



wwPDB EM Validation Summary Report ⓘ

Dec 26, 2024 – 10:00 AM EST

PDB ID : 6SCT
EMDB ID : EMD-0126
Title : Cryo-EM structure of the consensus triskelion hub of the clathrin coat complex
Authors : Morris, K.L.; Cameron, A.D.; Sessions, R.; Smith, C.J.
Deposited on : 2019-07-25
Resolution : 4.69 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.dev113
MolProbity : 4.02b-467
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) : 2.40

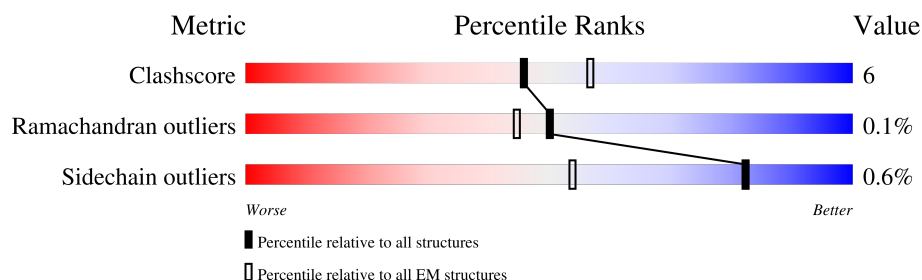
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.69 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	A	1675	<div> <div>17%</div> <div>20%</div> <div>77%</div> </div>
1	B	1675	<div> <div>35%</div> <div>34%</div> <div>6%</div> <div>60%</div> </div>
1	C	1675	<div> <div>24%</div> <div>22%</div> <div>5%</div> <div>74%</div> </div>
1	F	1675	<div> <div>17%</div> <div>19%</div> <div>77%</div> </div>
1	G	1675	<div> <div>35%</div> <div>34%</div> <div>6%</div> <div>60%</div> </div>
1	H	1675	<div> <div>24%</div> <div>22%</div> <div>74%</div> </div>
1	K	1675	<div> <div>17%</div> <div>19%</div> <div>77%</div> </div>
1	L	1675	<div> <div>35%</div> <div>34%</div> <div>6%</div> <div>60%</div> </div>

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Mol	Chain	Length	Quality of chain
1	M	1675	<div><div><div></div><div></div><div></div></div><div>24% 22% 74%</div></div>
2	D	229	<div><div><div></div><div></div><div></div></div><div>44% 38% 7% 55%</div></div>
2	E	229	<div><div><div></div><div></div><div></div></div><div>26% 23% 74%</div></div>
2	I	229	<div><div><div></div><div></div><div></div></div><div>44% 37% 8% 55%</div></div>
2	J	229	<div><div><div></div><div></div><div></div></div><div>26% 22% 74%</div></div>
2	N	229	<div><div><div></div><div></div><div></div></div><div>44% 38% 7% 55%</div></div>
2	O	229	<div><div><div></div><div></div><div></div></div><div>26% 22% 74%</div></div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 40680 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 Clathrin heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	379	Total	C	N	O	S	0	0
			3168	2037	528	584	19		
1	B	666	Total	C	N	O	S	0	0
			5405	3438	927	1015	25		
1	C	441	Total	C	N	O	S	0	0
			3598	2293	615	675	15		
1	F	379	Total	C	N	O	S	0	0
			3168	2037	528	584	19		
1	K	379	Total	C	N	O	S	0	0
			3168	2037	528	584	19		
1	G	666	Total	C	N	O	S	0	0
			5405	3438	927	1015	25		
1	L	666	Total	C	N	O	S	0	0
			5405	3438	927	1015	25		
1	H	441	Total	C	N	O	S	0	0
			3598	2293	615	675	15		
1	M	441	Total	C	N	O	S	0	0
			3598	2293	615	675	15		

- Molecule 2 is a protein called Clathrin light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	104	Total	C	N	O	S	0	0
			875	539	165	168	3		
2	E	59	Total	C	N	O		0	0
			514	312	101	101			
2	J	59	Total	C	N	O		0	0
			514	312	101	101			
2	O	59	Total	C	N	O		0	0
			514	312	101	101			
2	I	104	Total	C	N	O	S	0	0
			875	539	165	168	3		
2	N	104	Total	C	N	O	S	0	0
			875	539	165	168	3		

SER	VAL	ALA	VAL	PRO	GLN	ALA	PRO	PHE	GLY	TYR	GLY	TYR	THR	ALA	PRO	PRO	TYR	GLY	GLN	PRO	GLN	PRO	GLY	PHE	GLY	TYR	SER	MET
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MET	ALA	ALA	GLN	LEU	LEU	PRO	I LE	ARG	PHE	GLN	GLY	HIS	LEU	GLN	LEU	GLN	ASN	ASN	GLY	ILE	PRO	PRO	ALA	ALA	ASN	ILE	GLY	PHE	SER	SER	THR	LEU	LEU	THR	MET	MET	GLY	GLY	SER	SER	ASP	LYS	ILE	CYS	ILE	ARG	GLE	GLY	LYS	VAL	GLY	GLY	GLU	GLN	ALA	ALA	GLN	VAL	VAL	VAL	ILE	ILE	ASP	MET	ASN	ASP	PRO	SER	SEN
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- Molecule 1: Clathrin heavy chain



[illegible]

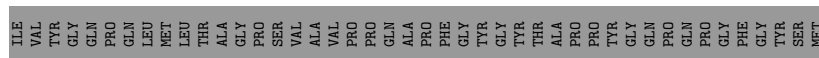
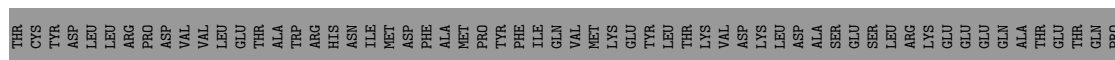
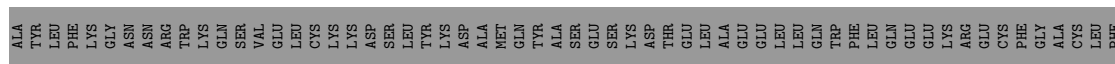
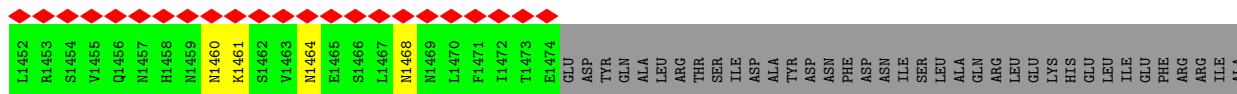
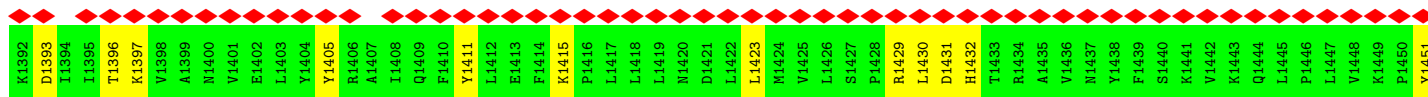
- Molecule 1: Clathrin heavy chain

[illegible]

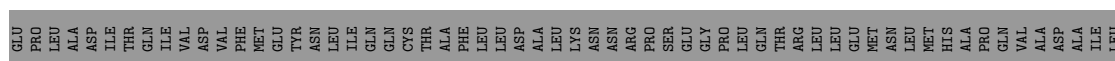
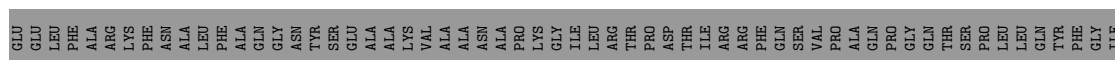
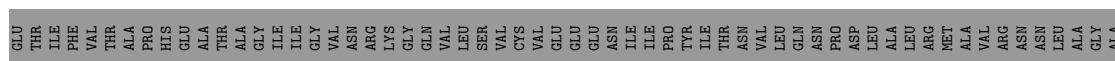
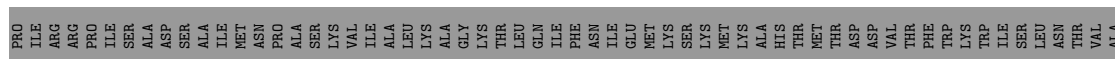
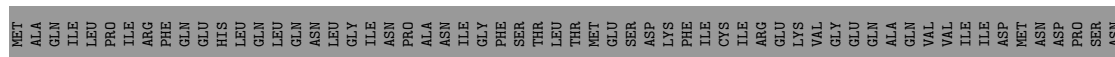
- Molecule 1: Clathrin heavy chain

