



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 11:49 PM UTC

PDB ID : 9UOY / pdb_00009uoy
EMDB ID : EMD-64385
Title : Structure of C. elegans piezo channel
Authors : Liu, Y.; Guo, Y.R.
Deposited on : 2025-04-27
Resolution : 3.40 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:

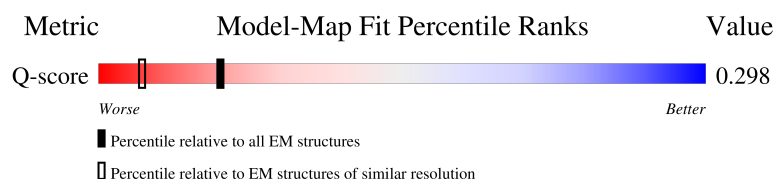
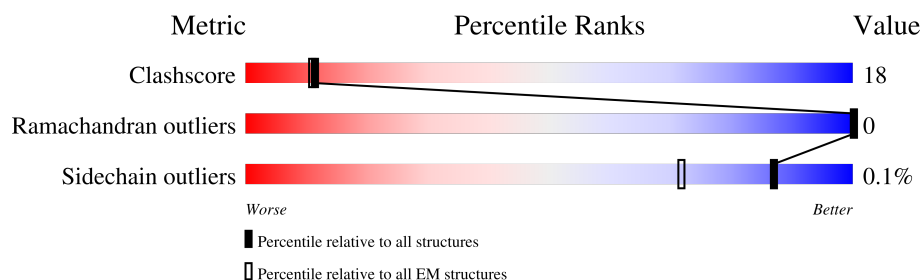
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.40 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	14717 (2.90 - 3.90)

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	2442	10% 49% 29% 21%
1	B	2442	11% 50% 29% 21%
1	C	2442	10% 50% 29% 21%

2 Entry composition

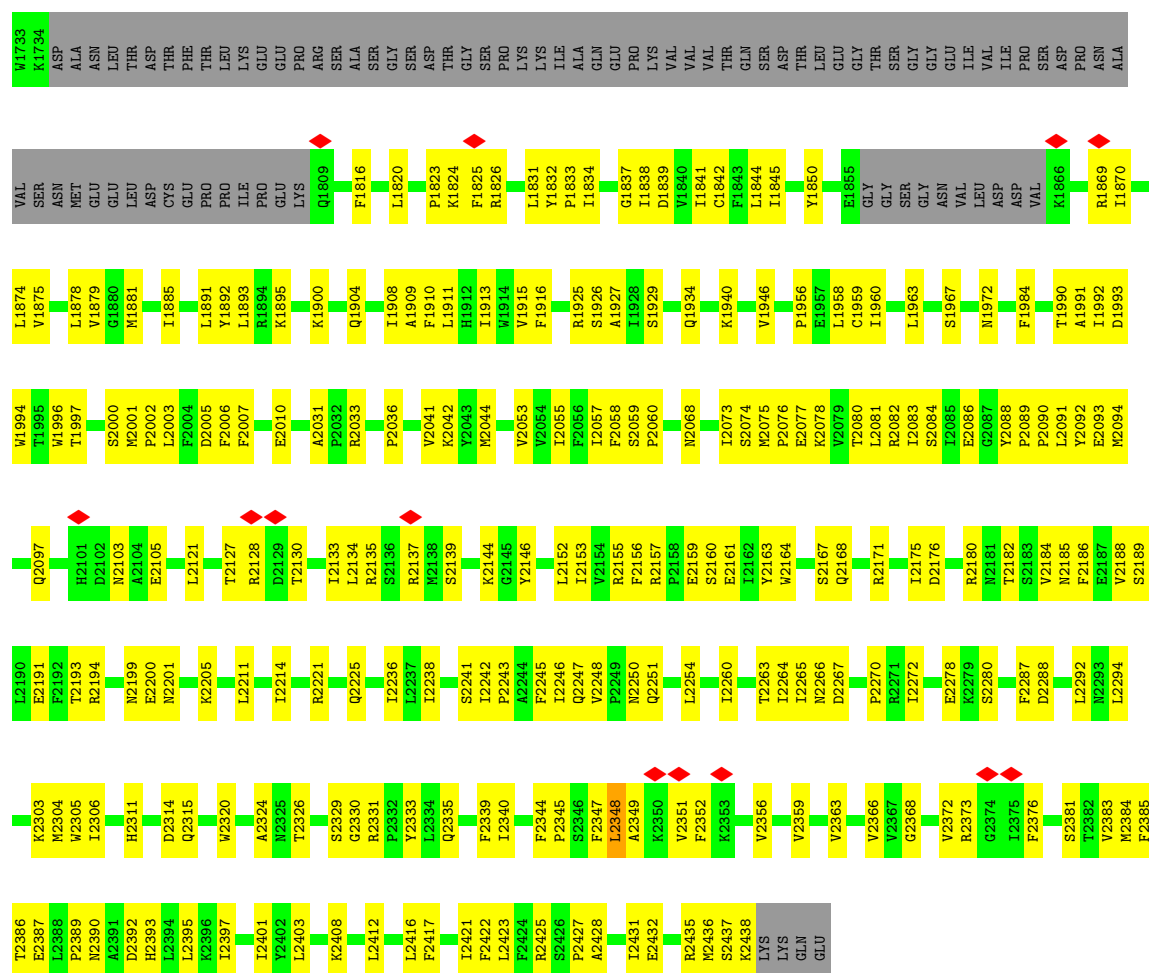
There is only 1 type of molecule in this entry. The entry contains 46695 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

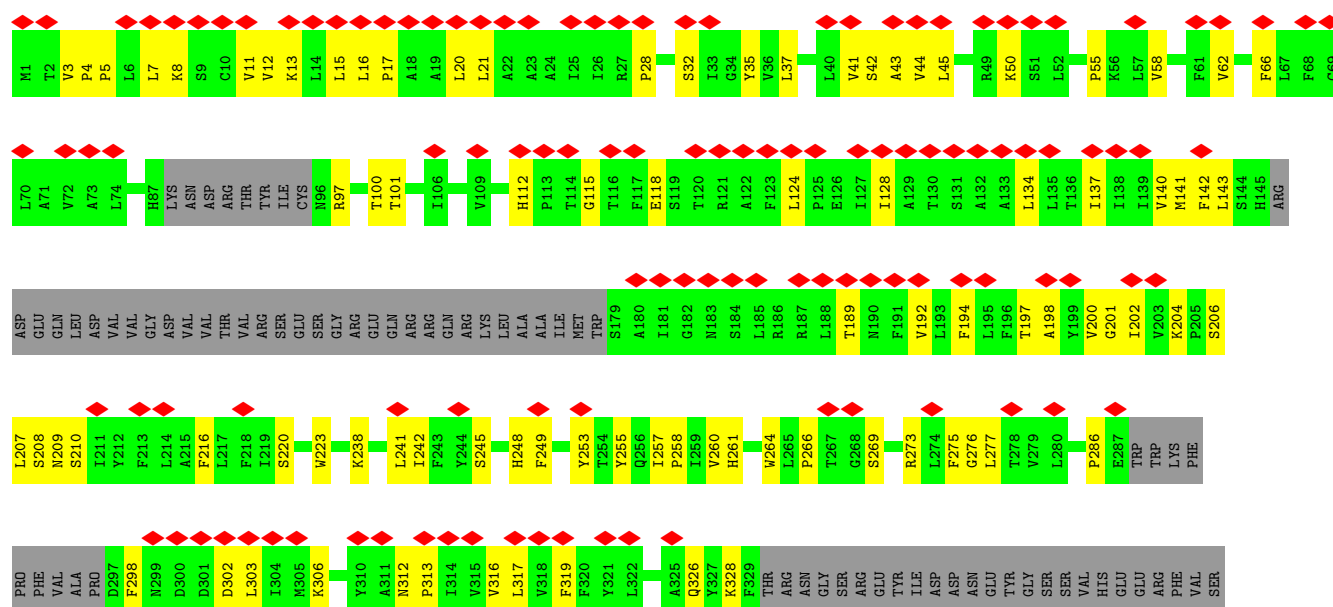
- Molecule 1 is a protein called Piezo-type mechanosensitive ion channel component 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1919	Total	C	N	O	S	0	0
			15565	10325	2510	2643	87		
1	B	1919	Total	C	N	O	S	0	0
			15565	10325	2510	2643	87		
1	C	1919	Total	C	N	O	S	0	0
			15565	10325	2510	2643	87		





