



Full wwPDB EM Validation Report ⓘ

Dec 8, 2025 – 05:19 pm GMT

PDB ID : 9QNT / pdb_00009qnt
EMDB ID : EMD-53250
Title : Connexin-32 (Cx32) in MSP2N2 nanodiscs with liver polar lipids
Authors : Korkhov, V.M.; Lavriha, P.
Deposited on : 2025-03-25
Resolution : 3.29 Å(reported)

This is a Full wwPDB EM Validation 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:

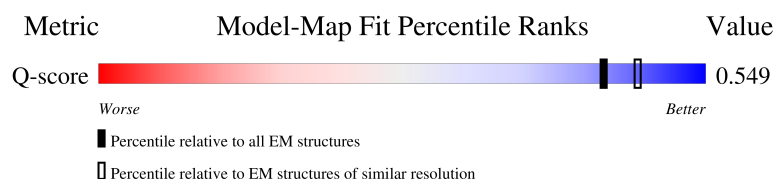
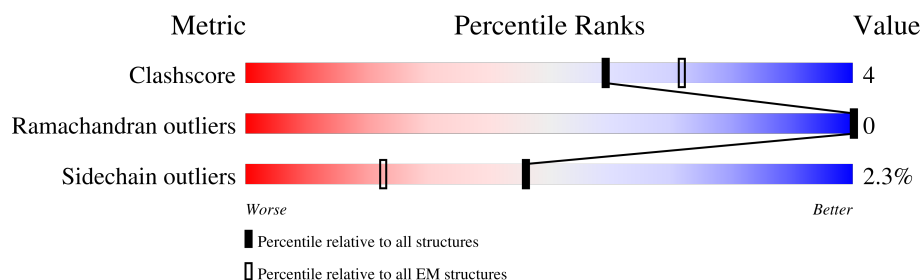
EMDB validation analysis : 0.0.1.dev129
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up 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) : 2.47

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 3.29 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	14466 (2.79 - 3.79)

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	566	
1	B	566	
1	C	566	
1	D	566	

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Mol	Chain	Length	Quality of chain
1	E	566	 30% • 65%
1	F	566	 31% •• 65%
1	G	566	 30% •• 65%
1	H	566	 30% •• 65%
1	I	566	 30% • 65%
1	J	566	 30% • 65%
1	K	566	 30% • 65%
1	L	566	 30% • 65%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19788 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 Gap junction beta-1 protein, Green fluorescent protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	196	Total	C	N	O	S	0	0
			1569	1041	252	261	15		
1	B	196	Total	C	N	O	S	0	0
			1569	1041	252	261	15		
1	C	196	Total	C	N	O	S	0	0
			1569	1041	252	261	15		
1	D	196	Total	C	N	O	S	0	0
			1569	1041	252	261	15		
1	E	196	Total	C	N	O	S	0	0
			1569	1041	252	261	15		
1	F	196	Total	C	N	O	S	0	0
			1569	1041	252	261	15		
1	G	196	Total	C	N	O	S	0	0
			1569	1041	252	261	15		
1	H	196	Total	C	N	O	S	0	0
			1569	1041	252	261	15		
1	I	196	Total	C	N	O	S	0	0
			1569	1041	252	261	15		
1	J	196	Total	C	N	O	S	0	0
			1569	1041	252	261	15		
1	K	196	Total	C	N	O	S	0	0
			1569	1041	252	261	15		
1	L	196	Total	C	N	O	S	0	0
			1569	1041	252	261	15		

There are 612 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	284	ALA	-	linker	UNP P08034
A	285	ALA	-	linker	UNP P08034
A	286	ALA	-	linker	UNP P08034
A	287	LEU	-	linker	UNP P08034
A	288	GLU	-	linker	UNP P08034
A	289	VAL	-	linker	UNP P08034

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Chain	Residue	Modelled	Actual	Comment	Reference
A	290	LEU	-	linker	UNP P08034
A	291	PHE	-	linker	UNP P08034
A	292	GLN	-	linker	UNP P08034
A	293	GLY	-	linker	UNP P08034
A	294	PRO	-	linker	UNP P08034
A	295	GLY	-	linker	UNP P08034
A	296	GLY	-	linker	UNP P08034
A	297	VAL	-	linker	UNP P08034
A	361	GLY	SER	conflict	UNP P42212
A	364	LEU	VAL	conflict	UNP P42212
A	368	ALA	SER	conflict	UNP P42212
A	499	TYR	THR	conflict	UNP P42212
A	527	LEU	HIS	conflict	UNP P42212
A	535	ALA	-	expression tag	UNP P42212
A	536	ALA	-	expression tag	UNP P42212
A	537	SER	-	expression tag	UNP P42212
A	538	ALA	-	expression tag	UNP P42212
A	539	TRP	-	expression tag	UNP P42212
A	540	SER	-	expression tag	UNP P42212
A	541	HIS	-	expression tag	UNP P42212
A	542	PRO	-	expression tag	UNP P42212
A	543	GLN	-	expression tag	UNP P42212
A	544	PHE	-	expression tag	UNP P42212
A	545	GLU	-	expression tag	UNP P42212
A	546	LYS	-	expression tag	UNP P42212
A	547	GLY	-	expression tag	UNP P42212
A	548	GLY	-	expression tag	UNP P42212
A	549	GLY	-	expression tag	UNP P42212
A	550	SER	-	expression tag	UNP P42212
A	551	GLY	-	expression tag	UNP P42212
A	552	GLY	-	expression tag	UNP P42212
A	553	GLY	-	expression tag	UNP P42212
A	554	SER	-	expression tag	UNP P42212
A	555	GLY	-	expression tag	UNP P42212
A	556	GLY	-	expression tag	UNP P42212
A	557	SER	-	expression tag	UNP P42212
A	558	ALA	-	expression tag	UNP P42212
A	559	TRP	-	expression tag	UNP P42212
A	560	SER	-	expression tag	UNP P42212
A	561	HIS	-	expression tag	UNP P42212
A	562	PRO	-	expression tag	UNP P42212
A	563	GLN	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	564	PHE	-	expression tag	UNP P42212
A	565	GLU	-	expression tag	UNP P42212
A	566	LYS	-	expression tag	UNP P42212
B	284	ALA	-	linker	UNP P08034
B	285	ALA	-	linker	UNP P08034
B	286	ALA	-	linker	UNP P08034
B	287	LEU	-	linker	UNP P08034
B	288	GLU	-	linker	UNP P08034
B	289	VAL	-	linker	UNP P08034
B	290	LEU	-	linker	UNP P08034
B	291	PHE	-	linker	UNP P08034
B	292	GLN	-	linker	UNP P08034
B	293	GLY	-	linker	UNP P08034
B	294	PRO	-	linker	UNP P08034
B	295	GLY	-	linker	UNP P08034
B	296	GLY	-	linker	UNP P08034
B	297	VAL	-	linker	UNP P08034
B	361	GLY	SER	conflict	UNP P42212
B	364	LEU	VAL	conflict	UNP P42212
B	368	ALA	SER	conflict	UNP P42212
B	499	TYR	THR	conflict	UNP P42212
B	527	LEU	HIS	conflict	UNP P42212
B	535	ALA	-	expression tag	UNP P42212
B	536	ALA	-	expression tag	UNP P42212
B	537	SER	-	expression tag	UNP P42212
B	538	ALA	-	expression tag	UNP P42212
B	539	TRP	-	expression tag	UNP P42212
B	540	SER	-	expression tag	UNP P42212
B	541	HIS	-	expression tag	UNP P42212
B	542	PRO	-	expression tag	UNP P42212
B	543	GLN	-	expression tag	UNP P42212
B	544	PHE	-	expression tag	UNP P42212
B	545	GLU	-	expression tag	UNP P42212
B	546	LYS	-	expression tag	UNP P42212
B	547	GLY	-	expression tag	UNP P42212
B	548	GLY	-	expression tag	UNP P42212
B	549	GLY	-	expression tag	UNP P42212
B	550	SER	-	expression tag	UNP P42212
B	551	GLY	-	expression tag	UNP P42212
B	552	GLY	-	expression tag	UNP P42212
B	553	GLY	-	expression tag	UNP P42212
B	554	SER	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
B	555	GLY	-	expression tag	UNP P42212
B	556	GLY	-	expression tag	UNP P42212
B	557	SER	-	expression tag	UNP P42212
B	558	ALA	-	expression tag	UNP P42212
B	559	TRP	-	expression tag	UNP P42212
B	560	SER	-	expression tag	UNP P42212
B	561	HIS	-	expression tag	UNP P42212
B	562	PRO	-	expression tag	UNP P42212
B	563	GLN	-	expression tag	UNP P42212
B	564	PHE	-	expression tag	UNP P42212
B	565	GLU	-	expression tag	UNP P42212
B	566	LYS	-	expression tag	UNP P42212
C	284	ALA	-	linker	UNP P08034
C	285	ALA	-	linker	UNP P08034
C	286	ALA	-	linker	UNP P08034
C	287	LEU	-	linker	UNP P08034
C	288	GLU	-	linker	UNP P08034
C	289	VAL	-	linker	UNP P08034
C	290	LEU	-	linker	UNP P08034
C	291	PHE	-	linker	UNP P08034
C	292	GLN	-	linker	UNP P08034
C	293	GLY	-	linker	UNP P08034
C	294	PRO	-	linker	UNP P08034
C	295	GLY	-	linker	UNP P08034
C	296	GLY	-	linker	UNP P08034
C	297	VAL	-	linker	UNP P08034
C	361	GLY	SER	conflict	UNP P42212
C	364	LEU	VAL	conflict	UNP P42212
C	368	ALA	SER	conflict	UNP P42212
C	499	TYR	THR	conflict	UNP P42212
C	527	LEU	HIS	conflict	UNP P42212
C	535	ALA	-	expression tag	UNP P42212
C	536	ALA	-	expression tag	UNP P42212
C	537	SER	-	expression tag	UNP P42212
C	538	ALA	-	expression tag	UNP P42212
C	539	TRP	-	expression tag	UNP P42212
C	540	SER	-	expression tag	UNP P42212
C	541	HIS	-	expression tag	UNP P42212
C	542	PRO	-	expression tag	UNP P42212
C	543	GLN	-	expression tag	UNP P42212
C	544	PHE	-	expression tag	UNP P42212
C	545	GLU	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
C	546	LYS	-	expression tag	UNP P42212
C	547	GLY	-	expression tag	UNP P42212
C	548	GLY	-	expression tag	UNP P42212
C	549	GLY	-	expression tag	UNP P42212
C	550	SER	-	expression tag	UNP P42212
C	551	GLY	-	expression tag	UNP P42212
C	552	GLY	-	expression tag	UNP P42212
C	553	GLY	-	expression tag	UNP P42212
C	554	SER	-	expression tag	UNP P42212
C	555	GLY	-	expression tag	UNP P42212
C	556	GLY	-	expression tag	UNP P42212
C	557	SER	-	expression tag	UNP P42212
C	558	ALA	-	expression tag	UNP P42212
C	559	TRP	-	expression tag	UNP P42212
C	560	SER	-	expression tag	UNP P42212
C	561	HIS	-	expression tag	UNP P42212
C	562	PRO	-	expression tag	UNP P42212
C	563	GLN	-	expression tag	UNP P42212
C	564	PHE	-	expression tag	UNP P42212
C	565	GLU	-	expression tag	UNP P42212
C	566	LYS	-	expression tag	UNP P42212
D	284	ALA	-	linker	UNP P08034
D	285	ALA	-	linker	UNP P08034
D	286	ALA	-	linker	UNP P08034
D	287	LEU	-	linker	UNP P08034
D	288	GLU	-	linker	UNP P08034
D	289	VAL	-	linker	UNP P08034
D	290	LEU	-	linker	UNP P08034
D	291	PHE	-	linker	UNP P08034
D	292	GLN	-	linker	UNP P08034
D	293	GLY	-	linker	UNP P08034
D	294	PRO	-	linker	UNP P08034
D	295	GLY	-	linker	UNP P08034
D	296	GLY	-	linker	UNP P08034
D	297	VAL	-	linker	UNP P08034
D	361	GLY	SER	conflict	UNP P42212
D	364	LEU	VAL	conflict	UNP P42212
D	368	ALA	SER	conflict	UNP P42212
D	499	TYR	THR	conflict	UNP P42212
D	527	LEU	HIS	conflict	UNP P42212
D	535	ALA	-	expression tag	UNP P42212
D	536	ALA	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
D	537	SER	-	expression tag	UNP P42212
D	538	ALA	-	expression tag	UNP P42212
D	539	TRP	-	expression tag	UNP P42212
D	540	SER	-	expression tag	UNP P42212
D	541	HIS	-	expression tag	UNP P42212
D	542	PRO	-	expression tag	UNP P42212
D	543	GLN	-	expression tag	UNP P42212
D	544	PHE	-	expression tag	UNP P42212
D	545	GLU	-	expression tag	UNP P42212
D	546	LYS	-	expression tag	UNP P42212
D	547	GLY	-	expression tag	UNP P42212
D	548	GLY	-	expression tag	UNP P42212
D	549	GLY	-	expression tag	UNP P42212
D	550	SER	-	expression tag	UNP P42212
D	551	GLY	-	expression tag	UNP P42212
D	552	GLY	-	expression tag	UNP P42212
D	553	GLY	-	expression tag	UNP P42212
D	554	SER	-	expression tag	UNP P42212
D	555	GLY	-	expression tag	UNP P42212
D	556	GLY	-	expression tag	UNP P42212
D	557	SER	-	expression tag	UNP P42212
D	558	ALA	-	expression tag	UNP P42212
D	559	TRP	-	expression tag	UNP P42212
D	560	SER	-	expression tag	UNP P42212
D	561	HIS	-	expression tag	UNP P42212
D	562	PRO	-	expression tag	UNP P42212
D	563	GLN	-	expression tag	UNP P42212
D	564	PHE	-	expression tag	UNP P42212
D	565	GLU	-	expression tag	UNP P42212
D	566	LYS	-	expression tag	UNP P42212
E	284	ALA	-	linker	UNP P08034
E	285	ALA	-	linker	UNP P08034
E	286	ALA	-	linker	UNP P08034
E	287	LEU	-	linker	UNP P08034
E	288	GLU	-	linker	UNP P08034
E	289	VAL	-	linker	UNP P08034
E	290	LEU	-	linker	UNP P08034
E	291	PHE	-	linker	UNP P08034
E	292	GLN	-	linker	UNP P08034
E	293	GLY	-	linker	UNP P08034
E	294	PRO	-	linker	UNP P08034
E	295	GLY	-	linker	UNP P08034

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Chain	Residue	Modelled	Actual	Comment	Reference
E	296	GLY	-	linker	UNP P08034
E	297	VAL	-	linker	UNP P08034
E	361	GLY	SER	conflict	UNP P42212
E	364	LEU	VAL	conflict	UNP P42212
E	368	ALA	SER	conflict	UNP P42212
E	499	TYR	THR	conflict	UNP P42212
E	527	LEU	HIS	conflict	UNP P42212
E	535	ALA	-	expression tag	UNP P42212
E	536	ALA	-	expression tag	UNP P42212
E	537	SER	-	expression tag	UNP P42212
E	538	ALA	-	expression tag	UNP P42212
E	539	TRP	-	expression tag	UNP P42212
E	540	SER	-	expression tag	UNP P42212
E	541	HIS	-	expression tag	UNP P42212
E	542	PRO	-	expression tag	UNP P42212
E	543	GLN	-	expression tag	UNP P42212
E	544	PHE	-	expression tag	UNP P42212
E	545	GLU	-	expression tag	UNP P42212
E	546	LYS	-	expression tag	UNP P42212
E	547	GLY	-	expression tag	UNP P42212
E	548	GLY	-	expression tag	UNP P42212
E	549	GLY	-	expression tag	UNP P42212
E	550	SER	-	expression tag	UNP P42212
E	551	GLY	-	expression tag	UNP P42212
E	552	GLY	-	expression tag	UNP P42212
E	553	GLY	-	expression tag	UNP P42212
E	554	SER	-	expression tag	UNP P42212
E	555	GLY	-	expression tag	UNP P42212
E	556	GLY	-	expression tag	UNP P42212
E	557	SER	-	expression tag	UNP P42212
E	558	ALA	-	expression tag	UNP P42212
E	559	TRP	-	expression tag	UNP P42212
E	560	SER	-	expression tag	UNP P42212
E	561	HIS	-	expression tag	UNP P42212
E	562	PRO	-	expression tag	UNP P42212
E	563	GLN	-	expression tag	UNP P42212
E	564	PHE	-	expression tag	UNP P42212
E	565	GLU	-	expression tag	UNP P42212
E	566	LYS	-	expression tag	UNP P42212
F	284	ALA	-	linker	UNP P08034
F	285	ALA	-	linker	UNP P08034
F	286	ALA	-	linker	UNP P08034

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Chain	Residue	Modelled	Actual	Comment	Reference
F	287	LEU	-	linker	UNP P08034
F	288	GLU	-	linker	UNP P08034
F	289	VAL	-	linker	UNP P08034
F	290	LEU	-	linker	UNP P08034
F	291	PHE	-	linker	UNP P08034
F	292	GLN	-	linker	UNP P08034
F	293	GLY	-	linker	UNP P08034
F	294	PRO	-	linker	UNP P08034
F	295	GLY	-	linker	UNP P08034
F	296	GLY	-	linker	UNP P08034
F	297	VAL	-	linker	UNP P08034
F	361	GLY	SER	conflict	UNP P42212
F	364	LEU	VAL	conflict	UNP P42212
F	368	ALA	SER	conflict	UNP P42212
F	499	TYR	THR	conflict	UNP P42212
F	527	LEU	HIS	conflict	UNP P42212
F	535	ALA	-	expression tag	UNP P42212
F	536	ALA	-	expression tag	UNP P42212
F	537	SER	-	expression tag	UNP P42212
F	538	ALA	-	expression tag	UNP P42212
F	539	TRP	-	expression tag	UNP P42212
F	540	SER	-	expression tag	UNP P42212
F	541	HIS	-	expression tag	UNP P42212
F	542	PRO	-	expression tag	UNP P42212
F	543	GLN	-	expression tag	UNP P42212
F	544	PHE	-	expression tag	UNP P42212
F	545	GLU	-	expression tag	UNP P42212
F	546	LYS	-	expression tag	UNP P42212
F	547	GLY	-	expression tag	UNP P42212
F	548	GLY	-	expression tag	UNP P42212
F	549	GLY	-	expression tag	UNP P42212
F	550	SER	-	expression tag	UNP P42212
F	551	GLY	-	expression tag	UNP P42212
F	552	GLY	-	expression tag	UNP P42212
F	553	GLY	-	expression tag	UNP P42212
F	554	SER	-	expression tag	UNP P42212
F	555	GLY	-	expression tag	UNP P42212
F	556	GLY	-	expression tag	UNP P42212
F	557	SER	-	expression tag	UNP P42212
F	558	ALA	-	expression tag	UNP P42212
F	559	TRP	-	expression tag	UNP P42212
F	560	SER	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
F	561	HIS	-	expression tag	UNP P42212
F	562	PRO	-	expression tag	UNP P42212
F	563	GLN	-	expression tag	UNP P42212
F	564	PHE	-	expression tag	UNP P42212
F	565	GLU	-	expression tag	UNP P42212
F	566	LYS	-	expression tag	UNP P42212
G	284	ALA	-	linker	UNP P08034
G	285	ALA	-	linker	UNP P08034
G	286	ALA	-	linker	UNP P08034
G	287	LEU	-	linker	UNP P08034
G	288	GLU	-	linker	UNP P08034
G	289	VAL	-	linker	UNP P08034
G	290	LEU	-	linker	UNP P08034
G	291	PHE	-	linker	UNP P08034
G	292	GLN	-	linker	UNP P08034
G	293	GLY	-	linker	UNP P08034
G	294	PRO	-	linker	UNP P08034
G	295	GLY	-	linker	UNP P08034
G	296	GLY	-	linker	UNP P08034
G	297	VAL	-	linker	UNP P08034
G	361	GLY	SER	conflict	UNP P42212
G	364	LEU	VAL	conflict	UNP P42212
G	368	ALA	SER	conflict	UNP P42212
G	499	TYR	THR	conflict	UNP P42212
G	527	LEU	HIS	conflict	UNP P42212
G	535	ALA	-	expression tag	UNP P42212
G	536	ALA	-	expression tag	UNP P42212
G	537	SER	-	expression tag	UNP P42212
G	538	ALA	-	expression tag	UNP P42212
G	539	TRP	-	expression tag	UNP P42212
G	540	SER	-	expression tag	UNP P42212
G	541	HIS	-	expression tag	UNP P42212
G	542	PRO	-	expression tag	UNP P42212
G	543	GLN	-	expression tag	UNP P42212
G	544	PHE	-	expression tag	UNP P42212
G	545	GLU	-	expression tag	UNP P42212
G	546	LYS	-	expression tag	UNP P42212
G	547	GLY	-	expression tag	UNP P42212
G	548	GLY	-	expression tag	UNP P42212
G	549	GLY	-	expression tag	UNP P42212
G	550	SER	-	expression tag	UNP P42212
G	551	GLY	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
G	552	GLY	-	expression tag	UNP P42212
G	553	GLY	-	expression tag	UNP P42212
G	554	SER	-	expression tag	UNP P42212
G	555	GLY	-	expression tag	UNP P42212
G	556	GLY	-	expression tag	UNP P42212
G	557	SER	-	expression tag	UNP P42212
G	558	ALA	-	expression tag	UNP P42212
G	559	TRP	-	expression tag	UNP P42212
G	560	SER	-	expression tag	UNP P42212
G	561	HIS	-	expression tag	UNP P42212
G	562	PRO	-	expression tag	UNP P42212
G	563	GLN	-	expression tag	UNP P42212
G	564	PHE	-	expression tag	UNP P42212
G	565	GLU	-	expression tag	UNP P42212
G	566	LYS	-	expression tag	UNP P42212
H	284	ALA	-	linker	UNP P08034
H	285	ALA	-	linker	UNP P08034
H	286	ALA	-	linker	UNP P08034
H	287	LEU	-	linker	UNP P08034
H	288	GLU	-	linker	UNP P08034
H	289	VAL	-	linker	UNP P08034
H	290	LEU	-	linker	UNP P08034
H	291	PHE	-	linker	UNP P08034
H	292	GLN	-	linker	UNP P08034
H	293	GLY	-	linker	UNP P08034
H	294	PRO	-	linker	UNP P08034
H	295	GLY	-	linker	UNP P08034
H	296	GLY	-	linker	UNP P08034
H	297	VAL	-	linker	UNP P08034
H	361	GLY	SER	conflict	UNP P42212
H	364	LEU	VAL	conflict	UNP P42212
H	368	ALA	SER	conflict	UNP P42212
H	499	TYR	THR	conflict	UNP P42212
H	527	LEU	HIS	conflict	UNP P42212
H	535	ALA	-	expression tag	UNP P42212
H	536	ALA	-	expression tag	UNP P42212
H	537	SER	-	expression tag	UNP P42212
H	538	ALA	-	expression tag	UNP P42212
H	539	TRP	-	expression tag	UNP P42212
H	540	SER	-	expression tag	UNP P42212
H	541	HIS	-	expression tag	UNP P42212
H	542	PRO	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
H	543	GLN	-	expression tag	UNP P42212
H	544	PHE	-	expression tag	UNP P42212
H	545	GLU	-	expression tag	UNP P42212
H	546	LYS	-	expression tag	UNP P42212
H	547	GLY	-	expression tag	UNP P42212
H	548	GLY	-	expression tag	UNP P42212
H	549	GLY	-	expression tag	UNP P42212
H	550	SER	-	expression tag	UNP P42212
H	551	GLY	-	expression tag	UNP P42212
H	552	GLY	-	expression tag	UNP P42212
H	553	GLY	-	expression tag	UNP P42212
H	554	SER	-	expression tag	UNP P42212
H	555	GLY	-	expression tag	UNP P42212
H	556	GLY	-	expression tag	UNP P42212
H	557	SER	-	expression tag	UNP P42212
H	558	ALA	-	expression tag	UNP P42212
H	559	TRP	-	expression tag	UNP P42212
H	560	SER	-	expression tag	UNP P42212
H	561	HIS	-	expression tag	UNP P42212
H	562	PRO	-	expression tag	UNP P42212
H	563	GLN	-	expression tag	UNP P42212
H	564	PHE	-	expression tag	UNP P42212
H	565	GLU	-	expression tag	UNP P42212
H	566	LYS	-	expression tag	UNP P42212
I	284	ALA	-	linker	UNP P08034
I	285	ALA	-	linker	UNP P08034
I	286	ALA	-	linker	UNP P08034
I	287	LEU	-	linker	UNP P08034
I	288	GLU	-	linker	UNP P08034
I	289	VAL	-	linker	UNP P08034
I	290	LEU	-	linker	UNP P08034
I	291	PHE	-	linker	UNP P08034
I	292	GLN	-	linker	UNP P08034
I	293	GLY	-	linker	UNP P08034
I	294	PRO	-	linker	UNP P08034
I	295	GLY	-	linker	UNP P08034
I	296	GLY	-	linker	UNP P08034
I	297	VAL	-	linker	UNP P08034
I	361	GLY	SER	conflict	UNP P42212
I	364	LEU	VAL	conflict	UNP P42212
I	368	ALA	SER	conflict	UNP P42212
I	499	TYR	THR	conflict	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
I	527	LEU	HIS	conflict	UNP P42212
I	535	ALA	-	expression tag	UNP P42212
I	536	ALA	-	expression tag	UNP P42212
I	537	SER	-	expression tag	UNP P42212
I	538	ALA	-	expression tag	UNP P42212
I	539	TRP	-	expression tag	UNP P42212
I	540	SER	-	expression tag	UNP P42212
I	541	HIS	-	expression tag	UNP P42212
I	542	PRO	-	expression tag	UNP P42212
I	543	GLN	-	expression tag	UNP P42212
I	544	PHE	-	expression tag	UNP P42212
I	545	GLU	-	expression tag	UNP P42212
I	546	LYS	-	expression tag	UNP P42212
I	547	GLY	-	expression tag	UNP P42212
I	548	GLY	-	expression tag	UNP P42212
I	549	GLY	-	expression tag	UNP P42212
I	550	SER	-	expression tag	UNP P42212
I	551	GLY	-	expression tag	UNP P42212
I	552	GLY	-	expression tag	UNP P42212
I	553	GLY	-	expression tag	UNP P42212
I	554	SER	-	expression tag	UNP P42212
I	555	GLY	-	expression tag	UNP P42212
I	556	GLY	-	expression tag	UNP P42212
I	557	SER	-	expression tag	UNP P42212
I	558	ALA	-	expression tag	UNP P42212
I	559	TRP	-	expression tag	UNP P42212
I	560	SER	-	expression tag	UNP P42212
I	561	HIS	-	expression tag	UNP P42212
I	562	PRO	-	expression tag	UNP P42212
I	563	GLN	-	expression tag	UNP P42212
I	564	PHE	-	expression tag	UNP P42212
I	565	GLU	-	expression tag	UNP P42212
I	566	LYS	-	expression tag	UNP P42212
J	284	ALA	-	linker	UNP P08034
J	285	ALA	-	linker	UNP P08034
J	286	ALA	-	linker	UNP P08034
J	287	LEU	-	linker	UNP P08034
J	288	GLU	-	linker	UNP P08034
J	289	VAL	-	linker	UNP P08034
J	290	LEU	-	linker	UNP P08034
J	291	PHE	-	linker	UNP P08034
J	292	GLN	-	linker	UNP P08034

