



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:03 PM UTC

PDB ID : 9L8W / pdb_00009l8w
EMDB ID : EMD-62892
Title : Human KCNQ2-CaM in complex with QO-58
Authors : Zhao, Y.W.; Yang, Z.N.; Du, X.N.; Guo, J.T.
Deposited on : 2024-12-28
Resolution : 2.90 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

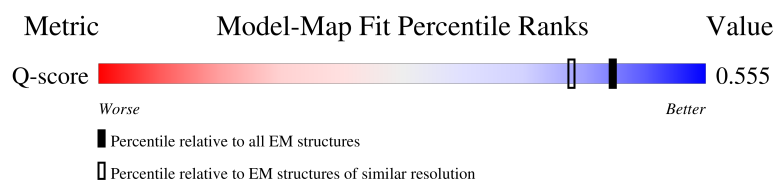
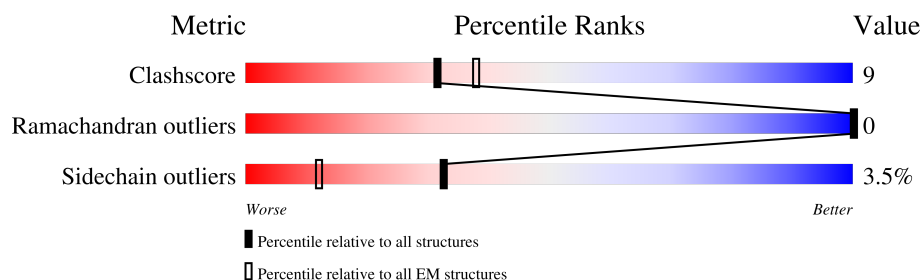
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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	13054 (2.40 - 3.40)

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	872	 22% 7% 70%
1	B	872	 24% 6% 70%
1	C	872	 23% 7% 70%
1	D	872	 23% 7% 70%

2 Entry composition [i](#)

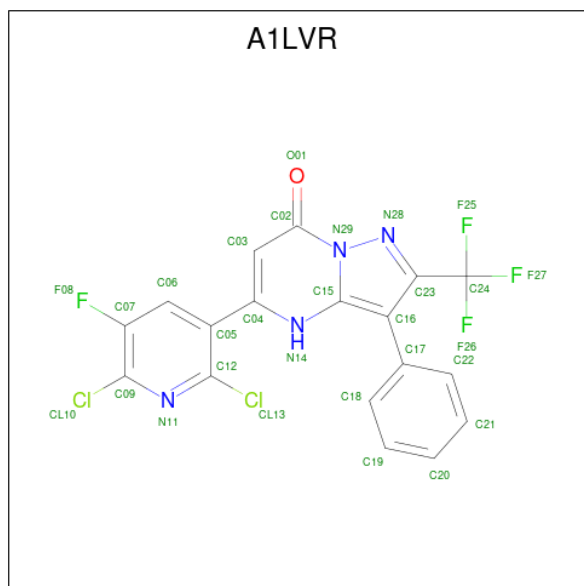
There are 2 unique types of molecules in this entry. The entry contains 8668 atoms, of which 64 are hydrogens and 0 are deuteriums.

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 Potassium voltage-gated channel subfamily KQT member 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	259	Total	C	N	O	S	0	0
			2093	1385	355	344	9		
1	B	259	Total	C	N	O	S	0	0
			2093	1385	355	344	9		
1	C	259	Total	C	N	O	S	0	0
			2093	1385	355	344	9		
1	D	259	Total	C	N	O	S	0	0
			2093	1385	355	344	9		

- Molecule 2 is QO-58 (CCD ID: A1LVR) (formula: $C_{18}H_8Cl_2F_4N_4O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							AltConf
2	A	1	Total	C	Cl	F	H	N	O	0
			37	18	2	4	8	4	1	
2	A	1	Total	C	Cl	F	H	N	O	0
			37	18	2	4	8	4	1	

Continued on next page...

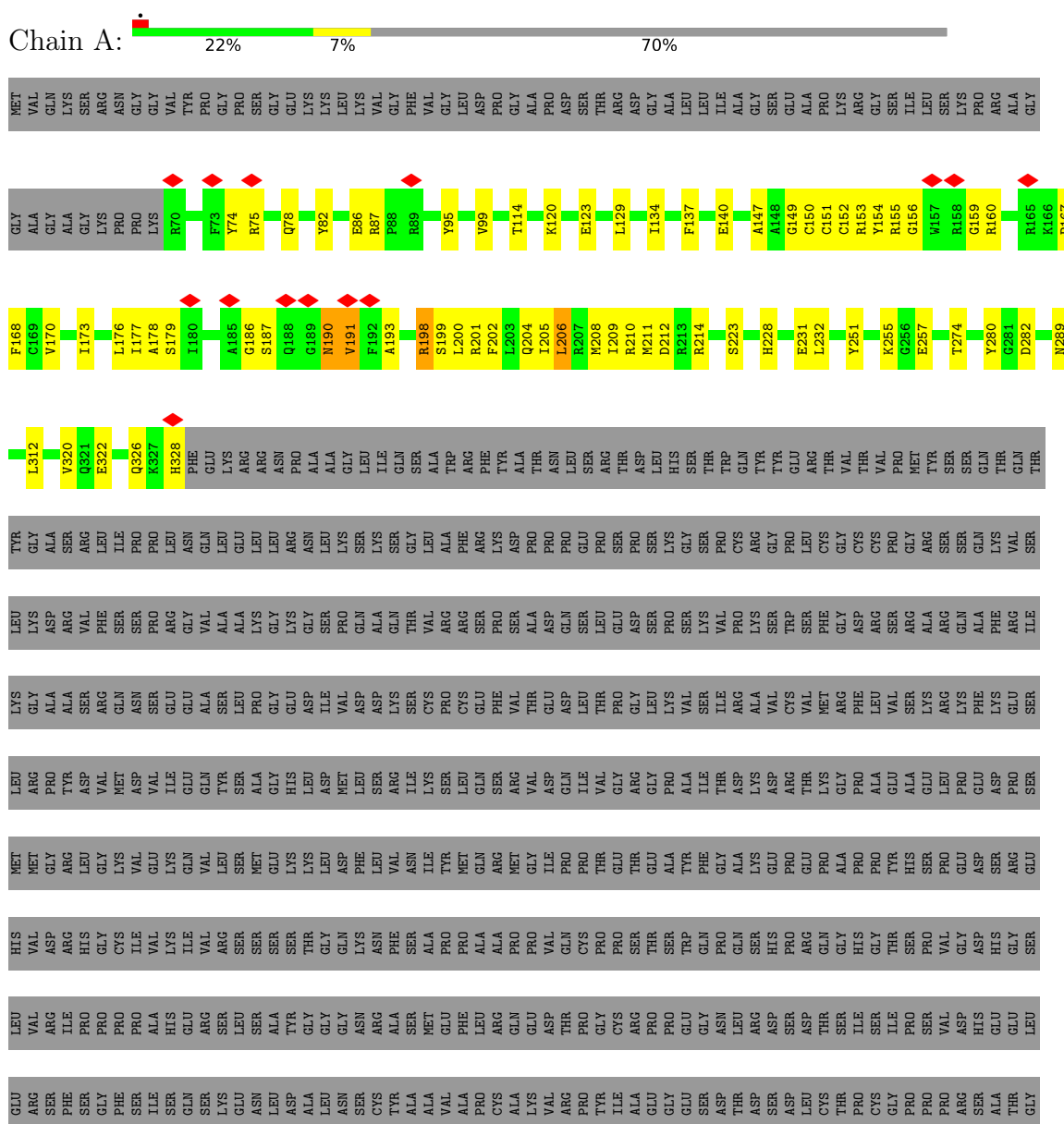
Continued from previous page...

Mol	Chain	Residues	Atoms							AltConf
2	A	1	Total	C	Cl	F	H	N	O	0
			37	18	2	4	8	4	1	
2	B	1	Total	C	Cl	F	H	N	O	0
			37	18	2	4	8	4	1	
2	B	1	Total	C	Cl	F	H	N	O	0
			37	18	2	4	8	4	1	
2	C	1	Total	C	Cl	F	H	N	O	0
			37	18	2	4	8	4	1	
2	D	1	Total	C	Cl	F	H	N	O	0
			37	18	2	4	8	4	1	
2	D	1	Total	C	Cl	F	H	N	O	0
			37	18	2	4	8	4	1	

3 Residue-property plots [i](#)

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: Potassium voltage-gated channel subfamily KQT member 2



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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	103232	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.066	Depositor
Minimum map value	-0.028	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0126	Depositor
Map size (Å)	223.2, 223.2, 223.2	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	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: A1LVR

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	0/2150	0.48	2/2913 (0.1%)
1	B	0.18	0/2150	0.35	0/2913
1	C	0.18	0/2150	0.35	0/2913
1	D	0.18	0/2150	0.35	0/2913
All	All	0.19	0/8600	0.39	2/11652 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	190	ASN	N-CA-C	-11.15	99.18	113.12
1	A	191	VAL	N-CA-C	8.14	122.31	110.09

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	2093	0	2127	49	0
1	B	2093	0	2127	32	0
1	C	2093	0	2127	37	0
1	D	2093	0	2127	36	0
2	A	87	24	0	7	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	58	16	0	3	0
2	C	29	8	0	0	0
2	D	58	16	0	1	0
All	All	8604	64	8508	148	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 9.

