



## wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 10:26 AM UTC

PDB ID : 8VAV / pdb\_00008vav  
EMDB ID : EMD-43106  
Title : Human Slo1 - human LRRC26 in presence of EDTA - GR masked  
Authors : Pal, K.; Kallure, G.S.; Chowdhury, S.  
Deposited on : 2023-12-11  
Resolution : 3.13 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

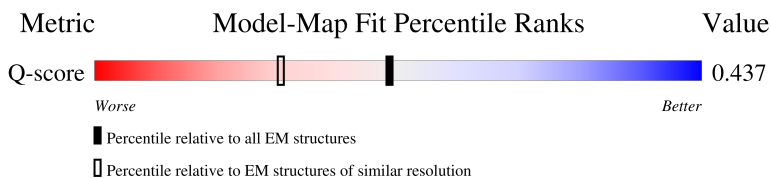
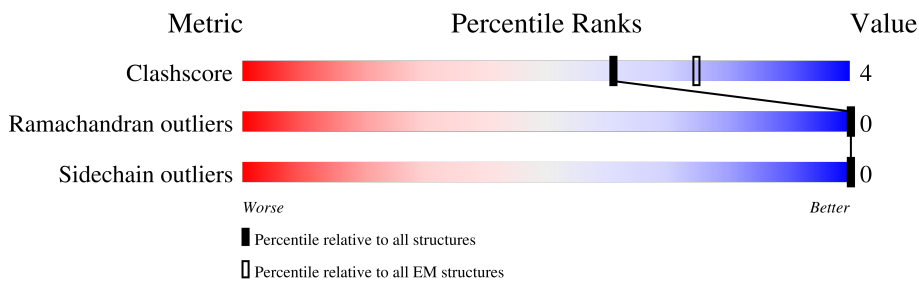
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*




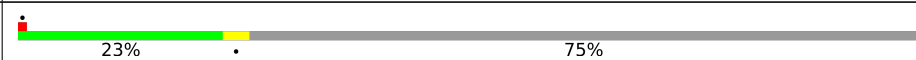
The reported resolution of this entry is 3.13 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



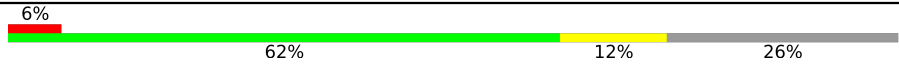

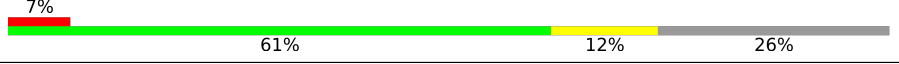

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14478 ( 2.63 - 3.63 )

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  $\geq 3$ , 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	1065	
1	B	1065	
1	C	1065	
1	D	1065	

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Mol	Chain	Length	Quality of chain
2	E	344	 6% 62% 12% 26%
2	F	344	 6% 62% 12% 26%
2	G	344	 7% 61% 12% 26%
2	H	344	 6% 62% 12% 26%

## 2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 18532 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 Calcium-activated potassium channel subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	271	2201	1476	342	371	12	0	0
1	B	271	2201	1476	342	371	12	0	0
1	C	271	2201	1476	342	371	12	0	0
1	D	271	2201	1476	342	371	12	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1057	SER	-	expression tag	UNP Q12791
A	1058	ASN	-	expression tag	UNP Q12791
A	1059	SER	-	expression tag	UNP Q12791
A	1060	LEU	-	expression tag	UNP Q12791
A	1061	GLU	-	expression tag	UNP Q12791
A	1062	VAL	-	expression tag	UNP Q12791
A	1063	LEU	-	expression tag	UNP Q12791
A	1064	PHE	-	expression tag	UNP Q12791
A	1065	GLN	-	expression tag	UNP Q12791
B	1057	SER	-	expression tag	UNP Q12791
B	1058	ASN	-	expression tag	UNP Q12791
B	1059	SER	-	expression tag	UNP Q12791
B	1060	LEU	-	expression tag	UNP Q12791
B	1061	GLU	-	expression tag	UNP Q12791
B	1062	VAL	-	expression tag	UNP Q12791
B	1063	LEU	-	expression tag	UNP Q12791
B	1064	PHE	-	expression tag	UNP Q12791
B	1065	GLN	-	expression tag	UNP Q12791
C	1057	SER	-	expression tag	UNP Q12791
C	1058	ASN	-	expression tag	UNP Q12791
C	1059	SER	-	expression tag	UNP Q12791
C	1060	LEU	-	expression tag	UNP Q12791

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1061	GLU	-	expression tag	UNP Q12791
C	1062	VAL	-	expression tag	UNP Q12791
C	1063	LEU	-	expression tag	UNP Q12791
C	1064	PHE	-	expression tag	UNP Q12791
C	1065	GLN	-	expression tag	UNP Q12791
D	1057	SER	-	expression tag	UNP Q12791
D	1058	ASN	-	expression tag	UNP Q12791
D	1059	SER	-	expression tag	UNP Q12791
D	1060	LEU	-	expression tag	UNP Q12791
D	1061	GLU	-	expression tag	UNP Q12791
D	1062	VAL	-	expression tag	UNP Q12791
D	1063	LEU	-	expression tag	UNP Q12791
D	1064	PHE	-	expression tag	UNP Q12791
D	1065	GLN	-	expression tag	UNP Q12791

- Molecule 2 is a protein called Leucine-rich repeat-containing protein 26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	253	1850	1177	343	319	11	0	0
2	F	253	1850	1177	343	319	11	0	0
2	G	253	1850	1177	343	319	11	0	0
2	H	253	1850	1177	343	319	11	0	0

There are 40 discrepancies between the modelled and reference sequences:

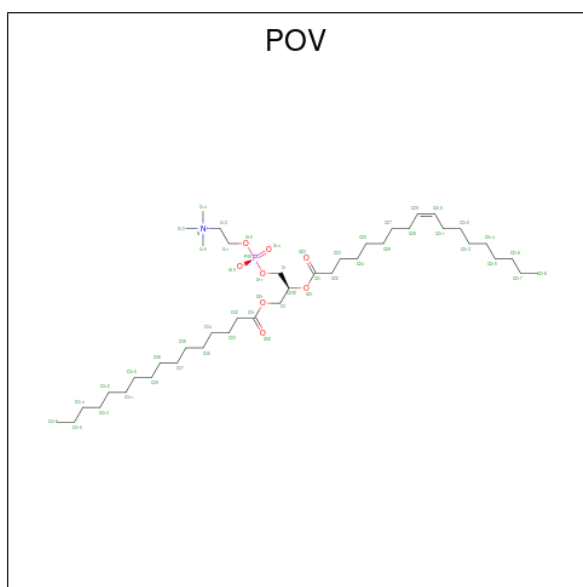
Chain	Residue	Modelled	Actual	Comment	Reference
E	335	ALA	-	expression tag	UNP Q2I0M4
E	336	ALA	-	expression tag	UNP Q2I0M4
E	337	ALA	-	expression tag	UNP Q2I0M4
E	338	GLY	-	expression tag	UNP Q2I0M4
E	339	LEU	-	expression tag	UNP Q2I0M4
E	340	GLU	-	expression tag	UNP Q2I0M4
E	341	VAL	-	expression tag	UNP Q2I0M4
E	342	LEU	-	expression tag	UNP Q2I0M4
E	343	PHE	-	expression tag	UNP Q2I0M4
E	344	GLN	-	expression tag	UNP Q2I0M4
F	335	ALA	-	expression tag	UNP Q2I0M4
F	336	ALA	-	expression tag	UNP Q2I0M4

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Chain	Residue	Modelled	Actual	Comment	Reference
F	337	ALA	-	expression tag	UNP Q2I0M4
F	338	GLY	-	expression tag	UNP Q2I0M4
F	339	LEU	-	expression tag	UNP Q2I0M4
F	340	GLU	-	expression tag	UNP Q2I0M4
F	341	VAL	-	expression tag	UNP Q2I0M4
F	342	LEU	-	expression tag	UNP Q2I0M4
F	343	PHE	-	expression tag	UNP Q2I0M4
F	344	GLN	-	expression tag	UNP Q2I0M4
G	335	ALA	-	expression tag	UNP Q2I0M4
G	336	ALA	-	expression tag	UNP Q2I0M4
G	337	ALA	-	expression tag	UNP Q2I0M4
G	338	GLY	-	expression tag	UNP Q2I0M4
G	339	LEU	-	expression tag	UNP Q2I0M4
G	340	GLU	-	expression tag	UNP Q2I0M4
G	341	VAL	-	expression tag	UNP Q2I0M4
G	342	LEU	-	expression tag	UNP Q2I0M4
G	343	PHE	-	expression tag	UNP Q2I0M4
G	344	GLN	-	expression tag	UNP Q2I0M4
H	335	ALA	-	expression tag	UNP Q2I0M4
H	336	ALA	-	expression tag	UNP Q2I0M4
H	337	ALA	-	expression tag	UNP Q2I0M4
H	338	GLY	-	expression tag	UNP Q2I0M4
H	339	LEU	-	expression tag	UNP Q2I0M4
H	340	GLU	-	expression tag	UNP Q2I0M4
H	341	VAL	-	expression tag	UNP Q2I0M4
H	342	LEU	-	expression tag	UNP Q2I0M4
H	343	PHE	-	expression tag	UNP Q2I0M4
H	344	GLN	-	expression tag	UNP Q2I0M4

- Molecule 3 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylammonio)ethyl phosphate (CCD ID: POV) (formula: C<sub>42</sub>H<sub>82</sub>NO<sub>8</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	AltConf
3	A	1	Total C O P 37 28 8 1	0
3	A	1	Total C O 10 9 1	0
3	A	1	Total C O P 36 27 8 1	0
3	A	1	Total C O 15 13 2	0
3	A	1	Total C O P 31 22 8 1	0
3	B	1	Total C O P 37 28 8 1	0
3	B	1	Total C O 10 9 1	0
3	B	1	Total C O P 36 27 8 1	0
3	B	1	Total C O 15 13 2	0
3	B	1	Total C O P 31 22 8 1	0
3	C	1	Total C O P 37 28 8 1	0
3	C	1	Total C O 10 9 1	0
3	C	1	Total C O P 36 27 8 1	0
3	C	1	Total C O 15 13 2	0

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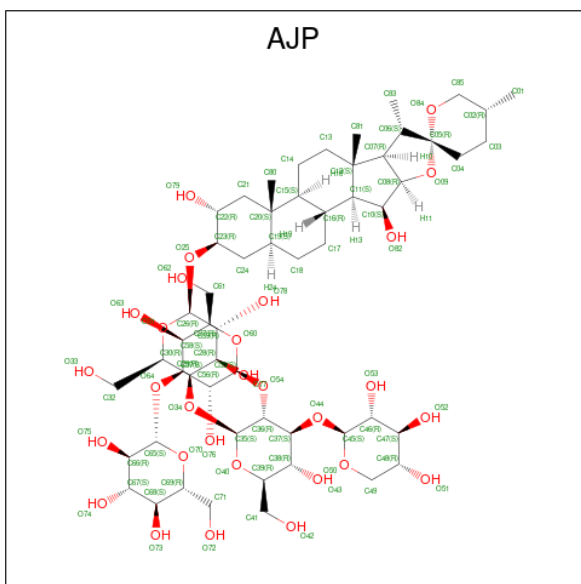
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Mol	Chain	Residues	Atoms				AltConf
3	C	1	Total	C	O	P	0
			31	22	8	1	
3	D	1	Total	C	O	P	0
			37	28	8	1	
3	D	1	Total	C	O	P	0
			36	27	8	1	
3	D	1	Total	C	O		0
			10	9	1		
3	D	1	Total	C	O		0
			15	13	2		
3	D	1	Total	C	O	P	0
			31	22	8	1	

- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	A	4	Total	K	0
			4	4	

- Molecule 5 is Digitonin (CCD ID: AJP) (formula: C<sub>56</sub>H<sub>92</sub>O<sub>29</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
5	A	1	Total	C	O	0
			54	39	15	

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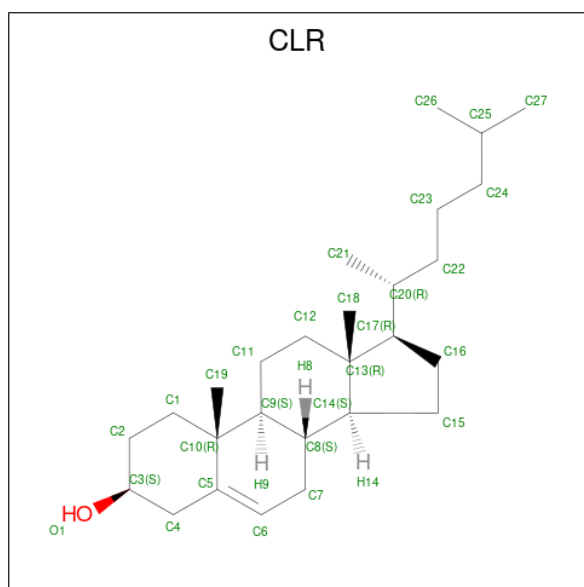
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
5	A	1	54	39	15	0
5	A	1	43	33	10	0
5	A	1	65	45	20	0
5	A	1	43	33	10	0
5	A	1	43	33	10	0
5	A	1	54	39	15	0
5	A	1	54	39	15	0
5	B	1	54	39	15	0
5	B	1	54	39	15	0
5	B	1	43	33	10	0
5	B	1	65	45	20	0
5	B	1	43	33	10	0
5	B	1	43	33	10	0
5	B	1	54	39	15	0
5	B	1	54	39	15	0
5	C	1	54	39	15	0
5	C	1	54	39	15	0
5	C	1	43	33	10	0
5	C	1	65	45	20	0
5	C	1	43	33	10	0
5	C	1	43	33	10	0

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Mol	Chain	Residues	Atoms			AltConf
5	C	1	Total	C	O	0
			54	39	15	
5	C	1	Total	C	O	0
			54	39	15	
5	D	1	Total	C	O	0
			54	39	15	
5	D	1	Total	C	O	0
			54	39	15	
5	D	1	Total	C	O	0
			43	33	10	
5	D	1	Total	C	O	0
			65	45	20	
5	D	1	Total	C	O	0
			43	33	10	
5	D	1	Total	C	O	0
			43	33	10	
5	D	1	Total	C	O	0
			54	39	15	
5	D	1	Total	C	O	0
			54	39	15	

- Molecule 6 is CHOLESTEROL (CCD ID: CLR) (formula: C<sub>27</sub>H<sub>46</sub>O) (labeled as "Ligand of Interest" by depositor).



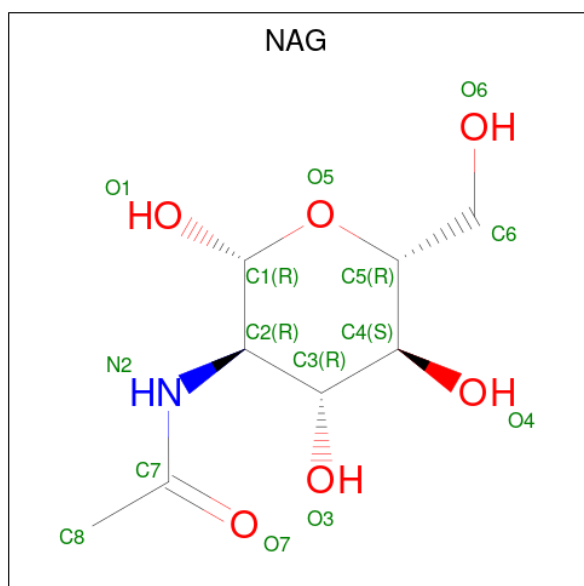
Mol	Chain	Residues	Atoms			AltConf
6	A	1	Total	C	O	0
			28	27	1	

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

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula:  $C_8H_{15}NO_6$ ) (labeled as "Ligand of Interest" by depositor).



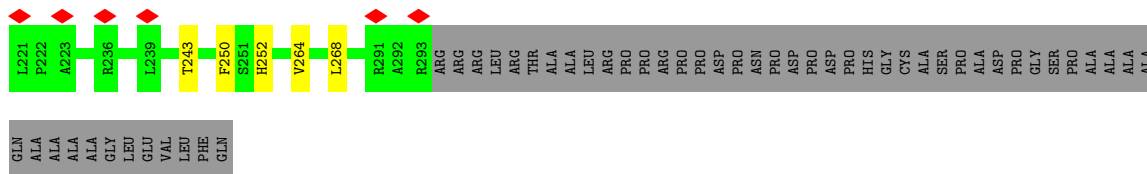
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
7	E	1	14	8	1	5	0
7	F	1	14	8	1	5	0
7	G	1	14	8	1	5	0
7	H	1	14	8	1	5	0



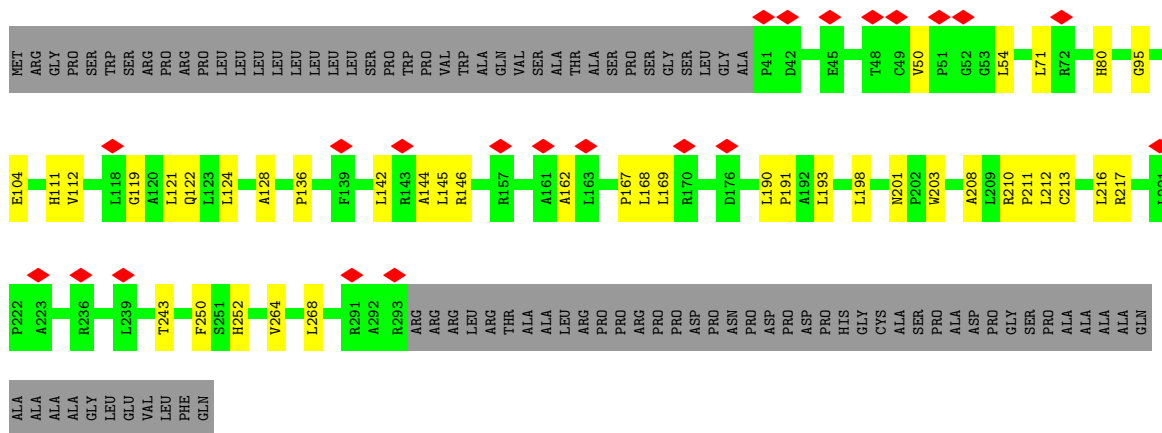




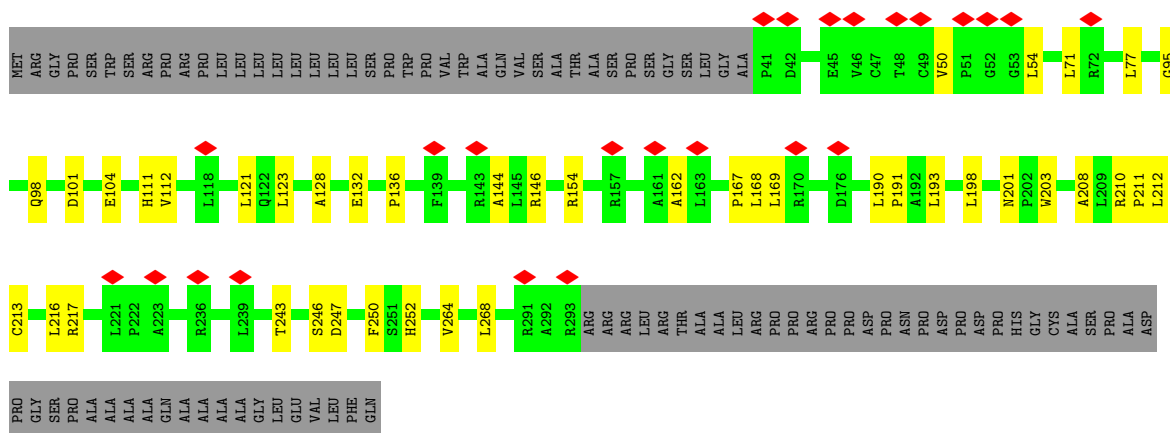




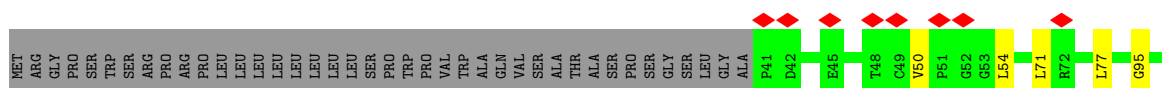
• Molecule 2: Leucine-rich repeat-containing protein 26

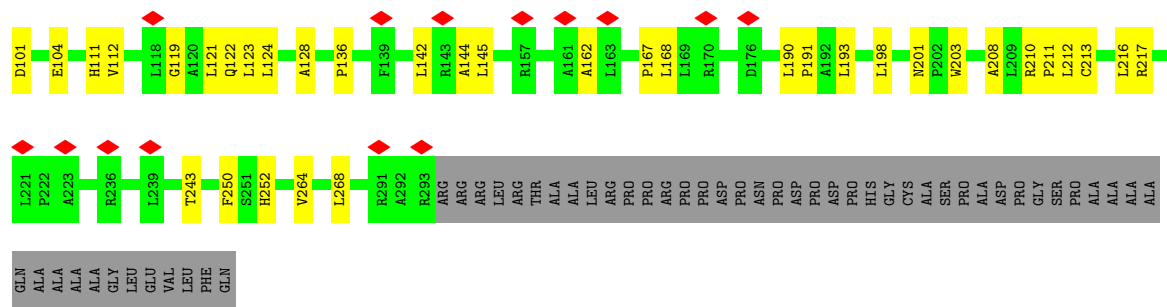


• Molecule 2: Leucine-rich repeat-containing protein 26



• Molecule 2: Leucine-rich repeat-containing protein 26





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	390830	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 ( $e^-/\text{\AA}^2$ )	72	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.432	Depositor
Minimum map value	-0.155	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	276.48, 276.48, 276.48	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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, K, NAG, AJP, 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	0.13	0/2264	0.29	0/3083
1	B	0.13	0/2264	0.30	0/3083
1	C	0.13	0/2264	0.29	0/3083
1	D	0.13	0/2264	0.30	0/3083
2	E	0.12	0/1892	0.32	0/2588
2	F	0.12	0/1892	0.32	0/2588
2	G	0.11	0/1892	0.30	0/2588
2	H	0.12	0/1892	0.32	0/2588
All	All	0.13	0/16624	0.30	0/22684

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	2201	0	2212	14	0
1	B	2201	0	2212	20	0
1	C	2201	0	2212	16	0
1	D	2201	0	2212	17	0
2	E	1850	0	1907	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1850	0	1907	23	0
2	G	1850	0	1907	23	0
2	H	1850	0	1907	24	0
3	A	129	0	157	1	0
3	B	129	0	157	1	0
3	C	129	0	157	2	0
3	D	129	0	157	1	0
4	A	4	0	0	0	0
5	A	410	0	0	0	0
5	B	410	0	0	0	0
5	C	410	0	0	0	0
5	D	410	0	0	0	0
6	A	28	0	46	1	0
6	B	28	0	46	1	0
6	C	28	0	46	1	0
6	D	28	0	46	1	0
7	E	14	0	13	1	0
7	F	14	0	13	0	0
7	G	14	0	13	1	0
7	H	14	0	13	1	0
All	All	18532	0	17340	156	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.

The worst 5 of 156 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)
2:F:119:GLY:HA2	2:F:142:LEU:HA	1.58	0.85
2:H:119:GLY:HA2	2:H:142:LEU:HA	1.64	0.80
2:E:119:GLY:HA2	2:E:142:LEU:HA	1.65	0.77
1:C:141:CYS:HG	2:G:252:HIS:HE2	1.38	0.70
2:G:144:ALA:HA	2:G:168:LEU:HD12	1.86	0.57

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	267/1065 (25%)	263 (98%)	4 (2%)	0	100	100
1	B	267/1065 (25%)	263 (98%)	4 (2%)	0	100	100
1	C	267/1065 (25%)	263 (98%)	4 (2%)	0	100	100
1	D	267/1065 (25%)	263 (98%)	4 (2%)	0	100	100
2	E	251/344 (73%)	246 (98%)	5 (2%)	0	100	100
2	F	251/344 (73%)	246 (98%)	5 (2%)	0	100	100
2	G	251/344 (73%)	247 (98%)	4 (2%)	0	100	100
2	H	251/344 (73%)	246 (98%)	5 (2%)	0	100	100
All	All	2072/5636 (37%)	2037 (98%)	35 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	239/937 (26%)	239 (100%)	0	100	100
1	B	239/937 (26%)	239 (100%)	0	100	100
1	C	239/937 (26%)	239 (100%)	0	100	100
1	D	239/937 (26%)	239 (100%)	0	100	100
2	E	190/260 (73%)	190 (100%)	0	100	100
2	F	190/260 (73%)	190 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	G	190/260 (73%)	190 (100%)	0	100	100
2	H	190/260 (73%)	190 (100%)	0	100	100
All	All	1716/4788 (36%)	1716 (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 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	98	GLN
2	E	122	GLN
2	H	122	GLN
2	G	122	GLN
2	H	98	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 64 ligands modelled in this entry, 4 are monoatomic - leaving 60 for Mogul analysis.

