



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:49 AM UTC

PDB ID : 9B3U / pdb_00009b3u
EMDB ID : EMD-44156
Title : Rat TRPV2 WT bound to probenecid
Authors : Rocereta, J.A.; Pumroy, R.A.; Moiseenkova-Bell, V.Y.
Deposited on : 2024-03-20
Resolution : 2.40 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

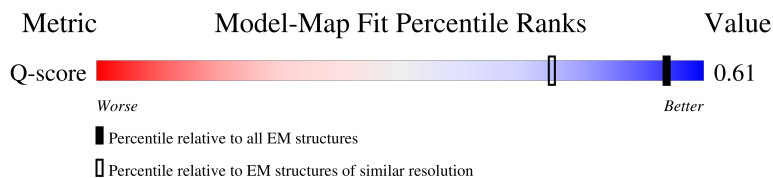
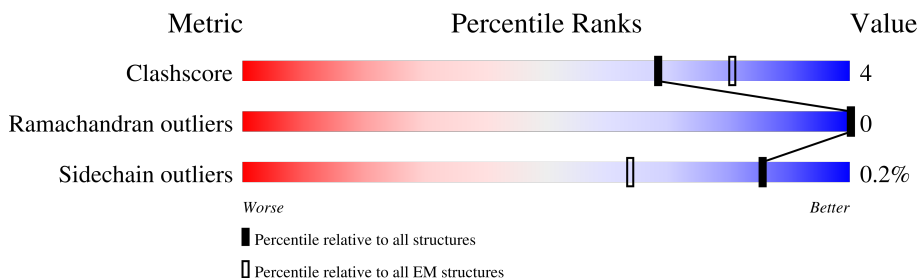
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5628 (1.90 - 2.90)

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	761	 73% 6% 20%
1	B	761	 73% 6% 20%
1	C	761	 73% 6% 20%
1	D	761	 73% 6% 20%

2 Entry composition [i](#)

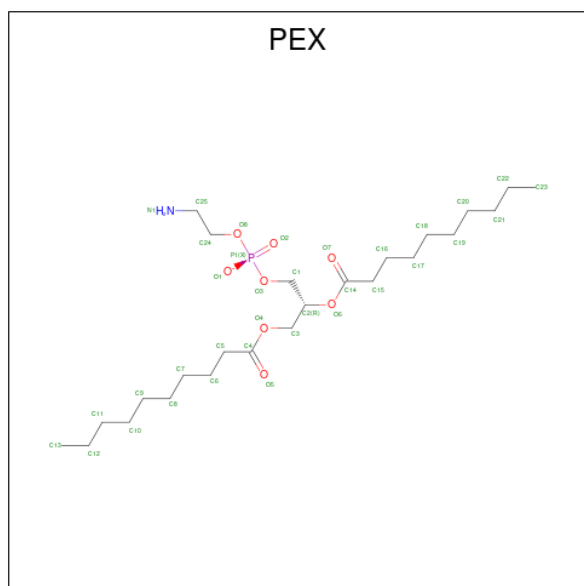
There are 3 unique types of molecules in this entry. The entry contains 19842 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Transient receptor potential cation channel subfamily V member 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	606	Total	C	N	O	S	0	0
			4863	3180	819	836	28		
1	B	607	Total	C	N	O	S	0	0
			4921	3220	826	847	28		
1	C	607	Total	C	N	O	S	0	0
			4921	3220	826	847	28		
1	D	607	Total	C	N	O	S	0	0
			4921	3220	826	847	28		

- Molecule 2 is 1,2-DIDECANOYL-SN-GLYCERO-3-PHOSPHOETHANOLAMINE (CCD ID: PEX) (formula: C₂₅H₄₉NO₈P).



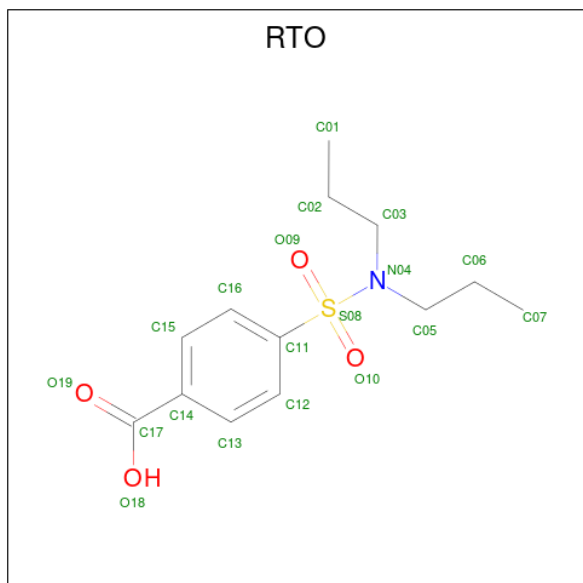
Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			35	25	1	8	1	
2	B	1	Total	C	N	O	P	0
			35	25	1	8	1	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf
2	C	1	Total	C	N	O	P	0
			35	25	1	8	1	
2	D	1	Total	C	N	O	P	0
			35	25	1	8	1	

- Molecule 3 is 4-(dipropylsulfamoyl)benzoic acid (CCD ID: RTO) (formula: $C_{13}H_{19}NO_4S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	S	0
			19	13	1	4	1	
3	A	1	Total	C	N	O	S	0
			19	13	1	4	1	
3	B	1	Total	C	N	O	S	0
			19	13	1	4	1	
3	C	1	Total	C	N	O	S	0
			19	13	1	4	1	

GLY	ASP62	Y228	PRO	ASP	GLU	THR	MET
PRO	ASP63	Y228	ASN	ASP	THR	THR	THR
ILE	PRO	H234	THR	THR	THR	ALA	ALA
GLY	ALA	Q235	LYS	LYS	ALA	SER	SER
ASN	PRO	L253	PRO	PRO	PRO	PRO	PRO
LYS	GLU	L256	SER	SER	SER	PRO	PRO
LYS	ASP	I256	ASN	GLN	ALA	PHE	PHE
ASN	ASN	A257	ASN	GLN	ALA	ARG	ARG
PRO	ASN	D258	GLU	GLU	ARG	LEU	LEU
THR	SER		PRO	PRO	LEU	GLU	GLU
SER	THR	I268	THR	ASP	THR	THR	THR
LYS	VAL	H269	VAL	R74			
PRO	THR	M270	GLY				
GLY	GLU	H313	GLY	G87			
LYS	GLN	I314	ASN	V88			
ASN	PRO	L315	THR	P89			
SER	THR		ALA	E90			
ALA	VAL	P377	GLY	E91			
SER	GLY	L378	GLU	L92			
GLY	GLN		GLU	T93			
GLU	GLU	L389	ASP				
ASP	GLU						
HIS	GLU						
LEU	LEU	F395	GLY	L96			
PRO	PRO	E407	ALA	Y98			
LEU	LEU	P589	GLY				
GLN	GLN		LYS				
VAL	VAL	E614	VAL	W101			
LEU	LEU	L417	LEU	M102			
GLN	GLN	ASP	GLN	S103			
SER	SER	F618	PRO	K104			
PRO	PRO	R619	ALA				
			ALA				
		E647	ILE	S115			
			PRO				
	N650		SER				
	H651		SER	L126			
			LYS	L128			
	V668		ALA	Q129			
			THR				
	R694			D145			
	G695						
ASP	ASP	I441		Q156			
GLY	GLY	S466		K181			
THR	THR						
	P699	Y471		V124			
	E708						
		H621					
	L719	I529		H191			
PRO	PRO			L192			
THR	THR			R193			
LEU	LEU	L534		H202			
SER	SER	R535					
GLY	GLY			T205			
ASP	ASP	R539		C206			
PRO	PRO						
SER	SER	E561		L212			
				T220			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	242931	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 ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.704	Depositor
Minimum map value	-1.679	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.076	Depositor
Recommended contour level	0.223	Depositor
Map size (Å)	265.6, 265.6, 265.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83000004, 0.83000004, 0.83000004	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: PEX, RTO

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	0.75	0/4981	1.25	2/6750 (0.0%)
1	B	0.75	0/5040	1.25	2/6830 (0.0%)
1	C	0.75	0/5040	1.25	2/6830 (0.0%)
1	D	0.75	0/5040	1.25	2/6830 (0.0%)
All	All	0.75	0/20101	1.25	8/27240 (0.0%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	617	ARG	N-CA-C	-6.17	100.52	110.32
1	B	617	ARG	N-CA-C	-6.17	100.52	110.32
1	C	617	ARG	N-CA-C	-6.17	100.52	110.32
1	D	617	ARG	N-CA-C	-6.17	100.52	110.32
1	A	193	ARG	CB-CA-C	-5.05	102.54	111.22

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	4863	0	4901	43	0
1	B	4921	0	4984	46	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4921	0	4984	45	0
1	D	4921	0	4984	46	0
2	A	35	0	49	1	0
2	B	35	0	49	1	0
2	C	35	0	49	1	0
2	D	35	0	49	1	0
3	A	38	0	0	0	0
3	B	19	0	0	0	0
3	C	19	0	0	0	0
All	All	19842	0	20049	146	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 4.

