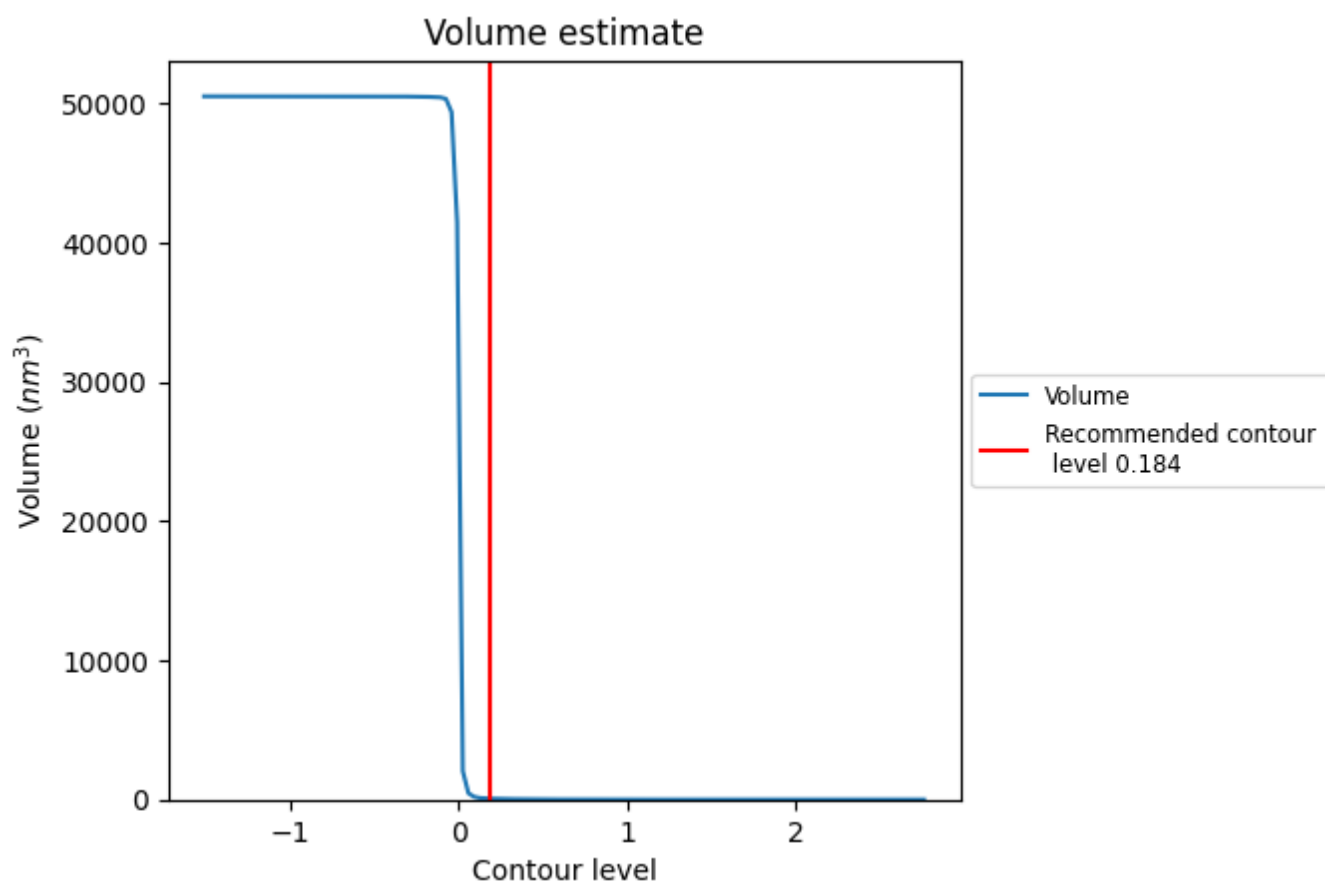
This section contains the results of statistical analysis of the map.

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.

