Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 04:30 PM EDT

PDB ID	:	6RFA / pdb_00006rfa
Title	:	Crystal structure of the H30K mutant of the light-driven sodium pump KR2 in the monomeric form, pH 8.0
Authors	:	Kovalev, K.; Polovinkin, V.; Gushchin, I.; Borshchevskiy, V.; Gordeliy, V.
Deposited on	:	2019-04-12
Resolution	:	2.20 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:

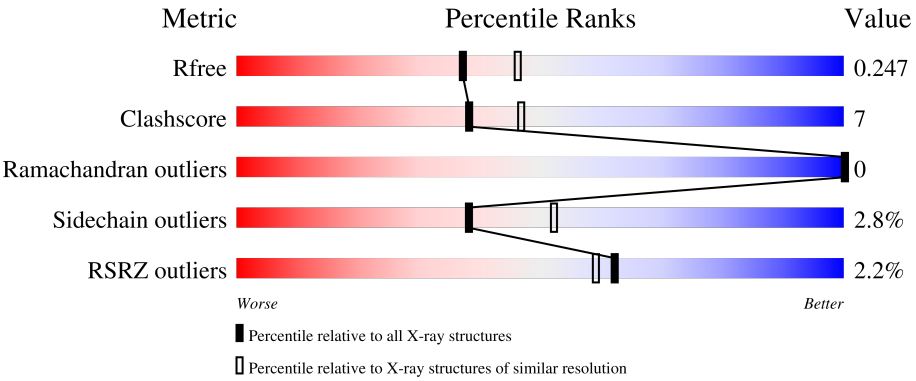
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 <=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	288	2% 84% 8% • 7%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2459 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
			2111	1414	318	370	9			

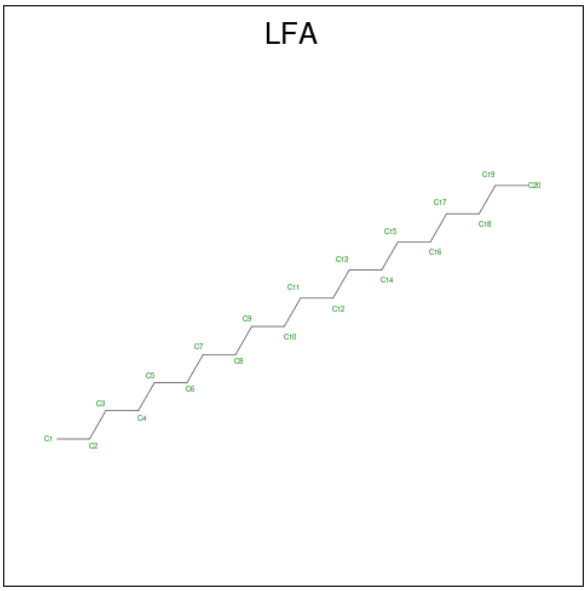
There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	LYS	HIS	engineered mutation	UNP N0DKS8
A	281	LEU	-	expression tag	UNP N0DKS8
A	282	GLU	-	expression tag	UNP N0DKS8
A	283	HIS	-	expression tag	UNP N0DKS8
A	284	HIS	-	expression tag	UNP N0DKS8
A	285	HIS	-	expression tag	UNP N0DKS8
A	286	HIS	-	expression tag	UNP N0DKS8
A	287	HIS	-	expression tag	UNP N0DKS8
A	288	HIS	-	expression tag	UNP N0DKS8

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		

- Molecule 3 is EICOSANE (CCD ID: LFA) (formula: $C_{20}H_{42}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C 8 8	0	0
3	A	1	Total C 9 9	0	0
3	A	1	Total C 6 6	0	0
3	A	1	Total C 5 5	0	0
3	A	1	Total C 13 13	0	0
3	A	1	Total C 10 10	0	0
3	A	1	Total C 8 8	0	0
3	A	1	Total C 8 8	0	0
3	A	1	Total C 12 12	0	0
3	A	1	Total C 16 16	0	0
3	A	1	Total C 5 5	0	0
3	A	1	Total C 10 10	0	0
3	A	1	Total C 5 5	0	0
3	A	1	Total C 5 5	0	0

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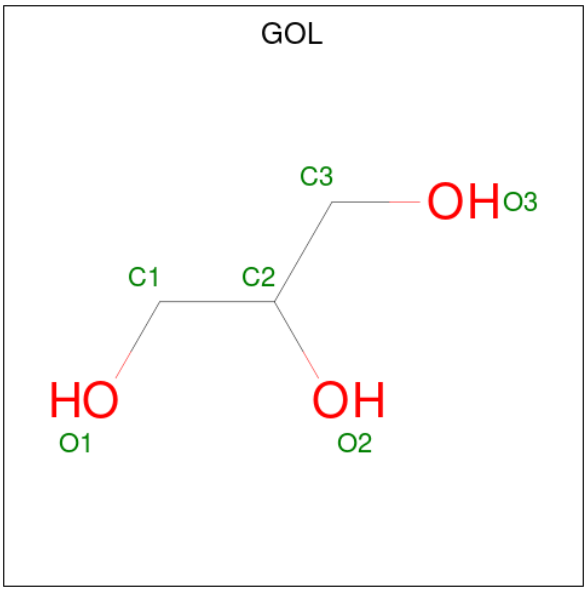
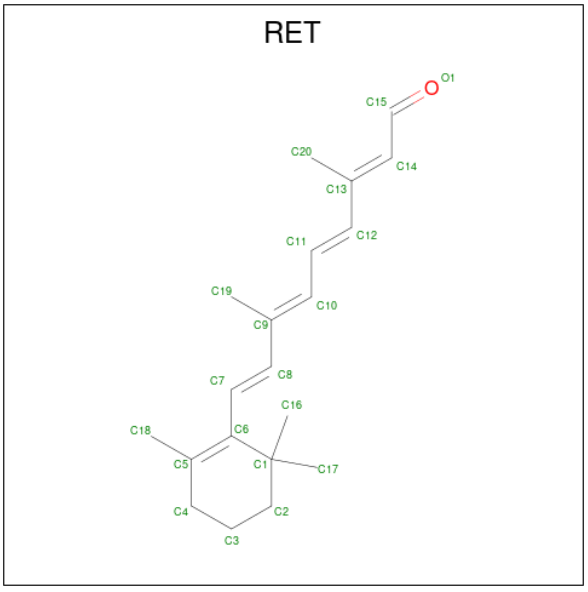
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C 11 11	0	0
3	A	1	Total C 12 12	0	0
3	A	1	Total C 10 10	0	0
3	A	1	Total C 6 6	0	0
3	A	1	Total C 5 5	0	0
3	A	1	Total C 6 6	0	0
3	A	1	Total C 4 4	0	0
3	A	1	Total C 6 6	0	0
3	A	1	Total C 6 6	0	0
3	A	1	Total C 10 10	0	0
3	A	1	Total C 7 7	0	0
3	A	1	Total C 3 3	0	0
3	A	1	Total C 5 5	0	0
3	A	1	Total C 11 11	0	0
3	A	1	Total C 4 4	0	0
3	A	1	Total C 5 5	0	0
3	A	1	Total C 10 10	0	0
3	A	1	Total C 12 12	0	0
3	A	1	Total C 10 10	0	0
3	A	1	Total C 20 20	0	0

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0

- Molecule 5 is RETINAL (CCD ID: RET) (formula: $C_{20}H_{28}O$).



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

- Molecule 6 is water.

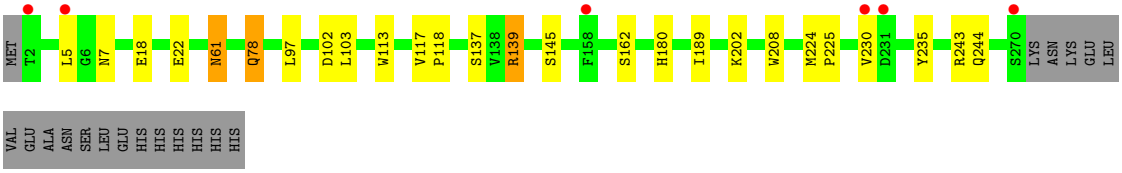
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	38	Total O 38 38	0	0

3 Residue-property plots (i)

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:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	40.74Å 84.18Å 234.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.89 – 2.20 19.89 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.6 (19.89-2.20) 99.6 (19.89-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.53 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.209 , 0.238 0.217 , 0.247	Depositor DCC
R_{free} test set	1013 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å^2)	35.8	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 39.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	2459	wwPDB-VP
Average B, all atoms (Å^2)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.68% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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, LFA, GOL, 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	0.52	0/2167	0.90	0/2947

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	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	139	ARG	Sidechain
1	A	235	TYR	Peptide
1	A	243	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2111	0	2080	21	0
2	A	1	0	0	0	0
3	A	283	0	517	11	0
4	A	6	0	8	0	0
5	A	20	0	27	7	0
6	A	38	0	0	3	0
All	All	2459	0	2632	35	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 7.

All (35) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:LYS:CB	6:A:436:HOH:O	2.13	0.97
1:A:230:VAL:HG23	3:A:308:LFA:C8	2.03	0.88
3:A:314:LFA:C2	3:A:315:LFA:C6	2.57	0.82
1:A:139:ARG:HH11	3:A:324:LFA:C6	1.97	0.77
5:A:337:RET:H161	5:A:337:RET:H8	1.68	0.74
1:A:61:ASN:H	1:A:61:ASN:HD22	1.44	0.66
3:A:321:LFA:H11	3:A:336:LFA:H201	1.81	0.62
3:A:330:LFA:C4	3:A:331:LFA:H32	2.30	0.61
3:A:304:LFA:H11	3:A:325:LFA:C10	2.32	0.59
1:A:189:ILE:HD13	1:A:208:TRP:HB2	1.85	0.59
1:A:230:VAL:HG12	1:A:230:VAL:O	2.03	0.58
5:A:337:RET:H161	5:A:337:RET:C8	2.35	0.57
1:A:5:LEU:HB3	1:A:97:LEU:HD23	1.89	0.54
1:A:102:ASP:O	1:A:103:LEU:CB	2.56	0.52
1:A:102:ASP:C	1:A:103:LEU:HG	2.35	0.51
1:A:102:ASP:O	1:A:103:LEU:HB2	2.12	0.50
5:A:337:RET:H8	5:A:337:RET:H171	1.93	0.50
3:A:317:LFA:H11	3:A:319:LFA:C6	2.42	0.49
1:A:61:ASN:HD22	1:A:61:ASN:N	2.10	0.48
3:A:321:LFA:C1	3:A:336:LFA:H201	2.44	0.48
1:A:7:ASN:C	1:A:7:ASN:N	2.71	0.47
1:A:78:GLN:NE2	6:A:405:HOH:O	2.48	0.47
1:A:230:VAL:O	1:A:230:VAL:CG1	2.64	0.45
1:A:117:VAL:N	1:A:118:PRO:HD2	2.32	0.45
5:A:337:RET:H181	5:A:337:RET:H7	1.67	0.44
5:A:337:RET:H11	5:A:337:RET:H191	1.91	0.44
1:A:244:GLN:HG2	6:A:401:HOH:O	2.18	0.44
1:A:224:MET:N	1:A:225:PRO:CD	2.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:SER:OG	1:A:180:HIS:HD2	2.02	0.42
1:A:139:ARG:NH1	3:A:324:LFA:C6	2.76	0.42
3:A:304:LFA:C1	3:A:325:LFA:C10	2.97	0.42
1:A:113:TRP:CD1	5:A:337:RET:H14	2.56	0.41
3:A:310:LFA:H72	3:A:310:LFA:H42	1.78	0.41
5:A:337:RET:C8	5:A:337:RET:H171	2.51	0.41
1:A:5:LEU:HD23	1:A:5:LEU:HA	1.84	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	266/288 (92%)	261 (98%)	5 (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	217/248 (88%)	211 (97%)	6 (3%)	38 52

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	GLU
1	A	22	GLU
1	A	61	ASN
1	A	78	GLN
1	A	137	SER
1	A	162	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	61	ASN
1	A	112	ASN
1	A	180	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 37 ligands modelled in this entry, 1 is monoatomic - leaving 36 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	$\#\|Z\|>2$
3	LFA	A	319	-	5,5,19	0.30	0	4,4,18	0.34	0
5	RET	A	337	1	20,20,21	0.80	1 (5%)	27,27,28	1.74	7 (25%)
3	LFA	A	329	-	10,10,19	0.28	0	9,9,18	0.48	0
3	LFA	A	305	-	4,4,19	0.27	0	3,3,18	0.40	0
3	LFA	A	313	-	9,9,19	0.34	0	8,8,18	0.41	0
3	LFA	A	324	-	5,5,19	0.29	0	4,4,18	0.37	0
3	LFA	A	318	-	9,9,19	0.27	0	8,8,18	0.51	0
3	LFA	A	302	-	7,7,19	0.27	0	6,6,18	0.45	0
3	LFA	A	303	-	8,8,19	0.31	0	7,7,18	0.45	0
3	LFA	A	308	-	7,7,19	0.29	0	6,6,18	0.42	0
3	LFA	A	312	-	4,4,19	0.31	0	3,3,18	0.36	0
3	LFA	A	320	-	4,4,19	0.28	0	3,3,18	0.35	0
3	LFA	A	309	-	7,7,19	0.31	0	6,6,18	0.41	0
3	LFA	A	328	-	4,4,19	0.35	0	3,3,18	0.34	0
3	LFA	A	322	-	3,3,19	0.37	0	2,2,18	0.62	0
3	LFA	A	304	-	5,5,19	0.30	0	4,4,18	0.33	0
4	GOL	A	335	-	5,5,5	0.29	0	5,5,5	0.32	0
3	LFA	A	323	-	5,5,19	0.34	0	4,4,18	0.29	0
3	LFA	A	332	-	9,9,19	0.33	0	8,8,18	0.34	0
3	LFA	A	327	-	2,2,19	0.21	0	1,1,18	0.01	0
3	LFA	A	325	-	9,9,19	0.29	0	8,8,18	0.49	0
3	LFA	A	326	-	6,6,19	0.34	0	5,5,18	0.33	0
3	LFA	A	336	-	19,19,19	0.27	0	18,18,18	0.56	0
3	LFA	A	315	-	4,4,19	0.35	0	3,3,18	0.33	0
3	LFA	A	330	-	3,3,19	0.35	0	2,2,18	0.63	0
3	LFA	A	311	-	15,15,19	0.30	0	14,14,18	0.50	0
3	LFA	A	317	-	11,11,19	0.26	0	10,10,18	0.53	0
3	LFA	A	331	-	4,4,19	0.38	0	3,3,18	0.30	0
3	LFA	A	334	-	9,9,19	0.28	0	8,8,18	0.45	0
3	LFA	A	321	-	5,5,19	0.34	0	4,4,18	0.27	0
3	LFA	A	310	-	11,11,19	0.31	0	10,10,18	0.39	0
3	LFA	A	314	-	4,4,19	0.35	0	3,3,18	0.31	0
3	LFA	A	333	-	11,11,19	0.29	0	10,10,18	0.48	0
3	LFA	A	316	-	10,10,19	0.33	0	9,9,18	0.42	0
3	LFA	A	306	-	12,12,19	0.26	0	11,11,18	0.53	0
3	LFA	A	307	-	9,9,19	0.29	0	8,8,18	0.45	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
3	LFA	A	319	-	-	1/3/3/17	-
5	RET	A	337	1	-	0/13/30/31	0/1/1/1
3	LFA	A	329	-	-	5/8/8/17	-
3	LFA	A	305	-	-	0/2/2/17	-
3	LFA	A	313	-	-	3/7/7/17	-
3	LFA	A	324	-	-	1/3/3/17	-
3	LFA	A	318	-	-	3/7/7/17	-
3	LFA	A	302	-	-	4/5/5/17	-
3	LFA	A	303	-	-	1/6/6/17	-
3	LFA	A	308	-	-	2/5/5/17	-
3	LFA	A	312	-	-	2/2/2/17	-
3	LFA	A	320	-	-	0/2/2/17	-
3	LFA	A	309	-	-	1/5/5/17	-
3	LFA	A	328	-	-	0/2/2/17	-
3	LFA	A	322	-	-	0/1/1/17	-
3	LFA	A	304	-	-	2/3/3/17	-
4	GOL	A	335	-	-	2/4/4/4	-
3	LFA	A	323	-	-	3/3/3/17	-
3	LFA	A	332	-	-	6/7/7/17	-
3	LFA	A	325	-	-	4/7/7/17	-
3	LFA	A	326	-	-	3/4/4/17	-
3	LFA	A	336	-	-	9/17/17/17	-
3	LFA	A	315	-	-	1/2/2/17	-
3	LFA	A	330	-	-	0/1/1/17	-
3	LFA	A	311	-	-	6/13/13/17	-
3	LFA	A	317	-	-	4/9/9/17	-
3	LFA	A	331	-	-	1/2/2/17	-
3	LFA	A	334	-	-	4/7/7/17	-
3	LFA	A	321	-	-	2/3/3/17	-
3	LFA	A	310	-	-	5/9/9/17	-
3	LFA	A	314	-	-	1/2/2/17	-
3	LFA	A	333	-	-	6/9/9/17	-
3	LFA	A	316	-	-	2/8/8/17	-
3	LFA	A	306	-	-	4/10/10/17	-
3	LFA	A	307	-	-	4/7/7/17	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	337	RET	C14-C13	2.30	1.35	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	337	RET	C18-C5-C6	-4.99	119.03	124.48
5	A	337	RET	C7-C8-C9	-2.90	121.95	126.23
5	A	337	RET	C11-C10-C9	-2.75	123.42	127.28
5	A	337	RET	C10-C11-C12	-2.27	116.61	123.20
5	A	337	RET	C19-C9-C8	2.23	121.50	118.09
5	A	337	RET	C1-C6-C7	2.10	121.34	115.65
5	A	337	RET	C7-C6-C5	-2.08	116.77	121.56