The worst 5 of 146 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:C:651:HIS:CE1	1:D:651:HIS:HD2	2.13	0.66
1:B:651:HIS:CE1	1:C:651:HIS:HD2	2.13	0.66
1:D:315:LEU:HD21	1:D:378:LEU:HD13	1.78	0.66
1:A:651:HIS:HD2	1:D:651:HIS:CE1	2.13	0.65
1:C:315:LEU:HD21	1:C:378:LEU:HD13	1.78	0.65

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	598/761 (79%)	586 (98%)	12 (2%)	0	100	100
1	B	599/761 (79%)	587 (98%)	12 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	599/761 (79%)	587 (98%)	12 (2%)	0	100	100
1	D	599/761 (79%)	587 (98%)	12 (2%)	0	100	100
All	All	2395/3044 (79%)	2347 (98%)	48 (2%)	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	523/676 (77%)	522 (100%)	1 (0%)	87	94
1	B	533/676 (79%)	532 (100%)	1 (0%)	87	94
1	C	533/676 (79%)	532 (100%)	1 (0%)	87	94
1	D	533/676 (79%)	532 (100%)	1 (0%)	87	94
All	All	2122/2704 (78%)	2118 (100%)	4 (0%)	85	94

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	234	HIS
1	B	234	HIS
1	C	234	HIS
1	D	234	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	259	ASN
1	D	156	GLN
1	C	354	ASN
1	C	651	HIS
1	D	203	GLN

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 ⓘ

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	PEX	A	801	-	34,34,34	0.70	0	37,39,39	0.49	0
3	RTO	B	802	-	19,19,19	1.76	5 (26%)	26,26,26	1.12	1 (3%)
3	RTO	A	802	-	19,19,19	1.76	5 (26%)	26,26,26	1.12	1 (3%)
3	RTO	C	802	-	19,19,19	1.76	5 (26%)	26,26,26	1.12	1 (3%)
2	PEX	C	801	-	34,34,34	0.70	0	37,39,39	0.49	0
3	RTO	A	803	-	19,19,19	1.76	5 (26%)	26,26,26	1.12	1 (3%)
2	PEX	D	801	-	34,34,34	0.70	0	37,39,39	0.49	0
2	PEX	B	801	-	34,34,34	0.70	0	37,39,39	0.49	0

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
2	PEX	A	801	-	-	5/38/38/38	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	RTO	B	802	-	-	1/22/22/22	0/1/1/1
3	RTO	A	802	-	-	1/22/22/22	0/1/1/1
3	RTO	C	802	-	-	1/22/22/22	0/1/1/1
2	PEX	C	801	-	-	5/38/38/38	-
3	RTO	A	803	-	-	1/22/22/22	0/1/1/1
2	PEX	D	801	-	-	5/38/38/38	-
2	PEX	B	801	-	-	5/38/38/38	-

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	802	RTO	S08-N04	3.71	1.68	1.63
3	A	803	RTO	S08-N04	3.71	1.68	1.63
3	B	802	RTO	S08-N04	3.71	1.68	1.63
3	C	802	RTO	S08-N04	3.71	1.68	1.63
3	A	802	RTO	O10-S08	3.24	1.47	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	802	RTO	C11-S08-N04	-3.50	103.05	107.28
3	A	803	RTO	C11-S08-N04	-3.50	103.05	107.28
3	B	802	RTO	C11-S08-N04	-3.50	103.05	107.28
3	C	802	RTO	C11-S08-N04	-3.50	103.05	107.28

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	PEX	C17-C18-C19-C20
2	B	801	PEX	C17-C18-C19-C20
2	C	801	PEX	C17-C18-C19-C20
2	D	801	PEX	C17-C18-C19-C20
3	A	802	RTO	C01-C02-C03-N04

There are no ring outliers.

4 monomers are involved in 4 short contacts:

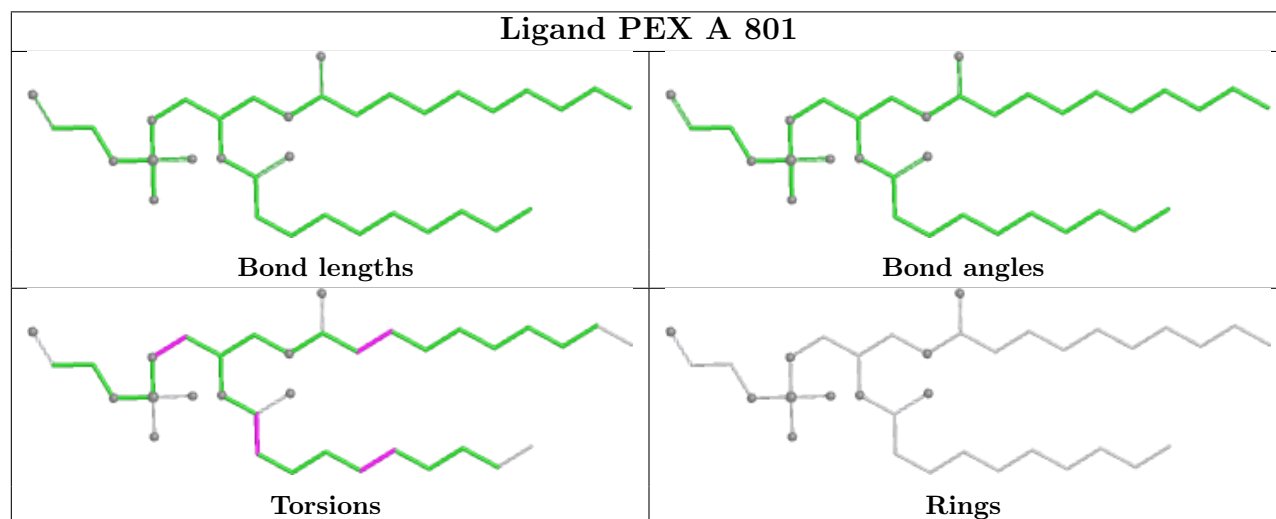
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	PEX	1	0

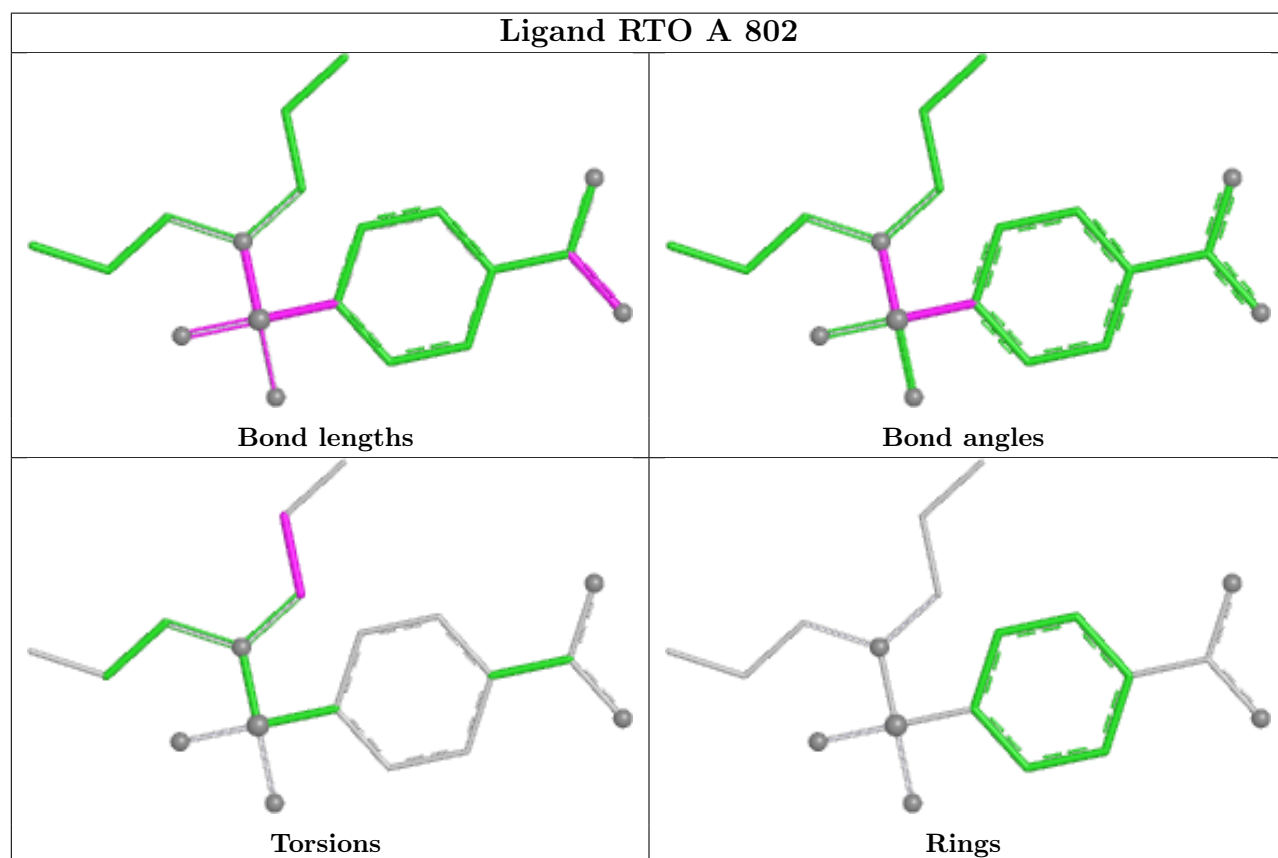
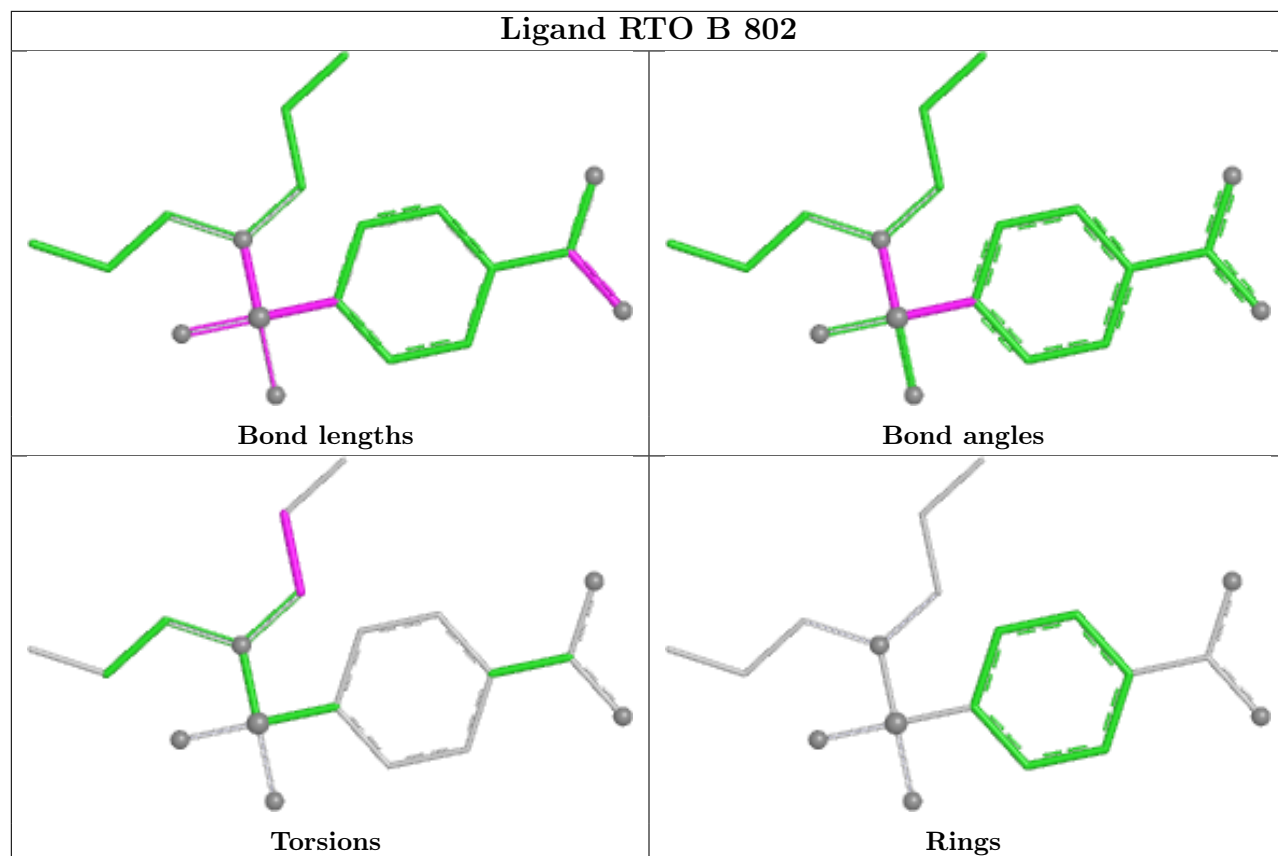
Continued on next page...