• Molecule 1: Piezo-type mechanosensitive ion channel component 1



G1383	M1299	S1212	F1111	L922	Y850	ASP	T695	PHE	V553	S483	GLU	ALA
A1384	I1300	T1213	F1112	K923	I851	PRO	S696	GLN	H554	I484	GLU	GLY
E1385	G1301	L1214	M1017	G924	P852	PRO	I697	ASP	A555	F485	GLN	THR
E1386	F1302	R1215	L1116	E925	L853	THR	V698	PRO	V556	C486	GLY	VAL
R1387	D1303	R1216	A1117	V926	V854	SER	I699	LYS	I557	C487	GLU	THR
Y1389	V1304	E1218	L1121	E927	S858	THR	I700	LYS	I558	I488	PRO	ASN
A1396	H1219	H1219	A1021	E928	I861	THR	Y705	GLU	L559	I489	LEU	VAL
L1397	T1220	T1220	A1022	T929	I861	GLU	F706	ALA	C560	L490	ARG	ASP
G1401	W1224	W1224	C1025	E930	P864	ALA	F707	ALA	V561	L491	VAL	ASP
F1404	Y1230	Y1230	L1028	Y933	S865	VAL	S711	ALA	S562	L492	THR	GLY
M1405	F1312	L1231	M1028	N934	A866	ALA	N717	SER	L564	T493	GLN	LEU
F1406	G1312	L1232	V1029	I935	I870	THR	T718	THR	L565	C494	ILE	LEU
D1409	R1315	F1233	F936	G937	F871	THR	S719	GLY	L567			
F1410	I1316	T1234	M1146	Q937	S872	GLY	L720	GLY	P568			
E1411	I1235	I1236	F1147	Q148	M875	THR	E723	THR	F499			
ASN	M1237	M1237	R1036	Y940		GLN	E724	GLN	R501			
ASP	L1241	L1241	D1153	L945	Y878	GLY	W734	GLY	K504			
ASP	Q1242	Q1242	T1154	A946	L879	ARG	A735	ARG	S505			
LEU	Y1329	Y1329	K1155	F947	F880	ALA	I736	ALA	F507			
VAL	R1330	I1243	X1156	Q948	F881	HIS	G737	ALA	A508			
GLU	S1331	F1244	S1157	S949	L881	ALA	E738	ALA	M509			
PRO	E1332	F1244	V1047	I950	V882	ALA	L730	ALA	A510			
VAL	V1247	V1247	V1159	Y951	L882	GLY	R734	GLY	P511			
ASP	F1248	F1248	D1160	A883	L884	ASP	A735	ASP	I512			
SER	L1249	L1249	Y1054	L884	L884	LEU	I736	LEU	I513			
PHE	F1252	F1252	L1053	M887	L887	THR	G737	THR	I514			
VAL	D1253	D1253	Q1057	L888	L889	THR	E738	THR	P515			
PRO	G1259	G1259	Y958	L891	L891	LEU	S739	LEU	V516			
ASP	L1262	L1262	V1062	L892	L892	LEU	A741	LEU	I517			
LYS	C1263	C1263	P1065	E895	L893	THR	L742	THR	E518			
ALA	I1264	I1264	P1066	L895	L895	THR	L743	THR	F519			
THR	V1265	V1265	D1067	L896	L896	THR	Q745	THR	L520			
ALA	R1266	R1266	S1068	L897	L897	THR	L746	THR	I452			
TVR	Q1267	Q1267	C1069	L898	L898	THR	L747	THR	M455			
ASP	L1268	L1268	I1070	L899	L899	THR	A748	THR	I456			
ARG	I1271	I1271	W1074	L900	L900	THR	P749	THR	H465			
LEU	V1274	V1274	W1077	L901	L901	THR	L750	THR	S468			
ASP	N1276	N1276	D1083	L902	L902	THR	A751	THR	I469			
GLY	E1277	E1277	R1086	L903	L903	THR	L752	THR	I470			
GLN	V1280	V1280	L1089	L904	L904	THR	V755	THR	A470			
MET	L1281	L1281	L1092	L905	L905	THR	L760	THR	L471			
ALA	K1282	K1282	L1093	L906	L906	THR	K761	THR	A472			
ALA	D1286	D1286	L1094	L907	L907	THR	A769	THR	A473			
THR	F1287	F1287	L1095	L908	L908	THR	V769	THR	M474			
ALA	C1291	C1291	Y1106	L909	L909	THR	S772	THR	M475			
ASP	E1294	E1294	D1110	L910	L910	THR	ARG	THR	M476			
LEU				L911	L911	THR	ALA	THR	T476			
				L912	L912	THR	GLY	THR	M477			
				L913	L913	THR	GLY	THR	A478			
				L914	L914	THR	GLY	THR	L480			
				L915	L915	THR	GLY	THR	M481			
				L916	L916	THR	GLY	THR	T481			
				L917	L917	THR	GLY	THR	M482			
				L918	L918	THR	GLY	THR	T483			
				L919	L919	THR	GLY	THR	M484			
				L920	L920	THR	GLY	THR	T485			
				L921	L921	THR	GLY	THR	M486			
				L922	L922	THR	GLY	THR	T487			
				L923	L923	THR	GLY	THR	M488			
				L924	L924	THR	GLY	THR	T489			
				L925	L925	THR	GLY	THR	M490			
				L926	L926	THR	GLY	THR	T491			
				L927	L927	THR	GLY	THR	M492			
				L928	L928	THR	GLY	THR	T493			
				L929	L929	THR	GLY	THR	M494			
				L930	L930	THR	GLY	THR	T495			
				L931	L931	THR	GLY	THR	M496			
				L932	L932	THR	GLY	THR	T497			
				L933	L933	THR	GLY	THR	M498			
				L934	L934	THR	GLY	THR	T499			
				L935	L935	THR	GLY	THR	M500			
				L936	L936	THR	GLY	THR	T501			
				L937	L937	THR	GLY	THR	M502			
				L938	L938	THR	GLY	THR	T503			
				L939	L939	THR	GLY	THR	M504			
				L940	L940	THR	GLY	THR	T505			
				L941	L941	THR	GLY	THR	M506			
				L942	L942	THR	GLY	THR	T507			
				L943	L943	THR	GLY	THR	M508			
				L944	L944	THR	GLY	THR	T509			
				L945	L945	THR	GLY	THR	M510			
				L946	L946	THR	GLY	THR	T511			
				L947	L947	THR	GLY	THR	M512			
				L948	L948	THR	GLY	THR	T513			
				L949	L949	THR	GLY	THR	M514			
				L950	L950	THR	GLY	THR	T515			
				L951	L951	THR	GLY	THR	M516			
				L952	L952	THR	GLY	THR	T517			
				L953	L953	THR	GLY	THR	M518			
				L954	L954	THR	GLY	THR	T519			
				L955	L955	THR	GLY	THR	M520			
				L956	L956	THR	GLY	THR	T521			
				L957	L957	THR	GLY	THR	M522			
				L958	L958	THR	GLY	THR	T523			
				L959	L959	THR	GLY	THR	M524			
				L960	L960	THR	GLY	THR	T525			
				L961	L961	THR	GLY	THR	M526			
				L962	L962	THR	GLY	THR	T527			
				L963	L963	THR	GLY	THR	M528			
				L964	L964	THR	GLY	THR	T529			
				L965	L965	THR	GLY	THR	M530			
				L966	L966	THR	GLY	THR	T531			
				L967	L967	THR	GLY	THR	M532			
				L968	L968	THR	GLY	THR	T533			
				L969	L969	THR	GLY	THR	M534			
				L970	L970	THR	GLY	THR	T535			
				L971	L971	THR	GLY	THR	M536			
				L972	L972	THR	GLY	THR	T537			
				L973	L973	THR	GLY	THR	M538			
				L974	L974	THR	GLY	THR	T539			
				L975	L975	THR	GLY	THR	M540			
				L976	L976	THR	GLY	THR	T541			
				L977	L977	THR	GLY	THR	M542			
				L978	L978	THR	GLY	THR	T543			
				L979	L979	THR	GLY	THR	M544			
				L980	L980	THR	GLY	THR	T545			
				L981	L981	THR	GLY	THR	M546			
				L982	L982	THR	GLY	THR	T547			
				L983	L983	THR	GLY	THR	M548			
				L984	L984	THR	GLY	THR	T549			
				L985	L985	THR	GLY	THR	M550			
				L986	L986	THR	GLY	THR	T551			
				L987	L987	THR	GLY	THR	M552			
				L988	L988	THR	GLY	THR	T553			
				L989	L989	THR	GLY	THR	M554			
				L990	L990	THR	GLY	THR	T555			
				L991	L991	THR	GLY	THR	M556			
				L992	L992	THR	GLY	THR	T557			
				L993	L993	THR	GLY	THR	M558			
				L994	L994	THR	GLY	THR	T559			
				L995	L995	THR	GLY	THR	M560			
				L996	L996	THR	GLY	THR	T561			
				L997	L997	THR	GLY	THR	M562			
				L998	L998	THR	GLY	THR	T563			
				L999	L999	THR	GLY	THR	M564			
				L1000	L1000	THR	GLY	THR	T565			
				L1001	L1001	THR	GLY	THR	M566			
				L1002	L1002	THR	GLY	THR	T567			
				L1003	L1003	THR	GLY	THR	M568			
				L1004	L1004	THR	GLY	THR	T569			
				L1005	L1005	THR	GLY	THR	M570			
				L1006	L1006	THR	GLY	THR	T571			
				L1007	L1007	THR	GLY	THR	M572			
				L1008	L1008	THR	GLY	THR	T573			
				L1009	L1009	THR	GLY	THR	M574			
				L1010								