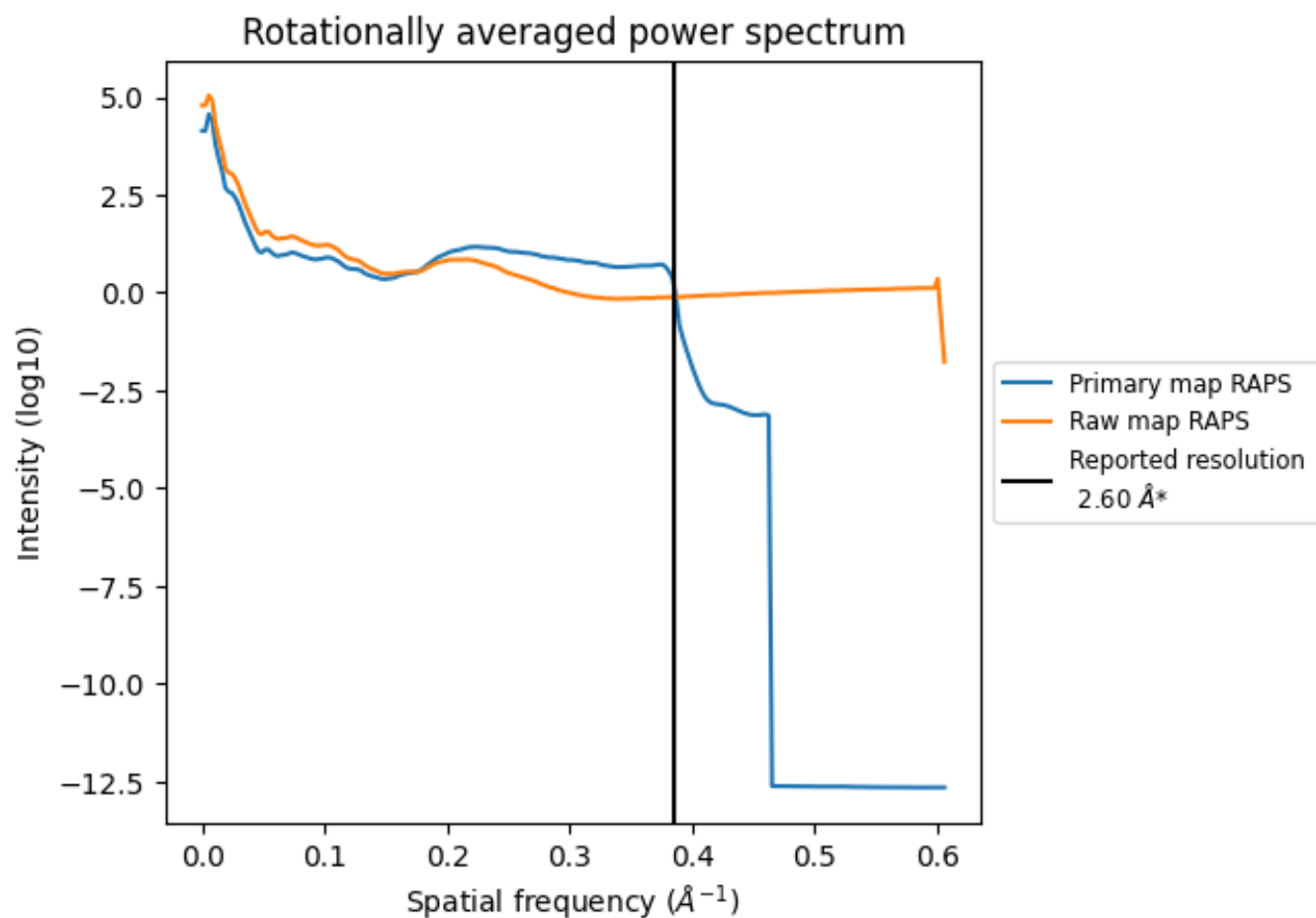
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 70 nm^3 ; this corresponds to an approximate mass of 63 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 ⓘ