The worst 5 of 148 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:D:168:PHE:HE2	1:D:210:ARG:HA	1.54	0.73
1:B:168:PHE:HE2	1:B:210:ARG:HA	1.54	0.72
1:C:168:PHE:HE2	1:C:210:ARG:HA	1.55	0.72
1:A:120:LYS:HA	1:A:120:LYS:HE2	1.73	0.69
1:D:257:GLU:N	1:D:257:GLU:OE1	2.26	0.68

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	257/872 (30%)	255 (99%)	2 (1%)	0	100	100
1	B	257/872 (30%)	254 (99%)	3 (1%)	0	100	100
1	C	257/872 (30%)	253 (98%)	4 (2%)	0	100	100
1	D	257/872 (30%)	254 (99%)	3 (1%)	0	100	100
All	All	1028/3488 (30%)	1016 (99%)	12 (1%)	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	214/728 (29%)	207 (97%)	7 (3%)	33	67
1	B	214/728 (29%)	207 (97%)	7 (3%)	33	67
1	C	214/728 (29%)	206 (96%)	8 (4%)	30	64
1	D	214/728 (29%)	206 (96%)	8 (4%)	30	64
All	All	856/2912 (29%)	826 (96%)	30 (4%)	32	66

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	99	VAL
1	D	206	LEU
1	C	190	ASN
1	D	328	HIS
1	D	152	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	204	GLN
1	D	71	ASN
1	C	71	ASN
1	B	204	GLN
1	C	204	GLN

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](#)

8 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	A1LVR	A	903	-	31,32,32	2.62	10 (32%)	42,49,49	2.38	15 (35%)
2	A1LVR	A	902	-	31,32,32	2.34	10 (32%)	42,49,49	2.75	21 (50%)
2	A1LVR	D	902	-	31,32,32	2.34	10 (32%)	42,49,49	2.75	21 (50%)
2	A1LVR	B	902	-	31,32,32	2.62	10 (32%)	42,49,49	2.38	15 (35%)
2	A1LVR	D	901	-	31,32,32	2.62	10 (32%)	42,49,49	2.38	15 (35%)
2	A1LVR	A	901	-	31,32,32	2.62	10 (32%)	42,49,49	2.38	15 (35%)
2	A1LVR	C	901	-	31,32,32	2.34	10 (32%)	42,49,49	2.75	21 (50%)
2	A1LVR	B	901	-	31,32,32	2.34	10 (32%)	42,49,49	2.75	21 (50%)

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	A1LVR	A	903	-	-	2/13/14/14	0/4/4/4
2	A1LVR	A	902	-	-	1/13/14/14	0/4/4/4
2	A1LVR	D	902	-	-	1/13/14/14	0/4/4/4
2	A1LVR	B	902	-	-	2/13/14/14	0/4/4/4
2	A1LVR	D	901	-	-	2/13/14/14	0/4/4/4
2	A1LVR	A	901	-	-	2/13/14/14	0/4/4/4
2	A1LVR	C	901	-	-	1/13/14/14	0/4/4/4
2	A1LVR	B	901	-	-	1/13/14/14	0/4/4/4

The worst 5 of 80 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	901	A1LVR	C03-C04	8.16	1.47	1.37
2	A	903	A1LVR	C03-C04	8.16	1.47	1.37
2	B	902	A1LVR	C03-C04	8.16	1.47	1.37
2	D	901	A1LVR	C03-C04	8.16	1.47	1.37
2	A	901	A1LVR	C15-N14	8.00	1.51	1.37

The worst 5 of 144 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	902	A1LVR	C24-C23-N28	7.46	127.33	118.50
2	B	901	A1LVR	C24-C23-N28	7.46	127.33	118.50
2	C	901	A1LVR	C24-C23-N28	7.46	127.33	118.50
2	D	902	A1LVR	C24-C23-N28	7.46	127.33	118.50
2	A	901	A1LVR	C24-C23-N28	6.26	125.92	118.50

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	A1LVR	C03-C04-C05-C06
2	A	901	A1LVR	C03-C04-C05-C12
2	A	903	A1LVR	C03-C04-C05-C06
2	A	903	A1LVR	C03-C04-C05-C12
2	B	902	A1LVR	C03-C04-C05-C06

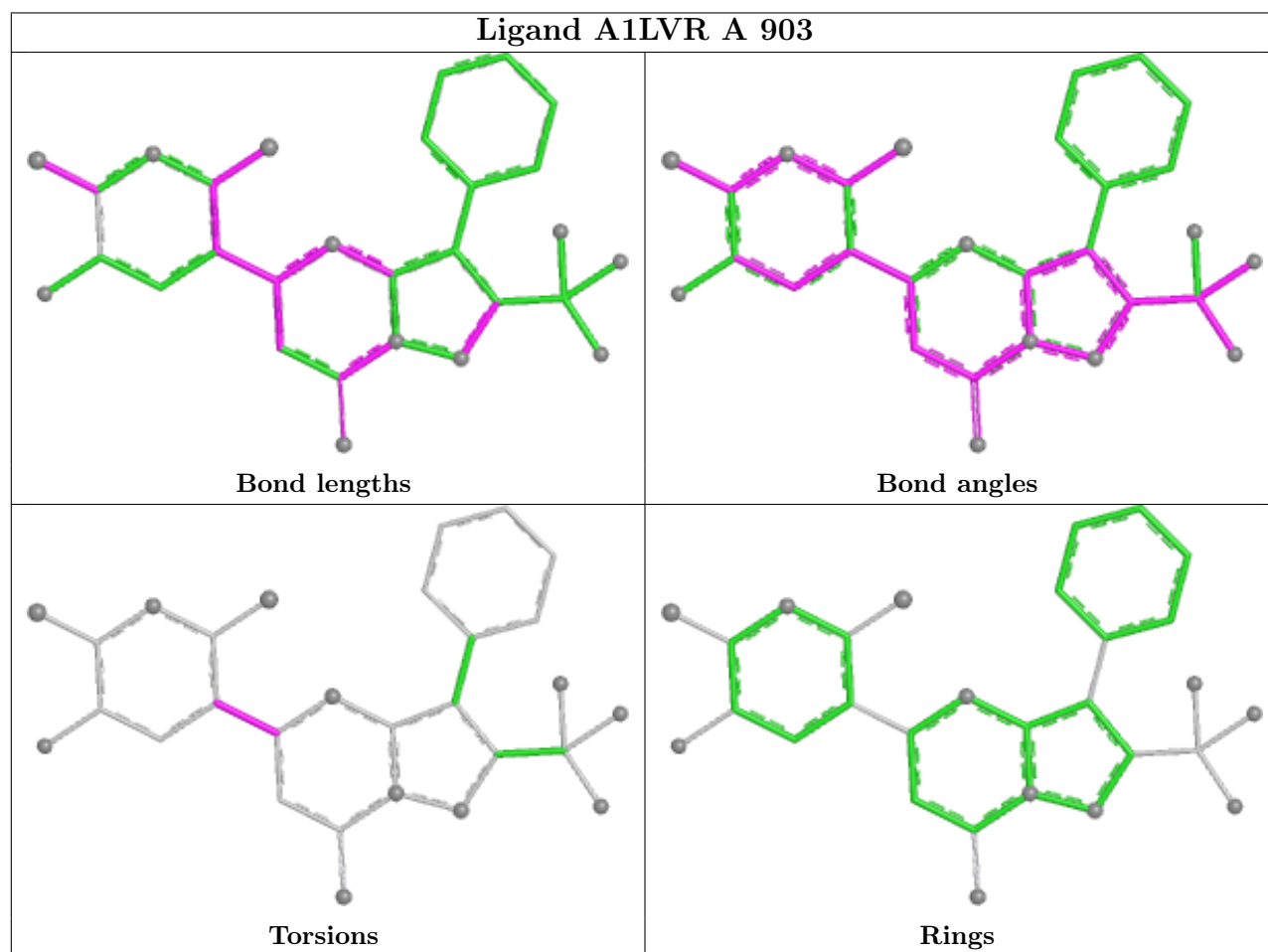
There are no ring outliers.

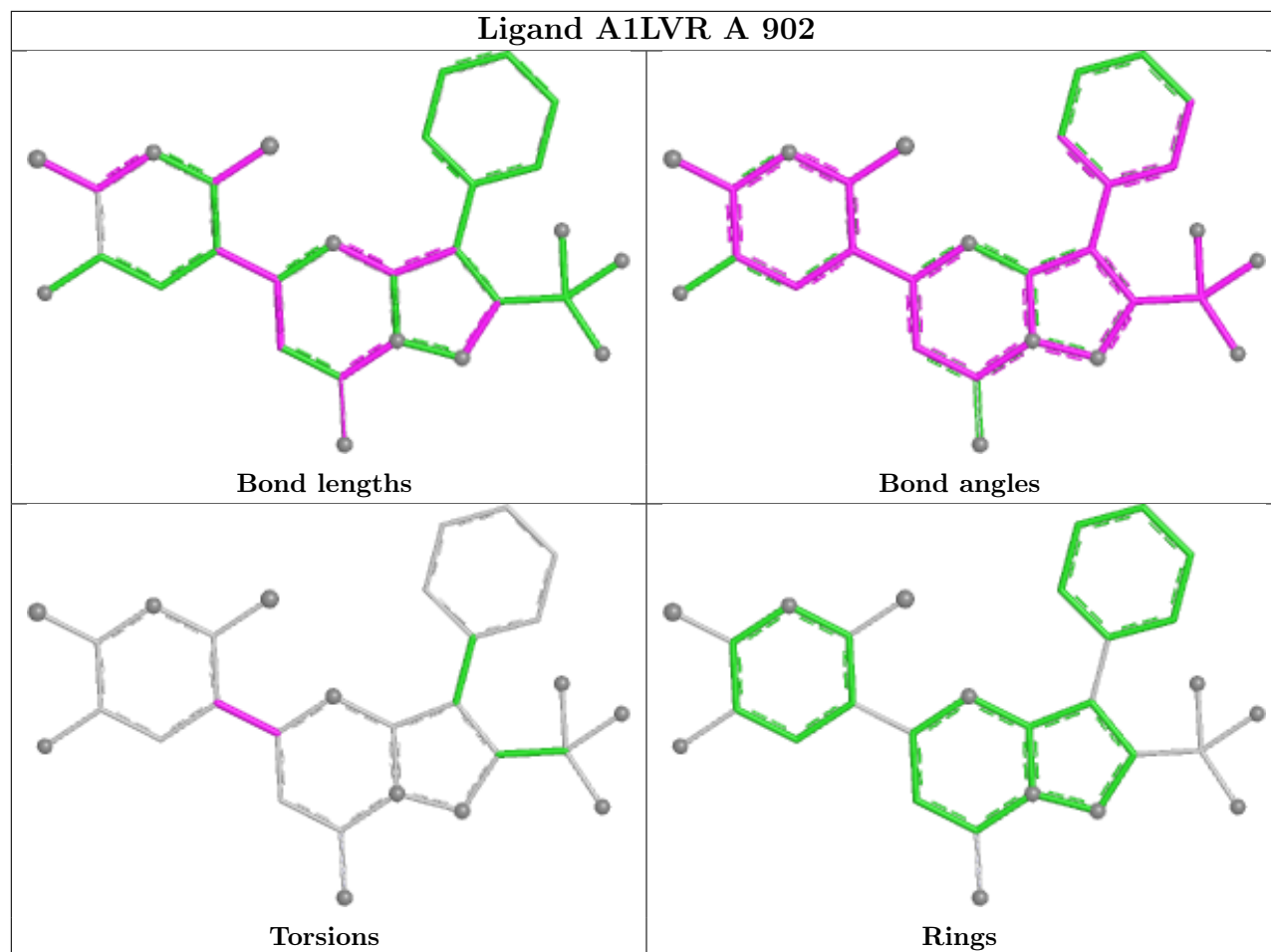
5 monomers are involved in 11 short contacts:

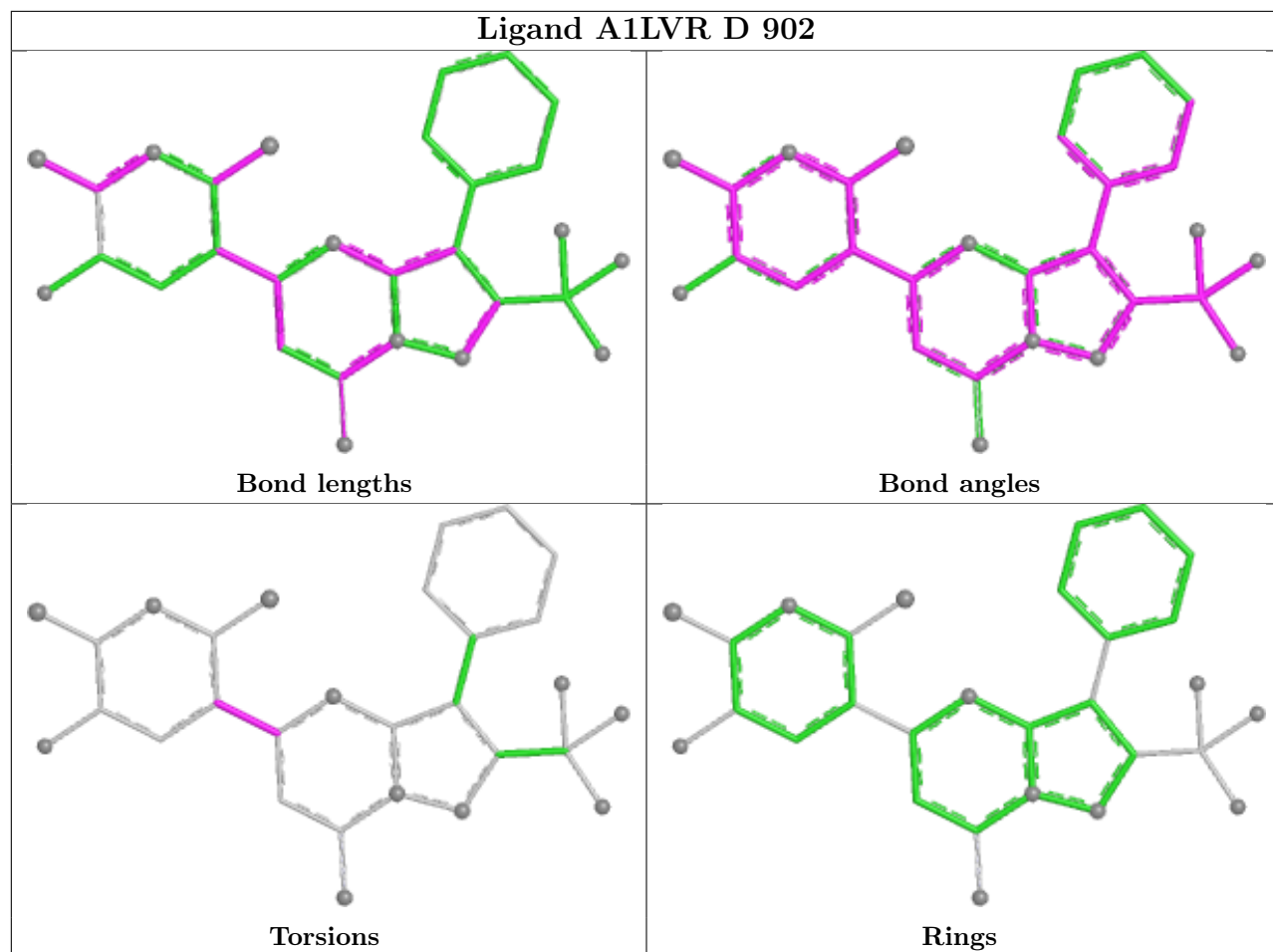
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	903	A1LVR	1	0
2	A	902	A1LVR	3	0
2	B	902	A1LVR	3	0
2	D	901	A1LVR	1	0
2	A	901	A1LVR	3	0

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

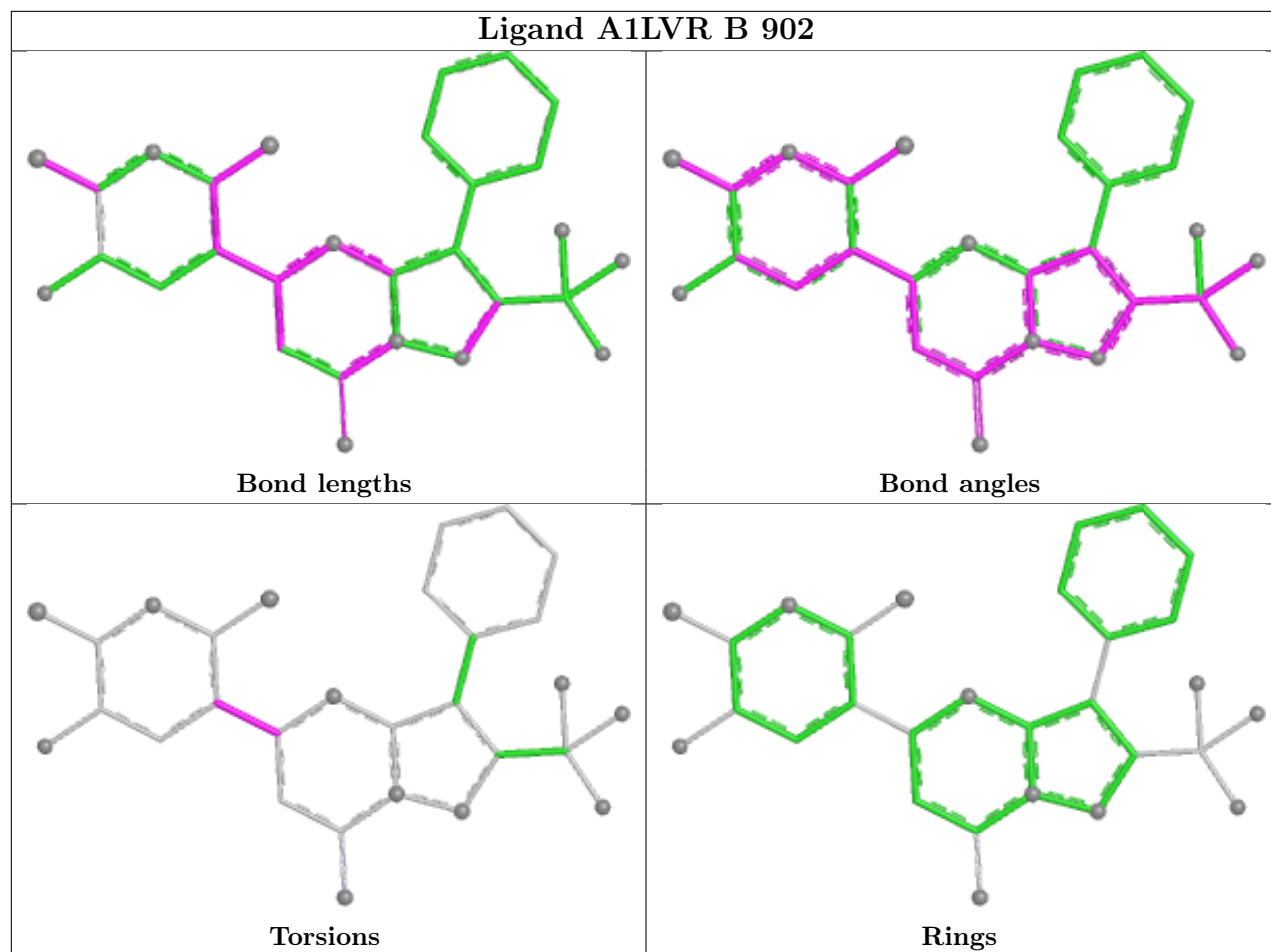
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

