



wwPDB EM Validation Summary Report ⓘ

Jan 7, 2025 – 12:16 PM JST

PDB ID : 8J7M
EMDB ID : EMD-36042
Title : ion channel
Authors : Chen, H.W.; Chen, H.W.
Deposited on : 2023-04-27
Resolution : 3.10 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.dev113
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

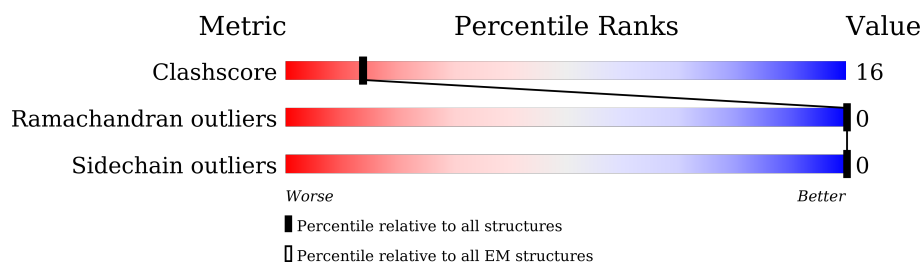
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY



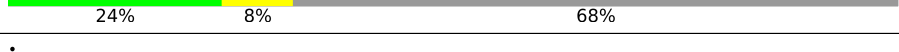
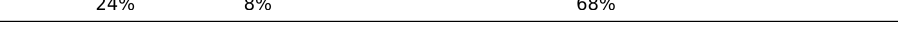
The reported resolution of this entry is 3.10 Å.

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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	803	 25% 7% 68%
1	B	803	 25% 7% 68%
1	C	803	 24% 8% 68%
1	D	803	 24% 8% 68%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8806 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 ion channel,Voltage dependent ion channel,Green fluorescent protein (Fragment),Voltage dependent ion channel,Green fluorescent protein (Fragment),Voltage dependent ion channel,Green fluorescent protein (Fragment).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	257	Total	C	N	O	S	0	0
			2096	1411	329	345	11		
1	D	257	Total	C	N	O	S	0	0
			2096	1411	329	345	11		
1	B	257	Total	C	N	O	S	0	0
			2096	1411	329	345	11		
1	C	257	Total	C	N	O	S	0	0
			2096	1411	329	345	11		

There are 176 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	543	ALA	-	linker	UNP R1FVI4
A	544	ALA	-	linker	UNP R1FVI4
A	545	ALA	-	linker	UNP R1FVI4
A	546	LEU	-	linker	UNP R1FVI4
A	547	GLU	-	linker	UNP R1FVI4
A	548	VAL	-	linker	UNP R1FVI4
A	549	LEU	-	linker	UNP R1FVI4
A	550	PHE	-	linker	UNP R1FVI4
A	551	GLN	-	linker	UNP R1FVI4
A	552	GLY	-	linker	UNP R1FVI4
A	553	PRO	-	linker	UNP R1FVI4
A	554	SER	-	linker	UNP R1FVI4
A	582	ARG	SER	conflict	UNP A0A059PIQ0
A	624	SER	ALA	conflict	UNP A0A059PIQ0
A	632	ARG	GLN	conflict	UNP A0A059PIQ0
A	758	VAL	ALA	conflict	UNP A0A059PIQ0
A	788	TRP	-	expression tag	UNP A0A059PIQ0
A	789	SER	-	expression tag	UNP A0A059PIQ0
A	790	HIS	-	expression tag	UNP A0A059PIQ0
A	791	PRO	-	expression tag	UNP A0A059PIQ0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	792	GLN	-	expression tag	UNP A0A059PIQ0
A	793	PHE	-	expression tag	UNP A0A059PIQ0
A	794	GLU	-	expression tag	UNP A0A059PIQ0
A	795	LYS	-	expression tag	UNP A0A059PIQ0
A	796	GLY	-	expression tag	UNP A0A059PIQ0
A	797	GLY	-	expression tag	UNP A0A059PIQ0
A	798	GLY	-	expression tag	UNP A0A059PIQ0
A	799	SER	-	expression tag	UNP A0A059PIQ0
A	800	GLY	-	expression tag	UNP A0A059PIQ0
A	801	GLY	-	expression tag	UNP A0A059PIQ0
A	802	GLY	-	expression tag	UNP A0A059PIQ0
A	803	SER	-	expression tag	UNP A0A059PIQ0
A	804	GLY	-	expression tag	UNP A0A059PIQ0
A	805	GLY	-	expression tag	UNP A0A059PIQ0
A	806	SER	-	expression tag	UNP A0A059PIQ0
A	807	ALA	-	expression tag	UNP A0A059PIQ0
A	808	TRP	-	expression tag	UNP A0A059PIQ0
A	809	SER	-	expression tag	UNP A0A059PIQ0
A	810	HIS	-	expression tag	UNP A0A059PIQ0
A	811	PRO	-	expression tag	UNP A0A059PIQ0
A	812	GLN	-	expression tag	UNP A0A059PIQ0
A	813	PHE	-	expression tag	UNP A0A059PIQ0
A	814	GLU	-	expression tag	UNP A0A059PIQ0
A	815	LYS	-	expression tag	UNP A0A059PIQ0
D	543	ALA	-	linker	UNP R1FVI4
D	544	ALA	-	linker	UNP R1FVI4
D	545	ALA	-	linker	UNP R1FVI4
D	546	LEU	-	linker	UNP R1FVI4
D	547	GLU	-	linker	UNP R1FVI4
D	548	VAL	-	linker	UNP R1FVI4
D	549	LEU	-	linker	UNP R1FVI4
D	550	PHE	-	linker	UNP R1FVI4
D	551	GLN	-	linker	UNP R1FVI4
D	552	GLY	-	linker	UNP R1FVI4
D	553	PRO	-	linker	UNP R1FVI4
D	554	SER	-	linker	UNP R1FVI4
D	582	ARG	SER	conflict	UNP A0A059PIQ0
D	624	SER	ALA	conflict	UNP A0A059PIQ0
D	632	ARG	GLN	conflict	UNP A0A059PIQ0
D	758	VAL	ALA	conflict	UNP A0A059PIQ0
D	788	TRP	-	expression tag	UNP A0A059PIQ0
D	789	SER	-	expression tag	UNP A0A059PIQ0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	790	HIS	-	expression tag	UNP A0A059PIQ0
D	791	PRO	-	expression tag	UNP A0A059PIQ0
D	792	GLN	-	expression tag	UNP A0A059PIQ0
D	793	PHE	-	expression tag	UNP A0A059PIQ0
D	794	GLU	-	expression tag	UNP A0A059PIQ0
D	795	LYS	-	expression tag	UNP A0A059PIQ0
D	796	GLY	-	expression tag	UNP A0A059PIQ0
D	797	GLY	-	expression tag	UNP A0A059PIQ0
D	798	GLY	-	expression tag	UNP A0A059PIQ0
D	799	SER	-	expression tag	UNP A0A059PIQ0
D	800	GLY	-	expression tag	UNP A0A059PIQ0
D	801	GLY	-	expression tag	UNP A0A059PIQ0
D	802	GLY	-	expression tag	UNP A0A059PIQ0
D	803	SER	-	expression tag	UNP A0A059PIQ0
D	804	GLY	-	expression tag	UNP A0A059PIQ0
D	805	GLY	-	expression tag	UNP A0A059PIQ0
D	806	SER	-	expression tag	UNP A0A059PIQ0
D	807	ALA	-	expression tag	UNP A0A059PIQ0
D	808	TRP	-	expression tag	UNP A0A059PIQ0
D	809	SER	-	expression tag	UNP A0A059PIQ0
D	810	HIS	-	expression tag	UNP A0A059PIQ0
D	811	PRO	-	expression tag	UNP A0A059PIQ0
D	812	GLN	-	expression tag	UNP A0A059PIQ0
D	813	PHE	-	expression tag	UNP A0A059PIQ0
D	814	GLU	-	expression tag	UNP A0A059PIQ0
D	815	LYS	-	expression tag	UNP A0A059PIQ0
B	543	ALA	-	linker	UNP R1FVI4
B	544	ALA	-	linker	UNP R1FVI4
B	545	ALA	-	linker	UNP R1FVI4
B	546	LEU	-	linker	UNP R1FVI4
B	547	GLU	-	linker	UNP R1FVI4
B	548	VAL	-	linker	UNP R1FVI4
B	549	LEU	-	linker	UNP R1FVI4
B	550	PHE	-	linker	UNP R1FVI4
B	551	GLN	-	linker	UNP R1FVI4
B	552	GLY	-	linker	UNP R1FVI4
B	553	PRO	-	linker	UNP R1FVI4
B	554	SER	-	linker	UNP R1FVI4
B	582	ARG	SER	conflict	UNP A0A059PIQ0
B	624	SER	ALA	conflict	UNP A0A059PIQ0
B	632	ARG	GLN	conflict	UNP A0A059PIQ0
B	758	VAL	ALA	conflict	UNP A0A059PIQ0

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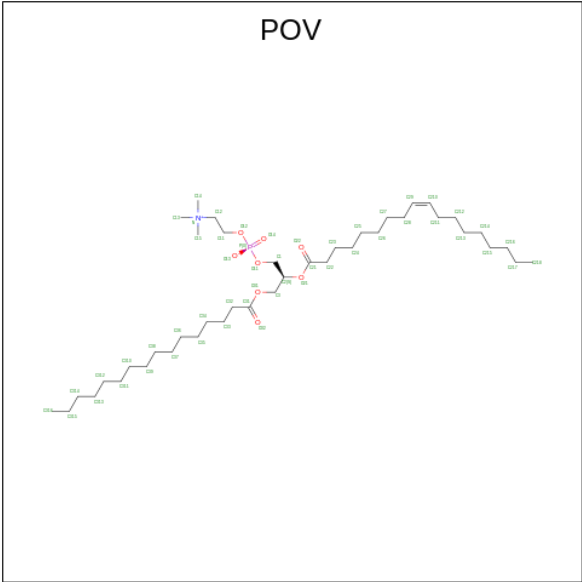
Chain	Residue	Modelled	Actual	Comment	Reference
B	788	TRP	-	expression tag	UNP A0A059PIQ0
B	789	SER	-	expression tag	UNP A0A059PIQ0
B	790	HIS	-	expression tag	UNP A0A059PIQ0
B	791	PRO	-	expression tag	UNP A0A059PIQ0
B	792	GLN	-	expression tag	UNP A0A059PIQ0
B	793	PHE	-	expression tag	UNP A0A059PIQ0
B	794	GLU	-	expression tag	UNP A0A059PIQ0
B	795	LYS	-	expression tag	UNP A0A059PIQ0
B	796	GLY	-	expression tag	UNP A0A059PIQ0
B	797	GLY	-	expression tag	UNP A0A059PIQ0
B	798	GLY	-	expression tag	UNP A0A059PIQ0
B	799	SER	-	expression tag	UNP A0A059PIQ0
B	800	GLY	-	expression tag	UNP A0A059PIQ0
B	801	GLY	-	expression tag	UNP A0A059PIQ0
B	802	GLY	-	expression tag	UNP A0A059PIQ0
B	803	SER	-	expression tag	UNP A0A059PIQ0
B	804	GLY	-	expression tag	UNP A0A059PIQ0
B	805	GLY	-	expression tag	UNP A0A059PIQ0
B	806	SER	-	expression tag	UNP A0A059PIQ0
B	807	ALA	-	expression tag	UNP A0A059PIQ0
B	808	TRP	-	expression tag	UNP A0A059PIQ0
B	809	SER	-	expression tag	UNP A0A059PIQ0
B	810	HIS	-	expression tag	UNP A0A059PIQ0
B	811	PRO	-	expression tag	UNP A0A059PIQ0
B	812	GLN	-	expression tag	UNP A0A059PIQ0
B	813	PHE	-	expression tag	UNP A0A059PIQ0
B	814	GLU	-	expression tag	UNP A0A059PIQ0
B	815	LYS	-	expression tag	UNP A0A059PIQ0
C	543	ALA	-	linker	UNP R1FVI4
C	544	ALA	-	linker	UNP R1FVI4
C	545	ALA	-	linker	UNP R1FVI4
C	546	LEU	-	linker	UNP R1FVI4
C	547	GLU	-	linker	UNP R1FVI4
C	548	VAL	-	linker	UNP R1FVI4
C	549	LEU	-	linker	UNP R1FVI4
C	550	PHE	-	linker	UNP R1FVI4
C	551	GLN	-	linker	UNP R1FVI4
C	552	GLY	-	linker	UNP R1FVI4
C	553	PRO	-	linker	UNP R1FVI4
C	554	SER	-	linker	UNP R1FVI4
C	582	ARG	SER	conflict	UNP A0A059PIQ0
C	624	SER	ALA	conflict	UNP A0A059PIQ0

