



wwPDB EM Validation Summary Report ⓘ

Apr 5, 2026 – 08:03 PM UTC

PDB ID : 9HEO / pdb_00009heo
EMDB ID : EMD-52085
Title : Open-state RyR1 in 0.05% POPC micelles, in complex with a nanobody and FKBP
Authors : Li, C.; Efremov, R.G.
Deposited on : 2024-11-14
Resolution : 3.40 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:

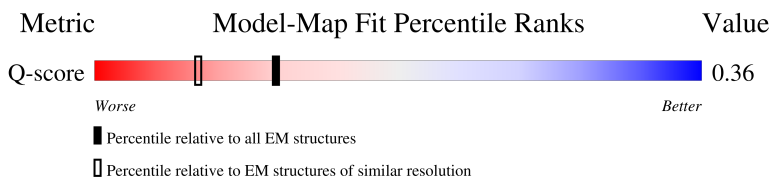
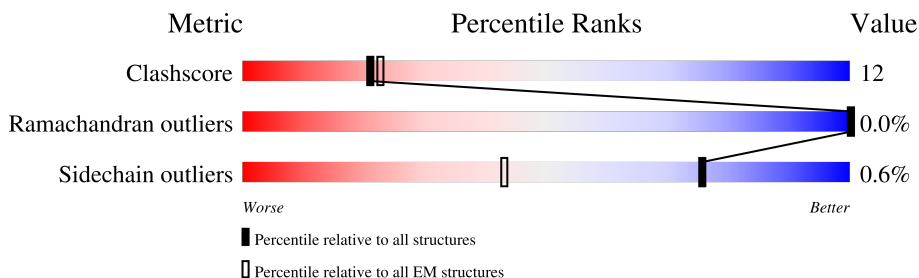
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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





The reported resolution of this entry is 3.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	5027	 63% 23% 14%
1	C	5027	 63% 23% 14%
1	G	5027	 63% 23% 14%
1	J	5027	 63% 23% 14%

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Mol	Chain	Length	Quality of chain
2	B	126	
2	D	126	
2	H	126	
2	K	126	
3	E	107	
3	F	107	
3	I	107	
3	L	107	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 146783 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 Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	4327	Total	C	N	O	S	1	0
			34225	21798	5895	6303	229		
1	C	4327	Total	C	N	O	S	1	0
			34225	21798	5895	6303	229		
1	G	4327	Total	C	N	O	S	1	0
			34225	21798	5895	6303	229		
1	J	4327	Total	C	N	O	S	1	0
			34224	21797	5895	6303	229		

- Molecule 2 is a protein called Nanobody 9657.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	126	Total	C	N	O	S	0	0
			961	594	167	195	5		
2	D	126	Total	C	N	O	S	0	0
			961	594	167	195	5		
2	H	126	Total	C	N	O	S	0	0
			961	594	167	195	5		
2	K	126	Total	C	N	O	S	0	0
			961	594	167	195	5		

- Molecule 3 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
3	F	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
3	I	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
3	L	107	Total	C	N	O	S	0	0
			818	516	144	154	4		

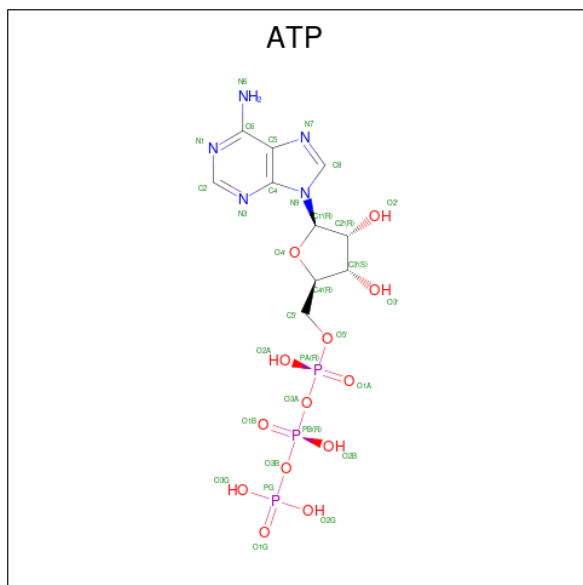
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	100	ASP	GLY	conflict	UNP Q8HYX6
F	100	ASP	GLY	conflict	UNP Q8HYX6
I	100	ASP	GLY	conflict	UNP Q8HYX6
L	100	ASP	GLY	conflict	UNP Q8HYX6

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	Zn	0
			1	1	
4	C	1	Total	Zn	0
			1	1	
4	G	1	Total	Zn	0
			1	1	
4	J	1	Total	Zn	0
			1	1	

- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



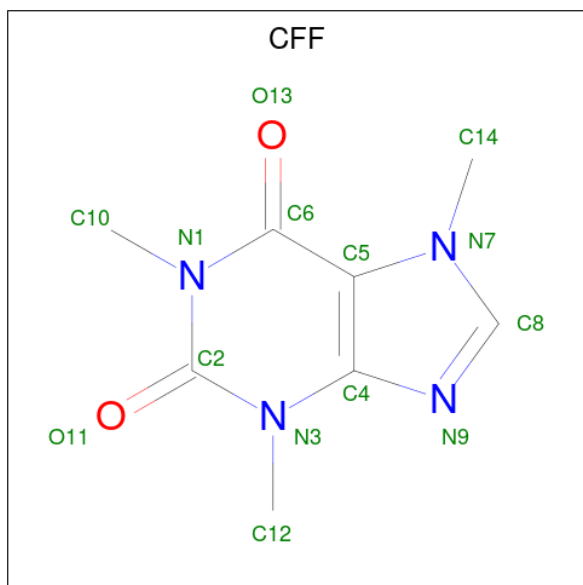
Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	G	1	Total	C	N	O	P	0
			31	10	5	13	3	

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Mol	Chain	Residues	Atoms					AltConf
5	J	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 6 is CAFFEINE (CCD ID: CFF) (formula: $C_8H_{10}N_4O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
6	A	1	Total	C	N	O	0
			14	8	4	2	
6	C	1	Total	C	N	O	0
			14	8	4	2	
6	G	1	Total	C	N	O	0
			14	8	4	2	
6	J	1	Total	C	N	O	0
			14	8	4	2	

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

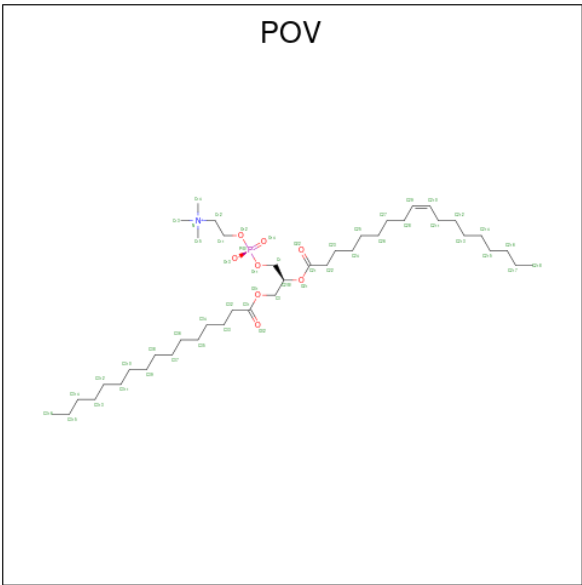
Mol	Chain	Residues	Atoms		AltConf
7	A	1	Total	Ca	0
			1	1	
7	C	1	Total	Ca	0
			1	1	
7	G	1	Total	Ca	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
7	J	1	Total	Ca	0
			1	1	

- Molecule 8 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylammonio)ethyl phosphate (CCD ID: POV) (formula: C₄₂H₈₂NO₈P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
8	A	1	Total	C	N	O	P	0
			49	39	1	8	1	
8	A	1	Total	C	N	O	P	0
			47	37	1	8	1	
8	A	1	Total	C	N	O	P	0
			50	40	1	8	1	
8	A	1	Total	C	N	O	P	0
			46	36	1	8	1	
8	A	1	Total	C	N	O	P	0
			20	11	1	7	1	
8	A	1	Total	C	N	O	P	0
			20	11	1	7	1	
8	A	1	Total	C	N	O	P	0
			20	12	1	6	1	
8	A	1	Total	C	N	O	P	0
			35	25	1	8	1	
8	A	1	Total	C	N	O	P	0
			28	18	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
8	A	1	Total	C	N	O	P	0
			24	15	1	7	1	
8	A	1	Total	C	N	O	P	0
			34	24	1	8	1	
8	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
8	A	1	Total	C	N	O	P	0
			47	37	1	8	1	
8	A	1	Total	C	N	O	P	0
			41	31	1	8	1	
8	A	1	Total	C	N	O	P	0
			31	21	1	8	1	
8	A	1	Total	C	N	O	P	0
			40	30	1	8	1	
8	A	1	Total	C	N	O	P	0
			48	38	1	8	1	
8	A	1	Total	C				0
			13	13				
8	C	1	Total	C	N	O	P	0
			40	30	1	8	1	
8	C	1	Total	C	N	O	P	0
			48	38	1	8	1	
8	C	1	Total	C				0
			13	13				
8	C	1	Total	C	N	O	P	0
			49	39	1	8	1	
8	C	1	Total	C	N	O	P	0
			47	37	1	8	1	
8	C	1	Total	C	N	O	P	0
			50	40	1	8	1	
8	C	1	Total	C	N	O	P	0
			46	36	1	8	1	
8	C	1	Total	C	N	O	P	0
			20	11	1	7	1	
8	C	1	Total	C	N	O	P	0
			20	11	1	7	1	
8	C	1	Total	C	N	O	P	0
			20	12	1	6	1	
8	C	1	Total	C	N	O	P	0
			35	25	1	8	1	
8	C	1	Total	C	N	O	P	0
			28	18	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
8	C	1	Total	C	N	O	P	0
			24	15	1	7	1	
8	C	1	Total	C	N	O	P	0
			34	24	1	8	1	
8	C	1	Total	C	N	O	P	0
			52	42	1	8	1	
8	C	1	Total	C	N	O	P	0
			47	37	1	8	1	
8	C	1	Total	C	N	O	P	0
			41	31	1	8	1	
8	C	1	Total	C	N	O	P	0
			31	21	1	8	1	
8	G	1	Total	C	N	O	P	0
			40	30	1	8	1	
8	G	1	Total	C	N	O	P	0
			48	38	1	8	1	
8	G	1	Total	C				0
			13	13				
8	G	1	Total	C	N	O	P	0
			49	39	1	8	1	
8	G	1	Total	C	N	O	P	0
			47	37	1	8	1	
8	G	1	Total	C	N	O	P	0
			50	40	1	8	1	
8	G	1	Total	C	N	O	P	0
			46	36	1	8	1	
8	G	1	Total	C	N	O	P	0
			20	11	1	7	1	
8	G	1	Total	C	N	O	P	0
			20	11	1	7	1	
8	G	1	Total	C	N	O	P	0
			20	12	1	6	1	
8	G	1	Total	C	N	O	P	0
			35	25	1	8	1	
8	G	1	Total	C	N	O	P	0
			28	18	1	8	1	
8	G	1	Total	C	N	O	P	0
			24	15	1	7	1	
8	G	1	Total	C	N	O	P	0
			34	24	1	8	1	
8	G	1	Total	C	N	O	P	0
			52	42	1	8	1	

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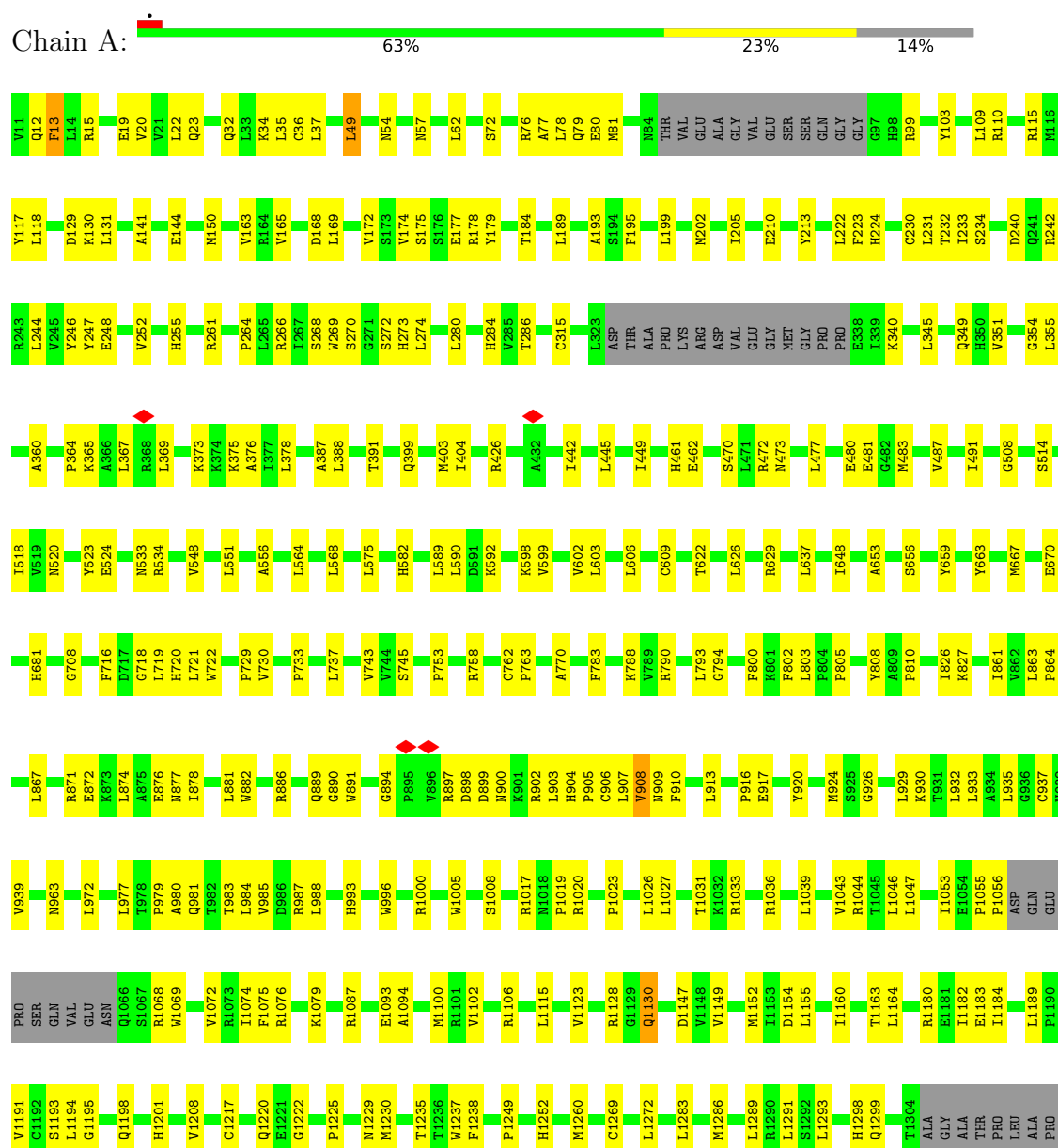
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Mol	Chain	Residues	Atoms					AltConf
8	G	1	Total	C	N	O	P	0
			47	37	1	8	1	
8	G	1	Total	C	N	O	P	0
			41	31	1	8	1	
8	G	1	Total	C	N	O	P	0
			31	21	1	8	1	
8	J	1	Total	C	N	O	P	0
			52	42	1	8	1	
8	J	1	Total	C	N	O	P	0
			47	37	1	8	1	
8	J	1	Total	C	N	O	P	0
			41	31	1	8	1	
8	J	1	Total	C	N	O	P	0
			31	21	1	8	1	
8	J	1	Total	C	N	O	P	0
			40	30	1	8	1	
8	J	1	Total	C	N	O	P	0
			48	38	1	8	1	
8	J	1	Total	C				0
			13	13				
8	J	1	Total	C	N	O	P	0
			49	39	1	8	1	
8	J	1	Total	C	N	O	P	0
			47	37	1	8	1	
8	J	1	Total	C	N	O	P	0
			50	40	1	8	1	
8	J	1	Total	C	N	O	P	0
			46	36	1	8	1	
8	J	1	Total	C	N	O	P	0
			20	11	1	7	1	
8	J	1	Total	C	N	O	P	0
			20	11	1	7	1	
8	J	1	Total	C	N	O	P	0
			20	12	1	6	1	
8	J	1	Total	C	N	O	P	0
			35	25	1	8	1	
8	J	1	Total	C	N	O	P	0
			28	18	1	8	1	
8	J	1	Total	C	N	O	P	0
			24	15	1	7	1	
8	J	1	Total	C	N	O	P	0
			34	24	1	8	1	

3 Residue-property plots

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

• Molecule 1: Ryanodine receptor 1

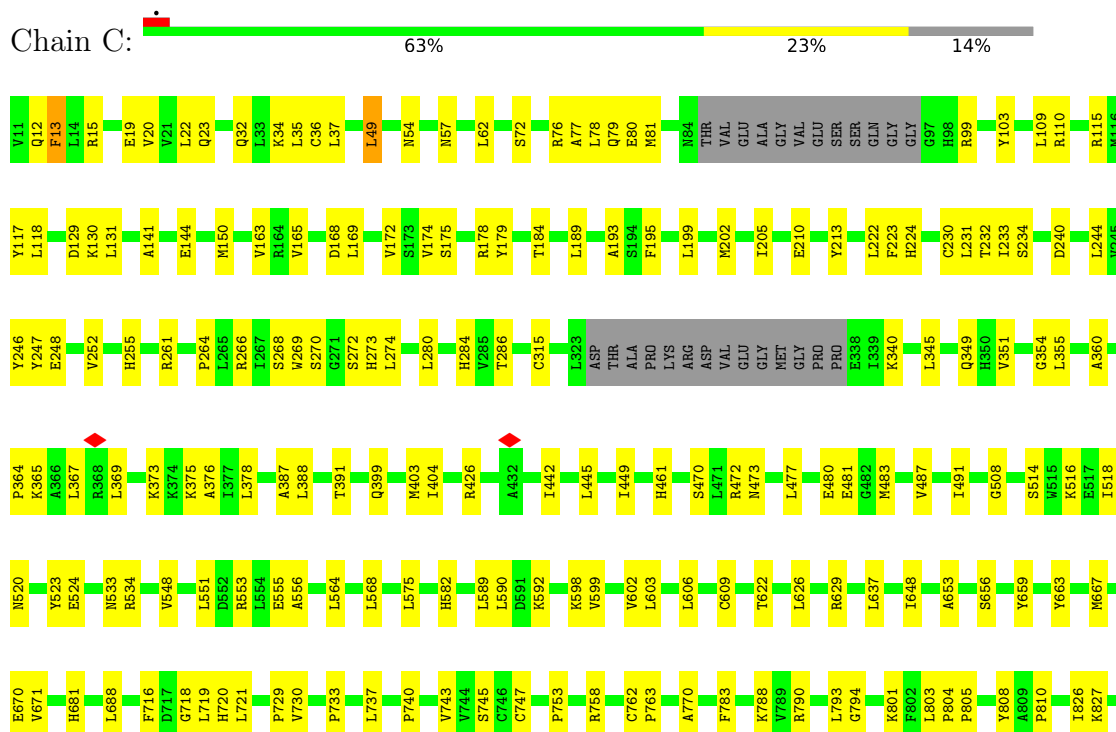


A2759	L2672	L2577	D2464	L2377	Y2256	L2094	Y1977	GLU	T1769	M1610	C1447	PRO
E2760	T2675	M2578	D2465	T2380	Y2259	L2097	M1981	GLU	S1770	W1626	V1448	GLY
Y2761	L2678	V2579	V2467	E2381	E2259	V2098	L2098	GLU	L1771	A1627	P1455	GLN
L2762	L2678	M2582	G2468	E2382	L2265	M2101	F2012	LYS	H1775	M1637	M1462	PRO
H2763	T2682	L2583	I2469	I2384	S2270	V2102	E2025	GLU	A1784	A1471	A1471	ALA
E2764	Y2691	R2588	P2477	I2386	T2271	V2111	R2028	ASP	A1785	C1647	THR	GLU
K2765	L2698	L2589	T2478	I2386	P2272	Q2112	L2031	GLU	L1786	M1476	LYS	ALA
W2766	S2590	R2590	L2479	R2392	L2273	S2113	L2031	GLU	P1787	L1650	LYS	ALA
A2767	L2595	R2591	D2482	R2395	D2274	S2117	L2031	GLU	ALA	L1651	ASN	ARG
F2768	Q2599	L2595	L2485	GLY	V2275	V2117	D2037	GLU	ALA	E1652	LYS	ALA
D2769	Q2599	Q2599	L2485	VAL	S2279	M2120	Q2045	LYS	GLY	H1665	ALA	ALA
K2770	Q2599	Q2599	Q2486	ARG	S2279	M2120	Q2045	LYS	VAL	H1665	ALA	ALA
I2771	T2703	T2603	Q2487	ARG	Q2291	L2123	GLU	ASP	E1793	R1668	PHE	PRO
Q2772	C2704	T2603	Q2488	ASP	E2292	L2124	GLY	ALA	F1500	F1500	LEU	PRO
N2773	T2706	D2605	K2489	ARG	Q2293	H2125	GLU	LYS	P1803	L1676	PHE	ASP
N2774	L2710	C2606	M2490	ARG	E2296	R2126	GLU	GLU	R1808	H1688	LYS	TYR
W2775	P2711	L2610	V2495	ARG	K2297	Q2127	GLU	GLU	Q1506	Q1506	ALA	GLU
S2776	Y2715	R2615	D2496	HIS	V2298	Y2128	GLU	GLU	G1507	G1507	LYS	ASN
Y2777	Y2715	P2616	D2497	PHE	V2298	Y2128	PRO	GLU	R1508	R1508	LEU	LEU
G2778	Y2719	P2616	A2500	GLY	G2306	L2131	GLU	ALA	L1694	L1694	ALA	ARG
E2779	Y2719	S2617	S2501	GLU	L2307	L2138	GLU	PRO	L1695	L1695	MET	ARG
N2780	E2724	M2618	M2502	GLU	K2316	L2144	GLU	GLU	H1696	H1696	MET	ALA
V2781	K2725	L2619	R2508	PRO	G2317	I2144	THR	GLY	H1702	H1702	GLY	GLY
D2782	LYS	H2621	T2512	GLU	Y2318	P2146	LEU	LYS	A1523	A1523	TRP	TRP
E2783	ALA	L2622	T2512	GLU	G2321	S2147	SER	ASP	L1526	L1526	GLY	GLY
THR	THR	L2623	F2517	M2414	G2322	S2148	ARG	ASP	H1511	H1511	ALA	ALA
VAL	VAL	R2624	L2518	H2417	W2323	T2152	LEU	LEU	L1519	L1519	ALA	ALA
ASP	ASP	L2625	L2518	L2418	W2323	M2153	ARG	LEU	F1540	F1540	GLY	GLY
ALA	ALA	L2626	L2522	L2422	G2327	M2153	ARG	LEU	LEU	LEU	GLY	GLY
GLU	GLY	V2627	F2526	L2422	G2327	I2167	LEU	LEU	P1544	P1544	LYS	LYS
GLY	GLY	D2628	F2526	L2422	G2327	I2167	LEU	LEU	F1549	F1549	GLU	GLU
N2734	R2738	D2629	M2530	L2429	Y2331	M2186	GLU	GLU	P1550	P1550	GLY	GLY
R2790	P2739	V2630	M2530	D2431	L2332	M2186	THR	THR	A1551	A1551	THR	THR
L2791	E2741	E2635	A2534	R2435	L2332	I2167	VAL	VAL	HIS	HIS	ALA	ALA
R2792	T2740	K2638	S2535	C2436	L2332	I2167	VAL	VAL	ASP	ASP	LYS	LYS
P2793	E2741	M2639	L2536	A2437	F2339	G2202	LYS	LYS	V1552	V1552	GLY	GLY
Y2794	T2742	P2640	L2536	E2439	F2340	M2203	LYS	LYS	V1554	V1554	VAL	VAL
K2795	L2743	K2642	F2541	E2439	F2340	M2203	LYS	LYS	L1555	L1555	PRO	PRO
L2796	W2744	L2643	F2541	E2439	F2340	M2203	LYS	LYS	I1562	I1562	GLY	GLY
F2797	V2745	L2644	W2546	M2440	R2354	T2206	GLU	GLU	Q1563	Q1563	ASP	ASP
S2798	V2745	T2645	A2547	L2442	R2355	V2210	PRO	PRO	F1564	F1564	THR	THR
E2799	L2746	T2645	L2548	L2443	T2358	W2211	LYS	LYS	Q1569	Q1569	GLN	GLN
K2800	L2747	Y2648	L2548	L2443	R2359	V2212	GLU	GLU	I1572	I1572	PRO	PRO
D2801	P2748	W2652	Y2553	K2447	E2362	M2228	GLU	GLU	Y1434	Y1434	VAL	VAL
E2749	E2749	W2652	Y2553	G2448	E2362	M2228	GLU	GLU	F1580	F1580	GLY	GLY
W2750	W2750	W2661	L2559	E2449	C2363	R1964	LEU	LEU	V1437	V1437	ALA	ALA
L2751	L2751	A2662	L2559	E2449	F2364	C2232	PRO	PRO	Y1437	Y1437	GLN	GLN
D2752	D2752	A2662	L2559	R2452	F2364	C2232	ALA	ALA	E1444	E1444	VAL	VAL
S2753	S2753	E2670	T2563	I2453	R2369	R2234	GLU	GLU	P1445	P1445	VAL	VAL
R2806	F2754	E2671	A2576	L2463	L2376	Q2247	GLU	GLU	S1446	S1446	GLY	GLY
W2807	F2755	E2671	A2576	L2463	L2376	Q2247	GLU	GLU				
P2808	W2756	E2671	A2576	L2463	L2376	Q2247	GLU	GLU				
I2809	K2757	E2671	A2576	L2463	L2376	Q2247	GLU	GLU				
K2810	F2758	E2671	A2576	L2463	L2376	Q2247	GLU	GLU				
E2811	F2758	E2671	A2576	L2463	L2376	Q2247	GLU	GLU				
S2812	F2758	E2671	A2576	L2463	L2376	Q2247	GLU	GLU				
L2813	F2758	E2671	A2576	L2463	L2376	Q2247	GLU	GLU				
K2814	F2758	E2671	A2576	L2463	L2376	Q2247	GLU	GLU				
A2815	F2758	E2671	A2576	L2463	L2376	Q2247	GLU	GLU				
M2816	F2758	E2671	A2576	L2463	L2376	Q2247	GLU	GLU				
I2817	F2758	E2671	A2576	L2463	L2376	Q2247	GLU	GLU				
A2818	F2758	E2671	A2576	L2463	L2376	Q2247	GLU	GLU				



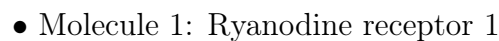
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L4884	M4887	I4897	G4898	I4901	R4913	L4914	V4915	F4916	D4917	I4918	F4922	F4923	V4924	I4925	I4927	I4931	I4932	Q4933	I4936	E4948	K4951	T4956	K4957	C4958	F4959	S4965	F4968	G4974	F4975	H4978	T4979	L4980	E4981	E4982	L4985	A4986	M4989	L4995	E5000																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
H5003	T5004	E5007	M5011	M5012	M5013	Q5015	M5019	D5020	D5026	C5027	F5028	R5029	K5030	S5037																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
SER	GLY	TRP	GLY	SER	GLY	ALA	GLY	GLU	GLU	GLU	GLU	GLY	M4626		F4631	E4640	D4641	T4651		A4654	F4655	I4658	I4659	V4666	I4670	F4671	K4672	L4673	E4674		K4680	L4681		L4686	Y4687	D4696	M4697	K4698	G4699	Q4700	V4705	M4716	D4717	K4718	M4723	H4724																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
PRO	PRO	GLU	PRO	LYS	LYS	ALA	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	GLY	GLY	ASP	ASP	GLU	GLU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
ASP	MET	ALA	ASP	THR	THR	PRO	ASP	ALA	ALA	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	VAL	VAL	VAL	VAL	VAL	VAL	ALA	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
LEU	TRP	ALA	VAL	VAL	ALA	ARG	ALA	ALA	ALA	GLY	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	VAL	GLU	LEU	LEU	LEU	ALA	GLY	MET	PRO	ASP	THR	GLU	ARG	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA

• Molecule 1: Ryanodine receptor 1





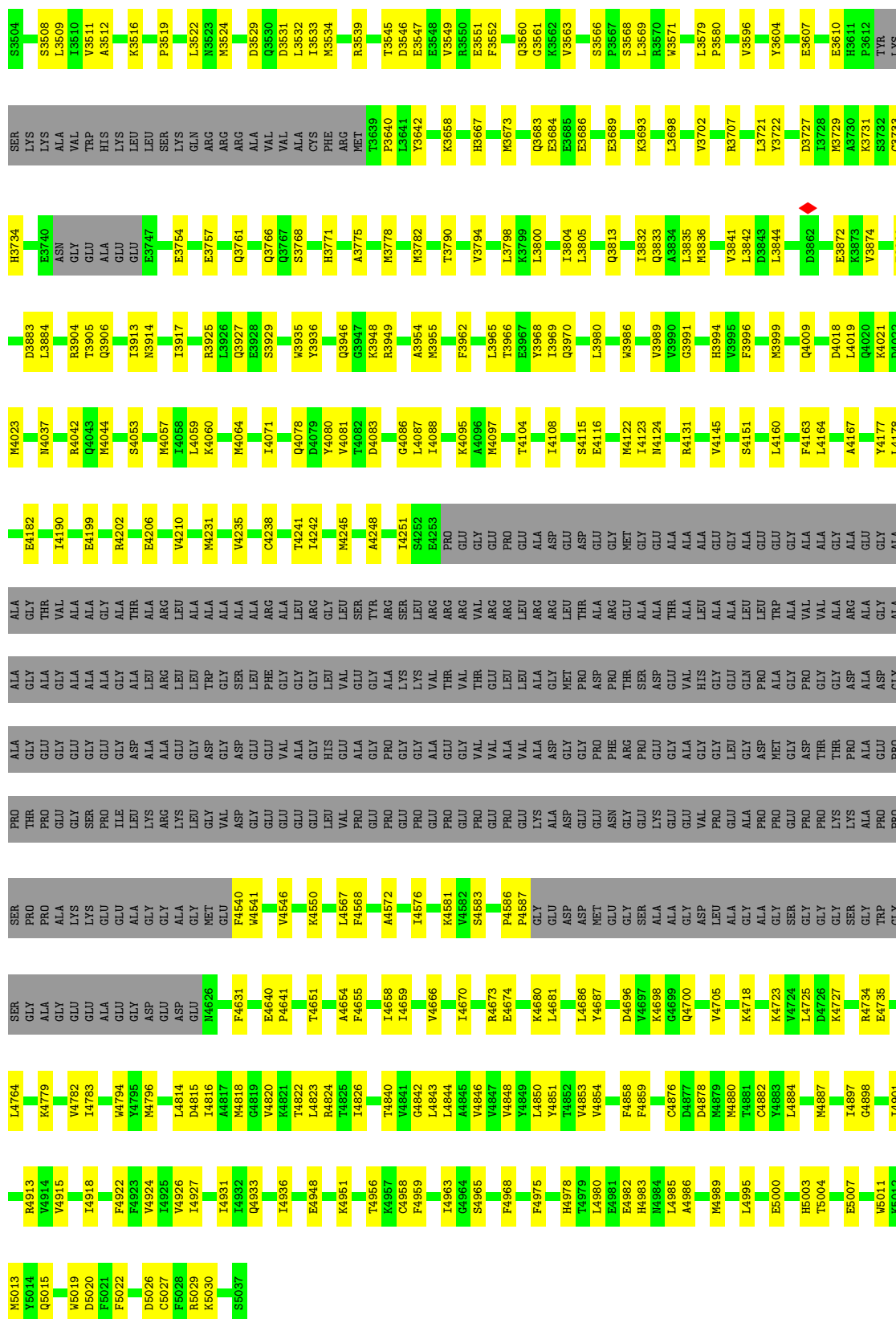
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L3698	L3379	ARG	V3183	Y3182	P2990	K2922	GLU	P2793	ALA	L2626	F2526
V3702	P3580	THR	R3403	L3277	H2991	A2923	Y2856	Y2794	GLY	F2627	R2530
V3707	V3596	LYS	Y3406	L3281	I2995	E2925	R2856	K2795	R2738	D2629	K2534
R3707	Q3597	LYS	P3262	P3282	K2996	L2927	P2857	T2796	P2739	V2630	S2535
D3719	Q3598	ARG	Y3409	L3103	L3002	K2928	Q2858	F2797	V2740	E2635	S2536
V3720	V3602	GLY	P3410	K3104	L3003	F2929	P2859	S2798	M2638	K2638	M2539
L3721	L3603	ASP	R3414	K3105	P3003	F2929	P2860	E2799	E2741	P2640	F2541
Y3722	Y3604	THR	Y3415	V3107	P3004	L2930	D2861	K2742	T2743	L2641	M2546
E3727	E3607	TTR	R3196	L3110	N3007	Q2931	L2862	L2743	L2743	K2642	A2547
D3727	E3610	S3504	R3420	R3111	Q3008	M2932	S2863	N2744	N2744	L2644	L2548
L3728	H3611	S3508	A3421	LEU	Y3009	M2933	G2864	V2745	V2745	T2645	R2552
K3729	P3612	T3610	H3422	GLY	F3010	G2934	V2865	I2746	I2746	Y2648	Y2553
A3730	TYR	L3316	W3423	LYS	C3014	Y2935	T2866	L2747	L2747	V2652	V2558
K3731	LYS	G3317	N3428	SER	L3018	A2936	L2867	P2748	P2748	W2652	L2559
S3732	SER	N3318	E3207	ALA	S3019	S2868	E2869	E2749	E2749	V2661	T2563
C3733	LYS	L3319	P3208	ARG	T3020	E2870	E2871	K2750	K2750	A2662	K2562
H3734	LYS	T3322	N3211	THR	P3021	GLY	L2871	L2751	L2751	Y2662	L2563
E3740	VAL	I3323	S3217	GLN	K3022	LYS	M2874	D2752	D2752	E2670	A2576
ASN	TRP	D3330	S3222	VAL	A3023	ASP	A2875	S2753	S2753	L2577	K2578
GLY	GLY	W3334	K3223	GLY	V3024	GLY	E2880	F2754	F2754	L2672	V2579
ALA	LEU	W3335	S3224	VAL	L3025	L2946	R2881	I2755	I2755	T2675	K2582
LEU	LEU	M3336	E3225	GLY	G3026	D2947	Y2882	K2756	K2756	L2678	L2583
SER	SER	R3337	R3226	R3127	A3031	T2948	W2886	F2758	F2758	I2682	R2588
GLN	GLN	V3340	E3226	N3128	S3032	GLY	K2890	E2760	E2760	Y2691	S2589
LYS	LYS	F3341	R3227	I3129	I3039	LYS	K2891	Y2761	Y2761	M2698	R2591
ARG	ARG	A3342	P3233	T3130	K3036	E2952	E2892	T2762	T2762	A2699	L2595
ALA	ALA	I3345	V3236	T3133	M3038	K2953	K2891	H2763	H2763	M2700	Q2599
VAL	VAL	R3350	P3244	P3138	I3039	R2954	K2891	E2764	E2764	P2701	C2702
ALA	ALA	R3350	V3245	H3146	L3049	G2955	K2891	K2765	K2765	R2600	D2602
CYS	CYS	L3354	L3246	H3150	H3052	L2961	E2895	W2766	W2766	L2703	V2605
PHE	PHE	L3354	L3246	Q3151	P3062	Q2962	A2896	A2767	A2767	C2704	V2602
ARG	ARG	G3363	L3249	F3152	V3065	L2963	K2897	F2768	F2768	I2706	E2604
MET	MET	R3366	M3250	R3152	N3066	L2964	E2898	D2769	D2769	L2710	C2606
LYS	LYS	K3367	A3251	D3155	L3067	L2965	K2899	K2770	K2770	P2711	L2610
ALA	ALA	A3369	I3253	Q3162	L3068	W2966	G2900	I2771	I2771	V2715	R2615
LYS	LYS	G3370	L3256	V3163	H3069	M2967	T2901	Q2772	Q2772	Y2719	P2616
ALA	ALA	K3371	R3262	C3164	L3070	S2970	H2902	K2773	K2773	M2617	S2617
GLY	GLY	V3372	S3262	V3166	L3071	F2973	P2903	N2774	N2774	E2724	L2619
ASP	ASP	V3373	A3251	R3167	S3074	L2974	L2904	W2775	W2775	K2725	L2622
GLN	GLN	L3379	D3265	T3168	L3075	L2976	L2905	S2776	S2776	LYS	L2623
SER	SER	A3387	M3266	T3168	L3075	L2977	P2906	Y2777	Y2777	ALA	
GLY	GLY	E3371	E3271	T3172	T3079	E2978	Y2908	Q2778	Q2778	THR	
GLY	GLY	I3272	I3272	A2979	K3082	A2979	L2911	E2779	E2779		
SER	SER	T3273	T3273	V2980		V2981	T2912	LYS	LYS		
							A2913	ILE	ILE		
							K2914	SER	SER		
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							K2916	THR	THR		
							A2917	ALA	ALA		
							R2918	GLN	GLN		
							D2919	THR	THR		
								TVR	TVR		
								L2785	L2785		
								K2786	K2786		
								T2787	T2787		
								H2788	H2788		
								P2789	P2789		
								M2790	M2790		



