



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 05:03 PM UTC

PDB ID : 3S8F / pdb_00003s8f
Title : 1.8 Å structure of ba3 cytochrome c oxidase from *Thermus thermophilus* in lipid environment
Authors : Tiefenbrunn, T.; Liu, W.; Chen, Y.; Katritch, V.; Stout, C.D.; Fee, J.A.; Cherezov, V.
Deposited on : 2011-05-27
Resolution : 1.80 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

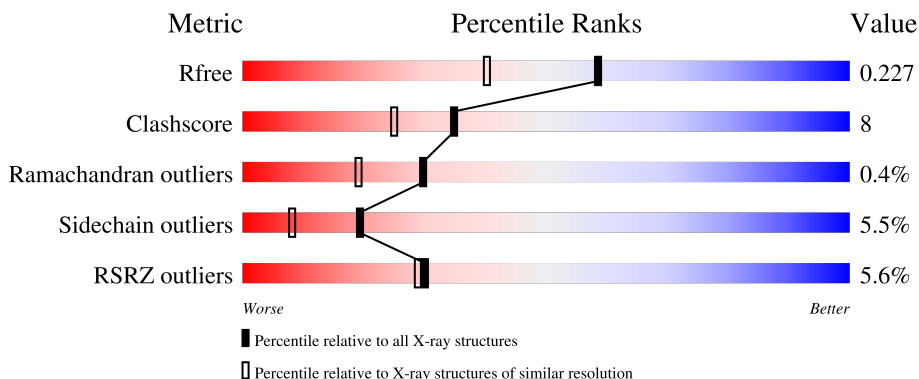
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


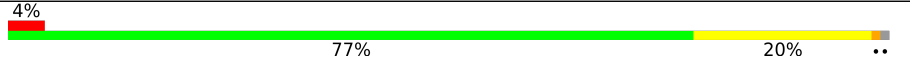
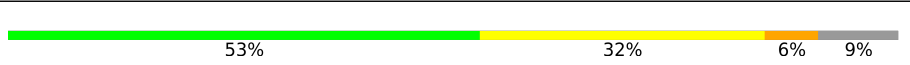
The reported resolution of this entry is 1.80 Å.

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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	569	
2	B	168	
3	C	34	

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
6	HAS	A	801	X	-	-	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 6567 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 Cytochrome c oxidase subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	554	4389	2979	699	695	16	0	5	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	expression tag	UNP Q5SJ79
A	-5	HIS	-	expression tag	UNP Q5SJ79
A	-4	HIS	-	expression tag	UNP Q5SJ79
A	-3	HIS	-	expression tag	UNP Q5SJ79
A	-2	HIS	-	expression tag	UNP Q5SJ79
A	-1	HIS	-	expression tag	UNP Q5SJ79
A	0	HIS	-	expression tag	UNP Q5SJ79
A	1	HIS	-	expression tag	UNP Q5SJ79

- Molecule 2 is a protein called Cytochrome c oxidase subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	166	1288	837	214	233	4	0	1	0

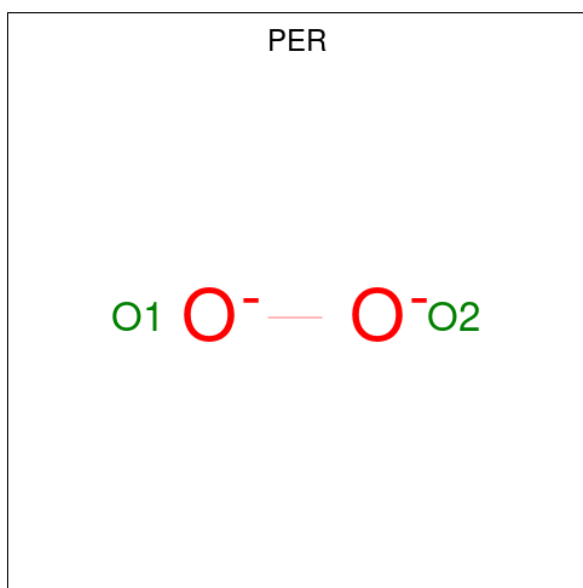
- Molecule 3 is a protein called Cytochrome c oxidase polypeptide 2A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	31	241	169	37	35	0	0	0

- Molecule 4 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

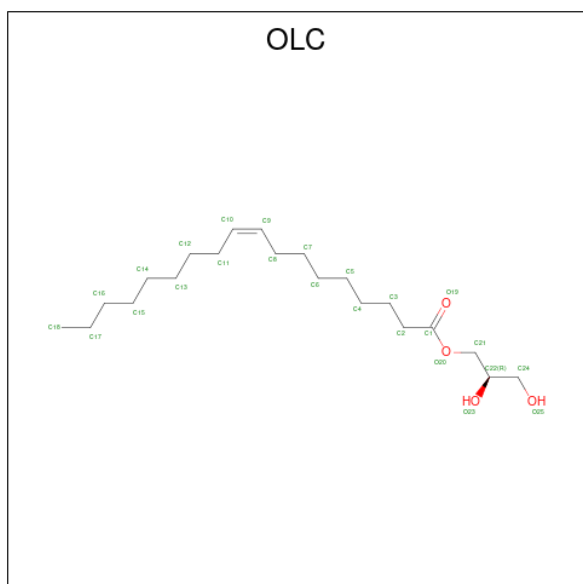
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cu	0	0
			1	1		

- Molecule 7 is PEROXIDE ION (CCD ID: PER) (formula: O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total O 2 2	0	0

- Molecule 8 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (CCD ID: OLC) (formula: C₂₁H₄₀O₄).



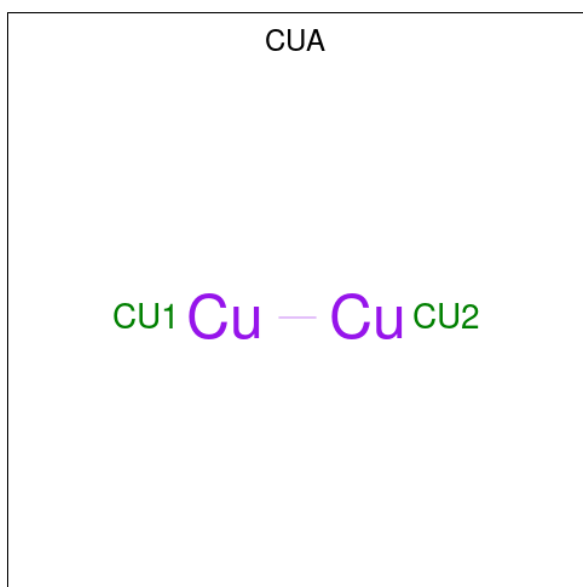
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C O 25 21 4	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			25	21	4		
8	A	1	Total	C	O	0	0
			23	19	4		
8	A	1	Total	C	O	0	0
			18	14	4		
8	A	1	Total	C	O	0	0
			17	13	4		
8	A	1	Total	C	O	0	0
			8	4	4		
8	A	1	Total	C	O	0	0
			15	11	4		
8	A	1	Total	C	O	0	0
			20	16	4		
8	A	1	Total	C	O	0	0
			25	21	4		
8	A	1	Total	C	O	0	0
			21	17	4		
8	A	1	Total	C	O	0	0
			25	21	4		
8	B	1	Total	C	O	0	0
			25	21	4		
8	B	1	Total	C	O	0	0
			25	21	4		
8	B	1	Total	C	O	0	0
			25	21	4		
8	B	1	Total	C	O	0	0
			21	19	2		
8	C	1	Total	C	O	0	0
			25	21	4		

- Molecule 9 is DINUCLEAR COPPER ION (CCD ID: CUA) (formula: Cu₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total Cu 2 2	0	0

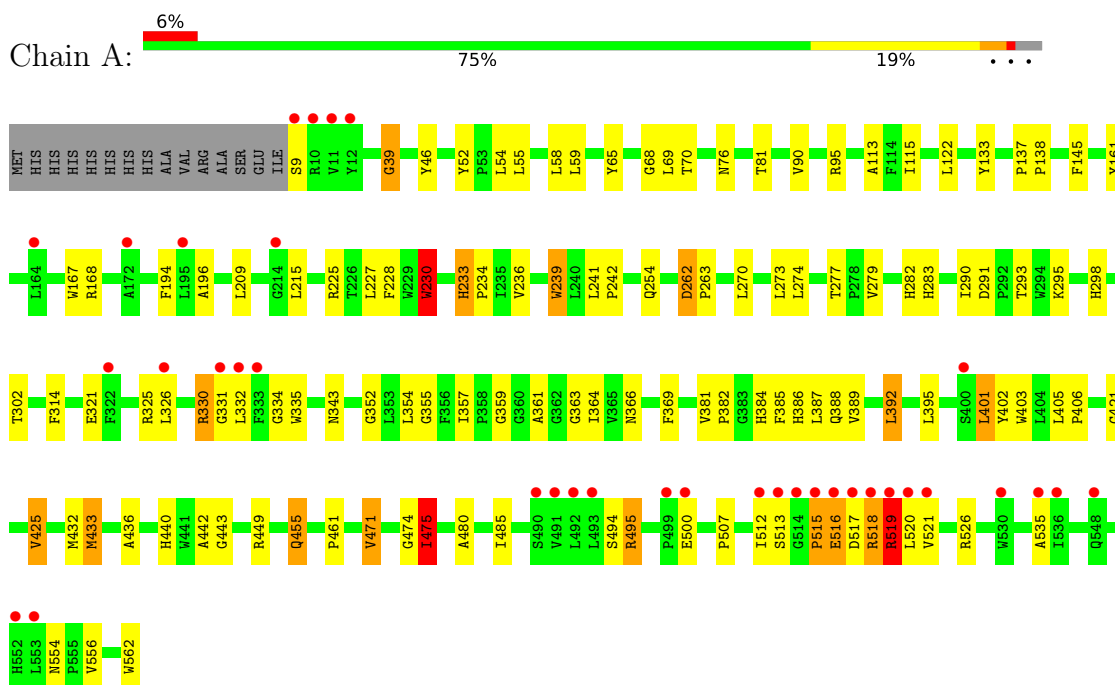
- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	117	Total O 117 117	0	0
10	B	71	Total O 71 71	0	0
10	C	5	Total O 5 5	0	0

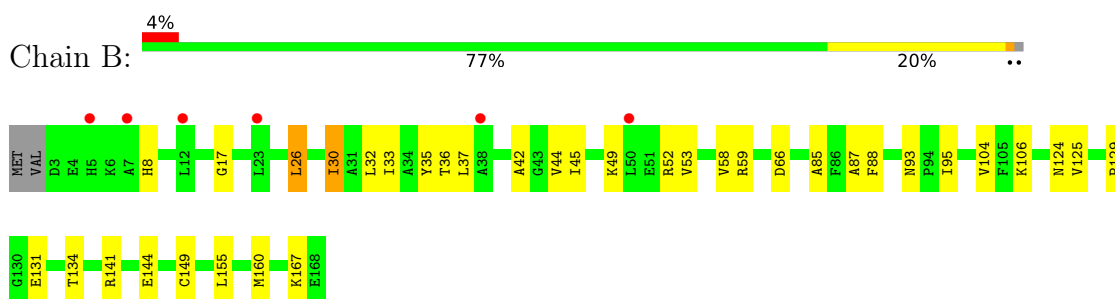
3 Residue-property plots [i](#)

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.