There are no chirality outliers.

All (92) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	335	GOL	O1-C1-C2-C3
3	A	310	LFA	C4-C5-C6-C7
3	A	317	LFA	C3-C4-C5-C6
3	A	321	LFA	C2-C3-C4-C5
3	A	329	LFA	C4-C5-C6-C7
3	A	306	LFA	C4-C5-C6-C7
3	A	323	LFA	C2-C3-C4-C5
3	A	333	LFA	C4-C5-C6-C7
3	A	318	LFA	C5-C6-C7-C8
3	A	332	LFA	C5-C6-C7-C8
3	A	336	LFA	C15-C16-C17-C18
3	A	311	LFA	C11-C10-C9-C8
3	A	302	LFA	C2-C3-C4-C5
3	A	311	LFA	C2-C3-C4-C5
3	A	334	LFA	C4-C5-C6-C7
3	A	310	LFA	C5-C6-C7-C8
3	A	317	LFA	C6-C7-C8-C9
3	A	333	LFA	C2-C3-C4-C5
3	A	316	LFA	C6-C7-C8-C9
3	A	306	LFA	C9-C10-C11-C12
3	A	336	LFA	C12-C13-C14-C15
3	A	333	LFA	C9-C10-C11-C12
3	A	333	LFA	C5-C6-C7-C8
3	A	306	LFA	C3-C4-C5-C6
3	A	334	LFA	C3-C4-C5-C6

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Mol	Chain	Res	Type	Atoms
3	A	336	LFA	C11-C12-C13-C14
3	A	329	LFA	C2-C3-C4-C5
3	A	329	LFA	C5-C6-C7-C8
3	A	302	LFA	C4-C5-C6-C7
3	A	325	LFA	C6-C7-C8-C9
3	A	310	LFA	C6-C7-C8-C9
3	A	333	LFA	C6-C7-C8-C9
3	A	310	LFA	C3-C4-C5-C6
3	A	332	LFA	C2-C3-C4-C5
3	A	317	LFA	C7-C8-C9-C10
3	A	308	LFA	C5-C6-C7-C8
3	A	336	LFA	C17-C18-C19-C20
3	A	311	LFA	C9-C10-C11-C12
3	A	315	LFA	C3-C4-C5-C6
3	A	318	LFA	C1-C2-C3-C4
3	A	311	LFA	C11-C12-C13-C14
3	A	325	LFA	C7-C8-C9-C10
3	A	304	LFA	C1-C2-C3-C4
4	A	335	GOL	O1-C1-C2-O2
3	A	324	LFA	C3-C4-C5-C6
3	A	317	LFA	C11-C10-C9-C8
3	A	307	LFA	C7-C8-C9-C10
3	A	310	LFA	C9-C10-C11-C12
3	A	312	LFA	C1-C2-C3-C4
3	A	329	LFA	C6-C7-C8-C9
3	A	318	LFA	C4-C5-C6-C7
3	A	334	LFA	C5-C6-C7-C8
3	A	313	LFA	C4-C5-C6-C7
3	A	319	LFA	C3-C4-C5-C6
3	A	336	LFA	C16-C17-C18-C19
3	A	311	LFA	C5-C6-C7-C8
3	A	336	LFA	C13-C14-C15-C16
3	A	307	LFA	C2-C3-C4-C5
3	A	307	LFA	C4-C5-C6-C7
3	A	313	LFA	C2-C3-C4-C5
3	A	329	LFA	C7-C8-C9-C10
3	A	332	LFA	C3-C4-C5-C6
3	A	302	LFA	C1-C2-C3-C4
3	A	336	LFA	C1-C2-C3-C4
3	A	332	LFA	C6-C7-C8-C9
3	A	326	LFA	C1-C2-C3-C4
3	A	311	LFA	C7-C8-C9-C10

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Mol	Chain	Res	Type	Atoms
3	A	306	LFA	C11-C10-C9-C8
3	A	314	LFA	C3-C4-C5-C6
3	A	302	LFA	C5-C6-C7-C8
3	A	316	LFA	C3-C4-C5-C6
3	A	323	LFA	C1-C2-C3-C4
3	A	321	LFA	C1-C2-C3-C4
3	A	336	LFA	C9-C10-C11-C12
3	A	334	LFA	C7-C8-C9-C10
3	A	325	LFA	C5-C6-C7-C8
3	A	303	LFA	C5-C6-C7-C8
3	A	307	LFA	C1-C2-C3-C4
3	A	309	LFA	C3-C4-C5-C6
3	A	323	LFA	C3-C4-C5-C6
3	A	332	LFA	C4-C5-C6-C7
3	A	326	LFA	C2-C3-C4-C5
3	A	332	LFA	C1-C2-C3-C4
3	A	336	LFA	C7-C8-C9-C10
3	A	333	LFA	C1-C2-C3-C4
3	A	325	LFA	C3-C4-C5-C6
3	A	308	LFA	C1-C2-C3-C4
3	A	313	LFA	C7-C8-C9-C10
3	A	312	LFA	C2-C3-C4-C5
3	A	331	LFA	C2-C3-C4-C5
3	A	326	LFA	C3-C4-C5-C6
3	A	304	LFA	C2-C3-C4-C5

There are no ring outliers.

14 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	319	LFA	1	0
5	A	337	RET	7	0
3	A	324	LFA	2	0
3	A	308	LFA	1	0
3	A	304	LFA	2	0
3	A	325	LFA	2	0
3	A	336	LFA	2	0
3	A	315	LFA	1	0
3	A	330	LFA	1	0
3	A	317	LFA	1	0
3	A	331	LFA	1	0
3	A	321	LFA	2	0

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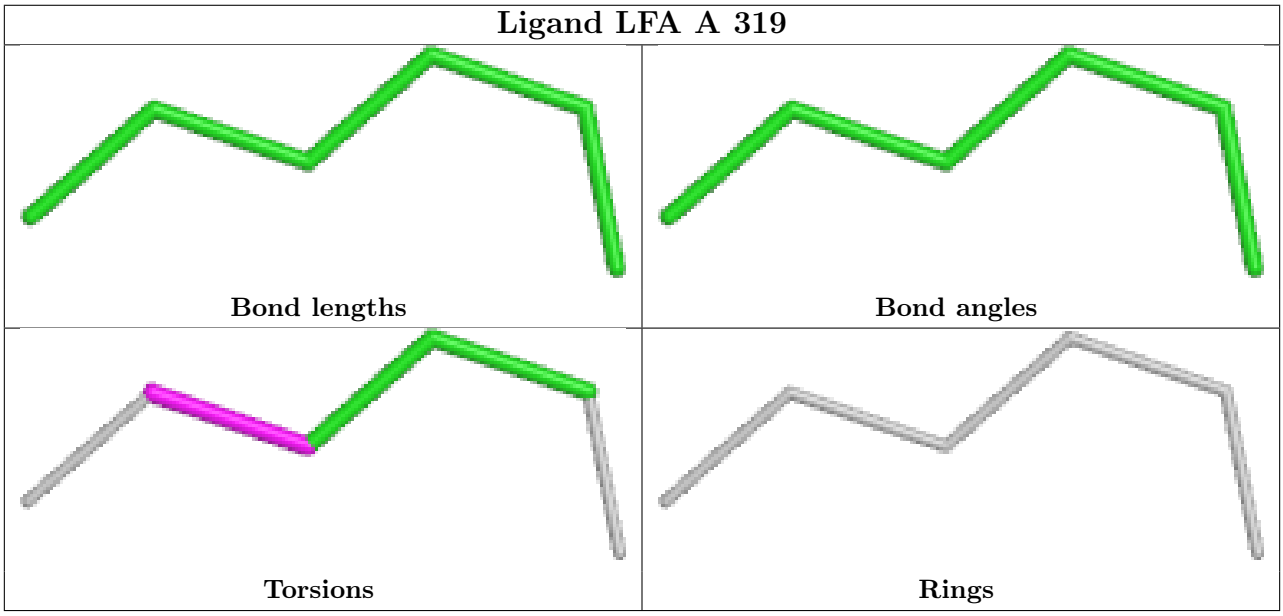
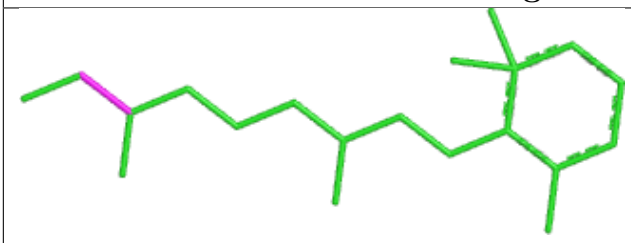
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	310	LFA	1	0
3	A	314	LFA	1	0

