



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:07 PM UTC

PDB ID : 6SCT / pdb_00006sct
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.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

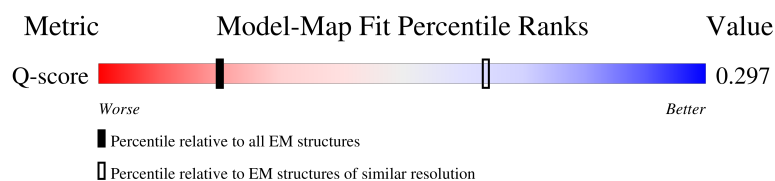
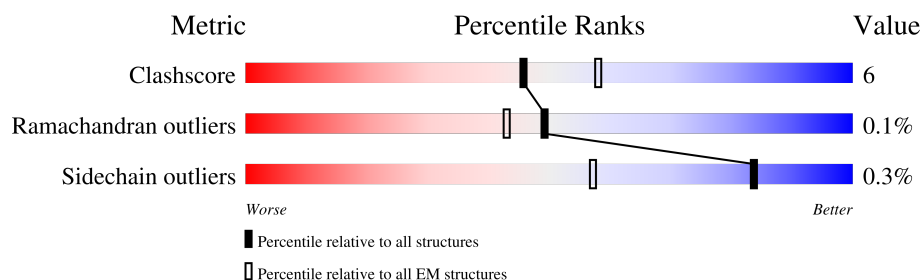
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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.



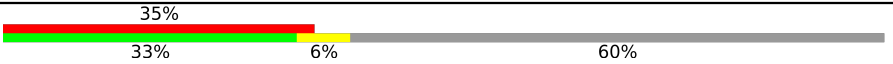
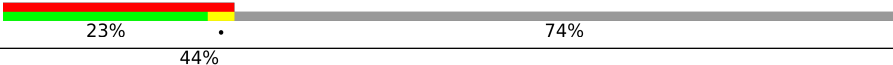
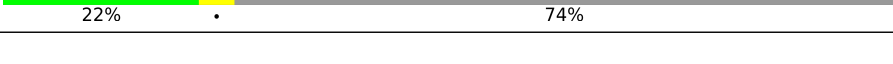
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	1970 (4.19 - 5.19)

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	
1	B	1675	
1	C	1675	
1	F	1675	

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Mol	Chain	Length	Quality of chain
1	G	1675	
1	H	1675	
1	K	1675	
1	L	1675	
1	M	1675	
2	D	229	
2	E	229	
2	I	229	
2	J	229	
2	N	229	
2	O	229	

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.

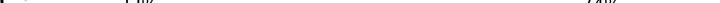
Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	104	Total	C	N	O	S	0	0
			875	539	165	168	3		
2	E	59	Total	C	N	O		0	0
			514	312	101	101			
2	J	59	Total	C	N	O		0	0
			514	312	101	101			
2	O	59	Total	C	N	O		0	0
			514	312	101	101			
2	I	104	Total	C	N	O	S	0	0
			875	539	165	168	3		
2	N	104	Total	C	N	O	S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

SER VAL ALA VAL PRO PRO GLN ALA PHE GLY TYR GLY TYR THR ALA PRO PRO PRO TYR GLY GLN PRO GLN PRO PRO GLY PHE GLY TYR SER MET

MET	ALA	ALA	GLN	ILE	LEU	PRO	ILE	ARG	PHE	GLN	GLY	HIS	LEU	GLN	LEU	GLN	ASN	ASN	GLY	ILE	GLY	GLY	ILE	ASP	THR	SER	LEU	THR	LEU	LEU	MET	MET	SER	SER	LYS	PHE	CYS	ILE	ARG	GLY	LYS	VAL	GLY	GLU	GLN	ALA	GLN	VAL	VAL	ILE	ILE	ASP	MET	ASN	ASP	PRO	SER	GLY
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[illegible]

Chain C: 



[illegible]

- Molecule 1: Clathrin heavy chain



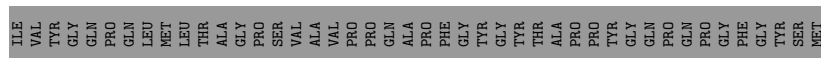
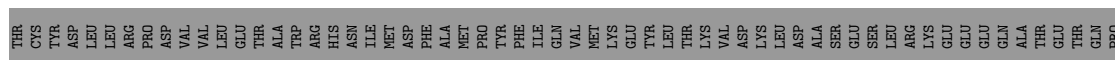
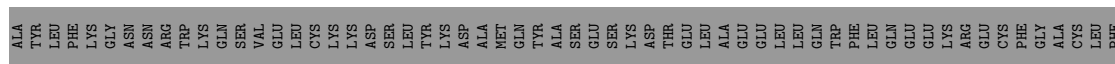
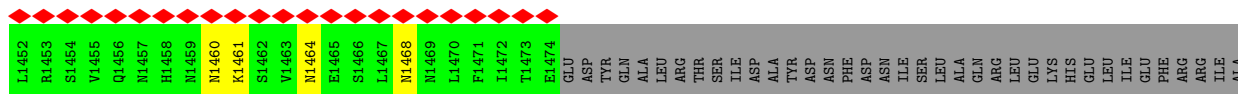
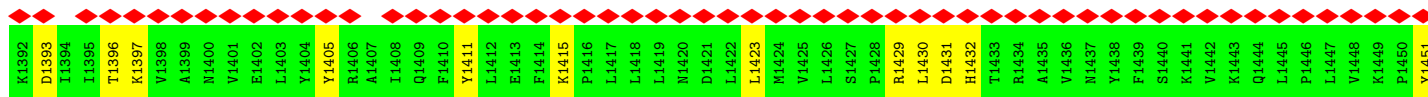
GLU	GLY	GLU	ARG	LEU	GLU	GLU	GLU	THR	GLN	MET	LEU	PRO	MET
ASP	ASN	PRO	ALA	LEU	GLU	GLU	THR	THR	PRO	GLN	VAL	ILE	ALA
SER	ASN	LEU	ASN	ASP	GLN	GLN	ILE	GLN	PHE	LEU	THR	ARG	ARG
LEU	MET	ALA	VAL	GLN	PHE	ALA	VAL	PHE	PRO	TYR	ASP	PRO	ILE
CYS	THR	ILE	ASN	GLN	ARG	ARG	THR	THR	LYS	VAL	ALA	ILE	PRO
LEU	HIS	THR	LYS	LEU	GLN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

