



Full wwPDB EM Validation Report ⓘ

Nov 8, 2022 – 06:12 AM JST

PDB ID : 5YDZ
EMDB ID : EMD-6823
Title : structure of endo-lysosomal TRPML1 channel inserting into amphipol: state 1
Authors : Yang, M.; Gao, N.
Deposited on : 2017-09-15
Resolution : 5.80 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

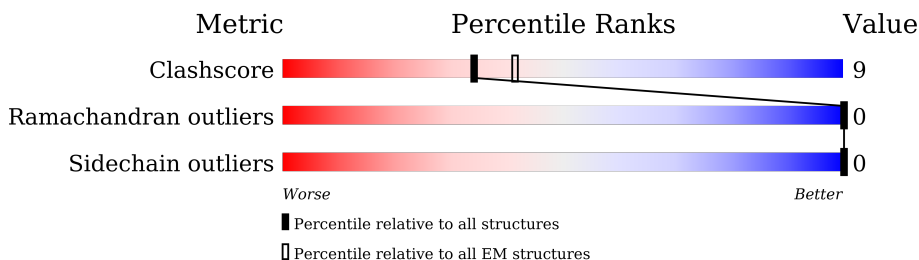
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.80 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	580	<div> <div>11%</div> <div>67%</div> <div>6%</div> <div>27%</div> </div>
1	B	580	<div> <div>11%</div> <div>67%</div> <div>6%</div> <div>27%</div> </div>
1	C	580	<div> <div>11%</div> <div>67%</div> <div>7%</div> <div>27%</div> </div>
1	D	580	<div> <div>11%</div> <div>67%</div> <div>6%</div> <div>27%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6888 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.

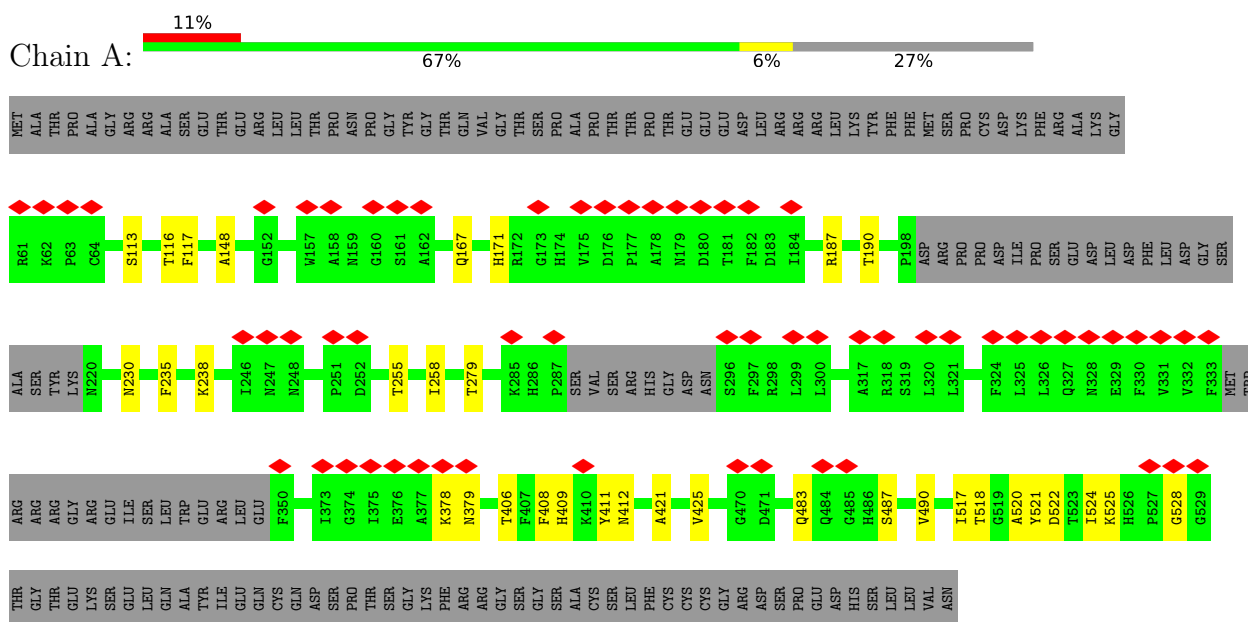
- Molecule 1 is a protein called mammalian endo-lysosomal TRPML1 channel.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	424	Total	C	N	O	0	0
			1722	870	426	426		
1	B	424	Total	C	N	O	0	0
			1722	870	426	426		
1	C	424	Total	C	N	O	0	0
			1722	870	426	426		
1	D	424	Total	C	N	O	0	0
			1722	870	426	426		