L70	A71	V72	A73	L74	H87	LYS	ASP	GLU	GLN	LEU	VAL	VAL	GLY	ASP	ASN	ASP	THR	THR	THR	ILE	CYS	N96	R97	T100	T101	I106	V109	H112	P113	T114	G115	T116	F117	E118	S119	T120	R121	A122	F123	L124	P125	E126	L127	I128	A129	T130	S131	A132	A133	L134	L135	T136	I137	I138	I139	V140	M141	F142	L143	S144	H145	ARG
ASP	GLU	THR	LEU	VAL	VAL	GLY	GLU	GLN	GLN	ASP	PRO	VAL	THR	ASN	VAL	VAL	THR	THR	ARG	SER	GLU	SER	GLY	ARG	GLN	ARG	GLN	ARG	ALA	ALA	ILE	MET	TRP	S179	A180	I181	G182	N183	S184	L185	R186	R187	L188	T189	N190	F191	V192	L193	F194	L195	F196	T197	A198	Y199	V200	G201	I202	V203	K204	P205	S206	
L207	S208	N209	S210	I211	Y212	F213	L214	A215	F216	L217	F218	I219	S220	W223	K238	L241	I242	F243	Y244	S245	H248	F249	Y253	T254	Y255	Q256	P258	I259	V260	H261	W264	L265	P266	T267	G268	S269	R273	L274	F275	G276	L277	T278	V279	L280	P286	E287	TRP	TRP	LYS	PHE												
PRO	PHE	VAL	ALA	PRO	D297	F298	N299	D300	D301	D302	L303	I304	M305	K306	Y310	A311	N312	P313	I314	V315	V316	L317	V318	F319	F320	Y321	L322	A325	Q326	Y327	K328	F329	THR	ARG	ASN	GLY	ARG	ARG	GLU	GLN	TYR	ILE	ASP	ASP	GLU	GLY	ARG	ALA	ASN	PRO	LEU	ARG	ASN	GLY								
ALA	GLY	THR	VAL	THR	ASN	VAL	VAL	ASP	ASP	VAL	GLY	GLN	LEU	ILE	ILE	GLU	THR	THR	ALA	ALA	PRO	SER	GLY	THR	GLY	THR	LEU	LEU	LEU	SER	ASN	ALA	SER	SER	SER	ALA	ASN	ASP	ASP	GLU	GLN	TYR	ILE	ASP	ASP	GLU	GLY	ARG	ALA	ASN	PRO	LEU	ARG	ASN	GLY							
GLU	GLU	GLN	GLY	SER	ILE	PRO	LEU	ARG	LYS	THR	THR	GLN	VAL	VAL	ASP	ARG	ASN	LYS	LEU	ASN	ILE	PHE	ASN	THR	THR	PRO	GLY	ASP	LYS	A449	A450	A451	A452	G453	G454	M455	I456	H465	S468	I469	A470	L471	T472	A473	M474	M475	T476	W477	A478	L479	I480	L481	H482									
S483	I484	F485	G486	L487	I488	L489	L490	L491	Q492	T493	C494	H497	I498	F499	A500	D501	K504	S505	F507	A508	M509	A510	P511	I512	I513	L514	M515	Y516	I517	E518	F519	L520	L521	L522	L523	Q524	Y525	F526	M529	D530	I531	H532	W540	M541	M542	F543	V544	E547	H548	T549	L550	L551	P552									
V553	H554	A555	V556	I557	I558	C559	V561	Q562	T563	L564	L565	L566	L567	P568	V569	F570	L571	L572	L573	R574	R578	E579	L581	F582	E583	SER	LEU	SER	ASP	TYR	GLU	ARG	GLN	ARG	ARG	ARG	ILE	ASN	TYR	GLY	THR	PHE	GLY	ALA	GLY	VAL	ALA	VAL	ALA	LYS												
PHE	GLN	ASP	PRO	LYS	S620	R621	K622	F623	A624	A625	Y629	K633	Y637	F638	L639	V641	V642	S643	V644	V645	L646	V649	F653	A654	P655	N656	F657	T660	L661	F662	F663	A664	L665	W666	L673	S676	L679	Y680	R681	Y685	A686	F687	W688	L689	T692	F693	Y694															
T695	S696	I697	V698	I699	I700	Y705	N717	T718	S719	L720	E723	W724	I728	G729	L730	R734	A735	I736	G737	E738	S739	G740	A741	L742	F743	L744	Q745	L746	L747	A748	P749	I750	A751	L752	V755	L760	K761	R769	A770	T771	S772	P773	ARG	ARG	ALA	GLY	VAL	ALA	VAL	ALA	LYS											
SER	THR	THR	GLU	ALA	ALA	VAL	ALA	SER	THR	GLY	THR	GLY	GLY	ARG	ALA	HIS	ALA	ALA	GLY	ASP	LEU	V808	I809	X810	L814	A815	Q817	L821	R824	F825	F826	E827	I830	V834	F835	V836	I837	I838	A839	I840	F841	I842	N847	A848	L849	Y850	I851	P852	L853													
V854	S858	I861	P864	S865	A866	G869	S872	M875	Y878	L879	F880	L881	V882	A883	L884	M887	I888	Y889	Q890	L891	D892	I893	E896	L821	R824	F825	F826	E827	I830	V834	F835	V836	I837	I838	A839	I840	F841	I842	N847	A848	L849	Y850	I851	P852	L853																	
V926	E927	G928	T929	E930	Y933	M934	L935	F936	G937	L945	A946	Q947	Q948	S949	Y950	I951	Q955	R956	H957	Y958	R959	G963	L964	P965	E966	S967	M968	R969	P974	D975	P976	H977	H978	S979	H980	R983	L1002	E1003	I1004	T1005	M1006	I1007	A1008	I1009	R1016	M1017	D1018	F1111	F1112													
A1022	I1023	Q1024	C1025	L1028	V1029	L1033	R1036	Y1037	F1038	I1042	W1043	V1047	L1053	Y1054	P1055	Q1057	F1058	V1062	G1063	L1064	P1065	L1066	D1067	S1068	C1069	I1070	W1074	W1077	D1083	R1086	L1089	L1092	L1093	N1094	L1095	S1104	A1105	Y1106	L1107	G1108	I1109	D1110	F1111	F1112																		