- Molecule 1: Clathrin heavy chain

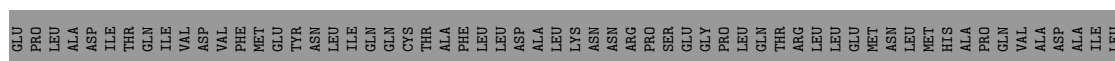
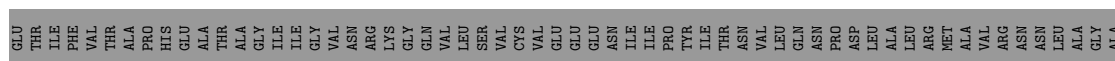
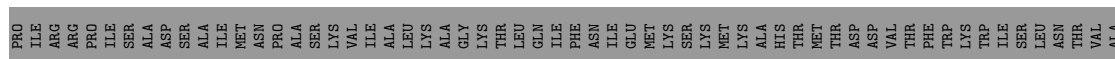
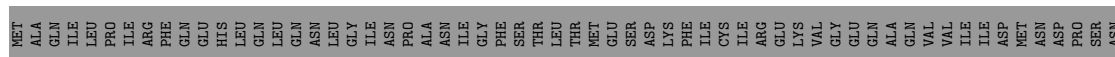
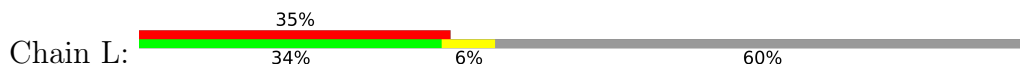
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M1271	Y1211	E1151	H1088	M1023	S963	S902	T842	ASP	ASP	PRO	ASN	ASP	PRO	GLN	ALA	LEU
C1272	D1212	E1152	I1089		N964	R903	D843	VAL	VAL	ASP	VAL	LEU	ALA	VAL	VAL	ASP
A1213	A1213	L1153	G1090	N1026	P965	V904	E844	HIS	HIS	ASP	ASP	CYS	ASP	ASN	GLN	GLY
A1214	A1214	V1154	N1091	L1027	Y966	V905	L845	LEU	LEU	VAL	THR	LEU	LEU	LYS	ASN	LEU
H1275	K1215	K1155	L1092	L1028	R967	G906	V846	VAL	VAL	HIS	THR	ARG	VAL	ILE	ASN	ASN
L1216	K1215	Y1156	D1093	I1029	R968	K907	A847	LEU	LEU	PHE	GLN	ALA	VAL	VAL	VAL	VAL
L1217	L1157	L1157	R1094	L1030	P969	Y908	E848	TYR	TYR	LYS	ARG	MET	VAL	GLN	TYR	TYR
Y1218	Q1158	Q1158	A1095	T1031	L870	C909	V849	LEU	LEU	ILE	HIS	SER	VAL	VAL	SER	SER
N1219	M1159	M1159	Y1096	A1032	I971	C910	E850	ARG	ARG	GLN	ILE	ALA	PHE	ALA	LEU	LEU
N1220	A1160	A1160	E1097	I1033	D972	K911	K851	ASN	ASN	ALA	ALA	ASN	GLU	GLU	GLU	GLU
D1281	R1161	R1161	F1098	K1034	Q973	R912	R852	ALA	ALA	ALA	ILE	ILE	THR	THR	THR	THR
E1282	K1162	K1162	A1099	A1035	V974	D913	N853	CYS	CYS	CYS	GLN	ARG	GLN	GLN	CYS	CYS
L1283	K1163	K1163	E1100	D1036	Q975	P914	L855	GLN	GLN	LYS	LYS	ASN	VAL	VAL	ARG	ARG
F1224	A1164	A1164	R1101	R1037	Q976	H915	R854	LYS	LYS	THR	GLY	ASN	LEU	VAL	VAL	PRO
G1225	R1165	R1165	G1102	T1038	T977	L916	L855	ILE	ILE	GLN	ALA	LYS	GLN	GLN	LEU	LEU
R1226	E1166	E1166	N1103	T1038	A978	A917	K856	ILE	ILE	ILE	ILE	GLN	GLN	ILE	ILE	GLN
L1287	S1167	S1167	E1104	R1039	L879	C918	L857	LYS	LYS	GLY	GLY	VAL	VAL	VAL	VAL	GLY
A1228	Y1168	Y1168	E1106		S980	V919	L858	VAL	VAL	GLU	GLN	VAL	VAL	VAL	ALA	ALA
S1229	Y1169	Y1169	P1106	E1042	E981	A920	L859	ARG	ARG	VAL	VAL	VAL	VAL	VAL	LYS	LYS
T1230	E1170	E1170		M1045	T982	Y921	P860	LYS	LYS	GLU	ALA	ALA	LEU	LEU	LYS	LYS
L1231	T1171	T1171	S1109	R1046	Q983	E922	W861	ILE	ILE	CYS	SER	SER	LEU	LEU	LEU	LEU
V1232	E1172	E1172	Q1110	R1047	D984	R923	L862	ASP	ASP	LYS	TYR	THR	GLU	VAL	VAL	VAL
H1233	L1111	L1111	L1111	L1047	P985	R924	E863	ARG	ARG	GLY	HIS	THR	GLU	GLY	GLY	GLY
L1234	A1112	A1112	A1112	D1048	E986	Q925	A864	SER	SER	GLU	GLY	GLU	LEU	LEU	THR	THR
G1235	K1113	K1113	K1113	M1049	E987	Q926	R865	ASN	ASN	ASN	THR	GLN	LEU	LEU	PRO	PRO
E1236	F1175	F1175		Y1050	V988	C926	R866	CYS	CYS	ASN	ASP	GLN	LEU	LEU	ASP	ASP
E1237	A1176	A1176	Q1117	D1051	S989	D927	H867	TYR	TYR	TYR	THR	SER	GLU	GLU	TRP	TRP
Q1238	L1177	L1177	Q1117	A1052	V990	L928	E868	ASP	ASP	ASP	THR	THR	GLU	GLU	GLU	GLU
L1299	A1178	A1178	K1118	P1053	T991	E929	E868	PRO	PRO	PRO	GLU	SER	GLU	GLU	LEU	LEU
A1239	K1179	K1179	G1119	D1054	V992	L930	G869	ARG	ARG	ARG	GLY	SER	GLU	GLU	GLU	GLU
A1240	T1180	T1180	G1119	I1055	K993	R931	C870	VAL	VAL	VAL	ALA	ILE	PRO	PRO	CYS	CYS
V1241	N1181	N1181	V1121	A1056	A994	N932	E871	LYS	LYS	LYS	VAL	GLU	GLU	GLU	ASN	ASN
D1242	Y1182	Y1182	K1122	M1057	F995	V933	E872	ASN	ASN	ASN	PHE	PHE	GLN	GLN	VAL	VAL
G1243	L1183	L1183	E1123	I1060	M996	C934	A874	LEU	LEU	LEU	LYS	SER	GLU	GLU	ARG	ARG
A1244	A1184	A1184	A1124		T997	E935	T875	ASP	ASP	ASP	GLU	PHE	GLU	GLU	ILE	ILE
R1245	E1185	E1185	I1125	S1061	A998	N936	H876	ALA	ALA	ALA	LYS	PHE	GLU	GLU	SER	SER
K1246	L1186	L1186	D1126	M1062	D999	N937		LEU	LEU	LEU	SER	ASP	VAL	VAL	VAL	VAL
A1247	E1187	E1187	S1127	E1063	L1000	S938	N877	THR	THR	THR	GLY	PHE	GLN	GLN	GLN	GLN
N1248	E1188	E1188	Y1128	F1065	P1001	L939	A878	ASP	ASP	ASP	GLY	GLY	LEU	LEU	MET	MET
S1249	F1189	F1189	I1129	E1066	N1002	F940	L879	GLN	GLN	GLN	THR	THR	LEU	LEU	GLN	GLN
T1250	I1190	I1190	K1130	E1067	E1003	K941	A880	LEU	LEU	LEU	VAL	VAL	VAL	VAL	PHO	PHO
R1251	N1191	N1191	A1131	E1067	L1004	S944	R881	THR	THR	THR	VAL	VAL	VAL	VAL	ALA	ALA
T1252	G1192	G1192	D1132	A1068	I1005	R945	L882	PRO	PRO	PRO	THR	THR	THR	THR	ALA	ALA
W1253	P1193	P1193	D1133	F1069	I1006	Y946	Y883	ILE	ILE	ILE	LEU	LEU	LEU	LEU	ALA	ALA
K1254	N1194	N1194	P1134	I1070	L1007	Y947	L884	VAL	VAL	VAL	GLY	GLY	GLY	GLY	VAL	VAL
E1255	N1195	N1195	S1135	I1071	L1008	V948	D885	CYS	CYS	CYS	ILE	ILE	ILE	ILE	GLN	GLN
V1256	A1196	A1196	S1136	F1072	E1009	R949	S886	ASP	ASP	ASP	THR	THR	THR	THR	ASP	ASP
F1257	H1197	H1197	Y1137	R1073	K1010	R949	N887	GLN	GLN	GLN	LEU	LEU	LEU	LEU	VAL	VAL
C1258	I1198	I1198	Y1137	K1074	I1011	R950	N888	LEU	LEU	LEU	VAL	VAL	VAL	VAL	GLN	GLN
F1258	I1198	I1198	M1138	F1075	V1012	K951	W835	THR	THR	THR	GLY	GLY	GLY	GLY	ASP	ASP
A1259	Q1199	Q1199	E1139	D1076	L1013	R954	V836	ASP	ASP	ASP	GLY	GLY	GLY	GLY	ASP	ASP
C1260	Q1200	Q1200	Q1142	V1077	D1014	P953	R837	GLN	GLN	GLN	THR	THR	THR	THR	ASP	ASP
V1261	V1201	V1201	A1143	M1078	N1015	E954	C838	VAL	VAL	VAL	THR	THR	THR	THR	ASP	ASP
L1322	G1202	G1202	A1144	T1079	S1016	L955	D839	VAL	VAL	VAL	THR	THR	THR	THR	ASP	ASP
L1323	D1203	D1203	N1145	T1079	V1017	W956	F893	VAL	VAL	VAL	THR	THR	THR	THR	ASP	ASP
L1264	C1204	C1204	T1146	S1080	F1018	Q957	L894	CYS	CYS	CYS	THR	THR	THR	THR	ASP	ASP
E1265	C1205	C1205	G1147	Q1083	E1019	S958	R895	VAL	VAL	VAL	THR	THR	THR	THR	ASP	ASP
F1266	Y1206	Y1206	S1147	V1084	E1020	V959	E896	VAL	VAL	VAL	THR	THR	THR	THR	ASP	ASP
R1267	D1207	D1207	G1148	L1085	E1020	L960	N897	VAL	VAL	VAL	THR	THR	THR	THR	ASP	ASP
L1268	E1208	E1208	N1149	I1086	H1021	L961	Y900	ARG	ARG	ARG	THR	THR	THR	THR	ASP	ASP
Q1330																



