



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:27 PM UTC

PDB ID : 7RHS / pdb_00007rhs
EMDB ID : EMD-24468
Title : Cryo-EM structure of apo-state of human CNGA3/CNGB3 channel
Authors : Zheng, X.; Yang, J.
Deposited on : 2021-07-18
Resolution : 2.93 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:

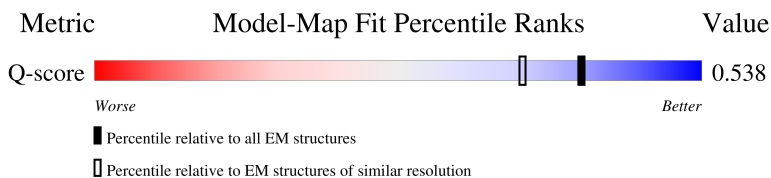
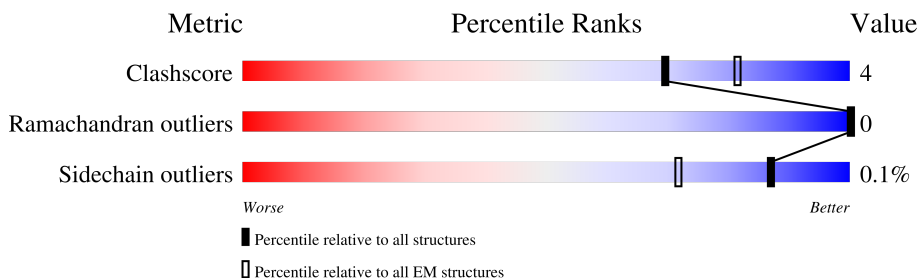
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.93 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	13037 (2.43 - 3.43)

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	706	
1	B	706	
1	C	706	
2	D	841	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14767 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 Cyclic nucleotide-gated cation channel alpha-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	456	Total	C	N	O	S	1	0
			3725	2433	603	674	15		
1	B	453	Total	C	N	O	S	0	0
			3692	2410	600	667	15		
1	C	454	Total	C	N	O	S	0	0
			3697	2413	601	668	15		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q16281
A	-2	PRO	-	expression tag	UNP Q16281
A	-1	GLY	-	expression tag	UNP Q16281
A	0	SER	-	expression tag	UNP Q16281
A	695	ASP	-	expression tag	UNP Q16281
A	696	TYR	-	expression tag	UNP Q16281
A	697	LYS	-	expression tag	UNP Q16281
A	698	ASP	-	expression tag	UNP Q16281
A	699	ASP	-	expression tag	UNP Q16281
A	700	ASP	-	expression tag	UNP Q16281
A	701	ASP	-	expression tag	UNP Q16281
A	702	LYS	-	expression tag	UNP Q16281
B	-3	GLY	-	expression tag	UNP Q16281
B	-2	PRO	-	expression tag	UNP Q16281
B	-1	GLY	-	expression tag	UNP Q16281
B	0	SER	-	expression tag	UNP Q16281
B	695	ASP	-	expression tag	UNP Q16281
B	696	TYR	-	expression tag	UNP Q16281
B	697	LYS	-	expression tag	UNP Q16281
B	698	ASP	-	expression tag	UNP Q16281
B	699	ASP	-	expression tag	UNP Q16281
B	700	ASP	-	expression tag	UNP Q16281
B	701	ASP	-	expression tag	UNP Q16281
B	702	LYS	-	expression tag	UNP Q16281

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP Q16281
C	-2	PRO	-	expression tag	UNP Q16281
C	-1	GLY	-	expression tag	UNP Q16281
C	0	SER	-	expression tag	UNP Q16281
C	695	ASP	-	expression tag	UNP Q16281
C	696	TYR	-	expression tag	UNP Q16281
C	697	LYS	-	expression tag	UNP Q16281
C	698	ASP	-	expression tag	UNP Q16281
C	699	ASP	-	expression tag	UNP Q16281
C	700	ASP	-	expression tag	UNP Q16281
C	701	ASP	-	expression tag	UNP Q16281
C	702	LYS	-	expression tag	UNP Q16281

- Molecule 2 is a protein called Cyclic nucleotide-gated cation channel beta-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	441	Total	C	N	O	S	1	0
			3610	2364	591	634	21		

There are 33 discrepancies between the modelled and reference sequences:

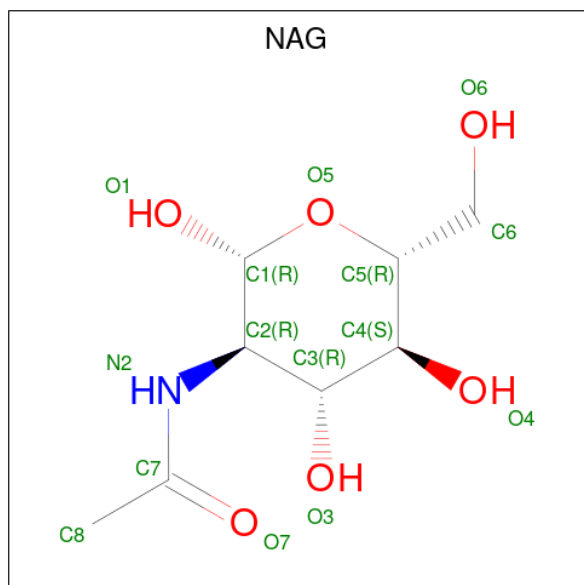
Chain	Residue	Modelled	Actual	Comment	Reference
D	-31	MET	-	initiating methionine	UNP Q9NQW8
D	-30	GLY	-	expression tag	UNP Q9NQW8
D	-29	SER	-	expression tag	UNP Q9NQW8
D	-28	TRP	-	expression tag	UNP Q9NQW8
D	-27	SER	-	expression tag	UNP Q9NQW8
D	-26	HIS	-	expression tag	UNP Q9NQW8
D	-25	PRO	-	expression tag	UNP Q9NQW8
D	-24	GLN	-	expression tag	UNP Q9NQW8
D	-23	PHE	-	expression tag	UNP Q9NQW8
D	-22	GLU	-	expression tag	UNP Q9NQW8
D	-21	LYS	-	expression tag	UNP Q9NQW8
D	-20	GLY	-	expression tag	UNP Q9NQW8
D	-19	GLY	-	expression tag	UNP Q9NQW8
D	-18	GLY	-	expression tag	UNP Q9NQW8
D	-17	SER	-	expression tag	UNP Q9NQW8
D	-16	GLY	-	expression tag	UNP Q9NQW8
D	-15	GLY	-	expression tag	UNP Q9NQW8
D	-14	GLY	-	expression tag	UNP Q9NQW8
D	-13	SER	-	expression tag	UNP Q9NQW8
D	-12	GLY	-	expression tag	UNP Q9NQW8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-11	GLY	-	expression tag	UNP Q9NQW8
D	-10	SER	-	expression tag	UNP Q9NQW8
D	-9	ALA	-	expression tag	UNP Q9NQW8
D	-8	TRP	-	expression tag	UNP Q9NQW8
D	-7	SER	-	expression tag	UNP Q9NQW8
D	-6	HIS	-	expression tag	UNP Q9NQW8
D	-5	PRO	-	expression tag	UNP Q9NQW8
D	-4	GLN	-	expression tag	UNP Q9NQW8
D	-3	PHE	-	expression tag	UNP Q9NQW8
D	-2	GLU	-	expression tag	UNP Q9NQW8
D	-1	LYS	-	expression tag	UNP Q9NQW8
D	0	GLY	-	expression tag	UNP Q9NQW8
D	1	SER	-	expression tag	UNP Q9NQW8

