



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2026 – 05:17 PM EDT

PDB ID : 7IN8 / pdb\_00007in8  
Title : Crystal structure of A2A in complex with 10 mM ZM241385 for 3h  
Authors : Huang, C.-Y.; Cheng, R.Y.K.; Metz, A.  
Deposited on : 2025-08-21  
Resolution : 2.52 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](mailto: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>.

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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

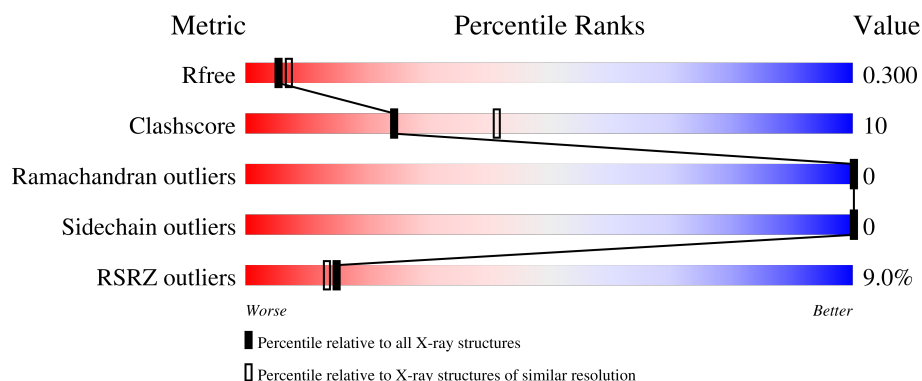
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.52 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	7383 (2.54-2.50)
Clashscore	190562	8079 (2.54-2.50)
Ramachandran outliers	187476	7944 (2.54-2.50)
Sidechain outliers	187428	7946 (2.54-2.50)
RSRZ outliers	180081	7387 (2.54-2.50)

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  $\geq 3$ , 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	433	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3686 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 Adenosine receptor A2a/Soluble cytochrome b562/Adenosine receptor A2a chimera.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	13	0
			3126	2035	532	536	23			

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	ASP	-	expression tag	UNP P29274
A	-7	TYR	-	expression tag	UNP P29274
A	-6	LYS	-	expression tag	UNP P29274
A	-5	ASP	-	expression tag	UNP P29274
A	-4	ASP	-	expression tag	UNP P29274
A	-3	ASP	-	expression tag	UNP P29274
A	-2	ASP	-	expression tag	UNP P29274
A	-1	GLY	-	expression tag	UNP P29274
A	0	ALA	-	expression tag	UNP P29274
A	1	PRO	-	expression tag	UNP P29274
A	54	LEU	ALA	engineered mutation	UNP P29274
A	88	ALA	THR	engineered mutation	UNP P29274
A	107	ALA	ARG	engineered mutation	UNP P29274
A	122	ALA	LYS	engineered mutation	UNP P29274
A	154	ALA	ASN	engineered mutation	UNP P29274
A	202	ALA	LEU	engineered mutation	UNP P29274
A	1007	TRP	MET	conflict	UNP P0ABE7
A	1102	ILE	-	linker	UNP P0ABE7
A	1103	GLN	-	linker	UNP P0ABE7
A	1104	LYS	-	linker	UNP P0ABE7
A	1105	TYR	-	linker	UNP P0ABE7
A	1106	LEU	-	linker	UNP P0ABE7
A	235	ALA	LEU	engineered mutation	UNP P29274
A	239	ALA	VAL	engineered mutation	UNP P29274
A	318	ALA	-	expression tag	UNP P29274
A	319	HIS	-	expression tag	UNP P29274

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Chain	Residue	Modelled	Actual	Comment	Reference
A	320	HIS	-	expression tag	UNP P29274
A	321	HIS	-	expression tag	UNP P29274
A	322	HIS	-	expression tag	UNP P29274
A	323	HIS	-	expression tag	UNP P29274
A	324	HIS	-	expression tag	UNP P29274
A	325	HIS	-	expression tag	UNP P29274
A	326	HIS	-	expression tag	UNP P29274
A	327	HIS	-	expression tag	UNP P29274
A	328	HIS	-	expression tag	UNP P29274

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

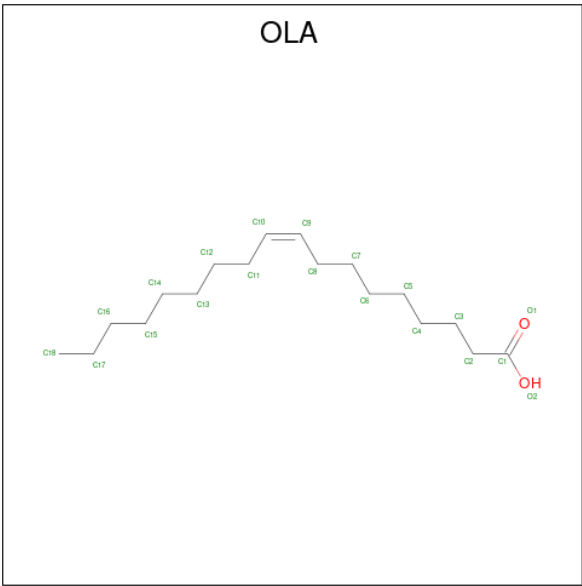
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Na 1 1	0	0

- Molecule 3 is CHOLESTEROL (CCD ID: CLR) (formula: C<sub>27</sub>H<sub>46</sub>O).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 28 27 1	0	0
3	A	1	Total C O 28 27 1	0	0
3	A	1	Total C O 28 27 1	0	0

- Molecule 4 is OLEIC ACID (CCD ID: OLA) (formula: C<sub>18</sub>H<sub>34</sub>O<sub>2</sub>).



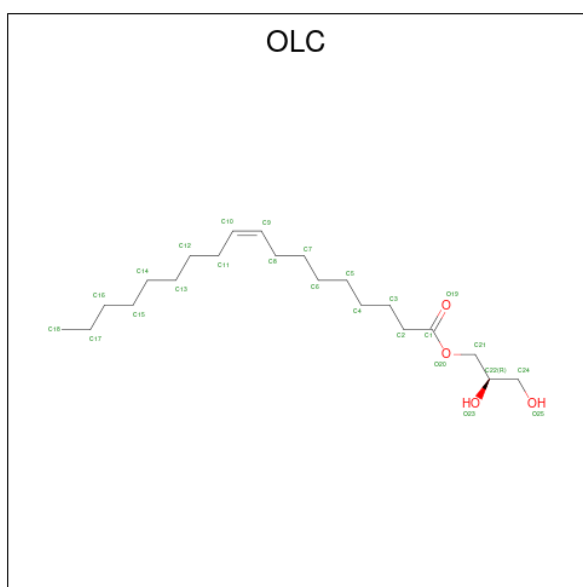
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			20	18	2		
4	A	1	Total	C	O	0	0
			10	8	2		
4	A	1	Total	C	O	0	0
			9	7	2		
4	A	1	Total	C	O	0	0
			18	16	2		
4	A	1	Total	C	O	0	0
			20	18	2		
4	A	1	Total	C	O	0	0
			20	18	2		
4	A	1	Total	C	O	0	0
			12	10	2		
4	A	1	Total	C	O	0	0
			8	6	2		
4	A	1	Total	C	O	0	0
			15	13	2		
4	A	1	Total	C	O	0	0
			11	9	2		
4	A	1	Total	C	O	0	0
			19	17	2		
4	A	1	Total	C	O	0	0
			20	18	2		
4	A	1	Total	C		0	0
			12	12			

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C 10 10	0	0
4	A	1	Total C 11 11	0	0
4	A	1	Total C 12 12	0	0
4	A	1	Total C 9 9	0	0
4	A	1	Total C 8 8	0	0
4	A	1	Total C O 15 13 2	0	0
4	A	1	Total C 15 15	0	0
4	A	1	Total C O 13 11 2	0	0
4	A	1	Total C O 20 18 2	0	0

- Molecule 5 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (CCD ID: OLC) (formula:  $C_{21}H_{40}O_4$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 16 12 4	0	0
5	A	1	Total C O 17 13 4	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			23	19	4		
5	A	1	Total	C	O	0	0
			23	19	4		
5	A	1	Total	C	O	0	0
			23	19	4		
5	A	1	Total	C	O	0	0
			18	14	4		
5	A	1	Total	C	O	0	0
			16	12	4		

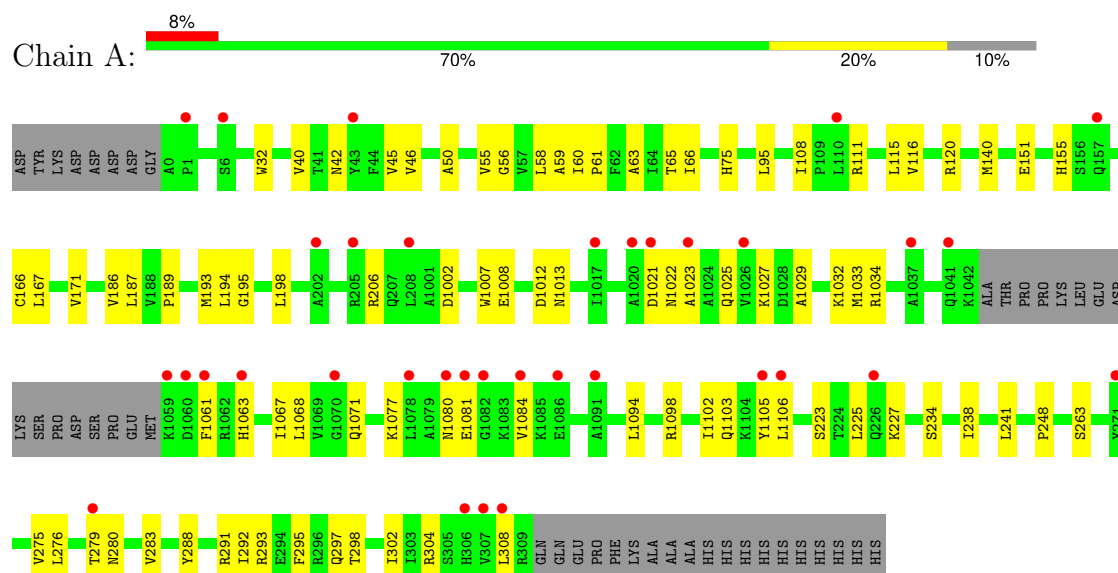
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	32	Total	O	0	0
			32	32		

### 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: Adenosine receptor A2a/Soluble cytochrome b562/Adenosine receptor A2a chimera





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	39.32Å 179.66Å 139.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.41 – 2.52 38.41 – 2.52	Depositor EDS
% Data completeness (in resolution range)	98.4 (38.41-2.52) 98.1 (38.41-2.52)	Depositor EDS
$R_{merge}$	0.51	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.89 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, $R_{free}$	0.251 , 0.300 0.252 , 0.300	Depositor DCC
$R_{free}$ test set	852 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.9	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 71.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	3686	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.73% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: OLC, CLR, OLA, NA

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	0.33	0/3191	0.45	0/4338

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	3126	0	3207	65	0
2	A	1	0	0	0	0
3	A	84	0	138	2	0
4	A	307	0	459	15	0
5	A	136	0	186	5	0
6	A	32	0	0	0	0
All	All	3686	0	3990	76	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 10.

