



wwPDB EM Validation Summary Report ⓘ

Jul 15, 2025 – 02:13 PM JST

PDB ID : 9JEE / pdb_00009jee
EMDB ID : EMD-61414
Title : Cryo-EM structure of human TRPV3 in complex with citral determined in MSP2N2 nanodisc
Authors : Lu, X.; Yao, J.
Deposited on : 2024-09-03
Resolution : 3.51 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

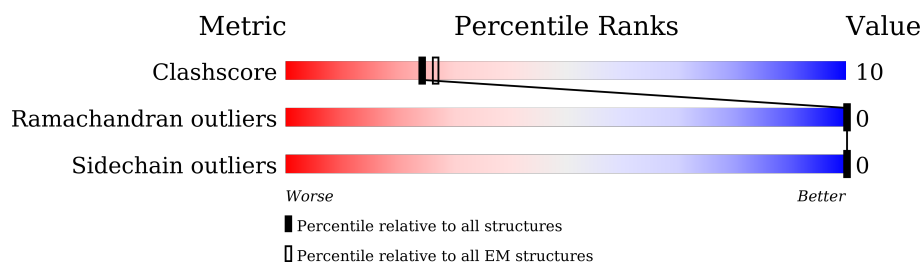
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.51 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	799	
1	B	799	
1	C	799	
1	D	799	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20660 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Transient receptor potential cation channel subfamily V member 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	612	Total	C	N	O	S	0	0
			4974	3241	819	883	31		
1	B	612	Total	C	N	O	S	0	0
			4974	3241	819	883	31		
1	C	612	Total	C	N	O	S	0	0
			4974	3241	819	883	31		
1	D	612	Total	C	N	O	S	0	0
			4974	3241	819	883	31		

There are 40 discrepancies between the modelled and reference sequences:

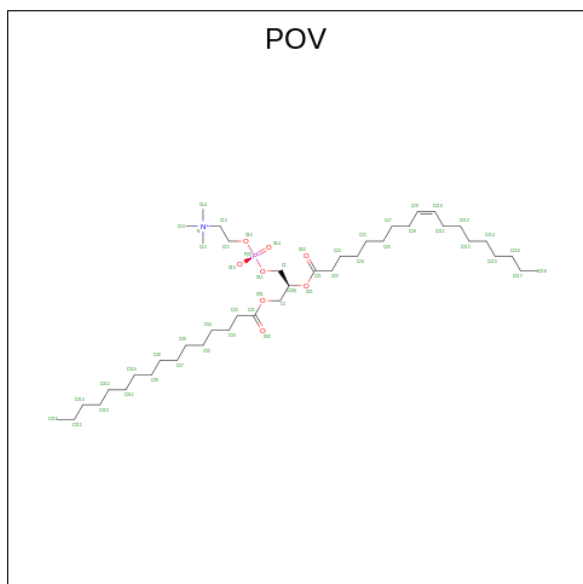
Chain	Residue	Modelled	Actual	Comment	Reference
A	25	VAL	ILE	variant	UNP Q8NET8
A	791	SER	-	expression tag	UNP Q8NET8
A	792	ASN	-	expression tag	UNP Q8NET8
A	793	SER	-	expression tag	UNP Q8NET8
A	794	LEU	-	expression tag	UNP Q8NET8
A	795	GLU	-	expression tag	UNP Q8NET8
A	796	VAL	-	expression tag	UNP Q8NET8
A	797	LEU	-	expression tag	UNP Q8NET8
A	798	PHE	-	expression tag	UNP Q8NET8
A	799	GLN	-	expression tag	UNP Q8NET8
B	25	VAL	ILE	variant	UNP Q8NET8
B	791	SER	-	expression tag	UNP Q8NET8
B	792	ASN	-	expression tag	UNP Q8NET8
B	793	SER	-	expression tag	UNP Q8NET8
B	794	LEU	-	expression tag	UNP Q8NET8
B	795	GLU	-	expression tag	UNP Q8NET8
B	796	VAL	-	expression tag	UNP Q8NET8
B	797	LEU	-	expression tag	UNP Q8NET8
B	798	PHE	-	expression tag	UNP Q8NET8
B	799	GLN	-	expression tag	UNP Q8NET8
C	25	VAL	ILE	variant	UNP Q8NET8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	791	SER	-	expression tag	UNP Q8NET8
C	792	ASN	-	expression tag	UNP Q8NET8
C	793	SER	-	expression tag	UNP Q8NET8
C	794	LEU	-	expression tag	UNP Q8NET8
C	795	GLU	-	expression tag	UNP Q8NET8
C	796	VAL	-	expression tag	UNP Q8NET8
C	797	LEU	-	expression tag	UNP Q8NET8
C	798	PHE	-	expression tag	UNP Q8NET8
C	799	GLN	-	expression tag	UNP Q8NET8
D	25	VAL	ILE	variant	UNP Q8NET8
D	791	SER	-	expression tag	UNP Q8NET8
D	792	ASN	-	expression tag	UNP Q8NET8
D	793	SER	-	expression tag	UNP Q8NET8
D	794	LEU	-	expression tag	UNP Q8NET8
D	795	GLU	-	expression tag	UNP Q8NET8
D	796	VAL	-	expression tag	UNP Q8NET8
D	797	LEU	-	expression tag	UNP Q8NET8
D	798	PHE	-	expression tag	UNP Q8NET8
D	799	GLN	-	expression tag	UNP Q8NET8

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



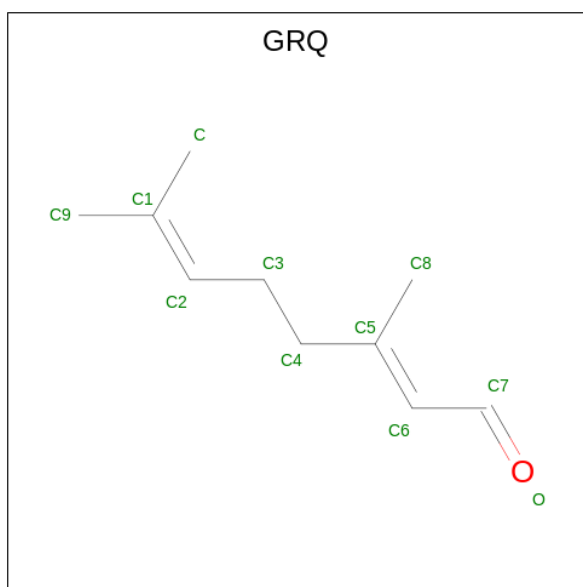
Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			32	22	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			36	26	1	8	1	
2	A	1	Total	C	N	O	P	0
			36	26	1	8	1	
2	A	1	Total	C	N	O	P	0
			44	34	1	8	1	
2	A	1	Total	C	N	O	P	0
			32	22	1	8	1	
2	B	1	Total	C	N	O	P	0
			32	22	1	8	1	
2	B	1	Total	C	N	O	P	0
			32	22	1	8	1	
2	B	1	Total	C	N	O	P	0
			36	26	1	8	1	
2	B	1	Total	C	N	O	P	0
			36	26	1	8	1	
2	B	1	Total	C	N	O	P	0
			44	34	1	8	1	
2	C	1	Total	C	N	O	P	0
			32	22	1	8	1	
2	C	1	Total	C	N	O	P	0
			32	22	1	8	1	
2	C	1	Total	C	N	O	P	0
			36	26	1	8	1	
2	C	1	Total	C	N	O	P	0
			36	26	1	8	1	
2	C	1	Total	C	N	O	P	0
			44	34	1	8	1	
2	D	1	Total	C	N	O	P	0
			44	34	1	8	1	
2	D	1	Total	C	N	O	P	0
			32	22	1	8	1	
2	D	1	Total	C	N	O	P	0
			32	22	1	8	1	
2	D	1	Total	C	N	O	P	0
			36	26	1	8	1	
2	D	1	Total	C	N	O	P	0
			36	26	1	8	1	

- Molecule 3 is Geranaldehyde (CCD ID: GRQ) (formula: C₁₀H₁₆O) (labeled as "Ligand of Interest" by depositor).

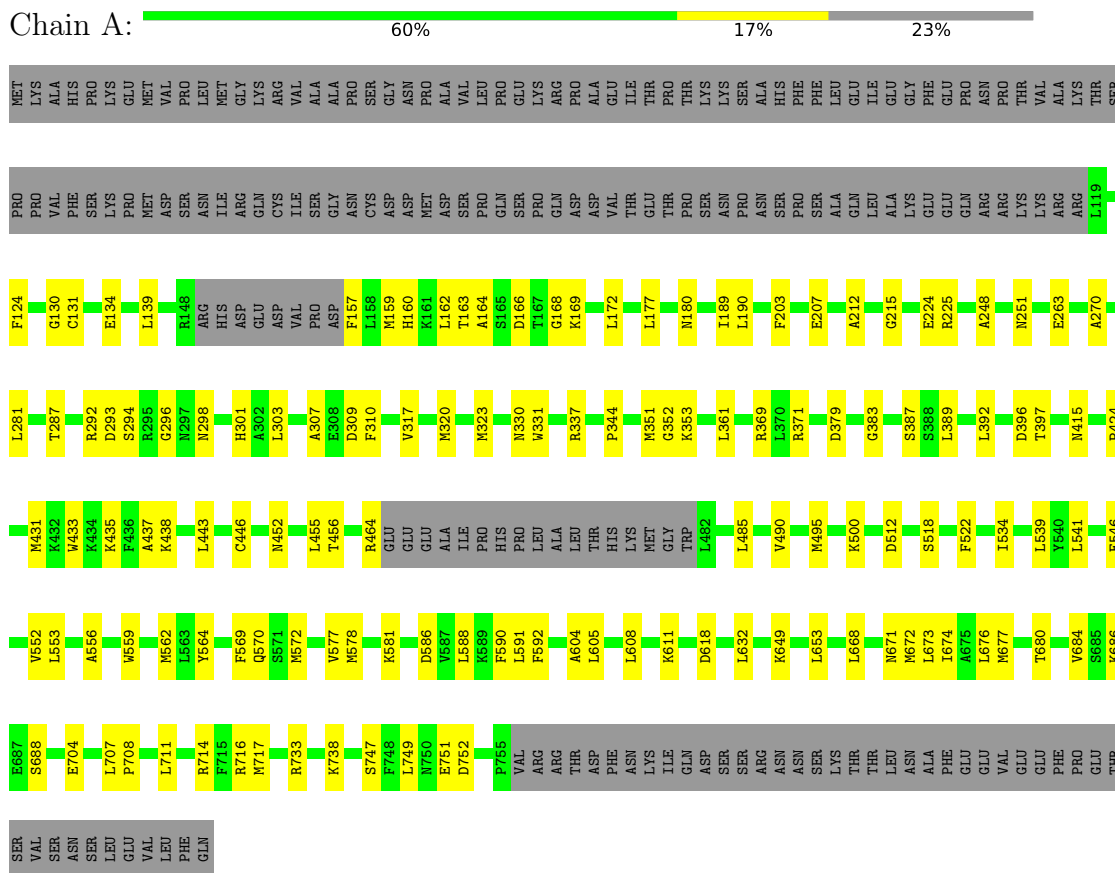


Mol	Chain	Residues	Atoms			AltConf
3	A	1	Total	C	O	0
			11	10	1	
3	B	1	Total	C	O	0
			11	10	1	
3	C	1	Total	C	O	0
			11	10	1	
3	D	1	Total	C	O	0
			11	10	1	