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
6	CLR	A	1118	-	31,31,31	0.40	0	48,48,48	0.65	0
5	AJP	B	1107	-	61,61,95	0.16	0	93,98,149	0.46	0
3	POV	D	1105	-	30,30,51	0.77	1 (3%)	33,35,59	0.90	2 (6%)
5	AJP	A	1116	-	61,61,95	0.14	0	93,98,149	0.35	0
3	POV	D	1101	-	36,36,51	0.70	1 (2%)	39,41,59	0.90	2 (5%)
3	POV	B	1103	-	35,35,51	0.72	1 (2%)	38,40,59	0.85	2 (5%)
5	AJP	D	1110	-	49,49,95	0.17	0	75,80,149	0.38	0
5	AJP	B	1110	-	49,49,95	0.16	0	75,80,149	0.37	0
5	AJP	D	1106	-	61,61,95	0.16	0	93,98,149	0.47	1 (1%)
5	AJP	A	1114	-	49,49,95	0.16	0	75,80,149	0.38	0
5	AJP	C	1106	-	61,61,95	0.16	0	93,98,149	0.47	1 (1%)
7	NAG	G	401	2	14,14,15	0.70	0	17,19,21	0.84	0
5	AJP	A	1110	-	61,61,95	0.16	0	93,98,149	0.47	1 (1%)
5	AJP	A	1113	-	73,73,95	0.15	0	111,116,149	0.44	0
7	NAG	F	401	2	14,14,15	0.64	0	17,19,21	1.56	1 (5%)
5	AJP	B	1112	-	61,61,95	0.14	0	93,98,149	0.35	0
5	AJP	B	1109	-	73,73,95	0.15	0	111,116,149	0.44	0
5	AJP	B	1111	-	49,49,95	0.16	0	75,80,149	0.44	0
5	AJP	C	1110	-	49,49,95	0.16	0	75,80,149	0.38	0
5	AJP	A	1115	-	49,49,95	0.16	0	75,80,149	0.44	0
3	POV	A	1102	-	9,9,51	0.59	0	8,8,59	0.29	0
7	NAG	E	401	2	14,14,15	0.70	0	17,19,21	0.81	0
6	CLR	B	1114	-	31,31,31	0.41	0	48,48,48	0.67	0
3	POV	B	1101	-	36,36,51	0.70	1 (2%)	39,41,59	0.91	2 (5%)
3	POV	C	1102	-	9,9,51	0.59	0	8,8,59	0.29	0
3	POV	D	1102	-	35,35,51	0.71	1 (2%)	38,40,59	0.85	2 (5%)
5	AJP	B	1108	-	49,49,95	0.16	0	75,80,149	0.46	0
5	AJP	A	1111	-	61,61,95	0.16	0	93,98,149	0.46	0
3	POV	A	1108	-	14,14,51	1.24	2 (14%)	14,14,59	1.43	2 (14%)
5	AJP	C	1109	-	73,73,95	0.15	0	111,116,149	0.44	0
5	AJP	C	1112	-	61,61,95	0.14	0	93,98,149	0.35	0
5	AJP	D	1111	-	49,49,95	0.16	0	75,80,149	0.43	0
5	AJP	D	1112	-	61,61,95	0.14	0	93,98,149	0.35	0
5	AJP	B	1106	-	61,61,95	0.16	0	93,98,149	0.47	1 (1%)
3	POV	C	1103	-	35,35,51	0.72	1 (2%)	38,40,59	0.85	2 (5%)
5	AJP	D	1107	-	61,61,95	0.16	0	93,98,149	0.46	0
3	POV	A	1101	-	36,36,51	0.70	1 (2%)	39,41,59	0.90	2 (5%)
5	AJP	C	1107	-	61,61,95	0.16	0	93,98,149	0.46	0
5	AJP	C	1111	-	49,49,95	0.15	0	75,80,149	0.44	0
3	POV	B	1104	-	14,14,51	1.24	2 (14%)	14,14,59	1.43	2 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	POV	C	1101	-	36,36,51	0.70	1 (2%)	39,41,59	0.91	2 (5%)
3	POV	D	1103	-	9,9,51	0.59	0	8,8,59	0.29	0
3	POV	B	1105	-	30,30,51	0.77	1 (3%)	33,35,59	0.91	2 (6%)
3	POV	A	1103	-	35,35,51	0.72	1 (2%)	38,40,59	0.85	2 (5%)
3	POV	D	1104	-	14,14,51	1.23	2 (14%)	14,14,59	1.42	2 (14%)
3	POV	A	1109	-	30,30,51	0.77	1 (3%)	33,35,59	0.91	2 (6%)
5	AJP	B	1113	-	61,61,95	0.17	0	93,98,149	0.48	1 (1%)
5	AJP	C	1108	-	49,49,95	0.17	0	75,80,149	0.46	0
6	CLR	C	1114	-	31,31,31	0.40	0	48,48,48	0.67	0
6	CLR	D	1114	-	31,31,31	0.41	0	48,48,48	0.67	0
5	AJP	D	1108	-	49,49,95	0.16	0	75,80,149	0.46	0
5	AJP	A	1112	-	49,49,95	0.17	0	75,80,149	0.46	0
5	AJP	D	1109	-	73,73,95	0.15	0	111,116,149	0.44	0
5	AJP	D	1113	-	61,61,95	0.17	0	93,98,149	0.48	1 (1%)
3	POV	B	1102	-	9,9,51	0.58	0	8,8,59	0.29	0
3	POV	C	1105	-	30,30,51	0.77	1 (3%)	33,35,59	0.91	2 (6%)
5	AJP	C	1113	-	61,61,95	0.17	0	93,98,149	0.48	1 (1%)
7	NAG	H	401	2	14,14,15	0.71	0	17,19,21	0.81	0
3	POV	C	1104	-	14,14,51	1.25	2 (14%)	14,14,59	1.43	2 (14%)
5	AJP	A	1117	-	61,61,95	0.17	0	93,98,149	0.47	1 (1%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	CLR	A	1118	-	-	2/10/68/68	0/4/4/4
5	AJP	B	1107	-	-	0/12/147/220	0/8/8/11
3	POV	D	1105	-	-	5/32/32/55	-
5	AJP	A	1116	-	-	1/12/147/220	0/8/8/11
3	POV	D	1101	-	-	15/38/38/55	-
3	POV	B	1103	-	-	4/37/37/55	-
5	AJP	D	1110	-	-	1/6/121/220	0/7/7/11
5	AJP	B	1110	-	-	1/6/121/220	0/7/7/11
5	AJP	D	1106	-	-	4/12/147/220	1/8/8/11
5	AJP	A	1114	-	-	1/6/121/220	0/7/7/11
5	AJP	C	1106	-	-	4/12/147/220	1/8/8/11
7	NAG	G	401	2	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	AJP	A	1110	-	-	4/12/147/220	1/8/8/11
5	AJP	A	1113	-	-	5/18/173/220	0/9/9/11
7	NAG	F	401	2	-	2/6/23/26	0/1/1/1
5	AJP	B	1112	-	-	1/12/147/220	0/8/8/11
5	AJP	B	1109	-	-	4/18/173/220	0/9/9/11
5	AJP	B	1111	-	-	2/6/121/220	0/7/7/11
5	AJP	C	1110	-	-	1/6/121/220	0/7/7/11
5	AJP	A	1115	-	-	2/6/121/220	0/7/7/11
3	POV	A	1102	-	-	0/7/7/55	-
7	NAG	E	401	2	-	2/6/23/26	0/1/1/1
6	CLR	B	1114	-	-	2/10/68/68	0/4/4/4
3	POV	B	1101	-	-	15/38/38/55	-
3	POV	C	1102	-	-	0/7/7/55	-
3	POV	D	1102	-	-	5/37/37/55	-
5	AJP	B	1108	-	-	1/6/121/220	0/7/7/11
5	AJP	A	1111	-	-	0/12/147/220	0/8/8/11
3	POV	A	1108	-	-	3/12/12/55	-
5	AJP	C	1109	-	-	4/18/173/220	0/9/9/11
5	AJP	C	1112	-	-	1/12/147/220	0/8/8/11
5	AJP	D	1111	-	-	2/6/121/220	0/7/7/11
5	AJP	D	1112	-	-	1/12/147/220	0/8/8/11
5	AJP	B	1106	-	-	4/12/147/220	1/8/8/11
3	POV	C	1103	-	-	5/37/37/55	-
5	AJP	D	1107	-	-	0/12/147/220	0/8/8/11
3	POV	A	1101	-	-	15/38/38/55	-
5	AJP	C	1107	-	-	0/12/147/220	0/8/8/11
5	AJP	C	1111	-	-	2/6/121/220	0/7/7/11
3	POV	B	1104	-	-	3/12/12/55	-
3	POV	C	1101	-	-	15/38/38/55	-
3	POV	D	1103	-	-	0/7/7/55	-
3	POV	B	1105	-	-	5/32/32/55	-
3	POV	A	1103	-	-	5/37/37/55	-
3	POV	D	1104	-	-	3/12/12/55	-
3	POV	A	1109	-	-	5/32/32/55	-
5	AJP	B	1113	-	-	6/12/147/220	1/8/8/11
5	AJP	C	1108	-	-	1/6/121/220	0/7/7/11

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	CLR	C	1114	-	-	2/10/68/68	0/4/4/4
6	CLR	D	1114	-	-	2/10/68/68	0/4/4/4
5	AJP	D	1108	-	-	1/6/121/220	0/7/7/11
5	AJP	A	1112	-	-	1/6/121/220	0/7/7/11
5	AJP	D	1109	-	-	4/18/173/220	0/9/9/11
5	AJP	D	1113	-	-	6/12/147/220	1/8/8/11
3	POV	B	1102	-	-	0/7/7/55	-
3	POV	C	1105	-	-	5/32/32/55	-
5	AJP	C	1113	-	-	6/12/147/220	1/8/8/11
7	NAG	H	401	2	-	2/6/23/26	0/1/1/1
3	POV	C	1104	-	-	3/12/12/55	-
5	AJP	A	1117	-	-	6/12/147/220	1/8/8/11

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1104	POV	O22-C21	3.49	1.33	1.22
3	A	1108	POV	O22-C21	3.49	1.33	1.22
3	B	1104	POV	O22-C21	3.48	1.33	1.22
3	D	1104	POV	O22-C21	3.46	1.33	1.22
3	A	1103	POV	P-O12	3.06	1.66	1.54

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	F	401	NAG	C1-O5-C5	5.56	119.63	112.19
3	C	1104	POV	O22-C21-C22	-3.82	110.98	123.09
3	A	1108	POV	O22-C21-C22	-3.82	110.99	123.09
3	B	1104	POV	O22-C21-C22	-3.81	111.00	123.09
3	D	1104	POV	O22-C21-C22	-3.80	111.03	123.09

There are no chirality outliers.

5 of 204 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1101	POV	C1-O11-P-O12
3	A	1101	POV	C1-O11-P-O13
3	A	1101	POV	C1-O11-P-O14
3	A	1103	POV	C1-O11-P-O13
3	A	1103	POV	O21-C2-C3-O31

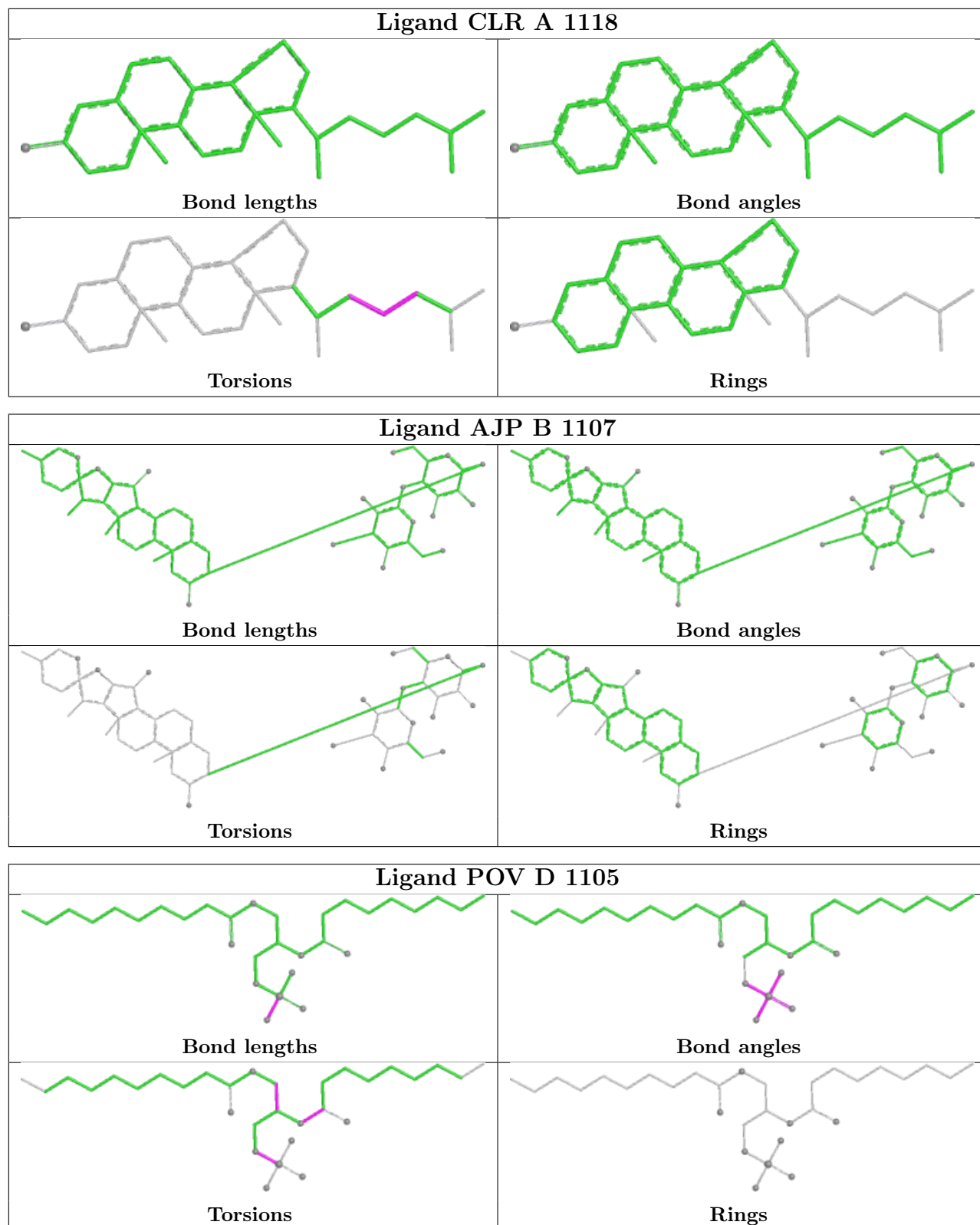
5 of 8 ring outliers are listed below:

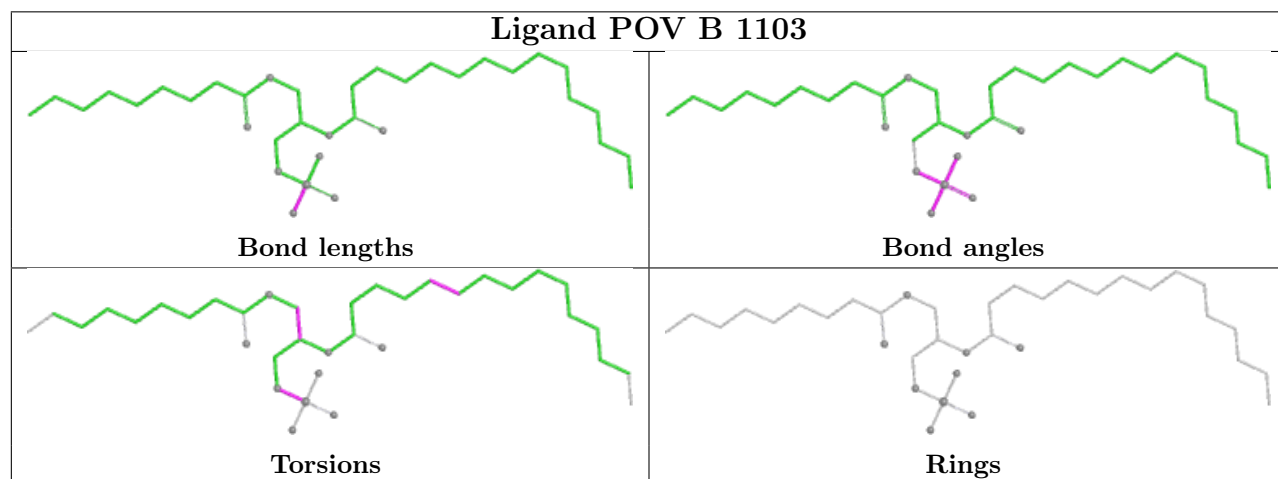
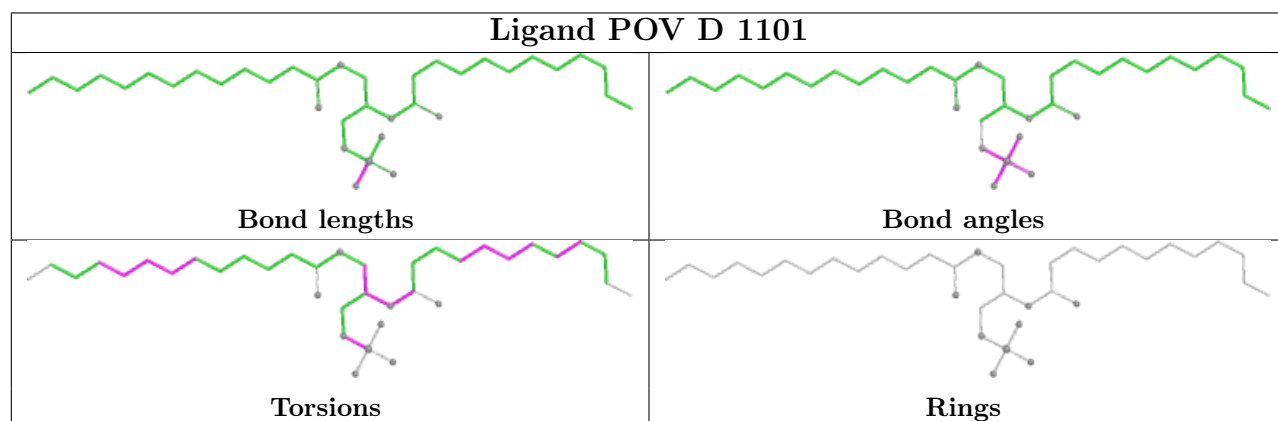
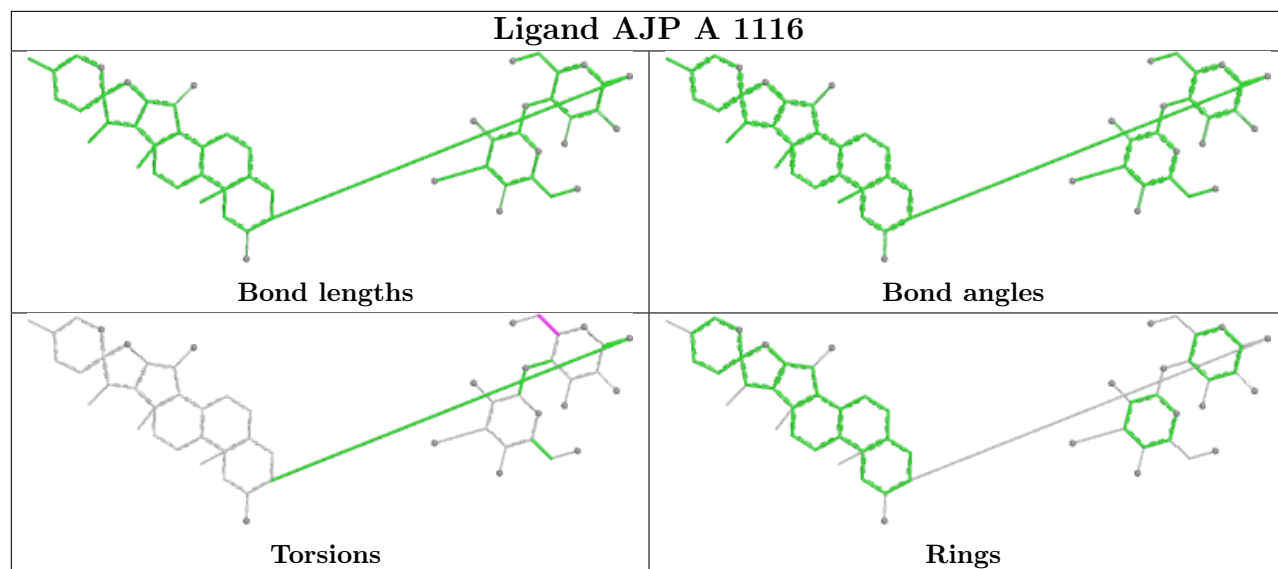
Mol	Chain	Res	Type	Atoms
5	C	1106	AJP	C19-C20-C21-C22-C23-C24
5	A	1110	AJP	C19-C20-C21-C22-C23-C24
5	B	1106	AJP	C19-C20-C21-C22-C23-C24
5	D	1106	AJP	C19-C20-C21-C22-C23-C24
5	A	1117	AJP	C19-C20-C21-C22-C23-C24

