



wwPDB EM Validation Summary Report ⓘ

Nov 30, 2025 – 12:08 AM JST

PDB ID : 9KDM / pdb_00009kdm
EMDB ID : EMD-62281
Title : Cryo-EM structure of LIPID-mediated human norepinephrine transporter NET in the presence of Levomilnacipran in an inward-open state at resolution of 2.46 angstrom.
Authors : Zhang, H.; Jiang, Y.; Xu, E.H.
Deposited on : 2024-11-03
Resolution : 2.46 Å(reported)

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

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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 Phenix2.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

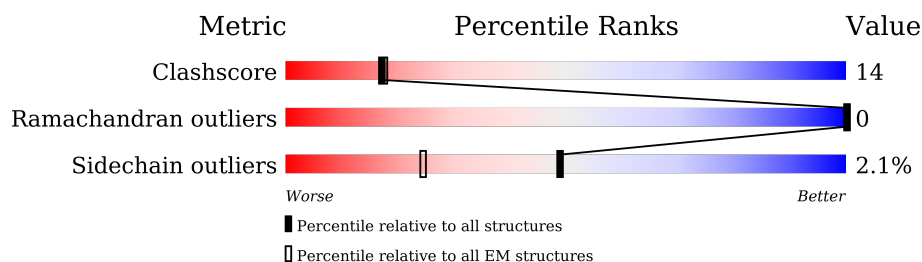
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.46 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	629	 66% 22% • 11%
1	B	629	 66% 21% • 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9462 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 Sodium-dependent noradrenaline transporter.

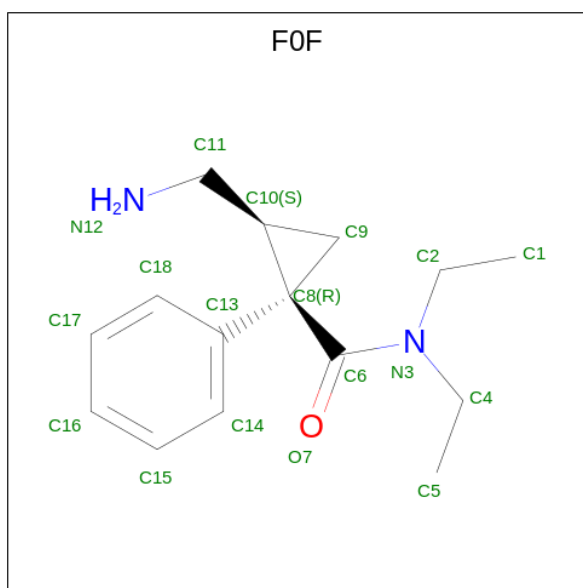
Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	557	Total	C	N	O	S	0	0
			4453	2985	695	753	20		
1	A	557	Total	C	N	O	S	0	0
			4453	2985	695	753	20		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-11	MET	-	initiating methionine	UNP P23975
B	-10	ASP	-	expression tag	UNP P23975
B	-9	TYR	-	expression tag	UNP P23975
B	-8	LYS	-	expression tag	UNP P23975
B	-7	ASP	-	expression tag	UNP P23975
B	-6	ASP	-	expression tag	UNP P23975
B	-5	ASP	-	expression tag	UNP P23975
B	-4	ASP	-	expression tag	UNP P23975
B	-3	LYS	-	expression tag	UNP P23975
B	-2	GLY	-	expression tag	UNP P23975
B	-1	SER	-	expression tag	UNP P23975
B	0	GLY	-	expression tag	UNP P23975
A	-11	MET	-	initiating methionine	UNP P23975
A	-10	ASP	-	expression tag	UNP P23975
A	-9	TYR	-	expression tag	UNP P23975
A	-8	LYS	-	expression tag	UNP P23975
A	-7	ASP	-	expression tag	UNP P23975
A	-6	ASP	-	expression tag	UNP P23975
A	-5	ASP	-	expression tag	UNP P23975
A	-4	ASP	-	expression tag	UNP P23975
A	-3	LYS	-	expression tag	UNP P23975
A	-2	GLY	-	expression tag	UNP P23975
A	-1	SER	-	expression tag	UNP P23975
A	0	GLY	-	expression tag	UNP P23975

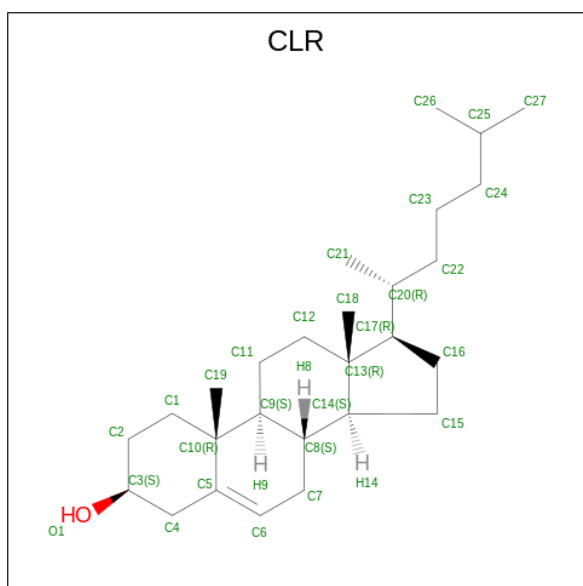
- Molecule 2 is (1R,2S)-2-(aminomethyl)-N,N-diethyl-1-phenyl-cyclopropane-1-carboxamide

(CCD ID: F0F) (formula: C₁₅H₂₂N₂O).



Mol	Chain	Residues	Atoms				AltConf
2	B	1	Total 18	C 15	N 2	O 1	0
2	A	1	Total 18	C 15	N 2	O 1	0

- Molecule 3 is CHOLESTEROL (CCD ID: CLR) (formula: $C_{27}H_{46}O$).



