



Full wwPDB EM Validation Report ⓘ

May 12, 2025 – 02:00 PM JST

PDB ID : 9KJC / pdb_00009kjc
EMDB ID : EMD-62366
Title : Cryo-EM structure of BL-bound atABCB19 in lipid nanodisc
Authors : Liu, Y.; Liao, M.
Deposited on : 2024-11-12
Resolution : 3.60 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev118
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

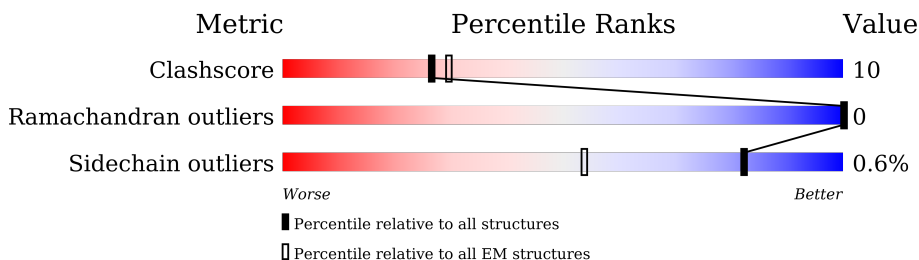
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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	1252	<div> <div>27%</div> <div>74%</div> <div>19%</div> <div>• 7%</div> </div>

2 Entry composition [i](#)

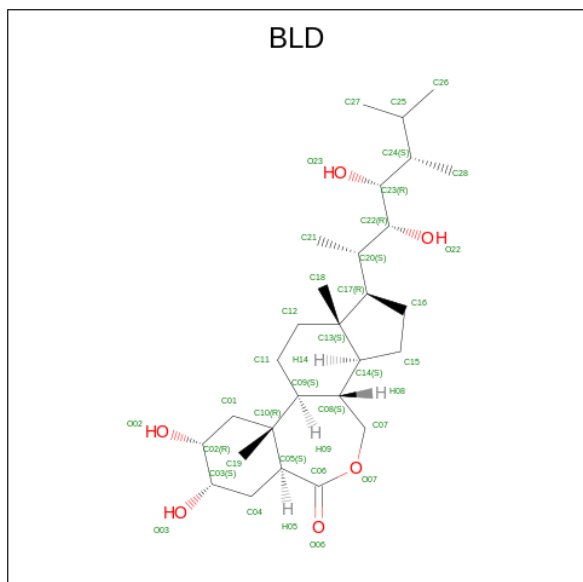
There are 2 unique types of molecules in this entry. The entry contains 9015 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ABC transporter B family member 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1168	8981	5761	1521	1662	37	0	0

- Molecule 2 is Brassinolide (CCD ID: BLD) (formula: $C_{28}H_{48}O_6$) (labeled as "Ligand of Interest" by depositor).

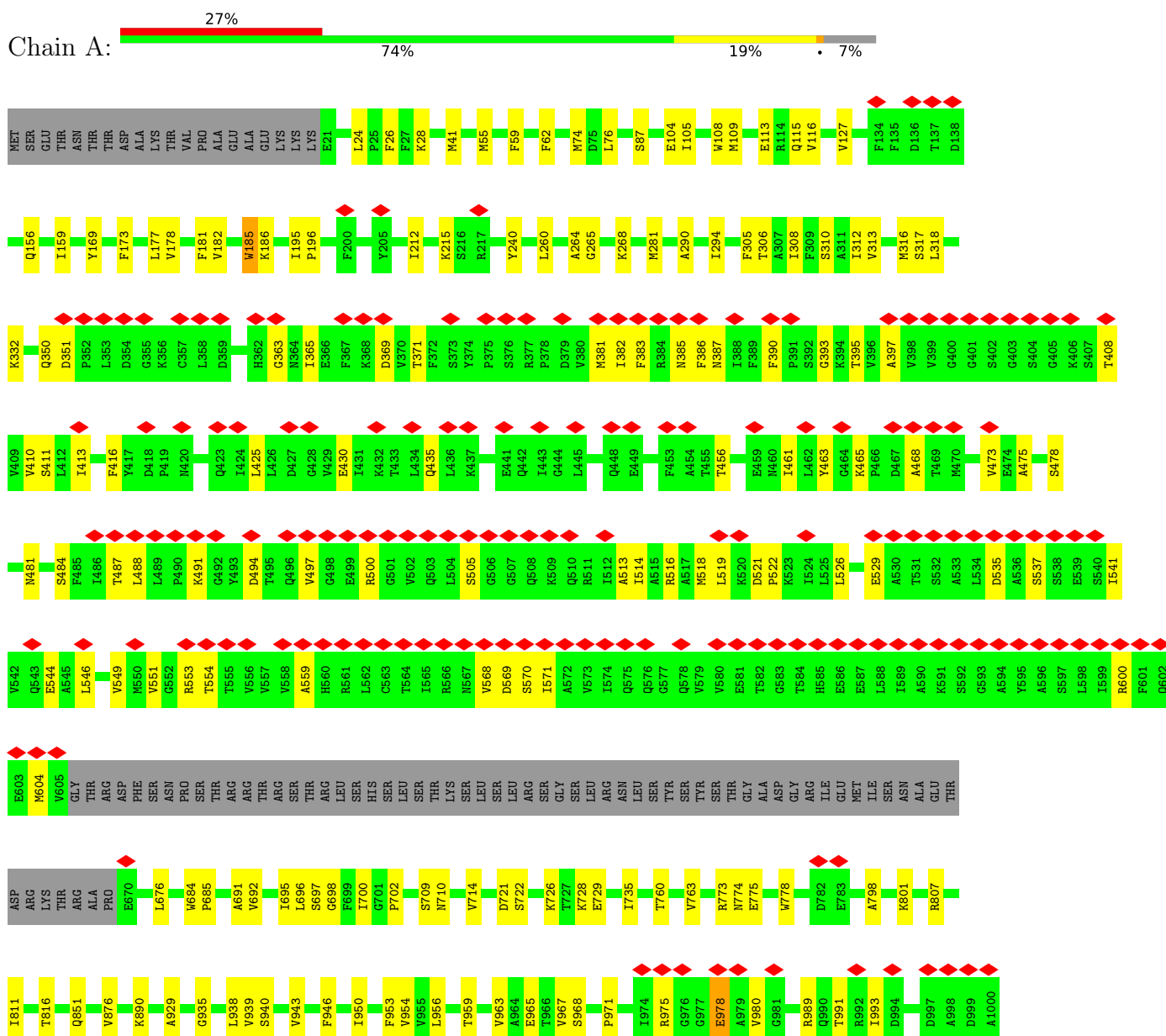


Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
2	A	1	34	28	6	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: ABC transporter B family member 19



S1208	T1209	I1210	R1211	G1212	V1213	D1214	G1215	I1216	G1217	V1218	I1219	Q1220	D1221	G1222	R1223	I1224	V1225	E1226	Q1227	G1228	S1229	H1230	S1231	E1232	V1234	S1235	R1236	P1237	E1238	G1239	A1240	Y1241	S1242	R1243	L1244	L1245	Q1246	L1247	Q1248	T1249	H1250	R1251	I1252																
P1141	V1142	G1143	E1144	R1145	G1146	V1147	Q1148	L1149	S1150	G1151	G1152	Q1153	K1154	Q1155	R1156	I1157	A1158	I1159	K1165	V1169	L1170	L1171	L1172	D1173	E1174	A1175	T1176	S1177	A1178	L1179	D1180	A1181	E1182	S1183	V1186	L1187	Q1188	E1189	A1190	L1191	E1192	R1193	L1194	M1195	R1196	G1197	R1198	T1199	T1200	V1201	V1202	V1203	A1204	H1205	R1206	L1207			
P1064	L1065	A1066	G1067	K1068	V1069	M1070	I1071	D1072	G1073	K1074	D1075	I1076	R1077	R1078	L1079		A1086	K1087	I1088		Q1083	E1094		L1097	F1098	A1099	A1100	T1101	I1102	F1103	D1104	N1105		K1110	D1111	G1112	A1113	T1114	E1115		I1119		A1124	A1125	N1126	A1127	H1128	G1129	F1130	I1131	S1132	G1133	L1134	P1135	E1136	G1137	Y1138	K1139	T1140
D1001	P1002	V1003	E1004	T1005	I1006	R1007	G1008	D1009	I1010	E1011	F1012	R1013	H1014	V1015	D1016	F1017	A1018	V1019	P1020	S1021	R1022	P1023	D1024	V1025	M1026	V1027	F1028	R1029	D1030	F1031	N1032	L1033	R1034	I1035	R1036	A1037	G1038	H1039	S1040	Q1041	A1042	L1043	V1044	G1045	A1046	S1047	G1048	S1049	G1050	K1051	S1052		I1055	A1056	M1057		R1060		N1063

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	191000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.610	Depositor
Minimum map value	-1.711	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.053	Depositor
Recommended contour level	0.28	Depositor
Map size (Å)	239.40001, 239.40001, 239.40001	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.855, 0.855, 0.855	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.19	0/9150	0.40	0/12381

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	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1243	ARG	Sidechain
1	A	1251	ARG	Sidechain
1	A	185	TRP	Peptide
1	A	978	GLU	Peptide

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	8981	0	9076	177	0
2	A	34	0	48	7	0
All	All	9015	0	9124	177	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 10.

