



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 06:41 AM UTC

PDB ID : 7ZKB / pdb_00007zkb
EMDB ID : EMD-14761
Title : ABCB1 V978C mutant (mABCB1) in the inward facing state
Authors : Parey, K.; Janulienė, D.; Gewering, T.; Moeller, A.
Deposited on : 2022-04-12
Resolution : 4.70 Å (reported)
Based on initial model : 6C0V

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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

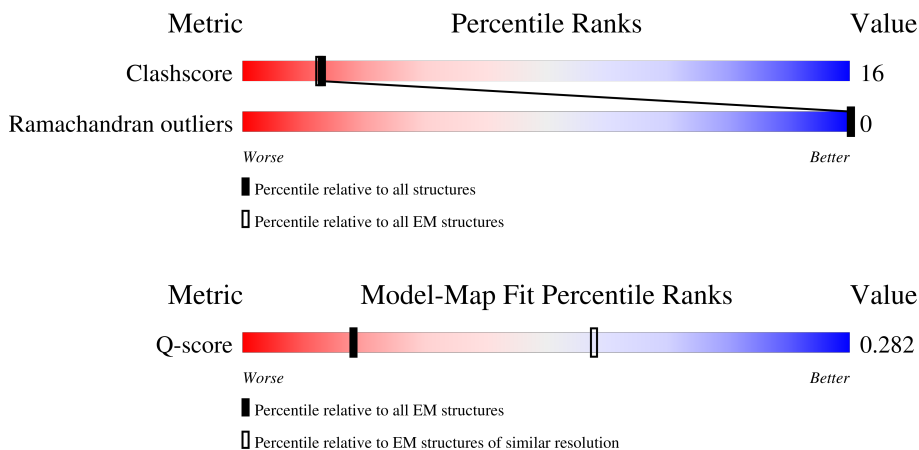
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 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	-
Q-score	-	25397	1989 (4.20 - 5.20)

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	1328	29% 58% 29% 13%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	JIZ	A	1401	-	X	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9043 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 ATP-dependent translocase ABCB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1157	Total	C	N	O	S	0	0
			8968	5764	1527	1647	30		

There are 65 discrepancies between the modelled and reference sequences:

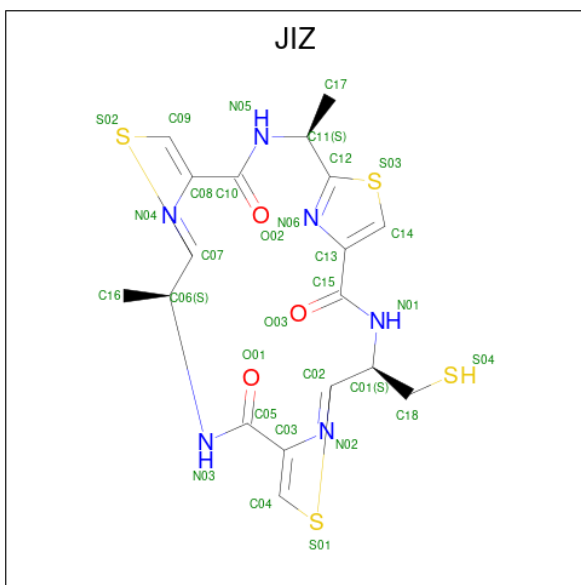
Chain	Residue	Modelled	Actual	Comment	Reference
A	83	GLN	ASN	engineered mutation	UNP P21447
A	87	GLN	ASN	engineered mutation	UNP P21447
A	90	GLN	ASN	engineered mutation	UNP P21447
A	133	ALA	CYS	engineered mutation	UNP P21447
A	427	GLY	CYS	engineered mutation	UNP P21447
A	638	GLY	CYS	engineered mutation	UNP P21447
A	669	THR	CYS	engineered mutation	UNP P21447
A	713	ALA	CYS	engineered mutation	UNP P21447
A	952	ALA	CYS	engineered mutation	UNP P21447
A	978	CYS	VAL	engineered mutation	UNP P21447
A	1070	GLY	CYS	engineered mutation	UNP P21447
A	1121	ARG	CYS	engineered mutation	UNP P21447
A	1223	VAL	CYS	engineered mutation	UNP P21447
A	1277	LEU	-	expression tag	UNP P21447
A	1278	GLU	-	expression tag	UNP P21447
A	1279	GLU	-	expression tag	UNP P21447
A	1280	ASN	-	expression tag	UNP P21447
A	1281	LEU	-	expression tag	UNP P21447
A	1282	TYR	-	expression tag	UNP P21447
A	1283	PHE	-	expression tag	UNP P21447
A	1284	GLN	-	expression tag	UNP P21447
A	1285	GLY	-	expression tag	UNP P21447
A	1286	GLY	-	expression tag	UNP P21447
A	1287	GLY	-	expression tag	UNP P21447
A	1288	ALA	-	expression tag	UNP P21447
A	1289	SER	-	expression tag	UNP P21447
A	1290	GLY	-	expression tag	UNP P21447
A	1291	GLY	-	expression tag	UNP P21447

Continued on next page...

Continued from previous page...

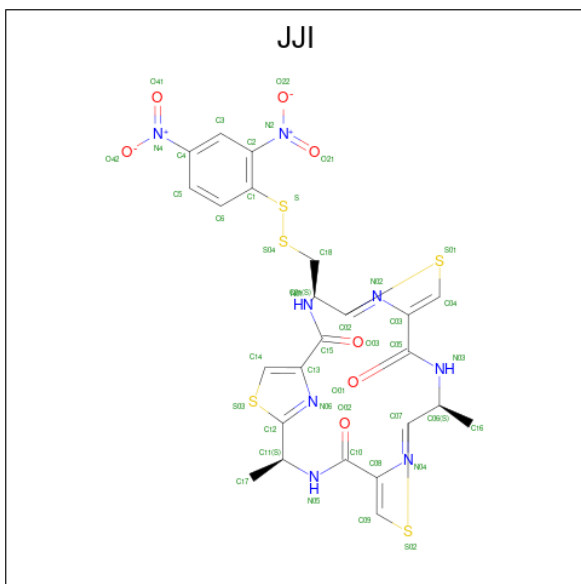
Chain	Residue	Modelled	Actual	Comment	Reference
A	1292	SER	-	expression tag	UNP P21447
A	1293	TRP	-	expression tag	UNP P21447
A	1294	SER	-	expression tag	UNP P21447
A	1295	HIS	-	expression tag	UNP P21447
A	1296	PRO	-	expression tag	UNP P21447
A	1297	GLN	-	expression tag	UNP P21447
A	1298	PHE	-	expression tag	UNP P21447
A	1299	GLU	-	expression tag	UNP P21447
A	1300	LYS	-	expression tag	UNP P21447
A	1301	ALA	-	expression tag	UNP P21447
A	1302	ALA	-	expression tag	UNP P21447
A	1303	ALA	-	expression tag	UNP P21447
A	1304	GLY	-	expression tag	UNP P21447
A	1305	GLY	-	expression tag	UNP P21447
A	1306	GLY	-	expression tag	UNP P21447
A	1307	SER	-	expression tag	UNP P21447
A	1308	GLY	-	expression tag	UNP P21447
A	1309	GLY	-	expression tag	UNP P21447
A	1310	GLY	-	expression tag	UNP P21447
A	1311	SER	-	expression tag	UNP P21447
A	1312	TRP	-	expression tag	UNP P21447
A	1313	SER	-	expression tag	UNP P21447
A	1314	HIS	-	expression tag	UNP P21447
A	1315	PRO	-	expression tag	UNP P21447
A	1316	GLN	-	expression tag	UNP P21447
A	1317	PHE	-	expression tag	UNP P21447
A	1318	GLU	-	expression tag	UNP P21447
A	1319	LYS	-	expression tag	UNP P21447
A	1320	GLY	-	expression tag	UNP P21447
A	1321	SER	-	expression tag	UNP P21447
A	1322	GLY	-	expression tag	UNP P21447
A	1323	HIS	-	expression tag	UNP P21447
A	1324	HIS	-	expression tag	UNP P21447
A	1325	HIS	-	expression tag	UNP P21447
A	1326	HIS	-	expression tag	UNP P21447
A	1327	HIS	-	expression tag	UNP P21447
A	1328	HIS	-	expression tag	UNP P21447