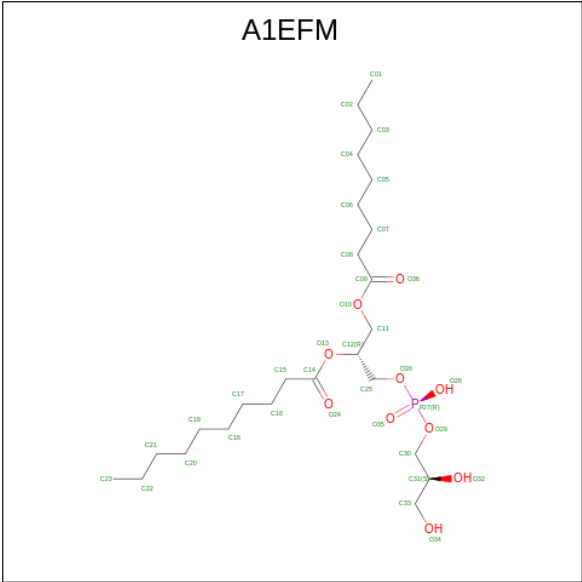
Mol	Chain	Residues	Atoms			AltConf
3	B	1	Total	C	O	0
			28	27	1	

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

- Molecule 4 is [(2 {R})-1-[(2 {S})-2,3-bis(oxidanyl)propoxy]-oxidanyl-phosphoryl]oxy-3-nonanoyloxy-propan-2-yl] decanoate (CCD ID: A1EFM) (formula: C₂₅H₄₉O₁₀P) (labeled as "Ligand of Interest" by depositor).



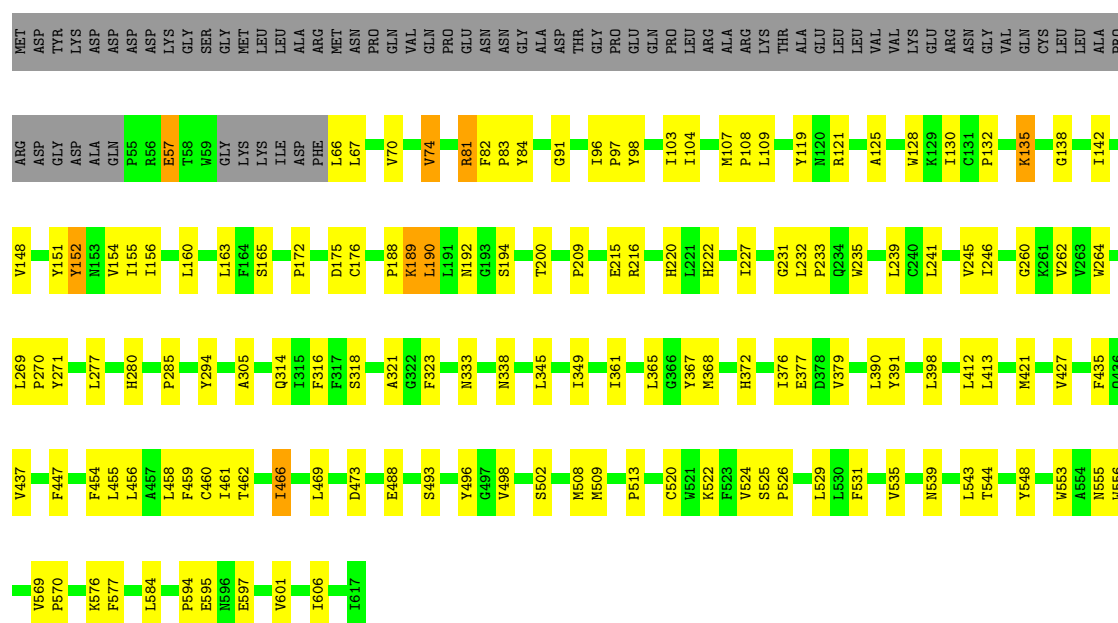
Mol	Chain	Residues	Atoms				AltConf
4	B	1	Total	C	O	P	0
			36	25	10	1	
4	A	1	Total	C	O	P	0
			36	25	10	1	

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.

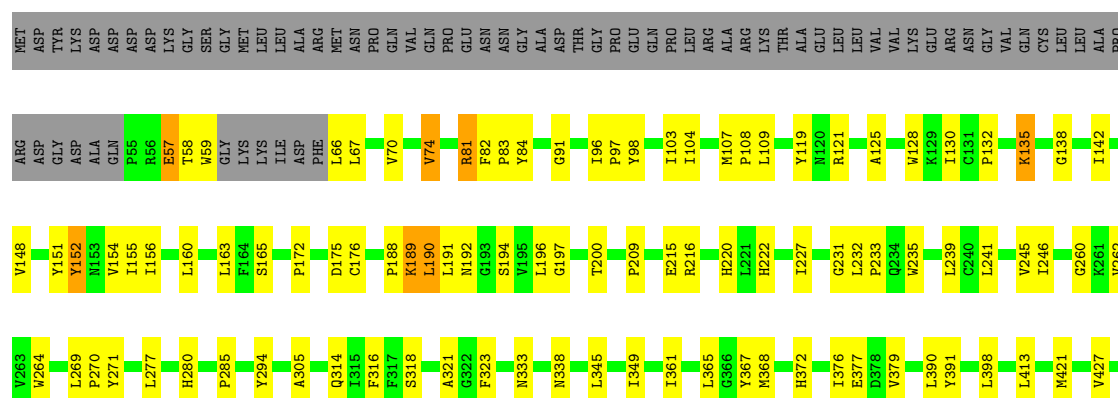
- Molecule 1: Sodium-dependent noradrenaline transporter

Chain B: 



- Molecule 1: Sodium-dependent noradrenaline transporter

Chain A: 



F435	Q436	V437	F447	F454	L455	L456	A457	F459	C460	I461	T462	I466	L469	D473	E488	S493	Y496	G497	V498	S502	M508	M509	P513	C520	W521	K522	F523	V524	S525	P526	L529	L530	F531	V535	N539	L543	T544	Y548	W553	A554
N555	W556	V569	P570	K576	F577	L584	P594	E595	N596	E597	V601	I606	I617																											

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	277385	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)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k 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: F0F, CLR, A1EFM

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	0.91	0/4598	1.14	0/6273
1	B	0.91	0/4598	1.14	0/6273
All	All	0.91	0/9196	1.14	0/12546

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	4453	0	4433	124	0
1	B	4453	0	4433	119	0
2	A	18	0	0	0	0
2	B	18	0	0	0	0
3	A	224	0	368	28	0
3	B	224	0	368	29	0
4	A	36	0	0	0	0
4	B	36	0	0	0	0
All	All	9462	0	9602	258	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 14.