K2303	D2197	H2101	V1996	M1881	G1695	PRO	GLN	ASP	E1381	M1299	S1212	L116
K2304	D2102	D2102	T1997	T1885	M1646	SER	LYS	LEU	R1382	I1300	T1213	T1213
V2306	P2198	N2103	S2000	L1891	L1647	GLN	ILE	ALA	A1384	G1301	L214	A1117
E2200	M2001	E2105	M2001	P1891	S1648	LEU	SER	THR	A1385	F1302	R1215	L1121
H2311	N2201	L2121	L2003	L1893	P1650	VAL	ALA	VAL	R1387	D1303	E1218	R1125
D2314	K2205	L2121	F2004	R1894	R1651	SER	LEU	GLN	Y1394	V1304	H219	H219
Q2315	L2211	T2127	P2006	K1895	M1660	ALA	ASP	VAL	Y1394	I1305	T2220	N1131
V2320	L2214	R2128	F2007	K1900	T1661	ASN	CYS	LYS	A1397	L1310	W1224	Y1135
A2324	R2221	T2130	E2010	Q1904	T1662	VAL	THR	GLY	A1397	F1312	W1224	N1136
K2325	Q2225	L2133	A2031	I1908	Y1663	GLU	VAL	ASP	G1401	Y1230	Y1230	D1137
T2326	Q2225	L2134	P2032	A1909	T1664	LYS	THR	THR	G1401	Q1313	T2231	G1138
S2329	R2230	R2135	R2033	F1910	E1685	MET	LEU	ILE	Y1404	I1314	L2232	N1146
G2330	L2236	S2136	F1910	L1911	C1686	GLU	LYS	ASP	H1405	R1315	F1233	P1147
R2331	L2237	R2137	P2036	L1912	V1687	THR	LEU	PRO	F1406	I1316	T2234	L2148
F2332	I2238	R2138	P2036	I1913	I1670	ALA	CYS	ASP	D1409	F1317	I1235	Q1148
L2334	S2241	S2139	V2041	W1914	V1673	VAL	ARG	SER	P1410	Q1323	M1237	D1153
Q2335	M2044	F1826	M2044	F1916	V1673	VAL	GLU	ARG	E1411	I1241	D1154	T1154
F2339	V2053	L1831	V2053	L1919	F1678	TRP	HIS	ALA	ASN	M1326	Q1242	K1155
I2340	V2054	P1833	V2054	L1919	P1679	ASP	ARG	ALA	ASP	R1330	L1243	K1156
F2344	I2246	Y1832	I2055	R1925	M1678	Q1594	TYR	ILE	ASP	S1331	F1244	S1157
Q2347	F2056	G1837	I2055	S1926	P1680	Q1595	VAL	ALA	ASP	E1332	V1247	V1159
P2346	I2057	L1838	I2057	A1927	Y1681	K1596	GLY	VAL	LEU	I1335	F1248	D1160
S2349	F2058	Y1840	F2058	L1928	Y1681	S1597	PHE	SER	GLU	L1335	L1249	Y1161
F2347	S2059	V1841	S2059	S1929	T1688	S1598	LEU	PRO	VAL	R1338	F1162	F1162
L2348	P2060	I1841	P2060	Q1934	E1689	R1601	LYS	ALA	SER	V1341	V1166	V1166
A2349	S2160	C1842	I1841	I1841	H1690	H1613	GLU	ARG	PHE	L1342	F1167	F1167
K2350	E2253	I1842	C1842	C1842	Q1691	T1614	LYS	LYS	VAL	L1343	H1172	H1172
V2351	L2162	I1845	I1845	I1845	M1692	I1616	GLY	GLY	PRO	K1343	G1269	G1269
F2352	Y2163	I1845	I1845	I1845	M1692	I1616	LEU	GLY	GLY	M1344	L1262	L1262
K2353	W2164	Y1850	Y1850	Y1946	P1694	Y1619	SER	THR	ASP	Q1345	C1263	C1263
V2356	S2167	E1855	E1855	P1956	F1701	F1620	GLU	GLU	PRO	K1349	I1264	I1264
I2263	Q2168	GLY	GLY	E1957	G1702	F1622	GLY	THR	LYS	E1350	V1265	V1265
I2265	R2171	SER	SER	L1958	D1707	I1623	ASP	GLY	ALA	M1351	R1266	R1266
N2266	R2171	ASN	ASN	C1959	S1708	T1625	LEU	ASP	THR	K1352	Q1267	Q1267
D2267	I2175	GLY	GLY	I1960	F1709	Q1626	SER	GLU	ASP	Q1354	L1268	L1268
G2268	D2176	VAL	VAL	L1963	A1710	V1627	LEU	GLU	ASP	N1355	I1183	I1183
N2269	R2180	LEU	LEU	S1967	L1711	M1628	SER	ASP	ARG	E1356	I1271	I1271
P2270	R2181	ASP	ASP	L1967	L1712	G1630	THR	ASP	GLN	K1359	V1274	V1274
I2272	R2182	ASP	ASP	M1972	D1713	G1631	ARG	LYS	ASP	E1359	N1275	N1275
E2278	S2183	VAL	VAL	F1984	I1714	G1632	LYS	ASP	GLY	D1364	E1277	E1277
K2279	V2184	K1866	K1866	F1984	V1715	L1632	LEU	SER	ILE	I1365	V1280	V1280
S2280	N2185	R1869	R1869	E1987	L1716	T1634	THR	LYS	MET	R1366	L1281	L1281
F2287	F2186	I1870	I1870	E1987	L1730	P1636	VAL	VAL	THR	R1367	K1282	K1282
D2288	R2188	L1874	L1874	A1991	G1741	P1637	SER	ARG	ALA	R1368	D1286	D1286
L2292	S2189	V1875	V1875	I1992	L1732	P1638	ALA	THR	ALA	R1373	F1287	F1287
N2293	L2190	L1878	L1878	L1992	W1733	I1639	ALA	ALA	ALA	Q1377	L1207	L1207
L2294	E2191	L1878	L1878	W1994	K1734	M1640	VAL	LYS	ALA	K1378	L1207	L1207
F2295	F2192	L1879	L1879	T1995	ASP	W1644	ASP	PHE	ASP	I1379	V1209	V1209
E2387	T2193	V1879	V1879	T1995	ALA	W1644	LEU	ILE	LEU	I1380	E1294	E1294
L2388	R2194	G1880	G1880	T1995	ASN	W1644	LEU	ILE	LEU	I1380	E1294	E1294

P2389	N2390	A2391	D2392	H2393	L2394	L2395	R2396	L2397	L2401	Y2402	L2403	K2408	L2412	L2416	F2417	I2421	F2422	L2423	F2424	R2425	S2426	P2427	I2431	E2432	R2435	N2436	S2437	K2438	LYS	LYS	GLN	GLU
-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	163221	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.401	Depositor
Minimum map value	-0.140	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.075	Depositor
Map size (Å)	532.0, 532.0, 532.0	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	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	0.15	0/16001	0.39	0/21741
1	B	0.15	0/16001	0.39	0/21741
1	C	0.15	0/16001	0.39	0/21741
All	All	0.15	0/48003	0.39	0/65223

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	15565	0	15810	581	0
1	B	15565	0	15810	593	0
1	C	15565	0	15810	582	0
All	All	46695	0	47430	1687	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 18.

The worst 5 of 1687 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:A:966:GLU:HG2	1:A:969:ARG:NH1	1.54	1.22

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:966:GLU:HG2	1:C:969:ARG:NH1	1.54	1.21
1:B:966:GLU:HG2	1:B:969:ARG:NH1	1.54	1.19
1:B:959:ARG:NH2	1:B:969:ARG:HD3	1.61	1.15
1:A:959:ARG:NH2	1:A:969:ARG:HD3	1.62	1.13

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	1897/2442 (78%)	1792 (94%)	105 (6%)	0	100	100
1	B	1897/2442 (78%)	1792 (94%)	105 (6%)	0	100	100
1	C	1897/2442 (78%)	1792 (94%)	105 (6%)	0	100	100
All	All	5691/7326 (78%)	5376 (94%)	315 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1698/2141 (79%)	1697 (100%)	1 (0%)	88	89
1	B	1698/2141 (79%)	1697 (100%)	1 (0%)	88	89
1	C	1698/2141 (79%)	1697 (100%)	1 (0%)	88	89

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	5094/6423 (79%)	5091 (100%)	3 (0%)	87 89

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2348	LEU
1	B	2348	LEU
1	C	2348	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	980	HIS
1	C	2201	ASN
1	C	1267	GLN
1	C	1682	ASN
1	A	2325	ASN

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 ⓘ

There are no chain breaks in this entry.

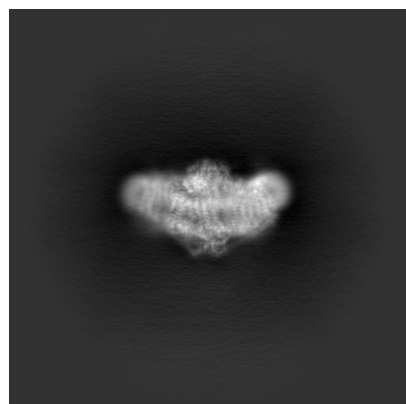
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64385. These allow visual inspection of the internal detail of the map and identification of artifacts.