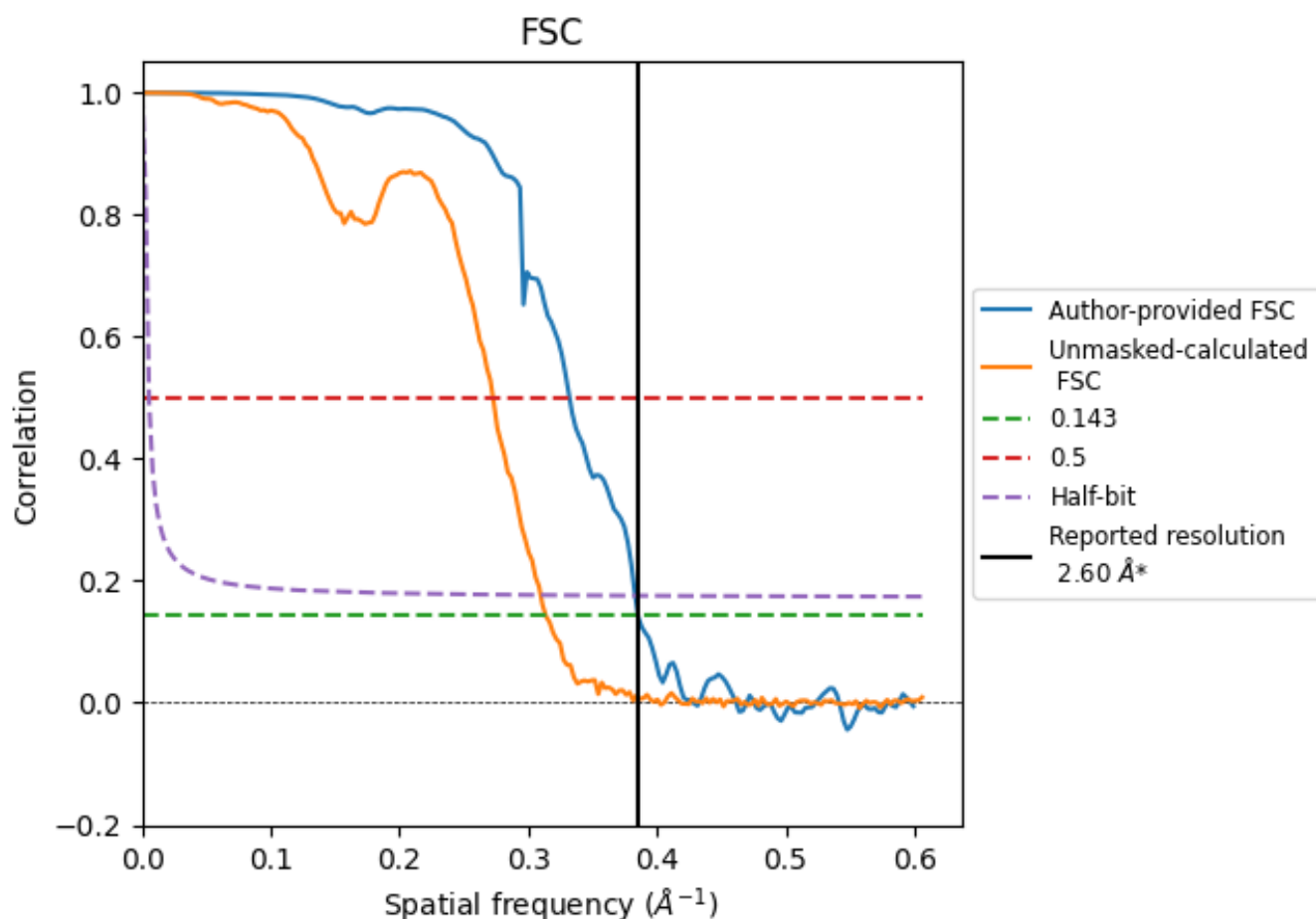


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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 $0.385 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

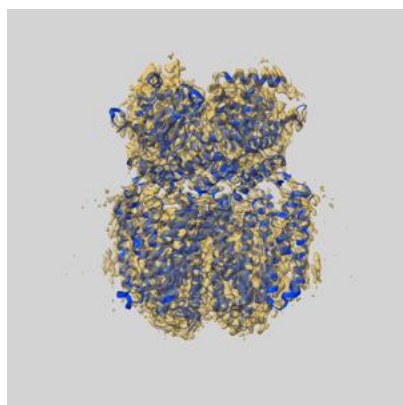
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.60	3.01	2.61
Unmasked-calculated*	3.19	3.67	3.23

*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 3.19 differs from the reported value 2.6 by more than 10 %

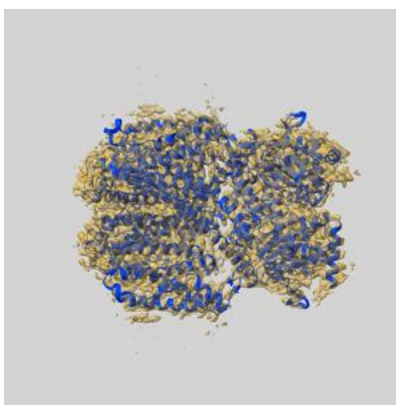
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-66432 and PDB model 9X0C. Per-residue inclusion information can be found in section [3](#) on page [5](#).