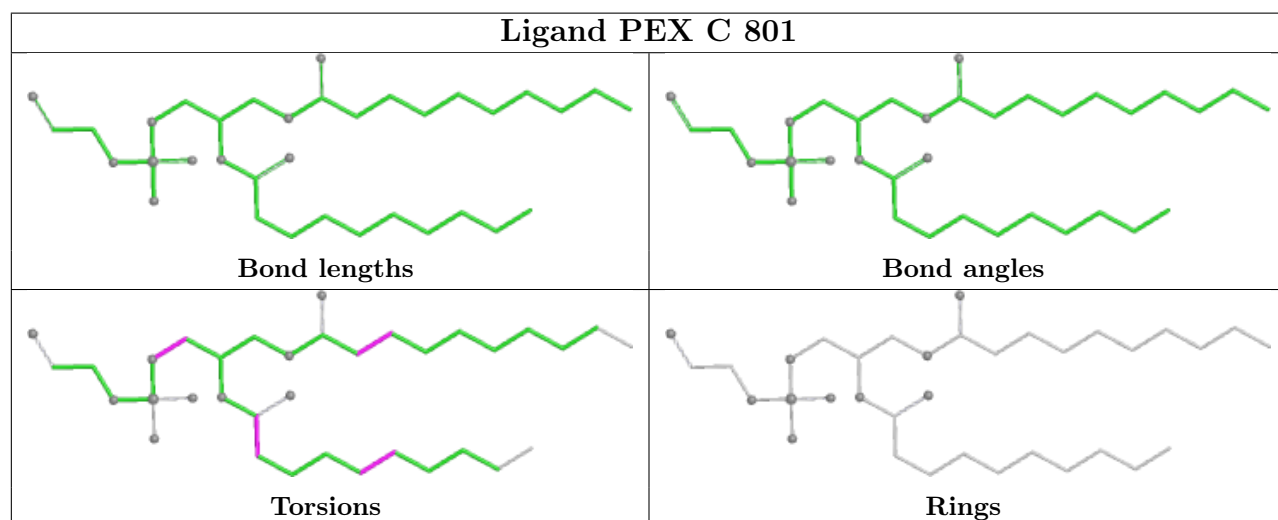
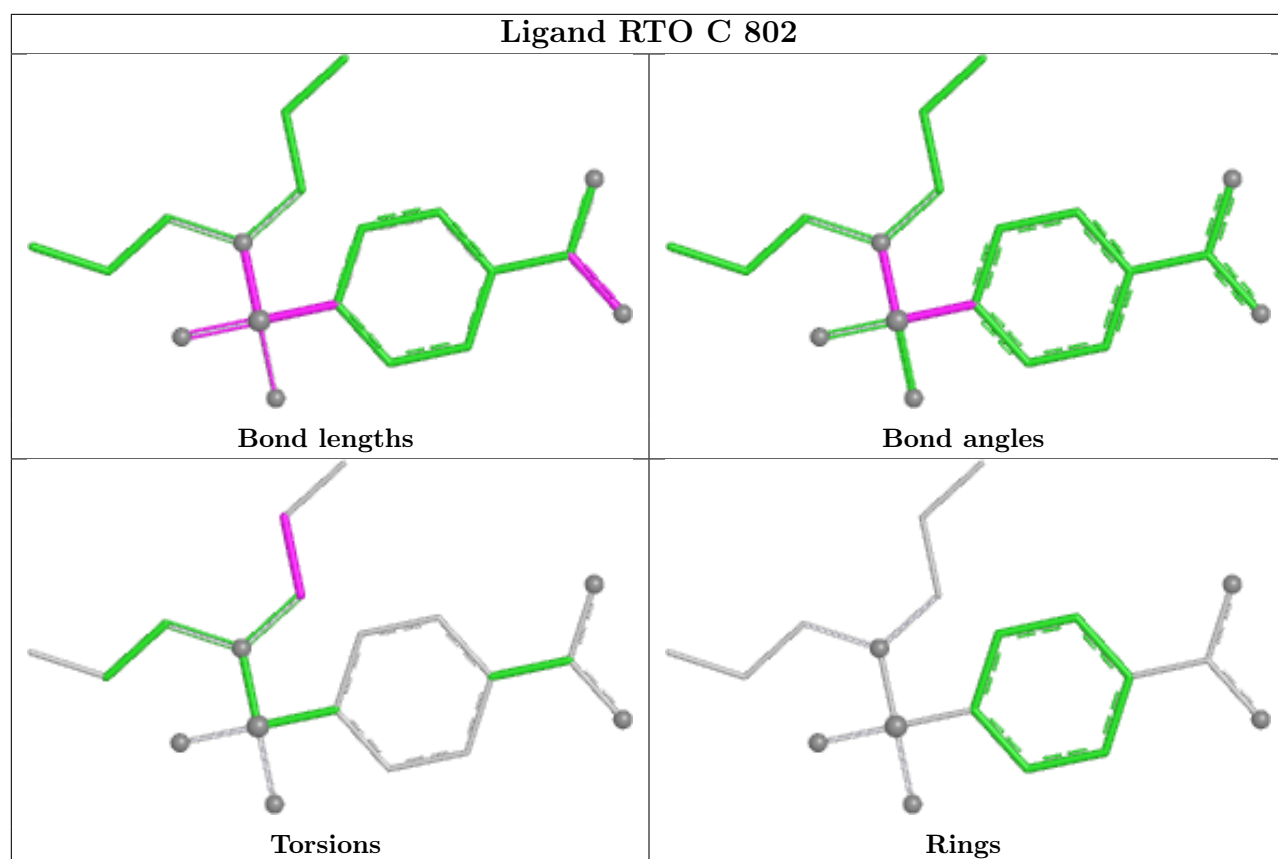
Continued from previous page...