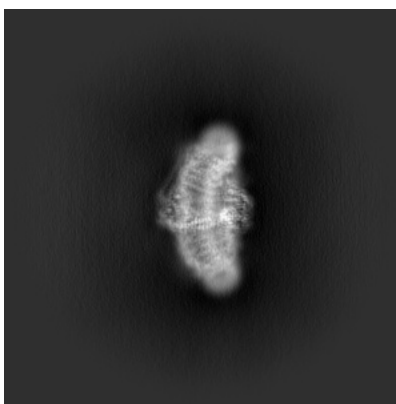
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

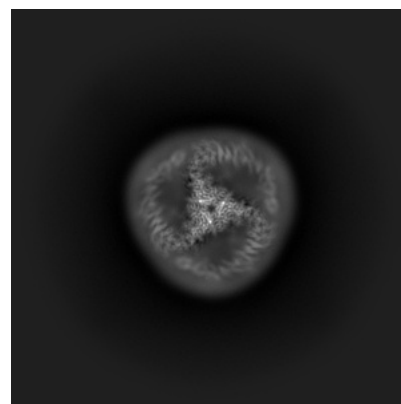
6.1.1 Primary map



X

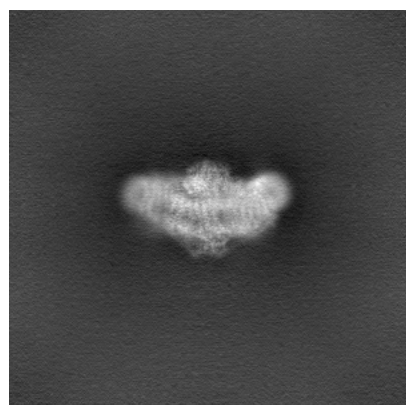


Y

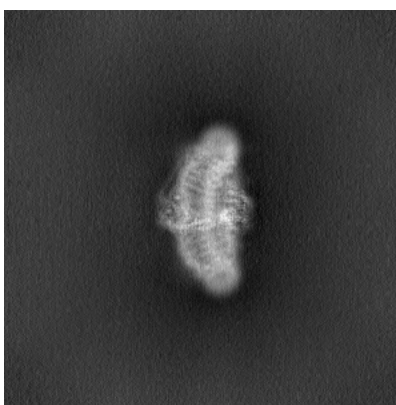


Z

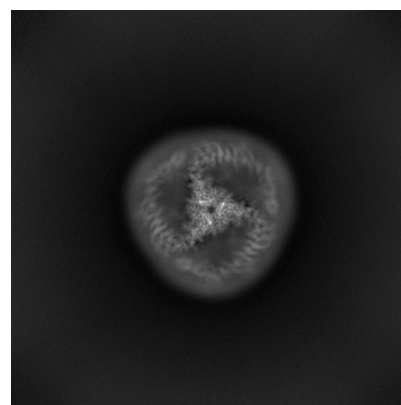
6.1.2 Raw map



X



Y

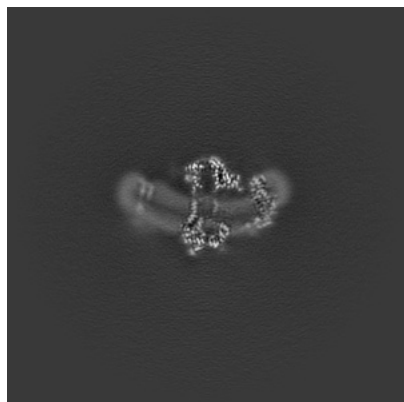


Z

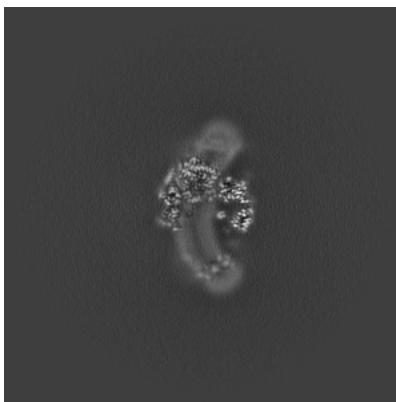
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

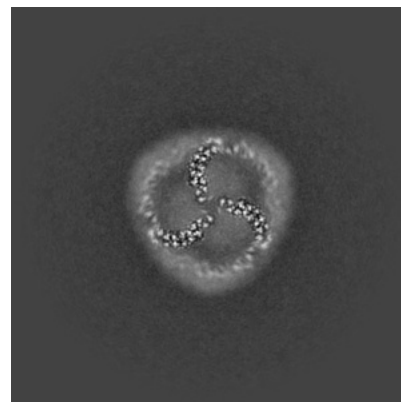
6.2.1 Primary map



X Index: 280



Y Index: 280

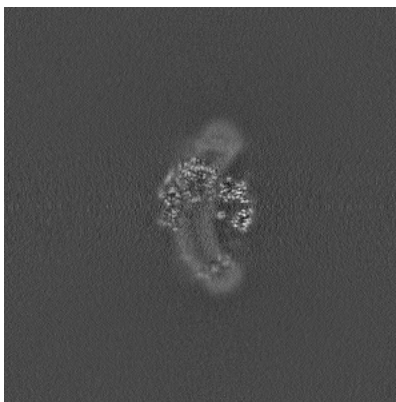


Z Index: 280

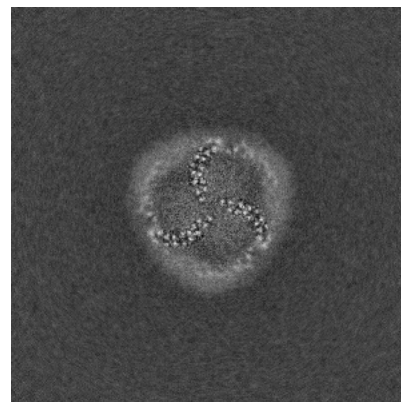
6.2.2 Raw map



X Index: 280



Y Index: 280

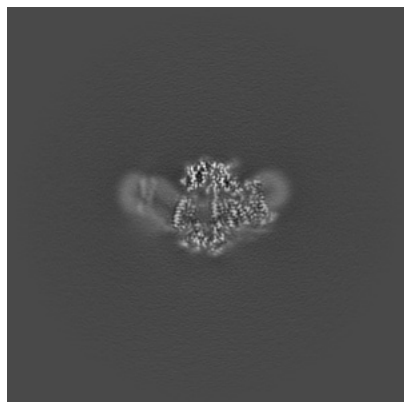


Z Index: 280

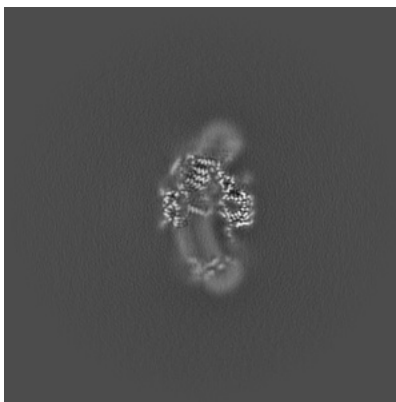
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

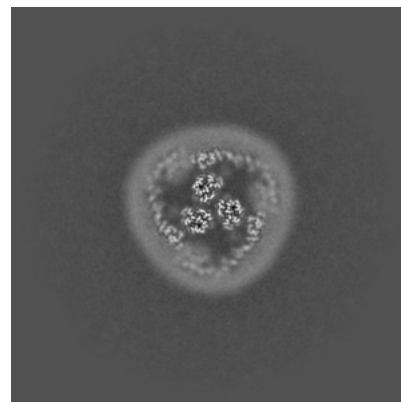
6.3.1 Primary map



X Index: 265

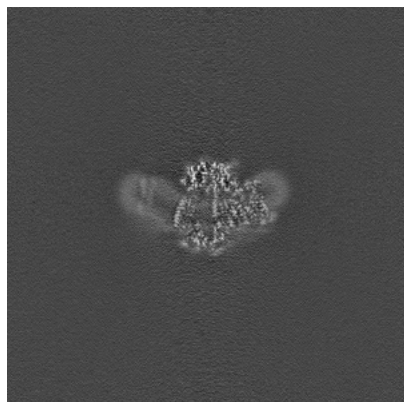


Y Index: 273

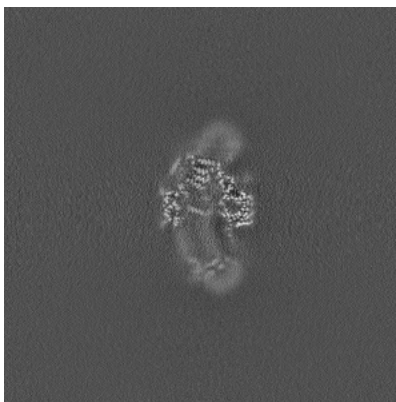


Z Index: 314

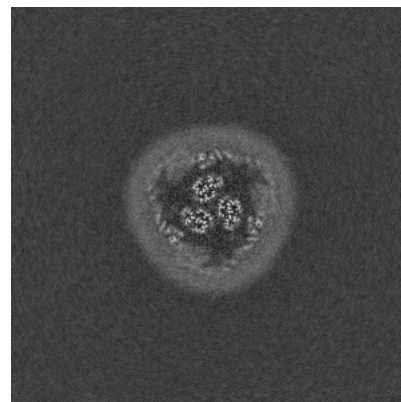
6.3.2 Raw map



X Index: 265



Y Index: 273

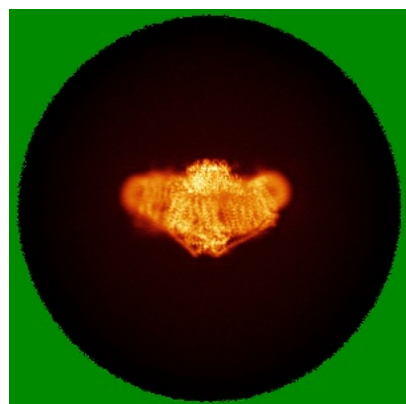


Z Index: 315

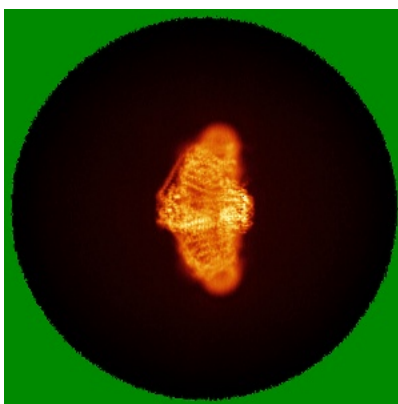
The images above show the largest variance slices of the map in three orthogonal directions.