E243	Y117	Y11
L244	L118	Q12
V245		F13
V246	D129	L14
Y247	K130	R15
E248	L131	
		E19
V252	A141	V20
		V21
H255	E144	L22
		Q23
R261	M150	
		Q32
P264	V163	L33
L265	R164	K34
R266	V165	L35
T267		C36
S268	D168	L37
T269	L169	
S270		L49
G271	V172	N54
S272	S173	
H273	V174	N57
L274	S175	
	S176	L62
	E177	
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H284	Y179	
		R76
T286	T184	A77
		L78
C315	L189	Q79
		E80
L323	A193	M81
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ALA		THR
PRO	L199	VAL
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ARG	M202	ALA
ASP		GLY
VAL	I205	VAL
GLU		GLU
GLY	E210	SER
MET		GLN
GLY	Y213	SER
PRO		GLY
PRO	L222	GLY
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I339	H224	H98
K340		R99
	C230	
	L231	Y103
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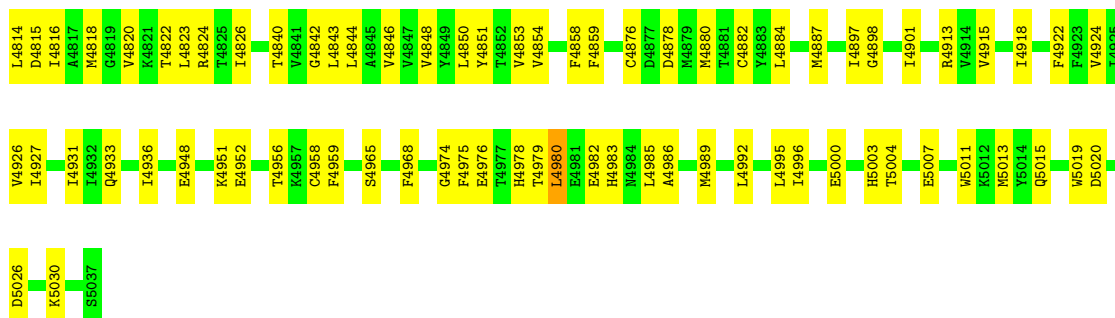
• Molecule 1: Ryanodine receptor 1

Chain J: 63% 23% 14%

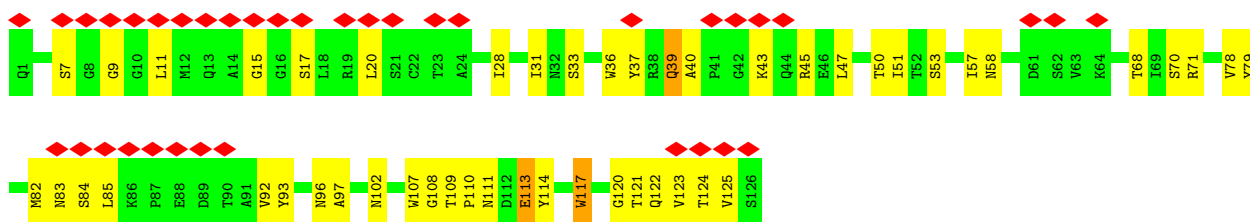




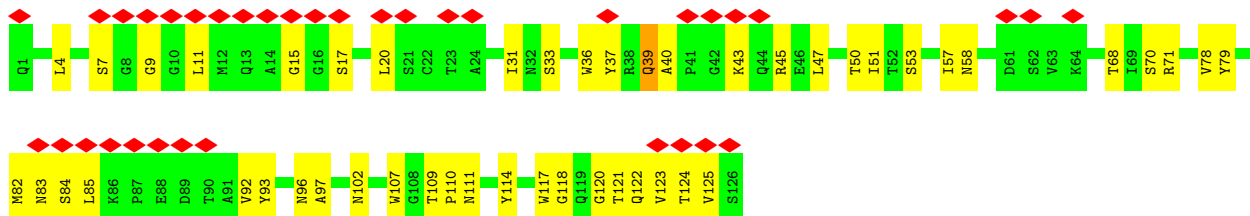
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PDB
PROTEIN DATA BANK



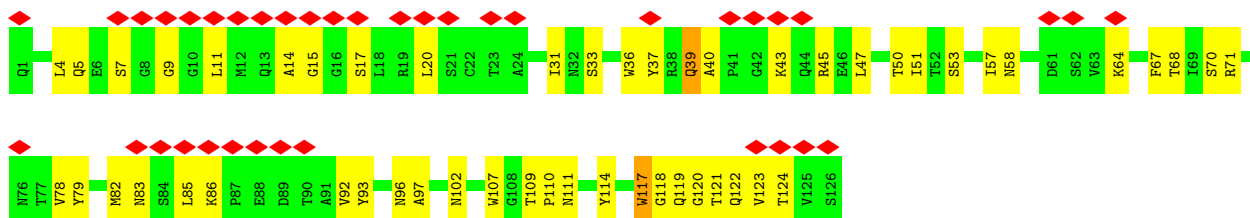
• Molecule 2: Nanobody 9657



• Molecule 2: Nanobody 9657



• Molecule 2: Nanobody 9657

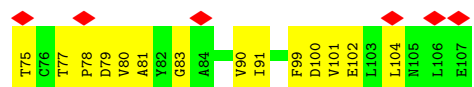
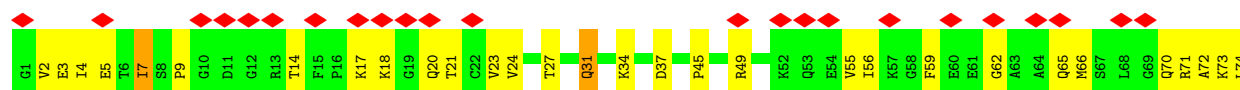


• Molecule 2: Nanobody 9657





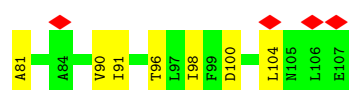
• Molecule 3: Peptidyl-prolyl cis-trans isomerase FKBP1B



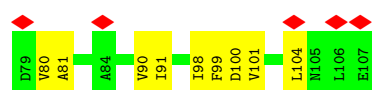
• Molecule 3: Peptidyl-prolyl cis-trans isomerase FKBP1B



• Molecule 3: Peptidyl-prolyl cis-trans isomerase FKBP1B



• Molecule 3: Peptidyl-prolyl cis-trans isomerase FKBP1B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	279776	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.280	Depositor
Minimum map value	-0.106	Depositor
Average map value	0.043	Depositor
Map value standard deviation	0.121	Depositor
Recommended contour level	0.3	Depositor
Map size (\AA)	479.136, 479.136, 479.136	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.426, 1.426, 1.426	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: POV, CFF, ZN, ATP, CA

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	0.26	0/35002	0.49	3/47442 (0.0%)
1	C	0.27	0/35002	0.50	1/47442 (0.0%)
1	G	0.28	0/35002	0.51	2/47442 (0.0%)
1	J	0.26	0/34999	0.49	2/47436 (0.0%)
2	B	0.38	0/981	0.66	1/1333 (0.1%)
2	D	0.35	0/981	0.65	1/1333 (0.1%)
2	H	0.48	0/981	0.72	1/1333 (0.1%)
2	K	0.52	0/981	0.74	1/1333 (0.1%)
3	E	0.59	0/834	0.93	3/1123 (0.3%)
3	F	0.57	0/834	0.87	0/1123
3	I	0.63	0/834	0.93	0/1123
3	L	0.66	0/834	0.90	0/1123
All	All	0.28	0/147265	0.52	15/199586 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	G	0	2
All	All	0	3

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3436	ARG	N-CA-C	7.07	118.99	111.28
1	A	1499	ASP	N-CA-C	-5.49	106.75	113.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	1499	ASP	N-CA-C	-5.41	106.85	113.50
1	G	1499	ASP	N-CA-C	-5.35	106.92	113.50
1	C	967	PRO	N-CA-CB	-5.32	98.29	102.28

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	5029	ARG	Sidechain
1	G	1033	ARG	Sidechain
1	G	5029	ARG	Sidechain

5.2 Too-close contacts

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	34225	0	33636	808	0
1	C	34225	0	33636	822	0
1	G	34225	0	33636	809	0
1	J	34224	0	33634	809	0
2	B	961	0	905	33	0
2	D	961	0	905	32	0
2	H	961	0	905	31	0
2	K	961	0	905	35	0
3	E	818	0	824	32	0
3	F	818	0	824	25	0
3	I	818	0	824	22	0
3	L	818	0	824	24	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	G	1	0	0	0	0
4	J	1	0	0	0	0
5	A	31	0	12	1	0
5	C	31	0	12	2	0
5	G	31	0	12	1	0
5	J	31	0	12	2	0
6	A	14	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	14	0	10	0	0
6	G	14	0	10	0	0
6	J	14	0	10	0	0
7	A	1	0	0	0	0
7	C	1	0	0	0	0
7	G	1	0	0	0	0
7	J	1	0	0	0	0
8	A	645	0	873	39	0
8	C	645	0	873	42	0
8	G	645	0	873	37	0
8	J	645	0	873	43	0
All	All	146783	0	145038	3476	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 12.

The worst 5 of 3476 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:G:3539:ARG:HH12	1:G:3552:PHE:HB2	1.24	1.00
1:C:3539:ARG:HH12	1:C:3552:PHE:HB2	1.24	1.00
1:J:3539:ARG:HH12	1:J:3552:PHE:HB2	1.24	0.99
1:C:3315:LEU:HD22	1:C:3345:ILE:HG12	1.51	0.91
1:G:3315:LEU:HD22	1:G:3345:ILE:HG12	1.51	0.91

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	4292/5027 (85%)	4162 (97%)	128 (3%)	2 (0%)	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	4292/5027 (85%)	4162 (97%)	129 (3%)	1 (0%)	100	100
1	G	4292/5027 (85%)	4164 (97%)	127 (3%)	1 (0%)	100	100
1	J	4290/5027 (85%)	4161 (97%)	127 (3%)	2 (0%)	100	100
2	B	124/126 (98%)	112 (90%)	12 (10%)	0	100	100
2	D	124/126 (98%)	111 (90%)	13 (10%)	0	100	100
2	H	124/126 (98%)	112 (90%)	12 (10%)	0	100	100
2	K	124/126 (98%)	109 (88%)	14 (11%)	1 (1%)	16	44
3	E	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
3	F	105/107 (98%)	99 (94%)	6 (6%)	0	100	100
3	I	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
3	L	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
All	All	18082/21040 (86%)	17493 (97%)	582 (3%)	7 (0%)	100	100

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	908	VAL
1	C	908	VAL
1	G	908	VAL
1	J	908	VAL
2	K	102	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	3688/4270 (86%)	3670 (100%)	18 (0%)	81	81
1	C	3688/4270 (86%)	3666 (99%)	22 (1%)	78	80
1	G	3688/4270 (86%)	3666 (99%)	22 (1%)	78	80
1	J	3688/4270 (86%)	3673 (100%)	15 (0%)	84	83
2	B	103/104 (99%)	100 (97%)	3 (3%)	37	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	103/104 (99%)	102 (99%)	1 (1%)	68	75
2	H	103/104 (99%)	101 (98%)	2 (2%)	50	66
2	K	103/104 (99%)	100 (97%)	3 (3%)	37	60
3	E	88/88 (100%)	85 (97%)	3 (3%)	32	57
3	F	88/88 (100%)	86 (98%)	2 (2%)	44	63
3	I	88/88 (100%)	84 (96%)	4 (4%)	24	51
3	L	88/88 (100%)	84 (96%)	4 (4%)	24	51
All	All	15516/17848 (87%)	15417 (99%)	99 (1%)	76	80

5 of 99 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	2192	TYR
2	H	68	THR
1	G	2308	GLN
1	G	3075	LEU
3	I	47	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 230 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	412	ASN
1	J	4020	GLN
1	G	2283	ASN
1	J	3869	GLN
1	J	1837	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 88 ligands modelled in this entry, 8 are monoatomic - leaving 80 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	POV	J	5115	-	45,45,51	0.52	0	51,53,59	0.48	0
8	POV	C	5122	-	30,30,51	0.75	1 (3%)	34,37,59	0.60	0
8	POV	C	5116	-	27,27,51	0.66	0	33,35,59	0.60	0
8	POV	C	5108	-	48,48,51	0.52	0	54,56,59	0.47	0
8	POV	G	5108	-	48,48,51	0.51	0	54,56,59	0.47	0
8	POV	J	5105	-	39,39,51	0.54	0	45,47,59	0.66	1 (2%)
8	POV	A	5115	-	33,33,51	0.34	0	39,41,59	0.39	0
8	POV	C	5114	-	19,19,51	0.66	0	24,25,59	0.58	0
8	POV	A	5107	-	49,49,51	0.50	0	55,57,59	0.48	0
8	POV	G	5112	-	19,19,51	0.73	0	24,26,59	0.72	0
8	POV	G	5114	-	19,19,51	0.66	0	24,25,59	0.58	0
8	POV	A	5120	-	39,39,51	0.55	0	45,47,59	0.65	1 (2%)
8	POV	C	5113	-	19,19,51	0.41	0	24,26,59	0.52	0
8	POV	C	5112	-	19,19,51	0.73	0	24,26,59	0.72	0
8	POV	C	5121	-	40,40,51	0.54	0	46,48,59	0.62	1 (2%)
8	POV	G	5121	-	40,40,51	0.54	0	46,48,59	0.62	1 (2%)
5	ATP	A	5102	-	32,33,33	0.53	0	48,52,52	0.59	0
8	POV	J	5113	-	46,46,51	0.52	0	52,54,59	0.49	0
8	POV	A	5109	-	19,19,51	0.73	0	24,26,59	0.72	0
8	POV	G	5111	-	45,45,51	0.52	0	51,53,59	0.48	0
8	POV	C	5115	-	34,34,51	0.60	0	40,42,59	0.56	0
8	POV	J	5102	-	46,46,51	0.31	0	52,54,59	0.29	0
8	POV	A	5122	-	12,12,51	0.22	0	11,11,59	0.23	0
8	POV	A	5116	-	51,51,51	0.50	0	57,59,59	0.47	0
6	CFF	J	5110	-	15,15,15	0.32	0	23,23,23	0.49	0
5	ATP	J	5109	-	32,33,33	0.53	0	48,52,52	0.59	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	ATP	C	5105	-	32,33,33	0.53	0	48,52,52	0.59	0
8	POV	J	5119	-	34,34,51	0.59	0	40,42,59	0.56	0
5	ATP	G	5105	-	32,33,33	0.53	0	48,52,52	0.59	0
8	POV	J	5104	-	30,30,51	0.75	1 (3%)	34,37,59	0.60	0
8	POV	C	5118	-	33,33,51	0.61	0	39,41,59	0.54	0
8	POV	C	5102	-	47,47,51	0.51	0	53,55,59	0.48	0
8	POV	J	5120	-	27,27,51	0.66	0	33,35,59	0.60	0
8	POV	A	5106	-	46,46,51	0.53	0	52,54,59	0.49	0
8	POV	G	5115	-	34,34,51	0.60	0	40,42,59	0.56	0
8	POV	A	5117	-	46,46,51	0.32	0	52,54,59	0.31	0
8	POV	G	5120	-	46,46,51	0.31	0	52,54,59	0.34	0
6	CFF	C	5106	-	15,15,15	0.33	0	23,23,23	0.49	0
8	POV	C	5120	-	46,46,51	0.31	0	52,54,59	0.31	0
8	POV	J	5117	-	19,19,51	0.39	0	24,26,59	0.51	0
8	POV	J	5107	-	12,12,51	0.23	0	11,11,59	0.23	0
8	POV	C	5109	-	46,46,51	0.53	0	52,54,59	0.49	0
8	POV	A	5110	-	19,19,51	0.38	0	24,26,59	0.53	0
8	POV	G	5109	-	46,46,51	0.53	0	52,54,59	0.49	0
8	POV	J	5103	-	40,40,51	0.54	0	46,48,59	0.62	1 (2%)
8	POV	J	5118	-	19,19,51	0.67	0	24,25,59	0.58	0
8	POV	J	5112	-	48,48,51	0.52	0	54,56,59	0.47	0
6	CFF	A	5103	-	15,15,15	0.32	0	23,23,23	0.49	0
8	POV	A	5105	-	48,48,51	0.52	0	54,56,59	0.47	0
8	POV	G	5102	-	47,47,51	0.51	0	53,55,59	0.48	0
8	POV	C	5119	-	51,51,51	0.50	0	57,59,59	0.47	0
8	POV	G	5116	-	27,27,51	0.66	0	33,35,59	0.60	0
8	POV	A	5108	-	45,45,51	0.52	0	51,53,59	0.48	0
8	POV	A	5111	-	19,19,51	0.66	0	24,25,59	0.58	0
8	POV	J	5106	-	47,47,51	0.51	0	53,55,59	0.48	0
8	POV	J	5122	-	33,33,51	0.61	0	39,41,59	0.54	0
8	POV	A	5113	-	27,27,51	0.66	0	33,35,59	0.60	0
8	POV	A	5112	-	34,34,51	0.60	0	40,42,59	0.56	0
8	POV	A	5114	-	23,23,51	0.67	0	28,30,59	0.68	0
8	POV	G	5122	-	30,30,51	0.74	1 (3%)	34,37,59	0.60	0
8	POV	G	5113	-	19,19,51	0.39	0	24,26,59	0.52	0
8	POV	C	5117	-	23,23,51	0.67	0	28,30,59	0.68	0
8	POV	G	5119	-	51,51,51	0.49	0	57,59,59	0.47	0
8	POV	A	5121	-	47,47,51	0.51	0	53,55,59	0.48	0
8	POV	J	5114	-	49,49,51	0.50	0	55,57,59	0.48	0
8	POV	G	5117	-	23,23,51	0.66	0	28,30,59	0.68	0
8	POV	G	5101	-	39,39,51	0.54	0	45,47,59	0.66	1 (2%)
6	CFF	G	5106	-	15,15,15	0.32	0	23,23,23	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	POV	J	5121	-	23,23,51	0.66	0	28,30,59	0.68	0
8	POV	C	5101	-	39,39,51	0.54	0	45,47,59	0.65	1 (2%)
8	POV	C	5103	-	12,12,51	0.22	0	11,11,59	0.23	0
8	POV	A	5118	-	40,40,51	0.54	0	46,48,59	0.62	1 (2%)
8	POV	C	5110	-	49,49,51	0.50	0	55,57,59	0.48	0
8	POV	G	5103	-	12,12,51	0.23	0	11,11,59	0.23	0
8	POV	J	5101	-	51,51,51	0.50	0	57,59,59	0.47	0
8	POV	G	5110	-	49,49,51	0.50	0	55,57,59	0.48	0
8	POV	G	5118	-	33,33,51	0.61	0	39,41,59	0.54	0
8	POV	A	5119	-	30,30,51	0.75	1 (3%)	34,37,59	0.60	0
8	POV	J	5116	-	19,19,51	0.72	0	24,26,59	0.72	0
8	POV	C	5111	-	45,45,51	0.52	0	51,53,59	0.48	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	POV	J	5115	-	-	10/49/49/55	-
8	POV	C	5122	-	-	14/33/33/55	-
8	POV	C	5116	-	-	9/31/31/55	-
8	POV	C	5108	-	-	23/52/52/55	-
8	POV	G	5108	-	-	23/52/52/55	-
8	POV	J	5105	-	-	10/43/43/55	-
8	POV	A	5115	-	-	9/37/37/55	-
8	POV	C	5114	-	-	7/20/20/55	-
8	POV	A	5107	-	-	23/53/53/55	-
8	POV	G	5112	-	-	8/22/22/55	-
8	POV	G	5114	-	-	7/20/20/55	-
8	POV	A	5120	-	-	10/43/43/55	-
8	POV	C	5113	-	-	6/22/22/55	-
8	POV	C	5112	-	-	8/22/22/55	-
8	POV	C	5121	-	-	15/44/44/55	-
8	POV	G	5121	-	-	15/44/44/55	-
5	ATP	A	5102	-	-	3/22/38/38	0/3/3/3
8	POV	J	5113	-	-	11/50/50/55	-
8	POV	A	5109	-	-	8/22/22/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	POV	G	5111	-	-	10/49/49/55	-
8	POV	C	5115	-	-	10/38/38/55	-
8	POV	J	5102	-	-	3/50/50/55	-
8	POV	A	5122	-	-	1/10/10/55	-
8	POV	A	5116	-	-	15/55/55/55	-
6	CFF	J	5110	-	-	-	0/2/2/2
5	ATP	J	5109	-	-	3/22/38/38	0/3/3/3
5	ATP	C	5105	-	-	3/22/38/38	0/3/3/3
8	POV	J	5119	-	-	10/38/38/55	-
5	ATP	G	5105	-	-	3/22/38/38	0/3/3/3
8	POV	J	5104	-	-	14/33/33/55	-
8	POV	C	5118	-	-	9/37/37/55	-
8	POV	C	5102	-	-	12/51/51/55	-
8	POV	J	5120	-	-	9/31/31/55	-
8	POV	A	5106	-	-	11/50/50/55	-
8	POV	G	5115	-	-	10/38/38/55	-
8	POV	A	5117	-	-	5/50/50/55	-
8	POV	G	5120	-	-	7/50/50/55	-
6	CFF	C	5106	-	-	-	0/2/2/2
8	POV	C	5120	-	-	5/50/50/55	-
8	POV	J	5117	-	-	9/22/22/55	-
8	POV	J	5107	-	-	1/10/10/55	-
8	POV	C	5109	-	-	11/50/50/55	-
8	POV	A	5110	-	-	6/22/22/55	-
8	POV	G	5109	-	-	11/50/50/55	-
8	POV	J	5103	-	-	15/44/44/55	-
8	POV	J	5118	-	-	7/20/20/55	-
8	POV	J	5112	-	-	23/52/52/55	-
6	CFF	A	5103	-	-	-	0/2/2/2
8	POV	A	5105	-	-	23/52/52/55	-
8	POV	G	5102	-	-	12/51/51/55	-
8	POV	C	5119	-	-	15/55/55/55	-
8	POV	G	5116	-	-	9/31/31/55	-
8	POV	A	5108	-	-	10/49/49/55	-
8	POV	A	5111	-	-	7/20/20/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	POV	J	5106	-	-	12/51/51/55	-
8	POV	J	5122	-	-	9/37/37/55	-
8	POV	A	5113	-	-	9/31/31/55	-
8	POV	A	5112	-	-	10/38/38/55	-
8	POV	A	5114	-	-	7/26/26/55	-
8	POV	G	5122	-	-	14/33/33/55	-
8	POV	G	5113	-	-	8/22/22/55	-
8	POV	C	5117	-	-	7/26/26/55	-
8	POV	G	5119	-	-	15/55/55/55	-
8	POV	A	5121	-	-	12/51/51/55	-
8	POV	J	5114	-	-	23/53/53/55	-
8	POV	G	5117	-	-	7/26/26/55	-
8	POV	G	5101	-	-	10/43/43/55	-
6	CFF	G	5106	-	-	-	0/2/2/2
8	POV	J	5121	-	-	7/26/26/55	-
8	POV	C	5101	-	-	10/43/43/55	-
8	POV	C	5103	-	-	1/10/10/55	-
8	POV	A	5118	-	-	15/44/44/55	-
8	POV	C	5110	-	-	23/53/53/55	-
8	POV	G	5103	-	-	1/10/10/55	-
8	POV	J	5101	-	-	15/55/55/55	-
8	POV	G	5110	-	-	23/53/53/55	-
8	POV	G	5118	-	-	9/37/37/55	-
8	POV	A	5119	-	-	14/33/33/55	-
8	POV	J	5116	-	-	8/22/22/55	-
8	POV	C	5111	-	-	10/49/49/55	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	5119	POV	O21-C2	-2.70	1.43	1.46
8	C	5122	POV	O21-C2	-2.70	1.43	1.46
8	J	5104	POV	O21-C2	-2.70	1.43	1.46
8	G	5122	POV	O21-C2	-2.61	1.43	1.46

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	5101	POV	C2-O21-C21	2.56	123.92	117.80
8	G	5101	POV	C2-O21-C21	2.56	123.92	117.80
8	J	5105	POV	C2-O21-C21	2.56	123.92	117.80
8	A	5120	POV	C2-O21-C21	2.55	123.90	117.80
8	C	5121	POV	C2-O21-C21	2.33	123.37	117.80

There are no chirality outliers.

5 of 797 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	5105	POV	C1-O11-P-O12
8	A	5105	POV	C1-O11-P-O14
8	A	5105	POV	C11-O12-P-O11
8	A	5105	POV	C11-O12-P-O14
8	A	5105	POV	O12-C11-C12-N

There are no ring outliers.

76 monomers are involved in 153 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	J	5115	POV	4	0
8	C	5122	POV	1	0
8	C	5116	POV	2	0
8	C	5108	POV	1	0
8	G	5108	POV	1	0
8	J	5105	POV	1	0
8	A	5115	POV	1	0
8	C	5114	POV	5	0
8	A	5107	POV	7	0
8	G	5112	POV	2	0
8	G	5114	POV	4	0
8	A	5120	POV	1	0
8	C	5113	POV	5	0
8	C	5112	POV	3	0
8	C	5121	POV	1	0
8	G	5121	POV	1	0
5	A	5102	ATP	1	0
8	J	5113	POV	2	0
8	A	5109	POV	2	0
8	G	5111	POV	4	0
8	C	5115	POV	5	0
8	J	5102	POV	3	0

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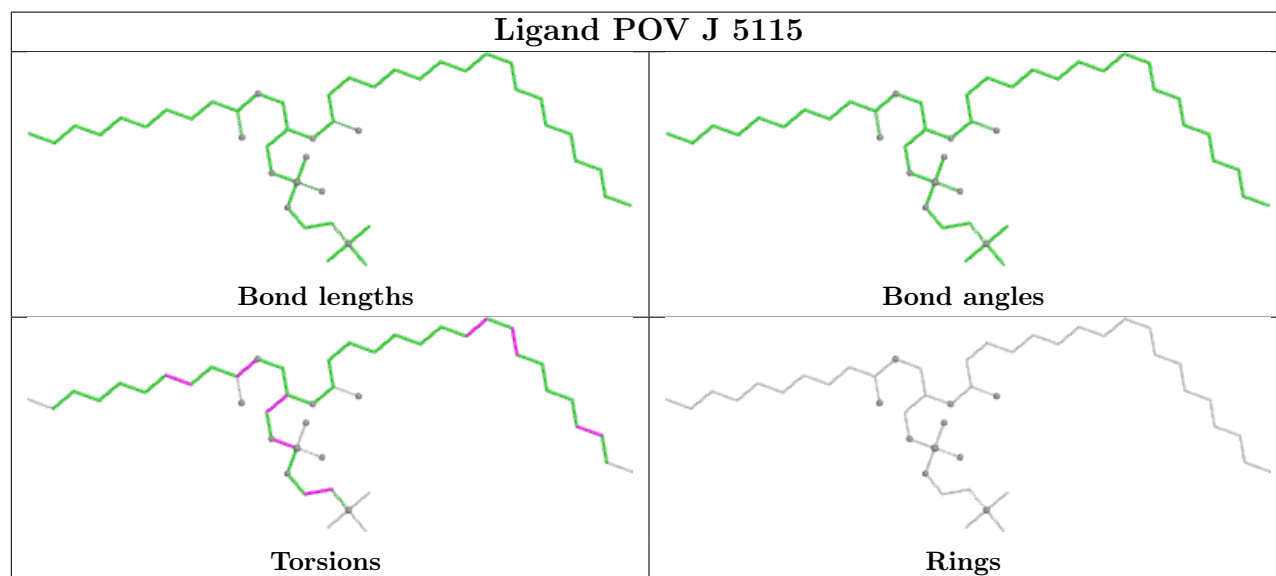
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	5122	POV	2	0
8	A	5116	POV	7	0
5	J	5109	ATP	2	0
5	C	5105	ATP	2	0
8	J	5119	POV	5	0
5	G	5105	ATP	1	0
8	J	5104	POV	1	0
8	C	5118	POV	1	0
8	C	5102	POV	2	0
8	J	5120	POV	1	0
8	A	5106	POV	1	0
8	G	5115	POV	4	0
8	A	5117	POV	3	0
8	G	5120	POV	1	0
8	C	5120	POV	4	0
8	J	5117	POV	5	0
8	J	5107	POV	2	0
8	C	5109	POV	1	0
8	A	5110	POV	2	0
8	G	5109	POV	2	0
8	J	5103	POV	1	0
8	J	5118	POV	5	0
8	J	5112	POV	2	0
8	A	5105	POV	2	0
8	G	5102	POV	2	0
8	C	5119	POV	5	0
8	G	5116	POV	1	0
8	A	5108	POV	3	0
8	A	5111	POV	4	0
8	J	5106	POV	2	0
8	J	5122	POV	1	0
8	A	5113	POV	1	0
8	A	5112	POV	5	0
8	A	5114	POV	2	0
8	G	5122	POV	1	0
8	G	5113	POV	3	0
8	C	5117	POV	3	0
8	G	5119	POV	4	0
8	A	5121	POV	3	0
8	J	5114	POV	7	0
8	G	5117	POV	3	0
8	G	5101	POV	1	0

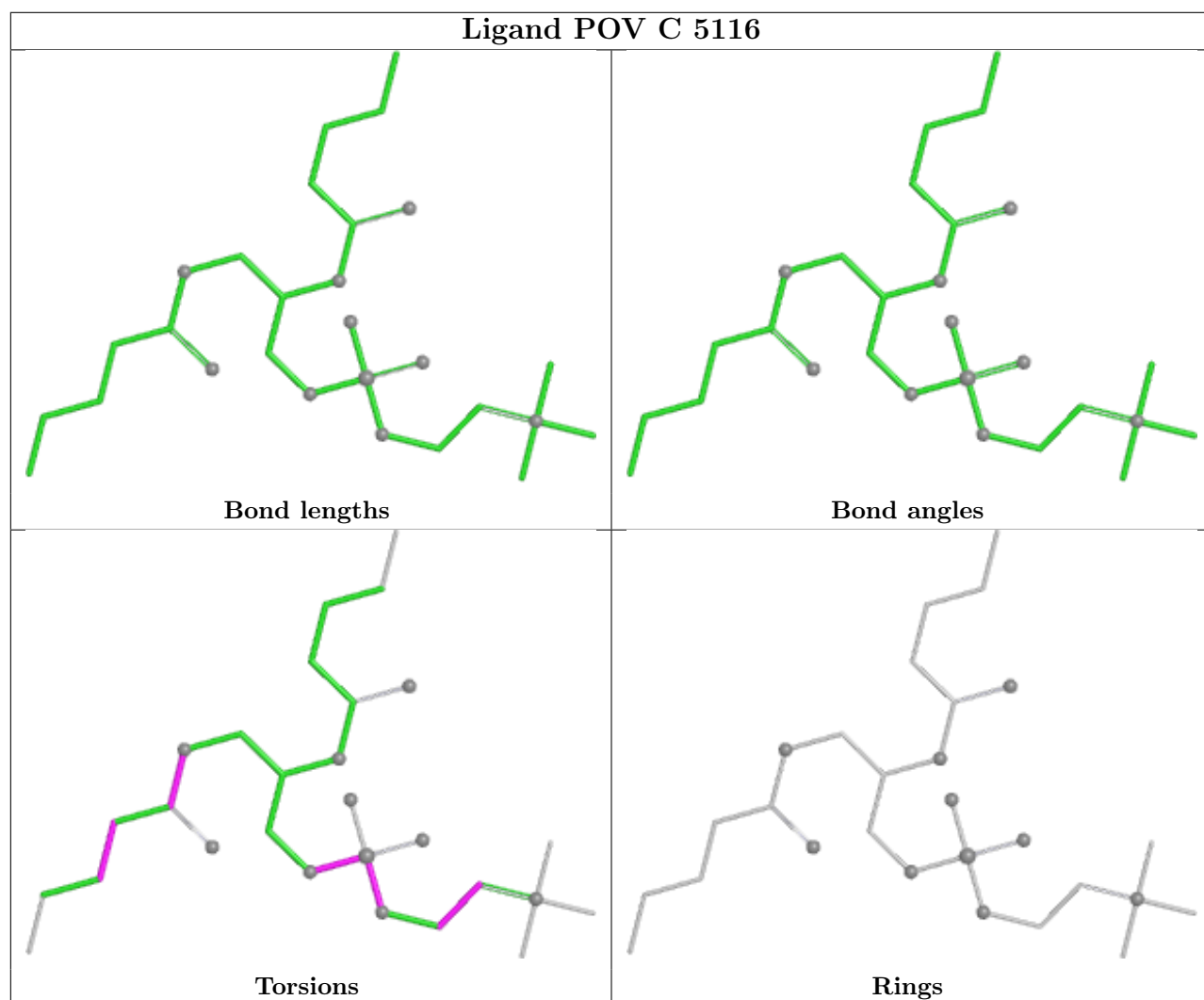
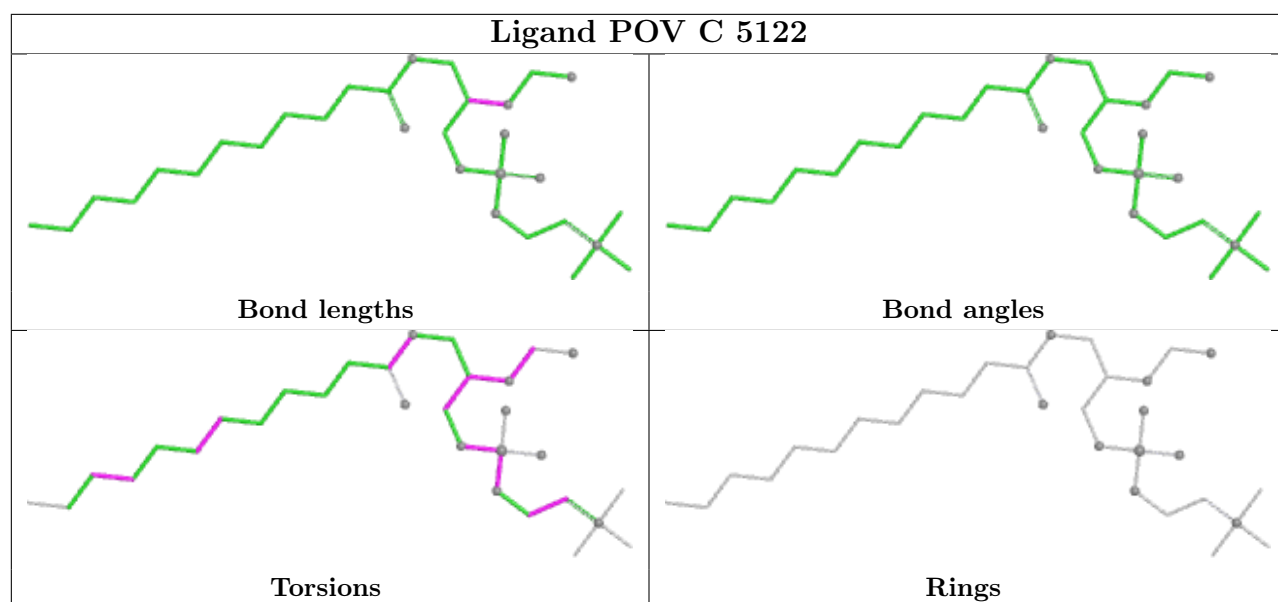
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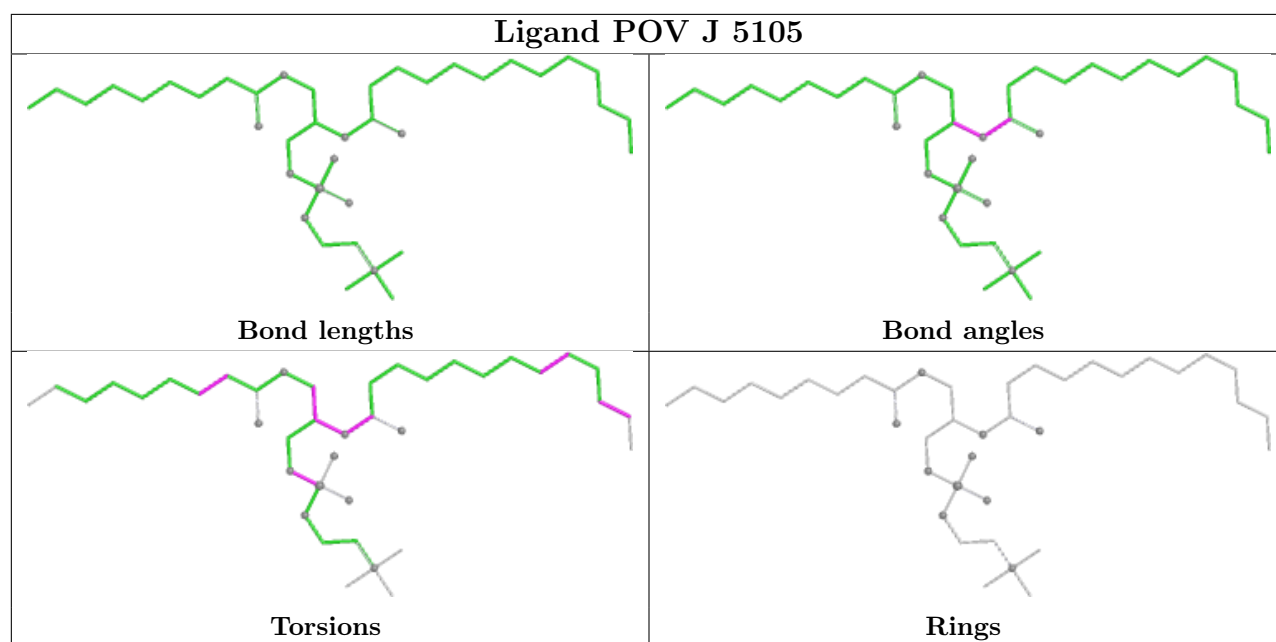
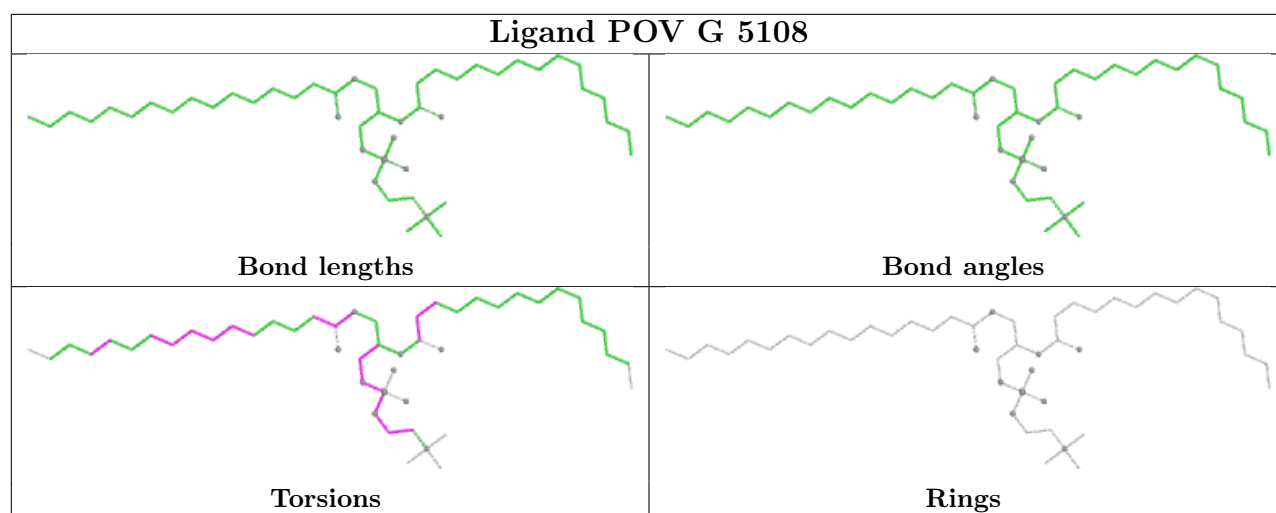
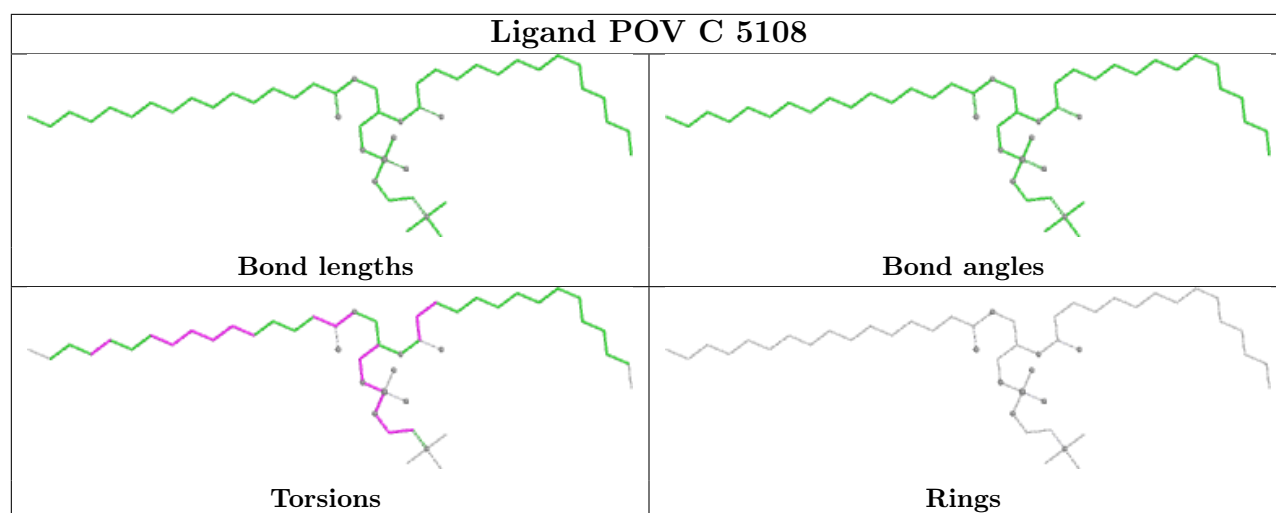
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	J	5121	POV	3	0
8	C	5101	POV	1	0
8	C	5103	POV	2	0
8	A	5118	POV	1	0
8	C	5110	POV	7	0
8	G	5103	POV	2	0
8	J	5101	POV	6	0
8	G	5110	POV	7	0
8	G	5118	POV	1	0
8	A	5119	POV	1	0
8	J	5116	POV	3	0
8	C	5111	POV	4	0

