



wwPDB EM Validation Summary Report ⓘ

Sep 3, 2023 – 05:31 AM EDT

PDB ID : 8CT9
EMDB ID : EMD-26984
Title : CryoEM structure of human S-OPA1 assembled on lipid membrane in membrane-distal state
Authors : Du Pont, K.E.; Aydin, H.
Deposited on : 2022-05-13
Resolution : 6.80 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev50
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

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 6.80 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	960	 17% 73% 27%
1	B	960	 17% 73% 27%
1	C	960	 17% 73% 27%
1	D	960	 17% 73% 27%
1	E	960	 18% 73% 27%
1	F	960	 17% 73% 27%
1	G	960	 17% 73% 27%
1	H	960	 17% 73% 27%
1	I	960	 17% 73% 27%

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Mol	Chain	Length	Quality of chain		
1	J	960	19%	73%	27%
1	K	960	16%	73%	27%
1	L	960	18%	73%	27%
1	M	960	16%	73%	27%
1	N	960	17%	73%	27%
1	O	960	17%	73%	27%
1	P	960	18%	73%	27%
1	Q	960	17%	73%	27%
1	R	960	17%	73%	27%
1	S	960	17%	73%	27%
1	T	960	17%	73%	27%
1	U	960	17%	73%	27%
1	V	960	17%	73%	27%
1	W	960	17%	73%	27%
1	X	960	18%	73%	27%
1	Y	960	17%	73%	27%
1	Z	960	18%	73%	27%
1	a	960	18%	73%	27%
1	b	960	16%	73%	27%
1	c	960	17%	73%	27%
1	d	960	18%	73%	27%
1	e	960	17%	73%	27%
1	f	960	16%	73%	27%
1	g	960	17%	73%	27%
1	h	960	20%	73%	27%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 203553 atoms, of which 5246 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 Dynamin-like 120 kDa protein, mitochondrial.

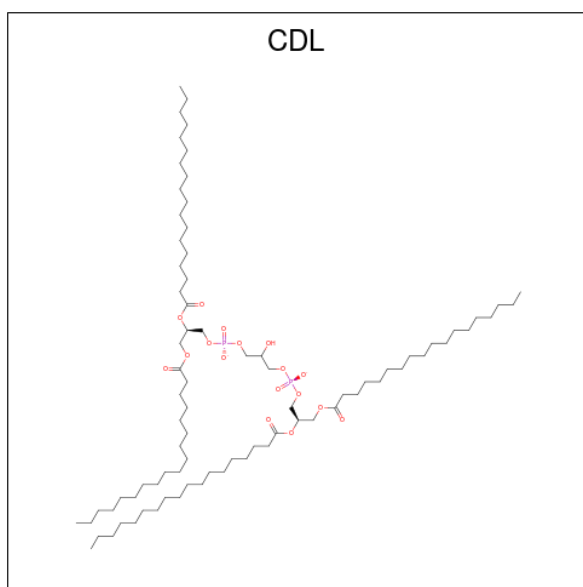
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	698	5685	3572	996	1091	26	0	0
1	B	698	5685	3572	996	1091	26	0	0
1	C	698	5685	3572	996	1091	26	0	0
1	D	698	5685	3572	996	1091	26	0	0
1	E	698	5685	3572	996	1091	26	0	0
1	F	698	5685	3572	996	1091	26	0	0
1	G	698	5685	3572	996	1091	26	0	0
1	H	698	5685	3572	996	1091	26	0	0
1	I	698	5685	3572	996	1091	26	0	0
1	J	698	5685	3572	996	1091	26	0	0
1	K	698	5685	3572	996	1091	26	0	0
1	L	698	5685	3572	996	1091	26	0	0
1	M	698	5685	3572	996	1091	26	0	0
1	N	698	5685	3572	996	1091	26	0	0
1	O	698	5685	3572	996	1091	26	0	0
1	P	698	5685	3572	996	1091	26	0	0
1	Q	698	5685	3572	996	1091	26	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	S	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	T	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	U	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	V	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	W	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	X	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	Y	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	Z	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	a	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	b	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	c	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	d	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	e	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	f	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	g	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	h	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		

- Molecule 2 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	O	P	
2	A	1	Total	C	H	O	P	0
			121	38	64	17	2	
2	A	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	A	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	B	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	B	1	Total	C	H	O	P	0
			121	38	64	17	2	
2	B	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	B	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	C	1	Total	C	H	O	P	0
			121	38	64	17	2	
2	C	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	C	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	C	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	D	1	Total	C	H	O	P	0
			121	38	64	17	2	
2	D	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	D	1	Total	C	H	O	P	0
			138	44	75	17	2	

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	O	P	
2	E	1	82	27	36	17	2	0
2	F	1	82	27	36	17	2	0
2	F	1	138	44	75	17	2	0
2	G	1	121	38	64	17	2	0
2	G	1	82	27	36	17	2	0
2	H	1	82	27	36	17	2	0
2	H	1	138	44	75	17	2	0
2	I	1	82	27	36	17	2	0
2	I	1	138	44	75	17	2	0
2	J	1	82	27	36	17	2	0
2	K	1	138	44	75	17	2	0
2	K	1	121	38	64	17	2	0
2	K	1	82	27	36	17	2	0
2	L	1	121	38	64	17	2	0
2	L	1	138	44	75	17	2	0
2	L	1	82	27	36	17	2	0
2	L	1	138	44	75	17	2	0
2	M	1	138	44	75	17	2	0
2	M	1	121	38	64	17	2	0
2	M	1	82	27	36	17	2	0
2	N	1	138	44	75	17	2	0

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Mol	Chain	Residues	Atoms					AltConf
2	N	1	Total	C	H	O	P	0
			121	38	64	17	2	
2	N	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	O	1	Total	C	H	O	P	0
			121	38	64	17	2	
2	O	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	O	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	P	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	P	1	Total	C	H	O	P	0
			121	38	64	17	2	
2	P	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	Q	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	Q	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	R	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	R	1	Total	C	H	O	P	0
			121	38	64	17	2	
2	R	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	S	1	Total	C	H	O	P	0
			121	38	64	17	2	
2	S	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	T	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	T	1	Total	C	H	O	P	0
			121	38	64	17	2	
2	T	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	U	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	U	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	V	1	Total	C	H	O	P	0
			82	27	36	17	2	

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	O	P	
2	V	1	Total 121	C 38	H 64	O 17	P 2	0
2	V	1	Total 138	C 44	H 75	O 17	P 2	0
2	W	1	Total 138	C 44	H 75	O 17	P 2	0
2	W	1	Total 82	C 27	H 36	O 17	P 2	0
2	X	1	Total 121	C 38	H 64	O 17	P 2	0
2	X	1	Total 138	C 44	H 75	O 17	P 2	0
2	X	1	Total 82	C 27	H 36	O 17	P 2	0
2	X	1	Total 138	C 44	H 75	O 17	P 2	0
2	Y	1	Total 138	C 44	H 75	O 17	P 2	0
2	Y	1	Total 121	C 38	H 64	O 17	P 2	0
2	Y	1	Total 82	C 27	H 36	O 17	P 2	0
2	Z	1	Total 121	C 38	H 64	O 17	P 2	0
2	Z	1	Total 82	C 27	H 36	O 17	P 2	0
2	Z	1	Total 138	C 44	H 75	O 17	P 2	0
2	a	1	Total 82	C 27	H 36	O 17	P 2	0
2	b	1	Total 121	C 38	H 64	O 17	P 2	0
2	b	1	Total 82	C 27	H 36	O 17	P 2	0
2	b	1	Total 138	C 44	H 75	O 17	P 2	0
2	c	1	Total 138	C 44	H 75	O 17	P 2	0
2	c	1	Total 121	C 38	H 64	O 17	P 2	0
2	c	1	Total 82	C 27	H 36	O 17	P 2	0

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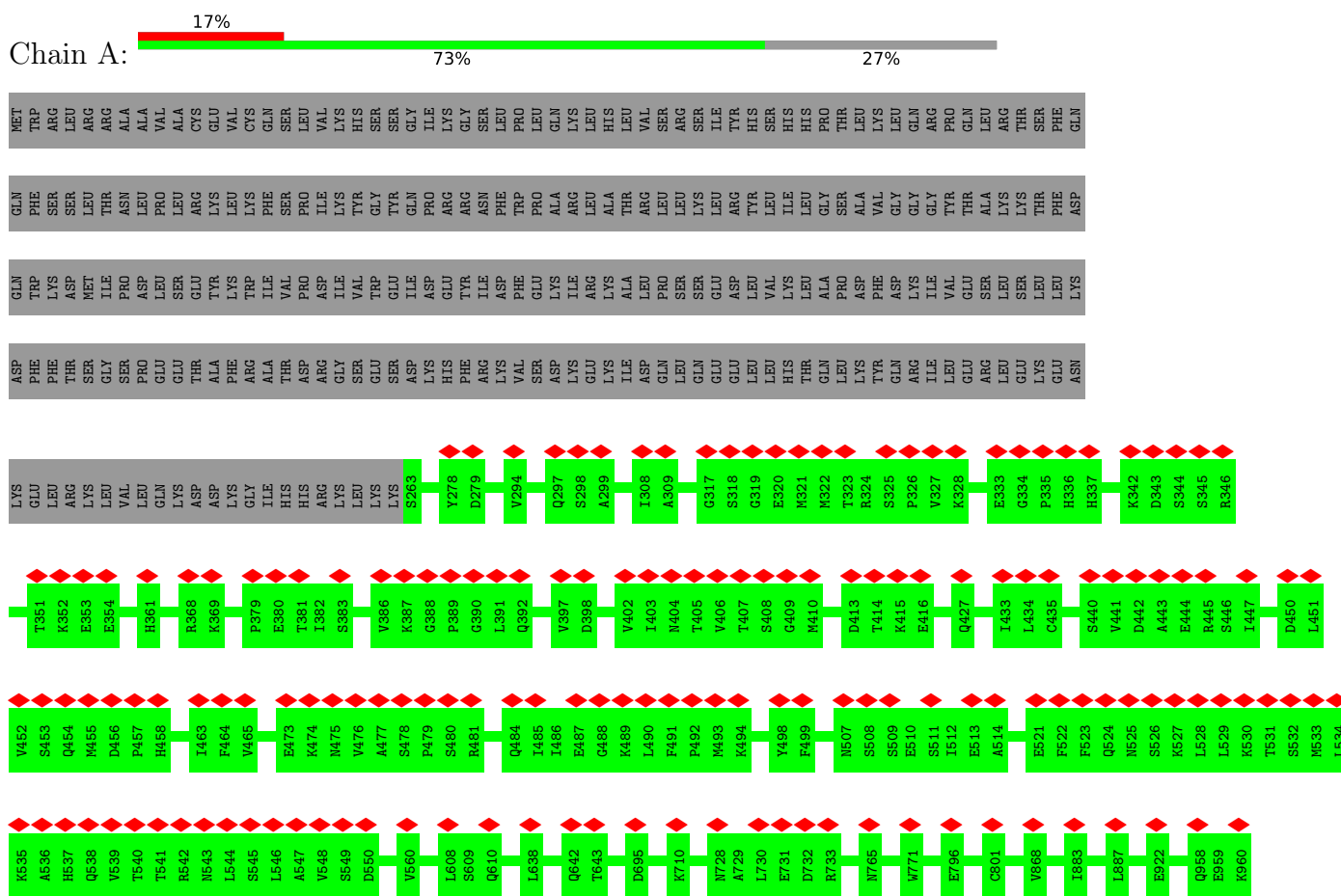
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Mol	Chain	Residues	Atoms					AltConf
2	d	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	d	1	Total	C	H	O	P	0
			121	38	64	17	2	
2	d	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	d	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	e	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	f	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	f	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	f	1	Total	C	H	O	P	0
			121	38	64	17	2	
2	g	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	g	1	Total	C	H	O	P	0
			82	27	36	17	2	
2	h	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	h	1	Total	C	H	O	P	0
			121	38	64	17	2	
2	h	1	Total	C	H	O	P	0
			138	44	75	17	2	
2	h	1	Total	C	H	O	P	0
			82	27	36	17	2	

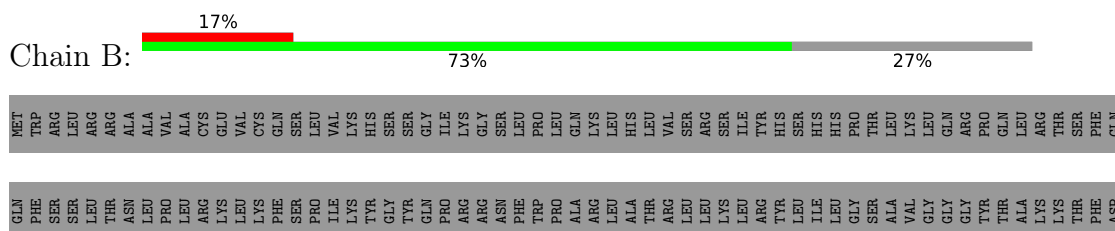
3 Residue-property plots

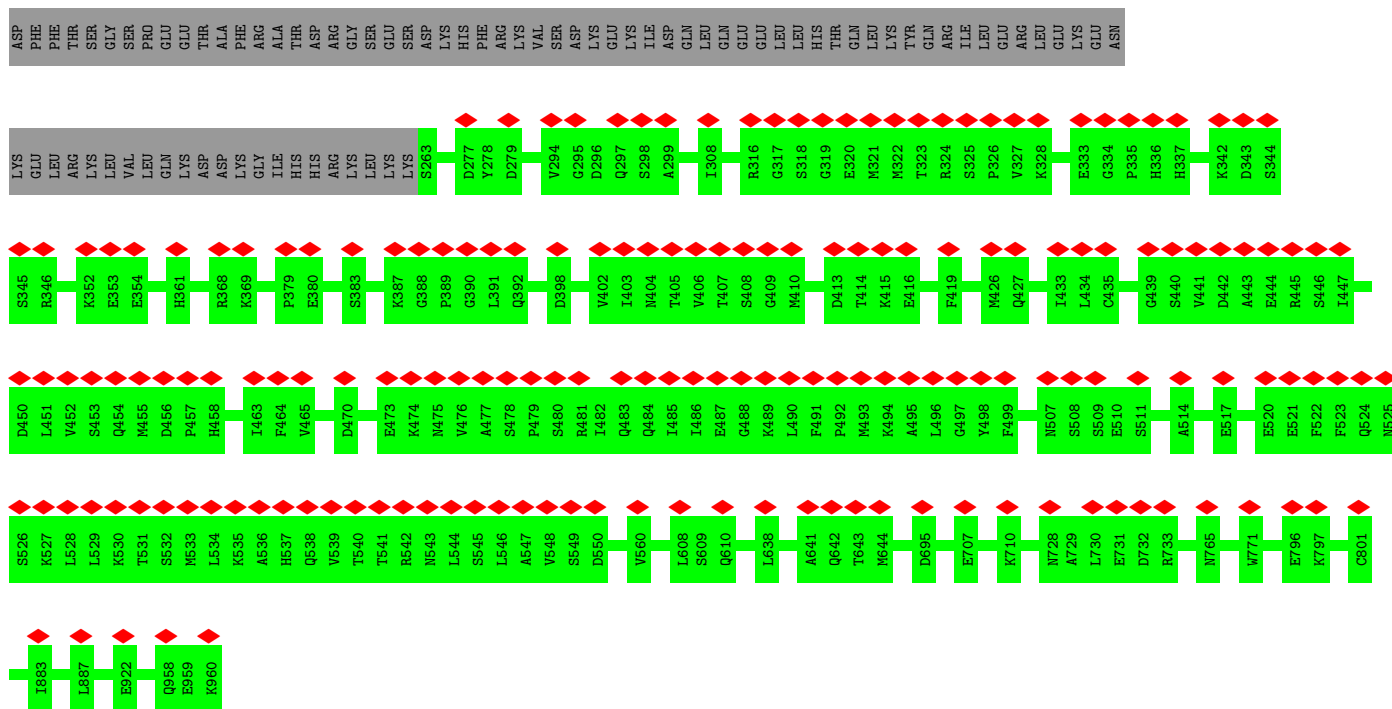
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

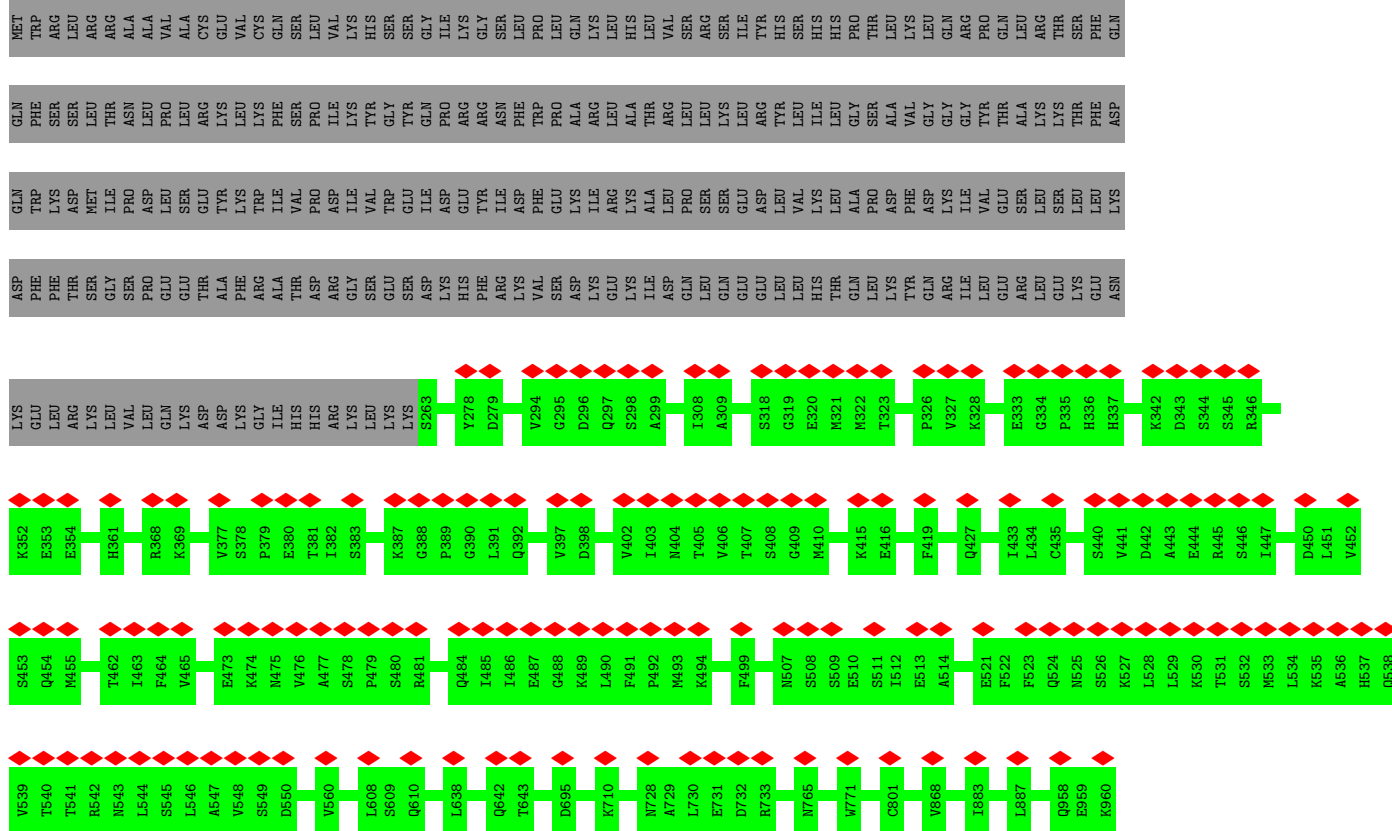
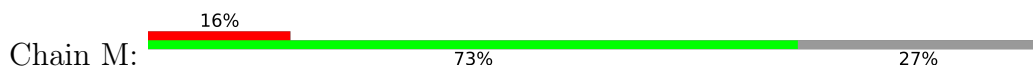


- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

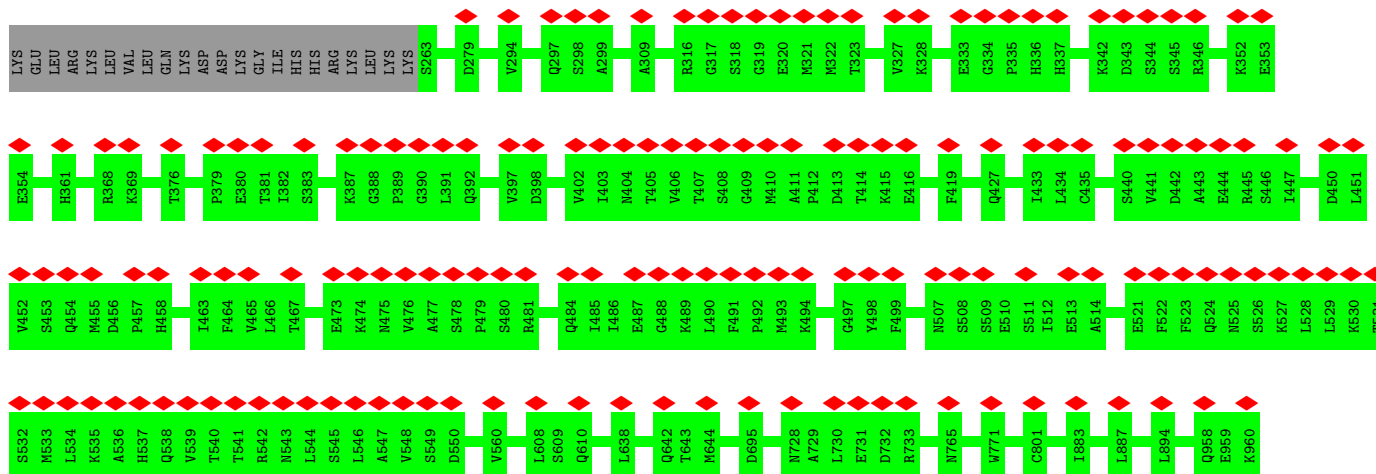




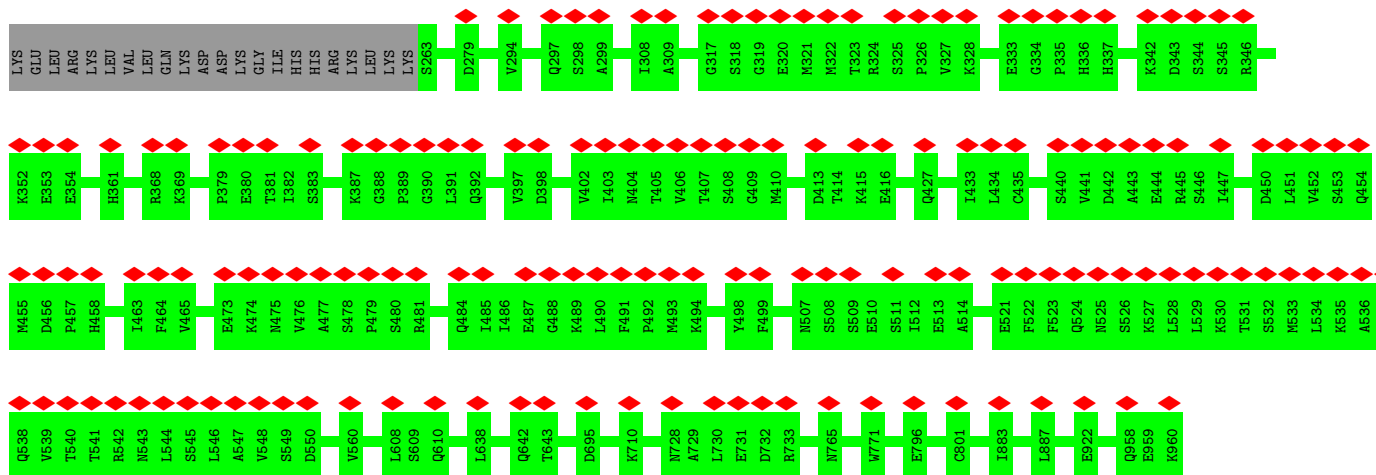
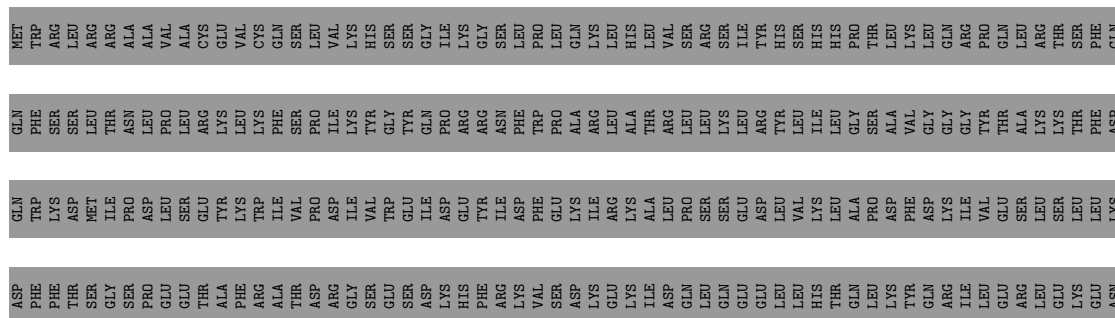
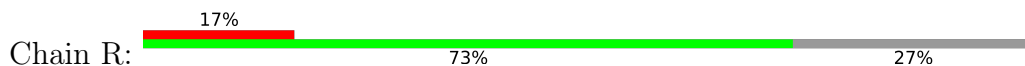
• Molecule 1: Dynamamin-like 120 kDa protein, mitochondrial



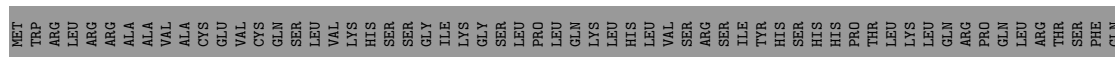
• Molecule 1: Dynamamin-like 120 kDa protein, mitochondrial

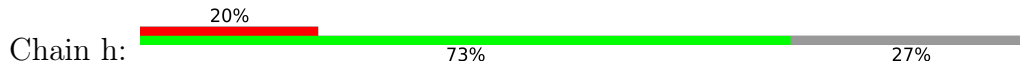


• Molecule 1: Dynamin-like 120 kDa protein, mitochondrial



• Molecule 1: Dynamin-like 120 kDa protein, mitochondrial





MET	GLN	LYS	S344	D442	A514	D732
TRP	GLU	GLU	S345	A443	E517	R733
ARG	SER	LEU	R346	E444	Y518	N765
LEU	THR	ARG	R352	R445	E519	N771
ARG	LEU	LEU	E353	S446	E520	C801
ALA	ASN	VAL	E354	I447	E521	V868
ALA	LEU	LEU	H361	D450	F522	D869
ALA	PRO	GLN	R368	L451	F523	I883
VAL	PRO	LYS	K369	V452	Q524	L887
ALA	THR	GLU	V377	S453	N525	E922
CYS	GLU	ASP	K378	Q454	S526	Q968
GLU	TYR	LYS	S379	M455	K527	E969
VAL	LEU	PHE	F379	D456	L528	R960
CYS	VAL	ARG	E380	P457	L529	
GLN	ILE	GLY	T381	H458	K530	
SER	THR	LYS	I382	I463	T531	
SER	ASP	ASP	S383	F464	S532	
LEU	VAL	LYS	K387	V465	M533	
VAL	PRO	ARG	G388	L466	L534	
VAL	ASP	GLY	F389	D470	K535	
ILE	ILE	LEU	G390	E473	A536	
GLY	GLU	LEU	L391	R474	H537	
GLY	TYR	LEU	Q392	M475	Q538	
ARG	ARG	LEU	V397	V476	T540	
GLY	ASN	LEU	D398	A477	T541	
LEU	ASP	LEU	V402	S478	R642	
LEU	PHE	LEU	I403	P479	N543	
LEU	TRP	LEU	N404	S480	L544	
LEU	PRO	LEU	T405	R481	S545	
LEU	GLN	LEU	V406	I482	L546	
LEU	LEU	LEU	T407	Q483	A547	
LEU	LEU	LEU	S408	Q484	V548	
LEU	VAL	LEU	G409	I485	S549	
LEU	VAL	LEU	M410	I486	D550	
LEU	ASP	LEU	D413	E487	V560	
LEU	ASP	LEU	T414	G488	L608	
LEU	VAL	LEU	R415	K489	S609	
LEU	THR	LEU	E416	F491	Q610	
LEU	THR	LEU	T417	P492	L638	
LEU	THR	LEU	I418	M493	A641	
LEU	ALA	LEU	F419	R494	Q642	
LEU	VAL	LEU	S420	A495	T643	
LEU	VAL	LEU	M426	L496	M644	
LEU	ASP	LEU	Q427	G497	D695	
LEU	ASP	LEU	I433	Y498	F499	
LEU	GLY	LEU	L434	A500	E707	
LEU	GLY	LEU	C435	V501	K710	
LEU	GLY	LEU	G439	S508	N728	
LEU	THR	LEU	S440	S509	A729	
LEU	THR	LEU	V441	E510	L730	
LEU	THR	LEU	E511	I512	E731	
LEU	PHE	LEU	E513			
LEU	GLN	LEU				

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=128.619°, rise=8.04 Å, axial sym=C1	Depositor
Number of segments used	96152	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	82	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.020	Depositor
Minimum map value	-0.014	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0025	Depositor
Map size (Å)	699.72003, 699.72003, 699.72003	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.6660001, 1.6660001, 1.6660001	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: CDL

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	0.23	0/5788	0.42	0/7811
1	B	0.23	0/5788	0.42	0/7811
1	C	0.23	0/5788	0.42	0/7811
1	D	0.23	0/5788	0.43	0/7811
1	E	0.23	0/5788	0.43	0/7811
1	F	0.23	0/5788	0.43	0/7811
1	G	0.23	0/5788	0.42	0/7811
1	H	0.23	0/5788	0.43	0/7811
1	I	0.23	0/5788	0.43	0/7811
1	J	0.23	0/5788	0.43	0/7811
1	K	0.23	0/5788	0.43	0/7811
1	L	0.23	0/5788	0.42	0/7811
1	M	0.23	0/5788	0.42	0/7811
1	N	0.23	0/5788	0.43	0/7811
1	O	0.23	0/5788	0.43	0/7811
1	P	0.23	0/5788	0.42	0/7811
1	Q	0.23	0/5788	0.43	0/7811
1	R	0.23	0/5788	0.43	0/7811
1	S	0.23	0/5788	0.42	0/7811
1	T	0.23	0/5788	0.42	0/7811
1	U	0.23	0/5788	0.42	0/7811
1	V	0.23	0/5788	0.43	0/7811
1	W	0.23	0/5788	0.42	0/7811
1	X	0.23	0/5788	0.42	0/7811
1	Y	0.23	0/5788	0.43	0/7811
1	Z	0.23	0/5788	0.42	0/7811
1	a	0.23	0/5788	0.43	0/7811
1	b	0.23	0/5788	0.43	0/7811
1	c	0.23	0/5788	0.43	0/7811
1	d	0.23	0/5788	0.43	0/7811
1	e	0.23	0/5788	0.42	0/7811
1	f	0.23	0/5788	0.42	0/7811

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	g	0.23	0/5788	0.43	0/7811
1	h	0.23	0/5788	0.42	0/7811
All	All	0.23	0/196792	0.43	0/265574

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](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	696/960 (72%)	686 (99%)	10 (1%)	0	100	100
1	B	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	C	696/960 (72%)	685 (98%)	11 (2%)	0	100	100
1	D	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	E	696/960 (72%)	686 (99%)	10 (1%)	0	100	100
1	F	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	G	696/960 (72%)	685 (98%)	11 (2%)	0	100	100
1	H	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	I	696/960 (72%)	686 (99%)	10 (1%)	0	100	100
1	J	696/960 (72%)	685 (98%)	11 (2%)	0	100	100
1	K	696/960 (72%)	686 (99%)	10 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	696/960 (72%)	686 (99%)	10 (1%)	0	100	100
1	M	696/960 (72%)	686 (99%)	10 (1%)	0	100	100
1	N	696/960 (72%)	686 (99%)	10 (1%)	0	100	100
1	O	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	P	696/960 (72%)	686 (99%)	10 (1%)	0	100	100
1	Q	696/960 (72%)	686 (99%)	10 (1%)	0	100	100
1	R	696/960 (72%)	685 (98%)	11 (2%)	0	100	100
1	S	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	T	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	U	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	V	696/960 (72%)	685 (98%)	11 (2%)	0	100	100
1	W	696/960 (72%)	685 (98%)	11 (2%)	0	100	100
1	X	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	Y	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	Z	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	a	696/960 (72%)	686 (99%)	10 (1%)	0	100	100
1	b	696/960 (72%)	686 (99%)	10 (1%)	0	100	100
1	c	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	d	696/960 (72%)	686 (99%)	10 (1%)	0	100	100
1	e	696/960 (72%)	686 (99%)	10 (1%)	0	100	100
1	f	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	g	696/960 (72%)	687 (99%)	9 (1%)	0	100	100
1	h	696/960 (72%)	686 (99%)	10 (1%)	0	100	100
All	All	23664/32640 (72%)	23332 (99%)	332 (1%)	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	633/874 (72%)	633 (100%)	0	100	100
1	B	633/874 (72%)	633 (100%)	0	100	100
1	C	633/874 (72%)	633 (100%)	0	100	100
1	D	633/874 (72%)	633 (100%)	0	100	100
1	E	633/874 (72%)	633 (100%)	0	100	100
1	F	633/874 (72%)	633 (100%)	0	100	100
1	G	633/874 (72%)	633 (100%)	0	100	100
1	H	633/874 (72%)	633 (100%)	0	100	100
1	I	633/874 (72%)	633 (100%)	0	100	100
1	J	633/874 (72%)	633 (100%)	0	100	100
1	K	633/874 (72%)	633 (100%)	0	100	100
1	L	633/874 (72%)	633 (100%)	0	100	100
1	M	633/874 (72%)	633 (100%)	0	100	100
1	N	633/874 (72%)	633 (100%)	0	100	100
1	O	633/874 (72%)	633 (100%)	0	100	100
1	P	633/874 (72%)	633 (100%)	0	100	100
1	Q	633/874 (72%)	633 (100%)	0	100	100
1	R	633/874 (72%)	633 (100%)	0	100	100
1	S	633/874 (72%)	633 (100%)	0	100	100
1	T	633/874 (72%)	633 (100%)	0	100	100
1	U	633/874 (72%)	633 (100%)	0	100	100
1	V	633/874 (72%)	633 (100%)	0	100	100
1	W	633/874 (72%)	633 (100%)	0	100	100
1	X	633/874 (72%)	633 (100%)	0	100	100
1	Y	633/874 (72%)	633 (100%)	0	100	100
1	Z	633/874 (72%)	633 (100%)	0	100	100
1	a	633/874 (72%)	633 (100%)	0	100	100
1	b	633/874 (72%)	633 (100%)	0	100	100
1	c	633/874 (72%)	633 (100%)	0	100	100
1	d	633/874 (72%)	633 (100%)	0	100	100
1	e	633/874 (72%)	633 (100%)	0	100	100
1	f	633/874 (72%)	633 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	g	633/874 (72%)	633 (100%)	0	100	100
1	h	633/874 (72%)	633 (100%)	0	100	100
All	All	21522/29716 (72%)	21522 (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. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