The worst 5 of 258 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:A:66:LEU:HD12	1:A:67:LEU:N	1.27	1.49
1:B:66:LEU:HD12	1:B:67:LEU:N	1.27	1.46
1:B:577:PHE:CZ	1:B:584:LEU:HD12	1.67	1.30
1:B:66:LEU:CD1	1:B:67:LEU:H	1.45	1.29
1:A:577:PHE:CZ	1:A:584:LEU:HD12	1.67	1.27

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	553/629 (88%)	536 (97%)	17 (3%)	0	100	100
1	B	553/629 (88%)	536 (97%)	17 (3%)	0	100	100
All	All	1106/1258 (88%)	1072 (97%)	34 (3%)	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	470/529 (89%)	460 (98%)	10 (2%)	48	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	470/529 (89%)	460 (98%)	10 (2%)	48 64
All	All	940/1058 (89%)	920 (98%)	20 (2%)	49 64

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	152	TYR
1	A	200	THR
1	A	576	LYS
1	A	466	ILE
1	B	190	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	220	HIS
1	A	539	ASN
1	A	610	GLN
1	A	555	ASN
1	A	441	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](#)

20 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	B	805	-	31,31,31	0.32	0	48,48,48	0.40	0
3	CLR	A	707	-	31,31,31	0.30	0	48,48,48	0.52	0
3	CLR	A	706	-	31,31,31	0.32	0	48,48,48	0.40	0
3	CLR	A	703	-	31,31,31	0.35	0	48,48,48	0.60	0
3	CLR	B	803	-	31,31,31	0.32	0	48,48,48	0.51	0
3	CLR	A	704	-	31,31,31	0.32	0	48,48,48	0.51	0
3	CLR	B	806	-	31,31,31	0.30	0	48,48,48	0.52	0
4	A1EFM	B	809	-	35,35,35	1.07	4 (11%)	38,41,41	1.42	3 (7%)
3	CLR	B	804	-	31,31,31	0.40	0	48,48,48	0.98	4 (8%)
2	F0F	A	702	-	19,19,19	2.49	5 (26%)	23,27,27	4.27	8 (34%)
3	CLR	A	701	-	31,31,31	0.33	0	48,48,48	0.54	0
3	CLR	A	708	-	31,31,31	0.33	0	48,48,48	0.59	0
3	CLR	B	808	-	31,31,31	0.30	0	48,48,48	0.58	0
3	CLR	B	807	-	31,31,31	0.34	0	48,48,48	0.59	0
2	F0F	B	801	-	19,19,19	2.49	5 (26%)	23,27,27	4.27	8 (34%)
3	CLR	A	709	-	31,31,31	0.31	0	48,48,48	0.58	0
3	CLR	B	802	-	31,31,31	0.35	0	48,48,48	0.59	0
3	CLR	A	705	-	31,31,31	0.40	0	48,48,48	0.98	4 (8%)
3	CLR	B	810	-	31,31,31	0.33	0	48,48,48	0.54	0
4	A1EFM	A	710	-	35,35,35	1.07	4 (11%)	38,41,41	1.42	3 (7%)

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	B	805	-	-	6/10/68/68	0/4/4/4
3	CLR	A	707	-	-	3/10/68/68	0/4/4/4
3	CLR	A	706	-	-	6/10/68/68	0/4/4/4
3	CLR	A	703	-	-	1/10/68/68	0/4/4/4
3	CLR	B	803	-	-	0/10/68/68	0/4/4/4
3	CLR	A	704	-	-	0/10/68/68	0/4/4/4
3	CLR	B	806	-	-	3/10/68/68	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A1EFM	B	809	-	-	20/40/40/40	-
3	CLR	B	804	-	-	6/10/68/68	0/4/4/4
2	F0F	A	702	-	-	4/22/30/30	0/2/2/2
3	CLR	A	701	-	-	0/10/68/68	0/4/4/4
3	CLR	A	708	-	-	5/10/68/68	0/4/4/4
3	CLR	B	808	-	-	6/10/68/68	0/4/4/4
3	CLR	B	807	-	-	5/10/68/68	0/4/4/4
2	F0F	B	801	-	-	4/22/30/30	0/2/2/2
3	CLR	A	709	-	-	6/10/68/68	0/4/4/4
3	CLR	B	802	-	-	1/10/68/68	0/4/4/4
3	CLR	A	705	-	-	6/10/68/68	0/4/4/4
3	CLR	B	810	-	-	0/10/68/68	0/4/4/4
4	A1EFM	A	710	-	-	20/40/40/40	-

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	F0F	C6-N3	9.11	1.50	1.35
2	A	702	F0F	C6-N3	9.11	1.50	1.35
2	B	801	F0F	C8-C6	3.57	1.57	1.52
2	A	702	F0F	C8-C6	3.56	1.57	1.52
4	B	809	A1EFM	O13-C12	-2.82	1.39	1.46

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	F0F	C9-C8-C13	-16.31	88.68	119.95
2	A	702	F0F	C9-C8-C13	-16.31	88.68	119.95
2	B	801	F0F	C9-C10-C11	-7.89	104.67	121.00
2	A	702	F0F	C9-C10-C11	-7.89	104.67	121.00
2	B	801	F0F	C13-C8-C6	-6.10	106.61	114.19

There are no chirality outliers.

5 of 102 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	801	F0F	C9-C10-C11-N12
2	B	801	F0F	N3-C6-C8-C9
2	B	801	F0F	O7-C6-C8-C9

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Mol	Chain	Res	Type	Atoms
2	A	702	F0F	C9-C10-C11-N12
2	A	702	F0F	N3-C6-C8-C9

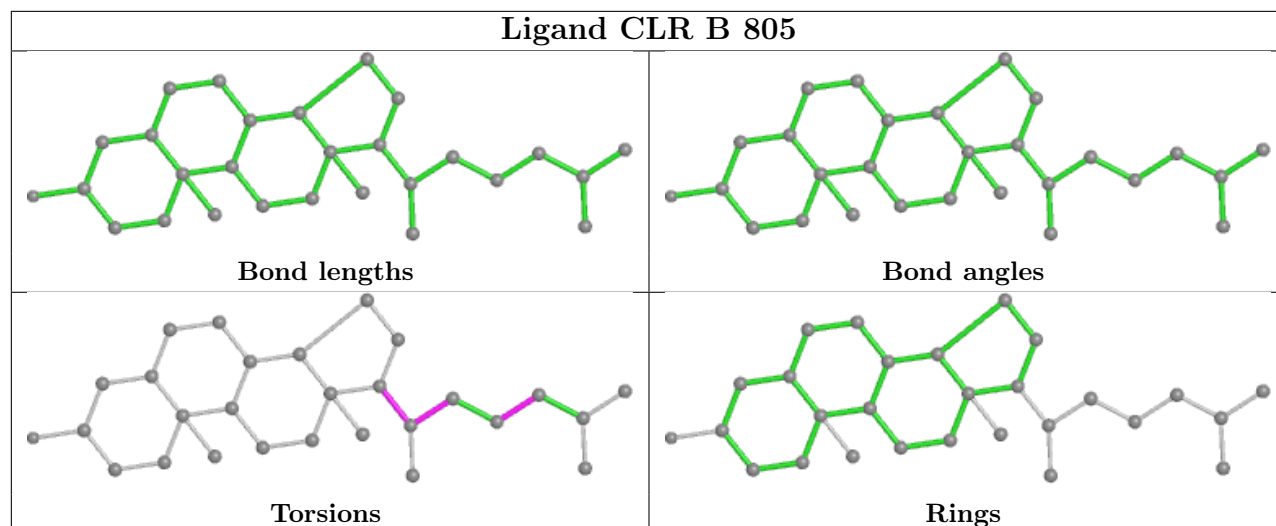
There are no ring outliers.