All (76) 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:206:ARG:NH1	1:A:1002:ASP:OD1	2.22	0.72
1:A:1013:ASN:HD21	1:A:1032:LYS:HB2	1.62	0.64
4:A:1222:OLA:H41	4:A:1224:OLA:H152	1.80	0.63
4:A:1222:OLA:H51	4:A:1226:OLA:H131	1.81	0.62
1:A:1007:TRP:CH2	1:A:1103:GLN:HG3	2.35	0.62
1:A:140[A]:MET:HE2	4:A:1225:OLA:H52	1.83	0.60
1:A:1007:TRP:HB2	1:A:1106:LEU:HD13	1.85	0.58
1:A:223:SER:O	1:A:227:LYS:HD3	2.04	0.58
4:A:1205:OLA:H161	5:A:1230:OLC:H14A	1.89	0.54
1:A:1008:GLU:HG2	1:A:1012:ASP:OD1	2.07	0.54
1:A:288:TYR:HA	1:A:292:ILE:HD12	1.89	0.54
1:A:1063:HIS:O	1:A:1067:ILE:HG13	2.07	0.54
1:A:1068:LEU:HD12	1:A:1094:LEU:HD22	1.91	0.53
1:A:1008:GLU:O	1:A:1012:ASP:OD1	2.27	0.53
1:A:1021:ASP:H	1:A:1025:GLN:HE22	1.57	0.53
1:A:1098:ARG:HA	1:A:1102:ILE:HB	1.91	0.53
1:A:1077:LYS:O	1:A:1081:GLU:HG3	2.09	0.53
1:A:75:HIS:CD2	4:A:1225:OLA:H22	2.44	0.53
1:A:66:ILE:CD1	1:A:166:CYS:SG	2.98	0.52
1:A:108:ILE:HG13	1:A:108:ILE:O	2.09	0.51
1:A:32:TRP:CE3	4:A:1215:OLA:H71	2.46	0.51
1:A:298:THR:O	1:A:302:ILE:HG13	2.11	0.51
1:A:55:VAL:HA	1:A:59:ALA:HB3	1.92	0.50
1:A:1029:ALA:O	1:A:1033:MET:HG3	2.12	0.49
1:A:1013:ASN:HD21	1:A:1032:LYS:CB	2.26	0.49
4:A:1209:OLA:H122	4:A:1216:OLA:H151	1.94	0.48
4:A:1209:OLA:H151	4:A:1216:OLA:H151	1.95	0.48
1:A:275[B]:VAL:O	1:A:279[B]:THR:HG23	2.13	0.48
4:A:1210:OLA:H183	4:A:1221:OLA:H121	1.94	0.48
1:A:1013:ASN:ND2	1:A:1029:ALA:O	2.48	0.47
1:A:58:LEU:C	1:A:61:PRO:HD2	2.40	0.47
1:A:241:LEU:HD23	1:A:241:LEU:HA	1.78	0.47
1:A:1007:TRP:HZ3	1:A:1102:ILE:HG22	1.81	0.46
1:A:40:VAL:HG11	1:A:116:VAL:CG1	2.45	0.46
1:A:50:ALA:HB2	5:A:1232:OLC:H7A	1.97	0.46
4:A:1225:OLA:H62	5:A:1233:OLC:H3A	1.97	0.46
1:A:167:LEU:O	1:A:171:VAL:HG22	2.15	0.46
1:A:1023:ALA:HB2	1:A:1084:VAL:HG22	1.99	0.45
1:A:234:SER:OG	1:A:291:ARG:NH1	2.43	0.45
1:A:42:ASN:HA	1:A:45:VAL:HB	1.98	0.45
1:A:279[A]:THR:HG23	4:A:1217:OLA:H131	1.99	0.45
1:A:1067:ILE:O	1:A:1071:GLN:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:LEU:O	1:A:120:ARG:NH1	2.51	0.44
1:A:1061:PHE:HB2	1:A:1105:TYR:HD2	1.82	0.44
1:A:225:LEU:HD23	1:A:225:LEU:HA	1.82	0.44
5:A:1229:OLC:H15	5:A:1230:OLC:H14	1.99	0.44
1:A:304:ARG:O	1:A:308:LEU:HB2	2.17	0.44
1:A:40:VAL:HG11	1:A:116:VAL:HG12	1.99	0.44
1:A:95:LEU:HD21	1:A:238:ILE:HG22	2.00	0.44
1:A:195:GLY:HA3	4:A:1206:OLA:H42	1.99	0.44
1:A:1022:ASN:ND2	1:A:1025:GLN:HE21	2.15	0.44
1:A:1027:LYS:HD2	1:A:1080:ASN:OD1	2.18	0.43
1:A:1034:ARG:HH11	1:A:1034:ARG:HG2	1.82	0.43
1:A:292:ILE:HG22	1:A:295:PHE:H	1.84	0.43
1:A:56:GLY:HA2	1:A:60:ILE:HD12	1.99	0.43
1:A:280:ASN:O	1:A:283:VAL:HG22	2.19	0.43
1:A:189:PRO:O	1:A:193:MET:HG3	2.19	0.43
1:A:1022:ASN:H	1:A:1025:GLN:NE2	2.16	0.43
1:A:293:ARG:HG2	1:A:297:GLN:OE1	2.19	0.42
1:A:187[B]:LEU:HD23	1:A:187[B]:LEU:HA	1.61	0.42
1:A:1021:ASP:H	1:A:1025:GLN:NE2	2.17	0.42
1:A:108:ILE:O	1:A:108:ILE:CG1	2.67	0.42
1:A:194:LEU:O	1:A:198:LEU:HG	2.19	0.42
4:A:1209:OLA:H21	4:A:1216:OLA:H32	2.01	0.42
1:A:111:ARG:HA	1:A:111:ARG:HD2	1.69	0.42
1:A:66:ILE:HD12	1:A:66:ILE:HA	1.73	0.42
4:A:1225:OLA:H32	4:A:1226:OLA:H41	2.02	0.41
1:A:263:SER:O	3:A:1203:CLR:O1	2.36	0.41
1:A:248:PRO:HG2	1:A:276:LEU:HD23	2.01	0.41
1:A:65:THR:OG1	4:A:1205:OLA:H62	2.21	0.41
1:A:151:GLU:O	1:A:155:HIS:ND1	2.54	0.41
1:A:46:VAL:HG12	5:A:1231:OLC:H4	2.03	0.41
1:A:186:VAL:C	1:A:189:PRO:HD2	2.45	0.41
1:A:63:ALA:O	1:A:66:ILE:HG22	2.21	0.41
3:A:1204:CLR:H162	3:A:1204:CLR:H222	1.77	0.41
1:A:187[A]:LEU:HD12	1:A:187[A]:LEU:HA	1.67	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	399/433 (92%)	393 (98%)	6 (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	329/354 (93%)	329 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	34	ASN
1	A	39	ASN
1	A	113	ASN
1	A	148	GLN
1	A	1013	ASN
1	A	1025	GLN
1	A	250	HIS
1	A	280	ASN
1	A	297	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 33 ligands modelled in this entry, 1 is monoatomic - leaving 32 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	OLA	A	1208	-	17,17,19	0.60	0	17,17,19	0.56	0
4	OLA	A	1212	-	7,7,19	0.98	0	7,7,19	0.89	0
4	OLA	A	1216	-	19,19,19	0.69	0	19,19,19	0.53	0
4	OLA	A	1222	-	7,7,19	0.20	0	6,6,19	0.29	0
5	OLC	A	1229	-	22,22,24	0.40	0	23,23,25	0.61	0
5	OLC	A	1230	-	22,22,24	0.47	0	23,23,25	0.55	0
4	OLA	A	1211	-	11,11,19	0.75	0	11,11,19	0.82	0
4	OLA	A	1225	-	12,12,19	0.78	0	12,12,19	0.68	0
4	OLA	A	1218	-	9,9,19	0.32	0	8,8,19	0.32	0
4	OLA	A	1226	-	19,19,19	0.59	0	19,19,19	0.56	0
5	OLC	A	1228	-	16,16,24	0.52	0	17,17,25	0.59	0
4	OLA	A	1214	-	10,10,19	0.73	0	10,10,19	0.97	1 (10%)
4	OLA	A	1209	-	19,19,19	0.63	0	19,19,19	0.60	0
3	CLR	A	1203	-	31,31,31	0.41	0	48,48,48	0.94	1 (2%)
4	OLA	A	1223	-	14,14,19	0.70	0	14,14,19	0.56	0
4	OLA	A	1220	-	11,11,19	0.35	0	10,10,19	0.33	0
3	CLR	A	1202	-	31,31,31	0.39	0	48,48,48	0.83	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	OLC	A	1233	-	15,15,24	0.58	0	16,16,25	0.70	0
4	OLA	A	1224	-	14,14,19	0.20	0	13,13,19	0.40	0
5	OLC	A	1231	-	22,22,24	0.45	0	23,23,25	0.51	0
4	OLA	A	1210	-	19,19,19	0.59	0	19,19,19	0.63	0
3	CLR	A	1204	-	31,31,31	0.38	0	48,48,48	0.67	0
4	OLA	A	1205	-	19,19,19	0.59	0	19,19,19	0.52	0
4	OLA	A	1213	-	14,14,19	0.66	0	14,14,19	0.62	0
5	OLC	A	1232	-	17,17,24	0.50	0	18,18,25	0.47	0
4	OLA	A	1221	-	8,8,19	0.14	0	7,7,19	0.57	0
4	OLA	A	1207	-	8,8,19	1.00	0	8,8,19	0.82	0
4	OLA	A	1219	-	10,10,19	0.32	0	9,9,19	0.34	0
5	OLC	A	1227	-	15,15,24	0.55	0	16,16,25	0.59	0
4	OLA	A	1215	-	18,18,19	0.67	0	18,18,19	0.62	0
4	OLA	A	1217	-	11,11,19	0.30	0	10,10,19	0.33	0
4	OLA	A	1206	-	9,9,19	0.83	0	9,9,19	0.67	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	OLA	A	1208	-	-	9/15/15/17	-
4	OLA	A	1212	-	-	1/5/5/17	-
4	OLA	A	1216	-	-	5/17/17/17	-
4	OLA	A	1222	-	-	0/5/5/17	-
5	OLC	A	1229	-	-	13/22/22/24	-
5	OLC	A	1230	-	-	11/22/22/24	-
4	OLA	A	1211	-	-	2/9/9/17	-
4	OLA	A	1225	-	-	5/10/10/17	-
4	OLA	A	1218	-	-	2/7/7/17	-
4	OLA	A	1226	-	-	9/17/17/17	-
5	OLC	A	1228	-	-	4/16/16/24	-
4	OLA	A	1214	-	-	4/8/8/17	-
4	OLA	A	1209	-	-	10/17/17/17	-
3	CLR	A	1203	-	-	0/10/68/68	0/4/4/4
4	OLA	A	1223	-	-	5/12/12/17	-
4	OLA	A	1220	-	-	3/9/9/17	-
3	CLR	A	1202	-	-	1/10/68/68	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	OLC	A	1233	-	-	4/15/15/24	-
4	OLA	A	1224	-	-	3/12/12/17	-
5	OLC	A	1231	-	-	9/22/22/24	-
4	OLA	A	1210	-	-	6/17/17/17	-
3	CLR	A	1204	-	-	4/10/68/68	0/4/4/4
4	OLA	A	1205	-	-	8/17/17/17	-
4	OLA	A	1213	-	-	4/12/12/17	-
5	OLC	A	1232	-	-	8/17/17/24	-
4	OLA	A	1221	-	-	3/6/6/17	-
4	OLA	A	1207	-	-	3/6/6/17	-
4	OLA	A	1219	-	-	6/8/8/17	-
5	OLC	A	1227	-	-	6/15/15/24	-
4	OLA	A	1215	-	-	5/16/16/17	-
4	OLA	A	1217	-	-	3/9/9/17	-
4	OLA	A	1206	-	-	2/7/7/17	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1214	OLA	O1-C1-C2	-2.24	116.00	123.09
3	A	1203	CLR	C19-C10-C9	2.11	114.02	111.66
3	A	1202	CLR	C19-C10-C9	2.01	113.91	111.66

There are no chirality outliers.

All (158) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1210	OLA	C6-C7-C8-C9
4	A	1213	OLA	C10-C11-C12-C13
4	A	1217	OLA	C6-C7-C8-C9
5	A	1227	OLC	O20-C21-C22-C24
5	A	1229	OLC	C21-C22-C24-O25
5	A	1229	OLC	O20-C21-C22-O23
5	A	1230	OLC	C21-C22-C24-O25
5	A	1230	OLC	O20-C21-C22-O23
5	A	1231	OLC	O20-C21-C22-C24
5	A	1232	OLC	O20-C21-C22-O23

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Mol	Chain	Res	Type	Atoms
5	A	1231	OLC	C2-C1-O20-C21
5	A	1232	OLC	C2-C1-O20-C21
5	A	1231	OLC	O19-C1-O20-C21
5	A	1232	OLC	O19-C1-O20-C21
5	A	1227	OLC	O20-C21-C22-O23
5	A	1231	OLC	O20-C21-C22-O23
5	A	1230	OLC	O20-C21-C22-C24
4	A	1223	OLA	C1-C2-C3-C4
5	A	1233	OLC	C1-C2-C3-C4
4	A	1225	OLA	C1-C2-C3-C4
3	A	1204	CLR	C20-C22-C23-C24
4	A	1215	OLA	C3-C4-C5-C6
5	A	1230	OLC	C2-C1-O20-C21
5	A	1230	OLC	C1-C2-C3-C4
5	A	1232	OLC	O20-C21-C22-C24
5	A	1230	OLC	O19-C1-O20-C21
4	A	1205	OLA	C2-C3-C4-C5
5	A	1229	OLC	C3-C4-C5-C6
5	A	1229	OLC	O23-C22-C24-O25
4	A	1223	OLA	C5-C6-C7-C8
4	A	1215	OLA	C5-C6-C7-C8
4	A	1223	OLA	C3-C4-C5-C6
4	A	1226	OLA	C15-C16-C17-C18
5	A	1232	OLC	C5-C6-C7-C8
4	A	1219	OLA	C11-C12-C13-C14
5	A	1228	OLC	C1-C2-C3-C4
5	A	1232	OLC	C6-C7-C8-C9
4	A	1226	OLA	C11-C12-C13-C14
4	A	1217	OLA	C12-C13-C14-C15
5	A	1229	OLC	O20-C21-C22-C24
5	A	1231	OLC	C4-C5-C6-C7
4	A	1216	OLA	C3-C4-C5-C6
5	A	1229	OLC	C4-C5-C6-C7
4	A	1209	OLA	C10-C11-C12-C13
4	A	1210	OLA	C15-C16-C17-C18
4	A	1214	OLA	C4-C5-C6-C7
4	A	1205	OLA	C14-C15-C16-C17
4	A	1207	OLA	C3-C4-C5-C6
4	A	1208	OLA	C6-C7-C8-C9
5	A	1229	OLC	C10-C11-C12-C13
5	A	1231	OLC	C6-C7-C8-C9
4	A	1226	OLA	C4-C5-C6-C7

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Mol	Chain	Res	Type	Atoms
4	A	1220	OLA	C4-C5-C6-C7
4	A	1208	OLA	C4-C5-C6-C7
4	A	1226	OLA	C3-C4-C5-C6
4	A	1219	OLA	C10-C11-C12-C13
4	A	1224	OLA	C6-C7-C8-C9
4	A	1209	OLA	C13-C14-C15-C16
4	A	1205	OLA	C10-C11-C12-C13
4	A	1216	OLA	C6-C7-C8-C9
4	A	1219	OLA	C12-C13-C14-C15
5	A	1233	OLC	C2-C3-C4-C5
4	A	1216	OLA	C5-C6-C7-C8
4	A	1225	OLA	C4-C5-C6-C7
5	A	1227	OLC	C2-C1-O20-C21
4	A	1205	OLA	C3-C4-C5-C6
4	A	1209	OLA	C14-C15-C16-C17
5	A	1231	OLC	C1-C2-C3-C4
5	A	1231	OLC	C5-C6-C7-C8
4	A	1211	OLA	C4-C5-C6-C7
5	A	1228	OLC	C3-C4-C5-C6
4	A	1219	OLA	C15-C16-C17-C18
5	A	1233	OLC	C6-C7-C8-C9
4	A	1205	OLA	C15-C16-C17-C18
4	A	1205	OLA	C11-C12-C13-C14
4	A	1205	OLA	C12-C13-C14-C15
5	A	1232	OLC	C3-C4-C5-C6
5	A	1227	OLC	C6-C7-C8-C9
4	A	1212	OLA	C1-C2-C3-C4
5	A	1229	OLC	C5-C6-C7-C8
5	A	1227	OLC	O23-C22-C24-O25
4	A	1226	OLA	C14-C15-C16-C17
4	A	1208	OLA	C1-C2-C3-C4
5	A	1233	OLC	C4-C5-C6-C7
4	A	1208	OLA	C13-C14-C15-C16
5	A	1227	OLC	O19-C1-O20-C21
4	A	1225	OLA	C5-C6-C7-C8
4	A	1206	OLA	C3-C4-C5-C6
4	A	1209	OLA	C11-C12-C13-C14
4	A	1209	OLA	C12-C13-C14-C15
4	A	1223	OLA	C6-C7-C8-C9
4	A	1218	OLA	C9-C10-C11-C12
5	A	1230	OLC	O23-C22-C24-O25
4	A	1210	OLA	C12-C13-C14-C15

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Mol	Chain	Res	Type	Atoms
5	A	1232	OLC	C4-C5-C6-C7
4	A	1208	OLA	C12-C13-C14-C15
4	A	1225	OLA	C6-C7-C8-C9
4	A	1205	OLA	C4-C5-C6-C7
3	A	1204	CLR	C22-C23-C24-C25
4	A	1210	OLA	C11-C12-C13-C14
4	A	1217	OLA	C11-C12-C13-C14
4	A	1226	OLA	C12-C13-C14-C15
4	A	1224	OLA	C12-C13-C14-C15
5	A	1230	OLC	C4-C5-C6-C7
4	A	1223	OLA	C2-C3-C4-C5
5	A	1230	OLC	C12-C13-C14-C15
4	A	1209	OLA	C3-C4-C5-C6
5	A	1229	OLC	C9-C10-C11-C12
4	A	1221	OLA	C15-C16-C17-C18
4	A	1219	OLA	C9-C10-C11-C12
4	A	1220	OLA	C9-C10-C11-C12
4	A	1221	OLA	C14-C15-C16-C17
5	A	1231	OLC	C3-C4-C5-C6
4	A	1213	OLA	C6-C7-C8-C9
4	A	1214	OLA	C1-C2-C3-C4
4	A	1213	OLA	C9-C10-C11-C12
4	A	1225	OLA	C7-C8-C9-C10
4	A	1211	OLA	C7-C8-C9-C10
5	A	1228	OLC	C4-C5-C6-C7
4	A	1208	OLA	C3-C4-C5-C6
5	A	1229	OLC	C11-C12-C13-C14
4	A	1215	OLA	C9-C10-C11-C12
4	A	1213	OLA	C3-C4-C5-C6
4	A	1209	OLA	C6-C7-C8-C9
4	A	1221	OLA	C12-C13-C14-C15
4	A	1210	OLA	C10-C11-C12-C13
4	A	1218	OLA	C6-C7-C8-C9
4	A	1207	OLA	O2-C1-C2-C3
4	A	1214	OLA	C3-C4-C5-C6
4	A	1226	OLA	C10-C11-C12-C13
4	A	1207	OLA	O1-C1-C2-C3
4	A	1226	OLA	C7-C8-C9-C10
4	A	1216	OLA	C7-C8-C9-C10
4	A	1220	OLA	C7-C8-C9-C10
4	A	1219	OLA	C13-C14-C15-C16
3	A	1202	CLR	C23-C24-C25-C27

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Mol	Chain	Res	Type	Atoms
4	A	1214	OLA	C6-C7-C8-C9
5	A	1230	OLC	C9-C10-C11-C12
4	A	1209	OLA	C7-C8-C9-C10
4	A	1209	OLA	C9-C10-C11-C12
5	A	1229	OLC	C2-C3-C4-C5
4	A	1208	OLA	C7-C8-C9-C10
5	A	1229	OLC	C12-C13-C14-C15
5	A	1230	OLC	C5-C6-C7-C8
4	A	1216	OLA	C13-C14-C15-C16
4	A	1215	OLA	O2-C1-C2-C3
4	A	1224	OLA	C14-C15-C16-C17
3	A	1204	CLR	C16-C17-C20-C22
4	A	1226	OLA	C6-C7-C8-C9
5	A	1229	OLC	C6-C7-C8-C9
4	A	1208	OLA	C2-C3-C4-C5
3	A	1204	CLR	C13-C17-C20-C21
4	A	1206	OLA	C5-C6-C7-C8
4	A	1215	OLA	O1-C1-C2-C3
4	A	1209	OLA	C4-C5-C6-C7
4	A	1208	OLA	O2-C1-C2-C3
4	A	1210	OLA	C1-C2-C3-C4
5	A	1228	OLC	C6-C7-C8-C9

There are no ring outliers.