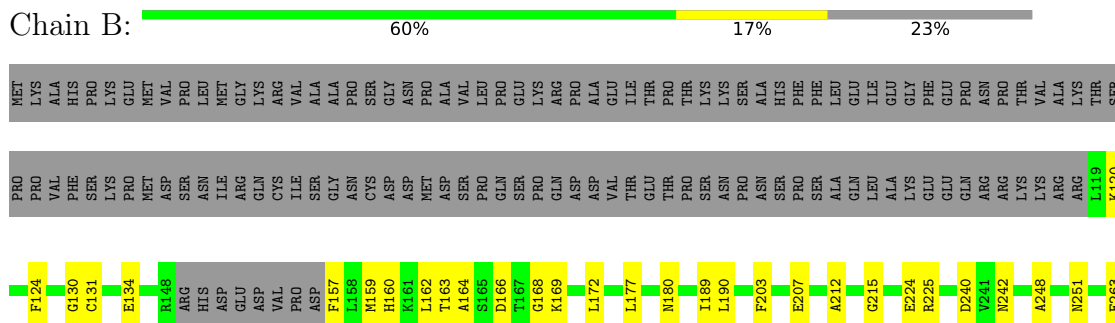
3 Residue-property plots

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. 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. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Transient receptor potential cation channel subfamily V member 3



- Molecule 1: Transient receptor potential cation channel subfamily V member 3





LEU	L707	M562	W433	R292	F124	PRO
GLU	P708	L563	K434	D293	G130	PRO
VAL	L711	F436	K435	S294	C131	VAL
LEU	L714	Y564	A437	R295	E134	PHE
PHE	R715	F569	K438	G296	R148	SER
GLN	R716	Q570	L443	R297	ARG	LYS
	R717	S571	C446	N298	HIS	PRO
	M572	M577	N452	H301	ASP	MET
	R733	M578	L455	L303	ASN	ASP
	K738	K581	T456	A307	ILE	ARG
	S747	D586	R464	E308	ASP	GLN
	F748	V587	GLU	D309	PRO	ARG
	L749	L588	GLU	F310	ASP	ILE
	N750	K589	GLU	F157	L158	SER
	E751	F590	ALA	M159	H160	GLY
	D752	F592	ILE	R161	T162	ASN
	P755	L604	PRO	L163	T163	CYS
VAL	ARG	L605	PRO	A164	ASP	ASP
ARG	ARG	L608	LEU	S165	D166	ASP
ARG	THR	K611	ALA	D167	G168	PRO
ASP	ASP	L615	THR	K169	L172	GLN
PHE	PHE	D618	HIS	M351	L177	GLN
ASN	ASN	L632	LYS	G352	N180	PRO
LYS	LYS	K649	MET	K353	L190	GLN
ILE	ILE	L653	GLY	L361	F203	ASP
GLN	GLN	L668	TRP	R369	E207	ASP
ASP	ASP	M671	L482	L370	A212	VAL
ASP	SER	M672	L485	R371	G215	THR
SER	SER	L673	V490	D379	E224	THR
ARG	ARG	I674	M495	G383	R225	PRO
ASN	ASN	A675	D512	S387	ALA	SER
ASN	ASN	L676	S518	S388	LEU	ALA
ASN	SER	M677	F522	L389	ALA	LYS
SER	LYS	T680	I534	L392	GLU	GLU
THR	THR	V684	L539	D396	GLU	GLU
LEU	LEU	S685	E546	T397	V241	GLN
ASN	ASN	K686	V552	N415	N242	ARG
ALA	ALA	E687	L553	P424	A248	ARG
PHE	PHE	S688	A556	M431	N251	LYS
GLU	GLU	E704	W559	K432	E263	LYS
VAL	VAL				A270	ARG
SER	SER					ARG
ASN	ASN					L119
SER	SER					

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	58795	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	-1300	Depositor
Maximum defocus (nm)	-1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	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: GRQ, 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	0.13	0/5080	0.37	0/6868
1	B	0.13	0/5080	0.37	0/6868
1	C	0.13	0/5080	0.37	0/6868
1	D	0.13	0/5080	0.37	0/6868
All	All	0.13	0/20320	0.37	0/27472

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	4974	0	5052	116	0
1	B	4974	0	5052	112	0
1	C	4974	0	5052	120	0
1	D	4974	0	5052	113	0
2	A	180	0	225	4	0
2	B	180	0	225	4	0
2	C	180	0	225	3	0
2	D	180	0	225	4	0
3	A	11	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	11	0	0	0	0
3	C	11	0	0	0	0
3	D	11	0	0	0	0
All	All	20660	0	21108	437	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 10.

The worst 5 of 437 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:B:392:LEU:HD13	1:B:396:ASP:HB2	1.27	1.16
1:D:392:LEU:HD13	1:D:396:ASP:HB2	1.27	1.14
1:A:392:LEU:HD13	1:A:396:ASP:HB2	1.27	1.11
1:C:392:LEU:HD13	1:C:396:ASP:HB2	1.27	1.09
1:D:172:LEU:HB2	1:D:203:PHE:CZ	1.95	1.01

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	606/799 (76%)	562 (93%)	44 (7%)	0	100	100
1	B	606/799 (76%)	563 (93%)	43 (7%)	0	100	100
1	C	606/799 (76%)	562 (93%)	44 (7%)	0	100	100
1	D	606/799 (76%)	562 (93%)	44 (7%)	0	100	100
All	All	2424/3196 (76%)	2249 (93%)	175 (7%)	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	542/712 (76%)	542 (100%)	0	100	100
1	B	542/712 (76%)	542 (100%)	0	100	100
1	C	542/712 (76%)	542 (100%)	0	100	100
1	D	542/712 (76%)	542 (100%)	0	100	100
All	All	2168/2848 (76%)	2168 (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 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	314	ASN
1	D	301	HIS
1	C	220	ASN
1	D	410	ASN
1	D	220	ASN

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

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$
2	POV	D	805	-	35,35,51	0.58	0	41,43,59	0.50	0
2	POV	B	806	-	43,43,51	0.53	0	49,51,59	0.49	0
2	POV	D	802	-	31,31,51	0.61	0	37,39,59	0.53	0
3	GRQ	C	805	-	10,10,10	1.89	2 (20%)	11,11,11	4.54	7 (63%)
2	POV	A	803	-	35,35,51	0.58	0	41,43,59	0.50	0
2	POV	D	804	-	35,35,51	0.59	0	41,43,59	0.52	0
2	POV	B	804	-	35,35,51	0.58	0	41,43,59	0.50	0
2	POV	A	802	-	35,35,51	0.59	0	41,43,59	0.52	0
2	POV	D	801	-	43,43,51	0.54	0	49,51,59	0.50	0
2	POV	A	801	-	31,31,51	0.62	0	37,39,59	0.55	0
2	POV	B	801	-	31,31,51	0.61	0	37,39,59	0.53	0
2	POV	A	806	-	31,31,51	0.61	0	37,39,59	0.53	0
2	POV	D	803	-	31,31,51	0.62	0	37,39,59	0.55	0
3	GRQ	B	805	-	10,10,10	1.88	2 (20%)	11,11,11	4.54	7 (63%)
2	POV	C	804	-	35,35,51	0.58	0	41,43,59	0.50	0
3	GRQ	A	804	-	10,10,10	1.88	2 (20%)	11,11,11	4.54	7 (63%)
2	POV	C	801	-	31,31,51	0.61	0	37,39,59	0.53	0
2	POV	B	803	-	35,35,51	0.59	0	41,43,59	0.52	0
2	POV	B	802	-	31,31,51	0.62	0	37,39,59	0.55	0
2	POV	A	805	-	43,43,51	0.54	0	49,51,59	0.50	0
3	GRQ	D	806	-	10,10,10	1.88	2 (20%)	11,11,11	4.54	7 (63%)
2	POV	C	803	-	35,35,51	0.60	0	41,43,59	0.52	0
2	POV	C	806	-	43,43,51	0.54	0	49,51,59	0.50	0
2	POV	C	802	-	31,31,51	0.62	0	37,39,59	0.55	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
2	POV	D	805	-	-	10/39/39/55	-
2	POV	B	806	-	-	14/47/47/55	-
2	POV	D	802	-	-	8/35/35/55	-
3	GRQ	C	805	-	-	1/9/9/9	-
2	POV	A	803	-	-	10/39/39/55	-
2	POV	D	804	-	-	13/39/39/55	-
2	POV	B	804	-	-	10/39/39/55	-
2	POV	A	802	-	-	13/39/39/55	-
2	POV	D	801	-	-	14/47/47/55	-
2	POV	A	801	-	-	10/35/35/55	-
2	POV	B	801	-	-	8/35/35/55	-
2	POV	A	806	-	-	8/35/35/55	-
2	POV	D	803	-	-	10/35/35/55	-
3	GRQ	B	805	-	-	1/9/9/9	-
2	POV	C	804	-	-	10/39/39/55	-
3	GRQ	A	804	-	-	1/9/9/9	-
2	POV	C	801	-	-	8/35/35/55	-
2	POV	B	803	-	-	13/39/39/55	-
2	POV	B	802	-	-	10/35/35/55	-
2	POV	A	805	-	-	14/47/47/55	-
3	GRQ	D	806	-	-	1/9/9/9	-
2	POV	C	803	-	-	13/39/39/55	-
2	POV	C	806	-	-	14/47/47/55	-
2	POV	C	802	-	-	10/35/35/55	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	804	GRQ	C6-C7	4.24	1.54	1.44
3	B	805	GRQ	C6-C7	4.24	1.54	1.44
3	C	805	GRQ	C6-C7	4.24	1.54	1.44
3	D	806	GRQ	C6-C7	4.24	1.54	1.44
3	A	804	GRQ	C4-C5	2.22	1.55	1.51

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	804	GRQ	C8-C5-C4	-11.55	95.84	115.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	805	GRQ	C8-C5-C4	-11.55	95.84	115.27
3	D	806	GRQ	C8-C5-C4	-11.55	95.84	115.27
3	C	805	GRQ	C8-C5-C4	-11.53	95.88	115.27
3	A	804	GRQ	C7-C6-C5	-6.81	111.04	125.60

There are no chirality outliers.