12 monomers are involved in 51 short contacts:

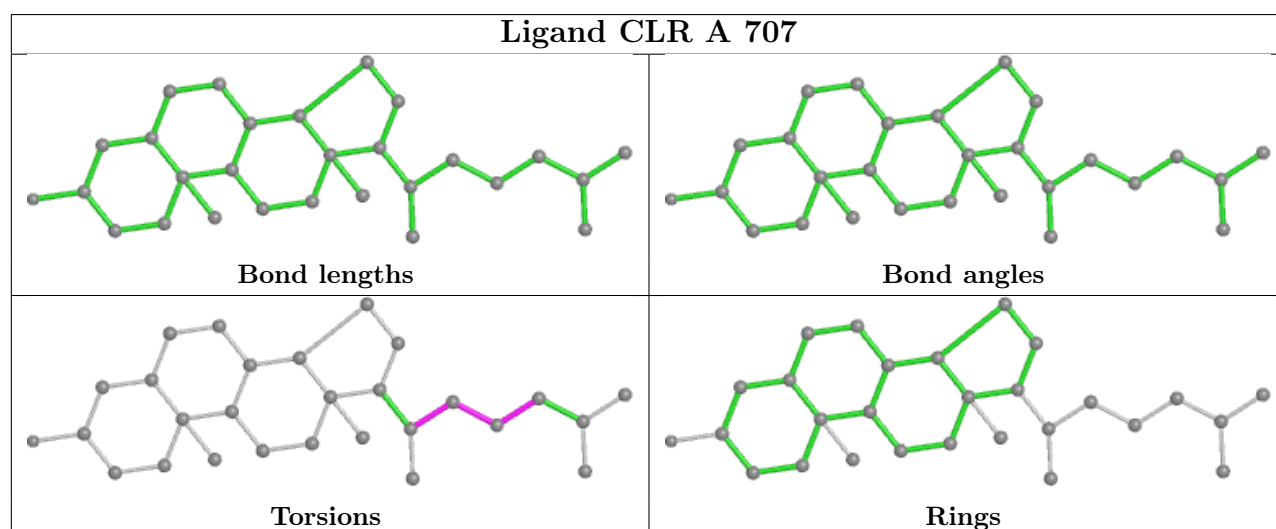
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	805	CLR	2	0
3	A	707	CLR	5	0
3	A	706	CLR	2	0
3	A	703	CLR	2	0
3	B	803	CLR	5	0
3	A	704	CLR	5	0
3	B	806	CLR	5	0
3	B	804	CLR	14	0
3	B	808	CLR	2	0
3	A	709	CLR	1	0
3	B	802	CLR	2	0
3	A	705	CLR	14	0