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	D	1	Total	Na	0
			1	1	

D576	K579	V589	L595	L616	L624	A642	L646	Lys	Gln	Lys	Ala	Lys	Lys	Thr	Ala	Glu	Ala	Thr	Pro	Arg	Lys	Asp	Leu	Ala	Leu	Leu	Phe	Pro	Pro	Lys	Glu	Glu	Thr	Pro	Lys	Leu	Gly	Gly	Thr	Gly	Lys	Ala	Ser	Leu	Ala	Arg	Leu		
Leu	Lys	Lys	Arg	Glu	Gln	Ala	Ala	Lys	Gln	Lys	Glu	Lys	Glu	Gly	Val	Lys	Asn	Glu	Asp	Lys	Gln	Lys	Glu	Asn	Lys	Leu	Lys	Gln	Lys	Glu	Asn	Lys	Asp	Gly	Lys	Glu	Glu	Asn	Lys	Arg	Gly	Pro	Glu	Lys	Gln	Pro	Arg	Leu	
Asp	Arg	Pro	Glu	Cys	Thr	Ala	Ser	Pro	Ile	Gln	Ala	Val	Glu	Thr	Val	Leu	Pro	Arg	Gly	Thr	Ser	Arg	Gln	Ser	Leu	Ile	Ile	Ser	Met	Ala	Pro	Ser	Ala	Glu	Gly	Gly	Glu	Glu	Val	Leu	Thr	Ile	Glu	Val	Lys	Lys	Ala	Lys	Gln

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	205492	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	57.63	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.771	Depositor
Minimum map value	-1.620	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.070	Depositor
Recommended contour level	0.4	Depositor
Map size ($\text{\AA}$)	296.892, 296.892, 296.892	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.8247, 0.8247, 0.8247	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, NA

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	0.33	2/3813 (0.1%)	0.62	2/5170 (0.0%)
1	B	0.31	1/3776 (0.0%)	0.61	2/5120 (0.0%)
1	C	0.27	0/3781	0.59	2/5127 (0.0%)
2	D	0.34	2/3704 (0.1%)	0.58	2/5027 (0.0%)
All	All	0.31	5/15074 (0.0%)	0.60	8/20444 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	163	PRO	N-CD	-8.51	1.35	1.47
2	D	442[A]	ARG	C-O	6.72	1.31	1.24
2	D	442[B]	ARG	C-O	6.72	1.31	1.24
1	A	392[A]	PHE	C-O	5.95	1.31	1.24
1	A	392[B]	PHE	C-O	5.95	1.31	1.24

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	442[A]	ARG	CA-C-O	8.41	129.46	120.55
2	D	442[B]	ARG	CA-C-O	8.41	129.46	120.55
1	B	560	SER	N-CA-C	8.38	120.19	111.14
1	A	392[A]	PHE	CA-C-O	6.24	127.05	119.31
1	A	392[B]	PHE	CA-C-O	6.24	127.05	119.31

There are no chirality outliers.

There are no planarity outliers.

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	3725	0	3779	32	0
1	B	3692	0	3749	35	0
1	C	3697	0	3754	28	0
2	D	3610	0	3629	24	0
3	A	14	0	13	0	0
3	B	14	0	13	0	0
3	C	14	0	13	0	0
4	D	1	0	0	0	0
All	All	14767	0	14950	108	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 108 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:182:ASN:O	1:A:186:LEU:HB2	1.65	0.95
1:B:182:ASN:O	1:B:186:LEU:HB2	1.67	0.94
1:C:182:ASN:O	1:C:186:LEU:HB2	1.70	0.92
1:B:559:LYS:HD3	1:B:610:ASN:HB2	1.52	0.91
1:B:260:ASP:O	1:B:263:TYR:HB2	1.88	0.73

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	455/706 (64%)	440 (97%)	15 (3%)	0	100	100
1	B	451/706 (64%)	437 (97%)	14 (3%)	0	100	100
1	C	452/706 (64%)	441 (98%)	11 (2%)	0	100	100
2	D	440/841 (52%)	430 (98%)	10 (2%)	0	100	100
All	All	1798/2959 (61%)	1748 (97%)	50 (3%)	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	412/618 (67%)	412 (100%)	0	100	100
1	B	408/618 (66%)	408 (100%)	0	100	100
1	C	408/618 (66%)	408 (100%)	0	100	100
2	D	392/737 (53%)	391 (100%)	1 (0%)	86	93
All	All	1620/2591 (62%)	1619 (100%)	1 (0%)	87	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	307	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	229	GLN
2	D	423	GLN
1	C	305	ASN
2	D	611	HIS
1	C	554	ASN

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, 1 is monoatomic - leaving 3 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	NAG	B	801	1	14,14,15	0.53	0	17,19,21	0.72	1 (5%)
3	NAG	C	801	1	14,14,15	0.56	0	17,19,21	0.75	1 (5%)
3	NAG	A	801	1	14,14,15	0.60	0	17,19,21	0.71	1 (5%)

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	NAG	B	801	1	-	2/6/23/26	0/1/1/1
3	NAG	C	801	1	-	2/6/23/26	0/1/1/1
3	NAG	A	801	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	801	NAG	C1-O5-C5	2.74	115.85	112.19
3	B	801	NAG	C1-O5-C5	2.62	115.70	112.19
3	A	801	NAG	C1-O5-C5	2.56	115.62	112.19

There are no chirality outliers.