- Molecule 2 is (4 {S},11 {S},18 {S})-4,11-dimethyl-18-(sulfanylmethyl)-6,13,20-trithia-3,10,17,22,23,24-hexazatetracyclo[17.2.1.1[^]{5,8}.1[^]{12,15}]tetracosa-1(21),5(24),7,12(23),14,19(22)-hexaene-2,9,16-trione (CCD ID: JIZ) (formula: C₁₈H₁₈N₆O₃S₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	S	0
			31	18	6	3	4	

- Molecule 3 is (4S,11S,18S)-4-[[[(2,4-dinitrophenyl)disulfanyl]methyl]-11,18-dimethyl-6,13,20-trithia-3,10,17,22,23,24-hexazatetracyclo[17.2.1.1^{5,8}.1^{12,15}]]tetracos-1(21),5(24),7,12(23),14,19(22)-hexaene-2,9,16-trione (CCD ID: JJI) (formula: C₂₄H₂₀N₈O₇S₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	S	0
			44	24	8	7	5	

TYR	ARG	ARG	ARG	THR	THR	LYS	SER	ILE	THR	GLY	PRO	HIS	ASP	GLN	ASP	ARG	LYS	SER	THR	LYS	GLU	ALA	ASP	GLU	ASP	VAL	P689	F693	M694	R695	K698	L699	N700	W704	P705	Y706	F707	G710	I711	A714	Q721	P722	A723	V726	I727	F728	S729	K730	V734										
P1158	D1159	K1160	Y1161	N1162	T1163	R1164	D1167	K1168	G1169	T1170	Q1171	L1172	G1175	Q1176	K1177	R1178	R1179	I1182	A1183	R1184	V1187	R1188	Q1189	P1190	H1191	I1192	L1193	L1194	L1195	D1196	E1197	A1198	T1199	S1200	A1201	L1202	D1203	T1204	E1205	S1206	K1208	V1209	Q1211	E1212	A1213	L1214	D1215	K1216	A1217	R1218	E1219	G1220	R1221						
T1222	V1223	I1224	V1225	I1226	A1227	H1228	R1229	L1230	S1231	T1232	I1233	Q1234	N1235	A1236	D1237	L1238	I1239	Y1240	V1241	I1242	Q1243	N1244	G1245	K1246	V1247	K1248	E1249	H1250	G1251	T1252	H1253	Q1254	Q1255	L1256	L1257	A1258	Q1259	K1260	GLY	ILE	TYR	PHE	SER	MET	VAL	SER	VAL	GLN	ALA	GLY	ALA	LYS	ARG	SER	GLU	LEU	GLU	ASN	LEU
G1088	S1089	V1090	F1091	D1093	G1094	K1095	E1096	I1097	K1098	Q1099	L1100	N1101	V1102	Q1103	W1104	L1105	R1106	Q1107	Q1108	L1109	S1113	Q1114	E1115	D1120	R1121	S1122	M1126	I1127	A1128	Y1129	G1130	D1131	N1132	S1133	R1134	V1135	Y1138	E1139	E1140	I1141	V1142	R1143	K1146	N1149	I1150	H1151	Q1152	I1153	D1155	G1156	L1157								
S1018	T1019	K1023	P1024	M1025	M1026	L1027	E1028	G1029	M1030	V1031	Q1032	F1033	S1034	G1035	V1036	R1043	P1044	S1045	I1046	P1047	Y1048	L1049	Q1050	G1051	L1052	S1053	L1054	E1055	V1056	K1057	K1058	G1059	Q1060	T1061	L1062	A1063	L1064	V1065	G1066	S1067	S1068	G1069	G1070	G1071	K1072	S1073	T1074	Q1077	L1078	R1081	F1082	P1085	M1086	A1087					
A943	M944	M945	Y946	F947	S948	A951	F955	G956	A957	Y958	L959	V960	T961	M965	E968	N969	L972	C978	F979	G980	A981	N982	A983	V984	G985	Q986	V987	S988	S989	F990	A991	P992	D993	Y994	A995	K996	A997	T998	V999	S1000	A1001	S1002	H1003	I1004	I1005	R1006	I1007	I1008	E1013	S1016	Y1017								
V631	A637	N638	T641	I644	S646	Y649	G650	L655	L656	L657	I661	T672	L680	L684	R685	V788	F789	K790	S791	M792	L793	R794	Q795	D796	V797	S798	M799	F800	D801	D802	F803	K804	N805	A809	L810	R813	N816	D817	Q820	G823	S827	R828	L829	A830															

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	343873	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 ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.801	Depositor
Minimum map value	-0.648	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	234.36, 234.36, 234.36	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.837, 0.837, 0.837	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.34	2/9132 (0.0%)	0.64	11/12343 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	245	LYS	C-O	5.68	1.30	1.24
1	A	269	GLU	C-O	5.63	1.31	1.24

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	306	TYR	N-CA-C	-11.79	98.42	111.28
1	A	249	VAL	N-CA-C	-7.82	102.65	110.62
1	A	244	ALA	O-C-N	-6.21	114.95	122.22
1	A	272	ARG	CA-C-N	-5.69	112.65	120.28
1	A	272	ARG	C-N-CA	-5.69	112.65	120.28

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	8968	0	9150	297	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	31	0	0	2	0
3	A	44	0	0	0	0
All	All	9043	0	9150	298	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 16.

The worst 5 of 298 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:79:ALA:O	1:A:83:GLN:HG3	1.36	1.23
1:A:482:GLU:HA	1:A:485:ARG:HG2	1.28	1.13
1:A:268:LYS:HD2	1:A:1132:ASN:HB2	1.36	1.05
1:A:223:LEU:O	1:A:227:ILE:HD12	1.63	0.98
1:A:268:LYS:CD	1:A:1132:ASN:HB2	1.96	0.95

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	817/1328 (62%)	761 (93%)	56 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 ligands are 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	$\# Z > 2$
3	JJI	A	1402	-	47,48,48	2.93	18 (38%)	56,69,69	2.90	19 (33%)
2	JIZ	A	1401	1	34,34,34	2.63	19 (55%)	45,49,49	4.41	26 (57%)

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
3	JJI	A	1402	-	-	23/46/50/50	0/5/5/5
2	JIZ	A	1401	1	-	22/38/38/38	1/4/4/4

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1402	JJI	O41-N4	10.50	1.40	1.22

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1402	JJI	O21-N2	10.45	1.40	1.22
2	A	1401	JIZ	C15-N01	6.57	1.47	1.34
2	A	1401	JIZ	C10-N05	6.09	1.46	1.34
3	A	1402	JJI	C15-N01	5.62	1.45	1.34

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1401	JIZ	C13-C15-N01	11.80	131.99	115.22
2	A	1401	JIZ	C01-C18-S04	9.59	124.97	114.16
2	A	1401	JIZ	C04-S01-C02	8.28	99.31	89.52
2	A	1401	JIZ	C14-S03-C12	7.12	97.95	89.52
2	A	1401	JIZ	C08-N04-C07	6.95	117.82	110.65

There are no chirality outliers.