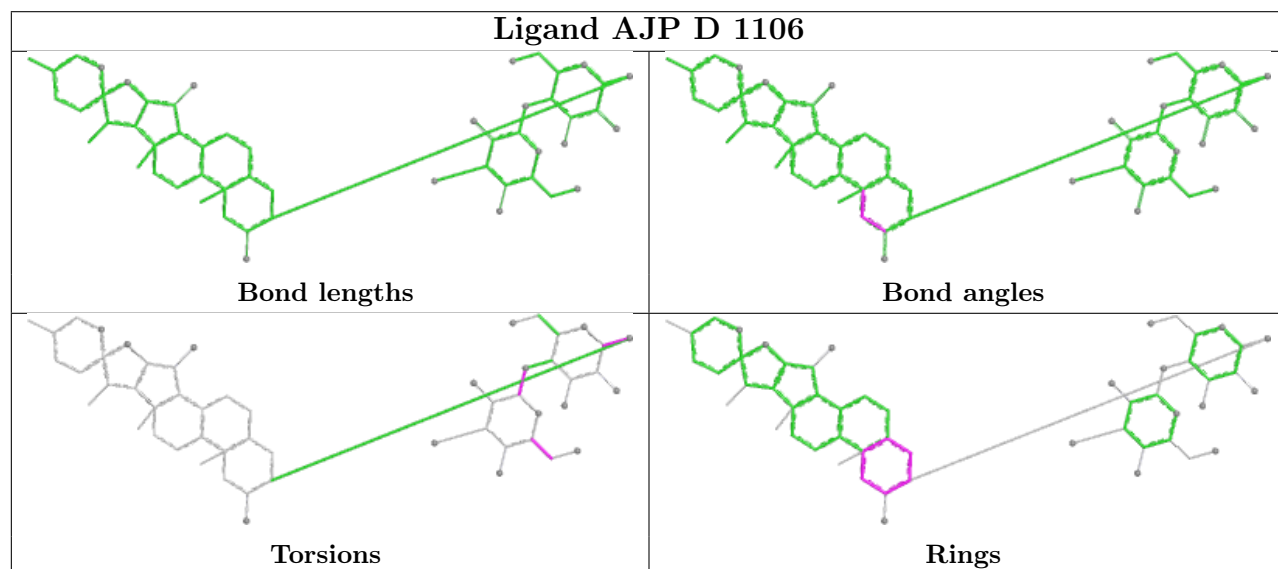
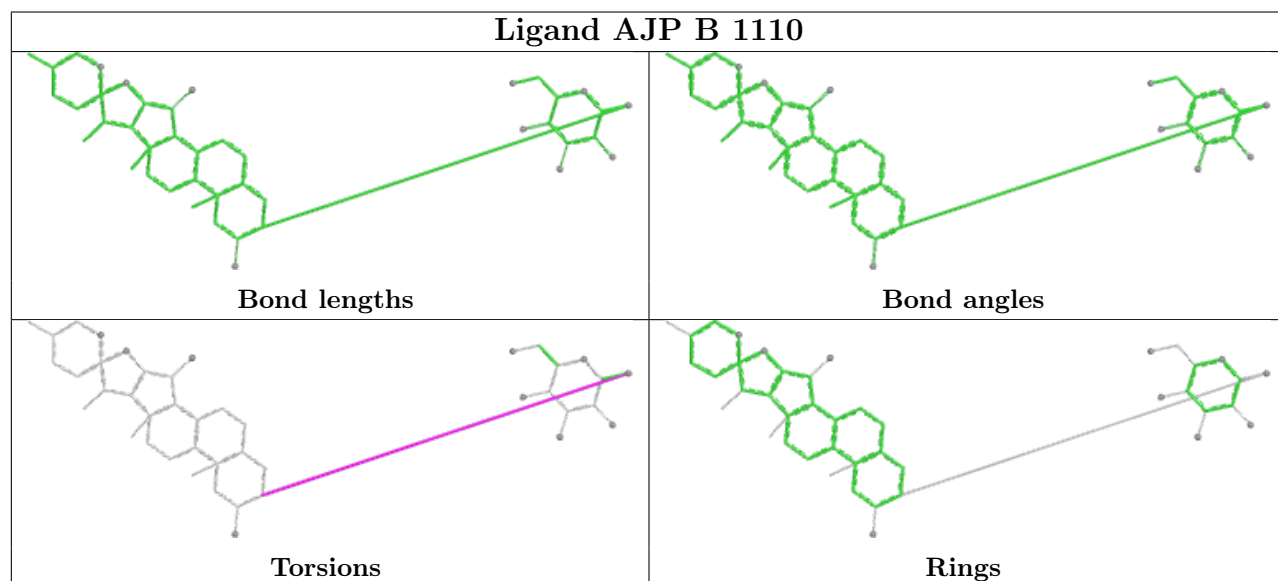
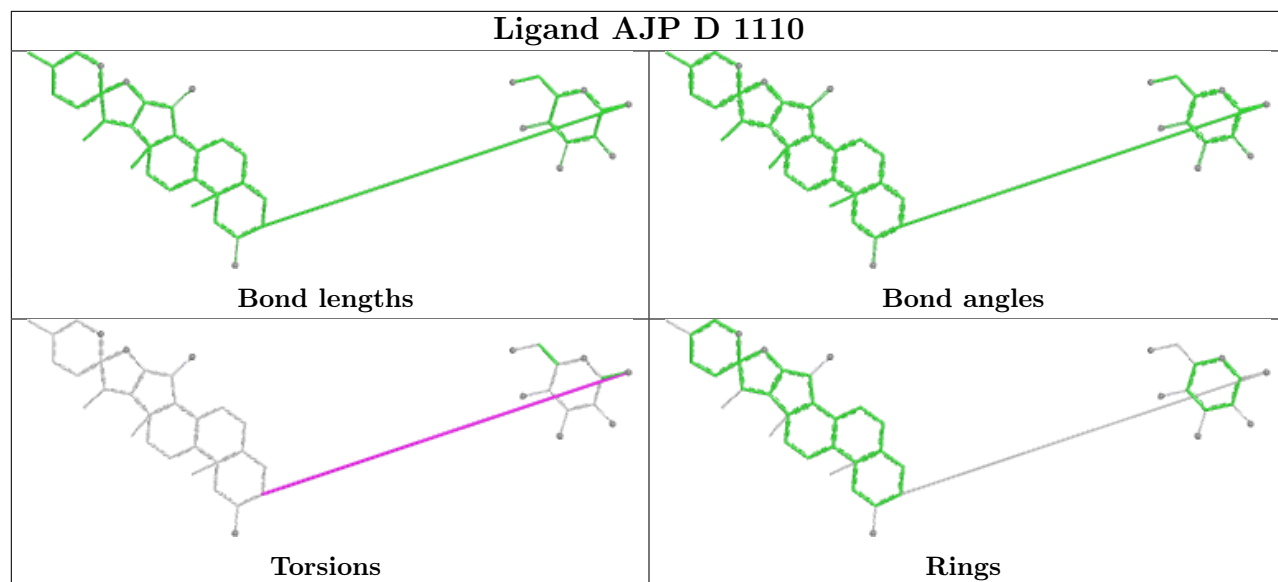
12 monomers are involved in 12 short contacts:

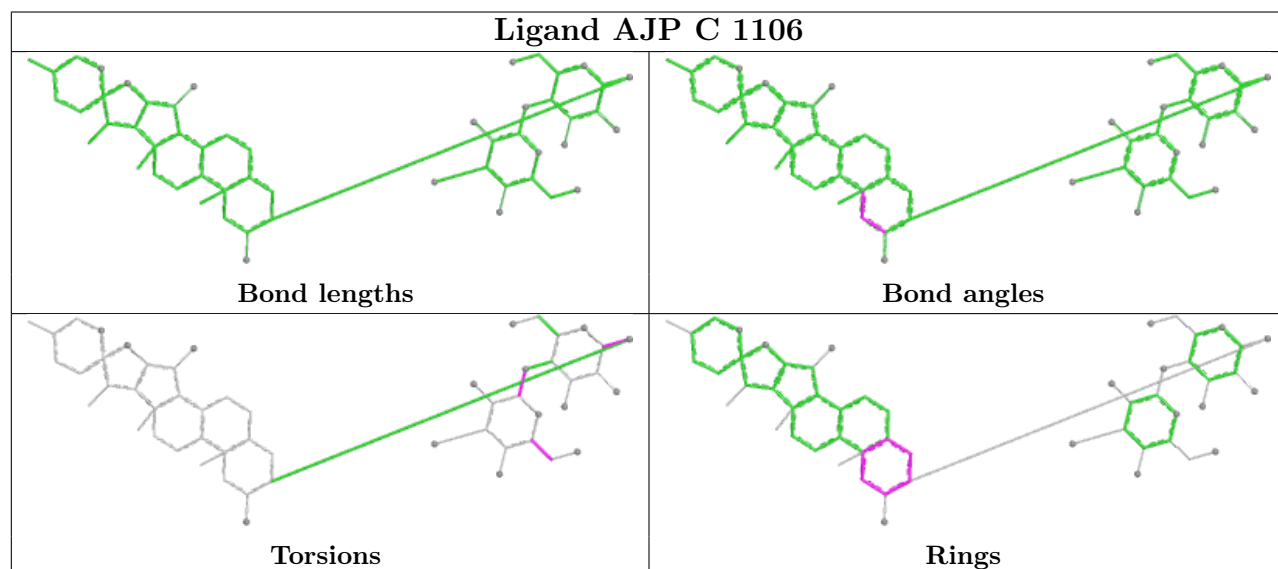
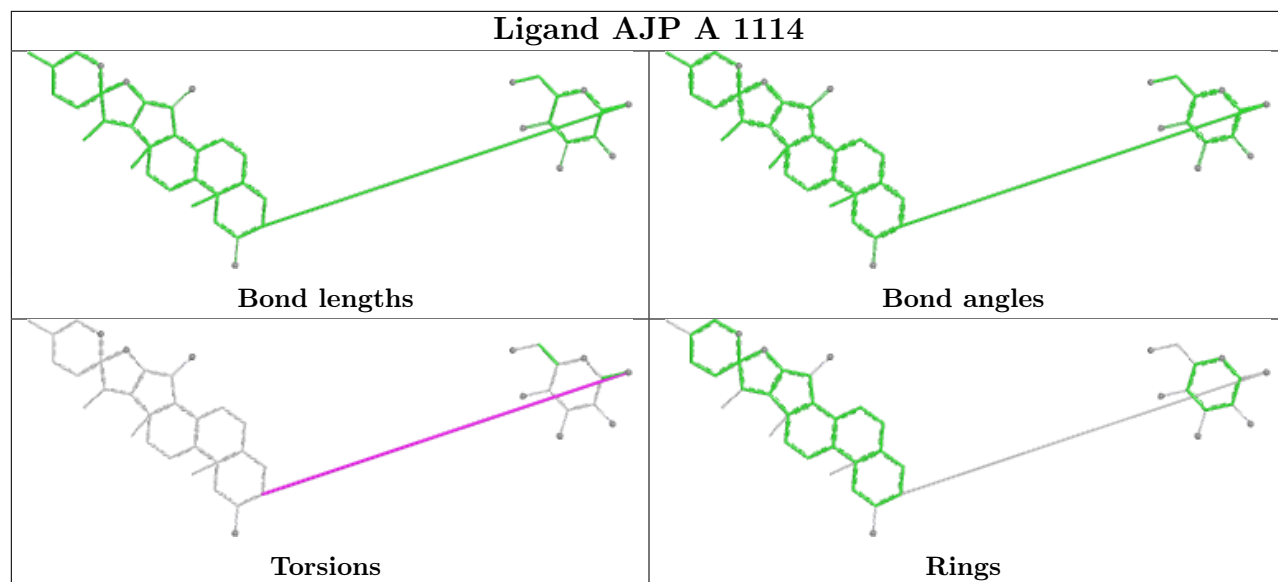
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1118	CLR	1	0
3	B	1103	POV	1	0
7	G	401	NAG	1	0
7	E	401	NAG	1	0
6	B	1114	CLR	1	0
3	D	1102	POV	1	0
3	C	1103	POV	1	0
3	C	1101	POV	1	0
3	A	1103	POV	1	0
6	C	1114	CLR	1	0
6	D	1114	CLR	1	0
7	H	401	NAG	1	0

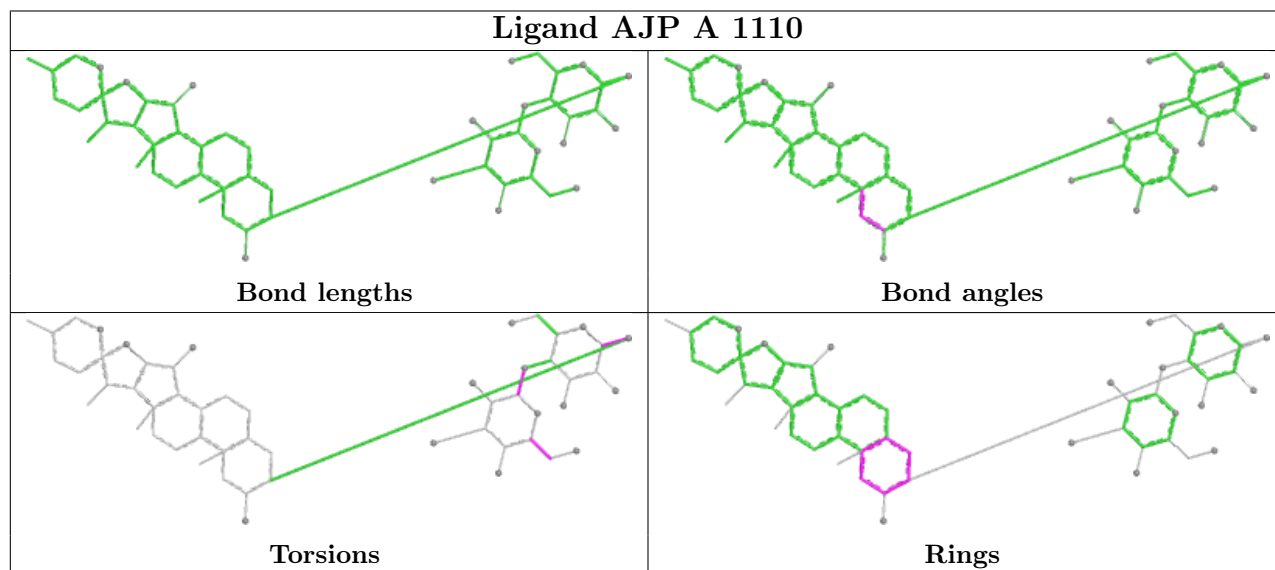
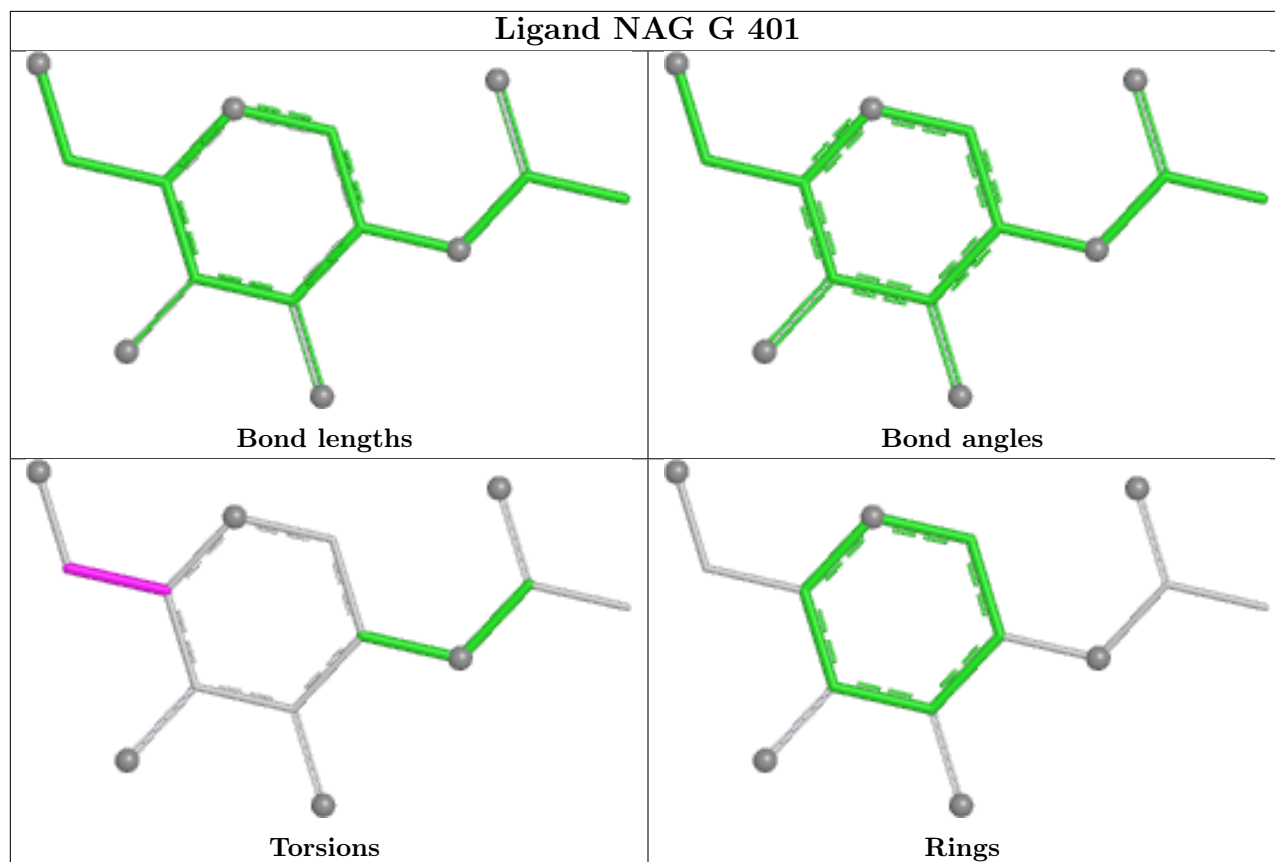
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

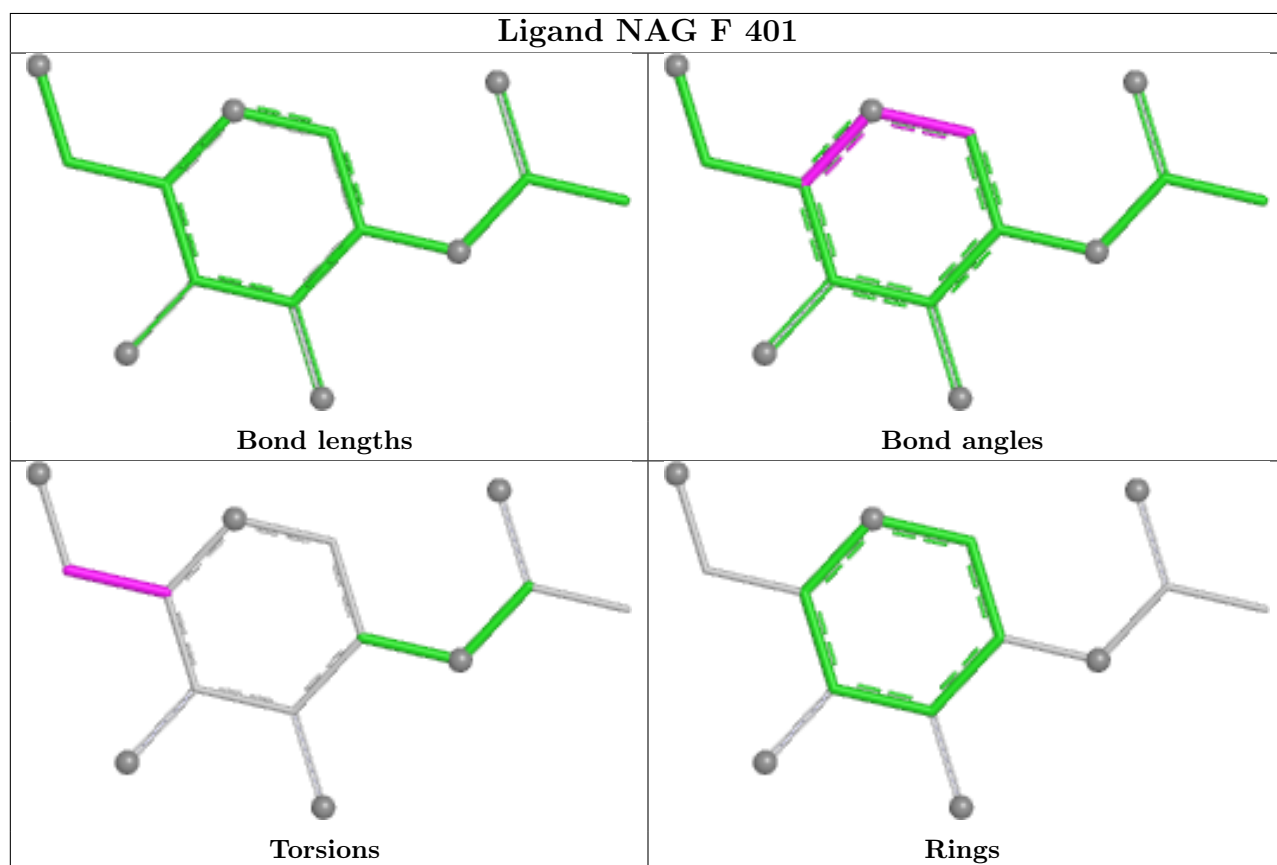
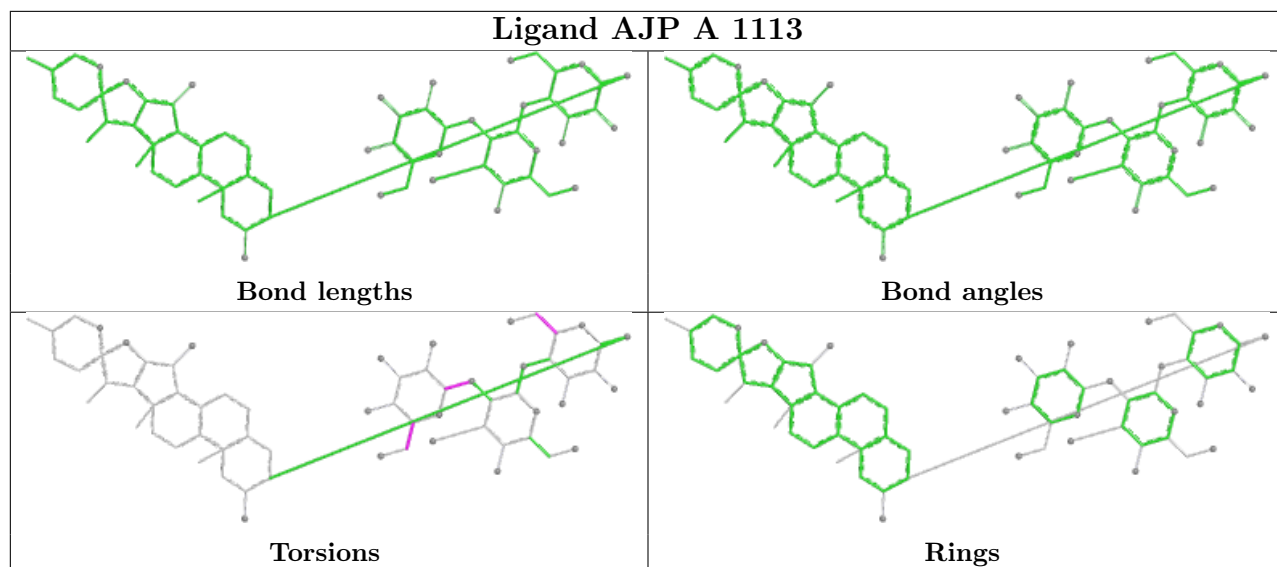


