



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:34 PM UTC

PDB ID : 8IEB / pdb_00008ieb
EMDB ID : EMD-35377
Title : Cryo-EM structure of GPR156 of GPR156-miniGo-scFv16 complex (local re-fine)
Authors : Shin, J.; Park, J.; Cho, Y.
Deposited on : 2023-02-15
Resolution : 3.03 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

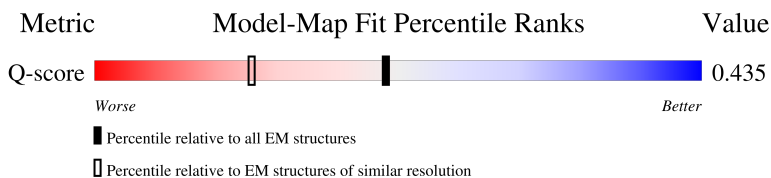
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.03 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	13929 (2.53 - 3.53)

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	598	
1	B	598	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4416 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 Probable G-protein coupled receptor 156.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	269	Total	C	N	O	S	0	0
			2062	1367	326	352	17		
1	B	289	Total	C	N	O	S	0	0
			2250	1483	363	386	18		

There are 82 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	558	SER	-	expression tag	UNP Q8NFN8
A	559	GLY	-	expression tag	UNP Q8NFN8
A	560	SER	-	expression tag	UNP Q8NFN8
A	561	GLY	-	expression tag	UNP Q8NFN8
A	562	SER	-	expression tag	UNP Q8NFN8
A	563	GLY	-	expression tag	UNP Q8NFN8
A	564	ARG	-	expression tag	UNP Q8NFN8
A	565	GLY	-	expression tag	UNP Q8NFN8
A	566	ARG	-	expression tag	UNP Q8NFN8
A	567	GLY	-	expression tag	UNP Q8NFN8
A	568	GLY	-	expression tag	UNP Q8NFN8
A	569	SER	-	expression tag	UNP Q8NFN8
A	570	GLU	-	expression tag	UNP Q8NFN8
A	571	ASN	-	expression tag	UNP Q8NFN8
A	572	LEU	-	expression tag	UNP Q8NFN8
A	573	TYR	-	expression tag	UNP Q8NFN8
A	574	PHE	-	expression tag	UNP Q8NFN8
A	575	GLN	-	expression tag	UNP Q8NFN8
A	576	GLY	-	expression tag	UNP Q8NFN8
A	577	GLY	-	expression tag	UNP Q8NFN8
A	578	SER	-	expression tag	UNP Q8NFN8
A	579	GLY	-	expression tag	UNP Q8NFN8
A	580	SER	-	expression tag	UNP Q8NFN8
A	581	GLY	-	expression tag	UNP Q8NFN8
A	582	GLY	-	expression tag	UNP Q8NFN8
A	583	ASP	-	expression tag	UNP Q8NFN8

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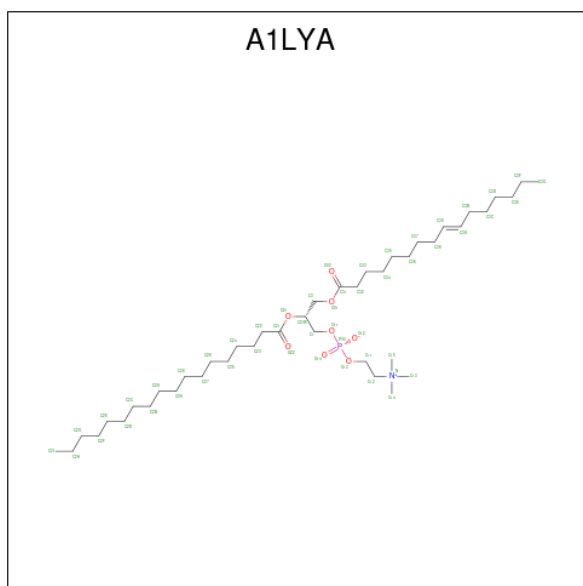
Chain	Residue	Modelled	Actual	Comment	Reference
A	584	TYR	-	expression tag	UNP Q8NFN8
A	585	LYS	-	expression tag	UNP Q8NFN8
A	586	ASP	-	expression tag	UNP Q8NFN8
A	587	ASP	-	expression tag	UNP Q8NFN8
A	588	ASP	-	expression tag	UNP Q8NFN8
A	589	ASP	-	expression tag	UNP Q8NFN8
A	590	LYS	-	expression tag	UNP Q8NFN8
A	591	ASP	-	expression tag	UNP Q8NFN8
A	592	TYR	-	expression tag	UNP Q8NFN8
A	593	LYS	-	expression tag	UNP Q8NFN8
A	594	ASP	-	expression tag	UNP Q8NFN8
A	595	ASP	-	expression tag	UNP Q8NFN8
A	596	ASP	-	expression tag	UNP Q8NFN8
A	597	ASP	-	expression tag	UNP Q8NFN8
A	598	LYS	-	expression tag	UNP Q8NFN8
B	558	SER	-	expression tag	UNP Q8NFN8
B	559	GLY	-	expression tag	UNP Q8NFN8
B	560	SER	-	expression tag	UNP Q8NFN8
B	561	GLY	-	expression tag	UNP Q8NFN8
B	562	SER	-	expression tag	UNP Q8NFN8
B	563	GLY	-	expression tag	UNP Q8NFN8
B	564	ARG	-	expression tag	UNP Q8NFN8
B	565	GLY	-	expression tag	UNP Q8NFN8
B	566	ARG	-	expression tag	UNP Q8NFN8
B	567	GLY	-	expression tag	UNP Q8NFN8
B	568	GLY	-	expression tag	UNP Q8NFN8
B	569	SER	-	expression tag	UNP Q8NFN8
B	570	GLU	-	expression tag	UNP Q8NFN8
B	571	ASN	-	expression tag	UNP Q8NFN8
B	572	LEU	-	expression tag	UNP Q8NFN8
B	573	TYR	-	expression tag	UNP Q8NFN8
B	574	PHE	-	expression tag	UNP Q8NFN8
B	575	GLN	-	expression tag	UNP Q8NFN8
B	576	GLY	-	expression tag	UNP Q8NFN8
B	577	GLY	-	expression tag	UNP Q8NFN8
B	578	SER	-	expression tag	UNP Q8NFN8
B	579	GLY	-	expression tag	UNP Q8NFN8
B	580	SER	-	expression tag	UNP Q8NFN8
B	581	GLY	-	expression tag	UNP Q8NFN8
B	582	GLY	-	expression tag	UNP Q8NFN8
B	583	ASP	-	expression tag	UNP Q8NFN8
B	584	TYR	-	expression tag	UNP Q8NFN8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	585	LYS	-	expression tag	UNP Q8NFN8
B	586	ASP	-	expression tag	UNP Q8NFN8
B	587	ASP	-	expression tag	UNP Q8NFN8
B	588	ASP	-	expression tag	UNP Q8NFN8
B	589	ASP	-	expression tag	UNP Q8NFN8
B	590	LYS	-	expression tag	UNP Q8NFN8
B	591	ASP	-	expression tag	UNP Q8NFN8
B	592	TYR	-	expression tag	UNP Q8NFN8
B	593	LYS	-	expression tag	UNP Q8NFN8
B	594	ASP	-	expression tag	UNP Q8NFN8
B	595	ASP	-	expression tag	UNP Q8NFN8
B	596	ASP	-	expression tag	UNP Q8NFN8
B	597	ASP	-	expression tag	UNP Q8NFN8
B	598	LYS	-	expression tag	UNP Q8NFN8