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand LFA A 319

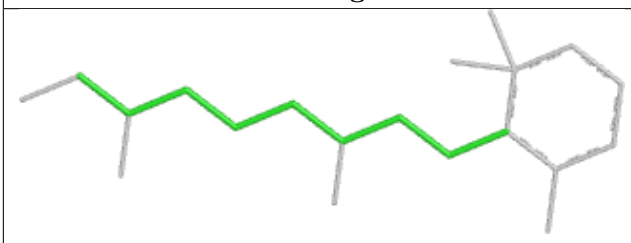


Ligand RET A 337

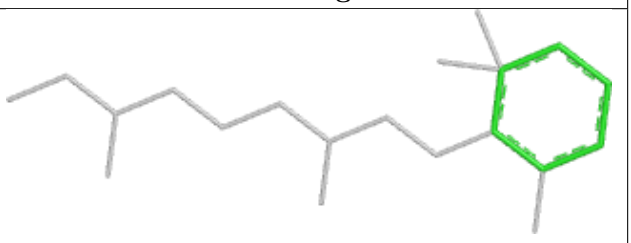


Bond lengths

Bond angles

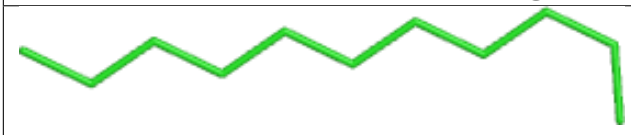


Torsions

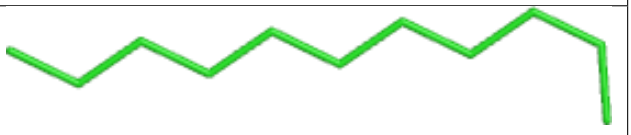


Rings

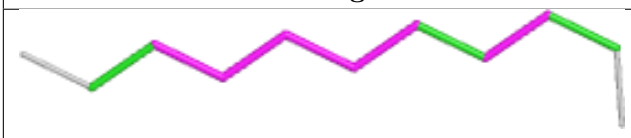
Ligand LFA A 329



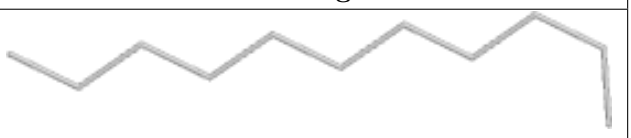
Bond lengths



Bond angles

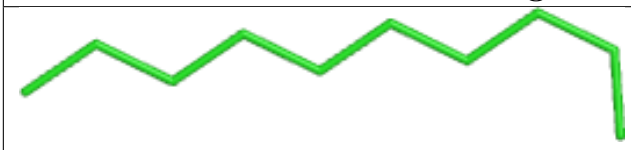


Torsions

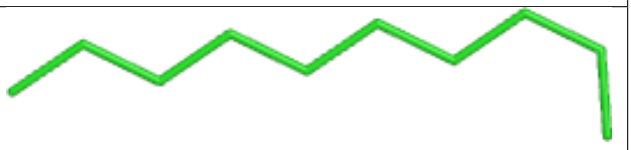


Rings

Ligand LFA A 313

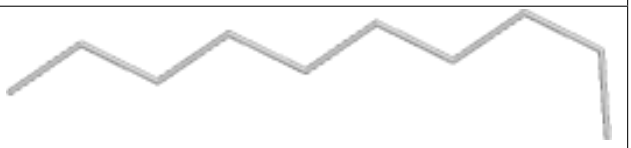


Bond lengths



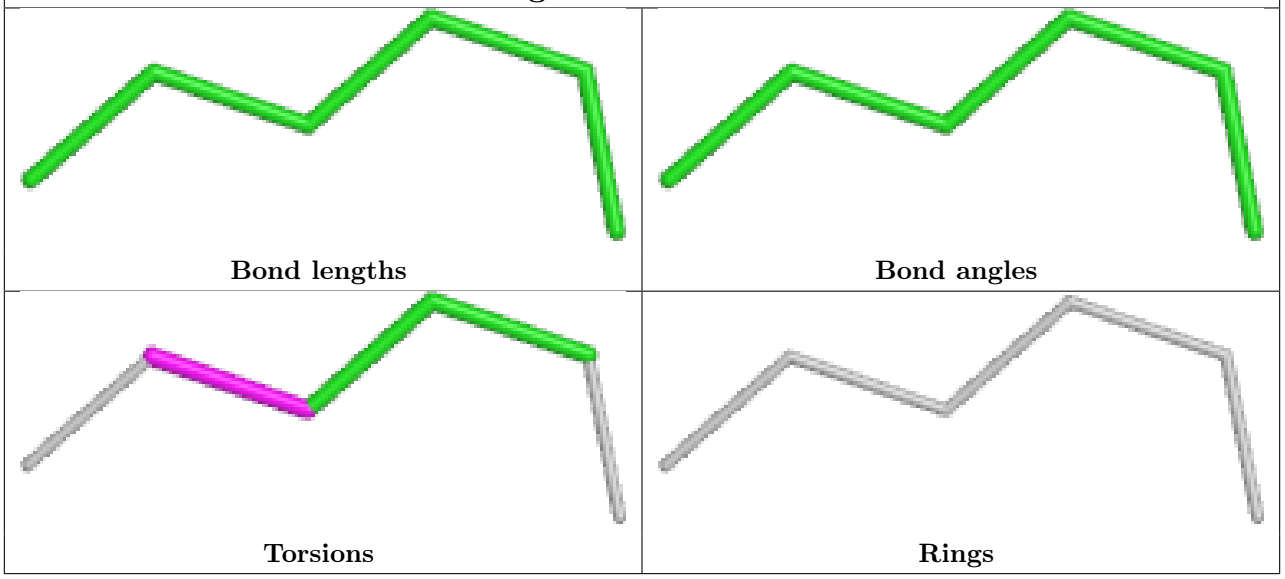
Bond angles

Torsions

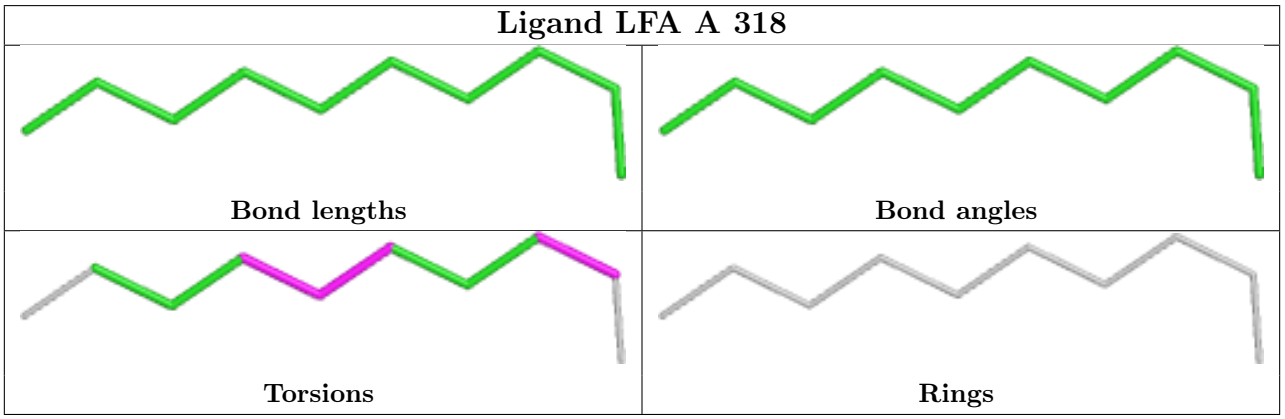


Rings

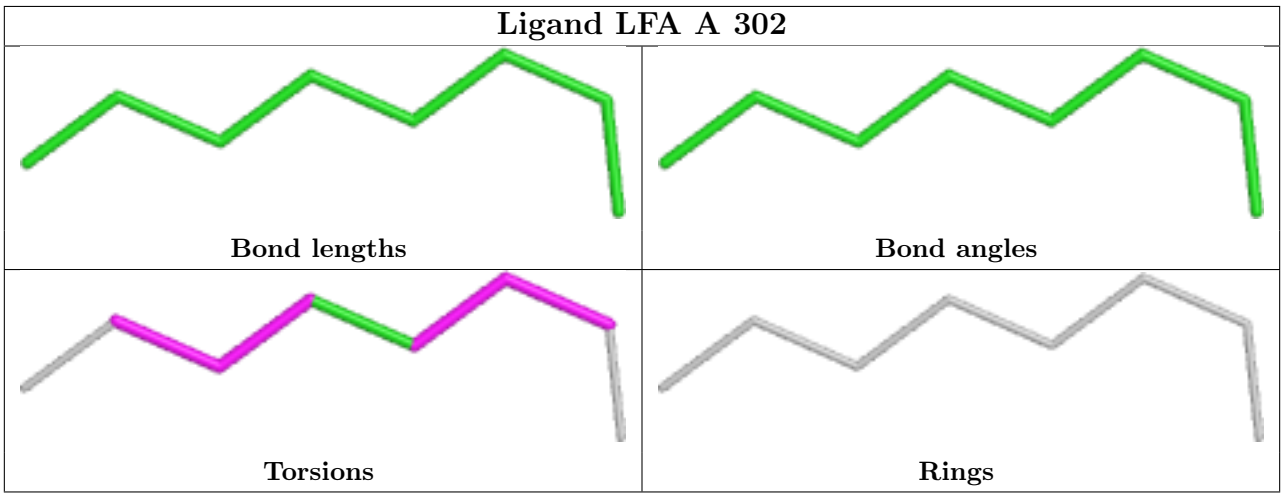
Ligand LFA A 324



Ligand LFA A 318



Ligand LFA A 302



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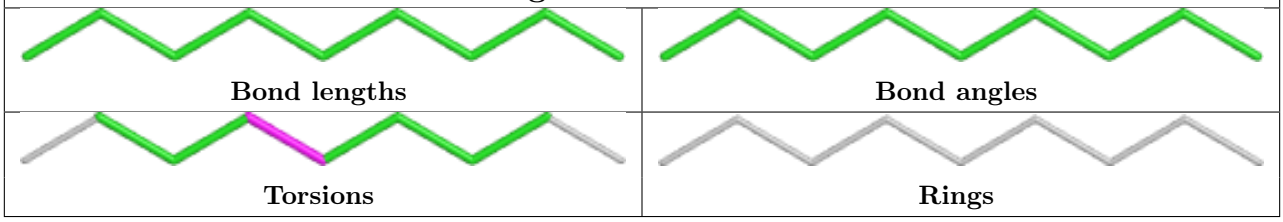

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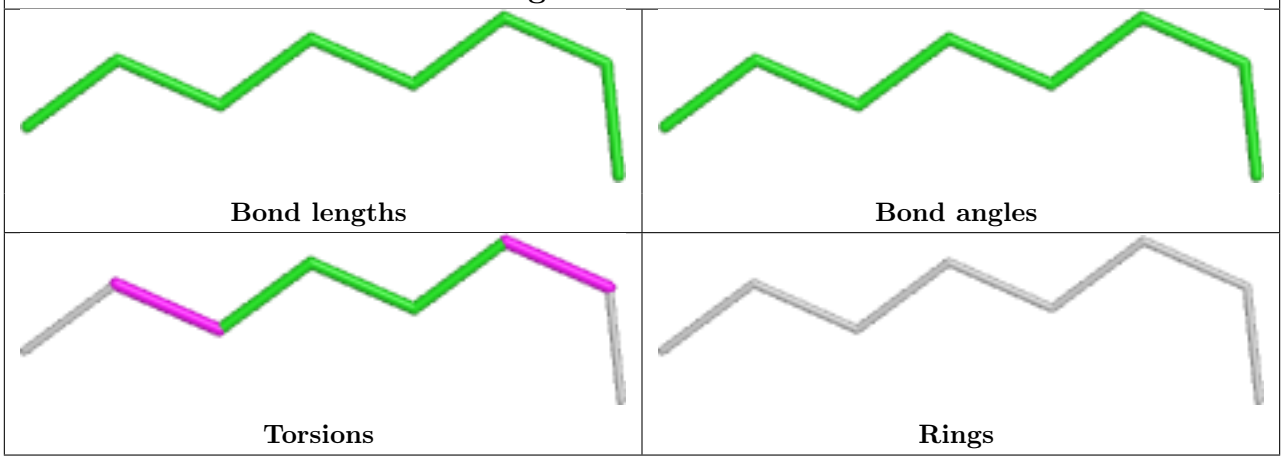
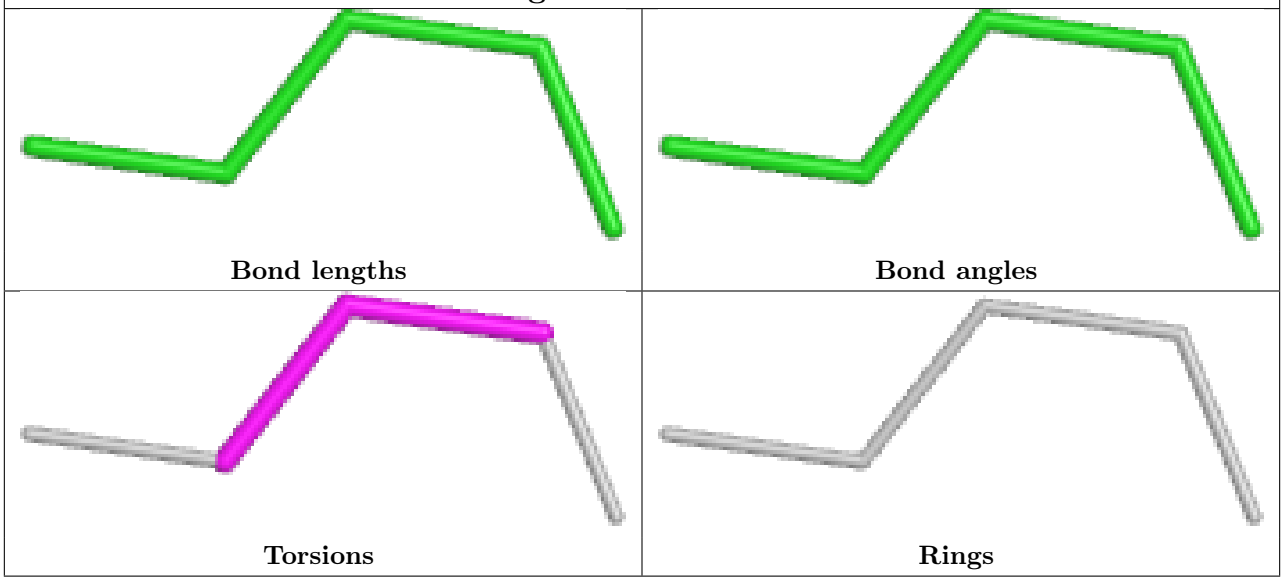


Ligand LFA A 312



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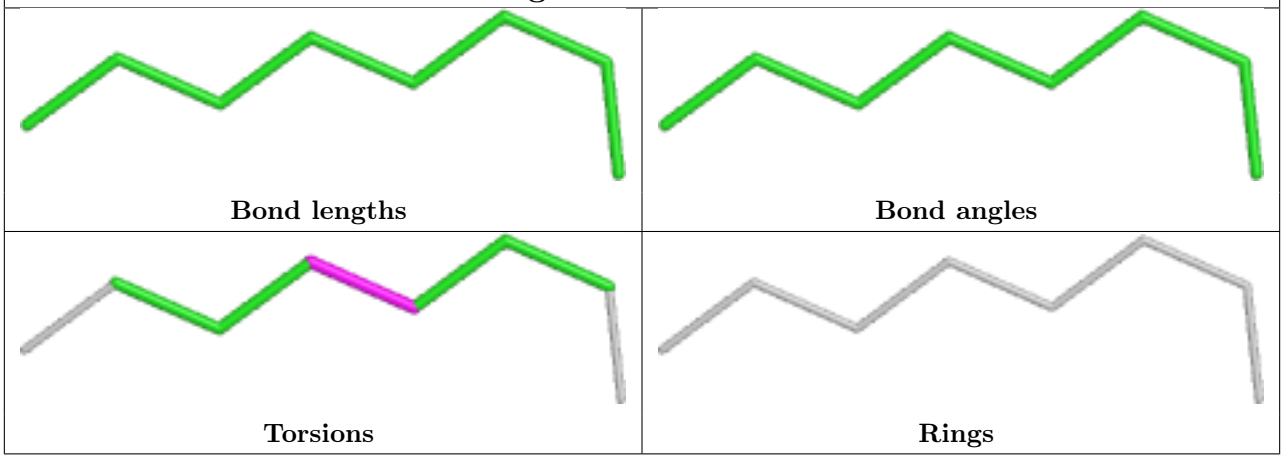

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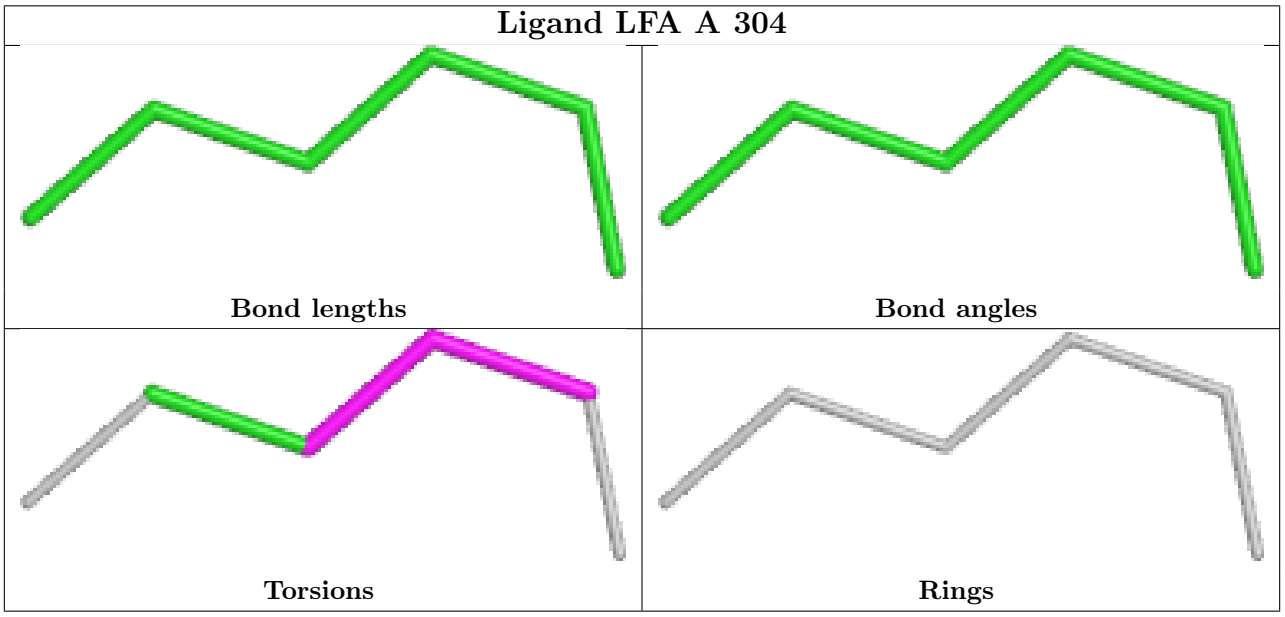

