



Full wwPDB EM Validation Report ⓘ

Apr 17, 2025 – 12:55 PM EDT

PDB ID : 8GMJ / pdb_00008gmj
EMDB ID : EMD-40227
Title : CryoEM structure of P-Glycoprotein in collapsed closed state under continuous turnover conditions with verapamil
Authors : Culbertson, A.; Liao, M.
Deposited on : 2023-03-26
Resolution : 4.40 Å(reported)

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

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A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
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) : 2.42

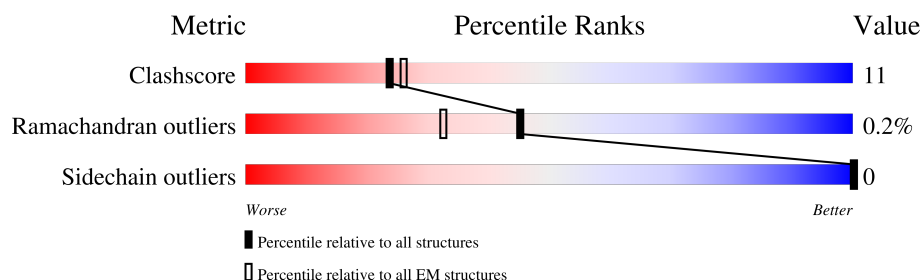
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
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	1280	<div> <div>38%</div> <div>81%</div> <div>9%</div> <div>11%</div> </div>

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
3	ATP	A	1304	-	-	X	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7960 atoms, of which 2194 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.

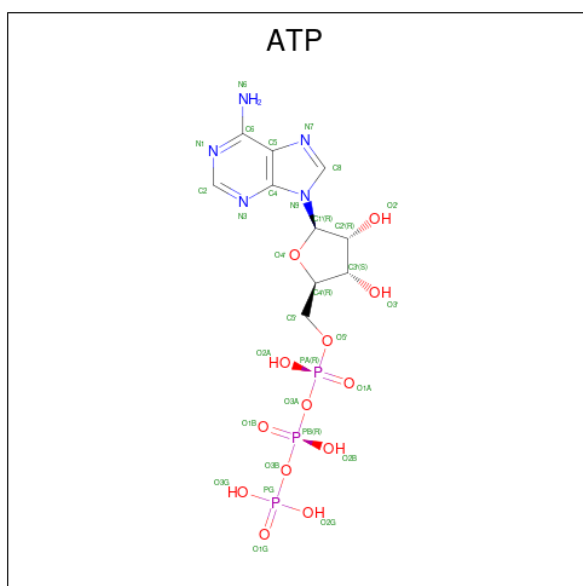
- Molecule 1 is a protein called ATP-dependent translocase ABCB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
1	A	1145	7872	3408	2170	1145	1149	0	0

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
2	A	2	2	2	0

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).

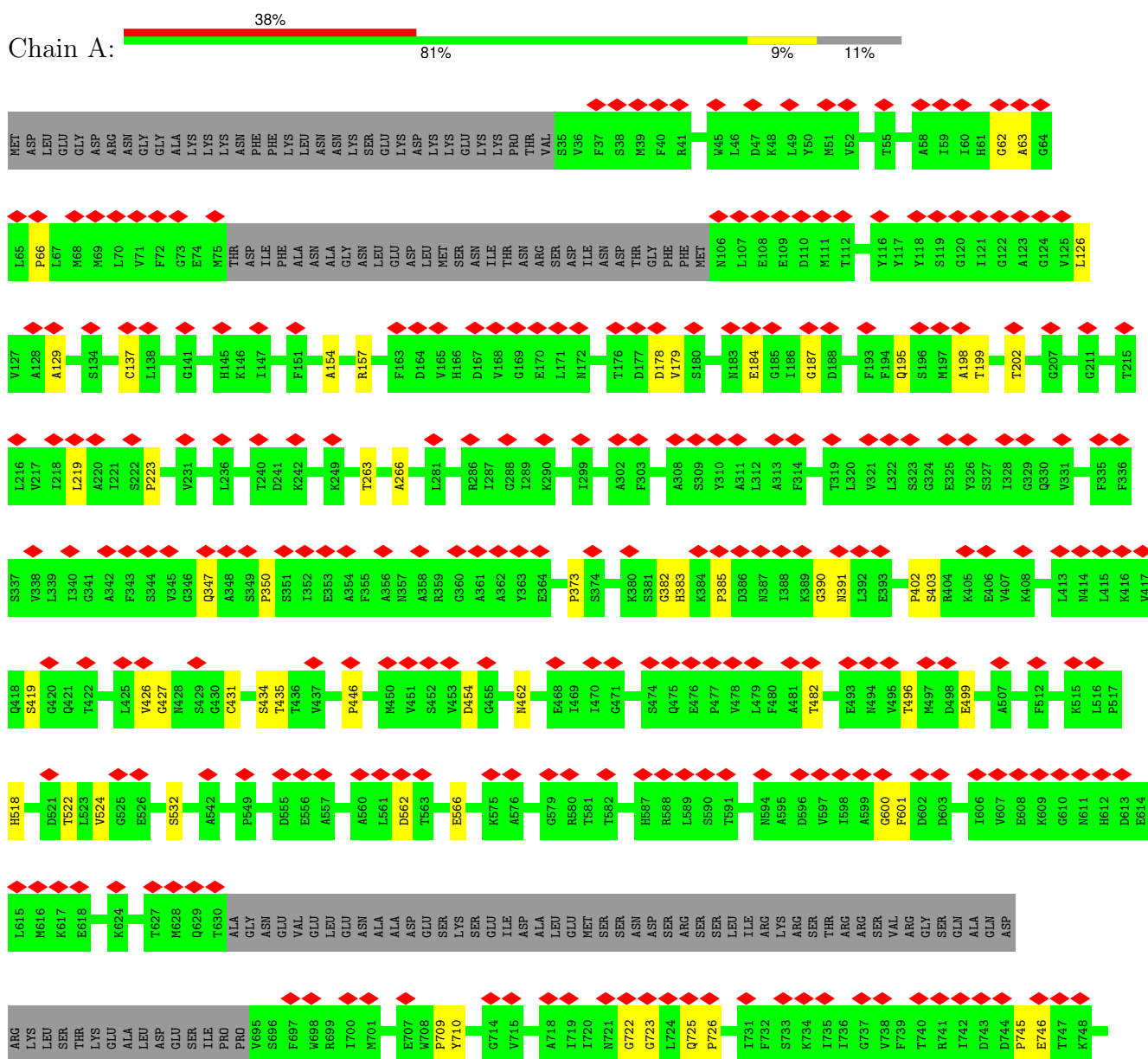


Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
3	A	1	43	10	12	5	13	3	0
3	A	1	43	10	12	5	13	3	0

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: ATP-dependent translocase ABCB1