19 monomers are involved in 20 short contacts:

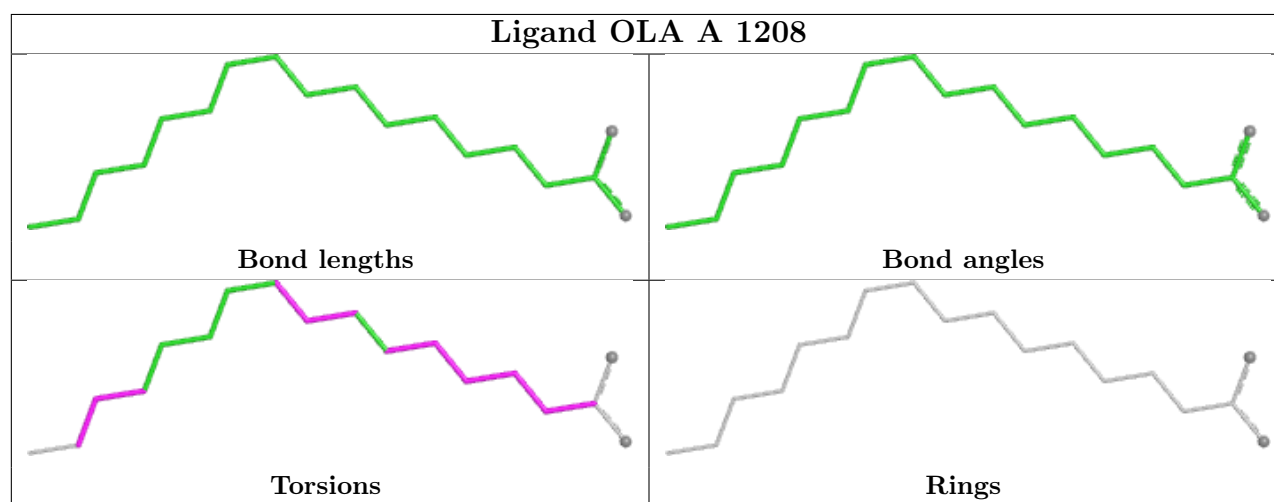
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1216	OLA	3	0
4	A	1222	OLA	2	0
5	A	1229	OLC	1	0
5	A	1230	OLC	2	0
4	A	1225	OLA	4	0
4	A	1226	OLA	2	0
4	A	1209	OLA	3	0
3	A	1203	CLR	1	0
5	A	1233	OLC	1	0
4	A	1224	OLA	1	0
5	A	1231	OLC	1	0
4	A	1210	OLA	1	0
3	A	1204	CLR	1	0
4	A	1205	OLA	2	0
5	A	1232	OLC	1	0

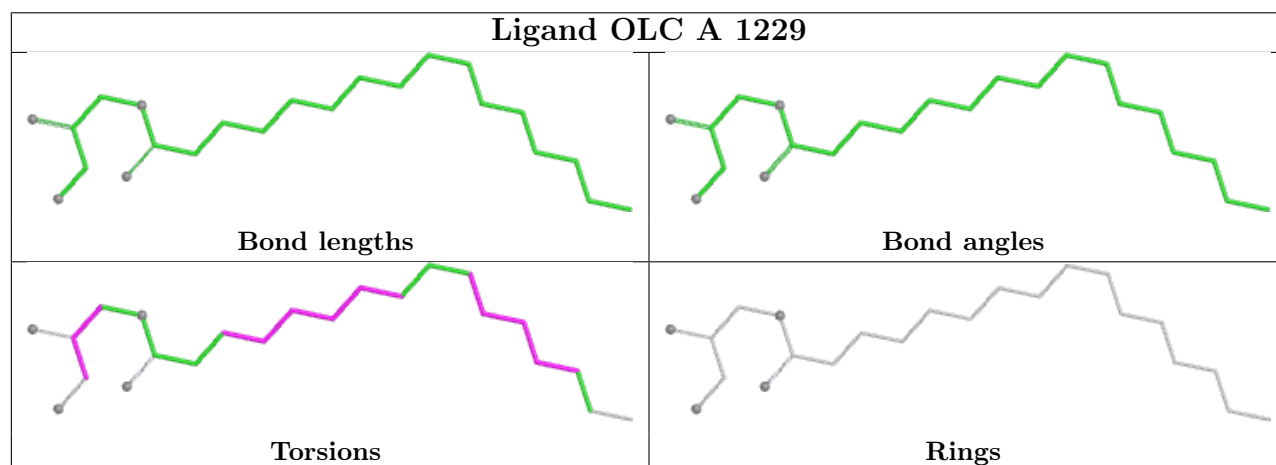
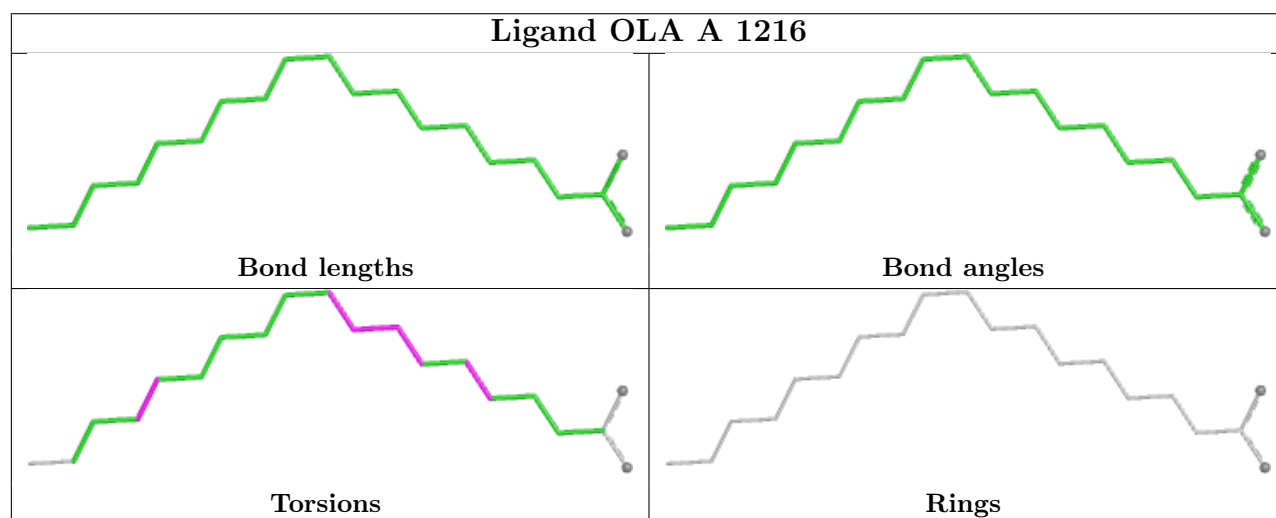
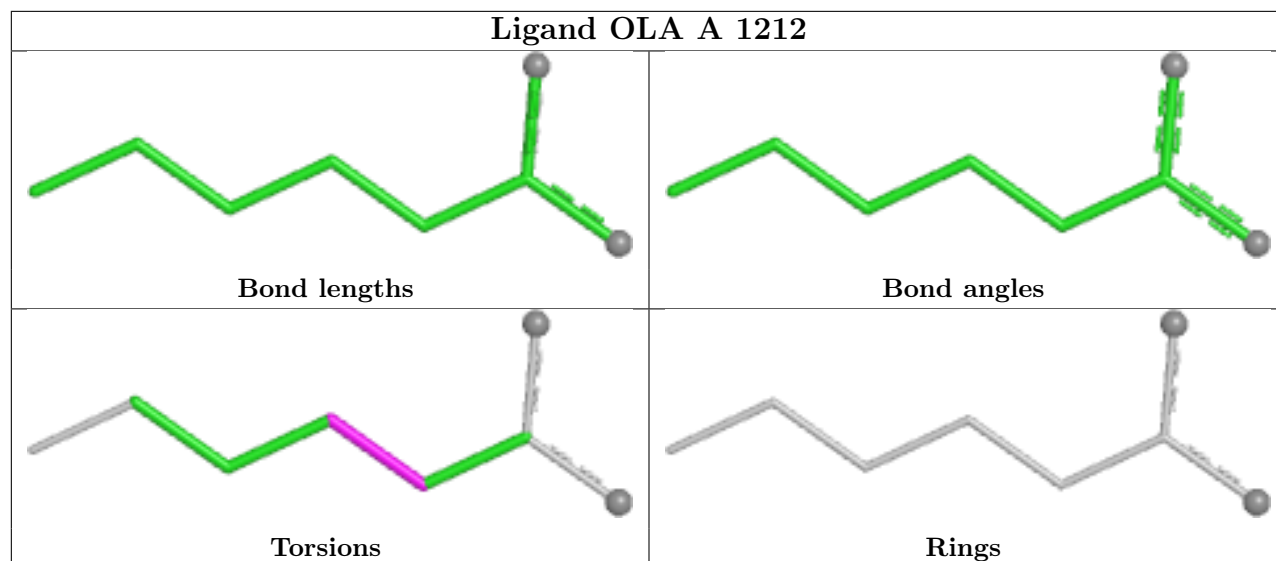
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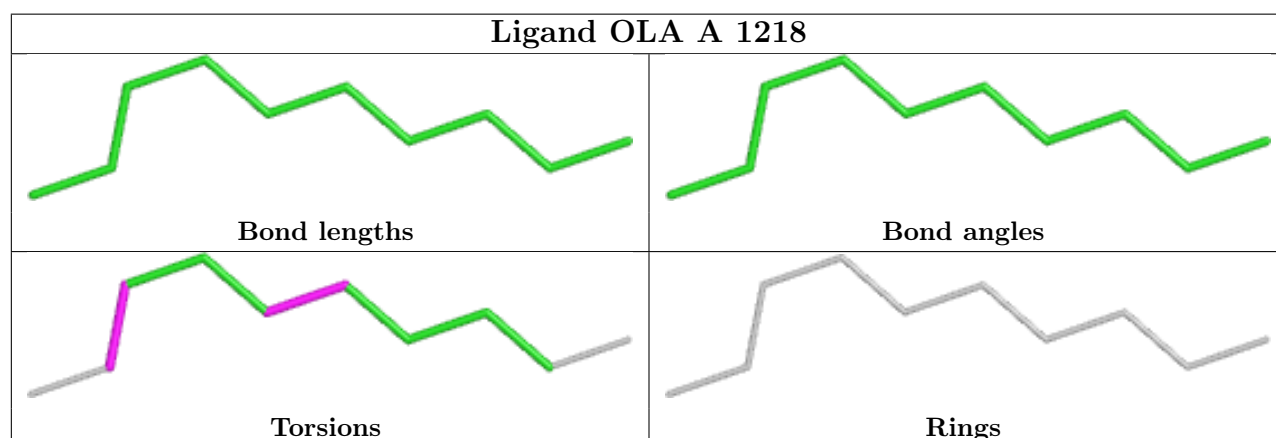
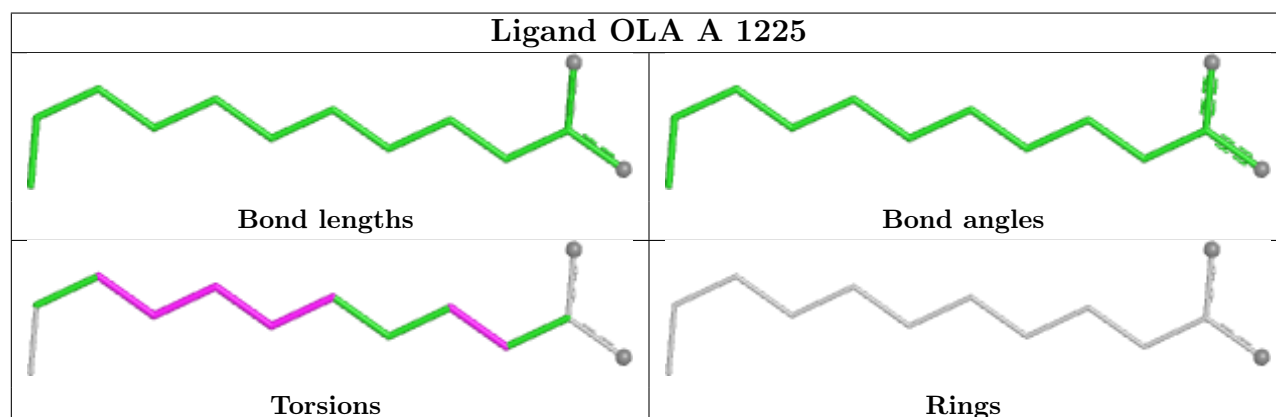
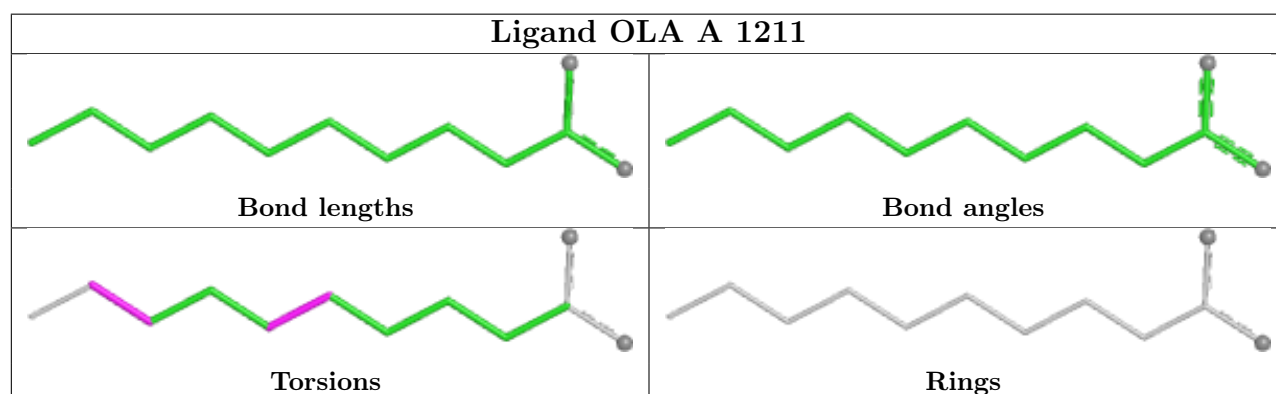
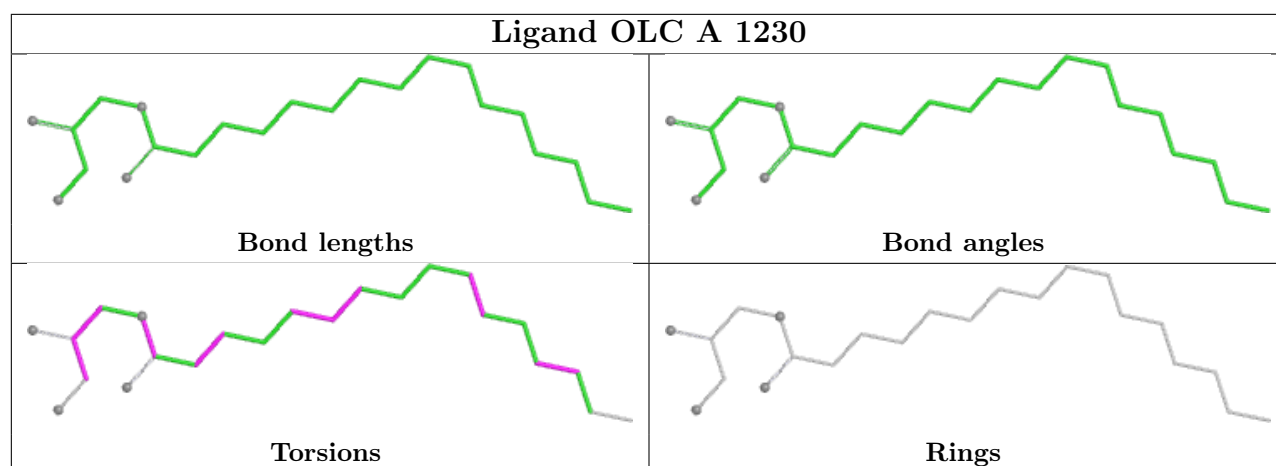
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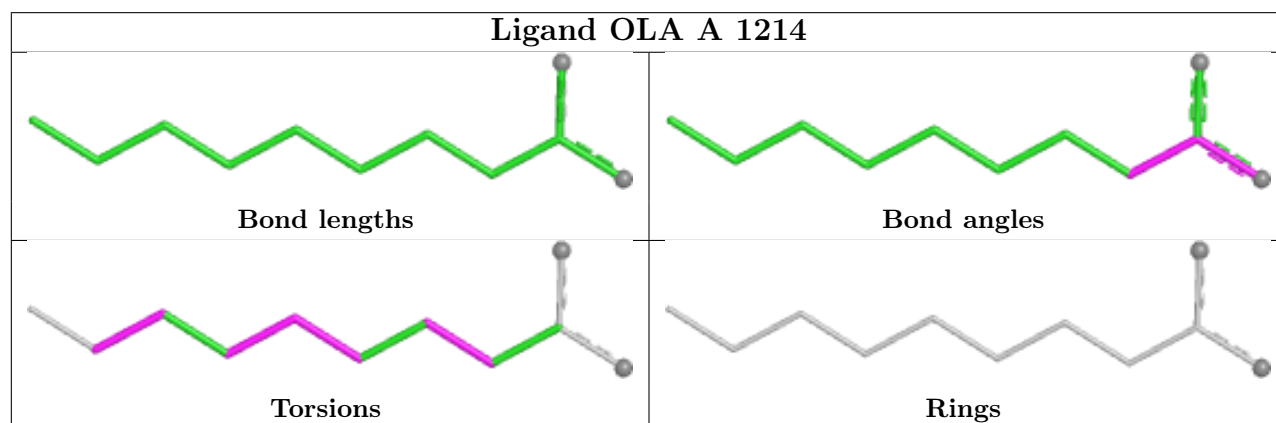
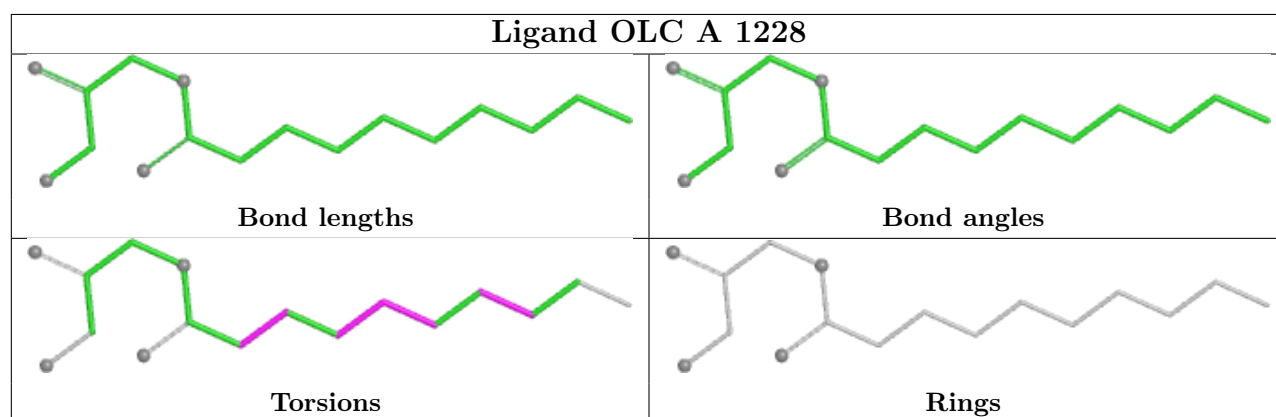
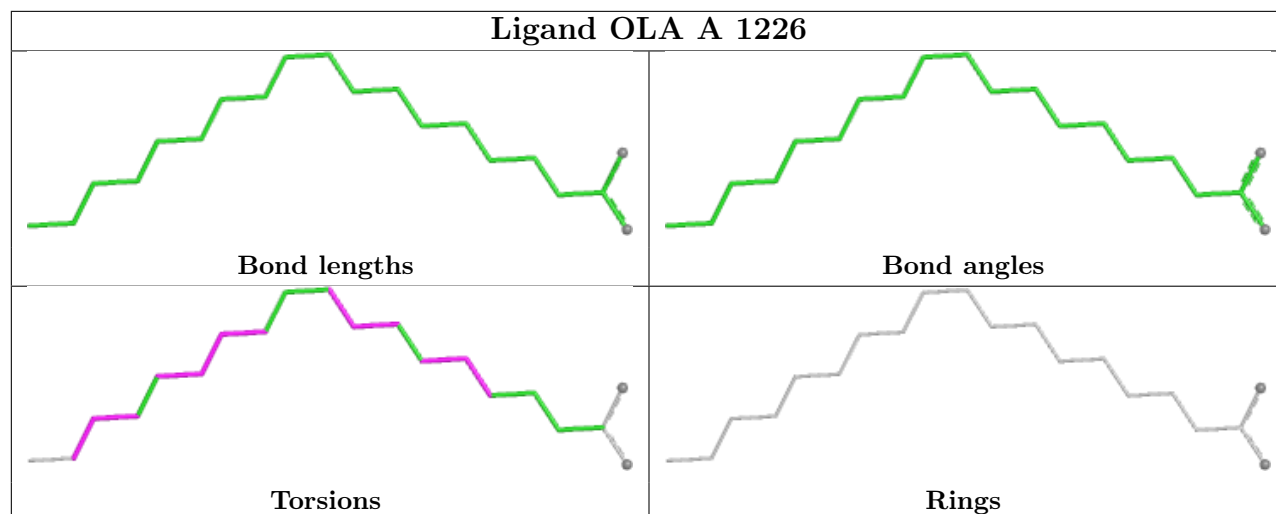
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1221	OLA	1	0
4	A	1215	OLA	1	0
4	A	1217	OLA	1	0
4	A	1206	OLA	1	0

