



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 24, 2022 – 03:37 pm GMT

PDB ID : 6RZ6
Title : Crystal structure of the human cysteinyl leukotriene receptor 2 in complex with ONO-2570366 (C2221 space group)
Authors : Gusach, A.; Luginina, A.; Marin, E.; Brouillette, R.L.; Besserer-Offroy, E.; Longpre, J.M.; Ishchenko, A.; Popov, P.; Fujimoto, T.; Maruyama, T.; Stauch, B.; Ergasheva, M.; Romanovskaya, D.; Stepko, A.; Kovalev, K.; Shevtsov, M.; Gordeliy, V.; Han, G.W.; Sarret, P.; Katritch, V.; Borshchevskiy, V.; Mishin, A.; Cherezov, V.
Deposited on : 2019-06-12
Resolution : 2.43 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.27
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.27

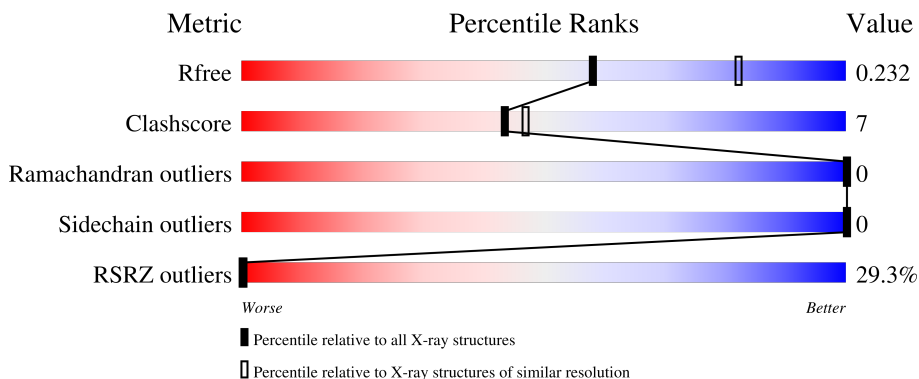
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.43 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1564 (2.46-2.42)
Clashscore	141614	1631 (2.46-2.42)
Ramachandran outliers	138981	1617 (2.46-2.42)
Sidechain outliers	138945	1617 (2.46-2.42)
RSRZ outliers	127900	1547 (2.46-2.42)

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

Mol	Chain	Length	Quality of chain
1	A	405	

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
4	TLA	A	2003	-	-	-	X
5	OLC	A	2015	-	-	-	X
5	OLC	A	2016	-	-	-	X
5	OLC	A	2017	-	-	-	X
7	1PE	A	2030	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 3326 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.

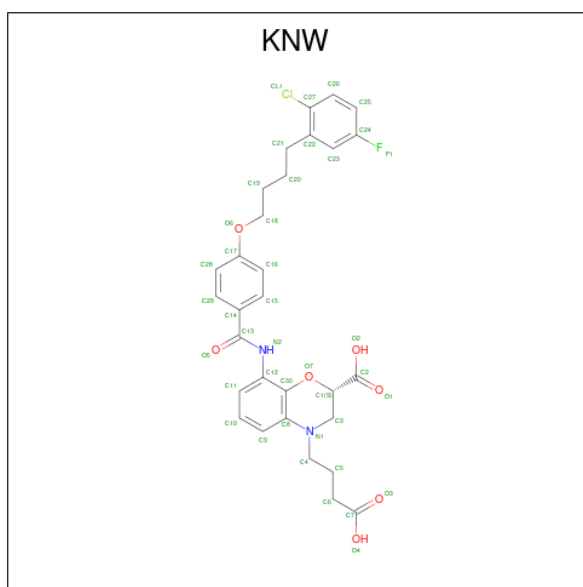
- Molecule 1 is a protein called Cysteinyl leukotriene receptor 2, Soluble cytochrome b562, Cysteinyl leukotriene receptor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	365	2798	1846	450	482	20	0	4	0

There are 6 discrepancies between the modelled and reference sequences:

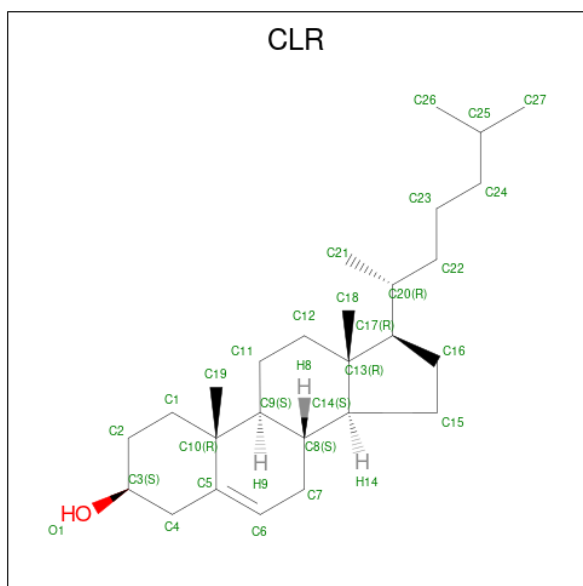
Chain	Residue	Modelled	Actual	Comment	Reference
A	51	VAL	TRP	engineered mutation	UNP Q9NS75
A	84	ASN	ASP	engineered mutation	UNP Q9NS75
A	137	TYR	PHE	engineered mutation	UNP Q9NS75
A	1007	TRP	MET	engineered mutation	UNP P0ABE7
A	1102	ILE	HIS	engineered mutation	UNP P0ABE7
A	1106	LEU	ARG	engineered mutation	UNP P0ABE7

- Molecule 2 is (2 {S})-8-[[4-[4-(2-chloranyl-5-fluoranyl-phenyl)butoxy]phenyl]carbonylamino]-4-(4-oxidanyl-4-oxidanylidene-butyl)-2,3-dihydro-1,4-benzoxazine-2-carboxylic acid (three-letter code: KNW) (formula: C₃₀H₃₀ClFN₂O₇) (labeled as "Ligand of Interest" by depositor).



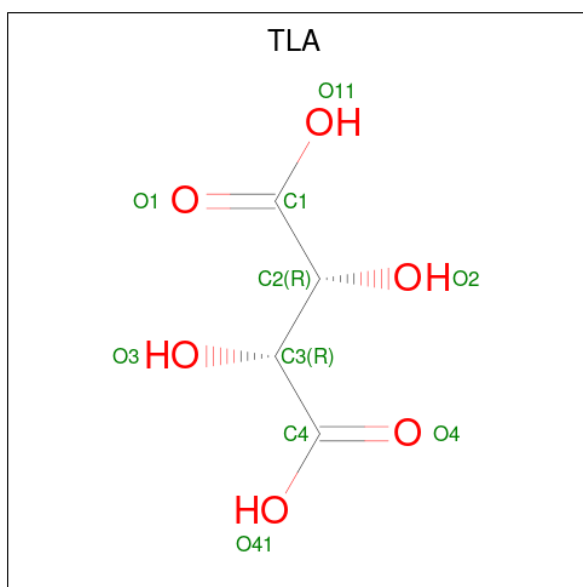
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	Cl	F	N			O
2	A	1	41	30	1	1	2	7	0	0

- Molecule 3 is CHOLESTEROL (three-letter code: CLR) (formula: $C_{27}H_{46}O$).



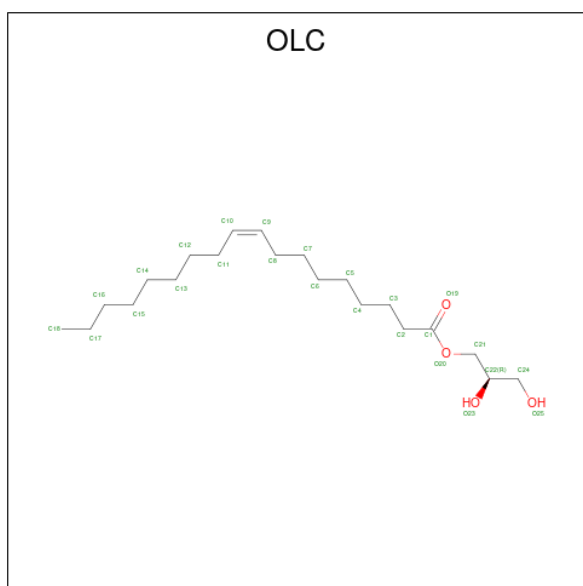
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	C O		
3	A	1	28	27 1	0	0

- Molecule 4 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula: $C_4H_6O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	4	6		

- Molecule 5 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLC) (formula: C₂₁H₄₀O₄).



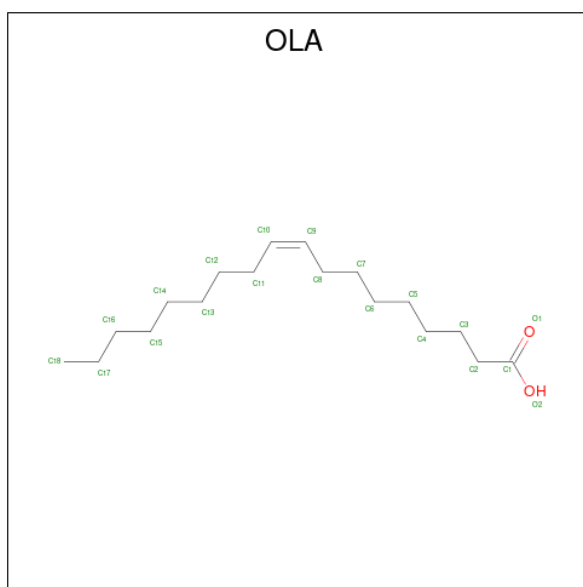
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			21	17	4		
5	A	1	Total	C	O	0	0
			21	17	4		

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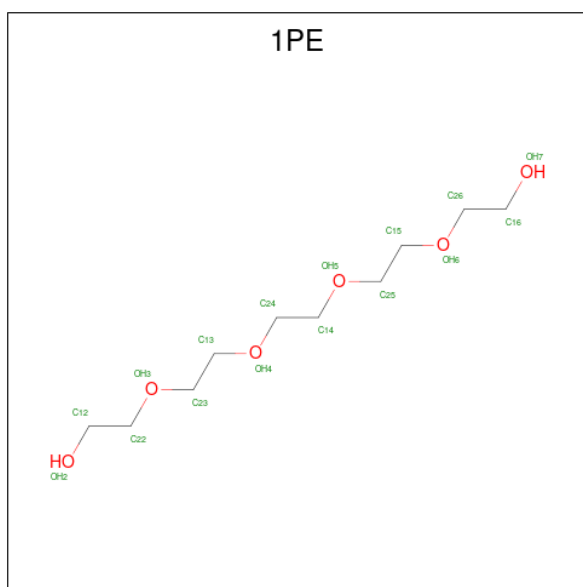
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 17 13 4	0	0
5	A	1	Total C 8 8	0	0
5	A	1	Total C 8 8	0	0
5	A	1	Total C O 25 21 4	0	0
5	A	1	Total C 8 8	0	0
5	A	1	Total C 12 12	0	0
5	A	1	Total C 11 11	0	0
5	A	1	Total C O 17 13 4	0	0
5	A	1	Total C 12 12	0	0
5	A	1	Total C 11 11	0	0
5	A	1	Total C O 16 12 4	0	0
5	A	1	Total C O 16 12 4	0	0
5	A	1	Total C 14 14	0	0
5	A	1	Total C 17 17	0	0

- Molecule 6 is OLEIC ACID (three-letter code: OLA) (formula: $C_{18}H_{34}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			16	14	2		
6	A	1	Total	C	O	0	0
			17	15	2		
6	A	1	Total	C	O	0	0
			12	10	2		
6	A	1	Total	C	O	0	0
			20	18	2		
6	A	1	Total	C	O	0	0
			20	18	2		
6	A	1	Total	C	O	0	0
			10	8	2		
6	A	1	Total	C	O	0	0
			19	17	2		
6	A	1	Total	C	O	0	0
			20	18	2		
6	A	1	Total	C	O	0	0
			20	18	2		
6	A	1	Total	C	O	0	0
			11	9	2		

- Molecule 7 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	C O	0	0
			15	10 5		

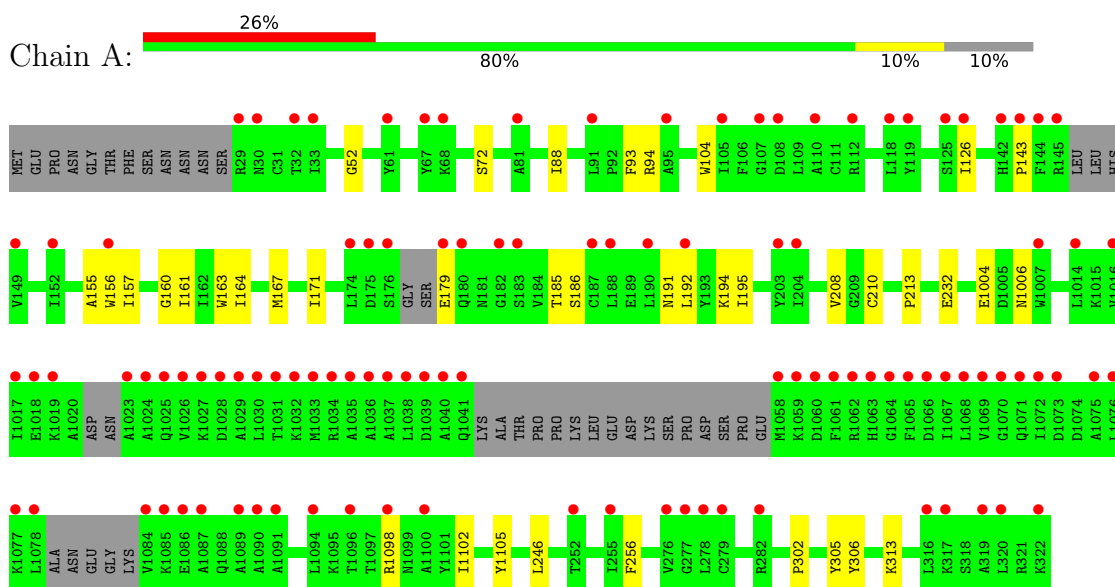
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	35	Total	O	0	0
			35	35		

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: Cysteinyl leukotriene receptor 2,Soluble cytochrome b562,Cysteinyl leukotriene receptor 2