91 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	CDL	F	1002	-	62,62,99	0.33	0	68,74,111	0.48	0
2	CDL	R	1002	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	c	1002	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	R	1001	-	62,62,99	0.34	0	68,74,111	0.48	0
2	CDL	N	1003	-	45,45,99	0.36	0	51,57,111	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CDL	H	1002	-	62,62,99	0.33	0	68,74,111	0.48	0
2	CDL	K	1001	-	62,62,99	0.34	0	68,74,111	0.48	0
2	CDL	L	1004	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	O	1002	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	T	1002	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	I	1001	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	U	1001	-	45,45,99	0.36	0	51,57,111	0.47	0
2	CDL	c	1001	-	62,62,99	0.33	0	68,74,111	0.48	0
2	CDL	h	1002	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	h	1004	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	C	1004	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	G	1002	-	45,45,99	0.36	0	51,57,111	0.47	0
2	CDL	b	1002	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	g	1002	-	45,45,99	0.36	0	51,57,111	0.47	0
2	CDL	D	1003	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	S	1002	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	O	1001	-	56,56,99	0.33	0	62,68,111	0.58	1 (1%)
2	CDL	C	1003	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	b	1003	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	V	1001	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	J	1001	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	h	1001	-	62,62,99	0.33	0	68,74,111	0.48	0
2	CDL	L	1001	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	Y	1001	-	62,62,99	0.34	0	68,74,111	0.49	0
2	CDL	C	1001	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	d	1001	-	62,62,99	0.33	0	68,74,111	0.48	0
2	CDL	f	1002	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	H	1001	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	b	1001	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	N	1001	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	P	1003	-	45,45,99	0.35	0	51,57,111	0.47	0
2	CDL	W	1002	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	d	1003	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	K	1003	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	g	1001	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	G	1001	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	F	1001	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	B	1004	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	A	1003	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	M	1003	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	e	1001	-	45,45,99	0.36	0	51,57,111	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CDL	W	1001	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	d	1002	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	X	1003	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	L	1003	-	45,45,99	0.35	0	51,57,111	0.47	0
2	CDL	V	1002	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	D	1001	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	K	1002	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	A	1002	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	M	1002	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	E	1001	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	A	1001	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	D	1002	-	45,45,99	0.35	0	51,57,111	0.46	0
2	CDL	I	1002	-	62,62,99	0.33	0	68,74,111	0.48	0
2	CDL	Z	1003	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	Z	1001	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	Q	1002	-	62,62,99	0.33	0	68,74,111	0.48	0
2	CDL	P	1001	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	B	1003	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	M	1001	-	62,62,99	0.33	0	68,74,111	0.48	0
2	CDL	d	1004	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	V	1003	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	P	1002	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	Y	1002	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	B	1001	-	62,62,99	0.33	0	68,74,111	0.48	0
2	CDL	X	1001	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	T	1003	-	45,45,99	0.36	0	51,57,111	0.47	0
2	CDL	c	1003	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	S	1001	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	B	1002	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	a	1001	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	X	1004	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	C	1002	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	L	1002	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	T	1001	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	U	1002	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	f	1001	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	X	1002	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	Y	1003	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	O	1003	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	R	1003	-	45,45,99	0.36	0	51,57,111	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CDL	f	1003	-	56,56,99	0.33	0	62,68,111	0.56	1 (1%)
2	CDL	Z	1002	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	Q	1001	-	45,45,99	0.36	0	51,57,111	0.46	0
2	CDL	h	1003	-	62,62,99	0.33	0	68,74,111	0.49	0
2	CDL	N	1002	-	56,56,99	0.33	0	62,68,111	0.56	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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CDL	F	1002	-	-	33/73/73/110	-
2	CDL	R	1002	-	-	23/67/67/110	-
2	CDL	c	1002	-	-	23/67/67/110	-
2	CDL	R	1001	-	-	34/73/73/110	-
2	CDL	N	1003	-	-	19/56/56/110	-
2	CDL	H	1002	-	-	33/73/73/110	-
2	CDL	K	1001	-	-	35/73/73/110	-
2	CDL	L	1004	-	-	34/73/73/110	-
2	CDL	O	1002	-	-	19/56/56/110	-
2	CDL	T	1002	-	-	23/67/67/110	-
2	CDL	I	1001	-	-	19/56/56/110	-
2	CDL	U	1001	-	-	19/56/56/110	-
2	CDL	c	1001	-	-	33/73/73/110	-
2	CDL	h	1002	-	-	23/67/67/110	-
2	CDL	h	1004	-	-	19/56/56/110	-
2	CDL	C	1004	-	-	34/73/73/110	-
2	CDL	G	1002	-	-	19/56/56/110	-
2	CDL	b	1002	-	-	19/56/56/110	-
2	CDL	g	1002	-	-	19/56/56/110	-
2	CDL	D	1003	-	-	34/73/73/110	-
2	CDL	S	1002	-	-	19/56/56/110	-
2	CDL	O	1001	-	-	24/67/67/110	-
2	CDL	C	1003	-	-	19/56/56/110	-
2	CDL	b	1003	-	-	34/73/73/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CDL	V	1001	-	-	19/56/56/110	-
2	CDL	J	1001	-	-	19/56/56/110	-
2	CDL	h	1001	-	-	35/73/73/110	-
2	CDL	L	1001	-	-	23/67/67/110	-
2	CDL	Y	1001	-	-	34/73/73/110	-
2	CDL	C	1001	-	-	23/67/67/110	-
2	CDL	d	1001	-	-	34/73/73/110	-
2	CDL	f	1002	-	-	19/56/56/110	-
2	CDL	H	1001	-	-	19/56/56/110	-
2	CDL	b	1001	-	-	23/67/67/110	-
2	CDL	N	1001	-	-	33/73/73/110	-
2	CDL	P	1003	-	-	19/56/56/110	-
2	CDL	W	1002	-	-	19/56/56/110	-
2	CDL	d	1003	-	-	38/73/73/110	-
2	CDL	K	1003	-	-	19/56/56/110	-
2	CDL	g	1001	-	-	34/73/73/110	-
2	CDL	G	1001	-	-	23/67/67/110	-
2	CDL	F	1001	-	-	19/56/56/110	-
2	CDL	B	1004	-	-	19/56/56/110	-
2	CDL	A	1003	-	-	34/73/73/110	-
2	CDL	M	1003	-	-	19/56/56/110	-
2	CDL	e	1001	-	-	19/56/56/110	-
2	CDL	W	1001	-	-	34/73/73/110	-
2	CDL	d	1002	-	-	23/67/67/110	-
2	CDL	X	1003	-	-	19/56/56/110	-
2	CDL	L	1003	-	-	19/56/56/110	-
2	CDL	V	1002	-	-	23/67/67/110	-
2	CDL	D	1001	-	-	23/67/67/110	-
2	CDL	K	1002	-	-	23/67/67/110	-
2	CDL	A	1002	-	-	19/56/56/110	-
2	CDL	M	1002	-	-	23/67/67/110	-
2	CDL	E	1001	-	-	19/56/56/110	-
2	CDL	A	1001	-	-	23/67/67/110	-
2	CDL	D	1002	-	-	19/56/56/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CDL	I	1002	-	-	34/73/73/110	-
2	CDL	Z	1003	-	-	34/73/73/110	-
2	CDL	Z	1001	-	-	23/67/67/110	-
2	CDL	Q	1002	-	-	33/73/73/110	-
2	CDL	P	1001	-	-	35/73/73/110	-
2	CDL	B	1003	-	-	37/73/73/110	-
2	CDL	M	1001	-	-	35/73/73/110	-
2	CDL	d	1004	-	-	19/56/56/110	-
2	CDL	V	1003	-	-	34/73/73/110	-
2	CDL	P	1002	-	-	23/67/67/110	-
2	CDL	Y	1002	-	-	23/67/67/110	-
2	CDL	B	1001	-	-	33/73/73/110	-
2	CDL	X	1001	-	-	23/67/67/110	-
2	CDL	T	1003	-	-	19/56/56/110	-
2	CDL	c	1003	-	-	19/56/56/110	-
2	CDL	S	1001	-	-	23/67/67/110	-
2	CDL	B	1002	-	-	23/67/67/110	-
2	CDL	a	1001	-	-	19/56/56/110	-
2	CDL	X	1004	-	-	34/73/73/110	-
2	CDL	C	1002	-	-	38/73/73/110	-
2	CDL	L	1002	-	-	38/73/73/110	-
2	CDL	T	1001	-	-	34/73/73/110	-
2	CDL	U	1002	-	-	34/73/73/110	-
2	CDL	f	1001	-	-	33/73/73/110	-
2	CDL	X	1002	-	-	38/73/73/110	-
2	CDL	Y	1003	-	-	19/56/56/110	-
2	CDL	O	1003	-	-	33/73/73/110	-
2	CDL	R	1003	-	-	19/56/56/110	-
2	CDL	f	1003	-	-	23/67/67/110	-
2	CDL	Z	1002	-	-	19/56/56/110	-
2	CDL	Q	1001	-	-	19/56/56/110	-
2	CDL	h	1003	-	-	38/73/73/110	-
2	CDL	N	1002	-	-	23/67/67/110	-

There are no bond length outliers.

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	1001	CDL	OA6-CA5-C11	2.11	116.06	111.50
2	C	1001	CDL	OA6-CA5-C11	2.07	115.96	111.50
2	X	1001	CDL	OA6-CA5-C11	2.07	115.96	111.50
2	P	1002	CDL	OA6-CA5-C11	2.07	115.95	111.50
2	Z	1001	CDL	OA6-CA5-C11	2.06	115.94	111.50

There are no chirality outliers.

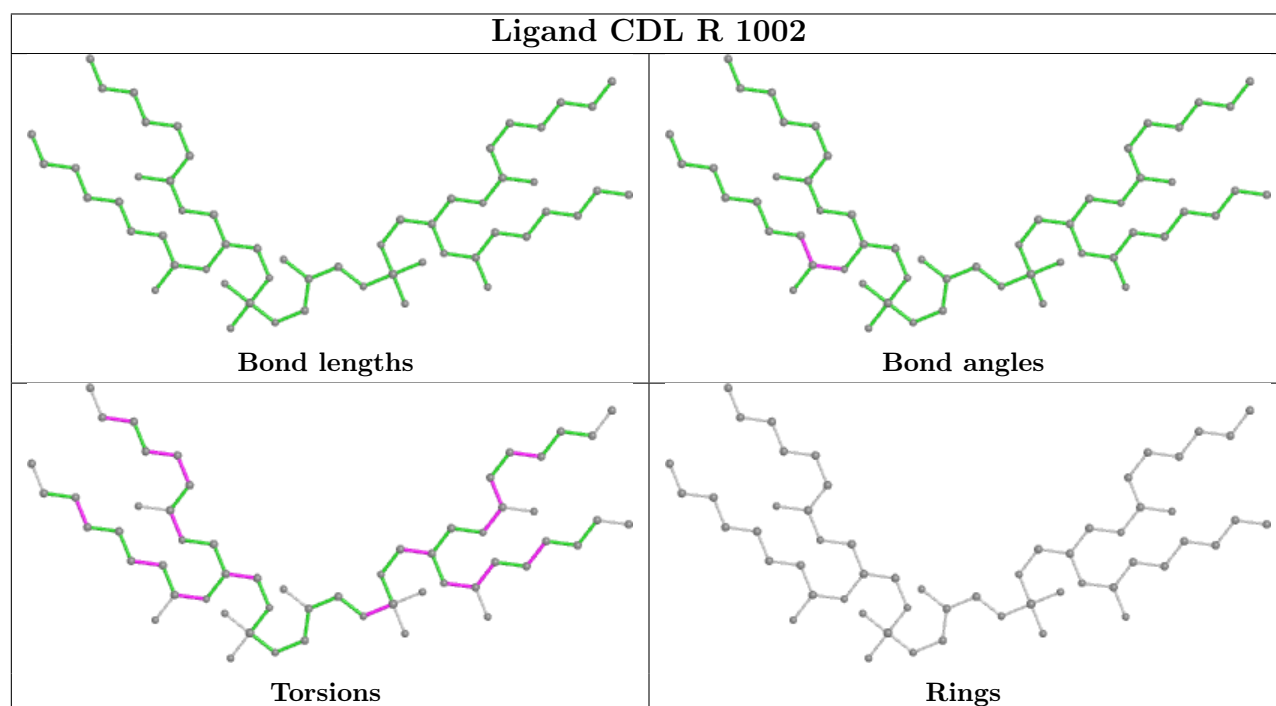
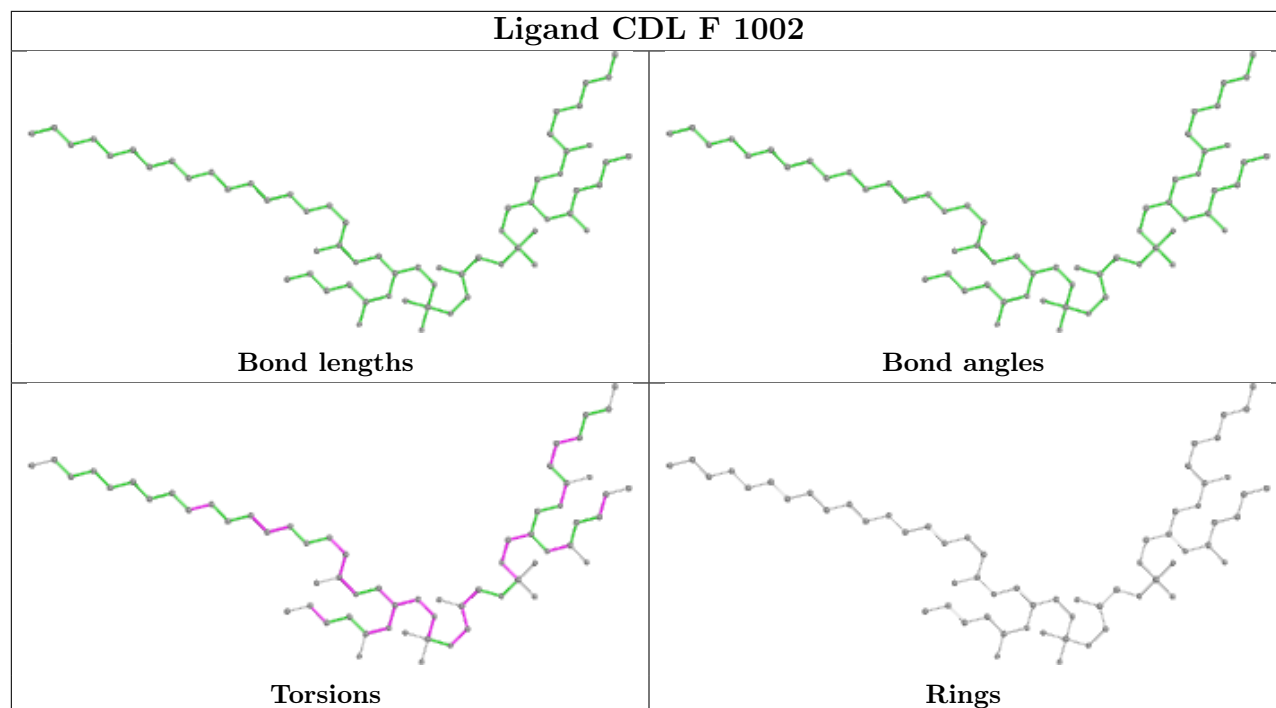
5 of 2351 torsion outliers are listed below:

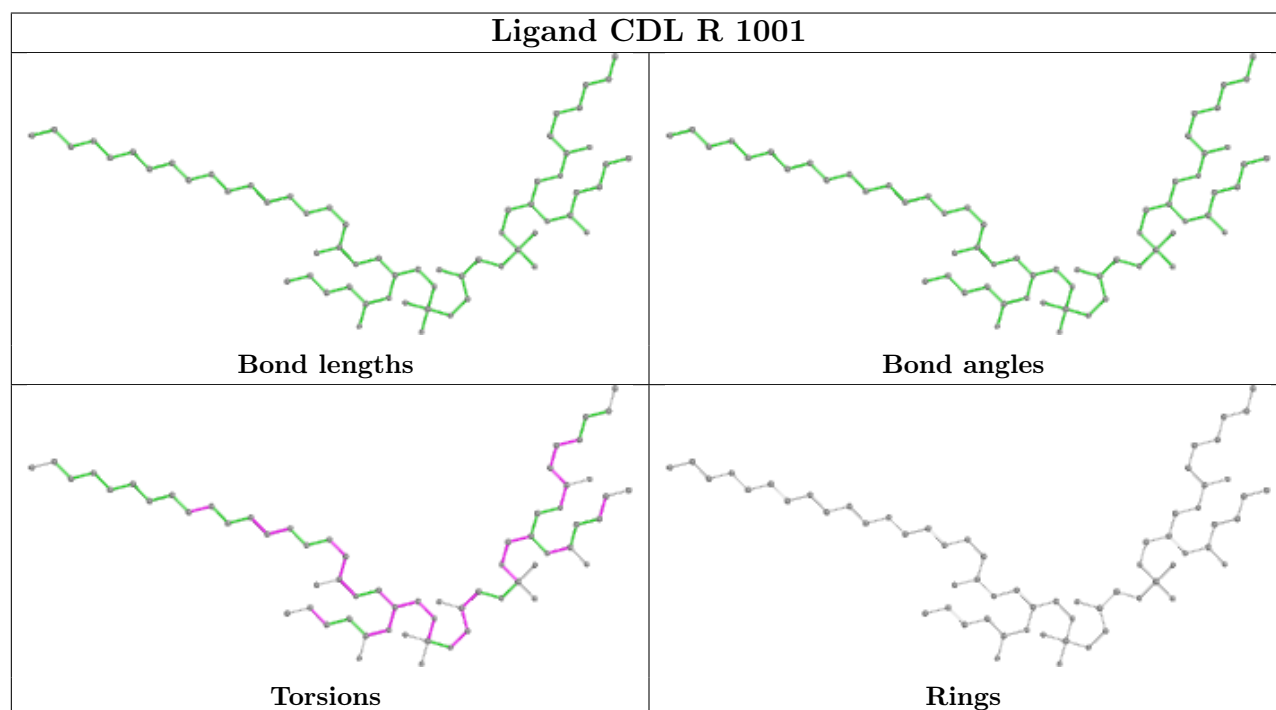
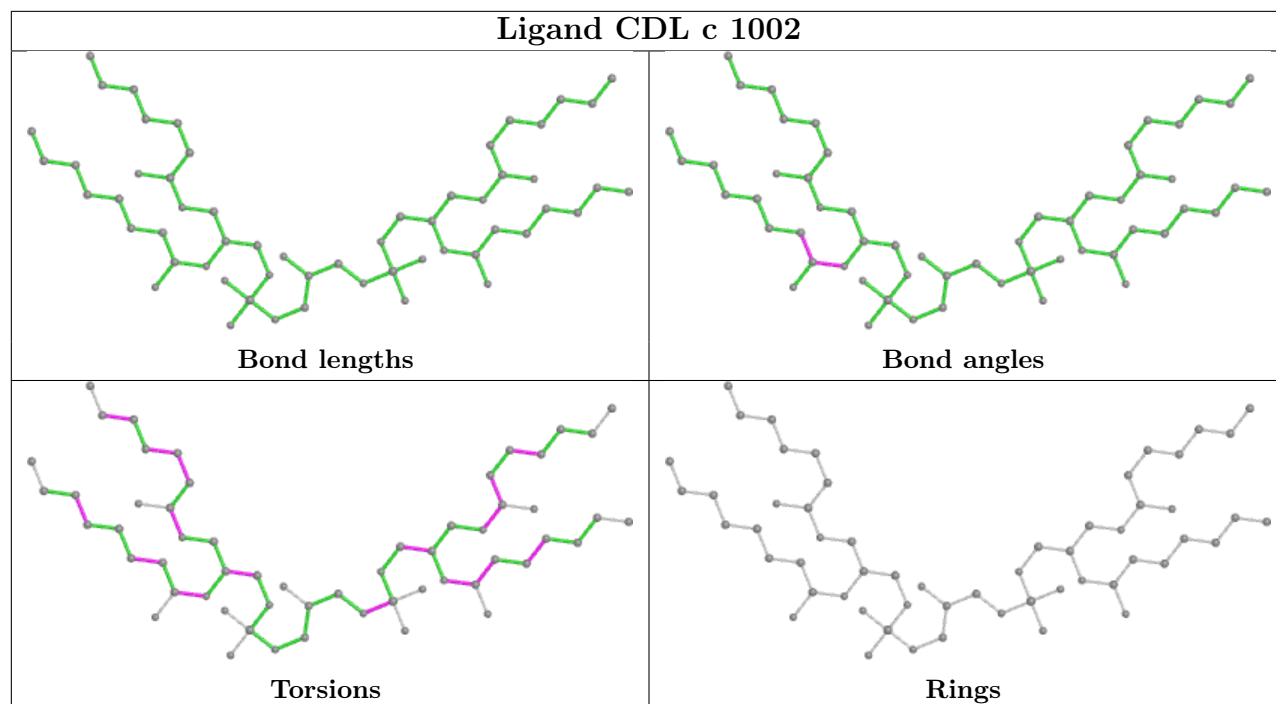
Mol	Chain	Res	Type	Atoms
2	A	1001	CDL	OA7-CA5-OA6-CA4
2	A	1001	CDL	C11-CA5-OA6-CA4
2	A	1001	CDL	OB7-CB5-OB6-CB4
2	A	1001	CDL	C51-CB5-OB6-CB4
2	A	1002	CDL	CA3-OA5-PA1-OA4

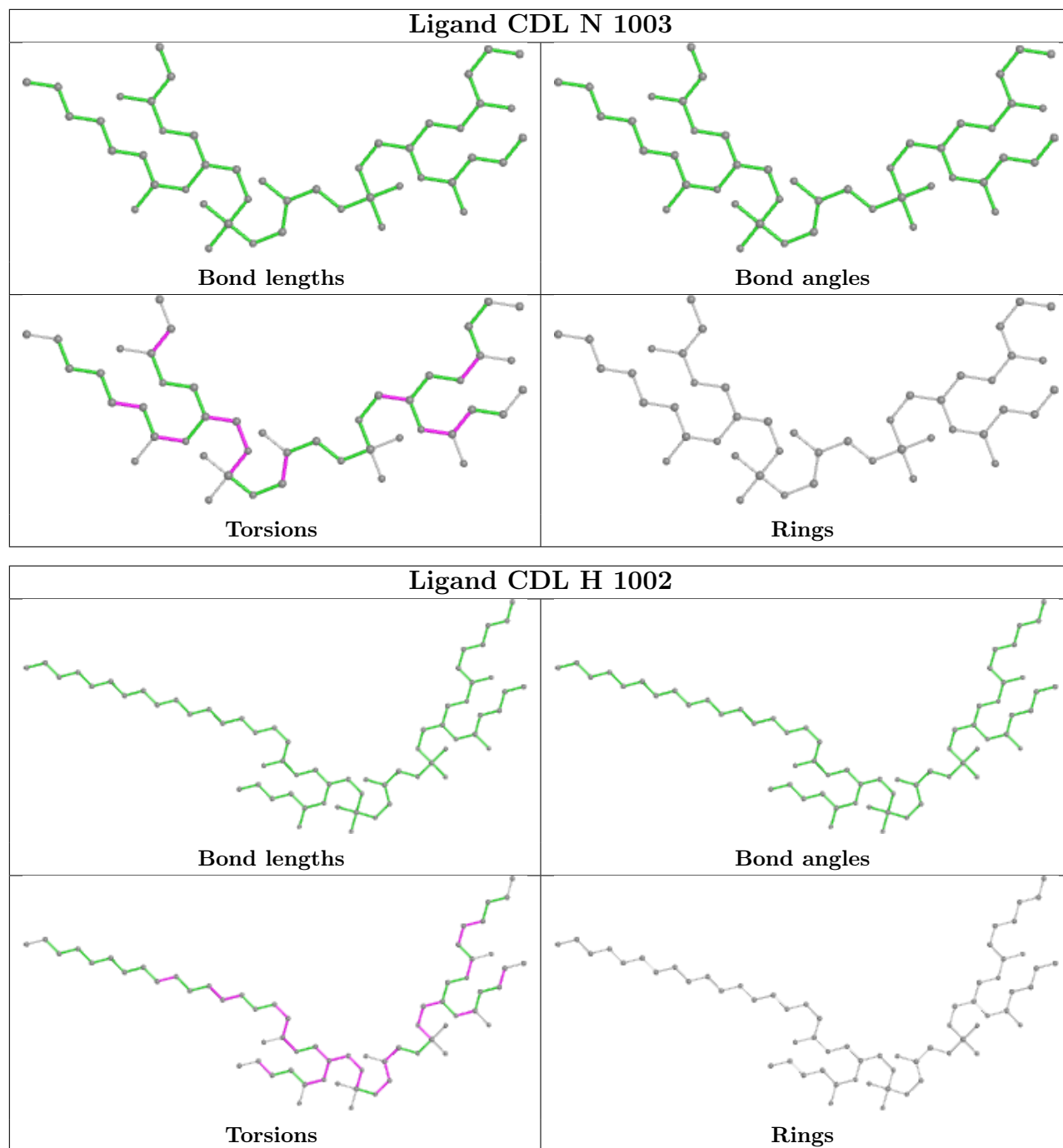
There are no ring outliers.

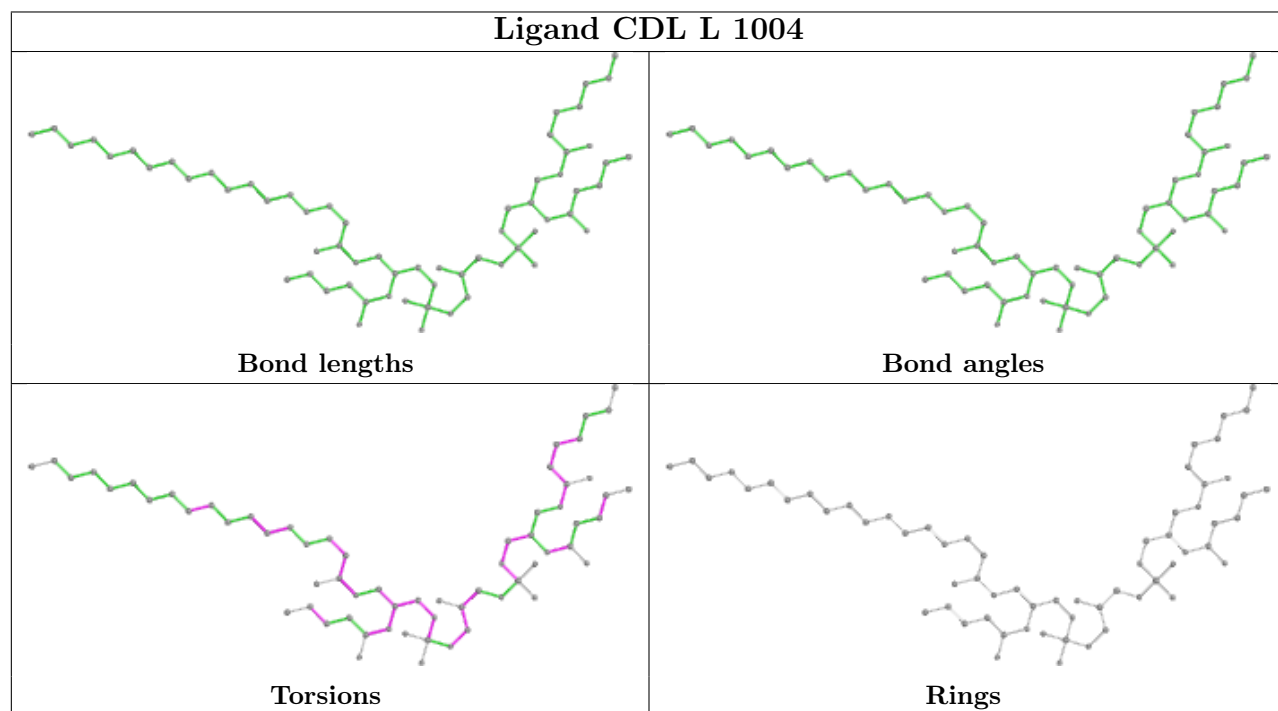
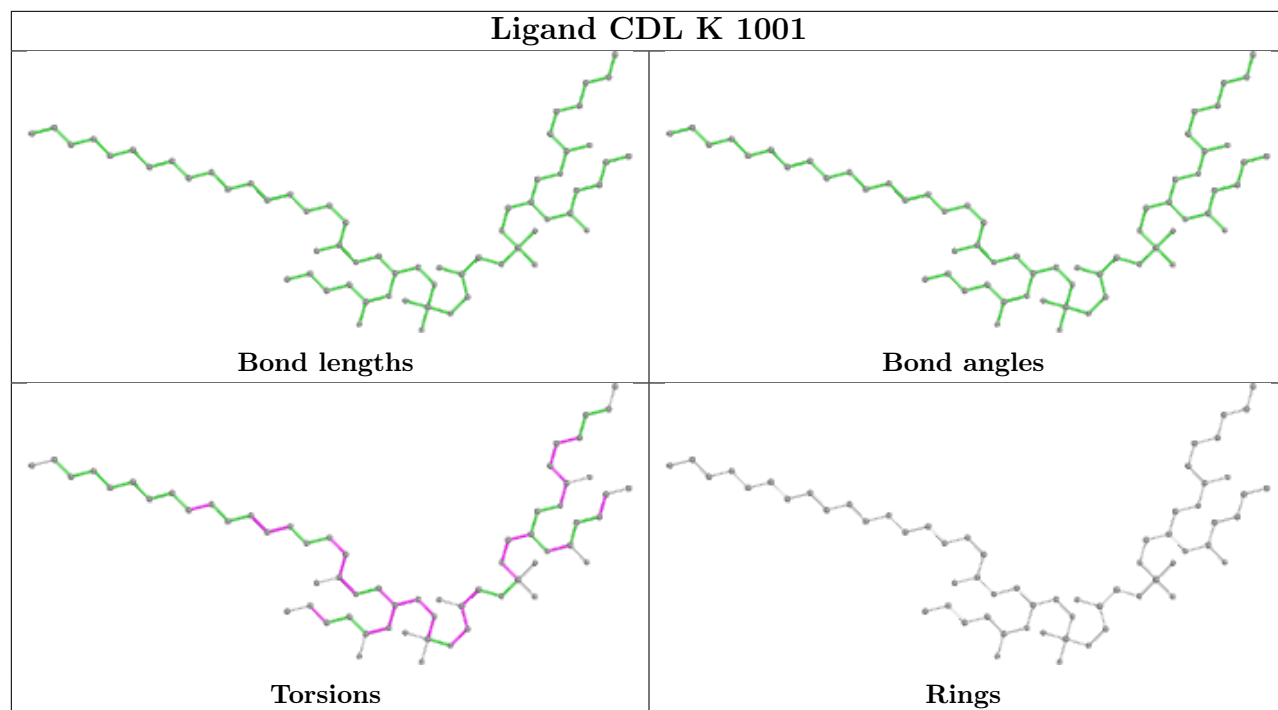
No monomer is involved in short contacts.

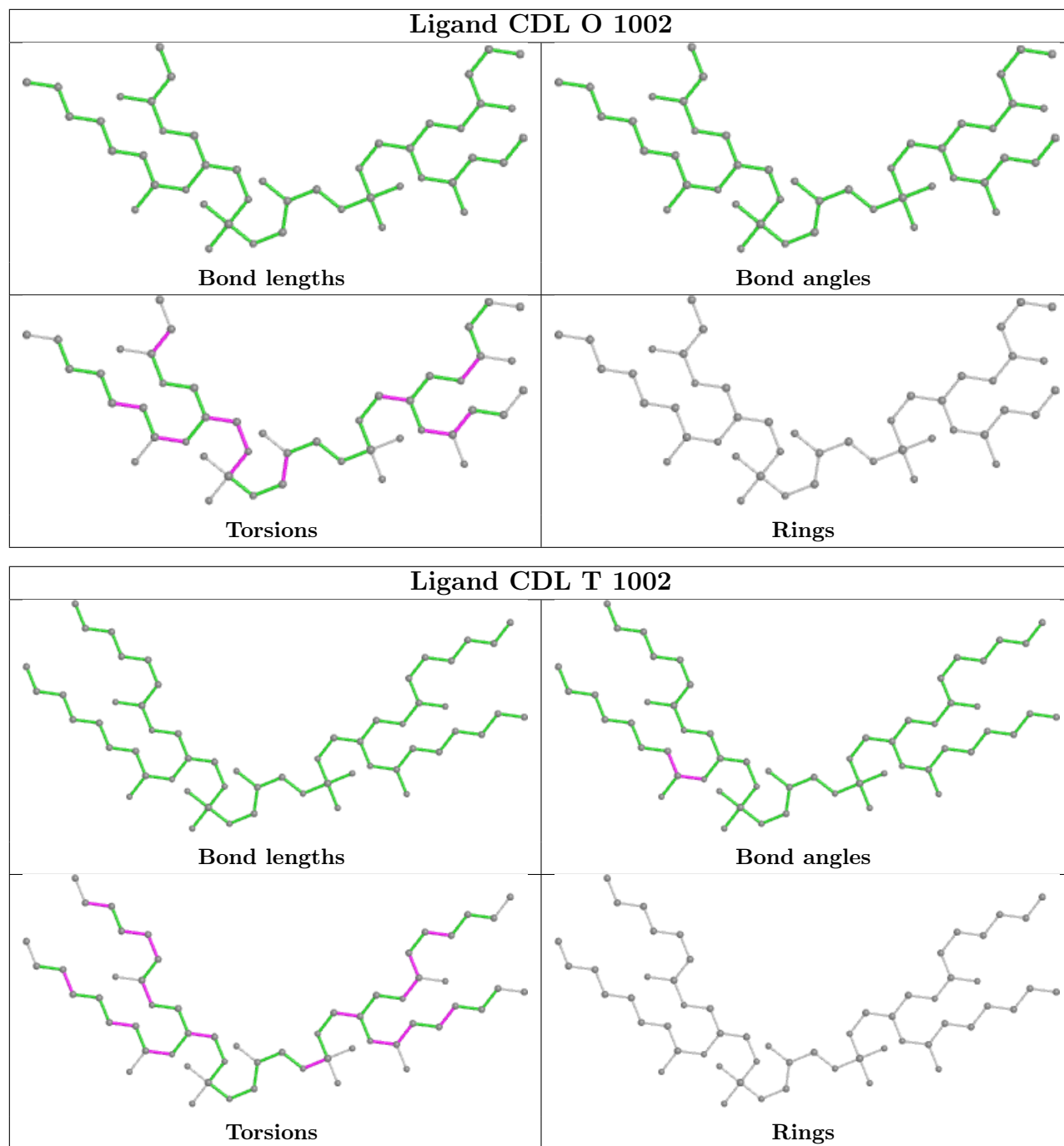
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

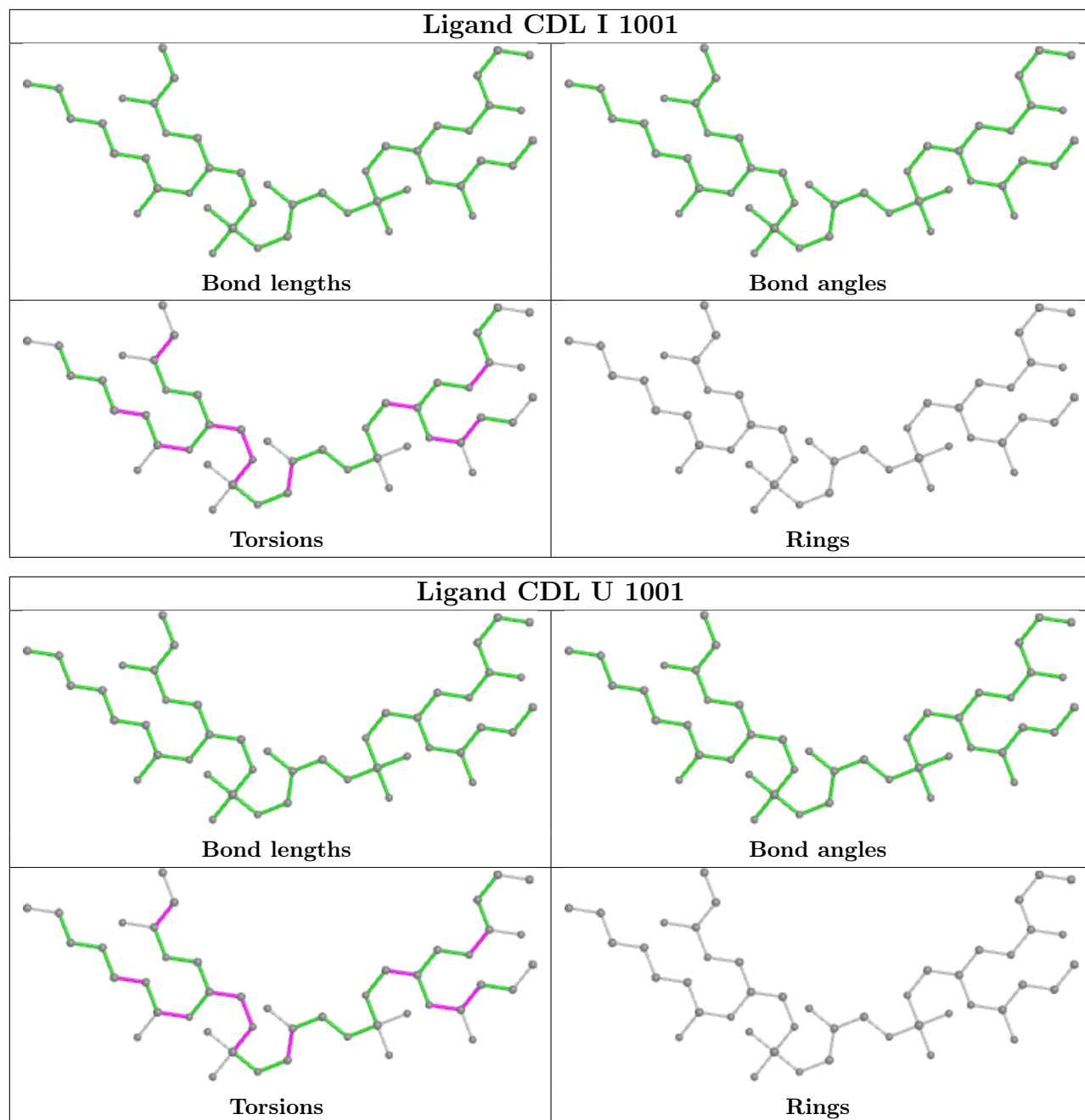


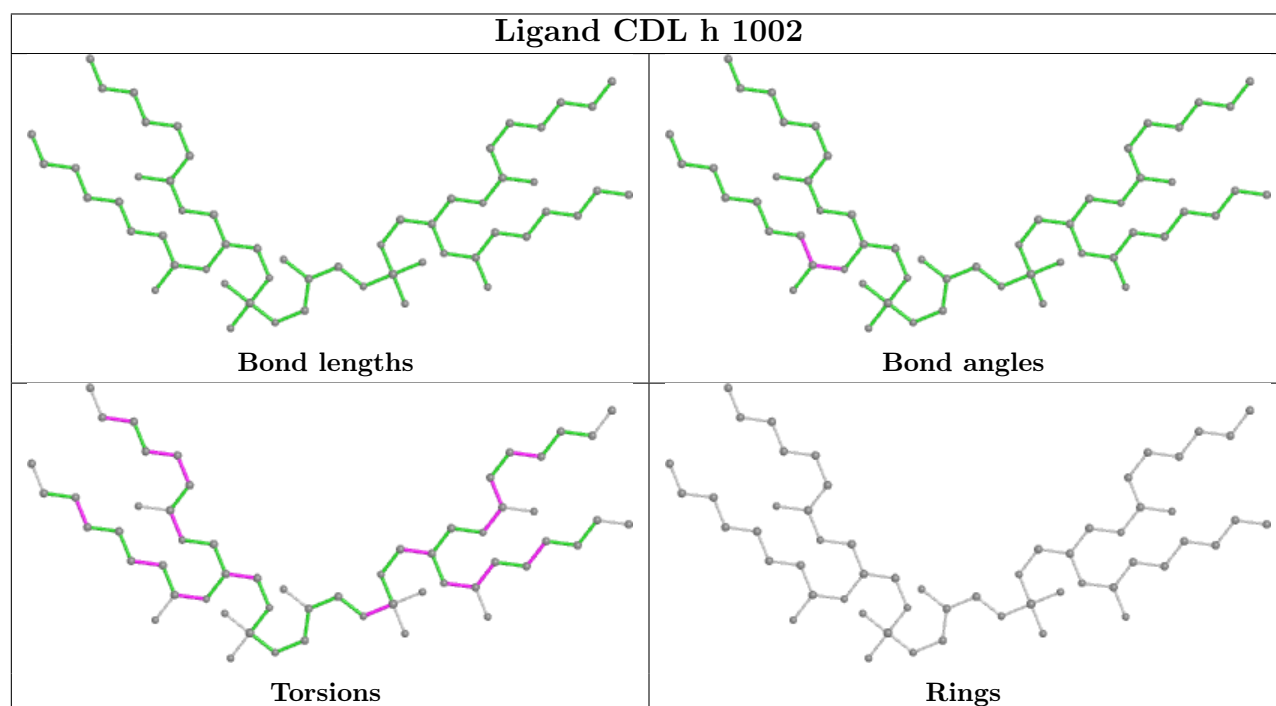
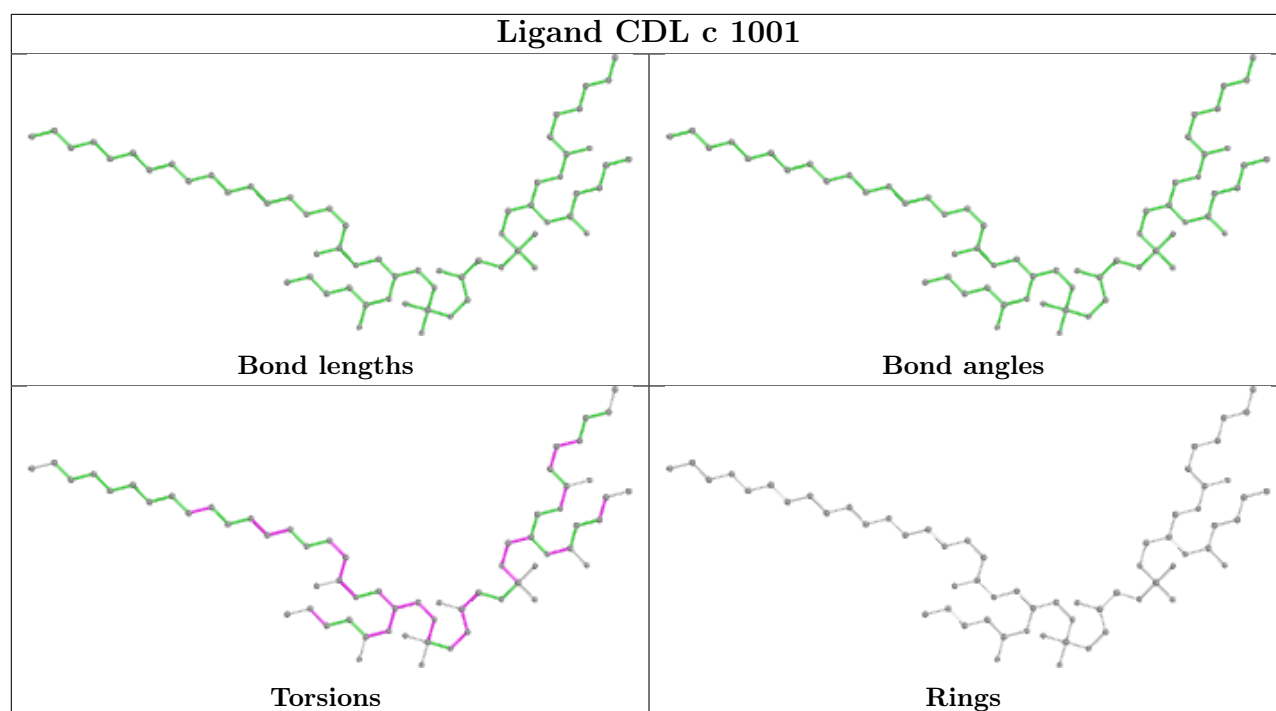


