



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 01:54 AM UTC

PDB ID : 8A6C / pdb_00008a6c

Title : 1 picosecond light activated crystal structure of bovine rhodopsin in Lipidic Cubic Phase

Authors : Gruhl, T.; Weinert, T.; Rodrigues, M.J.; Milne, C.J.; Ortolani, G.; Nass, K.; Nango, E.; Sen, S.; Johnson, P.J.M.; Cirelli, C.; Furrer, A.; Mous, S.; Skopintsev, P.; James, D.; Dworkowski, F.; Baath, P.; Kekilli, D.; Oserov, D.; Tanaka, R.; Glover, H.; Bacellar, C.; Bruenle, S.; Casadei, C.M.; Diethelm, A.D.; Gashi, D.; Gotthard, G.; Guixa-Gonzalez, R.; Joti, Y.; Kabanova, V.; Knopp, G.; Lesca, E.; Ma, P.; Martiel, I.; Muehle, J.; Owada, S.; Pamula, F.; Sarabi, D.; Tejero, O.; Tsai, C.J.; Varma, N.; Wach, A.; Boutet, S.; Tono, K.; Nogly, P.; Deupi, X.; Iwata, S.; Neutze, R.; Standfuss, J.; Schertler, G.F.X.; Panneels, V.

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

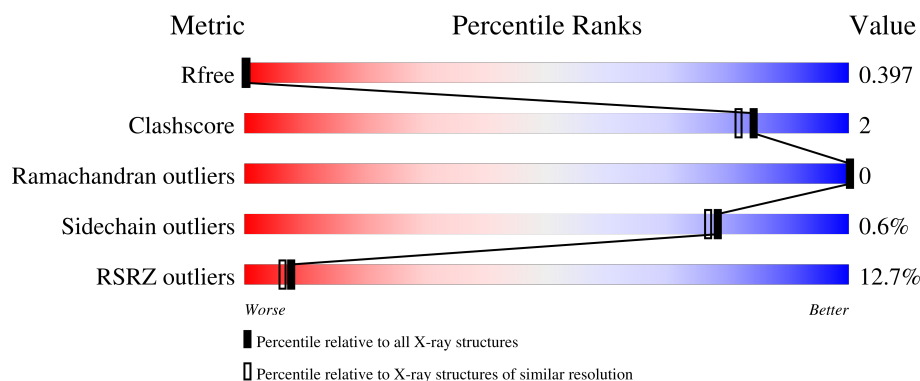
1 Overall quality at a glance

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	348	15% 85% • 13%
1	B	348	7% 82% 5% • 13%
2	C	2	100%
2	D	2	50% 50%

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 5490 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.

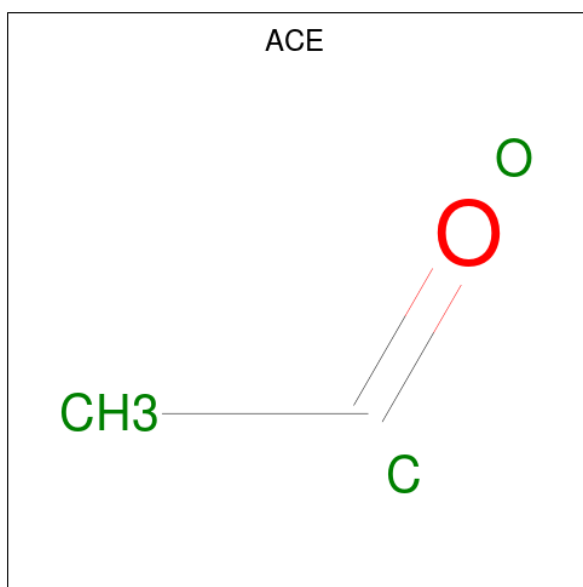
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	304	Total	C	N	O	S	0	11	0
			2490	1671	378	418	23			
1	B	304	Total	C	N	O	S	0	10	0
			2477	1664	373	416	24			

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



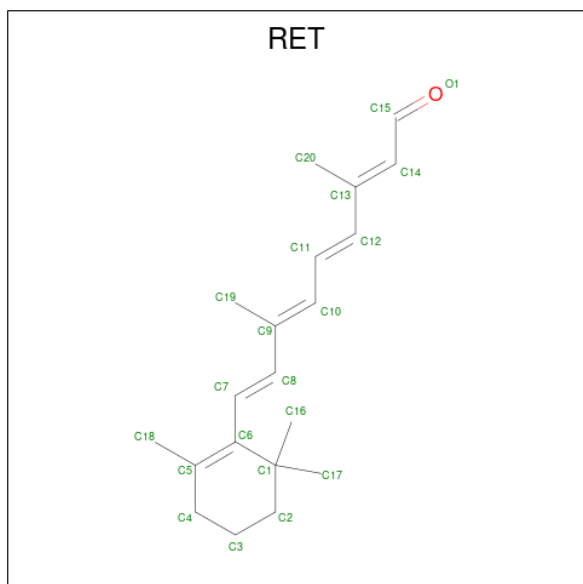
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is ACETYL GROUP (CCD ID: ACE) (formula: C₂H₄O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			3	2	1		
3	B	1	Total	C	O	0	0
			3	2	1		

- Molecule 4 is RETINAL (CCD ID: RET) (formula: $C_{20}H_{28}O$) (labeled as "Ligand of Interest" by depositor).