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Chain	Residue	Modelled	Actual	Comment	Reference
J	293	GLY	-	linker	UNP P08034
J	294	PRO	-	linker	UNP P08034
J	295	GLY	-	linker	UNP P08034
J	296	GLY	-	linker	UNP P08034
J	297	VAL	-	linker	UNP P08034
J	361	GLY	SER	conflict	UNP P42212
J	364	LEU	VAL	conflict	UNP P42212
J	368	ALA	SER	conflict	UNP P42212
J	499	TYR	THR	conflict	UNP P42212
J	527	LEU	HIS	conflict	UNP P42212
J	535	ALA	-	expression tag	UNP P42212
J	536	ALA	-	expression tag	UNP P42212
J	537	SER	-	expression tag	UNP P42212
J	538	ALA	-	expression tag	UNP P42212
J	539	TRP	-	expression tag	UNP P42212
J	540	SER	-	expression tag	UNP P42212
J	541	HIS	-	expression tag	UNP P42212
J	542	PRO	-	expression tag	UNP P42212
J	543	GLN	-	expression tag	UNP P42212
J	544	PHE	-	expression tag	UNP P42212
J	545	GLU	-	expression tag	UNP P42212
J	546	LYS	-	expression tag	UNP P42212
J	547	GLY	-	expression tag	UNP P42212
J	548	GLY	-	expression tag	UNP P42212
J	549	GLY	-	expression tag	UNP P42212
J	550	SER	-	expression tag	UNP P42212
J	551	GLY	-	expression tag	UNP P42212
J	552	GLY	-	expression tag	UNP P42212
J	553	GLY	-	expression tag	UNP P42212
J	554	SER	-	expression tag	UNP P42212
J	555	GLY	-	expression tag	UNP P42212
J	556	GLY	-	expression tag	UNP P42212
J	557	SER	-	expression tag	UNP P42212
J	558	ALA	-	expression tag	UNP P42212
J	559	TRP	-	expression tag	UNP P42212
J	560	SER	-	expression tag	UNP P42212
J	561	HIS	-	expression tag	UNP P42212
J	562	PRO	-	expression tag	UNP P42212
J	563	GLN	-	expression tag	UNP P42212
J	564	PHE	-	expression tag	UNP P42212
J	565	GLU	-	expression tag	UNP P42212
J	566	LYS	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
K	284	ALA	-	linker	UNP P08034
K	285	ALA	-	linker	UNP P08034
K	286	ALA	-	linker	UNP P08034
K	287	LEU	-	linker	UNP P08034
K	288	GLU	-	linker	UNP P08034
K	289	VAL	-	linker	UNP P08034
K	290	LEU	-	linker	UNP P08034
K	291	PHE	-	linker	UNP P08034
K	292	GLN	-	linker	UNP P08034
K	293	GLY	-	linker	UNP P08034
K	294	PRO	-	linker	UNP P08034
K	295	GLY	-	linker	UNP P08034
K	296	GLY	-	linker	UNP P08034
K	297	VAL	-	linker	UNP P08034
K	361	GLY	SER	conflict	UNP P42212
K	364	LEU	VAL	conflict	UNP P42212
K	368	ALA	SER	conflict	UNP P42212
K	499	TYR	THR	conflict	UNP P42212
K	527	LEU	HIS	conflict	UNP P42212
K	535	ALA	-	expression tag	UNP P42212
K	536	ALA	-	expression tag	UNP P42212
K	537	SER	-	expression tag	UNP P42212
K	538	ALA	-	expression tag	UNP P42212
K	539	TRP	-	expression tag	UNP P42212
K	540	SER	-	expression tag	UNP P42212
K	541	HIS	-	expression tag	UNP P42212
K	542	PRO	-	expression tag	UNP P42212
K	543	GLN	-	expression tag	UNP P42212
K	544	PHE	-	expression tag	UNP P42212
K	545	GLU	-	expression tag	UNP P42212
K	546	LYS	-	expression tag	UNP P42212
K	547	GLY	-	expression tag	UNP P42212
K	548	GLY	-	expression tag	UNP P42212
K	549	GLY	-	expression tag	UNP P42212
K	550	SER	-	expression tag	UNP P42212
K	551	GLY	-	expression tag	UNP P42212
K	552	GLY	-	expression tag	UNP P42212
K	553	GLY	-	expression tag	UNP P42212
K	554	SER	-	expression tag	UNP P42212
K	555	GLY	-	expression tag	UNP P42212
K	556	GLY	-	expression tag	UNP P42212
K	557	SER	-	expression tag	UNP P42212

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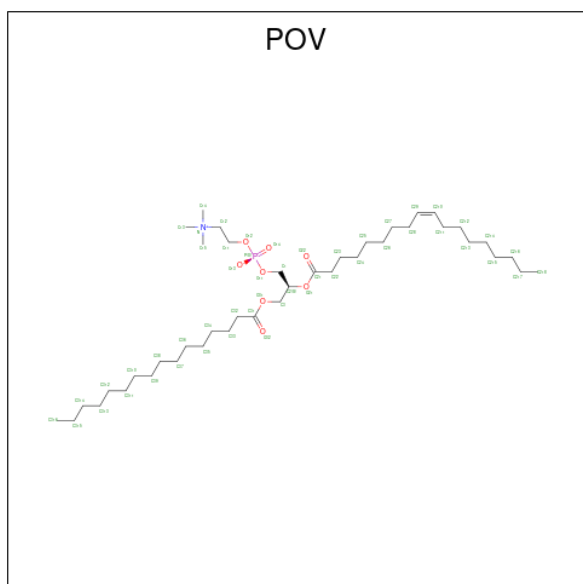
Chain	Residue	Modelled	Actual	Comment	Reference
K	558	ALA	-	expression tag	UNP P42212
K	559	TRP	-	expression tag	UNP P42212
K	560	SER	-	expression tag	UNP P42212
K	561	HIS	-	expression tag	UNP P42212
K	562	PRO	-	expression tag	UNP P42212
K	563	GLN	-	expression tag	UNP P42212
K	564	PHE	-	expression tag	UNP P42212
K	565	GLU	-	expression tag	UNP P42212
K	566	LYS	-	expression tag	UNP P42212
L	284	ALA	-	linker	UNP P08034
L	285	ALA	-	linker	UNP P08034
L	286	ALA	-	linker	UNP P08034
L	287	LEU	-	linker	UNP P08034
L	288	GLU	-	linker	UNP P08034
L	289	VAL	-	linker	UNP P08034
L	290	LEU	-	linker	UNP P08034
L	291	PHE	-	linker	UNP P08034
L	292	GLN	-	linker	UNP P08034
L	293	GLY	-	linker	UNP P08034
L	294	PRO	-	linker	UNP P08034
L	295	GLY	-	linker	UNP P08034
L	296	GLY	-	linker	UNP P08034
L	297	VAL	-	linker	UNP P08034
L	361	GLY	SER	conflict	UNP P42212
L	364	LEU	VAL	conflict	UNP P42212
L	368	ALA	SER	conflict	UNP P42212
L	499	TYR	THR	conflict	UNP P42212
L	527	LEU	HIS	conflict	UNP P42212
L	535	ALA	-	expression tag	UNP P42212
L	536	ALA	-	expression tag	UNP P42212
L	537	SER	-	expression tag	UNP P42212
L	538	ALA	-	expression tag	UNP P42212
L	539	TRP	-	expression tag	UNP P42212
L	540	SER	-	expression tag	UNP P42212
L	541	HIS	-	expression tag	UNP P42212
L	542	PRO	-	expression tag	UNP P42212
L	543	GLN	-	expression tag	UNP P42212
L	544	PHE	-	expression tag	UNP P42212
L	545	GLU	-	expression tag	UNP P42212
L	546	LYS	-	expression tag	UNP P42212
L	547	GLY	-	expression tag	UNP P42212
L	548	GLY	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
L	549	GLY	-	expression tag	UNP P42212
L	550	SER	-	expression tag	UNP P42212
L	551	GLY	-	expression tag	UNP P42212
L	552	GLY	-	expression tag	UNP P42212
L	553	GLY	-	expression tag	UNP P42212
L	554	SER	-	expression tag	UNP P42212
L	555	GLY	-	expression tag	UNP P42212
L	556	GLY	-	expression tag	UNP P42212
L	557	SER	-	expression tag	UNP P42212
L	558	ALA	-	expression tag	UNP P42212
L	559	TRP	-	expression tag	UNP P42212
L	560	SER	-	expression tag	UNP P42212
L	561	HIS	-	expression tag	UNP P42212
L	562	PRO	-	expression tag	UNP P42212
L	563	GLN	-	expression tag	UNP P42212
L	564	PHE	-	expression tag	UNP P42212
L	565	GLU	-	expression tag	UNP P42212
L	566	LYS	-	expression tag	UNP P42212

- Molecule 2 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylammonio)ethyl phosphate (CCD ID: POV) (formula: C₄₂H₈₂NO₈P) (labeled as "Ligand of Interest" by depositor).



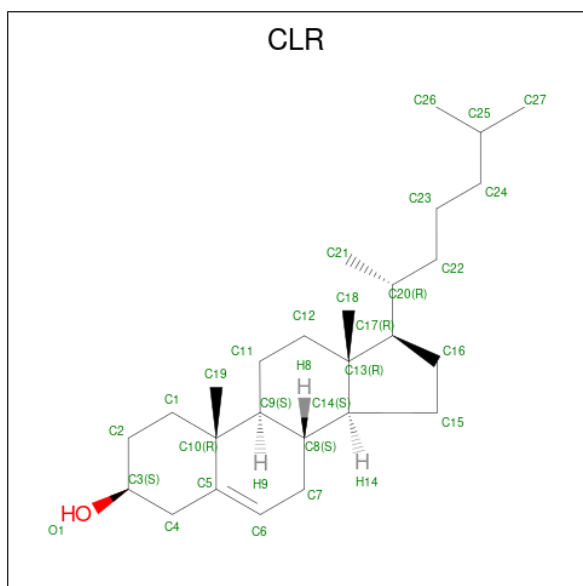
Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			52	42	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
2	B	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	C	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	D	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	E	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	F	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	G	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	H	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	I	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	J	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	K	1	Total	C	N	O	P	0
			52	42	1	8	1	
2	L	1	Total	C	N	O	P	0
			52	42	1	8	1	

- Molecule 3 is CHOLESTEROL (CCD ID: CLR) (formula: $C_{27}H_{46}O$) (labeled as "Ligand of Interest" by depositor).

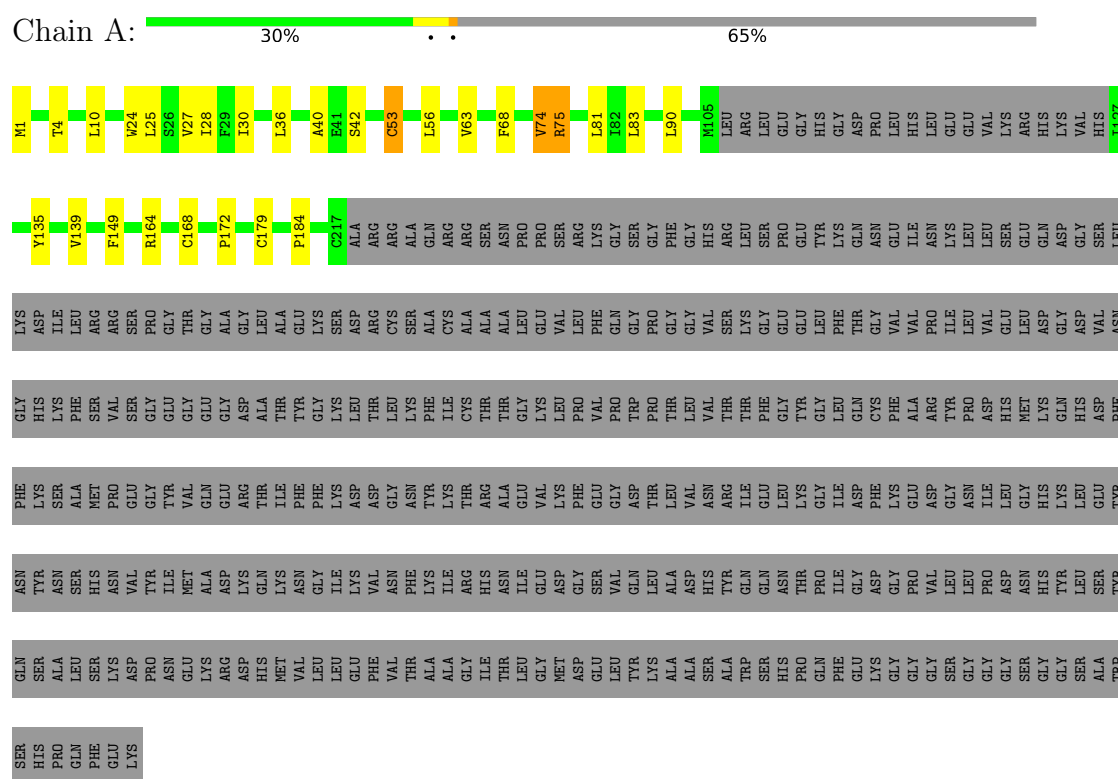


Mol	Chain	Residues	Atoms			AltConf
3	A	1	Total	C	O	0
			28	27	1	
3	B	1	Total	C	O	0
			28	27	1	
3	C	1	Total	C	O	0
			28	27	1	
3	D	1	Total	C	O	0
			28	27	1	
3	E	1	Total	C	O	0
			28	27	1	
3	F	1	Total	C	O	0
			28	27	1	
3	G	1	Total	C	O	0
			28	27	1	
3	H	1	Total	C	O	0
			28	27	1	
3	I	1	Total	C	O	0
			28	27	1	
3	J	1	Total	C	O	0
			28	27	1	
3	K	1	Total	C	O	0
			28	27	1	
3	L	1	Total	C	O	0
			28	27	1	

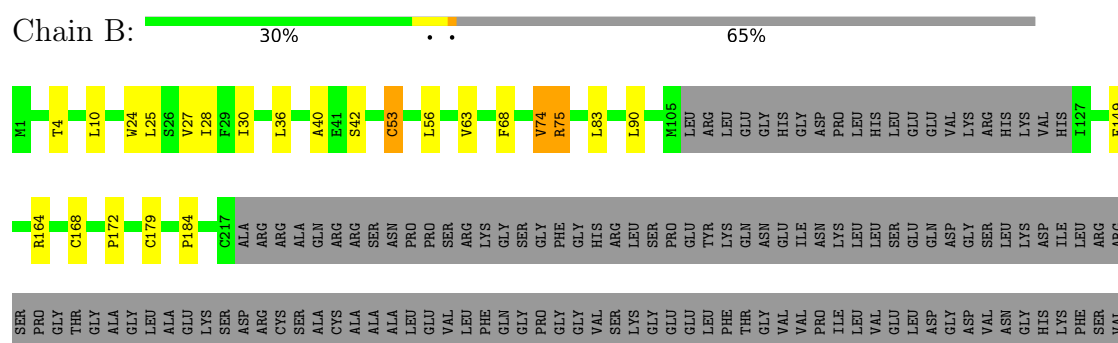
3 Residue-property plots

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: Gap junction beta-1 protein, Green fluorescent protein



- Molecule 1: Gap junction beta-1 protein, Green fluorescent protein



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

- Molecule 1: Gap junction beta-1 protein, Green fluorescent protein

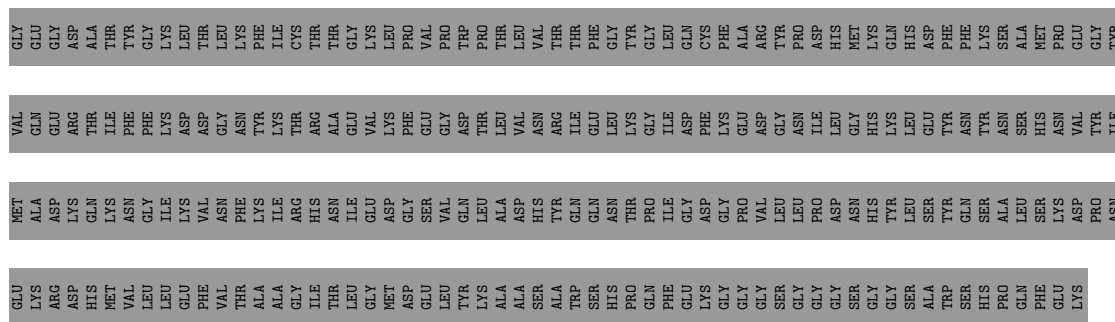
Chain C: 

HIS	PRO	ALA	TYR	LYS	HIS	ASP	Y135	MI
	PRO	GLN	ASN	SER	LYS	ILE	LEU	T4
	PHE	SER	HIS	MET	PHE	SER	ARG	L10
	GLU	LYS	ASN	PRO	VAL	LYS	ARG	W24
	LYS	ASP	VAL	GLU	SER	SER	ASP	W24
	PRO	PRO	TYR	TYR	GLY	PRO	GLY	V27
	GLU	ASN	ILE	VAL	GLY	THR	GLY	C168
	LYS	LYS	ALA	GLN	GLY	GLY	GLY	V29
	ARG	ASP	ASP	GLU	GLY	ALA	GLY	I30
	ASP	LYS	LYS	ARG	ASP	GLY	GLY	I30
HIS	HIS	HIS	GLN	THR	ALA	LEU	LEU	L36
	MET	MET	ASN	PHE	TYR	GLU	GLU	L36
	VAL	VAL	ASN	PHE	THR	GLU	GLU	L212
	LEU	GLY	GLY	PHE	GLY	LYS	LYS	C217
	LEU	ILE	ILE	LYS	LYS	SER	SER	F41
	GLU	LYS	LYS	ASP	LEU	ASP	ASP	S42
	PHE	VAL	VAL	ASP	THR	ARG	ARG	S42
	VAL	ASN	ASN	GLY	LEU	CYS	CYS	C53
	THR	PHE	PHE	ASN	LYS	SER	ALA	C53
	ALA	LYS	LYS	TYR	PHE	ALA	GLN	L56
HIS	ALA	ILE	ILE	LYS	ILE	CYS	ARG	L56
	GLY	ARG	THR	LYS	CYS	ALA	ARG	V63
	ILE	HIS	THR	ARG	THR	ALA	SER	V63
	THR	THR	ASN	ALA	THR	ALA	ASN	F68
	LEU	ILE	ILE	GLU	GLY	LEU	PRO	F68
	GLY	GLU	GLU	VAL	LYS	GLU	PRO	V74
	MET	ASP	ASP	LYS	LEU	VAL	SER	V74
	ASP	GLY	GLY	PHE	PRO	LEU	ARG	R75
	GLU	SER	SER	GLY	VAL	PHE	LYS	R81
	LEU	VAL	VAL	GLY	GLN	GLY	GLY	R81
HIS	TYR	TYR	GLN	ASP	TRP	GLN	SER	L83
	LYS	LYS	LEU	THR	PRO	PRO	GLY	L83
	ALA	ALA	ALA	LEU	THR	GLY	PHE	L90
	ALA	ASP	VAL	VAL	LEU	GLY	GLY	L90
	SER	HIS	HIS	ASN	VAL	VAL	HIS	MI05
	ALA	ALA	TYR	ARG	THR	SER	ARG	LEU
	TRP	ALA	GLN	ILE	THR	LYS	ARG	ARG
	SER	SER	GLN	GLY	PHE	GLY	SER	LEU
	PRO	HIS	ASN	LEU	GLY	GLY	PRO	GLU
	PRO	GLN	THR	LYS	TYR	GLU	GLU	GLY
HIS	PHE	ILE	ILE	ILE	LEU	PHE	TYR	GLY
	GLU	GLY	GLY	ASP	GLN	THR	LYS	GLY
	LYS	LYS	ASP	PHE	CYS	GLY	ASN	PRO
	GLY	GLY	GLY	LYS	PHE	VAL	GLU	LEU
	PRO	PRO	VAL	GLU	ALA	VAL	ILE	SER
	GLY	VAL	VAL	ASP	ARG	PRO	ASN	HIS
	SER	LEU	LEU	GLY	TYR	ILE	LYS	GLU
	GLY	LEU	ASN	ASN	PRO	LEU	LEU	VAL
	GLY	PRO	ILE	ILE	ASP	VAL	SER	LYS
	SER	ASN	GLY	GLY	MET	GLU	GLU	ARG
HIS	GLY	HIS	HIS	LYS	LYS	ASP	GLN	HIS
	GLY	TYR	TYR	LYS	GLN	GLY	ASP	LYS
	LEU	LEU	LEU	LEU	HIS	GLY	VAL	VAL
	ALA	SER	SER	GLU	ASP	VAL	SER	HIS
	TRP	TRP	TYR	TYR	PHE	ASN	LEU	I127
	SER	SER	GLN	ASN	PHE	GLY	LYS	I127
	PRO	PRO	GLN	ASN	THR	GLY	LYS	I127
	GLY	GLY	GLY	GLY	THR	GLY	LYS	I127
	GLY	GLY	GLY	GLY	THR	GLY	LYS	I127
	GLY	GLY	GLY	GLY	THR	GLY	LYS	I127