- 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	V904	E344	PRO
V1455	I1395	H1335	L1274	A1214	L1153	I1089	L1027	P966	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	E348	PHE
N1459	F1399	F1339	W1278	Y1218	M1159	D1093	T1031	P970	C909	V849	ALA
N1460	N1400	W1340	H1279	N1219	A1095	R1094	A1032	P971	E910	E850	LEU
V1461	V1401	S1341	A1280	N1220	R1161	R1095	I1033	D972	TYR	ARG	ILE
S1462	V1343	V1343	D1281	V1221	K1162	Y1096	K1034	Q973	ASN	GLN	ALA
V1463	L1403	L1283	E1282	N1223	K1163	F1098	D1036	Q974	ASN	ALA	ALA
Y1464	Y1404	I1345	E1284	F1224	A1099	E1097	R1037	Y975	R852	R852	ILE
E1465	Y1405	P1346	E1285	G1225	R1165	A1099	D1036	Y976	R853	R853	ARG
R1406	R1406	K1347	E1286	G1226	E1166	R1101	R1038	Y977	GLN	GLN	ASN
A1407	A1407	V1348	L1287	L1227	S1167	C1102	T1038	A978	TYR	GLY	GLN
T1408	T1408	L1349	N1288	L1228	Y1168	M1103	R1039	L979	ILE	ILE	ILE
Q1409	Q1409	R1350	Y1289	S1229	Y1169	E1104	V1040	S980	GLY	GLY	CYS
F1410	F1410	A1351	Y1290	T1230	E1170	E1104	M1041	E981	VAL	VAL	VAL
Y1411	Y1411	A1352	Q1291	L1231	T1171	P1105	E1042	T982	GLN	GLN	VAL
L1412	E1353	E1353	D1292	V1232	E1172	S1109	I1044	Q983	LYS	LYS	ALA
E1413	Q1354	Q1354	H1293	H1233	L1173	Q1110	N1045	D984	TYR	TYR	ILE
F1414	A1355	A1355	R1293	H1233	I1174	K1118	R1046	P985	ARG	GLU	GLU
K1415	H1356	H1356	G1294	L1234	I1174	A1112	L1047	E986	ASN	ASN	GLN
P1416	L1357	L1357	Y1295	G1235	F1175	K1113	D1048	E987	CYS	CYS	GLN
L1417	W1358	W1358	E1296	E1236	L1176		N1049	Y988	D927	I866	LEU
L1418	A1359	A1359	F1297	Y1237	L1177		Y1050	S989	L928	H867	THR
L1419	E1360	E1360	E1298	Q1238	A1178	Q1117	D1051	V990	L928	H867	ASP
L1420	L1361	L1361	L1299	A1239	K1179	K1118	A1052	T991	E868	V815	PRO
D1421	V1362	V1362	T1300	A1240	T1180	G1119	P1053	Y992	GLY	V815	GLY
L1422	F1363	F1363	M1302	Y1241	N1181	M1120	D1054	K993	N932	I816	LEU
L1423	L1364	L1364	M1302	D1242	R1182	V1121	I1055	A994	V933	G817	VAL
Y1365	Y1365	Y1365	E1304	G1243	L1183	E1125	A1056	P995	C934	L819	ASN
M1424	D1366	D1366	E1304	A1244	E1184	E1125	N1057	P996	E936	L820	LEU
V1425	K1367	K1367	A1305	R1245	A1185	K1122	I1055	T997	N937	D821	LYS
L1426	Y1368	Y1368	A1306	K1246	L1186	E1127	A1056	A998	E936	V822	ALA
S1427	S1427	S1427	L1307	K1247	E1187	S1127	N1062	D999	L939	D823	LYS
P1428	E1369	E1369	G1308	N1248	E1188	Y1128	E1063	P1001	F940	S825	THR
R1429	E1370	E1370	L1309	S1249	F1189	I1129	L1064	N1002	K941	E326	GLN
L1430	Y1371	Y1371	E1310	T1250	I1190	K1130	F1065	E1003	S944	L879	LEU
D1431	N1373	N1373	R1311	R1251	N1191	A1131	E1066	E1003	K881	A880	PHE
H1432	A1374	A1374	A1312	T1252	G1192	D1132	E1067	I1005	V828	D827	PRO
T1433	I1375	I1375	H1313	W1253	P1193	D1133	E1068	I1006	I829	I829	ILE
R1434	I1376	I1376	M1314	K1254	N1194	P1134	A1068	E1006	Y883	K830	GLY
A1435	T1377	T1377	G1315	E1255	N1195	L1136	F1069	L1007	I884	N831	SER
V1436	M1378	M1378	M1316	V1256	A1196	S1135	A1070	L1008	D885	L832	VAL
N1437	M1379	M1379	F1317	V1257	H1197	S1136	A1070	E1009	V948	S886	CYS
V1438	T1318	T1318	L1318	F1258	I1198	Y1137	I1071	I1009	R949	I833	VAL
F1439	E1319	E1319	Y1318	F1258	Q1199	W1138	R1072	K1010	R950	N887	ASN
S1440	P1382	P1382	L1320	A1259	Q1200	E1139	K1074	V1012	K951	L834	GLY
K1441	T1383	T1383	A1321	C1260	G1201	Q1142	F1075	V1013	D952	V836	PRO
K1442	L1384	L1384	I1322	V1261	G1202	Q1143	D1076	N1015	P953	R892	ILE
K1443	A1385	A1385	L1323	D1262	D1203	A1144	V1077	S1016	E954	R893	GLY
Q1444	W1386	W1386	Y1324	G1263	R1204	A1145	N1078	S1017	W956	L894	ILE
L1445	K1387	K1387	S1325	K1264	C1205	N1145	T1079	F1018	S958	R895	VAL
P1446	E1388	E1388	K1326	E1265	Y1206	T1146	S1080	S1019	V959	E896	CYS
L1447	Q1389	Q1389	F1327	F1266	D1207	S1147	Q1083	E1020	L960	N897	ASP
L1448				R1267	E1208	G1148	V1084	H1021	L961	P898	VAL
K1449				L1268	K1209					Y900	ARG
P1450				A1269							

PRO	ILE	VAL	TYR	GLY	GLN	PRO	GLN	LEU	MET	LEU	THR	ALA	GLY	PRO	SER	VAL	ALA	VAL	PRO	PRO	GLN	ALA	PRO	PHE	GLY	TYR	GLY	THR	ALA	PRO	PRO	TYR	GLY	GLN	PRO	GLN	PRO	GLY	PHE	GLY	TYR	SER	MET
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- Molecule 1: Clathrin heavy chain



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

GLY	ASN	GLN	MET	PHE	THR	HIS	TYR	ASP	ARG	ALA	HIS	ILE	ALA	GLN	LEU	CYS	GLU	LYS	ALA	GLY	GLU	LEU	GLN	ARG	ALA	LEU	HIS	GLU	PHE	THR	ASP	LEU	TYR	D635	T636	F637	R638	A639	V640	V641	H642	T643	H644	L645	L646	N647	F648	E649	V650	L651	V652	V653	V654	F655	G656	S657	L658	S659	V660
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D661	D662	D663	D664	D665	D666	D667	D668	D669	D670	D671	D672	D673	D674	D675	D676	D677	D678	D679	D680	D681	D682	D683	D684	D685	D686	D687	D688	D689	D690	D691	D692	D693	D694	D695	D696	D697	D698	D699	D700	D701	D702	D703	D704	D705	D706	D707	D708	D709	D710	D711	D712	D713	D714	D715	D716	D717	D718	D719	D720
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F721	S722	Q723	Q724	P725	D726	V727	H728	F729	K730	Y731	1732	Q733	A734	A735	C736	K737	T738	G739	Q740	1741	K742	E743	V744	E745	R746	1747	C748	R749	E750	S751	N752	C753	Y754	D755	P756	E757	F758	V759	K760	N761	F762	L763	K764	E765	A766	K767	L768	T769	D770	Q771	L772	P773	L774	1775	1776	V777	C778	D779	E780
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F781	D782	F783	V784	H785	D786		L789	V790	L791	V792	R793	N794	M795	L796	V797	K798	V799	I800	E801	I802		Q805	K806	V807	M808	P809	S810	R811	L812	P813	V814	V815	I816	G817	G818	L819	L820	D821	V822	D823	C824	S825	E826	D827	V828	T829	K830	M831	L832	L833	L834	V835	V836	R837	Q839	F840	S841
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GLU	GLN	ALA	GLY	THR	GLU	THR	GLN	PRO	PRO	ILE	CYS	VAL	TYR	GLY	GLN	GLY	THR	VAL	SER	PRO	THR	GLU	GLY	THR	VAL	ALA	THR	TYR	THR	ALA	GLY	GLN	PRO	PRO	PRO	GLY	PHE	GLY	TYR	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	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 1: Clathrin heavy chain