5 of 45 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1401	JIZ	C09-C08-C10-N05
2	A	1401	JIZ	N04-C08-C10-N05
2	A	1401	JIZ	C09-C08-C10-O02
2	A	1401	JIZ	N04-C08-C10-O02
2	A	1401	JIZ	C14-C13-C15-N01

All (1) ring outliers are listed below:

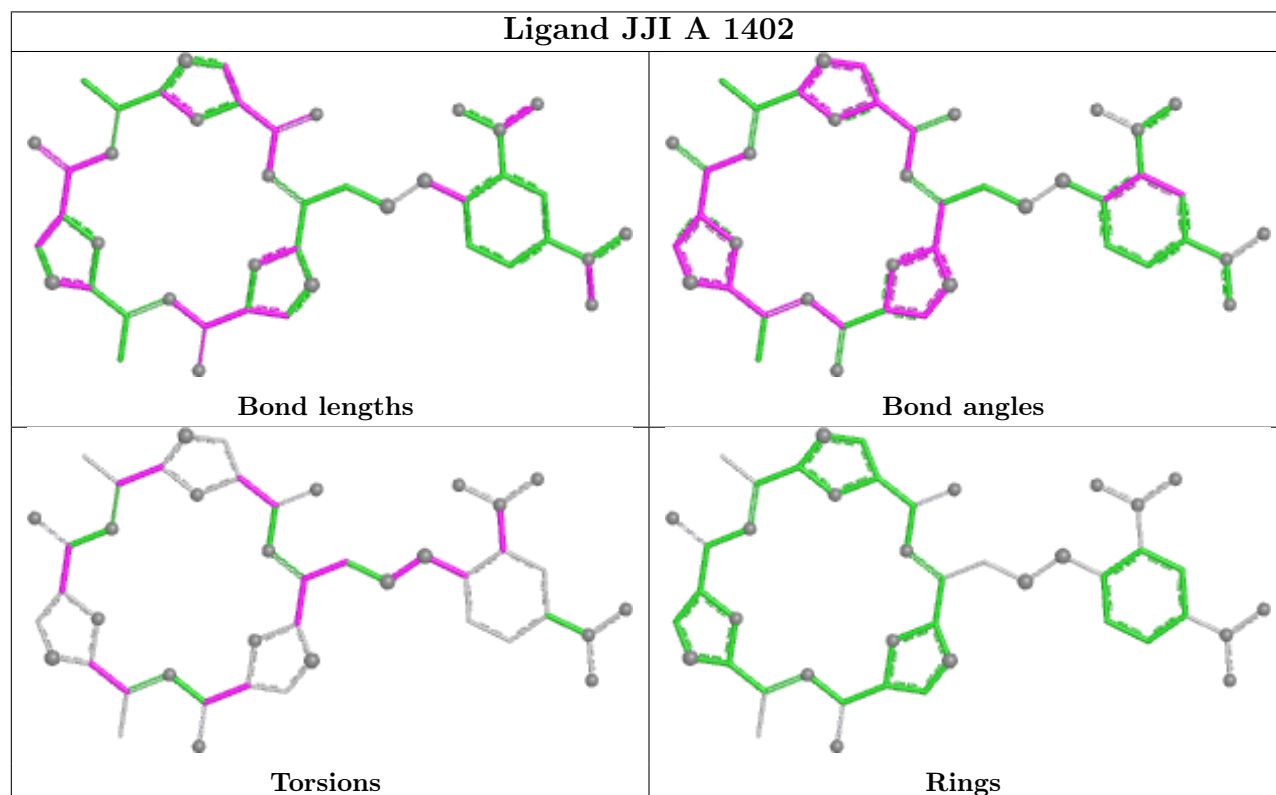
Mol	Chain	Res	Type	Atoms
2	A	1401	JIZ	C01-C02-C03-C05-C06-C07-C08-C10-C11-C12-C13-C15-N01-N02-N03-N04-I

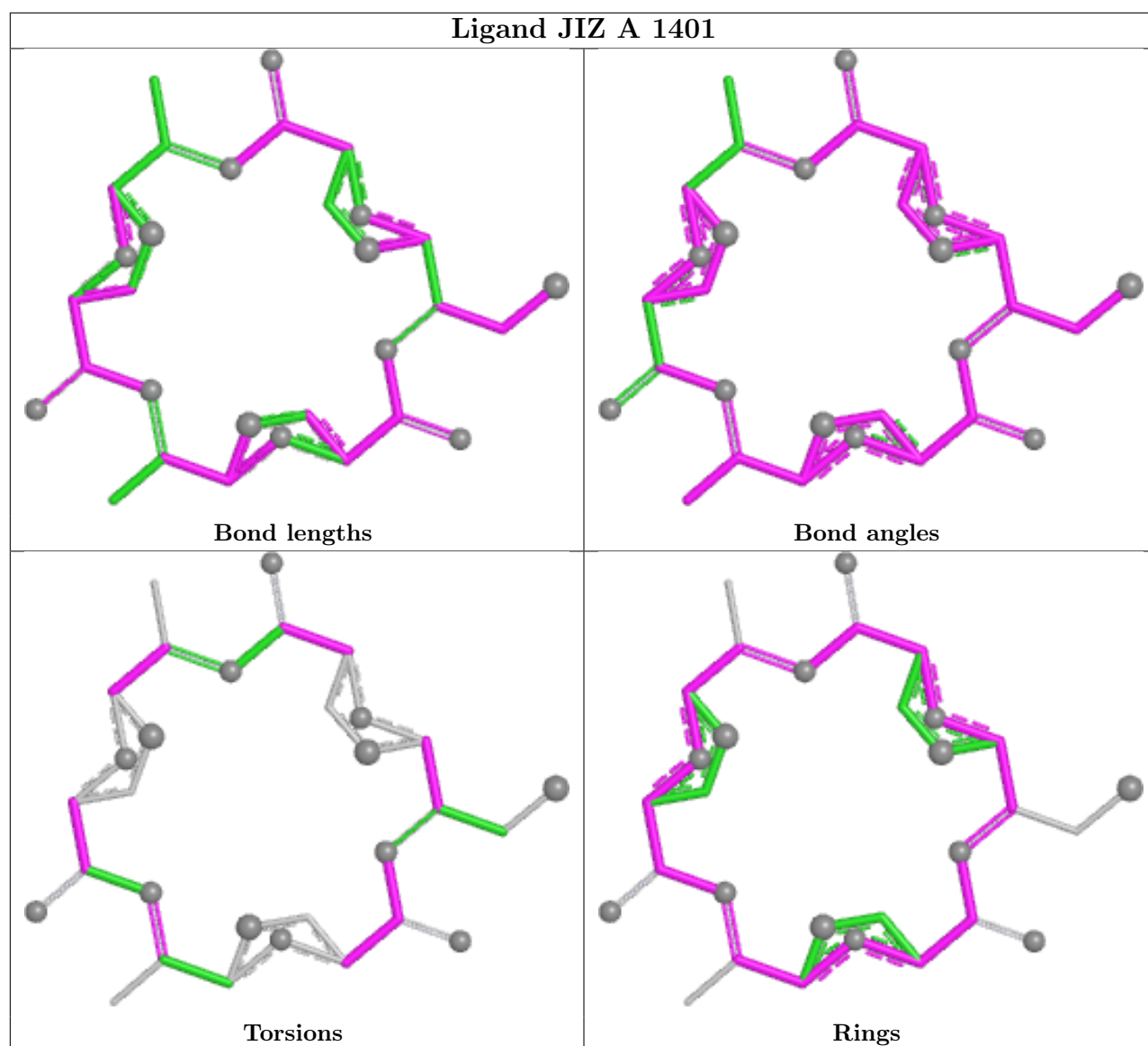
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1401	JIZ	2	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.

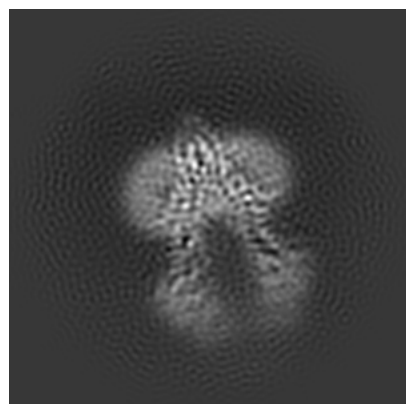
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14761. These allow visual inspection of the internal detail of the map and identification of artifacts.