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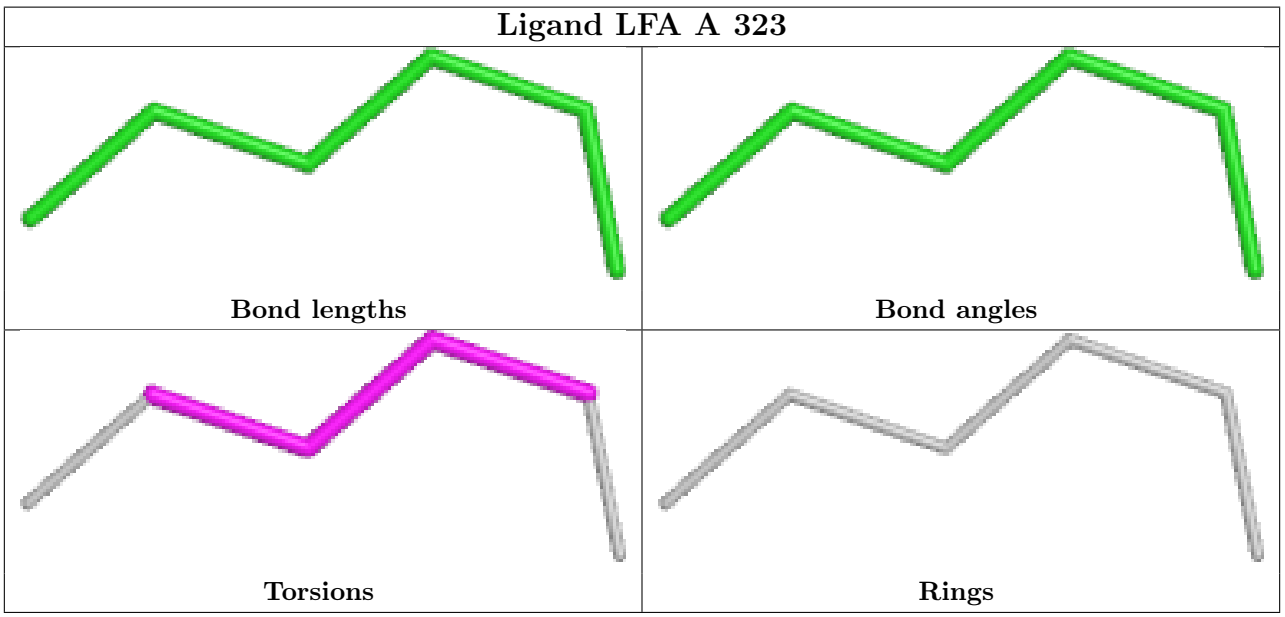

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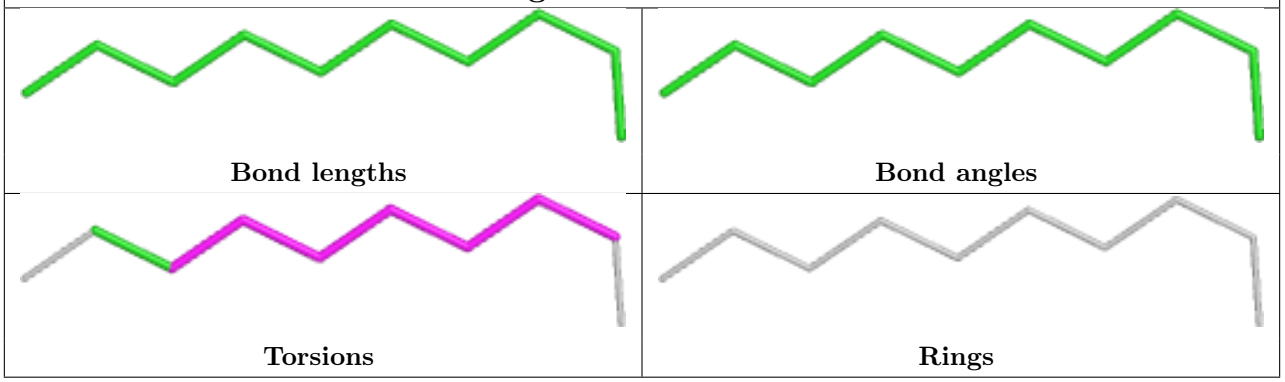

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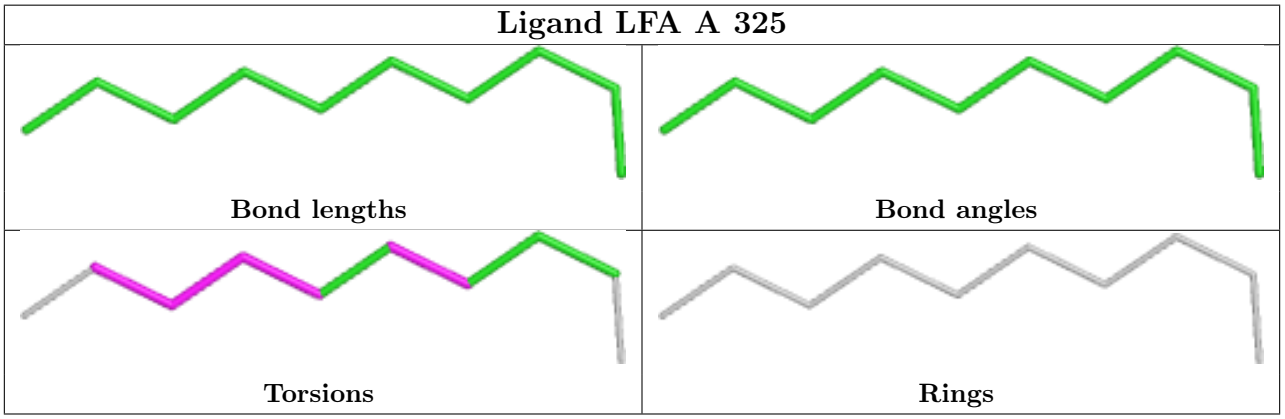

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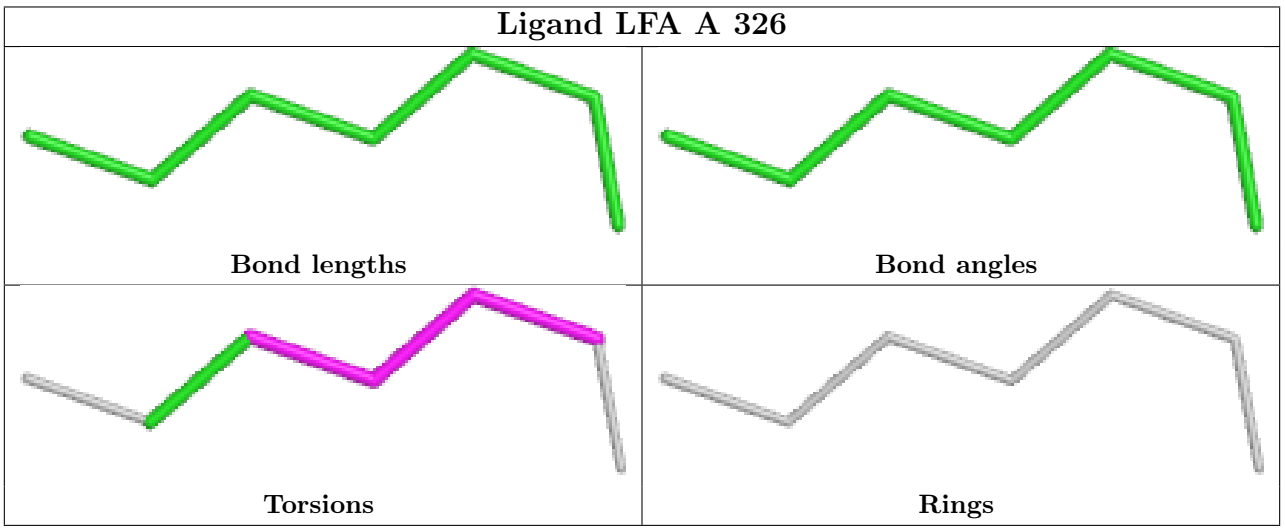

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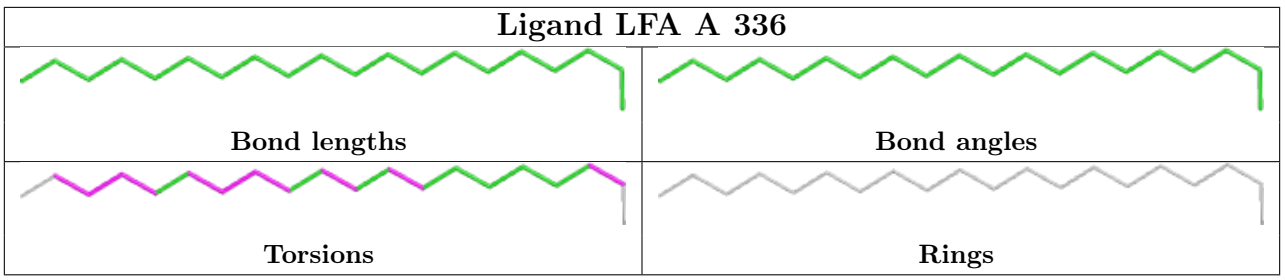

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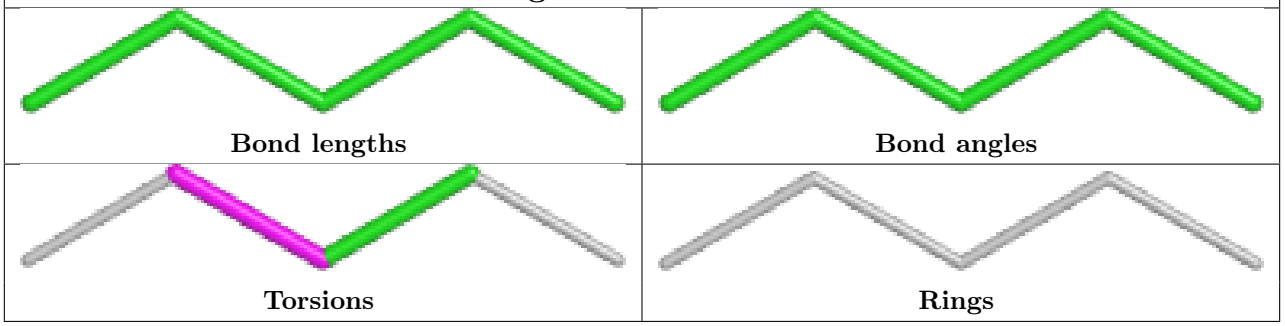

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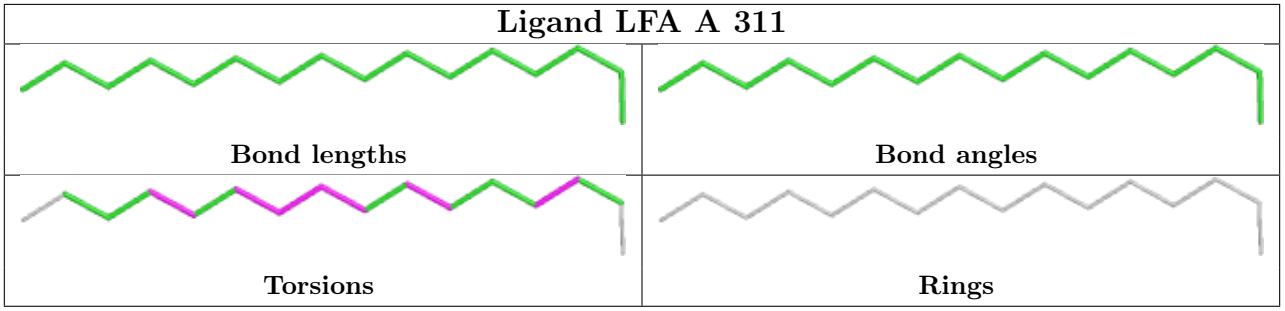

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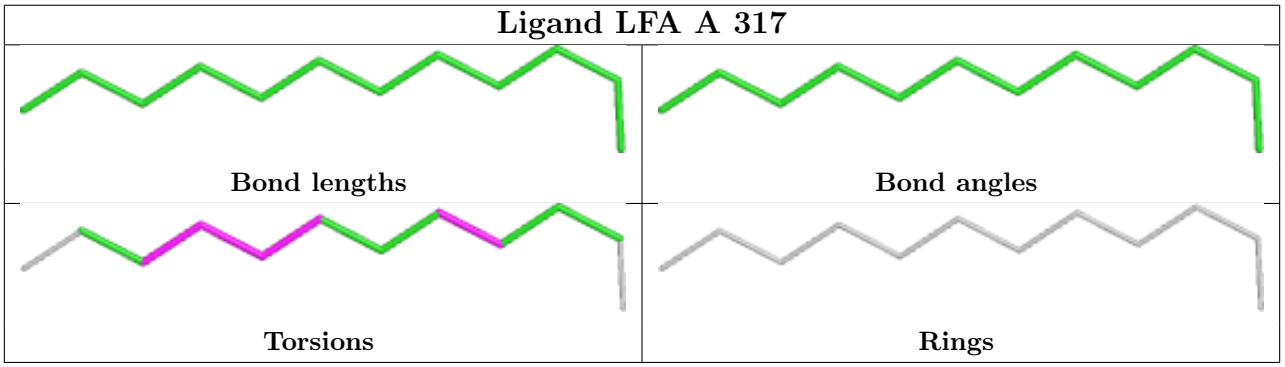

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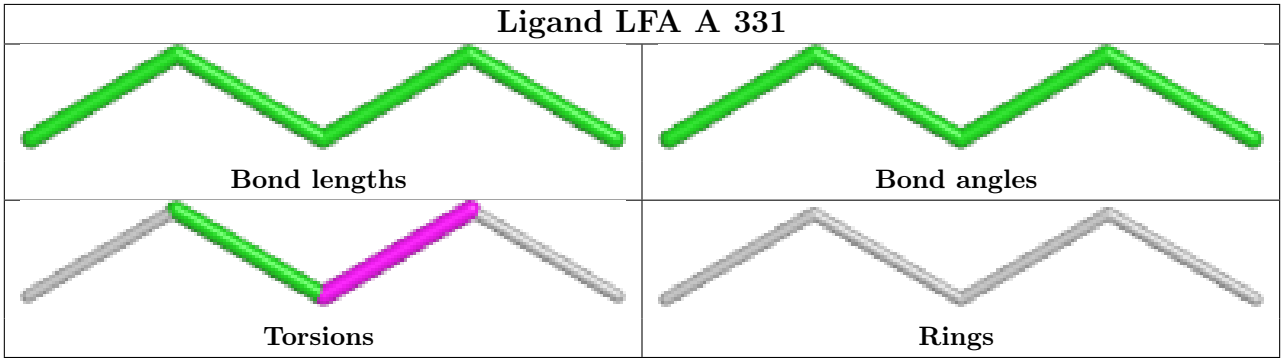