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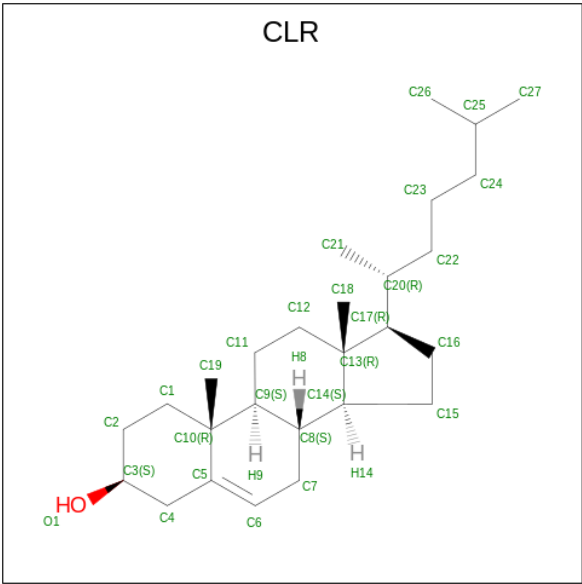
Chain	Residue	Modelled	Actual	Comment	Reference
C	632	ARG	GLN	conflict	UNP A0A059PIQ0
C	758	VAL	ALA	conflict	UNP A0A059PIQ0
C	788	TRP	-	expression tag	UNP A0A059PIQ0
C	789	SER	-	expression tag	UNP A0A059PIQ0
C	790	HIS	-	expression tag	UNP A0A059PIQ0
C	791	PRO	-	expression tag	UNP A0A059PIQ0
C	792	GLN	-	expression tag	UNP A0A059PIQ0
C	793	PHE	-	expression tag	UNP A0A059PIQ0
C	794	GLU	-	expression tag	UNP A0A059PIQ0
C	795	LYS	-	expression tag	UNP A0A059PIQ0
C	796	GLY	-	expression tag	UNP A0A059PIQ0
C	797	GLY	-	expression tag	UNP A0A059PIQ0
C	798	GLY	-	expression tag	UNP A0A059PIQ0
C	799	SER	-	expression tag	UNP A0A059PIQ0
C	800	GLY	-	expression tag	UNP A0A059PIQ0
C	801	GLY	-	expression tag	UNP A0A059PIQ0
C	802	GLY	-	expression tag	UNP A0A059PIQ0
C	803	SER	-	expression tag	UNP A0A059PIQ0
C	804	GLY	-	expression tag	UNP A0A059PIQ0
C	805	GLY	-	expression tag	UNP A0A059PIQ0
C	806	SER	-	expression tag	UNP A0A059PIQ0
C	807	ALA	-	expression tag	UNP A0A059PIQ0
C	808	TRP	-	expression tag	UNP A0A059PIQ0
C	809	SER	-	expression tag	UNP A0A059PIQ0
C	810	HIS	-	expression tag	UNP A0A059PIQ0
C	811	PRO	-	expression tag	UNP A0A059PIQ0
C	812	GLN	-	expression tag	UNP A0A059PIQ0
C	813	PHE	-	expression tag	UNP A0A059PIQ0
C	814	GLU	-	expression tag	UNP A0A059PIQ0
C	815	LYS	-	expression tag	UNP A0A059PIQ0

- Molecule 2 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylammonio)ethyl phosphate (three-letter code: POV) (formula: C₄₂H₈₂NO₈P).



Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	O	P	0
			36	27	8	1	
2	D	1	Total	C	O	P	0
			35	26	8	1	
2	B	1	Total	C	O	P	0
			35	26	8	1	
2	C	1	Total	C	O	P	0
			36	27	8	1	

- Molecule 3 is CHOLESTEROL (three-letter code: CLR) (formula: C₂₇H₄₆O).

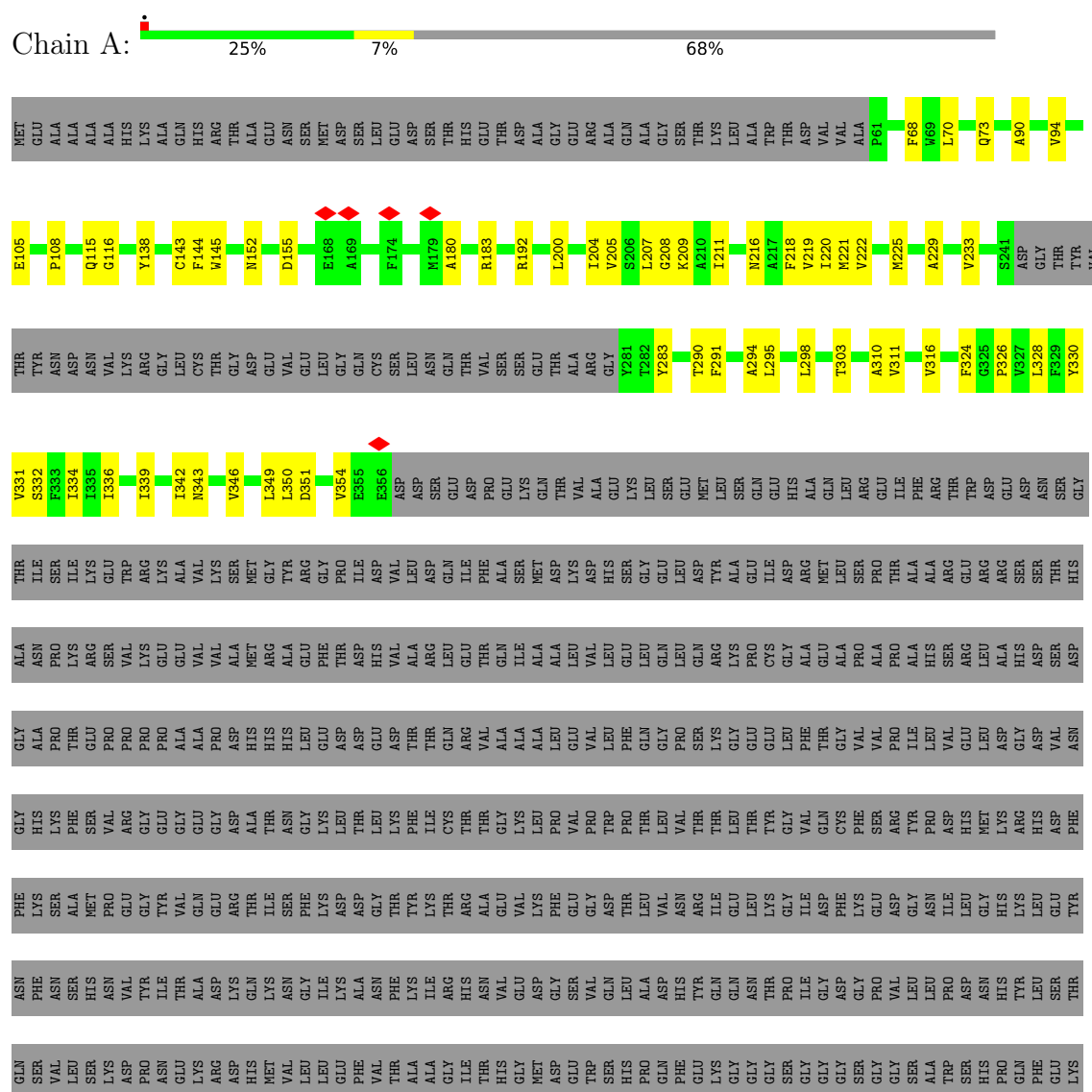


Mol	Chain	Residues	Atoms			AltConf
3	A	1	Total	C	O	0
			28	27	1	
3	A	1	Total	C	O	0
			28	27	1	
3	D	1	Total	C	O	0
			28	27	1	
3	D	1	Total	C	O	0
			28	27	1	
3	D	1	Total	C	O	0
			28	27	1	
3	B	1	Total	C	O	0
			28	27	1	
3	B	1	Total	C	O	0
			28	27	1	
3	C	1	Total	C	O	0
			28	27	1	
3	C	1	Total	C	O	0
			28	27	1	
3	C	1	Total	C	O	0
			28	27	1	

3 Residue-property plots

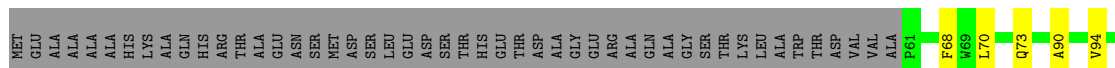
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

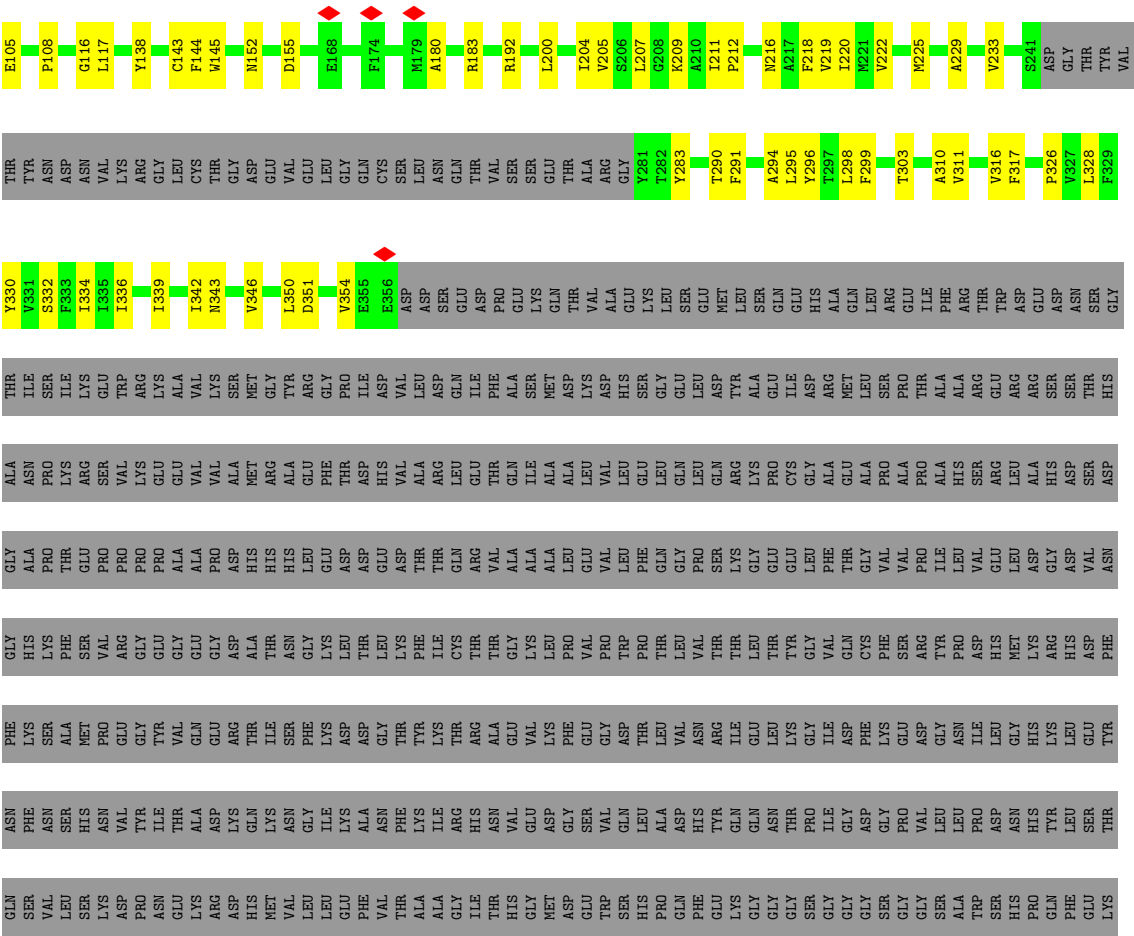
- Molecule 1: ion channel,Voltage dependent ion channel,Green fluorescent protein (Fragment),Voltage dependent ion channel,Green fluorescent protein (Fragment),Voltage dependent ion channel,Green fluorescent protein (Fragment)



