



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 01:22 AM UTC

PDB ID : 9D9Z / pdb_00009d9z
EMDB ID : EMD-46686
Title : Structure of human UBR4-KCMF1-CaM E3 ligase complex (Silencing Factor of the Integrated stress response, SiFI)
Authors : Yang, Z.; Rape, M.
Deposited on : 2024-08-21
Resolution : 3.40 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.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

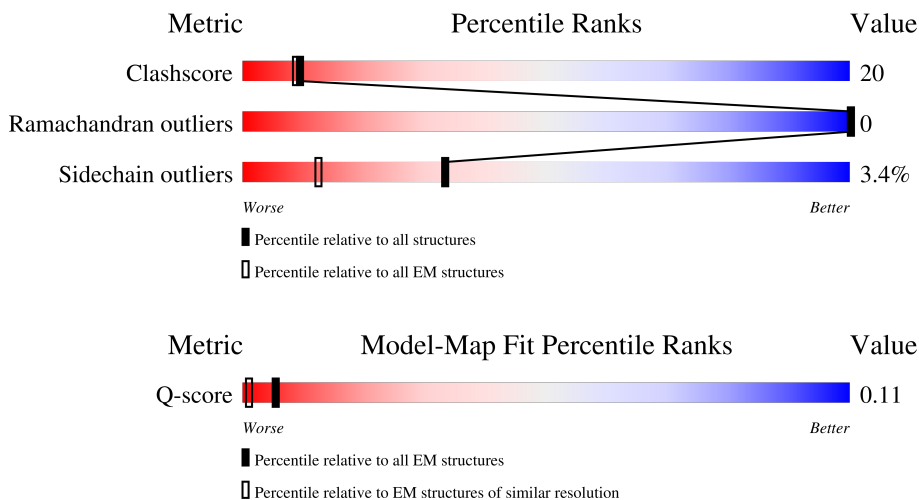
1 Overall quality at a glance i

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	5205	50% 45% 29% 25%
1	B	5205	50% 46% 28% 24%
2	C	149	83% 51% 43%
2	D	149	85% 47% 46%

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Mol	Chain	Length	Quality of chain
3	E	381	
3	F	381	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ZN	A	5202	-	-	X	-
4	ZN	B	5202	-	-	X	-
5	CA	D	202	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 66746 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 UBR4 (endogenously FLAG-tagged at the N-terminus),E3 ubiquitin-protein ligase UBR4,E3 ubiquitin-protein ligase UBR4,E3 ubiquitin-protein ligase UBR4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3917	Total	C	N	O	S	0	0
			30658	19475	5230	5749	204		
1	B	3946	Total	C	N	O	S	0	0
			30933	19647	5279	5802	205		

- Molecule 2 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	144	Total	C	N	O	S	0	0
			1134	696	182	247	9		
2	D	143	Total	C	N	O	S	0	0
			1127	692	181	245	9		

- Molecule 3 is a protein called E3 ubiquitin-protein ligase KCMF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	182	Total	C	N	O	S	0	0
			1435	881	250	288	16		
3	F	182	Total	C	N	O	S	0	0
			1435	881	250	288	16		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
4	A	6	Total	Zn	0
			6	6	
4	B	6	Total	Zn	0
			6	6	
4	E	4	Total	Zn	0
			4	4	

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Mol	Chain	Residues	Atoms		AltConf
4	F	4	Total	Zn	0
			4	4	

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
5	C	2	Total	Ca	0
			2	2	
5	D	2	Total	Ca	0
			2	2	



