



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 01:03 AM UTC

PDB ID : 4BOO / pdb_00004boo
EMDB ID : EMD-2381
Title : The structure and super-organization of acetylcholine receptor-rapsyn complexes class C
Authors : Zuber, B.; Unwin, N.
Deposited on : 2013-05-21
Resolution : 42.00 Å(reported)
Based on initial model : 2BG9

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

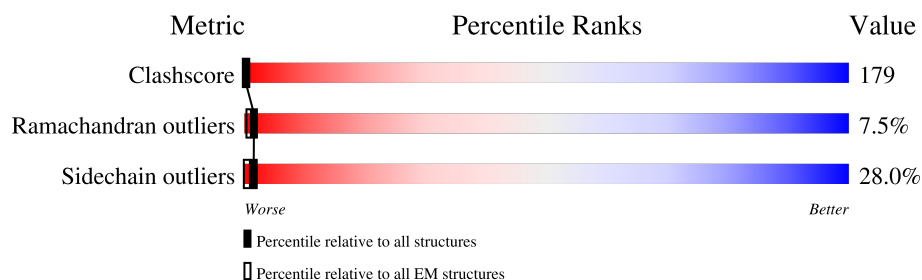
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 42.00 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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	461	8% 5% 40% 29% 6% 20%
1	D	461	9% 5% 44% 25% 6% 20%
2	B	493	6% • 42% 23% 5% 25%
3	C	522	5% 6% 37% 23% 5% 29%
4	E	505	• 5% 38% 25% 5% 27%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14924 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 ACETYLCHOLINE RECEPTOR SUBUNIT ALPHA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	370	Total	C	N	O	S	0	0
			2991	1954	478	540	19		
1	D	370	Total	C	N	O	S	0	0
			2991	1954	478	540	19		

- Molecule 2 is a protein called ACETYLCHOLINE RECEPTOR BETA SUBUNIT.

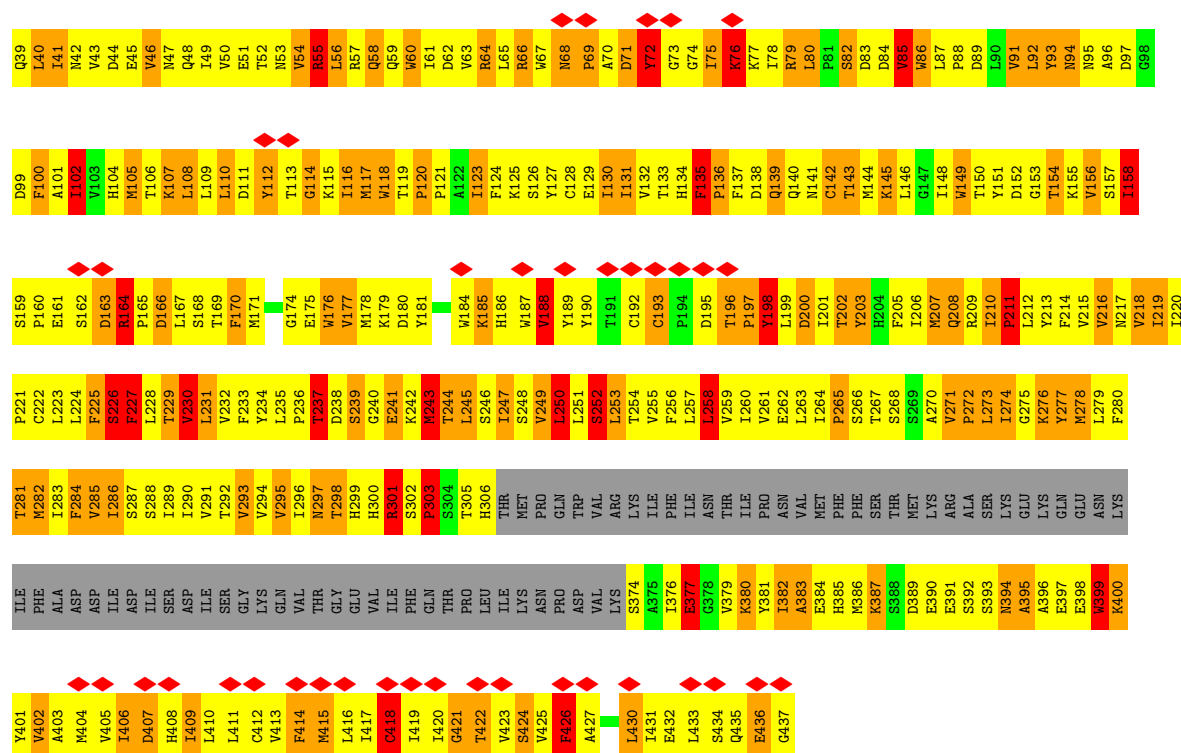
Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	370	Total	C	N	O	S	0	0
			2972	1938	465	554	15		

