



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 20, 2020 – 06:51 PM BST

PDB ID : 6REX
Title : Crystal structure of the light-driven sodium pump KR2 in the pentameric form, pH 6.0
Authors : Kovalev, K.; Polovinkin, V.; Gushchin, I.; Borshchevskiy, V.; Gordeliy, V.
Deposited on : 2019-04-12
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

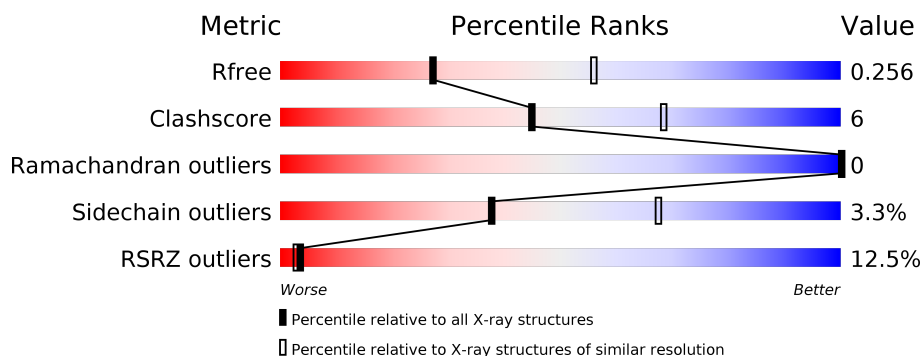
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 on 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	<div> <div>11%</div> <div> <div></div> <div>91%</div> <div>8%</div> </div> </div>
1	B	273	<div> <div>8%</div> <div> <div></div> <div>86%</div> <div>14%</div> </div> </div>
1	C	273	<div> <div>14%</div> <div> <div></div> <div>85%</div> <div>13%</div> <div>•</div> </div> </div>
1	D	273	<div> <div>13%</div> <div> <div></div> <div>89%</div> <div>11%</div> </div> </div>
1	E	273	<div> <div>16%</div> <div> <div></div> <div>86%</div> <div>13%</div> <div>•</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	OLC	B	305	-	-	-	X
2	OLC	C	303	-	-	-	X
2	OLC	C	309	-	-	-	X
2	OLC	D	303	-	-	-	X
2	OLC	D	305	-	-	-	X
2	OLC	E	304	-	-	-	X
3	LFA	A	311	-	-	-	X
3	LFA	B	302	-	-	-	X
3	LFA	B	306	-	-	-	X
3	LFA	C	313	-	-	-	X
3	LFA	C	314	-	-	-	X
3	LFA	D	306	-	-	-	X
3	LFA	D	312	-	-	-	X
5	BOG	A	310	-	-	-	X
5	BOG	B	312	-	-	-	X
5	BOG	C	317	-	-	-	X
5	BOG	D	314	-	-	-	X
5	BOG	E	312	-	-	-	X

2 Entry composition [i](#)

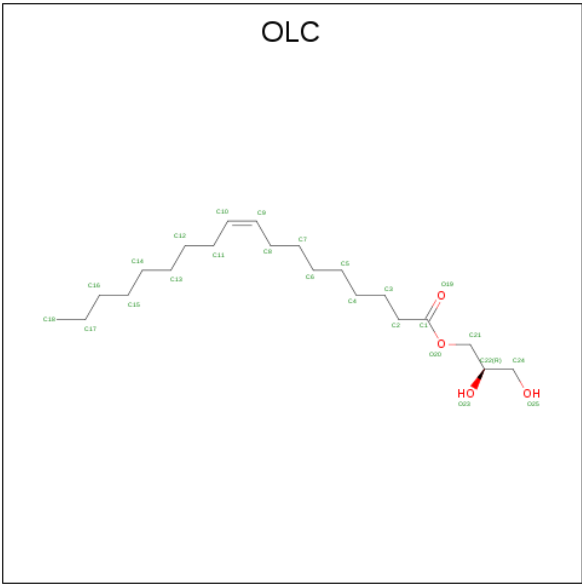
There are 7 unique types of molecules in this entry. The entry contains 12192 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	273	Total	C	N	O	S	0	1	0
			2179	1451	330	389	9			
1	B	273	Total	C	N	O	S	0	1	0
			2173	1446	331	387	9			
1	C	273	Total	C	N	O	S	0	1	0
			2178	1450	330	389	9			
1	D	273	Total	C	N	O	S	0	1	0
			2170	1445	330	386	9			
1	E	273	Total	C	N	O	S	0	1	0
			2172	1447	330	386	9			

- Molecule 2 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLC) (formula: C₂₁H₄₀O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			22	18	4		

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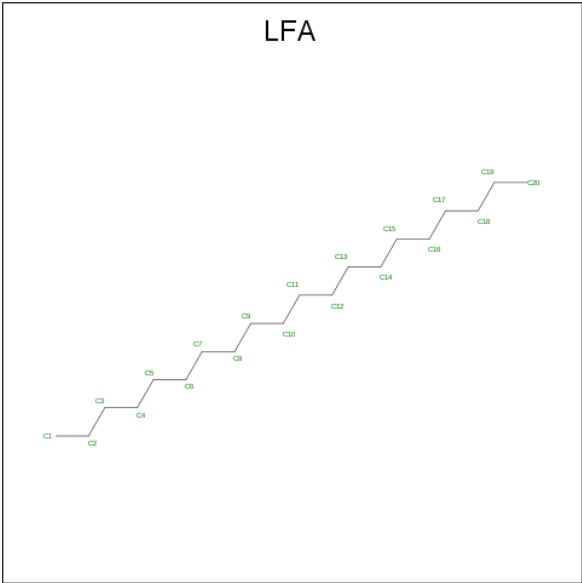
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	9	4		
2	A	1	Total	C	O	0	0
			15	11	4		
2	B	1	Total	C	O	0	0
			25	21	4		
2	B	1	Total	C	O	0	0
			20	16	4		
2	B	1	Total	C	O	0	0
			16	12	4		
2	B	1	Total	C	O	0	0
			17	13	4		
2	C	1	Total	C	O	0	0
			21	17	4		
2	C	1	Total	C	O	0	0
			20	16	4		
2	C	1	Total	C	O	0	0
			16	12	4		
2	C	1	Total	C	O	0	0
			23	19	4		
2	C	1	Total	C	O	0	0
			18	14	4		
2	C	1	Total	C	O	0	0
			15	11	4		
2	C	1	Total	C	O	0	0
			16	12	4		
2	C	1	Total	C	O	0	0
			16	12	4		
2	D	1	Total	C	O	0	0
			25	21	4		
2	D	1	Total	C	O	0	0
			18	14	4		
2	D	1	Total	C	O	0	0
			14	10	4		
2	D	1	Total	C	O	0	0
			25	21	4		
2	E	1	Total	C	O	0	0
			24	20	4		
2	E	1	Total	C	O	0	0
			25	21	4		
2	E	1	Total	C	O	0	0
			15	11	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	E	1	Total	C	O	0	0
			25	21	4		

- Molecule 3 is EICOSANE (three-letter code: LFA) (formula: C₂₀H₄₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	C	0	0
			8	8		
3	A	1	Total	C	0	0
			5	5		
3	A	1	Total	C	0	0
			8	8		
3	A	1	Total	C	0	0
			4	4		
3	A	1	Total	C	0	0
			6	6		
3	A	1	Total	C	0	0
			20	20		
3	B	1	Total	C	0	0
			20	20		
3	B	1	Total	C	0	0
			9	9		
3	B	1	Total	C	0	0
			5	5		
3	B	1	Total	C	0	0
			10	10		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C 7 7	0	0
3	B	1	Total C 6 6	0	0
3	C	1	Total C 20 20	0	0
3	C	1	Total C 7 7	0	0
3	C	1	Total C 8 8	0	0
3	C	1	Total C 12 12	0	0
3	C	1	Total C 11 11	0	0
3	C	1	Total C 4 4	0	0
3	C	1	Total C 6 6	0	0
3	D	1	Total C 20 20	0	0
3	D	1	Total C 20 20	0	0
3	D	1	Total C 20 20	0	0
3	D	1	Total C 8 8	0	0
3	D	1	Total C 17 17	0	0
3	D	1	Total C 7 7	0	0
3	D	1	Total C 6 6	0	0
3	D	1	Total C 20 20	0	0
3	E	1	Total C 8 8	0	0
3	E	1	Total C 6 6	0	0
3	E	1	Total C 14 14	0	0
3	E	1	Total C 4 4	0	0

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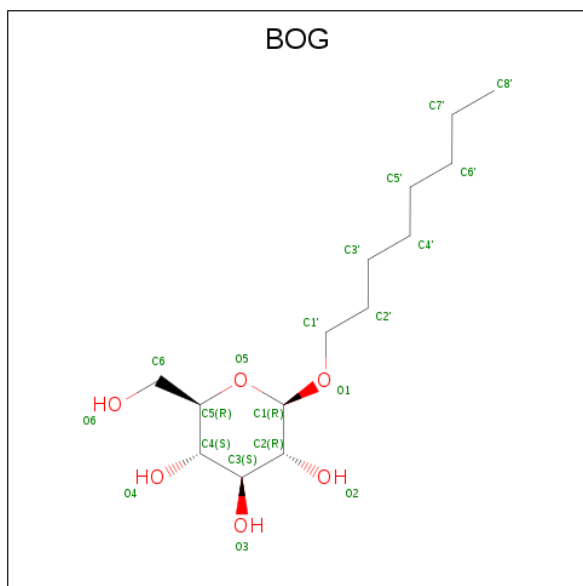
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	1	Total C 5 5	0	0
3	E	1	Total C 6 6	0	0
3	E	1	Total C 4 4	0	0
3	E	1	Total C 14 14	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

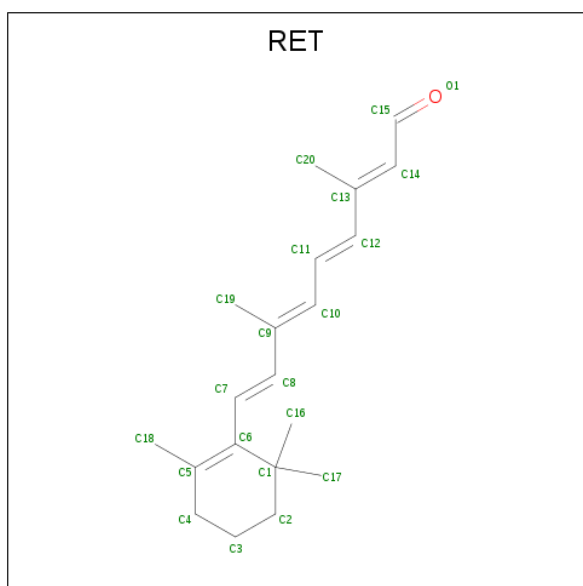
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Na 1 1	0	0
4	A	1	Total Na 1 1	0	0
4	D	1	Total Na 1 1	0	0
4	C	1	Total Na 1 1	0	0
4	E	1	Total Na 1 1	0	0

- Molecule 5 is octyl beta-D-glucopyranoside (three-letter code: BOG) (formula: C₁₄H₂₈O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			20	14	6		
5	B	1	Total	C	O	0	0
			20	14	6		
5	C	1	Total	C	O	0	0
			20	14	6		
5	D	1	Total	C	O	0	0
			20	14	6		
5	E	1	Total	C	O	0	0
			20	14	6		

- Molecule 6 is RETINAL (three-letter code: RET) (formula: C₂₀H₂₈O).



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

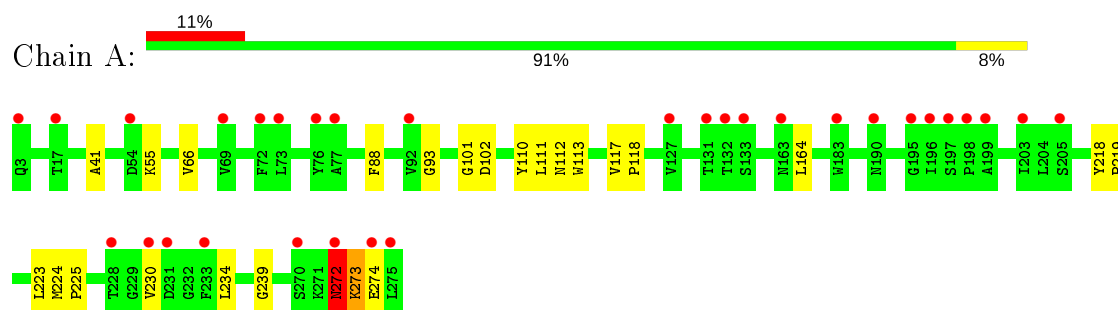
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	64	Total 64	O 64	0	0
7	B	66	Total 66	O 66	0	0
7	C	76	Total 76	O 76	0	0
7	D	41	Total 41	O 41	0	0
7	E	69	Total 69	O 69	0	0

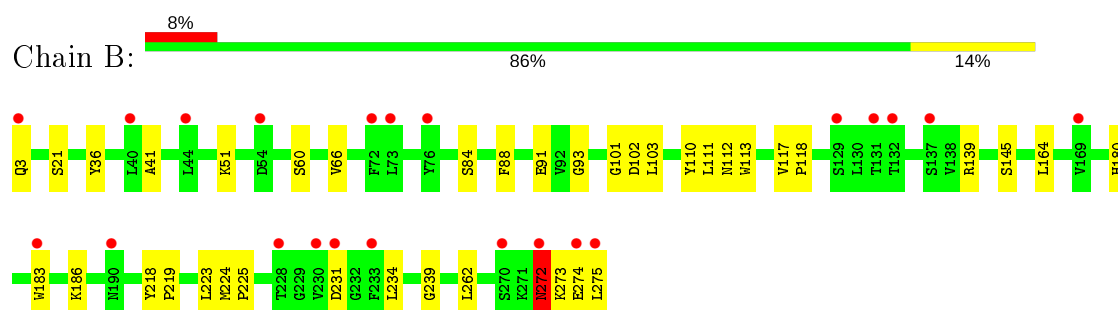
3 Residue-property plots

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.

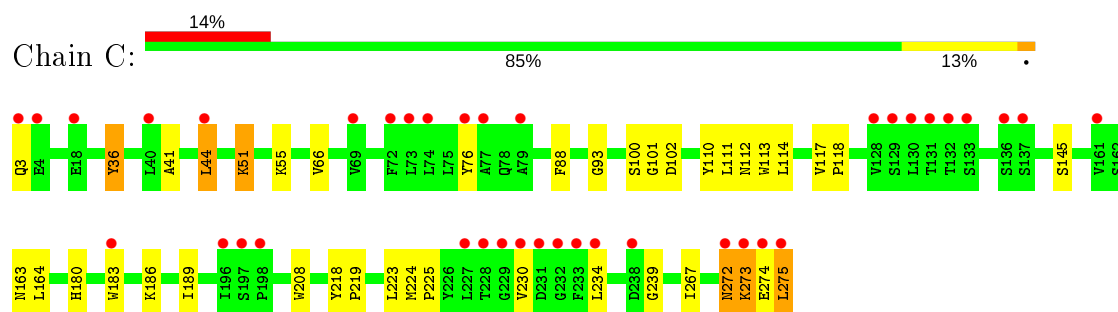
- Molecule 1: Sodium pumping rhodopsin



- Molecule 1: Sodium pumping rhodopsin

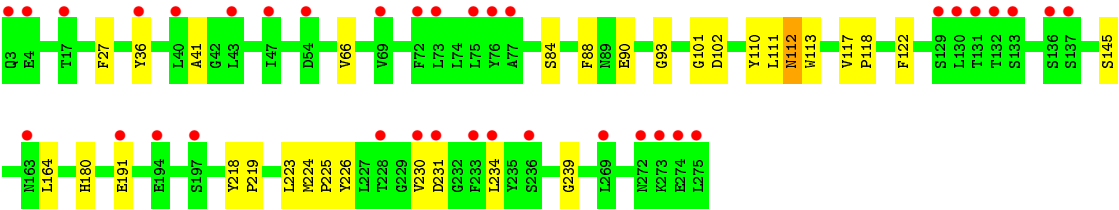


- Molecule 1: Sodium pumping rhodopsin

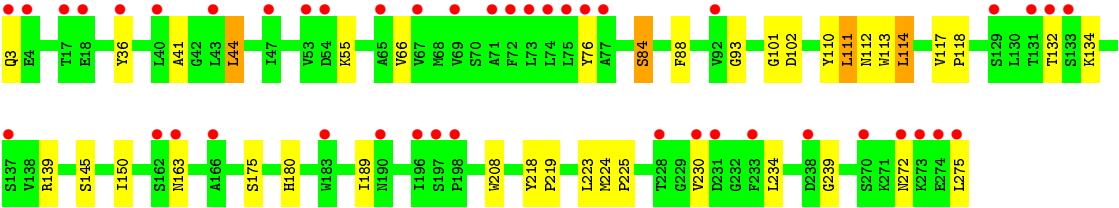
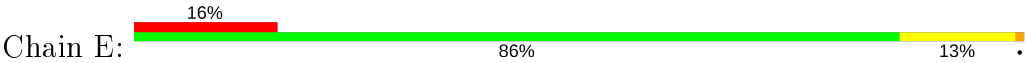


- Molecule 1: Sodium pumping rhodopsin





● Molecule 1: Sodium pumping rhodopsin



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	131.43Å 240.79Å 135.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.26 – 2.70 48.21 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.5 (48.26-2.70) 96.5 (48.21-2.70)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.223 , 0.250 0.232 , 0.256	Depositor DCC
R_{free} test set	2803 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	45.4	Xtriage
Anisotropy	0.565	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 51.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.000 for 1/2*h+1/2*k,3/2*h-1/2*k,-l 0.000 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12192	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.62% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, OLC, LFA, RET, BOG

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	0.27	0/2237	0.41	0/3041
1	B	0.27	0/2231	0.41	0/3034
1	C	0.26	0/2236	0.41	0/3040
1	D	0.26	0/2228	0.41	0/3029
1	E	0.26	0/2230	0.41	0/3032
All	All	0.27	0/11162	0.41	0/15176

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	E	0	2
All	All	0	5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	272	ASN	Peptide
1	B	272	ASN	Peptide
1	C	272	ASN	Peptide
1	E	139	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	E	272	ASN	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2179	0	2154	19	0
1	B	2173	0	2149	34	0
1	C	2178	0	2152	28	0
1	D	2170	0	2142	23	0
1	E	2172	0	2150	24	0
2	A	50	0	65	0	0
2	B	78	0	110	4	0
2	C	145	0	194	6	0
2	D	82	0	120	4	0
2	E	89	0	134	1	0
3	A	51	0	99	0	0
3	B	57	0	111	3	0
3	C	68	0	132	5	0
3	D	118	0	240	1	0
3	E	61	0	114	3	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
5	A	20	0	28	2	0
5	B	20	0	28	2	0
5	C	20	0	28	1	0
5	D	20	0	28	4	0
5	E	20	0	28	0	0
6	A	20	0	27	5	0
6	B	20	0	27	4	0
6	C	20	0	27	5	0
6	D	20	0	27	5	0
6	E	20	0	27	6	0
7	A	64	0	0	1	0
7	B	66	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	76	0	0	5	0
7	D	41	0	0	2	0
7	E	69	0	0	1	0
All	All	12192	0	12341	157	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 6.

The worst 5 of 157 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:272:ASN:N	1:B:272:ASN:HD22	1.66	0.90
1:A:272:ASN:HD22	1:A:272:ASN:N	1.69	0.89
6:E:315:RET:H161	6:E:315:RET:H8	1.59	0.85
6:D:315:RET:H8	6:D:315:RET:H161	1.60	0.84
6:A:312:RET:H161	6:A:312:RET:H8	1.60	0.83

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	272/273 (100%)	266 (98%)	6 (2%)	0	100	100
1	B	272/273 (100%)	264 (97%)	8 (3%)	0	100	100
1	C	272/273 (100%)	267 (98%)	5 (2%)	0	100	100
1	D	272/273 (100%)	266 (98%)	6 (2%)	0	100	100
1	E	272/273 (100%)	267 (98%)	5 (2%)	0	100	100
All	All	1360/1365 (100%)	1330 (98%)	30 (2%)	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	231/234 (99%)	224 (97%)	7 (3%)	41	70
1	B	231/234 (99%)	225 (97%)	6 (3%)	46	75
1	C	231/234 (99%)	221 (96%)	10 (4%)	29	57
1	D	229/234 (98%)	223 (97%)	6 (3%)	46	75
1	E	230/234 (98%)	219 (95%)	11 (5%)	25	53
All	All	1152/1170 (98%)	1112 (96%)	40 (4%)	38	65

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	112	ASN
1	C	275	LEU
1	E	132	THR
1	C	273	LYS
1	D	36	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	3	GLN
1	E	180	HIS
1	C	180	HIS
1	B	180	HIS
1	D	180	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 73 ligands modelled in this entry, 5 are monoatomic - leaving 68 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	$\# Z > 2$
2	OLC	C	303	-	15,15,24	1.23	1 (6%)	16,16,25	1.02	1 (6%)
3	LFA	A	307	-	3,3,19	0.38	0	2,2,18	0.58	0
3	LFA	D	312	-	19,19,19	0.38	0	18,18,18	0.35	0
3	LFA	A	308	-	5,5,19	0.29	0	4,4,18	0.32	0
2	OLC	D	305	-	24,24,24	0.94	1 (4%)	25,25,25	0.81	1 (4%)
2	OLC	B	301	-	24,24,24	0.94	1 (4%)	25,25,25	0.86	1 (4%)
3	LFA	D	311	-	5,5,19	0.32	0	4,4,18	0.31	0
3	LFA	C	315	-	5,5,19	0.31	0	4,4,18	0.30	0
5	BOG	A	310	-	20,20,20	0.59	1 (5%)	25,25,25	0.67	0
3	LFA	B	308	-	9,9,19	0.31	0	8,8,18	0.43	0
3	LFA	B	310	-	5,5,19	0.27	0	4,4,18	0.36	0
2	OLC	C	309	-	15,15,24	1.25	1 (6%)	16,16,25	1.04	1 (6%)
2	OLC	A	302	-	12,12,24	1.32	1 (8%)	13,13,25	1.23	2 (15%)
3	LFA	A	305	-	4,4,19	0.30	0	3,3,18	0.38	0
3	LFA	C	304	-	19,19,19	0.37	0	18,18,18	0.33	0
5	BOG	C	317	-	20,20,20	0.56	1 (5%)	25,25,25	0.62	0
3	LFA	E	313	-	3,3,19	0.39	0	2,2,18	0.57	0
3	LFA	E	308	-	3,3,19	0.37	0	2,2,18	0.60	0
3	LFA	E	314	-	13,13,19	0.29	0	12,12,18	0.50	0
5	BOG	E	312	-	20,20,20	0.57	1 (5%)	25,25,25	0.55	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	RET	A	312	1	20,20,21	0.72	0	27,27,28	1.62	4 (14%)
3	LFA	B	306	-	8,8,19	0.30	0	7,7,18	0.41	0
2	OLC	C	305	-	22,22,24	0.96	1 (4%)	23,23,25	0.87	2 (8%)
3	LFA	C	310	-	6,6,19	0.31	0	5,5,18	0.36	0
6	RET	D	315	1	20,20,21	0.71	0	27,27,28	1.59	4 (14%)
2	OLC	E	302	-	24,24,24	0.94	1 (4%)	25,25,25	0.89	1 (4%)
2	OLC	A	301	-	21,21,24	0.98	1 (4%)	22,22,25	0.87	2 (9%)
2	OLC	B	303	-	19,19,24	1.07	1 (5%)	20,20,25	0.90	1 (5%)
3	LFA	D	310	-	6,6,19	0.29	0	5,5,18	0.38	0
3	LFA	E	309	-	4,4,19	0.29	0	3,3,18	0.35	0
3	LFA	C	313	-	10,10,19	0.29	0	9,9,18	0.52	0
2	OLC	B	305	-	16,16,24	1.17	1 (6%)	17,17,25	0.97	1 (5%)
2	OLC	D	304	-	13,13,24	1.22	1 (7%)	14,14,25	1.02	2 (14%)
3	LFA	E	305	-	7,7,19	0.30	0	6,6,18	0.39	0
3	LFA	A	304	-	7,7,19	0.31	0	6,6,18	0.38	0
3	LFA	C	314	-	3,3,19	0.37	0	2,2,18	0.59	0
3	LFA	B	309	-	6,6,19	0.27	0	5,5,18	0.42	0
5	BOG	D	314	-	20,20,20	0.53	0	25,25,25	0.68	0
2	OLC	E	304	-	24,24,24	0.94	1 (4%)	25,25,25	0.82	2 (8%)
3	LFA	A	306	-	7,7,19	0.29	0	6,6,18	0.40	0
3	LFA	D	301	-	19,19,19	0.36	0	18,18,18	0.38	0
3	LFA	E	306	-	5,5,19	0.43	0	4,4,18	0.32	0
3	LFA	D	306	-	19,19,19	0.27	0	18,18,18	0.57	0
3	LFA	C	311	-	7,7,19	0.32	0	6,6,18	0.32	0
2	OLC	C	301	-	20,20,24	1.01	1 (5%)	21,21,25	0.95	1 (4%)
6	RET	C	318	1	20,20,21	0.73	0	27,27,28	1.59	3 (11%)
2	OLC	E	301	-	23,23,24	0.96	1 (4%)	24,24,25	0.87	1 (4%)
2	OLC	C	306	-	17,17,24	1.11	1 (5%)	18,18,25	0.98	1 (5%)
2	OLC	B	304	-	15,15,24	1.14	1 (6%)	16,16,25	1.05	2 (12%)
3	LFA	C	312	-	11,11,19	0.31	0	10,10,18	0.43	0
3	LFA	B	302	-	19,19,19	0.36	0	18,18,18	0.40	0
2	OLC	C	308	-	15,15,24	1.19	1 (6%)	16,16,25	0.92	1 (6%)
3	LFA	D	308	-	7,7,19	0.31	0	6,6,18	0.34	0
2	OLC	D	303	-	17,17,24	1.16	1 (5%)	18,18,25	1.03	1 (5%)
3	LFA	D	309	-	16,16,19	0.30	0	15,15,18	0.49	0
6	RET	B	313	1	20,20,21	0.76	0	27,27,28	1.63	5 (18%)
2	OLC	D	302	-	24,24,24	0.93	1 (4%)	25,25,25	0.87	1 (4%)
3	LFA	E	307	-	13,13,19	0.27	0	12,12,18	0.54	0
3	LFA	E	310	-	5,5,19	0.31	0	4,4,18	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	RET	E	315	1	20,20,21	0.74	0	27,27,28	1.56	4 (14%)
3	LFA	A	311	-	19,19,19	0.36	0	18,18,18	0.38	0
3	LFA	D	307	-	19,19,19	0.27	0	18,18,18	0.55	0
2	OLC	C	307	-	14,14,24	1.23	1 (7%)	15,15,25	1.01	1 (6%)
2	OLC	C	302	-	19,19,24	1.05	1 (5%)	20,20,25	0.92	2 (10%)
2	OLC	E	303	-	14,14,24	1.27	1 (7%)	15,15,25	1.05	1 (6%)
3	LFA	B	307	-	4,4,19	0.34	0	3,3,18	0.29	0
5	BOG	B	312	-	20,20,20	0.55	0	25,25,25	0.64	0
2	OLC	A	303	-	14,14,24	1.19	1 (7%)	15,15,25	1.05	2 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OLC	C	303	-	-	7/15/15/24	-
3	LFA	A	307	-	-	0/1/1/17	-
3	LFA	D	312	-	-	5/17/17/17	-
3	LFA	A	308	-	-	3/3/3/17	-
2	OLC	D	305	-	-	14/24/24/24	-
2	OLC	B	301	-	-	10/24/24/24	-
3	LFA	D	311	-	-	1/3/3/17	-
3	LFA	C	315	-	-	3/3/3/17	-
5	BOG	A	310	-	-	4/11/31/31	0/1/1/1
3	LFA	B	308	-	-	4/7/7/17	-
3	LFA	B	310	-	-	1/3/3/17	-
2	OLC	C	309	-	-	9/15/15/24	-
2	OLC	A	302	-	-	1/12/12/24	-
3	LFA	A	305	-	-	1/2/2/17	-
3	LFA	C	304	-	-	10/17/17/17	-
5	BOG	C	317	-	-	3/11/31/31	0/1/1/1
3	LFA	E	313	-	-	0/1/1/17	-
3	LFA	E	308	-	-	1/1/1/17	-
3	LFA	E	314	-	-	4/11/11/17	-
5	BOG	E	312	-	-	9/11/31/31	0/1/1/1
6	RET	A	312	1	-	0/13/30/31	0/1/1/1
3	LFA	B	306	-	-	3/6/6/17	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OLC	C	305	-	-	9/22/22/24	-
3	LFA	C	310	-	-	2/4/4/17	-
6	RET	D	315	1	-	0/13/30/31	0/1/1/1
2	OLC	E	302	-	-	13/24/24/24	-
2	OLC	A	301	-	-	9/21/21/24	-
2	OLC	B	303	-	-	7/19/19/24	-
3	LFA	D	310	-	-	3/4/4/17	-
3	LFA	E	309	-	-	1/2/2/17	-
3	LFA	C	313	-	-	3/8/8/17	-
2	OLC	B	305	-	-	9/16/16/24	-
2	OLC	D	304	-	-	9/13/13/24	-
3	LFA	E	305	-	-	0/5/5/17	-
3	LFA	A	304	-	-	2/5/5/17	-
3	LFA	C	314	-	-	1/1/1/17	-
3	LFA	B	309	-	-	0/4/4/17	-
5	BOG	D	314	-	-	1/11/31/31	0/1/1/1
2	OLC	E	304	-	-	15/24/24/24	-
3	LFA	A	306	-	-	3/5/5/17	-
3	LFA	D	301	-	-	8/17/17/17	-
3	LFA	E	306	-	-	1/3/3/17	-
3	LFA	D	306	-	-	10/17/17/17	-
3	LFA	C	311	-	-	5/5/5/17	-
2	OLC	C	301	-	-	9/20/20/24	-
6	RET	C	318	1	-	0/13/30/31	0/1/1/1
2	OLC	E	301	-	-	15/23/23/24	-
2	OLC	C	306	-	-	7/17/17/24	-
2	OLC	B	304	-	-	4/15/15/24	-
3	LFA	C	312	-	-	7/9/9/17	-
3	LFA	B	302	-	-	6/17/17/17	-
2	OLC	C	308	-	-	9/15/15/24	-
3	LFA	D	308	-	-	4/5/5/17	-
2	OLC	D	303	-	-	4/17/17/24	-
3	LFA	D	309	-	-	8/14/14/17	-
6	RET	B	313	1	-	0/13/30/31	0/1/1/1
2	OLC	D	302	-	-	10/24/24/24	-
3	LFA	E	307	-	-	7/11/11/17	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	LFA	E	310	-	-	1/3/3/17	-
6	RET	E	315	1	-	0/13/30/31	0/1/1/1
3	LFA	A	311	-	-	9/17/17/17	-
3	LFA	D	307	-	-	8/17/17/17	-
2	OLC	C	307	-	-	4/14/14/24	-
2	OLC	C	302	-	-	11/19/19/24	-
2	OLC	E	303	-	-	5/14/14/24	-
3	LFA	B	307	-	-	2/2/2/17	-
5	BOG	B	312	-	-	7/11/31/31	0/1/1/1
2	OLC	A	303	-	-	6/14/14/24	-

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	309	OLC	O20-C1	4.61	1.46	1.33
2	C	303	OLC	O20-C1	4.56	1.46	1.33
2	E	303	OLC	O20-C1	4.56	1.46	1.33
2	D	303	OLC	O20-C1	4.51	1.46	1.33
2	C	307	OLC	O20-C1	4.43	1.46	1.33

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	312	RET	C18-C5-C6	-4.64	119.32	124.53
6	B	313	RET	C18-C5-C6	-4.44	119.54	124.53
6	D	315	RET	C18-C5-C6	-4.40	119.58	124.53
6	C	318	RET	C18-C5-C6	-4.35	119.64	124.53
6	E	315	RET	C18-C5-C6	-4.35	119.65	124.53

There are no chirality outliers.