- Molecule 2 is [(2R)-3-[(E)-hexadec-9-enoyl]oxy-2-octadecanoyloxy-propyl] 2-(trimethylazaniumyl)ethyl phosphate (CCD ID: A1LYA) (formula: C₄₂H₈₂NO₈P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	

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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	205728	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 ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.936	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.0383	Depositor
Map size (Å)	332.1, 332.1, 332.1	wwPDB
Map dimensions	410, 410, 410	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.81, 0.81, 0.81	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: A1LYA

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	0.21	0/2107	0.43	0/2873
1	B	0.21	0/2299	0.38	0/3130
All	All	0.21	0/4406	0.41	0/6003

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2062	0	2166	22	0
1	B	2250	0	2367	20	0
2	A	52	0	0	0	0
2	B	52	0	0	0	0
All	All	4416	0	4533	41	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 41 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:259:THR:HG22	1:A:306:PHE:HB3	1.75	0.68
1:B:229:TRP:HE1	1:B:271:ALA:HB1	1.59	0.65
1:B:263:GLY:HA3	1:B:303:ILE:HD11	1.79	0.63
1:A:176:ASP:OD1	1:A:232:LYS:NZ	2.34	0.59
1:B:87:LEU:HB3	1:B:137:PRO:HB3	1.84	0.59

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	263/598 (44%)	255 (97%)	8 (3%)	0	100	100
1	B	285/598 (48%)	275 (96%)	10 (4%)	0	100	100
All	All	548/1196 (46%)	530 (97%)	18 (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	235/523 (45%)	235 (100%)	0	100	100
1	B	257/523 (49%)	257 (100%)	0	100	100
All	All	492/1046 (47%)	492 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	108	GLN
1	B	322	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](#)

2 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	A1LYA	B	601	-	51,51,51	1.17	4 (7%)	57,59,59	0.79	2 (3%)
2	A1LYA	A	601	-	51,51,51	1.15	4 (7%)	57,59,59	0.86	2 (3%)

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	A1LYA	B	601	-	-	22/55/55/55	-
2	A1LYA	A	601	-	-	29/55/55/55	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	A1LYA	O21-C2	-3.45	1.38	1.46
2	A	601	A1LYA	O21-C2	-3.44	1.38	1.46
2	B	601	A1LYA	O31-C31	3.33	1.43	1.33
2	A	601	A1LYA	O31-C31	3.06	1.42	1.33
2	B	601	A1LYA	P-O13	2.40	1.68	1.59

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	A1LYA	O21-C21-C22	3.74	119.56	111.48
2	B	601	A1LYA	O21-C21-C22	3.14	118.27	111.48
2	B	601	A1LYA	O31-C31-C32	2.58	119.69	111.83
2	A	601	A1LYA	O31-C31-C32	2.35	119.00	111.83

There are no chirality outliers.

5 of 51 torsion outliers are listed below:

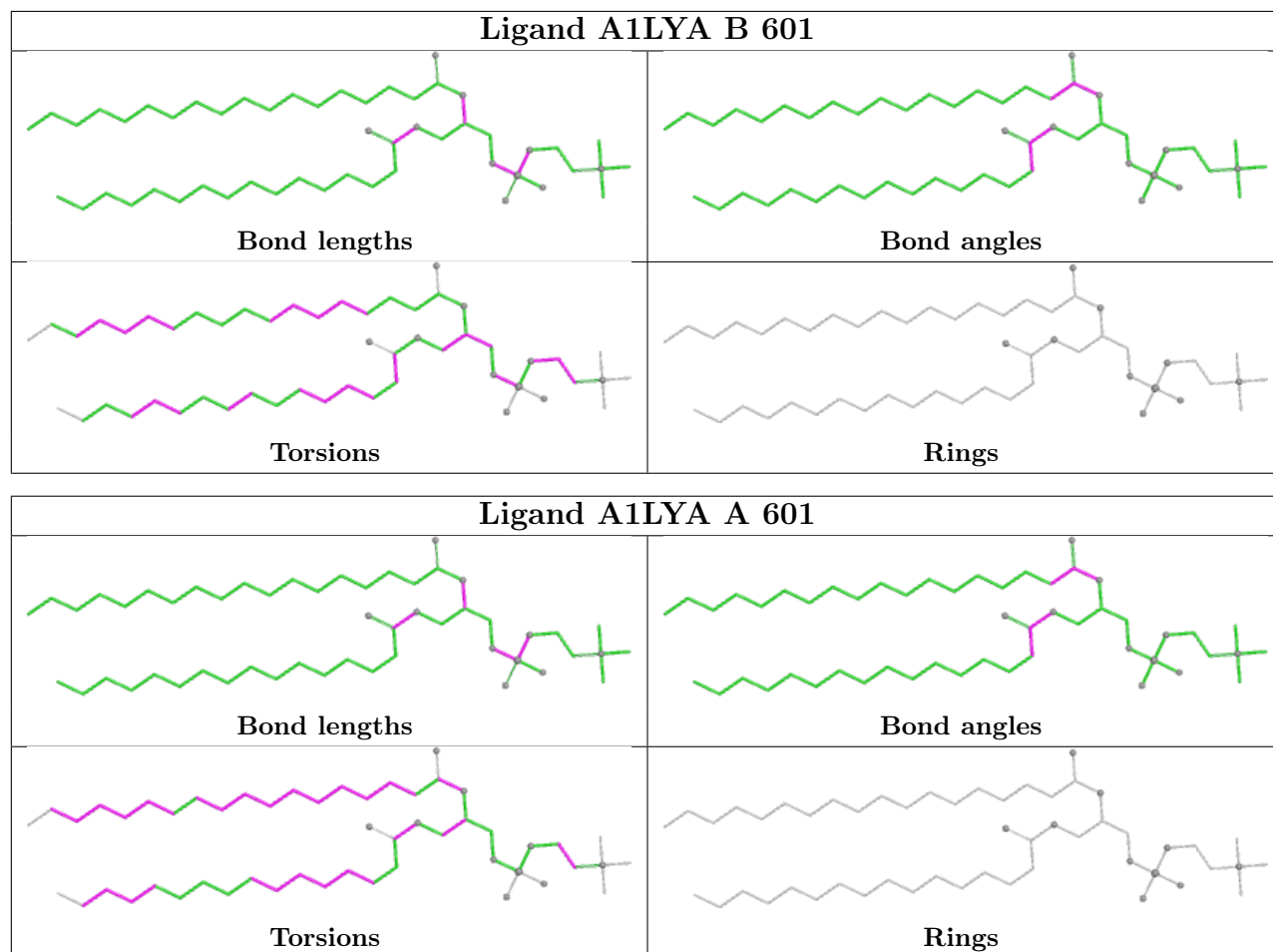
Mol	Chain	Res	Type	Atoms
2	B	601	A1LYA	O13-C11-C12-N
2	B	601	A1LYA	O21-C2-C3-O31
2	A	601	A1LYA	C32-C31-O31-C3
2	A	601	A1LYA	O32-C31-O31-C3
2	A	601	A1LYA	C21-C22-C23-C24

