



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:06 PM UTC

PDB ID : 4XTL / pdb_00004xtl
Title : Crystal structure of the light-driven sodium pump KR2 in the monomeric blue form, pH 4.3
Authors : Gushchin, I.; Shevchenko, V.; Polovinkin, V.; Gordeliy, V.
Deposited on : 2015-01-23
Resolution : 1.45 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

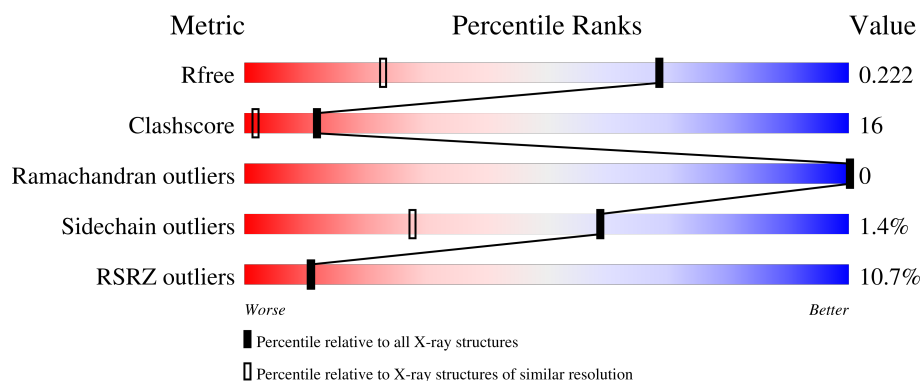
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.45 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	1756 (1.46-1.46)
Clashscore	190562	1795 (1.46-1.46)
Ramachandran outliers	187476	1776 (1.46-1.46)
Sidechain outliers	187428	1776 (1.46-1.46)
RSRZ outliers	180081	1756 (1.46-1.46)

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

Mol	Chain	Length	Quality of chain
1	A	288	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2722 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	271	Total	C	N	O	S	0	25	0
			2286	1554	330	388	14			

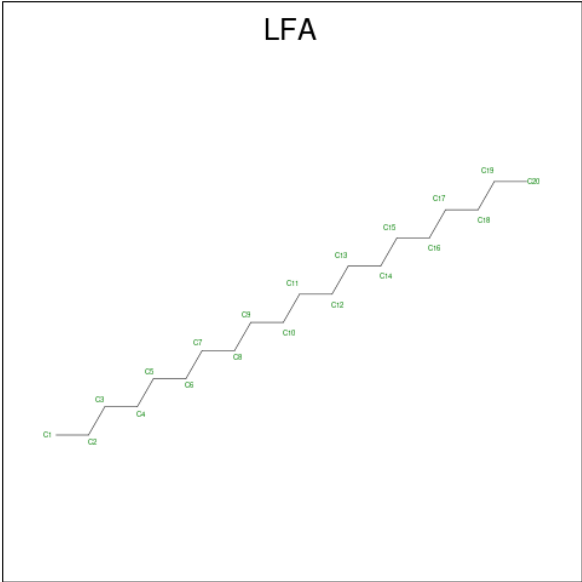
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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: C₂₀H₄₂).



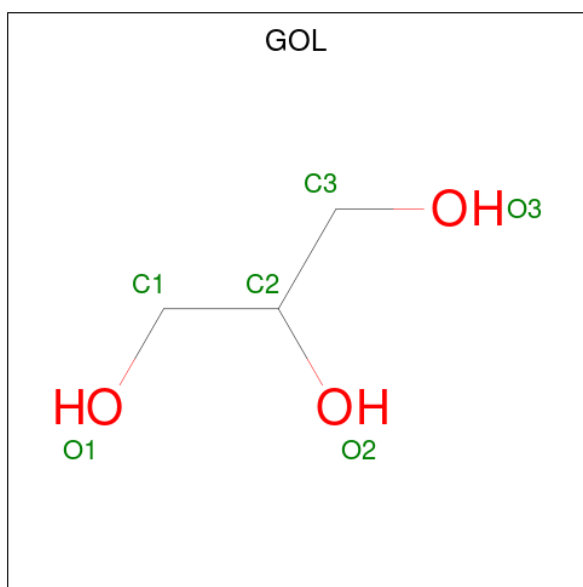
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C 16 16	0	0
3	A	1	Total C 8 8	0	0
3	A	1	Total C 9 9	0	0
3	A	1	Total C 6 6	0	0
3	A	1	Total C 5 5	0	0
3	A	1	Total C 13 13	0	0
3	A	1	Total C 10 10	0	0
3	A	1	Total C 8 8	0	0
3	A	1	Total C 8 8	0	0
3	A	1	Total C 12 12	0	0
3	A	1	Total C 16 16	0	0
3	A	1	Total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

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

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



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

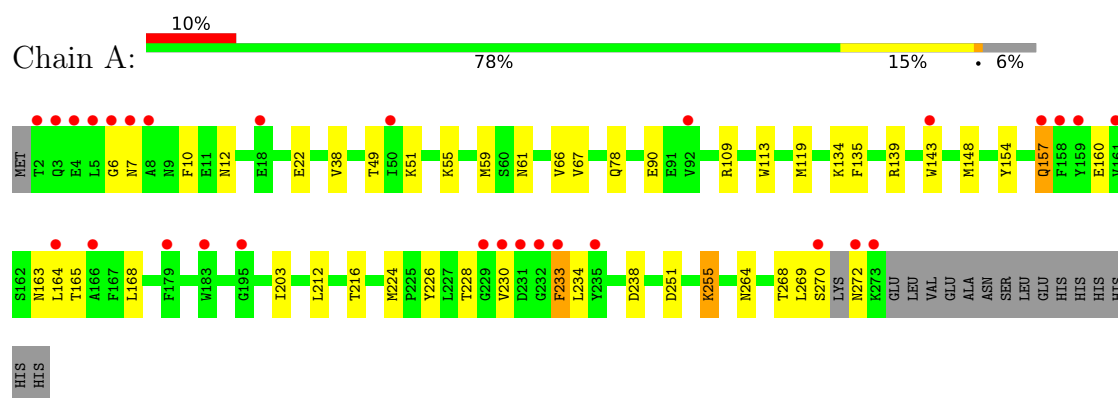
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	144	Total	O	0	0
			144	144		

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



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	40.18Å 80.84Å 232.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.40 – 1.45 40.40 – 1.45	Depositor EDS
% Data completeness (in resolution range)	99.7 (40.40-1.45) 99.7 (40.40-1.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 1.45Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.187 , 0.216 0.194 , 0.222	Depositor DCC
R_{free} test set	3221 reflections (4.68%)	wwPDB-VP
Wilson B-factor (Å ²)	21.1	Xtriage
Anisotropy	0.656	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 69.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2722	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.25% 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: LFA, GOL, NA, LYR

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	0.53	0/2394	0.70	0/3248

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2286	0	2326	62	0
2	A	1	0	0	0	0
3	A	279	0	506	41	0
4	A	12	0	16	3	0
5	A	144	0	0	14	0
All	All	2722	0	2848	85	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 16.

All (85) 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)
3:A:335:LFA:C10	4:A:336:GOL:O3	1.70	1.37
1:A:230:VAL:HG23	3:A:309:LFA:C8	1.71	1.20
1:A:59[B]:MET:HE1	3:A:328:LFA:H12	1.47	0.93
1:A:55:LYS:HE2	5:A:401:HOH:O	1.72	0.89
3:A:318:LFA:H11	3:A:320:LFA:C6	2.04	0.88
1:A:78[B]:GLN:NE2	5:A:442:HOH:O	2.00	0.84
3:A:315:LFA:C2	3:A:316:LFA:C6	2.62	0.78
1:A:59[B]:MET:HE1	3:A:328:LFA:C1	2.14	0.77
3:A:335:LFA:C10	4:A:336:GOL:HO3	1.99	0.76
1:A:233:PHE:CE2	1:A:238:ASP:OD2	2.39	0.75
1:A:255:LYR:H9	1:A:255:LYR:H183	1.71	0.73
1:A:269:LEU:HD23	5:A:414:HOH:O	1.87	0.72
1:A:270:SER:CB	5:A:527:HOH:O	2.37	0.72
1:A:160[A]:GLU:CG	1:A:226[A]:TYR:OH	2.39	0.71
1:A:264:ASN:O	1:A:268[A]:THR:HG23	1.91	0.70
1:A:230:VAL:CG2	3:A:309:LFA:C8	2.63	0.69
1:A:51:LYS:HB2	5:A:480:HOH:O	1.91	0.68
1:A:66:VAL:HB	1:A:119[B]:MET:HE1	1.76	0.68
3:A:305:LFA:C1	3:A:326:LFA:C10	2.74	0.66
1:A:66:VAL:CG1	1:A:119[B]:MET:HE1	2.26	0.65
1:A:139:ARG:HH11	3:A:325:LFA:C6	2.10	0.64
3:A:319:LFA:H61	3:A:325:LFA:C3	2.29	0.62
1:A:160[A]:GLU:OE1	1:A:226[A]:TYR:OH	2.16	0.61
1:A:59[A]:MET:HE2	3:A:319:LFA:H71	1.82	0.61
1:A:163:ASN:HD21	3:A:304:LFA:C10	2.14	0.60
1:A:134:LYS:CE	5:A:409:HOH:O	2.48	0.60
1:A:270:SER:O	1:A:272:ASN:N	2.35	0.59
3:A:305:LFA:H11	3:A:326:LFA:C10	2.32	0.59
1:A:59[B]:MET:CE	3:A:328:LFA:H12	2.28	0.59
3:A:319:LFA:H61	3:A:325:LFA:H32	1.83	0.59
1:A:164[B]:LEU:HD21	1:A:226[B]:TYR:CE2	2.38	0.59
1:A:148[B]:MET:HA	1:A:148[B]:MET:HE2	1.86	0.58
1:A:59[A]:MET:HE1	3:A:321:LFA:C1	2.34	0.57
1:A:66:VAL:CB	1:A:119[B]:MET:HE1	2.36	0.56
1:A:164[A]:LEU:HD22	3:A:335:LFA:H91	1.88	0.56
3:A:314:LFA:H62	3:A:330:LFA:C9	2.38	0.54
1:A:164[B]:LEU:HD13	1:A:168:LEU:HG	1.89	0.54
3:A:318:LFA:C1	3:A:320:LFA:C6	2.84	0.53
1:A:160[A]:GLU:HG3	1:A:226[A]:TYR:OH	2.07	0.53
1:A:270:SER:HB2	5:A:527:HOH:O	2.06	0.53
3:A:319:LFA:H13	5:A:407:HOH:O	2.09	0.53
1:A:59[B]:MET:HE3	3:A:319:LFA:H31	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:270:SER:HB3	5:A:527:HOH:O	2.03	0.53
3:A:309:LFA:H12	3:A:313:LFA:C5	2.39	0.52
1:A:55:LYS:HG3	5:A:401:HOH:O	2.09	0.52
1:A:38:VAL:HG22	3:A:302:LFA:H151	1.93	0.50
1:A:10:PHE:HB2	1:A:160[B]:GLU:OE1	2.11	0.50
3:A:319:LFA:C6	3:A:325:LFA:H31	2.42	0.50
1:A:61:ASN:H	1:A:61:ASN:HD22	1.59	0.49
3:A:314:LFA:H62	3:A:330:LFA:H91	1.95	0.49
3:A:319:LFA:H61	3:A:325:LFA:H31	1.93	0.49
3:A:321:LFA:H13	3:A:328:LFA:C3	2.42	0.49
1:A:135:PHE:CE1	3:A:325:LFA:H41	2.48	0.49
1:A:113:TRP:NE1	5:A:434:HOH:O	2.29	0.48
3:A:305:LFA:H12	3:A:326:LFA:C10	2.42	0.48
1:A:113:TRP:CD1	1:A:255:LYR:HC2	2.48	0.48
1:A:143:TRP:CZ2	3:A:333:LFA:H22	2.49	0.47
1:A:59[A]:MET:HE1	3:A:321:LFA:H11	1.95	0.47
1:A:255:LYR:H183	1:A:255:LYR:C9	2.40	0.47
1:A:49:THR:HG22	3:A:308:LFA:H22	1.97	0.47
1:A:228:THR:HG23	1:A:234:LEU:HD12	1.97	0.47
3:A:319:LFA:C1	5:A:407:HOH:O	2.62	0.47
1:A:224:MET:HE1	3:A:330:LFA:C11	2.45	0.46
1:A:90:GLU:CD	5:A:544:HOH:O	2.59	0.45
3:A:319:LFA:H72	3:A:325:LFA:H52	1.99	0.45
1:A:233:PHE:HE2	1:A:238:ASP:OD2	1.95	0.45
1:A:157[A]:GLN:HE21	1:A:157[A]:GLN:HB3	1.64	0.45
1:A:160[A]:GLU:CD	1:A:226[A]:TYR:HH	2.20	0.45
1:A:203:ILE:CD1	1:A:268[A]:THR:HG21	2.47	0.44
1:A:255:LYR:H9	1:A:255:LYR:H192	2.00	0.44
3:A:302:LFA:H141	3:A:317:LFA:H101	2.00	0.44
1:A:67:VAL:HG22	1:A:119[A]:MET:HE3	2.00	0.43
1:A:109[A]:ARG:NH2	1:A:251:ASP:OD2	2.51	0.43
1:A:7:ASN:C	1:A:7:ASN:N	2.76	0.43
3:A:333:LFA:H72	3:A:333:LFA:H42	1.81	0.43
3:A:307:LFA:H82	3:A:307:LFA:H112	1.94	0.42
1:A:165:THR:H	4:A:336:GOL:H11	1.83	0.42
3:A:320:LFA:H12	5:A:490:HOH:O	2.19	0.42
1:A:6:GLY:HA2	1:A:12:ASN:HB3	2.01	0.41
1:A:255:LYR:H81	1:A:255:LYR:H10	1.79	0.41
1:A:154:TYR:O	1:A:157[B]:GLN:HG3	2.20	0.41
1:A:160[A]:GLU:HG2	1:A:226[A]:TYR:OH	2.20	0.41
1:A:212:LEU:O	1:A:216[B]:THR:HG23	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216[B]:THR:OG1	3:A:330:LFA:H41	2.21	0.41