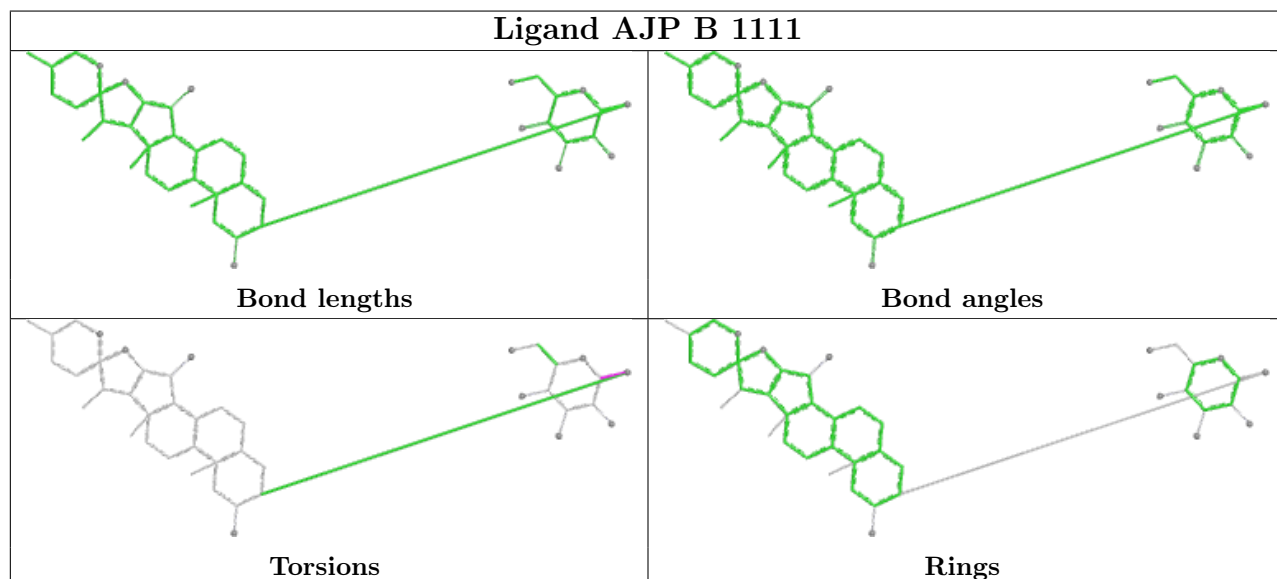
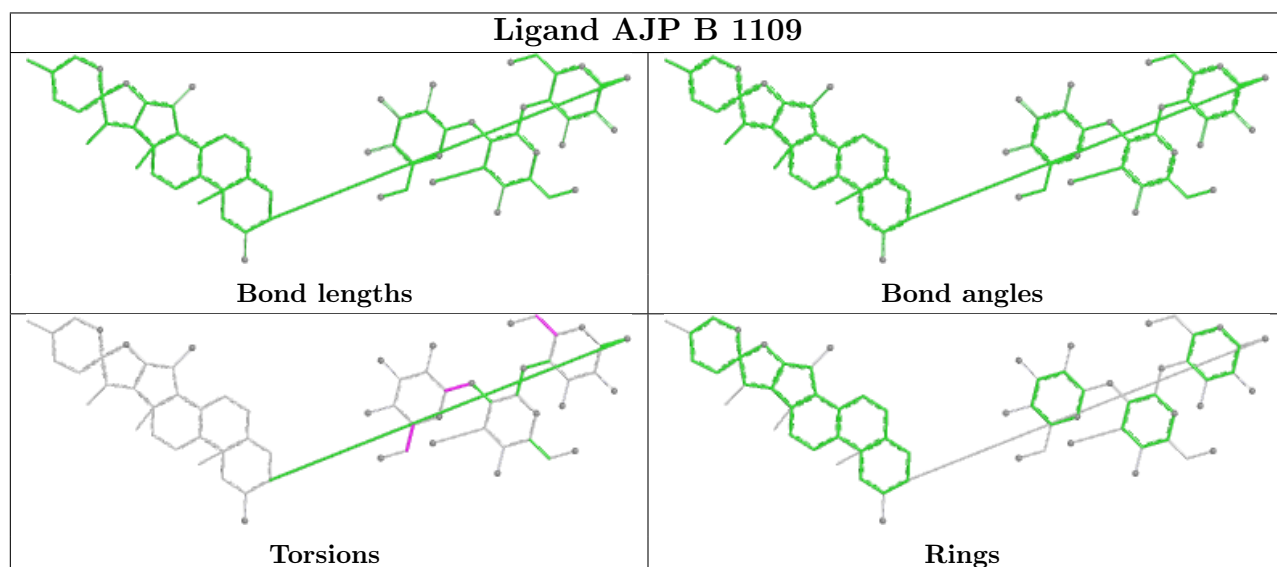
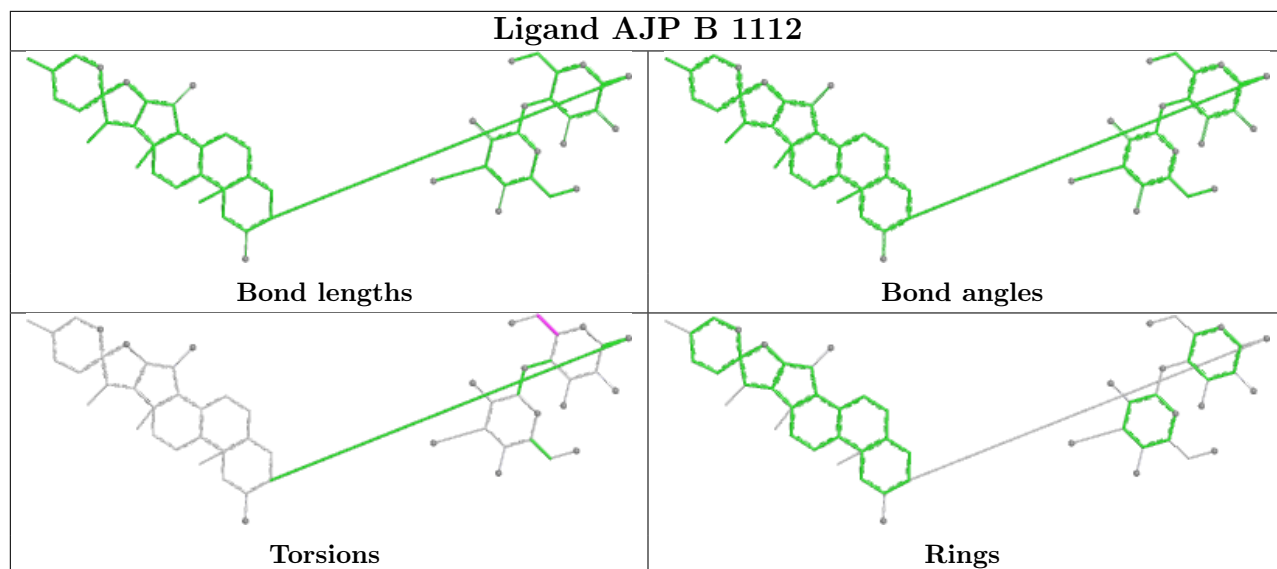


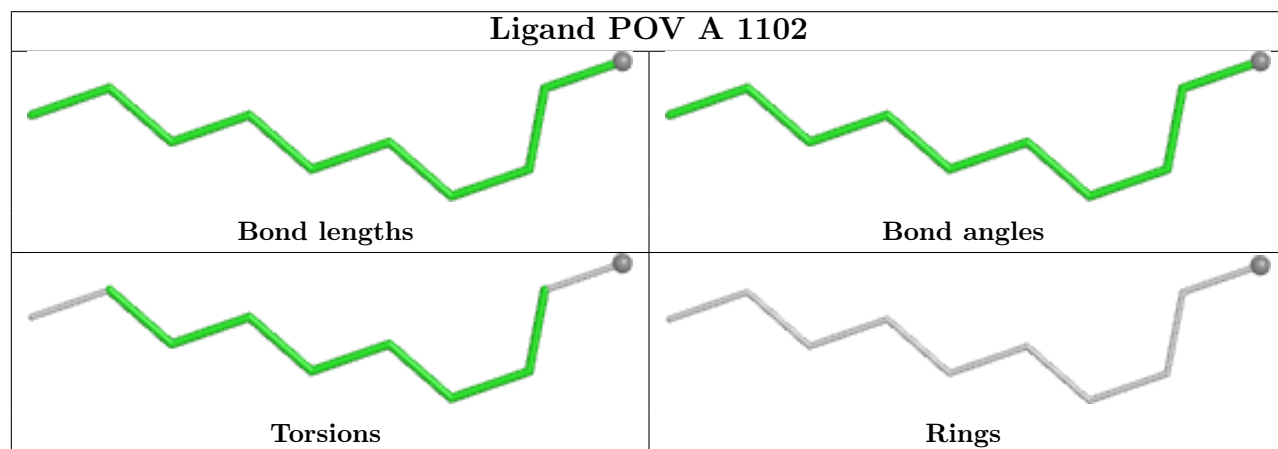
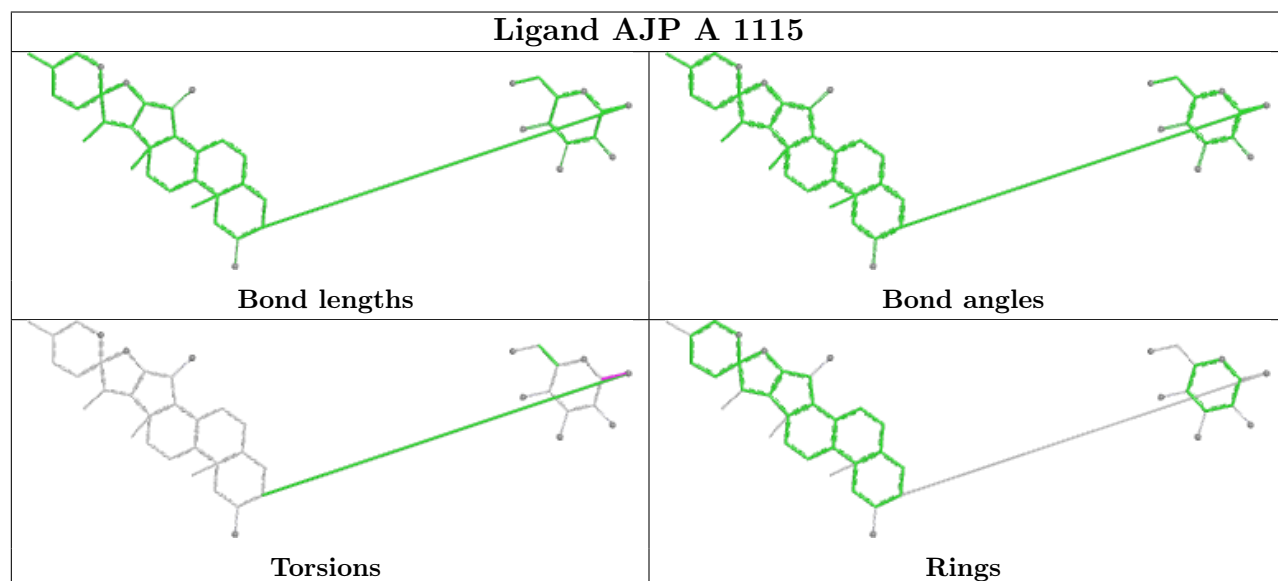
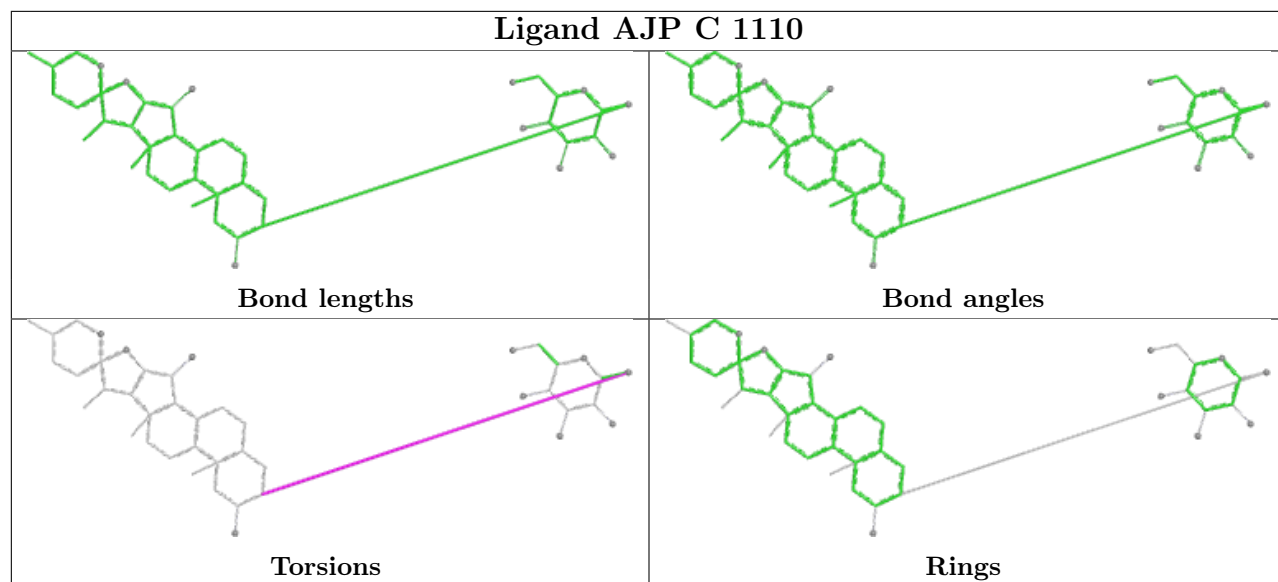


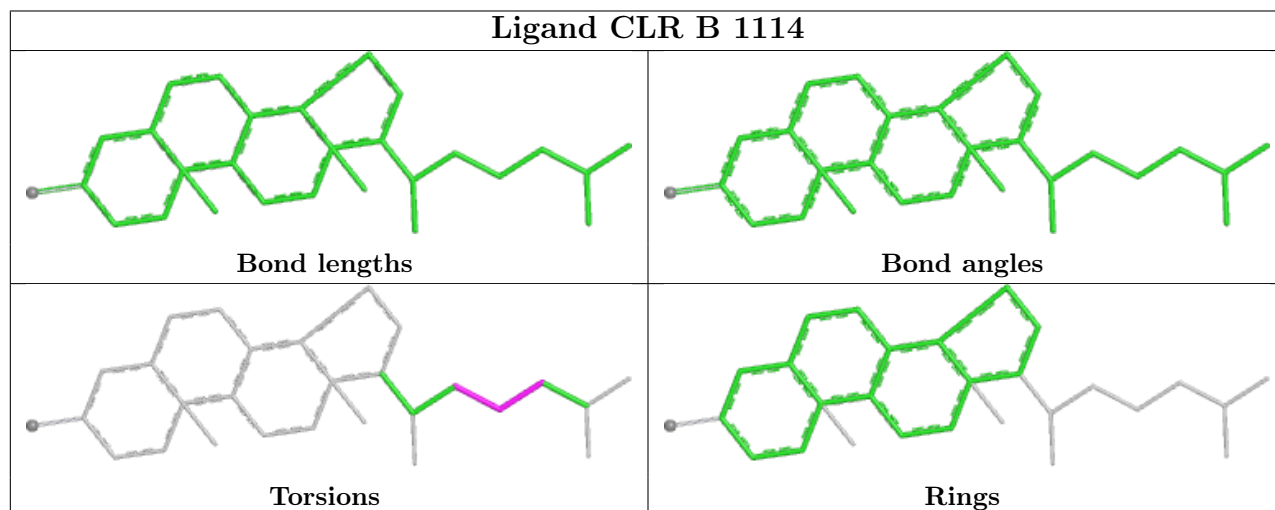
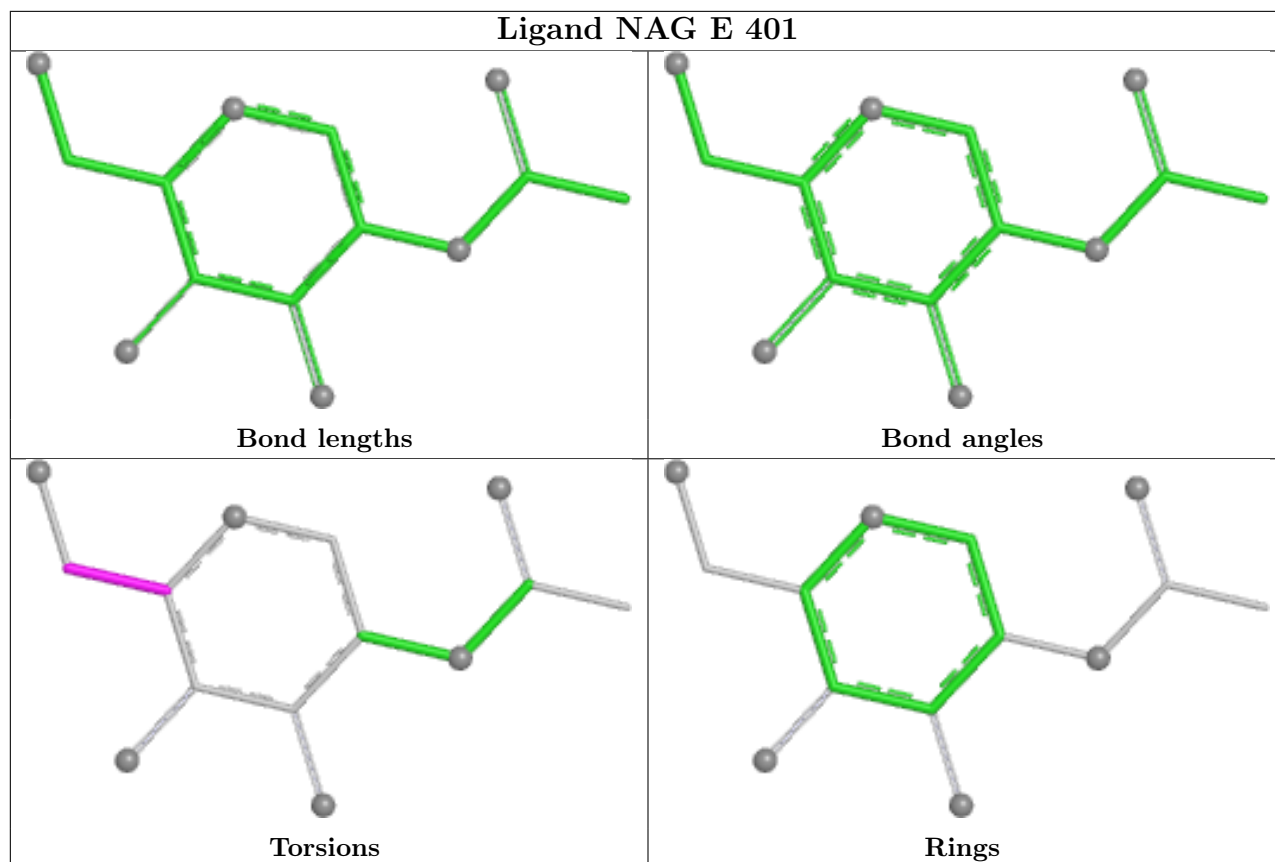


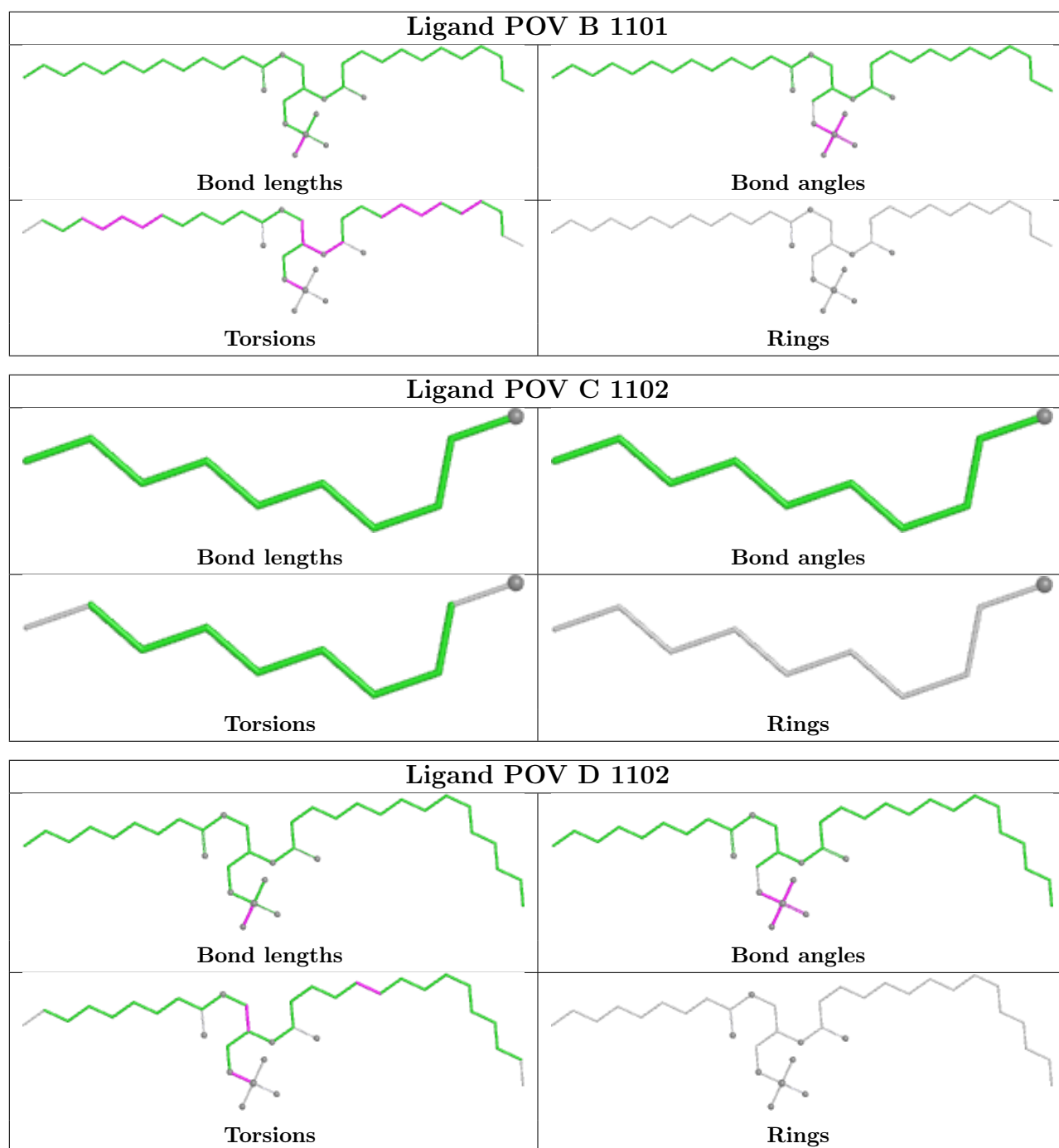


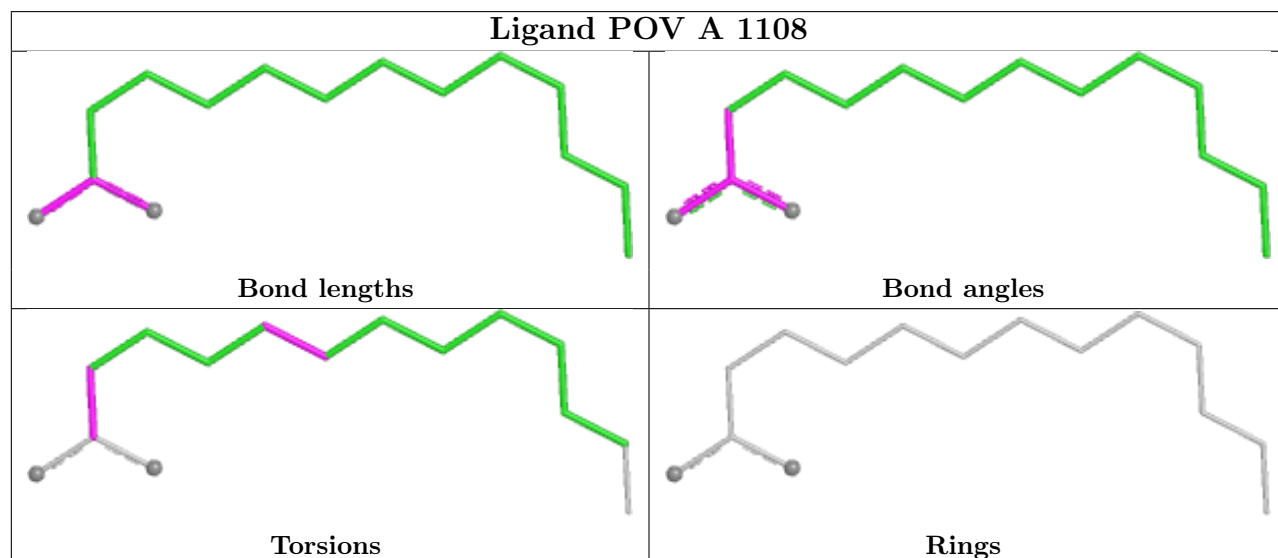
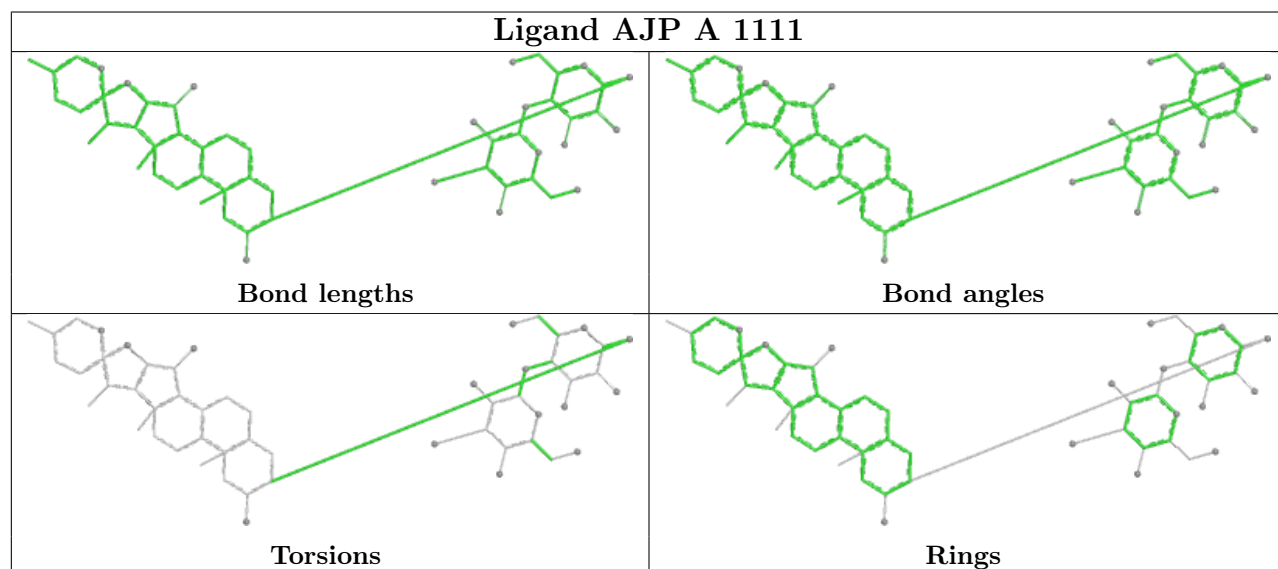
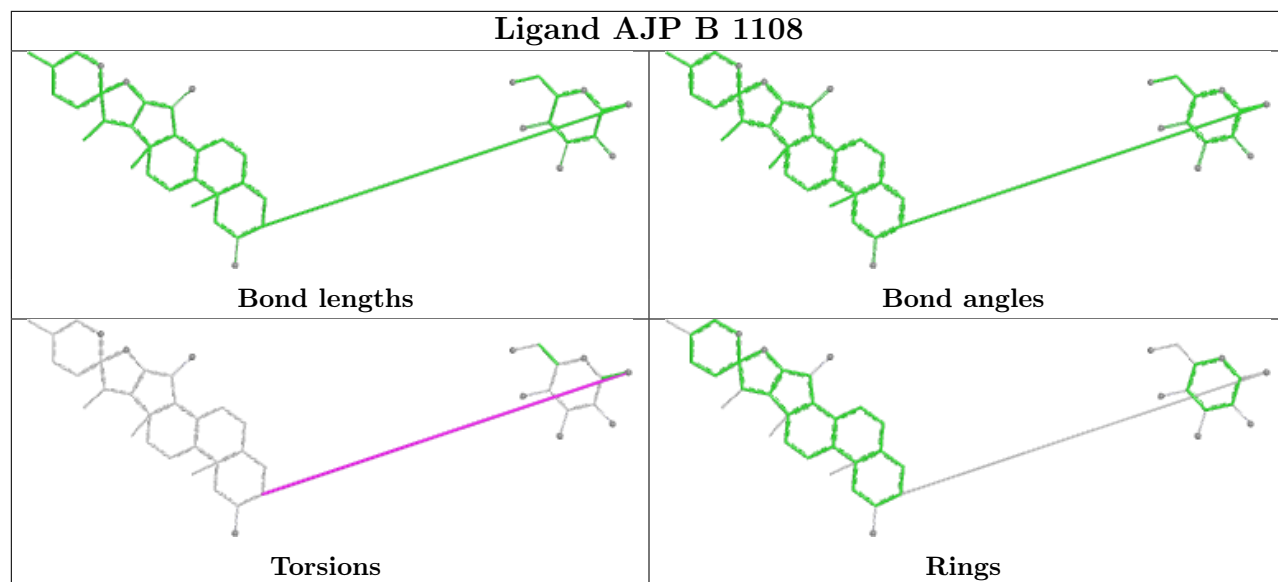


