



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:36 AM UTC

PDB ID : 8A6E / pdb_00008a6e
Title : 100 picosecond light activated crystal structure of bovine rhodopsin in Lipidic Cubic Phase (SACLA)
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Deposited on : 2022-06-17
Resolution : 1.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0

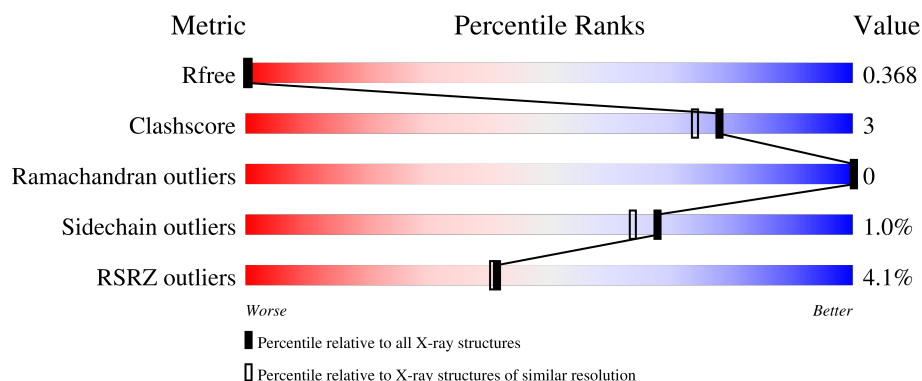
1 Overall quality at a glance

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.

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

Mol	Chain	Length	Quality of chain
1	A	349	4% 81% 6% 13%
1	B	349	3% 83% 5% 13%
2	C	2	50% 50%
2	D	2	100%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 5477 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 Rhodopsin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	304	Total	C	N	O	S	0	11	0
			2488	1668	377	420	23			
1	B	305	Total	C	N	O	S	5	10	0
			2484	1667	375	418	24			

There are 2 discrepancies between the modelled and reference sequences:

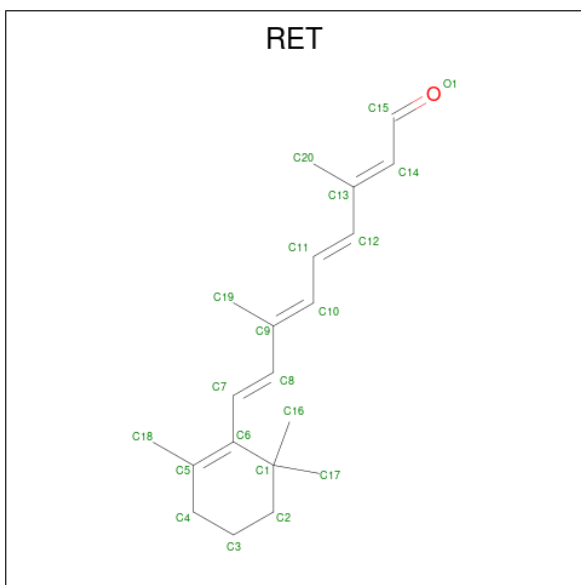
Chain	Residue	Modelled	Actual	Comment	Reference
A	401	ACE	-	acetylation	UNP P02699
B	401	ACE	-	acetylation	UNP P02699

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



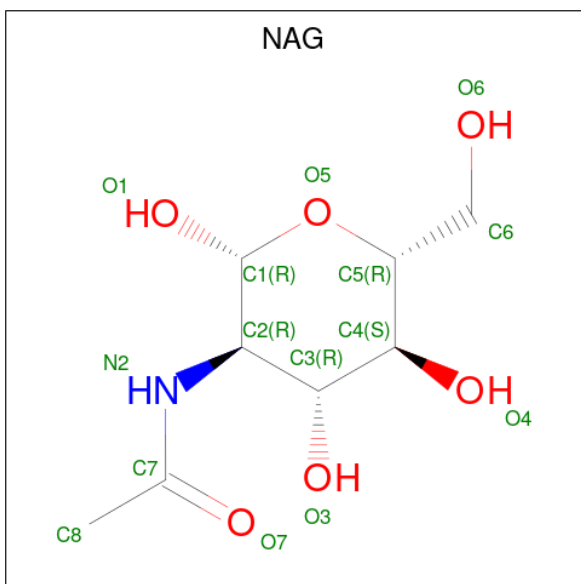
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is RETINAL (CCD ID: RET) (formula: C₂₀H₂₈O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C		0	0
			20	20			
3	B	1	Total	C		0	0
			20	20			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



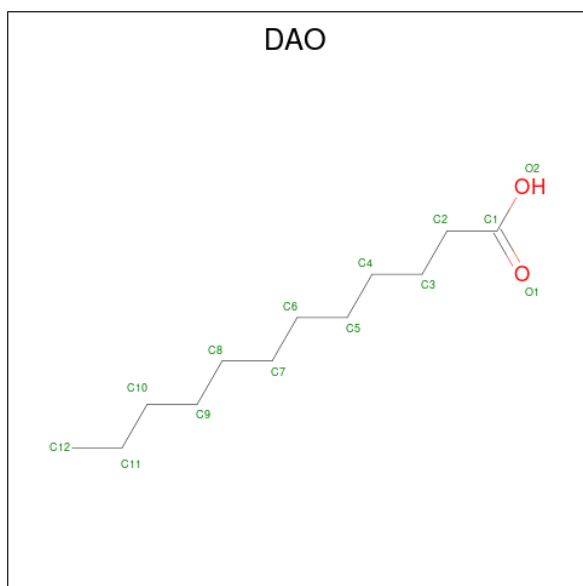
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		

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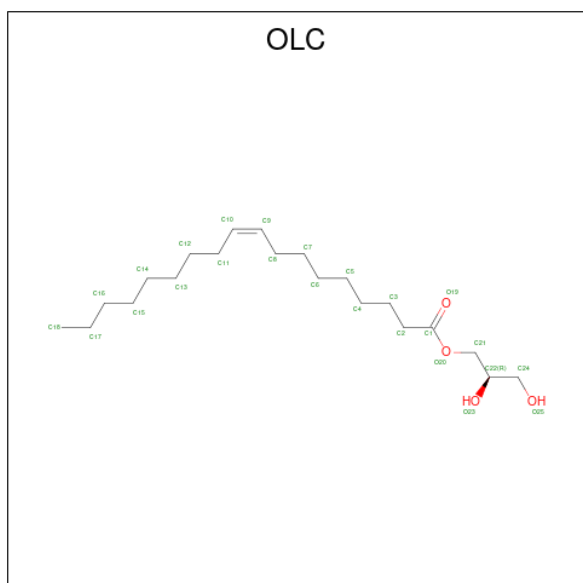
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is LAURIC ACID (CCD ID: DAO) (formula: $C_{12}H_{24}O_2$).



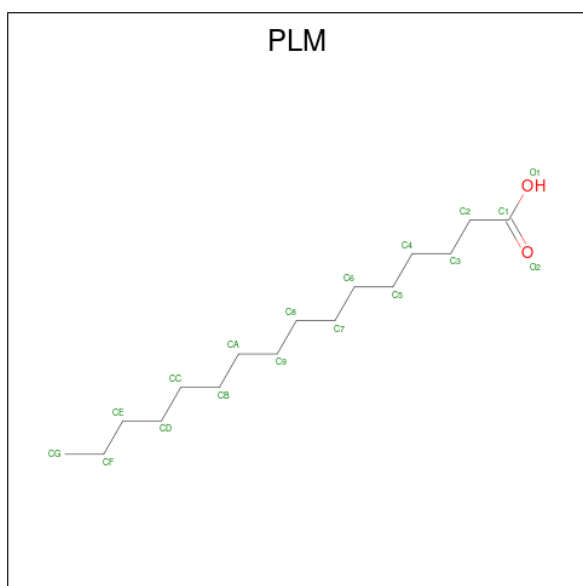
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			14	12	2		

- 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 25 21 4	0	0
6	A	1	Total C O 22 18 4	0	0
6	A	1	Total C 7 7	0	0
6	A	1	Total C 10 10	0	0
6	A	1	Total C 12 12	0	0
6	A	1	Total C O 10 8 2	0	0
6	A	1	Total C O 25 21 4	0	0
6	A	1	Total C O 10 8 2	0	0
6	A	1	Total C O 25 21 4	0	0
6	A	1	Total C 13 13	0	0
6	B	1	Total C O 19 17 2	0	0
6	B	1	Total C O 18 14 4	0	0
6	B	1	Total C 7 7	0	0

- Molecule 7 is PALMITIC ACID (CCD ID: PLM) (formula: C₁₆H₃₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			17	16	1		
7	B	1	Total	C	O	0	0
			7	6	1		

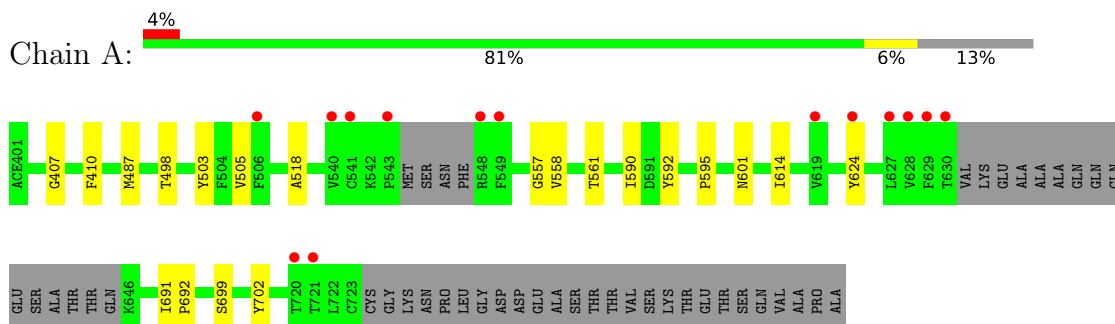
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	75	Total	O	0	0
			75	75		
8	B	65	Total	O	0	0
			65	65		