[illegible]





- Molecule 1: Clathrin heavy chain

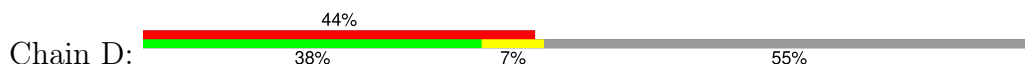


Y1451	F1391	K1331	Q1270	M1210	W1149	L1085	R1022	E962	D901	S841	PHE
L1452	K1392	M1332	M1271	Y1211	W1150	I1086	N1023	S963	S902	T842	ASP
R1453	D1393	R1333	C1272	D1212	E1151	E1087		R964	R903	D843	GLN
S1454	I1394	E1334	G1273	A1213	E1152	H1088	N1026	P965	P904	E344	PRO
V1455	I1395	H1335	L1274	A1214	L1153	I1089	L1027	R966	V905	V845	ASP
Q1456	T1396	L1336	H1275	K1215	V1154	G1090	L1028	R967	G906	V846	VAL
N1457	K1397	E1337	T1276	L1216	K1155	N1091	I1029	R968	K907	A847	HIS
H1458	V1398	L1338	V1277	L1217	Q1158	L1092	L1030	R969	Y908	LEU	PHE
N1459	F1399	F1339	H1278	Y1218	M1159	D1093	T1031	P970	LEU	TYR	LYS
N1460	M1400	W1340	H1279	N1219	A1160	R1094	A1032	P971	TYR	ARG	ILE
V1461	V1401	S1341	A1280	N1220	R1161	A1095	I1033	D972	ARG	E850	ALA
S1462	L1402	V1342	D1281	V1221	K1162	Y1096	K1034	Q973	ASN	E851	ALA
V1463	L1403	V1343	E1282	M1223	K1163	F1098	D1036	Q974	ASN	R852	ALA
N1464	Y1404	I1344	L1283	F1224	A1164	A1099	R1037	Y975	LEU	R853	CYS
E1465	Y1405	P1346	E1284	G1225	R1165	E1100	R1037	Q976	GLN	R854	LYS
R1406	R1407	K1347	E1285	G1226	E1166	R1101	T1038	Q977	TYR	L855	THR
L1408	T1408	V1348	I1287	L1227	S1167	C1102	R1039	Q978	ILE	K856	GLN
Q1409	F1410	R1350	M1288	A1228	Y1168	M1103	V1040	S980	GLU	L857	ILE
F1411	Y1411	A1351	Y1289	S1229	Y1169	E1104	M1041	E981	TYR	L858	CYS
L1412	L1412	A1352	Y1290	T1230	E1170	E1104	E1042	T982	VAL	L859	VAL
E1413	E1413	E1353	Q1291	L1231	T1171	S1109	I1044	Q983	LYS	P860	GLY
F1414	Q1354	Q1354	D1292	H1233	E1172	Q1110	N1045	D984	ASN	W861	ALA
K1415	F1414	A1355	R1293	H1233	L1173	K1118	R1046	P985	ARG	L862	ILE
P1416	F1415	H1356	G1294	L1234	I1174	G1119	L1047	E986	GLY	E863	GLY
L1417	P1416	L1357	Y1295	G1235	F1175	M1120	D1048	E987	ASN	A864	ASN
L1418	W1358	E1297	E1296	E1236	L1176	L1125	N1049	Y988	CYS	R865	GLN
L1419	A1359	E1297	F1297	Y1237	L1177	I1126	Y1050	S989	THR	I866	LEU
L1420	E1360	L1299	Q1238	Q1238	A1178	Q1117	D1051	V990	ASP	H867	THR
L1421	L1361	L1300	A1239	A1239	K1179	K1118	A1052	T991	PRO	V814	GLN
D1421	V1362	T1301	M1302	A1240	T1180	K1118	A1052	V992	GLY	V815	GLY
L1422	F1363	T1301	M1302	A1240	N1181	G1119	P1053	K993	ARG	I816	LEU
L1423	L1364	M1302	D1242	D1242	R1182	V1121	I1055	A994	VAL	G817	ILE
M1424	Y1365	E1304	G1304	G1304	L1183	K1122	A1056	P995	LYS	E871	GLY
V1425	K1366	A1305	A1244	A1244	E1185	E1123	N1057	M996	ASN	E872	ASN
L1426	K1367	A1306	R1245	R1245	A1184	K1122	I1055	T997	PHE	L819	PHE
S1427	Y1368	A1307	K1246	K1246	L1186	E1187	A1056	A998	LEU	L820	LEU
P1428	E1369	G1308	A1247	A1247	E1188	Y1128	E1063	P1001	GLY	D821	GLY
R1429	E1370	G1309	N1248	N1248	F1189	I1129	L1064	N1002	ALA	V822	ALA
L1430	Y1371	E1310	T1250	T1250	I1190	K1130	F1085	L1000	LYS	D823	LYS
D1431	N1372	R1311	R1251	R1251	N1191	A1131	E1066	E1003	THR	S825	THR
H1432	A1373	A1312	T1252	T1252	G1192	D1132	E1067	E1006	GLN	E826	GLN
T1433	I1374	H1313	W1253	W1253	P1193	D1133	E1068	I1005	LEU	D827	LEU
R1434	I1375	M1314	K1254	K1254	N1194	P1134	A1068	E1006	PRO	V829	PRO
A1435	I1376	G1315	E1255	E1255	N1195	P1134	F1069	L1007	ILE	I830	ILE
V1436	T1377	M1316	V1256	V1256	A1196	S1135	F1069	L1008	GLY	N831	GLY
N1437	M1378	F1317	V1257	V1257	H1197	S1136	A1070	E1009	VAL	L832	VAL
L1438	M1379	T1318	C1257	C1257	I1198	Y1137	I1071	E1009	ASP	I833	ASP
F1439	N1380	E1319	F1258	F1258	I1198	W1138	R1072	K1010	GLN	L834	GLN
S1440	H1381	L1320	A1259	A1259	Q1199	E1139	K1074	V1012	LEU	V835	LEU
T1382	P1382	L1320	C1260	C1260	Q1200	Q1142	F1075	V1013	THR	V836	THR
T1383	A1321	A1321	V1261	V1261	G1202	Q1143	D1076	N1015	ARG	R837	ARG
L1442	L1322	I1322	D1262	D1262	G1202	A1144	V1077	S1016	GLY	Q838	GLY
K1443	L1323	L1323	G1263	G1263	R1204	A1144	N1078	S1016	ILE	Q839	ILE
Q1444	Y1324	Y1324	K1264	K1264	C1205	T1145	T1079	V1017	CYS	F840	CYS
L1445	S1325	S1325	E1265	E1265	Y1206	T1146	S1080	E1019	VAL		
P1446	K1326	K1326	F1266	F1266	D1207	S1147	Q1083	E1020	ASP		
L1447	F1327	F1327	R1267	R1267	E1208	G1148	V1084	H1021	ARG		
L1448	Q1390	Q1390	L1268	L1268	K1209				Y900		



[illegible]