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

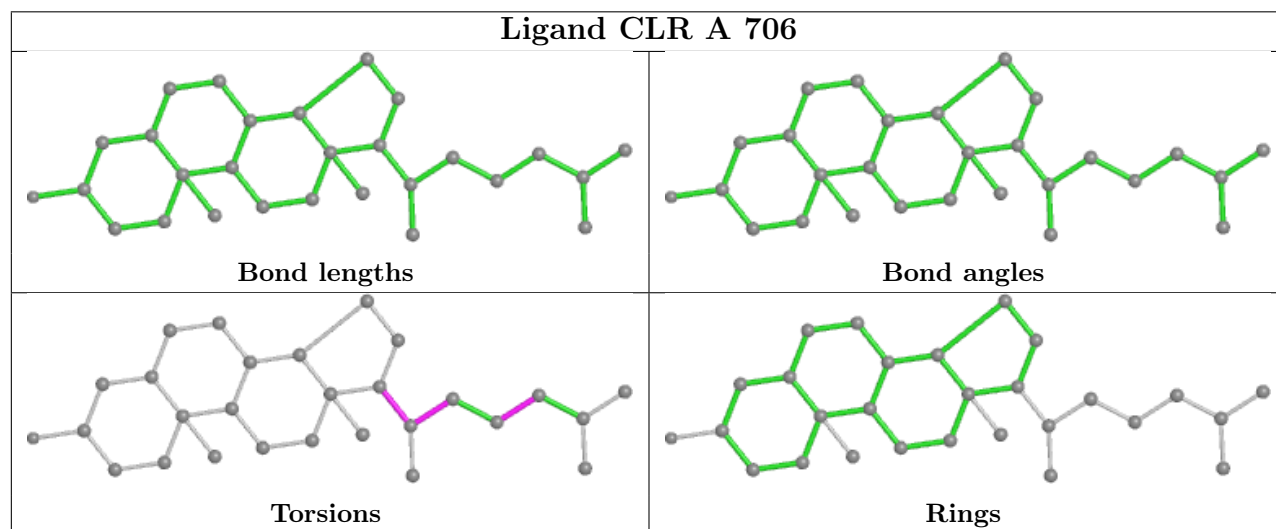
Ligand CLR B 805

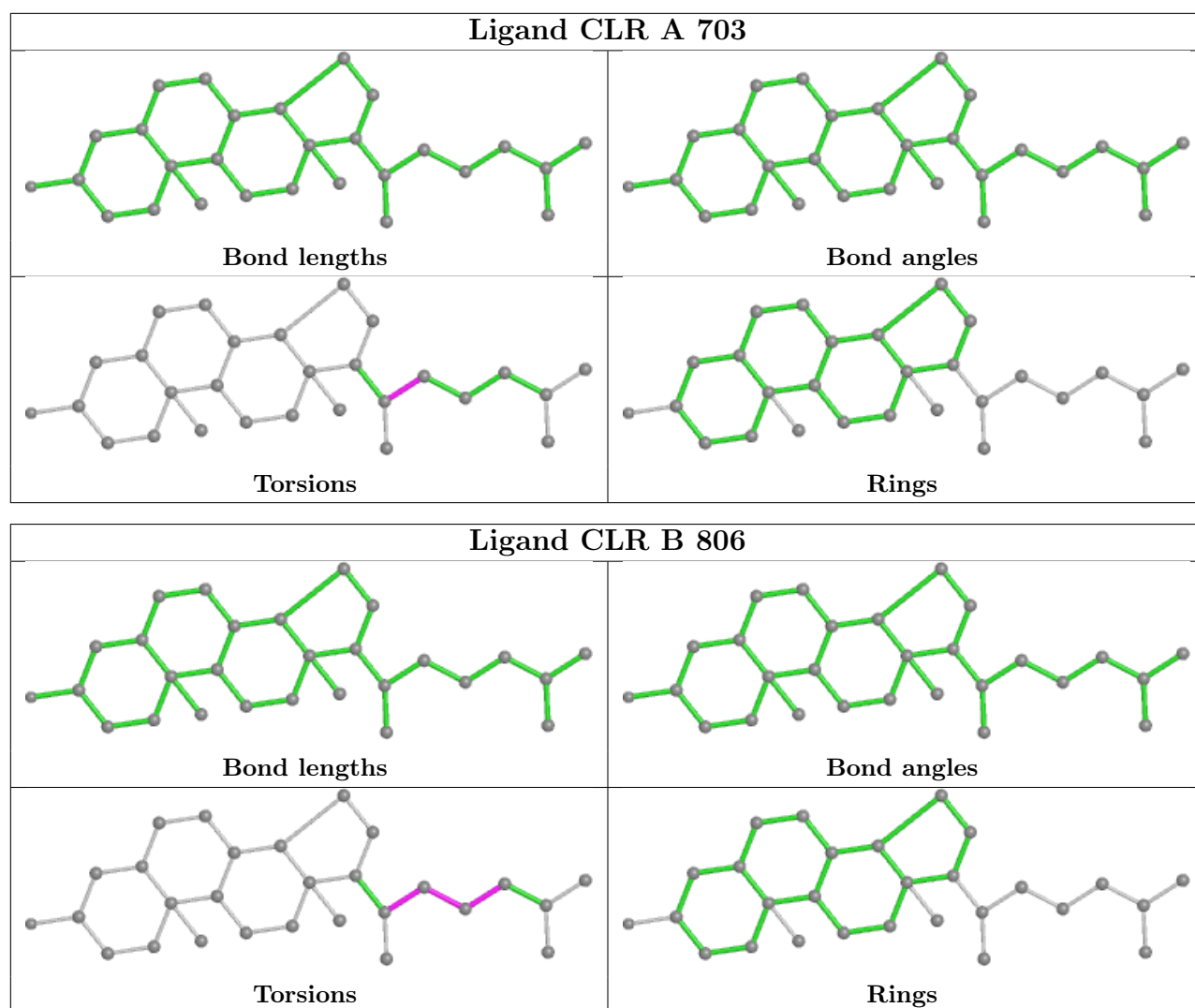


Ligand CLR A 707

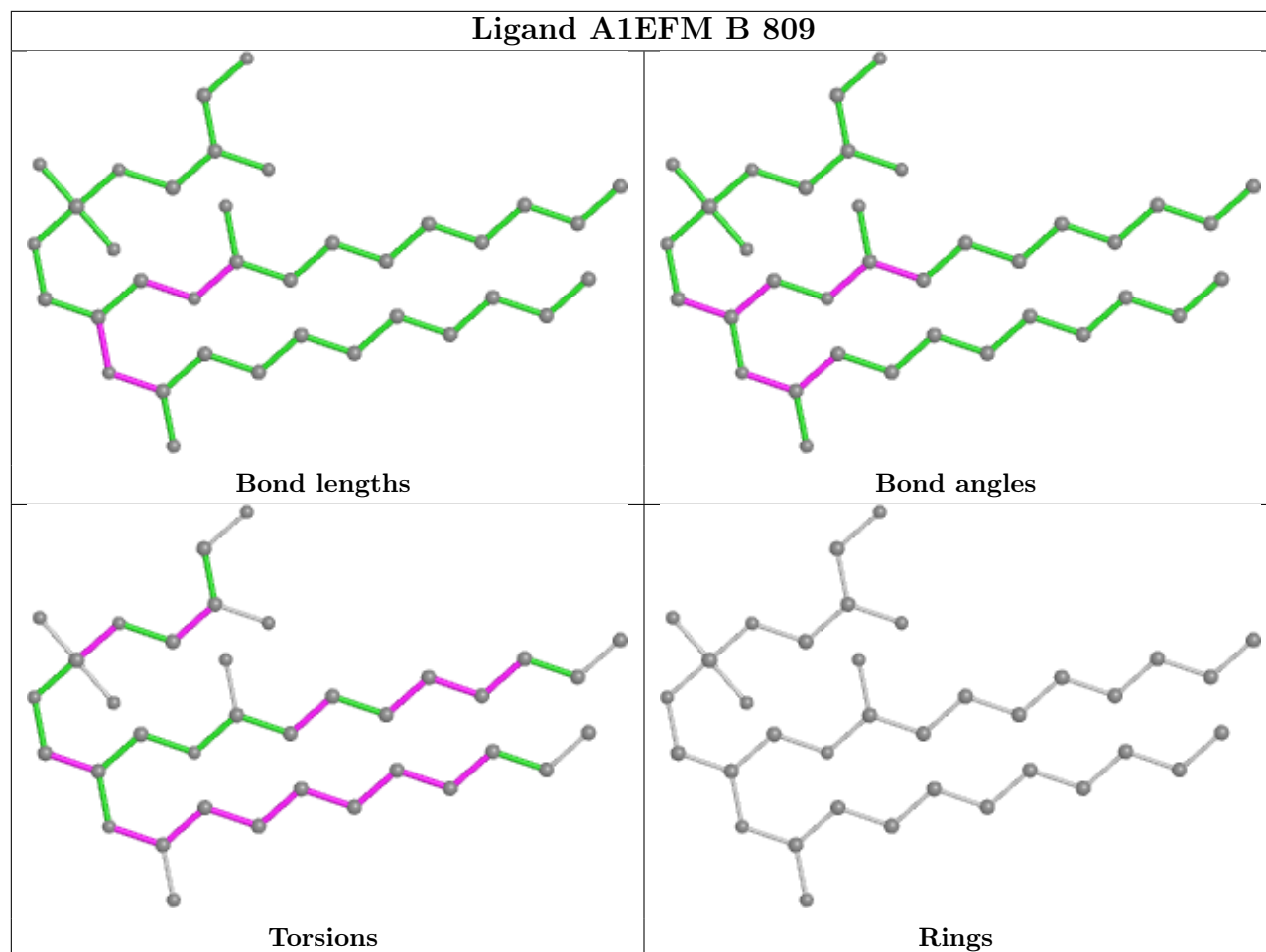