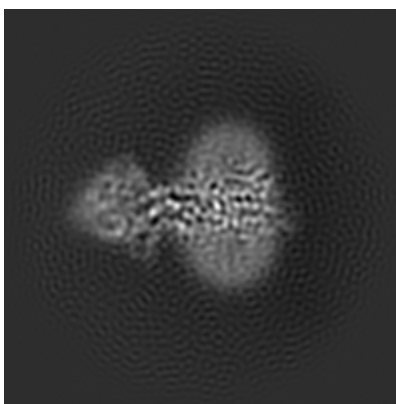
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

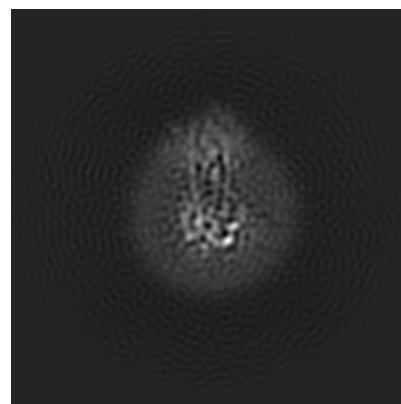
6.1.1 Primary map



X

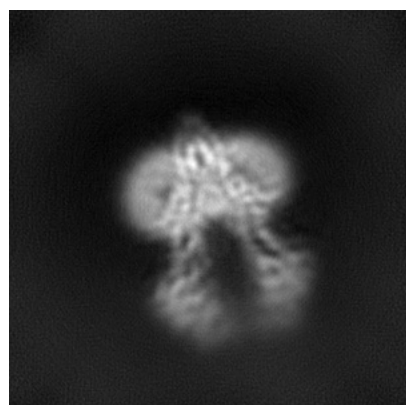


Y

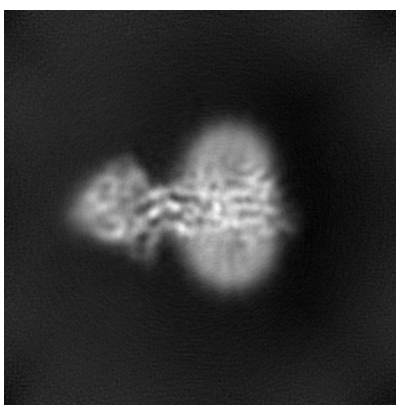


Z

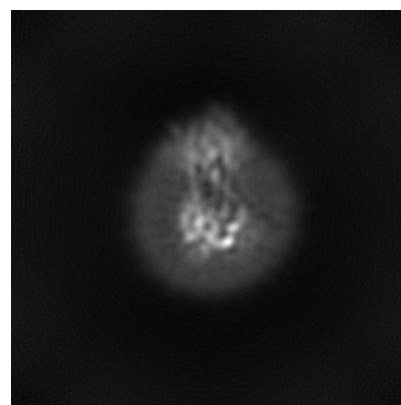
6.1.2 Raw map



X



Y

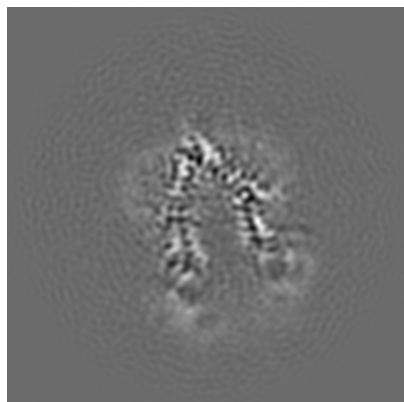


Z

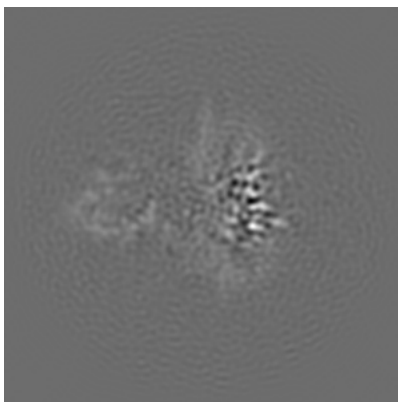
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

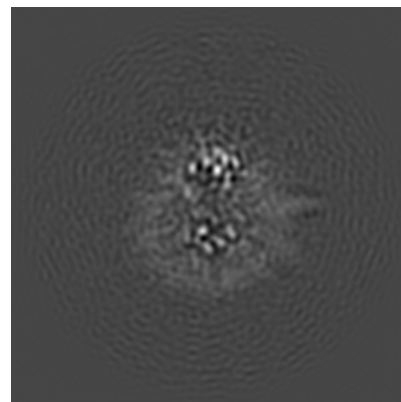
6.2.1 Primary map



X Index: 140

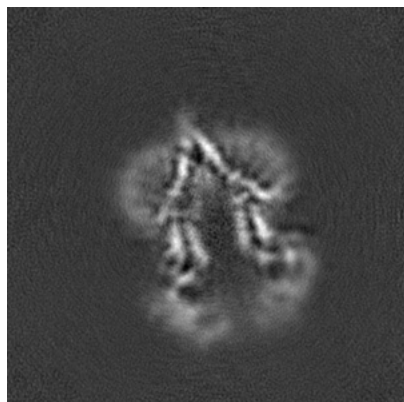


Y Index: 140

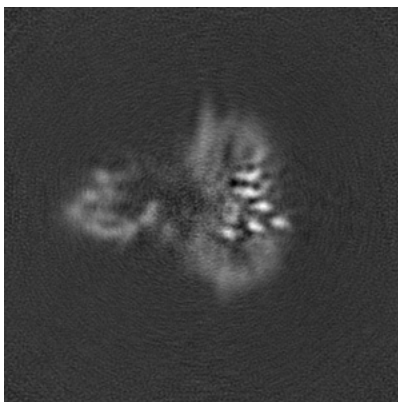


Z Index: 140

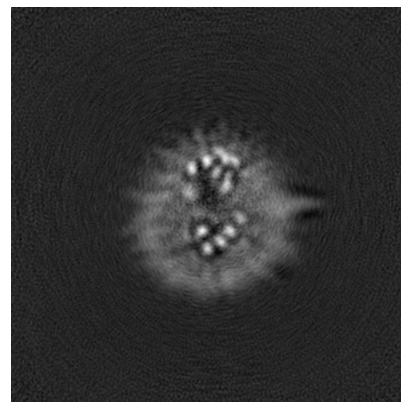
6.2.2 Raw map



X Index: 140



Y Index: 140

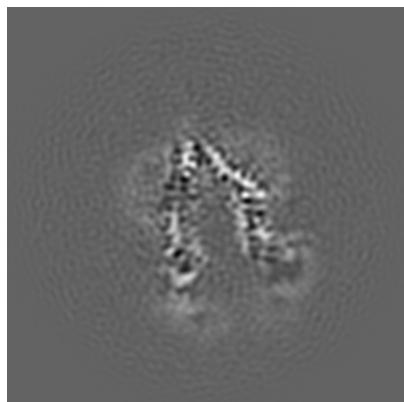


Z Index: 140

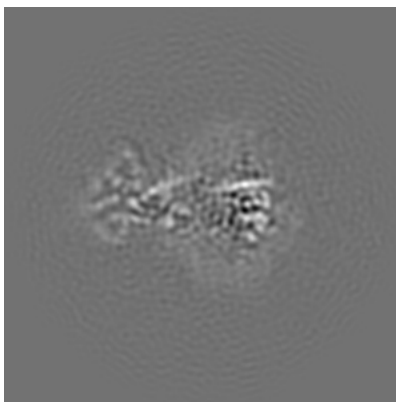
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