- Molecule 2: Clathrin light chain

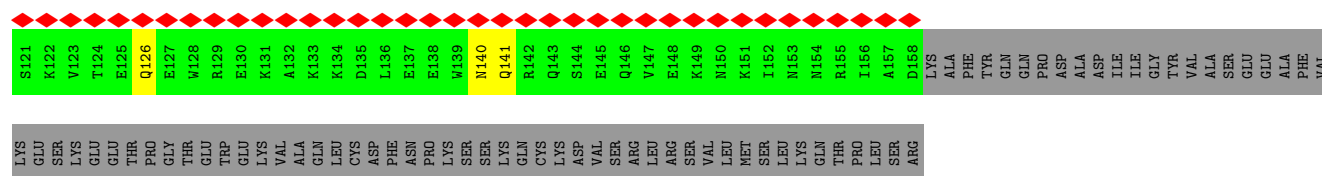


MET	LYS	GLU	SER	LYS	GLU	THR	PRO	G189	T190	E191	W192	K193	K194	V195	A196	Q197	L198	C199	F201	M202	P203	K204	S205	S206	K207	Q208	C209	K210	D211	V212	S213	R214	L215	R216	S217	V218	L219	M220	S221	L222	K223	Q224	T225	PRO	LEU	SER	ARG	SER	GLY	PHE	GLY	ASP	GLY	ALA	GLY	ASP	GLY	ASP	GLY	ALA	ASN	GLY	ILE	GLY	ILE	GLY	GLY	GLN	ALA	LEU	ALA	GLN	PRO	GLY	GLY	ALA	ALA	ASP	GLY	GLY	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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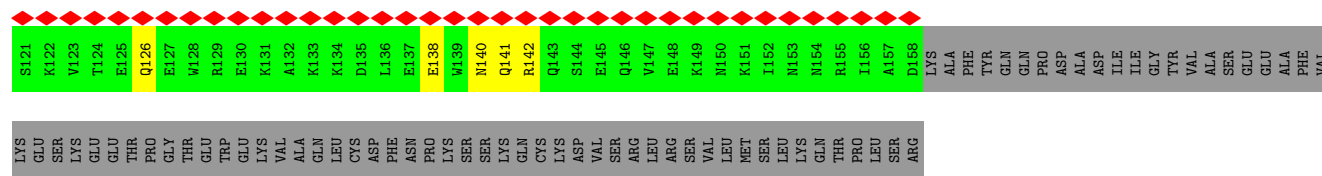
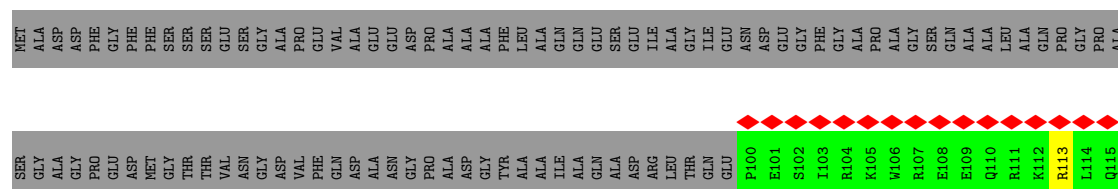
- Molecule 2: Clathrin light chain



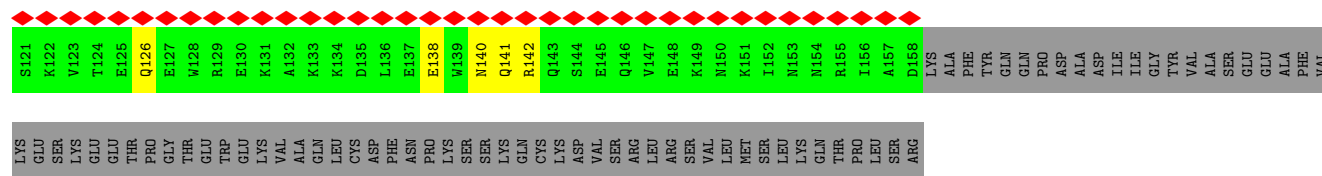
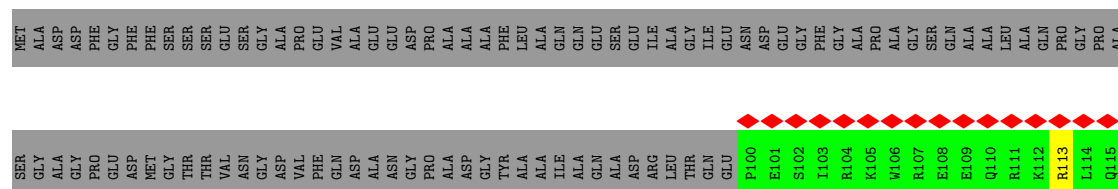
SER	GLY	ALA	GLY	GLU	ASP	MET	GLY	THR	THR	VAL	ASN	GLY	ASP	VAL	PHE	GLN	ASP	ALA	ALA	ASN	GLY	TYR	ALA	ALA	ILE	GLN	GLN	ALA	ASP	ARG	LEU	THR	GLU	<div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></d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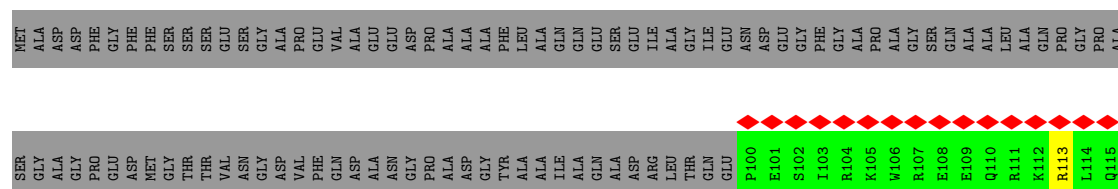
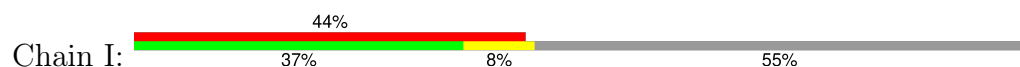
• Molecule 2: Clathrin light chain



• Molecule 2: Clathrin light chain



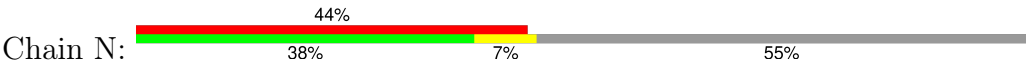
• Molecule 2: Clathrin light chain



S121	K122	V123	T124	E125	Q126	E127	W128	R129	E130	K131	A132	K133	K134	D135	L136	E137	E138	W139	N140	Q141	R142	Q143	S144	E145	Q146	V147	E148	K149	N150	K151	I152	N153	R154	R155	I156	A157	D158	K159	A160	F161	Y162	Q163	Q164	P165	D166	ALA	ASP	ILE	ILE	GLY	TYR	VAL	ALA	SER	GLU	GLU	ALA	PHE	VAL
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LYS	GLU	SER	LYS	GLU	GLU	THR	PRO	G189	T190	E191	W192	E193	K194	V195	A196	Q197	L198	C199	D200	F201	N202	P203	K204	S205	S206	K207	Q208	C209	I150	K210	D211	V212	S213	R214	L215	R216	S217	V218	L219	M220	S221	L222	K223	Q224	T225	PRO	LEU	SER	ARG
-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----

• Molecule 2: Clathrin light chain



MET	ALA	ASP	GLY	PHE	GLY	PHE	SER	SER	SER	GLU	SER	GLY	ALA	GLU	VAL	ALA	GLU	ASP	PRO	ALA	ALA	ALA	PHE	LEU	ALA	GLN	GLU	SER	GLU	ASP	I150	ALA	GLY	ILE	GLY	THR	GLN	GLU	P100	E101	S102	I103	R104	K105	W106	R107	E108	E109	Q110	R111	K112	R113	L114	Q115	E116	L117	D118	A119	A120
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

SER	GLY	ALA	GLY	PRO	GLU	ASP	MET	THR	THR	VAL	ASN	GLY	VAL	PHE	GLN	ASP	ALA	GLY	TYR	ALA	ILE	ALA	GLN	ALA	ARG	LEU	THR	GLN	GLU	P100	E101	S102	I103	R104	K105	W106	R107	E108	E109	Q110	R111	K112	R113	L114	Q115	E116	L117	D118	A119	A120
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S121	K122	V123	T124	E125	Q126	E127	W128	R129	E130	K131	A132	K133	K134	D135	L136	E137	E138	W139	N140	Q141	R142	Q143	S144	E145	Q146	V147	E148	K149	N150	K151	I152	N153	R154	R155	I156	A157	D158	K159	A160	F161	Y162	Q163	Q164	P165	D166	ALA	ASP	ILE	ILE	GLY	TYR	VAL	ALA	SER	GLU	GLU	ALA	PHE	VAL
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

LYS	GLU	SER	LYS	GLU	GLU	THR	PRO	G189	T190	E191	W192	E193	K194	V195	A196	Q197	L198	C199	D200	F201	N202	P203	K204	S205	S206	K207	Q208	C209	I150	K210	D211	V212	S213	R214	L215	R216	S217	V218	L219	M220	S221	L222	K223	Q224	T225	PRO	LEU	SER	ARG
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	313406	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	69	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	82111	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.374	Depositor
Minimum map value	-0.157	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.195	Depositor
Map size (Å)	436.48, 436.48, 436.48	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.705, 1.705, 1.705	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	0.30	0/3240	0.50	0/4375
1	B	0.28	0/5513	0.49	0/7468
1	C	0.29	0/3667	0.52	0/4970
1	F	0.30	0/3240	0.50	0/4375
1	G	0.29	0/5513	0.49	0/7468
1	H	0.29	0/3667	0.52	0/4970
1	K	0.30	0/3240	0.50	0/4375
1	L	0.29	0/5513	0.49	0/7468
1	M	0.29	0/3667	0.52	0/4970
2	D	0.28	0/887	0.51	0/1183
2	E	0.27	0/520	0.57	0/692
2	I	0.28	0/887	0.51	0/1183
2	J	0.28	0/520	0.56	0/692
2	N	0.28	0/887	0.51	0/1183
2	O	0.28	0/520	0.56	0/692
All	All	0.29	0/41481	0.51	0/56064