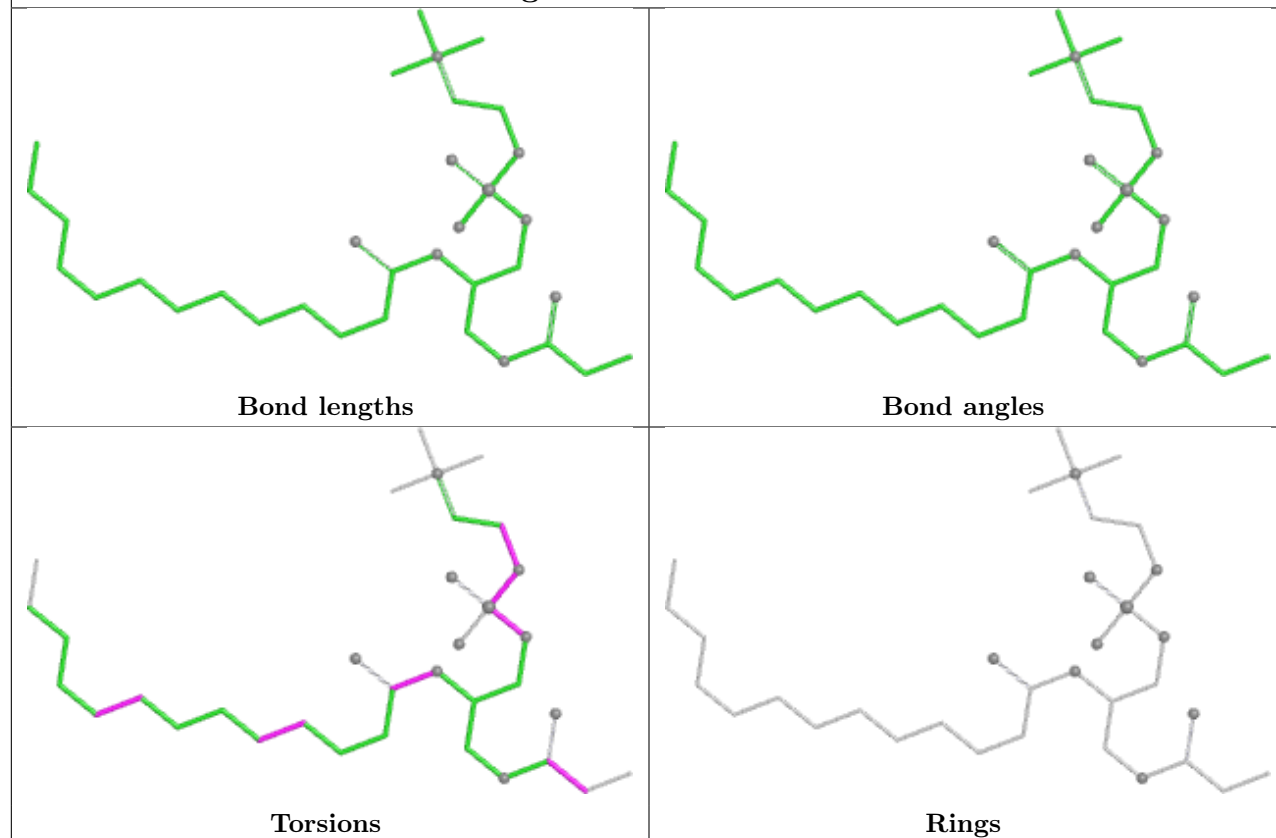
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



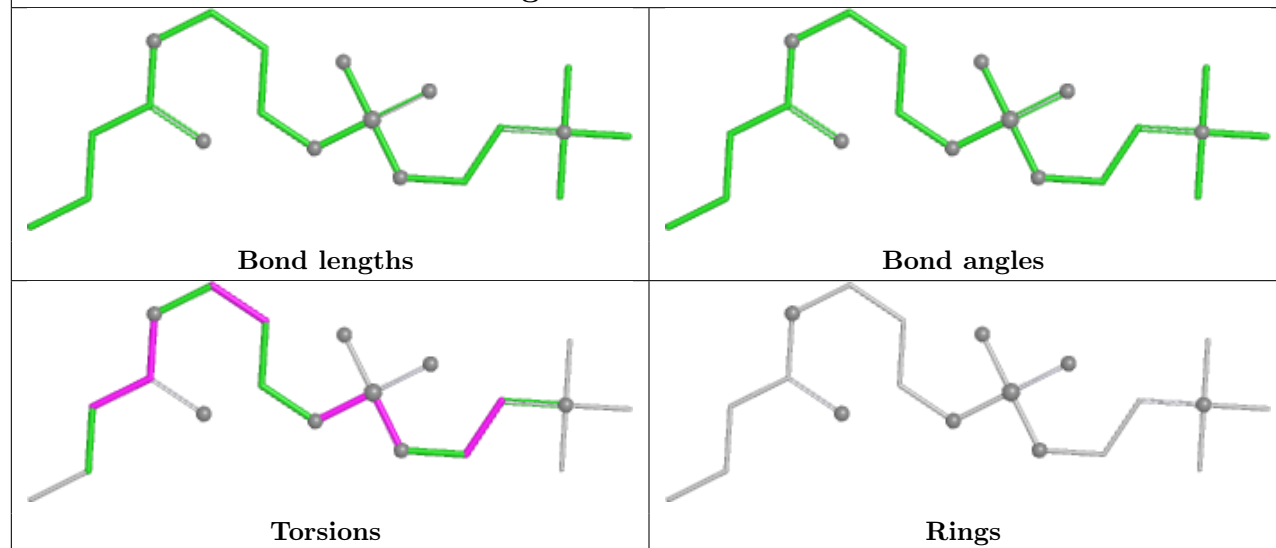


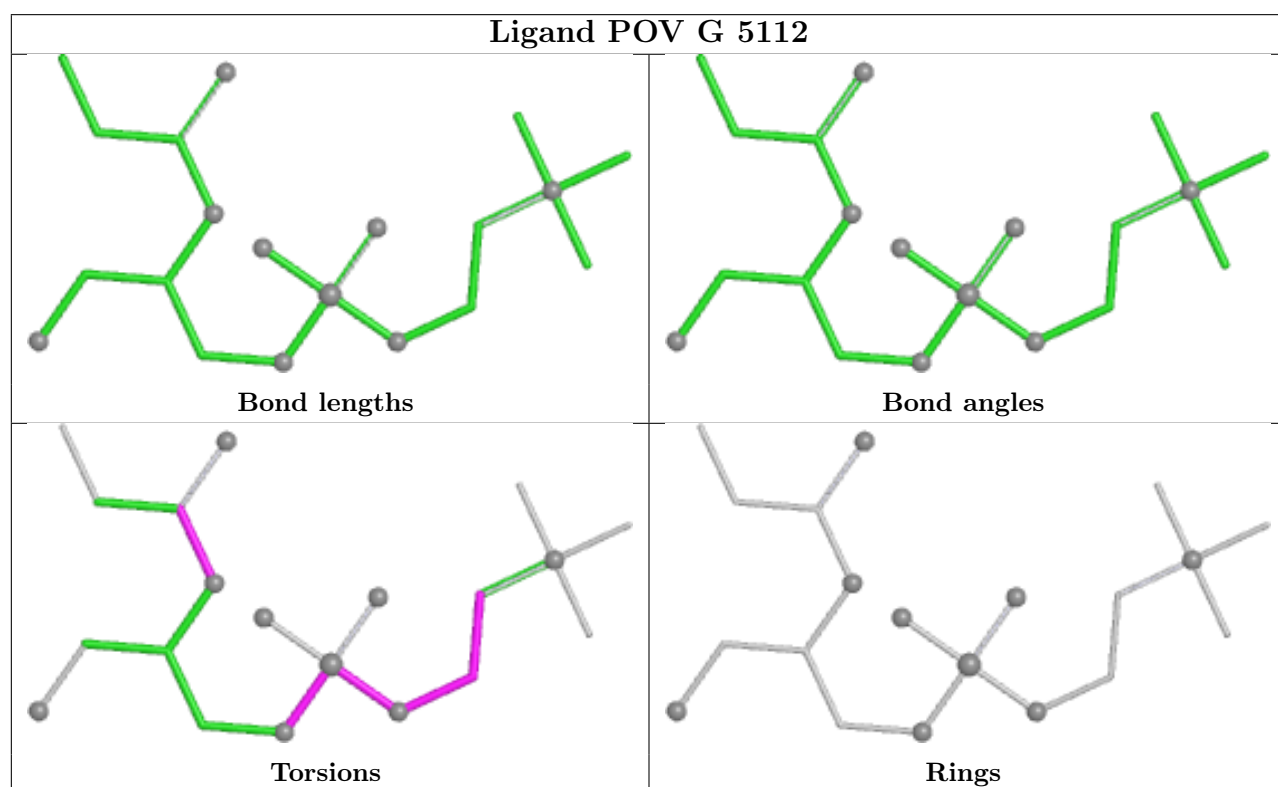
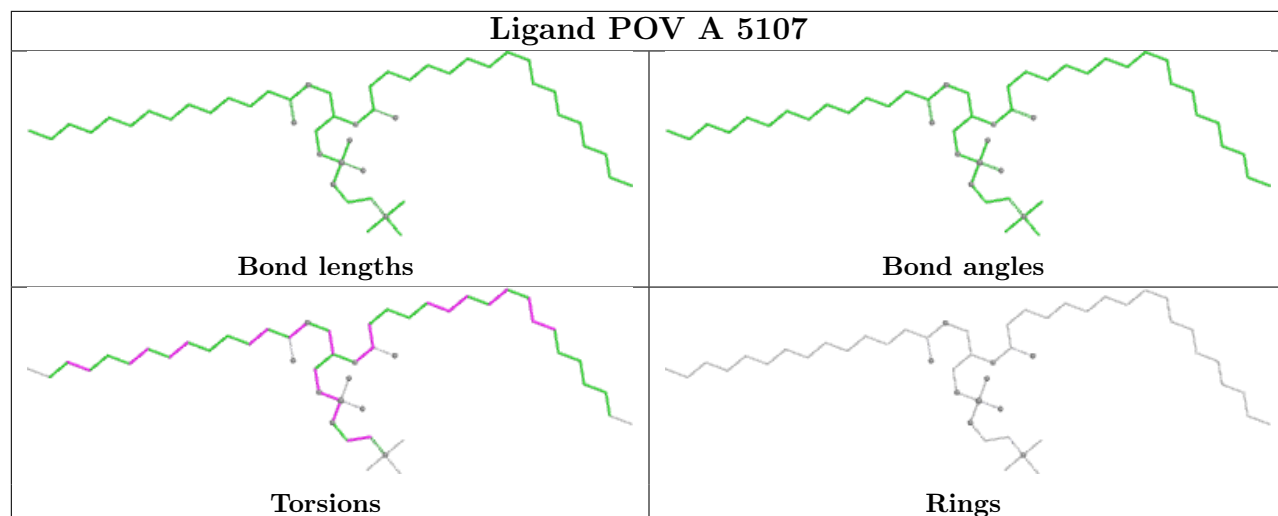


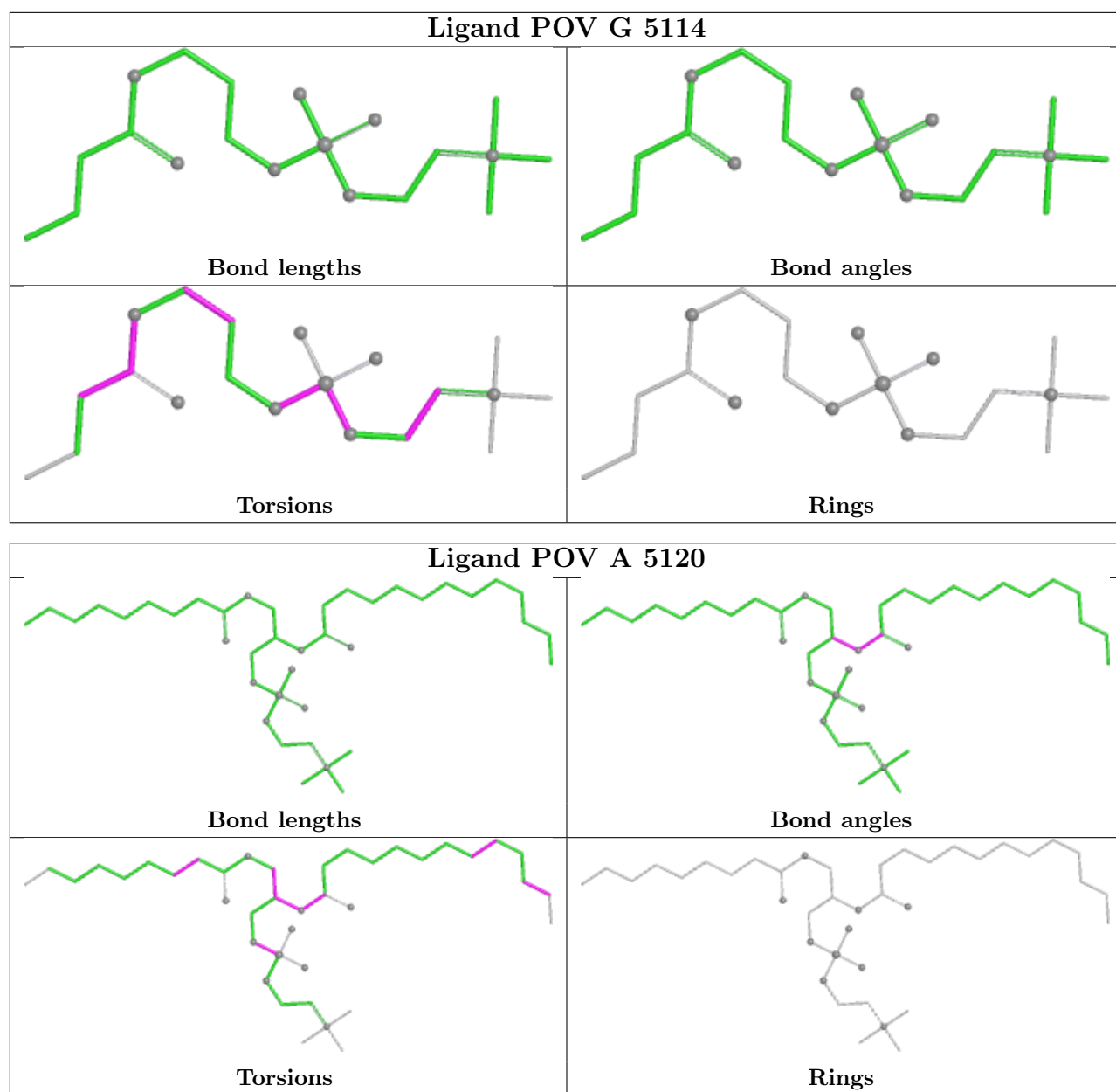
Ligand POV A 5115

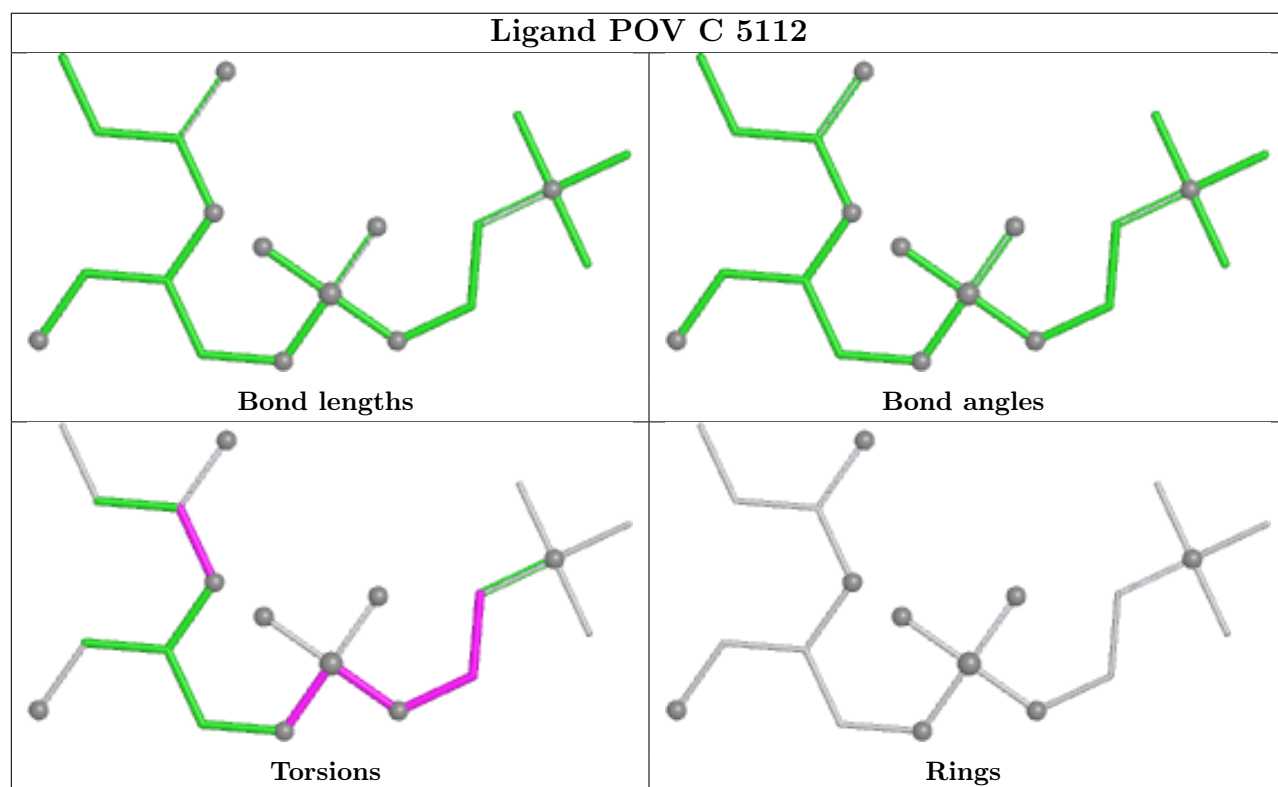
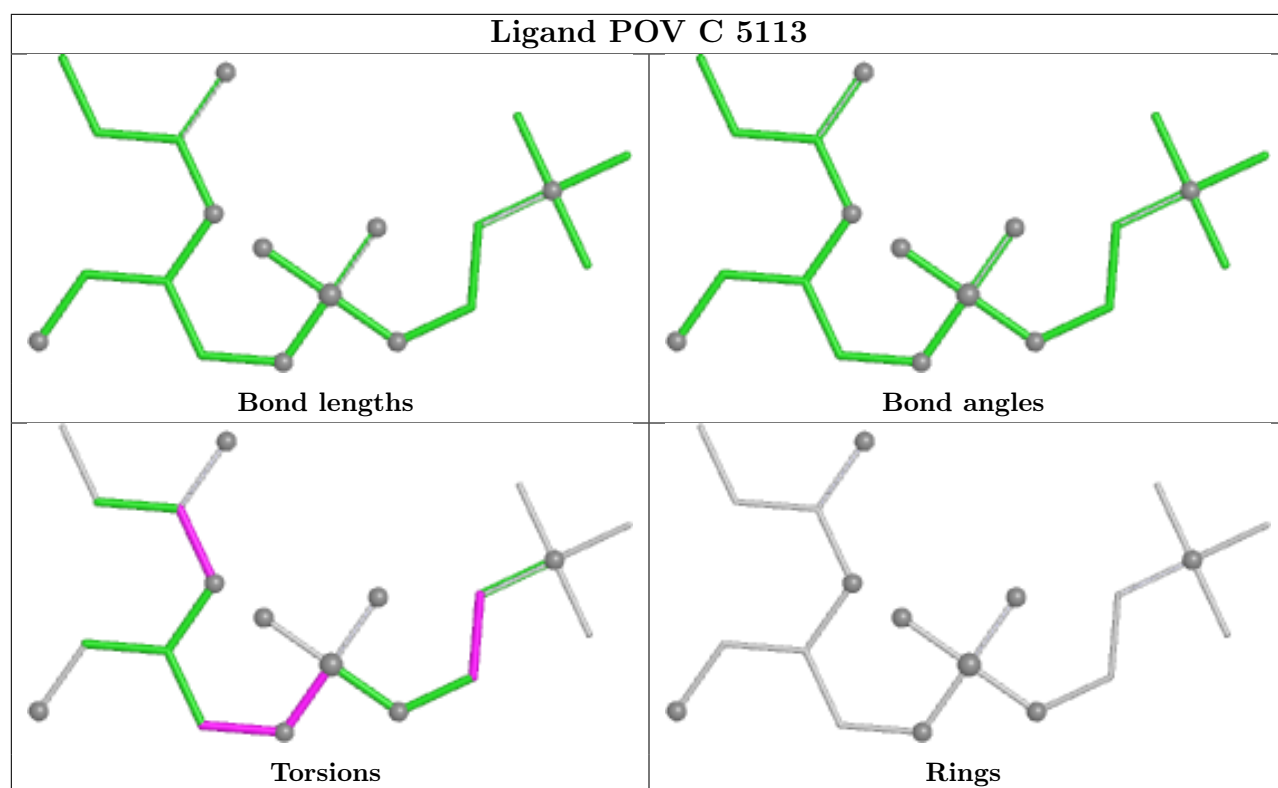


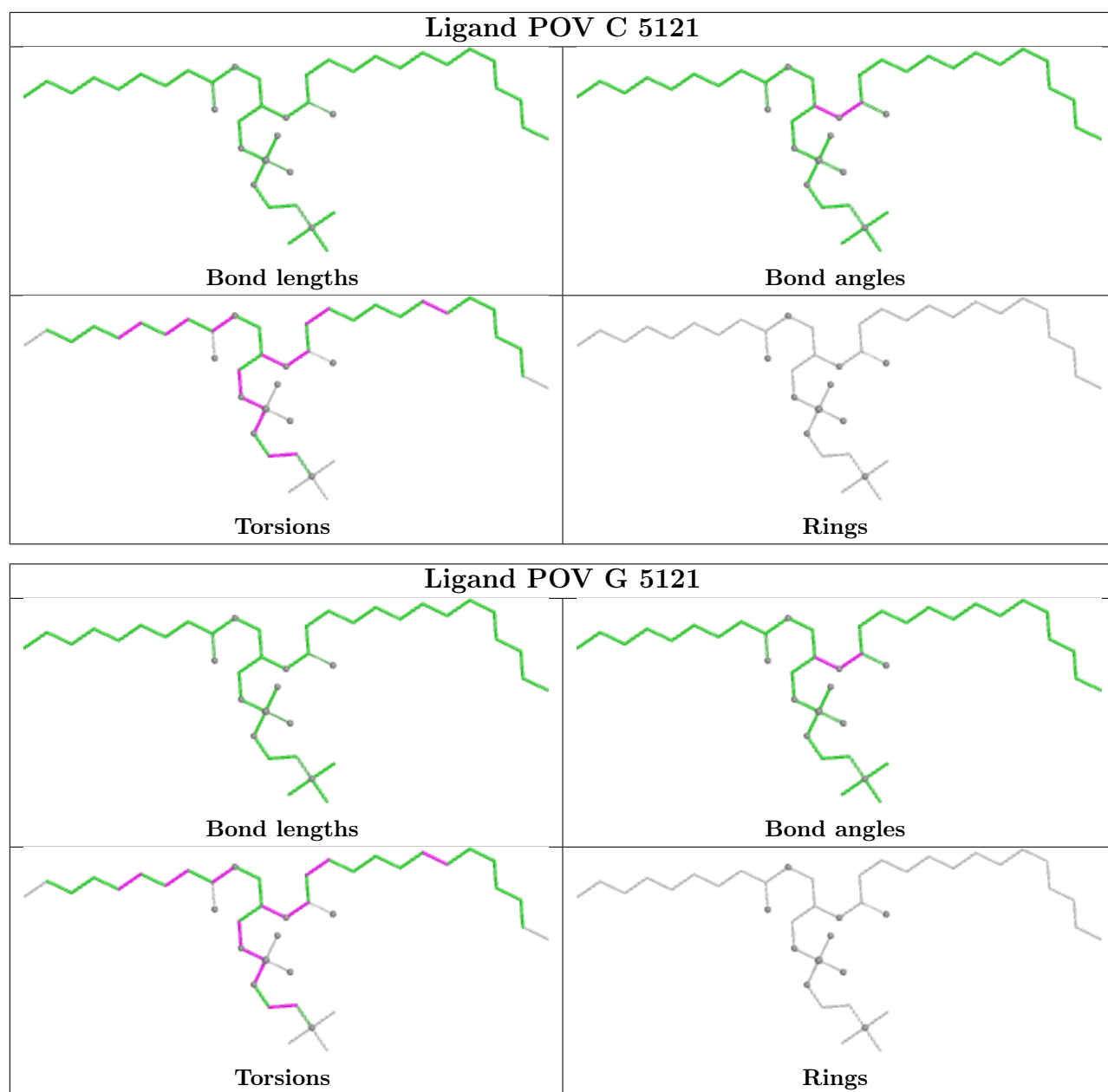
Ligand POV C 5114

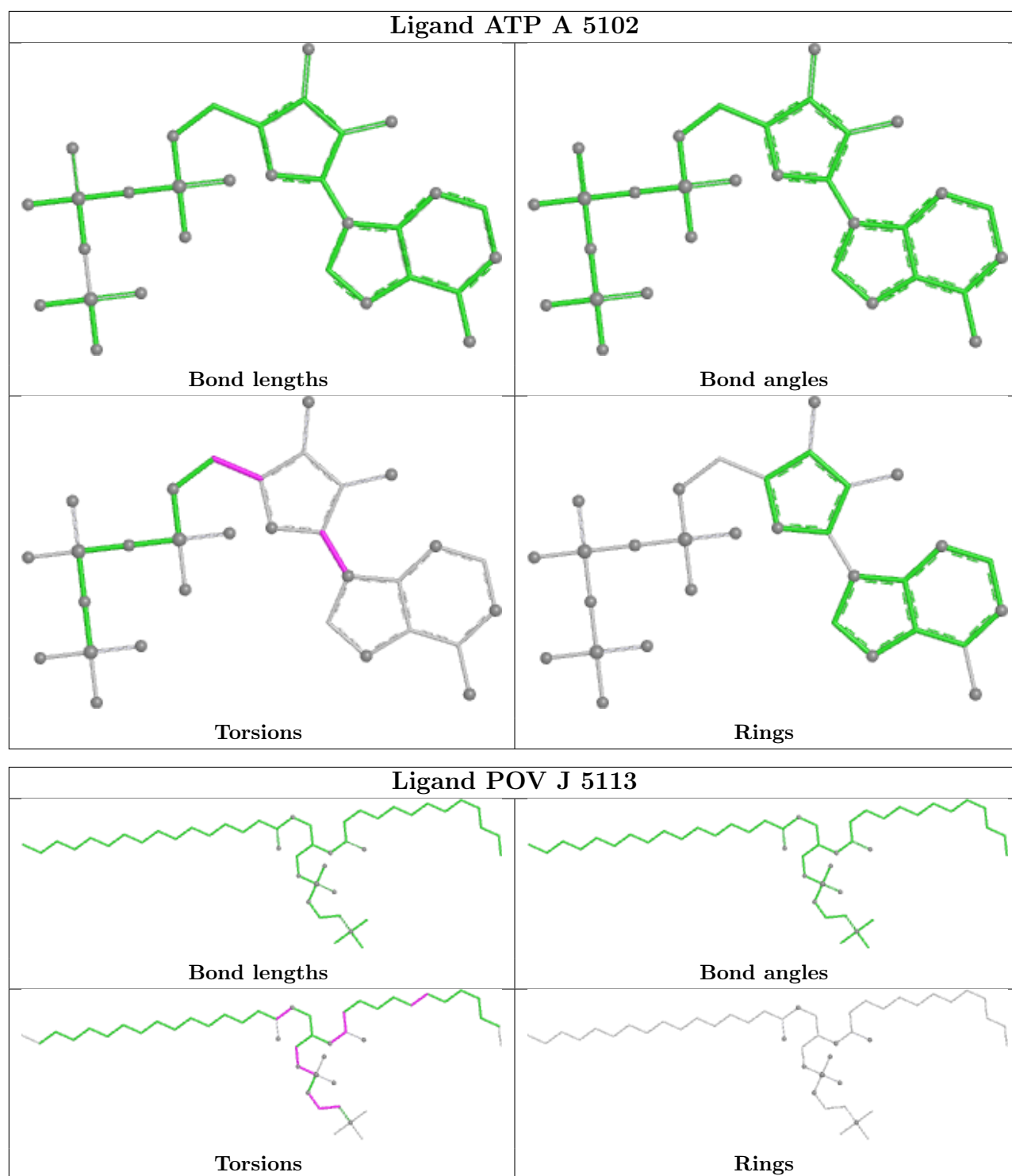


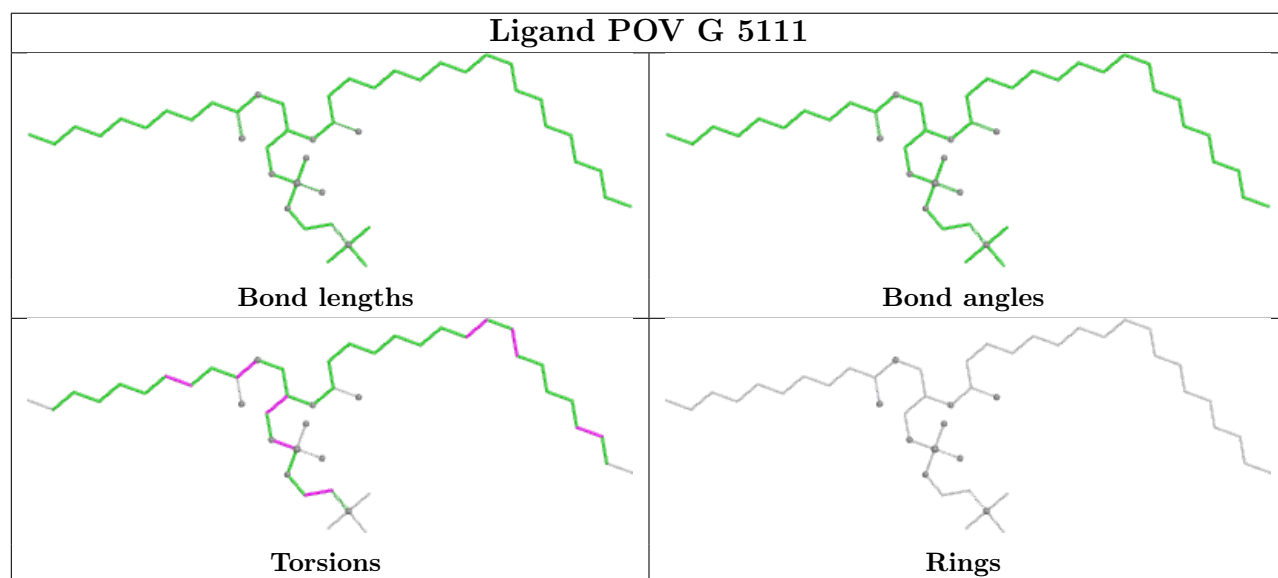
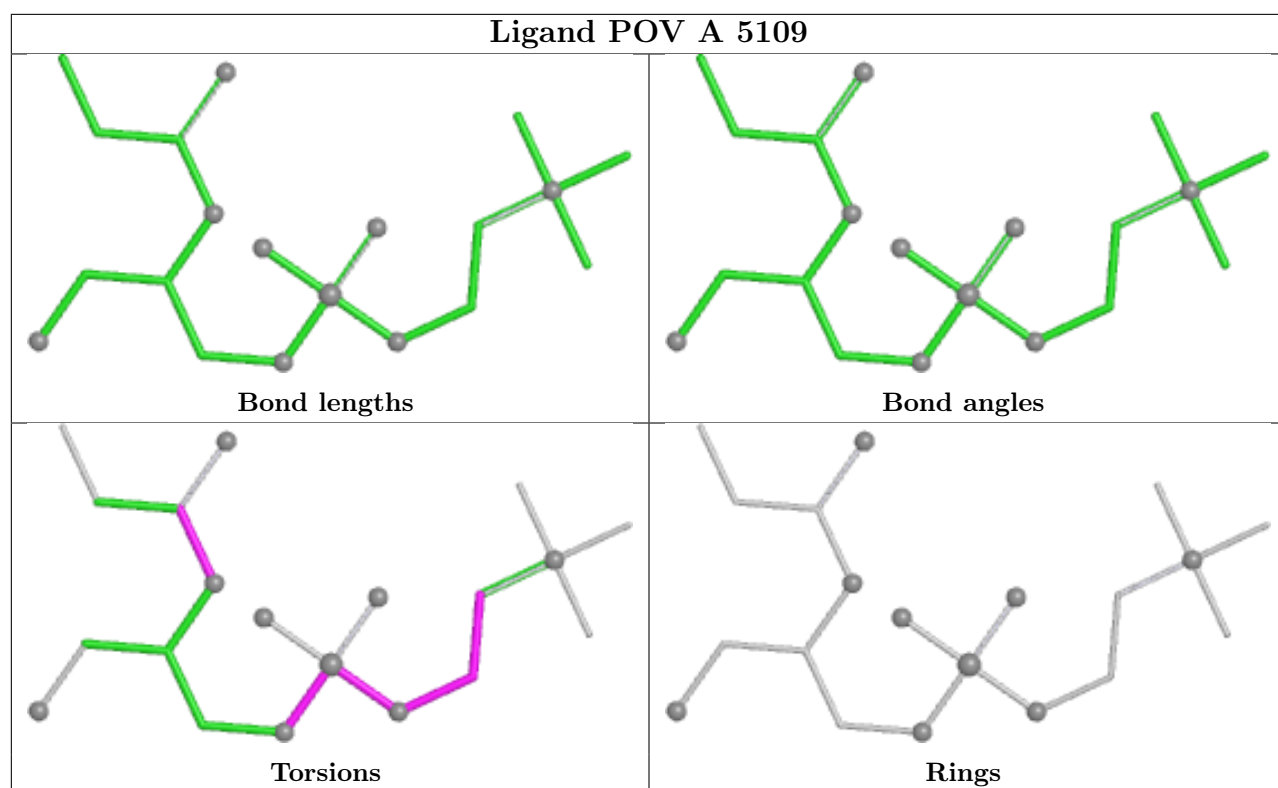