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

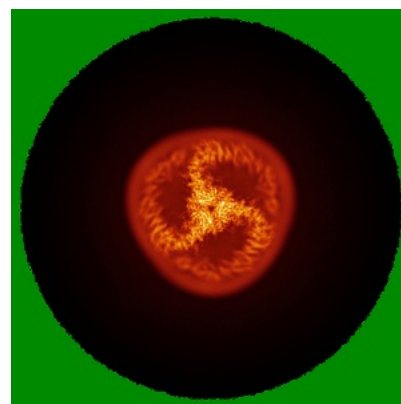
6.4.1 Primary map



X

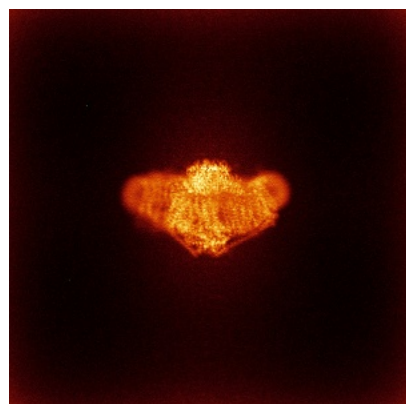


Y

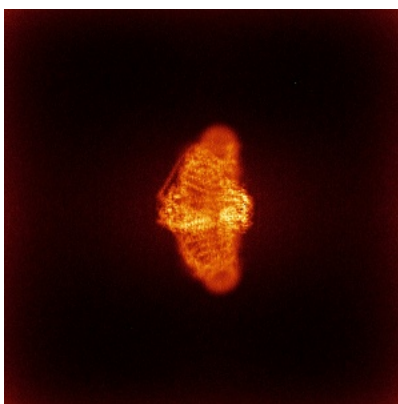


Z

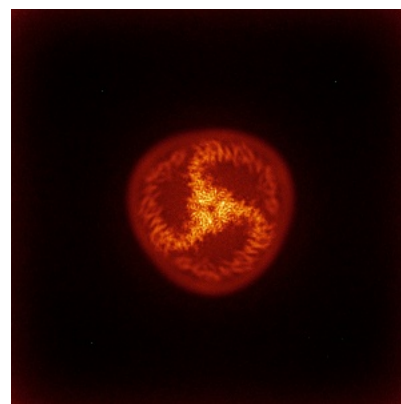
6.4.2 Raw map



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

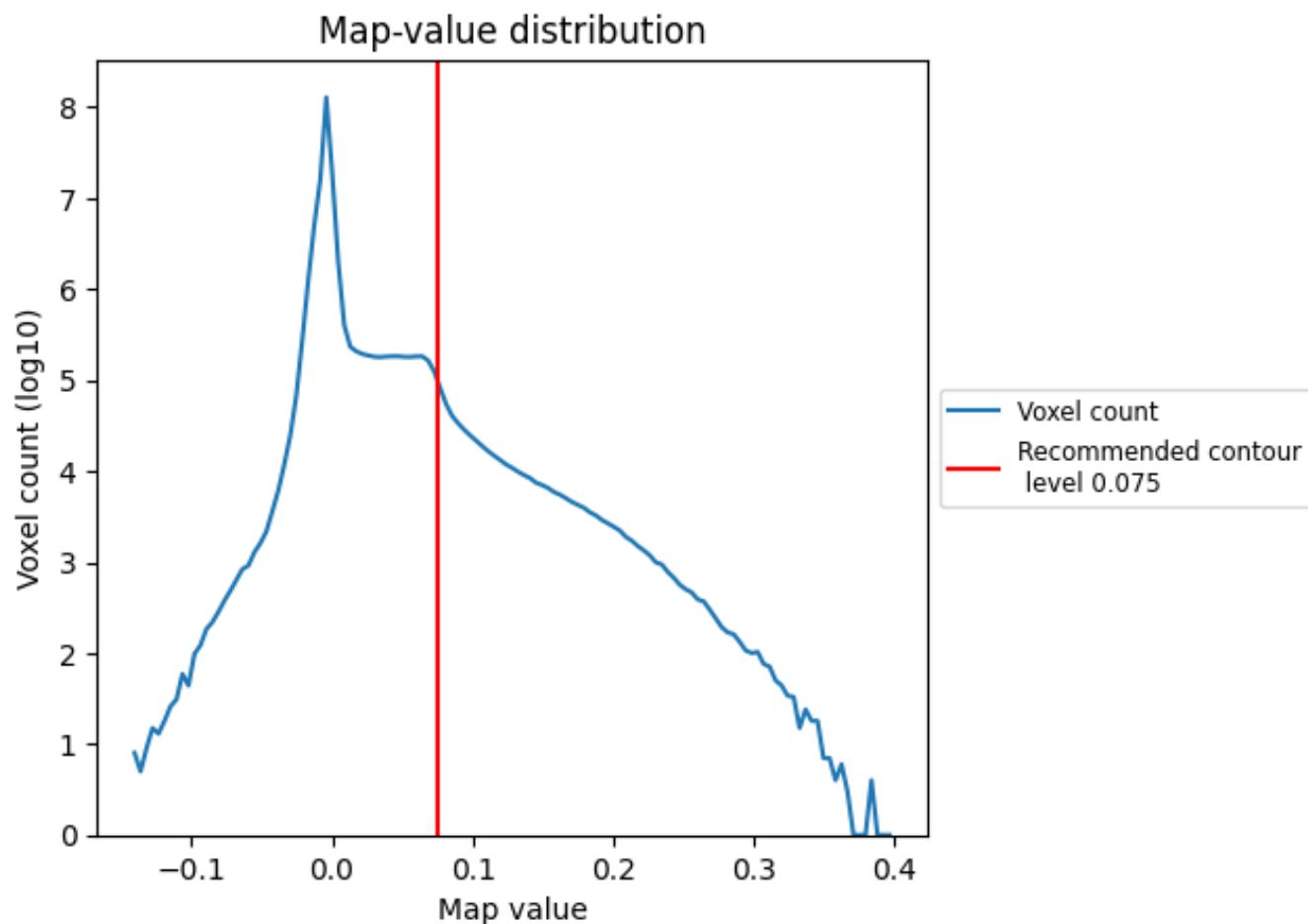
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