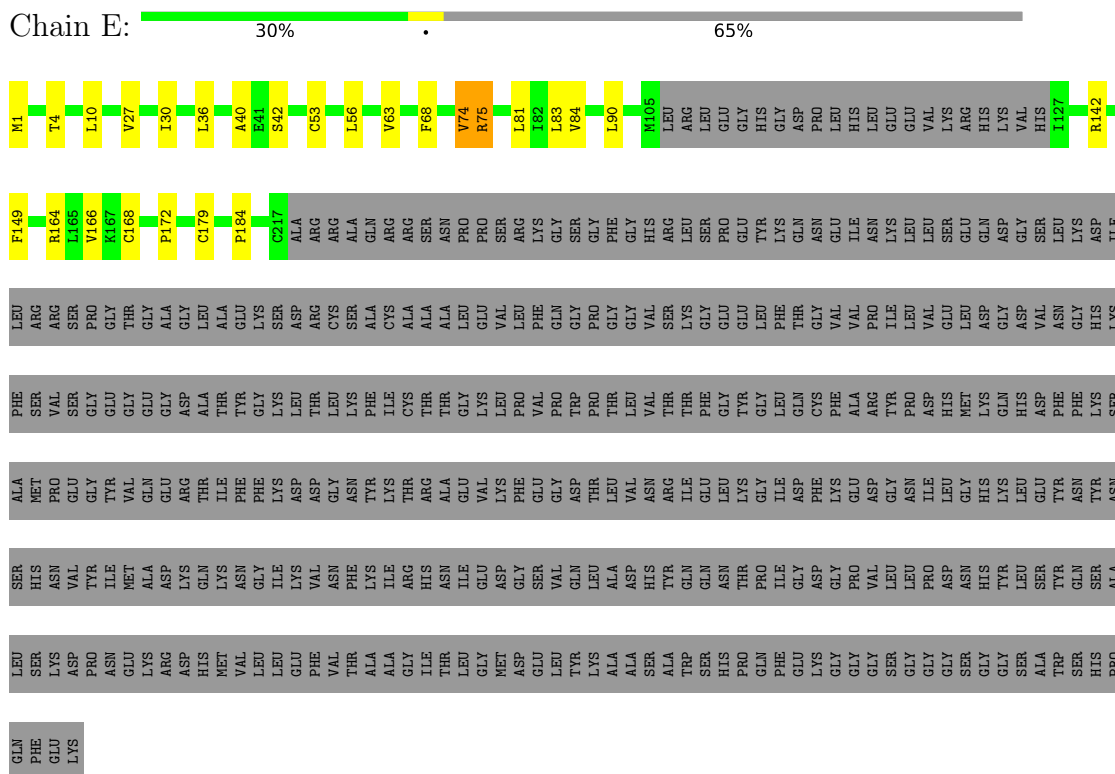
- Molecule 1: Gap junction beta-1 protein, Green fluorescent protein

Chain D: 31% 1% 65%

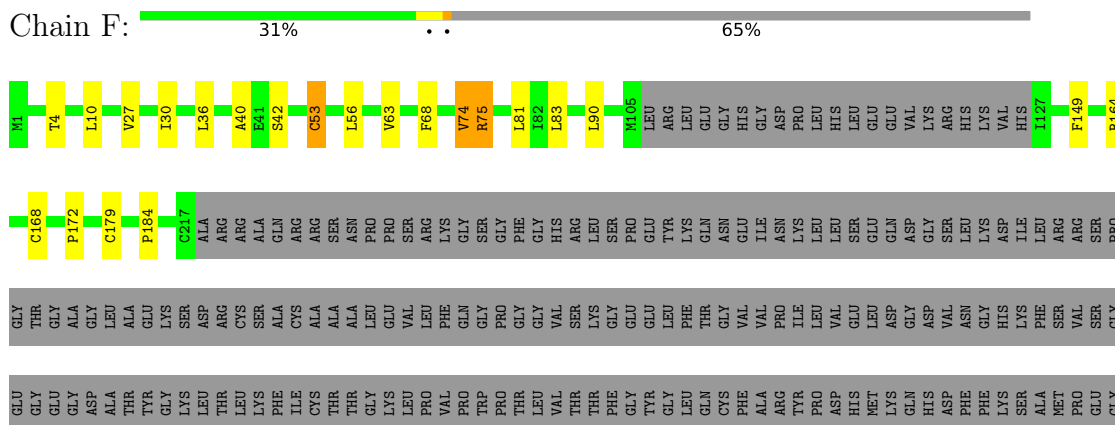
[illegible]



- Molecule 1: Gap junction beta-1 protein, Green fluorescent protein



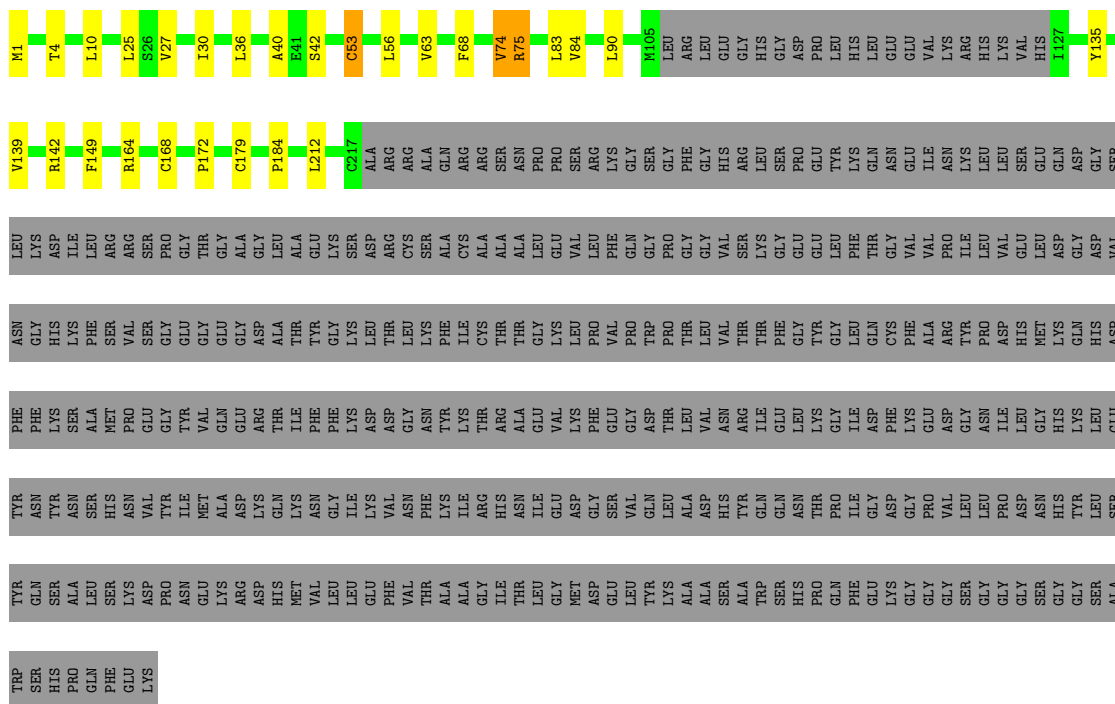
- Molecule 1: Gap junction beta-1 protein, Green fluorescent protein



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

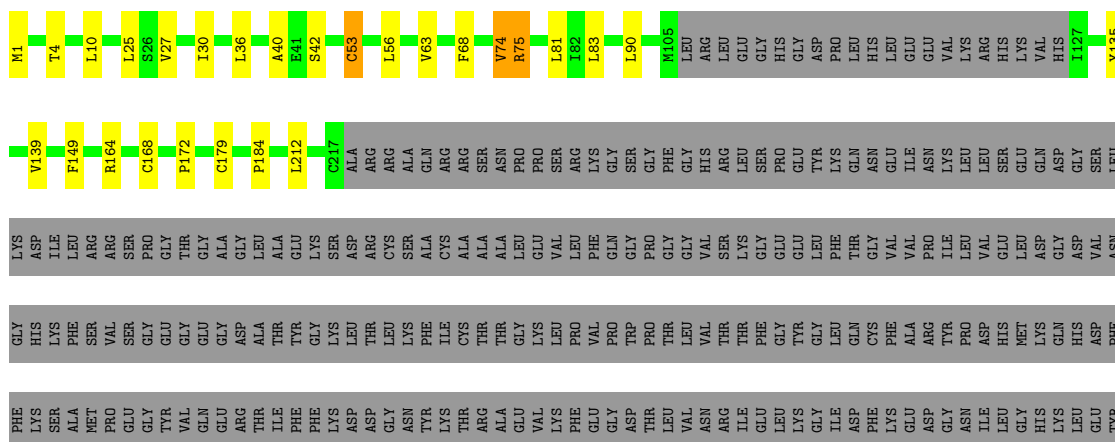
- Molecule 1: Gap junction beta-1 protein, Green fluorescent protein.

Chain G: 30% .. 65%



- Molecule 1: Gap junction beta-1 protein, Green fluorescent protein.

Chain H:  30% . . 65%

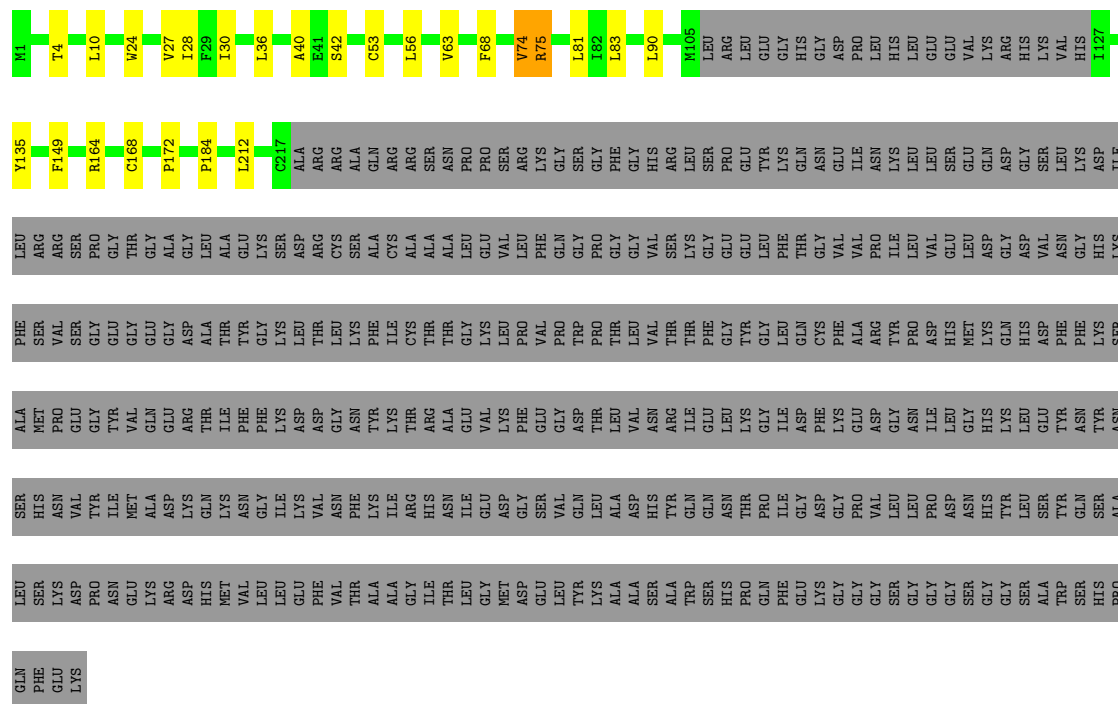




[illegible]

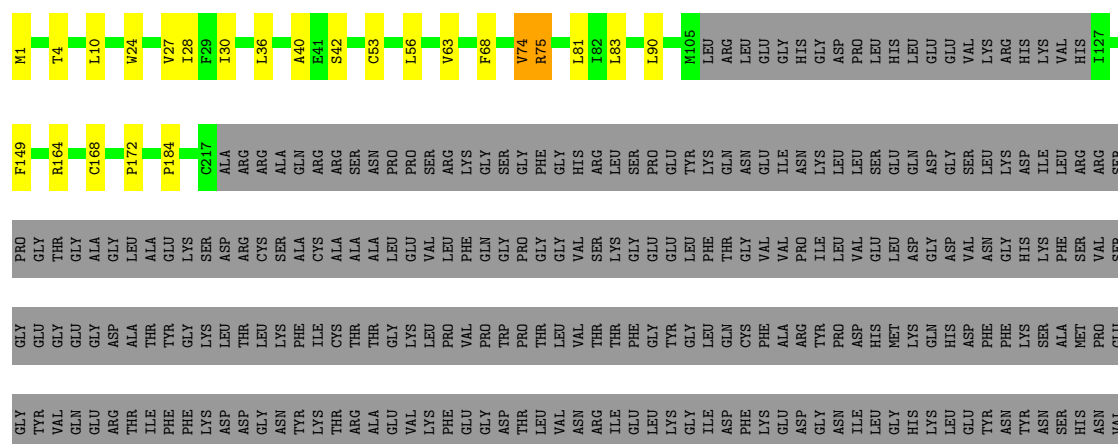
- Molecule 1: Gap junction beta-1 protein, Green fluorescent protein.

Chain K:  30% 5% 65%



- Molecule 1: Gap junction beta-1 protein, Green fluorescent protein

Chain L:  30% 65%



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D6	Depositor
Number of particles used	53450	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 ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.021	Depositor
Minimum map value	-0.011	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0022	Depositor
Map size (Å)	249.84033, 249.84033, 249.84033	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.6506259, 0.6506259, 0.6506259	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: CLR, POV

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	0.15	0/1612	0.27	0/2200
1	B	0.15	0/1612	0.28	0/2200
1	C	0.15	0/1612	0.27	0/2200
1	D	0.15	0/1612	0.27	0/2200
1	E	0.15	0/1612	0.27	0/2200
1	F	0.15	0/1612	0.28	0/2200
1	G	0.15	0/1612	0.28	0/2200
1	H	0.15	0/1612	0.27	0/2200
1	I	0.15	0/1612	0.27	0/2200
1	J	0.15	0/1612	0.27	0/2200
1	K	0.15	0/1612	0.28	0/2200
1	L	0.16	0/1612	0.27	0/2200
All	All	0.15	0/19344	0.27	0/26400

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1569	0	1600	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1569	0	1600	16	0
1	C	1569	0	1600	17	0
1	D	1569	0	1600	14	0
1	E	1569	0	1600	16	0
1	F	1569	0	1600	14	0
1	G	1569	0	1600	19	0
1	H	1569	0	1600	18	0
1	I	1569	0	1600	17	0
1	J	1569	0	1600	16	0
1	K	1569	0	1600	15	0
1	L	1569	0	1600	15	0
2	A	52	0	82	2	0
2	B	52	0	82	2	0
2	C	52	0	82	2	0
2	D	52	0	82	2	0
2	E	52	0	82	3	0
2	F	52	0	82	2	0
2	G	52	0	82	3	0
2	H	52	0	82	3	0
2	I	52	0	82	2	0
2	J	52	0	82	2	0
2	K	52	0	82	2	0
2	L	52	0	82	2	0
3	A	28	0	46	2	0
3	B	28	0	46	0	0
3	C	28	0	46	0	0
3	D	28	0	46	0	0
3	E	28	0	46	0	0
3	F	28	0	46	0	0
3	G	28	0	46	1	0
3	H	28	0	46	1	0
3	I	28	0	46	0	0
3	J	28	0	46	1	0
3	K	28	0	46	2	0
3	L	28	0	46	0	0
All	All	19788	0	20736	180	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 4.

