



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 07:08 PM UTC

PDB ID : 7L2J / pdb_00007l2j
EMDB ID : EMD-23130
Title : Cryo-EM structure of full-length TRPV1 at pH6c state
Authors : Zhang, K.; Julius, D.; Cheng, Y.
Deposited on : 2020-12-17
Resolution : 3.66 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

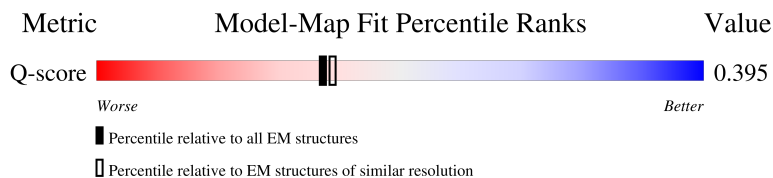
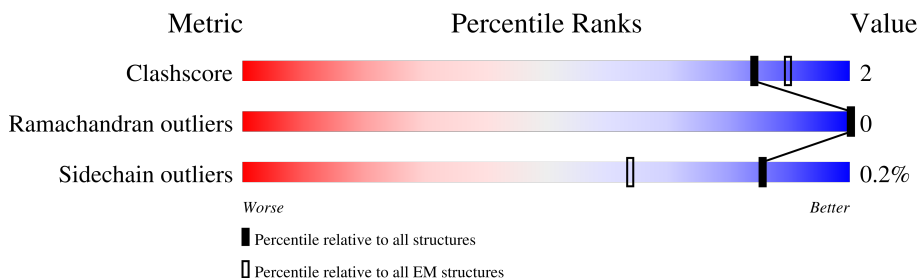
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.66 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	11491 (3.16 - 4.16)

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 17336 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.

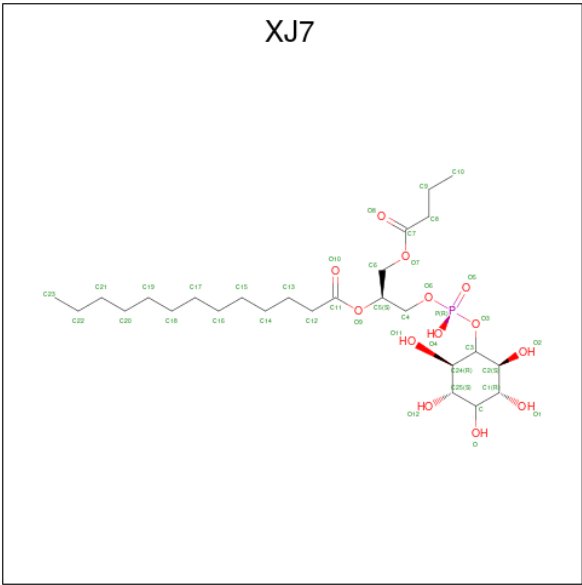
- Molecule 1 is a protein called Transient receptor potential cation channel subfamily V member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	529	Total	C	N	O	S	1	0
			4294	2814	695	760	25		
1	B	529	Total	C	N	O	S	1	0
			4294	2814	695	760	25		
1	C	529	Total	C	N	O	S	1	0
			4294	2814	695	760	25		
1	D	529	Total	C	N	O	S	1	0
			4294	2814	695	760	25		

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
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
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

- Molecule 2 is (2S)-1-(butanoyloxy)-3-{[(R)-hydroxy{[(1r,2R,3S,4S,5R,6S)-2,3,4,5,6-pentahydroxycyclohexyl]oxy}phosphoryl]oxy}propan-2-yl tridecanoate (CCD ID: XJ7) (formula: C₂₆H₄₉O₁₃P) (labeled as "Ligand of Interest" by depositor).

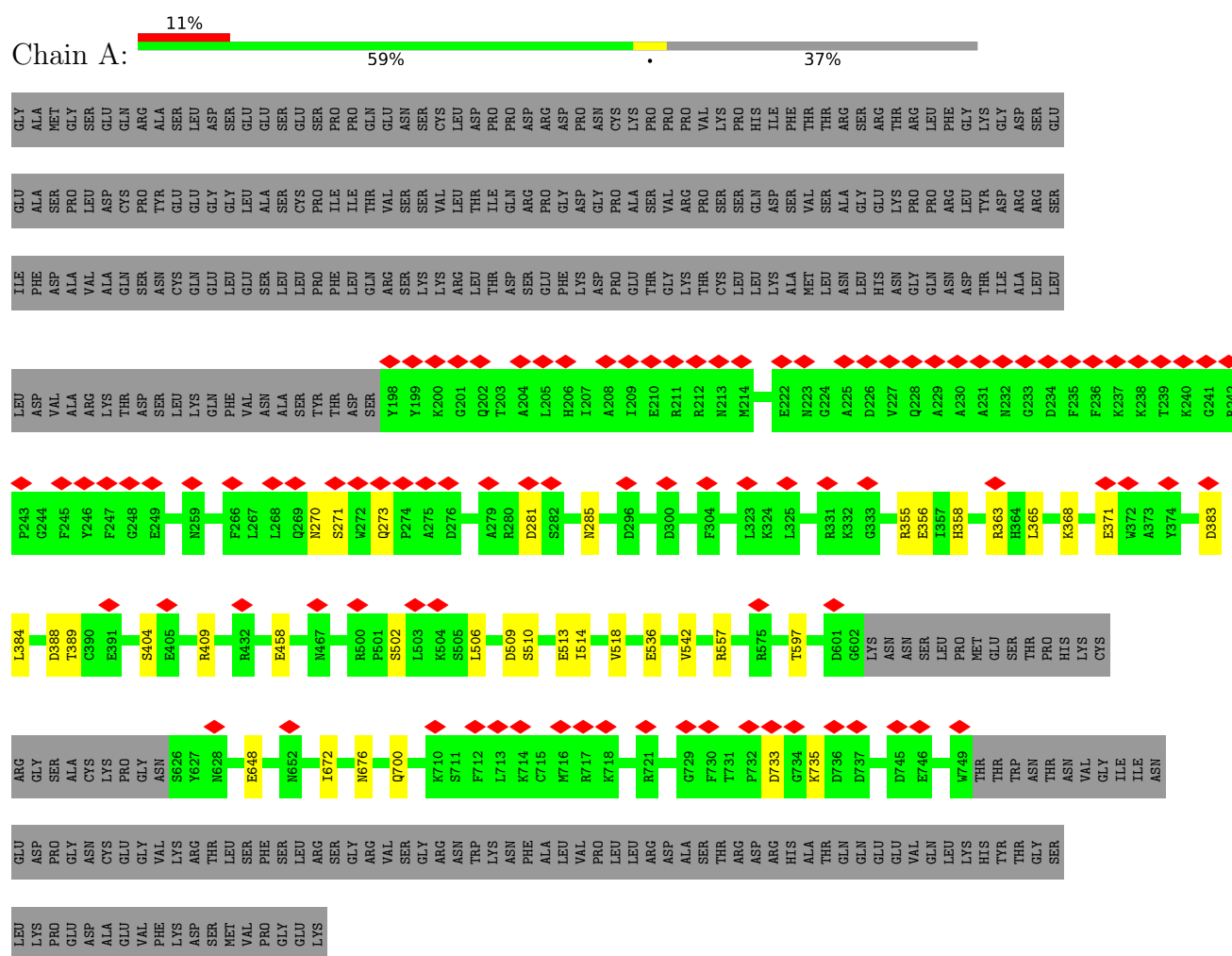


Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	O	P	0
			40	26	13	1	
2	B	1	Total	C	O	P	0
			40	26	13	1	
2	C	1	Total	C	O	P	0
			40	26	13	1	
2	D	1	Total	C	O	P	0
			40	26	13	1	