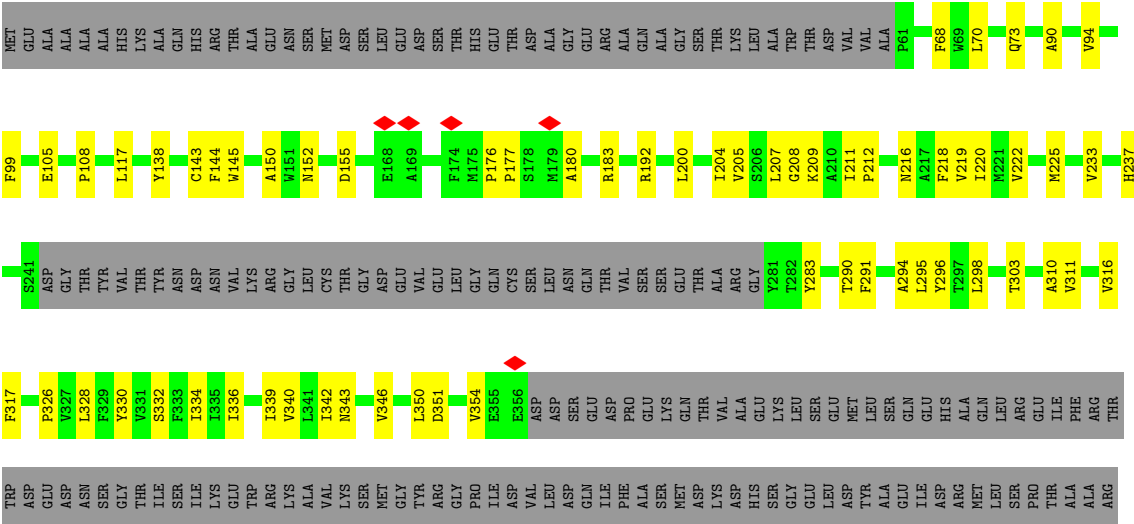
- [illegible]

- Chain B: 25% 7% 68%





● Molecule 1: ion channel, Voltage dependent ion channel, Green fluorescent protein (Fragment), Voltage dependent ion channel, Green fluorescent protein (Fragment), Voltage dependent ion channel, Green fluorescent protein (Fragment)



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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	81844	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	6.750	Depositor
Minimum map value	-4.127	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.128	Depositor
Recommended contour level	0.423	Depositor
Map size (\AA)	266.24, 266.24, 266.24	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.04, 1.04, 1.04	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: POV, CLR

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	0.48	0/2164	0.51	0/2947
1	B	0.51	0/2164	0.54	1/2947 (0.0%)
1	C	0.51	0/2164	0.56	1/2947 (0.0%)
1	D	0.52	0/2164	0.59	3/2947 (0.1%)
All	All	0.51	0/8656	0.55	5/11788 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	307	TRP	CB-CA-C	-5.86	98.69	110.40
1	C	336	ILE	CB-CA-C	-5.77	100.06	111.60
1	B	336	ILE	CB-CA-C	-5.76	100.08	111.60
1	D	308	SER	N-CA-CB	5.70	119.05	110.50
1	D	338	GLN	CB-CA-C	-5.65	99.10	110.40

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	2096	0	2065	62	0
1	B	2096	0	2065	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2096	0	2065	65	0
1	D	2096	0	2065	70	0
2	A	36	0	48	6	0
2	B	35	0	46	1	0
2	C	36	0	48	12	0
2	D	35	0	46	5	0
3	A	56	0	92	13	0
3	B	56	0	92	15	0
3	C	84	0	138	31	0
3	D	84	0	138	30	0
All	All	8806	0	8908	277	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 16.

The worst 5 of 277 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)
3:B:903:CLR:H222	3:B:903:CLR:H272	1.45	0.98
1:C:208:GLY:HA3	2:C:901:POV:H22	1.50	0.93
1:D:143:CYS:O	1:D:145:TRP:CE3	2.22	0.91
3:C:902:CLR:H183	3:C:902:CLR:H212	1.49	0.91
3:D:904:CLR:C16	3:D:904:CLR:H232	2.01	0.91

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	253/803 (32%)	228 (90%)	25 (10%)	0	100	100
1	B	253/803 (32%)	235 (93%)	18 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	253/803 (32%)	232 (92%)	21 (8%)	0	100	100
1	D	253/803 (32%)	233 (92%)	20 (8%)	0	100	100
All	All	1012/3212 (32%)	928 (92%)	84 (8%)	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	216/679 (32%)	216 (100%)	0	100	100
1	B	216/679 (32%)	216 (100%)	0	100	100
1	C	216/679 (32%)	216 (100%)	0	100	100
1	D	216/679 (32%)	216 (100%)	0	100	100
All	All	864/2716 (32%)	864 (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. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	72	HIS
1	B	126	ASN
1	C	343	ASN
1	C	72	HIS
1	A	343	ASN

5.3.3 RNA ⓘ

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](#)

14 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$
3	CLR	D	902	-	31,31,31	1.11	2 (6%)	48,48,48	2.14	15 (31%)
3	CLR	D	904	-	31,31,31	1.17	3 (9%)	48,48,48	1.93	15 (31%)
3	CLR	C	902	-	31,31,31	1.01	2 (6%)	48,48,48	1.97	12 (25%)
2	POV	C	901	-	35,35,51	1.08	2 (5%)	39,40,59	1.33	5 (12%)
3	CLR	A	903	-	31,31,31	1.15	3 (9%)	48,48,48	1.93	12 (25%)
3	CLR	B	903	-	31,31,31	1.17	3 (9%)	48,48,48	1.96	17 (35%)
2	POV	B	901	-	34,34,51	1.13	2 (5%)	38,39,59	1.32	5 (13%)
3	CLR	A	902	-	31,31,31	1.20	3 (9%)	48,48,48	1.97	15 (31%)
2	POV	A	901	-	35,35,51	1.11	2 (5%)	39,40,59	1.23	4 (10%)
2	POV	D	901	-	34,34,51	1.12	2 (5%)	38,39,59	1.22	4 (10%)
3	CLR	B	902	-	31,31,31	1.15	1 (3%)	48,48,48	1.92	12 (25%)
3	CLR	D	903	-	31,31,31	1.12	2 (6%)	48,48,48	1.91	13 (27%)
3	CLR	C	904	-	31,31,31	1.10	3 (9%)	48,48,48	1.66	10 (20%)
3	CLR	C	903	-	31,31,31	1.15	1 (3%)	48,48,48	1.92	12 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CLR	D	902	-	-	7/10/68/68	0/4/4/4
3	CLR	D	904	-	-	7/10/68/68	0/4/4/4
3	CLR	C	902	-	-	8/10/68/68	0/4/4/4
2	POV	C	901	-	-	20/37/37/55	-
3	CLR	A	903	-	-	3/10/68/68	0/4/4/4
3	CLR	B	903	-	-	3/10/68/68	0/4/4/4
2	POV	B	901	-	-	16/36/36/55	-
3	CLR	A	902	-	-	9/10/68/68	0/4/4/4
2	POV	A	901	-	-	18/37/37/55	-
2	POV	D	901	-	-	18/36/36/55	-
3	CLR	B	902	-	-	3/10/68/68	0/4/4/4
3	CLR	D	903	-	-	7/10/68/68	0/4/4/4
3	CLR	C	904	-	-	10/10/68/68	0/4/4/4
3	CLR	C	903	-	-	3/10/68/68	0/4/4/4

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	901	POV	O31-C31	4.25	1.45	1.33
2	D	901	POV	O31-C31	4.19	1.45	1.33
2	B	901	POV	O21-C21	4.18	1.46	1.34
2	B	901	POV	O31-C31	4.15	1.45	1.33
2	D	901	POV	O21-C21	4.04	1.45	1.34

The worst 5 of 151 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	902	CLR	C13-C14-C8	-5.88	105.67	114.38
3	A	903	CLR	C4-C5-C10	5.60	123.86	116.42
3	B	902	CLR	C4-C5-C10	5.59	123.84	116.42
3	C	903	CLR	C4-C5-C10	5.53	123.77	116.42
3	D	903	CLR	C4-C5-C10	5.46	123.67	116.42

There are no chirality outliers.

5 of 132 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	904	CLR	C13-C17-C20-C21
3	C	904	CLR	C13-C17-C20-C22

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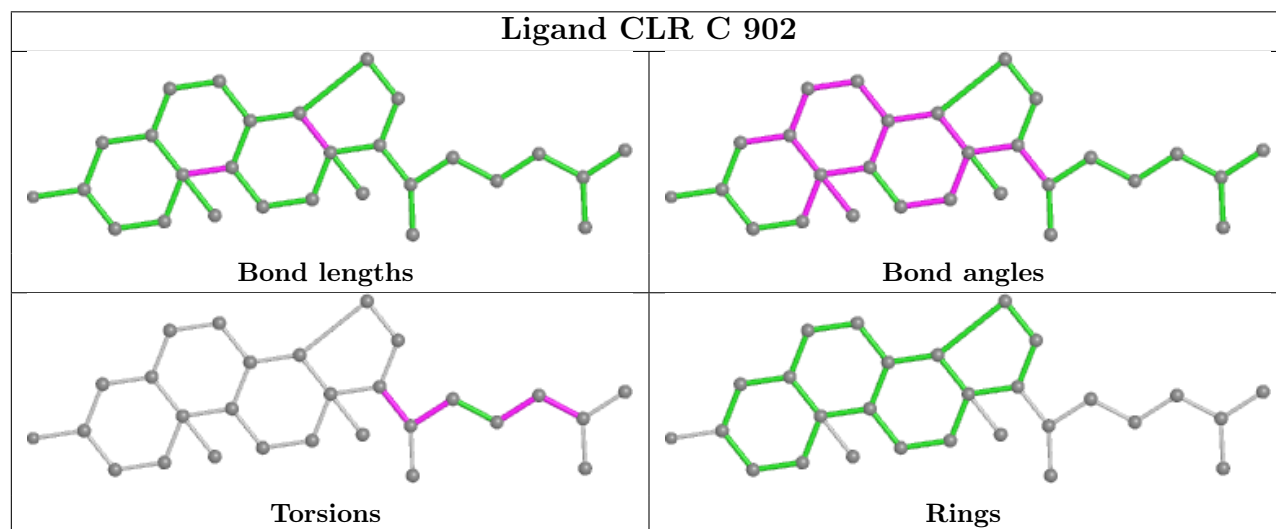
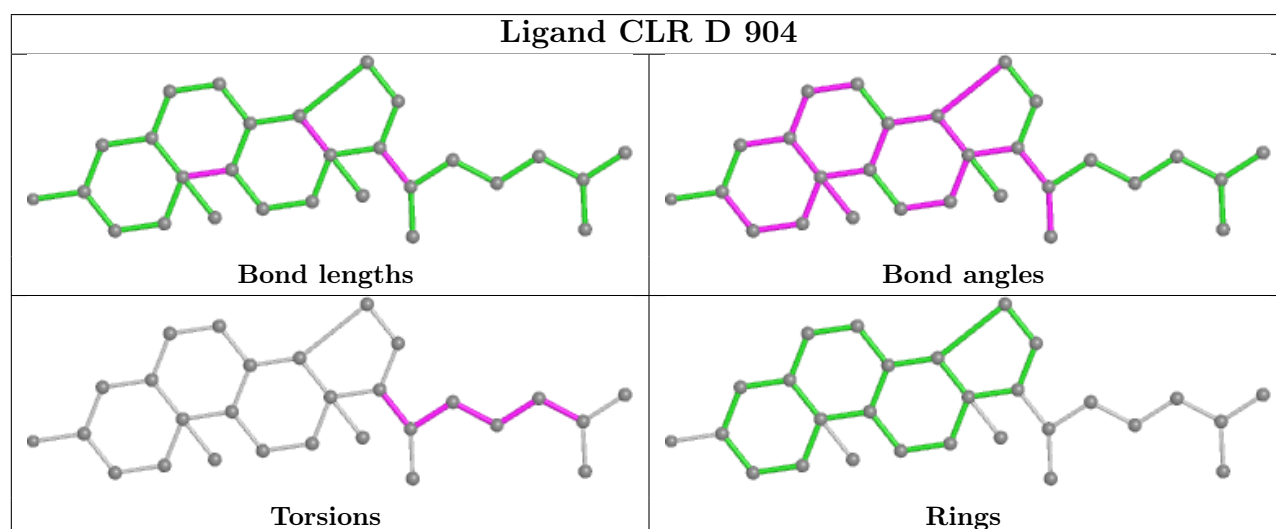
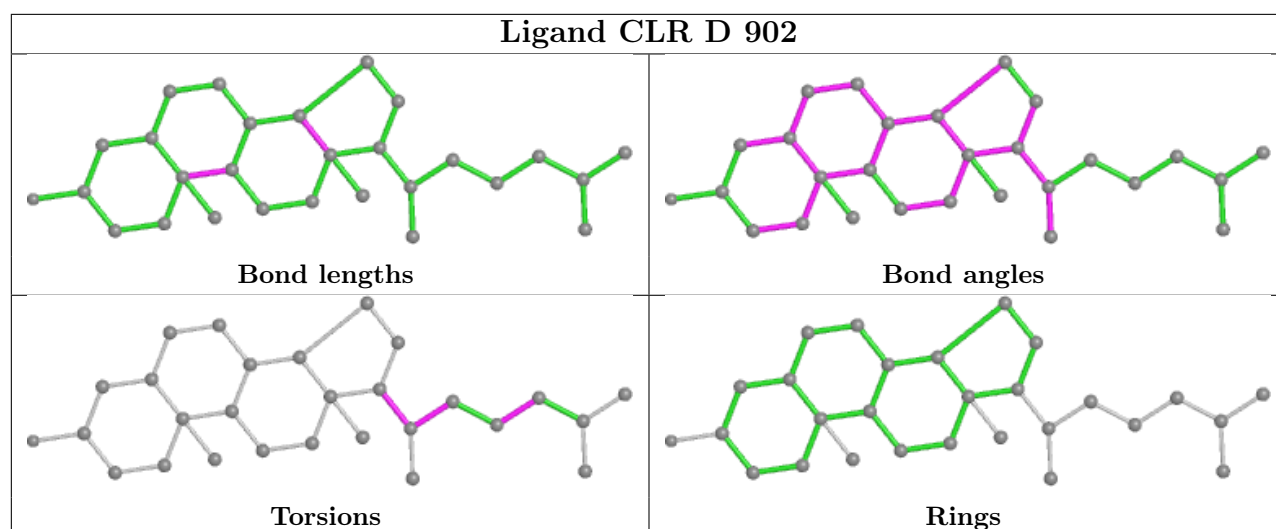
Mol	Chain	Res	Type	Atoms
3	C	904	CLR	C16-C17-C20-C22
2	A	901	POV	O32-C31-O31-C3
2	D	901	POV	O32-C31-O31-C3

