



wwPDB EM Validation Summary Report ⓘ

May 14, 2025 – 07:55 AM EDT

PDB ID : 9BAX / pdb_00009bax
EMDB ID : EMD-44413
Title : PI4KA complex bound to C-terminus of EFR3A
Authors : Shaw, A.L.; Suresh, S.; Yip, C.K.; Burke, J.E.
Deposited on : 2024-04-04
Resolution : 3.65 Å(reported)

This is a wwPDB EM Validation Summary 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

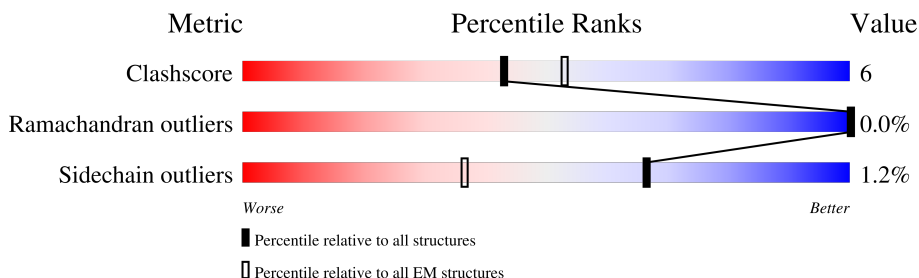
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.65 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	C	130	
1	H	130	
2	A	2102	
2	B	2102	
3	D	843	
3	F	843	
4	E	308	
4	G	308	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 42100 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 Protein EFR3 homolog A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	64	Total	C	N	O	S	0	0
			522	328	90	102	2		
1	H	64	Total	C	N	O	S	0	0
			522	328	90	102	2		

There are 118 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	662	MET	-	initiating methionine	UNP Q14156
C	663	ALA	-	expression tag	UNP Q14156
C	664	SER	-	expression tag	UNP Q14156
C	665	ALA	-	expression tag	UNP Q14156
C	666	TRP	-	expression tag	UNP Q14156
C	667	SER	-	expression tag	UNP Q14156
C	668	HIS	-	expression tag	UNP Q14156
C	669	PRO	-	expression tag	UNP Q14156
C	670	GLN	-	expression tag	UNP Q14156
C	671	PHE	-	expression tag	UNP Q14156
C	672	GLU	-	expression tag	UNP Q14156
C	673	LYS	-	expression tag	UNP Q14156
C	674	GLY	-	expression tag	UNP Q14156
C	675	GLY	-	expression tag	UNP Q14156
C	676	GLY	-	expression tag	UNP Q14156
C	677	SER	-	expression tag	UNP Q14156
C	678	GLY	-	expression tag	UNP Q14156
C	679	GLY	-	expression tag	UNP Q14156
C	680	GLY	-	expression tag	UNP Q14156
C	681	SER	-	expression tag	UNP Q14156
C	682	GLY	-	expression tag	UNP Q14156
C	683	GLY	-	expression tag	UNP Q14156
C	684	SER	-	expression tag	UNP Q14156
C	685	ALA	-	expression tag	UNP Q14156
C	686	TRP	-	expression tag	UNP Q14156
C	687	SER	-	expression tag	UNP Q14156

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Chain	Residue	Modelled	Actual	Comment	Reference
C	688	HIS	-	expression tag	UNP Q14156
C	689	PRO	-	expression tag	UNP Q14156
C	690	GLN	-	expression tag	UNP Q14156
C	691	PHE	-	expression tag	UNP Q14156
C	692	GLU	-	expression tag	UNP Q14156
C	693	LYS	-	expression tag	UNP Q14156
C	694	SER	-	expression tag	UNP Q14156
C	695	GLY	-	expression tag	UNP Q14156
C	696	MET	-	expression tag	UNP Q14156
C	697	HIS	-	expression tag	UNP Q14156
C	698	HIS	-	expression tag	UNP Q14156
C	699	HIS	-	expression tag	UNP Q14156
C	700	HIS	-	expression tag	UNP Q14156
C	701	HIS	-	expression tag	UNP Q14156
C	702	HIS	-	expression tag	UNP Q14156
C	703	HIS	-	expression tag	UNP Q14156
C	704	HIS	-	expression tag	UNP Q14156
C	705	HIS	-	expression tag	UNP Q14156
C	706	HIS	-	expression tag	UNP Q14156
C	707	GLY	-	expression tag	UNP Q14156
C	708	SER	-	expression tag	UNP Q14156
C	709	GLY	-	expression tag	UNP Q14156
C	710	GLY	-	expression tag	UNP Q14156
C	711	SER	-	expression tag	UNP Q14156
C	712	GLU	-	expression tag	UNP Q14156
C	713	ASN	-	expression tag	UNP Q14156
C	714	LEU	-	expression tag	UNP Q14156
C	715	TYR	-	expression tag	UNP Q14156
C	716	PHE	-	expression tag	UNP Q14156
C	717	GLN	-	expression tag	UNP Q14156
C	718	GLY	-	expression tag	UNP Q14156
C	719	ALA	-	expression tag	UNP Q14156
C	720	GLY	-	expression tag	UNP Q14156
H	662	MET	-	initiating methionine	UNP Q14156
H	663	ALA	-	expression tag	UNP Q14156
H	664	SER	-	expression tag	UNP Q14156
H	665	ALA	-	expression tag	UNP Q14156
H	666	TRP	-	expression tag	UNP Q14156
H	667	SER	-	expression tag	UNP Q14156
H	668	HIS	-	expression tag	UNP Q14156
H	669	PRO	-	expression tag	UNP Q14156
H	670	GLN	-	expression tag	UNP Q14156

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Chain	Residue	Modelled	Actual	Comment	Reference
H	671	PHE	-	expression tag	UNP Q14156
H	672	GLU	-	expression tag	UNP Q14156
H	673	LYS	-	expression tag	UNP Q14156
H	674	GLY	-	expression tag	UNP Q14156
H	675	GLY	-	expression tag	UNP Q14156
H	676	GLY	-	expression tag	UNP Q14156
H	677	SER	-	expression tag	UNP Q14156
H	678	GLY	-	expression tag	UNP Q14156
H	679	GLY	-	expression tag	UNP Q14156
H	680	GLY	-	expression tag	UNP Q14156
H	681	SER	-	expression tag	UNP Q14156
H	682	GLY	-	expression tag	UNP Q14156
H	683	GLY	-	expression tag	UNP Q14156
H	684	SER	-	expression tag	UNP Q14156
H	685	ALA	-	expression tag	UNP Q14156
H	686	TRP	-	expression tag	UNP Q14156
H	687	SER	-	expression tag	UNP Q14156
H	688	HIS	-	expression tag	UNP Q14156
H	689	PRO	-	expression tag	UNP Q14156
H	690	GLN	-	expression tag	UNP Q14156
H	691	PHE	-	expression tag	UNP Q14156
H	692	GLU	-	expression tag	UNP Q14156
H	693	LYS	-	expression tag	UNP Q14156
H	694	SER	-	expression tag	UNP Q14156
H	695	GLY	-	expression tag	UNP Q14156
H	696	MET	-	expression tag	UNP Q14156
H	697	HIS	-	expression tag	UNP Q14156
H	698	HIS	-	expression tag	UNP Q14156
H	699	HIS	-	expression tag	UNP Q14156
H	700	HIS	-	expression tag	UNP Q14156
H	701	HIS	-	expression tag	UNP Q14156
H	702	HIS	-	expression tag	UNP Q14156
H	703	HIS	-	expression tag	UNP Q14156
H	704	HIS	-	expression tag	UNP Q14156
H	705	HIS	-	expression tag	UNP Q14156
H	706	HIS	-	expression tag	UNP Q14156
H	707	GLY	-	expression tag	UNP Q14156
H	708	SER	-	expression tag	UNP Q14156
H	709	GLY	-	expression tag	UNP Q14156
H	710	GLY	-	expression tag	UNP Q14156
H	711	SER	-	expression tag	UNP Q14156
H	712	GLU	-	expression tag	UNP Q14156