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-35377. These allow visual inspection of the internal detail of the map and identification of artifacts.

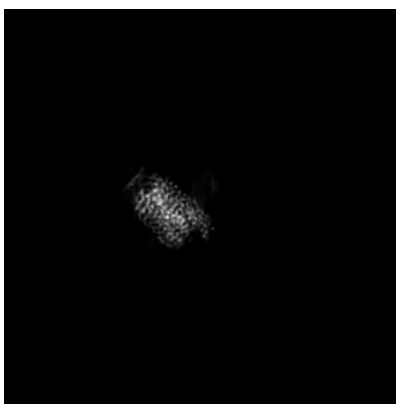
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

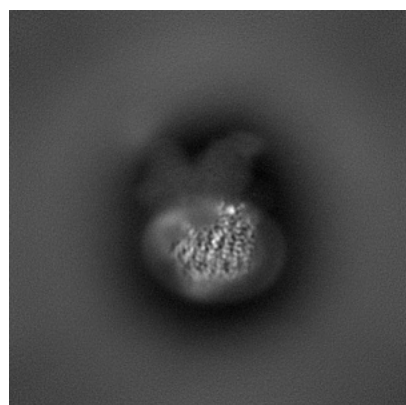


Y

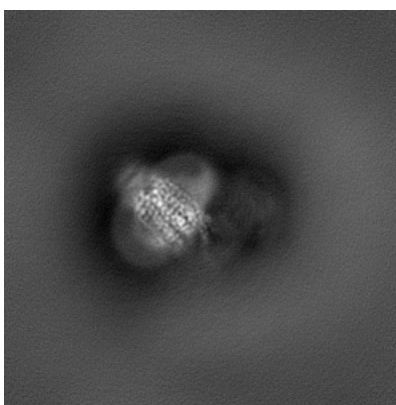


Z

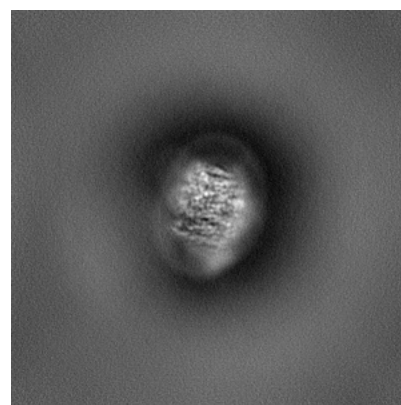
6.1.2 Raw map



X



Y

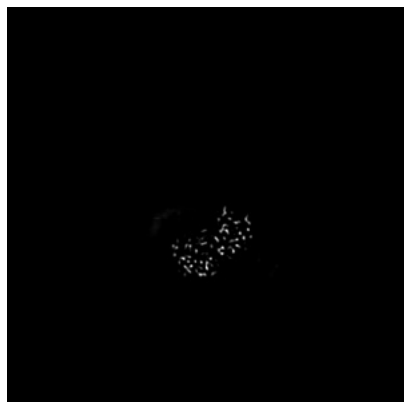


Z

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

6.2 Central slices [i](#)

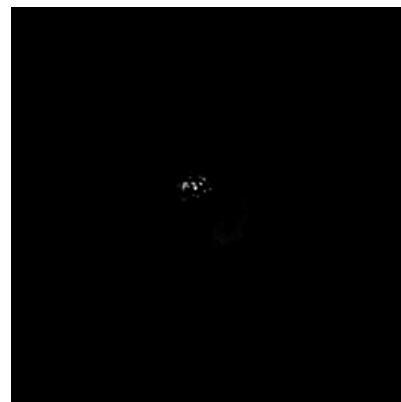
6.2.1 Primary map



X Index: 205

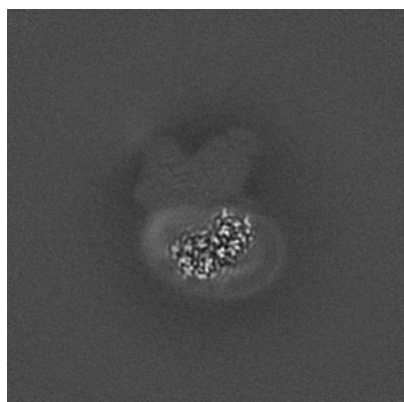


Y Index: 205

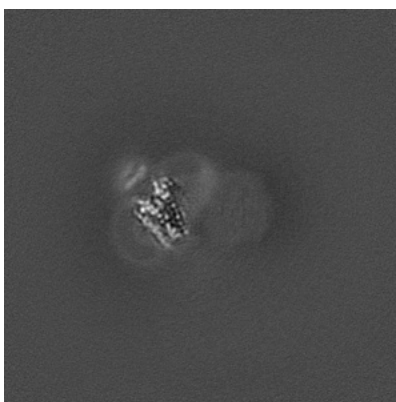


Z Index: 205

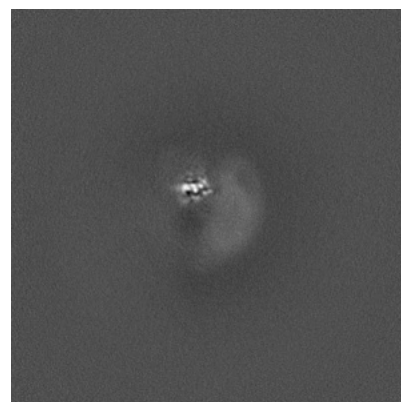
6.2.2 Raw map



X Index: 205



Y Index: 205

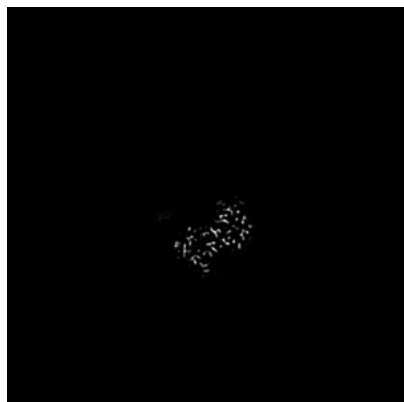