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	3168	0	3118	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	5405	0	5359	61	0
1	C	3598	0	3592	58	0
1	F	3168	0	3118	35	0
1	G	5405	0	5359	65	0
1	H	3598	0	3592	53	0
1	K	3168	0	3118	36	0
1	L	5405	0	5359	65	0
1	M	3598	0	3592	56	0
2	D	875	0	872	8	0
2	E	514	0	508	4	0
2	I	875	0	872	9	0
2	J	514	0	508	5	0
2	N	875	0	872	8	0
2	O	514	0	508	5	0
All	All	40680	0	40347	488	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 488 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:772:LEU:H	1:C:773:PRO:HD2	1.22	1.03
1:H:772:LEU:H	1:H:773:PRO:HD2	1.22	1.00
1:M:772:LEU:H	1:M:773:PRO:HD2	1.22	1.00
1:H:763:LEU:HB3	1:H:768:LEU:HD11	1.46	0.97
1:C:763:LEU:HB3	1:C:768:LEU:HD11	1.46	0.97

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	377/1675 (22%)	351 (93%)	26 (7%)	0	100	100
1	B	664/1675 (40%)	620 (93%)	44 (7%)	0	100	100
1	C	439/1675 (26%)	389 (89%)	48 (11%)	2 (0%)	25	64
1	F	377/1675 (22%)	351 (93%)	26 (7%)	0	100	100
1	G	664/1675 (40%)	620 (93%)	44 (7%)	0	100	100
1	H	439/1675 (26%)	391 (89%)	46 (10%)	2 (0%)	25	64
1	K	377/1675 (22%)	351 (93%)	26 (7%)	0	100	100
1	L	664/1675 (40%)	620 (93%)	44 (7%)	0	100	100
1	M	439/1675 (26%)	389 (89%)	48 (11%)	2 (0%)	25	64
2	D	100/229 (44%)	95 (95%)	5 (5%)	0	100	100
2	E	57/229 (25%)	57 (100%)	0	0	100	100
2	I	100/229 (44%)	95 (95%)	5 (5%)	0	100	100
2	J	57/229 (25%)	57 (100%)	0	0	100	100
2	N	100/229 (44%)	95 (95%)	5 (5%)	0	100	100
2	O	57/229 (25%)	57 (100%)	0	0	100	100
All	All	4911/16449 (30%)	4538 (92%)	367 (8%)	6 (0%)	50	83

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	772	LEU
1	H	772	LEU
1	M	772	LEU
1	C	773	PRO
1	H	773	PRO

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	A	342/1471 (23%)	341 (100%)	1 (0%)	91	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	587/1471 (40%)	585 (100%)	2 (0%)	91	92
1	C	405/1471 (28%)	401 (99%)	4 (1%)	73	82
1	F	342/1471 (23%)	341 (100%)	1 (0%)	91	92
1	G	587/1471 (40%)	585 (100%)	2 (0%)	91	92
1	H	405/1471 (28%)	401 (99%)	4 (1%)	73	82
1	K	342/1471 (23%)	341 (100%)	1 (0%)	91	92
1	L	587/1471 (40%)	585 (100%)	2 (0%)	91	92
1	M	405/1471 (28%)	401 (99%)	4 (1%)	73	82
2	D	96/184 (52%)	94 (98%)	2 (2%)	48	67
2	E	55/184 (30%)	55 (100%)	0	100	100
2	I	96/184 (52%)	95 (99%)	1 (1%)	73	82
2	J	55/184 (30%)	55 (100%)	0	100	100
2	N	96/184 (52%)	94 (98%)	2 (2%)	48	67
2	O	55/184 (30%)	55 (100%)	0	100	100
All	All	4455/14343 (31%)	4429 (99%)	26 (1%)	82	88

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	907	LYS
1	H	907	LYS
2	N	150	ASN
1	H	772	LEU
1	H	1045	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	889	ASN
1	M	889	ASN
2	I	150	ASN
2	I	153	ASN

5.3.3 RNA ⓘ

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.

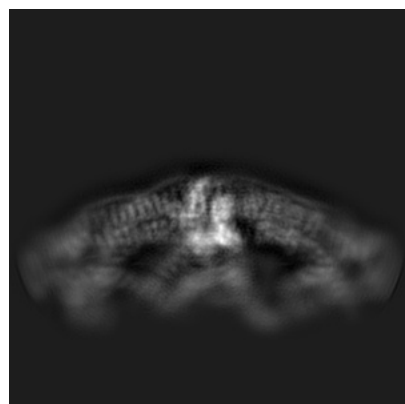
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0126. These allow visual inspection of the internal detail of the map and identification of artifacts.

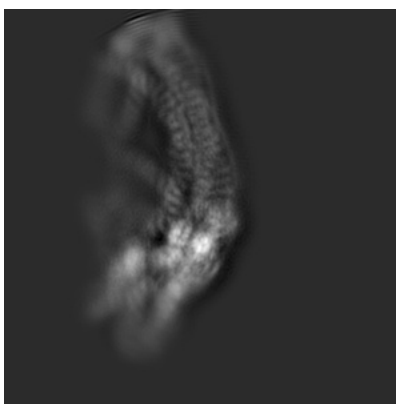
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

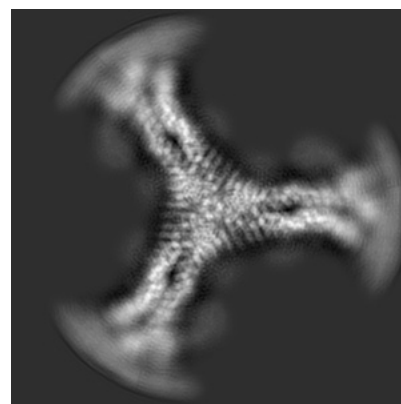
6.1.1 Primary map



X

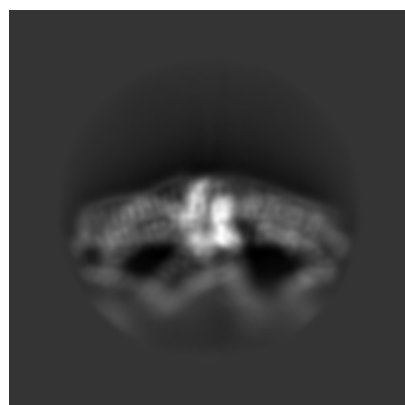


Y

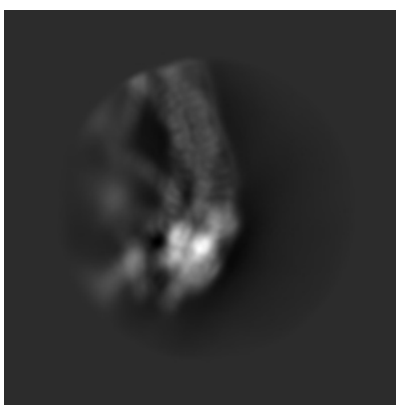


Z

6.1.2 Raw map



X



Y

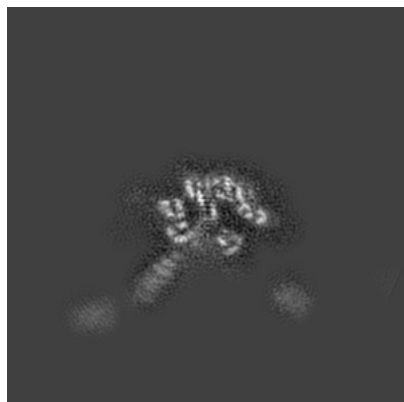


Z

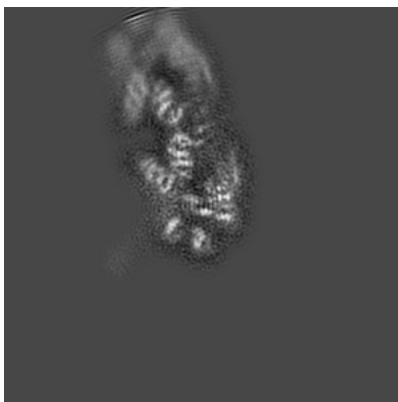
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