5 of 347 torsion outliers are listed below:

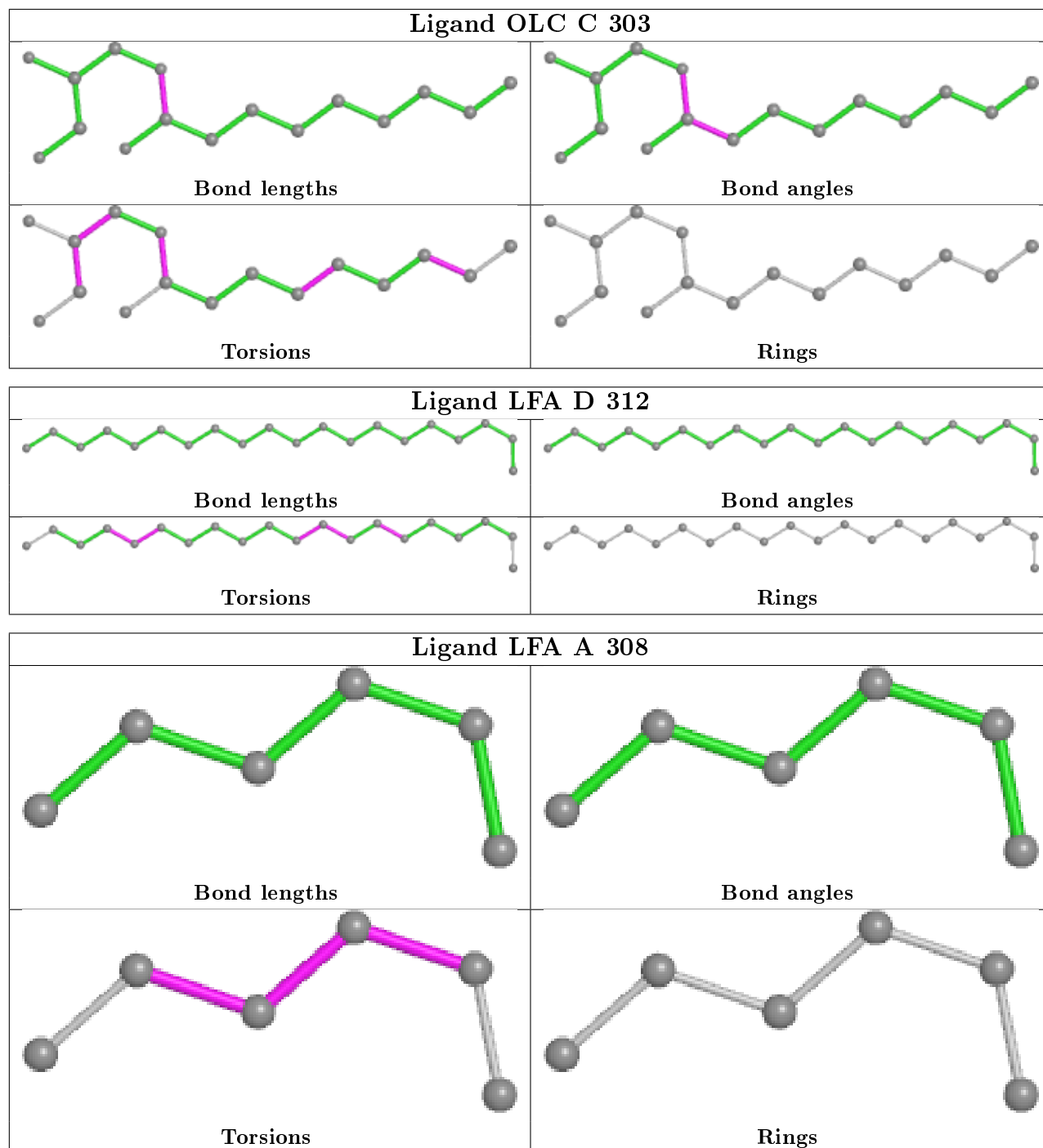
Mol	Chain	Res	Type	Atoms
2	C	303	OLC	C21-C22-C24-O25
5	A	310	BOG	C2'-C1'-O1-C1
2	C	309	OLC	O20-C21-C22-O23
5	E	312	BOG	C2-C1-O1-C1'
5	E	312	BOG	O5-C1-O1-C1'

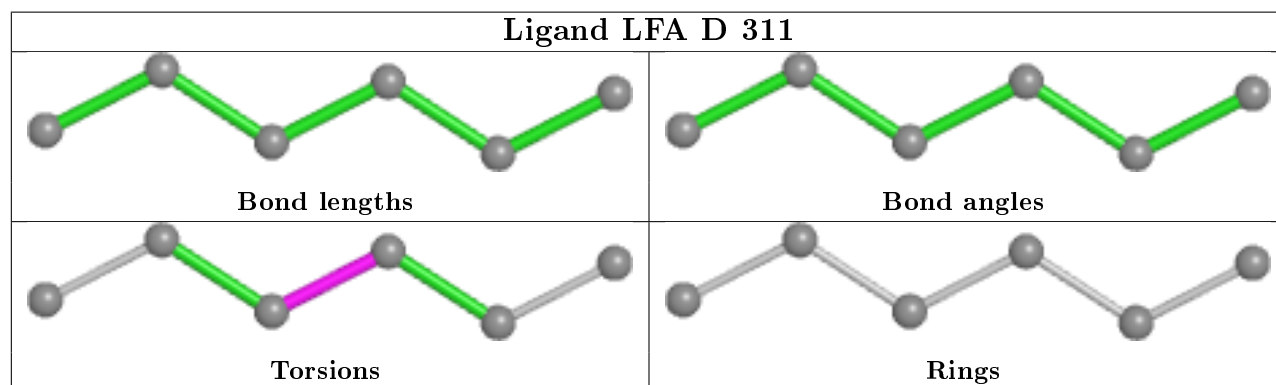
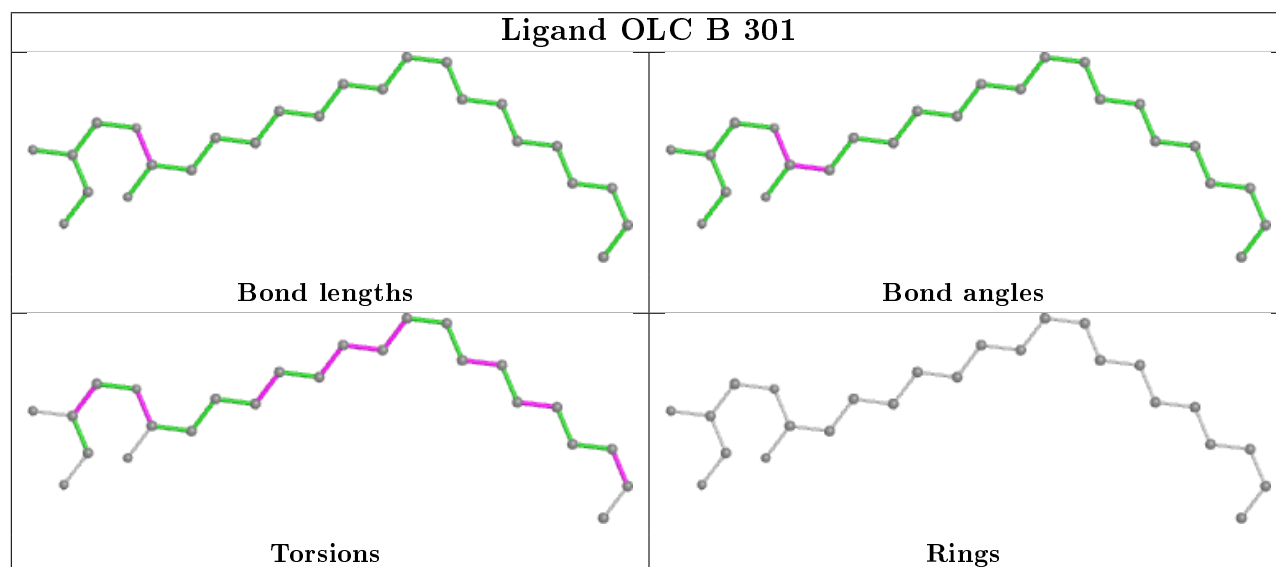
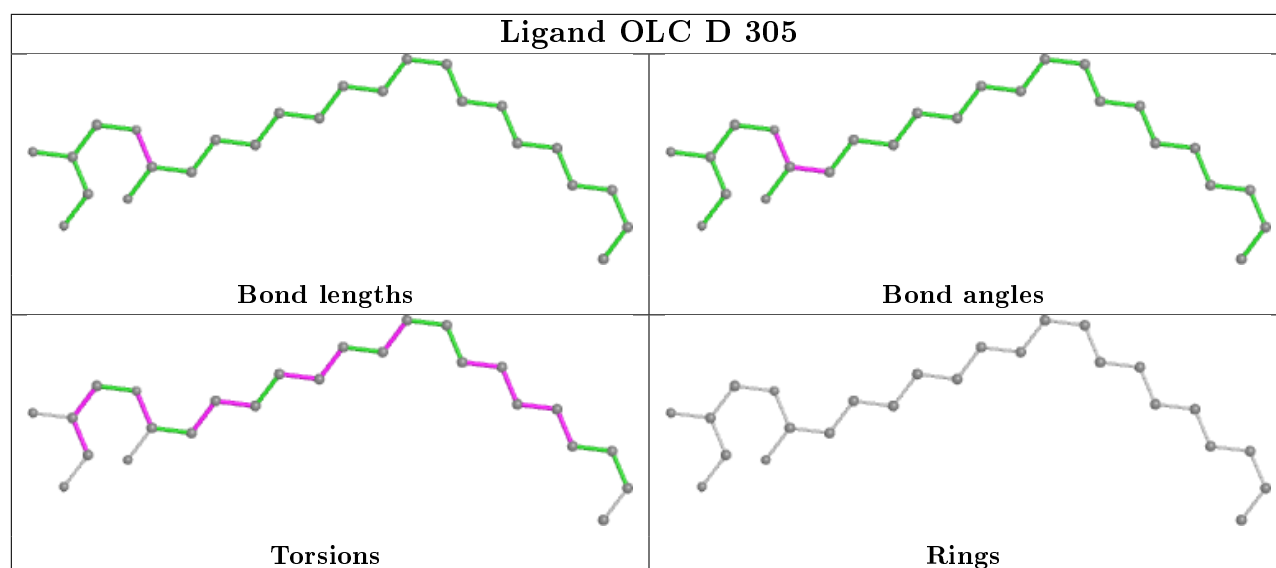
There are no ring outliers.

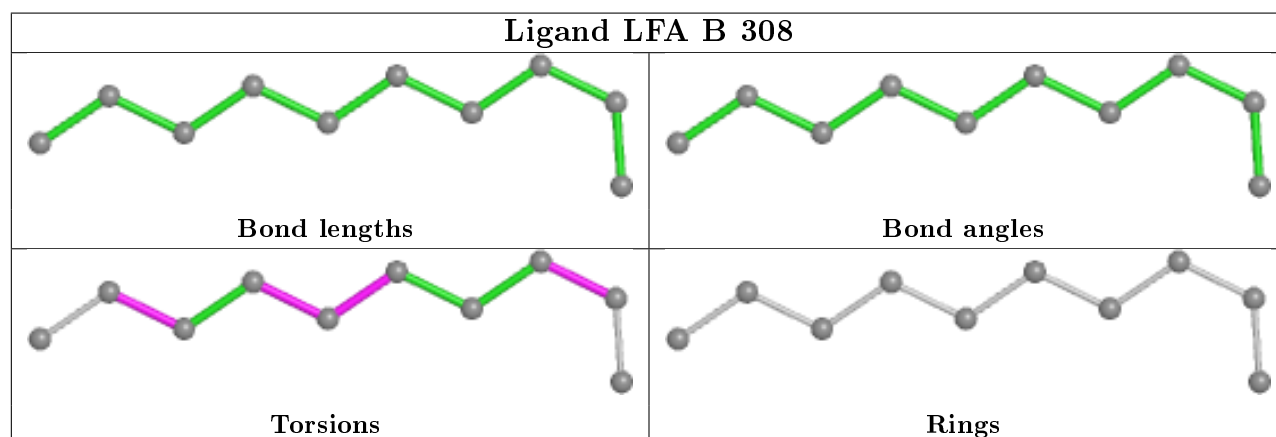
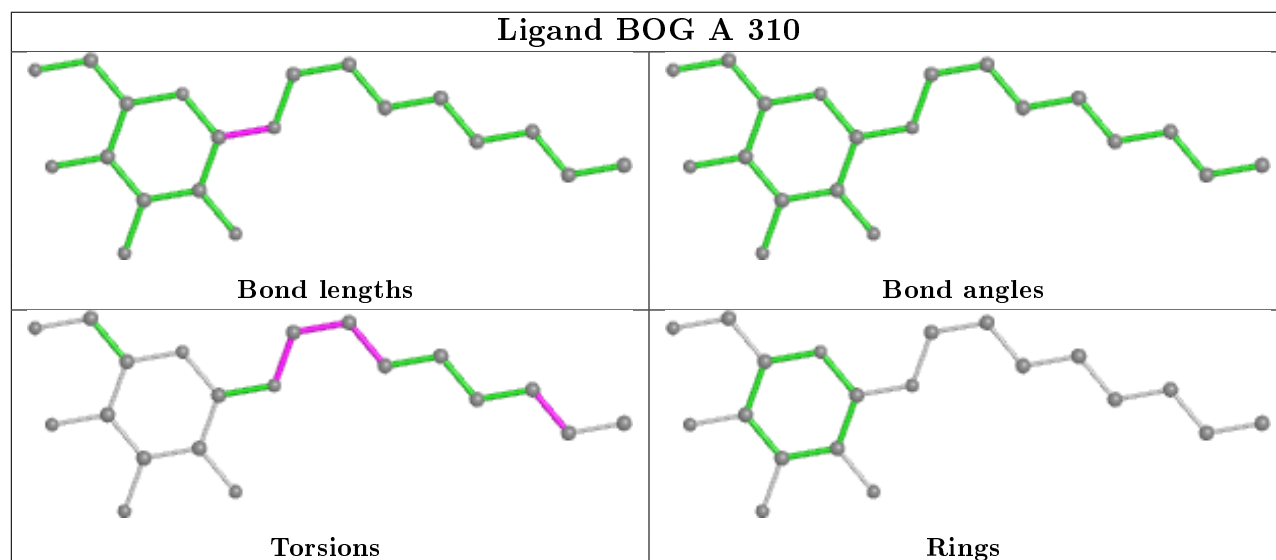
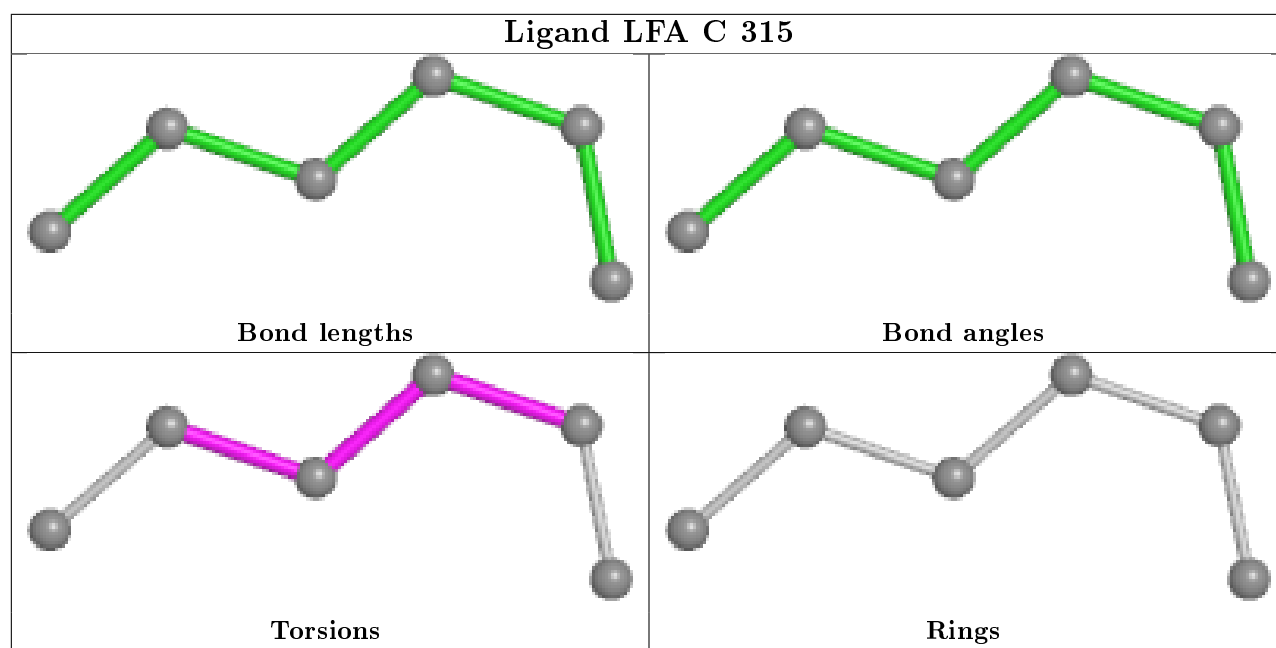
29 monomers are involved in 58 short contacts:

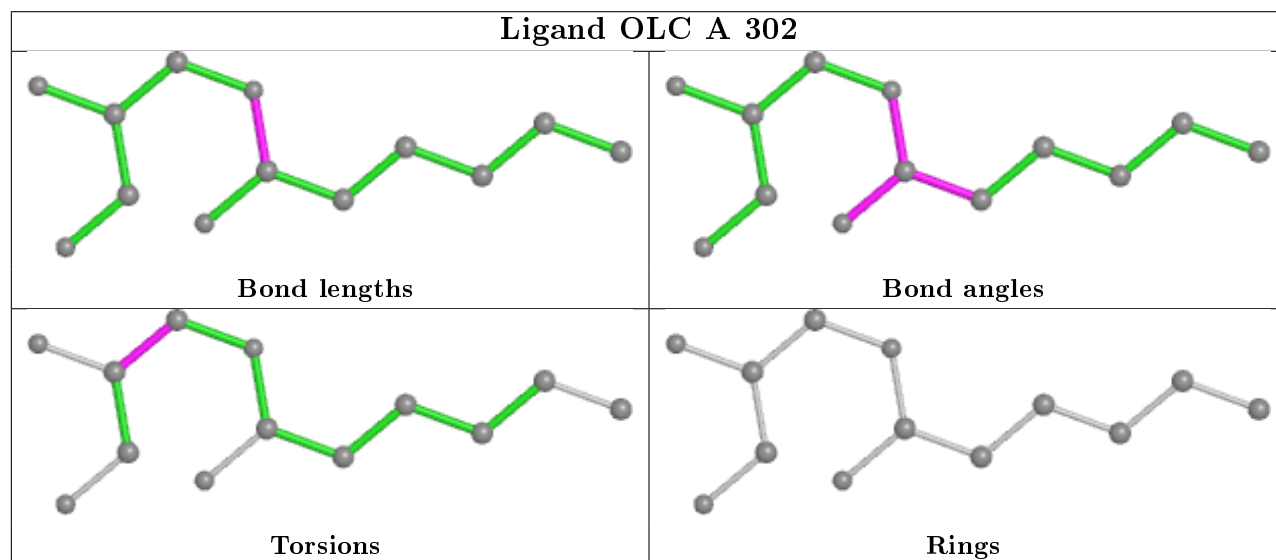
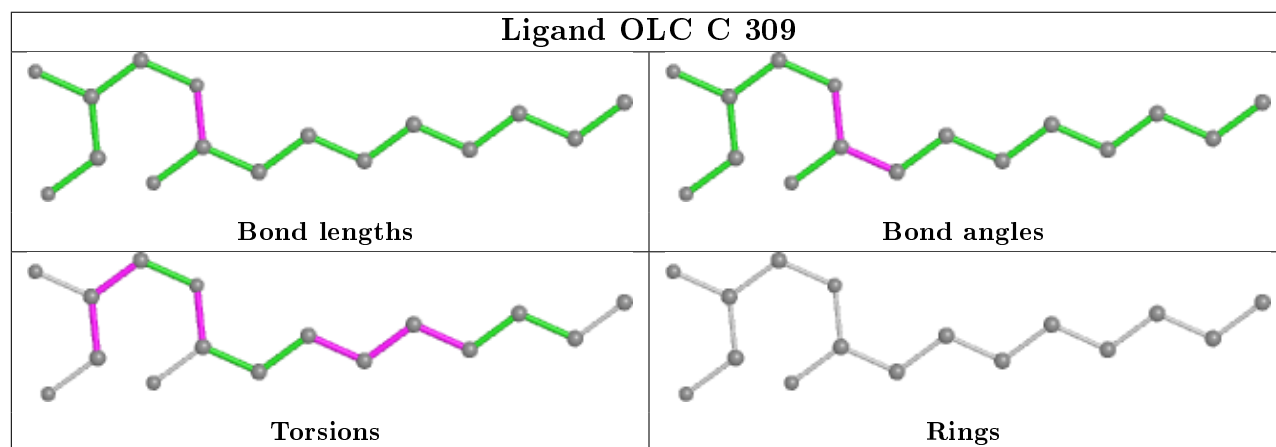
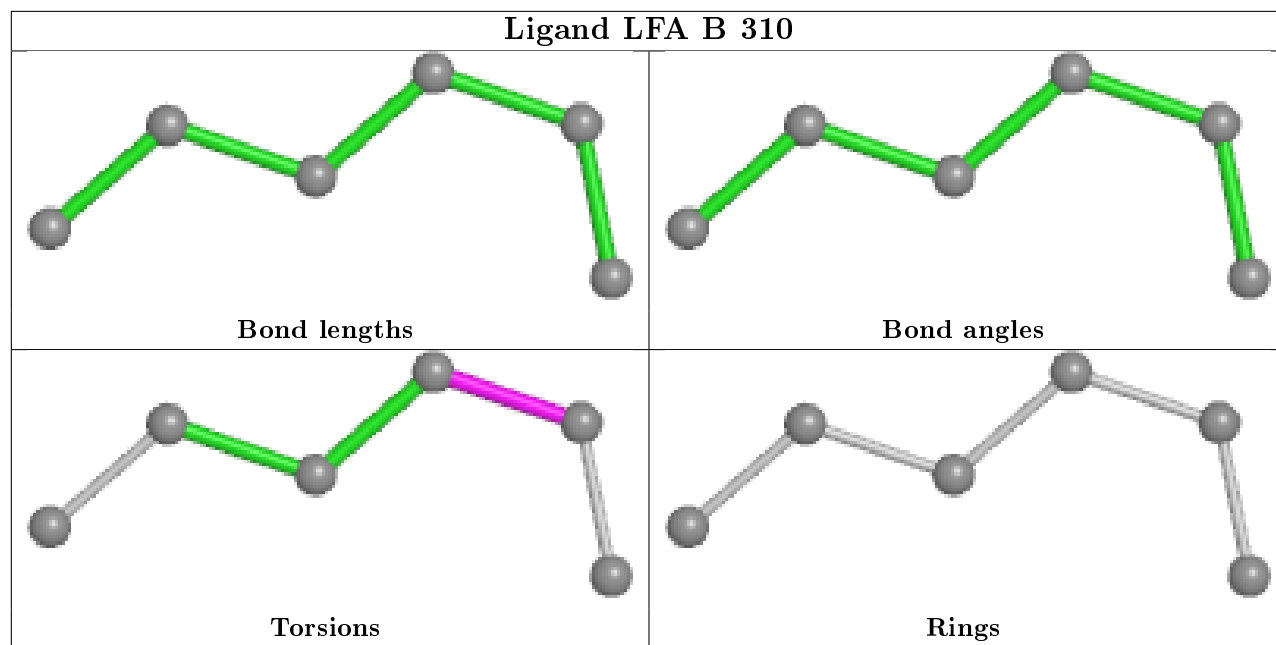
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	303	OLC	1	0
2	D	305	OLC	4	0
2	B	301	OLC	1	0
5	A	310	BOG	2	0
3	B	310	LFA	1	0
3	C	304	LFA	2	0
5	C	317	BOG	1	0
3	E	308	LFA	1	0
3	E	314	LFA	1	0
6	A	312	RET	5	0
3	B	306	LFA	2	0
2	C	305	OLC	2	0
3	C	310	LFA	3	0
6	D	315	RET	5	0
2	B	305	OLC	3	0
5	D	314	BOG	4	0
2	E	304	OLC	1	0
3	D	301	LFA	1	0
6	C	318	RET	5	0
2	C	306	OLC	2	0
2	C	308	OLC	2	0
6	B	313	RET	4	0
2	D	302	OLC	2	0
3	E	307	LFA	1	0
3	E	310	LFA	1	0
6	E	315	RET	6	0
2	C	307	OLC	1	0
2	C	302	OLC	1	0
5	B	312	BOG	2	0

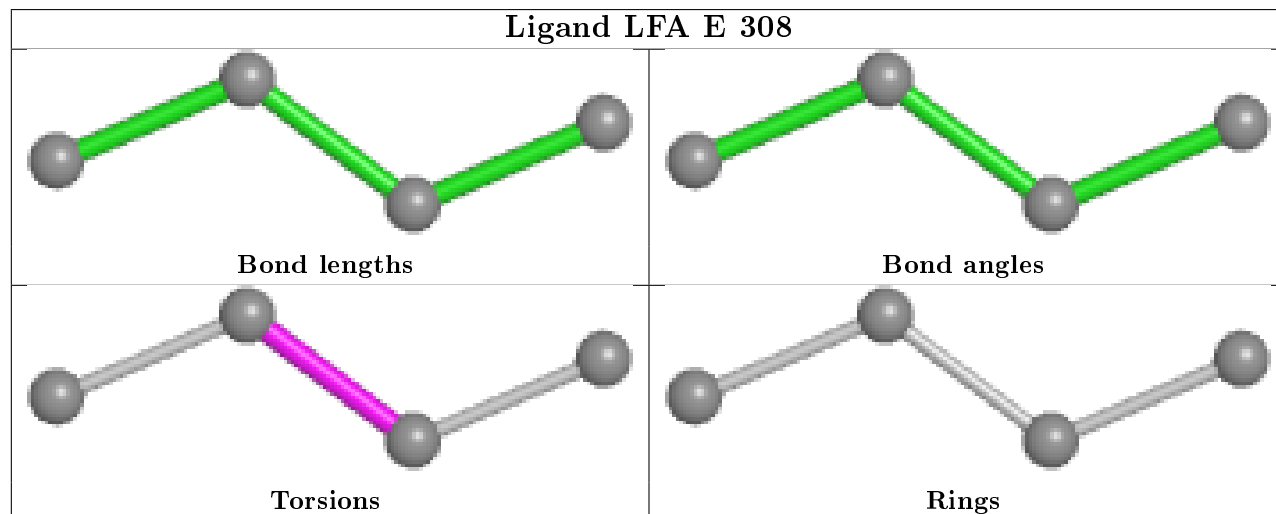
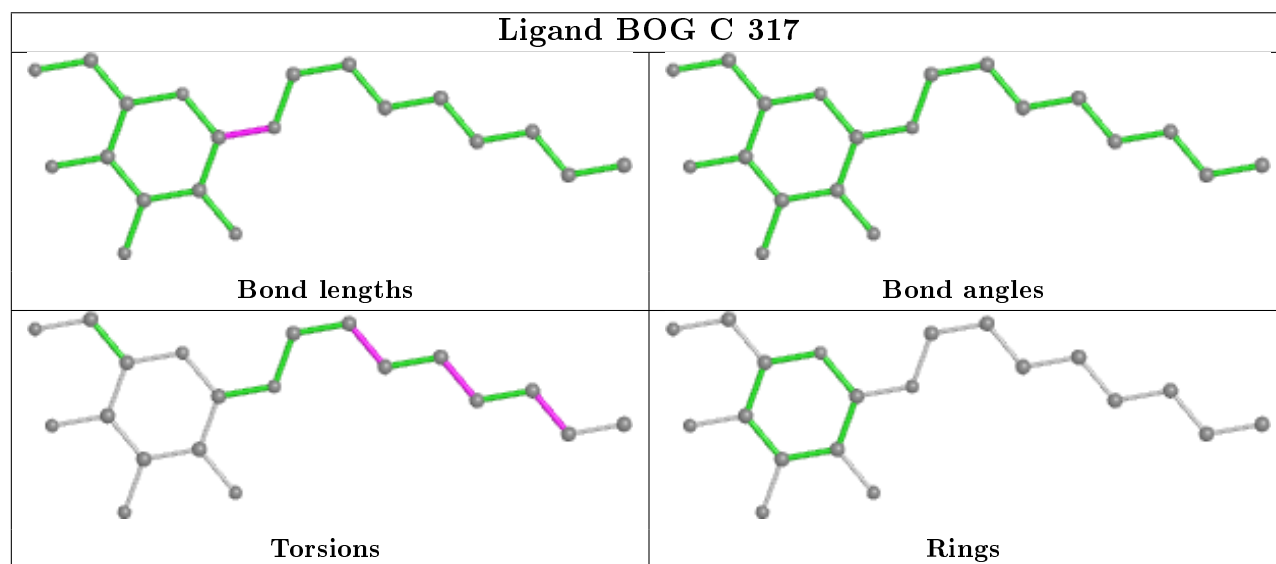
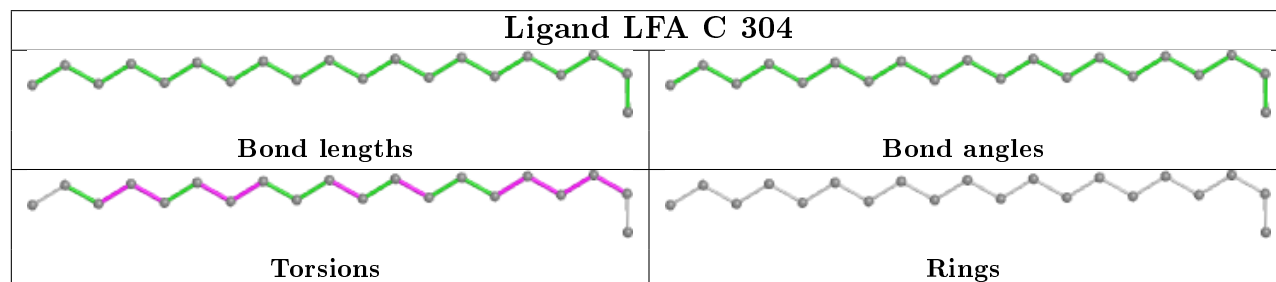
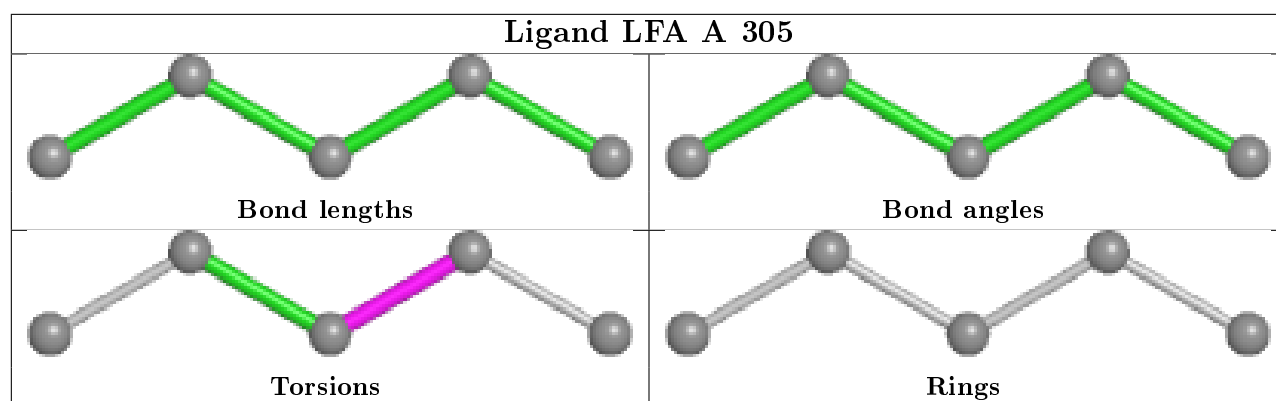
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

