



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2026 – 06:51 PM EDT

PDB ID : 7IP7 / pdb\_00007ip7  
Title : Crystal structure of A2A in complex with FU293-87  
Authors : Huang, C.-Y.; Cheng, R.Y.K.; Metz, A.  
Deposited on : 2025-08-21  
Resolution : 2.32 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

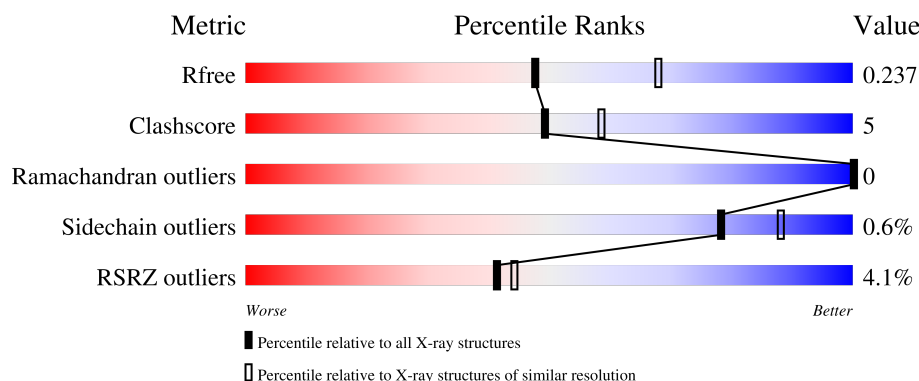
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.32 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	7754 (2.34-2.30)
Clashscore	190562	8383 (2.34-2.30)
Ramachandran outliers	187476	8303 (2.34-2.30)
Sidechain outliers	187428	8303 (2.34-2.30)
RSRZ outliers	180081	7760 (2.34-2.30)

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	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	TEP	A	1202	-	X	-	-

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 3730 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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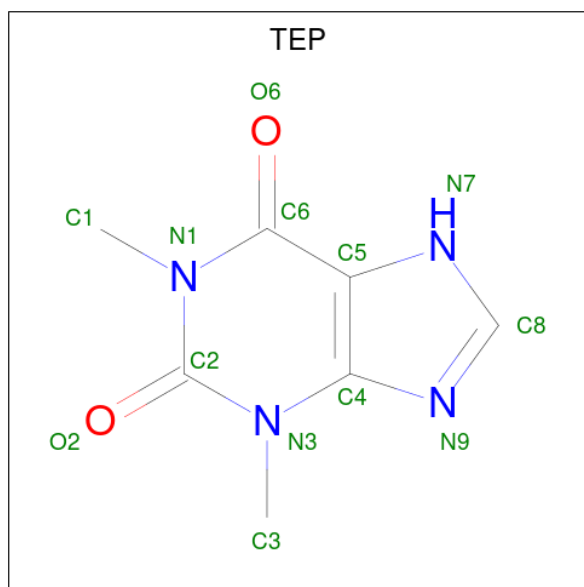
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Chain	Residue	Modelled	Actual	Comment	Reference
A	320	HIS	-	expression tag	UNP P29274
A	321	HIS	-	expression tag	UNP P29274
A	322	HIS	-	expression tag	UNP P29274
A	323	HIS	-	expression tag	UNP P29274
A	324	HIS	-	expression tag	UNP P29274
A	325	HIS	-	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).

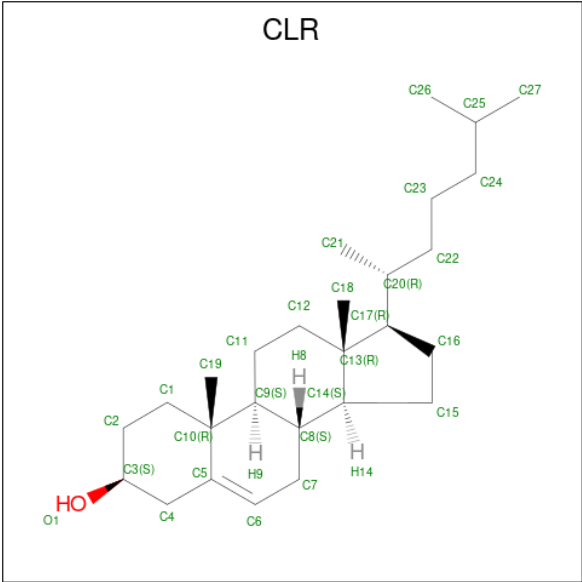
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		

- Molecule 3 is THEOPHYLLINE (CCD ID: TEP) (formula: C<sub>7</sub>H<sub>8</sub>N<sub>4</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



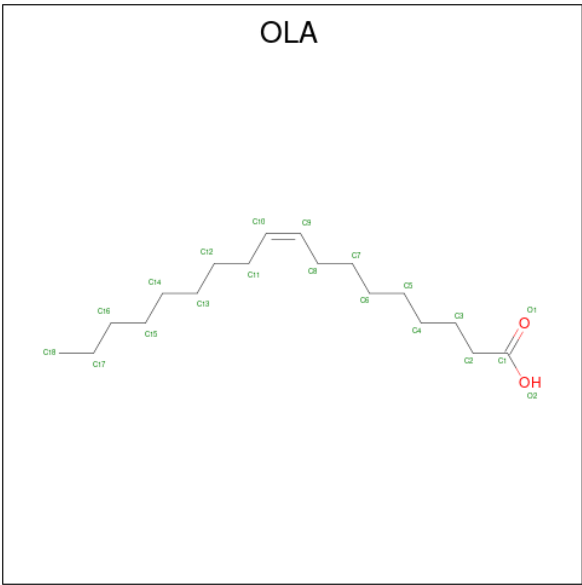
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			13	7	4	2		

- Molecule 4 is CHOLESTEROL (CCD ID: CLR) (formula: C<sub>27</sub>H<sub>46</sub>O).



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

- Molecule 5 is OLEIC ACID (CCD ID: OLA) (formula:  $C_{18}H_{34}O_2$ ).



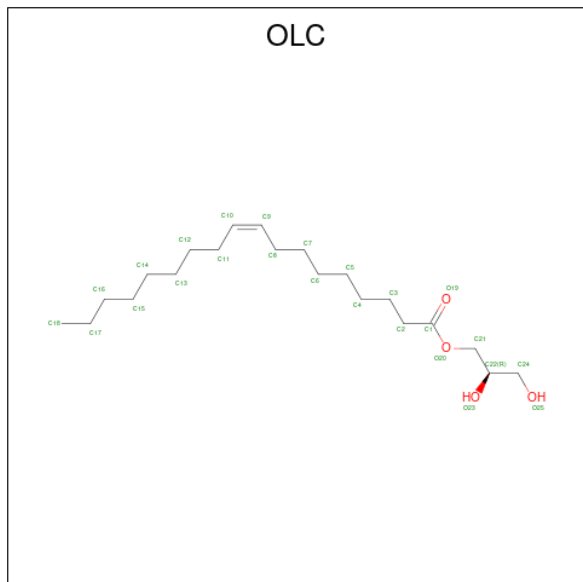
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			20	18	2		

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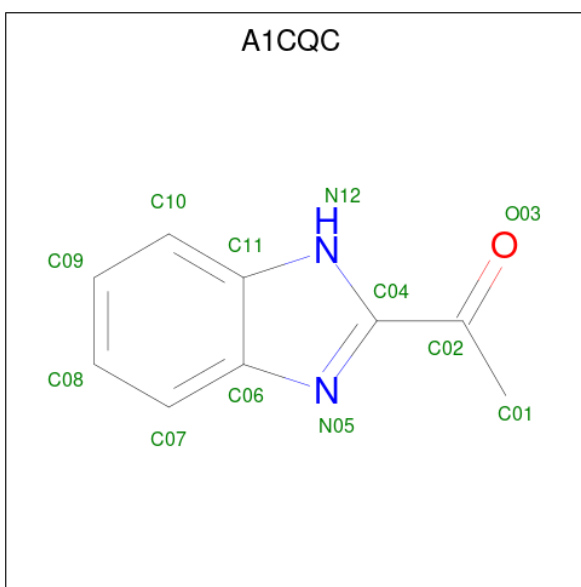
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 10 8 2	0	0
5	A	1	Total C O 9 7 2	0	0
5	A	1	Total C O 18 16 2	0	0
5	A	1	Total C O 20 18 2	0	0
5	A	1	Total C O 20 18 2	0	0
5	A	1	Total C O 12 10 2	0	0
5	A	1	Total C O 8 6 2	0	0
5	A	1	Total C O 15 13 2	0	0
5	A	1	Total C O 11 9 2	0	0
5	A	1	Total C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

- Molecule 6 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (CCD ID: OLC) (formula:  $C_{21}H_{40}O_4$ ).



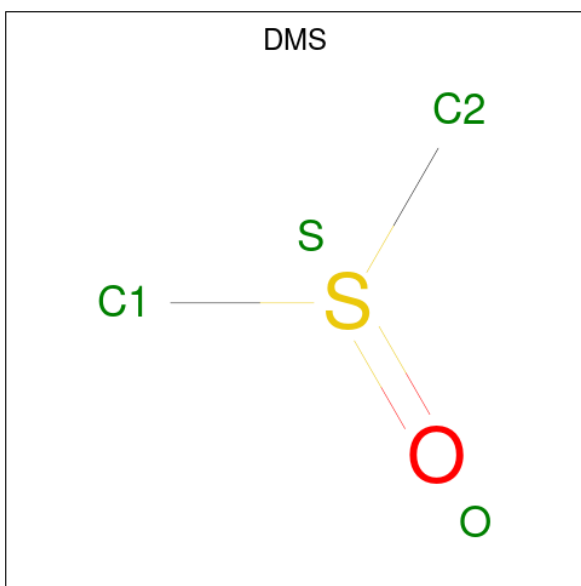
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			16	12	4		
6	A	1	Total	C	O	0	0
			17	13	4		
6	A	1	Total	C	O	0	0
			23	19	4		
6	A	1	Total	C	O	0	0
			23	19	4		
6	A	1	Total	C	O	0	0
			23	19	4		
6	A	1	Total	C	O	0	0
			18	14	4		
6	A	1	Total	C	O	0	0
			16	12	4		

- Molecule 7 is 1-(1H-1,3-benzimidazol-2-yl)ethan-1-one (CCD ID: A1CQC) (formula:  $C_9H_8N_2O$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			12	9	2	1		

- Molecule 8 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula:  $C_2H_6OS$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	O	S	0	1
			4	2	1	1		
8	A	1	Total	C	O	S	0	1
			4	2	1	1		

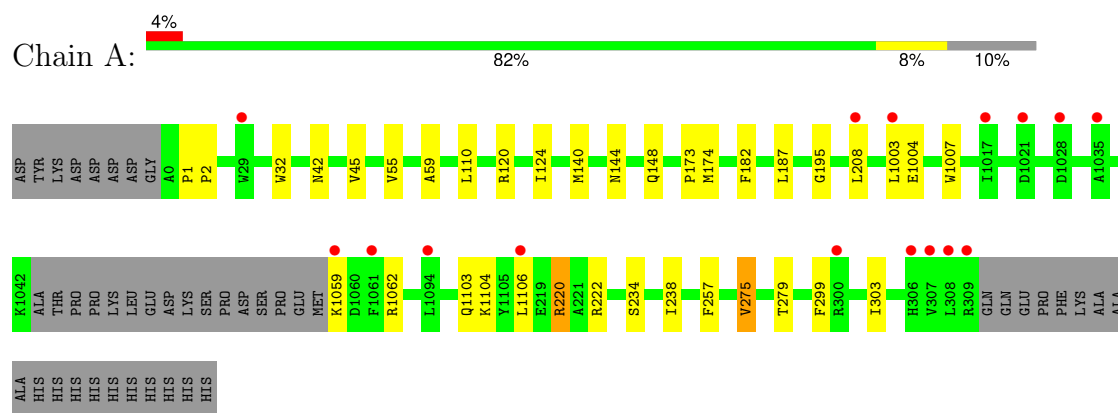
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	43	Total 43	O 43	0	0

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 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, $\alpha$ , $\beta$ , $\gamma$	39.24Å 179.36Å 139.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	89.68 – 2.32 89.68 – 2.32	Depositor EDS
% Data completeness (in resolution range)	85.1 (89.68-2.32) 85.4 (89.68-2.32)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.40 (at 2.32Å)	Xtriage
Refinement program	PHENIX (1.20_4459: ???)	Depositor
R, $R_{free}$	0.202 , 0.238 0.201 , 0.237	Depositor DCC
$R_{free}$ test set	921 reflections (4.18%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	40.6	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 53.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3730	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.36% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: A1CQC, TEP, NA, DMS, OLA, OLC, CLR

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	0.16	0/3191	0.34	1/4338 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	148	GLN	CA-CB-CG	-5.52	103.06	114.10

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3126	0	3206	27	0
2	A	1	0	0	0	0
3	A	13	0	8	0	0
4	A	84	0	138	0	0
5	A	307	0	459	15	0
6	A	136	0	186	5	0
7	A	12	0	0	0	0
8	A	8	0	12	0	0
9	A	43	0	0	0	0
All	All	3730	0	4009	42	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 5.

All (42) 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:1106:LEU:HD11	1:A:222:ARG:HH21	1.41	0.85
1:A:1059:LYS:HA	1:A:1062:ARG:HE	1.54	0.72
5:A:1223:OLA:H41	5:A:1225:OLA:H152	1.74	0.67
5:A:1210:OLA:H21	5:A:1217:OLA:H32	1.80	0.62
1:A:110:LEU:HD23	1:A:110:LEU:H	1.65	0.61
1:A:1062:ARG:HD3	1:A:1062:ARG:H	1.66	0.60
5:A:1226:OLA:H62	6:A:1234:OLC:H3A	1.84	0.58
1:A:1007:TRP:CH2	1:A:1103:GLN:HG3	2.38	0.58
1:A:1059:LYS:HA	1:A:1062:ARG:NE	2.19	0.57
1:A:275[B]:VAL:O	1:A:279[B]:THR:HG23	2.08	0.53
5:A:1211:OLA:H183	5:A:1222:OLA:H121	1.89	0.53
5:A:1223:OLA:H51	5:A:1227:OLA:H131	1.90	0.53
1:A:55:VAL:HA	1:A:59:ALA:HB3	1.91	0.53
1:A:140[A]:MET:HE2	5:A:1226:OLA:H52	1.90	0.53
6:A:1230:OLC:H4A	6:A:1231:OLC:H2	1.91	0.51
1:A:1106:LEU:HD11	1:A:222:ARG:NH2	2.21	0.48
1:A:140[B]:MET:HE3	5:A:1226:OLA:H71	1.97	0.46
1:A:32:TRP:CE3	5:A:1216:OLA:H71	2.52	0.45
1:A:174[A]:MET:HG3	1:A:257:PHE:HB2	1.97	0.45
1:A:42:ASN:HA	1:A:45:VAL:HB	1.98	0.45
5:A:1227:OLA:H82	5:A:1227:OLA:H112	1.74	0.44
1:A:220:ARG:HD3	1:A:220:ARG:HA	1.70	0.44
1:A:1004:GLU:OE2	1:A:222:ARG:NH2	2.49	0.44
1:A:120:ARG:O	1:A:124:ILE:HG13	2.17	0.44
6:A:1230:OLC:H15	6:A:1231:OLC:H14	2.00	0.43
1:A:1106:LEU:HD21	1:A:222:ARG:NH2	2.33	0.43
1:A:1104:LYS:HD3	1:A:1104:LYS:HA	1.66	0.43
6:A:1233:OLC:H2A	6:A:1233:OLC:H5A	1.75	0.43
5:A:1210:OLA:H61	5:A:1210:OLA:H9	1.84	0.42
5:A:1223:OLA:C9	5:A:1226:OLA:H72	2.49	0.42
1:A:299:PHE:O	1:A:303:ILE:HD12	2.19	0.42
5:A:1210:OLA:H122	5:A:1217:OLA:H151	2.02	0.42
1:A:208:LEU:HA	1:A:1003:LEU:HD12	2.01	0.42
1:A:182:PHE:CE1	1:A:187[B]:LEU:HG	2.55	0.41
1:A:234:SER:O	1:A:238:ILE:HG12	2.20	0.41
5:A:1210:OLA:H151	5:A:1217:OLA:H151	2.02	0.41
5:A:1211:OLA:H82	5:A:1211:OLA:H112	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1232:OLC:H10	6:A:1232:OLC:H13A	1.76	0.41
1:A:110:LEU:H	1:A:110:LEU:CD2	2.34	0.40
1:A:144:ASN:HA	1:A:173:PRO:HD3	2.04	0.40
1:A:1:PRO:HA	1:A:2:PRO:HD3	1.94	0.40
1:A:195:GLY:CA	5:A:1207:OLA:H42	2.50	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%)	395 (99%)	4 (1%)	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%)	326 (99%)	3 (1%)	70 83