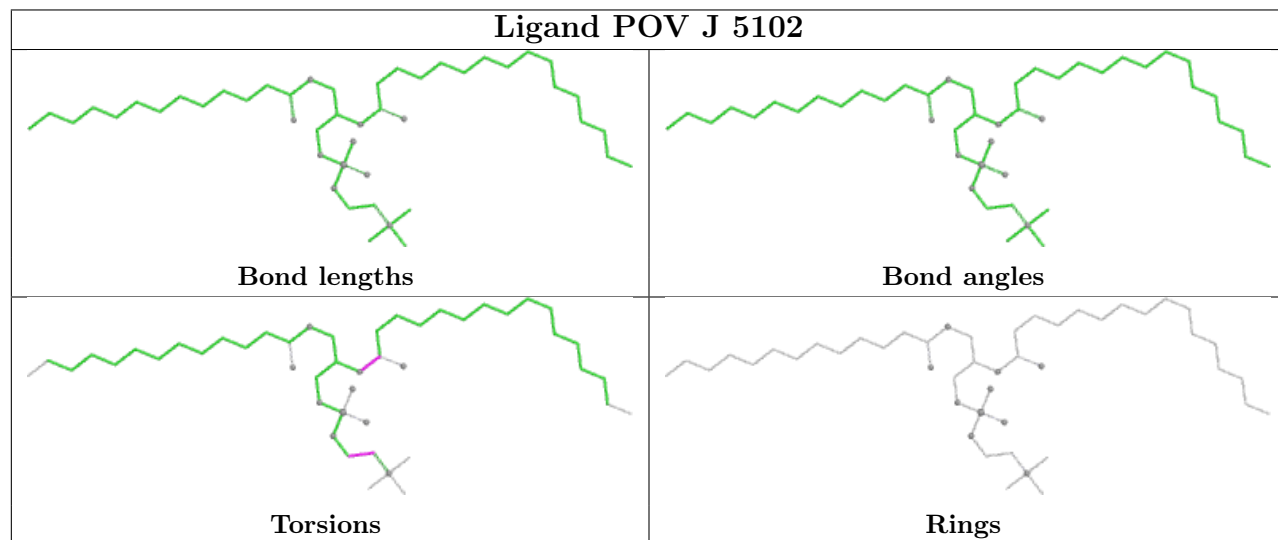
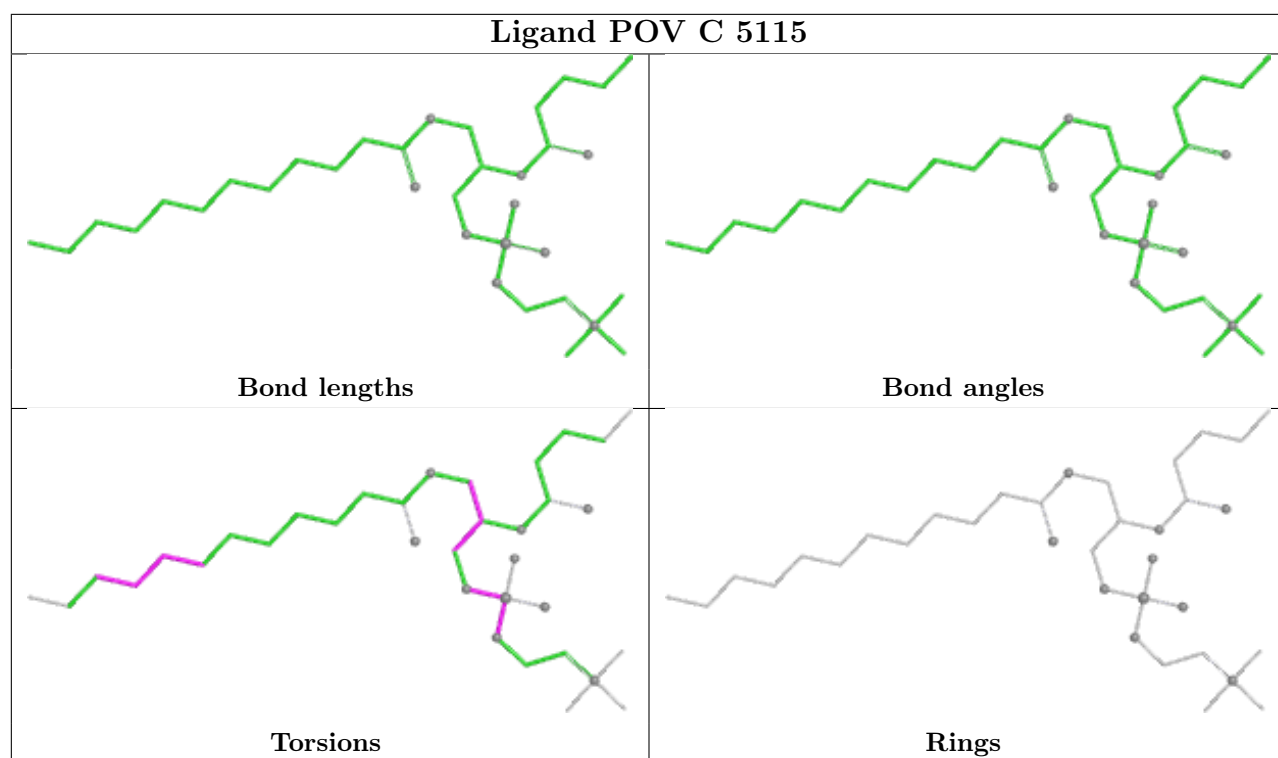


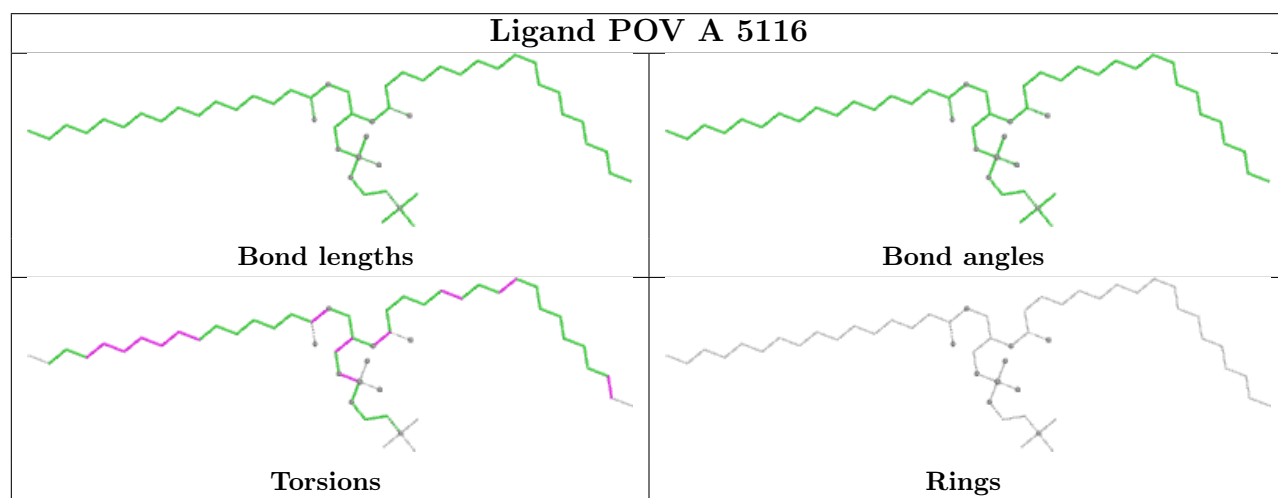
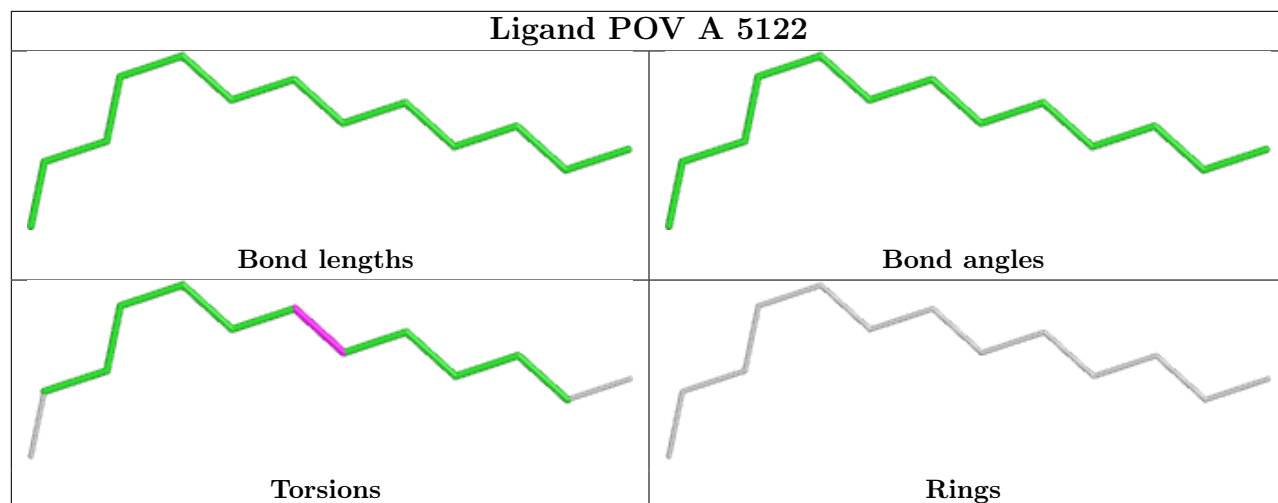


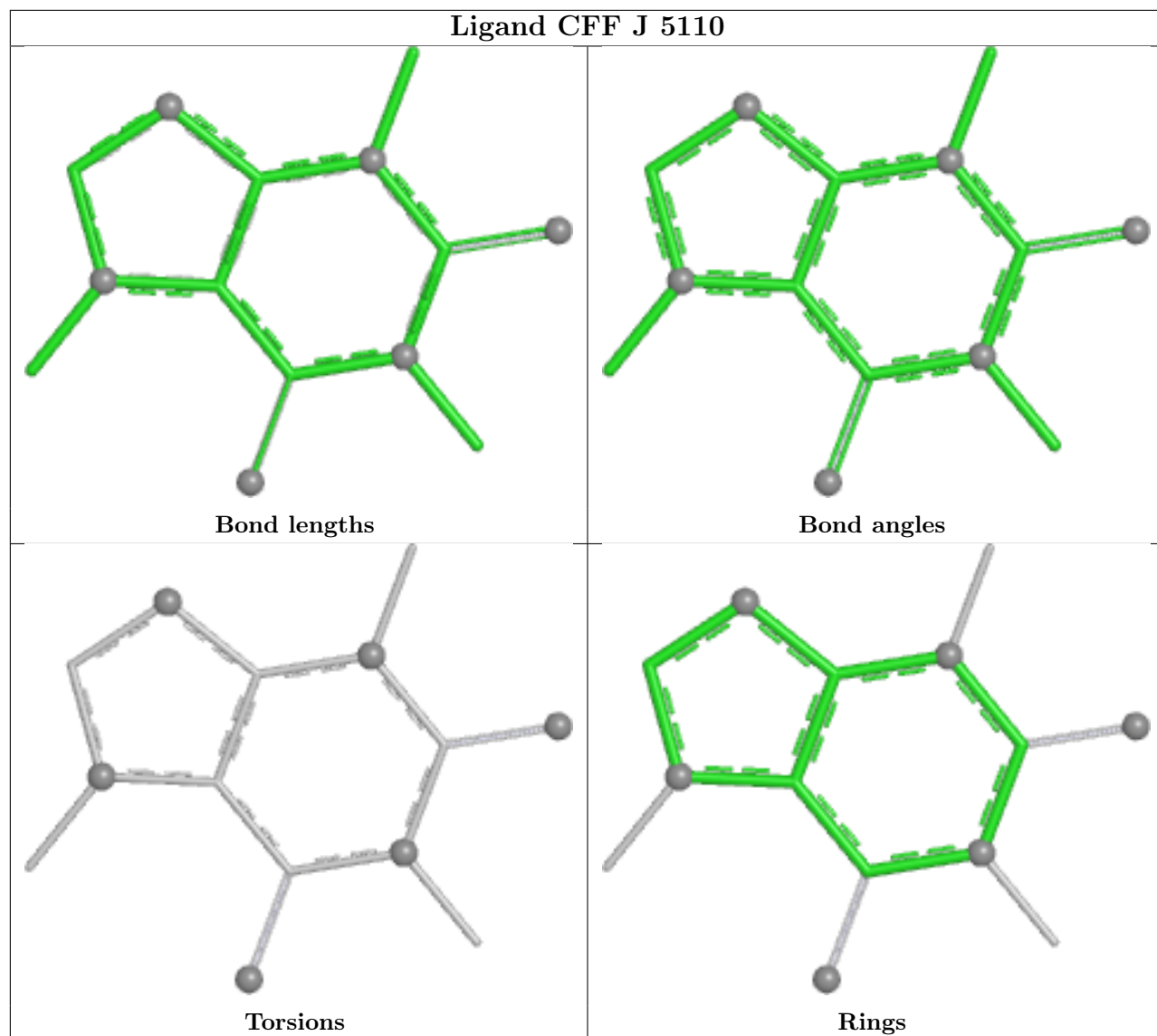


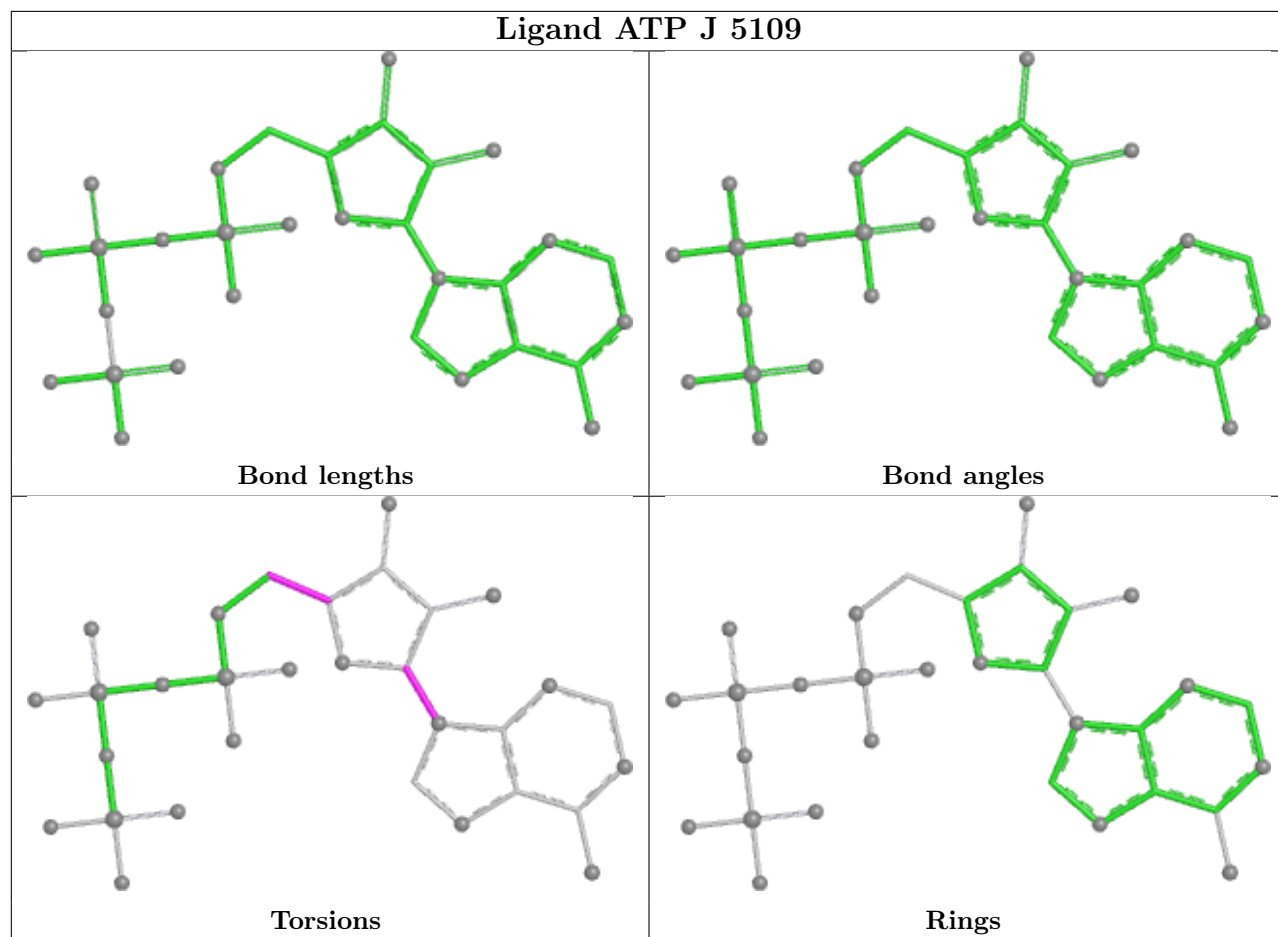


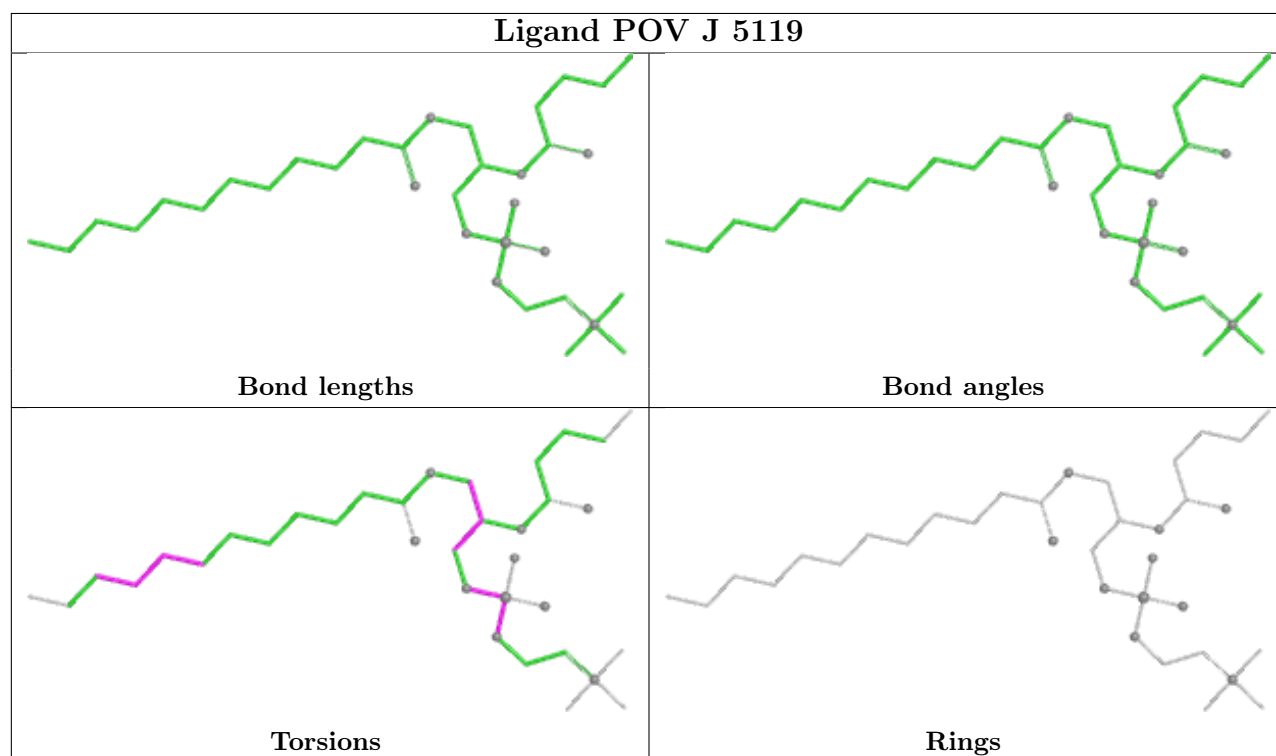
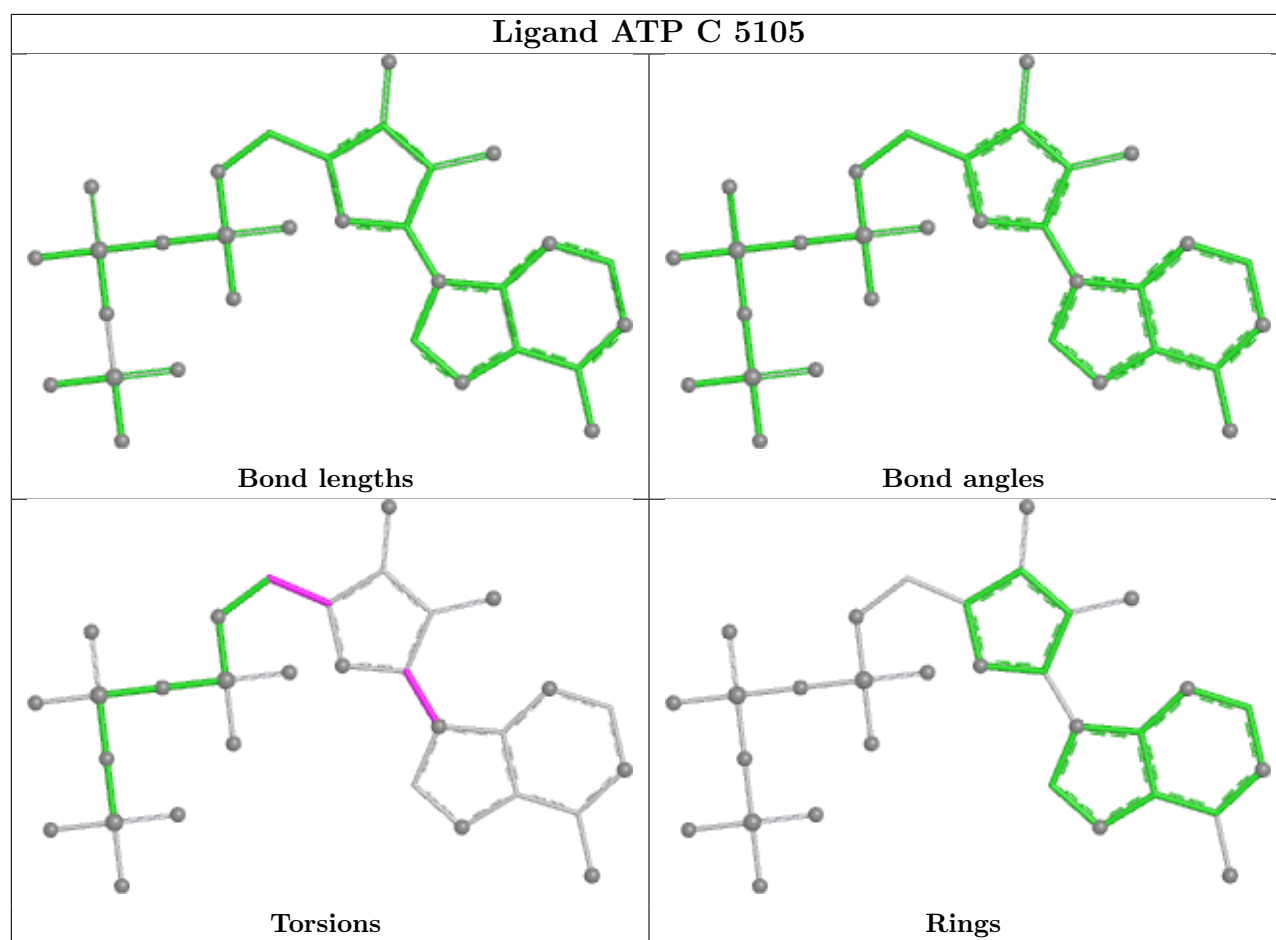


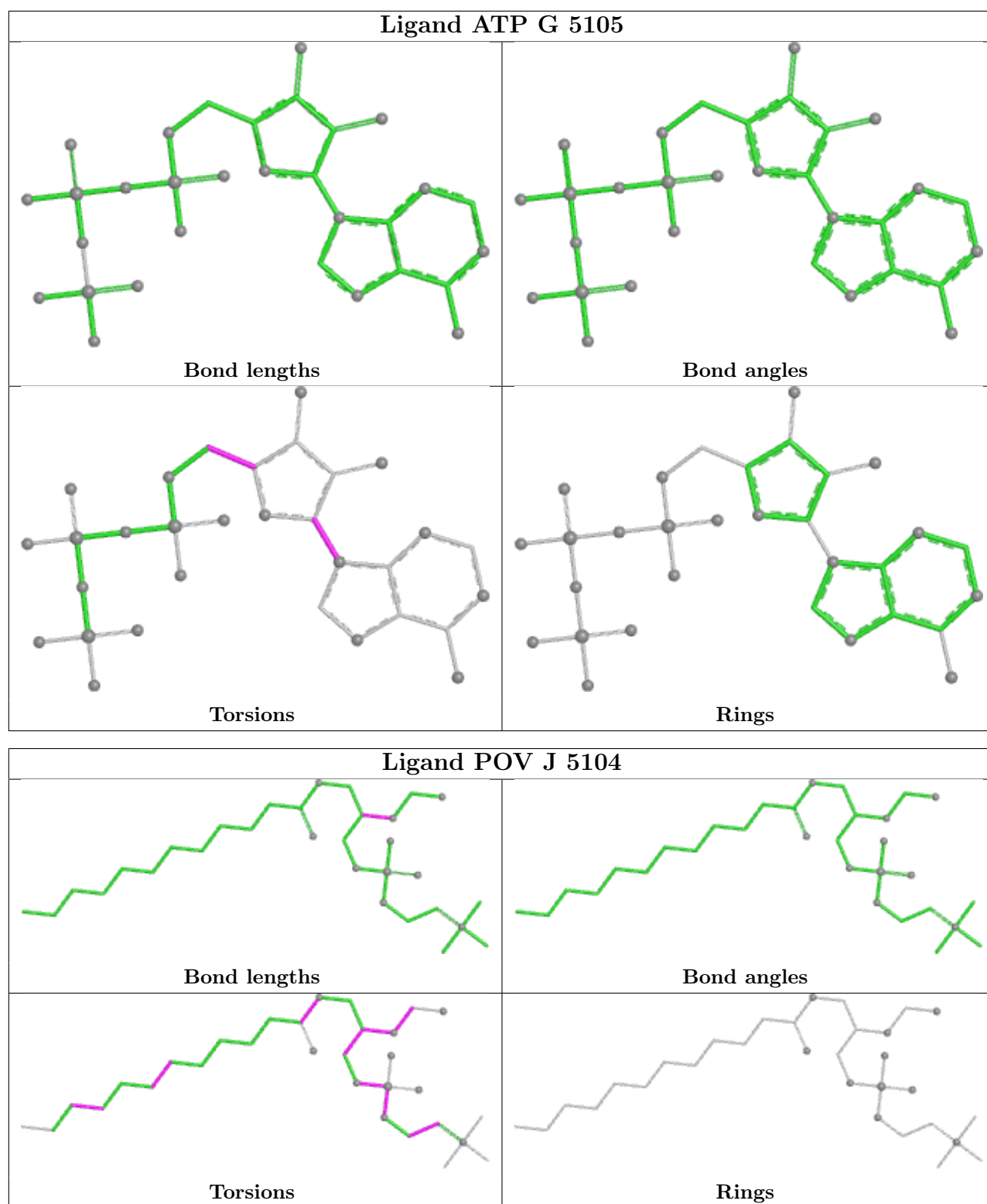


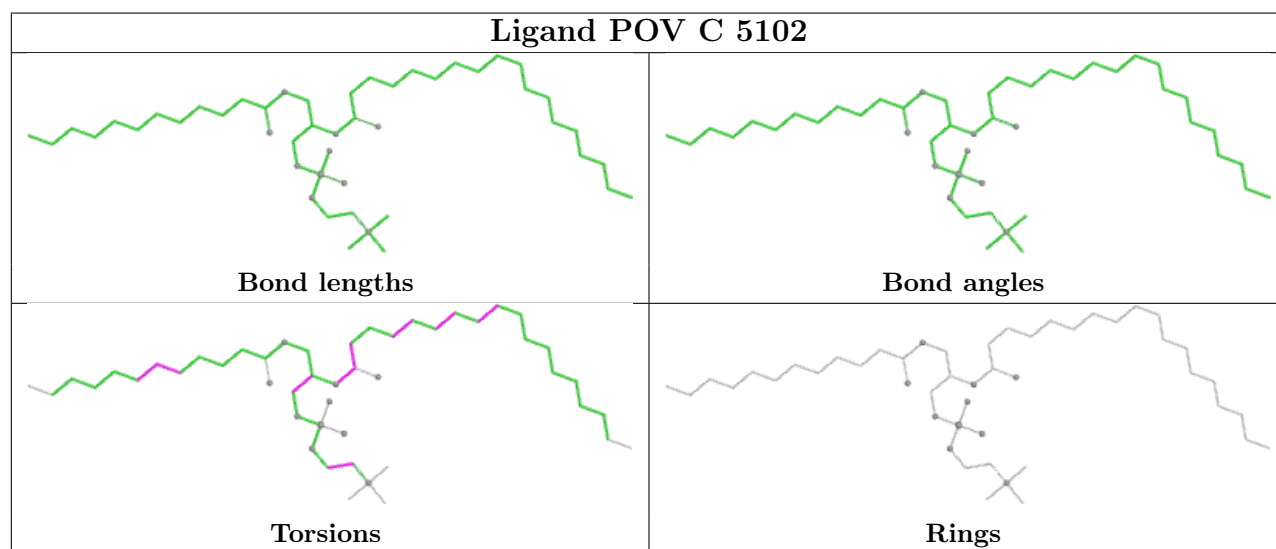
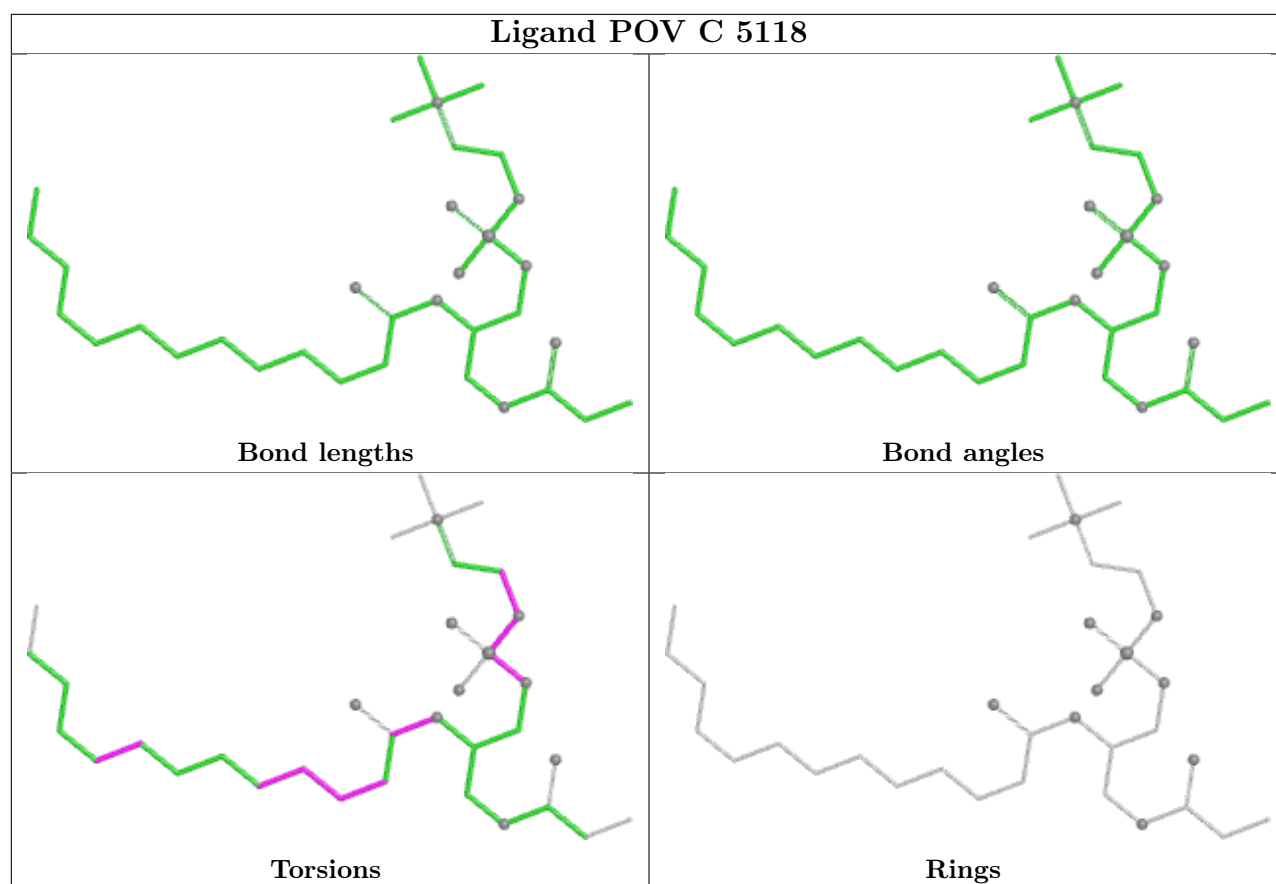