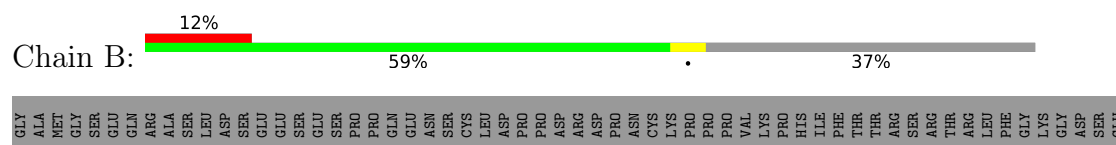
3 Residue-property plots

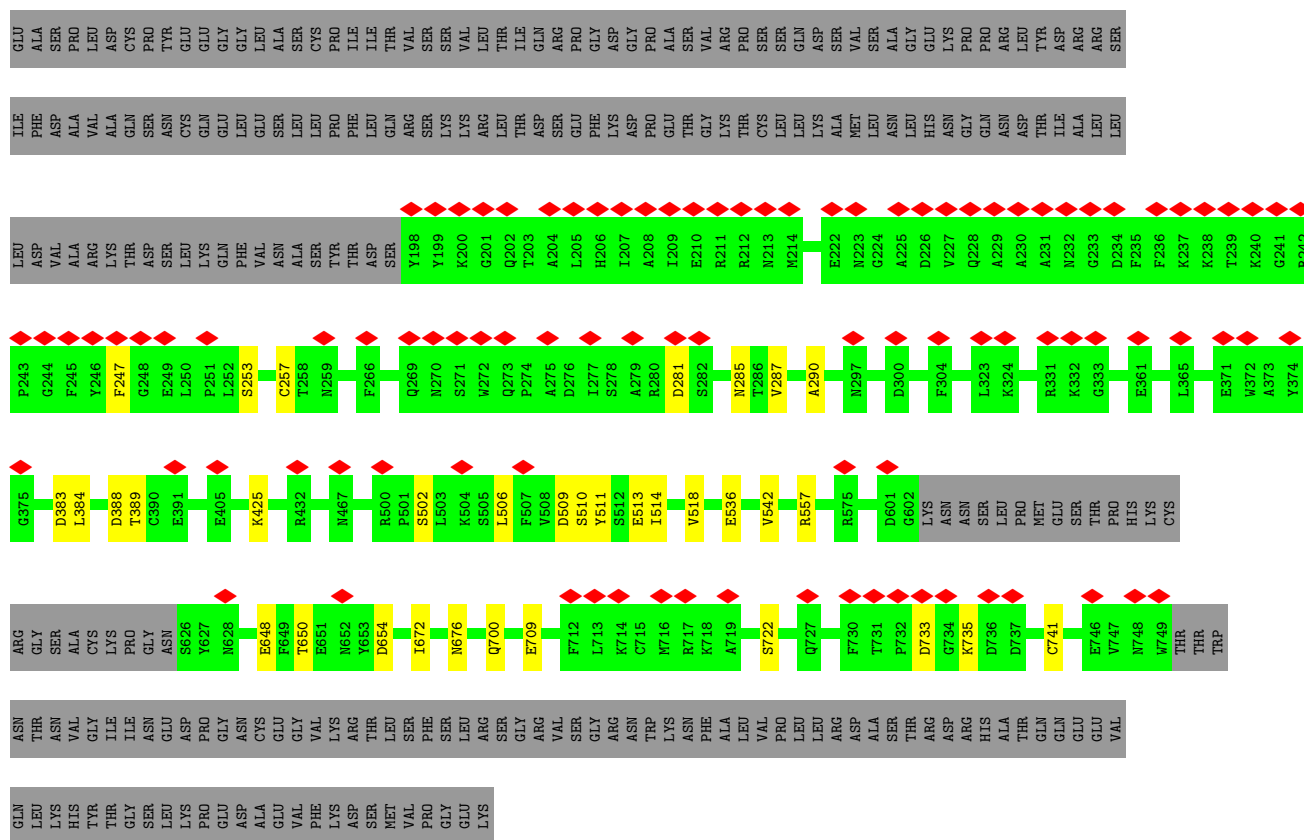
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

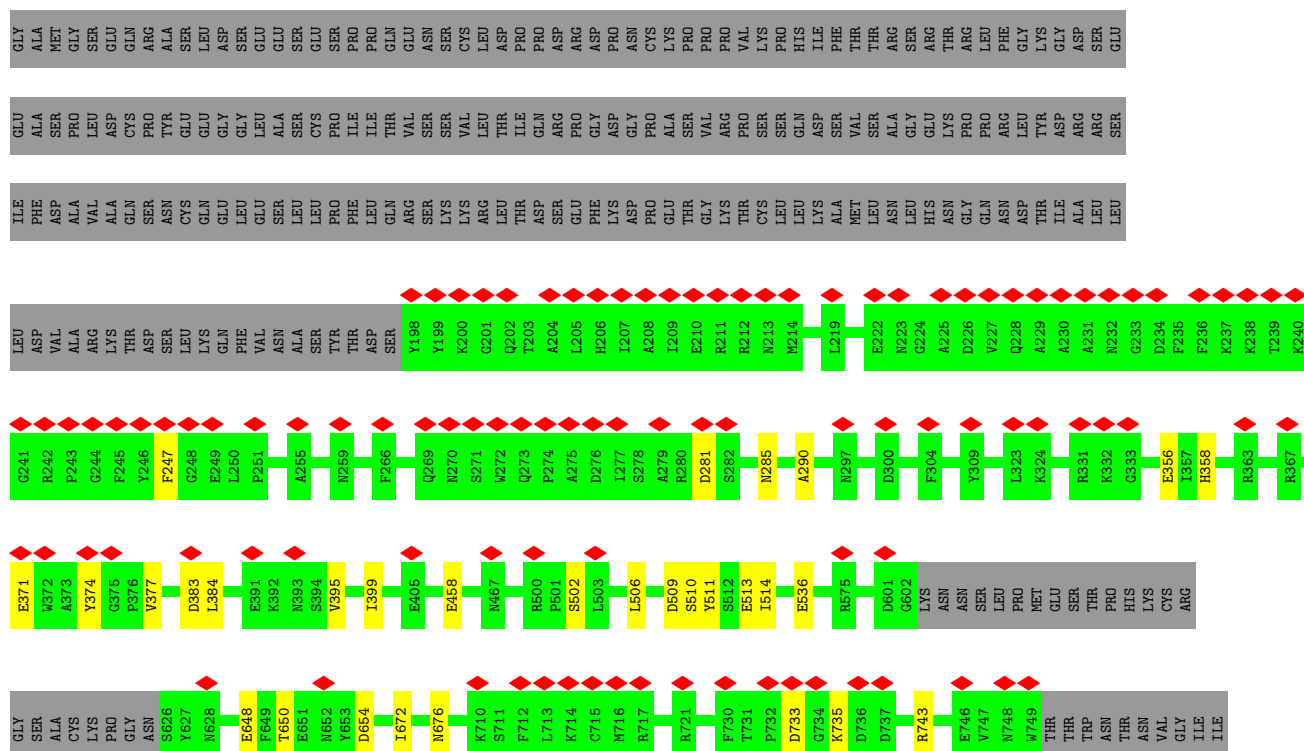


- Molecule 1: Transient receptor potential cation channel subfamily V member 1





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



[illegible]

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



GLY	ALA	MET	GLY	SER	GLU	GLN	ARG	ALA	SER	LEU	ASP	SER	GLU	SER	GLU	ASN	CYS	LEU	ASP	PRO	PRO	GLU	GLY	GLU	ASN	SER	SER	THR	THR	ARG	SER	ARG	THR	ARG	LEU	PHE	GLY	GLY	ASP	SER	GLU
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GLU	ALA	SER	PRO	LEU	ASP	CYS	PRO	PRO	TYR	GLU	GLY	GLY	LEU	ALA	SER	CYS	PRO	ILE	ILE	THR	VAL	SER	SER	VAL	LEU	THR	THR	ILE	ILE	GLN	ARG	ARG	PRO	GLY	GLY	ASP	PRO	ALA	SER	SER	VAL	VAL	ARG	ARG	PRO	SER	SER	GLN	ASP	SER	VAL	VAL	SER	ALA	ALA	GLY	GLU	LYS	PRO	PRO	PRO	ARG	TYR	ASP	ARG	ARG	SER	ARG	FER
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ILE	PHE	ASP	ALA	VAL	ALA	GLN	SER	ASN	CYS	GLN	GLU	LEU	GLU	SER	LEU	LEU	PRO	PHE	LEU	GLN	ARG	SER	LYS	LYS	ARG	LEU	THR	THR	SER	GLU	PHE	GLY	LYS	ASP	PRO	GLU	THR	THR	CYS	LEU	LEU	LYS	ALA	ALA	MET	LEU	ASN	ASN	GLN	ASN	ASP	THR	ILE	ALA	LEU	LEU
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[illegible]

P243	P244	P245	P246	P247	P248	P249	P250	P266	P267	P268	P269	P270	P271	P272	P273	P274	P275	P276	P277	P278	P279	P280	P281	P282	P285	P300	P304	L323	K324	R331	K332	G333	K355	K356	L357	K358	L365	K368	E371	K372	A373	Y374	V377	D383	L384	P388
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T389	C390	C391	S404	E405	R409	R432	R467	R500	P501	S502	L503	K504	S505	L506	F507	V508	D509	S510	E513	L514	V518	E536	R557	M572	R575	D576	T597	D601	G602	Lys	Asn	Asn	Asn	Ser	Ser	Leu	Pro	Met	GlU	Ser	Thr	Pro	HIS	Lys	Cys	Arg	Gly	Ser
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ALA	CYS	LYS	PRO	GLY	ASN	S626	T641	E648	F649	T650	S651	N652	Y653	D654	I672	L675	N676	F712	L713	K714	T715	M716	R717	K718	A719	T720	R721	S722	T727	F730	T731	P732	D733	G734	K735	D736	D737	C741	D745	E746	V747	N748	V749	THR	THR	TRP	TRP	ASN	ASN	THR	THR	ASN	ASN
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GLY ILE LEU ASN GLU ASP PRO GLY ASN CYS GLU VAL LYS ARG THR SER PHE SER LEU ARG GLY ARG VAL SER GLY ARG ASN TRP LYS ASN PHE LEU ALA LEU VAL PRO LEU LEU LEU ARG ASP ALA SER THR THR GLN GLN GLU VAL VAL GLN GLN LEU LEU LYS HIS

TYR	THR	GLY	SER	LEU	LYS	PRO	GLU	ASP	ALA	GLU	VAL	PHE	LYS	ASP	SER	MET	VAL	PRO	GLY	GLU	LYS
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	21512	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 ($e^-/\text{\AA}^2$)	76.8	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	0.125	Depositor
Minimum map value	-0.091	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.014	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: XJ7

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	0.30	0/4396	0.40	0/5950
1	B	0.33	2/4396 (0.0%)	0.41	0/5950
1	C	0.32	1/4396 (0.0%)	0.43	0/5950
1	D	0.33	1/4396 (0.0%)	0.41	0/5950
All	All	0.32	4/17584 (0.0%)	0.41	0/23800

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	654	ASP	C-N	-7.66	1.23	1.33
1	D	654	ASP	C-N	7.07	1.43	1.33
1	B	654	ASP	C-N	-5.69	1.26	1.33
1	B	511	TYR	C-N	-5.07	1.27	1.33

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	4294	0	4325	22	0
1	B	4294	0	4325	19	0
1	C	4294	0	4325	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	4294	0	4325	23	0
2	A	40	0	0	0	0
2	B	40	0	0	1	0
2	C	40	0	0	0	0
2	D	40	0	0	1	0
All	All	17336	0	17300	79	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 79 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:672:ILE:O	1:A:676:ASN:ND2	2.17	0.77
1:C:672:ILE:O	1:C:676:ASN:ND2	2.17	0.76
1:B:672:ILE:O	1:B:676:ASN:ND2	2.20	0.73
1:A:458:GLU:OE1	1:A:458:GLU:N	2.25	0.69
1:B:722:SER:OG	1:B:741:CYS:O	2.07	0.67