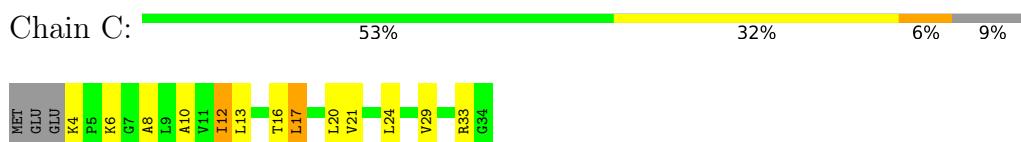
- Molecule 1: Cytochrome c oxidase subunit 1



- Molecule 2: Cytochrome c oxidase subunit 2



- Molecule 3: Cytochrome c oxidase polypeptide 2A



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	143.59Å 97.82Å 94.95Å 90.00° 128.30° 90.00°	Depositor
Resolution (Å)	37.26 – 1.80 37.26 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.2 (37.26-1.80) 97.2 (37.26-1.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 1.81Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.184 , 0.215 0.198 , 0.227	Depositor DCC
R_{free} test set	4656 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	27.5	Xtrriage
Anisotropy	0.146	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6567	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.08% 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, PER, CU, CUA, HEM, HAS

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	1.72	46/4562 (1.0%)	1.33	31/6263 (0.5%)
2	B	1.74	16/1330 (1.2%)	1.30	3/1817 (0.2%)
3	C	1.73	3/247 (1.2%)	1.35	1/335 (0.3%)
All	All	1.72	65/6139 (1.1%)	1.33	35/8415 (0.4%)

The worst 5 of 65 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	381	VAL	CA-CB	11.61	1.60	1.54
3	C	8	ALA	CA-CB	-8.34	1.40	1.53
1	A	352	GLY	CA-C	8.07	1.61	1.52
1	A	65	TYR	CA-C	7.98	1.63	1.52
1	A	480	ALA	CA-CB	7.74	1.65	1.53

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	233	HIS	N-CA-CB	11.17	121.00	110.39
1	A	227	LEU	N-CA-C	-8.11	102.01	112.23
1	A	331	GLY	N-CA-C	-7.41	104.07	111.56
1	A	359	GLY	N-CA-C	-7.37	103.95	112.50
1	A	270	LEU	N-CA-C	-7.23	103.48	111.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4389	0	4484	59	0
2	B	1288	0	1260	20	0
3	C	241	0	267	7	0
4	A	1	0	0	0	0
5	A	43	0	30	3	0
6	A	65	0	62	3	0
7	A	2	0	0	1	0
8	A	222	0	320	21	0
8	B	96	0	153	16	0
8	C	25	0	40	1	0
9	B	2	0	0	0	0
10	A	117	0	0	5	0
10	B	71	0	0	1	1
10	C	5	0	0	0	0
All	All	6567	0	6616	98	1

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 8.

The worst 5 of 98 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)
7:A:563:PER:O1	7:A:563:PER:O2	1.54	1.23
1:A:330[B]:ARG:HH11	1:A:330[B]:ARG:CG	1.49	1.21
1:A:330[B]:ARG:HG2	1:A:330[B]:ARG:NH1	1.41	1.13
1:A:516[A]:GLU:HG3	1:A:517:ASP:H	1.08	1.12
1:A:516[A]:GLU:HG3	1:A:517:ASP:N	1.55	1.11

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:175:HOH:O	10:B:201:HOH:O[2_556]	2.08	0.12

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	556/569 (98%)	536 (96%)	17 (3%)	3 (0%)	24	14
2	B	165/168 (98%)	162 (98%)	3 (2%)	0	100	100
3	C	29/34 (85%)	29 (100%)	0	0	100	100
All	All	750/771 (97%)	727 (97%)	20 (3%)	3 (0%)	30	19

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	515	PRO
1	A	519	ARG
1	A	369	PHE

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	450/463 (97%)	424 (94%)	26 (6%)	18	7
2	B	134/138 (97%)	129 (96%)	5 (4%)	30	18
3	C	24/27 (89%)	20 (83%)	4 (17%)	2	0
All	All	608/628 (97%)	573 (94%)	35 (6%)	19	7

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	49	LYS
2	B	144	GLU
3	C	17	LEU
1	A	401	LEU
1	A	332	LEU

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

Mol	Chain	Res	Type
1	A	407	ASN
1	A	455	GLN
2	B	40	HIS
2	B	91	GLN

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 21 ligands modelled in this entry, 1 is monoatomic - leaving 20 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	$\# Z > 2$
8	OLC	A	574	-	24,24,24	0.49	0	25,25,25	0.94	2 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	OLC	A	572	-	24,24,24	0.70	1 (4%)	25,25,25	0.96	1 (4%)
8	OLC	B	171	-	24,24,24	0.51	0	25,25,25	0.53	0
8	OLC	B	169	-	24,24,24	0.51	0	25,25,25	0.82	0
8	OLC	A	566	-	22,22,24	0.54	0	23,23,25	1.26	4 (17%)
6	HAS	A	801	1,7	72,72,72	2.33	26 (36%)	87,109,109	2.34	34 (39%)
9	CUA	B	802	2	0,1,1	-	-	-	-	-
8	OLC	A	564	-	24,24,24	0.53	0	25,25,25	0.72	0
8	OLC	B	170	-	24,24,24	0.85	1 (4%)	25,25,25	1.10	2 (8%)
8	OLC	A	565	-	24,24,24	0.47	0	25,25,25	0.83	0
7	PER	A	563	4,6	1,1,1	0.85	0	-	-	-
8	OLC	A	570	-	14,14,24	0.70	1 (7%)	15,15,25	0.58	0
8	OLC	A	573	-	20,20,24	0.54	0	21,21,25	0.87	1 (4%)
5	HEM	A	800	1	50,50,50	2.85	22 (44%)	67,82,82	3.64	33 (49%)
8	OLC	A	571	-	19,19,24	0.51	0	20,20,25	1.09	2 (10%)
8	OLC	B	172	-	20,20,24	0.65	1 (5%)	20,20,25	0.73	1 (5%)
8	OLC	C	35	-	24,24,24	0.52	0	25,25,25	0.51	0
8	OLC	A	567	-	17,17,24	0.58	0	18,18,25	0.66	0
8	OLC	A	569	-	7,7,24	0.42	0	6,7,25	0.92	0
8	OLC	A	568	-	16,16,24	0.75	0	17,17,25	0.70	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
8	OLC	B	169	-	-	11/24/24/24	-
8	OLC	A	566	-	-	10/22/22/24	-
6	HAS	A	801	1,7	1/1/8/18	6/42/82/82	-
8	OLC	A	570	-	-	5/14/14/24	-
8	OLC	A	572	-	-	15/24/24/24	-
8	OLC	A	574	-	-	8/24/24/24	-
8	OLC	A	573	-	-	10/20/20/24	-
8	OLC	A	564	-	-	13/24/24/24	-
8	OLC	A	571	-	-	7/19/19/24	-
8	OLC	B	170	-	-	10/24/24/24	-
8	OLC	B	172	-	-	9/19/19/24	-
8	OLC	C	35	-	-	12/24/24/24	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	OLC	A	567	-	-	6/17/17/24	-
8	OLC	B	171	-	-	10/24/24/24	-
5	HEM	A	800	1	-	0/14/54/54	-
8	OLC	A	565	-	-	11/24/24/24	-
8	OLC	A	569	-	-	4/6/6/24	-
8	OLC	A	568	-	-	6/16/16/24	-

The worst 5 of 52 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	800	HEM	C3C-C4C	-8.19	1.31	1.46
5	A	800	HEM	C1C-C2C	-7.00	1.31	1.45
5	A	800	HEM	CHC-C1C	6.45	1.51	1.38
6	A	801	HAS	CHC-C1C	6.19	1.53	1.39
5	A	800	HEM	CHA-C1A	5.29	1.51	1.39

The worst 5 of 80 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	800	HEM	CHD-C1D-ND	9.71	134.87	124.42
5	A	800	HEM	C4C-C3C-C2C	-9.50	98.58	106.81
5	A	800	HEM	CHA-C4D-ND	9.28	135.84	124.37
5	A	800	HEM	C4D-ND-C1D	8.87	115.71	105.21
5	A	800	HEM	CHC-C4B-NB	8.60	133.67	124.42

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	801	HAS	NA

5 of 153 torsion outliers are listed below:

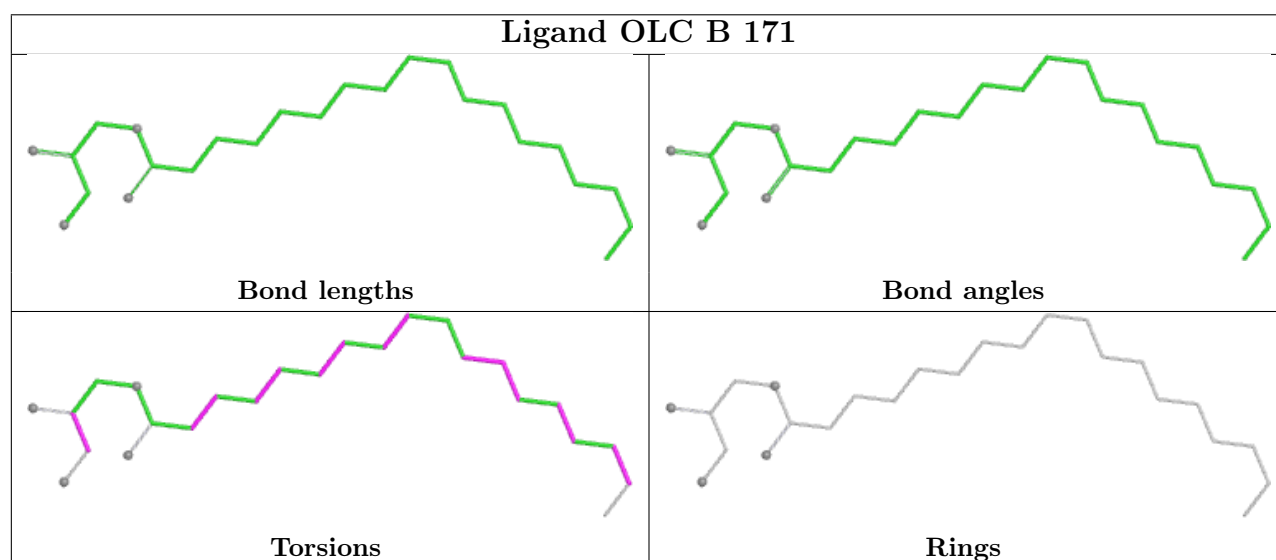
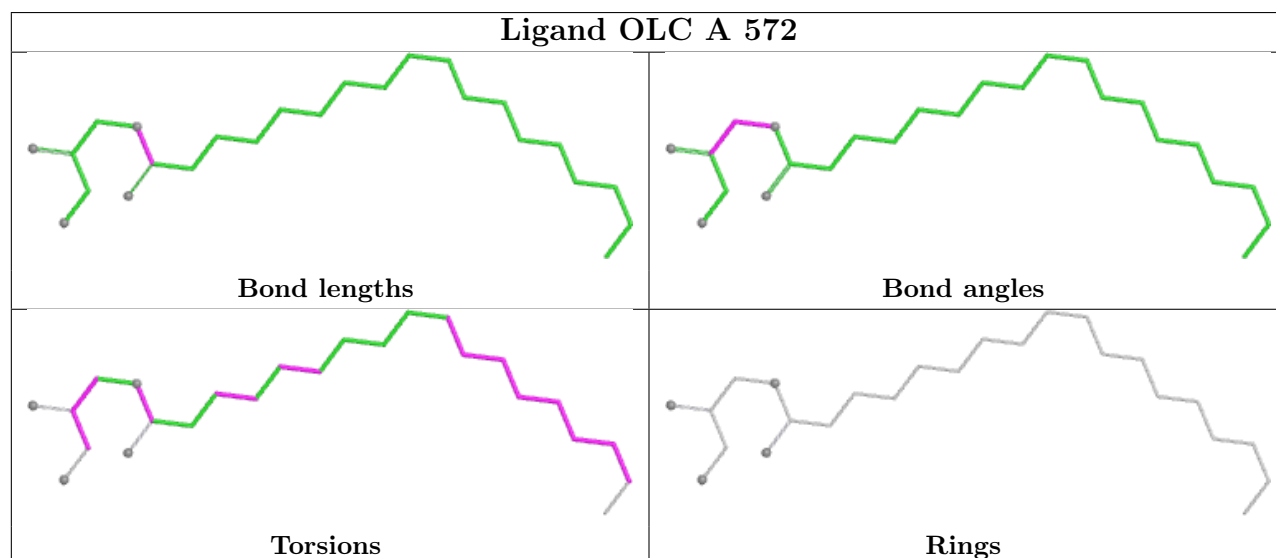
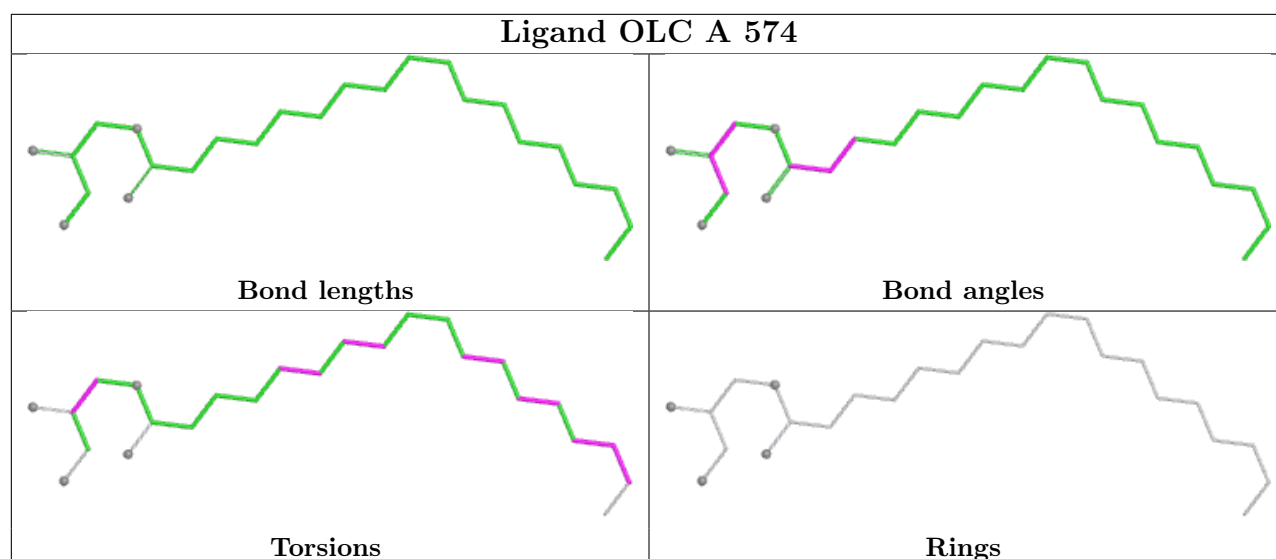
Mol	Chain	Res	Type	Atoms
8	A	565	OLC	O20-C21-C22-C24
8	A	565	OLC	O20-C21-C22-O23
8	A	566	OLC	C21-C22-C24-O25
8	A	566	OLC	O23-C22-C24-O25
8	A	569	OLC	O19-C1-O20-C21

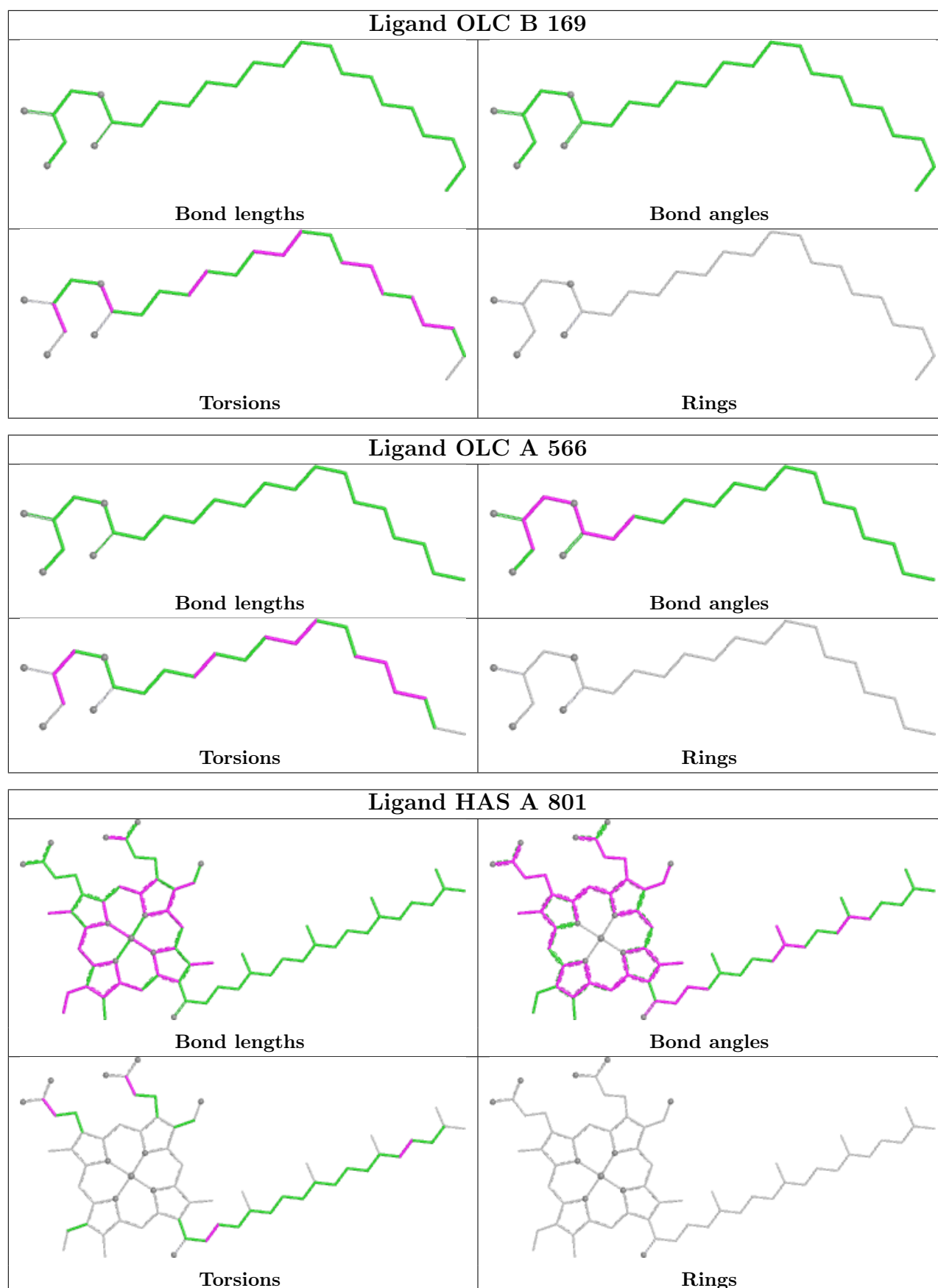
There are no ring outliers.