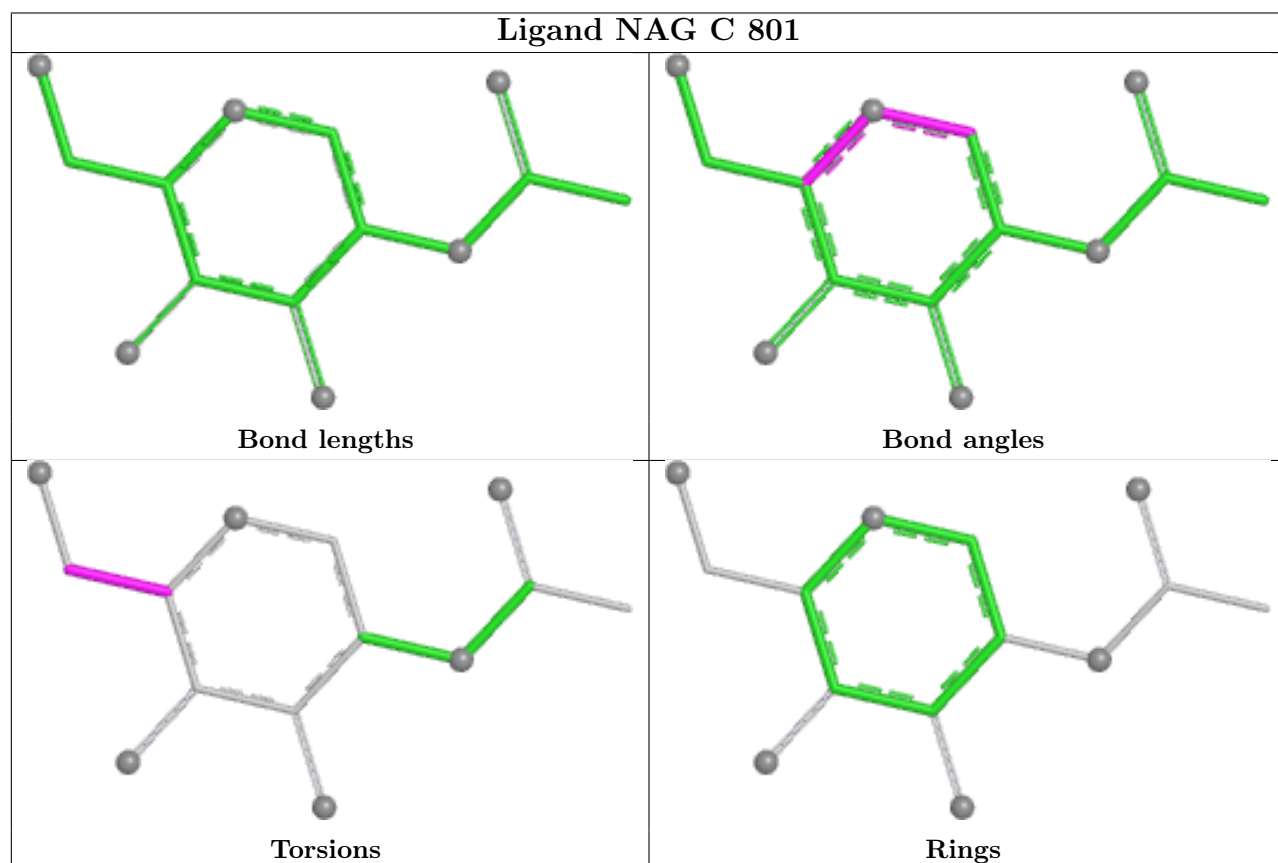
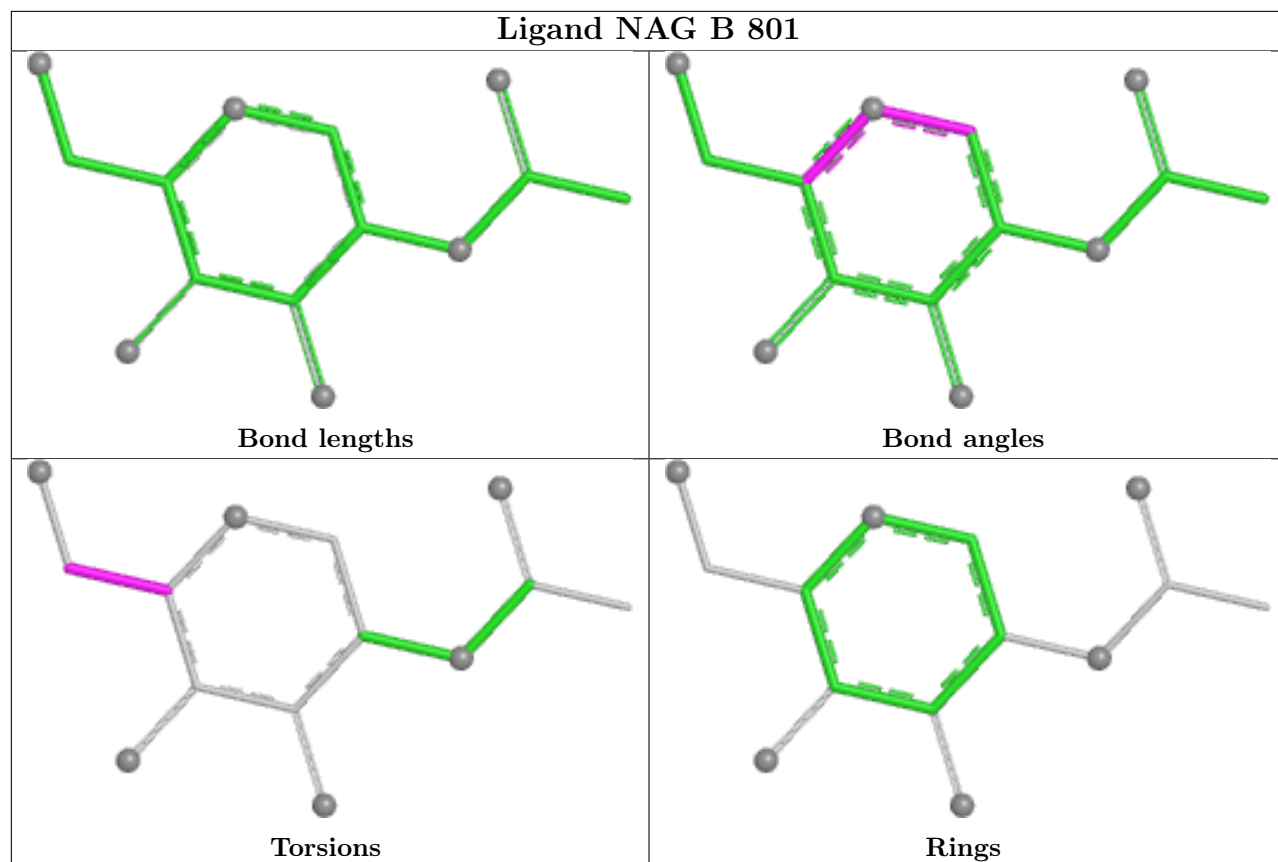
5 of 6 torsion outliers are listed below:

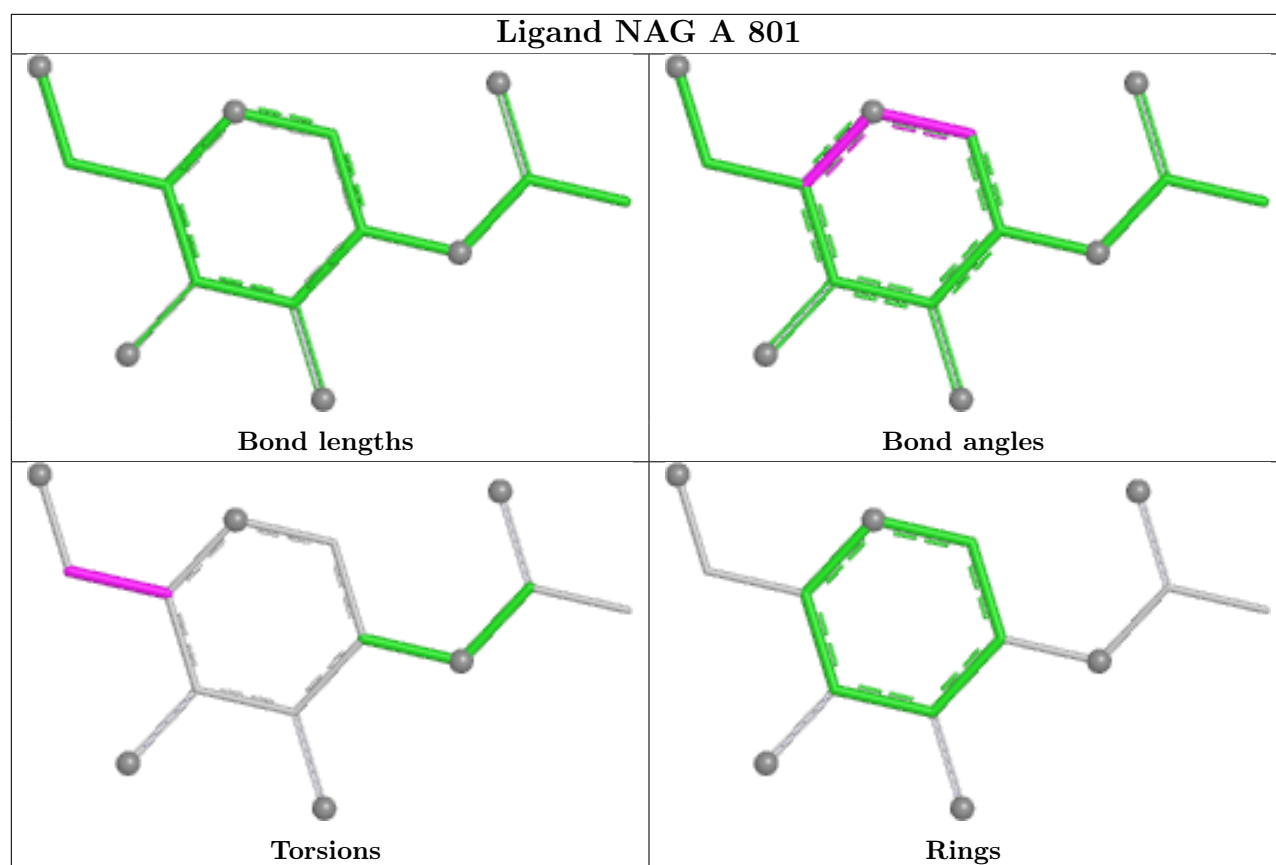
Mol	Chain	Res	Type	Atoms
3	A	801	NAG	O5-C5-C6-O6
3	B	801	NAG	O5-C5-C6-O6
3	C	801	NAG	O5-C5-C6-O6
3	A	801	NAG	C4-C5-C6-O6
3	B	801	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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.

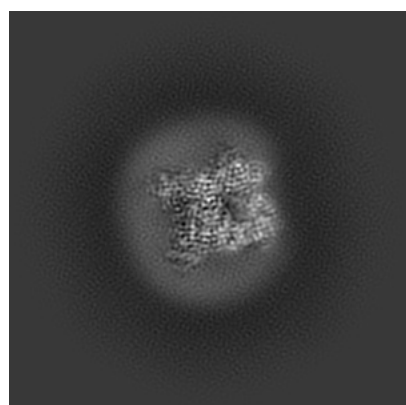
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24468. These allow visual inspection of the internal detail of the map and identification of artifacts.