- Molecule 3 is a protein called ACETYLCHOLINE RECEPTOR DELTA SUBUNIT.

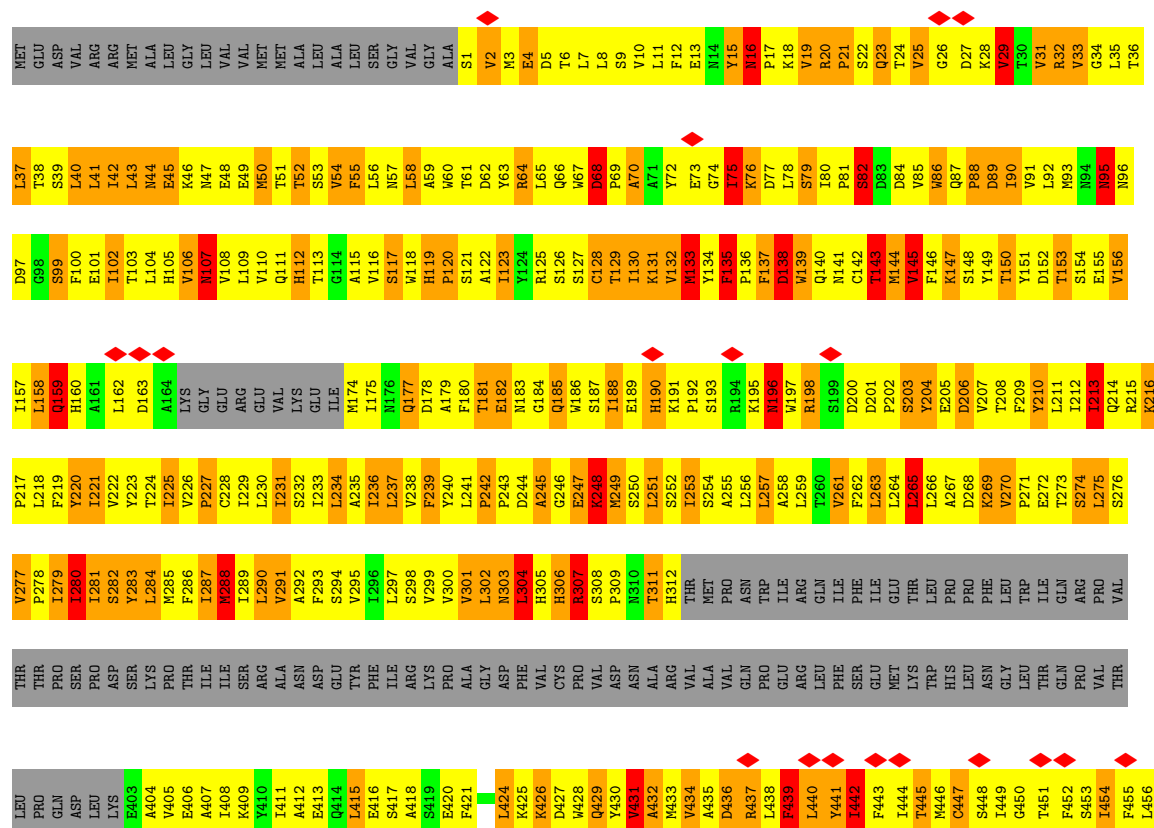
Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	370	Total	C	N	O	S	0	1
			2983	1944	489	536	14		

- Molecule 4 is a protein called ACETYLCHOLINE RECEPTOR GAMMA SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	371	Total	C	N	O	S	0	1
			2987	1948	478	551	10		