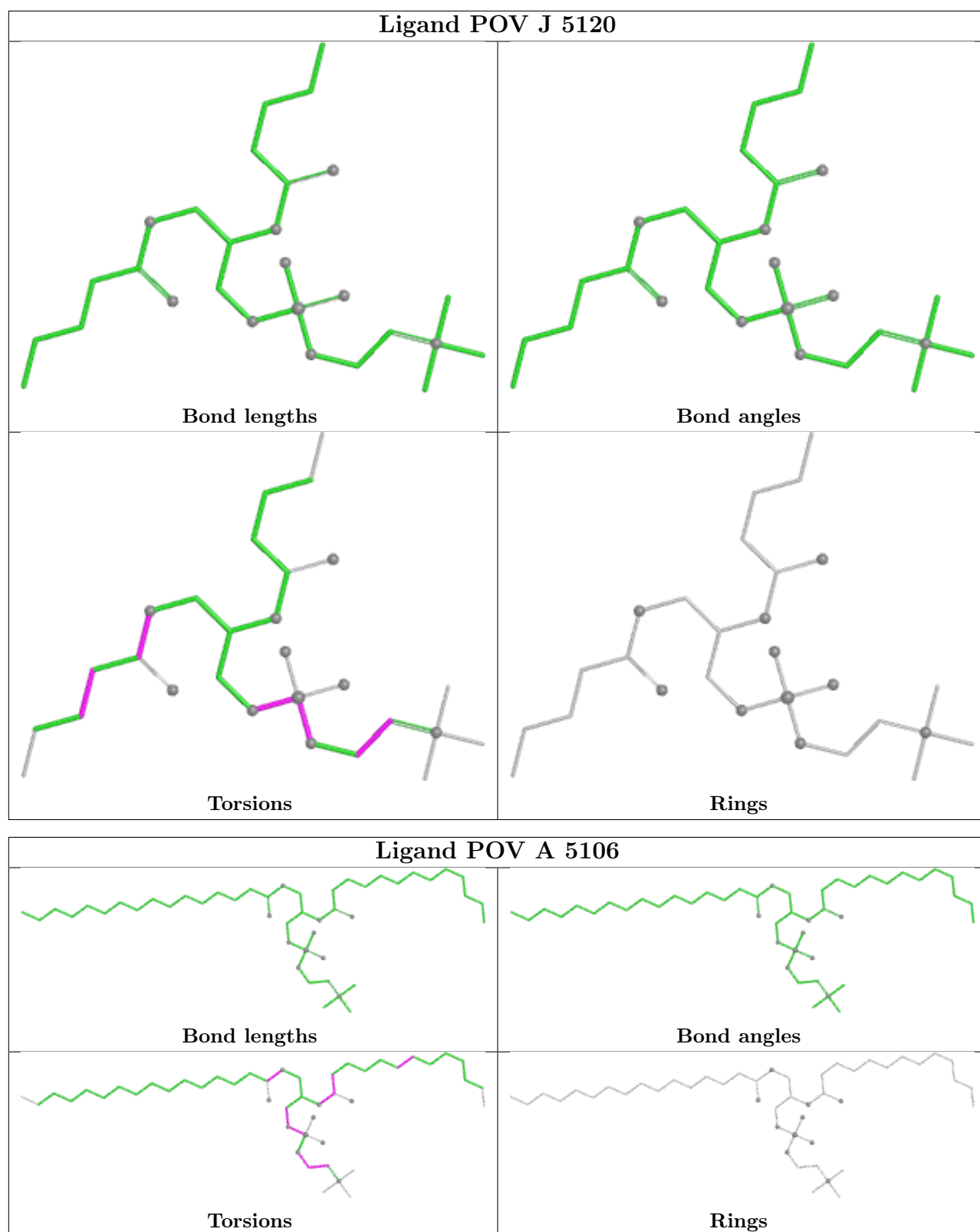


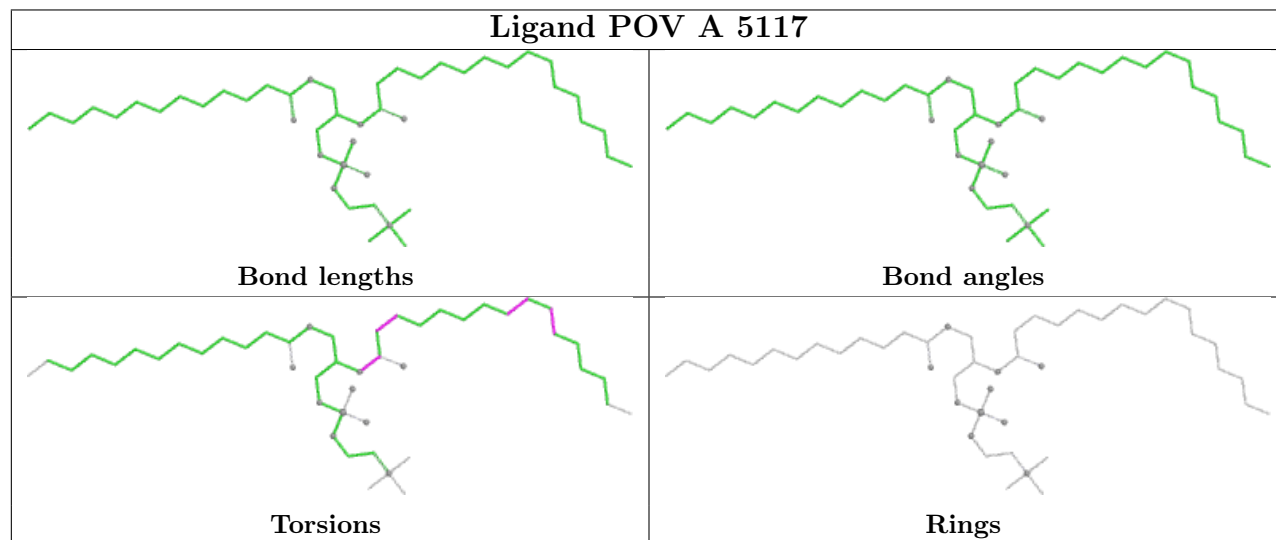
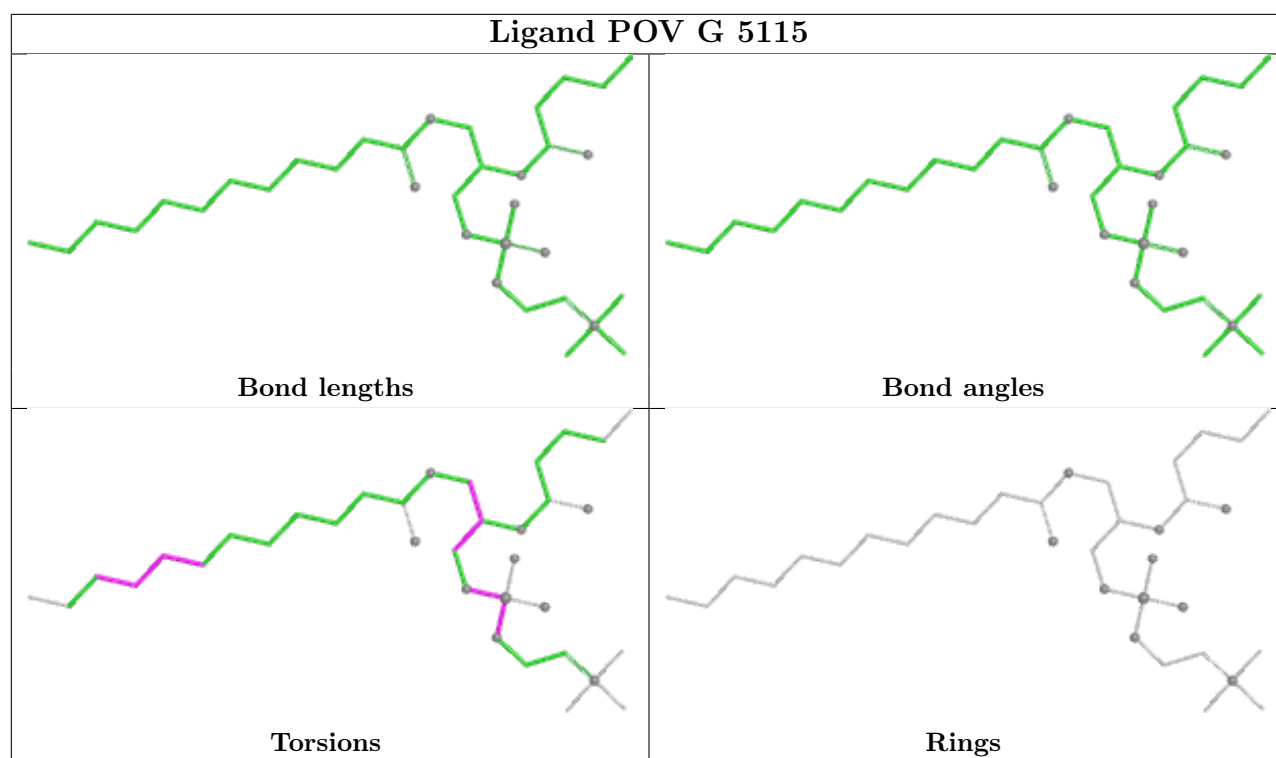


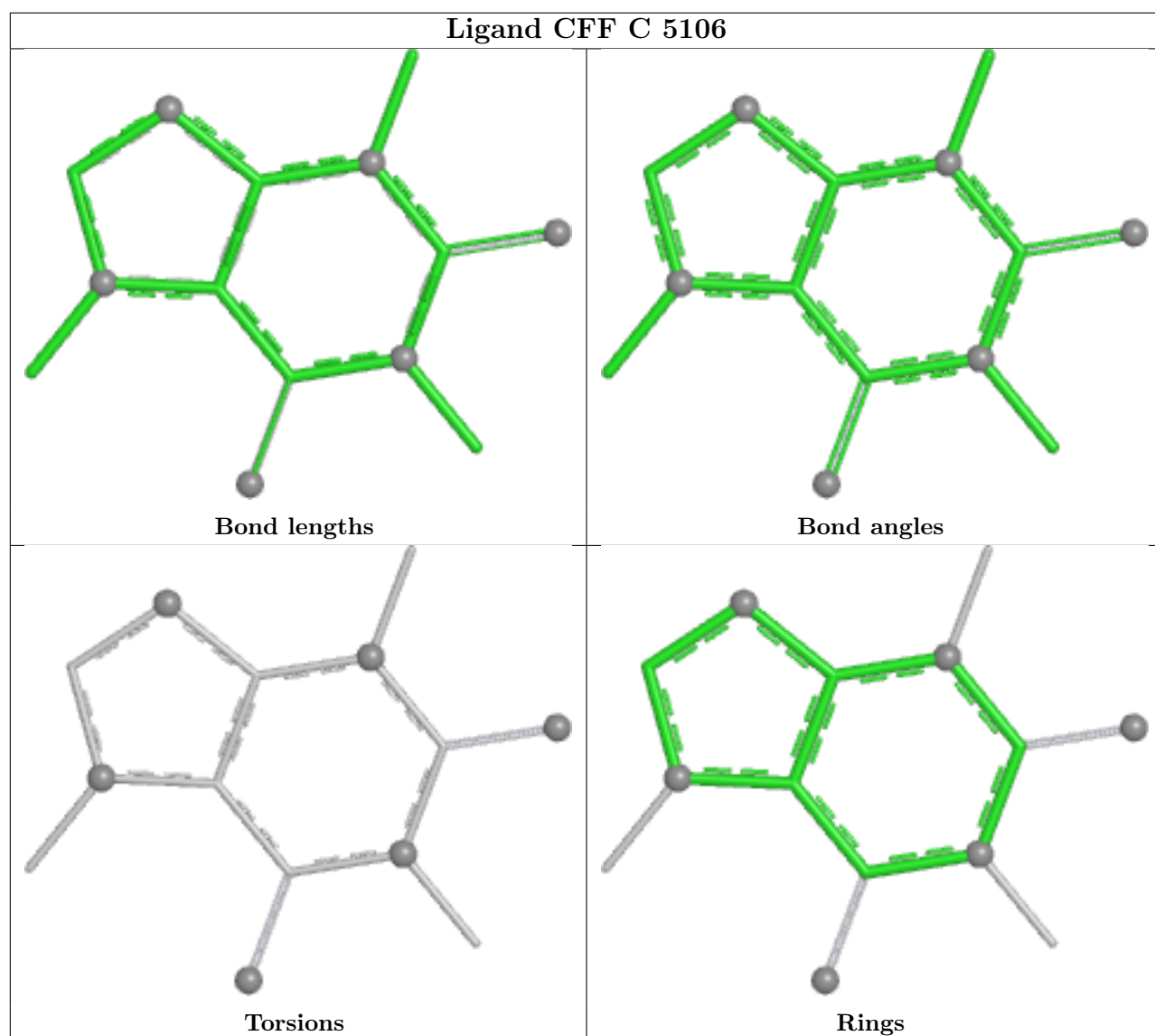
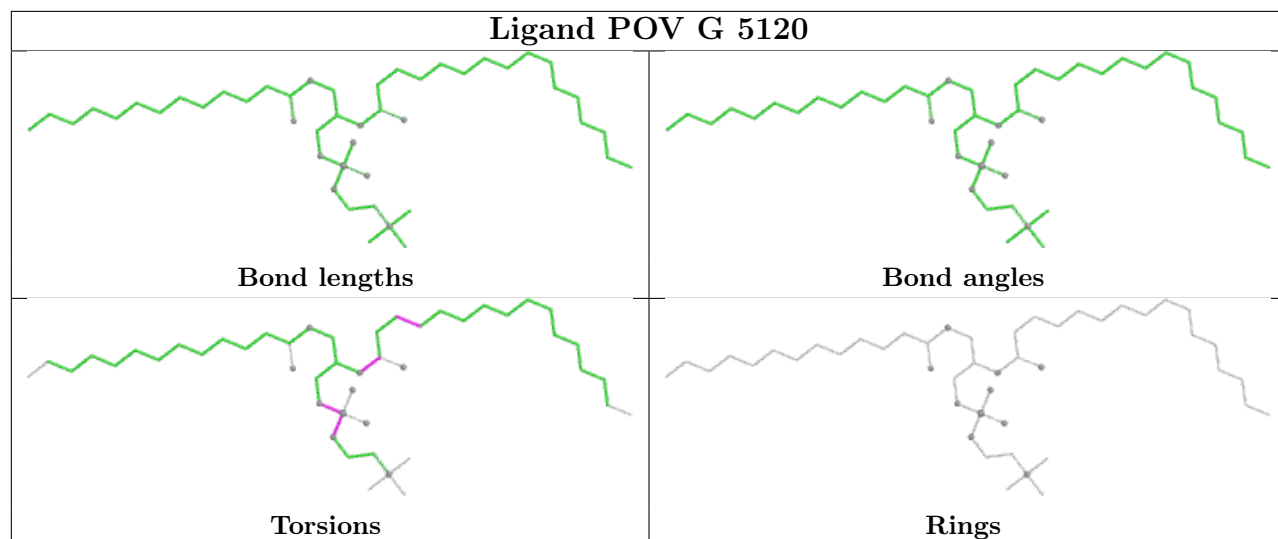


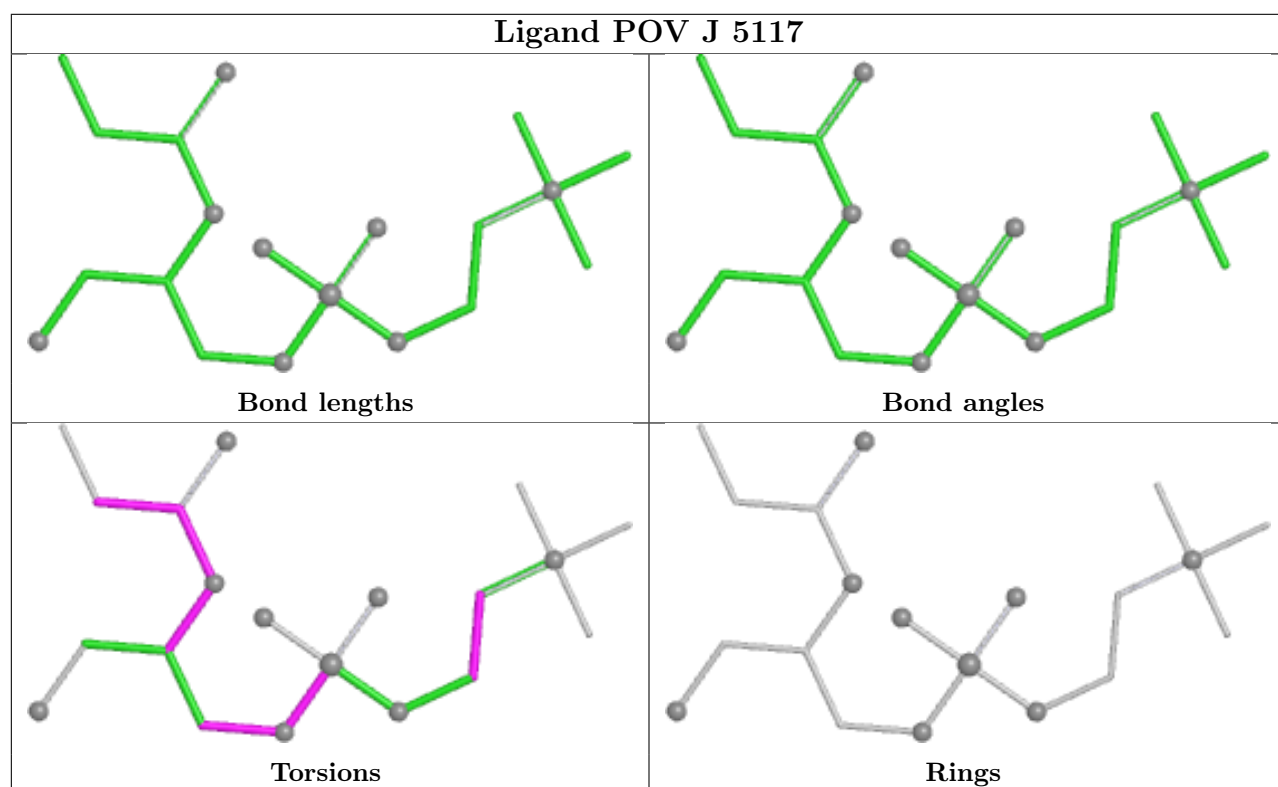
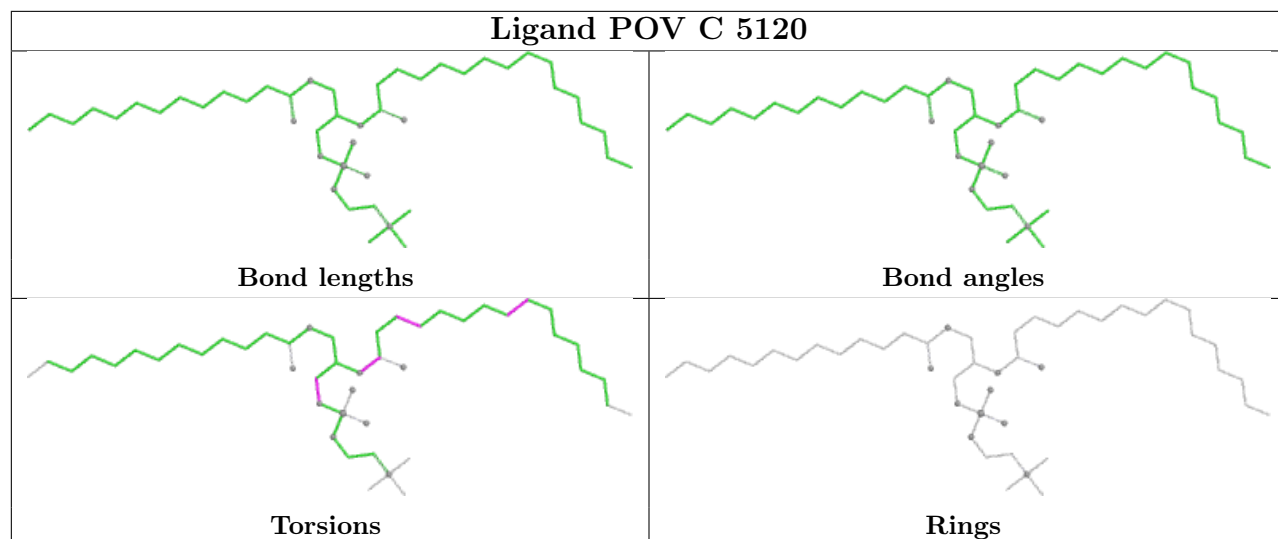


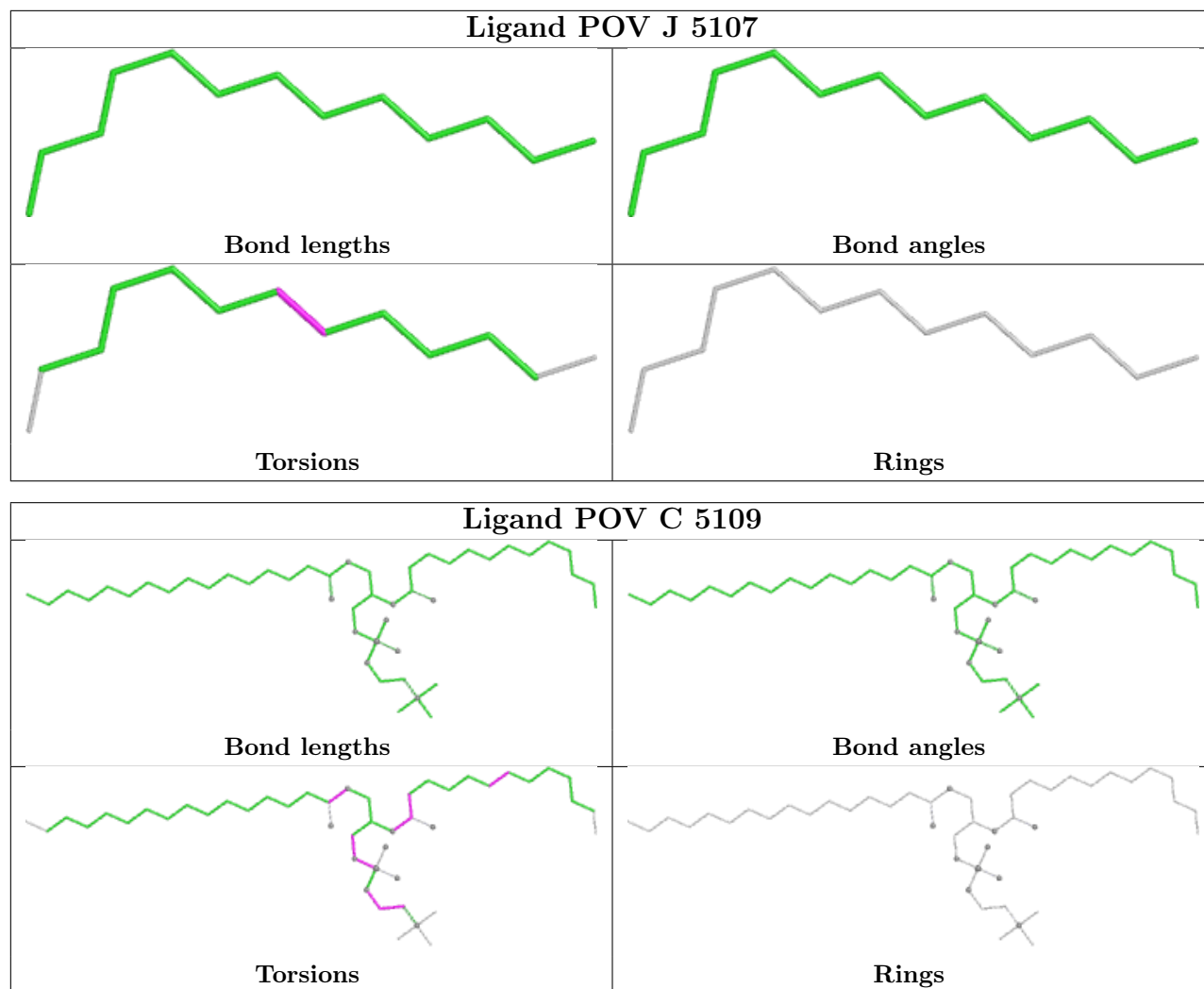


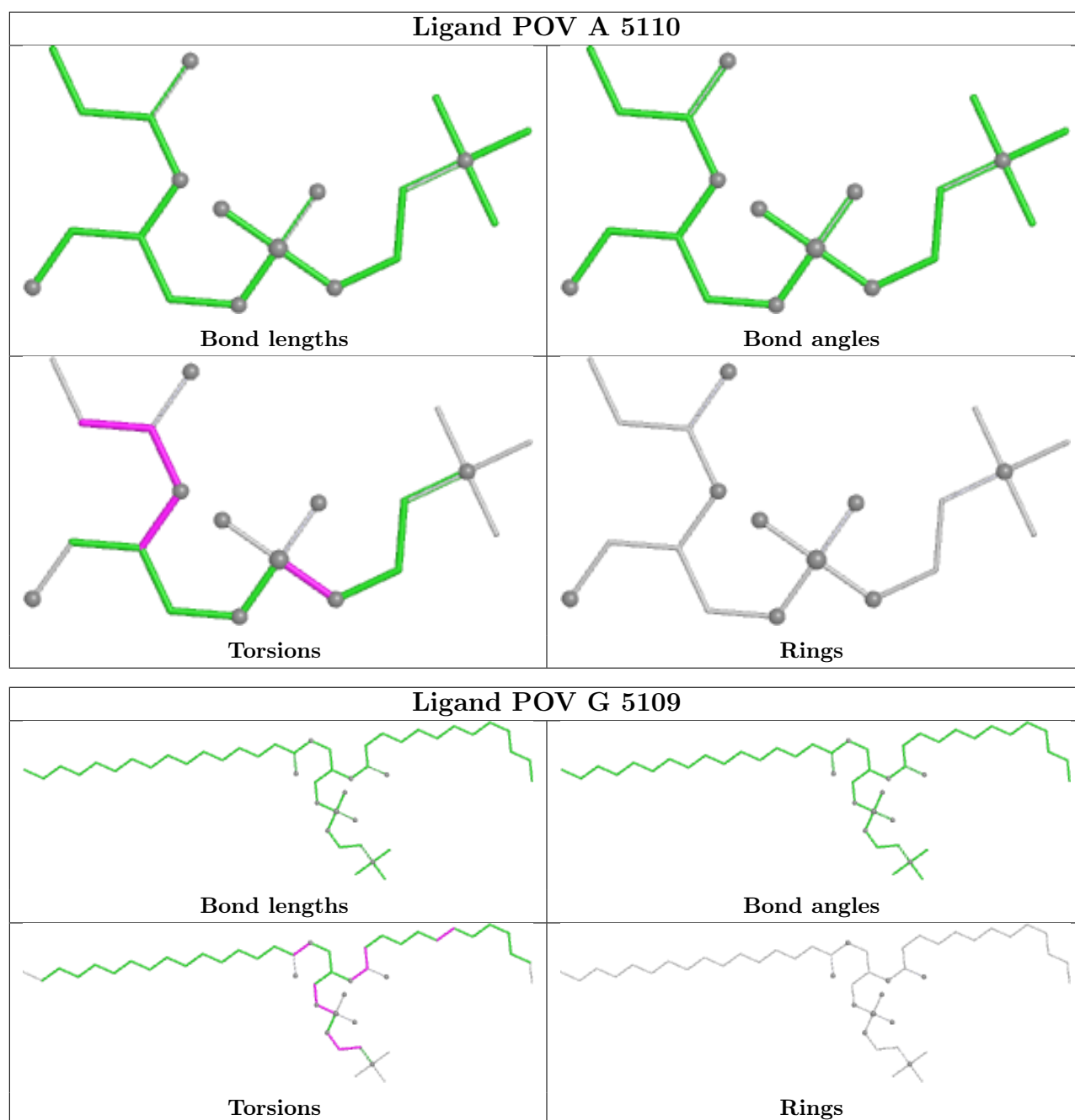


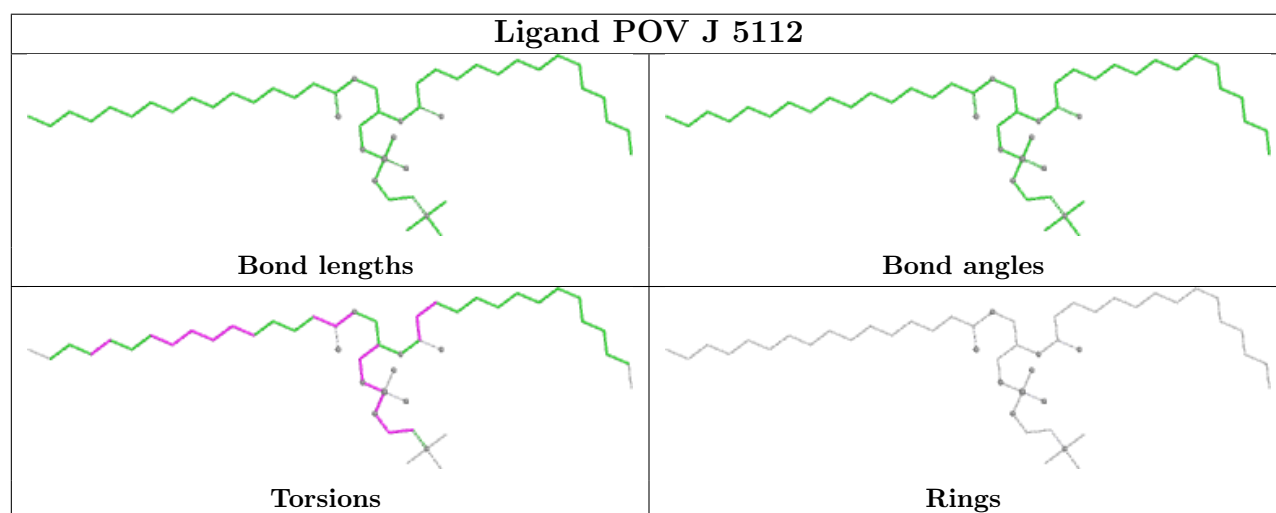
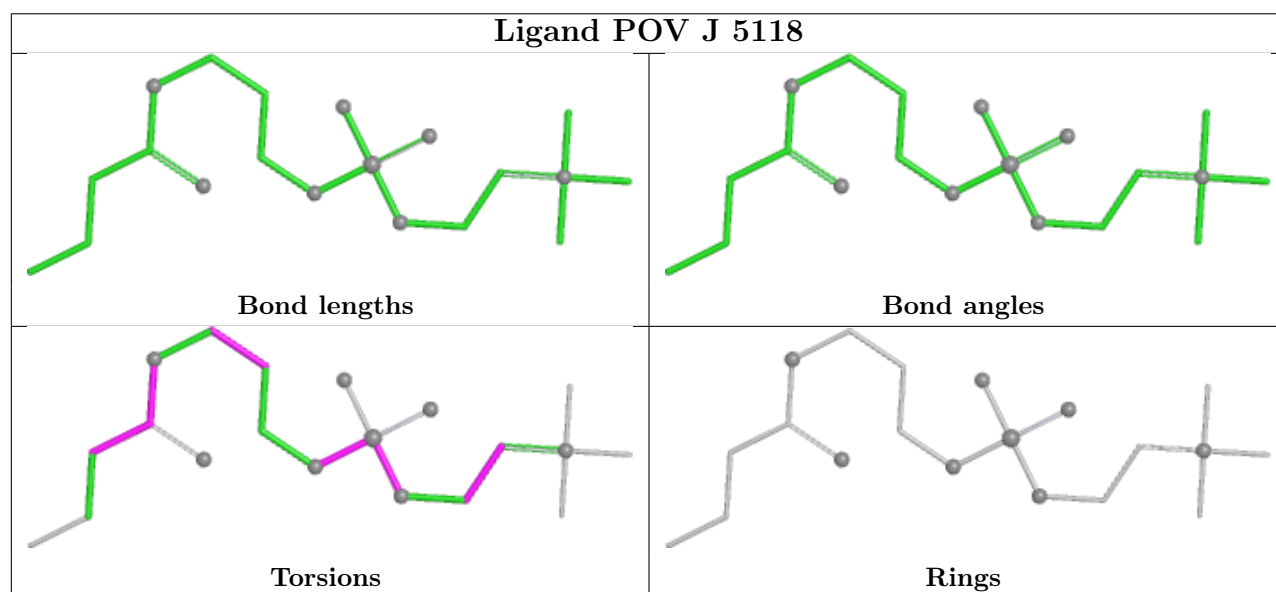
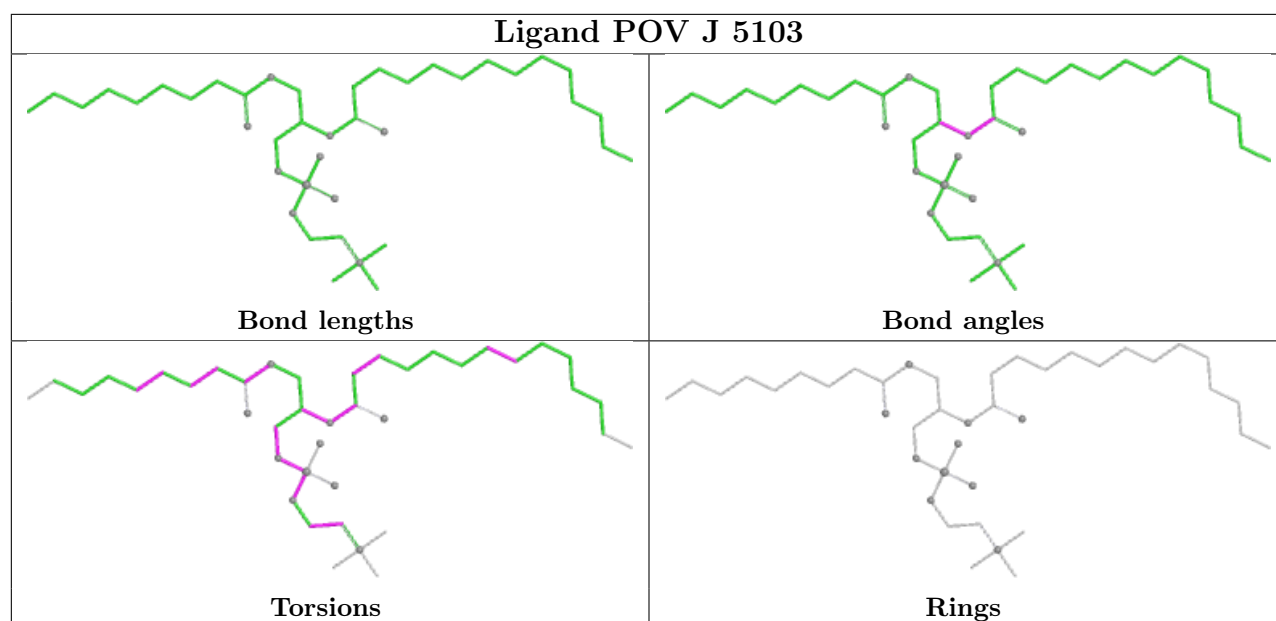