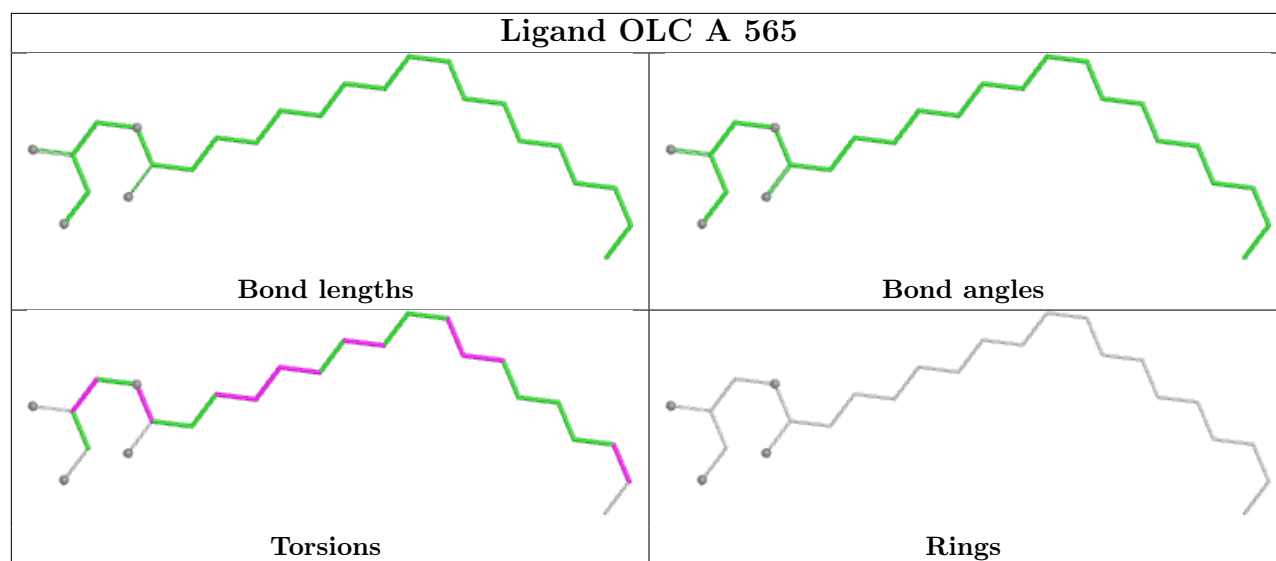
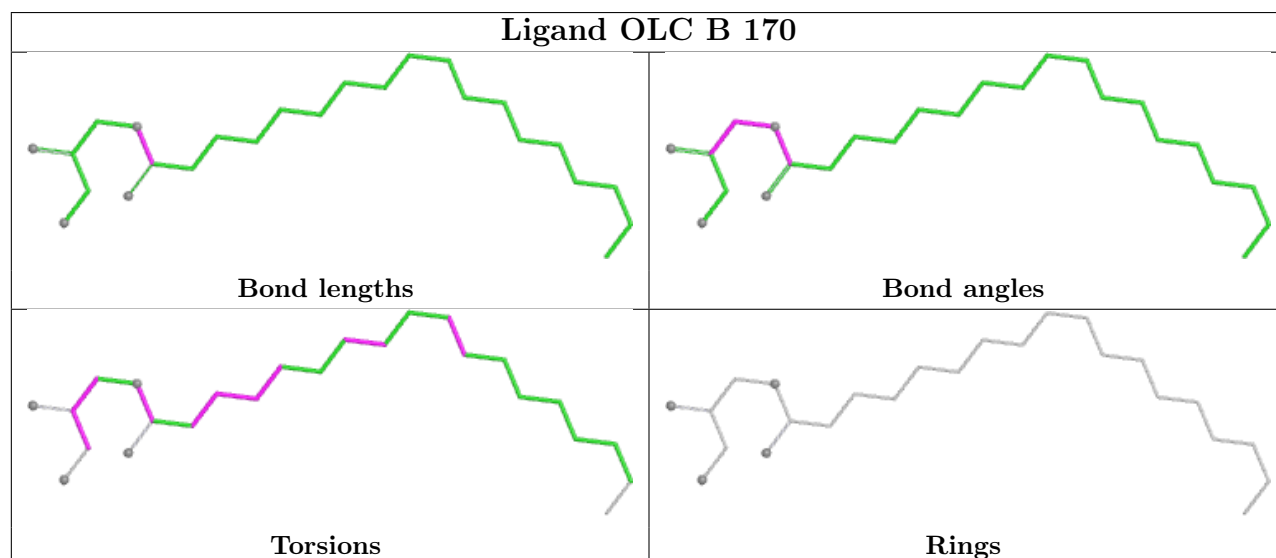
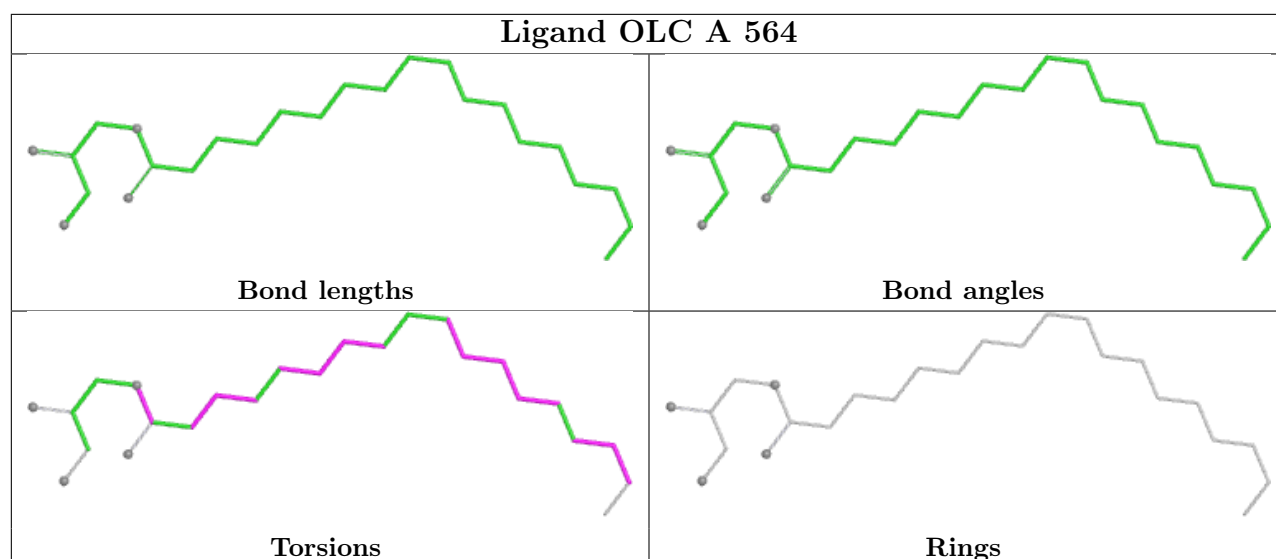
16 monomers are involved in 44 short contacts:

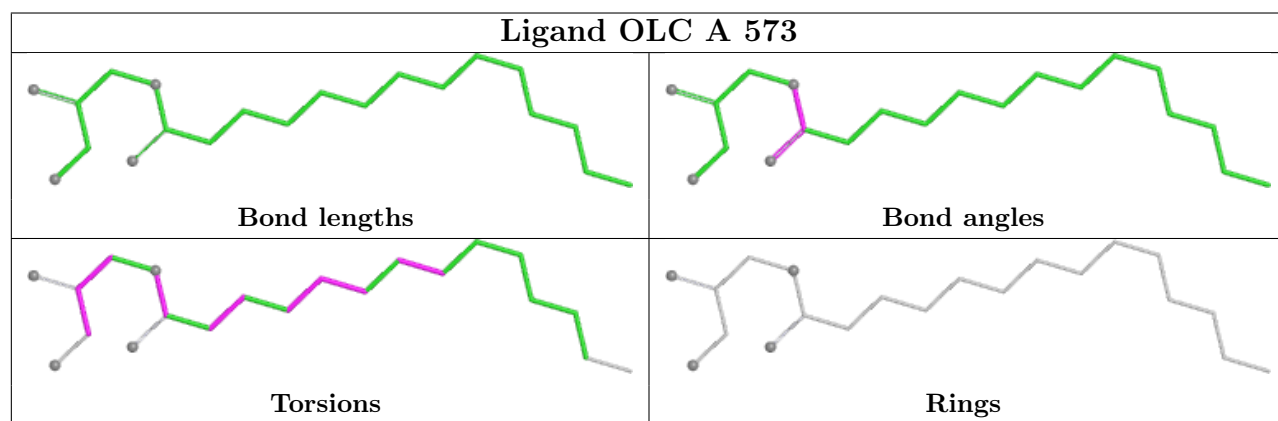
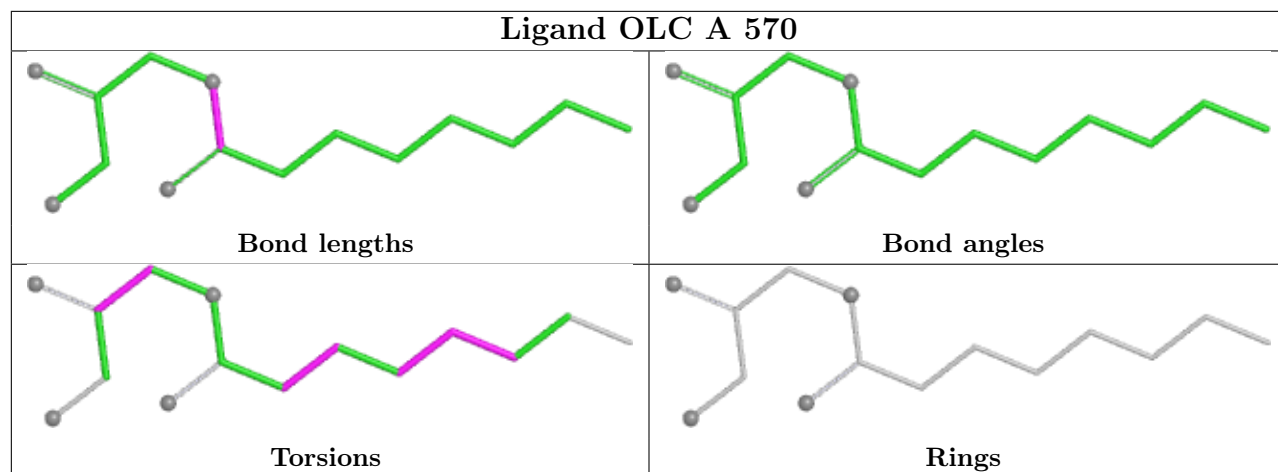
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	574	OLC	1	0
8	A	572	OLC	6	0
8	B	171	OLC	1	0
8	B	169	OLC	4	0
8	A	566	OLC	2	0
6	A	801	HAS	3	0
8	A	564	OLC	1	0
8	B	170	OLC	10	0
8	A	565	OLC	4	0
7	A	563	PER	1	0
8	A	570	OLC	7	0
5	A	800	HEM	3	0
8	A	571	OLC	2	0
8	B	172	OLC	1	0
8	C	35	OLC	1	0
8	A	569	OLC	4	0