THR LYS ARG GLN	E1201	D1088	K1014	R833	G830	H751
	A1202	P1089	T1015	K934	A834	S752
	T1203	L1090	L1017	H836	W835	F755
	S1204	A1091	I1018	I937	I836	S756
	A1205	G1092	D1019	F938	T837	L757
	L1206	K1093	S1020	S943	Q838	L758
D1207	V1094	T1023	F944	A841	F759	
T1208	L1095	E1024	T945	M842	L760	
K1220	L1096	G1025	Q946	L843	A761	
A1221	D1097	L1026	A947	G844	L762	
G1224	G1098	M948	M948	T845	G763	
C1227	E1100	M949	M949	G846	I764	
	I1228	I1101	P1028	I847	I765	
	H1232	K1102	N1029	I848	S766	
R1233	R1103	T1030	S952	I849	F767	
L1234	L1104	L1031	Y953	S850	I768	
S1235	L1109	E1032	A954	F851	I769	
T1236	R1110	G1033	G955	I852	F770	
N1239	A1111	N1034	C956	Y853	F771	
	H1112	A1111	F957	G854	L772	
	L1113	T1036	R958	W855	Q773	
A1240	V1116	F1037	F959	I857	G774	
D1241	S1117	Y1040	G960	T858	F775	
L1242	Q1118	V1041	A961	I776	F777	
I1243	E1119	Y1044	Y962	L859	G778	
V1244	P1120	P1045	V964	L862	G781	
V1245	F1233	T1046	A965	I863		
F1246	D1124	R1047	H966	I864	L784	
Q1247	C1125	P1048	K967	P866	Y790	
N1248	G1134	D1049	L968	I867		
G1249	R1250	I1050	M969	I868	D800	
R1250	D1135	P1051	S970	A869	V801	
V1251	N1136	G1055	F971	I870	D805	
K1252	S1137	L1056	E972	A871		
E1253	A1150	S1057	A980	G872	D806	
H1254	E1151	L1058	V981	V873	P807	
G1255	A1152	E1059	V982	G881	K808	
T1256	T1256	V1060	F983	Q882	N809	
H1257	L1161	K1061	G984	A883	T810	
Q1258	A1168	T1065	A985	L884	T811	
Q1259	V1169	L1066	M986	K895	G812	
L1260	G1170	A1067	A987	G894	A813	
L1261	D1171	L1068	V988	R905	L814	
A1262	K1172	V1069	G989	Q922	T815	
Q1263	G1173	G1070	Q990	S923	T816	
K1264	T1174	S1071	V991	I924	A819	
G1265	Q1175	S1072	S992	L924	N820	
I1266	P1194	G1073	A995	P927	A823	
S1269	L1198	C1074	P996	Y928	Q824	
M1270	L1199	K1075	D997	Y998	V825	
V1271	D1200	S1077	A999	K1000	K826	
S1272	GLN	T1078	A1001	A1001	G827	
V1273		L1082	I829			
ALA	GLY					

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	33409	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 ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.133	Depositor
Minimum map value	-0.068	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.049	Depositor
Map size (Å)	128.26, 126.13999, 155.81999	wwPDB
Map dimensions	121, 119, 147	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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: ATP, MG

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	0/5727	0.49	0/7978

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5702	2170	2848	92	0
2	A	2	0	0	0	0
3	A	62	24	24	12	0
All	All	5766	2194	2872	92	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 11.

All (92) 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:1077:SER:HB2	3:A:1304:ATP:PA	2.16	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:726:PRO:HB3	1:A:846:GLY:HA2	1.58	0.83
1:A:996:PRO:HD2	1:A:997:ASP:H	1.48	0.79
1:A:726:PRO:HG3	1:A:845:THR:C	2.02	0.78
1:A:62:GLY:HA3	1:A:195:GLN:O	1.83	0.78
1:A:63:ALA:HB2	1:A:198:ALA:HB1	1.67	0.75
1:A:435:THR:N	3:A:1303:ATP:O2A	2.19	0.75
1:A:126:LEU:CB	1:A:947:ALA:HB2	2.20	0.72
1:A:391:ASN:O	1:A:454:ASP:N	2.23	0.71
1:A:726:PRO:CB	1:A:846:GLY:HA2	2.20	0.70
1:A:709:PRO:HD2	1:A:710:TYR:H	1.57	0.70
1:A:1040:VAL:C	1:A:1055:GLY:HA2	2.14	0.68
1:A:828:ALA:HB2	1:A:1001:ALA:HB2	1.75	0.68
1:A:382:GLY:HA3	1:A:462:ASN:HA	1.73	0.68
1:A:1096:LEU:N	1:A:1099:LYS:O	2.26	0.68
1:A:402:PRO:HD2	1:A:403:SER:H	1.57	0.67
1:A:390:GLY:O	1:A:419:SER:N	2.29	0.66
1:A:745:PRO:HD2	1:A:746:GLU:H	1.59	0.66
1:A:426:VAL:O	1:A:600:GLY:HA2	1.98	0.62
1:A:726:PRO:HG3	1:A:846:GLY:N	2.14	0.62
1:A:1041:VAL:O	1:A:1091:ALA:N	2.26	0.61
1:A:927:PRO:HD2	1:A:928:TYR:H	1.66	0.61
1:A:963:LEU:O	1:A:967:LYS:N	2.35	0.60
1:A:1077:SER:HB2	3:A:1304:ATP:O1A	2.01	0.59
1:A:1075:GLY:HA2	3:A:1304:ATP:H5'1	1.88	0.56
1:A:828:ALA:CB	1:A:1001:ALA:HB2	2.35	0.55
1:A:1041:VAL:N	1:A:1091:ALA:O	2.33	0.54
1:A:722:GLY:HA3	1:A:841:ALA:HB1	1.89	0.54
1:A:1077:SER:HB2	3:A:1304:ATP:O2A	2.07	0.54
1:A:865:VAL:N	1:A:866:PRO:HD2	2.22	0.54
1:A:1069:VAL:O	1:A:1246:PHE:N	2.41	0.54
1:A:924:LEU:O	1:A:927:PRO:HD2	2.08	0.53
1:A:1116:VAL:N	1:A:1198:LEU:O	2.38	0.53
1:A:1044:TYR:HB2	1:A:1047:ARG:CB	2.38	0.53
1:A:723:GLY:HA2	1:A:845:THR:CB	2.39	0.53
1:A:482:THR:O	1:A:524:VAL:N	2.40	0.52
1:A:383:HIS:O	1:A:462:ASN:N	2.35	0.52
1:A:1073:GLY:HA2	3:A:1304:ATP:O1B	2.10	0.52
1:A:66:PRO:HG3	1:A:199:THR:O	2.09	0.52
1:A:66:PRO:HG2	1:A:202:THR:CB	2.40	0.51
1:A:1112:HIS:O	1:A:1194:PRO:HB3	2.10	0.50
1:A:722:GLY:HA3	1:A:841:ALA:C	2.32	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:810:THR:H	1:A:813:ALA:HB3	1.75	0.49
1:A:518:HIS:O	1:A:522:THR:N	2.46	0.49
1:A:745:PRO:HD2	1:A:746:GLU:N	2.27	0.49
1:A:1123:PHE:O	1:A:1125:CYS:N	2.46	0.49
1:A:1075:GLY:O	1:A:1078:THR:N	2.45	0.49
1:A:402:PRO:HD2	1:A:403:SER:N	2.25	0.49
1:A:996:PRO:HD2	1:A:997:ASP:N	2.22	0.48
1:A:722:GLY:HA3	1:A:841:ALA:CB	2.44	0.48
1:A:434:SER:HB2	3:A:1303:ATP:O2A	2.14	0.47
1:A:178:ASP:O	1:A:179:VAL:C	2.52	0.47
1:A:726:PRO:HB3	1:A:846:GLY:CA	2.37	0.47
1:A:427:GLY:HA3	1:A:601:PHE:CB	2.43	0.47
1:A:709:PRO:HD2	1:A:710:TYR:N	2.28	0.47
1:A:850:SER:O	1:A:854:GLY:N	2.44	0.47
1:A:828:ALA:CB	1:A:1001:ALA:CB	2.93	0.46
1:A:154:ALA:O	1:A:157:ARG:N	2.49	0.46
1:A:562:ASP:O	1:A:566:GLU:N	2.32	0.46
1:A:810:THR:N	1:A:813:ALA:HB3	2.30	0.46
1:A:385:PRO:HD2	1:A:385:PRO:O	2.15	0.46
1:A:1047:ARG:N	1:A:1048:PRO:CD	2.78	0.46
1:A:137:CYS:CB	1:A:935:ALA:HB1	2.45	0.46
1:A:1113:LEU:HA	1:A:1194:PRO:HB2	1.96	0.46
1:A:129:ALA:HB3	1:A:943:SER:CB	2.46	0.45
1:A:1120:PRO:O	1:A:1120:PRO:HD2	2.17	0.45
1:A:446:PRO:HD2	1:A:446:PRO:O	2.17	0.45
1:A:62:GLY:O	1:A:66:PRO:HD2	2.17	0.45
1:A:1076:LYS:CB	3:A:1304:ATP:O2B	2.65	0.45
1:A:263:THR:O	1:A:266:ALA:HB3	2.17	0.45
1:A:1073:GLY:CA	3:A:1304:ATP:O1B	2.64	0.45
1:A:347:GLN:O	1:A:350:PRO:HD2	2.17	0.44
1:A:1066:LEU:O	1:A:1228:ILE:HA	2.17	0.44
1:A:431:CYS:CB	1:A:601:PHE:CB	2.95	0.44
1:A:373:PRO:O	1:A:373:PRO:HD2	2.18	0.44
1:A:1045:PRO:O	1:A:1048:PRO:HD3	2.17	0.44
1:A:826:LYS:O	1:A:830:GLY:N	2.51	0.43
1:A:1070:GLY:HA3	1:A:1246:PHE:CB	2.49	0.43
1:A:1175:GLN:O	3:A:1303:ATP:C4	2.71	0.43
1:A:1069:VAL:N	1:A:1244:VAL:O	2.39	0.42
1:A:219:LEU:O	1:A:223:PRO:HD2	2.19	0.42
1:A:1194:PRO:O	1:A:1194:PRO:HD2	2.20	0.42
1:A:996:PRO:CD	1:A:997:ASP:H	2.26	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:GLY:HA3	1:A:195:GLN:C	2.40	0.41
1:A:129:ALA:HB3	1:A:943:SER:HA	2.02	0.41
1:A:532:SER:CB	3:A:1304:ATP:O5'	2.68	0.41
1:A:927:PRO:HD2	1:A:928:TYR:N	2.32	0.41
1:A:1044:TYR:CB	3:A:1304:ATP:C2	3.03	0.41
1:A:725:GLN:CB	1:A:726:PRO:CD	2.98	0.41
1:A:126:LEU:CB	1:A:947:ALA:CB	2.93	0.40
1:A:722:GLY:O	1:A:726:PRO:HD2	2.22	0.40
1:A:496:THR:O	1:A:499:GLU:N	2.53	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	1139/1280 (89%)	1091 (96%)	46 (4%)	2 (0%)	44 78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	GLU
1	A	187	GLY