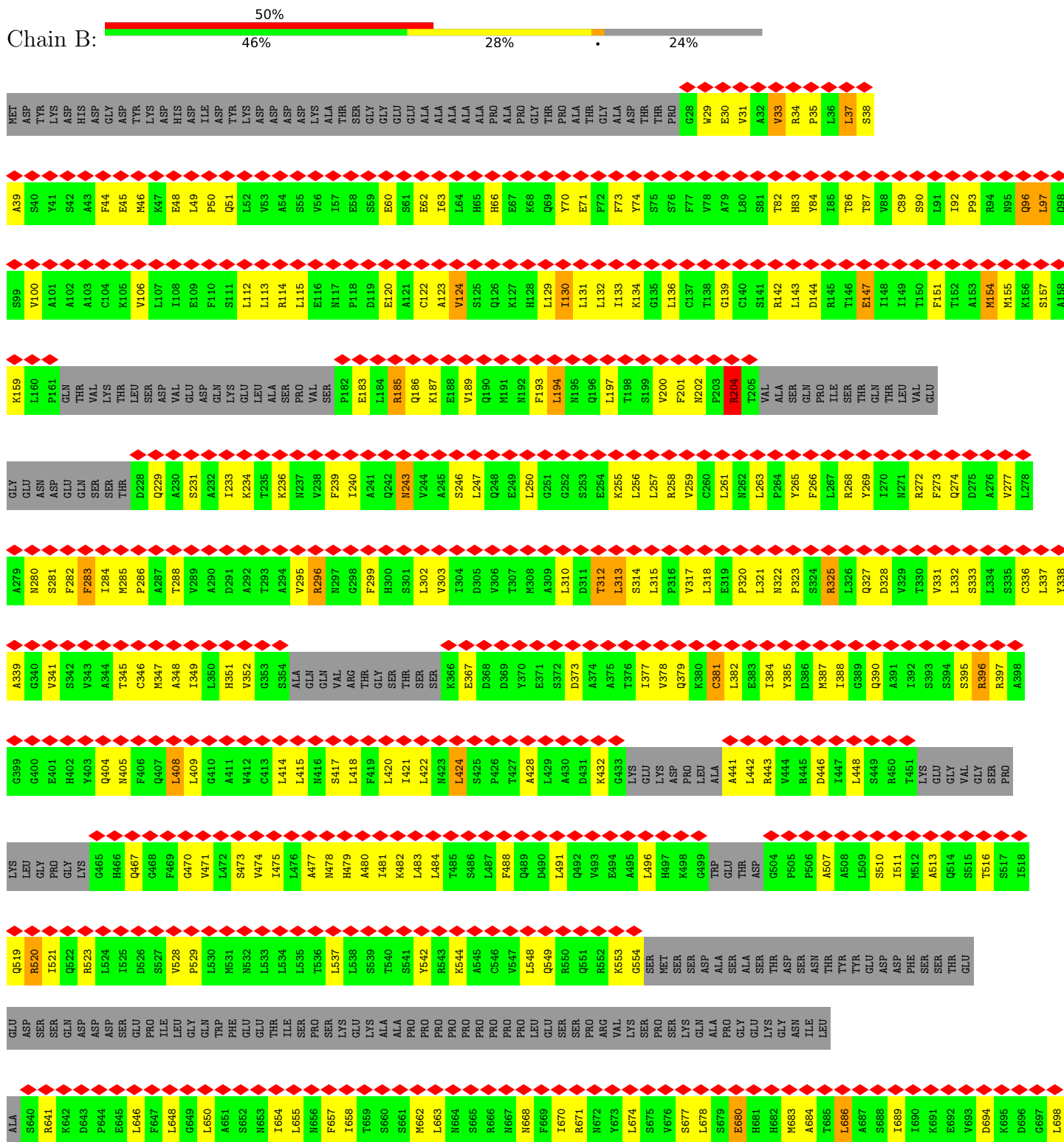






VAL	ASP	LEU	LEU	ILE	TYR	LEU	LYS	ARG	ILE	D4680	I4620	E4560	L4485	Q4364	Y4169
ASP	LEU	LEU	ILE	TYR	LEU	LEU	VAL	GLN	I4681	I4681	P4621	Q4561	E4486	G4365	L4170
ILE	ILE	TRP	ARG	LEU	ARG	LEU	ALA	ALA	I4682	I4682	Y4622	L4562	C4487	G4366	L4173
ASN	ASN	ILE	HIS	GLY	GLY	GLY	GLY	GLY	I4683	I4683	L4623	L4563	M4488	M4367	E4303
ASN	ASN	ASN	HIS	THR	THR	THR	THR	THR	Q4684	Q4684	P4624	S4564	L4489	T4306	L4186
THR	THR	THR	THR	THR	THR	THR	THR	THR	Q4685	Q4685	GLY	L4565	M4490	K4307	Y4187
THR	THR	THR	THR	THR	THR	THR	THR	THR	K4686	K4686	GLY	M4566	R4491	A4308	
THR	THR	THR	THR	THR	THR	THR	THR	THR	I4687	I4687	VAL	E4567	L4492	F4309	T4191
THR	THR	THR	THR	THR	THR	THR	THR	THR	VAL	VAL	GLU	L4568	I4495	M4310	
THR	THR	THR	THR	THR	THR	THR	THR	THR	GLU	GLU	GLU	T4569	T4431	H4195	H4195
THR	THR	THR	THR	THR	THR	THR	THR	THR	T4688	T4688	K4630	L4570	Y4372	C4313	H4196
THR	THR	THR	THR	THR	THR	THR	THR	THR	Q4689	Q4689	M4631	D4571	S4373	I4314	
THR	THR	THR	THR	THR	THR	THR	THR	THR	N4690	N4690	Q4632	E4572	S4374	Y4199	
THR	THR	THR	THR	THR	THR	THR	THR	THR	I4691	I4691	I4633	S4573	E4316	L4200	
THR	THR	THR	THR	THR	THR	THR	THR	THR	E4752	E4752	I4634	M4574	A4317	A4201	
THR	THR	THR	THR	THR	THR	THR	THR	THR	L4693	L4693	V4635	A4575	E4376	V4205	
THR	THR	THR	THR	THR	THR	THR	THR	THR	Y4694	Y4694	E4636	L4505	P4377	H4205	
THR	THR	THR	THR	THR	THR	THR	THR	THR	M4695	M4695	E4636	T4506	G4378	TYR	
THR	THR	THR	THR	THR	THR	THR	THR	THR	S4755	S4755	E4636	V4507	G4378	ASN	L4228
THR	THR	THR	THR	THR	THR	THR	THR	THR	S4756	S4756	E4637	L4508	T4379	LEU	L4228
THR	THR	THR	THR	THR	THR	THR	THR	THR	D4757	D4757	F4638	L4509	G4380	ASP	T4229
THR	THR	THR	THR	THR	THR	THR	THR	THR	E4758	E4758	K4639	K4510	P4381	D4231	D4231
THR	THR	THR	THR	THR	THR	THR	THR	THR	D4759	D4759	P4640	L4511	L4382	L4232	L4232
THR	THR	THR	THR	THR	THR	THR	THR	THR	I4699	I4699	Y4641	Y4514	M4384	Q4234	Q4234
THR	THR	THR	THR	THR	THR	THR	THR	THR	P4700	P4700	C4642	GLY	R4384	L4238	L4238
THR	THR	THR	THR	THR	THR	THR	THR	THR	S4701	S4701	N4643	ASN	D4385	I4331	L4244
THR	THR	THR	THR	THR	THR	THR	THR	THR	A4702	A4702	F4644	LEU	T4386	F4332	L4245
THR	THR	THR	THR	THR	THR	THR	THR	THR	K4703	K4703	D4645	LEU	K4387		
THR	THR	THR	THR	THR	THR	THR	THR	THR	N4704	N4704	T4646	GLY	N4388		
THR	THR	THR	THR	THR	THR	THR	THR	THR	L4705	L4705	K4646	GLY	I4339		
THR	THR	THR	THR	THR	THR	THR	THR	THR	D4706	D4706	Y4647	GLY	T4390		
THR	THR	THR	THR	THR	THR	THR	THR	THR	L4707	L4707	D4648	GLY	T4390		
THR	THR	THR	THR	THR	THR	THR	THR	THR	D4708	D4708	E4649	GLY	T4390		
THR	THR	THR	THR	THR	THR	THR	THR	THR	L4709	L4709	H4651	GLY	T4390		
THR	THR	THR	THR	THR	THR	THR	THR	THR	N4710	N4710	S4652	GLY	T4390		

- Molecule 1: UBR4 (endogenously FLAG-tagged at the N-terminus), E3 ubiquitin-protein ligase UBR4, E3 ubiquitin-protein ligase UBR4, E3 ubiquitin-protein ligase UBR4



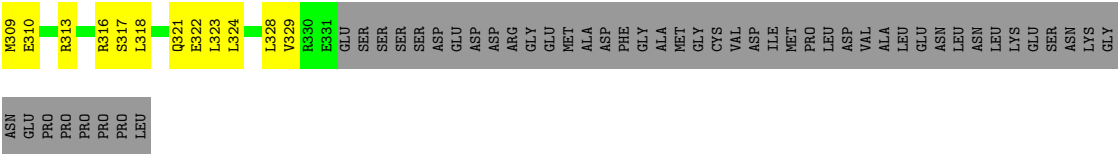
L1419	L1420	A1421	K1422	F1423	C1424	N1425	R1426	V1427	L1428	P1429	N1430	F1431	T1432	L1433	L1434	F1435	Q1436	L1437	T1438	E1439	C1440	S1441	P1442	M1443	P1444	S1445	L1446	L1447	L1448	L1449	C1450	G1451	L1452	L1453	A1454	Q1455	A1456	A1457	C1458	V1459	E1460	P1461	V1462	R1463	L1464	Q1465	A1466	W1467	L1468	T1469	R1470	M1471	T1472	T1473	S1474	P1475	PRO	LYS	ASP	
Y1359	N1360	I1361	L1362	A1363	N1364	H1365	A1366	D1367	P1368	N1369	S1370	G1371	L1372	D1373	E1374	S1375	I1376	L1377	E1378	E1379	C1380	L1381	Q1382	Y1383	L1384	E1385	K1386	Q1387	L1388	E1389	S1390	S1391	Q1392	A1393	R1394	K1395	A1396	M1397	E1398	F1399	F1400	F1401	S1402	D1403	S1404	G1405	E1406	L1407	L1408	Q1409	I1410	M1411	M1412	A1413	T1414	A1415	P1416	PRO	LYS	ASP
I1299	V1300	W1301	S1302	D1303	E1304	M1305	N1306	P1307	P1308	Q1309	V1310	I1311	R1312	T1313	L1314	L1315	P1316	L1317	L1318	L1319	E1320	S1321	S1322	T1323	E1324	S1325	V1326	A1327	E1328	I1329	S1330	S1331	S1332	S1333	L1334	E1335	R1336	I1337	L1338	G1339	P1340	A1341	E1342	S1343	D1344	E1345	F1346	L1347	L1348	R1349	V1350	Y1351	E1352	K1353	L1354	L1355	T1356	G1357	C1358	
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Q1179	N1180	F1181	N1182	GLU	GLU	GLY	THR	E1188	P1189	P1190	S1191	K1192	E1193	K1194	L1195	Q1196	G1197	F1198	A1199	A1200	V1201	L1202	K1141	M1142	A1143	ALA	GLU	THR	ASP	PRO	HIS	LYS	S1151	S1152	E1153	I1154	T1155	K1156	N1157	L1158	P1159	A1160	T1162	L1163	L1165	I1166	D1167	T1168	Y1169	A1170	S1171	F1172	T1173	R1174	A1175	Y1176	L1177	L1178		
I1069	K1060	Q1061	G1062	M1063	K1064	A1065	E1066	H1067	A1068	S1069	S1070	L1071	L1072	E1073	L1074	A1075	S1076	T1077	L1078	K1079	C1080	S1081	S1082	V1083	K1084	Y1085	D1086	V1087	E1088	I1089	V1090	E1091	E1092	Y1093	F1094	A1095	L1096	Q1097	I1098	S1099	F1101	C1102	S1103	I1104	D1105	C1106	T1107	T1108	I1109	L1110	Q1111	L1112	H1113	E1114	T1115	P1116	S1117	L1118		
L999	Q1000	Y1001	Y1002	F1003	L1004	I1005	L1006	W1007	R1008	I1009	L1010	G1011	I1012	L1013	P1014	P1015	S1016	T1017	T1018	Y1019	I1020	N1021	Q1022	L1023	S1024	M1025	N1026	S1027	P1028	E1029	M1030	S1031	E1032	C1033	D1034	I1035	L1036	H1037	T1038	L1039	R1040	W1041	S1042	S1043	R1044	L1045	R1046	I1047	N998	S1049	Y1050	V1051	N1052	W1053	I1054	K1055	D1056	H1057	L1058	
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Q879	V880	Q881	H882	N883	L884	L885	S886	P887	P888	F889	G890	TRP	ALA	GLY	SER	GLN	ASP	SER	ASN	SER	ARG	ARG	A903	T904	T905	P906	L907	Y908	H909	G910	F911	K912	E913	V914	E915	E916	N917	W918	S919	K920	H921	F922	S923	SER	ASP	ALA	VAL	PRO	HIS	P930	R931	F932	Y933	C934	V935	K936	L936	S937	P938	
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R759	L760	L761	L762	I763	W764	Q765	H766	K767	A768	S769	A770	Q771	Q772	D773	P774	D775	P776	P777	E778	C779	L780	K781	W782	W783	D784	R785	F786	L787	S788	T789	M790	K791	Q792	N793	A794	L795	Q796	G797	W798	V799	P800	S801	E802	T803	E804	D805	L806	N807	Y808	E809	H810	L811	Q812	M813	L814	L815	L816	I817	F818	
K699	G700	S701	S702	D703	E704	E705	F706	A707	A708	A709	L710	Y711	H712	F713	N714	H715	S716	L717	V718	T719	S720	D721	W722	Q723	S724	P725	N726	L727	Q728	N729	T730	L731	L732	Q733	Q734	L735	G736	V737	A738	P739	F740	S741	E742	G743	P744	W745	P746	L747	Y748	I749	H750	P751	Q752	S753	L754	S755	V756	L757	S758	