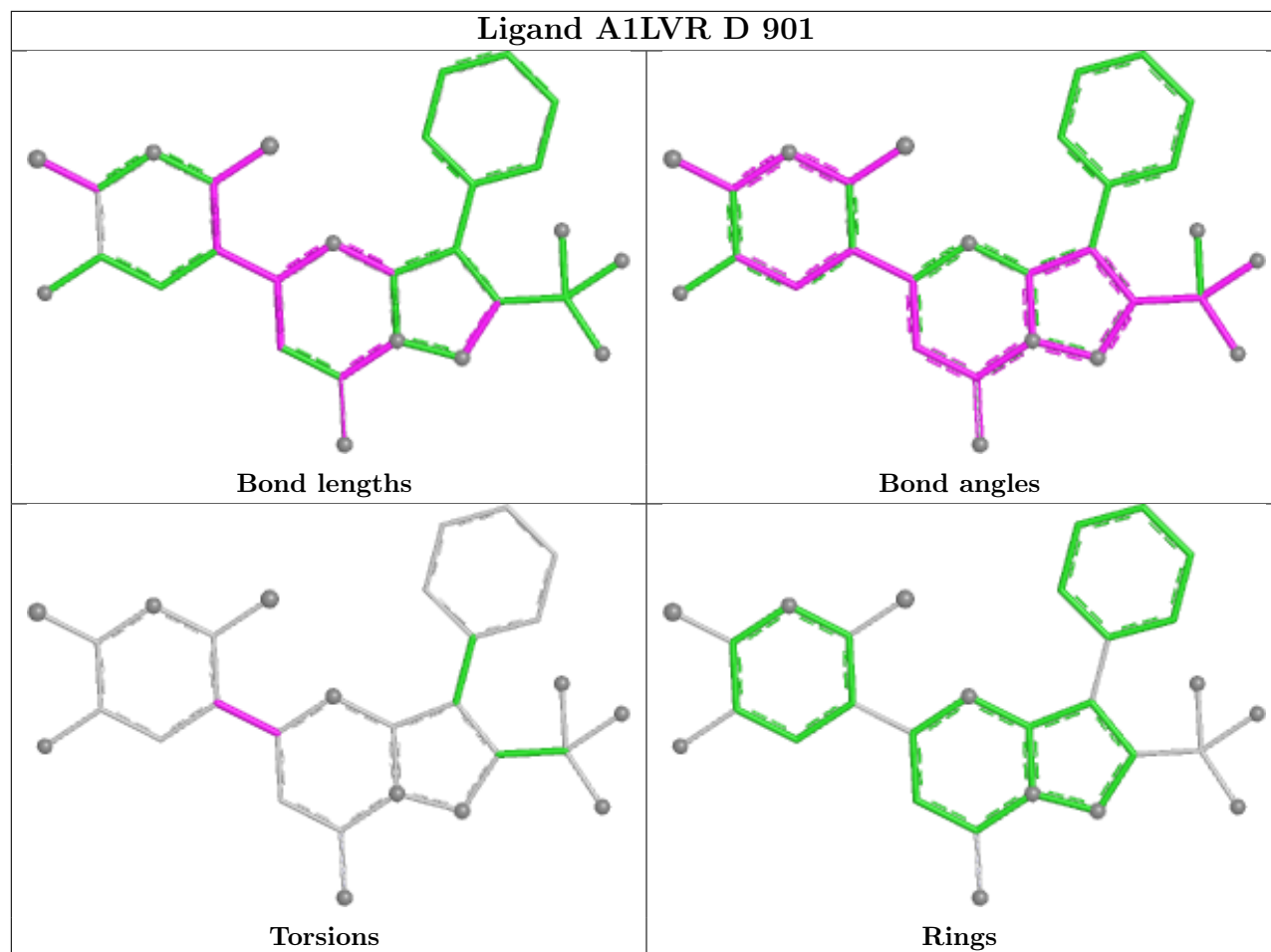




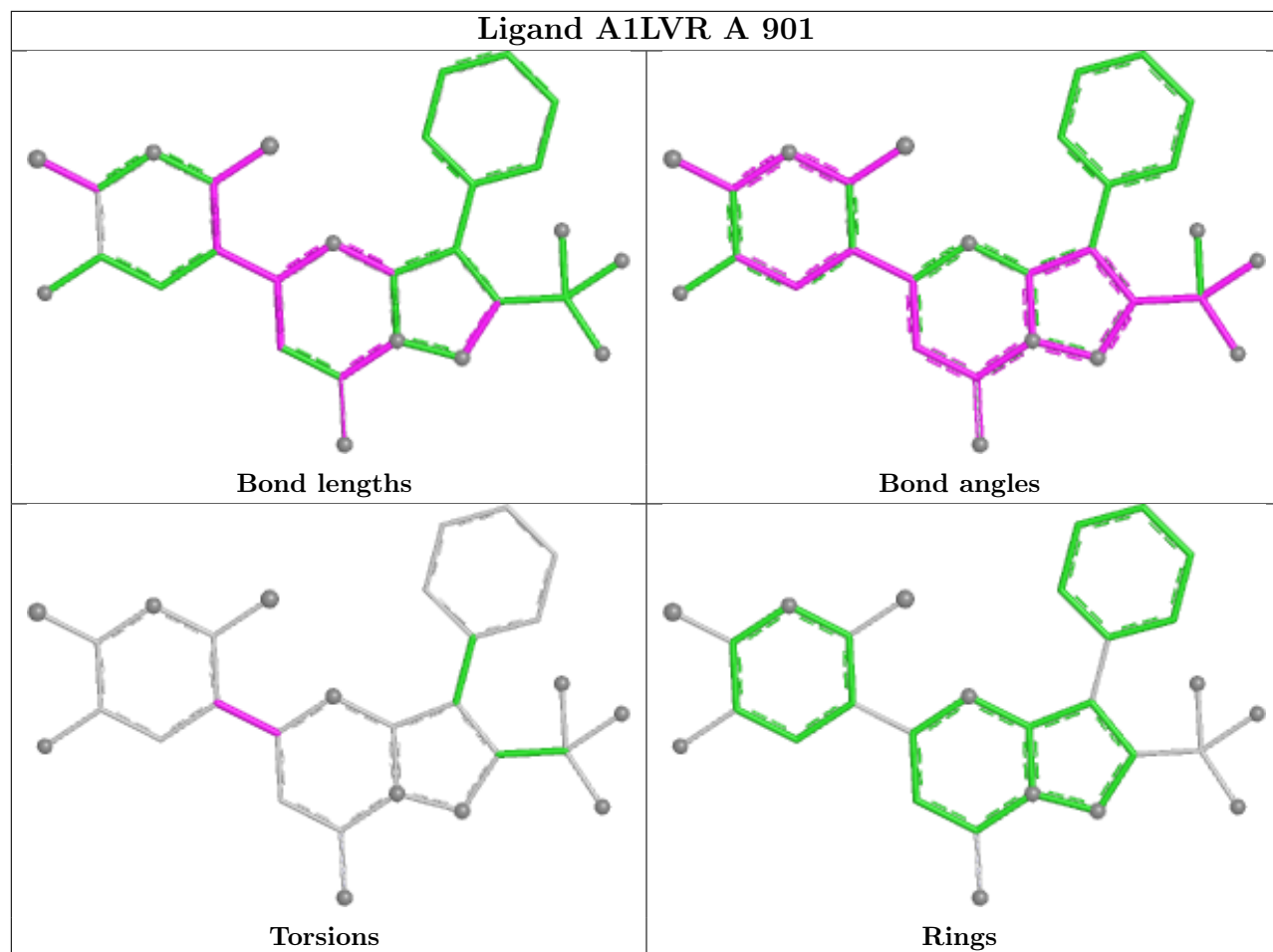


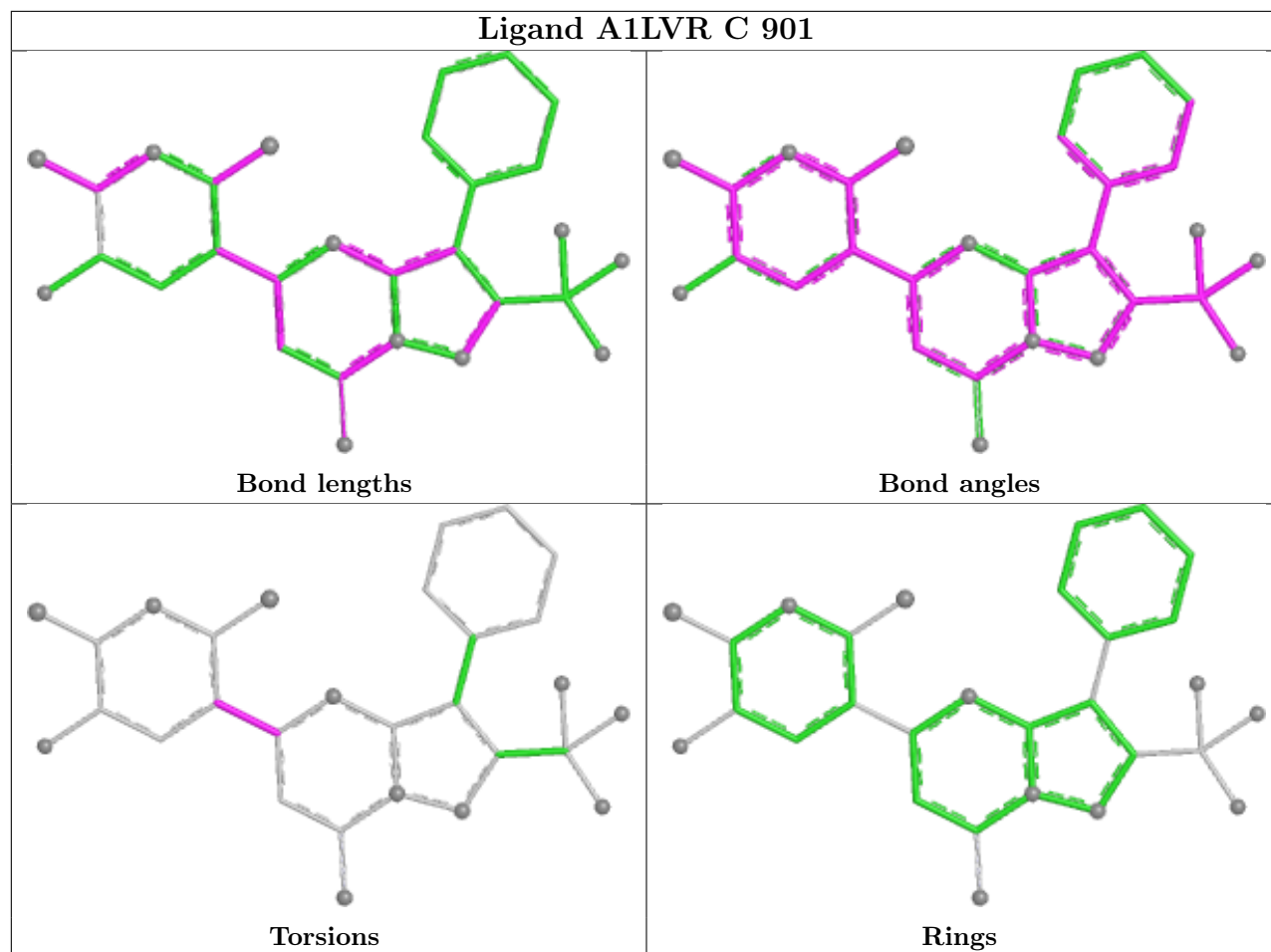
Ligand A1LVR B 902

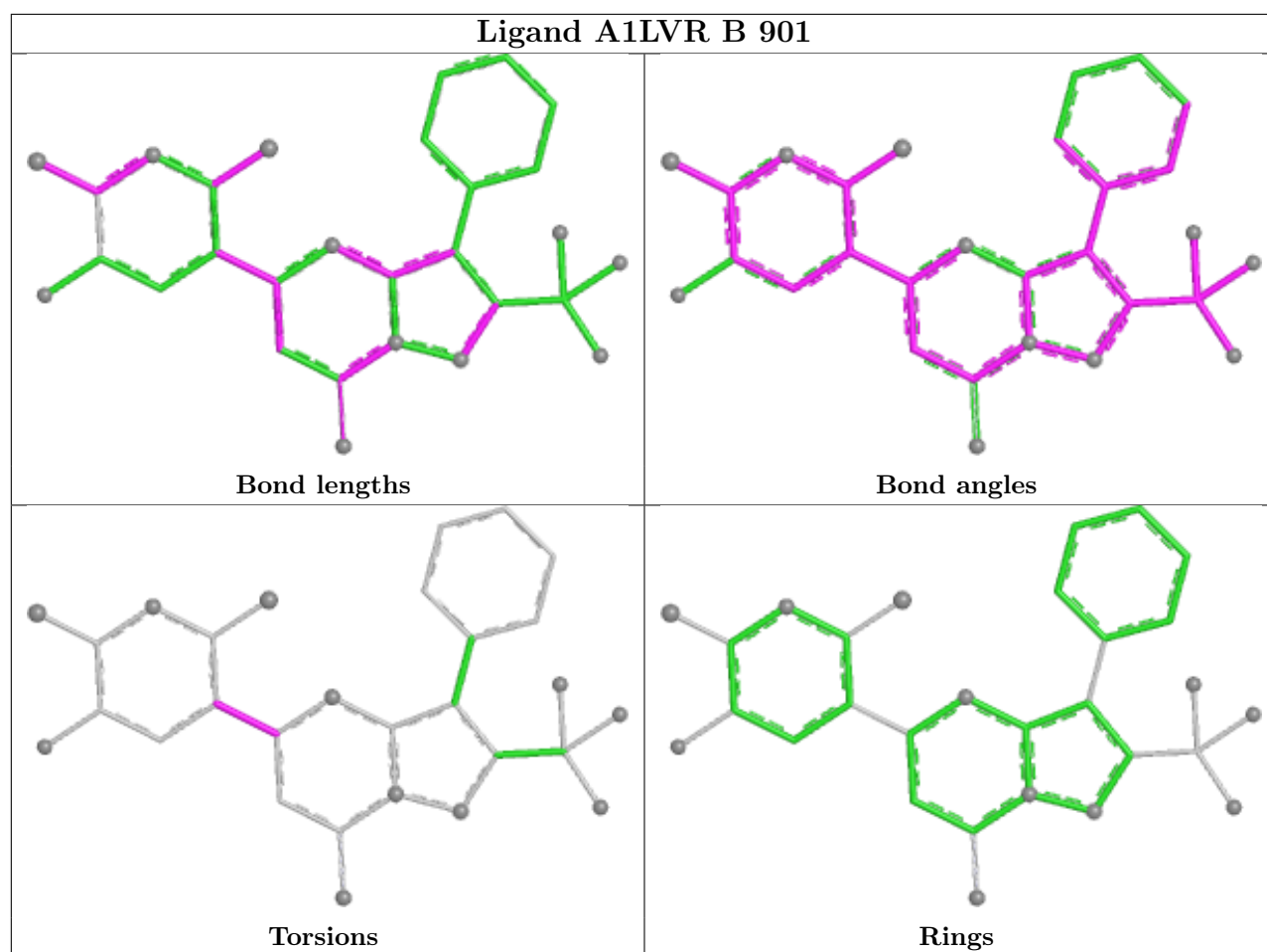




Ligand A1LVR A 901







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.

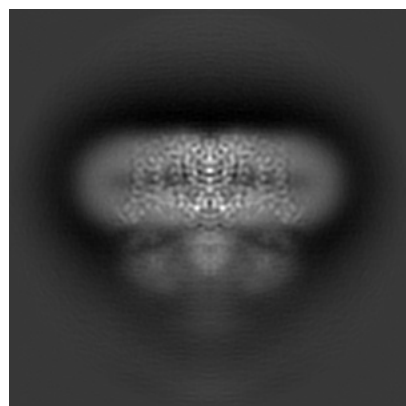
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62892. These allow visual inspection of the internal detail of the map and identification of artifacts.