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	220	ARG

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Mol	Chain	Res	Type
1	A	275[A]	VAL
1	A	275[B]	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	36	ASN
1	A	157	GLN
1	A	1013	ASN
1	A	226	GLN
1	A	280	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no 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	$\# Z  > 2$
5	OLA	A	1221	-	11,11,19	0.39	0	10,10,19	0.80	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	OLA	A	1222	-	8,8,19	0.30	0	7,7,19	0.84	0
5	OLA	A	1218	-	11,11,19	0.36	0	10,10,19	0.66	0
5	OLA	A	1223	-	7,7,19	0.30	0	6,6,19	0.84	0
6	OLC	A	1234	-	15,15,24	1.25	1 (6%)	16,16,25	0.98	1 (6%)
5	OLA	A	1214	-	14,14,19	0.65	0	14,14,19	1.16	1 (7%)
5	OLA	A	1206	-	19,19,19	0.58	0	19,19,19	1.03	1 (5%)
6	OLC	A	1230	-	22,22,24	1.07	1 (4%)	23,23,25	1.30	1 (4%)
5	OLA	A	1217	-	19,19,19	0.61	0	19,19,19	0.86	0
4	CLR	A	1204	-	31,31,31	0.30	0	48,48,48	0.42	0
6	OLC	A	1228	-	15,15,24	1.25	1 (6%)	16,16,25	1.34	1 (6%)
5	OLA	A	1208	-	8,8,19	0.83	0	8,8,19	1.25	0
6	OLC	A	1232	-	22,22,24	1.11	1 (4%)	23,23,25	1.32	2 (8%)
5	OLA	A	1210	-	19,19,19	0.61	0	19,19,19	0.97	1 (5%)
6	OLC	A	1233	-	17,17,24	1.27	1 (5%)	18,18,25	1.30	2 (11%)
5	OLA	A	1212	-	11,11,19	0.75	0	11,11,19	1.16	0
5	OLA	A	1224	-	14,14,19	0.68	0	14,14,19	1.01	0
5	OLA	A	1226	-	12,12,19	0.73	0	12,12,19	1.13	0
5	OLA	A	1219	-	9,9,19	0.41	0	8,8,19	0.72	0
6	OLC	A	1231	-	22,22,24	1.05	1 (4%)	23,23,25	1.37	3 (13%)
5	OLA	A	1209	-	17,17,19	0.59	0	17,17,19	1.06	0
5	OLA	A	1227	-	19,19,19	0.58	0	19,19,19	1.09	0
4	CLR	A	1203	-	31,31,31	0.31	0	48,48,48	0.46	0
5	OLA	A	1213	-	7,7,19	0.86	0	7,7,19	1.28	1 (14%)
4	CLR	A	1205	-	31,31,31	0.28	0	48,48,48	0.40	0
5	OLA	A	1211	-	19,19,19	0.58	0	19,19,19	1.04	1 (5%)
5	OLA	A	1216	-	18,18,19	0.60	0	18,18,19	1.04	1 (5%)
5	OLA	A	1215	-	10,10,19	0.71	0	10,10,19	1.28	0
5	OLA	A	1220	-	10,10,19	0.44	0	9,9,19	0.77	0
5	OLA	A	1225	-	14,14,19	0.38	0	13,13,19	0.64	0
3	TEP	A	1202	-	14,14,14	1.80	4 (28%)	21,21,21	3.26	12 (57%)
5	OLA	A	1207	-	9,9,19	0.78	0	9,9,19	1.14	0
7	A1CQC	A	1235	-	13,13,13	1.53	2 (15%)	18,18,18	1.81	3 (16%)
6	OLC	A	1229	-	16,16,24	1.31	1 (6%)	17,17,25	1.29	2 (11%)

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
5	OLA	A	1221	-	-	3/9/9/17	-
5	OLA	A	1222	-	-	2/6/6/17	-
5	OLA	A	1218	-	-	4/9/9/17	-
5	OLA	A	1223	-	-	1/5/5/17	-
6	OLC	A	1234	-	-	4/15/15/24	-
5	OLA	A	1214	-	-	4/12/12/17	-
5	OLA	A	1206	-	-	10/17/17/17	-
6	OLC	A	1230	-	-	11/22/22/24	-
5	OLA	A	1217	-	-	7/17/17/17	-
4	CLR	A	1204	-	-	0/10/68/68	0/4/4/4
6	OLC	A	1228	-	-	8/15/15/24	-
5	OLA	A	1208	-	-	3/6/6/17	-
6	OLC	A	1232	-	-	12/22/22/24	-
5	OLA	A	1210	-	-	12/17/17/17	-
6	OLC	A	1233	-	-	8/17/17/24	-
5	OLA	A	1212	-	-	5/9/9/17	-
5	OLA	A	1224	-	-	5/12/12/17	-
5	OLA	A	1226	-	-	6/10/10/17	-
5	OLA	A	1219	-	-	1/7/7/17	-
6	OLC	A	1231	-	-	12/22/22/24	-
5	OLA	A	1209	-	-	8/15/15/17	-
5	OLA	A	1227	-	-	12/17/17/17	-
4	CLR	A	1203	-	-	0/10/68/68	0/4/4/4
5	OLA	A	1213	-	-	1/5/5/17	-
4	CLR	A	1205	-	-	1/10/68/68	0/4/4/4
5	OLA	A	1211	-	-	8/17/17/17	-
5	OLA	A	1216	-	-	2/16/16/17	-
5	OLA	A	1215	-	-	3/8/8/17	-
5	OLA	A	1220	-	-	5/8/8/17	-
5	OLA	A	1225	-	-	2/12/12/17	-
3	TEP	A	1202	-	-	-	0/2/2/2
5	OLA	A	1207	-	-	3/7/7/17	-
7	A1CQC	A	1235	-	-	1/4/4/4	0/2/2/2
6	OLC	A	1229	-	-	8/16/16/24	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1202	TEP	C6-N1	-3.48	1.33	1.40
6	A	1233	OLC	O20-C1	3.00	1.42	1.33
6	A	1229	OLC	O20-C1	2.99	1.42	1.33
6	A	1234	OLC	O20-C1	2.97	1.42	1.33
6	A	1228	OLC	O20-C1	2.96	1.42	1.33
6	A	1232	OLC	O20-C1	2.91	1.41	1.33
6	A	1230	OLC	O20-C1	2.83	1.41	1.33
6	A	1231	OLC	O20-C1	2.73	1.41	1.33
3	A	1202	TEP	C5-N7	-2.43	1.34	1.38
7	A	1235	A1CQC	C04-N12	-2.21	1.33	1.36
3	A	1202	TEP	O2-C2	-2.11	1.18	1.22
3	A	1202	TEP	C5-C6	-2.11	1.38	1.42
7	A	1235	A1CQC	C02-C04	2.07	1.53	1.49

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1202	TEP	C4-C5-N7	6.23	108.36	105.29
3	A	1202	TEP	C5-C6-N1	5.72	119.74	112.07
3	A	1202	TEP	C8-N9-C4	5.55	107.17	103.45
3	A	1202	TEP	C5-C4-N9	-4.66	108.36	111.63
7	A	1235	A1CQC	C06-N05-C04	4.16	108.90	104.68
7	A	1235	A1CQC	N12-C04-N05	-4.14	108.79	113.22
3	A	1202	TEP	C5-C4-N3	-3.96	119.49	121.73
3	A	1202	TEP	C6-N1-C2	-3.75	119.56	125.66
3	A	1202	TEP	N3-C4-N9	3.74	132.14	126.27
6	A	1232	OLC	C8-C9-C10	3.59	151.69	124.83
6	A	1230	OLC	C8-C9-C10	3.58	151.66	124.83
3	A	1202	TEP	C6-C5-C4	-3.47	120.39	123.13
6	A	1229	OLC	C8-C9-C10	3.47	151.95	126.65
3	A	1202	TEP	O6-C6-C5	-3.45	119.61	126.64
3	A	1202	TEP	N7-C8-N9	-3.44	108.99	112.98
6	A	1228	OLC	O20-C1-C2	3.39	122.17	111.83
6	A	1231	OLC	C8-C9-C10	3.20	148.81	124.83
3	A	1202	TEP	N3-C2-N1	2.96	120.84	117.14
6	A	1233	OLC	C8-C9-C10	2.89	152.34	130.48
6	A	1232	OLC	O20-C1-C2	2.78	120.31	111.83
6	A	1233	OLC	O20-C1-C2	2.59	119.72	111.83
6	A	1231	OLC	O20-C1-C2	2.53	119.54	111.83
6	A	1234	OLC	O20-C1-C2	2.49	119.42	111.83
6	A	1229	OLC	O20-C1-C2	2.44	119.29	111.83
6	A	1231	OLC	C11-C10-C9	-2.25	108.00	124.83
7	A	1235	A1CQC	C02-C04-N12	2.22	125.62	121.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1206	OLA	C3-C2-C1	-2.22	108.72	114.51
5	A	1214	OLA	C3-C2-C1	-2.18	108.81	114.51
5	A	1211	OLA	C3-C2-C1	-2.17	108.85	114.51
3	A	1202	TEP	O2-C2-N3	-2.07	118.48	121.33
5	A	1216	OLA	O2-C1-C2	2.04	120.46	114.00
5	A	1210	OLA	O2-C1-C2	2.01	120.37	114.00
5	A	1213	OLA	O2-C1-C2	2.01	120.36	114.00

There are no chirality outliers.

All (172) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1211	OLA	C6-C7-C8-C9
5	A	1218	OLA	C6-C7-C8-C9
6	A	1230	OLC	C21-C22-C24-O25
6	A	1231	OLC	C21-C22-C24-O25
6	A	1231	OLC	O20-C21-C22-O23
6	A	1232	OLC	O20-C21-C22-C24
6	A	1233	OLC	O20-C21-C22-O23
6	A	1233	OLC	O19-C1-O20-C21
6	A	1233	OLC	C2-C1-O20-C21
6	A	1232	OLC	C2-C1-O20-C21
6	A	1232	OLC	O19-C1-O20-C21
5	A	1226	OLA	C1-C2-C3-C4
6	A	1228	OLC	O20-C21-C22-O23
6	A	1232	OLC	O20-C21-C22-O23
5	A	1224	OLA	C1-C2-C3-C4
6	A	1234	OLC	C1-C2-C3-C4
6	A	1232	OLC	C10-C11-C12-C13
6	A	1228	OLC	O20-C21-C22-C24
6	A	1231	OLC	O20-C21-C22-C24
4	A	1205	CLR	C20-C22-C23-C24
5	A	1227	OLA	C11-C12-C13-C14
6	A	1232	OLC	C1-C2-C3-C4
6	A	1231	OLC	C12-C13-C14-C15
6	A	1230	OLC	O23-C22-C24-O25
6	A	1231	OLC	O23-C22-C24-O25
5	A	1216	OLA	C5-C6-C7-C8
5	A	1218	OLA	C12-C13-C14-C15
6	A	1230	OLC	C3-C4-C5-C6
6	A	1233	OLC	C5-C6-C7-C8
6	A	1229	OLC	C1-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
5	A	1220	OLA	C11-C12-C13-C14
5	A	1224	OLA	C5-C6-C7-C8
5	A	1209	OLA	C6-C7-C8-C9
6	A	1230	OLC	C10-C11-C12-C13
6	A	1233	OLC	C6-C7-C8-C9
5	A	1211	OLA	C1-C2-C3-C4
5	A	1227	OLA	C1-C2-C3-C4
6	A	1233	OLC	C3-C4-C5-C6
5	A	1227	OLA	C15-C16-C17-C18
5	A	1215	OLA	C4-C5-C6-C7
6	A	1231	OLC	C1-C2-C3-C4
5	A	1209	OLA	C4-C5-C6-C7
5	A	1224	OLA	C3-C4-C5-C6
6	A	1229	OLC	C4-C5-C6-C7
5	A	1206	OLA	C2-C3-C4-C5
6	A	1232	OLC	C4-C5-C6-C7
5	A	1217	OLA	C5-C6-C7-C8
5	A	1206	OLA	C14-C15-C16-C17
5	A	1210	OLA	C10-C11-C12-C13
5	A	1220	OLA	C10-C11-C12-C13
6	A	1234	OLC	C2-C3-C4-C5
5	A	1217	OLA	C3-C4-C5-C6
6	A	1230	OLC	C4-C5-C6-C7
5	A	1225	OLA	C6-C7-C8-C9
5	A	1227	OLA	C6-C7-C8-C9
6	A	1231	OLC	C10-C11-C12-C13
6	A	1232	OLC	C6-C7-C8-C9
5	A	1212	OLA	C4-C5-C6-C7
5	A	1227	OLA	C12-C13-C14-C15
6	A	1233	OLC	O20-C21-C22-C24
5	A	1211	OLA	C15-C16-C17-C18
5	A	1227	OLA	C4-C5-C6-C7
5	A	1206	OLA	C6-C7-C8-C9
5	A	1226	OLA	C6-C7-C8-C9
5	A	1207	OLA	C3-C4-C5-C6
5	A	1217	OLA	C11-C12-C13-C14
5	A	1214	OLA	C10-C11-C12-C13
5	A	1208	OLA	C3-C4-C5-C6
6	A	1233	OLC	C4-C5-C6-C7
5	A	1211	OLA	C10-C11-C12-C13
6	A	1230	OLC	C12-C13-C14-C15
5	A	1215	OLA	C1-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
6	A	1231	OLC	C2-C1-O20-C21
5	A	1206	OLA	C11-C12-C13-C14
5	A	1206	OLA	C15-C16-C17-C18
6	A	1234	OLC	C6-C7-C8-C9
6	A	1228	OLC	C2-C1-O20-C21
6	A	1229	OLC	C2-C1-O20-C21
5	A	1226	OLA	C2-C3-C4-C5
5	A	1206	OLA	C4-C5-C6-C7
6	A	1229	OLC	C3-C4-C5-C6
5	A	1210	OLA	C6-C7-C8-C9
5	A	1210	OLA	C14-C15-C16-C17
5	A	1222	OLA	C12-C13-C14-C15
6	A	1229	OLC	C2-C3-C4-C5
5	A	1210	OLA	C12-C13-C14-C15
5	A	1226	OLA	C5-C6-C7-C8
6	A	1234	OLC	C4-C5-C6-C7
5	A	1220	OLA	C12-C13-C14-C15
5	A	1225	OLA	C12-C13-C14-C15
5	A	1206	OLA	C12-C13-C14-C15
5	A	1210	OLA	C13-C14-C15-C16
5	A	1221	OLA	C4-C5-C6-C7
5	A	1218	OLA	C11-C12-C13-C14
5	A	1219	OLA	C9-C10-C11-C12
5	A	1227	OLA	C14-C15-C16-C17
6	A	1231	OLC	O19-C1-O20-C21
6	A	1229	OLC	O19-C1-O20-C21
6	A	1229	OLC	O20-C21-C22-O23
6	A	1229	OLC	C7-C8-C9-C10
6	A	1228	OLC	O19-C1-O20-C21
6	A	1232	OLC	C3-C4-C5-C6
5	A	1209	OLA	C12-C13-C14-C15
5	A	1210	OLA	C3-C4-C5-C6
5	A	1210	OLA	C4-C5-C6-C7
5	A	1224	OLA	C2-C3-C4-C5
5	A	1209	OLA	C3-C4-C5-C6
5	A	1210	OLA	C11-C12-C13-C14
5	A	1222	OLA	C15-C16-C17-C18
5	A	1206	OLA	C10-C11-C12-C13
5	A	1226	OLA	C4-C5-C6-C7
6	A	1231	OLC	C5-C6-C7-C8
5	A	1213	OLA	C2-C3-C4-C5
6	A	1230	OLC	C2-C3-C4-C5

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Mol	Chain	Res	Type	Atoms
6	A	1232	OLC	C5-C6-C7-C8
5	A	1221	OLA	C7-C8-C9-C10
5	A	1212	OLA	C1-C2-C3-C4
5	A	1211	OLA	C5-C6-C7-C8
5	A	1221	OLA	C9-C10-C11-C12
6	A	1232	OLC	C2-C3-C4-C5
5	A	1220	OLA	C15-C16-C17-C18
5	A	1212	OLA	C5-C6-C7-C8
5	A	1209	OLA	C10-C11-C12-C13
5	A	1217	OLA	C6-C7-C8-C9
5	A	1224	OLA	C4-C5-C6-C7
7	A	1235	A1CQC	C01-C02-C04-N05
5	A	1211	OLA	C12-C13-C14-C15
6	A	1231	OLC	C4-C5-C6-C7
5	A	1210	OLA	O1-C1-C2-C3
6	A	1228	OLC	C1-C2-C3-C4
6	A	1228	OLC	C3-C4-C5-C6
5	A	1209	OLA	O2-C1-C2-C3
5	A	1210	OLA	O2-C1-C2-C3
5	A	1212	OLA	C3-C4-C5-C6
6	A	1230	OLC	C5-C6-C7-C8
5	A	1214	OLA	C4-C5-C6-C7
6	A	1230	OLC	O19-C1-O20-C21
6	A	1228	OLC	C6-C7-C8-C9
5	A	1223	OLA	C5-C6-C7-C8
5	A	1217	OLA	C7-C8-C9-C10
5	A	1214	OLA	C9-C10-C11-C12
6	A	1230	OLC	C9-C10-C11-C12
6	A	1230	OLC	C2-C1-O20-C21
5	A	1209	OLA	O1-C1-C2-C3
5	A	1214	OLA	C7-C8-C9-C10
6	A	1232	OLC	C9-C10-C11-C12
5	A	1208	OLA	O2-C1-C2-C3
5	A	1227	OLA	C5-C6-C7-C8
5	A	1210	OLA	C9-C10-C11-C12
5	A	1227	OLA	C3-C4-C5-C6
5	A	1220	OLA	C9-C10-C11-C12
5	A	1226	OLA	C7-C8-C9-C10
5	A	1208	OLA	O1-C1-C2-C3
5	A	1216	OLA	C3-C4-C5-C6
5	A	1210	OLA	C7-C8-C9-C10
5	A	1212	OLA	C7-C8-C9-C10