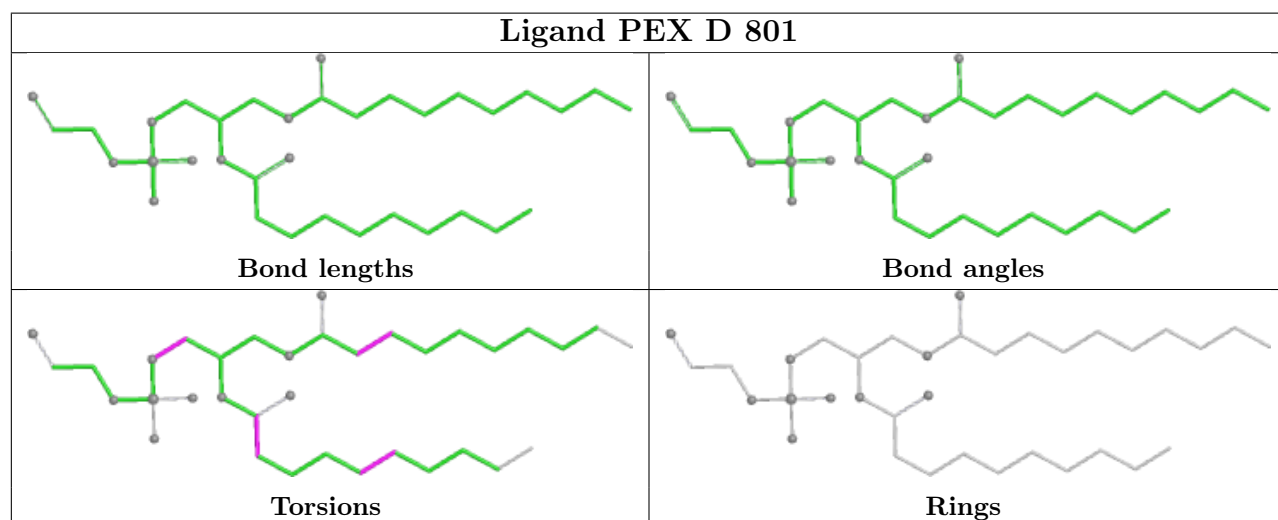
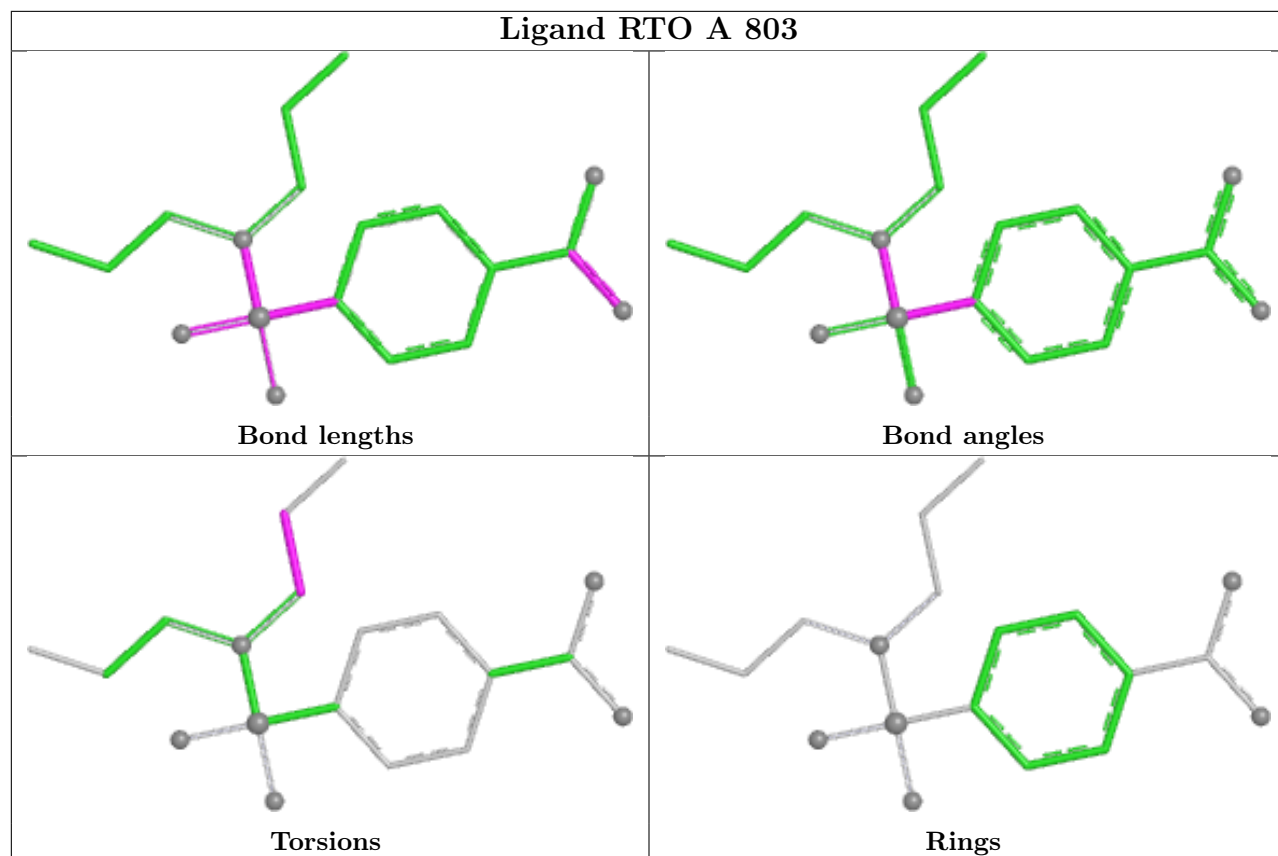
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	801	PEX	1	0
2	D	801	PEX	1	0
2	B	801	PEX	1	0

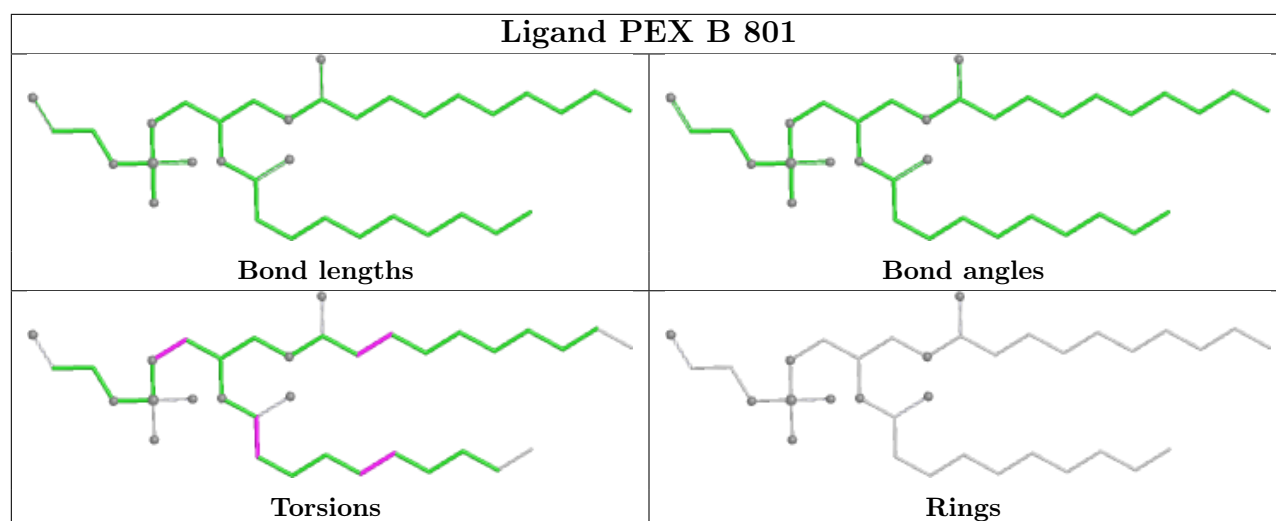
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

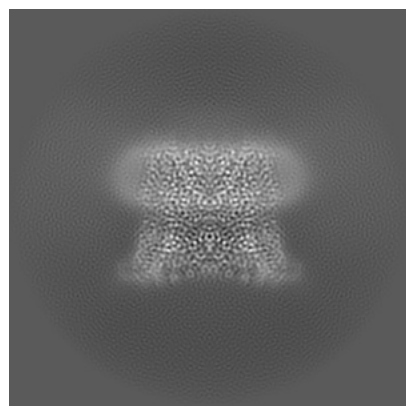
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44156. These allow visual inspection of the internal detail of the map and identification of artifacts.