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	30/1064 (3%)	30 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	ATP	A	1304	2	28,33,33	0.78	0	34,52,52	0.84	1 (2%)
3	ATP	A	1303	2	28,33,33	0.91	2 (7%)	34,52,52	0.98	3 (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
3	ATP	A	1304	2	-	5/18/38/38	0/3/3/3
3	ATP	A	1303	2	-	5/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1303	ATP	PA-O3A	-2.37	1.56	1.59
3	A	1303	ATP	PB-O3B	-2.04	1.57	1.59

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1303	ATP	C5-C6-N6	2.31	123.83	120.31
3	A	1303	ATP	O3'-C3'-C2'	-2.19	104.79	111.82
3	A	1303	ATP	O2'-C2'-C3'	-2.19	104.80	111.82
3	A	1304	ATP	C5-C6-N6	2.19	123.64	120.31

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1303	ATP	PB-O3B-PG-O3G
3	A	1303	ATP	C5'-O5'-PA-O1A
3	A	1303	ATP	C5'-O5'-PA-O3A
3	A	1304	ATP	PB-O3B-PG-O2G
3	A	1304	ATP	PA-O3A-PB-O3B
3	A	1303	ATP	C5'-O5'-PA-O2A
3	A	1303	ATP	O4'-C4'-C5'-O5'
3	A	1304	ATP	C3'-C4'-C5'-O5'
3	A	1304	ATP	PA-O3A-PB-O1B
3	A	1304	ATP	O4'-C4'-C5'-O5'

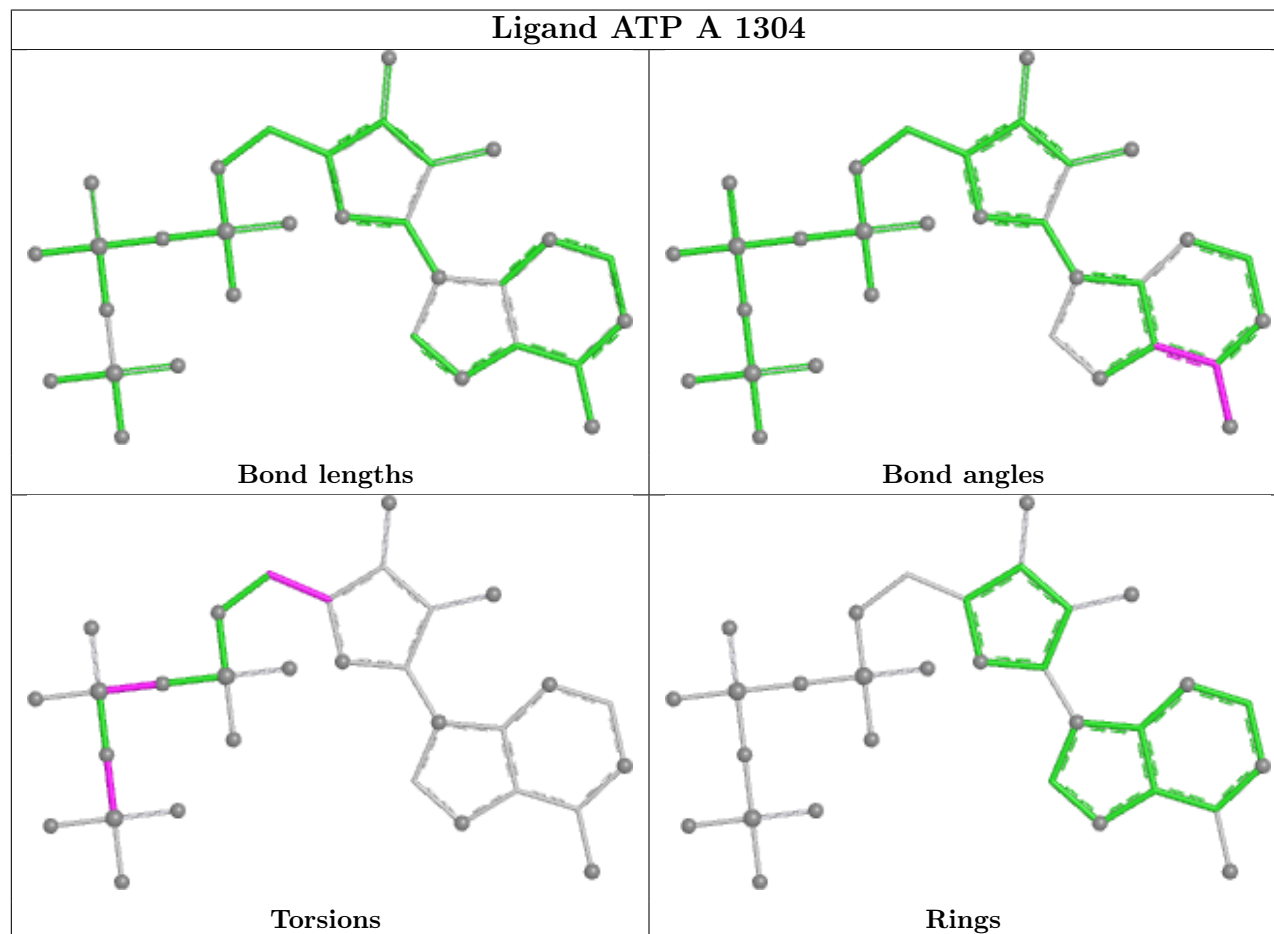
There are no ring outliers.