D2213	M2214	V2215	A2216	L2217	H2218	S2153	S2154	G2155	G2157	S2158	K2159	T2160	S2161	P2162	A2163	L2164	M2171	M2172	H2173	T2174	G2175	L2176	C2178	S2179	V2180	L2239	R2240	T2241	Y2242	M2243	A2244	M2245	V2246	E2247	L2189	F2123	F2124	S2125	T2126	G2127	Q2128	Q2129	K2130	S2131	F2132	A2133	A2134	T2135	L2136	S2137	R2138	T2139	T2140	K2206	A2209	K2210	L2211	Q2212		D2213	M2214	V2215	A2216	L2217	H2218	S2219	T2220	A2221	C2222	M2223	E2224	Q2225	K2226	T2227	T2228	M2230	T2231	L2232	L2233	C2234	E2235	D2236	G2237	S2238	L2239	R2240	T2241	Y2242	M2243	A2244	M2245	V2246	E2247	L2248	T2249	S2250	Y2251	M2252	Q2253	L2254	P2255	S2256	L2257	E2201	P2259	K2260	T2261	L2262	S2263	A2264	T2265	K2266	A2267	PRD	VAL	ARG	LYS	ARG																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N2054	E2055	E2056	G2057	K2058	N2059	I2060	T2061	V2062	Q2063	M2064	S2065	S2066	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	M2075	T2076	E2077	A2078	S2079	S2080	A2081		Q2082	Q2083	G2084	P2085	F2086	Y2087	V2088	T2089	M2090	V2091	L2092	E2093	L2094	M2095	H2096	E2097	T2098	F2039	L2040	L2041	P2042	S2043	S2044	S2045	L2046	D2047	D2048	V2049	T2050	F2051	L2052	T2053	N20

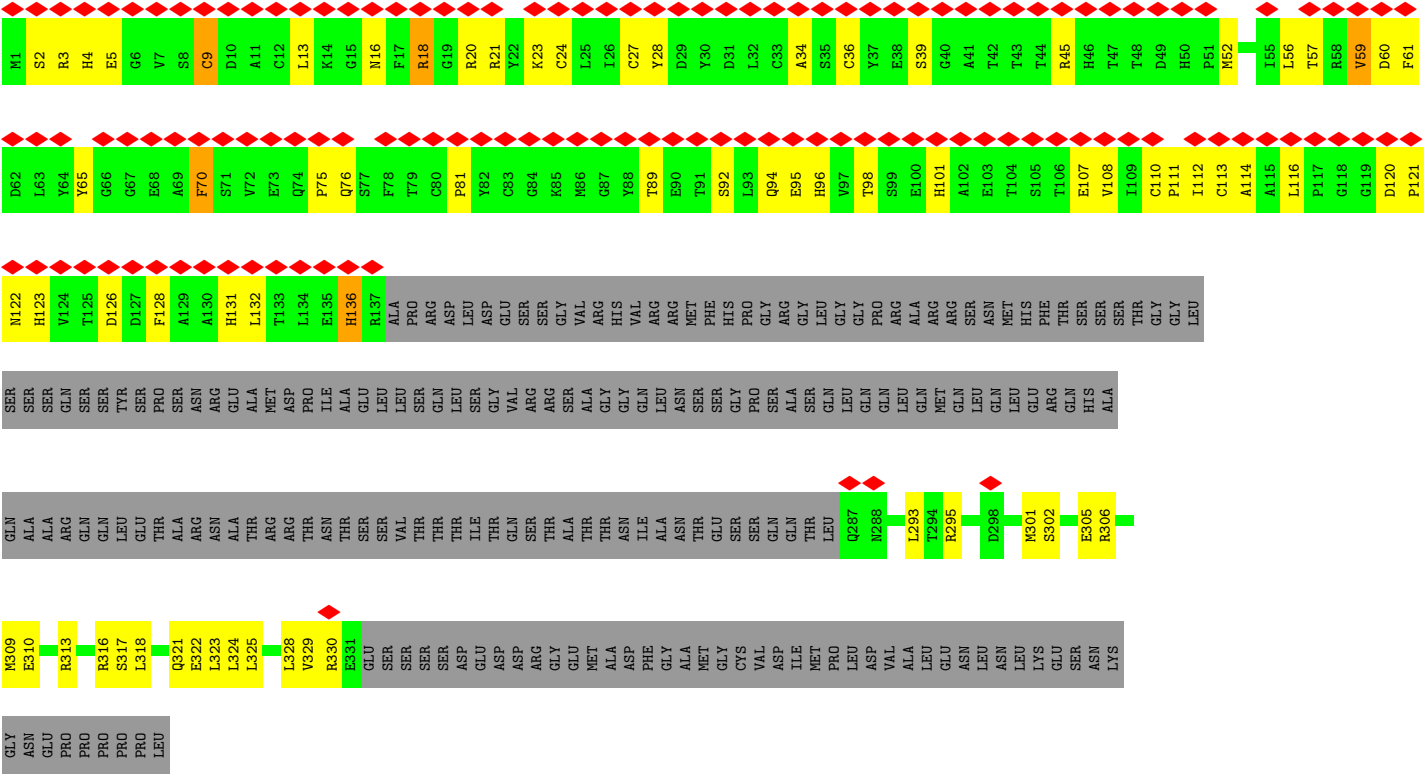
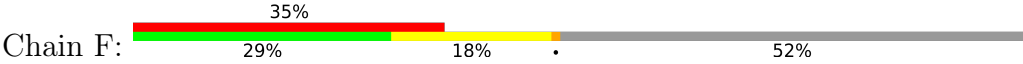
[illegible]

[illegible]

- Molecule 2: Calmodulin-1



● Molecule 3: E3 ubiquitin-protein ligase KCMF1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	126380	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.255	Depositor
Minimum map value	-0.578	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.13	Depositor
Map size ($\text{\AA}$)	440.16, 440.16, 440.16	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.048, 1.048, 1.048	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.88	39/31195 (0.1%)	1.04	1/42247 (0.0%)
1	B	0.91	36/31477 (0.1%)	1.10	2/42619 (0.0%)
2	C	0.97	0/1146	1.24	0/1539
2	D	0.98	0/1138	1.25	0/1526
3	E	1.01	12/1463 (0.8%)	0.99	0/1978
3	F	1.00	13/1463 (0.9%)	1.01	0/1978
All	All	0.91	100/67882 (0.1%)	1.08	3/91887 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	19
1	B	0	25
2	D	0	1
3	E	0	1
3	F	0	2
All	All	0	48

The worst 5 of 100 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1682	HIS	C-N	-10.20	1.20	1.33
1	B	1993	HIS	C-N	8.77	1.43	1.34
1	A	2290	ASP	C-N	-8.62	1.22	1.33
1	B	1865	SER	C-N	8.21	1.44	1.33
1	A	1894	LEU	C-N	-8.11	1.21	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1282	ALA	N-CA-C	-6.39	104.32	111.28
1	B	1131	VAL	N-CA-CB	5.70	117.22	110.55
1	B	529	PRO	N-CA-C	-5.06	102.05	112.47

There are no chirality outliers.

5 of 48 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1008	ARG	Sidechain
1	A	325	ARG	Sidechain
1	A	849	ARG	Sidechain
1	A	94	ARG	Sidechain
1	A	985	ARG	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	30658	0	31020	1288	0
1	B	30933	0	31316	1262	0
2	C	1134	0	1063	68	0
2	D	1127	0	1055	61	0
3	E	1435	0	1344	44	0
3	F	1435	0	1344	52	0
4	A	6	0	0	2	0
4	B	6	0	0	3	0
4	E	4	0	0	0	0
4	F	4	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	2	0
All	All	66746	0	67142	2687	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 20.