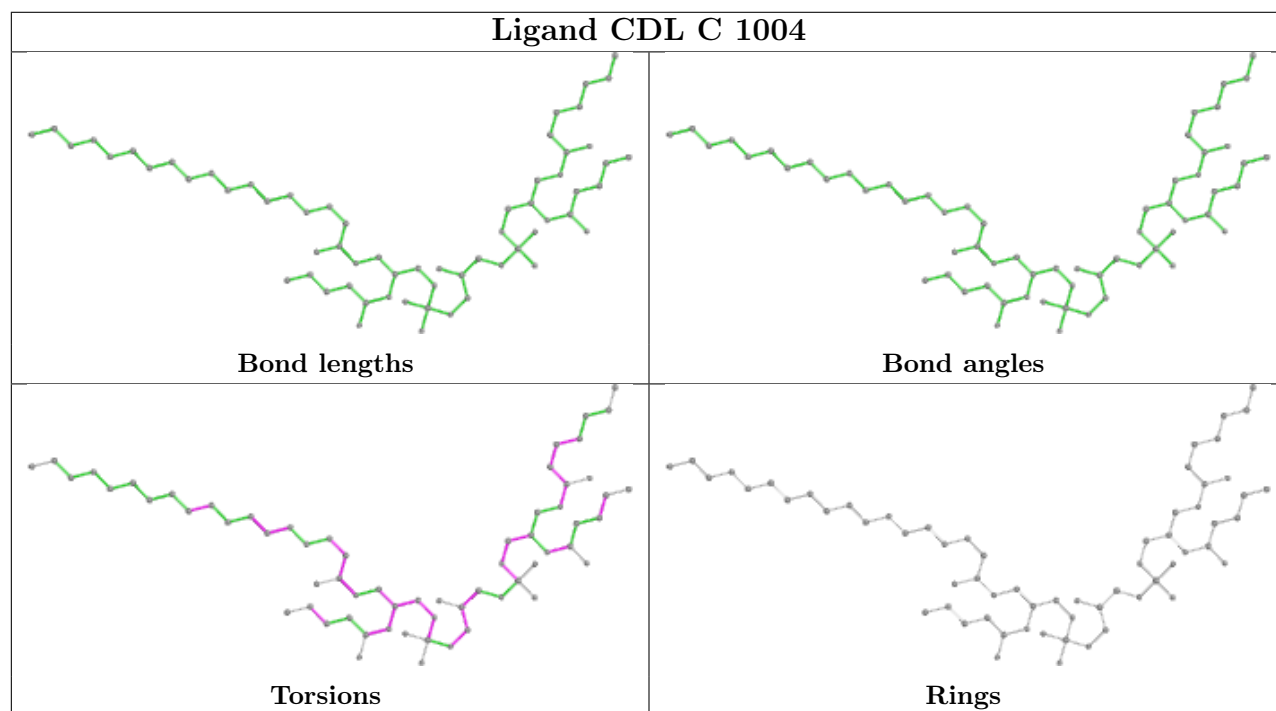
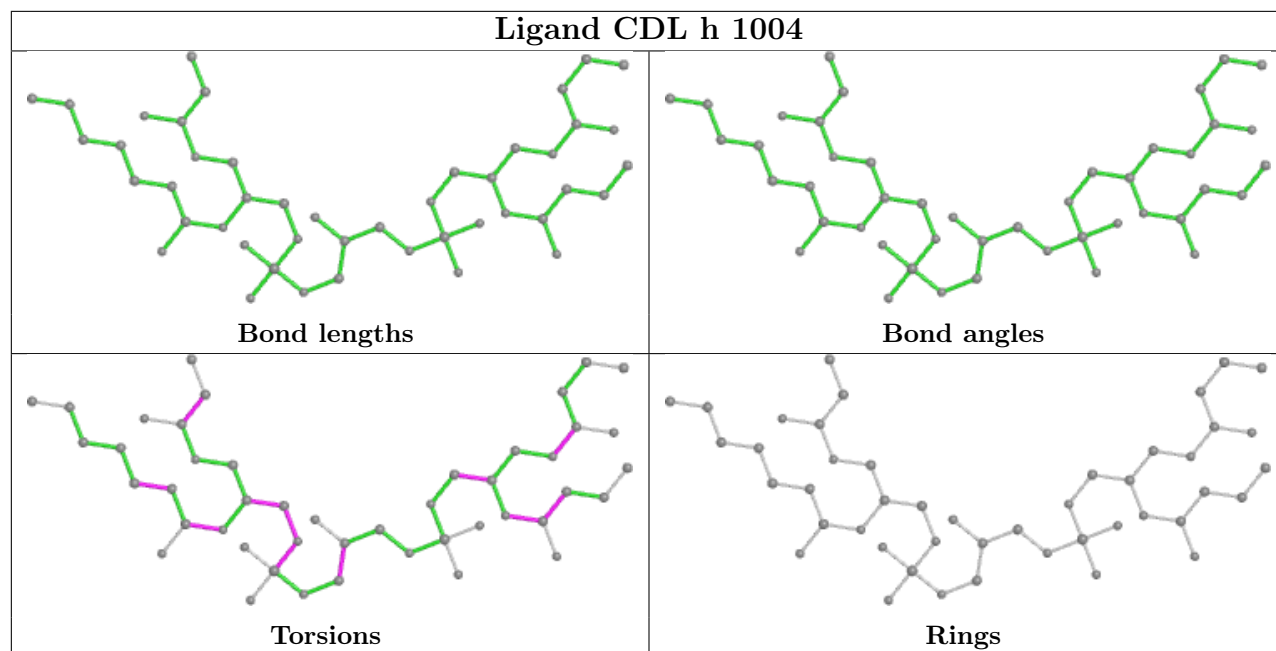


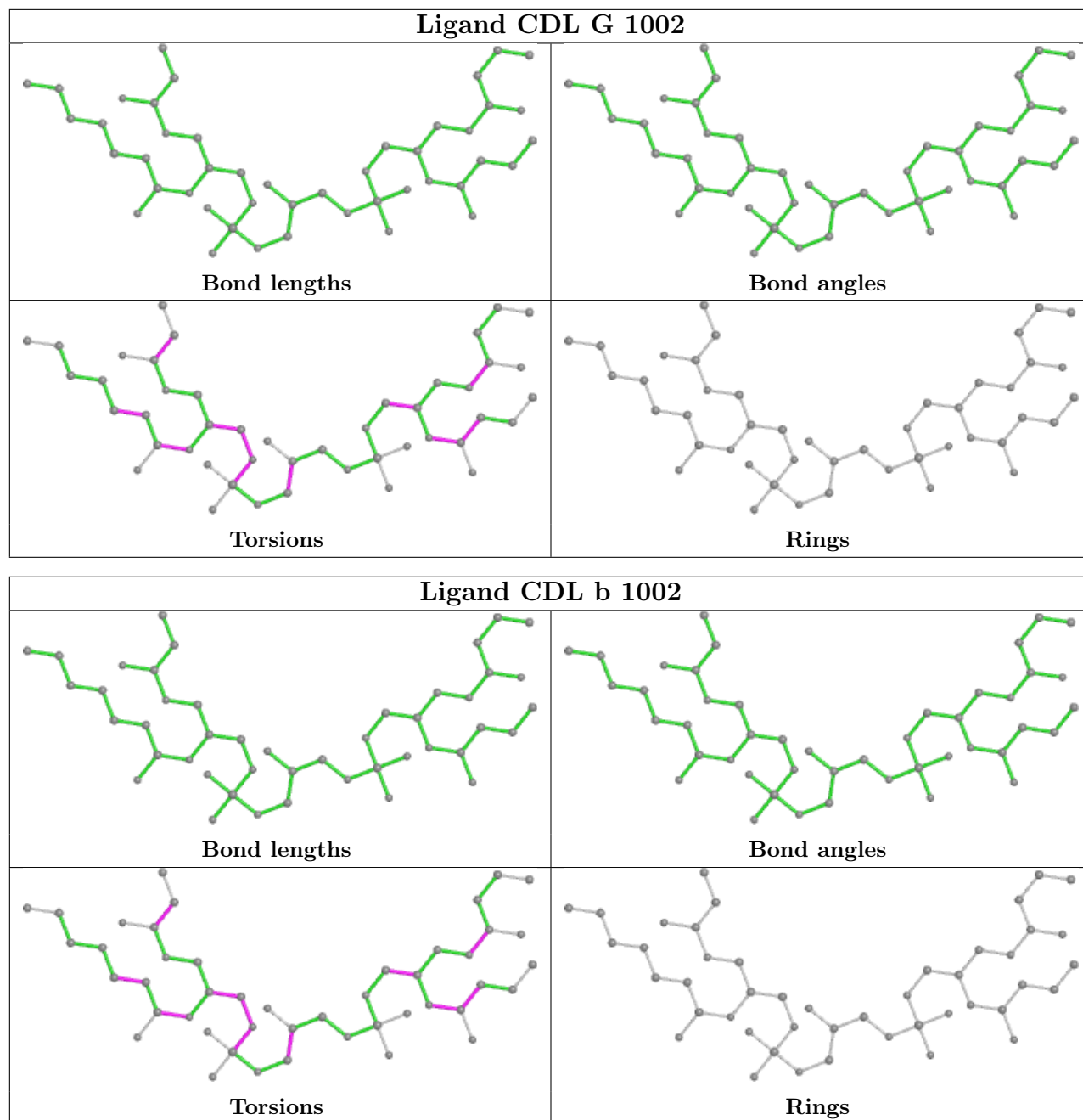


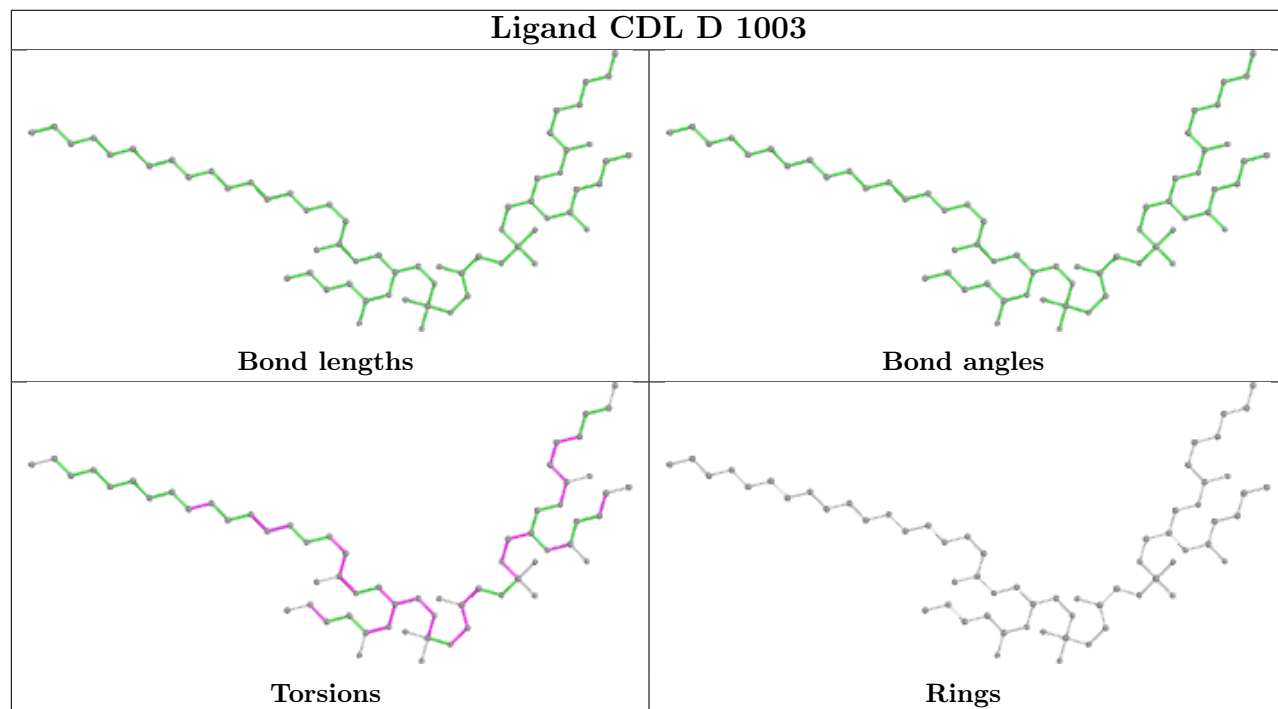
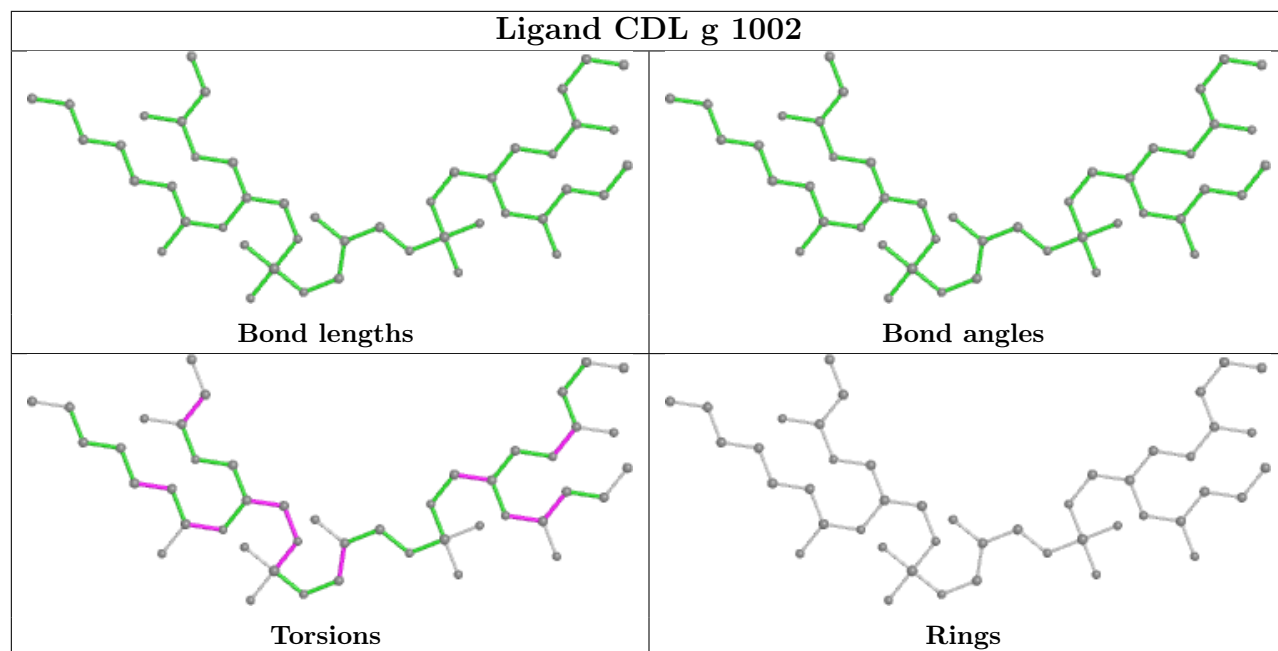


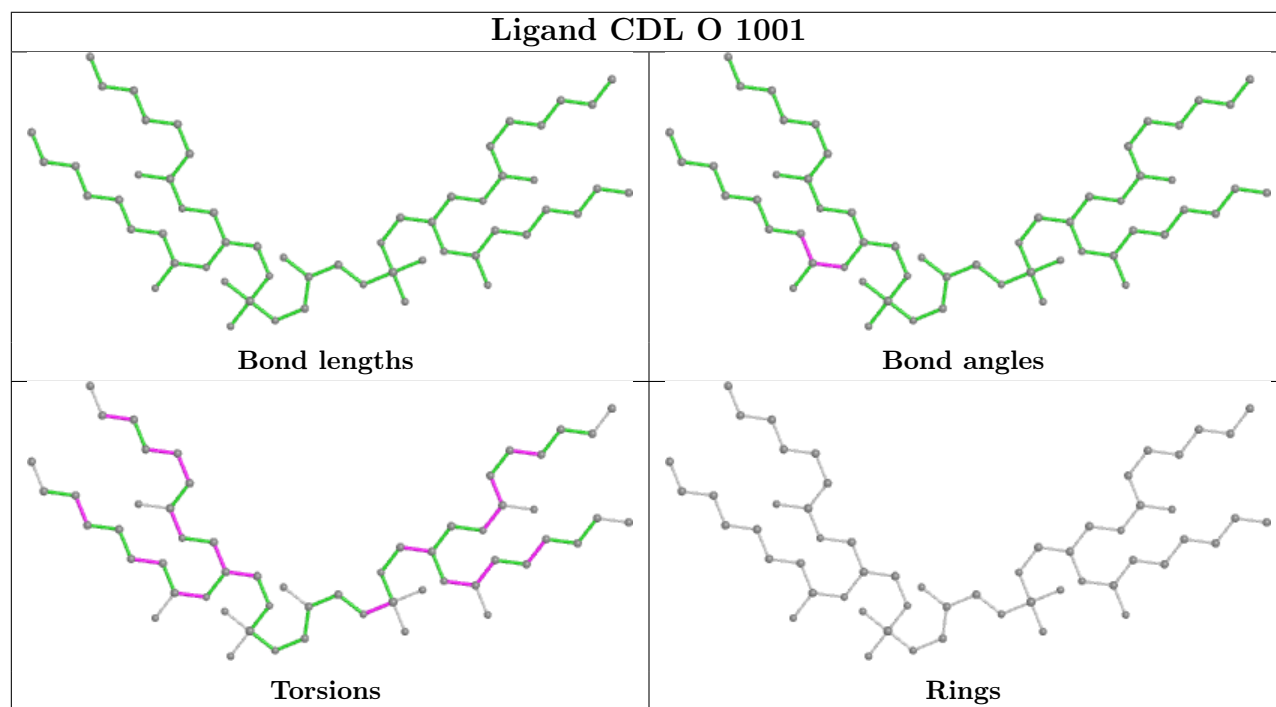
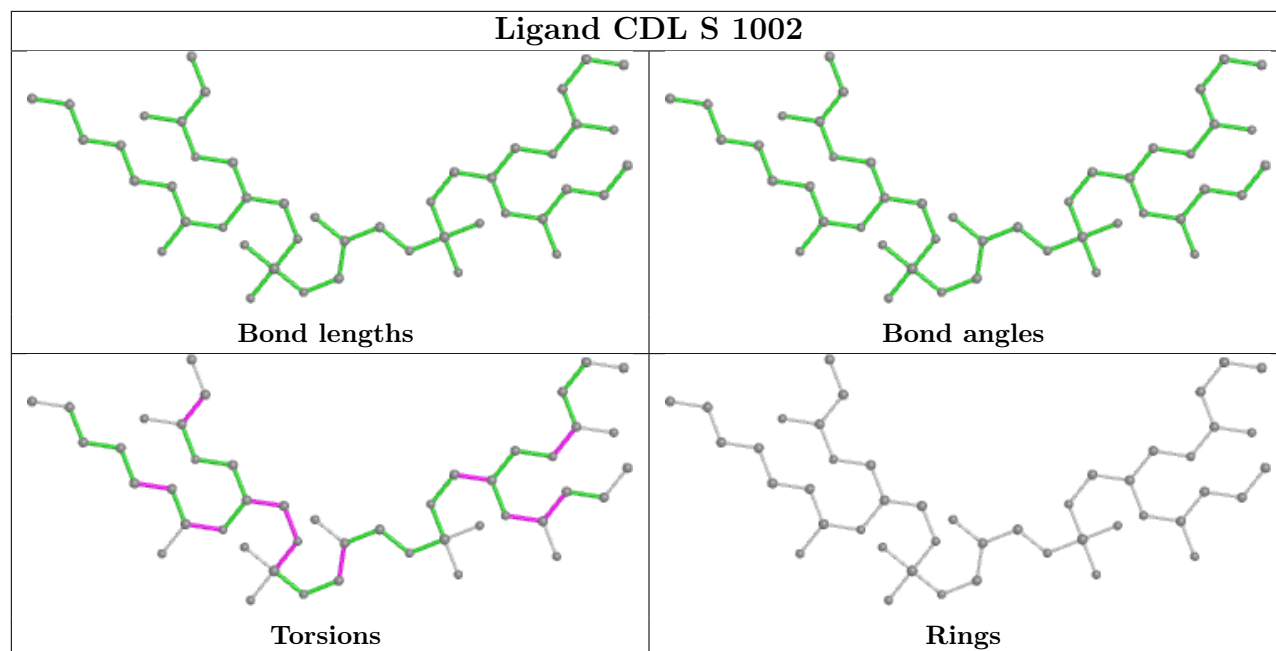


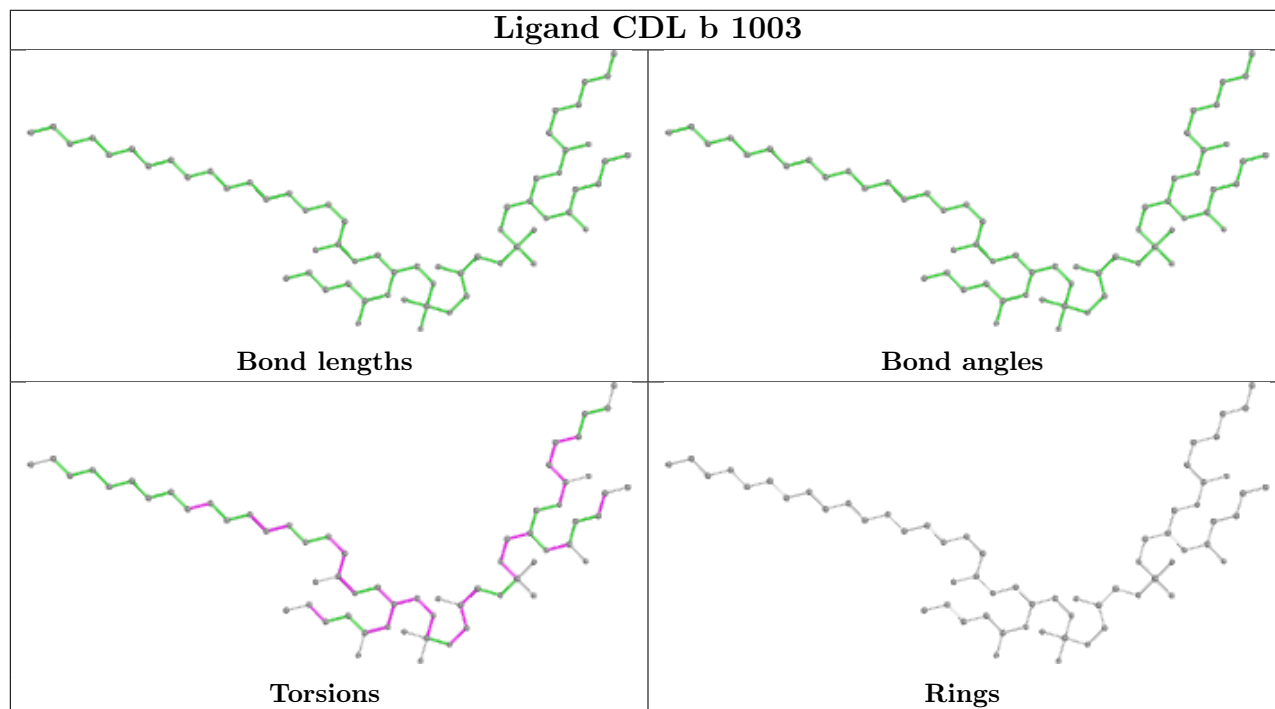
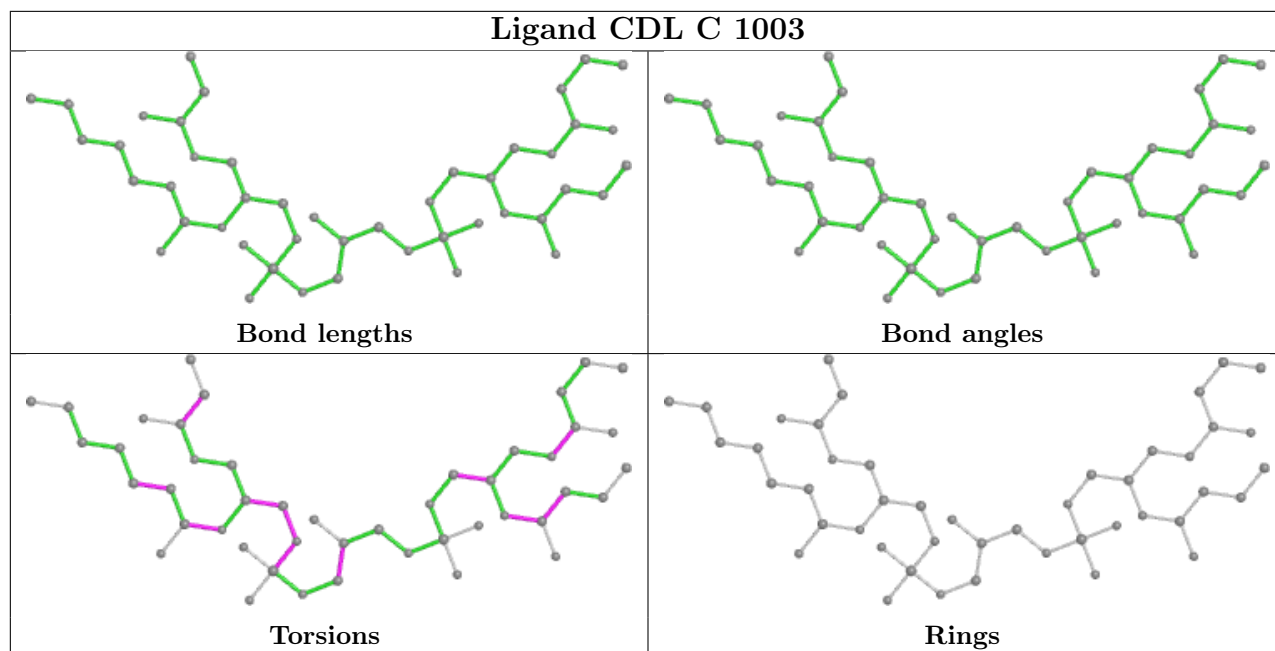


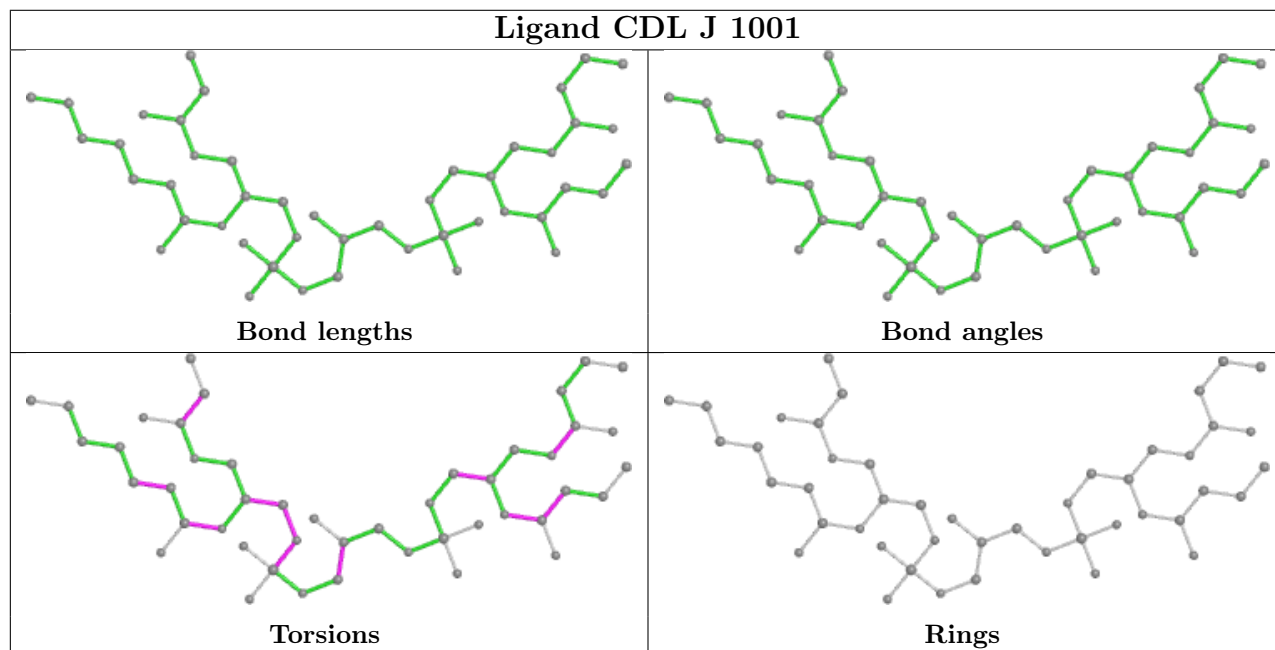
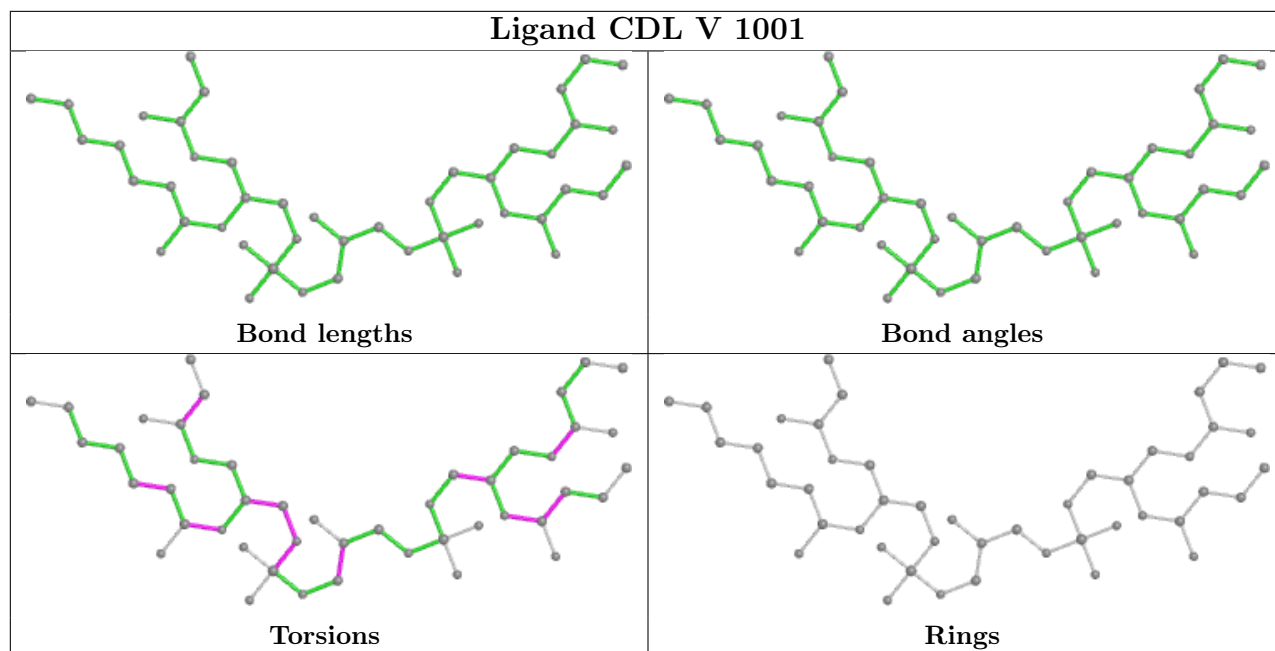


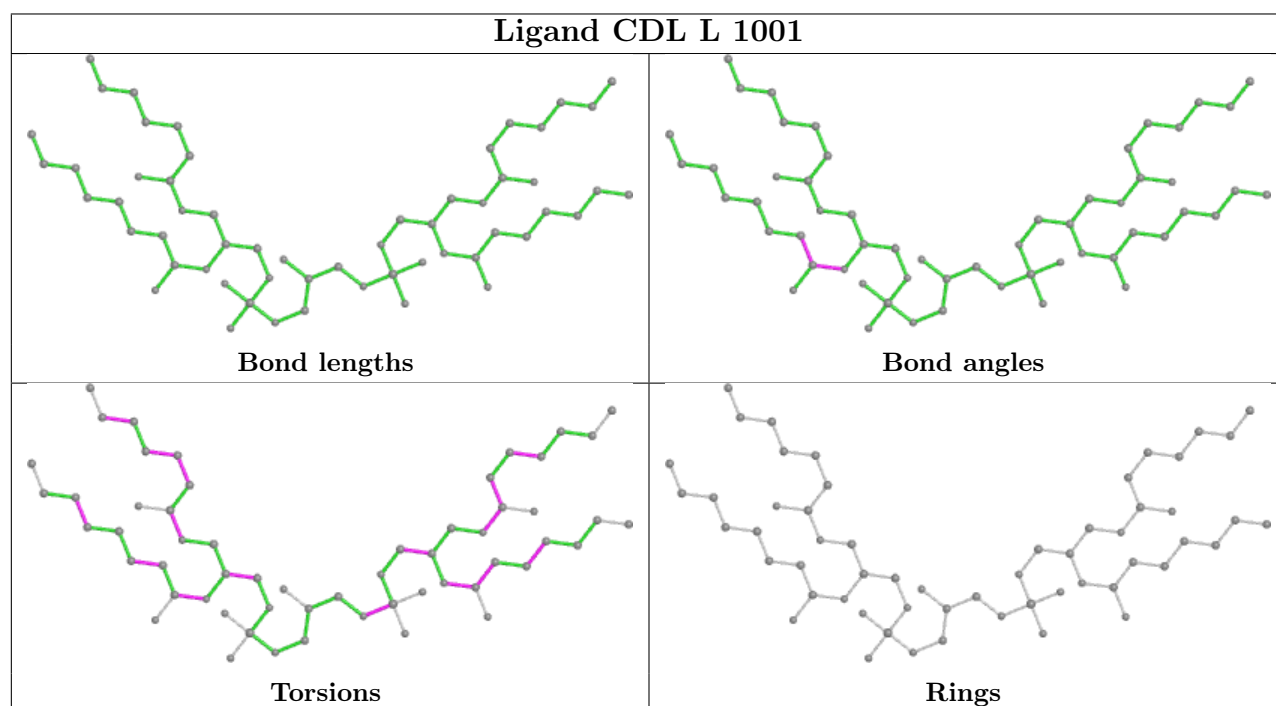
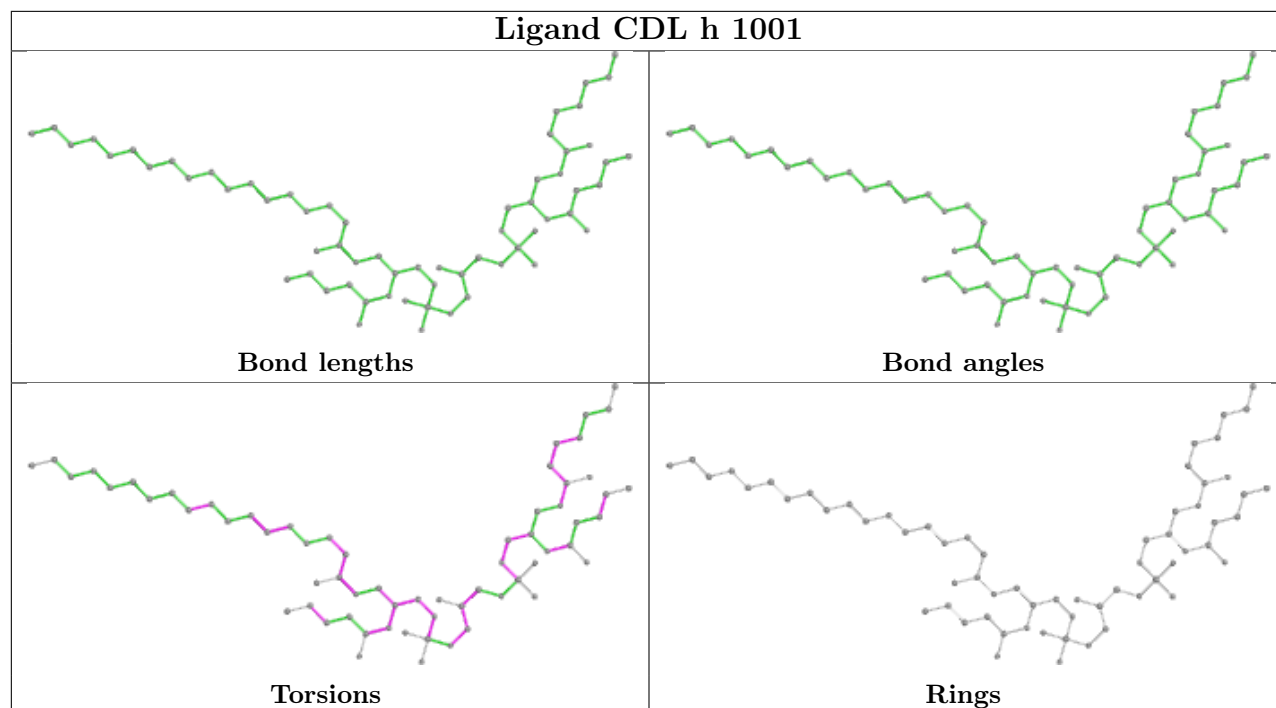