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	291/288 (101%)	286 (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	243/247 (98%)	239 (98%)	4 (2%)	55	23

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	GLU
1	A	157[A]	GLN
1	A	157[B]	GLN
1	A	233	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	61	ASN
1	A	106	ASN
1	A	206	ASN
1	A	272	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	LYR	A	255	1	27,29,30	1.30	4 (14%)	30,37,39	1.82	9 (30%)

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
1	LYR	A	255	1	-	2/22/40/42	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	255	LYR	C2-C3	3.63	1.42	1.33
1	A	255	LYR	C5-C3	-2.19	1.41	1.46
1	A	255	LYR	C1-C2	-2.14	1.37	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	255	LYR	C7-C80	2.07	1.40	1.35

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	255	LYR	C1-NZ-CE	4.74	122.47	112.85
1	A	255	LYR	C7-C6-C5	-3.90	111.91	123.20
1	A	255	LYR	C13-C12-C11	-3.41	120.77	124.48
1	A	255	LYR	C10-C9-C80	-3.12	121.61	126.23
1	A	255	LYR	C6-C7-C80	-2.39	123.93	127.28
1	A	255	LYR	C15-C14-C12	-2.19	110.15	114.06
1	A	255	LYR	C14-C12-C11	2.11	125.56	122.70
1	A	255	LYR	C8-C80-C7	-2.04	119.51	122.82
1	A	255	LYR	C17-C11-C10	2.02	121.13	115.65

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	255	LYR	C2-C1-NZ-CE
1	A	255	LYR	CE-CD-CG-CB

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	255	LYR	5	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	324	-	5,5,19	0.28	0	4,4,18	0.36	0
3	LFA	A	311	-	11,11,19	0.29	0	10,10,18	0.42	0
3	LFA	A	332	-	4,4,19	0.33	0	3,3,18	0.38	0
3	LFA	A	309	-	7,7,19	0.25	0	6,6,18	0.49	0
3	LFA	A	316	-	4,4,19	0.29	0	3,3,18	0.38	0
3	LFA	A	326	-	9,9,19	0.24	0	8,8,18	0.54	0
3	LFA	A	327	-	6,6,19	0.26	0	5,5,18	0.43	0
3	LFA	A	325	-	5,5,19	0.23	0	4,4,18	0.45	0
3	LFA	A	320	-	5,5,19	0.24	0	4,4,18	0.43	0
3	LFA	A	308	-	9,9,19	0.27	0	8,8,18	0.45	0
3	LFA	A	335	-	9,9,19	0.29	0	8,8,18	0.40	0
3	LFA	A	329	-	4,4,19	0.31	0	3,3,18	0.42	0
3	LFA	A	319	-	9,9,19	0.25	0	8,8,18	0.50	0
3	LFA	A	322	-	5,5,19	0.28	0	4,4,18	0.35	0
3	LFA	A	323	-	3,3,19	0.35	0	2,2,18	0.62	0
3	LFA	A	318	-	11,11,19	0.28	0	10,10,18	0.48	0
3	LFA	A	331	-	3,3,19	0.36	0	2,2,18	0.62	0
3	LFA	A	312	-	15,15,19	0.23	0	14,14,18	0.57	0
3	LFA	A	328	-	2,2,19	0.26	0	1,1,18	0.05	0
3	LFA	A	334	-	11,11,19	0.26	0	10,10,18	0.51	0
4	GOL	A	336	-	5,5,5	0.39	0	5,5,5	0.18	0
3	LFA	A	304	-	8,8,19	0.28	0	7,7,18	0.50	0
4	GOL	A	337	-	5,5,5	0.33	0	5,5,5	0.27	0
3	LFA	A	307	-	12,12,19	0.24	0	11,11,18	0.54	0
3	LFA	A	333	-	9,9,19	0.29	0	8,8,18	0.39	0
3	LFA	A	315	-	4,4,19	0.26	0	3,3,18	0.39	0
3	LFA	A	330	-	10,10,19	0.24	0	9,9,18	0.49	0
3	LFA	A	317	-	10,10,19	0.27	0	9,9,18	0.55	0
3	LFA	A	314	-	9,9,19	0.25	0	8,8,18	0.55	0
3	LFA	A	321	-	4,4,19	0.27	0	3,3,18	0.39	0
3	LFA	A	305	-	5,5,19	0.28	0	4,4,18	0.33	0
3	LFA	A	313	-	4,4,19	0.30	0	3,3,18	0.37	0
3	LFA	A	306	-	4,4,19	0.28	0	3,3,18	0.35	0
3	LFA	A	303	-	7,7,19	0.25	0	6,6,18	0.43	0
3	LFA	A	310	-	7,7,19	0.28	0	6,6,18	0.39	0
3	LFA	A	302	-	15,15,19	0.25	0	14,14,18	0.48	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
 '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	LFA	A	324	-	-	3/3/3/17	-
3	LFA	A	311	-	-	6/9/9/17	-
3	LFA	A	332	-	-	0/2/2/17	-
3	LFA	A	309	-	-	2/5/5/17	-
3	LFA	A	316	-	-	0/2/2/17	-
3	LFA	A	326	-	-	3/7/7/17	-
3	LFA	A	327	-	-	3/4/4/17	-
3	LFA	A	325	-	-	1/3/3/17	-
3	LFA	A	320	-	-	1/3/3/17	-
3	LFA	A	308	-	-	3/7/7/17	-
3	LFA	A	335	-	-	3/7/7/17	-
3	LFA	A	329	-	-	0/2/2/17	-
3	LFA	A	319	-	-	3/7/7/17	-
3	LFA	A	322	-	-	2/3/3/17	-
3	LFA	A	323	-	-	0/1/1/17	-
3	LFA	A	318	-	-	6/9/9/17	-
3	LFA	A	331	-	-	0/1/1/17	-
3	LFA	A	312	-	-	8/13/13/17	-
3	LFA	A	334	-	-	6/9/9/17	-
4	GOL	A	336	-	-	3/4/4/4	-
3	LFA	A	304	-	-	3/6/6/17	-
4	GOL	A	337	-	-	2/4/4/4	-
3	LFA	A	307	-	-	6/10/10/17	-
3	LFA	A	333	-	-	7/7/7/17	-
3	LFA	A	315	-	-	1/2/2/17	-
3	LFA	A	330	-	-	6/8/8/17	-
3	LFA	A	317	-	-	3/8/8/17	-
3	LFA	A	314	-	-	3/7/7/17	-
3	LFA	A	321	-	-	1/2/2/17	-
3	LFA	A	305	-	-	0/3/3/17	-
3	LFA	A	313	-	-	1/2/2/17	-
3	LFA	A	306	-	-	1/2/2/17	-
3	LFA	A	303	-	-	2/5/5/17	-
3	LFA	A	310	-	-	2/5/5/17	-
3	LFA	A	302	-	-	4/13/13/17	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (95) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	336	GOL	C1-C2-C3-O3
4	A	337	GOL	C1-C2-C3-O3
4	A	336	GOL	O2-C2-C3-O3
3	A	307	LFA	C11-C10-C9-C8
3	A	312	LFA	C11-C10-C9-C8
3	A	318	LFA	C3-C4-C5-C6
3	A	330	LFA	C5-C6-C7-C8
3	A	330	LFA	C7-C8-C9-C10
3	A	307	LFA	C9-C10-C11-C12
3	A	334	LFA	C5-C6-C7-C8
3	A	335	LFA	C4-C5-C6-C7
3	A	335	LFA	C5-C6-C7-C8
3	A	322	LFA	C2-C3-C4-C5
3	A	327	LFA	C2-C3-C4-C5
3	A	333	LFA	C6-C7-C8-C9
4	A	337	GOL	O2-C2-C3-O3
3	A	334	LFA	C2-C3-C4-C5
3	A	311	LFA	C6-C7-C8-C9
3	A	311	LFA	C3-C4-C5-C6
3	A	311	LFA	C2-C3-C4-C5
3	A	330	LFA	C4-C5-C6-C7
3	A	302	LFA	C12-C13-C14-C15
3	A	324	LFA	C2-C3-C4-C5
3	A	326	LFA	C3-C4-C5-C6
3	A	310	LFA	C4-C5-C6-C7
3	A	334	LFA	C4-C5-C6-C7
3	A	333	LFA	C4-C5-C6-C7
3	A	318	LFA	C11-C10-C9-C8
3	A	319	LFA	C3-C4-C5-C6
3	A	330	LFA	C6-C7-C8-C9
3	A	330	LFA	C2-C3-C4-C5
3	A	311	LFA	C5-C6-C7-C8
3	A	333	LFA	C2-C3-C4-C5
3	A	307	LFA	C6-C7-C8-C9
3	A	307	LFA	C4-C5-C6-C7
3	A	333	LFA	C5-C6-C7-C8
3	A	335	LFA	C3-C4-C5-C6

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Mol	Chain	Res	Type	Atoms
3	A	334	LFA	C1-C2-C3-C4
3	A	302	LFA	C11-C10-C9-C8
3	A	312	LFA	C9-C10-C11-C12
3	A	303	LFA	C4-C5-C6-C7
3	A	327	LFA	C3-C4-C5-C6
3	A	308	LFA	C7-C8-C9-C10
3	A	309	LFA	C5-C6-C7-C8
3	A	318	LFA	C9-C10-C11-C12
3	A	317	LFA	C9-C10-C11-C12
3	A	333	LFA	C1-C2-C3-C4
3	A	304	LFA	C6-C7-C8-C9
3	A	311	LFA	C9-C10-C11-C12
3	A	324	LFA	C1-C2-C3-C4
3	A	327	LFA	C4-C5-C6-C7
3	A	304	LFA	C5-C6-C7-C8
3	A	312	LFA	C11-C12-C13-C14
3	A	311	LFA	C11-C10-C9-C8
3	A	318	LFA	C6-C7-C8-C9
3	A	314	LFA	C5-C6-C7-C8
3	A	308	LFA	C6-C7-C8-C9
3	A	330	LFA	C11-C10-C9-C8
4	A	336	GOL	O1-C1-C2-O2
3	A	306	LFA	C2-C3-C4-C5
3	A	303	LFA	C2-C3-C4-C5
3	A	313	LFA	C2-C3-C4-C5
3	A	312	LFA	C3-C4-C5-C6
3	A	326	LFA	C6-C7-C8-C9
3	A	318	LFA	C7-C8-C9-C10
3	A	312	LFA	C2-C3-C4-C5
3	A	334	LFA	C6-C7-C8-C9
3	A	308	LFA	C2-C3-C4-C5
3	A	314	LFA	C4-C5-C6-C7
3	A	310	LFA	C1-C2-C3-C4
3	A	325	LFA	C3-C4-C5-C6
3	A	326	LFA	C5-C6-C7-C8
3	A	319	LFA	C1-C2-C3-C4
3	A	320	LFA	C1-C2-C3-C4
3	A	304	LFA	C7-C8-C9-C10
3	A	333	LFA	C3-C4-C5-C6
3	A	334	LFA	C7-C8-C9-C10
3	A	324	LFA	C3-C4-C5-C6
3	A	322	LFA	C3-C4-C5-C6

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Mol	Chain	Res	Type	Atoms
3	A	321	LFA	C2-C3-C4-C5
3	A	307	LFA	C3-C4-C5-C6
3	A	307	LFA	C10-C11-C12-C13
3	A	317	LFA	C6-C7-C8-C9
3	A	319	LFA	C7-C8-C9-C10
3	A	309	LFA	C1-C2-C3-C4
3	A	302	LFA	C13-C14-C15-C16
3	A	302	LFA	C11-C12-C13-C14
3	A	333	LFA	C7-C8-C9-C10
3	A	312	LFA	C13-C14-C15-C16
3	A	318	LFA	C2-C3-C4-C5
3	A	314	LFA	C3-C4-C5-C6
3	A	312	LFA	C7-C8-C9-C10
3	A	317	LFA	C5-C6-C7-C8
3	A	315	LFA	C3-C4-C5-C6
3	A	312	LFA	C4-C5-C6-C7

There are no ring outliers.