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Chain	Residue	Modelled	Actual	Comment	Reference
H	713	ASN	-	expression tag	UNP Q14156
H	714	LEU	-	expression tag	UNP Q14156
H	715	TYR	-	expression tag	UNP Q14156
H	716	PHE	-	expression tag	UNP Q14156
H	717	GLN	-	expression tag	UNP Q14156
H	718	GLY	-	expression tag	UNP Q14156
H	719	ALA	-	expression tag	UNP Q14156
H	720	GLY	-	expression tag	UNP Q14156

- Molecule 2 is a protein called Phosphatidylinositol 4-kinase alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1724	Total	C	N	O	S	0	0
			13842	8951	2305	2489	97		
2	A	1724	Total	C	N	O	S	0	0
			13842	8951	2305	2489	97		

- Molecule 3 is a protein called Tetratricopeptide repeat protein 7B.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	592	Total	C	N	O	S	0	0
			4676	2983	811	855	27		
3	D	592	Total	C	N	O	S	0	0
			4676	2983	811	855	27		

- Molecule 4 is a protein called Hyccin.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	252	Total	C	N	O	S	0	0
			2010	1309	323	366	12		
4	E	252	Total	C	N	O	S	0	0
			2010	1309	323	366	12		

F1980	G1986	M1987	L1988	E1991	L1996	M2000	M2004	M2008	L2025	M2031	R2050	P2063	I2074	V2077	L2083	SER	ASN	ARG	SER	THR	THR	ASP	MET	ILE	GLN	TYR	GLN	ASN	ASP	PRO	TYR														
R1823	C1824	ARG	ASP	ASP	SER	GLU	ASP	GLU	CYS	SER	THR	GLN	GLU	ALA	ASP	GLY	GLN	G1852	D1853	D1854	L1862	T1865	D1866	L1867	L1874	A1890	P1891	G1892	C1893	I1899	D1906	Q1911	F1920	I1940	L1949	R1958	G1961	M1964	L1965	D1966	H1970	D1975			
LEU	GLU	GLU	GLU	GLY	VAL	ARG	ARG	ARG	ARG	PHE	ASN	ASP	PHE	ARG	SER	ILE	PRO	SER	SER	LEU	PRO	SER	ASN	VAL	K416	ILE	LEU	PRO	HIS	ASP	ALA	ASP	ARG	ILE	ASN	HIS	PRO	ASP	GLU	LEU	VAL	THR	LEU	GLY	SER
ALA	PHE	HIS	TYR	PHE	GLU	ALA	SER	CYS	LEU	PRO	ASP	THR	ALA	LEU	E296	E296	S305	S309	VAL	SER	LEU	THR	PHE	VAL	CYS	GLN	GLY	THR	THR	LEU	LEU	ARG	ARG	ILE	SER	ILE	SER	GLN	VAL	THR	PRO	PRO	GLY	SER	
ASP	L364	M377	F378	K379	R382	S385	L386	Y387	M388	H400	D401	F402	V403	L404	E405	K416	ILE	LEU	PRO	HIS	ASP	ALA	ASP	ARG	ILE	ASN	HIS	PRO	ASP	GLU	LEU	VAL	K432	C435	Q436	M457	K461	E464	S468	LYS	THR	ALA	L478	L479	
P480	L507	V512	I513	PRO	S515	K523	TYR	HIS	SER	GLN	TYR	HIS	VAL	ALA	GLY	ASN	ASP	ILE	LYS	ILE	SER	VAL	THR	GLN	THR	LEU	ASN	SER	GLU	LEU	THR	LYS	GLY	GLY	VAL	MET	PRO	PRO	PRO	PRO	PRO	PRO	PRO	GLY	SER
L577	K578	E589	L592	R598	I601	GLN	GLU	GLU	SER	ASP	ASP	ASP	ALA	HIS	L611	I612	P613	L620	G621	H622	R628	D629	T630	PRO	K632	V633	M634	E635	L638	Q639	I640	L641	Q642	Q643	K644	F645	C646	S650	L655	I656	I657	I665	T666	Y670	Q673
N677	A686	SER	SER	VAL	VAL	TYR	SER	ALA	THR	LYS	ASP	TYR	LYS	ASP	GLY	Y702	A708	N715	N719	D722	L725	PRO	HIS	ASN	ASP	E735	L742	GLU	LYS	ARG	ALA	GLU	ALA	ALA	SER	GLU	LYS	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
P772	K788	P789	R790	G811	SER	GLY	W815	W819	L832	F835	PRO	HIS	GLY	Y702	A708	N715	N719	D722	L725	PRO	HIS	ASN	ASP	E735	L742	GLU	LYS	ARG	ALA	GLU	ALA	ALA	SER	GLU	LYS	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
SER	GLY	M933	V943	K956	E963	R966	F970	V973	K980	R981	L982	R983	R984	L1007	M1010	I1013	I1034	I1041	M1063	I1064	L1065	Q1066	K1077	Q1088	Q1096	H1097	L1100	L1108	M1114	K1115	Q1116	A1122	THR	GLN	LEU	SER	GLU	ARG							
PRO	ALA	CYS	VAL	K1133	K1134	D1135	F1159	SER	GLY	THR	GLY	GLN	MET	SER	D1168	L1169	N1170	R1183	H1188	A1198	I1201	D1207	P1208	Q1209	L1210	M1221	F1222	N1223	G1240	F1264	D1275	P1276	L1277	P1285	V1292	V1303	Y1311	V1317	L1330	M1331	I1332	SER			
L1355	G1356	L1357	V1364	V1365	P1366	N1367	R1371	N1372	R1401	D1417	K1418	Y1420	L1421	S1424	GLN	R1483	LEU	VAL	H1188	A1198	I1201	D1207	P1208	Q1209	L1210	M1221	F1222	N1223	G1240	F1264	D1275	P1276	L1277	P1285	V1292	V1303	Y1311	V1317	L1330	M1331	I1332	SER			
THR	ILE	SER	LYS	LYS	SER	GLY	LYS	LYS	THR	R1477	K1483	Y1484	Y1485	M1486	K1487	N1508	P1509	L1510	E1516	R1529	Y1532	T1565	E1566	A1567	E1571	R1574	V1586	P1587	E1588	T1595	W1596	A1601	D1602	E1605	L1606	S1607	H1608	V1612	A1613	P1614	T1615	M1616	SER		
P1629	V1639	L1651	I1654	V1658	M1666	G1667	Y1668	A1684	I1688	N1689	N1690	M1691	K1692	T1693	L1697	G1701	H1702	D1705	D1710	L1715	K1749	L1765	S1766	V1770	I1787	D1788	Y1789	P1794	S1797	ALA	ALA	K1800	A1801	P1802	Y1803	E1816	K1819	E1820	D1975						

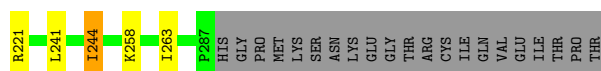
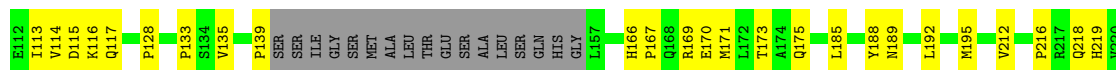
● Molecule 3: Tetratricopeptide repeat protein 7B





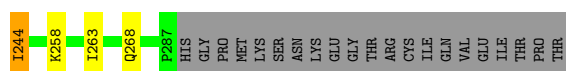
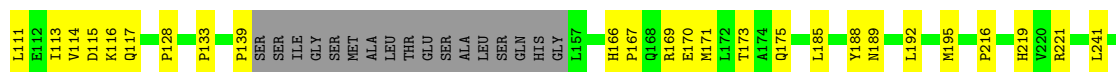
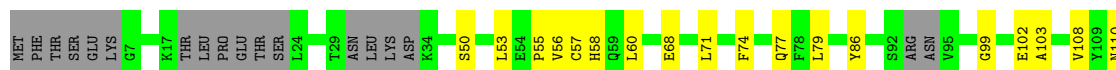
• Molecule 4: Hyccin