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	69.81Å 170.88Å 85.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.90 – 2.43 28.90 – 2.43	Depositor EDS
% Data completeness (in resolution range)	99.6 (28.90-2.43) 90.0 (28.90-2.43)	Depositor EDS
R_{merge}	0.28	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.05 (at 2.42Å)	Xtriage
Refinement program	PHENIX 1.12-2829	Depositor
R, R_{free}	0.194 , 0.232 0.195 , 0.232	Depositor DCC
R_{free} test set	984 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	45.1	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3326	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.28% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: OLC, KNW, 1PE, TLA, OLA, 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	0.38	0/2851	0.56	0/3881

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 [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	2798	0	2769	30	0
2	A	41	0	0	2	0
3	A	28	0	46	1	0
4	A	10	0	4	0	0
5	A	234	0	343	17	0
6	A	165	0	247	7	0
7	A	15	0	19	4	0
8	A	35	0	0	1	0
All	All	3326	0	3428	45	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 45 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)
6:A:2028:OLA:H9	6:A:2029:OLA:H71	1.61	0.81
1:A:179:GLU:HA	1:A:185:THR:HG23	1.72	0.70
1:A:179:GLU:N	1:A:186:SER:O	2.26	0.69
2:A:2001:KNW:C26	5:A:2015:OLC:H17	2.25	0.65
5:A:2013:OLC:H8	6:A:2028:OLA:H41	1.78	0.64

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	357/405 (88%)	353 (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	282/356 (79%)	282 (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. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

30 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	CLR	A	2002	-	31,31,31	0.63	0	48,48,48	1.22	3 (6%)
5	OLC	A	2013	-	16,16,24	0.72	0	17,17,25	1.05	1 (5%)
6	OLA	A	2027	-	16,19,19	0.23	0	15,19,19	0.67	0
2	KNW	A	2001	-	38,44,44	0.48	1 (2%)	48,60,60	0.69	1 (2%)
5	OLC	A	2012	-	10,10,24	0.36	0	9,9,25	0.63	0
5	OLC	A	2004	-	20,20,24	0.66	0	21,21,25	1.04	1 (4%)
4	TLA	A	2003	-	3,9,9	0.55	0	6,12,12	0.74	0
5	OLC	A	2014	-	11,11,24	0.38	0	9,10,25	0.79	0
5	OLC	A	2016	-	15,15,24	0.72	0	16,16,25	1.09	1 (6%)
5	OLC	A	2011	-	11,11,24	0.35	0	10,10,25	0.65	0
5	OLC	A	2015	-	10,10,24	0.36	0	9,9,25	0.93	0
6	OLA	A	2024	-	16,19,19	0.26	0	15,19,19	0.55	0
5	OLC	A	2019	-	16,16,24	0.35	0	15,15,25	0.75	0
5	OLC	A	2009	-	24,24,24	0.61	0	25,25,25	0.98	1 (4%)
6	OLA	A	2026	-	15,18,19	0.23	0	14,18,19	0.57	0
5	OLC	A	2006	-	16,16,24	0.69	0	17,17,25	1.05	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	OLC	A	2017	-	15,15,24	0.73	0	16,16,25	1.04	1 (6%)
6	OLA	A	2022	-	8,11,19	0.35	0	7,11,19	0.67	0
6	OLA	A	2025	-	6,9,19	0.22	0	5,9,19	0.56	0
6	OLA	A	2021	-	13,16,19	0.22	0	12,16,19	0.67	0
5	OLC	A	2018	-	13,13,24	0.36	0	12,12,25	0.71	0
6	OLA	A	2029	-	7,10,19	0.18	0	6,10,19	0.67	0
6	OLA	A	2028	-	16,19,19	0.29	0	15,19,19	0.48	0
5	OLC	A	2007	-	7,7,24	0.41	0	5,6,25	0.75	0
5	OLC	A	2005	-	20,20,24	0.66	0	21,21,25	1.06	1 (4%)
5	OLC	A	2010	-	7,7,24	0.33	0	6,6,25	0.69	0
5	OLC	A	2008	-	7,7,24	0.45	0	6,6,25	0.73	0
6	OLA	A	2020	-	12,15,19	0.19	0	11,15,19	0.73	0
7	1PE	A	2030	-	14,14,15	0.43	0	13,13,14	0.41	0
6	OLA	A	2023	-	16,19,19	0.23	0	15,19,19	0.55	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CLR	A	2002	-	-	7/10/68/68	0/4/4/4
5	OLC	A	2013	-	-	9/16/16/24	-
6	OLA	A	2027	-	-	8/15/17/17	-
2	KNW	A	2001	-	-	0/20/38/38	0/4/4/4
5	OLC	A	2012	-	-	3/8/8/24	-
5	OLC	A	2004	-	-	6/20/20/24	-
4	TLA	A	2003	-	-	0/4/12/12	-
5	OLC	A	2014	-	-	1/9/9/24	-
5	OLC	A	2016	-	-	11/15/15/24	-
5	OLC	A	2011	-	-	2/9/9/24	-
5	OLC	A	2015	-	-	5/8/8/24	-
6	OLA	A	2024	-	-	9/15/17/17	-
5	OLC	A	2019	-	-	5/14/14/24	-
5	OLC	A	2009	-	-	7/24/24/24	-
6	OLA	A	2026	-	-	8/14/16/17	-
5	OLC	A	2006	-	-	6/16/16/24	-
5	OLC	A	2017	-	-	9/15/15/24	-
6	OLA	A	2022	-	-	4/7/9/17	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	OLA	A	2025	-	-	4/5/7/17	-
6	OLA	A	2021	-	-	6/12/14/17	-
5	OLC	A	2018	-	-	6/11/11/24	-
6	OLA	A	2029	-	-	4/6/8/17	-
6	OLA	A	2028	-	-	7/15/17/17	-
5	OLC	A	2007	-	-	3/5/5/24	-
5	OLC	A	2005	-	-	9/20/20/24	-
5	OLC	A	2010	-	-	0/5/5/24	-
5	OLC	A	2008	-	-	2/5/5/24	-
6	OLA	A	2020	-	-	8/11/13/17	-
7	1PE	A	2030	-	-	8/12/12/13	-
6	OLA	A	2023	-	-	8/15/17/17	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2001	KNW	C8-N1	-2.13	1.38	1.43

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2002	CLR	C21-C20-C22	-5.14	102.30	110.36
5	A	2004	OLC	O20-C1-C2	3.13	121.73	111.91
5	A	2005	OLC	O20-C1-C2	3.10	121.63	111.91
5	A	2009	OLC	O20-C1-C2	2.96	121.20	111.91
5	A	2017	OLC	O20-C1-C2	2.88	120.94	111.91

There are no chirality outliers.

5 of 165 torsion outliers are listed below:

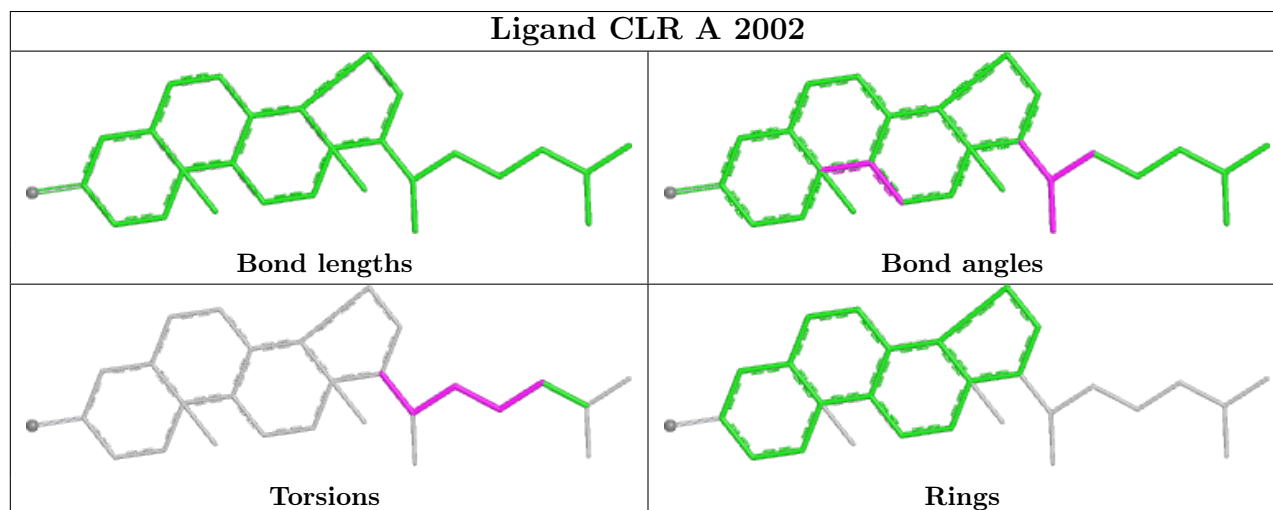
Mol	Chain	Res	Type	Atoms
5	A	2005	OLC	C21-C22-C24-O25
5	A	2006	OLC	O20-C21-C22-C24
5	A	2009	OLC	C21-C22-C24-O25
5	A	2017	OLC	C21-C22-C24-O25
5	A	2017	OLC	O20-C21-C22-C24

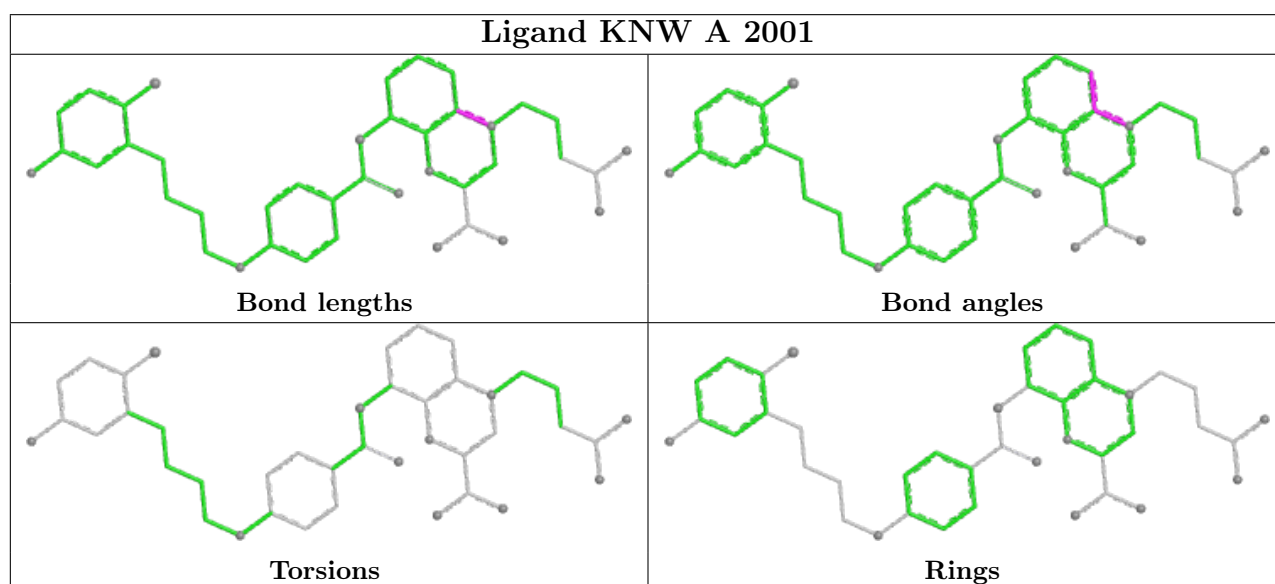
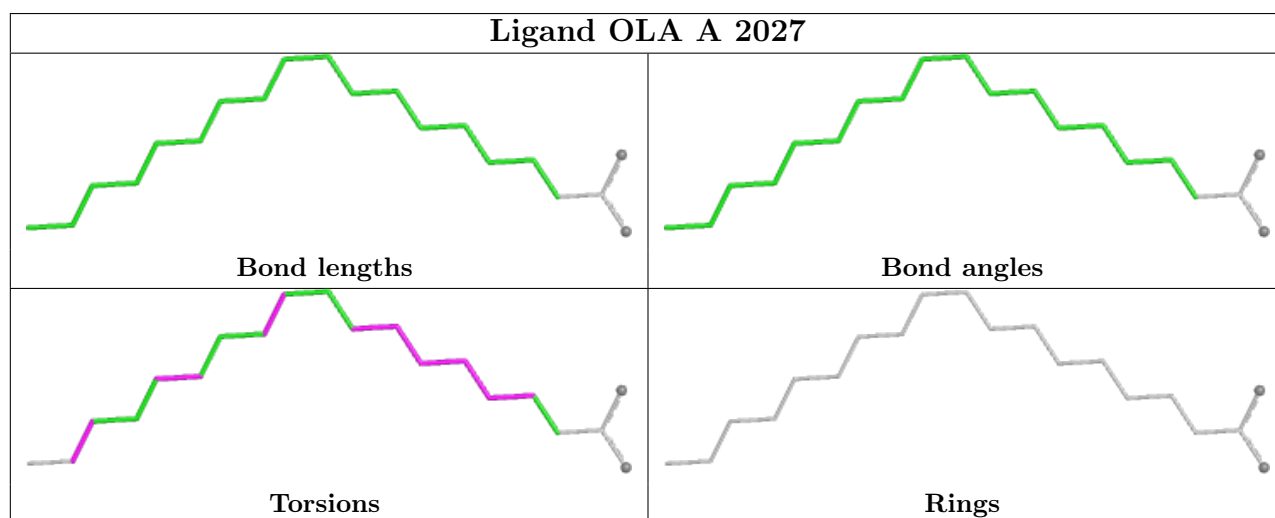
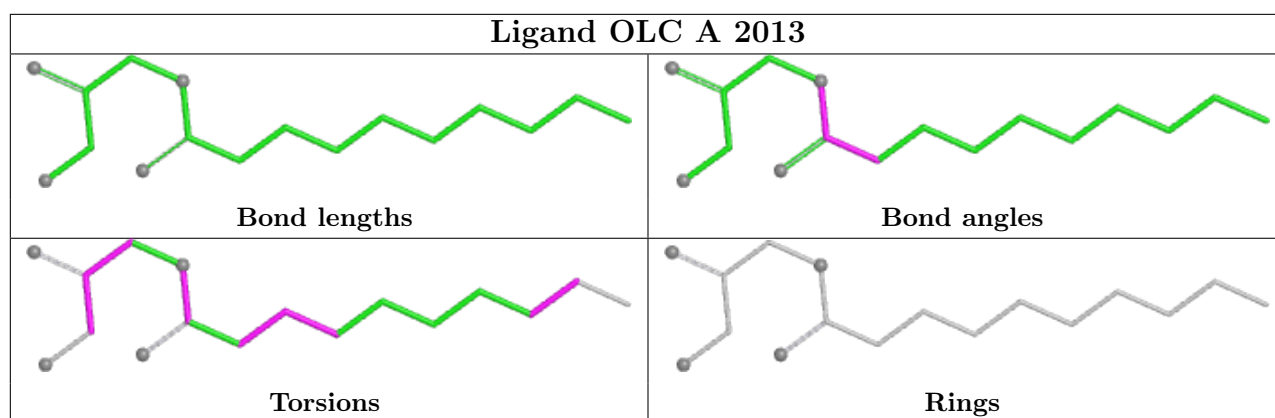
There are no ring outliers.

