



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:58 PM UTC

PDB ID : 7L2O / pdb_00007l2o
EMDB ID : EMD-23135
Title : Cryo-EM structure of RTX-bound full-length TRPV1 at pH 5.5
Authors : Zhang, K.; Julius, D.; Cheng, Y.
Deposited on : 2020-12-17
Resolution : 3.64 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

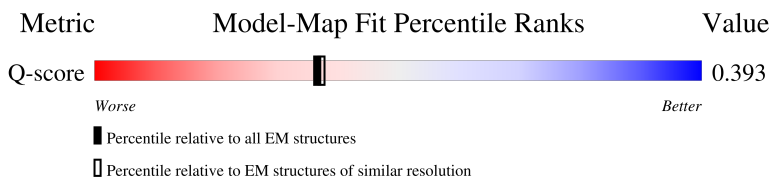
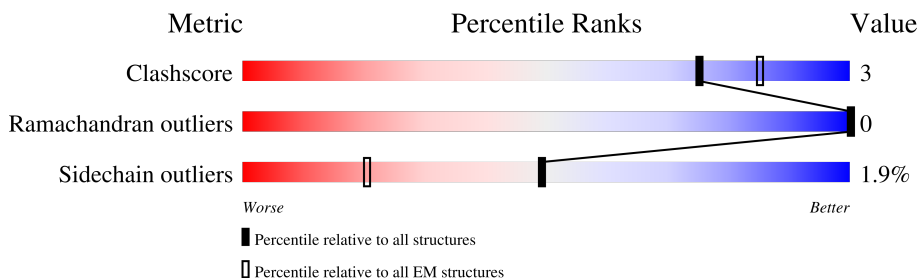
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.64 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	11633 (3.14 - 4.14)

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	842	
1	B	842	
1	C	842	
1	D	842	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 15800 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 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	480	Total	C	N	O	S	0	0
			3904	2567	623	690	24		
1	C	480	Total	C	N	O	S	0	0
			3904	2567	623	690	24		
1	D	480	Total	C	N	O	S	0	0
			3904	2567	623	690	24		
1	B	480	Total	C	N	O	S	0	0
			3904	2567	623	690	24		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP O35433
A	-2	ALA	-	expression tag	UNP O35433
A	-1	MET	-	expression tag	UNP O35433
A	0	GLY	-	expression tag	UNP O35433
A	1	SER	-	expression tag	UNP O35433
C	-3	GLY	-	expression tag	UNP O35433
C	-2	ALA	-	expression tag	UNP O35433
C	-1	MET	-	expression tag	UNP O35433
C	0	GLY	-	expression tag	UNP O35433
C	1	SER	-	expression tag	UNP O35433
D	-3	GLY	-	expression tag	UNP O35433
D	-2	ALA	-	expression tag	UNP O35433
D	-1	MET	-	expression tag	UNP O35433
D	0	GLY	-	expression tag	UNP O35433
D	1	SER	-	expression tag	UNP O35433
B	-3	GLY	-	expression tag	UNP O35433
B	-2	ALA	-	expression tag	UNP O35433
B	-1	MET	-	expression tag	UNP O35433
B	0	GLY	-	expression tag	UNP O35433
B	1	SER	-	expression tag	UNP O35433

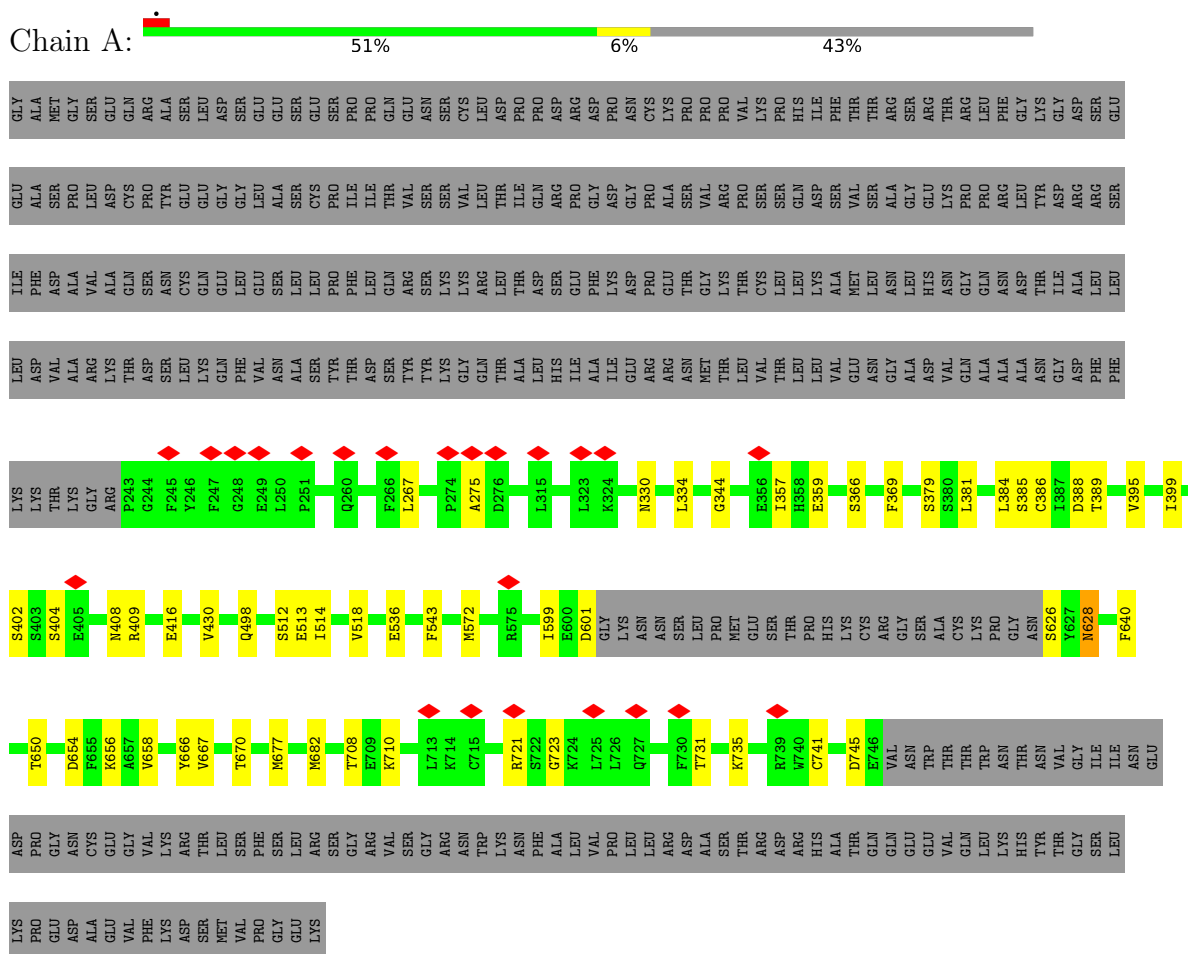
- [illegible]

Mol	Chain	Residues	Atoms			AltConf
2	A	1	Total 46	C 37	O 9	0
2	C	1	Total 46	C 37	O 9	0
2	D	1	Total 46	C 37	O 9	0
2	B	1	Total 46	C 37	O 9	0

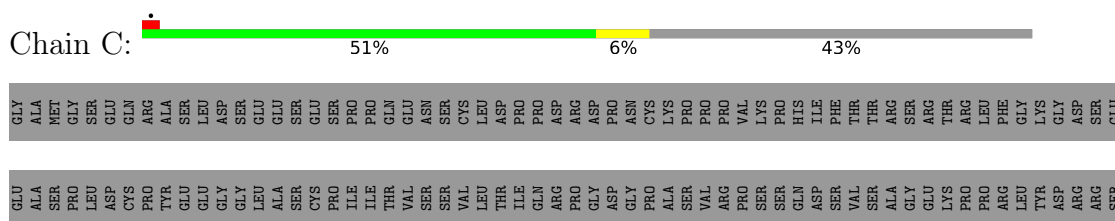
3 Residue-property plots

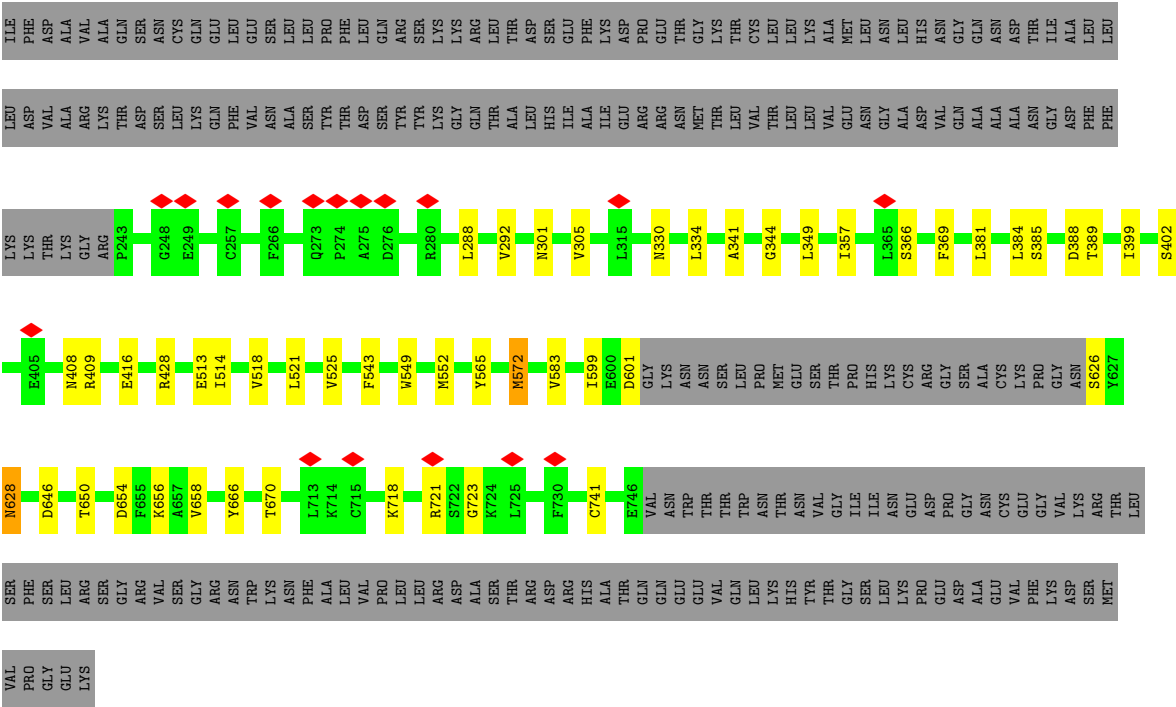
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Transient receptor potential cation channel subfamily V member 1