Chain G: 66% 15% 18%



• Molecule 4: Hyccin

Chain E: 67% 15% 18%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	135126	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)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	165000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.208	Depositor
Minimum map value	-0.100	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0284	Depositor
Map size (Å)	462.0, 462.0, 462.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.77, 0.77, 0.77	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	C	0.11	0/526	0.28	0/701
1	H	0.11	0/526	0.28	0/701
2	A	0.10	0/14149	0.26	1/19141 (0.0%)
2	B	0.10	0/14149	0.26	1/19141 (0.0%)
3	D	0.09	0/4762	0.24	0/6443
3	F	0.09	0/4762	0.24	0/6443
4	E	0.10	0/2058	0.27	0/2793
4	G	0.10	0/2058	0.27	0/2793
All	All	0.10	0/42990	0.26	2/58156 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1419	LYS	N-CA-C	-5.95	104.87	114.09
2	A	1419	LYS	N-CA-C	-5.92	104.91	114.09

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	C	522	0	536	9	0
1	H	522	0	536	10	0
2	A	13842	0	13974	171	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	13842	0	13974	171	0
3	D	4676	0	4734	67	0
3	F	4676	0	4734	64	0
4	E	2010	0	2017	31	0
4	G	2010	0	2017	31	0
All	All	42100	0	42522	539	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.

The worst 5 of 539 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:A:1667:GLY:HA3	3:D:347:ARG:HH22	1.49	0.78
2:B:1667:GLY:HA3	3:F:347:ARG:HH22	1.50	0.77
3:D:222:LEU:O	3:D:241:ARG:NH2	2.21	0.74
3:F:222:LEU:O	3:F:241:ARG:NH2	2.21	0.73
2:B:1596:TRP:HE1	2:B:1602:ASP:H	1.37	0.73

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	C	62/130 (48%)	61 (98%)	1 (2%)	0	100	100
1	H	62/130 (48%)	61 (98%)	1 (2%)	0	100	100
2	A	1676/2102 (80%)	1596 (95%)	79 (5%)	1 (0%)	48	78
2	B	1676/2102 (80%)	1596 (95%)	79 (5%)	1 (0%)	48	78
3	D	580/843 (69%)	567 (98%)	13 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F	580/843 (69%)	567 (98%)	13 (2%)	0	100	100
4	E	242/308 (79%)	234 (97%)	8 (3%)	0	100	100
4	G	242/308 (79%)	234 (97%)	8 (3%)	0	100	100
All	All	5120/6766 (76%)	4916 (96%)	202 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1980	PHE
2	A	1980	PHE

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	C	56/104 (54%)	55 (98%)	1 (2%)	54	71
1	H	56/104 (54%)	55 (98%)	1 (2%)	54	71
2	A	1527/1841 (83%)	1509 (99%)	18 (1%)	67	79
2	B	1527/1841 (83%)	1509 (99%)	18 (1%)	67	79
3	D	494/712 (69%)	487 (99%)	7 (1%)	62	77
3	F	494/712 (69%)	487 (99%)	7 (1%)	62	77
4	E	227/277 (82%)	226 (100%)	1 (0%)	89	93
4	G	227/277 (82%)	226 (100%)	1 (0%)	89	93
All	All	4608/5868 (78%)	4554 (99%)	54 (1%)	66	79

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	464	GLU
2	A	1264	PHE
3	D	569	LEU
2	A	577	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A	913	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	611	GLN
3	D	724	ASN
3	F	611	GLN
3	F	570	ASN
3	D	811	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.

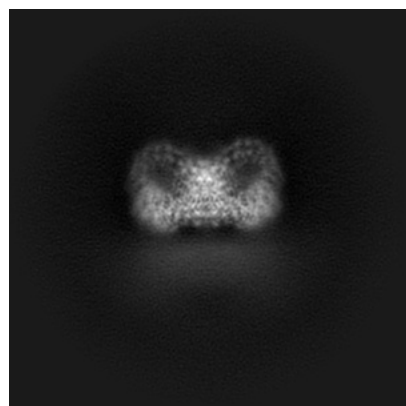
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44413. These allow visual inspection of the internal detail of the map and identification of artifacts.

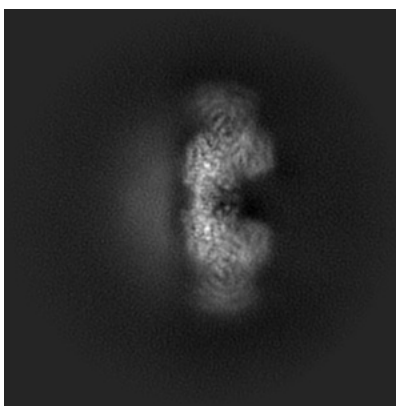
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

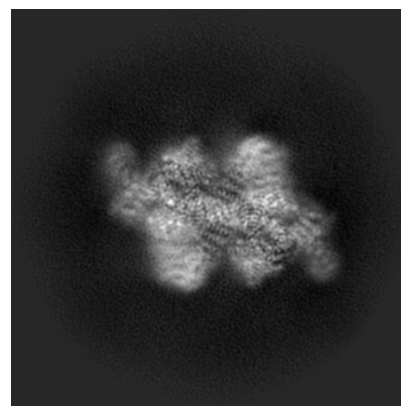
6.1.1 Primary map



X

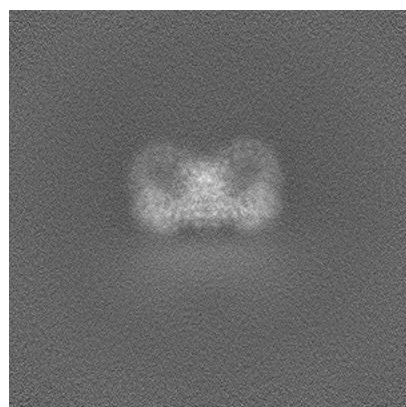


Y

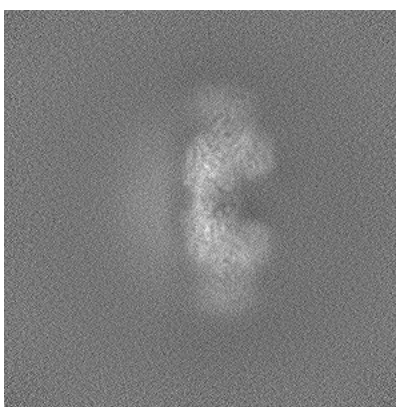


Z

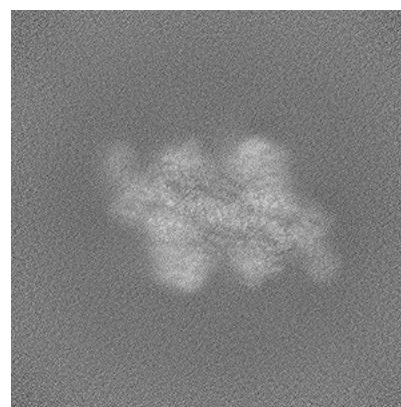
6.1.2 Raw map



X



Y

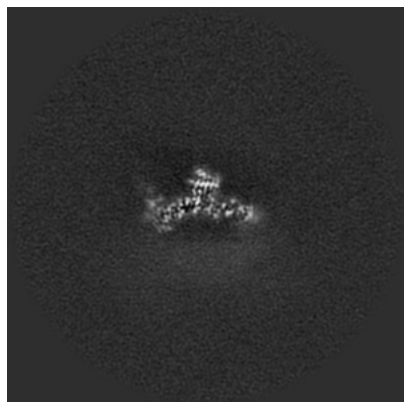


Z

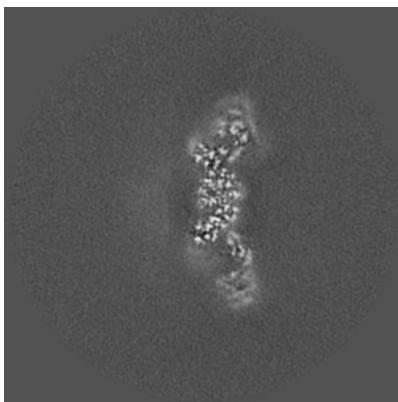
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

