



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:54 PM UTC

PDB ID : 9I6H / pdb_00009i6h
Title : Room temperature structure of KR2 rhodopsin in pentameric form at 95% relative humidity
Authors : Zabelskii, D.; Round, E.; Han, H.; von Stetten, D.; Melo, D.; de Wijn, R.; Bean, R.; Round, A.
Deposited on : 2025-01-30
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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/XrayValidationReportHelp>

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:

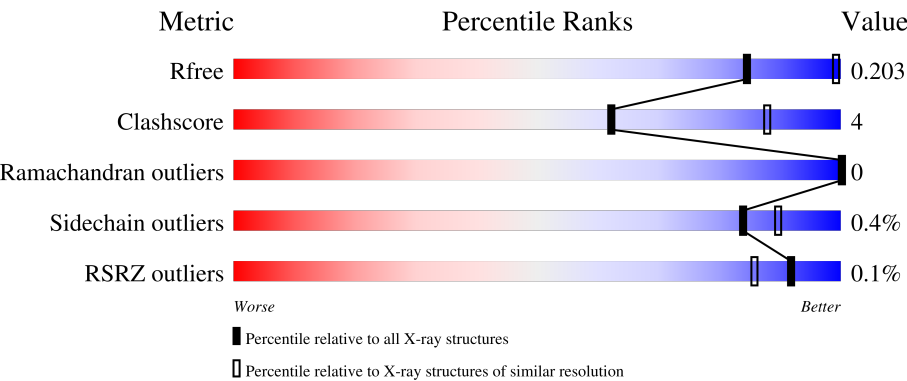
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	273	90%8%
1	B	273	% 91%7%
1	C	273	89%8%
1	D	273	89%10%

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Mol	Chain	Length	Quality of chain
1	E	273	 A horizontal bar chart showing the quality of chain E. The bar is divided into three segments: a green segment representing 86%, a yellow segment representing 12%, and a small grey segment at the end. The percentages '86%' and '12%' are printed below the green and yellow segments respectively. A small black dot is visible at the end of the grey segment.

2 Entry composition [i](#)

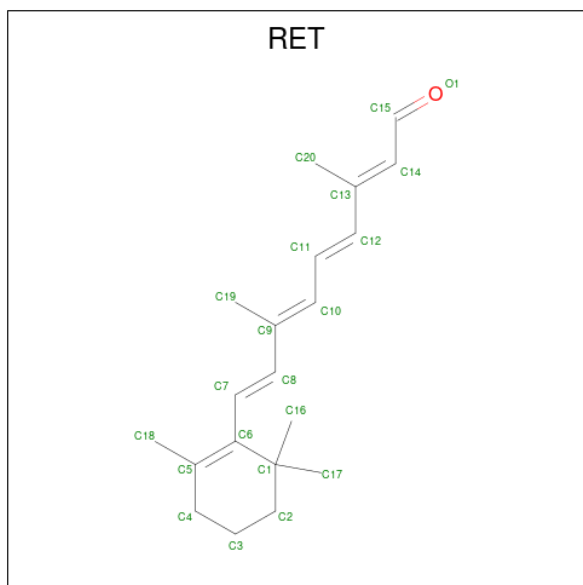
There are 6 unique types of molecules in this entry. The entry contains 11939 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Sodium pumping rhodopsin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	269	Total	C	N	O	S	0	0	0
			2133	1424	322	378	9			
1	B	269	Total	C	N	O	S	0	0	0
			2130	1421	323	377	9			
1	C	268	Total	C	N	O	S	0	0	0
			2127	1420	321	377	9			
1	D	268	Total	C	N	O	S	0	0	0
			2120	1415	321	375	9			
1	E	268	Total	C	N	O	S	0	0	0
			2126	1419	322	376	9			

- Molecule 2 is RETINAL (CCD ID: RET) (formula: $C_{20}H_{28}O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	C	0	0
			20	20		

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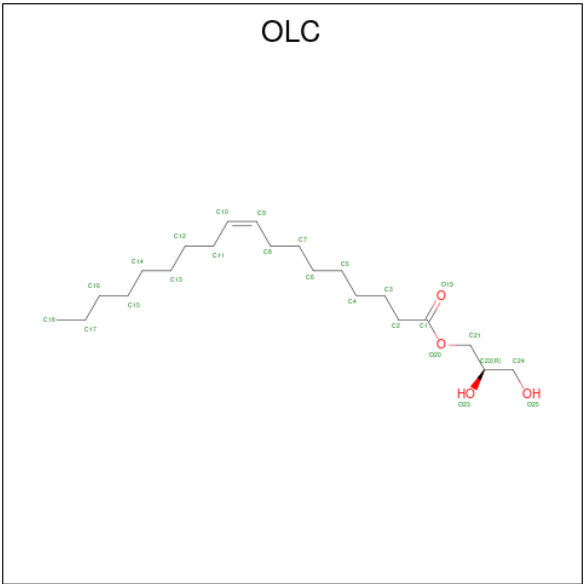
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C 20 20	0	0
2	C	1	Total C 20 20	0	0
2	D	1	Total C 20 20	0	0
2	E	1	Total C 20 20	0	0

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Na 1 1	0	0
3	B	1	Total Na 1 1	0	0
3	C	1	Total Na 1 1	0	0
3	D	1	Total Na 1 1	0	0
3	E	1	Total Na 1 1	0	0

- Molecule 4 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (CCD ID: OLC) (formula: C₂₁H₄₀O₄).



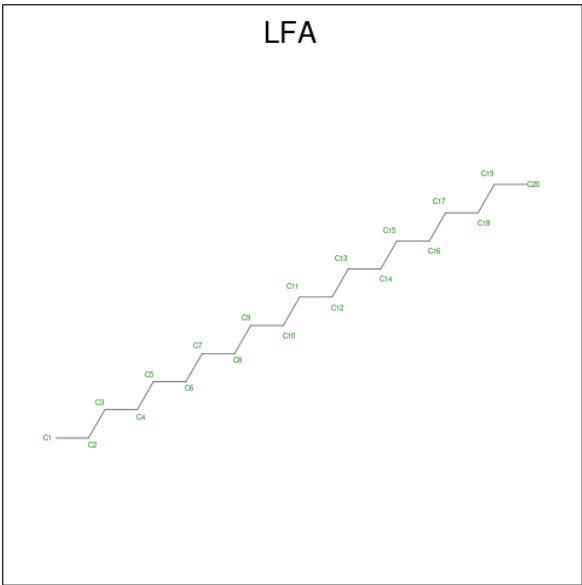
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 16 14 2	0	0
4	A	1	Total C O 23 21 2	0	0
4	A	1	Total C 9 9	0	0
4	A	1	Total C O 19 18 1	0	0
4	A	1	Total C O 23 21 2	0	0
4	A	1	Total C O 12 9 3	0	0
4	A	1	Total C O 20 19 1	0	0
4	A	1	Total C O 14 11 3	0	0
4	A	1	Total C 7 7	0	0
4	A	1	Total C O 15 12 3	0	0
4	A	1	Total C O 19 18 1	0	0
4	A	1	Total C O 22 20 2	0	0
4	B	1	Total C O 20 17 3	0	0
4	B	1	Total C 13 13	0	0
4	B	1	Total C 14 14	0	0
4	B	1	Total C O 13 11 2	0	0
4	B	1	Total C O 20 17 3	0	0
4	B	1	Total C O 19 16 3	0	0
4	B	1	Total C O 17 15 2	0	0
4	C	1	Total C O 22 20 2	0	0
4	C	1	Total C O 22 19 3	0	0
4	C	1	Total C O 21 18 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C O 16 13 3	0	0
4	C	1	Total C 6 6	0	0
4	C	1	Total C O 16 14 2	0	0
4	C	1	Total C O 15 12 3	0	0
4	C	1	Total C O 23 21 2	0	0
4	D	1	Total C O 17 14 3	0	0
4	D	1	Total C 18 18	0	0
4	D	1	Total C O 16 14 2	0	0
4	D	1	Total C O 13 10 3	0	0
4	D	1	Total C 7 7	0	0
4	D	1	Total C O 24 21 3	0	0
4	E	1	Total C 18 18	0	0
4	E	1	Total C 8 8	0	0
4	E	1	Total C 16 16	0	0
4	E	1	Total C O 19 16 3	0	0
4	E	1	Total C O 14 11 3	0	0
4	E	1	Total C 6 6	0	0
4	E	1	Total C O 19 17 2	0	0
4	E	1	Total C O 22 20 2	0	0
4	E	1	Total C O 18 17 1	0	0

- Molecule 5 is EICOSANE (CCD ID: LFA) (formula: C₂₀H₄₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C 7 7	0	0
5	A	1	Total C 8 8	0	0
5	A	1	Total C 8 8	0	0
5	A	1	Total C 4 4	0	0
5	A	1	Total C 6 6	0	0
5	A	1	Total C 16 16	0	0
5	A	1	Total C 9 9	0	0
5	B	1	Total C 9 9	0	0
5	B	1	Total C 8 8	0	0
5	B	1	Total C 10 10	0	0
5	B	1	Total C 7 7	0	0
5	B	1	Total C 11 11	0	0
5	B	1	Total C 11 11	0	0
5	C	1	Total C 8 8	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total C 20 20	0	0
5	C	1	Total C 5 5	0	0
5	C	1	Total C 4 4	0	0
5	C	1	Total C 6 6	0	0
5	C	1	Total C 5 5	0	0
5	D	1	Total C 20 20	0	0
5	D	1	Total C 20 20	0	0
5	D	1	Total C 17 17	0	0
5	D	1	Total C 7 7	0	0
5	D	1	Total C 6 6	0	0
5	D	1	Total C 7 7	0	0
5	E	1	Total C 10 10	0	0
5	E	1	Total C 8 8	0	0
5	E	1	Total C 14 14	0	0
5	E	1	Total C 4 4	0	0
5	E	1	Total C 5 5	0	0
5	E	1	Total C 7 7	0	0
5	E	1	Total C 6 6	0	0
5	E	1	Total C 10 10	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	34	Total 34	O 34	0	0
6	B	45	Total 45	O 45	0	0
6	C	40	Total 40	O 40	0	0
6	D	43	Total 43	O 43	0	0
6	E	42	Total 42	O 42	0	0

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Sodium pumping rhodopsin

Chain A:  90% 8% .



• Molecule 1: Sodium pumping rhodopsin

Chain B:  91% 7% .



• Molecule 1: Sodium pumping rhodopsin

Chain C:  89% 8% .



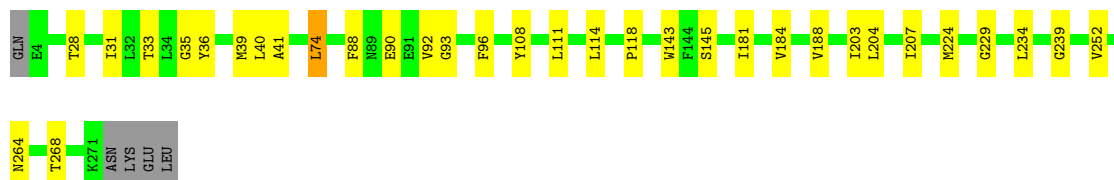
• Molecule 1: Sodium pumping rhodopsin

Chain D:  89% 10% .



• Molecule 1: Sodium pumping rhodopsin

Chain E:  86% 12% .



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	136.10Å 240.90Å 138.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.25 – 3.00 69.25 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (69.25-3.00) 99.9 (69.25-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.171 , 0.203 0.171 , 0.203	Depositor DCC
R_{free} test set	3796 reflections (4.56%)	wwPDB-VP
Wilson B-factor (Å ²)	55.9	Xtriage
Anisotropy	0.106	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 78.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.005 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.006 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11939	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.85% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: OLC, NA, LFA, RET

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	0.18	0/2191	0.34	0/2981
1	B	0.19	0/2188	0.35	0/2977
1	C	0.20	0/2185	0.38	0/2973
1	D	0.19	0/2178	0.36	0/2965
1	E	0.23	0/2184	0.39	0/2971
All	All	0.20	0/10926	0.36	0/14867

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2133	0	2104	15	0
1	B	2130	0	2106	14	0
1	C	2127	0	2100	18	0
1	D	2120	0	2090	17	0
1	E	2126	0	2105	23	0
2	A	20	0	27	0	0
2	B	20	0	27	1	0
2	C	20	0	27	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	20	0	27	1	0
2	E	20	0	27	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
4	A	199	0	299	6	0
4	B	116	0	166	5	0
4	C	141	0	207	9	0
4	D	95	0	144	5	0
4	E	140	0	213	8	0
5	A	58	0	109	0	0
5	B	56	0	103	1	0
5	C	48	0	87	0	0
5	D	77	0	151	1	0
5	E	64	0	117	2	0
6	A	34	0	0	0	0
6	B	45	0	0	1	0
6	C	40	0	0	0	0
6	D	43	0	0	0	0
6	E	42	0	0	0	0
All	All	11939	0	12236	98	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (98) 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:C:74:LEU:HD21	1:C:108:TYR:HB3	1.63	0.79
1:A:41:ALA:HB1	1:B:66:VAL:HG13	1.80	0.64
4:C:303:OLC:H16A	4:E:318:OLC:H14	1.87	0.55
1:B:41:ALA:HB1	1:C:66:VAL:HG13	1.89	0.55
1:B:88:PHE:CZ	1:B:93:GLY:HA2	2.42	0.54
1:C:41:ALA:HB1	1:D:66:VAL:HG13	1.90	0.54
4:D:308:OLC:H18A	4:E:304:OLC:H8A	1.88	0.54
4:D:308:OLC:H8	1:E:114:LEU:HD13	1.89	0.54
1:E:88:PHE:CZ	1:E:93:GLY:HA2	2.43	0.53
1:A:169:VAL:HG11	4:A:308:OLC:H3	1.91	0.53
4:D:308:OLC:H18	4:E:305:OLC:H3A	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:33:THR:HA	1:C:36:TYR:CE2	2.44	0.53
1:C:264:ASN:O	1:C:268:THR:HG23	2.10	0.51
1:E:33:THR:HA	1:E:36:TYR:CE2	2.46	0.51
1:C:111:LEU:O	1:C:114:LEU:HB2	2.10	0.51
1:E:74:LEU:HD21	1:E:108:TYR:HB3	1.92	0.51
1:A:33:THR:HA	1:A:36:TYR:CE2	2.47	0.50
1:E:111:LEU:O	1:E:114:LEU:HB2	2.11	0.50
1:D:74:LEU:HD21	1:D:108:TYR:HB3	1.92	0.50
1:C:88:PHE:CZ	1:C:93:GLY:HA2	2.47	0.49
1:E:229:GLY:HA3	5:E:316:LFA:H181	1.94	0.49
1:A:144:PHE:HA	4:A:305:OLC:H11	1.95	0.49
1:C:219:PRO:HD3	2:C:301:RET:H7	1.95	0.48
1:C:90:GLU:CD	1:D:99:PRO:HG2	2.38	0.48
1:A:28:THR:HG23	1:A:244:GLN:HG3	1.95	0.48
1:A:66:VAL:HG13	1:E:41:ALA:HB1	1.95	0.48
1:D:33:THR:HA	1:D:36:TYR:CE2	2.49	0.48
1:A:109:ARG:NH1	1:A:251:ASP:OD2	2.38	0.47
1:A:74:LEU:HD21	1:A:108:TYR:HB3	1.97	0.47
1:B:264:ASN:O	1:B:268:THR:HG23	2.14	0.47
1:D:163:ASN:HD22	4:D:306:OLC:H22	1.80	0.47
4:C:312:OLC:H2	4:C:312:OLC:H21	1.70	0.47
1:C:145:SER:OG	1:C:180:HIS:ND1	2.43	0.47
1:A:264:ASN:O	1:A:268:THR:HG23	2.15	0.46
1:B:74:LEU:HD21	1:B:108:TYR:HB3	1.97	0.46
5:B:307:LFA:H203	5:B:307:LFA:H172	1.81	0.46
1:A:111:LEU:O	1:A:114:LEU:HB2	2.16	0.46
1:D:88:PHE:CZ	1:D:93:GLY:HA2	2.51	0.46
4:B:312:OLC:H10	1:C:114:LEU:HD22	1.96	0.45
1:D:133:SER:OG	1:D:191:GLU:OE2	2.28	0.45
1:D:219:PRO:HB3	2:D:301:RET:H42	1.99	0.45
4:A:306:OLC:H2A	4:A:306:OLC:H21A	1.69	0.45
4:C:304:OLC:H2	4:C:304:OLC:H21	1.59	0.45
4:C:303:OLC:H11A	4:C:316:OLC:H14A	1.99	0.45
4:B:311:OLC:H7	4:B:311:OLC:H4A	1.62	0.45
1:B:139:ARG:NH2	4:B:303:OLC:O23	2.50	0.45
4:A:306:OLC:H2	1:B:122:PHE:HE2	1.82	0.45
1:D:35:GLY:O	1:D:39:MET:HG2	2.17	0.44
1:E:264:ASN:O	1:E:268:THR:HG23	2.17	0.44
1:C:256:VAL:HG11	4:C:304:OLC:H9	1.99	0.44
1:B:33:THR:HA	1:B:36:TYR:CE2	2.52	0.44
1:D:28:THR:HG23	1:D:244:GLN:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:304:OLC:H5A	4:A:304:OLC:H8	1.80	0.44
1:C:25:TYR:OH	1:D:102:ASP:OD2	2.32	0.44
1:D:264:ASN:O	1:D:268:THR:HG23	2.17	0.43
1:D:110:TYR:HA	1:D:113:TRP:CE3	2.52	0.43
1:D:169:VAL:HG11	4:D:305:OLC:H2	2.00	0.43
1:C:219:PRO:HB3	2:C:301:RET:H42	2.00	0.43
4:C:316:OLC:H18A	4:C:316:OLC:H15	1.79	0.43
1:E:118:PRO:HB3	1:E:143:TRP:CD1	2.54	0.43
4:E:304:OLC:H12	4:E:304:OLC:H15A	1.50	0.43
1:E:28:THR:O	1:E:31:ILE:HG22	2.19	0.43
4:C:312:OLC:H3	4:C:312:OLC:H6A	1.70	0.43
4:C:303:OLC:H10	4:E:318:OLC:H6A	2.00	0.43
1:A:73:LEU:HD11	1:E:40:LEU:HD23	2.00	0.43
1:E:234:LEU:O	1:E:239:GLY:HA3	2.19	0.42
1:A:91:GLU:H	1:A:91:GLU:HG2	1.45	0.42
1:C:120:LEU:O	1:C:123:GLN:HG2	2.19	0.42
1:E:145:SER:HB3	1:E:181:ILE:HG13	2.01	0.42
1:E:74:LEU:HD22	1:E:74:LEU:HA	1.78	0.42
1:B:234:LEU:O	1:B:239:GLY:HA3	2.19	0.42
1:D:44:LEU:HD13	4:E:318:OLC:H4A	2.02	0.42
1:E:252:VAL:HG11	4:E:319:OLC:H15	2.02	0.42
1:E:35:GLY:O	1:E:39:MET:HG2	2.20	0.42
1:E:92:VAL:HG21	1:E:96:PHE:HE2	1.84	0.42
4:C:304:OLC:H2A	4:C:304:OLC:H5A	1.80	0.41
2:E:301:RET:H161	2:E:301:RET:H8	2.02	0.41
1:D:68:MET:HE1	1:D:255:LYS:HB3	2.02	0.41
4:B:311:OLC:H10	4:B:312:OLC:H5A	2.03	0.41
4:A:311:OLC:H8	4:A:311:OLC:H5A	1.65	0.41
1:B:219:PRO:HB3	2:B:301:RET:H42	2.03	0.41
1:C:28:THR:HG23	1:C:244:GLN:HG3	2.01	0.41
1:E:204:LEU:HD23	1:E:204:LEU:HA	1.87	0.41
1:B:28:THR:O	1:B:31:ILE:HG22	2.21	0.41
1:A:110:TYR:HA	1:A:113:TRP:CE3	2.56	0.41
1:D:216:THR:HG21	5:D:312:LFA:H151	2.03	0.41
4:E:318:OLC:H3	4:E:318:OLC:H6	1.62	0.41
1:A:31:ILE:HD12	1:A:31:ILE:HA	1.96	0.41
1:E:92:VAL:HG21	1:E:96:PHE:CE2	2.56	0.41
1:B:90:GLU:HG2	1:C:99:PRO:HG3	2.03	0.41
1:E:203:ILE:O	1:E:207:ILE:HG13	2.22	0.41
1:B:94:ARG:NH1	6:B:404:HOH:O	2.43	0.40
1:C:28:THR:O	1:C:31:ILE:HG22	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:ILE:HD11	1:B:7:ASN:HD22	1.85	0.40
1:E:40:LEU:HD12	1:E:40:LEU:HA	1.95	0.40
1:E:184:VAL:O	1:E:188:VAL:HG23	2.21	0.40
1:E:224:MET:HE1	5:E:312:LFA:H171	2.02	0.40
4:B:315:OLC:H5A	4:B:315:OLC:H21A	2.04	0.40

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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	267/273 (98%)	260 (97%)	7 (3%)	0	100	100
1	B	267/273 (98%)	261 (98%)	6 (2%)	0	100	100
1	C	266/273 (97%)	258 (97%)	8 (3%)	0	100	100
1	D	266/273 (97%)	259 (97%)	7 (3%)	0	100	100
1	E	266/273 (97%)	259 (97%)	7 (3%)	0	100	100
All	All	1332/1365 (98%)	1297 (97%)	35 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	224/234 (96%)	222 (99%)	2 (1%)	70	85
1	B	225/234 (96%)	225 (100%)	0	100	100
1	C	224/234 (96%)	223 (100%)	1 (0%)	84	90
1	D	223/234 (95%)	223 (100%)	0	100	100
1	E	225/234 (96%)	223 (99%)	2 (1%)	70	85
All	All	1121/1170 (96%)	1116 (100%)	5 (0%)	84	90

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	90	GLU
1	A	91	GLU
1	C	74	LEU
1	E	74	LEU
1	E	90	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	GLN
1	A	141	GLN
1	B	123	GLN
1	C	123	GLN
1	C	141	GLN
1	D	123	GLN
1	E	7	ASN
1	E	112	ASN
1	E	141	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 85 ligands modelled in this entry, 5 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	$\# Z > 2$
4	OLC	E	305	-	7,7,24	0.91	0	6,6,25	0.72	0
4	OLC	B	312	-	18,18,24	0.87	0	18,18,25	1.22	1 (5%)
4	OLC	C	304	-	21,21,24	0.86	0	21,21,25	1.17	1 (4%)
5	LFA	B	309	-	9,9,19	0.31	0	8,8,18	0.79	0
5	LFA	D	313	-	5,5,19	0.32	0	4,4,18	0.63	0
4	OLC	A	319	-	18,18,24	0.87	0	17,17,25	1.28	1 (5%)
4	OLC	D	303	-	16,16,24	0.92	0	16,16,25	1.18	1 (6%)
5	LFA	C	310	-	4,4,19	0.33	0	3,3,18	0.58	0
2	RET	E	301	-	20,20,21	0.65	0	27,27,28	1.50	7 (25%)
4	OLC	D	308	-	23,23,24	0.85	0	23,23,25	1.15	1 (4%)
4	OLC	A	307	-	22,22,24	0.82	0	21,21,25	1.25	1 (4%)
4	OLC	D	304	-	17,17,24	0.88	0	16,16,25	1.28	1 (6%)
5	LFA	B	307	-	8,8,19	0.31	0	7,7,18	0.74	0
5	LFA	E	311	-	7,7,19	0.31	0	6,6,18	0.75	0
5	LFA	E	312	-	13,13,19	0.30	0	12,12,18	0.83	0
5	LFA	A	314	-	7,7,19	0.31	0	6,6,18	0.74	0
5	LFA	C	313	-	5,5,19	0.32	0	4,4,18	0.61	0
5	LFA	D	314	-	6,6,19	0.31	0	5,5,18	0.67	0
5	LFA	A	317	-	5,5,19	0.32	0	4,4,18	0.62	0
4	OLC	A	305	-	8,8,24	0.95	0	7,7,25	1.86	1 (14%)
4	OLC	E	304	-	17,17,24	0.89	0	16,16,25	1.25	1 (6%)
4	OLC	E	308	-	13,13,24	0.82	0	13,13,25	0.78	0
4	OLC	B	303	-	19,19,24	0.88	0	19,19,25	1.21	1 (5%)
4	OLC	A	306	-	18,18,24	0.85	0	17,17,25	1.28	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	LFA	B	314	-	10,10,19	0.30	0	9,9,18	0.81	0
2	RET	D	301	1	20,20,21	0.65	0	27,27,28	1.41	6 (22%)
4	OLC	C	303	-	21,21,24	0.82	0	20,20,25	1.33	2 (10%)
4	OLC	E	318	-	21,21,24	0.82	0	20,20,25	1.25	1 (5%)
4	OLC	A	309	-	19,19,24	0.86	0	18,18,25	1.38	2 (11%)
4	OLC	E	319	-	17,17,24	0.88	0	16,16,25	1.32	1 (6%)
4	OLC	C	305	-	20,20,24	0.87	0	20,20,25	1.16	1 (5%)
4	OLC	A	310	-	13,13,24	0.81	0	13,13,25	0.79	0
4	OLC	C	306	-	15,15,24	0.94	0	15,15,25	1.21	1 (6%)
4	OLC	C	316	-	22,22,24	0.82	0	21,21,25	1.27	1 (4%)
5	LFA	A	320	-	8,8,19	0.30	0	7,7,18	0.80	0
5	LFA	E	317	-	9,9,19	0.31	0	8,8,18	0.75	0
2	RET	C	301	1	20,20,21	0.66	0	27,27,28	1.43	7 (25%)
5	LFA	D	309	-	19,19,19	0.28	0	18,18,18	0.91	0
5	LFA	C	309	-	19,19,19	0.29	0	18,18,18	0.88	0
5	LFA	D	310	-	19,19,19	0.29	0	18,18,18	0.92	0
5	LFA	E	313	-	3,3,19	0.40	0	2,2,18	0.74	0
4	OLC	B	306	-	12,12,24	0.83	0	11,11,25	0.94	0
4	OLC	A	312	-	14,14,24	0.85	0	14,14,25	0.79	0
5	LFA	E	315	-	6,6,19	0.31	0	5,5,18	0.70	0
5	LFA	D	311	-	16,16,19	0.29	0	15,15,18	0.88	0
4	OLC	C	307	-	5,5,24	0.91	0	4,4,25	0.58	0
5	LFA	E	314	-	4,4,19	0.33	0	3,3,18	0.58	0
4	OLC	B	315	-	16,16,24	0.87	0	15,15,25	1.48	3 (20%)
4	OLC	B	305	-	13,13,24	0.93	0	12,12,25	1.36	1 (8%)
5	LFA	A	315	-	7,7,19	0.31	0	6,6,18	0.73	0
4	OLC	E	307	-	18,18,24	0.86	0	18,18,25	1.21	1 (5%)
5	LFA	E	303	-	9,9,19	0.30	0	8,8,18	0.81	0
4	OLC	A	303	-	15,15,24	0.89	0	14,14,25	1.36	2 (14%)
5	LFA	A	318	-	15,15,19	0.30	0	14,14,18	0.87	0
4	OLC	A	321	-	21,21,24	0.83	0	20,20,25	1.28	2 (10%)
4	OLC	A	308	-	11,11,24	0.78	0	11,11,25	0.75	0
5	LFA	D	312	-	6,6,19	0.31	0	5,5,18	0.71	0
4	OLC	E	310	-	18,18,24	0.85	0	17,17,25	1.34	1 (5%)
5	LFA	A	316	-	3,3,19	0.40	0	2,2,18	0.75	0
2	RET	B	301	1	20,20,21	0.66	0	27,27,28	1.43	6 (22%)
5	LFA	C	311	-	3,3,19	0.40	0	2,2,18	0.75	0
4	OLC	D	305	-	15,15,24	0.90	0	14,14,25	1.29	1 (7%)
4	OLC	B	311	-	19,19,24	0.87	0	19,19,25	1.19	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	LFA	C	308	-	7,7,19	0.31	0	6,6,18	0.73	0
2	RET	A	301	1	20,20,21	0.63	0	27,27,28	1.44	6 (22%)
4	OLC	D	306	-	12,12,24	0.79	0	12,12,25	0.78	0
4	OLC	E	306	-	15,15,24	0.90	0	14,14,25	1.31	1 (7%)
5	LFA	A	313	-	6,6,19	0.32	0	5,5,18	0.68	0
4	OLC	A	311	-	6,6,24	0.93	0	5,5,25	0.65	0
4	OLC	C	315	-	14,14,24	0.85	0	14,14,25	0.81	0
5	LFA	B	308	-	7,7,19	0.32	0	6,6,18	0.74	0
4	OLC	D	307	-	6,6,24	0.89	0	5,5,25	0.67	0
4	OLC	A	304	-	22,22,24	0.82	0	21,21,25	1.26	2 (9%)
5	LFA	B	313	-	10,10,19	0.31	0	9,9,18	0.78	0
5	LFA	C	314	-	4,4,19	0.33	0	3,3,18	0.59	0
4	OLC	E	309	-	5,5,24	0.89	0	4,4,25	0.57	0
4	OLC	B	304	-	12,12,24	0.93	0	11,11,25	1.40	1 (9%)
4	OLC	C	312	-	15,15,24	0.90	0	14,14,25	1.34	2 (14%)
5	LFA	E	316	-	5,5,19	0.32	0	4,4,18	0.61	0
5	LFA	B	310	-	6,6,19	0.31	0	5,5,18	0.71	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
4	OLC	E	305	-	-	4/5/5/24	-
4	OLC	B	312	-	-	10/17/17/24	-
4	OLC	C	304	-	-	15/20/20/24	-
5	LFA	B	309	-	-	3/7/7/17	-
5	LFA	D	313	-	-	0/3/3/17	-
4	OLC	A	319	-	-	11/16/16/24	-
4	OLC	D	303	-	-	3/15/15/24	-
5	LFA	C	310	-	-	2/2/2/17	-
2	RET	E	301	-	-	1/13/30/31	0/1/1/1
4	OLC	D	308	-	-	7/22/22/24	-
4	OLC	A	307	-	-	14/20/20/24	-
4	OLC	D	304	-	-	6/15/15/24	-
5	LFA	B	307	-	-	3/6/6/17	-
5	LFA	E	311	-	-	1/5/5/17	-
5	LFA	E	312	-	-	2/11/11/17	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	LFA	A	314	-	-	4/5/5/17	-
5	LFA	C	313	-	-	0/3/3/17	-
5	LFA	D	314	-	-	2/4/4/17	-
5	LFA	A	317	-	-	1/3/3/17	-
4	OLC	A	305	-	-	3/6/6/24	-
4	OLC	E	304	-	-	9/15/15/24	-
4	OLC	E	308	-	-	9/12/12/24	-
4	OLC	B	303	-	-	13/18/18/24	-
4	OLC	A	306	-	-	12/16/16/24	-
5	LFA	B	314	-	-	4/8/8/17	-
2	RET	D	301	1	-	4/13/30/31	0/1/1/1
4	OLC	C	303	-	-	8/19/19/24	-
4	OLC	E	318	-	-	9/19/19/24	-
4	OLC	A	309	-	-	8/17/17/24	-
4	OLC	E	319	-	-	8/15/15/24	-
4	OLC	C	305	-	-	11/19/19/24	-
4	OLC	A	310	-	-	5/12/12/24	-
4	OLC	C	306	-	-	9/14/14/24	-
4	OLC	C	316	-	-	9/20/20/24	-
5	LFA	A	320	-	-	0/6/6/17	-
5	LFA	E	317	-	-	1/7/7/17	-
2	RET	C	301	1	-	4/13/30/31	0/1/1/1
5	LFA	D	309	-	-	9/17/17/17	-
5	LFA	C	309	-	-	7/17/17/17	-
5	LFA	D	310	-	-	4/17/17/17	-
5	LFA	E	313	-	-	1/1/1/17	-
4	OLC	B	306	-	-	7/10/10/24	-
4	OLC	A	312	-	-	8/13/13/24	-
5	LFA	E	315	-	-	1/4/4/17	-
5	LFA	D	311	-	-	7/14/14/17	-
4	OLC	C	307	-	-	1/3/3/24	-
5	LFA	E	314	-	-	0/2/2/17	-
4	OLC	B	315	-	-	7/14/14/24	-
4	OLC	B	305	-	-	3/11/11/24	-
5	LFA	A	315	-	-	0/5/5/17	-
4	OLC	E	307	-	-	10/17/17/24	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	LFA	E	303	-	-	3/7/7/17	-
4	OLC	A	303	-	-	8/13/13/24	-
5	LFA	A	318	-	-	3/13/13/17	-
4	OLC	A	321	-	-	12/19/19/24	-
4	OLC	A	308	-	-	3/10/10/24	-
5	LFA	D	312	-	-	0/4/4/17	-
4	OLC	E	310	-	-	7/16/16/24	-
5	LFA	A	316	-	-	0/1/1/17	-
2	RET	B	301	1	-	4/13/30/31	0/1/1/1
5	LFA	C	311	-	-	1/1/1/17	-
4	OLC	D	305	-	-	6/13/13/24	-
4	OLC	B	311	-	-	8/18/18/24	-
5	LFA	C	308	-	-	2/5/5/17	-
2	RET	A	301	1	-	4/13/30/31	0/1/1/1
4	OLC	D	306	-	-	7/11/11/24	-
4	OLC	E	306	-	-	6/13/13/24	-
5	LFA	A	313	-	-	2/4/4/17	-
4	OLC	A	311	-	-	3/4/4/24	-
4	OLC	C	315	-	-	7/13/13/24	-
5	LFA	B	308	-	-	2/5/5/17	-
4	OLC	D	307	-	-	2/4/4/24	-
4	OLC	A	304	-	-	10/20/20/24	-
5	LFA	B	313	-	-	6/8/8/17	-
5	LFA	C	314	-	-	0/2/2/17	-
4	OLC	E	309	-	-	1/3/3/24	-
4	OLC	B	304	-	-	4/10/10/24	-
4	OLC	C	312	-	-	8/13/13/24	-
5	LFA	E	316	-	-	2/3/3/17	-
5	LFA	B	310	-	-	1/4/4/17	-