5 of 224 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	POV	O22-C21-O21-C2
2	A	802	POV	C1-O11-P-O14
2	A	802	POV	O12-C11-C12-N
2	A	803	POV	O12-C11-C12-N
2	A	803	POV	C22-C21-O21-C2

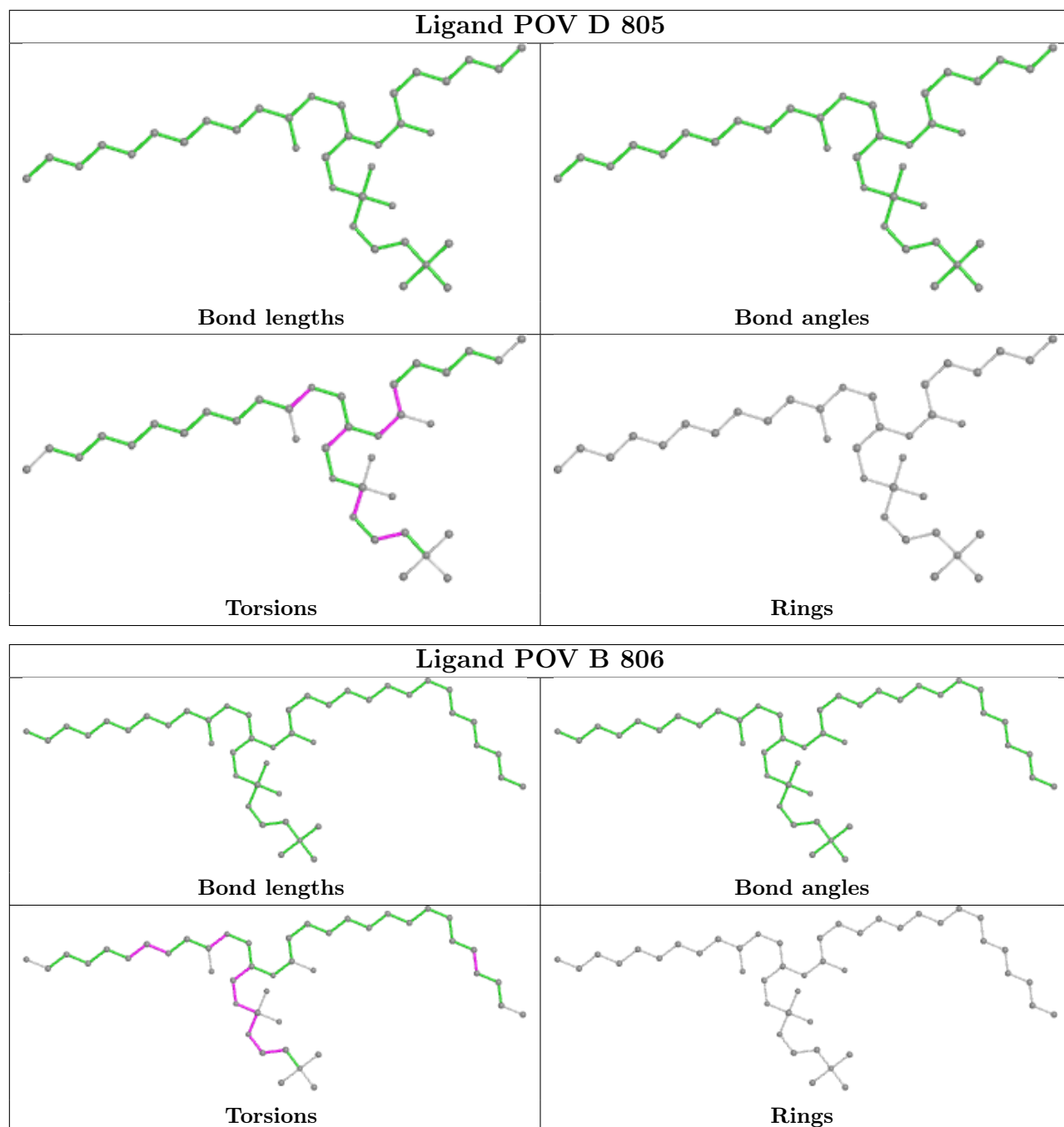
There are no ring outliers.

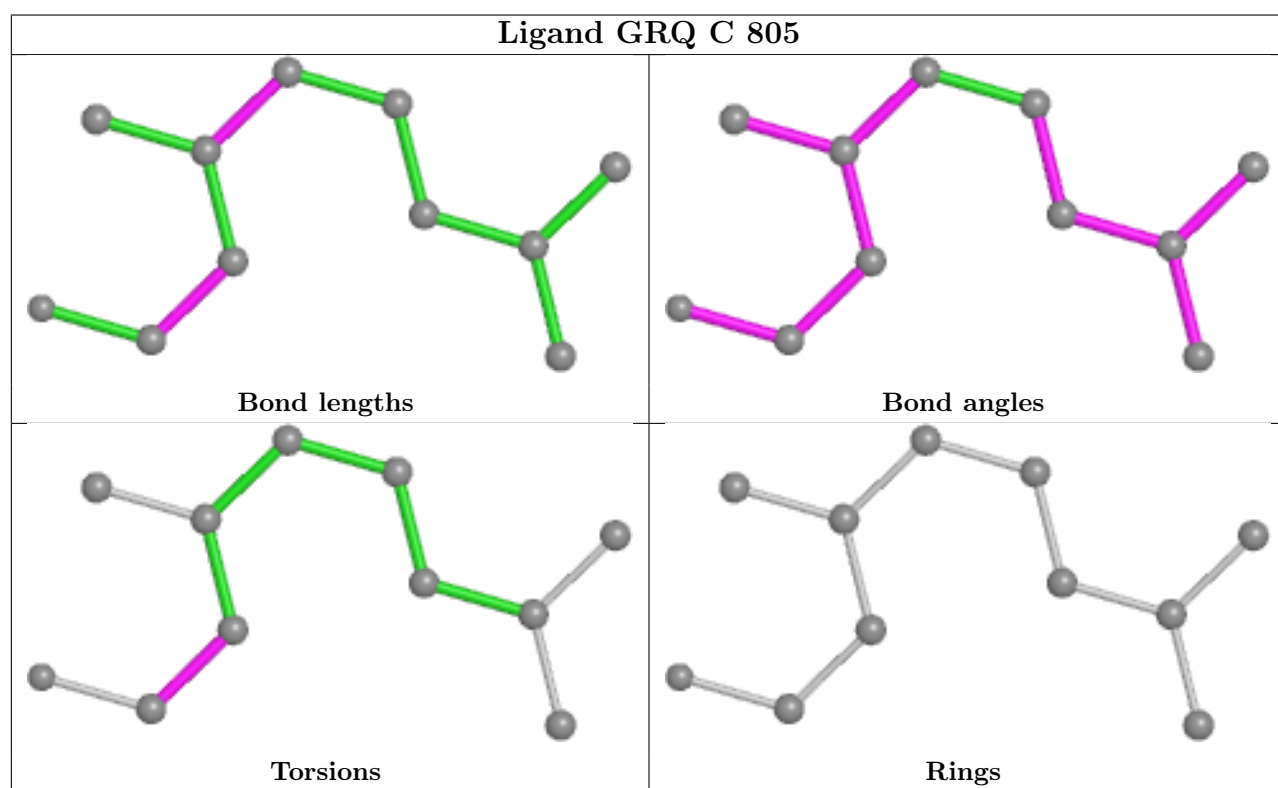
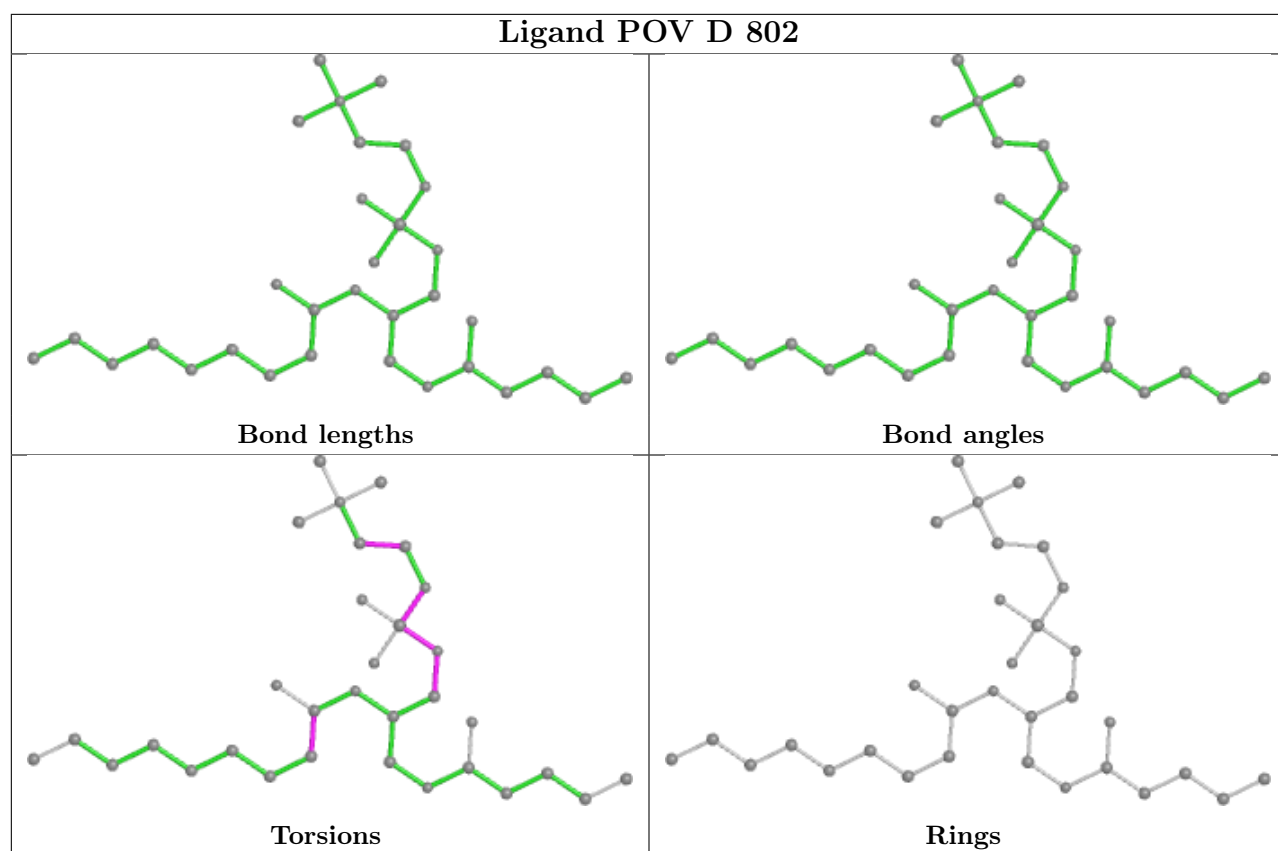
11 monomers are involved in 15 short contacts:

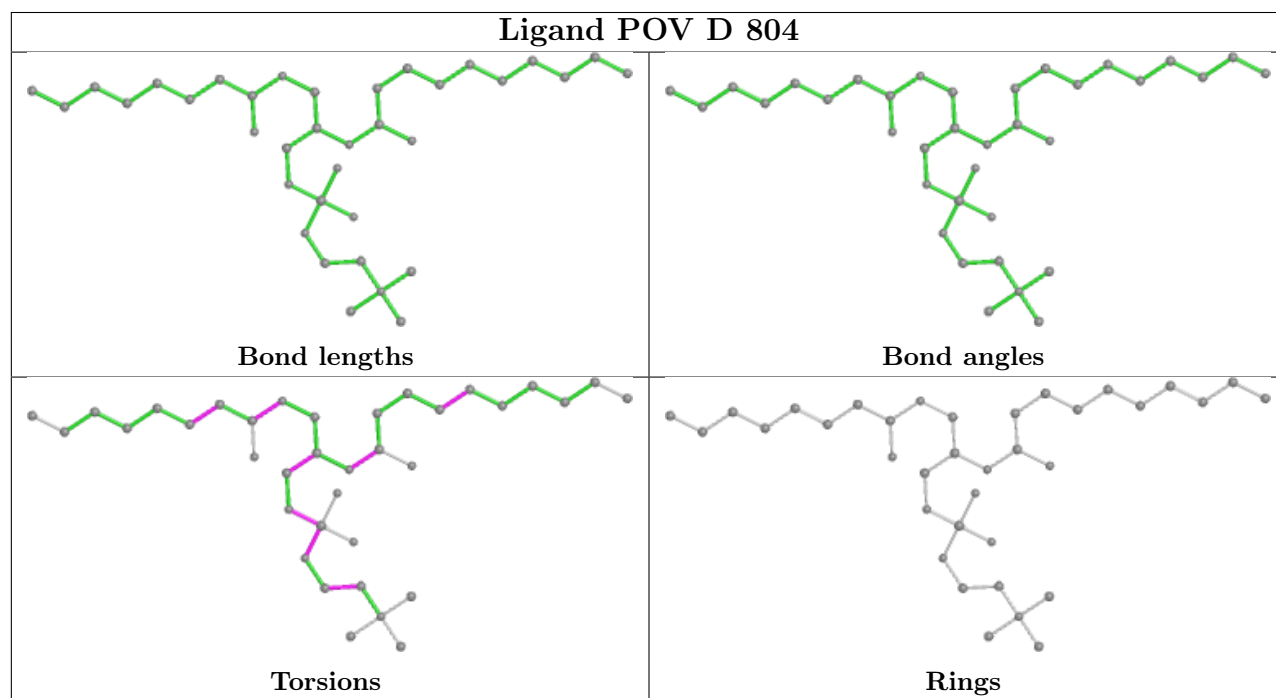
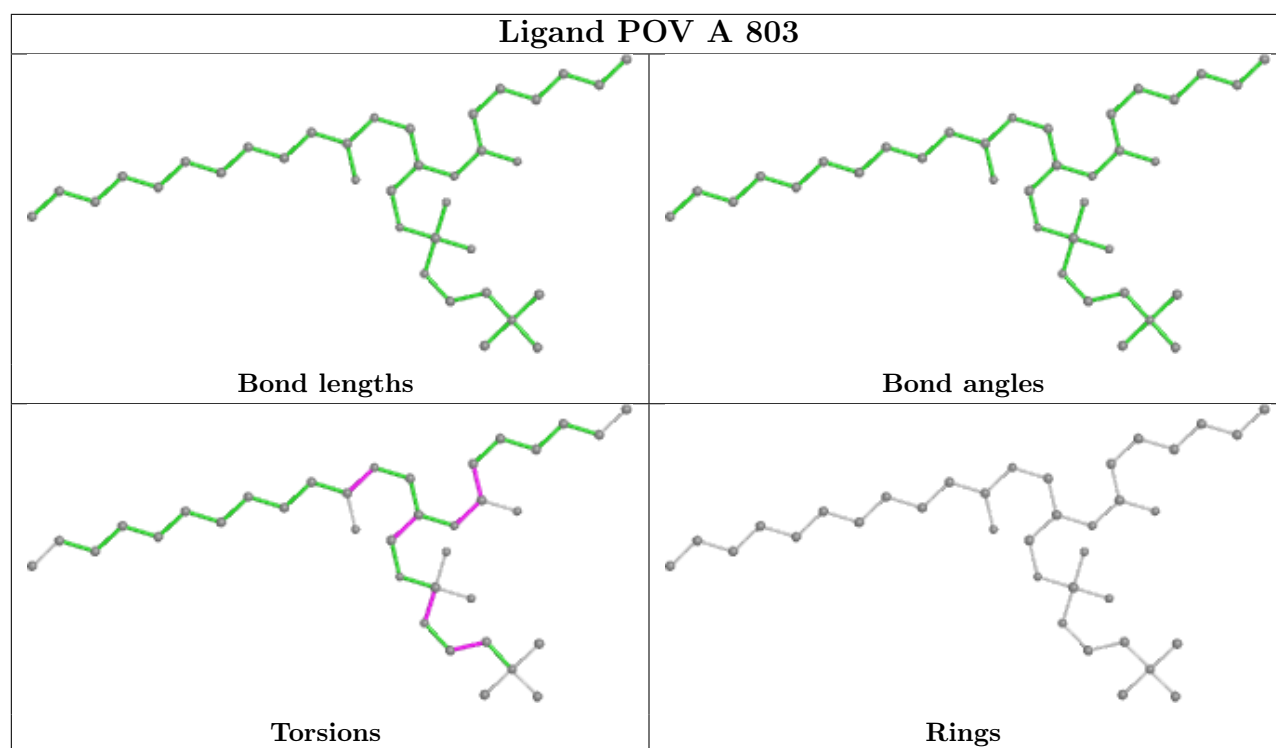
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	805	POV	2	0
2	B	806	POV	1	0
2	D	802	POV	1	0
2	A	803	POV	2	0
2	D	804	POV	1	0
2	B	804	POV	2	0
2	A	802	POV	1	0
2	A	806	POV	1	0
2	C	804	POV	2	0
2	B	803	POV	1	0
2	C	803	POV	1	0

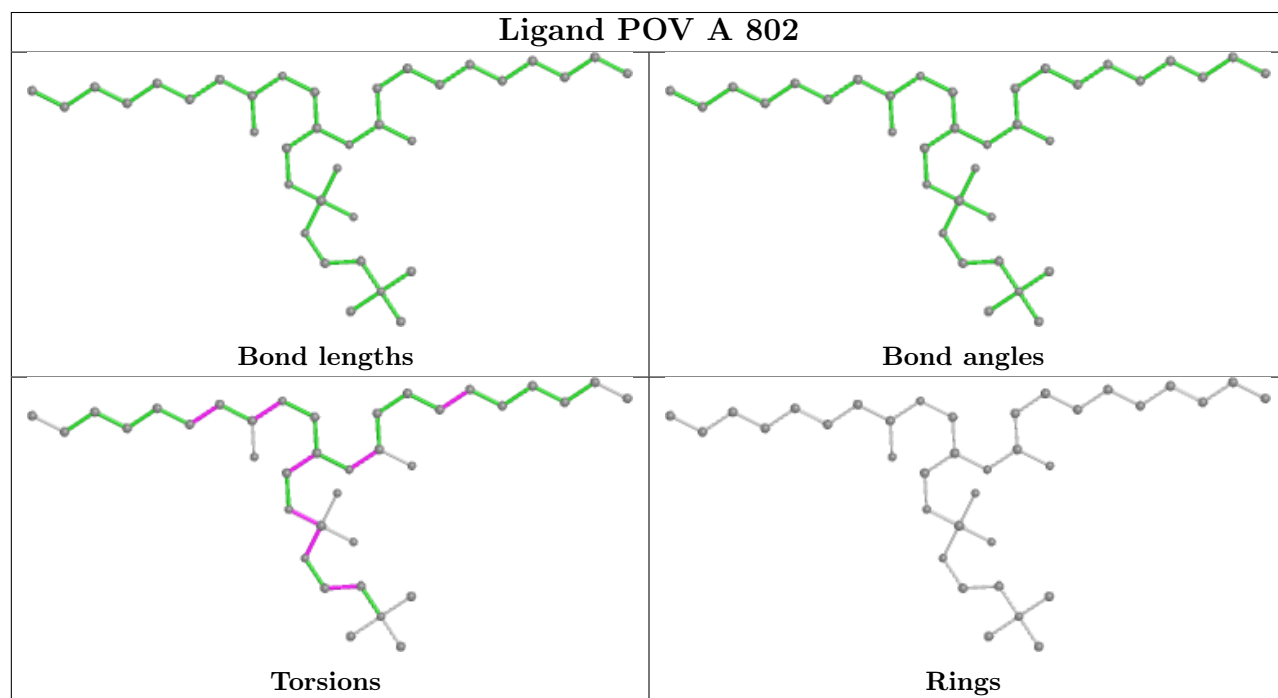
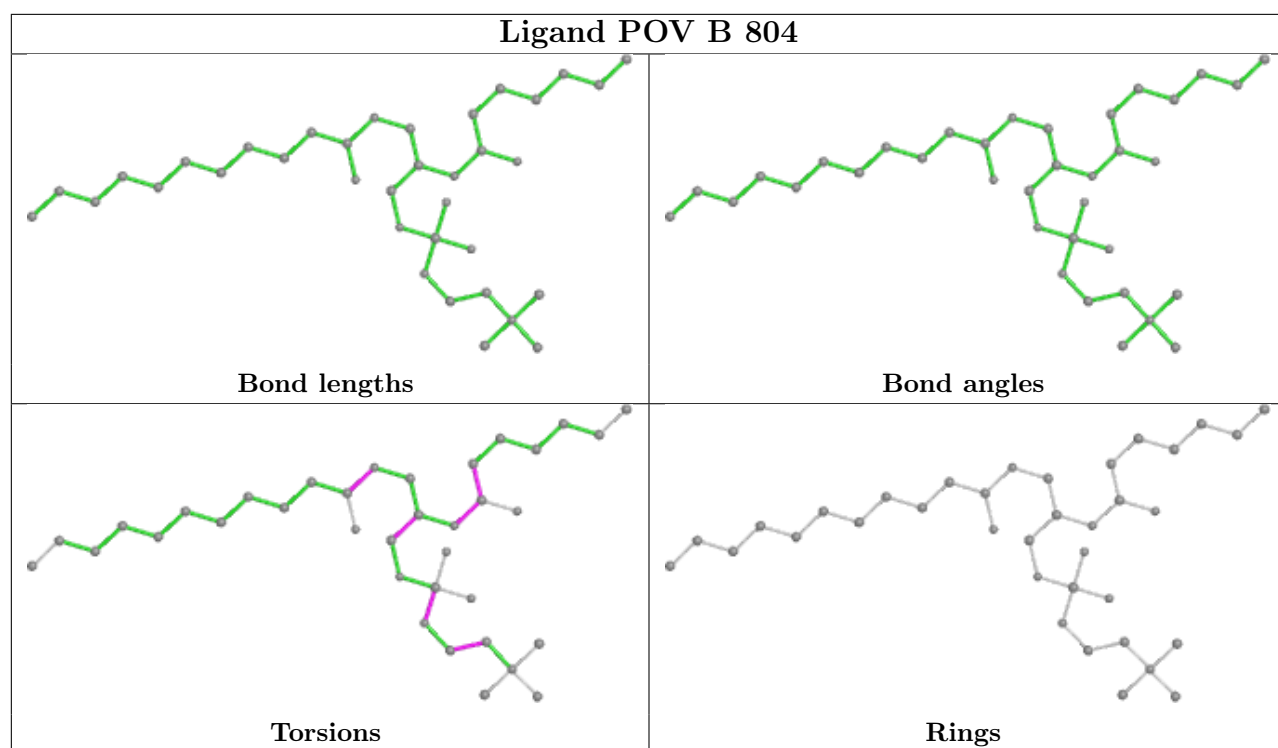
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