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Mol	Chain	Res	Type	Atoms
5	A	1206	OLA	C1-C2-C3-C4
5	A	1215	OLA	C5-C6-C7-C8
5	A	1227	OLA	C13-C14-C15-C16
6	A	1231	OLC	C9-C10-C11-C12
5	A	1211	OLA	O2-C1-C2-C3
5	A	1218	OLA	C14-C15-C16-C17
5	A	1217	OLA	C12-C13-C14-C15
5	A	1227	OLA	C2-C3-C4-C5
6	A	1228	OLC	C5-C6-C7-C8
5	A	1211	OLA	O1-C1-C2-C3
5	A	1206	OLA	O2-C1-C2-C3
5	A	1209	OLA	C5-C6-C7-C8
5	A	1207	OLA	O2-C1-C2-C3
5	A	1217	OLA	C4-C5-C6-C7
5	A	1227	OLA	C7-C8-C9-C10
5	A	1207	OLA	O1-C1-C2-C3

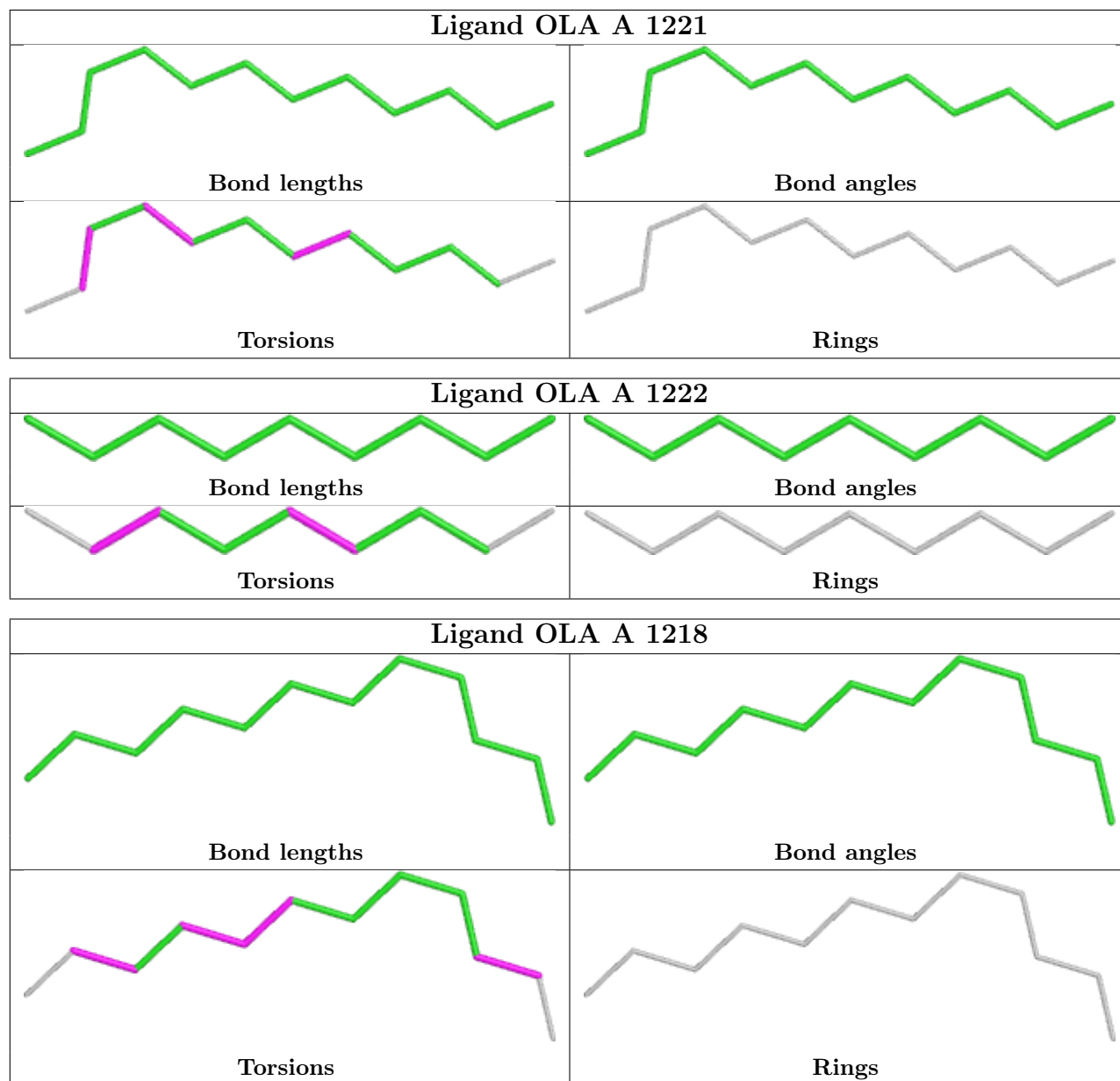
There are no ring outliers.

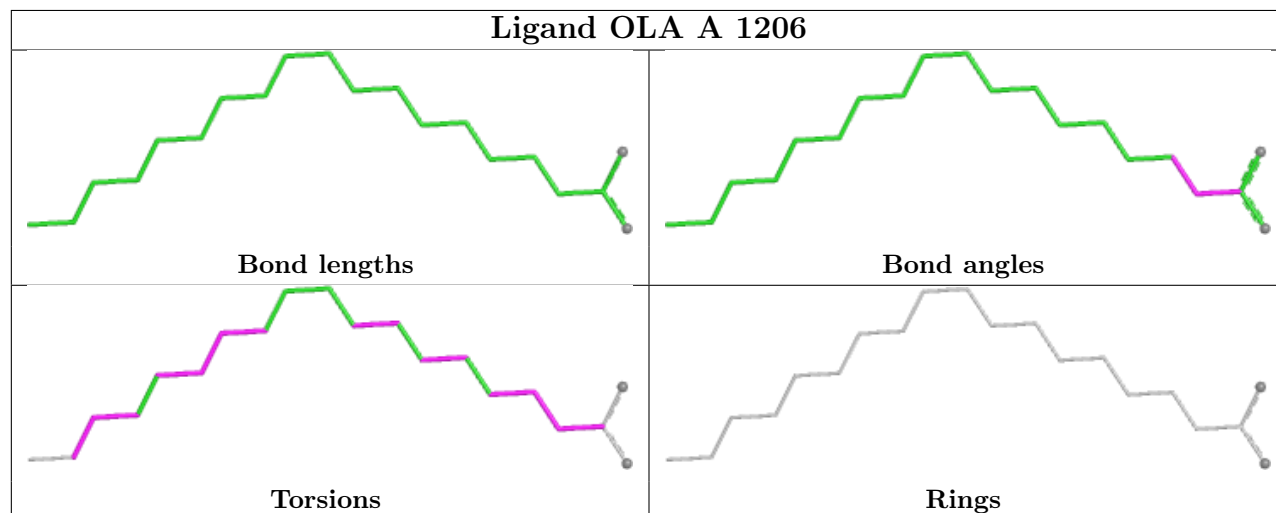
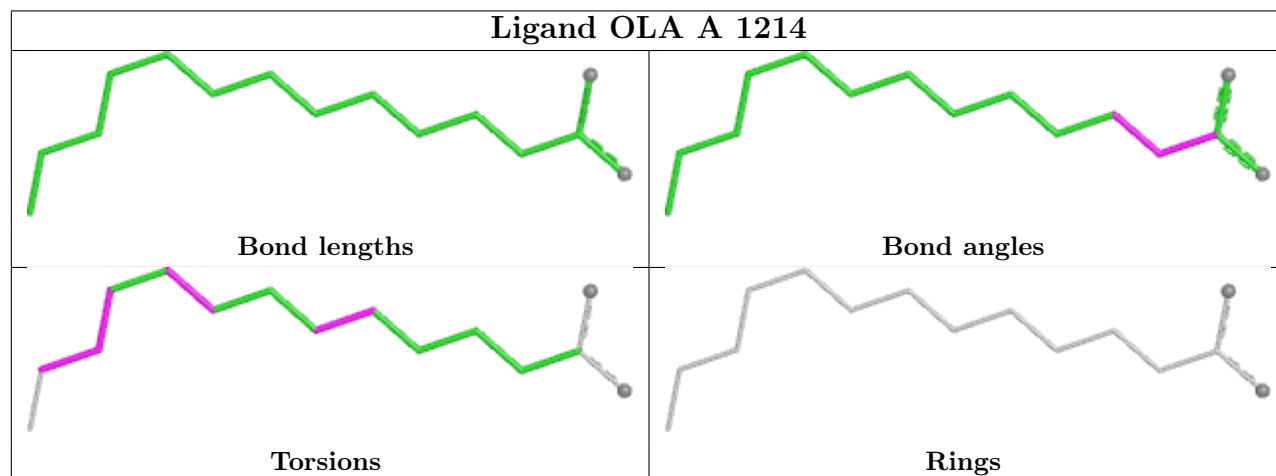
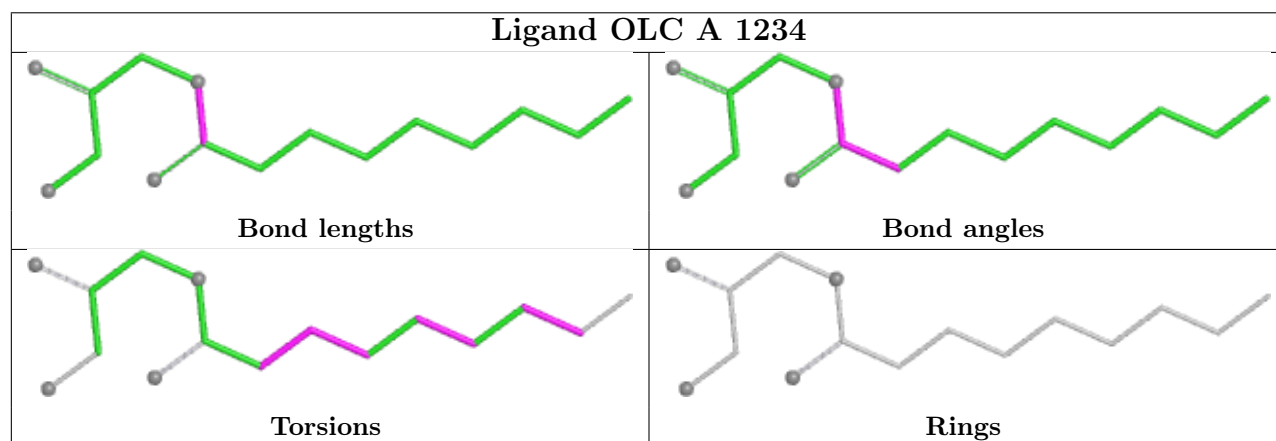
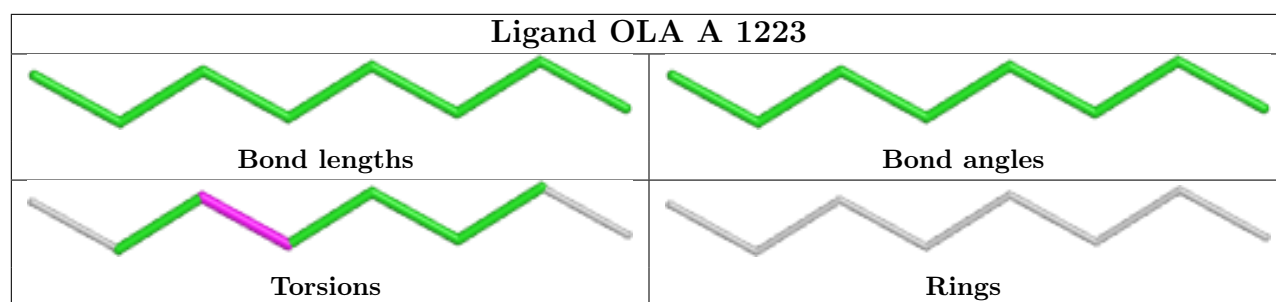
15 monomers are involved in 19 short contacts:

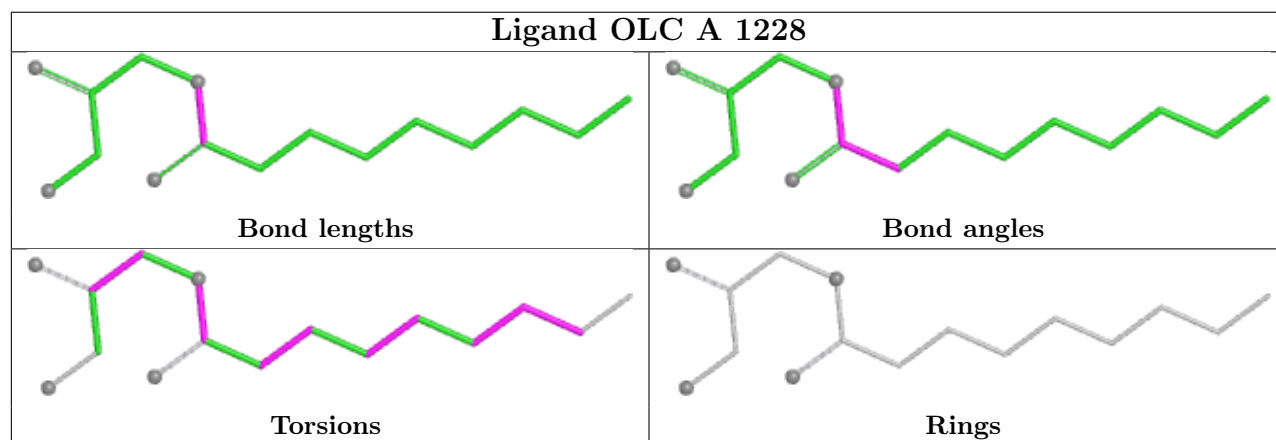
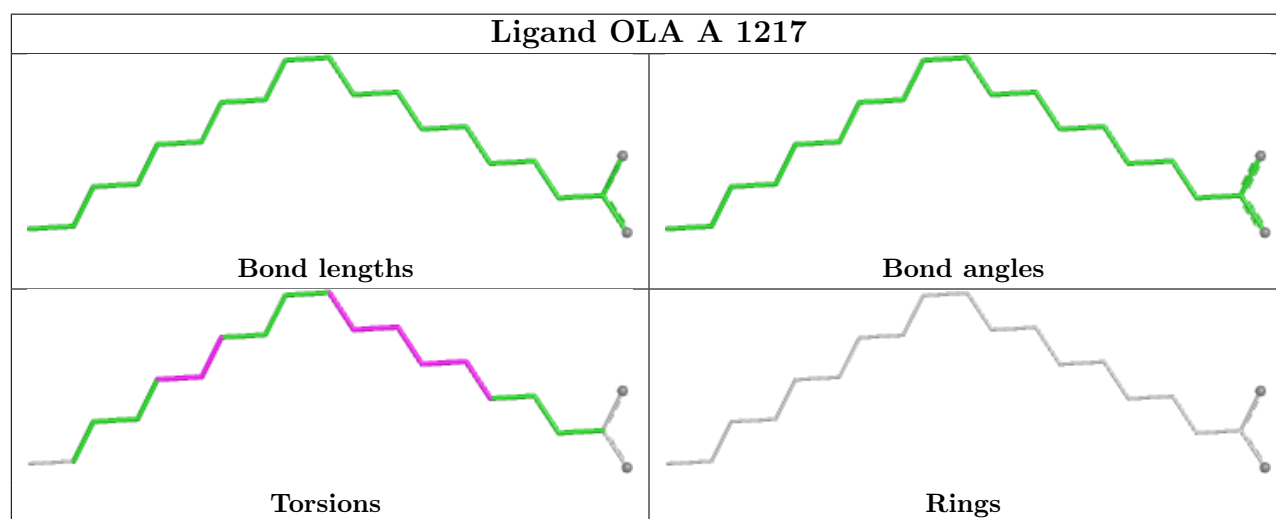
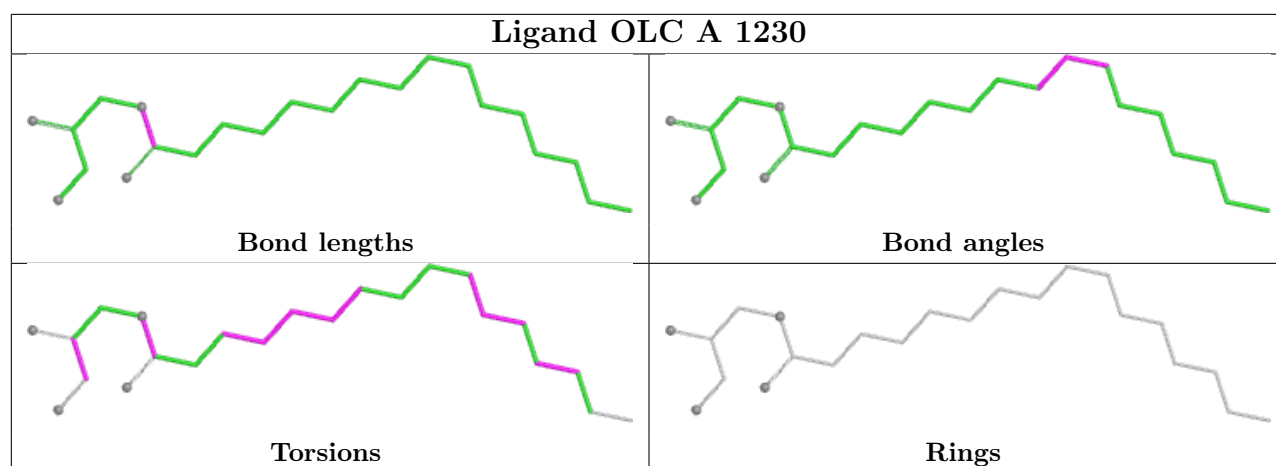
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1222	OLA	1	0
5	A	1223	OLA	3	0
6	A	1234	OLC	1	0
6	A	1230	OLC	2	0
5	A	1217	OLA	3	0
6	A	1232	OLC	1	0
5	A	1210	OLA	4	0
6	A	1233	OLC	1	0
5	A	1226	OLA	4	0
6	A	1231	OLC	2	0
5	A	1227	OLA	2	0
5	A	1211	OLA	2	0
5	A	1216	OLA	1	0
5	A	1225	OLA	1	0
5	A	1207	OLA	1	0