All (177) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:PHE:CZ	2:A:1301:BLD:H126	1.38	1.51
1:A:1249:THR:HA	1:A:1252:ILE:CD1	1.61	1.29
1:A:305:PHE:HZ	2:A:1301:BLD:C26	1.54	1.21
1:A:305:PHE:CZ	2:A:1301:BLD:C26	2.25	1.20
1:A:1249:THR:HA	1:A:1252:ILE:HD11	1.09	1.03
1:A:1249:THR:O	1:A:1252:ILE:HD12	1.60	1.00
1:A:1249:THR:CA	1:A:1252:ILE:HD11	1.97	0.94
1:A:1249:THR:CA	1:A:1252:ILE:CD1	2.47	0.92
1:A:1249:THR:HA	1:A:1252:ILE:HD12	1.58	0.84
1:A:1248:GLN:O	1:A:1252:ILE:HG13	1.80	0.81
1:A:281:MET:HE1	1:A:735:ILE:HG12	1.65	0.78
1:A:676:LEU:HD11	1:A:980:VAL:HG21	1.66	0.75
1:A:1207:LEU:HD12	1:A:1210:ILE:HD11	1.70	0.74
1:A:1249:THR:C	1:A:1252:ILE:HD12	2.15	0.71
1:A:410:VAL:HG12	1:A:526:LEU:HD12	1.71	0.71
1:A:1249:THR:CA	1:A:1252:ILE:HD12	2.17	0.71
1:A:312:ILE:HG22	1:A:316:MET:HE1	1.72	0.70
1:A:1152:GLY:O	1:A:1155:GLN:NE2	2.25	0.68
1:A:350:GLN:HG2	1:A:435:GLN:HB2	1.78	0.66
1:A:522:PRO:O	1:A:553:ARG:NH1	2.29	0.66
1:A:684:TRP:CD1	1:A:685:PRO:HD3	2.31	0.65
1:A:305:PHE:CE1	2:A:1301:BLD:C26	2.81	0.63
1:A:461:ILE:HG21	1:A:473:VAL:HG13	1.80	0.63
1:A:195:ILE:HG13	1:A:196:PRO:HD3	1.81	0.62
1:A:1172:LEU:HD12	1:A:1202:VAL:HG22	1.79	0.62
1:A:697:SER:HA	1:A:700:ILE:HD12	1.80	0.62
1:A:305:PHE:HZ	2:A:1301:BLD:H126	0.64	0.61
1:A:240:TYR:HD1	1:A:1165:LYS:HZ3	1.46	0.61
1:A:978:GLU:O	1:A:980:VAL:N	2.34	0.61
1:A:1060:ARG:NH2	1:A:1063:ASP:OD1	2.32	0.61
1:A:1127:ALA:HB2	1:A:1156:ARG:HD3	1.82	0.60
1:A:1141:PRO:HB2	1:A:1146:GLY:HA3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:365:ILE:HB	1:A:390:PHE:HB2	1.82	0.60
1:A:481:ASN:ND2	1:A:544:GLU:OE2	2.34	0.60
1:A:393:GLY:H	1:A:554:THR:HG22	1.67	0.59
1:A:395:THR:OG1	1:A:569:ASP:OD1	2.21	0.59
1:A:413:ILE:HG21	1:A:526:LEU:HD11	1.85	0.59
1:A:281:MET:HE3	1:A:281:MET:HA	1.84	0.58
1:A:774:ASN:HA	1:A:991:THR:HG21	1.86	0.58
1:A:1068:LYS:HG2	1:A:1077:ARG:HH21	1.68	0.57
1:A:1170:LEU:HD12	1:A:1171:LEU:H	1.69	0.57
1:A:491:LYS:HE2	1:A:494:ASP:HB3	1.87	0.57
1:A:1009:ASP:HB3	1:A:1072:ASP:H	1.70	0.56
1:A:1245:LEU:O	1:A:1249:THR:HG23	2.05	0.56
1:A:465:LYS:HE3	1:A:519:LEU:HD21	1.88	0.56
1:A:938:LEU:HD23	1:A:943:VAL:HG23	1.88	0.55
1:A:116:VAL:HG21	1:A:156:GLN:HB2	1.88	0.55
1:A:760:THR:HA	1:A:763:VAL:HG12	1.87	0.55
1:A:500:ARG:NH1	1:A:505:SER:OG	2.40	0.55
1:A:691:ALA:O	1:A:695:ILE:HD12	2.07	0.55
1:A:371:THR:HG22	1:A:385:ASN:H	1.72	0.54
1:A:381:MET:HA	1:A:381:MET:HE3	1.89	0.54
1:A:26:PHE:HB2	1:A:332:LYS:HD3	1.89	0.53
1:A:397:ALA:HB3	1:A:571:ILE:HG23	1.91	0.53
1:A:692:VAL:O	1:A:696:LEU:HG	2.10	0.52
1:A:1011:GLU:HG3	1:A:1034:ARG:HG3	1.92	0.52
1:A:1159:ILE:HG23	1:A:1194:LEU:HD11	1.91	0.52
1:A:369:ASP:N	1:A:387:ASN:OD1	2.37	0.51
1:A:546:LEU:O	1:A:549:VAL:HG12	2.10	0.51
1:A:1017:PHE:HB3	1:A:1028:PHE:HD2	1.76	0.51
1:A:1060:ARG:HG2	1:A:1060:ARG:HH11	1.76	0.50
1:A:993:ILE:HG23	1:A:1060:ARG:HE	1.77	0.50
1:A:41:MET:HE1	1:A:115:GLN:NE2	2.27	0.50
1:A:127:VAL:HG11	1:A:876:VAL:HG22	1.94	0.50
1:A:465:LYS:HD3	1:A:468:ALA:N	2.26	0.50
1:A:529:GLU:HG3	1:A:559:ALA:HA	1.93	0.49
1:A:956:LEU:HA	1:A:959:THR:HG22	1.95	0.49
1:A:104:GLU:HG3	1:A:105:ILE:N	2.27	0.49
1:A:351:ASP:N	1:A:351:ASP:OD1	2.44	0.49
1:A:55:MET:HE3	1:A:59:PHE:CE2	2.49	0.48
1:A:851:GLN:HE22	1:A:965:GLU:HG3	1.77	0.48
1:A:1029:ARG:HH12	1:A:1223:ARG:HD2	1.78	0.48
1:A:290:ALA:O	1:A:294:ILE:HD12	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:395:THR:O	1:A:570:SER:OG	2.30	0.48
1:A:946:PHE:CE1	1:A:950:ILE:HG13	2.48	0.48
1:A:1012:PHE:HB2	1:A:1033:LEU:H	1.78	0.48
1:A:726:LYS:HA	1:A:729:GLU:OE1	2.14	0.48
1:A:1015:VAL:HG13	1:A:1064:PRO:HB3	1.96	0.48
1:A:1174:GLU:O	1:A:1204:ALA:HA	2.13	0.48
1:A:465:LYS:HD3	1:A:468:ALA:H	1.79	0.48
1:A:1102:ILE:HD11	1:A:1142:VAL:HG11	1.96	0.47
1:A:798:ALA:O	1:A:801:LYS:HG3	2.14	0.47
1:A:305:PHE:CE1	2:A:1301:BLD:H326	2.49	0.47
1:A:568:VAL:HG12	1:A:570:SER:H	1.78	0.47
1:A:721:ASP:N	1:A:721:ASP:OD1	2.46	0.47
1:A:1110:LYS:HD2	1:A:1111:ASP:N	2.29	0.47
1:A:62:PHE:CE2	2:A:1301:BLD:H226	2.49	0.47
1:A:41:MET:HG2	1:A:108:TRP:CH2	2.50	0.47
1:A:475:ALA:O	1:A:478:SER:OG	2.28	0.47
1:A:521:ASP:OD1	1:A:553:ARG:NH2	2.47	0.47
1:A:1093:GLN:HE22	1:A:1175:ALA:H	1.61	0.47
1:A:1242:SER:O	1:A:1243:ARG:C	2.56	0.47
1:A:980:VAL:HG13	1:A:980:VAL:O	2.15	0.47
1:A:1153:GLN:HA	1:A:1156:ARG:HD2	1.96	0.47
1:A:1248:GLN:O	1:A:1252:ILE:CG1	2.58	0.46
1:A:1007:ARG:HH12	1:A:1009:ASP:HB2	1.80	0.46
1:A:109:MET:HE3	1:A:109:MET:HB2	1.82	0.46
1:A:215:LYS:HB3	1:A:260:LEU:HD21	1.96	0.46
1:A:484:SER:O	1:A:487:THR:OG1	2.29	0.46
1:A:185:TRP:HD1	1:A:186:LYS:H	1.64	0.46
1:A:1170:LEU:HD12	1:A:1171:LEU:N	2.30	0.46
1:A:169:TYR:O	1:A:317:SER:HB3	2.16	0.46
1:A:1244:LEU:HD13	1:A:1244:LEU:HA	1.76	0.46
1:A:383:PHE:HB3	1:A:386:PHE:HB2	1.97	0.45
1:A:1016:ASP:OD1	1:A:1016:ASP:N	2.49	0.45
1:A:212:ILE:HD12	1:A:264:ALA:HB1	1.98	0.45
1:A:773:ARG:HD3	1:A:773:ARG:HA	1.70	0.45
1:A:968:SER:O	1:A:971:PRO:HD2	2.16	0.45
1:A:74:MET:HE3	1:A:74:MET:HA	1.99	0.45
1:A:87:SER:HB2	1:A:929:ALA:HB1	1.97	0.45
1:A:488:LEU:O	1:A:488:LEU:HD23	2.17	0.45
1:A:775:GLU:HG2	1:A:778:TRP:H	1.82	0.45
1:A:62:PHE:HE1	1:A:953:PHE:HE2	1.63	0.45
1:A:698:GLY:O	1:A:702:PRO:HD2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:PHE:CG	1:A:318:LEU:HD21	2.52	0.45
1:A:313:VAL:HA	1:A:316:MET:HE2	1.99	0.45
1:A:807:ARG:O	1:A:811:ILE:HG12	2.17	0.45
1:A:1101:THR:HB	1:A:1139:LYS:HA	1.99	0.45
1:A:156:GLN:HA	1:A:159:ILE:HG22	1.99	0.45
1:A:514:ILE:O	1:A:518:MET:HG2	2.16	0.45
1:A:535:ASP:N	1:A:535:ASP:OD1	2.50	0.45
1:A:178:VAL:O	1:A:182:VAL:HG12	2.17	0.45
1:A:722:SER:O	1:A:726:LYS:HG3	2.17	0.45
1:A:946:PHE:HE1	1:A:950:ILE:HG13	1.82	0.45
1:A:1076:ILE:HG23	1:A:1077:ARG:HG3	1.99	0.45
1:A:1175:ALA:HA	1:A:1205:HIS:HD2	1.80	0.45
1:A:308:ILE:O	1:A:312:ILE:HG13	2.16	0.44
1:A:709:SER:HB2	1:A:954:VAL:HG11	1.99	0.44
1:A:537:SER:O	1:A:541:ILE:HG12	2.17	0.44
1:A:1243:ARG:CZ	1:A:1243:ARG:HA	2.48	0.44
1:A:1124:ALA:HA	1:A:1193:ARG:HH11	1.83	0.44
1:A:306:THR:O	1:A:310:SER:OG	2.31	0.44
1:A:1241:TYR:O	1:A:1244:LEU:HB2	2.18	0.44
1:A:363:GLY:HA3	1:A:554:THR:HG21	1.98	0.44
1:A:600:ARG:O	1:A:604:MET:HE3	2.18	0.44
1:A:1042:ALA:O	1:A:1216:ILE:HG13	2.18	0.44
1:A:971:PRO:O	1:A:975:ARG:N	2.50	0.44
1:A:1251:ARG:O	1:A:1252:ILE:C	2.60	0.43
1:A:28:LYS:HE2	1:A:28:LYS:HB2	1.77	0.43
1:A:177:LEU:O	1:A:181:PHE:HD2	2.02	0.43
1:A:513:ALA:O	1:A:516:ARG:HG2	2.18	0.43
1:A:1126:ASN:O	1:A:1156:ARG:NH1	2.52	0.43
1:A:600:ARG:HG2	1:A:604:MET:HE2	2.00	0.43
1:A:695:ILE:HG23	1:A:816:THR:HG21	2.01	0.43
1:A:696:LEU:O	1:A:700:ILE:HG13	2.18	0.43
1:A:775:GLU:CD	1:A:989:ARG:HH22	2.24	0.43
1:A:1030:ASP:OD2	1:A:1223:ARG:NH1	2.52	0.43
1:A:935:GLY:O	1:A:939:VAL:HG23	2.18	0.42
1:A:1110:LYS:HD2	1:A:1111:ASP:H	1.84	0.42
1:A:1242:SER:HA	1:A:1245:LEU:HG	2.01	0.42
1:A:1252:ILE:HG13	1:A:1252:ILE:H	1.42	0.42
1:A:456:THR:OG1	1:A:494:ASP:HA	2.20	0.42
1:A:425:LEU:HA	1:A:430:GLU:HA	2.01	0.42
1:A:1012:PHE:CD2	1:A:1033:LEU:HB2	2.55	0.42
1:A:411:SER:O	1:A:416:PHE:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:549:VAL:O	1:A:551:VAL:N	2.50	0.42
1:A:1088:ILE:HG12	1:A:1169:VAL:HB	2.02	0.42
1:A:24:LEU:O	1:A:332:LYS:HD2	2.20	0.41
1:A:382:ILE:HG22	1:A:383:PHE:CD1	2.54	0.41
1:A:463:TYR:HE1	1:A:890:LYS:HD2	1.85	0.41
1:A:1097:LEU:HD22	1:A:1105:ASN:HB3	2.01	0.41
1:A:497:VAL:HA	1:A:500:ARG:HH21	1.85	0.41
1:A:383:PHE:CZ	1:A:408:THR:HB	2.54	0.41
1:A:946:PHE:O	1:A:946:PHE:CG	2.74	0.41
1:A:1170:LEU:O	1:A:1200:THR:HA	2.20	0.41
1:A:76:LEU:HD21	1:A:940:SER:HA	2.01	0.41
1:A:993:ILE:HG23	1:A:1060:ARG:HH21	1.86	0.41
1:A:728:LYS:HB2	1:A:728:LYS:HE3	1.71	0.41
1:A:1006:ILE:H	1:A:1087:LYS:HE2	1.86	0.41
1:A:1036:ARG:HD3	1:A:1036:ARG:H	1.84	0.41
1:A:1007:ARG:NH1	1:A:1009:ASP:HB2	2.36	0.41
1:A:963:VAL:O	1:A:967:VAL:HG23	2.21	0.40
1:A:113:GLU:OE2	1:A:156:GLN:NE2	2.54	0.40
1:A:62:PHE:CE1	1:A:953:PHE:HE2	2.38	0.40
1:A:185:TRP:CD1	1:A:186:LYS:H	2.40	0.40
1:A:265:GLY:HA2	1:A:268:LYS:HG2	2.04	0.40
1:A:710:ASN:O	1:A:714:VAL:HG23	2.22	0.40