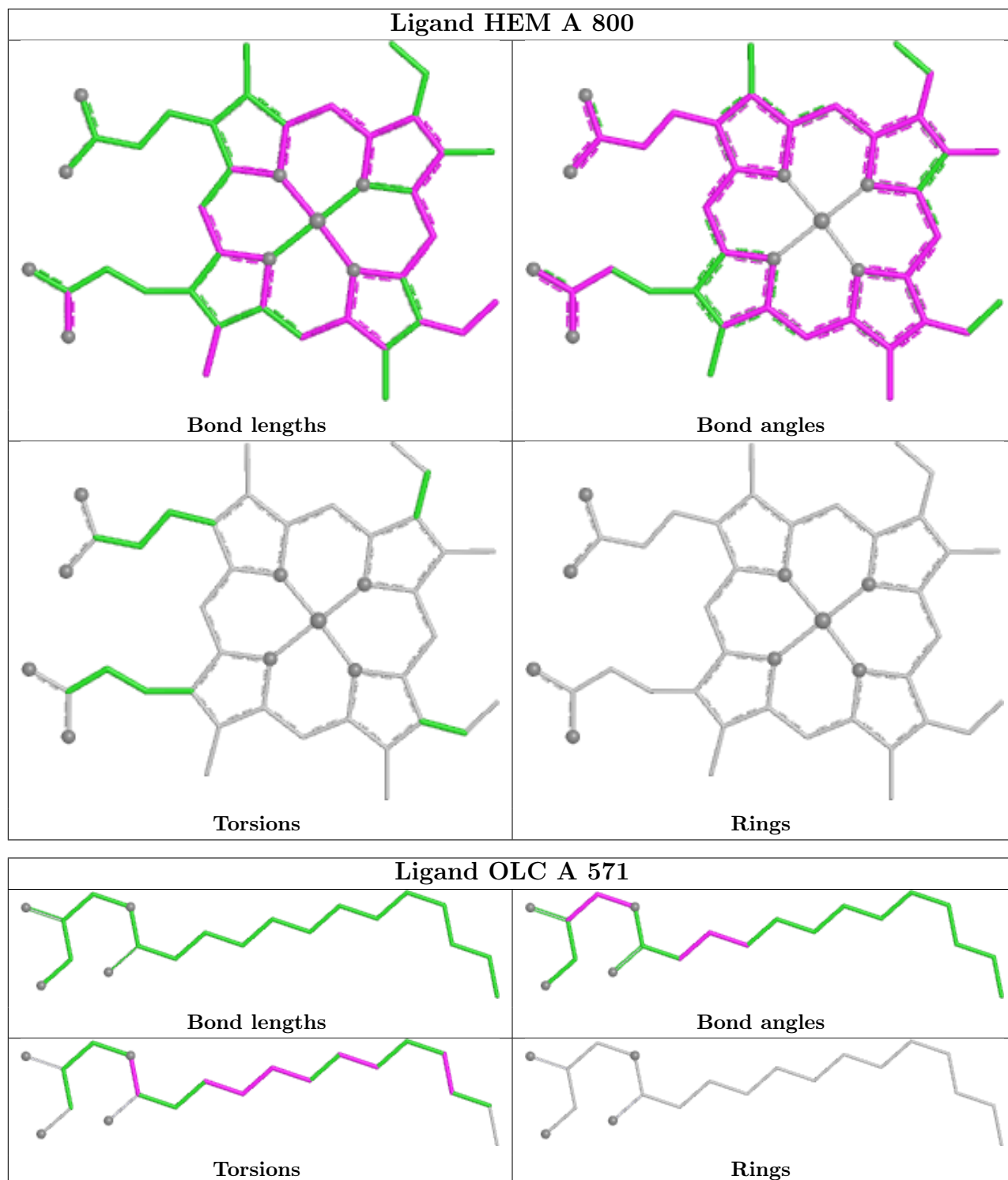
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

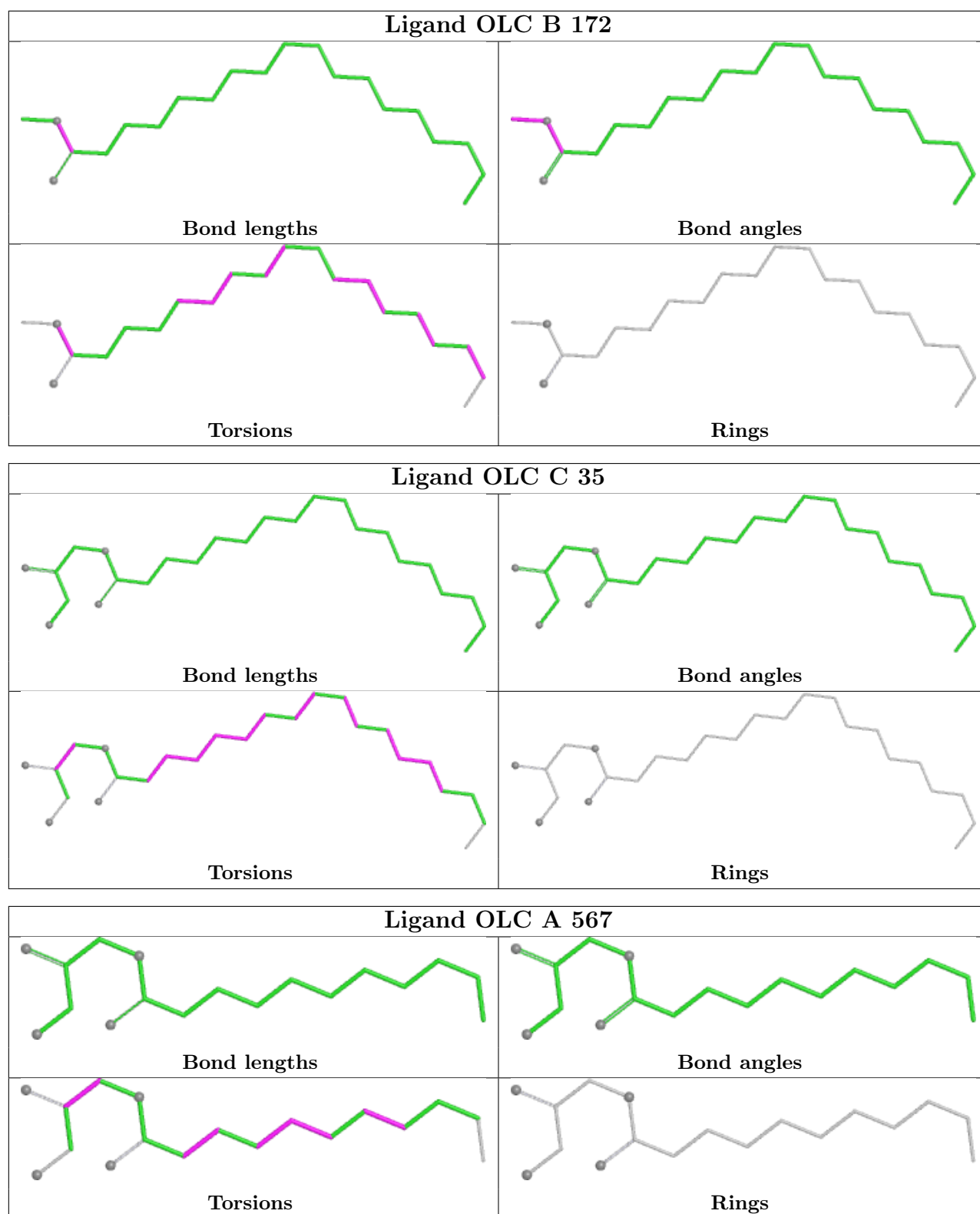


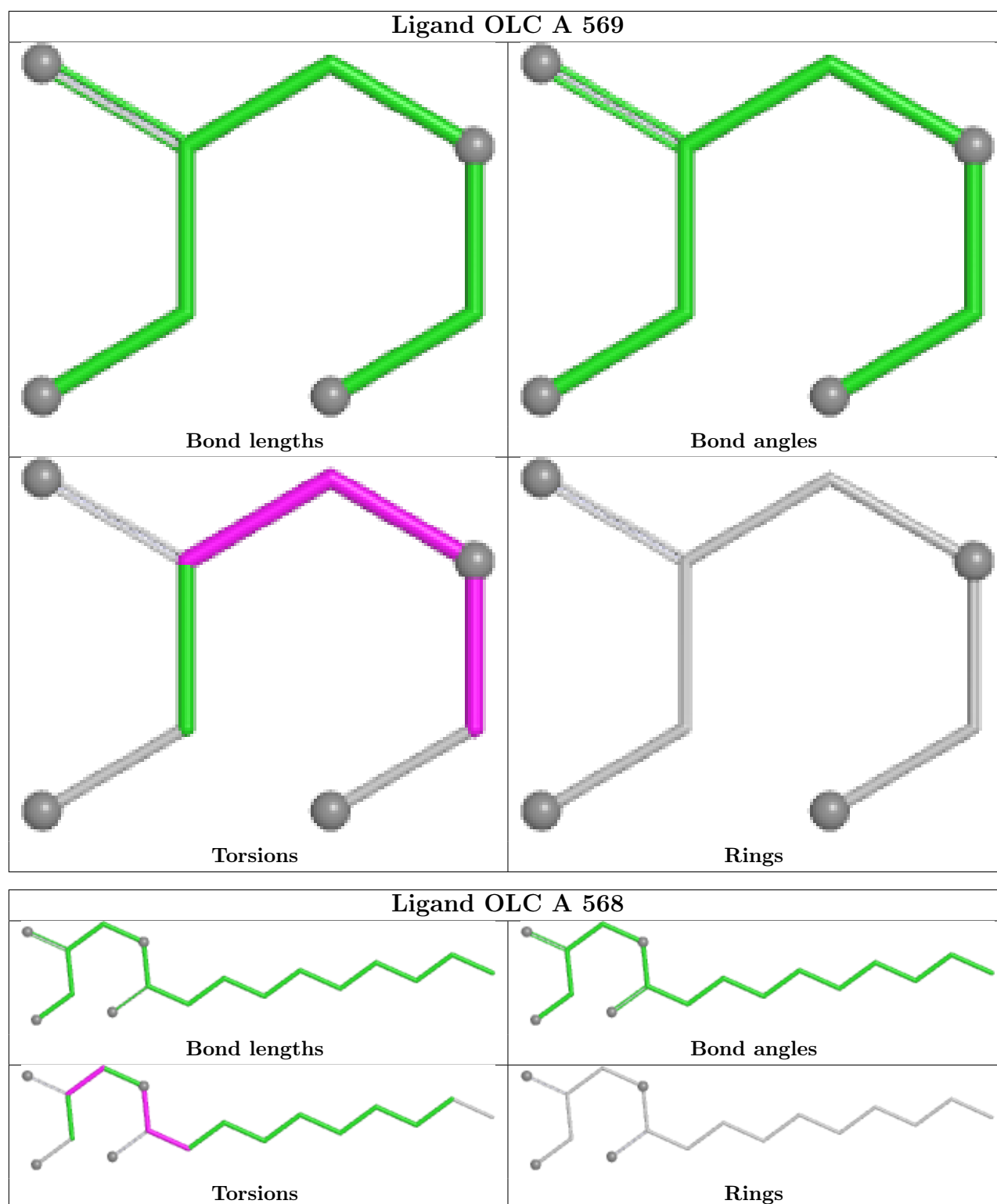












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

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	554/569 (97%)	0.34	36 (6%) 25 23	15, 29, 53, 84	4 (0%)
2	B	166/168 (98%)	0.28	6 (3%) 46 46	16, 30, 48, 65	1 (0%)
3	C	31/34 (91%)	0.35	0 100 100	24, 30, 40, 55	0
All	All	751/771 (97%)	0.33	42 (5%) 30 29	15, 29, 51, 84	5 (0%)