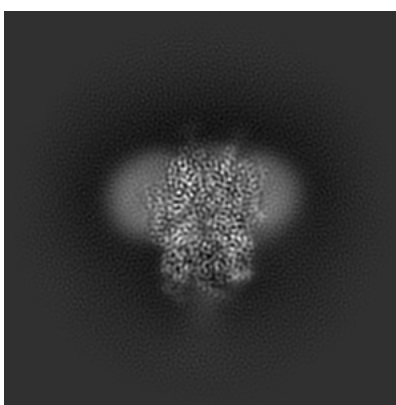
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

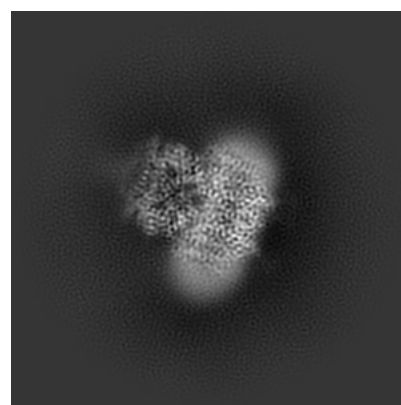
6.1.1 Primary map



X



Y

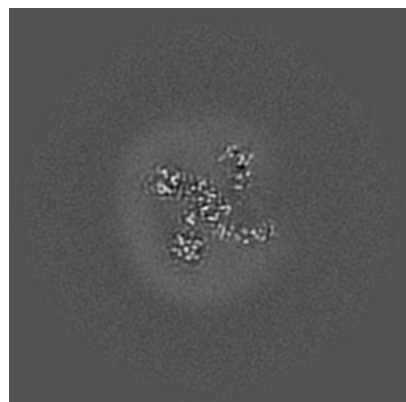


Z

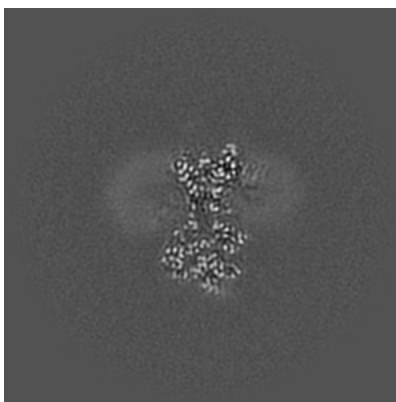
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

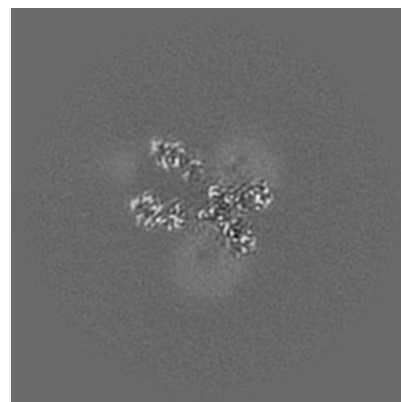
6.2.1 Primary map



X Index: 180



Y Index: 180

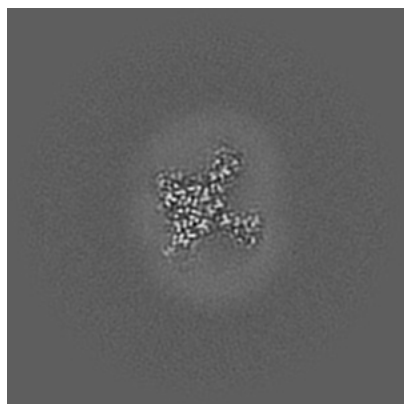


Z Index: 180

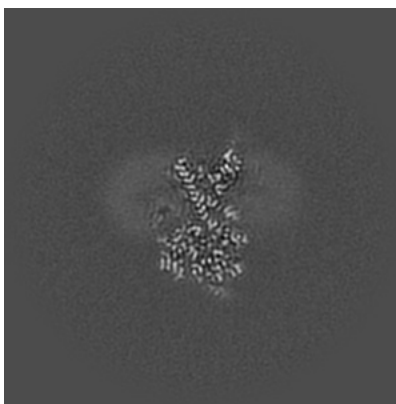
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

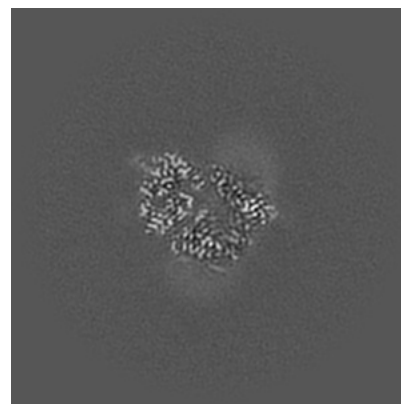
6.3.1 Primary map



X Index: 204



Y Index: 176

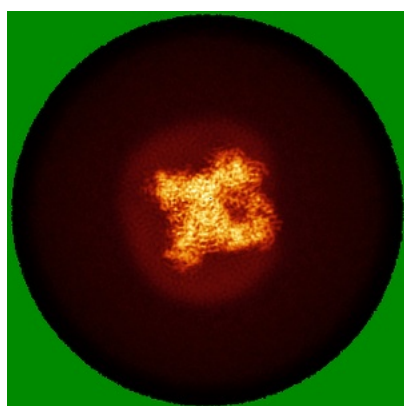


Z Index: 206

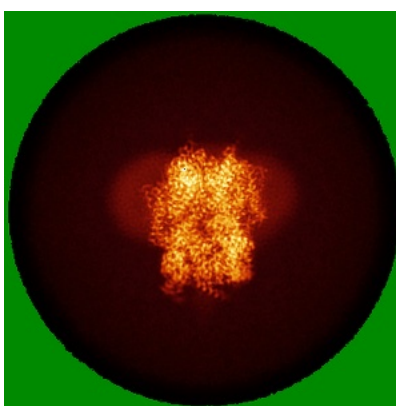
The images above show the largest variance slices of the map in three orthogonal directions.