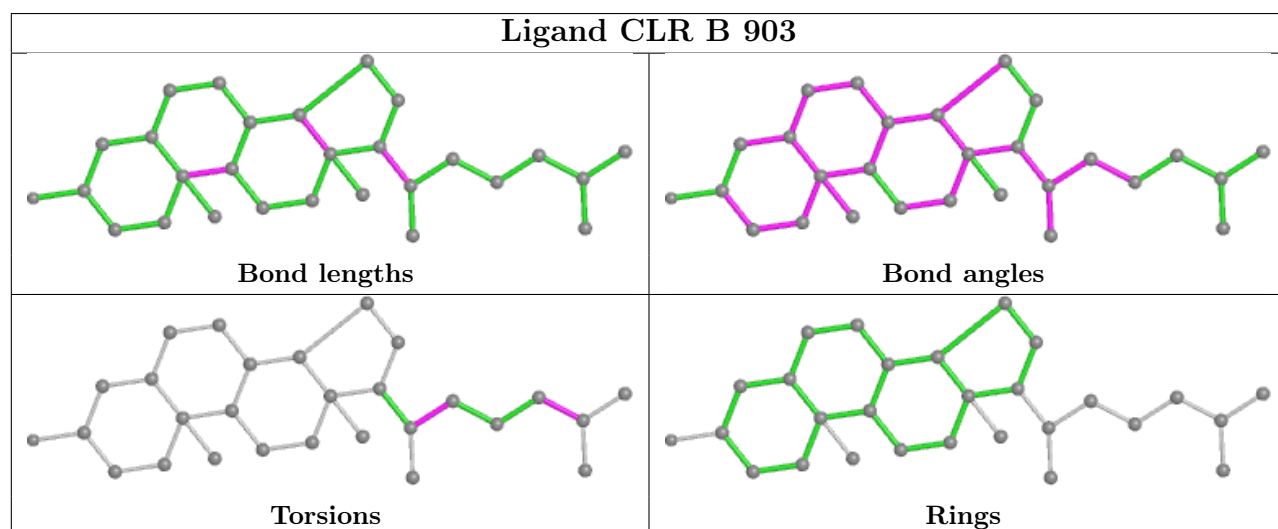
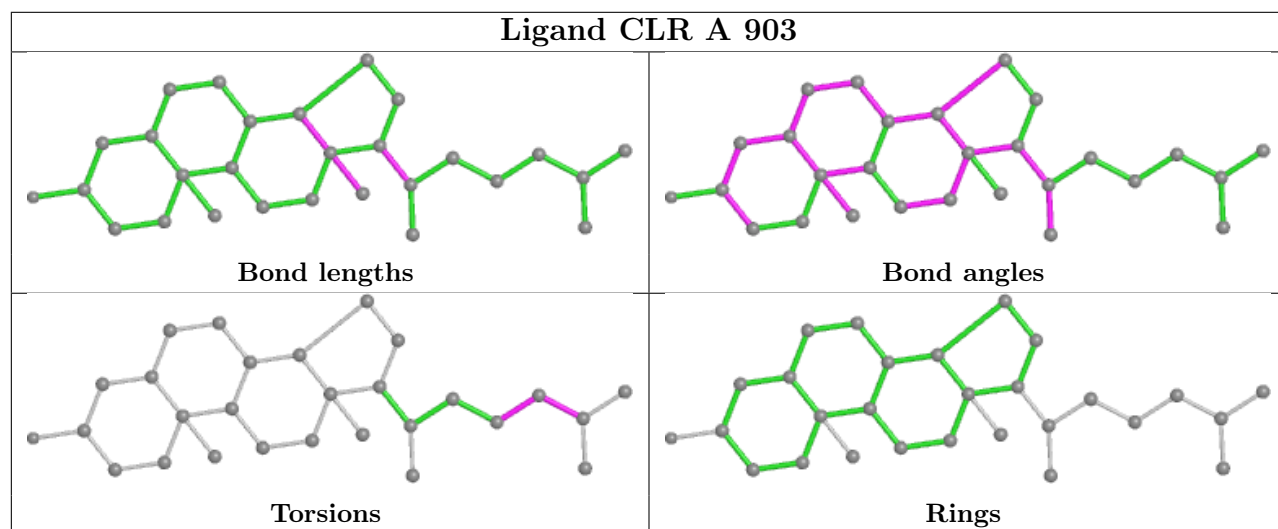
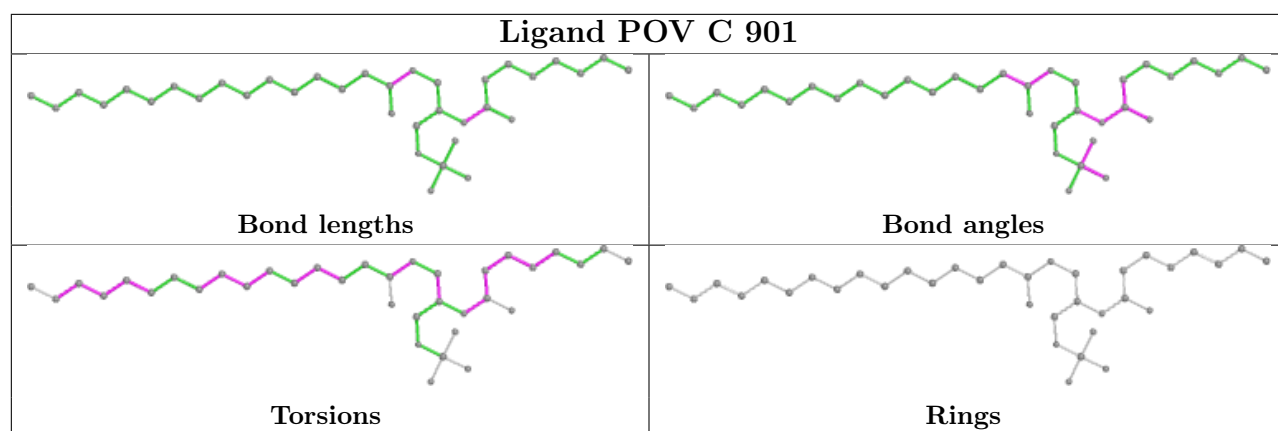
There are no ring outliers.

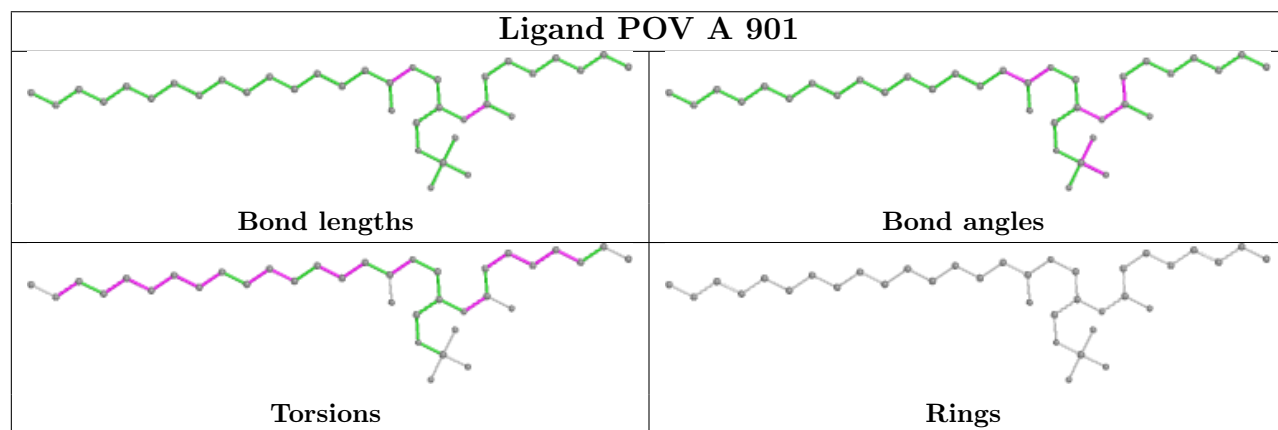
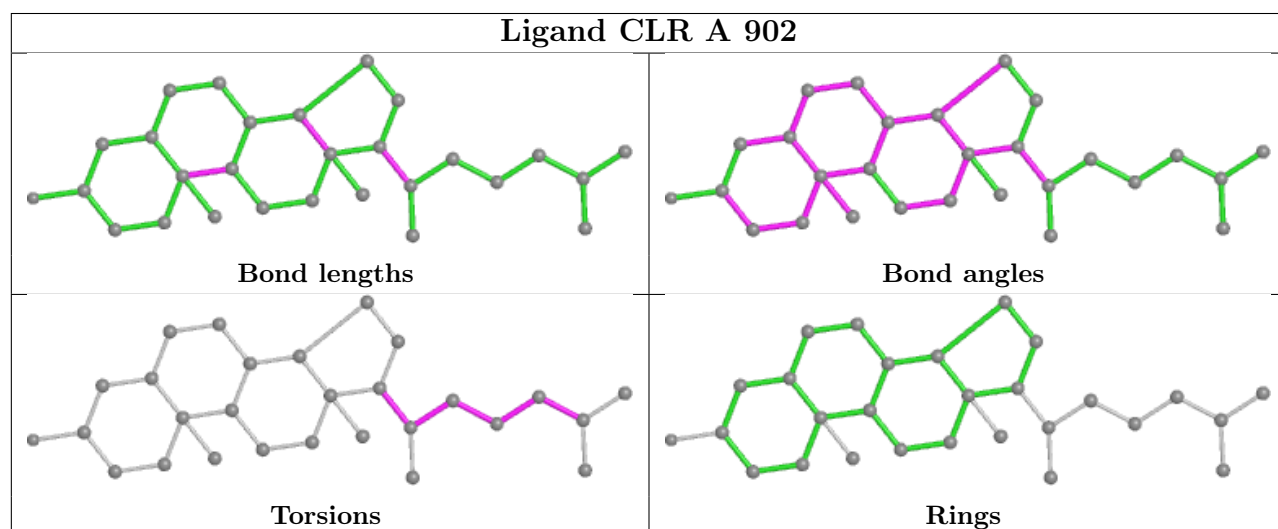
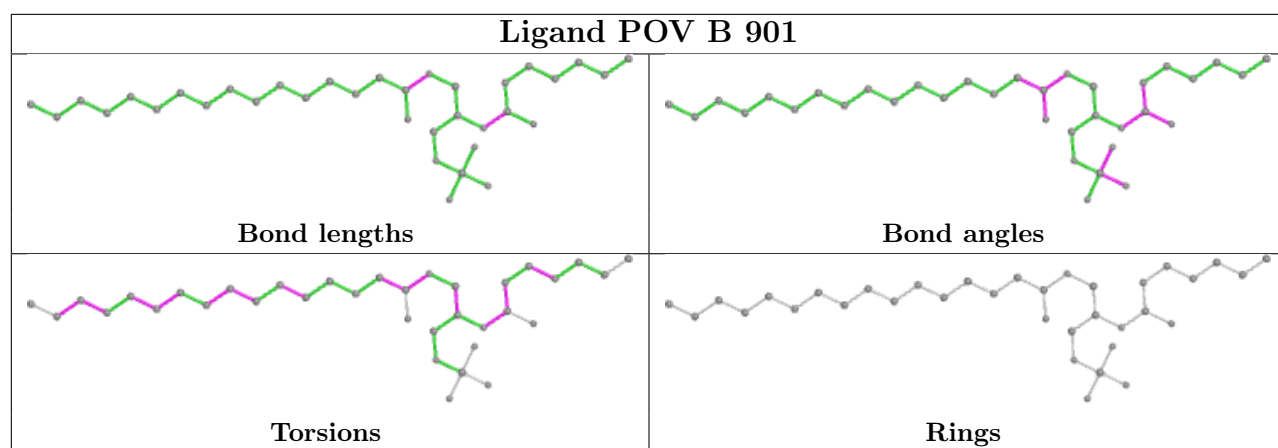
14 monomers are involved in 111 short contacts:

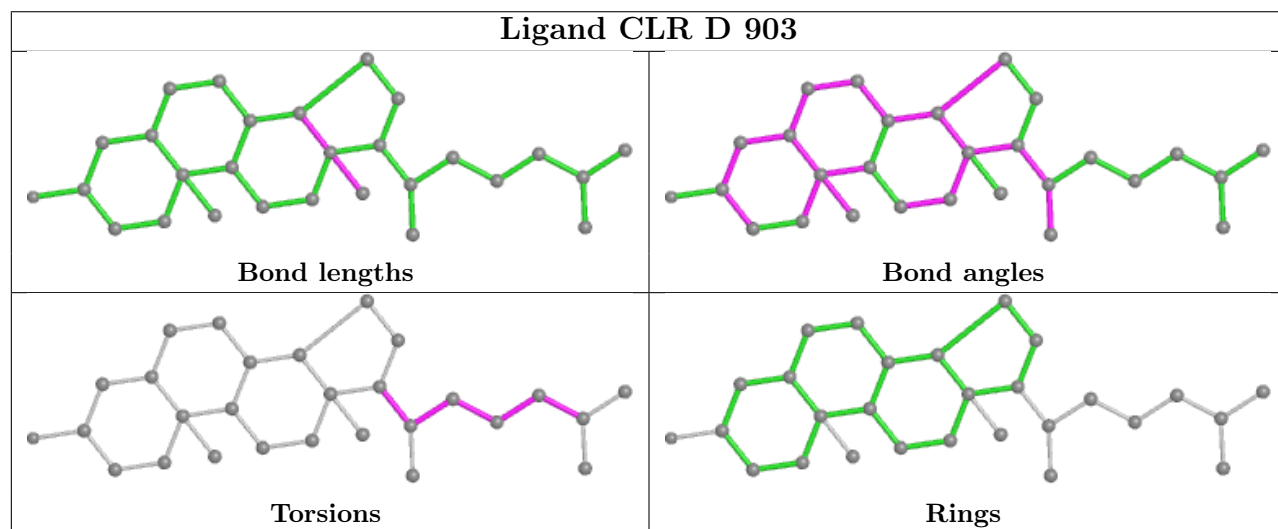
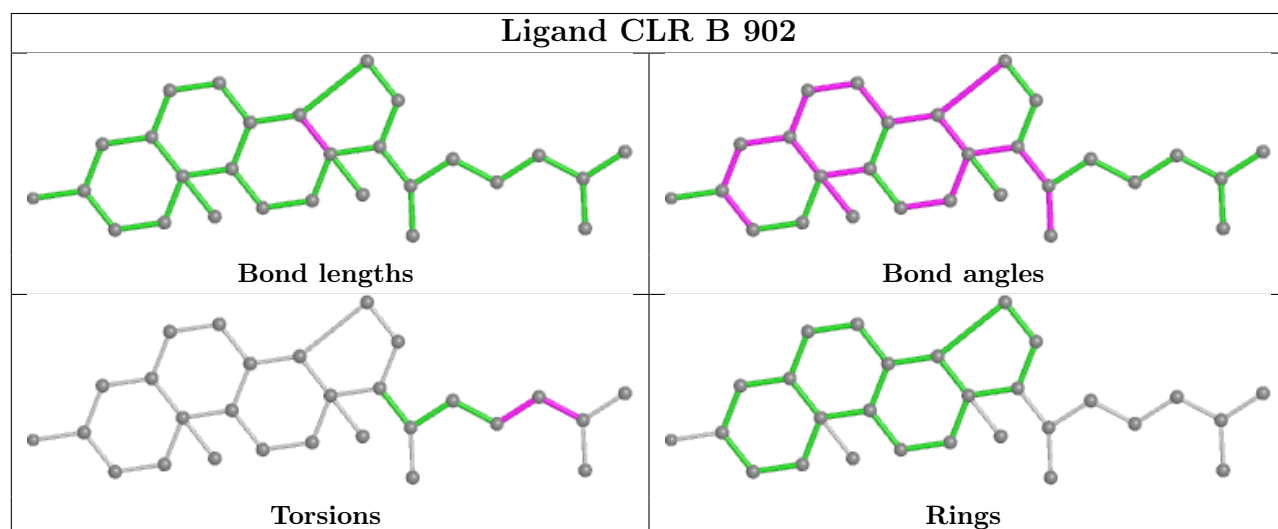
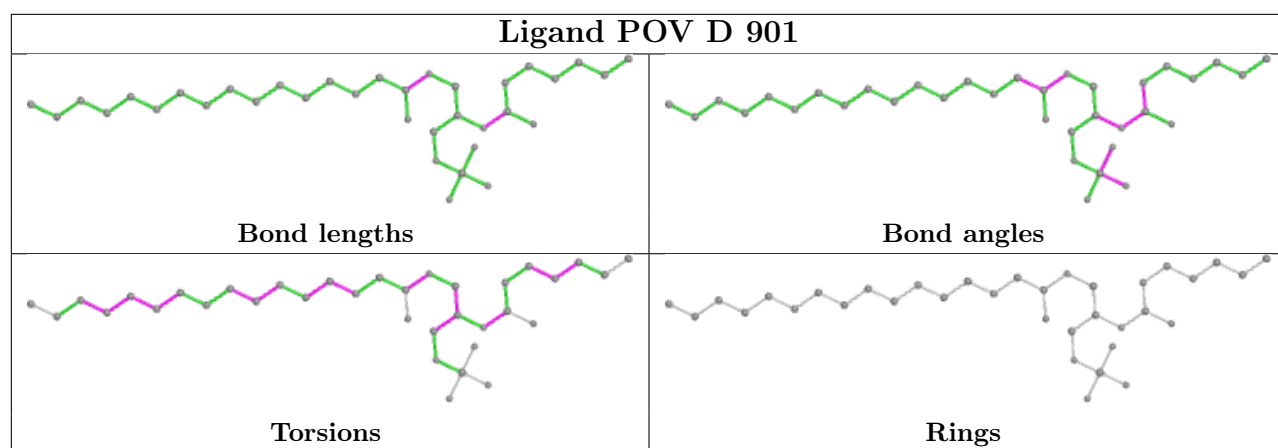
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	902	CLR	3	0
3	D	904	CLR	15	0
3	C	902	CLR	17	0
2	C	901	POV	12	0
3	A	903	CLR	9	0
3	B	903	CLR	4	0
2	B	901	POV	1	0
3	A	902	CLR	4	0
2	A	901	POV	6	0
2	D	901	POV	5	0
3	B	902	CLR	11	0
3	D	903	CLR	12	0
3	C	904	CLR	3	0
3	C	903	CLR	11	0

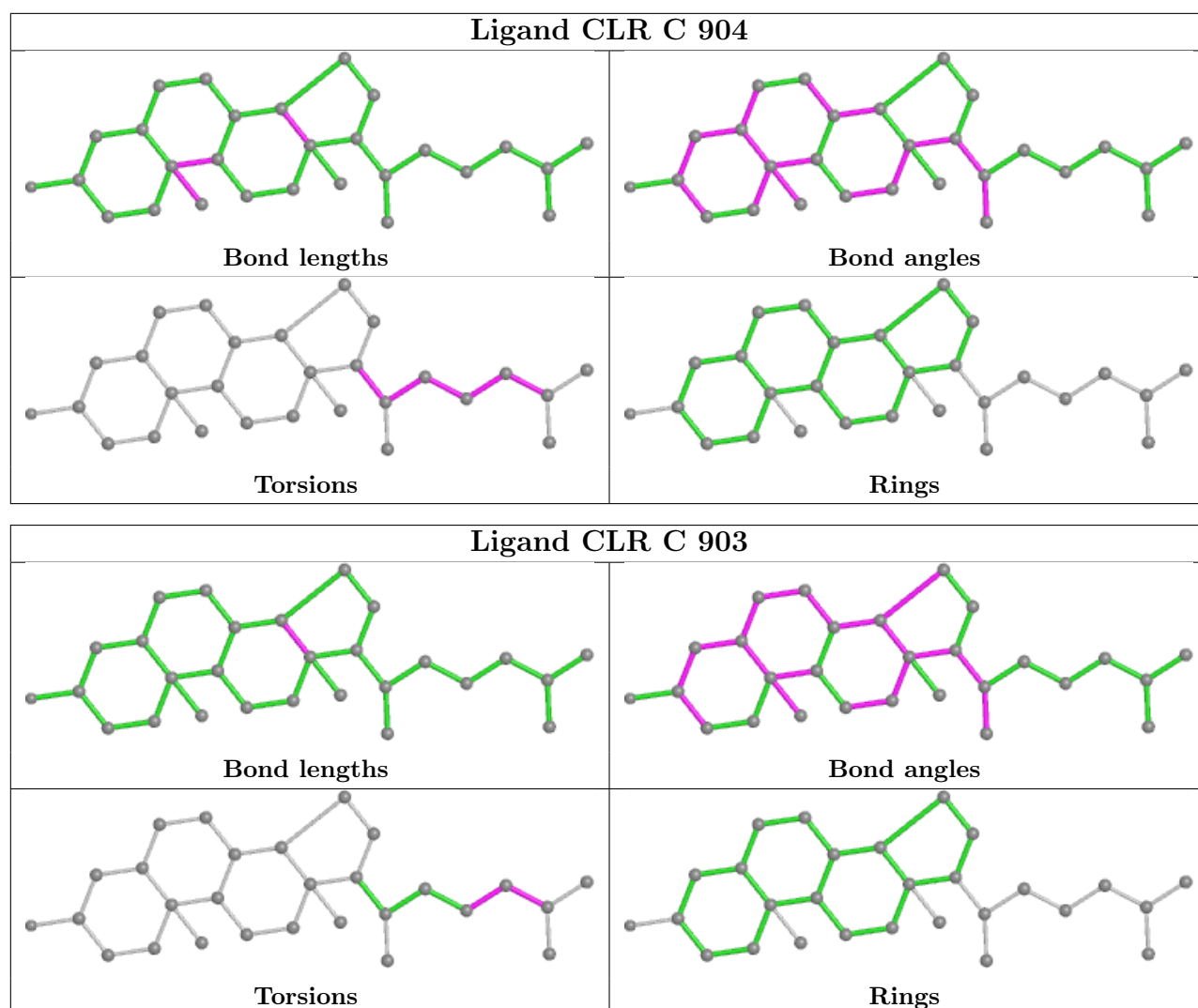
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

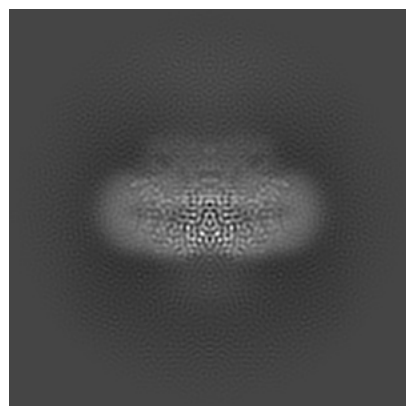
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36042. These allow visual inspection of the internal detail of the map and identification of artifacts.