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	1164/1252 (93%)	1074 (92%)	90 (8%)	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	951/1027 (93%)	945 (99%)	6 (1%)	84	92

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1243	ARG
1	A	1244	LEU
1	A	1245	LEU
1	A	1246	GLN
1	A	1248	GLN
1	A	1252	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	680	ASN
1	A	814	ASN
1	A	850	GLN
1	A	865	HIS
1	A	888	GLN
1	A	921	GLN
1	A	1092	GLN
1	A	1153	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	BLD	A	1301	-	36,37,37	0.43	0	46,59,59	1.35	4 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BLD	A	1301	-	-	7/20/85/85	1/4/4/4

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1301	BLD	O07-C06-O06	5.11	124.70	116.72
2	A	1301	BLD	C12-C11-C09	4.38	120.70	113.11
2	A	1301	BLD	C05-C04-C03	-3.87	106.48	111.90
2	A	1301	BLD	C14-C08-C09	2.04	111.82	109.09

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1301	BLD	C13-C17-C20-C22
2	A	1301	BLD	C16-C17-C20-C22

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Mol	Chain	Res	Type	Atoms
2	A	1301	BLD	C20-C22-C23-C24
2	A	1301	BLD	C13-C17-C20-C21
2	A	1301	BLD	O23-C23-C24-C28
2	A	1301	BLD	C16-C17-C20-C21
2	A	1301	BLD	O22-C22-C23-O23