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

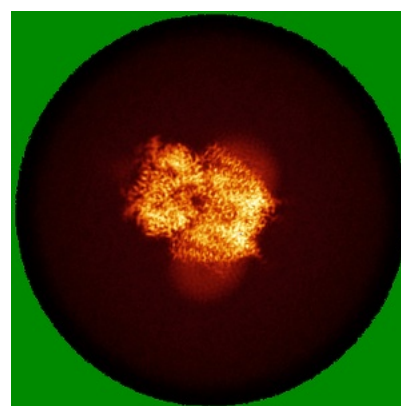
6.4.1 Primary map



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

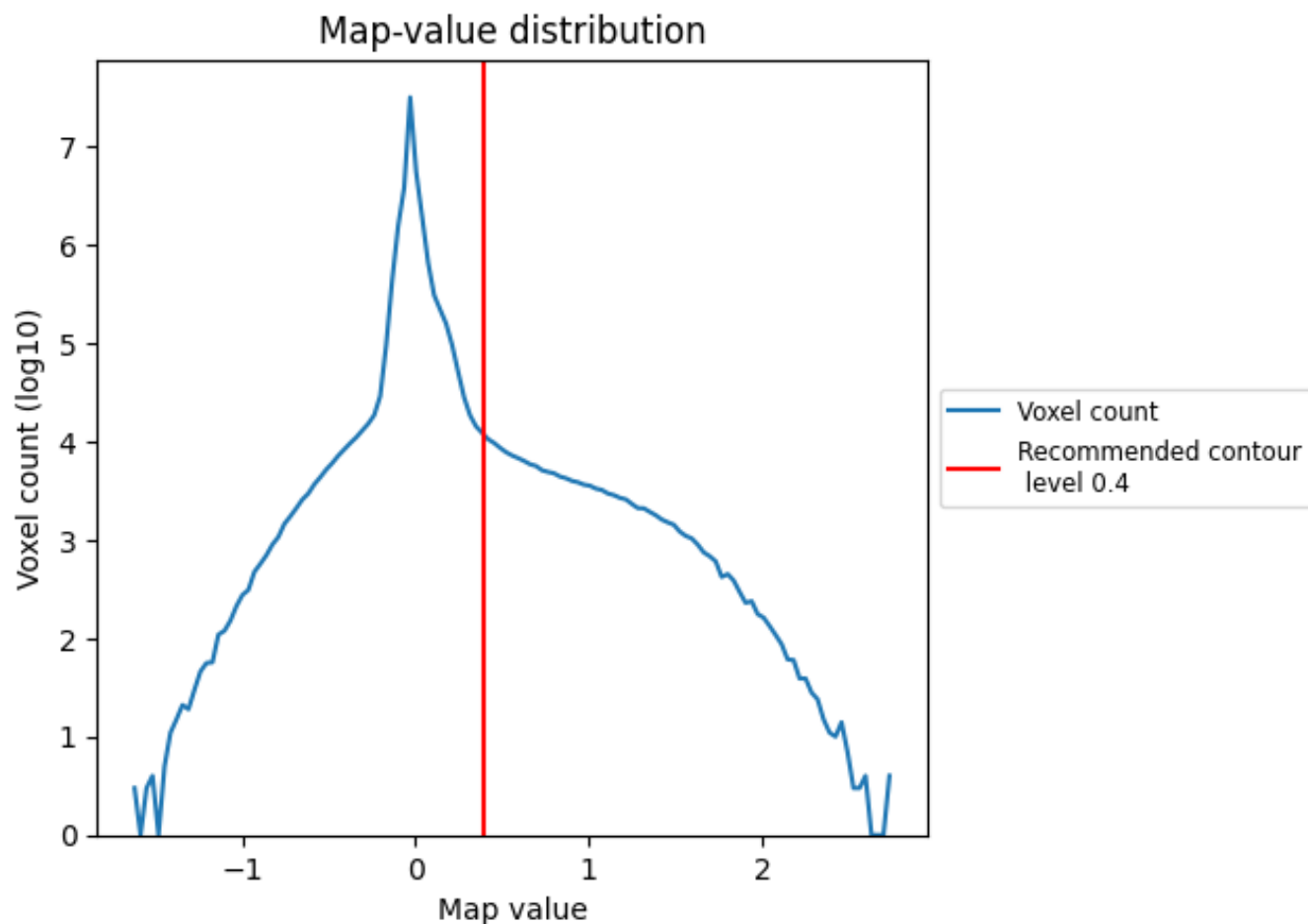
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

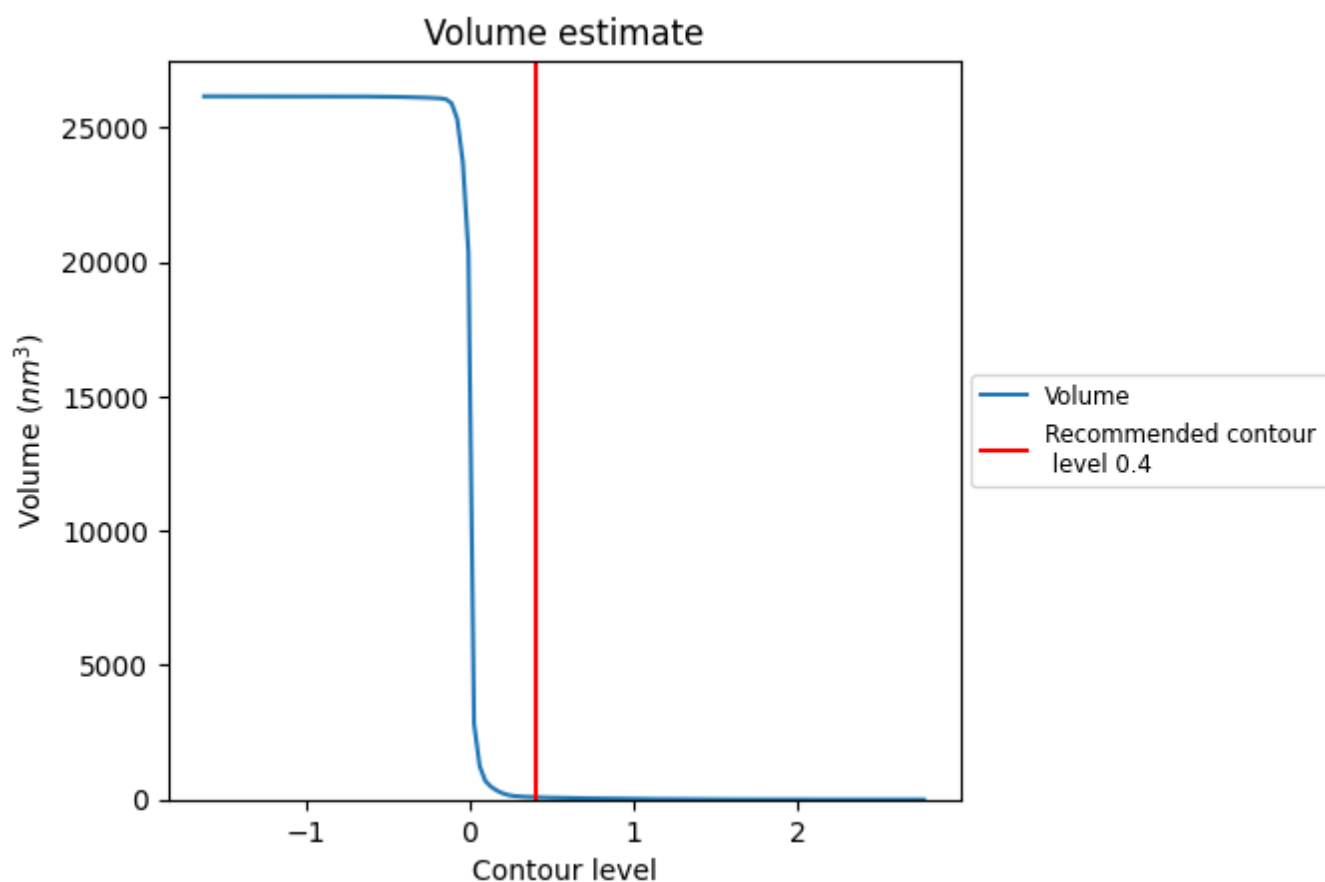
This section contains the results of statistical analysis of the map.