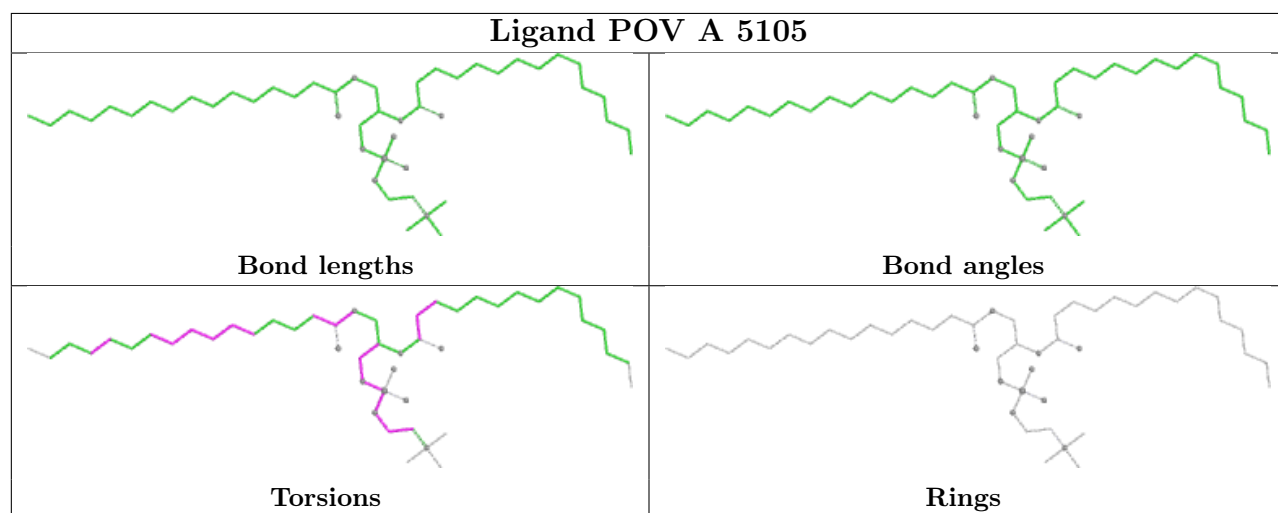
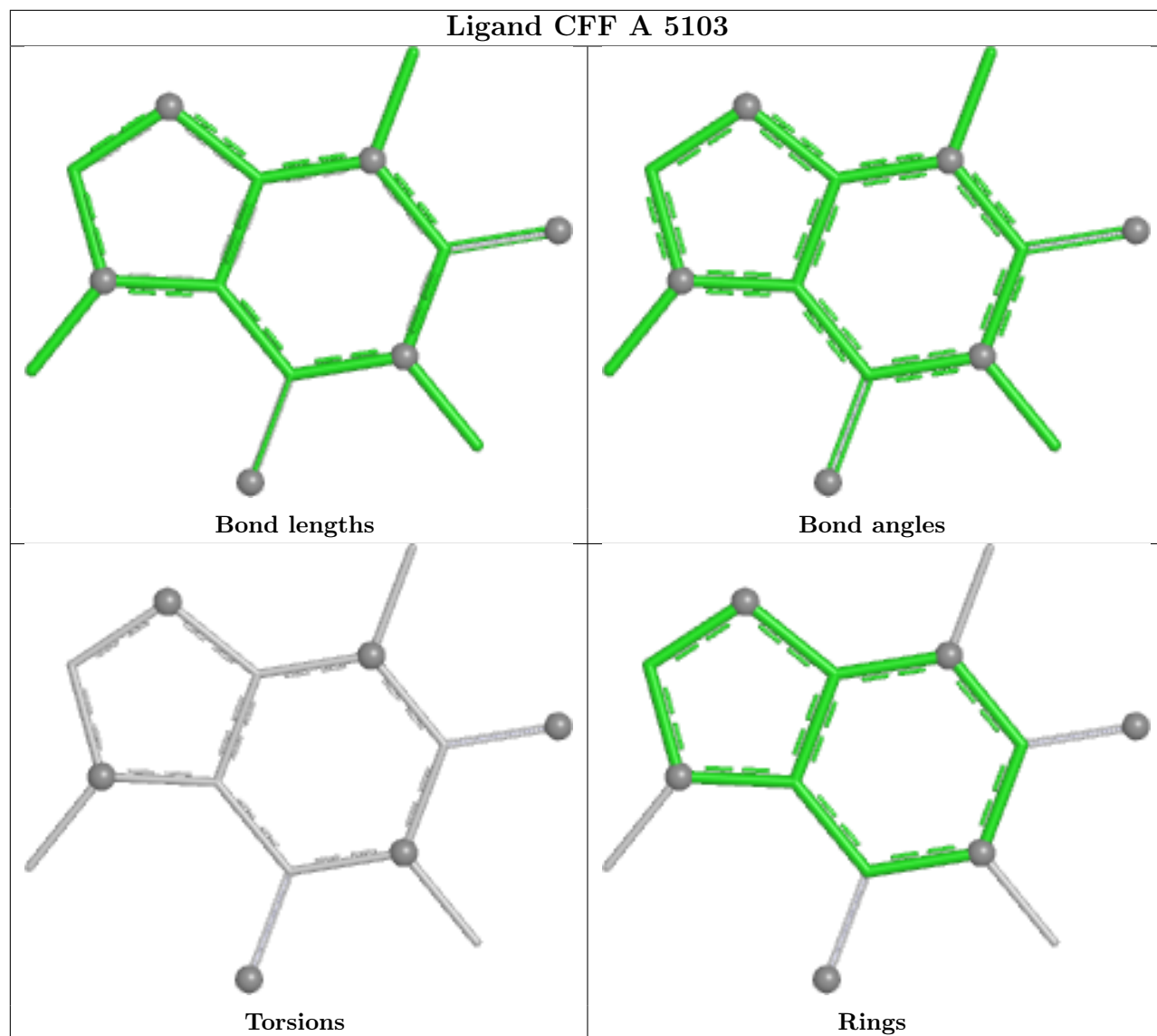


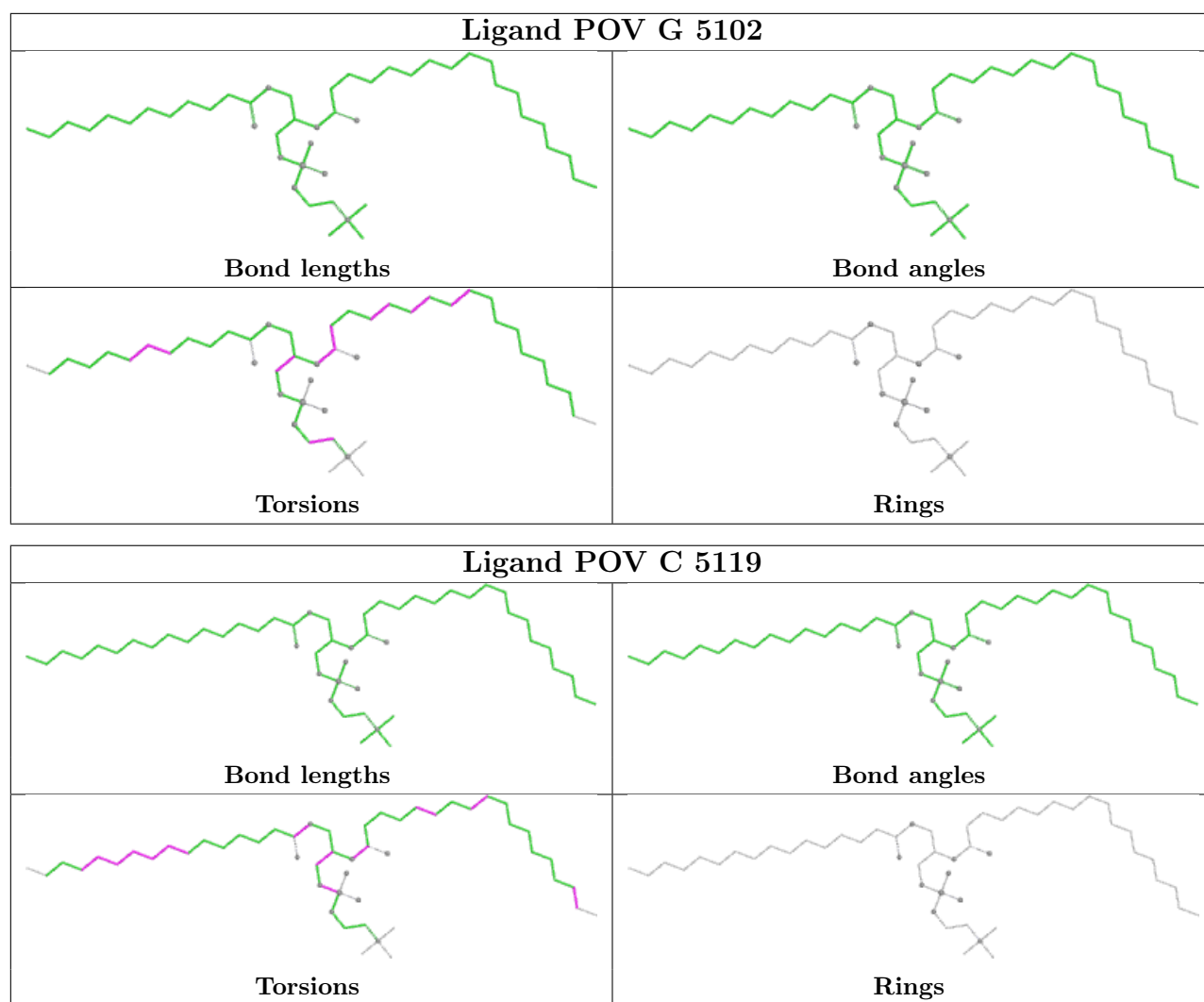




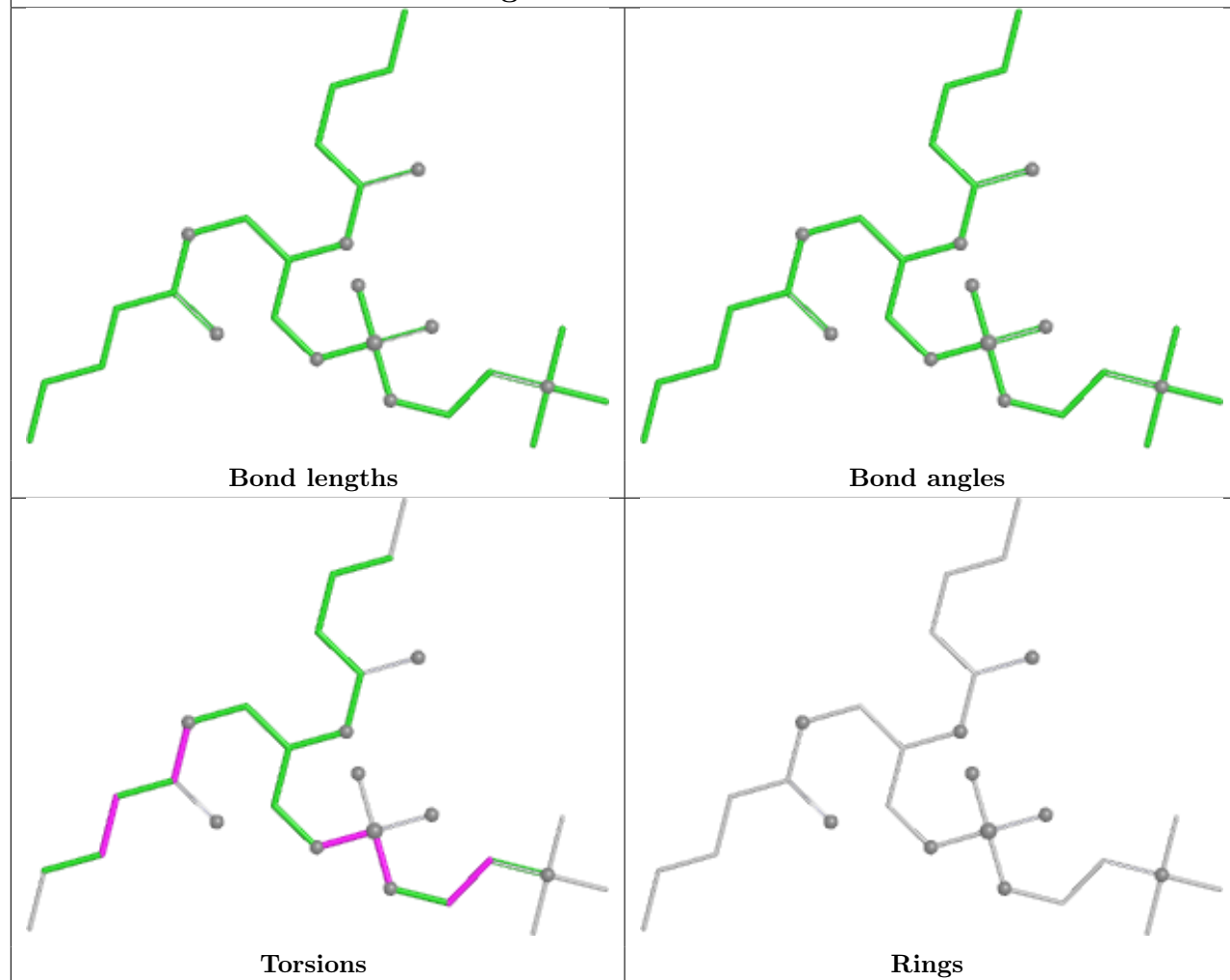




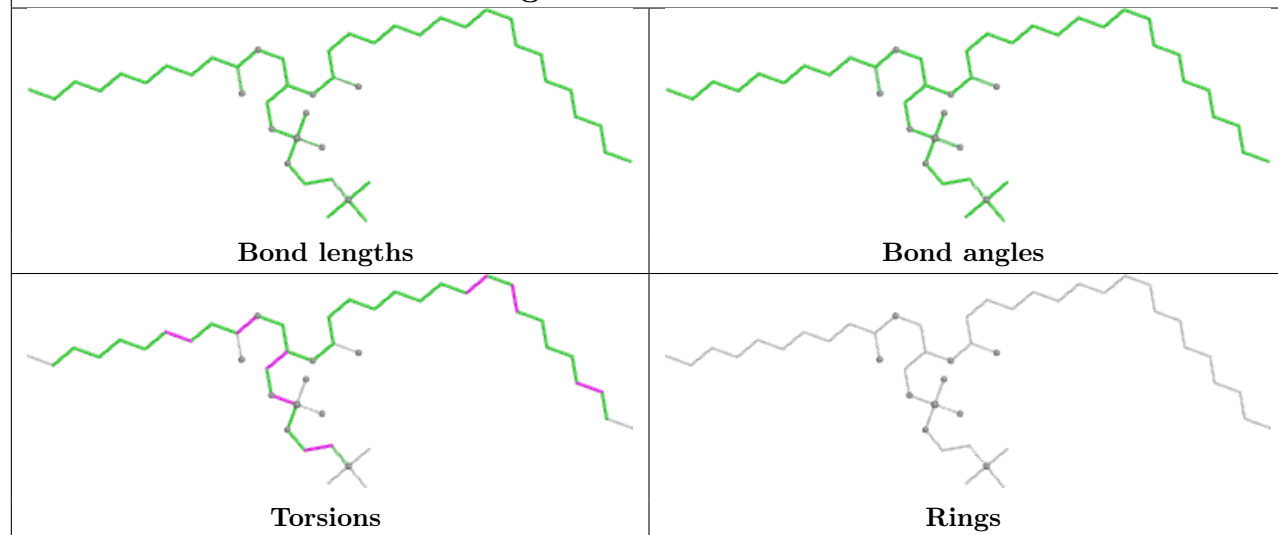


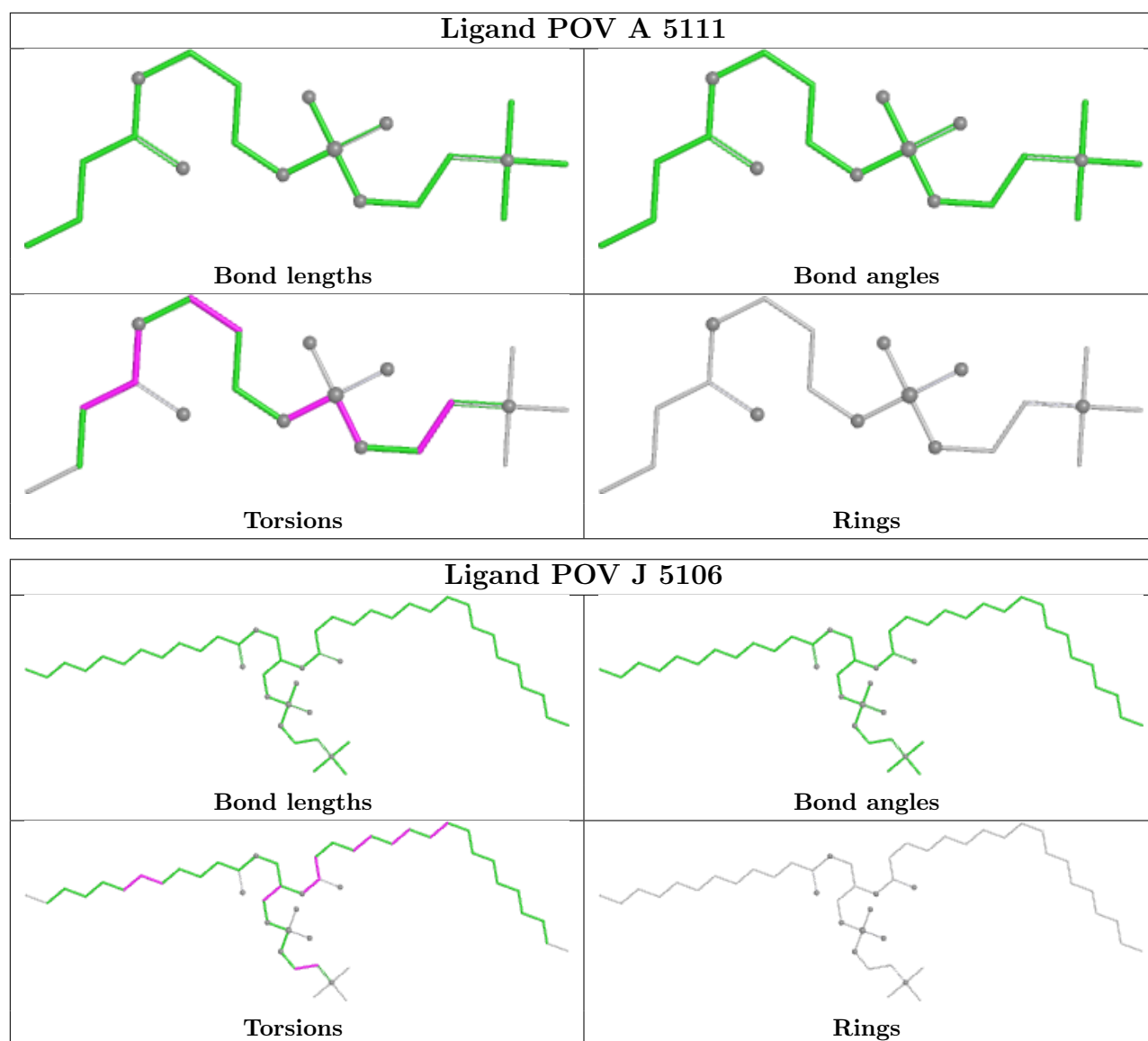


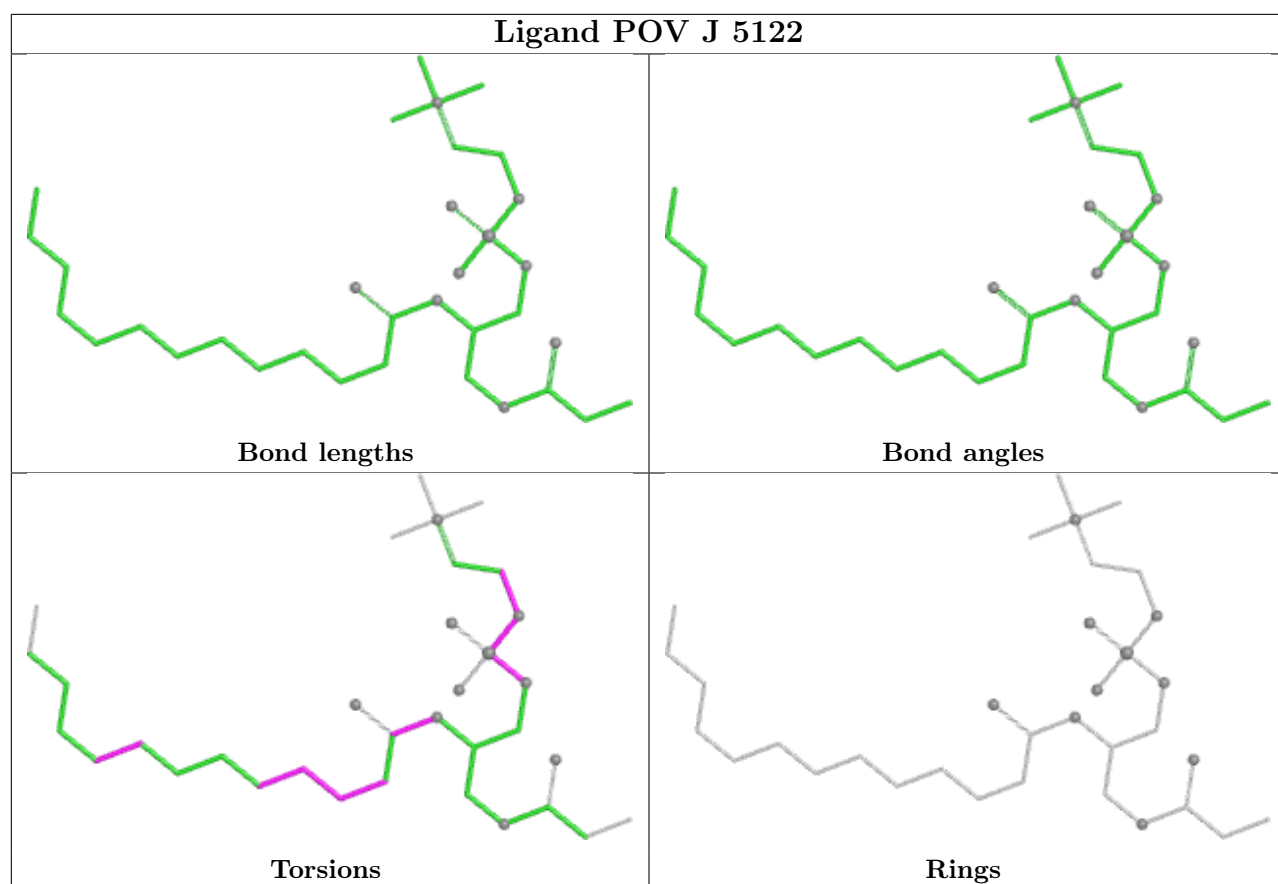
Ligand POV G 5116

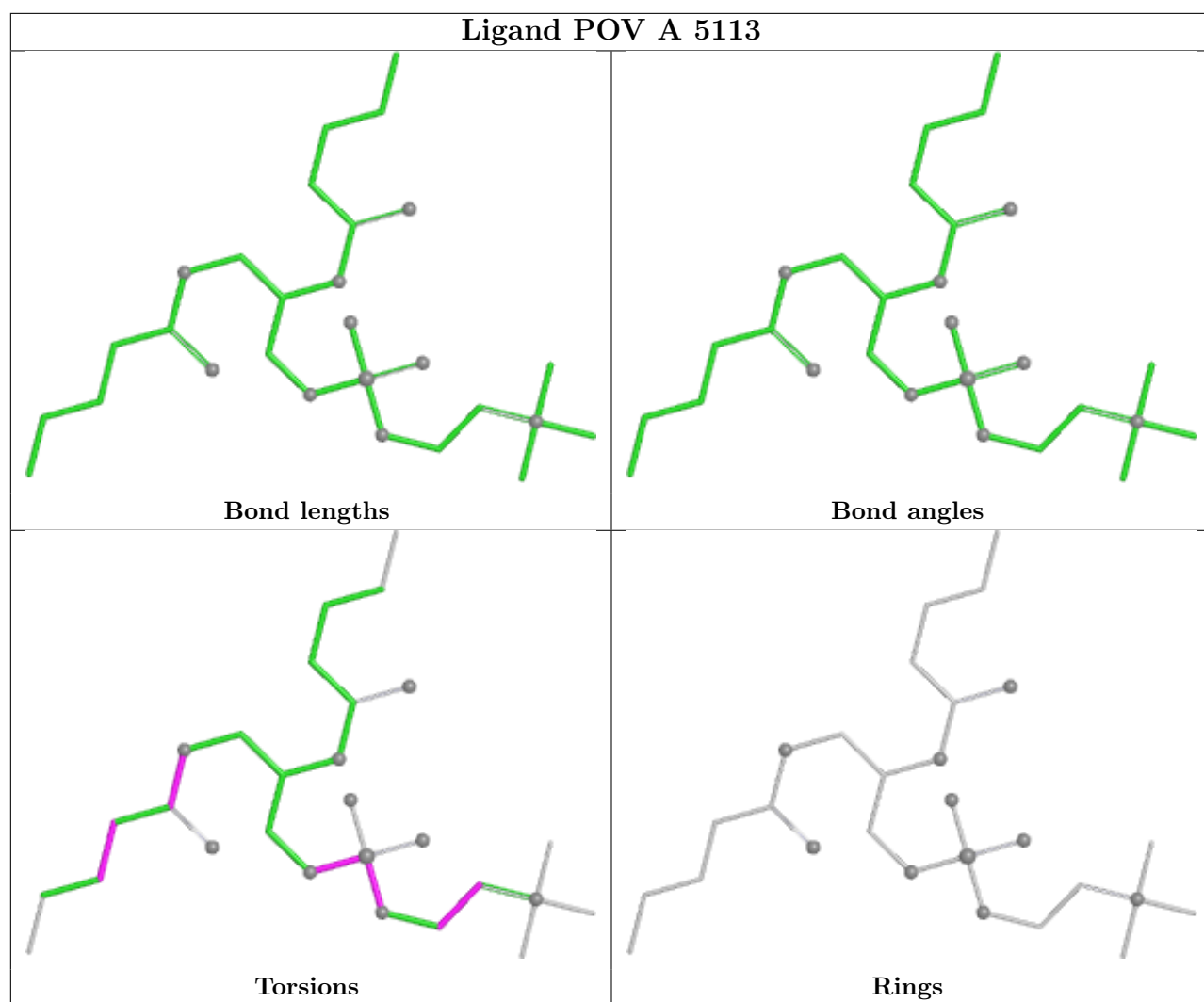


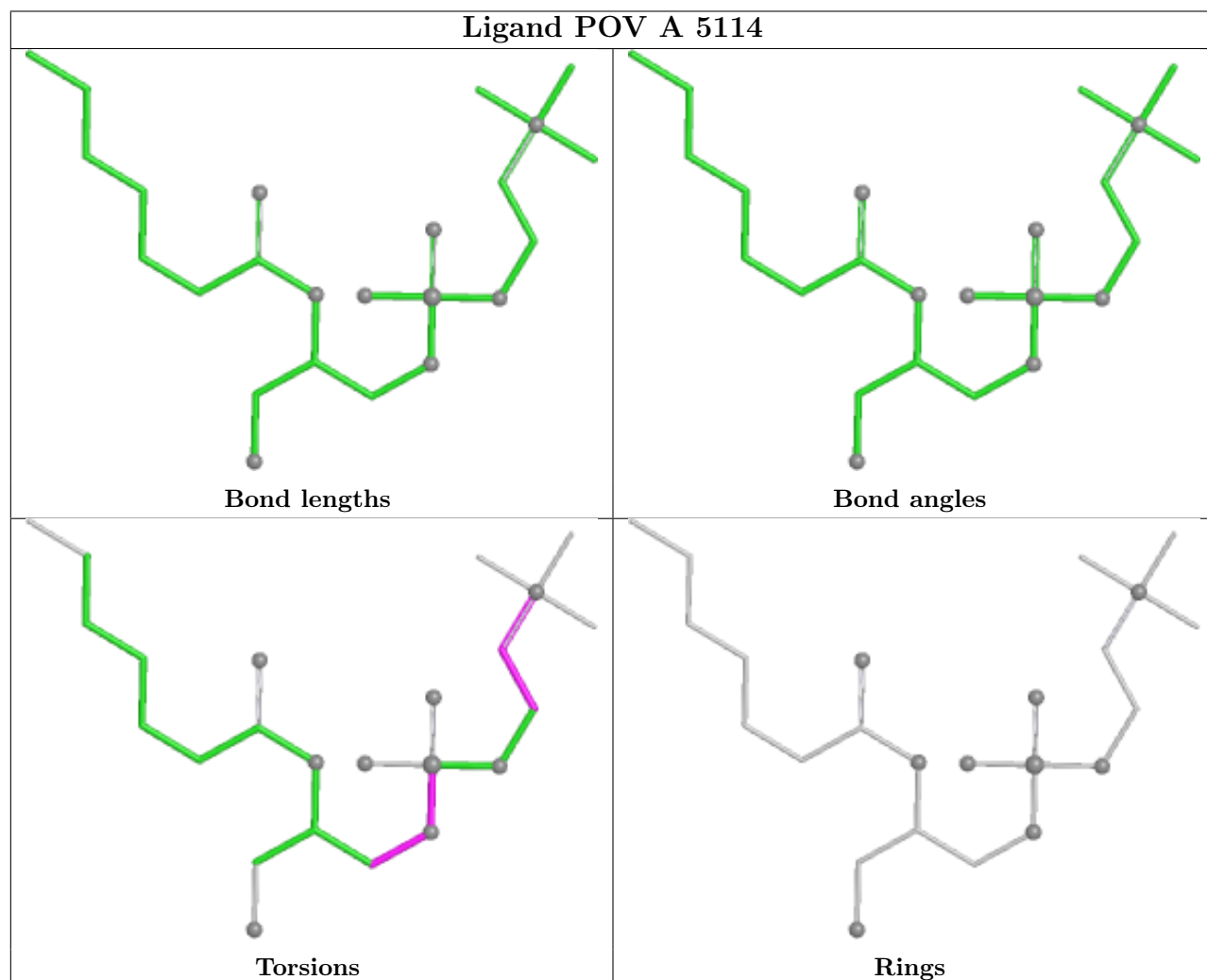
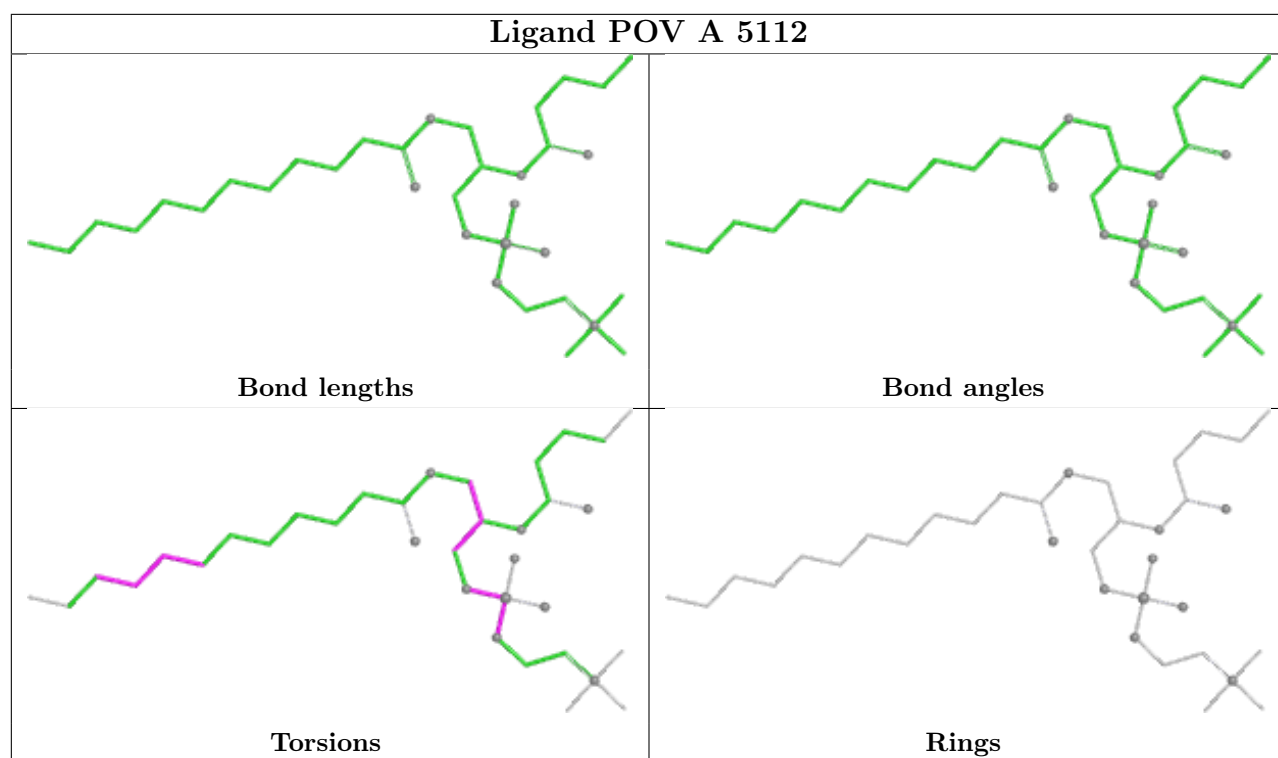
Ligand POV A 5108

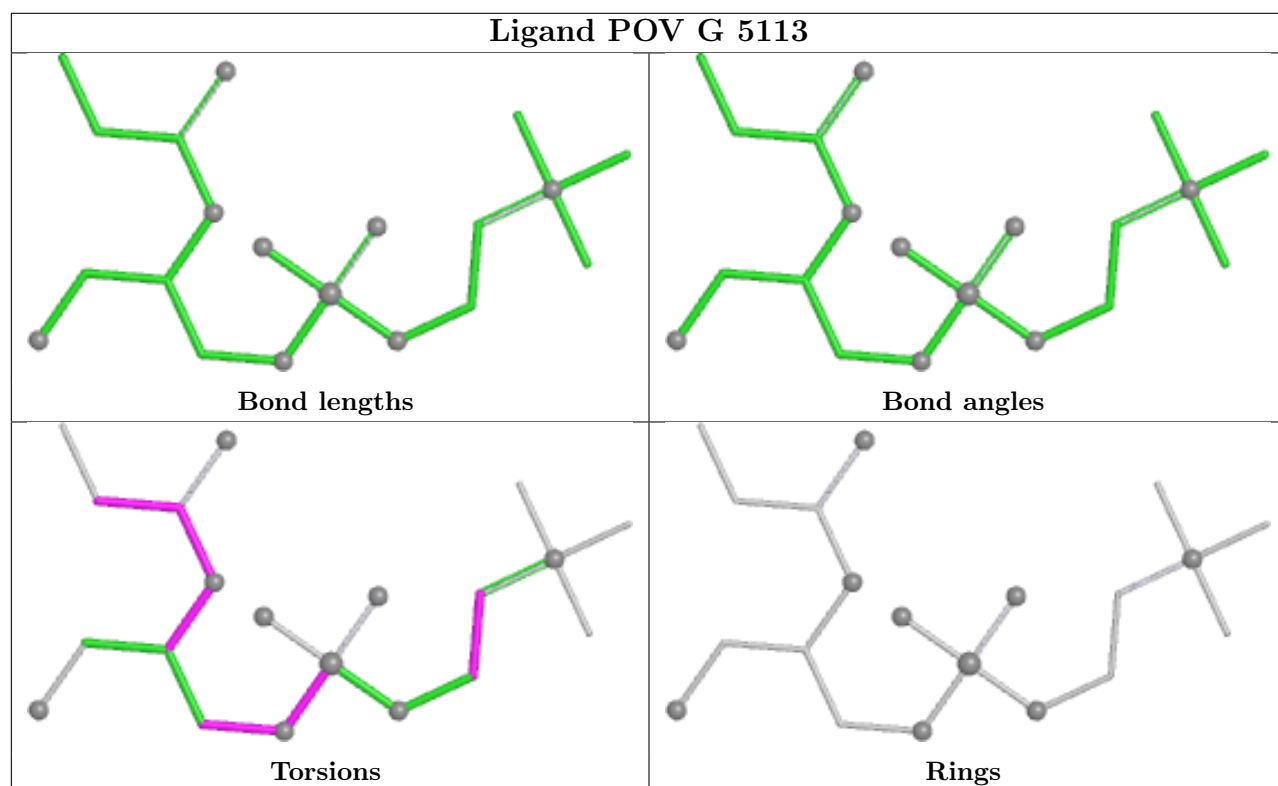
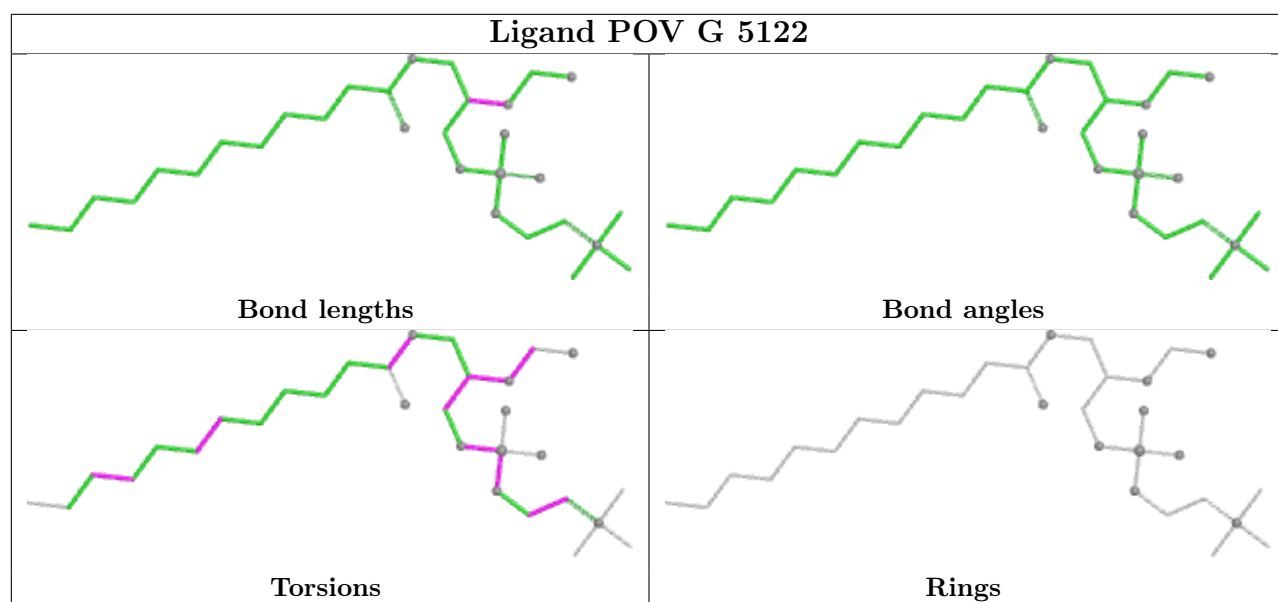