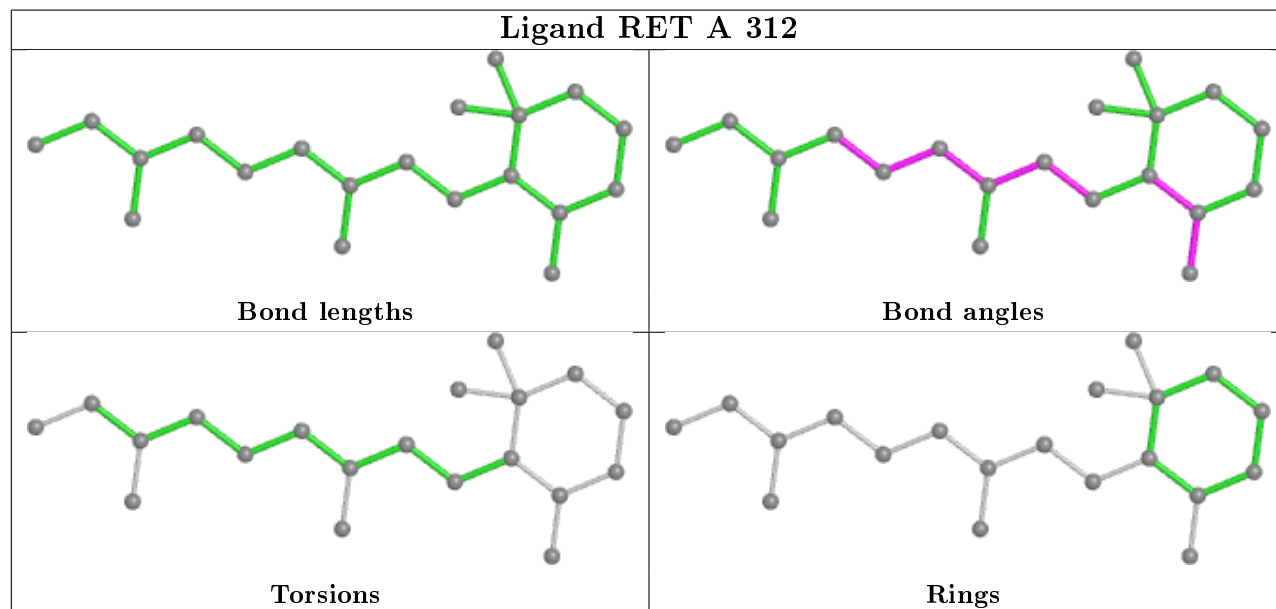
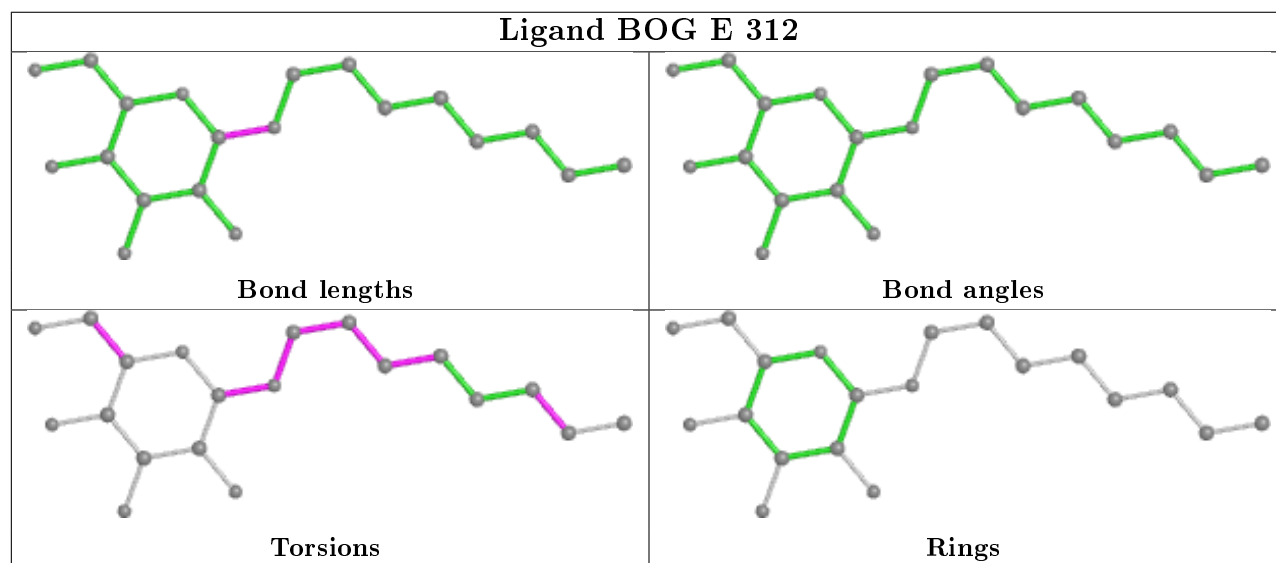
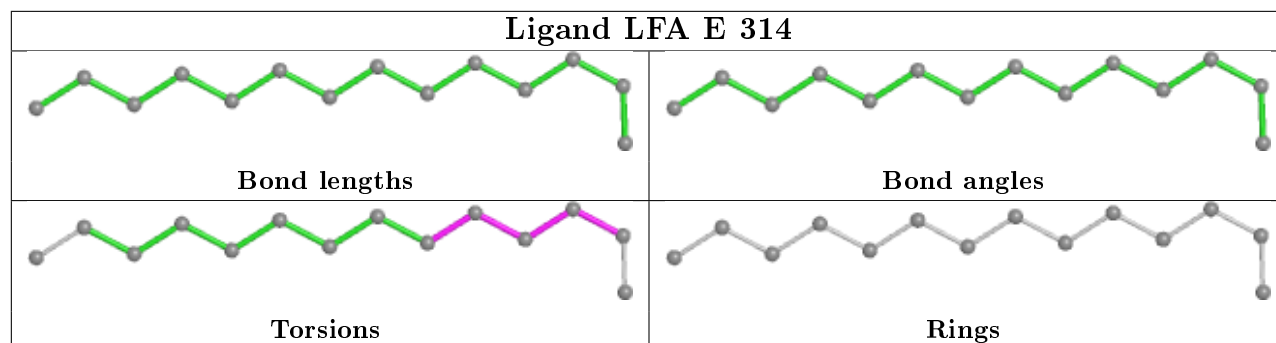


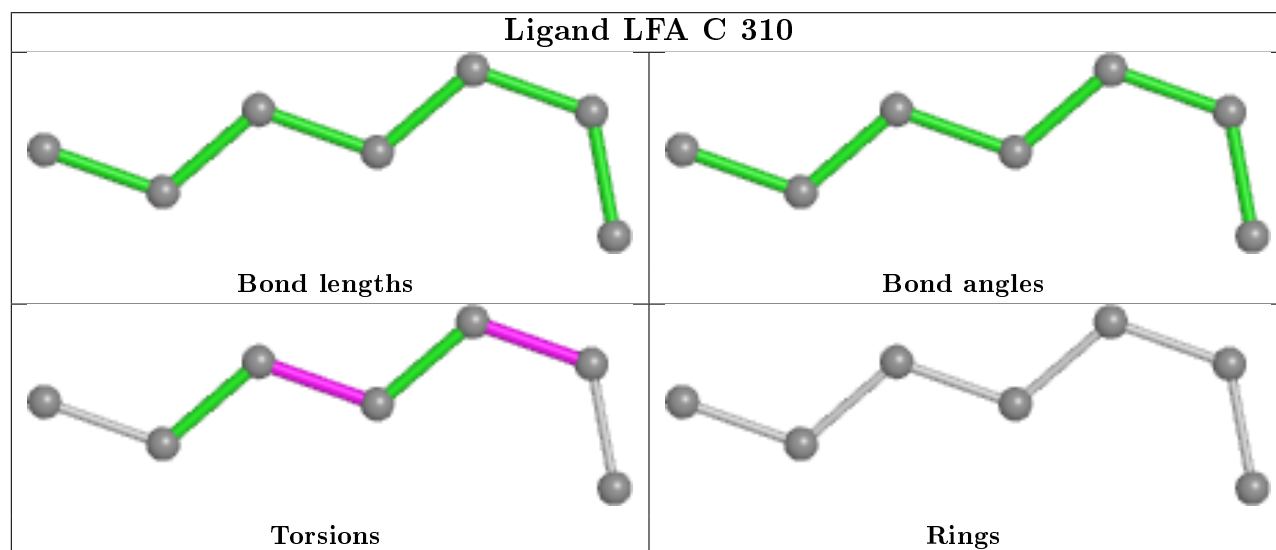
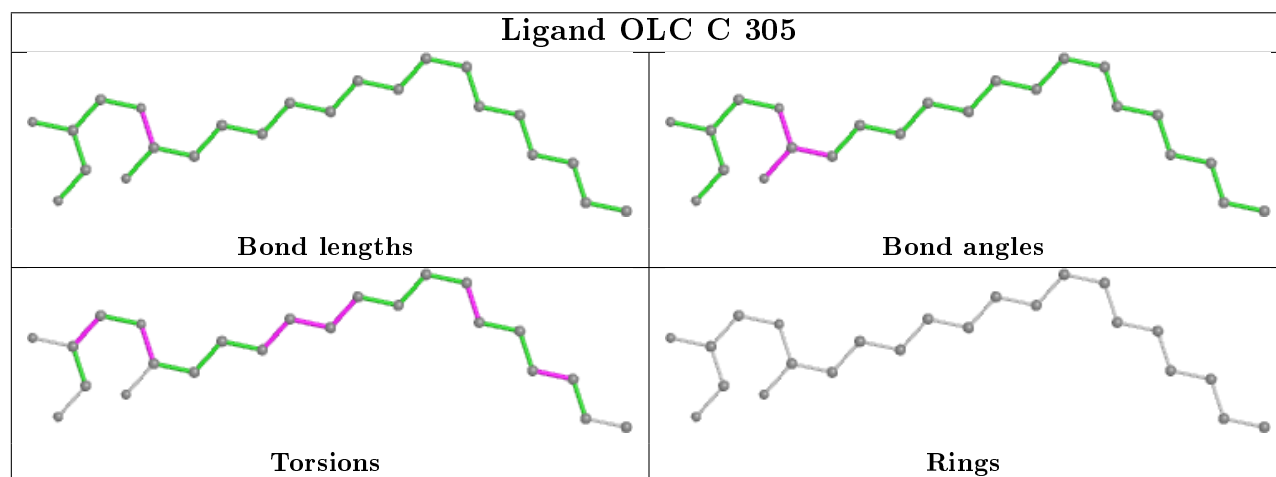
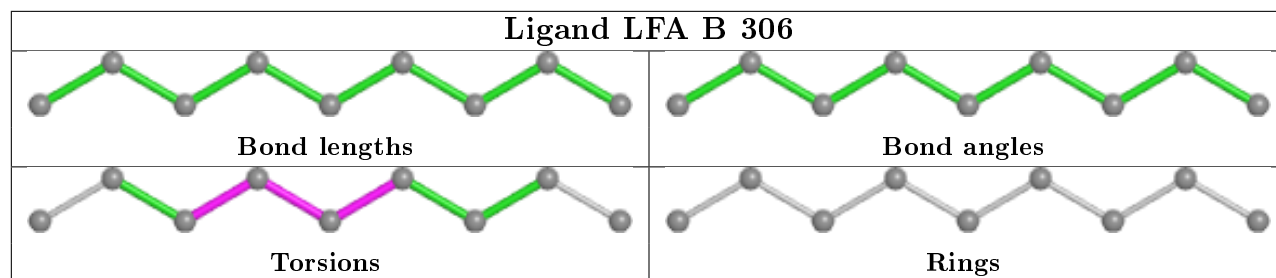


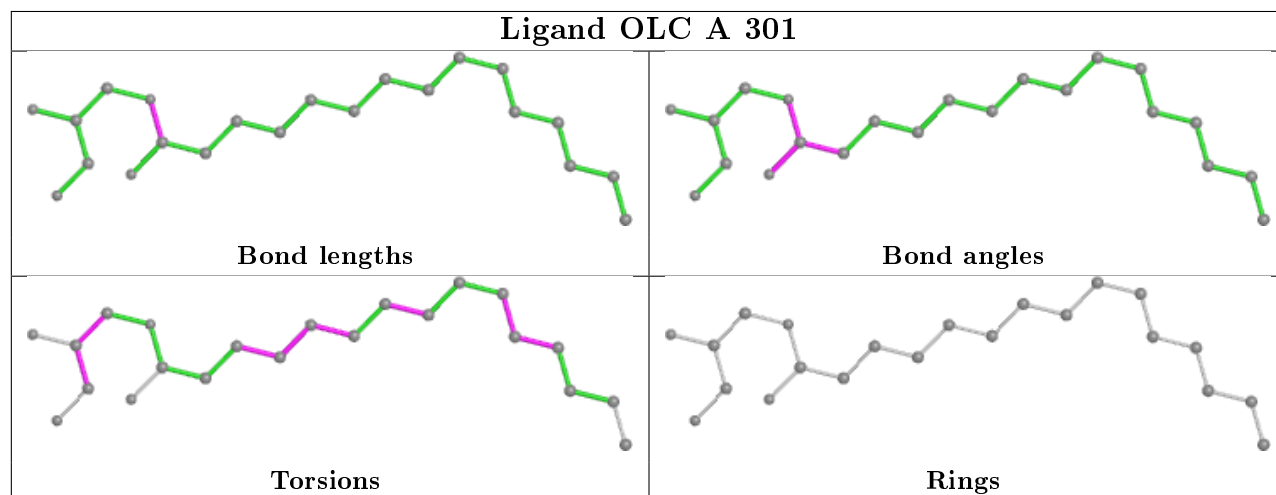
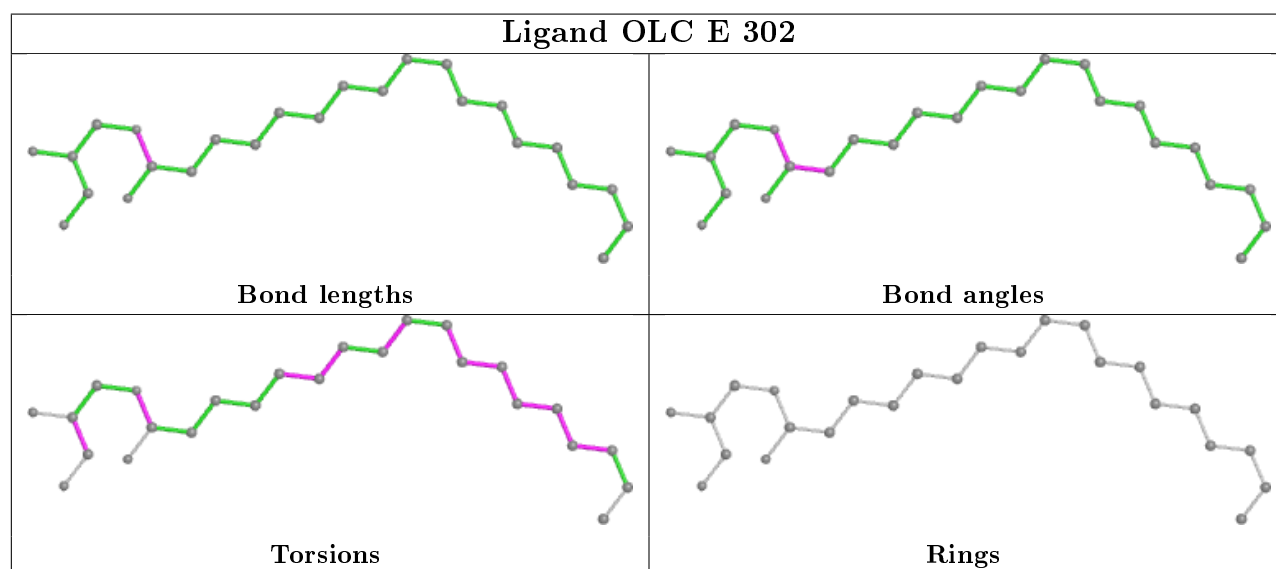
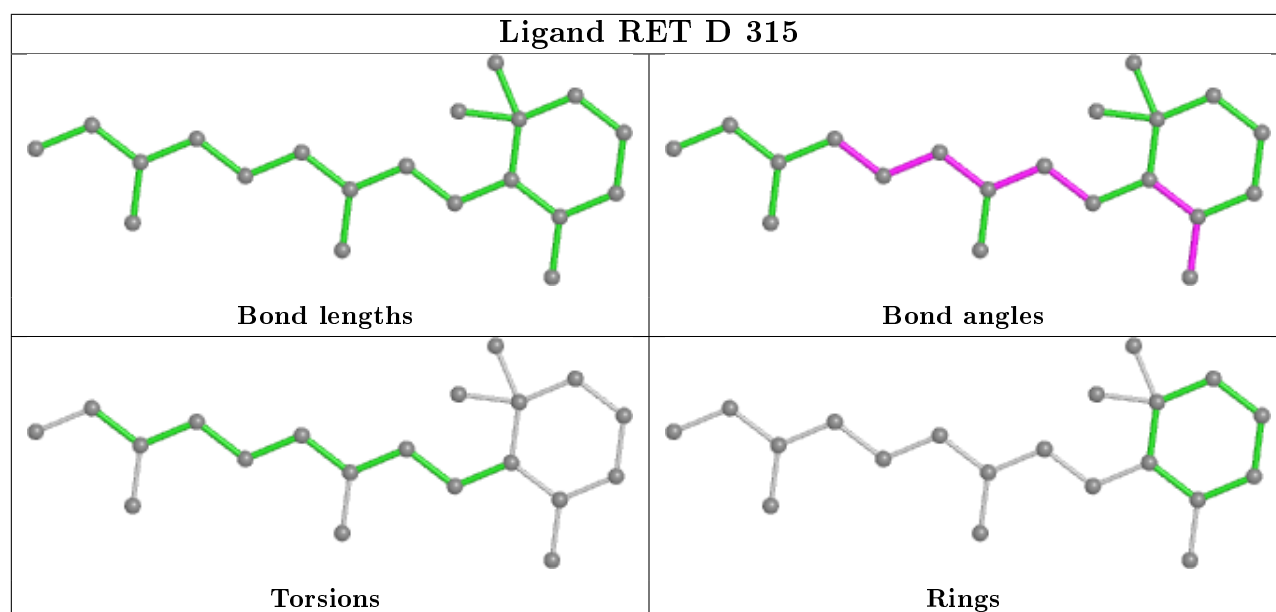


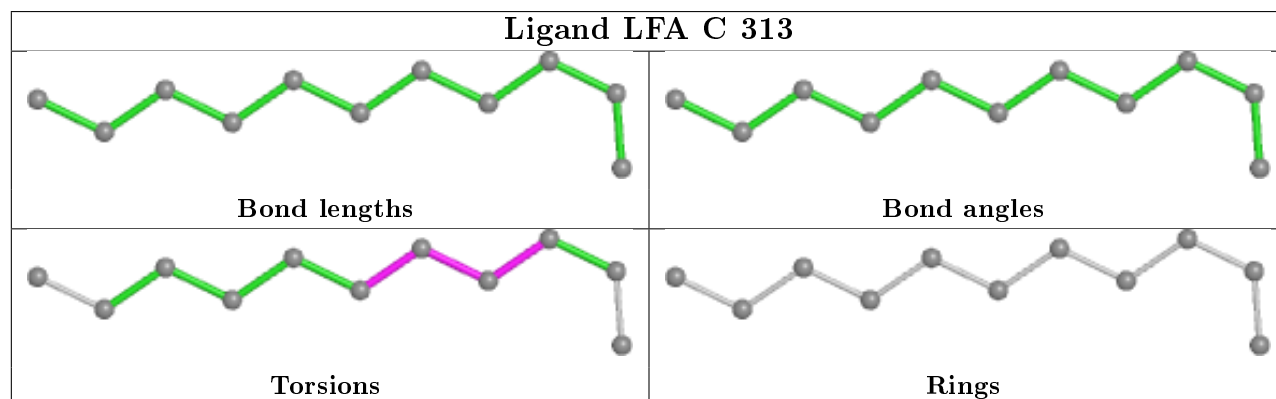
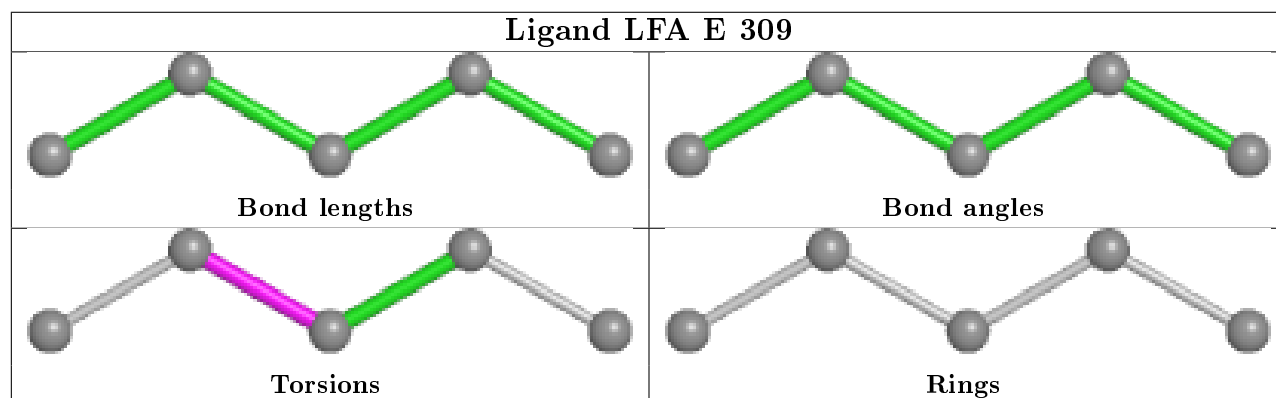
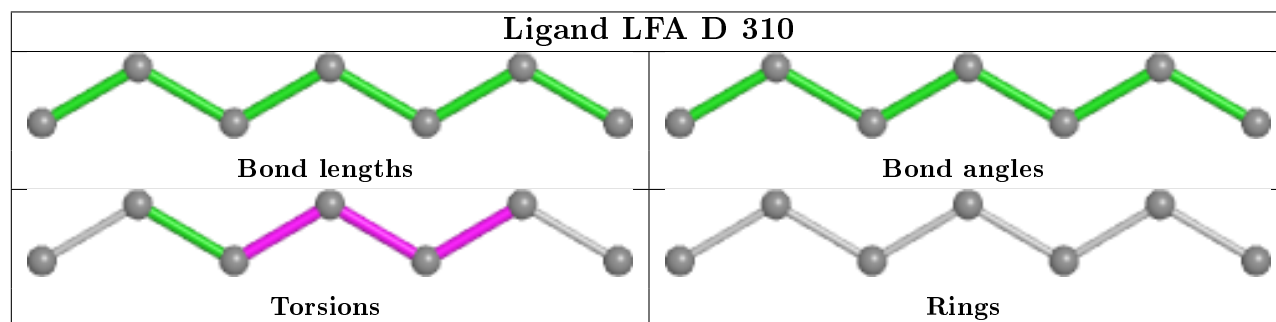
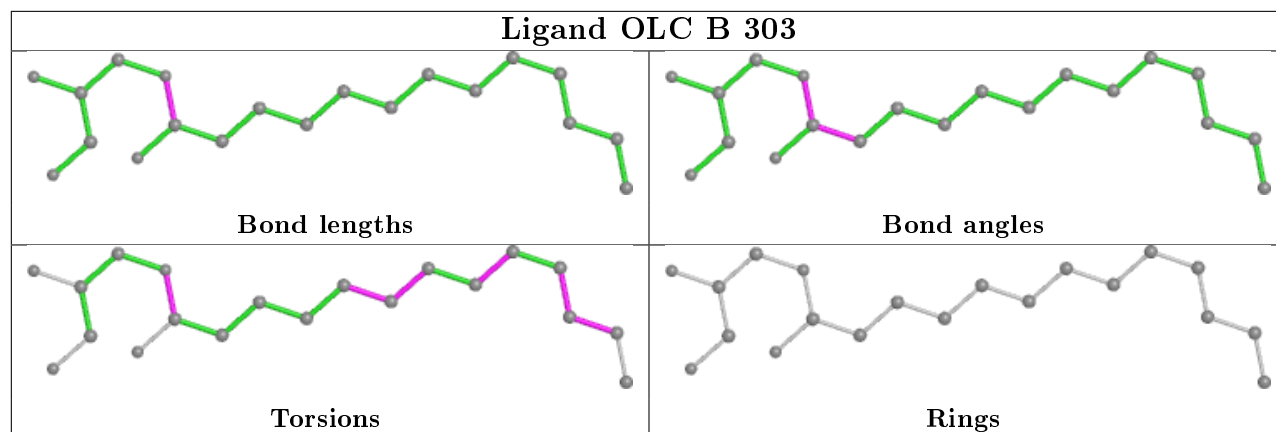


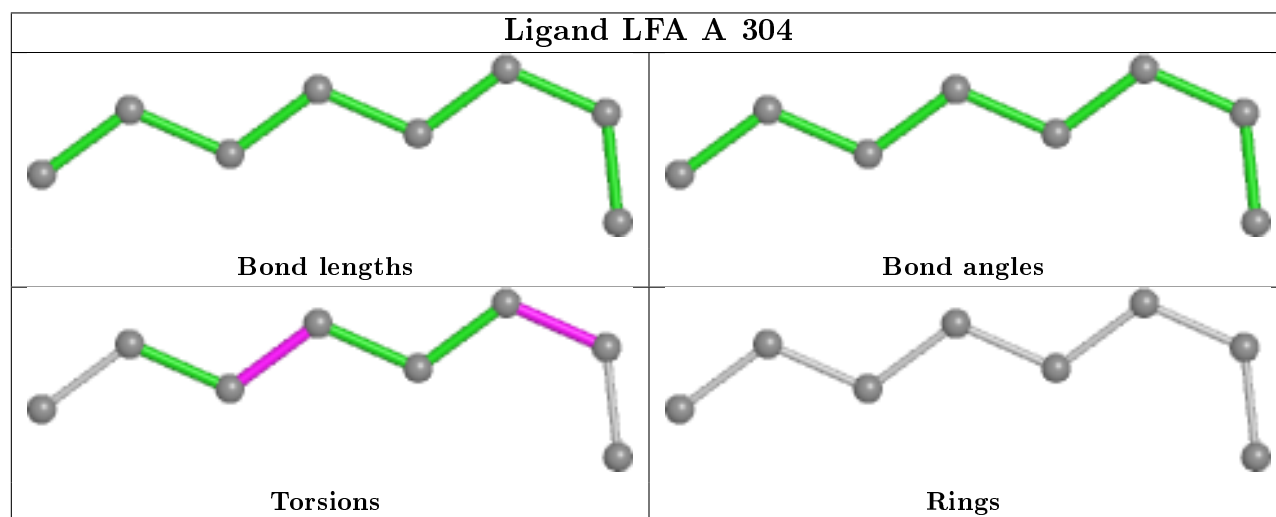
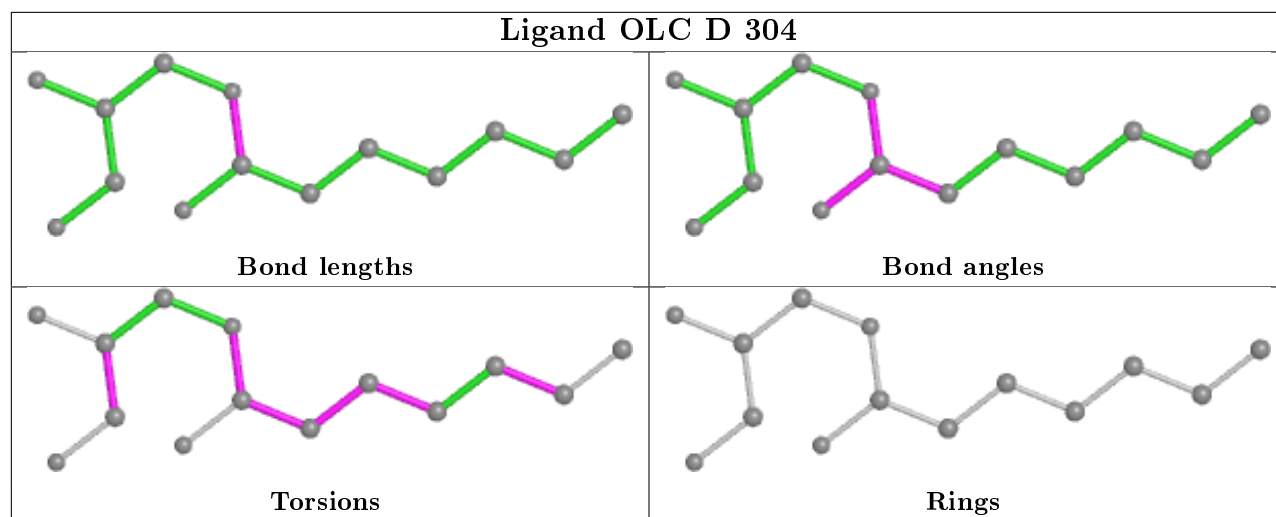
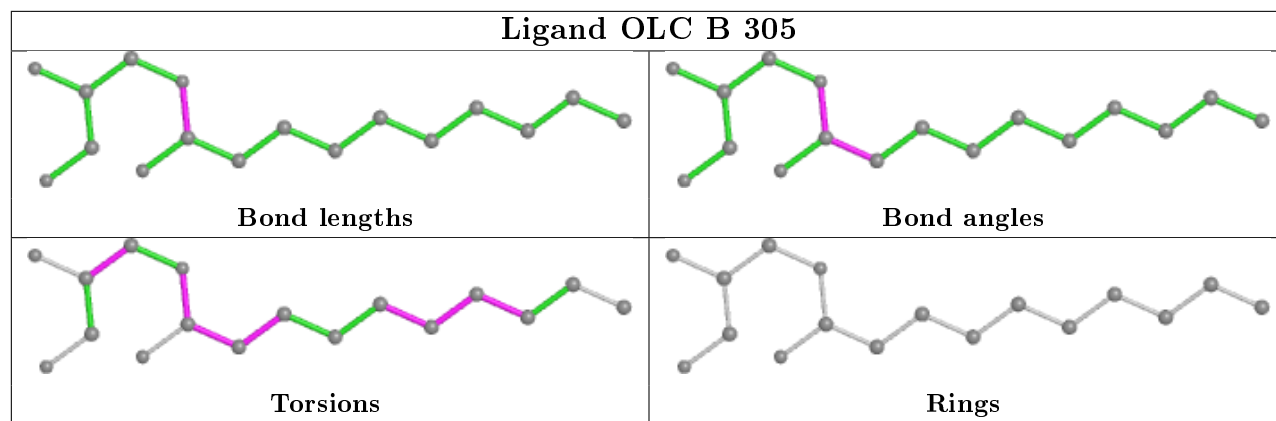