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	12	TYR	6.0
1	A	513	SER	5.2
1	A	515	PRO	4.7
1	A	10	ARG	4.2
1	A	492	LEU	4.1

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 [i](#)

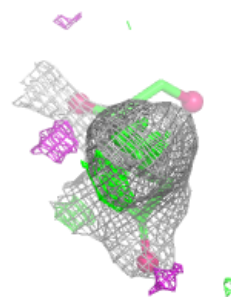
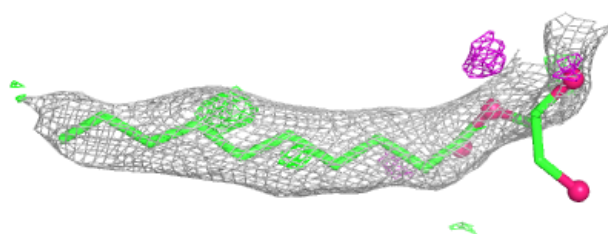
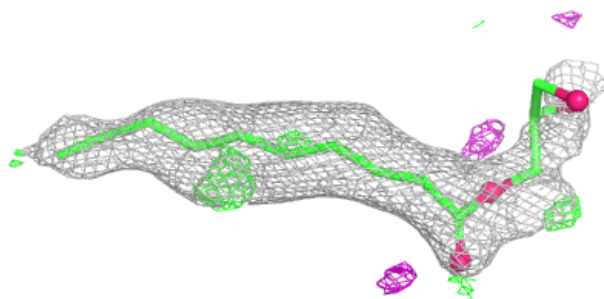
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	OLC	A	568	17/25	0.68	0.26	59,63,79,80	0
8	OLC	B	172	21/25	0.74	0.20	60,63,76,79	0
8	OLC	C	35	25/25	0.74	0.17	67,81,92,93	0
8	OLC	B	170	25/25	0.76	0.21	56,63,72,76	0
8	OLC	A	569	8/25	0.80	0.14	68,68,70,71	0
8	OLC	B	171	25/25	0.80	0.17	65,68,73,74	0
8	OLC	A	567	18/25	0.82	0.17	47,60,73,74	0
8	OLC	B	169	25/25	0.82	0.15	54,65,72,73	0
8	OLC	A	564	25/25	0.82	0.17	45,55,73,76	0
8	OLC	A	572	25/25	0.83	0.18	48,59,64,68	0
8	OLC	A	571	20/25	0.84	0.16	54,66,71,71	0
8	OLC	A	565	25/25	0.84	0.16	44,65,90,92	0
8	OLC	A	573	21/25	0.84	0.15	56,66,81,82	0
8	OLC	A	570	15/25	0.84	0.18	47,64,76,77	0
8	OLC	A	574	25/25	0.85	0.14	51,58,68,70	0
8	OLC	A	566	23/25	0.87	0.13	30,45,65,66	0
7	PER	A	563	2/2	0.96	0.05	19,19,19,21	0
6	HAS	A	801	65/65	0.98	0.06	11,20,34,39	0
4	CU	A	803	1/1	0.99	0.02	22,22,22,22	0
5	HEM	A	800	43/43	0.99	0.05	10,15,19,21	0
9	CUA	B	802	2/2	0.99	0.03	20,20,20,21	0

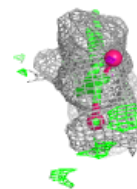
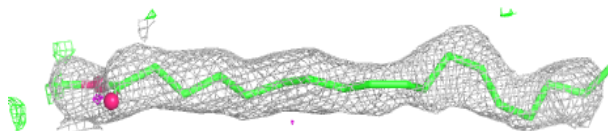
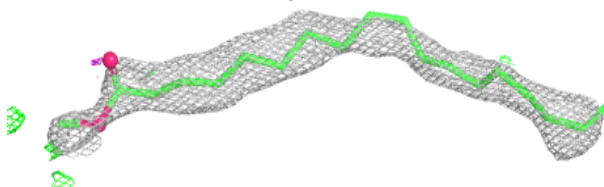
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around OLC A 568:

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

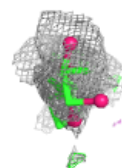
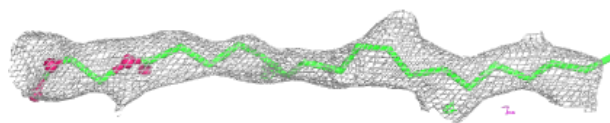
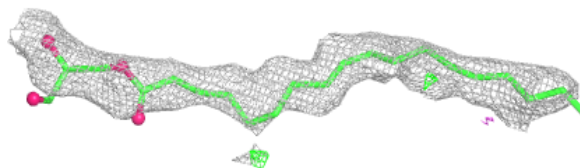
**Electron density around OLC B 172:**

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

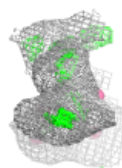
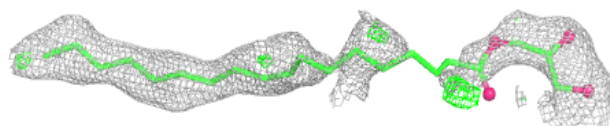
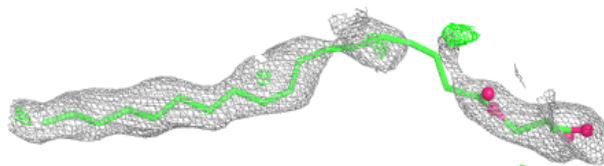


Electron density around OLC C 35:

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

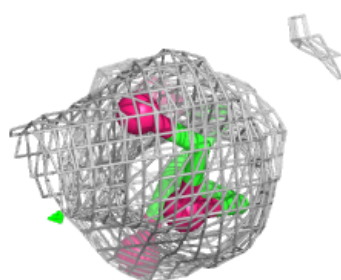
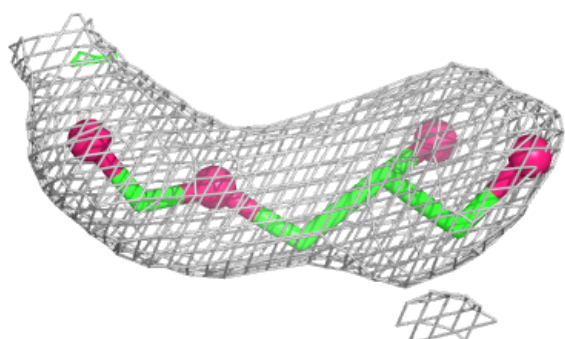
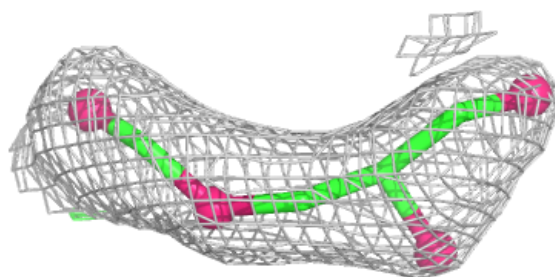
**Electron density around OLC B 170:**

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

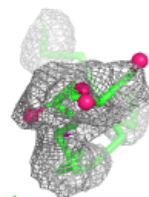
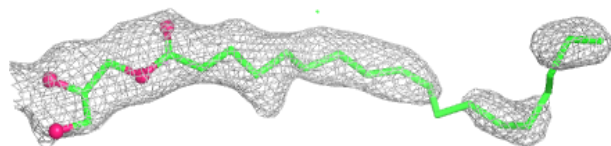
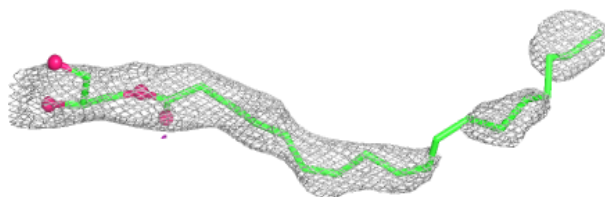


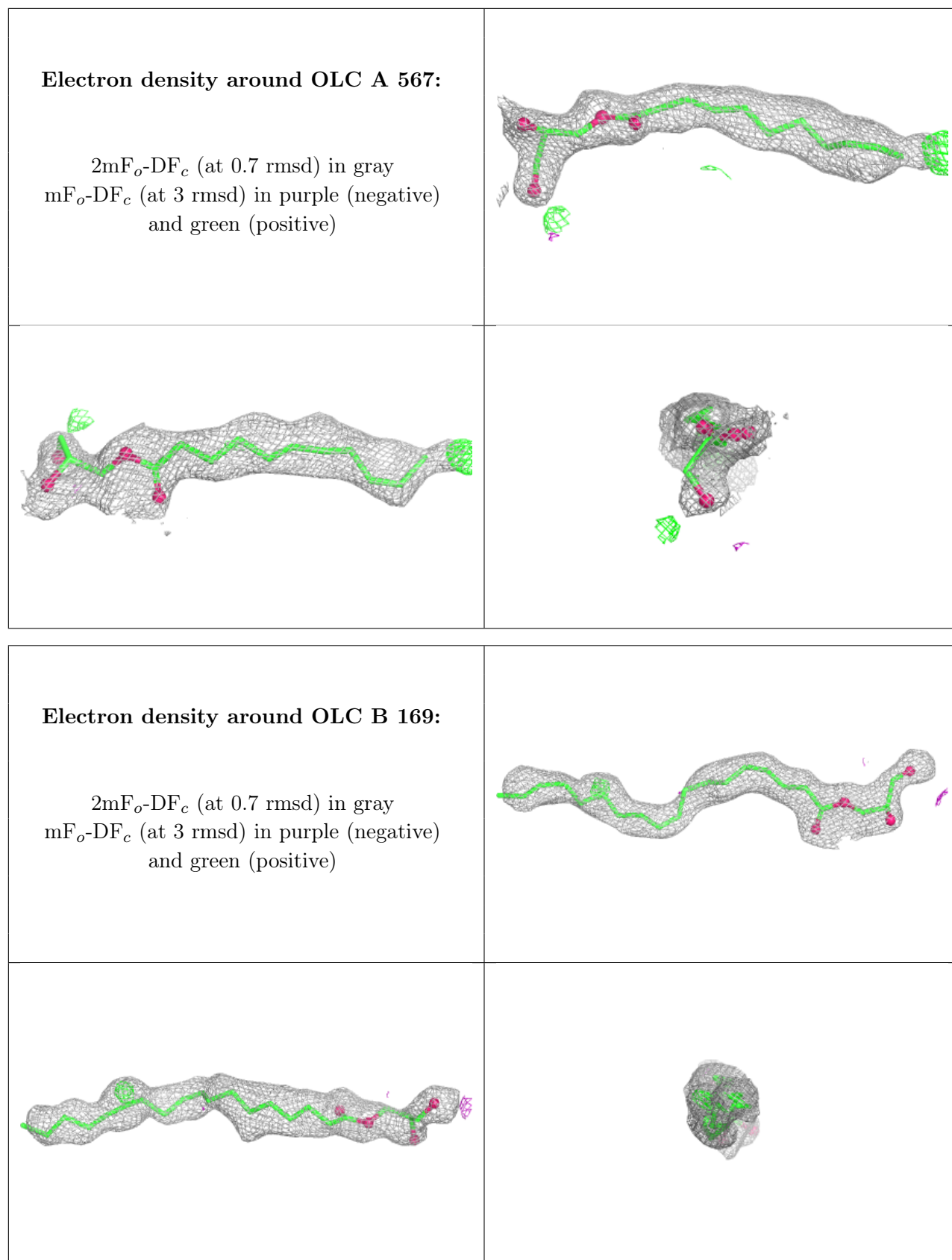
Electron density around OLC A 569:

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

**Electron density around OLC B 171:**

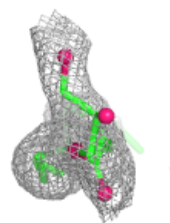
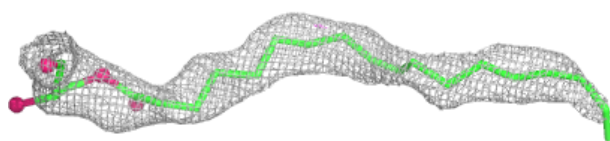
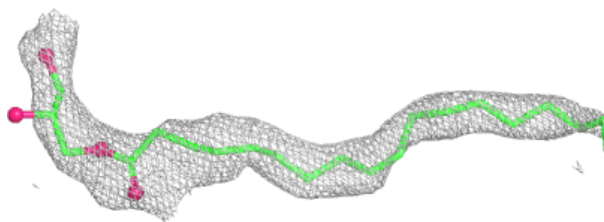
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



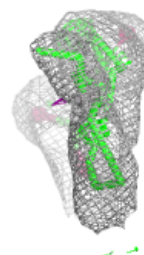
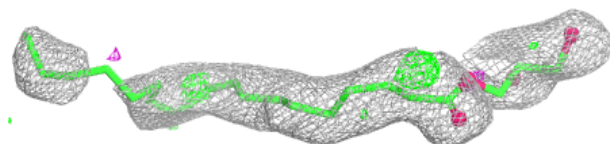
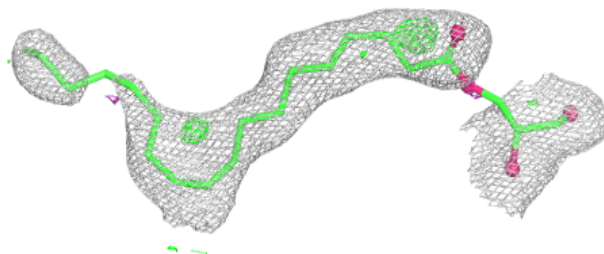


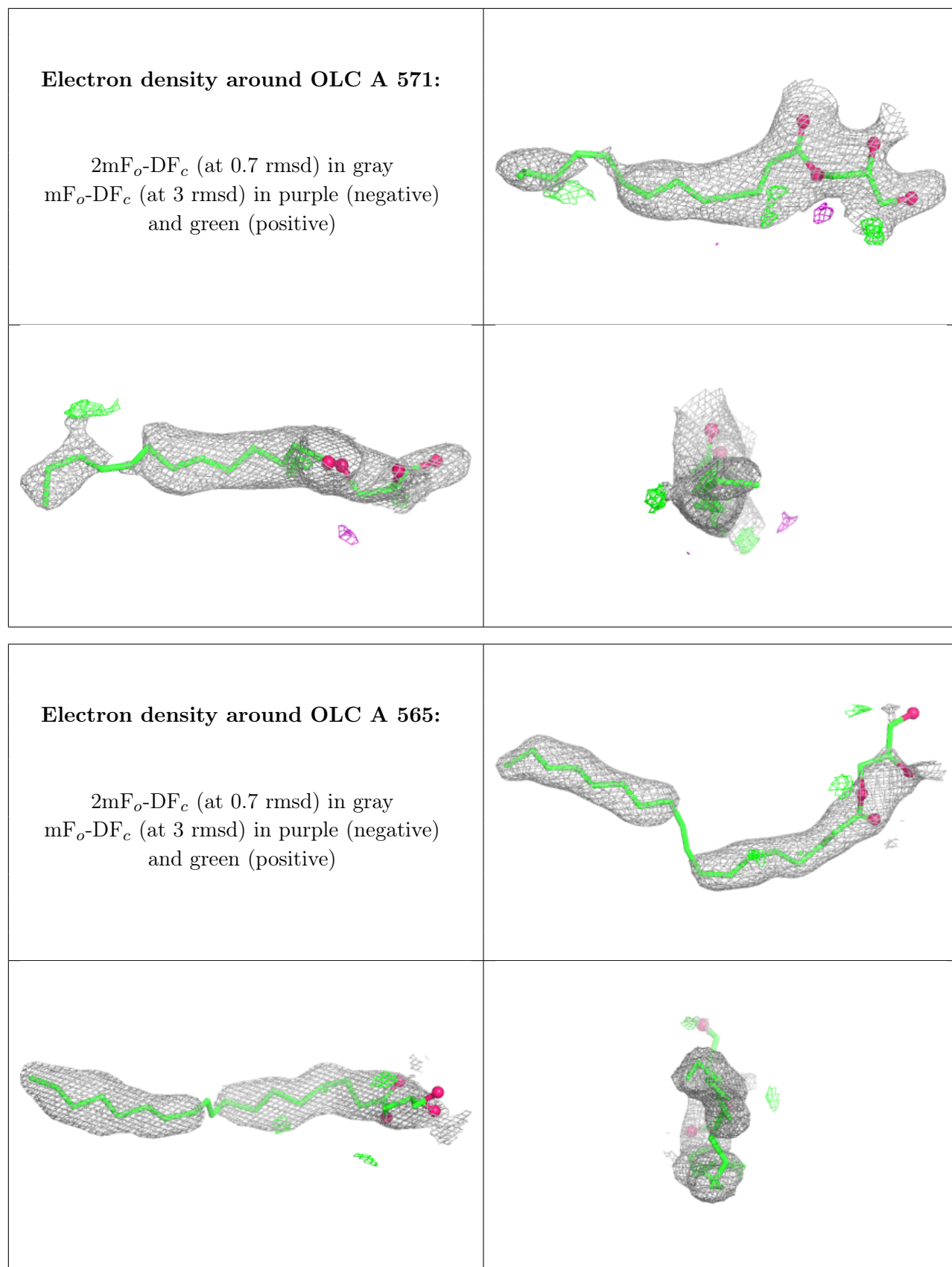
Electron density around OLC A 564:

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

**Electron density around OLC A 572:**

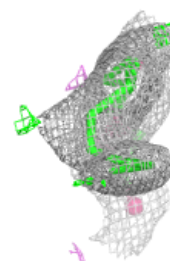
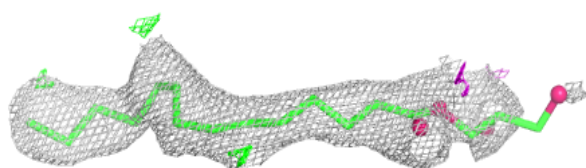
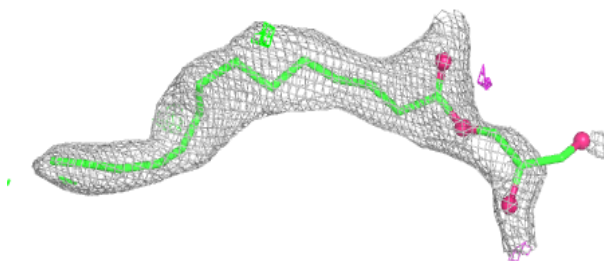
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



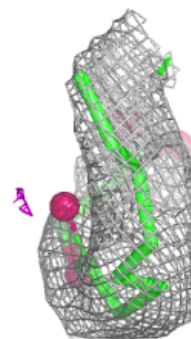
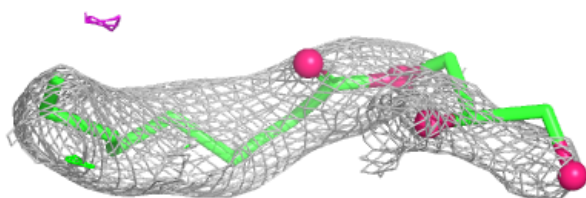
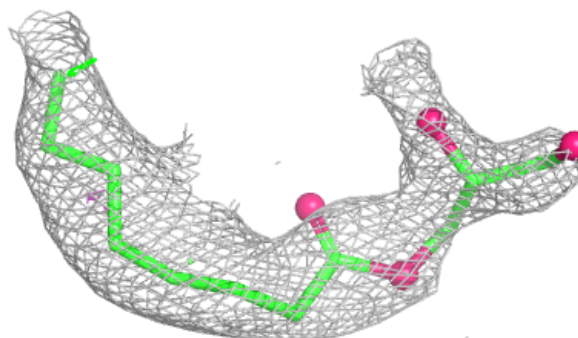