All (180) 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:C:56:LEU:HD13	1:I:56:LEU:HD13	1.88	0.55
1:B:56:LEU:HD13	1:J:56:LEU:HD13	1.89	0.54
1:H:56:LEU:HD13	1:K:56:LEU:HD13	1.89	0.54
1:F:56:LEU:HD13	1:L:56:LEU:HD13	1.91	0.53
1:A:56:LEU:HD13	1:E:56:LEU:HD13	1.90	0.53
1:D:56:LEU:HD13	1:G:56:LEU:HD13	1.89	0.53
1:J:40:ALA:HA	1:J:74:VAL:HG11	1.91	0.53
1:A:40:ALA:HA	1:A:74:VAL:HG11	1.91	0.53
1:D:40:ALA:HA	1:D:74:VAL:HG11	1.91	0.52
1:H:40:ALA:HA	1:H:74:VAL:HG11	1.92	0.52
1:C:40:ALA:HA	1:C:74:VAL:HG11	1.92	0.52
1:B:40:ALA:HA	1:B:74:VAL:HG11	1.92	0.52
1:K:40:ALA:HA	1:K:74:VAL:HG11	1.92	0.52
1:F:40:ALA:HA	1:F:74:VAL:HG11	1.92	0.52
1:G:40:ALA:HA	1:G:74:VAL:HG11	1.92	0.52
1:L:40:ALA:HA	1:L:74:VAL:HG11	1.92	0.52
1:I:40:ALA:HA	1:I:74:VAL:HG11	1.93	0.51
1:H:164:ARG:HG2	1:H:184:PRO:HG3	1.93	0.51
1:A:164:ARG:HG2	1:A:184:PRO:HG3	1.93	0.51
1:E:40:ALA:HA	1:E:74:VAL:HG11	1.93	0.51
1:F:164:ARG:HG2	1:F:184:PRO:HG3	1.93	0.50
1:B:164:ARG:HG2	1:B:184:PRO:HG3	1.94	0.50
1:C:164:ARG:HG2	1:C:184:PRO:HG3	1.94	0.50
1:D:164:ARG:HG2	1:D:184:PRO:HG3	1.93	0.49
1:L:164:ARG:HG2	1:L:184:PRO:HG3	1.94	0.49
1:J:164:ARG:HG2	1:J:184:PRO:HG3	1.93	0.49
1:I:164:ARG:HG2	1:I:184:PRO:HG3	1.94	0.49
1:G:164:ARG:HG2	1:G:184:PRO:HG3	1.95	0.49
1:K:164:ARG:HG2	1:K:184:PRO:HG3	1.95	0.48
1:E:164:ARG:HG2	1:E:184:PRO:HG3	1.95	0.48
1:G:63:VAL:HG21	1:G:172:PRO:HD2	1.96	0.47
2:K:602:POV:H36A	2:L:601:POV:H38	1.97	0.47
1:K:63:VAL:HG21	1:K:172:PRO:HD2	1.97	0.47
1:E:63:VAL:HG21	1:E:172:PRO:HD2	1.97	0.47
1:D:63:VAL:HG21	1:D:172:PRO:HD2	1.98	0.46
1:B:63:VAL:HG21	1:B:172:PRO:HD2	1.98	0.46
1:C:63:VAL:HG21	1:C:172:PRO:HD2	1.98	0.46
1:I:63:VAL:HG21	1:I:172:PRO:HD2	1.98	0.46
1:J:63:VAL:HG21	1:J:172:PRO:HD2	1.98	0.46
1:J:42:SER:HB2	1:K:75:ARG:CZ	2.46	0.45
2:B:601:POV:H36A	2:C:602:POV:H38	1.98	0.45
2:A:601:POV:H38	2:L:601:POV:H36A	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:601:POV:H38	2:H:601:POV:H36A	1.98	0.45
1:F:27:VAL:HG21	1:H:90:LEU:HD23	1.98	0.45
2:F:602:POV:H36A	2:H:601:POV:H38	1.99	0.45
2:E:602:POV:H36A	2:F:602:POV:H38	1.99	0.45
1:B:90:LEU:HD23	1:H:27:VAL:HG21	1.98	0.45
1:C:27:VAL:HG21	1:D:90:LEU:HD23	1.99	0.45
1:F:81:LEU:HD12	1:F:81:LEU:HA	1.86	0.45
1:H:63:VAL:HG21	1:H:172:PRO:HD2	1.98	0.45
2:J:602:POV:H36A	2:K:602:POV:H38	1.99	0.45
1:E:36:LEU:O	1:E:40:ALA:HB2	2.17	0.44
1:F:63:VAL:HG21	1:F:172:PRO:HD2	1.98	0.44
1:G:27:VAL:HG21	1:I:90:LEU:HD23	1.99	0.44
2:G:602:POV:H36A	2:I:602:POV:H38	2.00	0.44
1:A:63:VAL:HG21	1:A:172:PRO:HD2	1.98	0.44
2:I:602:POV:H36A	2:J:602:POV:H38	2.00	0.44
1:J:1:MET:HE2	3:K:601:CLR:H6	1.99	0.44
1:H:36:LEU:O	1:H:40:ALA:HB2	2.17	0.44
1:L:63:VAL:HG21	1:L:172:PRO:HD2	1.98	0.44
1:A:90:LEU:HD23	1:L:27:VAL:HG21	2.00	0.44
1:F:42:SER:HB2	1:H:75:ARG:CZ	2.48	0.44
1:D:27:VAL:HG21	1:E:90:LEU:HD23	1.99	0.44
1:A:81:LEU:HD12	1:A:81:LEU:HA	1.86	0.44
1:B:42:SER:HB2	1:C:75:ARG:CZ	2.48	0.43
3:A:602:CLR:H6	1:L:1:MET:HE2	2.01	0.43
2:C:602:POV:H36A	2:D:602:POV:H38	2.01	0.43
1:E:27:VAL:HG21	1:F:90:LEU:HD23	2.00	0.43
1:J:36:LEU:O	1:J:40:ALA:HB2	2.18	0.43
1:K:42:SER:HB2	1:L:75:ARG:CZ	2.48	0.43
1:D:36:LEU:O	1:D:40:ALA:HB2	2.19	0.43
1:G:36:LEU:O	1:G:40:ALA:HB2	2.19	0.43
1:H:81:LEU:HD12	1:H:81:LEU:HA	1.86	0.43
2:A:601:POV:H36A	2:G:602:POV:H38	2.01	0.43
1:E:42:SER:HB2	1:F:75:ARG:CZ	2.48	0.43
1:I:1:MET:HE2	3:J:601:CLR:H6	2.00	0.43
2:D:602:POV:H36A	2:E:602:POV:H38	2.00	0.43
1:F:36:LEU:O	1:F:40:ALA:HB2	2.19	0.43
1:K:36:LEU:O	1:K:40:ALA:HB2	2.19	0.43
1:A:27:VAL:HG21	1:G:90:LEU:HD23	2.00	0.43
1:I:36:LEU:O	1:I:40:ALA:HB2	2.18	0.43
1:B:36:LEU:O	1:B:40:ALA:HB2	2.19	0.43
1:B:75:ARG:CZ	1:H:42:SER:HB2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:42:SER:HB2	1:I:75:ARG:CZ	2.48	0.43
1:D:83:LEU:HD23	1:D:83:LEU:HA	1.88	0.43
1:A:42:SER:HB2	1:G:75:ARG:CZ	2.49	0.42
1:J:83:LEU:HD12	1:J:149:PHE:CE2	2.53	0.42
1:K:27:VAL:HG21	1:L:90:LEU:HD23	2.00	0.42
1:C:42:SER:HB2	1:D:75:ARG:CZ	2.50	0.42
1:I:27:VAL:HG21	1:J:90:LEU:HD23	2.01	0.42
1:J:27:VAL:HG21	1:K:90:LEU:HD23	2.01	0.42
3:A:602:CLR:H162	3:A:602:CLR:H222	1.89	0.42
1:F:83:LEU:HD12	1:F:149:PHE:CE2	2.55	0.42
1:H:1:MET:HB3	2:H:601:POV:H22	2.02	0.42
3:H:602:CLR:H162	3:H:602:CLR:H222	1.89	0.42
1:A:36:LEU:O	1:A:40:ALA:HB2	2.18	0.42
1:C:83:LEU:HD12	1:C:149:PHE:CE2	2.55	0.42
1:H:68:PHE:HE2	1:H:168:CYS:HB2	1.84	0.42
1:I:42:SER:HB2	1:J:75:ARG:CZ	2.50	0.42
1:I:83:LEU:HD12	1:I:149:PHE:CE2	2.55	0.42
1:L:36:LEU:O	1:L:40:ALA:HB2	2.19	0.42
1:L:83:LEU:HD12	1:L:149:PHE:CE2	2.55	0.42
1:H:53:CYS:HA	1:H:179:CYS:HA	2.02	0.42
1:I:68:PHE:HE2	1:I:168:CYS:HB2	1.84	0.42
1:D:42:SER:HB2	1:E:75:ARG:CZ	2.49	0.42
1:L:81:LEU:HD12	1:L:81:LEU:HA	1.86	0.42
1:A:75:ARG:CZ	1:L:42:SER:HB2	2.50	0.42
1:B:10:LEU:HD11	1:B:30:ILE:HD11	2.02	0.42
1:C:68:PHE:HE2	1:C:168:CYS:HB2	1.84	0.42
1:B:83:LEU:HD12	1:B:149:PHE:CE2	2.55	0.41
1:C:36:LEU:O	1:C:40:ALA:HB2	2.19	0.41
1:E:83:LEU:HD12	1:E:149:PHE:CE2	2.55	0.41
1:B:83:LEU:HD23	1:B:83:LEU:HA	1.87	0.41
1:C:24:TRP:O	1:C:28:ILE:HG12	2.20	0.41
1:H:83:LEU:HD12	1:H:149:PHE:CE2	2.55	0.41
1:D:10:LEU:HD11	1:D:30:ILE:HD11	2.03	0.41
1:D:83:LEU:HD12	1:D:149:PHE:CE2	2.54	0.41
1:G:83:LEU:HD23	1:G:83:LEU:HA	1.88	0.41
1:L:68:PHE:HE2	1:L:168:CYS:HB2	1.85	0.41
1:B:25:LEU:HD23	1:B:25:LEU:HA	1.95	0.41
1:A:83:LEU:HD12	1:A:149:PHE:CE2	2.55	0.41
1:B:24:TRP:O	1:B:28:ILE:HG12	2.20	0.41
1:E:10:LEU:HD11	1:E:30:ILE:HD11	2.03	0.41
1:G:83:LEU:HD12	1:G:149:PHE:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:83:LEU:HD23	1:I:83:LEU:HA	1.87	0.41
1:K:68:PHE:HE2	1:K:168:CYS:HB2	1.85	0.41
1:C:83:LEU:HD23	1:C:83:LEU:HA	1.87	0.41
1:D:24:TRP:O	1:D:28:ILE:HG12	2.21	0.41
1:A:1:MET:HE2	3:G:601:CLR:H6	2.03	0.41
1:A:10:LEU:HD11	1:A:30:ILE:HD11	2.02	0.41
1:E:166:VAL:HG23	1:E:179:CYS:HB2	2.02	0.41
1:I:81:LEU:HD12	1:I:81:LEU:HA	1.85	0.41
1:J:10:LEU:HD11	1:J:30:ILE:HD11	2.03	0.41
1:E:1:MET:HB3	2:E:602:POV:H22	2.03	0.41
1:H:25:LEU:HD23	1:H:25:LEU:HA	1.94	0.41
1:A:25:LEU:HD23	1:A:25:LEU:HA	1.94	0.41
1:A:68:PHE:HE2	1:A:168:CYS:HB2	1.85	0.41
1:B:53:CYS:HA	1:B:179:CYS:HA	2.03	0.41
1:B:68:PHE:HE2	1:B:168:CYS:HB2	1.85	0.41
1:E:84:VAL:HG13	1:E:142:ARG:HG3	2.02	0.41
1:G:10:LEU:HD11	1:G:30:ILE:HD11	2.03	0.41
1:G:53:CYS:HA	1:G:179:CYS:HA	2.03	0.41
1:H:10:LEU:HD11	1:H:30:ILE:HD11	2.03	0.41
1:I:10:LEU:HD11	1:I:30:ILE:HD11	2.03	0.41
1:I:24:TRP:O	1:I:28:ILE:HG12	2.21	0.41
1:K:10:LEU:HD11	1:K:30:ILE:HD11	2.03	0.41
1:K:81:LEU:HD12	1:K:81:LEU:HA	1.86	0.41
1:B:27:VAL:HG21	1:C:90:LEU:HD23	2.03	0.41
1:C:81:LEU:HD12	1:C:81:LEU:HA	1.86	0.41
1:F:10:LEU:HD11	1:F:30:ILE:HD11	2.03	0.41
1:G:1:MET:HB3	2:G:602:POV:H22	2.03	0.41
1:K:83:LEU:HD12	1:K:149:PHE:CE2	2.56	0.41
3:K:601:CLR:H162	3:K:601:CLR:H222	1.89	0.41
1:C:10:LEU:HD11	1:C:30:ILE:HD11	2.03	0.40
1:C:135:TYR:CE2	1:C:212:LEU:HD11	2.56	0.40
1:F:68:PHE:HE2	1:F:168:CYS:HB2	1.86	0.40
1:G:25:LEU:HD23	1:G:25:LEU:HA	1.95	0.40
1:H:135:TYR:O	1:H:139:VAL:HG23	2.21	0.40
1:J:135:TYR:CE2	1:J:212:LEU:HD11	2.56	0.40
1:L:24:TRP:O	1:L:28:ILE:HG12	2.21	0.40
1:A:24:TRP:O	1:A:28:ILE:HG12	2.21	0.40
1:E:68:PHE:HE2	1:E:168:CYS:HB2	1.85	0.40
1:J:68:PHE:HE2	1:J:168:CYS:HB2	1.85	0.40
1:A:53:CYS:HA	1:A:179:CYS:HA	2.04	0.40
1:A:135:TYR:O	1:A:139:VAL:HG23	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:68:PHE:HE2	1:G:168:CYS:HB2	1.86	0.40
1:I:135:TYR:CE2	1:I:212:LEU:HD11	2.57	0.40
1:K:135:TYR:CE2	1:K:212:LEU:HD11	2.56	0.40
1:L:10:LEU:HD11	1:L:30:ILE:HD11	2.03	0.40
1:C:135:TYR:O	1:C:139:VAL:HG23	2.21	0.40
1:E:81:LEU:HD12	1:E:81:LEU:HA	1.86	0.40
1:G:135:TYR:CE2	1:G:212:LEU:HD11	2.56	0.40
1:H:135:TYR:CE2	1:H:212:LEU:HD11	2.56	0.40
1:D:135:TYR:O	1:D:139:VAL:HG23	2.21	0.40
1:F:53:CYS:HA	1:F:179:CYS:HA	2.03	0.40
1:G:84:VAL:HG13	1:G:142:ARG:HG3	2.03	0.40
1:G:135:TYR:O	1:G:139:VAL:HG23	2.22	0.40
1:J:24:TRP:O	1:J:28:ILE:HG12	2.22	0.40
1:J:135:TYR:O	1:J:139:VAL:HG23	2.21	0.40
1:K:24:TRP:O	1:K:28:ILE:HG12	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	192/566 (34%)	188 (98%)	4 (2%)	0	100	100
1	B	192/566 (34%)	187 (97%)	5 (3%)	0	100	100
1	C	192/566 (34%)	188 (98%)	4 (2%)	0	100	100
1	D	192/566 (34%)	188 (98%)	4 (2%)	0	100	100
1	E	192/566 (34%)	188 (98%)	4 (2%)	0	100	100
1	F	192/566 (34%)	188 (98%)	4 (2%)	0	100	100
1	G	192/566 (34%)	187 (97%)	5 (3%)	0	100	100
1	H	192/566 (34%)	188 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	192/566 (34%)	188 (98%)	4 (2%)	0	100	100
1	J	192/566 (34%)	188 (98%)	4 (2%)	0	100	100
1	K	192/566 (34%)	188 (98%)	4 (2%)	0	100	100
1	L	192/566 (34%)	188 (98%)	4 (2%)	0	100	100
All	All	2304/6792 (34%)	2254 (98%)	50 (2%)	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	176/482 (36%)	172 (98%)	4 (2%)	45	68
1	B	176/482 (36%)	172 (98%)	4 (2%)	45	68
1	C	176/482 (36%)	172 (98%)	4 (2%)	45	68
1	D	176/482 (36%)	172 (98%)	4 (2%)	45	68
1	E	176/482 (36%)	172 (98%)	4 (2%)	45	68
1	F	176/482 (36%)	172 (98%)	4 (2%)	45	68
1	G	176/482 (36%)	172 (98%)	4 (2%)	45	68
1	H	176/482 (36%)	172 (98%)	4 (2%)	45	68
1	I	176/482 (36%)	172 (98%)	4 (2%)	45	68
1	J	176/482 (36%)	172 (98%)	4 (2%)	45	68
1	K	176/482 (36%)	172 (98%)	4 (2%)	45	68
1	L	176/482 (36%)	172 (98%)	4 (2%)	45	68
All	All	2112/5784 (36%)	2064 (98%)	48 (2%)	46	68

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	THR

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Mol	Chain	Res	Type
1	A	53	CYS
1	A	74	VAL
1	A	75	ARG
1	B	4	THR
1	B	53	CYS
1	B	74	VAL
1	B	75	ARG
1	C	4	THR
1	C	53	CYS
1	C	74	VAL
1	C	75	ARG
1	D	4	THR
1	D	53	CYS
1	D	74	VAL
1	D	75	ARG
1	E	4	THR
1	E	53	CYS
1	E	74	VAL
1	E	75	ARG
1	F	4	THR
1	F	53	CYS
1	F	74	VAL
1	F	75	ARG
1	G	4	THR
1	G	53	CYS
1	G	74	VAL
1	G	75	ARG
1	H	4	THR
1	H	53	CYS
1	H	74	VAL
1	H	75	ARG
1	I	4	THR
1	I	53	CYS
1	I	74	VAL
1	I	75	ARG
1	J	4	THR
1	J	53	CYS
1	J	74	VAL
1	J	75	ARG
1	K	4	THR
1	K	53	CYS
1	K	74	VAL

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Mol	Chain	Res	Type
1	K	75	ARG
1	L	4	THR
1	L	53	CYS
1	L	74	VAL
1	L	75	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	16	HIS
1	J	16	HIS
1	K	16	HIS

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](#)

24 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	F	601	-	31,31,31	0.36	0	48,48,48	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	CLR	A	602	-	31,31,31	0.35	0	48,48,48	0.51	0
3	CLR	K	601	-	31,31,31	0.35	0	48,48,48	0.52	0
3	CLR	B	602	-	31,31,31	0.36	0	48,48,48	0.52	0
2	POV	D	602	-	51,51,51	0.50	0	57,59,59	0.48	0
3	CLR	H	602	-	31,31,31	0.36	0	48,48,48	0.51	0
2	POV	A	601	-	51,51,51	0.50	0	57,59,59	0.48	0
2	POV	C	602	-	51,51,51	0.50	0	57,59,59	0.48	0
3	CLR	J	601	-	31,31,31	0.36	0	48,48,48	0.52	0
2	POV	B	601	-	51,51,51	0.49	0	57,59,59	0.48	0
2	POV	H	601	-	51,51,51	0.50	0	57,59,59	0.48	0
2	POV	E	602	-	51,51,51	0.50	0	57,59,59	0.48	0
2	POV	G	602	-	51,51,51	0.50	0	57,59,59	0.48	0
3	CLR	C	601	-	31,31,31	0.36	0	48,48,48	0.53	0
3	CLR	E	601	-	31,31,31	0.36	0	48,48,48	0.52	0
2	POV	F	602	-	51,51,51	0.50	0	57,59,59	0.48	0
3	CLR	I	601	-	31,31,31	0.36	0	48,48,48	0.51	0
3	CLR	D	601	-	31,31,31	0.36	0	48,48,48	0.52	0
2	POV	J	602	-	51,51,51	0.50	0	57,59,59	0.48	0
3	CLR	L	602	-	31,31,31	0.36	0	48,48,48	0.52	0
2	POV	I	602	-	51,51,51	0.50	0	57,59,59	0.48	0
3	CLR	G	601	-	31,31,31	0.36	0	48,48,48	0.51	0
2	POV	K	602	-	51,51,51	0.50	0	57,59,59	0.48	0
2	POV	L	601	-	51,51,51	0.50	0	57,59,59	0.48	0

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	F	601	-	-	5/10/68/68	0/4/4/4
3	CLR	A	602	-	-	4/10/68/68	0/4/4/4
3	CLR	K	601	-	-	4/10/68/68	0/4/4/4
3	CLR	B	602	-	-	4/10/68/68	0/4/4/4
2	POV	D	602	-	-	15/55/55/55	-
3	CLR	H	602	-	-	5/10/68/68	0/4/4/4
2	POV	A	601	-	-	14/55/55/55	-
2	POV	C	602	-	-	15/55/55/55	-
3	CLR	J	601	-	-	4/10/68/68	0/4/4/4
2	POV	B	601	-	-	15/55/55/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	POV	H	601	-	-	16/55/55/55	-
2	POV	E	602	-	-	16/55/55/55	-
2	POV	G	602	-	-	14/55/55/55	-
3	CLR	C	601	-	-	4/10/68/68	0/4/4/4
3	CLR	E	601	-	-	5/10/68/68	0/4/4/4
2	POV	F	602	-	-	15/55/55/55	-
3	CLR	I	601	-	-	4/10/68/68	0/4/4/4
3	CLR	D	601	-	-	4/10/68/68	0/4/4/4
2	POV	J	602	-	-	15/55/55/55	-
3	CLR	L	602	-	-	4/10/68/68	0/4/4/4
2	POV	I	602	-	-	15/55/55/55	-
3	CLR	G	601	-	-	4/10/68/68	0/4/4/4
2	POV	K	602	-	-	14/55/55/55	-
2	POV	L	601	-	-	14/55/55/55	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (229) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	POV	C1-O11-P-O13
2	A	601	POV	C11-O12-P-O11
2	A	601	POV	C12-C11-O12-P
2	B	601	POV	C1-O11-P-O13
2	B	601	POV	C11-O12-P-O11
2	B	601	POV	C12-C11-O12-P
2	C	602	POV	C1-O11-P-O13
2	C	602	POV	C11-O12-P-O11
2	C	602	POV	C12-C11-O12-P
2	D	602	POV	C1-O11-P-O13
2	D	602	POV	C11-O12-P-O11
2	D	602	POV	C12-C11-O12-P
2	E	602	POV	C1-O11-P-O13
2	E	602	POV	C11-O12-P-O11
2	E	602	POV	C12-C11-O12-P
2	F	602	POV	C1-O11-P-O13
2	F	602	POV	C11-O12-P-O11

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Mol	Chain	Res	Type	Atoms
2	F	602	POV	C12-C11-O12-P
2	G	602	POV	C1-O11-P-O13
2	G	602	POV	C11-O12-P-O11
2	G	602	POV	C12-C11-O12-P
2	H	601	POV	C1-O11-P-O13
2	H	601	POV	C11-O12-P-O11
2	H	601	POV	C12-C11-O12-P
2	I	602	POV	C1-O11-P-O13
2	I	602	POV	C11-O12-P-O11
2	I	602	POV	C12-C11-O12-P
2	J	602	POV	C1-O11-P-O13
2	J	602	POV	C11-O12-P-O11
2	J	602	POV	C12-C11-O12-P
2	K	602	POV	C1-O11-P-O13
2	K	602	POV	C11-O12-P-O11
2	K	602	POV	C12-C11-O12-P
2	L	601	POV	C1-O11-P-O13
2	L	601	POV	C11-O12-P-O11
2	L	601	POV	C12-C11-O12-P
2	G	602	POV	C36-C37-C38-C39
2	D	602	POV	C36-C37-C38-C39
2	E	602	POV	C36-C37-C38-C39
2	I	602	POV	C36-C37-C38-C39
2	J	602	POV	C36-C37-C38-C39
2	A	601	POV	C36-C37-C38-C39
2	F	602	POV	C36-C37-C38-C39
2	H	601	POV	C36-C37-C38-C39
2	B	601	POV	C36-C37-C38-C39
2	C	602	POV	C36-C37-C38-C39
2	K	602	POV	C36-C37-C38-C39
2	L	601	POV	C36-C37-C38-C39
2	A	601	POV	C32-C31-O31-C3
2	L	601	POV	C32-C31-O31-C3
2	B	601	POV	C32-C31-O31-C3
2	C	602	POV	C32-C31-O31-C3
2	D	602	POV	C32-C31-O31-C3
2	E	602	POV	C32-C31-O31-C3
2	F	602	POV	C32-C31-O31-C3
2	G	602	POV	C32-C31-O31-C3
2	H	601	POV	C32-C31-O31-C3
2	I	602	POV	C32-C31-O31-C3
2	J	602	POV	C32-C31-O31-C3

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Mol	Chain	Res	Type	Atoms
2	K	602	POV	C32-C31-O31-C3
2	A	601	POV	O32-C31-O31-C3
2	C	602	POV	O32-C31-O31-C3
2	G	602	POV	O32-C31-O31-C3
2	L	601	POV	O32-C31-O31-C3
2	I	602	POV	O32-C31-O31-C3
2	B	601	POV	O32-C31-O31-C3
2	D	602	POV	O32-C31-O31-C3
2	E	602	POV	O32-C31-O31-C3
2	F	602	POV	O32-C31-O31-C3
2	H	601	POV	O32-C31-O31-C3
2	K	602	POV	O32-C31-O31-C3
2	J	602	POV	O32-C31-O31-C3
3	J	601	CLR	C13-C17-C20-C21
3	F	601	CLR	C13-C17-C20-C21
3	D	601	CLR	C13-C17-C20-C22
3	F	601	CLR	C13-C17-C20-C22
3	J	601	CLR	C13-C17-C20-C22
3	D	601	CLR	C13-C17-C20-C21
3	A	602	CLR	C13-C17-C20-C22
3	C	601	CLR	C13-C17-C20-C22
3	H	602	CLR	C13-C17-C20-C22
2	J	602	POV	O11-C1-C2-C3
3	A	602	CLR	C13-C17-C20-C21
3	B	602	CLR	C13-C17-C20-C21
3	C	601	CLR	C13-C17-C20-C21
3	H	602	CLR	C13-C17-C20-C21
3	B	602	CLR	C13-C17-C20-C22
3	K	601	CLR	C13-C17-C20-C22
3	K	601	CLR	C13-C17-C20-C21
2	A	601	POV	C2-C1-O11-P
2	B	601	POV	C2-C1-O11-P
2	C	602	POV	C2-C1-O11-P
2	E	602	POV	C2-C1-O11-P
2	F	602	POV	C2-C1-O11-P
2	H	601	POV	C2-C1-O11-P
2	J	602	POV	C2-C1-O11-P
2	K	602	POV	C2-C1-O11-P
2	L	601	POV	C2-C1-O11-P
2	J	602	POV	O11-C1-C2-O21
3	E	601	CLR	C13-C17-C20-C21
3	G	601	CLR	C13-C17-C20-C21

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Mol	Chain	Res	Type	Atoms
3	I	601	CLR	C13-C17-C20-C21
3	L	602	CLR	C13-C17-C20-C21
3	J	601	CLR	C16-C17-C20-C22
3	E	601	CLR	C13-C17-C20-C22
3	J	601	CLR	C16-C17-C20-C21
3	G	601	CLR	C13-C17-C20-C22
3	I	601	CLR	C13-C17-C20-C22
3	L	602	CLR	C13-C17-C20-C22
3	F	601	CLR	C16-C17-C20-C22
2	D	602	POV	C2-C1-O11-P
2	G	602	POV	C2-C1-O11-P
2	I	602	POV	C2-C1-O11-P
2	A	601	POV	C11-O12-P-O13
2	B	601	POV	C11-O12-P-O13
2	C	602	POV	C11-O12-P-O13
2	D	602	POV	C11-O12-P-O13
2	E	602	POV	C11-O12-P-O13
2	F	602	POV	C11-O12-P-O13
2	G	602	POV	C11-O12-P-O13
2	H	601	POV	C11-O12-P-O13
2	I	602	POV	C11-O12-P-O13
2	J	602	POV	C11-O12-P-O13
2	K	602	POV	C11-O12-P-O13
2	L	601	POV	C11-O12-P-O13
2	B	601	POV	O11-C1-C2-C3
2	D	602	POV	O11-C1-C2-C3
2	G	602	POV	O11-C1-C2-C3
2	H	601	POV	O11-C1-C2-C3
2	I	602	POV	O11-C1-C2-C3
2	K	602	POV	O11-C1-C2-C3
2	L	601	POV	O11-C1-C2-C3
3	A	602	CLR	C16-C17-C20-C22
3	D	601	CLR	C16-C17-C20-C22
3	F	601	CLR	C16-C17-C20-C21
3	H	602	CLR	C16-C17-C20-C22
3	D	601	CLR	C16-C17-C20-C21
2	A	601	POV	O11-C1-C2-O21
2	B	601	POV	O11-C1-C2-O21
2	C	602	POV	O11-C1-C2-O21
2	D	602	POV	O11-C1-C2-O21
2	E	602	POV	O11-C1-C2-O21
2	F	602	POV	O11-C1-C2-O21

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Mol	Chain	Res	Type	Atoms
2	G	602	POV	O11-C1-C2-O21
2	H	601	POV	O11-C1-C2-O21
2	I	602	POV	O11-C1-C2-O21
2	K	602	POV	O11-C1-C2-O21
2	L	601	POV	O11-C1-C2-O21
3	B	602	CLR	C16-C17-C20-C22
3	C	601	CLR	C16-C17-C20-C22
3	K	601	CLR	C16-C17-C20-C22
3	C	601	CLR	C16-C17-C20-C21
3	H	602	CLR	C16-C17-C20-C21
3	A	602	CLR	C16-C17-C20-C21
3	E	601	CLR	C16-C17-C20-C22
3	I	601	CLR	C16-C17-C20-C22
3	G	601	CLR	C16-C17-C20-C22
3	L	602	CLR	C16-C17-C20-C22
3	B	602	CLR	C16-C17-C20-C21
2	J	602	POV	C32-C33-C34-C35
2	A	601	POV	O11-C1-C2-C3
2	C	602	POV	O11-C1-C2-C3
2	E	602	POV	O11-C1-C2-C3
2	F	602	POV	O11-C1-C2-C3
3	K	601	CLR	C16-C17-C20-C21
2	H	601	POV	C32-C33-C34-C35
3	E	601	CLR	C16-C17-C20-C21
3	I	601	CLR	C16-C17-C20-C21
3	L	602	CLR	C16-C17-C20-C21
2	K	602	POV	C32-C33-C34-C35
3	G	601	CLR	C16-C17-C20-C21
2	E	602	POV	C32-C33-C34-C35
2	D	602	POV	C210-C211-C212-C213
2	F	602	POV	C210-C211-C212-C213
2	H	601	POV	C210-C211-C212-C213
2	F	602	POV	C32-C33-C34-C35
2	A	601	POV	C32-C33-C34-C35
2	K	602	POV	C312-C313-C314-C315
2	D	602	POV	C32-C33-C34-C35
2	B	601	POV	C32-C33-C34-C35
2	I	602	POV	C32-C33-C34-C35
2	I	602	POV	C1-O11-P-O12
2	J	602	POV	C312-C313-C314-C315
2	L	601	POV	C32-C33-C34-C35
2	F	602	POV	C312-C313-C314-C315