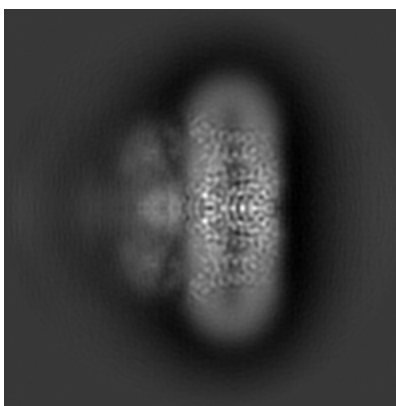
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

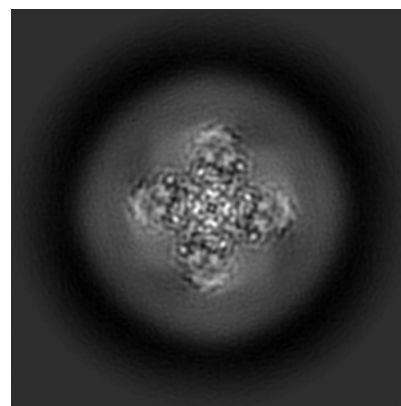
6.1.1 Primary map



X

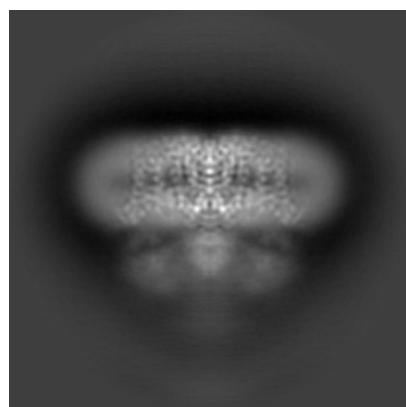


Y

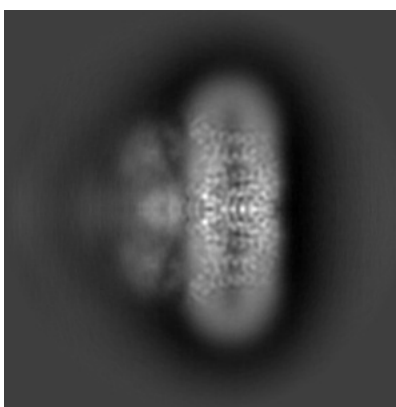


Z

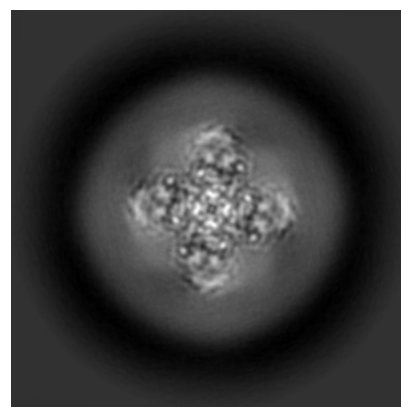
6.1.2 Raw map



X



Y

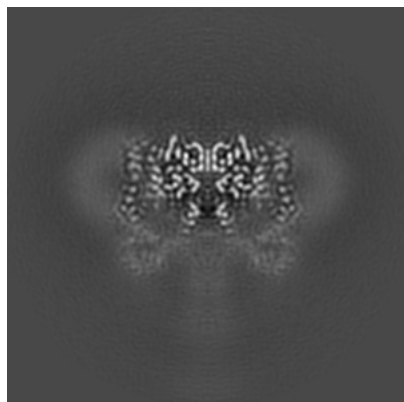


Z

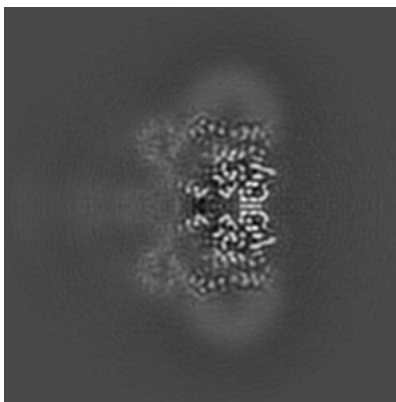
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