Ligand CLR A 706

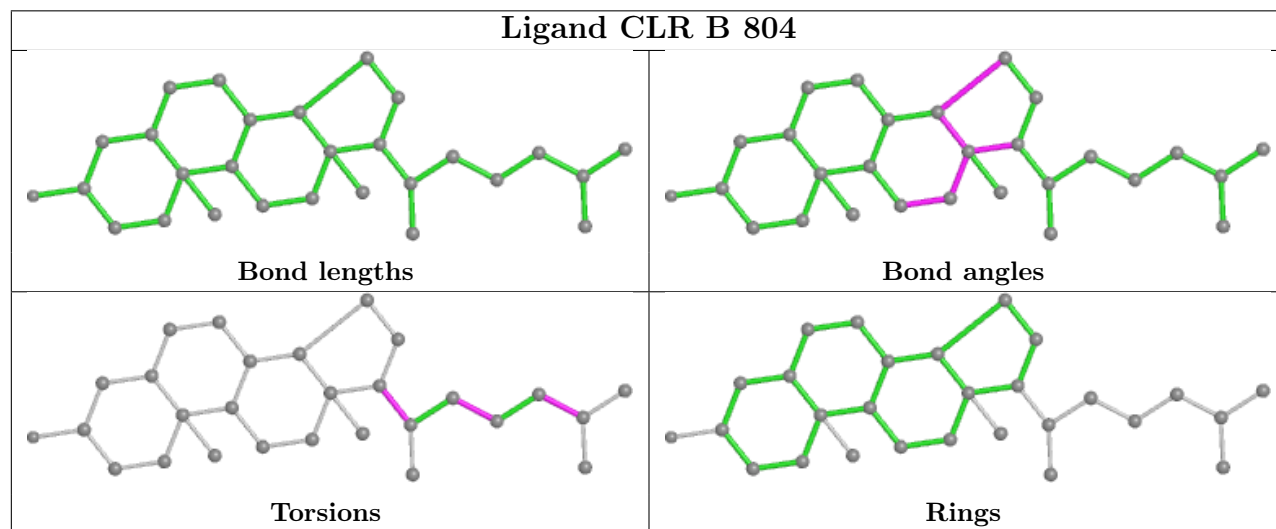


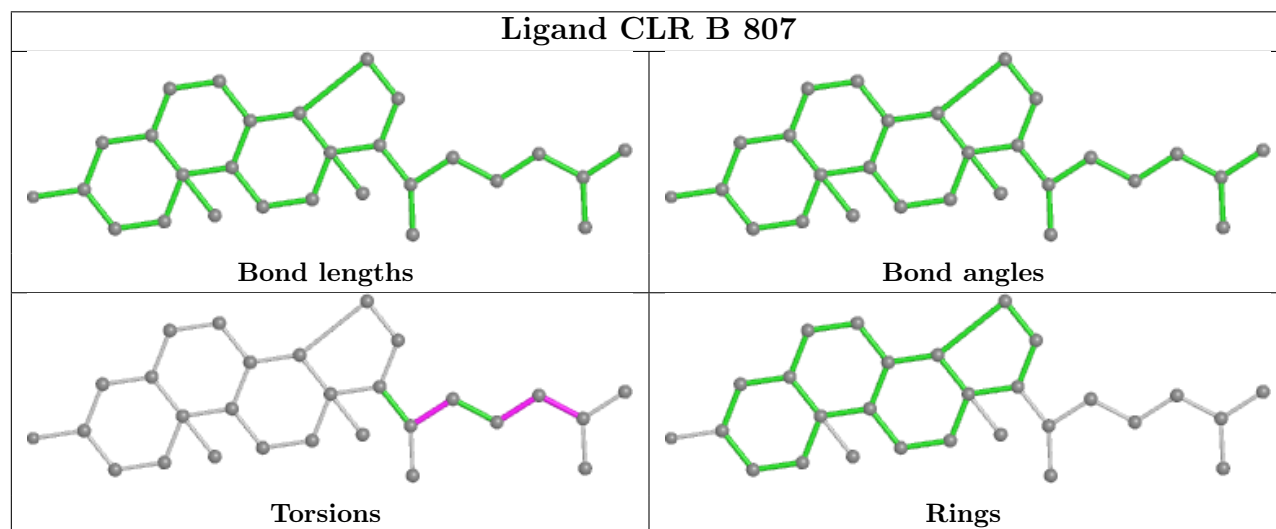
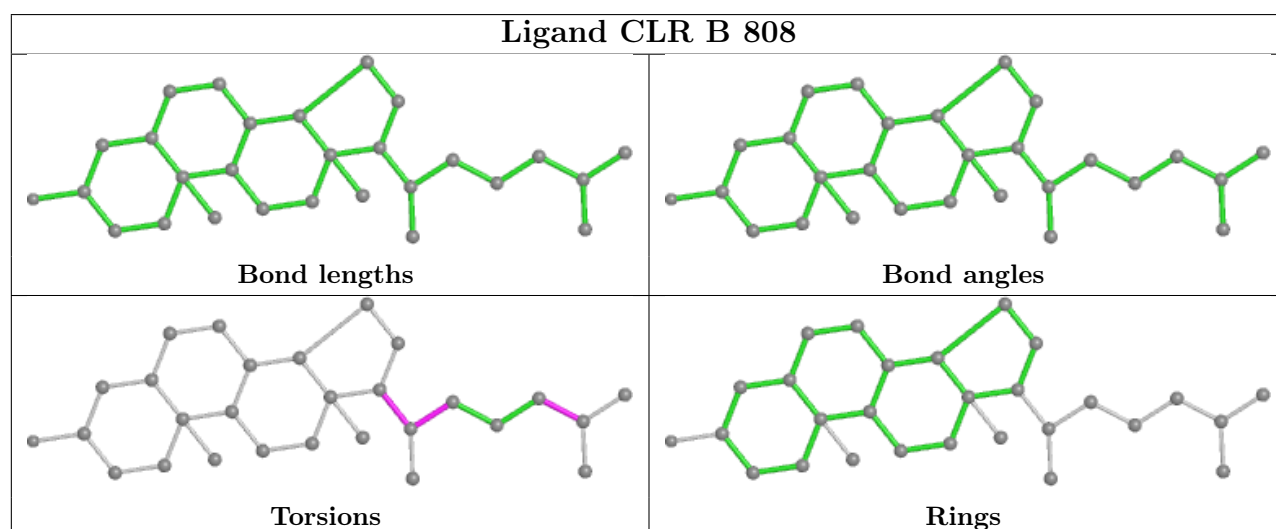
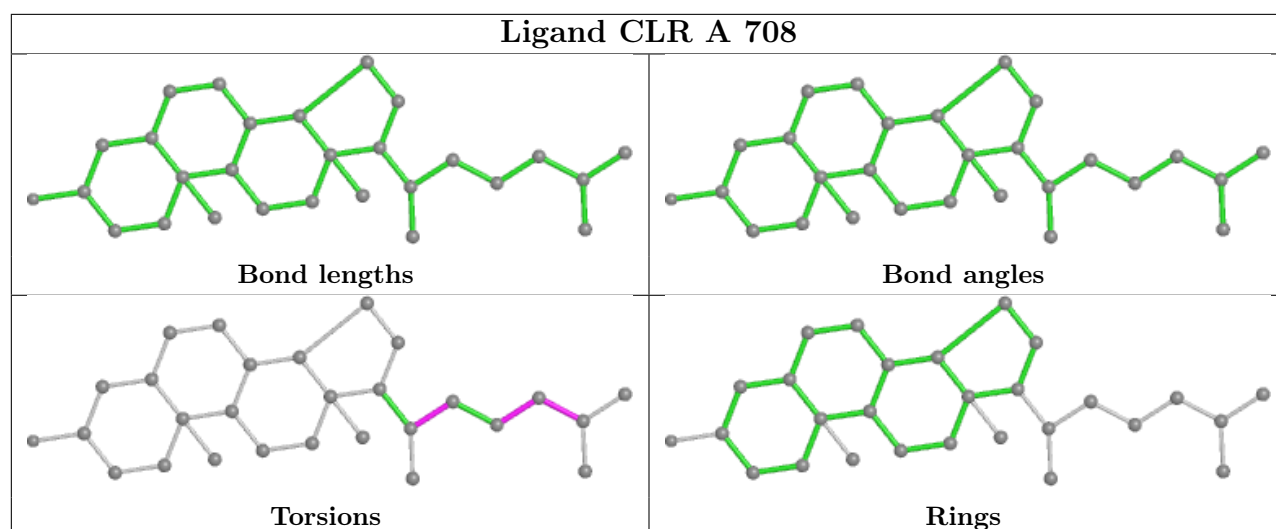