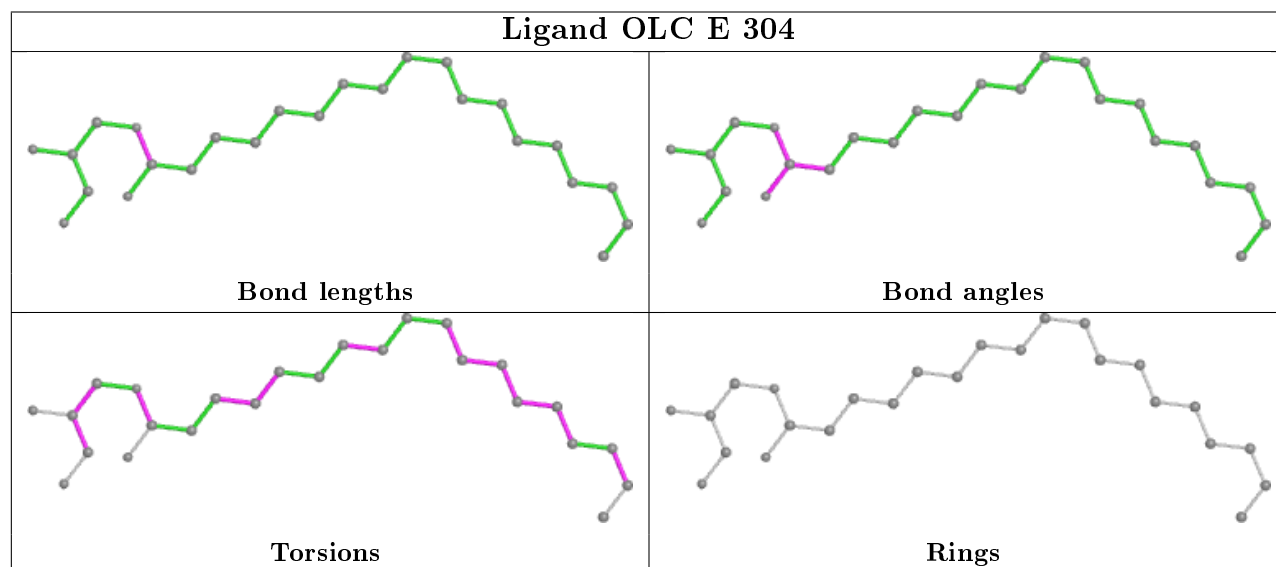
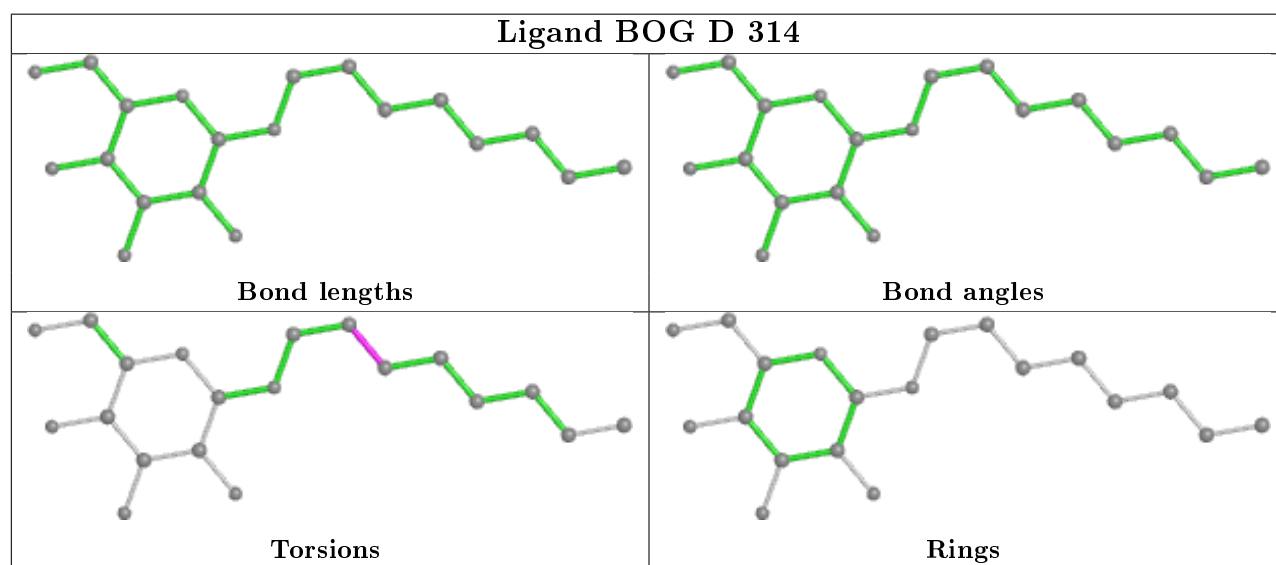
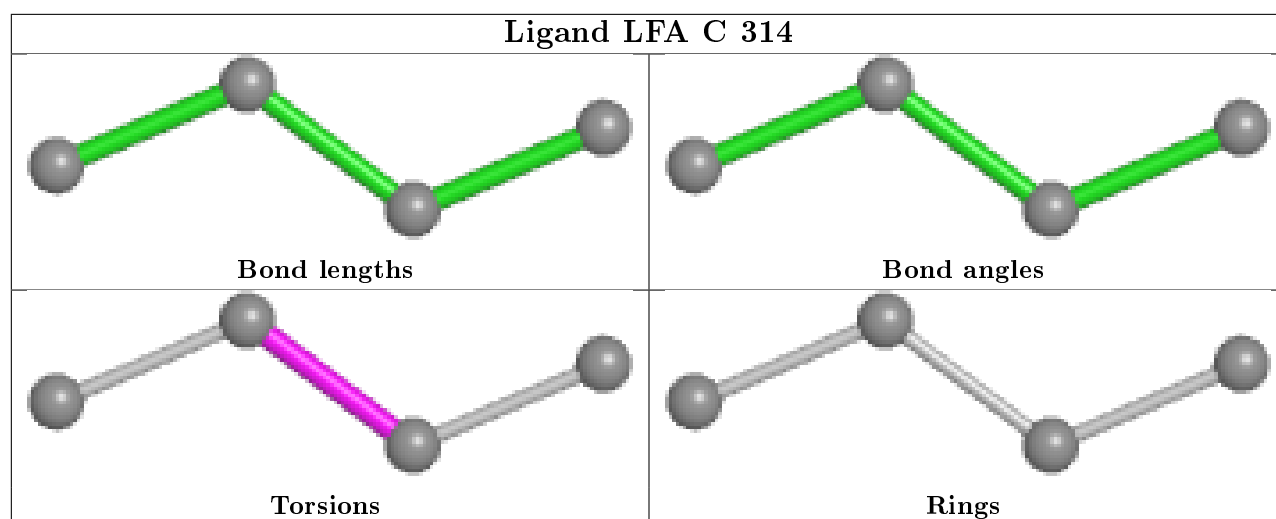


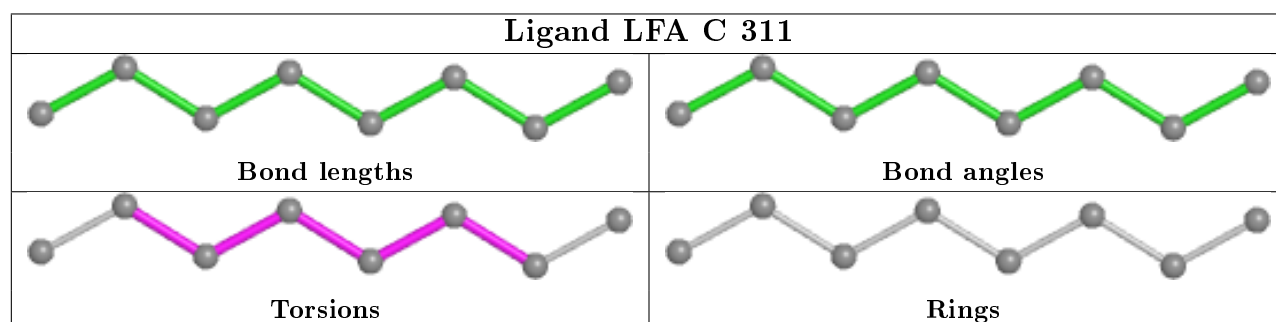
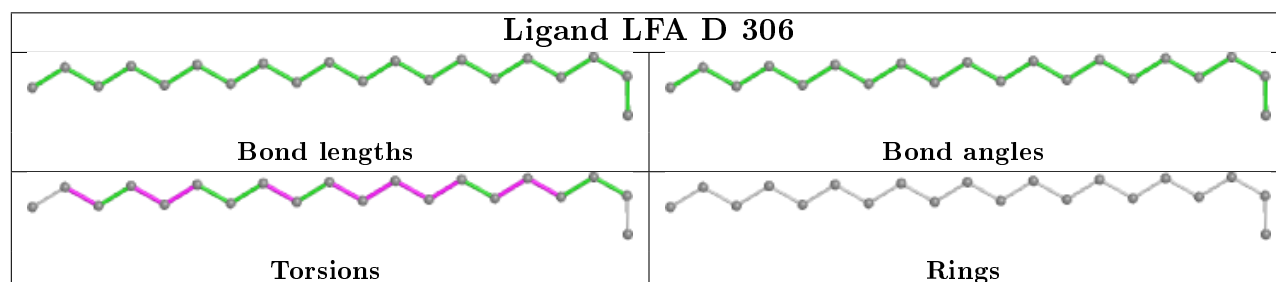
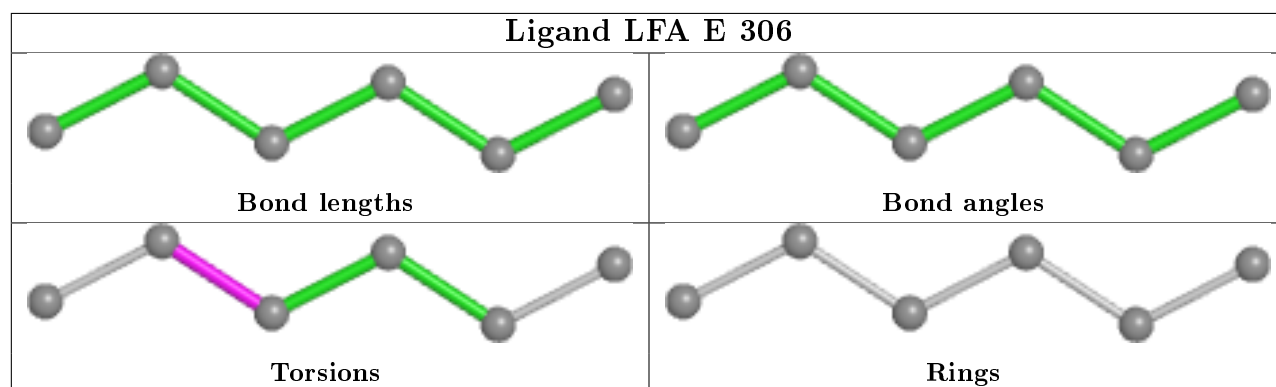
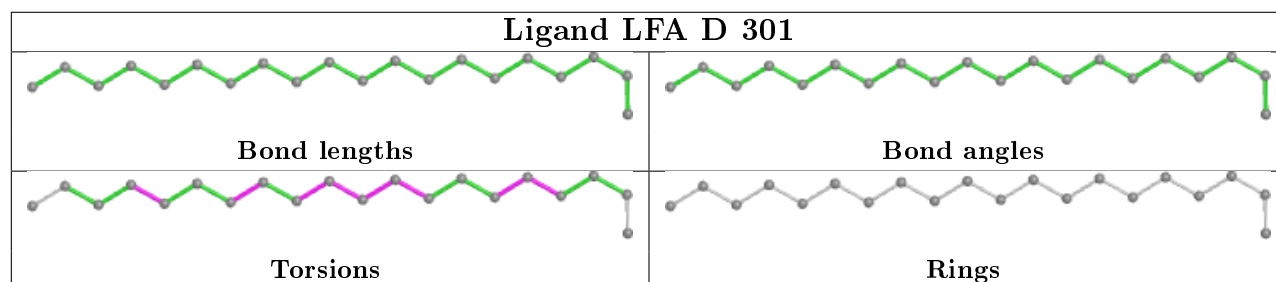
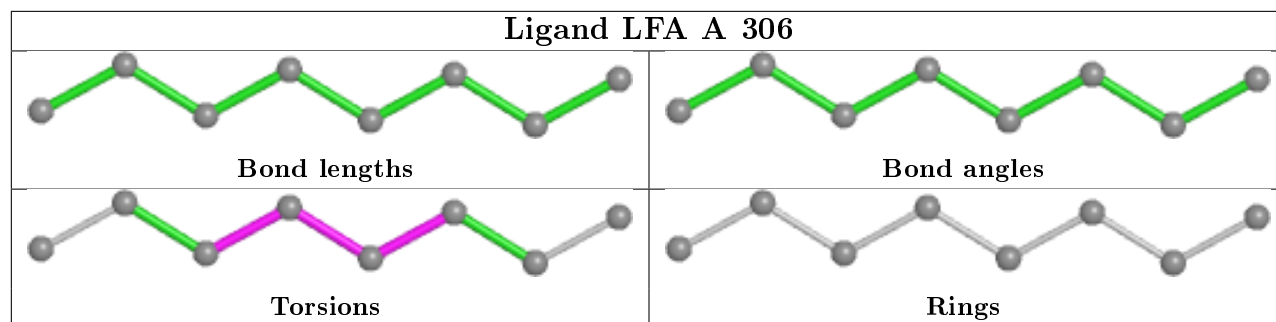


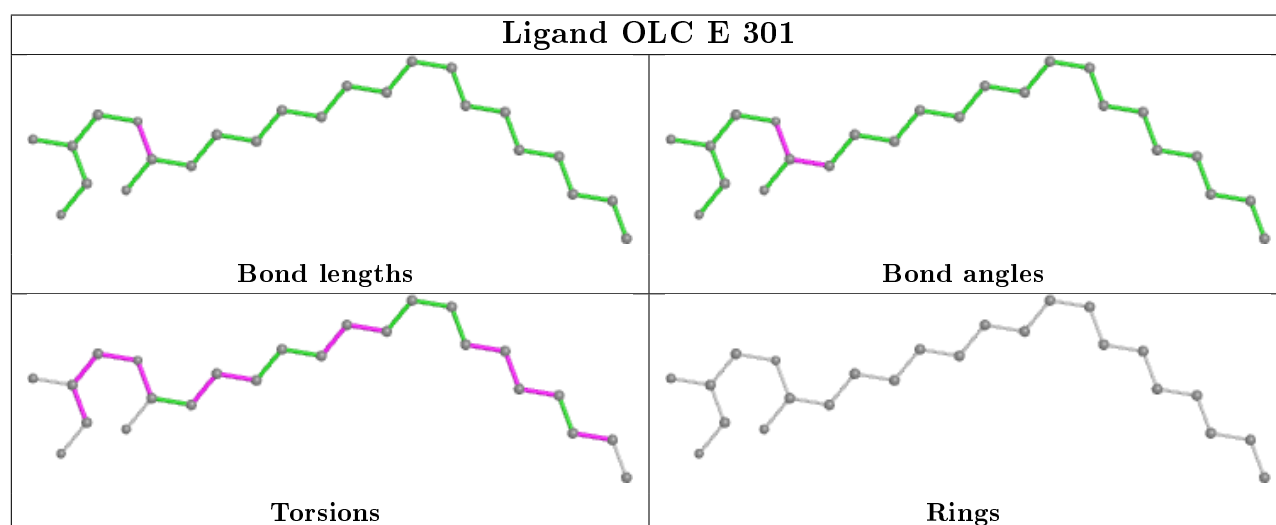
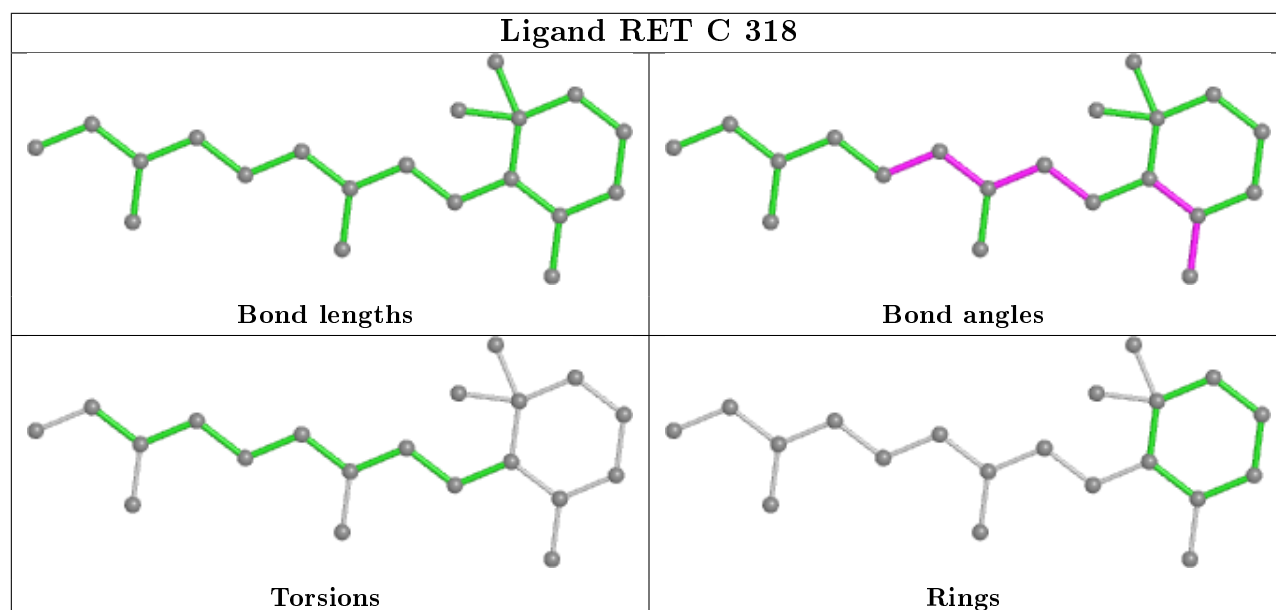
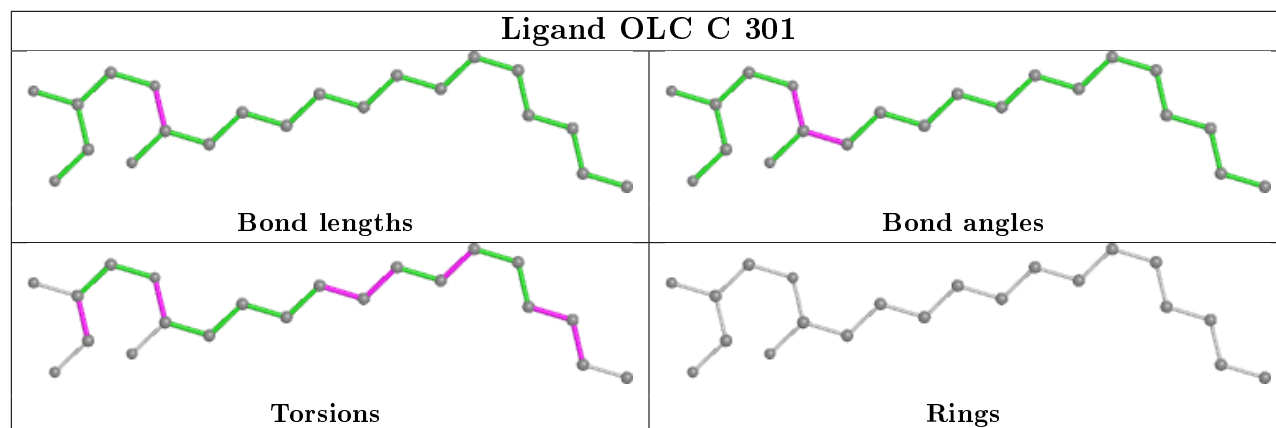


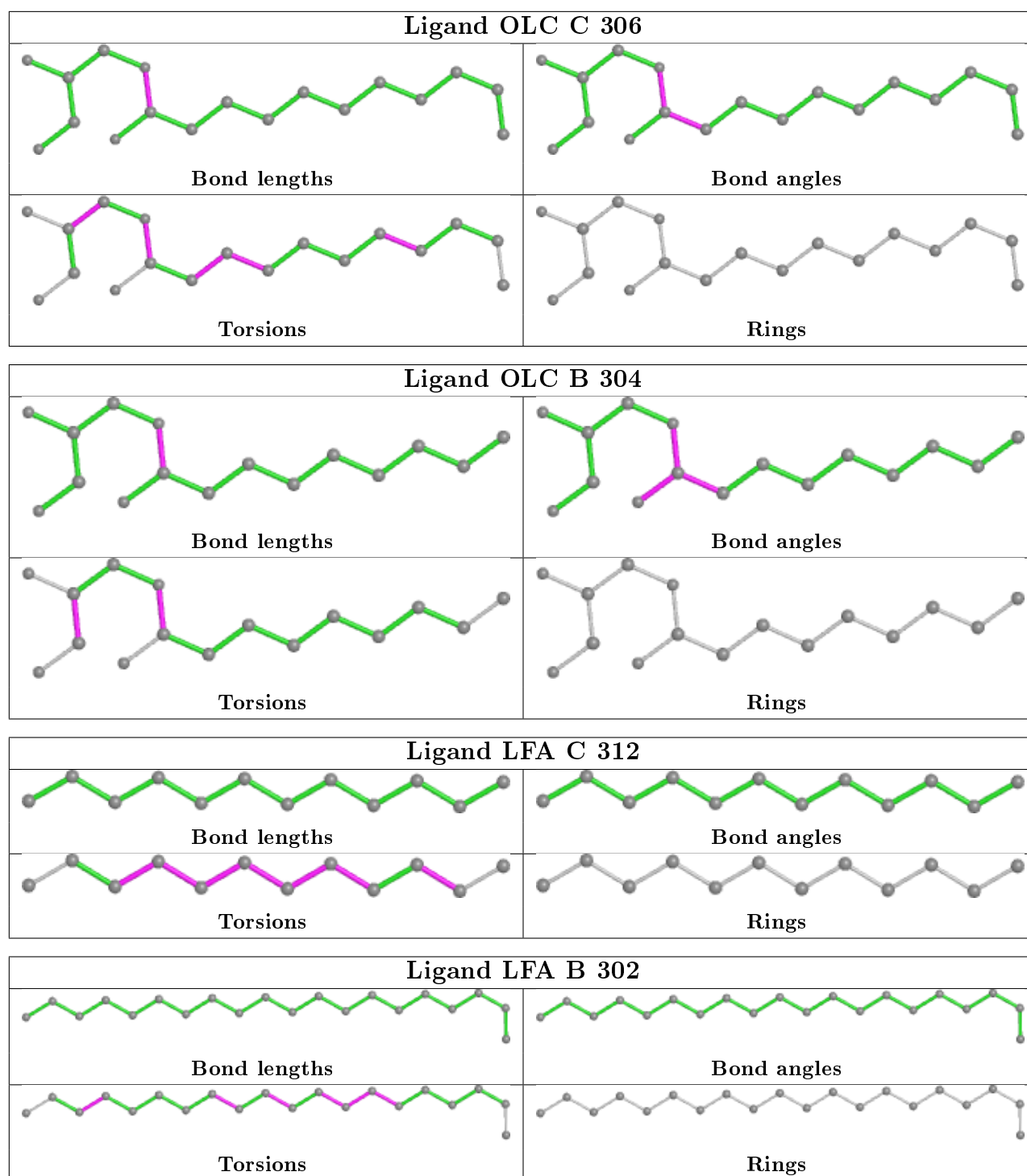


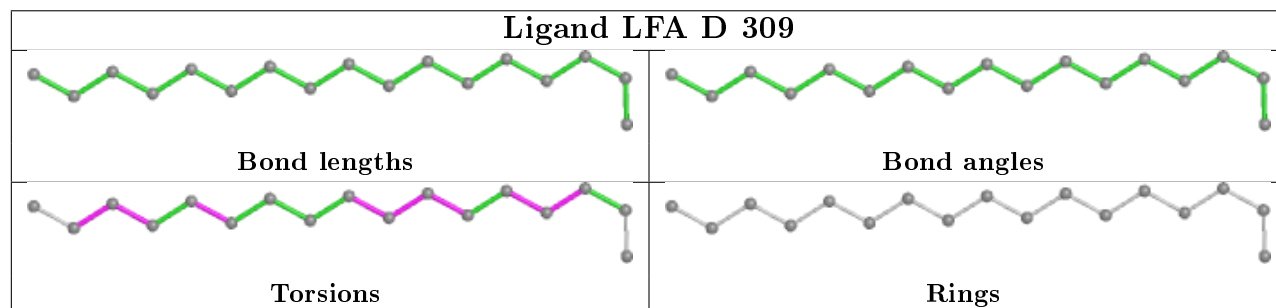
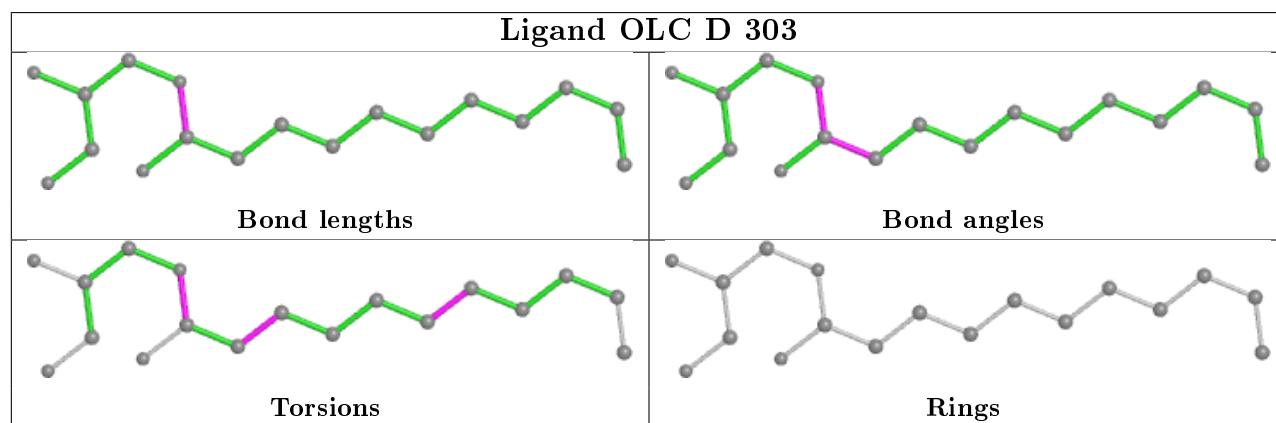
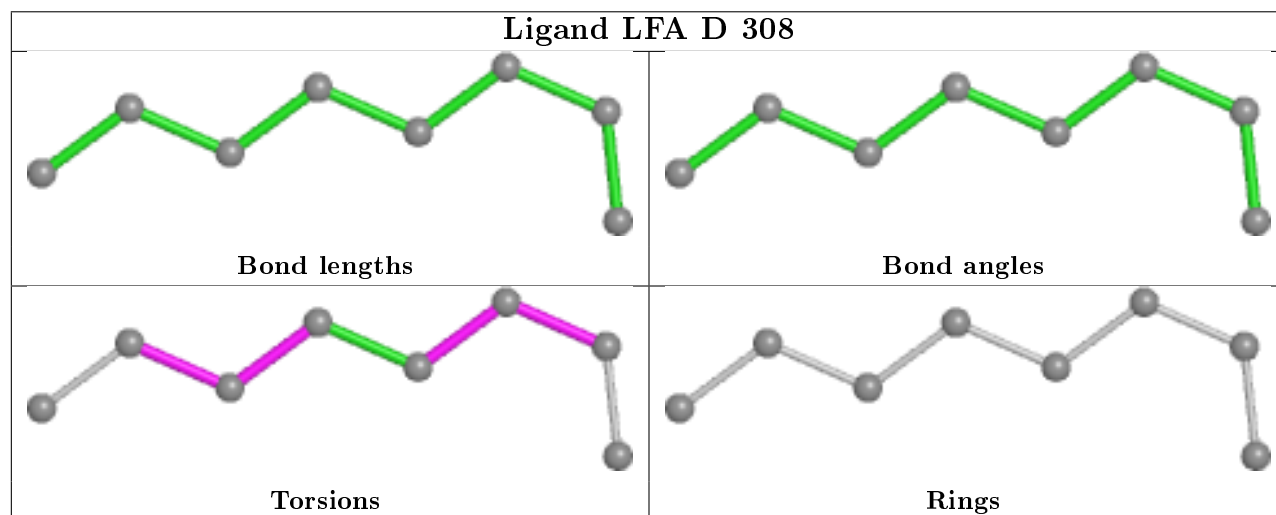
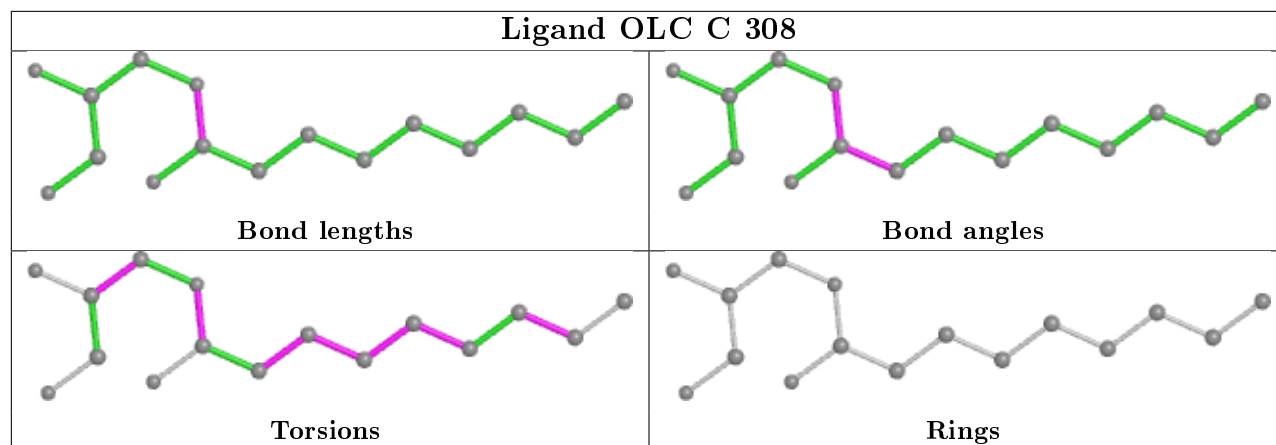