Z Index: 205

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: 196

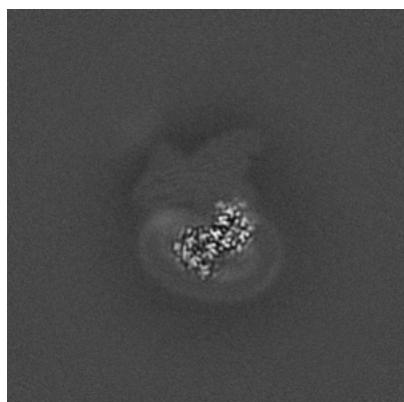


Y Index: 222

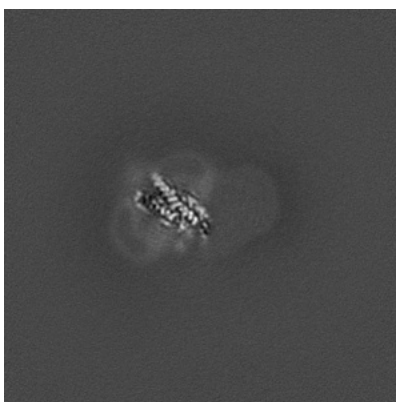


Z Index: 167

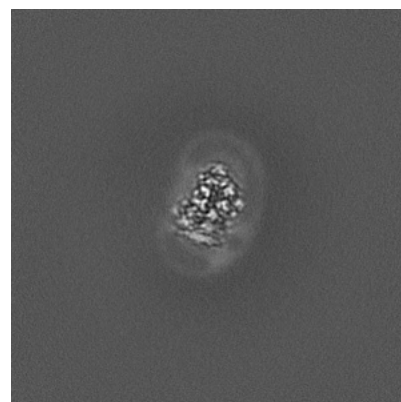
6.3.2 Raw map



X Index: 196



Y Index: 222

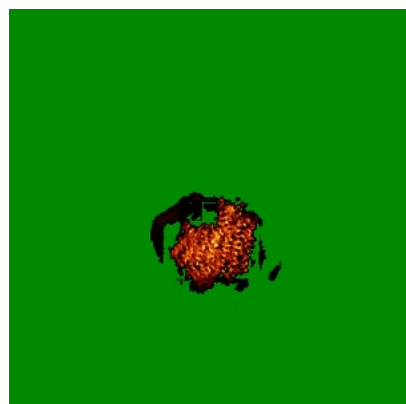


Z Index: 167

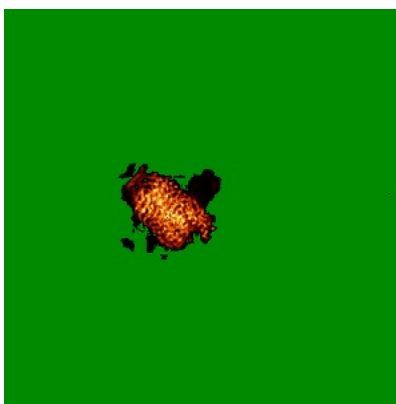
The images above show the largest variance slices of the map in three orthogonal directions.

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

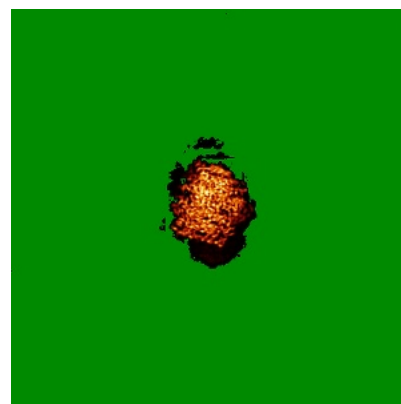
6.4.1 Primary map



X

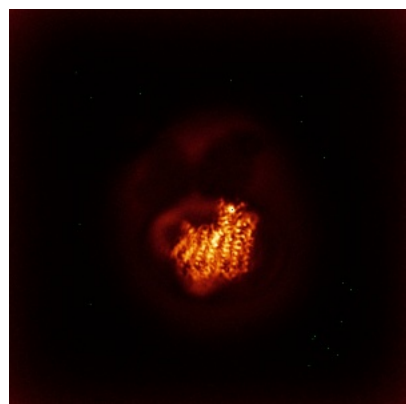


Y

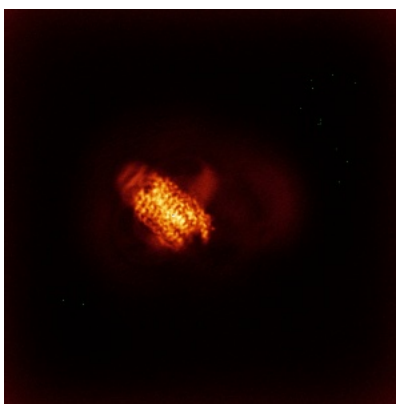


Z

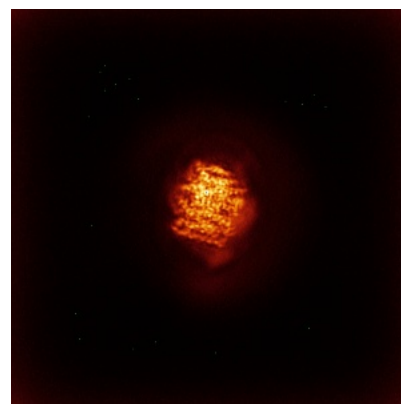
6.4.2 Raw map



X



Y

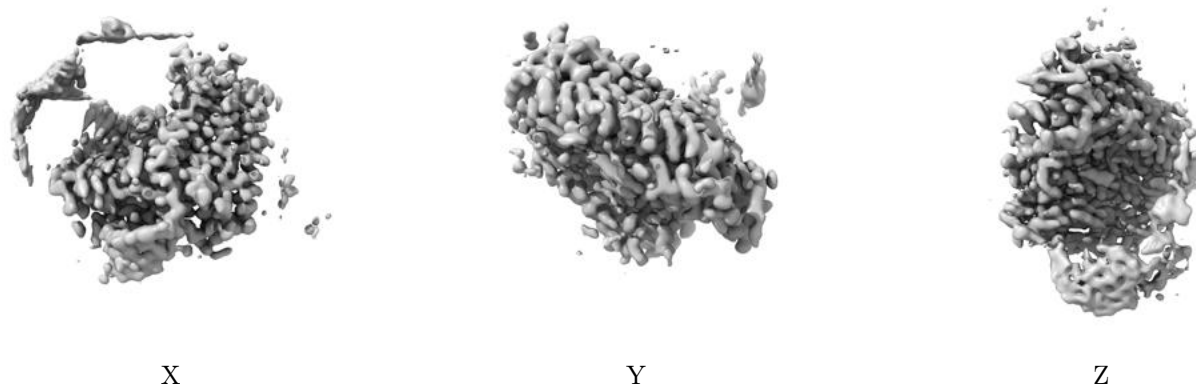


Z

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.