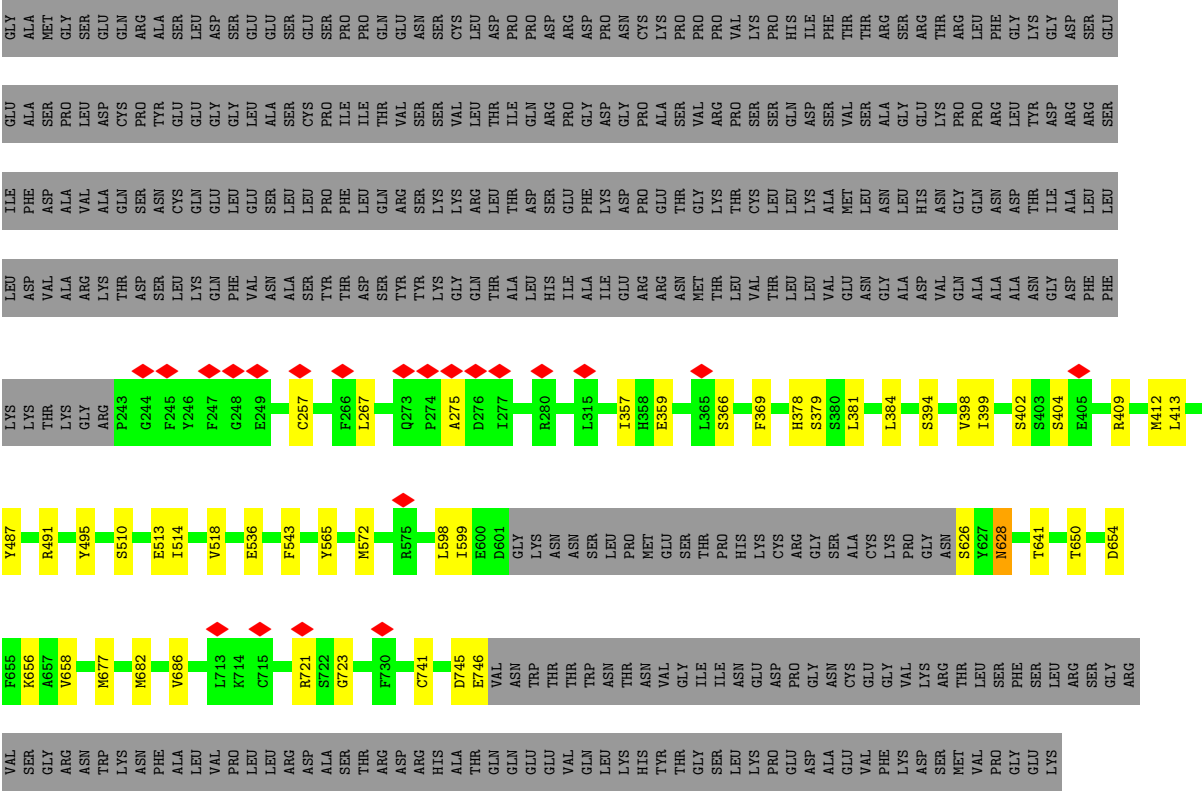


- Molecule 1: Transient receptor potential cation channel subfamily V member 1





• Molecule 1: Transient receptor potential cation channel subfamily V member 1



• Molecule 1: Transient receptor potential cation channel subfamily V member 1

Category	Percentage
Very bad	52%
Bad	5%
Good	43%

VAL	PRO	PRO	GLY	GLU	LYS	SER	GLY	ASN	D388	LYS	LEU	ILE	GLU	GLY
			ASN	S626	S627	PHE	ASN	T389	THR	LYS	ASP	PHE	ALA	ALA
			LEU	NG28	NG28	LEU	LEU	Y627	LYS	ALA	VAL	ALA	SER	MET
			SER			ARG	ARG	X393	GLY	ALA	LYS	VAL	LEU	GLY
			GLY	T650	T650	SER	SER	I399	ARG	THR	THR	ALA	ASP	GLJ
			ARG			ARG	ARG	S402	P243	THR	GLN	CYS	PRO	GLN
			VAL	D654	D654	SER	SER	S403	Q244	ASN	TYR	ALA	ARG	ALA
			GLY	K656	K656	GLY	GLY	E404	P247	LEU	CYS	GLN	GLY	SER
			ARG	A657	A657	ARG	ARG	E405	Q248	GLN	GLN	GLY	GLY	ASP
			ASN	V658	V658	ASN	ASN	R409	E249	VAL	VAL	LEU	LEU	SER
			TRP			TRP	TRP			ASN	SER	ALA	ALA	GLU
			LYS	M677	M677	LYS	LYS	M412	L254	ASN	GLN	SER	ALA	GLU
			ASN			ASN	ASN		A255	LEU	LEU	CYS	LEU	SER
			PHE			PHE	PHE	Y495	A256	SER	PRO	PRO	PRO	GLU
			ALA	L713	L713	ALA	ALA	K714	Q257	THR	PHE	ILE	ILE	PRO
			LEU	K715	K715	LEU	LEU		T258	ASP	LEU	THR	THR	GLN
			VAL			VAL	VAL	S510	N259	SER	GLN	ARG	VAL	GLU
			LEU	R721	R721	LEU	LEU	E513	Q260	TYR	ARG	THR	VAL	GLU
			LEU			LEU	LEU	1514		TYR	SER	SER	SER	ASN
			ARG			ARG	ARG	V518	T266	LYS	LYS	LYS	SER	SER
			ASP	L725	L725	ASP	ASP		L267	LYS	VAL	VAL	VAL	CYS
			ALA	F730	F730	ALA	ALA	F543	L268	GLN	ARG	LEU	LEU	LEU
			THR			THR	THR		Q269	ALA	THR	THR	ILE	PRO
			ARG	D733	D733	ARG	ARG	F559	Q273	LEU	ASP	GLN	ARG	PRO
			ASP	G734	G734	ASP	ASP	G563	P274	HIS	SER	ARG	ARG	ASP
			ARG	K735	K735	ARG	ARG		A275	ILE	GLU	GLY	GLY	ASP
			HIS			HIS	HIS	M572	Q276	ILE	LYS	ASP	PRO	PRO
			ALA	R739	R739	ALA	ALA		1277	GLU	ASP	GLY	PRO	CYS
			THR			THR	THR	V583		ARG	PRO	PRO	ALA	LYS
			GLN	E746	E746	GLN	GLN		L288	ARG	GLU	ALA	ALA	LYS
			GLU	ASN	ASN	GLU	GLU	1599		ASN	THR	SER	SER	PRO
			GLJ	TRP	TRP	GLJ	GLJ	E600	V292	MET	GLY	VAL	VAL	PRO
			VAL	THR	THR	VAL	VAL	D601		THR	LYS	ARG	ARG	PRO
			GLN	THR	THR	GLN	GLN	GLY	N301	LEU	THR	THR	PRO	VAL
			LEU	ASN	ASN	LEU	LEU	ASN	V305	VAL	CYS	SER	SER	LYS
			LYS	THR	THR	LYS	LYS	ASN		THR	LYS	THR	GLN	PRO
			HIS	ASN	ASN	HIS	HIS	SER	K324	LEU	LYS	ILE	GLN	ARG
			THR	VAL	VAL	THR	THR	LEU		VAL	ALA	ALA	THR	PHE
			GLY	GLY	GLY	GLY	GLY	PRO	N330	GLU	MET	VAL	VAL	GLY
			SER	ILE	ILE	SER	SER	MET		ASN	LEU	SER	SER	THR
			LEU	GLJ	GLJ	LEU	LEU	GLJ	L334	GLY	ASN	ALA	ALA	ARG
			LEU	ASN	ASN	LEU	LEU	SER		ALA	HIS	SER	GLY	THR
			PRO	GLU	GLU	PRO	PRO	THR	E356	ASP	ASN	LYS	LYS	THR
			GLU	ASP	ASP	GLU	GLU	HIS	1357	VAL	GLN	GLY	PRO	LEU
			ALA	GLY	GLY	ALA	ALA	LYS	H358	GLN	GLN	GLY	PRO	ARG
			GLJ	ASN	ASN	GLJ	CYS	CYS	E359	ALA	ALA	ASP	ARG	PHE
			VAL	CYS	CYS	VAL	VAL	ARG		ALA	THR	THR	LEU	GLY
			PHE	GLU	GLU	PHE	GLY	GLY	F369	ASN	ASP	ILE	TYR	LYS
			LYS	GLY	GLY	LYS	GLY	SER		GLY	GLY	ILE	GLY	GLY
			ASP	VAL	VAL	ASP	ALA	ALA		ASP	ARG	ALA	ARG	ASP
			SER	LYS	LYS	SER	CYS	CYS	Y374	PHE		LEU	ARG	SER

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39056	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	64	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	0.129	Depositor
Minimum map value	-0.082	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.008	Depositor
Map size ($\text{\AA}$)	257.6, 257.6, 257.6	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.15, 1.15, 1.15	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: 6EU

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	0.42	0/3999	0.49	0/5413
1	B	0.42	0/3999	0.50	0/5413
1	C	0.43	0/3999	0.50	0/5413
1	D	0.43	0/3999	0.50	0/5413
All	All	0.42	0/15996	0.50	0/21652

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 [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	3904	0	3937	30	0
1	B	3904	0	3937	25	0
1	C	3904	0	3937	28	0
1	D	3904	0	3937	24	0
2	A	46	0	0	0	0
2	B	46	0	0	0	0
2	C	46	0	0	0	0
2	D	46	0	0	0	0
All	All	15800	0	15748	98	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 3.