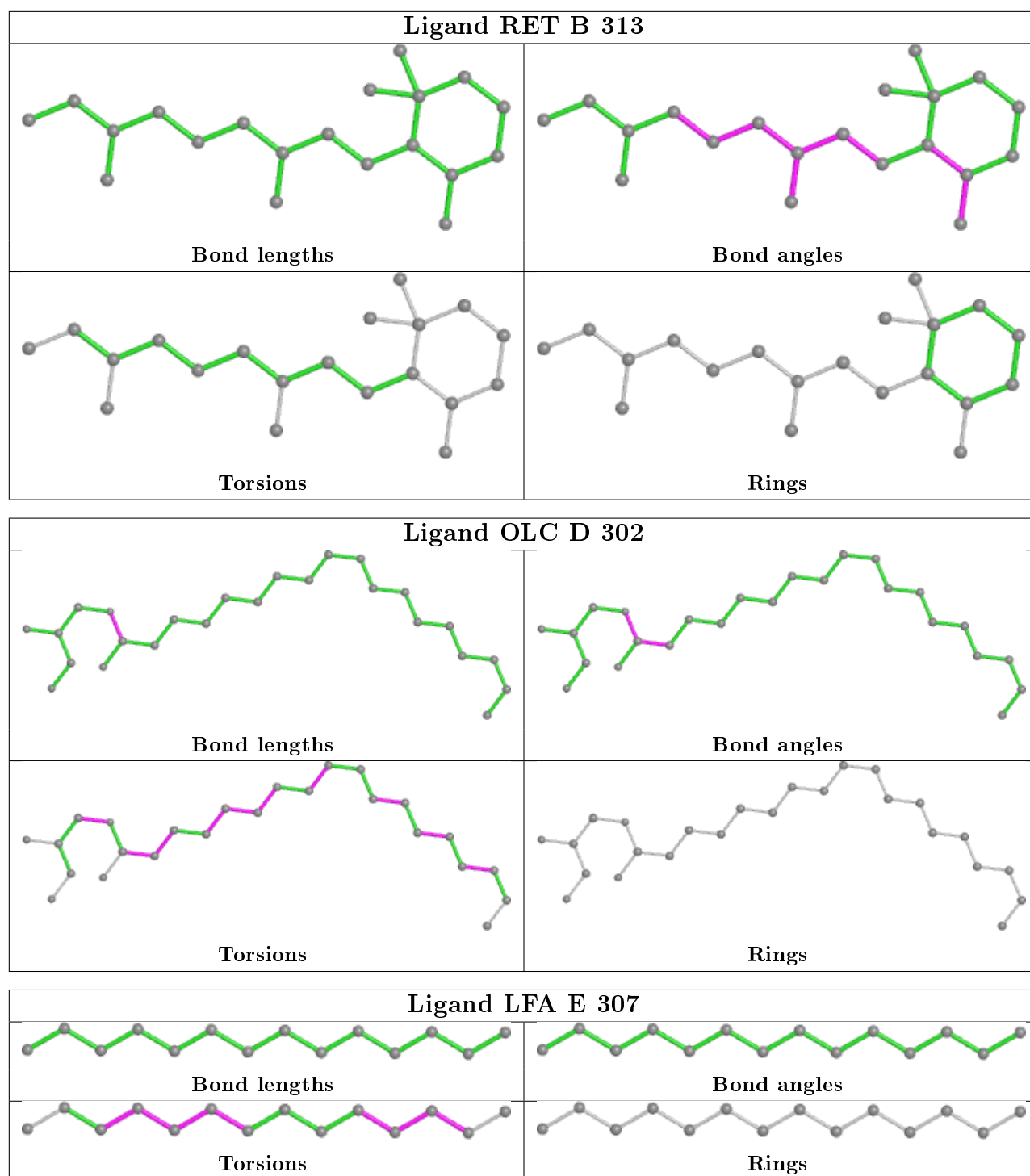


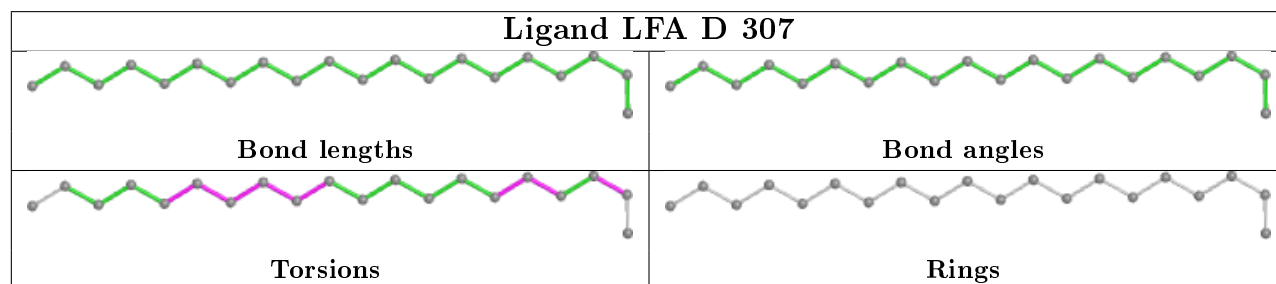
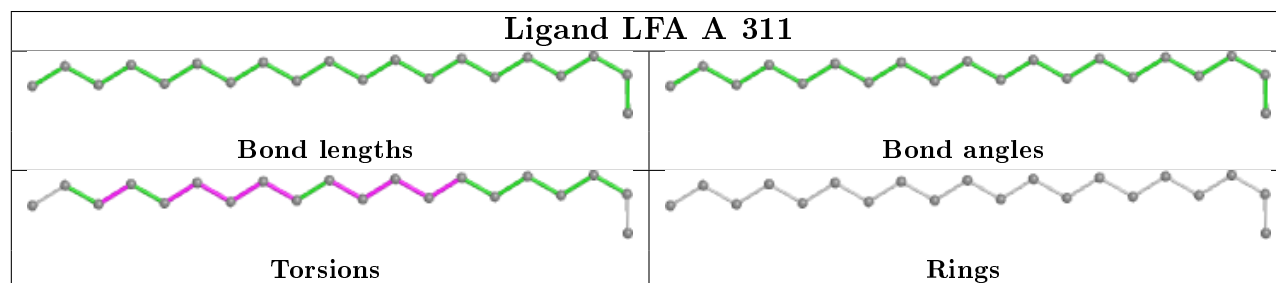
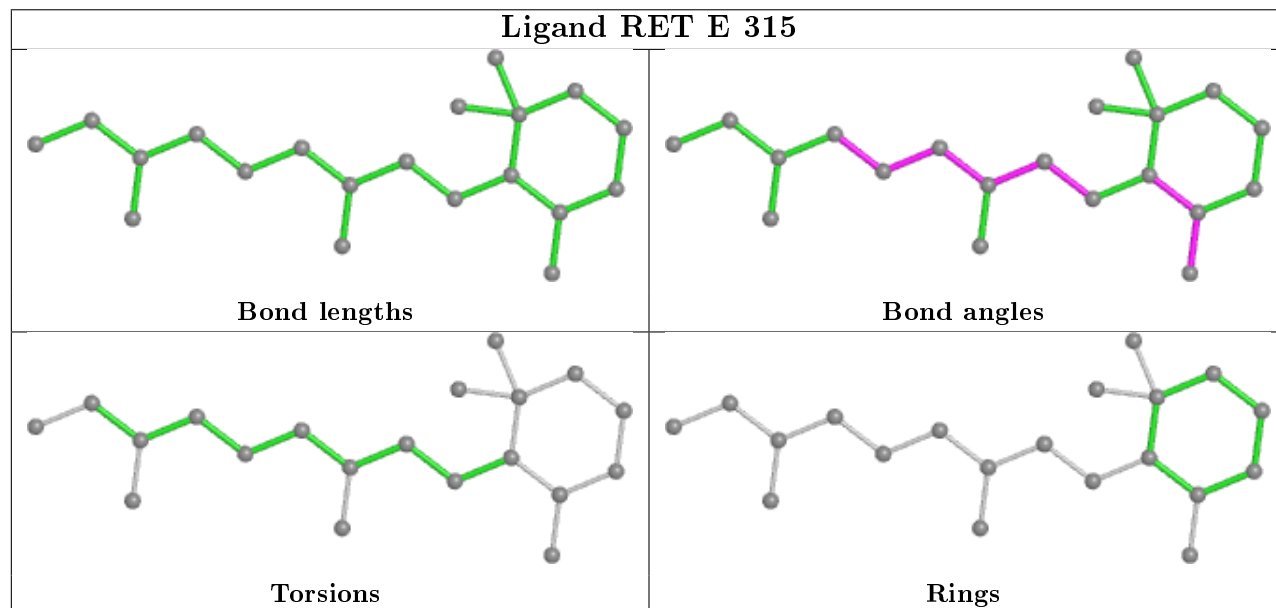
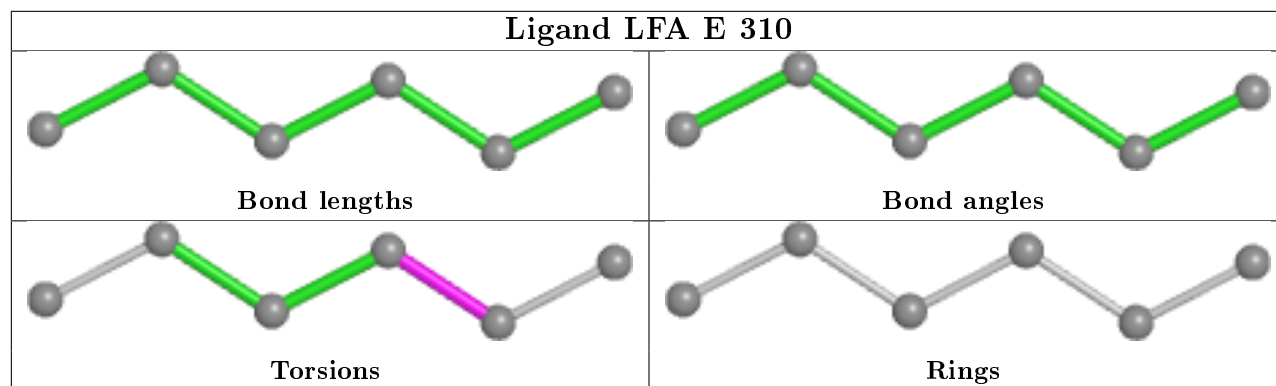


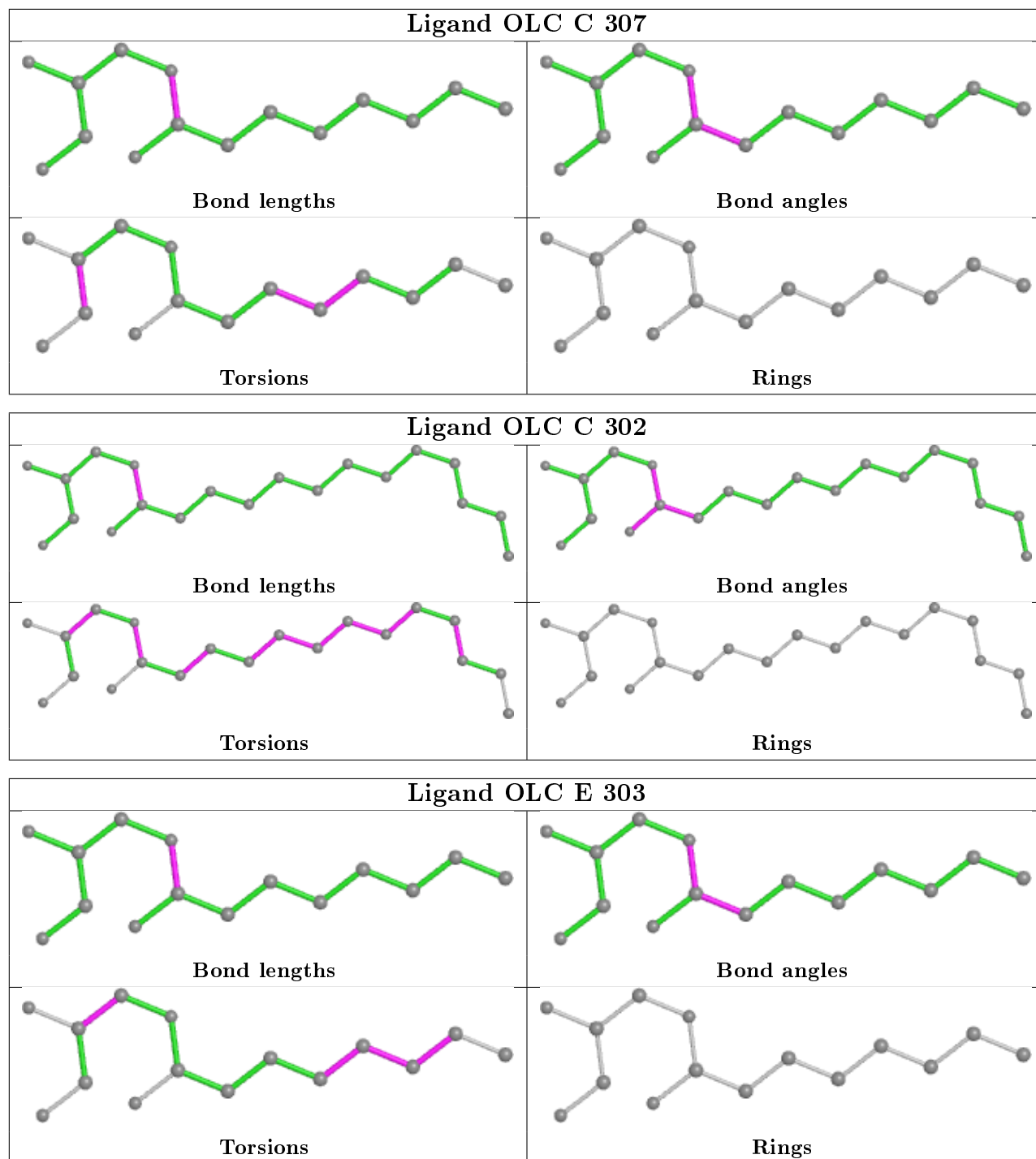


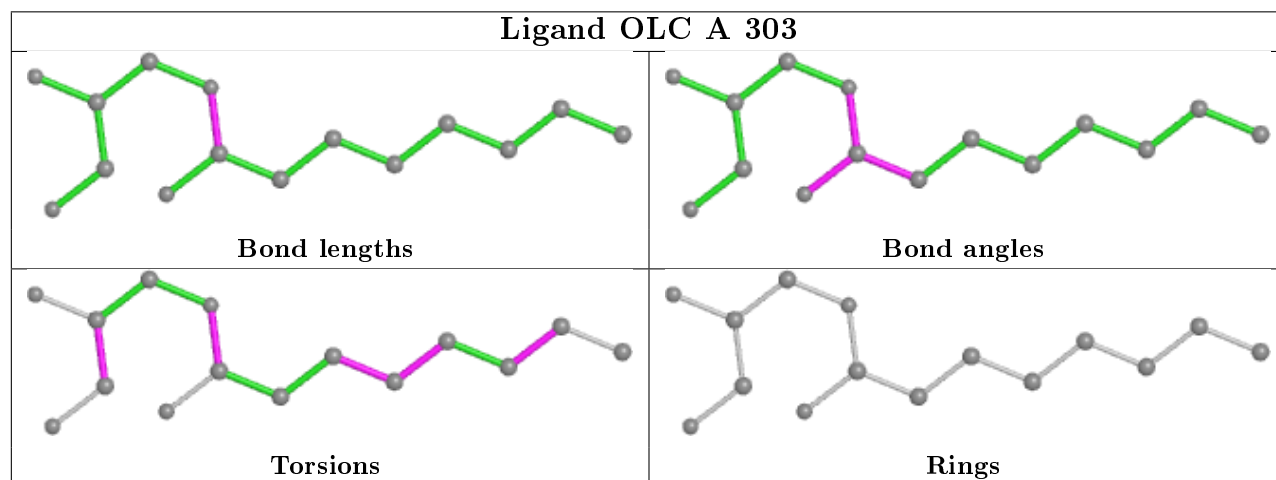
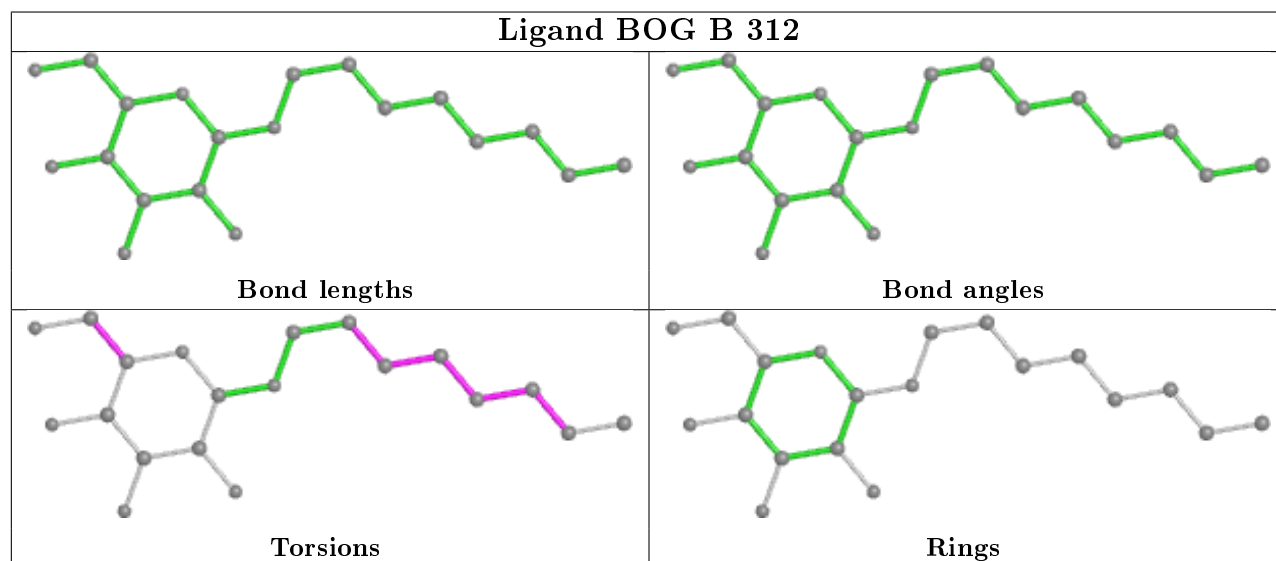
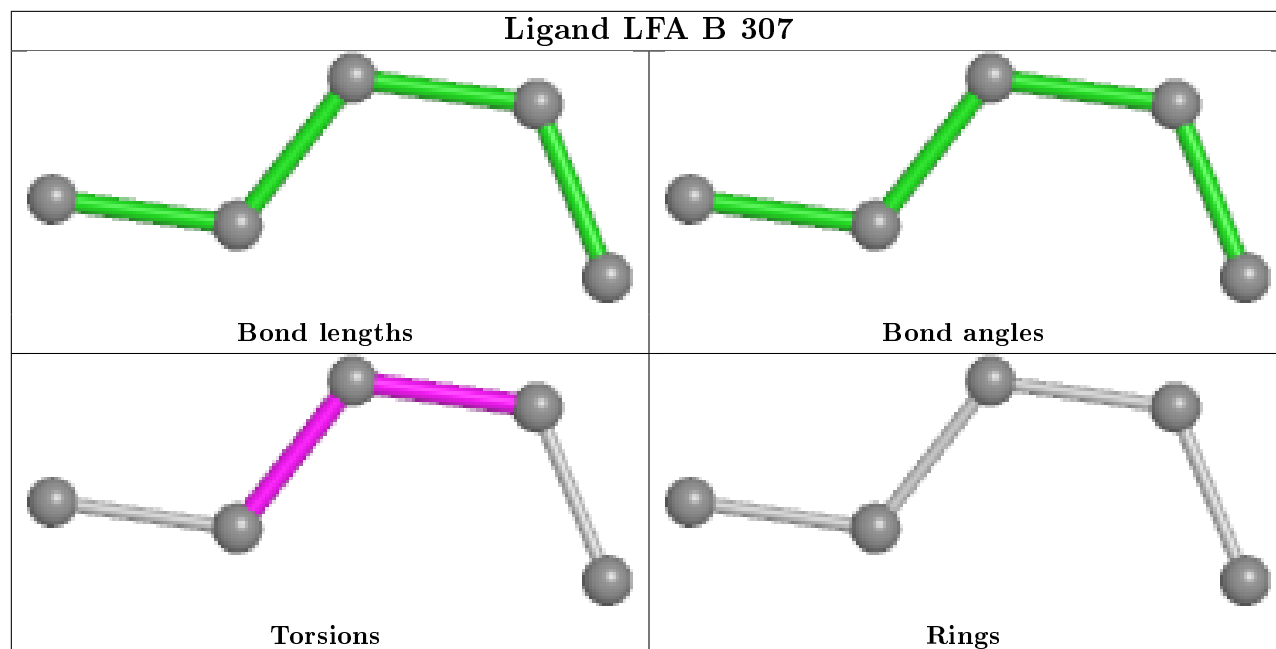












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	273/273 (100%)	0.77	31 (11%) 5 4	23, 34, 59, 110	0
1	B	273/273 (100%)	0.69	22 (8%) 12 10	23, 35, 59, 95	0
1	C	273/273 (100%)	0.80	38 (13%) 2 2	22, 35, 58, 117	0
1	D	273/273 (100%)	0.79	36 (13%) 3 2	21, 36, 60, 140	0
1	E	273/273 (100%)	0.75	44 (16%) 1 1	22, 36, 59, 121	0
All	All	1365/1365 (100%)	0.76	171 (12%) 3 3	21, 35, 59, 140	0

The worst 5 of 171 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	274	GLU	7.7
1	D	275	LEU	7.2
1	D	131	THR	6.2
1	C	230	VAL	6.0
1	A	272	ASN	6.0

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 monosaccharides 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(Å ²)	Q<0.9
2	OLC	C	309	16/25	0.55	0.47	55,75,96,106	0
3	LFA	A	306	8/20	0.60	0.32	49,72,86,89	0
5	BOG	A	310	20/20	0.61	0.59	53,78,98,102	0
2	OLC	D	305	25/25	0.62	0.52	63,78,95,109	0
3	LFA	B	306	9/20	0.63	0.44	71,81,86,88	0
3	LFA	C	314	4/20	0.65	0.56	64,65,68,69	0
3	LFA	C	313	11/20	0.65	0.47	58,77,93,93	0
5	BOG	E	312	20/20	0.68	0.43	50,86,110,114	0
3	LFA	B	302	20/20	0.68	1.19	43,63,75,78	0
3	LFA	C	310	7/20	0.69	0.33	51,58,67,69	0
2	OLC	C	303	16/25	0.69	0.41	63,76,93,104	0
5	BOG	B	312	20/20	0.69	0.70	66,87,108,108	0
3	LFA	D	312	20/20	0.69	1.13	42,58,75,80	0
3	LFA	B	308	10/20	0.70	0.33	54,69,81,82	0
5	BOG	C	317	20/20	0.71	0.52	57,84,95,101	0
3	LFA	D	308	8/20	0.71	0.31	55,74,88,94	0
2	OLC	C	307	15/25	0.74	0.30	48,63,81,87	0
3	LFA	C	312	12/20	0.74	0.33	60,65,76,79	0
3	LFA	E	307	14/20	0.74	0.27	47,71,88,93	0
3	LFA	A	311	20/20	0.75	1.02	34,65,78,78	0
2	OLC	E	302	25/25	0.77	0.34	62,78,114,119	0
3	LFA	C	311	8/20	0.77	0.30	42,59,64,65	0
2	OLC	D	302	25/25	0.77	0.34	55,76,110,116	0
2	OLC	B	305	17/25	0.77	0.42	49,79,102,104	0
3	LFA	E	305	8/20	0.77	0.30	61,67,71,72	0
3	LFA	D	310	7/20	0.77	0.30	53,59,69,71	0
2	OLC	A	301	22/25	0.78	0.34	38,51,92,94	0
3	LFA	D	306	20/20	0.78	0.46	64,86,95,95	0
2	OLC	D	303	18/25	0.78	0.42	47,71,84,106	0
2	OLC	E	301	24/25	0.78	0.35	41,52,91,94	0
2	OLC	B	303	20/25	0.79	0.35	46,58,87,92	0
3	LFA	B	309	7/20	0.79	0.32	56,59,73,78	0
2	OLC	C	306	18/25	0.79	0.31	57,71,86,90	0
5	BOG	D	314	20/20	0.79	0.51	66,84,88,90	0
2	OLC	E	304	25/25	0.79	0.47	42,72,104,111	0
3	LFA	E	309	5/20	0.79	0.28	61,65,69,72	0
3	LFA	C	304	20/20	0.80	0.99	34,51,62,64	0
3	LFA	E	308	4/20	0.80	0.31	62,62,63,67	0
2	OLC	E	303	15/25	0.80	0.36	56,67,75,77	0
2	OLC	C	302	20/25	0.81	0.29	55,68,73,81	0

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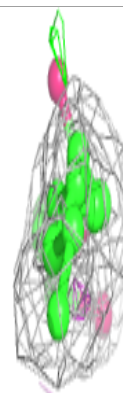
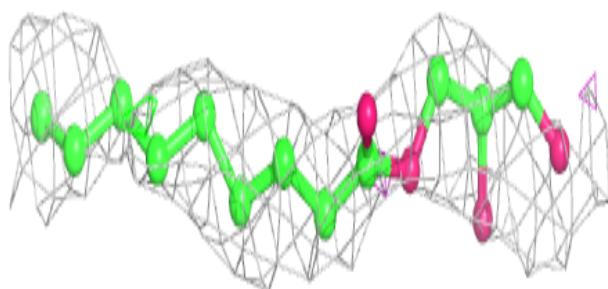
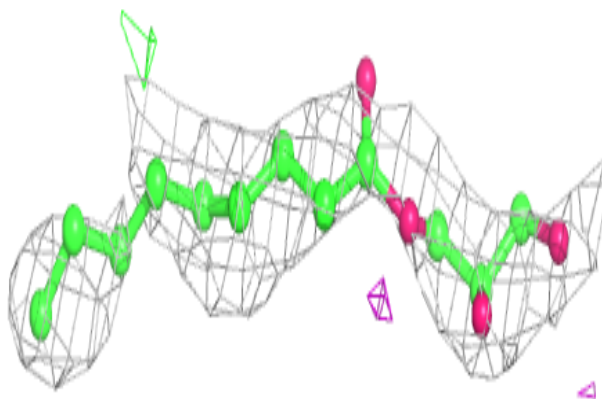
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	LFA	D	307	20/20	0.81	0.32	56,70,85,90	0
3	LFA	A	304	8/20	0.81	0.30	52,58,66,67	0
2	OLC	C	305	23/25	0.82	0.36	34,45,95,121	0
3	LFA	D	301	20/20	0.82	0.91	34,53,63,65	0
4	NA	E	311	1/1	0.82	0.20	34,34,34,34	0
3	LFA	B	307	5/20	0.83	0.23	30,35,40,42	0
3	LFA	E	314	14/20	0.83	1.30	86,97,101,105	0
3	LFA	A	307	4/20	0.84	0.35	52,58,59,63	0
3	LFA	B	310	6/20	0.84	0.34	49,51,53,54	0
2	OLC	C	301	21/25	0.84	0.33	39,46,63,83	0
3	LFA	E	306	6/20	0.85	0.51	53,58,61,61	0
3	LFA	A	305	5/20	0.85	0.29	50,51,56,57	0
2	OLC	A	302	13/25	0.85	0.36	47,59,65,79	0
3	LFA	D	311	6/20	0.86	0.26	37,41,44,47	0
2	OLC	A	303	15/25	0.86	0.30	50,56,78,81	0
2	OLC	B	301	25/25	0.87	0.29	60,77,94,100	0
2	OLC	B	304	16/25	0.87	0.31	54,61,67,71	0
3	LFA	E	313	4/20	0.88	1.65	59,63,67,70	0
2	OLC	D	304	14/25	0.89	0.30	46,68,75,77	0
3	LFA	D	309	17/20	0.89	0.39	37,45,50,50	0
3	LFA	C	315	6/20	0.89	0.32	39,42,45,45	0
6	RET	A	312	20/21	0.90	0.21	26,31,36,40	0
6	RET	E	315	20/21	0.90	0.22	24,28,38,38	0
2	OLC	C	308	16/25	0.90	0.25	41,58,71,77	0
6	RET	B	313	20/21	0.91	0.22	25,32,35,40	0
3	LFA	A	308	6/20	0.91	0.24	43,44,45,47	0
4	NA	B	311	1/1	0.91	0.13	33,33,33,33	0
6	RET	C	318	20/21	0.92	0.22	27,31,38,38	0
3	LFA	E	310	6/20	0.93	0.20	46,50,51,55	0
6	RET	D	315	20/21	0.93	0.19	29,34,40,41	0
4	NA	A	309	1/1	0.94	0.20	36,36,36,36	0
4	NA	D	313	1/1	0.96	0.09	34,34,34,34	0
4	NA	C	316	1/1	0.97	0.07	25,25,25,25	0

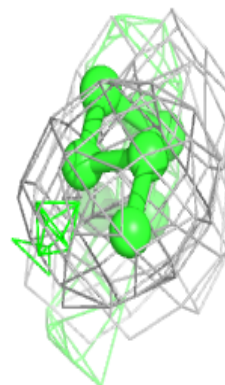
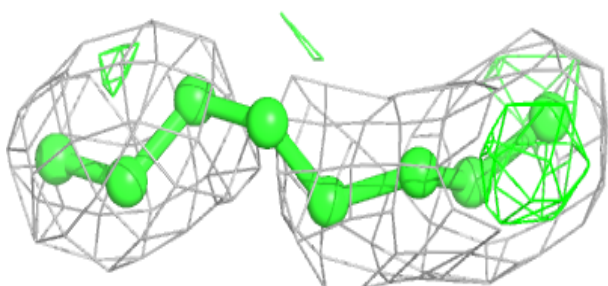
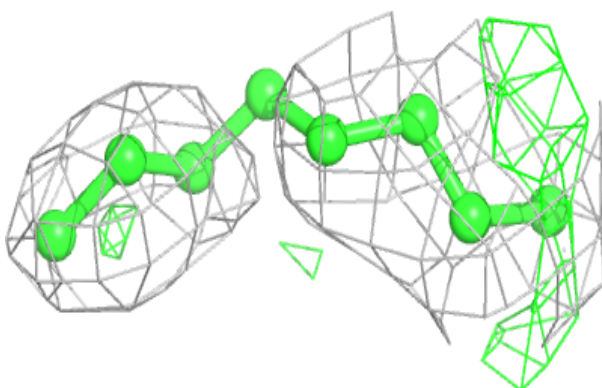
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around OLC 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)

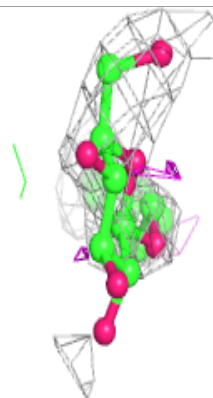
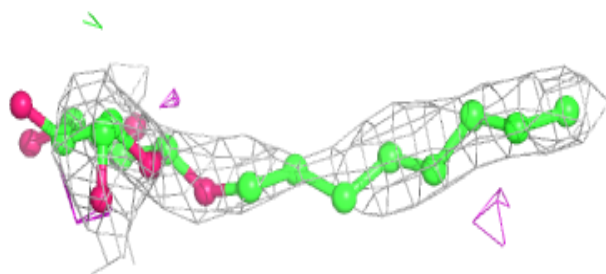
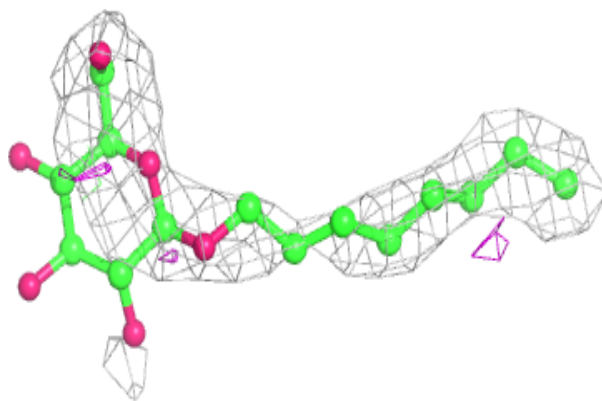
**Electron density around LFA A 306:**

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

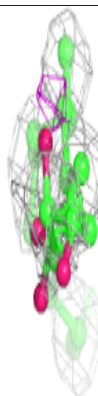
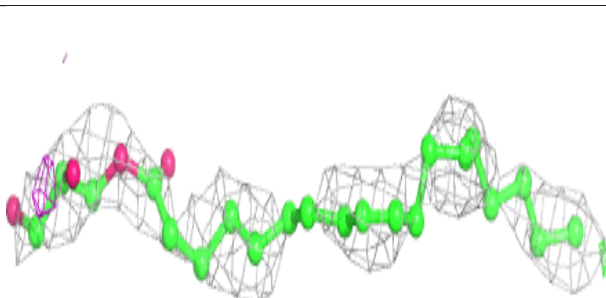
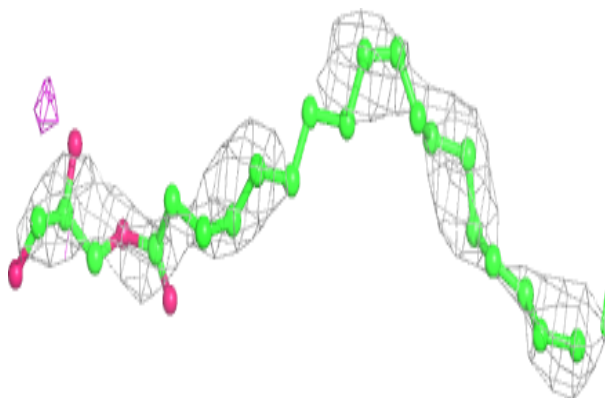


Electron density around BOG A 310:

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

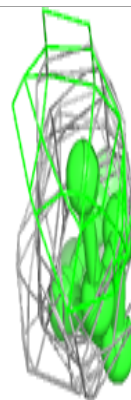
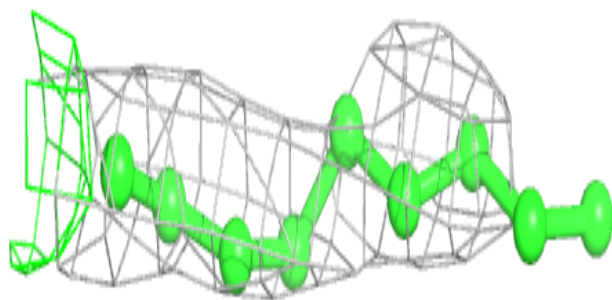
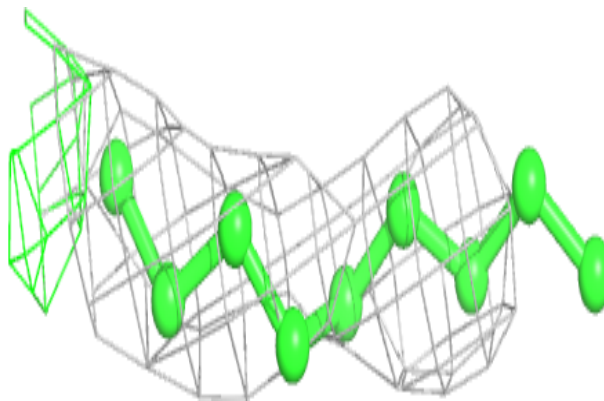
**Electron density around OLC D 305:**