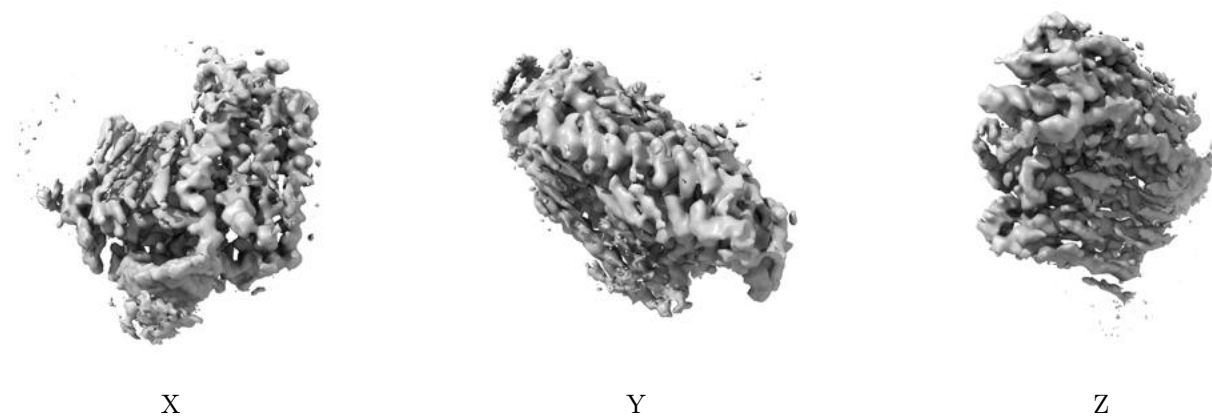
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0383. 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.

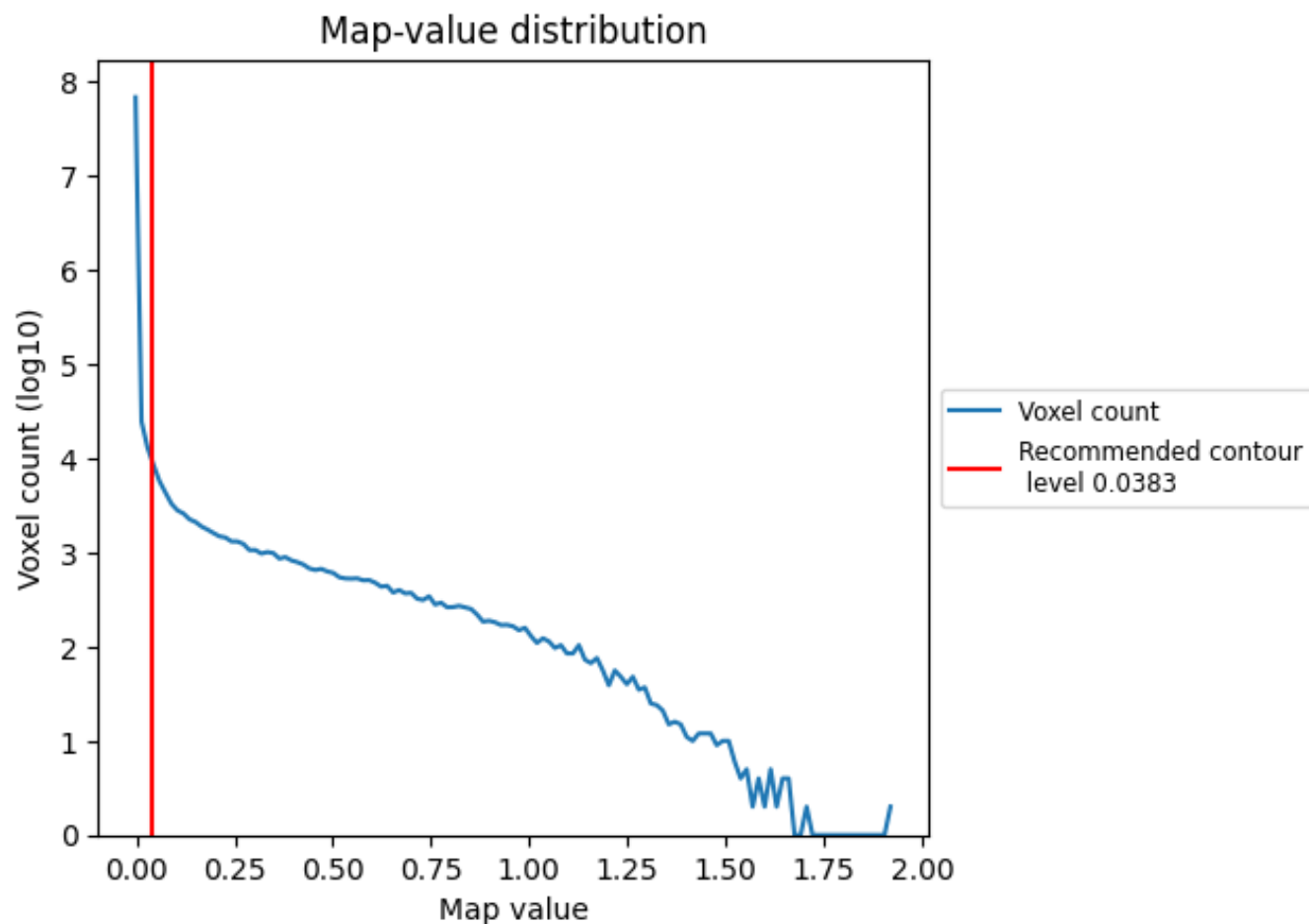
6.6 Mask visualisation [i](#)