There are no bond length outliers.

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	305	OLC	C8-C9-C10	4.34	152.54	126.42
4	B	303	OLC	C8-C9-C10	3.85	153.65	124.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	319	OLC	C8-C9-C10	3.82	153.45	124.83
4	C	303	OLC	C8-C9-C10	3.76	153.01	124.83
4	E	319	OLC	C8-C9-C10	3.76	152.97	124.83
4	E	310	OLC	C8-C9-C10	3.75	152.90	124.83
4	A	306	OLC	C8-C9-C10	3.74	152.85	124.83
4	B	312	OLC	C8-C9-C10	3.73	152.79	124.83
4	E	307	OLC	C8-C9-C10	3.73	152.78	124.83
4	D	304	OLC	C8-C9-C10	3.73	152.75	124.83
4	B	304	OLC	C8-C9-C10	3.73	152.74	124.83
4	A	309	OLC	C8-C9-C10	3.72	152.69	124.83
4	C	304	OLC	C8-C9-C10	3.70	152.58	124.83
4	B	311	OLC	C8-C9-C10	3.70	152.52	124.83
4	A	321	OLC	C8-C9-C10	3.69	152.50	124.83
4	E	304	OLC	C8-C9-C10	3.69	152.50	124.83
4	C	316	OLC	C8-C9-C10	3.69	152.45	124.83
4	E	306	OLC	C8-C9-C10	3.69	152.44	124.83
4	A	307	OLC	C8-C9-C10	3.69	152.44	124.83
4	A	304	OLC	C8-C9-C10	3.68	152.44	124.83
4	B	315	OLC	C8-C9-C10	3.67	152.30	124.83
4	E	318	OLC	C8-C9-C10	3.65	152.19	124.83
4	D	308	OLC	C8-C9-C10	3.64	152.07	124.83
4	C	305	OLC	C8-C9-C10	3.63	152.06	124.83
4	B	305	OLC	C8-C9-C10	3.63	152.01	124.83
4	C	306	OLC	C8-C9-C10	3.56	152.61	126.65
2	A	301	RET	C16-C1-C6	3.34	115.48	110.24
2	E	301	RET	C16-C1-C6	3.33	115.46	110.24
2	B	301	RET	C16-C1-C6	3.21	115.27	110.24
2	D	301	RET	C16-C1-C6	3.16	115.20	110.24
2	C	301	RET	C16-C1-C6	3.16	115.20	110.24
2	E	301	RET	C1-C6-C5	-2.99	118.55	122.64
4	A	303	OLC	C8-C9-C10	2.99	153.13	130.48
4	D	305	OLC	C8-C9-C10	2.96	152.91	130.48
4	D	303	OLC	C8-C9-C10	2.92	152.62	130.48
4	C	312	OLC	C8-C9-C10	2.88	152.30	130.48
2	C	301	RET	C1-C6-C5	-2.85	118.74	122.64
2	D	301	RET	C1-C6-C5	-2.83	118.77	122.64
4	A	309	OLC	O20-C1-C2	2.76	120.61	109.79
2	B	301	RET	C1-C6-C5	-2.73	118.90	122.64
2	A	301	RET	C1-C6-C5	-2.68	118.97	122.64
2	E	301	RET	C18-C5-C4	-2.49	108.30	113.60
2	B	301	RET	C18-C5-C4	-2.45	108.38	113.60
2	A	301	RET	C18-C5-C4	-2.45	108.38	113.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301	RET	C16-C1-C2	-2.42	99.65	108.95
2	B	301	RET	C1-C6-C7	2.42	122.20	115.65
2	A	301	RET	C1-C6-C7	2.41	122.20	115.65
2	E	301	RET	C1-C6-C7	2.39	122.13	115.65
2	C	301	RET	C16-C1-C2	-2.36	99.89	108.95
2	C	301	RET	C1-C6-C7	2.36	122.05	115.65
2	B	301	RET	C16-C1-C2	-2.36	99.90	108.95
2	A	301	RET	C16-C1-C2	-2.36	99.90	108.95
2	D	301	RET	C18-C5-C4	-2.35	108.59	113.60
2	D	301	RET	C16-C1-C2	-2.31	100.08	108.95
4	B	315	OLC	C11-C10-C9	-2.31	112.52	126.42
2	D	301	RET	C1-C6-C7	2.24	121.73	115.65
4	C	312	OLC	C21-C22-C24	-2.17	109.27	113.55
4	C	303	OLC	C21-C22-C24	-2.12	109.36	113.55
2	C	301	RET	C18-C5-C4	-2.12	109.07	113.60
2	B	301	RET	C7-C6-C5	-2.08	116.77	121.56
2	C	301	RET	C4-C5-C6	2.08	125.51	122.70
2	D	301	RET	C7-C6-C5	-2.07	116.80	121.56
4	B	315	OLC	C21-C22-C24	-2.06	109.47	113.55
2	C	301	RET	C7-C6-C5	-2.05	116.83	121.56
2	E	301	RET	C7-C6-C5	-2.05	116.83	121.56
4	A	303	OLC	C21-C22-C24	-2.04	109.52	113.55
2	A	301	RET	C7-C6-C5	-2.03	116.87	121.56
4	A	304	OLC	C21-C22-C24	-2.03	109.55	113.55
4	A	321	OLC	C21-C22-C24	-2.01	109.58	113.55
2	E	301	RET	C4-C5-C6	2.00	125.41	122.70

There are no chirality outliers.

All (402) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	303	OLC	C21-C22-C24-O25
4	A	304	OLC	C21-C22-C24-O25
4	A	309	OLC	C2-C1-O20-C21
4	A	312	OLC	C21-C22-C24-O25
4	B	312	OLC	O20-C21-C22-C24
4	C	304	OLC	O20-C21-C22-C24
4	C	304	OLC	O20-C21-C22-O23
4	C	306	OLC	C21-C22-C24-O25
4	C	306	OLC	O20-C21-C22-C24
4	C	306	OLC	O20-C21-C22-O23
4	C	312	OLC	C21-C22-C24-O25

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Mol	Chain	Res	Type	Atoms
4	C	315	OLC	O20-C21-C22-O23
4	C	316	OLC	C21-C22-C24-O25
4	D	305	OLC	C21-C22-C24-O25
4	E	307	OLC	C10-C11-C12-C13
4	E	307	OLC	C21-C22-C24-O25
4	E	308	OLC	O20-C21-C22-O23
5	E	313	LFA	C17-C18-C19-C20
4	B	312	OLC	O20-C21-C22-O23
4	B	306	OLC	C2-C1-O20-C21
4	C	304	OLC	C2-C1-O20-C21
4	D	303	OLC	C2-C1-O20-C21
4	A	307	OLC	O20-C21-C22-C24
4	E	318	OLC	C3-C4-C5-C6
4	A	306	OLC	C2-C1-O20-C21
4	C	312	OLC	C2-C1-O20-C21
4	A	307	OLC	C1-C2-C3-C4
4	E	307	OLC	O20-C21-C22-C24
4	E	304	OLC	C12-C13-C14-C15
4	A	303	OLC	O20-C1-C2-C3
4	E	308	OLC	O23-C22-C24-O25
4	C	304	OLC	C10-C11-C12-C13
4	C	316	OLC	C3-C4-C5-C6
4	A	309	OLC	O20-C1-C2-C3
4	A	306	OLC	O20-C1-C2-C3
4	E	307	OLC	C2-C1-O20-C21
4	A	319	OLC	C5-C6-C7-C8
4	B	303	OLC	O20-C1-C2-C3
4	A	307	OLC	C6-C7-C8-C9
4	A	312	OLC	O20-C21-C22-O23
4	E	307	OLC	O20-C21-C22-O23
4	A	312	OLC	O20-C1-C2-C3
4	B	312	OLC	O20-C1-C2-C3
4	D	306	OLC	O20-C1-C2-C3
4	C	304	OLC	O20-C1-C2-C3
4	A	306	OLC	O20-C21-C22-C24
4	A	304	OLC	O20-C1-C2-C3
4	A	307	OLC	O20-C1-C2-C3
4	A	308	OLC	O20-C1-C2-C3
4	A	312	OLC	O20-C21-C22-C24
4	C	315	OLC	O20-C21-C22-C24
4	E	318	OLC	O20-C21-C22-C24
4	B	312	OLC	C10-C11-C12-C13

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Mol	Chain	Res	Type	Atoms
4	A	310	OLC	C21-C22-C24-O25
4	C	304	OLC	C21-C22-C24-O25
4	D	306	OLC	C21-C22-C24-O25
4	E	308	OLC	C21-C22-C24-O25
4	B	306	OLC	O20-C21-C22-O23
4	E	318	OLC	C1-C2-C3-C4
4	C	312	OLC	C3-C4-C5-C6
4	C	303	OLC	O20-C1-C2-C3
4	A	311	OLC	C5-C6-C7-C8
5	D	309	LFA	C16-C17-C18-C19
4	A	321	OLC	C1-C2-C3-C4
4	D	305	OLC	C1-C2-C3-C4
4	E	304	OLC	C3-C4-C5-C6
4	E	319	OLC	C5-C6-C7-C8
5	A	318	LFA	C11-C12-C13-C14
4	D	304	OLC	C3-C4-C5-C6
4	A	310	OLC	O23-C22-C24-O25
4	C	304	OLC	O23-C22-C24-O25
4	C	306	OLC	O23-C22-C24-O25
4	D	306	OLC	O23-C22-C24-O25
4	A	319	OLC	C2-C3-C4-C5
4	E	319	OLC	C13-C14-C15-C16
5	D	310	LFA	C4-C5-C6-C7
4	E	310	OLC	O20-C1-C2-C3
4	C	305	OLC	C5-C6-C7-C8
4	A	306	OLC	C3-C4-C5-C6
5	B	313	LFA	C3-C4-C5-C6
4	A	304	OLC	C2-C3-C4-C5
4	B	304	OLC	C2-C3-C4-C5
4	A	321	OLC	C2-C3-C4-C5
4	C	305	OLC	C4-C5-C6-C7
4	D	306	OLC	C1-C2-C3-C4
4	E	319	OLC	C2-C3-C4-C5
4	B	304	OLC	C3-C4-C5-C6
5	B	307	LFA	C14-C15-C16-C17
4	C	303	OLC	C3-C4-C5-C6
4	B	303	OLC	C2-C3-C4-C5
4	C	305	OLC	C2-C3-C4-C5
4	A	304	OLC	C1-C2-C3-C4
4	A	306	OLC	C1-C2-C3-C4
4	C	316	OLC	C12-C13-C14-C15
4	E	304	OLC	C14-C15-C16-C17

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Mol	Chain	Res	Type	Atoms
5	C	309	LFA	C6-C7-C8-C9
5	E	317	LFA	C14-C15-C16-C17
4	C	303	OLC	C2-C3-C4-C5
5	B	314	LFA	C7-C8-C9-C10
5	D	311	LFA	C6-C7-C8-C9
4	C	304	OLC	C3-C4-C5-C6
4	C	315	OLC	C5-C6-C7-C8
4	D	306	OLC	C2-C3-C4-C5
2	A	301	RET	C1-C6-C7-C8
2	B	301	RET	C1-C6-C7-C8
2	C	301	RET	C1-C6-C7-C8
2	D	301	RET	C1-C6-C7-C8
2	E	301	RET	C1-C6-C7-C8
4	E	306	OLC	C6-C7-C8-C9
4	C	306	OLC	C5-C6-C7-C8
5	B	314	LFA	C3-C4-C5-C6
4	C	306	OLC	C3-C4-C5-C6
5	E	311	LFA	C16-C17-C18-C19
5	D	309	LFA	C7-C8-C9-C10
5	D	311	LFA	C5-C6-C7-C8
4	E	308	OLC	O20-C21-C22-C24
4	E	318	OLC	C11-C12-C13-C14
4	A	321	OLC	O20-C1-C2-C3
4	E	307	OLC	C2-C3-C4-C5
4	C	315	OLC	C3-C4-C5-C6
5	B	313	LFA	C6-C7-C8-C9
4	B	315	OLC	C9-C10-C11-C12
4	C	305	OLC	O20-C1-C2-C3
5	C	308	LFA	C15-C16-C17-C18
4	B	311	OLC	C6-C7-C8-C9
4	B	312	OLC	C6-C7-C8-C9
4	C	303	OLC	C6-C7-C8-C9
4	E	304	OLC	C10-C11-C12-C13
4	B	315	OLC	C3-C4-C5-C6
5	B	309	LFA	C5-C6-C7-C8
4	D	306	OLC	C3-C4-C5-C6
4	C	303	OLC	C4-C5-C6-C7
4	A	312	OLC	C3-C4-C5-C6
4	E	304	OLC	C13-C14-C15-C16
4	A	303	OLC	C3-C4-C5-C6
4	B	303	OLC	C6-C7-C8-C9
4	B	311	OLC	C10-C11-C12-C13

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Mol	Chain	Res	Type	Atoms
4	C	305	OLC	C6-C7-C8-C9
4	D	303	OLC	C6-C7-C8-C9
4	E	318	OLC	C6-C7-C8-C9
4	C	307	OLC	C6-C7-C8-C9
4	A	309	OLC	C5-C6-C7-C8
4	E	306	OLC	C12-C13-C14-C15
4	A	304	OLC	C7-C8-C9-C10
4	A	304	OLC	C3-C4-C5-C6
4	D	305	OLC	C5-C6-C7-C8
5	D	311	LFA	C7-C8-C9-C10
4	B	315	OLC	C4-C5-C6-C7
4	A	309	OLC	C12-C13-C14-C15
4	E	305	OLC	C5-C6-C7-C8
4	D	305	OLC	C4-C5-C6-C7
4	E	309	OLC	C5-C6-C7-C8
4	A	321	OLC	C3-C4-C5-C6
4	B	306	OLC	C3-C4-C5-C6
4	A	312	OLC	O23-C22-C24-O25
4	E	307	OLC	O23-C22-C24-O25
5	E	303	LFA	C6-C7-C8-C9
4	A	306	OLC	C6-C7-C8-C9
4	E	319	OLC	C6-C7-C8-C9
4	B	303	OLC	C3-C4-C5-C6
4	E	306	OLC	C3-C4-C5-C6
4	B	315	OLC	C1-C2-C3-C4
4	E	306	OLC	C5-C6-C7-C8
4	B	311	OLC	C22-C21-O20-C1
4	E	319	OLC	C12-C13-C14-C15
5	B	313	LFA	C4-C5-C6-C7
4	A	321	OLC	C13-C14-C15-C16
4	A	304	OLC	C13-C14-C15-C16
4	B	306	OLC	C2-C3-C4-C5
5	D	314	LFA	C15-C16-C17-C18
4	C	304	OLC	C12-C13-C14-C15
4	A	319	OLC	C10-C11-C12-C13
4	B	305	OLC	C6-C7-C8-C9
4	C	316	OLC	C10-C11-C12-C13
4	D	305	OLC	C6-C7-C8-C9
4	E	318	OLC	C10-C11-C12-C13
4	E	319	OLC	C10-C11-C12-C13
4	A	307	OLC	C21-C22-C24-O25
4	B	312	OLC	C3-C4-C5-C6

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Mol	Chain	Res	Type	Atoms
4	D	308	OLC	C11-C12-C13-C14
4	A	319	OLC	C12-C13-C14-C15
2	C	301	RET	C7-C8-C9-C19
4	C	312	OLC	O20-C1-C2-C3
4	A	309	OLC	C2-C3-C4-C5
4	A	319	OLC	C4-C5-C6-C7
4	B	303	OLC	O20-C21-C22-O23
5	B	314	LFA	C11-C10-C9-C8
4	A	304	OLC	C10-C11-C12-C13
4	A	307	OLC	C11-C12-C13-C14
4	D	308	OLC	C4-C5-C6-C7
5	C	309	LFA	C13-C14-C15-C16
4	D	304	OLC	C5-C6-C7-C8
5	B	313	LFA	C5-C6-C7-C8
4	A	307	OLC	C5-C6-C7-C8
5	A	313	LFA	C17-C18-C19-C20
5	D	309	LFA	C3-C4-C5-C6
4	E	310	OLC	C2-C3-C4-C5
4	A	306	OLC	C2-C3-C4-C5
5	D	311	LFA	C3-C4-C5-C6
4	C	315	OLC	C6-C7-C8-C9
5	B	308	LFA	C1-C2-C3-C4
4	B	303	OLC	C1-C2-C3-C4
4	A	311	OLC	C6-C7-C8-C9
4	B	303	OLC	C11-C12-C13-C14
5	D	311	LFA	C1-C2-C3-C4
4	C	312	OLC	C1-C2-C3-C4
4	B	303	OLC	C4-C5-C6-C7
4	A	310	OLC	C5-C6-C7-C8
4	B	304	OLC	C5-C6-C7-C8
4	A	307	OLC	C13-C14-C15-C16
4	D	303	OLC	C1-C2-C3-C4
4	C	304	OLC	C2-C3-C4-C5
4	B	303	OLC	O20-C21-C22-C24
4	B	306	OLC	O20-C1-C2-C3
4	D	304	OLC	C10-C11-C12-C13
5	D	309	LFA	C5-C6-C7-C8
4	B	312	OLC	C5-C6-C7-C8
4	C	305	OLC	C11-C12-C13-C14
4	A	307	OLC	C15-C16-C17-C18
4	A	308	OLC	C3-C4-C5-C6
4	E	305	OLC	C6-C7-C8-C9

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Mol	Chain	Res	Type	Atoms
5	A	314	LFA	C1-C2-C3-C4
4	B	311	OLC	C4-C5-C6-C7
4	A	303	OLC	C7-C8-C9-C10
4	C	305	OLC	C12-C13-C14-C15
4	A	319	OLC	O20-C1-C2-C3
2	D	301	RET	C7-C8-C9-C19
4	B	311	OLC	C5-C6-C7-C8
4	D	308	OLC	C2-C3-C4-C5
4	B	311	OLC	O20-C1-C2-C3
4	E	307	OLC	C4-C5-C6-C7
5	A	314	LFA	C5-C6-C7-C8
4	E	308	OLC	C1-C2-C3-C4
5	B	309	LFA	C7-C8-C9-C10
4	B	303	OLC	C10-C11-C12-C13
4	A	321	OLC	C12-C13-C14-C15
5	A	317	LFA	C2-C3-C4-C5
4	A	308	OLC	C2-C3-C4-C5
5	E	315	LFA	C15-C16-C17-C18
5	B	309	LFA	C1-C2-C3-C4
4	B	305	OLC	C2-C3-C4-C5
4	A	307	OLC	C2-C3-C4-C5
4	A	309	OLC	C7-C8-C9-C10
4	A	312	OLC	C6-C7-C8-C9
4	E	304	OLC	C5-C6-C7-C8
4	A	310	OLC	C2-C3-C4-C5
4	A	305	OLC	C7-C8-C9-C10
5	D	311	LFA	C14-C15-C16-C17
4	A	305	OLC	C11-C12-C13-C14
5	C	308	LFA	C16-C17-C18-C19
2	A	301	RET	C7-C8-C9-C19
4	A	309	OLC	C11-C12-C13-C14
4	B	315	OLC	C5-C6-C7-C8
4	C	304	OLC	C7-C8-C9-C10
5	E	316	LFA	C17-C18-C19-C20
4	D	304	OLC	C1-C2-C3-C4
4	A	303	OLC	O20-C21-C22-C24
4	C	305	OLC	C3-C4-C5-C6
4	B	312	OLC	C1-C2-C3-C4
4	B	312	OLC	C2-C3-C4-C5
4	E	308	OLC	C4-C5-C6-C7
4	C	315	OLC	O20-C1-C2-C3
4	A	306	OLC	C7-C8-C9-C10

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Mol	Chain	Res	Type	Atoms
4	C	303	OLC	C1-C2-C3-C4
4	A	307	OLC	C2-C1-O20-C21
4	D	308	OLC	C5-C6-C7-C8
4	C	306	OLC	C1-C2-C3-C4
5	E	303	LFA	C11-C10-C9-C8
4	E	310	OLC	C22-C21-O20-C1
2	B	301	RET	C7-C8-C9-C19
4	D	308	OLC	C3-C4-C5-C6
2	C	301	RET	C7-C8-C9-C10
4	A	309	OLC	C9-C10-C11-C12
5	A	314	LFA	C4-C5-C6-C7
4	C	312	OLC	C5-C6-C7-C8
4	B	303	OLC	C2-C1-O20-C21
4	C	316	OLC	C13-C14-C15-C16
5	A	318	LFA	C3-C4-C5-C6
5	B	313	LFA	C11-C10-C9-C8
5	C	309	LFA	C12-C13-C14-C15
4	D	304	OLC	C14-C15-C16-C17
5	D	310	LFA	C7-C8-C9-C10
5	C	311	LFA	C17-C18-C19-C20
4	A	303	OLC	C2-C3-C4-C5
5	D	309	LFA	C10-C11-C12-C13
5	C	310	LFA	C7-C8-C9-C10
4	A	304	OLC	C11-C12-C13-C14
4	D	308	OLC	C12-C13-C14-C15
4	E	318	OLC	C14-C15-C16-C17
4	E	304	OLC	C15-C16-C17-C18
5	D	309	LFA	C12-C13-C14-C15
5	E	312	LFA	C14-C15-C16-C17
4	D	307	OLC	C2-C3-C4-C5
4	A	307	OLC	C3-C4-C5-C6
4	A	321	OLC	C4-C5-C6-C7
5	B	313	LFA	C2-C3-C4-C5
5	D	314	LFA	C16-C17-C18-C19
4	E	306	OLC	C10-C11-C12-C13
4	E	305	OLC	C2-C3-C4-C5
4	C	316	OLC	C2-C1-O20-C21
4	D	305	OLC	C2-C1-O20-C21
4	A	306	OLC	C12-C13-C14-C15
4	C	304	OLC	C5-C6-C7-C8
4	A	303	OLC	C2-C1-O20-C21
4	B	315	OLC	C2-C1-O20-C21

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Mol	Chain	Res	Type	Atoms
5	B	307	LFA	C16-C17-C18-C19
4	B	306	OLC	C1-C2-C3-C4
4	B	304	OLC	C9-C10-C11-C12
4	E	308	OLC	O20-C1-C2-C3
4	B	311	OLC	C2-C3-C4-C5
4	A	311	OLC	C3-C4-C5-C6
5	A	318	LFA	C4-C5-C6-C7
4	A	319	OLC	C1-C2-C3-C4
4	A	312	OLC	C2-C1-O20-C21
5	C	309	LFA	C15-C16-C17-C18
4	C	306	OLC	C7-C8-C9-C10
4	E	319	OLC	O20-C1-C2-C3
4	D	308	OLC	O20-C1-C2-C3
4	C	305	OLC	C2-C1-O20-C21
4	E	318	OLC	C13-C14-C15-C16
4	E	307	OLC	C22-C21-O20-C1
4	A	307	OLC	C9-C10-C11-C12
2	A	301	RET	C7-C8-C9-C10
2	D	301	RET	C7-C8-C9-C10
5	D	309	LFA	C17-C18-C19-C20
5	D	309	LFA	C15-C16-C17-C18
4	C	304	OLC	C22-C21-O20-C1
4	A	321	OLC	C14-C15-C16-C17
5	C	309	LFA	C3-C4-C5-C6
4	A	319	OLC	C11-C12-C13-C14
5	E	303	LFA	C7-C8-C9-C10
5	A	313	LFA	C16-C17-C18-C19
4	D	307	OLC	C3-C4-C5-C6
2	B	301	RET	C7-C8-C9-C10
5	B	307	LFA	C12-C13-C14-C15
4	A	321	OLC	C5-C6-C7-C8
4	E	308	OLC	C3-C4-C5-C6
5	C	309	LFA	C14-C15-C16-C17
2	C	301	RET	C5-C6-C7-C8
4	B	312	OLC	C9-C10-C11-C12
4	C	304	OLC	C6-C7-C8-C9
4	E	318	OLC	C4-C5-C6-C7
4	C	305	OLC	O20-C21-C22-O23
4	A	319	OLC	C15-C16-C17-C18
5	A	314	LFA	C2-C3-C4-C5
4	A	321	OLC	C11-C12-C13-C14
5	D	310	LFA	C11-C12-C13-C14

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Mol	Chain	Res	Type	Atoms
4	E	310	OLC	C5-C6-C7-C8
4	A	304	OLC	C6-C7-C8-C9
4	B	306	OLC	C6-C7-C8-C9
4	A	306	OLC	C10-C11-C12-C13
4	A	321	OLC	C21-C22-C24-O25
4	B	303	OLC	C22-C21-O20-C1
4	A	307	OLC	C10-C11-C12-C13
5	E	316	LFA	C16-C17-C18-C19
4	C	306	OLC	C2-C1-O20-C21
4	C	315	OLC	C2-C1-O20-C21
4	E	308	OLC	C2-C1-O20-C21
4	A	319	OLC	C7-C8-C9-C10
4	B	305	OLC	C9-C10-C11-C12
4	B	315	OLC	C7-C8-C9-C10
4	E	306	OLC	C7-C8-C9-C10
4	E	305	OLC	C3-C4-C5-C6
4	C	305	OLC	C22-C21-O20-C1
4	C	316	OLC	C14-C15-C16-C17
4	D	304	OLC	C7-C8-C9-C10
4	E	310	OLC	C7-C8-C9-C10
4	A	321	OLC	C7-C8-C9-C10
4	B	303	OLC	C7-C8-C9-C10
4	C	316	OLC	C9-C10-C11-C12
4	E	310	OLC	C9-C10-C11-C12
4	E	310	OLC	C6-C7-C8-C9
4	A	319	OLC	C9-C10-C11-C12
4	A	310	OLC	C3-C4-C5-C6
5	D	311	LFA	C4-C5-C6-C7
4	E	307	OLC	C9-C10-C11-C12
5	B	310	LFA	C15-C16-C17-C18
4	D	306	OLC	C4-C5-C6-C7
2	A	301	RET	C5-C6-C7-C8
2	B	301	RET	C5-C6-C7-C8
2	D	301	RET	C5-C6-C7-C8
4	C	304	OLC	C9-C10-C11-C12
4	E	304	OLC	C7-C8-C9-C10
5	D	309	LFA	C11-C12-C13-C14
5	B	308	LFA	C2-C3-C4-C5
4	E	319	OLC	C14-C15-C16-C17
4	E	304	OLC	C6-C7-C8-C9
4	A	306	OLC	C5-C6-C7-C8
5	C	309	LFA	C4-C5-C6-C7

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Mol	Chain	Res	Type	Atoms
5	B	314	LFA	C6-C7-C8-C9
5	D	310	LFA	C5-C6-C7-C8
4	C	303	OLC	C7-C8-C9-C10
5	E	312	LFA	C7-C8-C9-C10
4	C	312	OLC	C2-C3-C4-C5
4	C	303	OLC	C5-C6-C7-C8
4	B	311	OLC	C7-C8-C9-C10
5	C	310	LFA	C6-C7-C8-C9
4	A	305	OLC	C12-C13-C14-C15
4	A	306	OLC	C9-C10-C11-C12
4	C	312	OLC	C7-C8-C9-C10
4	C	316	OLC	C22-C21-O20-C1
4	A	303	OLC	C4-C5-C6-C7

There are no ring outliers.