• Molecule 2: ACETYLCHOLINE RECEPTOR BETA SUBUNIT





4 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of tilted images used	3564	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	3000	Depositor
Maximum defocus (nm)	6000	Depositor
Magnification	80213	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum voxel value	1.092	Depositor
Minimum voxel value	-0.624	Depositor
Average voxel value	0.000	Depositor
Voxel value standard deviation	0.066	Depositor
Recommended contour level	0.248	Depositor
Tomogram size ($\text{\AA}$)	448.8, 448.8, 448.8	wwPDB
Tomogram dimensions	60, 60, 60	wwPDB
Tomogram angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Grid spacing ($\text{\AA}$)	7.48, 7.48, 7.48	Depositor

5 Model quality

5.1 Standard geometry

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	0.96	9/3069 (0.3%)	1.55	69/4186 (1.6%)
1	D	0.98	13/3069 (0.4%)	1.49	56/4186 (1.3%)
2	B	1.05	18/3048 (0.6%)	1.51	60/4162 (1.4%)
3	C	0.97	13/3059 (0.4%)	1.55	72/4175 (1.7%)
4	E	0.96	13/3057 (0.4%)	1.50	72/4174 (1.7%)
All	All	0.99	66/15302 (0.4%)	1.52	329/20883 (1.6%)

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	D	0	2
3	C	0	2
All	All	0	4

The worst 5 of 66 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	129	THR	C-N	-18.31	1.14	1.34
1	D	208	GLN	C-N	12.73	1.51	1.33
4	E	182	GLU	C-N	12.47	1.44	1.33
3	C	265	LEU	C-N	10.80	1.48	1.33
4	E	306	VAL	C-N	-8.77	1.22	1.33

The worst 5 of 329 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	122	PRO	CA-C-N	13.66	134.58	119.83
3	C	122	PRO	C-N-CA	13.66	134.58	119.83
3	C	460	ILE	N-CA-C	-13.48	100.98	111.90
4	E	238	LEU	N-CA-C	-13.47	96.08	111.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	441	TYR	N-CA-C	-12.76	97.06	112.89

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	63	TYR	Sidechain
3	C	74	TYR	Sidechain
1	D	277	TYR	Sidechain
1	D	72	TYR	Sidechain

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	2991	0	3006	1102	0
1	D	2991	0	3006	1091	0
2	B	2972	0	2954	1121	0
3	C	2983	0	2987	1191	0
4	E	2987	0	2994	1110	0
All	All	14924	0	14947	5345	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 179.

The worst 5 of 5345 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)
4:E:183:TRP:CB	4:E:216:ARG:HG2	1.33	1.50
1:A:167:LEU:HD12	1:A:178:MET:CB	1.43	1.48
2:B:134:TYR:CE1	2:B:213:ILE:HG13	1.44	1.47
1:A:167:LEU:CD1	1:A:178:MET:HB2	1.46	1.45
3:C:316:THR:CG2	3:C:317:PRO:HD2	1.53	1.39

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	366/461 (79%)	289 (79%)	48 (13%)	29 (8%)	1	10
1	D	366/461 (79%)	294 (80%)	41 (11%)	31 (8%)	0	9
2	B	364/493 (74%)	273 (75%)	59 (16%)	32 (9%)	0	8
3	C	364/522 (70%)	288 (79%)	58 (16%)	18 (5%)	1	16
4	E	365/505 (72%)	281 (77%)	58 (16%)	26 (7%)	1	11
All	All	1825/2442 (75%)	1425 (78%)	264 (14%)	136 (8%)	1	10

5 of 136 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	27	HIS
1	A	76	LYS
1	A	83	ASP
1	A	102	ILE

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	343/427 (80%)	236 (69%)	107 (31%)	0	2
1	D	343/427 (80%)	247 (72%)	96 (28%)	0	3
2	B	340/449 (76%)	261 (77%)	79 (23%)	1	5
3	C	335/475 (70%)	240 (72%)	95 (28%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	E	337/463 (73%)	238 (71%)	99 (29%)	0	2
All	All	1698/2241 (76%)	1222 (72%)	476 (28%)	1	3