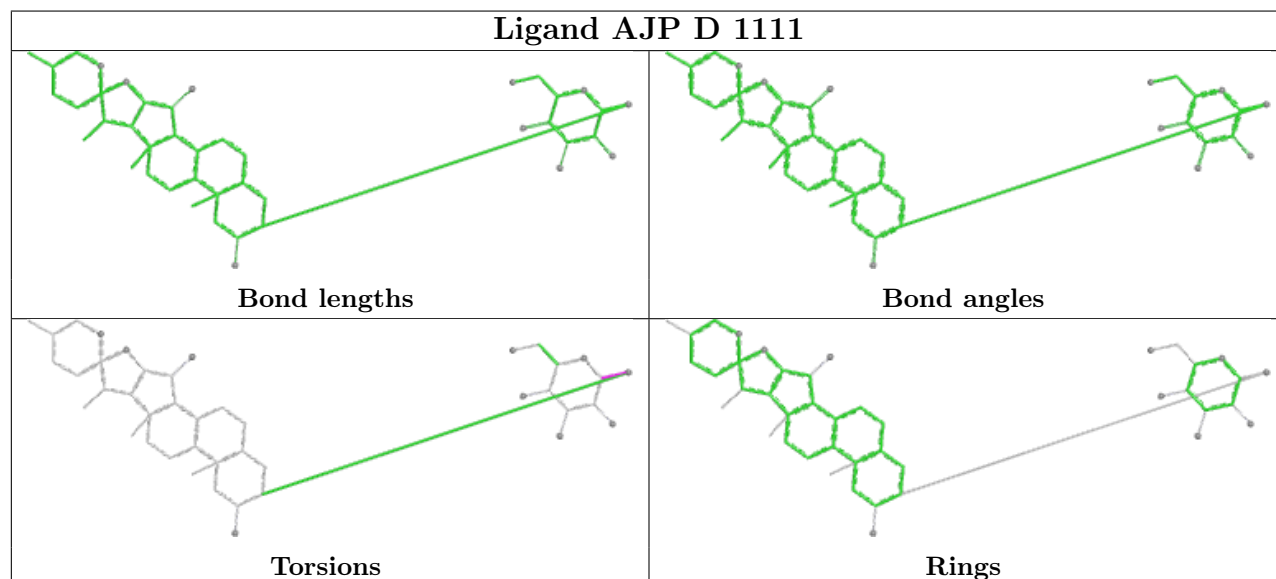
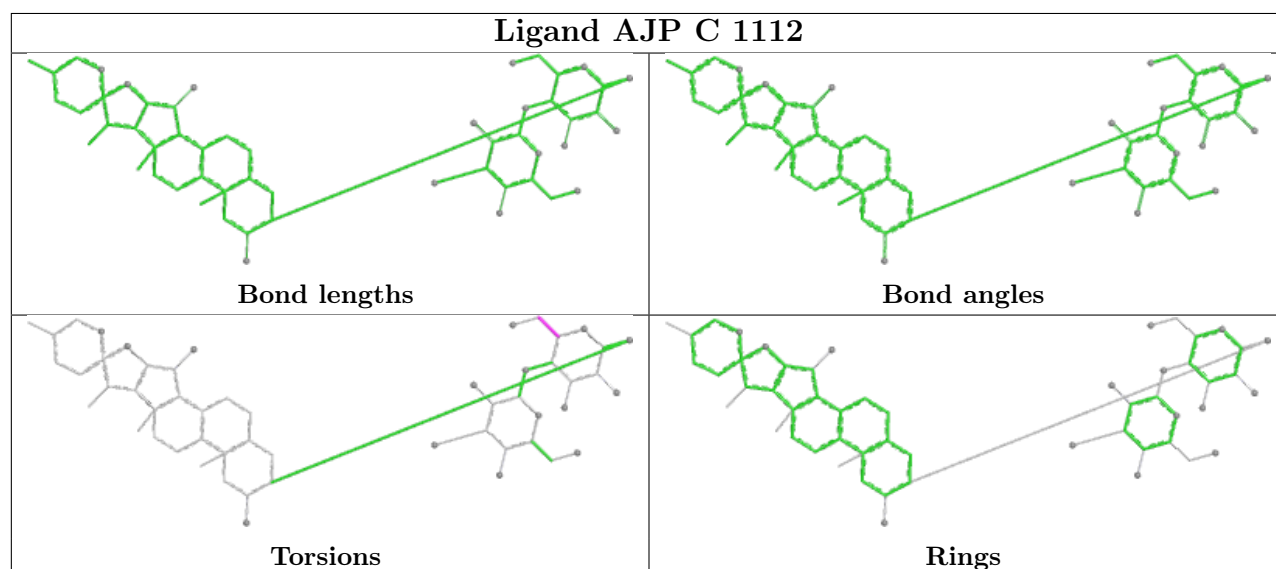
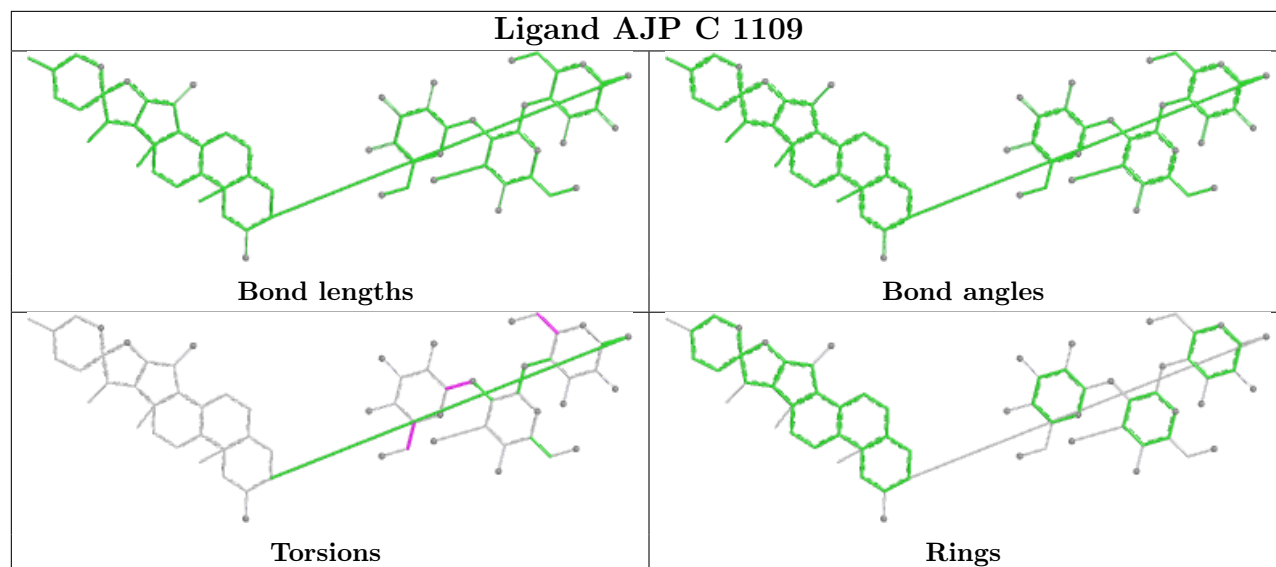


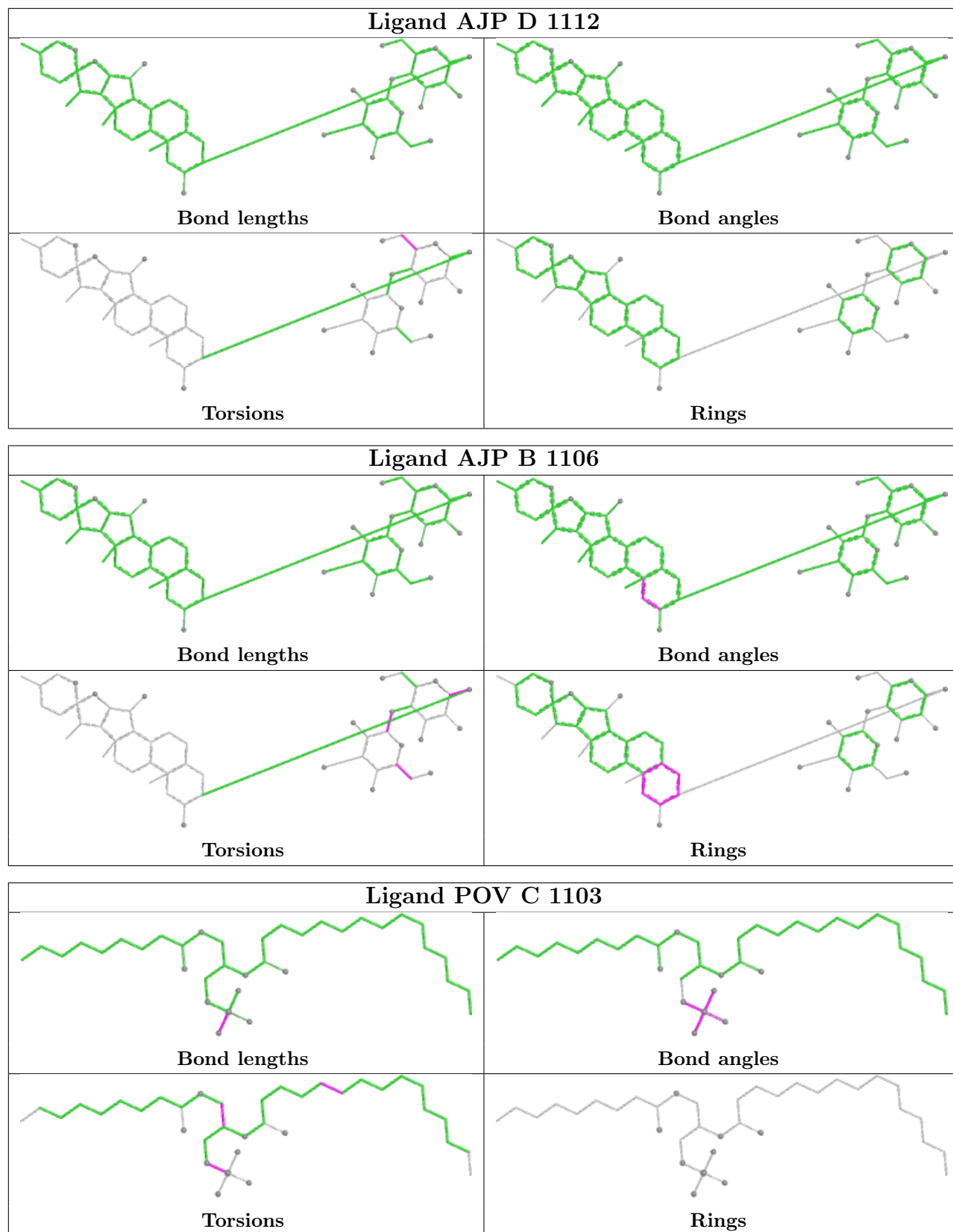


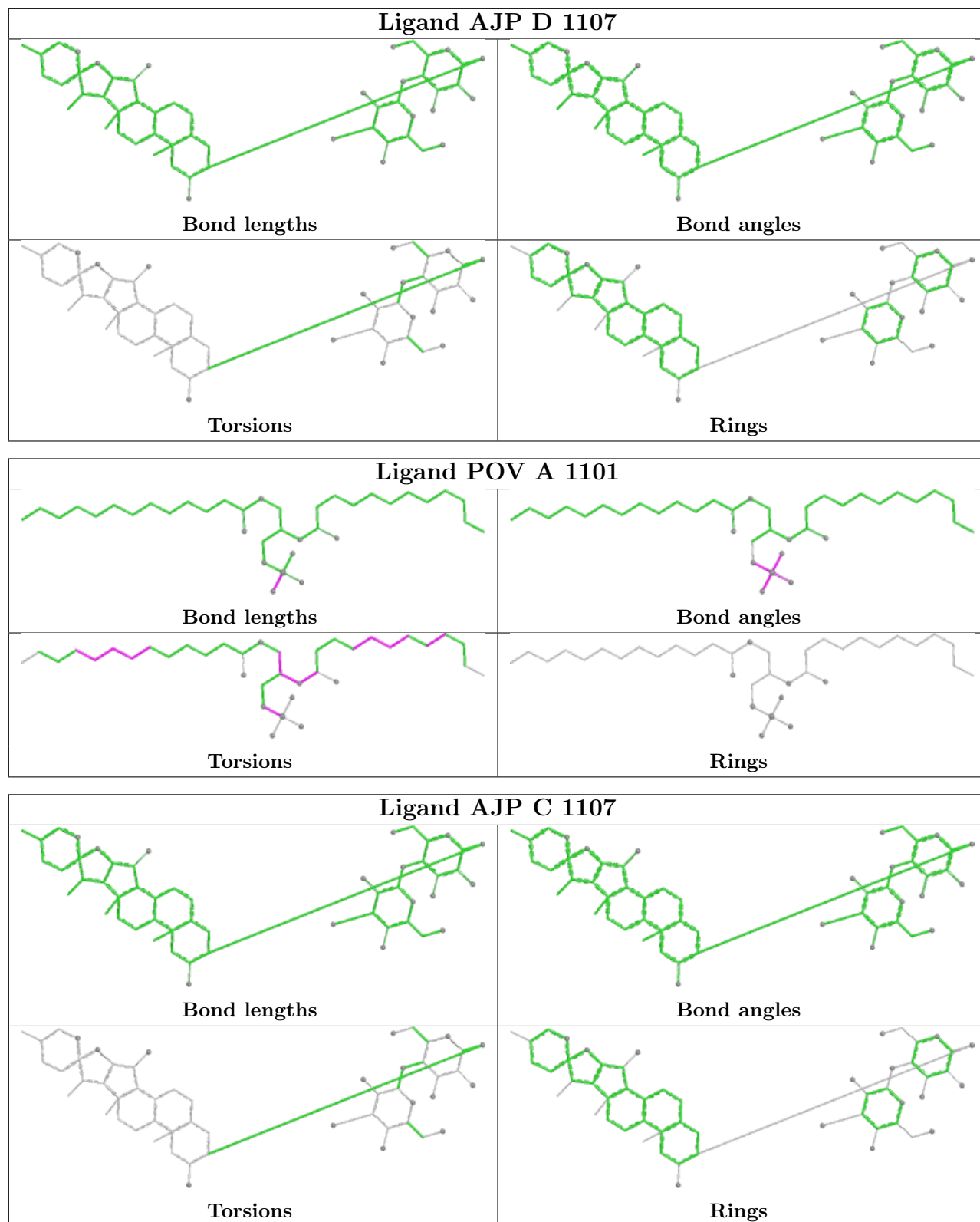


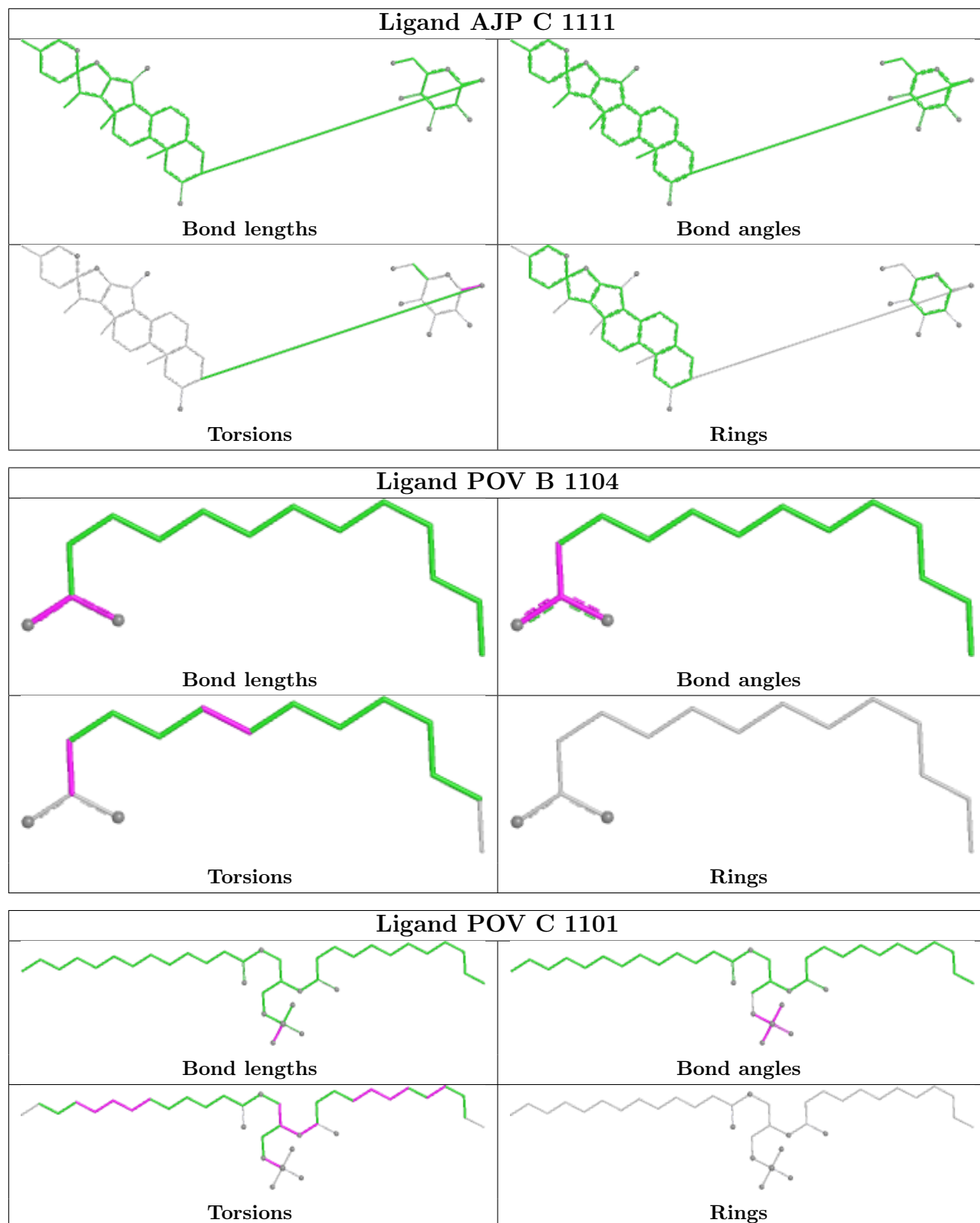


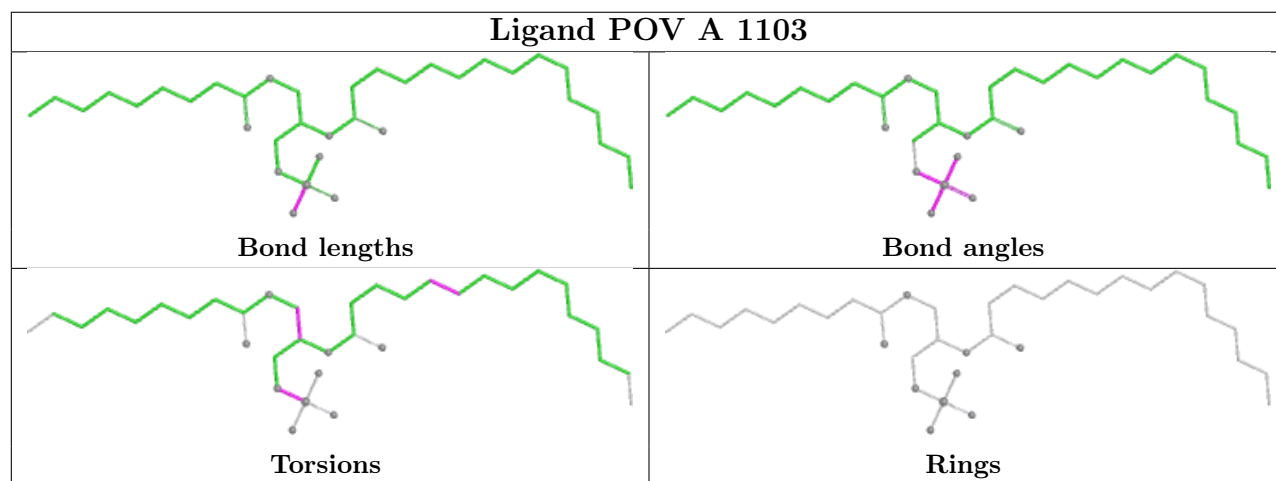
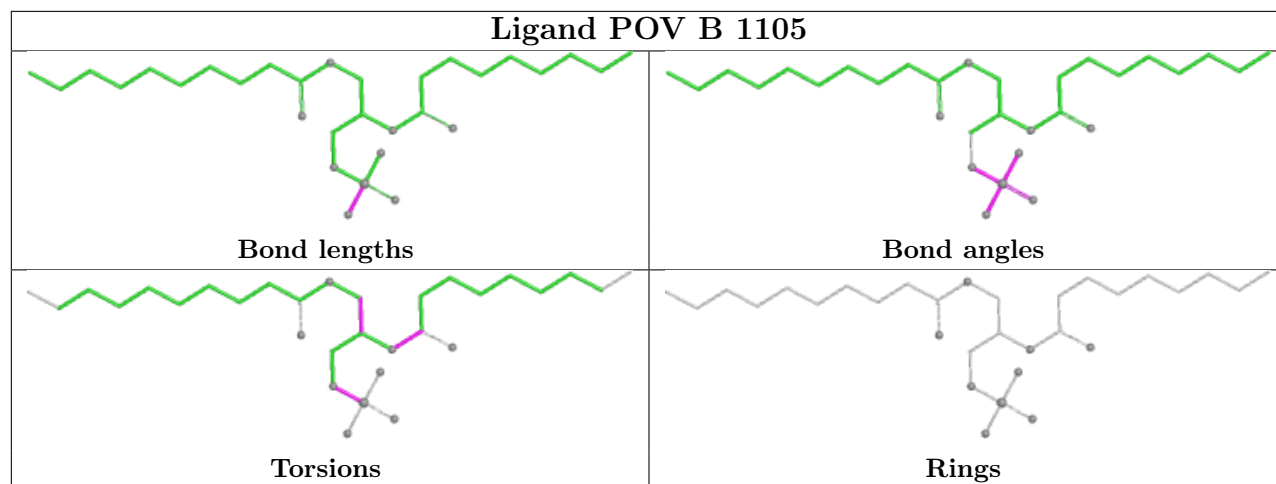
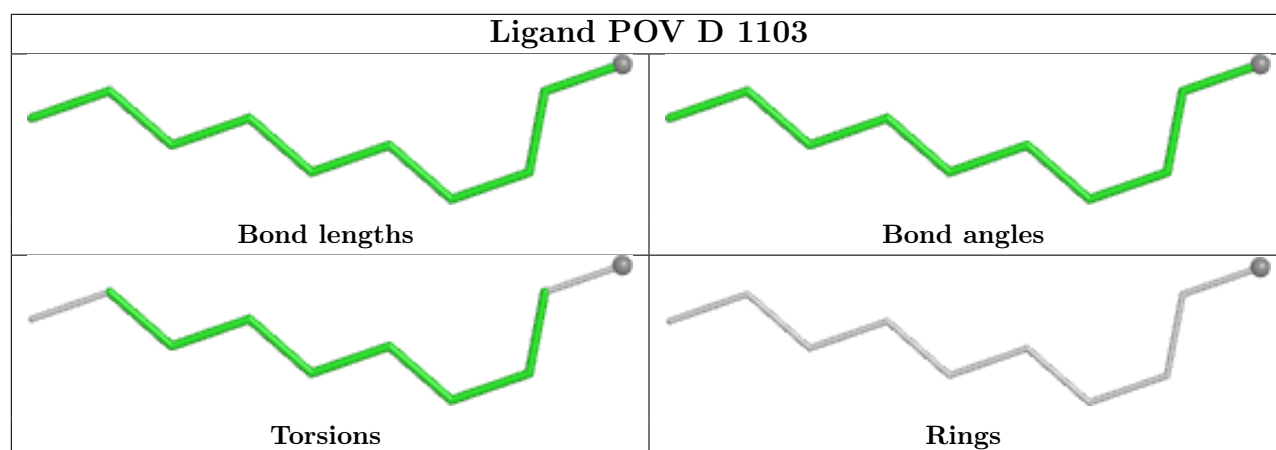