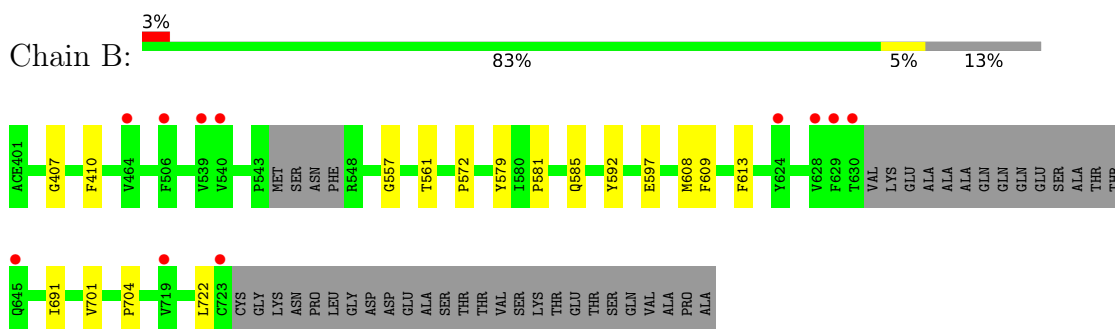
3 Residue-property plots [i](#)

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: Rhodopsin



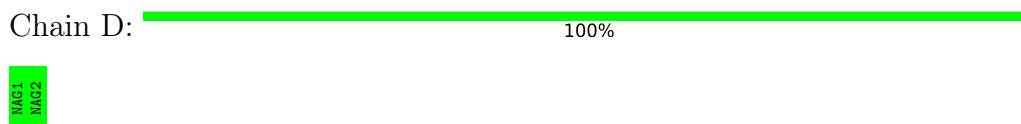
- Molecule 1: Rhodopsin



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	61.29Å 90.81Å 150.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.47 – 1.80 10.47 – 1.80	Depositor EDS
% Data completeness (in resolution range)	87.1 (10.47-1.80) 86.5 (10.47-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 1.80Å)	Xtriage
Refinement program	PHENIX 1.20_4459	Depositor
R, R_{free}	0.332 , 0.369 0.332 , 0.368	Depositor DCC
R_{free} test set	988 reflections (1.27%)	wwPDB-VP
Wilson B-factor (Å ²)	22.2	Xtriage
Anisotropy	0.401	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 89.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5477	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 59.77 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.6815e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OLC, NAG, RET, PLM, DAO, ACE

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	0.12	0/2564	0.33	0/3503
1	B	0.12	0/2563	0.32	0/3499
All	All	0.12	0/5127	0.32	0/7002

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2488	0	2449	13	0
1	B	2484	0	2443	11	0
2	C	28	0	25	0	0
2	D	28	0	25	0	0
3	A	20	0	27	3	0
3	B	20	0	27	1	0
4	A	14	0	13	0	0
4	B	14	0	13	0	0
5	A	14	0	23	1	0
6	A	159	0	235	4	0
6	B	44	0	57	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	17	0	31	0	0
7	B	7	0	8	0	0
8	A	75	0	0	0	0
8	B	65	0	0	0	0
All	All	5477	0	5376	30	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 3.

All (30) 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:B:613:PHE:HE2	6:B:806:OLC:H11	1.66	0.61
3:A:801:RET:H8	3:A:801:RET:H181	1.83	0.58
1:A:692:PRO:HG3	5:A:803:DAO:H31	1.88	0.55
1:A:699:SER:HA	1:A:702:TYR:CE2	2.46	0.51
1:A:407:GLY:HA3	1:A:410:PHE:CZ	2.46	0.50
1:A:558:VAL:HG11	6:A:805:OLC:H7	1.95	0.49
1:B:557:GLY:O	1:B:561:THR:HG23	2.13	0.49
3:B:801:RET:H8	3:B:801:RET:H181	1.95	0.48
1:A:699:SER:HA	1:A:702:TYR:CD2	2.48	0.48
1:A:557:GLY:O	1:A:561:THR:HG23	2.14	0.48
1:B:701:VAL:O	1:B:704:PRO:HD2	2.15	0.47
1:B:613:PHE:CE2	6:B:806:OLC:H11	2.48	0.47
1:A:614[A]:ILE:HD11	6:A:806:OLC:H9	1.97	0.46
1:B:572:PRO:HB2	1:B:579:TYR:CE2	2.51	0.46
1:B:407:GLY:HA3	1:B:410:PHE:CZ	2.52	0.45
3:A:801:RET:H8	3:A:801:RET:C18	2.48	0.44
1:B:691[B]:ILE:HG22	6:B:804:OLC:H2A	2.00	0.44
6:A:805:OLC:H21	6:A:805:OLC:H2	1.58	0.43
1:A:595:PRO:O	1:A:601:ASN:HB2	2.18	0.43
1:B:581:PRO:HB2	1:B:585:GLN:OE1	2.20	0.42
1:A:691[A]:ILE:HB	1:A:692:PRO:HD3	2.02	0.41
6:A:811:OLC:H2A	6:A:811:OLC:H21	1.83	0.41
1:B:608:MET:HE2	1:B:608:MET:HB3	1.92	0.41
1:B:609:PHE:O	1:B:613:PHE:HB3	2.21	0.41
1:A:503:TYR:CZ	1:A:505:VAL:HG22	2.56	0.41
3:A:801:RET:H181	3:A:801:RET:C8	2.50	0.41
1:A:498:THR:HG23	1:A:503:TYR:C	2.46	0.40
1:A:487:MET:HE3	1:A:518:ALA:HA	2.01	0.40
1:B:691[A]:ILE:HG22	6:B:804:OLC:H2A	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:590:ILE:HD13	1:A:590:ILE:HA	1.89	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	309/349 (88%)	298 (96%)	11 (4%)	0	100	100
1	B	309/349 (88%)	298 (96%)	11 (4%)	0	100	100
All	All	618/698 (88%)	596 (96%)	22 (4%)	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	265/296 (90%)	263 (99%)	2 (1%)	73	70
1	B	263/296 (89%)	260 (99%)	3 (1%)	65	60
All	All	528/592 (89%)	523 (99%)	5 (1%)	68	67

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	592	TYR
1	A	624	TYR
1	B	592	TYR
1	B	597	GLU
1	B	722	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	703	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

4 monosaccharides 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	$\# Z > 2$
2	NAG	C	1	1,2	14,14,15	0.26	0	17,19,21	0.63	1 (5%)
2	NAG	C	2	2	14,14,15	0.26	0	17,19,21	0.45	0
2	NAG	D	1	1,2	14,14,15	0.47	0	17,19,21	0.41	0
2	NAG	D	2	2	14,14,15	0.42	0	17,19,21	0.47	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
2	NAG	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	NAG	C1-O5-C5	2.15	115.06	112.19

There are no chirality outliers.

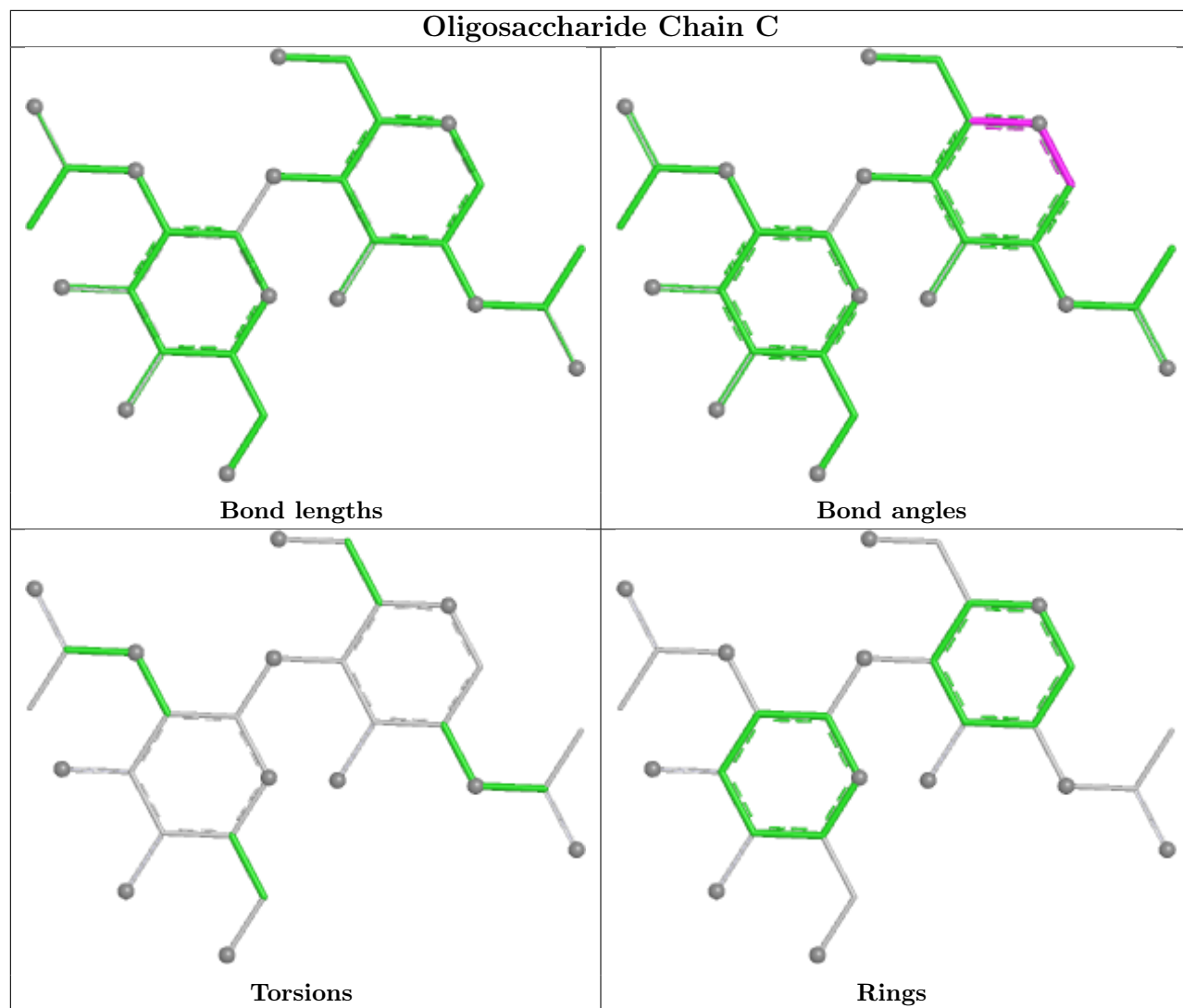
All (2) torsion outliers are listed below:

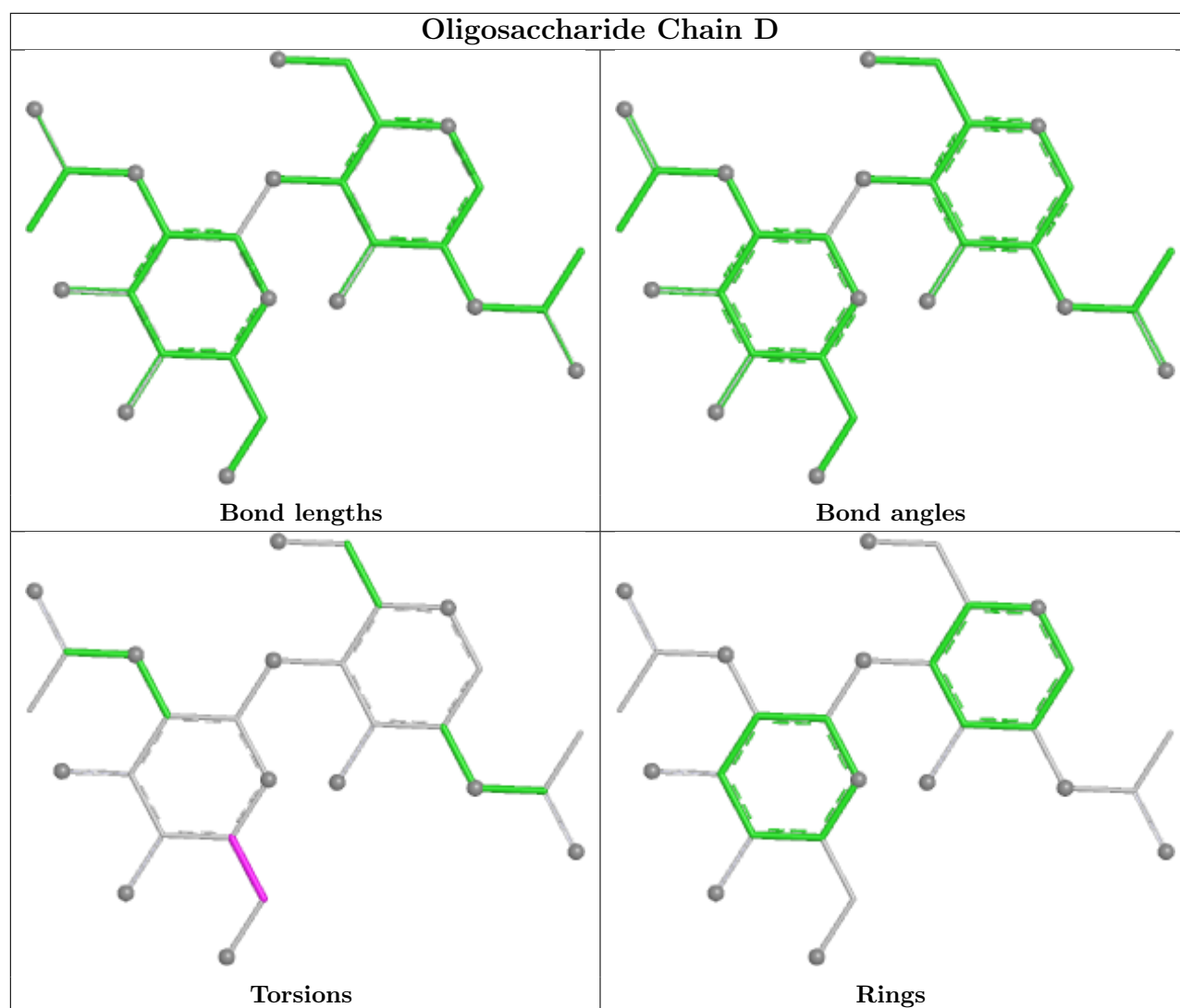
Mol	Chain	Res	Type	Atoms
2	D	2	NAG	O5-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





5.6 Ligand geometry [i](#)

20 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	$\# Z > 2$
6	OLC	A	806	-	6,6,24	0.18	0	5,5,25	0.22	0
6	OLC	A	813	-	24,24,24	0.24	0	25,25,25	0.23	0
6	OLC	A	812	-	9,9,24	1.53	2 (22%)	9,9,25	1.71	2 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	OLC	A	811	-	24,24,24	0.22	0	25,25,25	0.25	0
4	NAG	B	802	1	14,14,15	0.21	0	17,19,21	0.61	0
6	OLC	A	805	-	21,21,24	0.25	0	22,22,25	0.25	0
6	OLC	A	814	-	12,12,24	0.23	0	11,11,25	0.12	0
7	PLM	A	809	1	15,16,17	0.51	0	14,15,17	0.35	0
4	NAG	A	802	1	14,14,15	0.25	0	17,19,21	0.49	0
6	OLC	B	803	-	18,18,24	0.32	0	18,18,25	0.22	0
3	RET	B	801	1	20,20,21	2.45	5 (25%)	27,27,28	1.10	2 (7%)
3	RET	A	801	1	20,20,21	2.03	5 (25%)	27,27,28	1.26	3 (11%)
6	OLC	B	806	-	6,6,24	0.19	0	5,5,25	0.13	0
6	OLC	B	804	-	17,17,24	0.24	0	18,18,25	0.34	0
6	OLC	A	810	-	9,9,24	1.55	2 (22%)	9,9,25	1.73	2 (22%)
6	OLC	A	808	-	11,11,24	0.22	0	10,10,25	0.26	0
6	OLC	A	804	-	24,24,24	0.26	0	25,25,25	0.27	0
5	DAO	A	803	-	13,13,13	0.72	0	13,13,13	0.63	0
6	OLC	A	807	-	9,9,24	0.26	0	8,8,25	0.14	0
7	PLM	B	805	1	5,6,17	0.66	0	4,5,17	0.63	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
6	OLC	A	806	-	-	1/4/4/24	-
6	OLC	A	813	-	-	1/24/24/24	-
6	OLC	A	812	-	-	2/7/7/24	-
6	OLC	A	811	-	-	4/24/24/24	-
4	NAG	B	802	1	-	0/6/23/26	0/1/1/1
6	OLC	A	805	-	-	4/21/21/24	-
6	OLC	A	814	-	-	2/10/10/24	-
7	PLM	A	809	1	-	6/14/14/15	-
4	NAG	A	802	1	-	0/6/23/26	0/1/1/1
6	OLC	B	803	-	-	4/17/17/24	-
3	RET	B	801	1	-	4/13/30/31	0/1/1/1
3	RET	A	801	1	-	6/13/30/31	0/1/1/1
6	OLC	B	806	-	-	1/4/4/24	-
6	OLC	B	804	-	-	4/17/17/24	-
6	OLC	A	810	-	-	2/7/7/24	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	OLC	A	808	-	-	2/9/9/24	-
6	OLC	A	804	-	-	4/24/24/24	-
5	DAO	A	803	-	-	6/11/11/11	-
6	OLC	A	807	-	-	0/7/7/24	-
7	PLM	B	805	1	-	0/4/4/15	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	801	RET	C14-C13	8.97	1.39	1.33
3	A	801	RET	C14-C13	6.41	1.38	1.33
6	A	810	OLC	O19-C1	3.45	1.33	1.22
6	A	812	OLC	O19-C1	3.44	1.33	1.22
6	A	810	OLC	O20-C1	-3.03	1.20	1.30
6	A	812	OLC	O20-C1	-3.00	1.20	1.30
3	B	801	RET	C8-C9	-2.91	1.39	1.46
3	A	801	RET	C15-C14	-2.91	1.38	1.49
3	A	801	RET	C8-C9	-2.81	1.39	1.46
3	B	801	RET	C15-C14	-2.76	1.39	1.49
3	A	801	RET	C10-C9	2.64	1.41	1.35
3	A	801	RET	C12-C13	-2.52	1.40	1.46
3	B	801	RET	C12-C13	-2.41	1.40	1.46
3	B	801	RET	C10-C9	2.17	1.40	1.35

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	810	OLC	O19-C1-C2	-3.69	111.40	123.09
6	A	812	OLC	O19-C1-C2	-3.65	111.53	123.09
6	A	810	OLC	O20-C1-C2	3.61	125.39	114.00
6	A	812	OLC	O20-C1-C2	3.56	125.24	114.00
3	B	801	RET	C19-C9-C10	-3.25	117.55	122.82
3	A	801	RET	C19-C9-C10	-2.70	118.44	122.82
3	A	801	RET	C7-C8-C9	2.52	129.96	126.23
3	A	801	RET	C19-C9-C8	2.52	121.93	118.09
3	B	801	RET	C19-C9-C8	2.36	121.69	118.09

There are no chirality outliers.