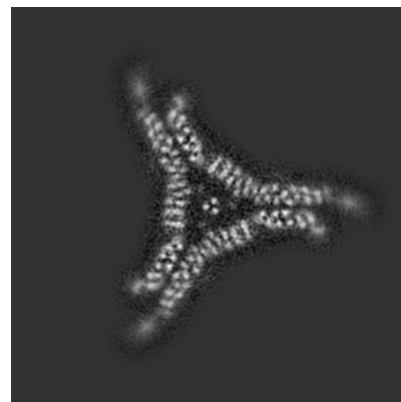
6.2.1 Primary map



X Index: 128

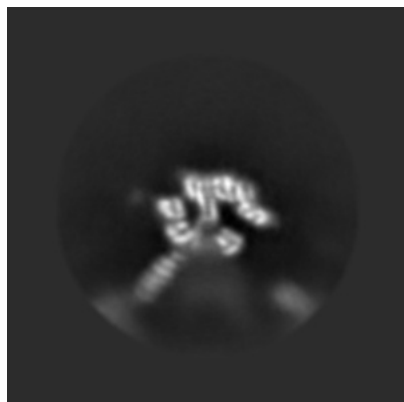


Y Index: 128

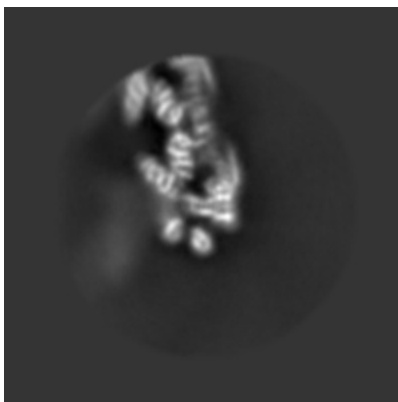


Z Index: 128

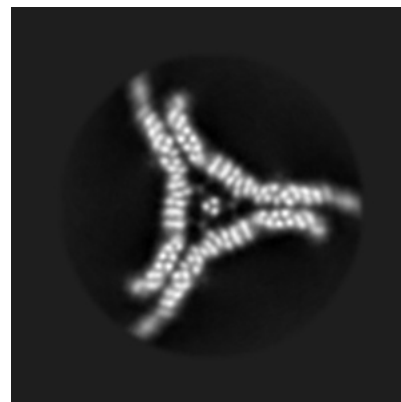
6.2.2 Raw map



X Index: 128



Y Index: 128

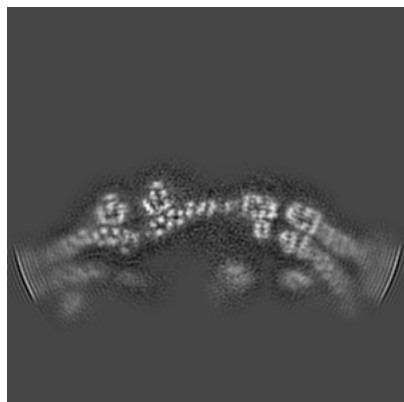


Z Index: 128

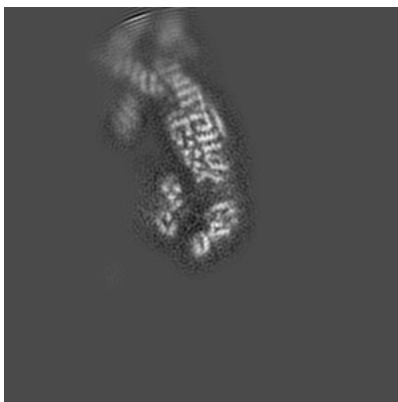
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

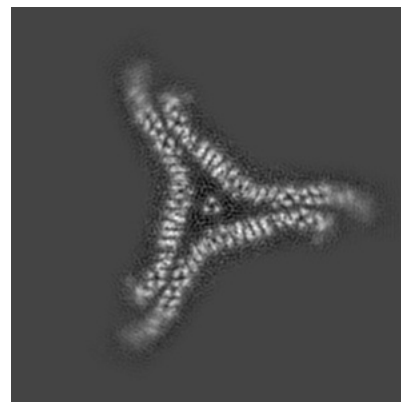
6.3.1 Primary map



X Index: 101



Y Index: 117



Z Index: 124

6.3.2 Raw map



X Index: 100



Y Index: 120



Z Index: 124

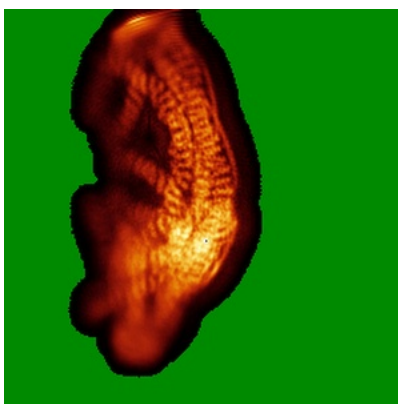
The images above show the largest variance slices of the map in three orthogonal directions.

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

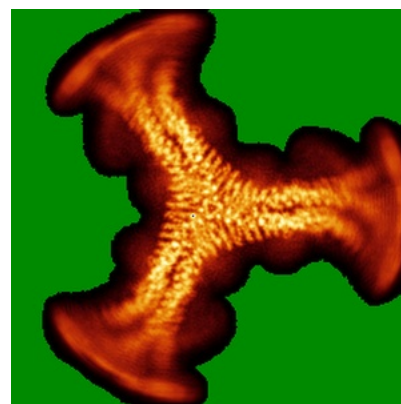
6.4.1 Primary map



X



Y

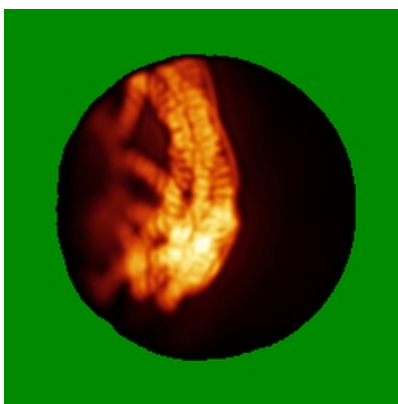


Z

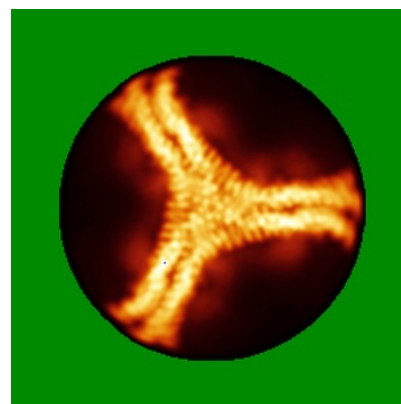
6.4.2 Raw map



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 0.195. 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.

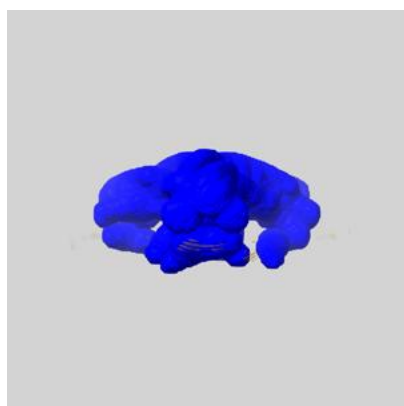
6.6 Mask visualisation [i](#)

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

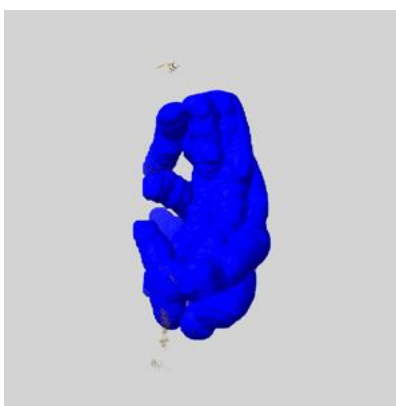
A mask typically either:

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

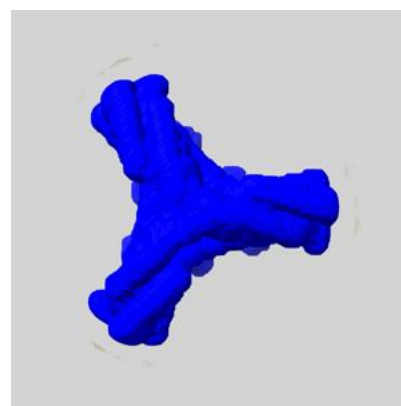
6.6.1 emd_0126_msk_1.map [i](#)