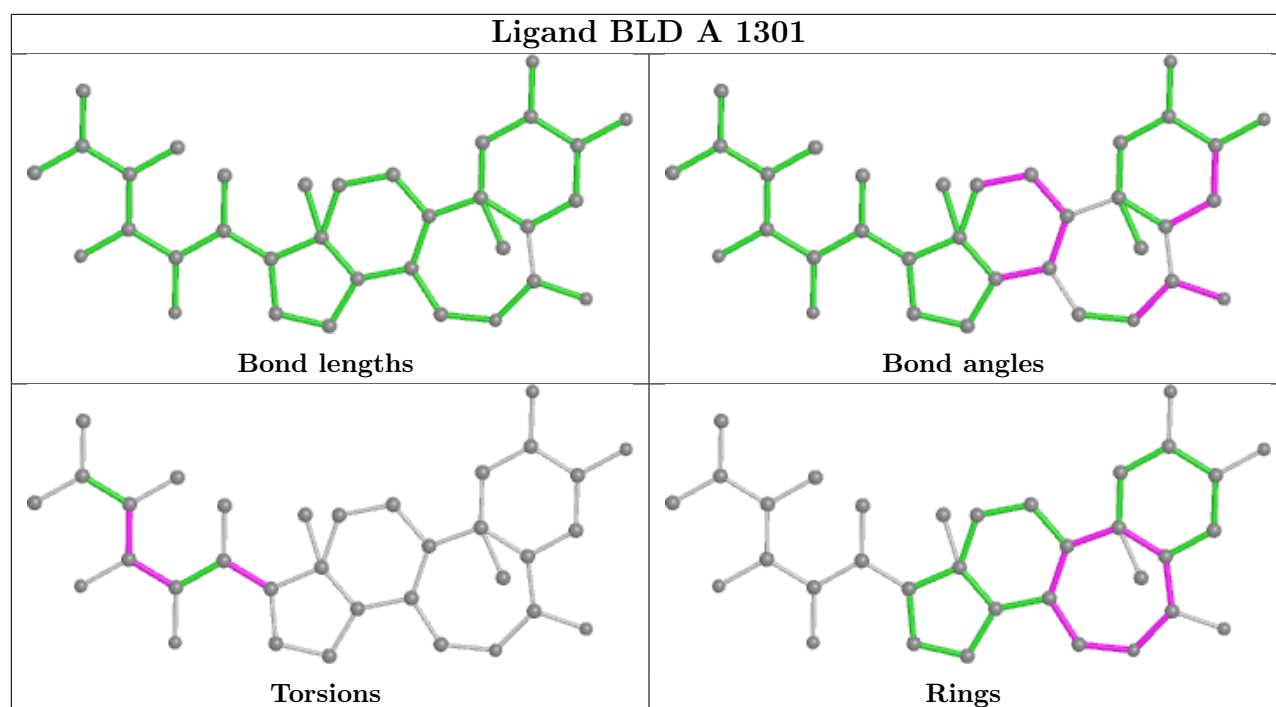
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1301	BLD	C05-C06-C07-C08-C09-C10-O07

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1301	BLD	7	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

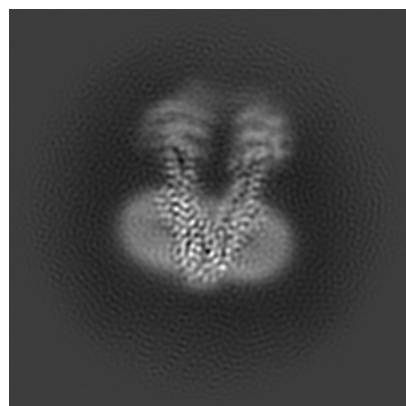
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62366. These allow visual inspection of the internal detail of the map and identification of artifacts.

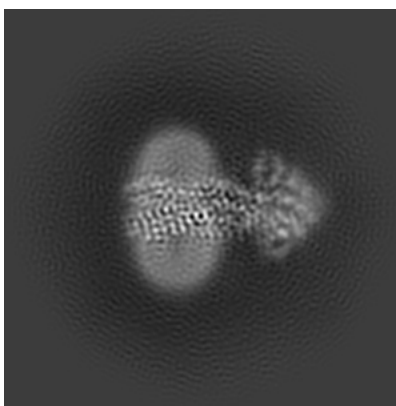
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

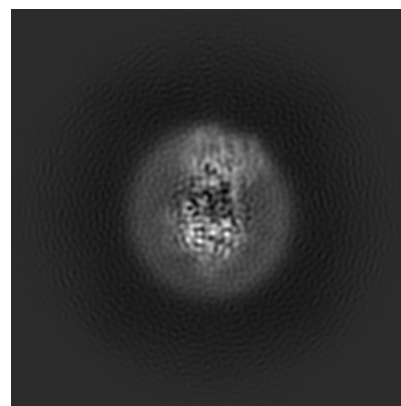
6.1.1 Primary map



X

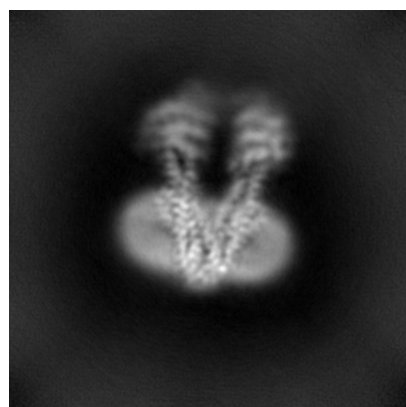


Y

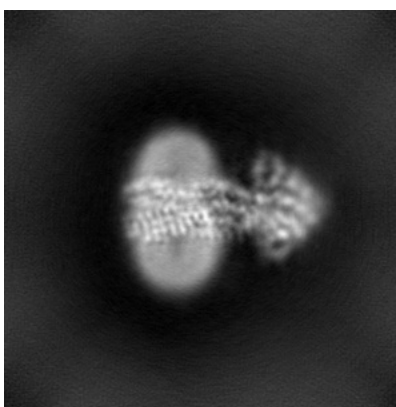


Z

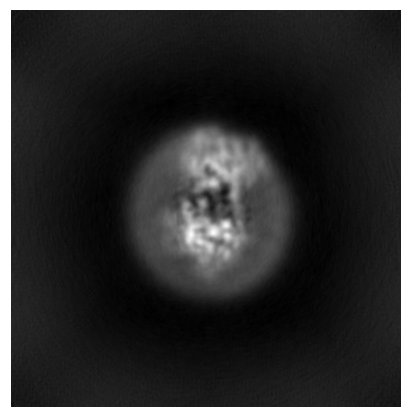
6.1.2 Raw map



X



Y

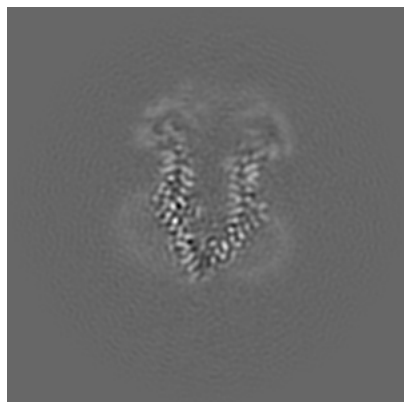


Z

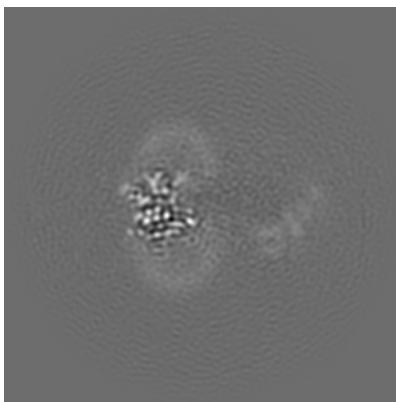
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

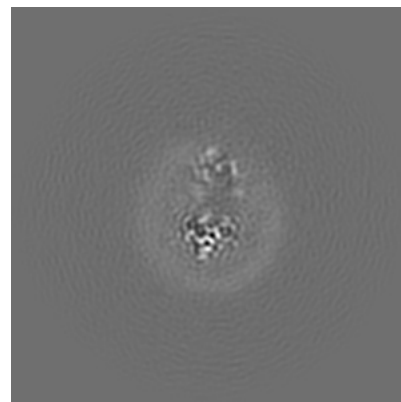
6.2.1 Primary map



X Index: 140

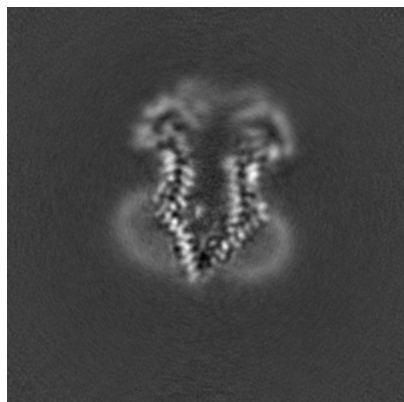


Y Index: 140

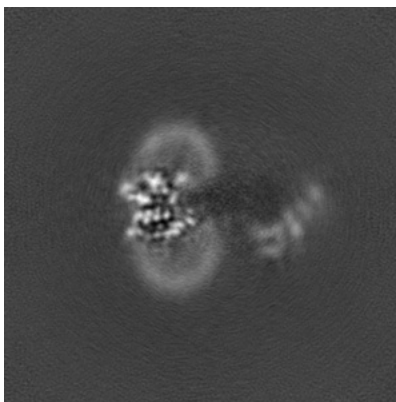


Z Index: 140

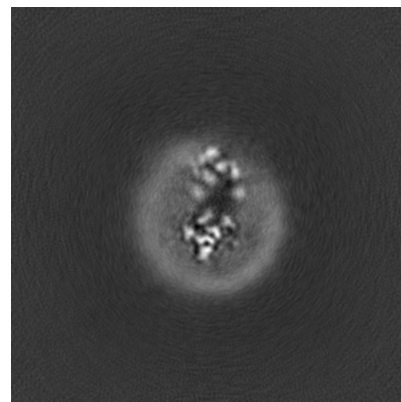
6.2.2 Raw map



X Index: 140



Y Index: 140

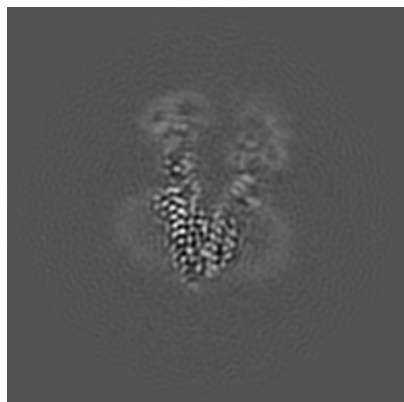


Z Index: 140

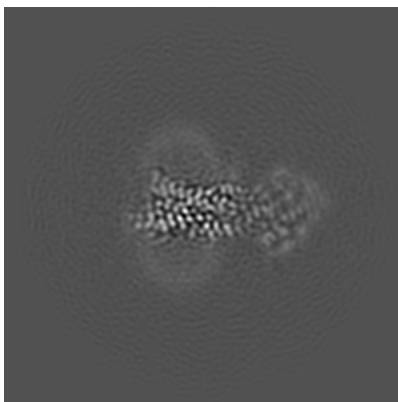
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