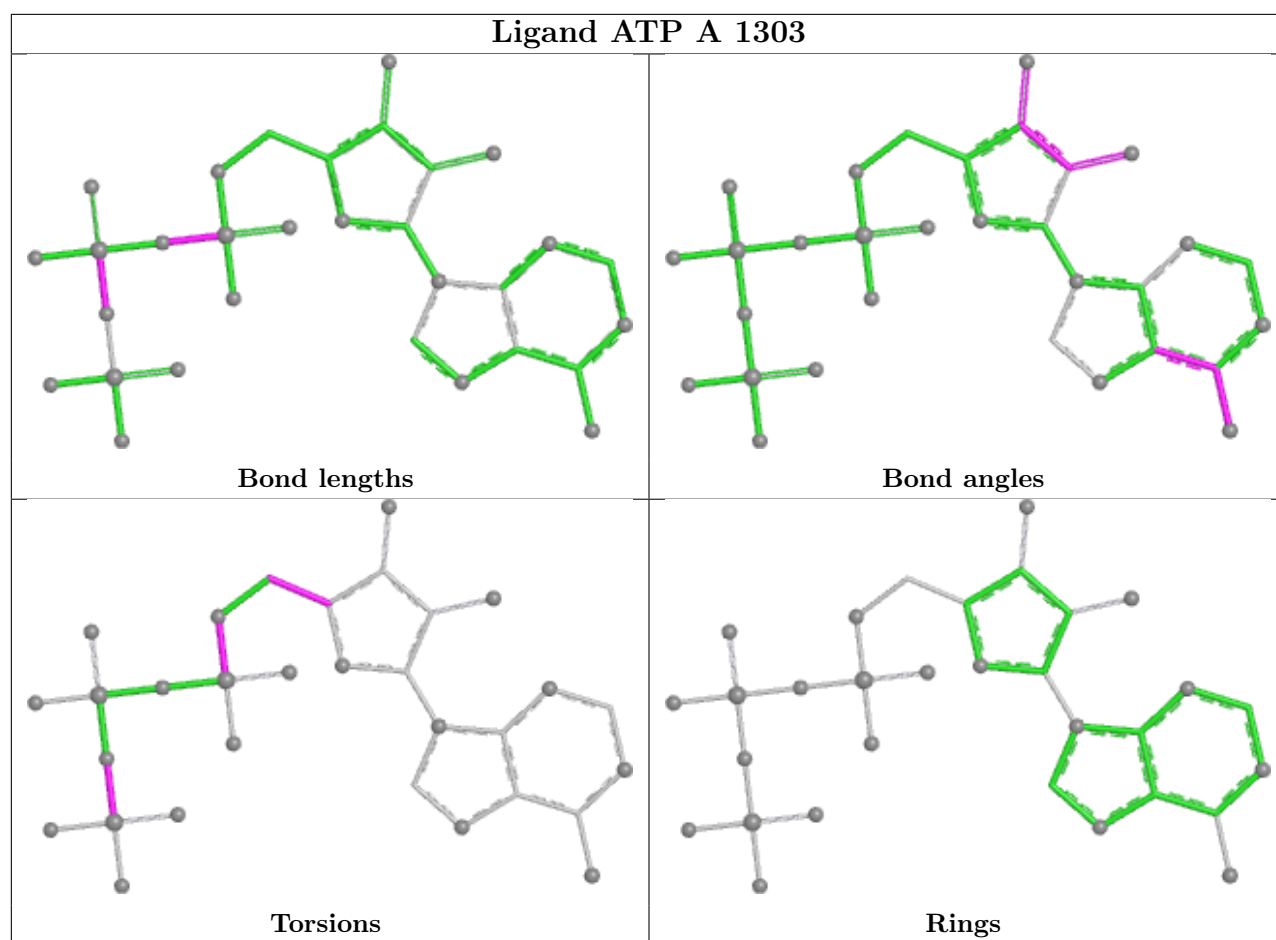
2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1304	ATP	9	0
3	A	1303	ATP	3	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.

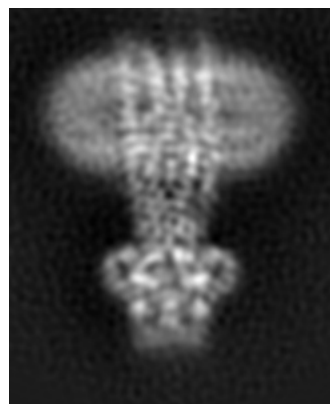
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40227. These allow visual inspection of the internal detail of the map and identification of artifacts.

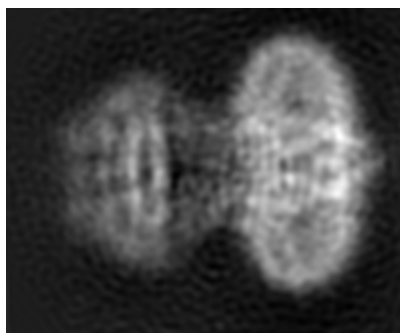
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

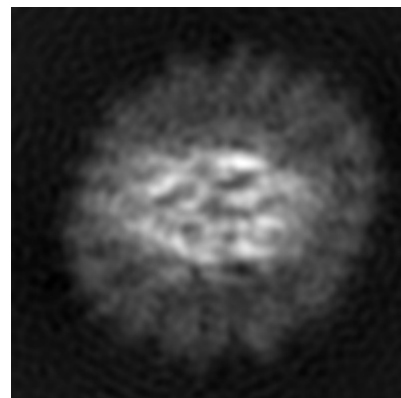
6.1.1 Primary map



X

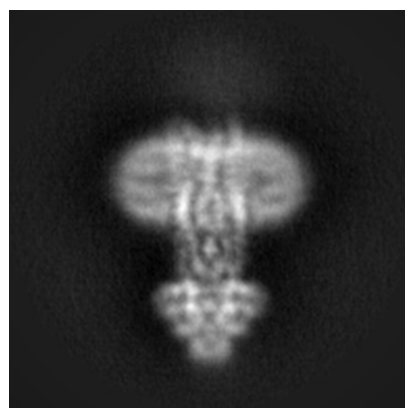


Y

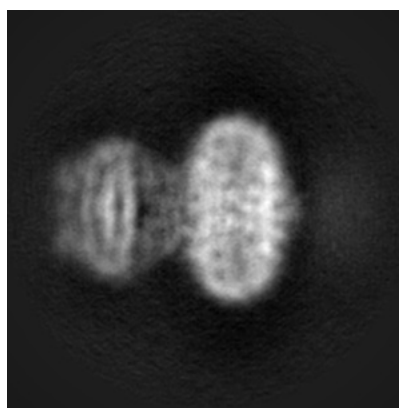


Z

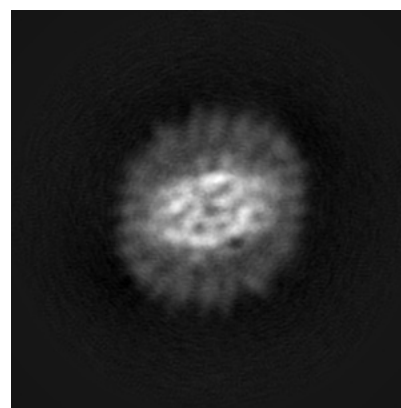
6.1.2 Raw map



X



Y



Z

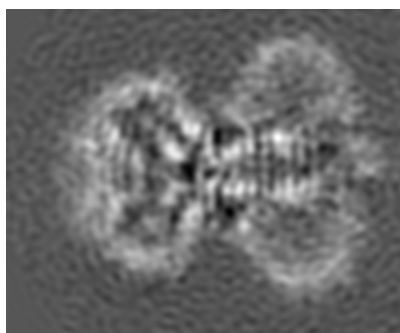
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