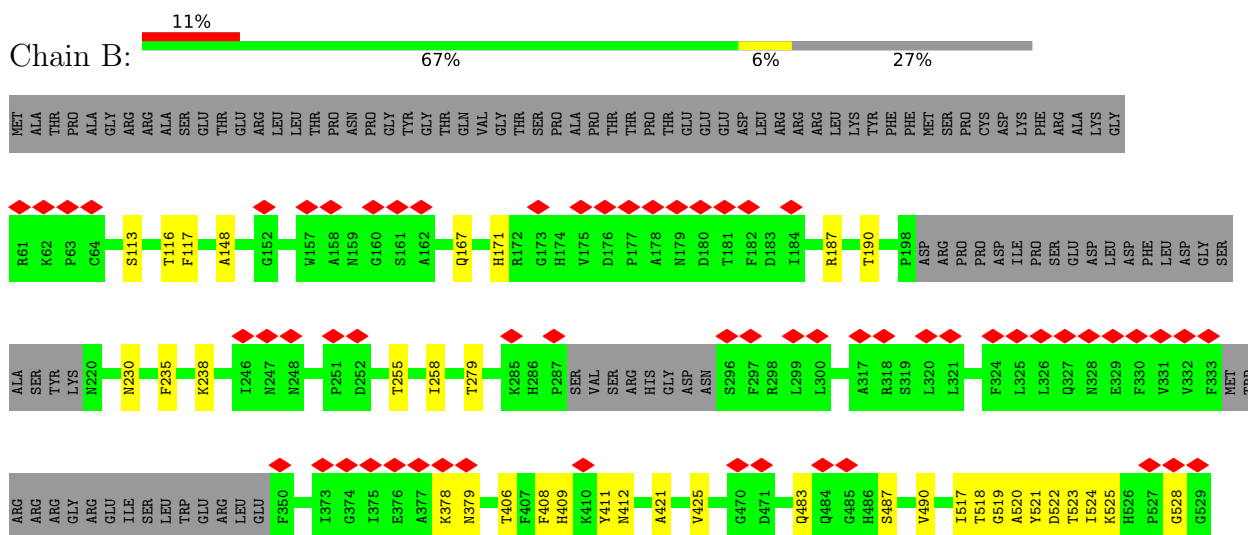
3 Residue-property plots

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: mammalian endo-lysosomal TRPML1 channel



- Molecule 1: mammalian endo-lysosomal TRPML1 channel



THR GLY THR THR LYS SER GLU LEU LEU GLN ALA ALA THR TYR GLU LEU LEU GLN THR TYR ILE GLU GLN CYS ASP SER PRO THR THR SER GLY LYS PHE ARG ARG GLY SER GLY SER ALA CYS SER SER PHE CYS CYS GLY ARG ASP SER SER PRO GLU ASP HIS LEU LEU VAL ASN

- Molecule 1: mammalian endo-lysosomal TRPML1 channel

Chain C: 

MET ALA THR PRO THR GLY ARG ARG ALA SER GLU THR GLU ARG LEU LEU THR PRO ASN PRO THR GLY TYR GLY THR GLN VAL THR GLY SER PRO ALA PRO SER SER THR D176 D177 D178 D179 D180 D181 D182 D183 D184 R187 T190 P198 ASP ARG PRO CYS ASP ILE PRO SER GLU ASP LEU PHE LEU MET SER PRO CYS ASP LYS PHE ARG ALA LYS GLY

R61 K62 P63 C64 S113 T116 F117 A148 G152 W157 A158 N159 G160 S161 A162 Q167 H171 R172 G173 H174 V175 D176 P177 A178 N179 D180 T181 F182 D183 I184 R187 T190 P198 ASP ARG PRO CYS ASP ILE PRO SER GLU ASP LEU PHE LEU MET SER PRO CYS ASP LYS PHE ARG ALA LYS GLY

ALA SER TYR LYS N220 N230 F235 K238 I246 N247 N248 P251 D252 T255 T258 T279 K285 H286 P287 SER VAL SER ARG HIS GLY ASP ASN S296 F297 R298 L299 L300 A317 R318 S319 L320 L321 F324 L325 L326 Q327 N328 F330 T329 V331 V332 F333 MET TRP

ARG ARG ARG GLU ILE SER LEU TRP GLU ARG GLU F350 I373 G374 I375 E376 A377 K378 N379 T406 F407 F408 H409 K410 Y411 N412 A421 V425 G470 D471 D472 T476 Q483 Q484 G485 H486 S487 V490 I517 T518 G519 Y521 D522 T523 I524 K525 H526

F527 G528 G529 THR THR GLU LYS SER TRP GLU LEU GLN ALA TYR ILE GLU GLN CYS GLN ASP SER PRO THR SER GLY PHE ARG ARG GLY SER GLY PHE ARG ARG GLY SER GLY SER ALA CYS SER LEU PHE CYS GLY ARG ASP SER PRO PHE ASP HIS SER LEU VAL ASN

- Molecule 1: mammalian endo-lysosomal TRPML1 channel

Chain D: 

MET ALA THR PRO THR GLY ARG ARG ALA SER GLU THR GLU ARG LEU LEU THR PRO ASN PRO THR GLY TYR GLY THR GLN VAL THR GLY SER PRO ALA PRO SER SER THR D176 D177 D178 D179 D180 D181 D182 D183 D184 R187 T190 P198 ASP ARG PRO CYS ASP ILE PRO SER GLU ASP LEU PHE LEU MET SER PRO CYS ASP LYS PHE ARG ALA LYS GLY

R61 K62 P63 C64 S113 T116 F117 A148 G152 W157 A158 N159 G160 S161 A162 Q167 H171 R172 G173 H174 V175 D176 P177 A178 N179 D180 T181 F182 D183 I184 R187 T190 P198 ASP ARG PRO CYS ASP ILE PRO SER GLU ASP LEU PHE LEU MET SER PRO CYS ASP LYS PHE ARG ALA LYS GLY

ALA SER TYR LYS N220 N230 F235 K238 I246 N247 N248 P251 D252 T255 T258 T279 K285 H286 P287 SER VAL SER ARG HIS GLY ASP ASN S296 F297 R298 L299 L300 A317 R318 S319 L320 L321 F324 L325 L326 Q327 N328 F330 T329 V331 V332 F333 MET TRP

ARG ARG ARG GLU ILE SER LEU TRP GLU ARG GLU F350 I373 G374 I375 E376 A377 K378 N379 T406 F407 F408 H409 K410 Y411 N412 A421 V425 G470 D471 D472 T476 Q483 Q484 G485 H486 S487 V490 I517 T518 G519 Y521 D522 T523 I524 K525 H526 P527 G528 G529

THR GLY THR THR LYS SER GLU LEU LEU GLN ALA ALA THR TYR GLU LEU LEU GLN THR TYR ILE GLU GLN CYS ASP SER PRO THR THR SER GLY LYS PHE ARG ARG GLY SER GLY SER ALA CYS SER SER PHE CYS CYS GLY ARG ASP SER SER PRO GLU ASP HIS LEU LEU VAL ASN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	167000	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	19.836	Depositor
Minimum map value	-12.523	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.0	Depositor
Map size (Å)	184.8, 184.8, 184.8	wwPDB
Map dimensions	70, 70, 70	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.64, 2.64, 2.64	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	0.51	0/1718	0.62	0/2156
1	B	0.51	0/1718	0.62	0/2156
1	C	0.51	0/1718	0.62	0/2156
1	D	0.51	0/1718	0.62	0/2156
All	All	0.51	0/6872	0.62	0/8624