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	526/842 (62%)	501 (95%)	25 (5%)	0	100	100
1	B	526/842 (62%)	503 (96%)	23 (4%)	0	100	100
1	C	526/842 (62%)	499 (95%)	27 (5%)	0	100	100
1	D	526/842 (62%)	498 (95%)	28 (5%)	0	100	100
All	All	2104/3368 (62%)	2001 (95%)	103 (5%)	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	466/743 (63%)	466 (100%)	0	100	100
1	B	466/743 (63%)	465 (100%)	1 (0%)	87	84
1	C	466/743 (63%)	465 (100%)	1 (0%)	87	84
1	D	466/743 (63%)	465 (100%)	1 (0%)	87	84
All	All	1864/2972 (63%)	1861 (100%)	3 (0%)	85	84

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	650	THR
1	C	650	THR
1	D	650	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	364	HIS
1	D	310	ASN
1	D	519	GLN
1	B	310	ASN
1	B	408	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	XJ7	D	901	-	40,40,40	1.07	3 (7%)	49,52,52	1.15	3 (6%)
2	XJ7	C	901	-	40,40,40	1.07	3 (7%)	49,52,52	1.15	3 (6%)
2	XJ7	A	901	-	40,40,40	1.07	3 (7%)	49,52,52	1.15	3 (6%)
2	XJ7	B	901	-	40,40,40	1.07	3 (7%)	49,52,52	1.14	3 (6%)

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	XJ7	D	901	-	-	15/35/59/59	0/1/1/1
2	XJ7	C	901	-	-	15/35/59/59	0/1/1/1
2	XJ7	A	901	-	-	15/35/59/59	0/1/1/1
2	XJ7	B	901	-	-	15/35/59/59	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	XJ7	O7-C7	2.68	1.41	1.33
2	C	901	XJ7	O7-C7	2.67	1.41	1.33
2	D	901	XJ7	O9-C11	2.66	1.41	1.34
2	A	901	XJ7	O7-C7	2.65	1.41	1.33
2	D	901	XJ7	O7-C7	2.65	1.41	1.33

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	901	XJ7	O9-C11-C12	4.48	121.16	111.48
2	A	901	XJ7	O9-C11-C12	4.46	121.14	111.48
2	B	901	XJ7	O9-C11-C12	4.44	121.09	111.48
2	D	901	XJ7	O9-C11-C12	4.44	121.09	111.48
2	D	901	XJ7	O7-C7-C8	2.90	120.68	111.83

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

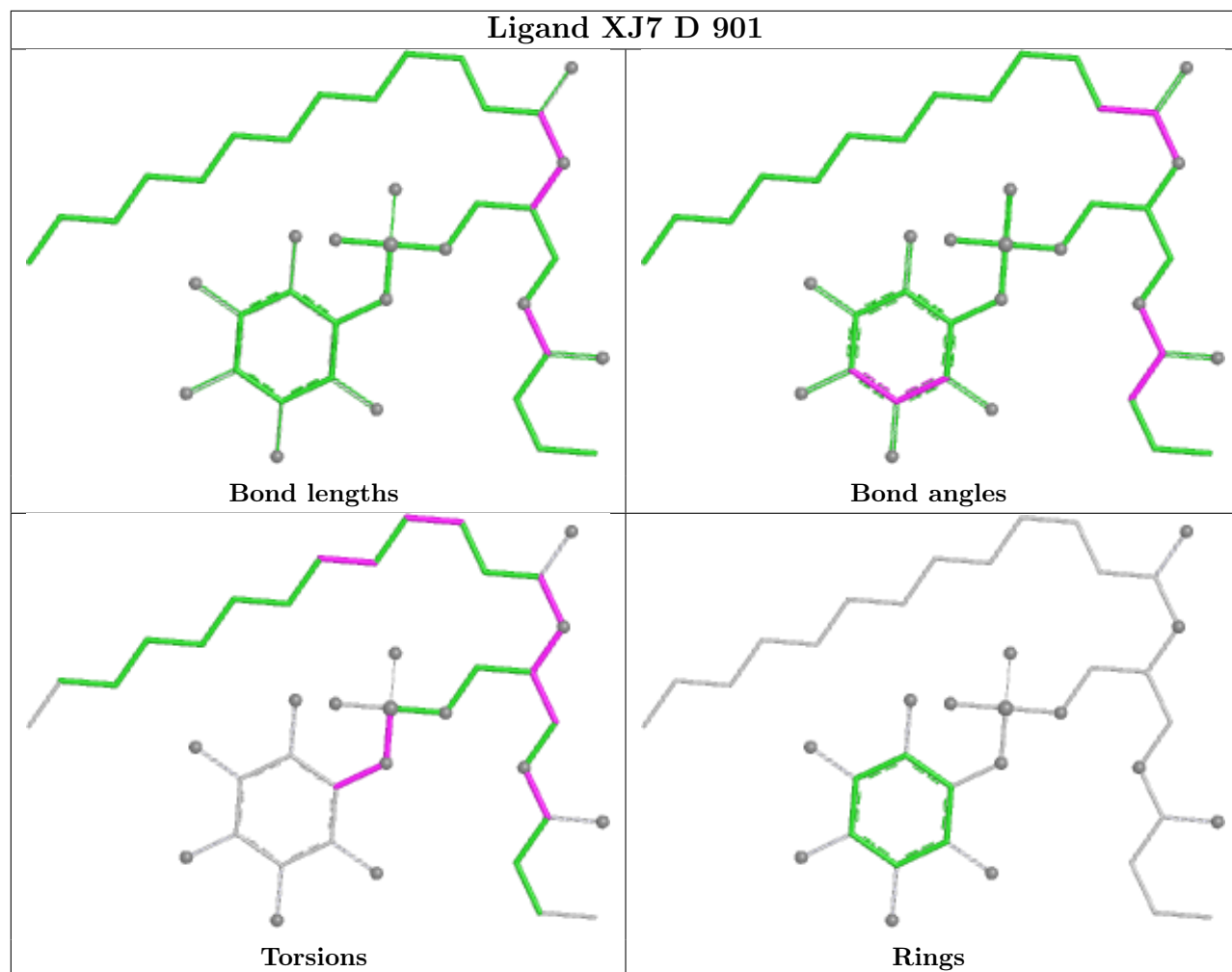
Mol	Chain	Res	Type	Atoms
2	A	901	XJ7	O10-C11-O9-C5
2	A	901	XJ7	C3-O3-P-O4
2	A	901	XJ7	C3-O3-P-O6
2	B	901	XJ7	O10-C11-O9-C5
2	B	901	XJ7	C3-O3-P-O4

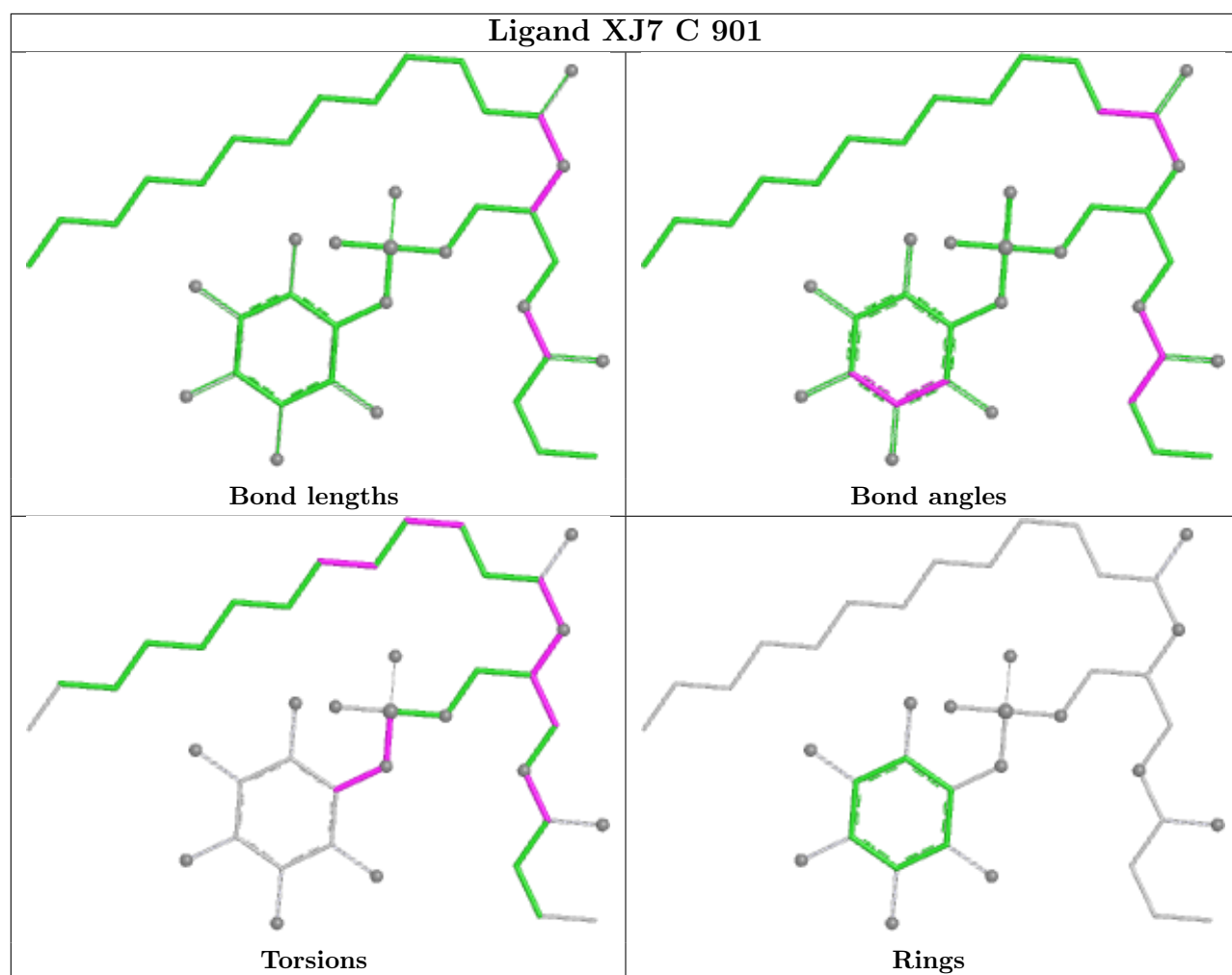
There are no ring outliers.