22 monomers are involved in 42 short contacts:

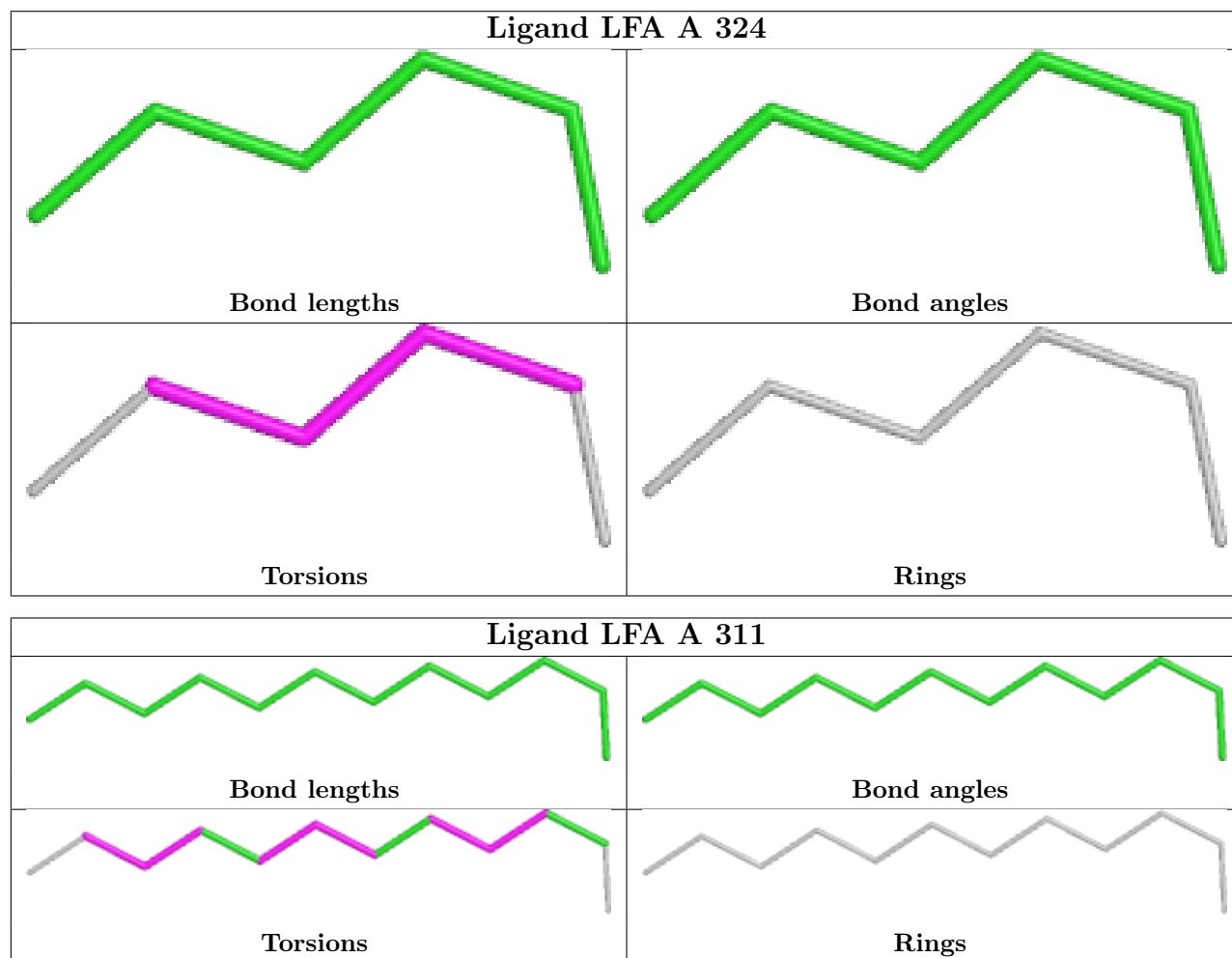
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	309	LFA	3	0
3	A	316	LFA	1	0
3	A	326	LFA	3	0
3	A	325	LFA	7	0
3	A	320	LFA	3	0
3	A	308	LFA	1	0
3	A	335	LFA	3	0
3	A	319	LFA	9	0
3	A	318	LFA	2	0
3	A	328	LFA	4	0
4	A	336	GOL	3	0
3	A	304	LFA	1	0
3	A	307	LFA	1	0
3	A	333	LFA	2	0
3	A	315	LFA	1	0
3	A	330	LFA	4	0
3	A	317	LFA	1	0
3	A	314	LFA	2	0
3	A	321	LFA	3	0
3	A	305	LFA	3	0
3	A	313	LFA	1	0

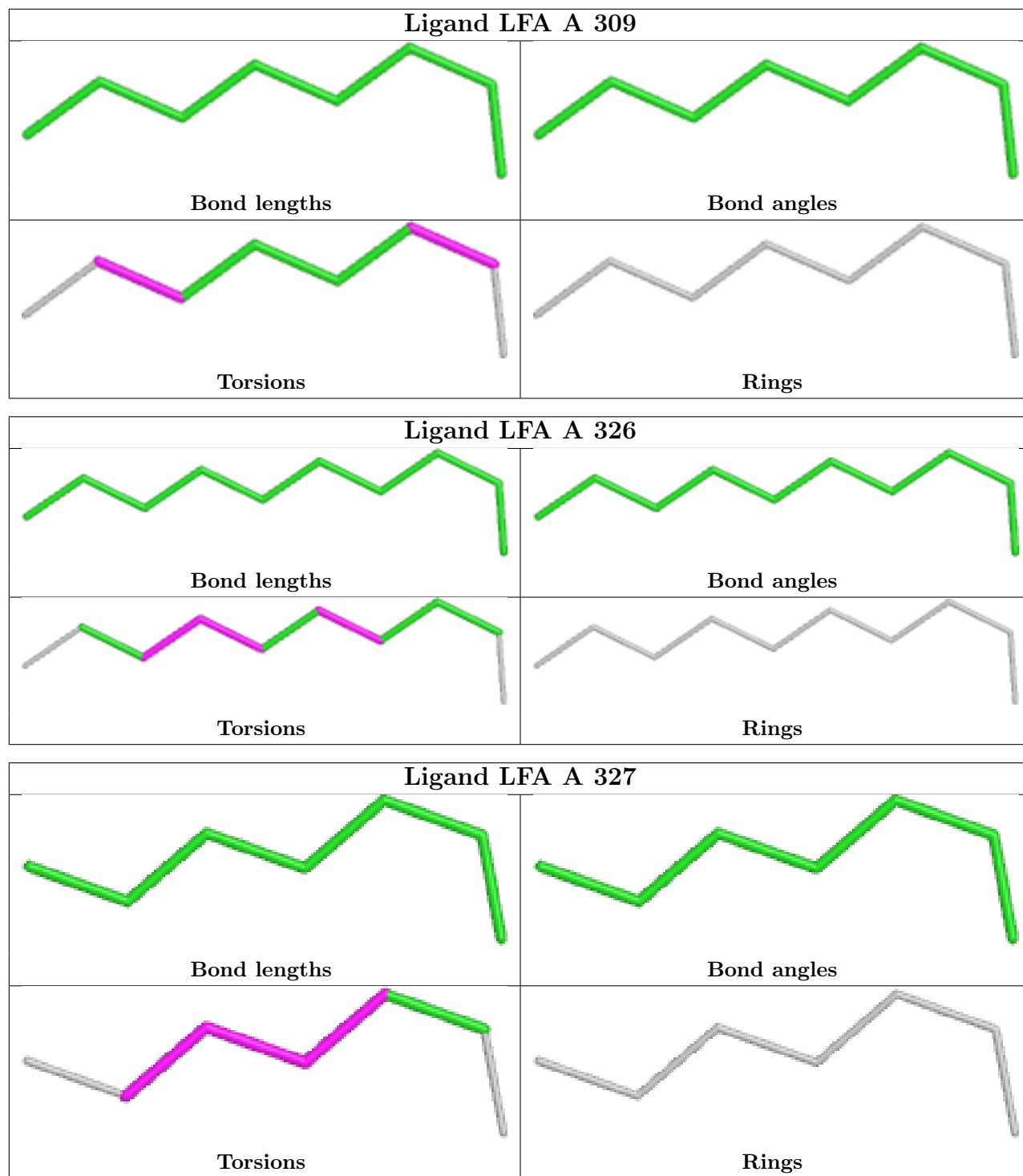
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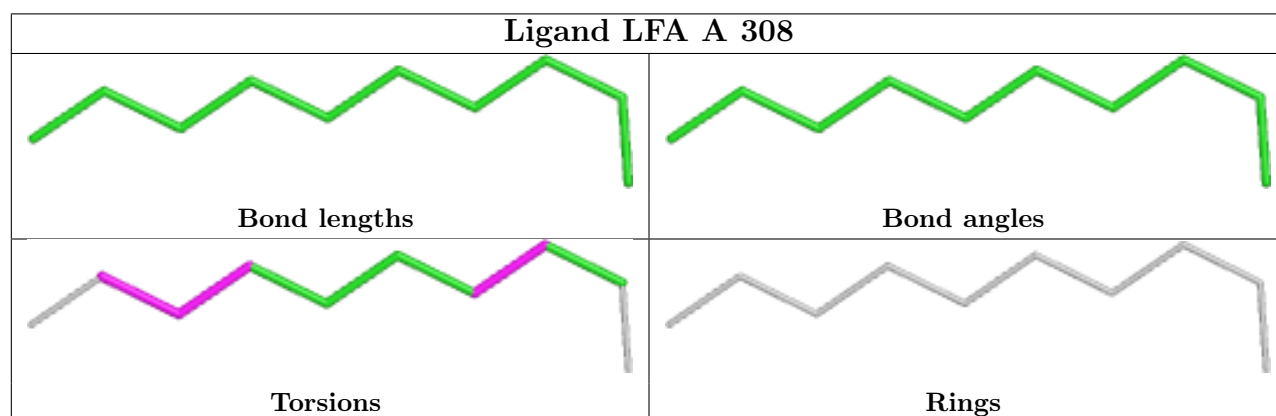
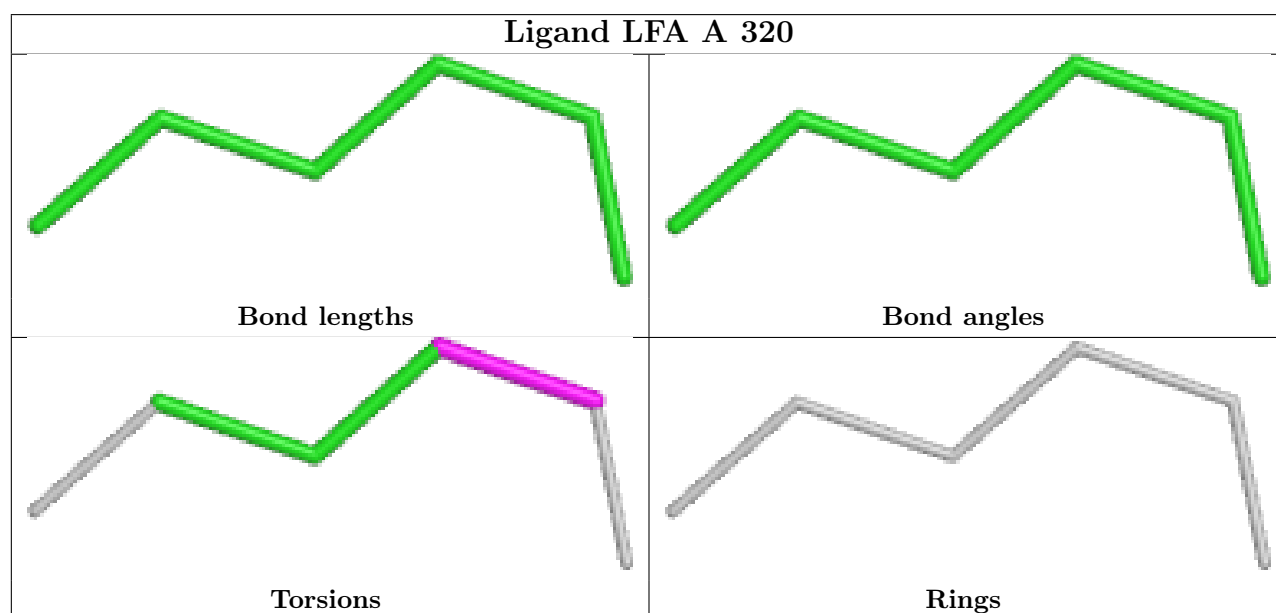
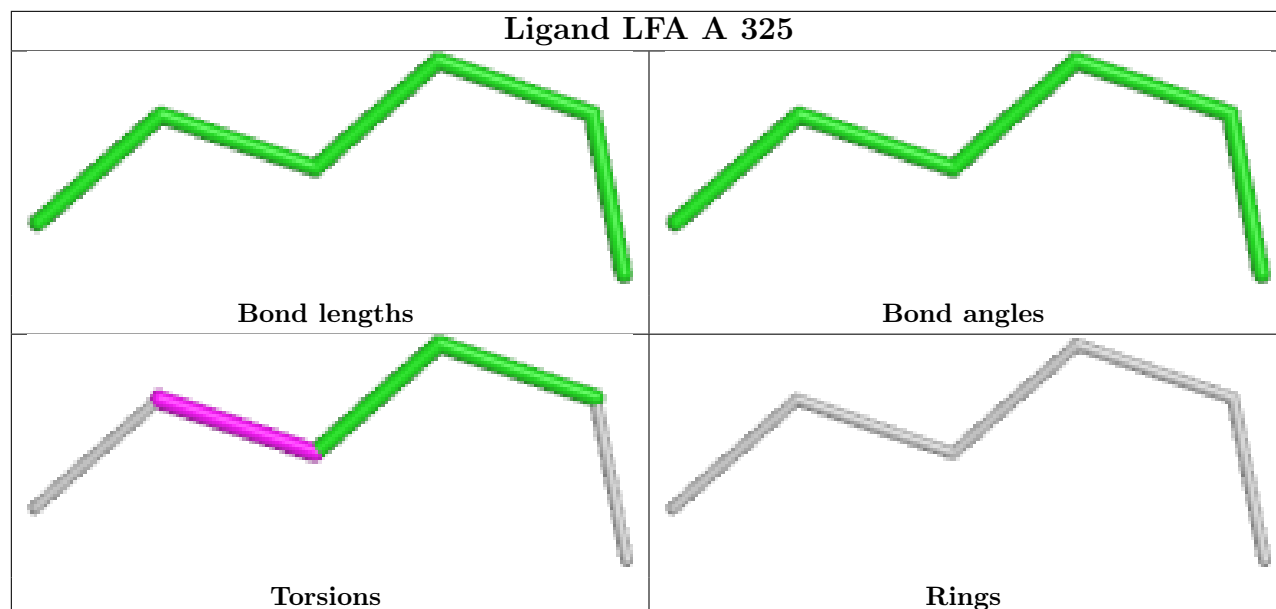
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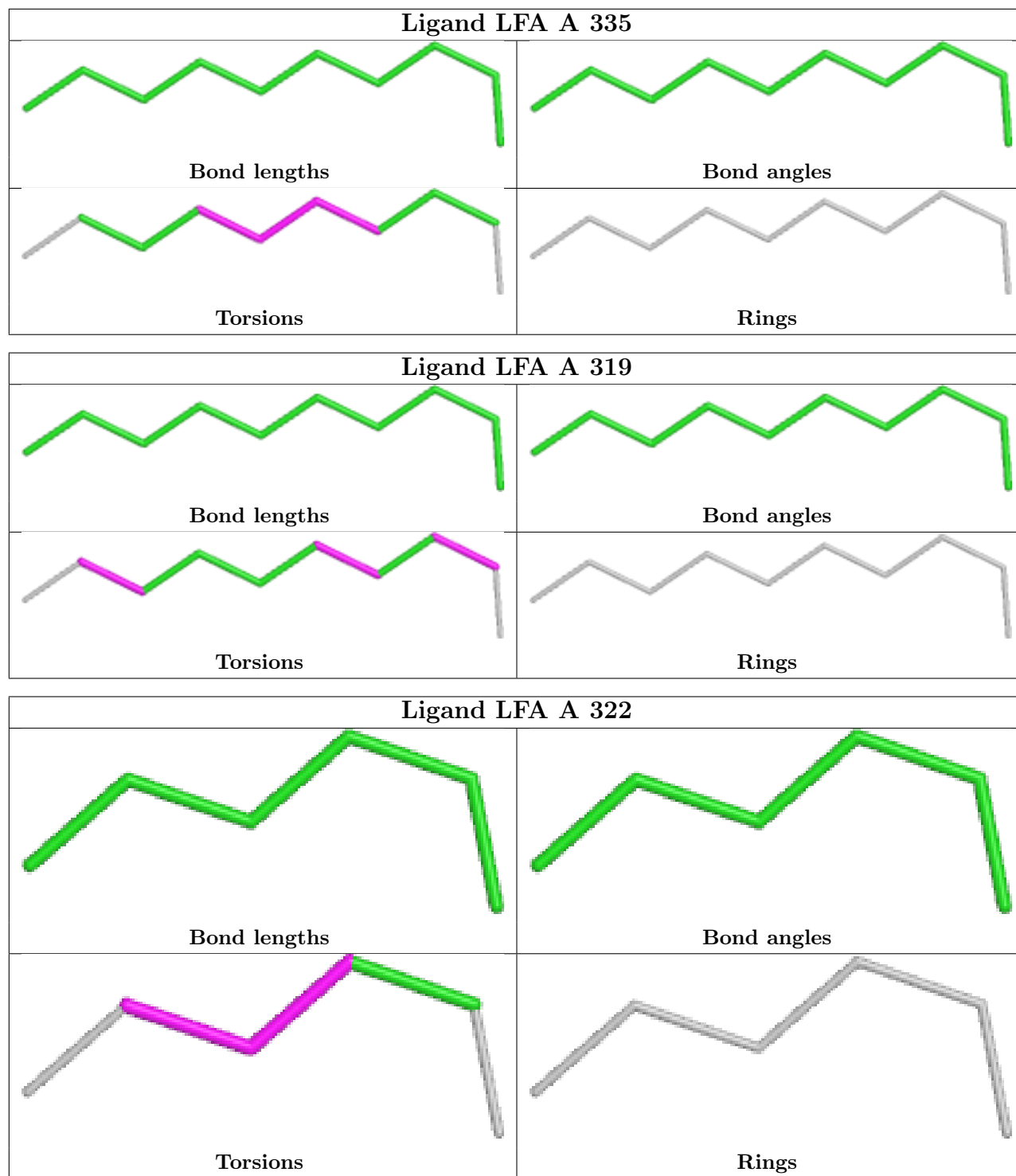
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	302	LFA	2	0