28 monomers are involved in 38 short contacts:

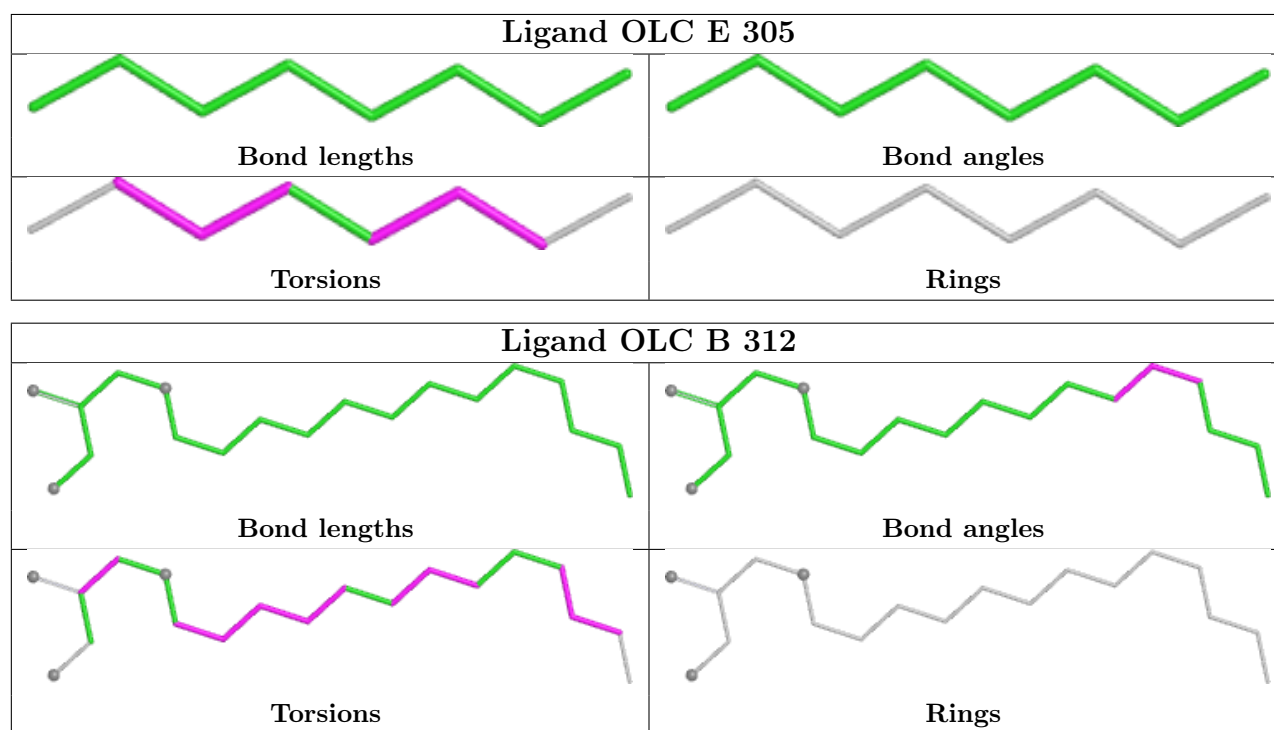
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	305	OLC	1	0
4	B	312	OLC	2	0
4	C	304	OLC	3	0
2	E	301	RET	1	0
4	D	308	OLC	3	0
5	B	307	LFA	1	0
5	E	312	LFA	1	0
4	A	305	OLC	1	0
4	E	304	OLC	2	0
4	B	303	OLC	1	0
4	A	306	OLC	2	0
2	D	301	RET	1	0
4	C	303	OLC	3	0
4	E	318	OLC	4	0
4	E	319	OLC	1	0
4	C	316	OLC	2	0
2	C	301	RET	2	0
4	B	315	OLC	1	0
4	A	308	OLC	1	0
5	D	312	LFA	1	0
2	B	301	RET	1	0
4	D	305	OLC	1	0
4	B	311	OLC	2	0
4	D	306	OLC	1	0

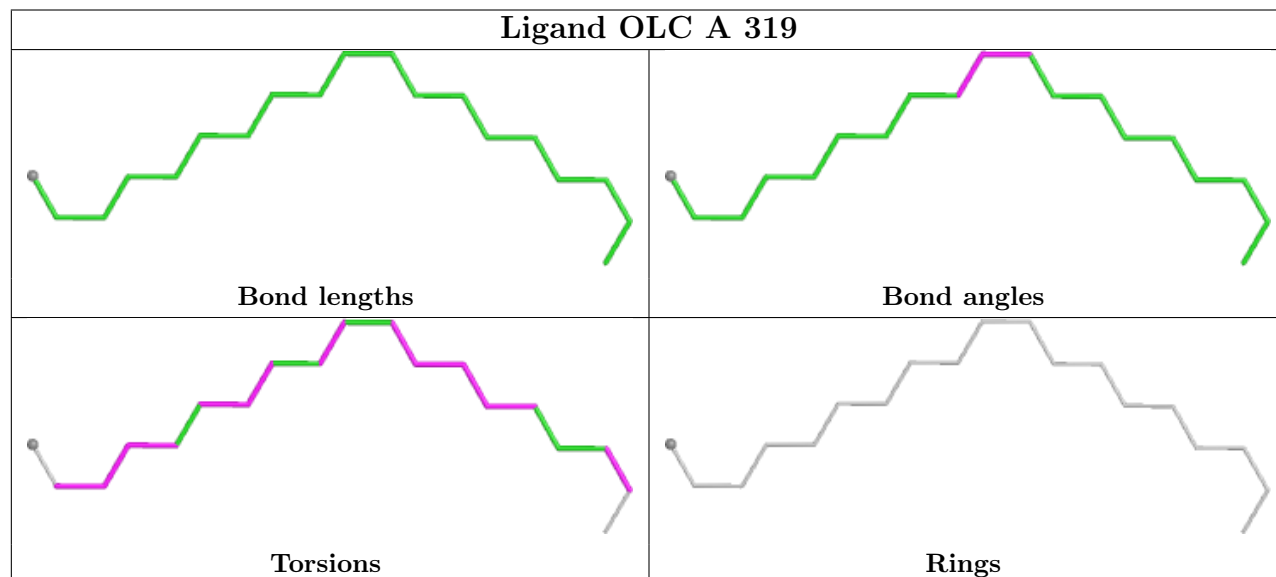
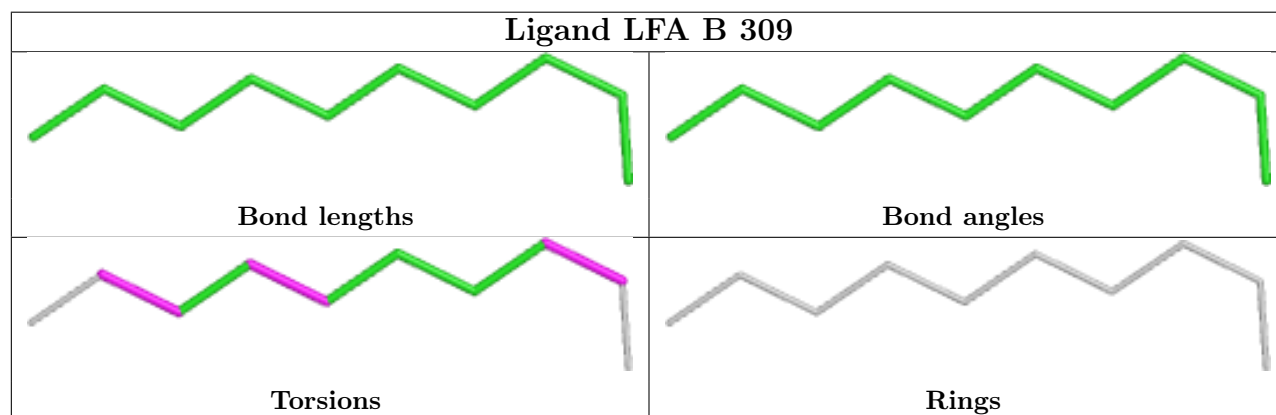
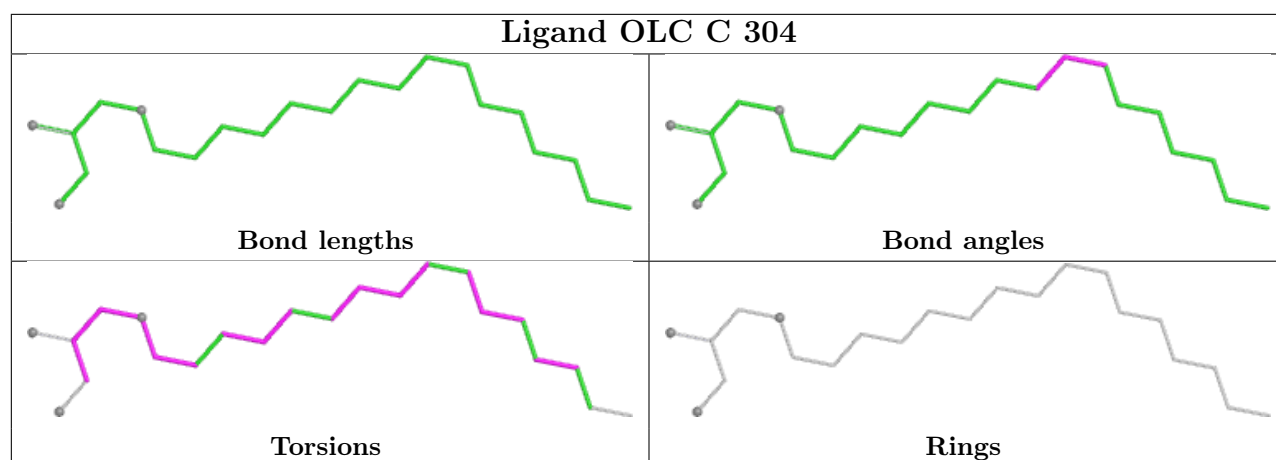
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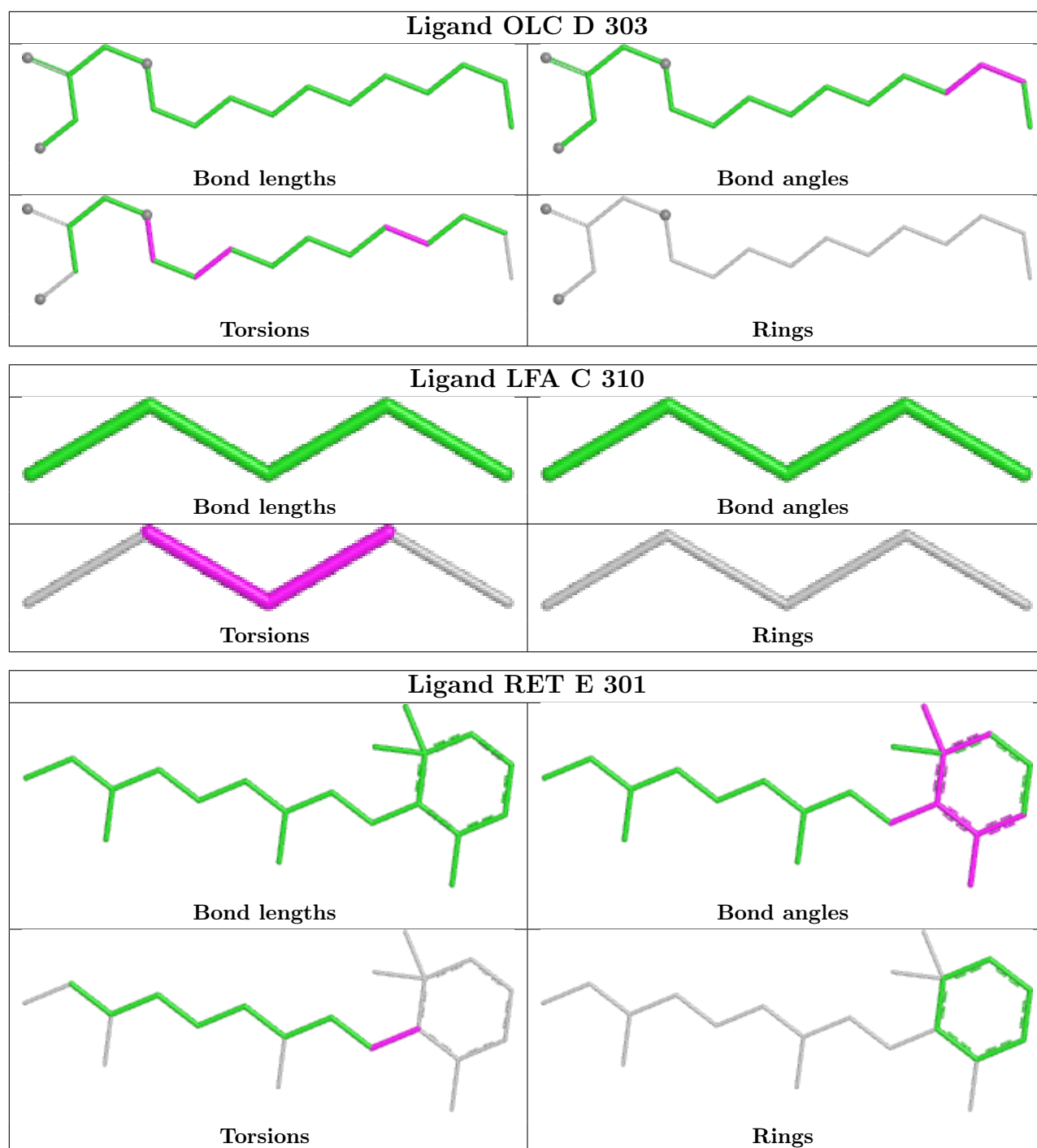
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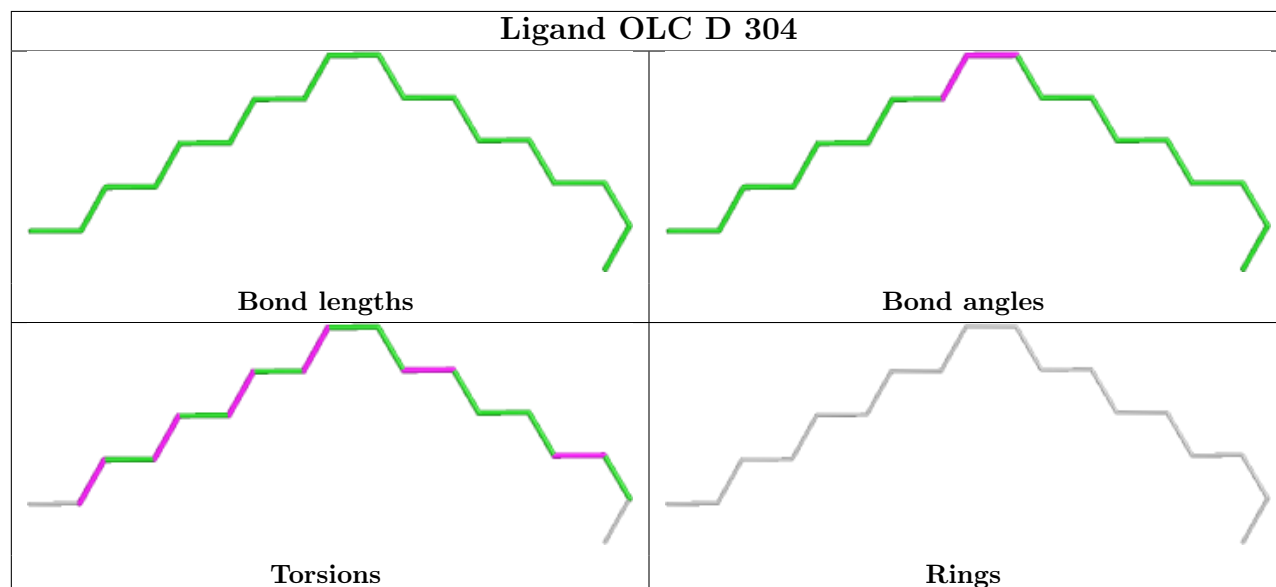
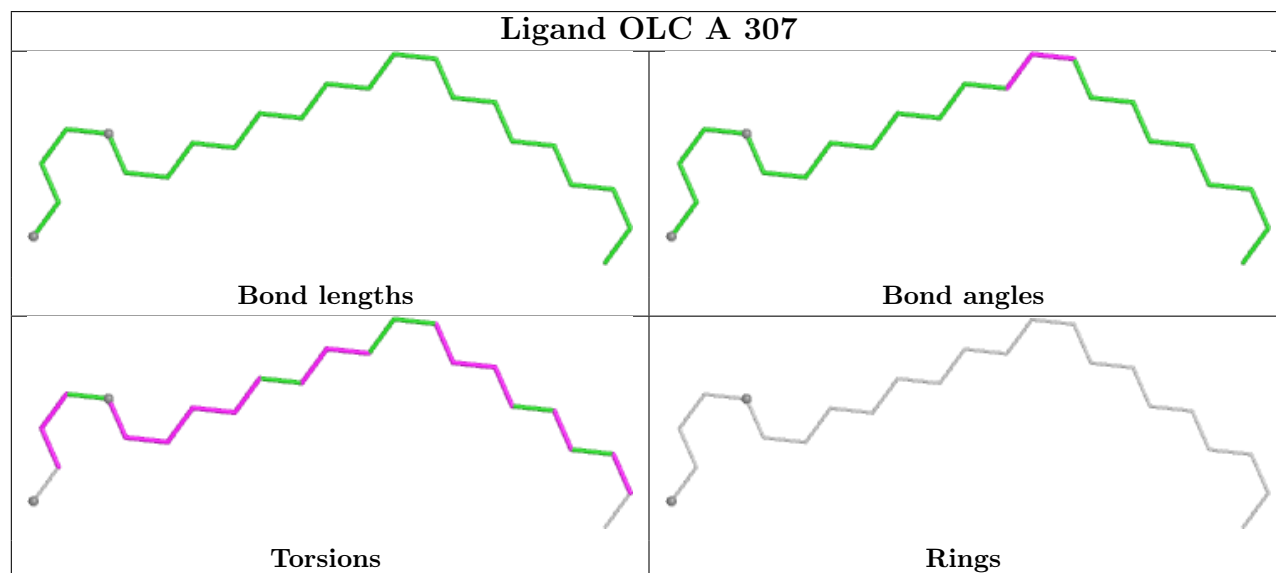
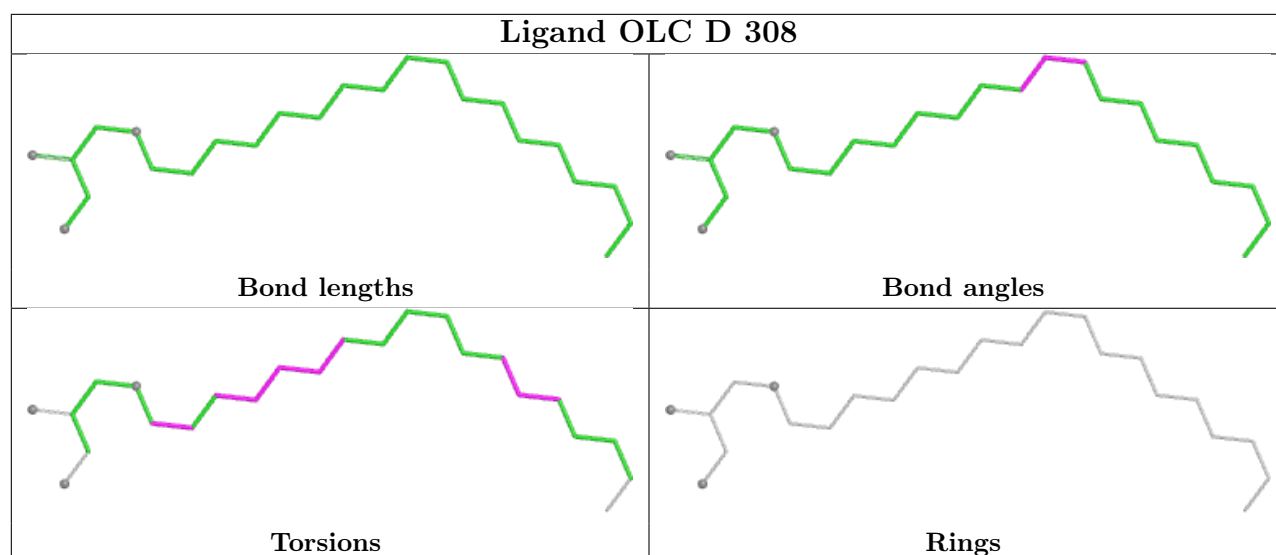
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	311	OLC	1	0
4	A	304	OLC	1	0
4	C	312	OLC	2	0
5	E	316	LFA	1	0

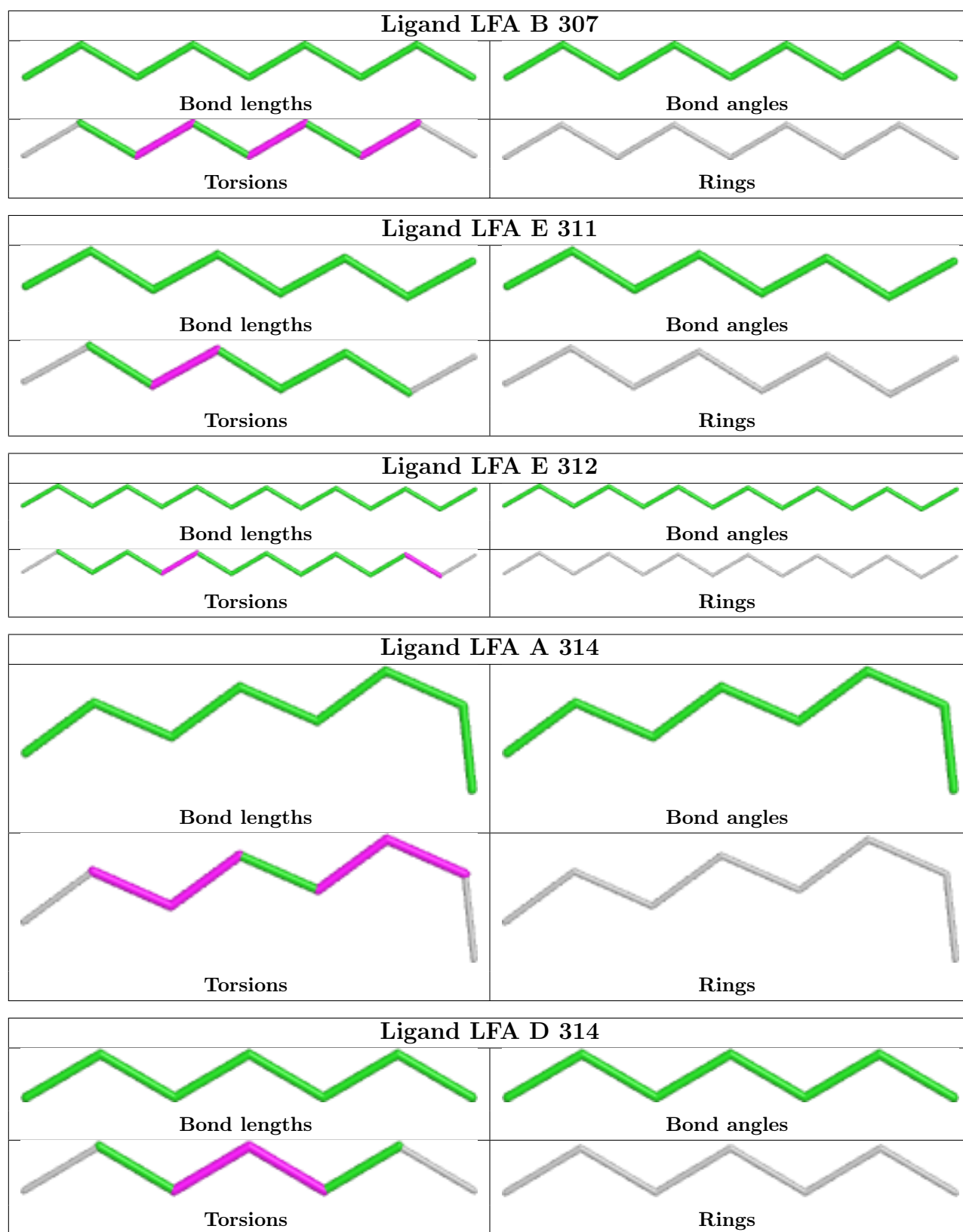
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