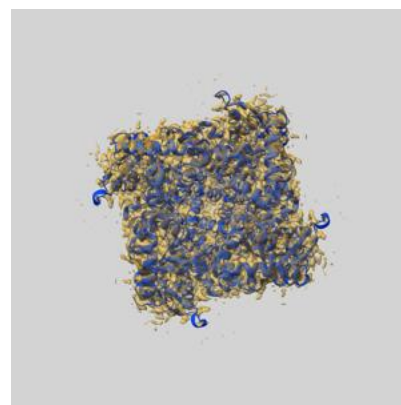
9.1 Map-model overlay [i](#)



X



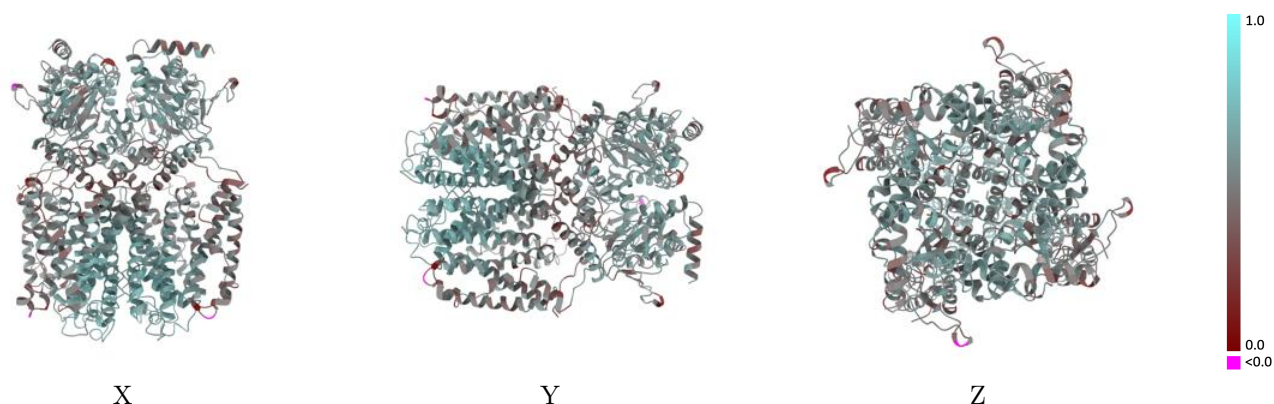
Y



Z

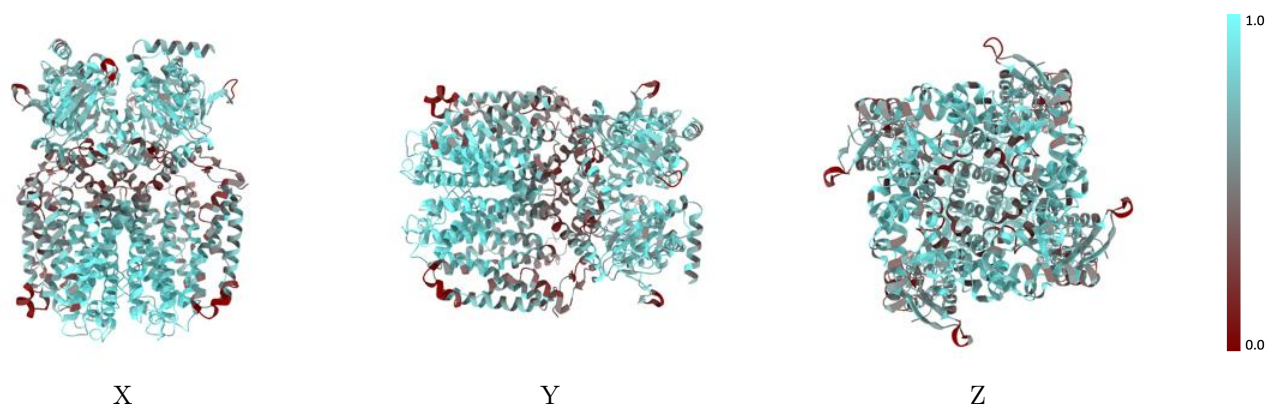
The images above show the 3D surface view of the map at the recommended contour level 0.184 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