X



Y

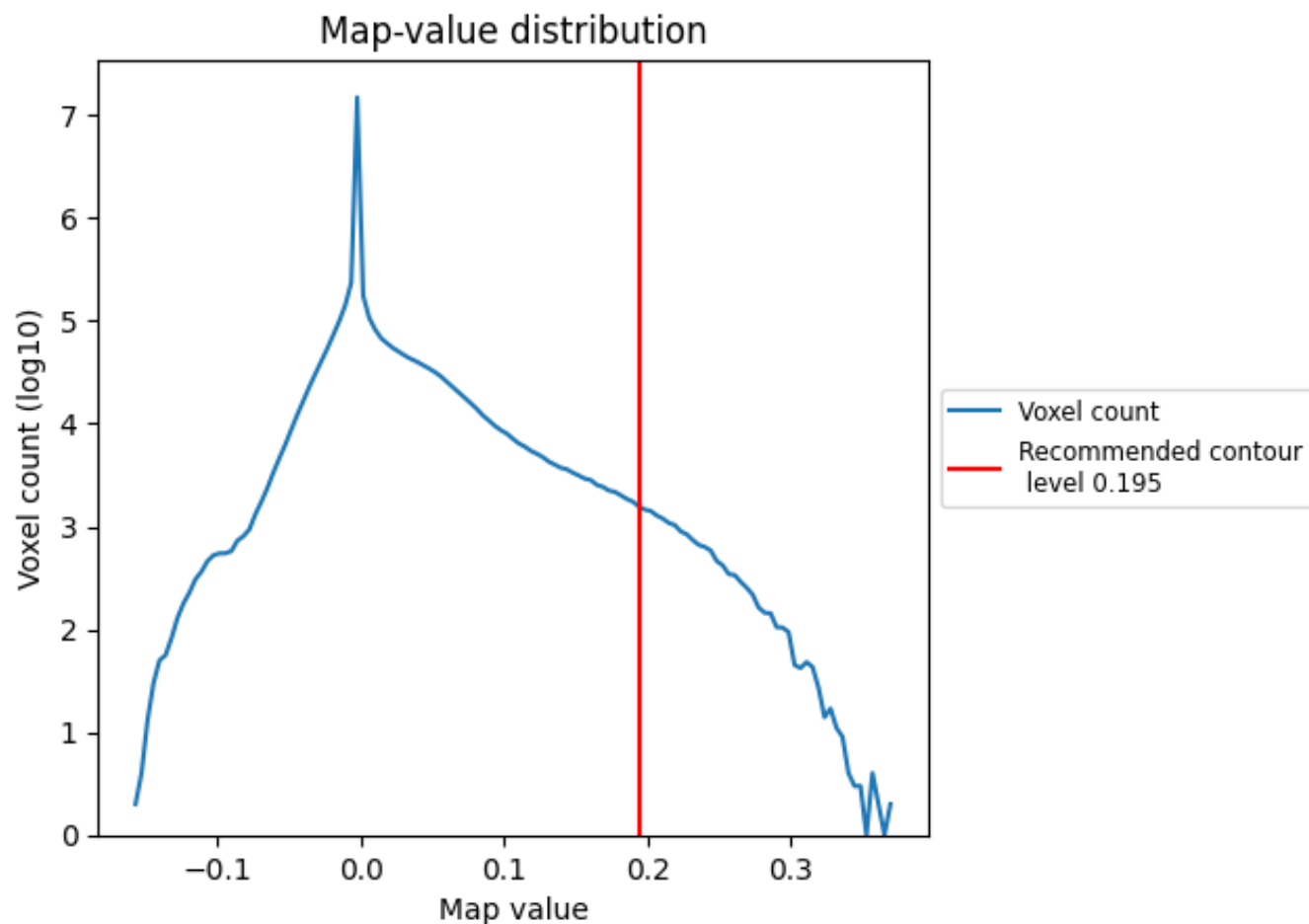


Z

7 Map analysis [i](#)

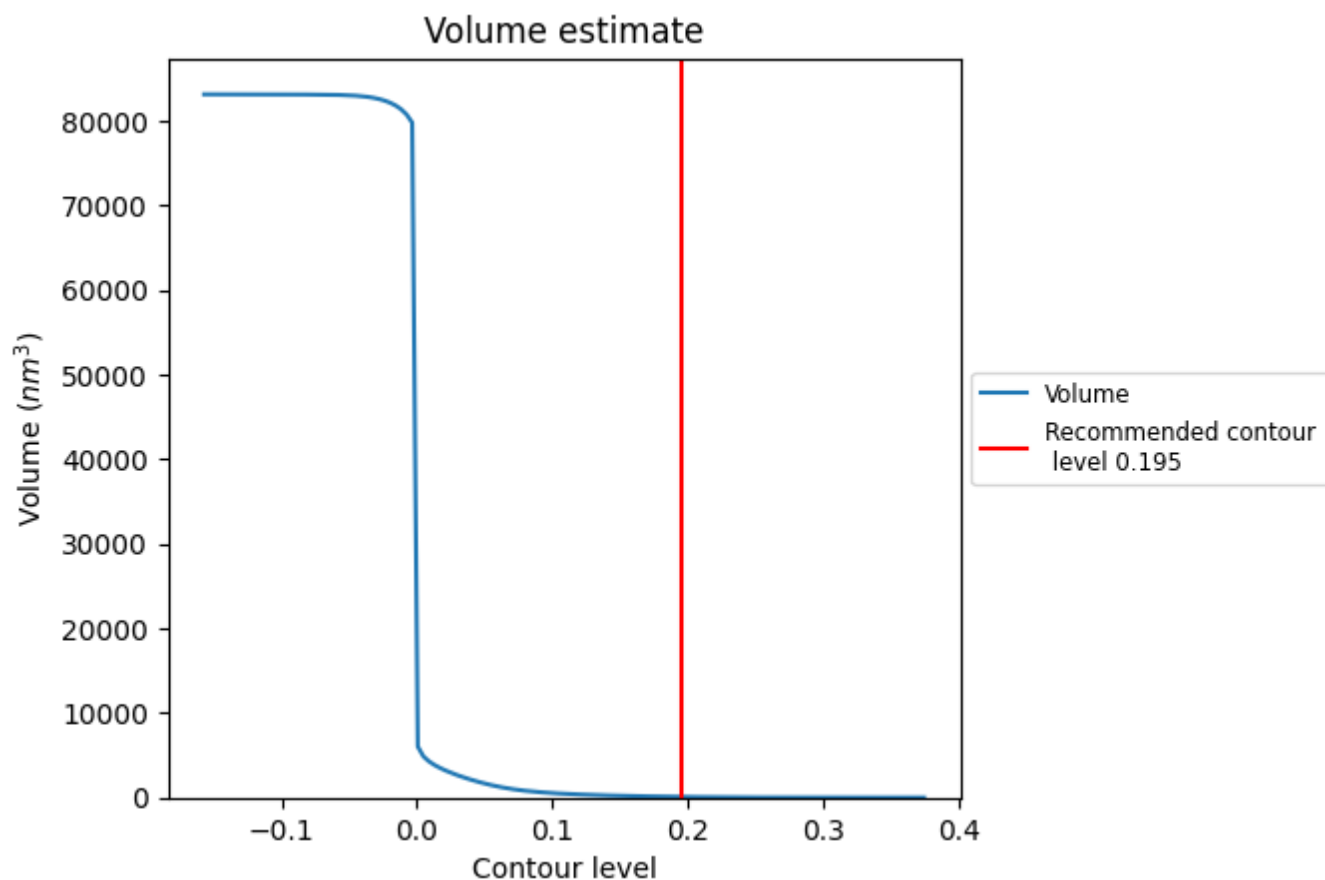
This section contains the results of statistical analysis of the map.

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.