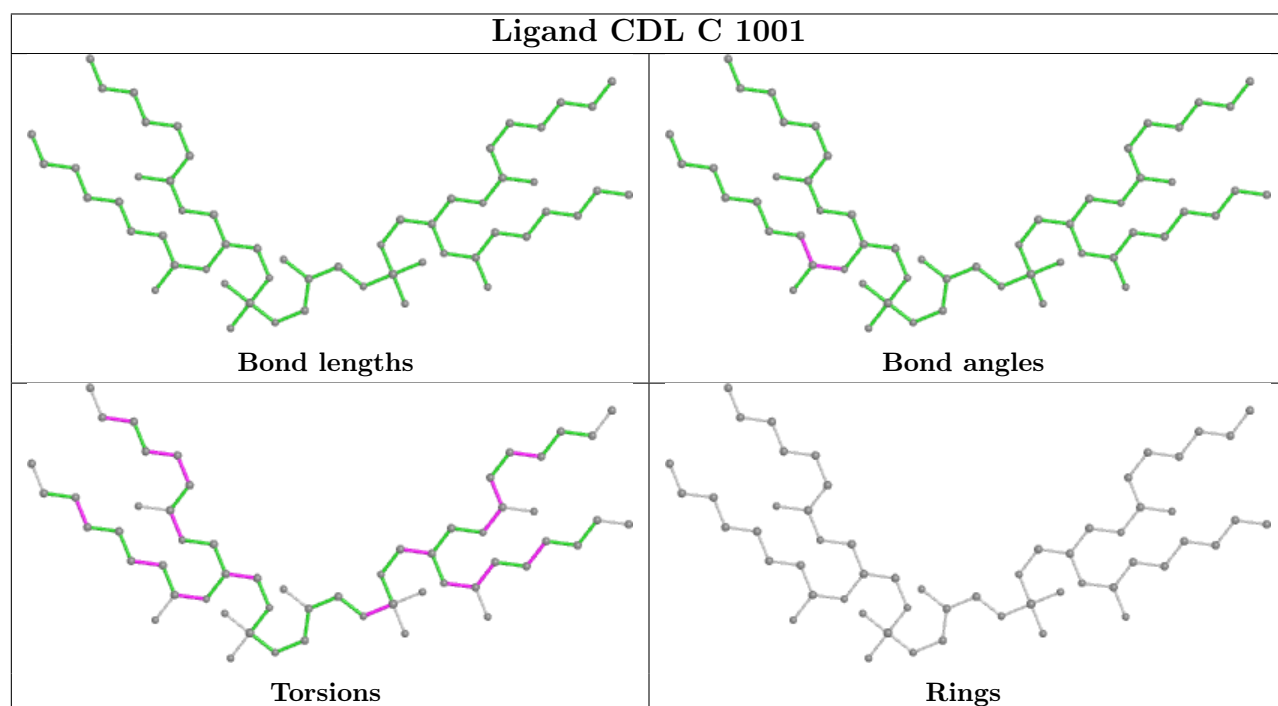
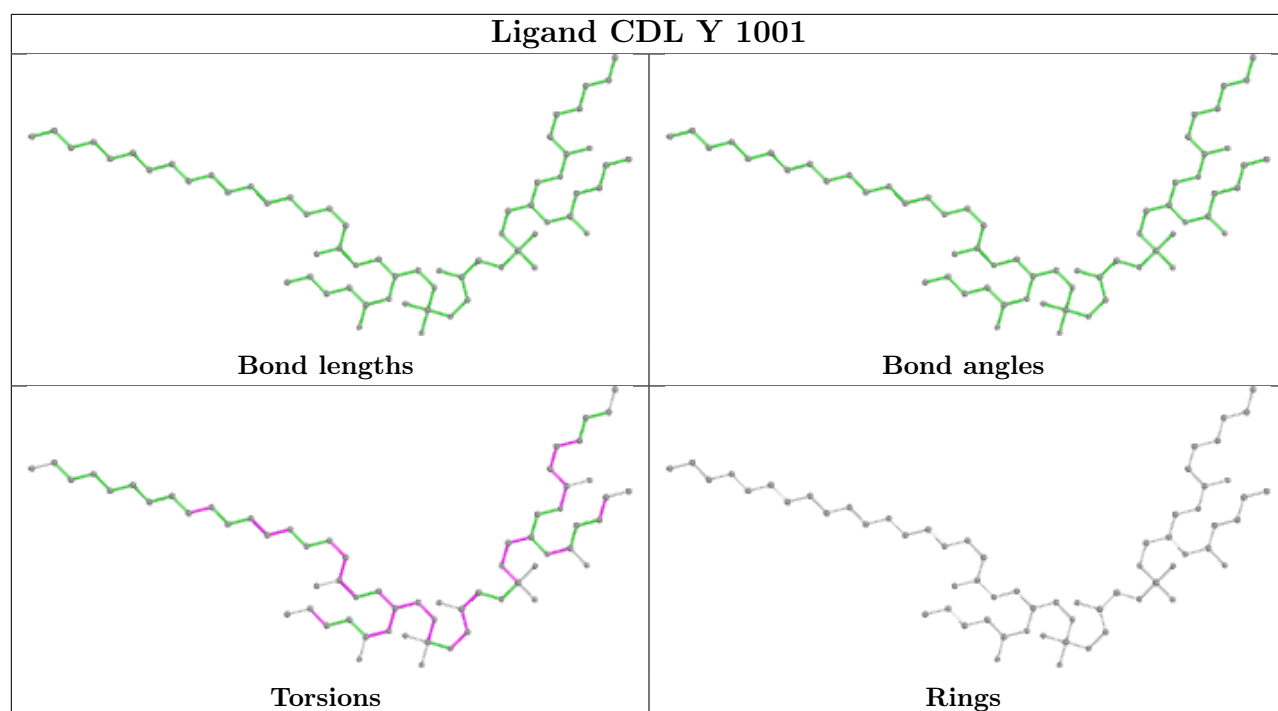


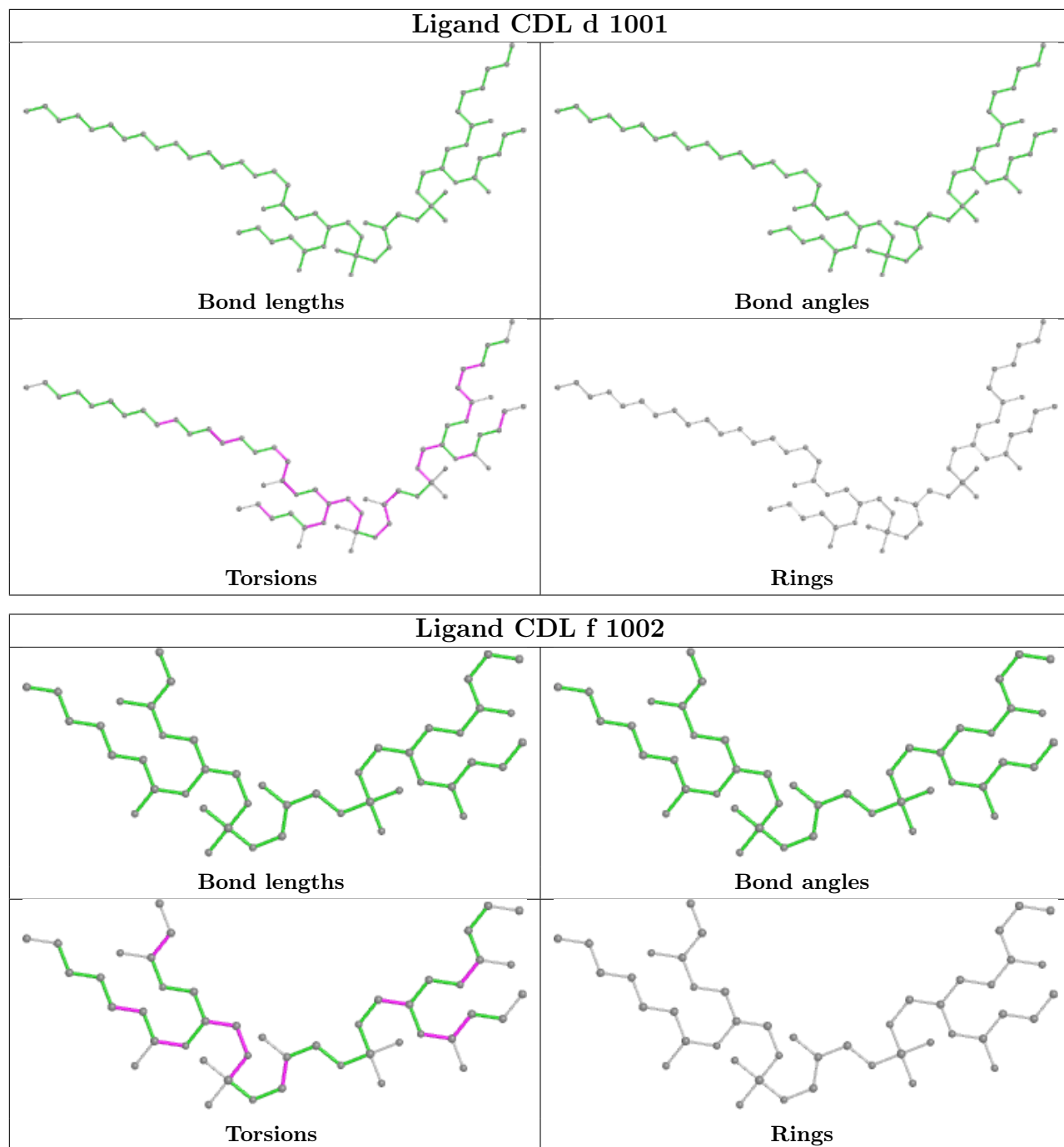


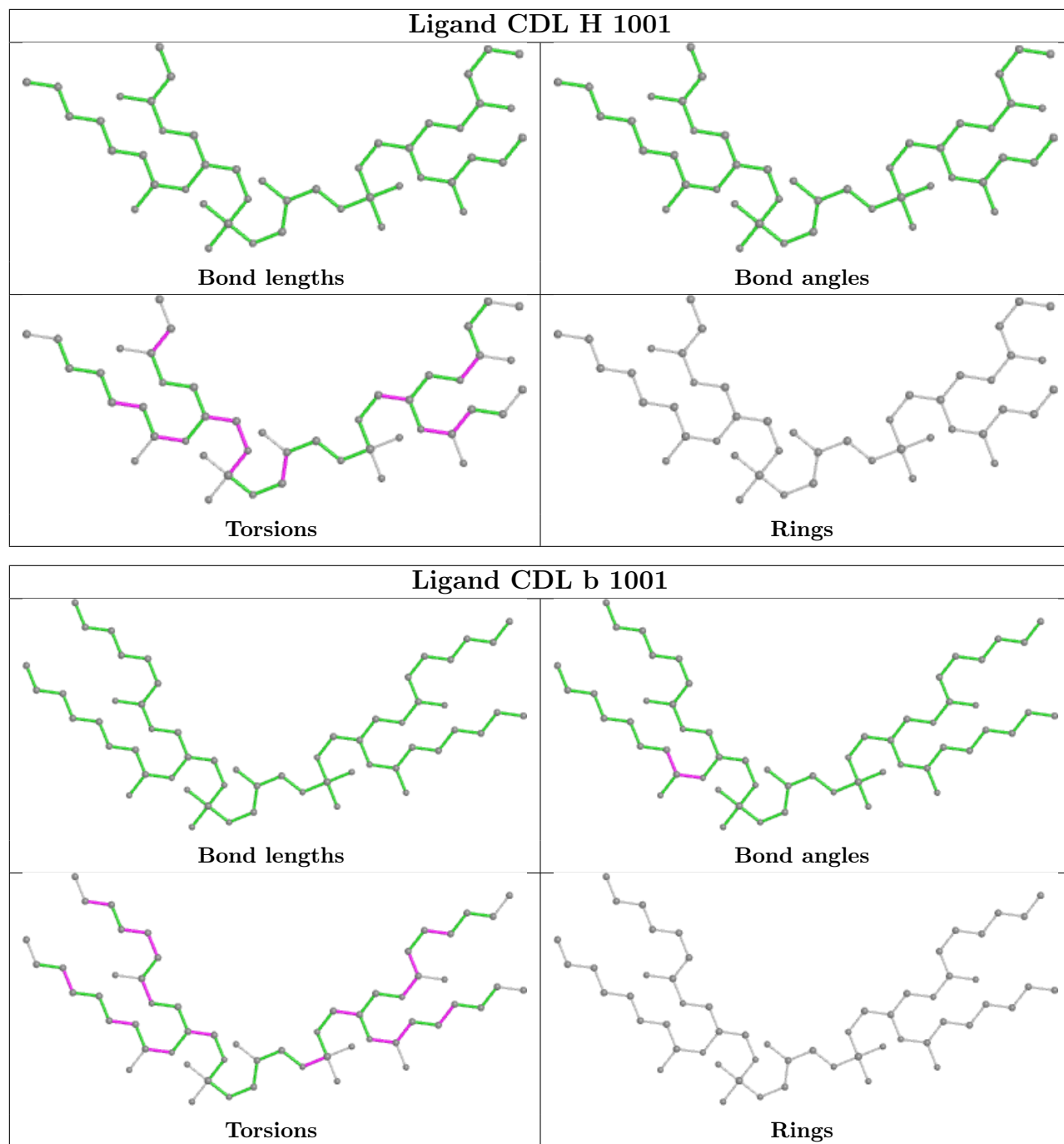


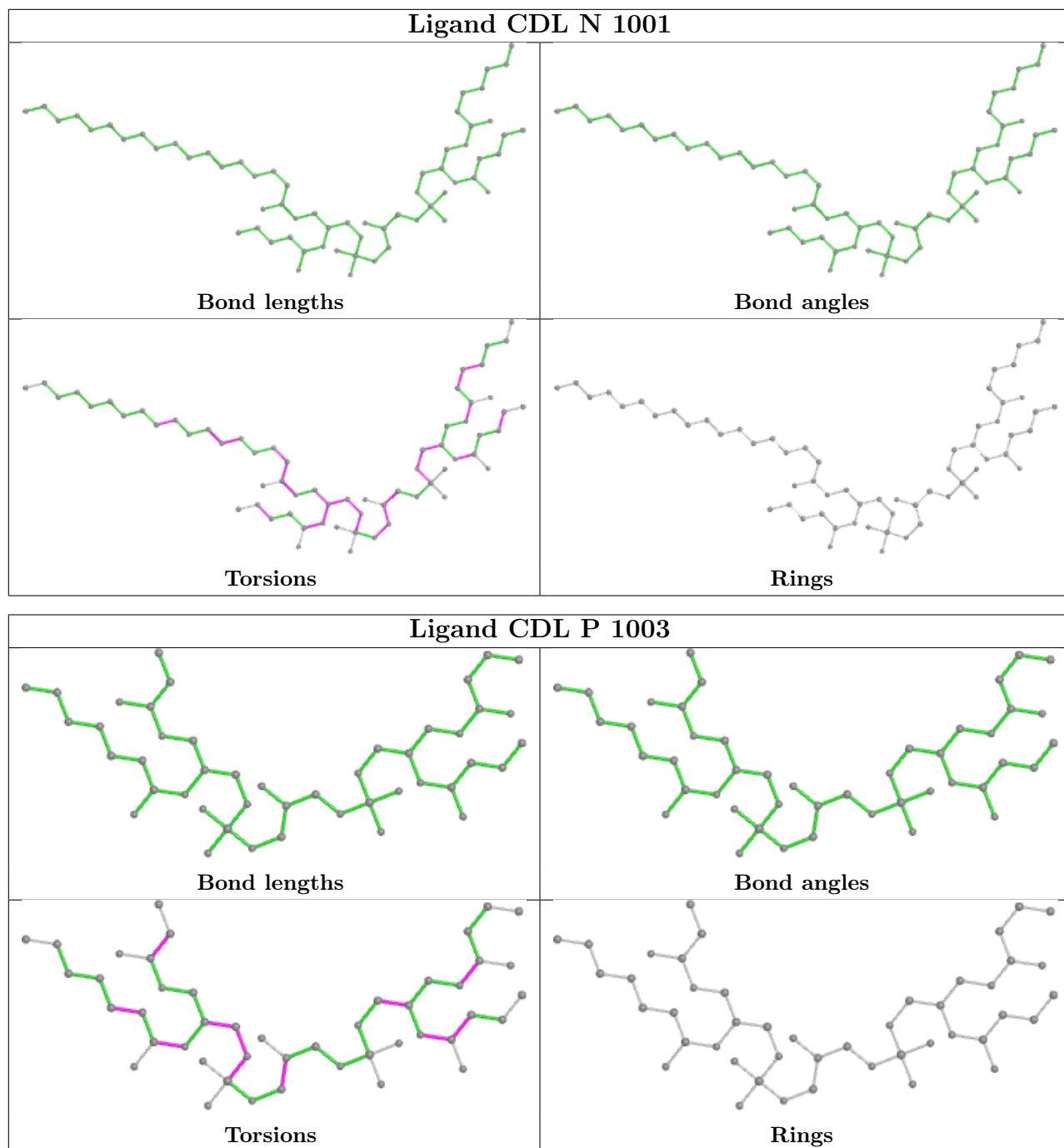


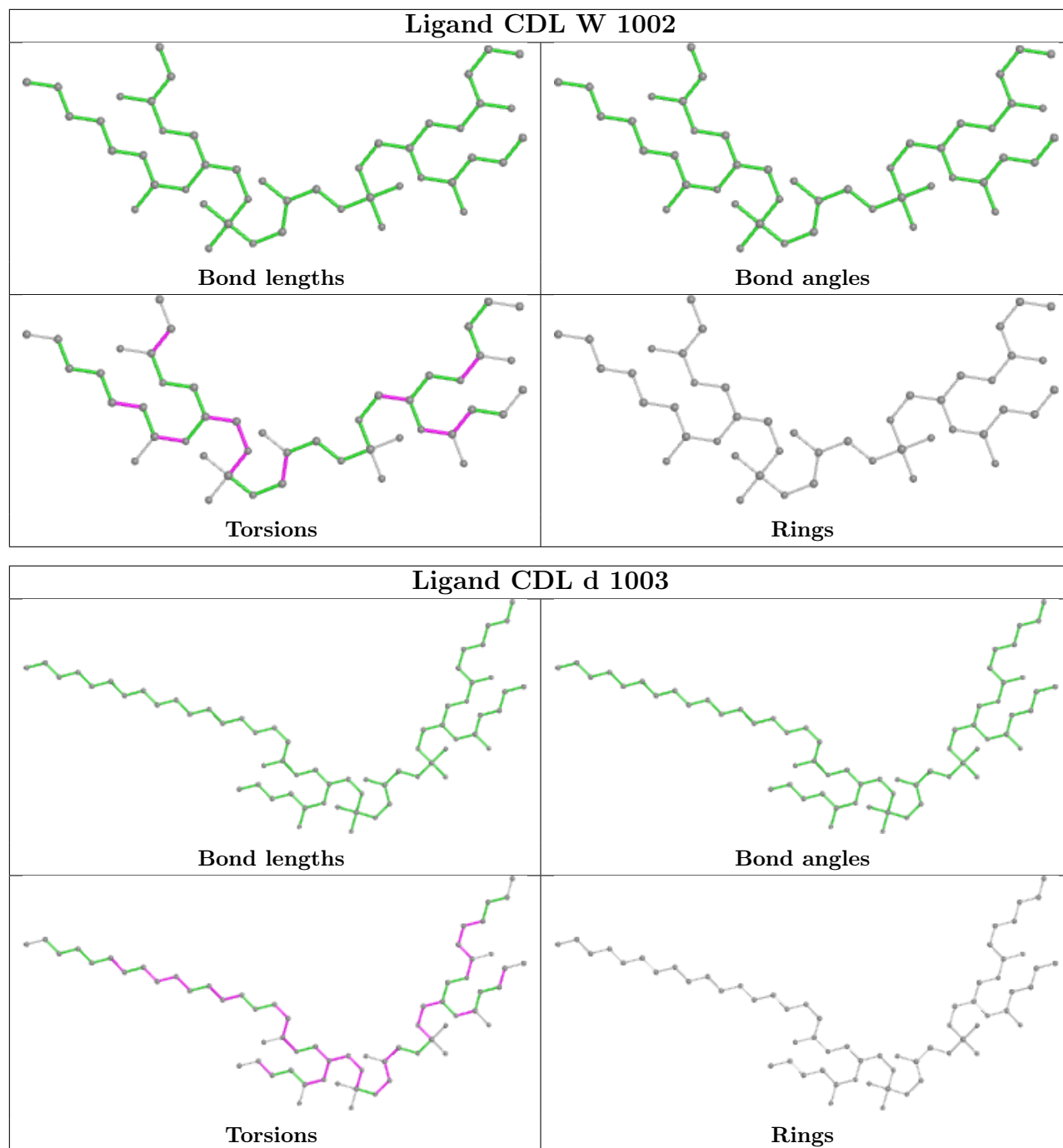


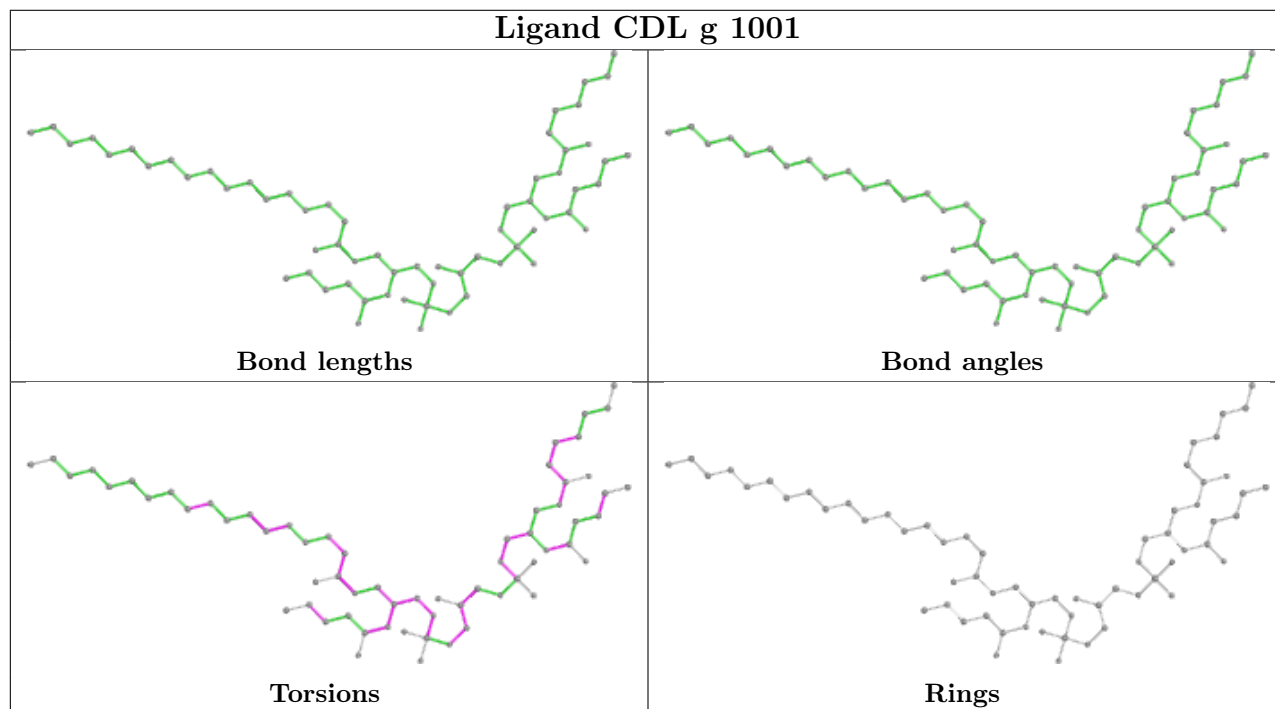
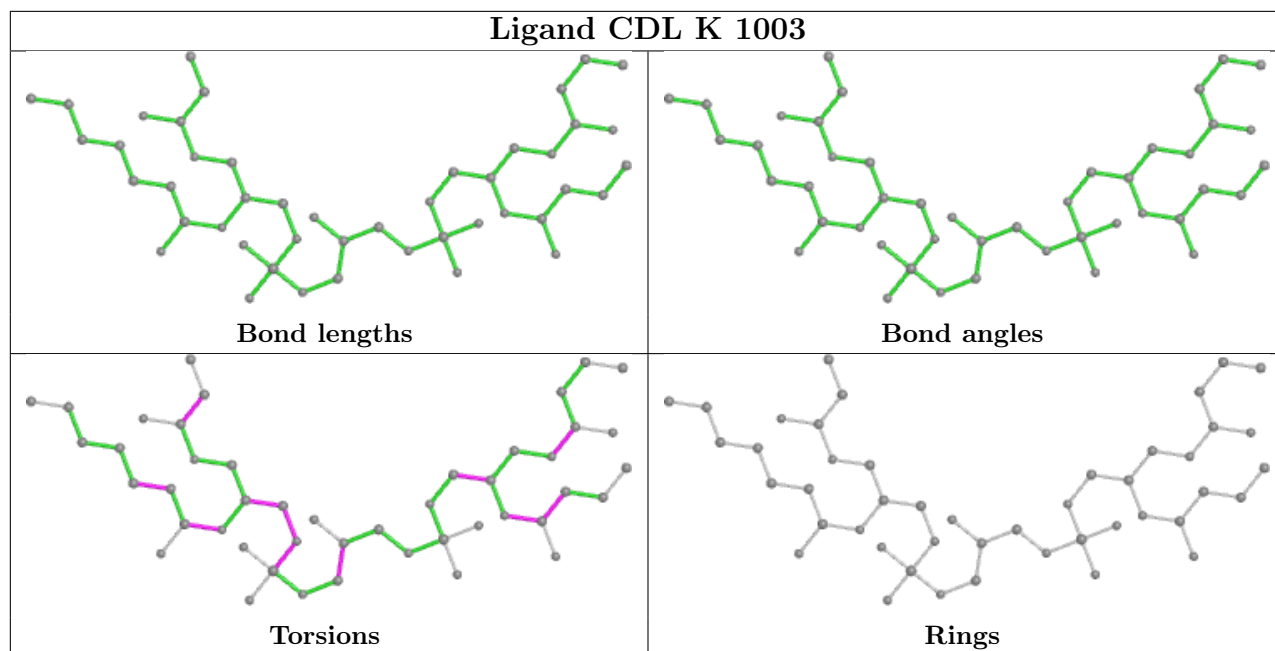


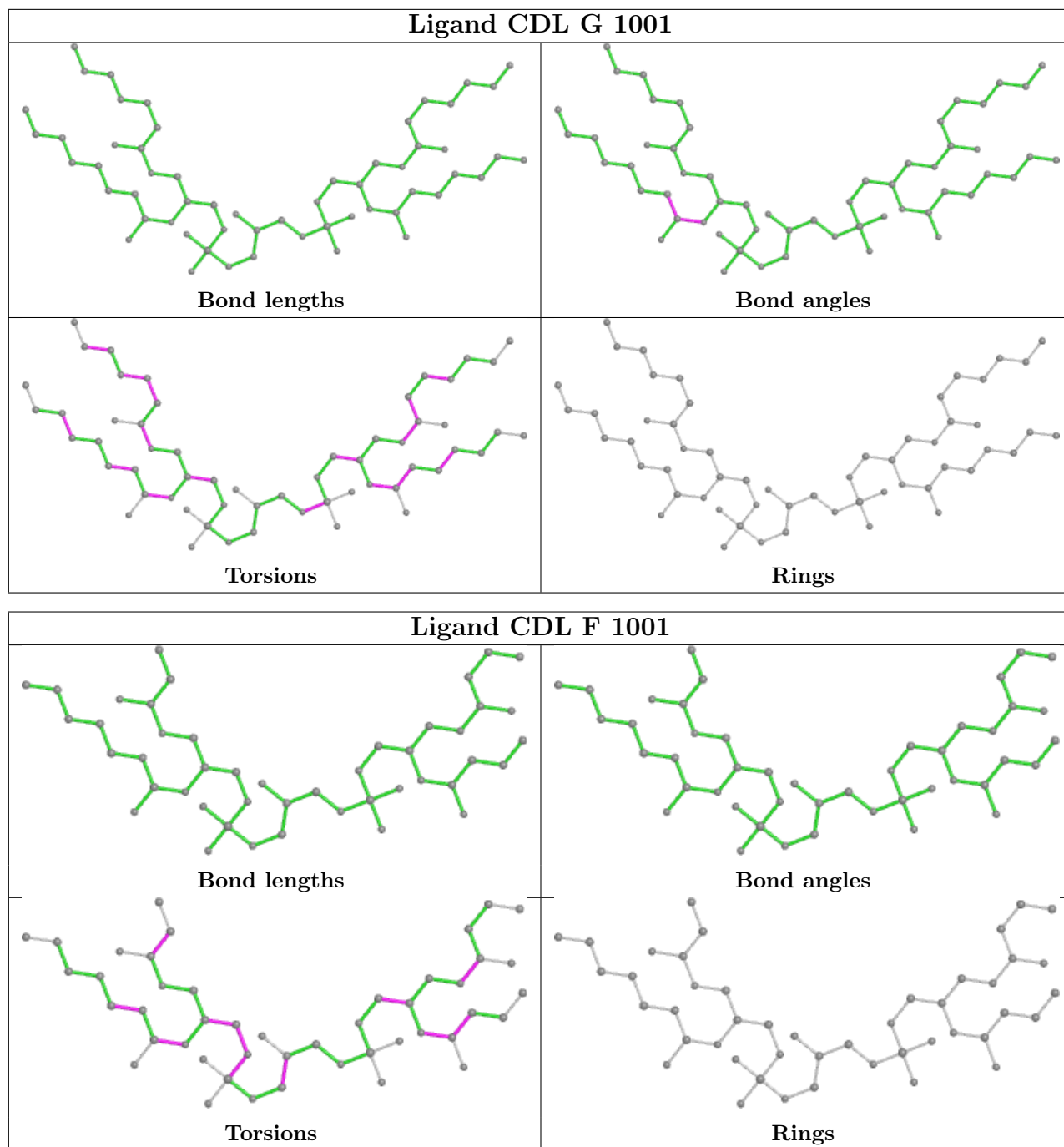


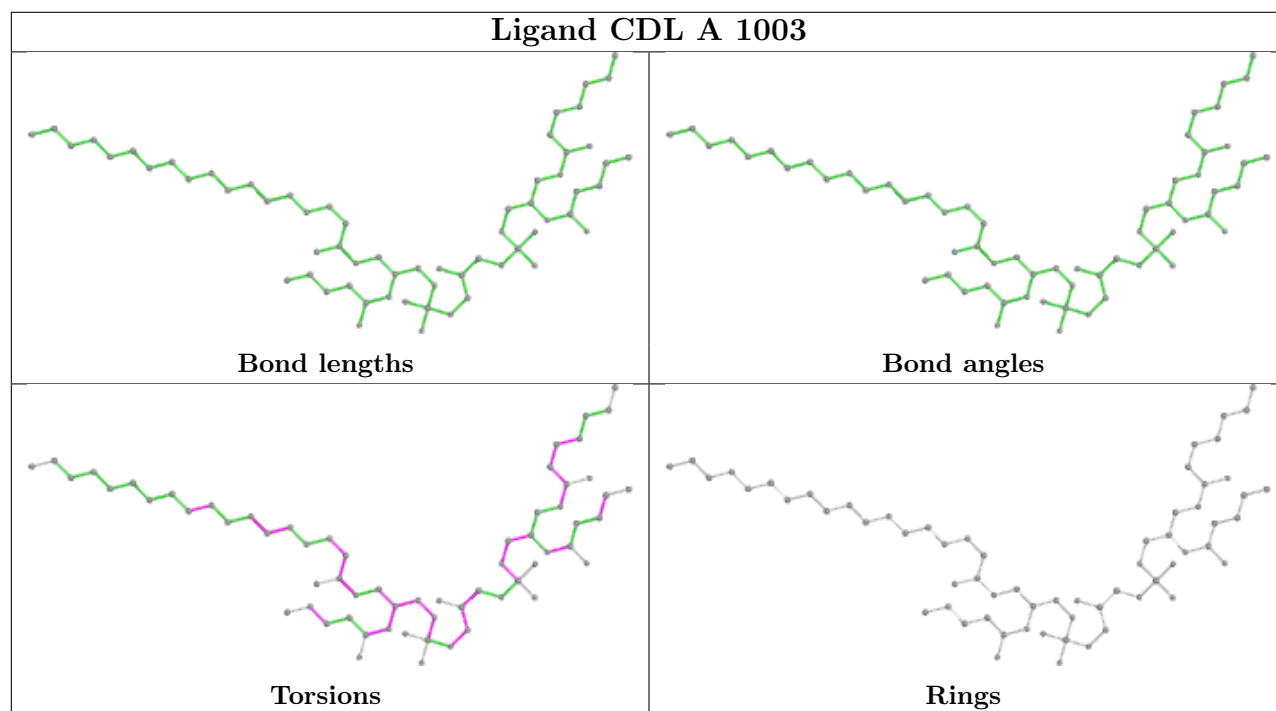
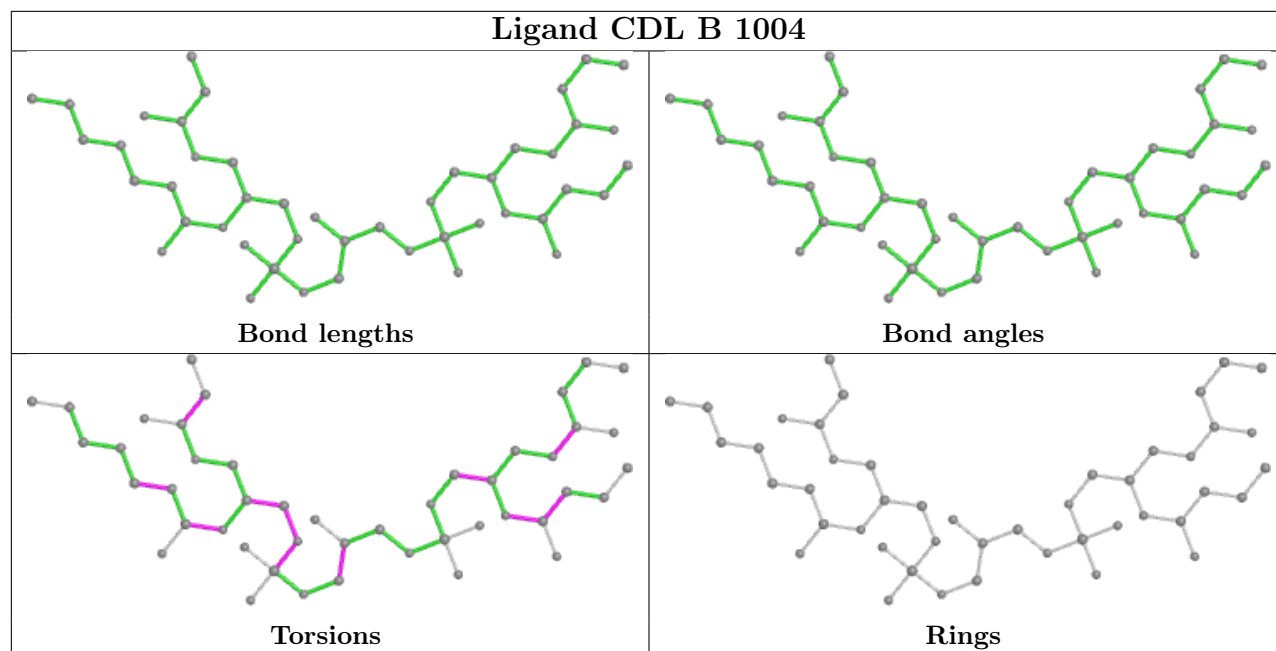