The worst 5 of 2687 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3270:ILE:CD1	1:B:3632:PRO:HG2	1.66	1.25
1:A:3270:ILE:CD1	1:A:3632:PRO:HG2	1.66	1.23
1:B:3087:ALA:CB	1:B:3181:ILE:HG21	1.73	1.19
1:A:73:PHE:CD1	1:A:159:LYS:HA	1.80	1.15
2:D:98:ASN:HB2	5:D:202:CA:CA	1.06	1.15

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	3853/5205 (74%)	3738 (97%)	115 (3%)	0	100	100
1	B	3884/5205 (75%)	3762 (97%)	122 (3%)	0	100	100
2	C	142/149 (95%)	136 (96%)	6 (4%)	0	100	100
2	D	139/149 (93%)	132 (95%)	7 (5%)	0	100	100
3	E	178/381 (47%)	175 (98%)	3 (2%)	0	100	100
3	F	178/381 (47%)	170 (96%)	8 (4%)	0	100	100
All	All	8374/11470 (73%)	8113 (97%)	261 (3%)	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	3438/4542 (76%)	3329 (97%)	109 (3%)	34	58
1	B	3474/4542 (76%)	3347 (96%)	127 (4%)	30	55
2	C	123/127 (97%)	118 (96%)	5 (4%)	27	52
2	D	122/127 (96%)	115 (94%)	7 (6%)	18	45
3	E	162/330 (49%)	161 (99%)	1 (1%)	78	80
3	F	162/330 (49%)	159 (98%)	3 (2%)	50	66
All	All	7481/9998 (75%)	7229 (97%)	252 (3%)	33	57

5 of 252 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	97	LEU
1	B	4228	LEU
1	B	703	ASP
1	B	3968	LEU
2	C	33	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 140 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	3397	ASN
1	B	3639	ASN
1	B	4766	ASN
1	A	3536	ASN
1	A	3491	GLN

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

Of 24 ligands modelled in this entry, 24 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

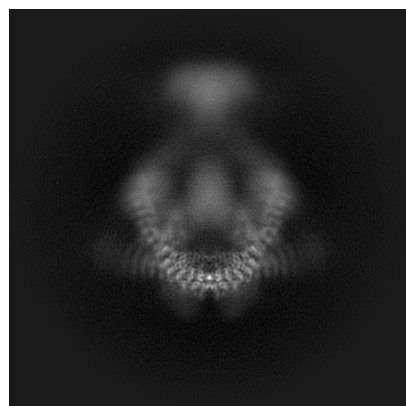
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46686. These allow visual inspection of the internal detail of the map and identification of artifacts.

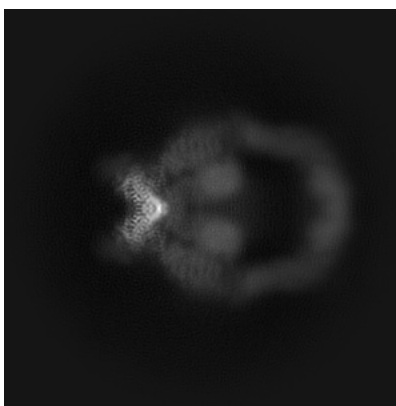
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

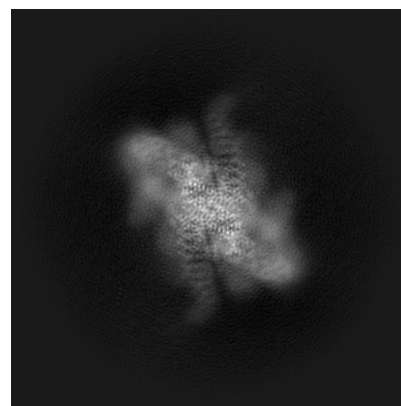
6.1.1 Primary map



X

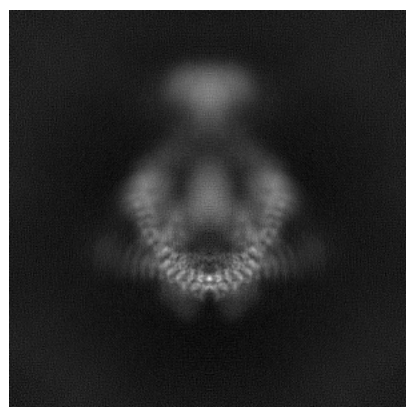


Y

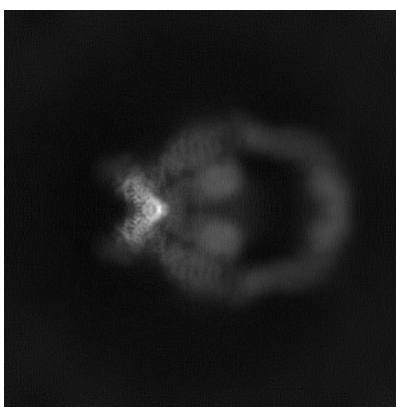


Z

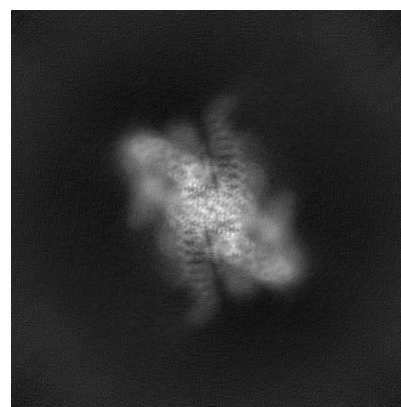
6.1.2 Raw map



X



Y

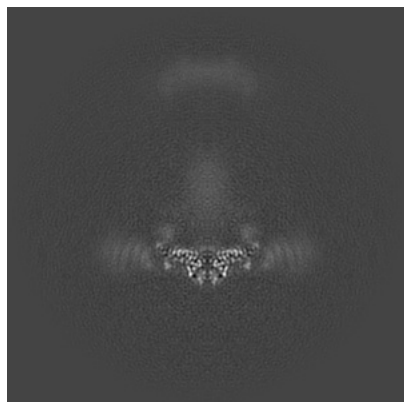


Z

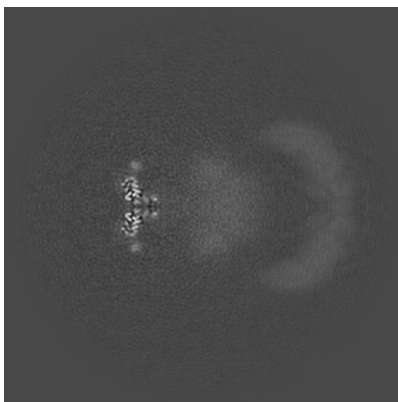
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

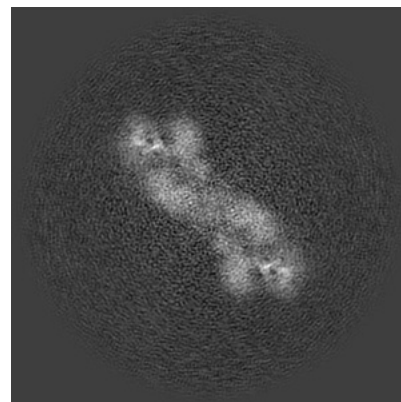
6.2.1 Primary map



X Index: 210



Y Index: 210

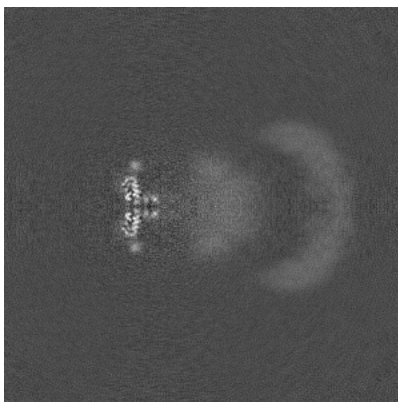


Z Index: 210

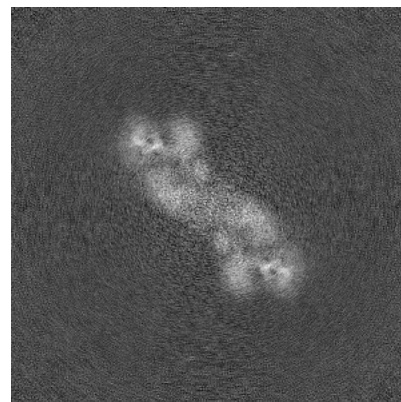
6.2.2 Raw map



X Index: 210



Y Index: 210



Z Index: 210

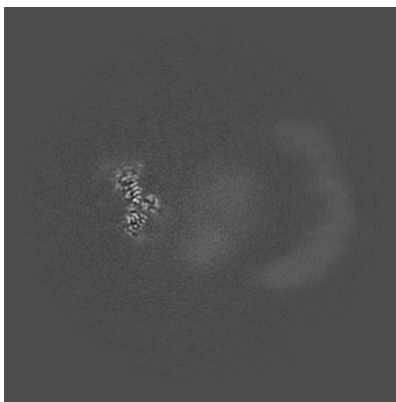
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