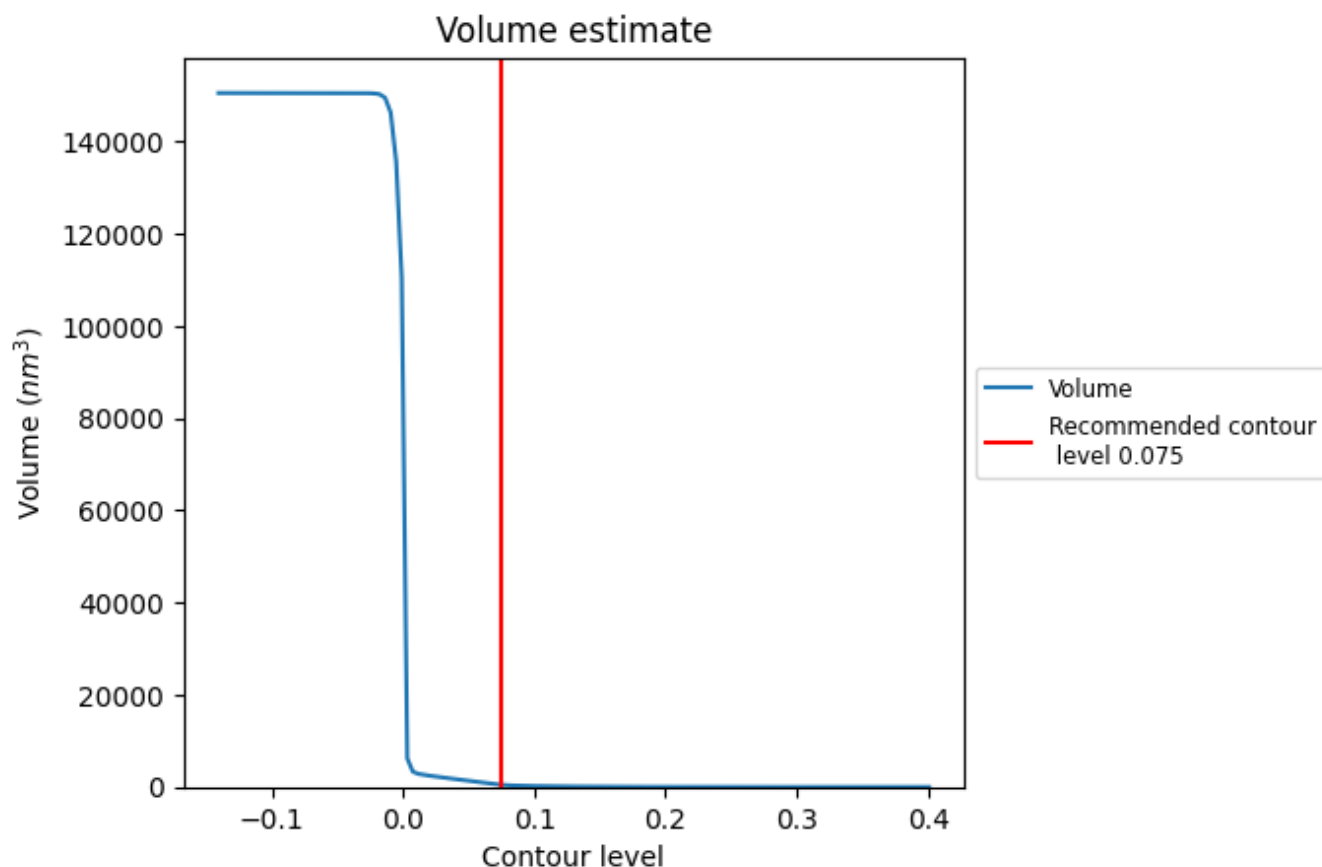
This section contains the results of statistical analysis of the map.

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.

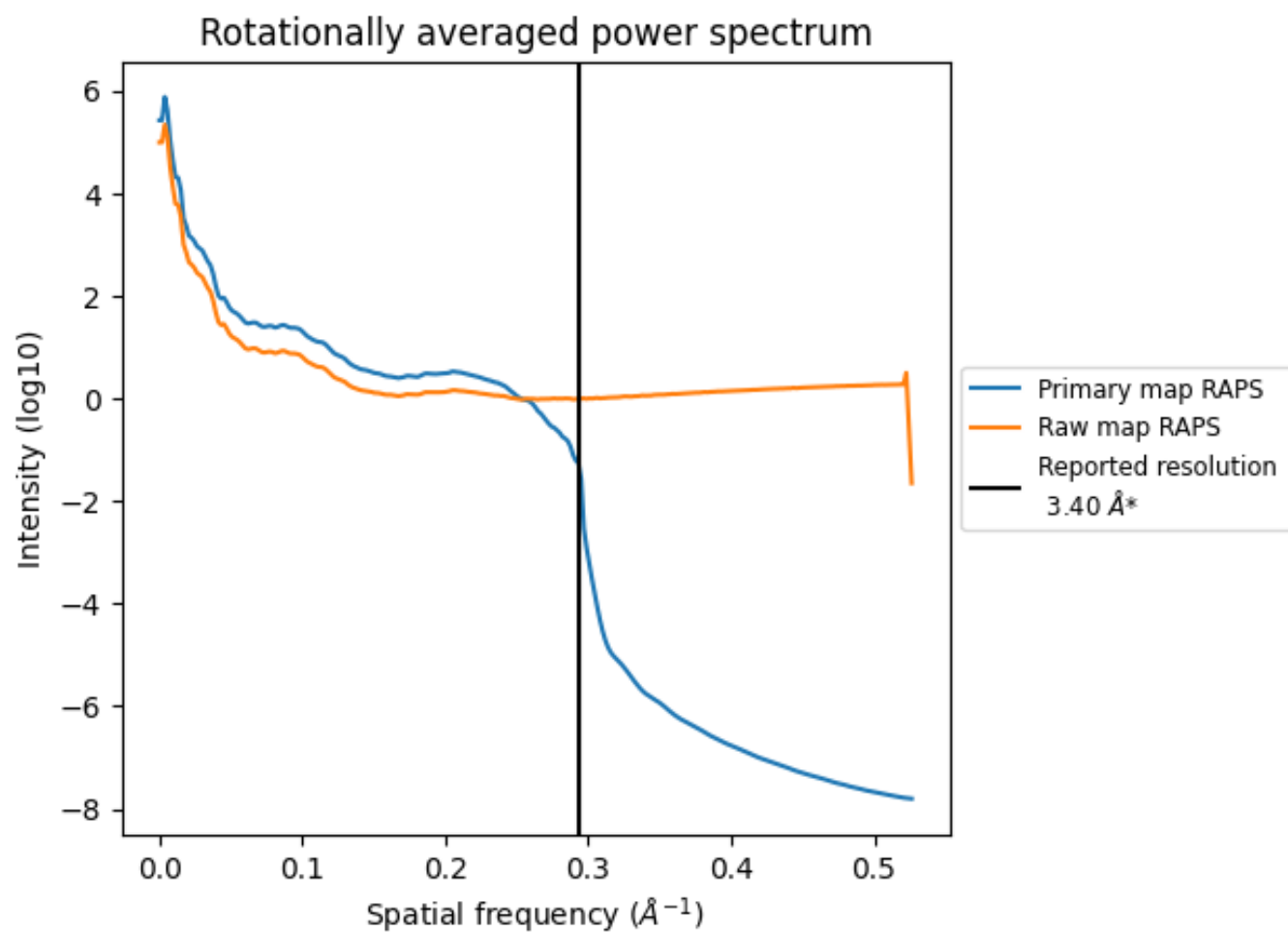
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 458 nm³; this corresponds to an approximate mass of 414 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 ⓘ

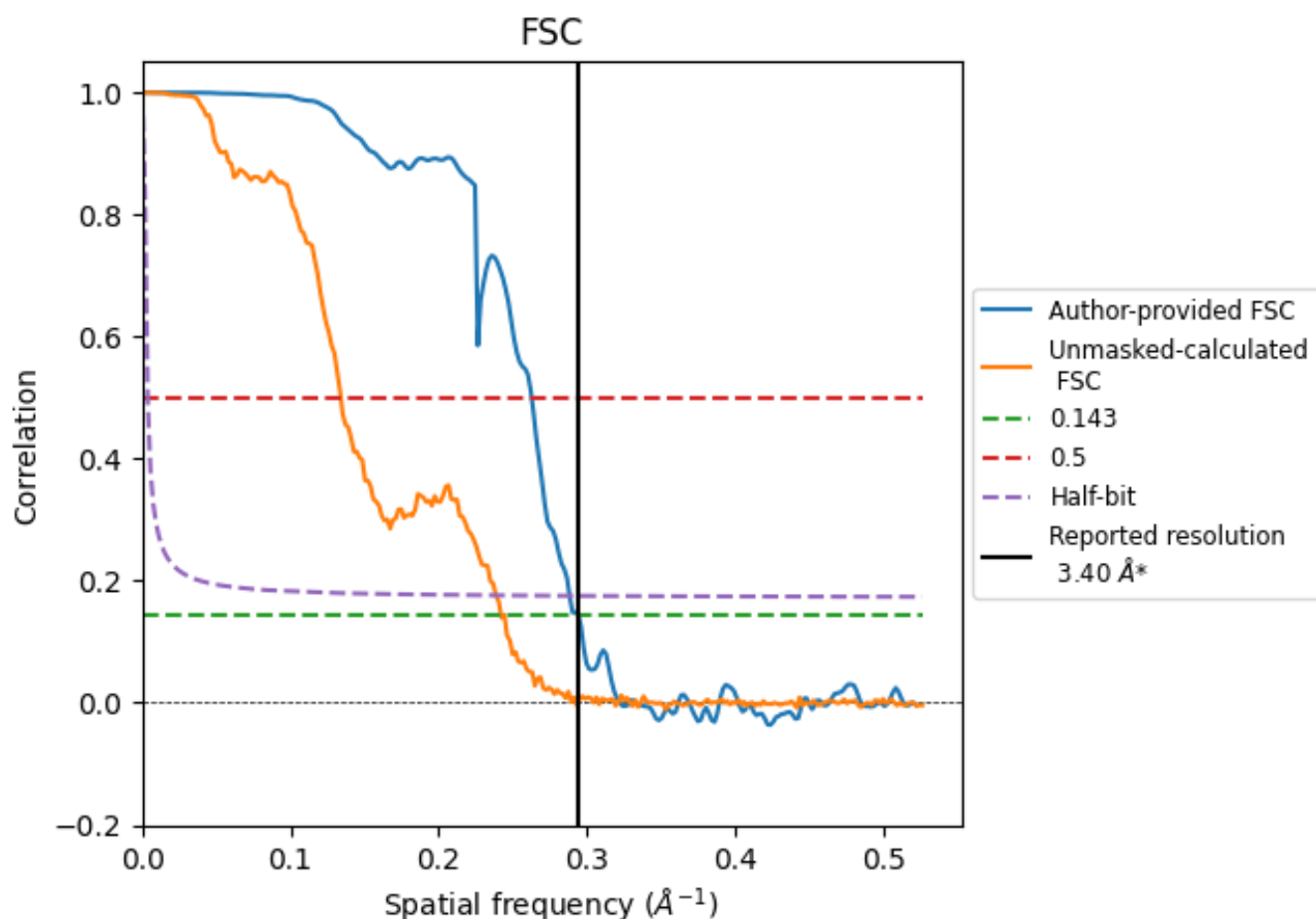


*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.40	3.81	3.47
Unmasked-calculated*	4.13	7.46	4.19