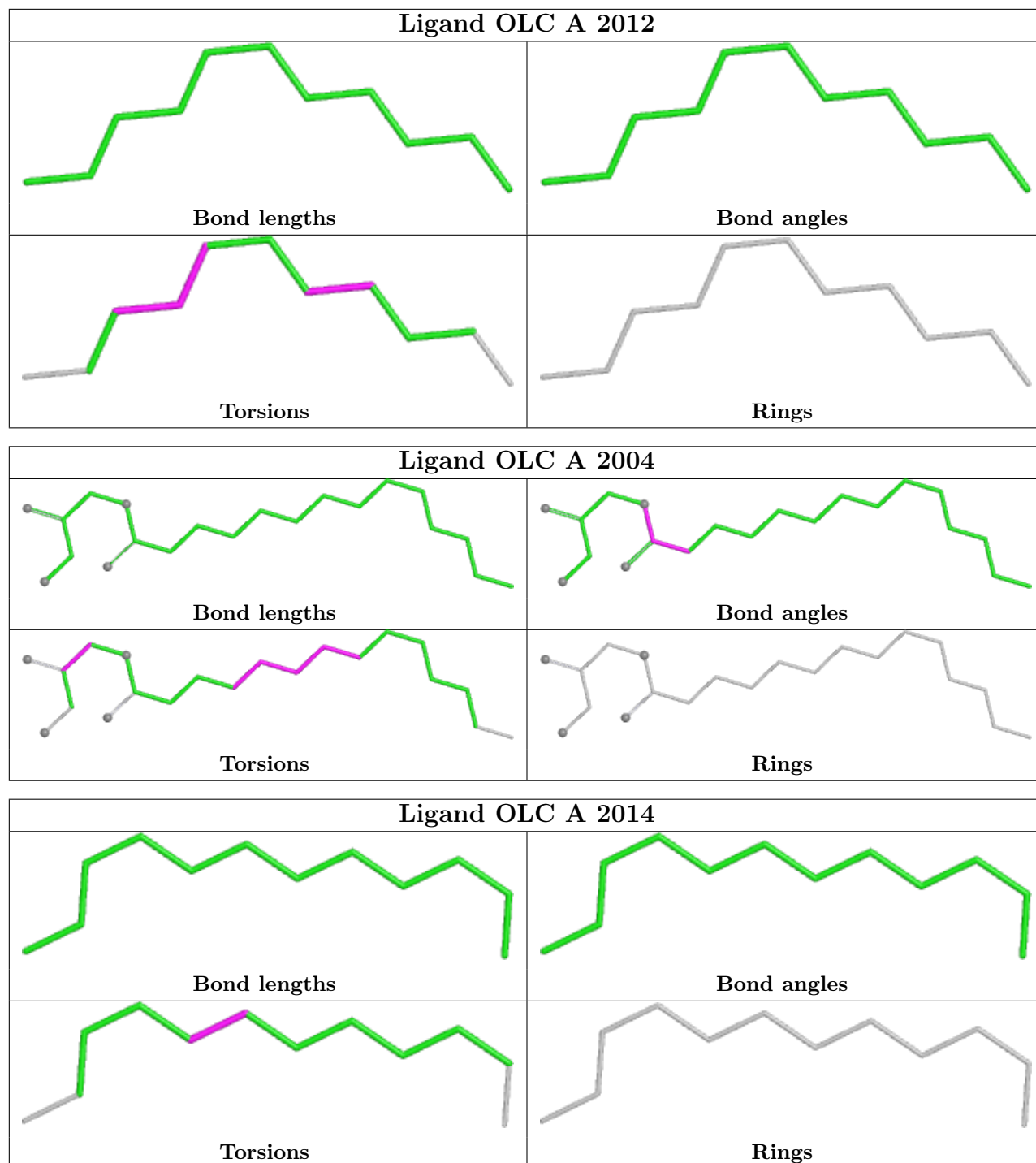
17 monomers are involved in 26 short contacts:

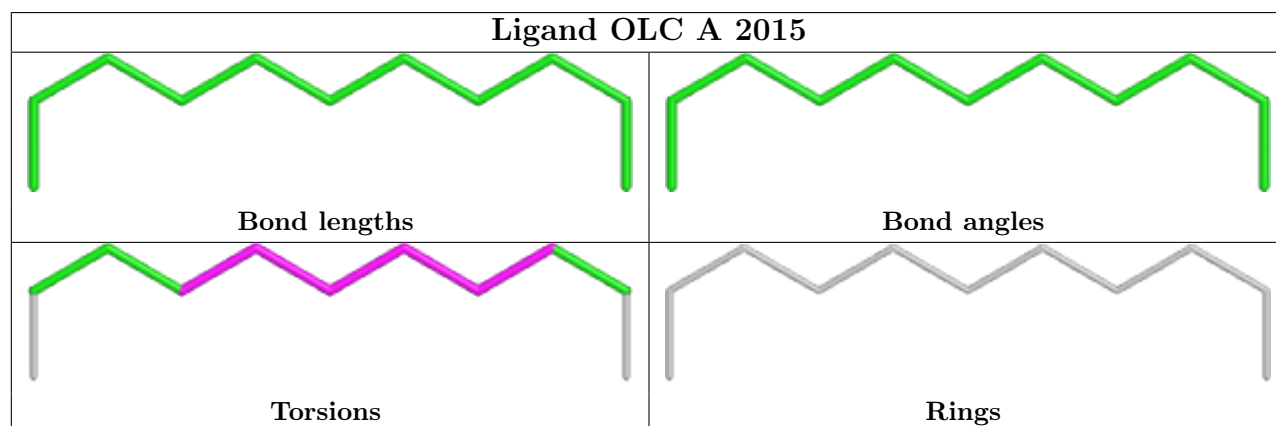
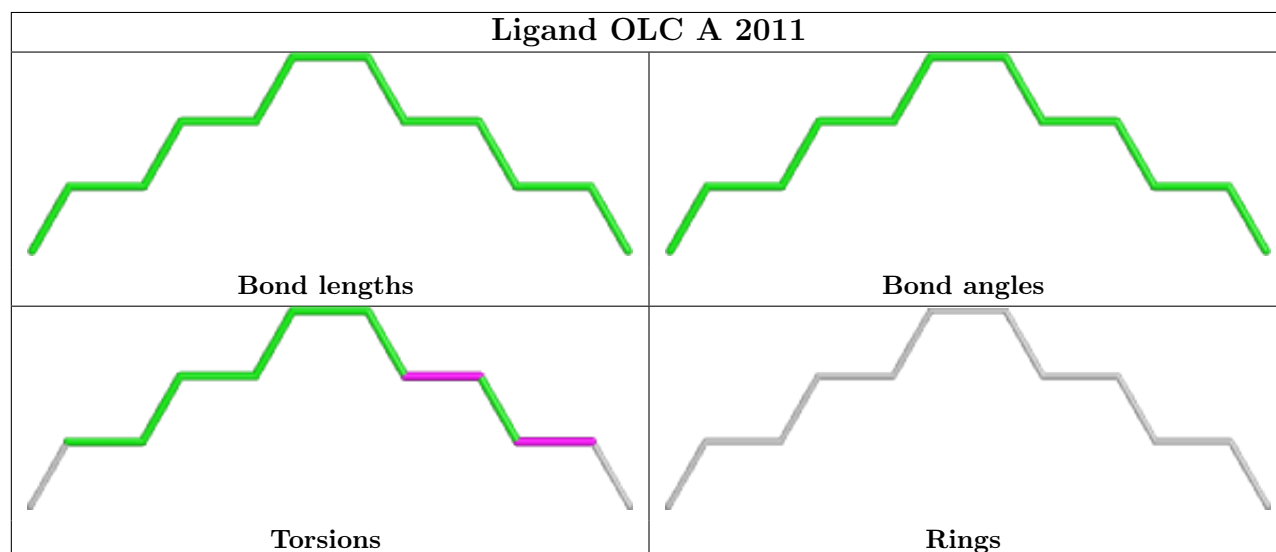
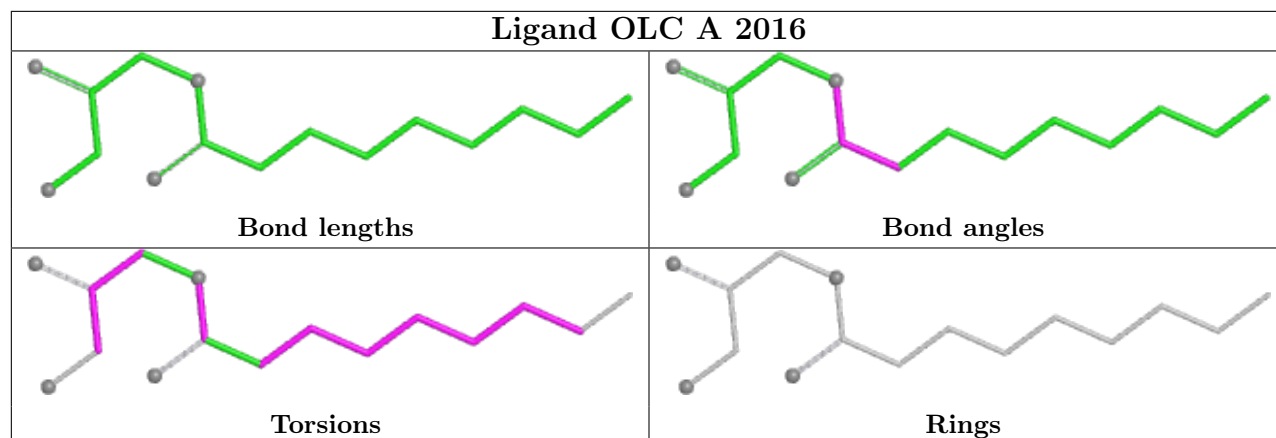
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2002	CLR	1	0
5	A	2013	OLC	4	0
6	A	2027	OLA	2	0
2	A	2001	KNW	2	0
5	A	2012	OLC	1	0
5	A	2004	OLC	1	0
5	A	2016	OLC	1	0
5	A	2011	OLC	2	0
5	A	2015	OLC	4	0
5	A	2019	OLC	3	0
5	A	2009	OLC	1	0
6	A	2029	OLA	1	0
6	A	2028	OLA	4	0
5	A	2005	OLC	1	0
5	A	2008	OLC	2	0
6	A	2020	OLA	1	0
7	A	2030	1PE	4	0

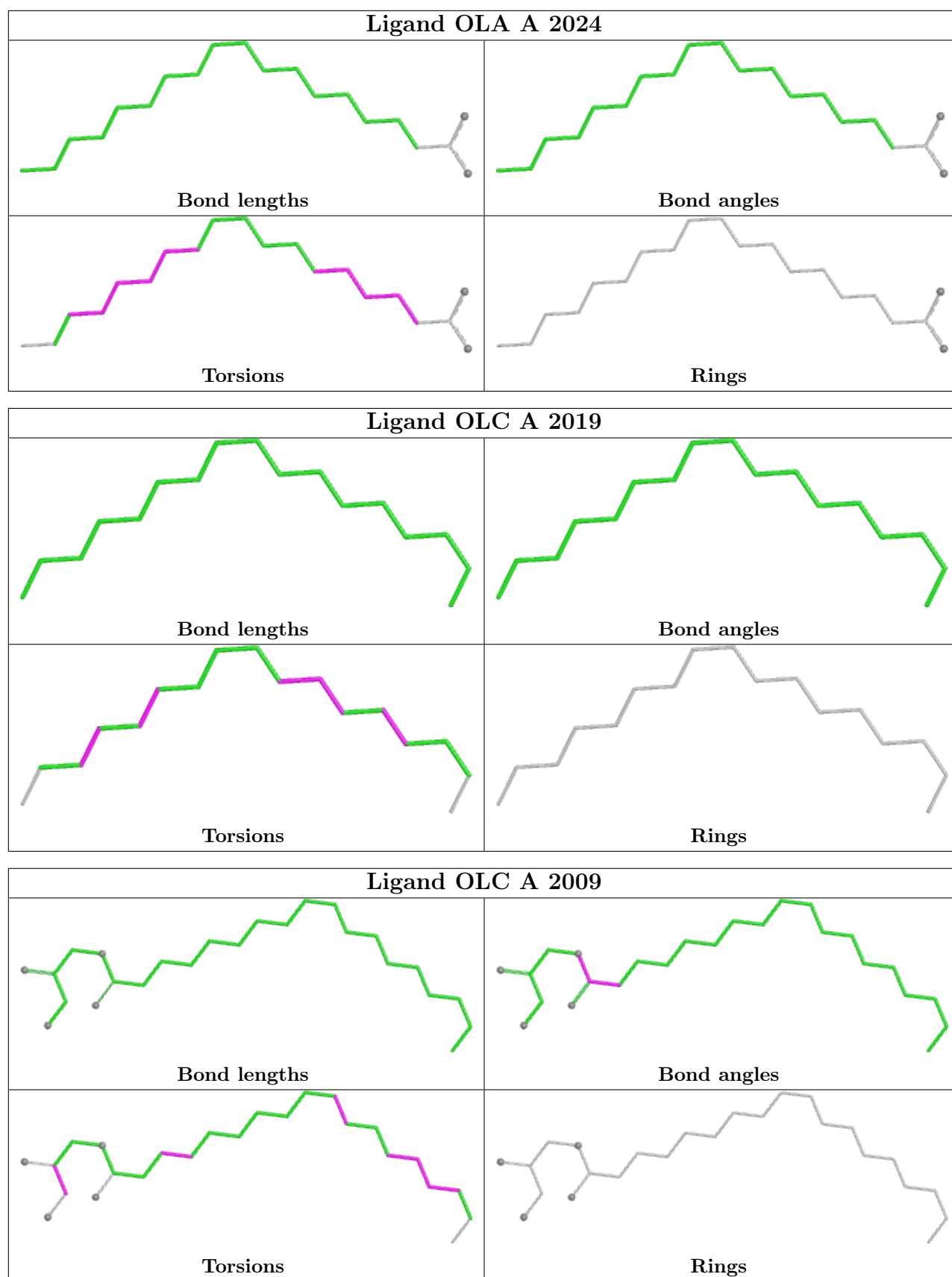
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