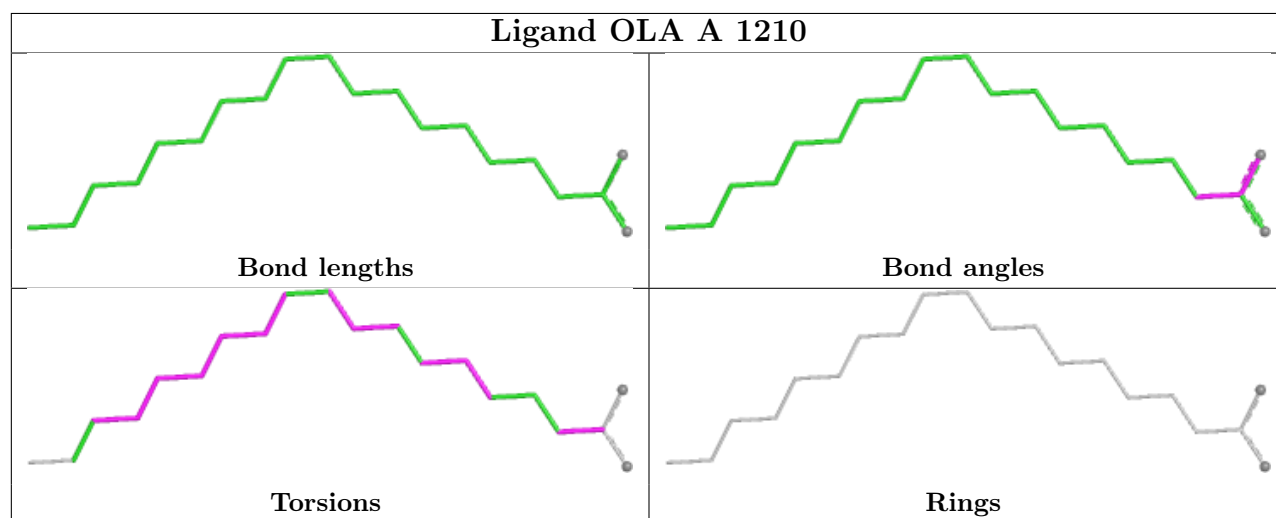
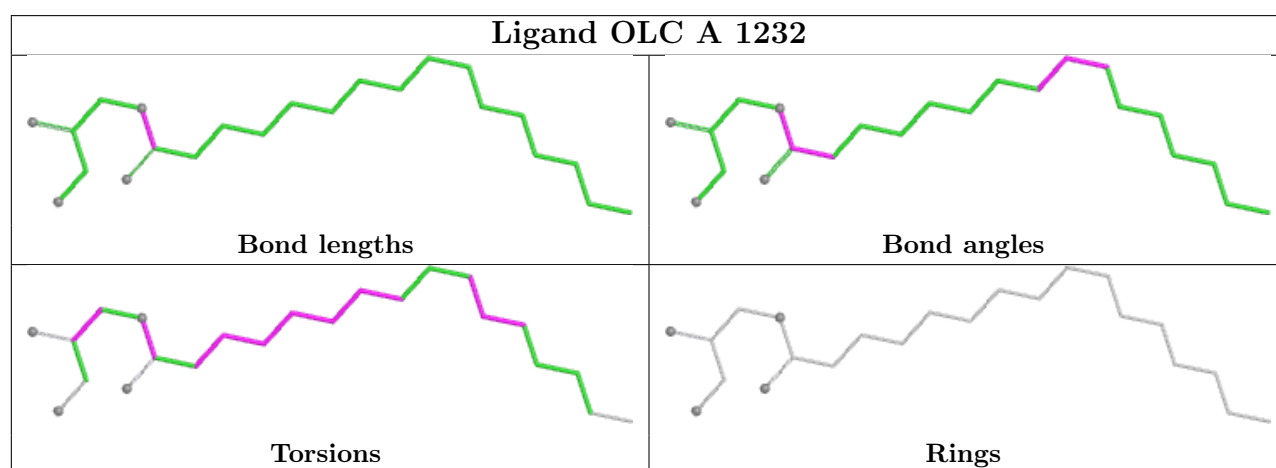
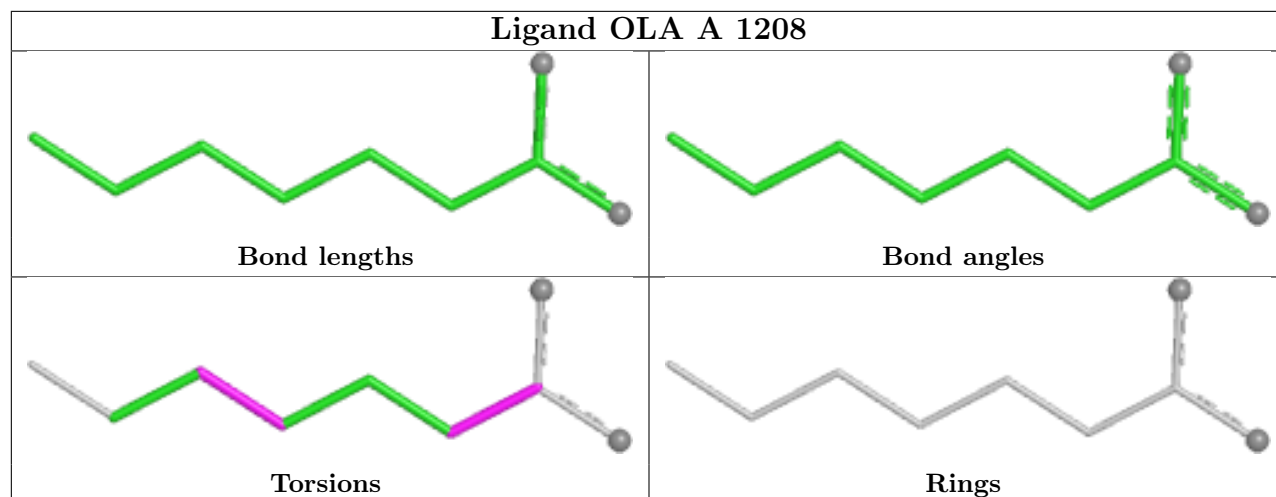
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

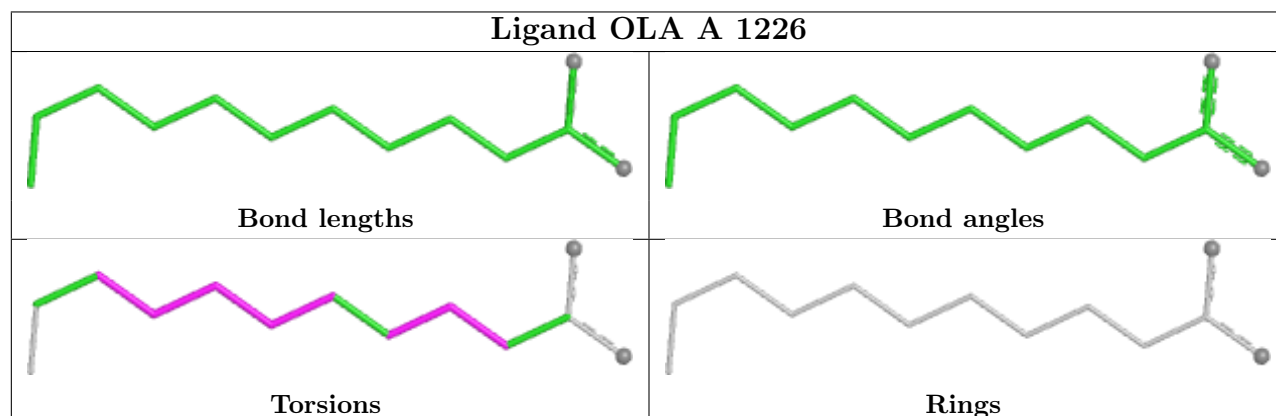
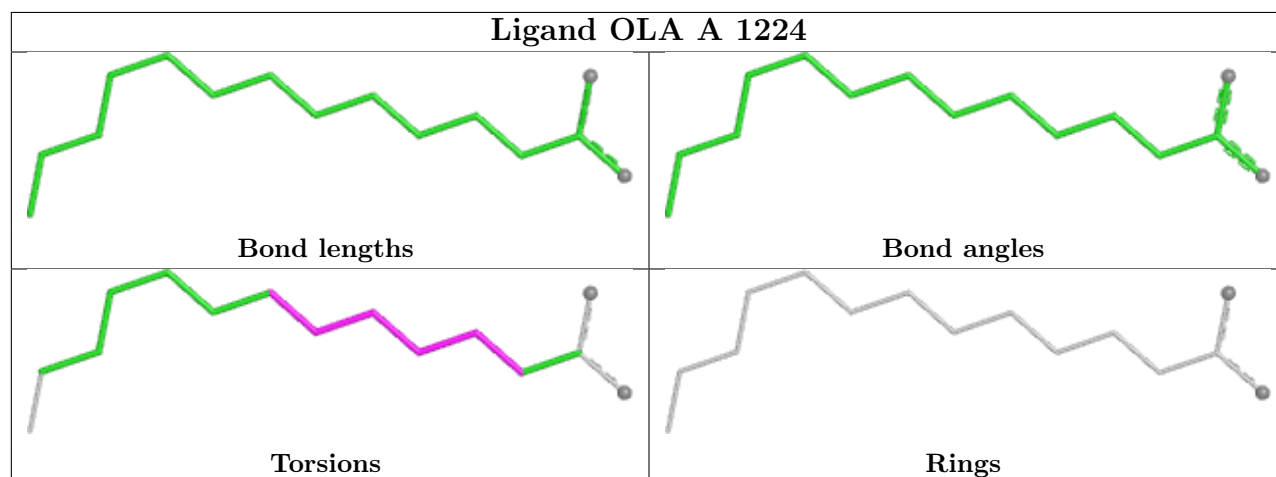
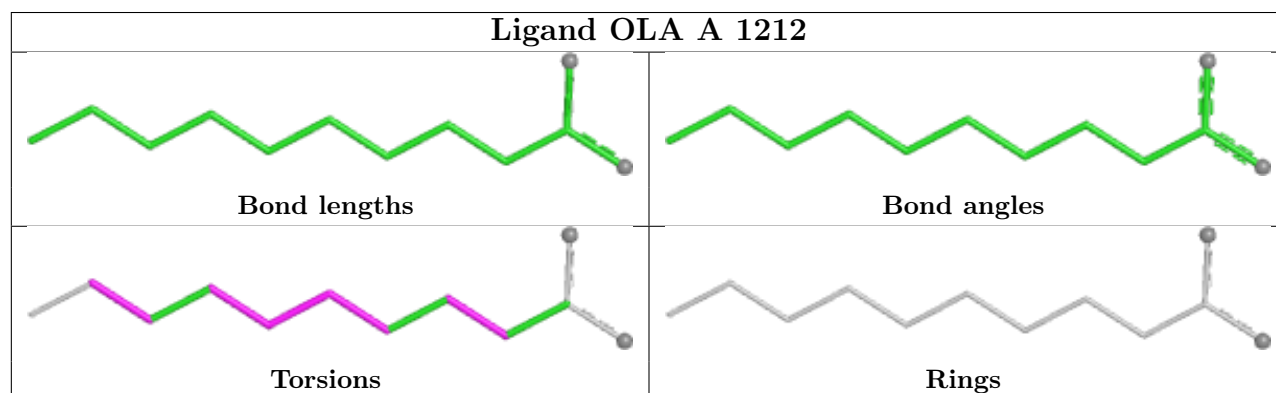
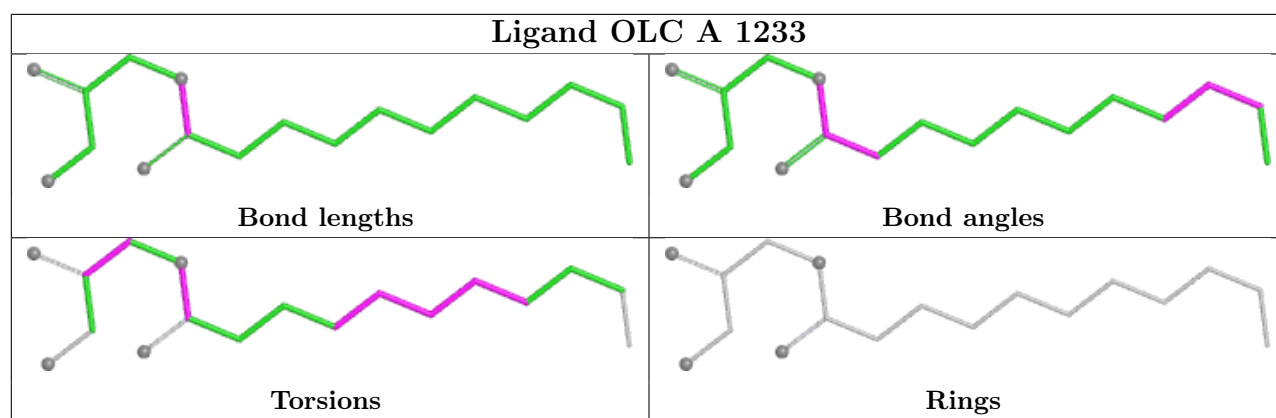
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD 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.

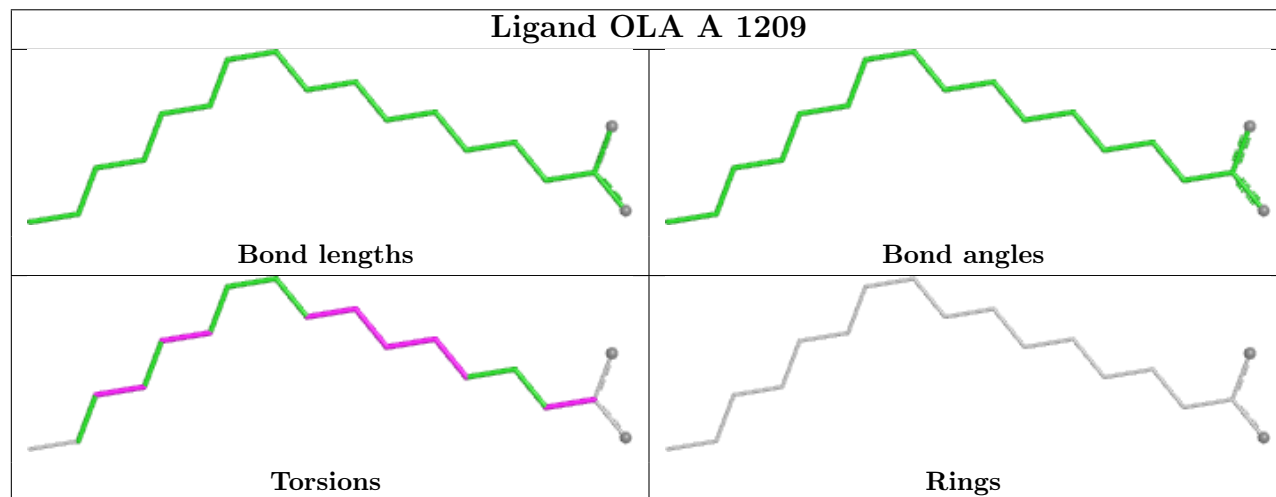
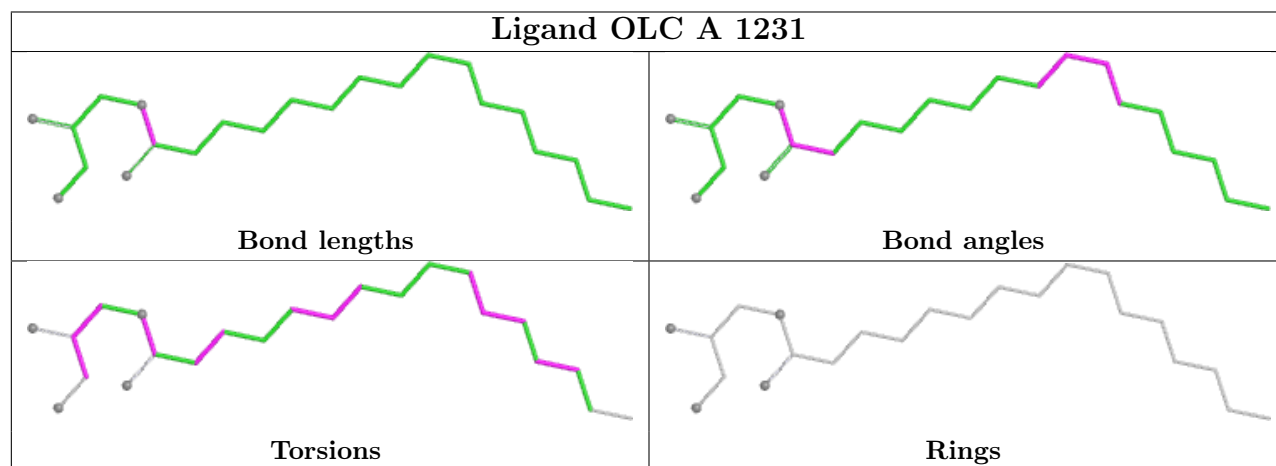
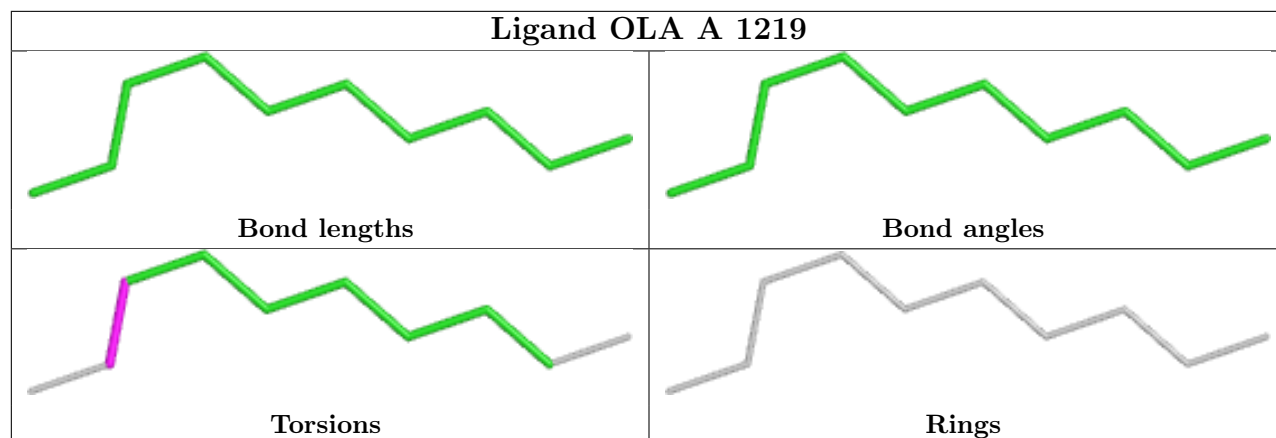