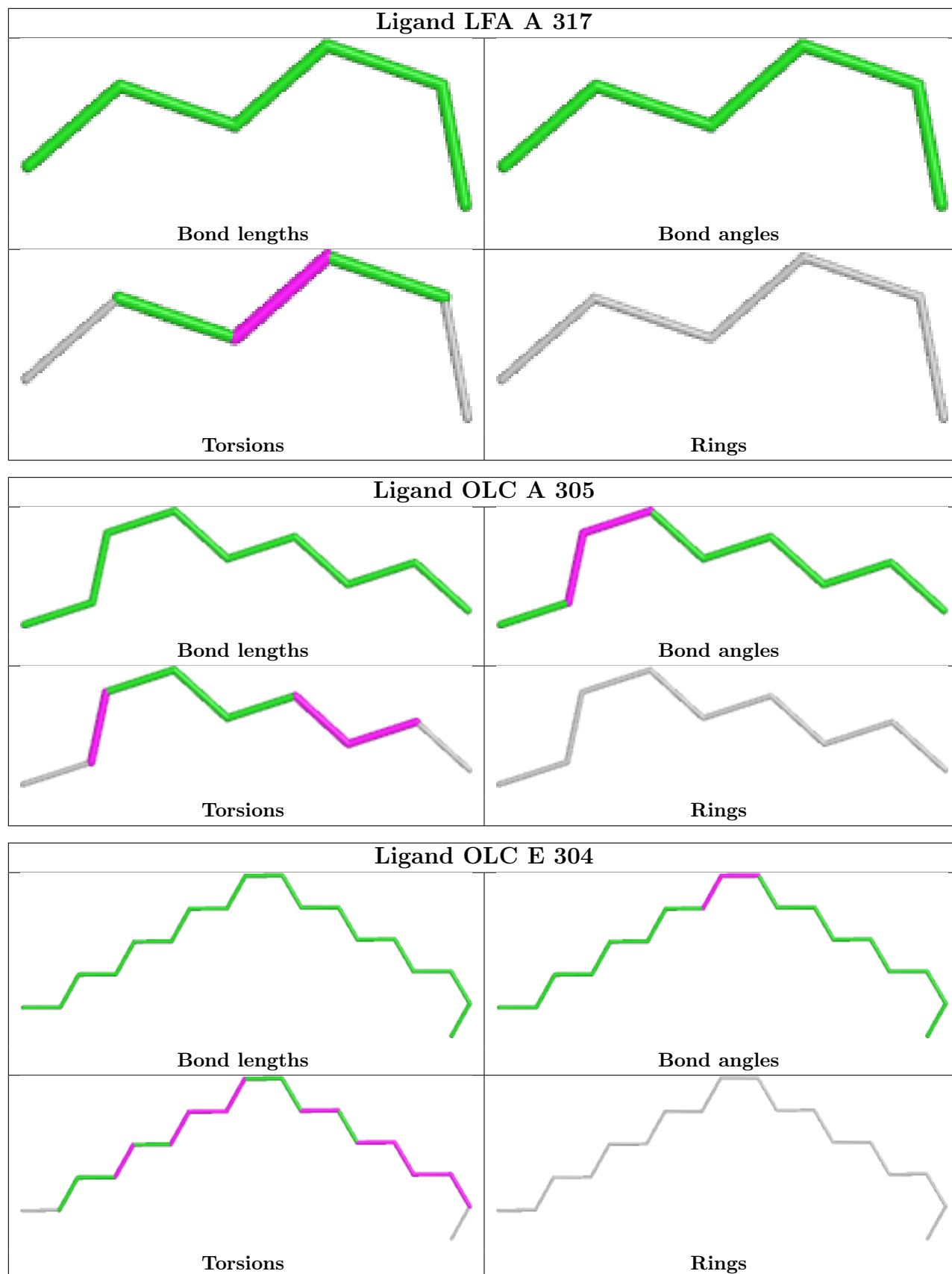


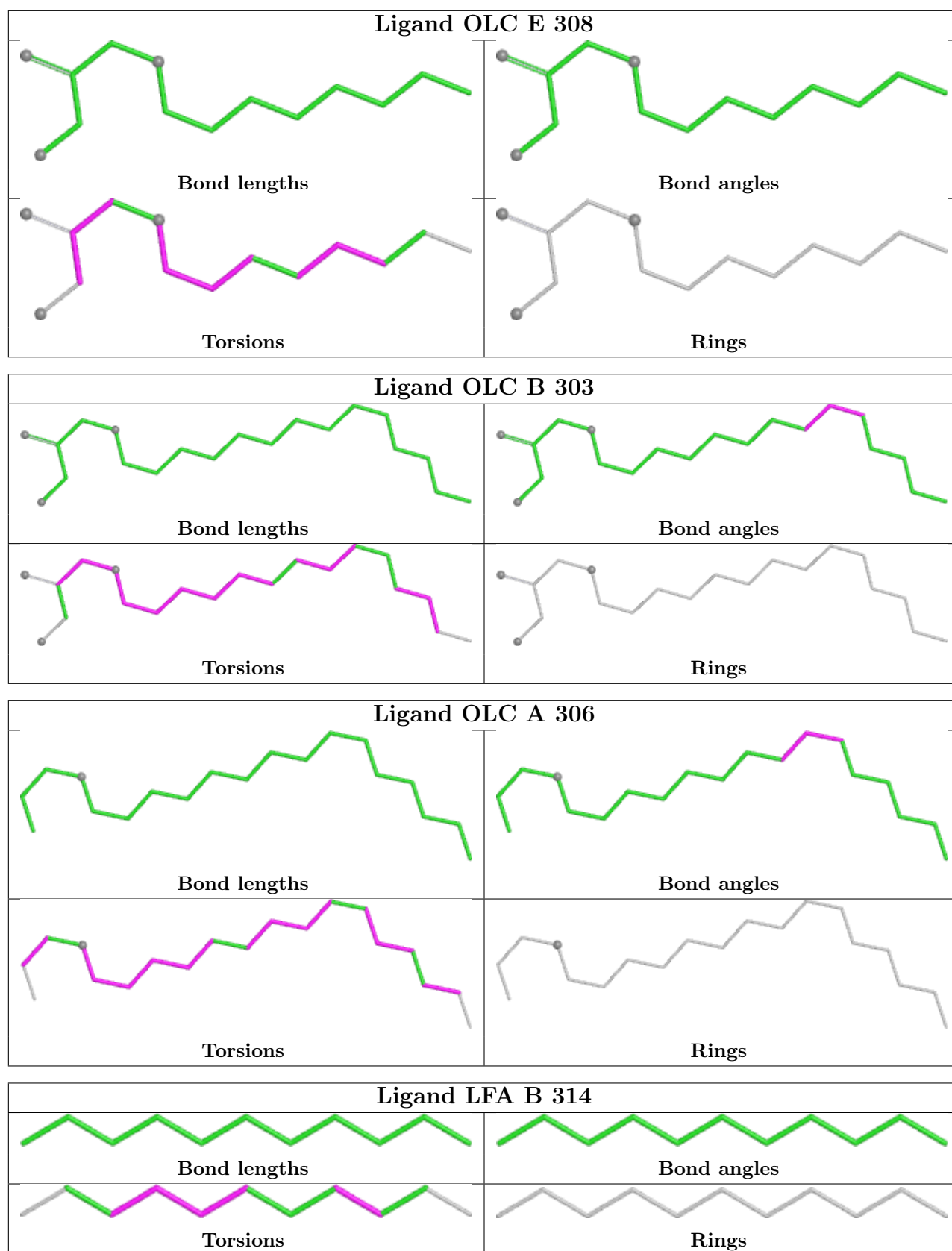


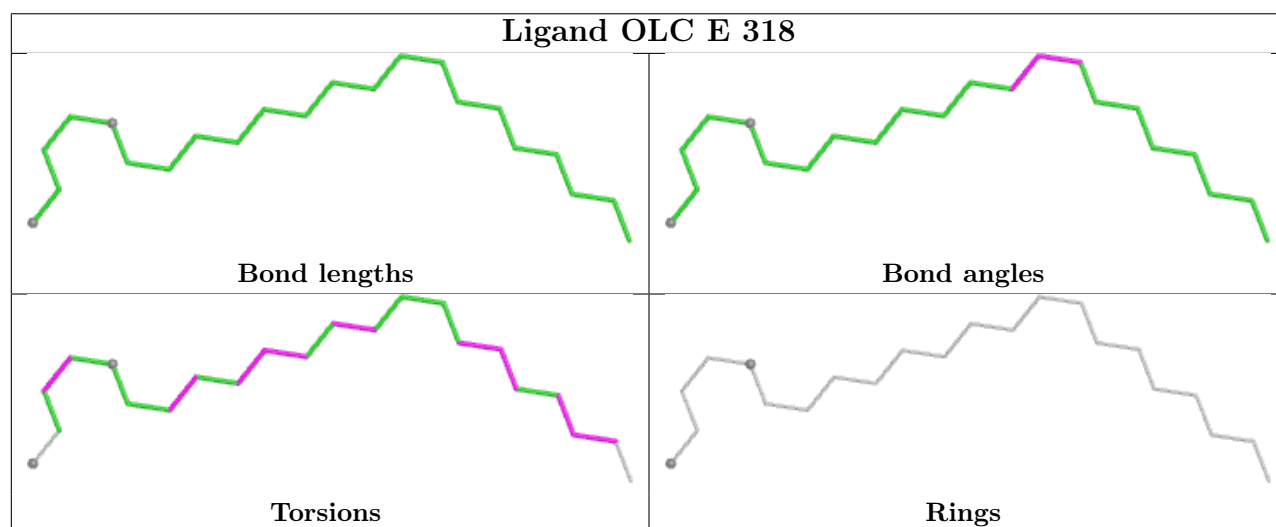
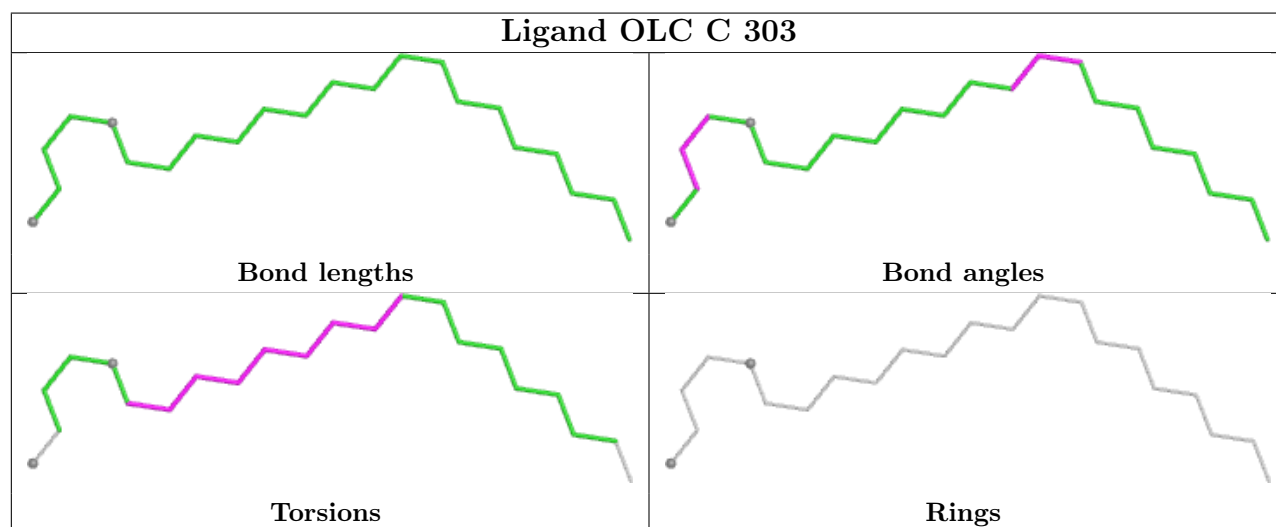
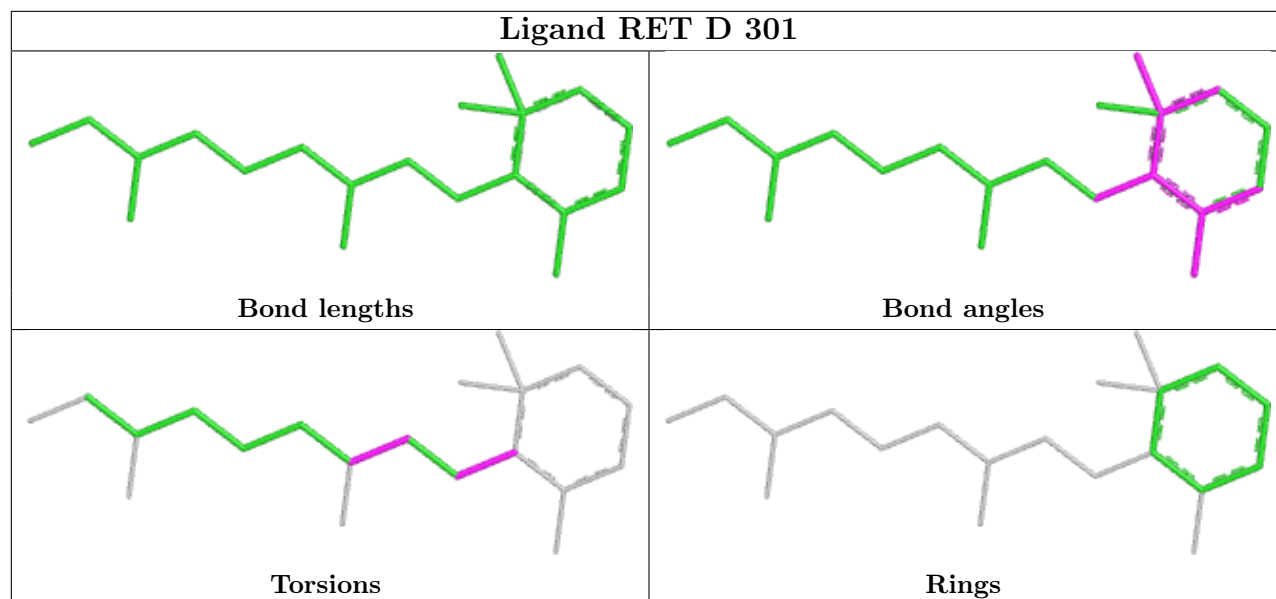


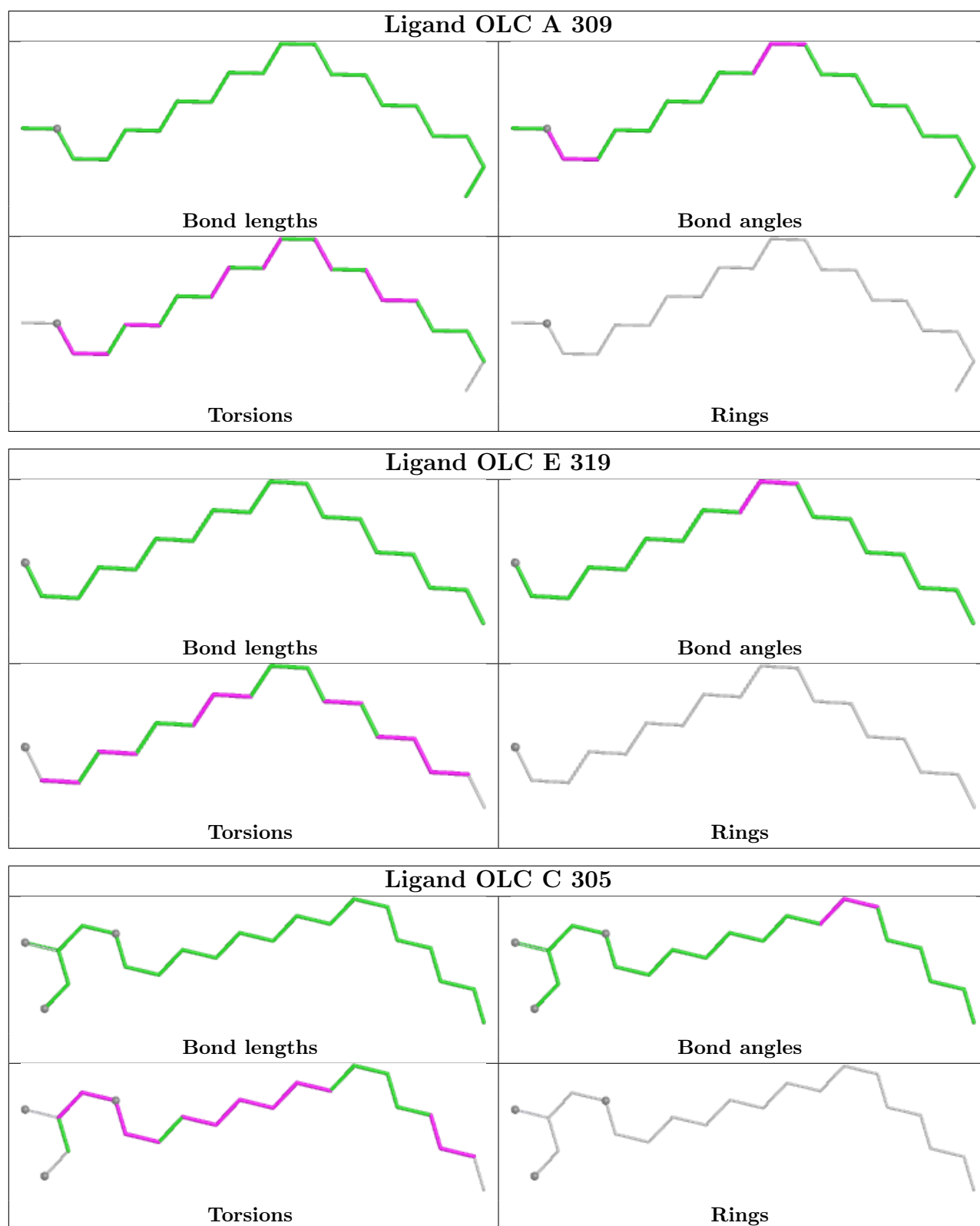


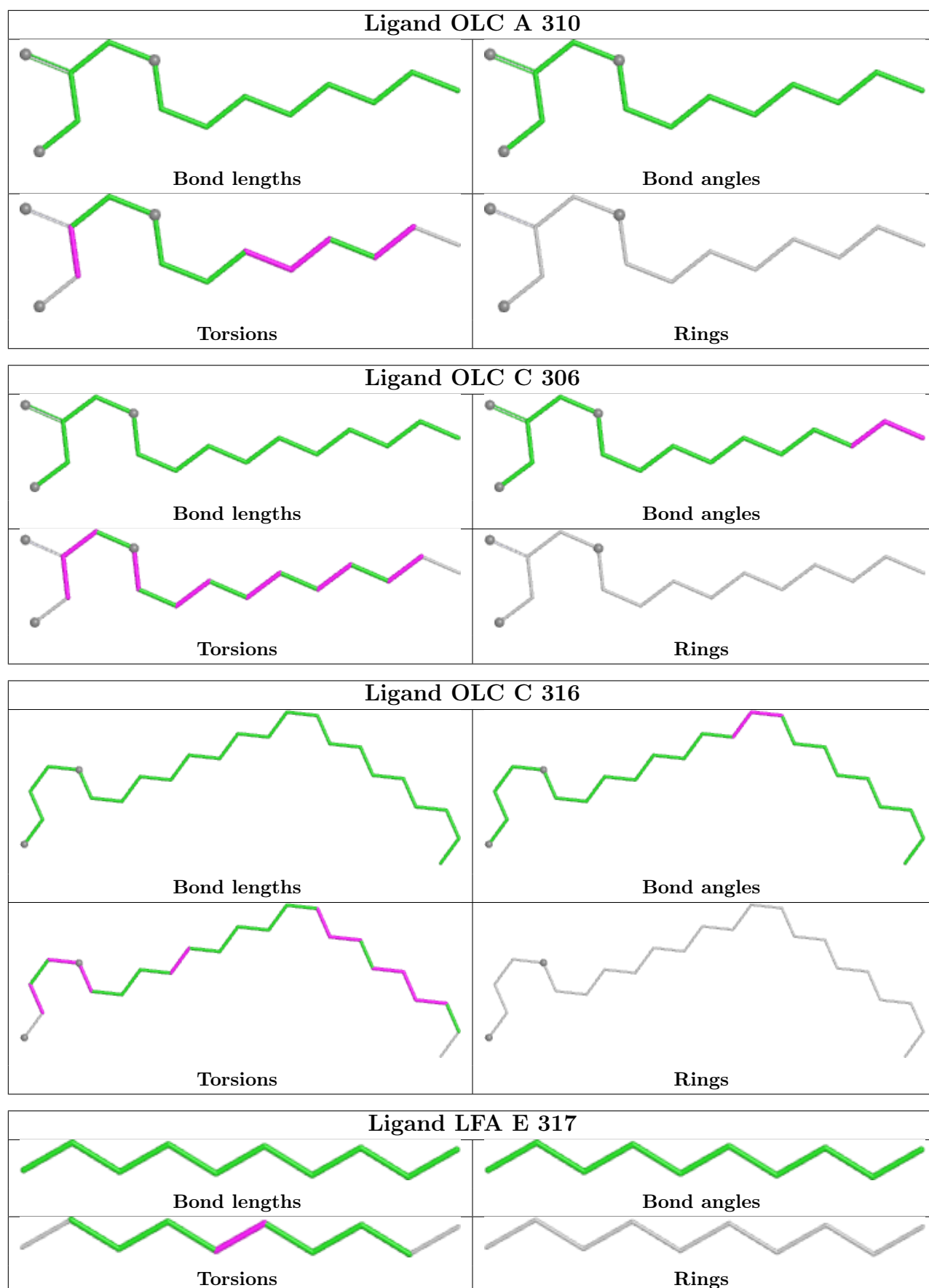


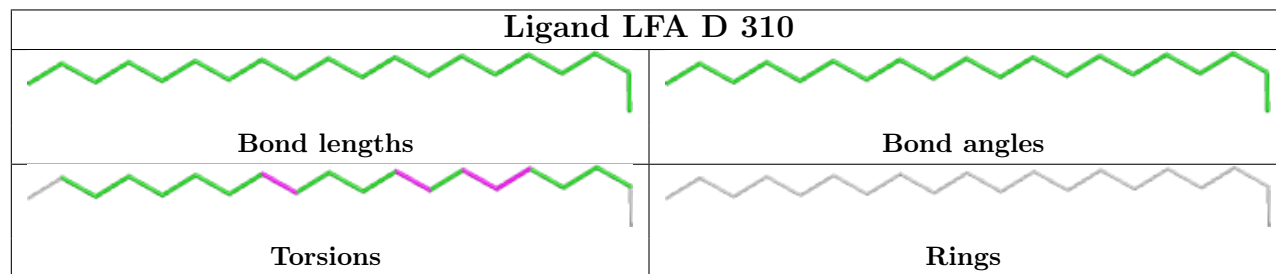
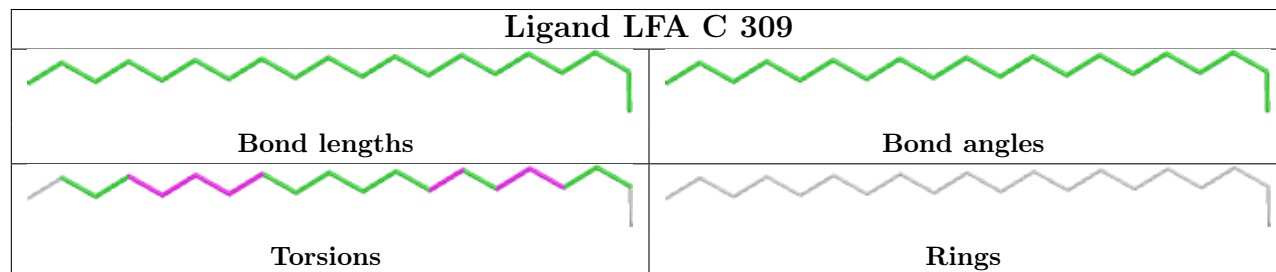
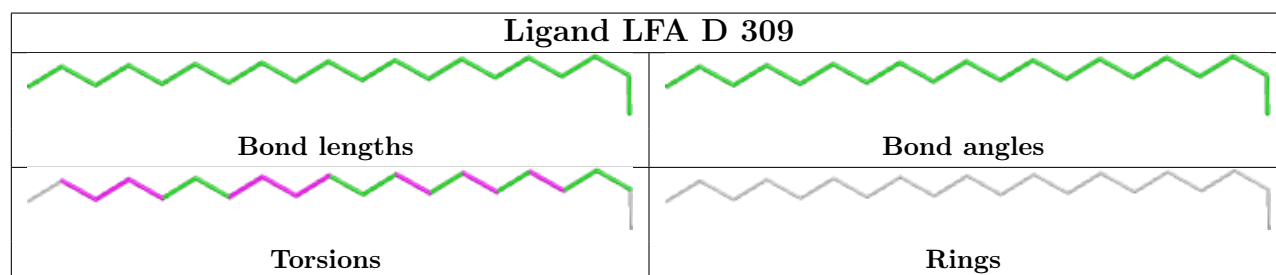
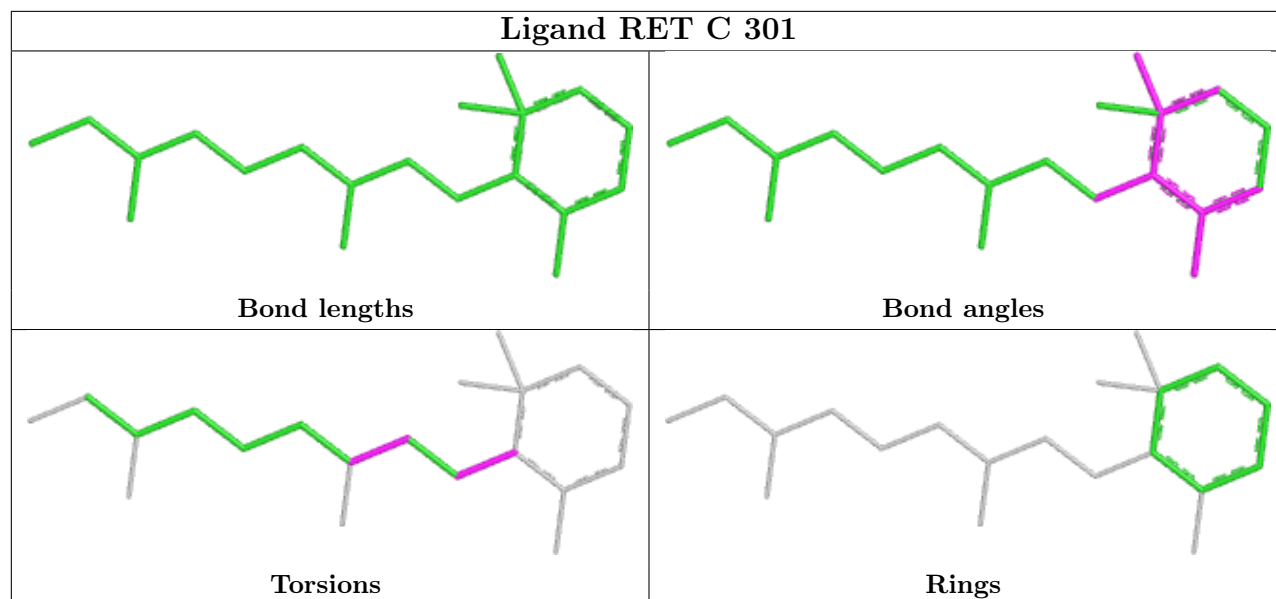