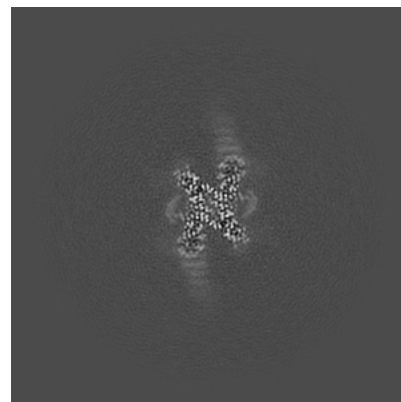
6.3.1 Primary map



X Index: 193

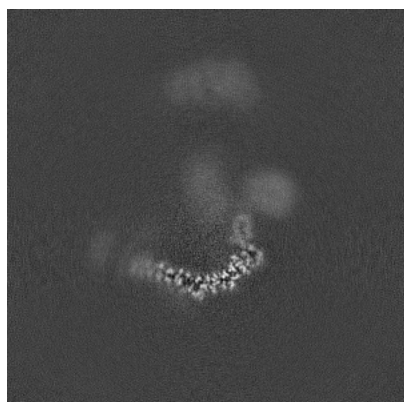


Y Index: 221

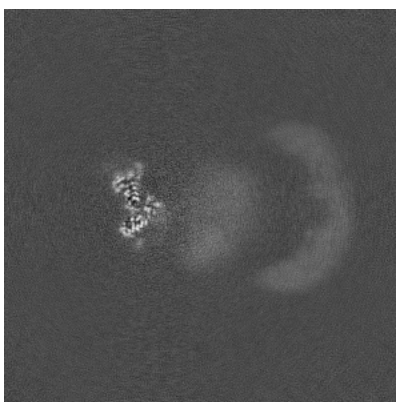


Z Index: 140

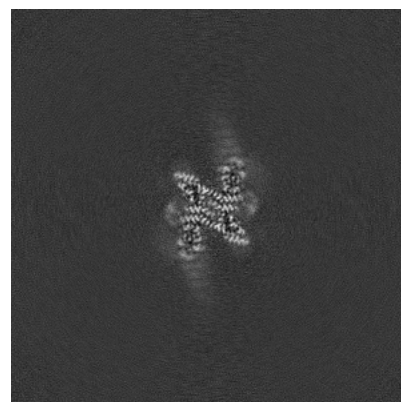
6.3.2 Raw map



X Index: 188



Y Index: 218

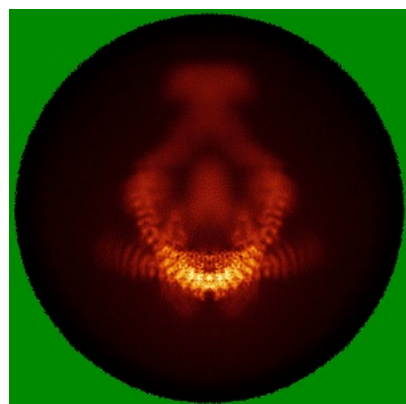


Z Index: 138

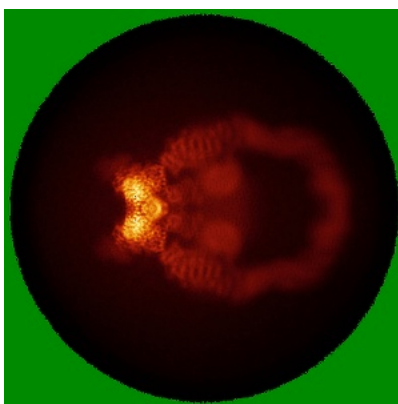
The images above show the largest variance slices of the map in three orthogonal directions.

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

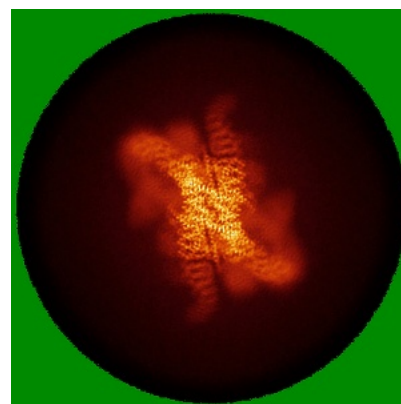
6.4.1 Primary map



X

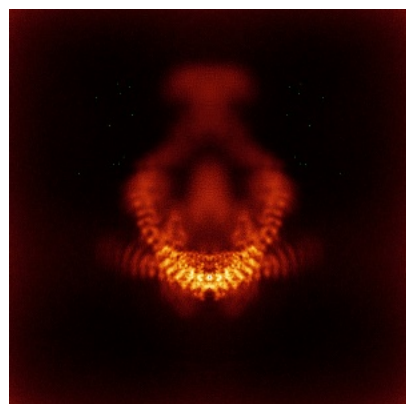


Y

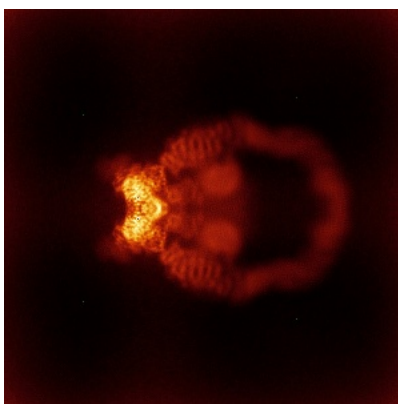


Z

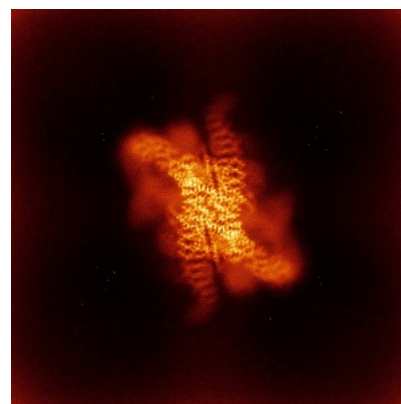
6.4.2 Raw map



X



Y

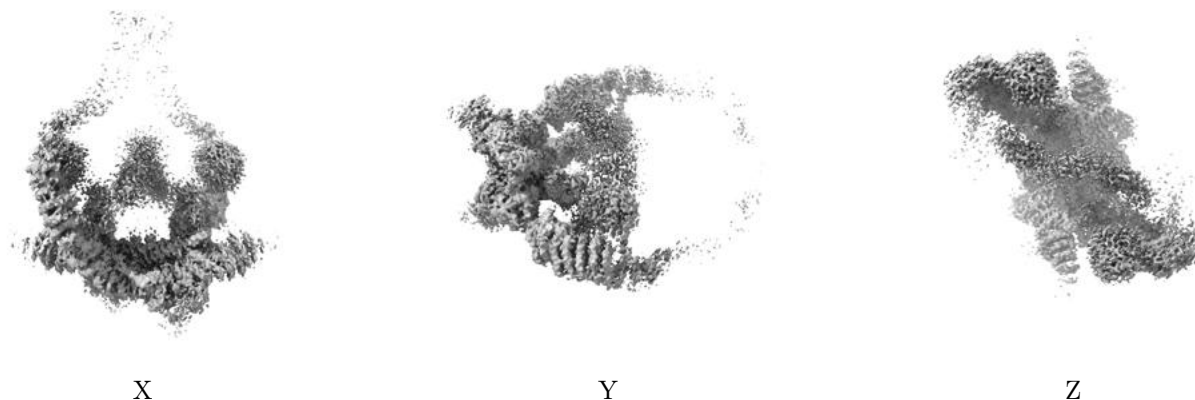


Z

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.

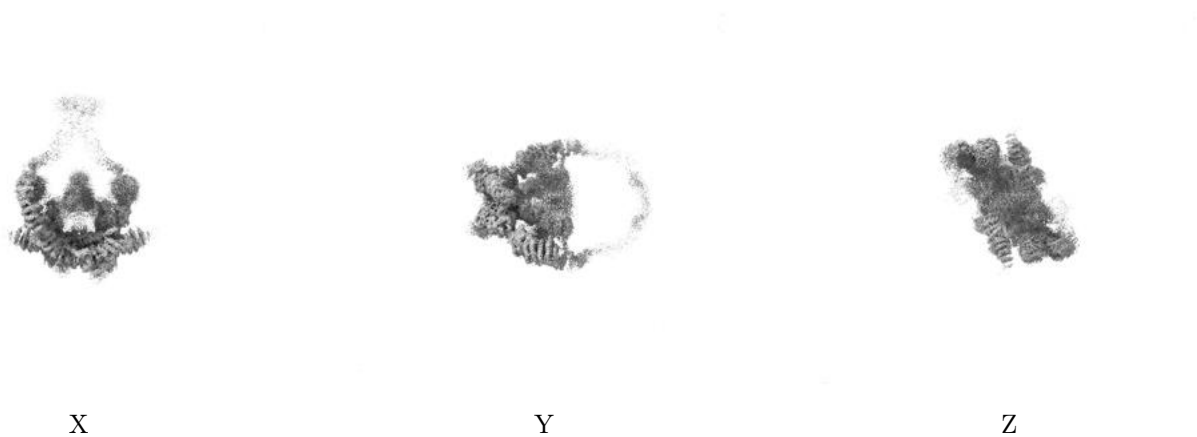
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

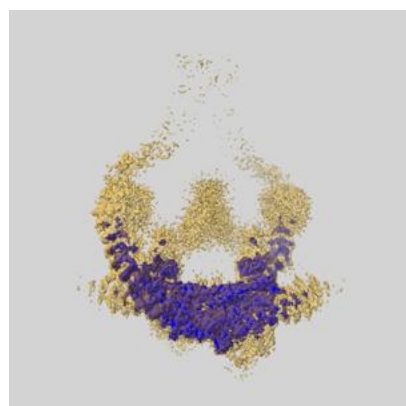
6.6 Mask visualisation [i](#)