The worst 5 of 98 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:495:TYR:HH	1:B:510:SER:HG	1.12	0.84
1:A:384:LEU:O	1:A:721:ARG:NH2	2.13	0.82
1:B:384:LEU:O	1:B:721:ARG:NH2	2.16	0.78
1:A:626:SER:N	1:A:628:ASN:OD1	2.19	0.75
1:A:498:GLN:OE1	1:A:710:LYS:NZ	2.20	0.74

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	476/842 (56%)	453 (95%)	23 (5%)	0	100	100
1	B	476/842 (56%)	451 (95%)	25 (5%)	0	100	100
1	C	476/842 (56%)	451 (95%)	25 (5%)	0	100	100
1	D	476/842 (56%)	454 (95%)	22 (5%)	0	100	100
All	All	1904/3368 (56%)	1809 (95%)	95 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	428/743 (58%)	420 (98%)	8 (2%)	50	64
1	B	428/743 (58%)	421 (98%)	7 (2%)	55	65
1	C	428/743 (58%)	421 (98%)	7 (2%)	55	65
1	D	428/743 (58%)	418 (98%)	10 (2%)	44	61
All	All	1712/2972 (58%)	1680 (98%)	32 (2%)	49	64

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	628	ASN
1	B	650	THR
1	C	650	THR
1	C	628	ASN
1	B	654	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	259	ASN
1	A	700	GLN
1	C	700	GLN
1	D	393	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 ⓘ

4 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	6EU	A	901	-	45,52,52	0.83	1 (2%)	44,83,83	1.87	9 (20%)
2	6EU	C	901	-	45,52,52	0.83	1 (2%)	44,83,83	1.87	9 (20%)
2	6EU	B	901	-	45,52,52	0.83	1 (2%)	44,83,83	1.87	9 (20%)
2	6EU	D	901	-	45,52,52	0.83	1 (2%)	44,83,83	1.87	9 (20%)

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	6EU	A	901	-	-	10/20/101/101	0/8/7/7
2	6EU	C	901	-	-	10/20/101/101	0/8/7/7
2	6EU	B	901	-	-	10/20/101/101	0/8/7/7
2	6EU	D	901	-	-	10/20/101/101	0/8/7/7

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	901	6EU	OAF-CBK	4.10	1.45	1.33
2	D	901	6EU	OAF-CBK	4.10	1.45	1.33
2	A	901	6EU	OAF-CBK	4.08	1.45	1.33
2	B	901	6EU	OAF-CBK	4.08	1.45	1.33

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	6EU	OAF-CBK-CBM	5.74	120.18	111.21
2	D	901	6EU	OAF-CBK-CBM	5.73	120.16	111.21
2	C	901	6EU	OAF-CBK-CBM	5.71	120.13	111.21
2	A	901	6EU	OAF-CBK-CBM	5.69	120.09	111.21
2	A	901	6EU	CAQ-CAY-CBE	-4.99	107.74	113.60

There are no chirality outliers.

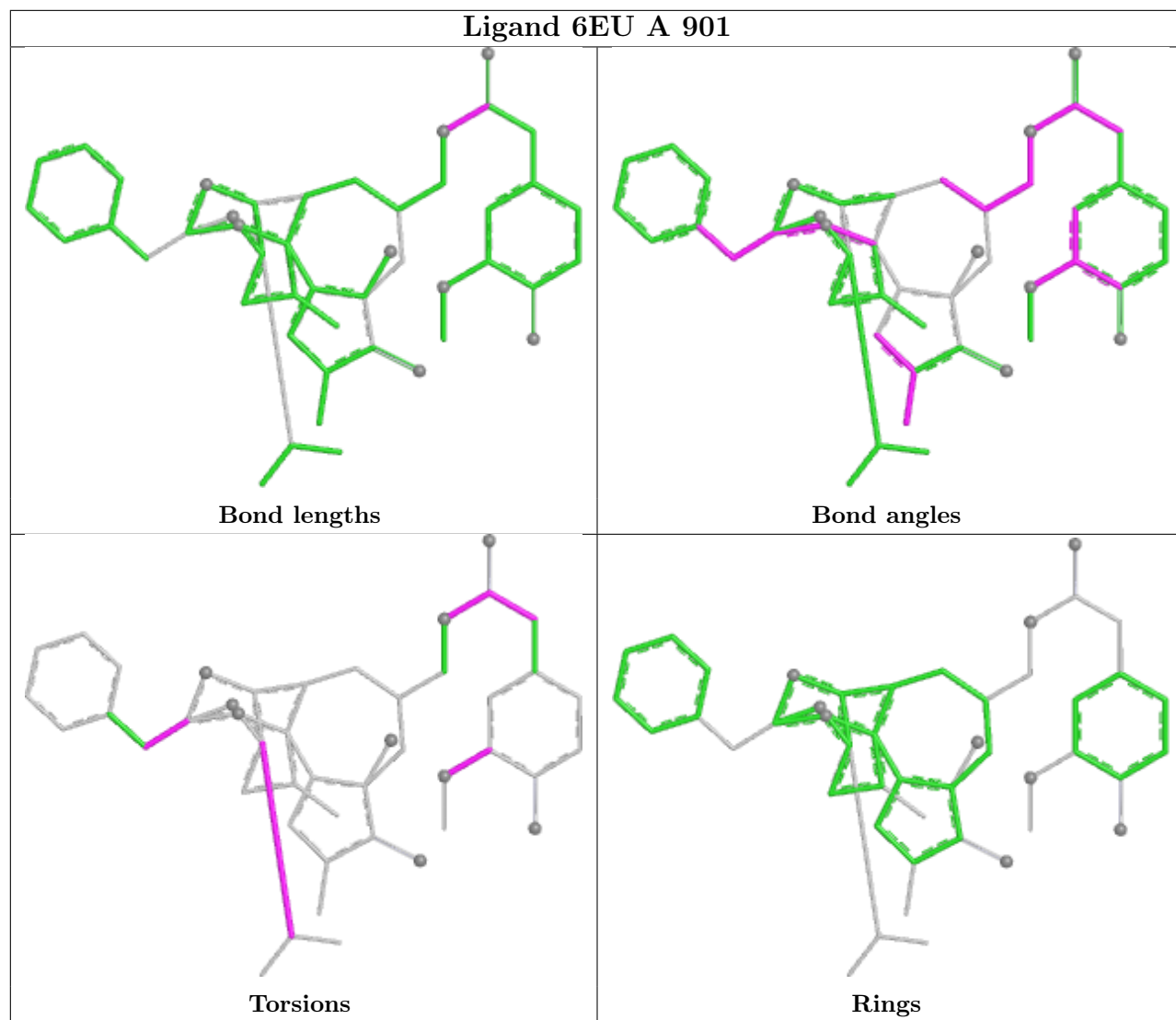
5 of 40 torsion outliers are listed below:

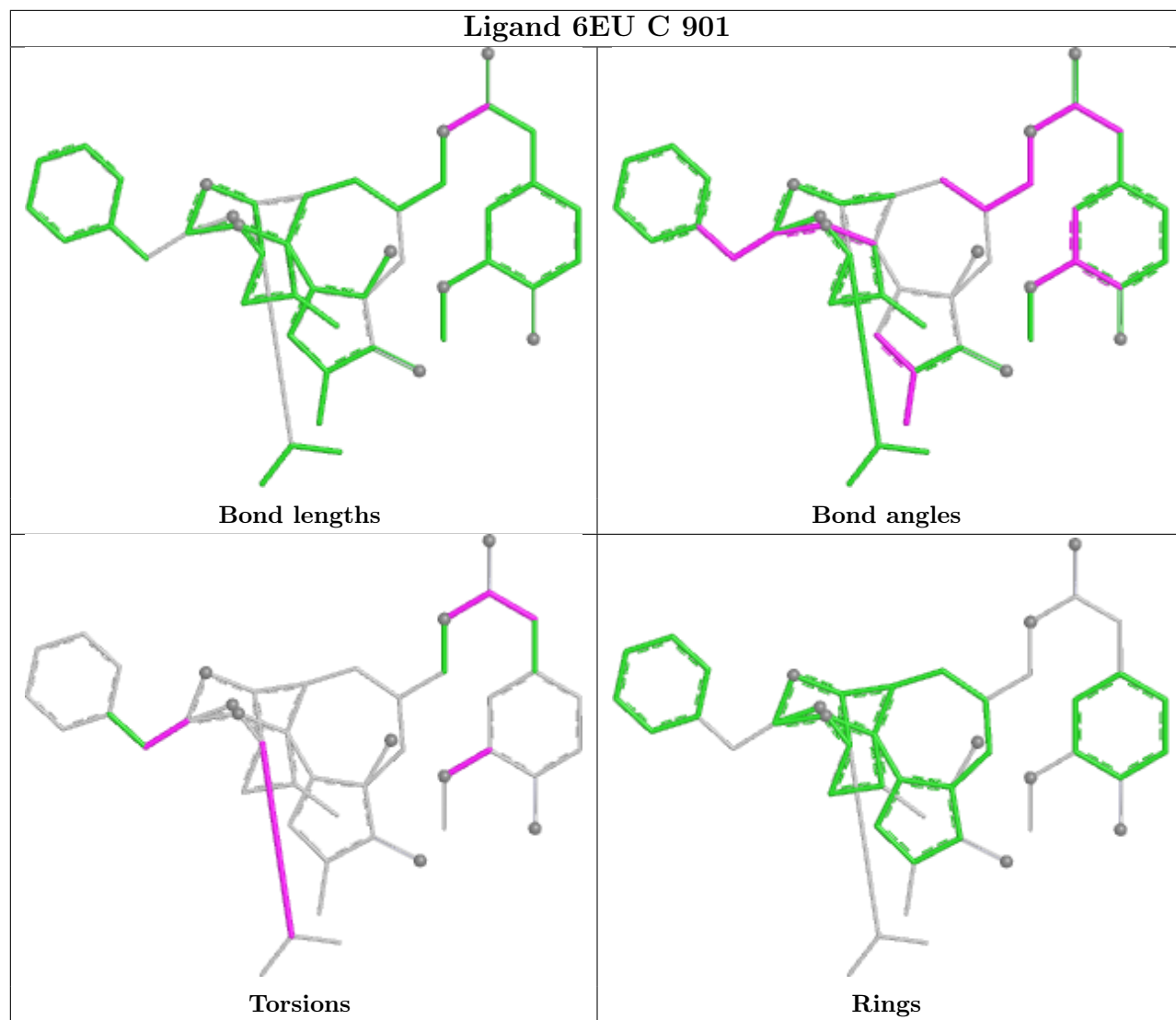
Mol	Chain	Res	Type	Atoms
2	A	901	6EU	OAC-CAM-CAV-CBB
2	A	901	6EU	OAC-CAM-CAV-CBD
2	A	901	6EU	OAC-CAQ-CAY-CBE
2	A	901	6EU	OAB-CAQ-CAY-CBE
2	C	901	6EU	OAC-CAM-CAV-CBB

