



Full wwPDB EM Validation Report ⓘ

Aug 5, 2026 – 06:27 AM EDT

PDB ID : 7SI6 / pdb_00007si6
EMDB ID : EMD-25138
Title : Structure of ATP7B in state 1
Authors : Bitter, R.M.; Oh, S.C.; Hite, R.K.; Yuan, P.
Deposited on : 2021-10-12
Resolution : 3.32 Å(reported)
Based on initial model : 3RFU

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.dev133
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) : 2.50

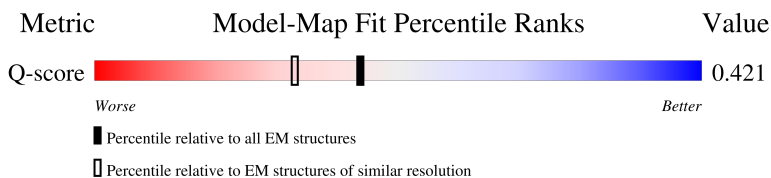
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.32 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14518 (2.82 - 3.82)

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	1467	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13515 atoms, of which 6910 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 P-type Cu(+) transporter.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	873	13509	4239	6910	1109	1202	49	0	0

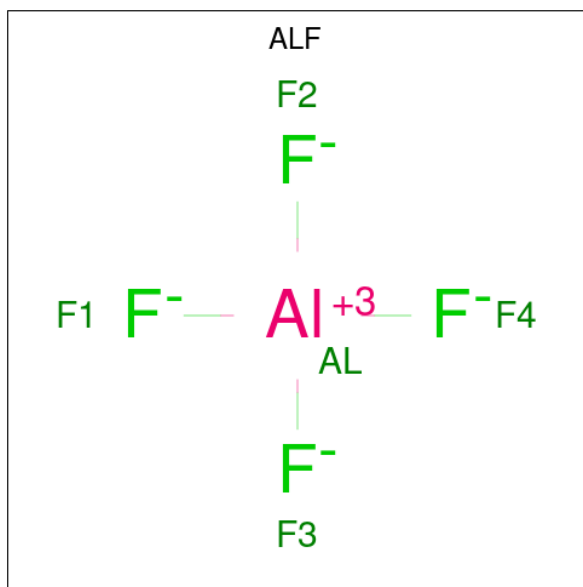
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	271	HIS	ARG	conflict	UNP A0A6I8R0A5
A	359	ILE	MET	conflict	UNP A0A6I8R0A5
A	497	ILE	ALA	conflict	UNP A0A6I8R0A5

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	Mg	0
			1	1	

- Molecule 3 is TETRAFLUOROALUMINATE ION (CCD ID: ALF) (formula: AlF_4) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
			Total	Al	F	
3	A	1	5	1	4	0

ARG	HIS	GLY	SER	LEU	VAL	GLU	GLN	GLN	ASP	LYS	TRP	SER	LEU	LEU	ILE	ASN	ASN	GLU	THR	HIS	GLU	ASP	MET	ILE																																				
P1351	A1352	V1355	L1356	Q1357	M1365	K1384	P1385	D1386	S1387	D1388	R1389	Y1390	E1391	A1392	R1393	A1394	Q1395	G1396	H1397	M1398	K1399	S1404	H1409	D1413	D1414	R1415	W1416	R1417	ASP	LEU	PRO	LYS	THR	LYS	ALA	TRP	ASP	GLN	ILE	SER	TYR	ILE	SER	GLN	VAL	SER	ARG	ALA	ALA	PRO	D1312	V1313	S1316	I1336	Y1337	N1338	M1350			
H1166	I1167	S1168	T1169	D1170	V1171	D1172	E1173	A1174	M1175	S1176	S1177	H1178	E1179	M1180	K1181	G1182	Q1183	T1184	A1185	V1186	L1187	V1188	A1189	I1190	D1191	G1192	E1193	L1194	C1195	G1196	M1197	I1198	A1199	I1200	A1201	I1236	A1237	V1240	G1241	V1258	M1276	A1301	D1302	D1312	V1313	S1316	I1336	Y1337	N1338	M1350										
T1106	E1107	S1108	V1109	L1110	V1111	Q1112	ASN	GLU	GLU	GLY	LEU	ASN	GLN	SER	TYR	ARG	ASN	SER	LEU	ILE	GLY	THR	ASP	SER	SER	LEU	ILE	THR	PRO	GLU	LEU	LEU	ALA	GLN	ALA	PRO	LEU	ALA	H1150	T1151	V1152	L1153	I1154	G1155	M1156	R1157	E1158	W1159	M1160	R1161	R1162	M1163	G1164	L1165						
V1046	K1047	M1048	P1049	L1050	K1051	R1052	M1053	L1054	A1055	V1056	V1057	G1058	T1059	A1060	E1061	A1062	S1063	S1064	E1065	R956	H1066	P1067	L1068	G1069	M1070	A1071	V1072	T1073	K1074	Y1075	C1076	K1077	E1078	E1079	L1080	G1081	T1082	E1083	L1084	L1085	G1086	Y1087	C1088	T1089	D1090	F1091	Q1092	A1093	V1094	P1095	G1096	C1097	G1098	I1099	S1100	C1101	K1102	V1103	N1104	N1105
A871	G872	S873	N874	A875	A876	H877	V880	V897	E901	I925	I926	W936	D945	Y954	S955	R956	N957	I958	F962	Q970	I973	T974	C980	P981	C982	V998	N1002	K1007	M1022	F1023	D1024	K1025	T1026	M1037	R1038	V1039	L1040	L1041	L1042	GLY	ASP	VAL																		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	138790	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	61	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	22.522	Depositor
Minimum map value	-14.195	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size (Å)	102.850006, 99.450005, 148.75	wwPDB
Map dimensions	175, 117, 121	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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: MG, ALF