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

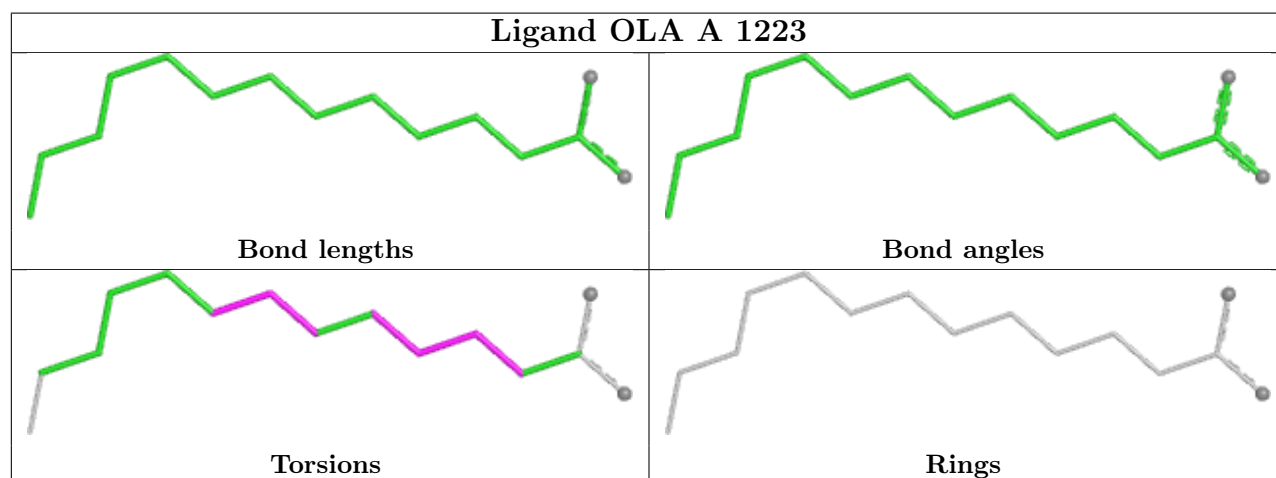
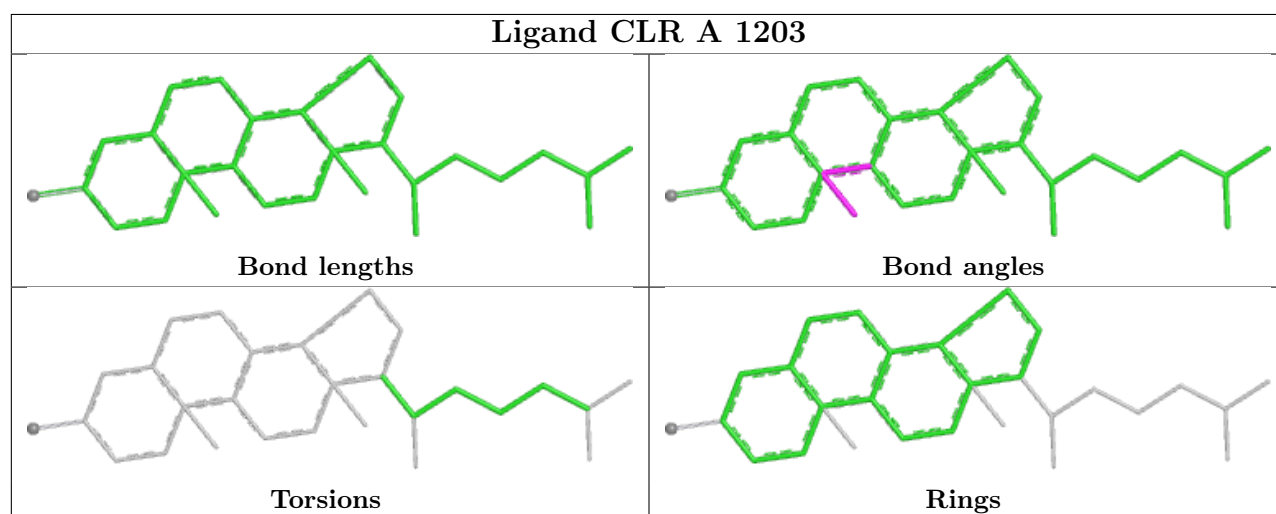
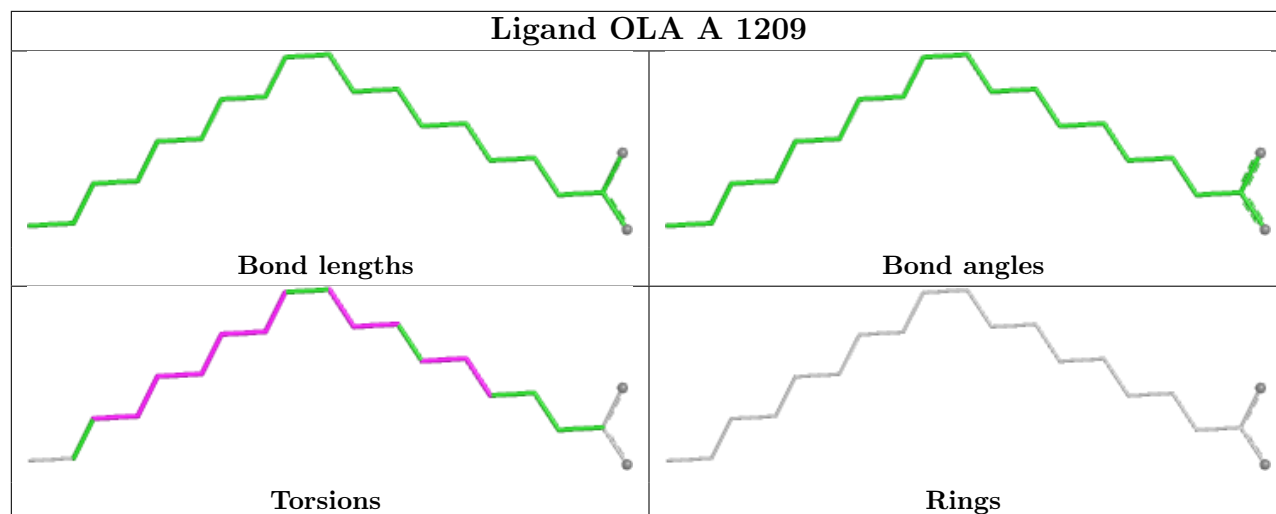


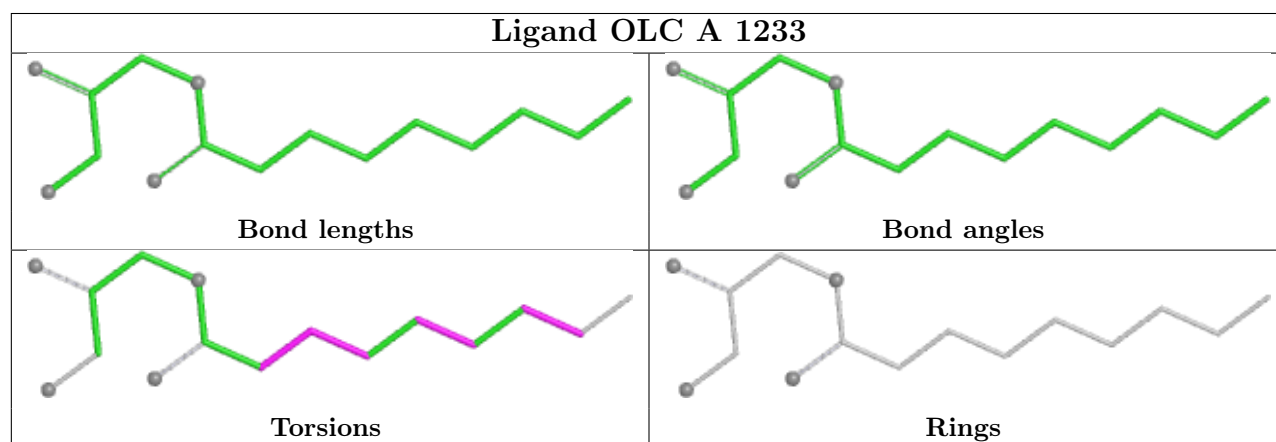
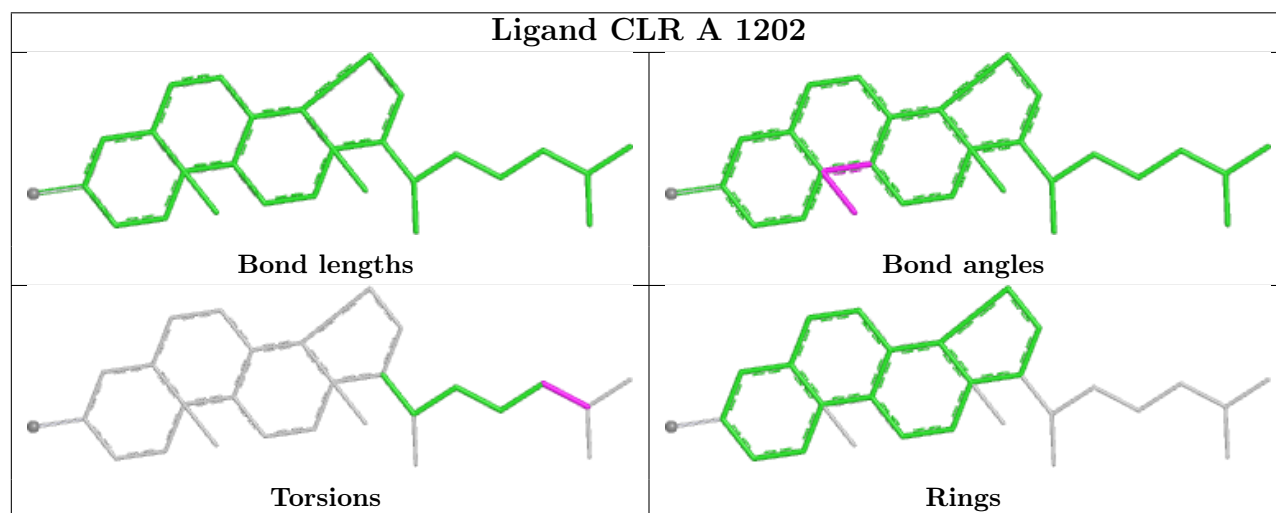
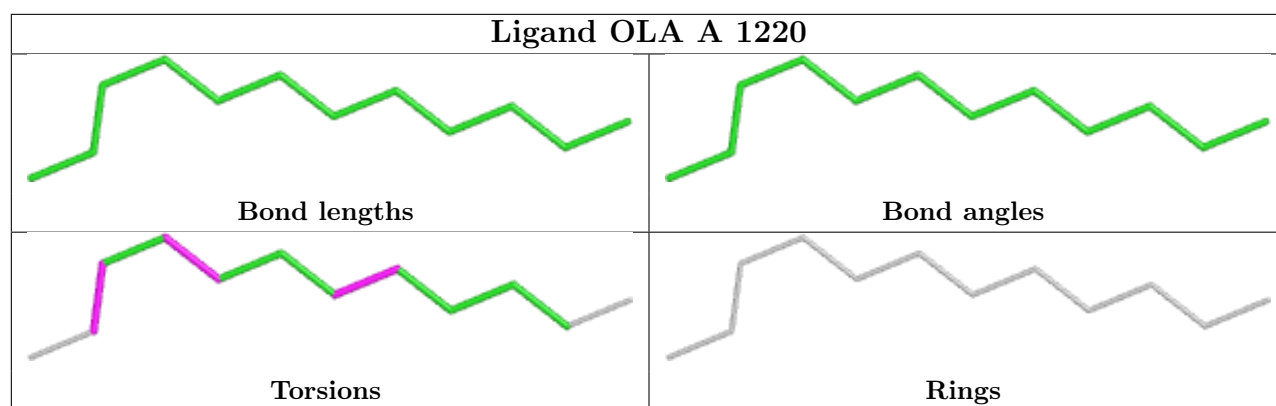