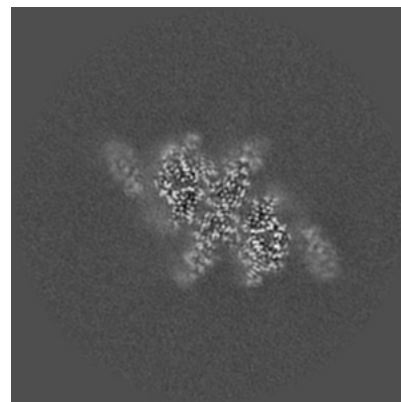
6.2.1 Primary map



X Index: 300

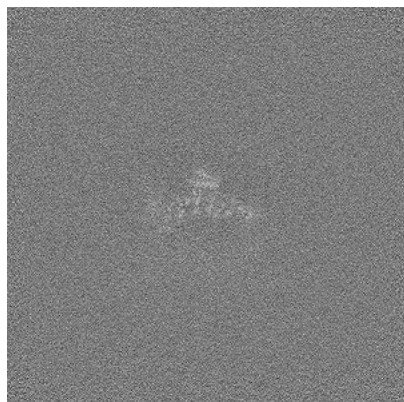


Y Index: 300

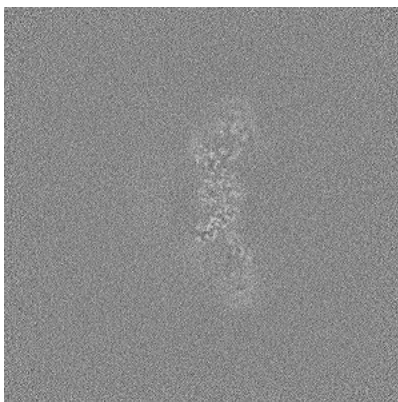


Z Index: 300

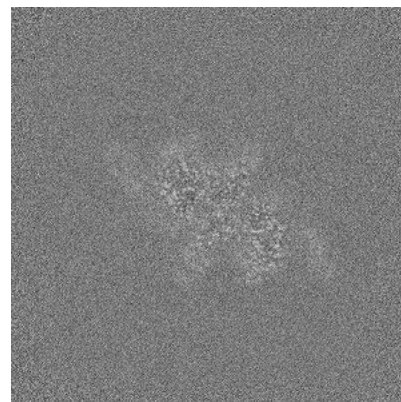
6.2.2 Raw map



X Index: 300



Y Index: 300

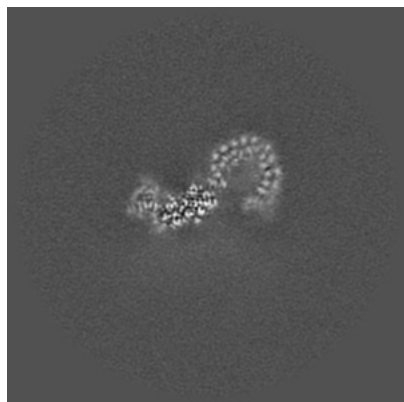


Z Index: 300

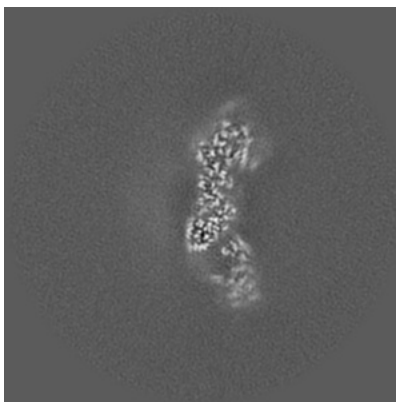
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

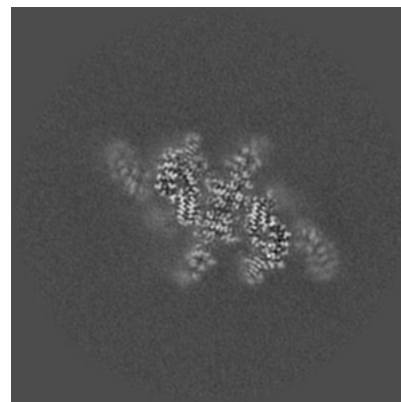
6.3.1 Primary map



X Index: 366

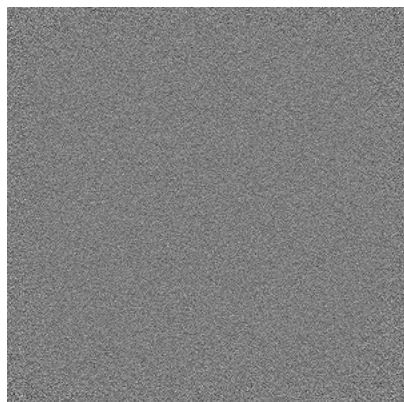


Y Index: 308

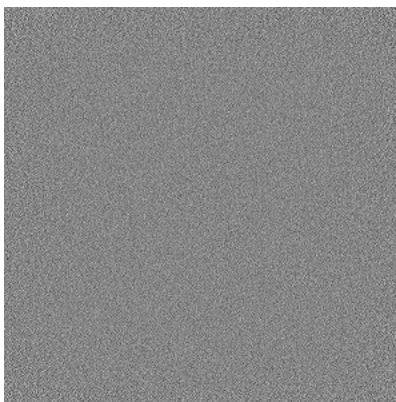


Z Index: 305

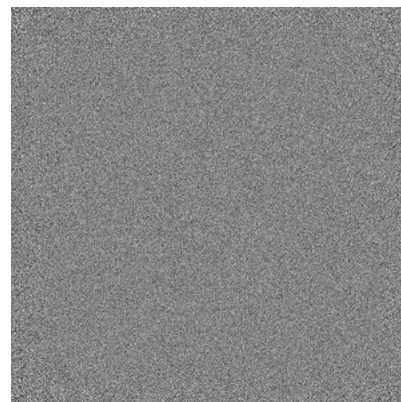
6.3.2 Raw map



X Index: 0



Y Index: 0

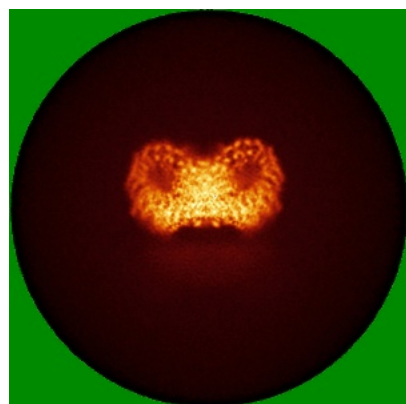


Z Index: 0

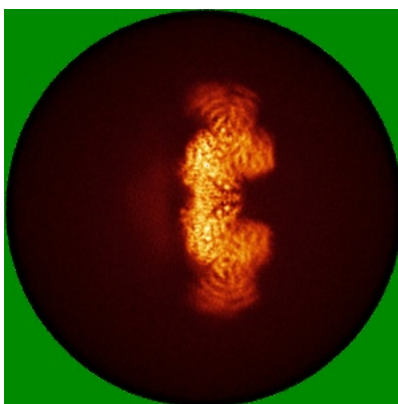
The images above show the largest variance slices of the map in three orthogonal directions.