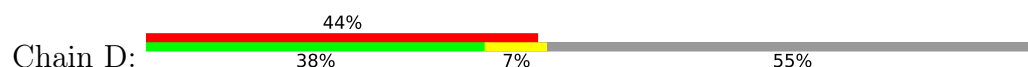


MET	ALA	ILE	GLN	ILE	PRO	ILE	ARG	PHE	GLN	GLY	HIS	ILE	GLN	GLY	ASN	PRO	GLY	GLN	GLY	ILE	ASN	THR	PHE	GLY	GLY	THR	GLY	GLY	ASP	GLY	GLN	ALA	GLN	GLN	VAL	VAL	ILE	ILE	ASP	MET	ASN	ASN	ASP	PRO	THR	SER	ALA	
PRO	ILE	ARG	ASP	PRO	ILE	SER	ALA	ASP	SER	ASN	MET	ILE	ASN	ASN	PRO	VAL	VAL	VAL	VAL	ILE	ALA	GLY	LYS	THR	GLY	GLY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



[illegible]

- Molecule 2: Clathrin light chain

[illegible]

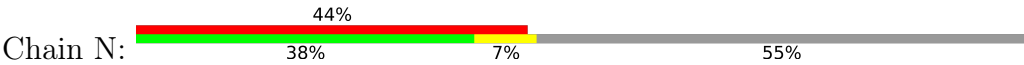
- Molecule 2: Clathrin light chain

[illegible]

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	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	K210	D211	V212	S213	R214	L215	R216	S217	V218	L219	M220	S221	L222	K223	Q224	T225	PRO	LEU	SER	ARG
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• Molecule 2: Clathrin light chain



MET	ALA	ASP	GLY	PHE	GLY	PHE	SER	SER	THR	GLU	SER	GLY	ALA	GLU	VAL	GLU	ALA	GLU	ASP	PRO	ALA	ALA	ALA	PHE	LEU	ALA	GLN	GLN	GLU	SER	GLU	ASP	ILE	ALA	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
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SER	GLY	ALA	GLY	PRO	GLU	ASP	MET	THR	VAL	ASN	GLY	VAL	PHE	GLN	ASP	ALA	GLY	TYR	ALA	ILE	ALA	GLN	ALA	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	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	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	0.22	0/3240	0.45	0/4375
1	B	0.20	0/5513	0.43	0/7468
1	C	0.23	0/3667	0.48	1/4970 (0.0%)
1	F	0.22	0/3240	0.45	0/4375
1	G	0.21	0/5513	0.43	0/7468
1	H	0.23	0/3667	0.48	1/4970 (0.0%)
1	K	0.22	0/3240	0.45	0/4375
1	L	0.21	0/5513	0.43	0/7468
1	M	0.23	0/3667	0.48	1/4970 (0.0%)
2	D	0.20	0/887	0.40	0/1183
2	E	0.21	0/520	0.45	0/692
2	I	0.20	0/887	0.40	0/1183
2	J	0.21	0/520	0.45	0/692
2	N	0.20	0/887	0.40	0/1183
2	O	0.21	0/520	0.45	0/692
All	All	0.21	0/41481	0.45	3/56064 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	769	THR	CB-CA-C	5.30	120.97	110.42
1	C	769	THR	CB-CA-C	5.29	120.94	110.42
1	M	769	THR	CB-CA-C	5.27	120.91	110.42

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	37	0
1	B	5405	0	5359	64	0
1	C	3598	0	3592	58	0
1	F	3168	0	3118	34	0
1	G	5405	0	5359	68	0
1	H	3598	0	3592	55	0
1	K	3168	0	3118	36	0
1	L	5405	0	5359	66	0
1	M	3598	0	3592	59	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	500	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 500 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%)	24	63
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%)	24	63
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%)	24	63
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%)	49	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%)	342 (100%)	0	100	100
1	B	587/1471 (40%)	586 (100%)	1 (0%)	87	86
1	C	405/1471 (28%)	403 (100%)	2 (0%)	81	82
1	F	342/1471 (23%)	342 (100%)	0	100	100
1	G	587/1471 (40%)	586 (100%)	1 (0%)	87	86
1	H	405/1471 (28%)	403 (100%)	2 (0%)	81	82
1	K	342/1471 (23%)	342 (100%)	0	100	100
1	L	587/1471 (40%)	586 (100%)	1 (0%)	87	86
1	M	405/1471 (28%)	403 (100%)	2 (0%)	81	82
2	D	96/184 (52%)	95 (99%)	1 (1%)	68	76
2	E	55/184 (30%)	55 (100%)	0	100	100
2	I	96/184 (52%)	95 (99%)	1 (1%)	68	76
2	J	55/184 (30%)	55 (100%)	0	100	100
2	N	96/184 (52%)	95 (99%)	1 (1%)	68	76
2	O	55/184 (30%)	55 (100%)	0	100	100
All	All	4455/14343 (31%)	4443 (100%)	12 (0%)	84	84

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	772	LEU
1	M	767	LYS
2	N	205	SER
1	M	772	LEU
2	D	205	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	973	GLN
1	H	876	HIS
1	H	761	ASN
1	H	1049	ASN
1	C	876	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

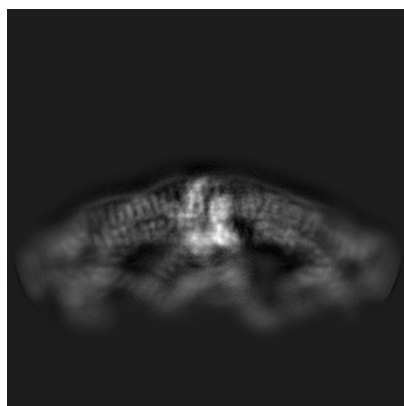
6 Map visualisation [i](#)

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

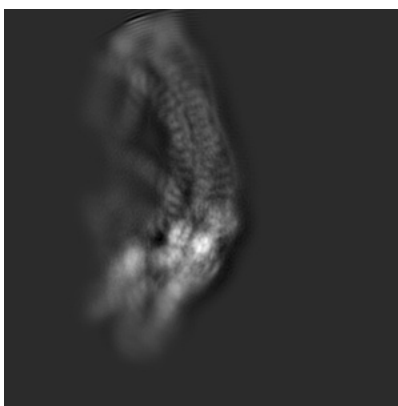
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

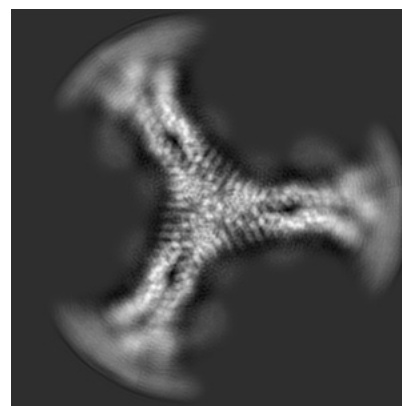
6.1.1 Primary map



X

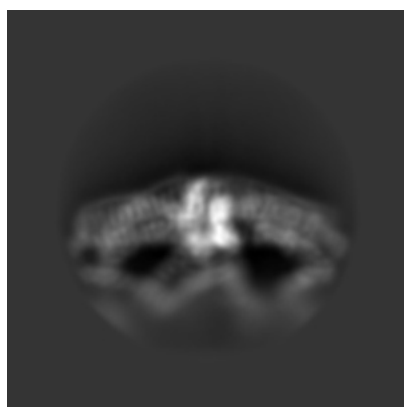


Y

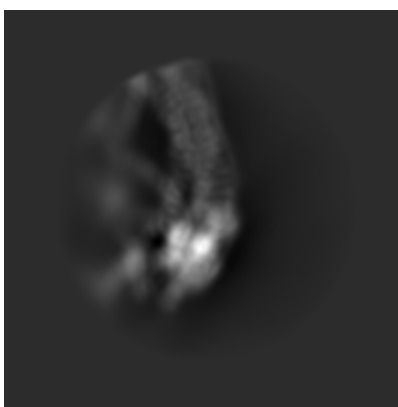


Z

6.1.2 Raw map



X



Y

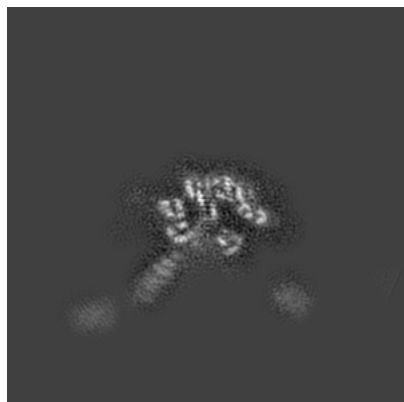


Z

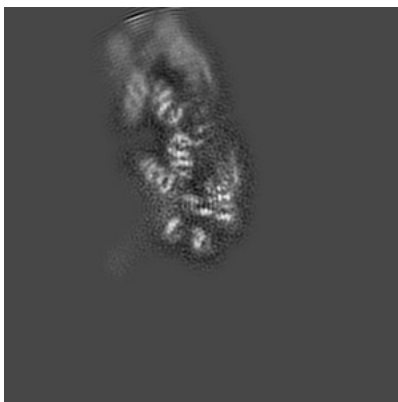
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