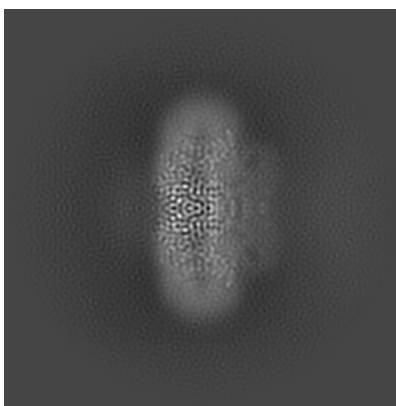
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

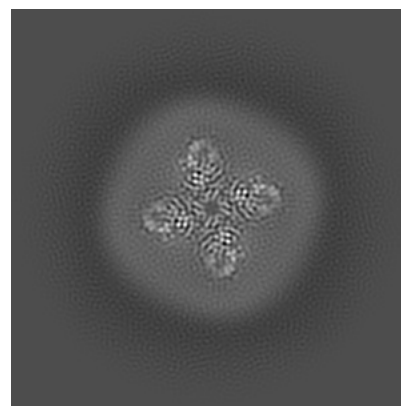
6.1.1 Primary map



X

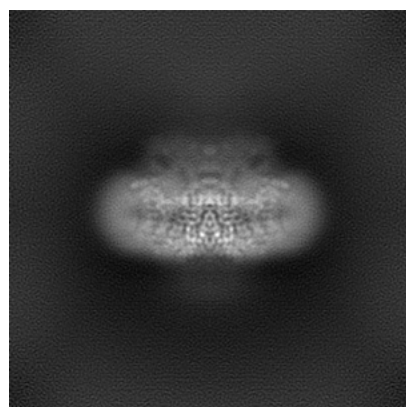


Y

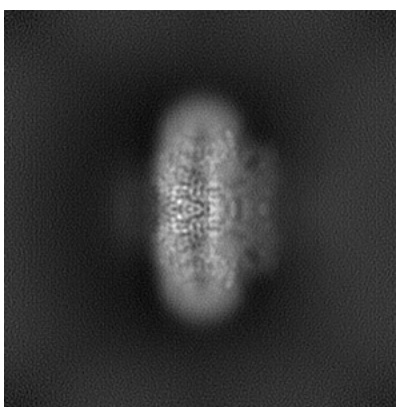


Z

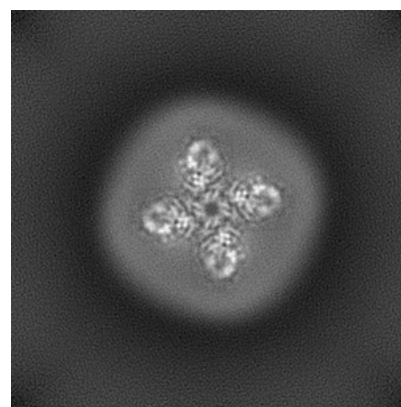
6.1.2 Raw map



X



Y

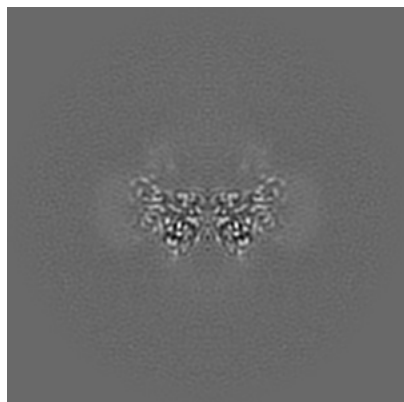


Z

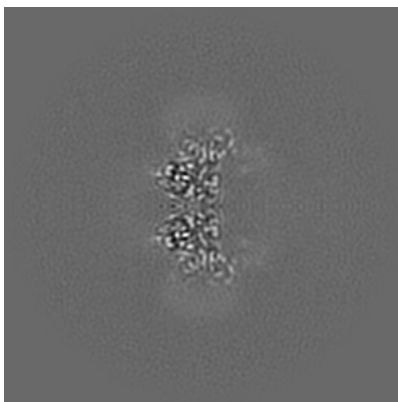
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

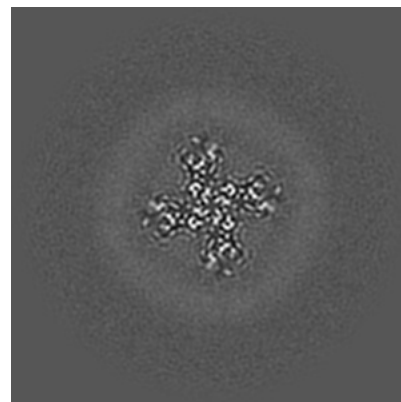
6.2.1 Primary map



X Index: 128

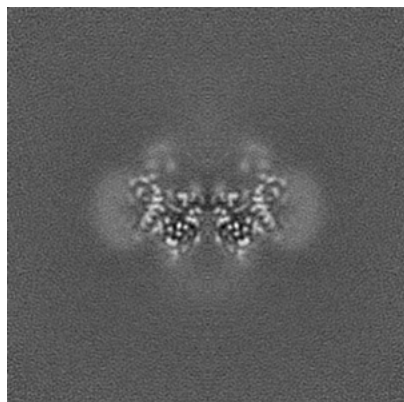


Y Index: 128

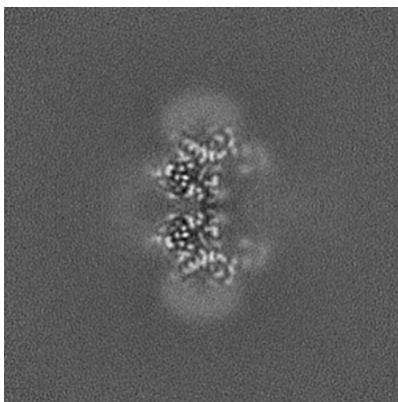


Z Index: 128

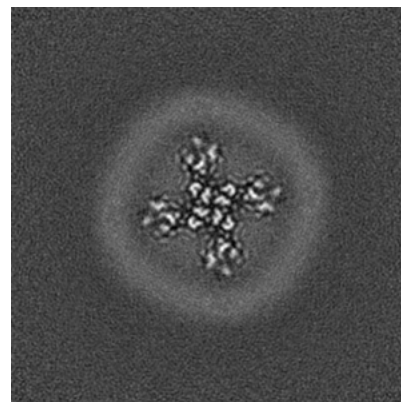
6.2.2 Raw map



X Index: 128



Y Index: 128

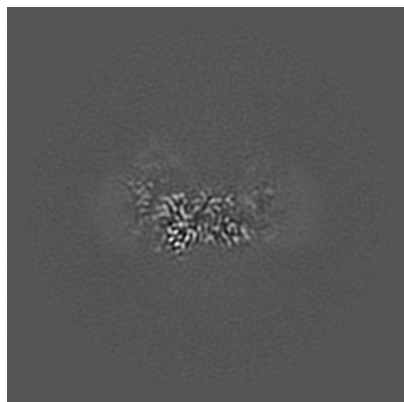


Z Index: 128

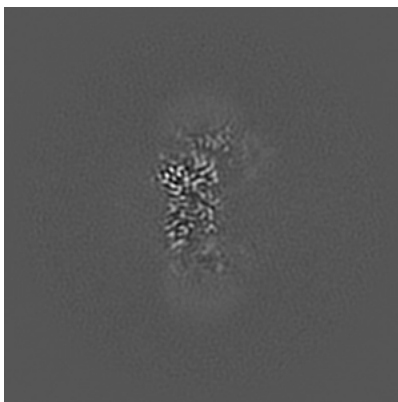
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

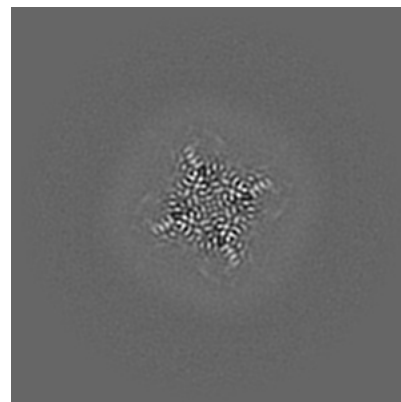
6.3.1 Primary map



X Index: 134

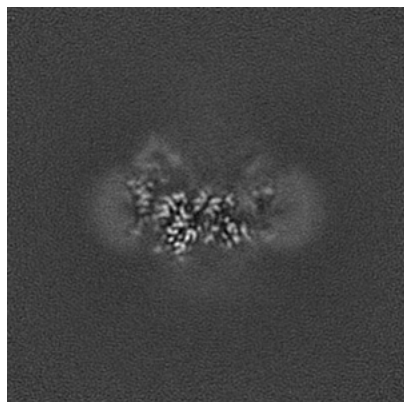


Y Index: 134

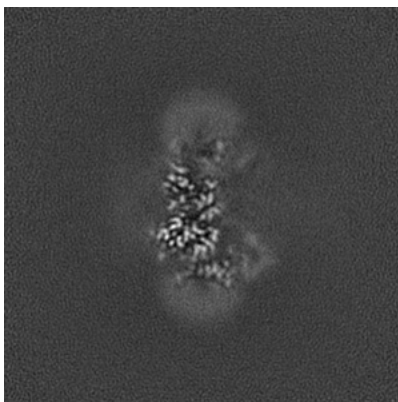


Z Index: 109

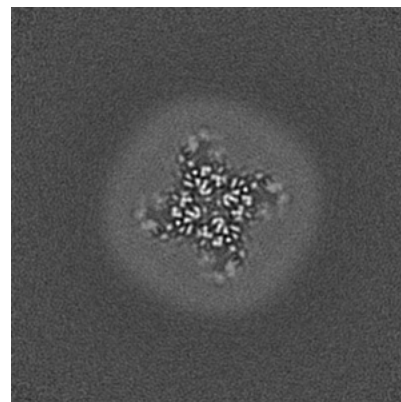
6.3.2 Raw map



X Index: 134



Y Index: 122

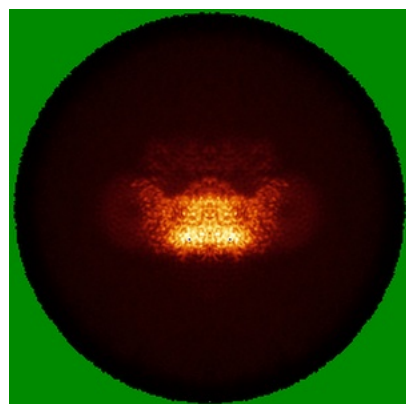


Z Index: 111

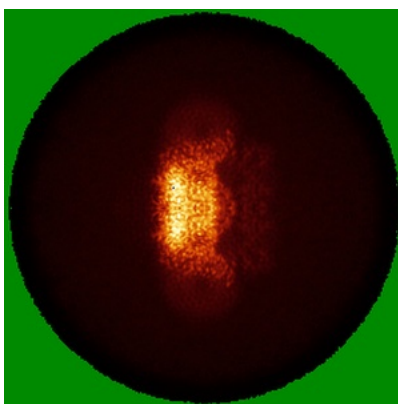
The images above show the largest variance slices of the map in three orthogonal directions.

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

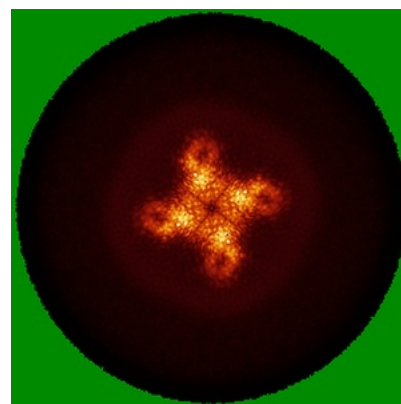
6.4.1 Primary map



X

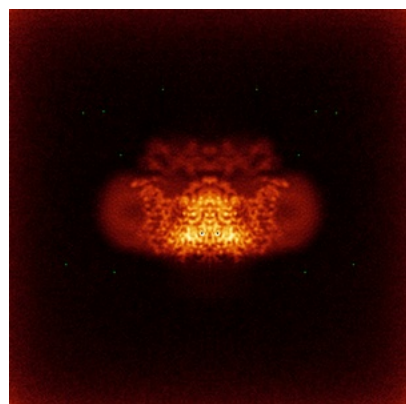


Y

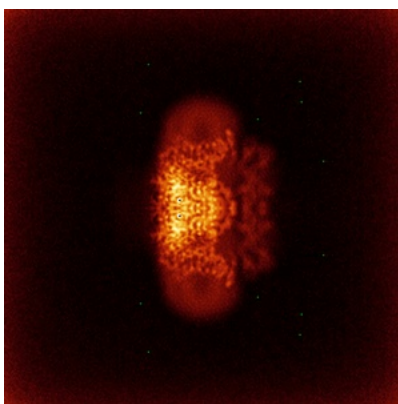


Z

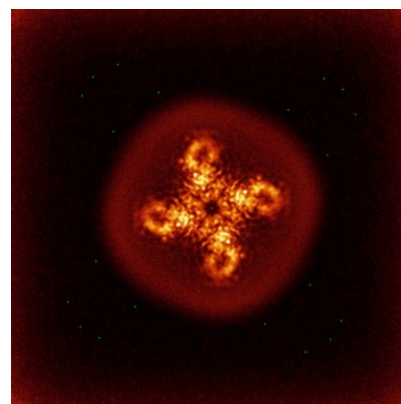
6.4.2 Raw map



X



Y

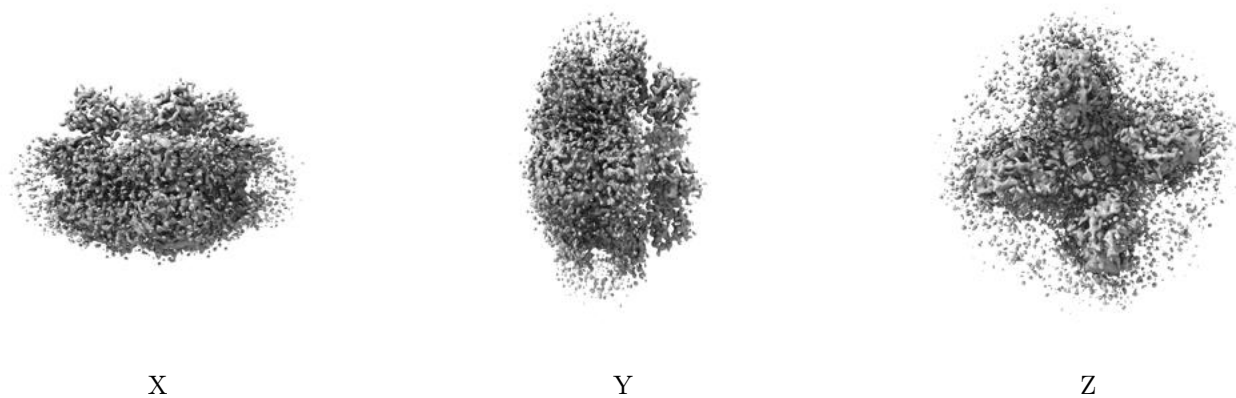


Z

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 0.423. 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.