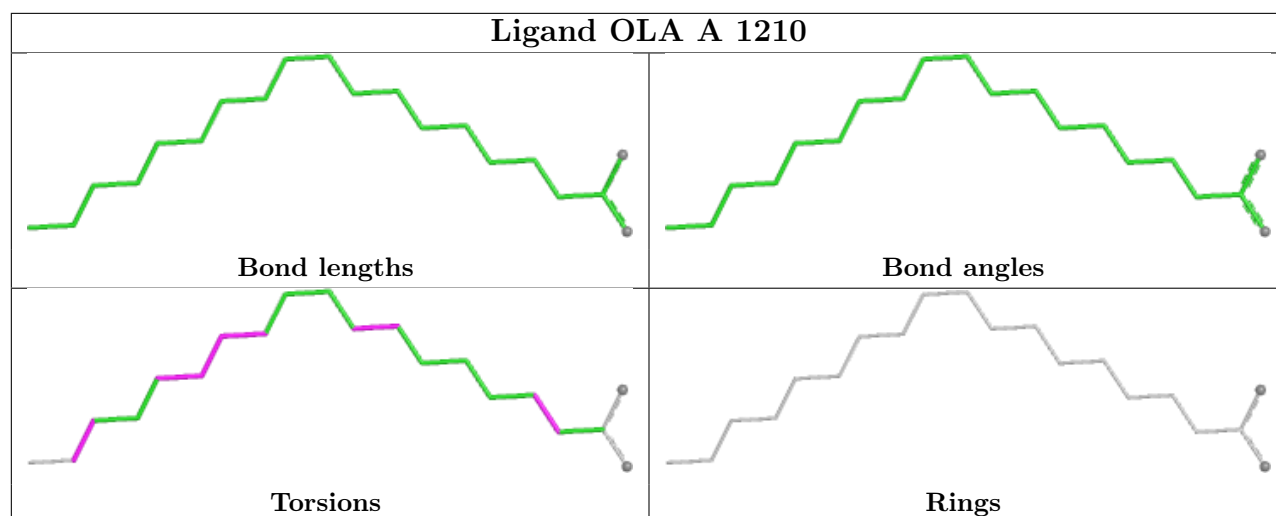
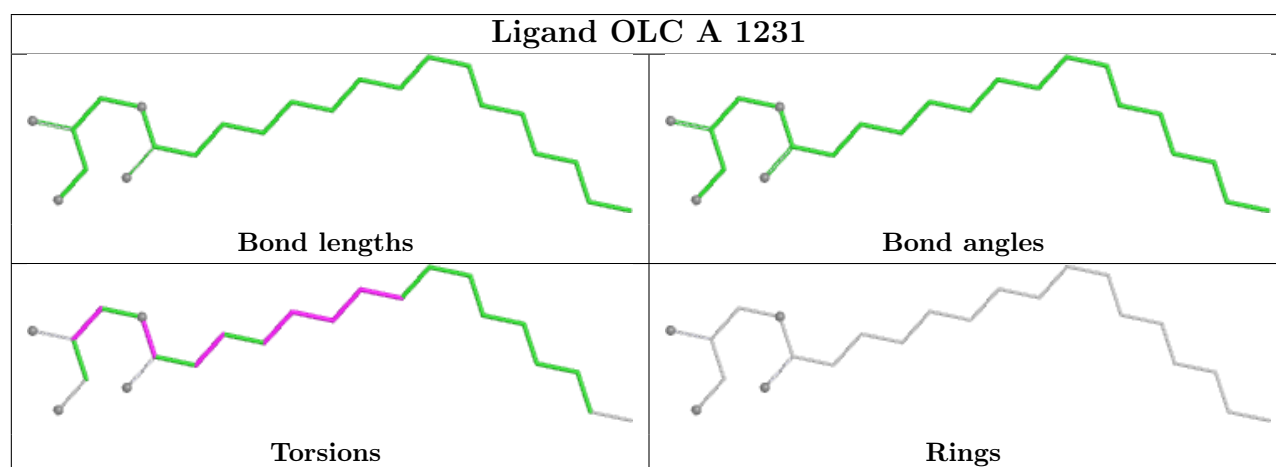
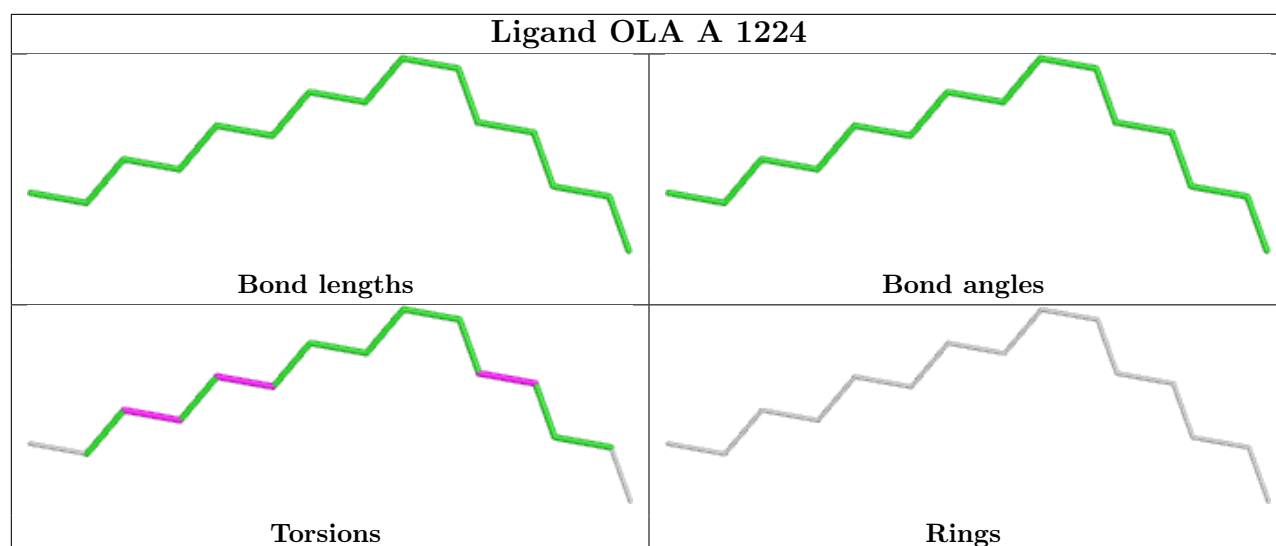


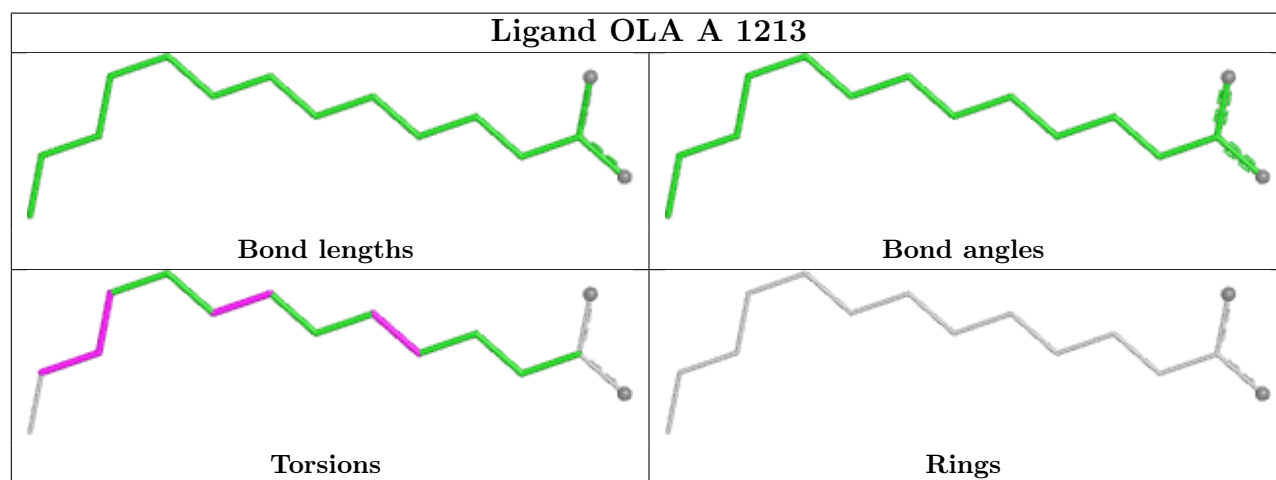
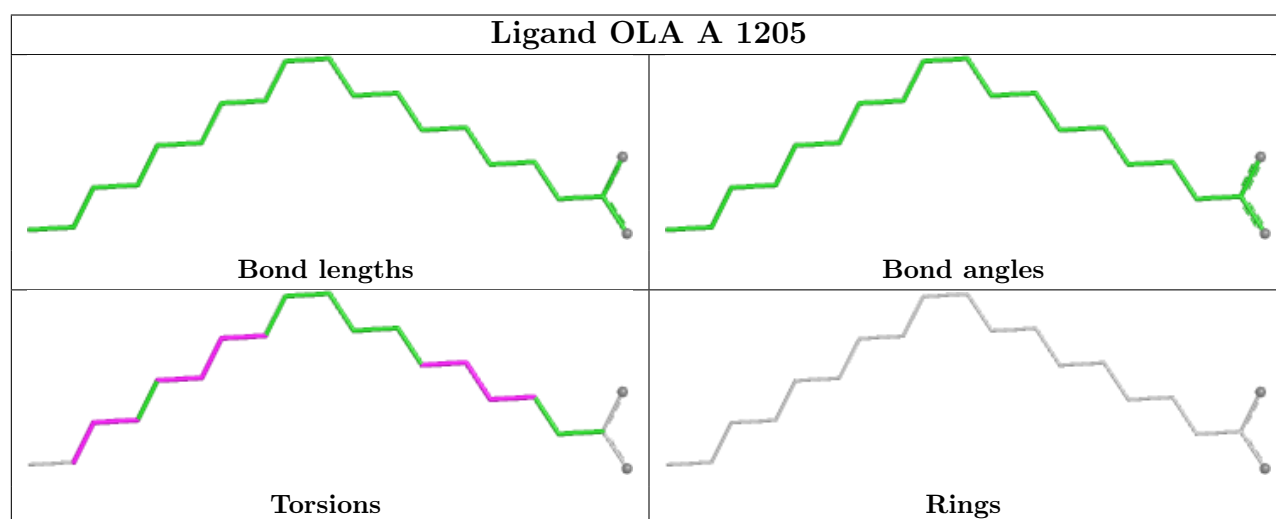
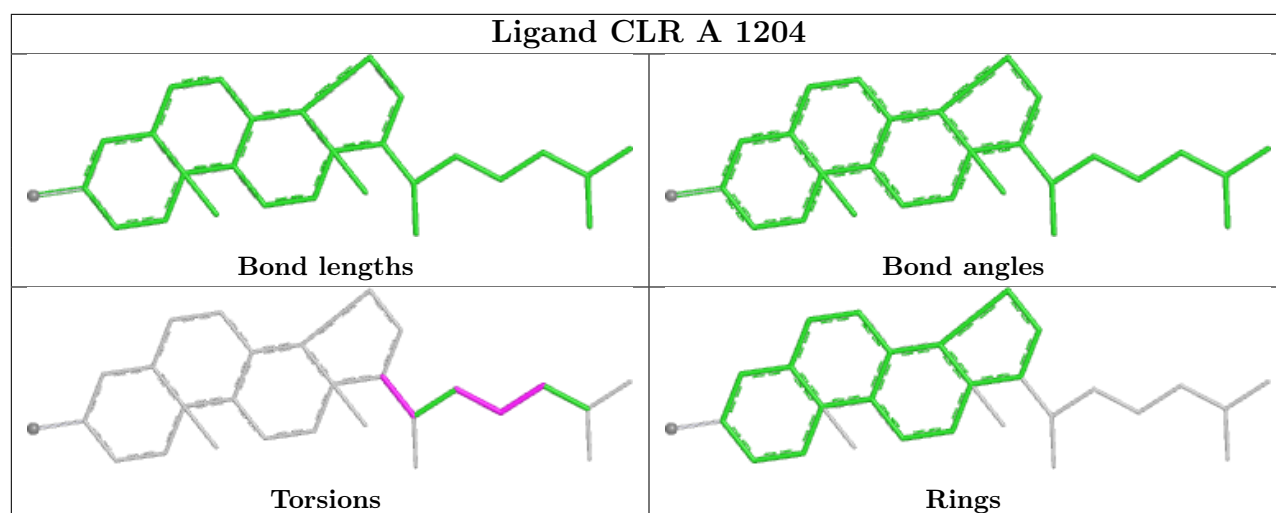


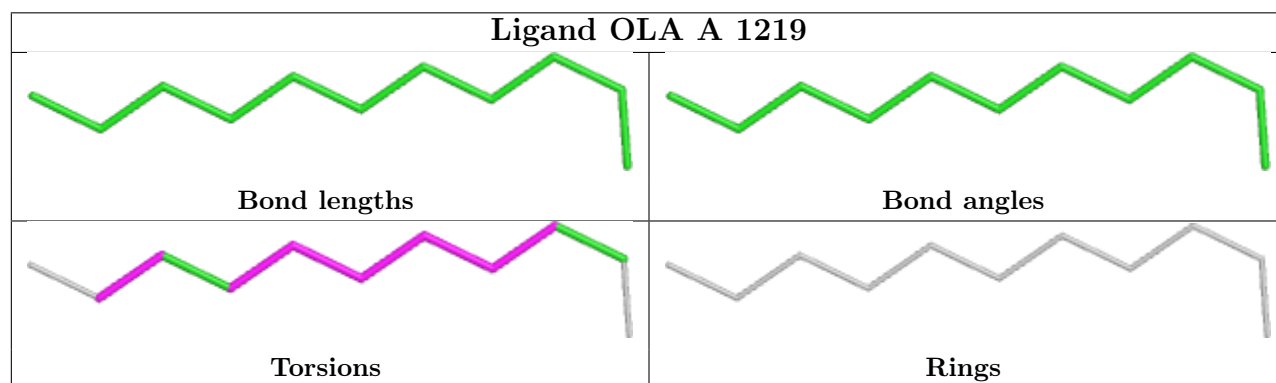
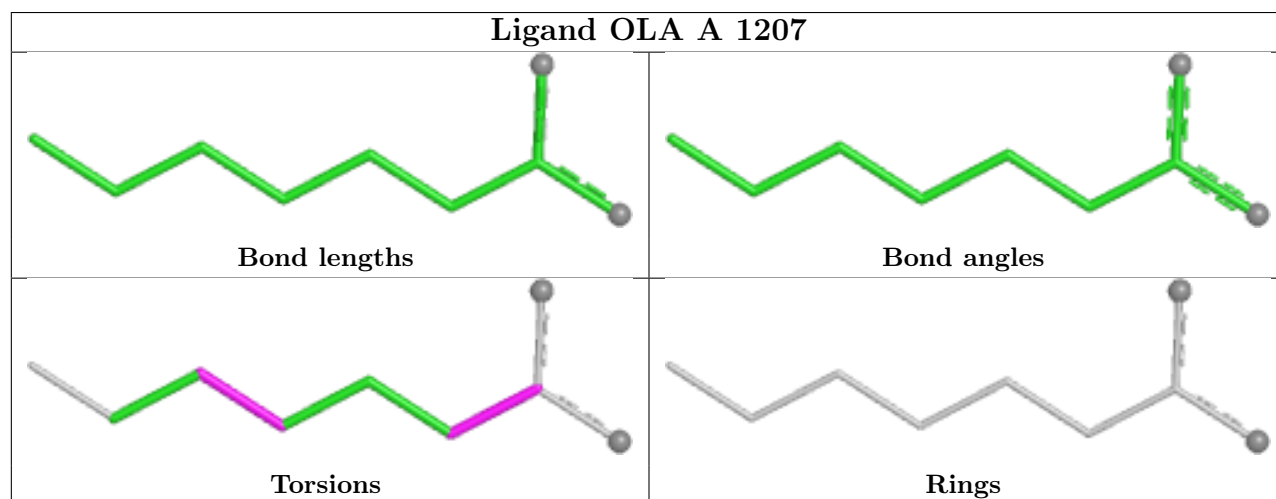
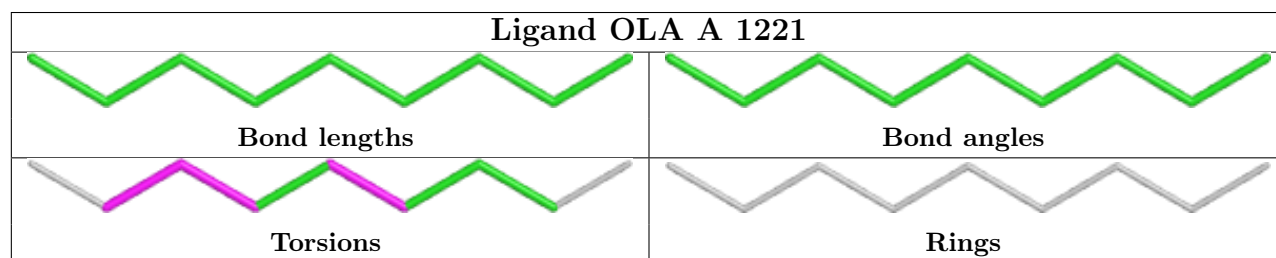
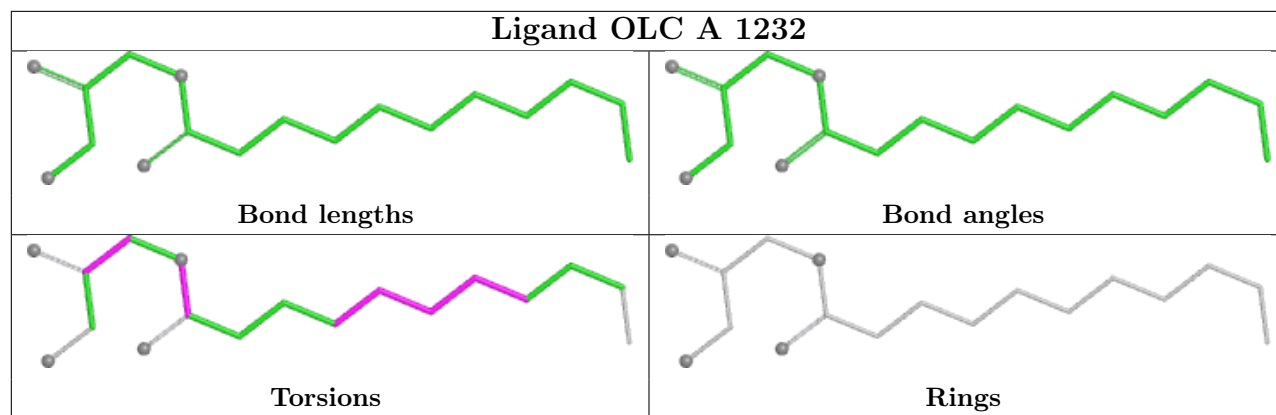