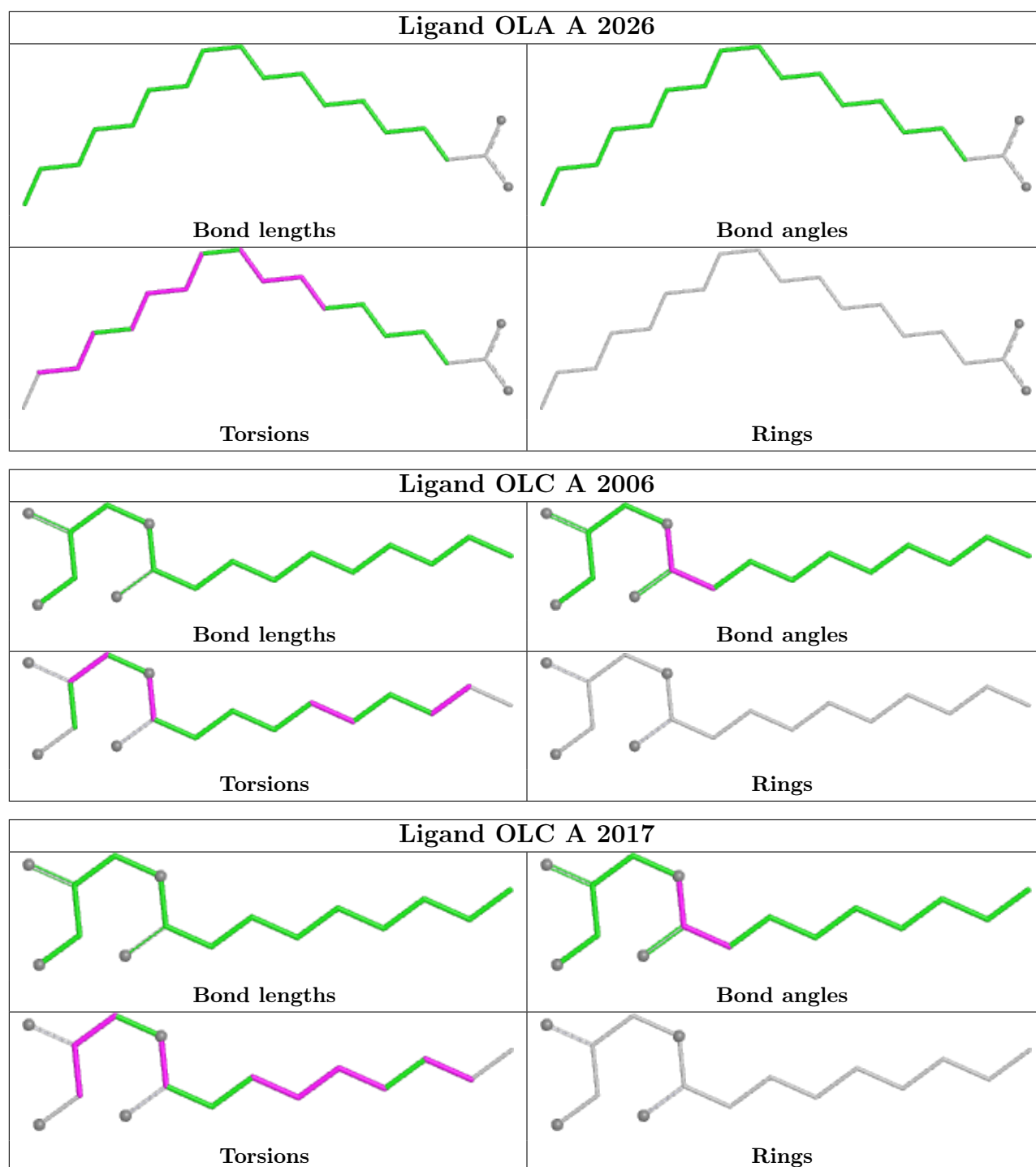


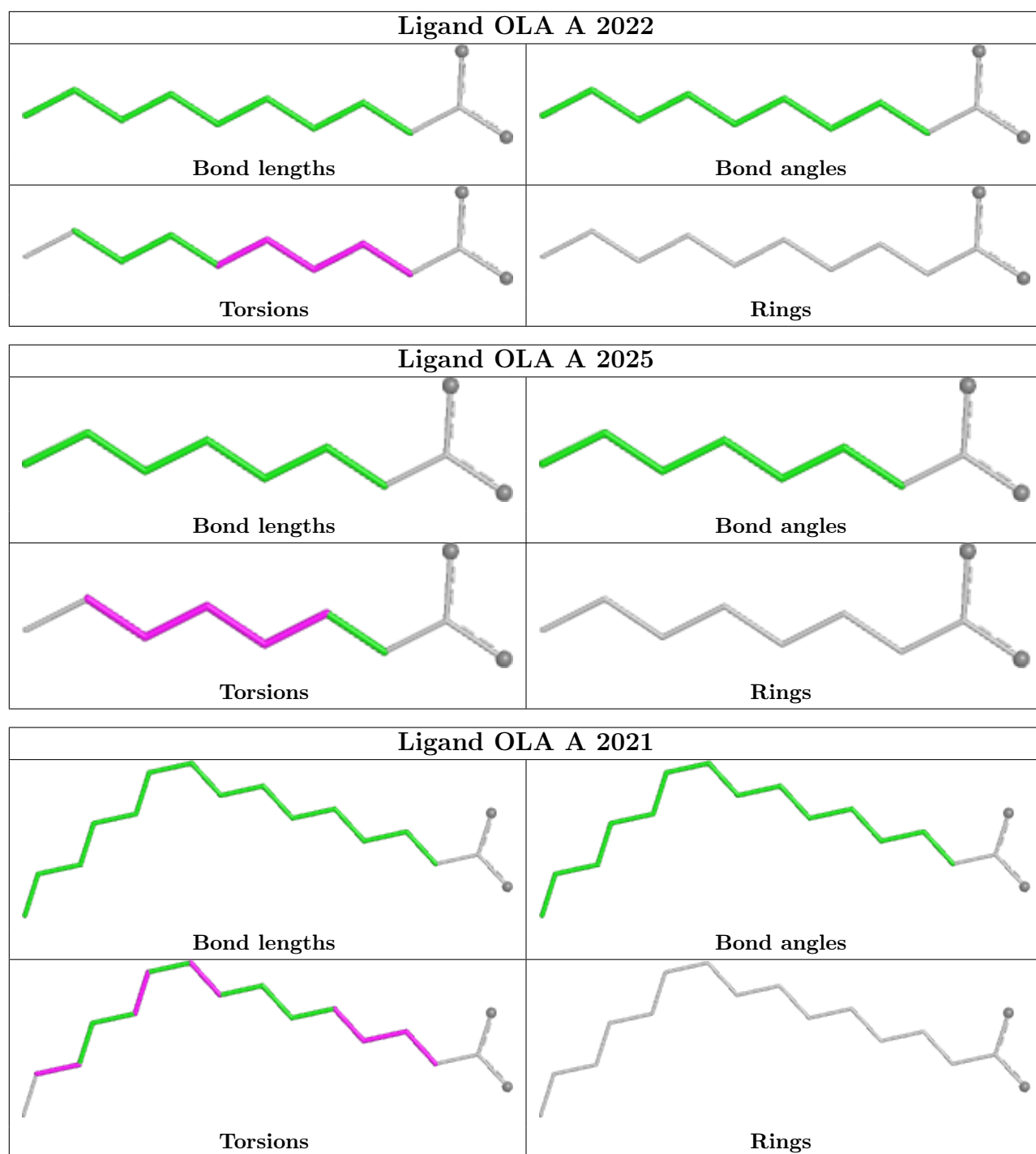


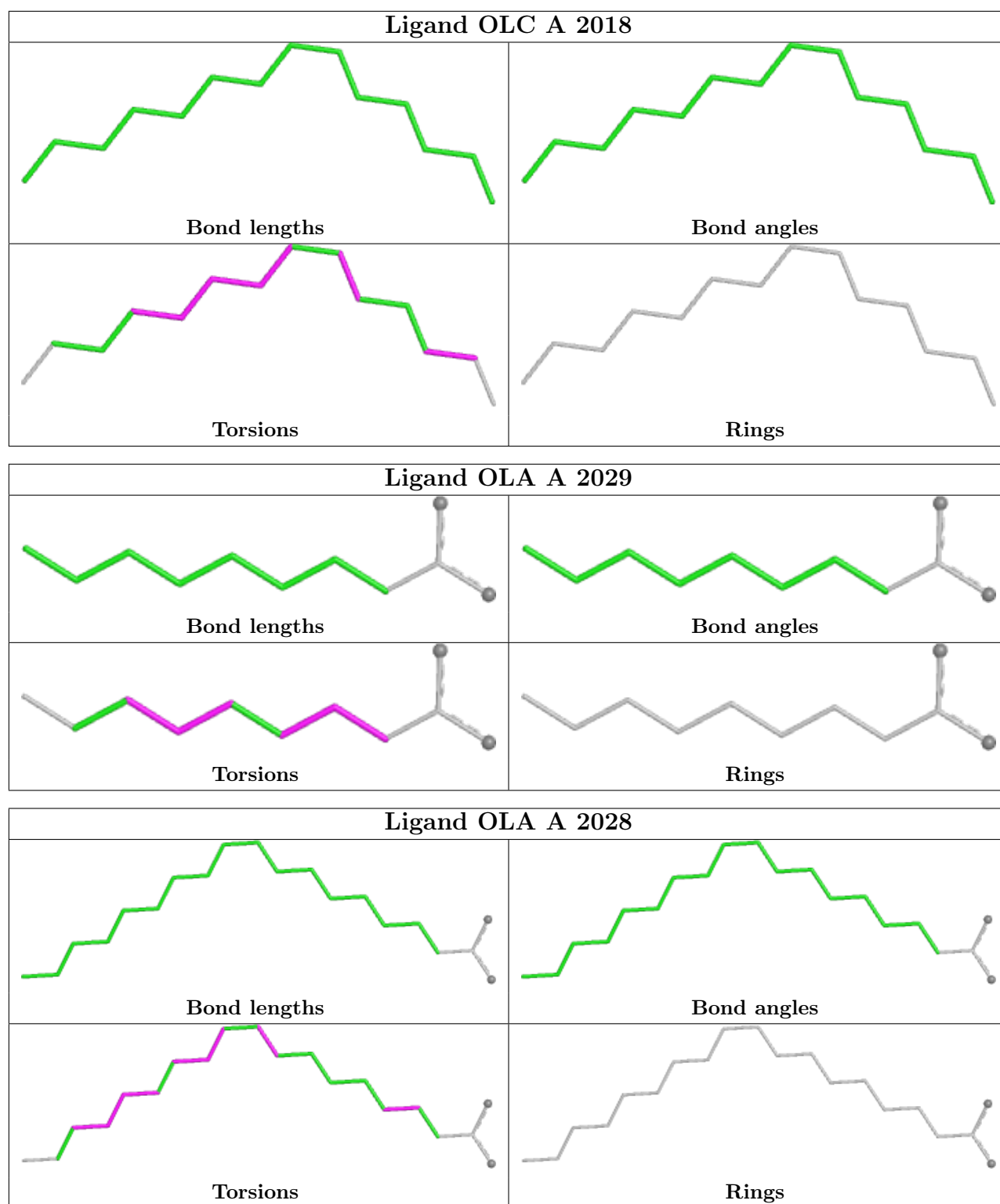


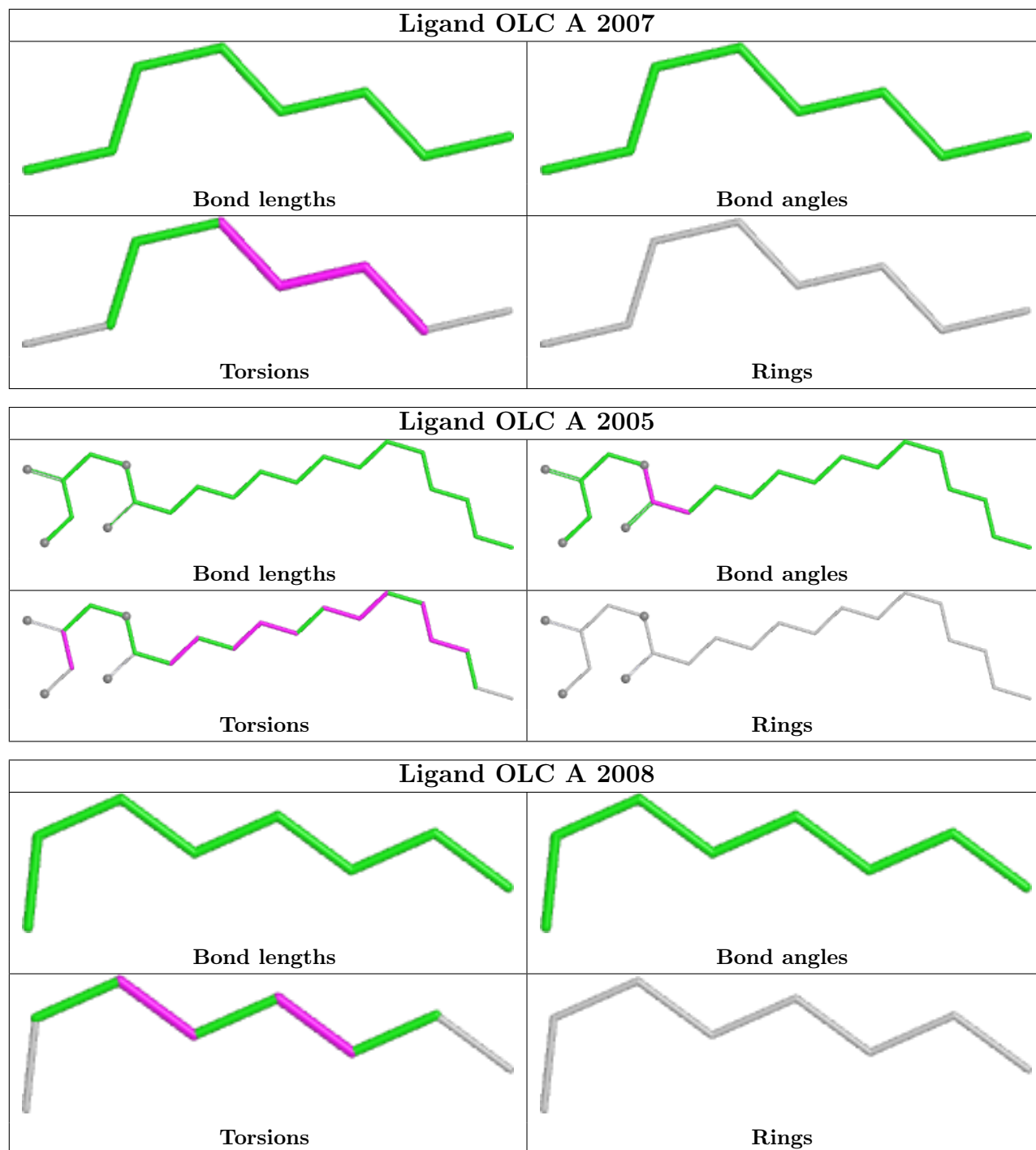


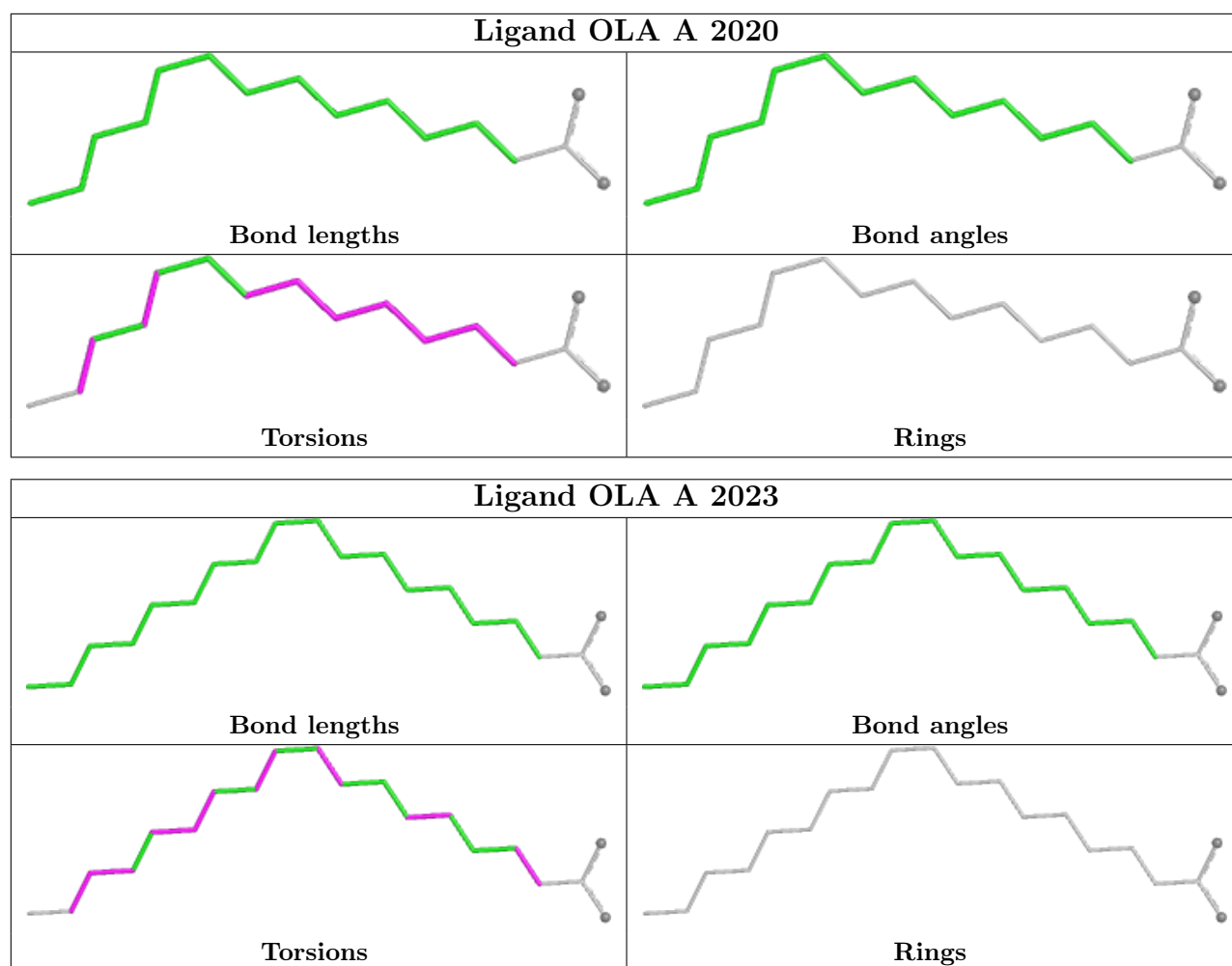












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	365/405 (90%)	1.77	107 (29%) 0 0	36, 55, 148, 185	0

The worst 5 of 107 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1076	LEU	19.5
1	A	1035	ALA	12.9
1	A	1085	LYS	10.6
1	A	1072	ILE	9.7
1	A	1077	LYS	9.7

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	OLA	A	2022	12/20	0.40	0.27	76,100,117,122	0
4	TLA	A	2003	10/10	0.44	0.51	113,116,117,117	0

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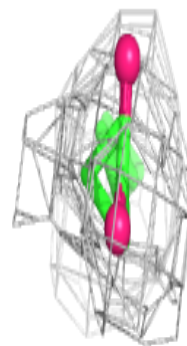
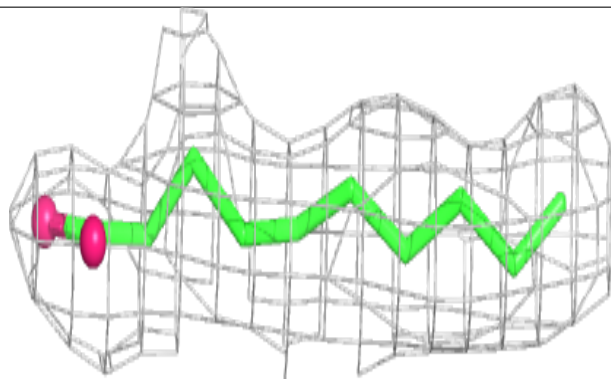
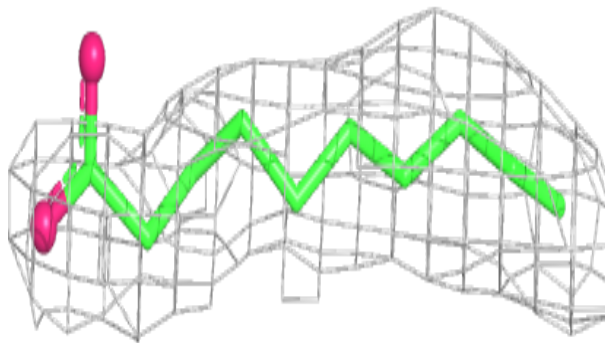
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	OLA	A	2027	20/20	0.44	0.35	56,75,91,93	0
6	OLA	A	2029	11/20	0.52	0.36	91,96,106,106	0
6	OLA	A	2026	19/20	0.54	0.31	75,91,108,110	0
5	OLC	A	2019	17/25	0.56	0.36	81,87,89,89	0
6	OLA	A	2028	20/20	0.57	0.26	80,89,102,102	0
5	OLC	A	2016	16/25	0.58	0.43	82,109,119,121	0
6	OLA	A	2024	20/20	0.58	0.37	62,87,104,104	0
5	OLC	A	2012	11/25	0.58	0.28	88,90,94,94	0
7	1PE	A	2030	15/16	0.60	0.41	102,107,117,117	0
5	OLC	A	2013	17/25	0.61	0.33	79,84,87,92	0
6	OLA	A	2021	17/20	0.63	0.24	87,97,109,110	0