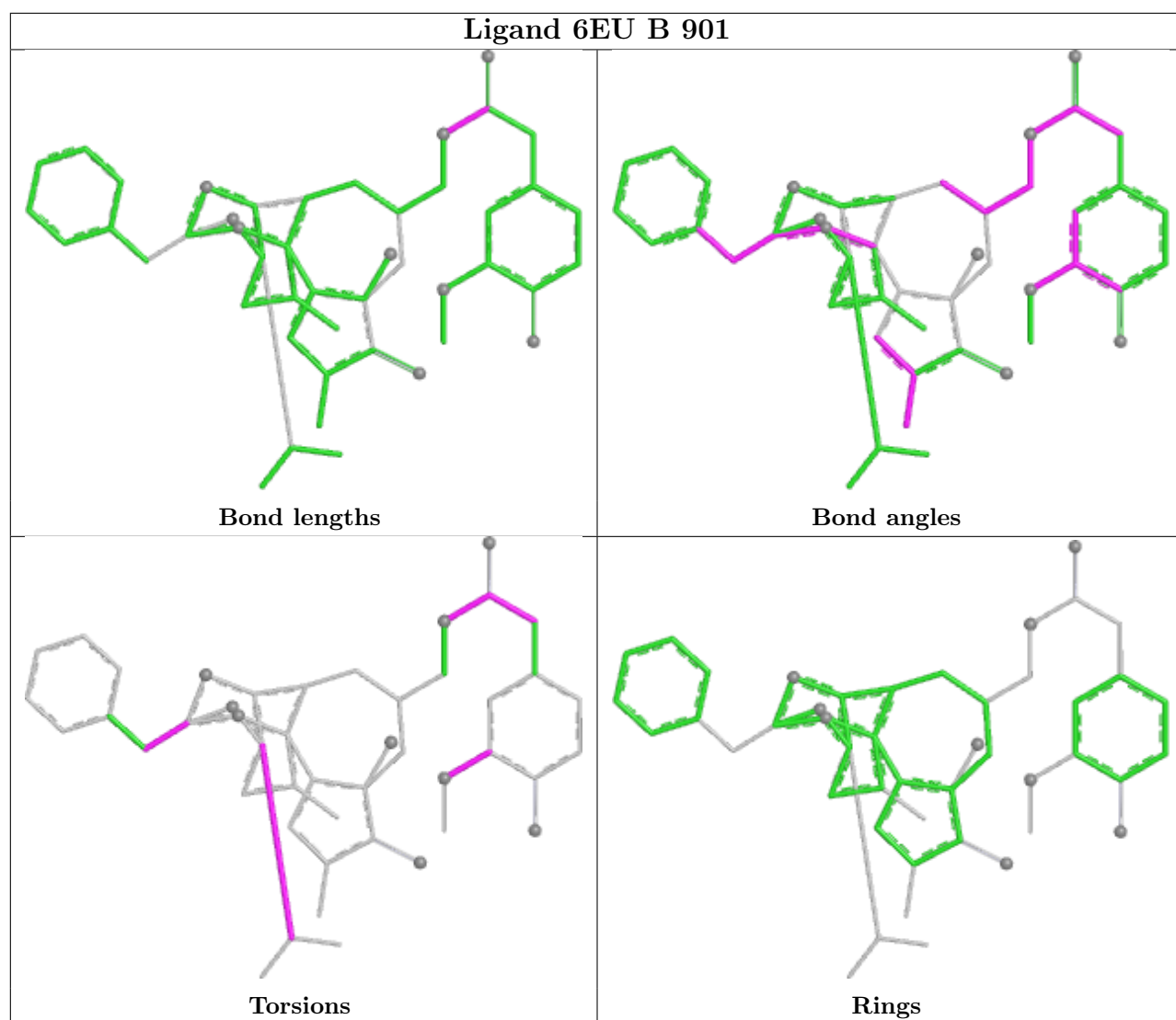
There are no ring outliers.

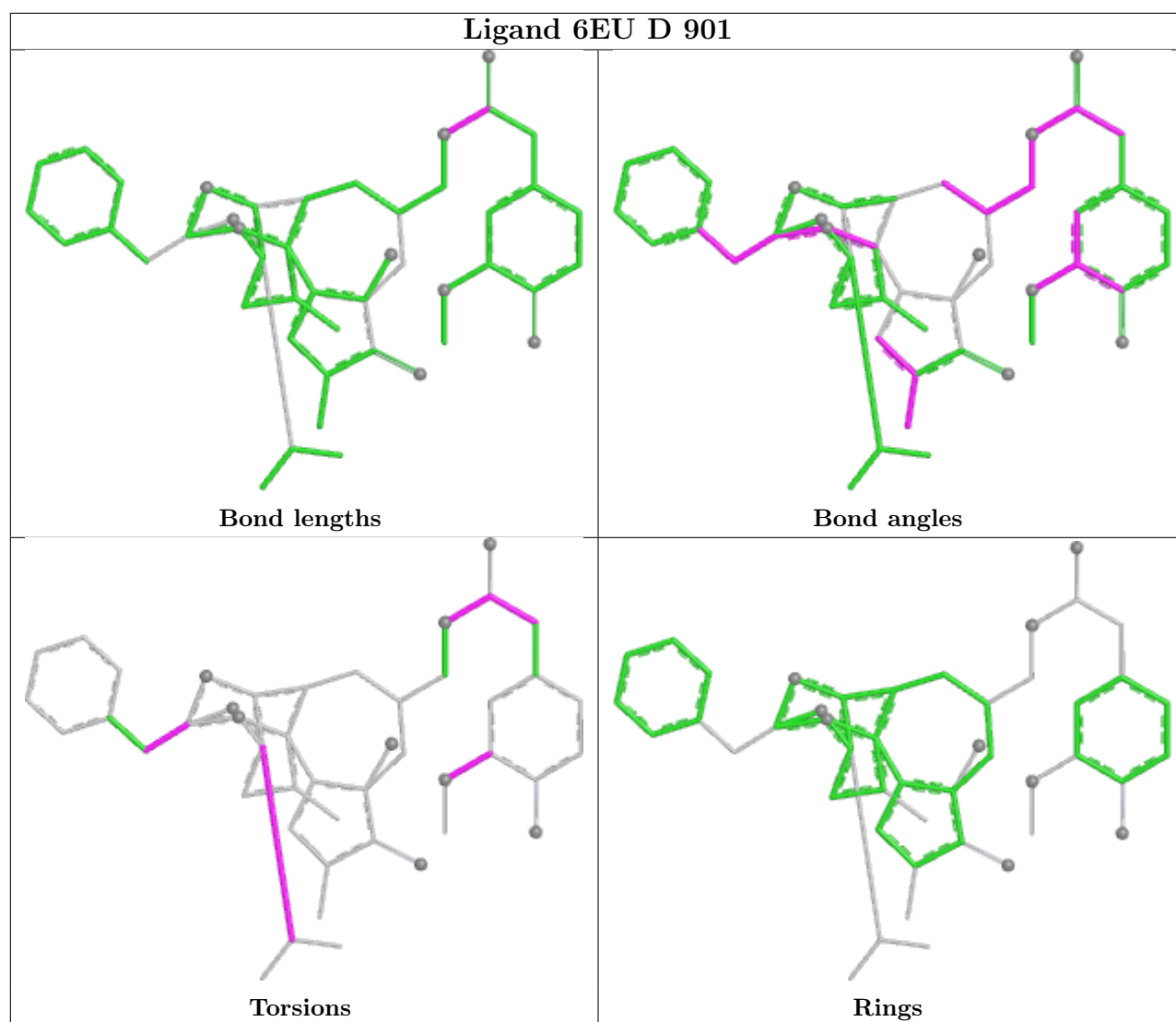
No monomer is involved in short contacts.

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.

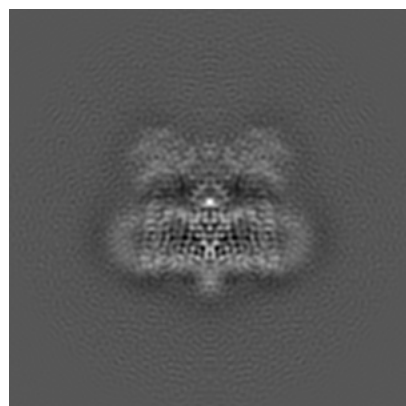
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23135. These allow visual inspection of the internal detail of the map and identification of artifacts.