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	3
1	C	0	3
1	D	0	3
All	All	0	12

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	378	LYS	Peptide
1	A	379	ASN	Peptide
1	A	483	GLN	Peptide
1	B	378	LYS	Peptide
1	B	379	ASN	Peptide
1	B	483	GLN	Peptide
1	C	378	LYS	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	C	379	ASN	Peptide
1	C	483	GLN	Peptide
1	D	378	LYS	Peptide
1	D	379	ASN	Peptide
1	D	483	GLN	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1722	0	491	19	0
1	B	1722	0	491	20	0
1	C	1722	0	491	21	0
1	D	1722	0	491	19	0
All	All	6888	0	1964	79	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 9.

All (79) 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:B:255:THR:O	1:B:279:THR:HA	1.84	0.78
1:D:255:THR:O	1:D:279:THR:HA	1.84	0.77
1:A:255:THR:O	1:A:279:THR:HA	1.84	0.77
1:C:255:THR:O	1:C:279:THR:HA	1.84	0.77
1:B:521:TYR:O	1:B:525:LYS:N	2.32	0.63
1:C:521:TYR:O	1:C:525:LYS:N	2.32	0.63
1:A:521:TYR:O	1:A:525:LYS:N	2.32	0.62
1:C:520:ALA:O	1:C:524:ILE:N	2.32	0.62
1:A:520:ALA:O	1:A:524:ILE:N	2.32	0.61
1:A:171:HIS:N	1:A:187:ARG:O	2.30	0.61
1:B:520:ALA:O	1:B:524:ILE:N	2.32	0.61
1:D:521:TYR:O	1:D:525:LYS:N	2.32	0.61
1:D:520:ALA:O	1:D:524:ILE:N	2.32	0.61
1:D:171:HIS:N	1:D:187:ARG:O	2.30	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:SER:O	1:A:117:PHE:N	2.36	0.59
1:D:148:ALA:O	1:D:238:LYS:N	2.35	0.59
1:A:517:ILE:O	1:A:521:TYR:N	2.35	0.59
1:B:113:SER:O	1:B:117:PHE:N	2.36	0.59
1:D:113:SER:O	1:D:117:PHE:N	2.36	0.59
1:C:113:SER:O	1:C:117:PHE:N	2.36	0.59
1:D:518:THR:O	1:D:522:ASP:N	2.37	0.58
1:B:517:ILE:O	1:B:521:TYR:N	2.35	0.57
1:A:524:ILE:O	1:A:528:GLY:N	2.37	0.57
1:D:524:ILE:O	1:D:528:GLY:N	2.37	0.57
1:A:148:ALA:O	1:A:238:LYS:N	2.35	0.56
1:C:148:ALA:O	1:C:238:LYS:N	2.35	0.56
1:C:517:ILE:O	1:C:521:TYR:N	2.35	0.56
1:C:518:THR:O	1:C:522:ASP:N	2.37	0.56
1:B:148:ALA:O	1:B:238:LYS:N	2.34	0.56
1:B:518:THR:O	1:B:522:ASP:N	2.37	0.56
1:C:524:ILE:O	1:C:528:GLY:N	2.37	0.56
1:B:171:HIS:N	1:B:187:ARG:O	2.30	0.55
1:A:518:THR:O	1:A:522:ASP:N	2.37	0.54
1:D:517:ILE:O	1:D:521:TYR:N	2.35	0.54
1:B:524:ILE:O	1:B:528:GLY:N	2.37	0.54
1:C:113:SER:O	1:C:116:THR:N	2.43	0.52
1:C:235:PHE:O	1:C:258:ILE:CB	2.58	0.52
1:A:408:PHE:O	1:A:412:ASN:N	2.43	0.52
1:D:235:PHE:O	1:D:258:ILE:CB	2.58	0.52
1:C:408:PHE:O	1:C:412:ASN:N	2.44	0.51
1:B:235:PHE:O	1:B:258:ILE:CB	2.58	0.51
1:B:408:PHE:O	1:B:412:ASN:N	2.43	0.51
1:C:171:HIS:N	1:C:187:ARG:O	2.30	0.51
1:D:113:SER:O	1:D:116:THR:N	2.43	0.51
1:A:235:PHE:O	1:A:258:ILE:CB	2.58	0.51
1:B:487:SER:O	1:B:490:VAL:N	2.38	0.51
1:D:408:PHE:O	1:D:412:ASN:N	2.43	0.51
1:B:113:SER:O	1:B:116:THR:N	2.43	0.50
1:D:487:SER:O	1:D:490:VAL:N	2.38	0.49
1:A:113:SER:O	1:A:116:THR:N	2.43	0.49
1:D:167:GLN:O	1:D:190:THR:CA	2.62	0.48
1:C:167:GLN:O	1:C:190:THR:CA	2.62	0.47
1:C:487:SER:O	1:C:490:VAL:N	2.38	0.47
1:A:148:ALA:N	1:A:238:LYS:O	2.47	0.47
1:B:148:ALA:N	1:B:238:LYS:O	2.47	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:148:ALA:N	1:D:238:LYS:O	2.48	0.47
1:C:148:ALA:N	1:C:238:LYS:O	2.47	0.47
1:A:487:SER:O	1:A:490:VAL:N	2.38	0.47
1:B:167:GLN:O	1:B:190:THR:CA	2.62	0.47
1:A:167:GLN:O	1:A:190:THR:CA	2.62	0.47
1:B:421:ALA:O	1:B:425:VAL:N	2.46	0.46
1:C:421:ALA:O	1:C:425:VAL:N	2.46	0.45
1:A:230:ASN:N	1:A:230:ASN:OD1	2.49	0.44
1:D:421:ALA:O	1:D:425:VAL:N	2.46	0.43
1:D:230:ASN:N	1:D:230:ASN:OD1	2.49	0.43
1:B:519:GLY:O	1:B:523:THR:N	2.46	0.43
1:C:230:ASN:OD1	1:C:230:ASN:N	2.49	0.43
1:B:230:ASN:N	1:B:230:ASN:OD1	2.49	0.43
1:C:519:GLY:O	1:C:523:THR:N	2.46	0.42
1:A:408:PHE:O	1:A:411:TYR:N	2.53	0.42
1:C:408:PHE:O	1:C:411:TYR:N	2.53	0.42
1:D:408:PHE:O	1:D:411:TYR:N	2.53	0.42
1:B:408:PHE:O	1:B:411:TYR:N	2.53	0.41
1:D:406:THR:C	1:D:409:HIS:H	2.24	0.41
1:A:421:ALA:O	1:A:425:VAL:N	2.46	0.41
1:A:406:THR:C	1:A:409:HIS:H	2.24	0.41
1:C:472:ASP:O	1:C:476:THR:N	2.33	0.41
1:B:406:THR:C	1:B:409:HIS:H	2.24	0.41
1:C:406:THR:C	1:C:409:HIS:H	2.24	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	416/580 (72%)	382 (92%)	34 (8%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	416/580 (72%)	382 (92%)	34 (8%)	0	100	100
1	C	416/580 (72%)	382 (92%)	34 (8%)	0	100	100
1	D	416/580 (72%)	382 (92%)	34 (8%)	0	100	100
All	All	1664/2320 (72%)	1528 (92%)	136 (8%)	0	100	100