5	OLC	A	2006	17/25	0.64	0.28	79,94,116,120	0
5	OLC	A	2010	8/25	0.67	0.28	82,87,91,93	0
3	CLR	A	2002	28/28	0.67	0.27	37,51,69,74	0
5	OLC	A	2017	16/25	0.67	0.51	60,96,109,112	0
5	OLC	A	2014	12/25	0.70	0.23	75,80,85,85	0
5	OLC	A	2011	12/25	0.72	0.26	67,80,86,86	0
5	OLC	A	2018	14/25	0.73	0.20	69,73,85,87	0
5	OLC	A	2004	21/25	0.73	0.25	64,78,89,95	0
5	OLC	A	2009	25/25	0.75	0.27	65,77,86,97	0
5	OLC	A	2015	11/25	0.75	0.53	50,55,77,78	0
5	OLC	A	2005	21/25	0.77	0.22	63,77,87,93	0
6	OLA	A	2023	20/20	0.79	0.29	59,67,80,82	0
6	OLA	A	2020	16/20	0.80	0.22	73,77,87,89	0
6	OLA	A	2025	10/20	0.82	0.14	75,88,118,118	0
5	OLC	A	2007	8/25	0.82	0.38	73,75,78,81	0
2	KNW	A	2001	41/41	0.90	0.19	40,48,57,63	0
5	OLC	A	2008	8/25	0.95	0.18	64,66,67,67	0

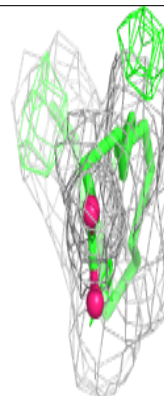
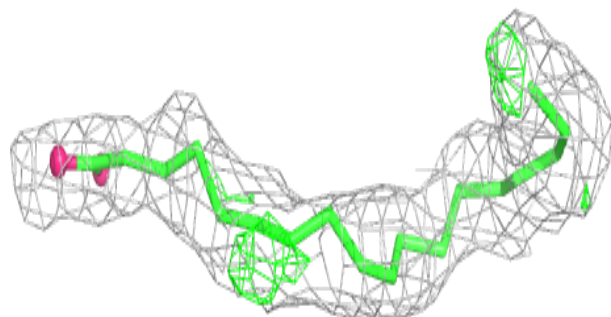
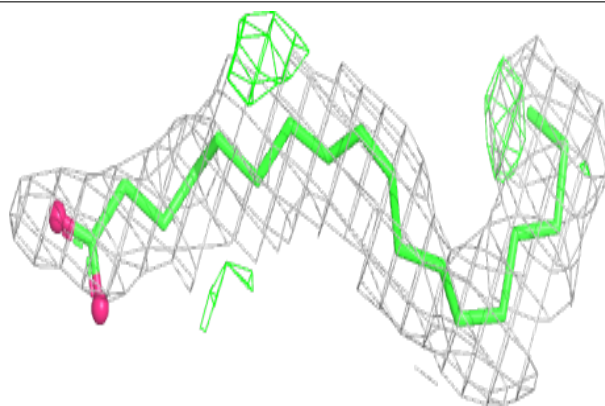
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around OLA A 2022:

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

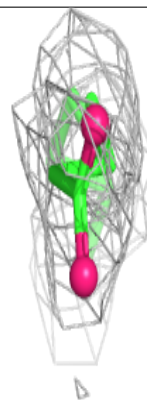
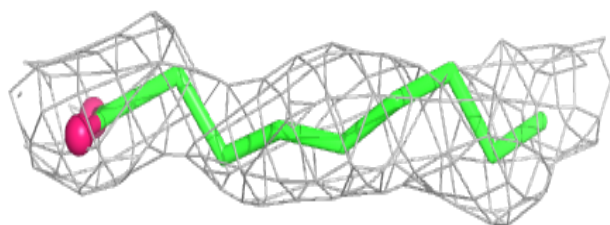
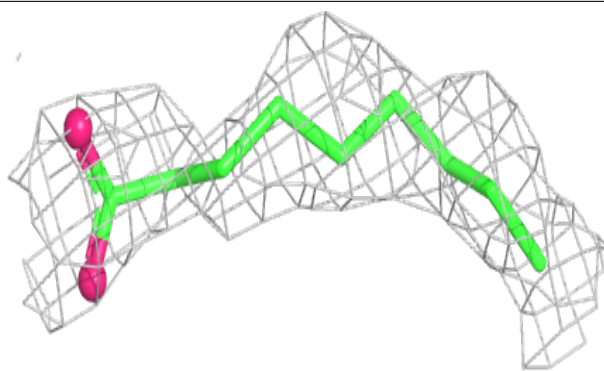
**Electron density around OLA A 2027:**

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

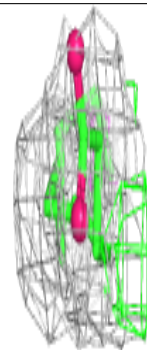
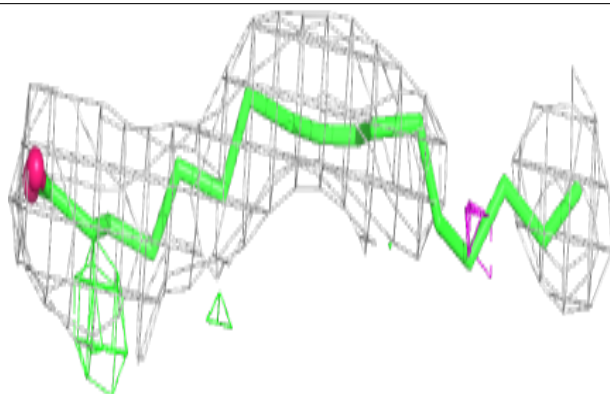
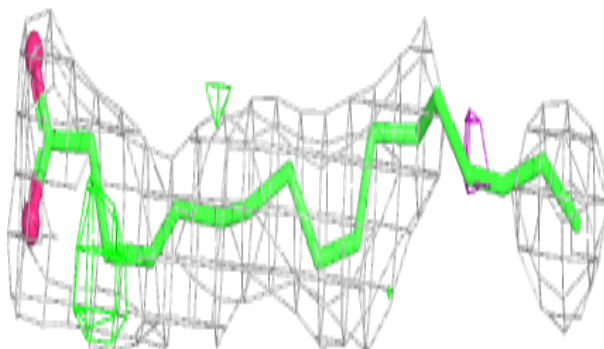