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

7 Map analysis ⓘ

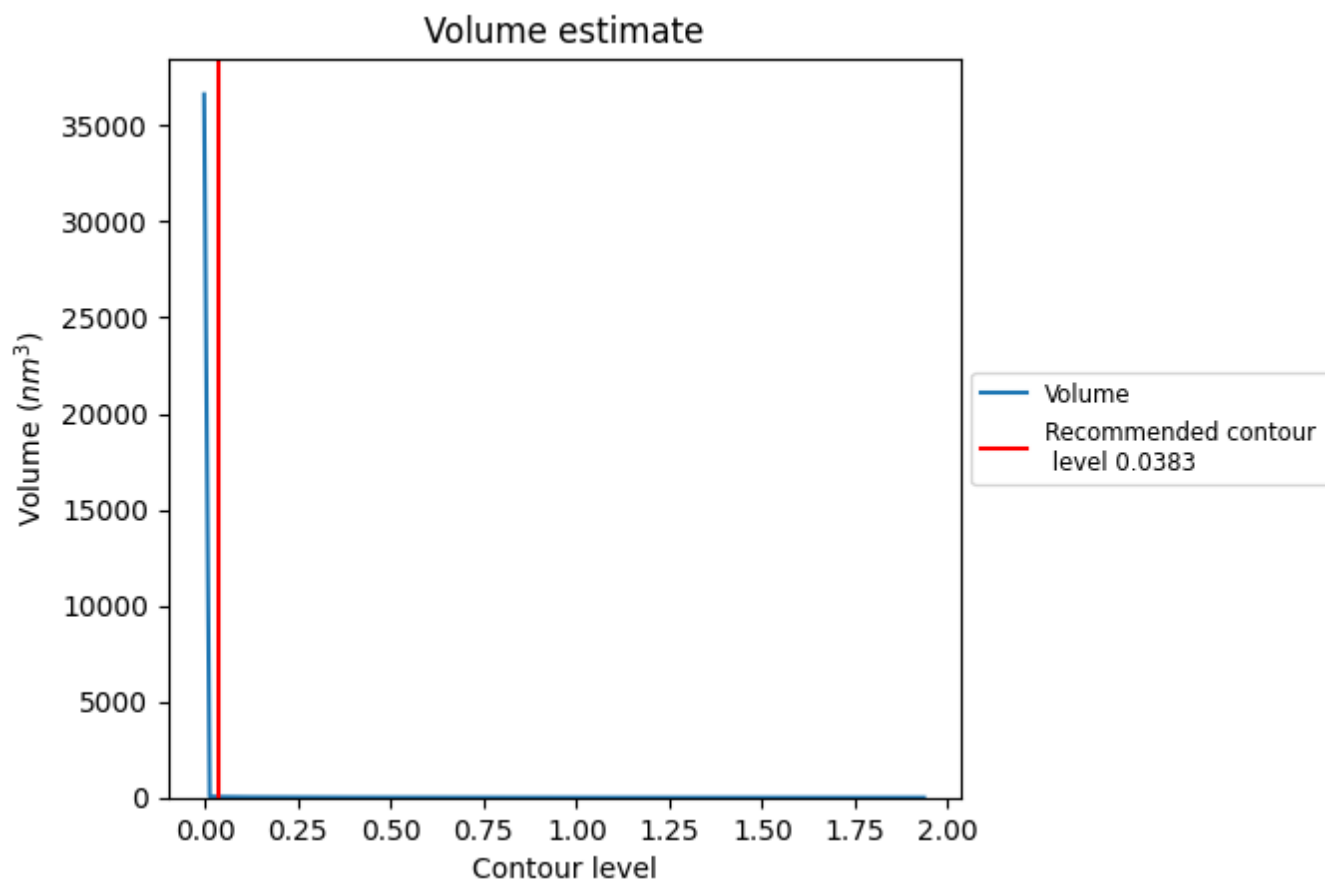
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

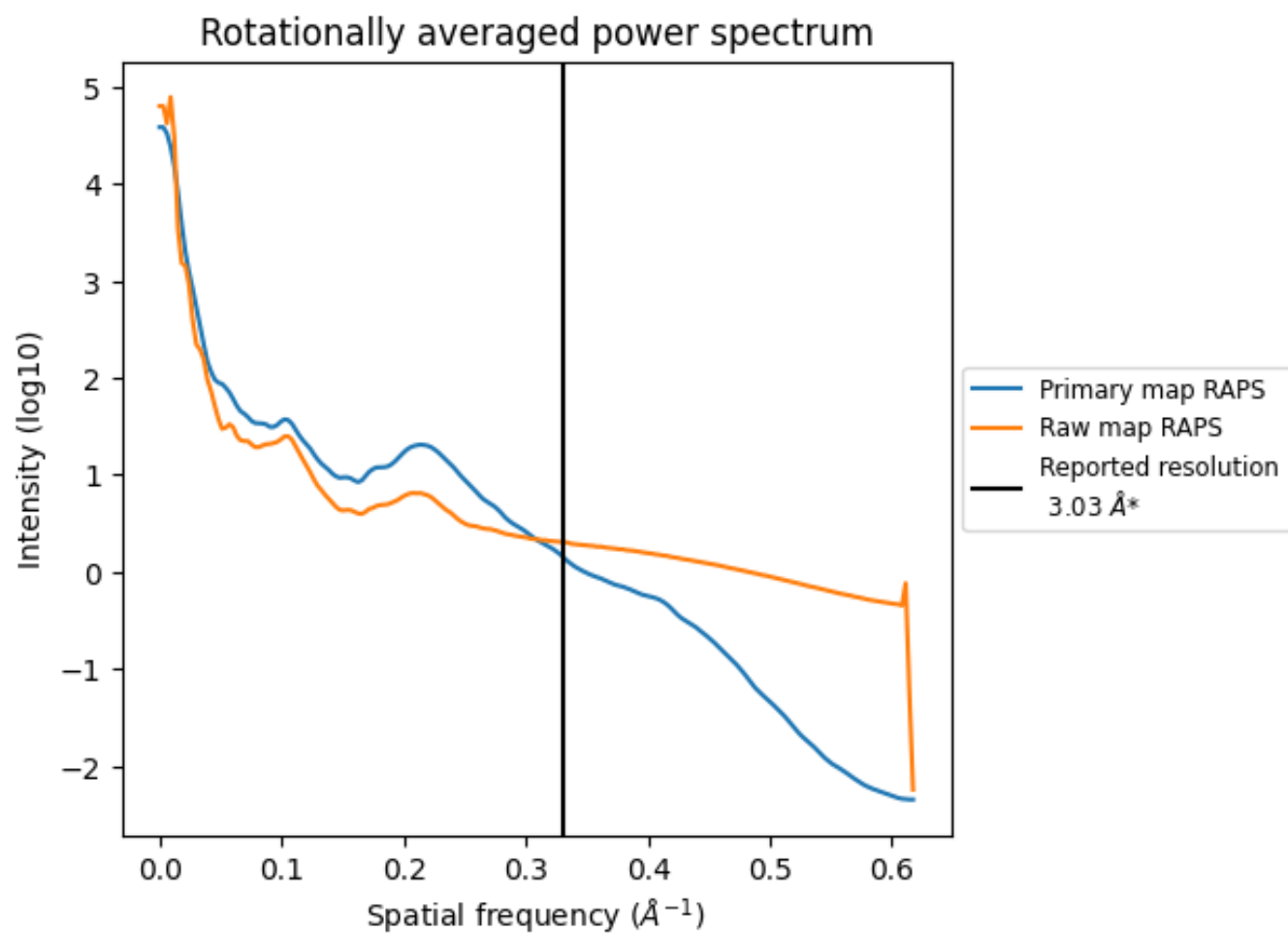
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 39 nm^3 ; this corresponds to an approximate mass of 35 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 ⓘ