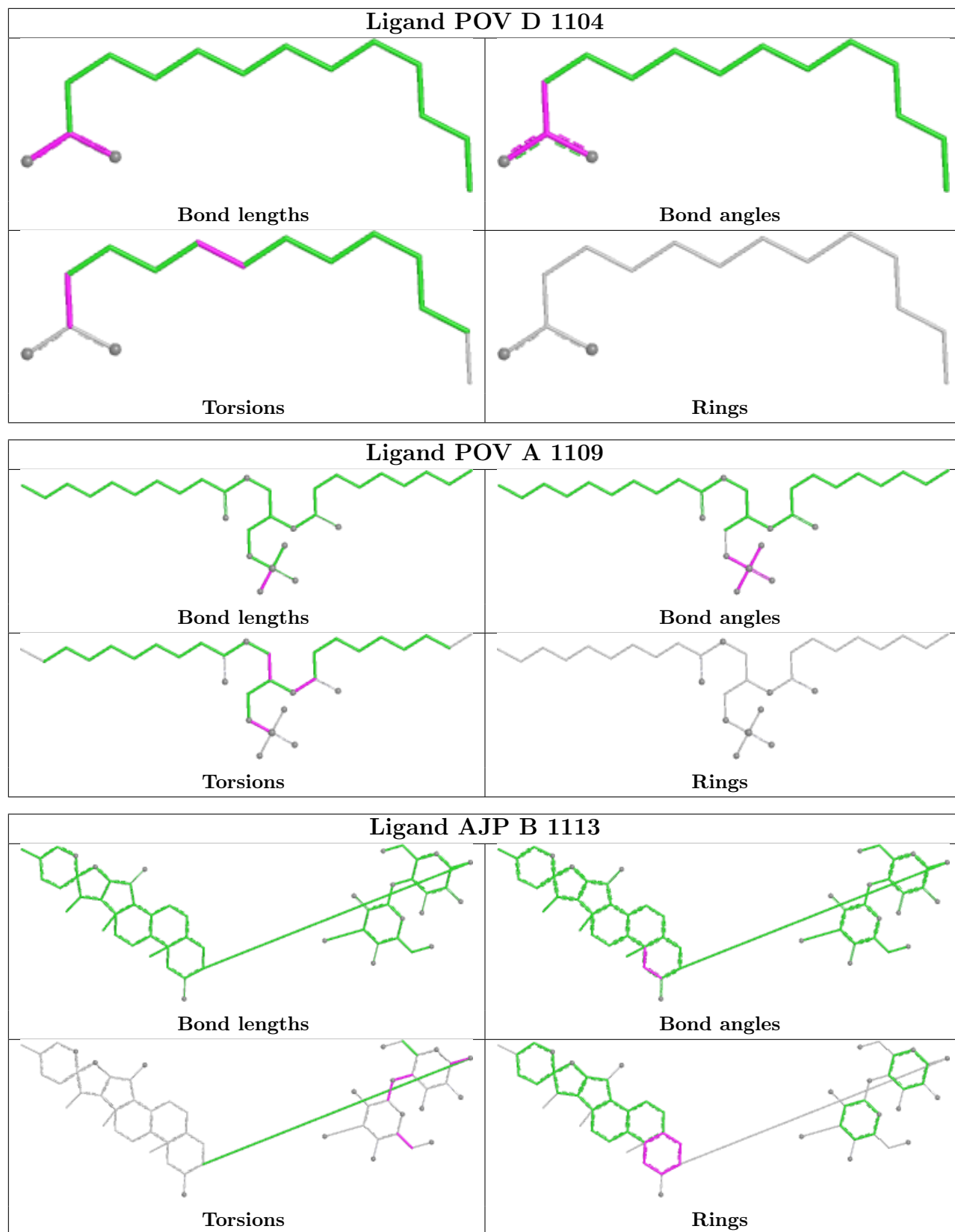


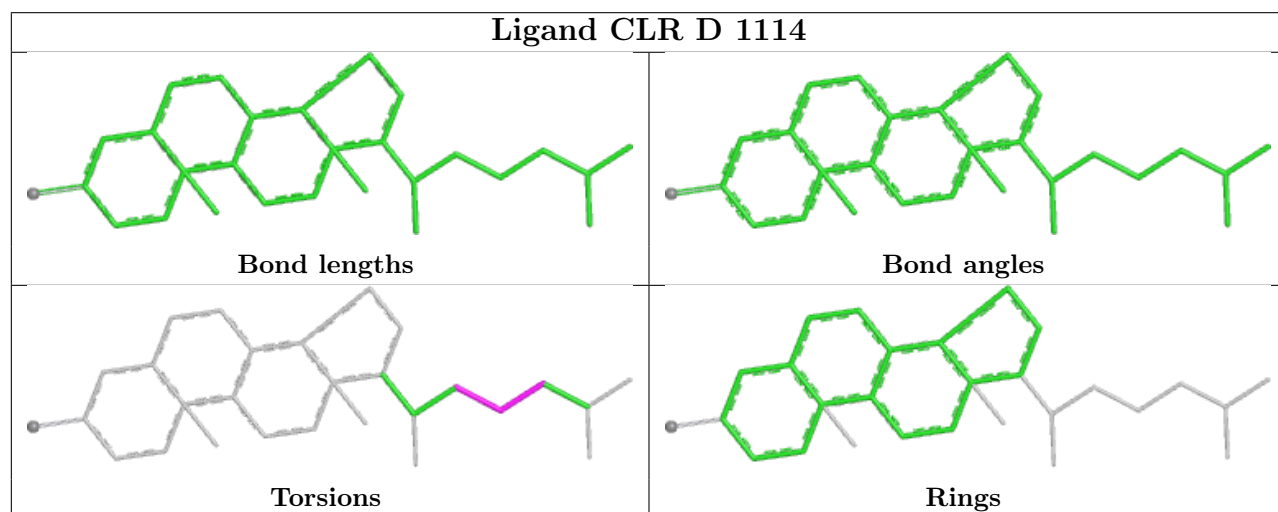
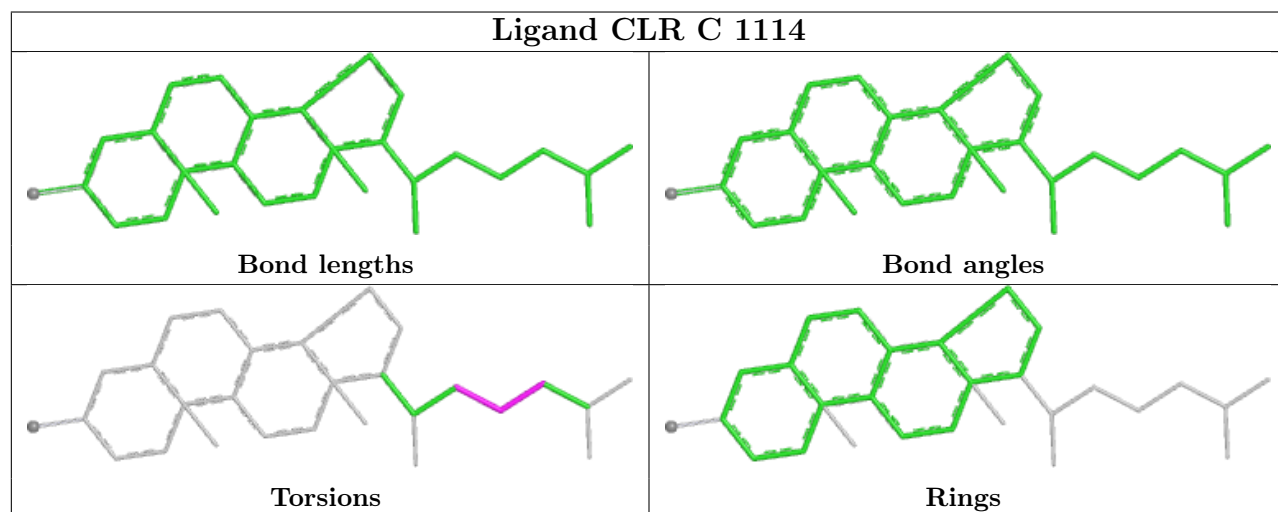
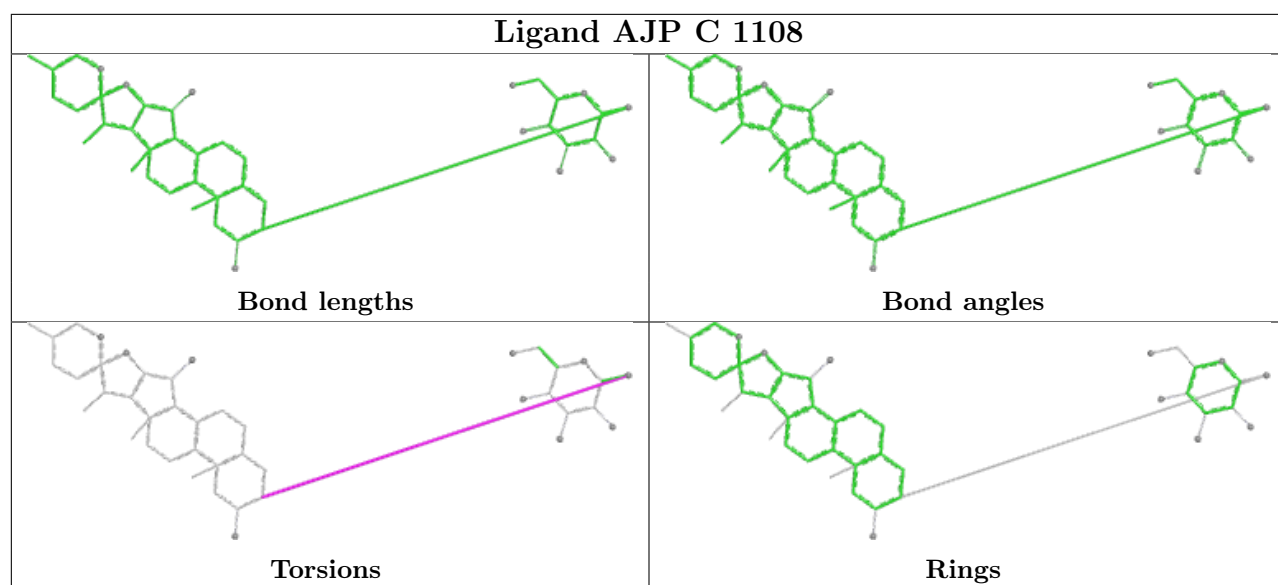


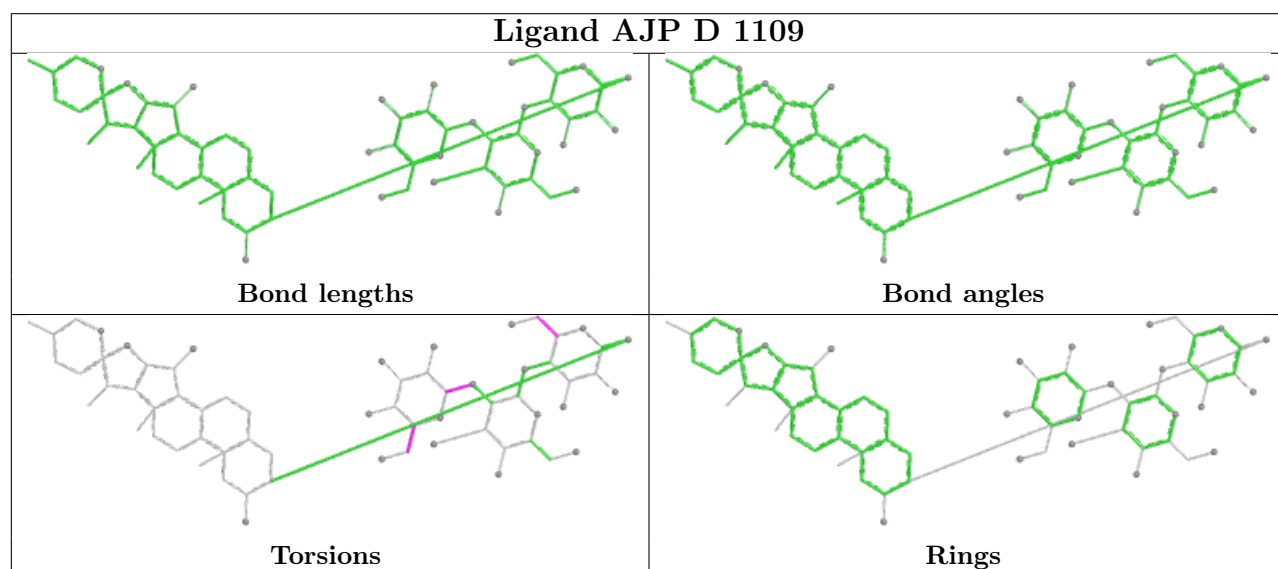
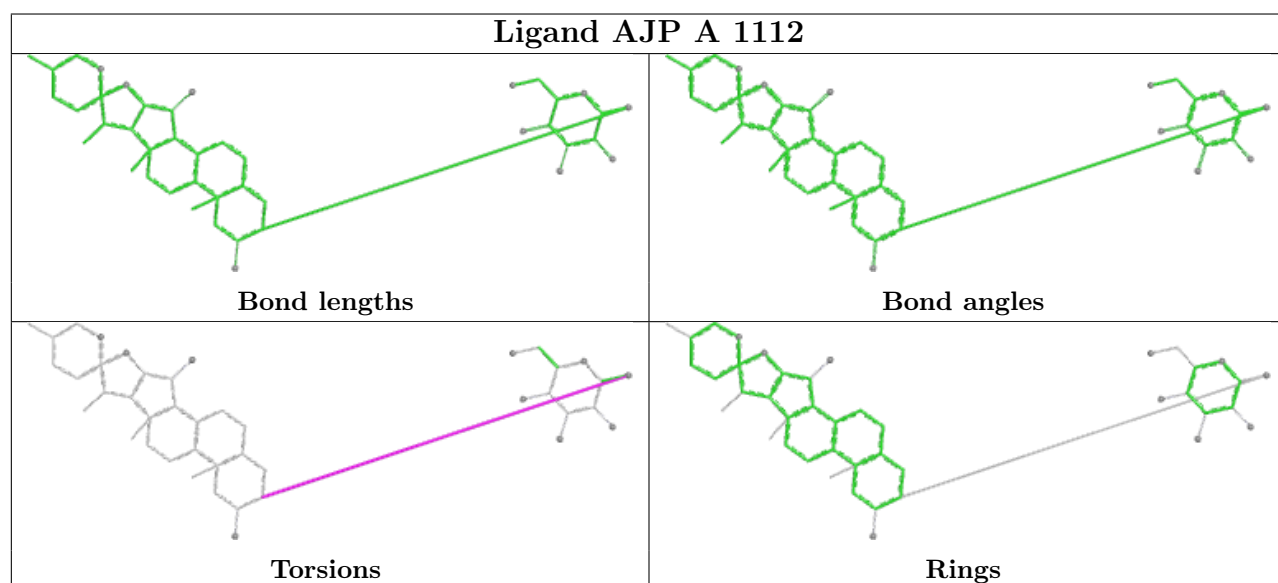
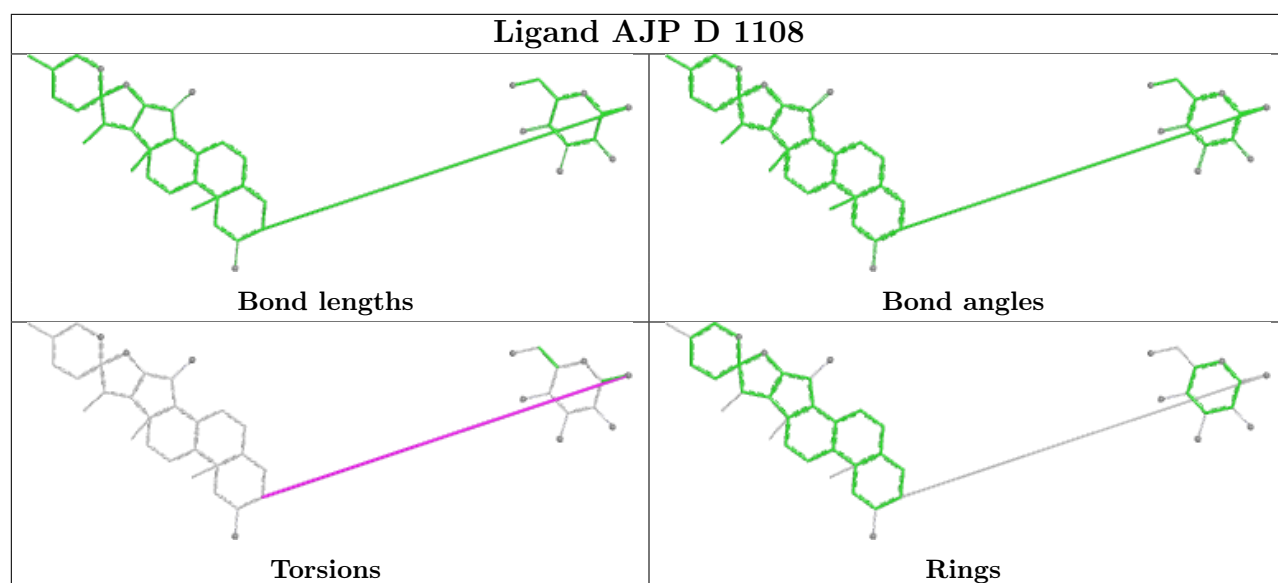


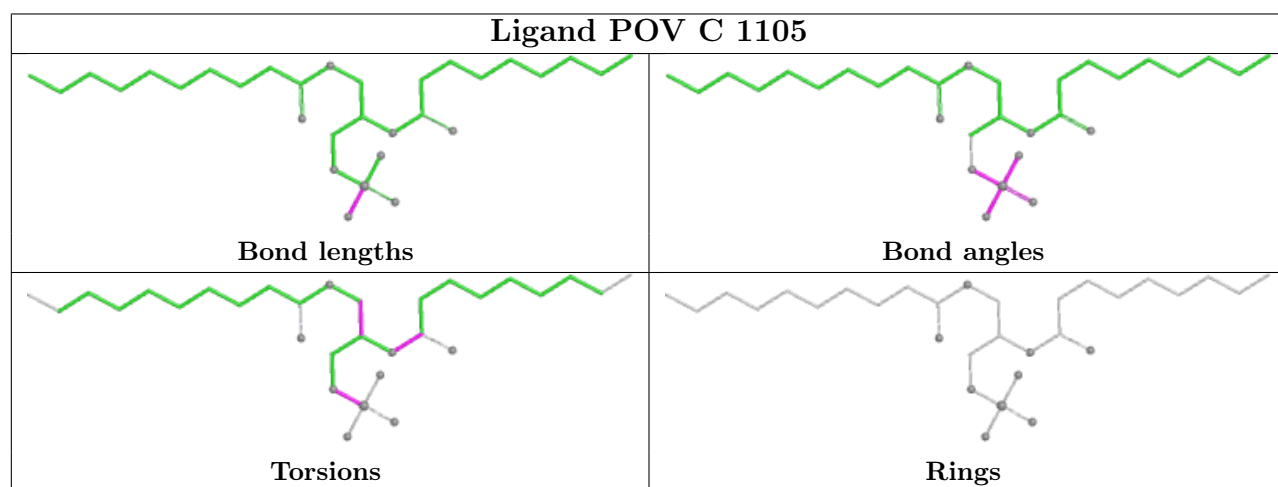
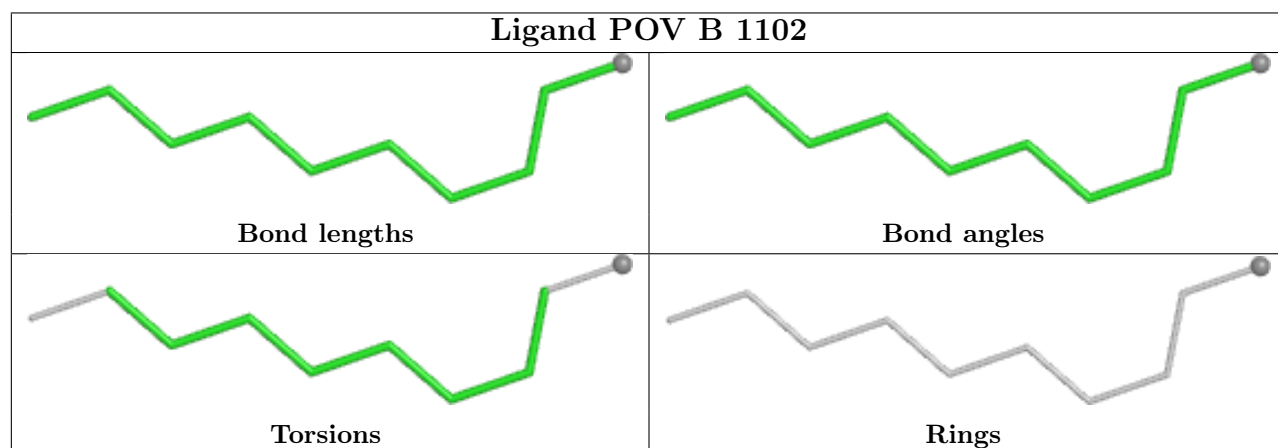
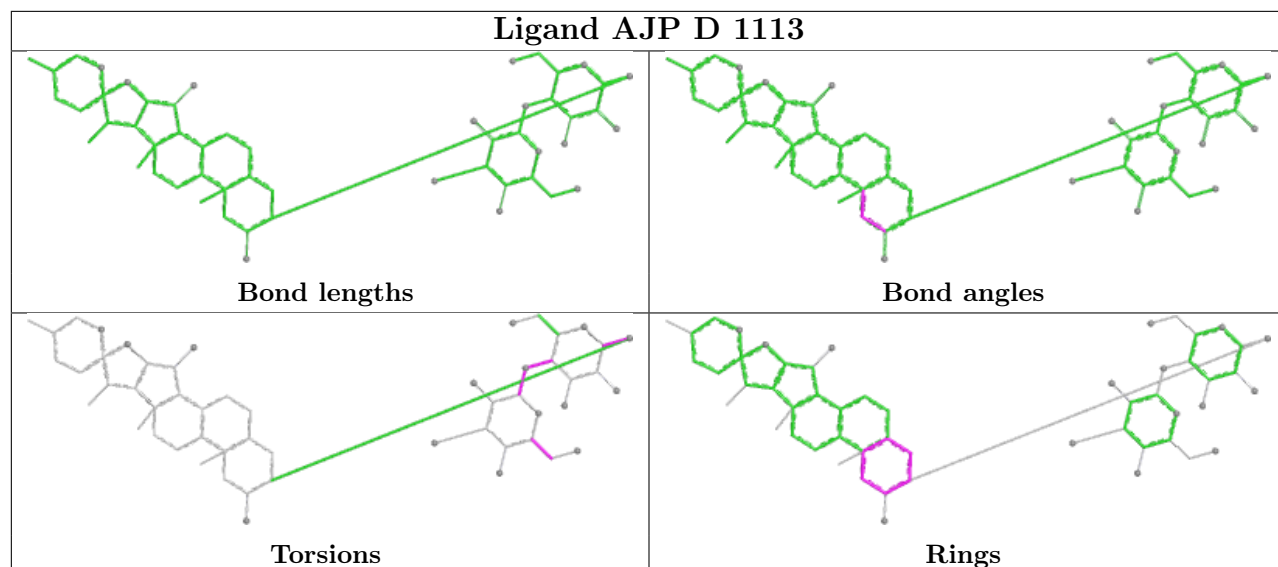