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

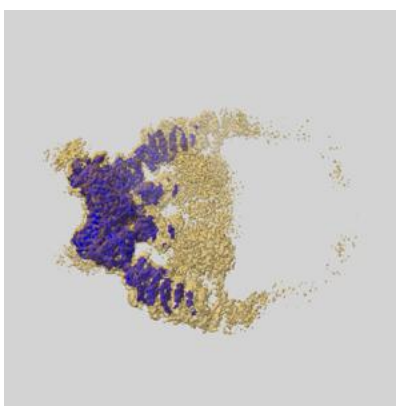
A mask typically either:

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

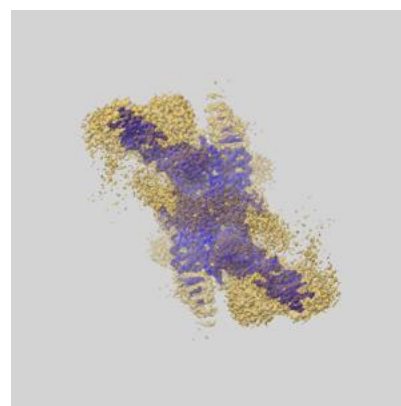
6.6.1 emd_46686_msk_1.map [i](#)



X



Y

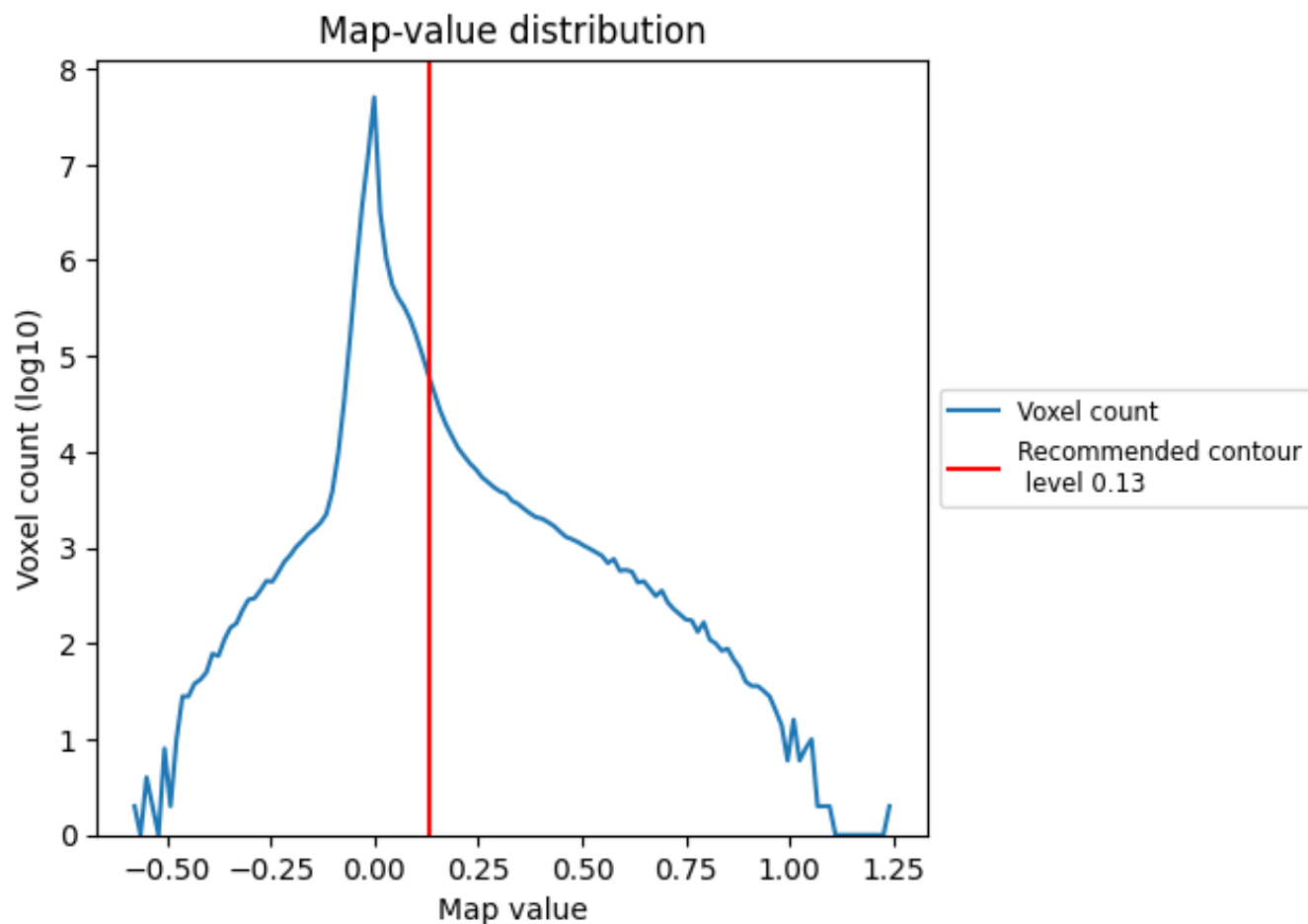


Z

7 Map analysis [i](#)

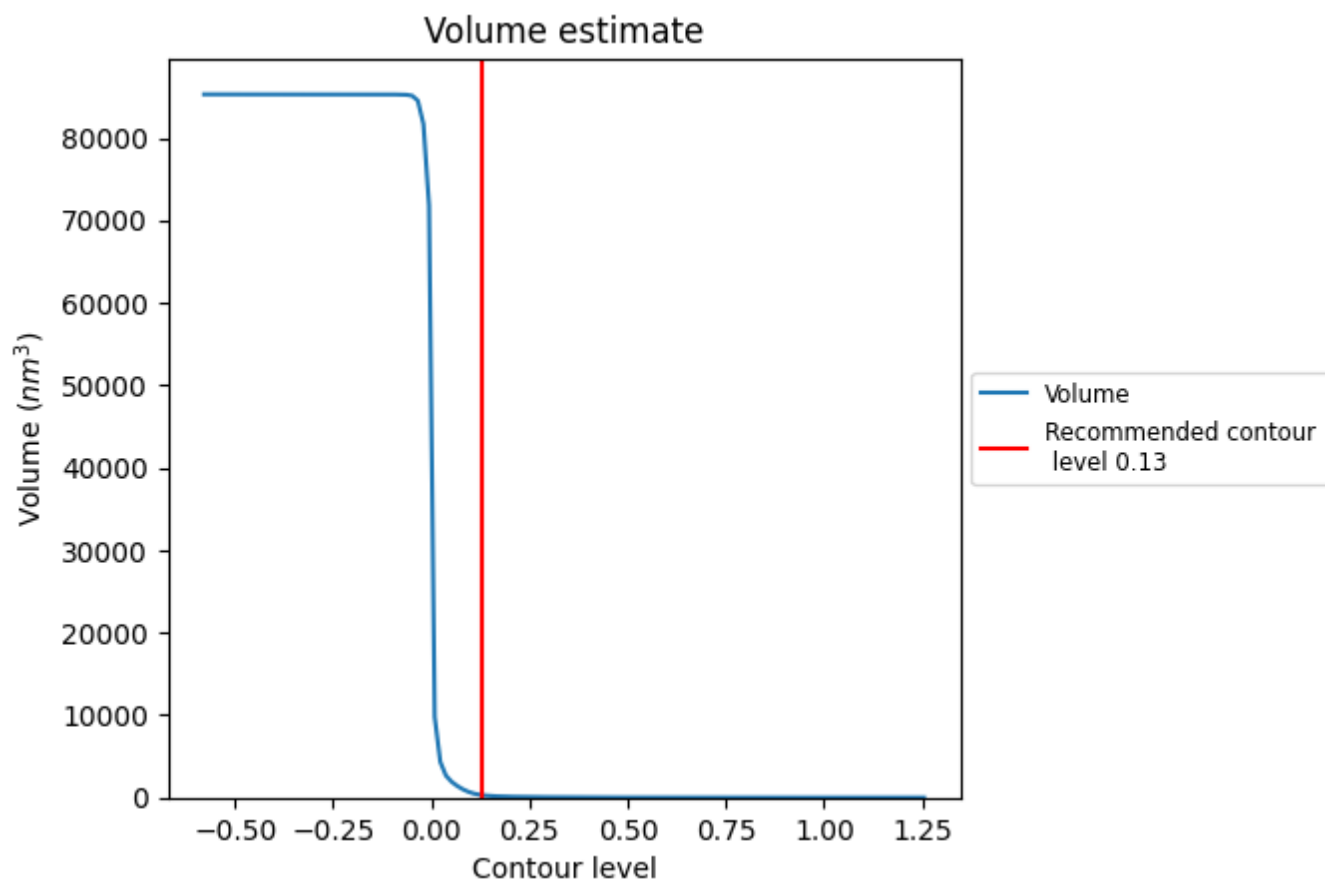
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