5 of 476 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	206	PHE
4	E	252	THR
1	D	25	HIS
4	E	231	LEU
4	E	472	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
4	E	140	ASN
4	E	153	HIS
4	E	249	GLN
3	C	20	HIS
3	C	15	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	1

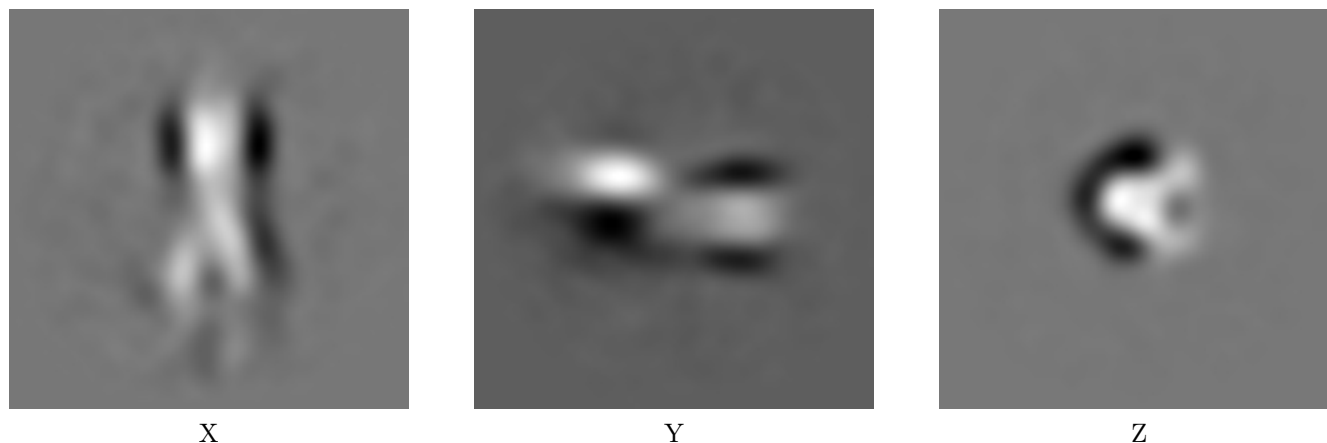
All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	129:THR	C	130:ILE	N	1.14

6 Tomogram visualisation [i](#)

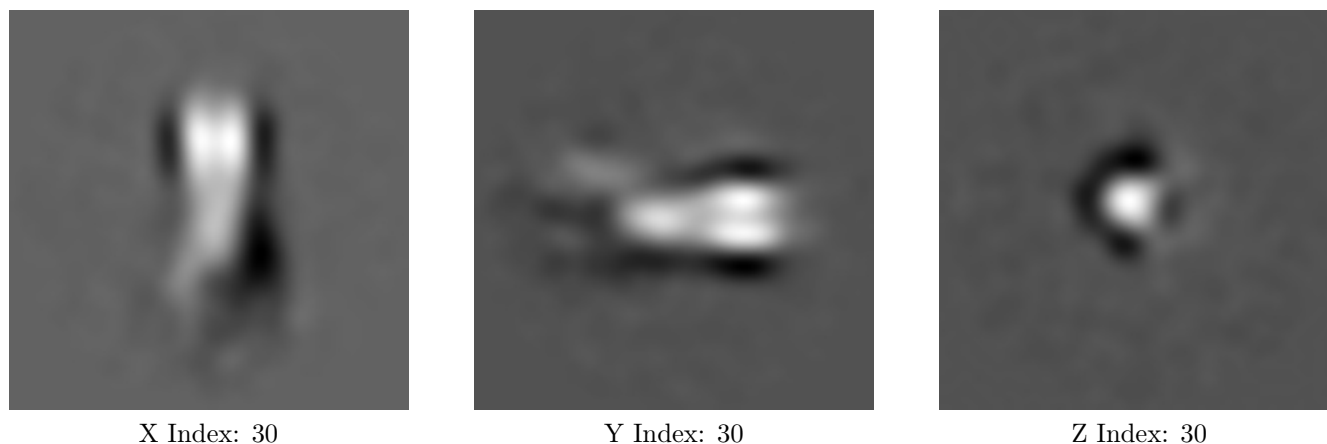
This section contains visualisations of the EMDB entry EMD-2381. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