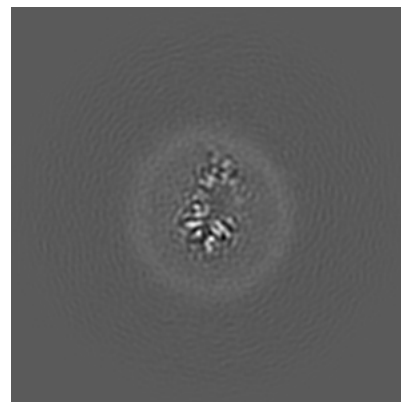
6.3.1 Primary map



X Index: 132

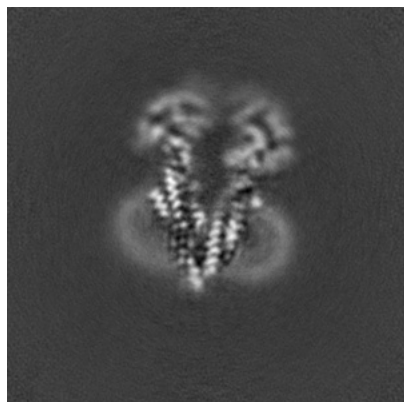


Y Index: 122

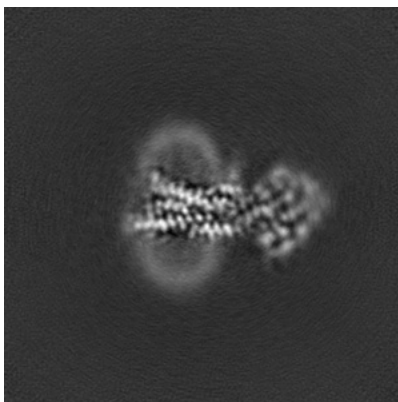


Z Index: 130

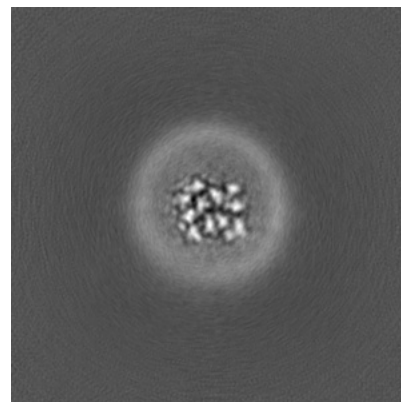
6.3.2 Raw map



X Index: 135



Y Index: 122



Z Index: 106

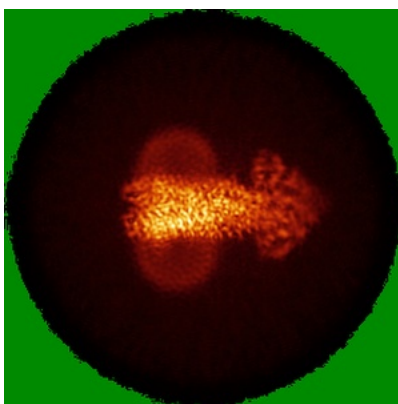
The images above show the largest variance slices of the map in three orthogonal directions.

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

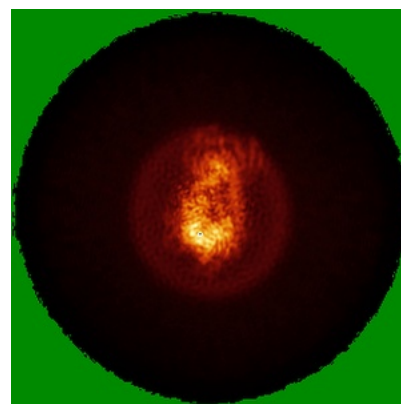
6.4.1 Primary map



X

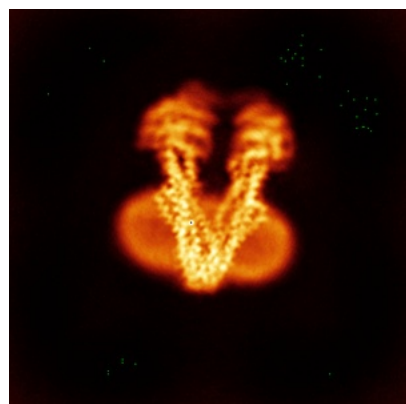


Y

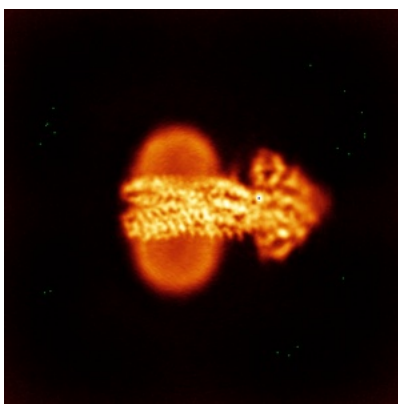


Z

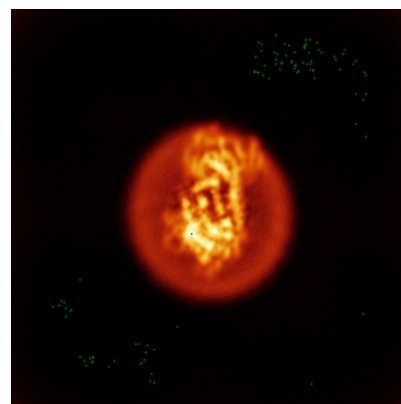
6.4.2 Raw map



X



Y

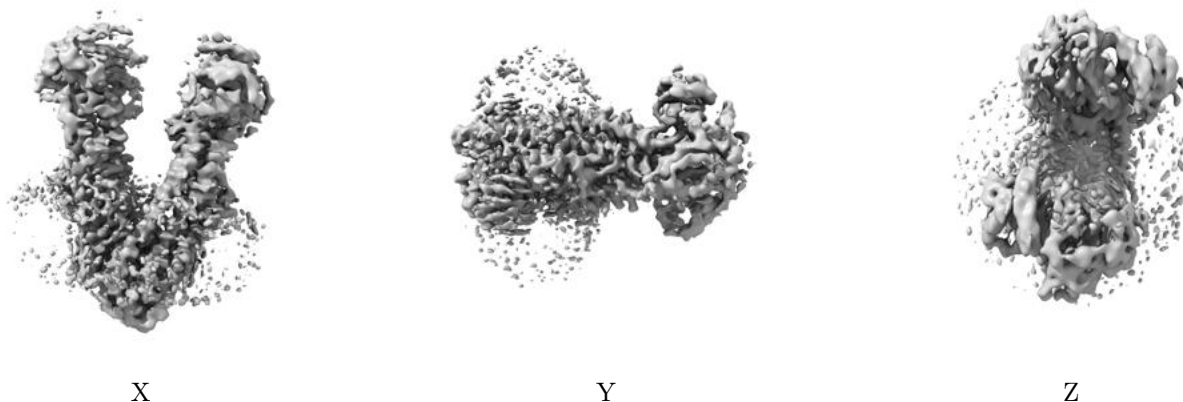


Z

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.

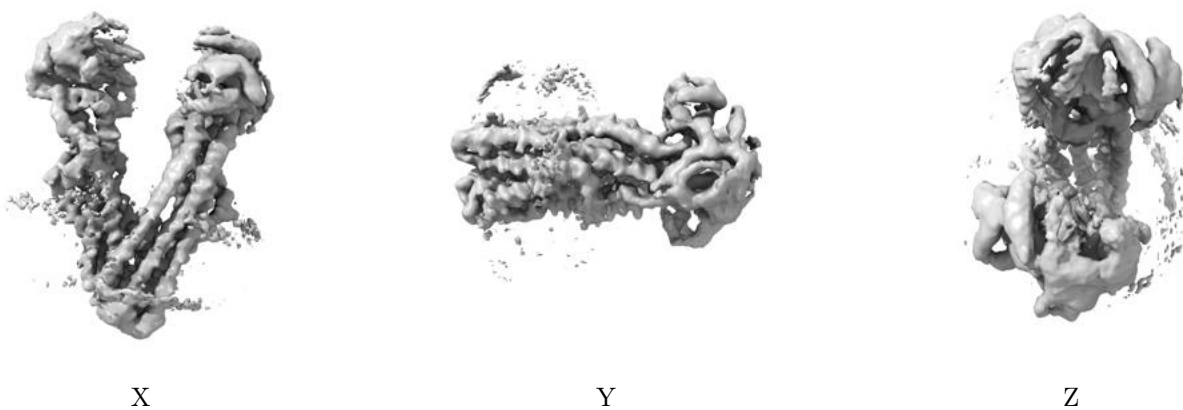
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.28. 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.