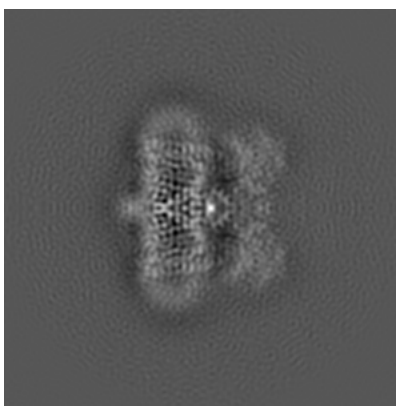
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

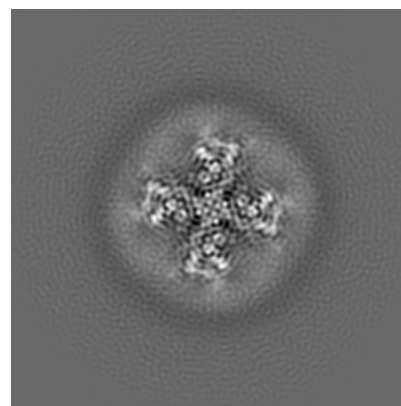
6.1.1 Primary map



X

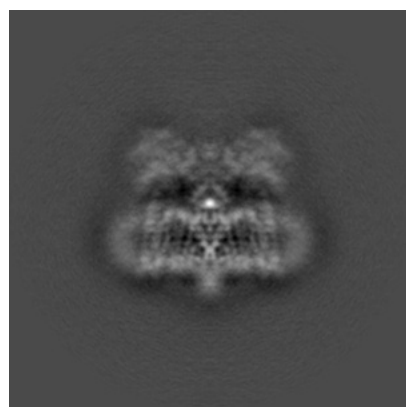


Y

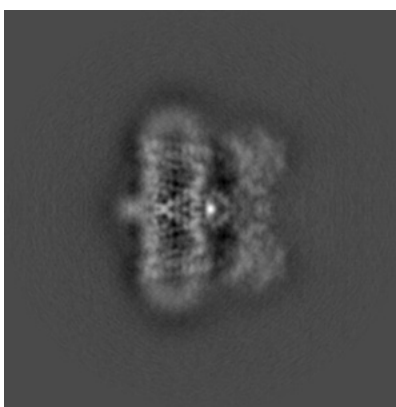


Z

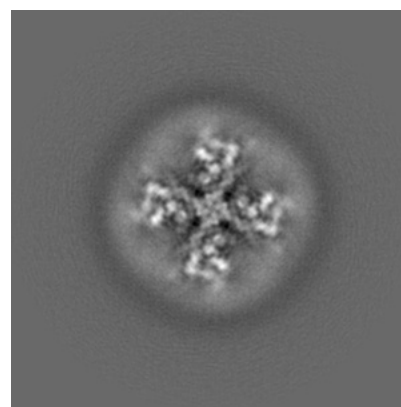
6.1.2 Raw map



X



Y

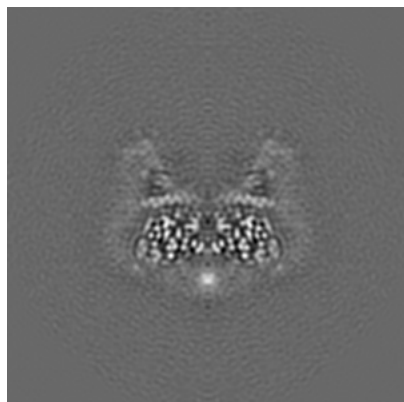


Z

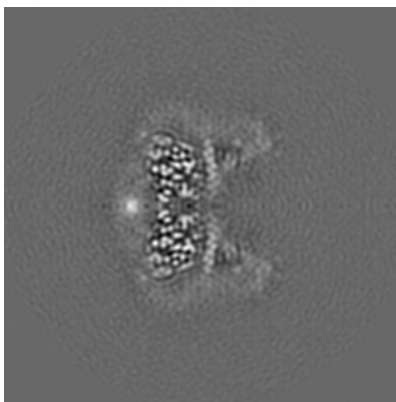
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

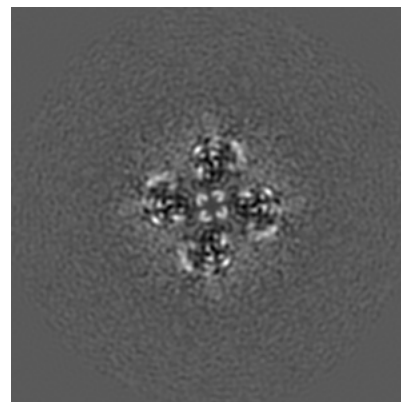
6.2.1 Primary map



X Index: 112

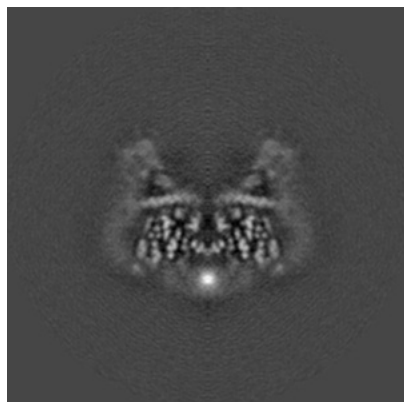


Y Index: 112

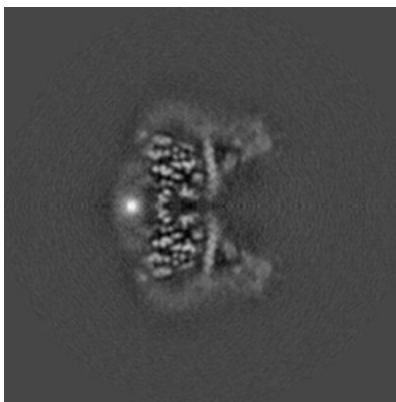


Z Index: 112

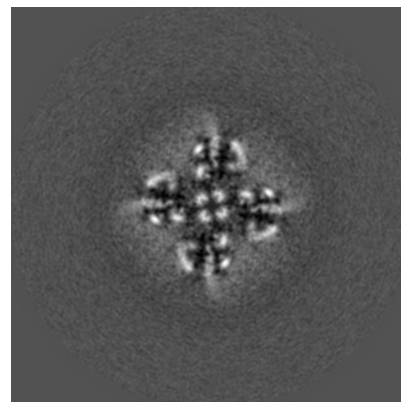
6.2.2 Raw map



X Index: 112



Y Index: 112

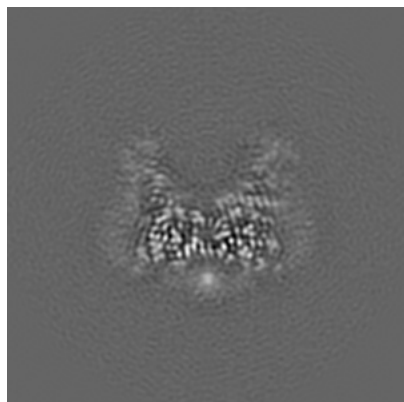


Z Index: 112

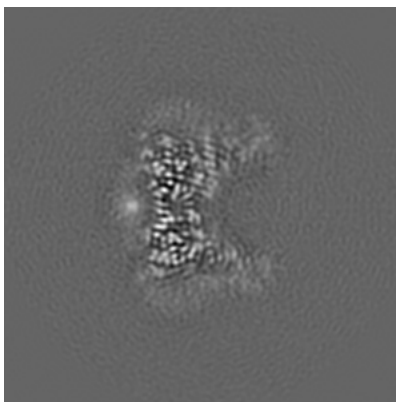
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

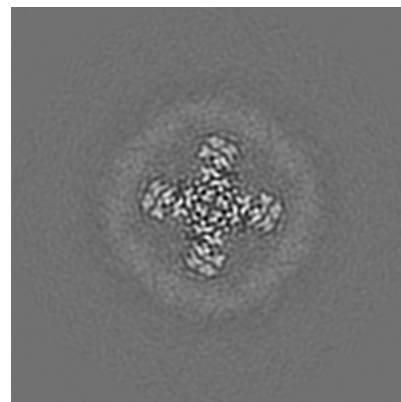
6.3.1 Primary map



X Index: 114

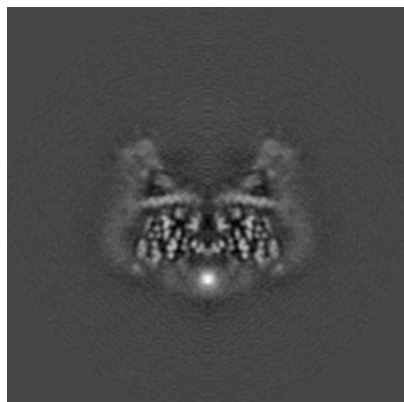


Y Index: 110

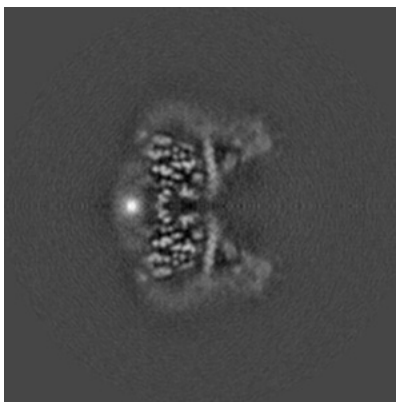


Z Index: 92

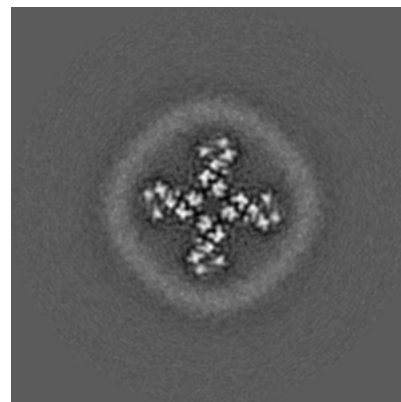
6.3.2 Raw map



X Index: 112



Y Index: 112

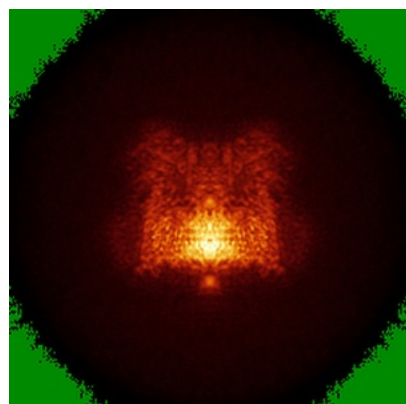


Z Index: 97

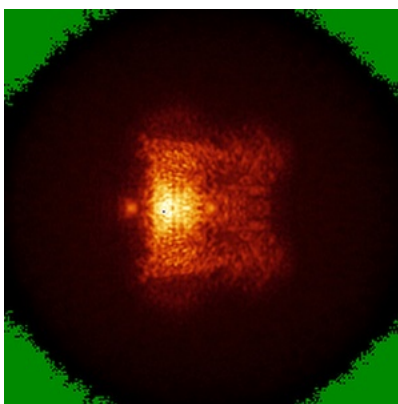
The images above show the largest variance slices of the map in three orthogonal directions.