6.1 Orthogonal projections [i](#)



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

6.2 Central slices [i](#)

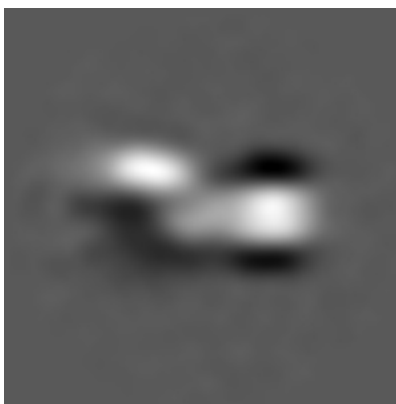


The images above show central slices of the tomogram in three orthogonal directions.

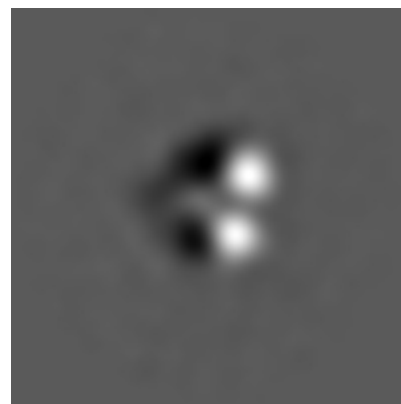
6.3 Largest variance slices [i](#)