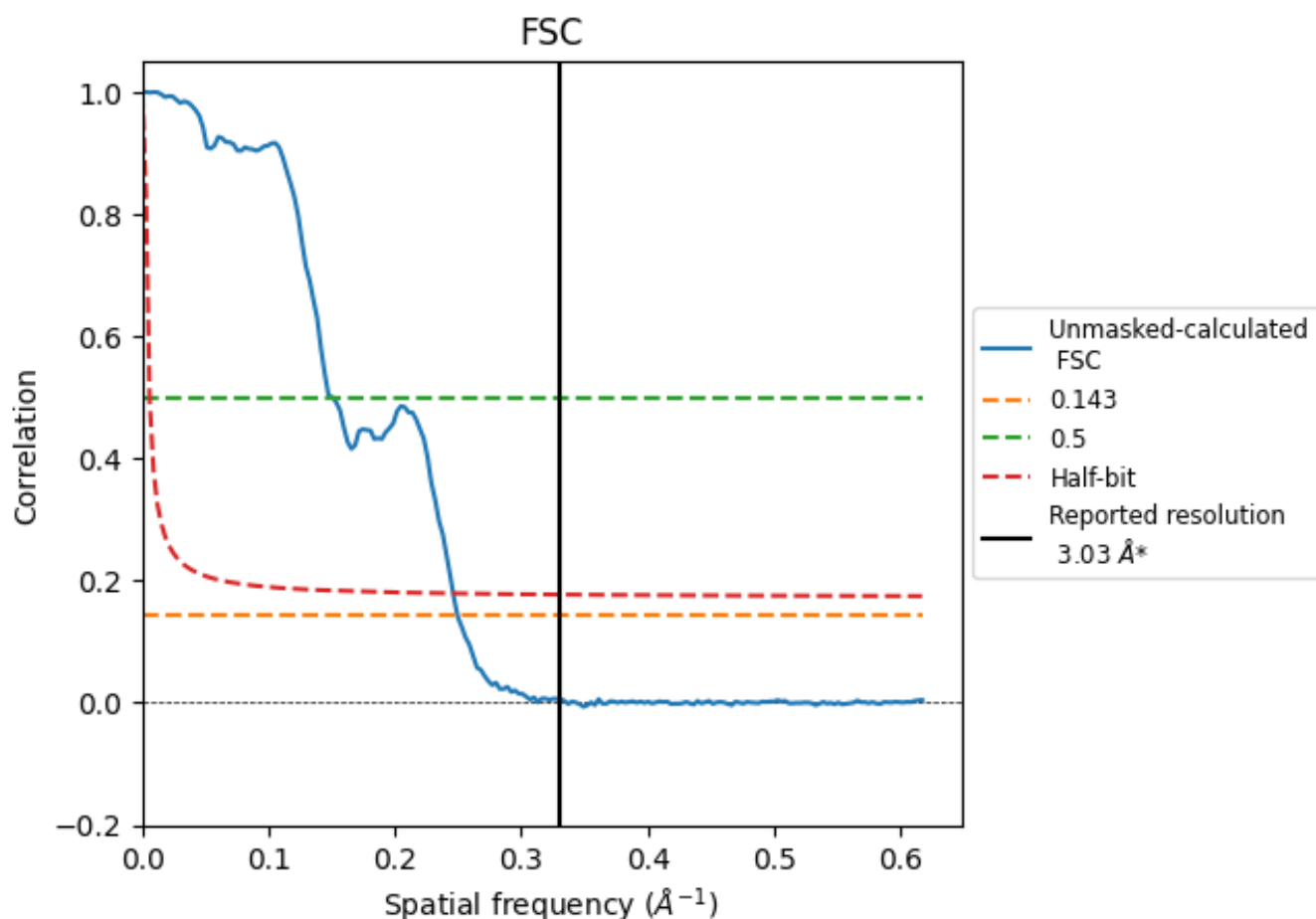


*Reported resolution corresponds to spatial frequency of 0.330 $\text{\AA}^{-1}$

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 0.330 Å⁻¹

8.2 Resolution estimates [i](#)

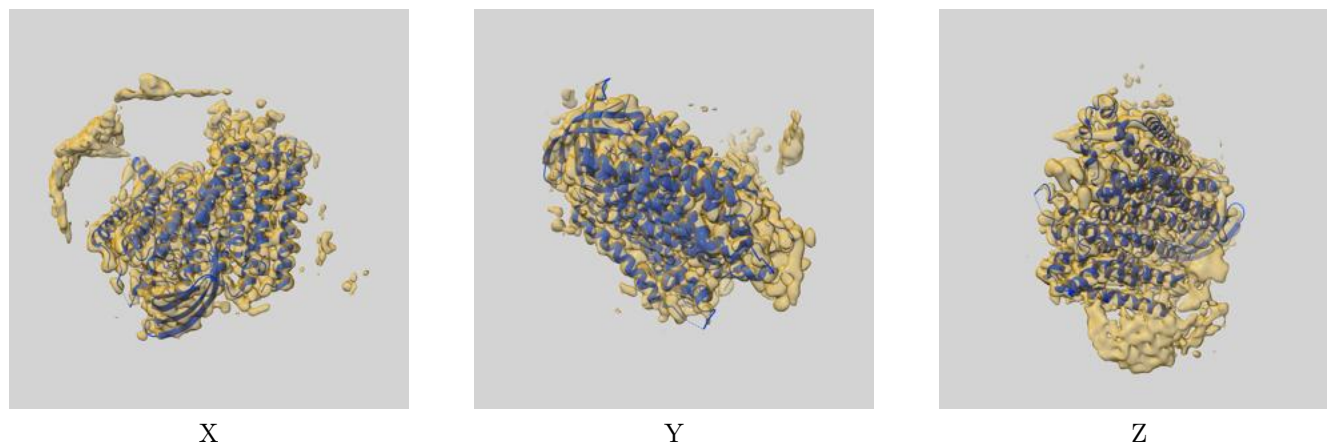
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.03	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.01	6.64	4.06

*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 4.01 differs from the reported value 3.03 by more than 10 %