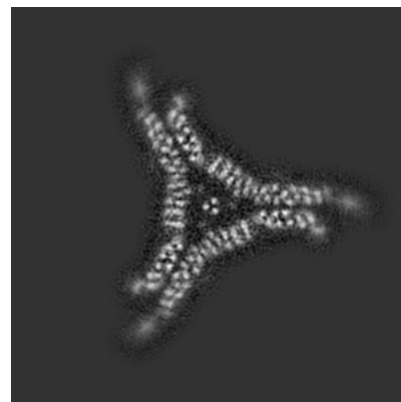
6.2.1 Primary map



X Index: 128

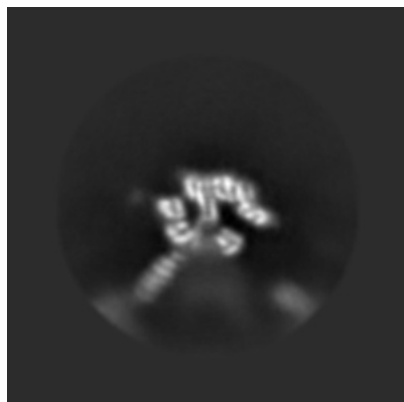


Y Index: 128

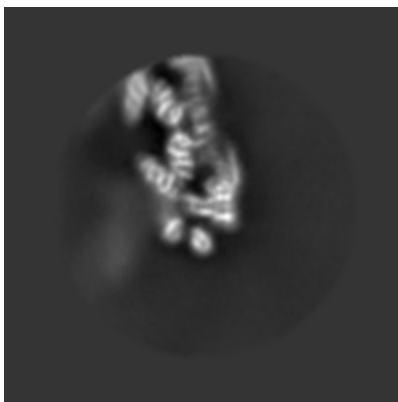


Z Index: 128

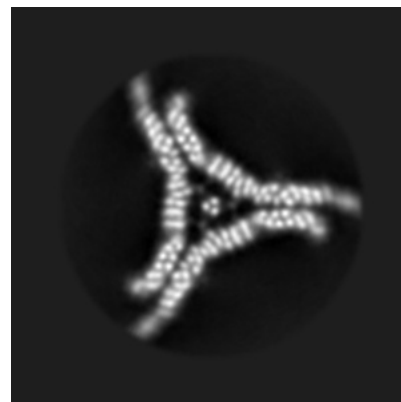
6.2.2 Raw map



X Index: 128



Y Index: 128

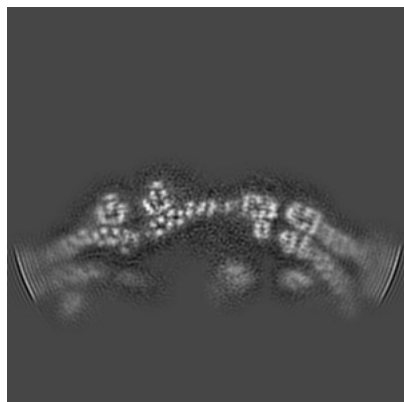


Z Index: 128

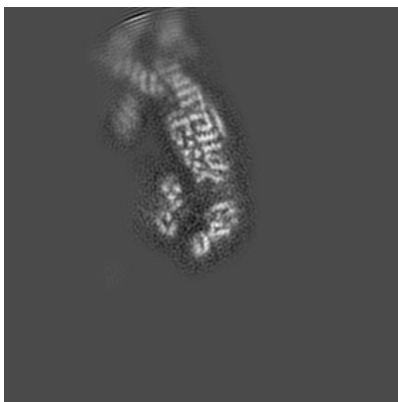
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

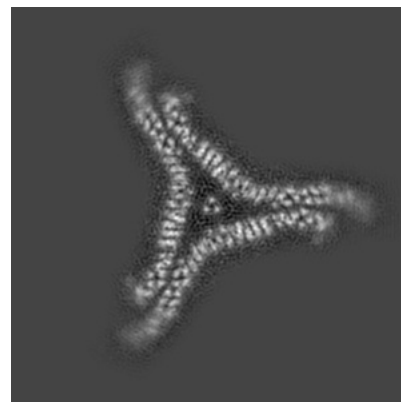
6.3.1 Primary map



X Index: 101



Y Index: 117



Z Index: 124

6.3.2 Raw map



X Index: 100



Y Index: 120



Z Index: 124

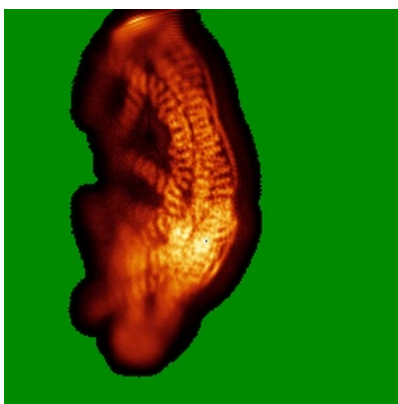
The images above show the largest variance slices of the map in three orthogonal directions.

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

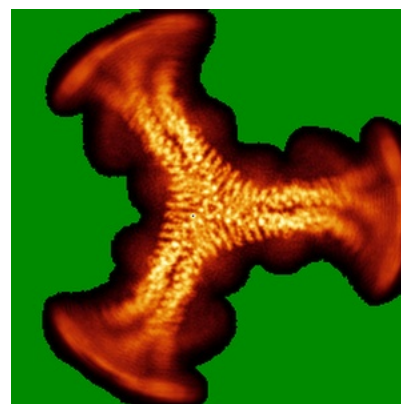
6.4.1 Primary map



X



Y

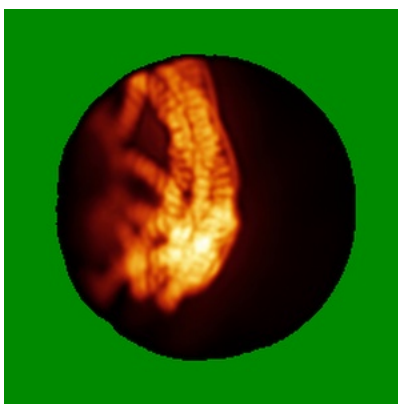


Z

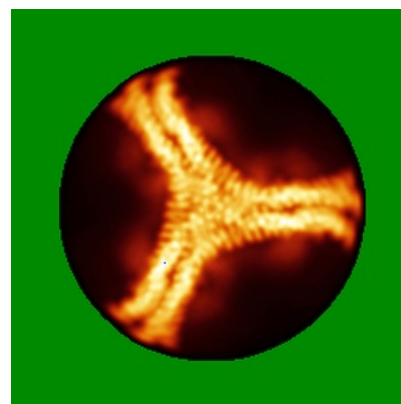
6.4.2 Raw map



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.

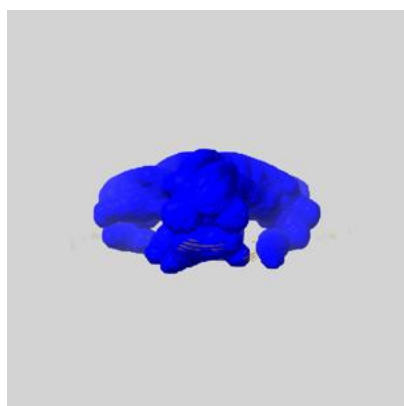
6.6 Mask visualisation [i](#)

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

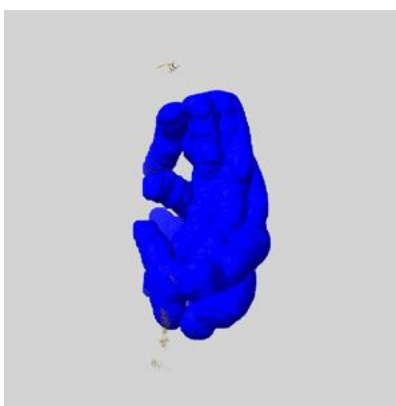
A mask typically either:

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

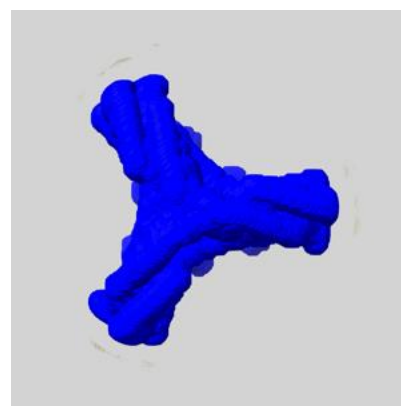
6.6.1 emd_0126_msk_1.map [i](#)



X



Y

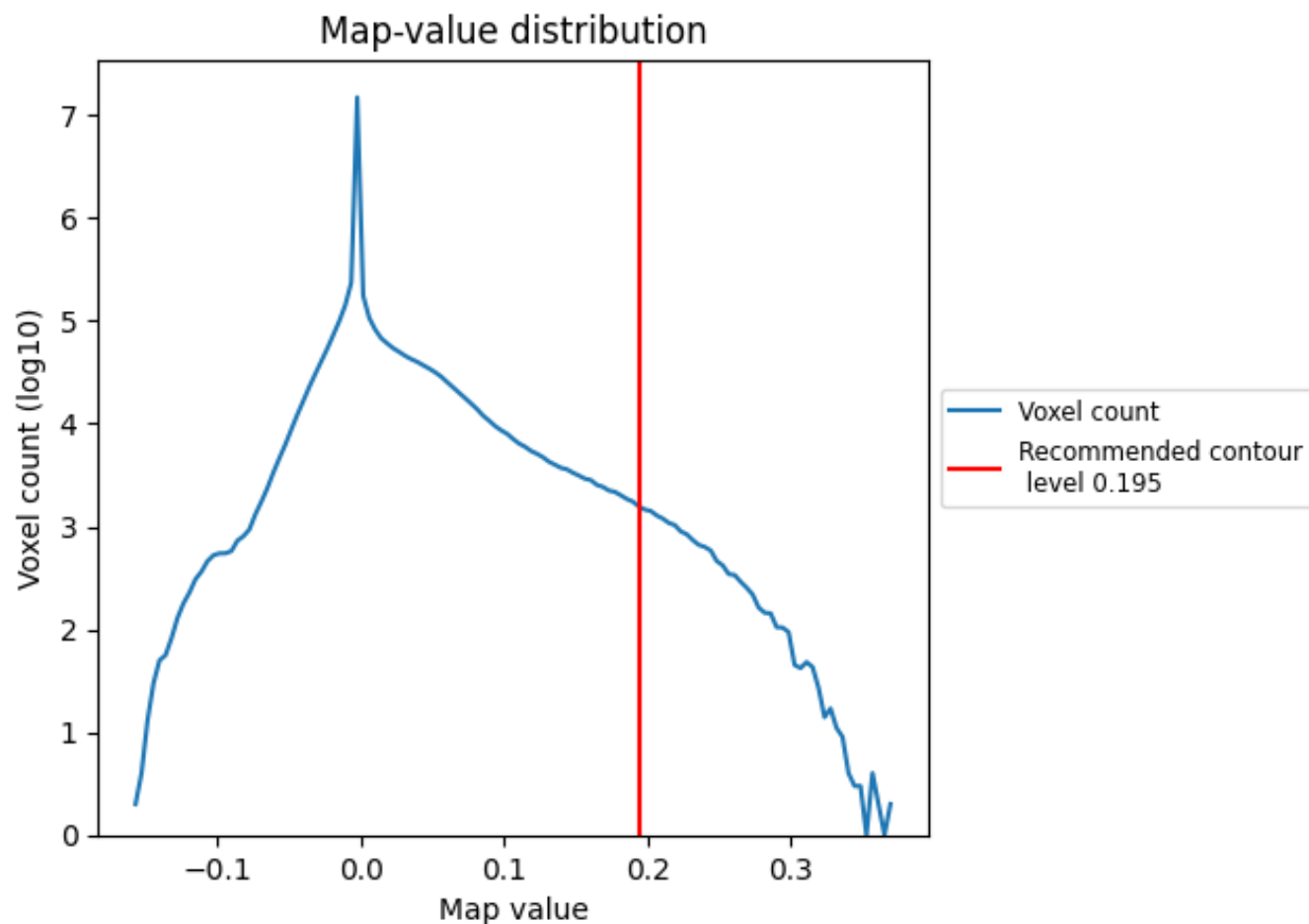


Z

7 Map analysis [i](#)

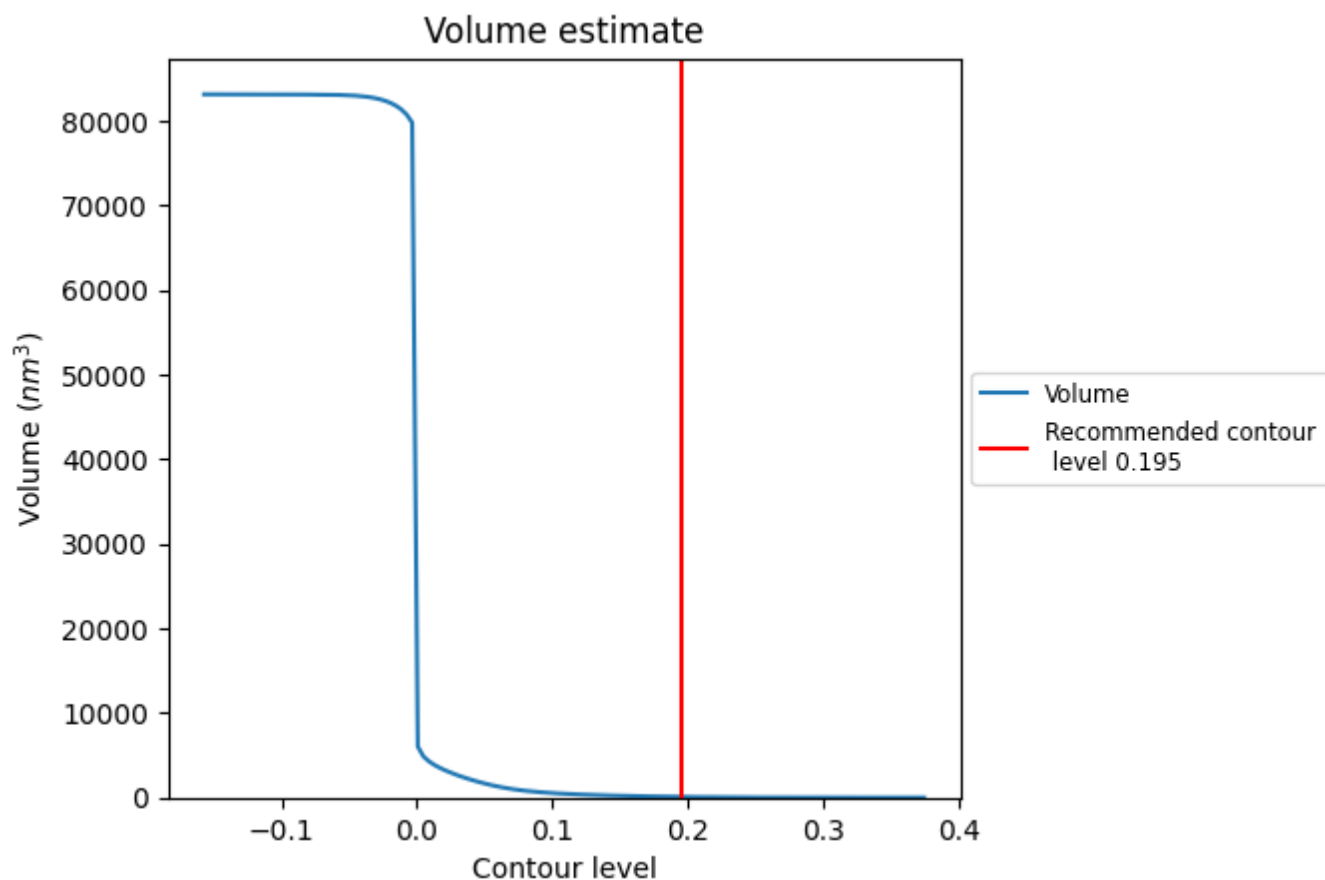
This section contains the results of statistical analysis of the map.

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.