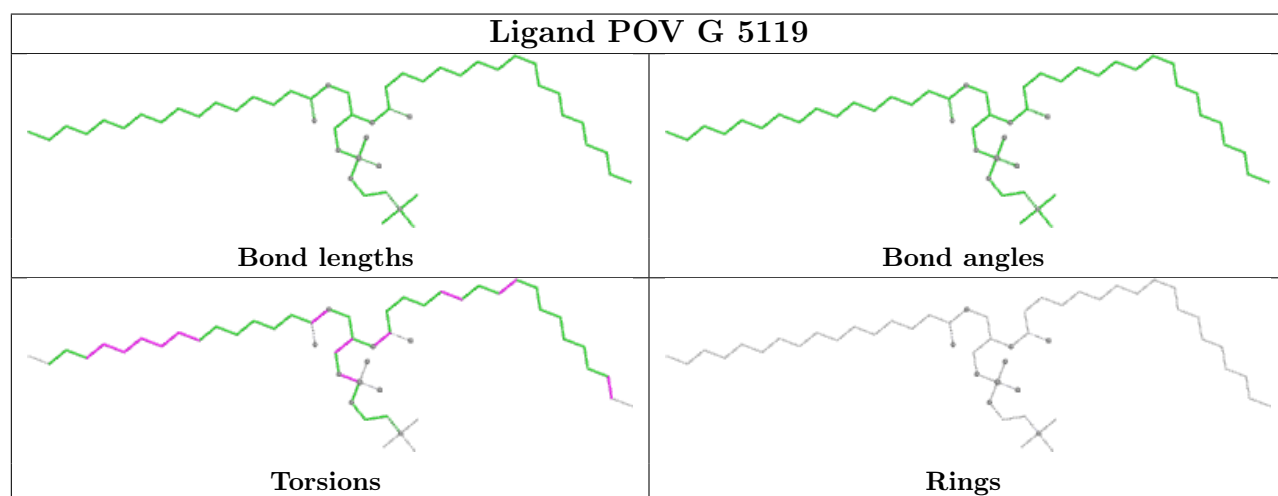
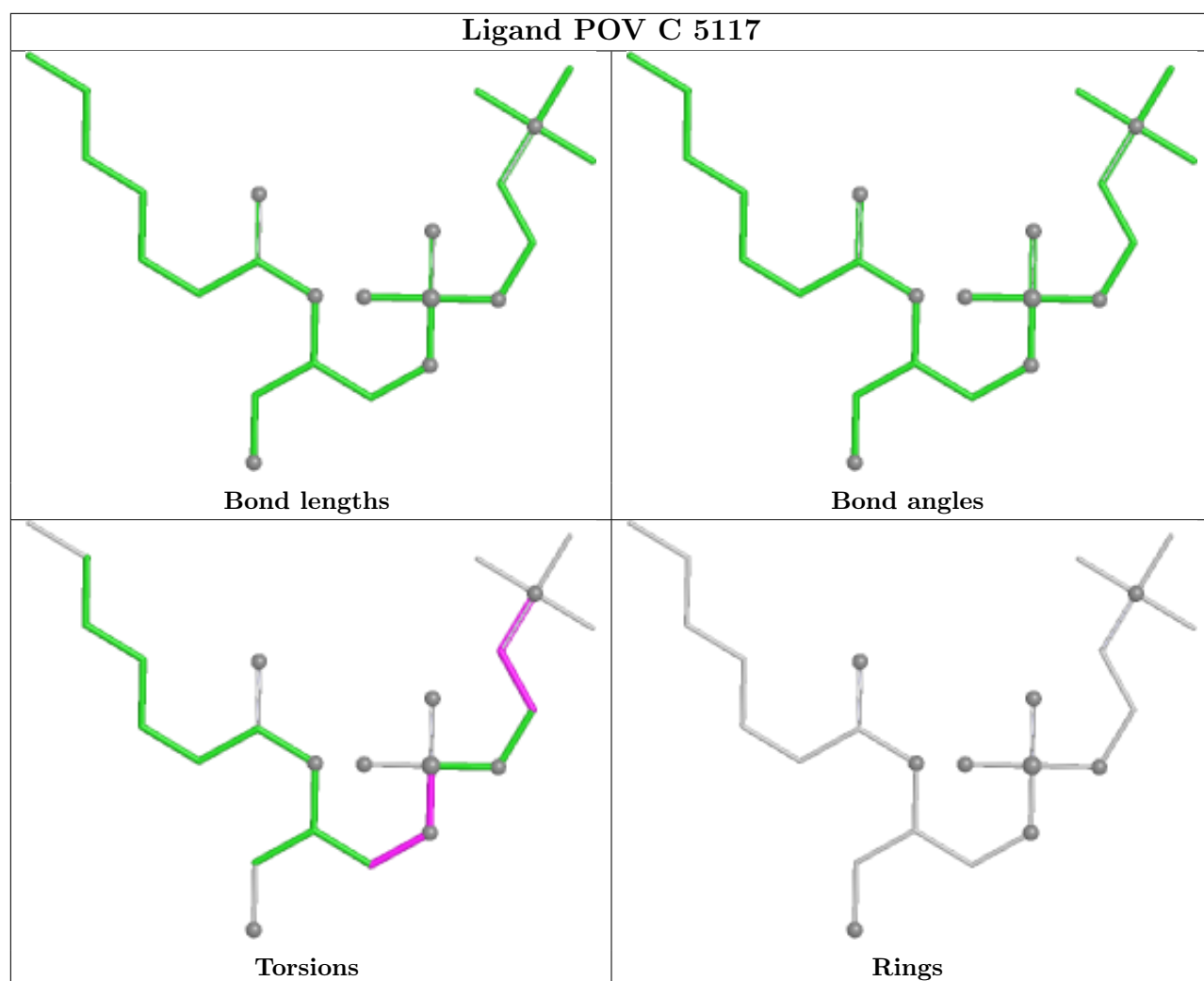


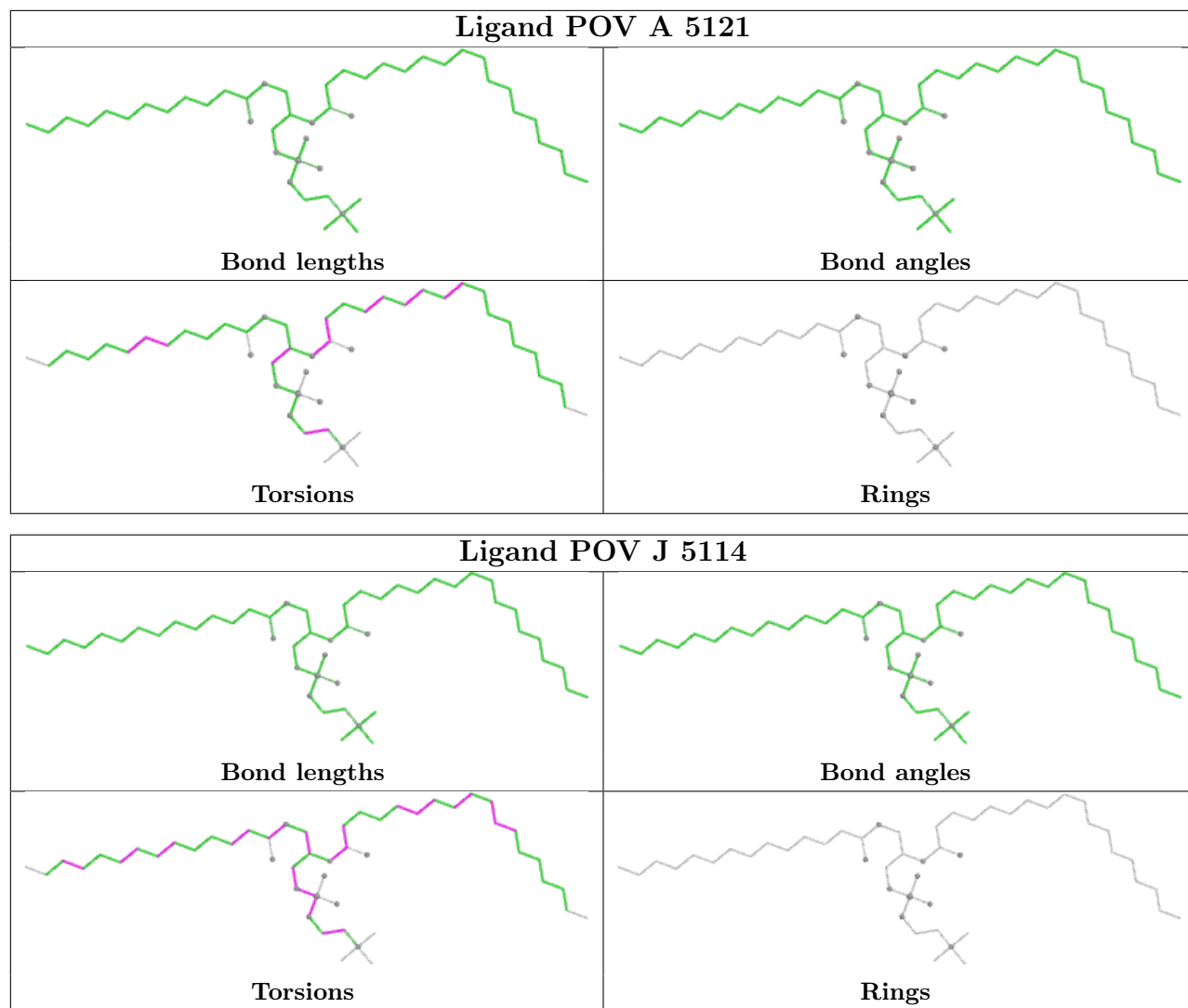


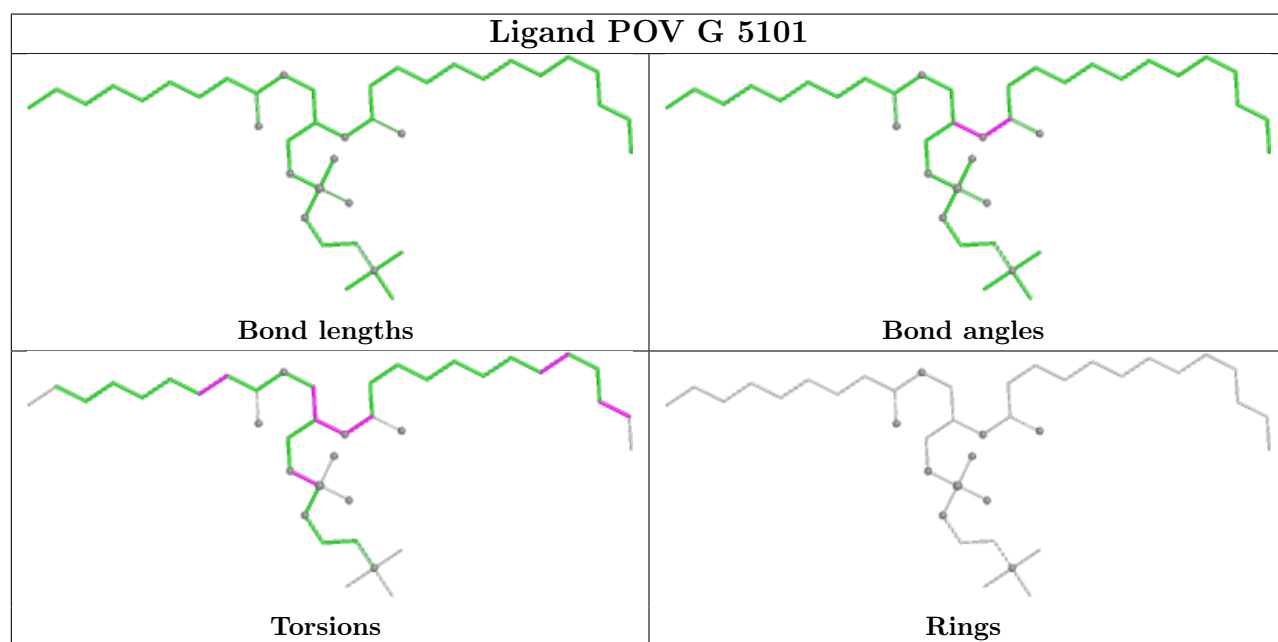
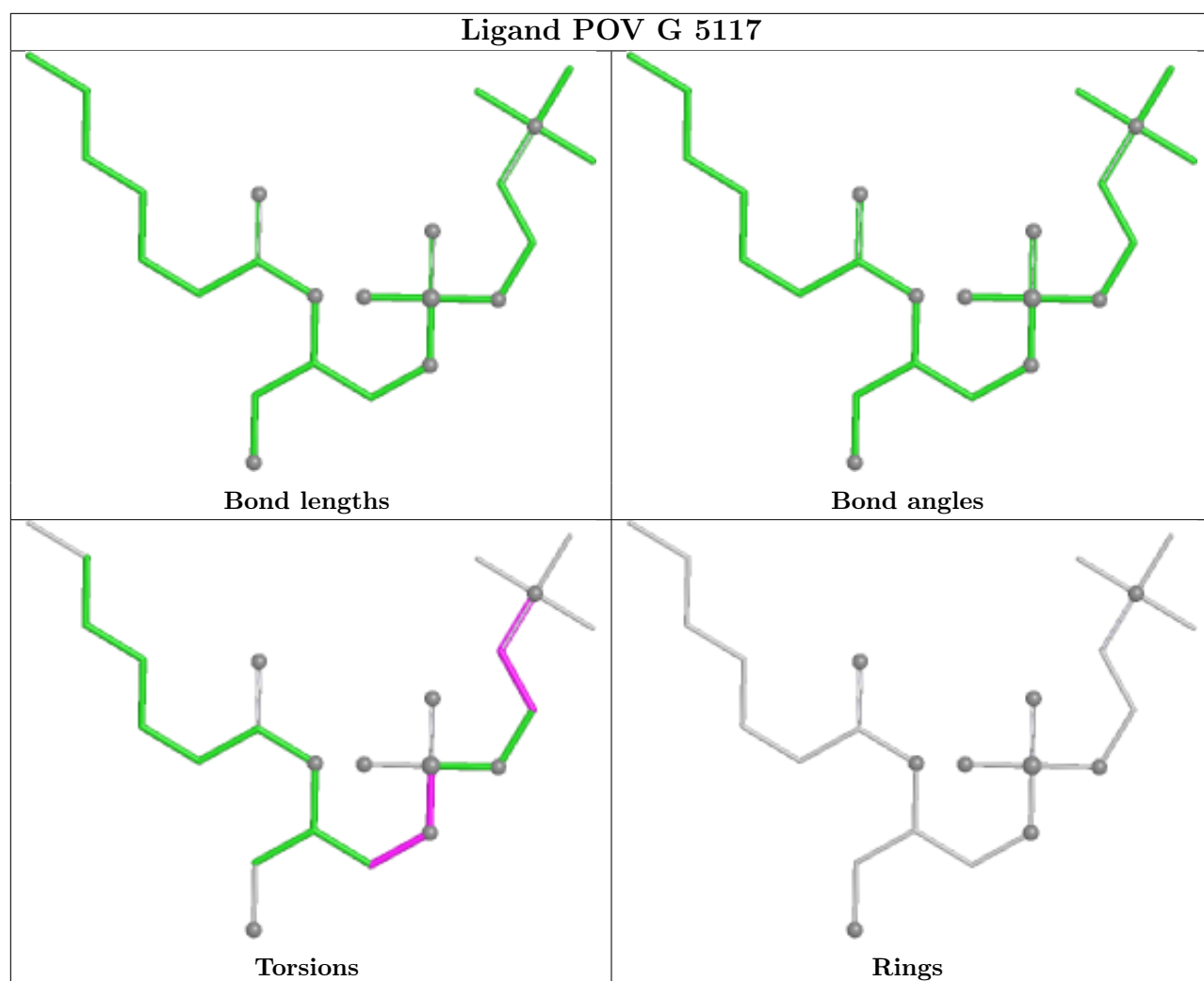


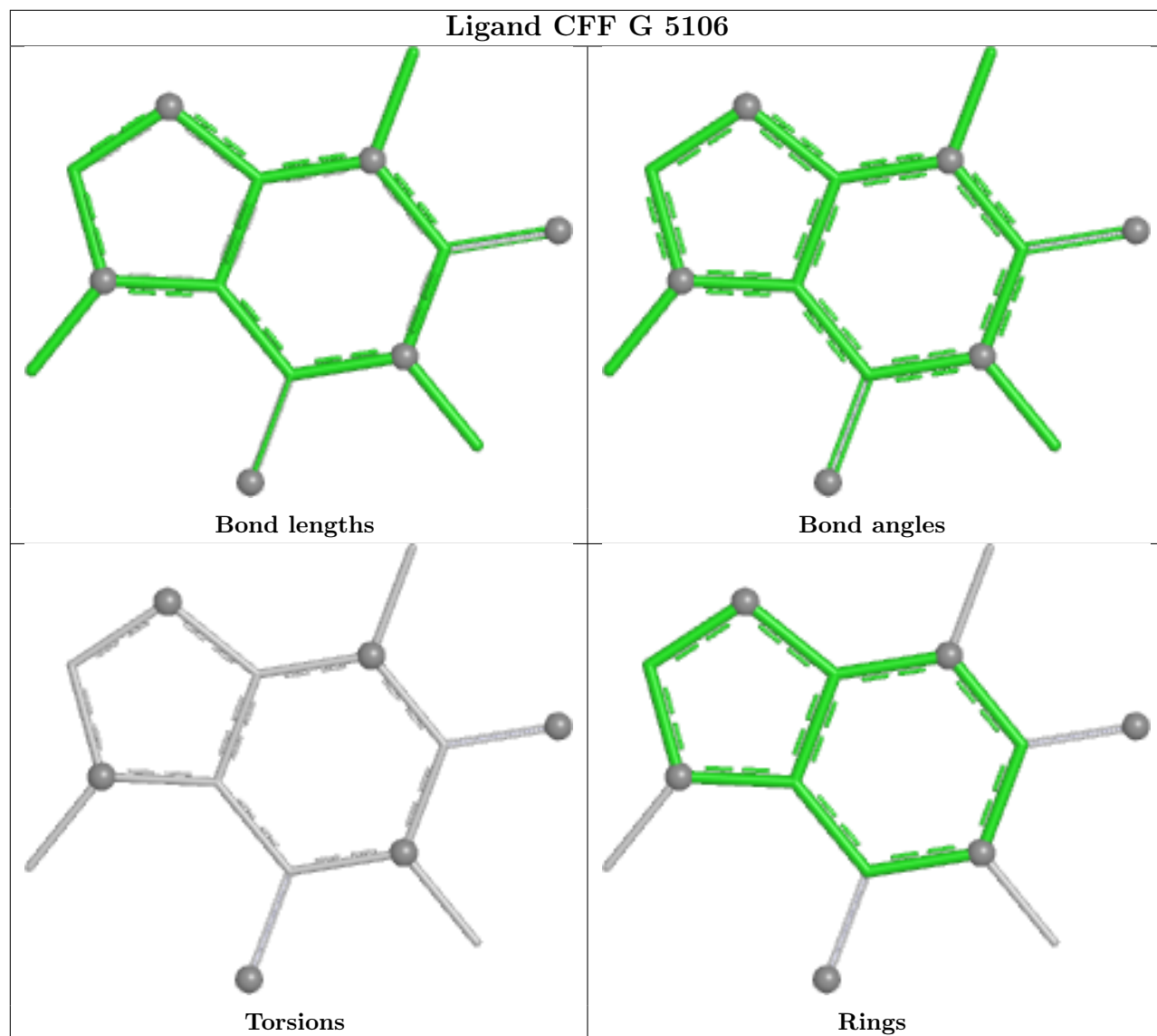


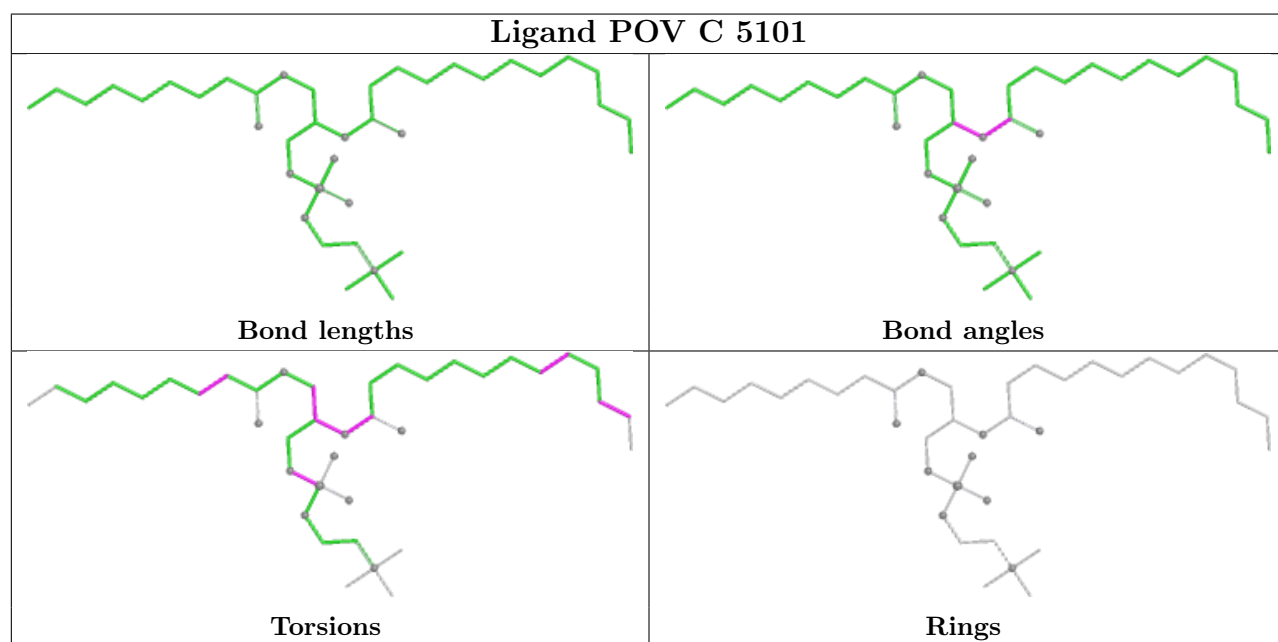
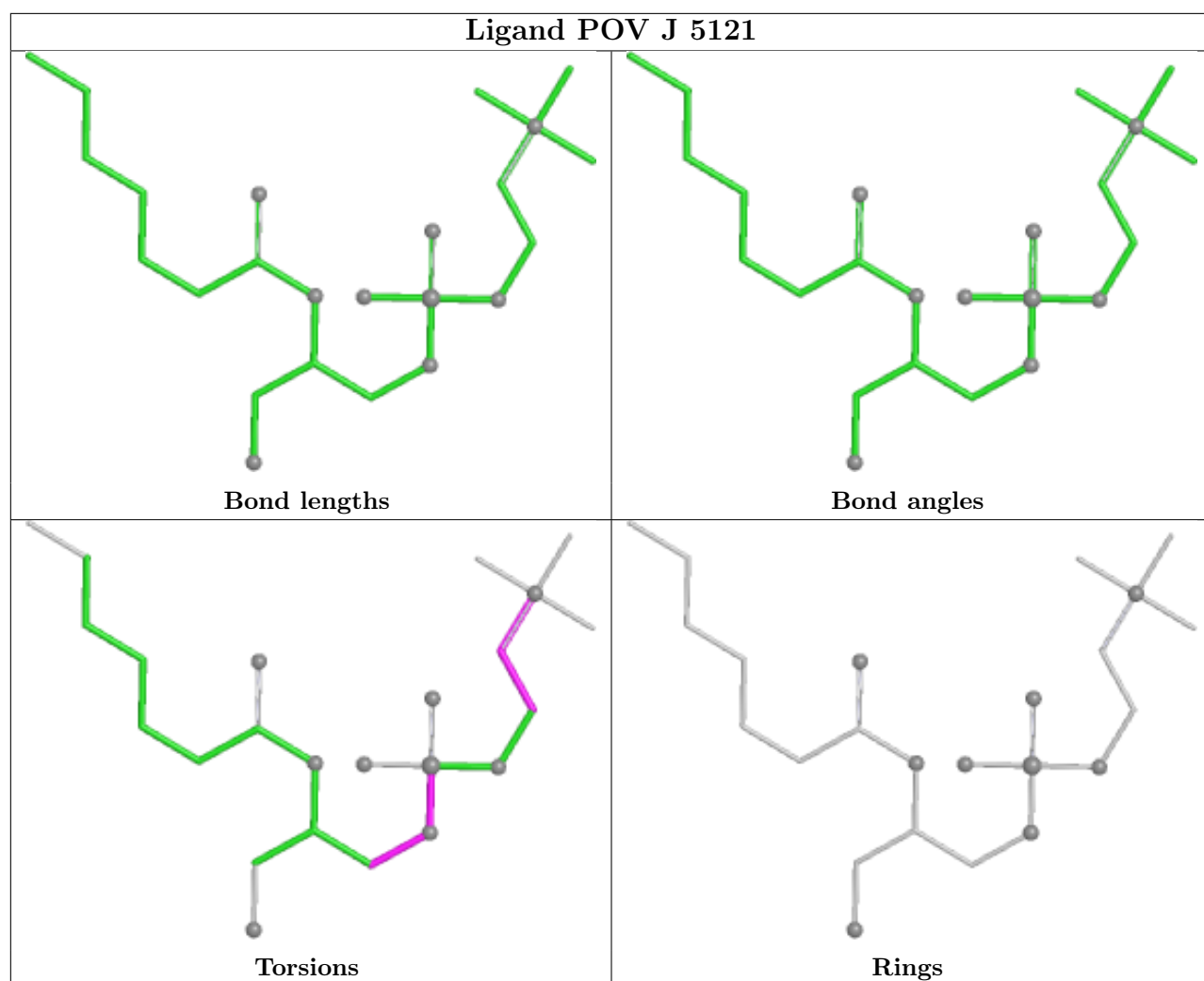


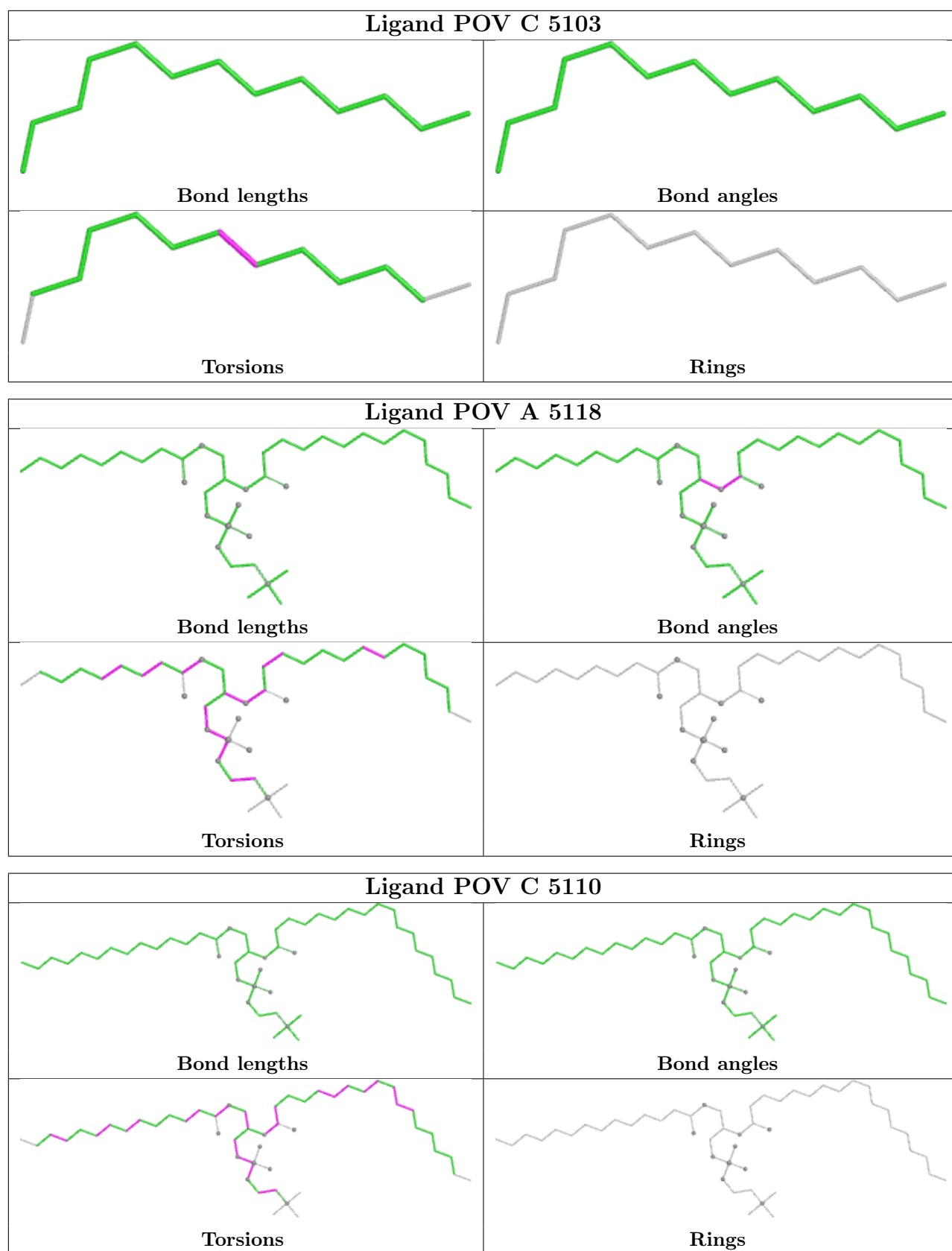


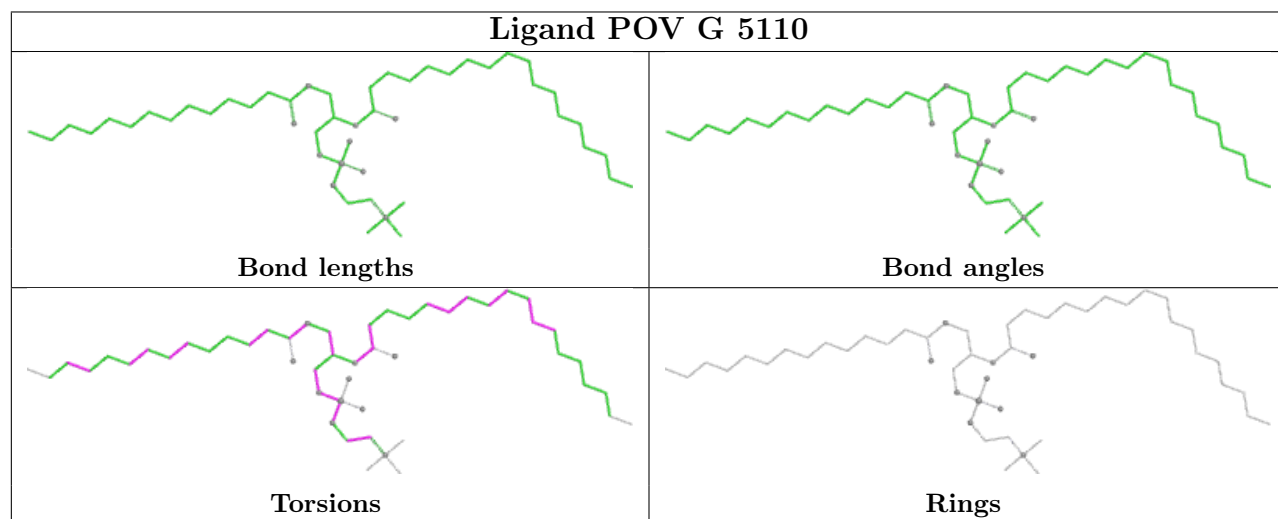
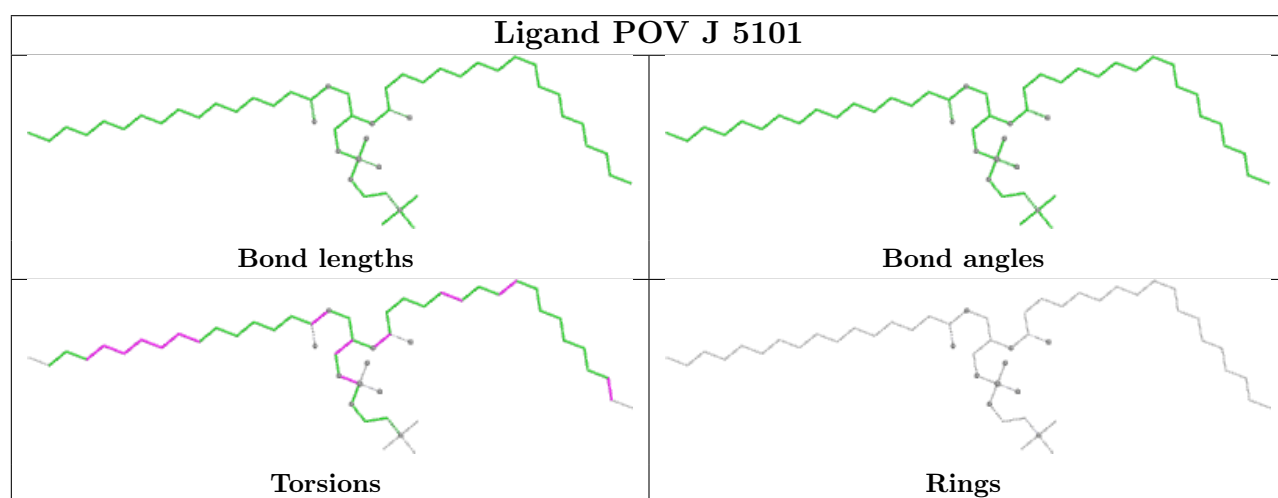
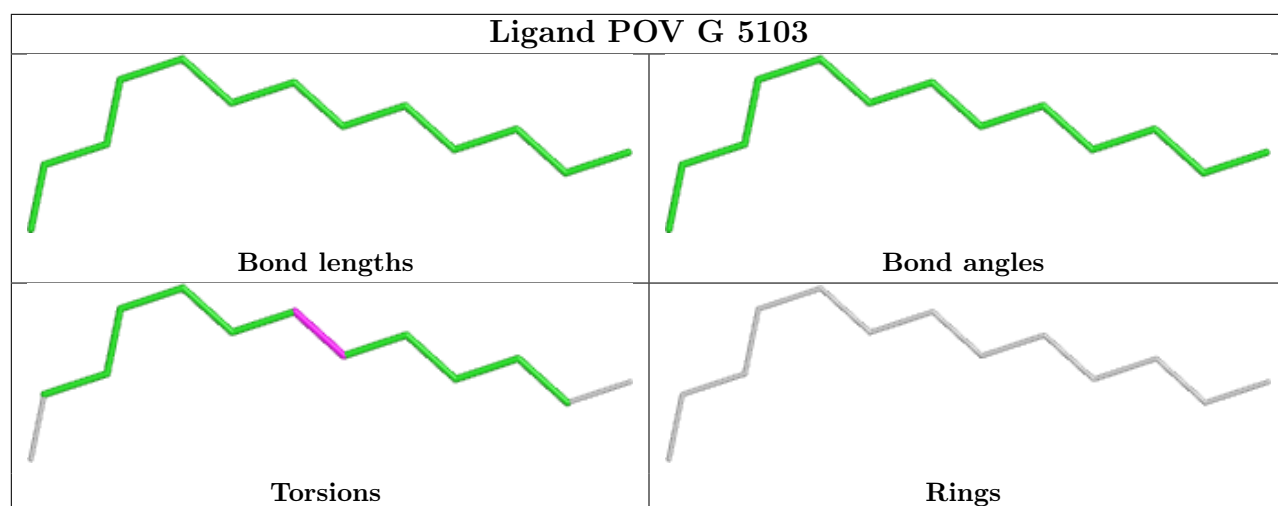