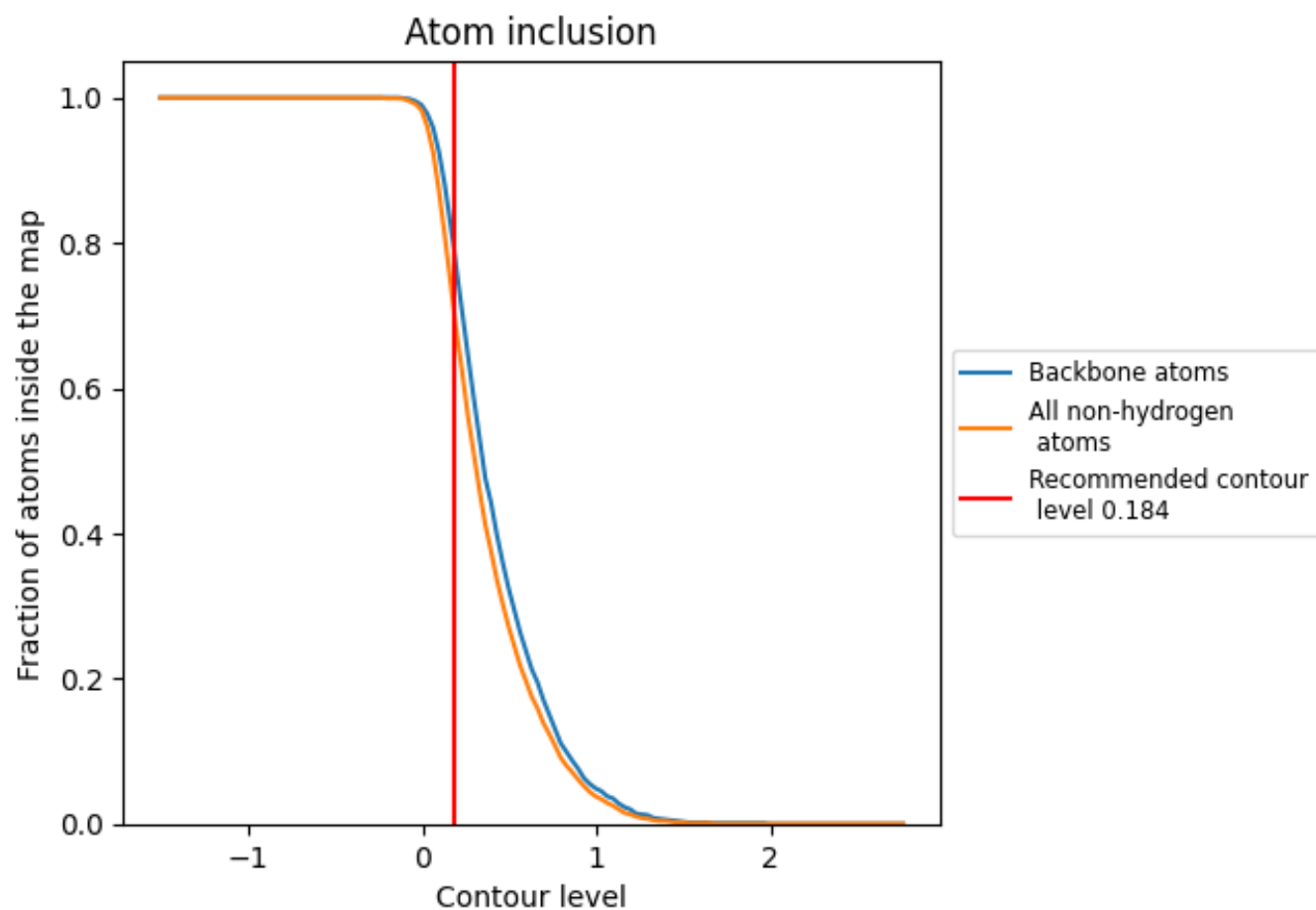
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.184).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% 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 (0.184) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7010	0.5290
A	0.7010	0.5300
B	0.6970	0.5260
C	0.7040	0.5300
D	0.7030	0.5300