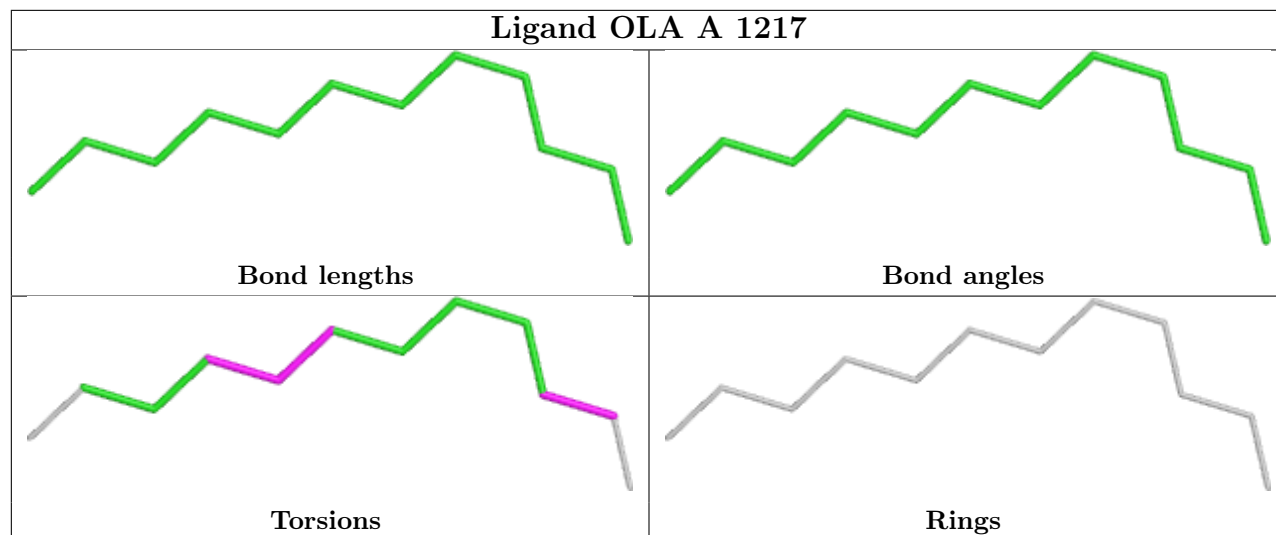
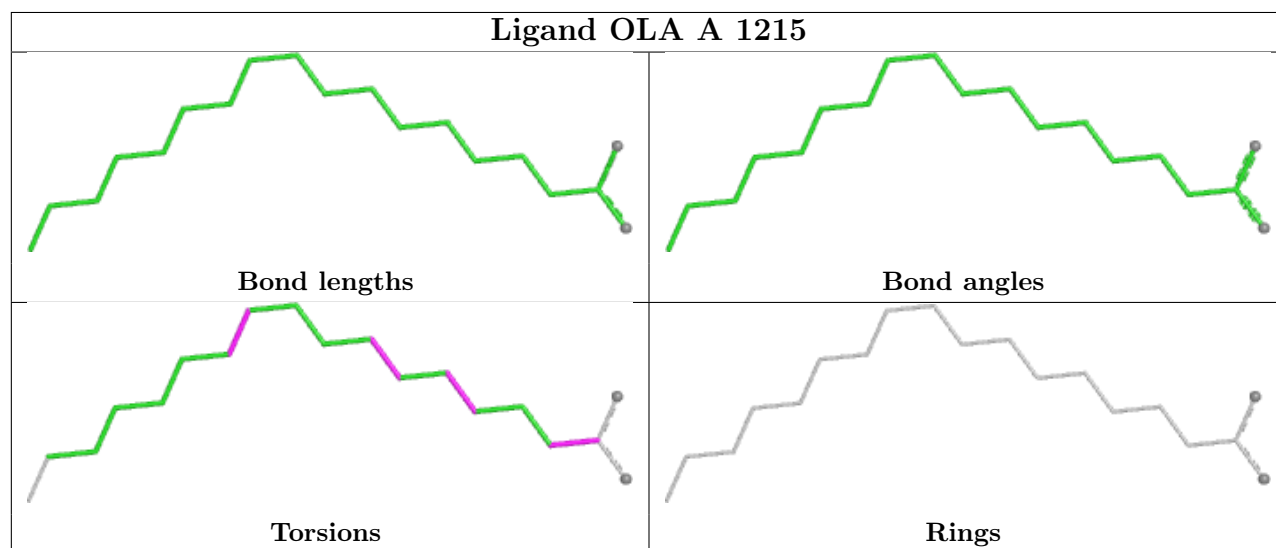
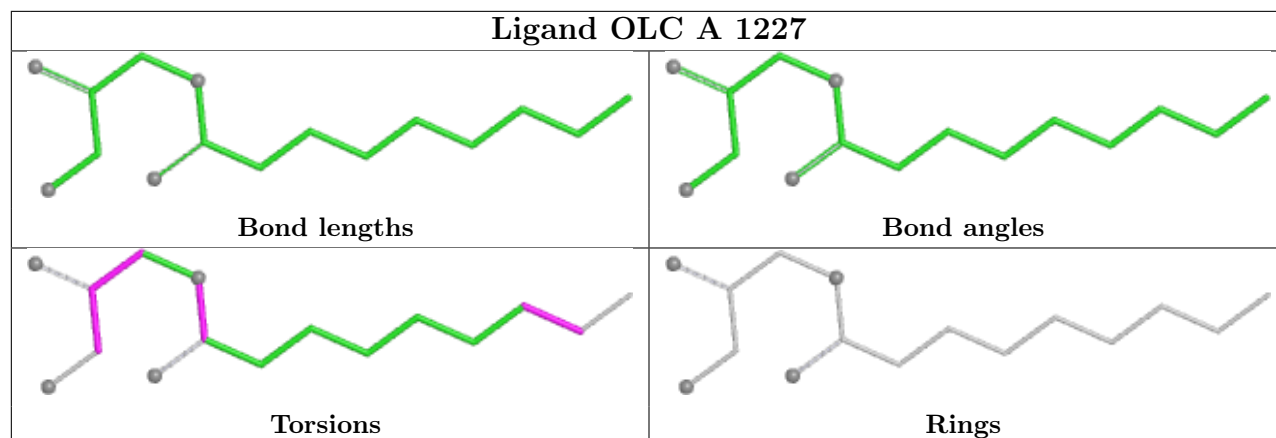


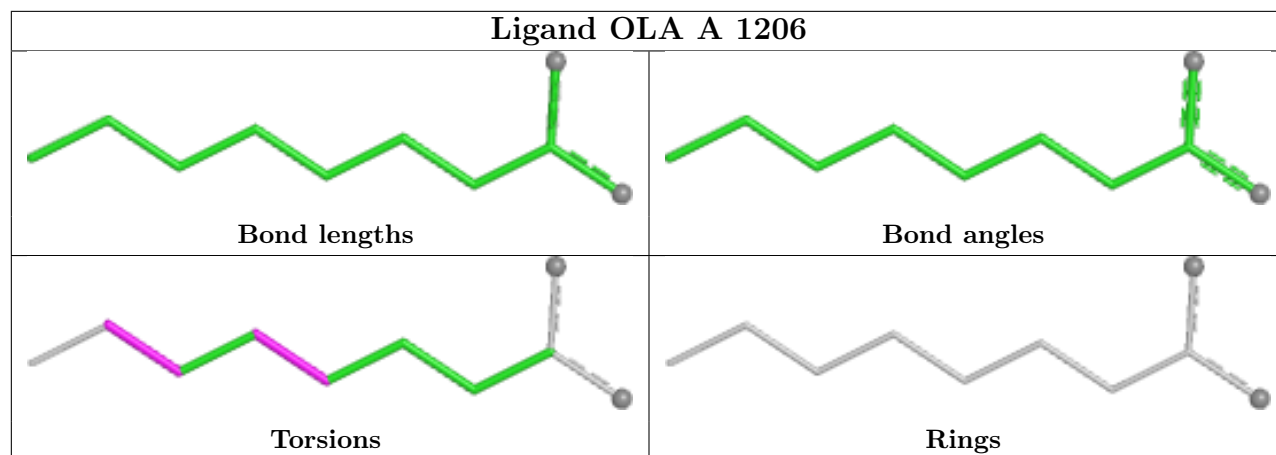












## 5.7 Other polymers [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	390/433 (90%)	0.85	35 (8%) 15 13	25, 67, 103, 130	14 (3%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	6[A]	SER	3.8
1	A	1017	ILE	3.8
1	A	1061	PHE	3.6
1	A	271	TYR	3.6
1	A	1059	LYS	3.5
1	A	1086	GLU	3.2
1	A	1021	ASP	3.2
1	A	1037	ALA	3.0
1	A	208	LEU	3.0
1	A	1026	VAL	3.0
1	A	1080	ASN	2.8
1	A	1084	VAL	2.8
1	A	306	HIS	2.8
1	A	308	LEU	2.8
1	A	1020	ALA	2.7
1	A	226	GLN	2.6
1	A	1082	GLY	2.5
1	A	1106	LEU	2.5
1	A	1060	ASP	2.5
1	A	307	VAL	2.4
1	A	1063	HIS	2.4
1	A	1105	TYR	2.4
1	A	43	TYR	2.3
1	A	157	GLN	2.2
1	A	1041	GLN	2.2
1	A	1023	ALA	2.2
1	A	1091	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1081	GLU	2.2
1	A	110	LEU	2.2
1	A	1078	LEU	2.2
1	A	1	PRO	2.1
1	A	202	ALA	2.0
1	A	205[A]	ARG	2.0
1	A	279[A]	THR	2.0
1	A	1070	GLY	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
4	OLA	A	1226	20/20	0.70	0.24	74,86,100,107	0
4	OLA	A	1206	10/20	0.71	0.18	72,87,98,110	0
4	OLA	A	1214	11/20	0.73	0.20	56,75,90,93	0
4	OLA	A	1216	20/20	0.74	0.19	56,77,91,94	0
4	OLA	A	1208	18/20	0.75	0.18	58,79,97,105	0
4	OLA	A	1212	8/20	0.76	0.15	66,71,81,81	0
4	OLA	A	1220	12/20	0.76	0.21	64,71,78,86	0
4	OLA	A	1207	9/20	0.76	0.21	49,62,83,88	0
4	OLA	A	1215	19/20	0.77	0.20	70,83,91,93	0
4	OLA	A	1225	13/20	0.77	0.16	60,79,97,105	0
4	OLA	A	1211	12/20	0.77	0.18	68,81,84,85	0
5	OLC	A	1231	23/25	0.77	0.17	61,75,106,109	0
5	OLC	A	1228	17/25	0.78	0.17	69,86,99,103	0
4	OLA	A	1223	15/20	0.78	0.21	64,76,95,106	0
4	OLA	A	1210	20/20	0.79	0.17	64,80,93,101	0

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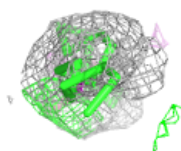
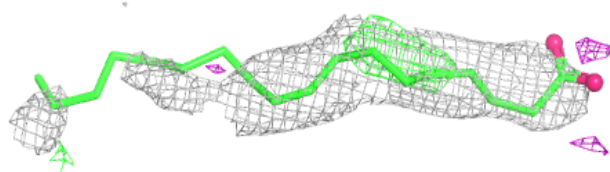
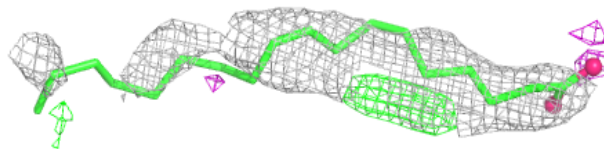
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	OLA	A	1209	20/20	0.79	0.15	50,81,92,94	0
4	OLA	A	1213	15/20	0.80	0.16	67,78,98,98	0
4	OLA	A	1217	12/20	0.80	0.19	67,76,83,89	0
4	OLA	A	1221	9/20	0.81	0.20	61,75,86,92	0
5	OLC	A	1232	18/25	0.81	0.18	62,81,104,109	0
4	OLA	A	1218	10/20	0.82	0.18	65,72,78,78	0
4	OLA	A	1222	8/20	0.83	0.16	67,74,78,79	0
4	OLA	A	1224	15/20	0.84	0.14	57,67,74,76	0
5	OLC	A	1229	23/25	0.85	0.15	63,71,100,102	0
4	OLA	A	1219	11/20	0.86	0.17	55,66,73,76	0
2	NA	A	1201	1/1	0.86	0.10	72,72,72,72	0
5	OLC	A	1233	16/25	0.86	0.15	53,73,81,82	0
5	OLC	A	1230	23/25	0.87	0.17	53,73,83,85	0
4	OLA	A	1205	20/20	0.89	0.16	56,69,89,97	0
5	OLC	A	1227	16/25	0.90	0.13	50,68,79,86	0
3	CLR	A	1202	28/28	0.92	0.15	55,63,71,77	0
3	CLR	A	1204	28/28	0.93	0.12	49,58,69,74	0
3	CLR	A	1203	28/28	0.93	0.13	44,57,69,77	0