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Mol	Chain	Res	Type	Atoms
2	E	602	POV	C312-C313-C314-C315
2	I	602	POV	C312-C313-C314-C315
2	C	602	POV	C32-C33-C34-C35
2	B	601	POV	C210-C211-C212-C213
2	C	602	POV	C210-C211-C212-C213
2	E	602	POV	C210-C211-C212-C213
2	B	601	POV	C312-C313-C314-C315
2	H	601	POV	C312-C313-C314-C315
2	L	601	POV	C34-C35-C36-C37
2	C	602	POV	C34-C35-C36-C37
2	G	602	POV	C32-C33-C34-C35
2	L	601	POV	C312-C313-C314-C315
2	B	601	POV	C34-C35-C36-C37
2	D	602	POV	C312-C313-C314-C315
2	G	602	POV	C312-C313-C314-C315
2	A	601	POV	C34-C35-C36-C37
2	F	602	POV	C34-C35-C36-C37
2	C	602	POV	C312-C313-C314-C315
2	I	602	POV	C34-C35-C36-C37
2	G	602	POV	C34-C35-C36-C37
2	H	601	POV	C34-C35-C36-C37
2	D	602	POV	C34-C35-C36-C37
2	K	602	POV	C34-C35-C36-C37
2	E	602	POV	C34-C35-C36-C37
2	A	601	POV	C312-C313-C314-C315
2	E	602	POV	C1-O11-P-O12
2	H	601	POV	C1-O11-P-O12
2	J	602	POV	C1-O11-P-O12
2	A	601	POV	C1-O11-P-O14
2	B	601	POV	C1-O11-P-O14
2	C	602	POV	C1-O11-P-O14
2	D	602	POV	C1-O11-P-O14
2	E	602	POV	C1-O11-P-O14
2	F	602	POV	C1-O11-P-O14
2	G	602	POV	C1-O11-P-O14
2	H	601	POV	C1-O11-P-O14
2	I	602	POV	C1-O11-P-O14
2	J	602	POV	C1-O11-P-O14
2	K	602	POV	C1-O11-P-O14
2	L	601	POV	C1-O11-P-O14
3	E	601	CLR	C20-C22-C23-C24
3	F	601	CLR	C20-C22-C23-C24

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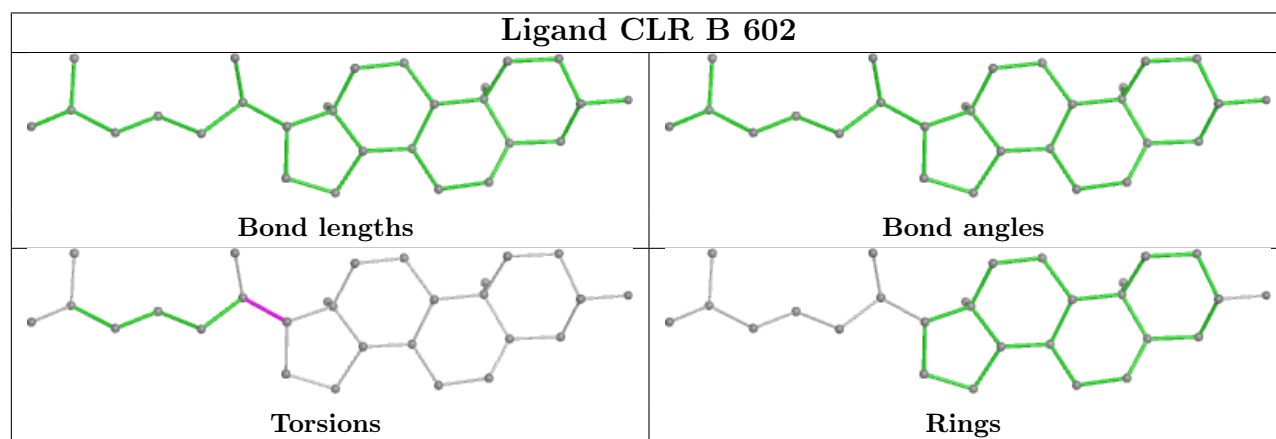
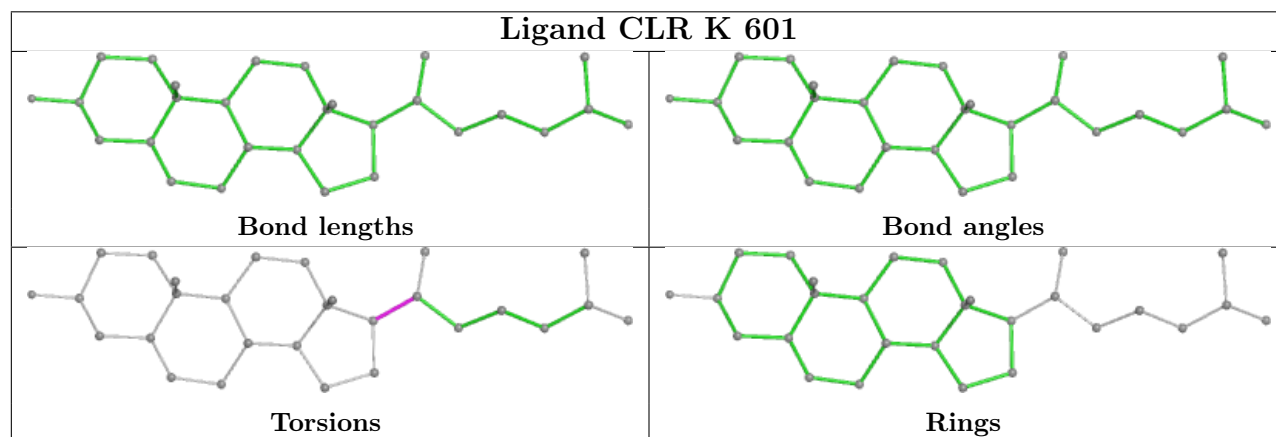
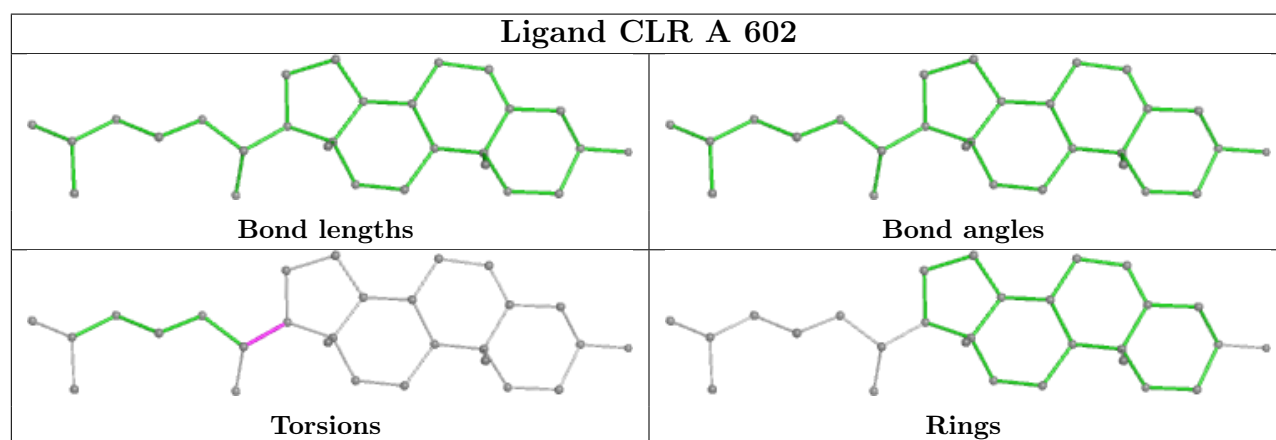
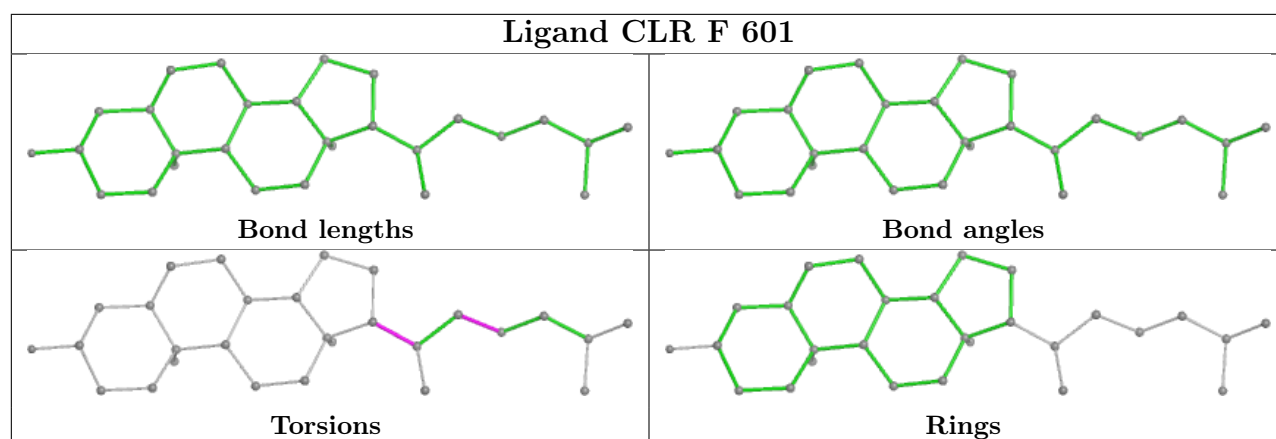
Mol	Chain	Res	Type	Atoms
3	H	602	CLR	C20-C22-C23-C24
2	J	602	POV	C34-C35-C36-C37

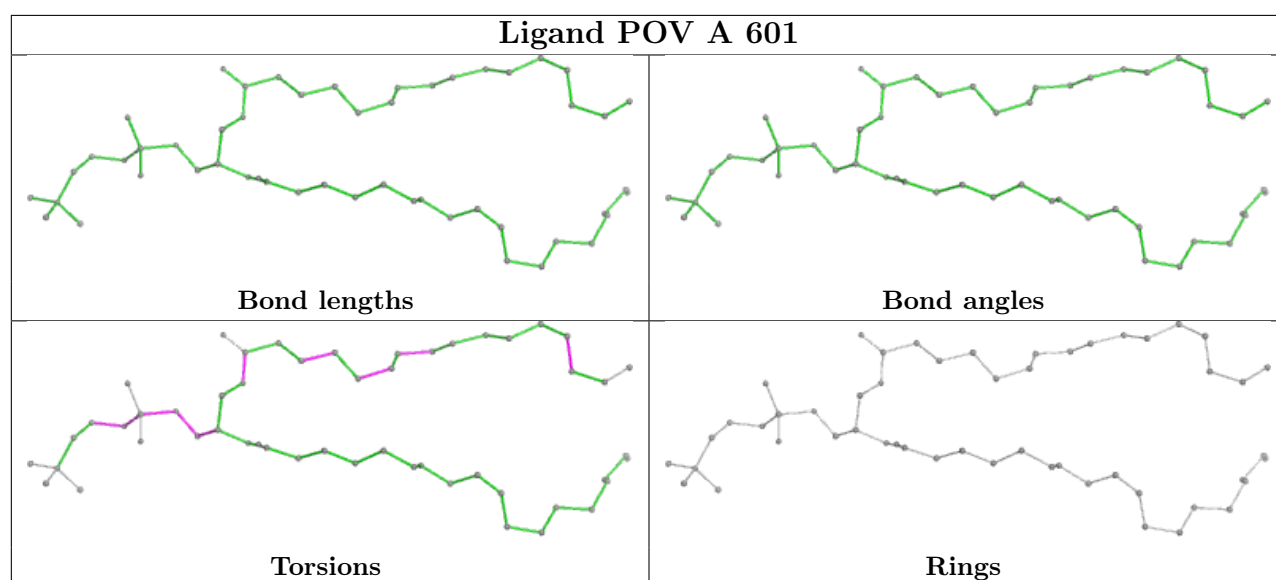
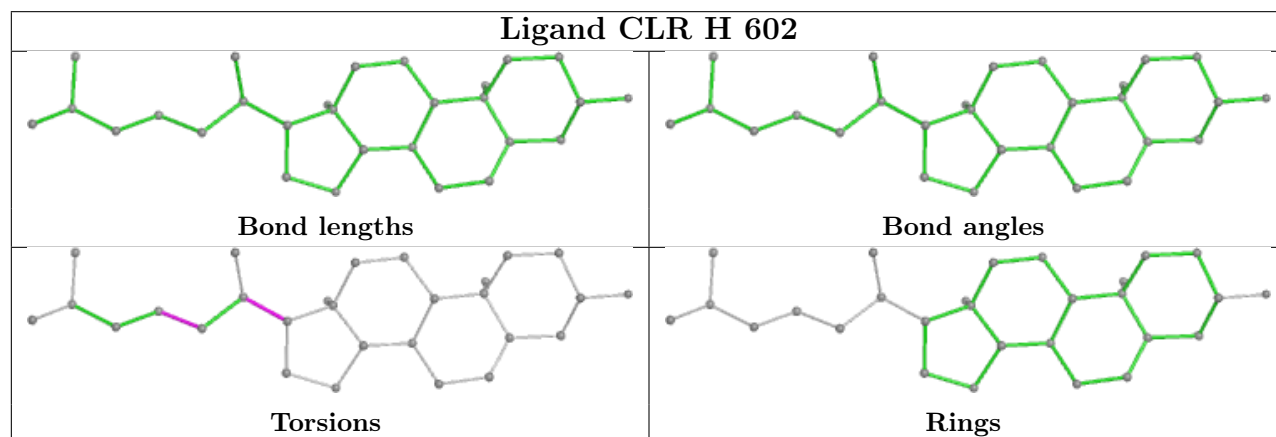
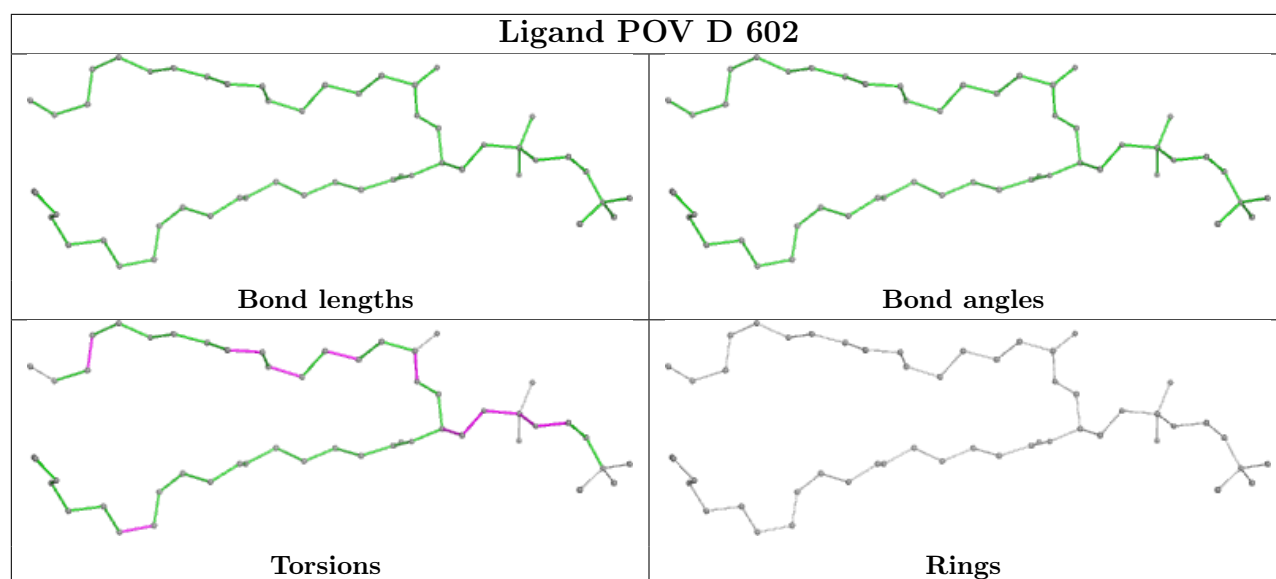
There are no ring outliers.

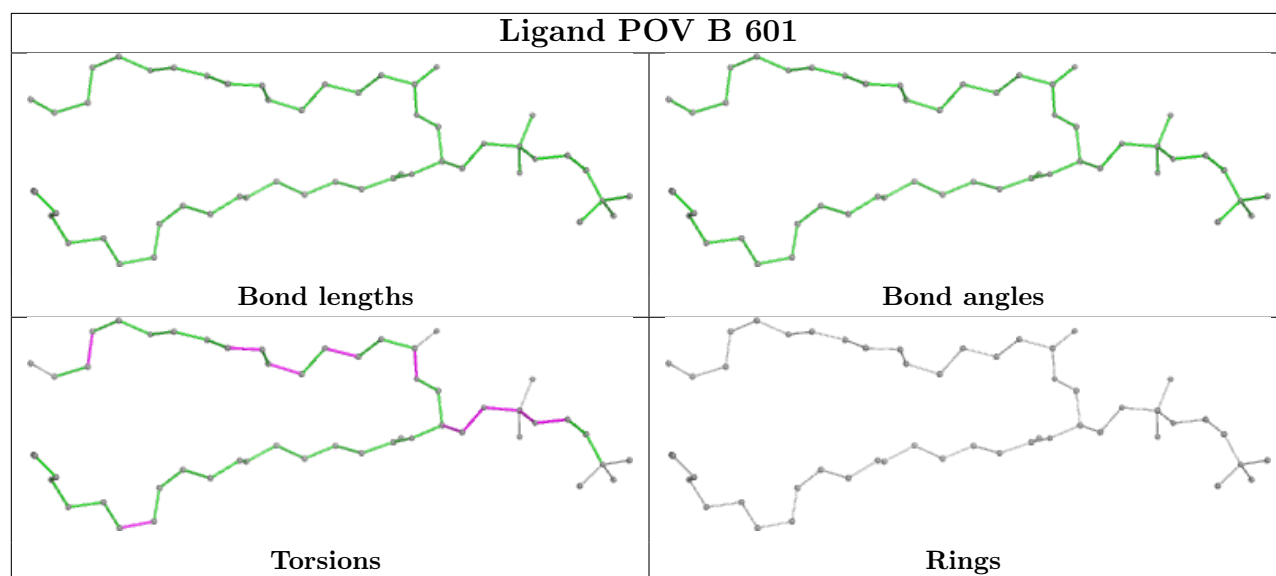
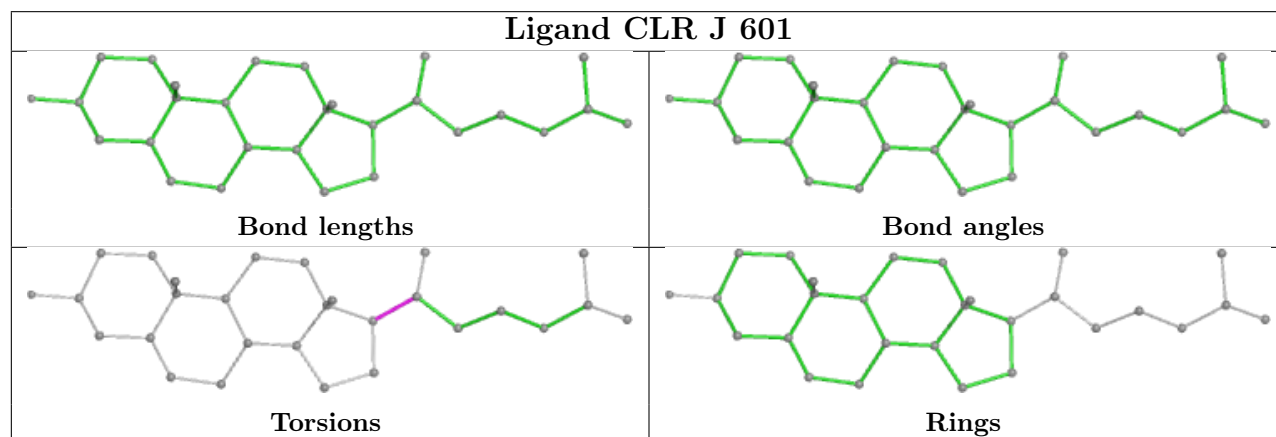
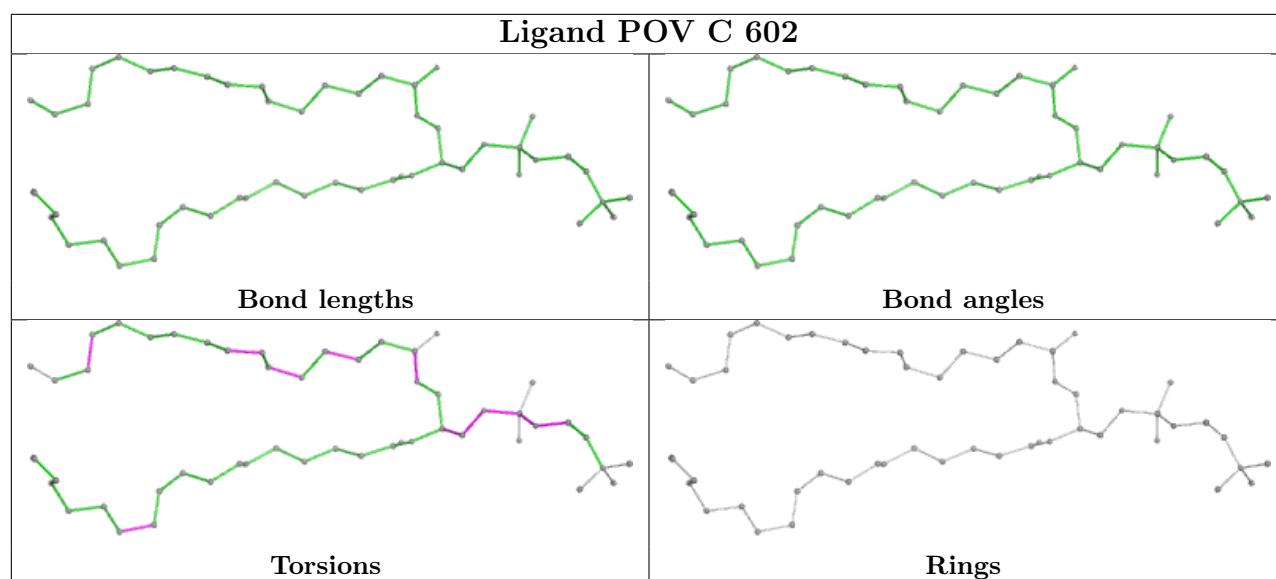
17 monomers are involved in 22 short contacts:

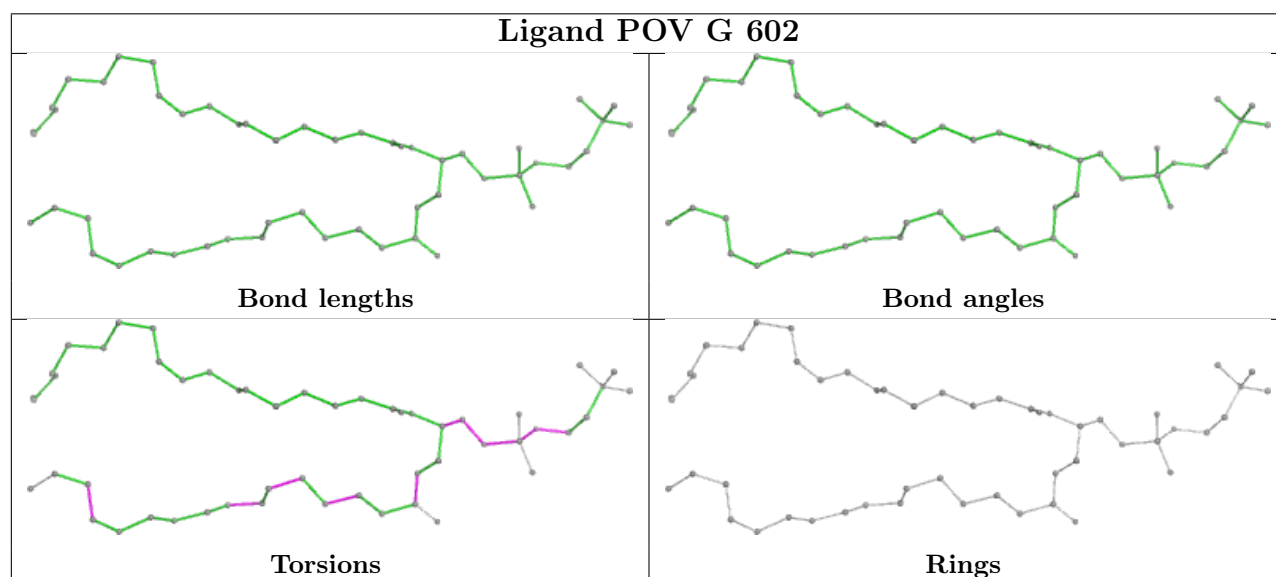
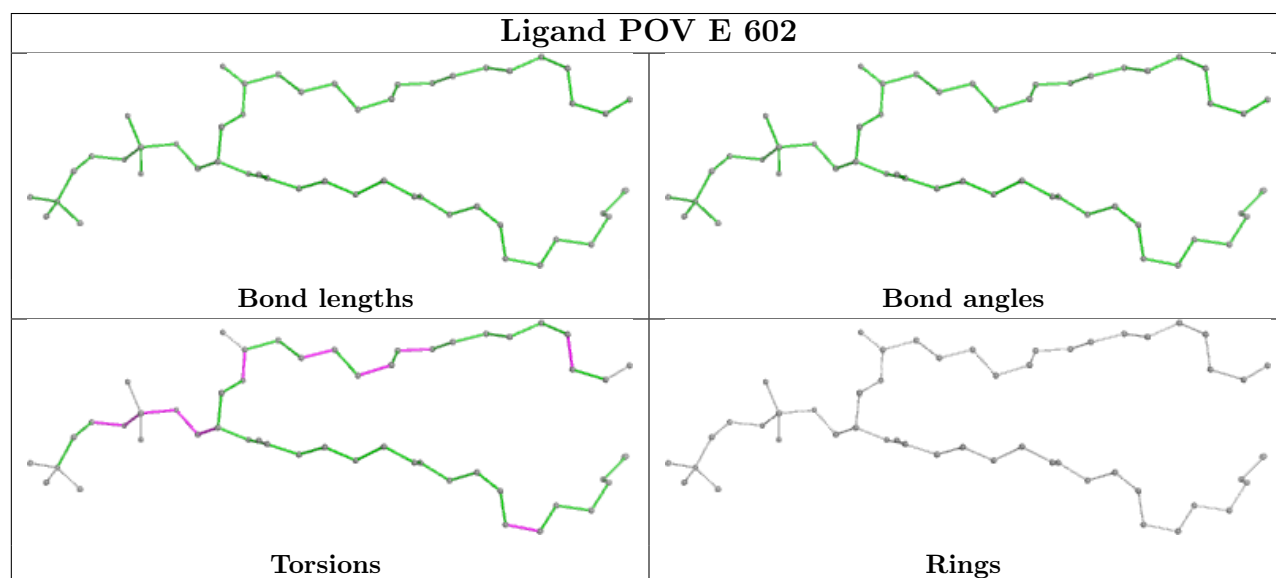
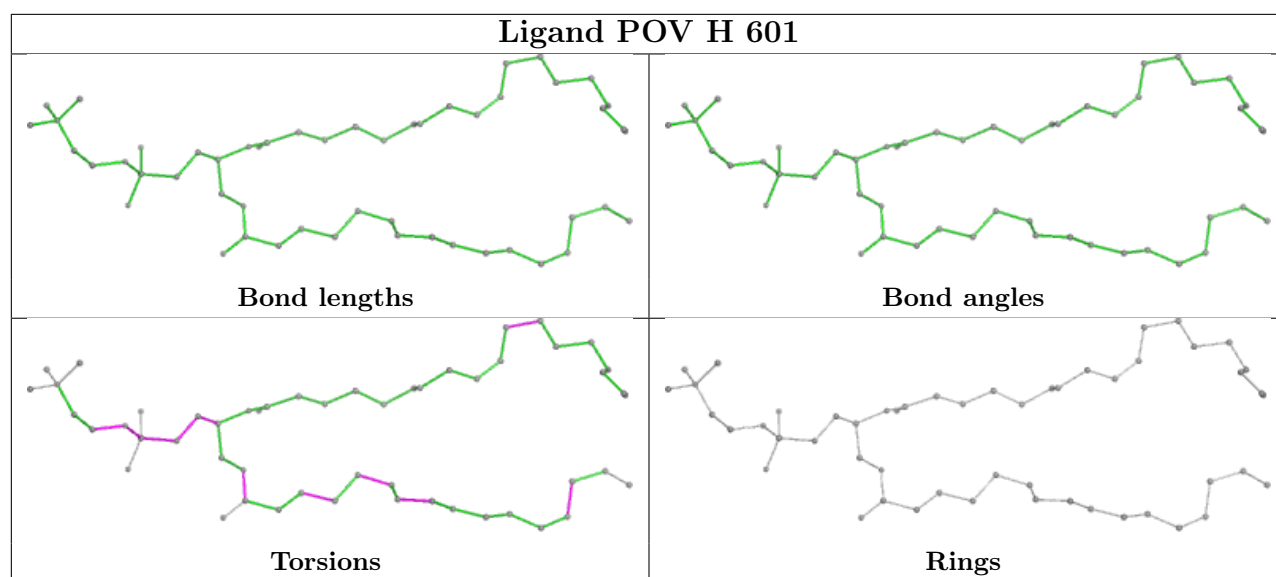
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	602	CLR	2	0
3	K	601	CLR	2	0
2	D	602	POV	2	0
3	H	602	CLR	1	0
2	A	601	POV	2	0
2	C	602	POV	2	0
3	J	601	CLR	1	0
2	B	601	POV	2	0
2	H	601	POV	3	0
2	E	602	POV	3	0
2	G	602	POV	3	0
2	F	602	POV	2	0
2	J	602	POV	2	0
2	I	602	POV	2	0
3	G	601	CLR	1	0
2	K	602	POV	2	0
2	L	601	POV	2	0

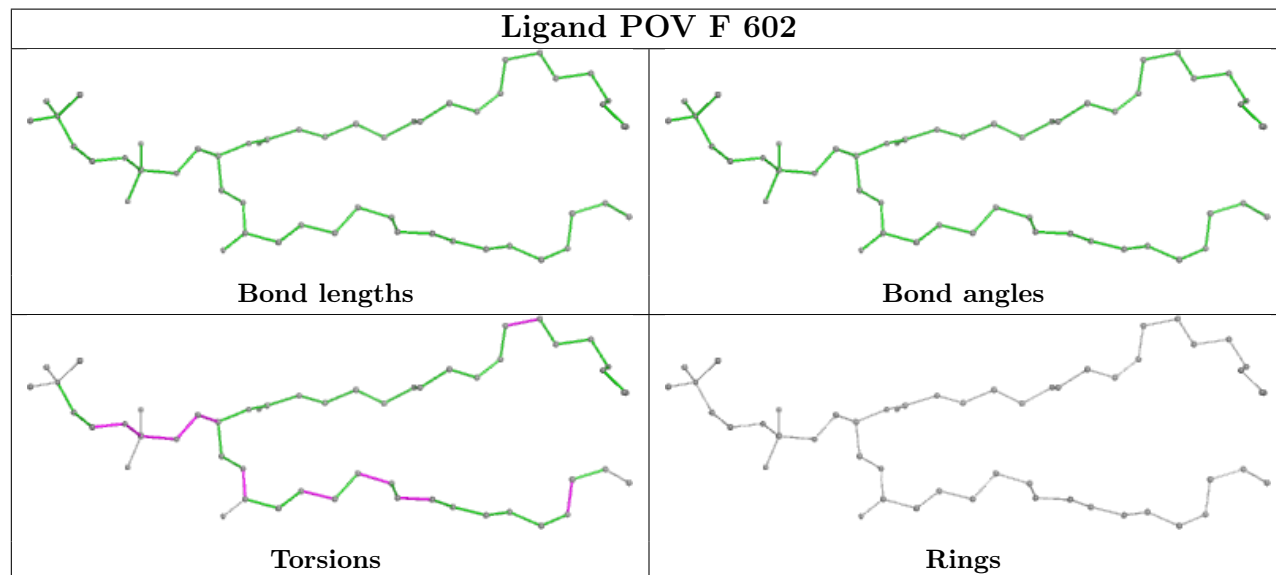
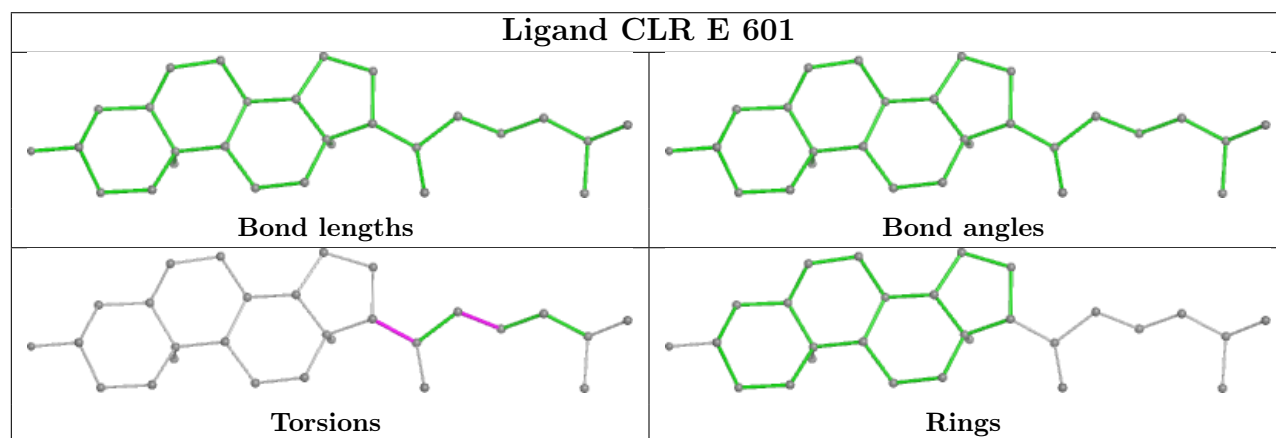
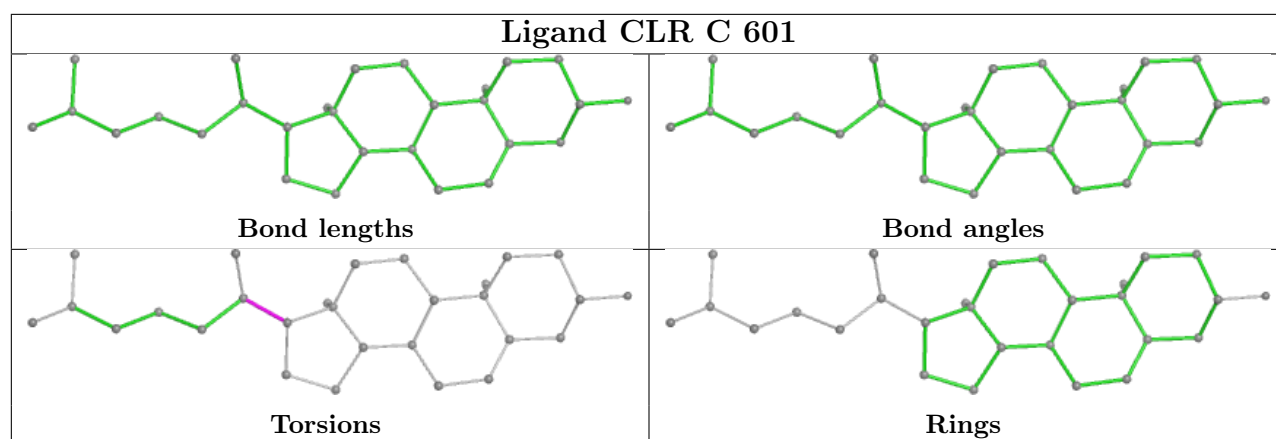
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

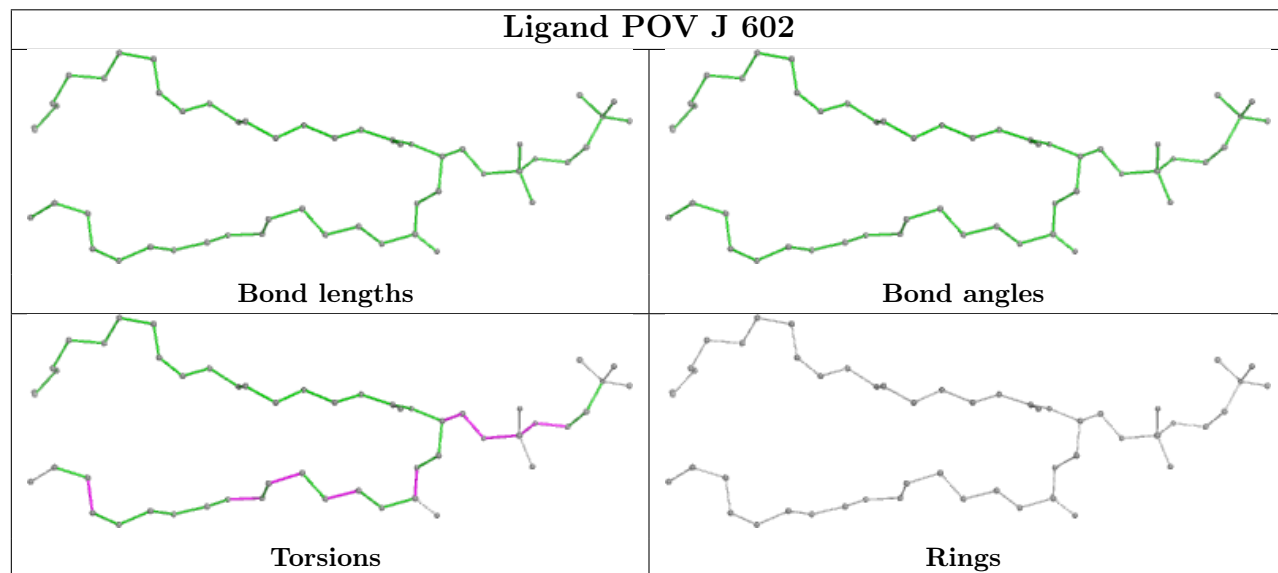
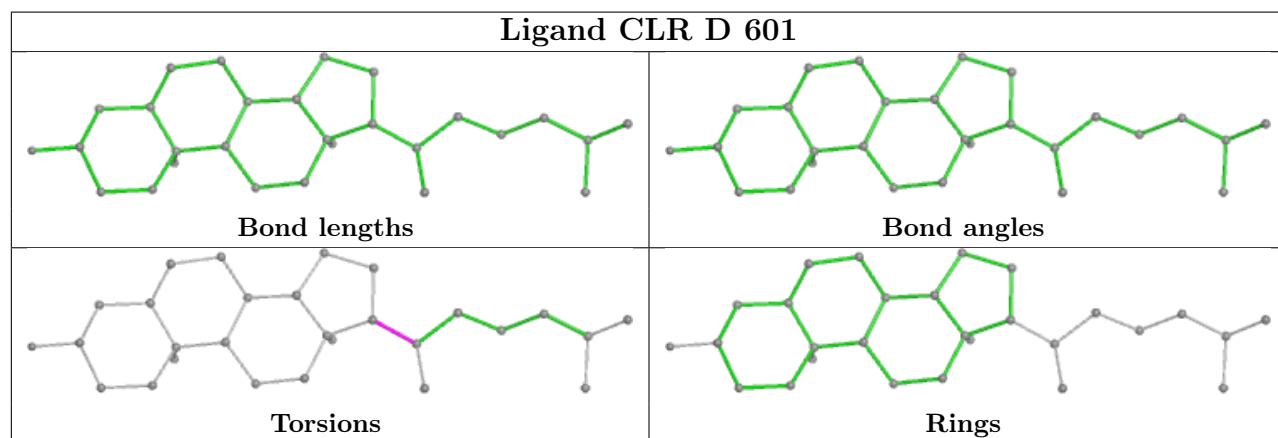
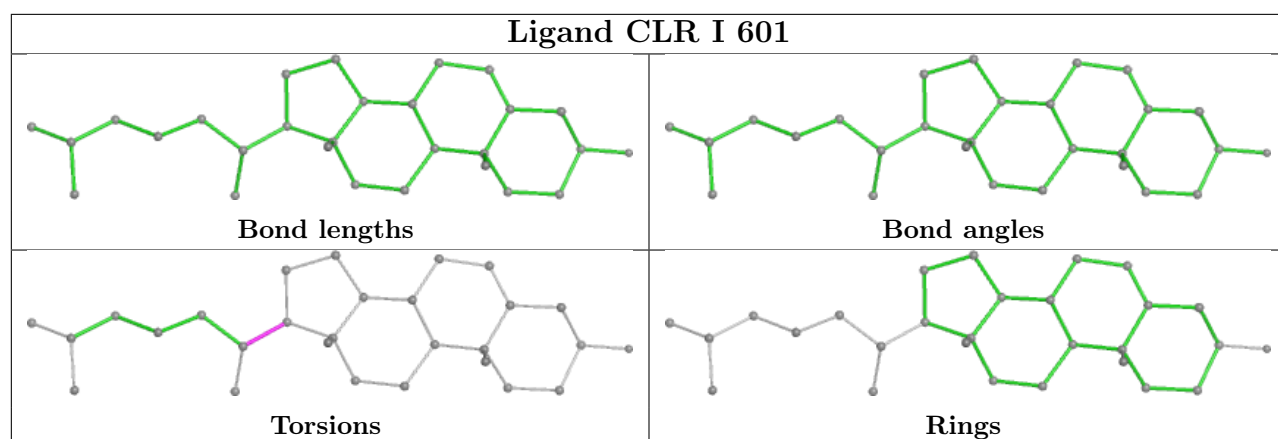


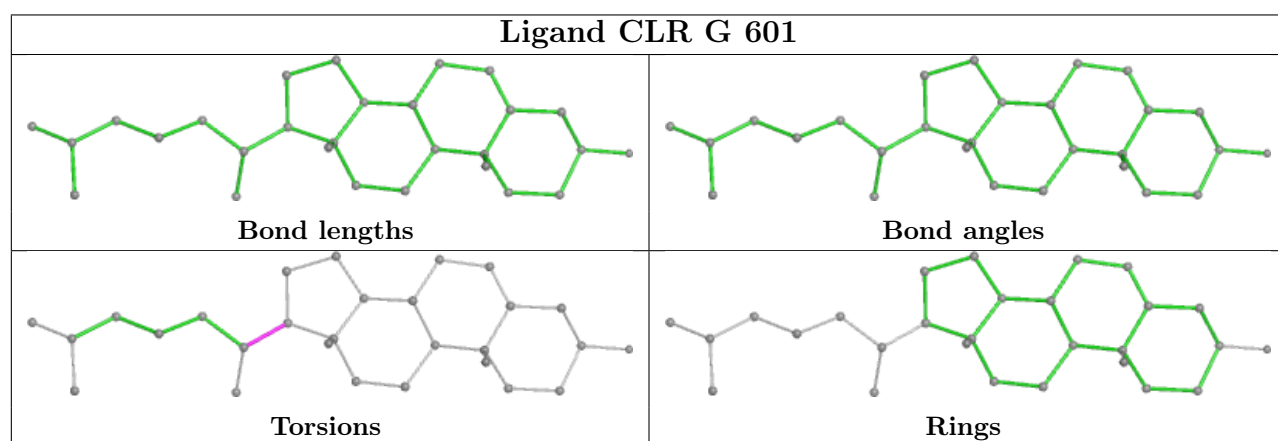
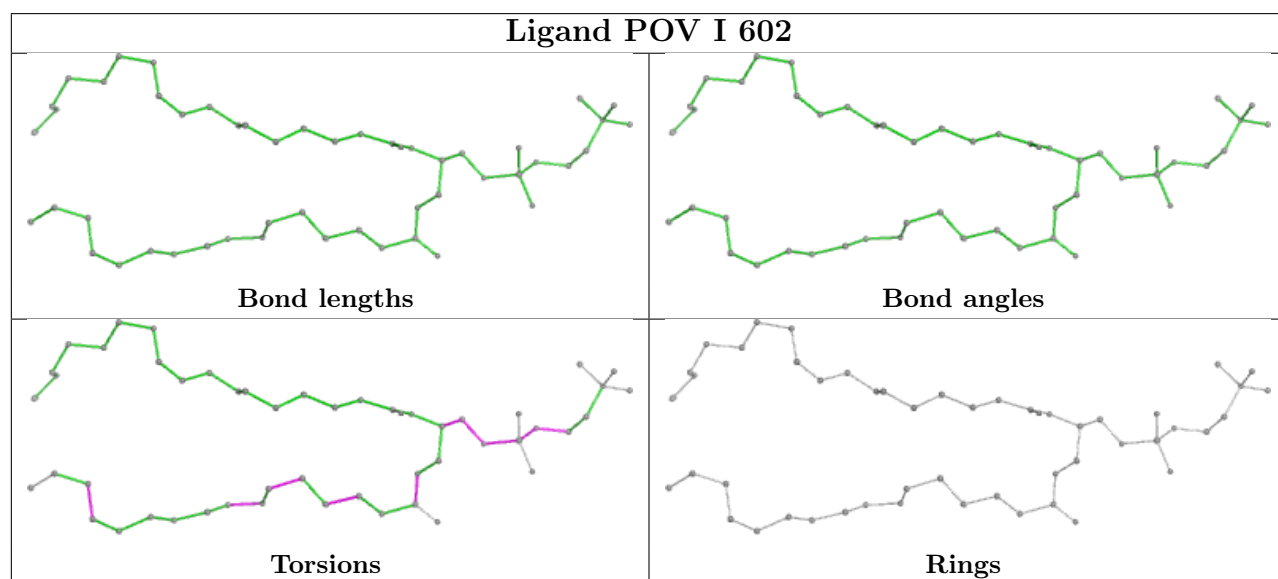
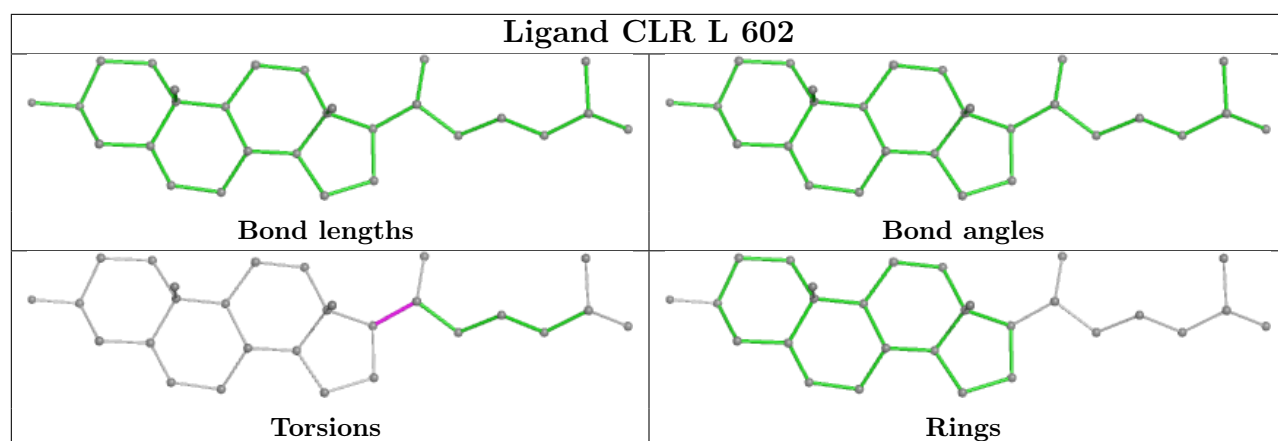