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

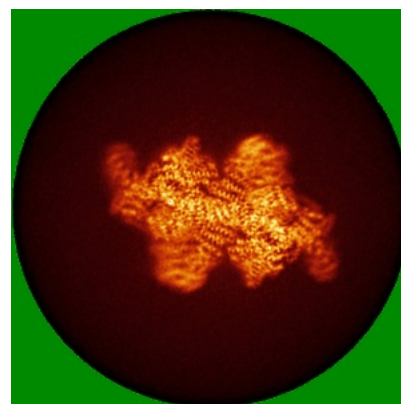
6.4.1 Primary map



X

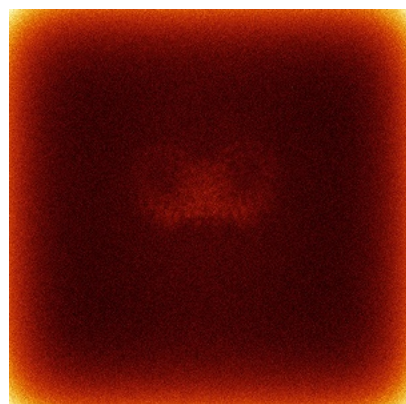


Y

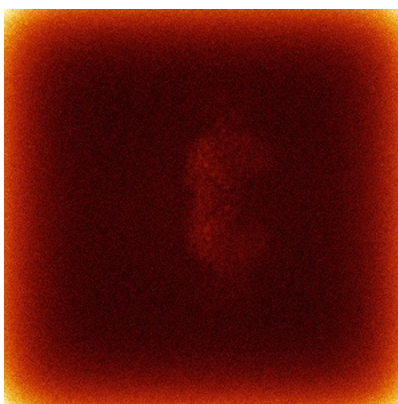


Z

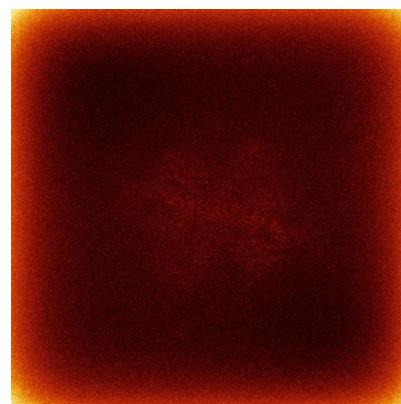
6.4.2 Raw map



X



Y

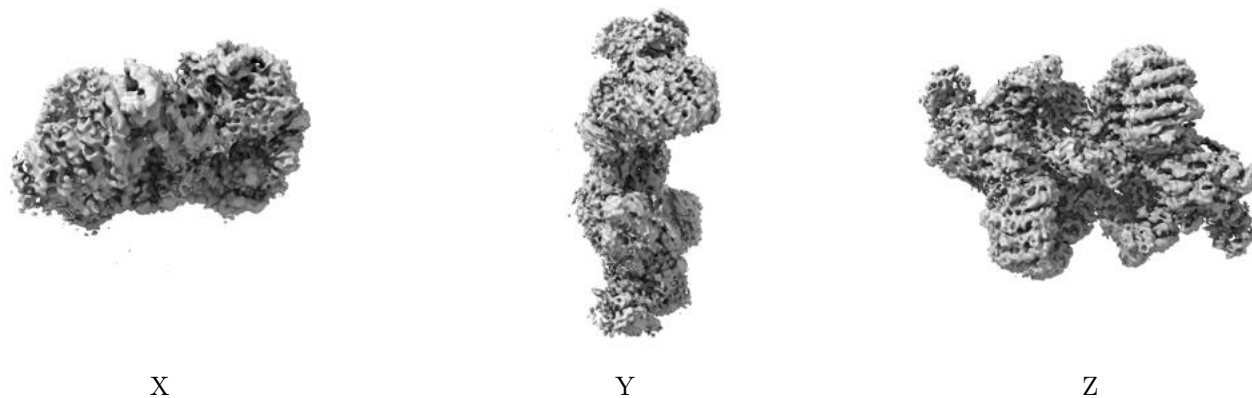


Z

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.

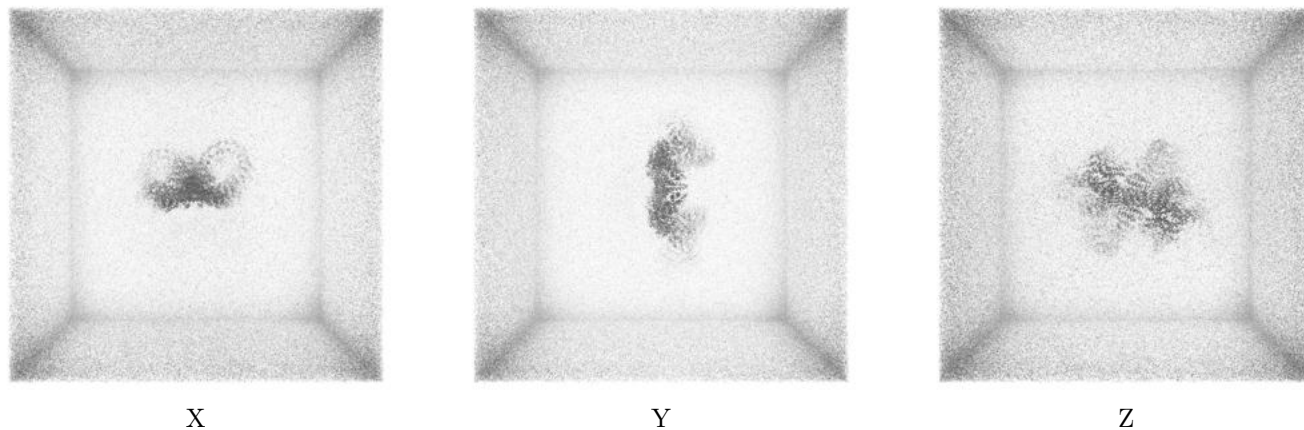
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0284. 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.

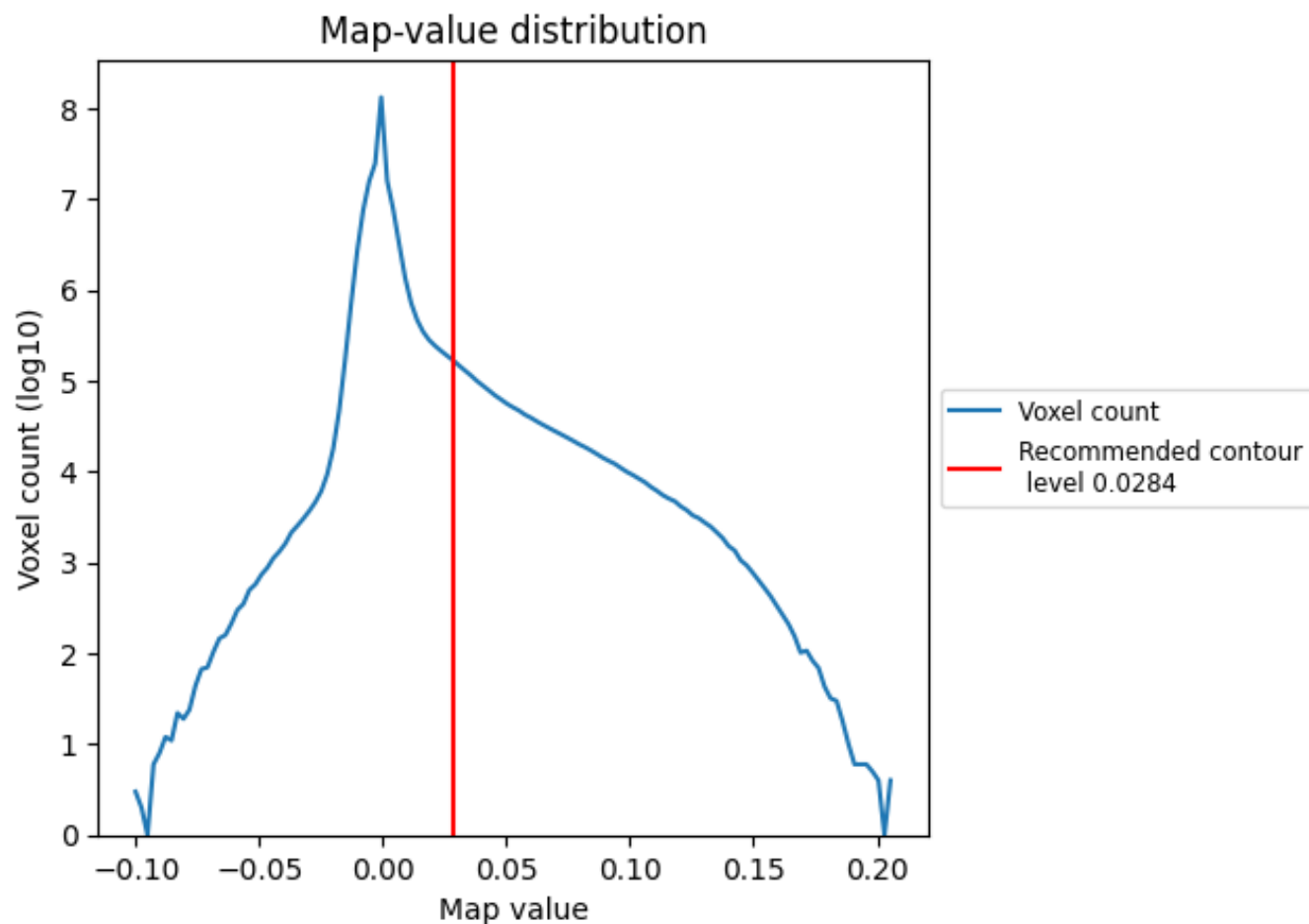
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