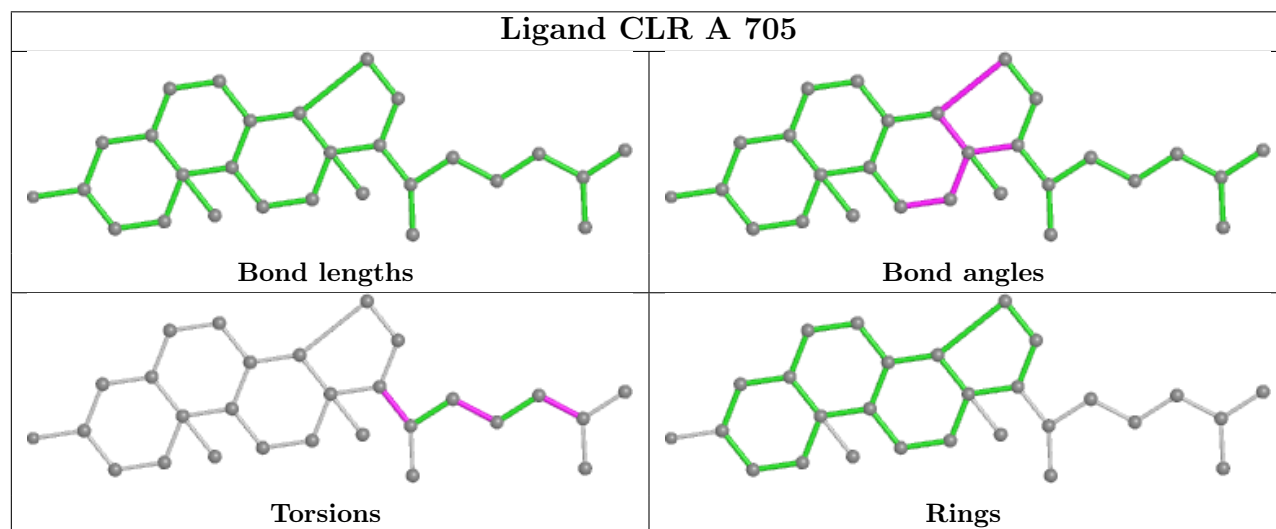
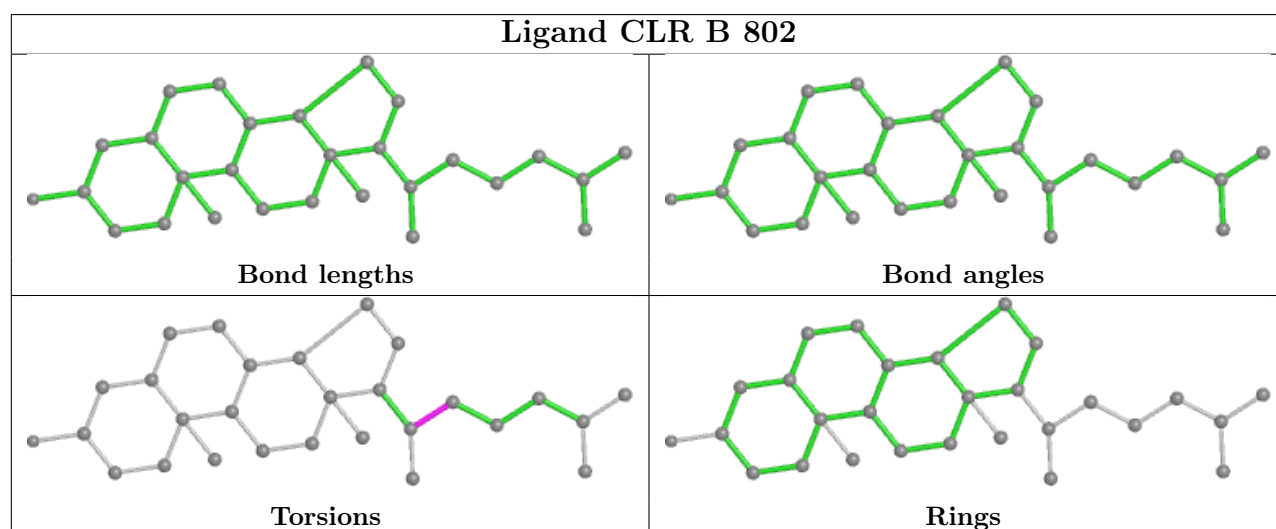
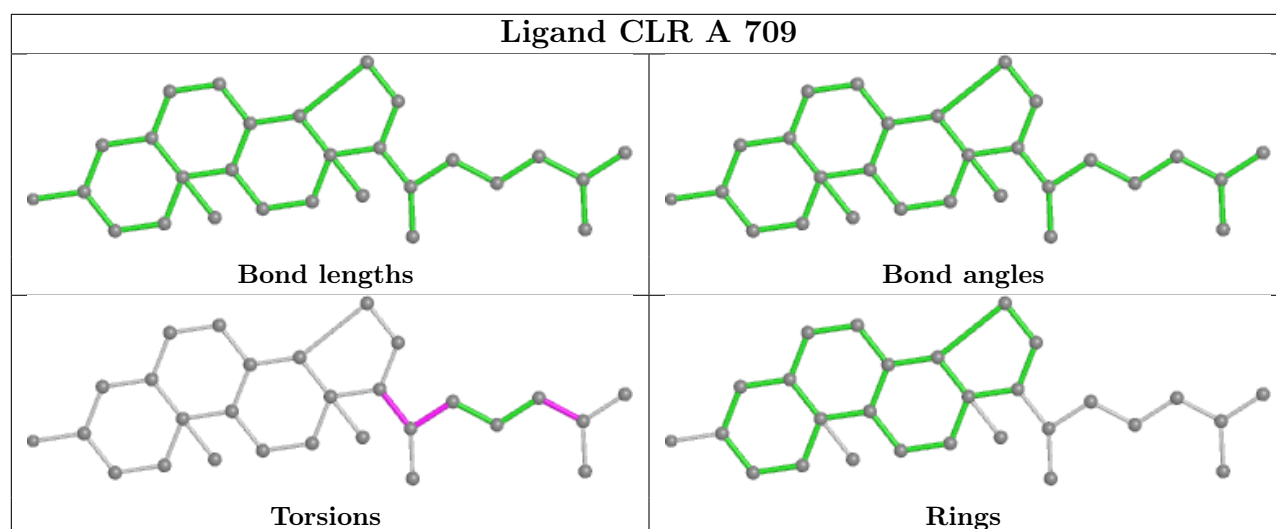
Ligand A1EFM B 809