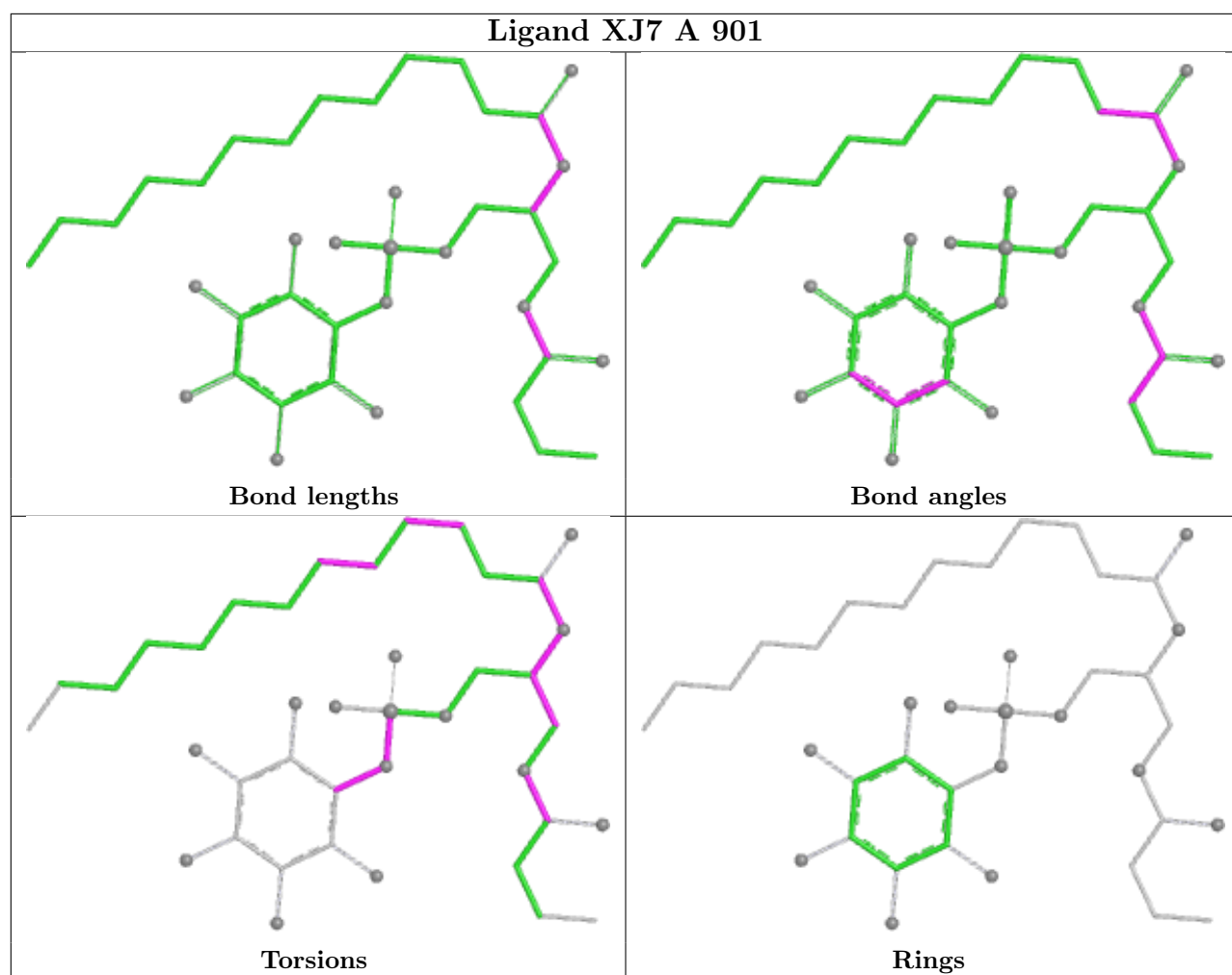
2 monomers are involved in 2 short contacts:

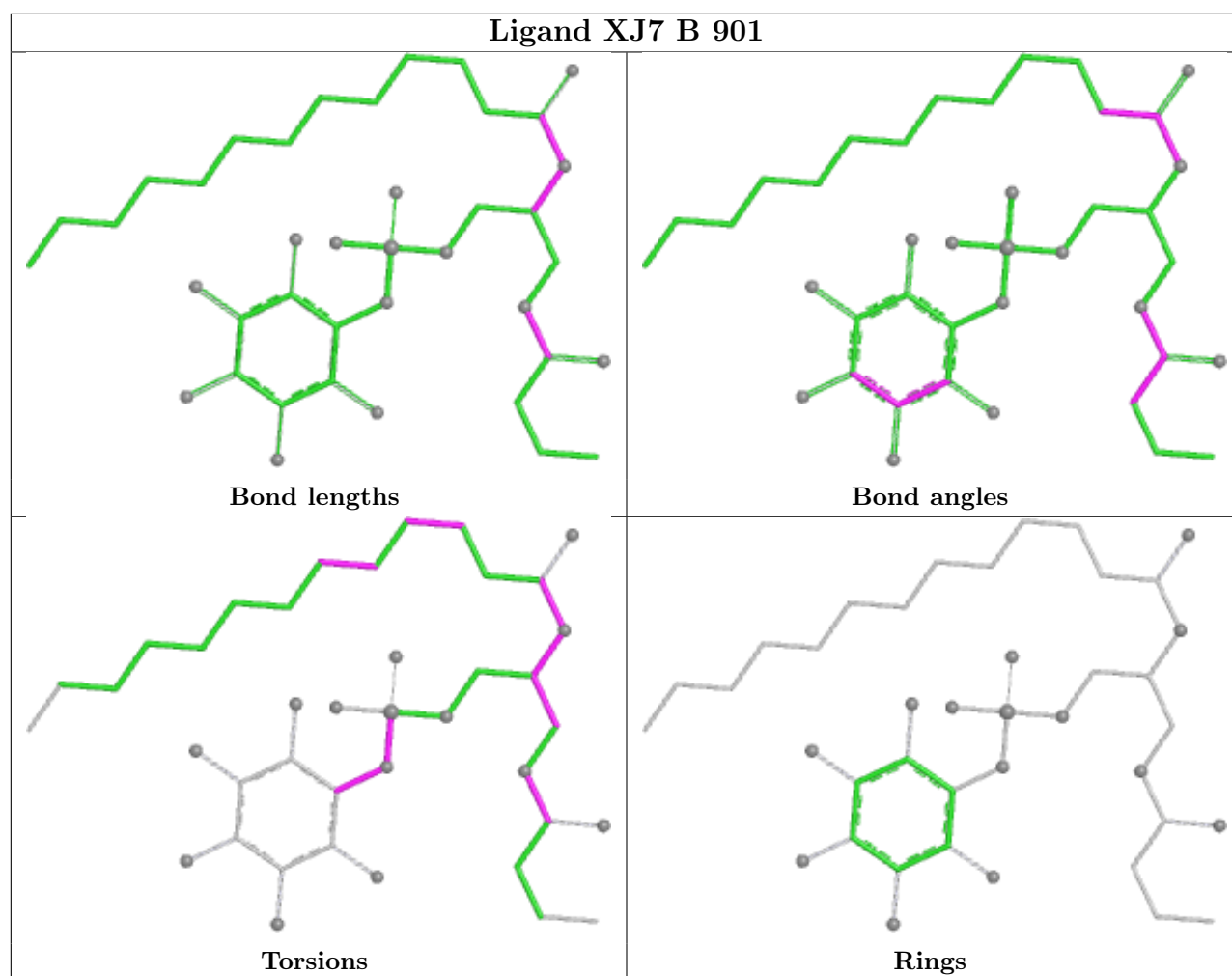
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	901	XJ7	1	0
2	B	901	XJ7	1	0

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.

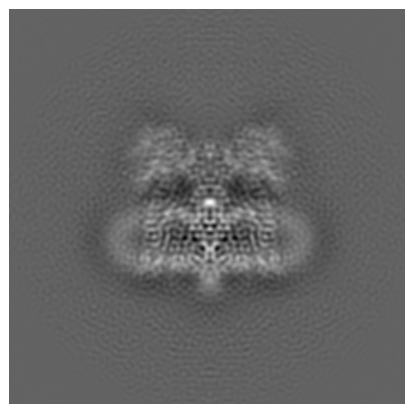
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23130. These allow visual inspection of the internal detail of the map and identification of artifacts.