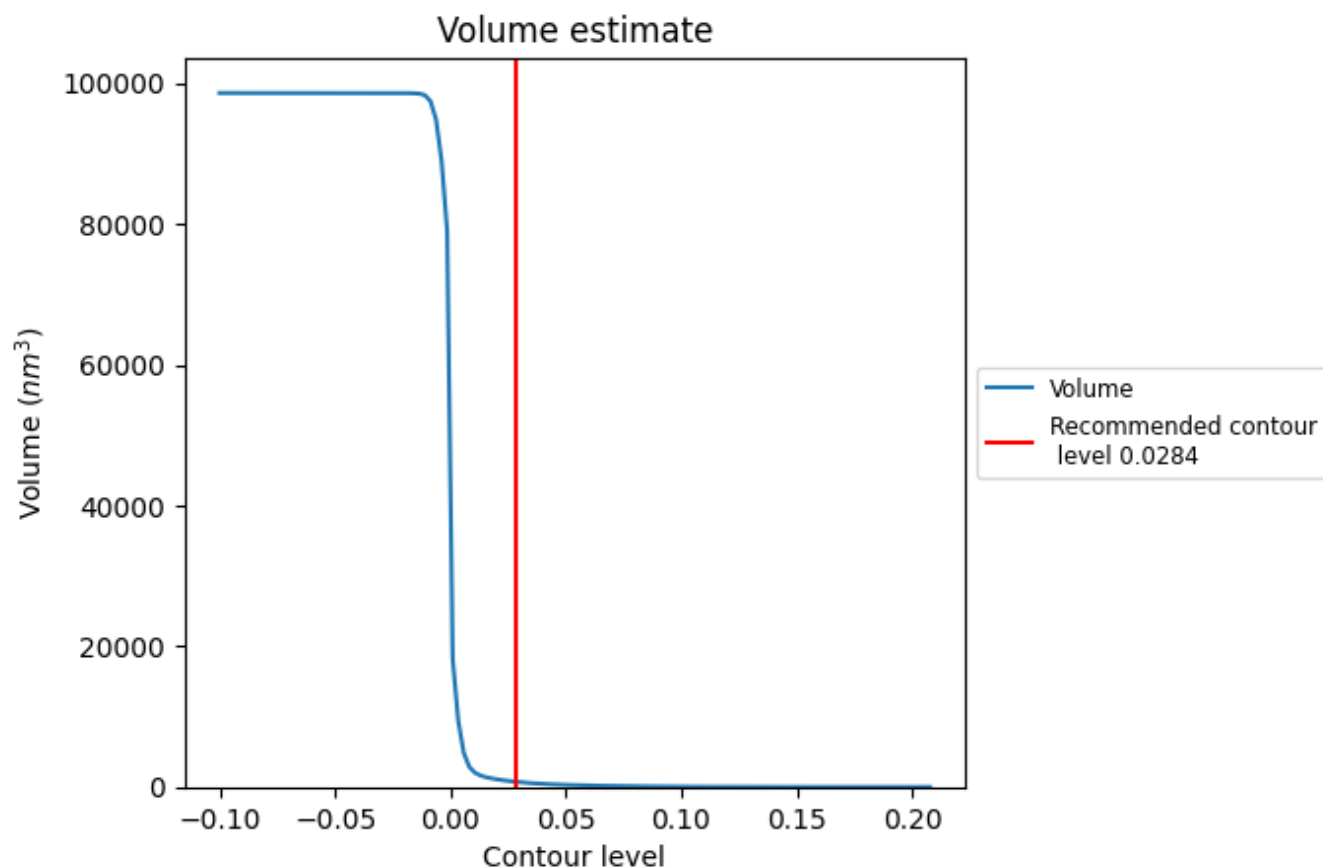
This section contains the results of statistical analysis of the map.

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.

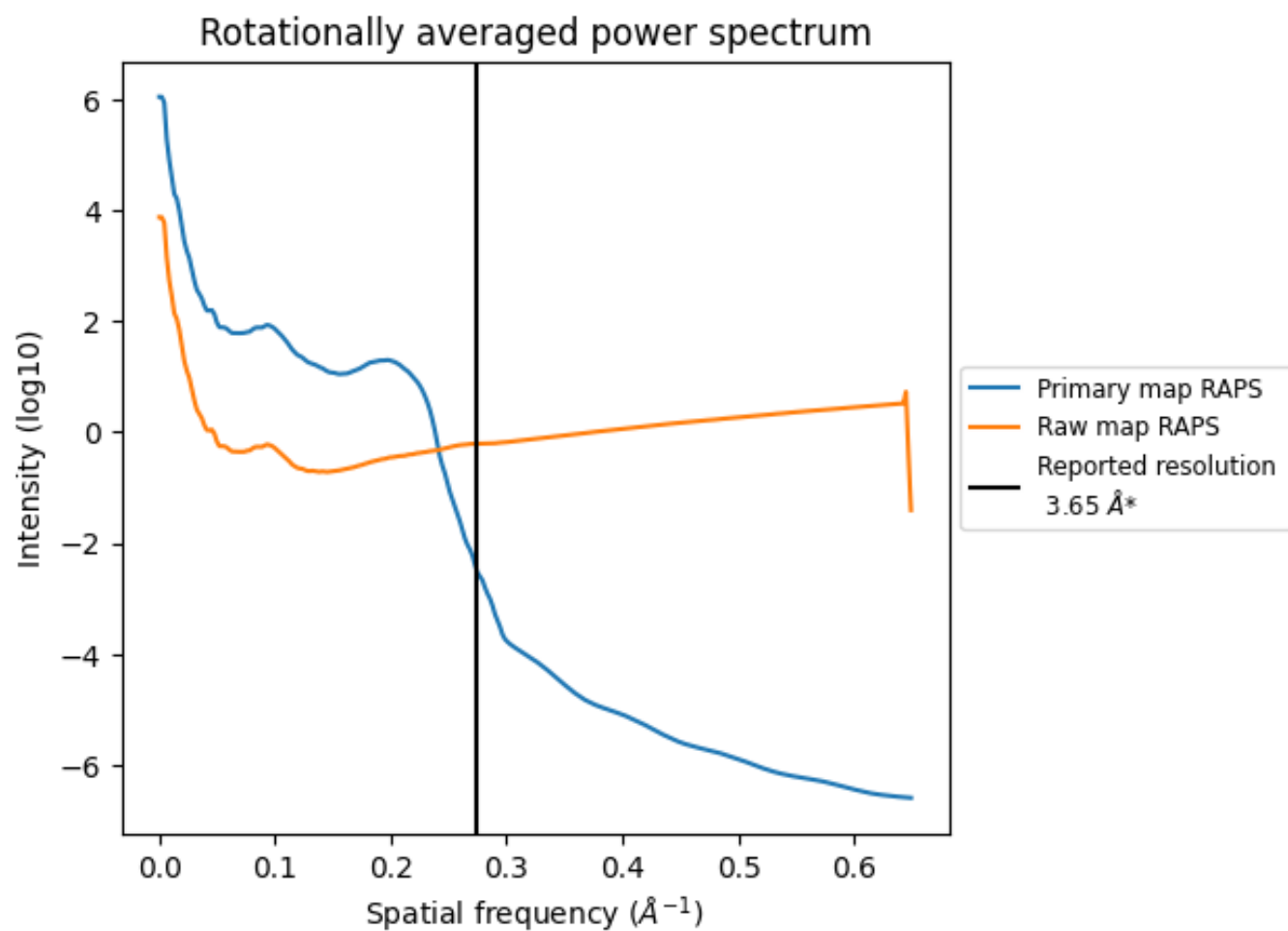
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 736 nm³; this corresponds to an approximate mass of 665 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 ⓘ