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	0.10	0/6700	0.25	0/9075

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	6599	6910	6909	63	0
2	A	1	0	0	0	0
3	A	5	0	0	1	0
All	All	6605	6910	6909	63	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 5.

All (63) 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:496:CYS:SG	1:A:499:CYS:N	2.52	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:980:CYS:O	1:A:1338:ASN:ND2	2.17	0.78
1:A:1312:ASP:OD2	1:A:1384:LYS:NZ	2.19	0.74
1:A:855:THR:HG22	1:A:857:GLU:OE1	1.88	0.71
1:A:1046:VAL:N	1:A:1048:MET:SD	2.68	0.66
1:A:1409:HIS:ND1	1:A:1414:ASP:OD2	2.33	0.62
1:A:850:ASP:O	1:A:873:SER:OG	2.15	0.61
1:A:875:ASN:OD1	1:A:876:ALA:N	2.33	0.60
1:A:1026:THR:OG1	3:A:1502:ALF:F2	2.10	0.60
1:A:1355:VAL:O	1:A:1357:GLN:NE2	2.35	0.60
1:A:970:GLN:O	1:A:974:THR:HG23	2.03	0.59
1:A:811:ILE:HG23	1:A:811:ILE:O	2.04	0.58
1:A:1022:MET:HE1	1:A:1258:VAL:HG22	1.84	0.57
1:A:712:TYR:OH	1:A:735:THR:OG1	2.23	0.56
1:A:1153:LEU:HD13	1:A:1159:TRP:HZ2	1.71	0.55
1:A:784:LYS:NZ	1:A:1302:ASP:OD1	2.40	0.54
1:A:1022:MET:HE1	1:A:1258:VAL:CG2	2.39	0.53
1:A:1099:ILE:HB	1:A:1154:ILE:HG22	1.91	0.53
1:A:1183:GLN:CB	1:A:1201:ALA:HB2	2.39	0.53
1:A:685:ILE:HD11	1:A:691:ILE:HG13	1.92	0.52
1:A:1048:MET:SD	1:A:1048:MET:N	2.83	0.51
1:A:839:ASP:OD1	1:A:871:ALA:N	2.38	0.51
1:A:1313:VAL:O	1:A:1316:SER:OG	2.19	0.49
1:A:500:VAL:HG13	1:A:518:VAL:CG1	2.42	0.48
1:A:1007:LYS:NZ	1:A:1301:ALA:O	2.23	0.48
1:A:776:TRP:CE2	1:A:780:ILE:HD11	2.48	0.48
1:A:1022:MET:CE	1:A:1258:VAL:HG22	2.44	0.48
1:A:842:VAL:HG13	1:A:880:VAL:HG13	1.96	0.47
1:A:1092:GLN:O	1:A:1099:ILE:HG23	2.15	0.47
1:A:655:LEU:O	1:A:659:ILE:HG12	2.15	0.46
1:A:516:VAL:HG13	1:A:527:VAL:HG22	1.98	0.46
1:A:1336:ILE:HG23	1:A:1337:TYR:N	2.31	0.46
1:A:1067:PRO:HA	1:A:1070:MET:HE2	1.97	0.46
1:A:925:ILE:HG13	1:A:926:ILE:N	2.30	0.45
1:A:851:GLU:OE2	1:A:861:VAL:HG21	2.17	0.45
1:A:1237:ALA:O	1:A:1241:GLY:N	2.50	0.45
1:A:734:THR:HG22	1:A:764:PRO:HA	1.98	0.44
1:A:877:HIS:ND1	1:A:877:HIS:O	2.51	0.44
1:A:767:LEU:HD23	1:A:982:CYS:SG	2.58	0.44
1:A:1024:ASP:OD1	1:A:1025:LYS:N	2.51	0.43
1:A:685:ILE:H	1:A:685:ILE:HD12	1.82	0.43
1:A:710:TYR:HA	1:A:713:VAL:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:619:ILE:HG22	1:A:624:PHE:O	2.19	0.43
1:A:789:LEU:HD13	1:A:897:VAL:HG13	2.00	0.43
1:A:1183:GLN:HB2	1:A:1201:ALA:HB2	1.99	0.43
1:A:740:TYR:CG	1:A:973:ILE:HD13	2.54	0.43
1:A:744:ILE:HD11	1:A:759:THR:HG22	2.01	0.42
1:A:483:ALA:HB3	1:A:484:PRO:HD3	2.01	0.42
1:A:715:ALA:O	1:A:719:LEU:HD13	2.19	0.42
1:A:1236:ILE:O	1:A:1240:VAL:HG22	2.20	0.42
1:A:811:ILE:HD11	1:A:814:GLU:OE2	2.20	0.42
1:A:766:MET:HG2	1:A:1365:MET:SD	2.60	0.41
1:A:936:TRP:CH2	1:A:1350:MET:HE1	2.55	0.41
1:A:1355:VAL:HG12	1:A:1356:LEU:N	2.36	0.41
1:A:764:PRO:HB2	1:A:765:PRO:HD3	2.02	0.41
1:A:1154:ILE:HD13	1:A:1188:VAL:HG22	2.02	0.41
1:A:1276:ASN:N	1:A:1276:ASN:OD1	2.54	0.41
1:A:729:LEU:CD1	1:A:925:ILE:HD13	2.51	0.41
1:A:877:HIS:O	1:A:877:HIS:CG	2.74	0.41
1:A:658:GLY:O	1:A:661:VAL:HG12	2.21	0.41
1:A:789:LEU:HD11	1:A:901:GLU:HG2	2.01	0.40
1:A:998:VAL:O	1:A:1002:ASN:ND2	2.52	0.40
1:A:789:LEU:HD11	1:A:901:GLU:CG	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	861/1467 (59%)	849 (99%)	12 (1%)	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	724/1254 (58%)	724 (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. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	684	ASN
1	A	721	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	ALF	A	1502	1	4,4,4	1.37	0	-		