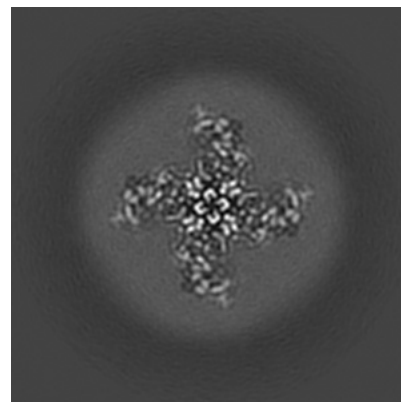
6.2.1 Primary map



X Index: 120

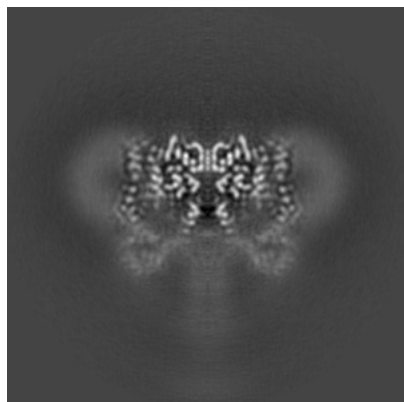


Y Index: 120

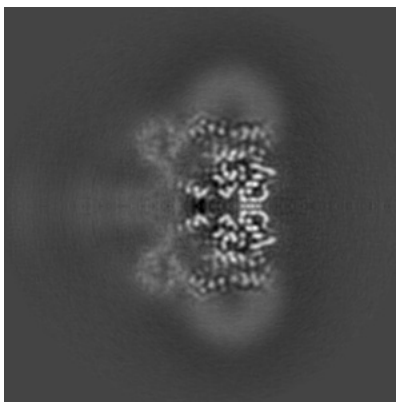


Z Index: 120

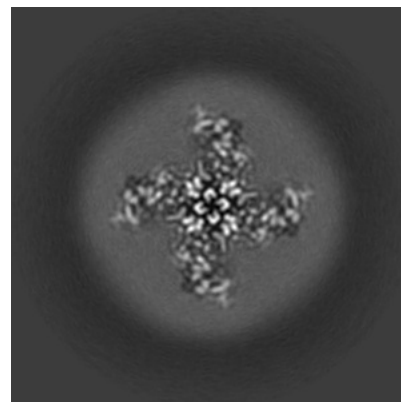
6.2.2 Raw map



X Index: 120



Y Index: 120

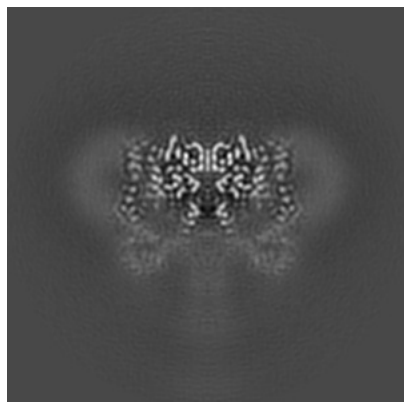


Z Index: 120

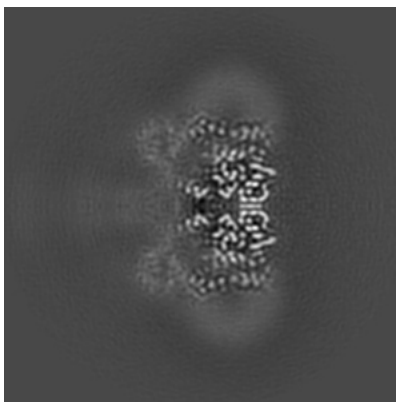
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

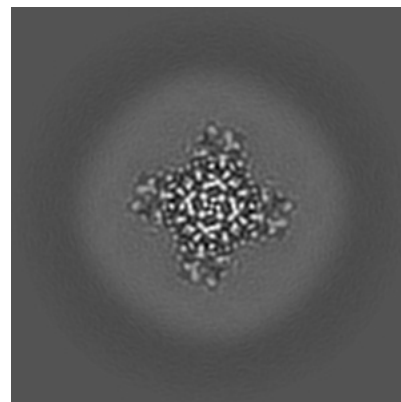
6.3.1 Primary map



X Index: 120

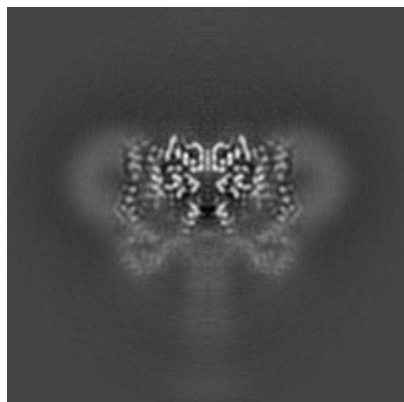


Y Index: 120

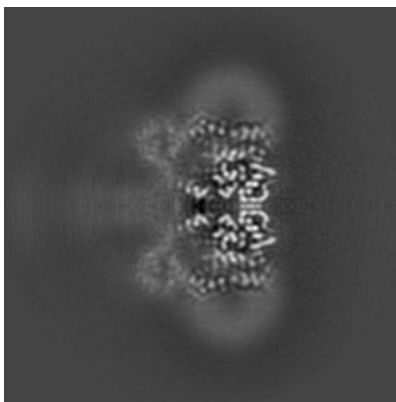


Z Index: 151

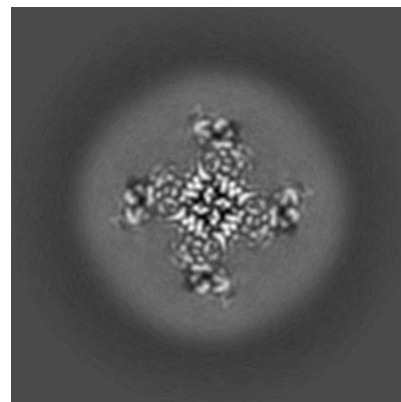
6.3.2 Raw map



X Index: 120



Y Index: 120

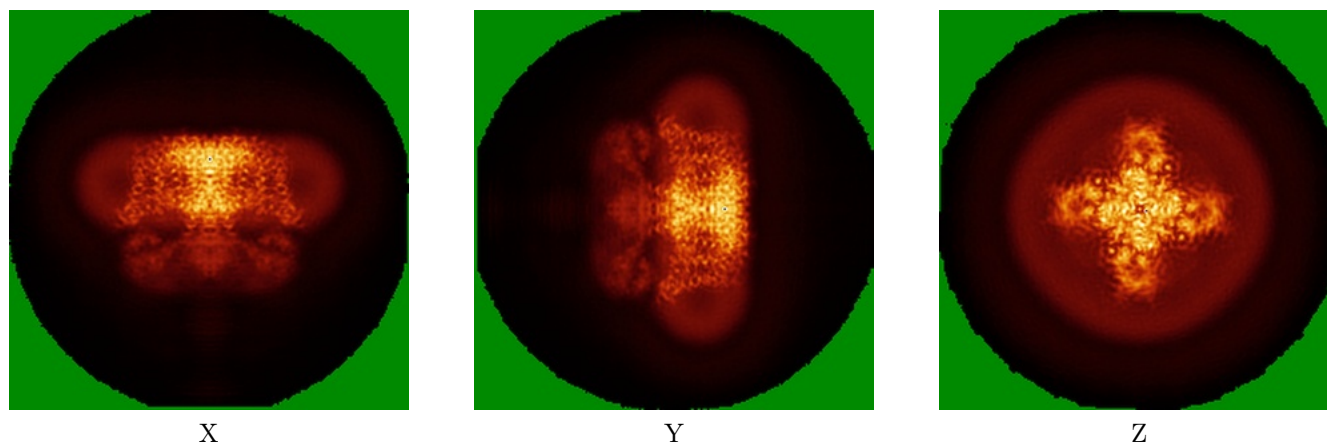


Z Index: 121

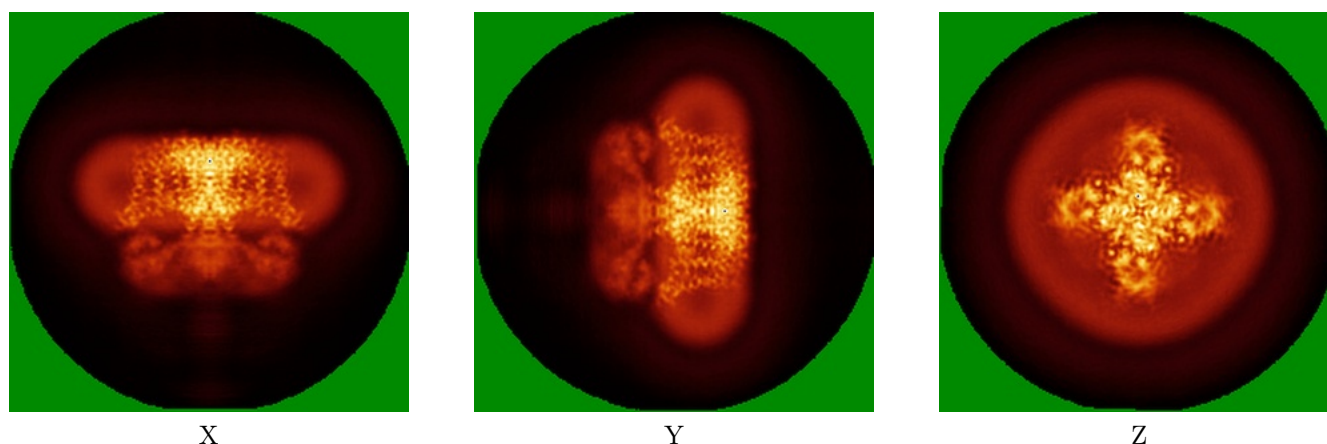
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