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

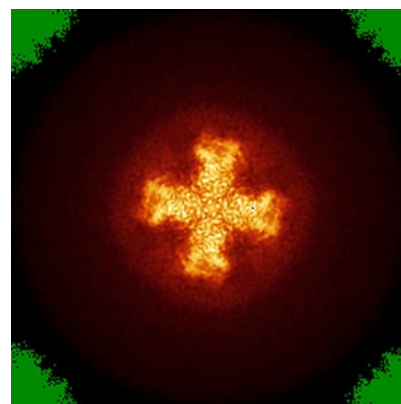
6.4.1 Primary map



X

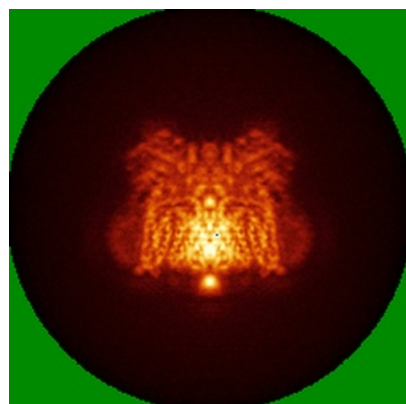


Y

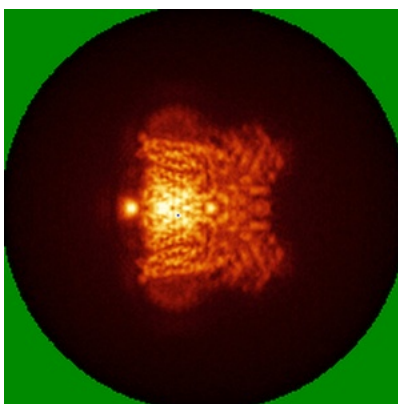


Z

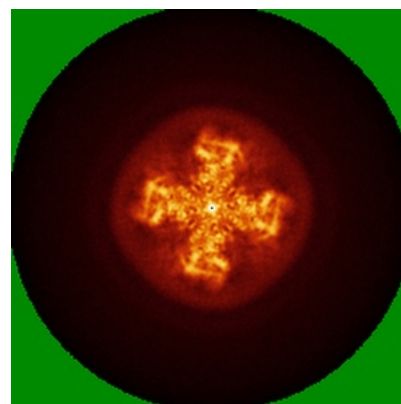
6.4.2 Raw map



X



Y

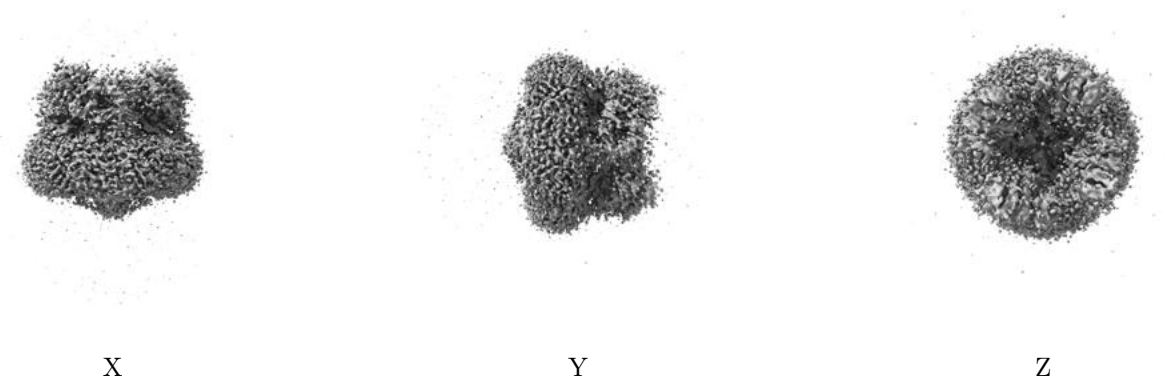


Z

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.

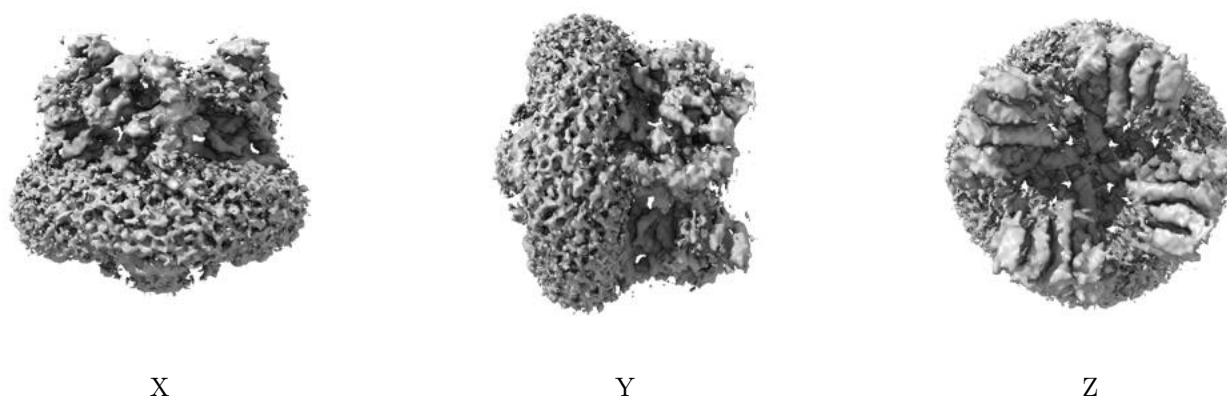
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. 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.

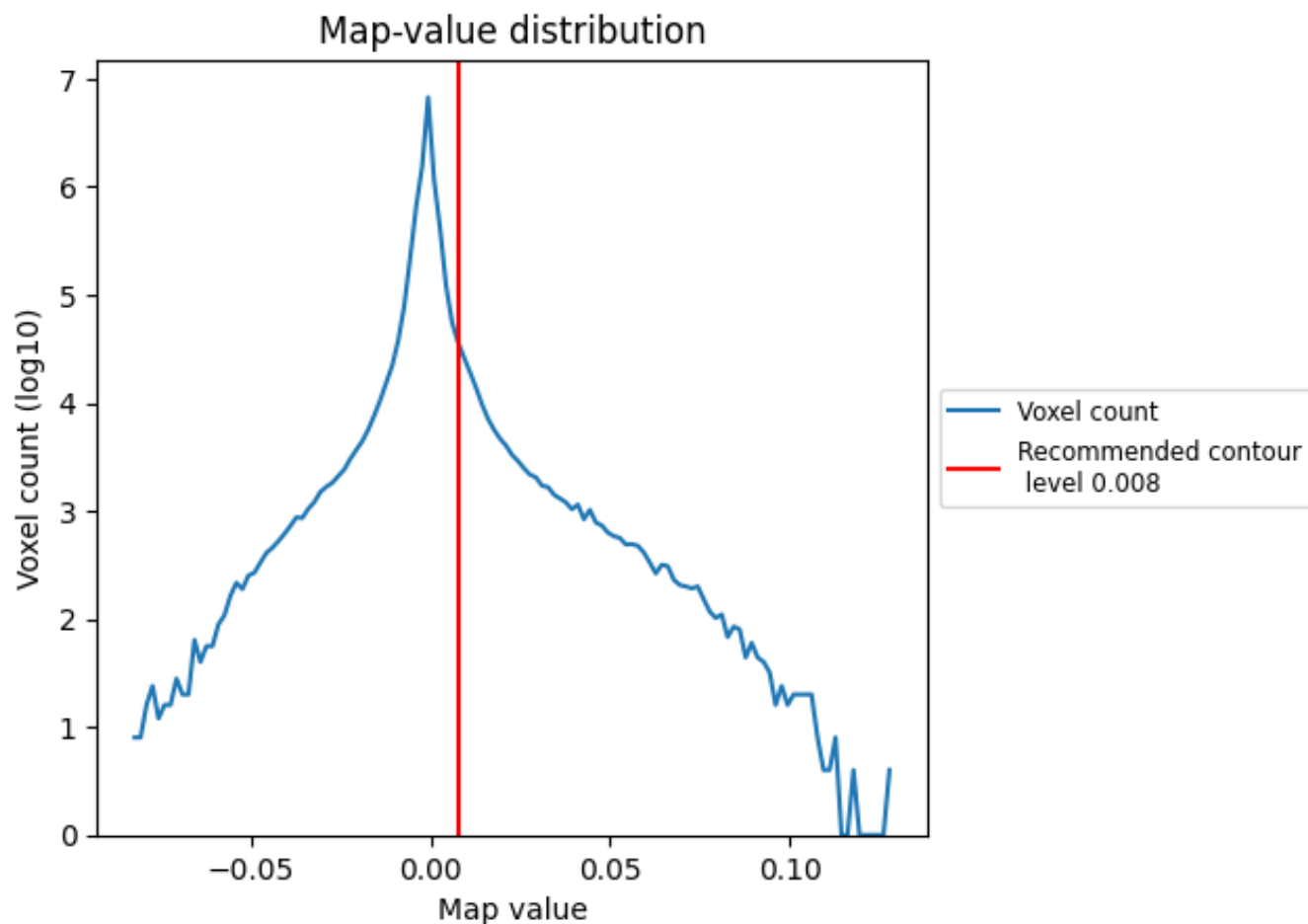
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