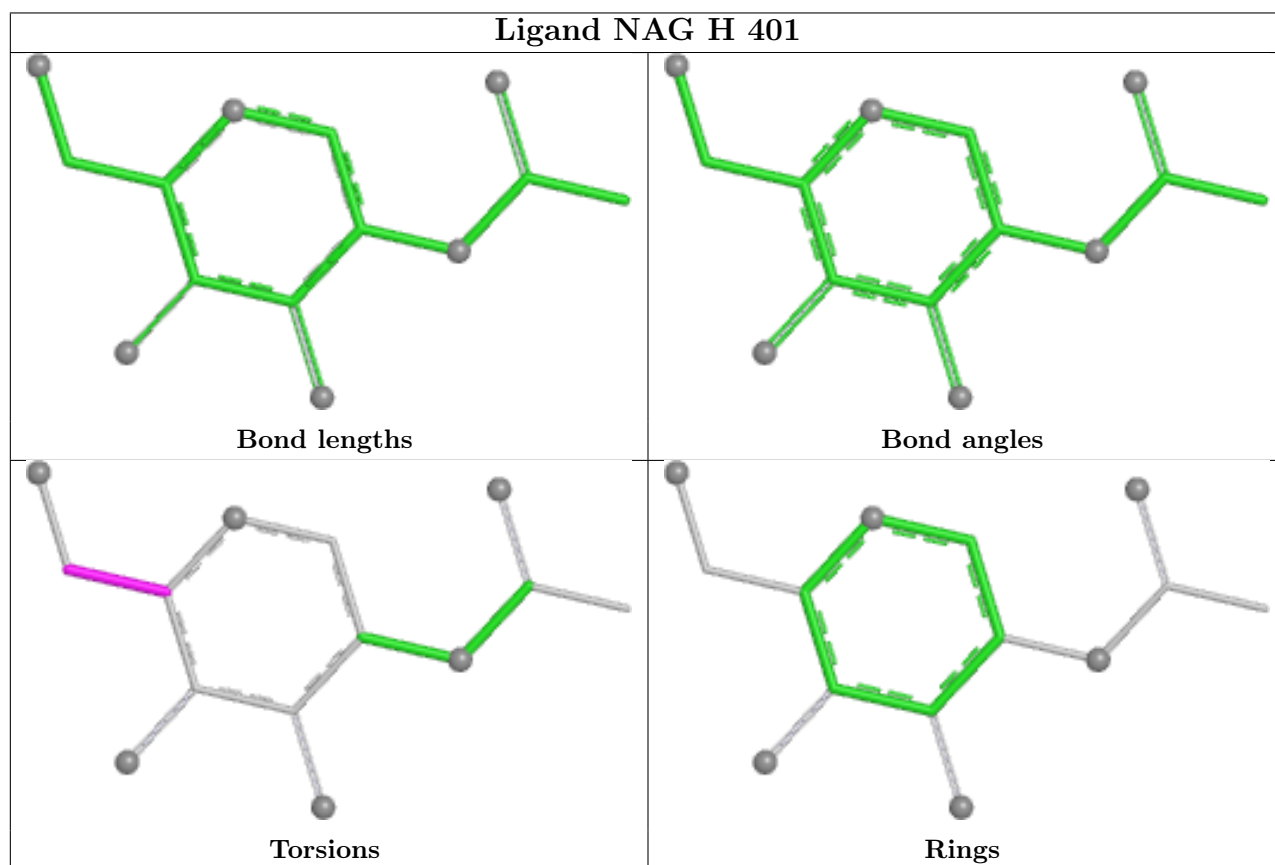
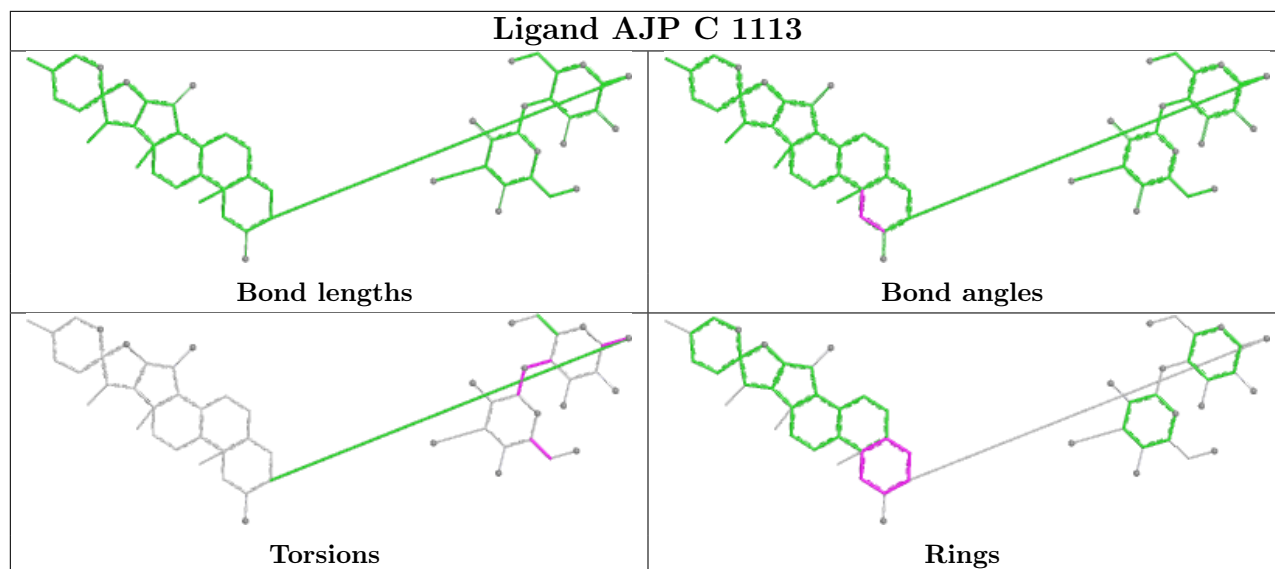


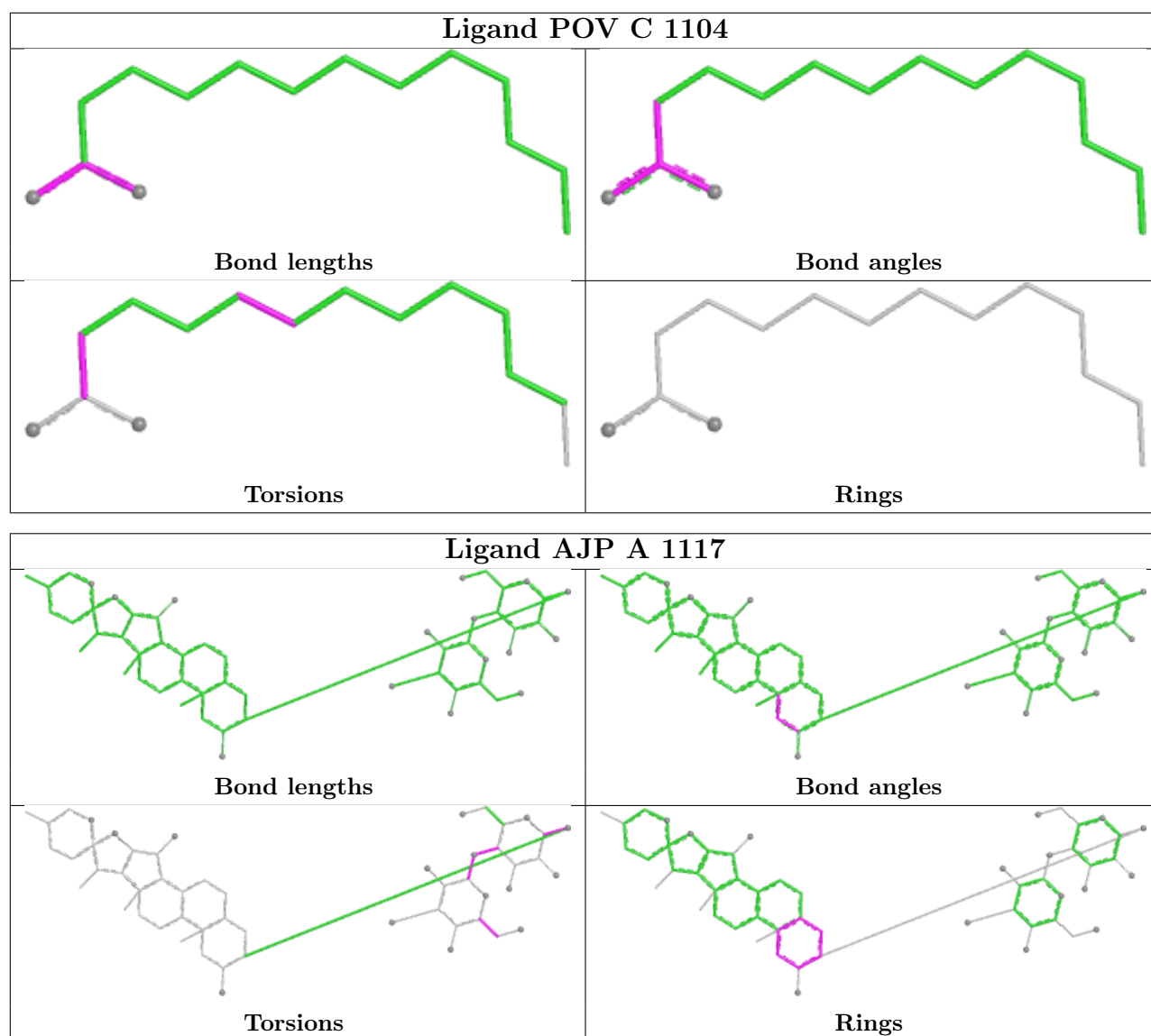












## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

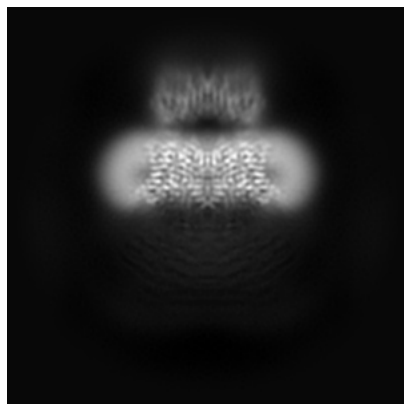
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43106. These allow visual inspection of the internal detail of the map and identification of artifacts.

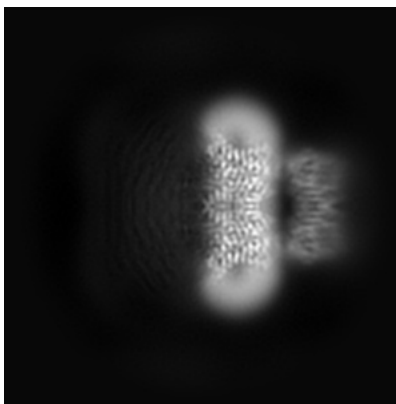
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

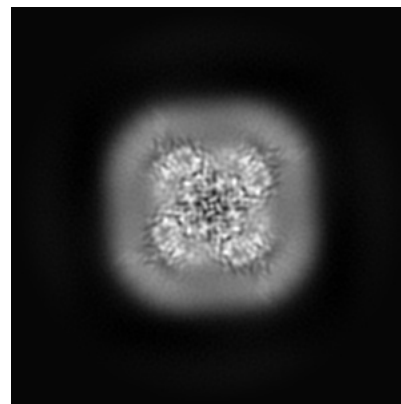
#### 6.1.1 Primary map



X

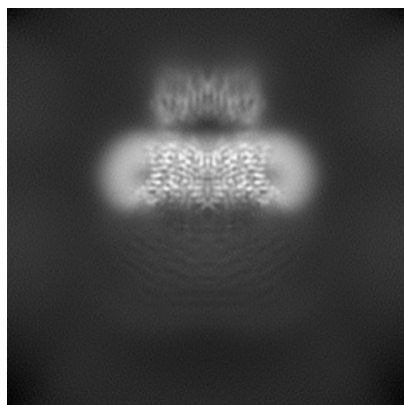


Y

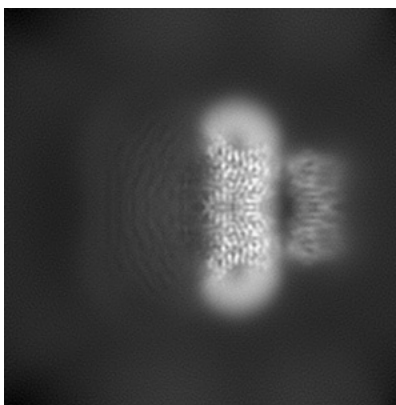


Z

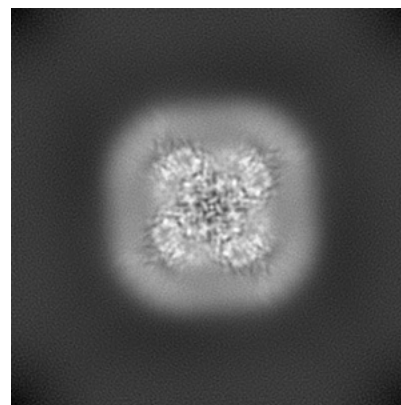
#### 6.1.2 Raw map



X



Y



Z

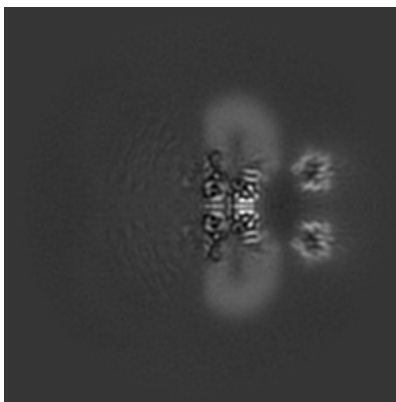
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

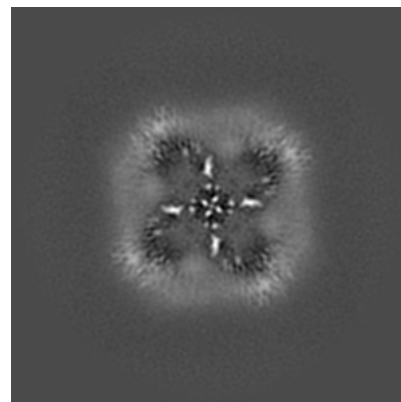
### 6.2.1 Primary map



X Index: 128

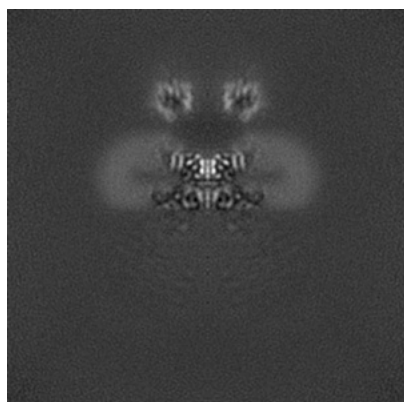


Y Index: 128

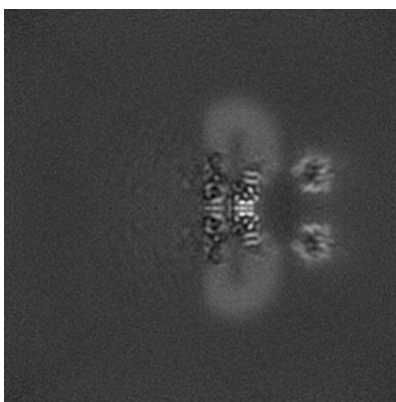


Z Index: 128

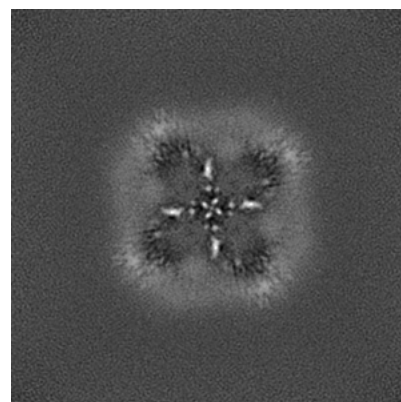
### 6.2.2 Raw map



X Index: 128



Y Index: 128

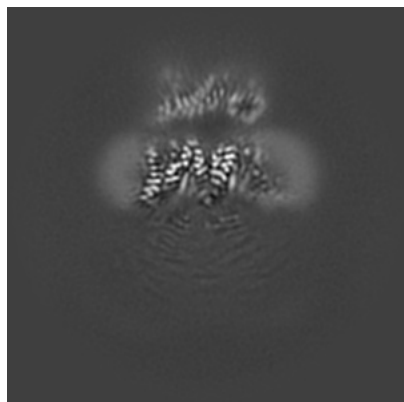


Z Index: 128

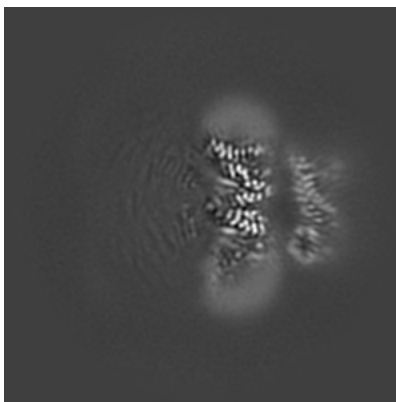
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

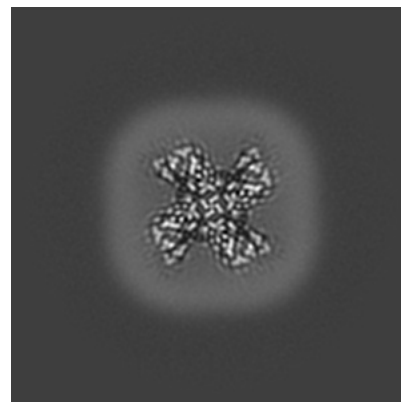
### 6.3.1 Primary map



X Index: 143

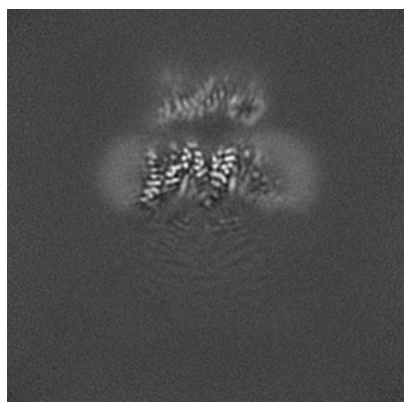


Y Index: 143

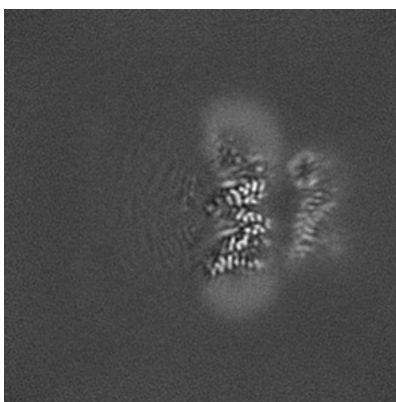


Z Index: 157

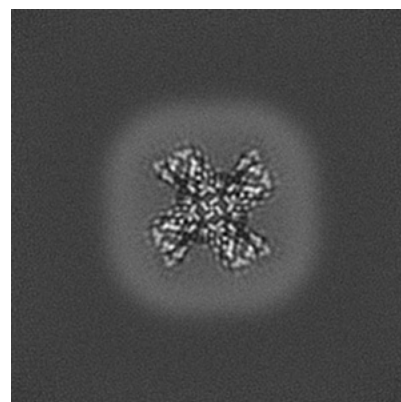
### 6.3.2 Raw map



X Index: 143



Y Index: 113

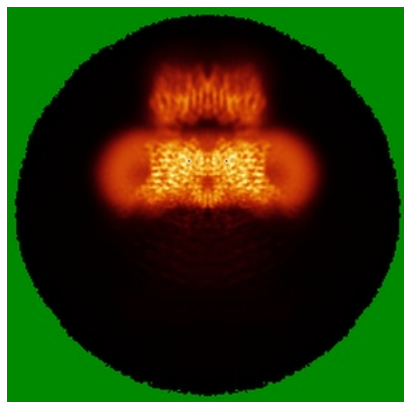


Z Index: 157

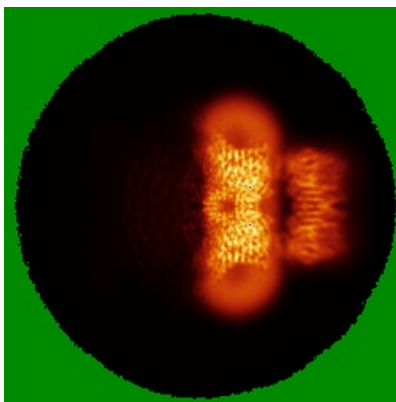
The images above show the largest variance slices of the map in three orthogonal directions.

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

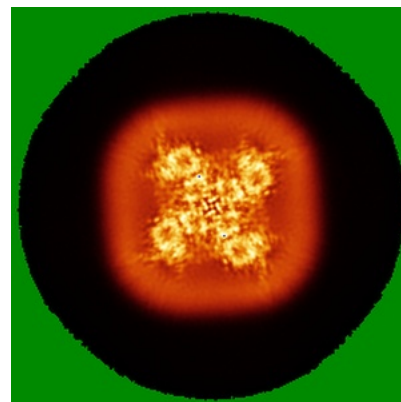
### 6.4.1 Primary map



X

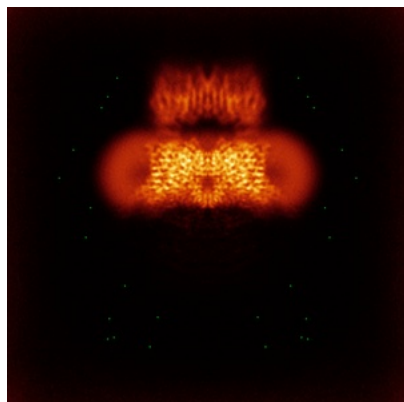


Y

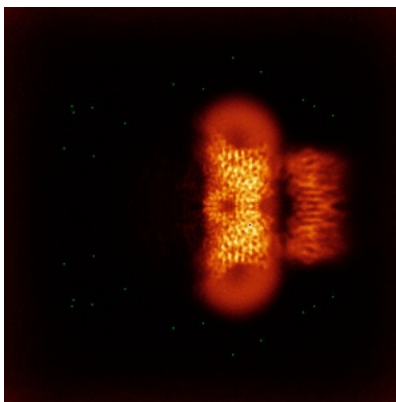


Z

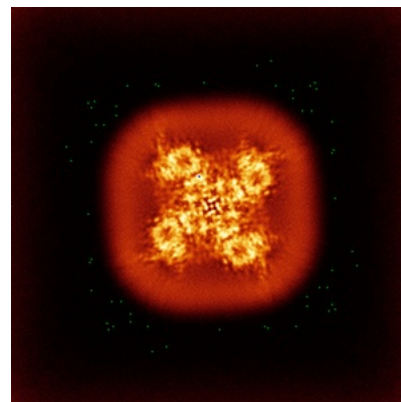
### 6.4.2 Raw map



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](#)

This section was not generated.