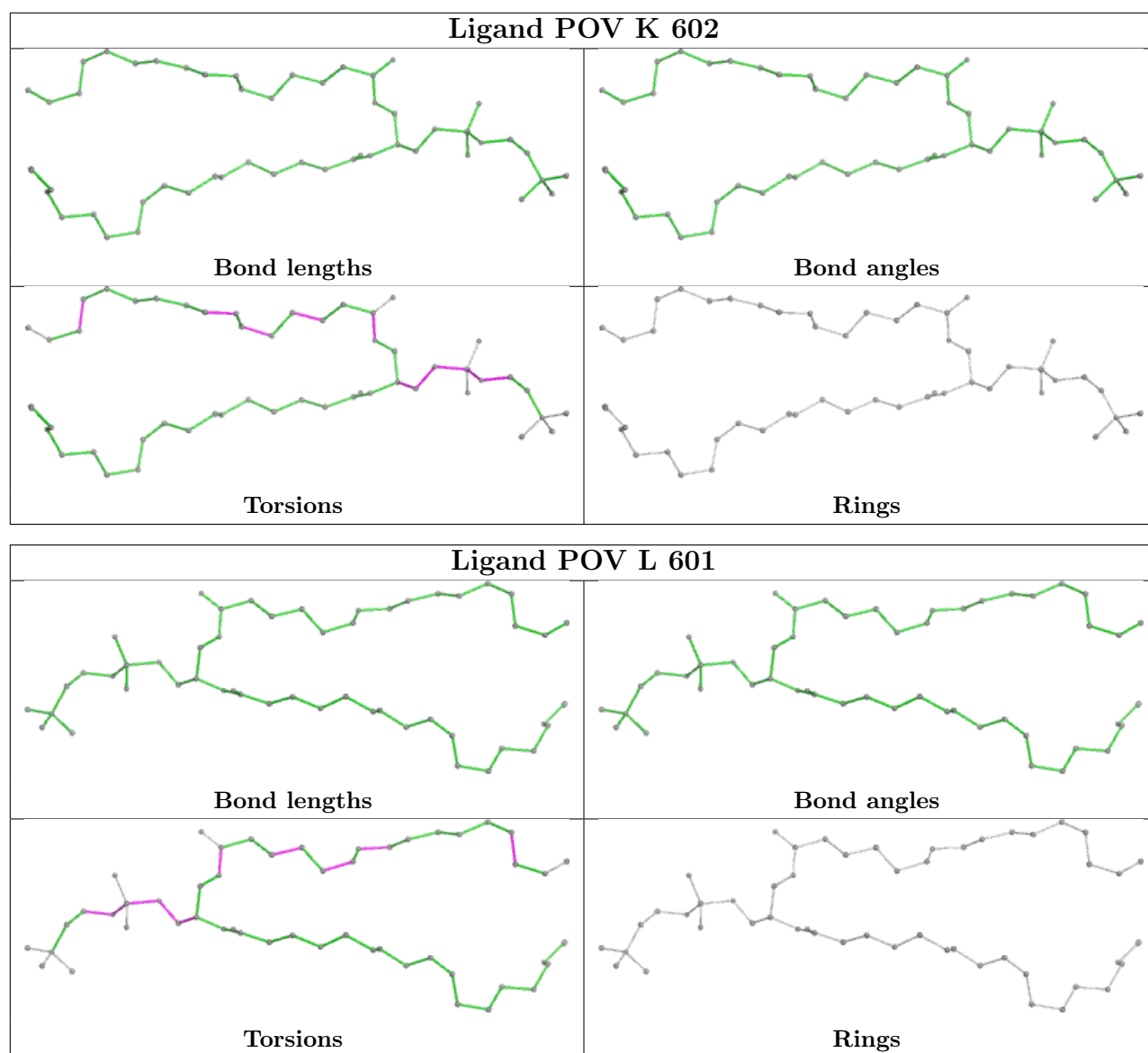












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

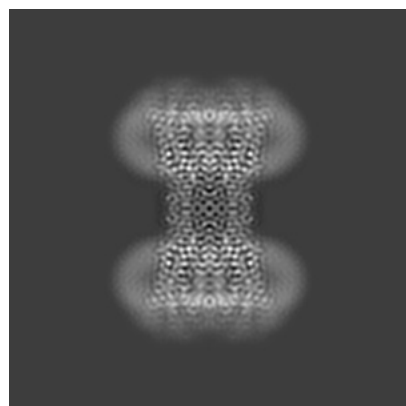
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53250. These allow visual inspection of the internal detail of the map and identification of artifacts.

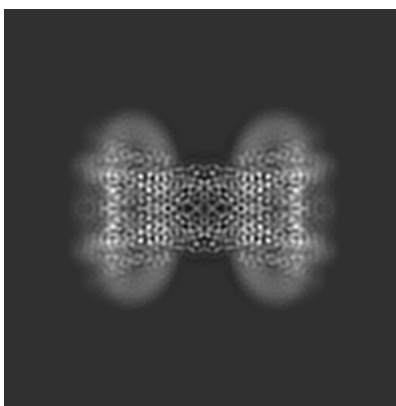
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

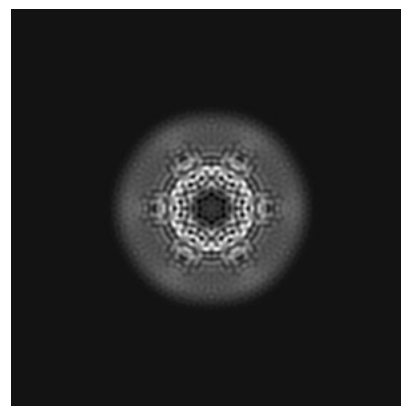
6.1.1 Primary map



X

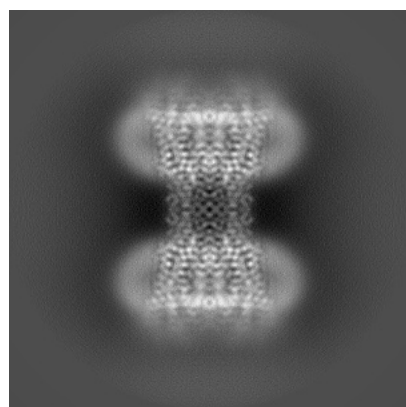


Y

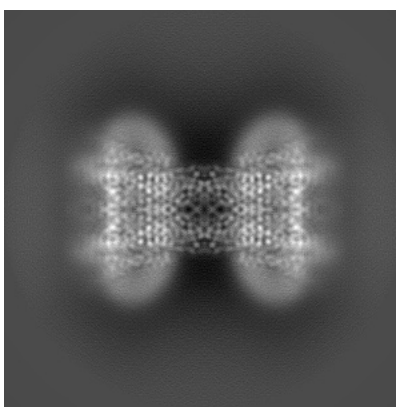


Z

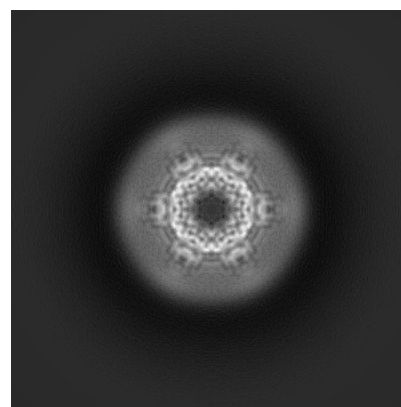
6.1.2 Raw map



X



Y

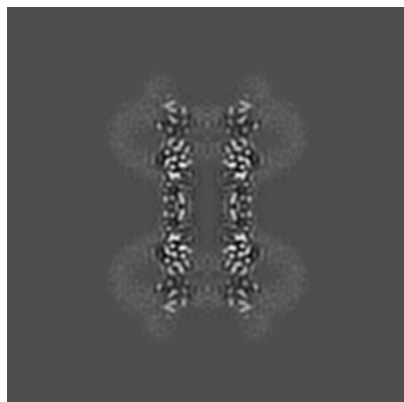


Z

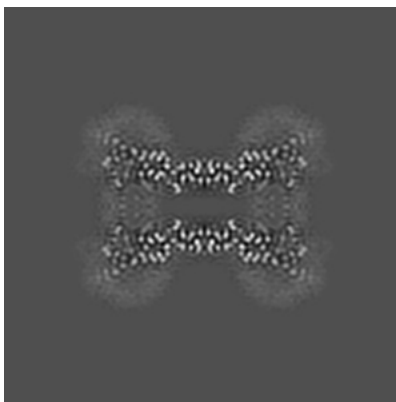
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

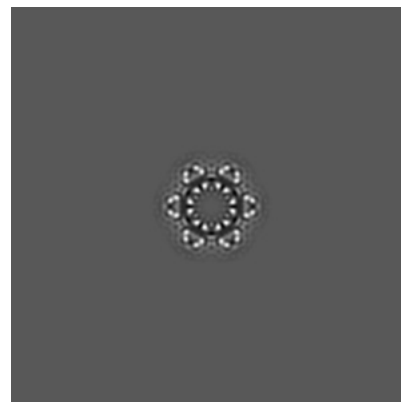
6.2.1 Primary map



X Index: 192

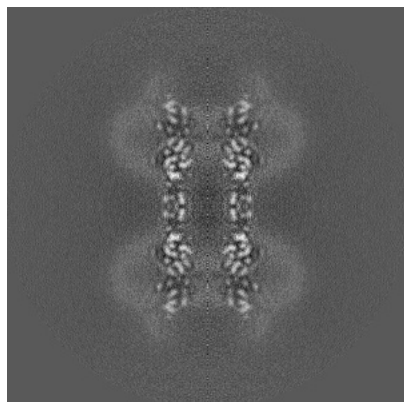


Y Index: 192

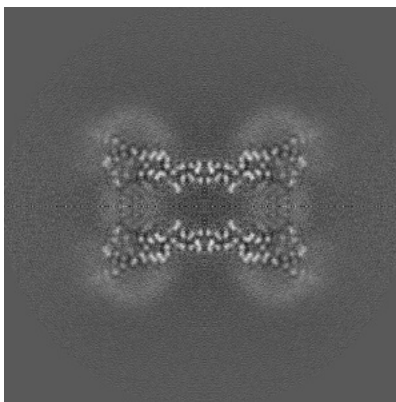


Z Index: 192

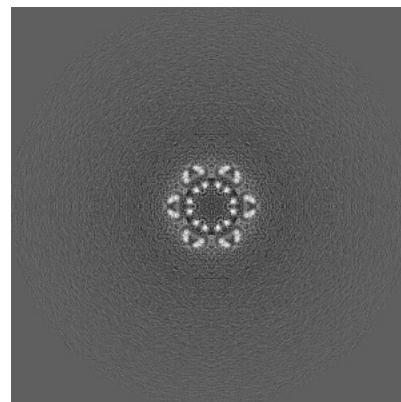
6.2.2 Raw map



X Index: 192



Y Index: 192

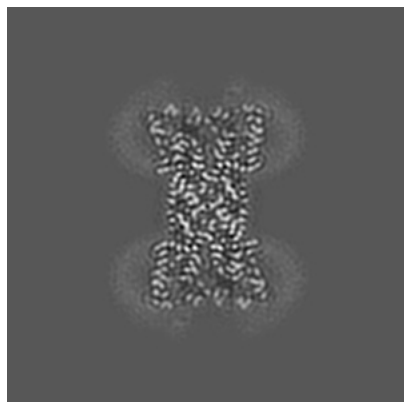


Z Index: 192

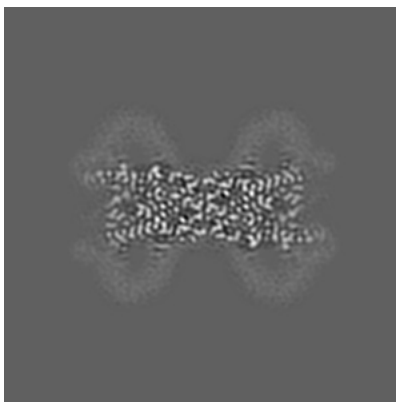
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

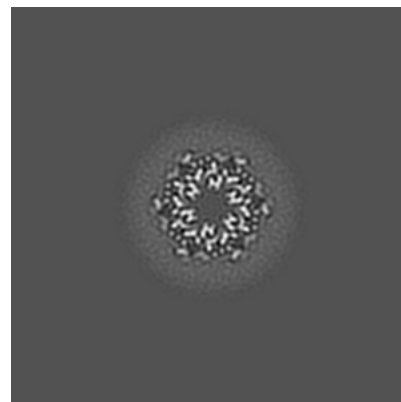
6.3.1 Primary map



X Index: 171

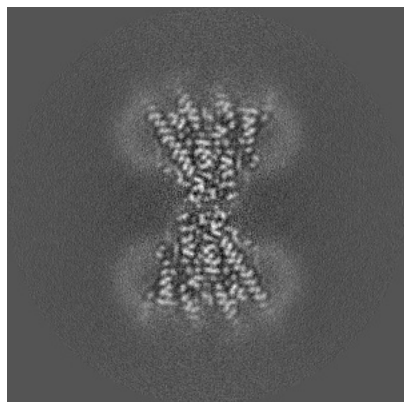


Y Index: 217

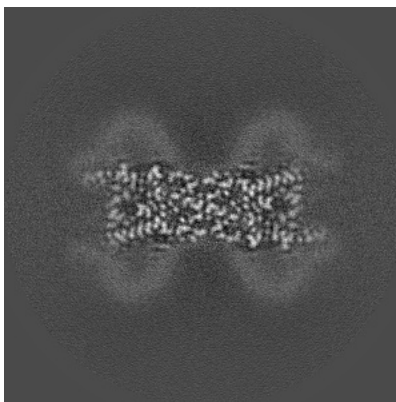


Z Index: 231

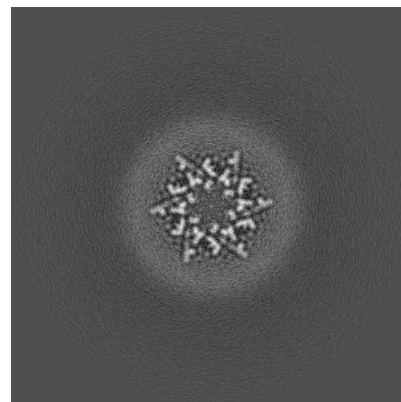
6.3.2 Raw map



X Index: 224



Y Index: 217

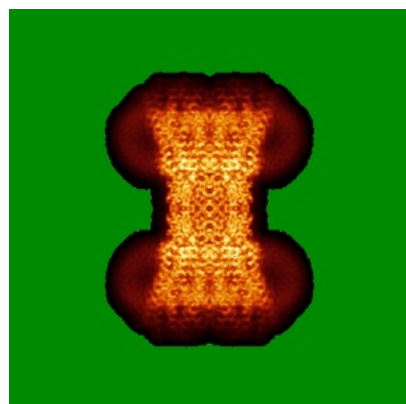


Z Index: 146

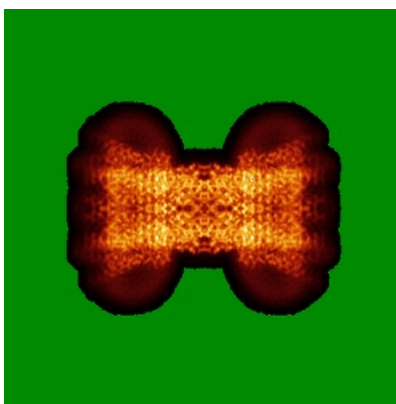
The images above show the largest variance slices of the map in three orthogonal directions.

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

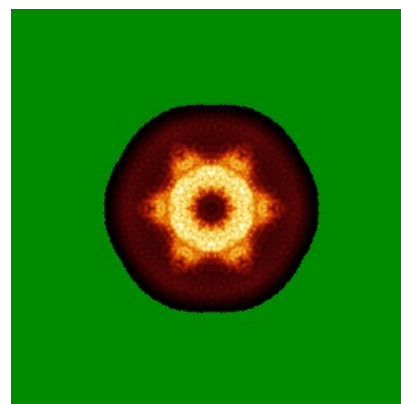
6.4.1 Primary map



X

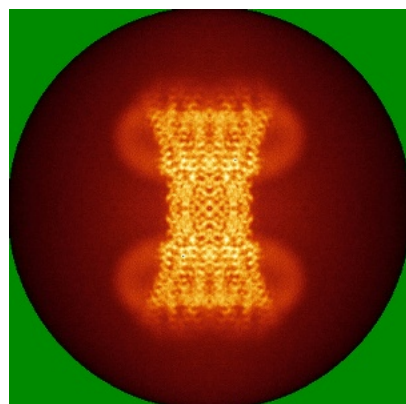


Y

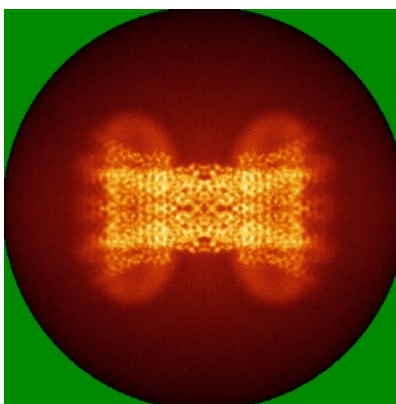


Z

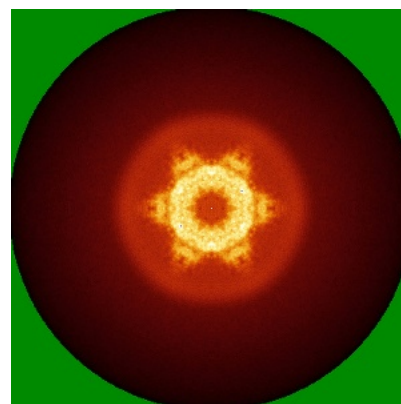
6.4.2 Raw map



X



Y

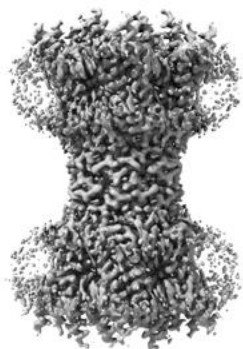


Z

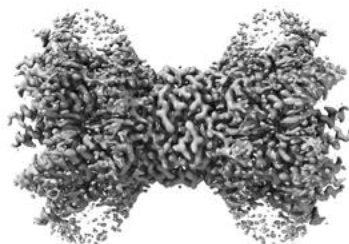
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

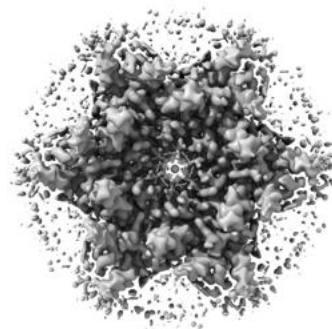
6.5.1 Primary map



X



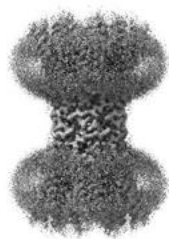
Y



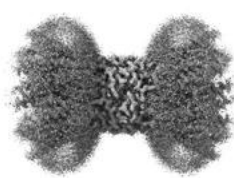
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0022. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

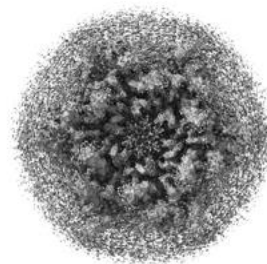
6.5.2 Raw map



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.

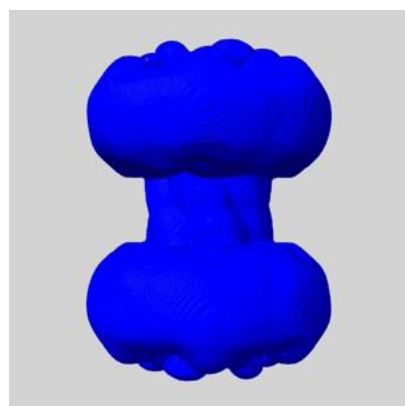
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

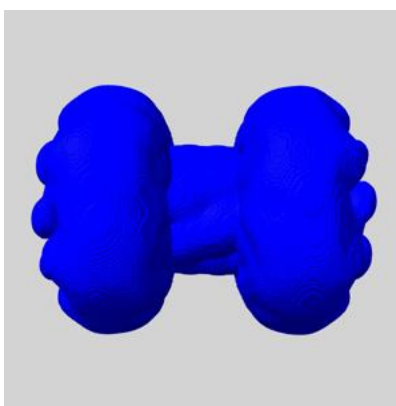
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

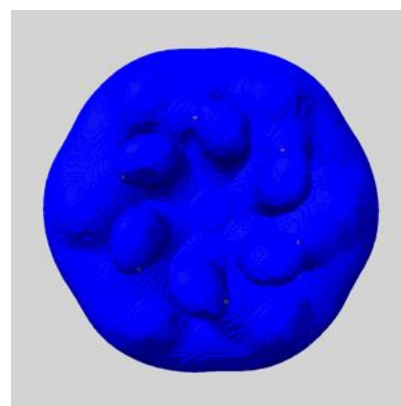
6.6.1 emd_53250_msk_1.map [i](#)