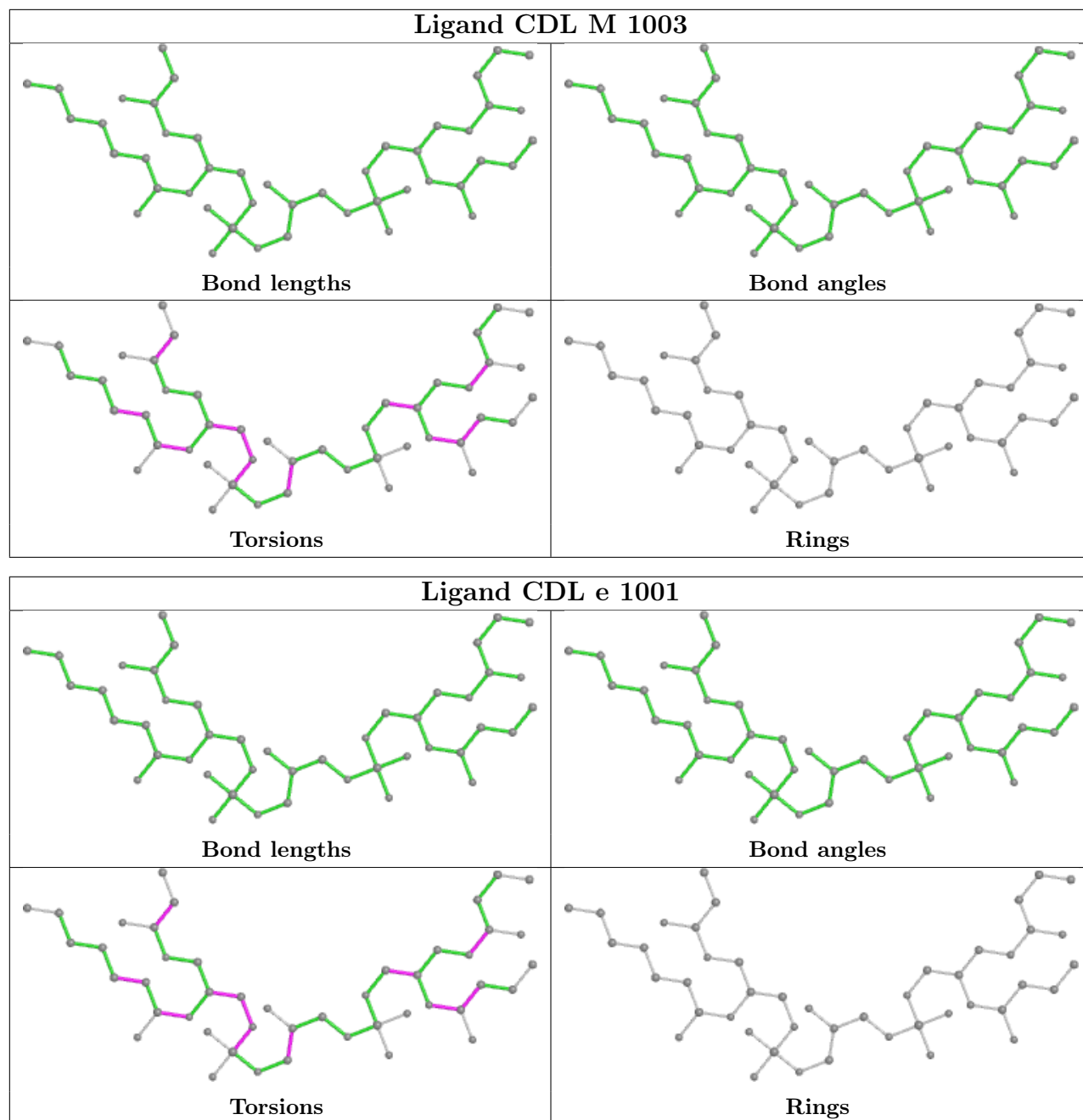


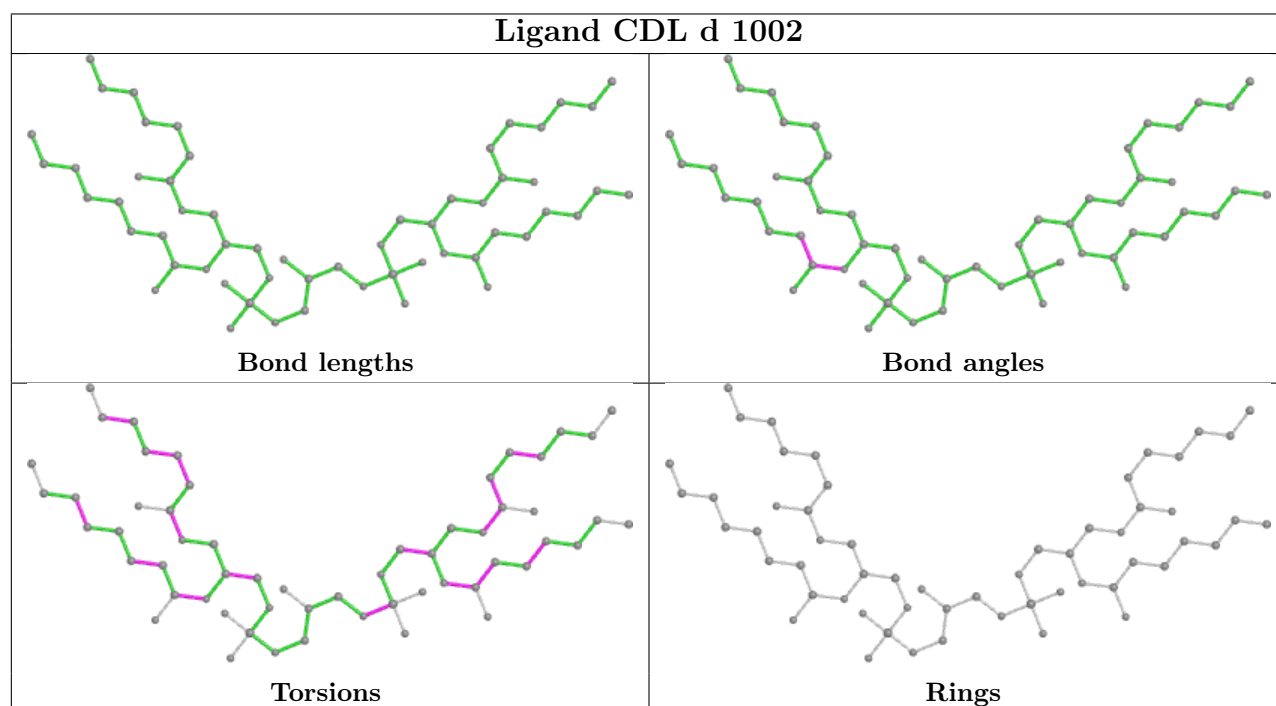
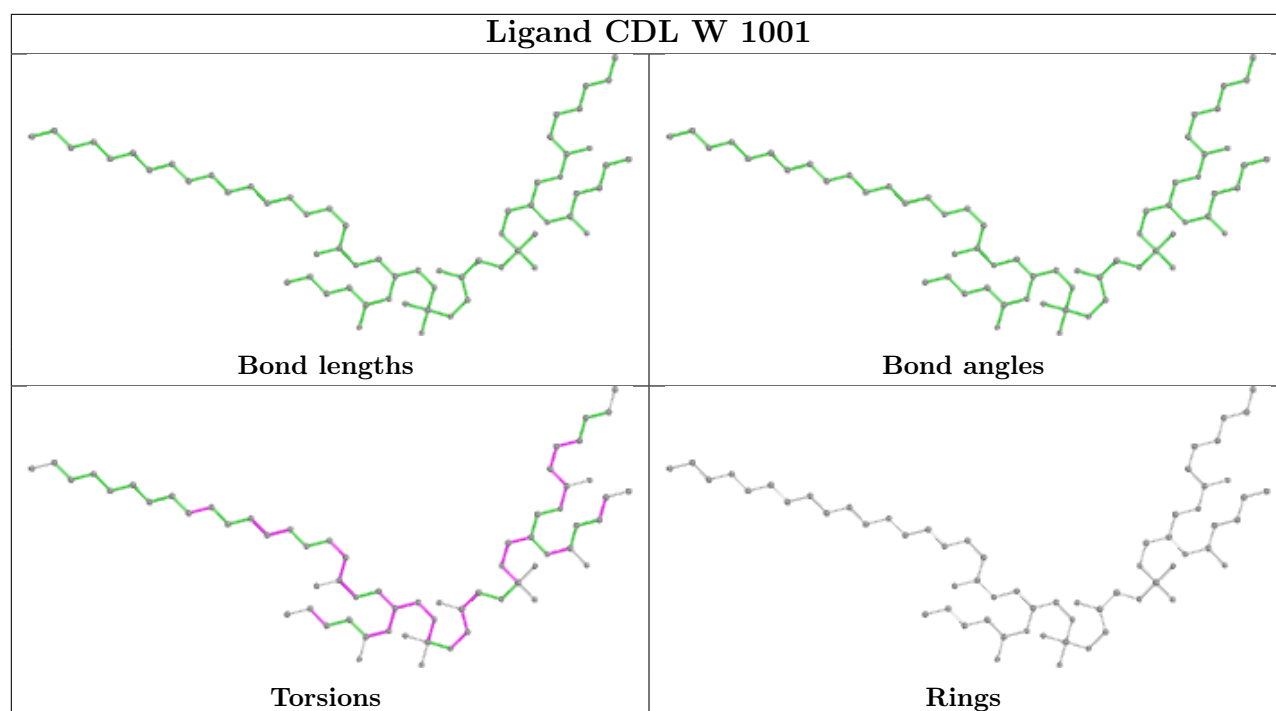


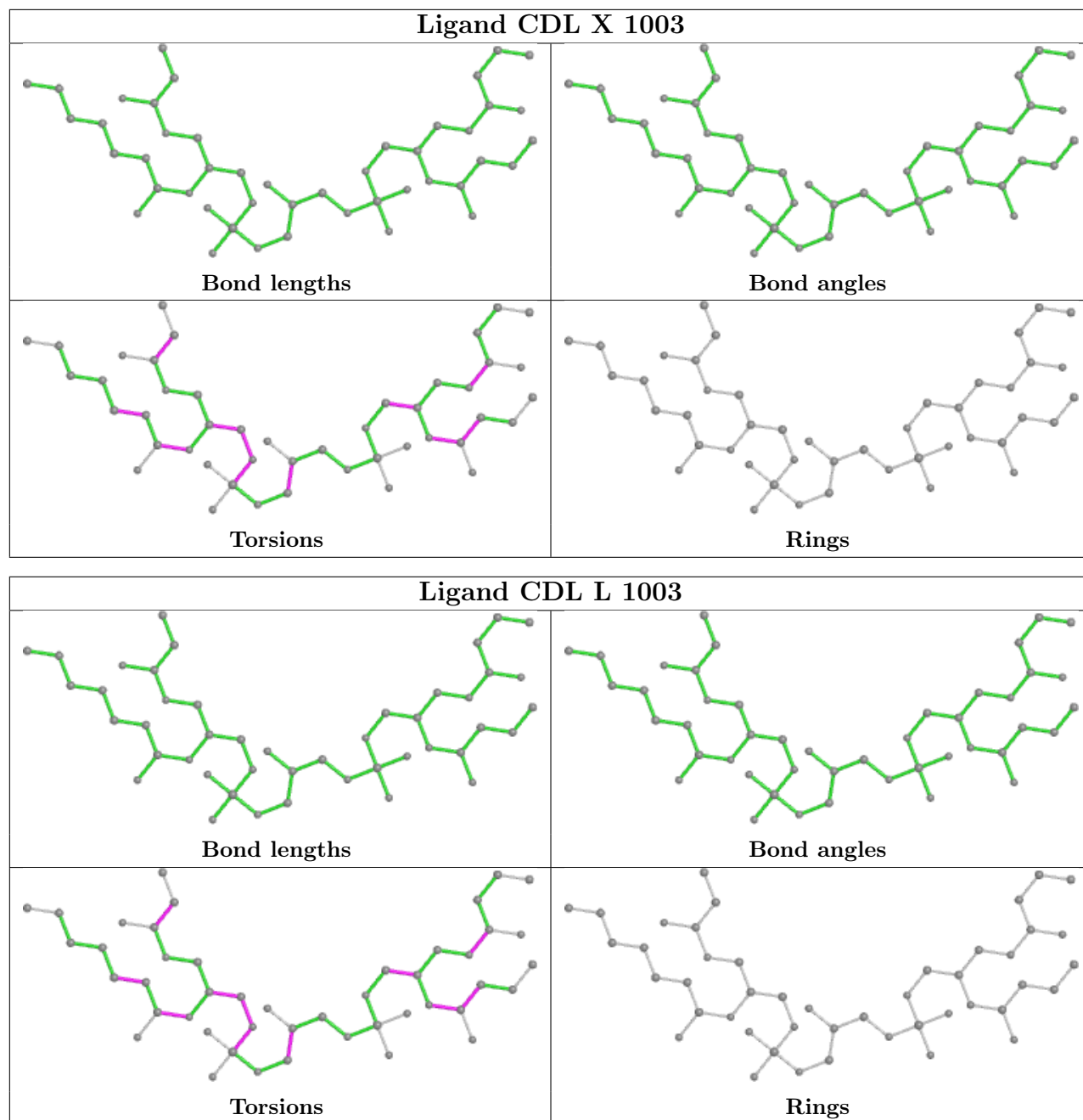


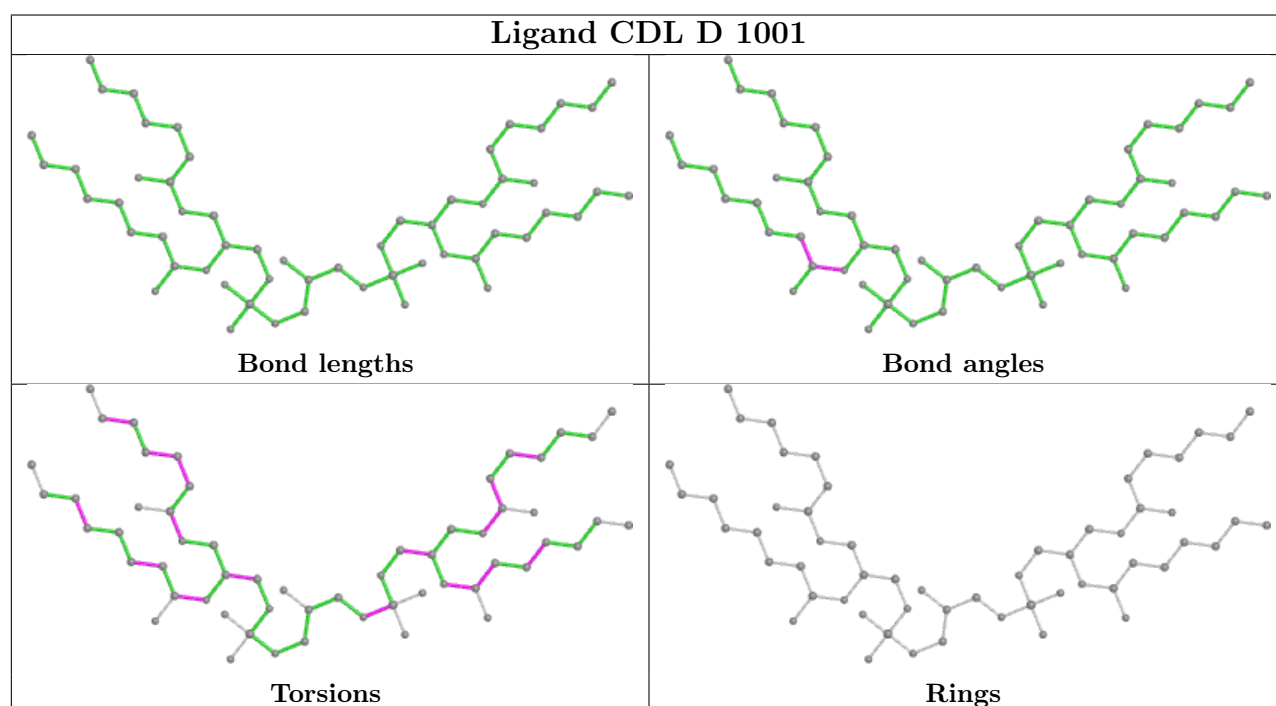
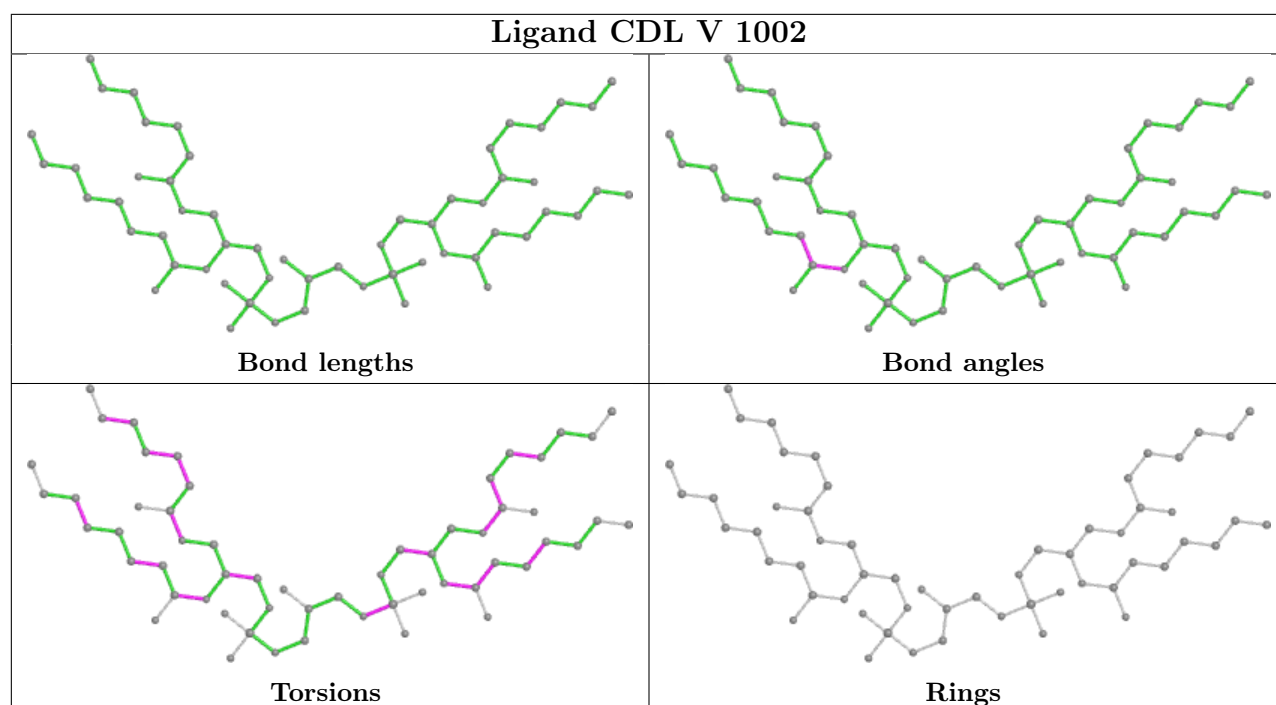


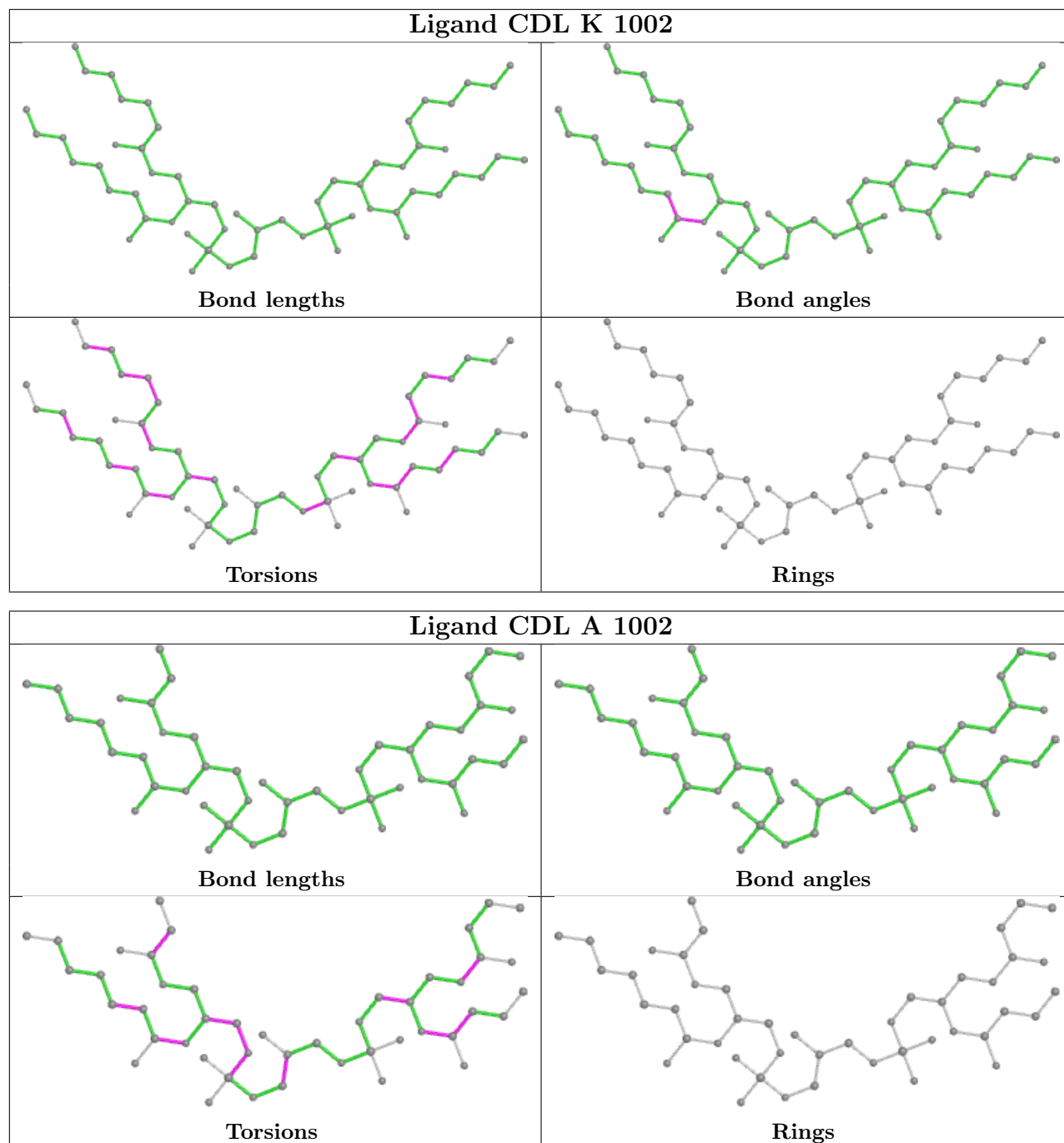


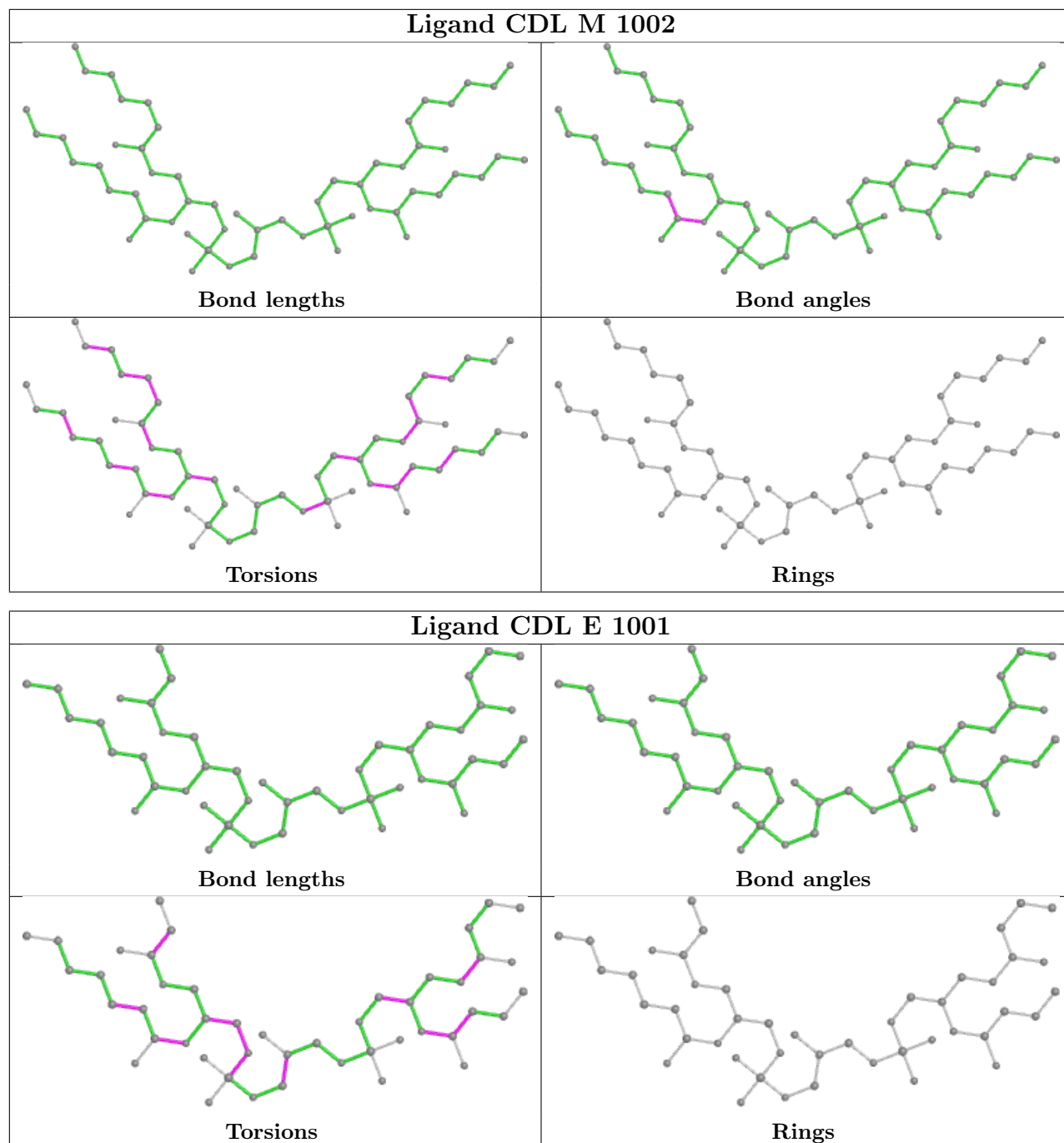


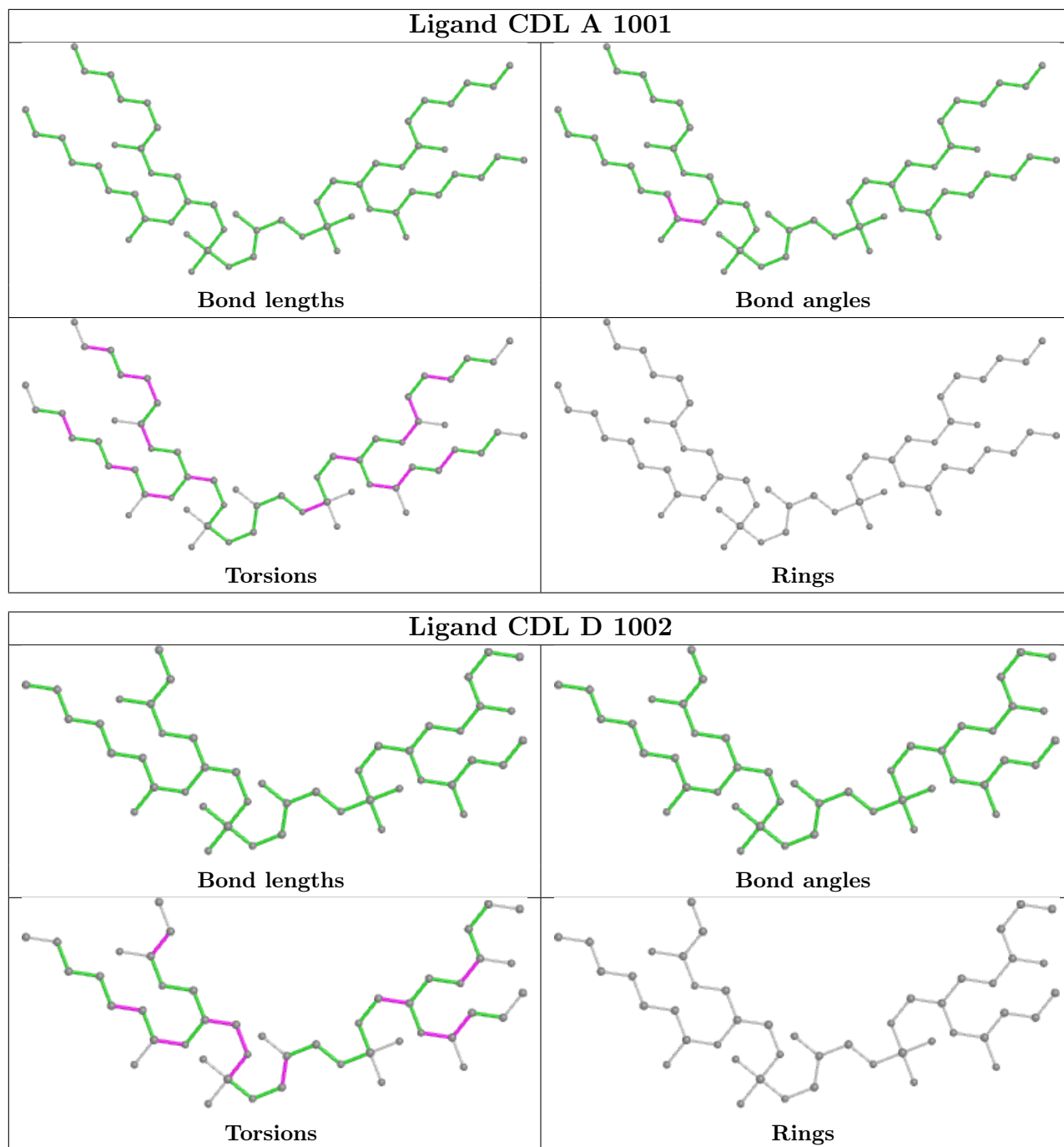


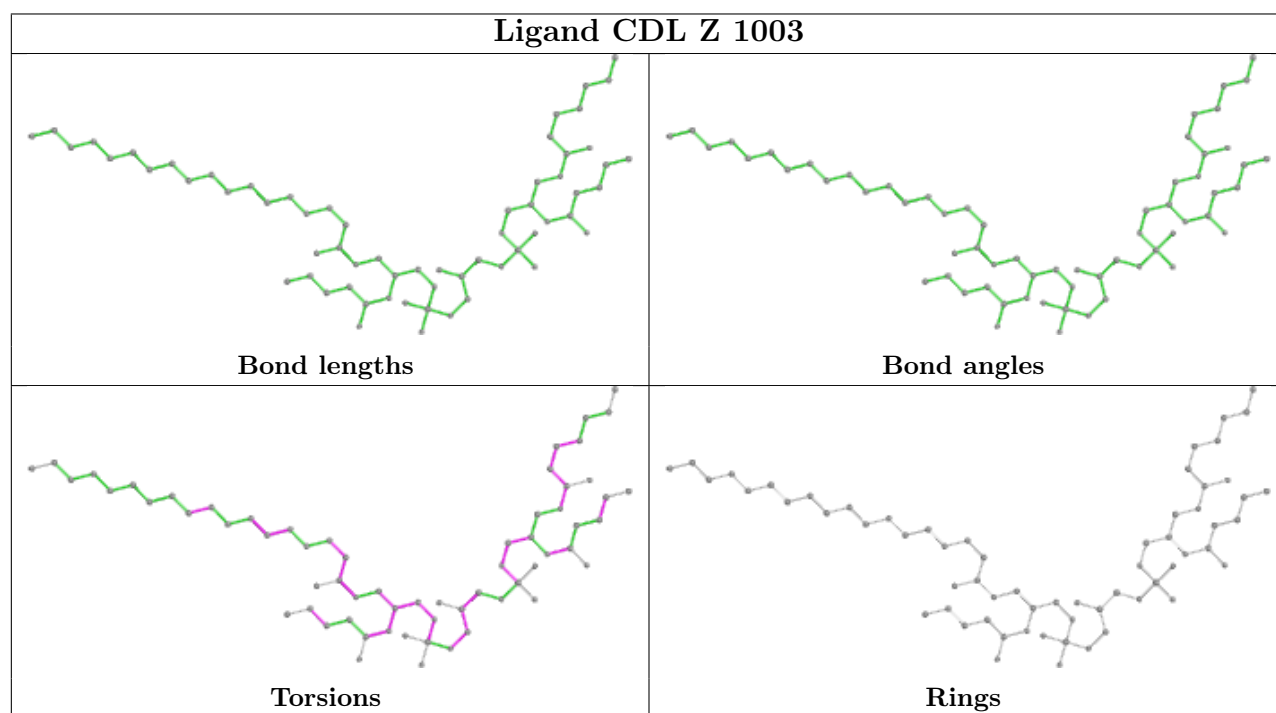
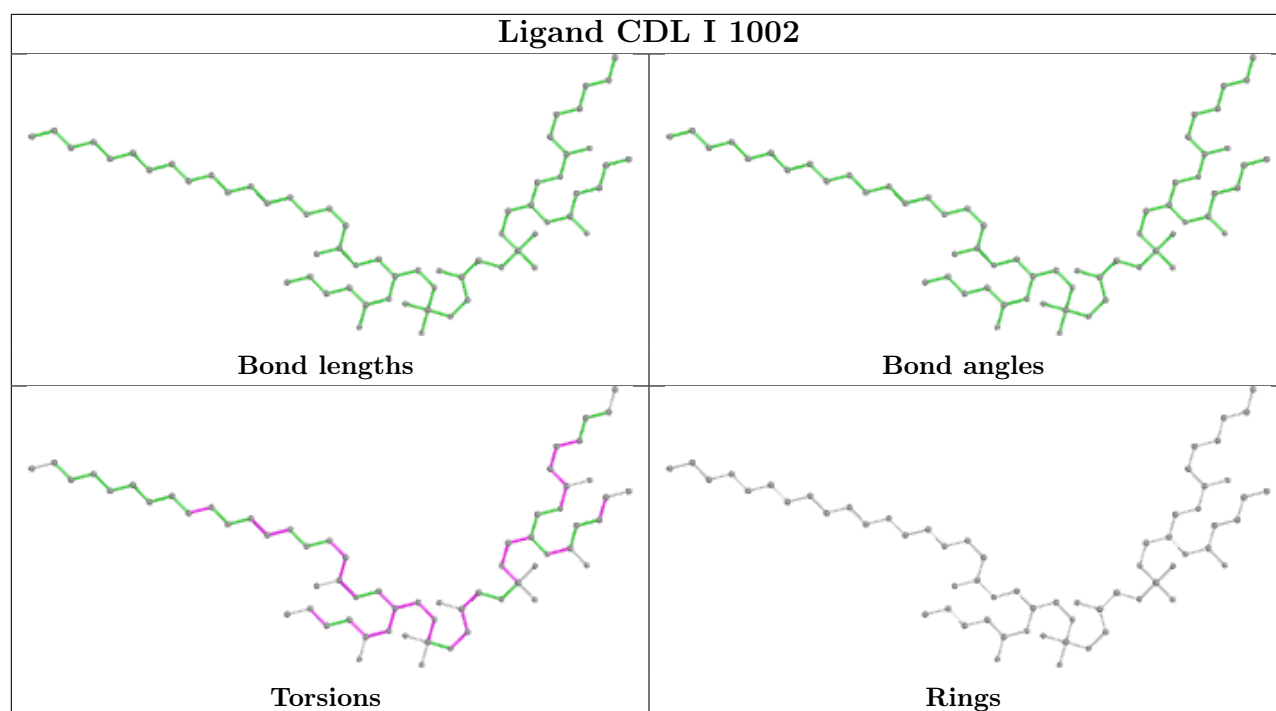