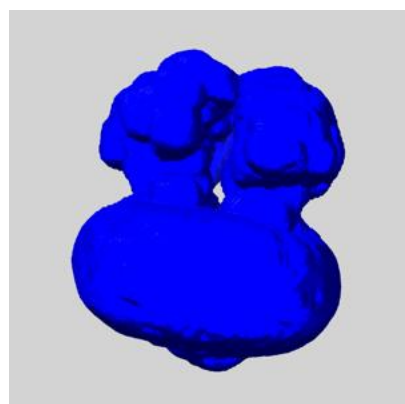
6.6 Mask visualisation [i](#)

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

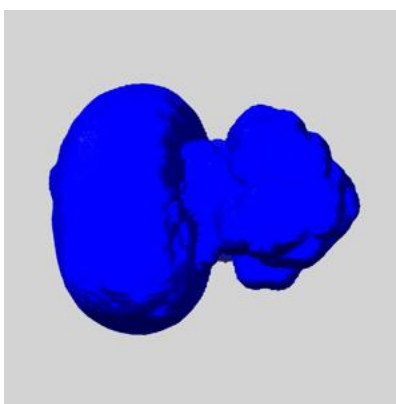
A mask typically either:

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

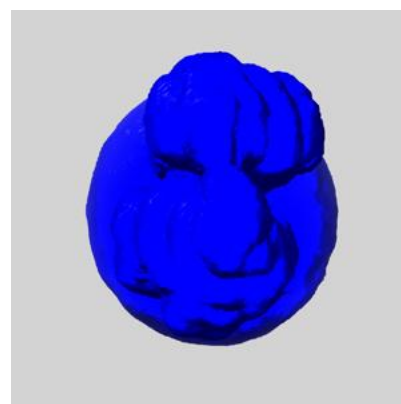
6.6.1 emd_62366_msk_1.map [i](#)



X



Y

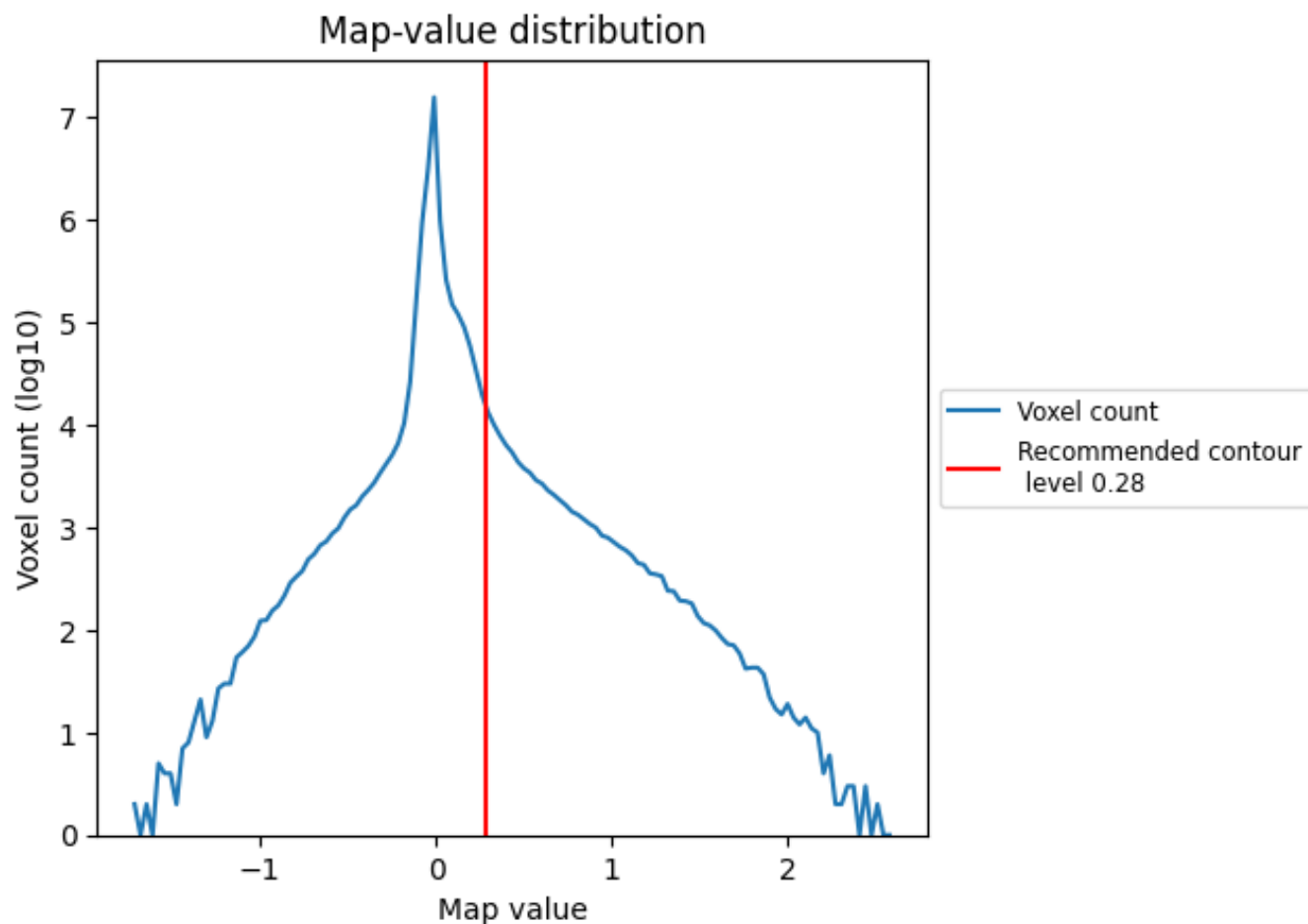


Z

7 Map analysis [i](#)

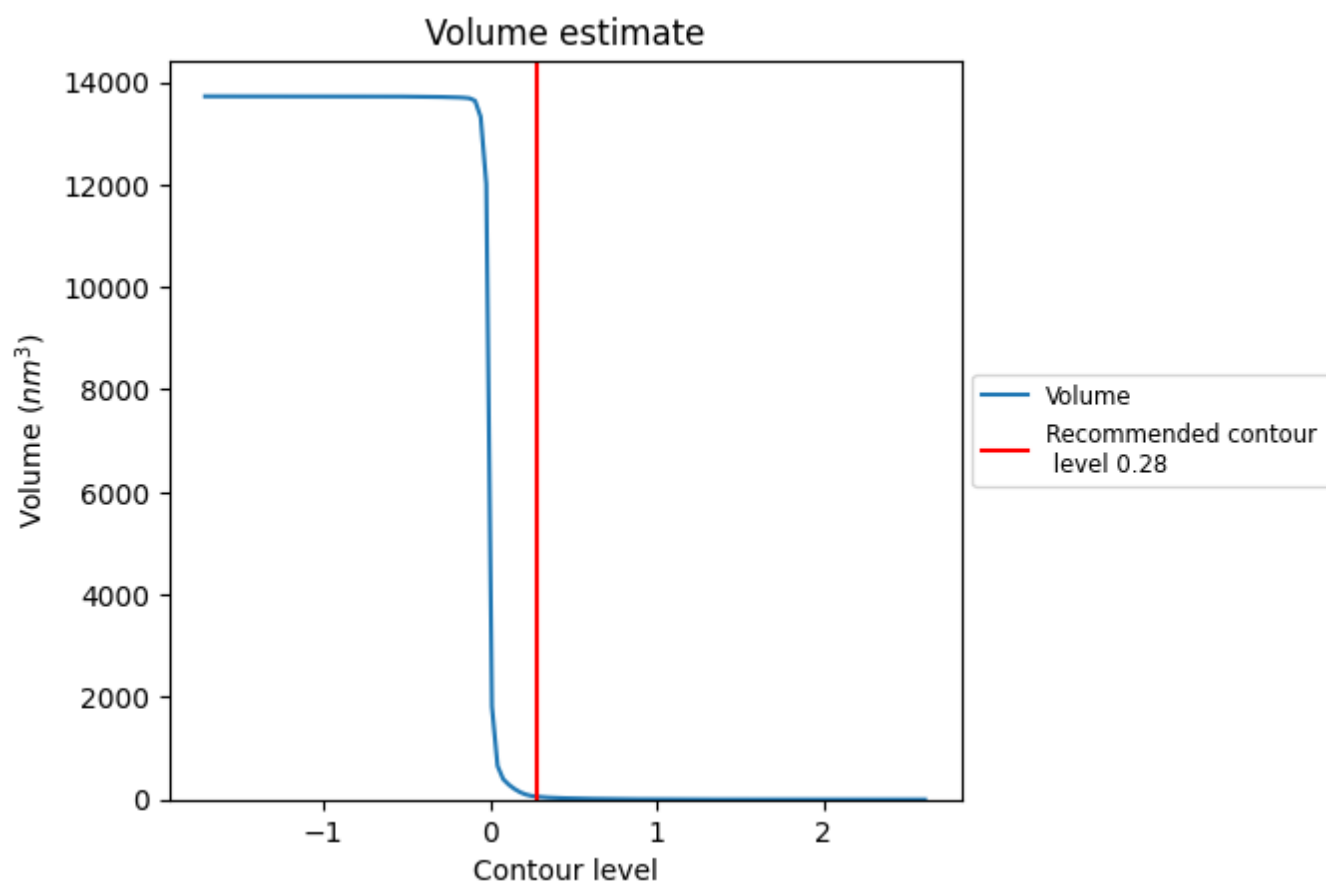
This section contains the results of statistical analysis of the map.