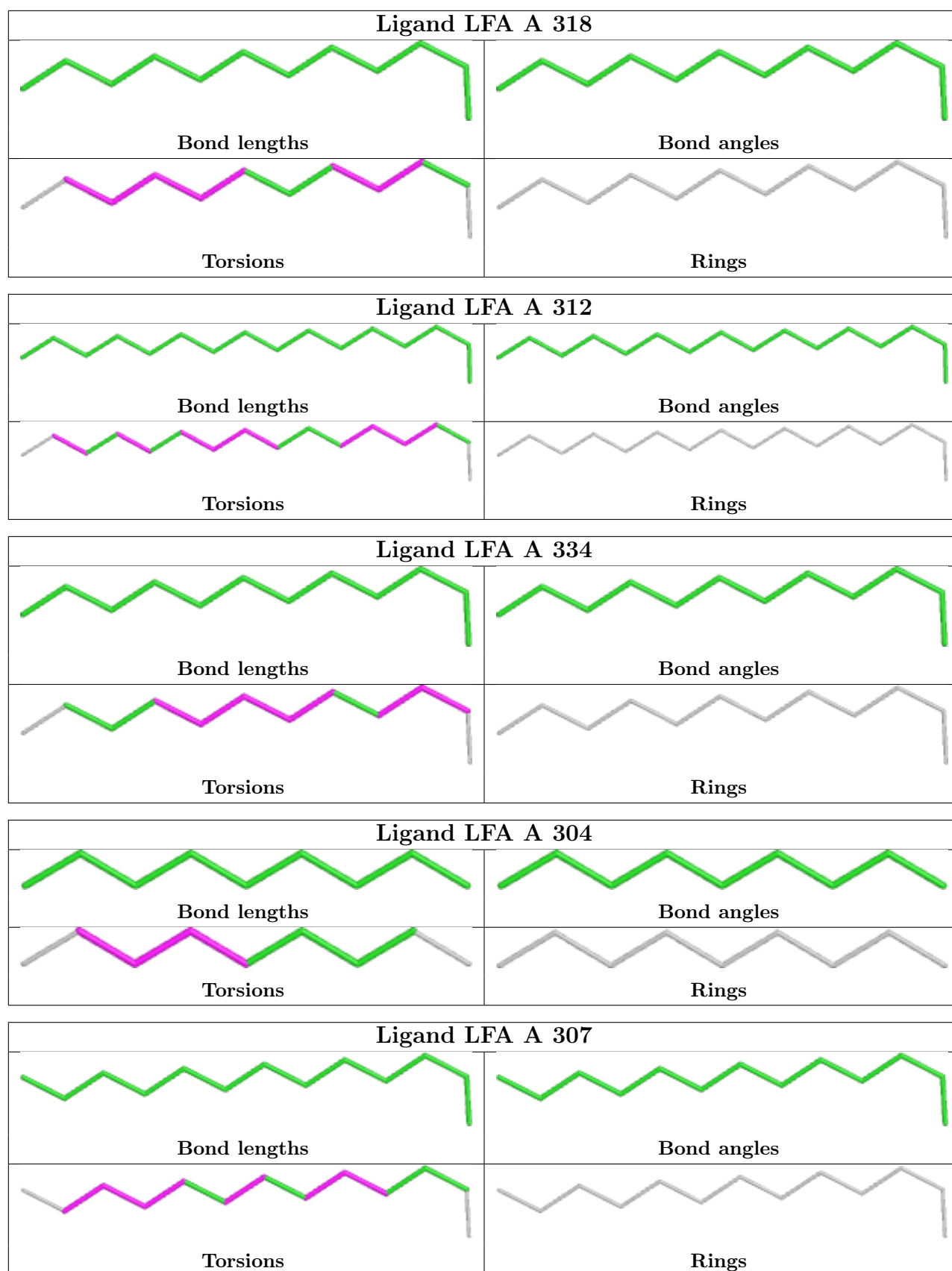
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

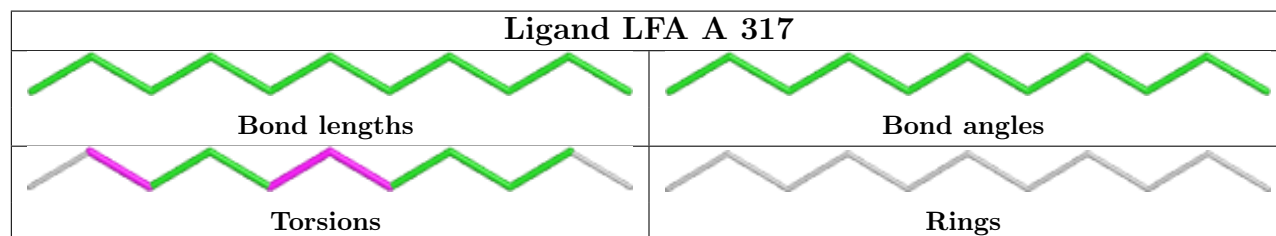
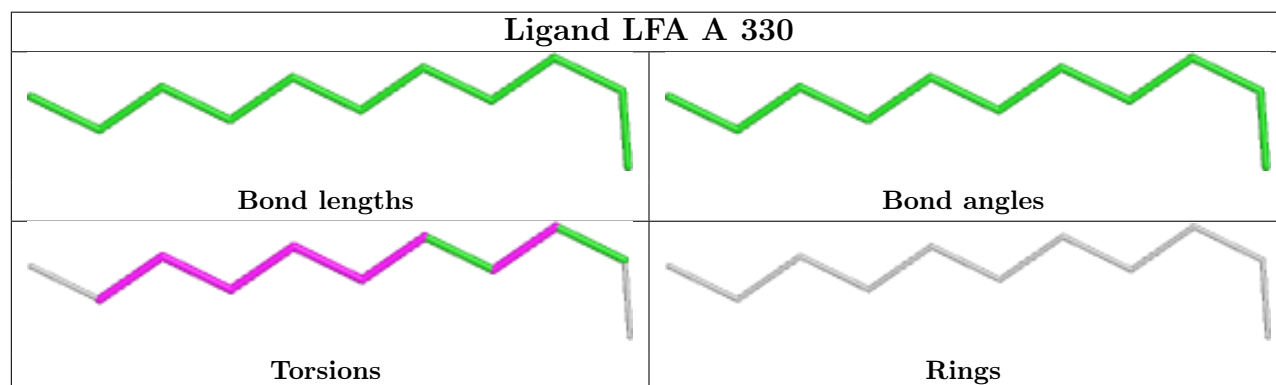
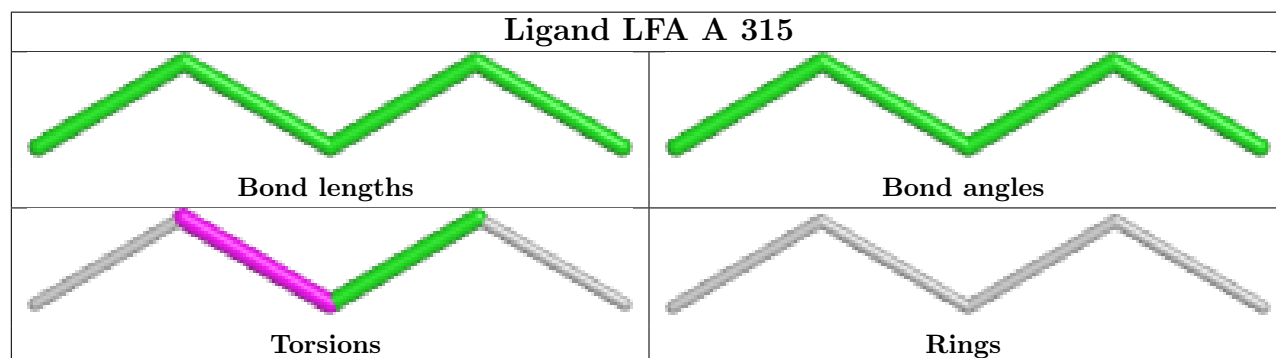
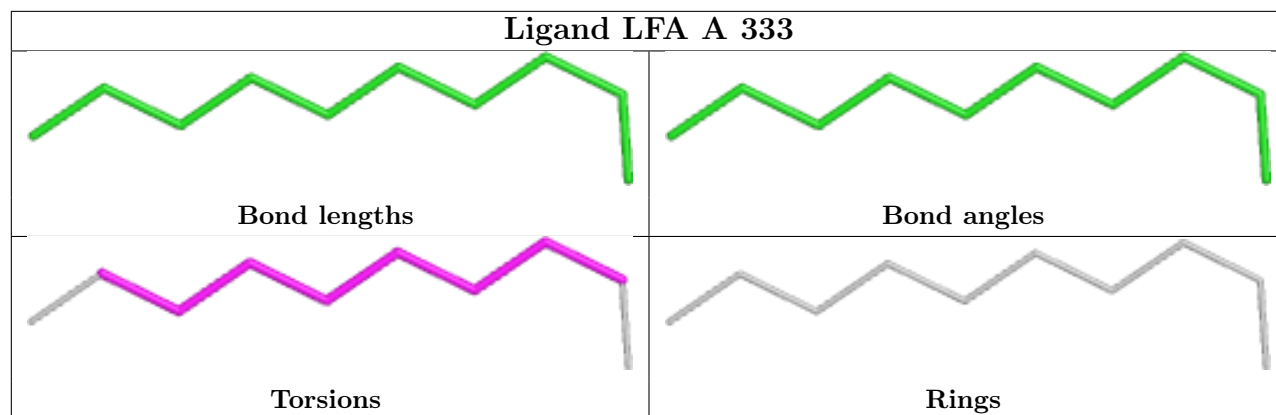