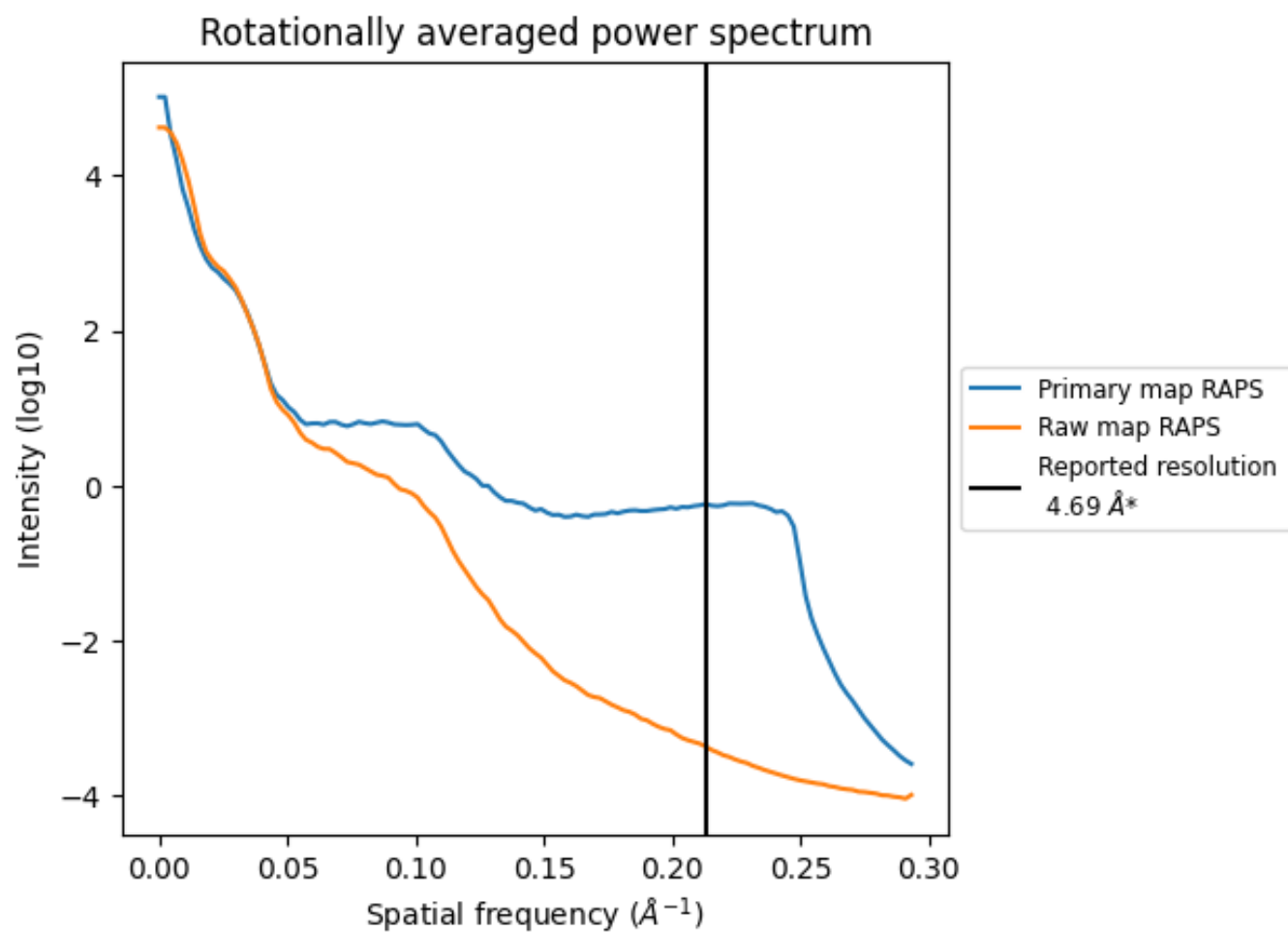
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 82 nm³; this corresponds to an approximate mass of 74 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 ⓘ

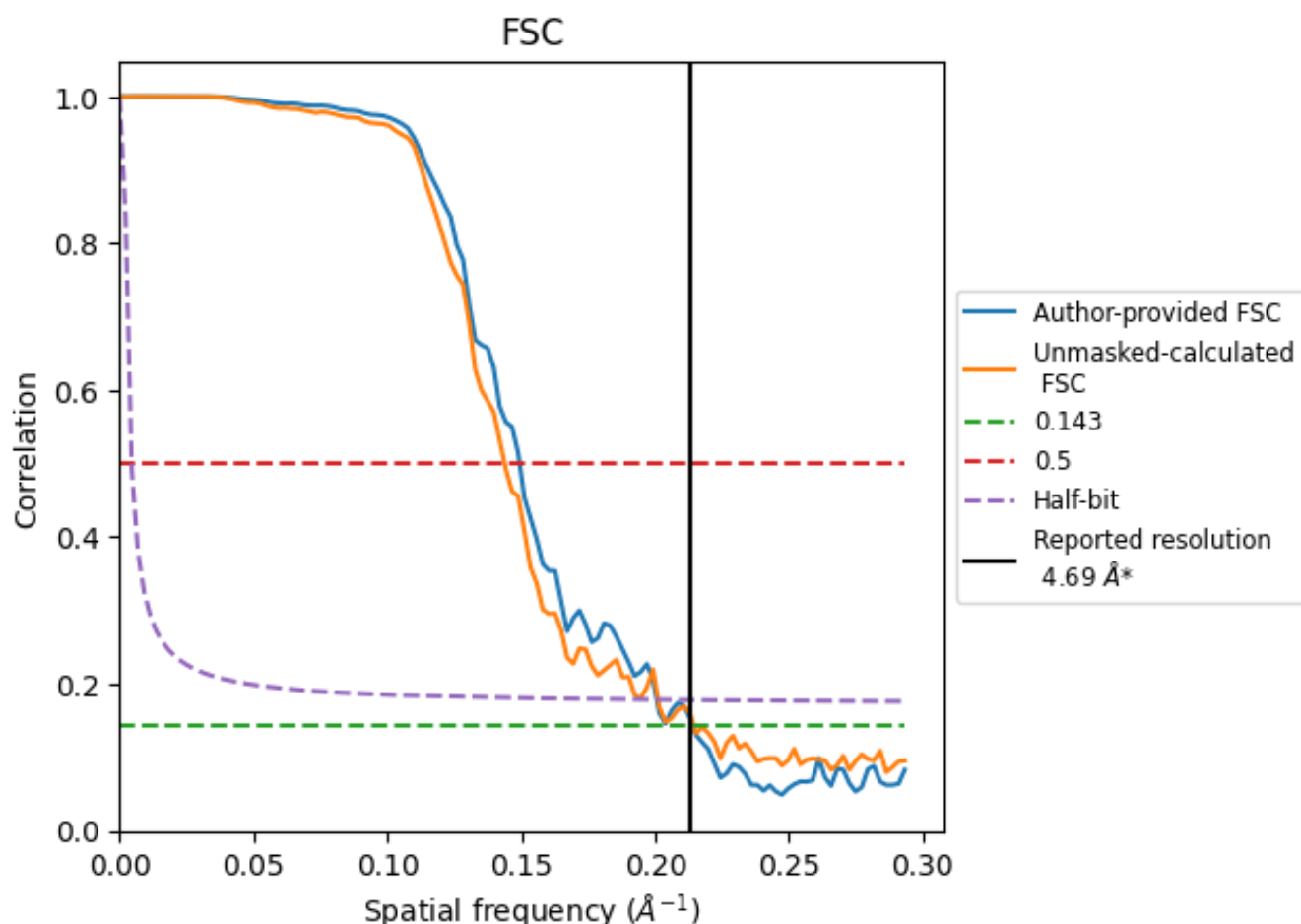


*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

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 0.213 \AA^{-1}

8.2 Resolution estimates [i](#)

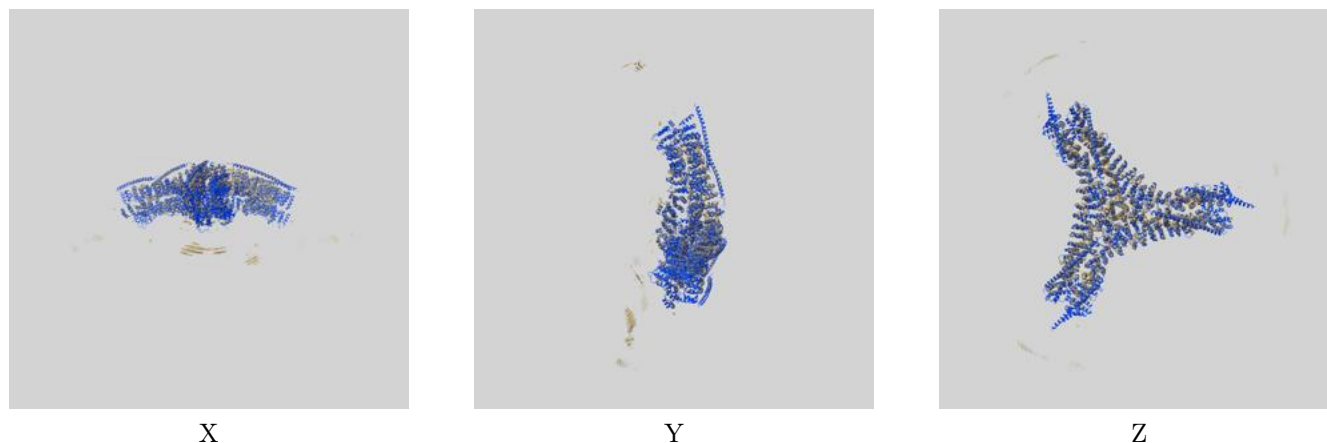
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.69	-	-
Author-provided FSC curve	4.67	6.69	4.98
Unmasked-calculated*	4.66	6.95	4.97