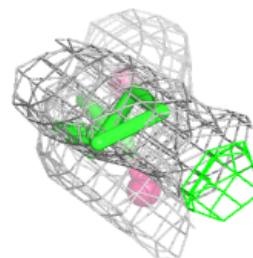
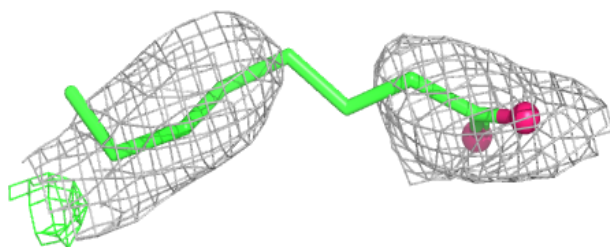
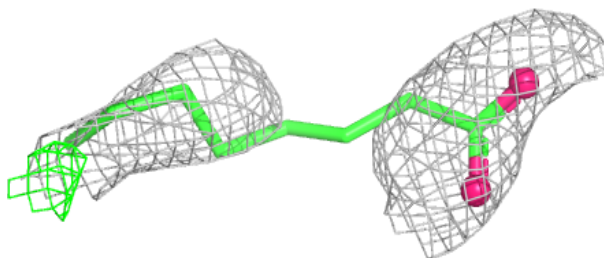
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around OLA A 1226:**

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

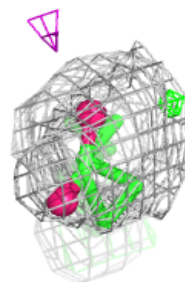
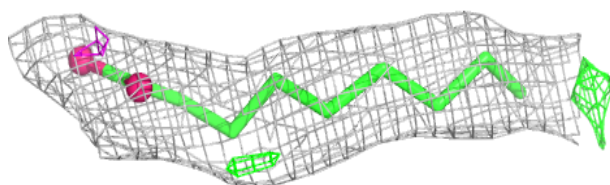
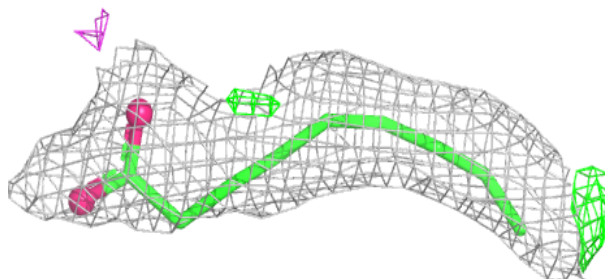
**Electron density around OLA A 1206:**

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

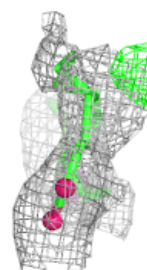
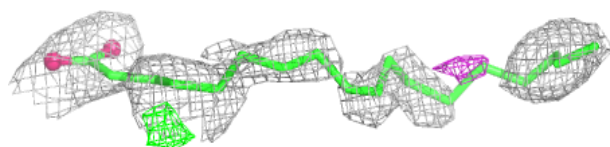
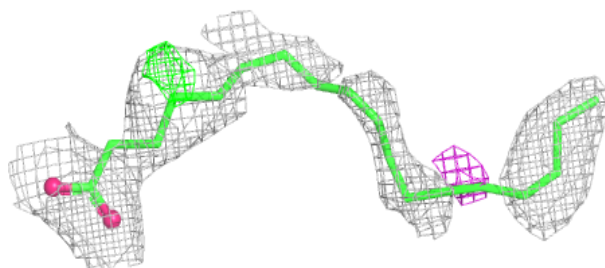


**Electron density around OLA A 1214:**

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

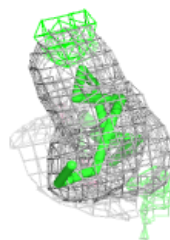
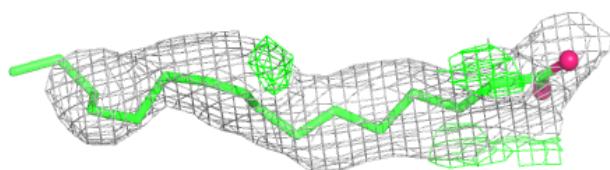
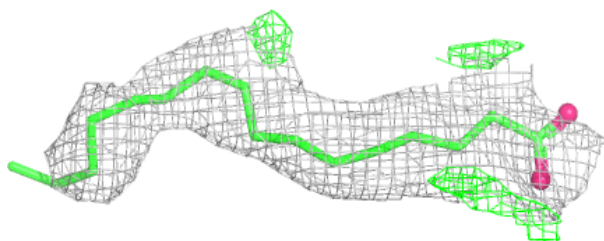
**Electron density around OLA A 1216:**

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

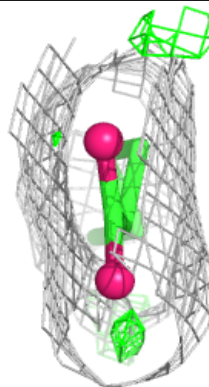
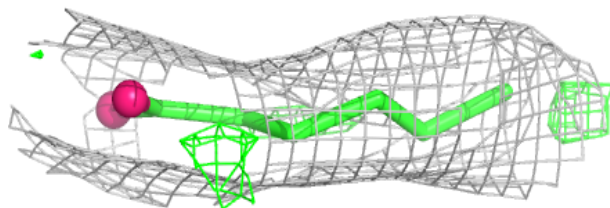
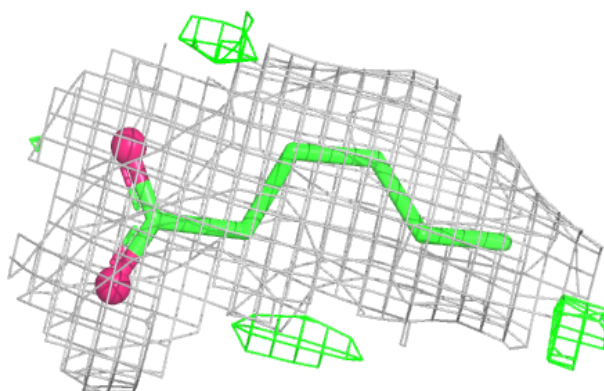


**Electron density around OLA A 1208:**

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

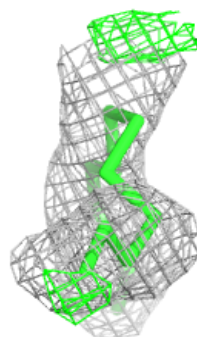
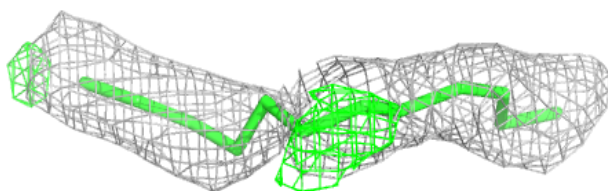
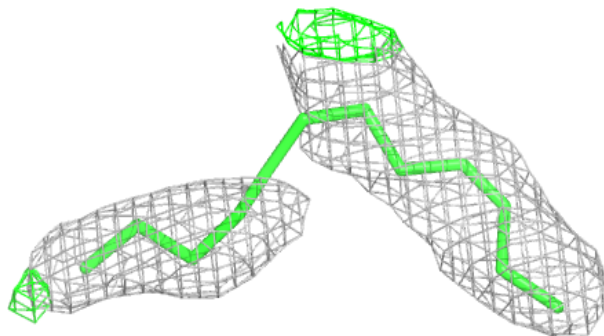
**Electron density around OLA A 1212:**

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

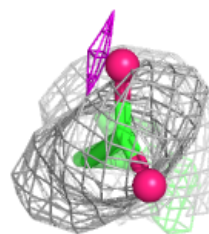
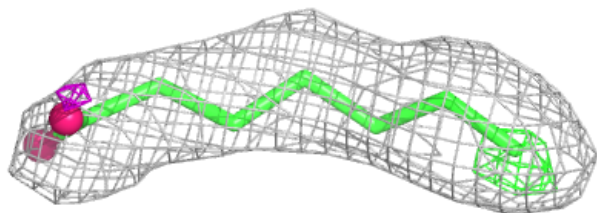
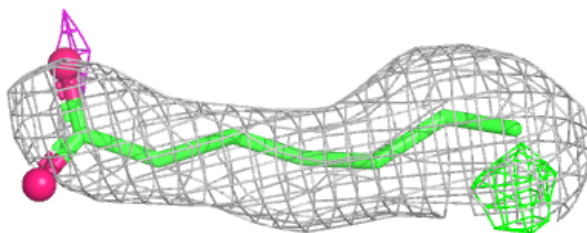


**Electron density around OLA A 1220:**

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

**Electron density around OLA A 1207:**

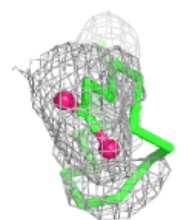
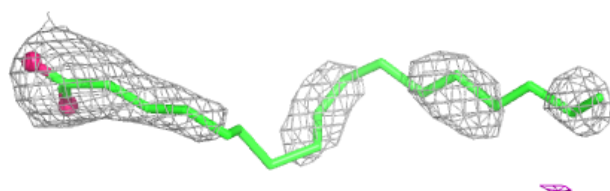
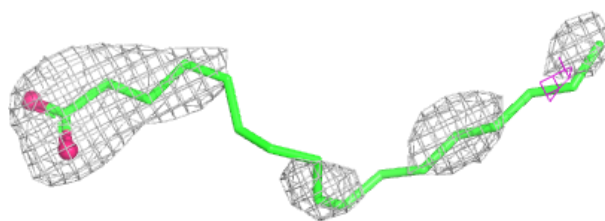
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



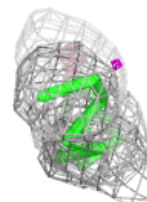
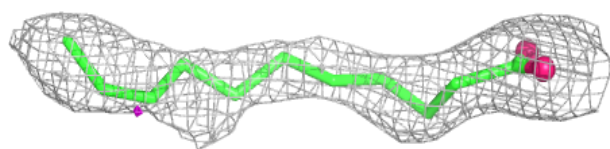
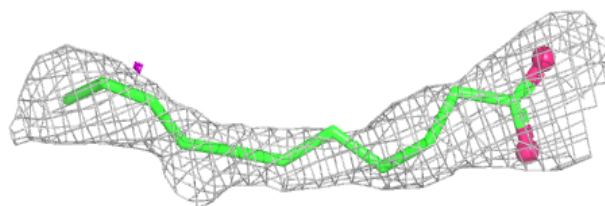


**Electron density around OLA A 1215:**

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

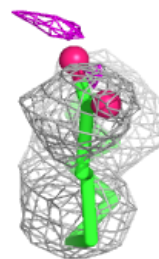
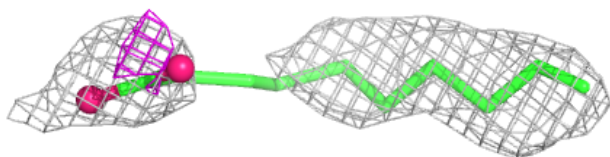
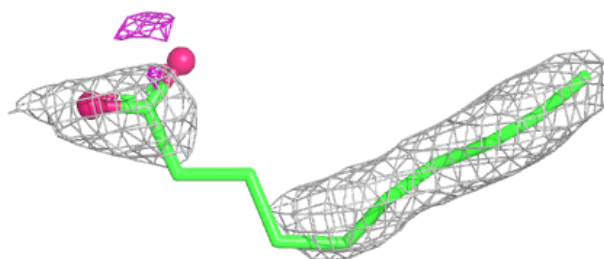
**Electron density around OLA A 1225:**

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and green (positive)

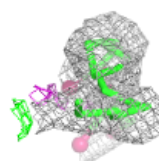
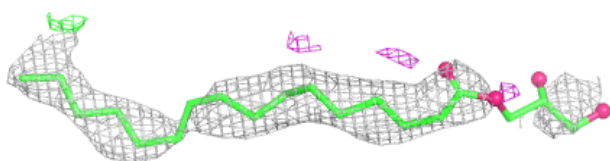
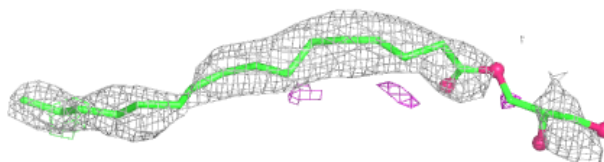


**Electron density around OLA A 1211:**

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

**Electron density around OLC A 1231:**

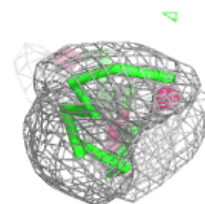
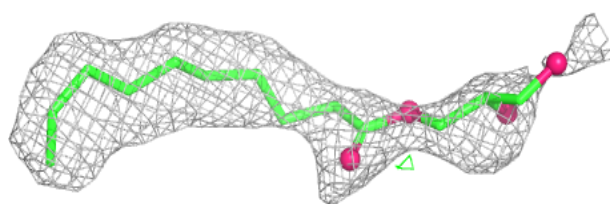
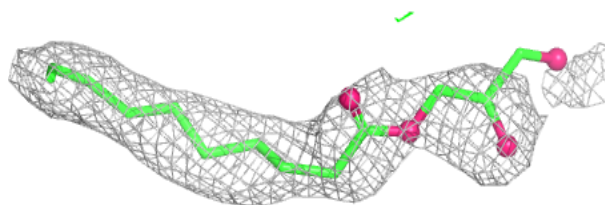
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



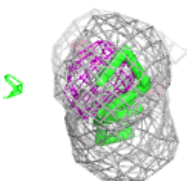
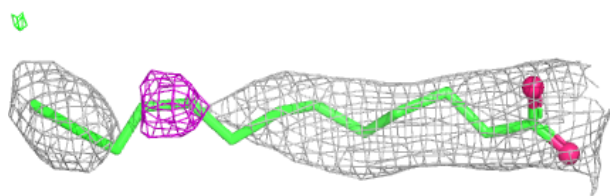
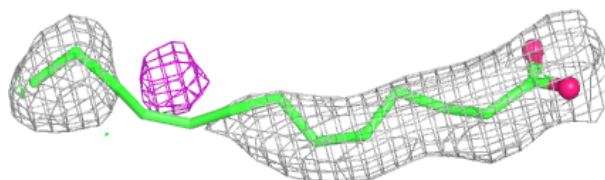


**Electron density around OLC A 1228:**

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and green (positive)

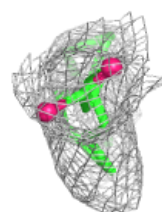
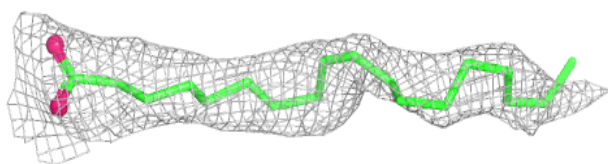
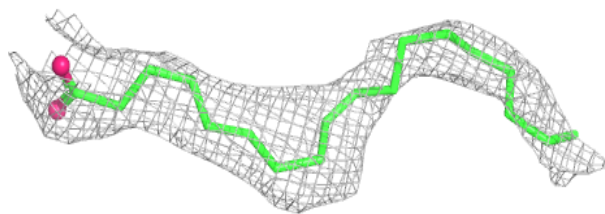
**Electron density around OLA A 1223:**

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and green (positive)

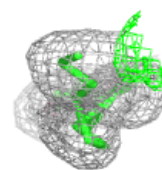
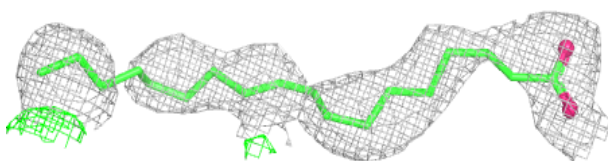
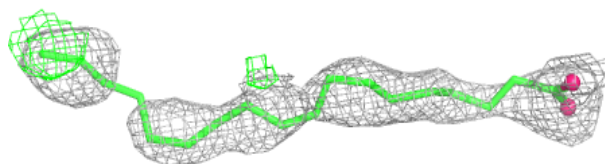


**Electron density around OLA A 1210:**

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

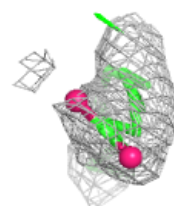
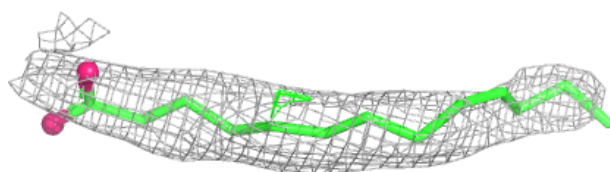
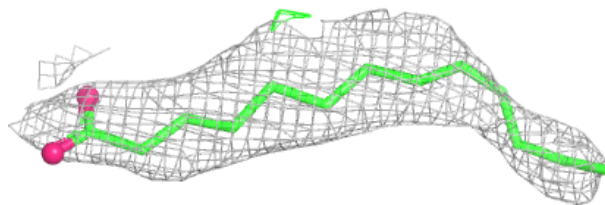
**Electron density around OLA A 1209:**