X



Y

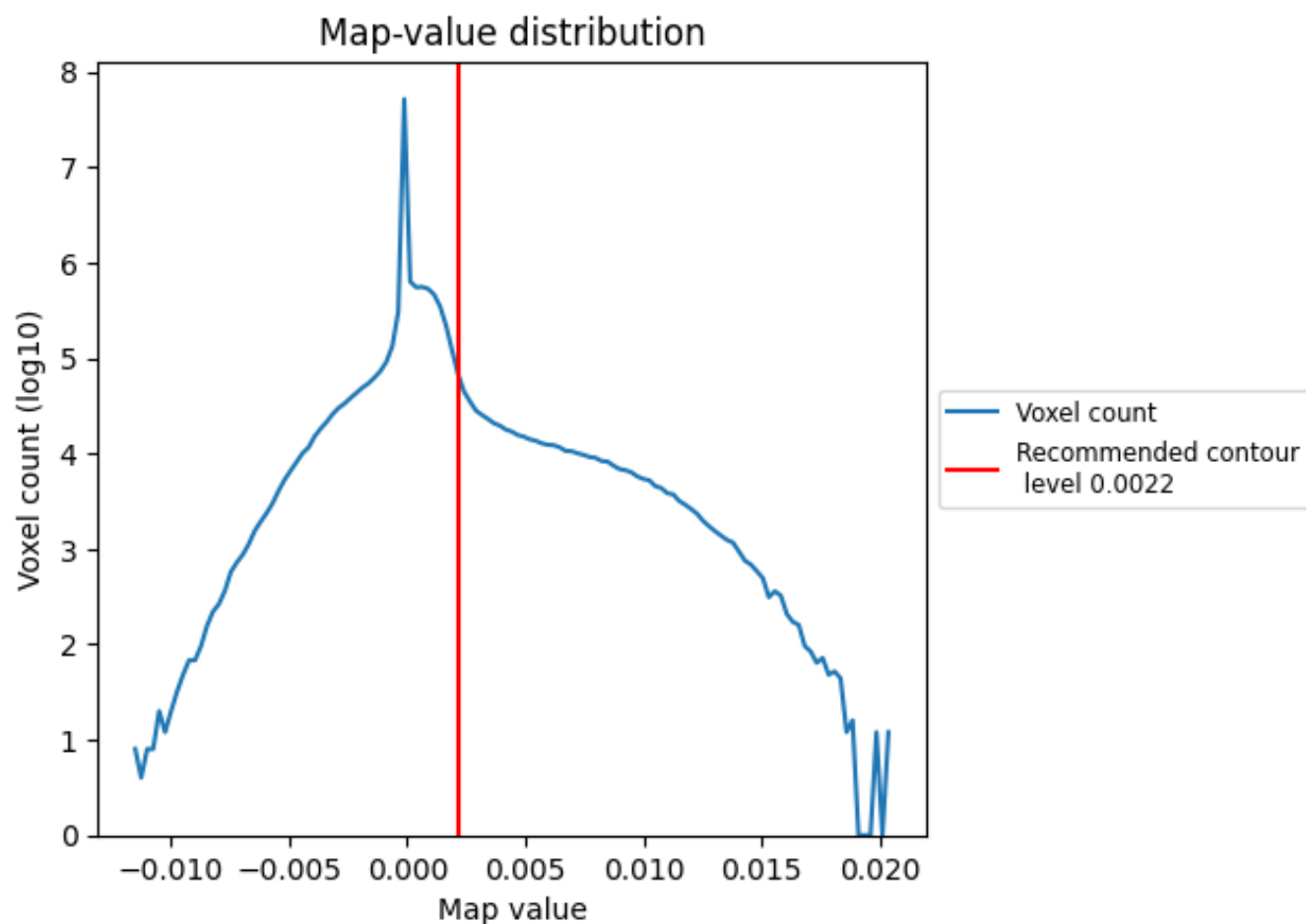


Z

7 Map analysis [i](#)

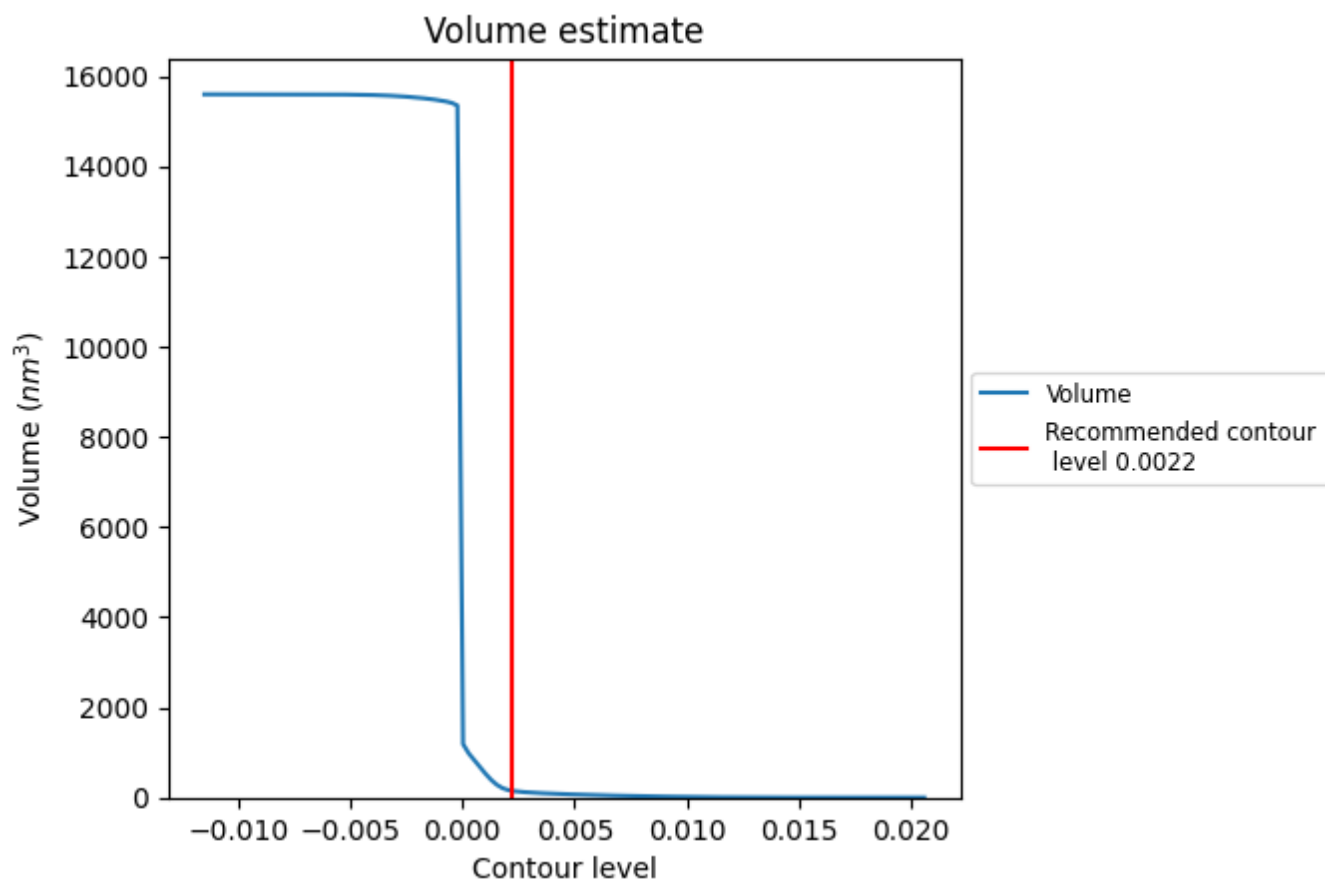
This section contains the results of statistical analysis of the map.

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.

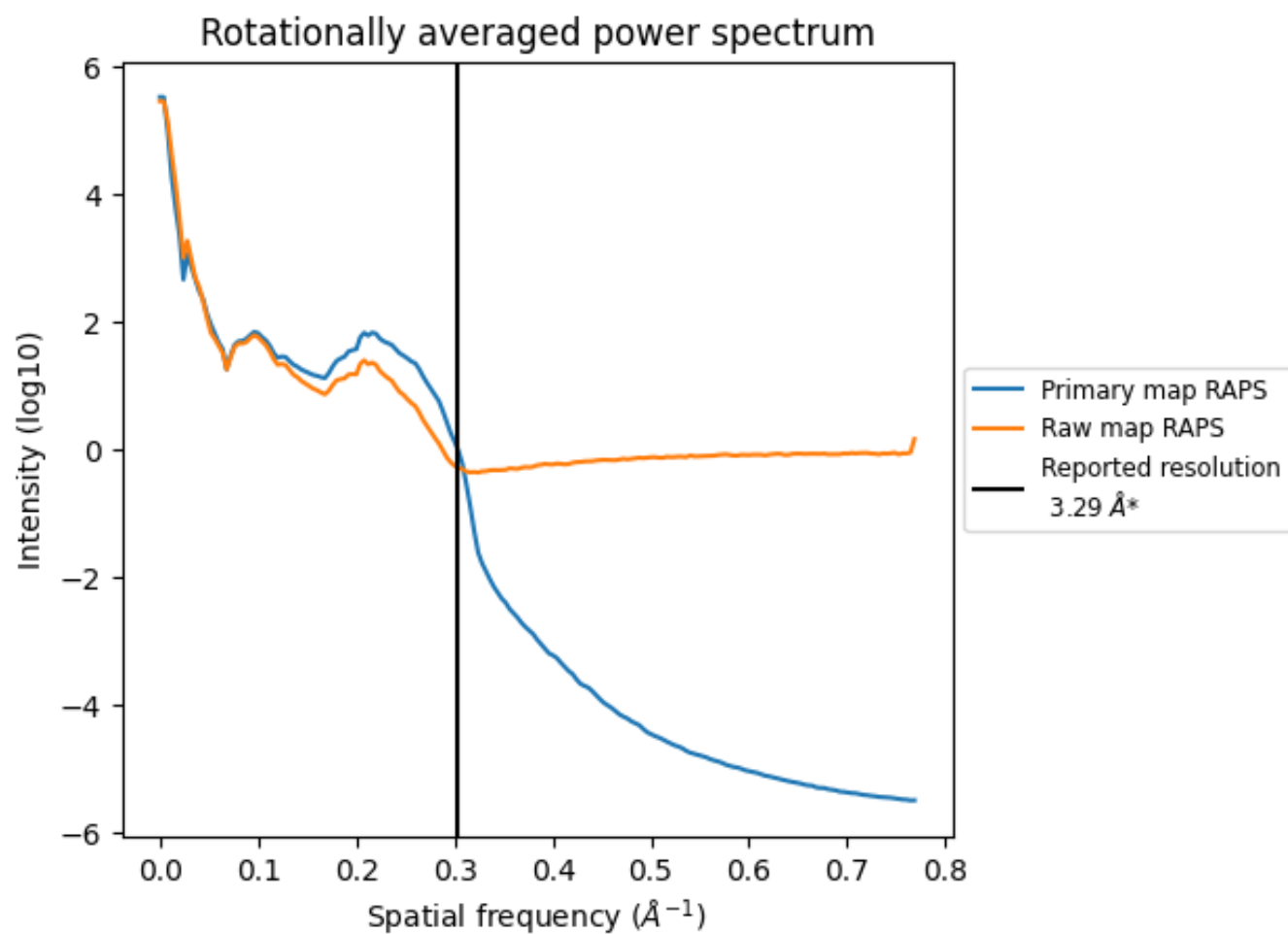
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 153 nm³; this corresponds to an approximate mass of 138 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 ⓘ

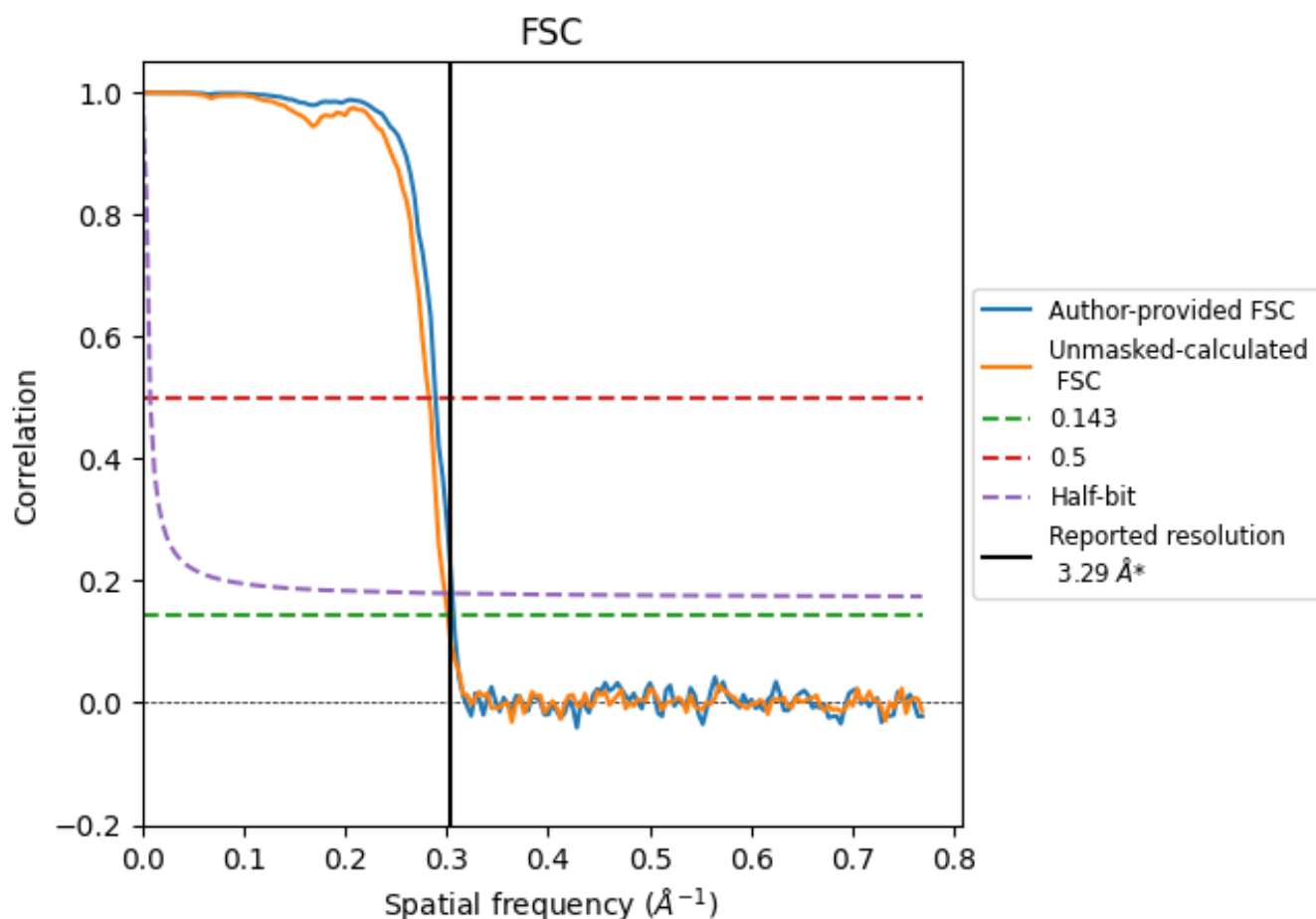


*Reported resolution corresponds to spatial frequency of 0.304 Å⁻¹

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 0.304 \AA^{-1}

8.2 Resolution estimates [i](#)

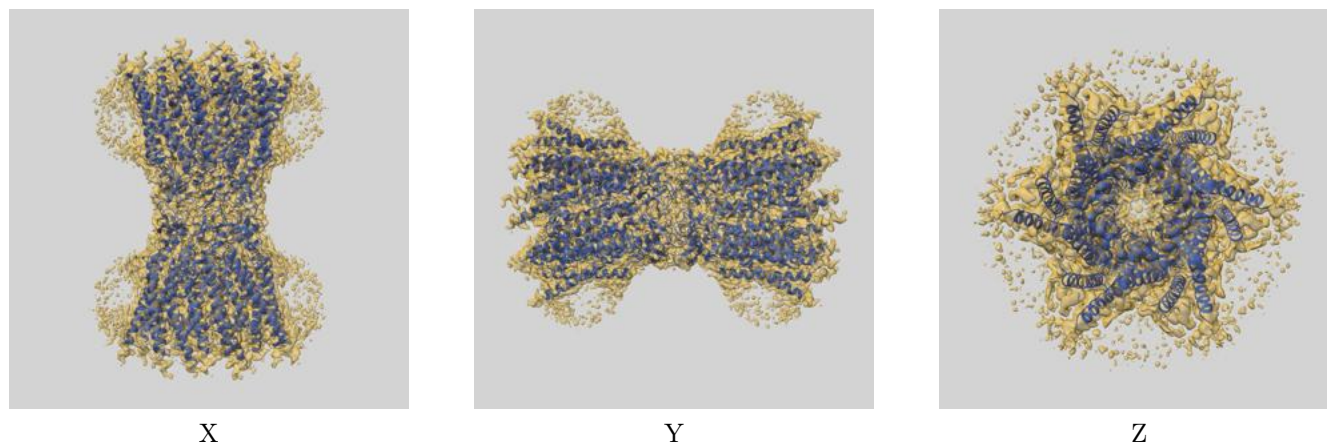
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.29	-	-
Author-provided FSC curve	3.26	3.46	3.27
Unmasked-calculated*	3.32	3.54	3.35

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

9 Map-model fit [i](#)

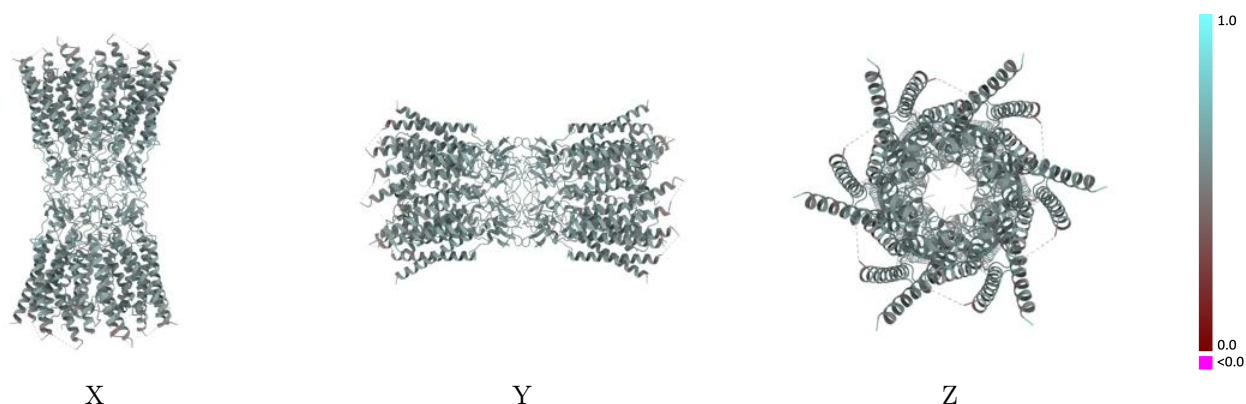
This section contains information regarding the fit between EMDB map EMD-53250 and PDB model 9QNT. Per-residue inclusion information can be found in section [3](#) on page [22](#).

9.1 Map-model overlay [i](#)



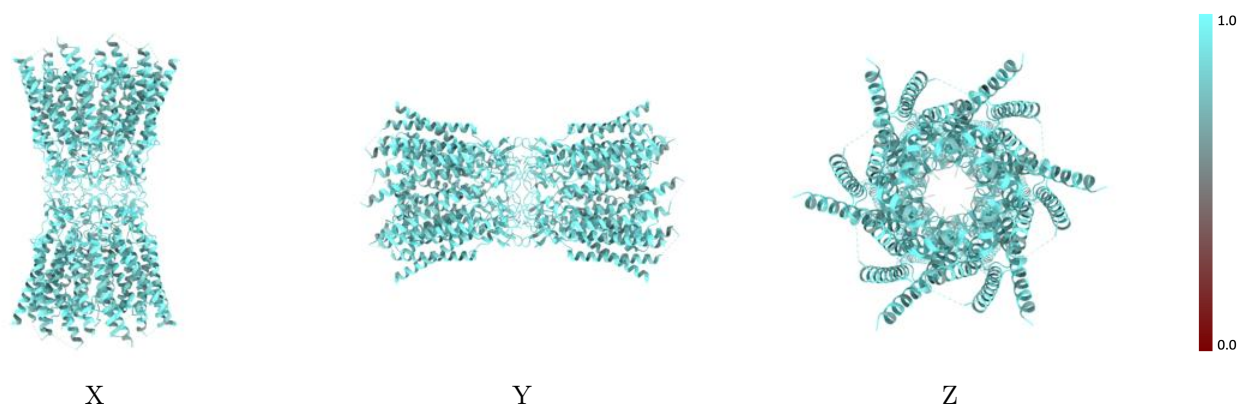
The images above show the 3D surface view of the map at the recommended contour level 0.0022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



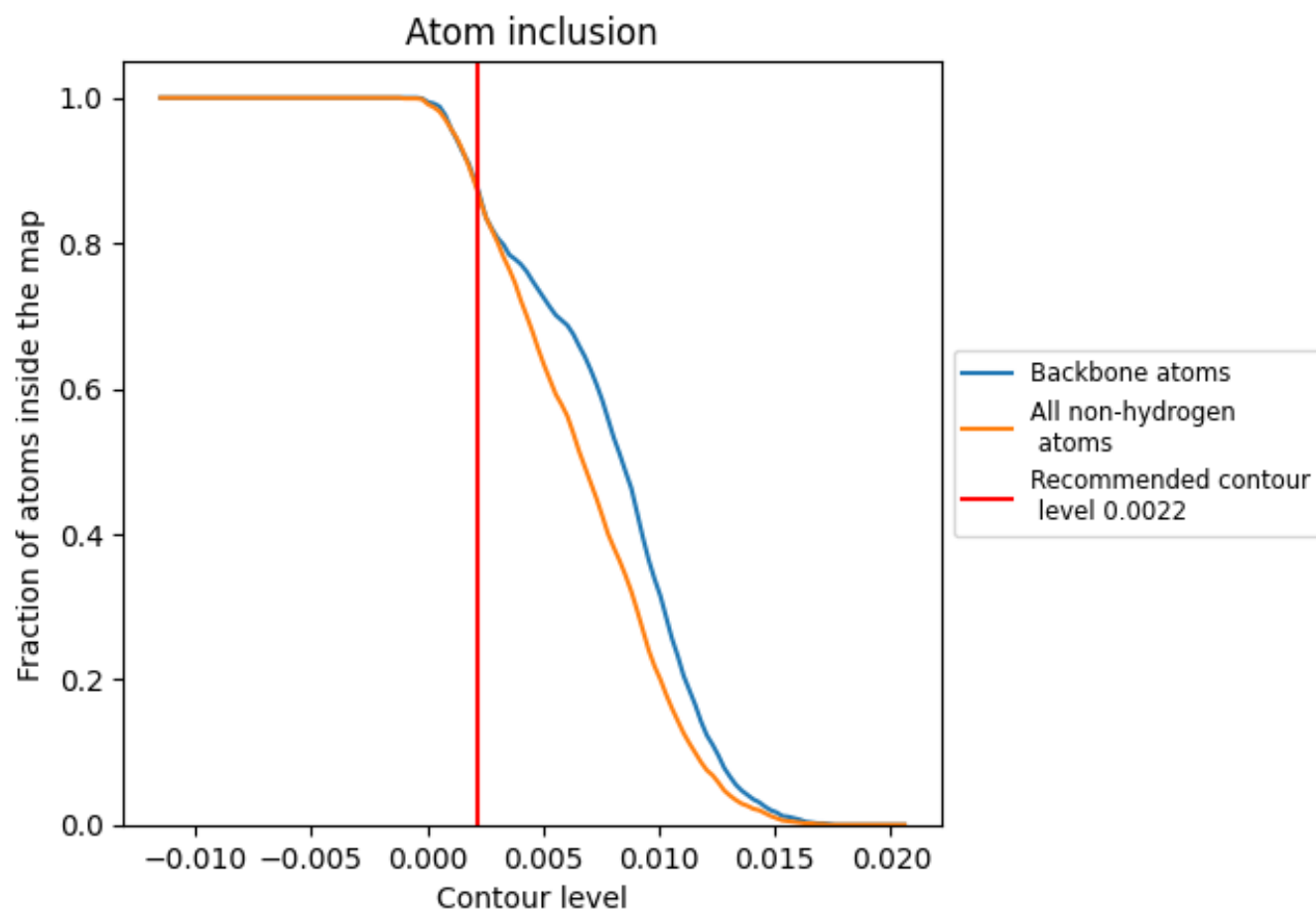
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0022).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 87% 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 (0.0022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8700	<div><div></div></div> 0.5490
A	<div><div></div></div> 0.8680	<div><div></div></div> 0.5470
B	<div><div></div></div> 0.8710	<div><div></div></div> 0.5490
C	<div><div></div></div> 0.8710	<div><div></div></div> 0.5490
D	<div><div></div></div> 0.8720	<div><div></div></div> 0.5490
E	<div><div></div></div> 0.8700	<div><div></div></div> 0.5470
F	<div><div></div></div> 0.8700	<div><div></div></div> 0.5500
G	<div><div></div></div> 0.8710	<div><div></div></div> 0.5490
H	<div><div></div></div> 0.8710	<div><div></div></div> 0.5490
I	<div><div></div></div> 0.8680	<div><div></div></div> 0.5480
J	<div><div></div></div> 0.8680	<div><div></div></div> 0.5470
K	<div><div></div></div> 0.8710	<div><div></div></div> 0.5480
L	<div><div></div></div> 0.8690	<div><div></div></div> 0.5490

1.0

0.0

<0.0