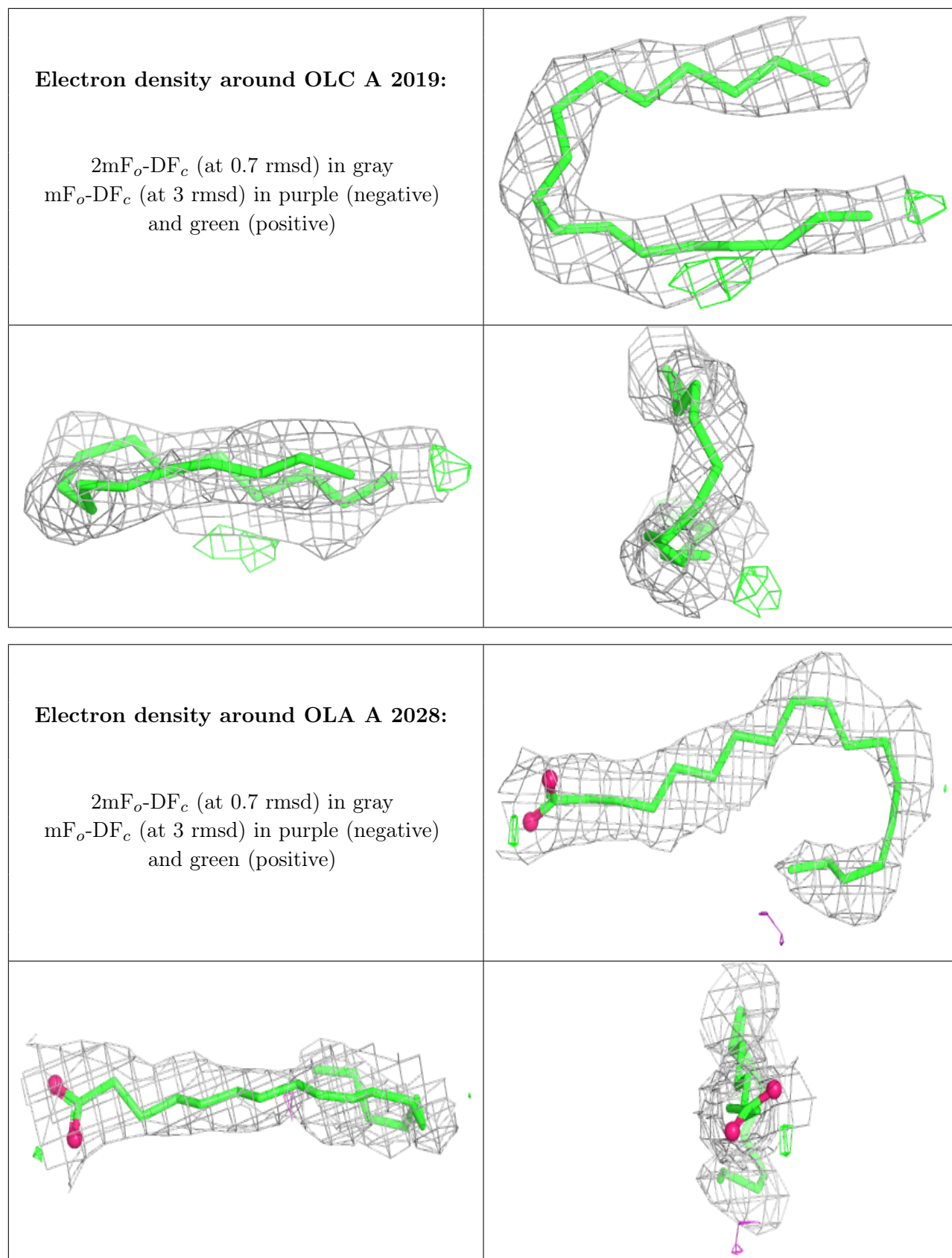
Electron density around OLA A 2029:

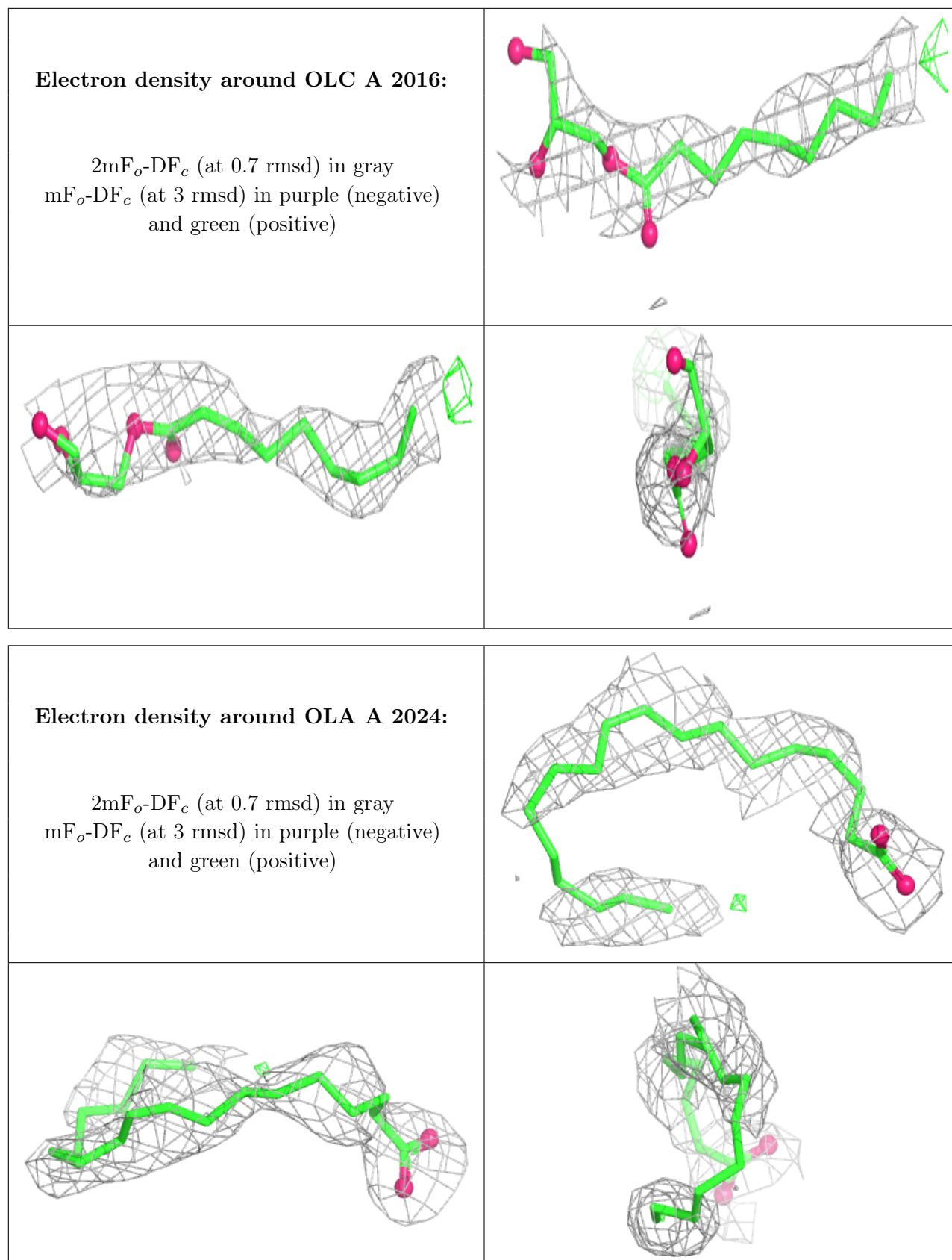
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

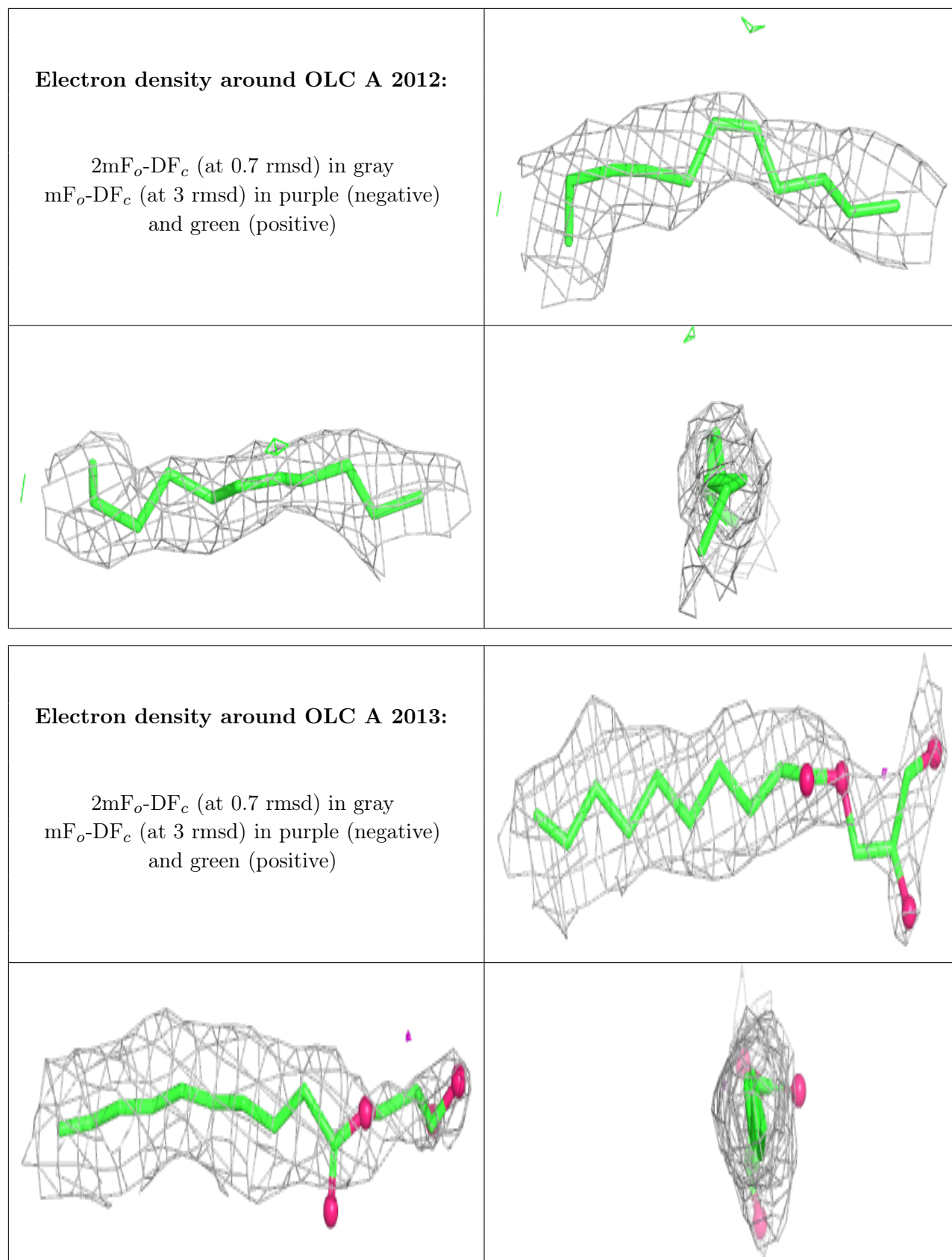
**Electron density around OLA A 2026:**

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



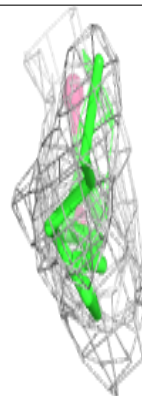
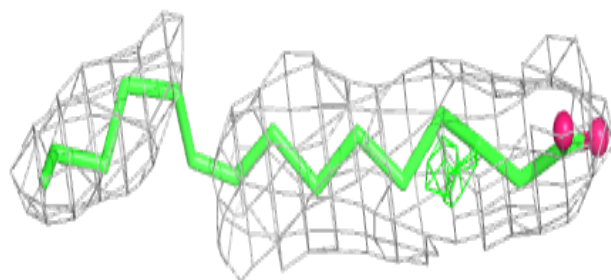
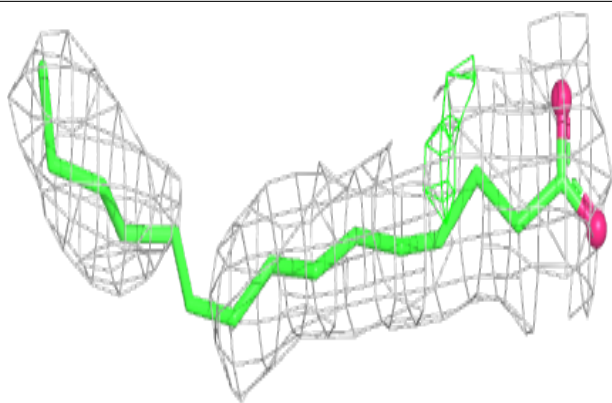




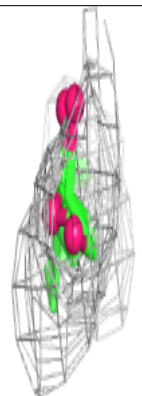
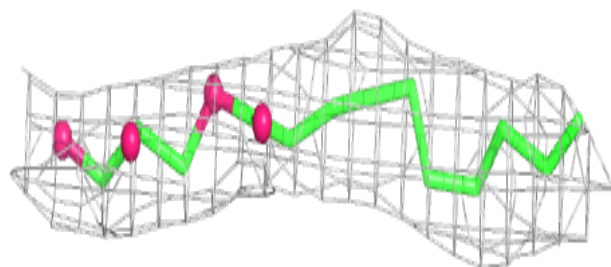
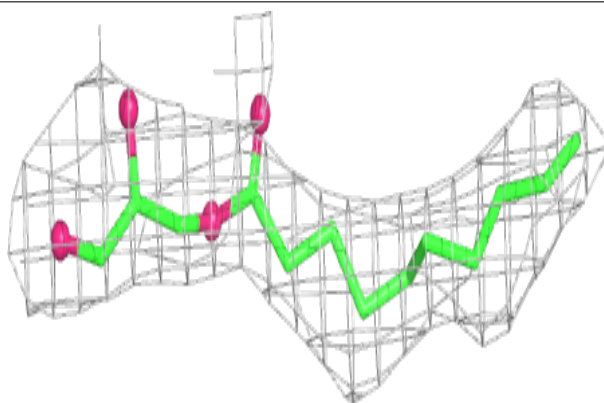