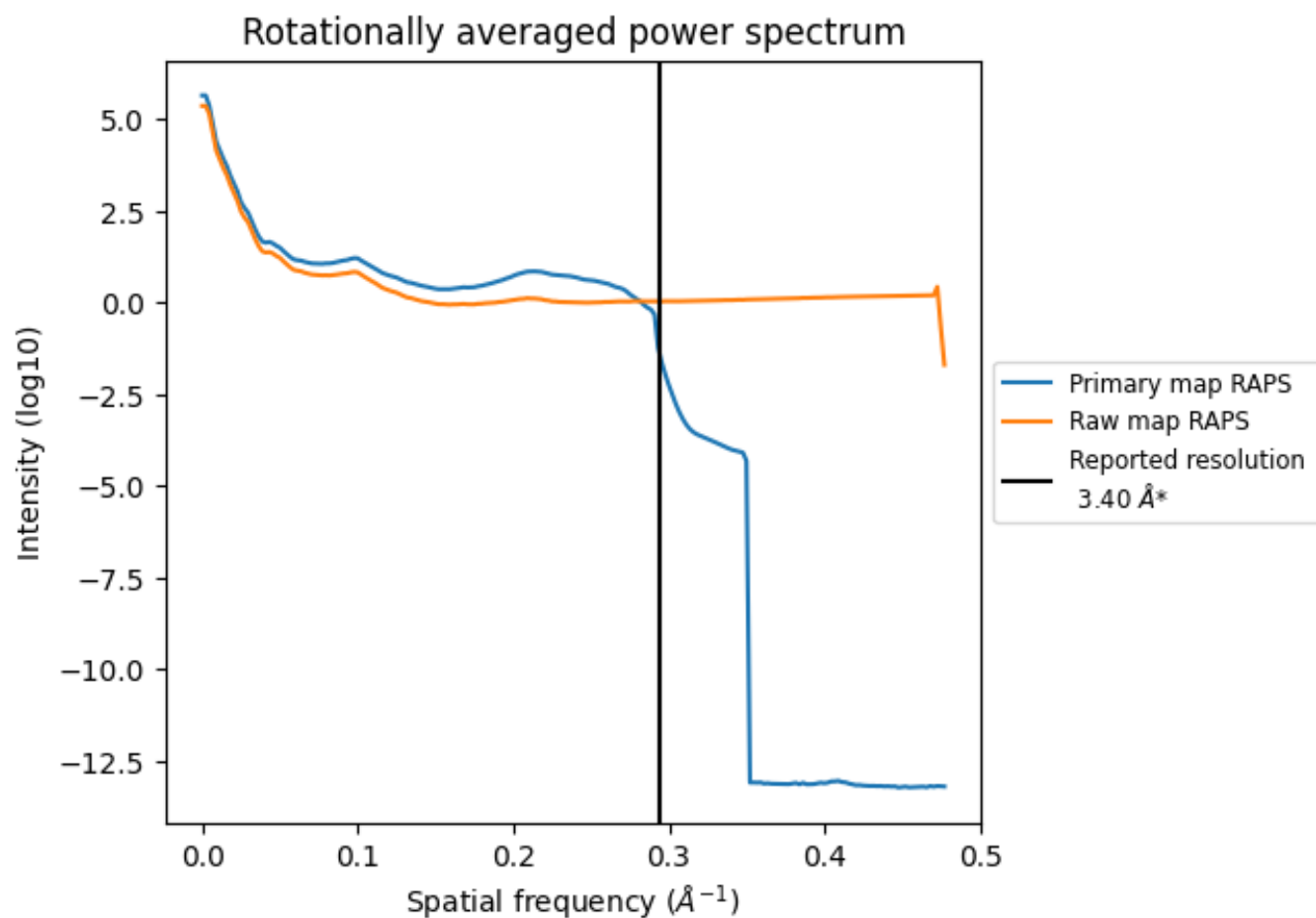
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 296 nm^3 ; this corresponds to an approximate mass of 268 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 ⓘ

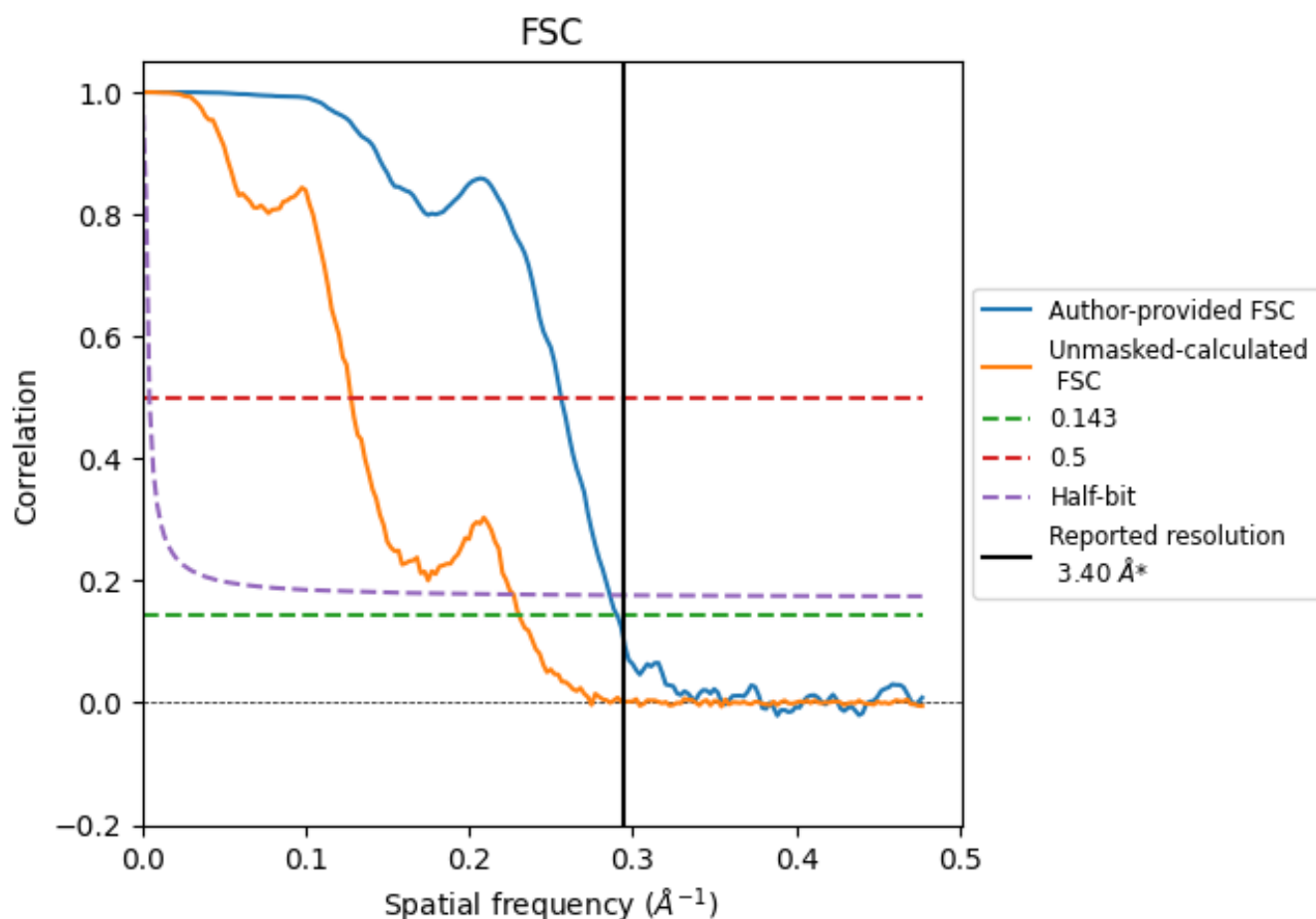


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 $0.294 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