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

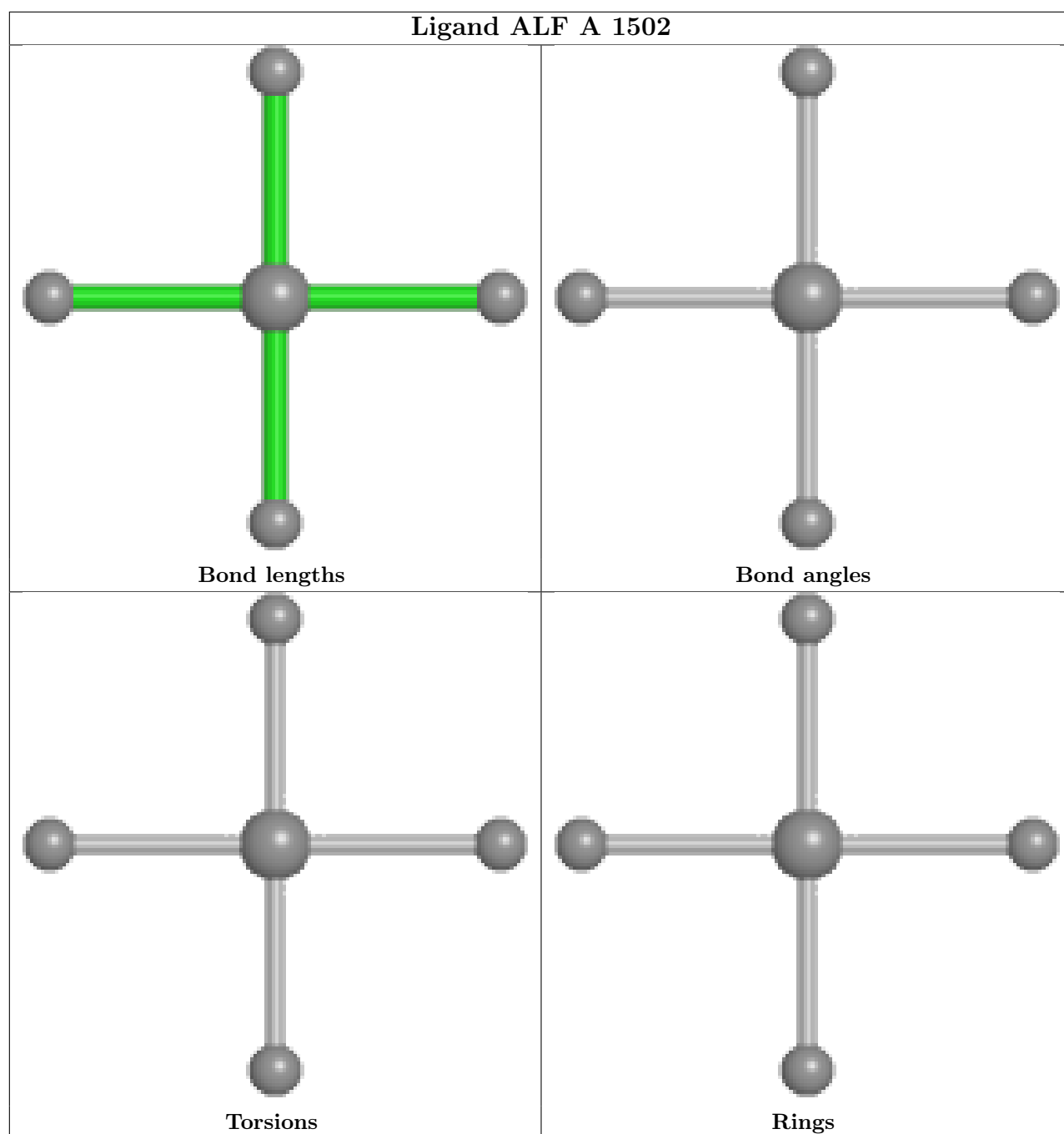
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1502	ALF	1	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.