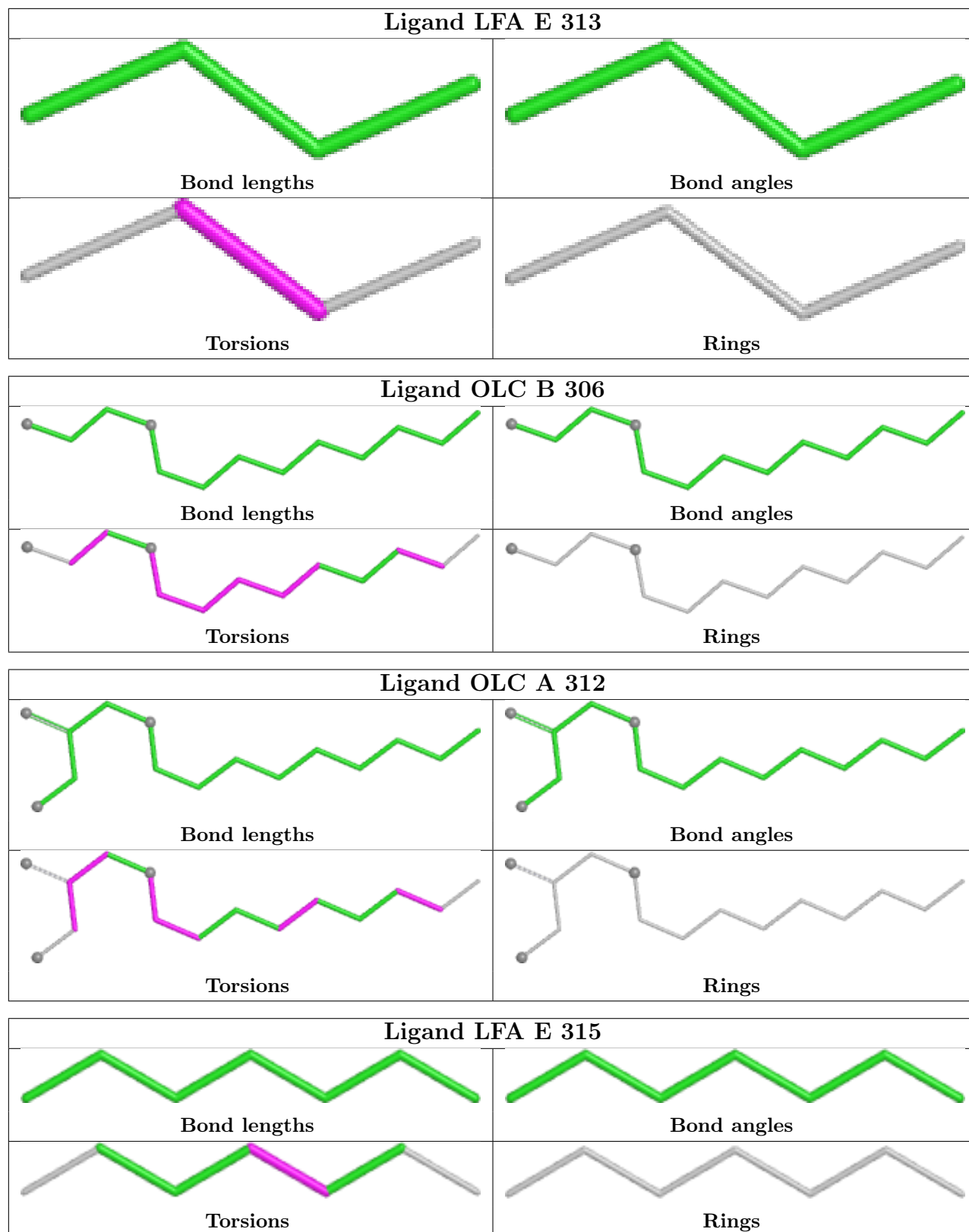


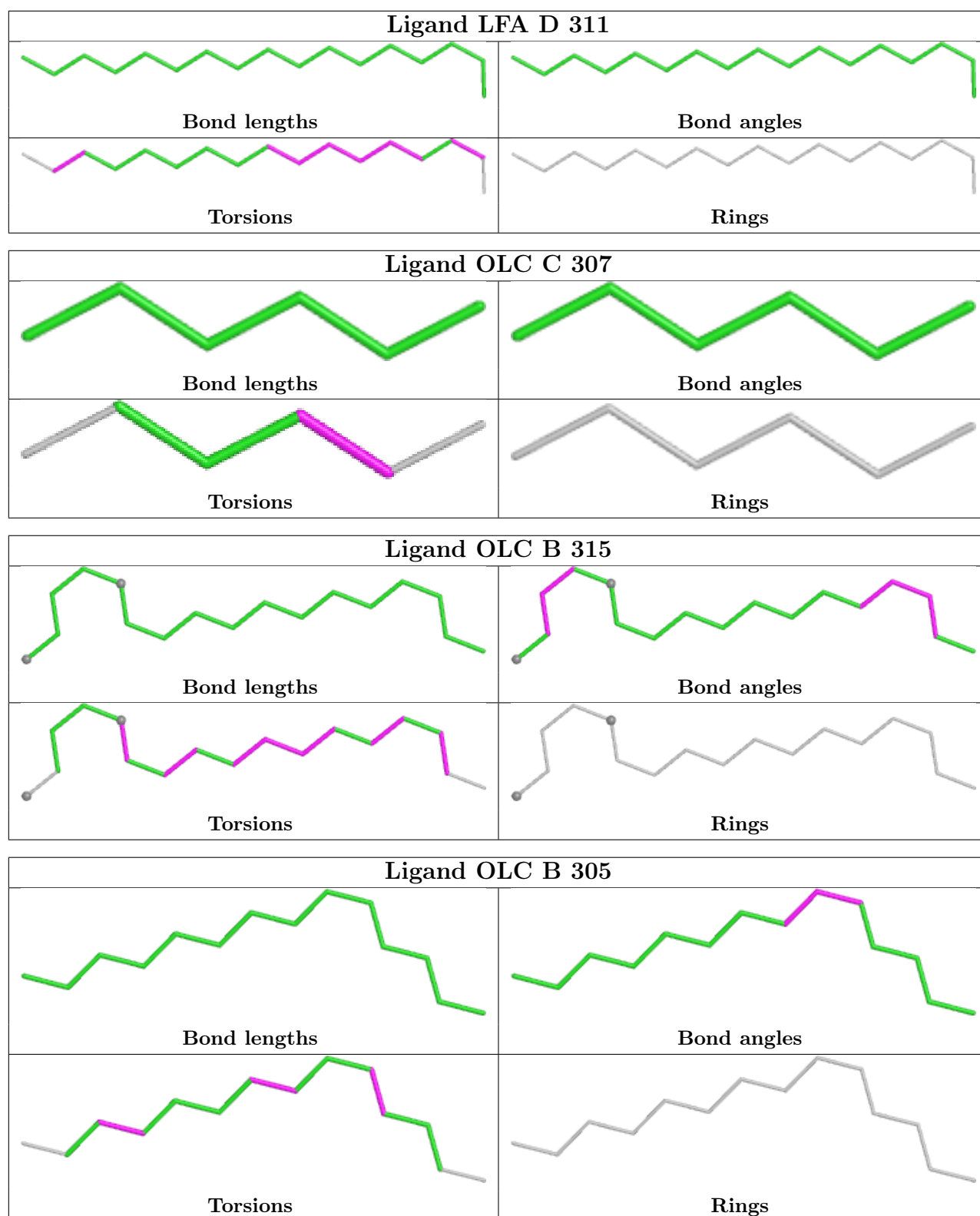


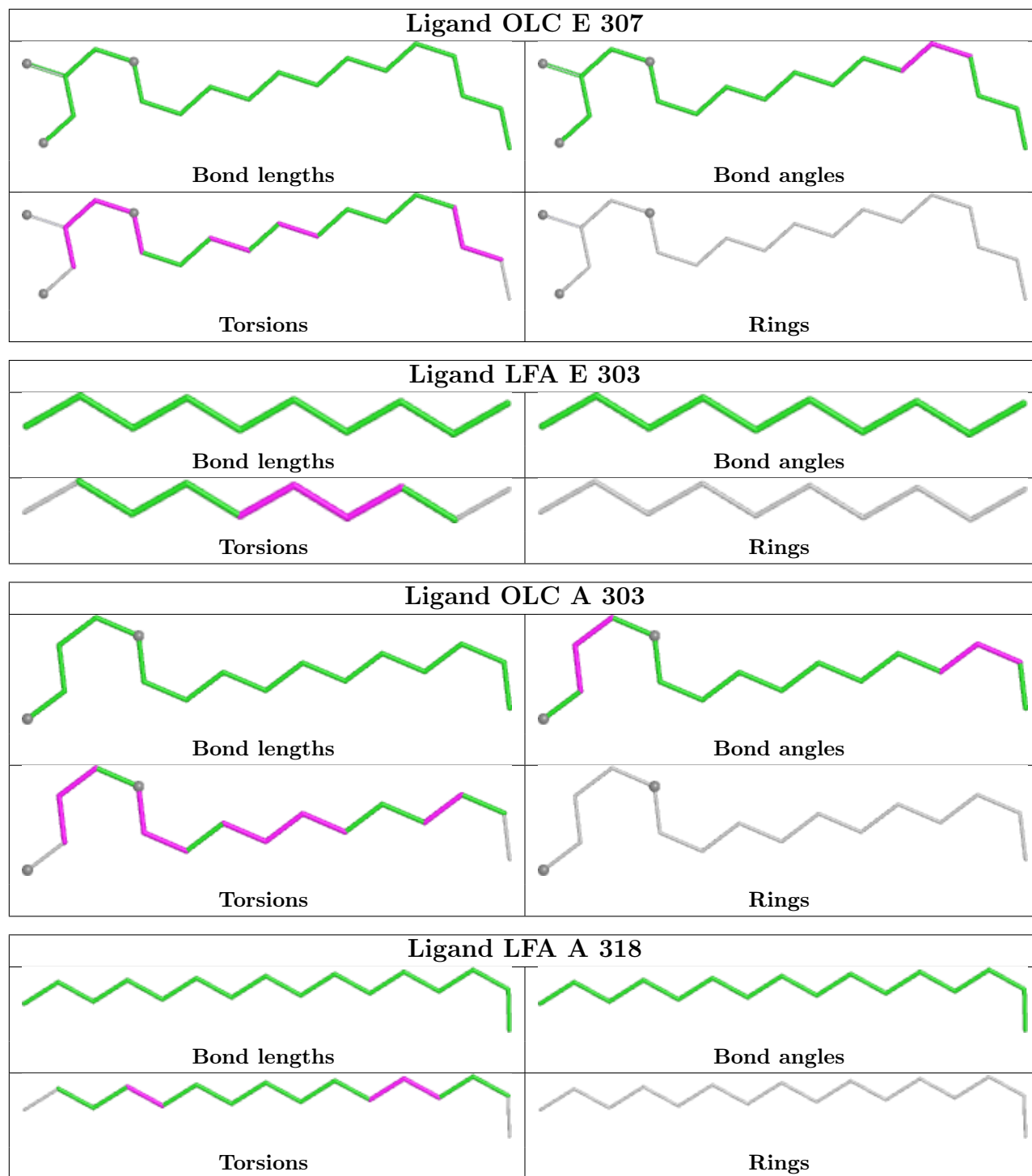


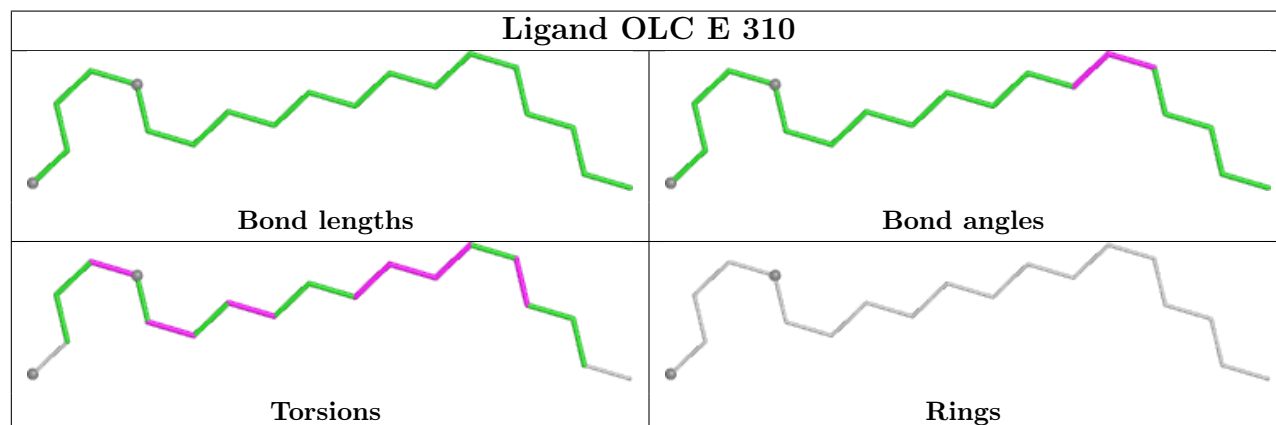
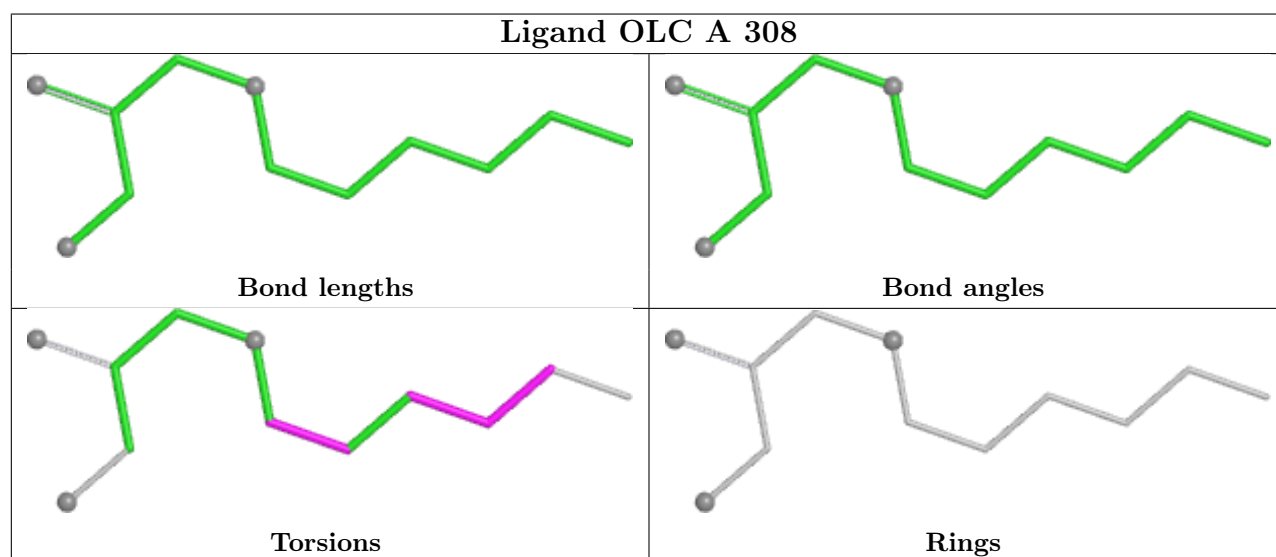
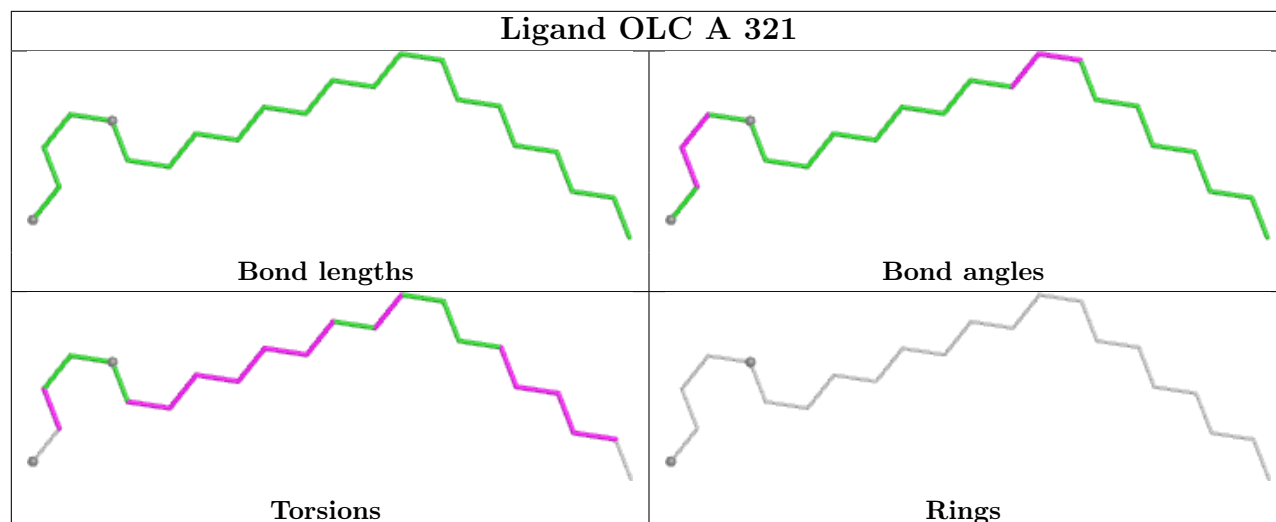


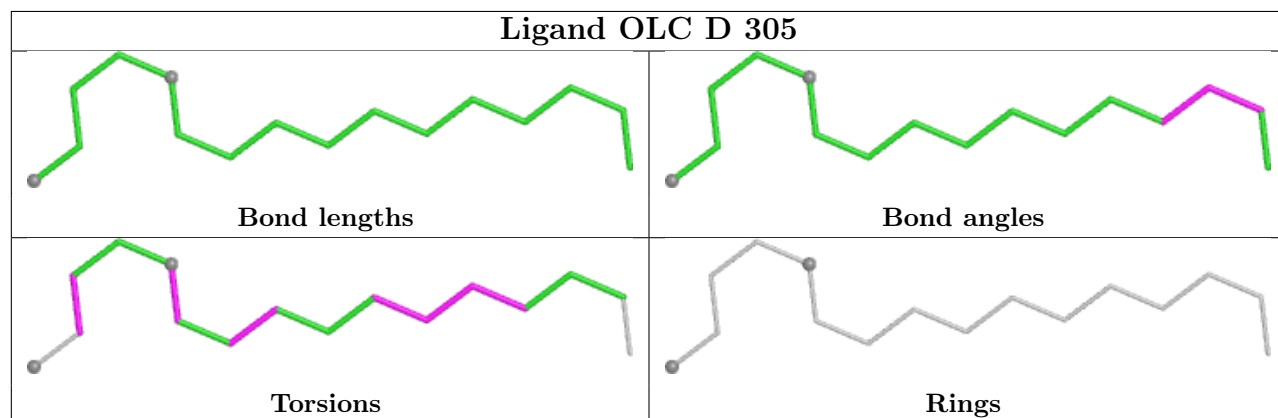
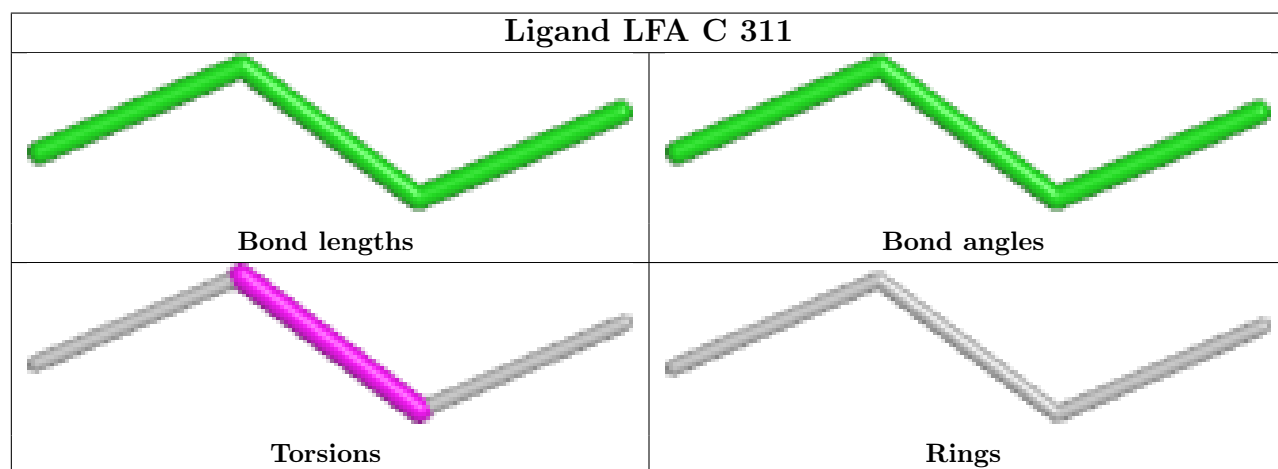
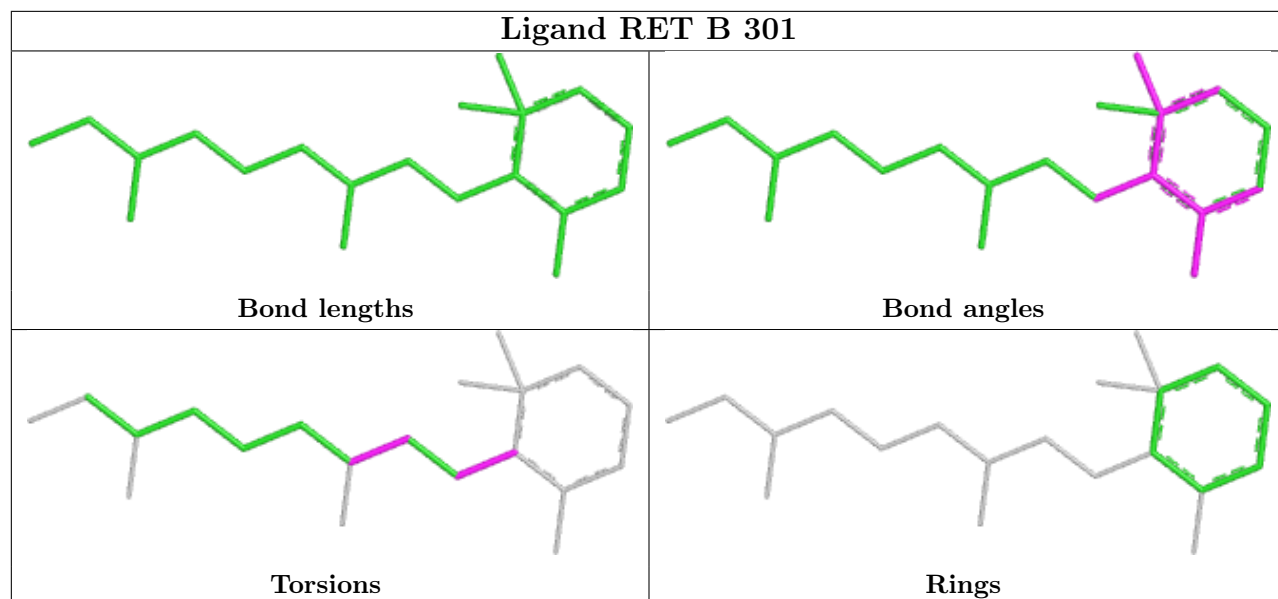


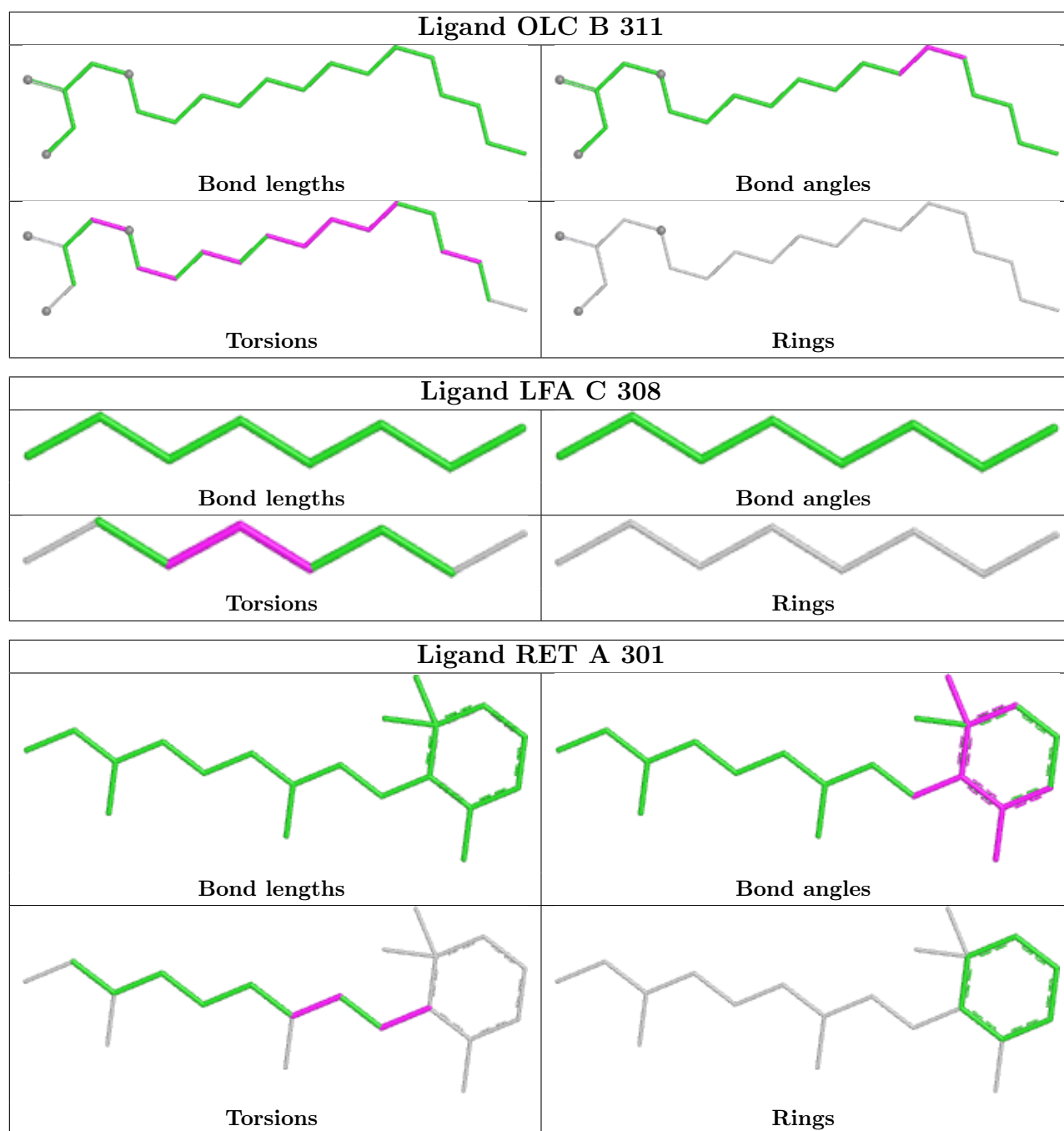


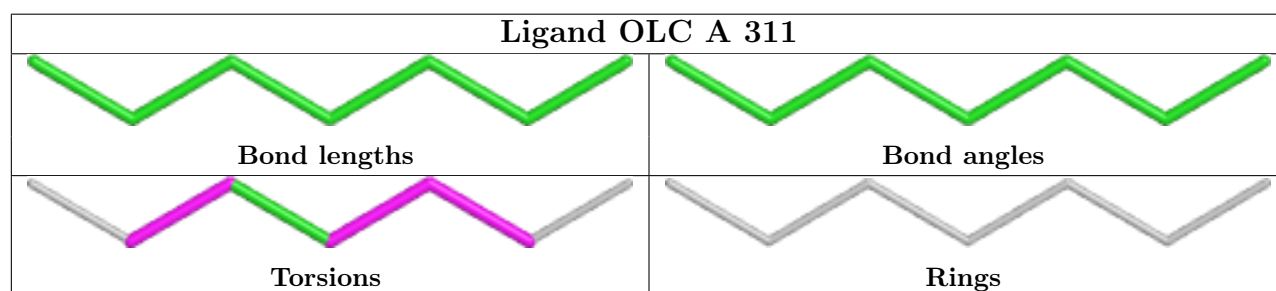
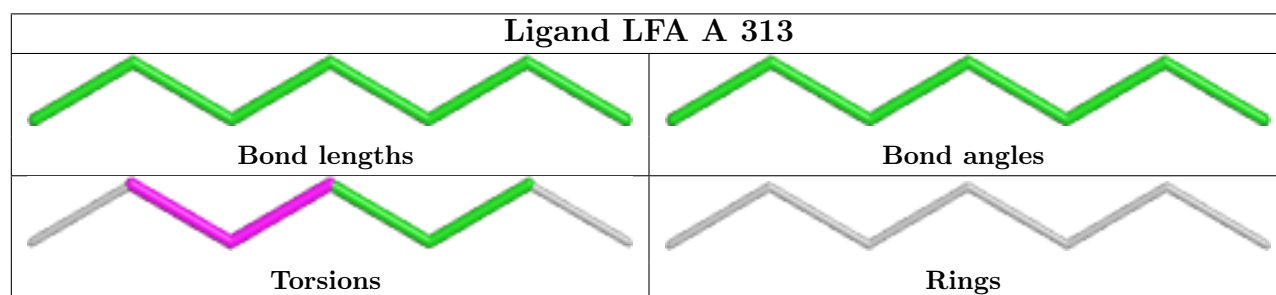
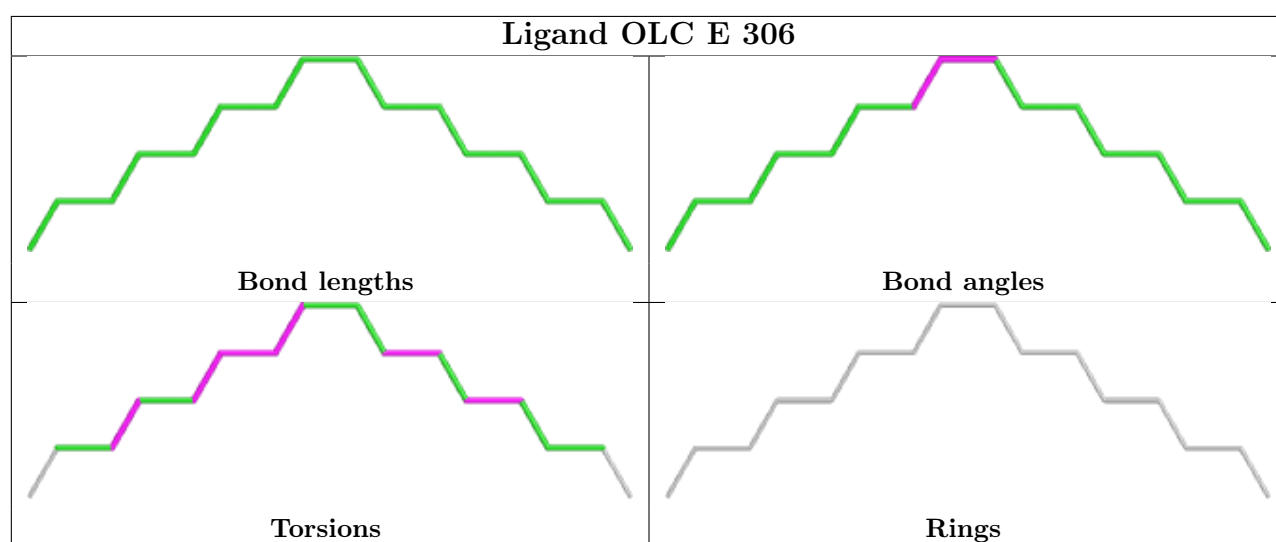
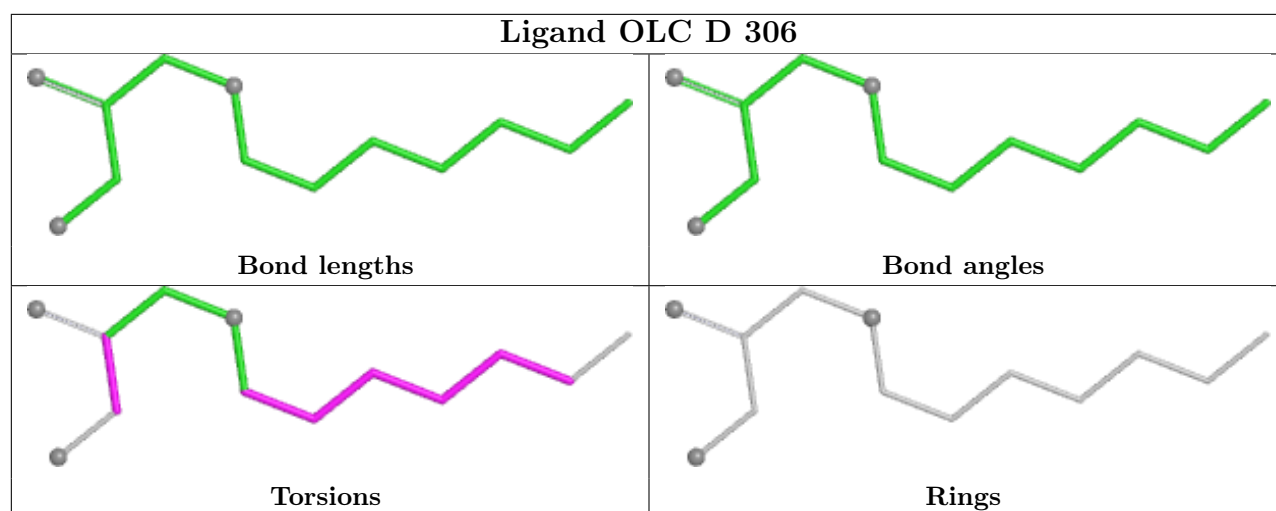