All (53) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	801	RET	C11-C10-C9-C8
3	A	801	RET	C11-C10-C9-C19
3	B	801	RET	C11-C10-C9-C8
3	B	801	RET	C11-C10-C9-C19
3	B	801	RET	C10-C11-C12-C13
6	A	805	OLC	C2-C1-O20-C21
6	A	805	OLC	O19-C1-O20-C21
6	B	803	OLC	C2-C1-O20-C21
6	B	803	OLC	O19-C1-O20-C21
6	A	811	OLC	O19-C1-O20-C21
6	A	811	OLC	C2-C1-O20-C21
3	A	801	RET	C10-C11-C12-C13
3	A	801	RET	C6-C7-C8-C9
5	A	803	DAO	C1-C2-C3-C4
6	A	813	OLC	C5-C6-C7-C8
7	A	809	PLM	C4-C5-C6-C7
6	B	803	OLC	C3-C4-C5-C6
6	A	804	OLC	C2-C1-O20-C21
3	A	801	RET	C5-C6-C7-C8
6	A	811	OLC	C5-C6-C7-C8
6	B	804	OLC	O20-C21-C22-O23
6	A	804	OLC	C2-C3-C4-C5
3	B	801	RET	C6-C7-C8-C9
6	A	806	OLC	C7-C8-C9-C10
7	A	809	PLM	CB-CC-CD-CE
6	A	804	OLC	O19-C1-O20-C21
6	A	804	OLC	C9-C10-C11-C12
6	B	804	OLC	O20-C21-C22-C24
6	A	814	OLC	C7-C8-C9-C10
7	A	809	PLM	C5-C6-C7-C8
6	A	808	OLC	C9-C10-C11-C12
6	A	811	OLC	C7-C8-C9-C10
6	B	806	OLC	C9-C10-C11-C12
6	A	808	OLC	C7-C8-C9-C10
7	A	809	PLM	C8-C9-CA-CB
6	A	814	OLC	C9-C10-C11-C12
5	A	803	DAO	C11-C10-C9-C8
6	A	805	OLC	C6-C7-C8-C9
6	B	803	OLC	C7-C8-C9-C10
5	A	803	DAO	C2-C3-C4-C5
5	A	803	DAO	O1-C1-C2-C3
6	A	810	OLC	O19-C1-C2-C3
5	A	803	DAO	C5-C6-C7-C8

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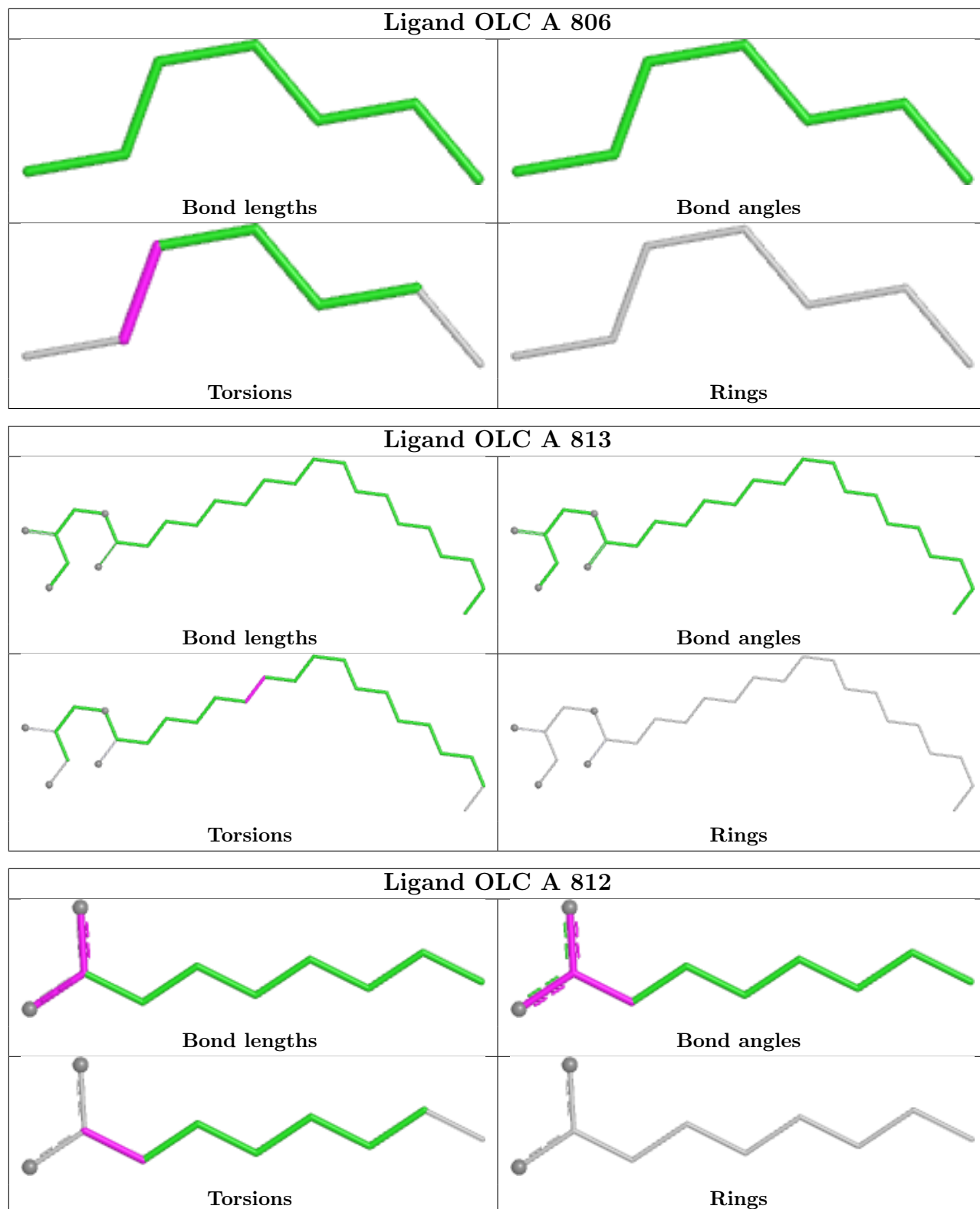
Mol	Chain	Res	Type	Atoms
6	A	810	OLC	O20-C1-C2-C3
5	A	803	DAO	O2-C1-C2-C3
6	A	812	OLC	O20-C1-C2-C3
6	A	812	OLC	O19-C1-C2-C3
3	A	801	RET	C1-C6-C7-C8
6	A	805	OLC	C4-C5-C6-C7
6	B	804	OLC	O19-C1-O20-C21
6	B	804	OLC	C21-C22-C24-O25
7	A	809	PLM	C6-C7-C8-C9
7	A	809	PLM	CC-CD-CE-CF

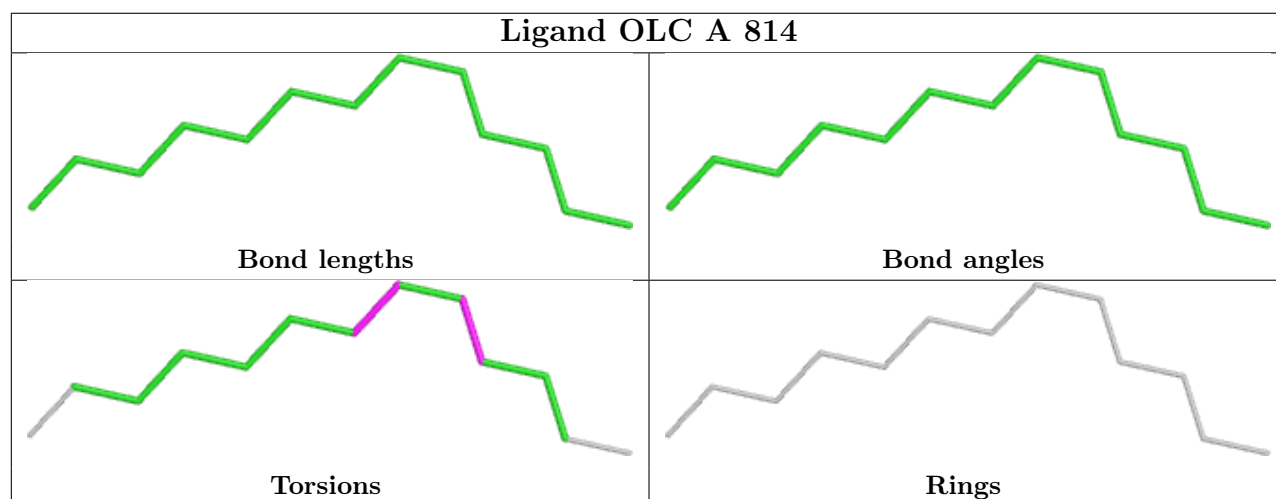
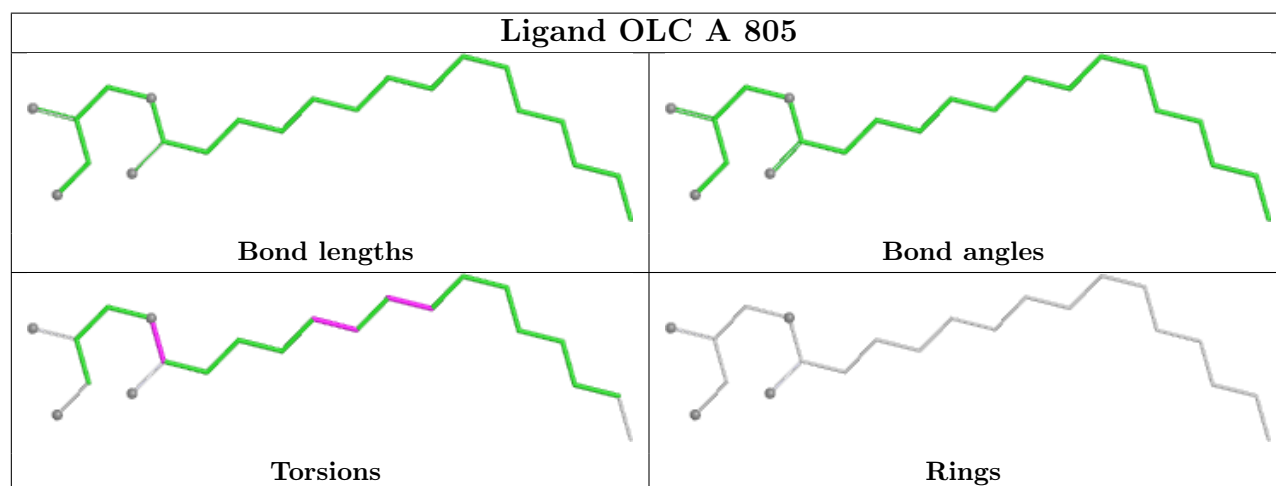
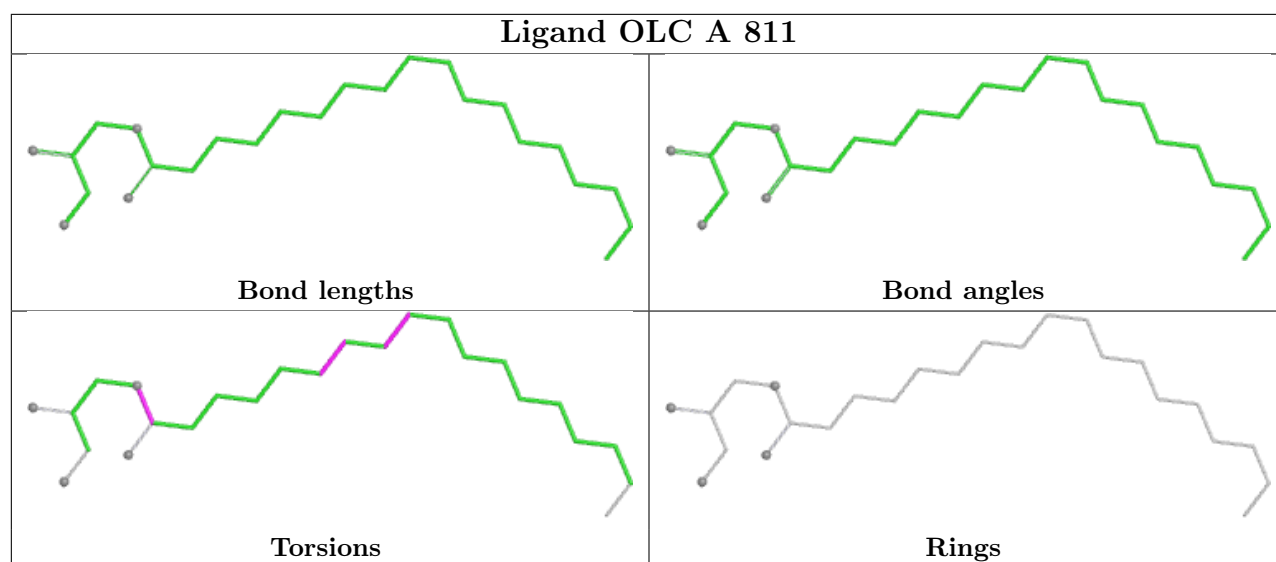
There are no ring outliers.