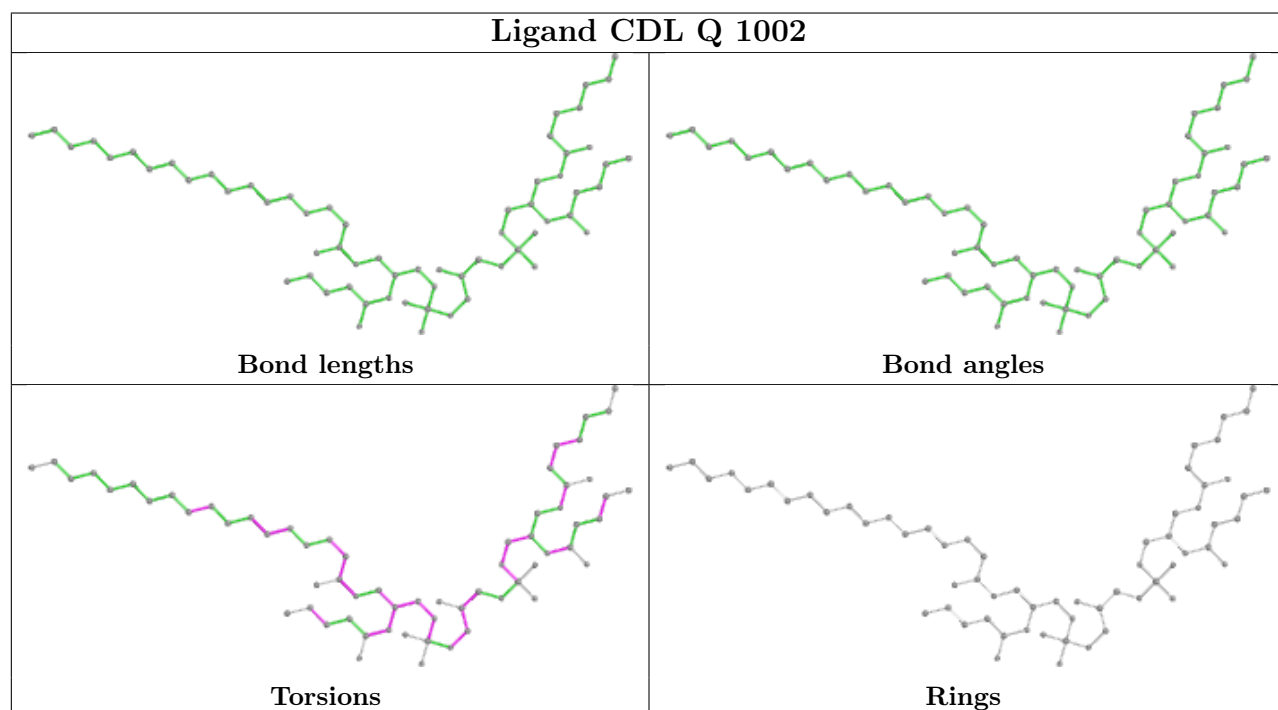
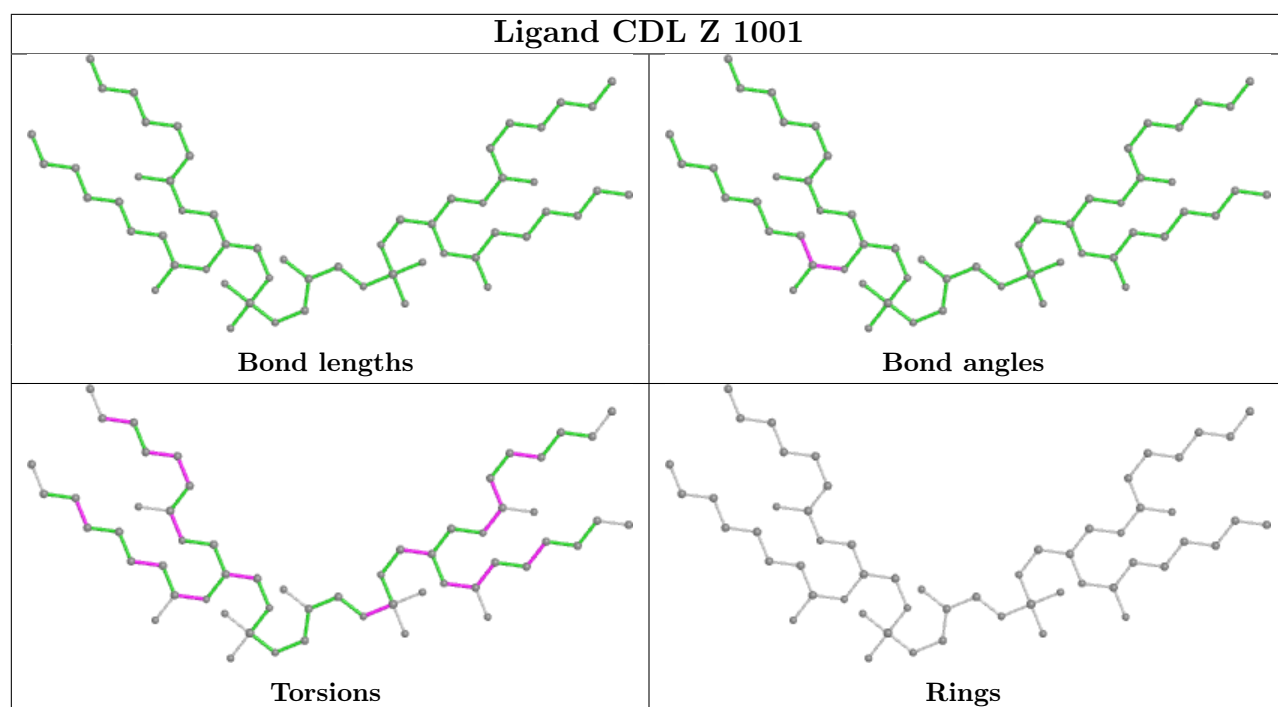


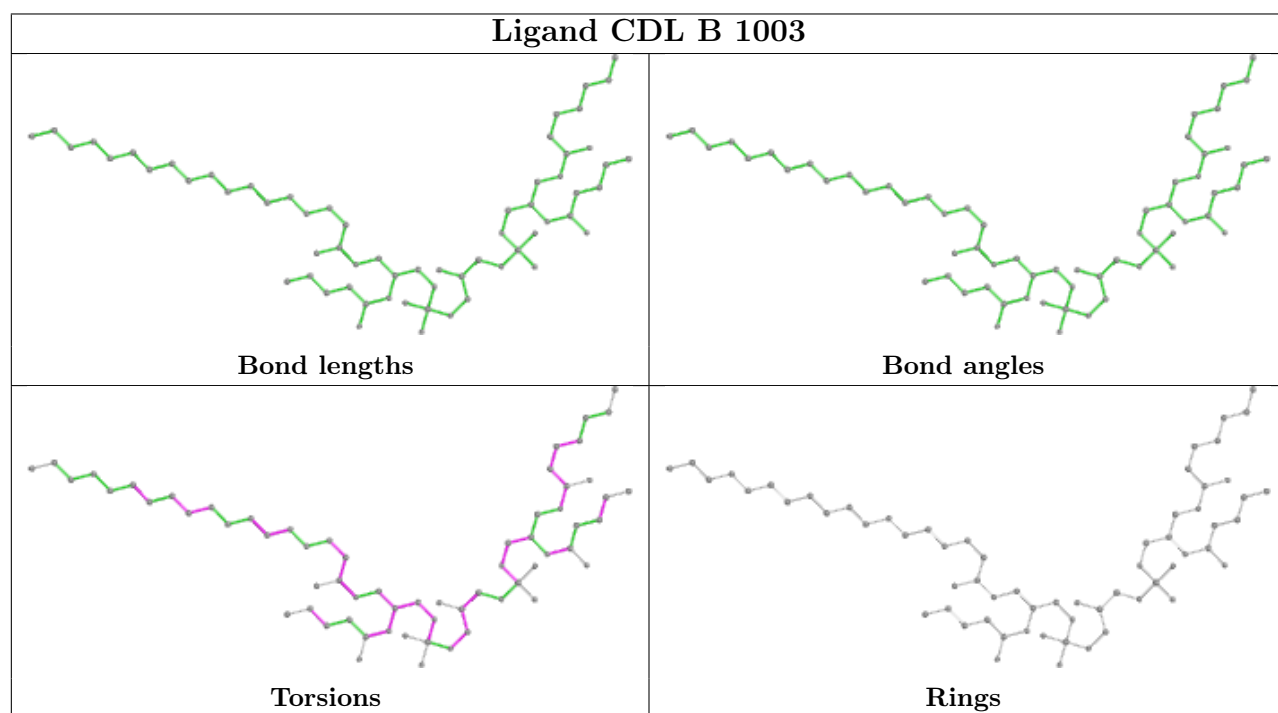
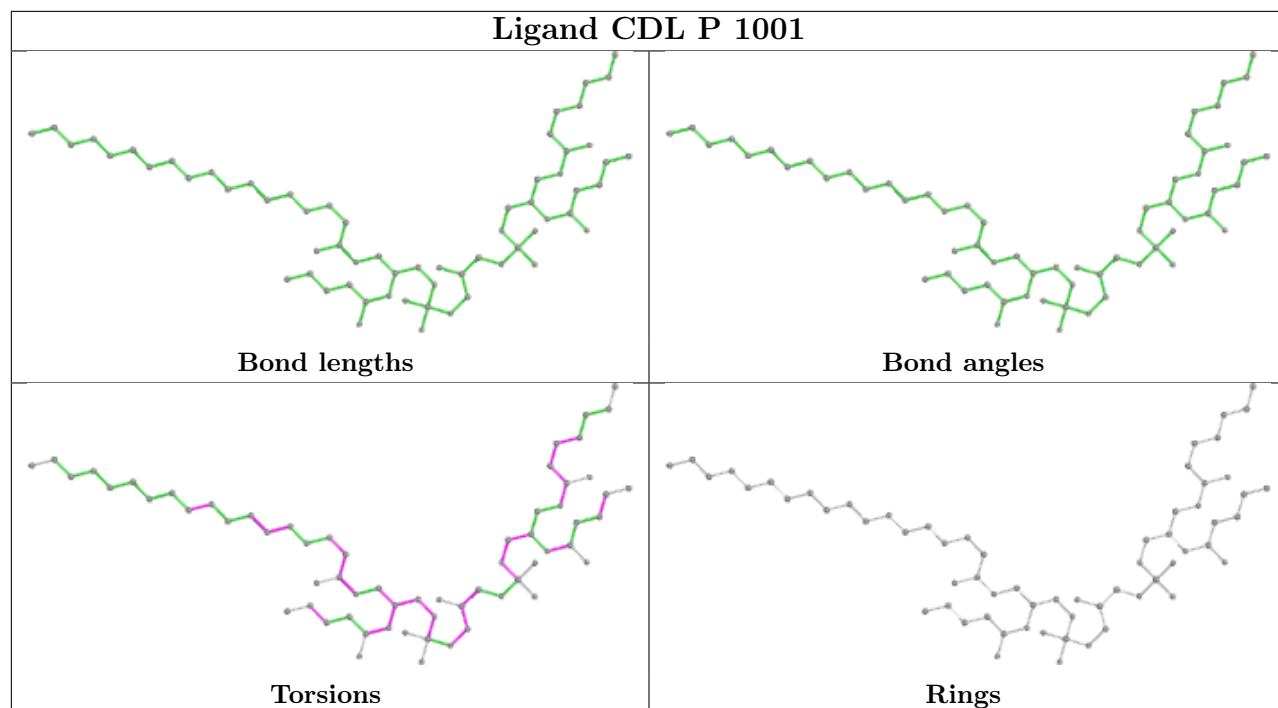


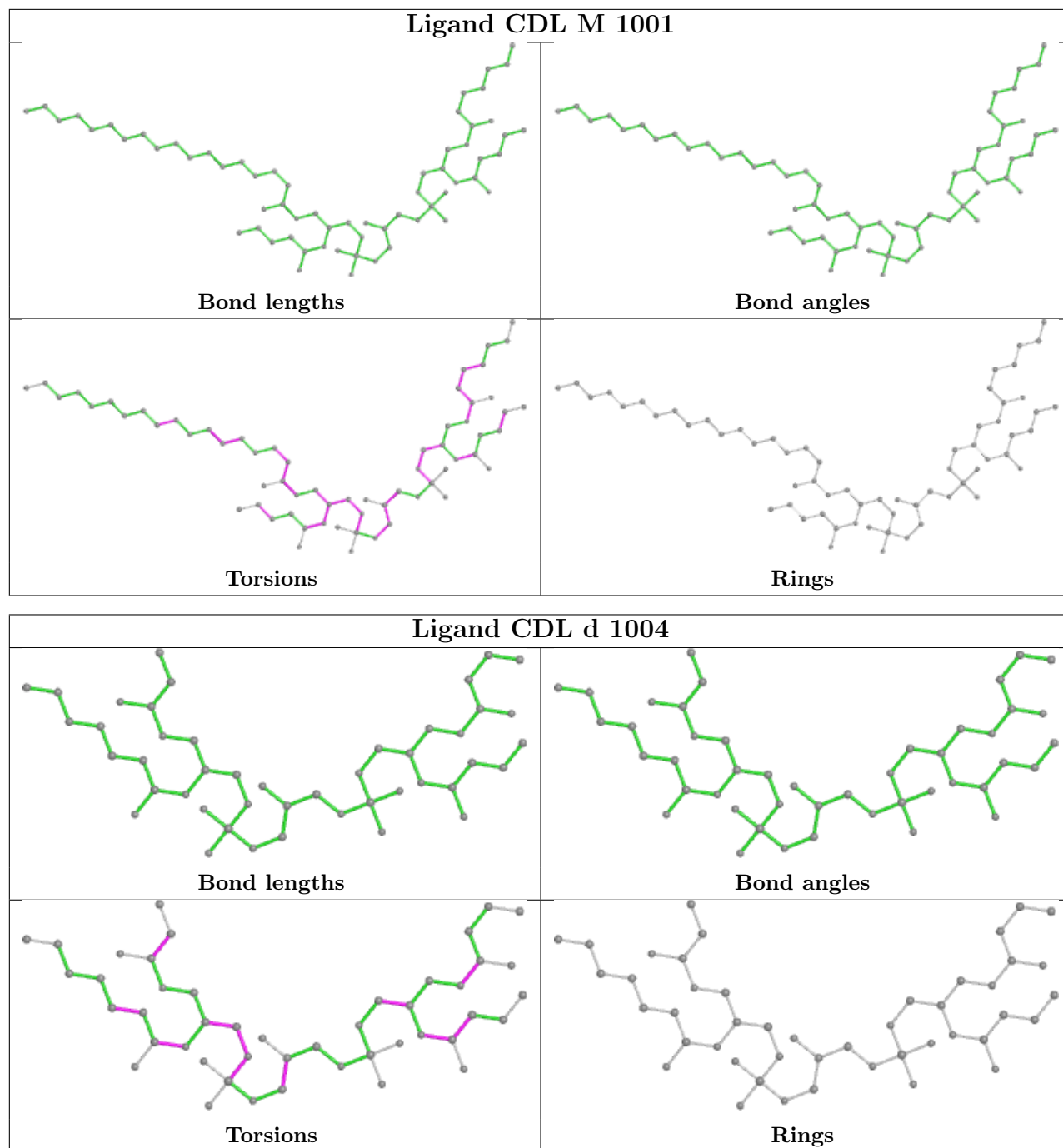


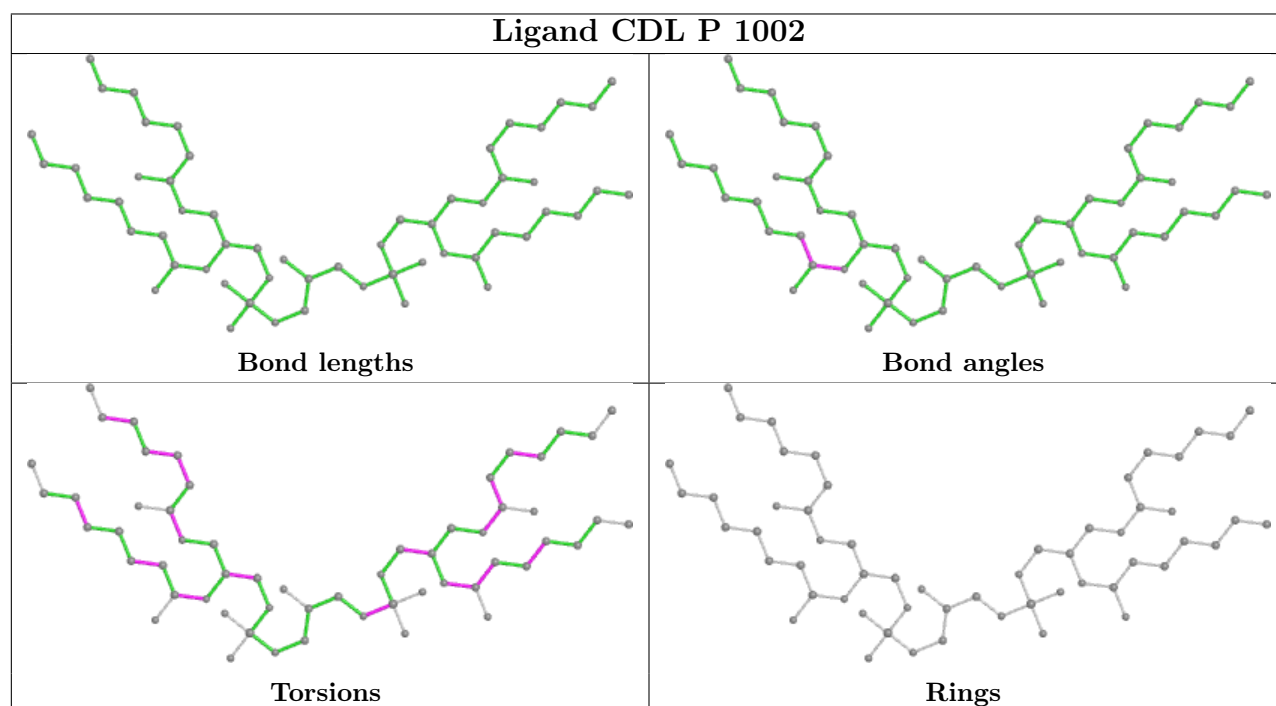
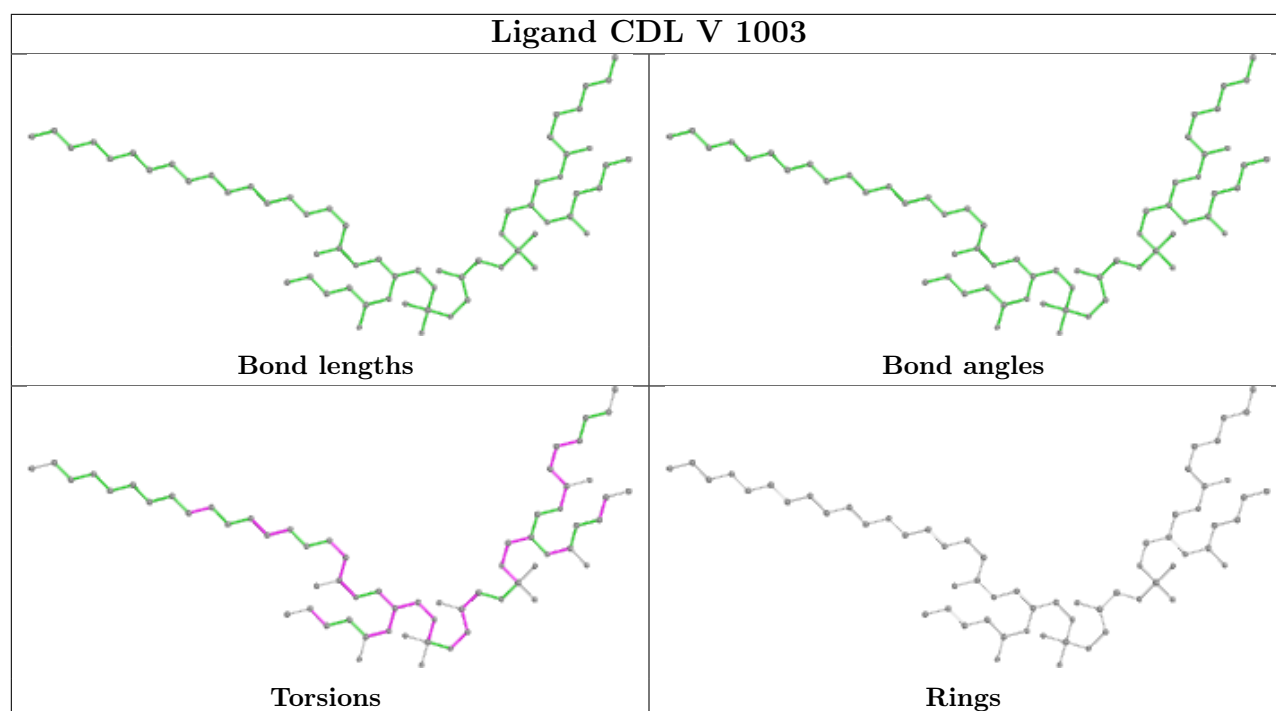


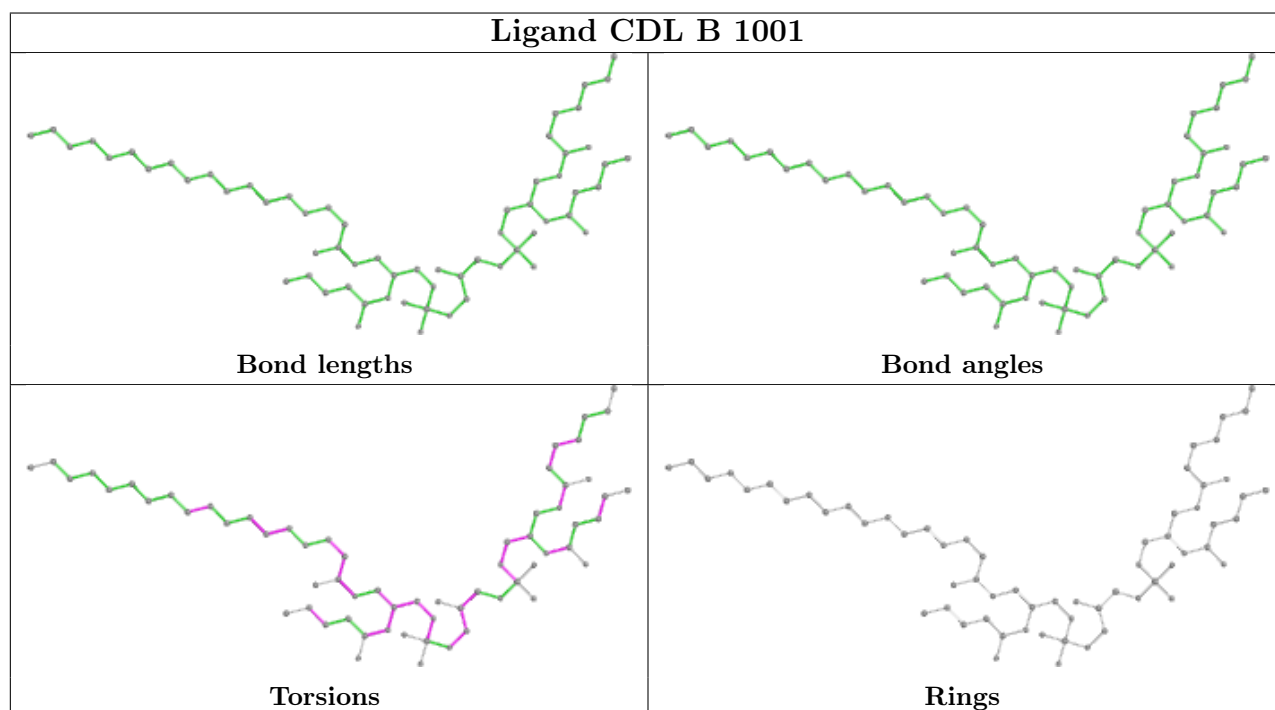
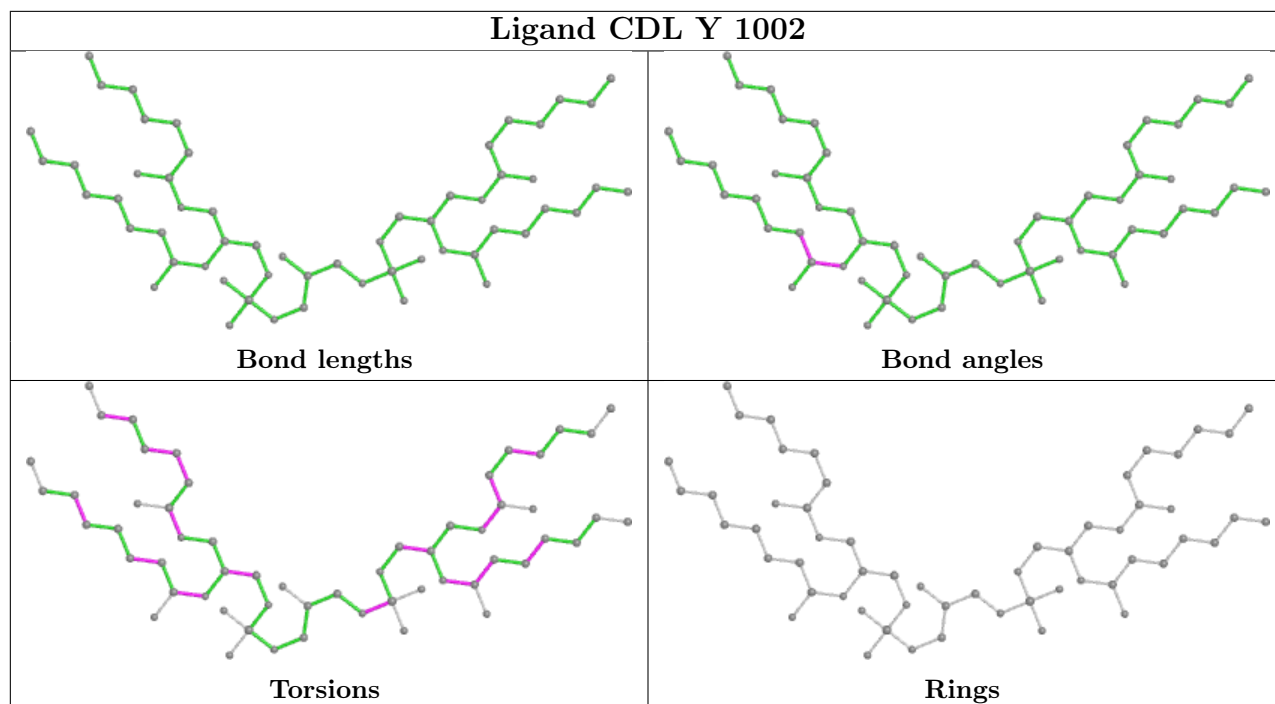


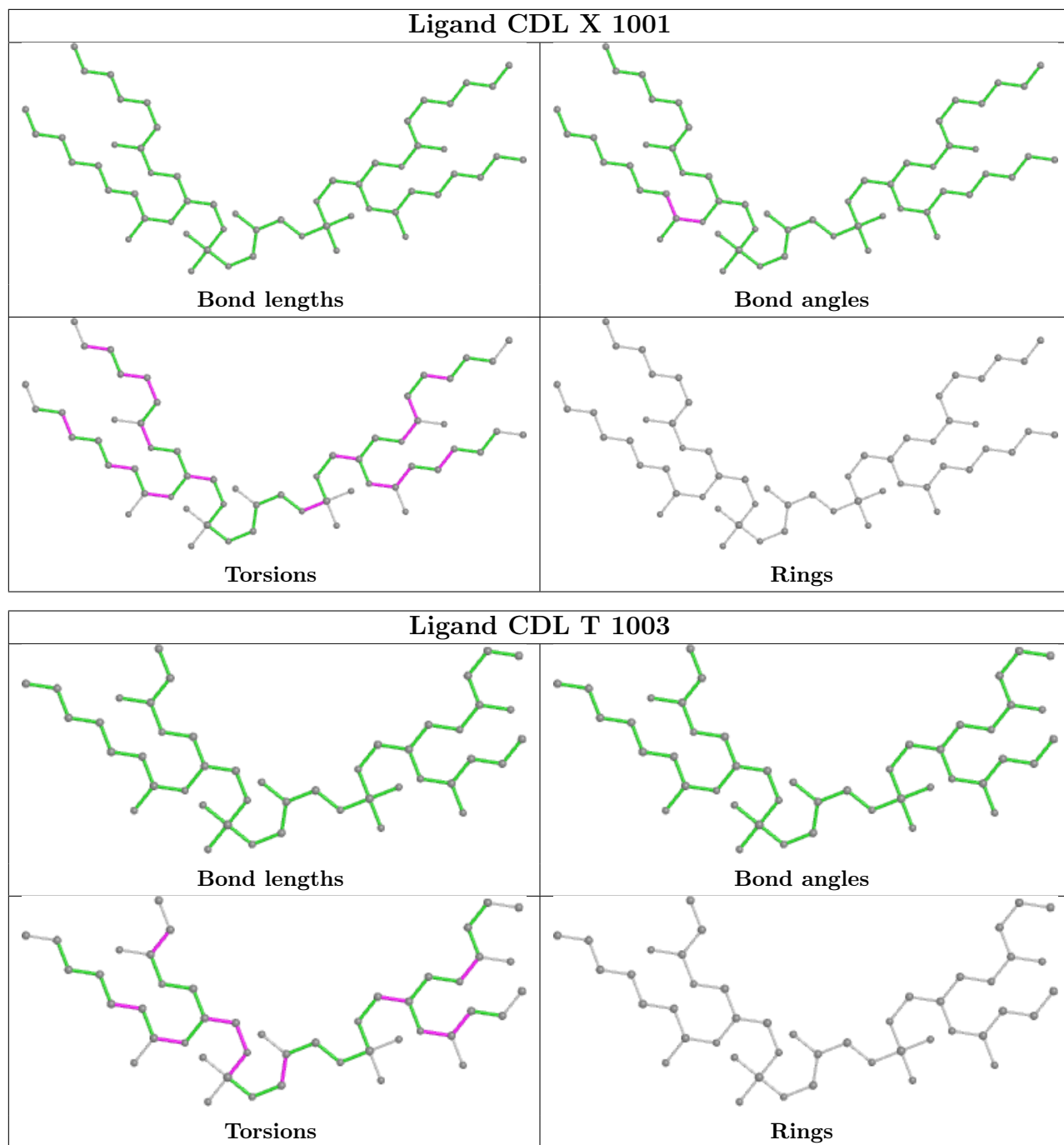


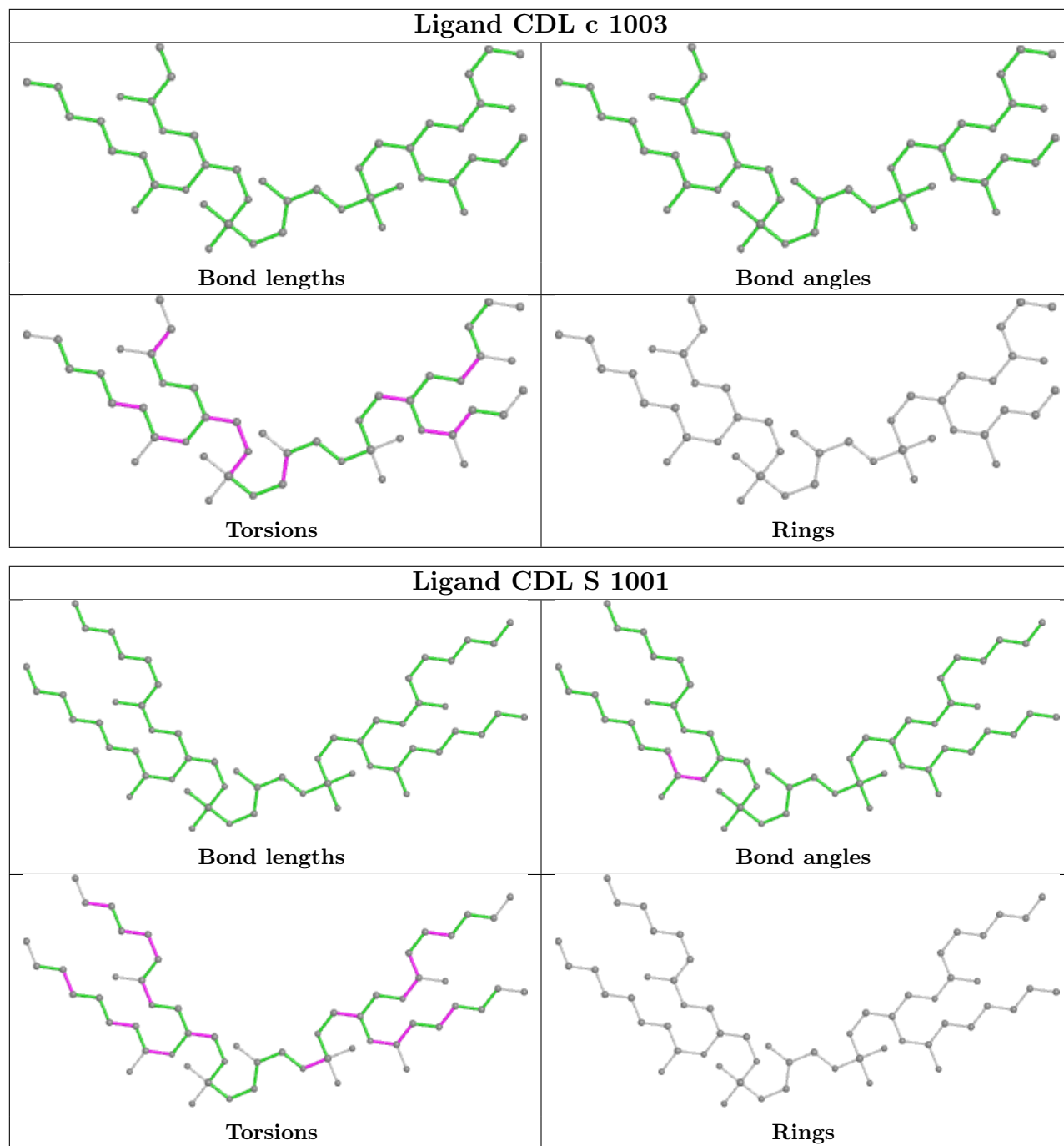


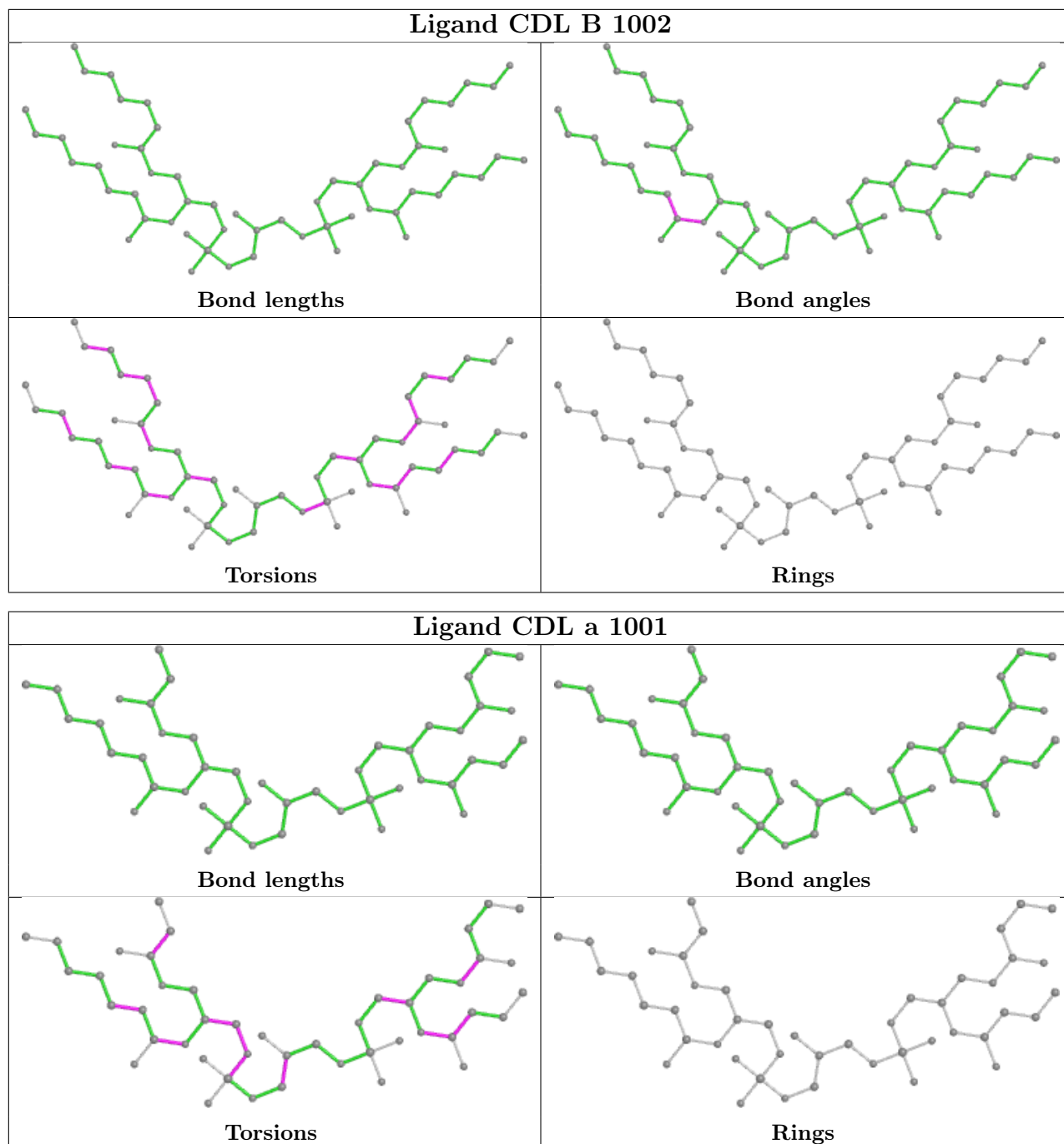


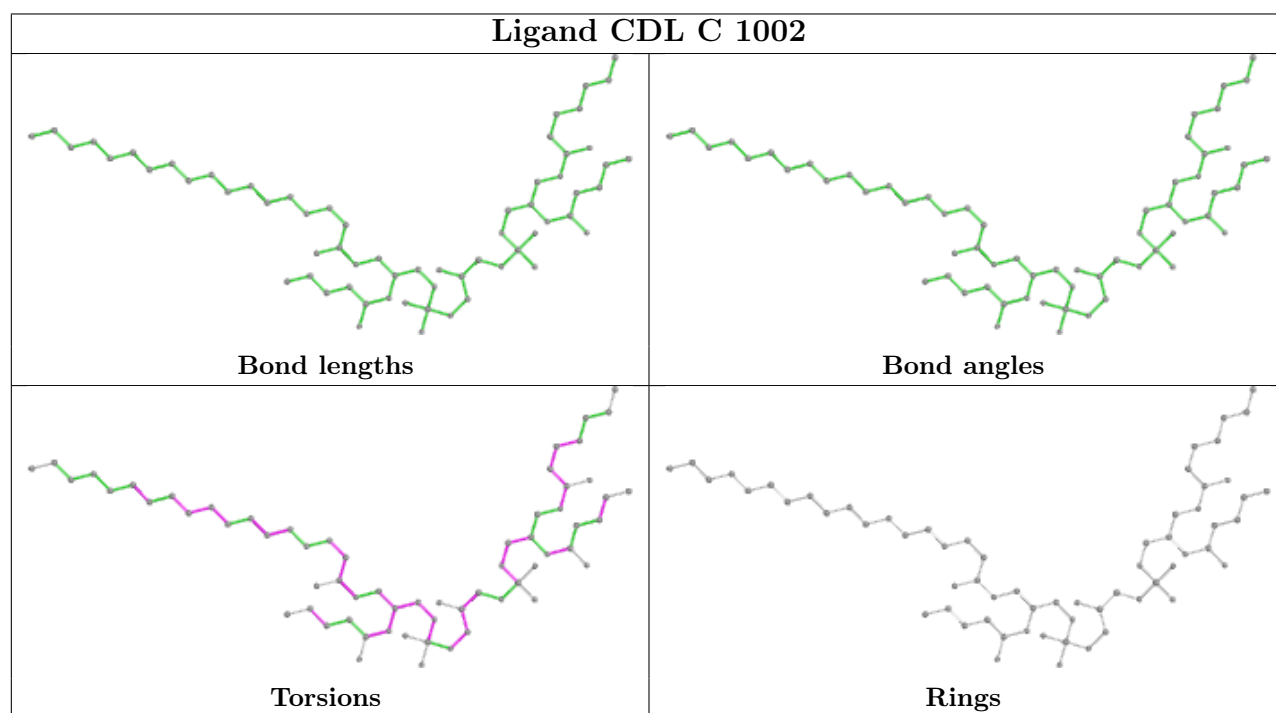
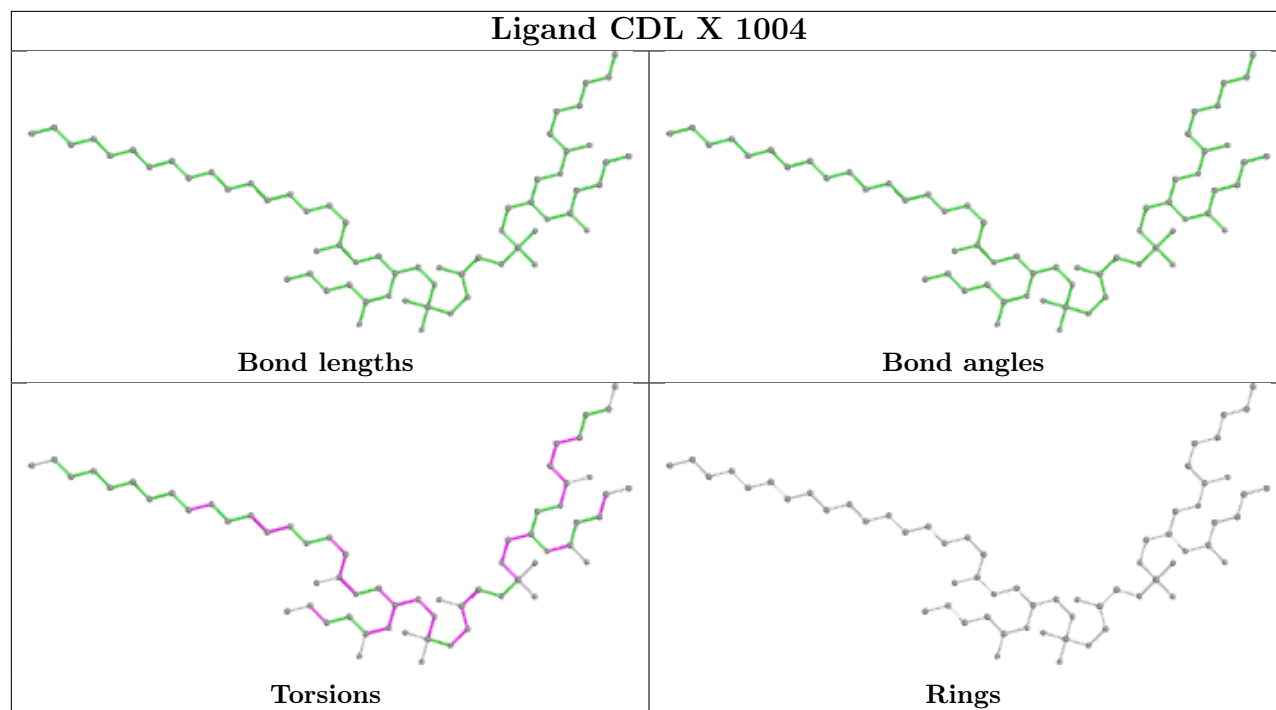