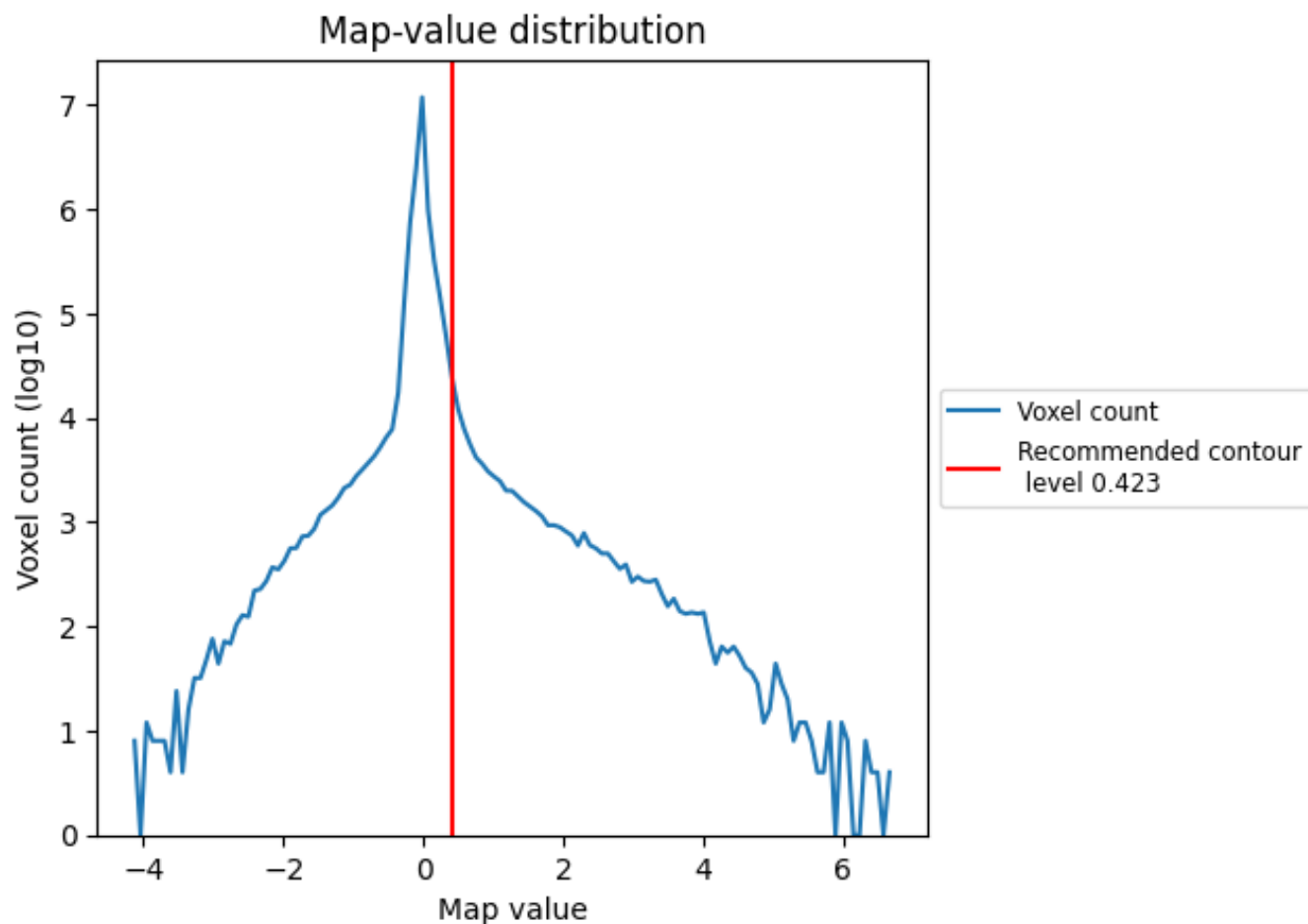
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

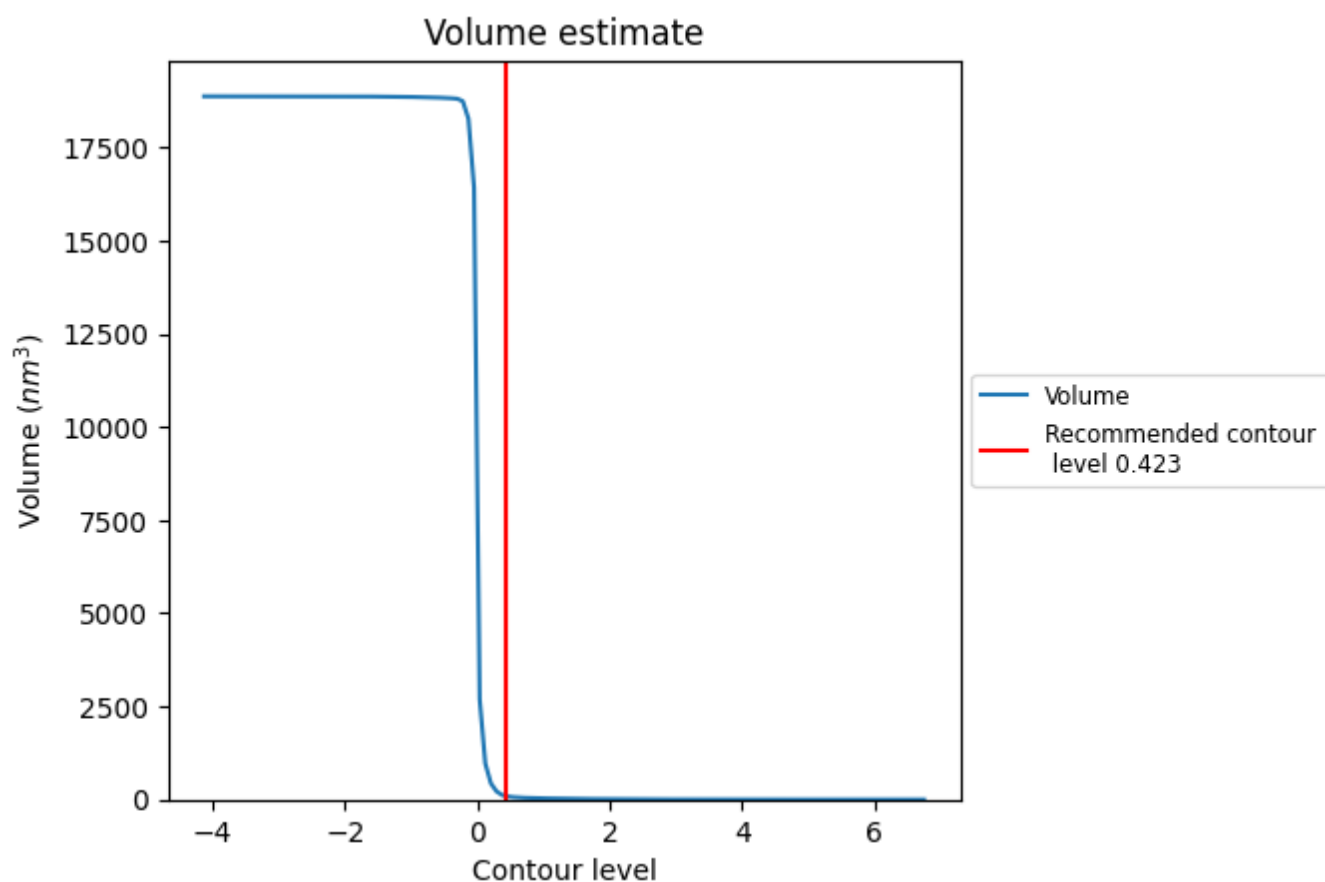
This section contains the results of statistical analysis of the map.

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.

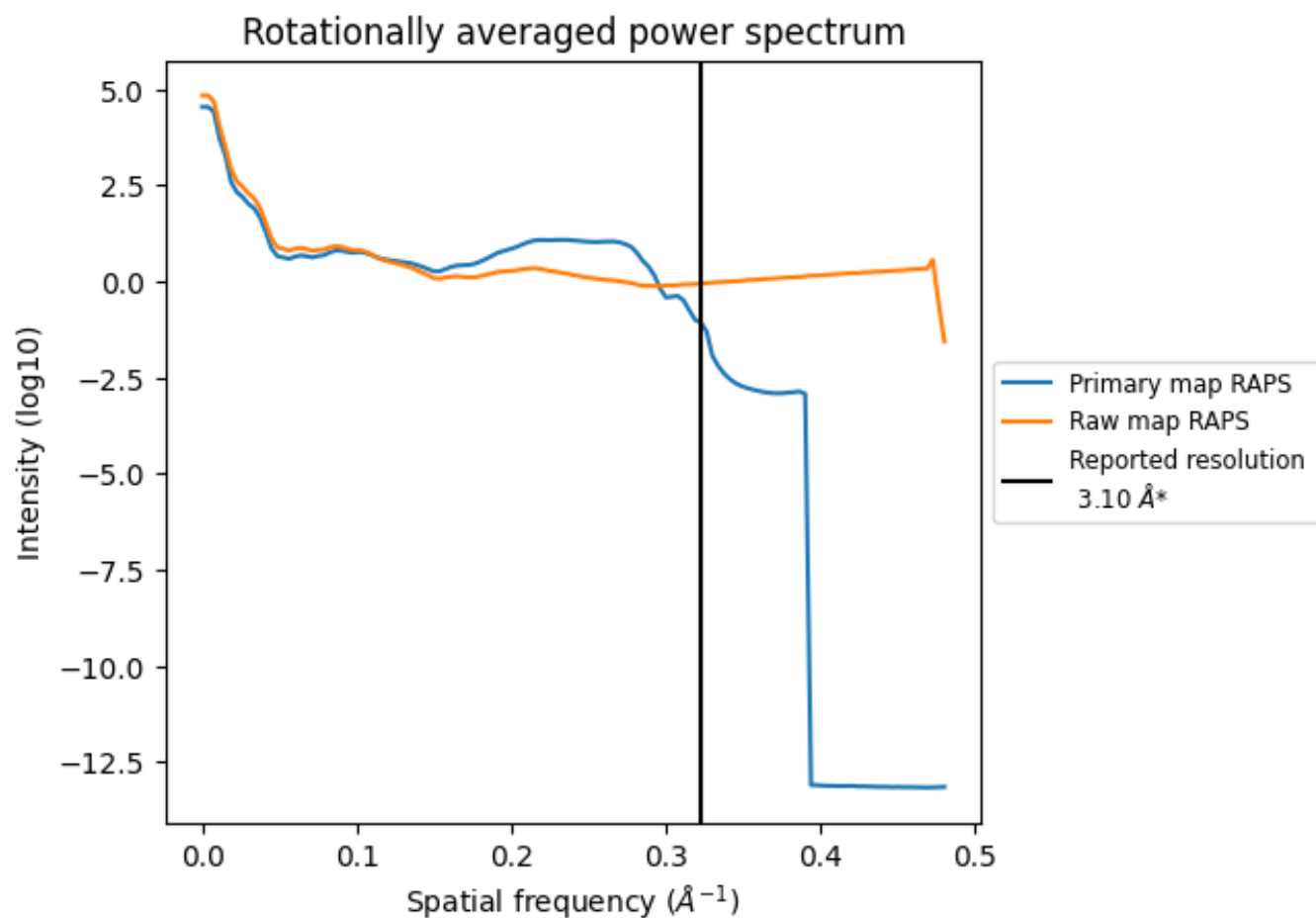
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 100 nm³; this corresponds to an approximate mass of 90 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 ⓘ