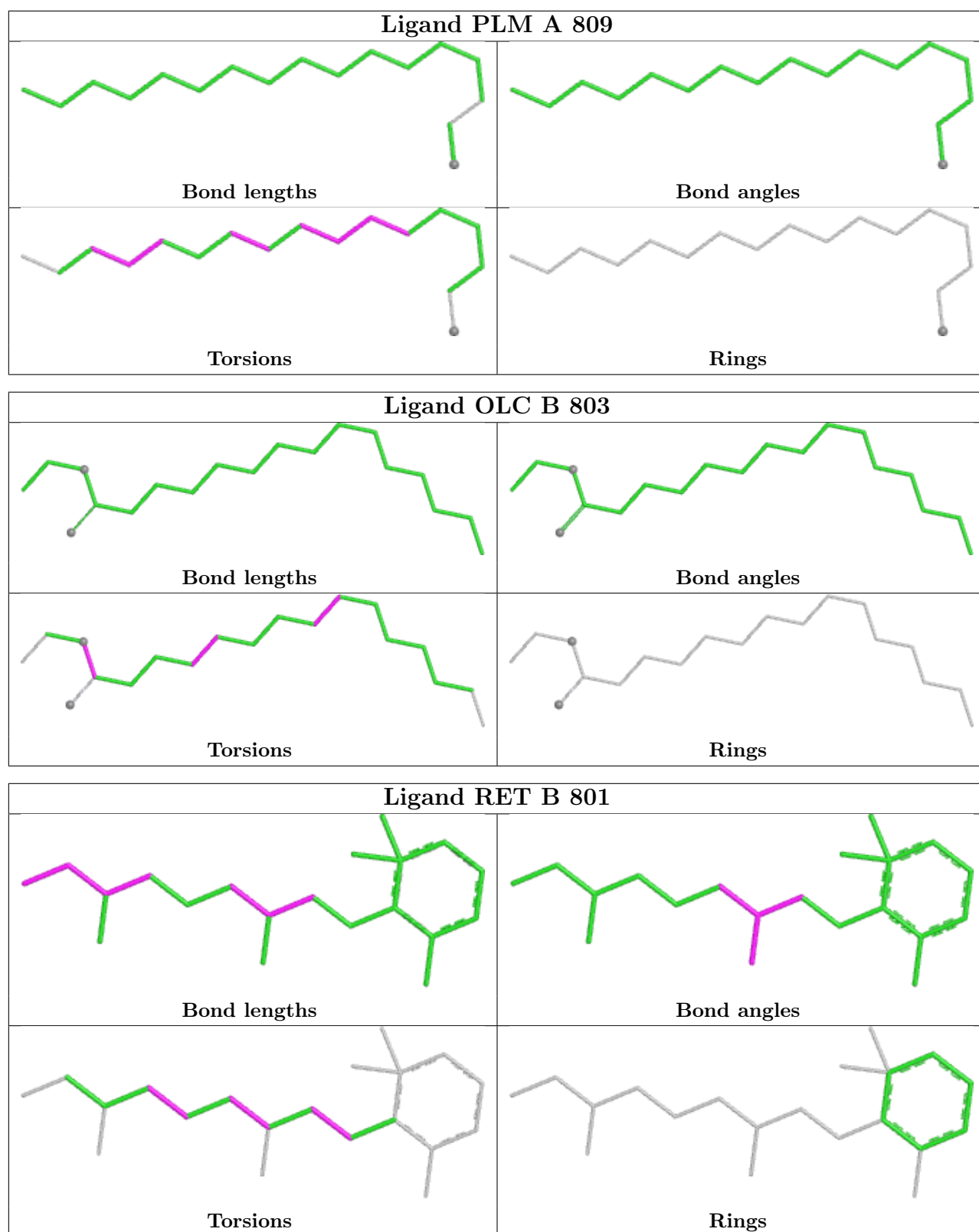
8 monomers are involved in 13 short contacts:

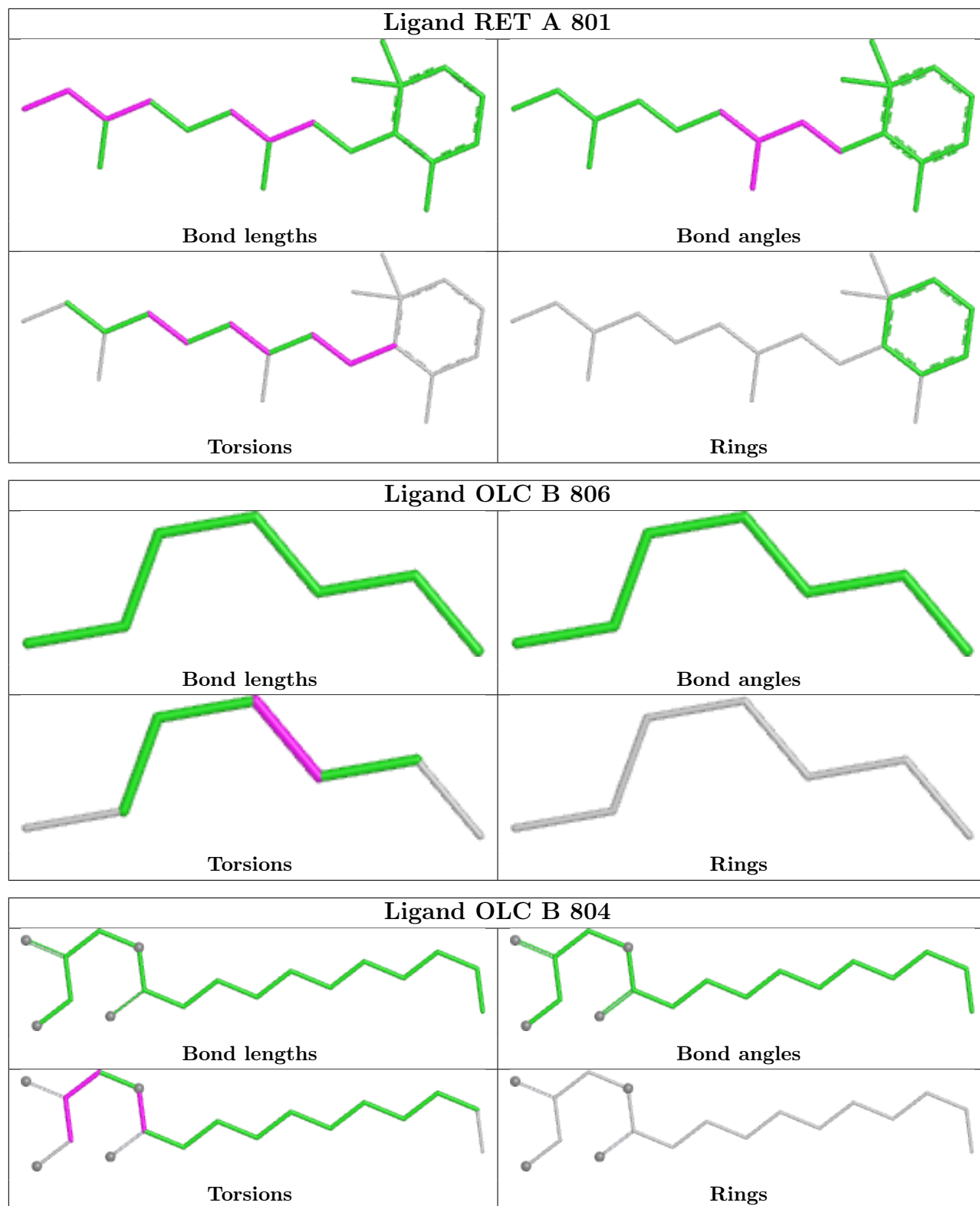
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	806	OLC	1	0
6	A	811	OLC	1	0
6	A	805	OLC	2	0
3	B	801	RET	1	0
3	A	801	RET	3	0
6	B	806	OLC	2	0
6	B	804	OLC	2	0
5	A	803	DAO	1	0