There are no Ramachandran outliers to report.

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	2/512 (0%)	2 (100%)	0	100	100
1	B	2/512 (0%)	2 (100%)	0	100	100
1	C	2/512 (0%)	2 (100%)	0	100	100
1	D	2/512 (0%)	2 (100%)	0	100	100
All	All	8/2048 (0%)	8 (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 [i](#)

There are no monosaccharides 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](#)

There are no chain breaks in this entry.

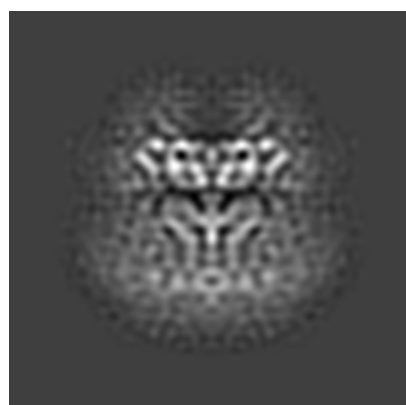
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6823. These allow visual inspection of the internal detail of the map and identification of artifacts.

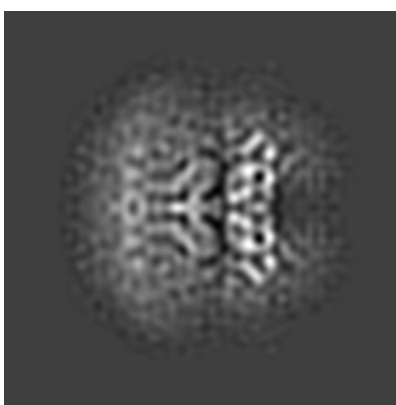
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

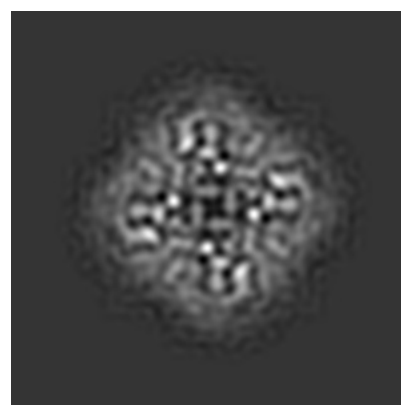
6.1.1 Primary map



X



Y



Z

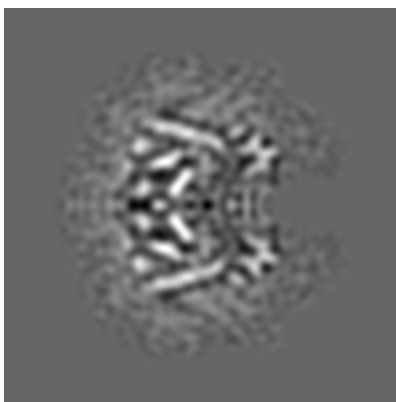
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

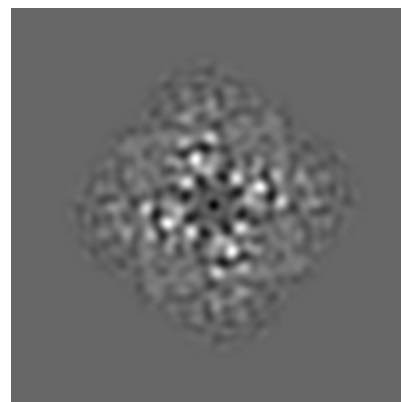
6.2.1 Primary map



X Index: 35



Y Index: 35

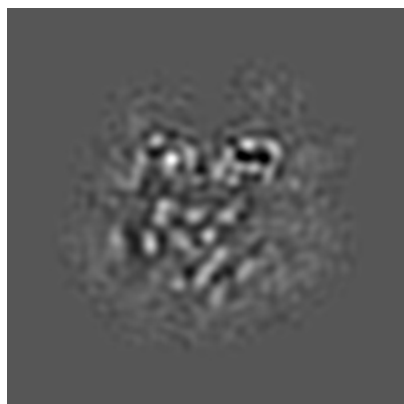


Z Index: 35

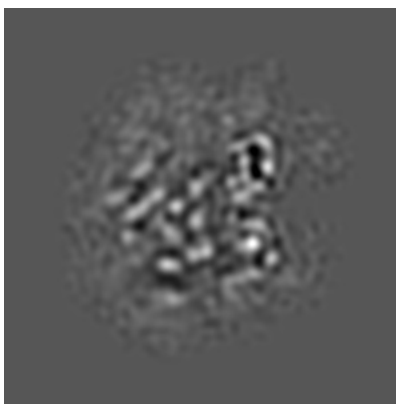
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