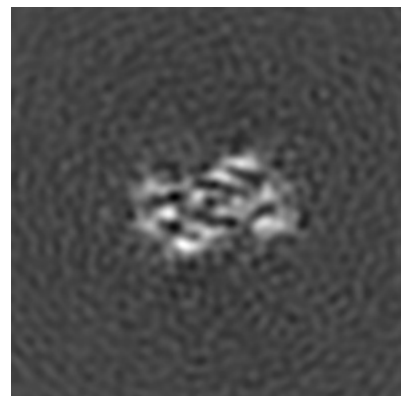
6.2.1 Primary map



X Index: 60



Y Index: 59

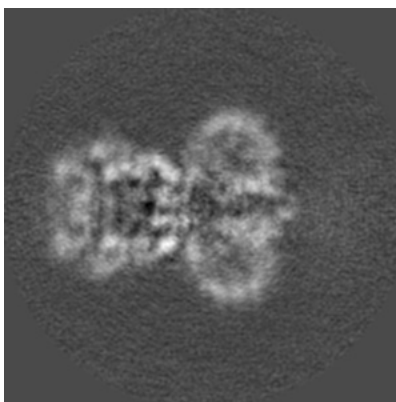


Z Index: 73

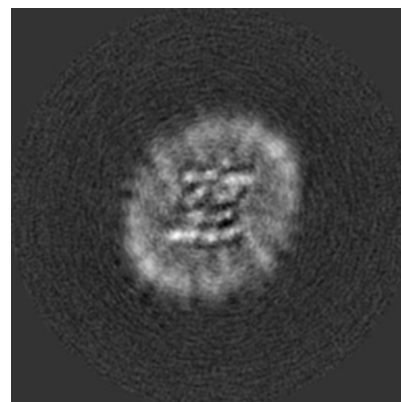
6.2.2 Raw map



X Index: 96



Y Index: 96

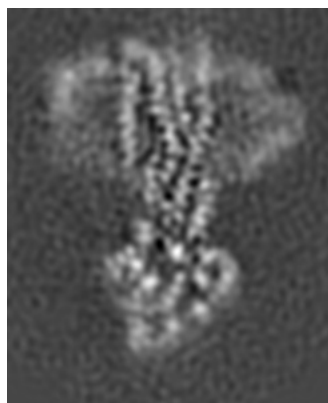


Z Index: 96

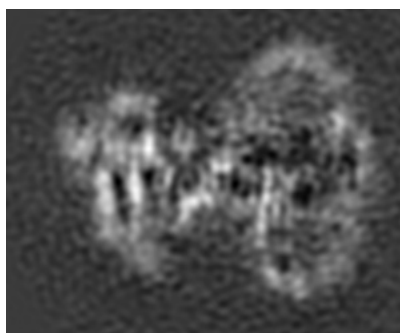
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

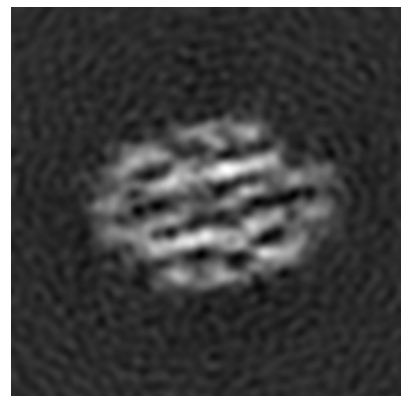
6.3.1 Primary map



X Index: 72

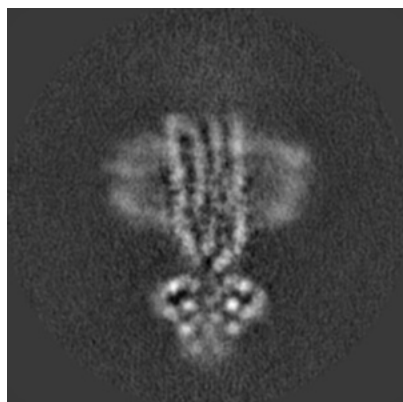


Y Index: 48

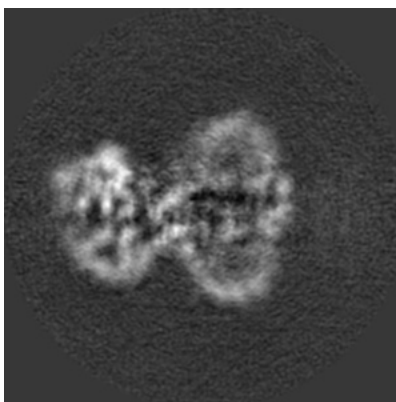


Z Index: 47

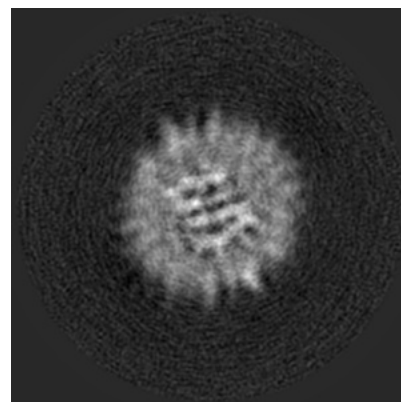
6.3.2 Raw map



X Index: 98



Y Index: 87

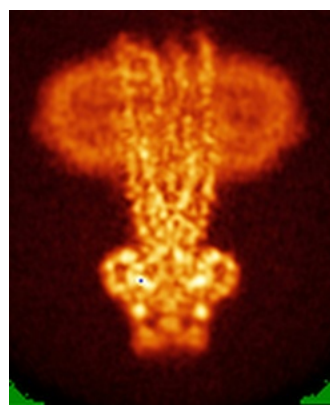


Z Index: 124

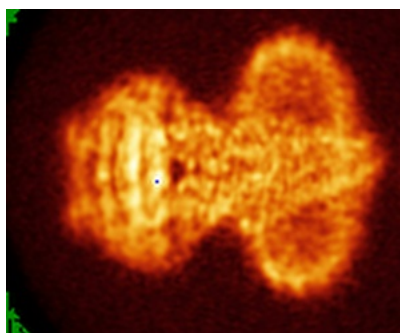
The images above show the largest variance slices of the map in three orthogonal directions.

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

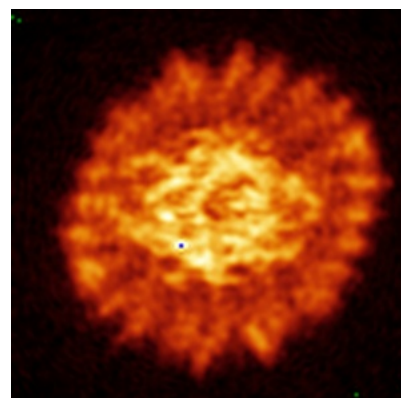
6.4.1 Primary map



X



Y

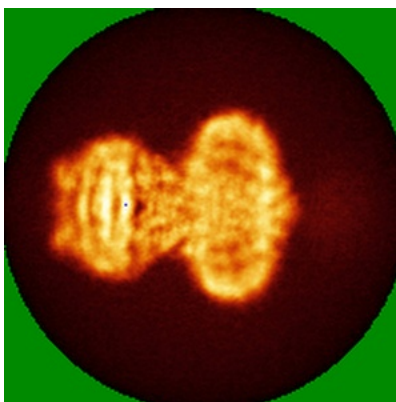


Z

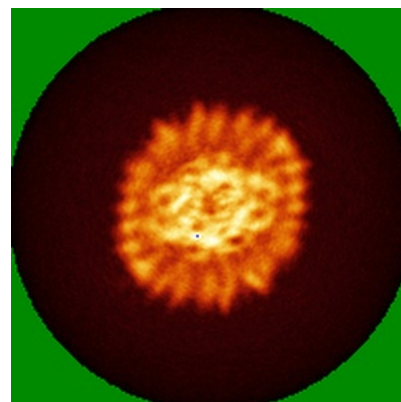
6.4.2 Raw map



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.