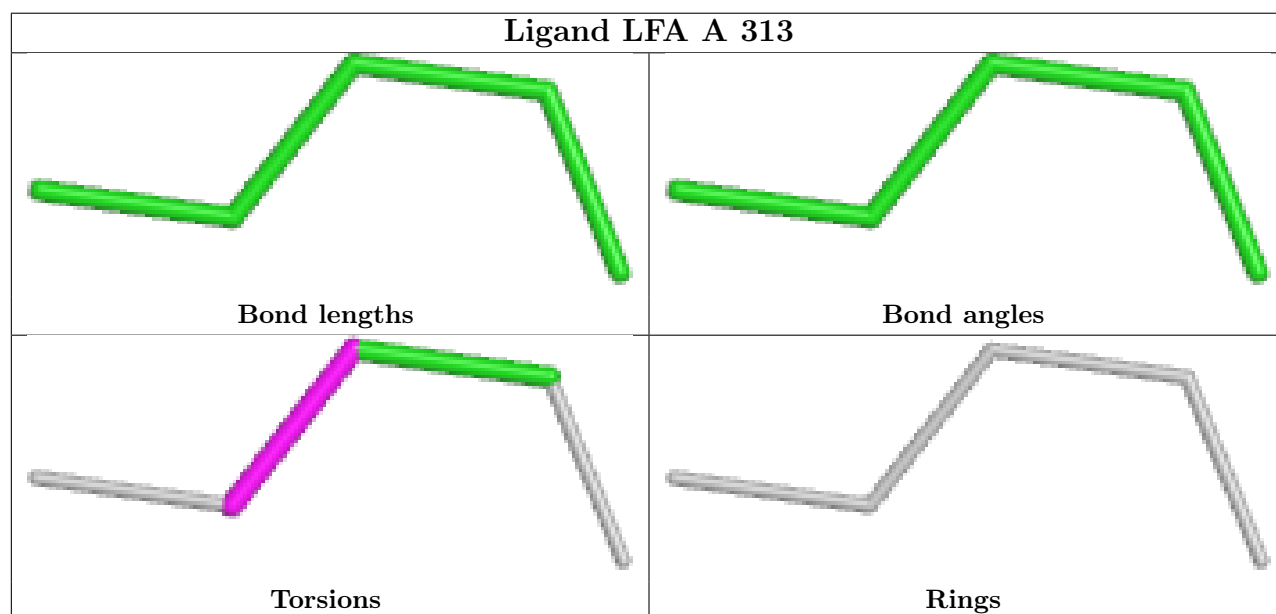
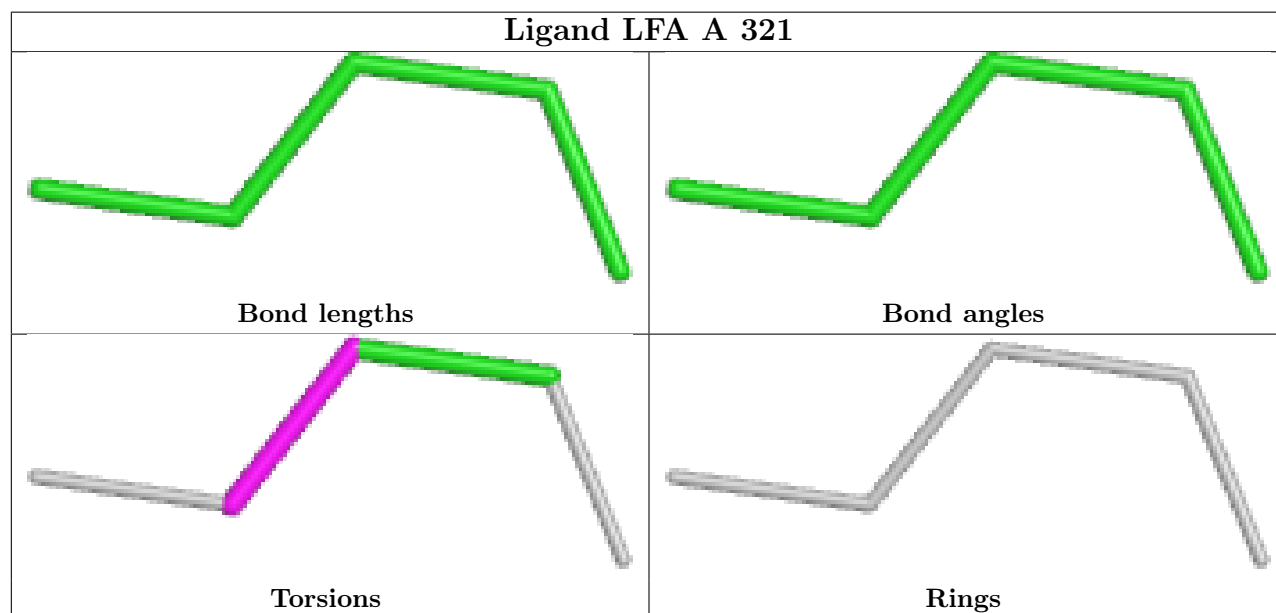
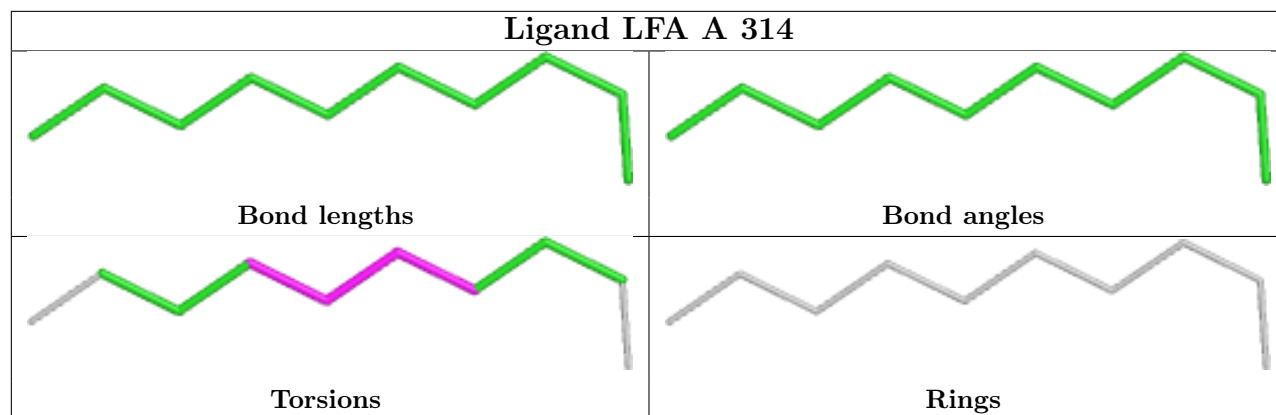


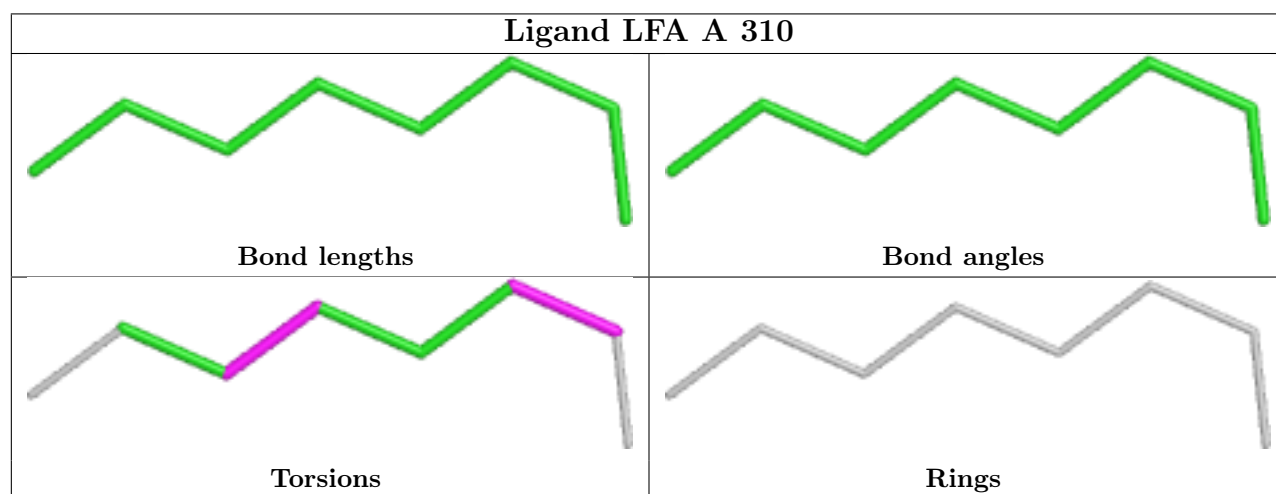
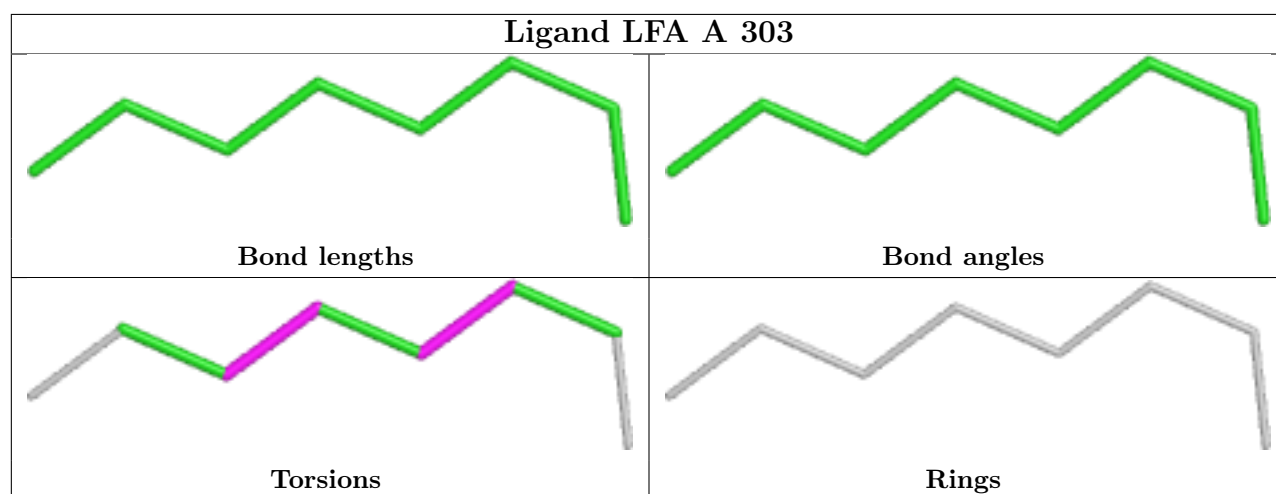
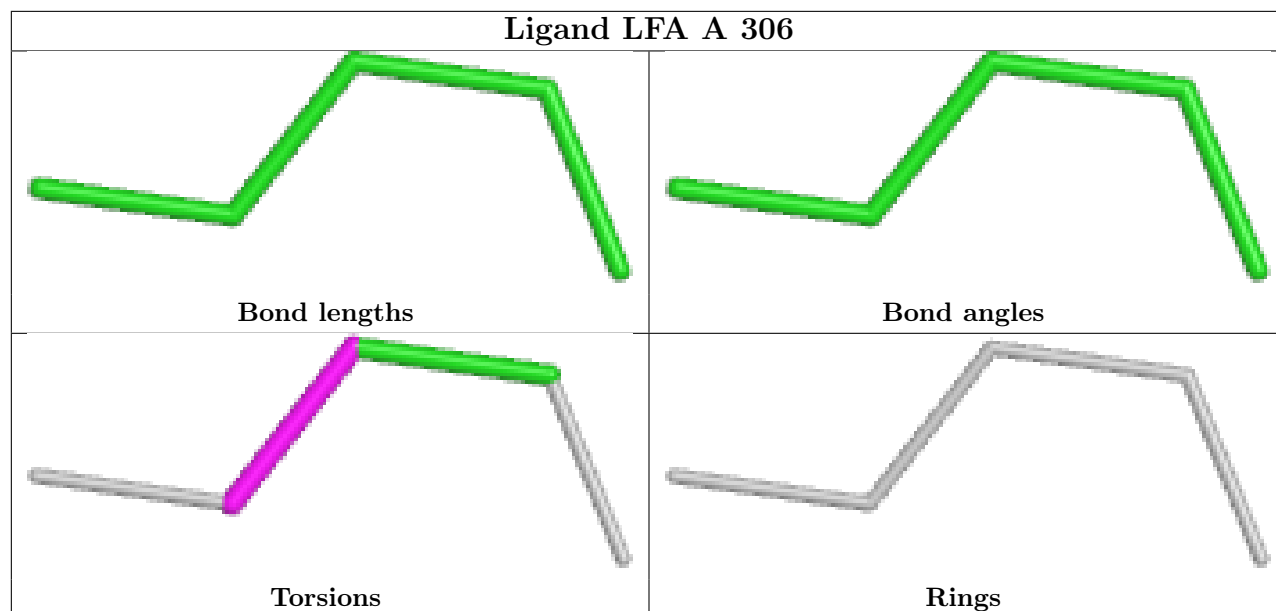