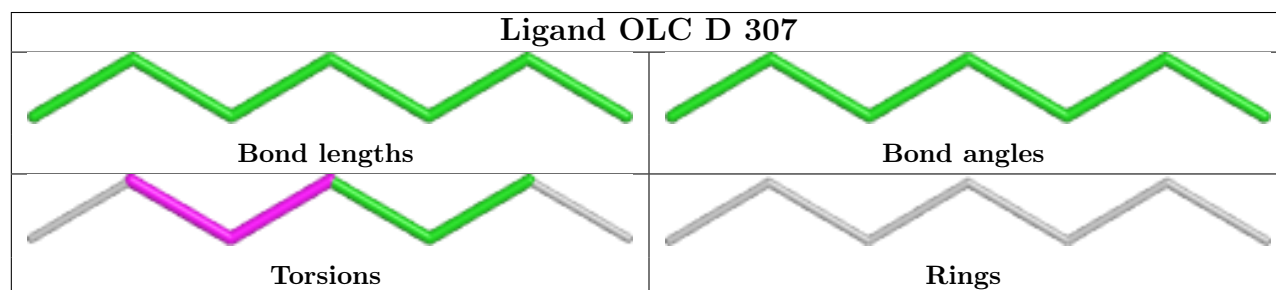
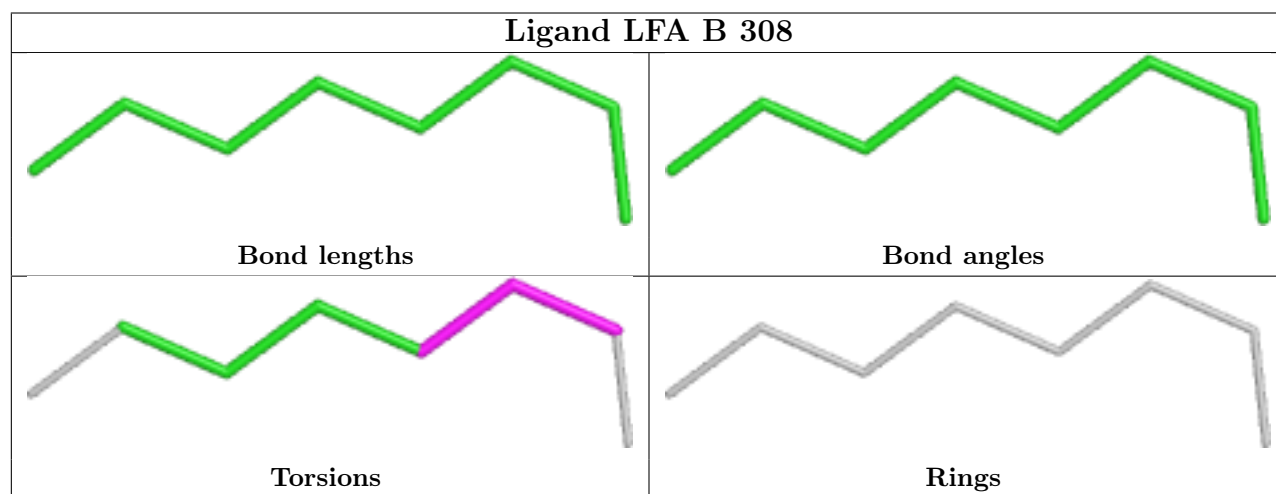
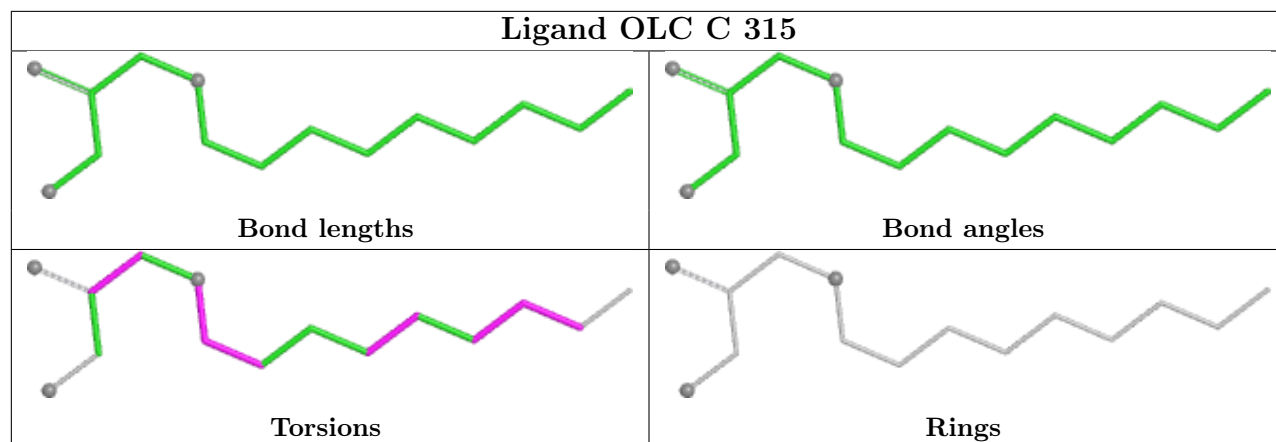


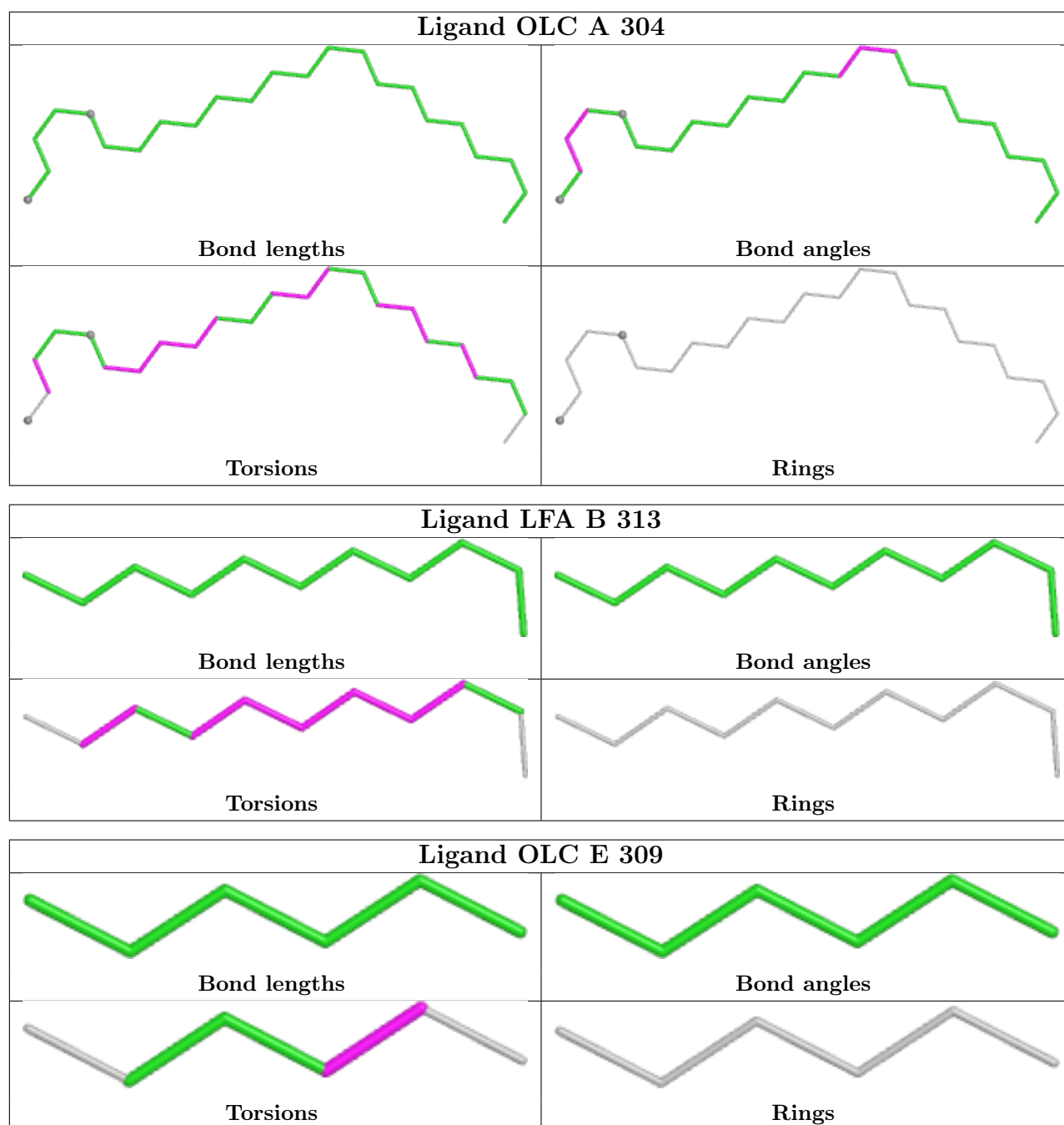


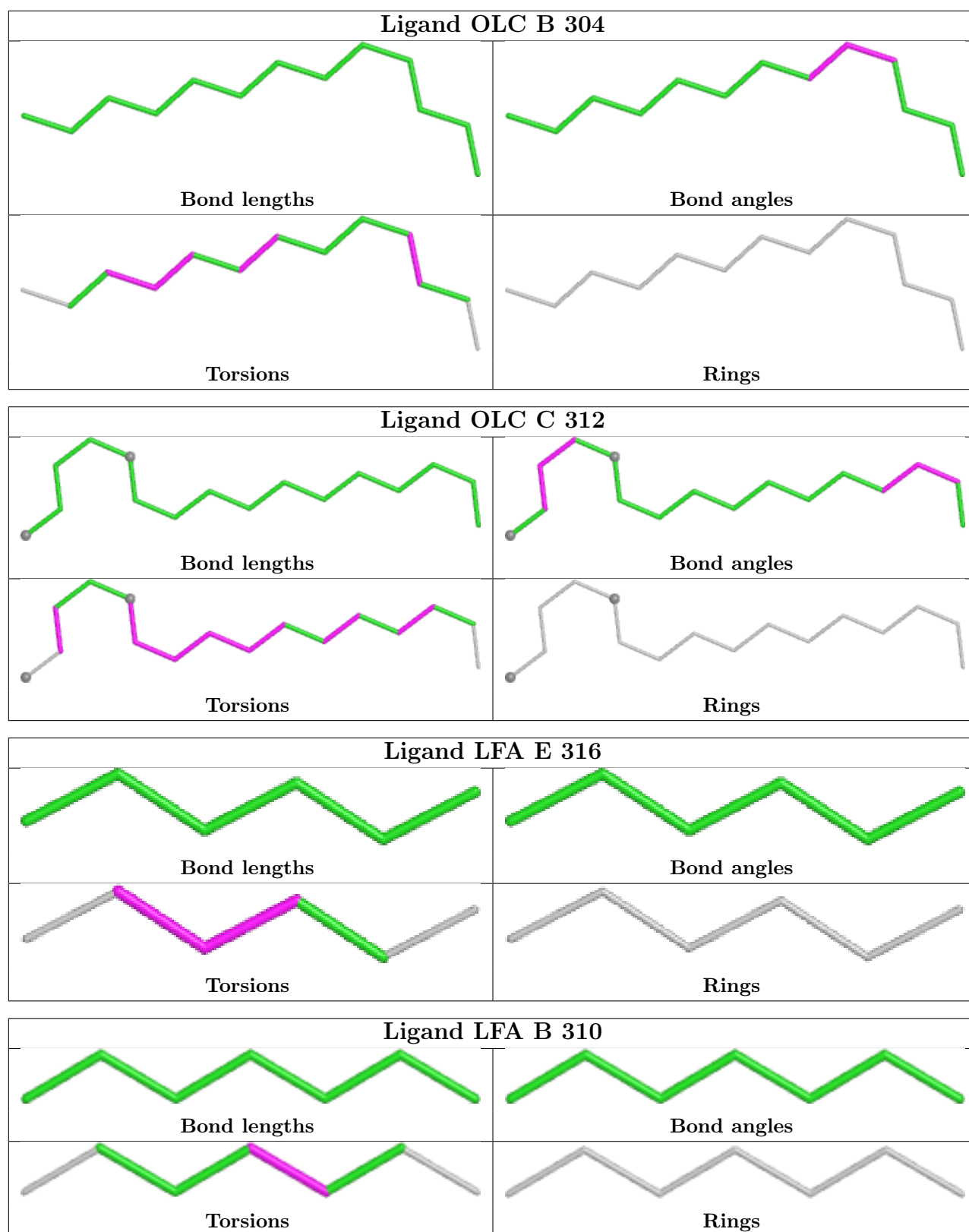












5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	269/273 (98%)	-0.51	0 100 100	38, 49, 71, 92	0
1	B	269/273 (98%)	-0.52	2 (0%) 84 66	39, 49, 67, 99	0
1	C	268/273 (98%)	-0.47	0 100 100	37, 50, 69, 111	0
1	D	268/273 (98%)	-0.48	0 100 100	38, 52, 74, 94	0
1	E	268/273 (98%)	-0.53	0 100 100	38, 51, 69, 100	0
All	All	1342/1365 (98%)	-0.50	2 (0%) 92 86	37, 50, 71, 111	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3	GLN	3.0
1	B	271	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	LFA	E	316	6/20	0.59	0.34	75,83,84,88	0
5	LFA	A	316	4/20	0.70	0.27	62,67,69,69	0
5	LFA	C	314	5/20	0.78	0.27	69,74,85,91	0
4	OLC	E	309	6/25	0.79	0.28	61,68,85,86	0
5	LFA	B	307	9/20	0.79	0.23	69,82,93,94	0
5	LFA	A	318	16/20	0.81	0.22	69,77,82,85	0
5	LFA	A	315	8/20	0.81	0.28	67,87,94,95	0
5	LFA	E	317	10/20	0.81	0.22	65,82,91,95	0
5	LFA	B	314	11/20	0.82	0.23	70,80,90,97	0
4	OLC	E	307	19/25	0.84	0.17	71,84,91,93	0
5	LFA	A	313	7/20	0.85	0.24	66,73,77,79	0
5	LFA	B	313	11/20	0.85	0.19	72,74,81,82	0
4	OLC	C	312	16/25	0.85	0.18	67,73,100,100	0
4	OLC	E	305	8/25	0.86	0.19	63,67,73,75	0
4	OLC	A	308	12/25	0.86	0.13	57,76,82,100	0
4	OLC	A	309	20/25	0.86	0.17	66,77,85,86	0
5	LFA	A	320	9/20	0.86	0.19	77,82,91,92	0
4	OLC	A	307	23/25	0.86	0.17	66,77,83,91	0
5	LFA	C	311	4/20	0.87	0.21	70,71,72,73	0
5	LFA	B	310	7/20	0.87	0.21	60,65,70,72	0
5	LFA	D	312	7/20	0.87	0.22	74,78,82,85	0
5	LFA	D	314	7/20	0.87	0.19	64,69,75,79	0
4	OLC	B	305	14/25	0.87	0.20	59,82,87,93	0
4	OLC	C	305	21/25	0.87	0.16	55,81,90,93	0
4	OLC	D	306	13/25	0.88	0.16	67,76,85,91	0
4	OLC	D	307	7/25	0.88	0.18	57,66,70,75	0
5	LFA	D	310	20/20	0.88	0.18	73,82,90,90	0
5	LFA	B	309	10/20	0.88	0.20	74,81,88,90	0
4	OLC	A	312	15/25	0.88	0.18	63,73,86,92	0
4	OLC	B	315	17/25	0.88	0.16	59,73,83,91	0
4	OLC	E	308	14/25	0.88	0.13	60,75,88,95	0
5	LFA	A	314	8/20	0.89	0.15	54,59,66,68	0
4	OLC	C	307	6/25	0.89	0.18	65,69,71,72	0
4	OLC	B	303	20/25	0.89	0.15	65,78,91,95	0
5	LFA	E	303	10/20	0.89	0.26	79,83,89,90	0
5	LFA	E	312	14/20	0.89	0.18	59,81,92,94	0
5	LFA	C	313	6/20	0.89	0.17	70,73,74,74	0
4	OLC	C	306	16/25	0.89	0.15	65,76,96,102	0
4	OLC	C	303	22/25	0.90	0.20	54,75,82,85	0
4	OLC	B	304	13/25	0.90	0.16	64,72,89,90	0
4	OLC	E	306	16/25	0.90	0.16	64,77,88,91	0
5	LFA	D	309	20/20	0.90	0.16	73,79,85,88	0
4	OLC	A	310	14/25	0.90	0.13	74,80,88,92	0

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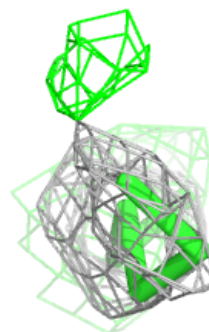
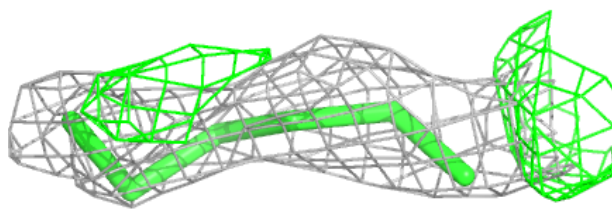
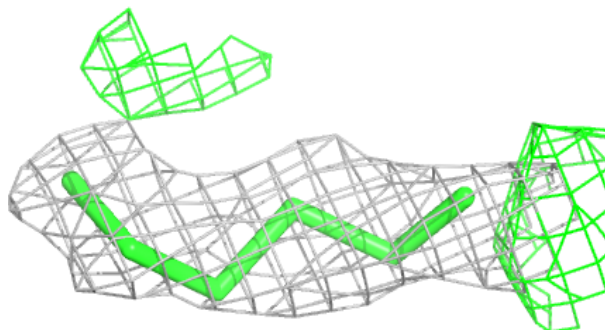
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	OLC	B	306	13/25	0.90	0.15	70,77,85,88	0
4	OLC	B	312	19/25	0.90	0.15	54,65,85,86	0
4	OLC	E	310	19/25	0.90	0.17	57,68,87,98	0
4	OLC	D	304	18/25	0.90	0.17	66,75,85,88	0
4	OLC	A	311	7/25	0.90	0.17	60,65,67,69	0
5	LFA	C	308	8/20	0.90	0.20	57,76,79,79	0
4	OLC	D	308	24/25	0.91	0.17	63,73,78,84	0
5	LFA	A	317	6/20	0.91	0.20	53,69,81,85	0
4	OLC	A	305	9/25	0.91	0.17	56,68,79,80	0
4	OLC	A	319	19/25	0.91	0.17	53,66,73,76	0
5	LFA	C	310	5/20	0.91	0.17	47,48,55,56	0
3	NA	D	302	1/1	0.91	0.09	42,42,42,42	0
5	LFA	E	314	5/20	0.91	0.20	63,63,73,75	0
5	LFA	B	308	8/20	0.91	0.19	60,70,73,83	0
4	OLC	A	303	16/25	0.91	0.17	63,70,79,80	0
4	OLC	E	304	18/25	0.92	0.17	60,69,82,83	0
5	LFA	E	311	8/20	0.92	0.15	49,69,75,75	0
4	OLC	E	318	22/25	0.92	0.16	52,69,80,81	0
5	LFA	E	313	4/20	0.92	0.20	67,68,68,75	0
4	OLC	C	316	23/25	0.92	0.17	56,76,83,89	0
5	LFA	D	313	6/20	0.92	0.18	51,64,69,70	0
4	OLC	D	303	17/25	0.92	0.15	63,69,90,90	0
4	OLC	A	321	22/25	0.93	0.14	51,70,79,83	0
4	OLC	D	305	16/25	0.93	0.13	62,70,79,82	0
5	LFA	E	315	7/20	0.93	0.16	49,65,68,75	0
4	OLC	C	315	15/25	0.93	0.14	60,70,75,81	0
5	LFA	C	309	20/20	0.93	0.14	59,68,84,85	0
5	LFA	D	311	17/20	0.94	0.13	45,55,60,61	0
4	OLC	C	304	22/25	0.94	0.13	47,58,84,87	0
4	OLC	A	306	19/25	0.94	0.13	39,53,79,80	0
4	OLC	A	304	23/25	0.94	0.15	60,70,82,84	0
2	RET	C	301	20/21	0.95	0.12	38,48,54,55	0
2	RET	D	301	20/21	0.95	0.11	45,49,55,56	0
2	RET	E	301	20/21	0.96	0.10	42,49,56,57	0
4	OLC	B	311	20/25	0.96	0.10	44,55,65,70	0
4	OLC	E	319	18/25	0.96	0.11	43,53,59,59	0
2	RET	A	301	20/21	0.97	0.10	39,45,52,54	0
2	RET	B	301	20/21	0.97	0.09	40,46,52,53	0
3	NA	E	302	1/1	0.97	0.04	39,39,39,39	0
3	NA	A	302	1/1	0.98	0.07	42,42,42,42	0
3	NA	C	302	1/1	0.99	0.03	41,41,41,41	0
3	NA	B	302	1/1	0.99	0.03	38,38,38,38	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

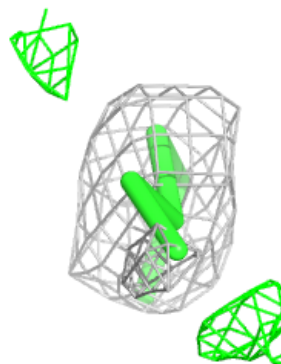
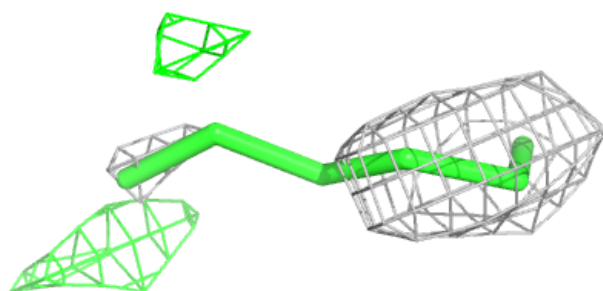
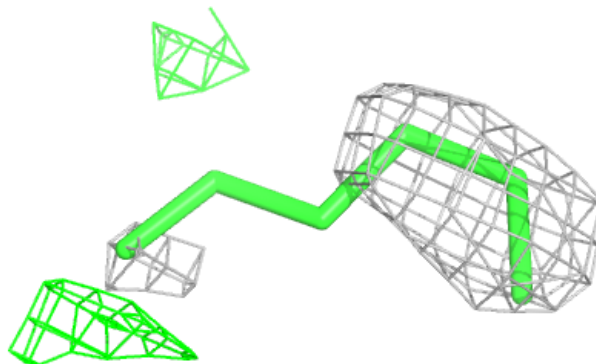
Electron density around LFA E 316:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

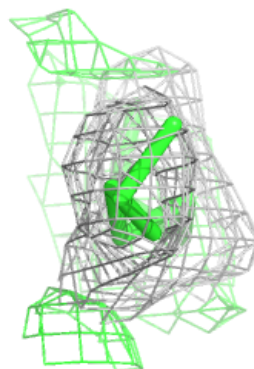
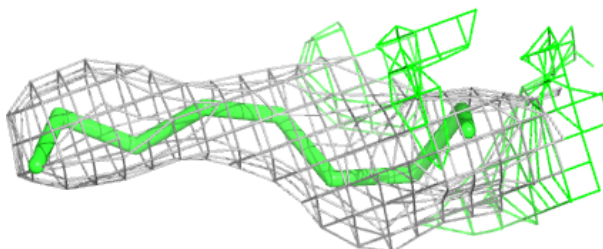
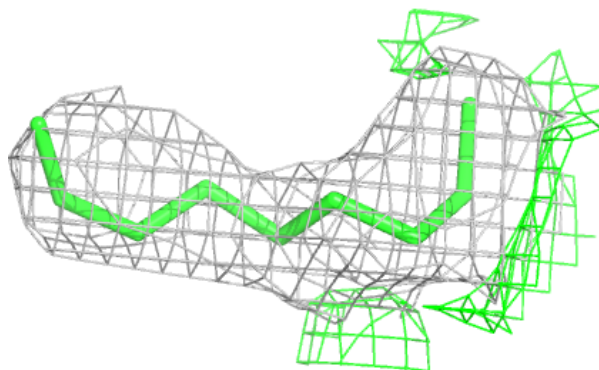


Electron density around OLC E 309:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

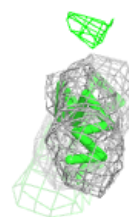
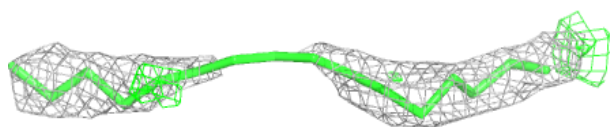
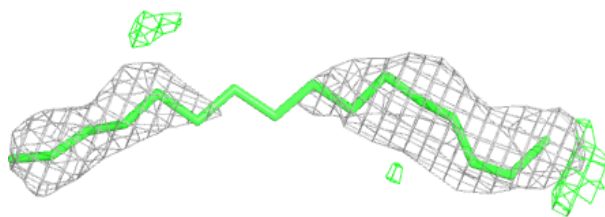
**Electron density around LFA B 307:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

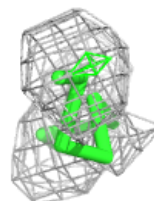
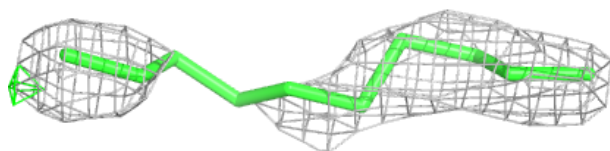
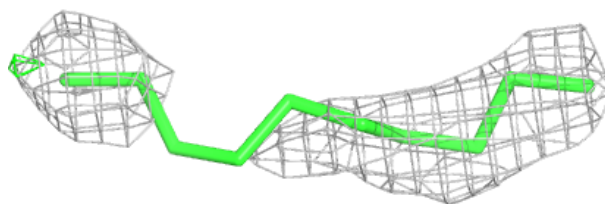


Electron density around LFA A 318:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

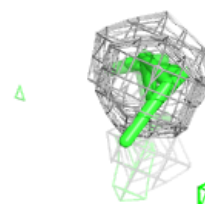
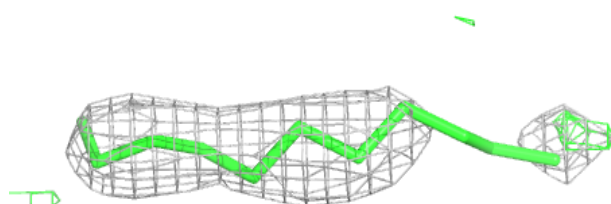
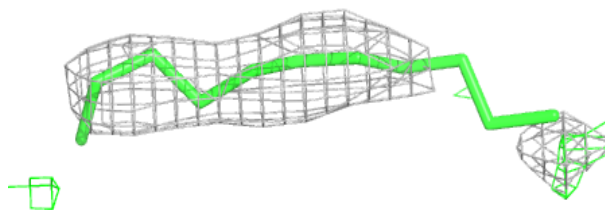
**Electron density around LFA E 317:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

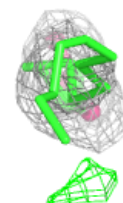
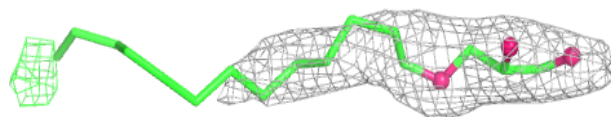
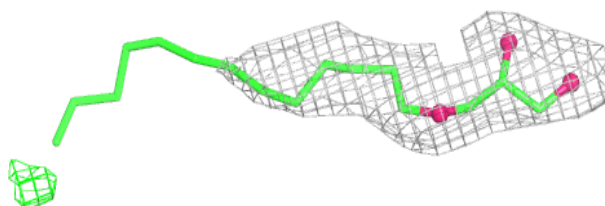


Electron density around LFA B 314:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

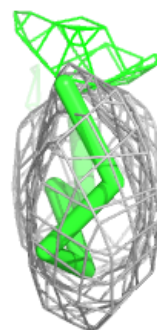
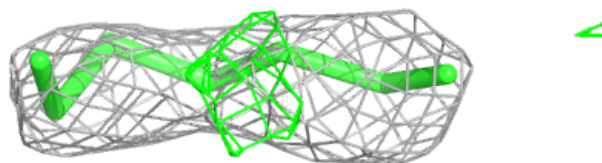
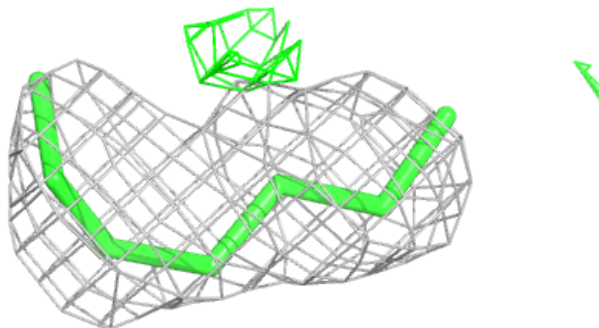
**Electron density around OLC E 307:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