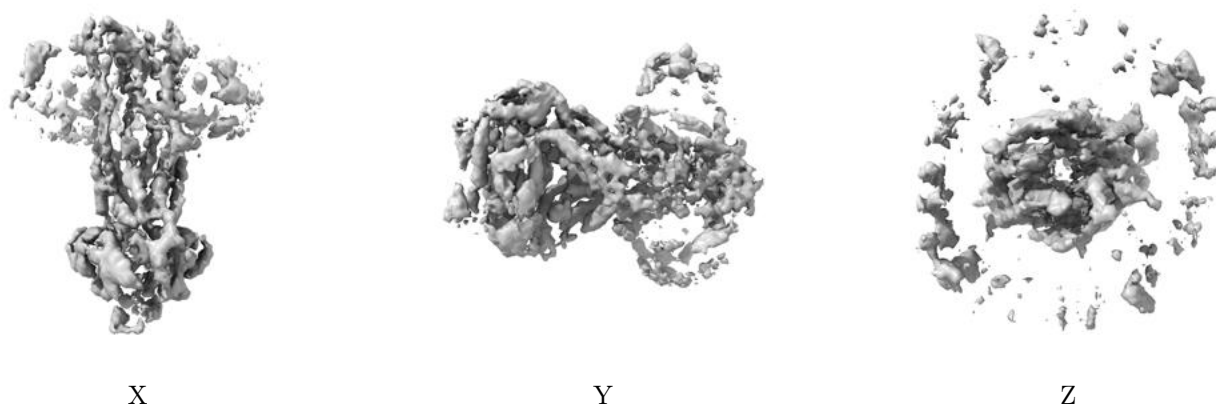
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.049. 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.

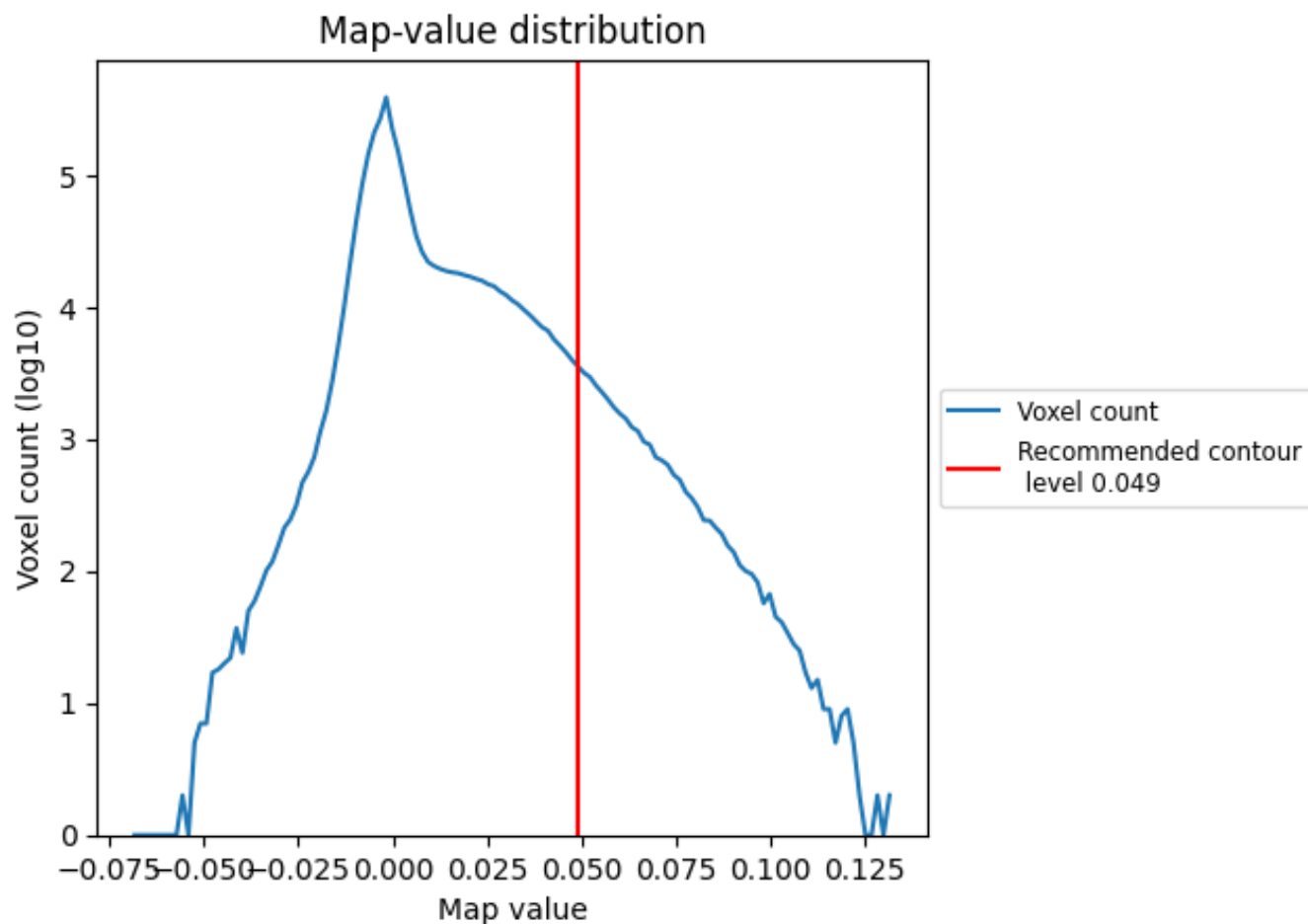
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