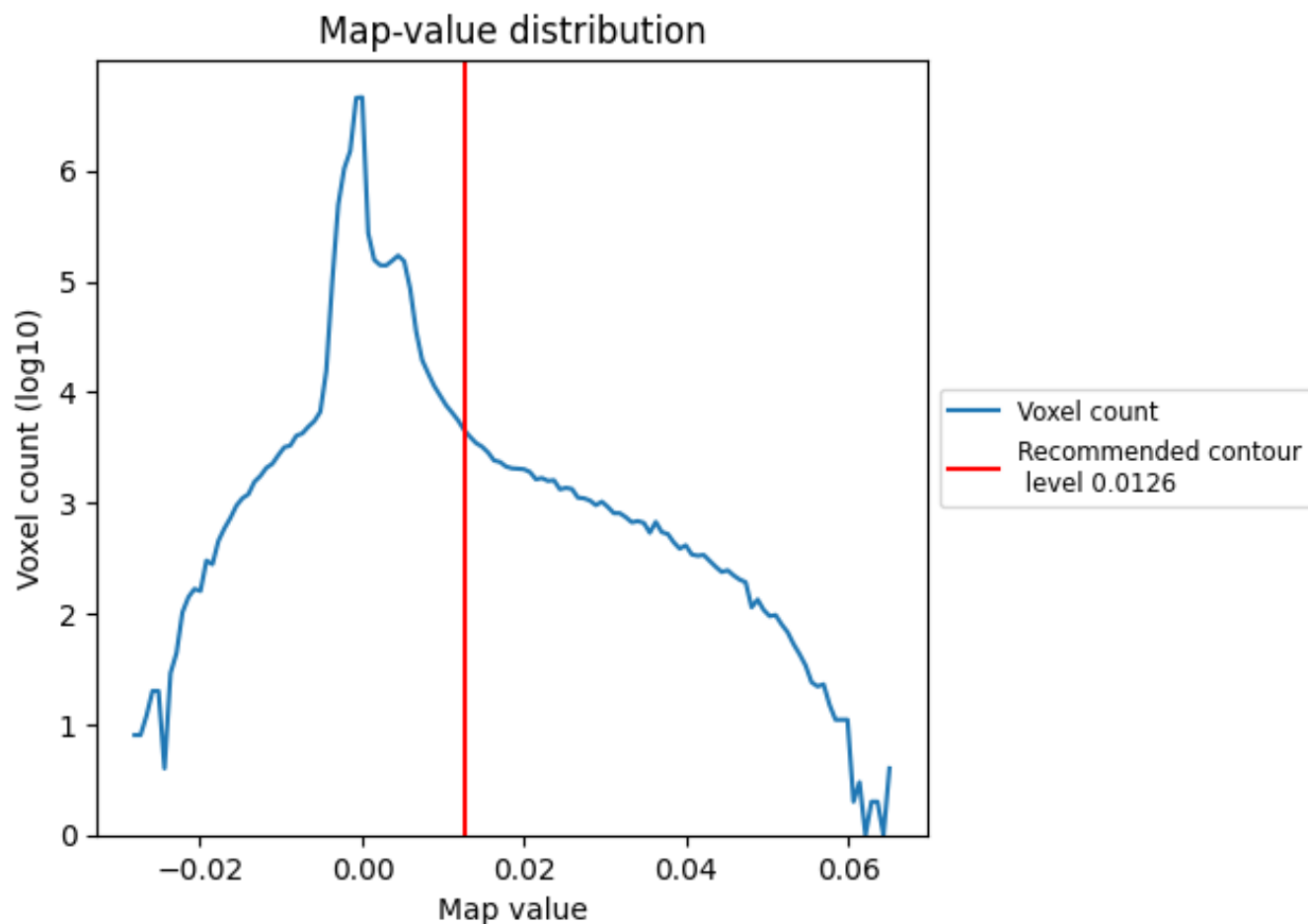
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

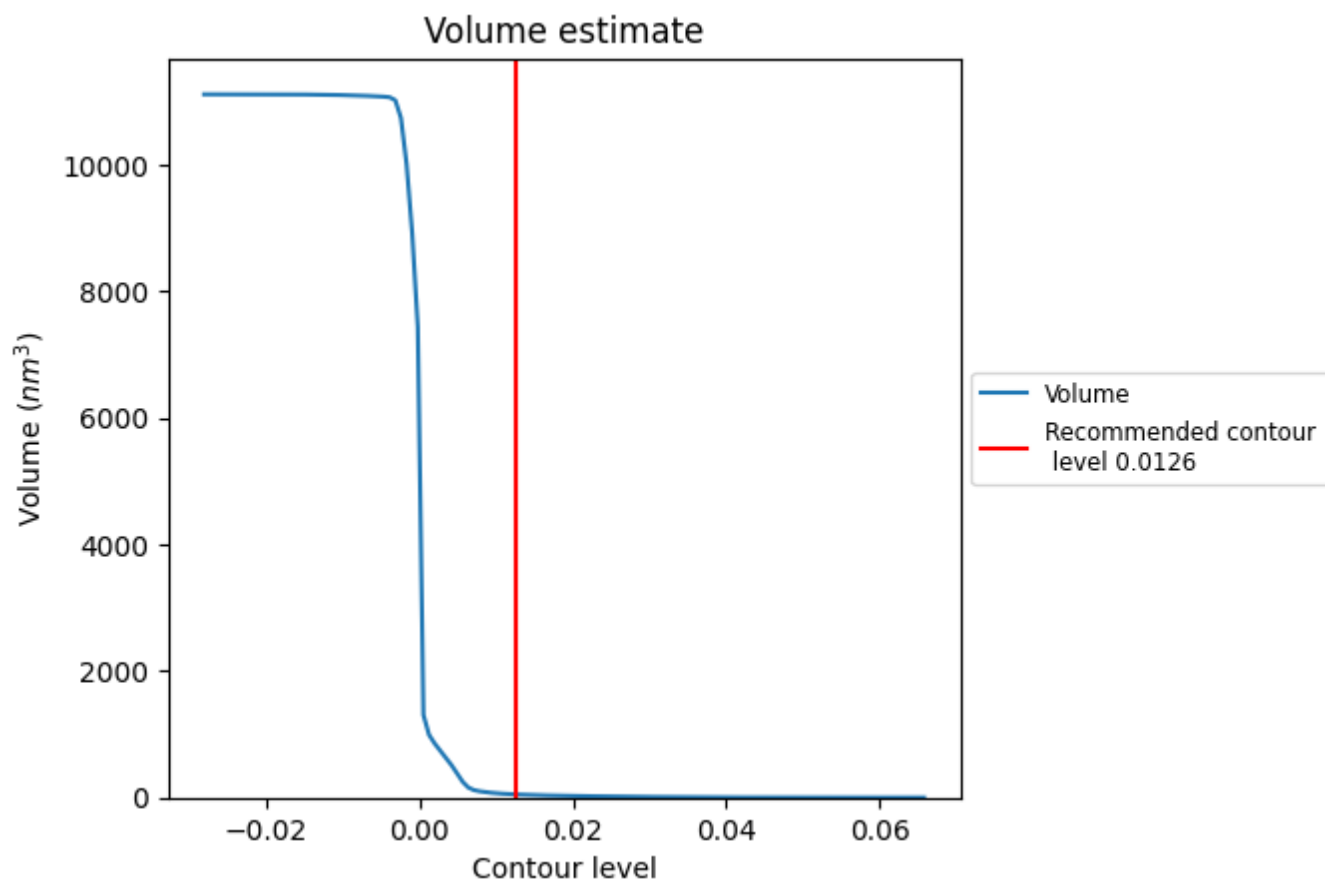
This section contains the results of statistical analysis of the map.

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.

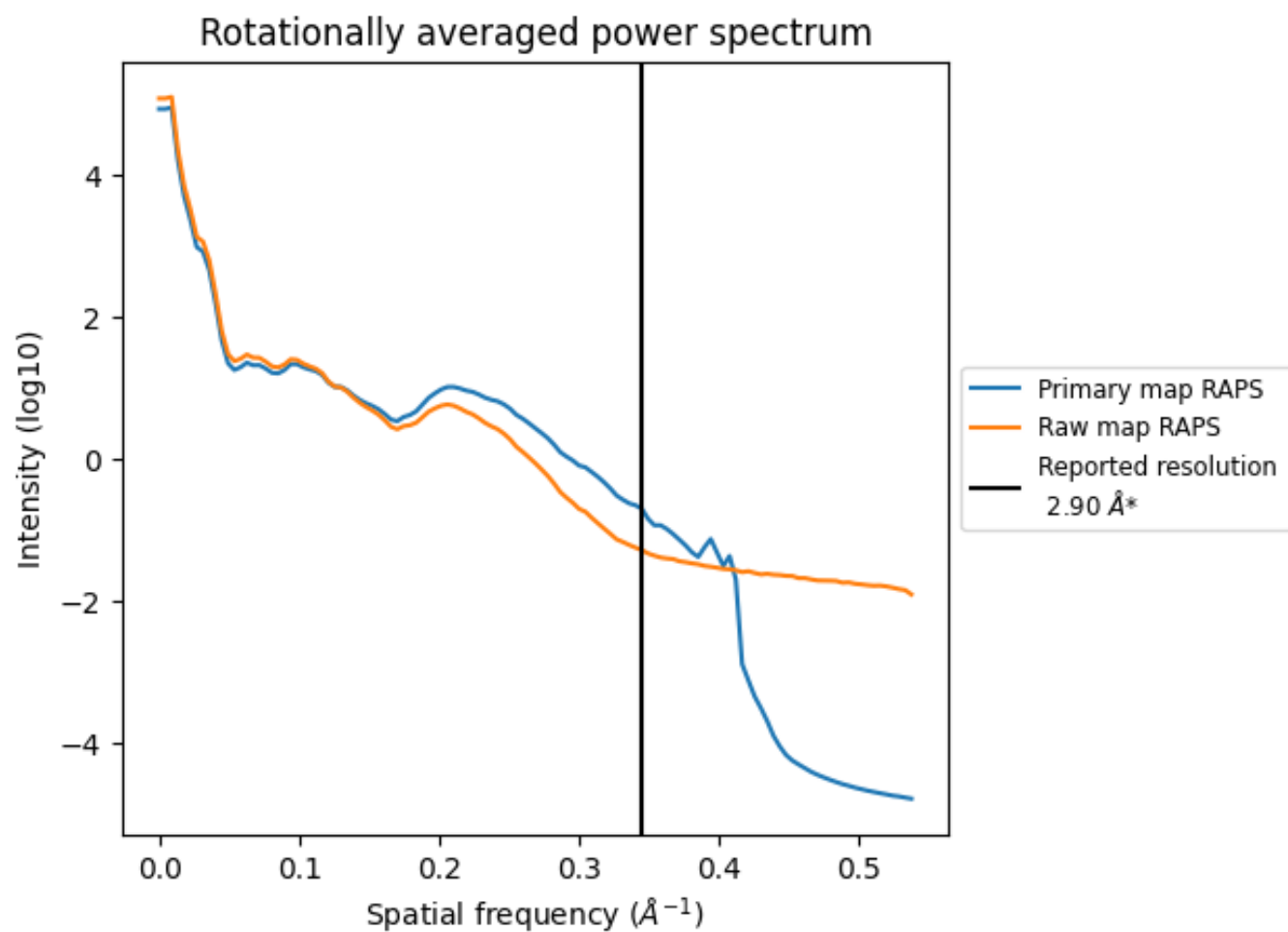
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 49 nm^3 ; this corresponds to an approximate mass of 44 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 ⓘ