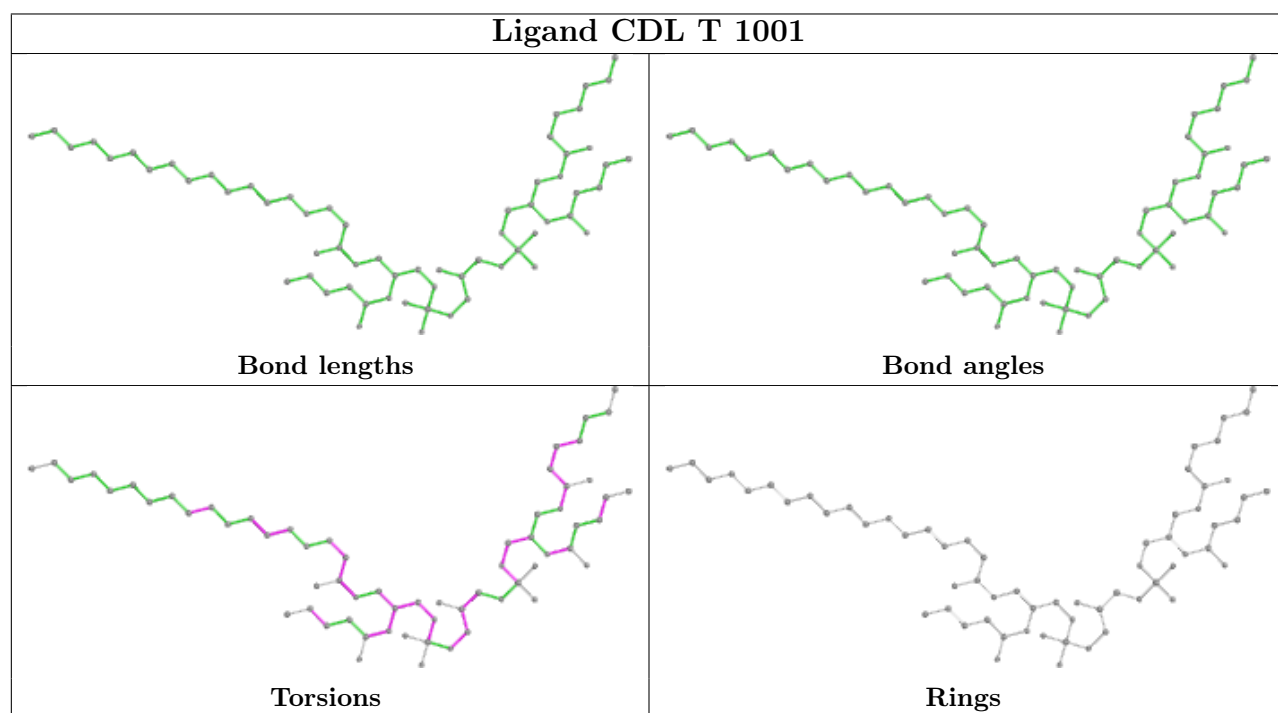
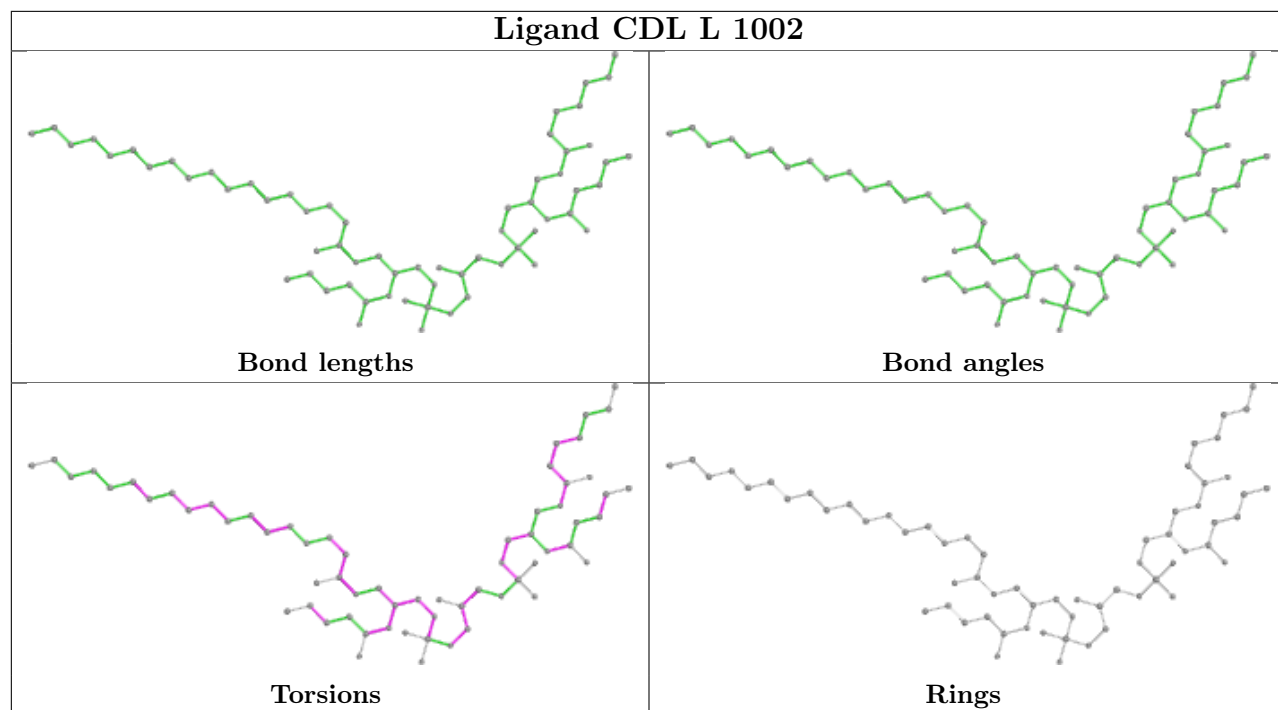


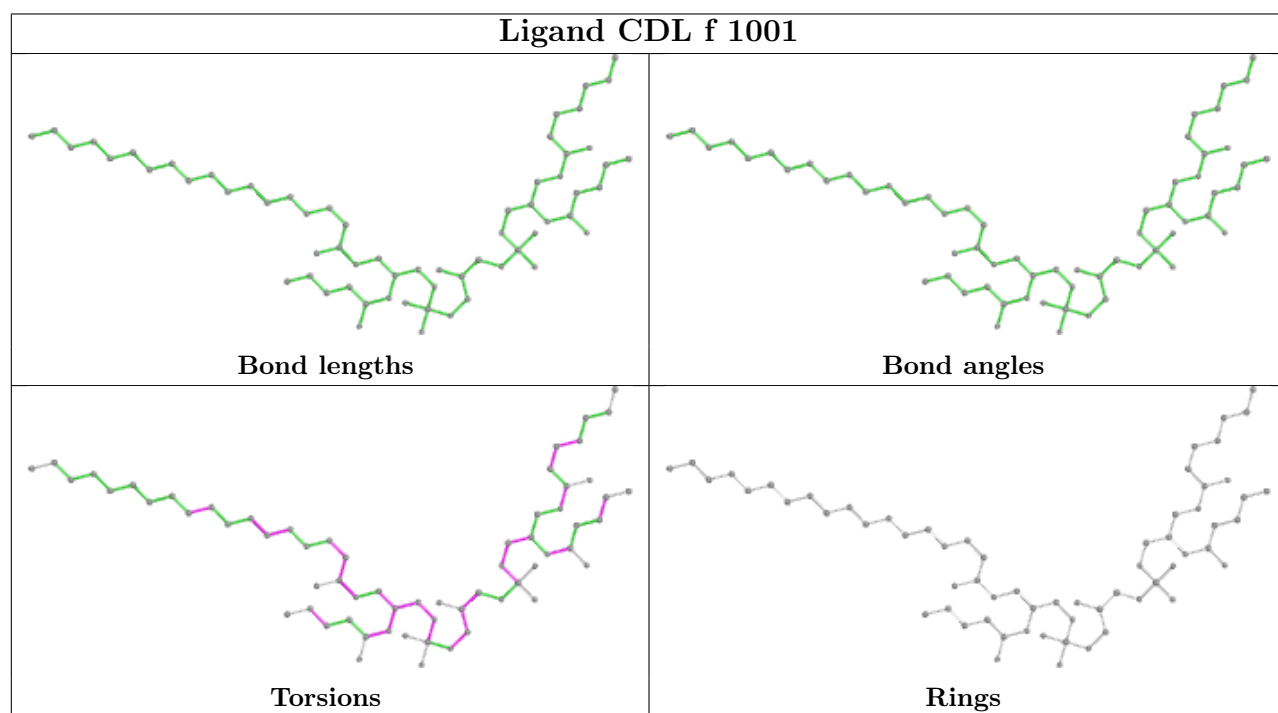
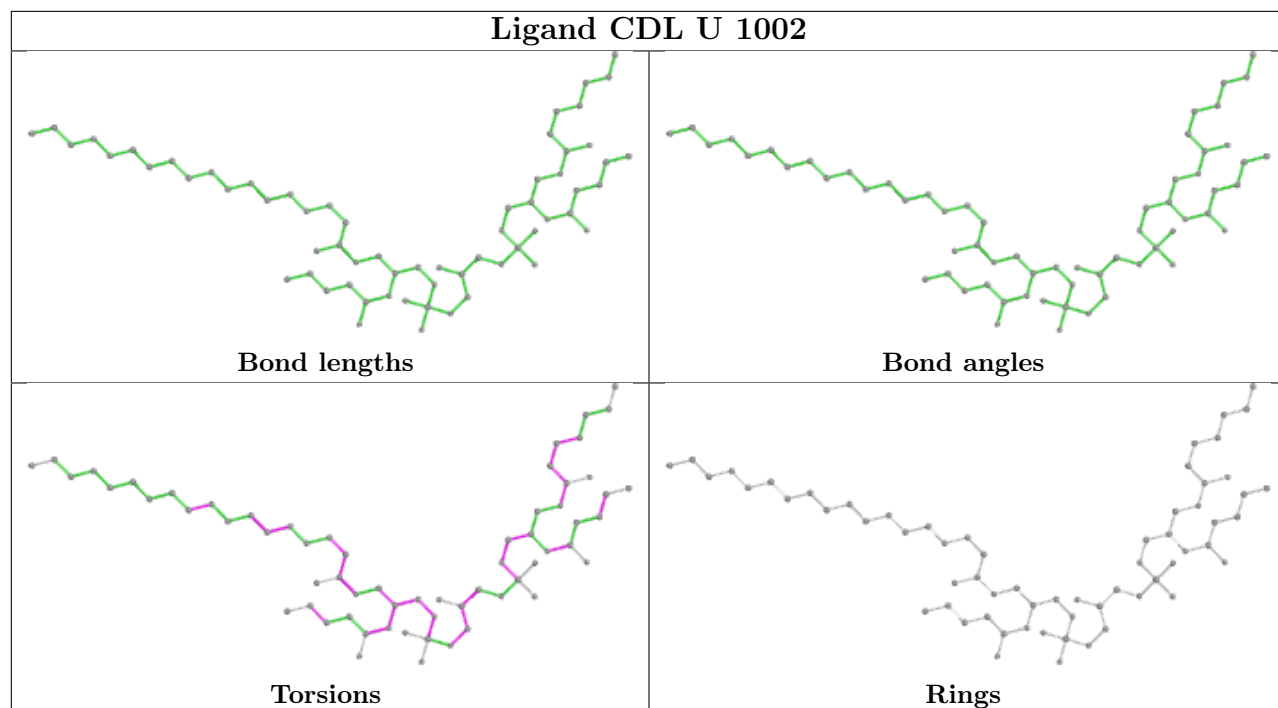


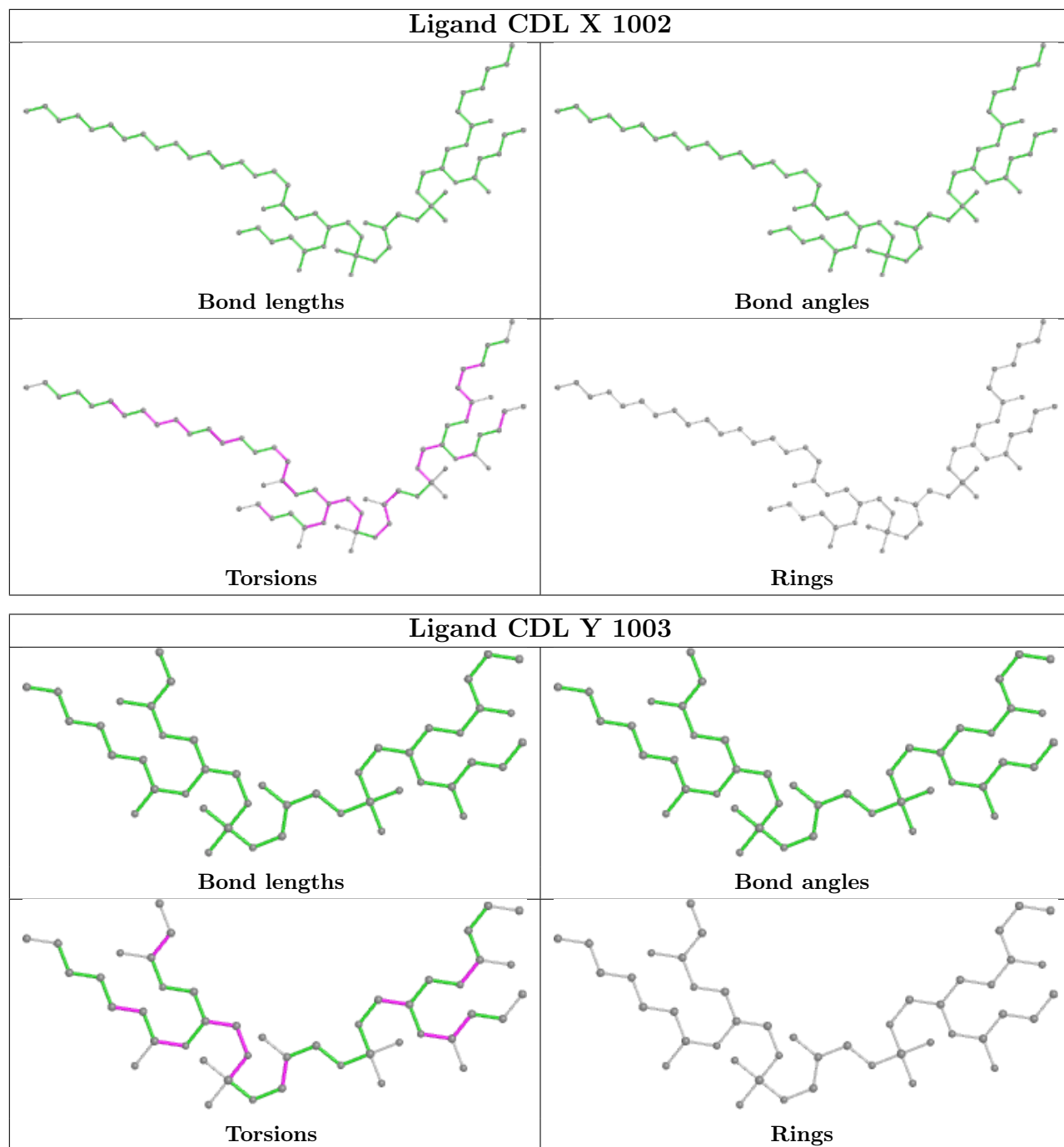


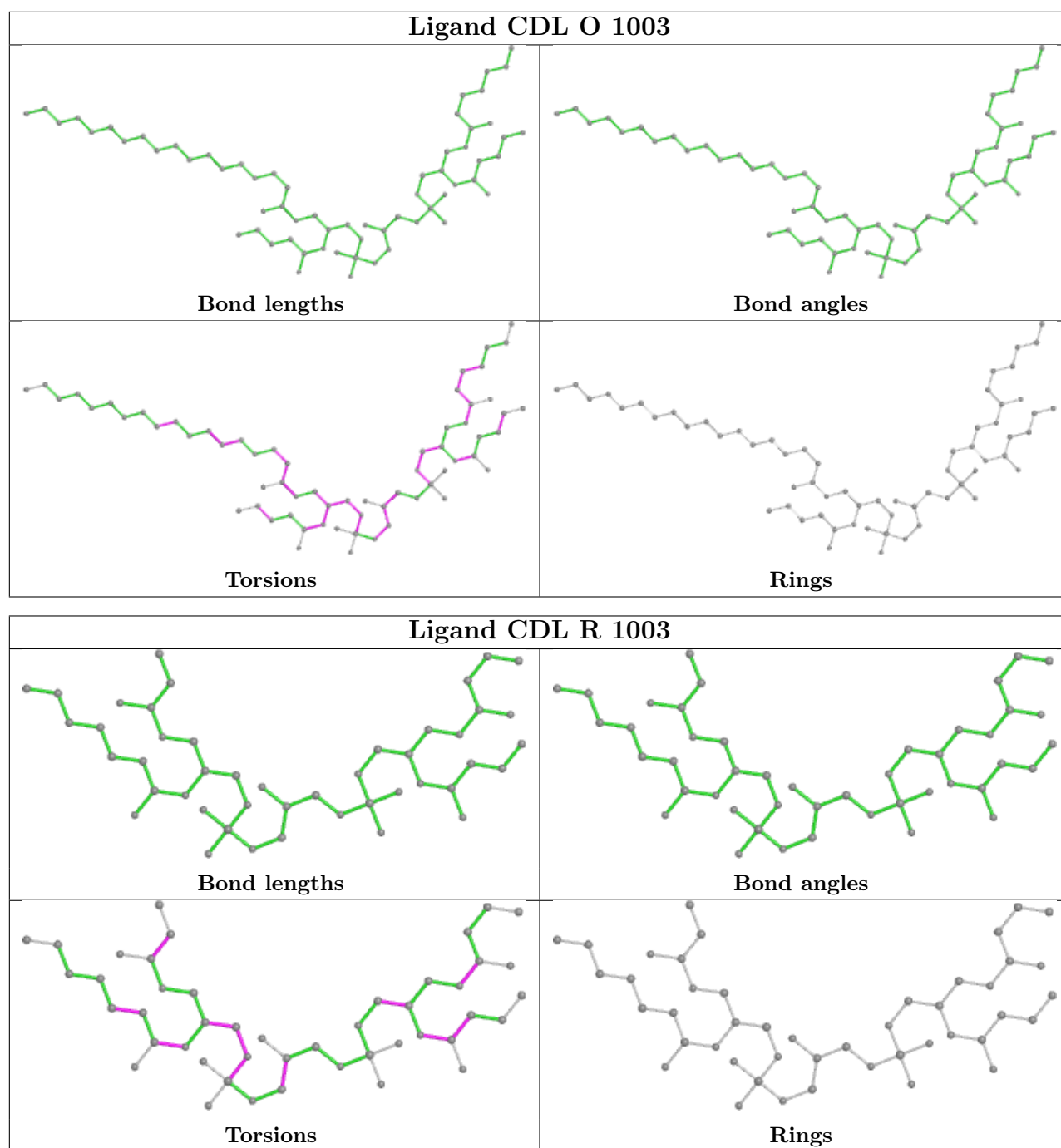


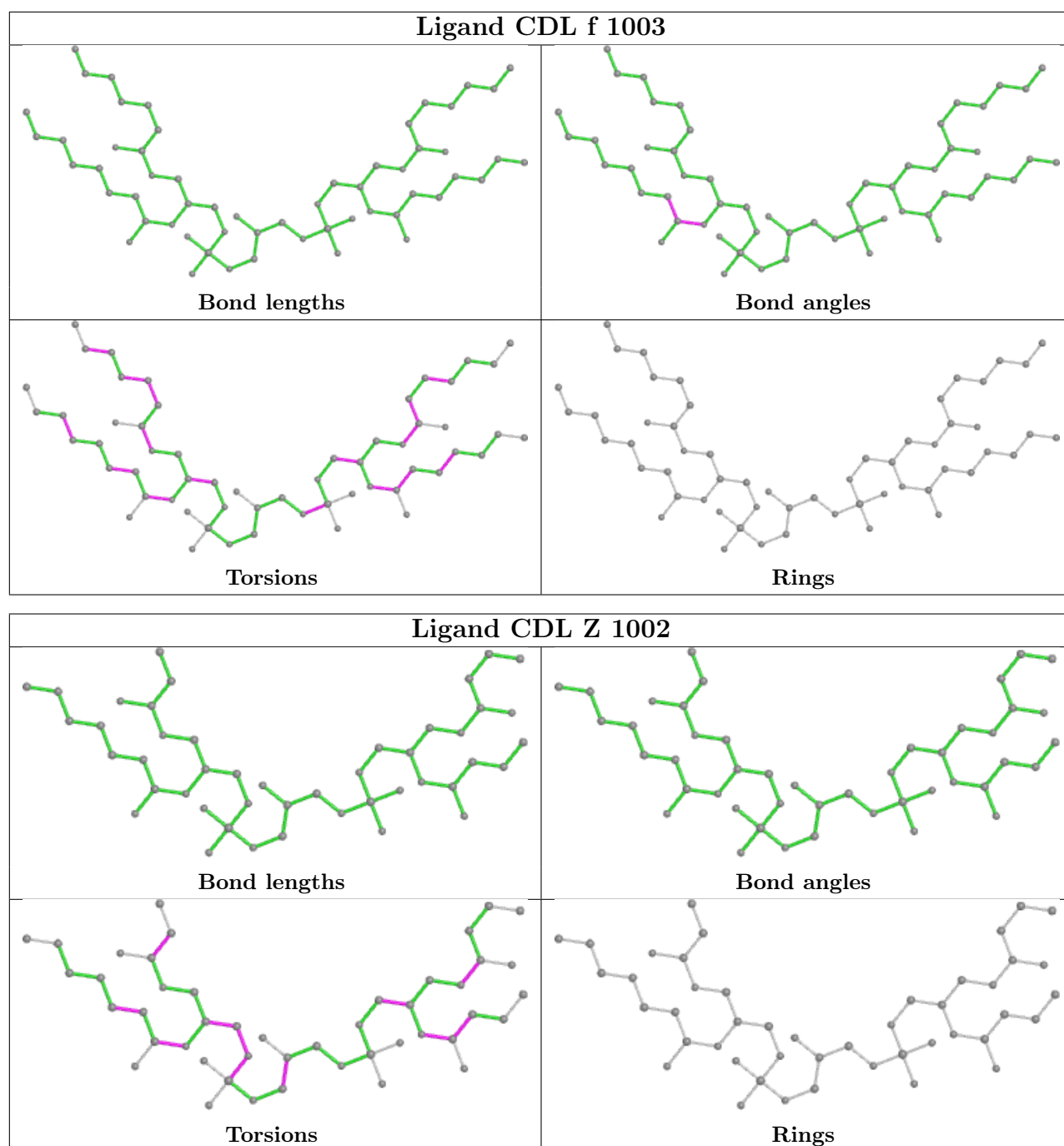


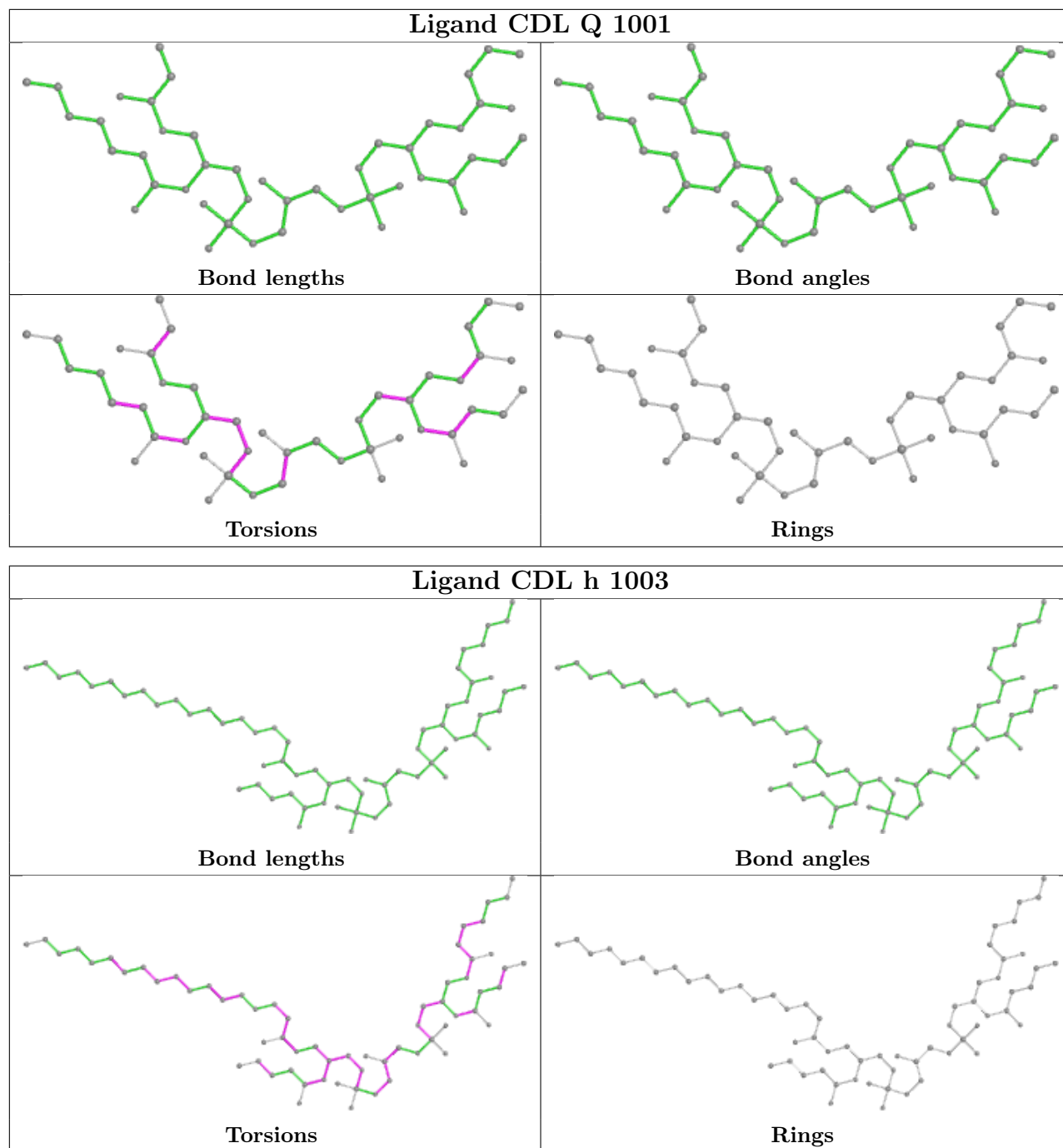


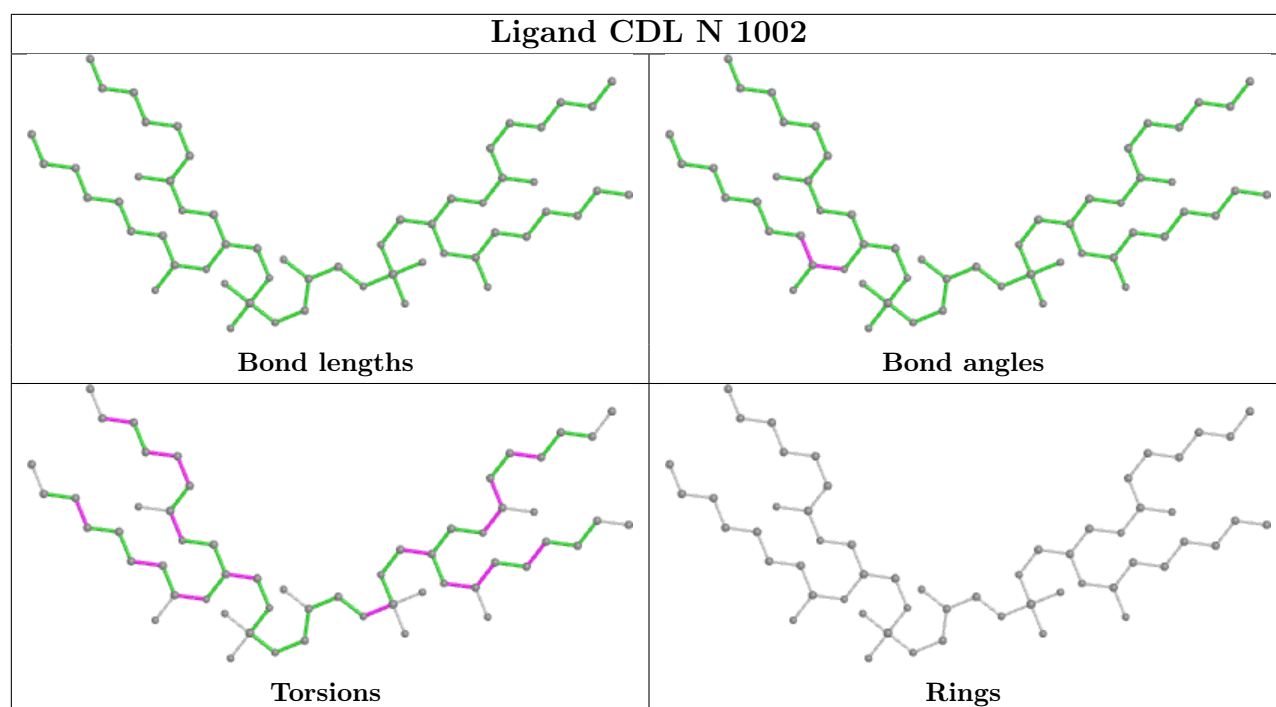












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

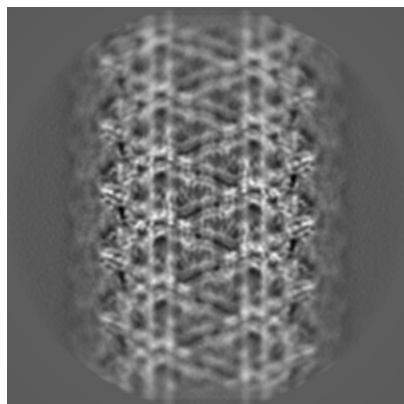
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26984. These allow visual inspection of the internal detail of the map and identification of artifacts.