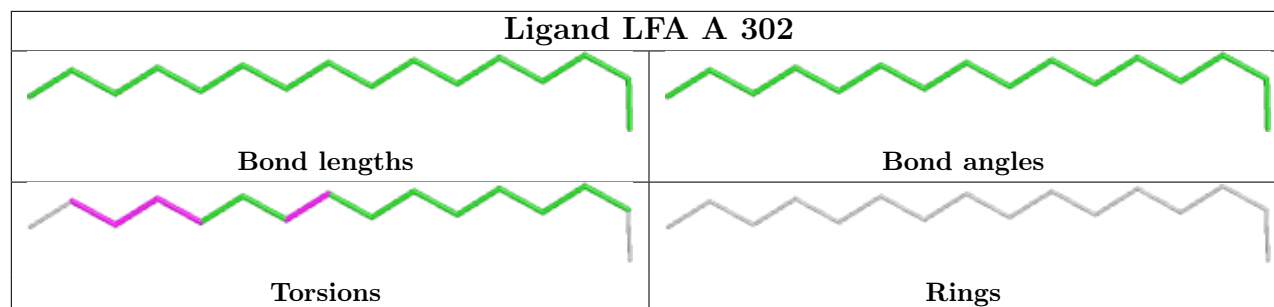












5.7 Other polymers [i](#)

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 ⓘ

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, 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	270/288 (93%)	0.64	29 (10%) 11 11	9, 27, 50, 106	29 (10%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	230	VAL	12.7
1	A	2	THR	6.3
1	A	5	LEU	4.8
1	A	229	GLY	4.2
1	A	233	PHE	4.1
1	A	8	ALA	4.0
1	A	195	GLY	3.9
1	A	179[A]	PHE	3.5
1	A	7	ASN	3.3
1	A	158[A]	PHE	3.1
1	A	3	GLN	3.0
1	A	272	ASN	2.8
1	A	6	GLY	2.8
1	A	231	ASP	2.7
1	A	4	GLU	2.7
1	A	273	LYS	2.7
1	A	183	TRP	2.6
1	A	161	VAL	2.6
1	A	232	GLY	2.6
1	A	18	GLU	2.5
1	A	270	SER	2.5
1	A	166	ALA	2.4
1	A	143	TRP	2.3
1	A	50	ILE	2.3
1	A	159	TYR	2.3
1	A	157[A]	GLN	2.2
1	A	164[A]	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	235	TYR	2.1
1	A	92	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	LYR	A	255	29/30	0.96	0.07	18,23,29,33	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	LFA	A	325	6/20	0.62	0.26	40,66,68,70	0
3	LFA	A	331	4/20	0.68	0.23	62,68,73,75	0
4	GOL	A	336	6/6	0.72	0.14	48,70,71,77	0
3	LFA	A	332	5/20	0.73	0.26	60,75,76,77	0
3	LFA	A	335	10/20	0.74	0.25	67,73,82,83	0
3	LFA	A	329	5/20	0.74	0.24	69,70,74,74	0
3	LFA	A	308	10/20	0.75	0.22	55,61,74,77	0
3	LFA	A	322	6/20	0.76	0.24	60,63,70,76	0
3	LFA	A	323	4/20	0.77	0.24	69,76,76,78	0
3	LFA	A	328	3/20	0.78	0.20	35,35,52,55	0
3	LFA	A	316	5/20	0.78	0.19	51,54,62,63	0
3	LFA	A	333	10/20	0.79	0.21	60,66,72,72	0
3	LFA	A	324	6/20	0.79	0.23	66,68,73,73	0
3	LFA	A	317	11/20	0.79	0.20	61,74,87,92	0
3	LFA	A	319	10/20	0.80	0.19	37,71,83,85	0

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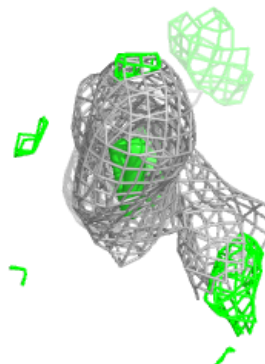
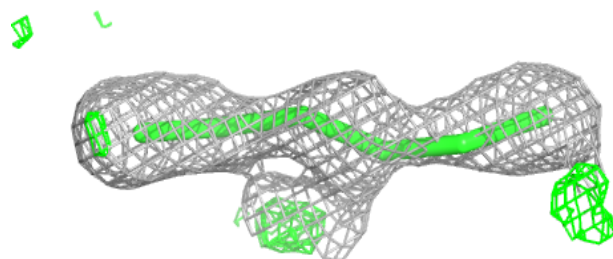
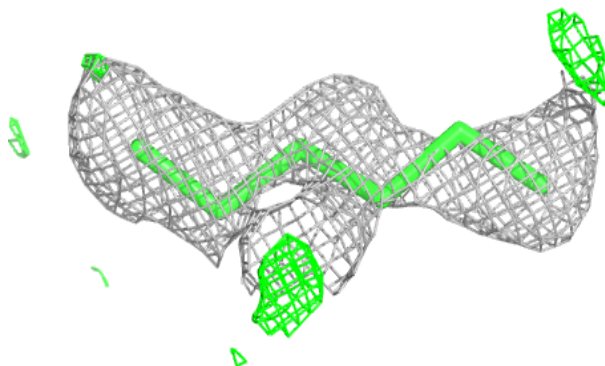
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	GOL	A	337	6/6	0.80	0.18	70,76,84,92	0
3	LFA	A	310	8/20	0.81	0.23	60,65,71,76	0
3	LFA	A	305	6/20	0.81	0.20	46,50,54,63	0
3	LFA	A	313	5/20	0.82	0.19	36,41,53,53	0
3	LFA	A	314	10/20	0.82	0.19	60,73,79,79	0
3	LFA	A	334	12/20	0.82	0.19	46,60,67,70	0
3	LFA	A	321	5/20	0.83	0.23	66,74,81,85	0
3	LFA	A	326	10/20	0.83	0.19	60,63,72,73	0
3	LFA	A	327	7/20	0.83	0.20	66,68,76,79	0
3	LFA	A	311	12/20	0.83	0.21	43,64,91,101	0
3	LFA	A	318	12/20	0.83	0.17	58,66,72,74	0
3	LFA	A	304	9/20	0.83	0.18	59,60,72,73	0
3	LFA	A	320	6/20	0.84	0.18	52,60,62,69	0
3	LFA	A	306	5/20	0.85	0.17	57,62,65,71	0
3	LFA	A	312	16/20	0.86	0.19	51,64,81,85	0
3	LFA	A	302	16/20	0.86	0.18	37,47,68,76	0
3	LFA	A	309	8/20	0.86	0.18	52,57,64,66	0
3	LFA	A	307	13/20	0.87	0.20	39,55,66,67	0
3	LFA	A	330	11/20	0.88	0.18	51,65,71,75	0
3	LFA	A	315	5/20	0.88	0.14	49,53,54,56	0
3	LFA	A	303	8/20	0.90	0.12	28,32,35,37	8
2	NA	A	301	1/1	0.98	0.11	31,31,31,31	0

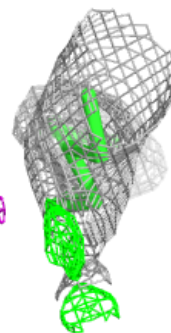
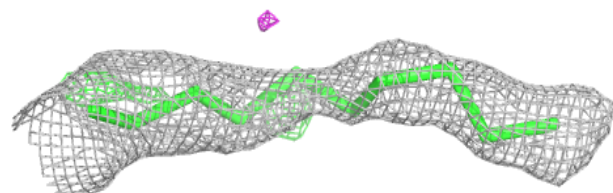
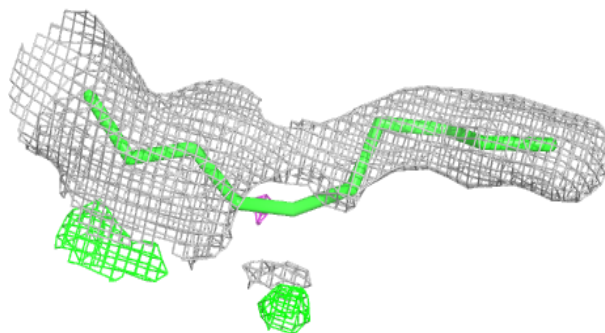
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around LFA A 325:

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

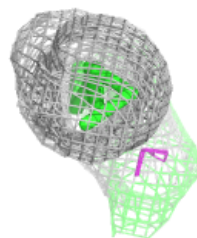
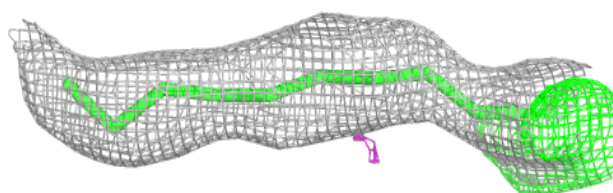
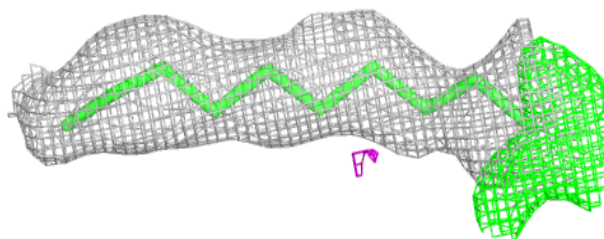
**Electron density around LFA A 335:**

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

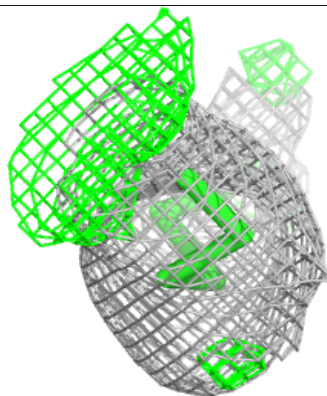
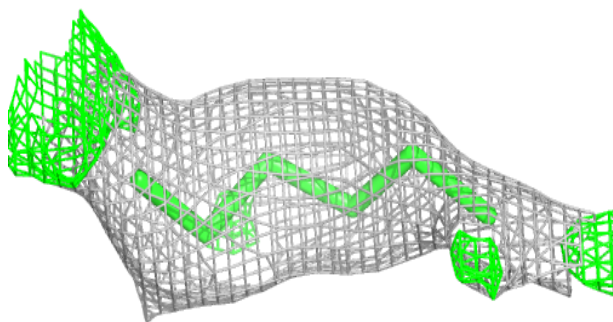
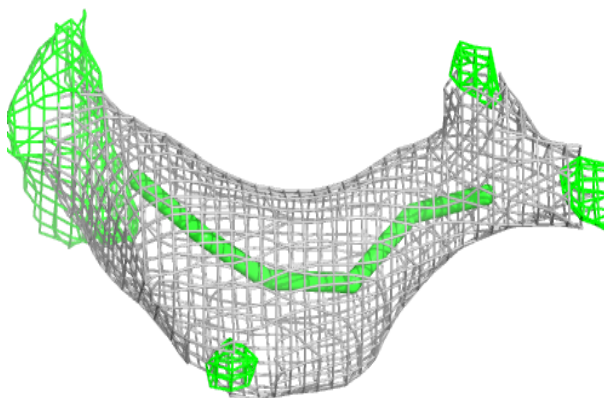


Electron density around LFA A 308:

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

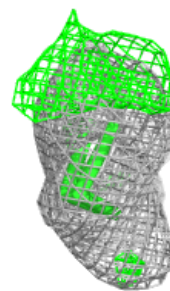
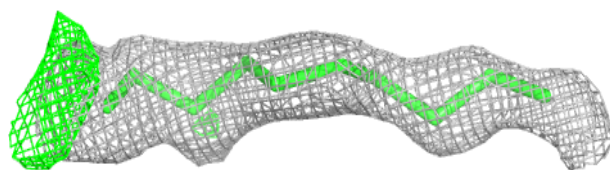
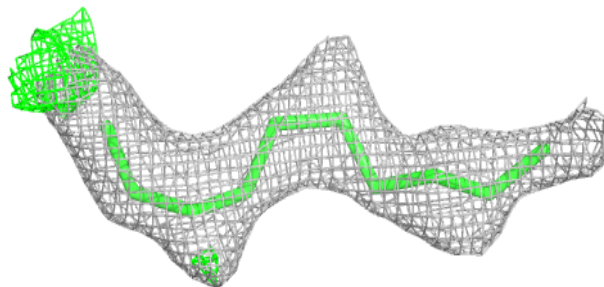
**Electron density around LFA A 322:**