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.

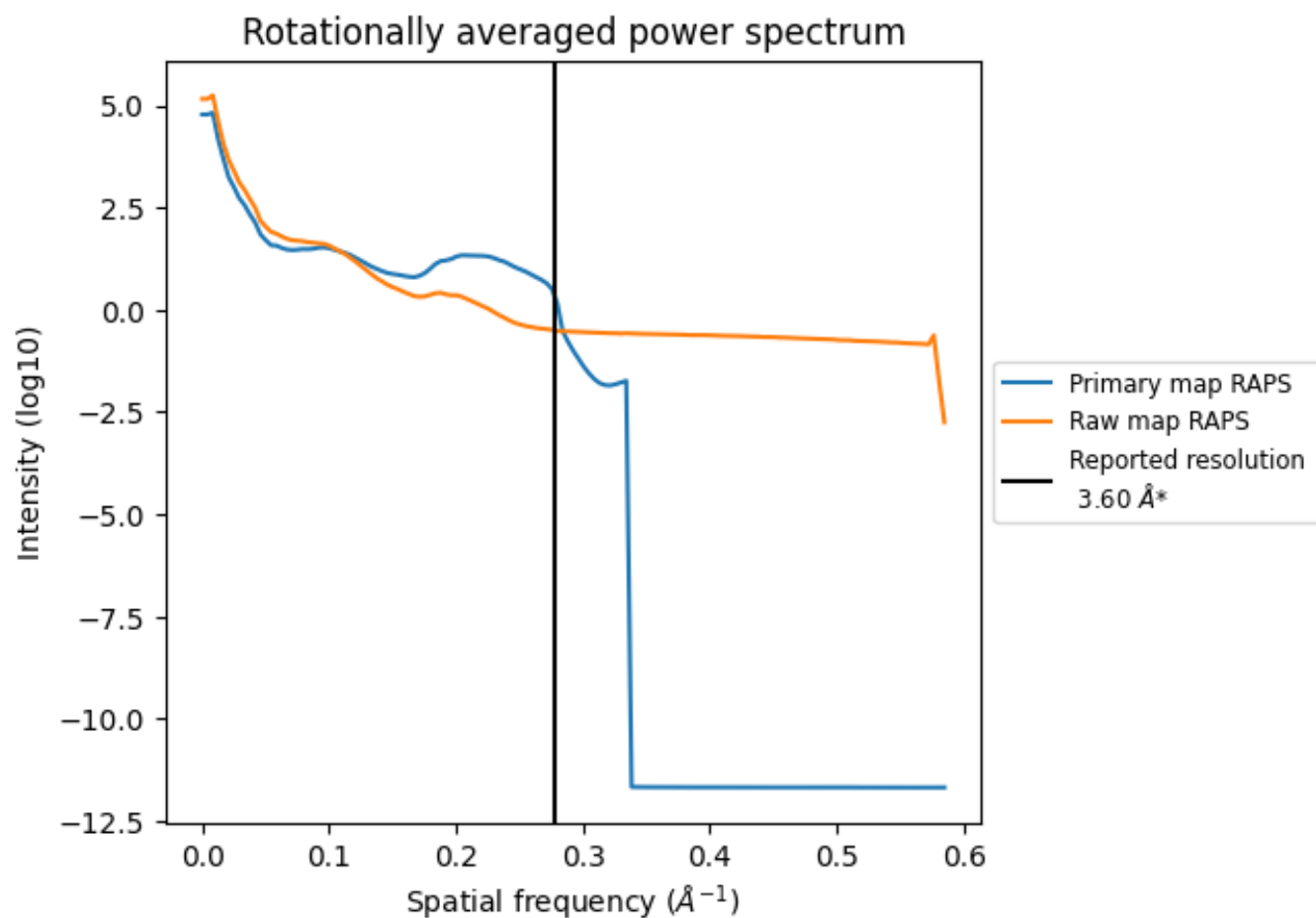
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 57 nm³; this corresponds to an approximate mass of 51 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 ⓘ