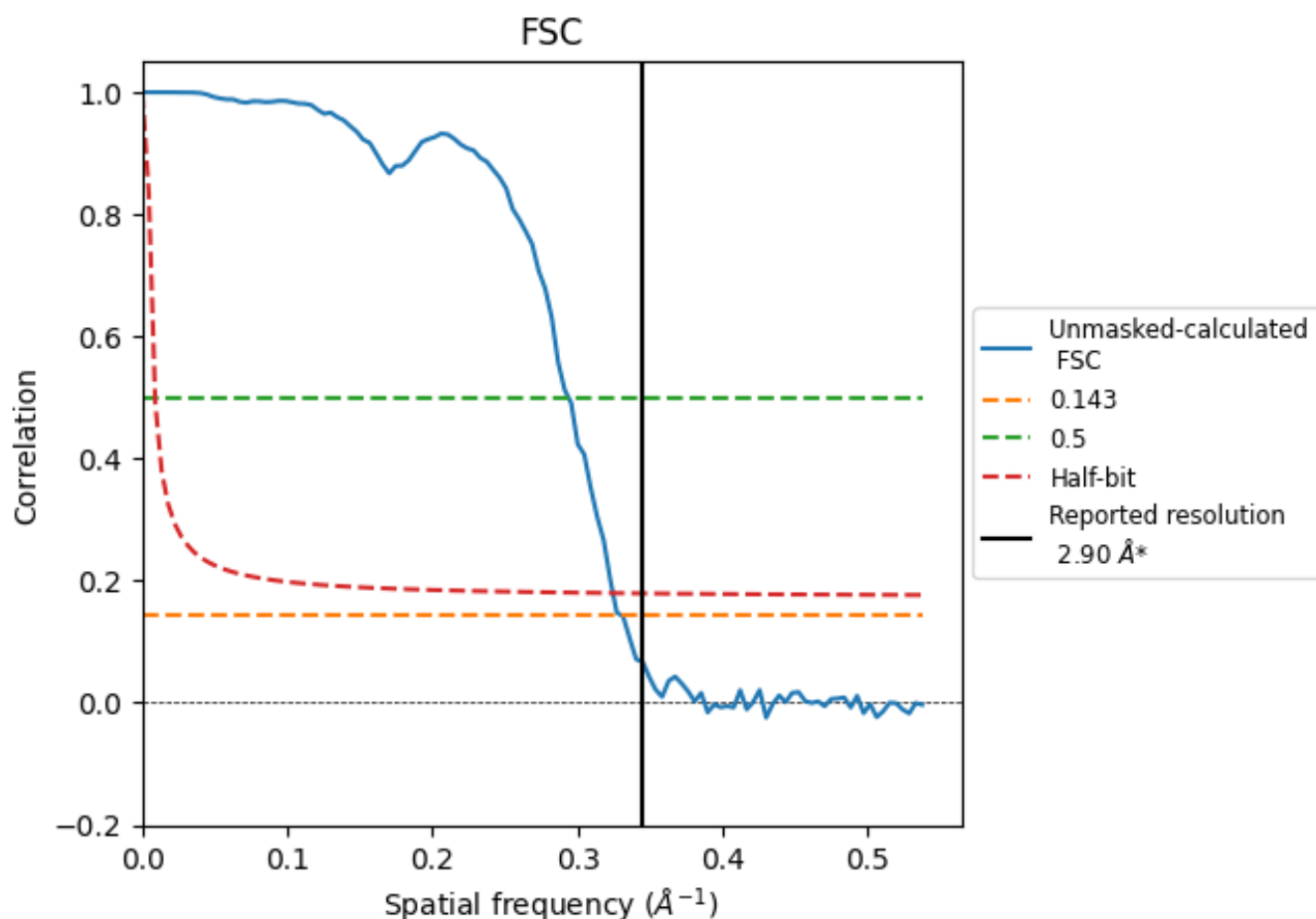


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.03	3.40	3.08

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

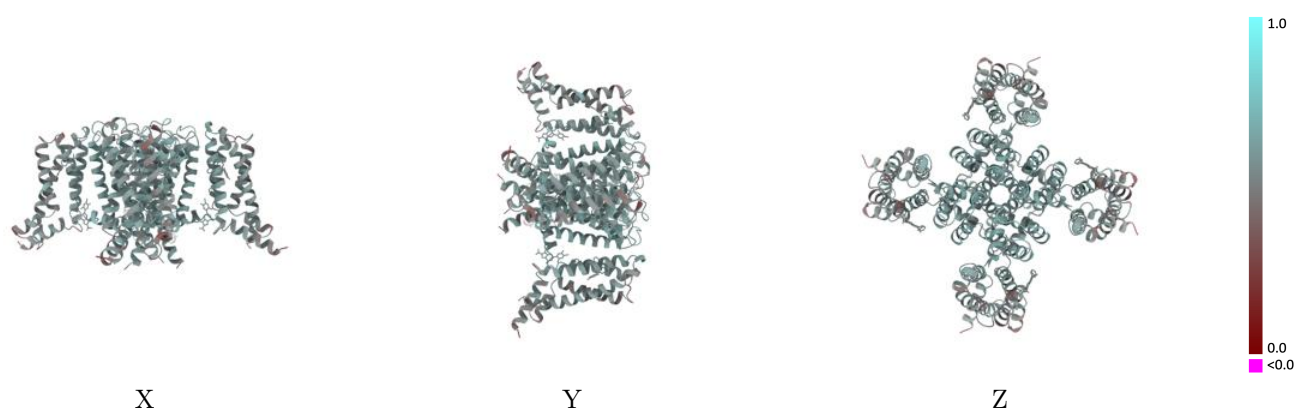
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-62892 and PDB model 9L8W. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)

This section was not generated.

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

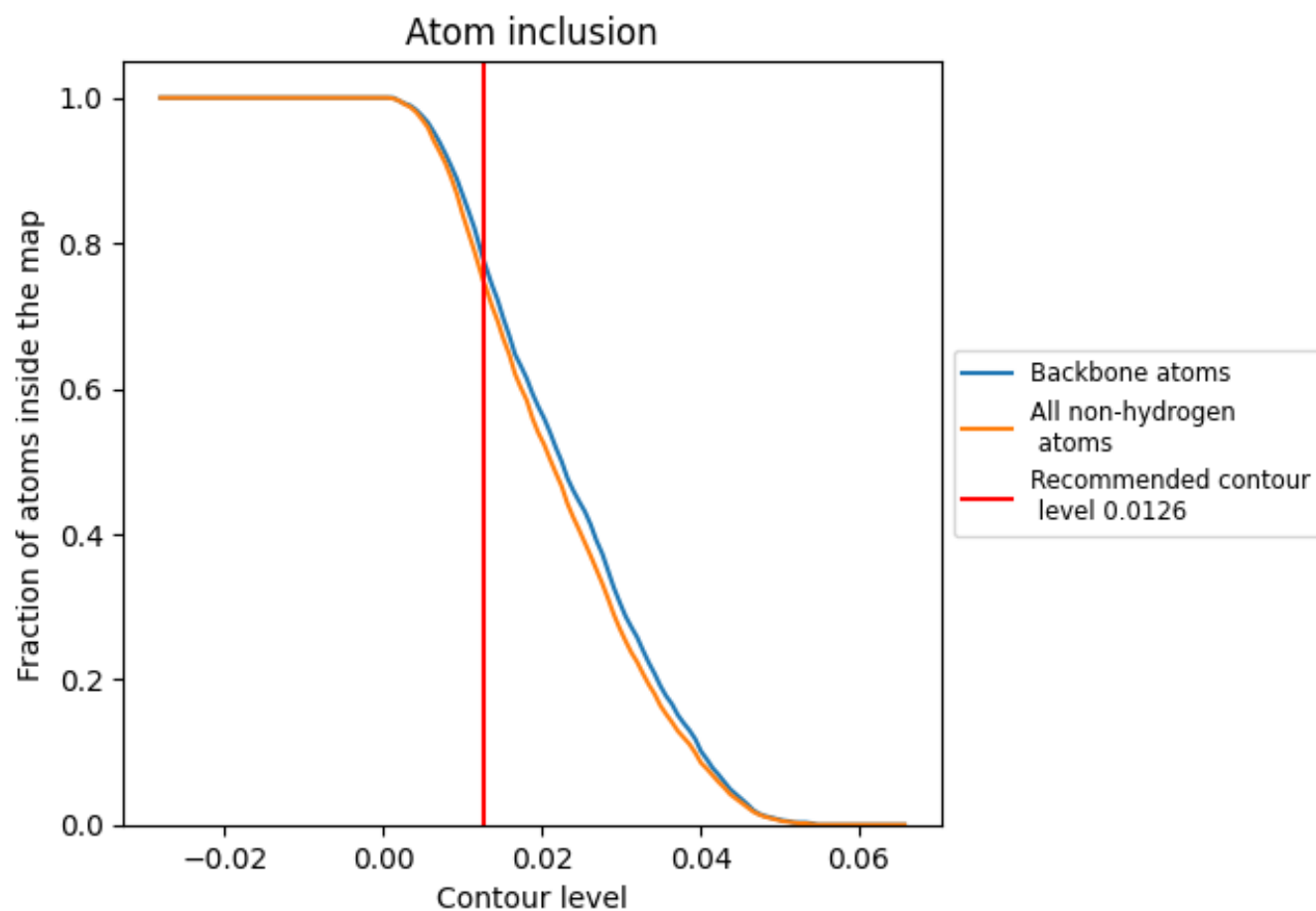


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 75% 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 (0.0126) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7490	0.5550
A	0.7540	0.5520
B	0.7570	0.5560
C	0.7570	0.5550
D	0.7580	0.5570