9 Map-model fit [i](#)

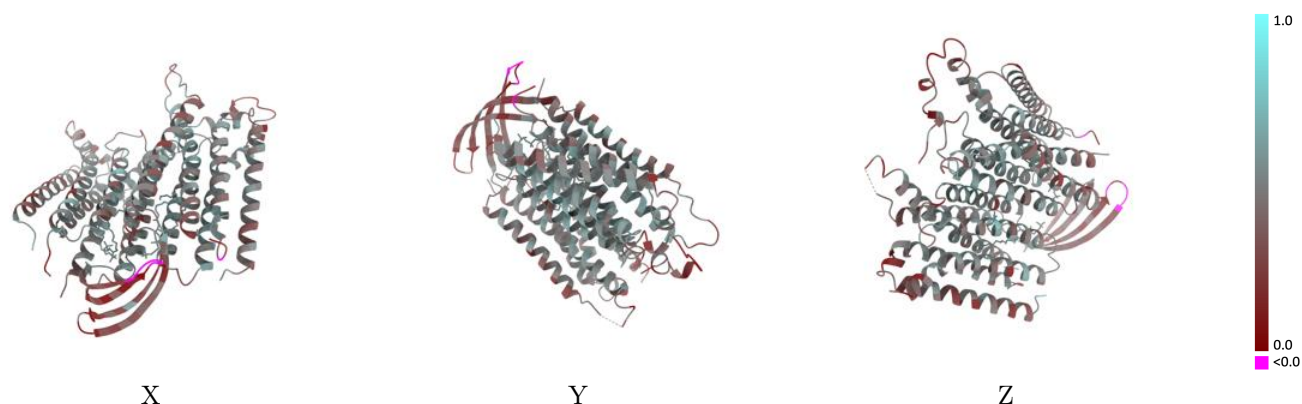
This section contains information regarding the fit between EMDB map EMD-35377 and PDB model 8IEB. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



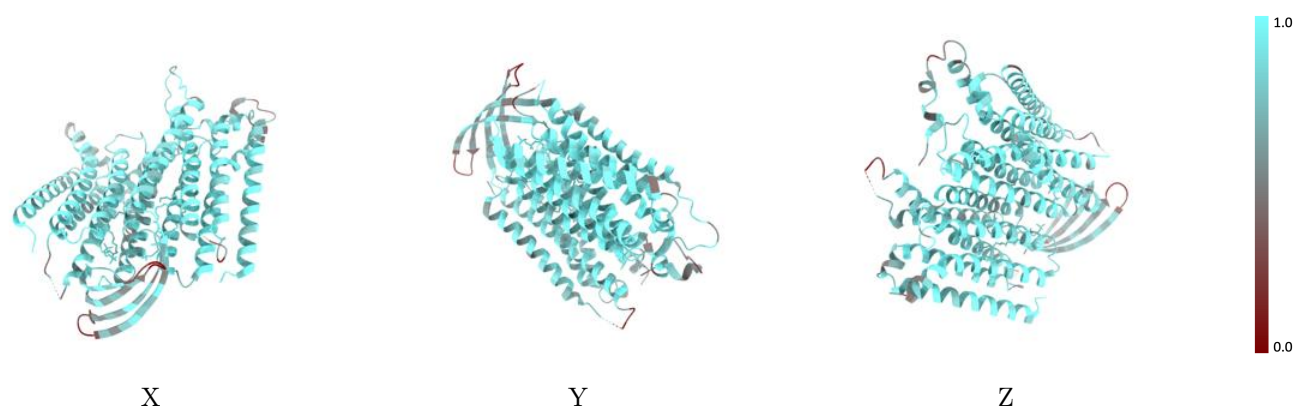
The images above show the 3D surface view of the map at the recommended contour level 0.0383 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



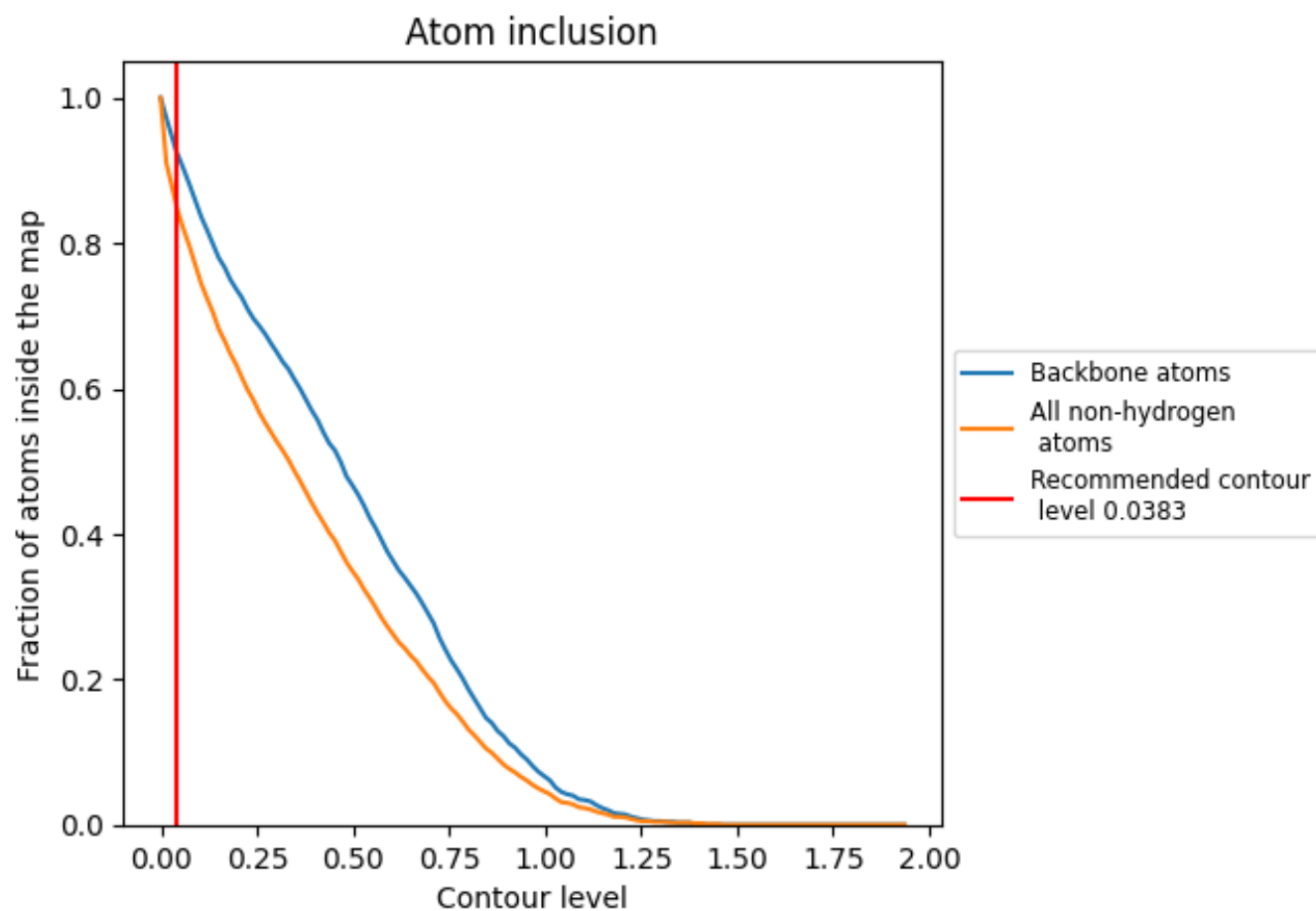
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0383).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 85% 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 (0.0383) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8530	0.4350
A	0.8520	0.4250
B	0.8530	0.4440