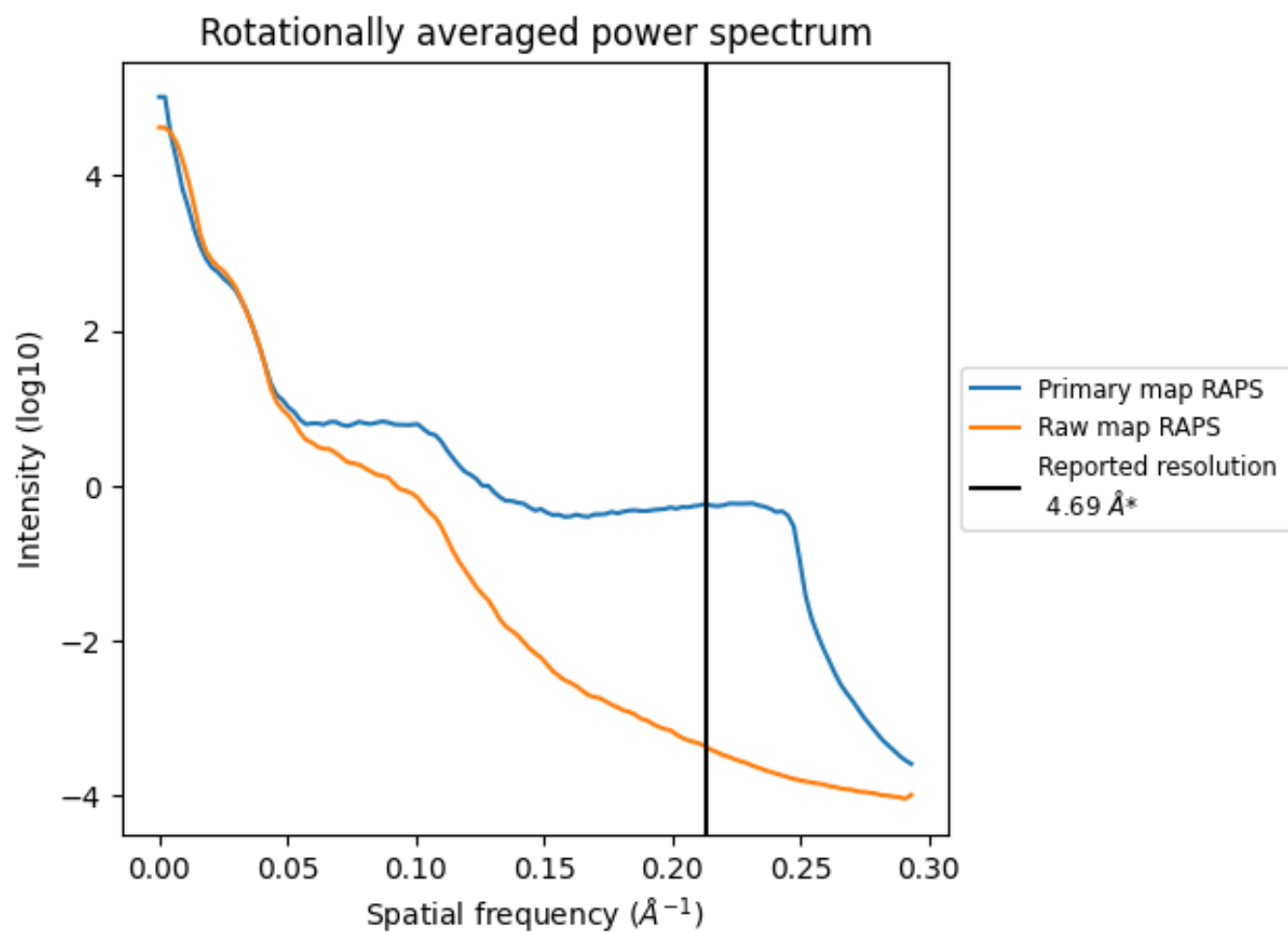
7.2 Volume estimate [i](#)



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 ⓘ

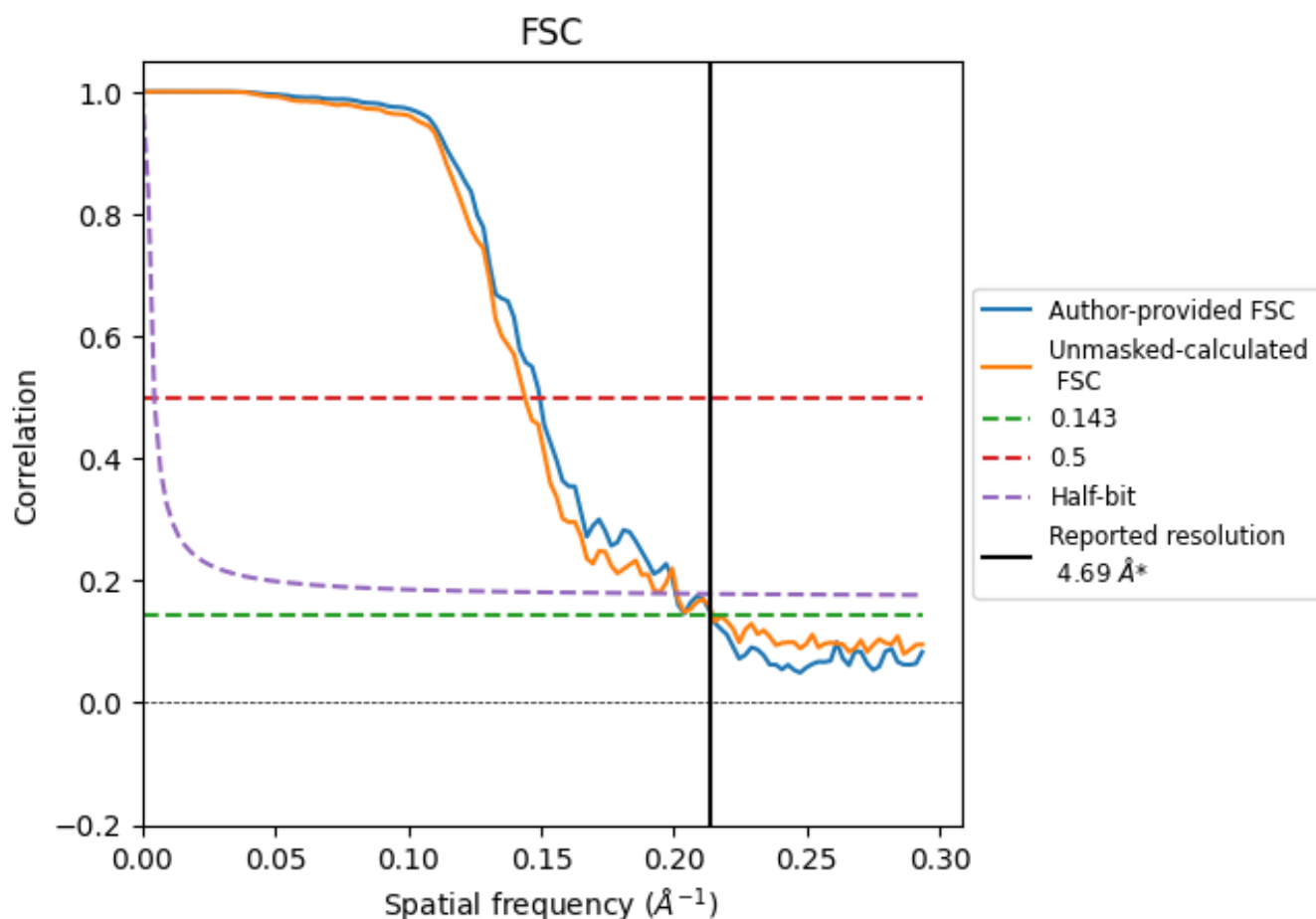


*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

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

8.2 Resolution estimates [i](#)

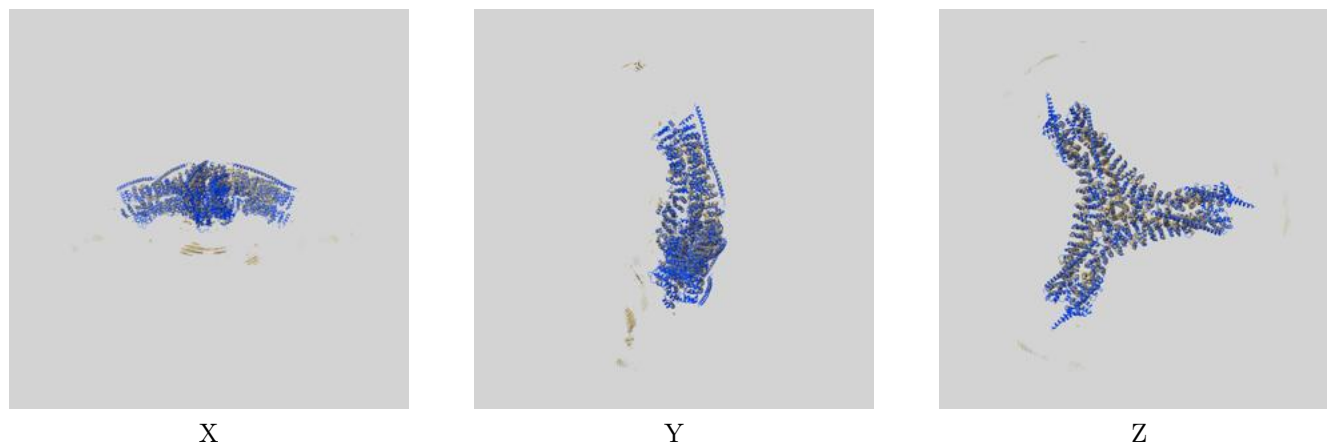
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.69	-	-
Author-provided FSC curve	4.67	6.69	4.98
Unmasked-calculated*	4.66	6.95	4.97