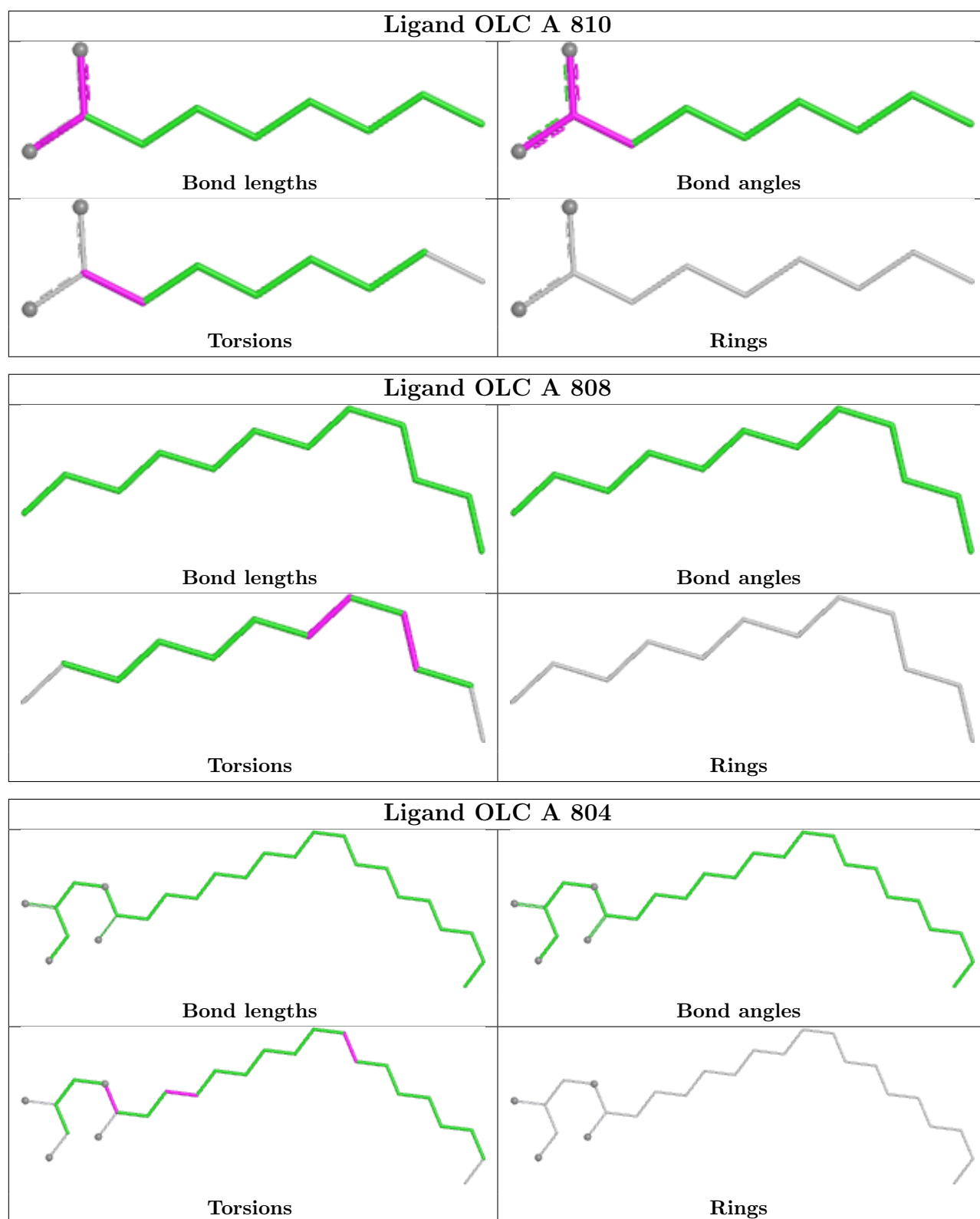
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

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

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	303/349 (86%)	0.31	14 (4%) 37 36	11, 27, 46, 72	11 (3%)
1	B	304/349 (87%)	0.39	11 (3%) 46 46	12, 26, 47, 74	10 (3%)
All	All	607/698 (86%)	0.35	25 (4%) 41 41	11, 26, 47, 74	21 (3%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	624	TYR	5.9
1	A	630	THR	4.0
1	B	624	TYR	3.9
1	A	629	PHE	3.5
1	B	540	VAL	3.4
1	A	627	LEU	3.2
1	B	464	VAL	3.1
1	B	719	VAL	2.9
1	B	506	PHE	2.9
1	A	543	PRO	2.8
1	B	630	THR	2.8
1	A	619	VAL	2.6
1	B	629	PHE	2.6
1	B	628	VAL	2.5
1	A	548	ARG	2.5
1	A	540	VAL	2.5
1	A	506	PHE	2.4
1	A	721	THR	2.4
1	B	645	GLN	2.4
1	B	723	CYS	2.3
1	A	549	PHE	2.3
1	A	541	CYS	2.2
1	A	720	THR	2.2
1	A	628	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	539	VAL	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](#)

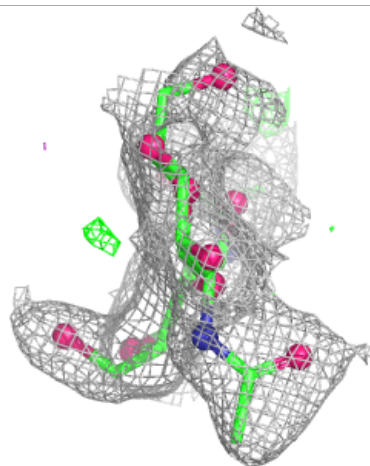
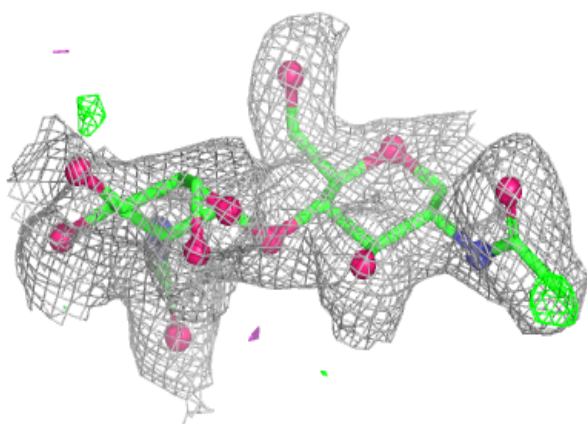
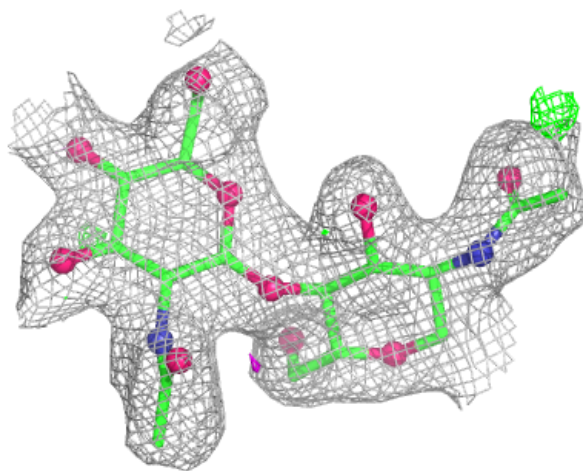
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

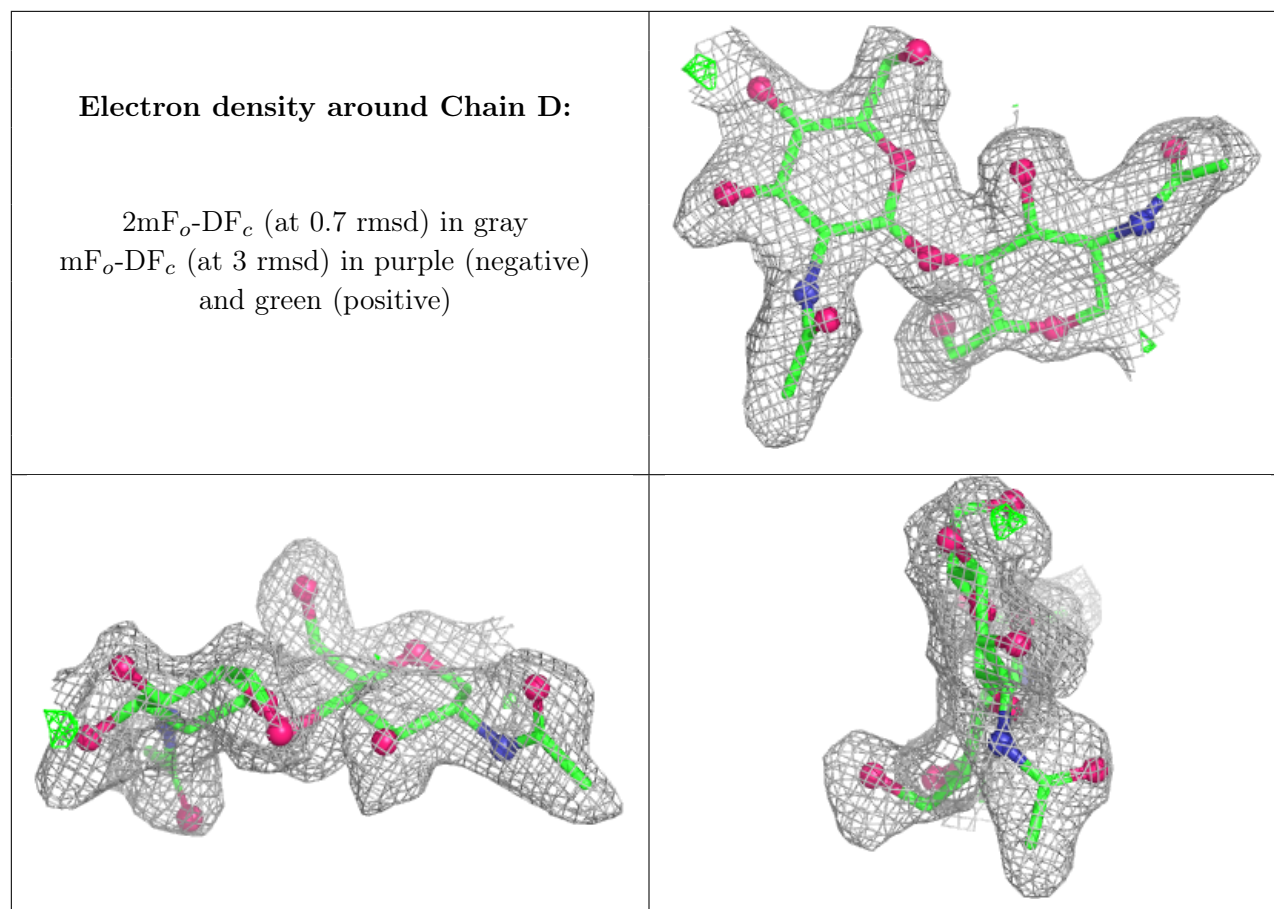
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	D	2	14/15	0.80	0.10	39,47,60,60	0
2	NAG	D	1	14/15	0.81	0.11	25,35,39,54	0
2	NAG	C	2	14/15	0.85	0.10	38,45,58,59	0
2	NAG	C	1	14/15	0.86	0.09	23,33,38,41	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