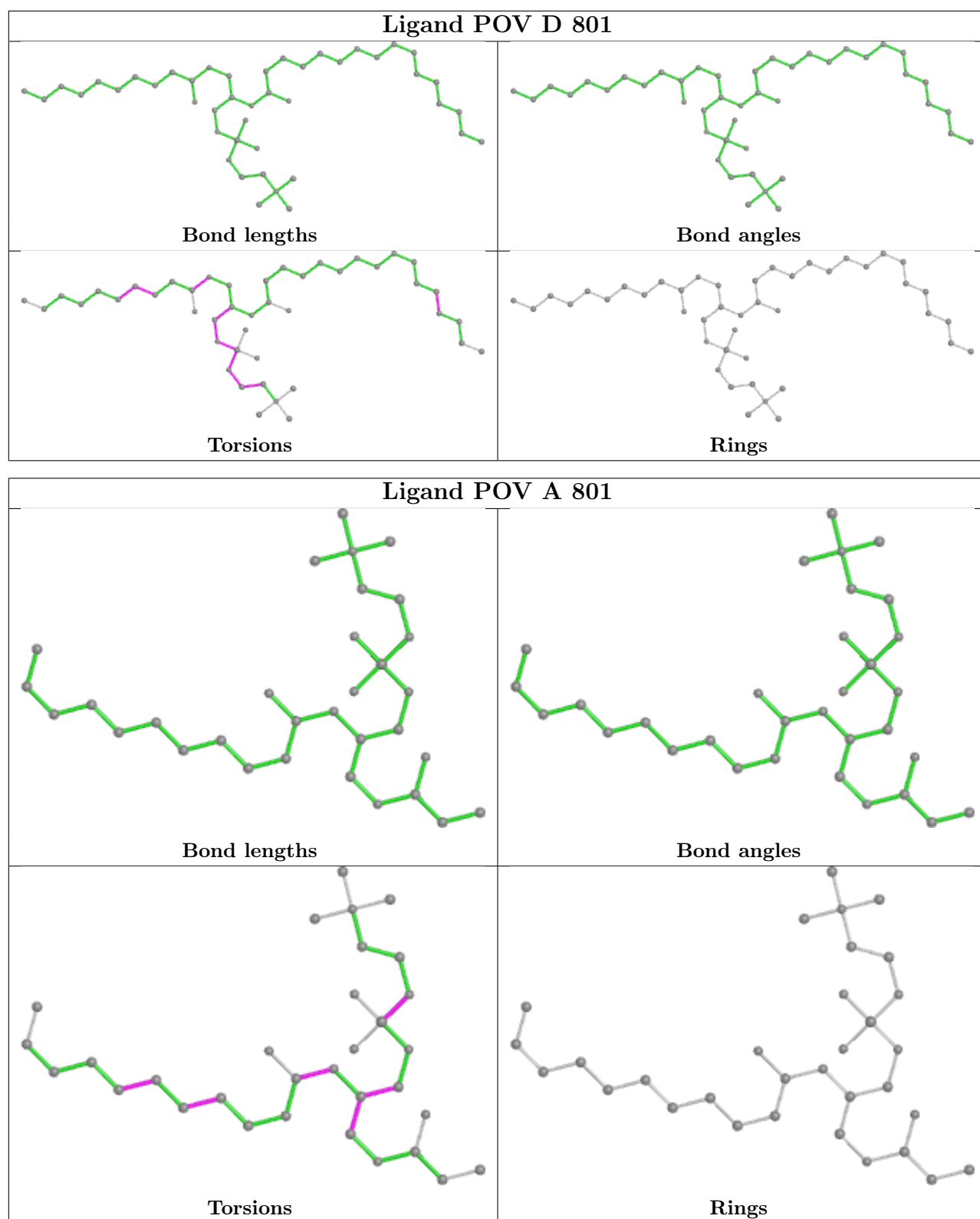
equivalents in the CSD to analyse the geometry.

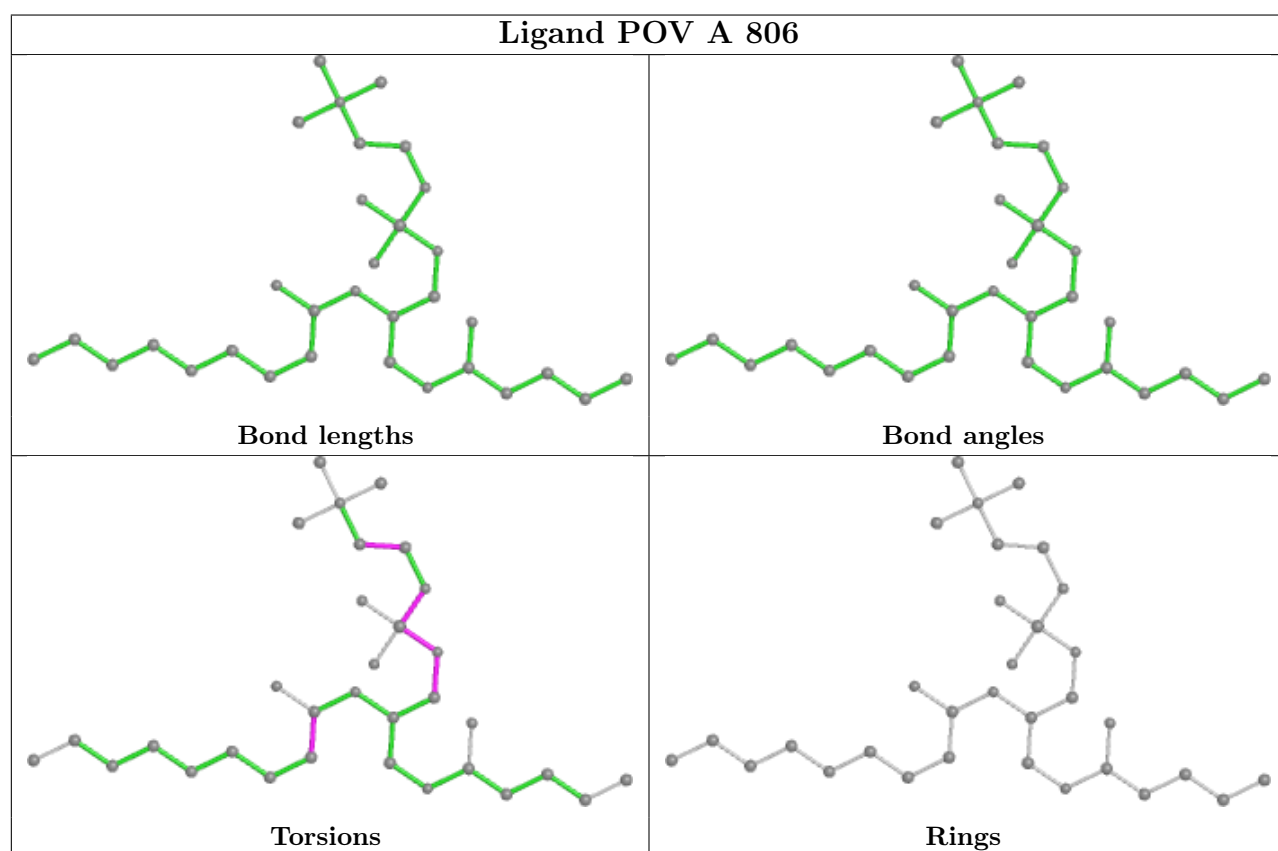
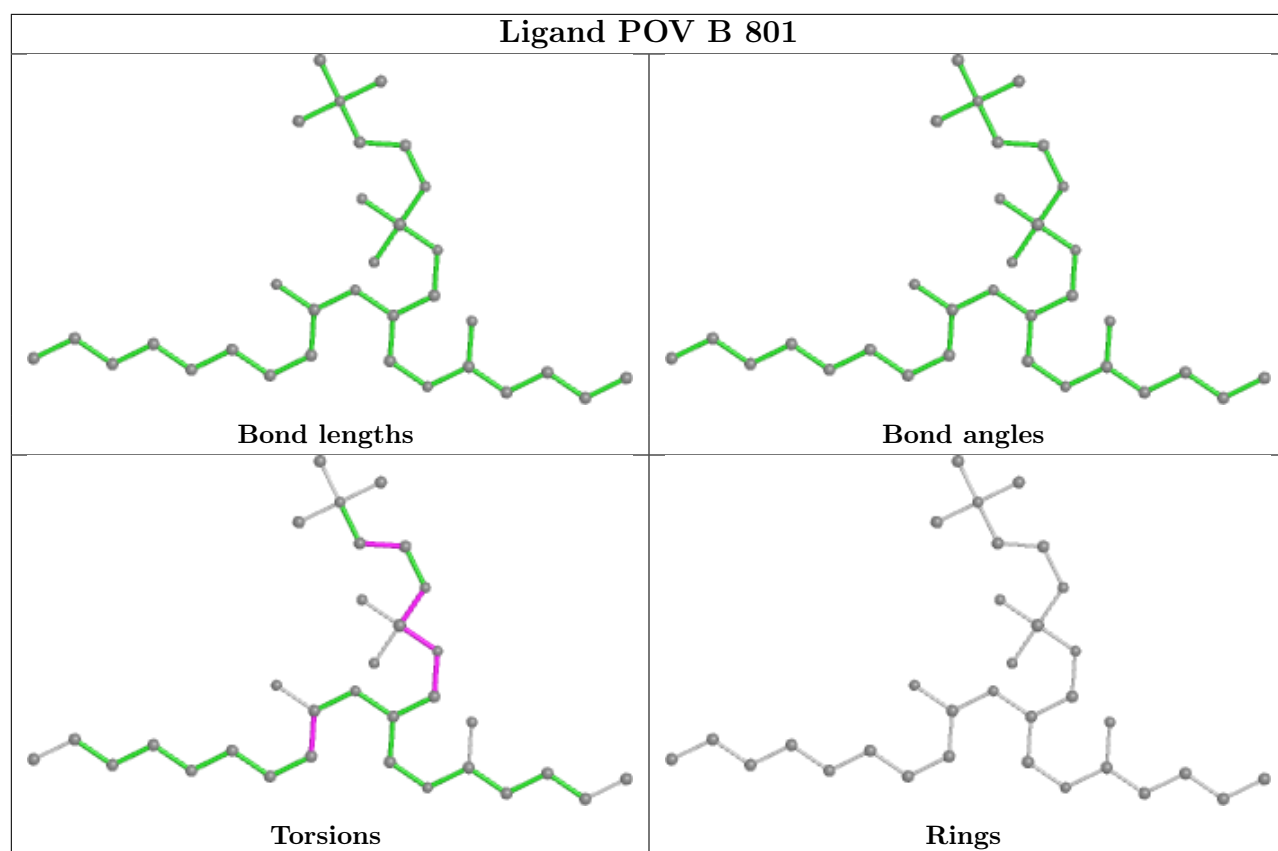