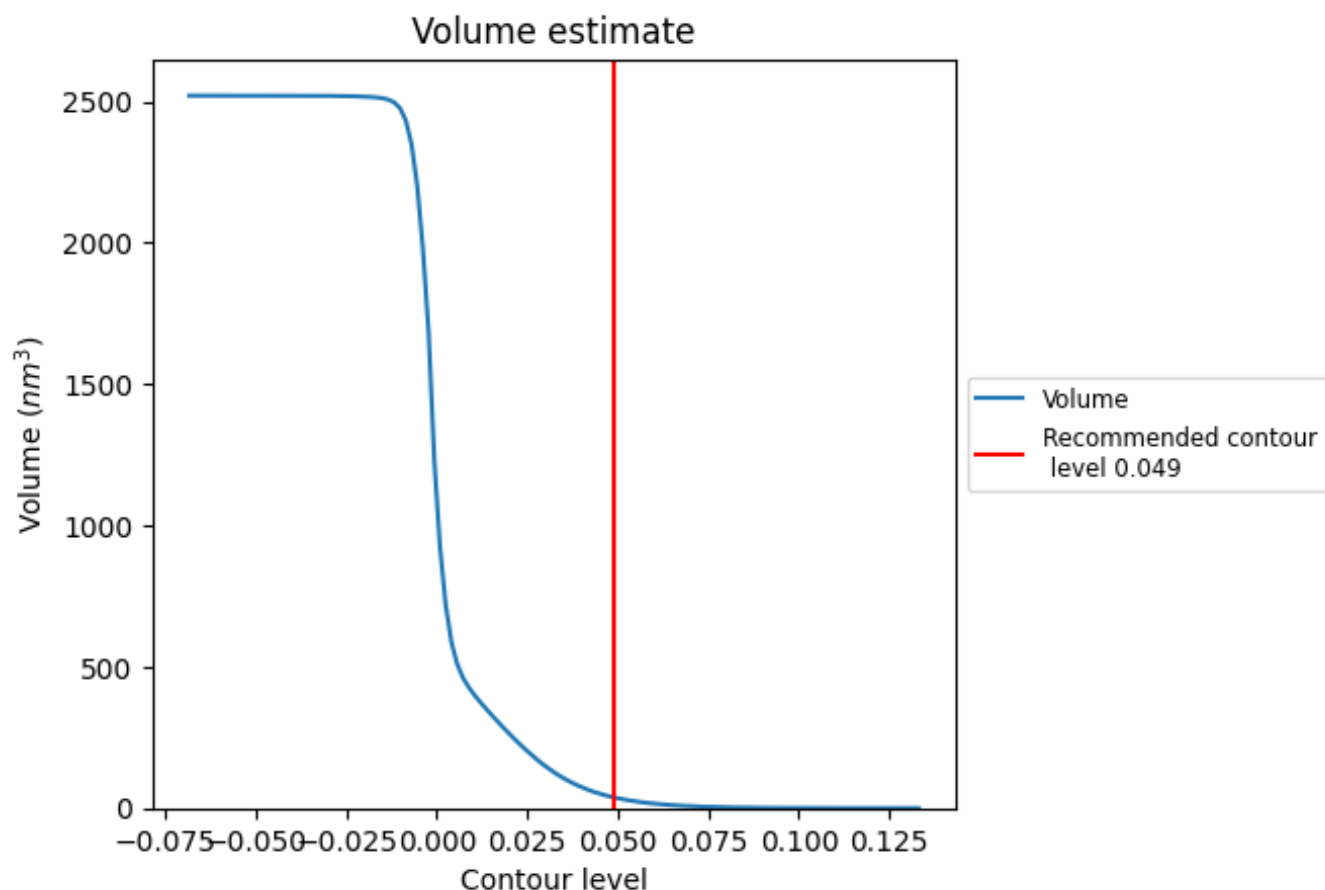
This section contains the results of statistical analysis of the map.

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 38 nm³; this corresponds to an approximate mass of 34 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.

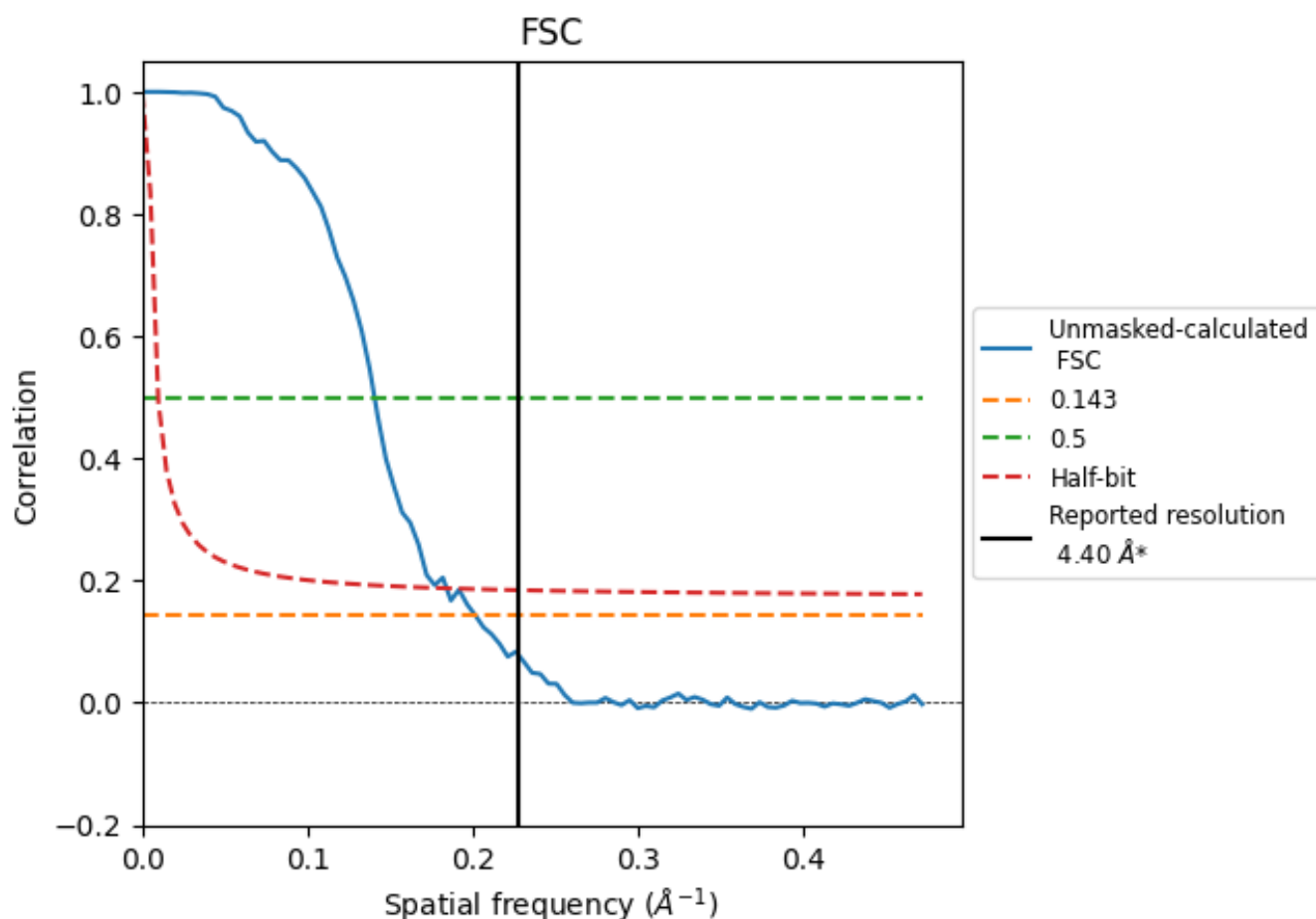
7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

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 0.227 \AA^{-1}

8.2 Resolution estimates [i](#)

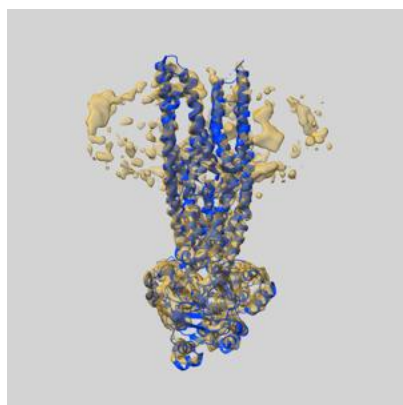
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.97	7.12	5.43

*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 4.97 differs from the reported value 4.4 by more than 10 %

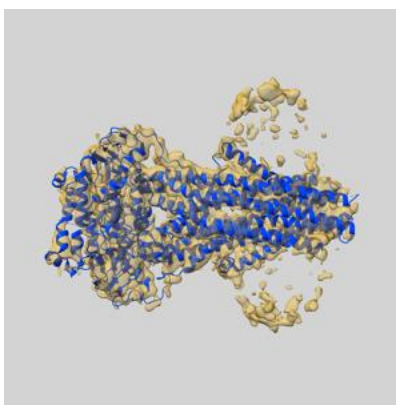
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40227 and PDB model 8GMJ. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

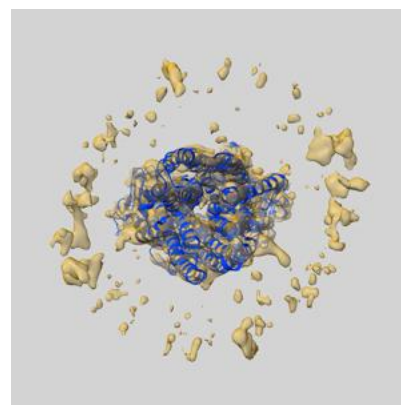
9.1 Map-model overlay [i](#)