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.

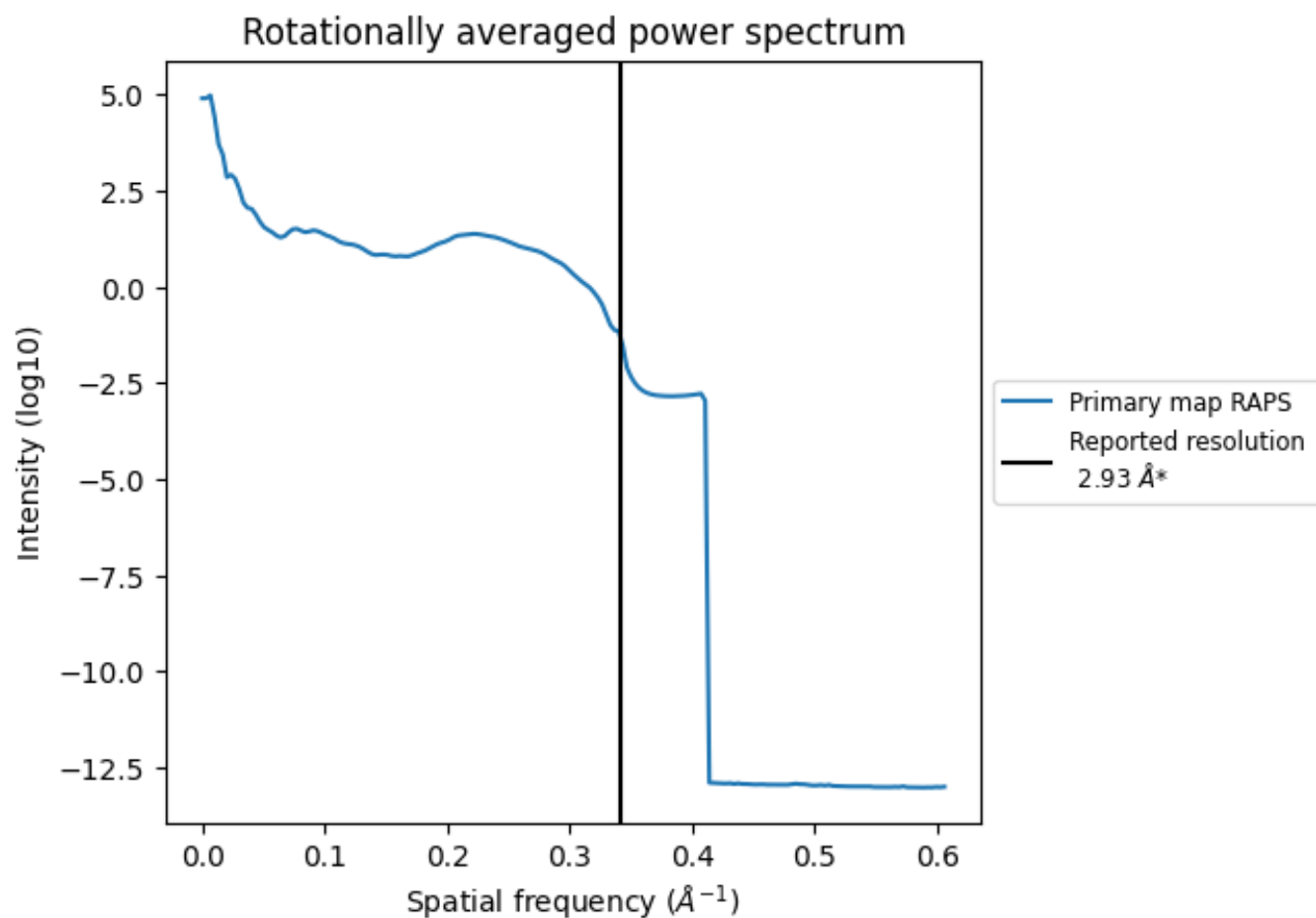
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 87 nm³; this corresponds to an approximate mass of 79 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 0.341 Å⁻¹

8 Fourier-Shell correlation

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

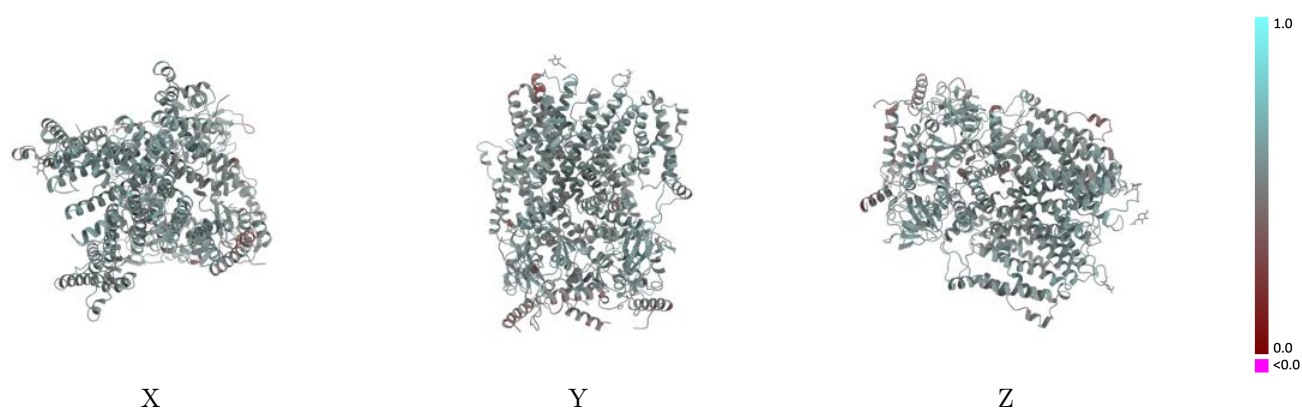
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24468 and PDB model 7RHS. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