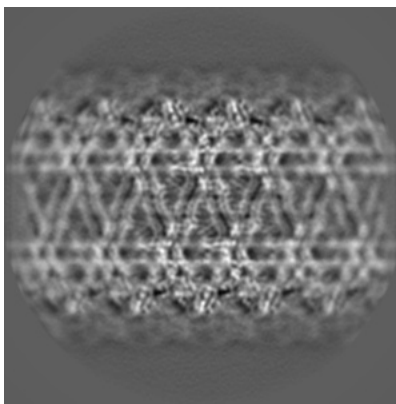
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

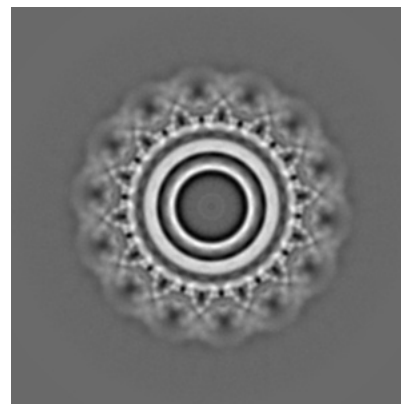
6.1.1 Primary map



X

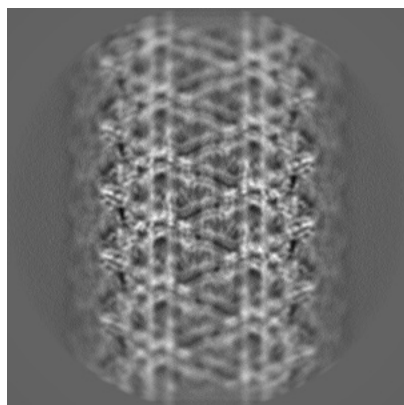


Y

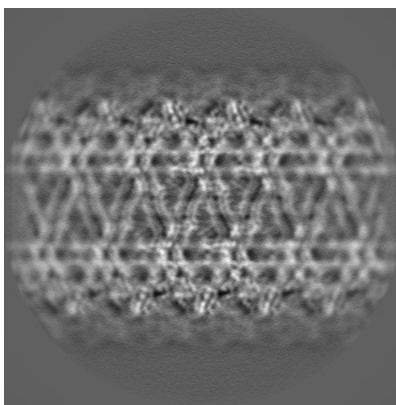


Z

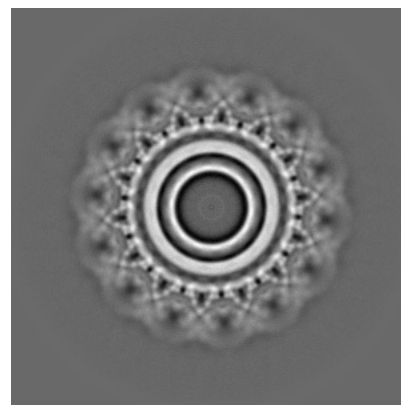
6.1.2 Raw map



X



Y

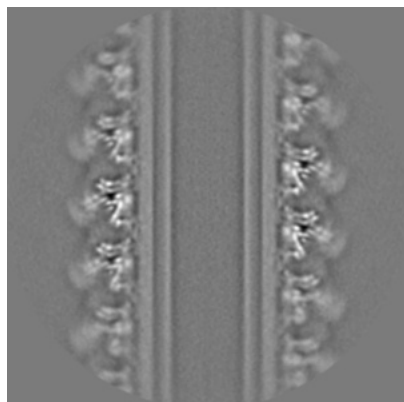


Z

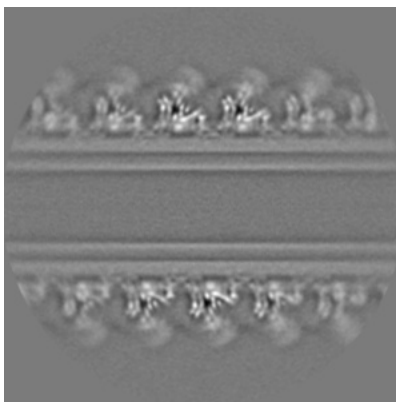
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

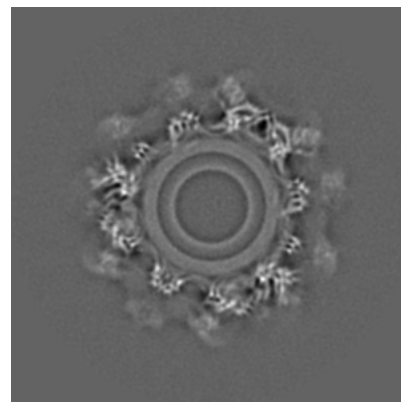
6.2.1 Primary map



X Index: 210

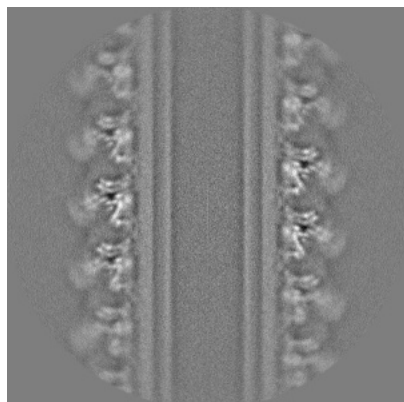


Y Index: 210

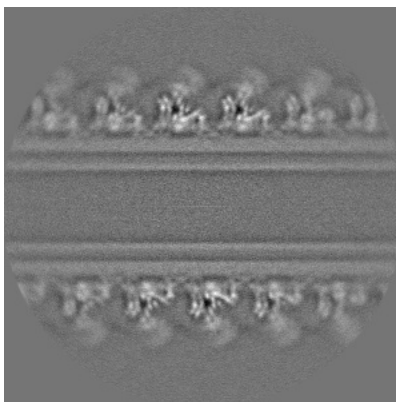


Z Index: 210

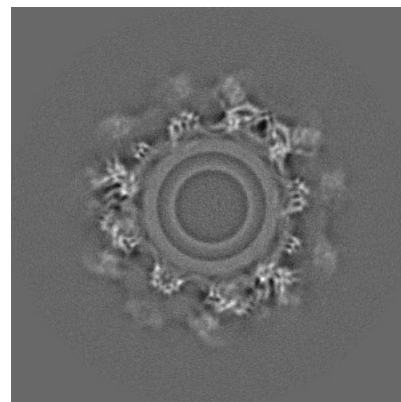
6.2.2 Raw map



X Index: 210



Y Index: 210

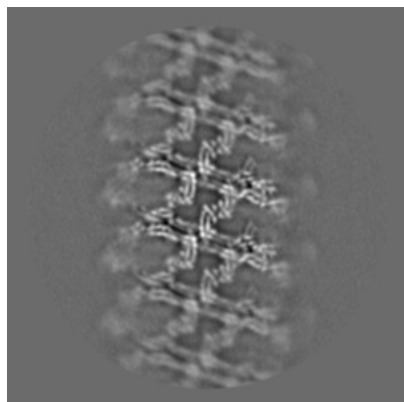


Z Index: 210

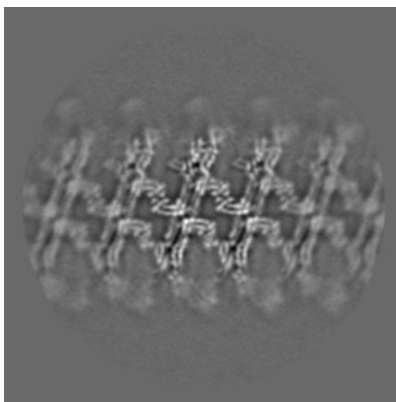
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

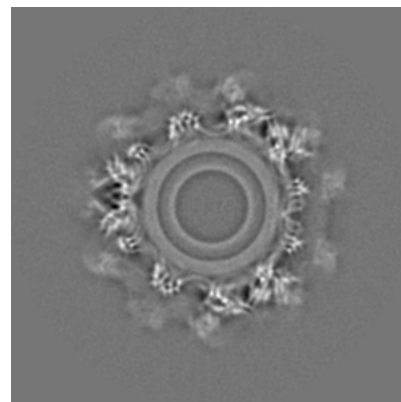
6.3.1 Primary map



X Index: 302

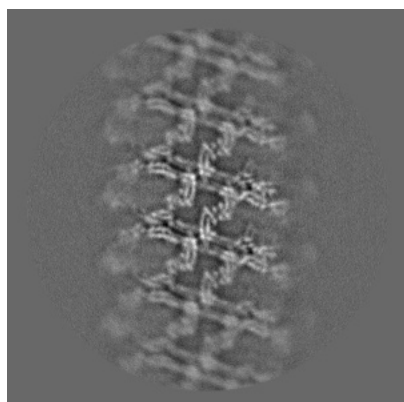


Y Index: 302

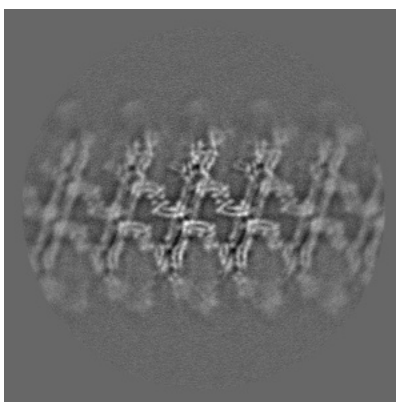


Z Index: 212

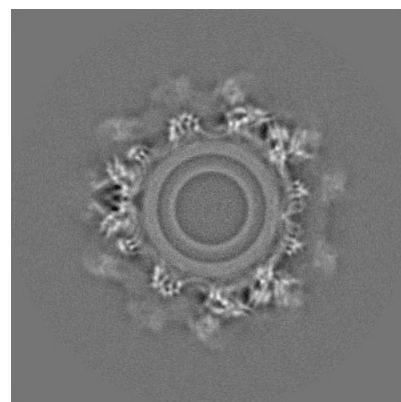
6.3.2 Raw map



X Index: 302



Y Index: 302

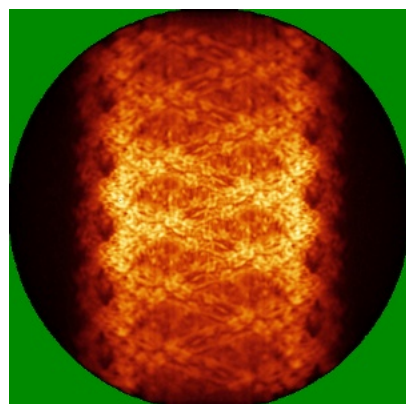


Z Index: 212

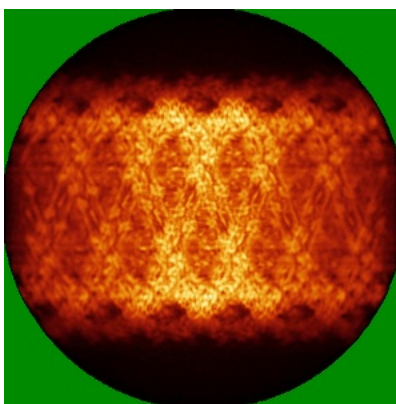
The images above show the largest variance slices of the map in three orthogonal directions.

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

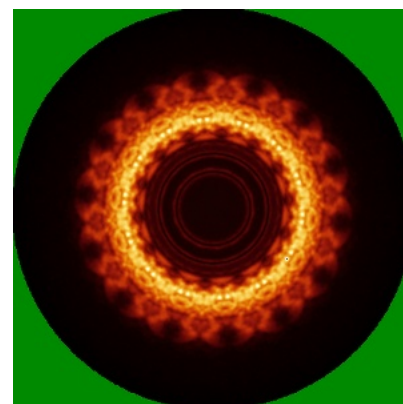
6.4.1 Primary map



X

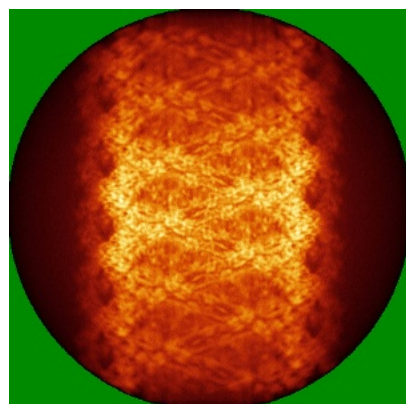


Y

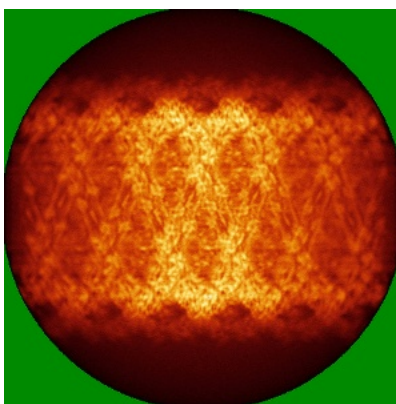


Z

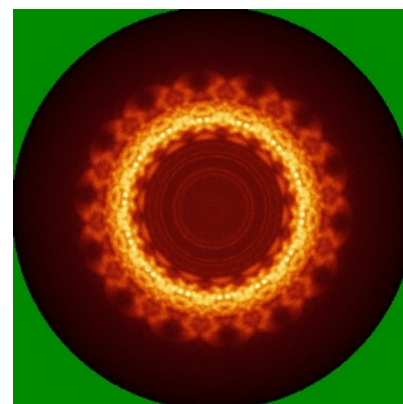
6.4.2 Raw map



X



Y

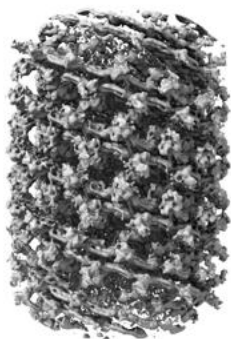


Z

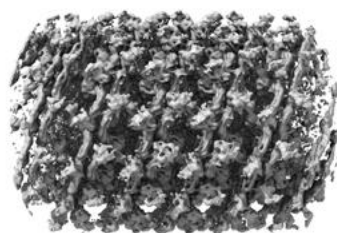
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

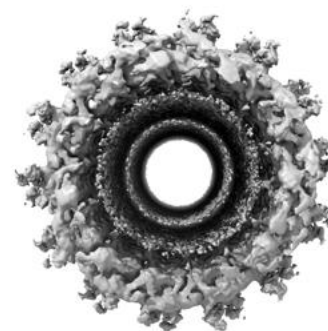
6.5.1 Primary map



X



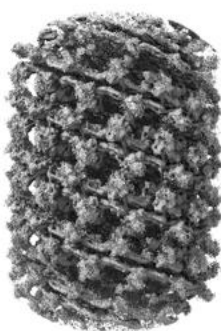
Y



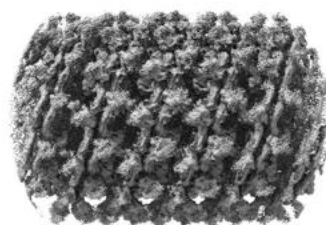
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

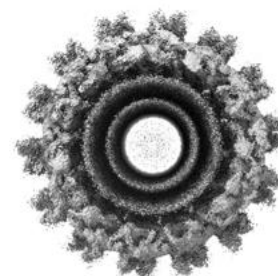
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

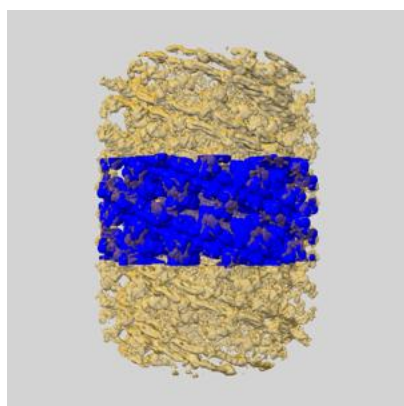
6.6 Mask visualisation [i](#)

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

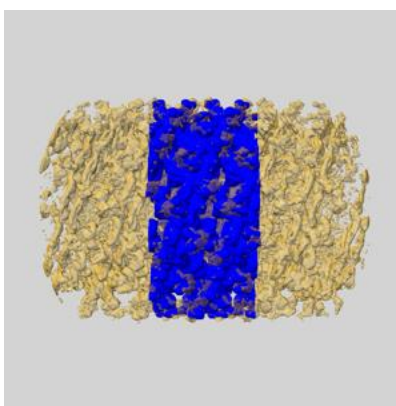
A mask typically either:

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

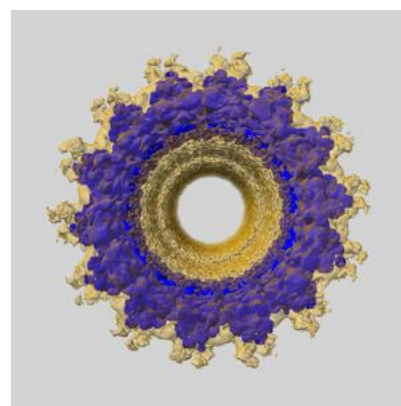
6.6.1 emd_26984_msk_1.map [i](#)



X



Y

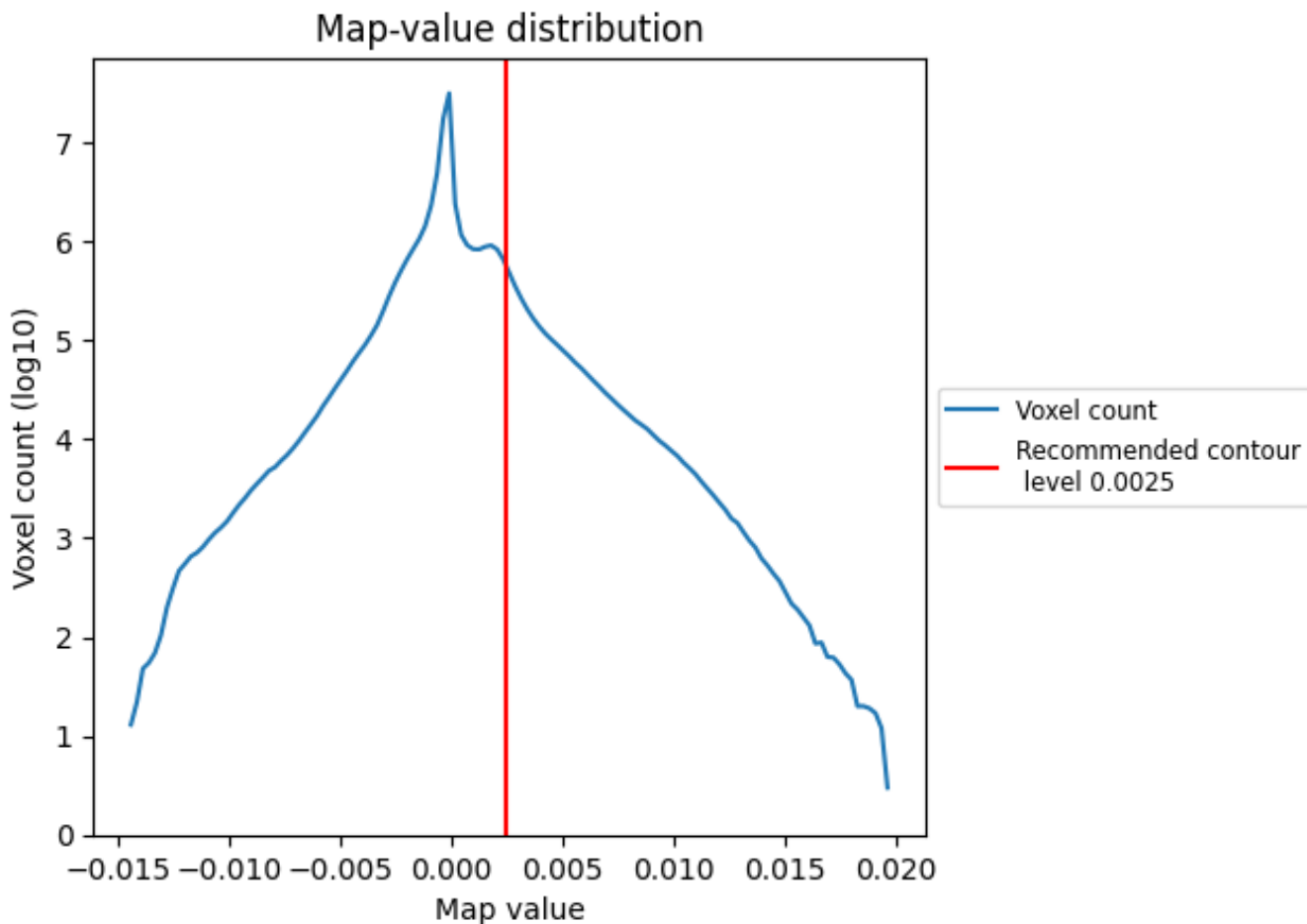


Z

7 Map analysis [i](#)

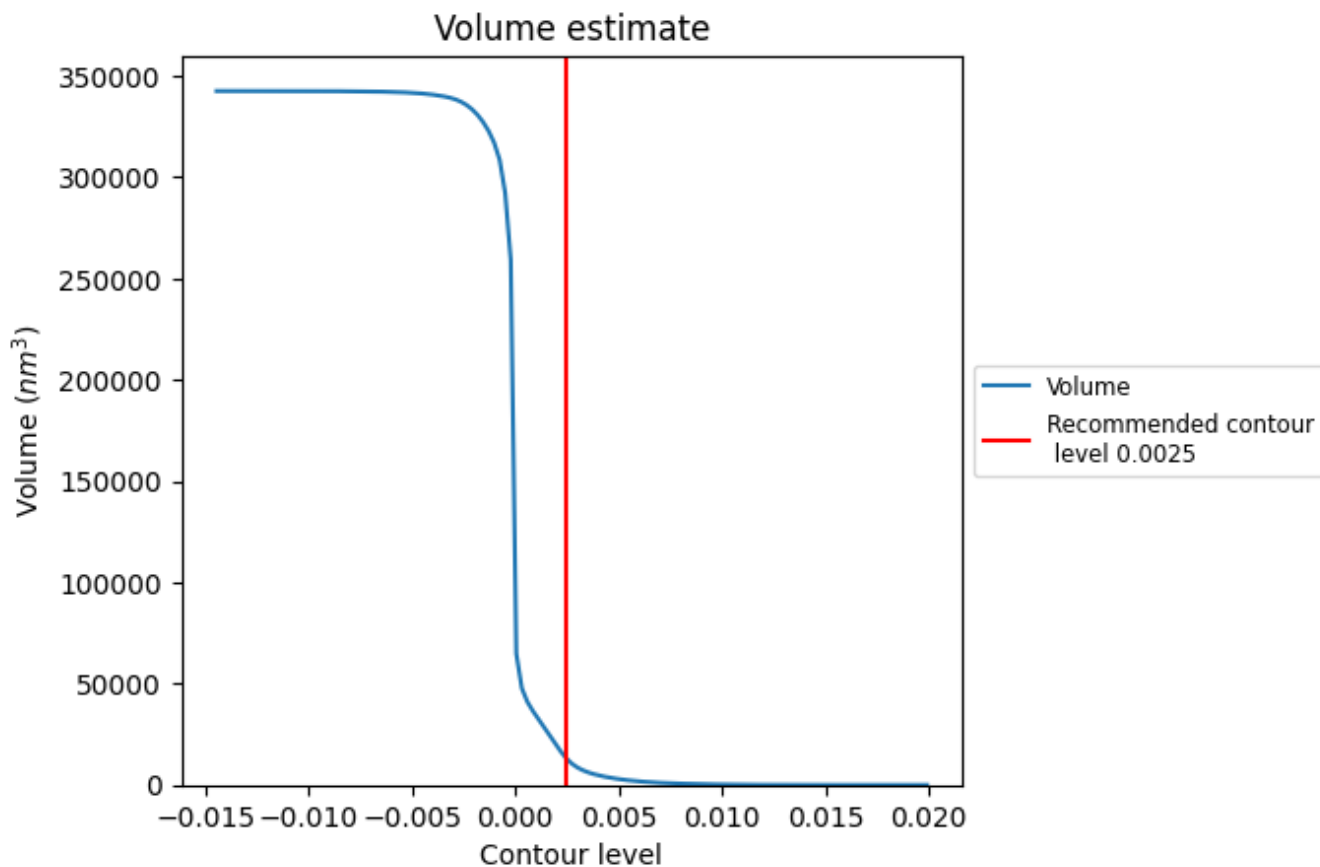
This section contains the results of statistical analysis of the map.

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.

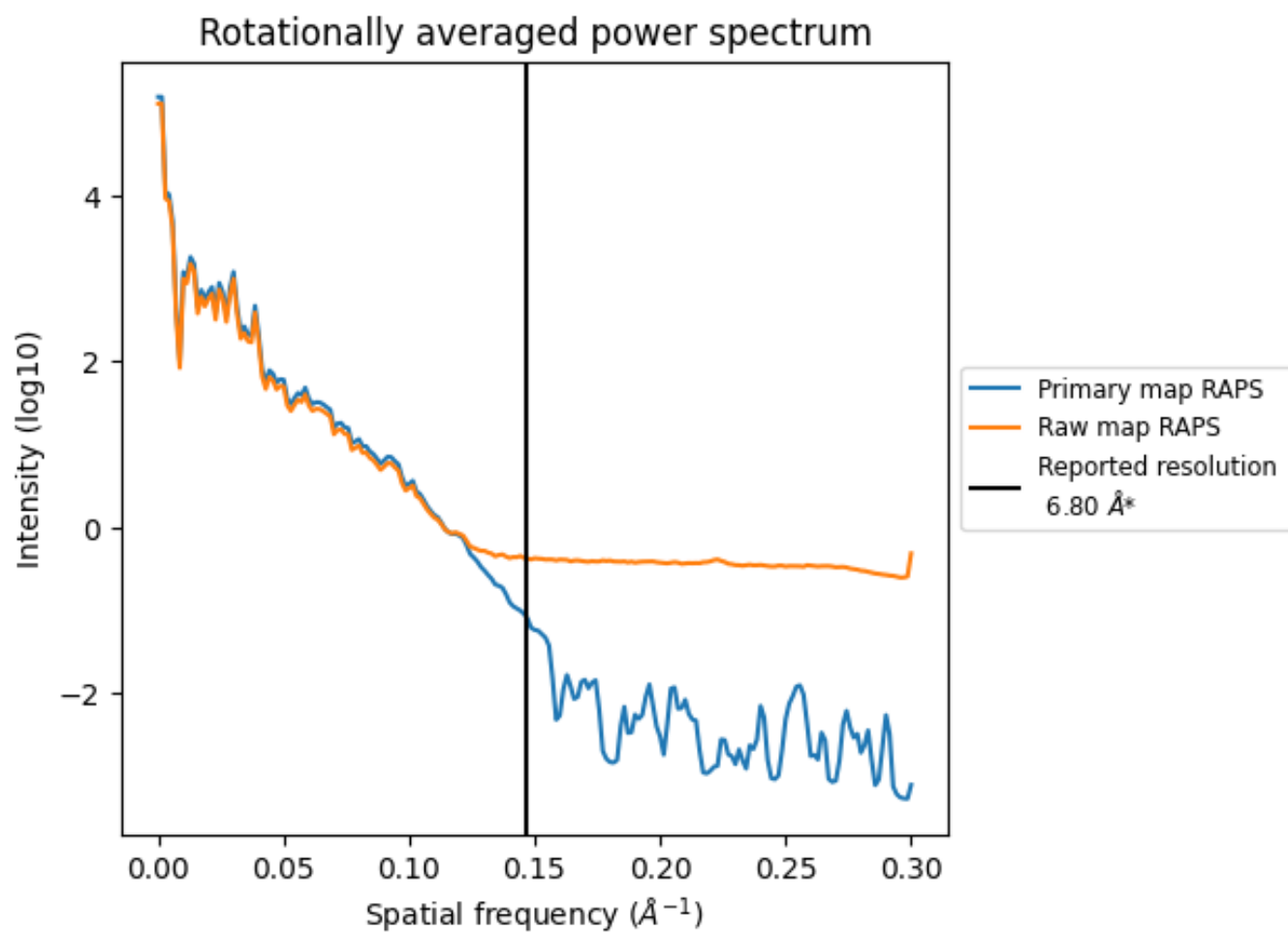
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 12869 nm³; this corresponds to an approximate mass of 11625 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](#)

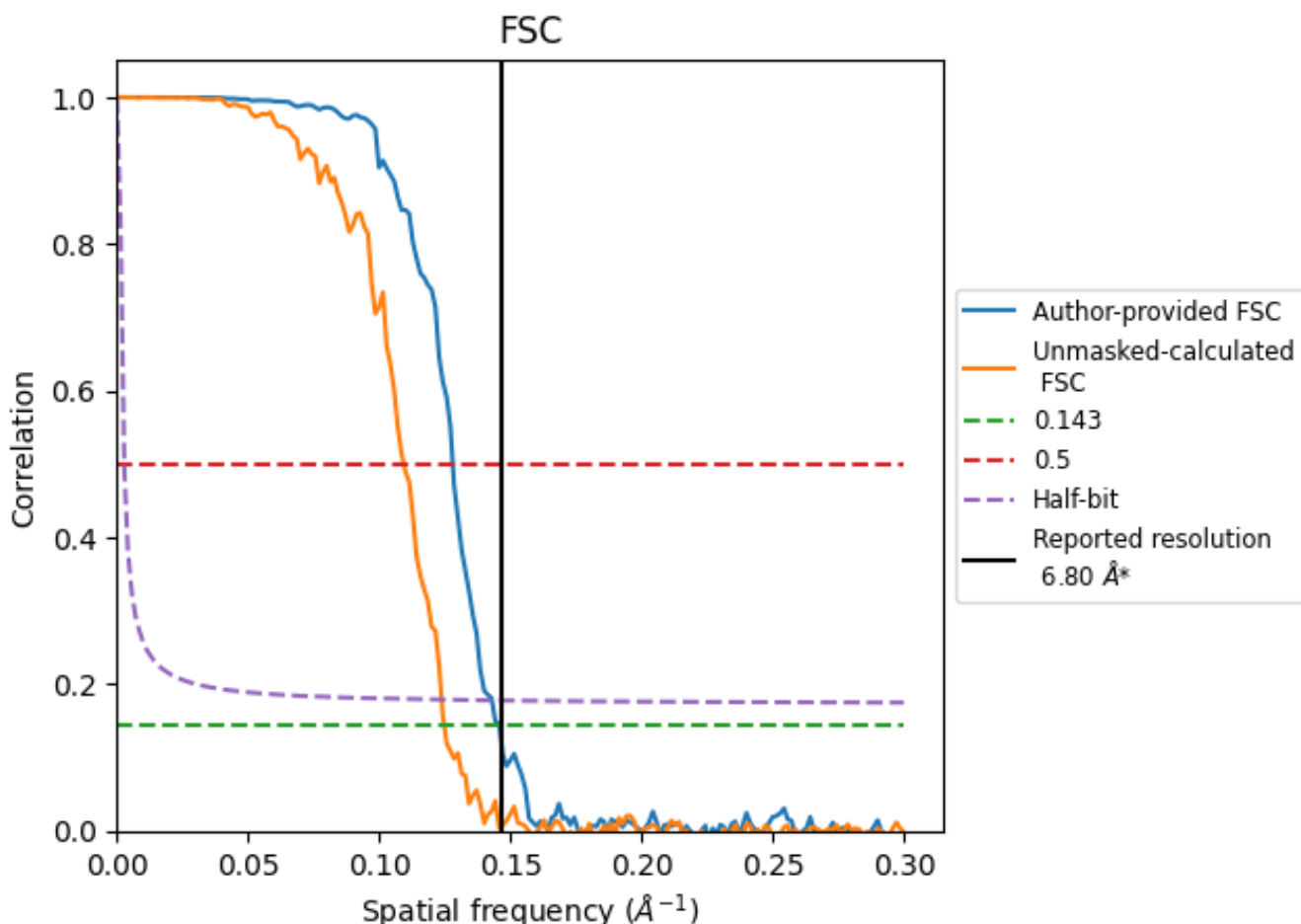


*Reported resolution corresponds to spatial frequency of 0.147 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.147 Å⁻¹

8.2 Resolution estimates [i](#)

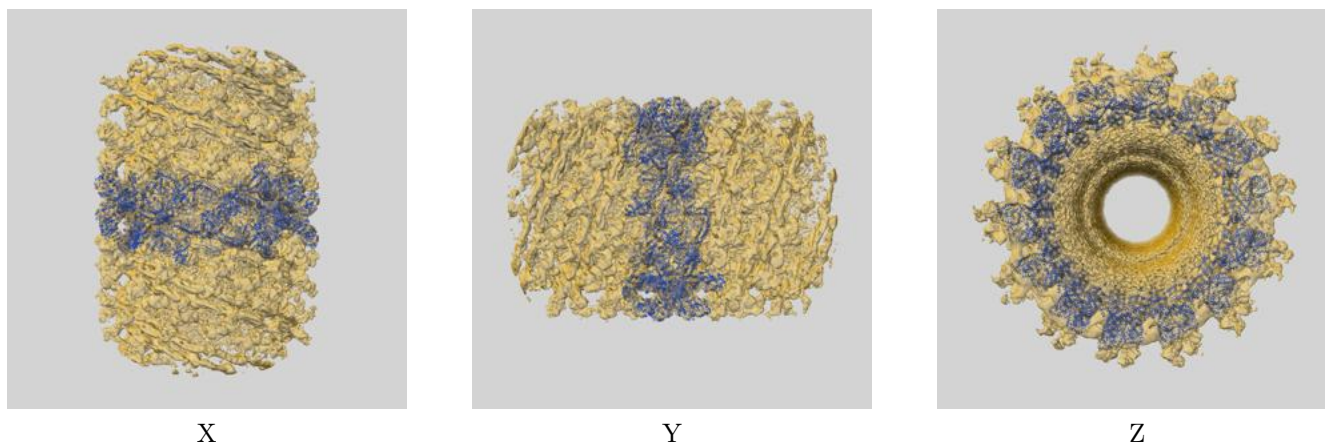
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.80	-	-
Author-provided FSC curve	6.86	7.81	6.99
Unmasked-calculated*	8.01	9.14	8.07

*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 8.01 differs from the reported value 6.8 by more than 10 %

9 Map-model fit [i](#)

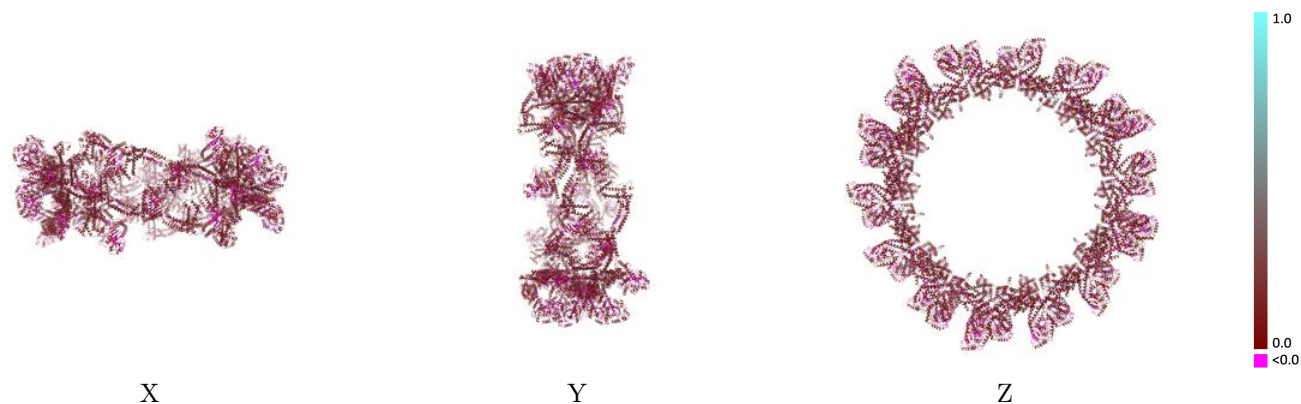
This section contains information regarding the fit between EMDB map EMD-26984 and PDB model 8CT9. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



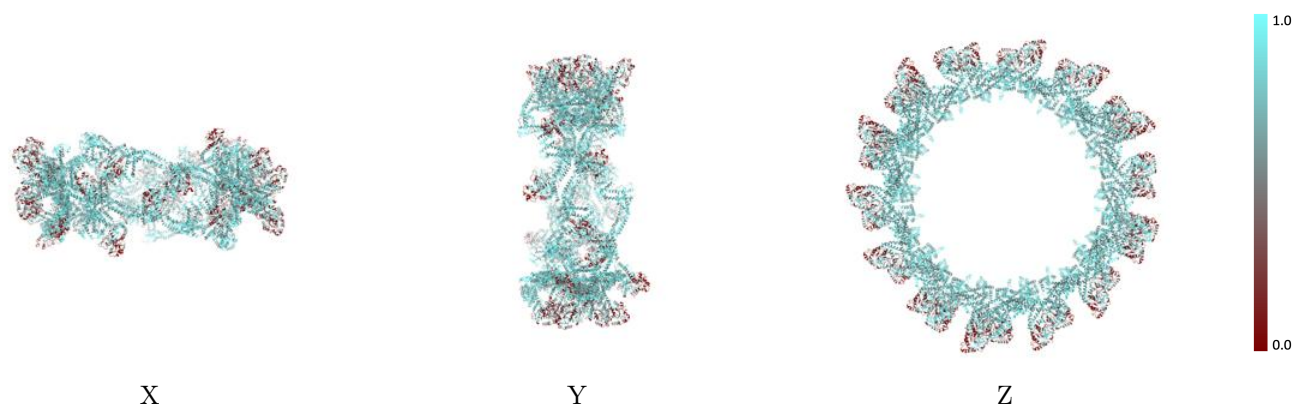
The images above show the 3D surface view of the map at the recommended contour level 0.0025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



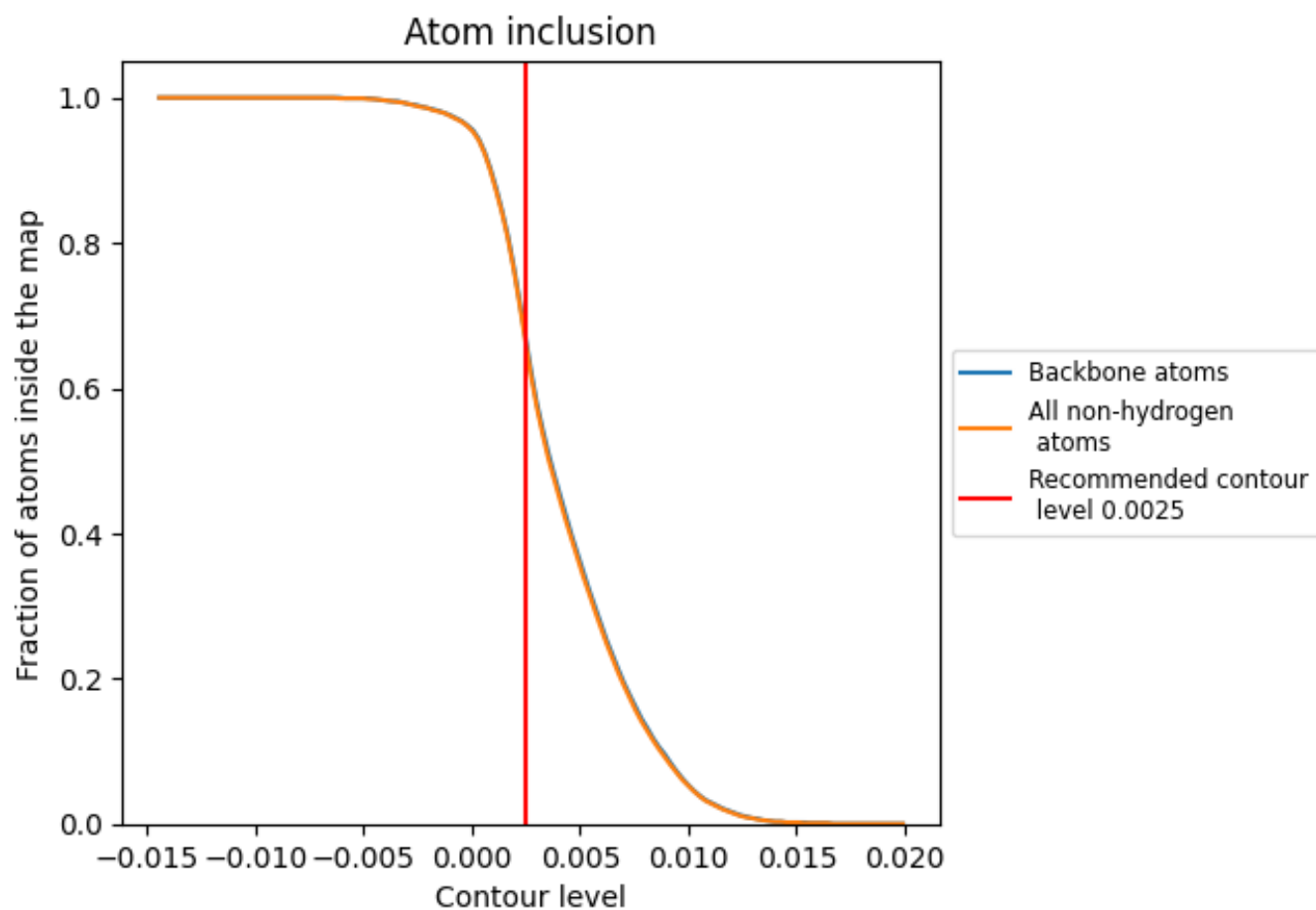
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0025).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 66% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6600	 0.1330
A	 0.6670	 0.1340
B	 0.6650	 0.1370
C	 0.6640	 0.1350
D	 0.6690	 0.1330
E	 0.6510	 0.1290
F	 0.6640	 0.1330
G	 0.6620	 0.1310
H	 0.6680	 0.1320
I	 0.6620	 0.1300
J	 0.6470	 0.1280
K	 0.6700	 0.1350
L	 0.6560	 0.1330
M	 0.6680	 0.1330
N	 0.6670	 0.1340
O	 0.6660	 0.1360
P	 0.6560	 0.1330
Q	 0.6630	 0.1330
R	 0.6700	 0.1350
S	 0.6620	 0.1320
T	 0.6680	 0.1330
U	 0.6660	 0.1310
V	 0.6680	 0.1330
W	 0.6670	 0.1330
X	 0.6570	 0.1330
Y	 0.6680	 0.1350
Z	 0.6640	 0.1340
a	 0.6550	 0.1300
b	 0.6710	 0.1330
c	 0.6680	 0.1370
d	 0.6590	 0.1360
e	 0.6550	 0.1300
f	 0.6700	 0.1340
g	 0.6660	 0.1340
h	 0.6370	 0.1320