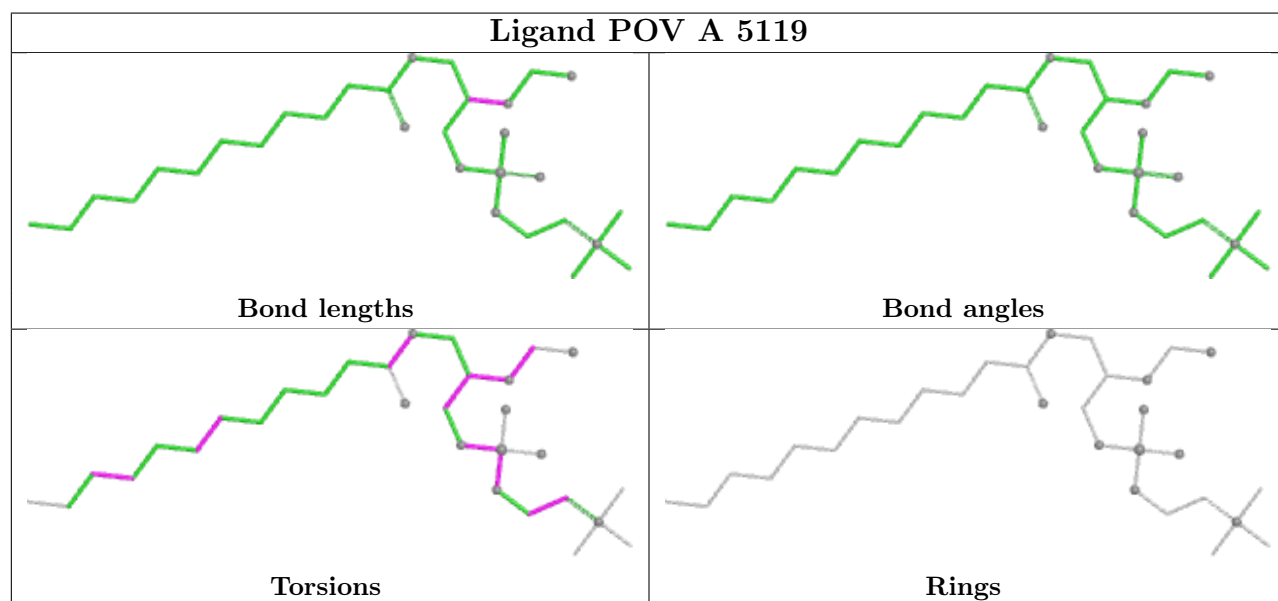
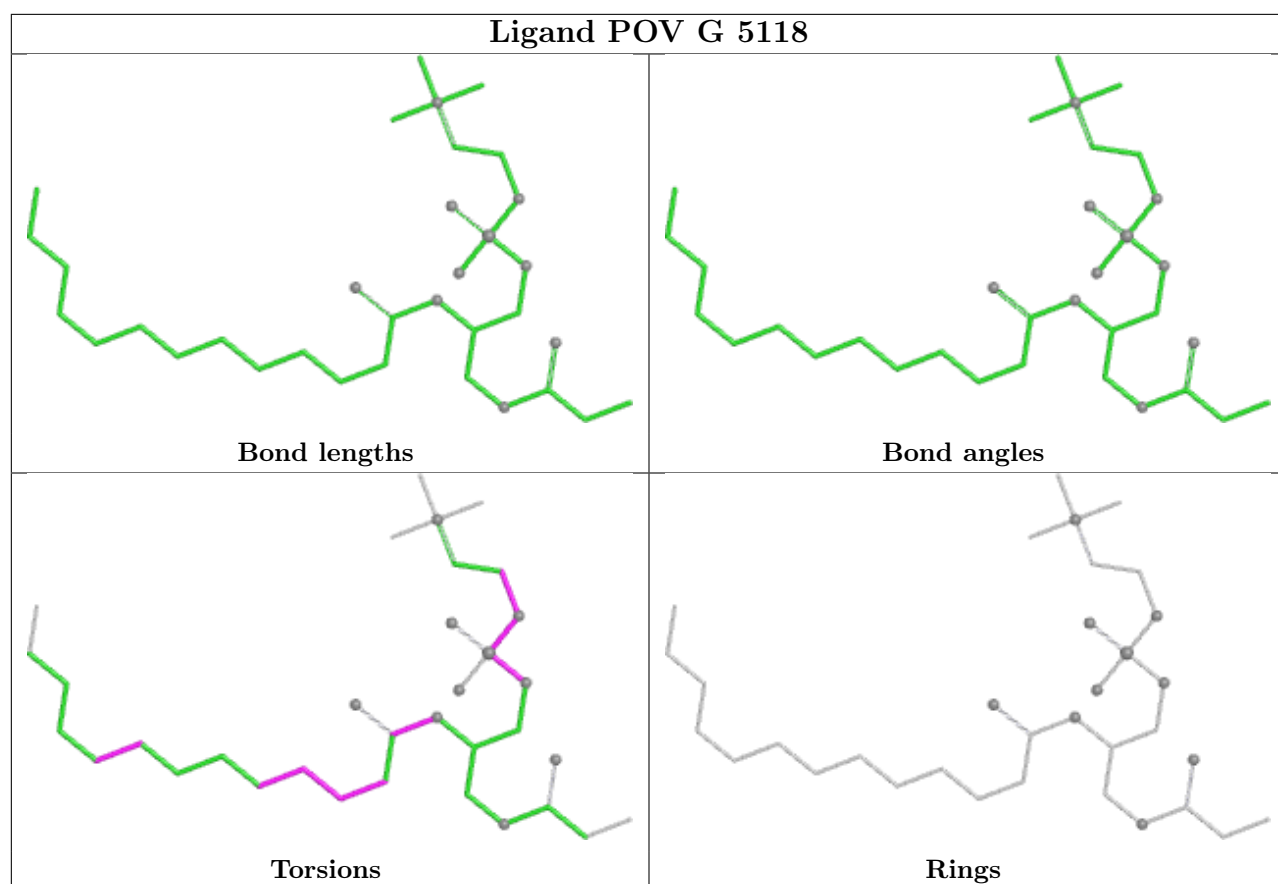


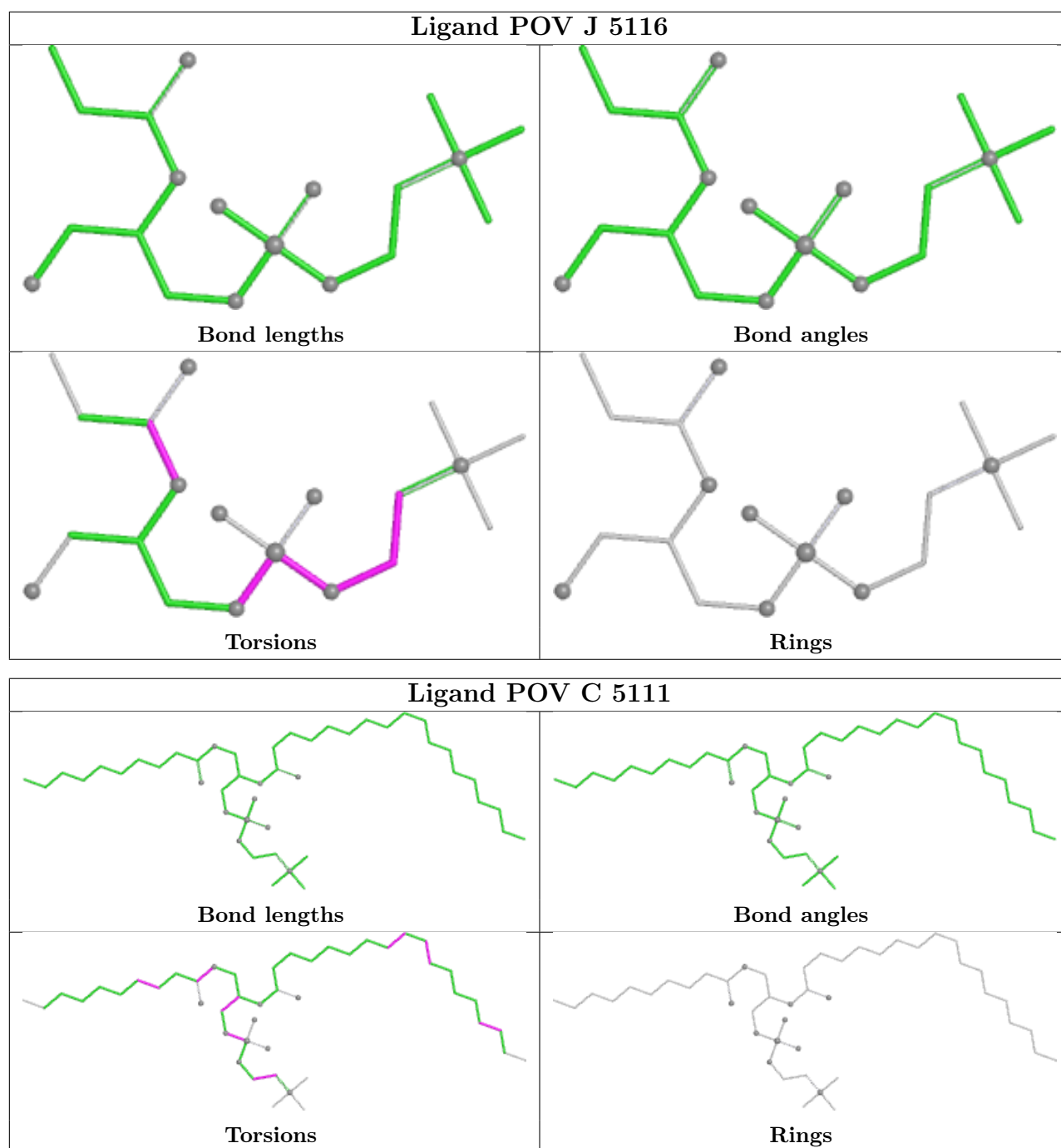












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

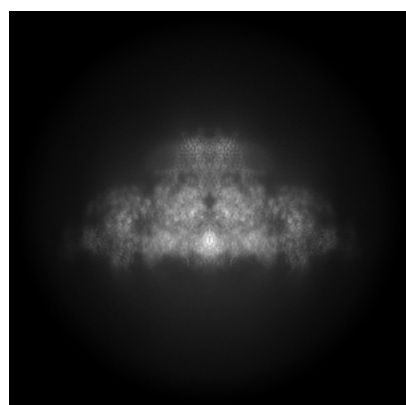
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52085. These allow visual inspection of the internal detail of the map and identification of artifacts.

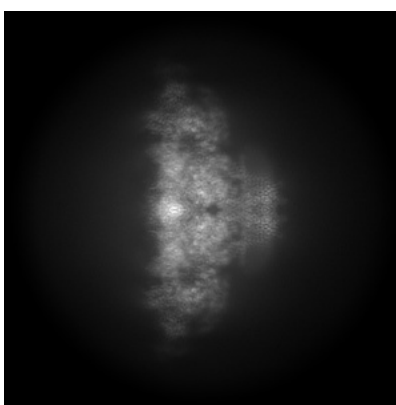
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

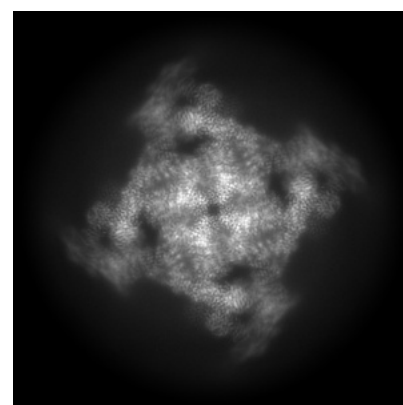
6.1.1 Primary map



X



Y



Z

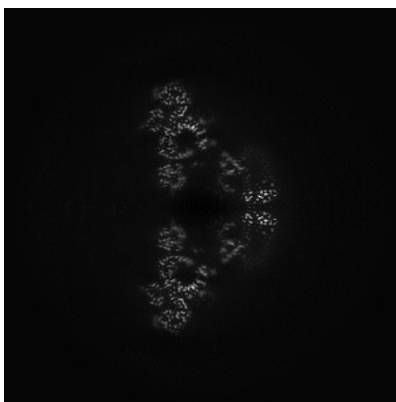
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

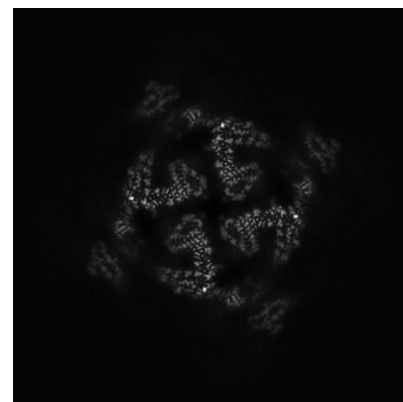
6.2.1 Primary map



X Index: 168



Y Index: 168



Z Index: 168

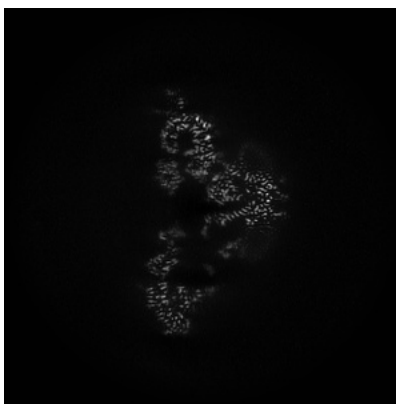
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

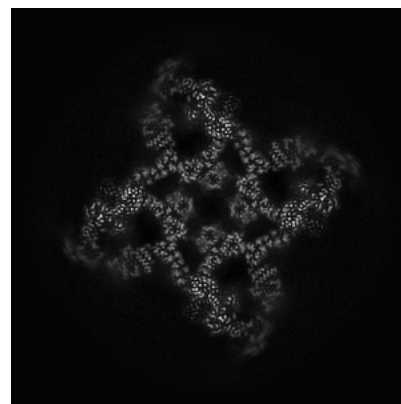
6.3.1 Primary map



X Index: 161



Y Index: 161

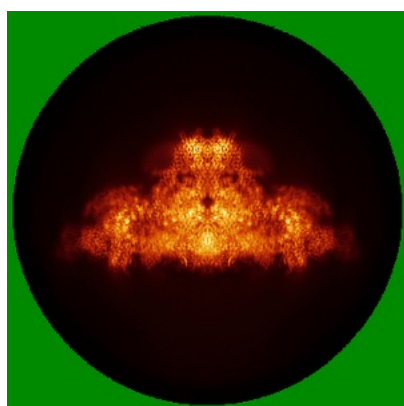


Z Index: 144

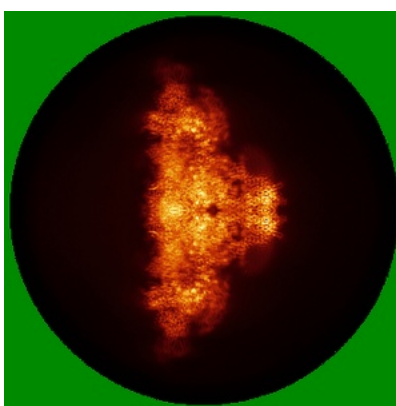
The images above show the largest variance slices of the map in three orthogonal directions.

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

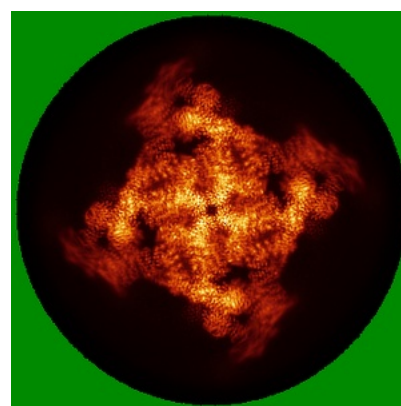
6.4.1 Primary map



X



Y

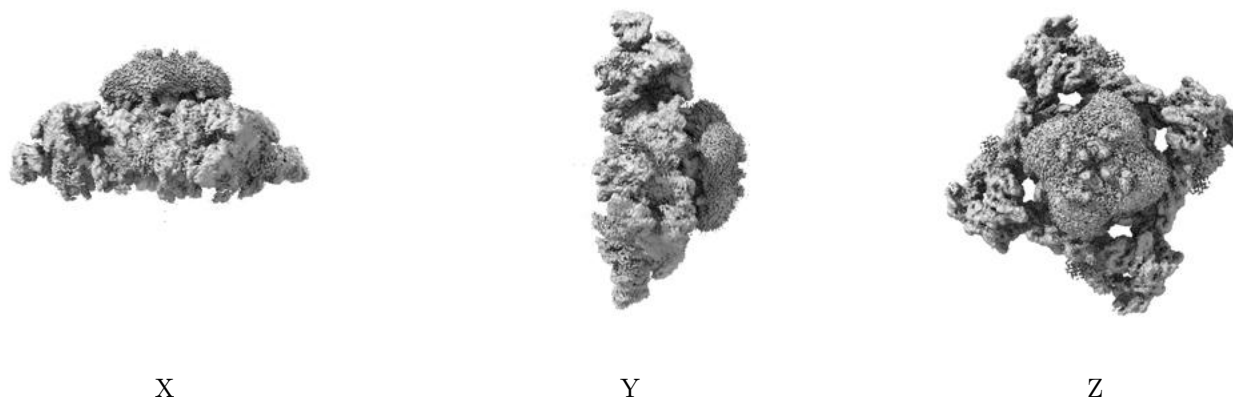


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

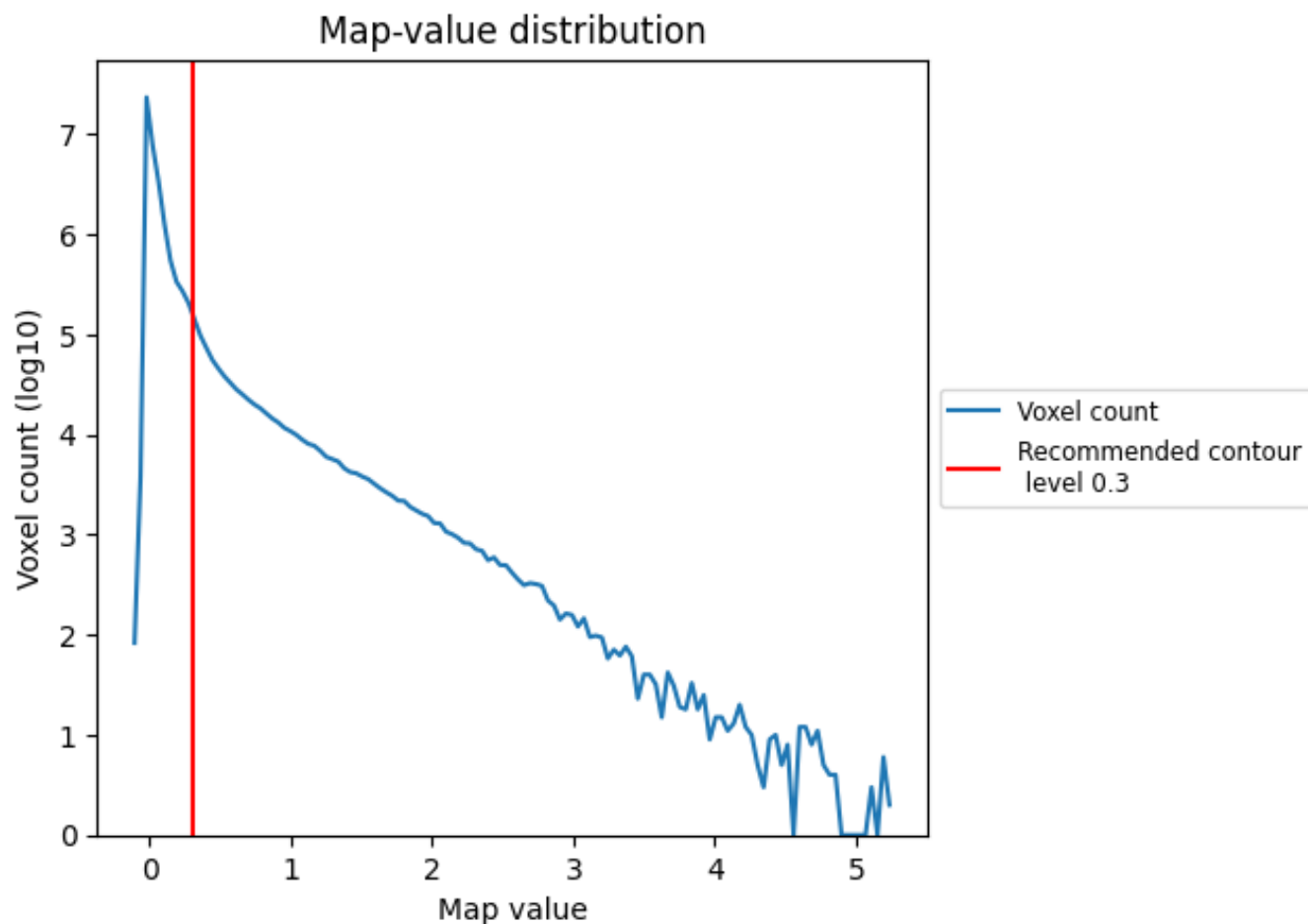
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

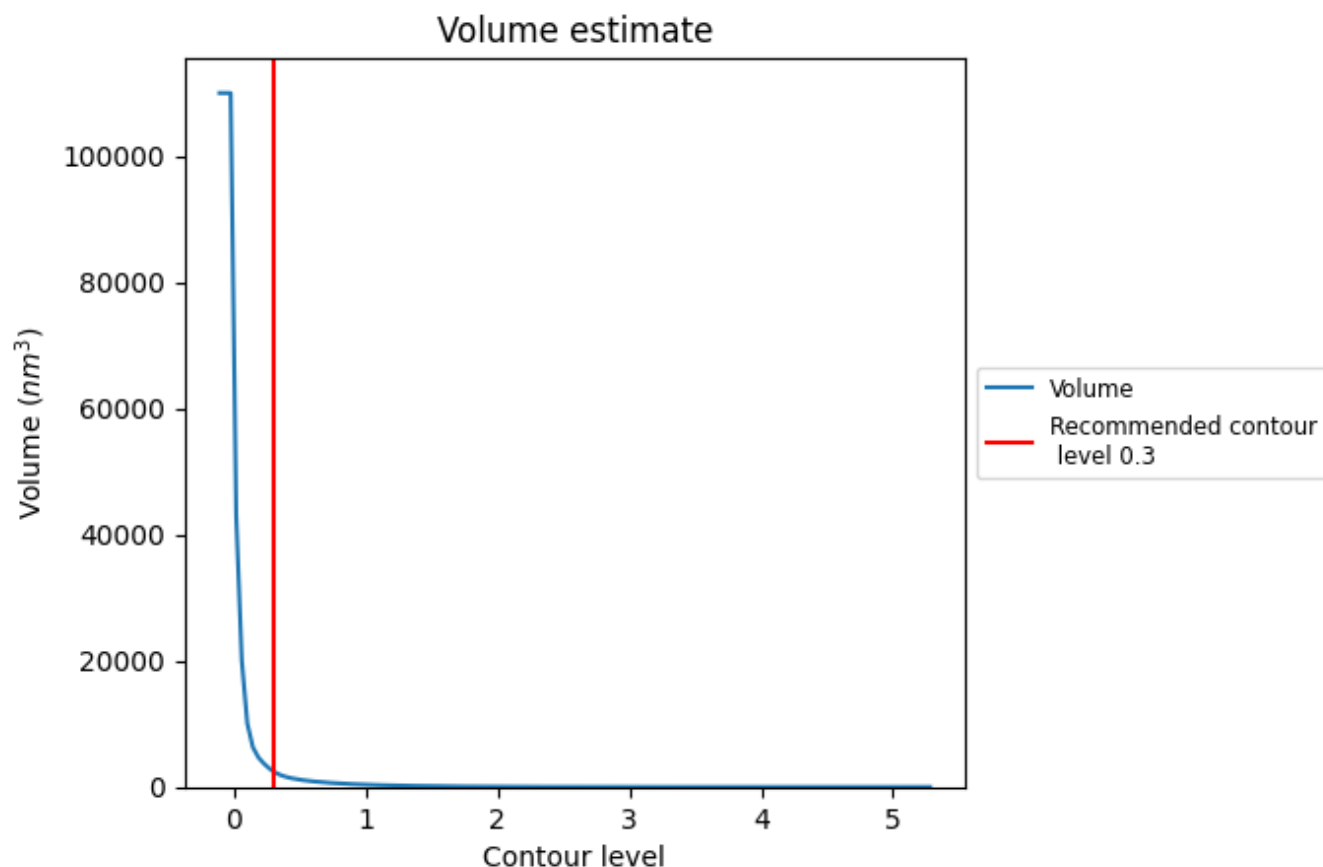
This section contains the results of statistical analysis of the map.

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.

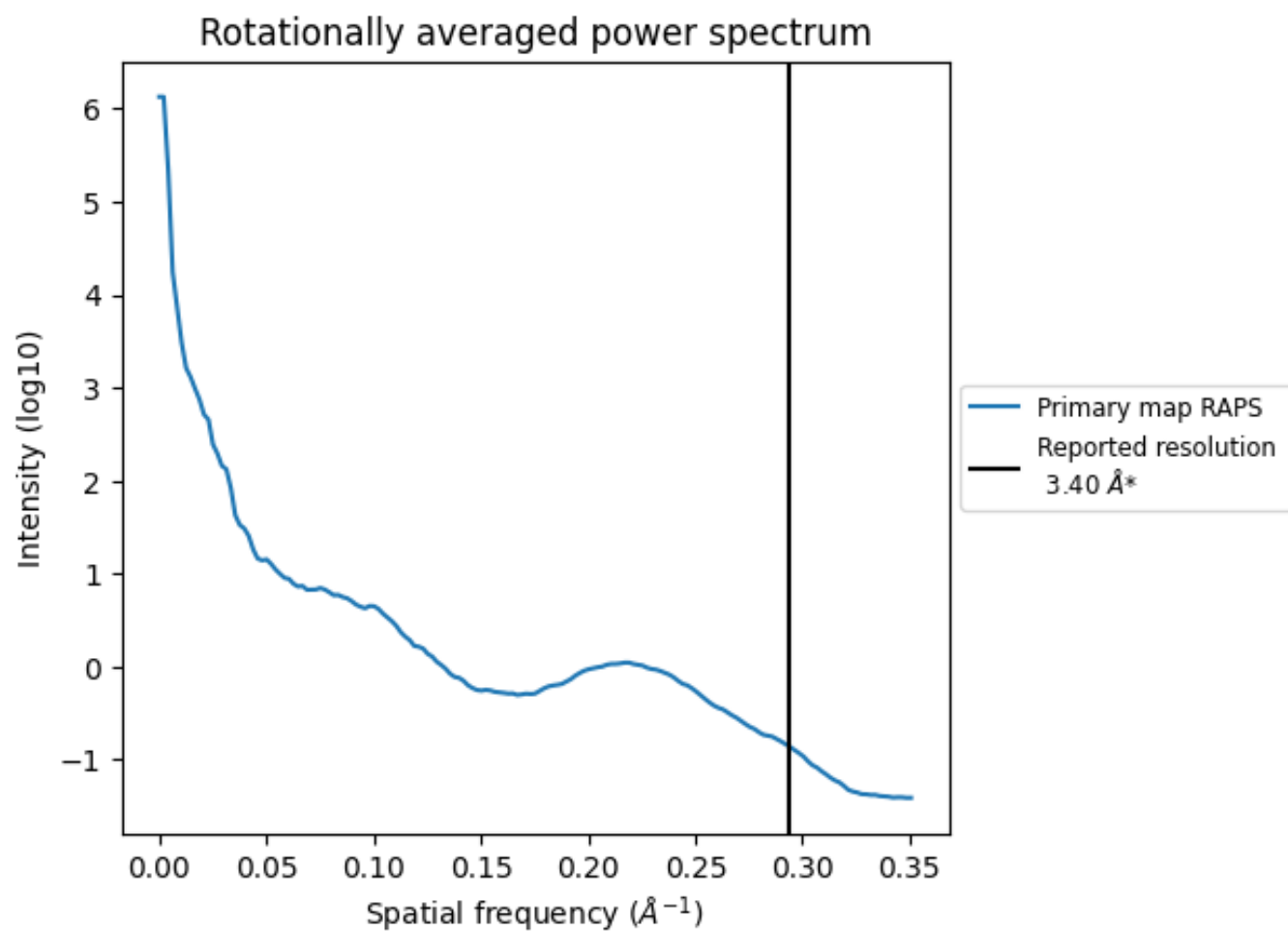
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2518 nm^3 ; this corresponds to an approximate mass of 2275 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

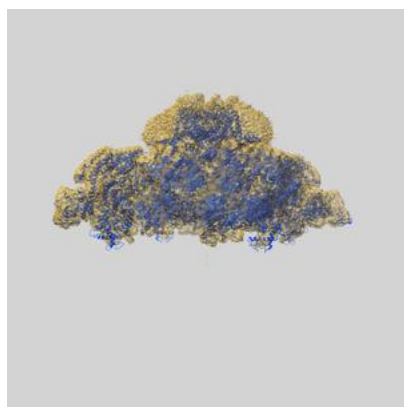
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

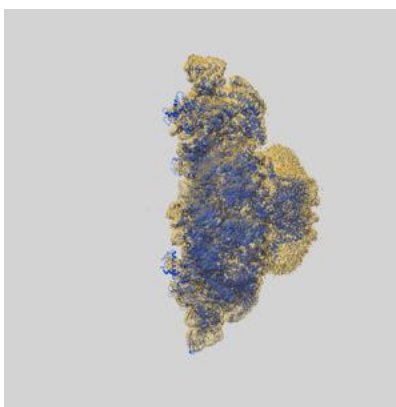
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-52085 and PDB model 9HEO. Per-residue inclusion information can be found in section [3](#) on page [11](#).

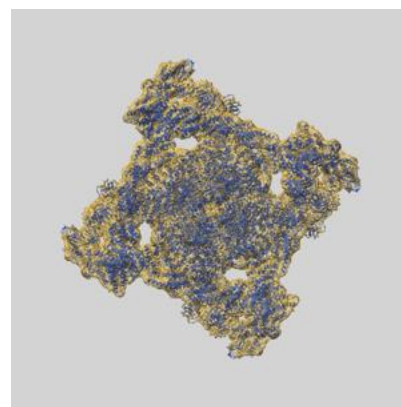
9.1 Map-model overlay [i](#)



X



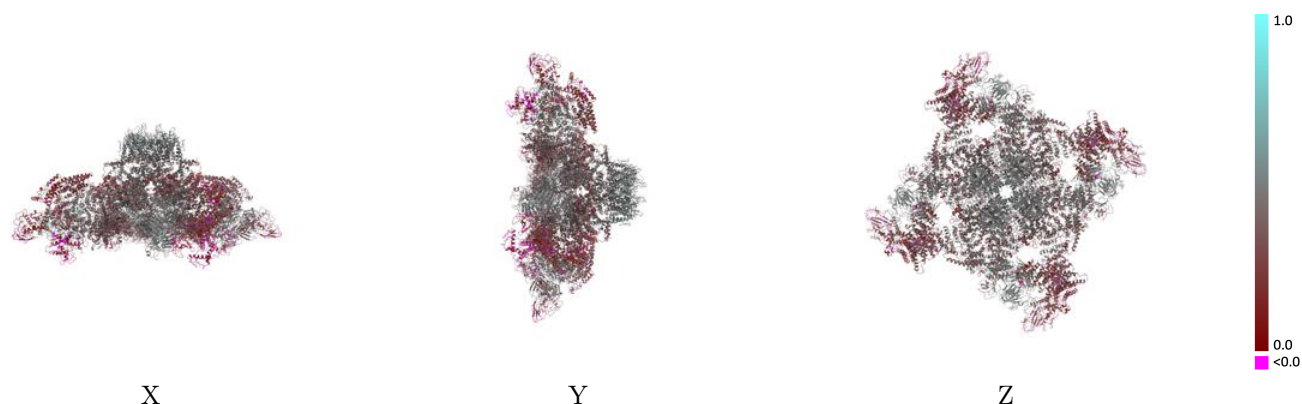
Y



Z

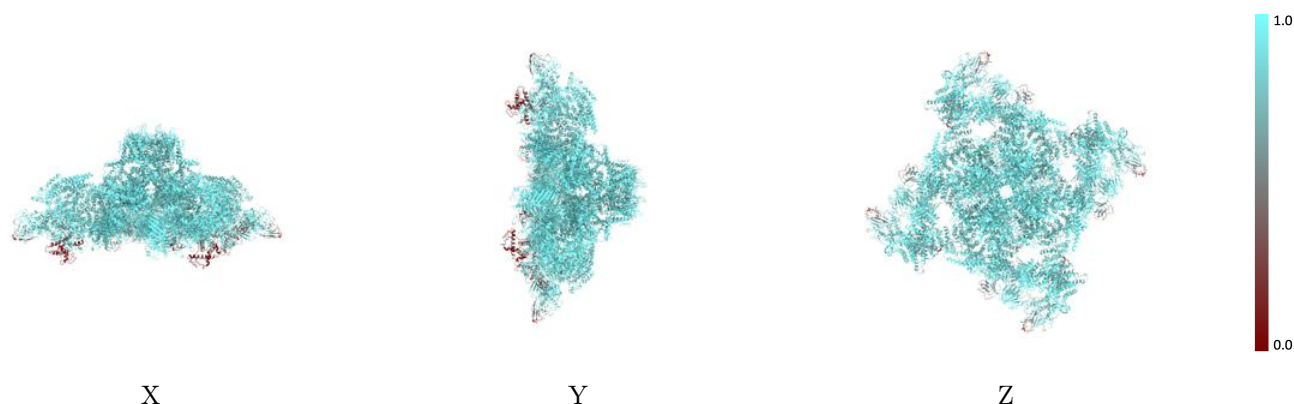
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



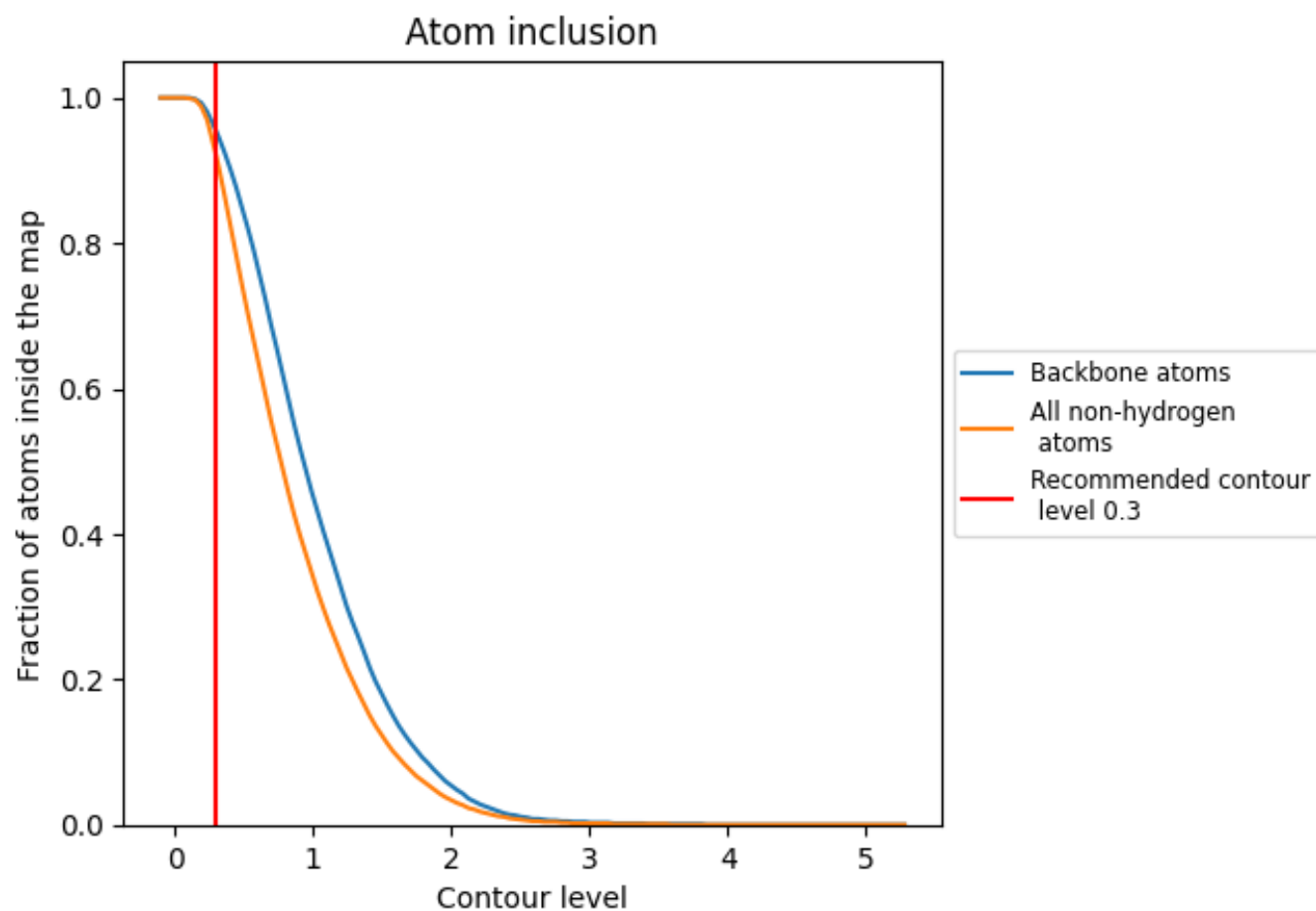
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 92% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9180	<div></div> 0.3600
A	<div></div> 0.9340	<div></div> 0.3650
B	<div></div> 0.6020	<div></div> 0.1630
C	<div></div> 0.9340	<div></div> 0.3660
D	<div></div> 0.6020	<div></div> 0.1660
E	<div></div> 0.6010	<div></div> 0.3560
F	<div></div> 0.5980	<div></div> 0.3610
G	<div></div> 0.9340	<div></div> 0.3650
H	<div></div> 0.6160	<div></div> 0.1670
I	<div></div> 0.6080	<div></div> 0.3710
J	<div></div> 0.9340	<div></div> 0.3650
K	<div></div> 0.6030	<div></div> 0.1660
L	<div></div> 0.6080	<div></div> 0.3670