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



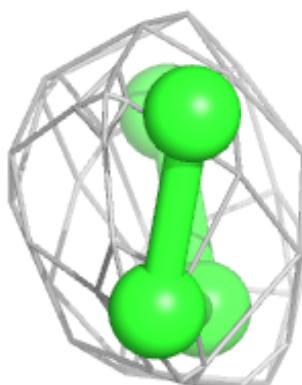
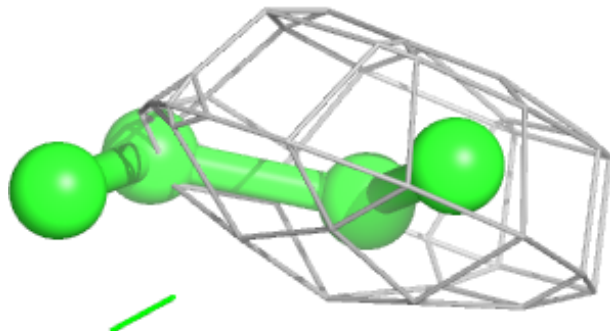
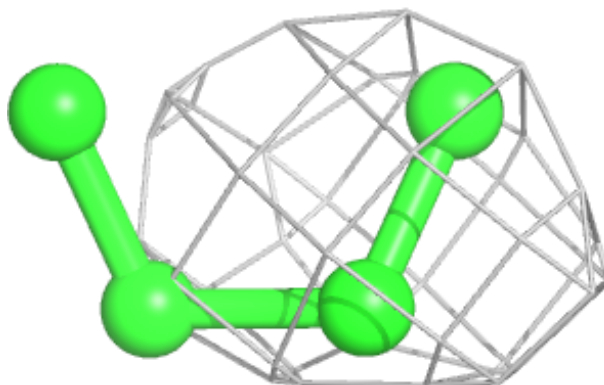
Electron density around LFA B 306:

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



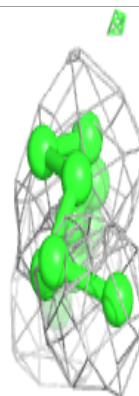
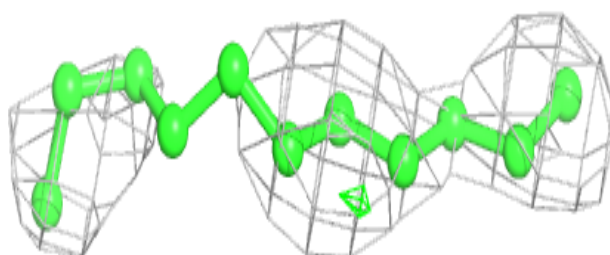
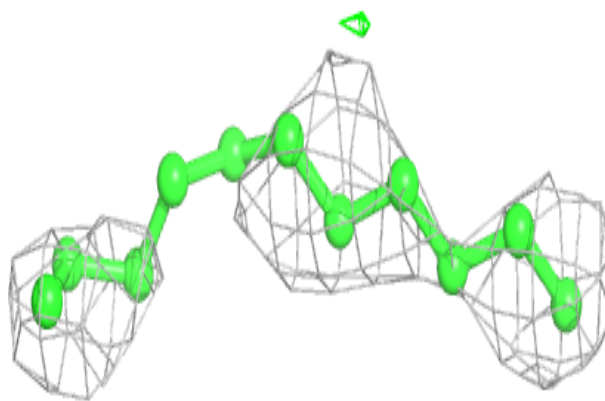
Electron density around LFA C 314:

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

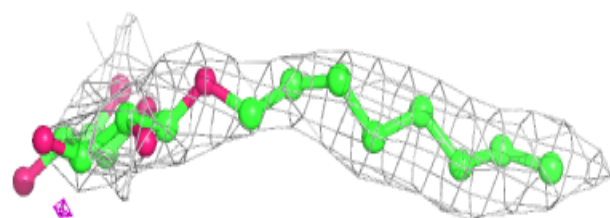
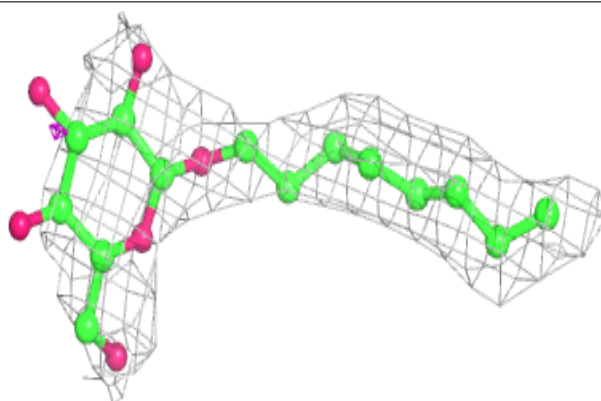


Electron density around LFA C 313:

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

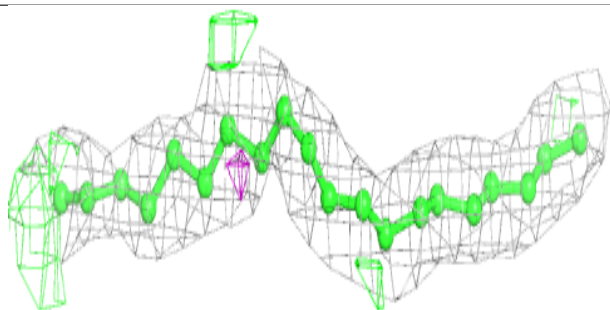
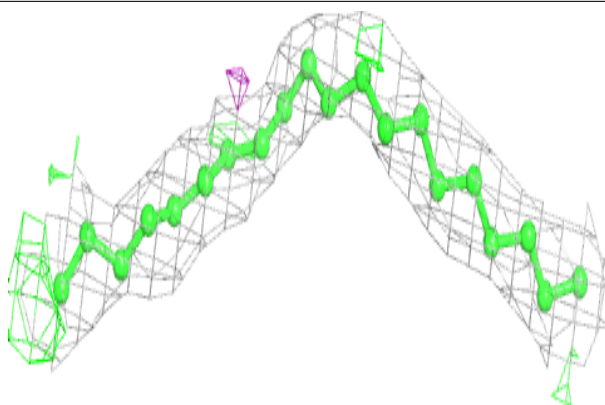
**Electron density around BOG E 312:**

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

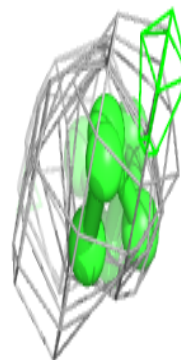
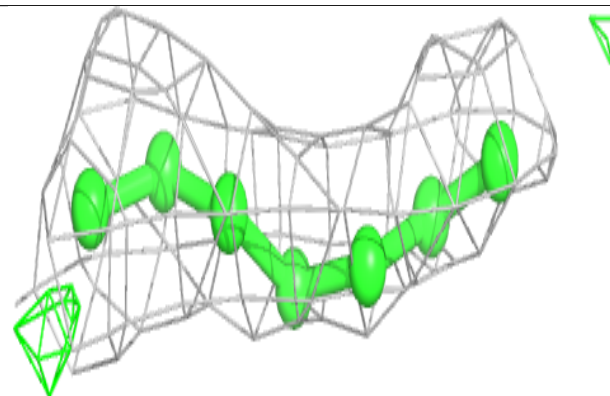
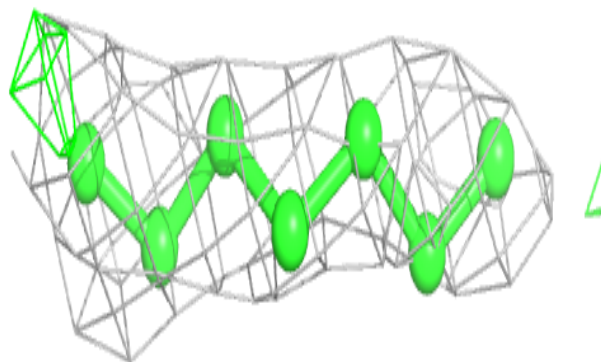


Electron density around LFA B 302:

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

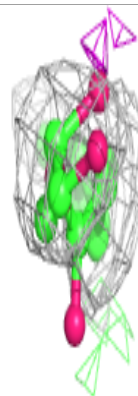
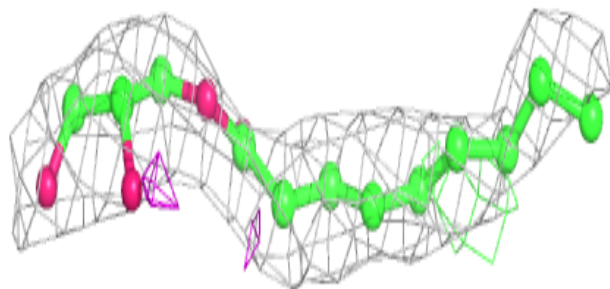
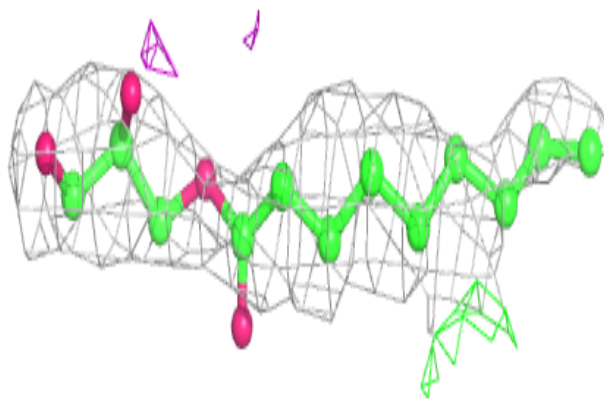
**Electron density around LFA C 310:**

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

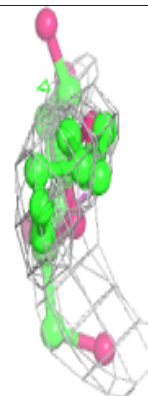
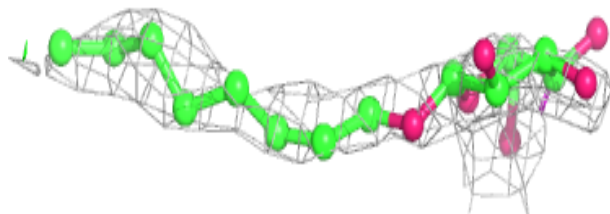
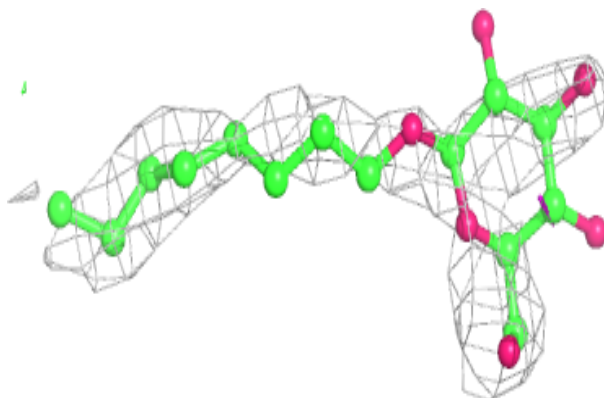


Electron density around OLC C 303:

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

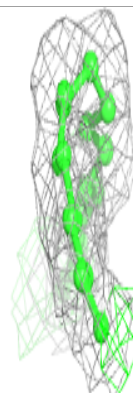
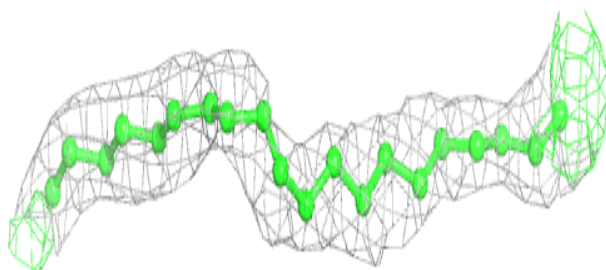
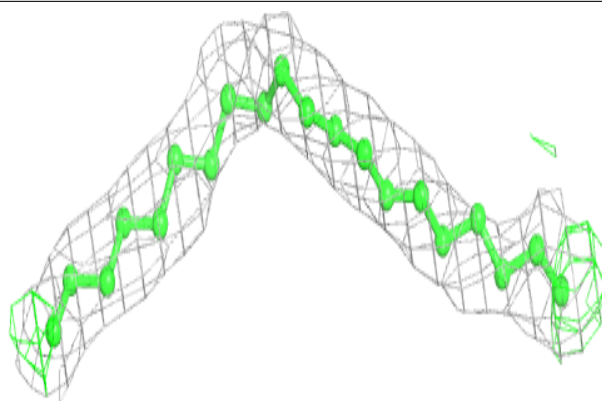
**Electron density around BOG B 312:**

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

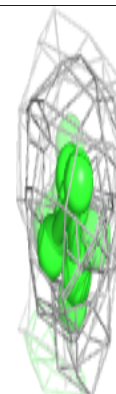
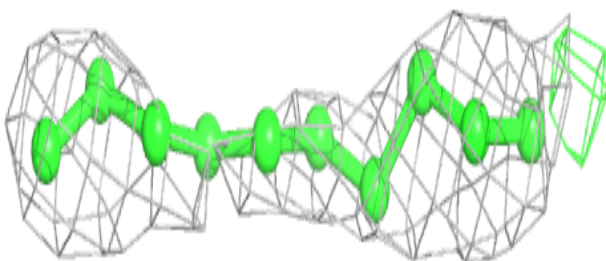
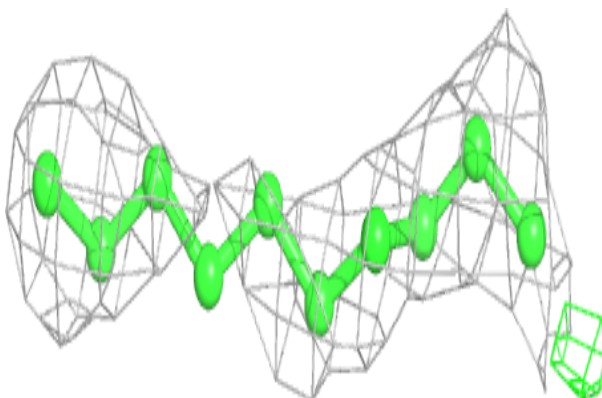


Electron density around LFA D 312:

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

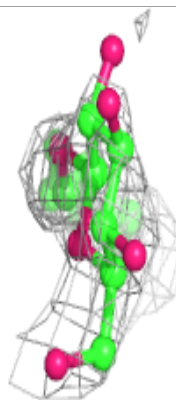
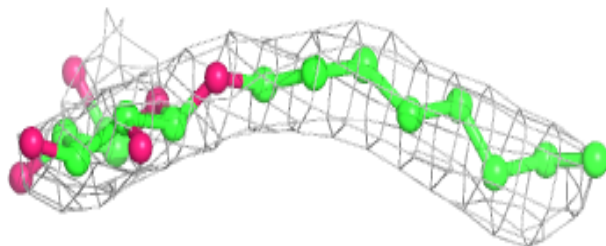
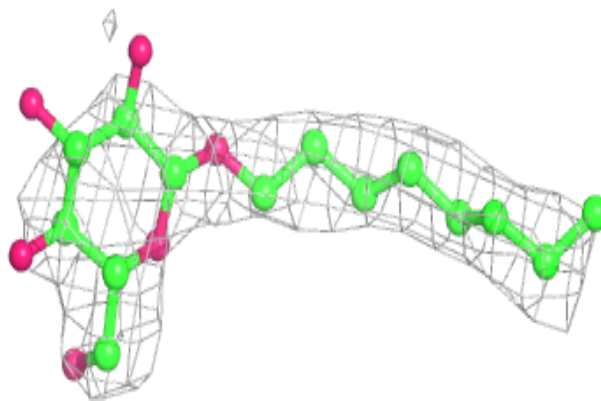
**Electron density around LFA B 308:**

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

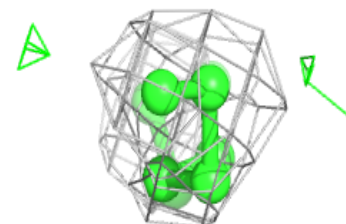
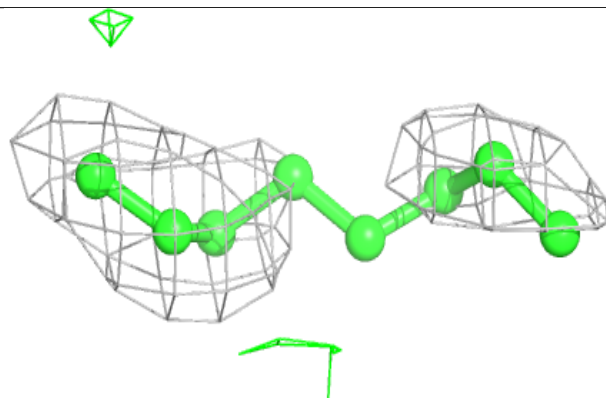
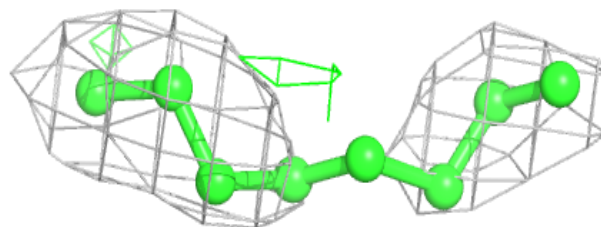


Electron density around BOG C 317:

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

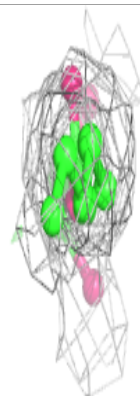
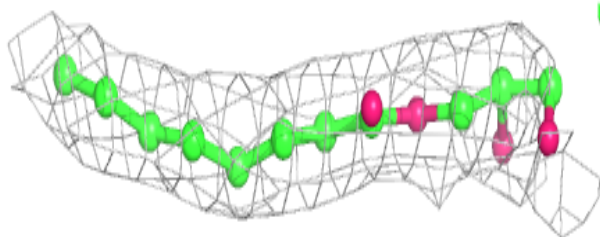
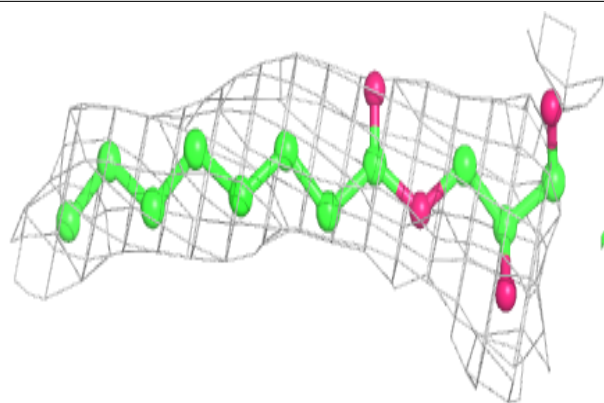
**Electron density around LFA D 308:**

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

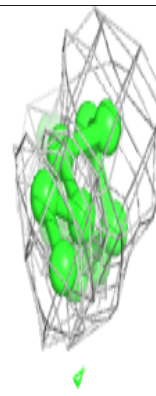
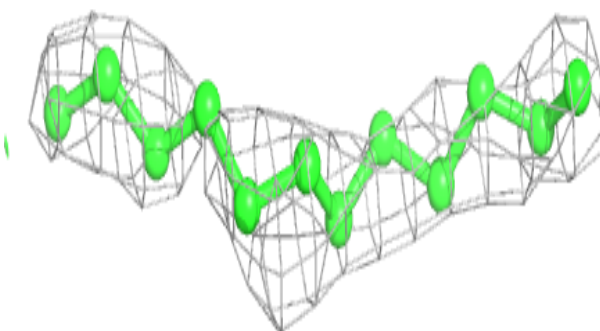
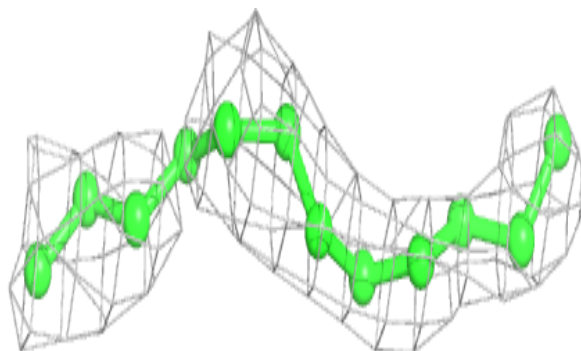


Electron density around OLC C 307:

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

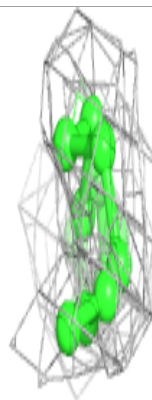
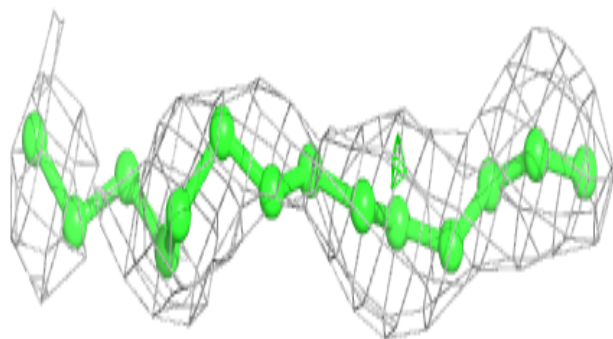
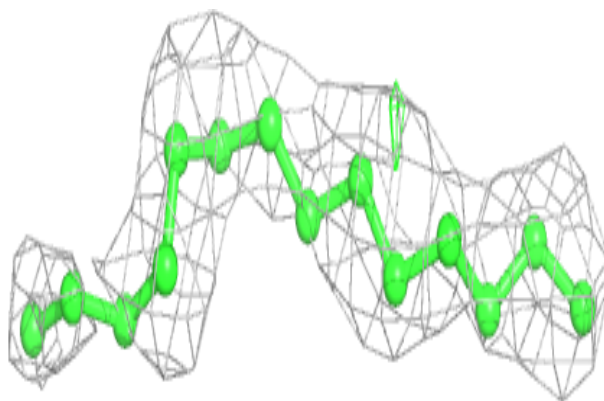
**Electron density around LFA C 312:**

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

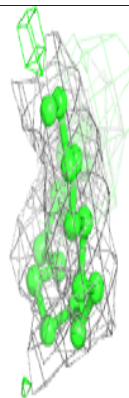
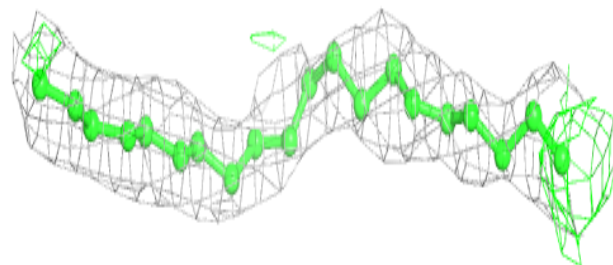
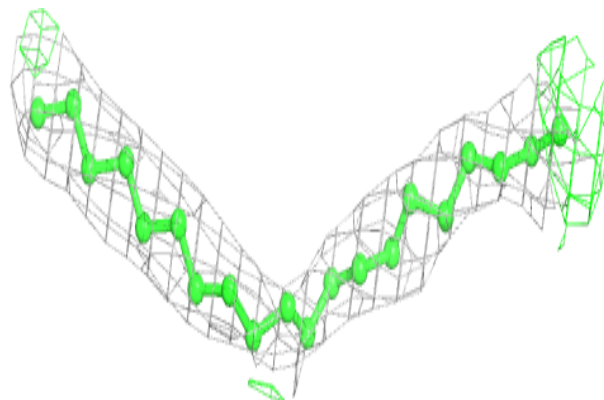


Electron density around LFA E 307:

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

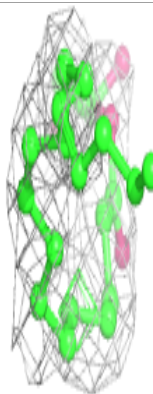
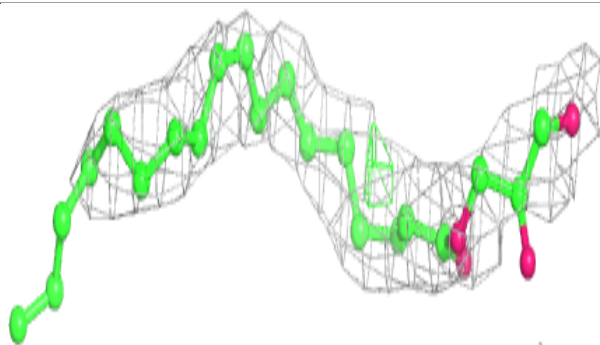
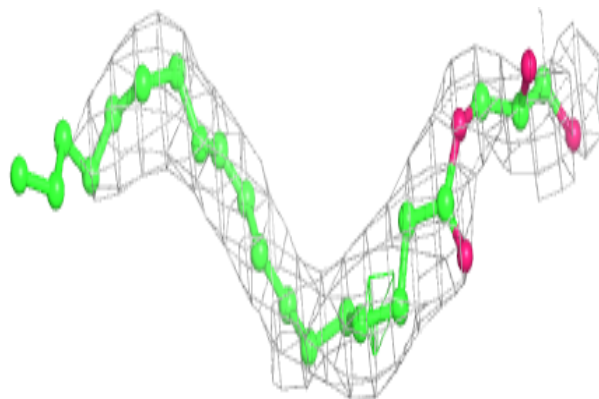
**Electron density around LFA A 311:**

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

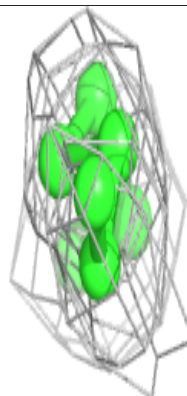
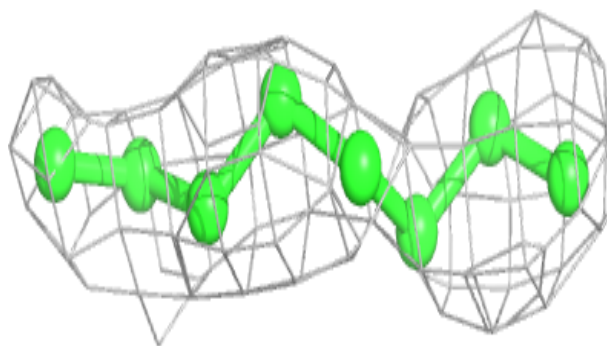
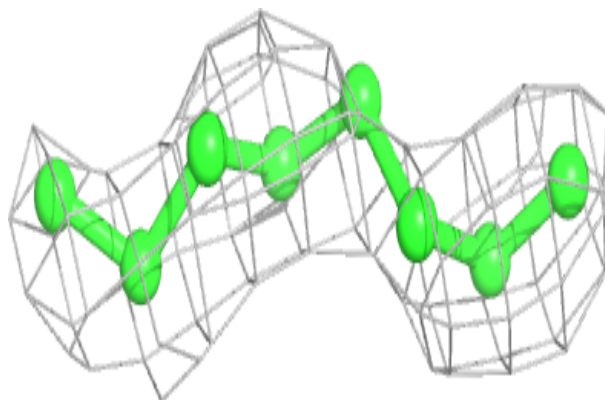


Electron density around OLC E 302:

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

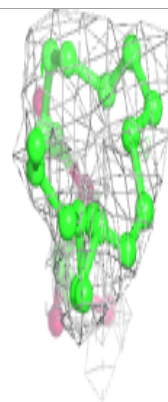
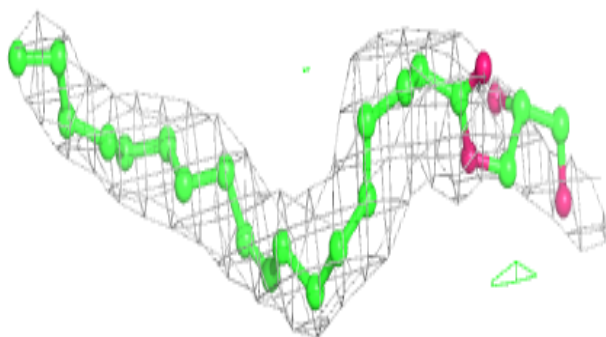
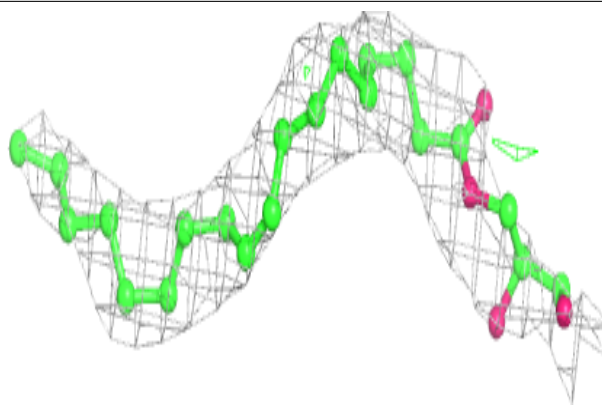
**Electron density around LFA C 311:**

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

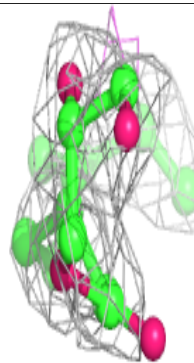
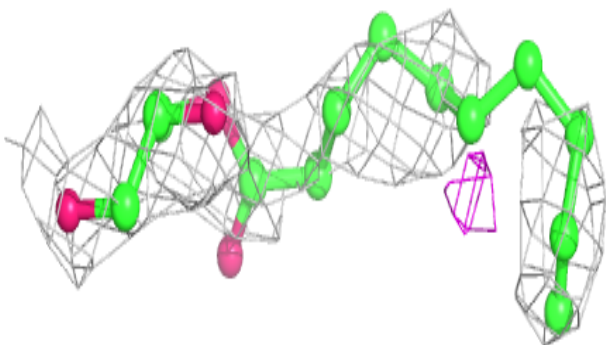
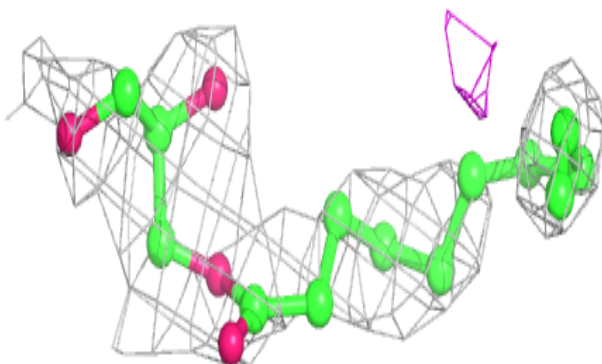


Electron density around OLC D 302:

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

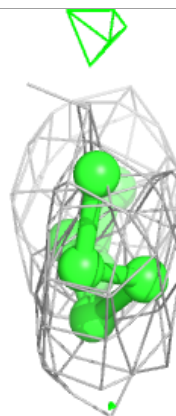
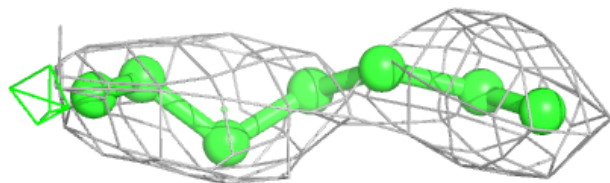
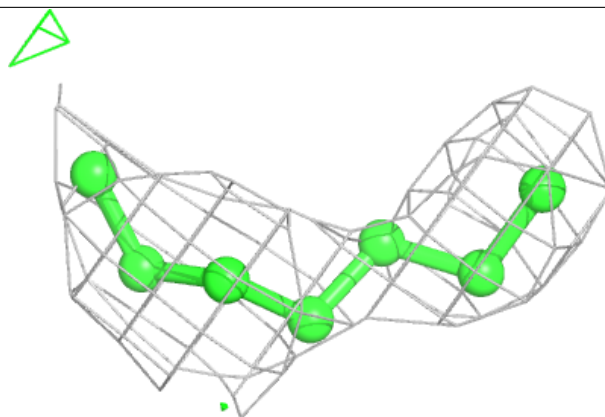
**Electron density around OLC B 305:**