X Index: 28



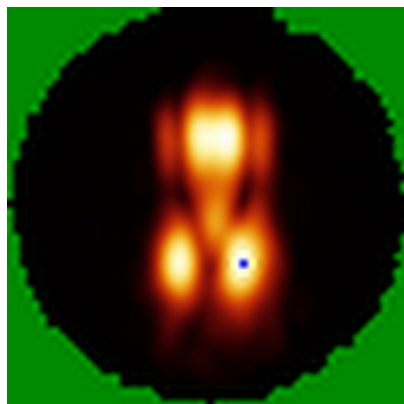
Y Index: 33



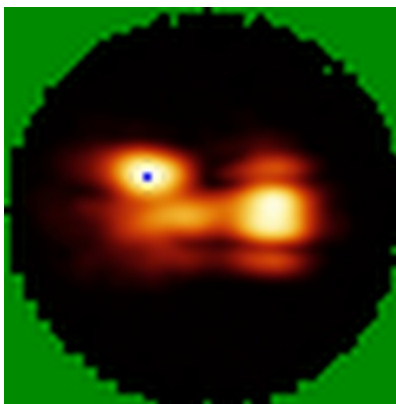
Z Index: 21

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

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



X



Y



Z

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

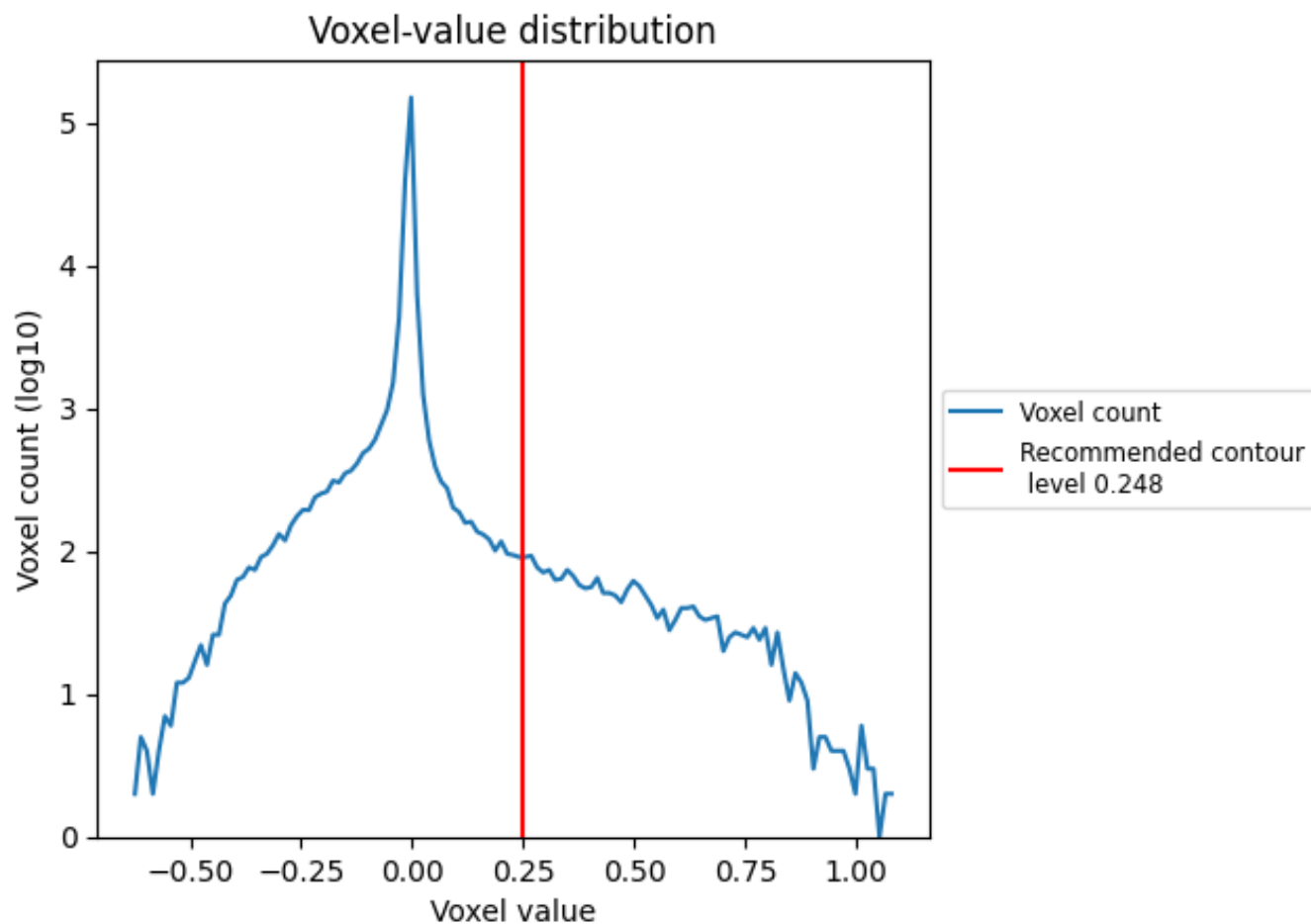
6.5 Mask visualisation [i](#)

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

7 Tomogram analysis [i](#)

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

7.1 Voxel-value distribution [i](#)



The voxel-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic.

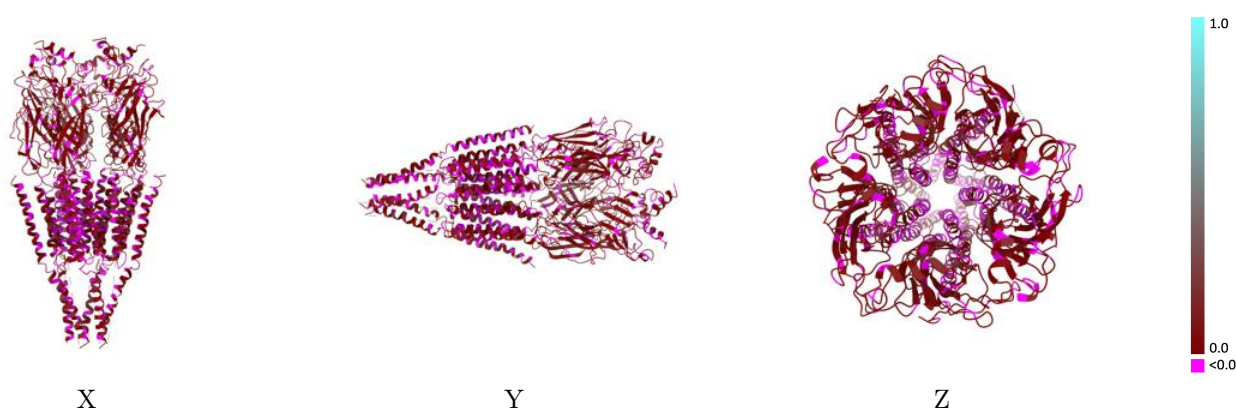
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2381 and PDB model 4BOO. Per-residue inclusion information can be found in section [3](#) on page [4](#).