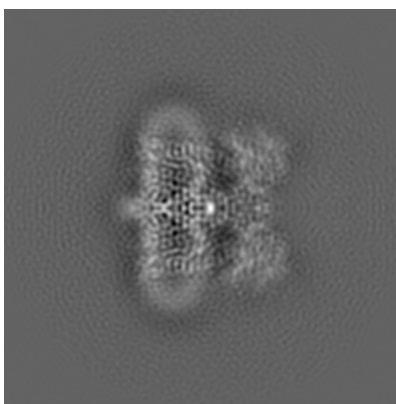
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

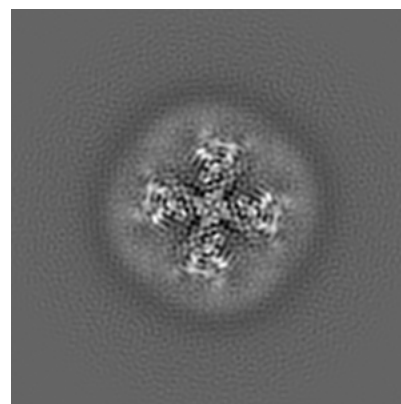
6.1.1 Primary map



X

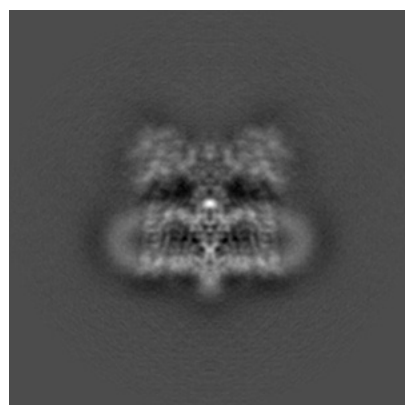


Y

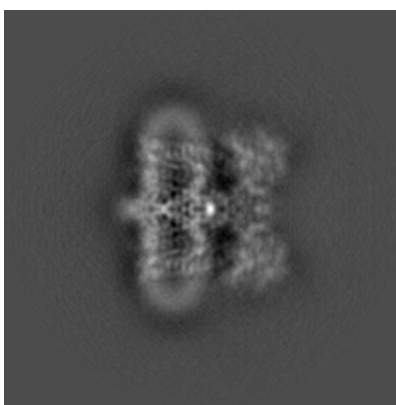


Z

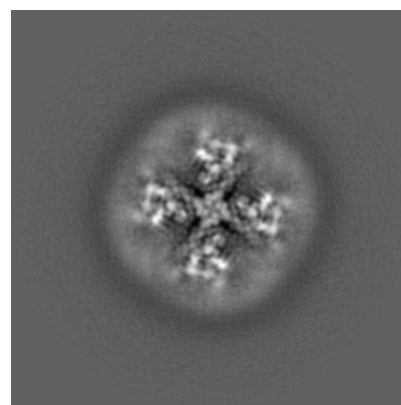
6.1.2 Raw map



X



Y

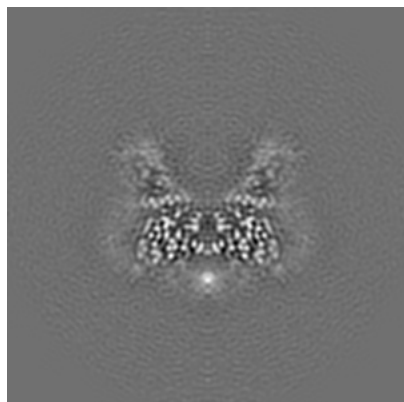


Z

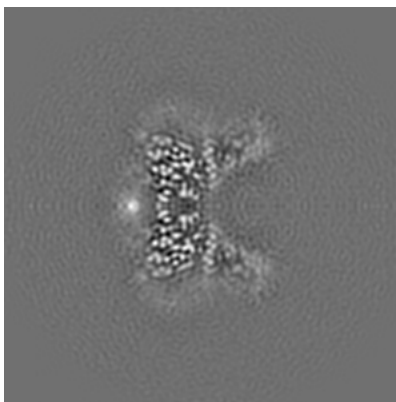
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

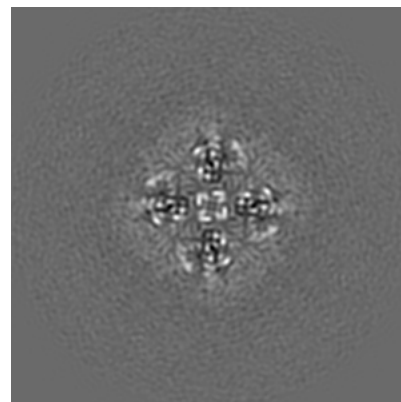
6.2.1 Primary map



X Index: 112

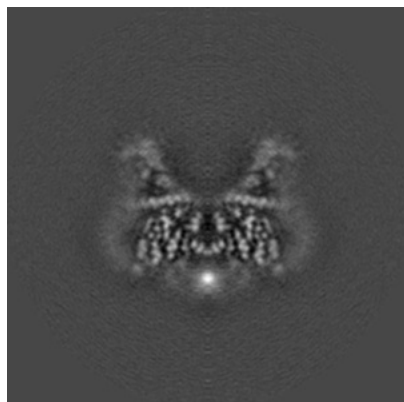


Y Index: 112

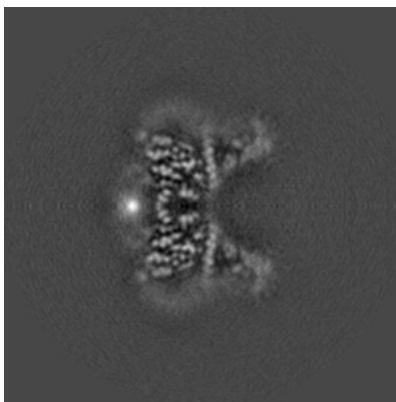


Z Index: 112

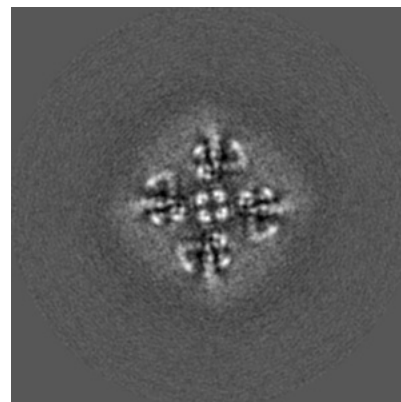
6.2.2 Raw map



X Index: 112



Y Index: 112

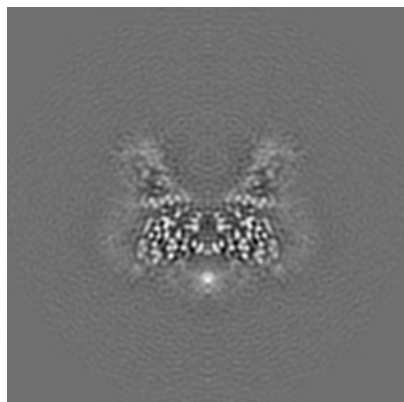


Z Index: 112

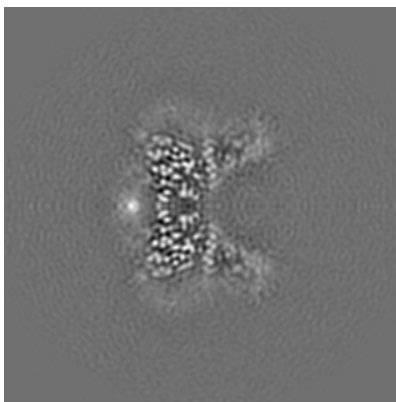
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

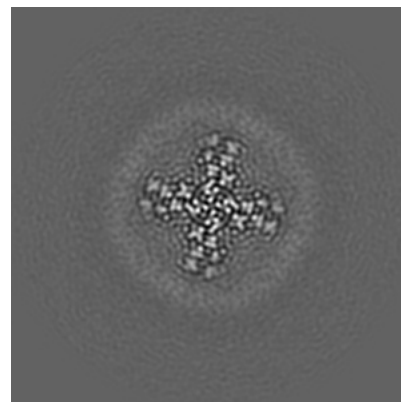
6.3.1 Primary map



X Index: 112

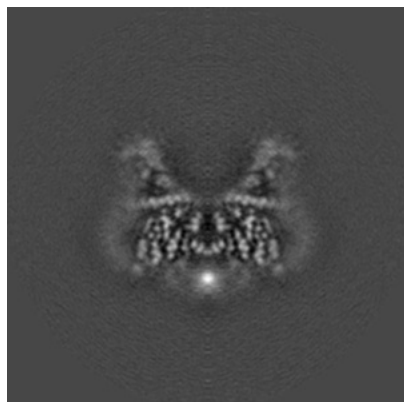


Y Index: 112

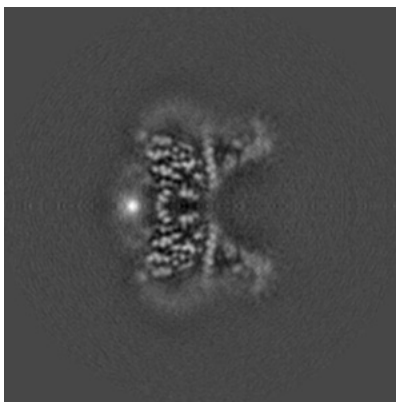


Z Index: 89

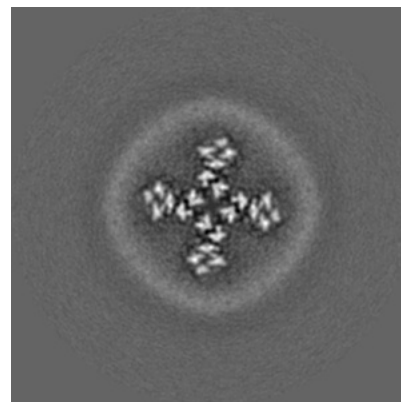
6.3.2 Raw map



X Index: 112



Y Index: 112

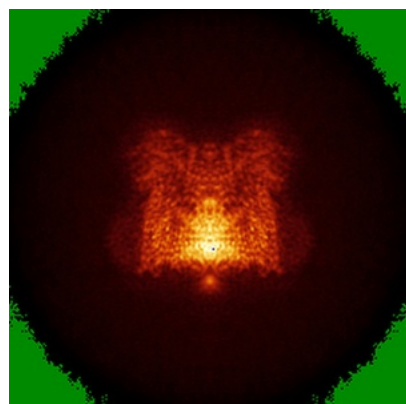


Z Index: 96

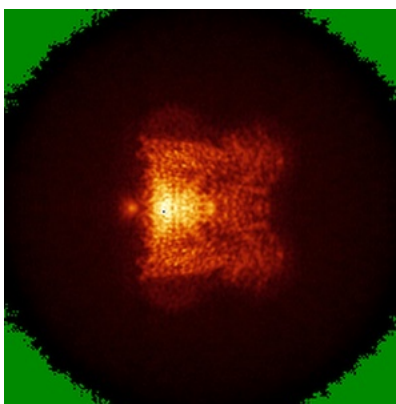
The images above show the largest variance slices of the map in three orthogonal directions.