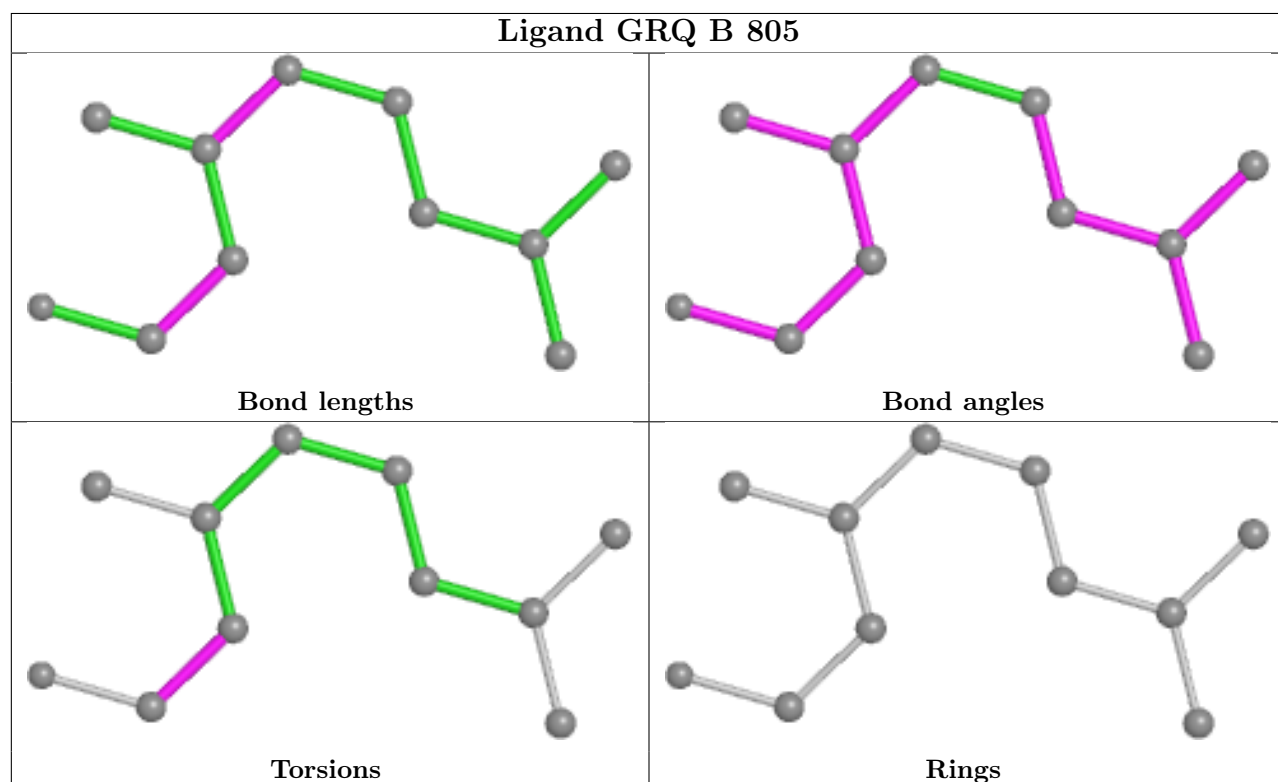
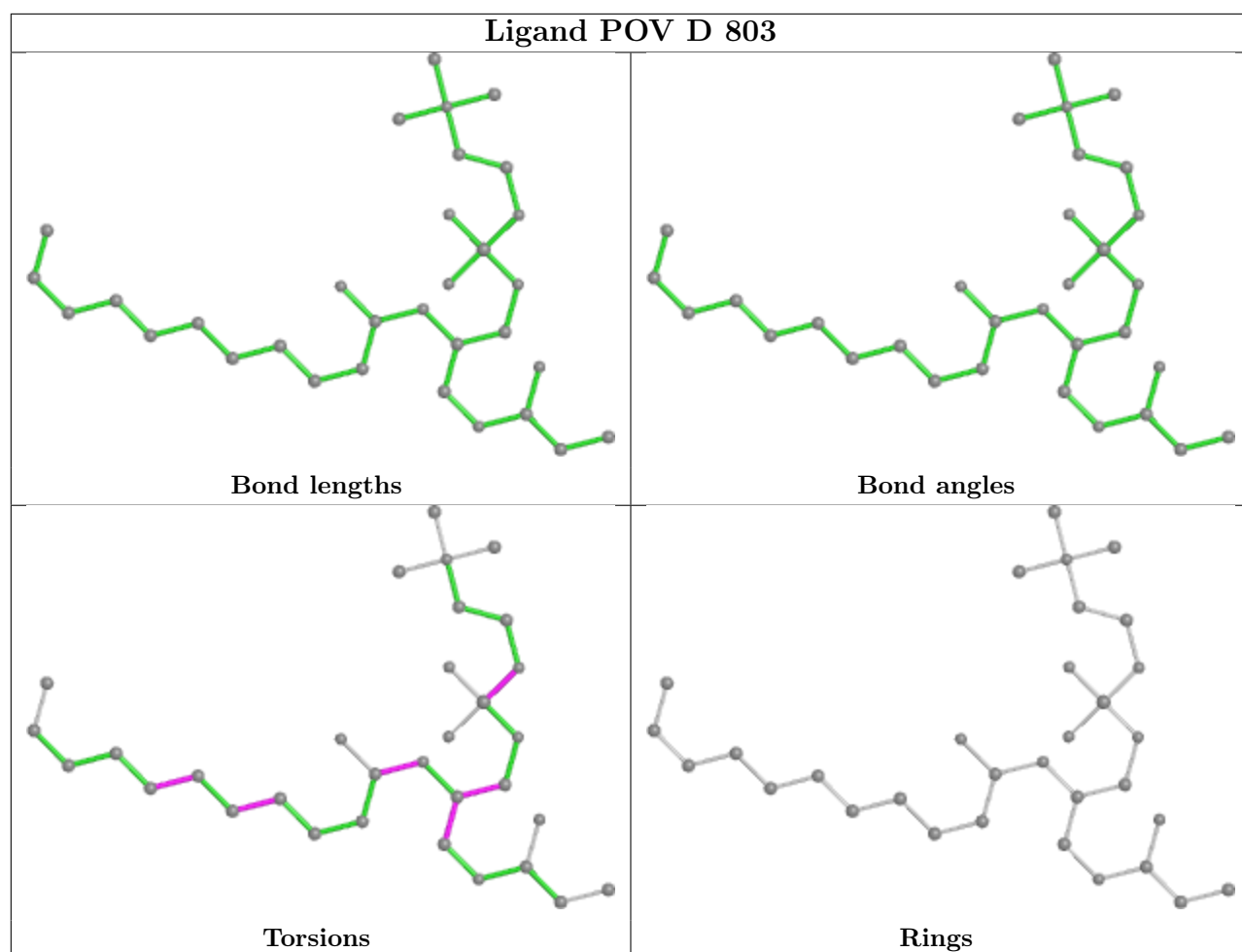


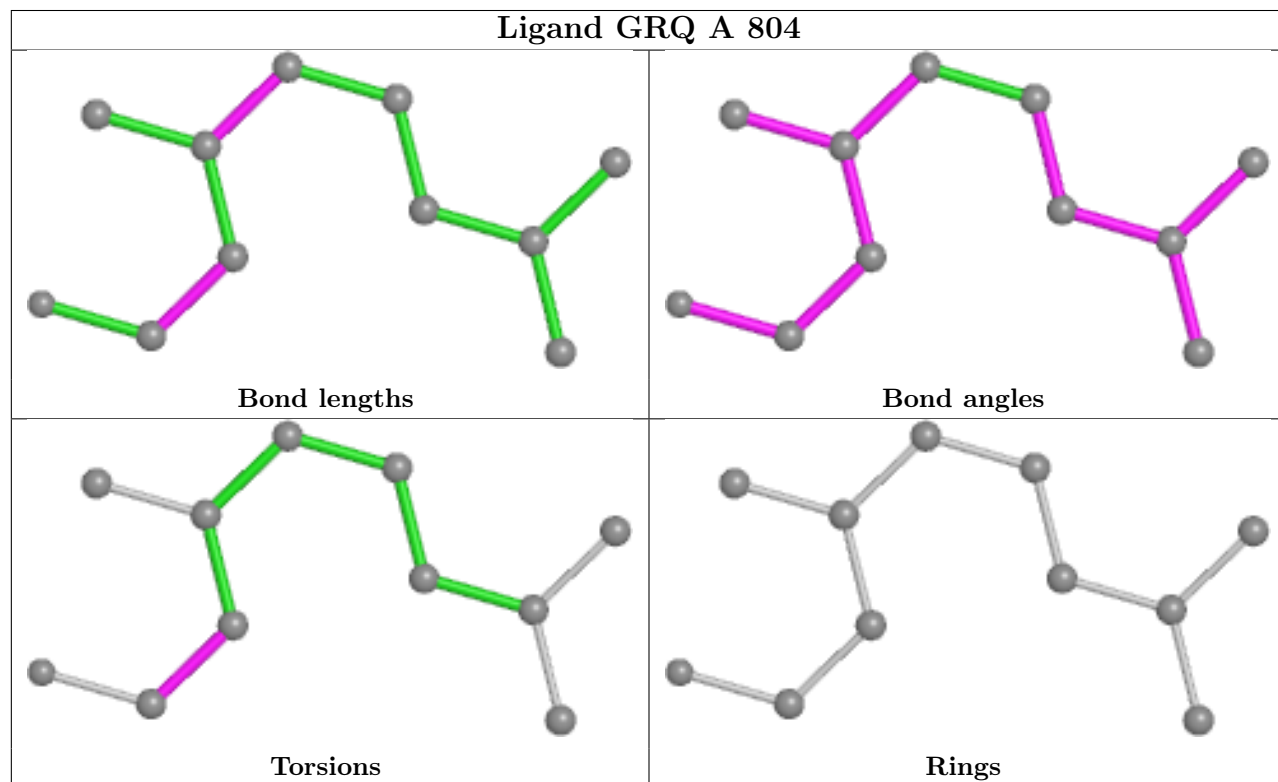
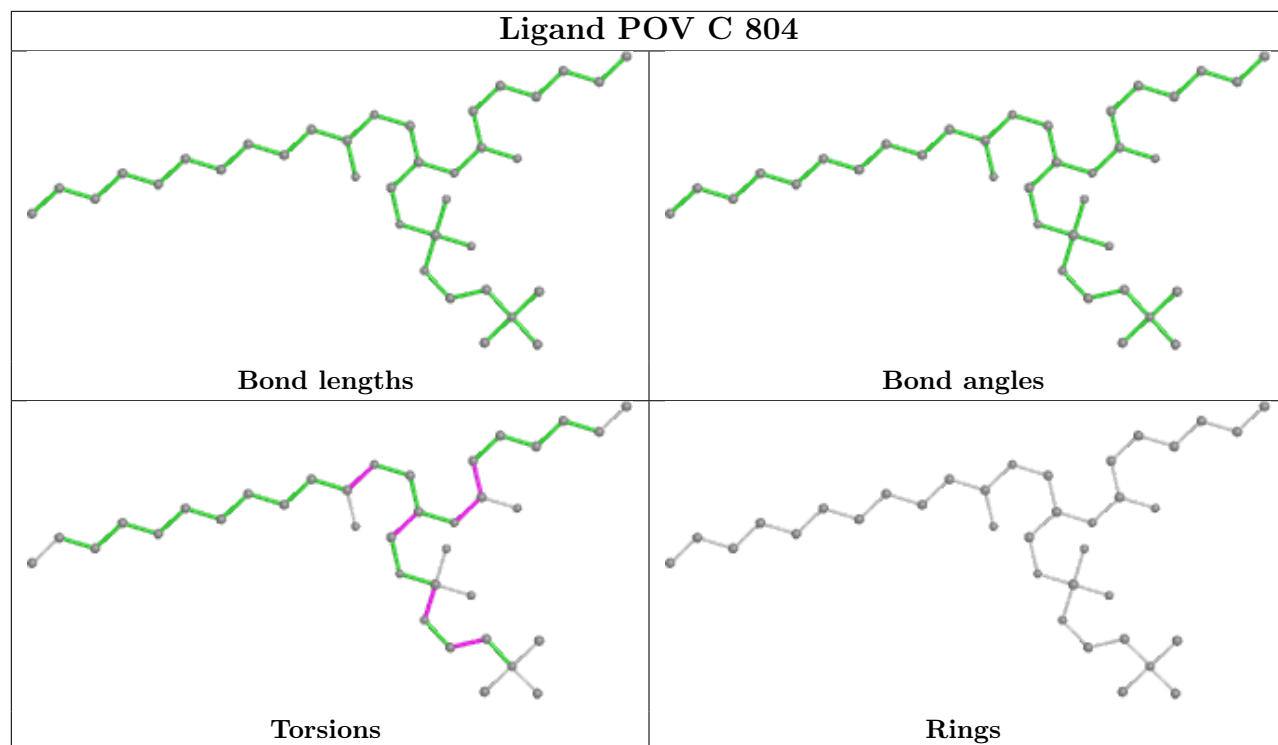