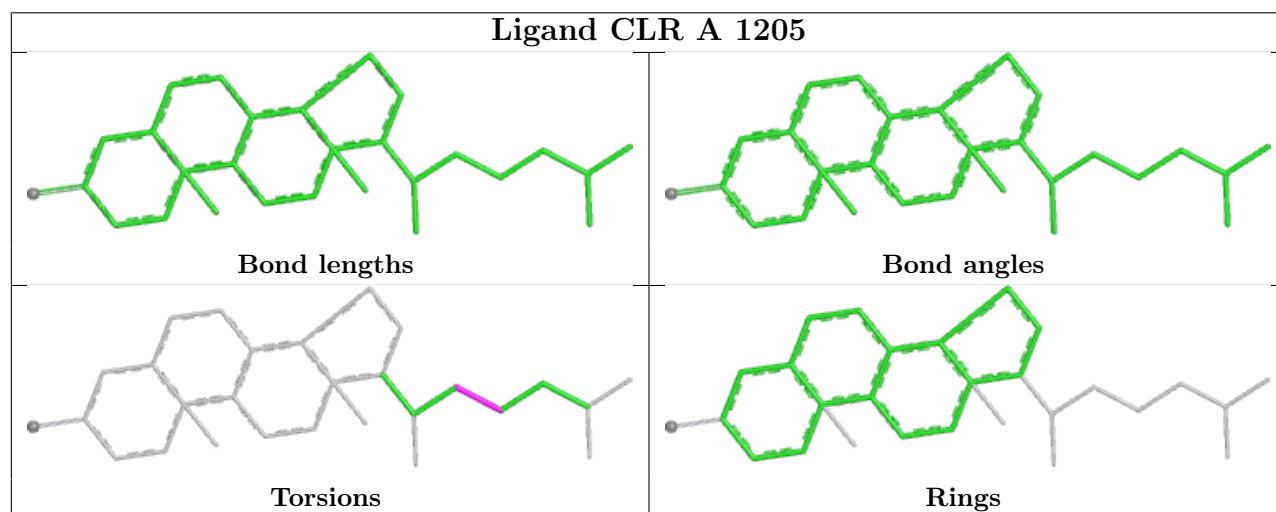
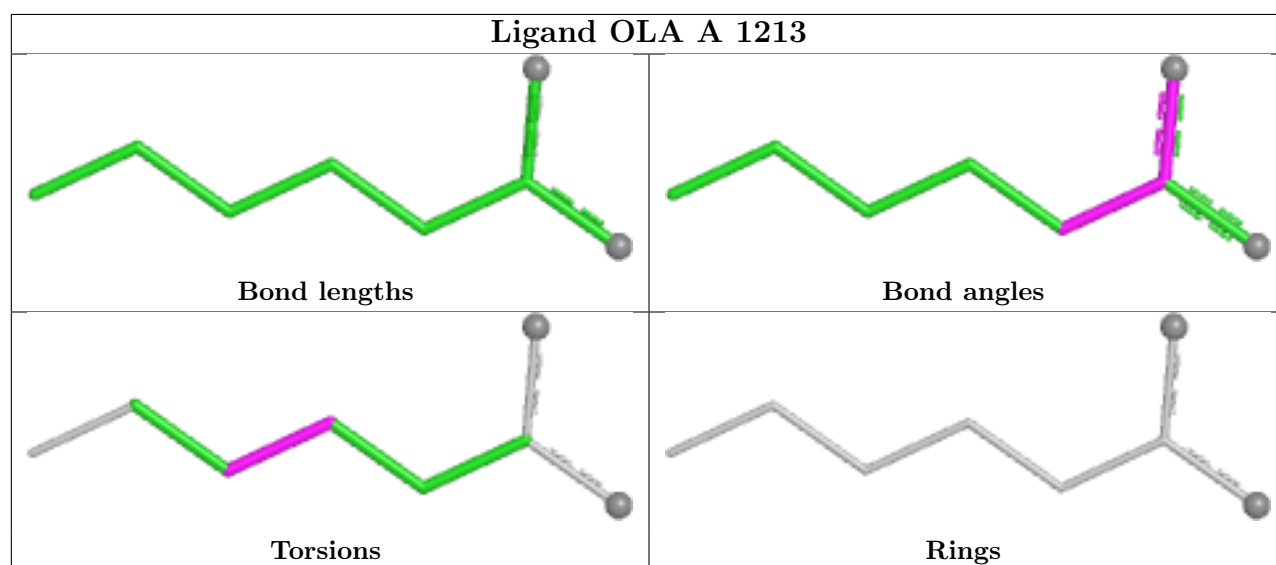
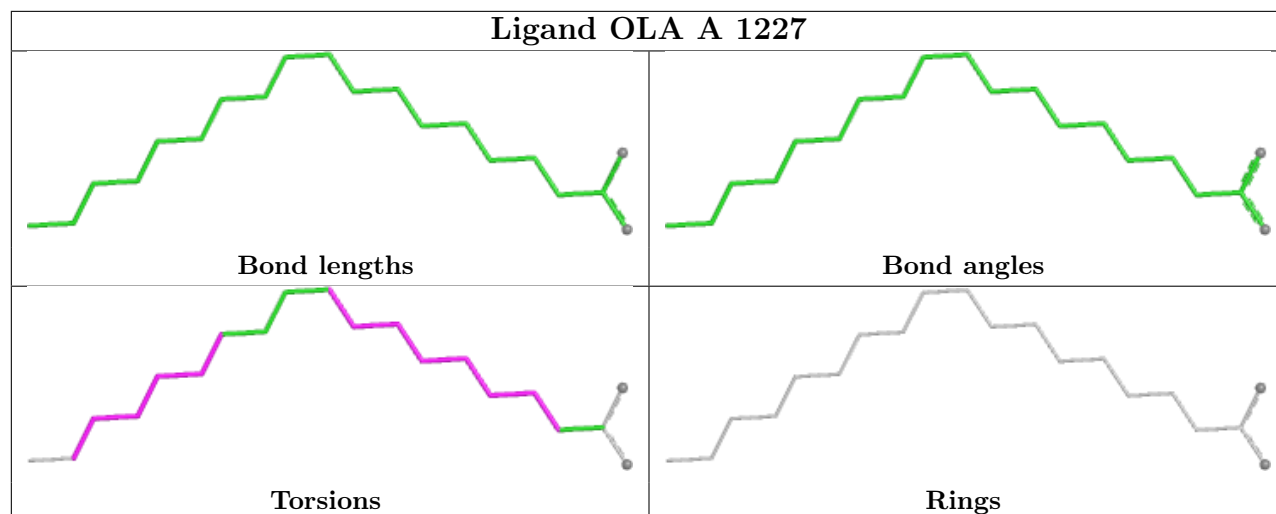


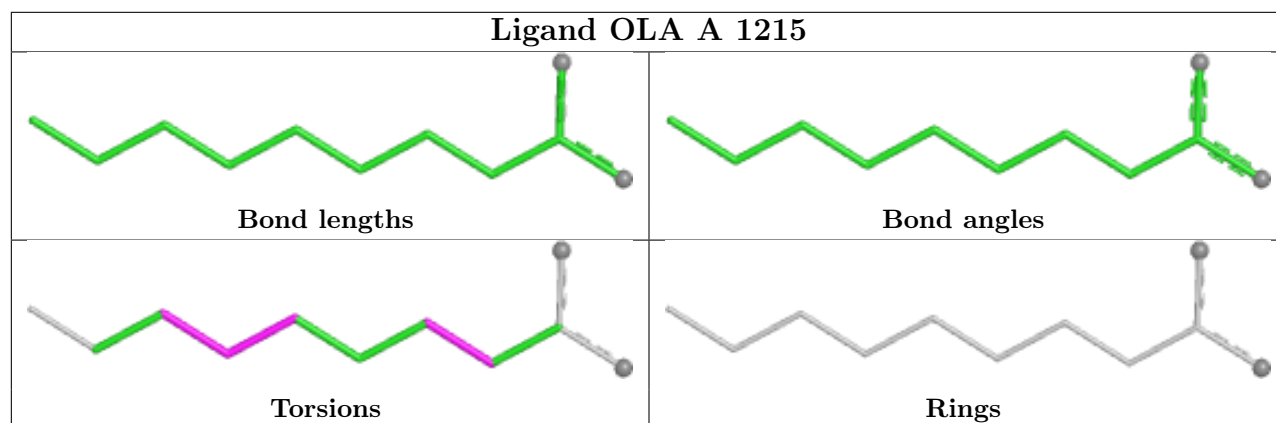
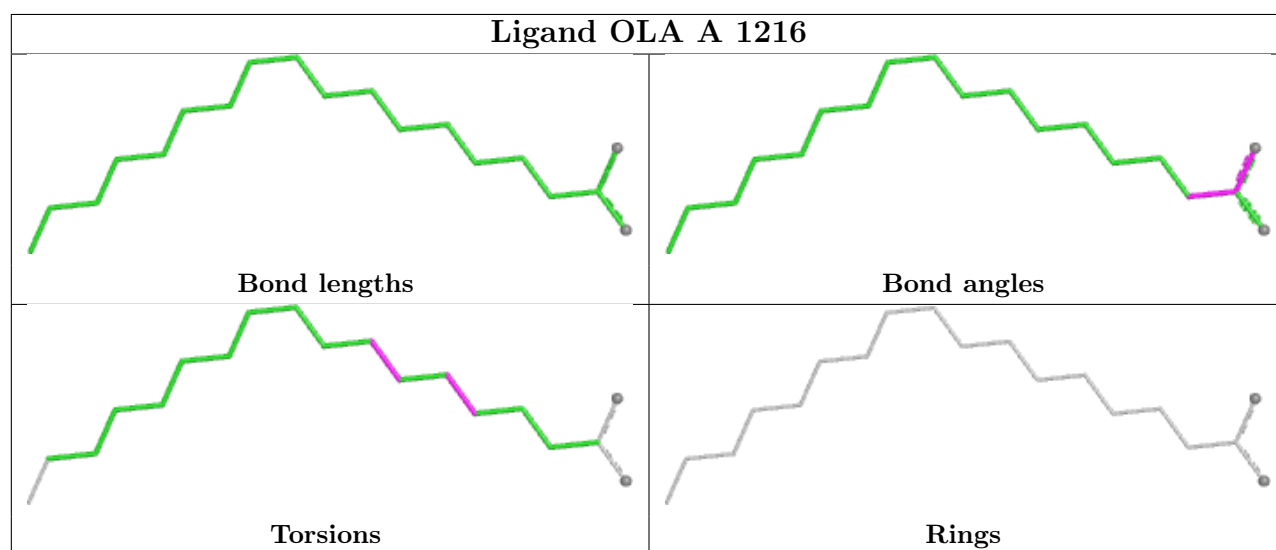
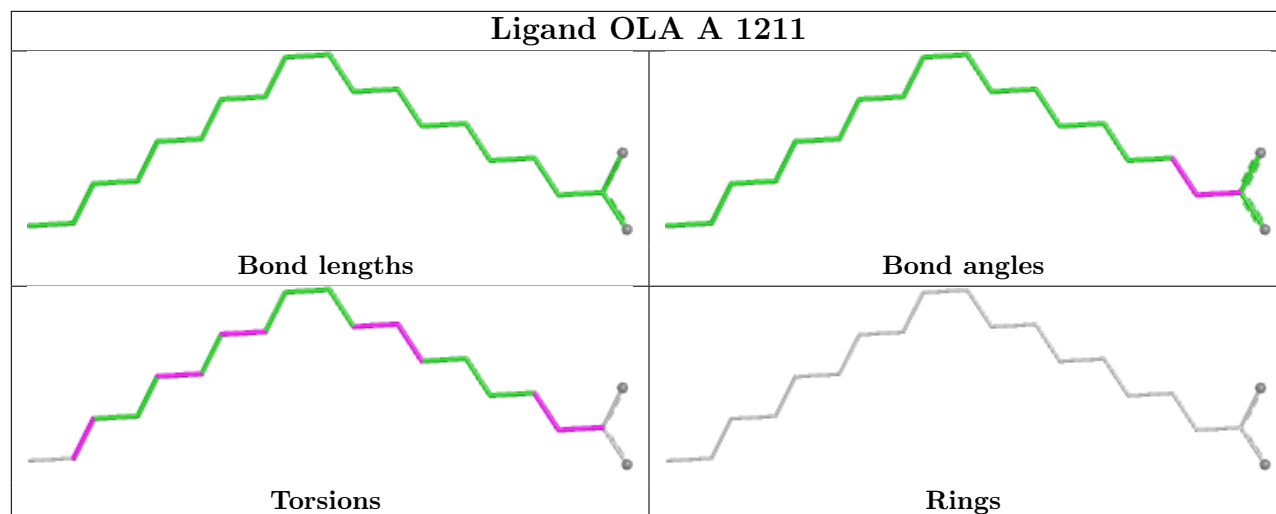