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

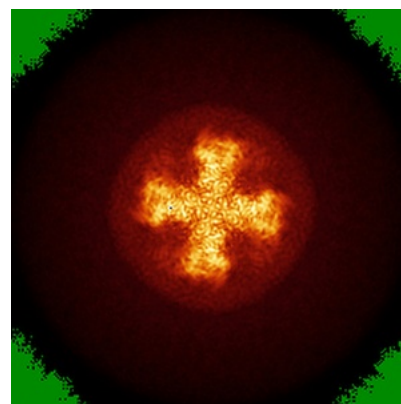
6.4.1 Primary map



X

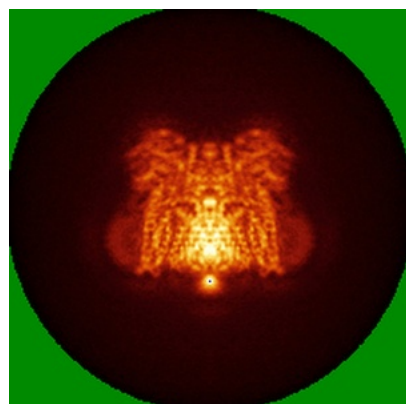


Y

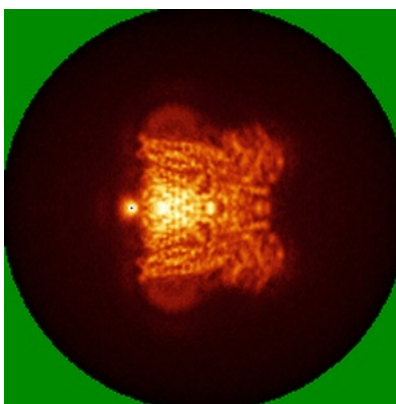


Z

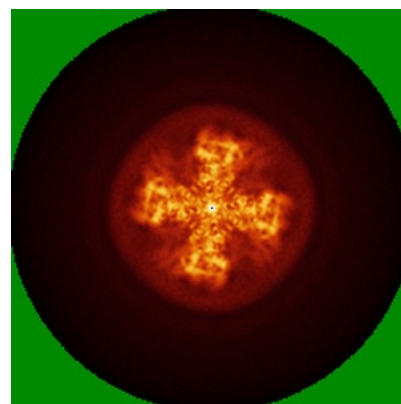
6.4.2 Raw map



X



Y

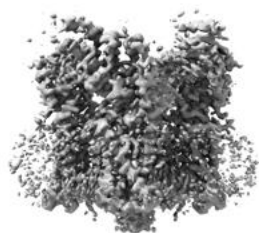


Z

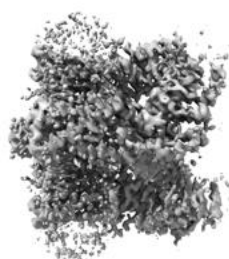
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

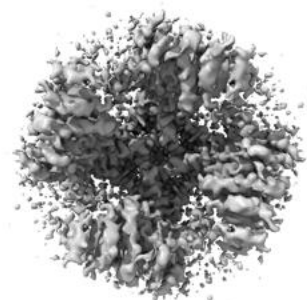
6.5.1 Primary map



X



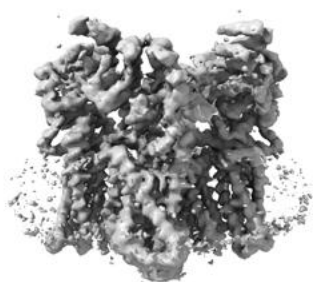
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.014. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

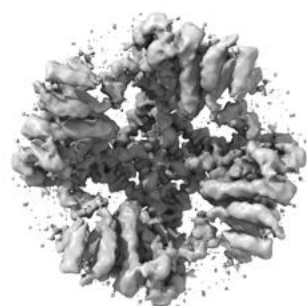
6.5.2 Raw map



X



Y



Z

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.

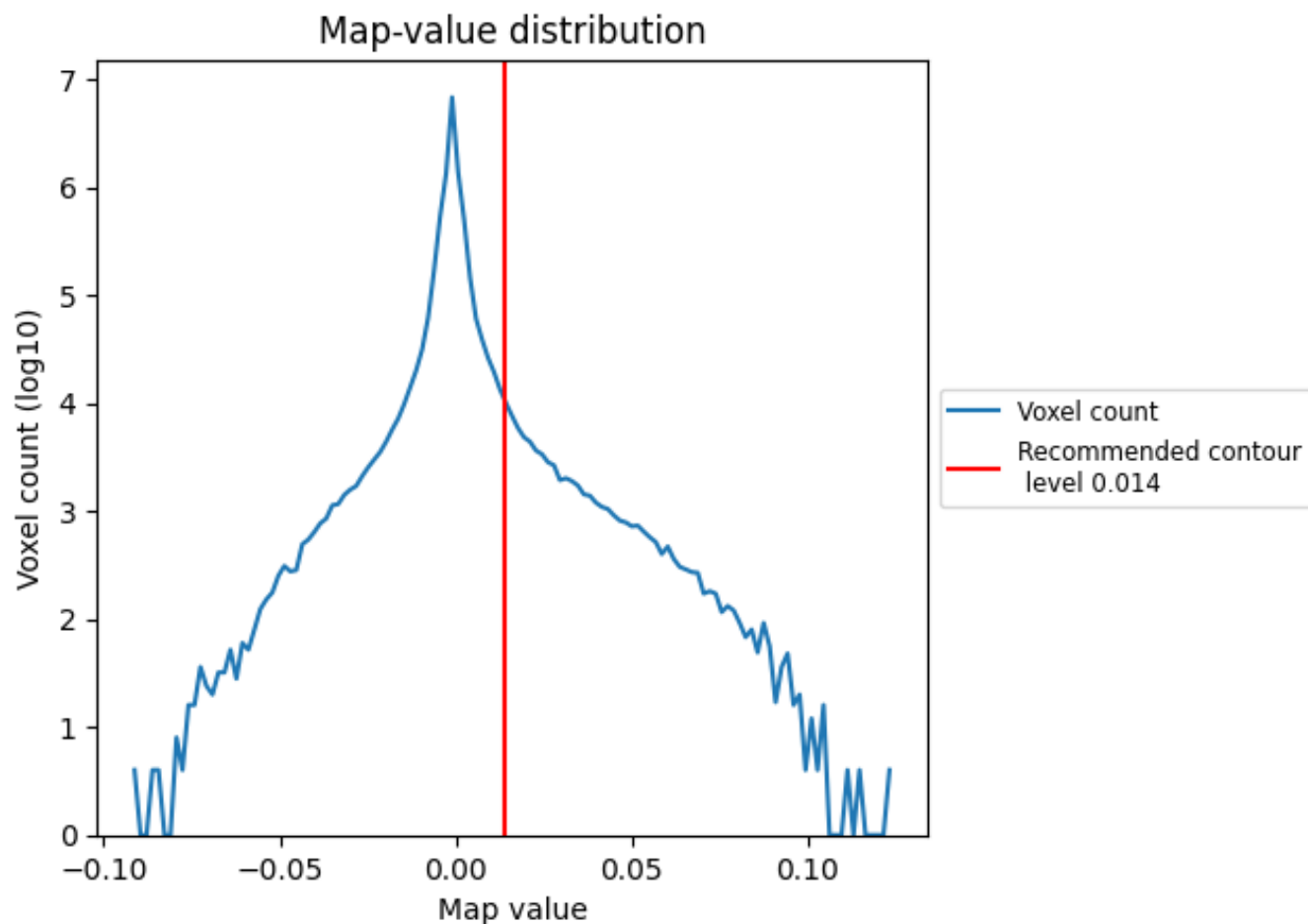
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