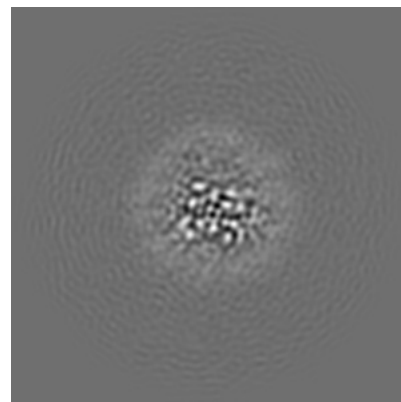
6.3.1 Primary map



X Index: 142

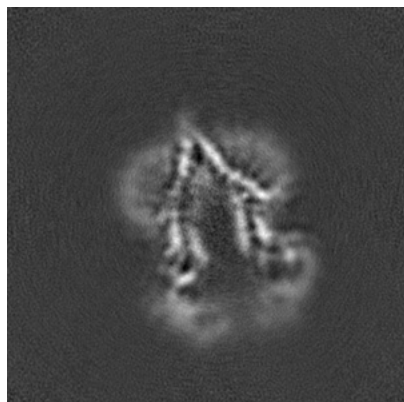


Y Index: 127

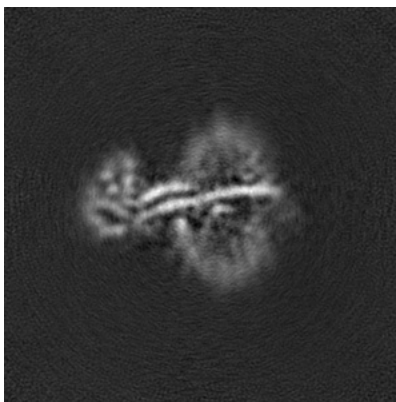


Z Index: 171

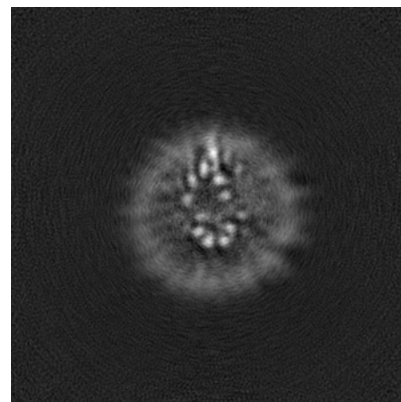
6.3.2 Raw map



X Index: 141



Y Index: 117

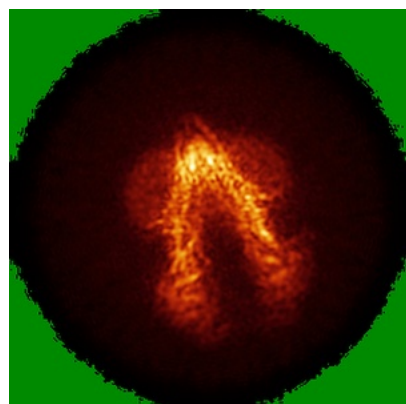


Z Index: 149

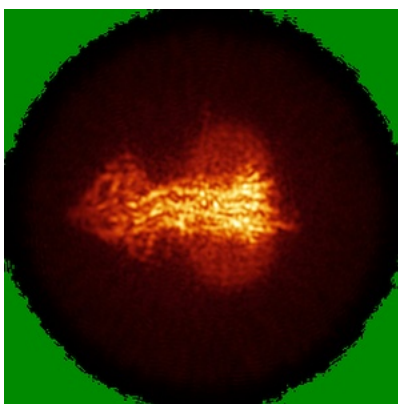
The images above show the largest variance slices of the map in three orthogonal directions.

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

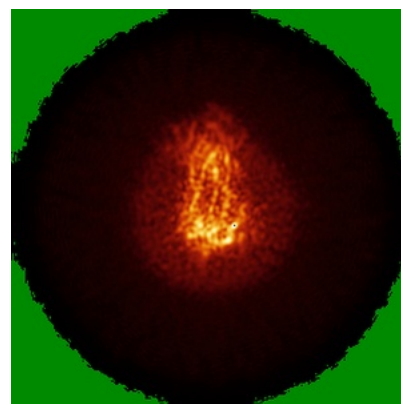
6.4.1 Primary map



X

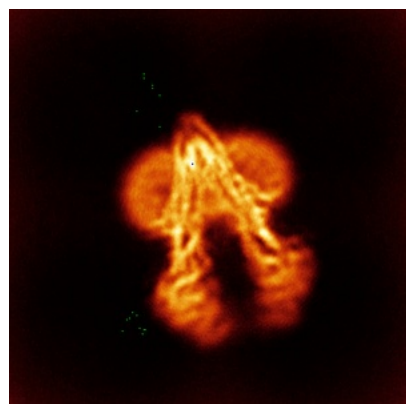


Y

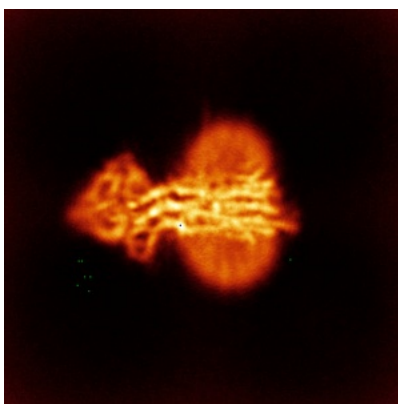


Z

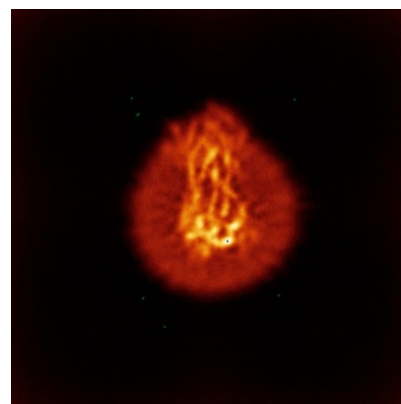
6.4.2 Raw map



X



Y

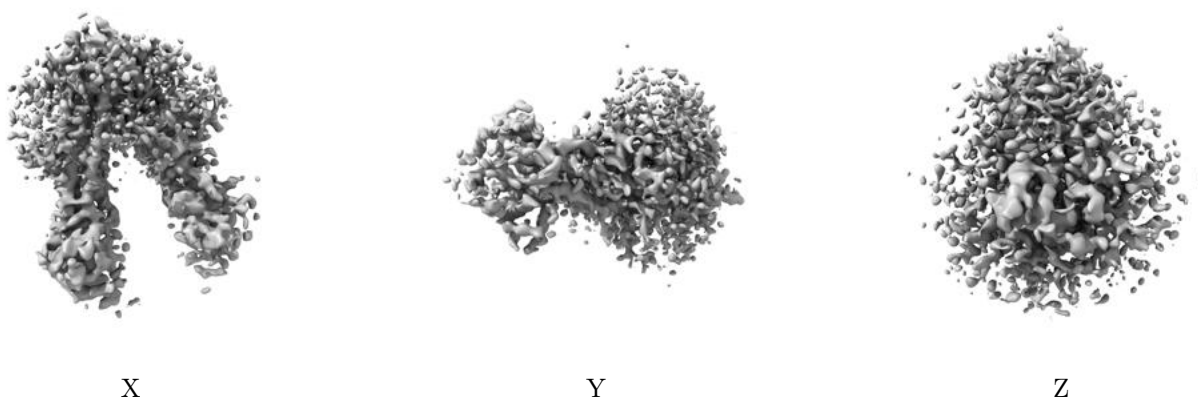


Z

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.

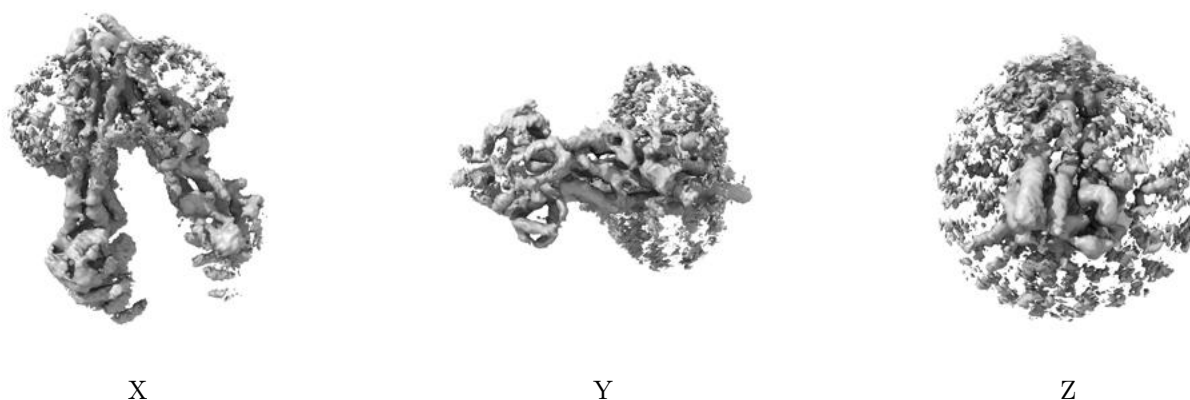
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. 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.