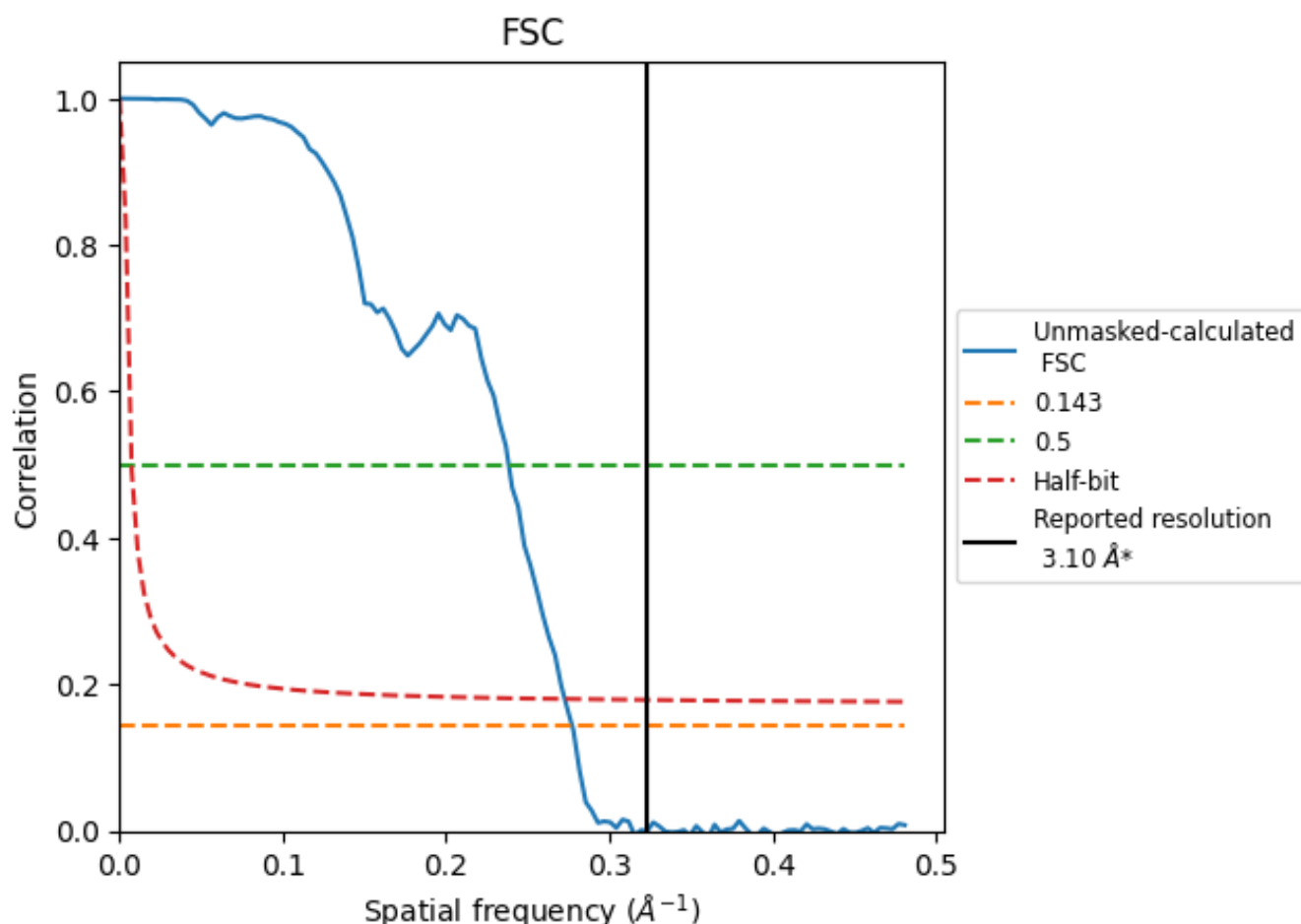


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

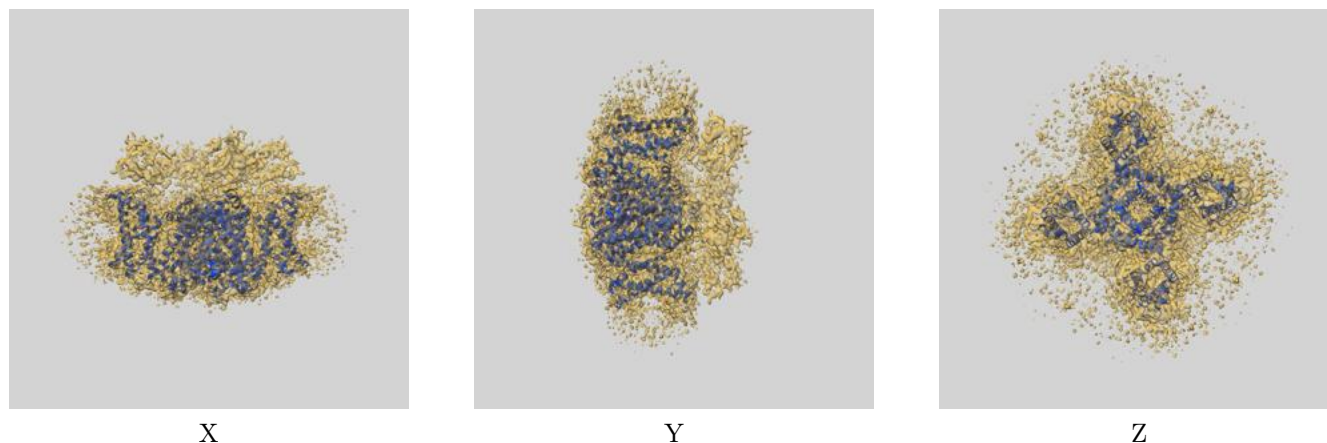
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.61	4.20	3.67

*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 3.61 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

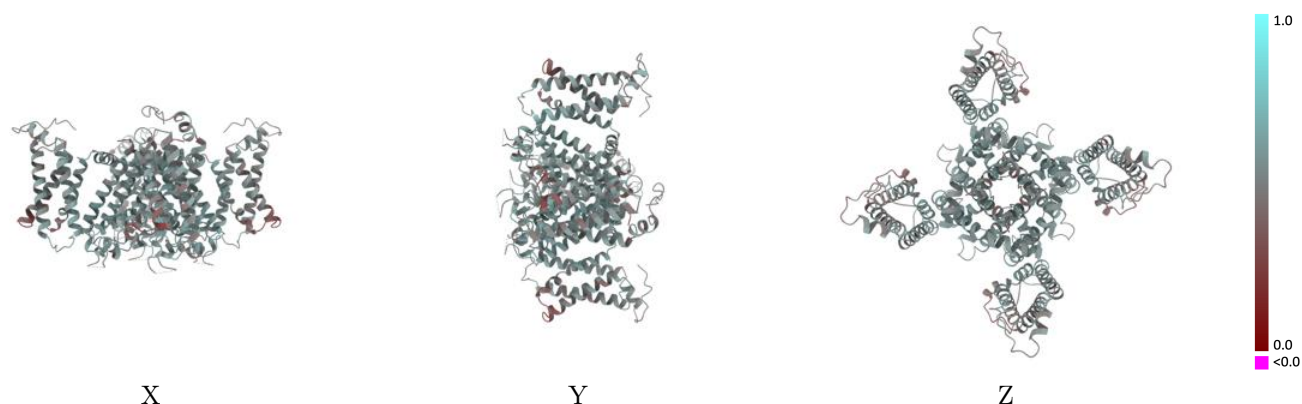
This section contains information regarding the fit between EMDB map EMD-36042 and PDB model 8J7M. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



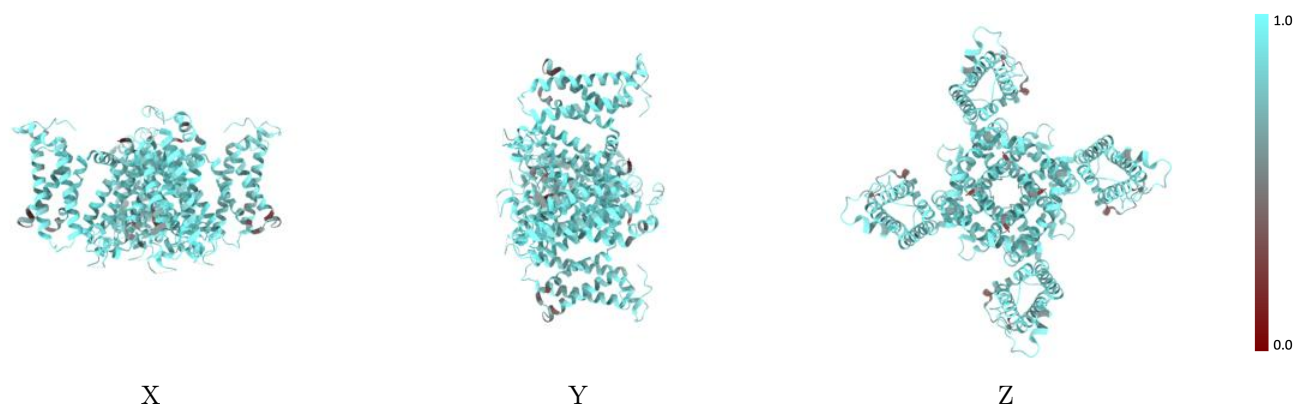
The images above show the 3D surface view of the map at the recommended contour level 0.423 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



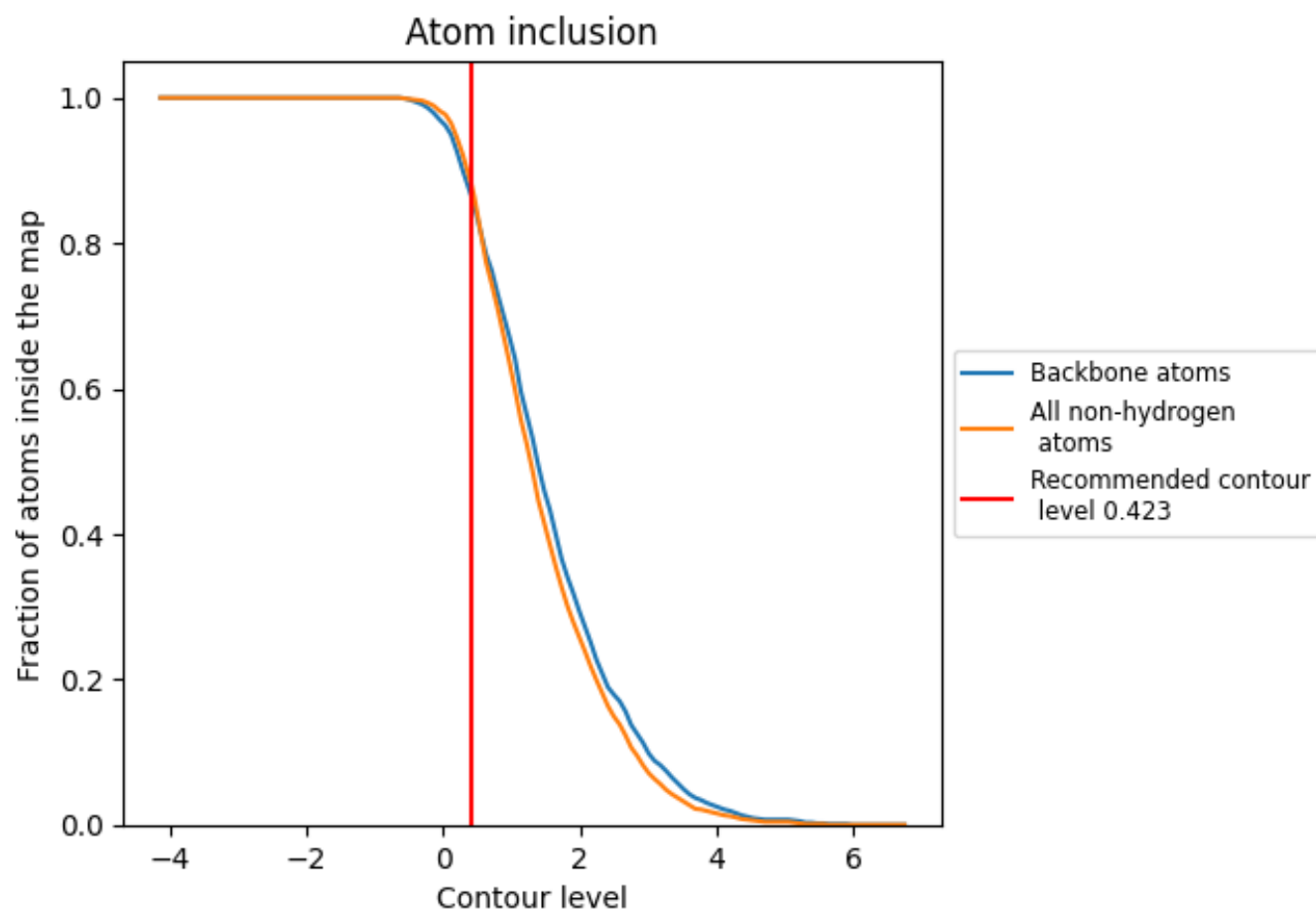
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.423).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 88% 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 (0.423) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8790	<div></div> 0.5300
A	<div></div> 0.8780	<div></div> 0.5300
B	<div></div> 0.8800	<div></div> 0.5290
C	<div></div> 0.8800	<div></div> 0.5290
D	<div></div> 0.8780	<div></div> 0.5310