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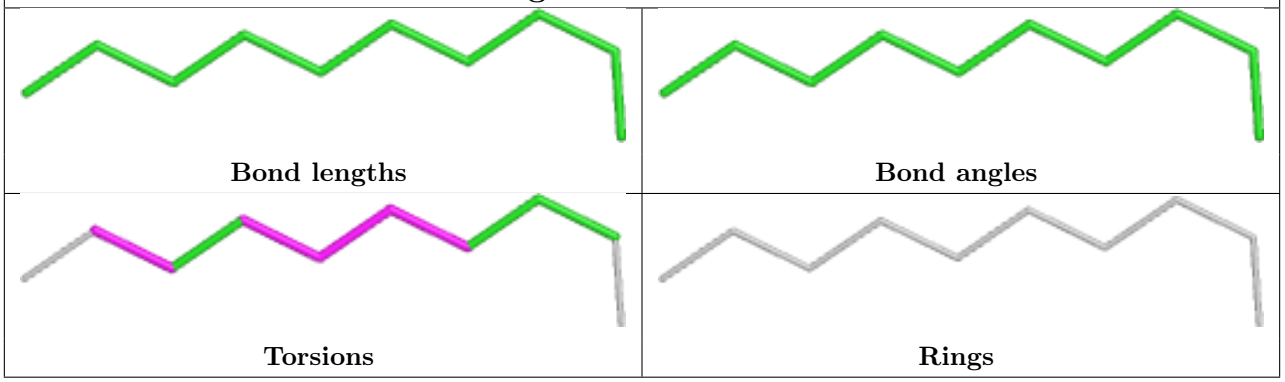

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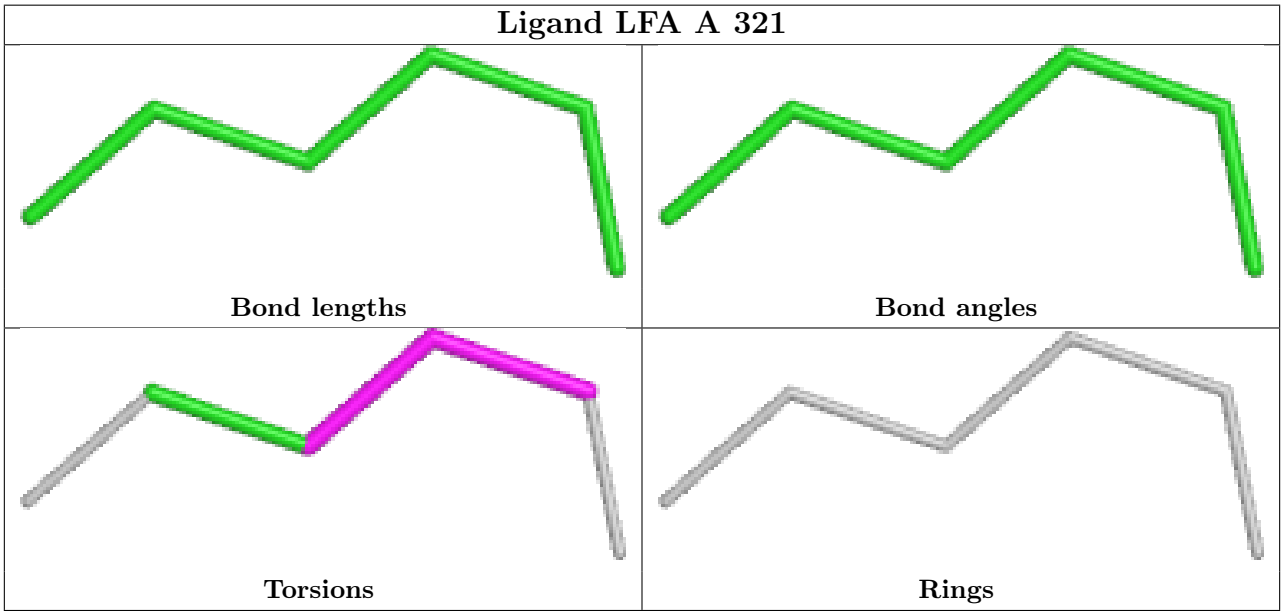

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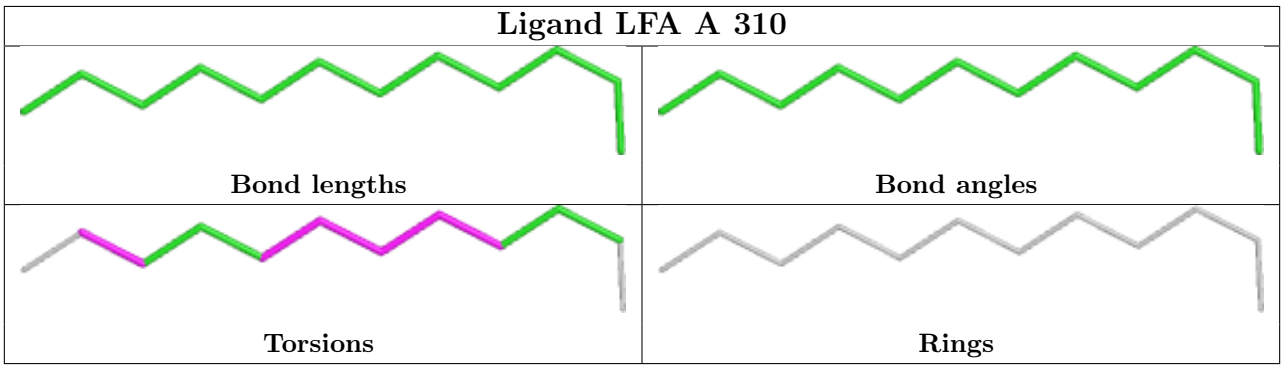
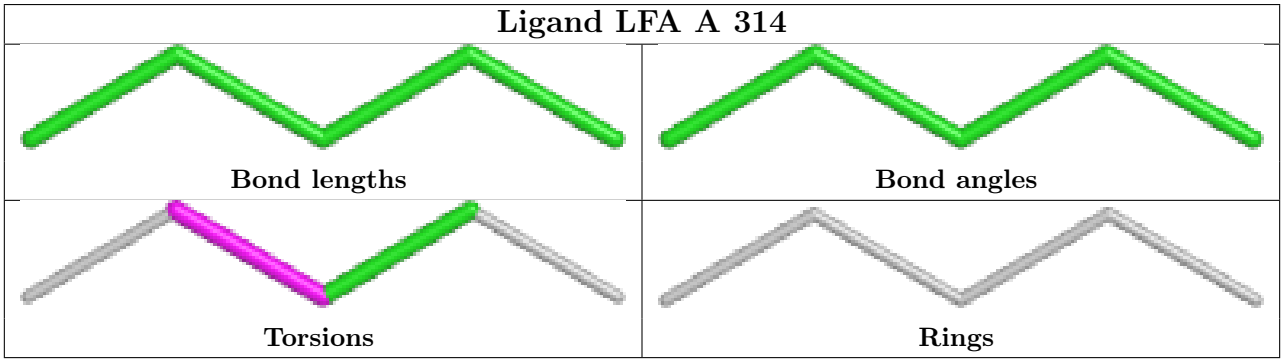
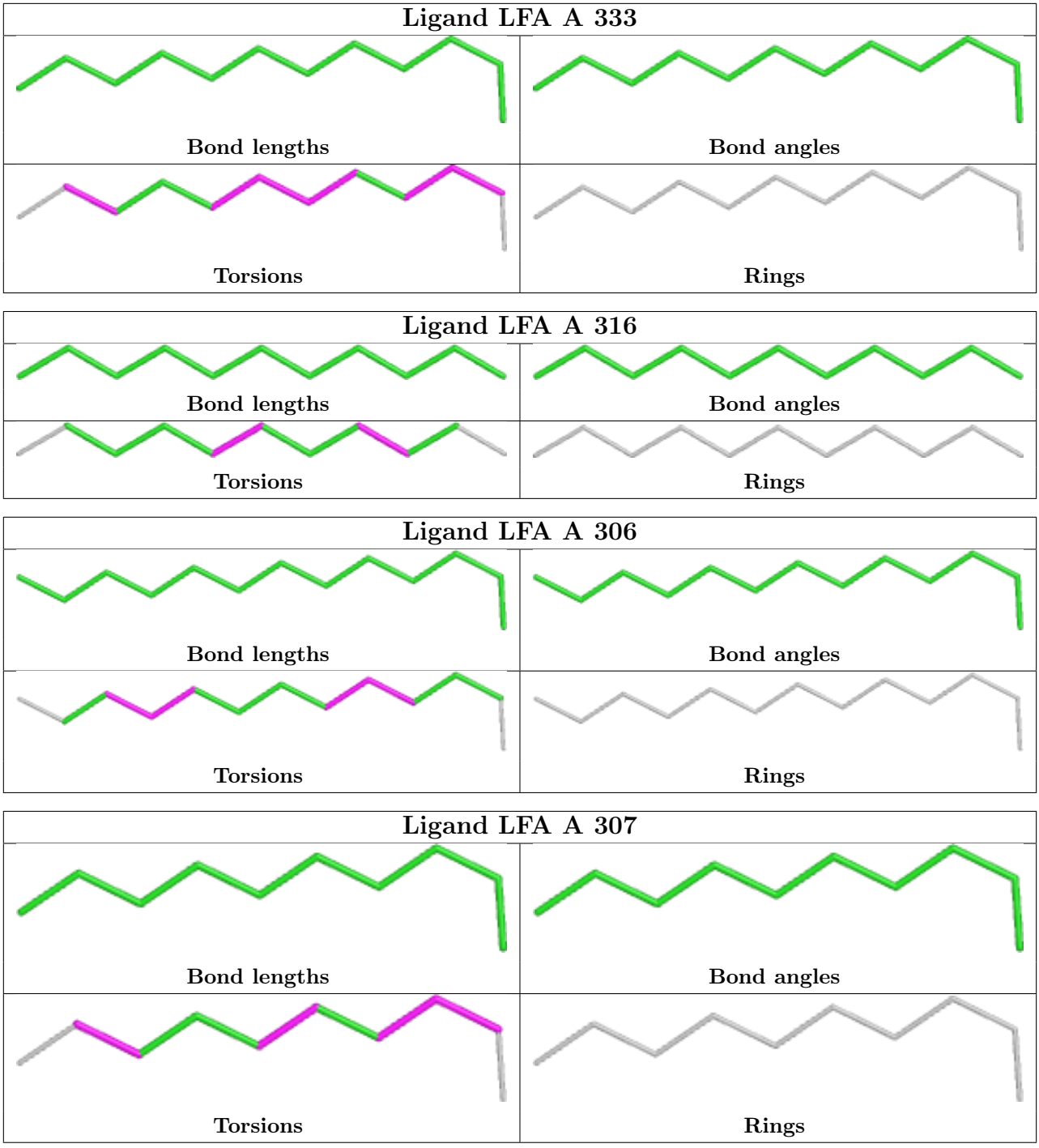


Ligand LFA A 314





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

6.1 Protein, DNA and RNA chains

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, 95^{th} 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	269/288 (93%)	-0.24	6 (2%)	62	59	22, 35, 63, 87	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	THR	3.5
1	A	270	SER	2.6
1	A	5	LEU	2.5
1	A	230	VAL	2.5
1	A	158	PHE	2.2
1	A	231	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands

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, 95^{th} 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
3	LFA	A	324	6/20	0.39	0.25	46,82,85,86	0

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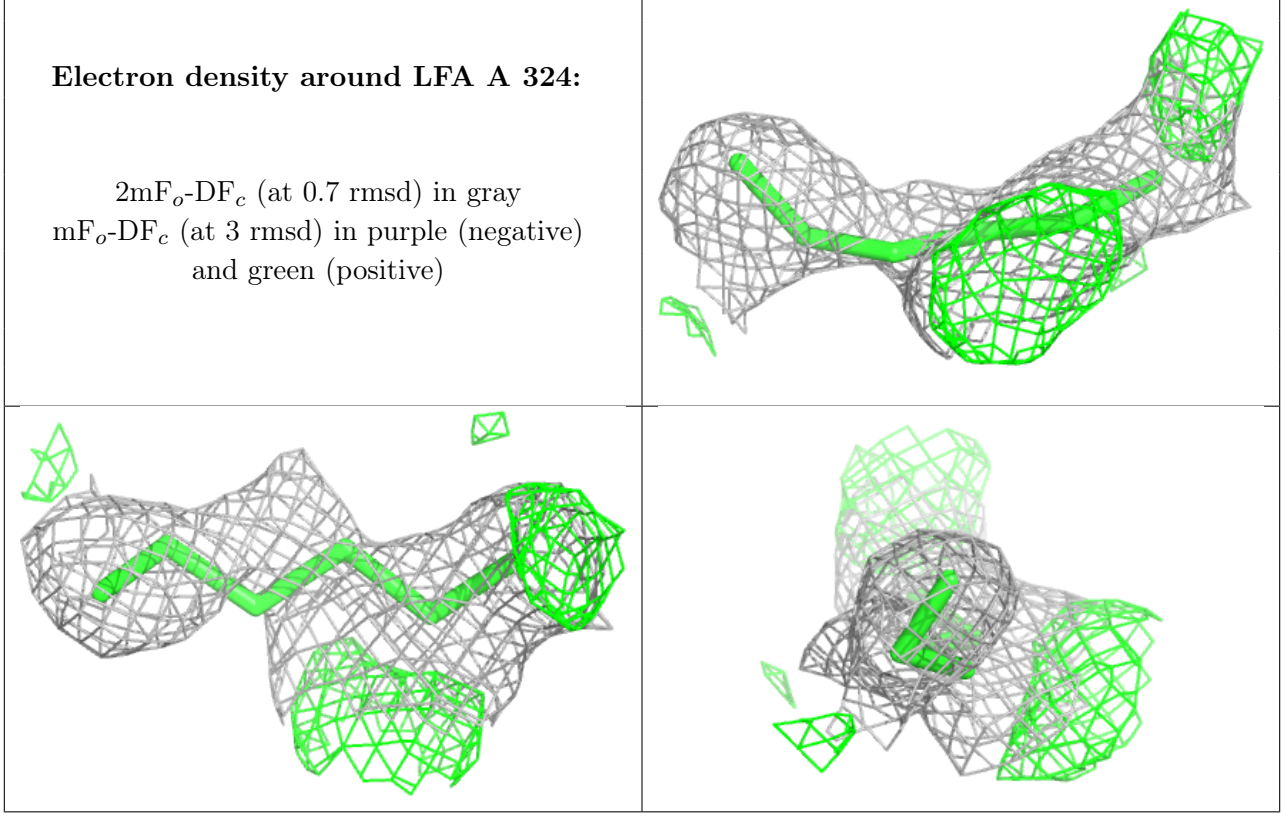
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	LFA	A	331	5/20	0.52	0.21	65,66,82,83	0
4	GOL	A	335	6/6	0.53	0.18	100,125,137,140	0
3	LFA	A	328	5/20	0.57	0.23	71,72,76,79	0
3	LFA	A	326	7/20	0.60	0.21	67,75,81,82	0
3	LFA	A	330	4/20	0.61	0.22	78,82,82,84	0
3	LFA	A	316	11/20	0.65	0.17	72,80,93,104	0
3	LFA	A	321	6/20	0.65	0.20	66,72,78,80	0
3	LFA	A	334	10/20	0.67	0.20	65,91,106,110	0
3	LFA	A	332	10/20	0.68	0.23	71,81,92,96	0
3	LFA	A	322	4/20	0.69	0.21	49,60,60,65	0
3	LFA	A	325	10/20	0.71	0.17	66,81,89,95	0
3	LFA	A	318	10/20	0.71	0.18	76,85,88,91	0
3	LFA	A	323	6/20	0.72	0.17	57,65,71,71	0
3	LFA	A	313	10/20	0.72	0.23	56,77,98,106	0
3	LFA	A	319	6/20	0.74	0.20	51,59,66,71	0
3	LFA	A	327	3/20	0.74	0.21	63,63,73,73	0
3	LFA	A	308	8/20	0.75	0.17	61,66,88,88	0
3	LFA	A	310	12/20	0.75	0.18	58,83,93,102	0
3	LFA	A	317	12/20	0.75	0.22	81,91,116,120	0
3	LFA	A	320	5/20	0.76	0.20	75,78,82,86	0
3	LFA	A	311	16/20	0.77	0.14	64,69,90,92	0
3	LFA	A	309	8/20	0.78	0.14	55,62,70,75	0
3	LFA	A	303	9/20	0.79	0.15	58,64,67,67	0
3	LFA	A	314	5/20	0.79	0.16	55,57,62,66	0
3	LFA	A	304	6/20	0.80	0.14	50,68,72,76	0
3	LFA	A	305	5/20	0.81	0.14	67,70,72,75	0
3	LFA	A	336	20/20	0.82	0.13	43,69,83,85	0
3	LFA	A	312	5/20	0.83	0.14	57,58,64,65	0
3	LFA	A	307	10/20	0.83	0.13	41,51,78,81	0
3	LFA	A	333	12/20	0.84	0.15	63,68,78,79	0
3	LFA	A	329	11/20	0.84	0.14	55,60,76,77	0
3	LFA	A	315	5/20	0.85	0.13	53,55,60,60	0
2	NA	A	301	1/1	0.86	0.16	60,60,60,60	0
3	LFA	A	302	8/20	0.88	0.20	31,33,75,272	8
3	LFA	A	306	13/20	0.88	0.16	48,51,76,77	0
5	RET	A	337	20/21	0.92	0.09	27,31,35,37	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.