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





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($\text{\AA}^2$)	Q<0.9
7	PLM	A	809	17/18	0.62	0.14	35,49,57,66	0
6	OLC	B	803	19/25	0.66	0.13	41,54,64,68	0
6	OLC	A	812	10/25	0.66	0.13	45,55,61,61	0
6	OLC	A	811	25/25	0.67	0.16	49,53,61,70	0
6	OLC	A	805	22/25	0.68	0.13	52,65,73,78	0
6	OLC	A	810	10/25	0.68	0.14	62,68,69,77	0
6	OLC	A	808	12/25	0.71	0.15	46,52,67,70	0
6	OLC	B	804	18/25	0.74	0.13	44,48,61,62	0
4	NAG	A	802	14/15	0.74	0.16	46,54,67,67	0
7	PLM	B	805	7/18	0.74	0.10	47,51,54,56	0
6	OLC	A	807	10/25	0.76	0.10	39,47,54,55	0
6	OLC	A	814	13/25	0.76	0.12	35,42,53,59	0
6	OLC	A	804	25/25	0.76	0.11	47,52,60,63	0

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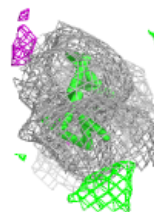
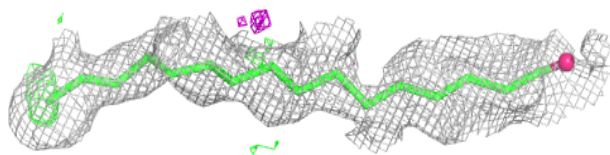
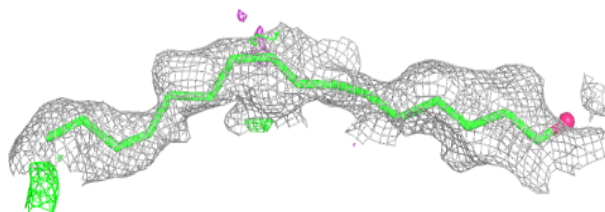
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	OLC	A	813	25/25	0.77	0.13	35,48,72,76	0
5	DAO	A	803	14/14	0.79	0.11	35,44,52,55	0
6	OLC	B	806	7/25	0.81	0.11	31,31,40,43	0
6	OLC	A	806	7/25	0.82	0.10	35,38,44,45	0
4	NAG	B	802	14/15	0.85	0.10	24,34,40,43	0
3	RET	A	801	20/21	0.87	0.09	16,19,32,34	0
3	RET	B	801	20/21	0.89	0.08	16,23,35,37	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.

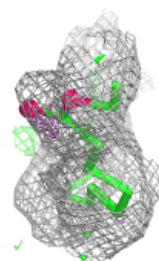
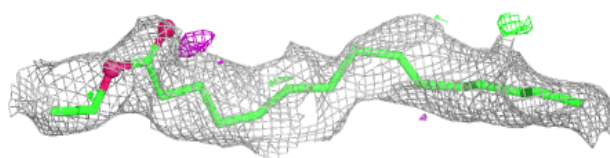
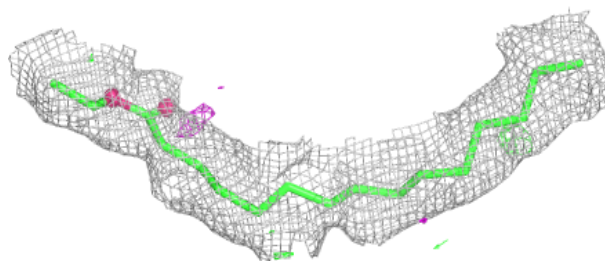
Electron density around PLM A 809:

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

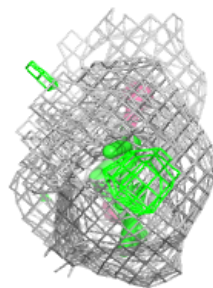
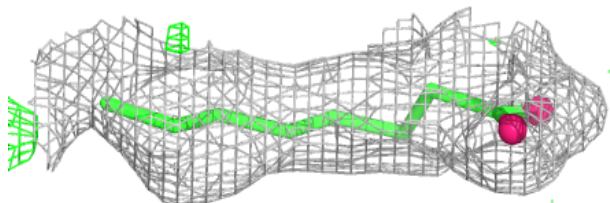
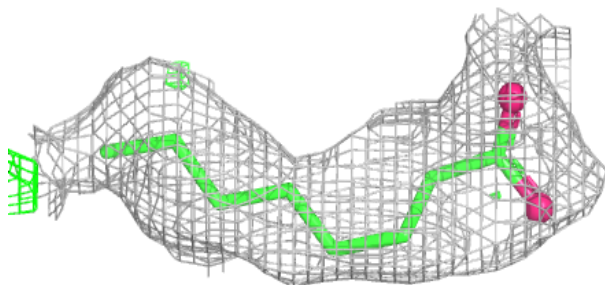


Electron density around OLC B 803:

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

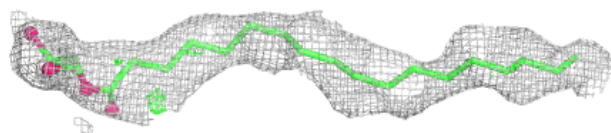
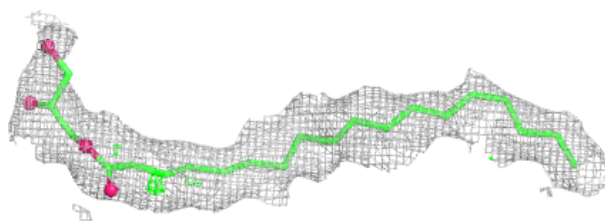
**Electron density around OLC A 812:**

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and green (positive)

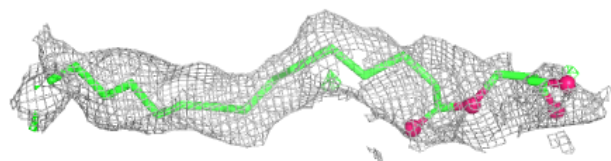
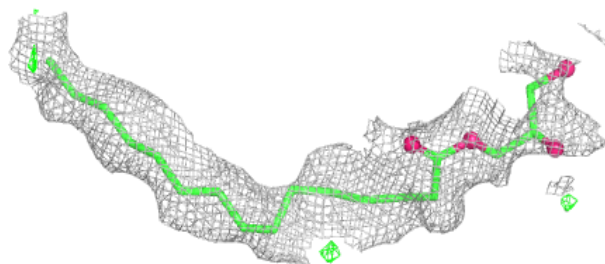


Electron density around OLC A 811:

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and green (positive)

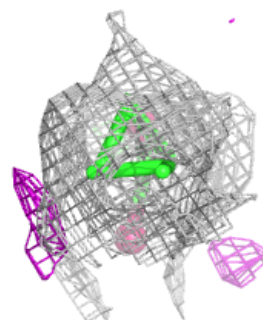
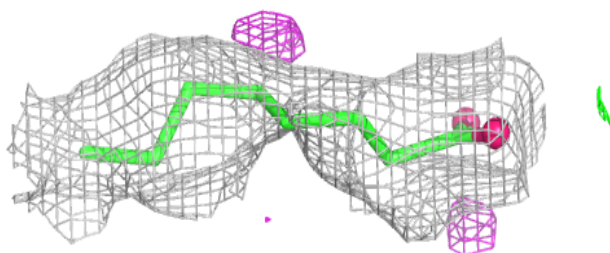
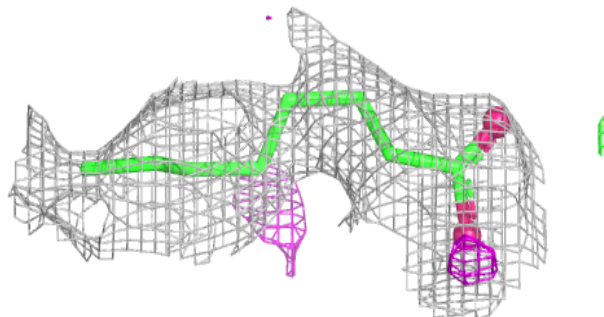
**Electron density around OLC A 805:**

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and green (positive)