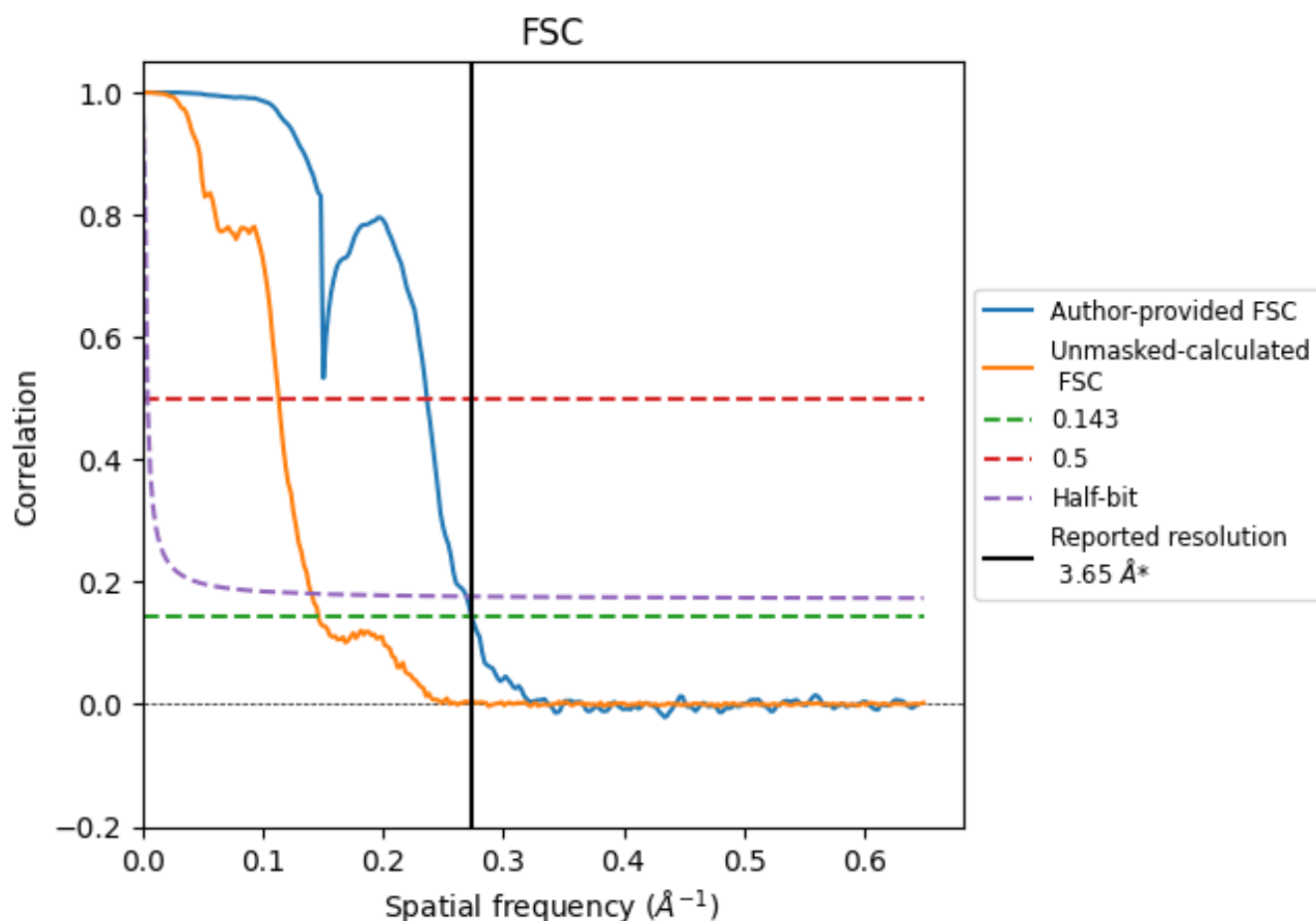


*Reported resolution corresponds to spatial frequency of 0.274 Å⁻¹

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 0.274 \AA^{-1}

8.2 Resolution estimates [i](#)

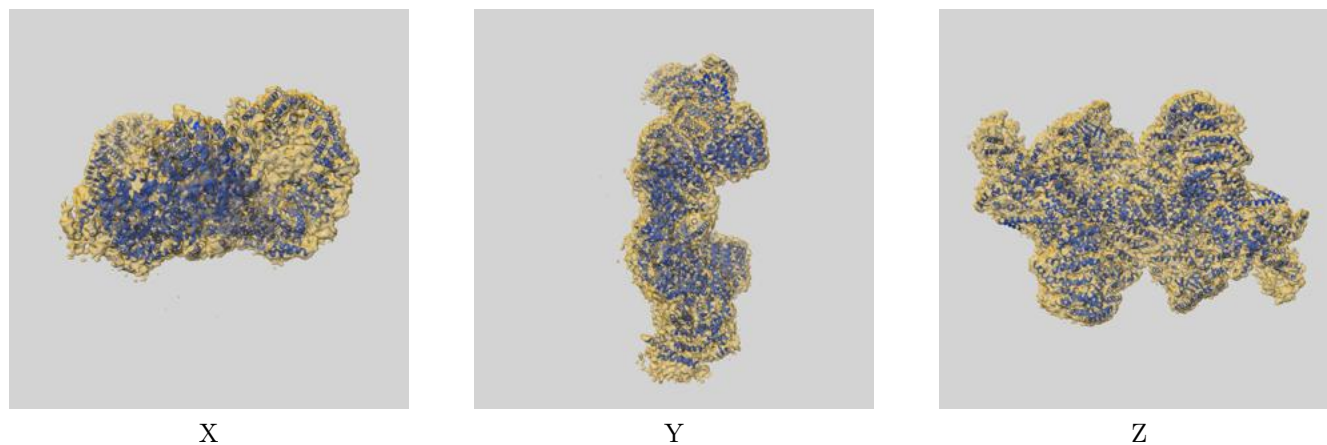
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.65	-	-
Author-provided FSC curve	3.65	4.23	3.71
Unmasked-calculated*	6.83	8.83	7.11

*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 6.83 differs from the reported value 3.65 by more than 10 %