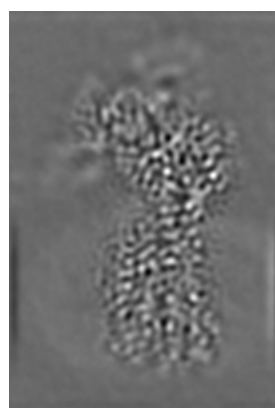
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25138. These allow visual inspection of the internal detail of the map and identification of artifacts.

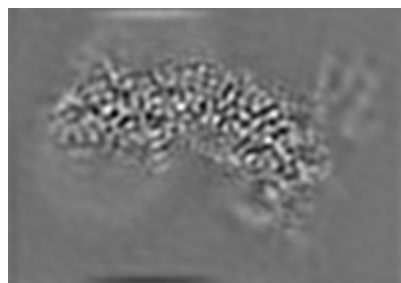
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

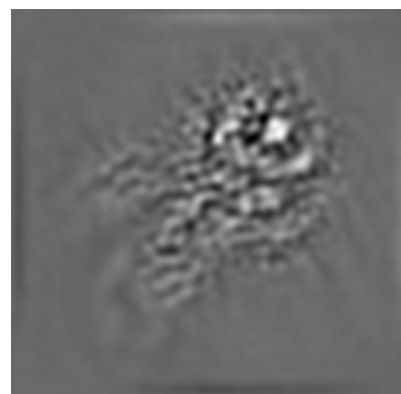
6.1.1 Primary map



X



Y

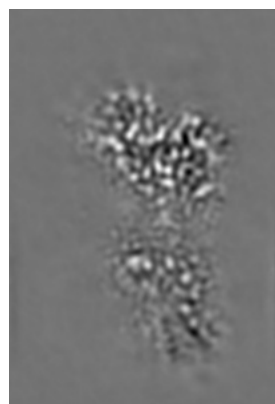


Z

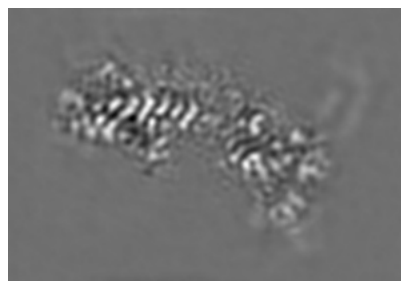
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

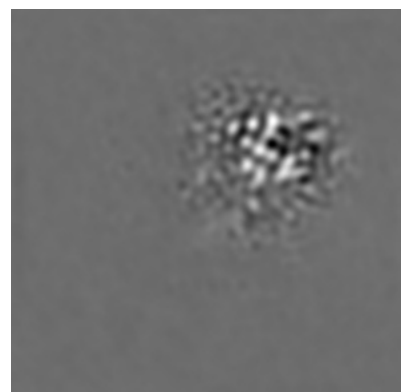
6.2.1 Primary map



X Index: 60



Y Index: 58

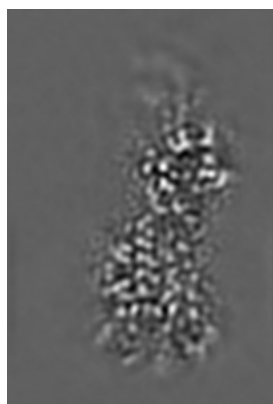


Z Index: 87

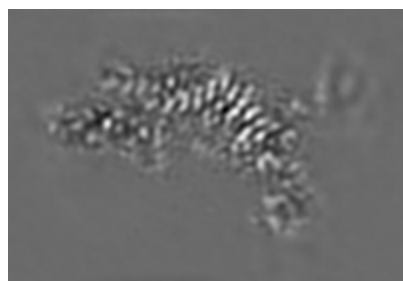
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