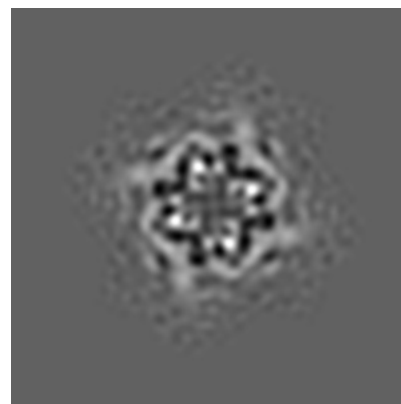
6.3.1 Primary map



X Index: 38



Y Index: 32

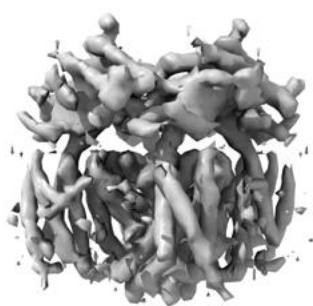


Z Index: 43

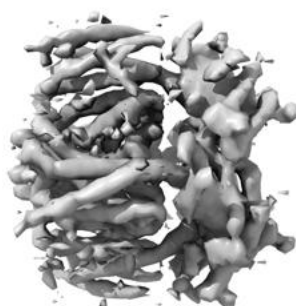
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

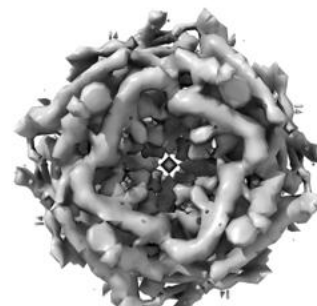
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