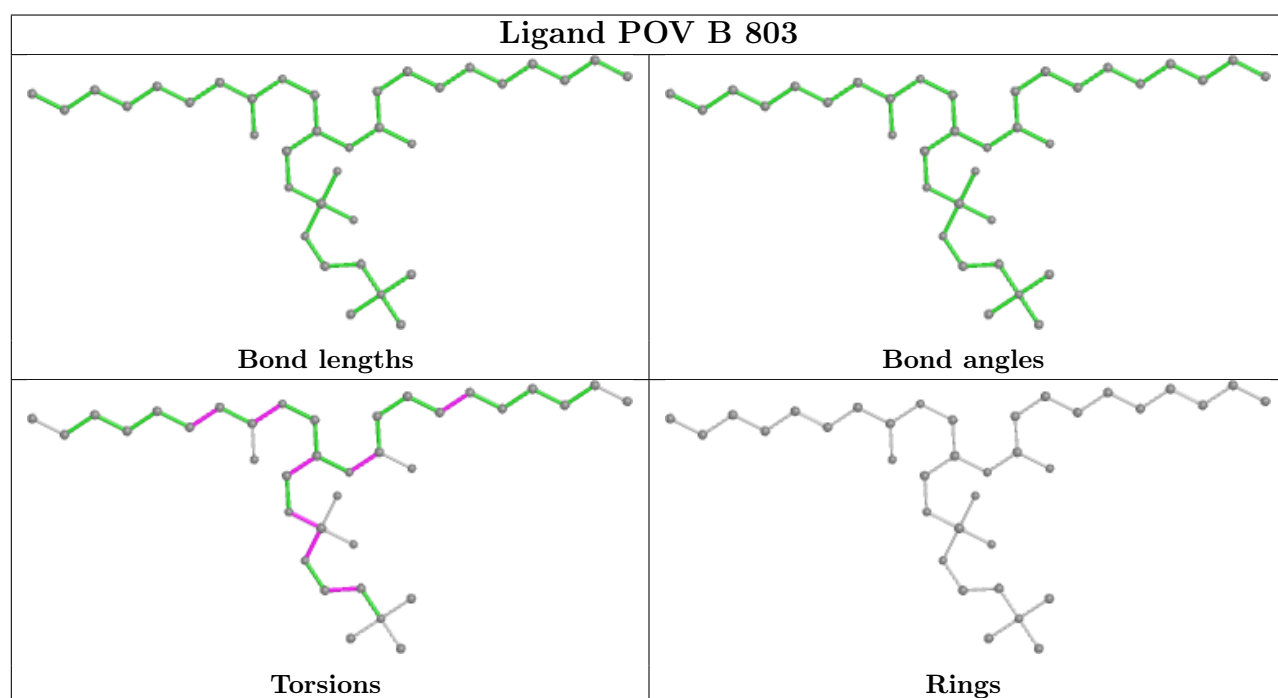
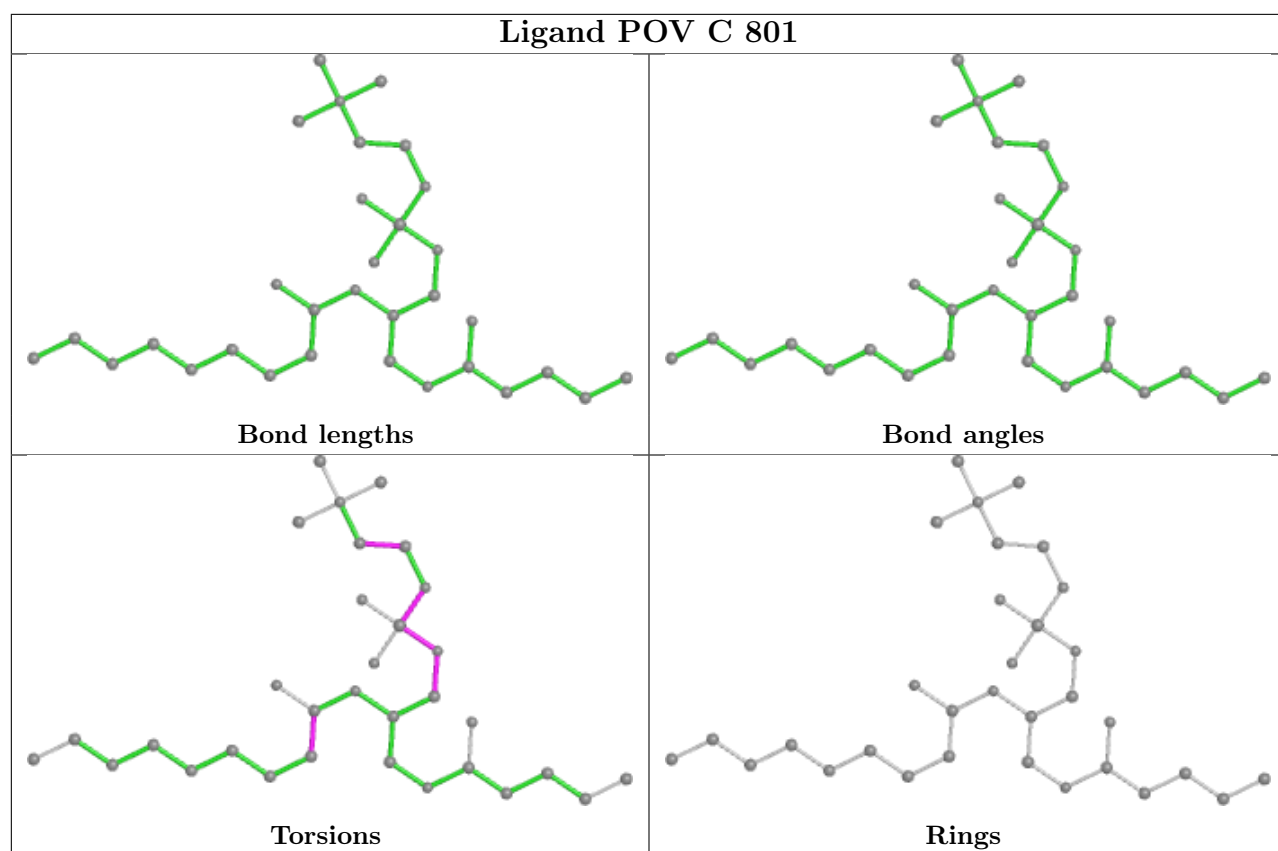