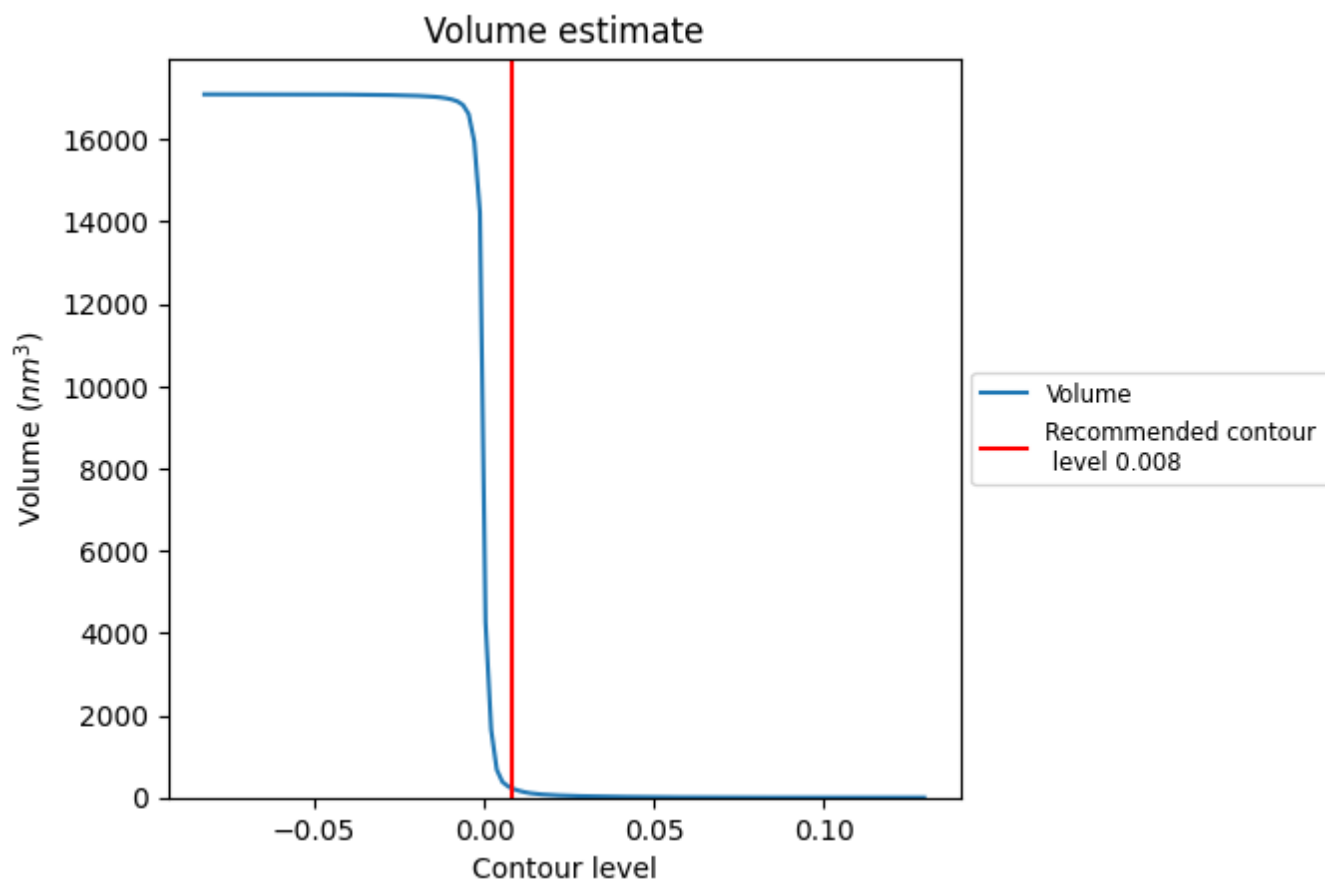
This section contains the results of statistical analysis of the map.

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.

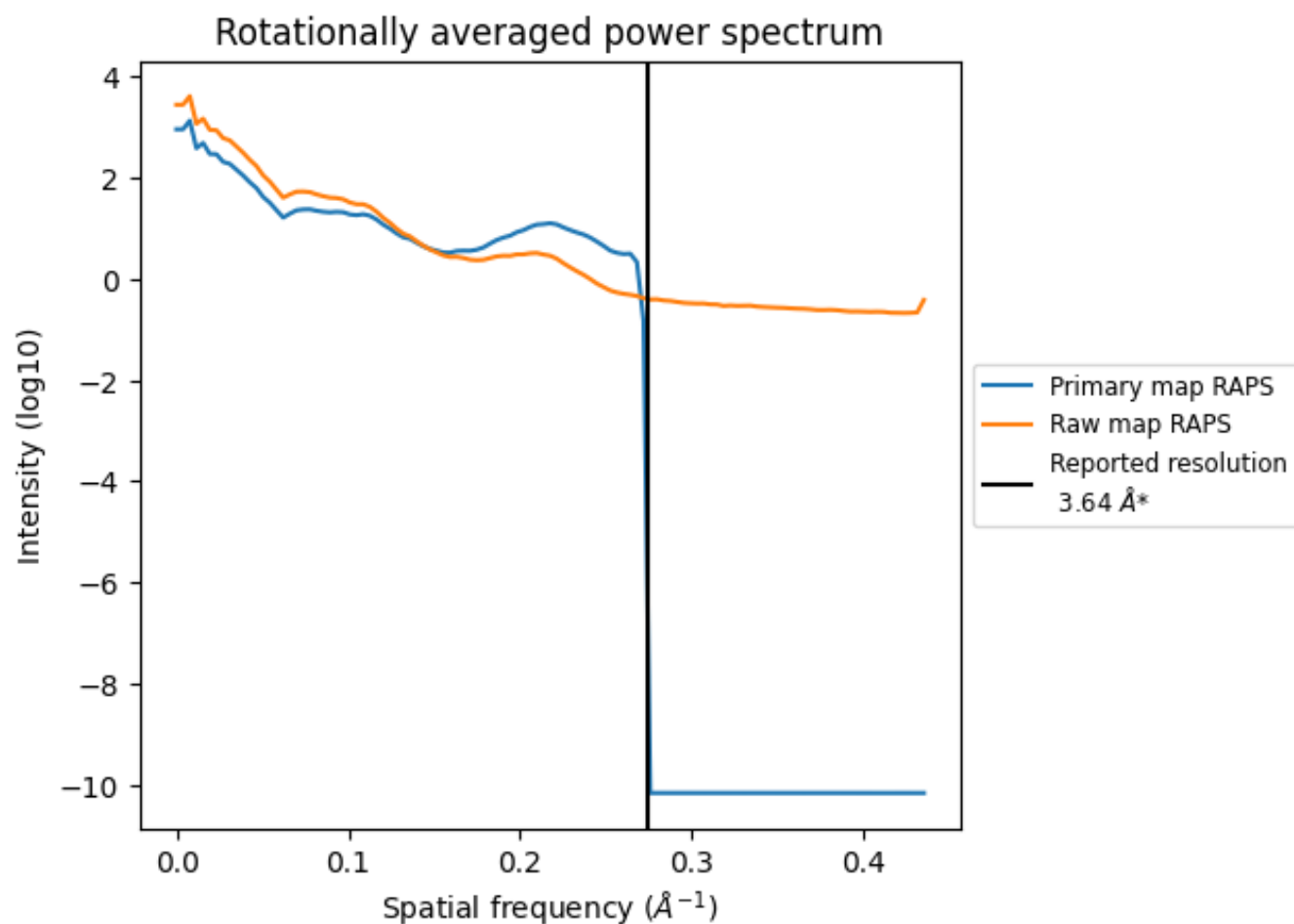
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 234 nm^3 ; this corresponds to an approximate mass of 211 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 ⓘ

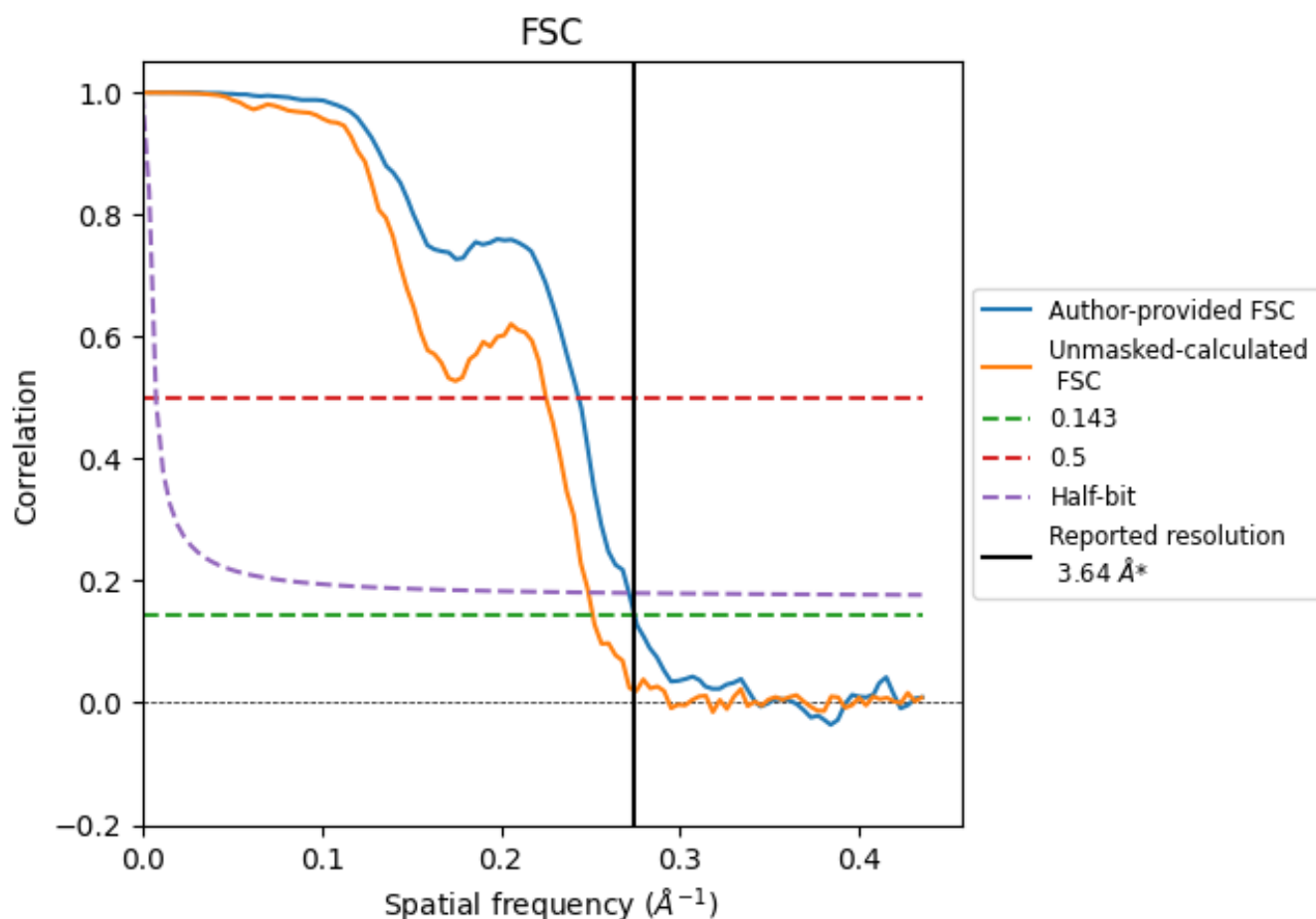


*Reported resolution corresponds to spatial frequency of 0.275 Å⁻¹

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 $0.275 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