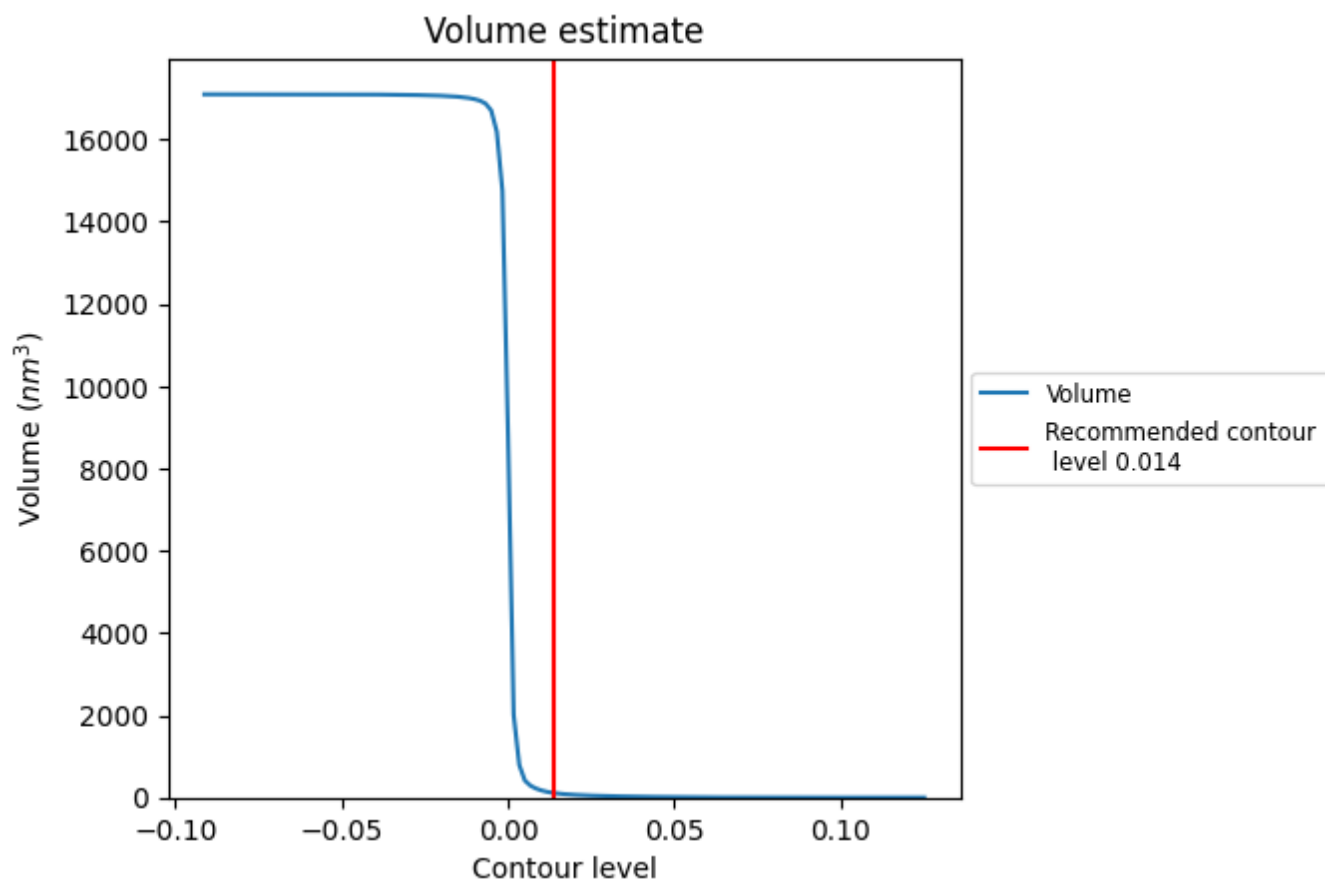
This section contains the results of statistical analysis of the map.

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.

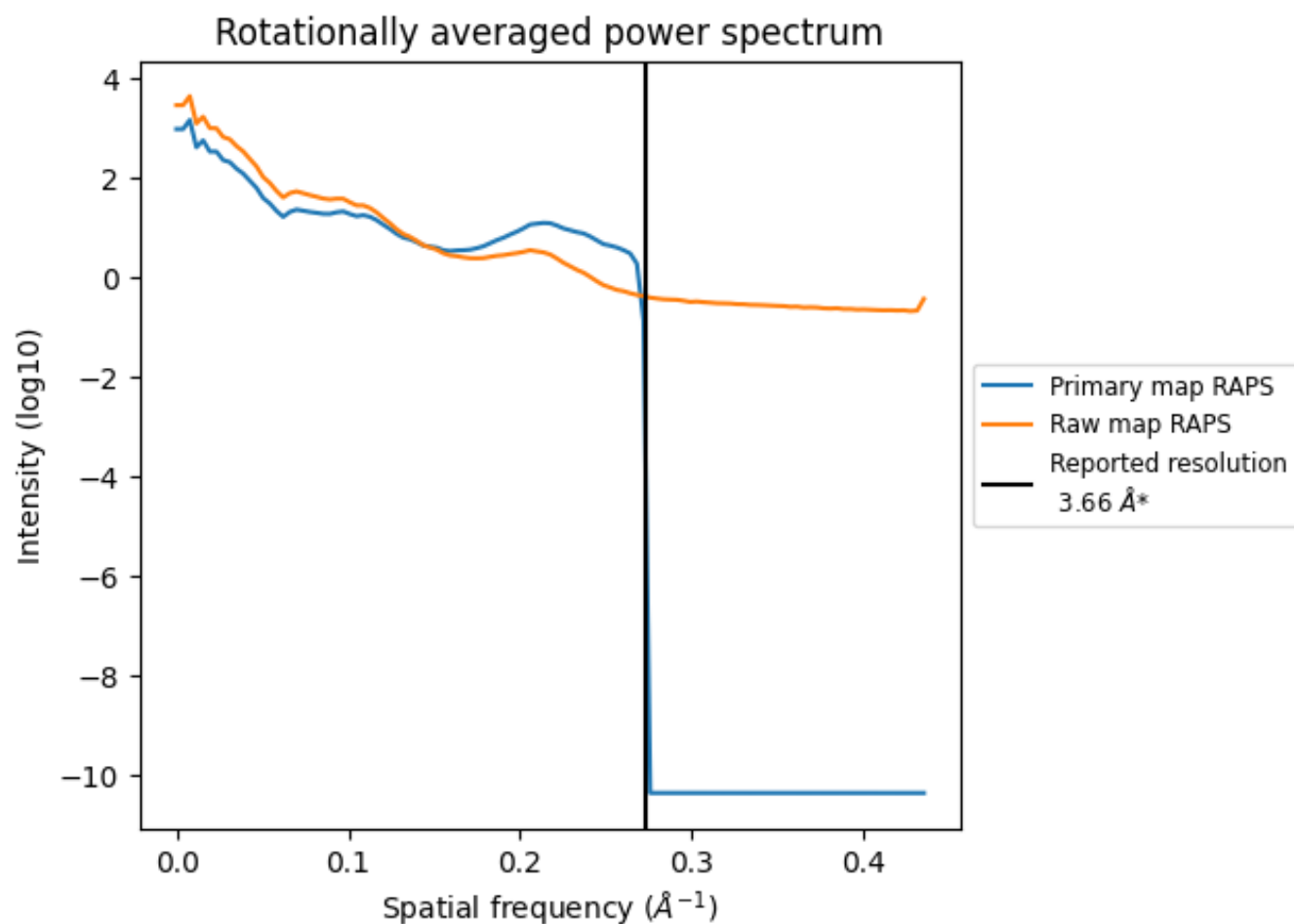
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 108 nm^3 ; this corresponds to an approximate mass of 98 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 ⓘ

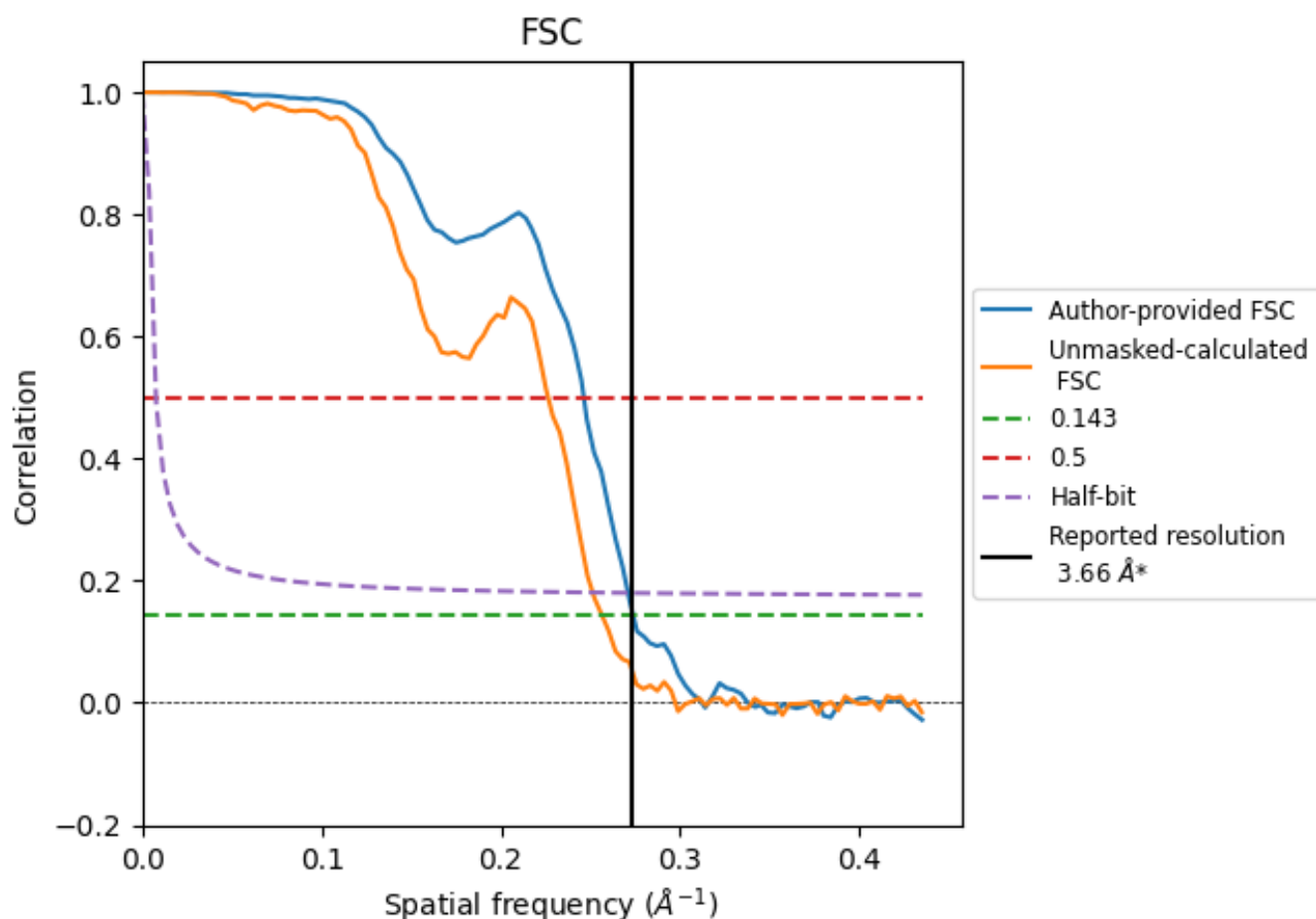


*Reported resolution corresponds to spatial frequency of 0.273 Å⁻¹

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 0.273 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