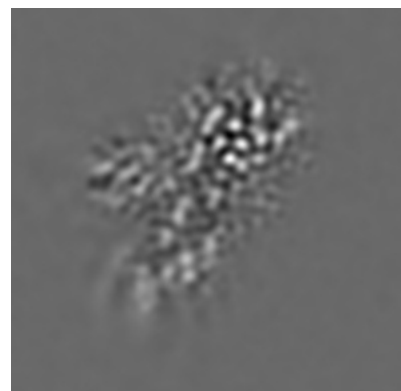
6.3.1 Primary map



X Index: 75



Y Index: 68

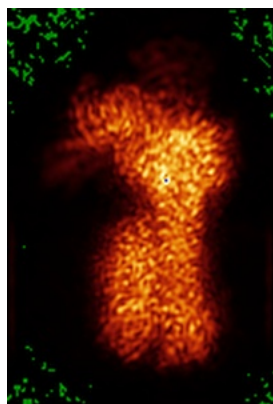


Z Index: 116

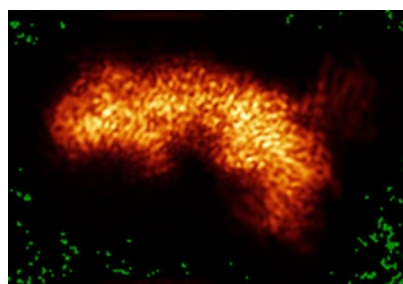
The images above show the largest variance slices of the map in three orthogonal directions.

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

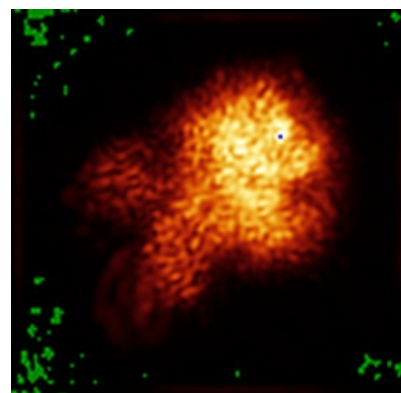
6.4.1 Primary map



X



Y

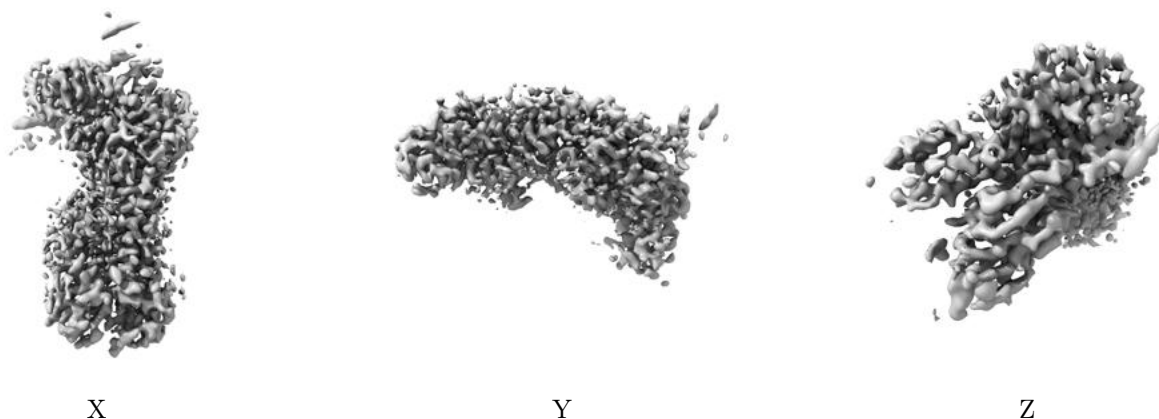


Z

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 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

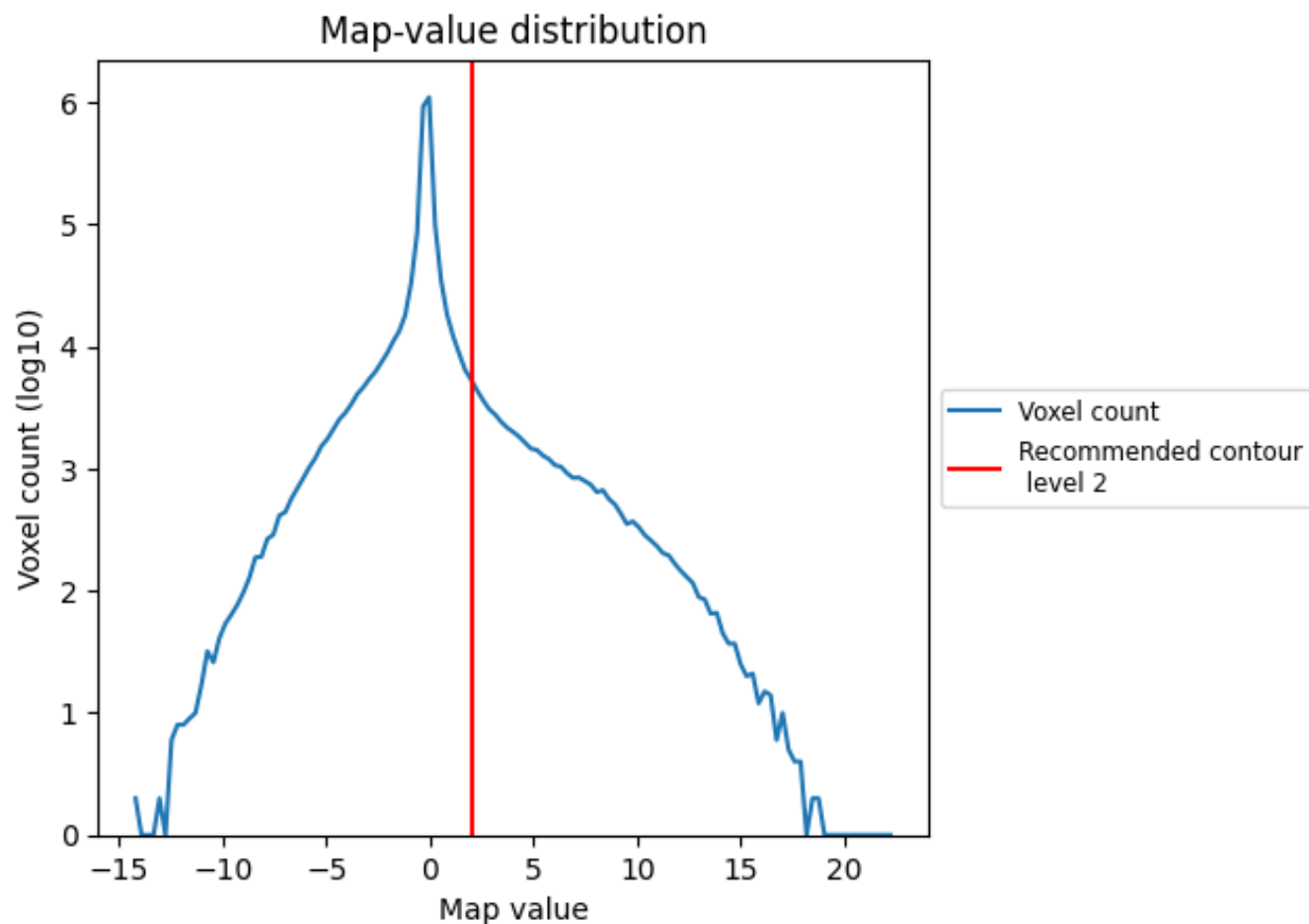
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