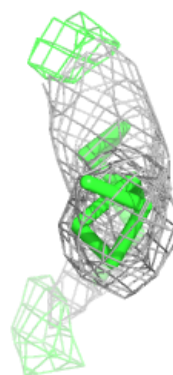
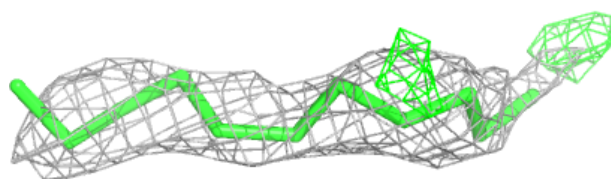
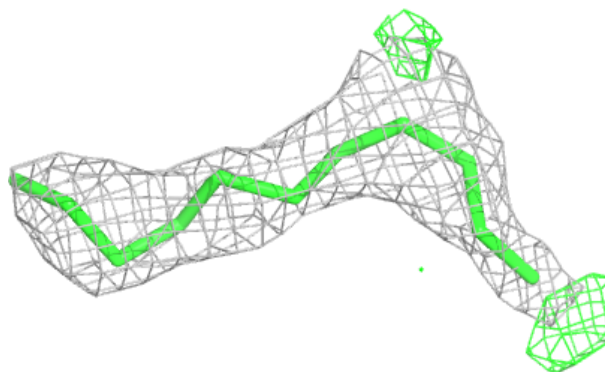


Electron density around LFA A 313:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

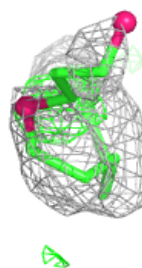
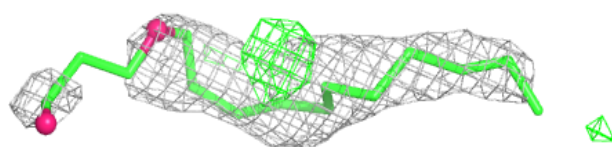
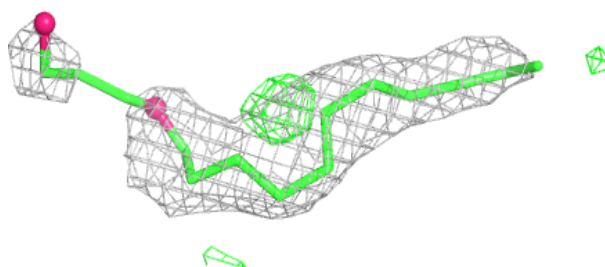
**Electron density around LFA B 313:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

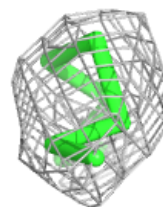
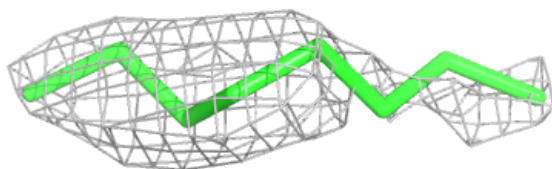
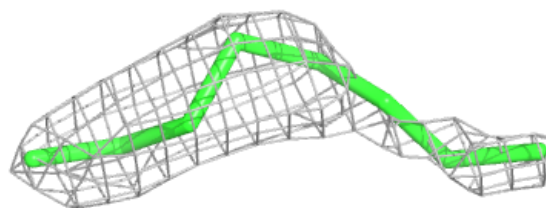


Electron density around OLC C 312:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

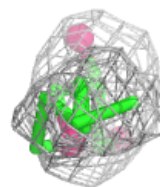
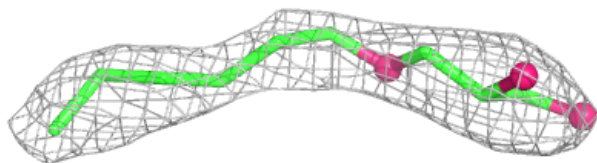
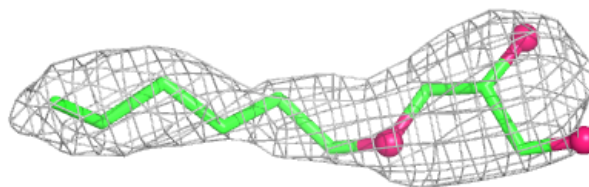
**Electron density around OLC E 305:**

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and green (positive)

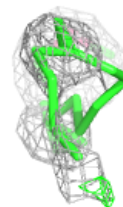
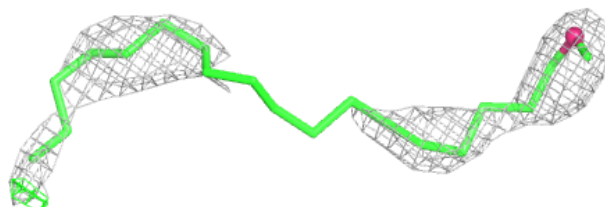


Electron density around OLC A 308:

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and green (positive)

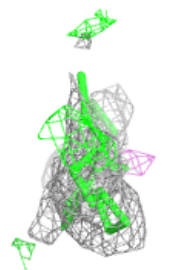
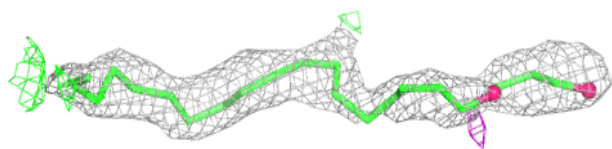
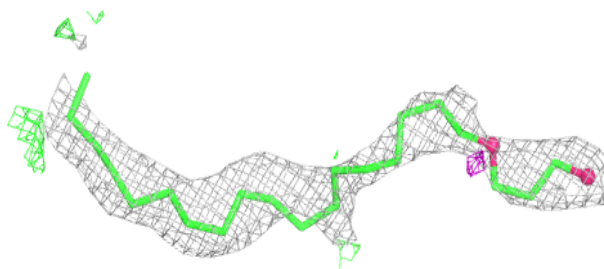
**Electron density around OLC A 309:**

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and green (positive)

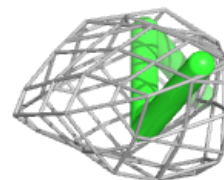
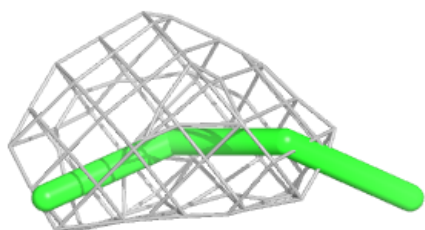
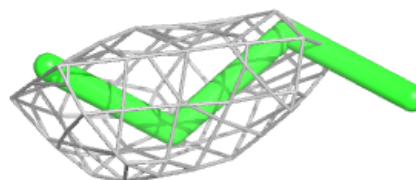


Electron density around OLC A 307:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

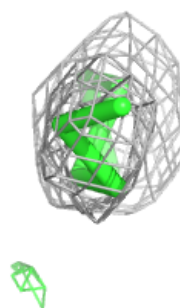
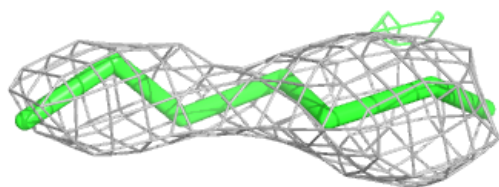
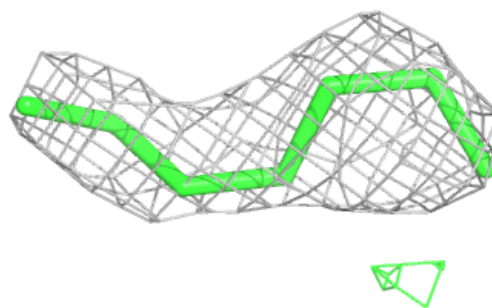
**Electron density around LFA C 311:**

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and green (positive)

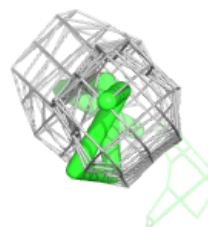
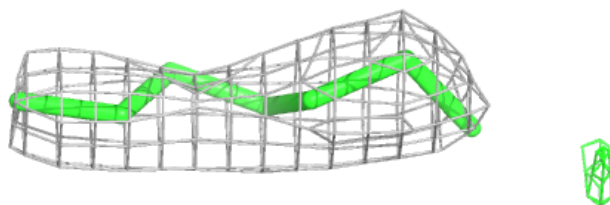
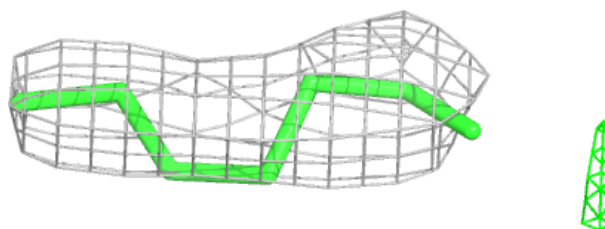


Electron density around LFA B 310:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

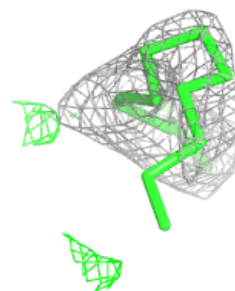
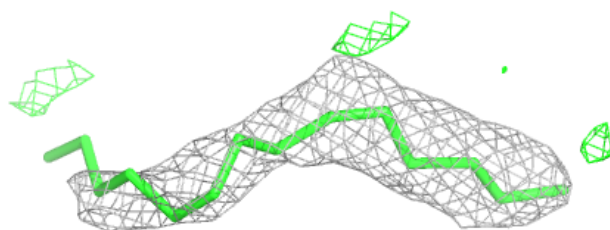
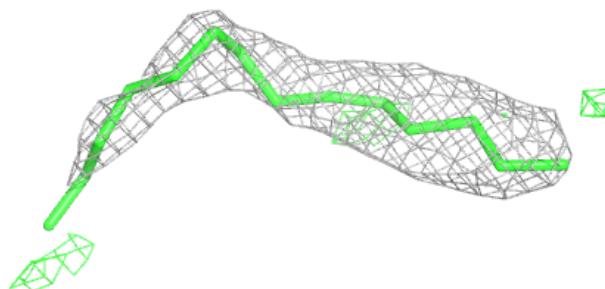
**Electron density around LFA D 314:**

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and green (positive)

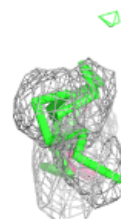
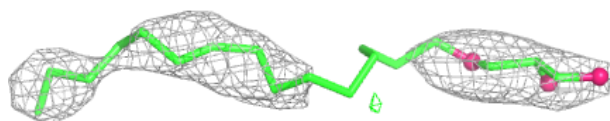
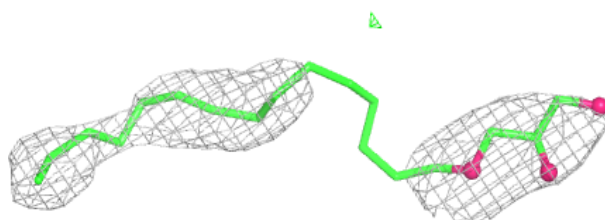


Electron density around OLC B 305:

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and green (positive)

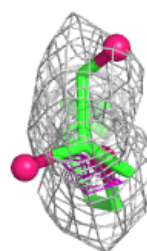
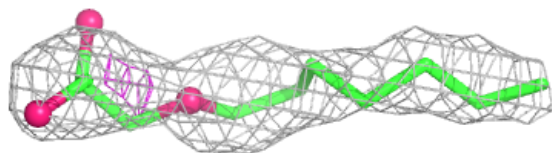
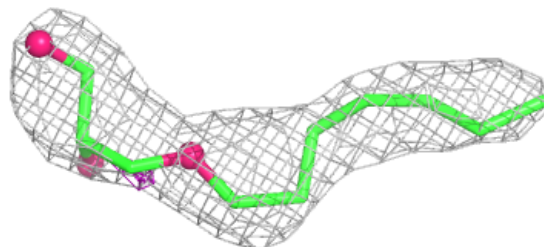
**Electron density around OLC C 305:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

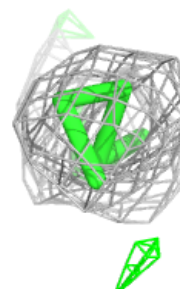
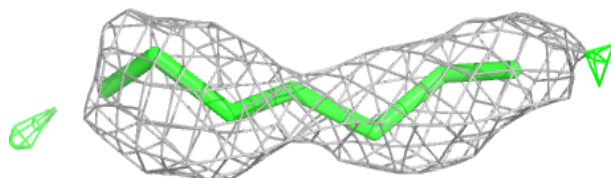
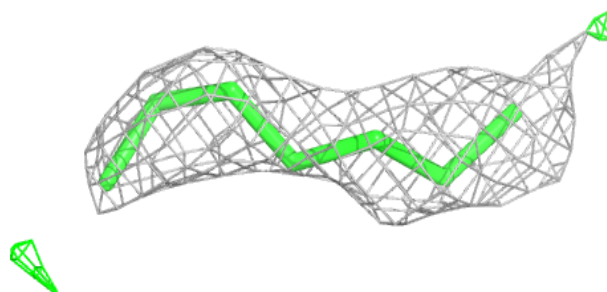


Electron density around OLC D 306:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

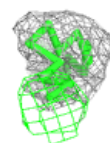
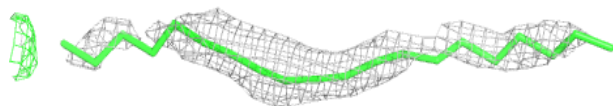
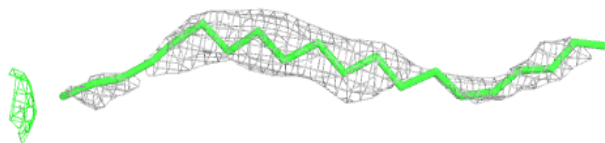
**Electron density around OLC D 307:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

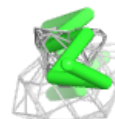
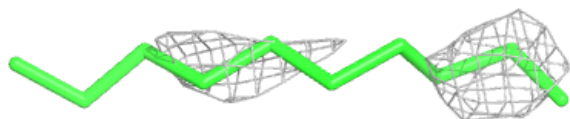
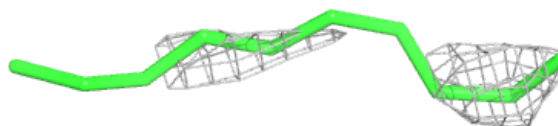


Electron density around LFA D 310:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

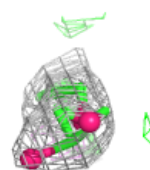
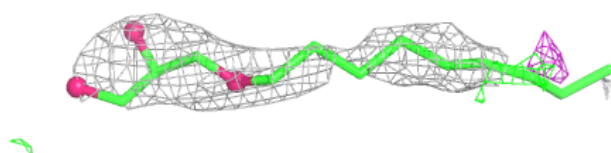
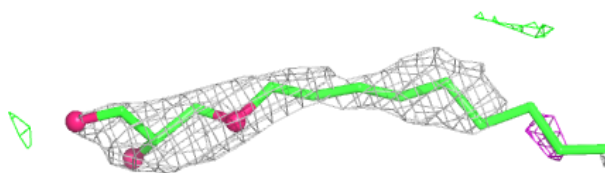
**Electron density around LFA B 309:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



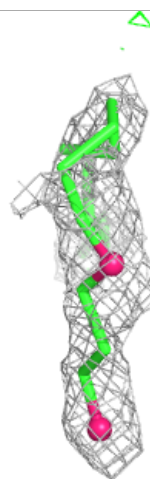
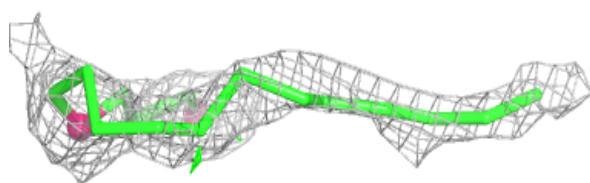
Electron density around OLC A 312:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



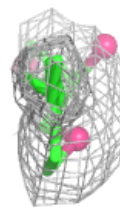
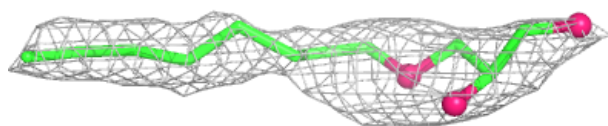
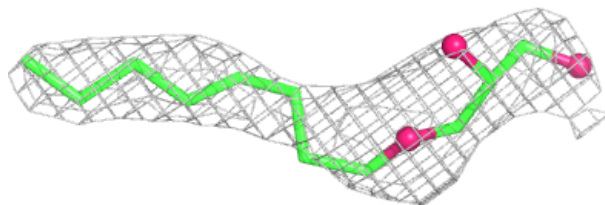
Electron density around OLC B 315:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

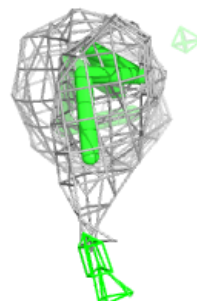
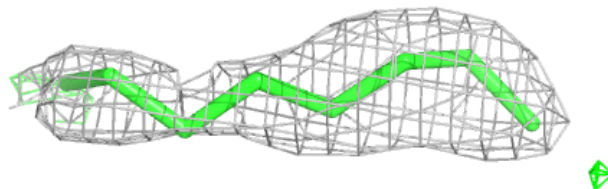
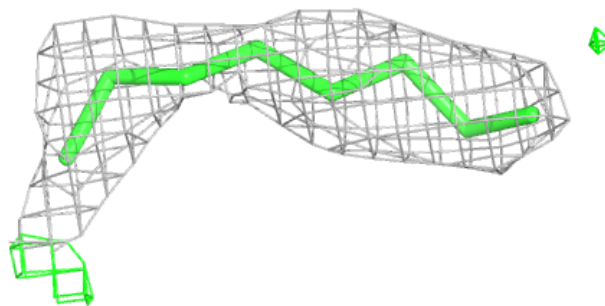


Electron density around OLC E 308:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

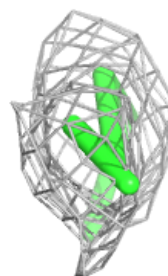
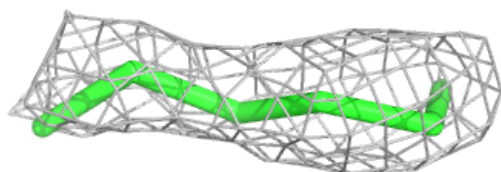
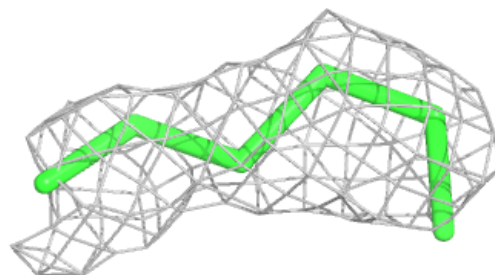
**Electron density around LFA A 314:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

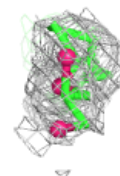
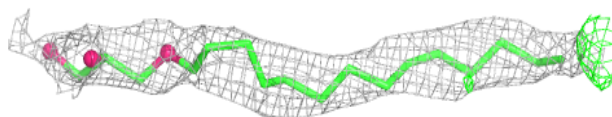
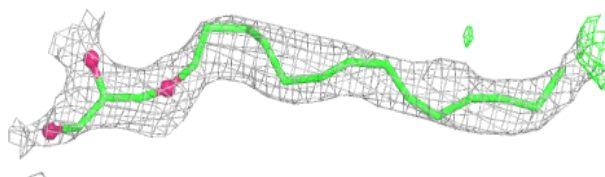


Electron density around OLC C 307:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

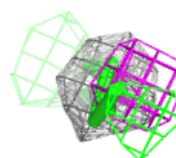
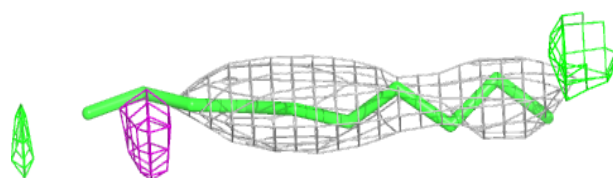
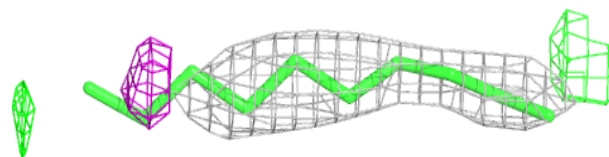
**Electron density around OLC B 303:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

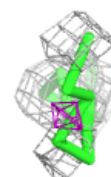
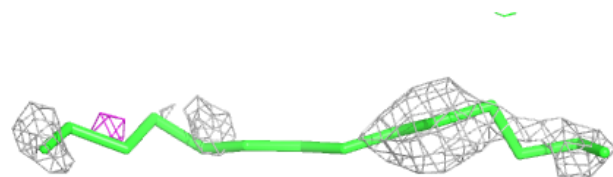
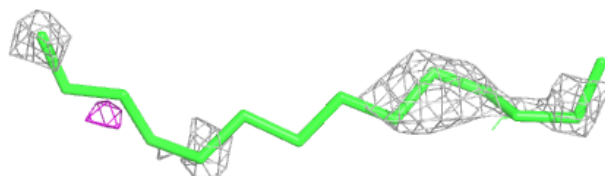


Electron density around LFA E 303:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

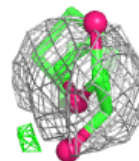
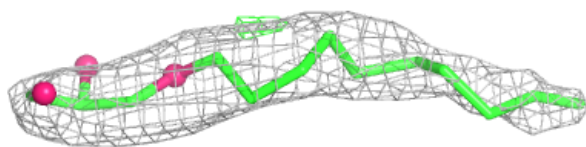
**Electron density around LFA E 312:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

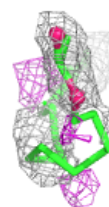
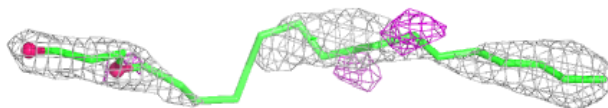
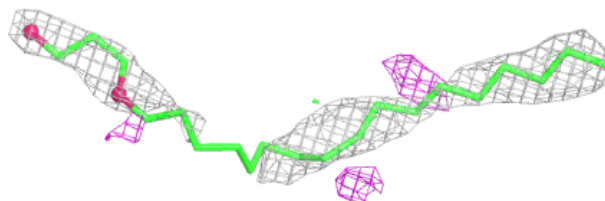


Electron density around OLC C 306:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

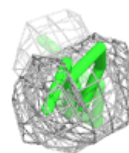
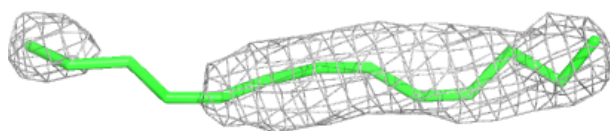
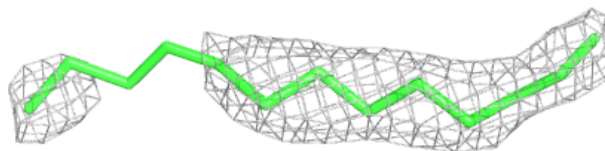
**Electron density around OLC C 303:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

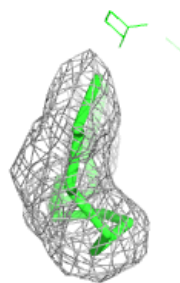
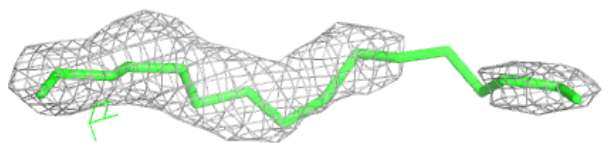
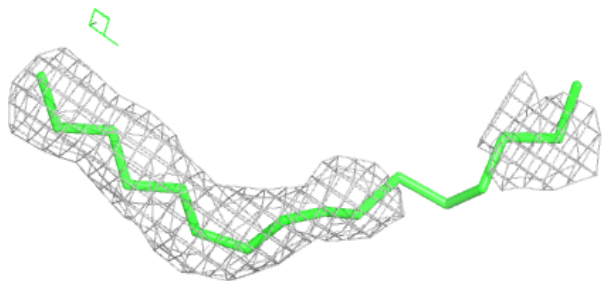


Electron density around OLC B 304:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

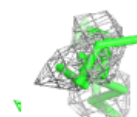
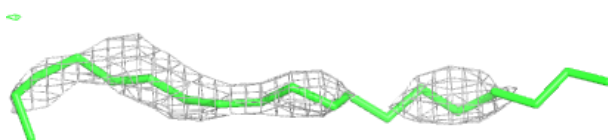
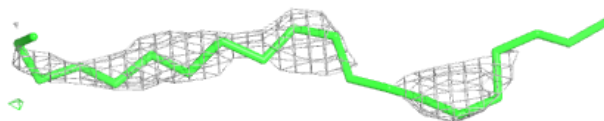
**Electron density around OLC E 306:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

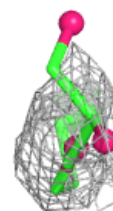
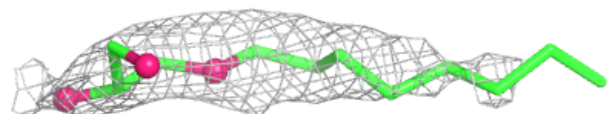
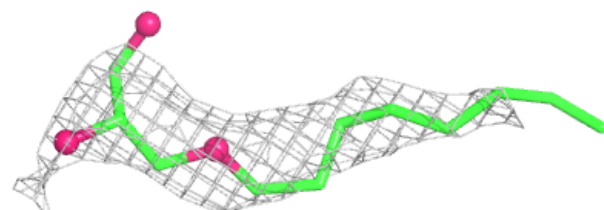


Electron density around LFA D 309:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

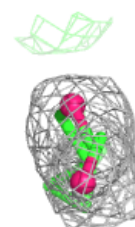
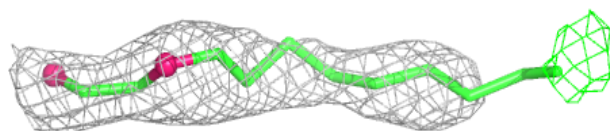
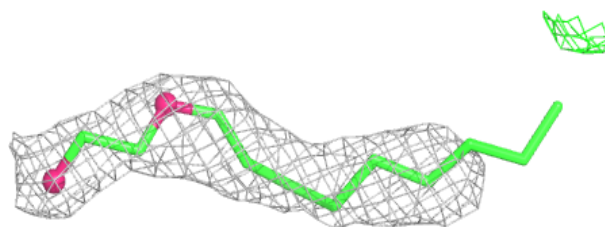
**Electron density around OLC A 310:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

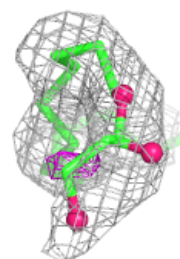
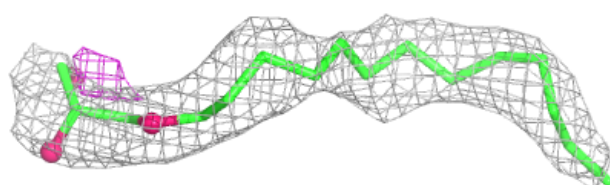
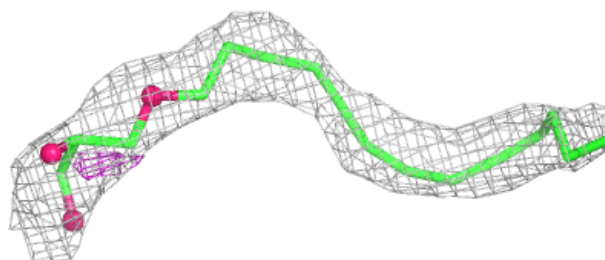


Electron density around OLC B 306:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

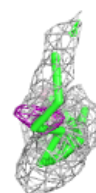
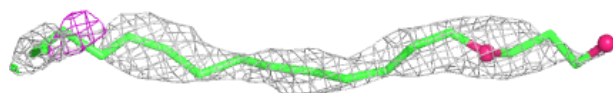
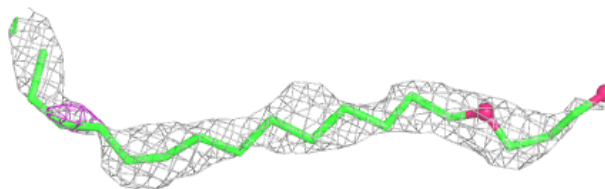
**Electron density around OLC B 312:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

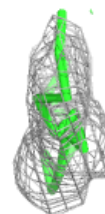
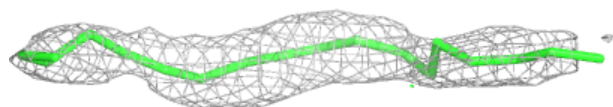
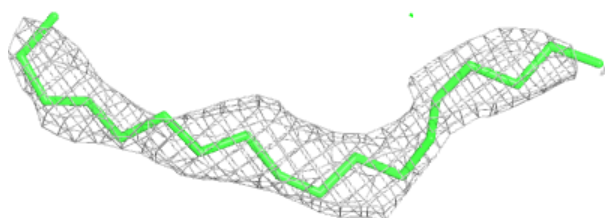


Electron density around OLC E 310:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