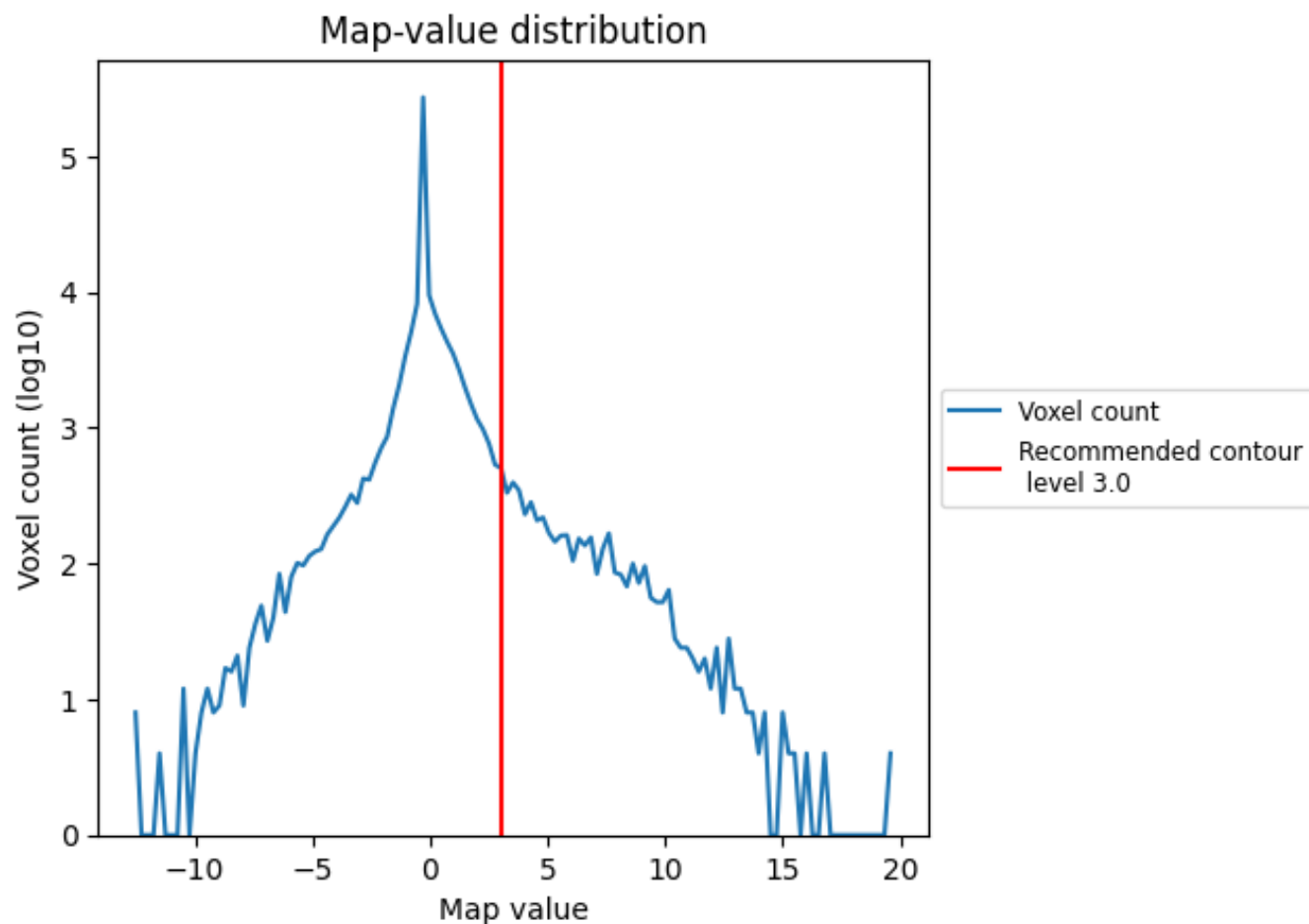
6.5 Mask visualisation

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

7 Map analysis [i](#)

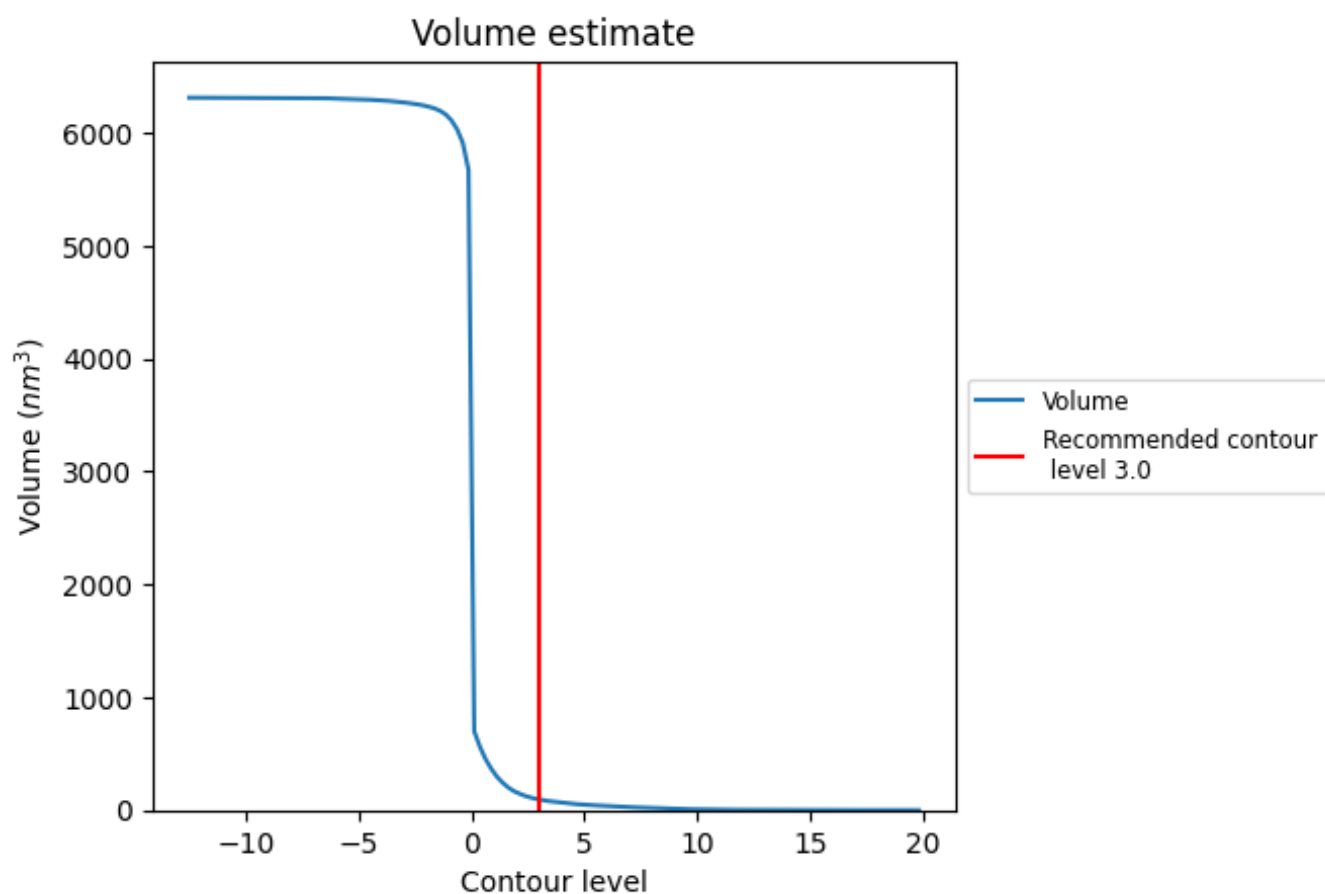
This section contains the results of statistical analysis of the map.

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.