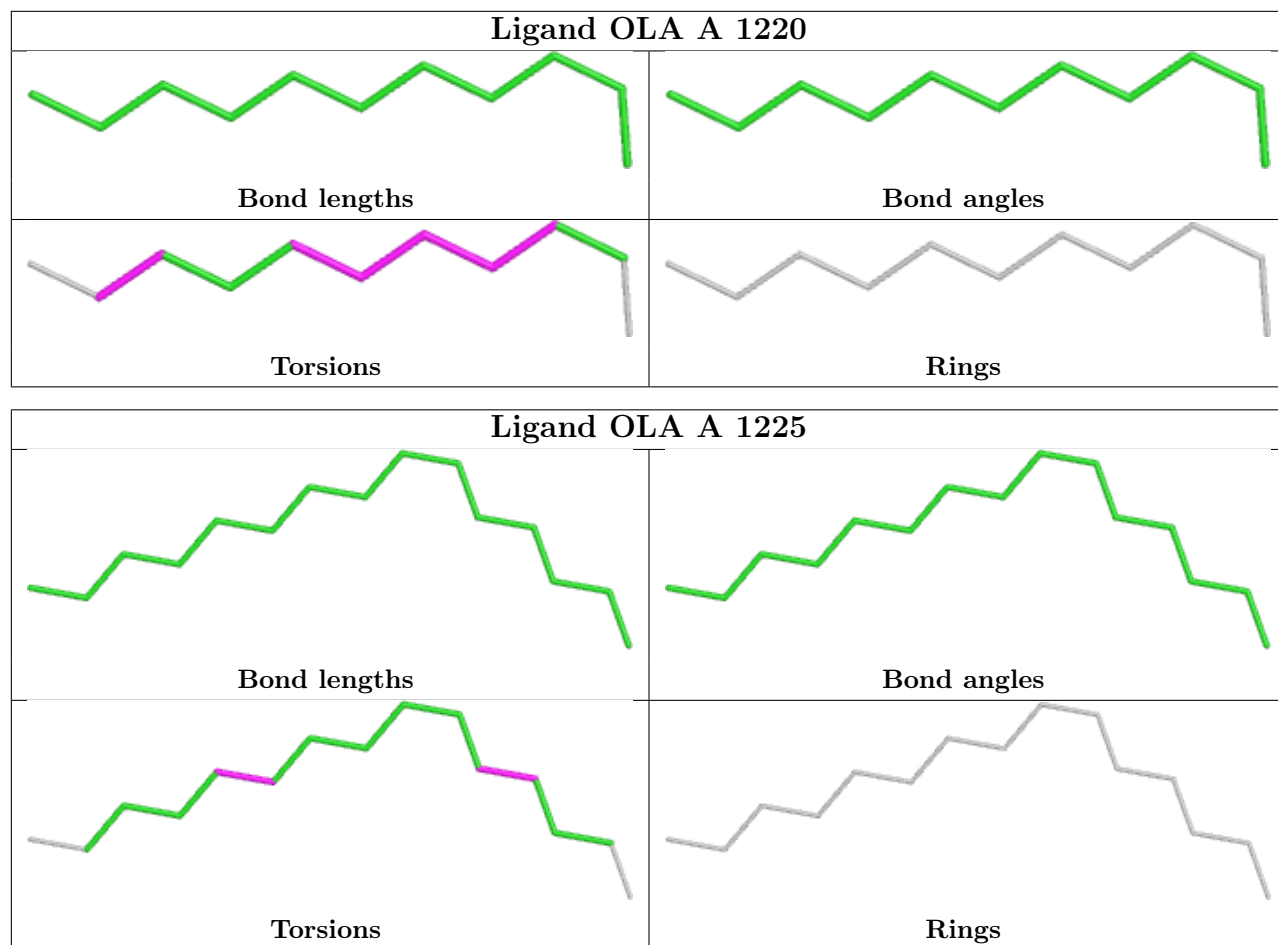


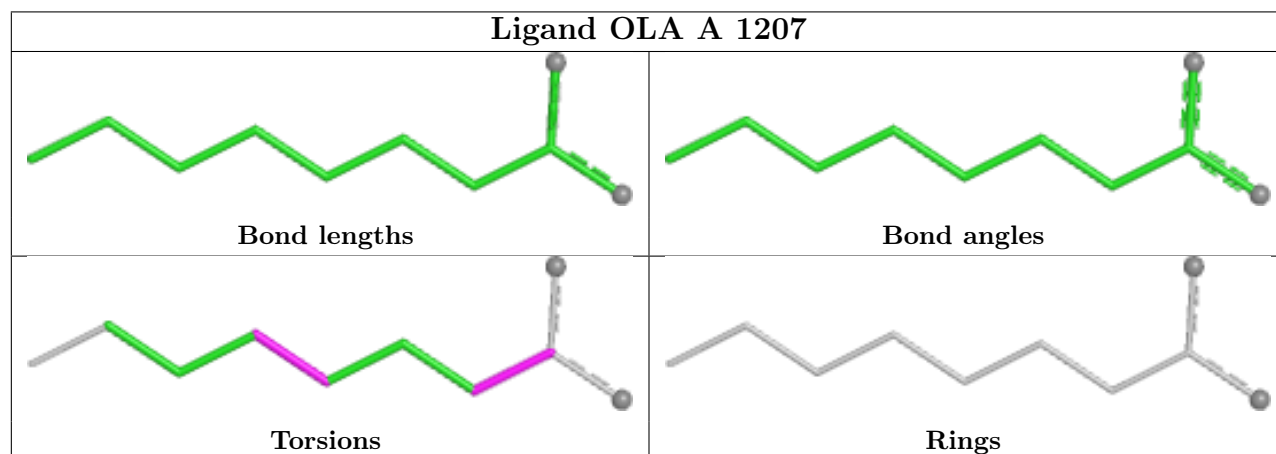
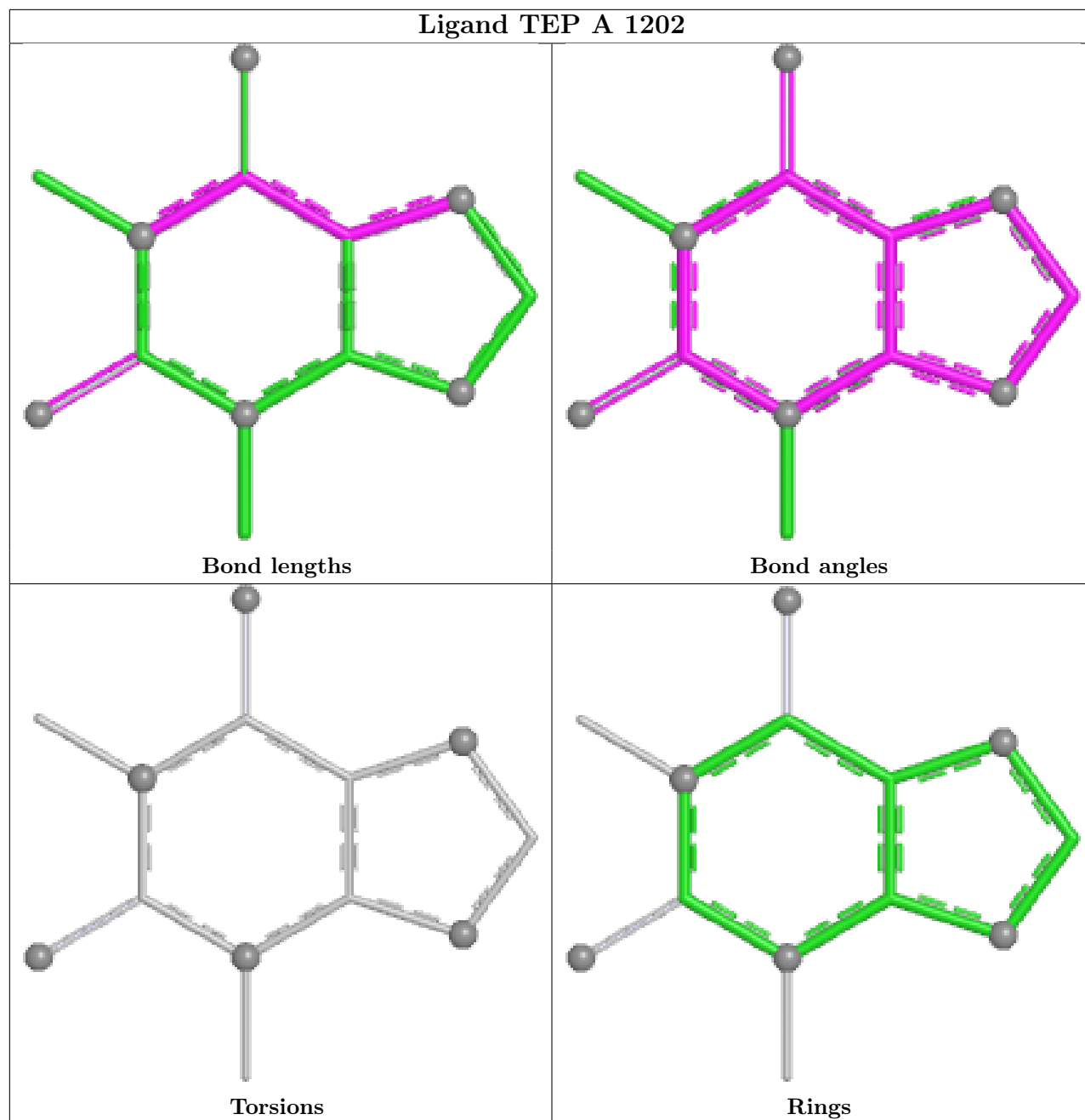


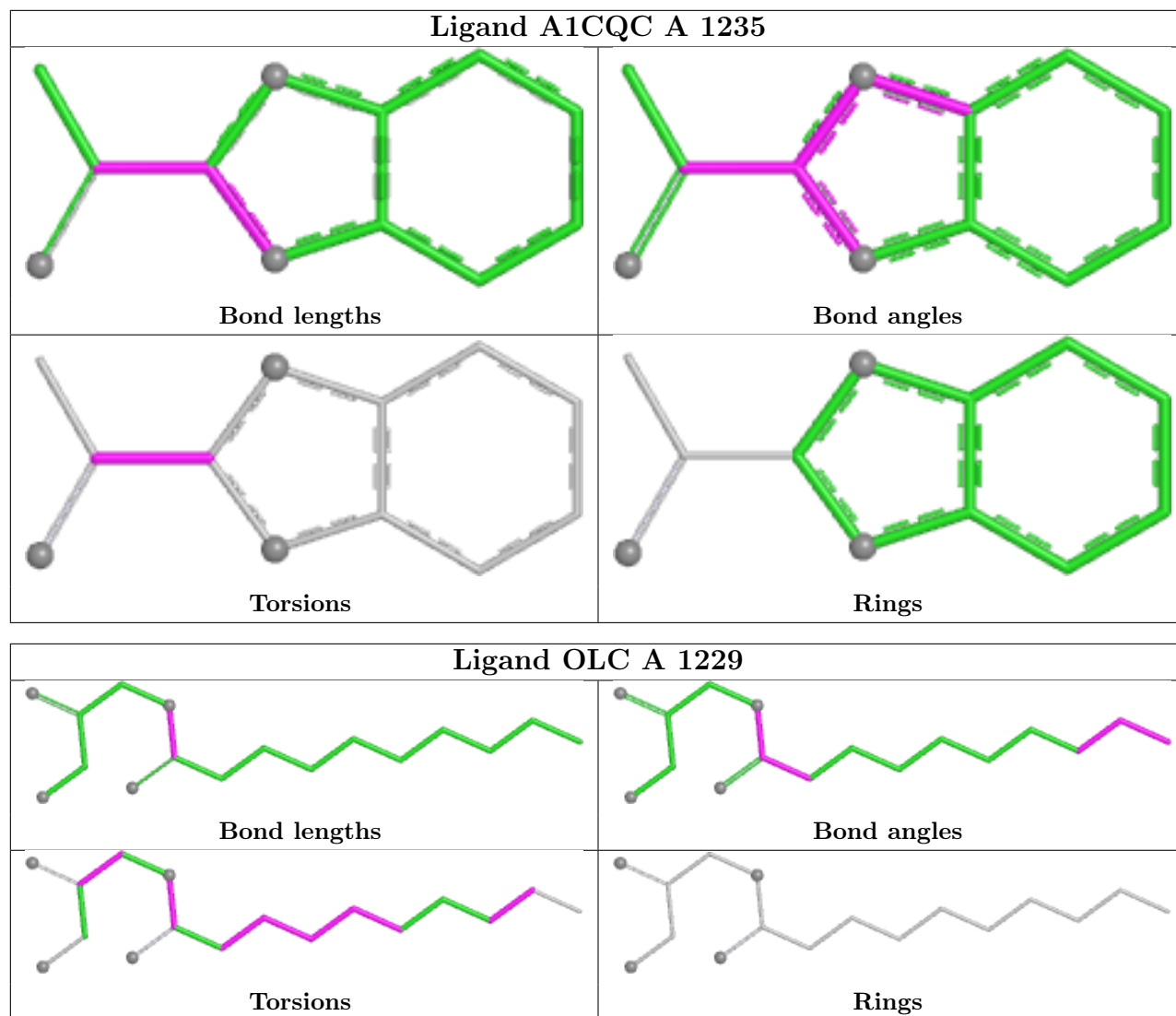












## 5.7 Other polymers [i](#)

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 [i](#)

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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%)	0.32	16 (4%) 41 44	14, 41, 79, 118	14 (3%)

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1061	PHE	6.0
1	A	1021	ASP	4.6
1	A	306	HIS	3.8
1	A	1106	LEU	3.8
1	A	307	VAL	3.6
1	A	1003	LEU	3.3
1	A	1028	ASP	3.1
1	A	308	LEU	2.9
1	A	309	ARG	2.4
1	A	208	LEU	2.4
1	A	1094	LEU	2.4
1	A	29	TRP	2.3
1	A	1017	ILE	2.2
1	A	1035	ALA	2.2
1	A	1059	LYS	2.1
1	A	300[A]	ARG	2.1

### 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](#)

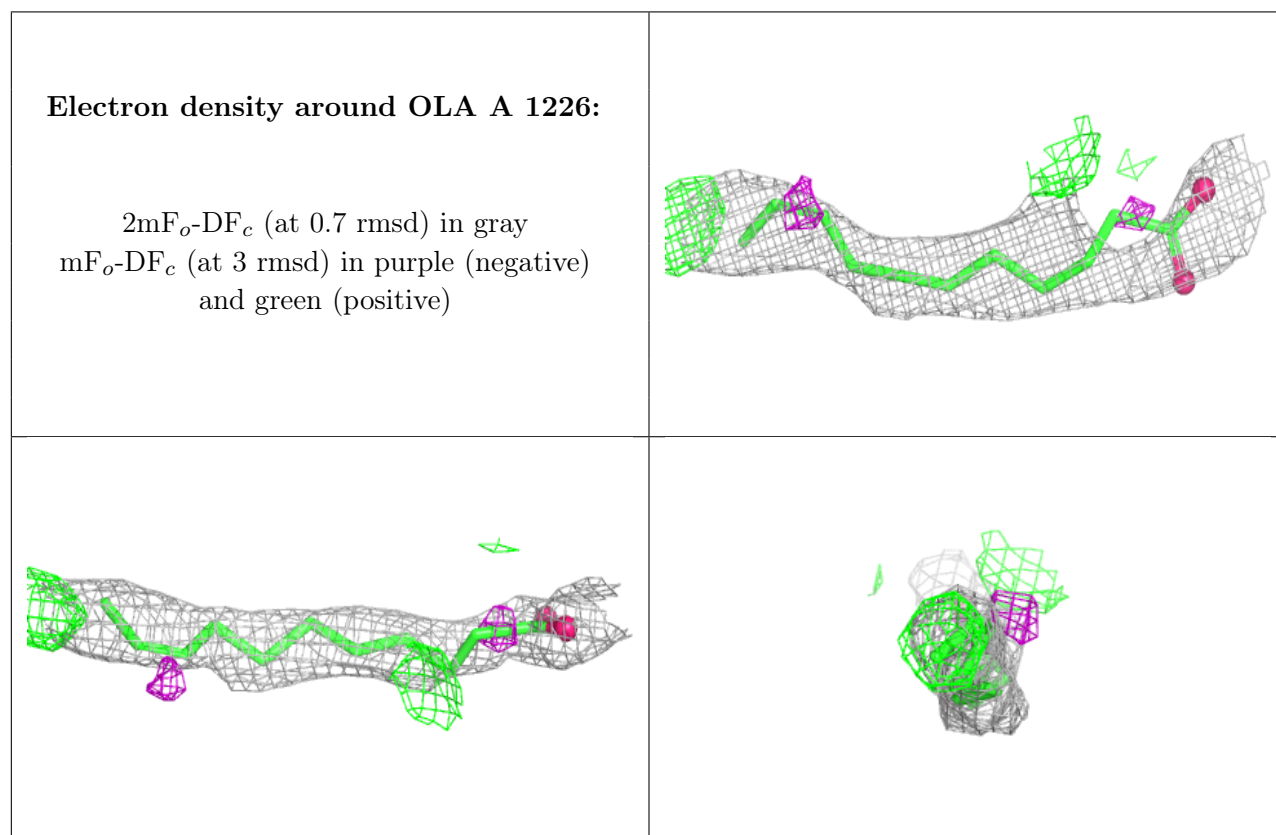
There are no oligosaccharides in this entry.

## 6.4 Ligands ⓘ

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.

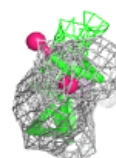
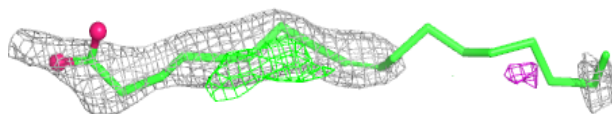
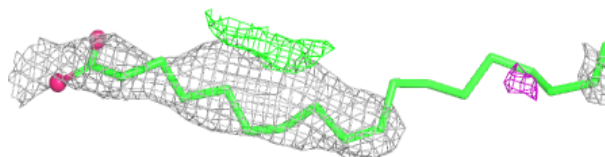
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
8	DMS	A	1237[S]	4/4	0.55	0.28	68,77,80,98	0
8	DMS	A	1236[S]	4/4	0.60	0.31	67,75,81,113	0
5	OLA	A	1226	13/20	0.70	0.19	45,55,79,83	0
5	OLA	A	1227	20/20	0.70	0.22	55,68,77,94	0
5	OLA	A	1215	11/20	0.71	0.18	45,49,66,77	0
5	OLA	A	1221	12/20	0.71	0.21	47,55,60,62	0
5	OLA	A	1214	15/20	0.75	0.19	56,62,69,70	0
5	OLA	A	1224	15/20	0.75	0.22	51,62,76,81	0
5	OLA	A	1217	20/20	0.75	0.20	42,64,67,67	0
5	OLA	A	1207	10/20	0.76	0.18	57,69,79,90	0
5	OLA	A	1218	12/20	0.76	0.19	37,48,57,59	0
5	OLA	A	1219	10/20	0.76	0.23	47,62,67,69	0
5	OLA	A	1216	19/20	0.76	0.20	49,58,68,69	0
5	OLA	A	1222	9/20	0.76	0.24	46,59,74,77	0
5	OLA	A	1209	18/20	0.78	0.18	39,52,74,77	0
5	OLA	A	1210	20/20	0.80	0.17	40,59,71,74	0
6	OLC	A	1229	17/25	0.80	0.16	55,66,78,78	0
6	OLC	A	1230	23/25	0.81	0.17	45,56,75,79	0
6	OLC	A	1232	23/25	0.81	0.17	42,51,76,85	0
5	OLA	A	1213	8/20	0.81	0.14	55,59,61,65	0
5	OLA	A	1223	8/20	0.81	0.19	51,56,58,59	0
5	OLA	A	1211	20/20	0.82	0.18	52,61,76,78	0
5	OLA	A	1208	9/20	0.83	0.16	39,44,63,65	0
6	OLC	A	1233	18/25	0.84	0.16	46,56,70,79	0
6	OLC	A	1234	16/25	0.84	0.14	39,47,60,64	0
5	OLA	A	1220	11/20	0.84	0.17	39,46,61,66	0
5	OLA	A	1212	12/20	0.84	0.16	39,57,66,70	0
5	OLA	A	1225	15/20	0.85	0.16	44,50,55,56	0
3	TEP	A	1202	13/13	0.88	0.11	24,33,39,40	0
5	OLA	A	1206	20/20	0.89	0.15	43,52,64,65	0
6	OLC	A	1231	23/25	0.90	0.14	35,52,64,67	0
6	OLC	A	1228	16/25	0.91	0.13	36,48,59,61	0
7	A1CQC	A	1235	12/12	0.91	0.11	39,50,63,64	0
2	NA	A	1201	1/1	0.92	0.14	39,39,39,39	0
4	CLR	A	1203	28/28	0.92	0.11	34,40,57,63	0
4	CLR	A	1204	28/28	0.94	0.11	35,44,50,52	0
4	CLR	A	1205	28/28	0.95	0.08	30,36,45,56	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.