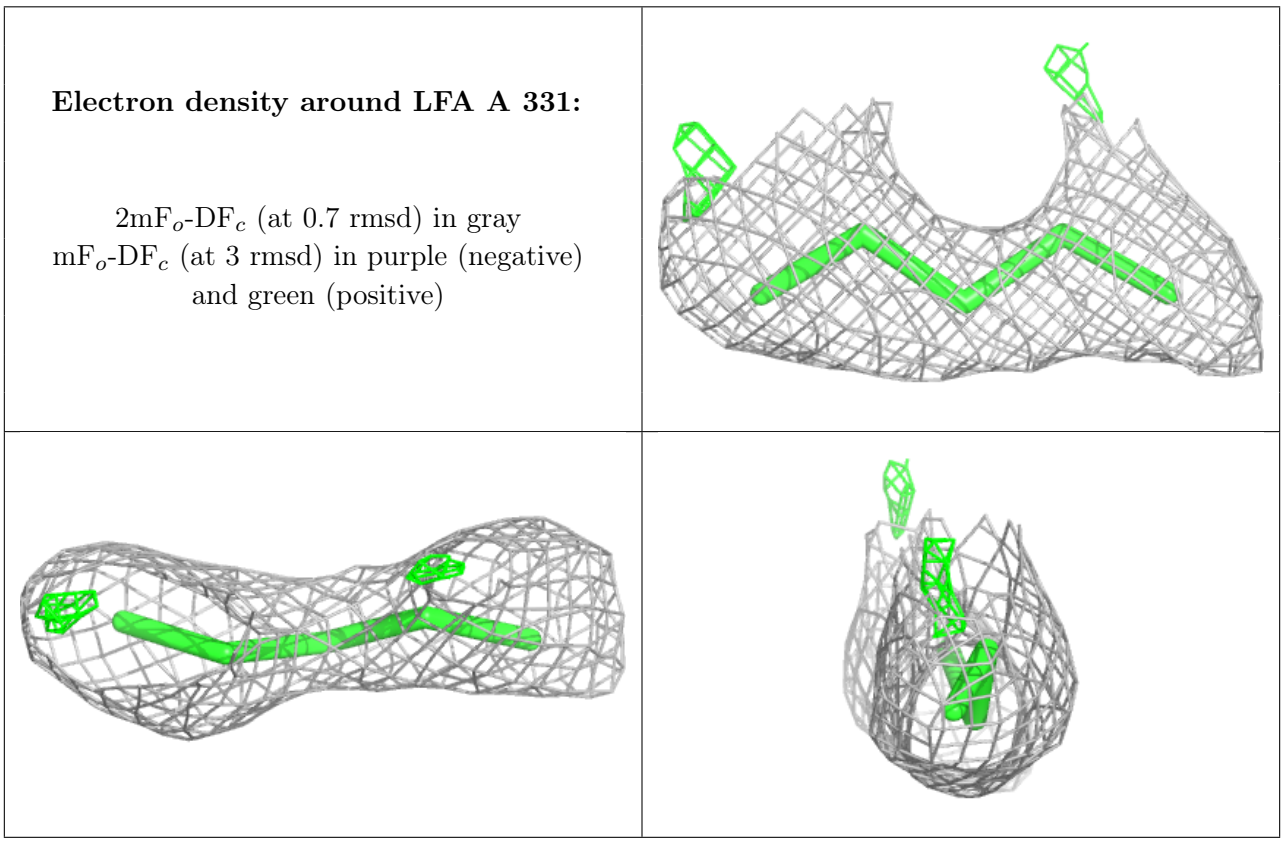
Electron density around LFA A 324:

$2mF_o$-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 331:

$2mF_o$-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 326:

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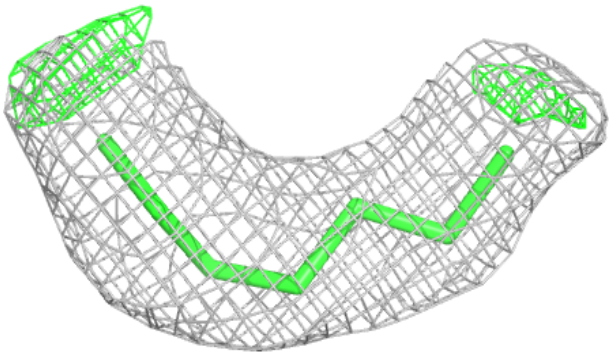
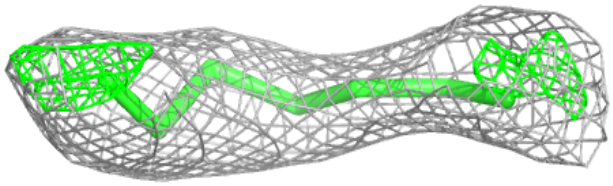
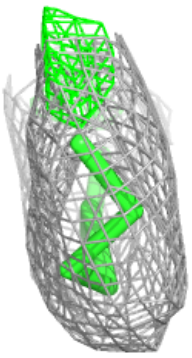
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

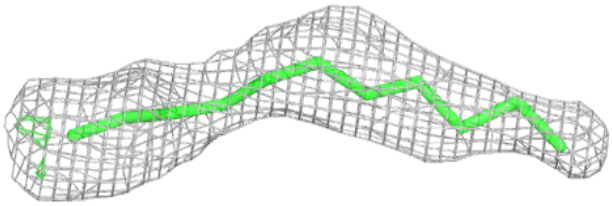


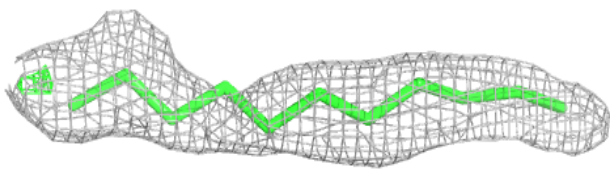


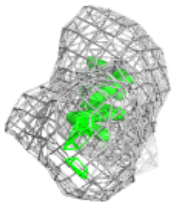


Electron density around LFA A 316:

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

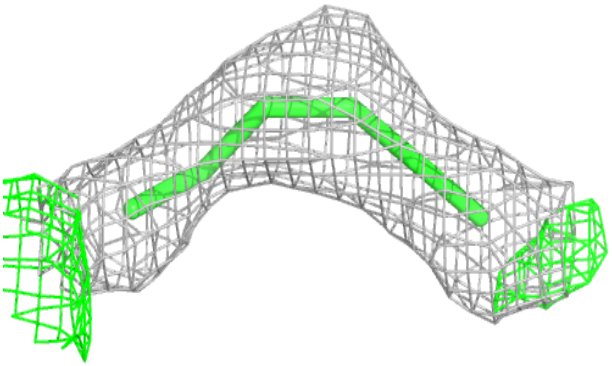


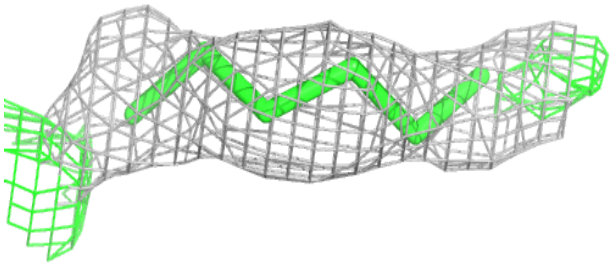


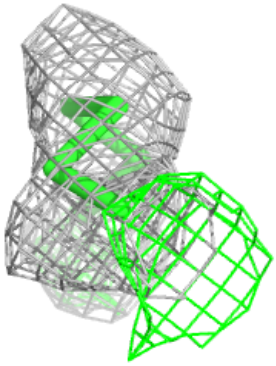


Electron density around LFA A 321:

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

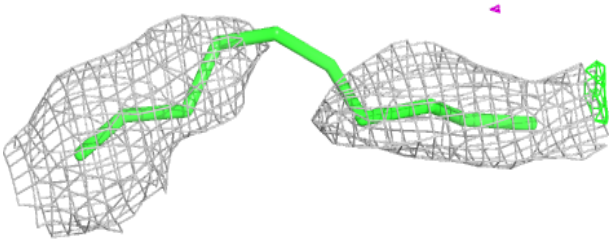


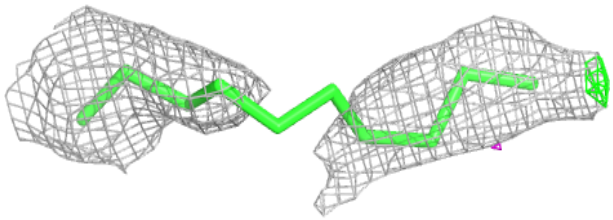


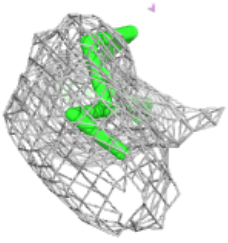


Electron density around LFA A 334:

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

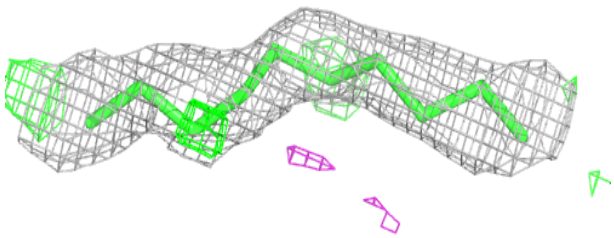


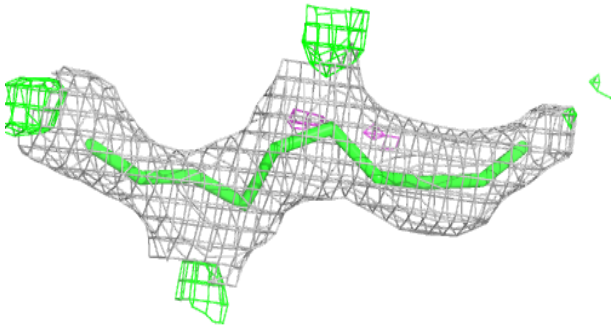


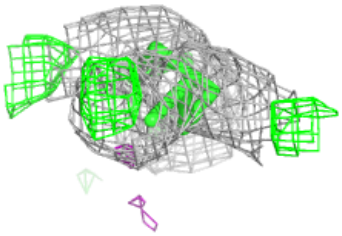


Electron density around LFA A 332:

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

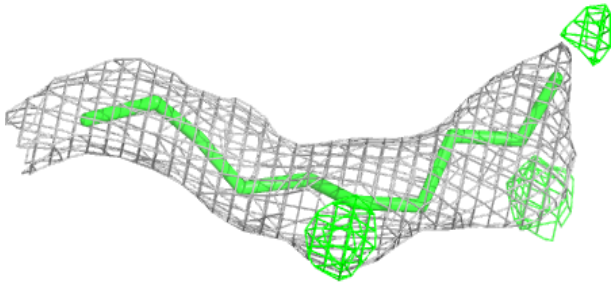


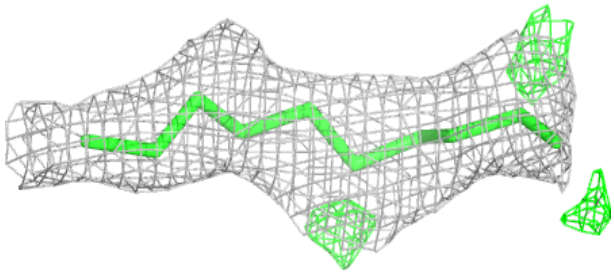


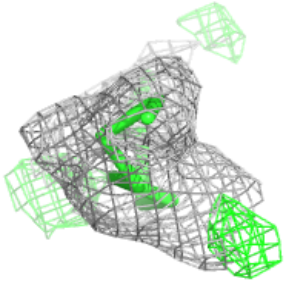


Electron density around LFA A 325:

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

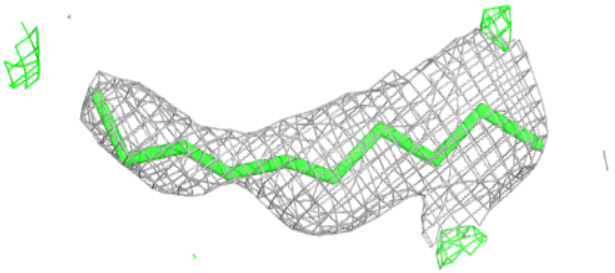


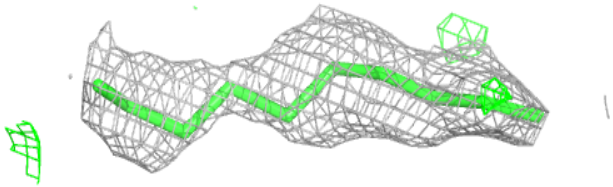


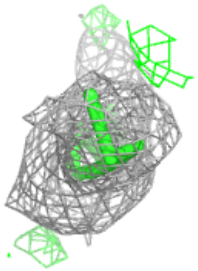


Electron density around LFA A 318:

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

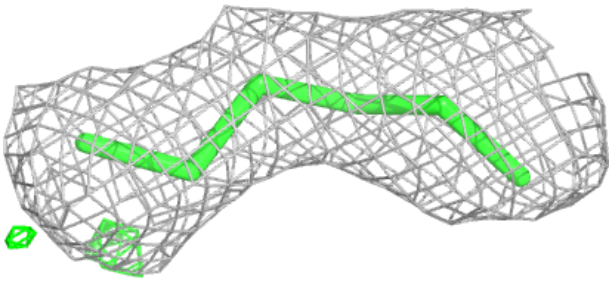


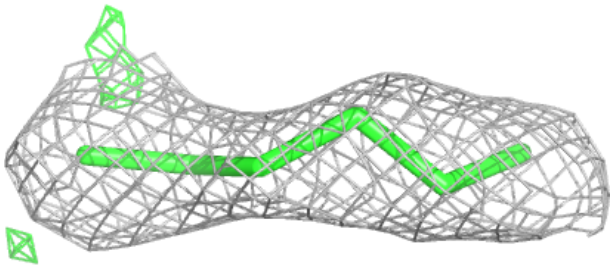


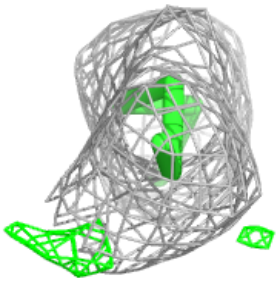


Electron density around LFA A 323:

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

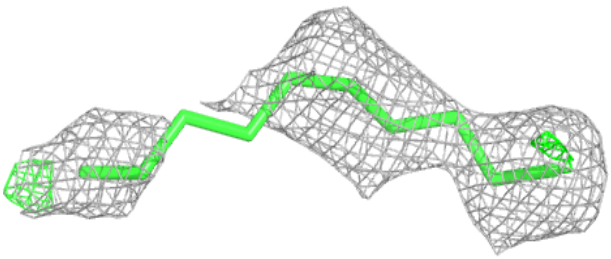


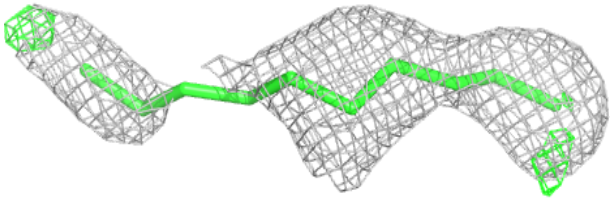


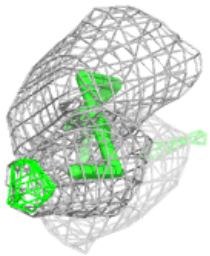


Electron density around LFA A 313:

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

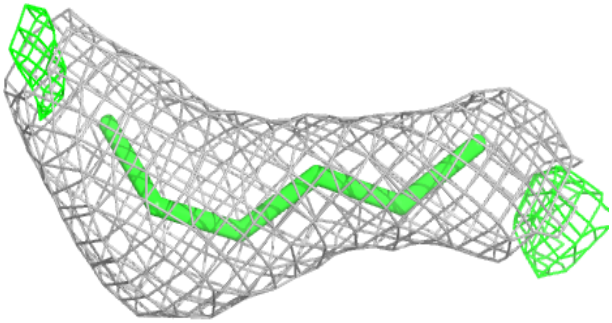


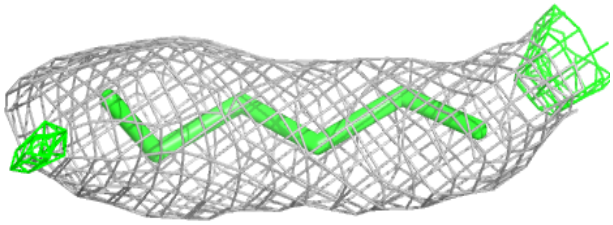


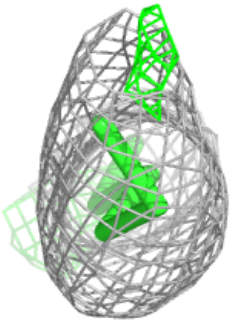


Electron density around LFA A 319:

$2mF_o$-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 A 308:

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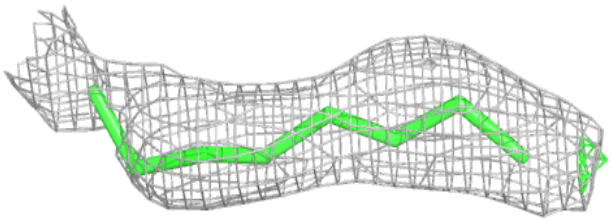
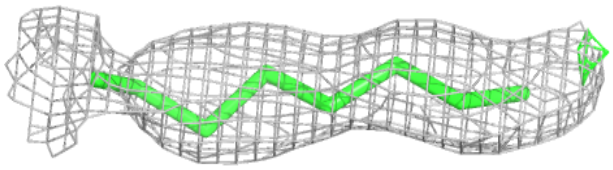
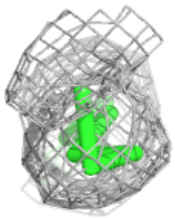
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

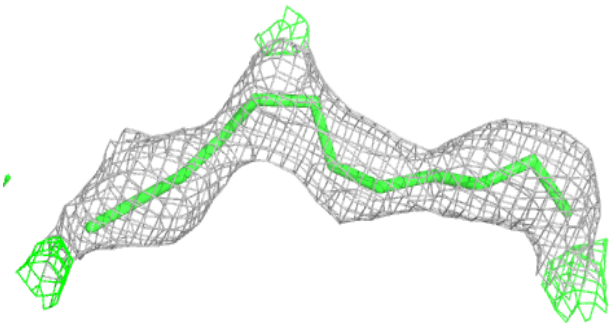


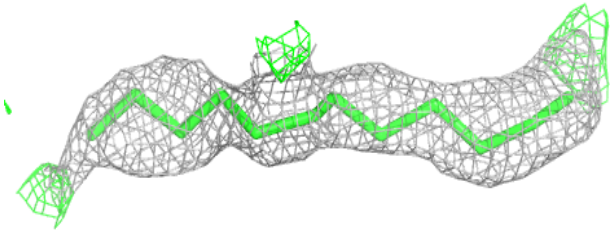


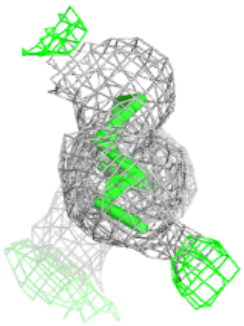


Electron density around LFA A 310:

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

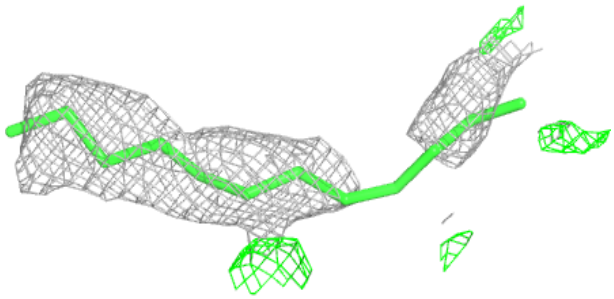


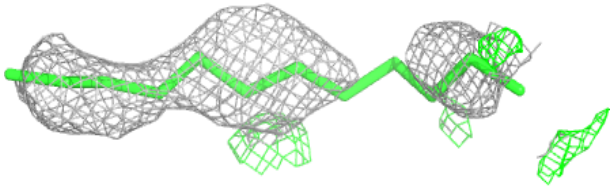


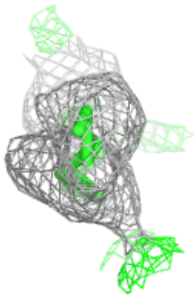


Electron density around LFA A 317:

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

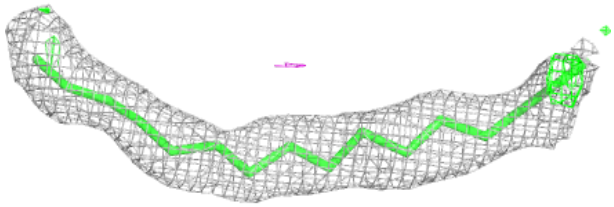


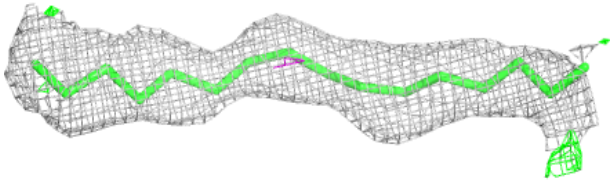


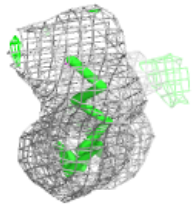


Electron density around LFA A 311:

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

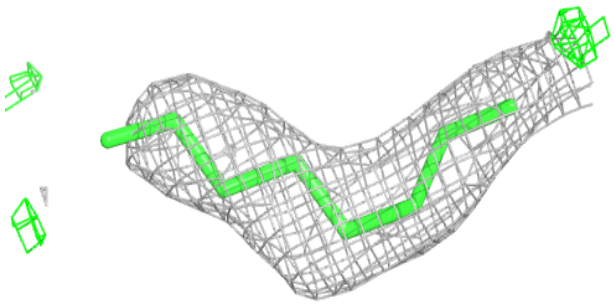


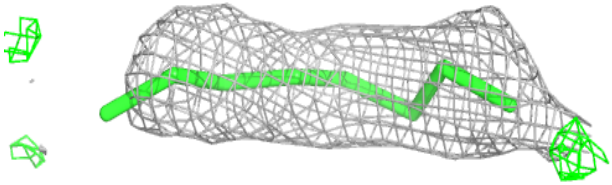


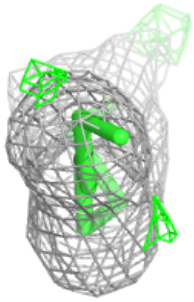


Electron density around LFA A 309:

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

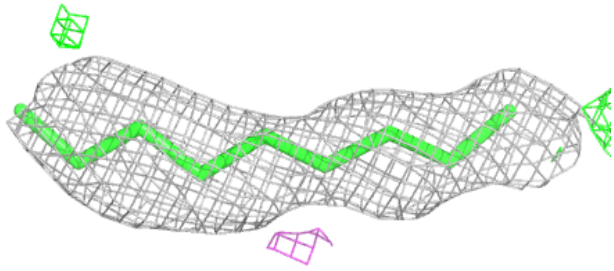


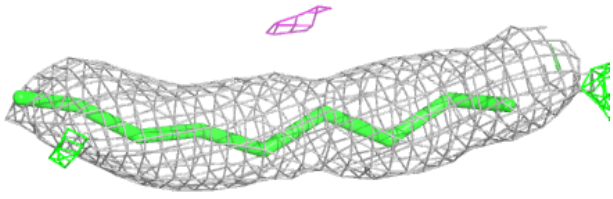


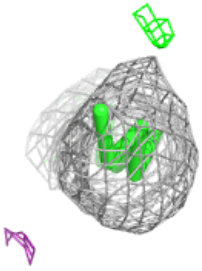


Electron density around LFA A 303:

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

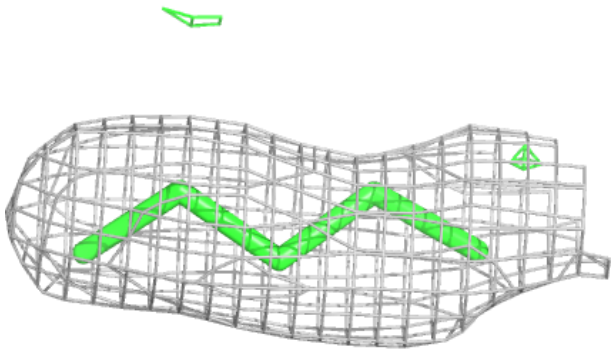


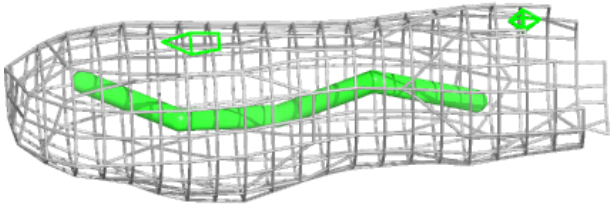


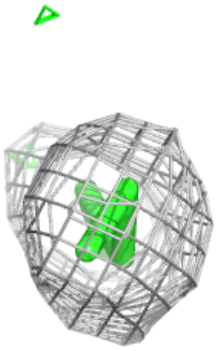


Electron density around LFA A 314:

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

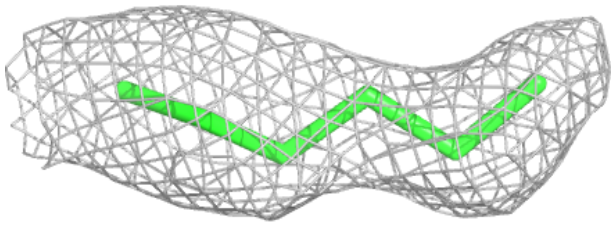


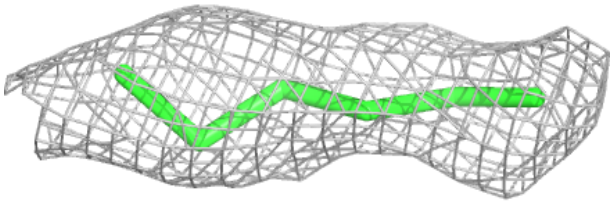


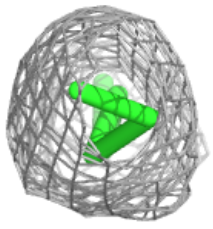


Electron density around LFA A 304:

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

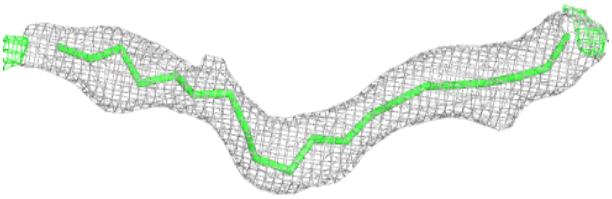


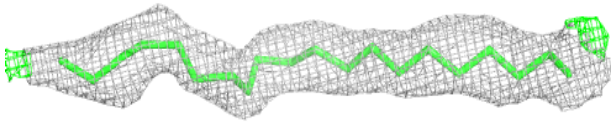


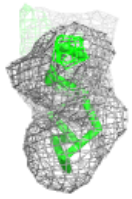


Electron density around LFA A 336:

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

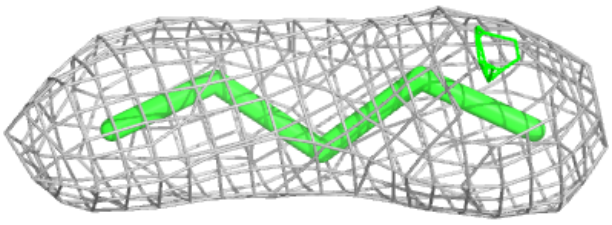


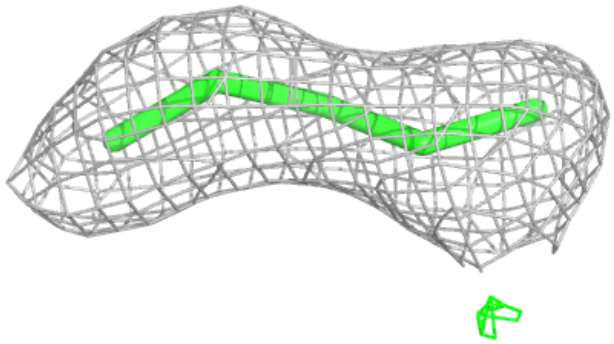


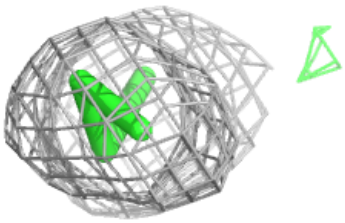


Electron density around LFA A 312:

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

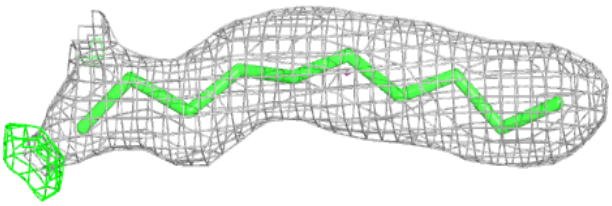


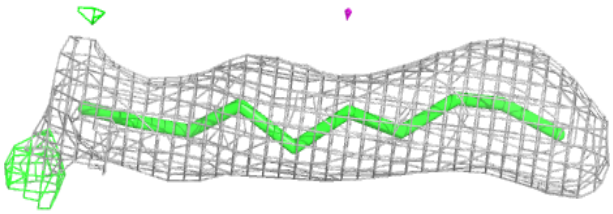


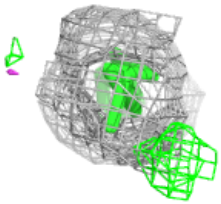


Electron density around LFA A 307:

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

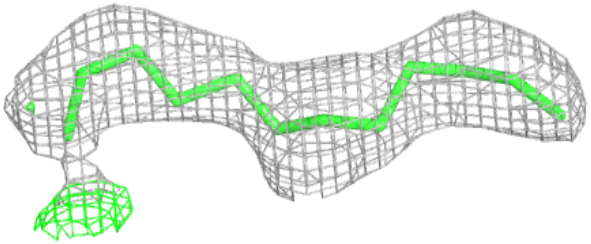


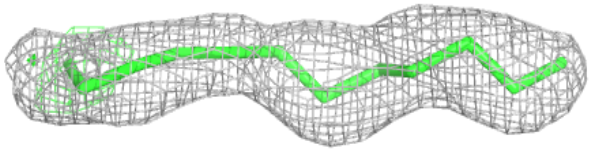


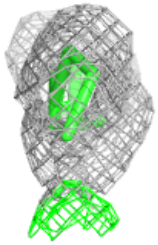


Electron density around LFA A 333:

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

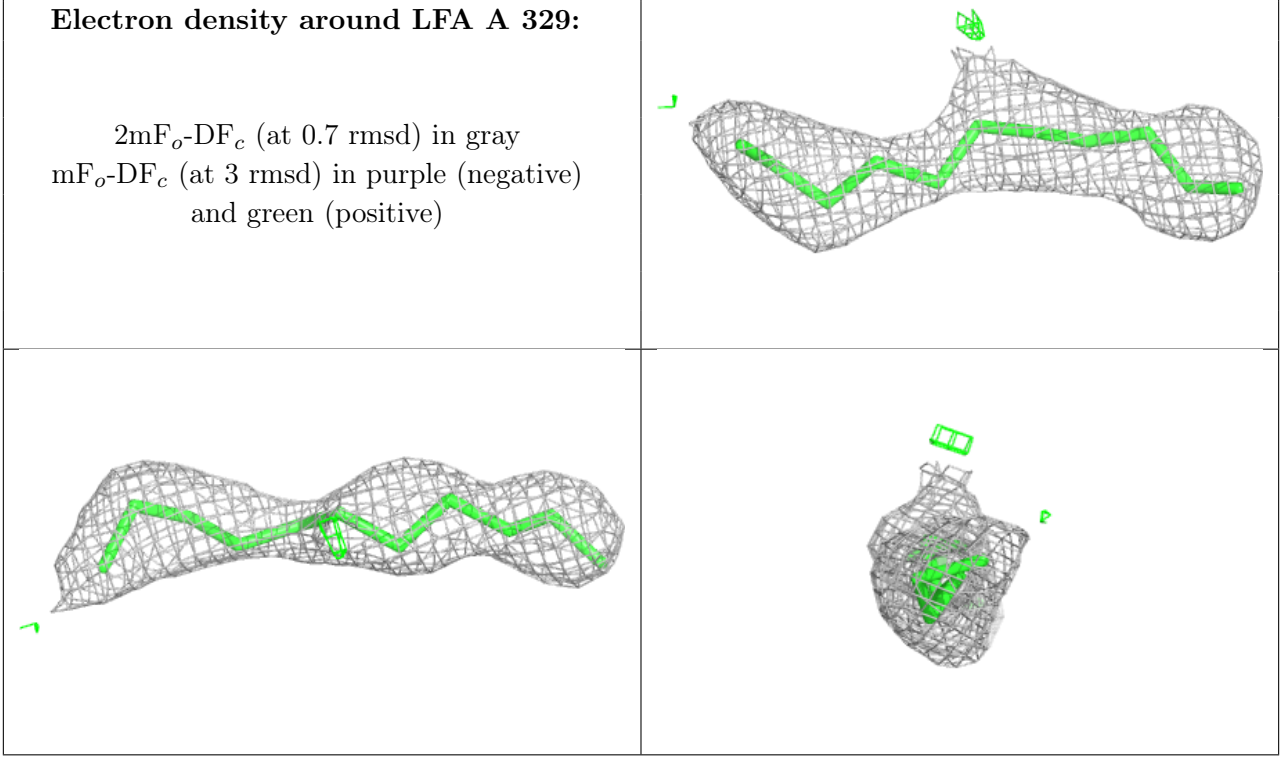






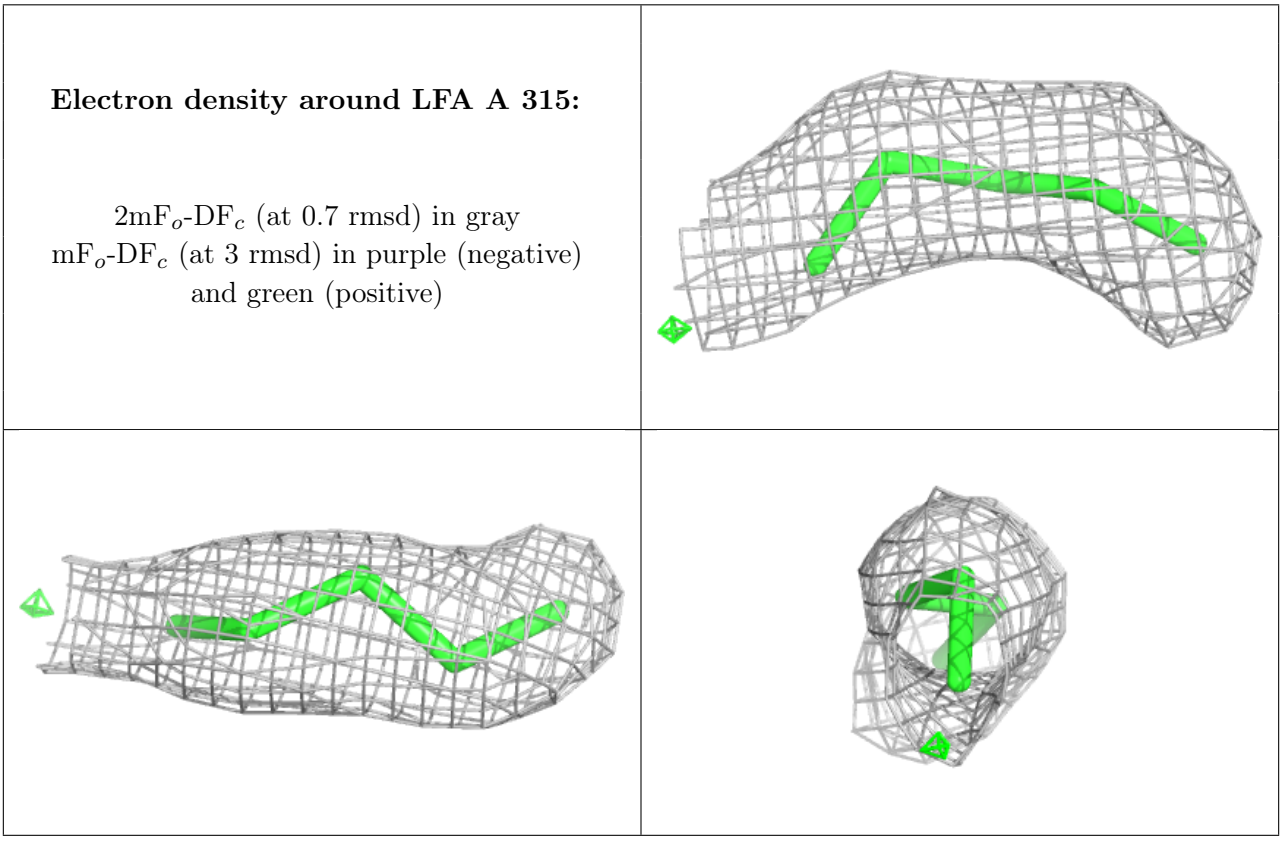
Electron density around LFA A 329:

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



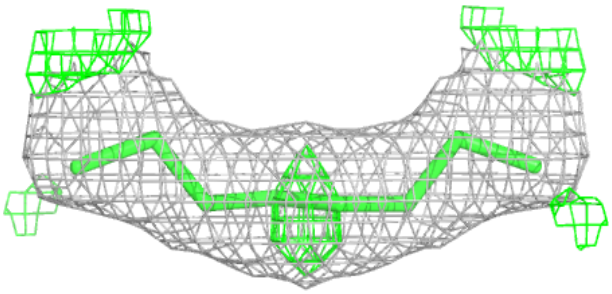
Electron density around LFA A 315:

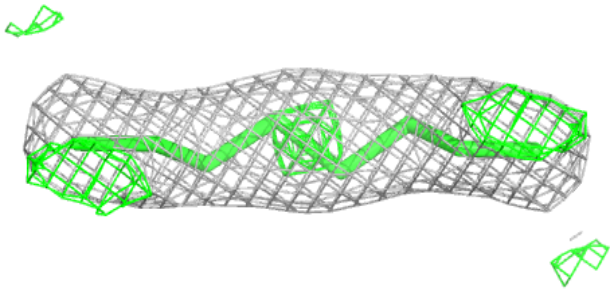
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

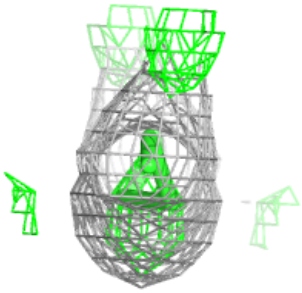


Electron density around LFA A 302:

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

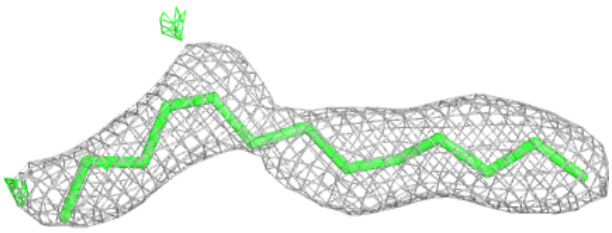


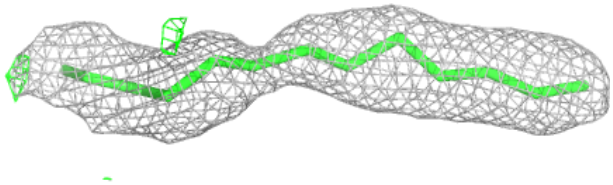


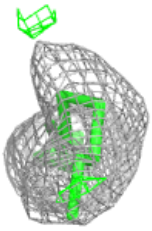


Electron density around LFA A 306:

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

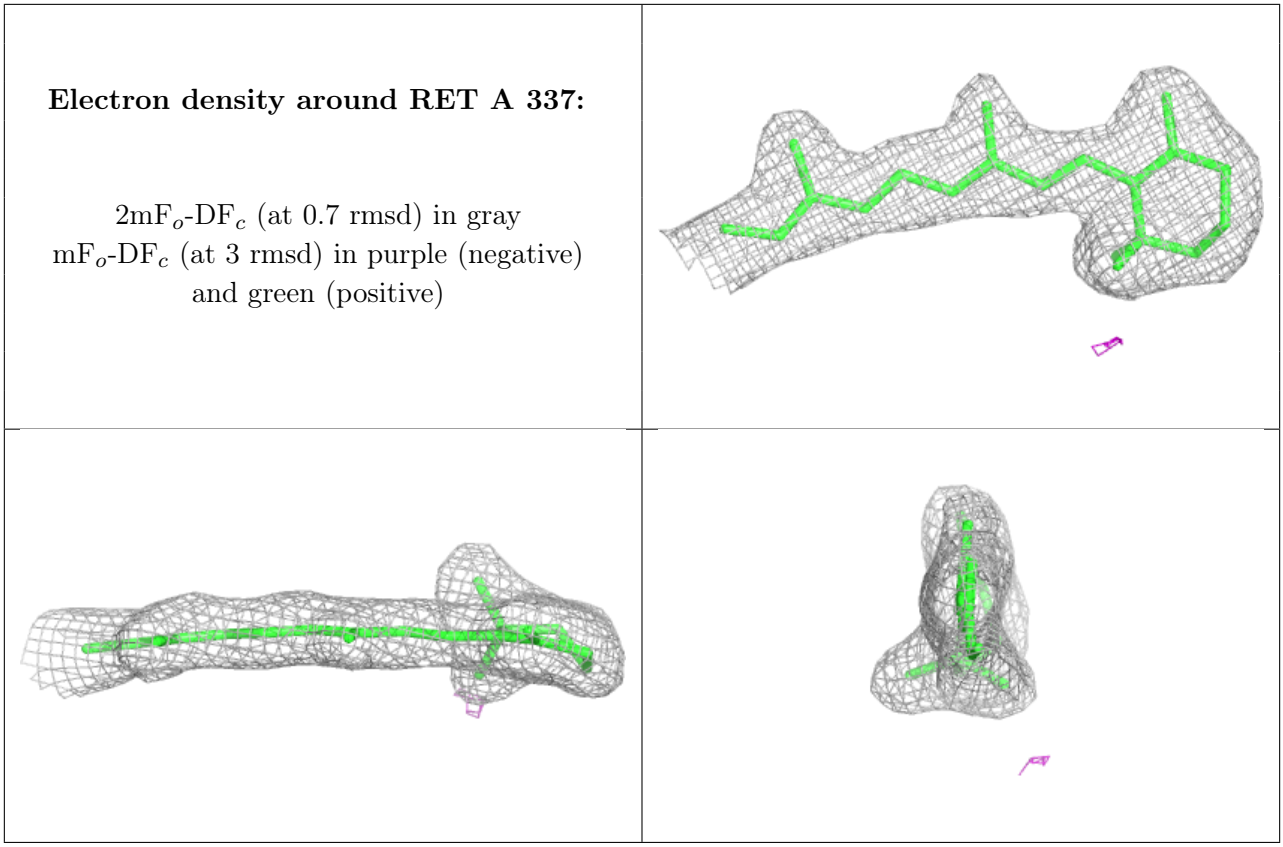






Electron density around RET A 337:

$2mF_o$-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

There are no such residues in this entry.