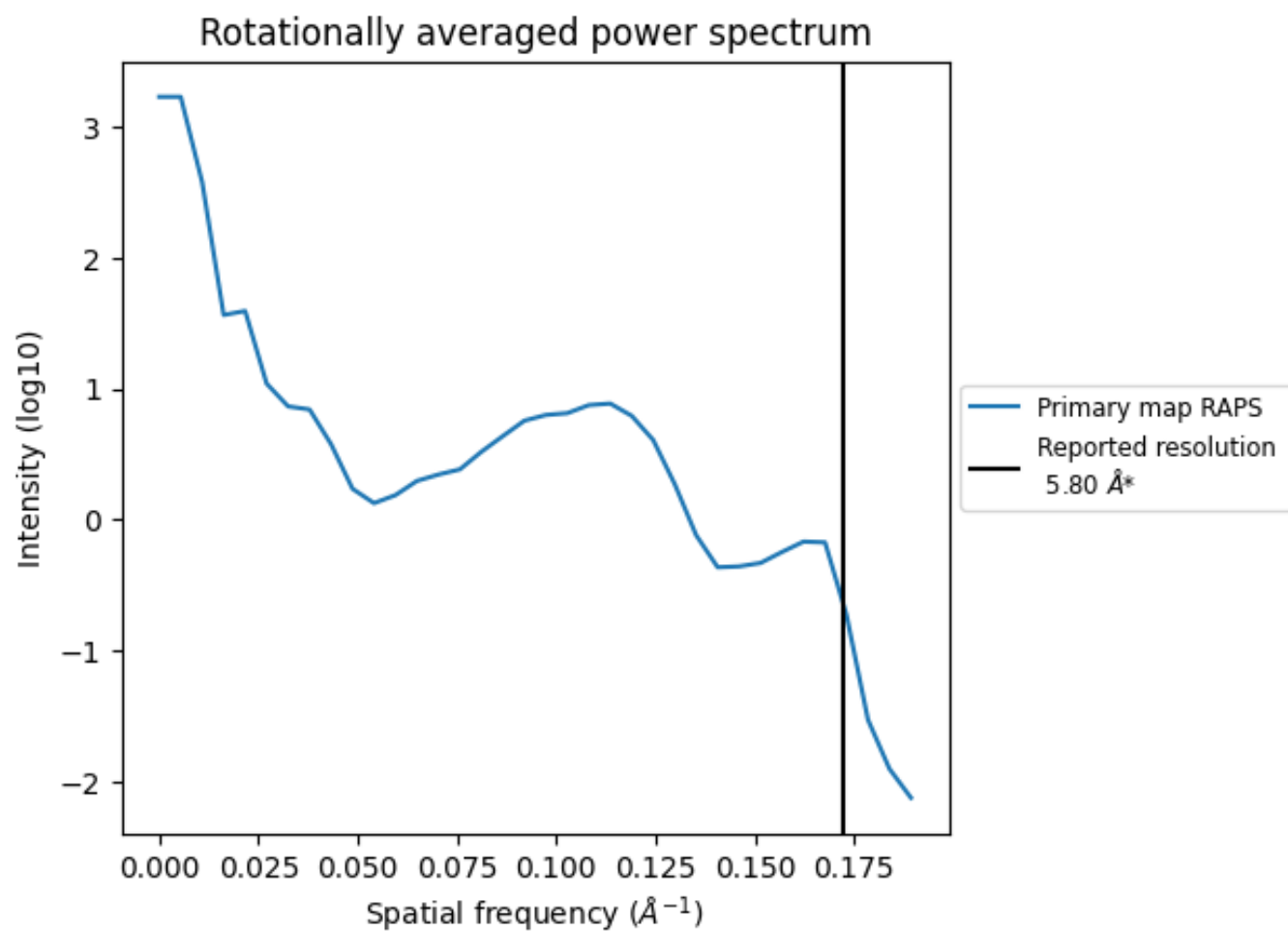
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 95 nm³; this corresponds to an approximate mass of 85 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 0.172 Å⁻¹

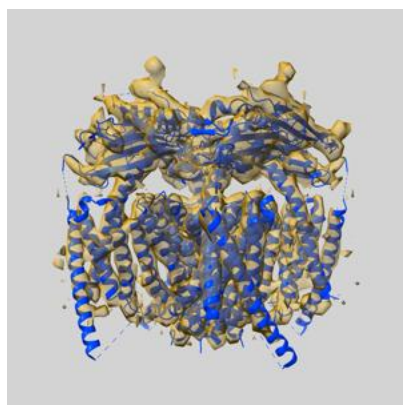
8 Fourier-Shell correlation

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

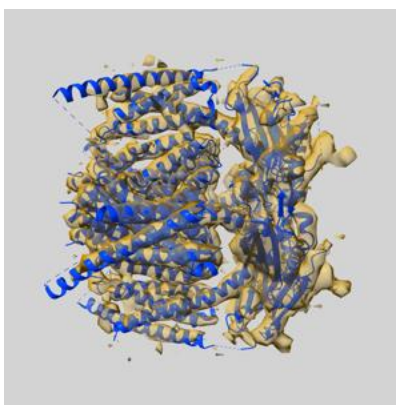
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6823 and PDB model 5YDZ. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

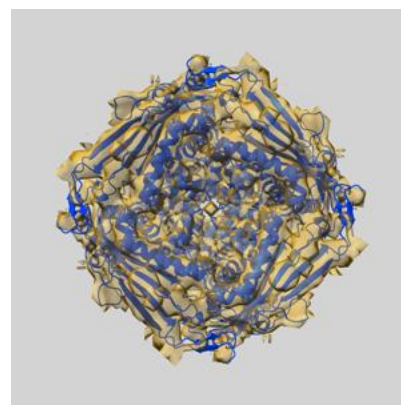
9.1 Map-model overlay [i](#)