X



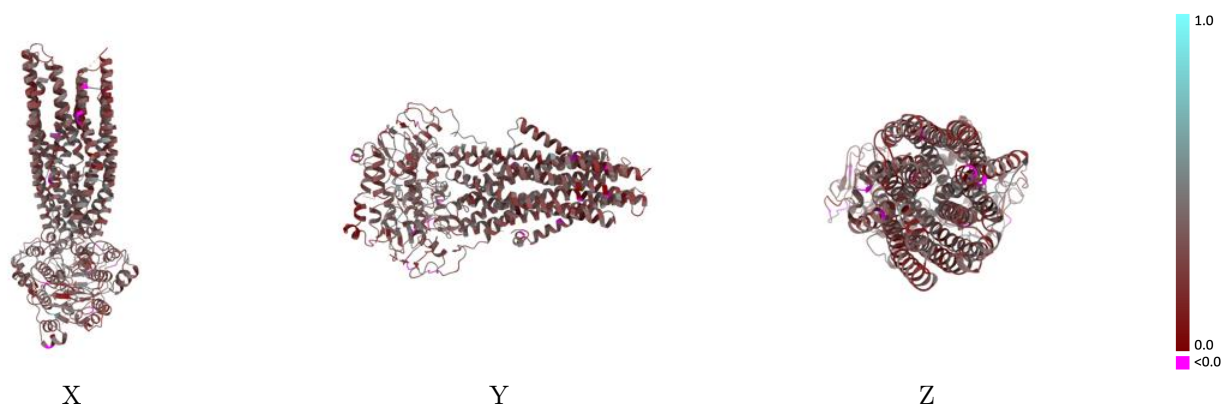
Y



Z

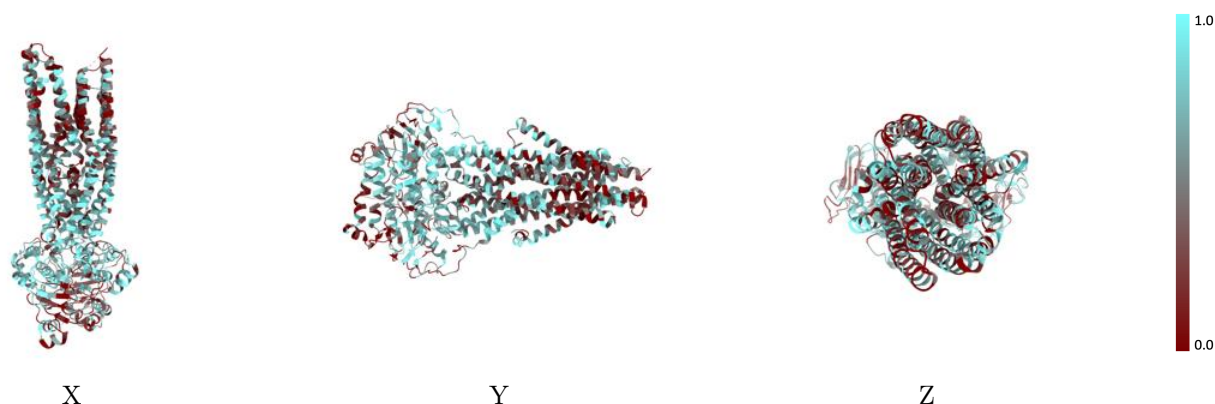
The images above show the 3D surface view of the map at the recommended contour level 0.049 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



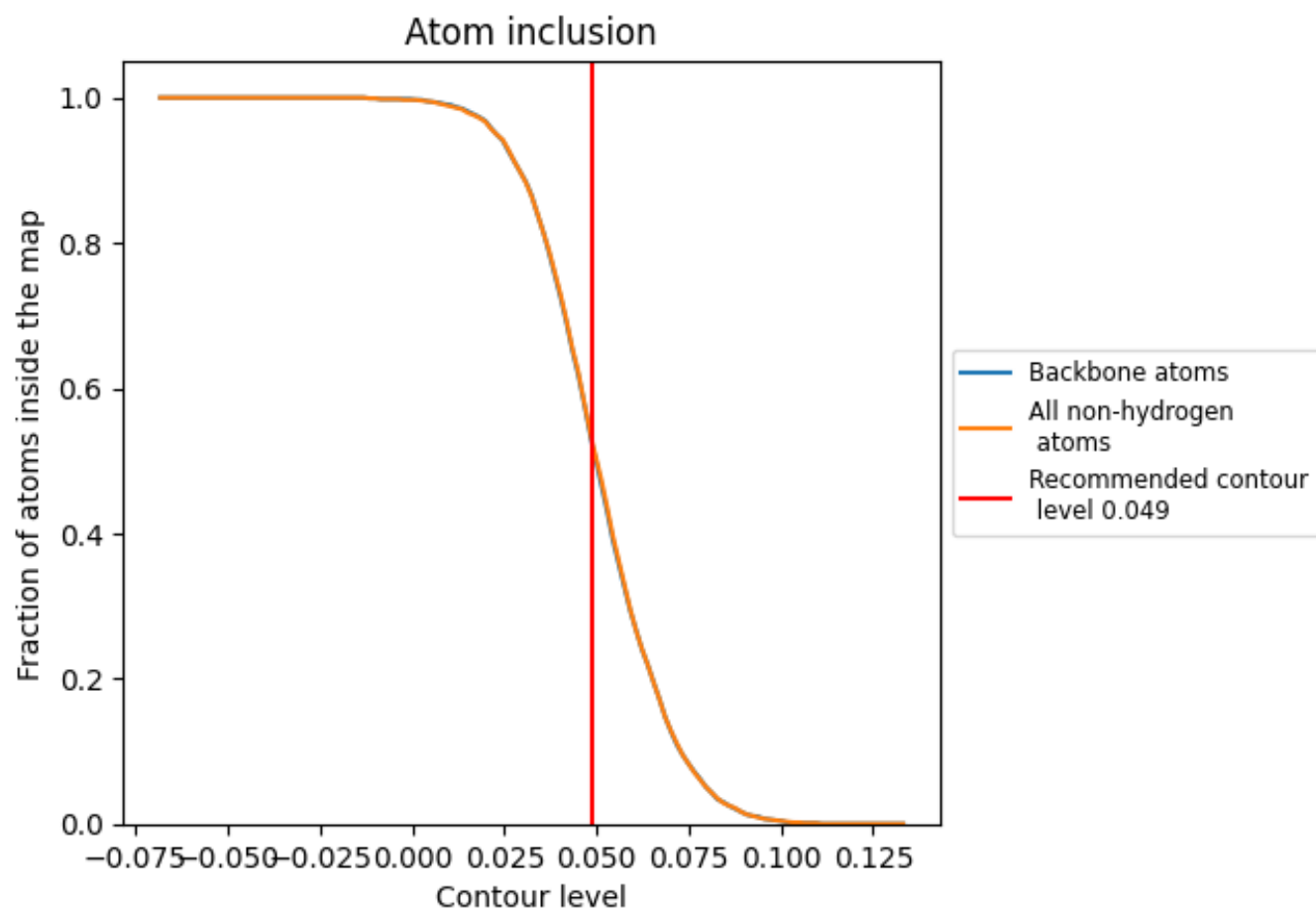
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.049).

9.4 Atom inclusion [i](#)



At the recommended contour level, 52% 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 (0.049) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5210	<div></div> 0.3180
A	<div></div> 0.5270	<div></div> 0.3180