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

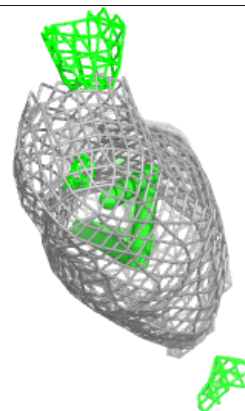
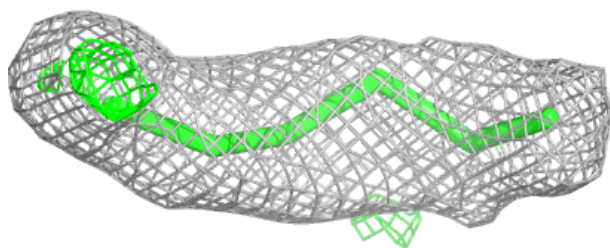
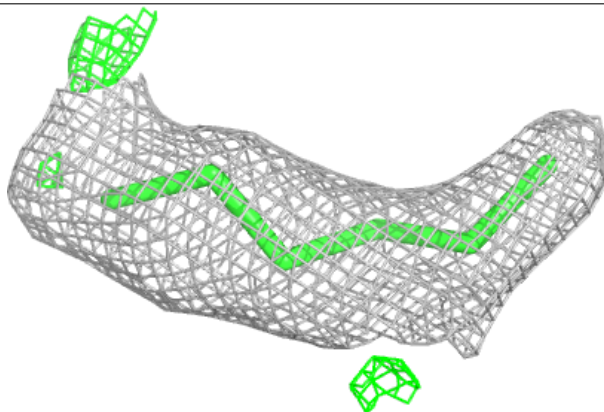


Electron density around LFA A 333:

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

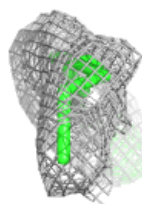
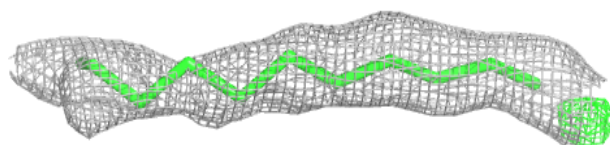
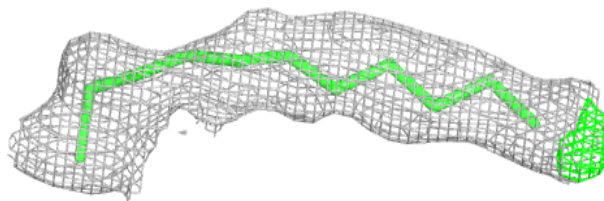
**Electron density around LFA A 324:**

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

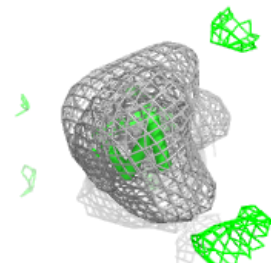
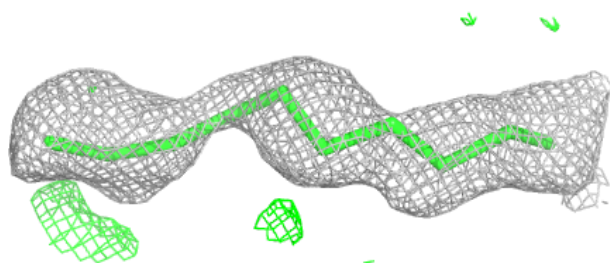
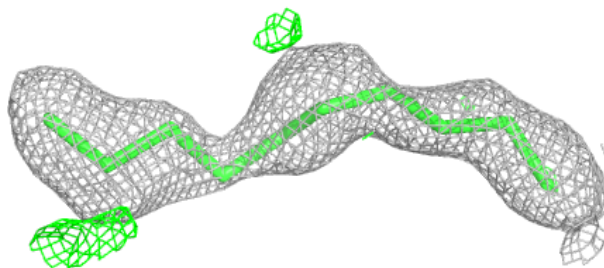


Electron density around LFA A 317:

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

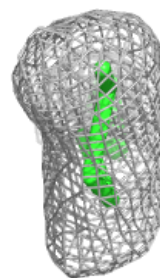
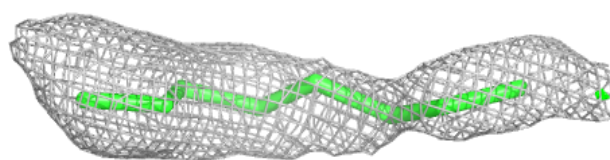
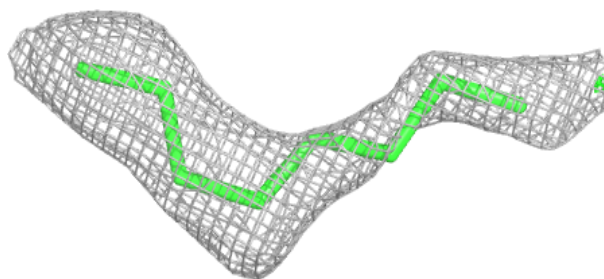
**Electron density around LFA A 319:**

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

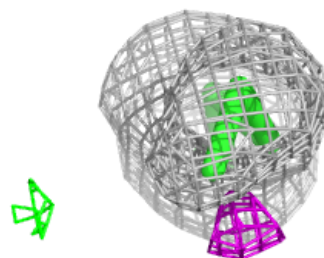
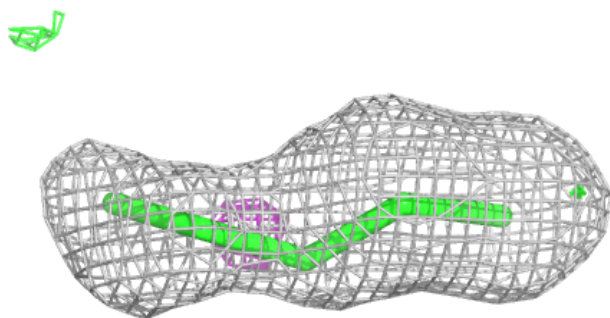
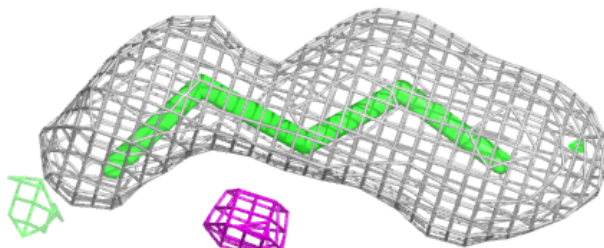


Electron density around LFA A 310:

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

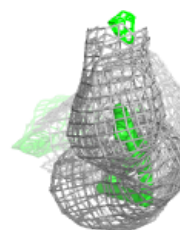
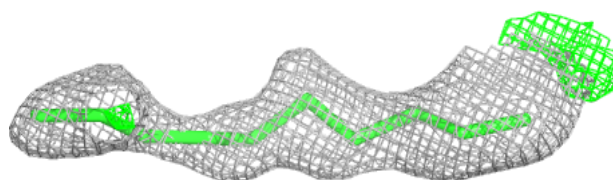
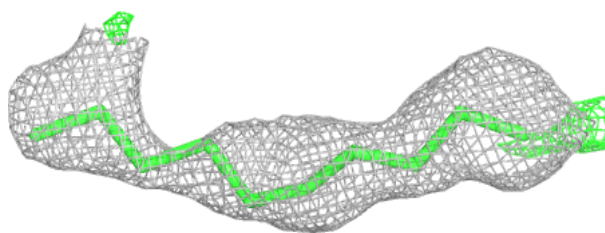
**Electron density around LFA A 313:**

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

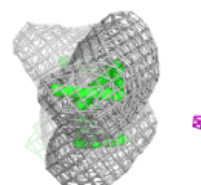
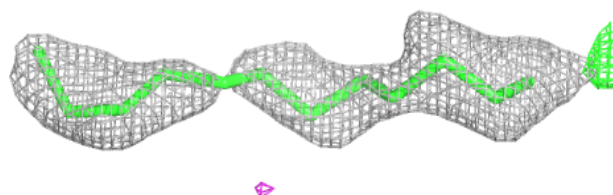
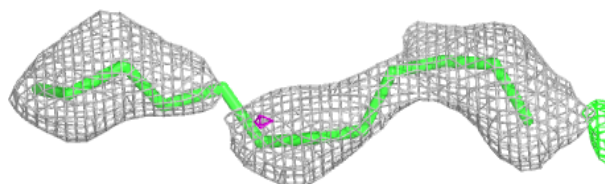


Electron density around LFA A 314:

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

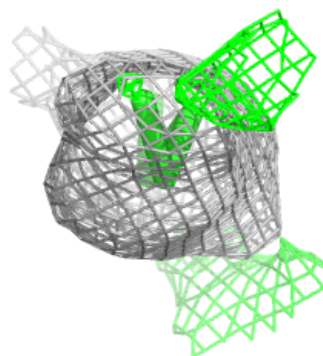
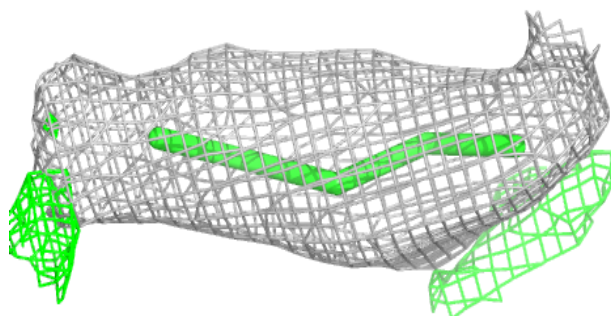
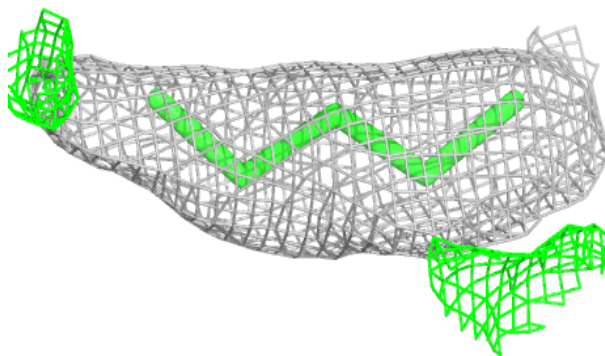
**Electron density around LFA A 334:**

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

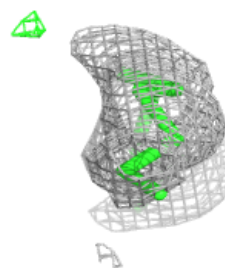
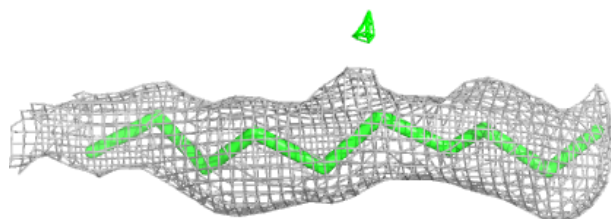
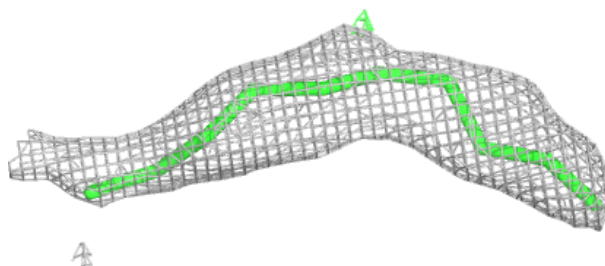


Electron density around LFA A 321:

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

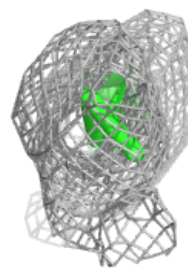
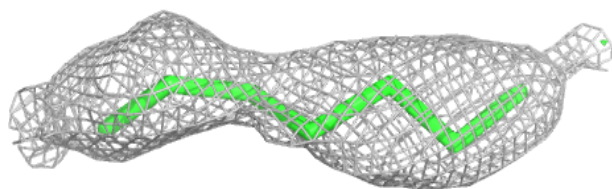
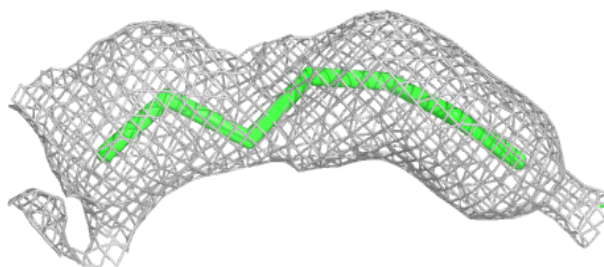
**Electron density around LFA A 326:**

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

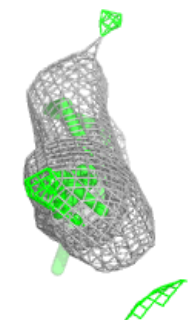
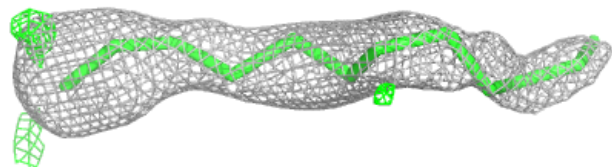
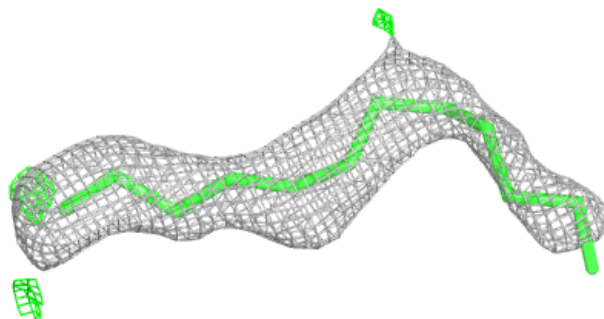


Electron density around LFA A 327:

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

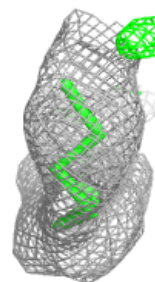
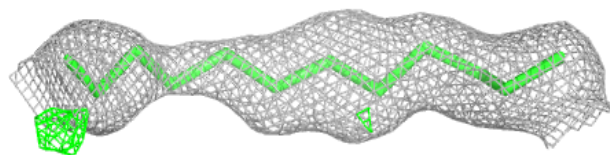
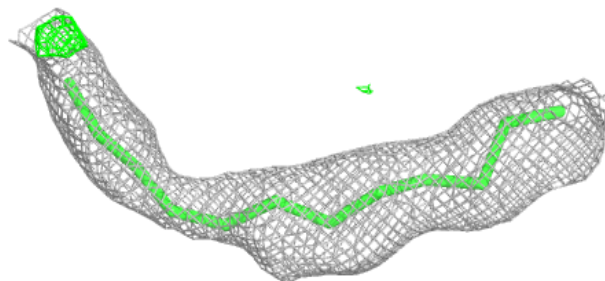
**Electron density around LFA A 311:**

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

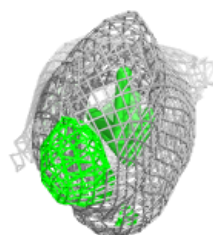
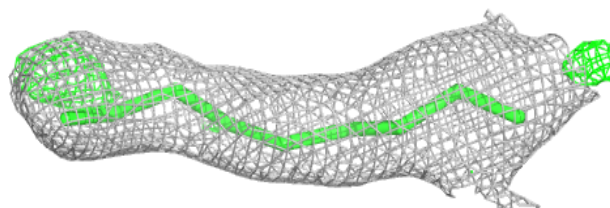
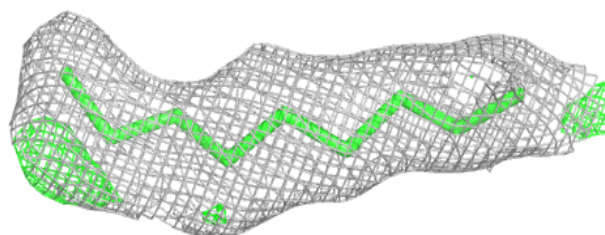


Electron density around LFA A 318:

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

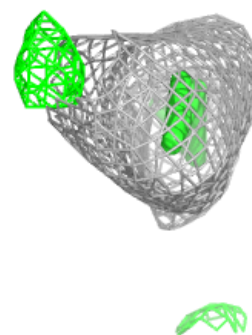
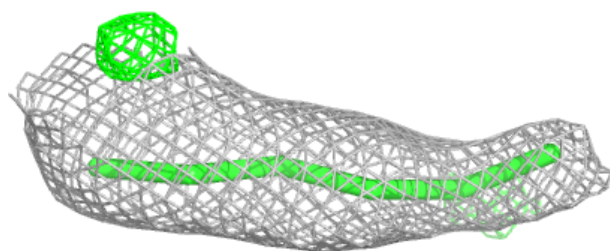
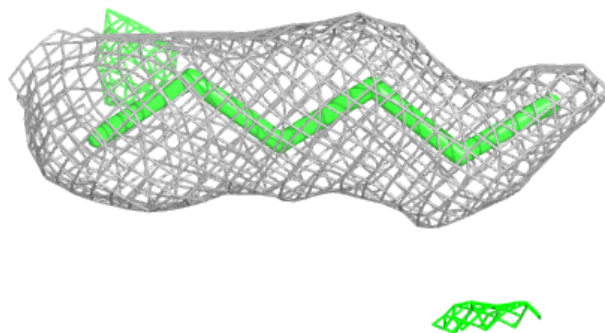
**Electron density around LFA A 304:**

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

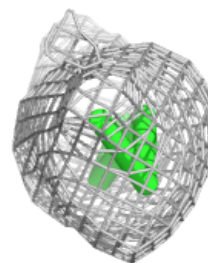
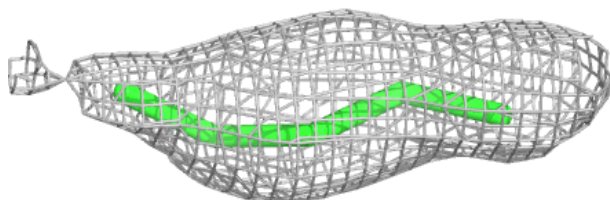
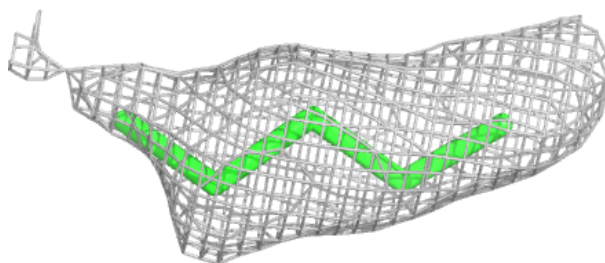


Electron density around LFA A 320:

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

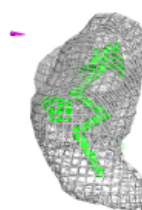
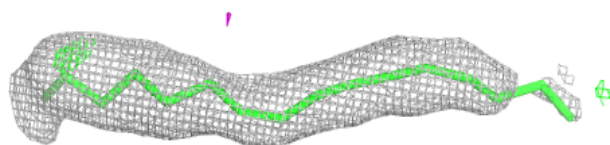
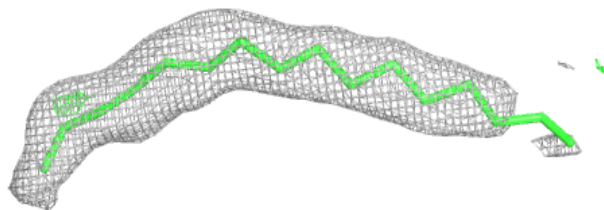
**Electron density around LFA A 306:**

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

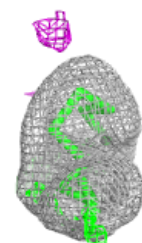
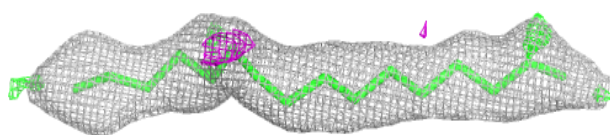
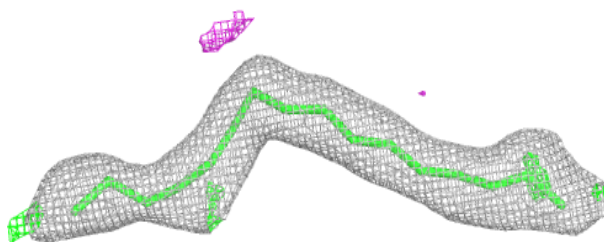


Electron density around LFA A 312:

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

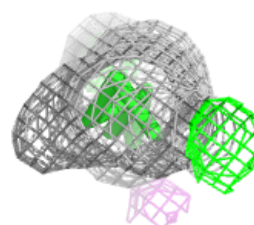
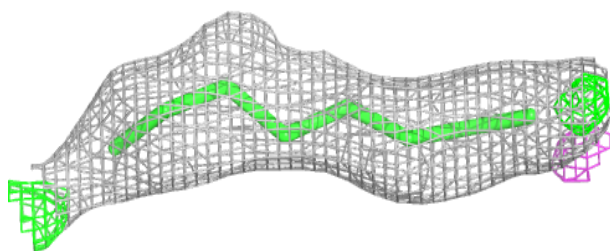
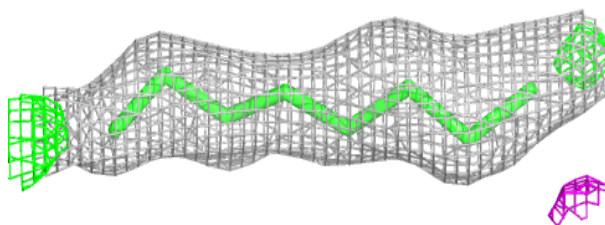
**Electron density around LFA A 302:**

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

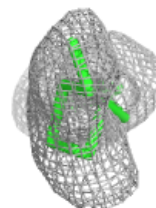
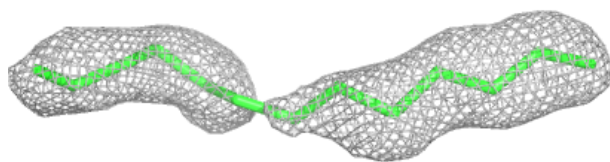
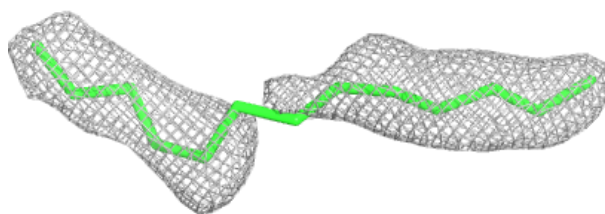


Electron density around LFA A 309:

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

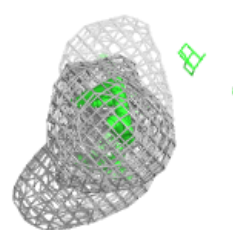
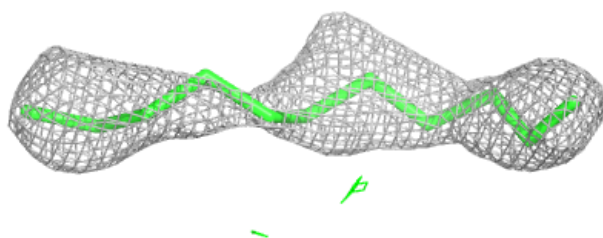
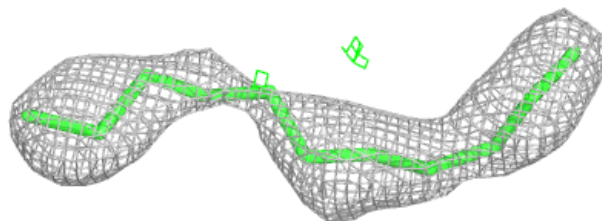
**Electron density around LFA A 307:**

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

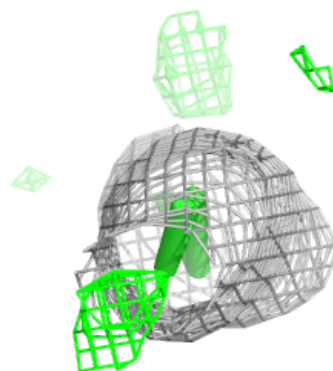
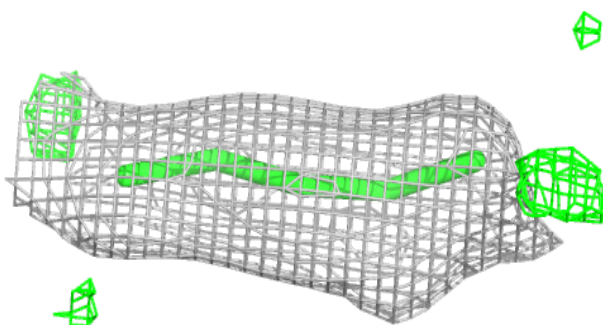
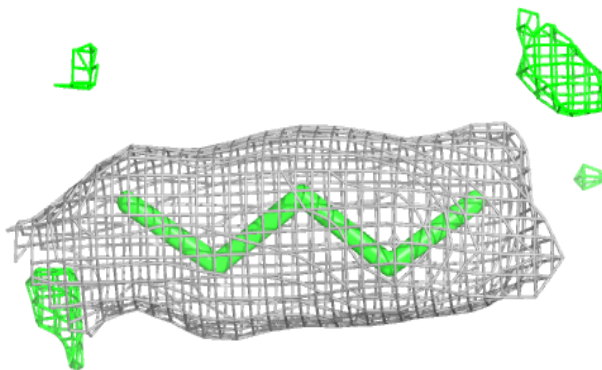


Electron density around LFA A 330:

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

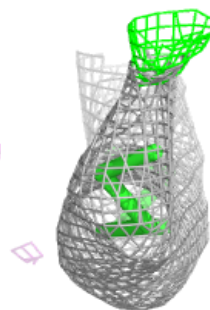
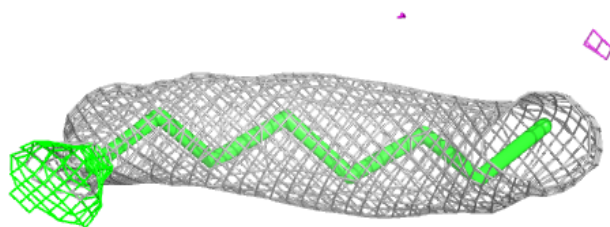
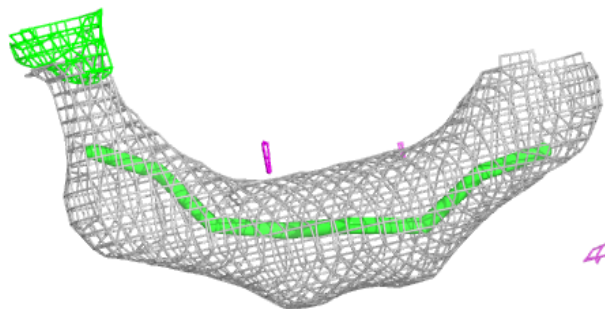
**Electron density around LFA A 315:**

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



Electron density around LFA A 303:

$2mF_o-DF_c$ (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.