X



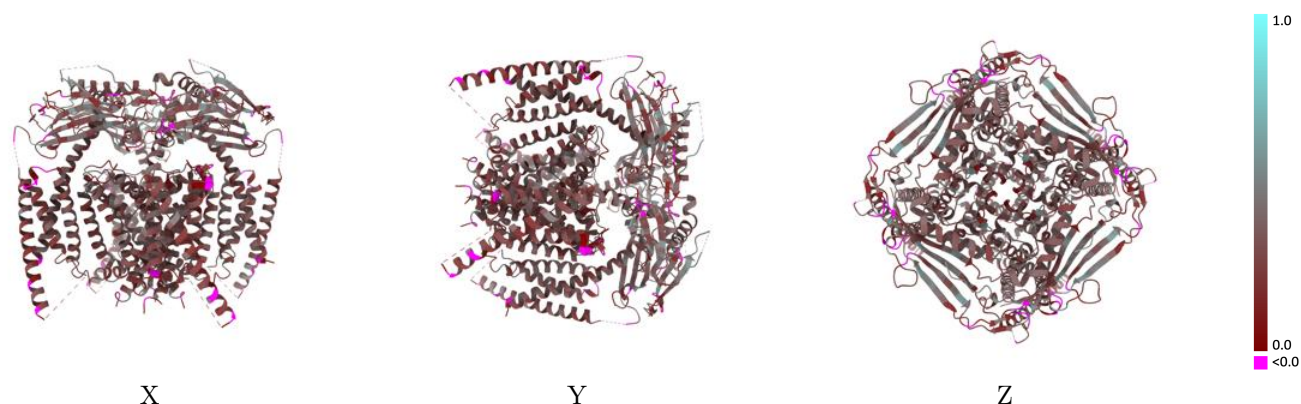
Y



Z

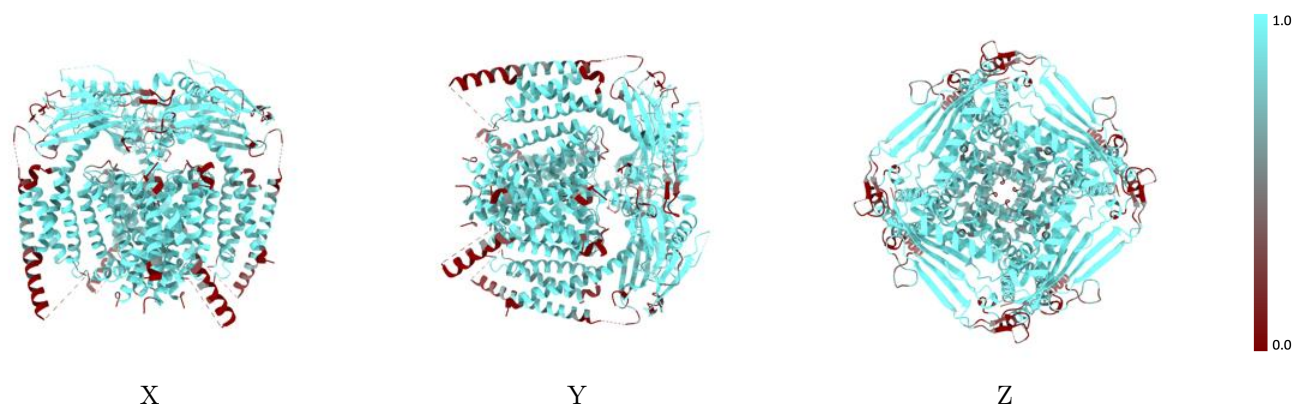
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



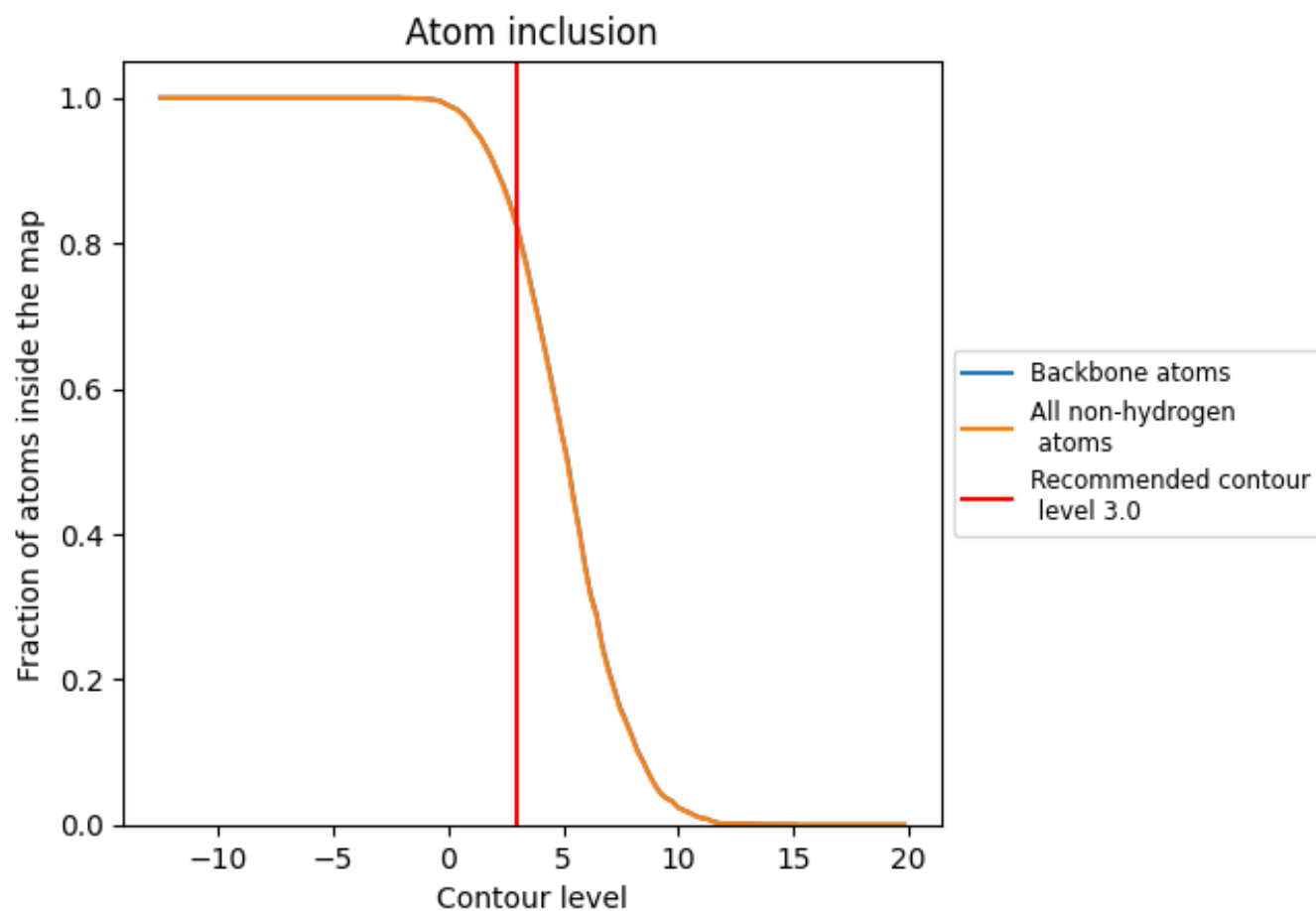
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.0).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 82% 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 (3.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8197	<div></div> 0.3000
A	<div></div> 0.8206	<div></div> 0.2990
B	<div></div> 0.8194	<div></div> 0.3010
C	<div></div> 0.8194	<div></div> 0.3010
D	<div></div> 0.8194	<div></div> 0.3000