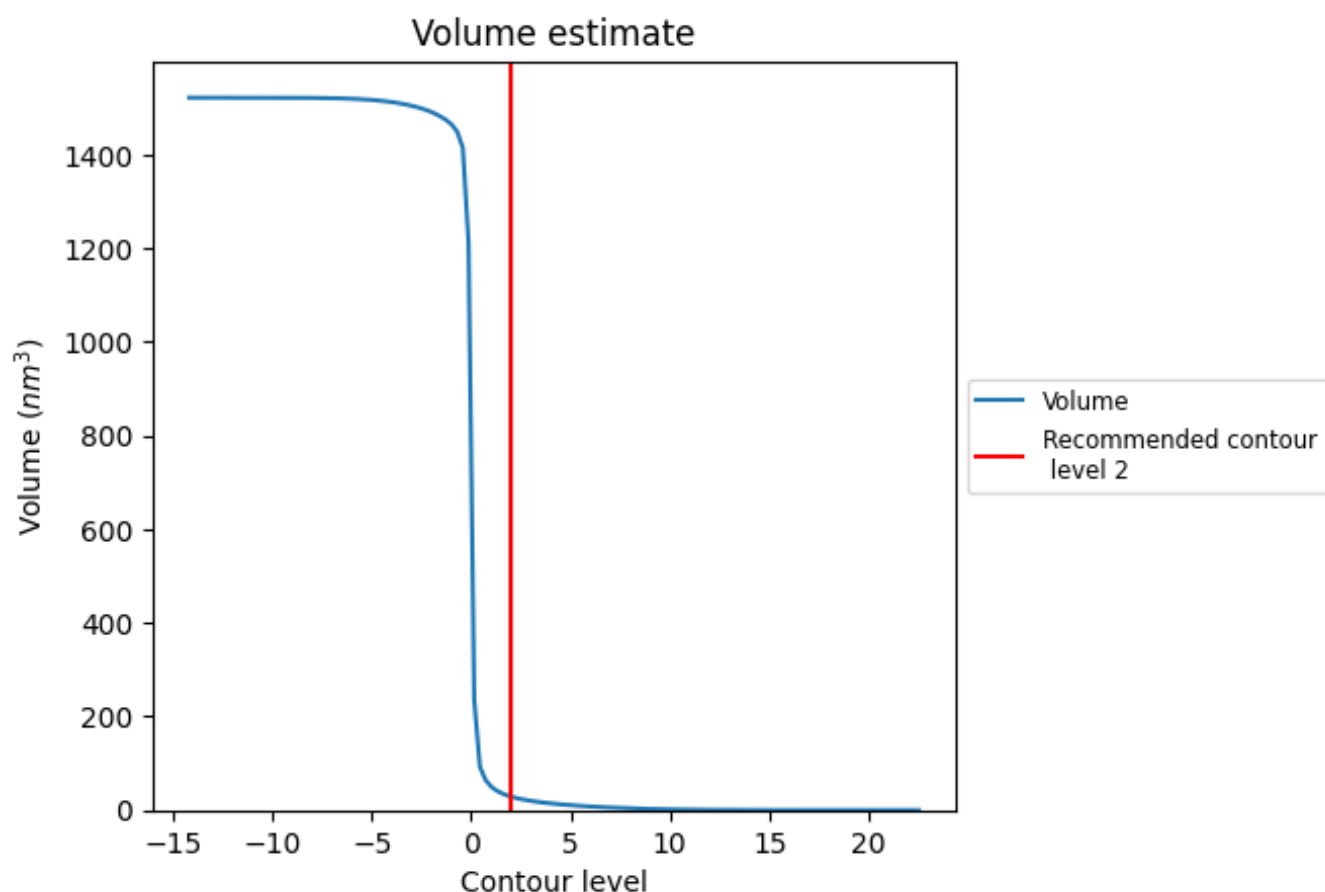
This section contains the results of statistical analysis of the map.