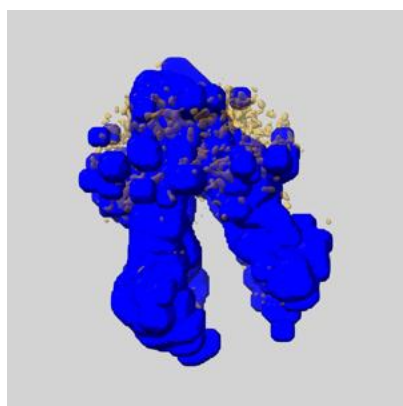
6.6 Mask visualisation [i](#)

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

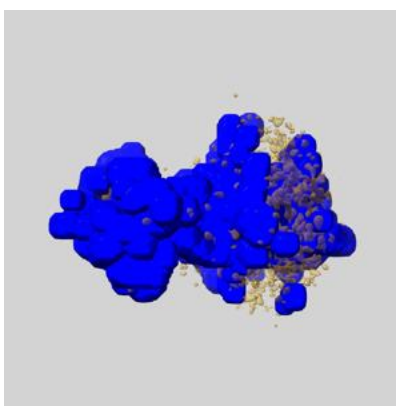
A mask typically either:

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

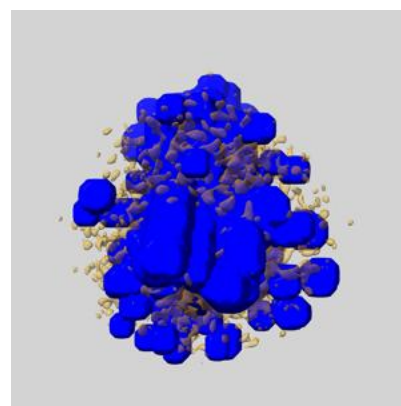
6.6.1 emd_14761_msk_1.map [i](#)



X



Y

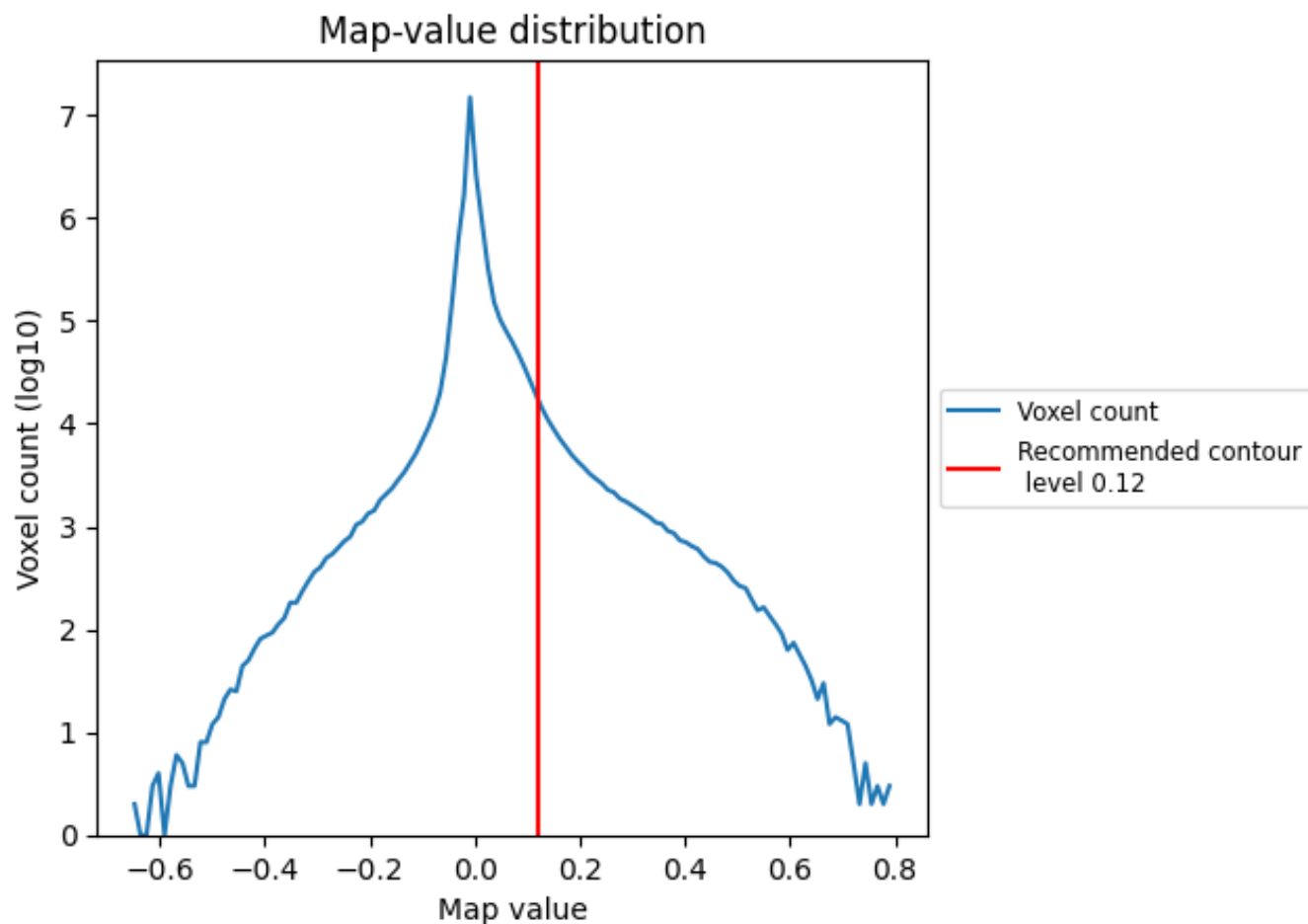


Z

7 Map analysis [i](#)

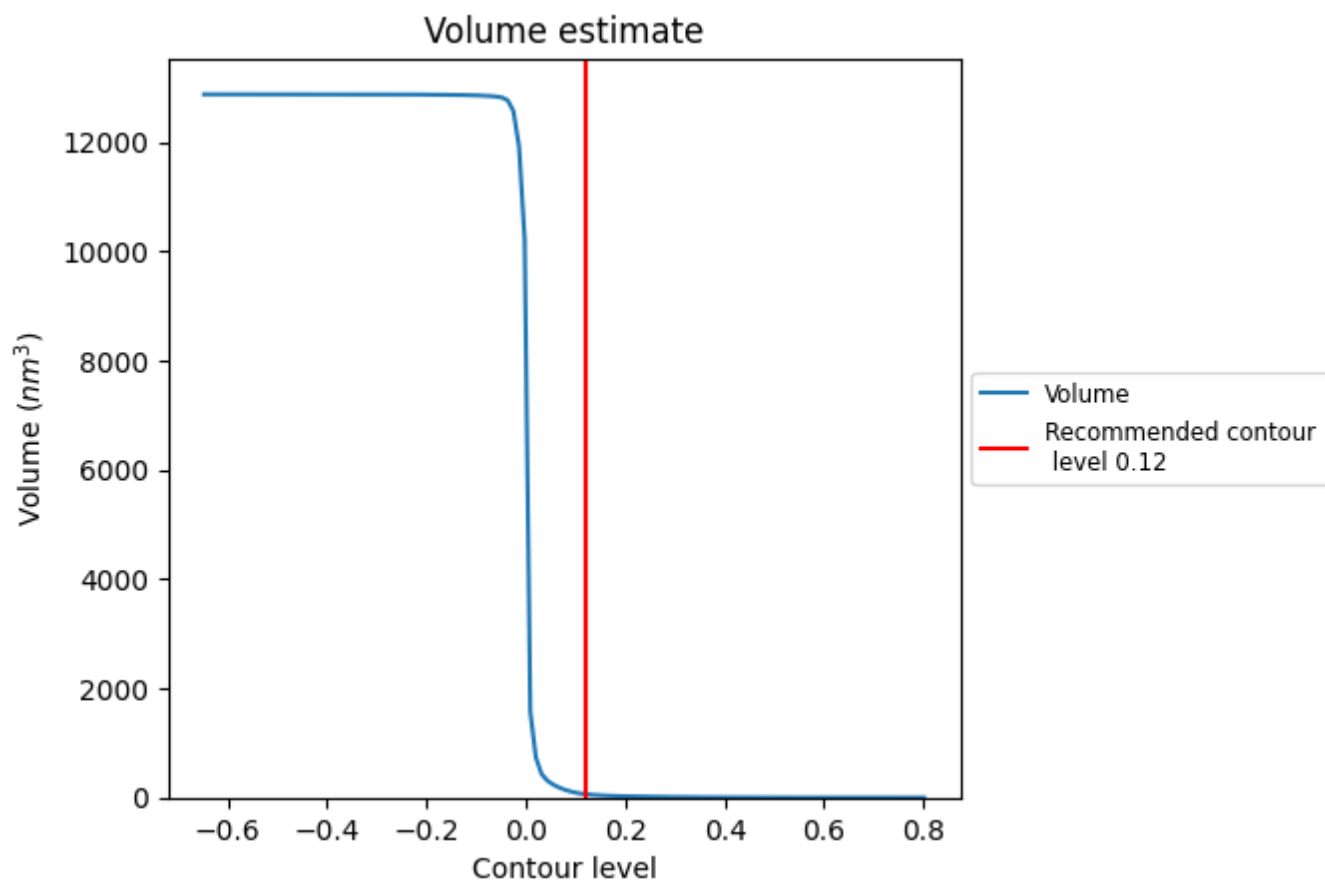
This section contains the results of statistical analysis of the map.