9 Map-model fit [i](#)

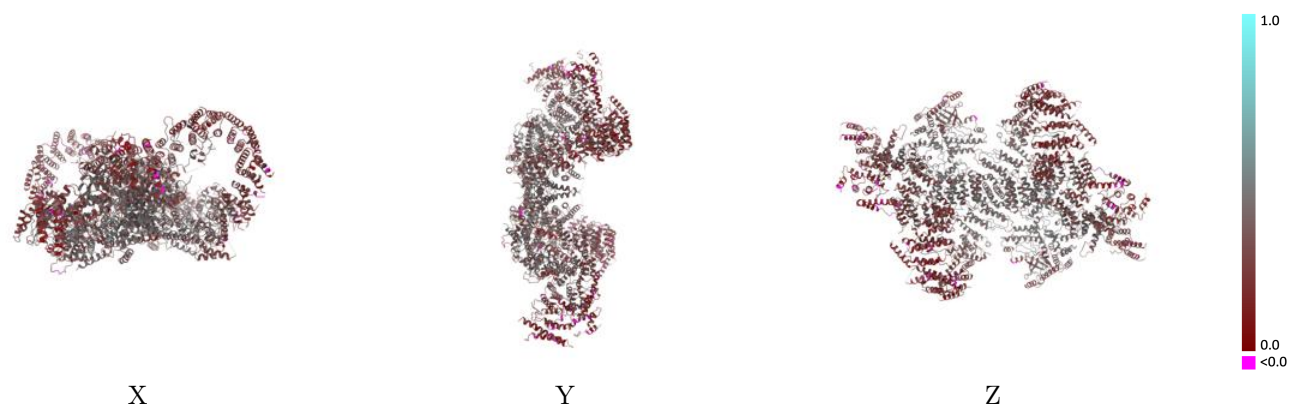
This section contains information regarding the fit between EMDB map EMD-44413 and PDB model 9BAX. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



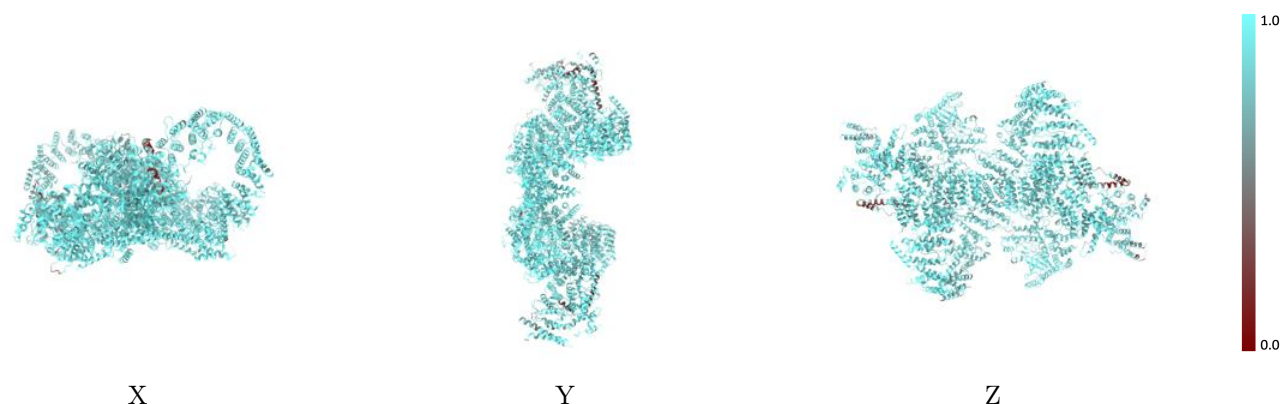
The images above show the 3D surface view of the map at the recommended contour level 0.0284 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



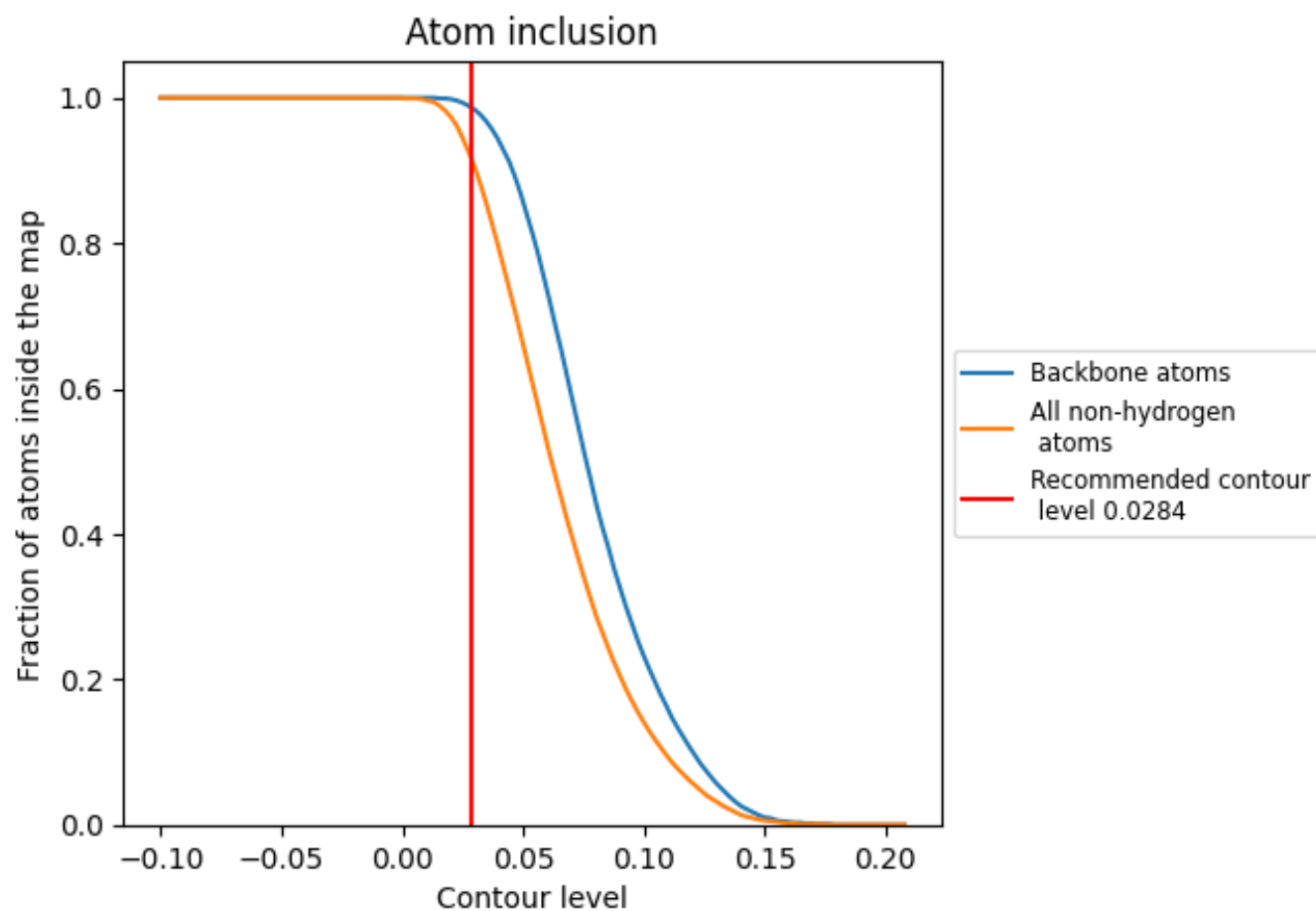
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0284).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 92% 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 (0.0284) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9180	<div></div> 0.3270
A	<div></div> 0.9450	<div></div> 0.3530
B	<div></div> 0.9320	<div></div> 0.3360
C	<div></div> 0.6030	<div></div> 0.1460
D	<div></div> 0.9110	<div></div> 0.3320
E	<div></div> 0.8820	<div></div> 0.2860
F	<div></div> 0.8950	<div></div> 0.3070
G	<div></div> 0.9160	<div></div> 0.2500
H	<div></div> 0.5520	<div></div> 0.1770

1.0

0.0

<0.0