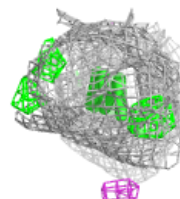
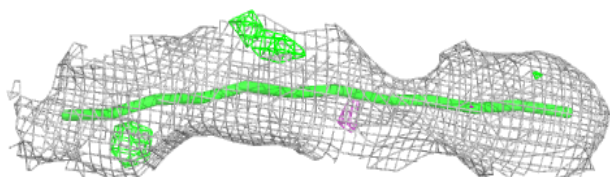
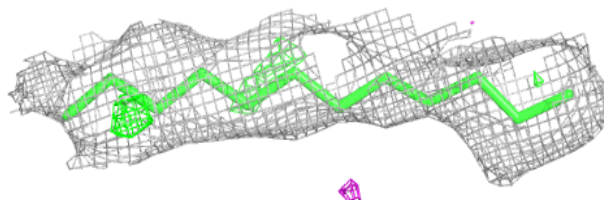


Electron density around OLC A 810:

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

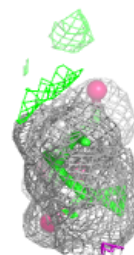
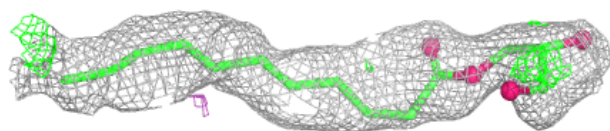
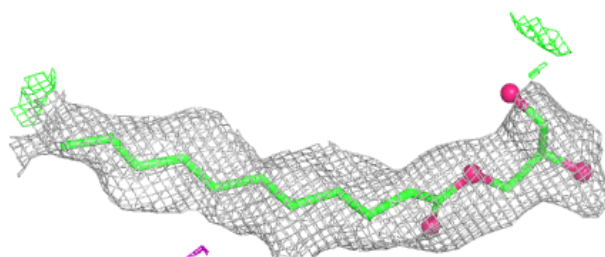
**Electron density around OLC A 808:**

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

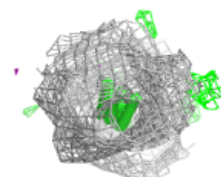
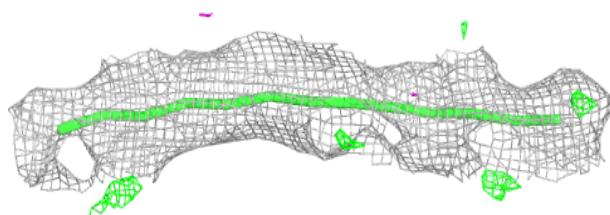
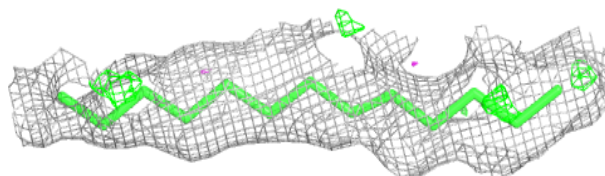


Electron density around OLC B 804:

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

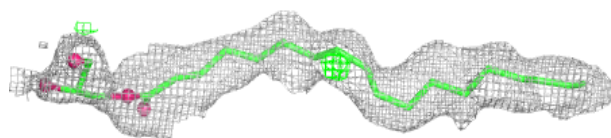
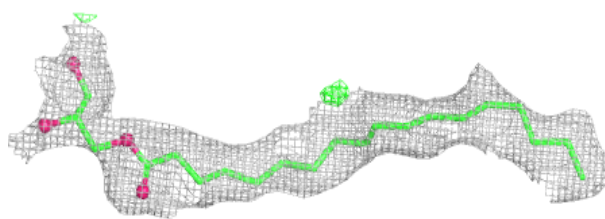
**Electron density around OLC A 814:**

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

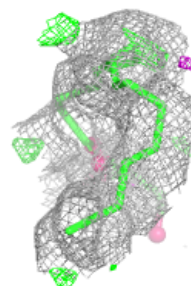
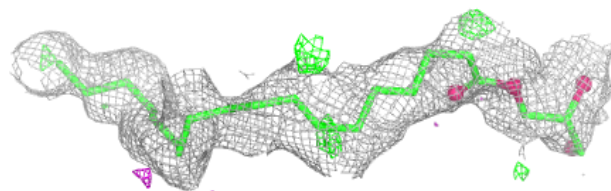
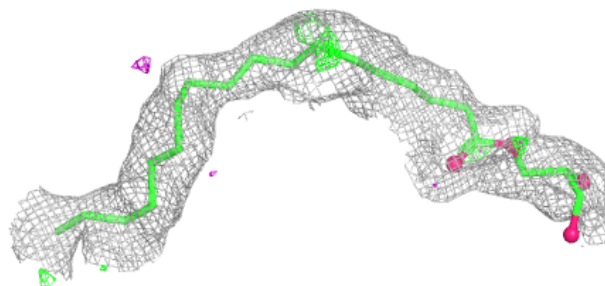


Electron density around OLC A 804:

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

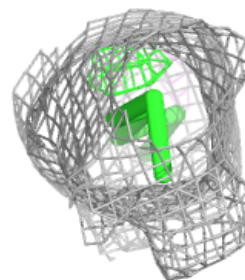
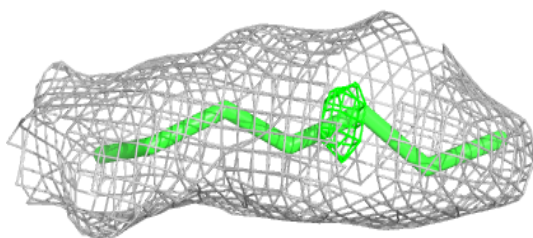
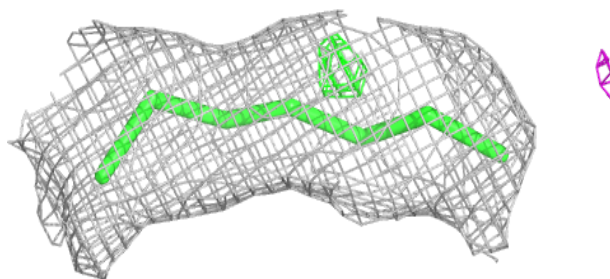
**Electron density around OLC A 813:**

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

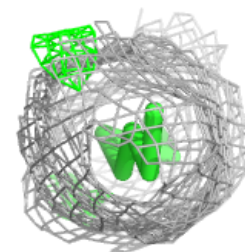
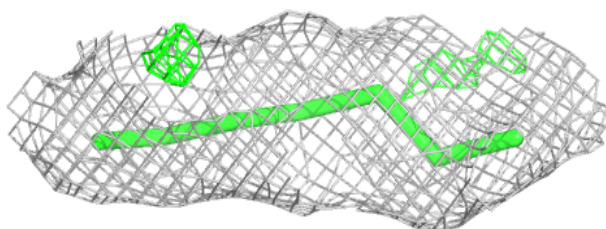
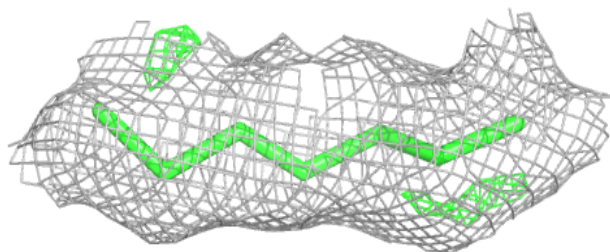


Electron density around OLC B 806:

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

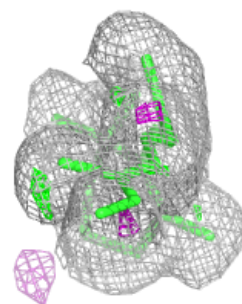
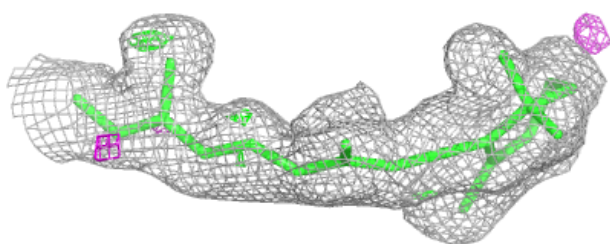
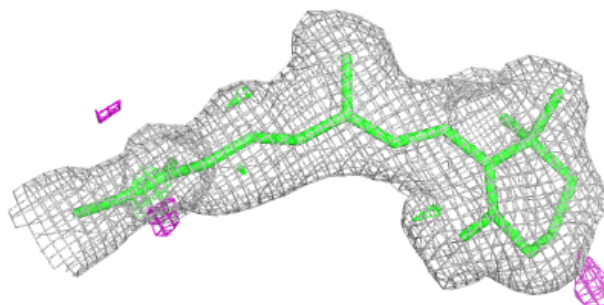
**Electron density around OLC A 806:**

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

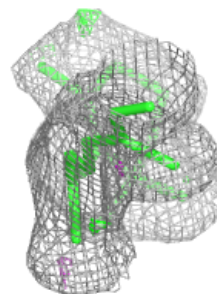
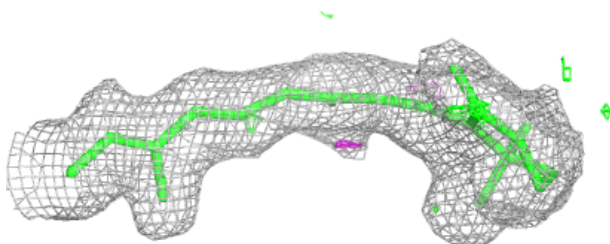
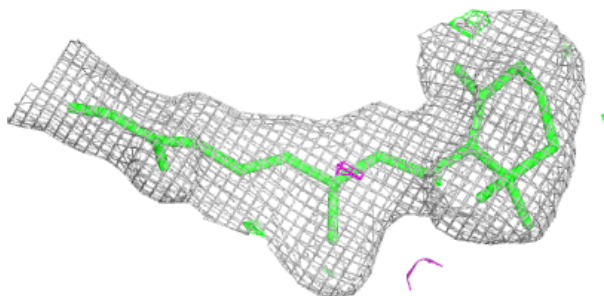


Electron density around RET A 801:

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

**Electron density around RET B 801:**

$2mF_o-DF_c$ (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.