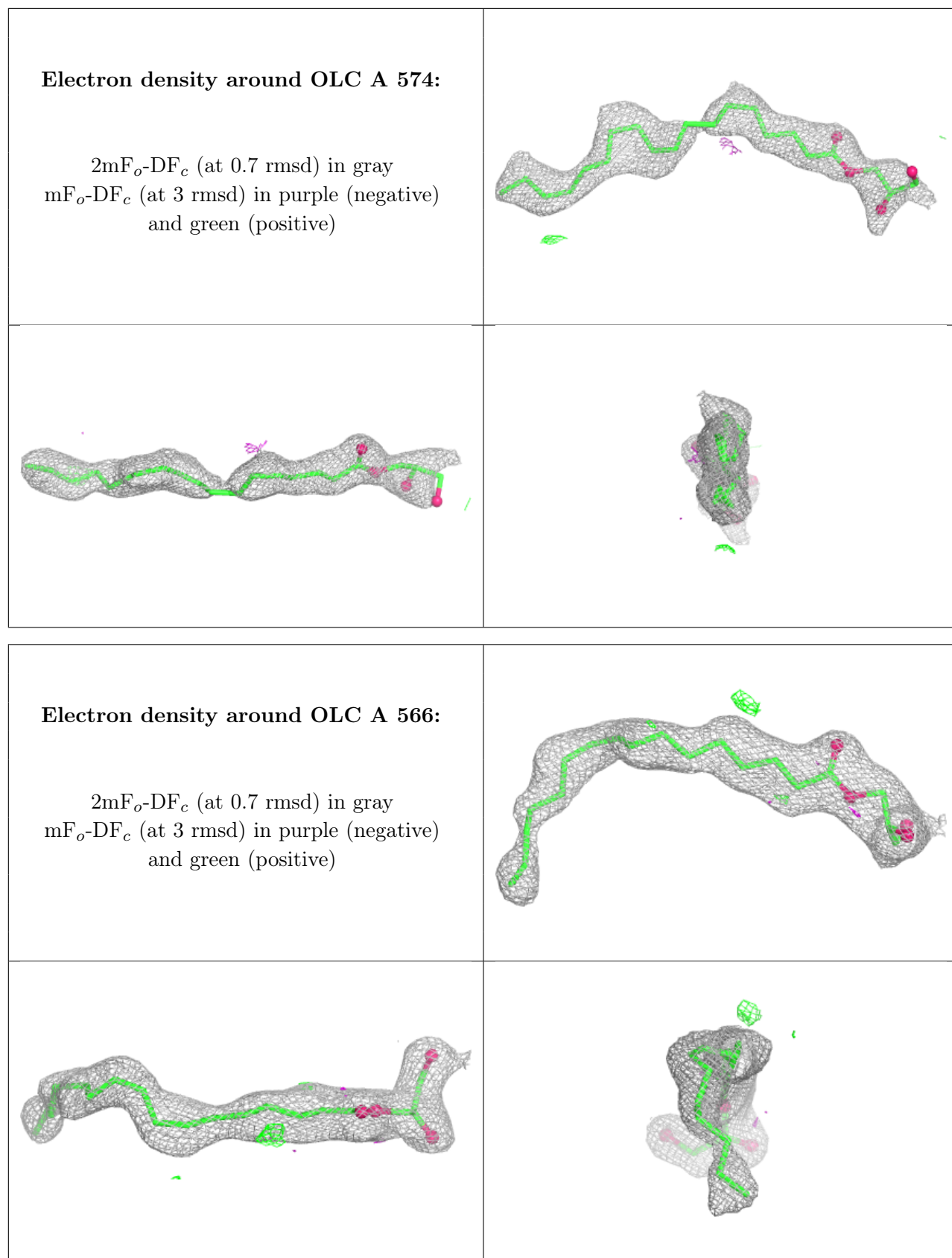
Electron density around OLC A 573:

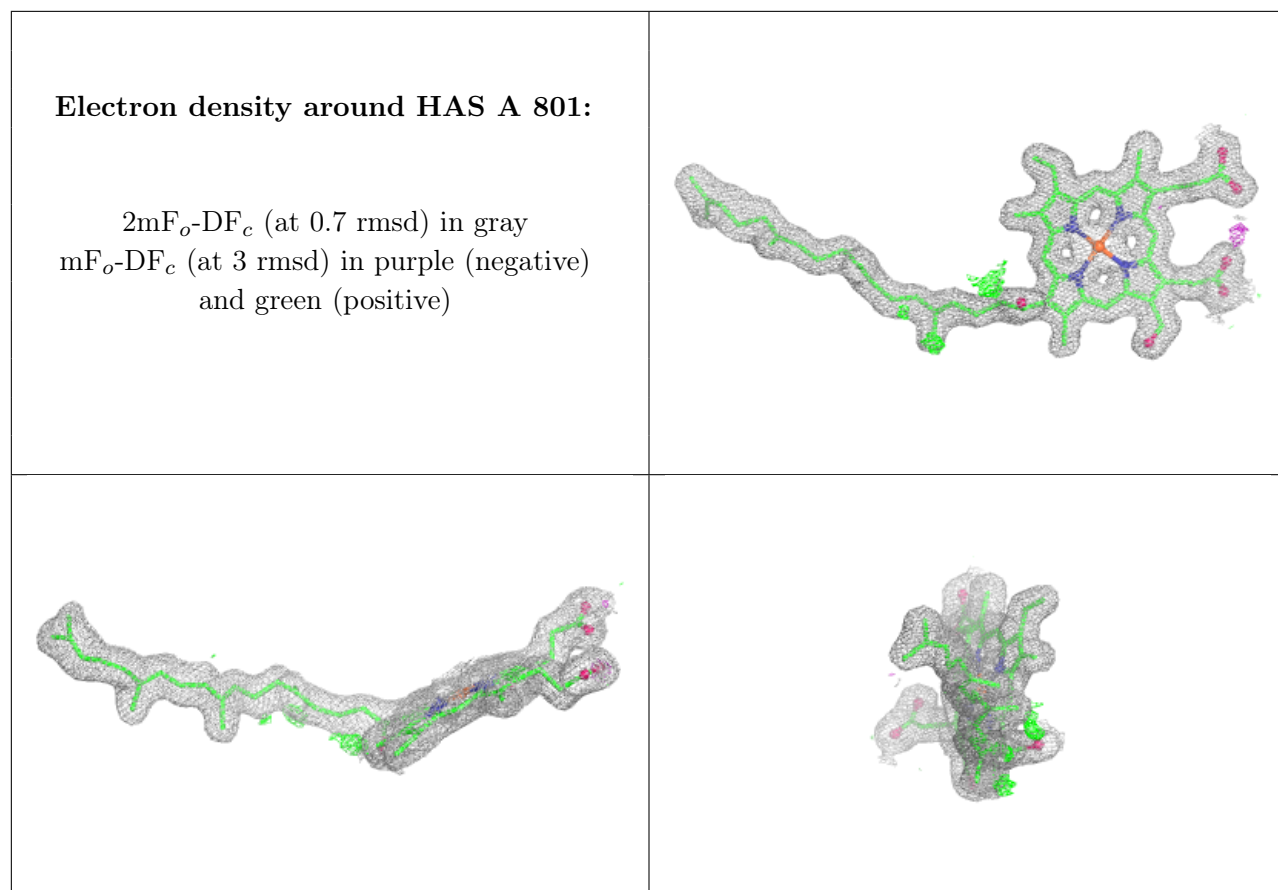
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

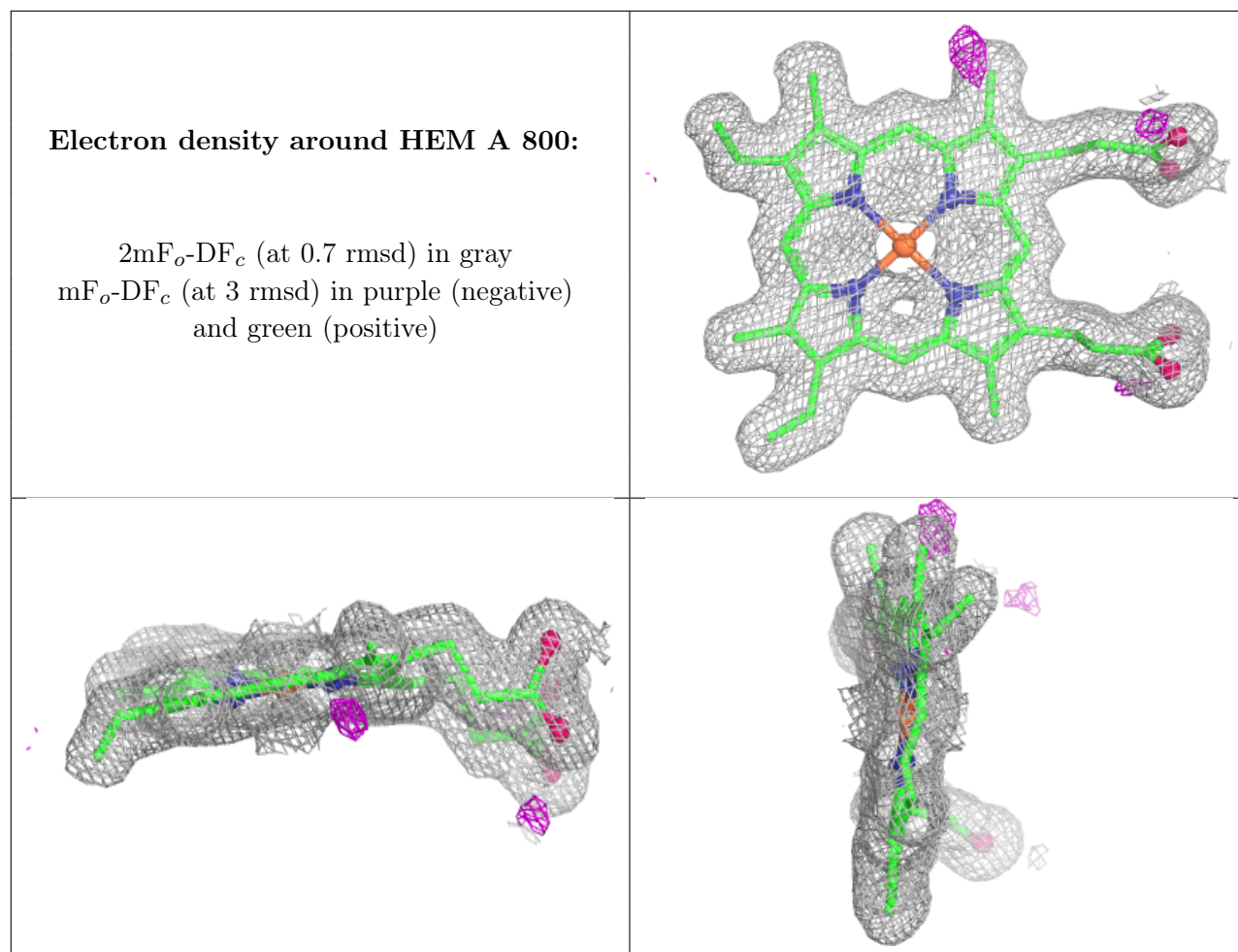
**Electron density around OLC A 570:**

$2mF_o-DF_c$ (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.