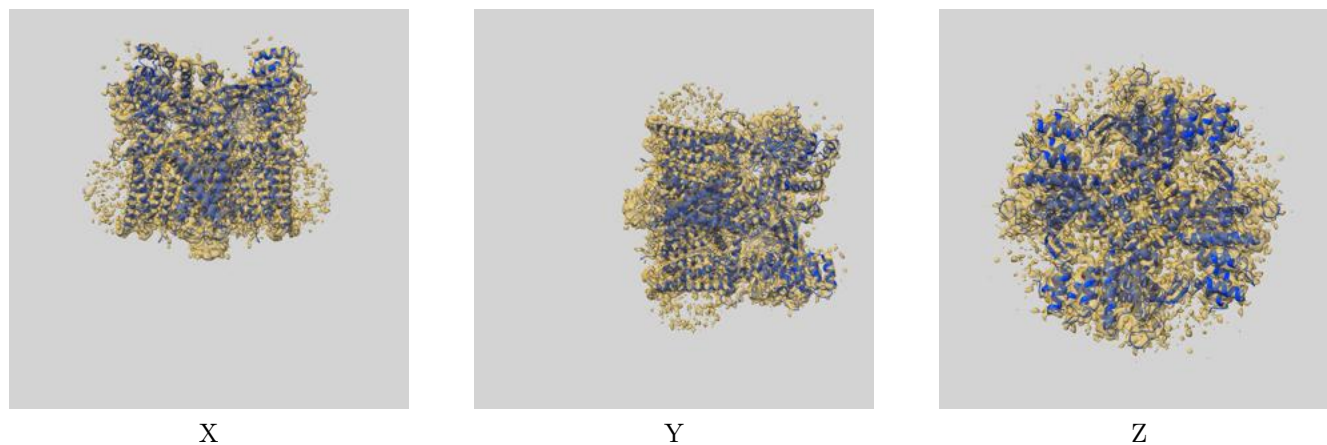
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.66	-	-
Author-provided FSC curve	3.65	4.06	3.69
Unmasked-calculated*	3.90	4.42	3.98

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

9 Map-model fit [i](#)

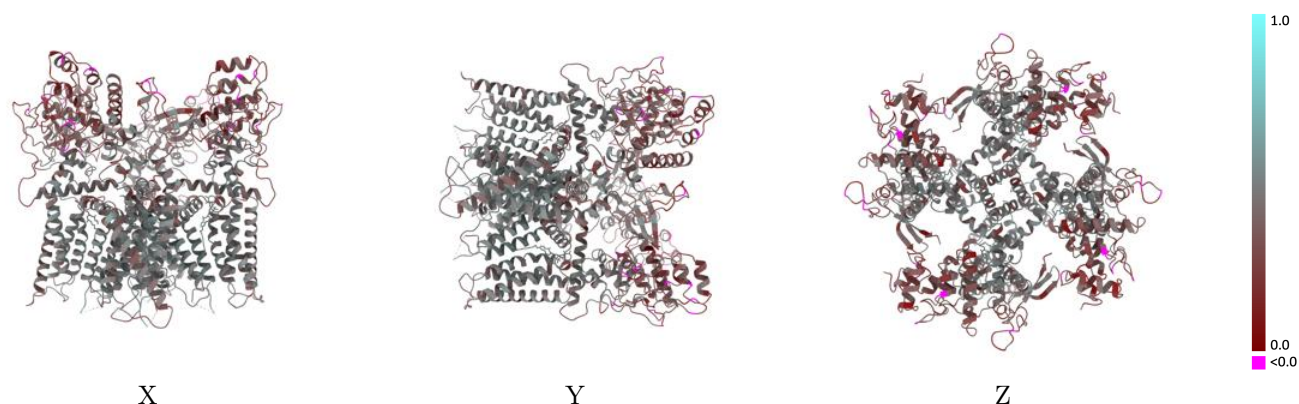
This section contains information regarding the fit between EMDB map EMD-23130 and PDB model 7L2J. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



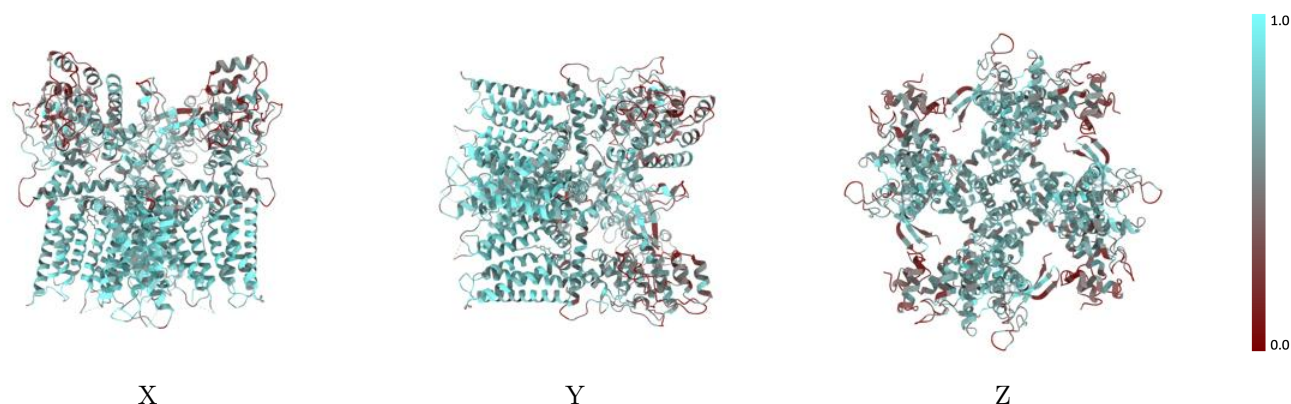
The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



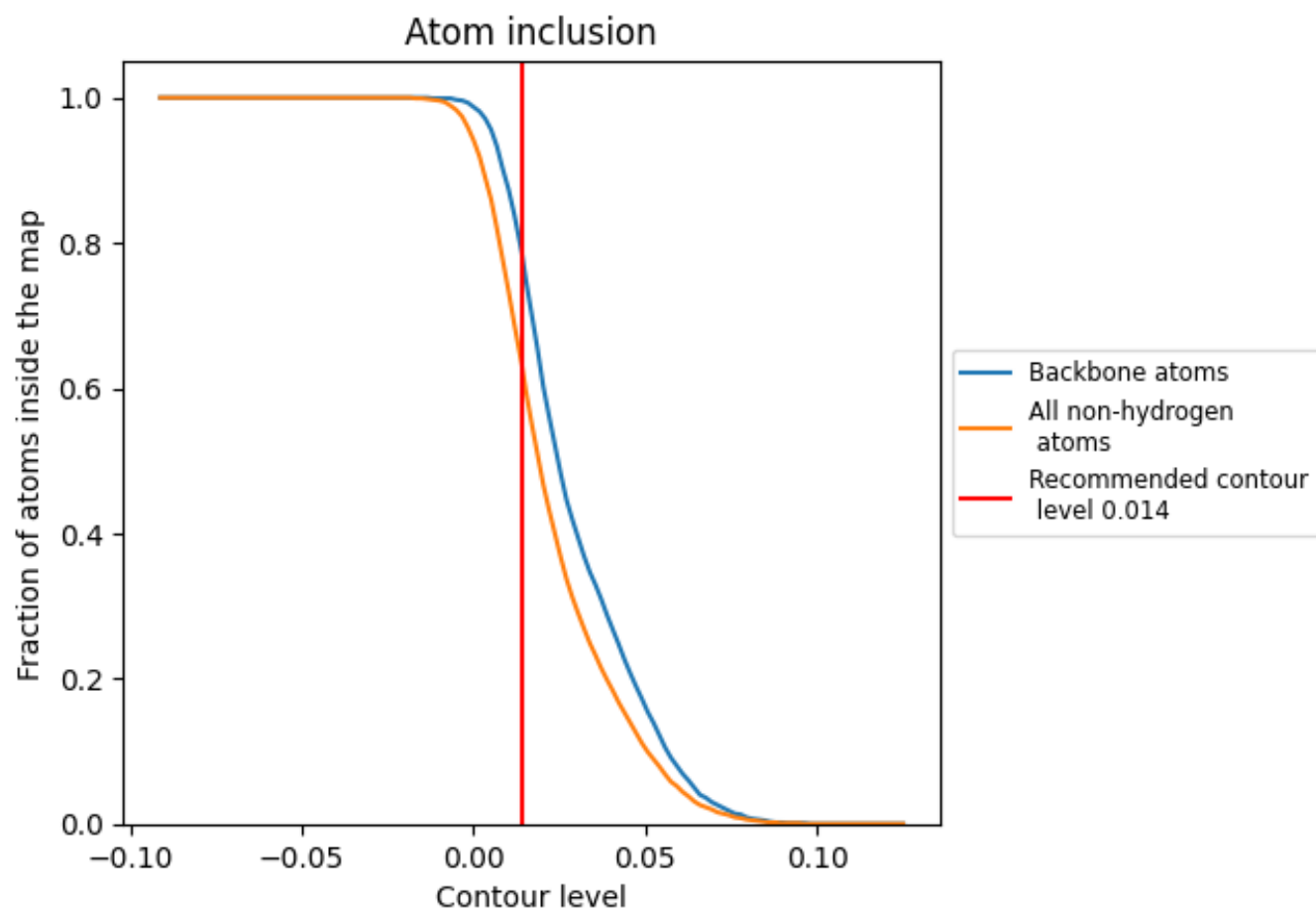
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 63% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6330	0.3950
A	0.6330	0.3960
B	0.6340	0.3970
C	0.6300	0.3940
D	0.6340	0.3940