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

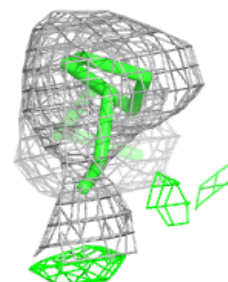
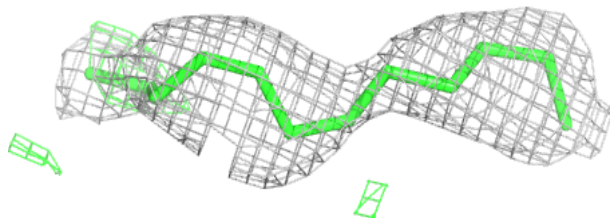
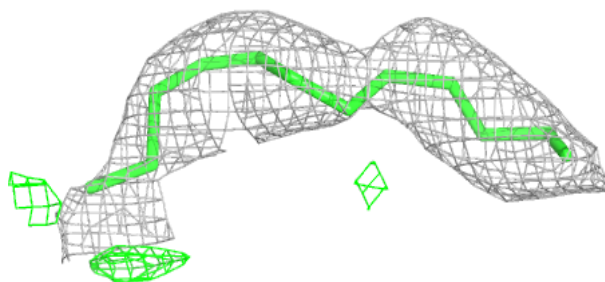


**Electron density around OLA A 1213:**

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

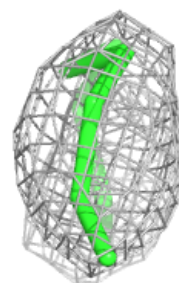
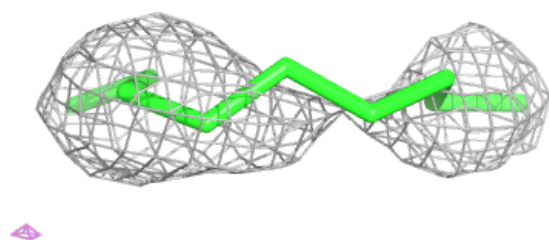
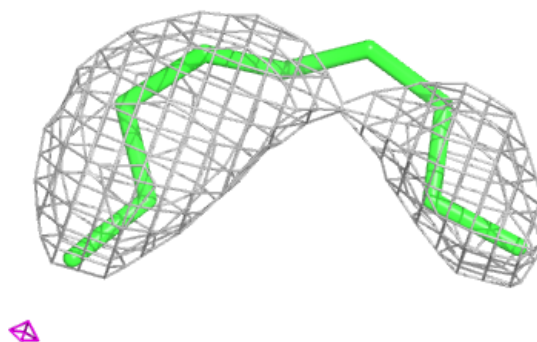
**Electron density around OLA A 1217:**

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

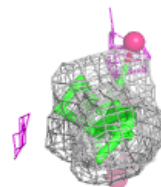
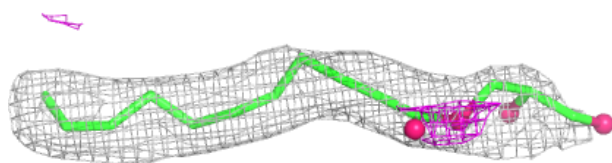
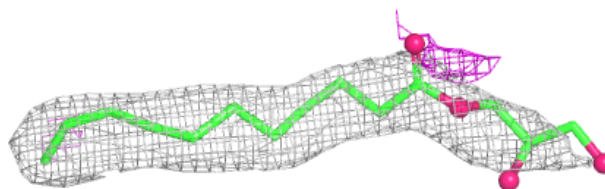


**Electron density around OLA A 1221:**

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

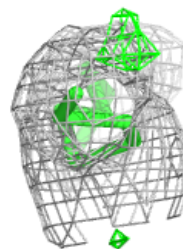
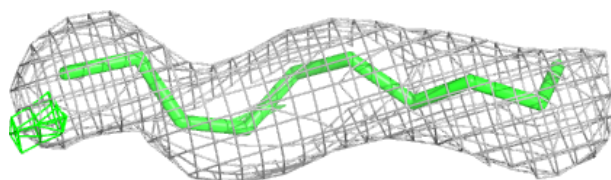
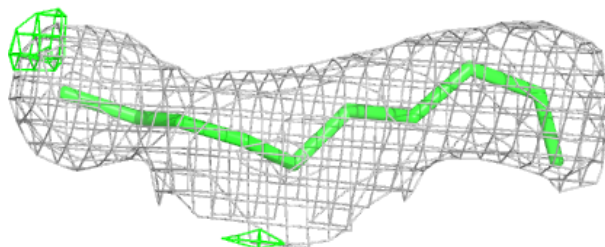
**Electron density around OLC A 1232:**

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

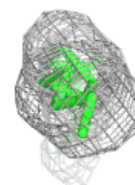
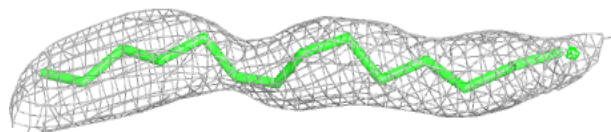
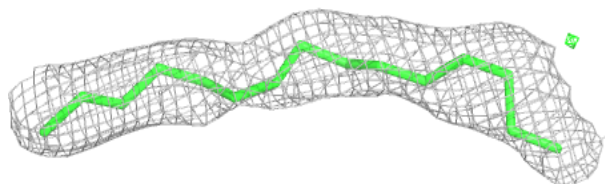


**Electron density around OLA A 1218:**

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

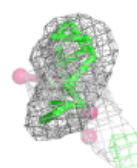
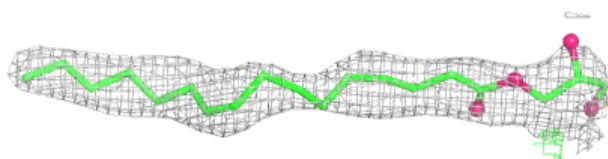
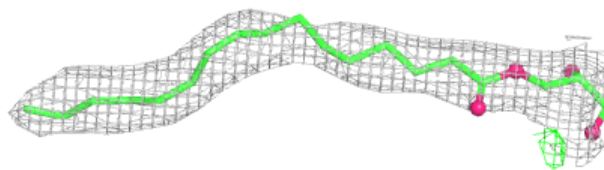
**Electron density around OLA A 1224:**

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

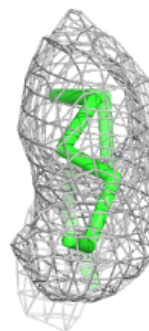
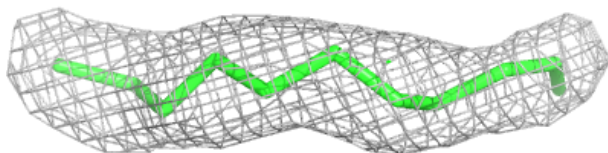
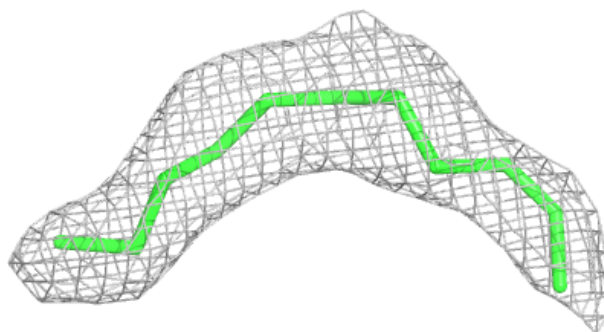


**Electron density around OLC A 1229:**

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

**Electron density around OLA A 1219:**

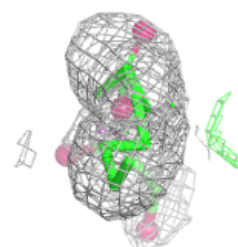
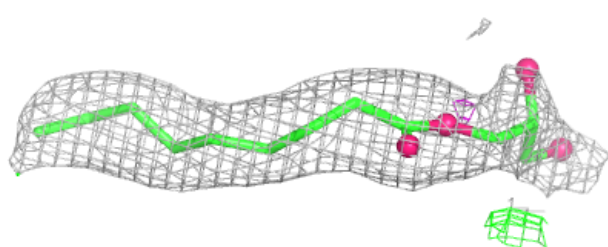
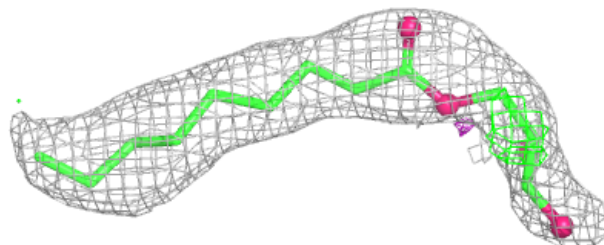
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



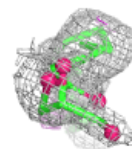
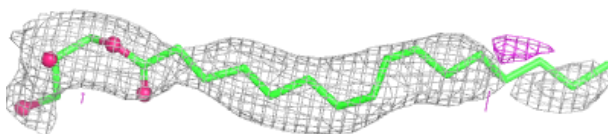
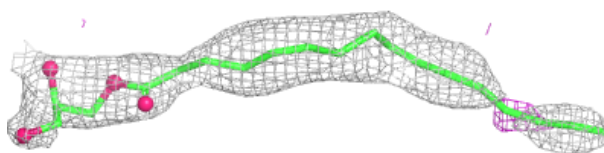


**Electron density around OLC A 1233:**

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

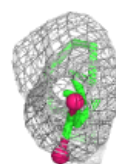
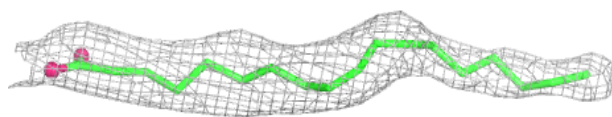
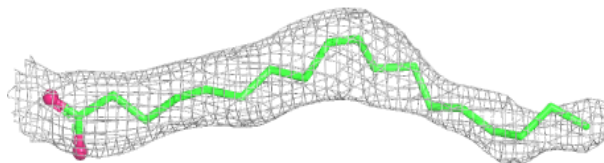
**Electron density around OLC A 1230:**

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

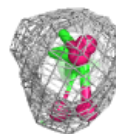
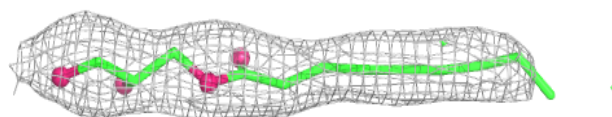
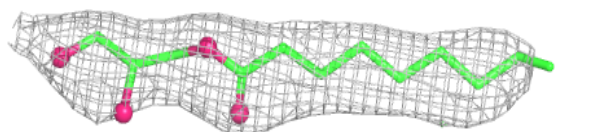


**Electron density around OLA A 1205:**

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

**Electron density around OLC A 1227:**

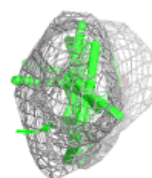
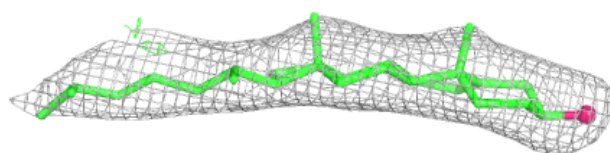
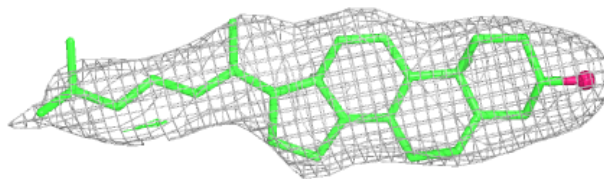
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



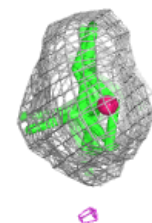
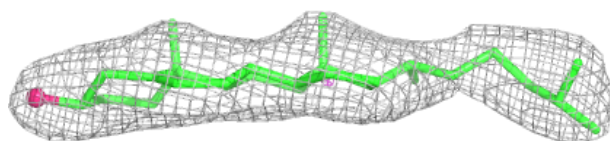
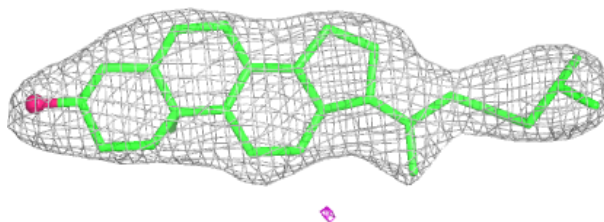


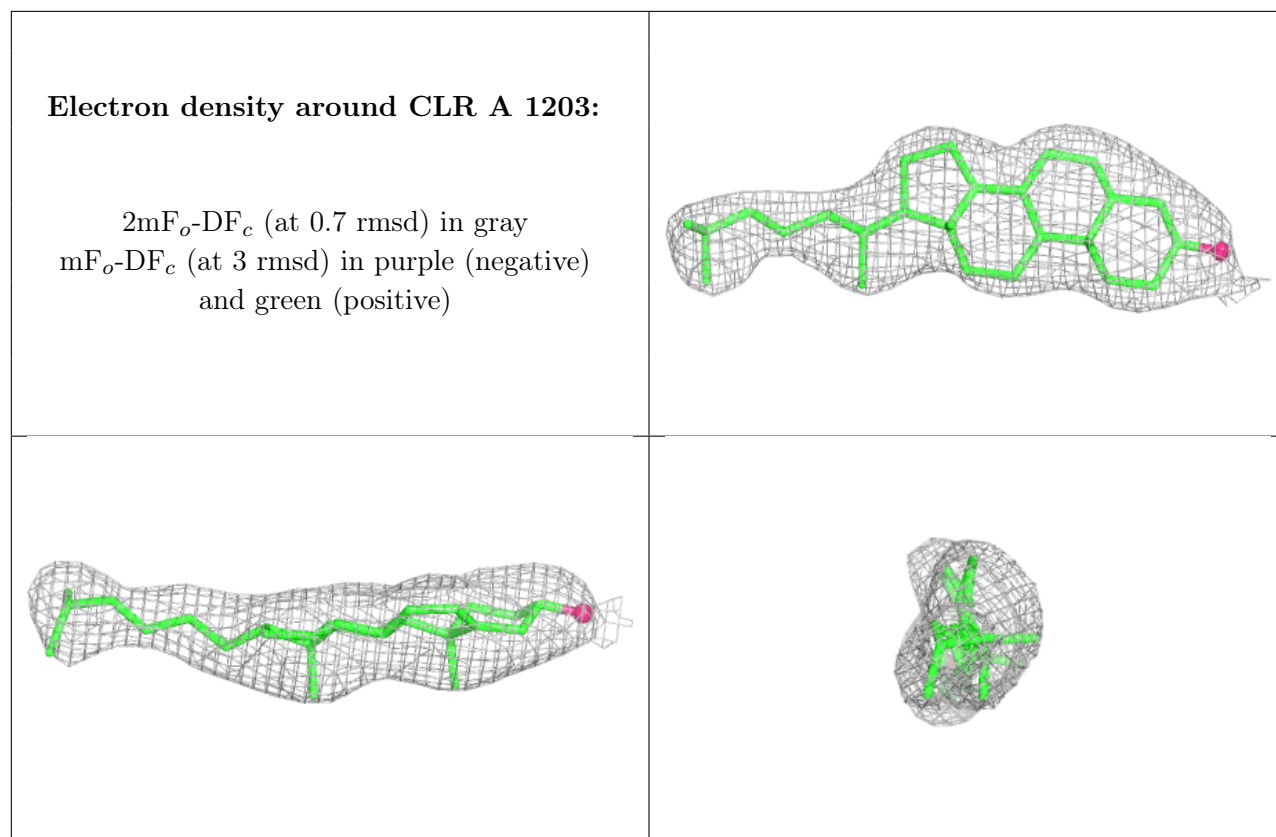
**Electron density around CLR A 1202:**

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

**Electron density around CLR A 1204:**

$2mF_o-DF_c$  (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.