Electron density around OLA A 2021:

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

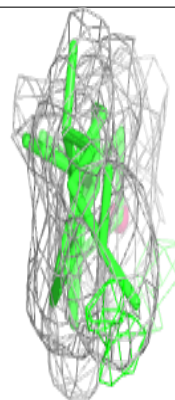
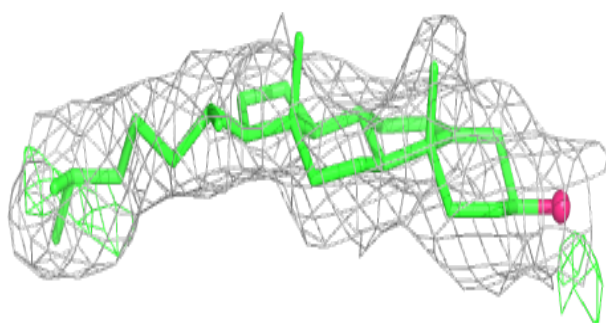
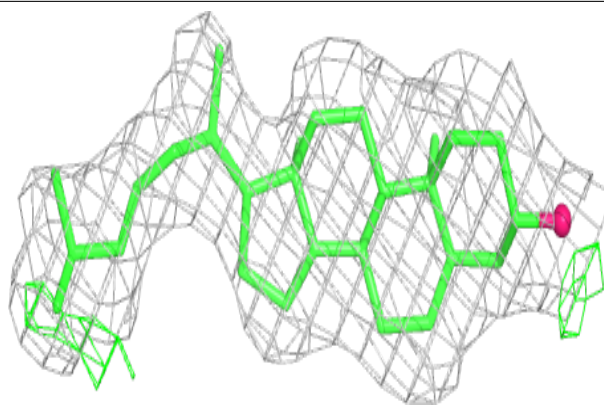
**Electron density around OLC A 2006:**

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

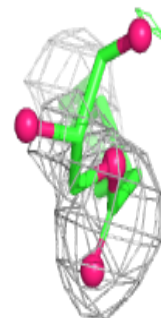
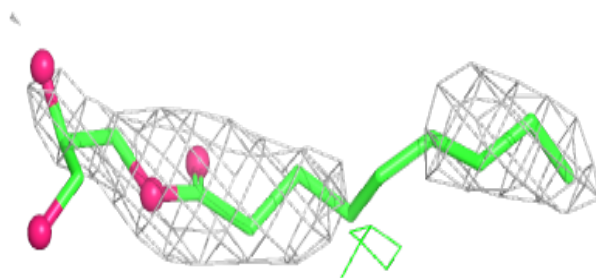
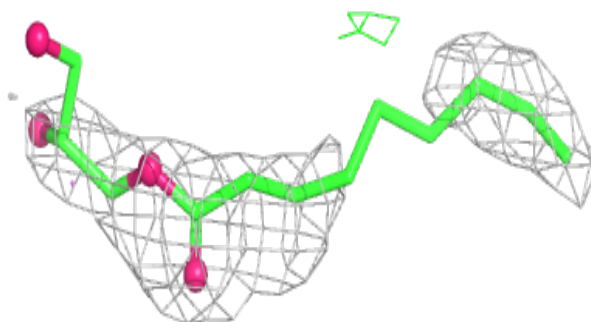


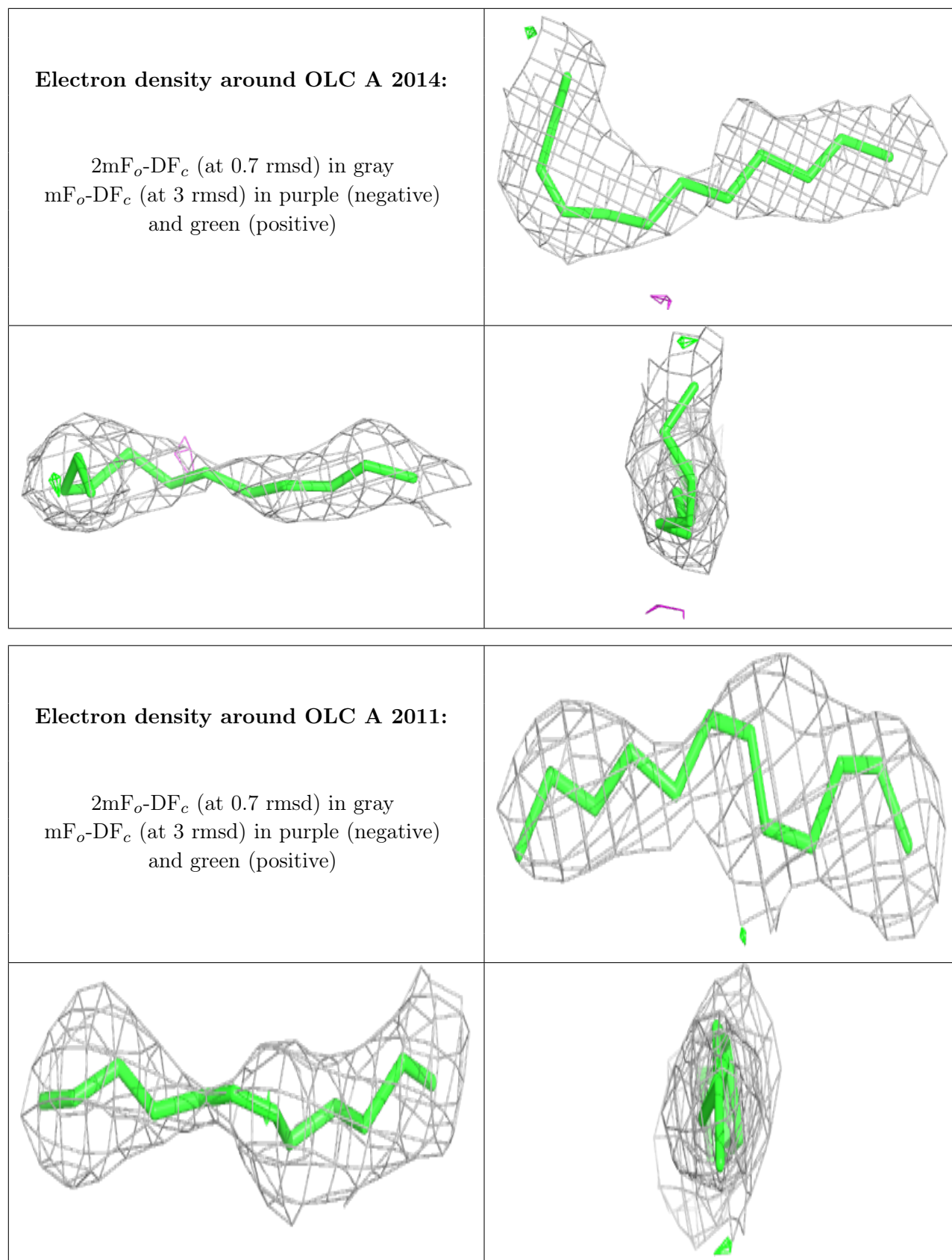
Electron density around CLR A 2002:

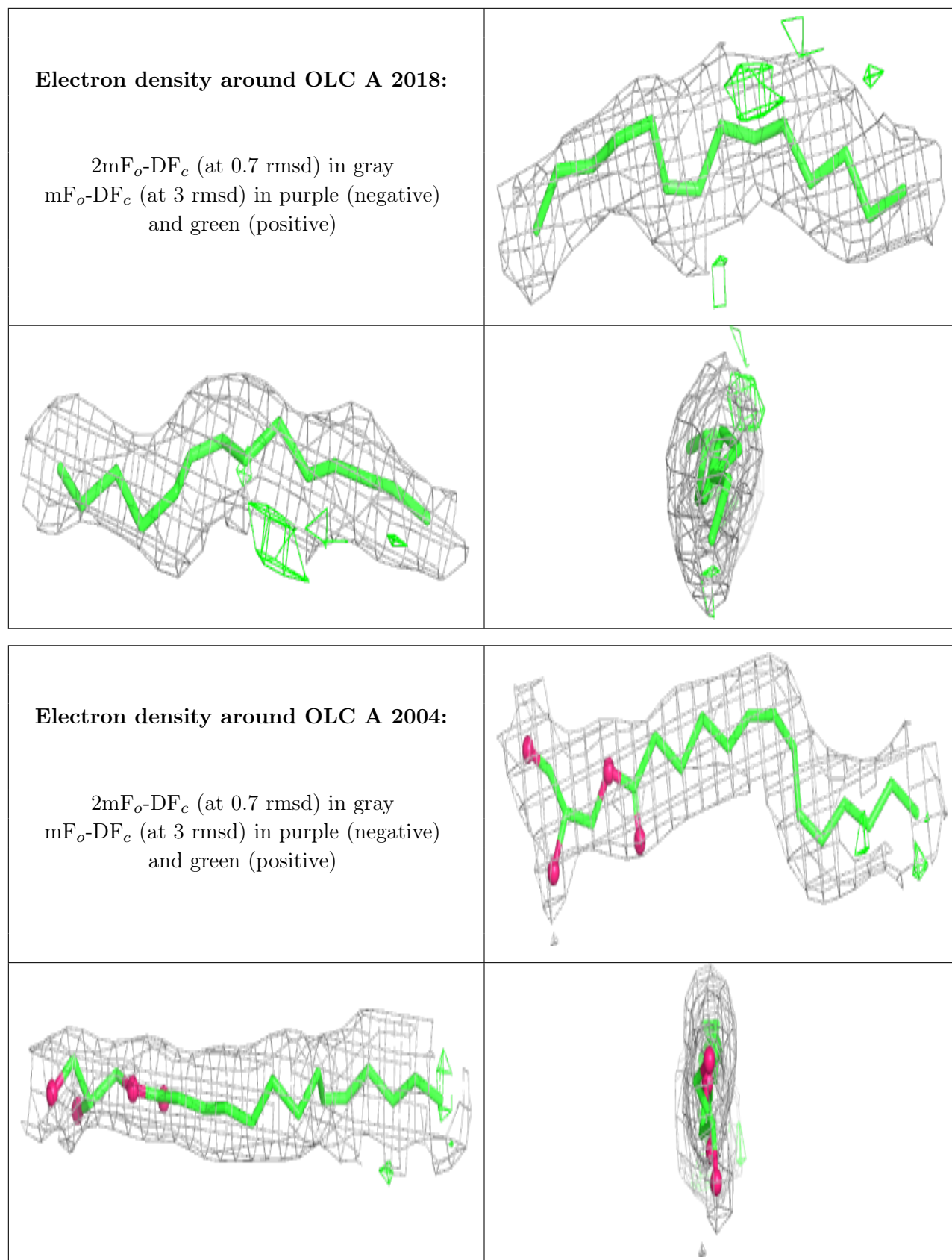
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