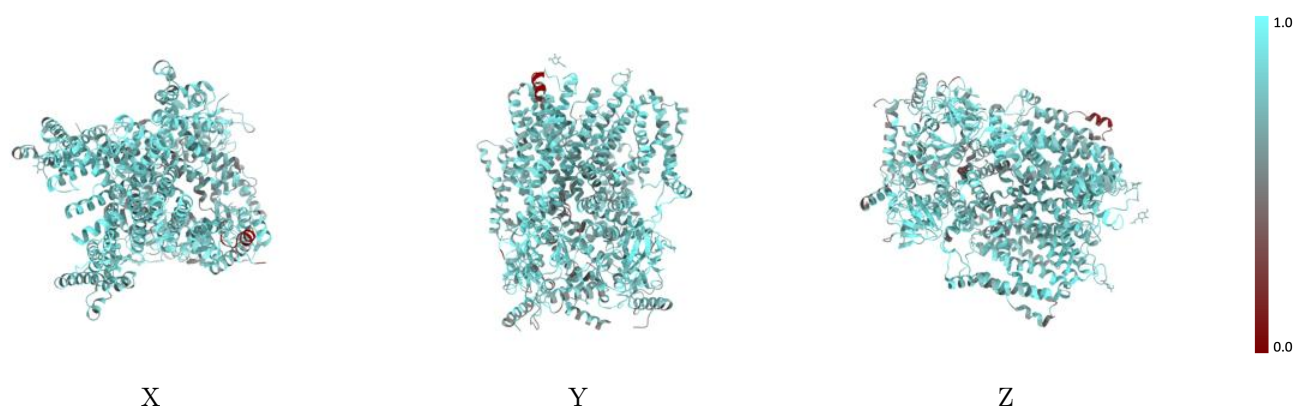
This section was not generated.

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



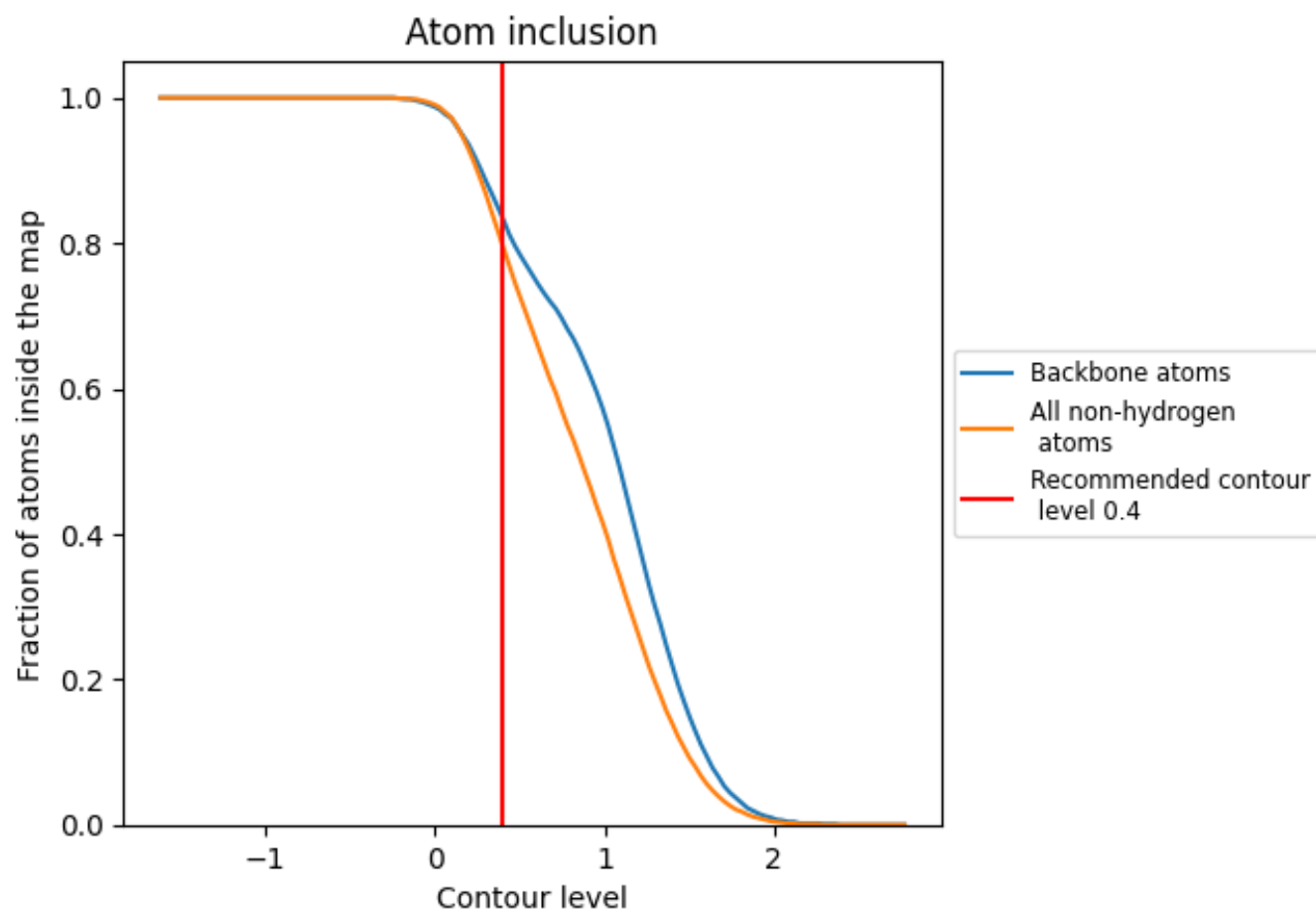
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 80% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7960	0.5380
A	0.7980	0.5400
B	0.7910	0.5370
C	0.7760	0.5290
D	0.8200	0.5460