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.

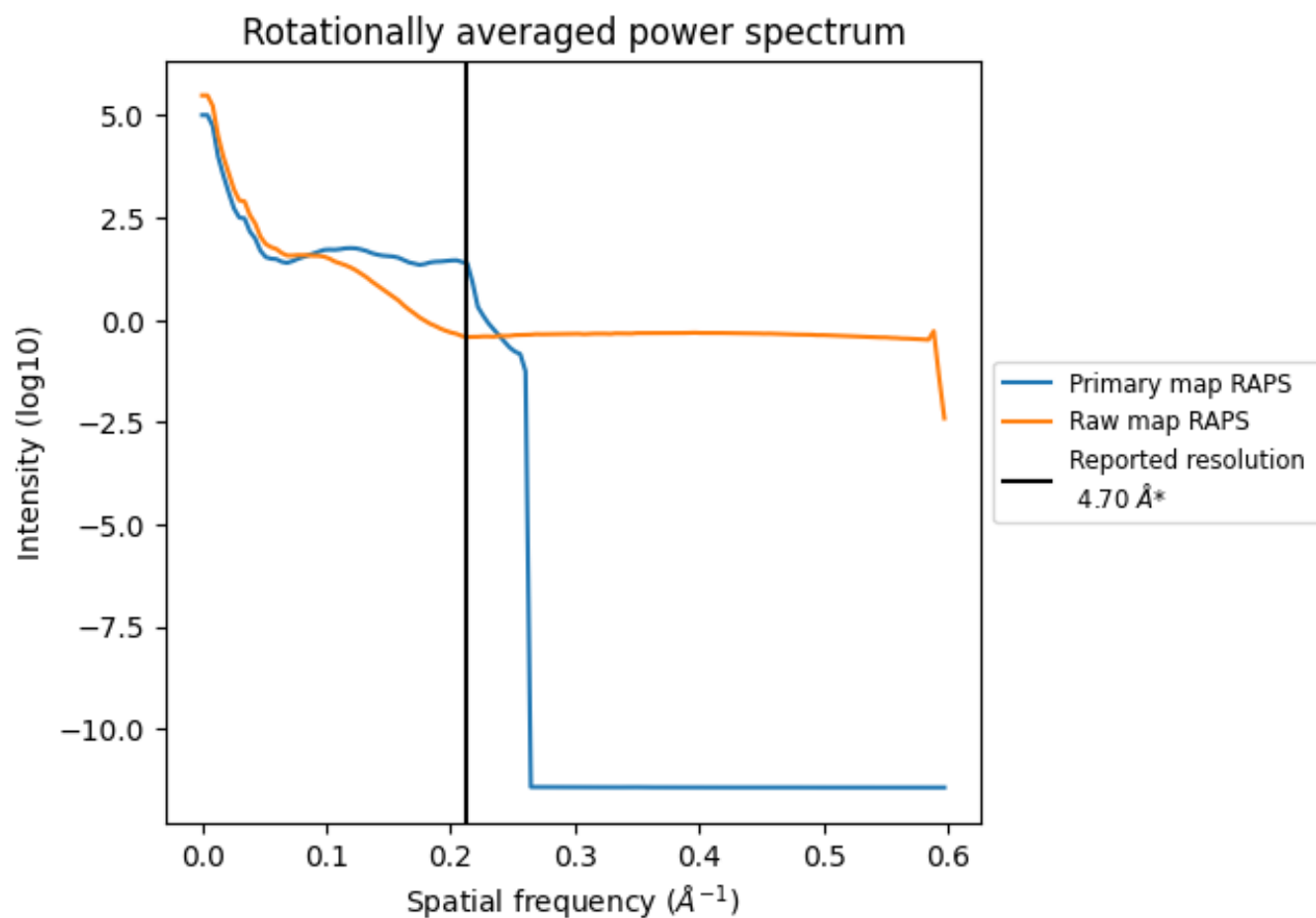
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 63 nm³; this corresponds to an approximate mass of 56 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 ⓘ

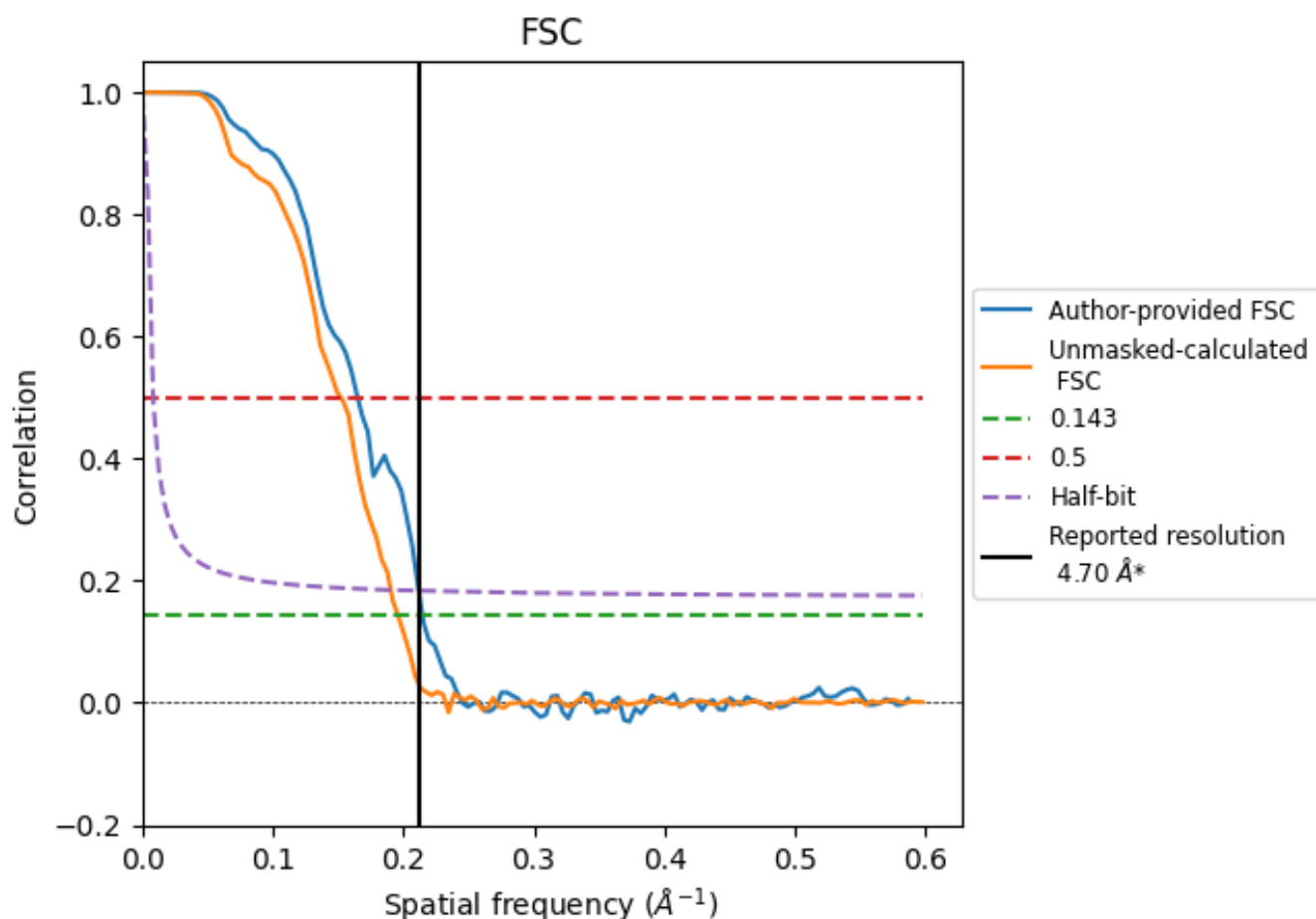


*Reported resolution corresponds to spatial frequency of 0.213 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