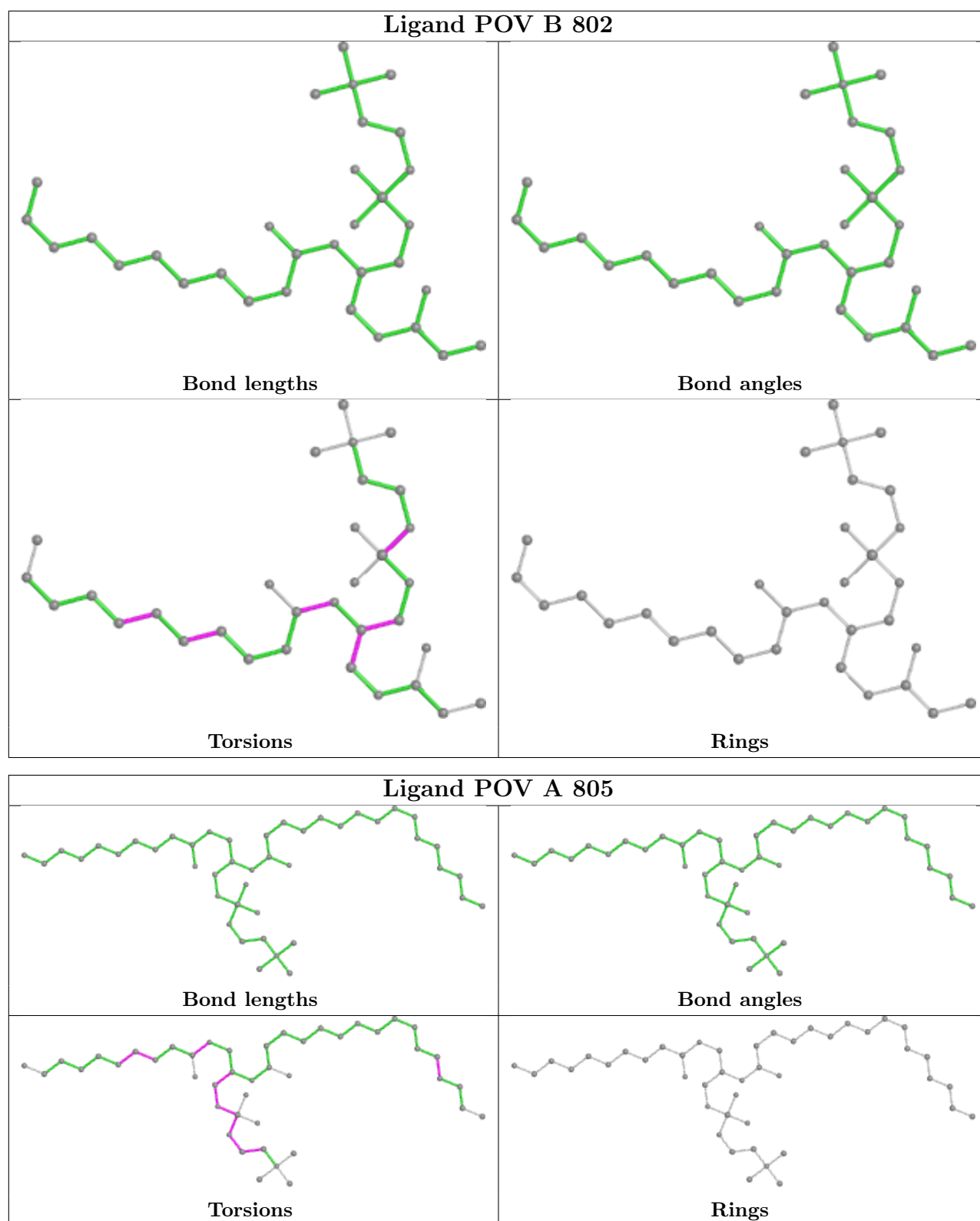


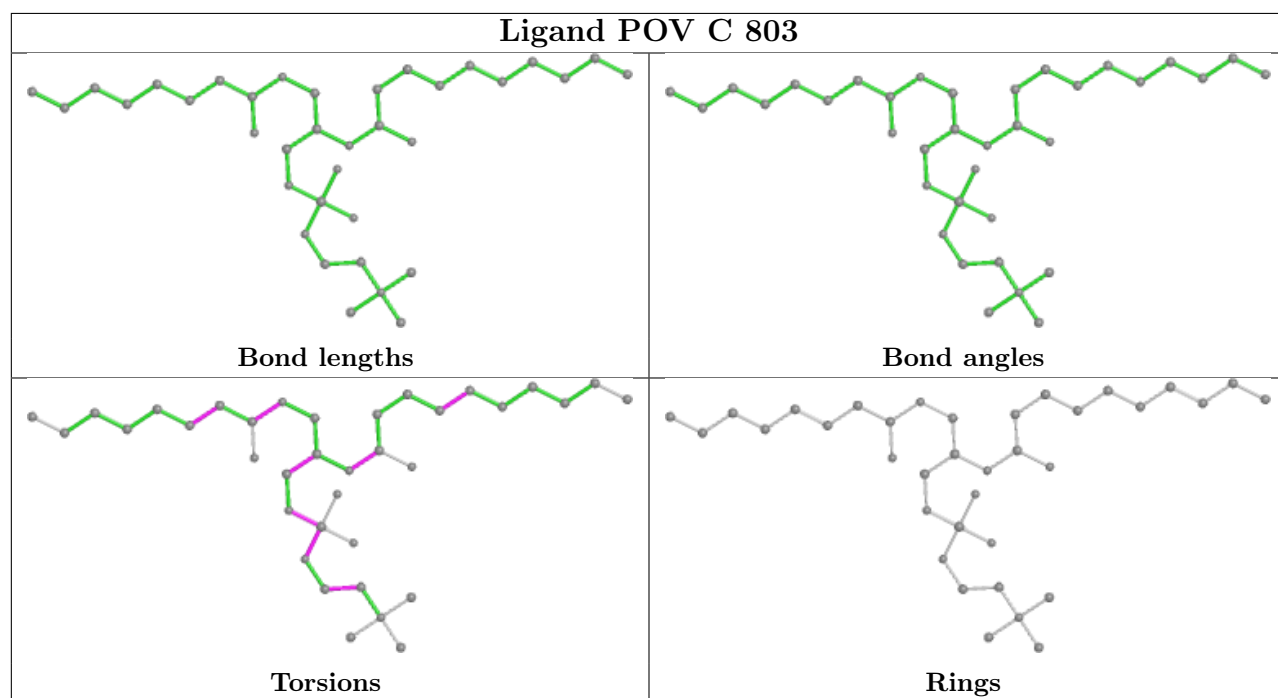
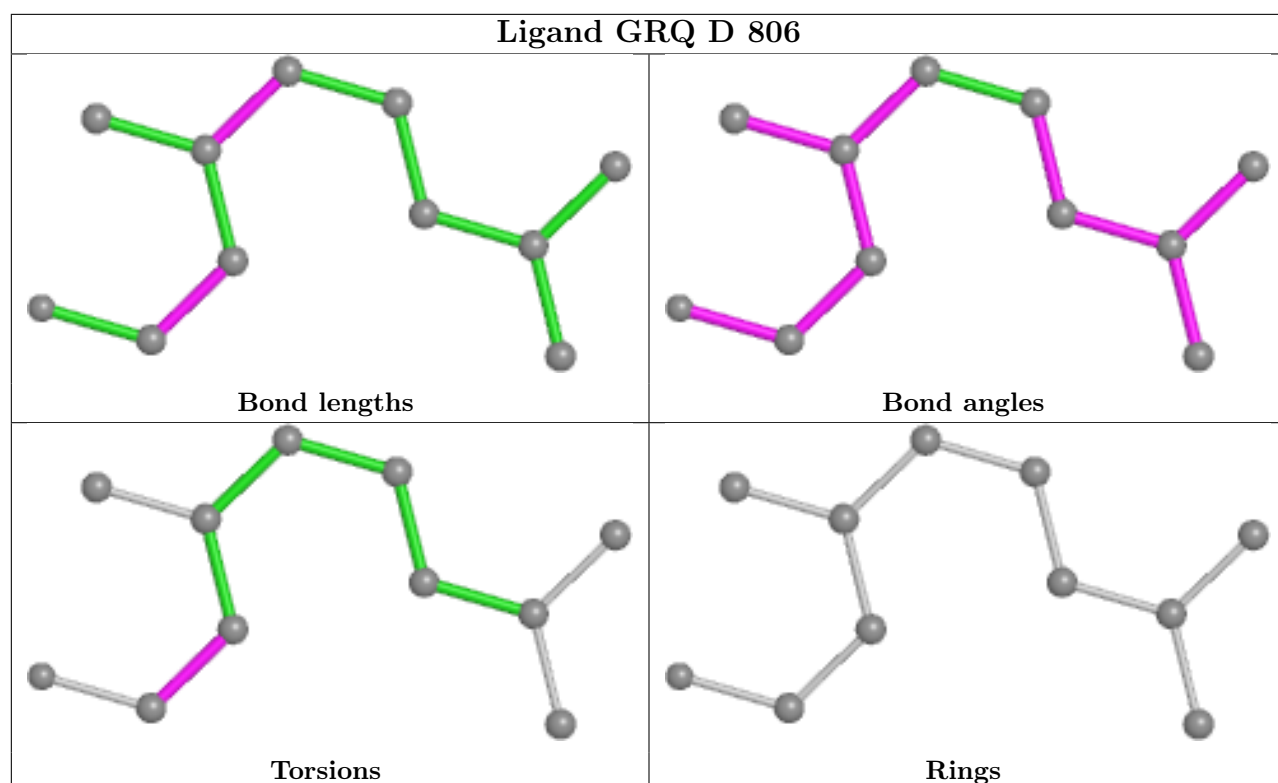


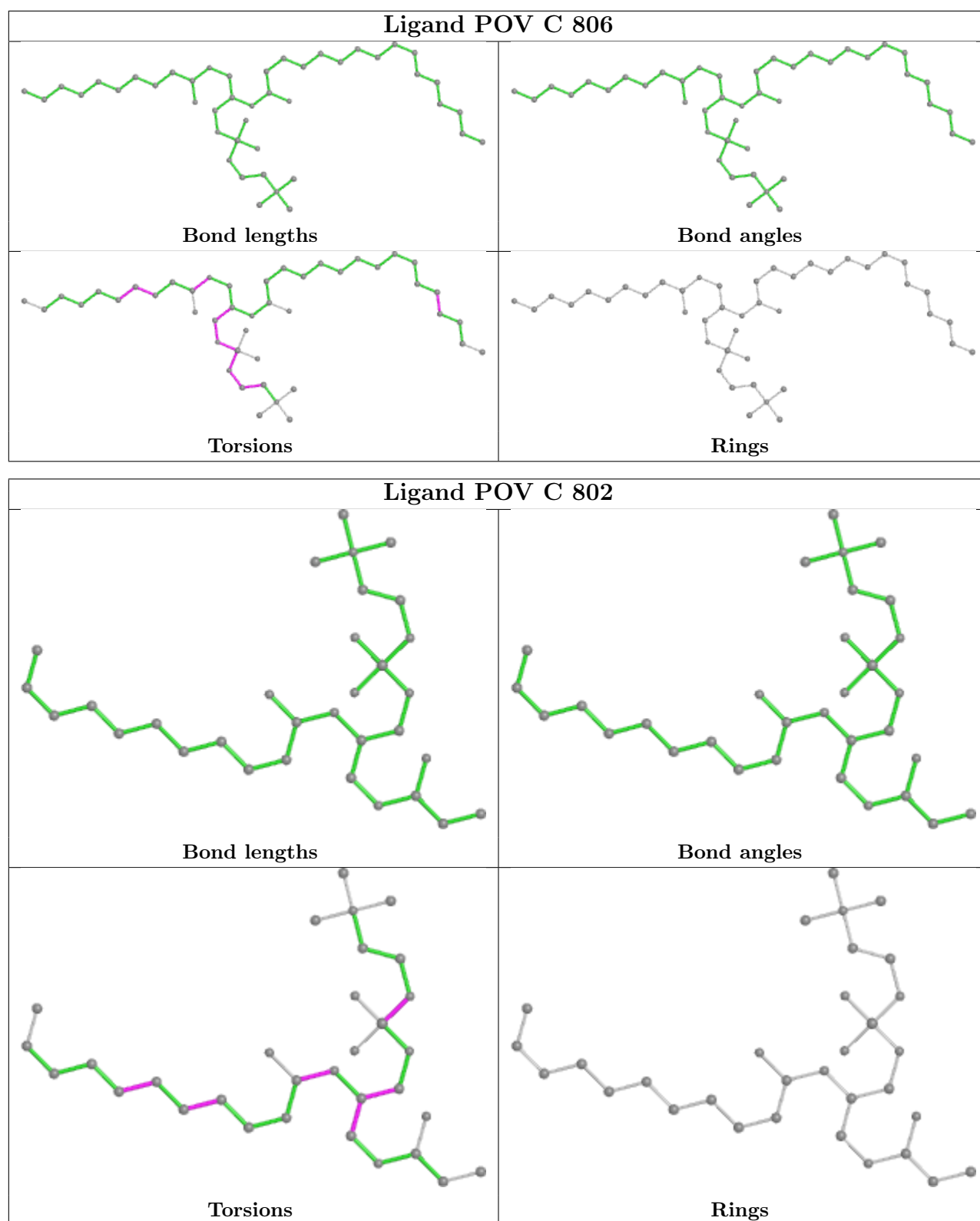












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.