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 29 nm³; this corresponds to an approximate mass of 26 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.

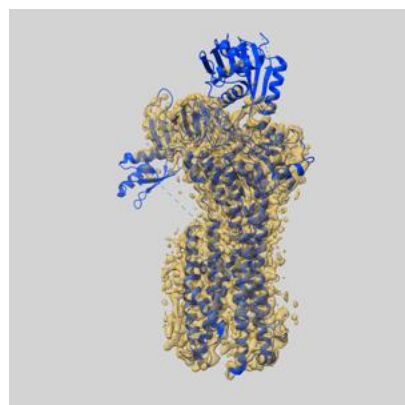
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

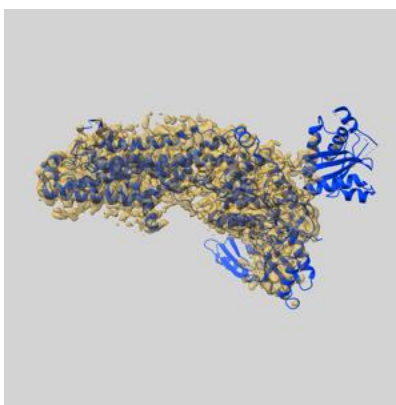
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25138 and PDB model 7SI6. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

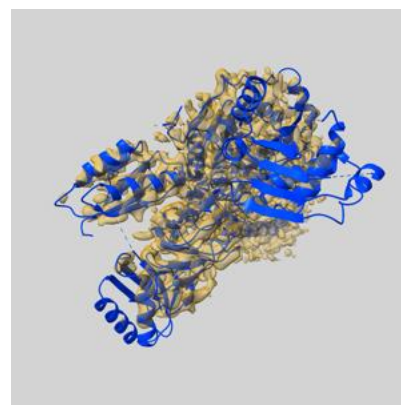
9.1 Map-model overlay [i](#)