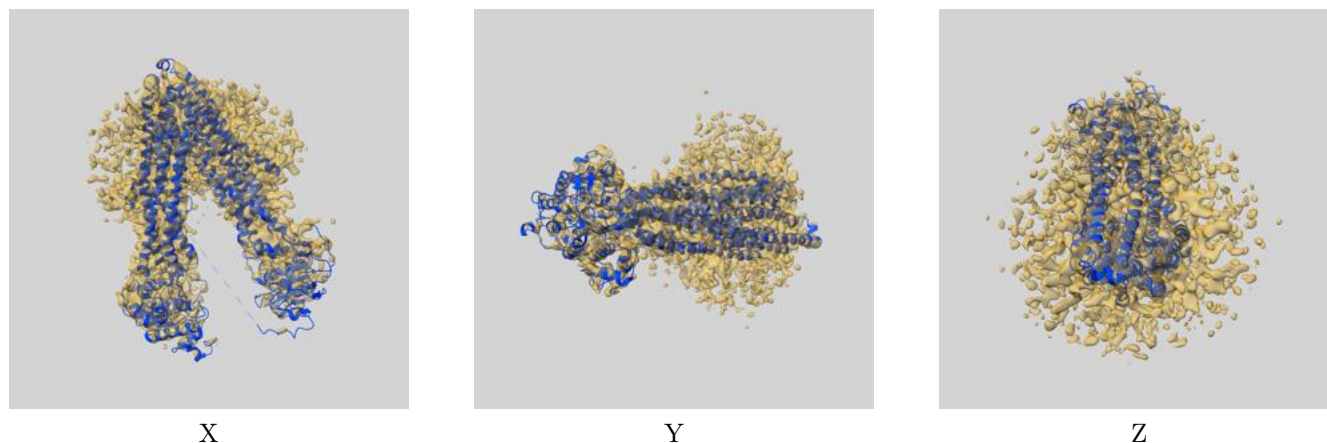
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.66	6.06	4.72
Unmasked-calculated*	5.10	6.57	5.25

*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-14761 and PDB model 7ZKB. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



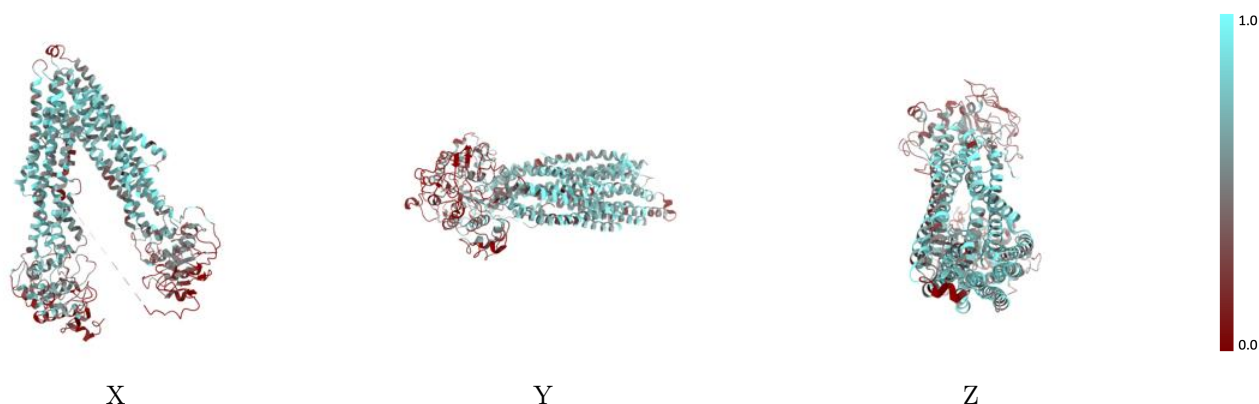
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



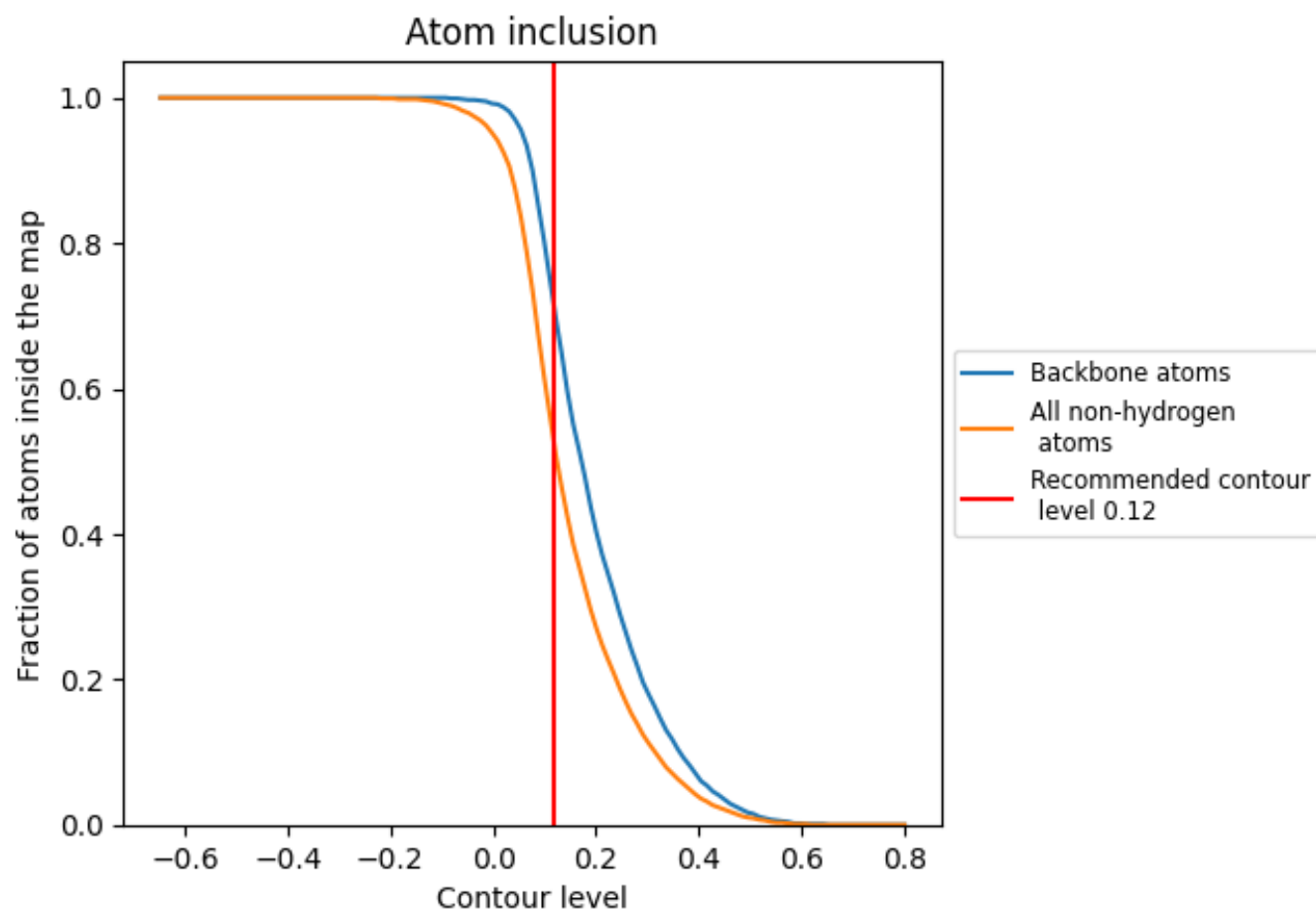
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 52% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5180	0.2820
A	0.5180	0.2820