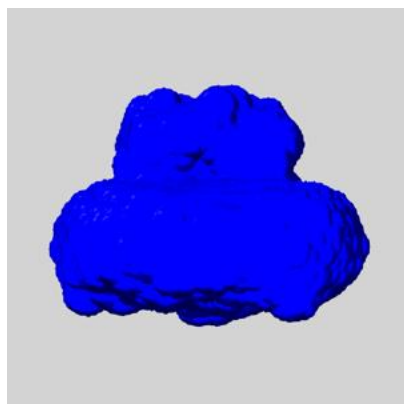
## 6.6 Mask visualisation [i](#)

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

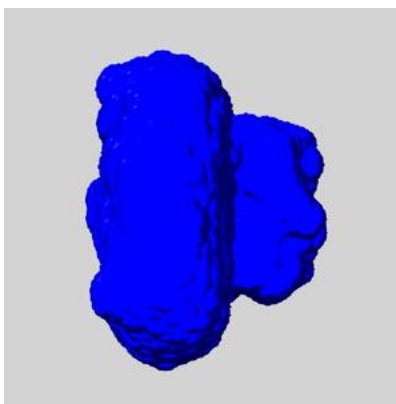
A mask typically either:

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

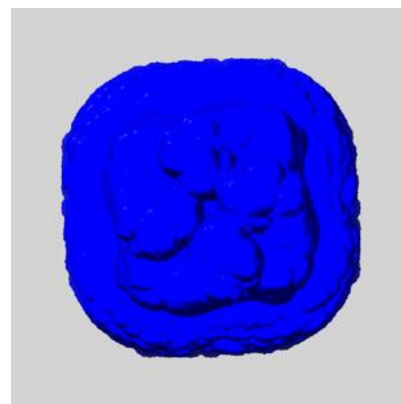
### 6.6.1 emd\_43106\_msk\_1.map [i](#)



X



Y

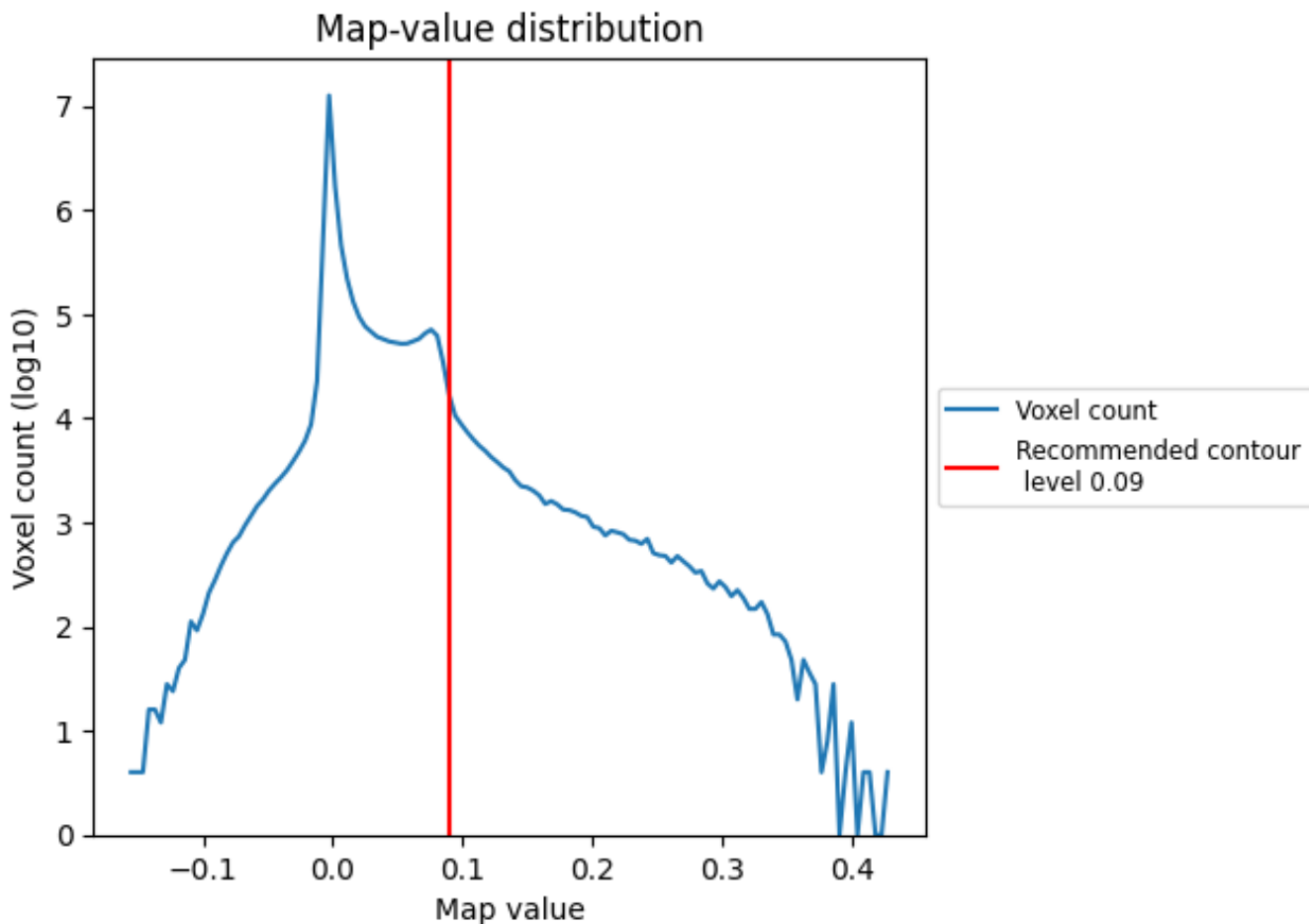


Z

## 7 Map analysis [i](#)

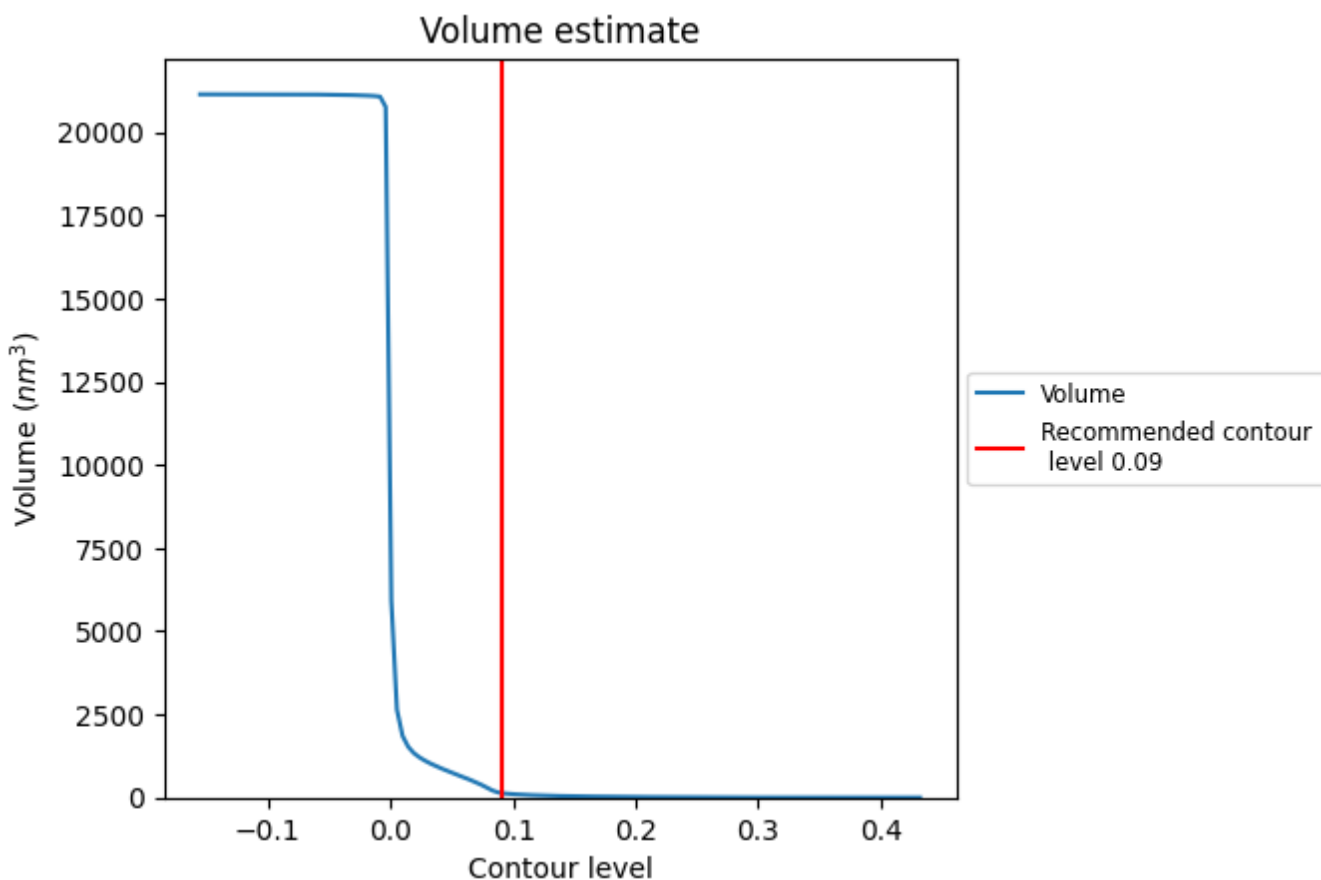
This section contains the results of statistical analysis of the map.

### 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.

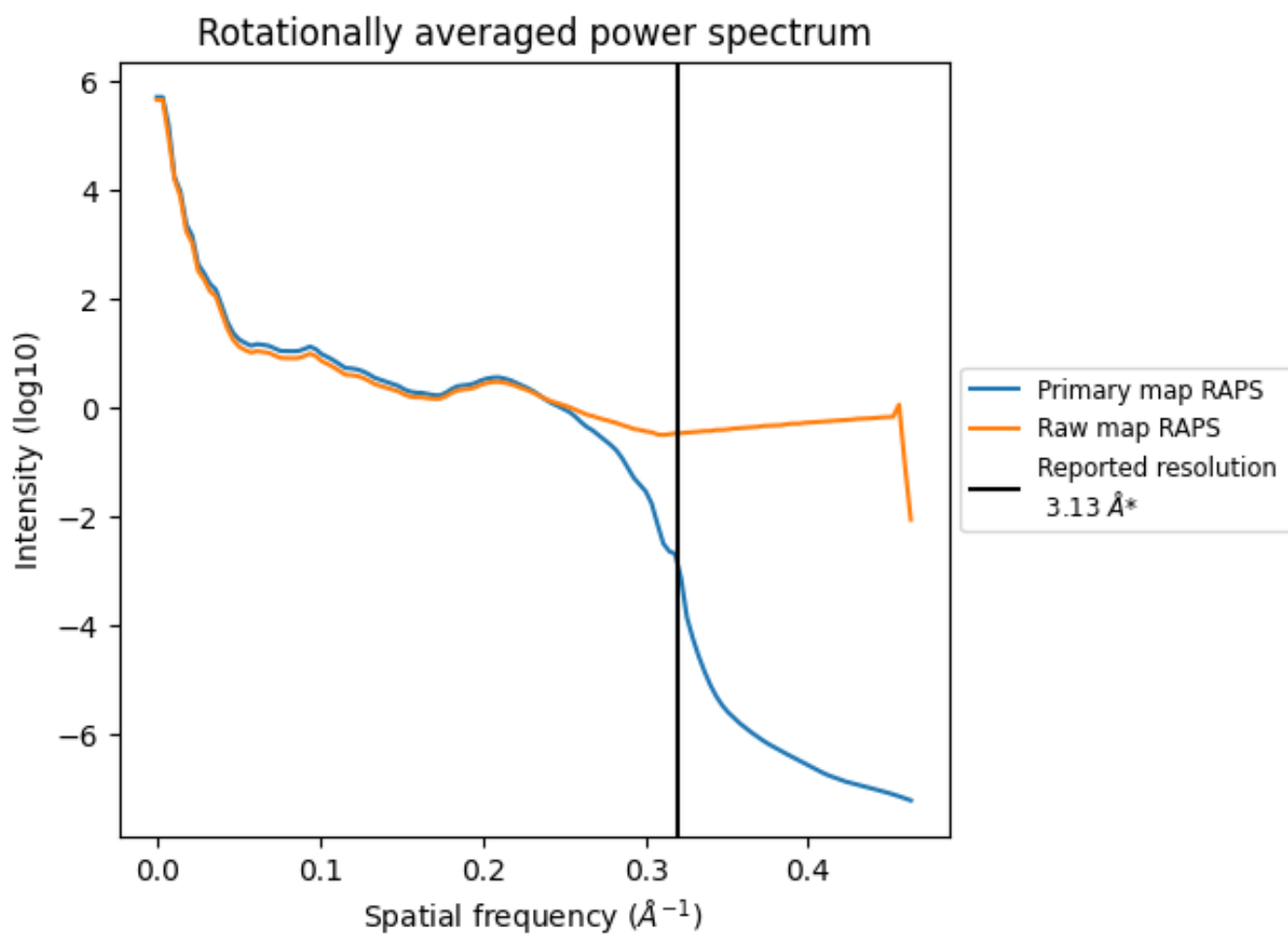
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 140  $\text{nm}^3$ ; this corresponds to an approximate mass of 126 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 [i](#)

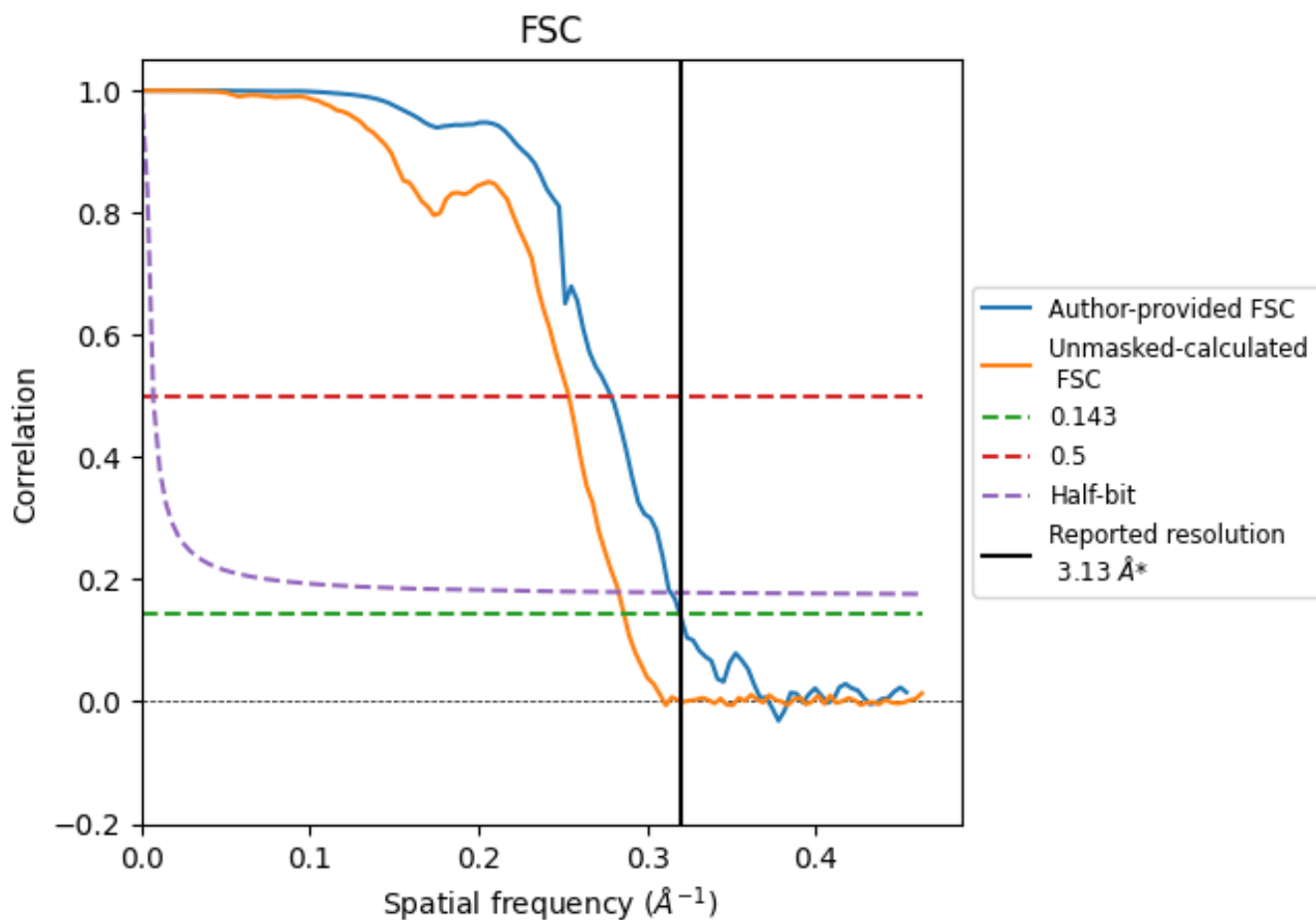


\*Reported resolution corresponds to spatial frequency of 0.319 Å<sup>-1</sup>

## 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 0.319 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

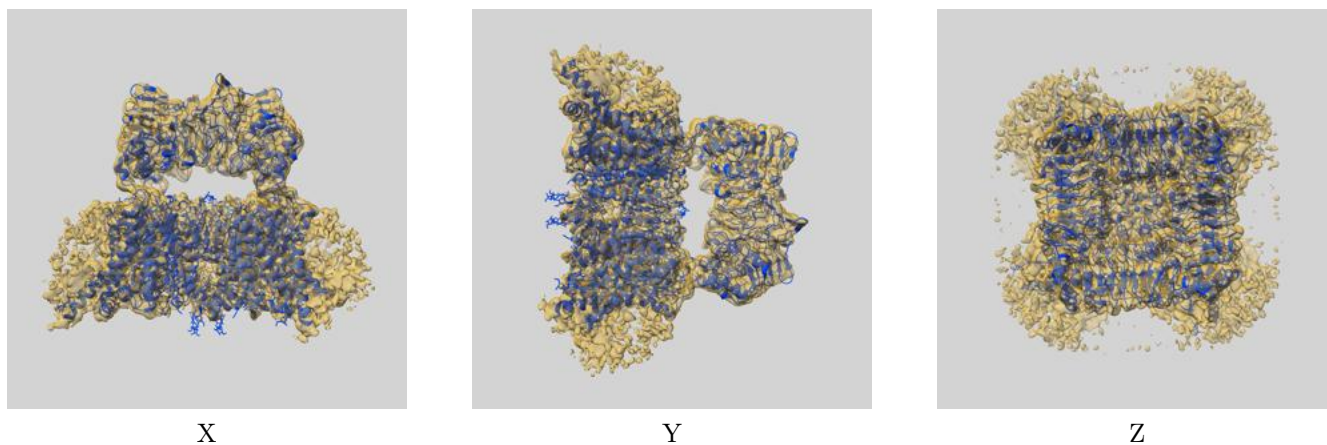
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.13	-	-
Author-provided FSC curve	3.13	3.59	3.18
Unmasked-calculated*	3.49	3.94	3.53

\*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 3.49 differs from the reported value 3.13 by more than 10 %

## 9 Map-model fit [i](#)

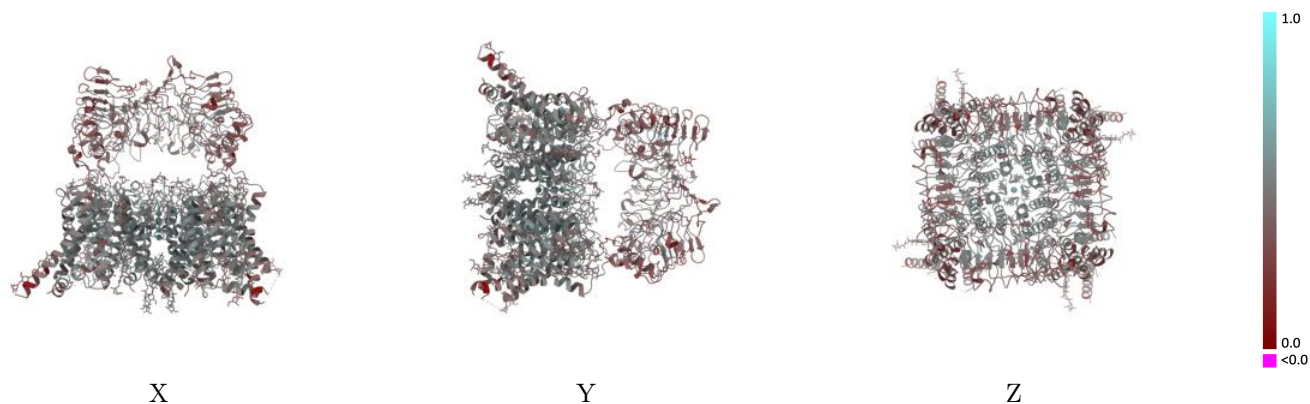
This section contains information regarding the fit between EMDB map EMD-43106 and PDB model 8VAV. Per-residue inclusion information can be found in section 3 on page 12.

### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.09 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](#)

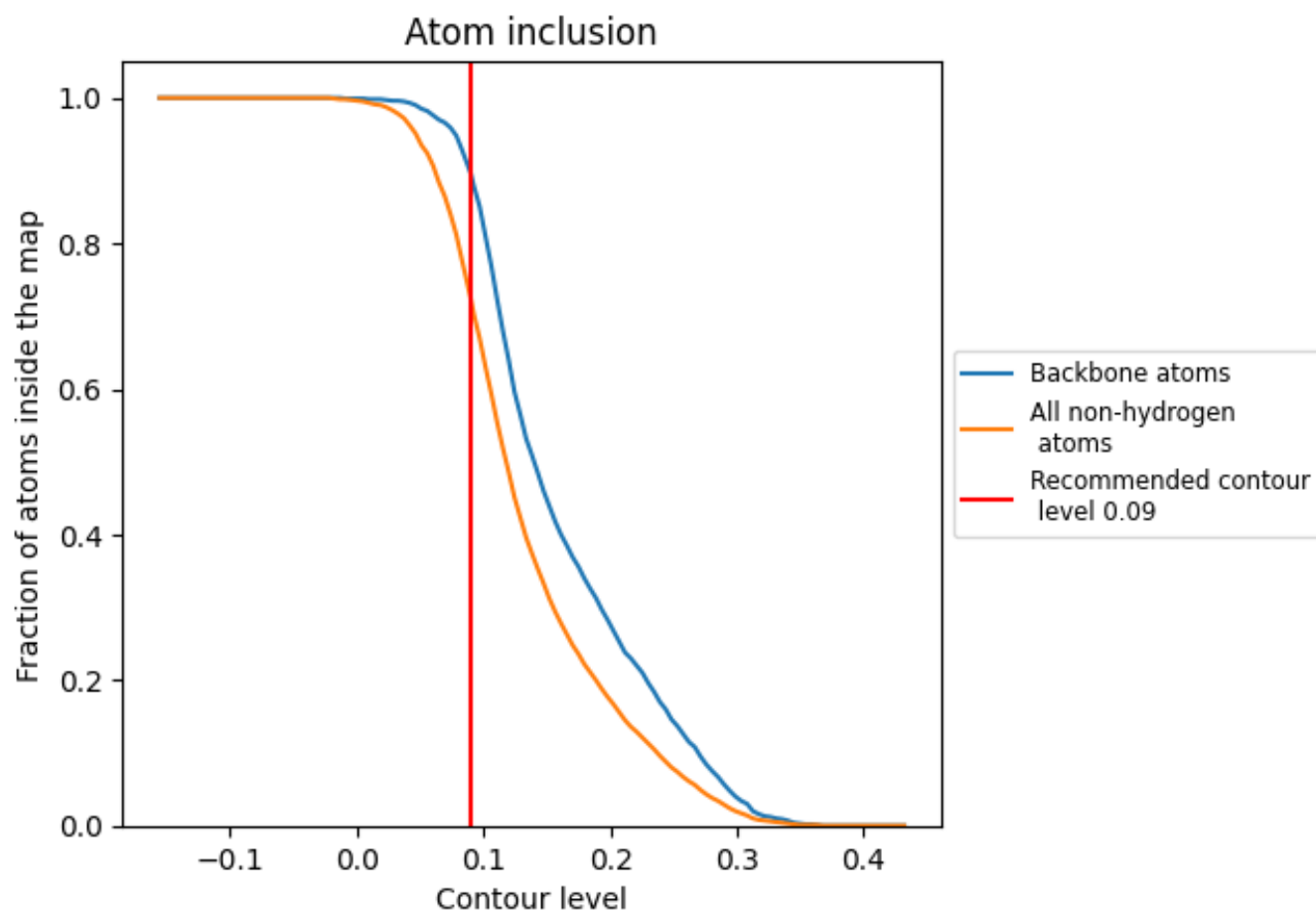


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.



















## 9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7240	 0.4370
A	 0.7570	 0.4750
B	 0.7570	 0.4730
C	 0.7560	 0.4740
D	 0.7570	 0.4740
E	 0.6740	 0.3820
F	 0.6760	 0.3830
G	 0.6750	 0.3830
H	 0.6740	 0.3810