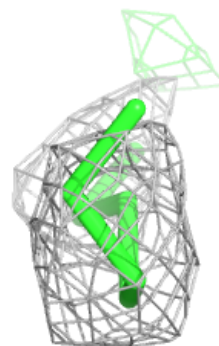
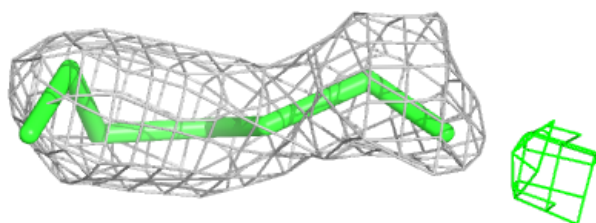
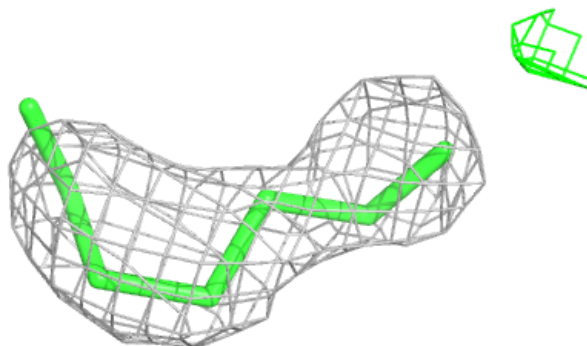
**Electron density around OLC D 304:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

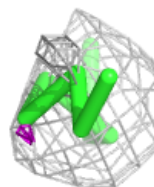
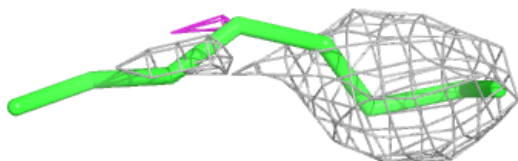
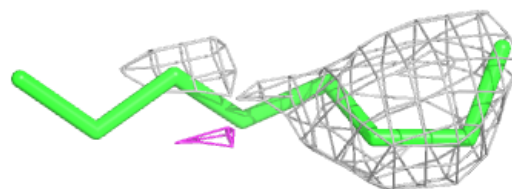


Electron density around OLC A 311:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

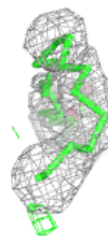
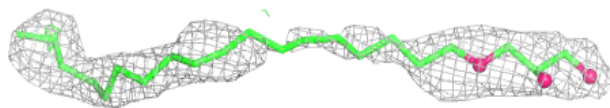
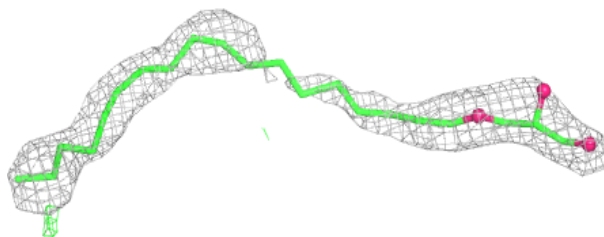
**Electron density around LFA C 308:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

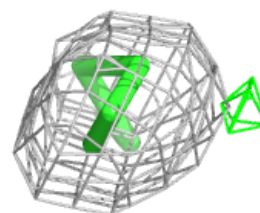
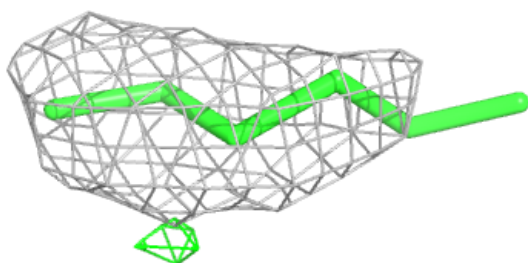
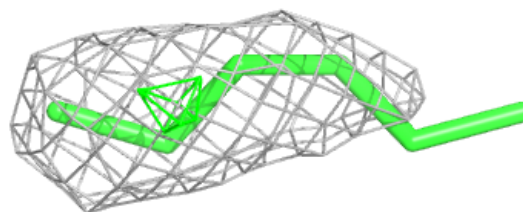


Electron density around OLC D 308:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

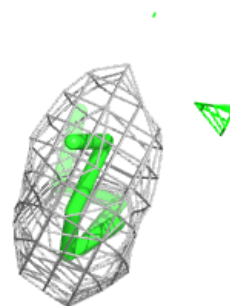
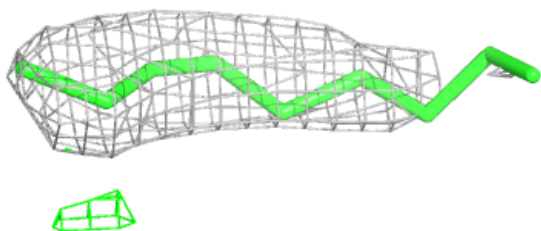
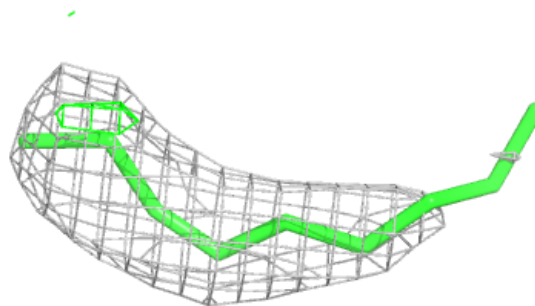
**Electron density around LFA A 317:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

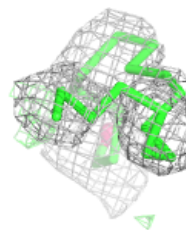
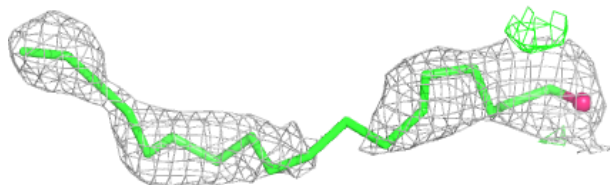
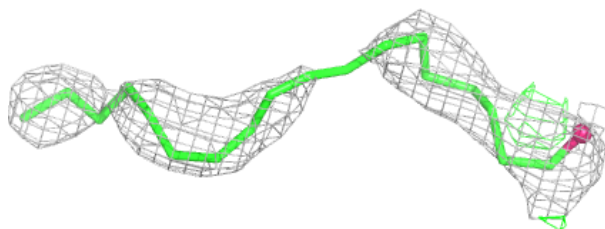


Electron density around OLC A 305:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

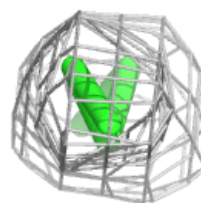
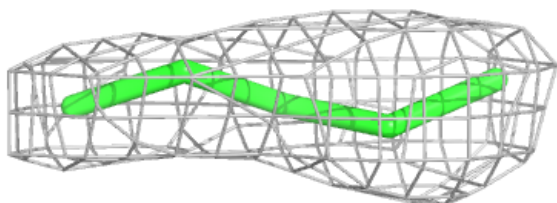
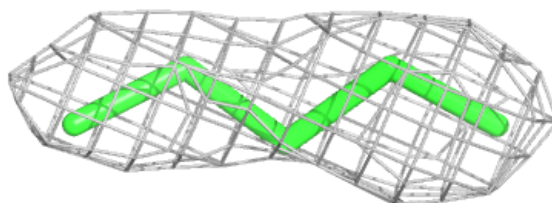
**Electron density around OLC A 319:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

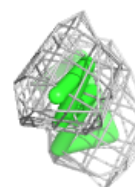
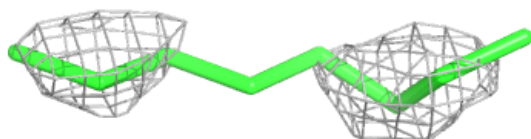
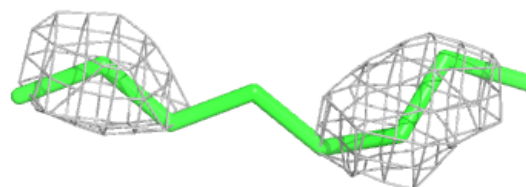


Electron density around LFA C 310:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

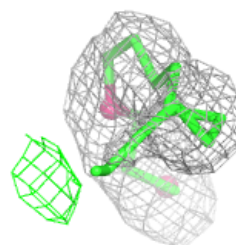
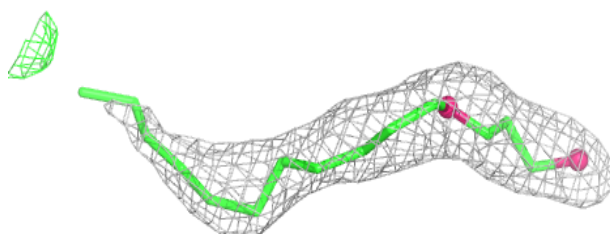
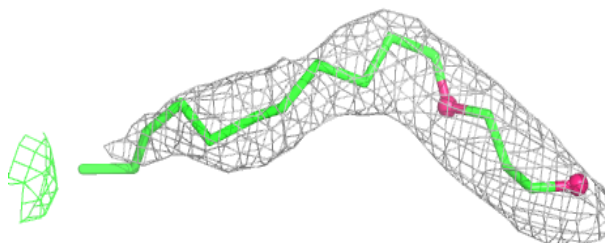
**Electron density around LFA B 308:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

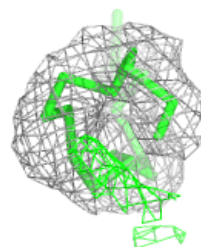
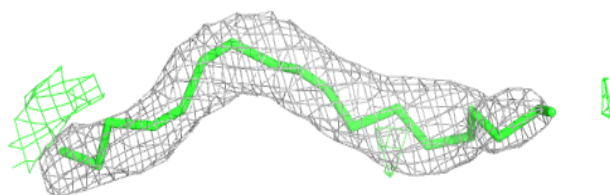
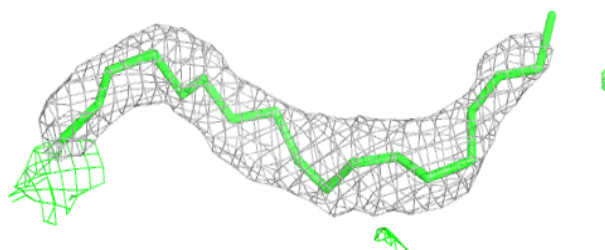


Electron density around OLC A 303:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

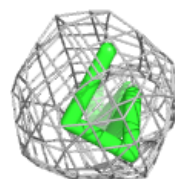
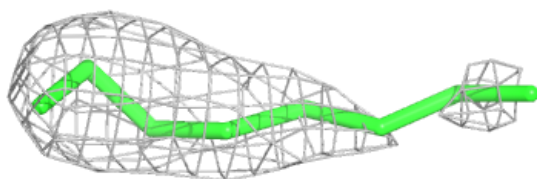
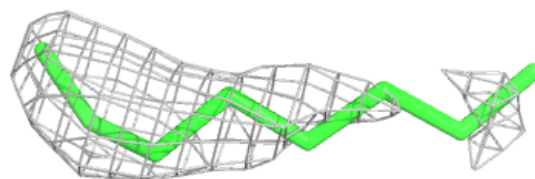
**Electron density around OLC E 304:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

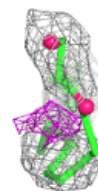
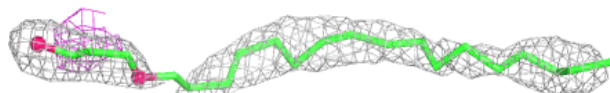
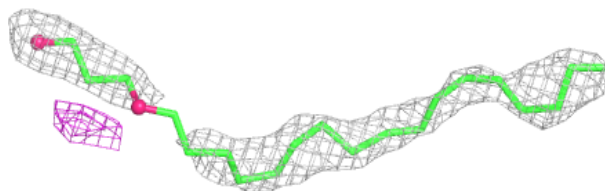


Electron density around LFA E 311:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

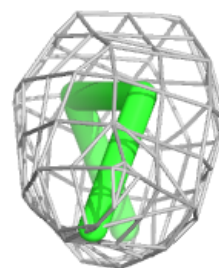
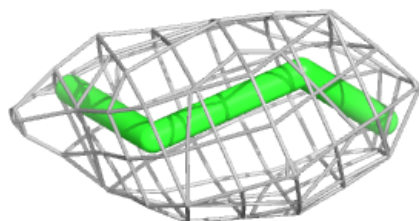
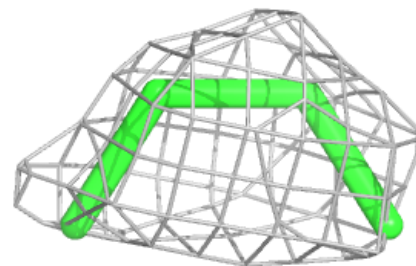
**Electron density around OLC E 318:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

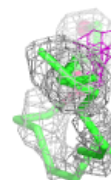
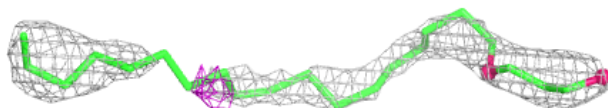
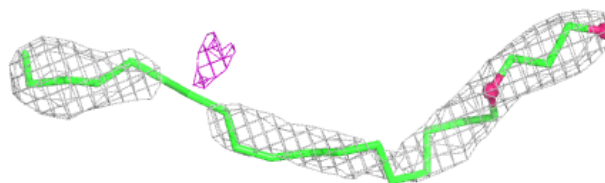


Electron density around LFA E 313:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

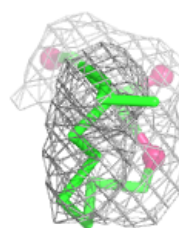
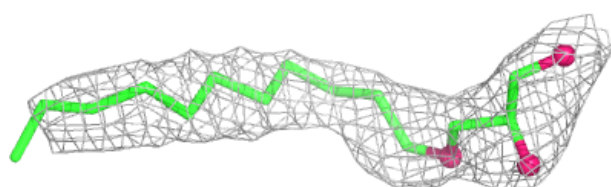
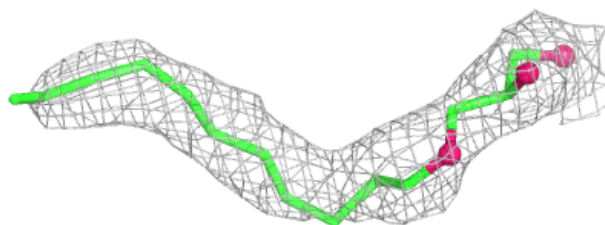
**Electron density around OLC C 316:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

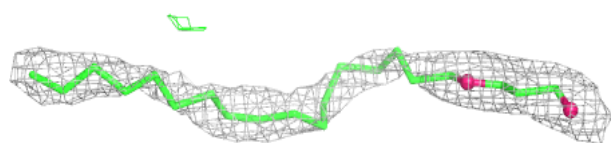
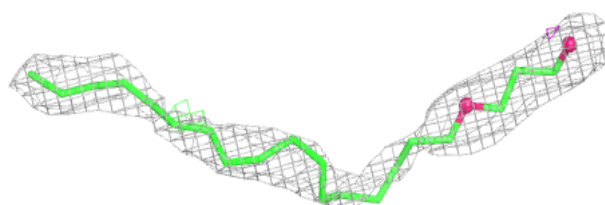


Electron density around OLC D 303:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

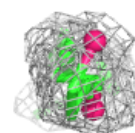
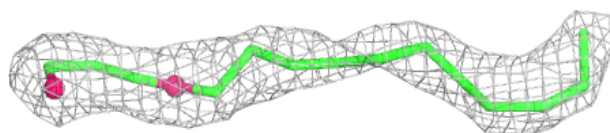
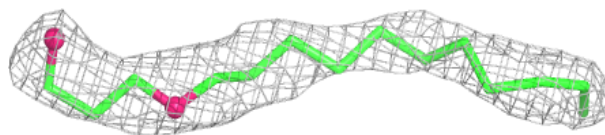
**Electron density around OLC A 321:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

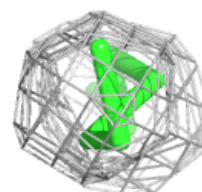
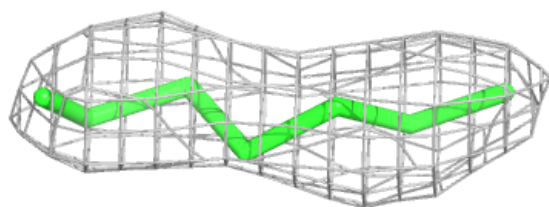
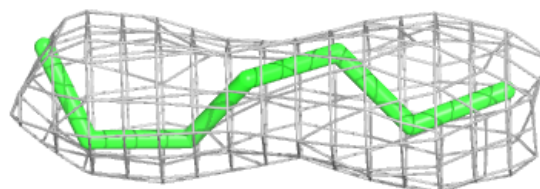


Electron density around OLC D 305:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

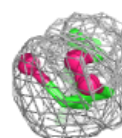
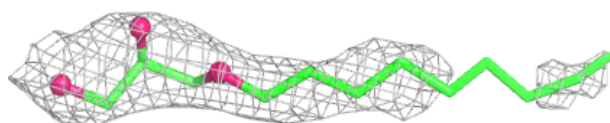
**Electron density around LFA E 315:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

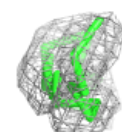
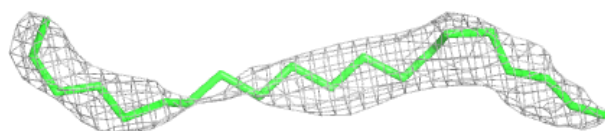


Electron density around OLC C 315:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

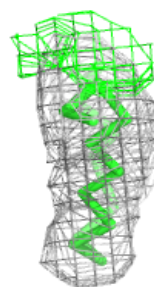
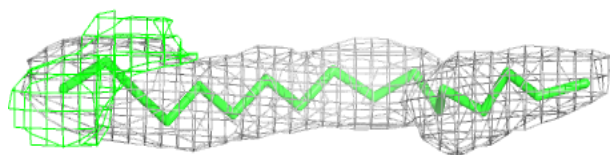
**Electron density around LFA C 309:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

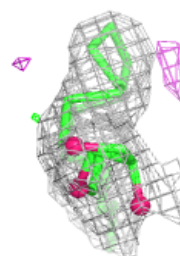
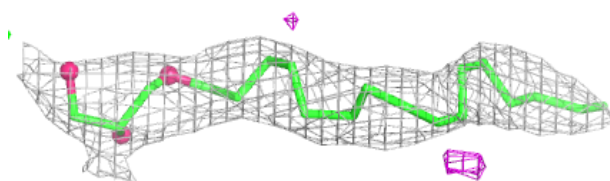


Electron density around LFA D 311:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

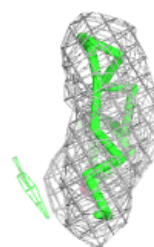
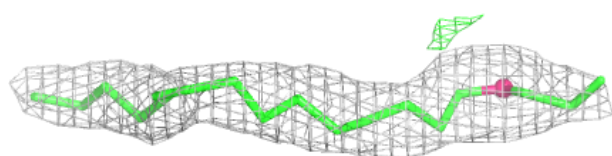
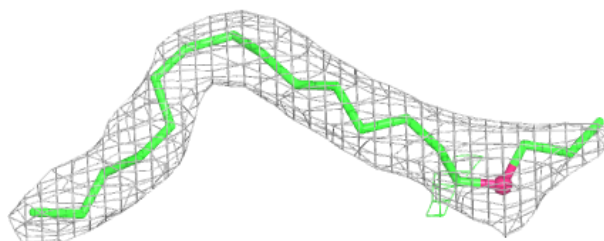
**Electron density around OLC C 304:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

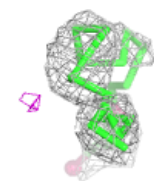
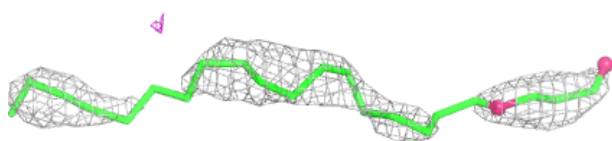
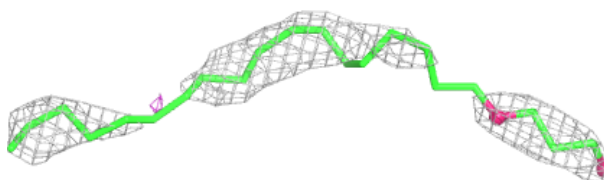


Electron density around OLC A 306:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

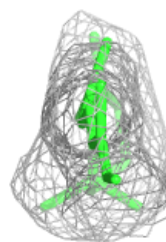
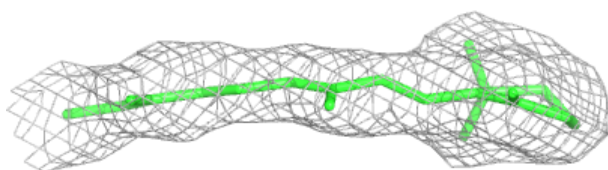
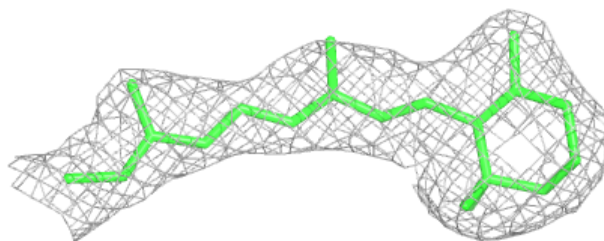
**Electron density around OLC A 304:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

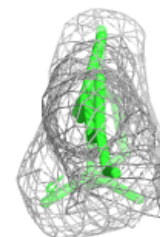
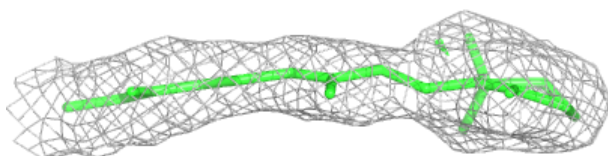
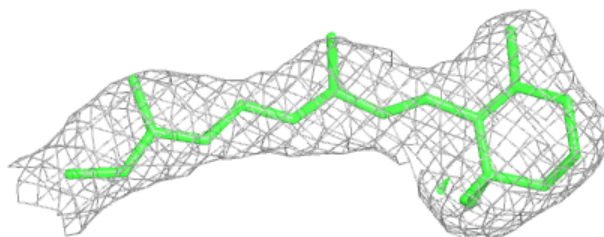


Electron density around RET C 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

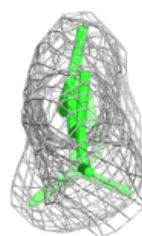
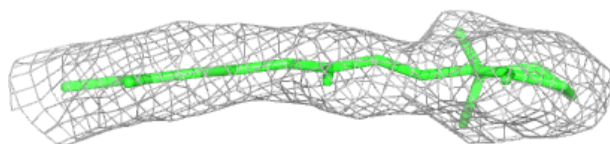
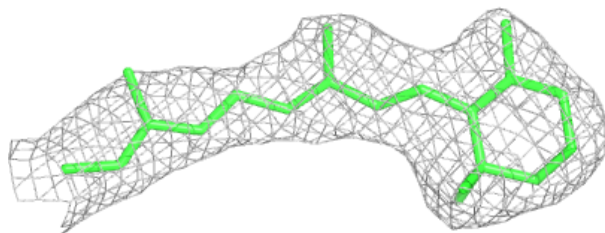
**Electron density around RET D 301:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

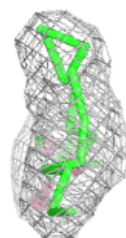
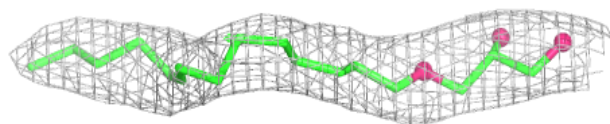
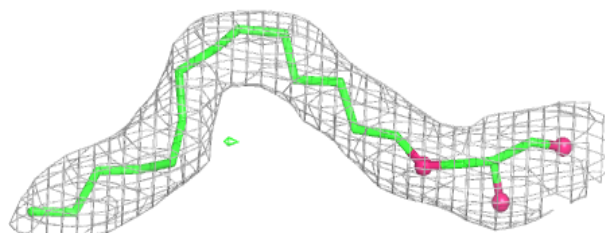


Electron density around RET E 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

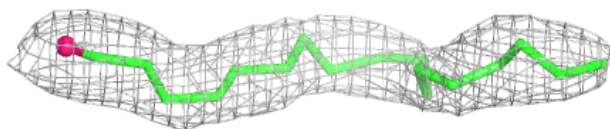
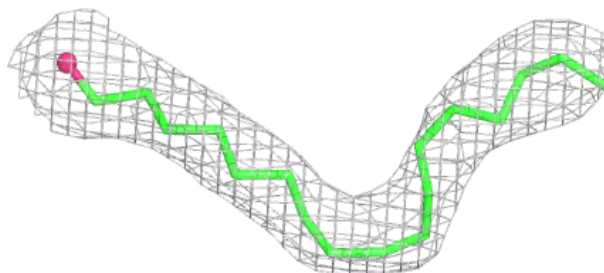
**Electron density around OLC B 311:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

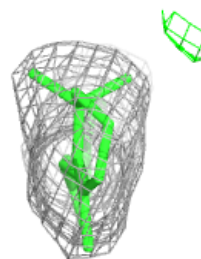
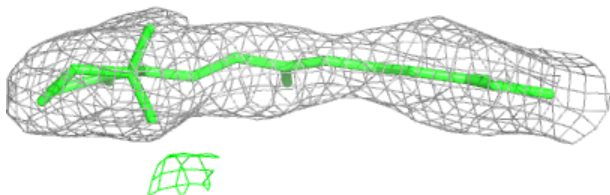
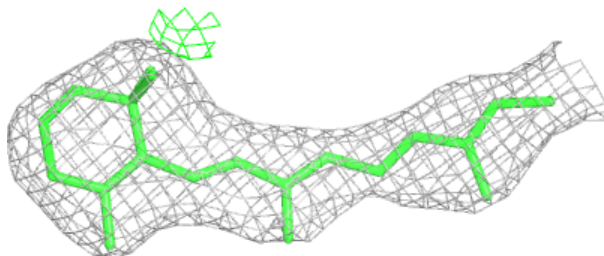


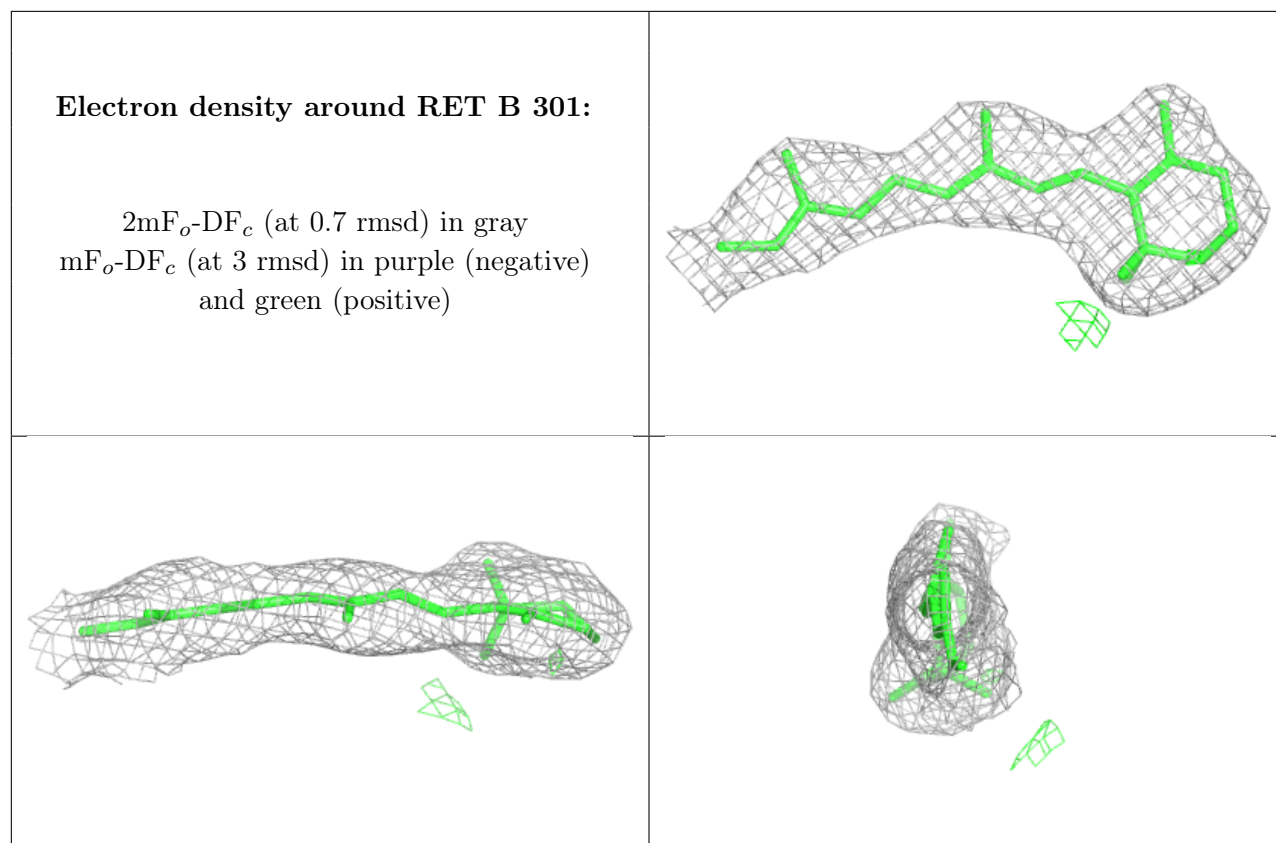
Electron density around OLC E 319:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around RET A 301:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.