8.1 Map-model overlay [i](#)

This section was not generated.

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

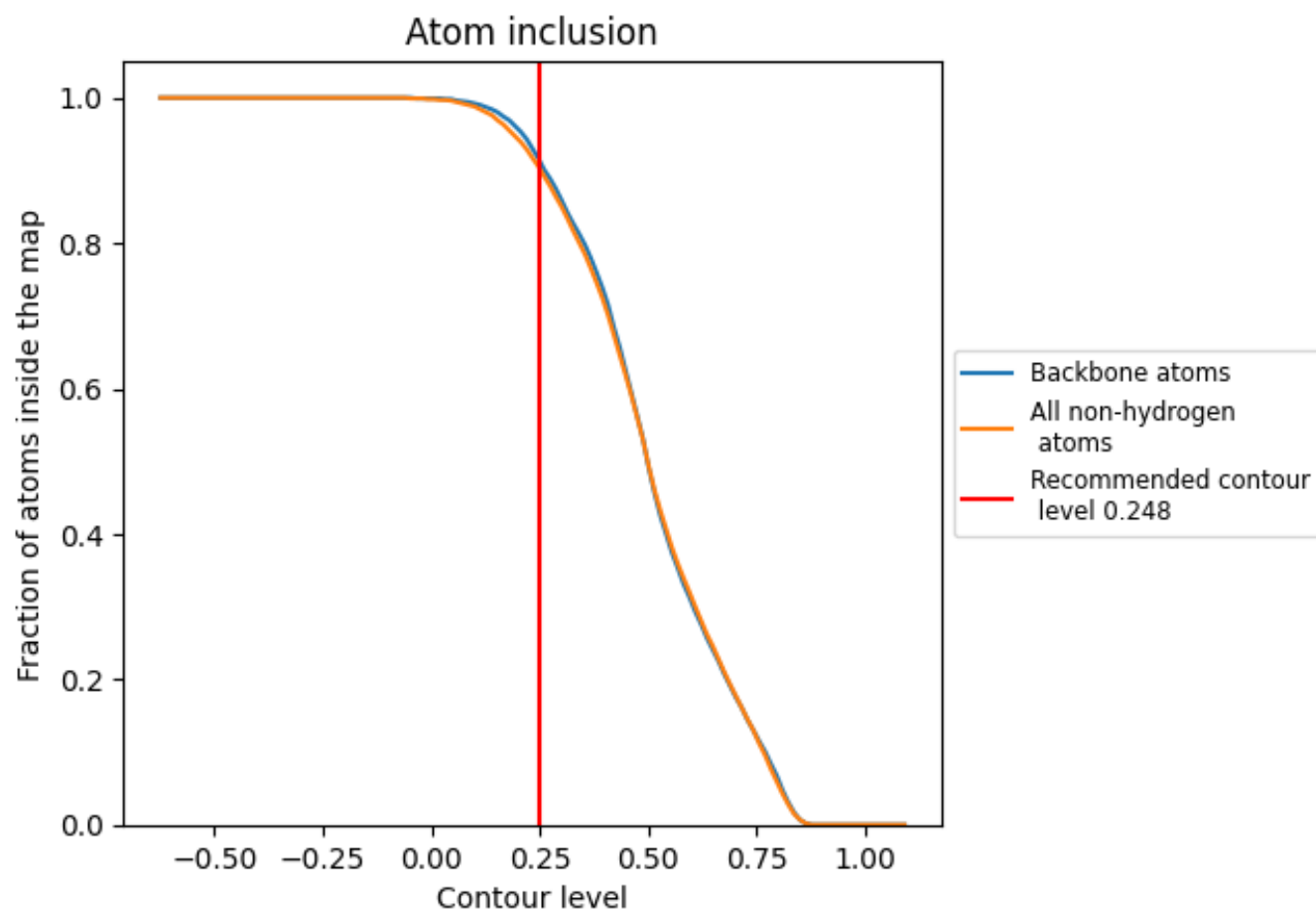


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

8.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.248) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9050	0.0420
A	0.8890	0.0460
B	0.9090	0.0470
C	0.9140	0.0410
D	0.8770	0.0300
E	0.9330	0.0470