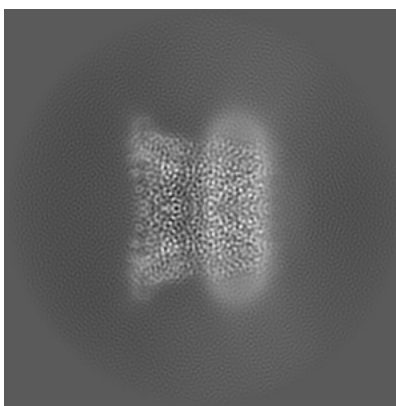
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

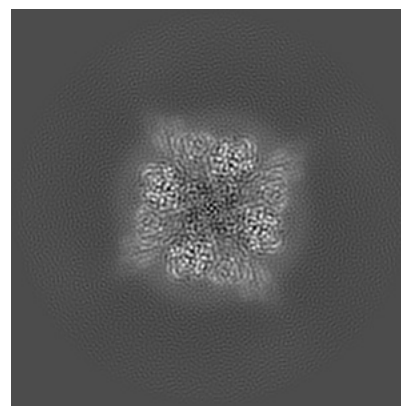
6.1.1 Primary map



X

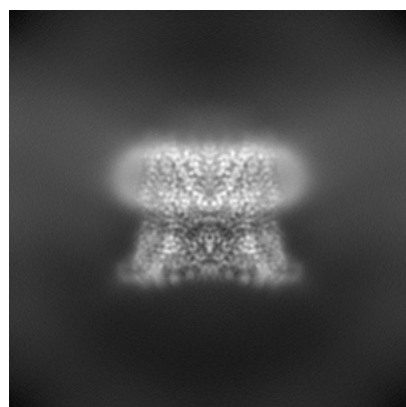


Y

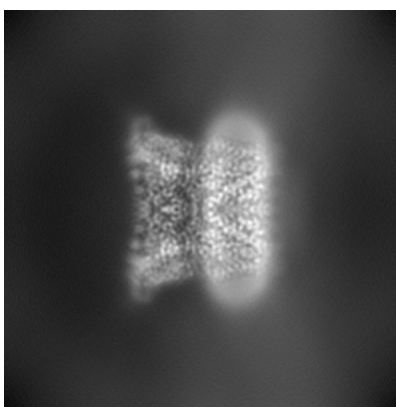


Z

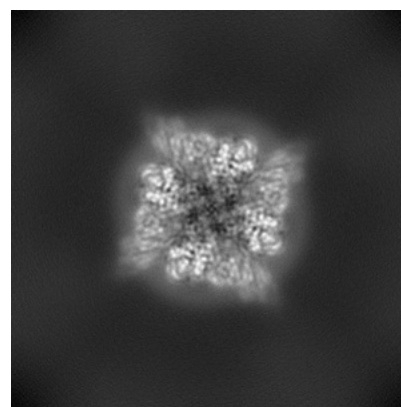
6.1.2 Raw map



X



Y

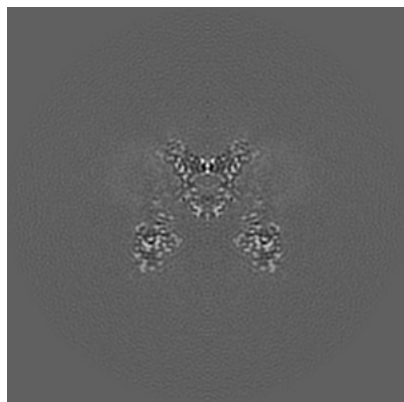


Z

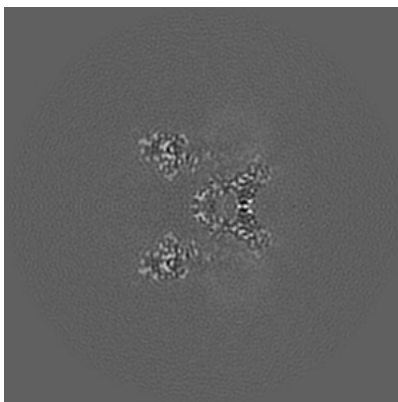
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

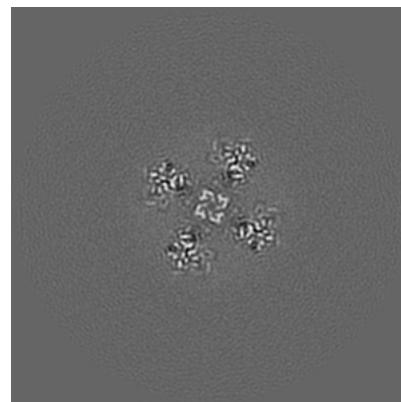
6.2.1 Primary map



X Index: 160

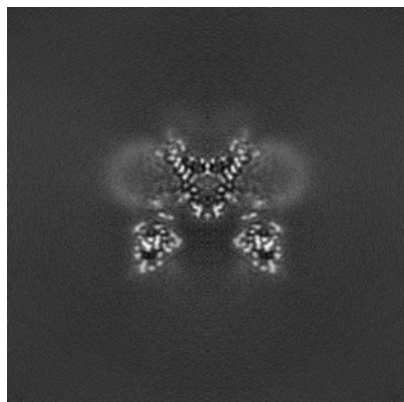


Y Index: 160

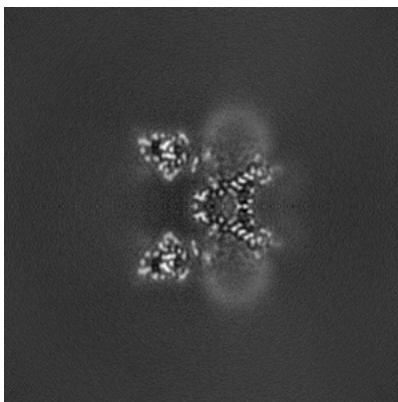


Z Index: 160

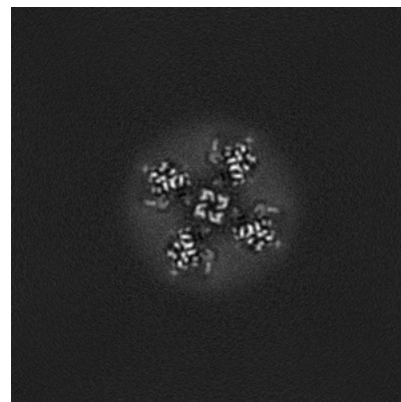
6.2.2 Raw map



X Index: 160



Y Index: 160

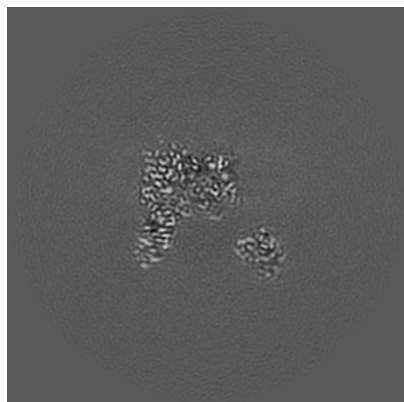


Z Index: 160

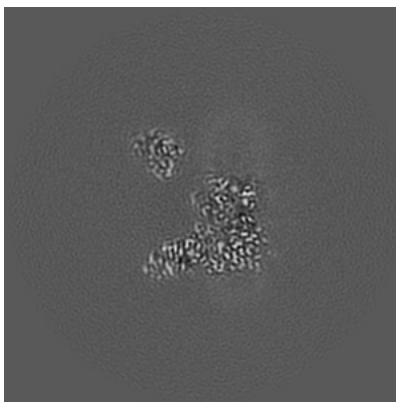
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

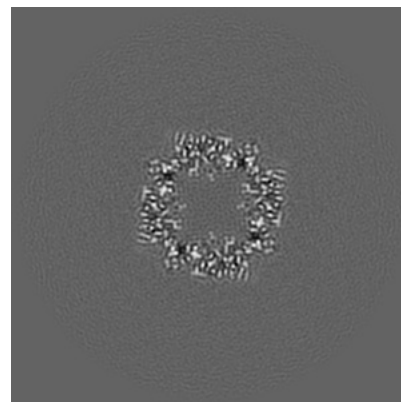
6.3.1 Primary map



X Index: 148

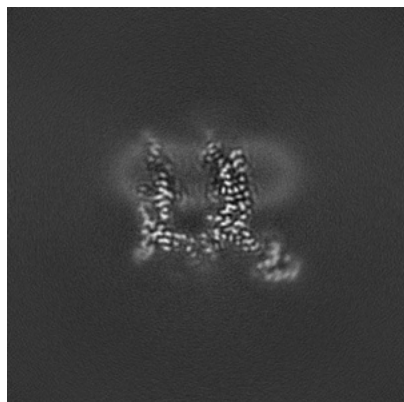


Y Index: 172

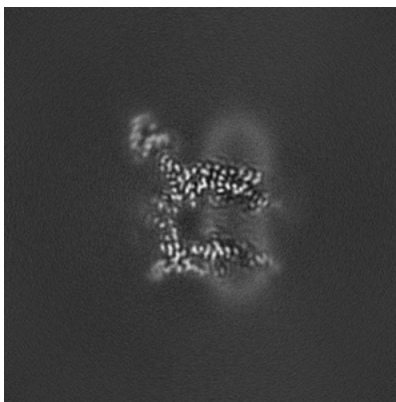


Z Index: 133

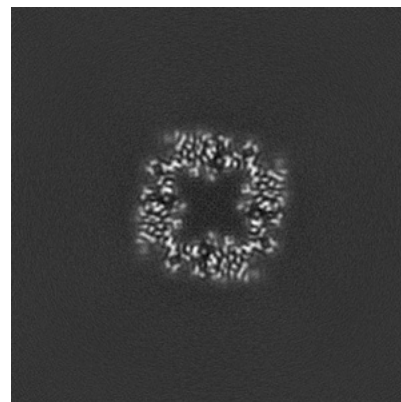
6.3.2 Raw map



X Index: 129



Y Index: 191

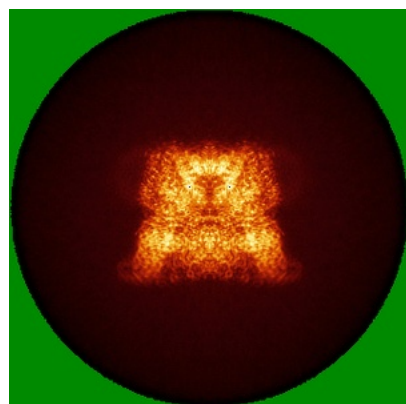


Z Index: 132

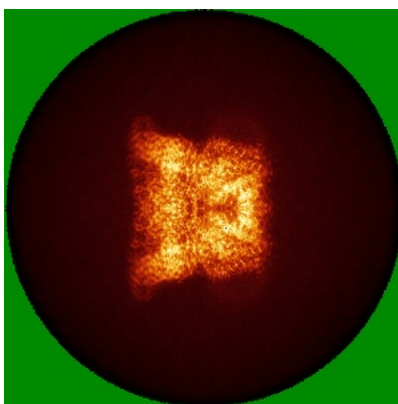
The images above show the largest variance slices of the map in three orthogonal directions.