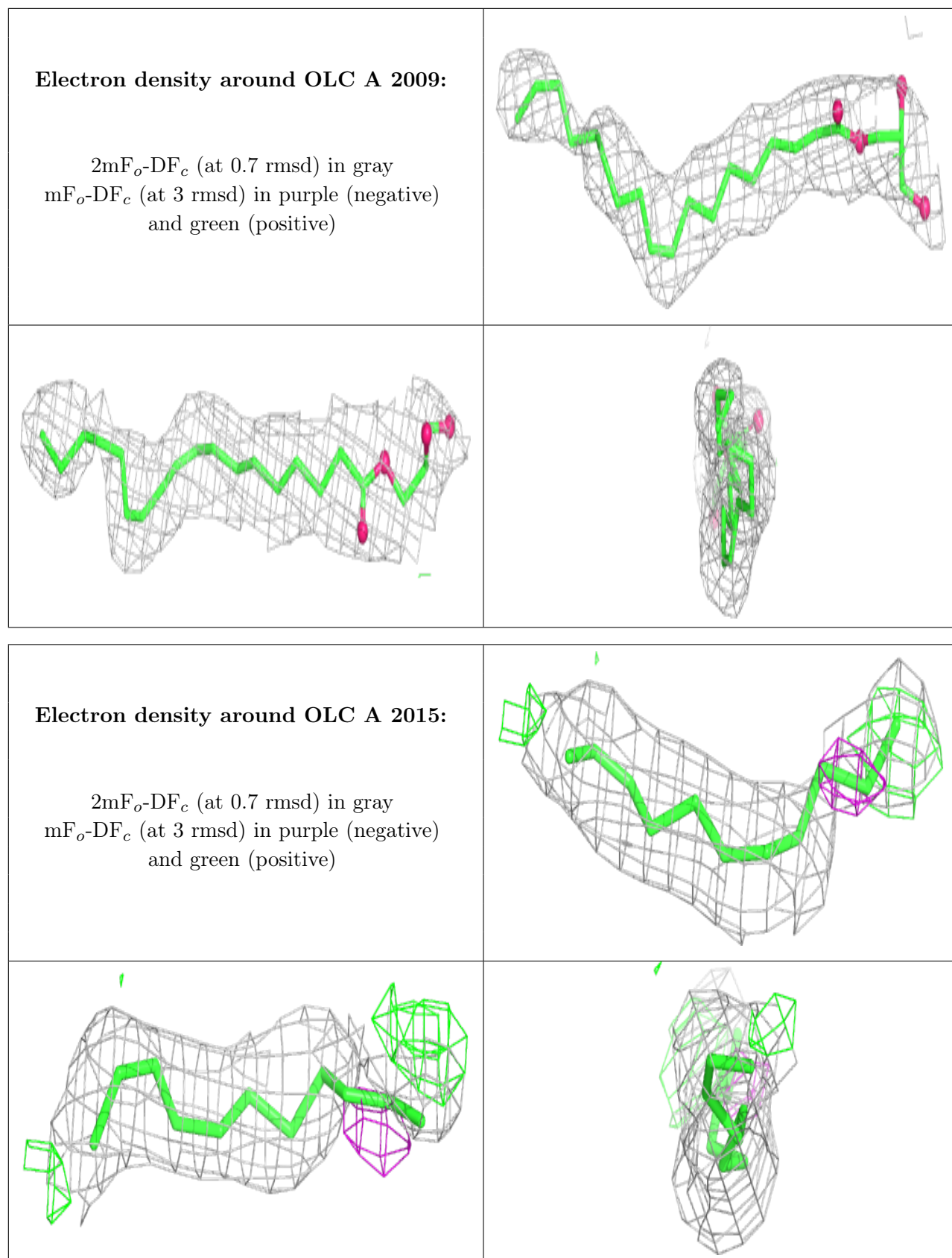
**Electron density around OLC A 2017:**

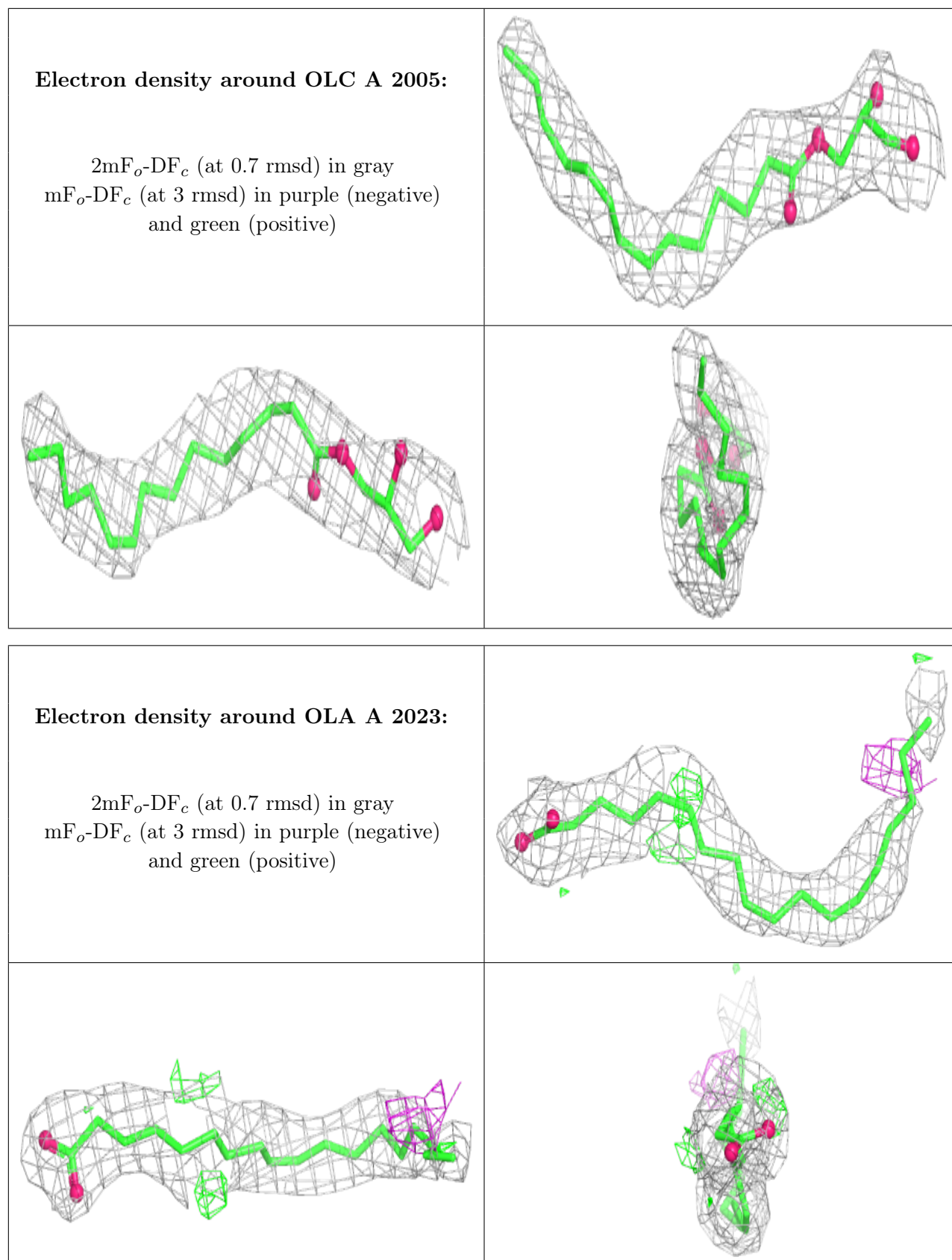
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





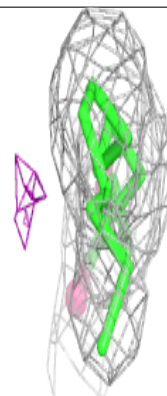
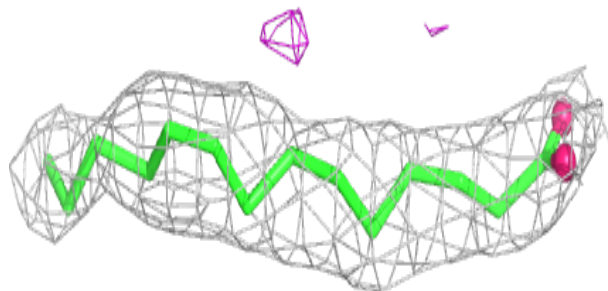
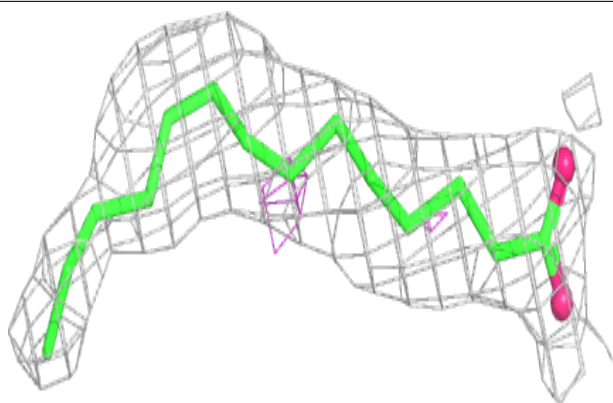




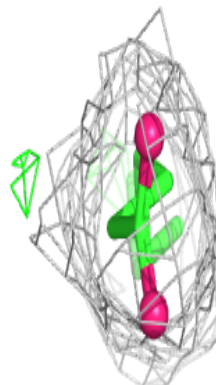
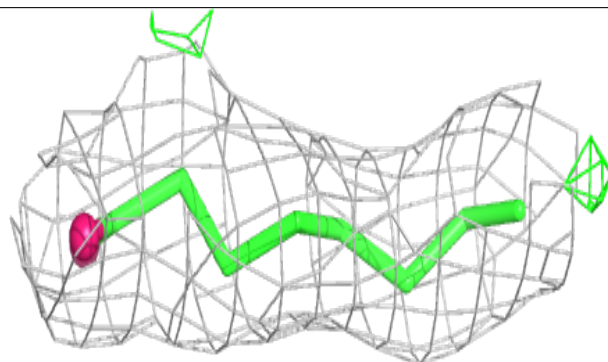
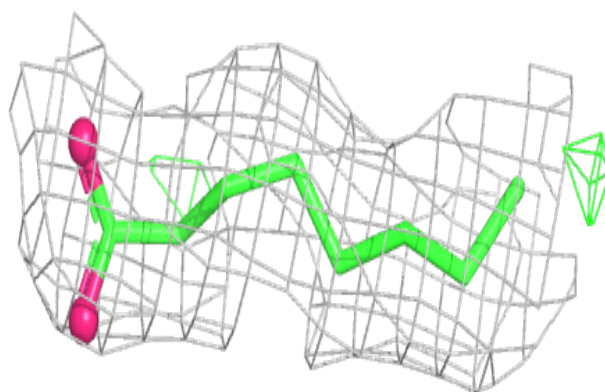


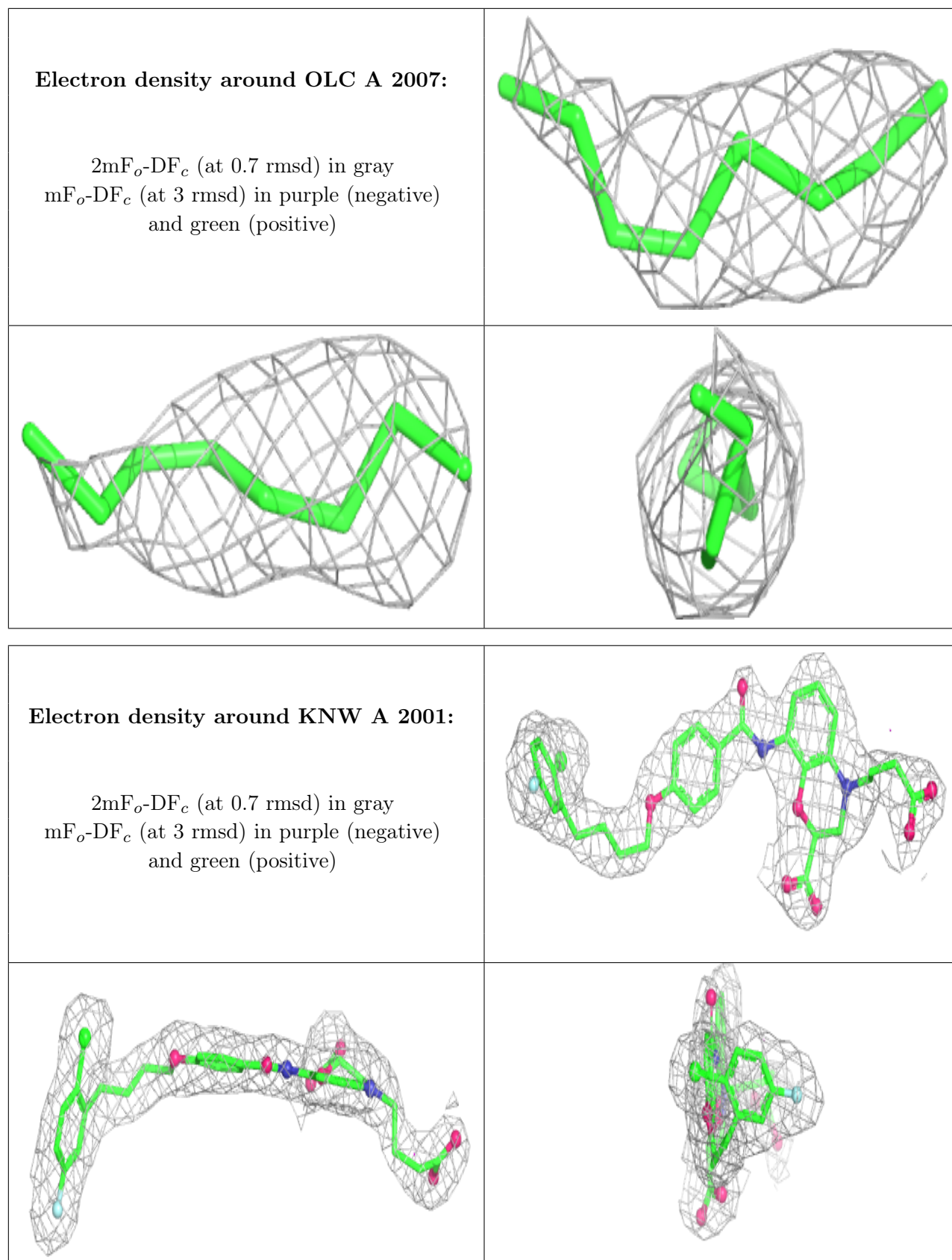
Electron density around OLA A 2020:

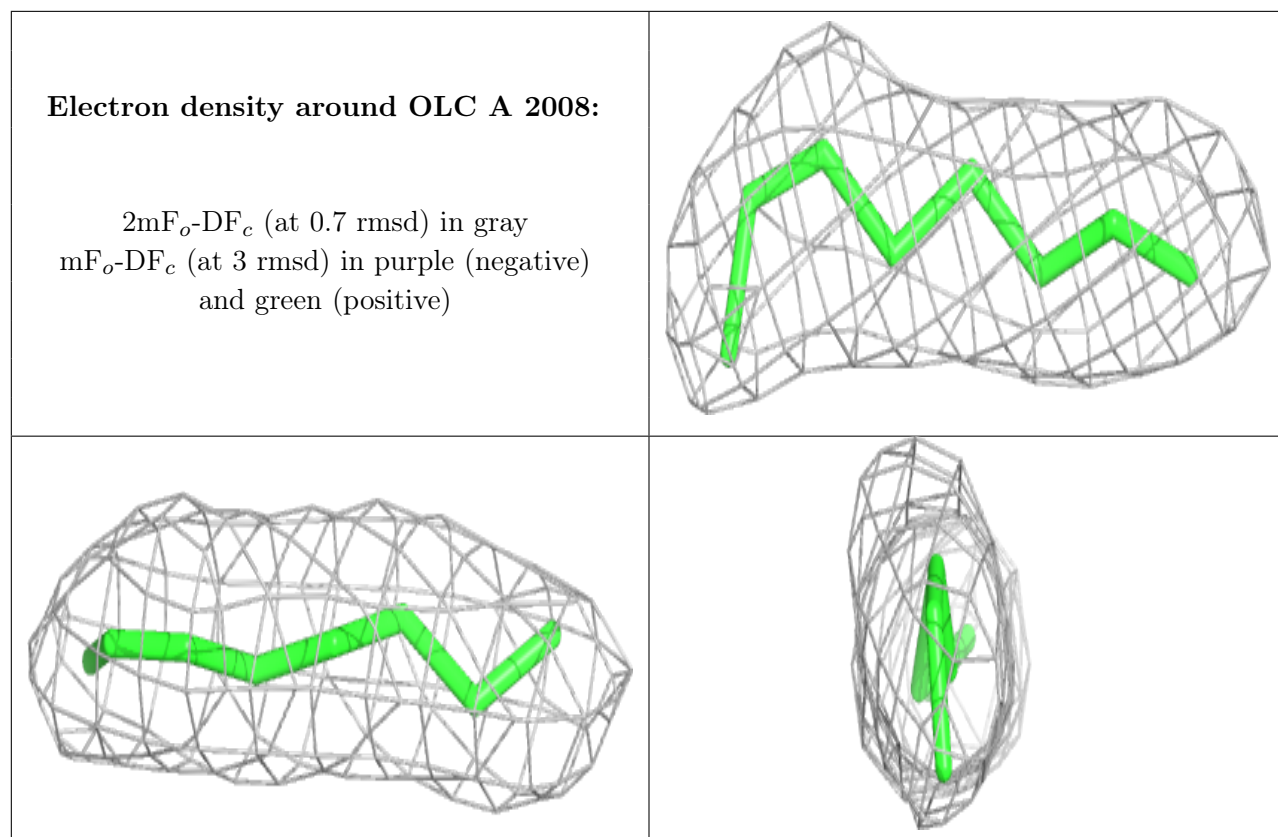
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around OLA A 2025:**

$2mF_o-DF_c$ (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.