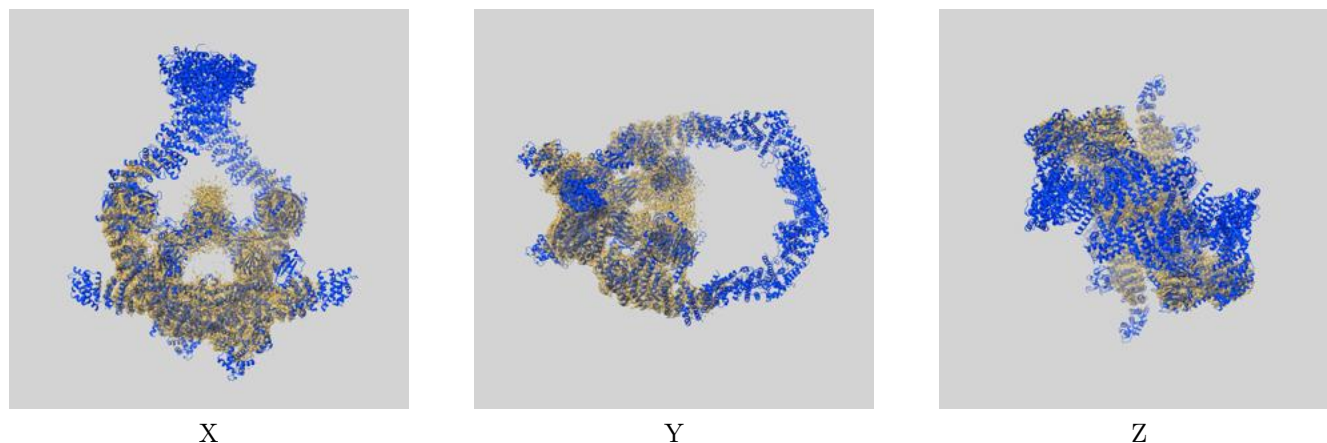
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.44	3.90	3.50
Unmasked-calculated*	4.34	7.83	4.40

*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 4.34 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

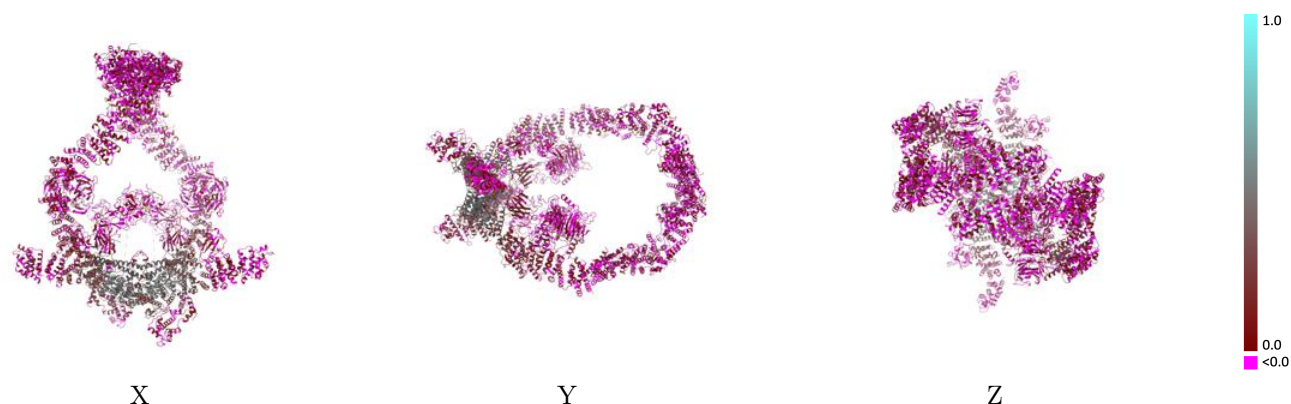
This section contains information regarding the fit between EMDB map EMD-46686 and PDB model 9D9Z. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



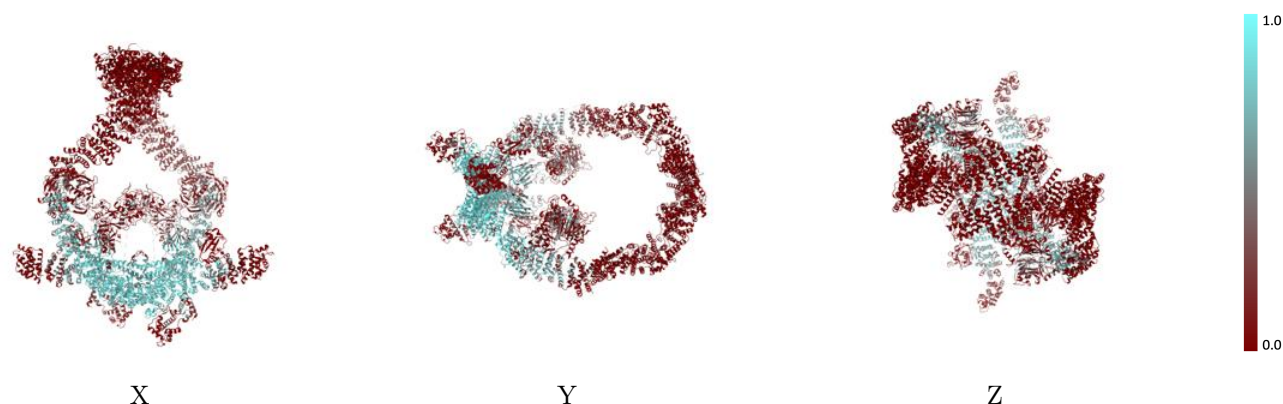
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



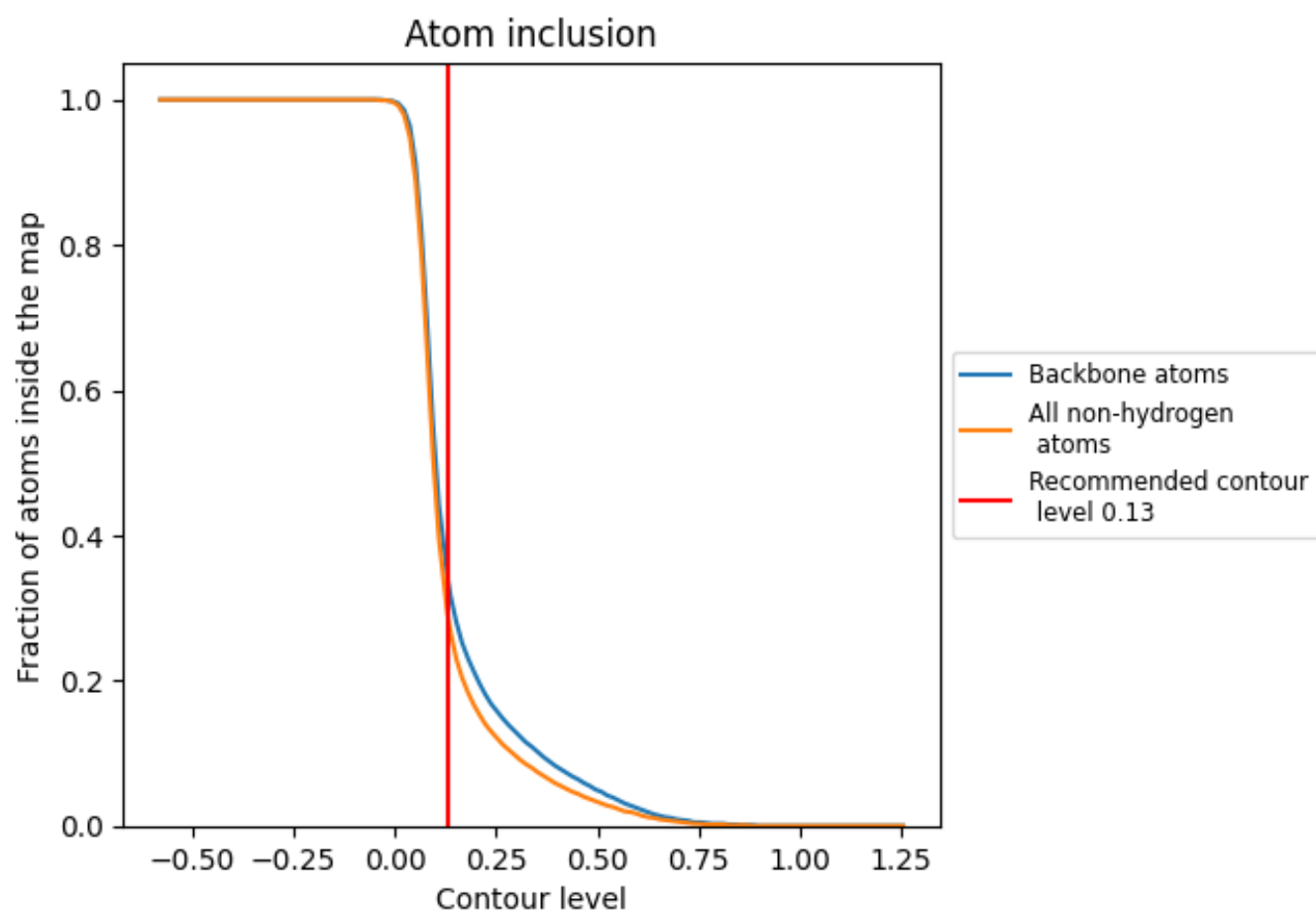
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 34% of all backbone atoms, 29% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.2930	0.1100
A	0.3000	0.1120
B	0.2990	0.1130
C	0.1500	0.0740
D	0.1350	0.0820
E	0.2720	0.0850
F	0.2740	0.0890

1.0

0.0

<0.0