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

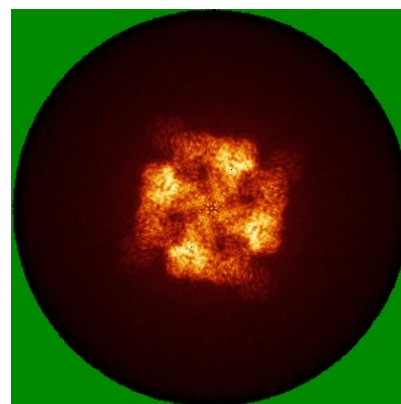
6.4.1 Primary map



X

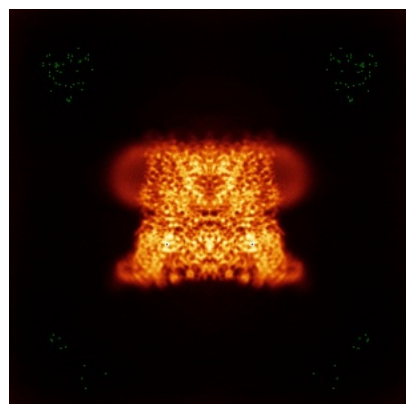


Y

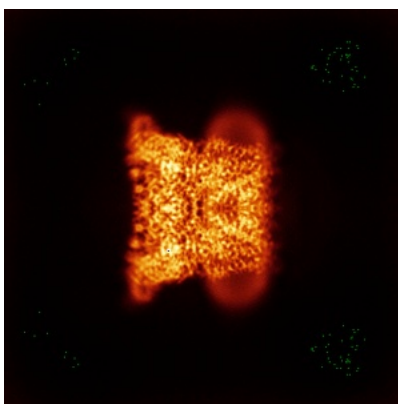


Z

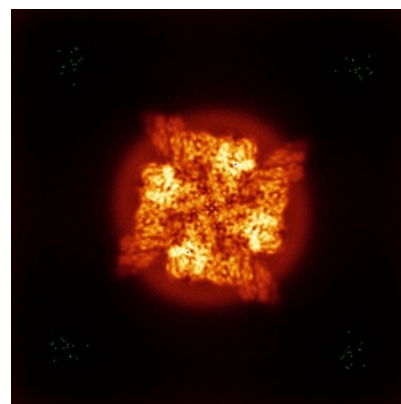
6.4.2 Raw map



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.

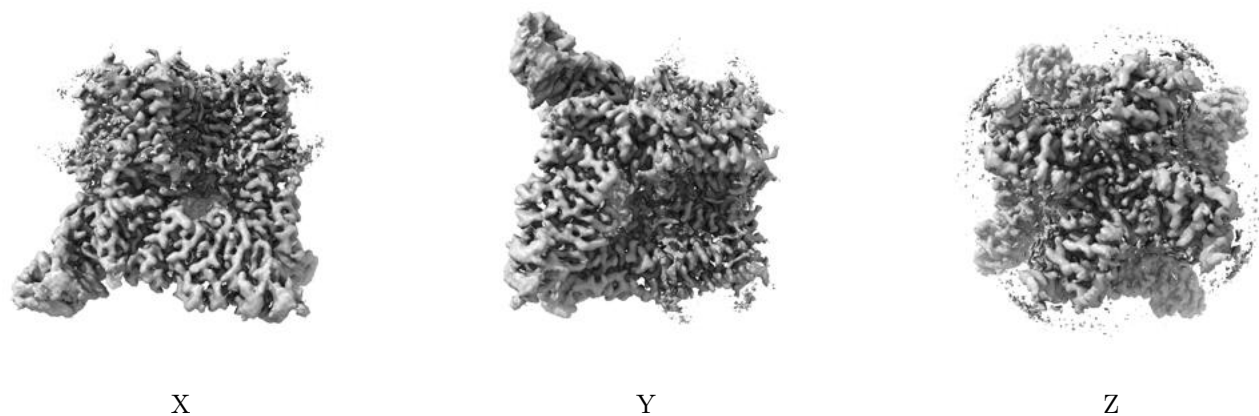
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.223. 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.

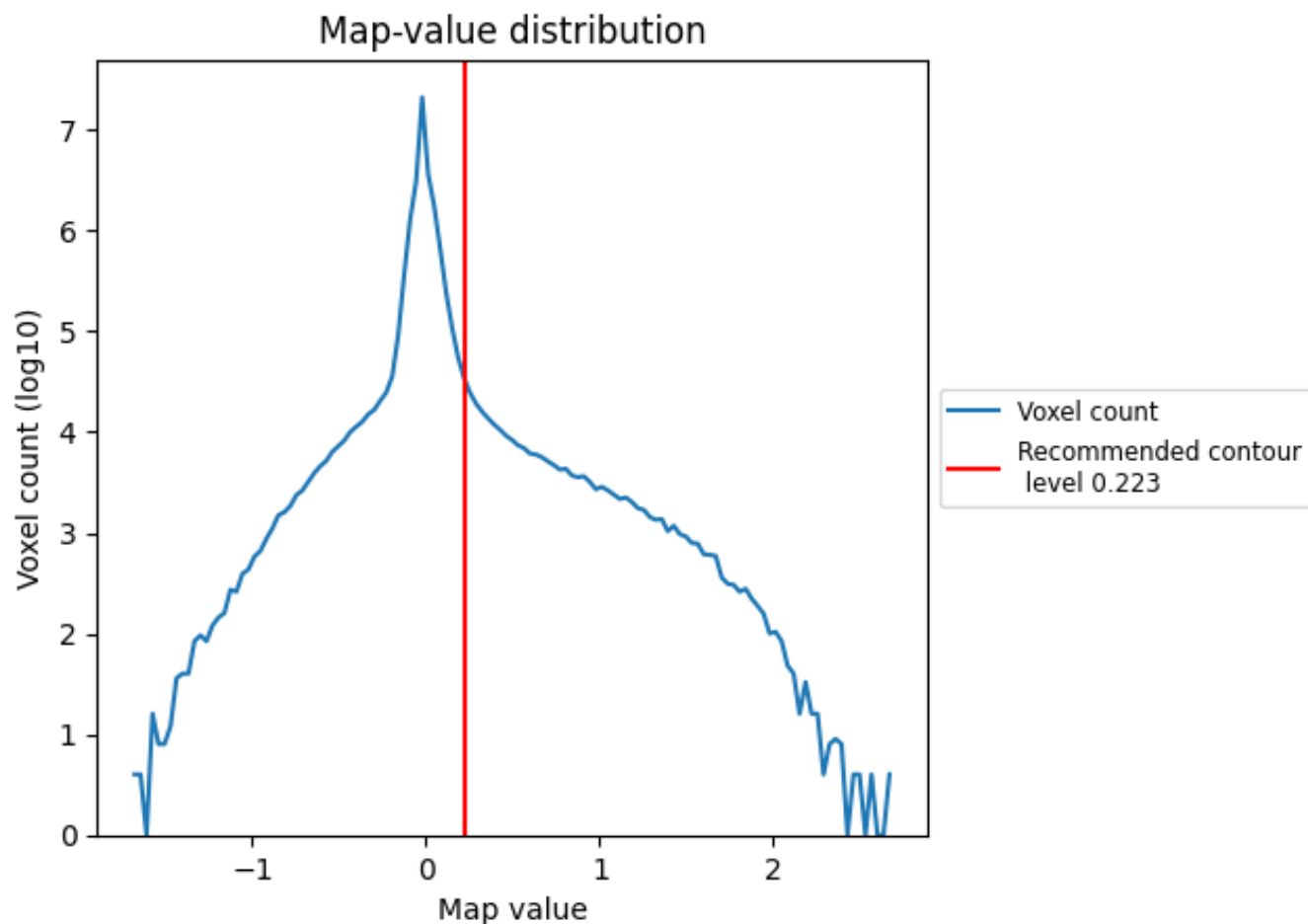
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