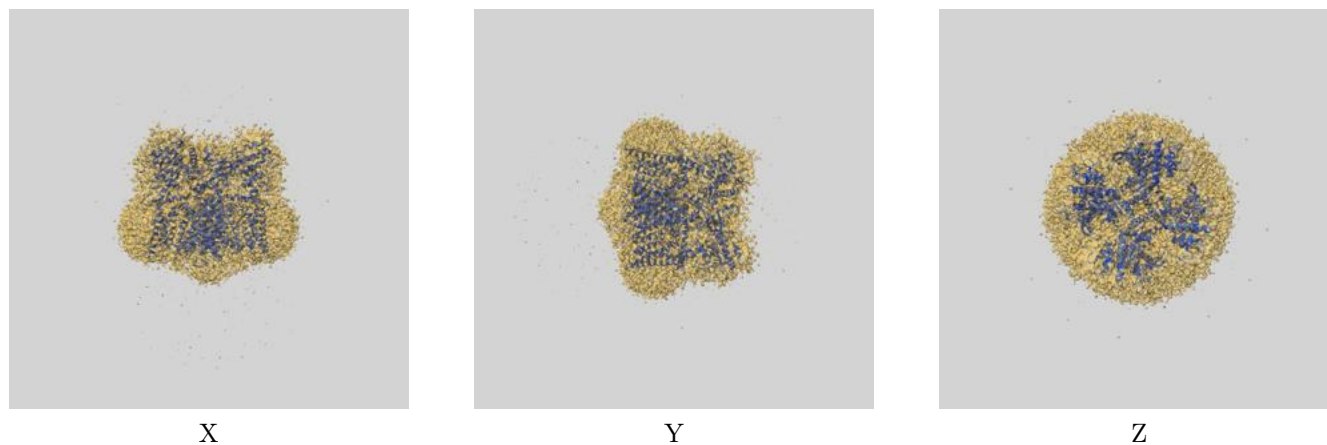
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.64	-	-
Author-provided FSC curve	3.64	4.11	3.68
Unmasked-calculated*	3.98	4.44	4.02

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

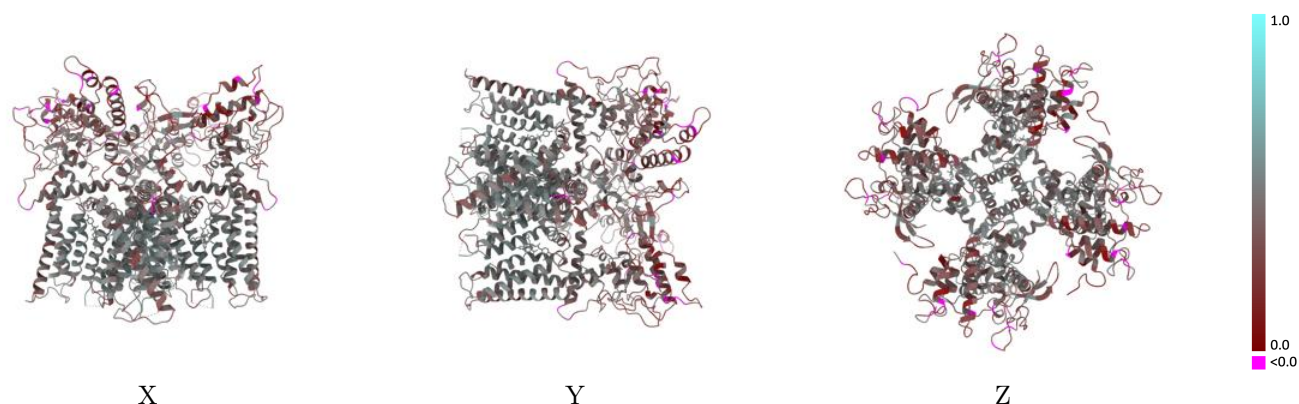
This section contains information regarding the fit between EMDB map EMD-23135 and PDB model 7L2O. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



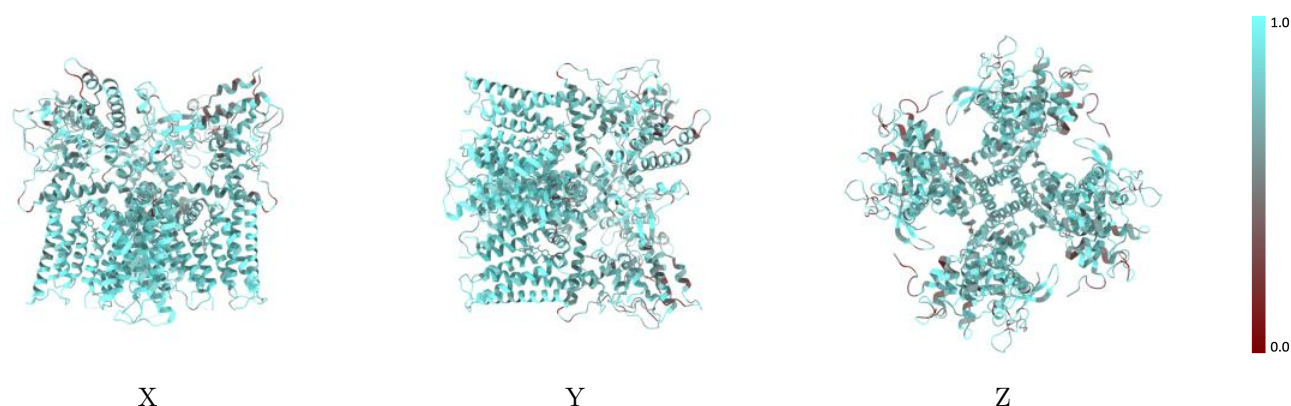
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



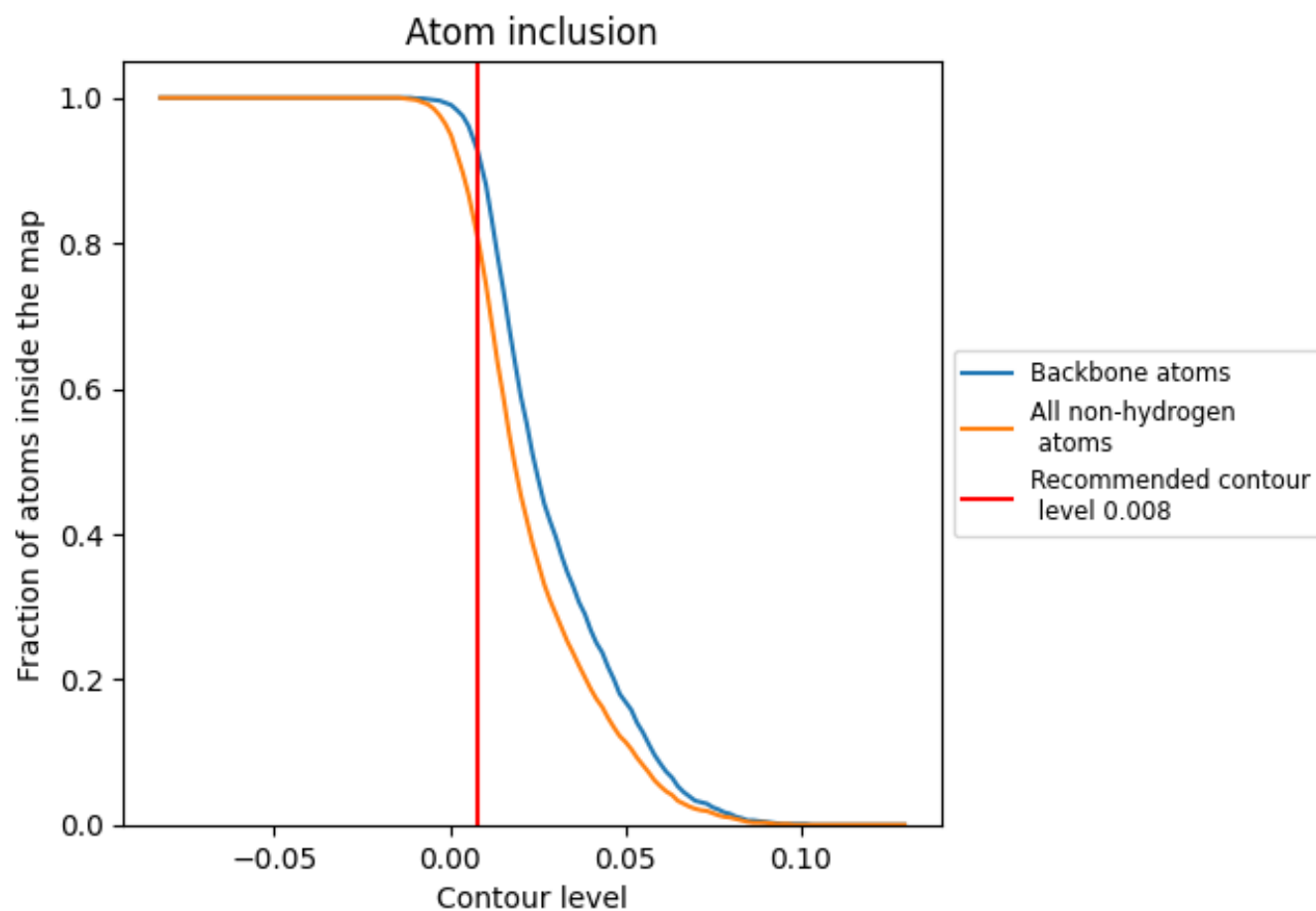
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 81% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8060	0.3930
A	0.8030	0.3920
B	0.8050	0.3920
C	0.8100	0.3920
D	0.8080	0.3950