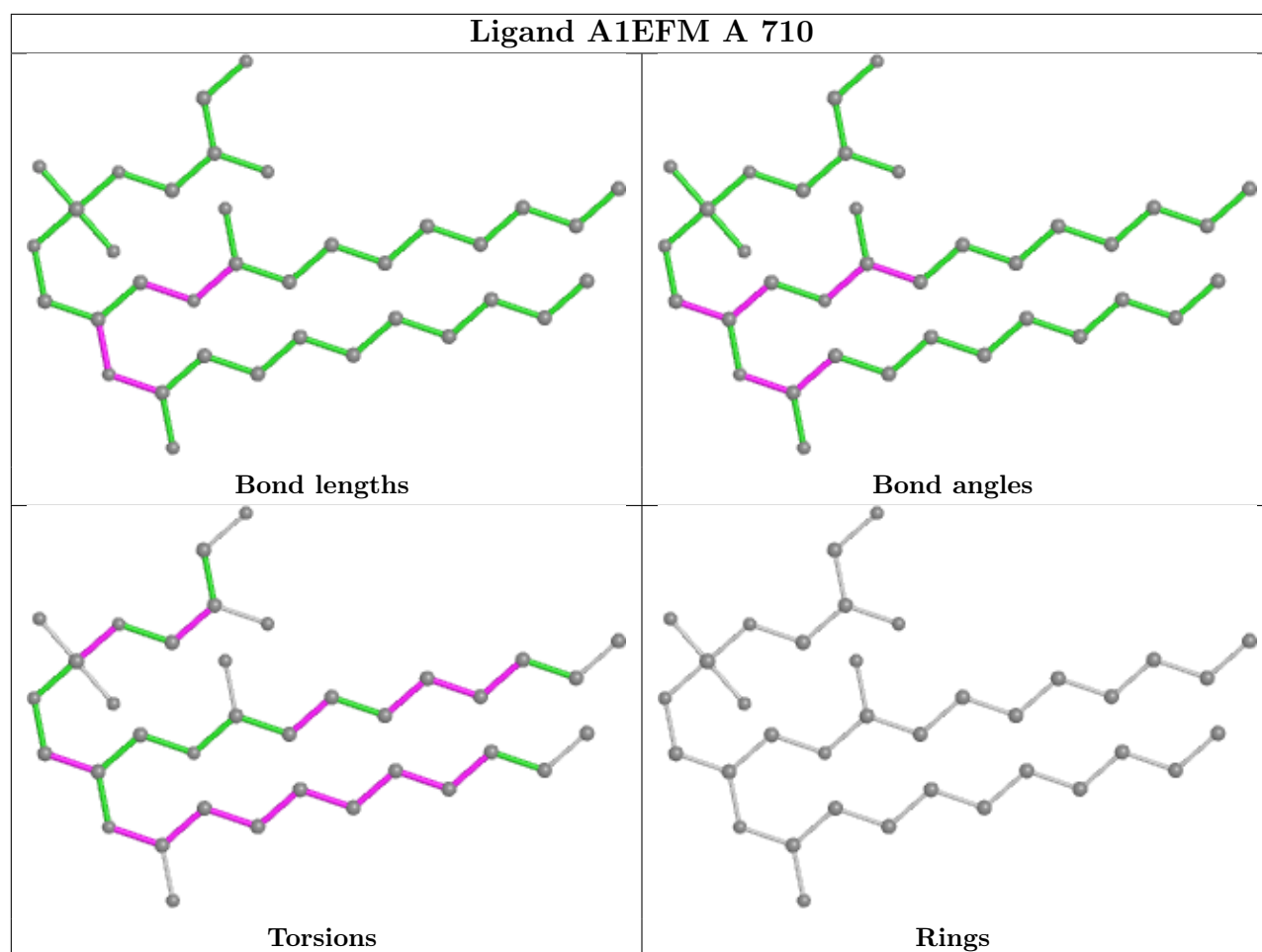


Ligand CLR B 804









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.