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

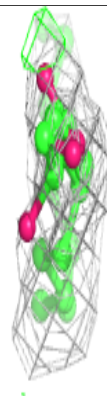
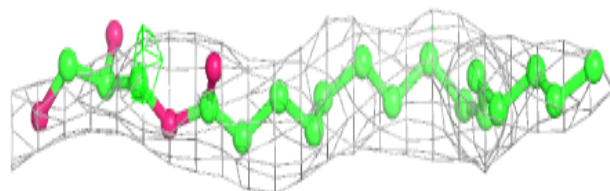
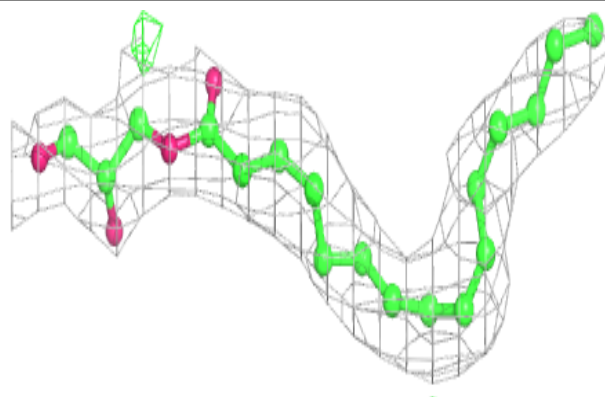


Electron density around LFA D 310:

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

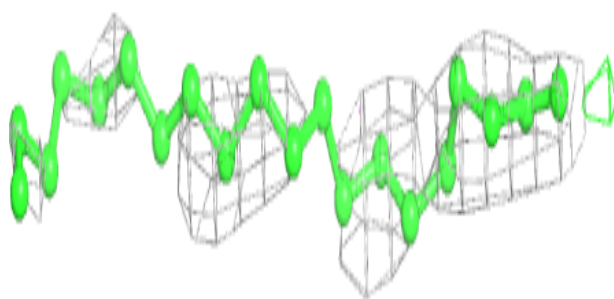
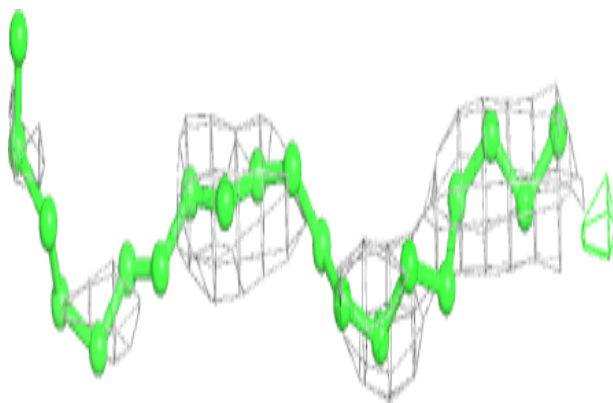
**Electron density around OLC A 301:**

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

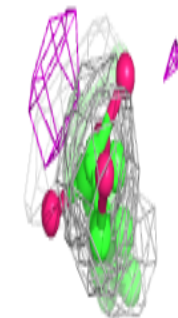
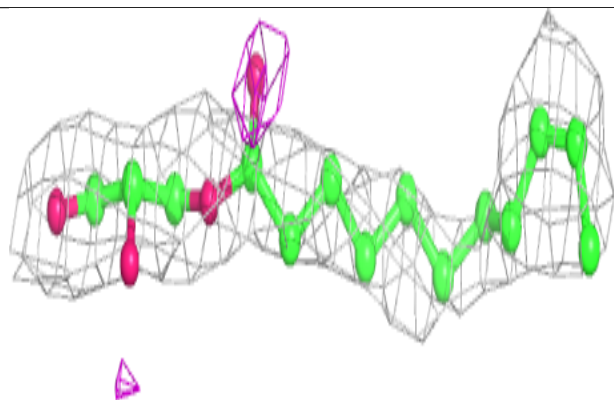
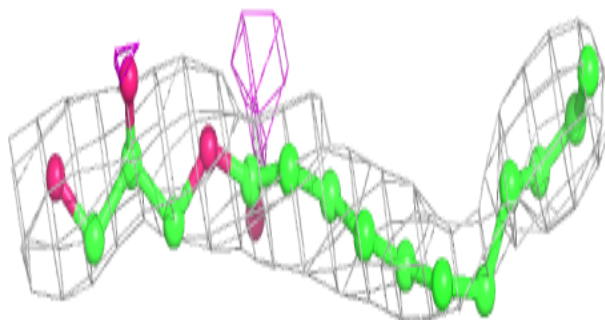


Electron density around LFA D 306:

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

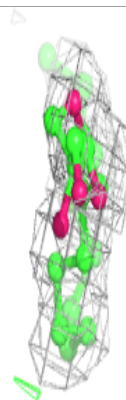
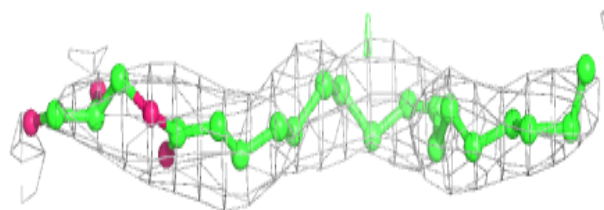
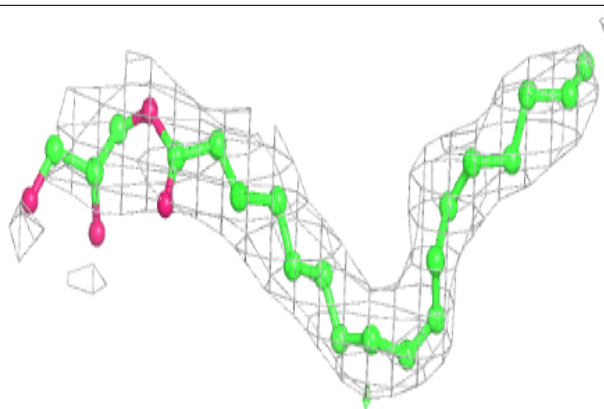
**Electron density around OLC D 303:**

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

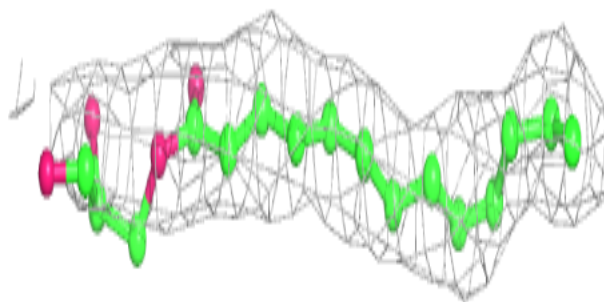
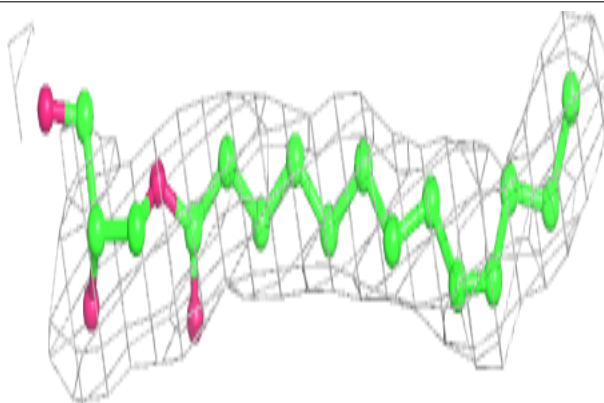


Electron density around OLC E 301:

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

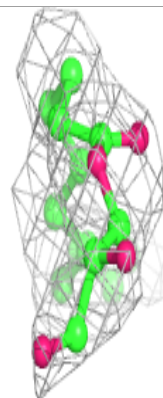
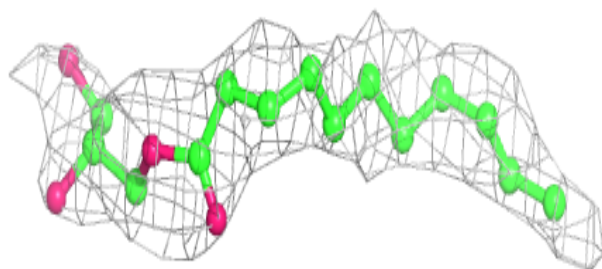
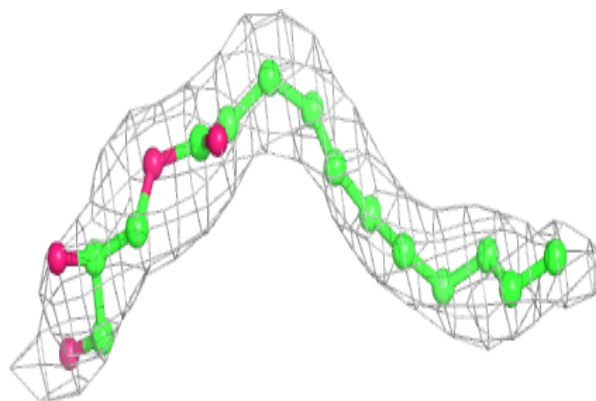
**Electron density around OLC B 303:**

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

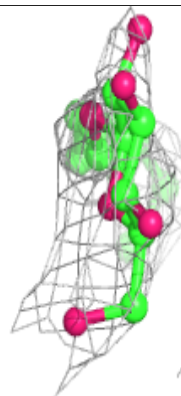
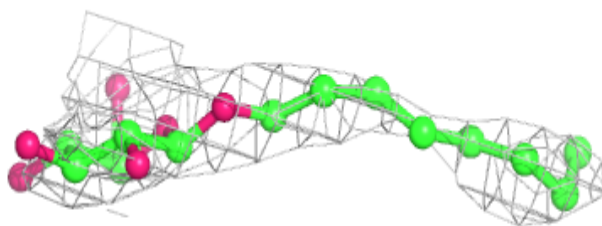
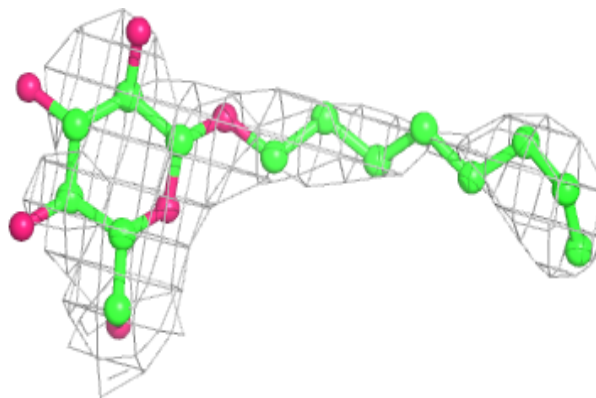


Electron density around OLC C 306:

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

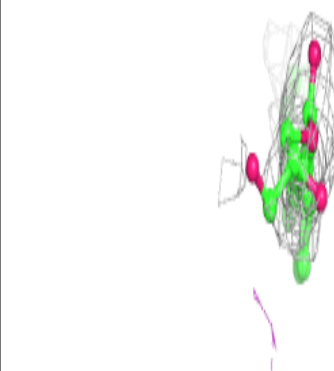
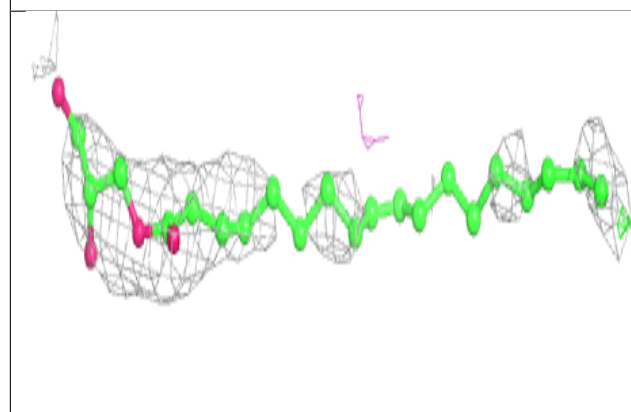
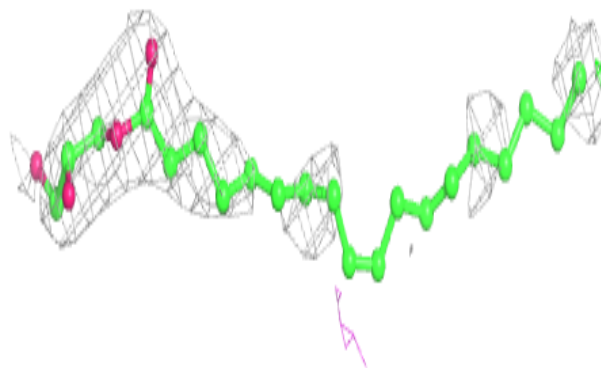
**Electron density around BOG D 314:**

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

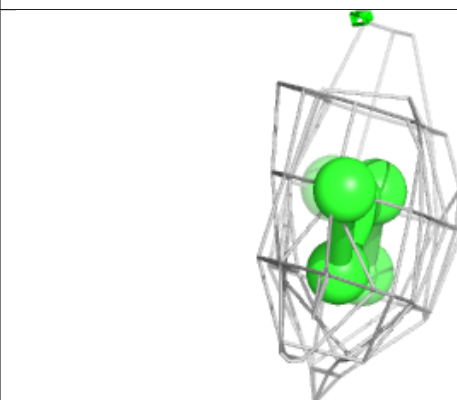
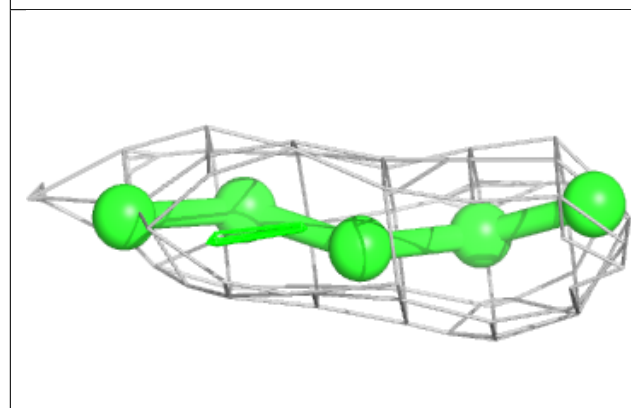
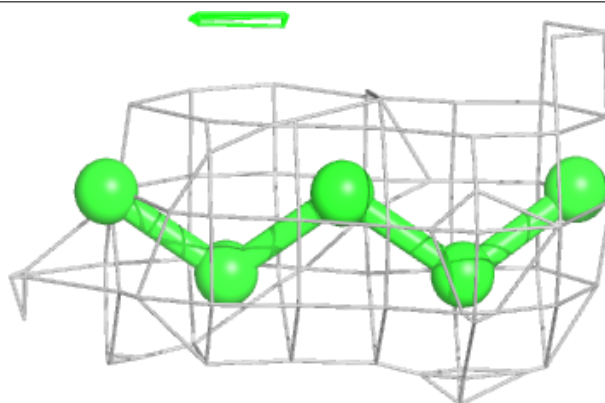


Electron density around OLC E 304:

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

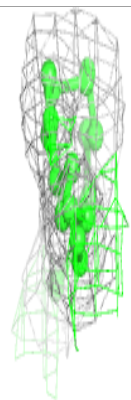
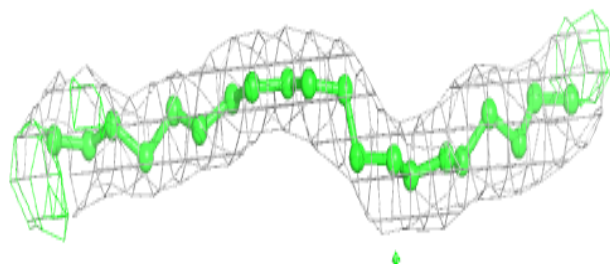
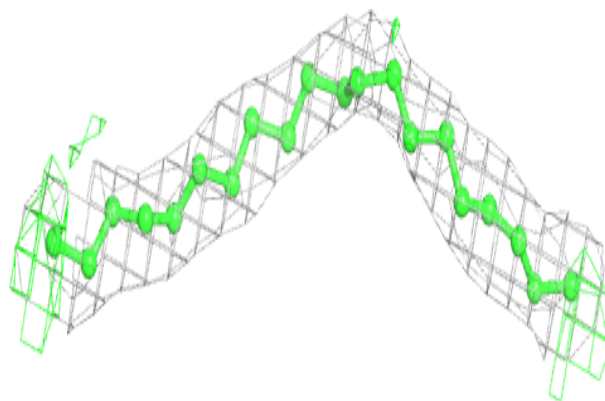
**Electron density around LFA E 309:**

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

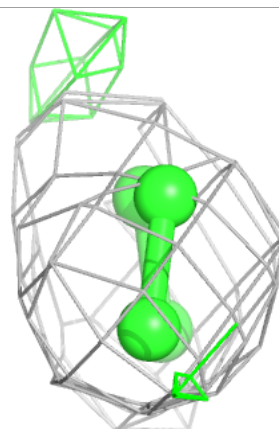
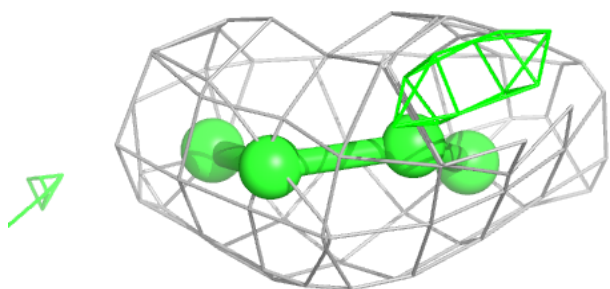
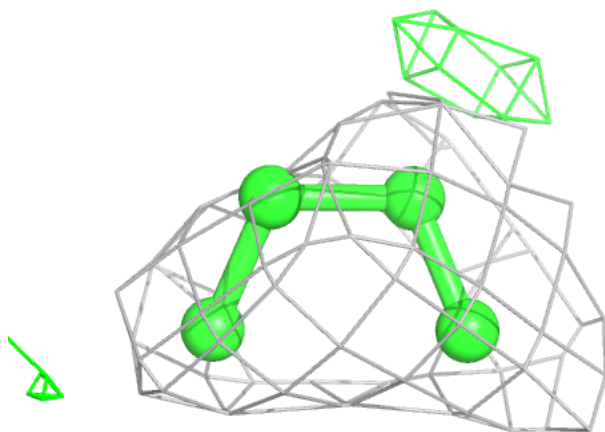


Electron density around LFA C 304:

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

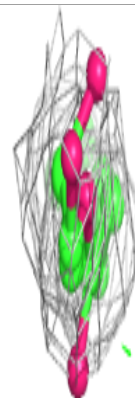
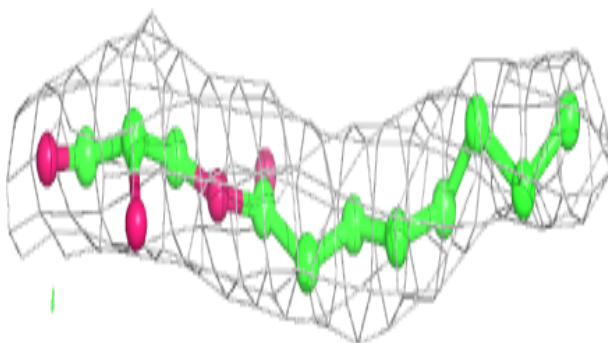
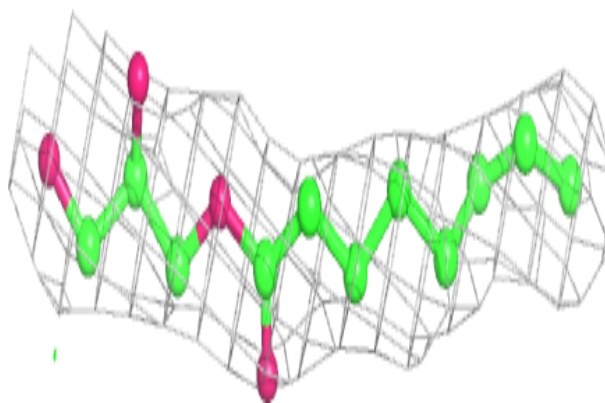
**Electron density around LFA E 308:**

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

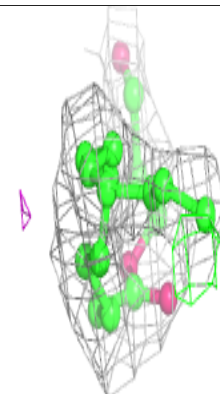
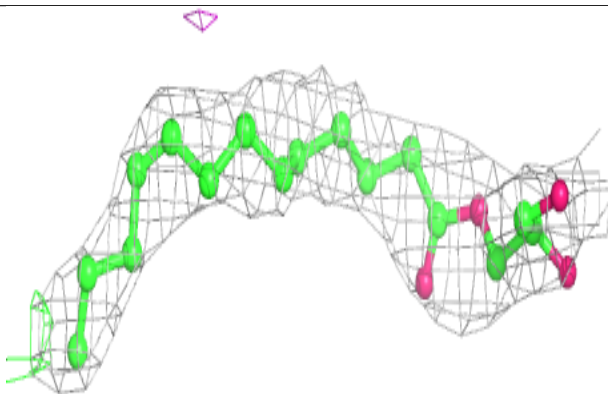
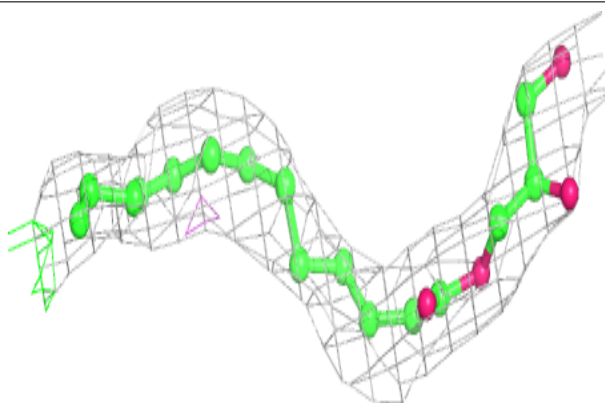


Electron density around OLC E 303:

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

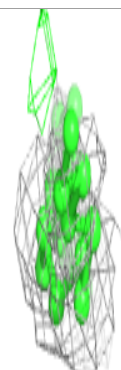
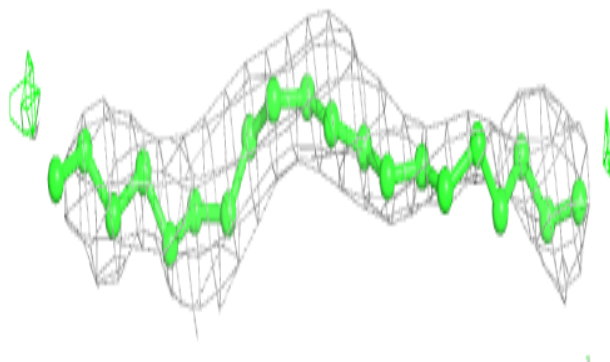
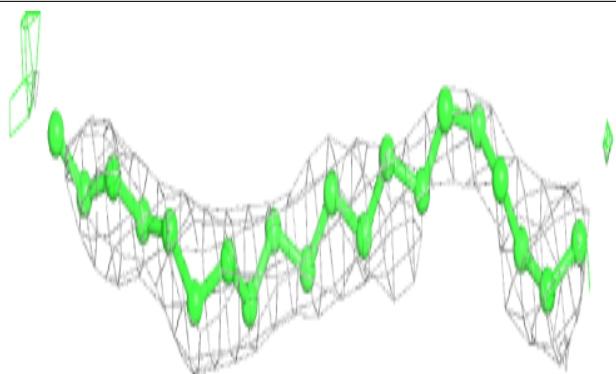
**Electron density around OLC C 302:**

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

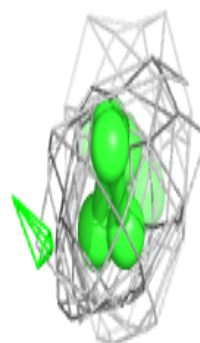
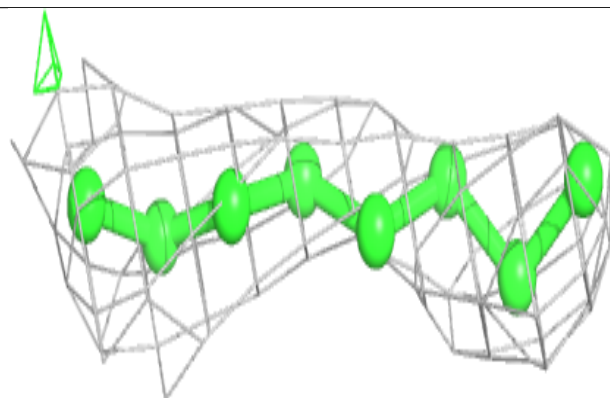
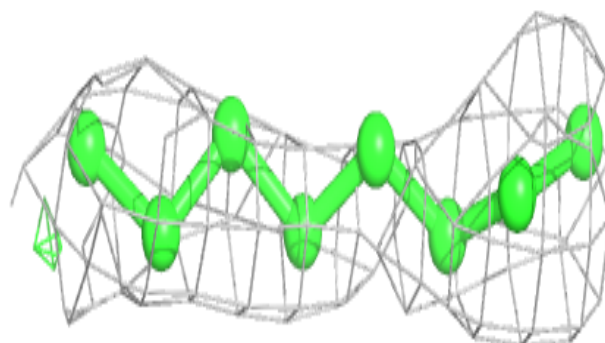


Electron density around LFA D 307:

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

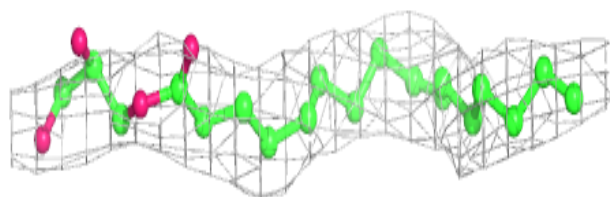
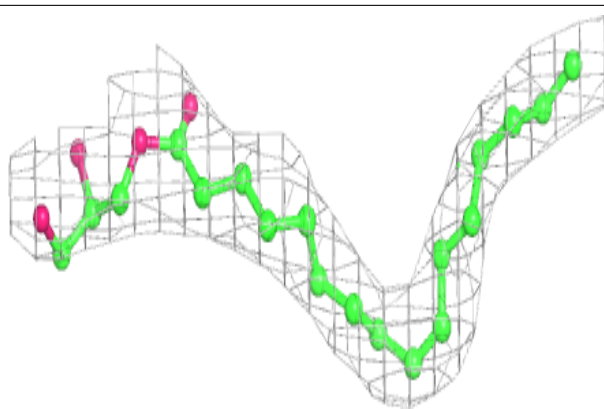
**Electron density around LFA A 304:**

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

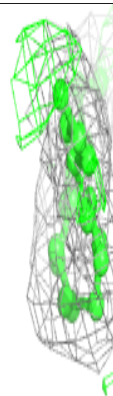
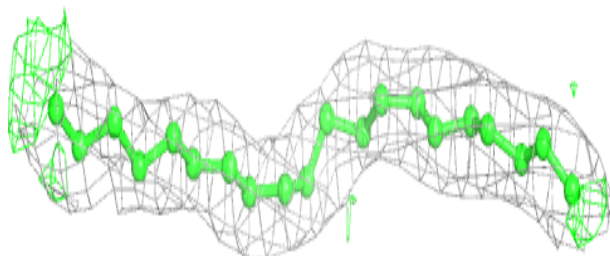
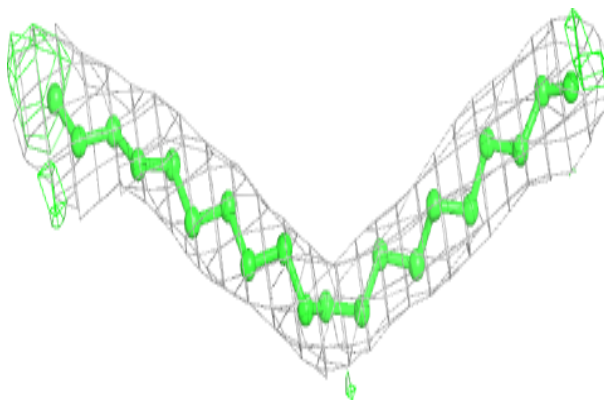


Electron density around OLC C 305:

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

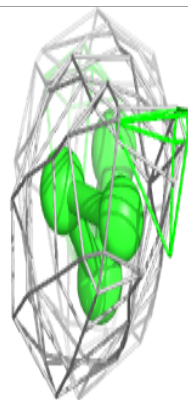
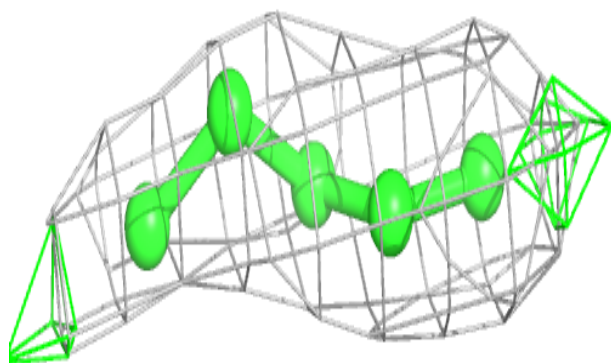
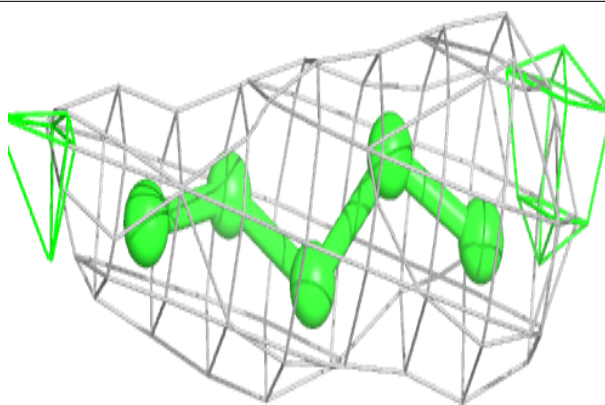
**Electron density around LFA D 301:**

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

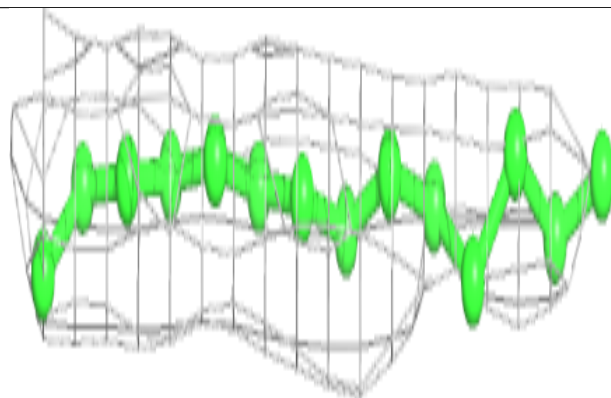
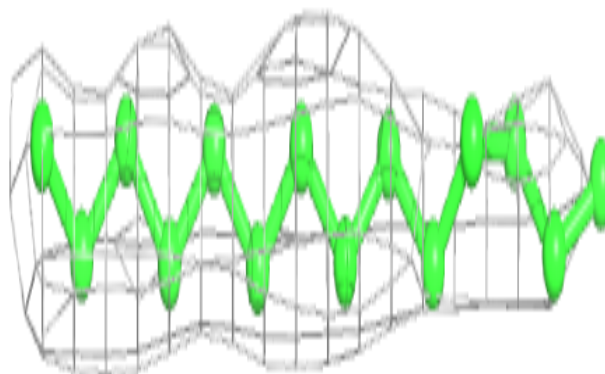


Electron density around LFA B 307:

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

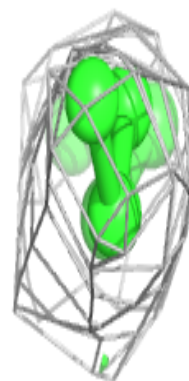
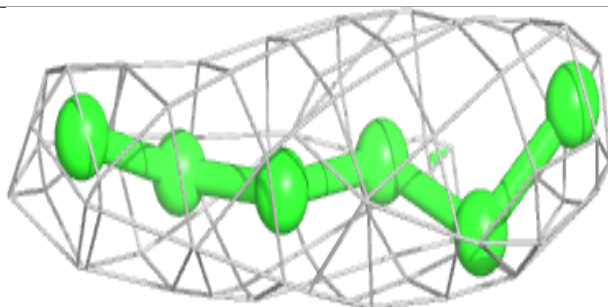
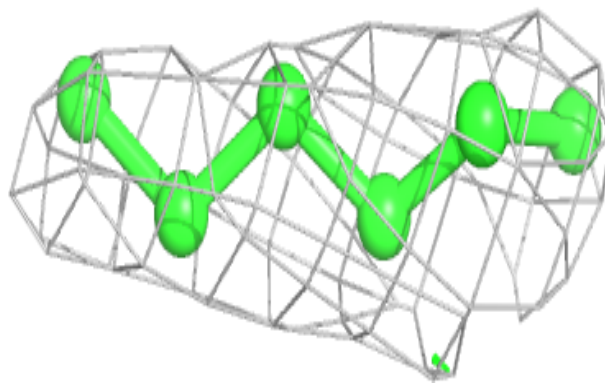
**Electron density around LFA E 314:**

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

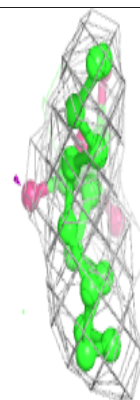
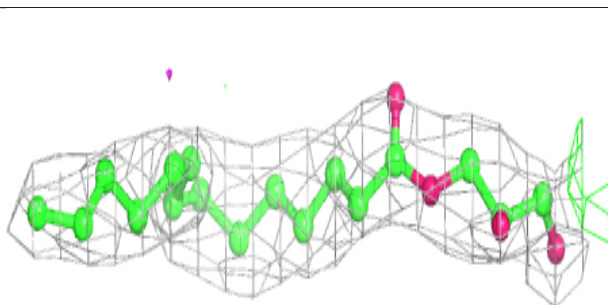
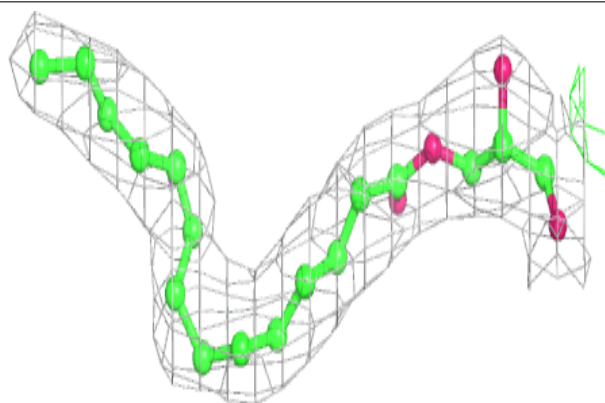


Electron density around LFA B 310:

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

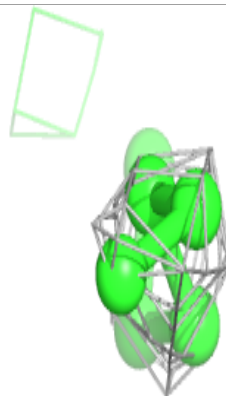
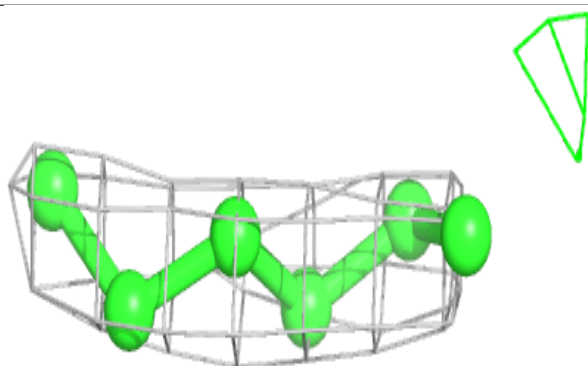
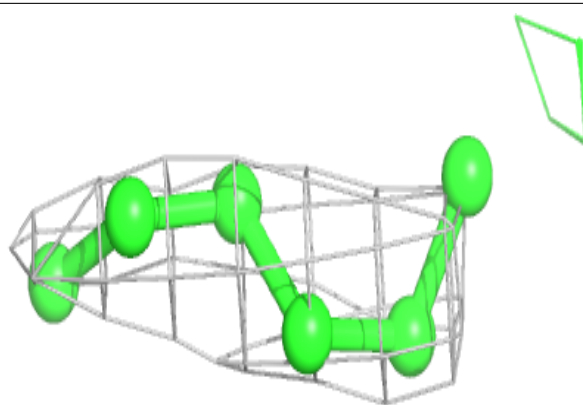
**Electron density around OLC C 301:**

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

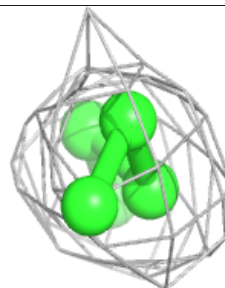
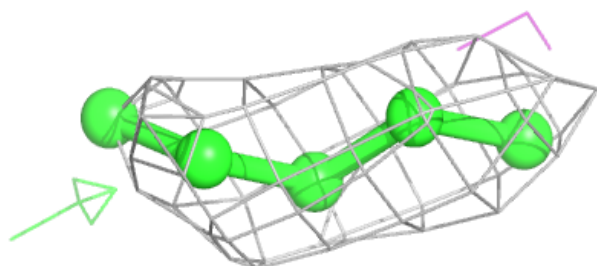
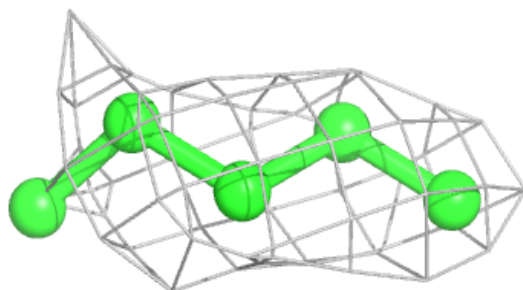


Electron density around LFA E 306:

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

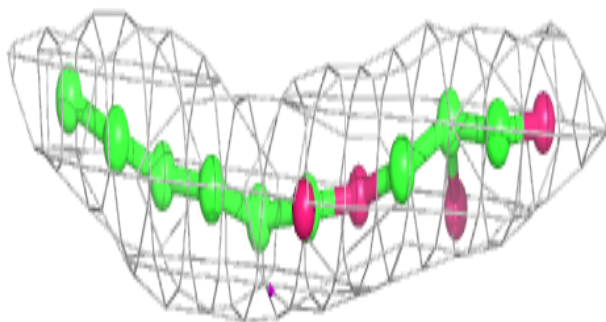
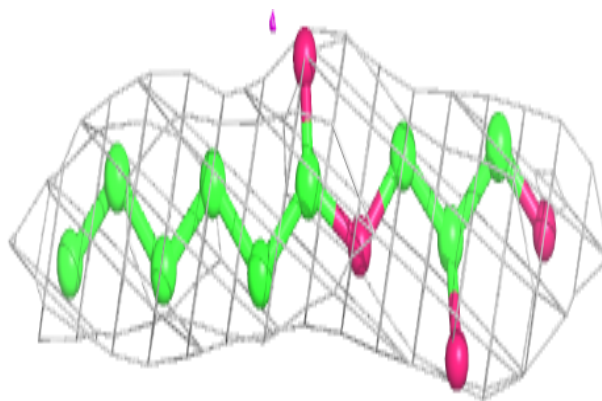
**Electron density around LFA A 305:**

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

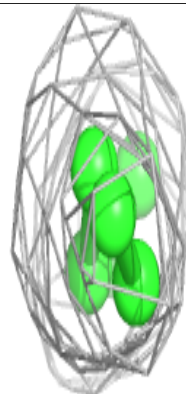
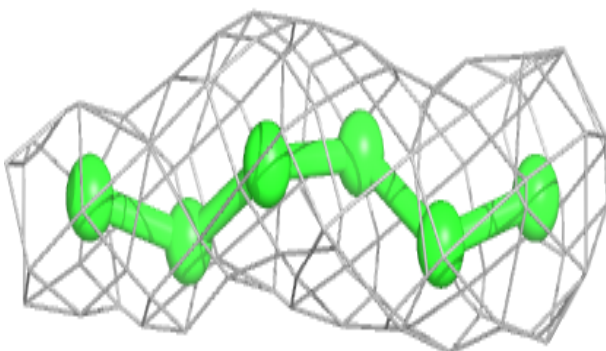
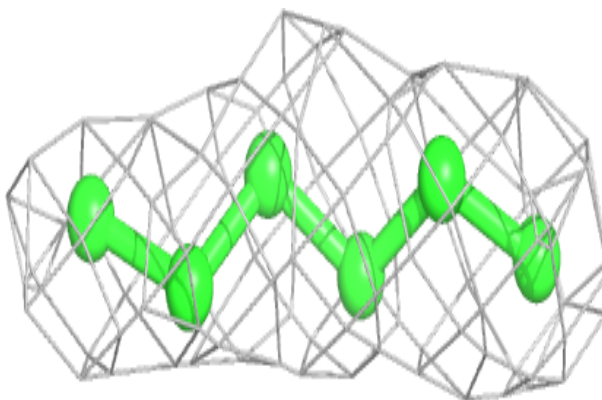


Electron density around OLC A 302:

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

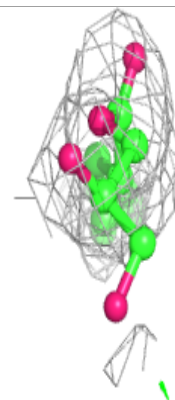
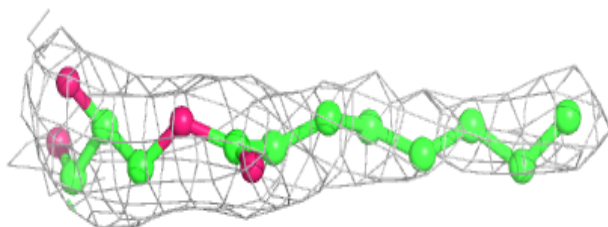
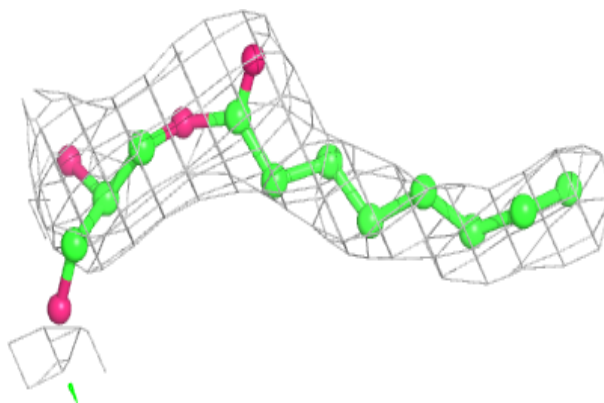
**Electron density around LFA D 311:**

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

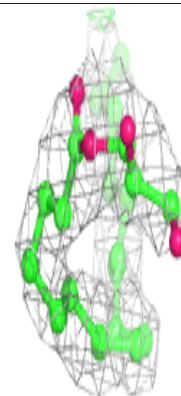
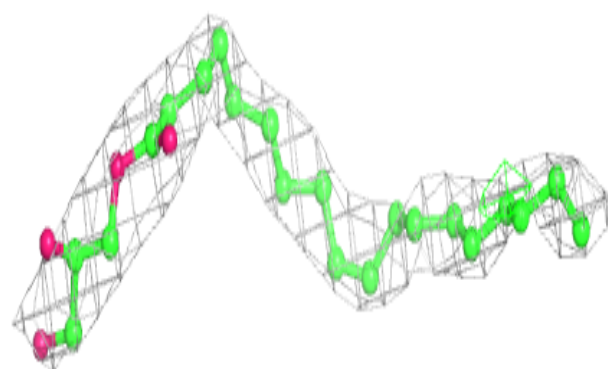
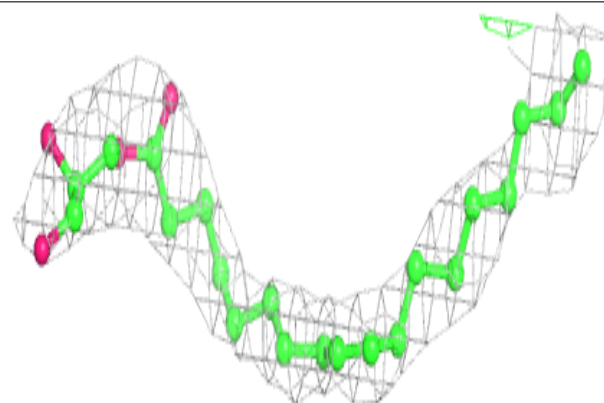


Electron density around OLC A 303:

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

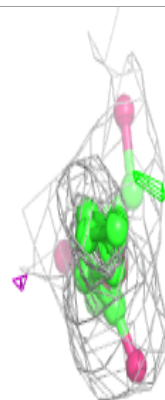
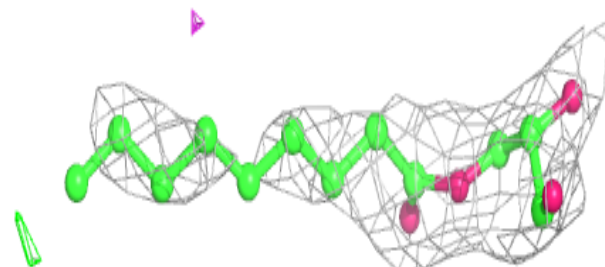
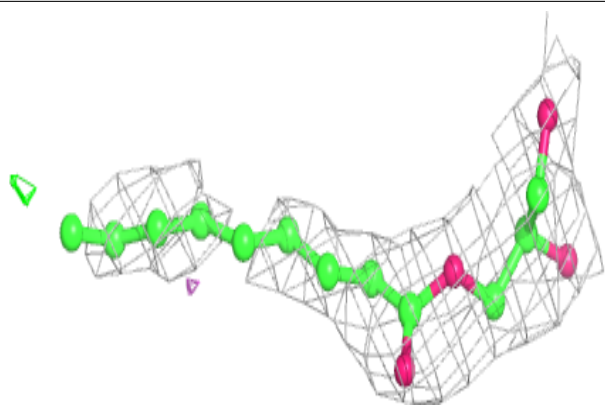
**Electron density around OLC B 301:**

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

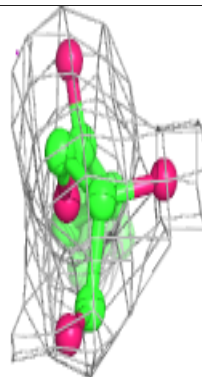
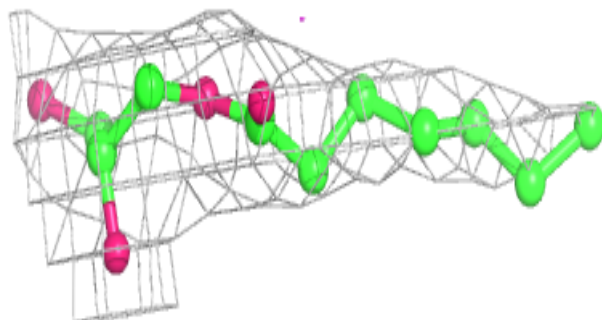
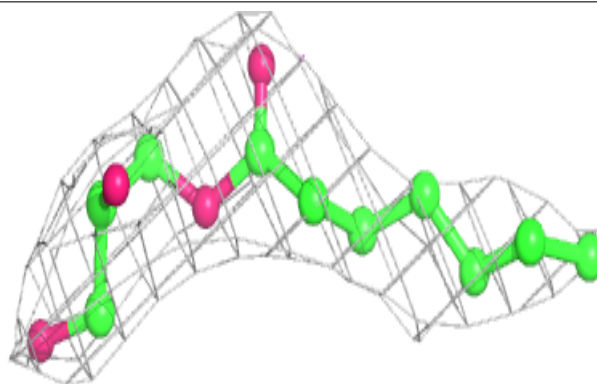


Electron density around OLC B 304:

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

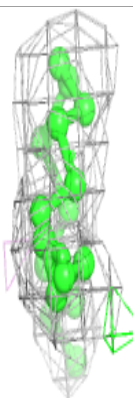
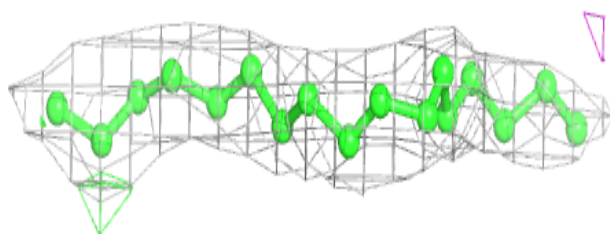
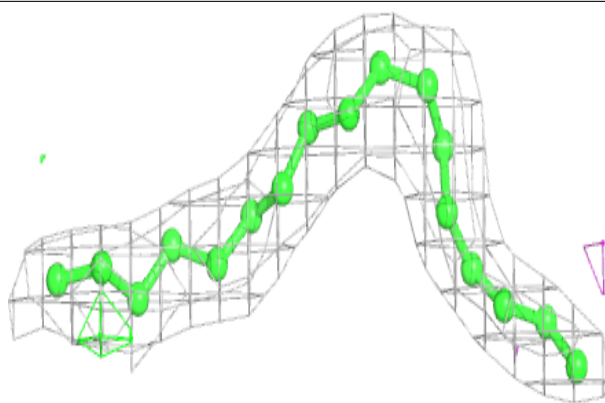
**Electron density around OLC D 304:**

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

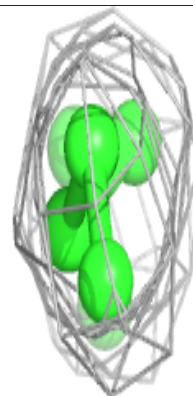
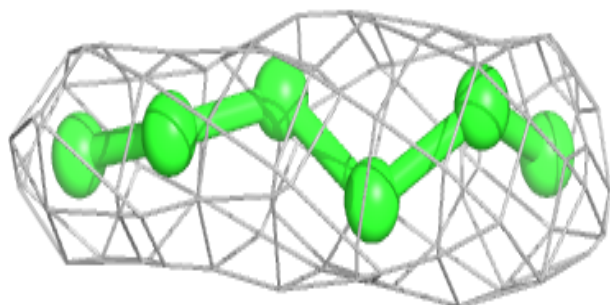
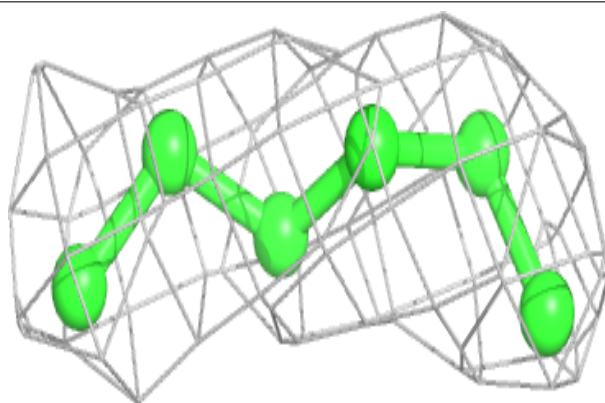


Electron density around LFA D 309:

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

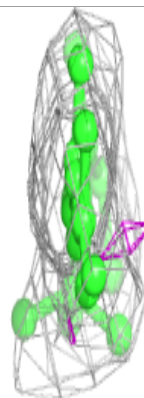
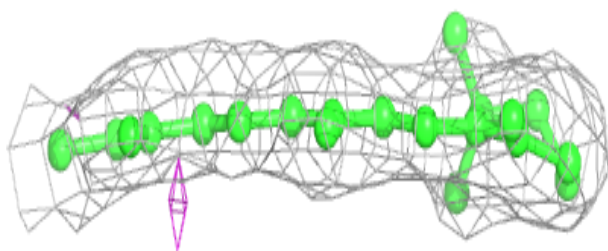
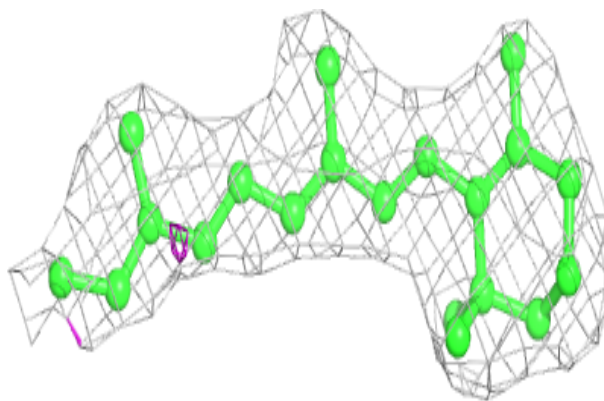
**Electron density around LFA C 315:**

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

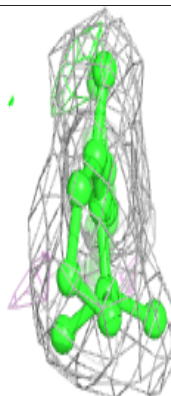
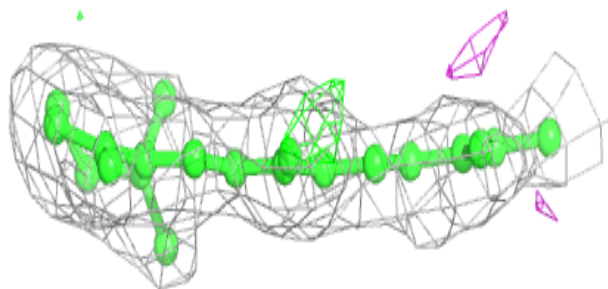
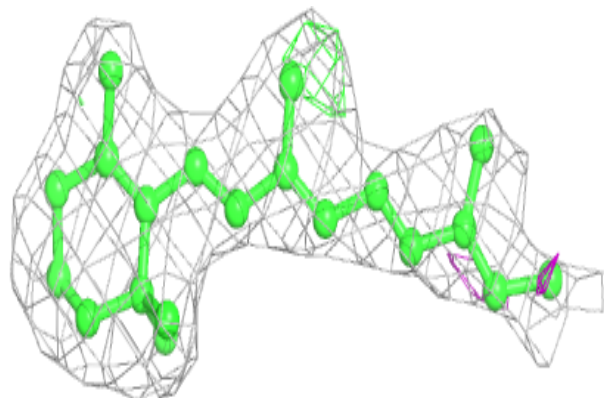


Electron density around RET A 312:

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

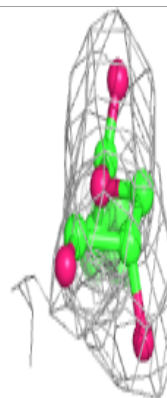
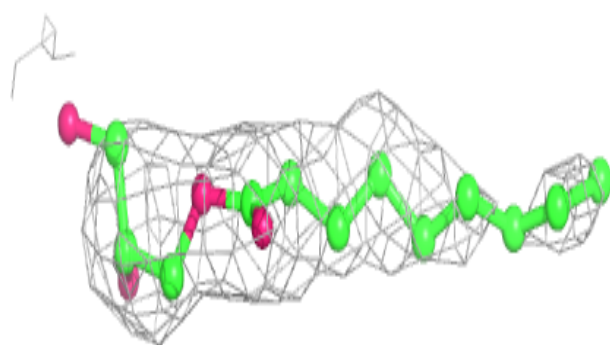
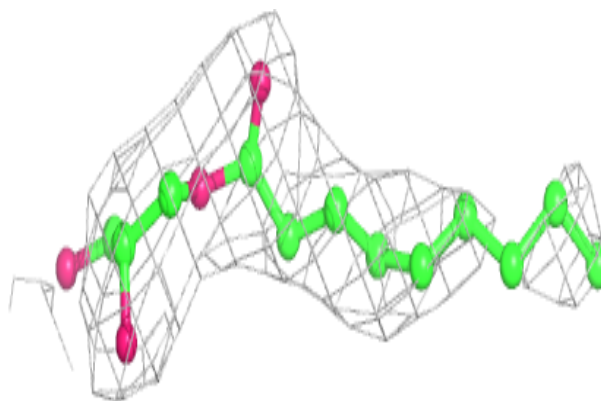
**Electron density around RET E 315:**

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

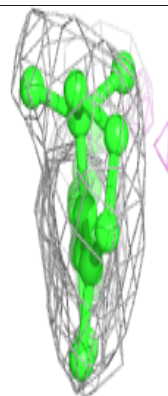
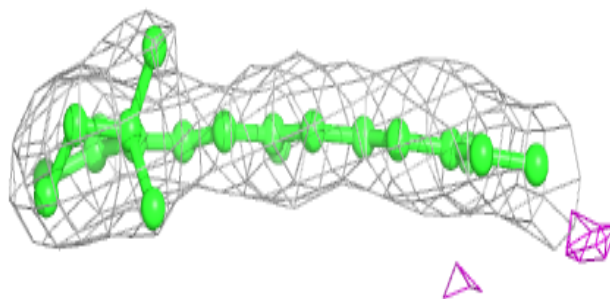
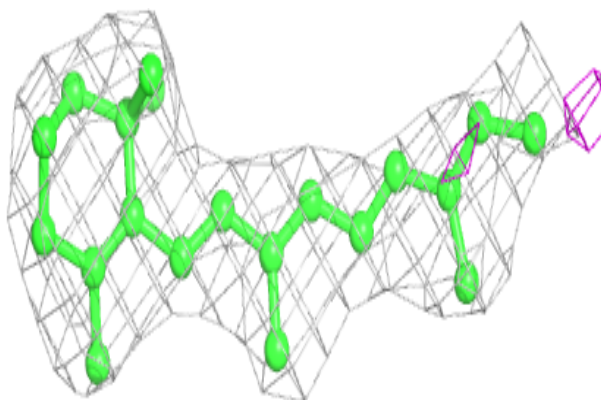


Electron density around OLC C 308:

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

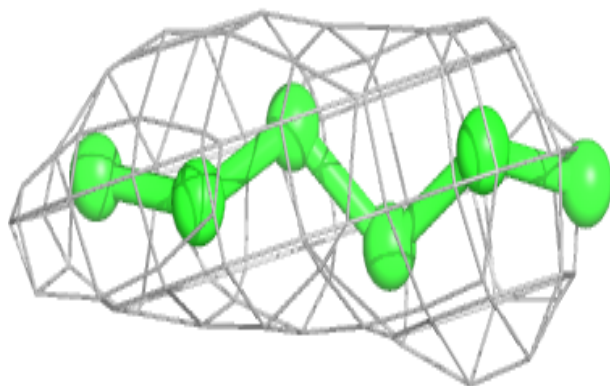
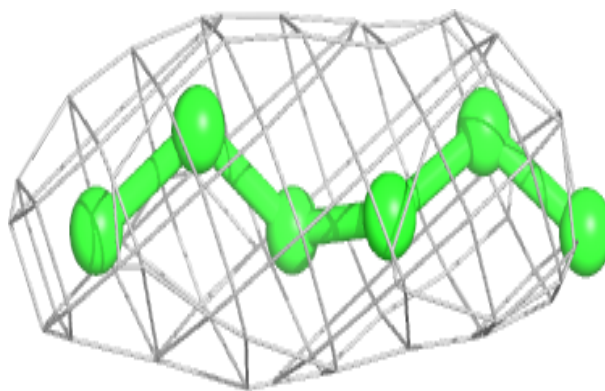
**Electron density around RET B 313:**

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

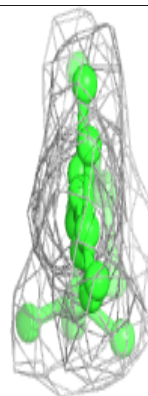
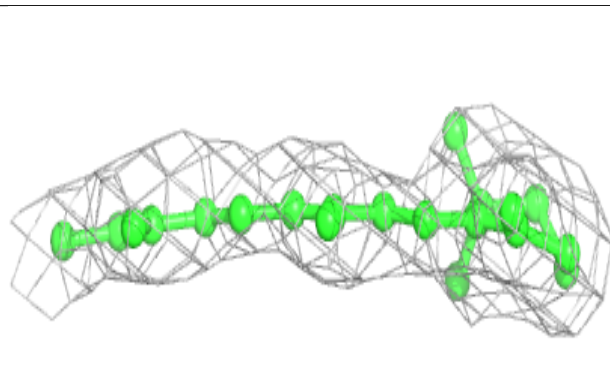
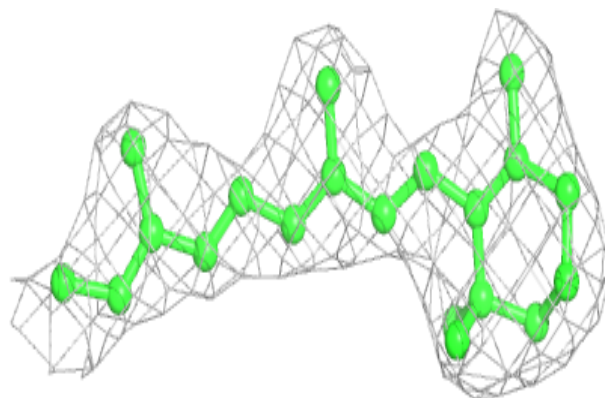


Electron density around LFA A 308:

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

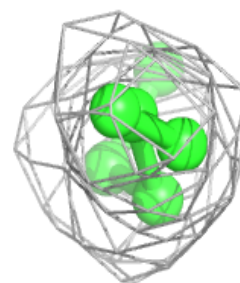
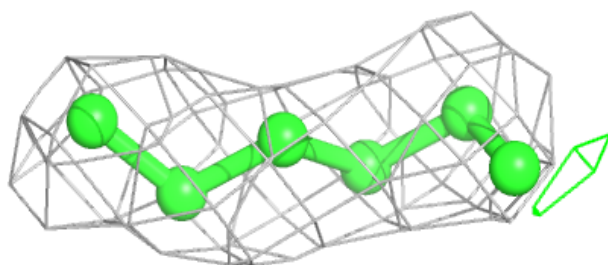
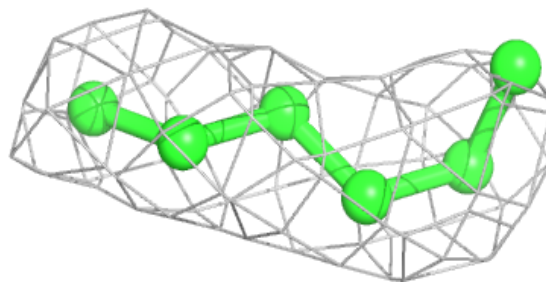
**Electron density around RET C 318:**

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

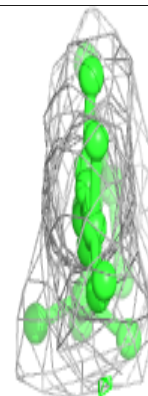
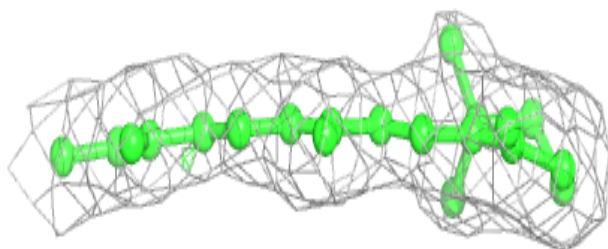
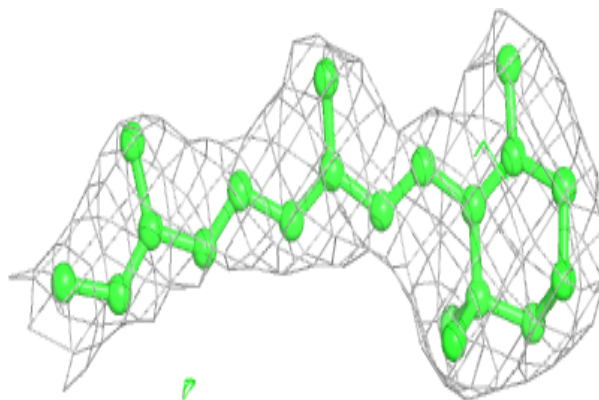


Electron density around LFA E 310:

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

**Electron density around RET D 315:**

$2mF_o-DF_c$ (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.