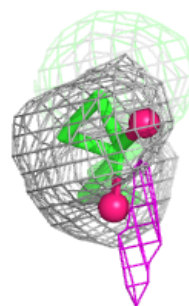
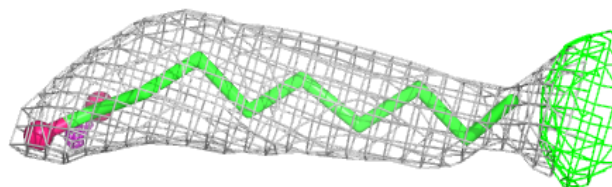
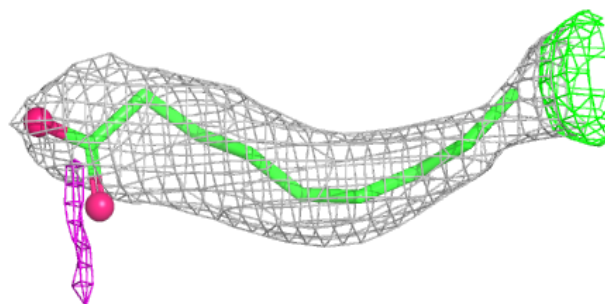


**Electron density around OLA A 1227:**

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

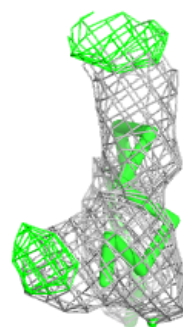
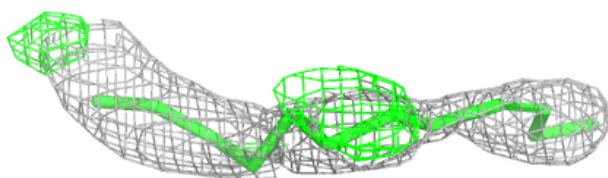
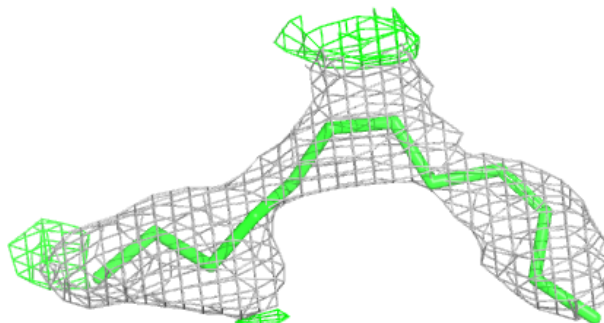
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and green (positive)

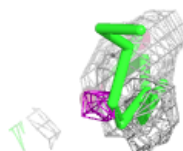
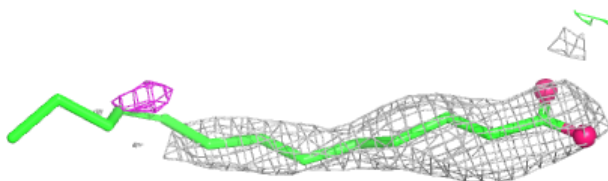
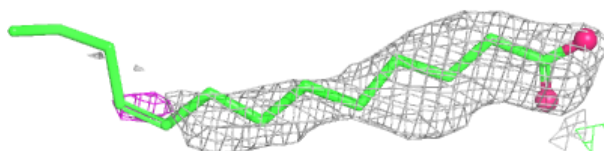


**Electron density around OLA A 1221:**

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

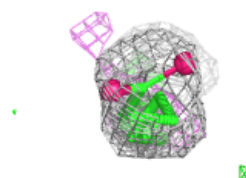
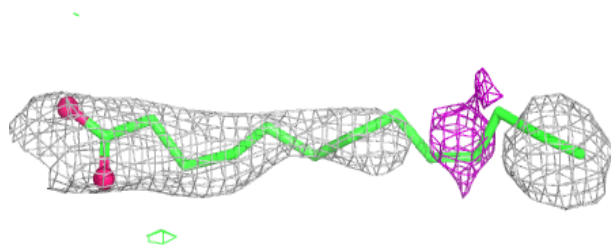
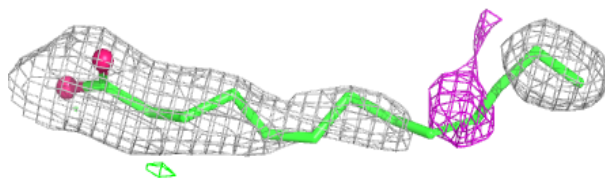
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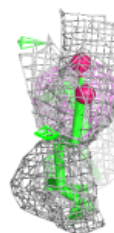
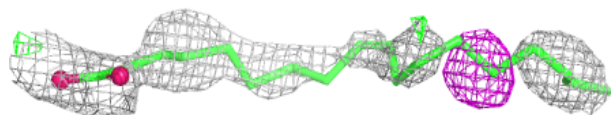
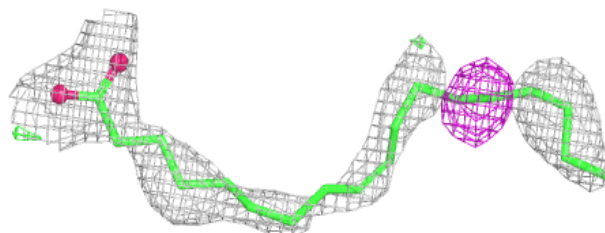


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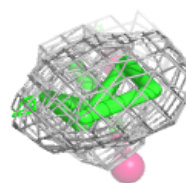
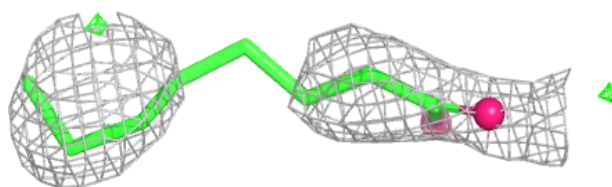
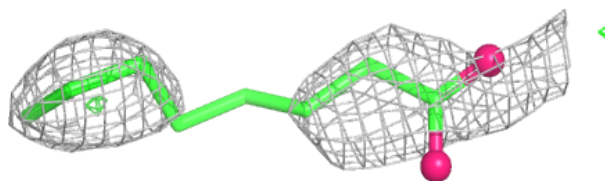
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and green (positive)

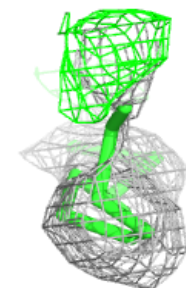
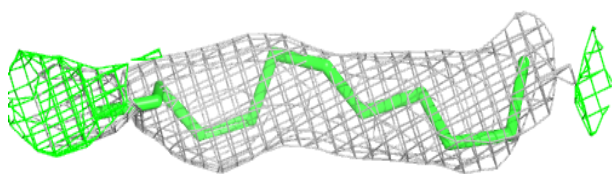
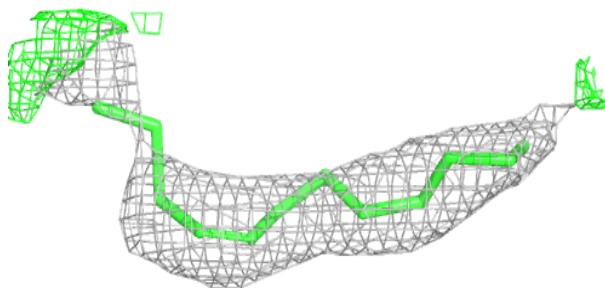


**Electron density around OLA A 1207:**

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and green (positive)

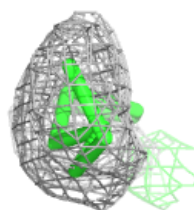
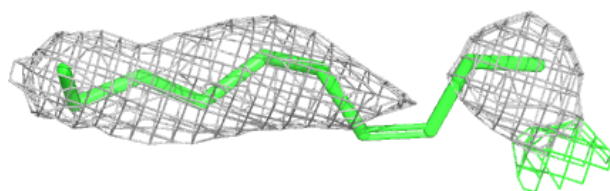
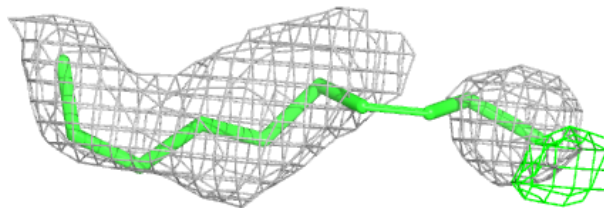
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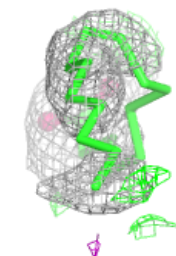
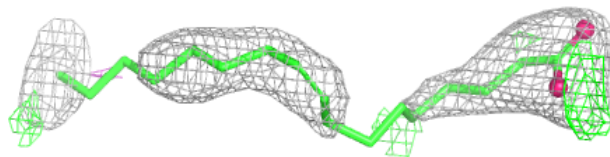
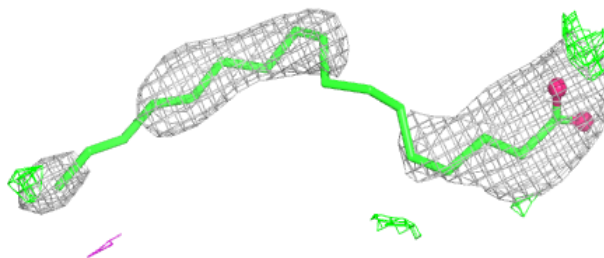


**Electron density around OLA A 1219:**

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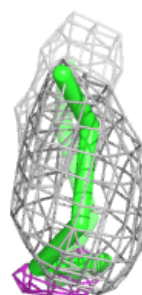
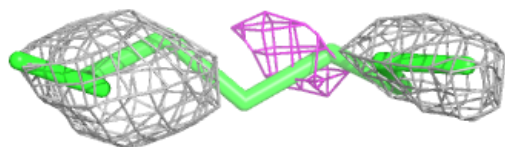
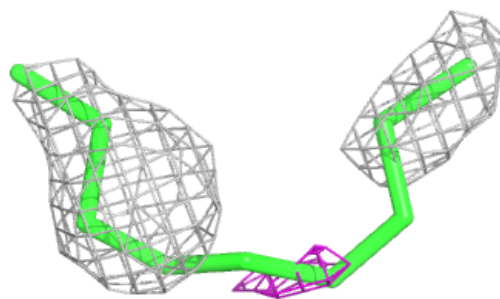
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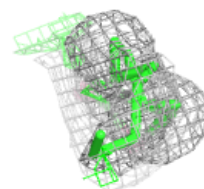
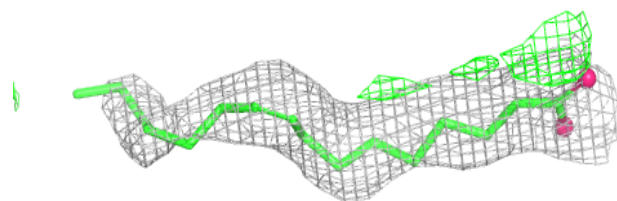
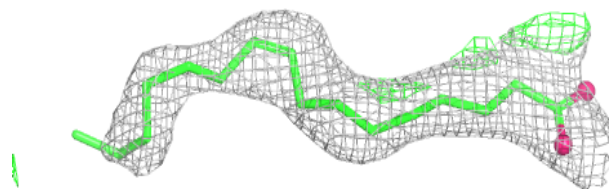


**Electron density around OLA A 1222:**

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

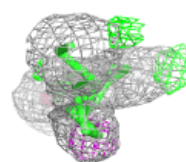
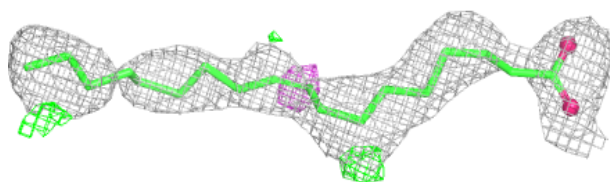
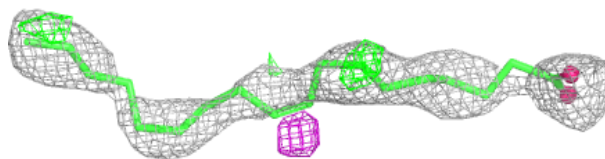
**Electron density around OLA A 1209:**

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

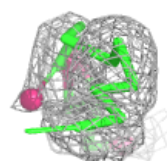
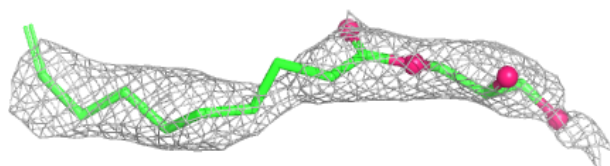
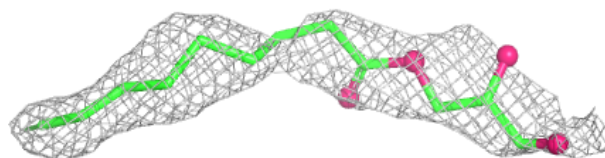


**Electron density around OLA A 1210:**

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

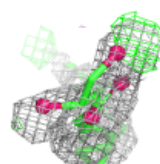
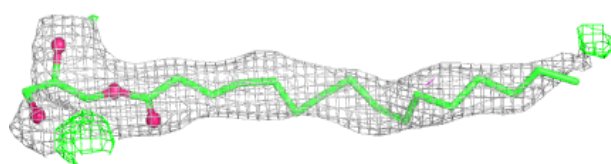
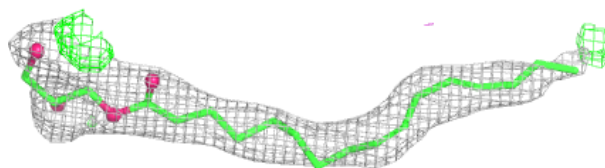
**Electron density around OLC A 1229:**

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

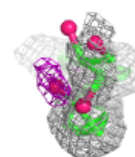
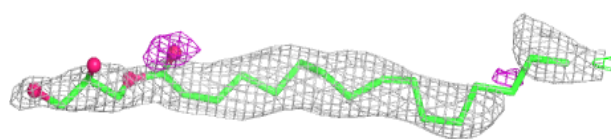
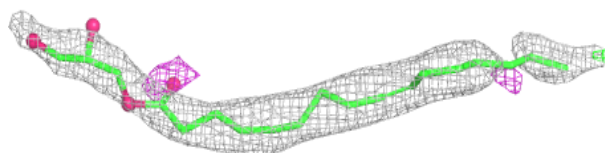


**Electron density around OLC A 1230:**

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

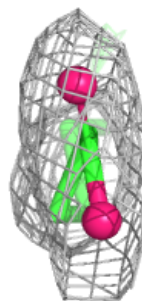
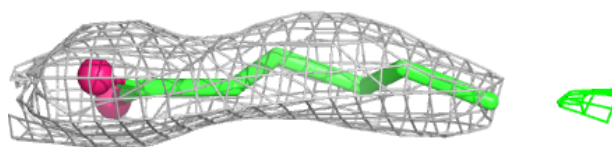
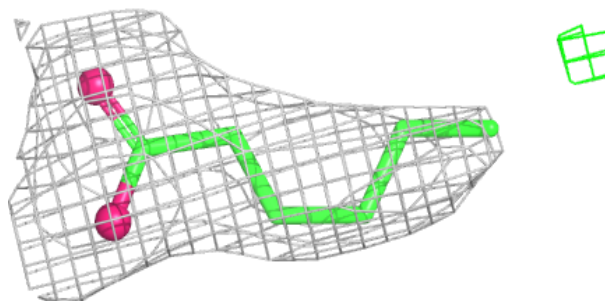
**Electron density around OLC A 1232:**

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

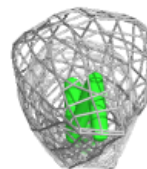
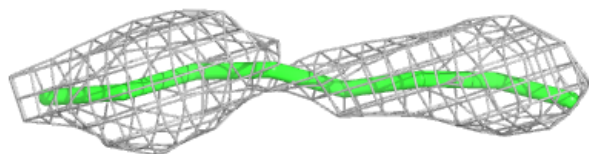
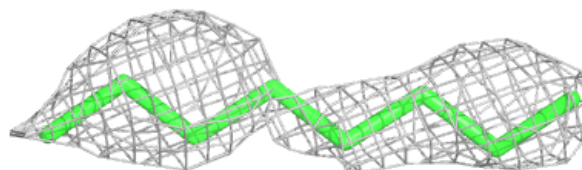