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

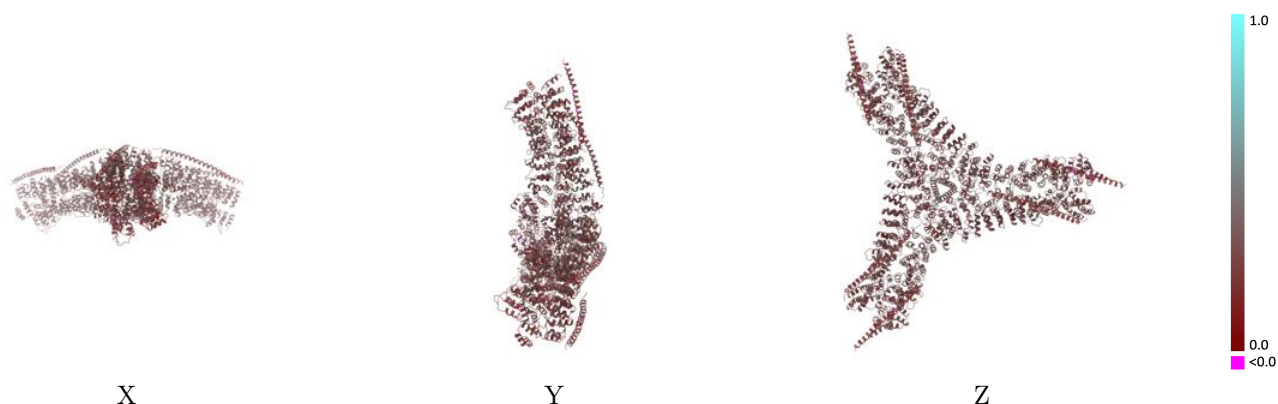
This section contains information regarding the fit between EMDB map EMD-0126 and PDB model 6SCT. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



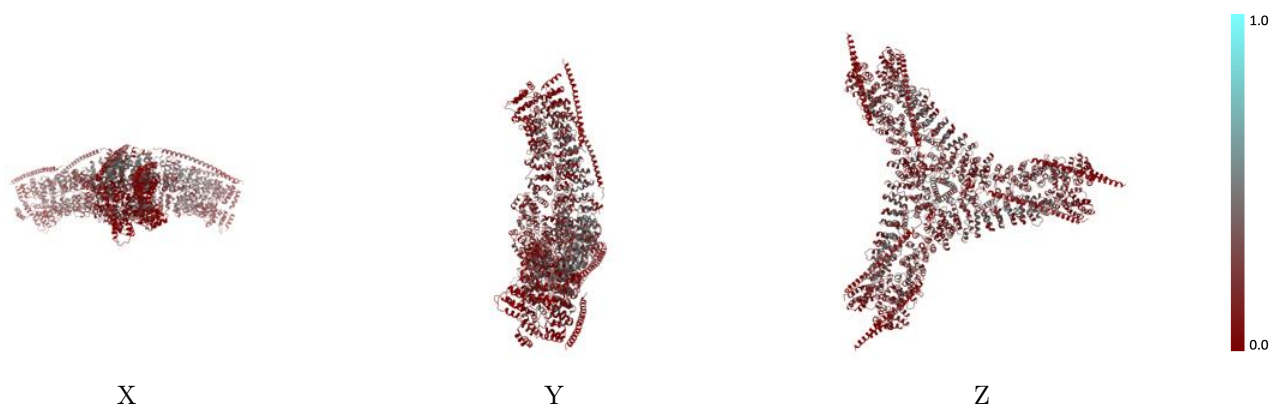
The images above show the 3D surface view of the map at the recommended contour level 0.195 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



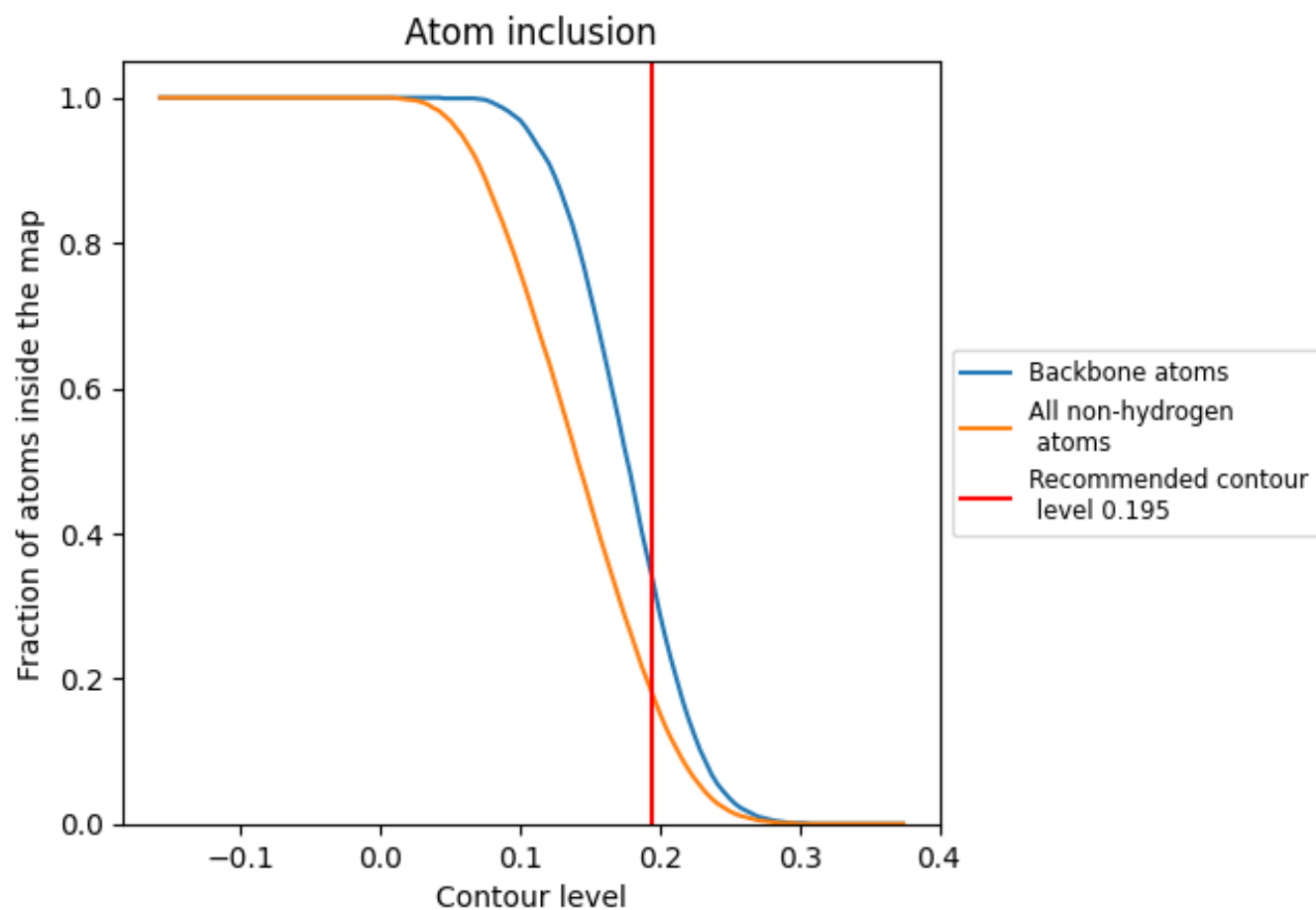
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.195).

9.4 Atom inclusion [i](#)



At the recommended contour level, 34% of all backbone atoms, 18% 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 (0.195) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.1780	<div></div> 0.2970
A	<div></div> 0.2840	<div></div> 0.3140
B	<div></div> 0.1680	<div></div> 0.2980
C	<div></div> 0.1370	<div></div> 0.2890
D	<div></div> 0.1160	<div></div> 0.2920
E	<div></div> 0.0220	<div></div> 0.2180
F	<div></div> 0.2860	<div></div> 0.3160
G	<div></div> 0.1690	<div></div> 0.2990
H	<div></div> 0.1360	<div></div> 0.2910
I	<div></div> 0.1150	<div></div> 0.2890
J	<div></div> 0.0260	<div></div> 0.2210
K	<div></div> 0.2860	<div></div> 0.3170
L	<div></div> 0.1680	<div></div> 0.2980
M	<div></div> 0.1390	<div></div> 0.2890
N	<div></div> 0.1100	<div></div> 0.2910
O	<div></div> 0.0340	<div></div> 0.2180

1.0

0.0

<0.0