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

9 Map-model fit [i](#)

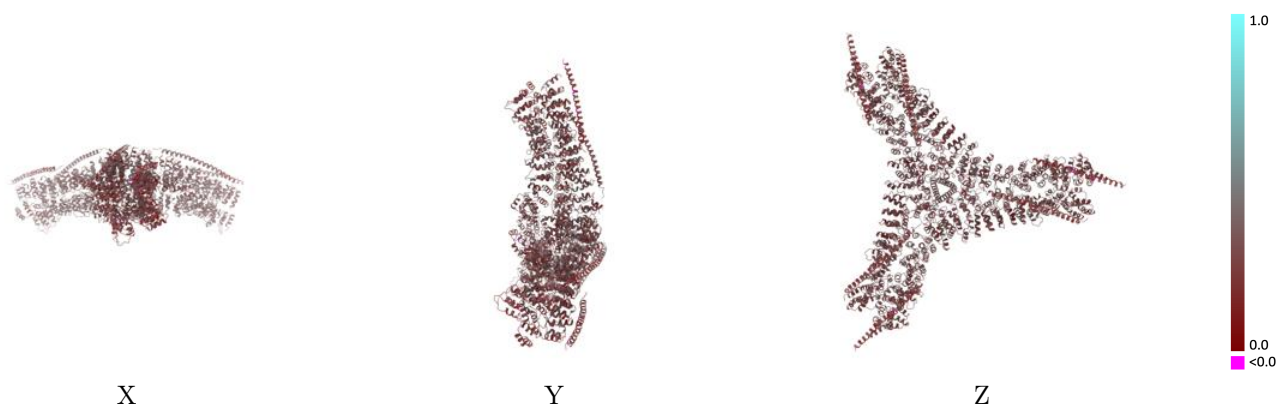
This section contains information regarding the fit between EMDB map EMD-0126 and PDB model 6SCT. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



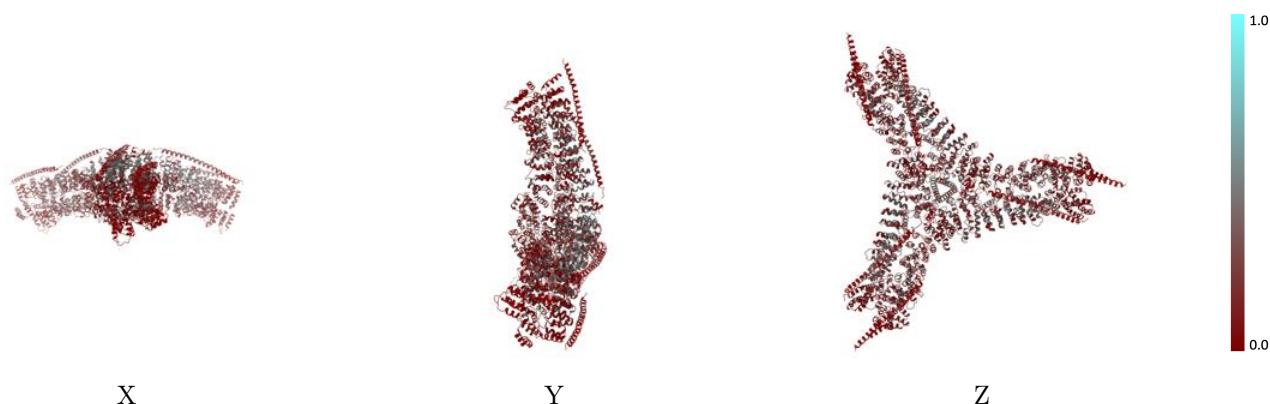
The images above show the 3D surface view of the map at the recommended contour level 0.195 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



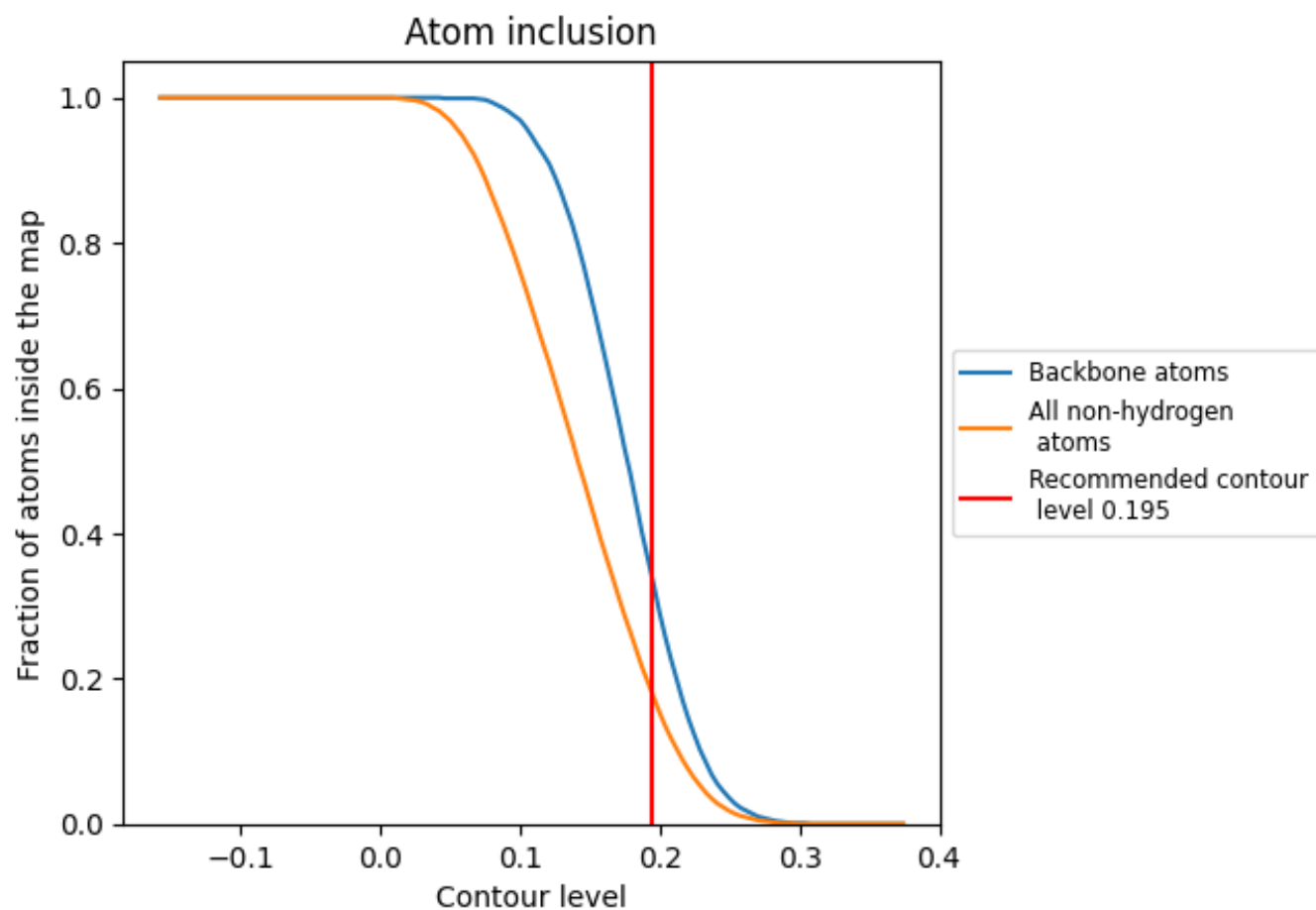
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	0.1780	0.2970
A	0.2840	0.3140
B	0.1680	0.2980
C	0.1370	0.2890
D	0.1160	0.2920
E	0.0220	0.2180
F	0.2860	0.3160
G	0.1690	0.2990
H	0.1360	0.2910
I	0.1150	0.2890
J	0.0260	0.2210
K	0.2860	0.3170
L	0.1680	0.2980
M	0.1390	0.2890
N	0.1100	0.2910
O	0.0340	0.2180

1.0

0.0

<0.0