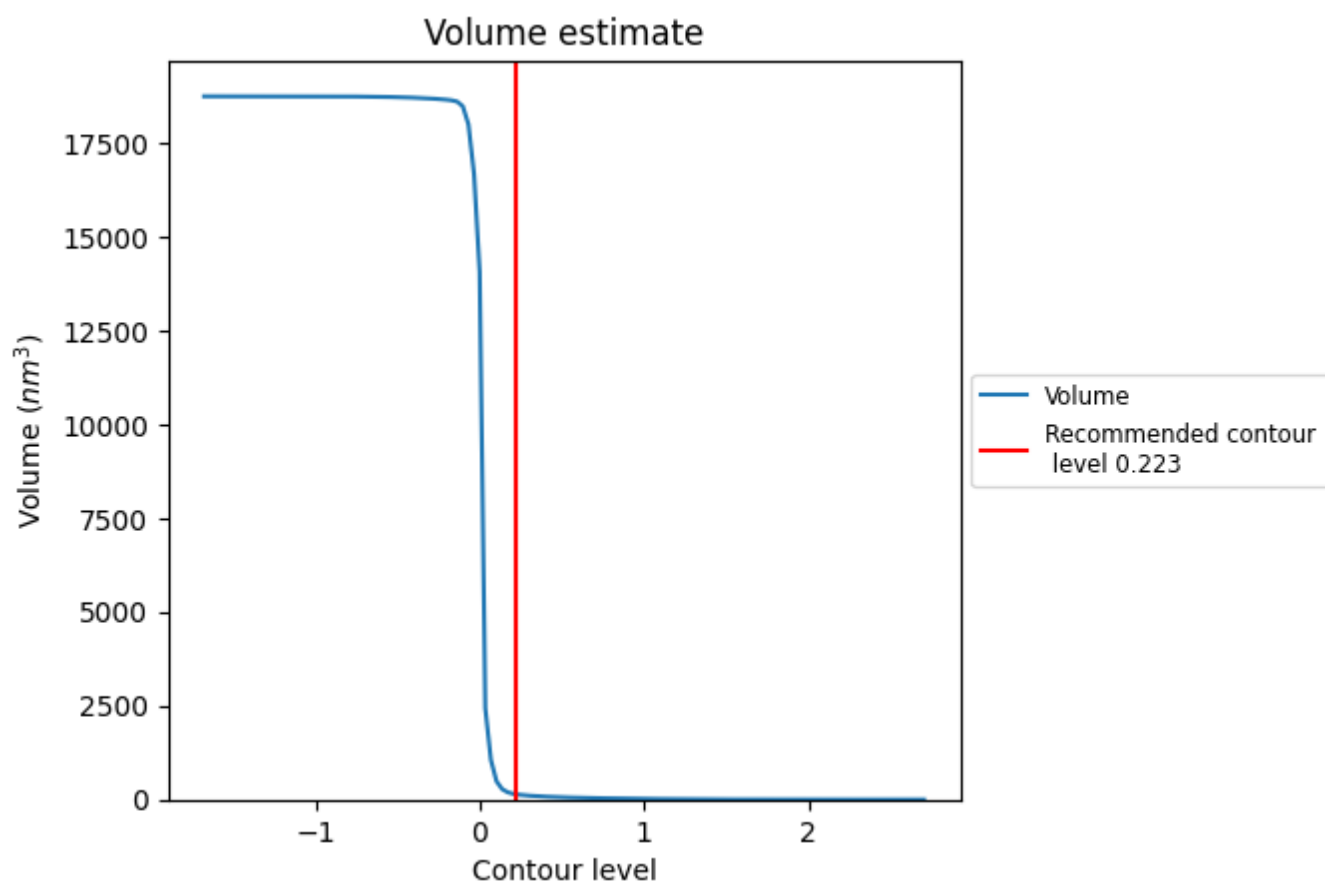
This section contains the results of statistical analysis of the map.

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.

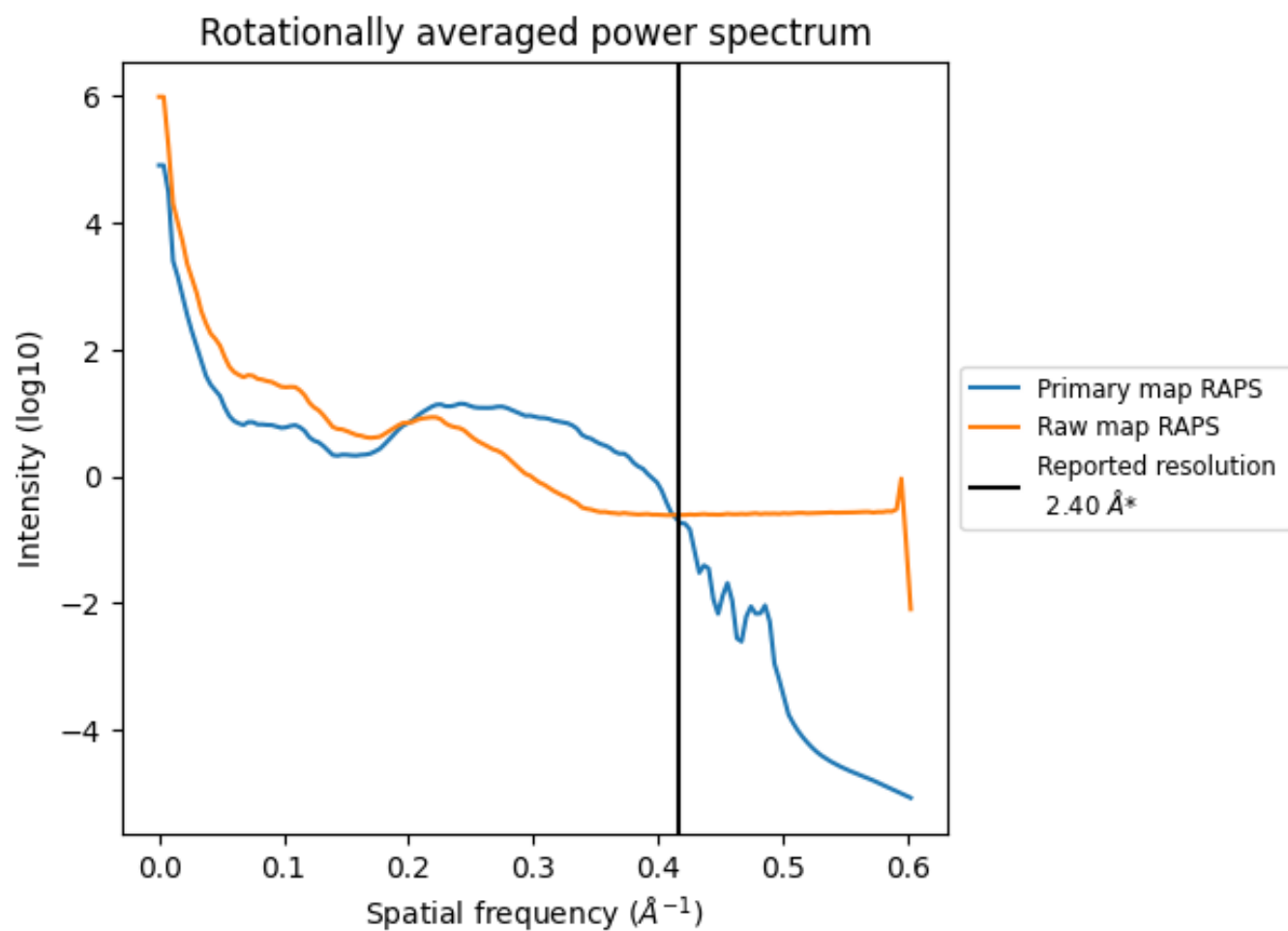
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 140 nm³; this corresponds to an approximate mass of 126 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 ⓘ