**Electron density around OLA A 1213:**

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

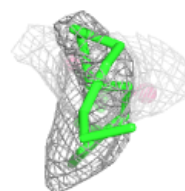
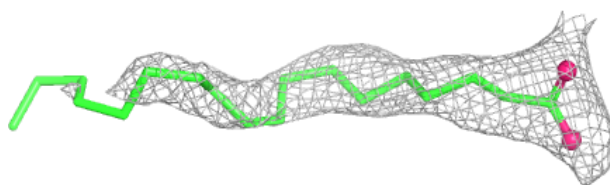
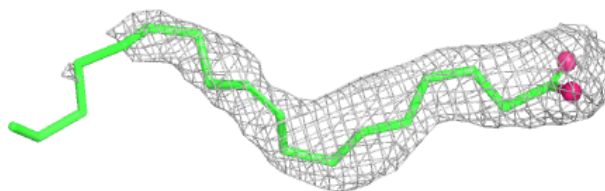
**Electron density around OLA A 1223:**

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

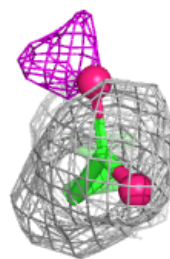
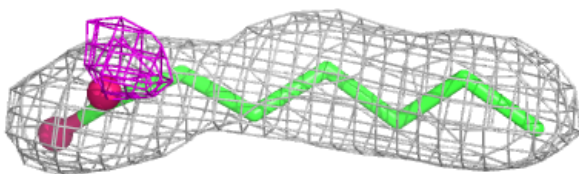
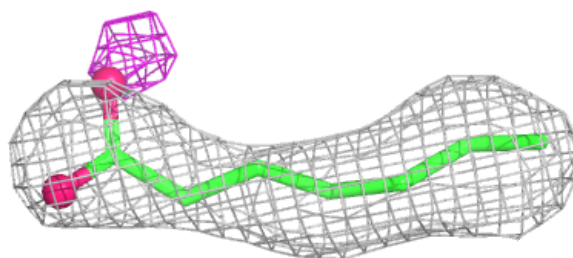


**Electron density around OLA A 1211:**

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

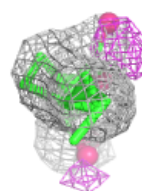
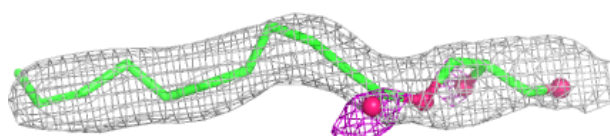
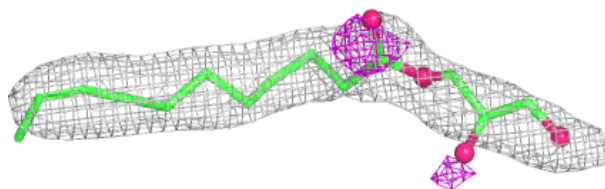
**Electron density around OLA A 1208:**

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

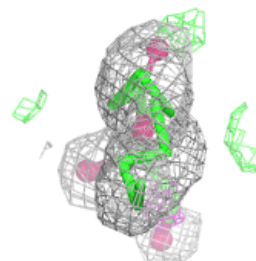
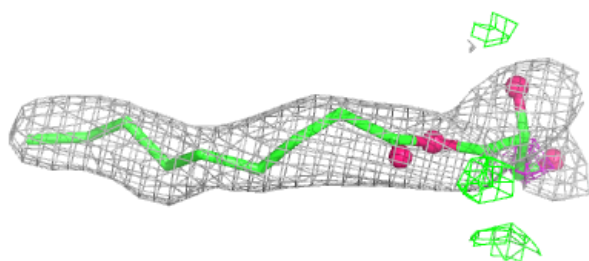
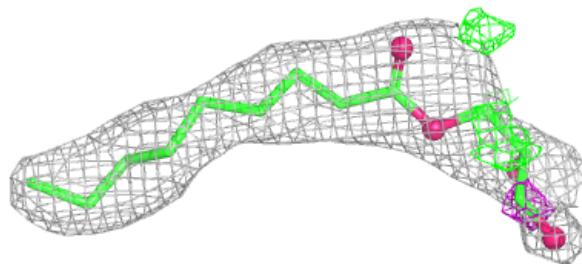


**Electron density around OLC A 1233:**

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

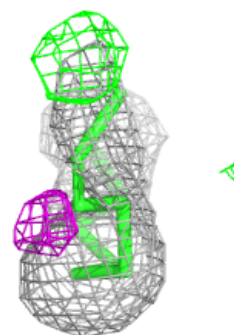
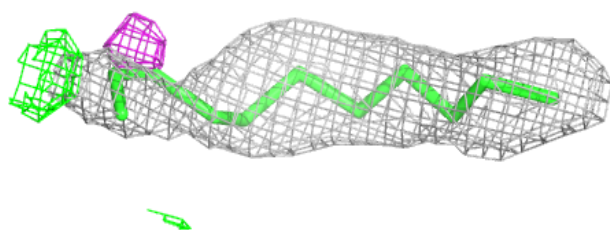
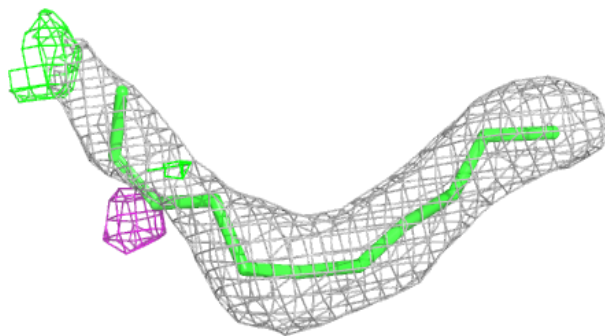
**Electron density around OLC A 1234:**

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

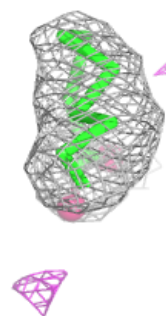
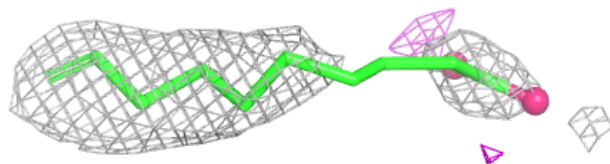
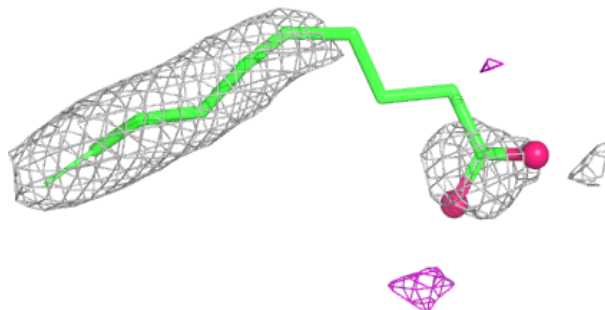


**Electron density around OLA A 1220:**

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

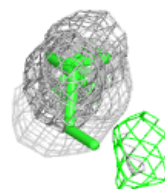
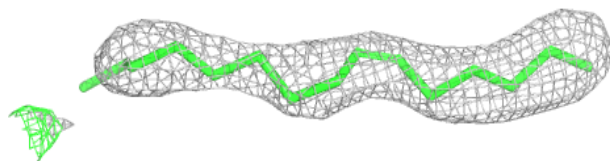
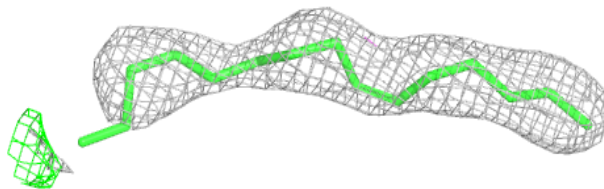
**Electron density around OLA A 1212:**

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



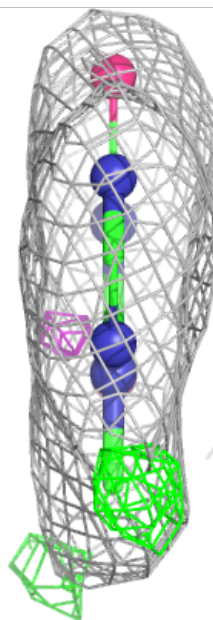
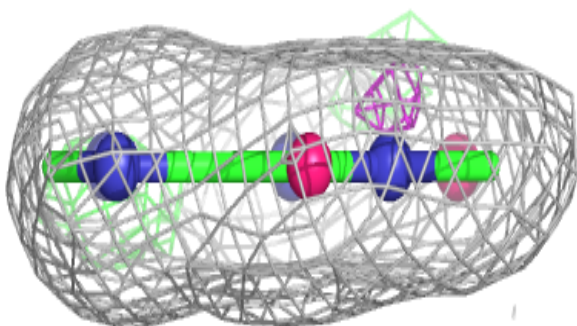
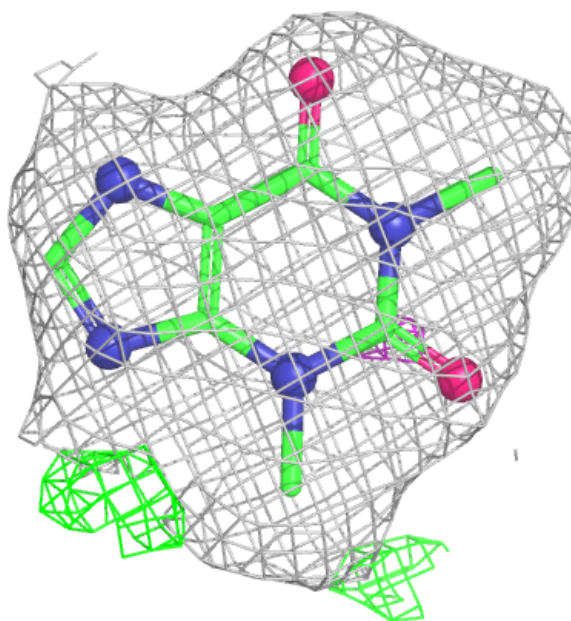
**Electron density around OLA A 1225:**

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



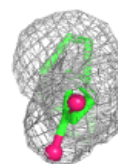
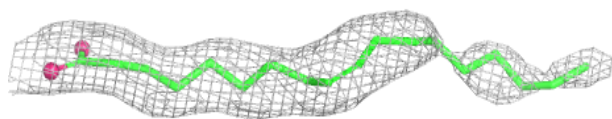
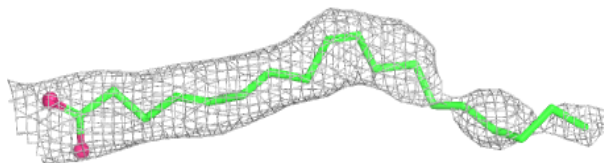
**Electron density around TEP A 1202:**

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

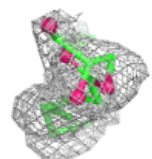
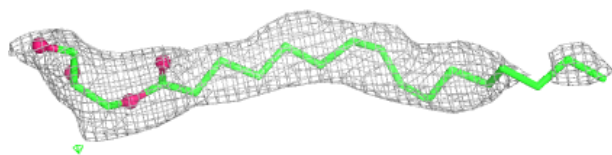
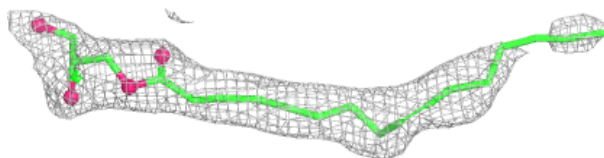


**Electron density around OLA A 1206:**

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

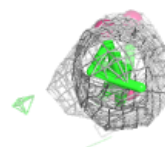
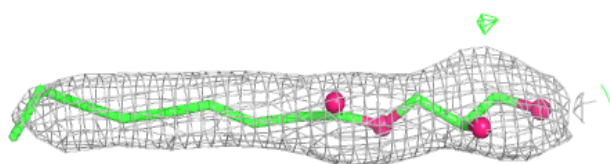
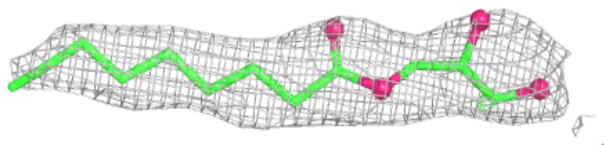
**Electron density around OLC A 1231:**

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

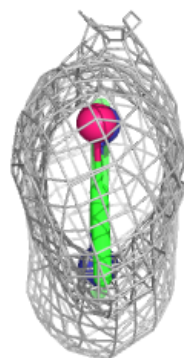
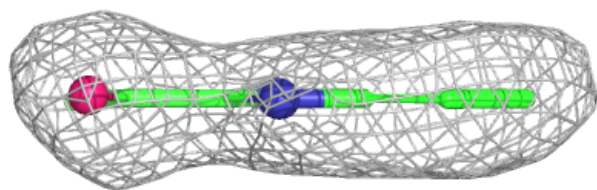
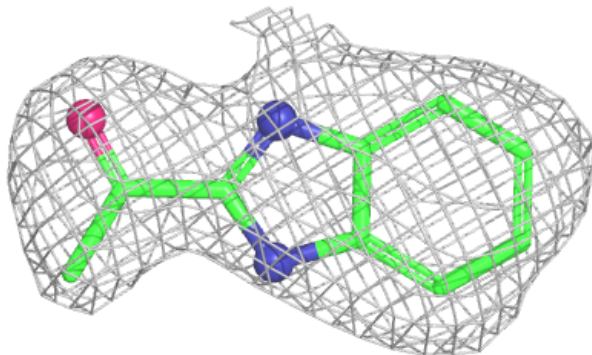


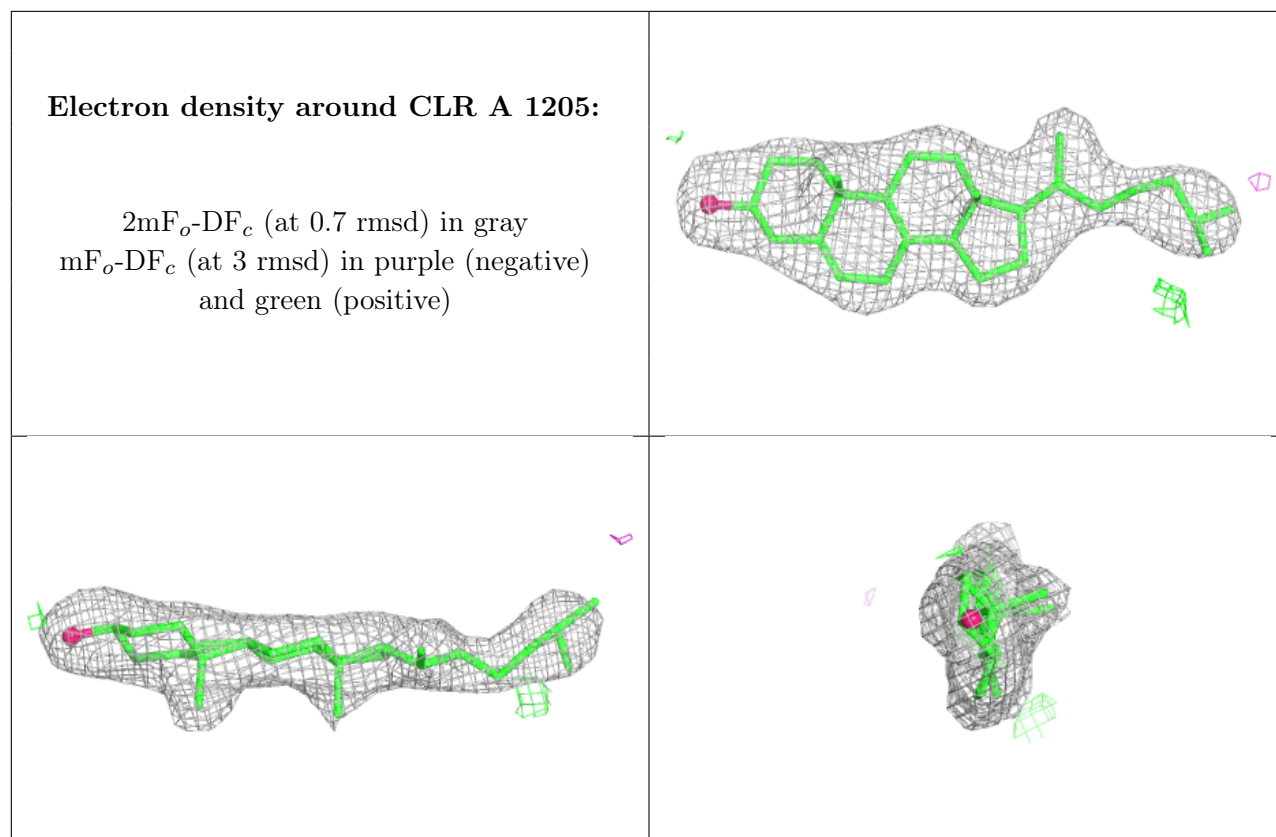
**Electron density around OLC A 1228:**

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

**Electron density around A1CQC A 1235:**

$2mF_o-DF_c$  (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.