X



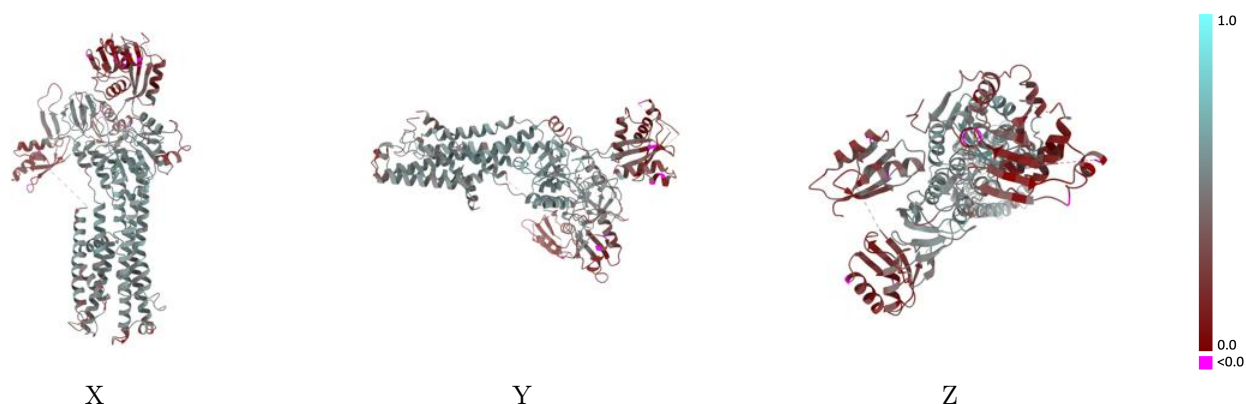
Y



Z

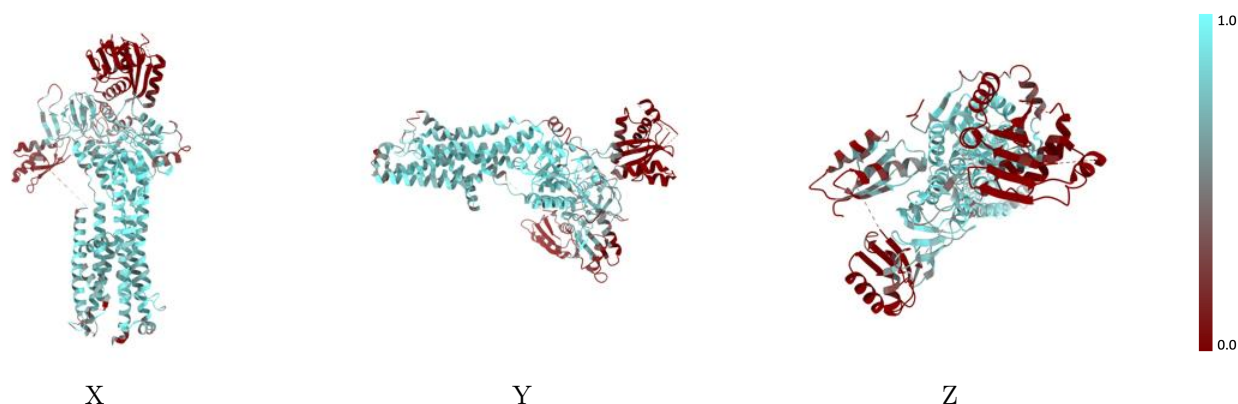
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



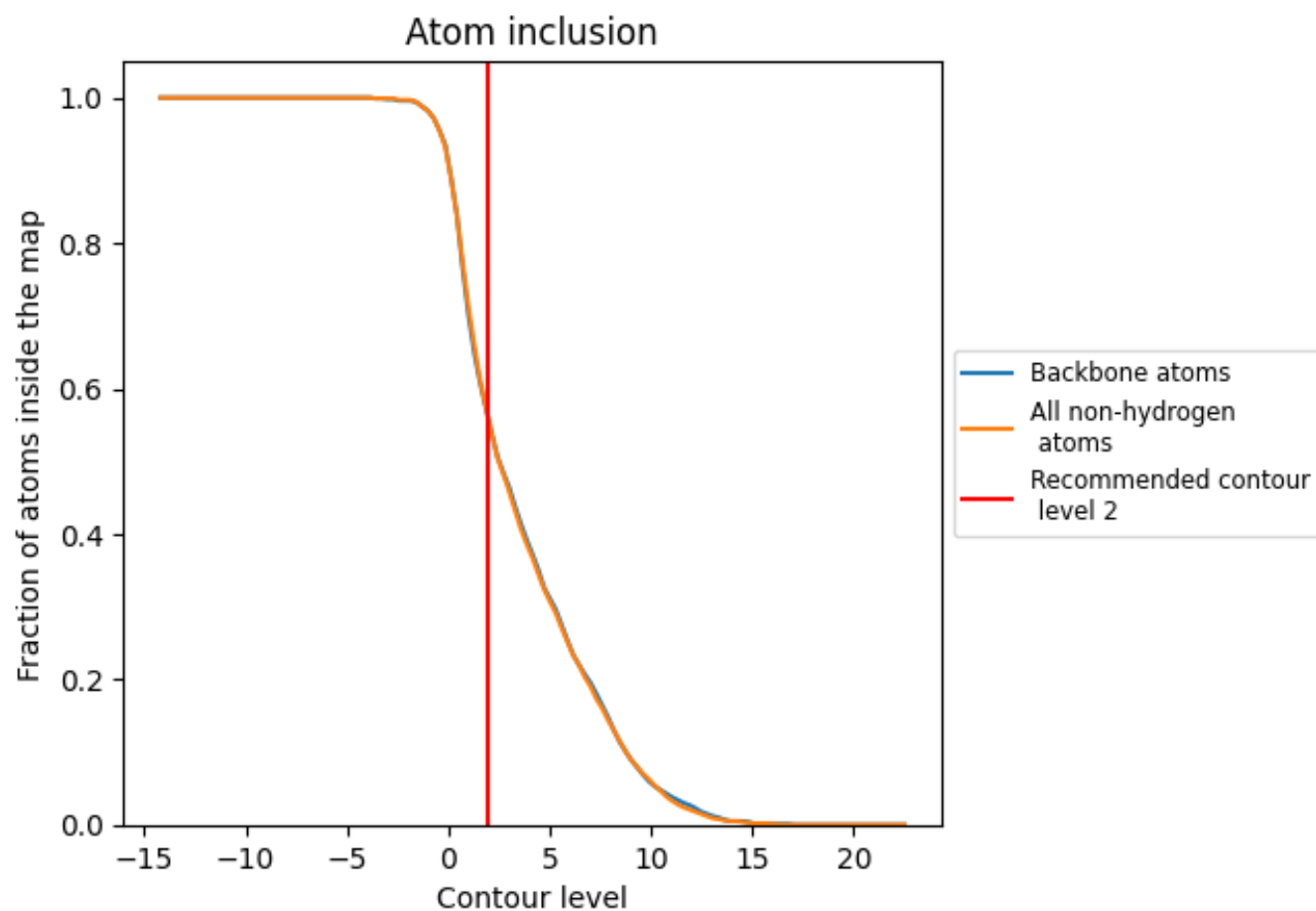
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 56% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5560	0.4210
A	0.5590	0.4210