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.13 differs from the reported value 3.4 by more than 10 %

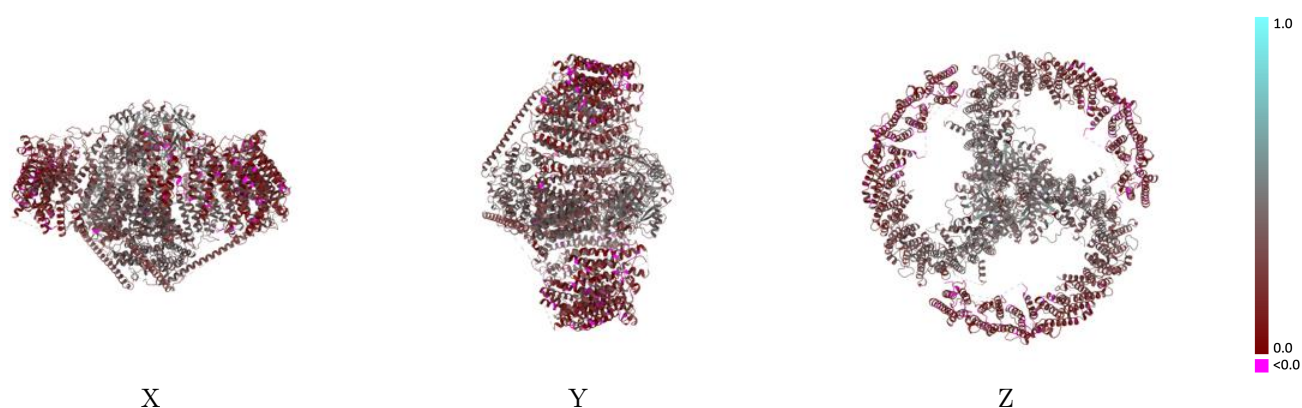
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-64385 and PDB model 9UOY. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

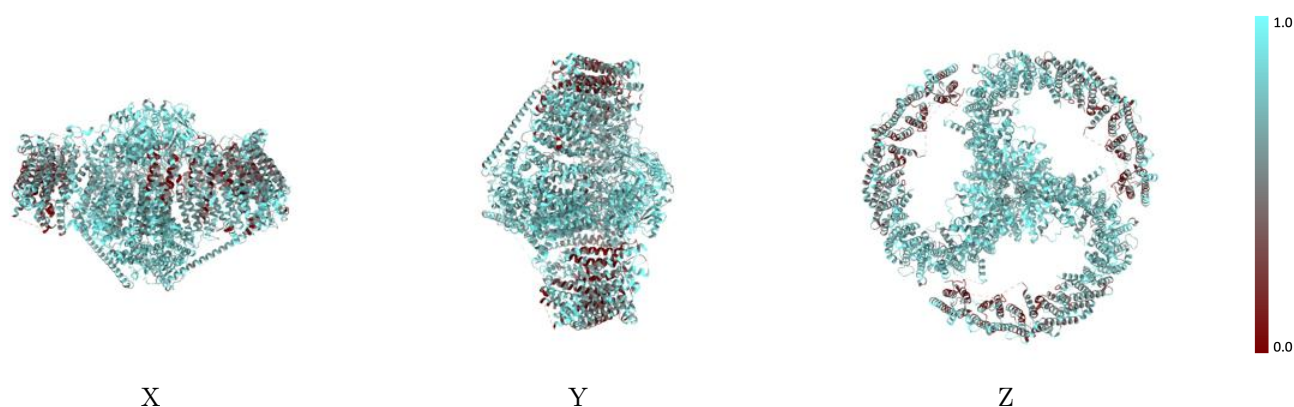
This section was not generated.

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



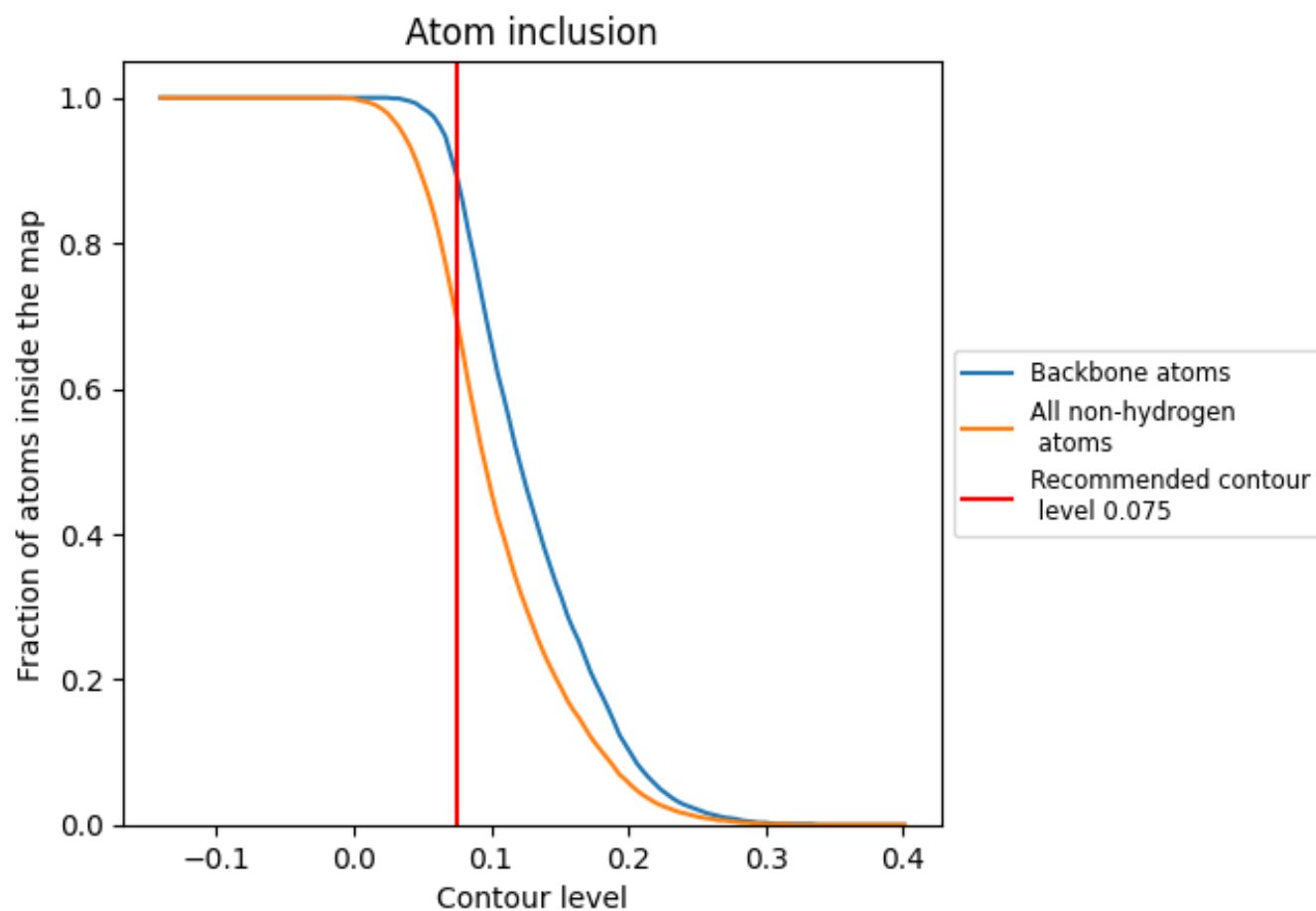
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.075).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% 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 (0.075) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6960	0.2980
A	0.6960	0.2970
B	0.6960	0.2980
C	0.6970	0.2980