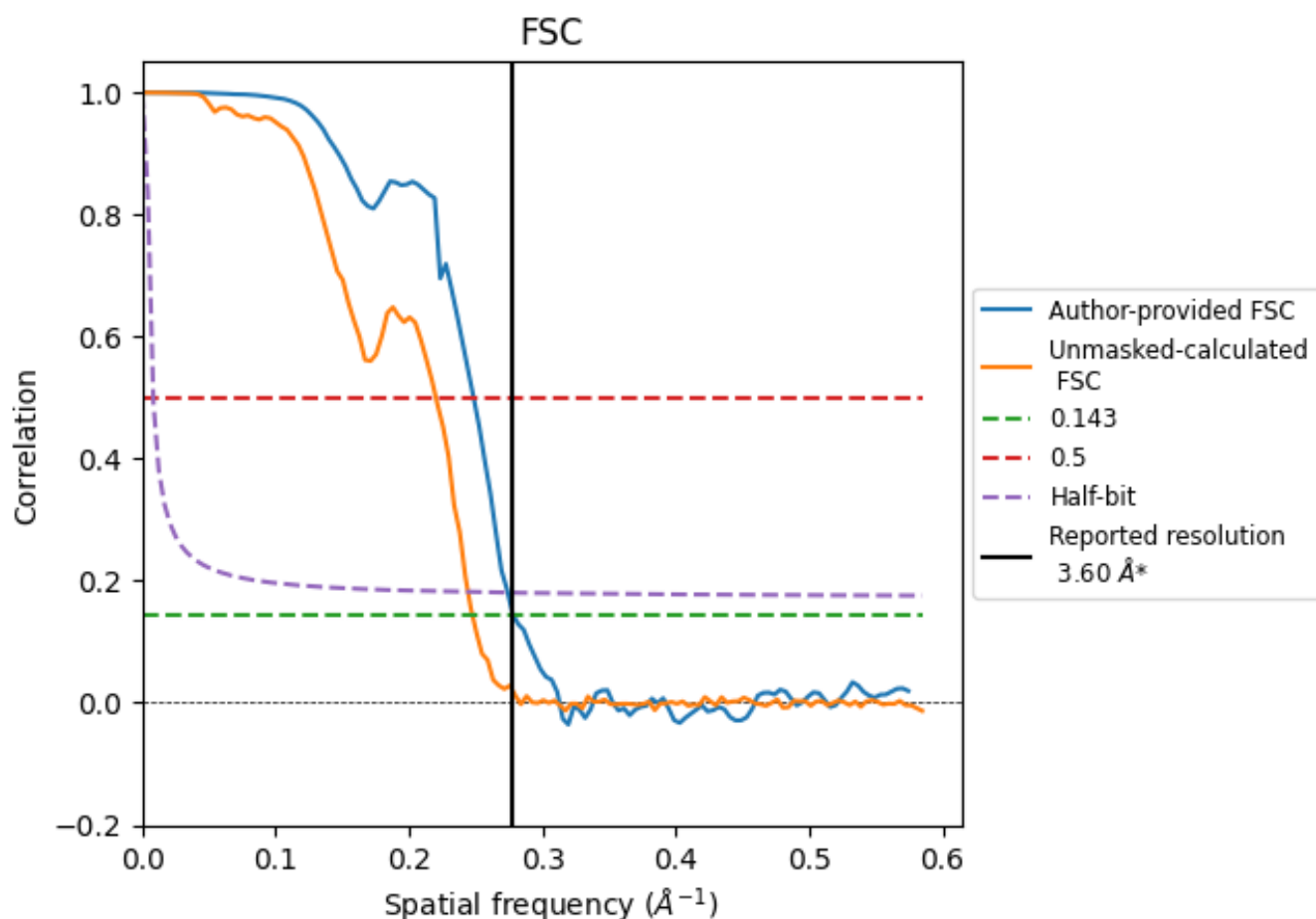


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 \AA^{-1}

8.2 Resolution estimates [i](#)

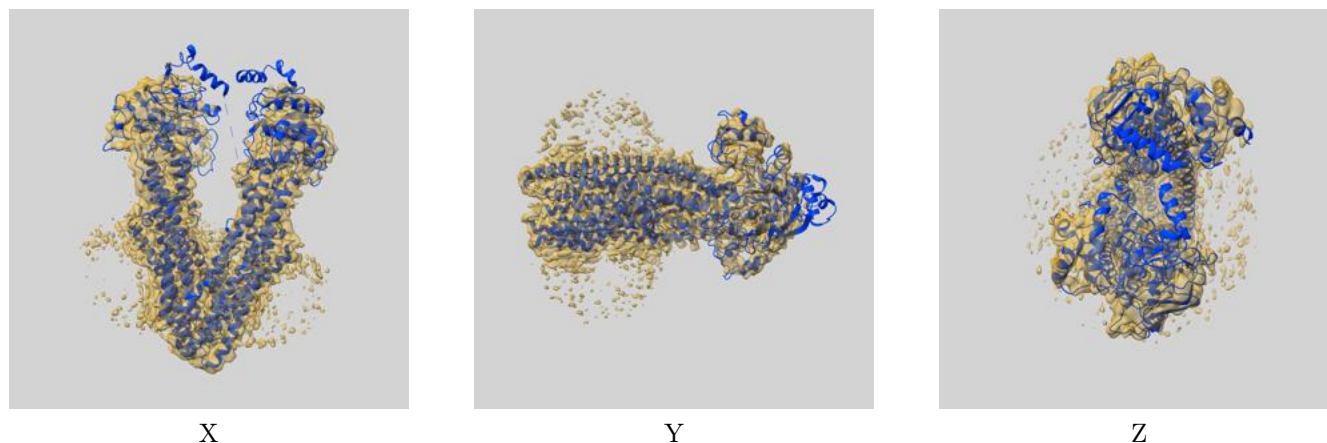
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.59	4.02	3.65
Unmasked-calculated*	4.04	4.54	4.09

*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 4.04 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

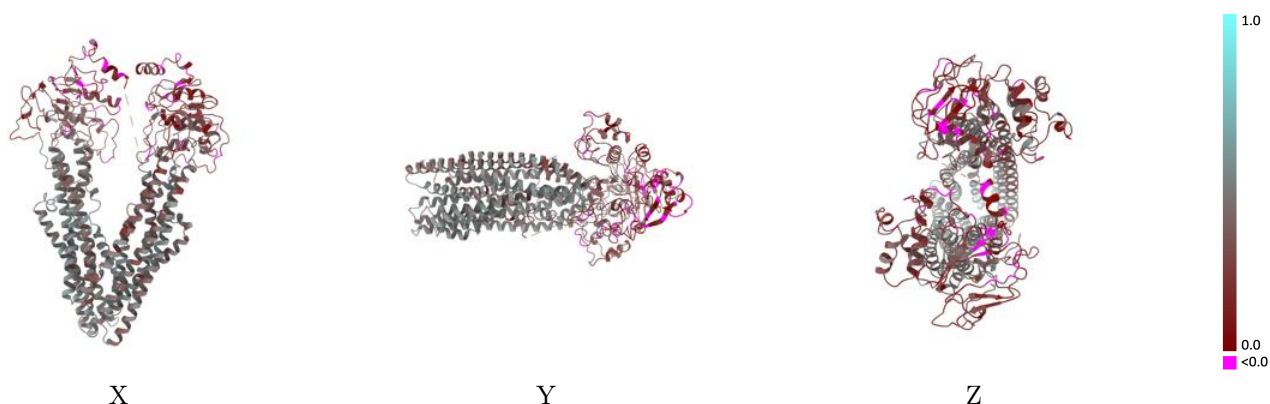
This section contains information regarding the fit between EMDB map EMD-62366 and PDB model 9KJC. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



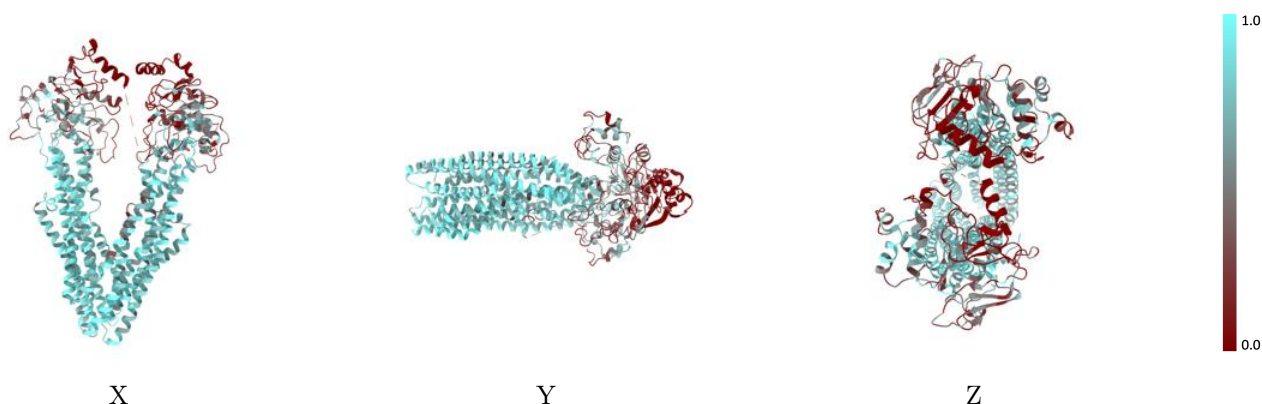
The images above show the 3D surface view of the map at the recommended contour level 0.28 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



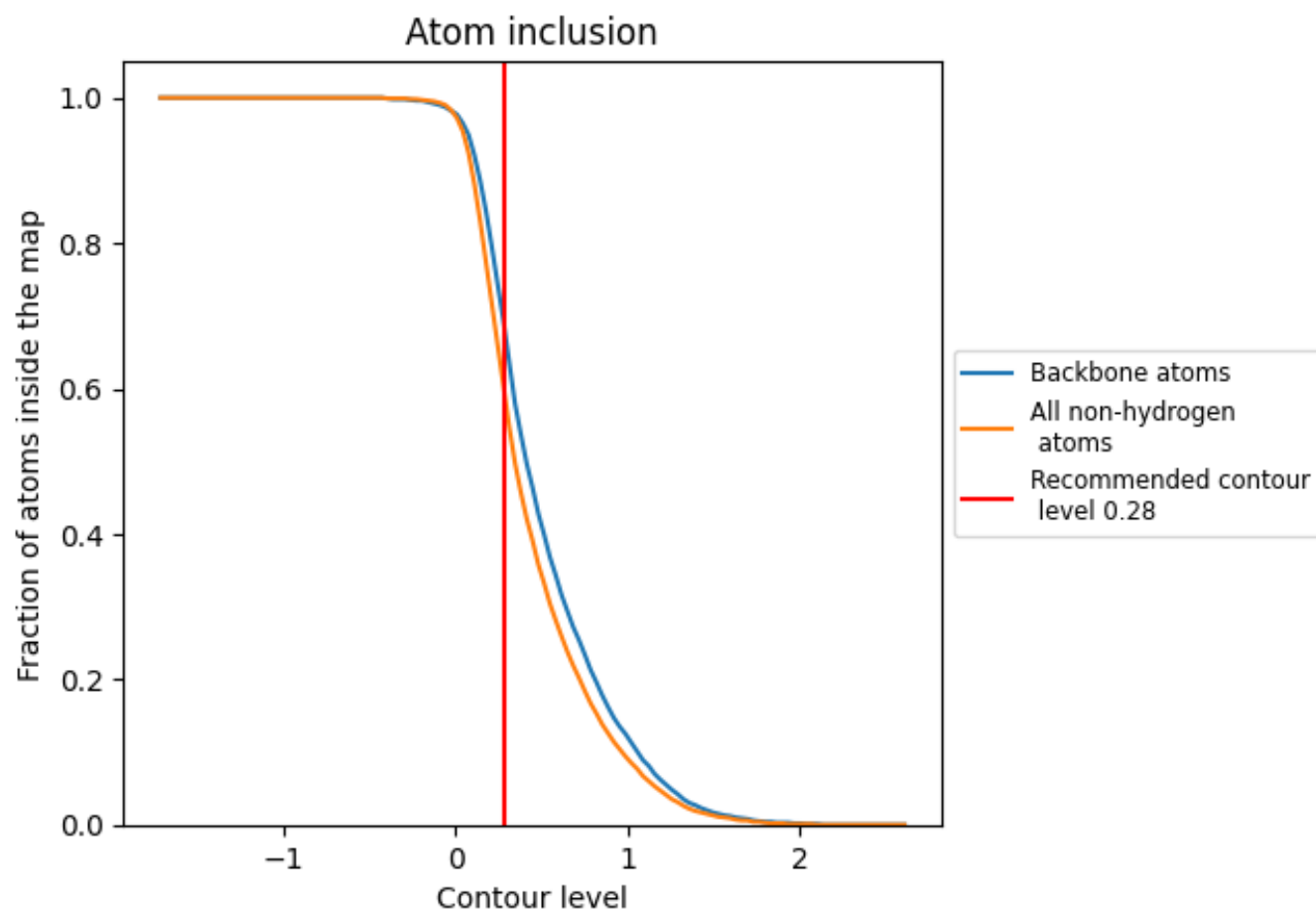
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.28).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 60% 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 (0.28) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6040	<div></div> 0.3470
A	<div></div> 0.6040	<div></div> 0.3470