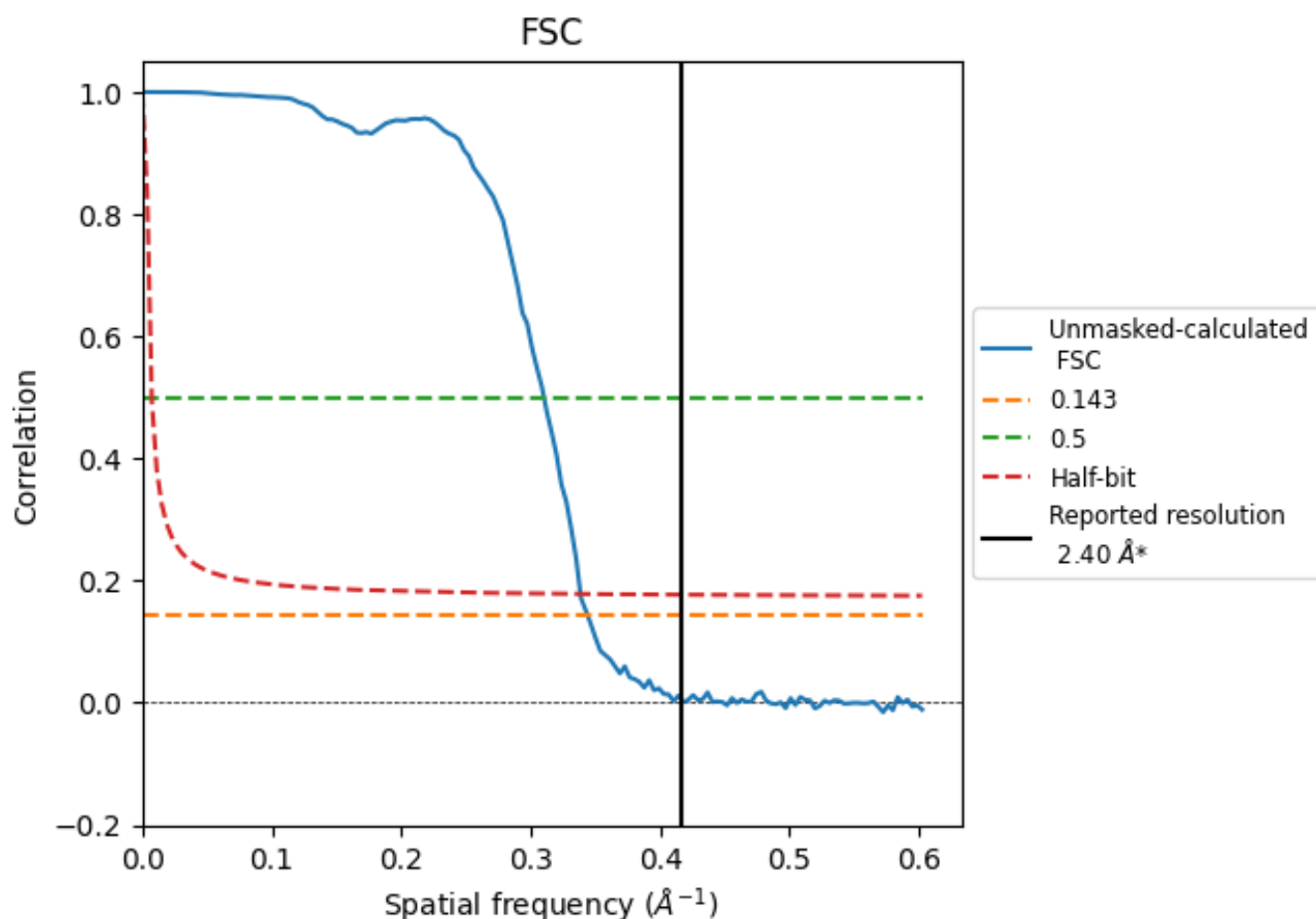


*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8.2 Resolution estimates [i](#)

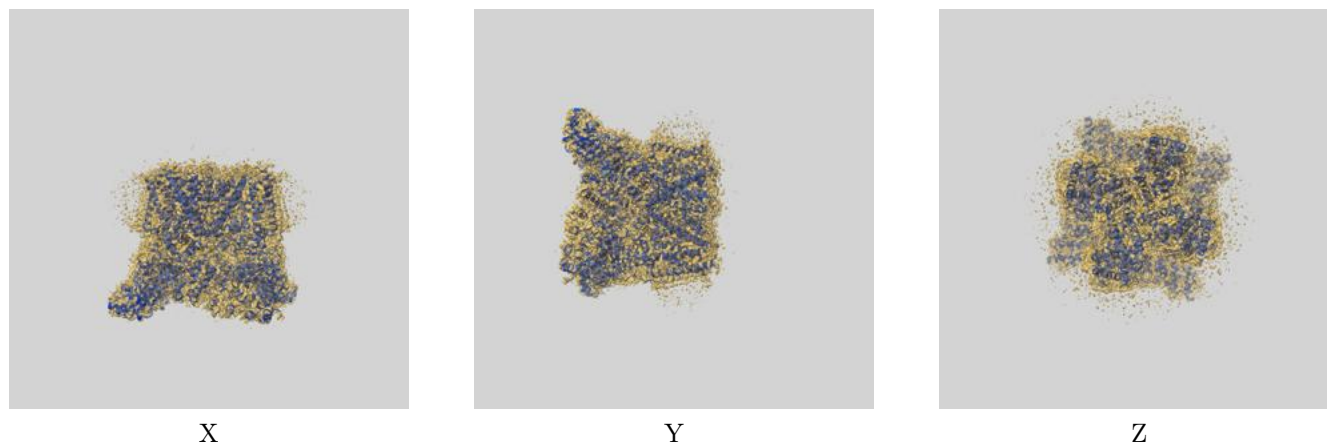
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.91	3.22	2.95

*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 2.91 differs from the reported value 2.4 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-44156 and PDB model 9B3U. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



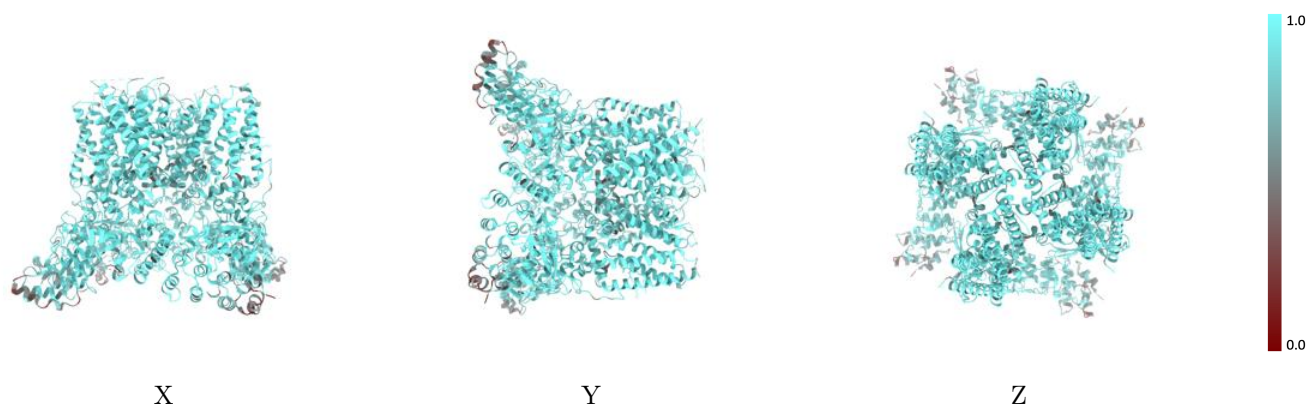
The images above show the 3D surface view of the map at the recommended contour level 0.223 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



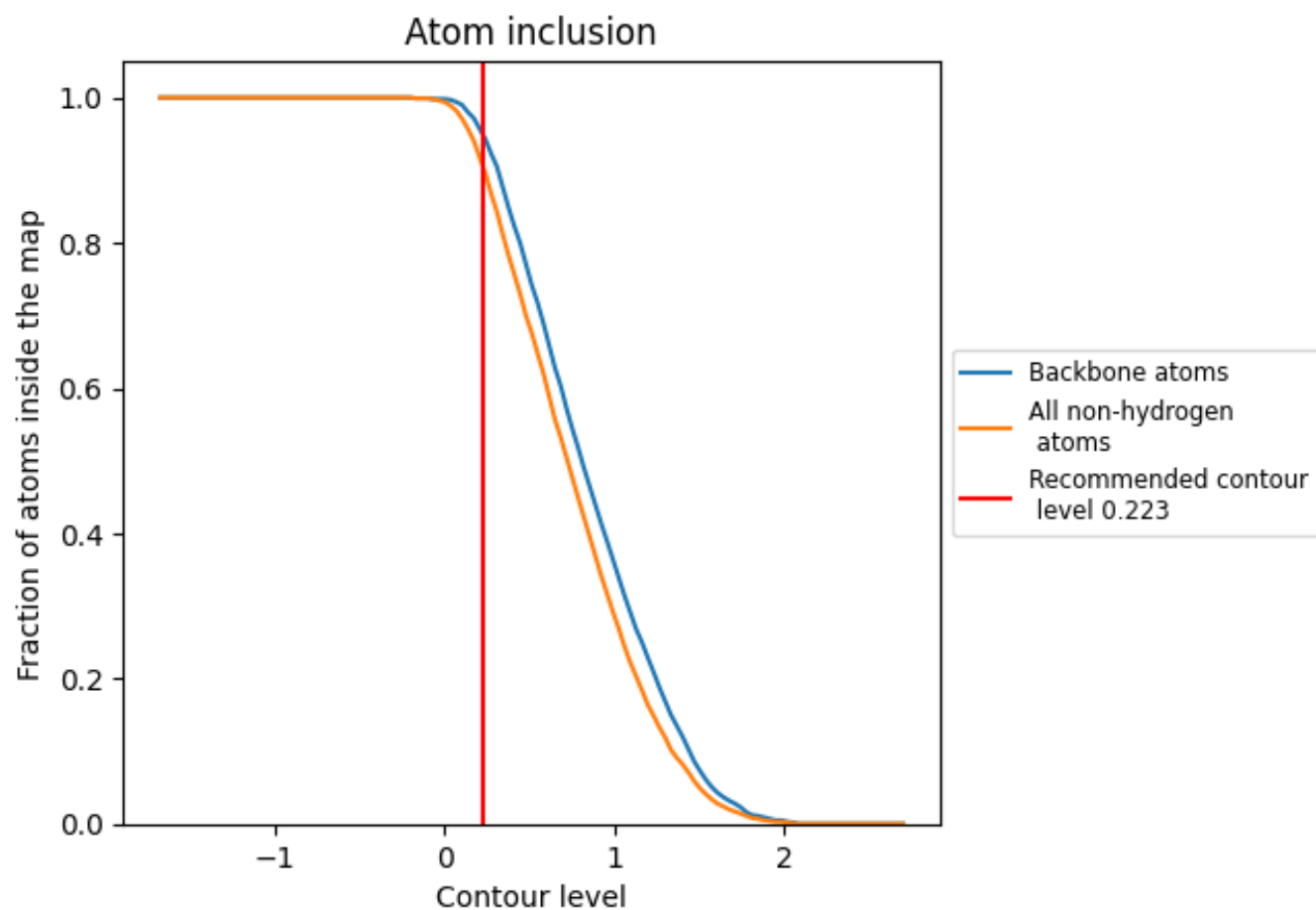
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.223).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 91% 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 (0.223) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9060	0.6100
A	0.9130	0.6130
B	0.9040	0.6100
C	0.9040	0.6100
D	0.9030	0.6090