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

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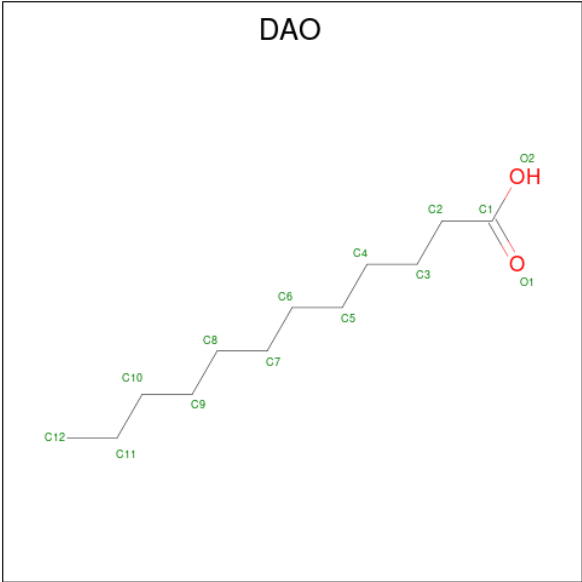
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C		0	0
			20	20			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



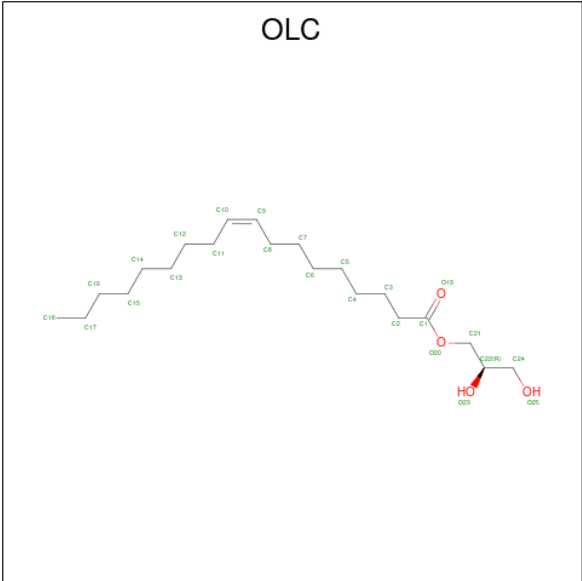
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is LAURIC ACID (CCD ID: DAO) (formula: $C_{12}H_{24}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			13	11	2		

- Molecule 7 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (CCD ID: OLC) (formula: $C_{21}H_{40}O_4$).



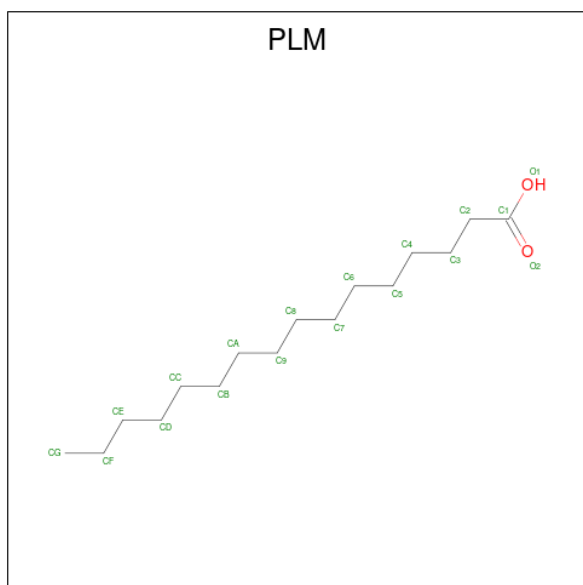
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			25	21	4		
7	A	1	Total	C	O	0	0
			17	15	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C 7 7	0	0
7	A	1	Total C 10 10	0	0
7	A	1	Total C 12 12	0	0
7	A	1	Total C O 10 8 2	0	0
7	A	1	Total C O 25 21 4	0	0
7	A	1	Total C 13 13	0	0
7	B	1	Total C O 19 17 2	0	0
7	B	1	Total C O 10 8 2	0	0
7	B	1	Total C O 18 14 4	0	0
7	B	1	Total C 17 17	0	0
7	B	1	Total C 7 7	0	0

- Molecule 8 is PALMITIC ACID (CCD ID: PLM) (formula: C₁₆H₃₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			12	11	1		
8	B	1	Total	C	O	0	0
			7	6	1		

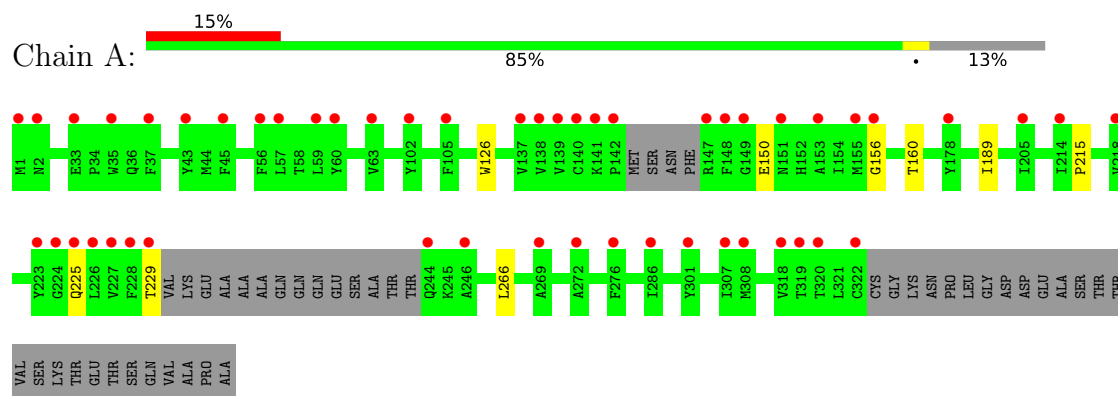
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	88	Total	O	0	0
			88	88		
9	B	83	Total	O	0	0
			83	83		

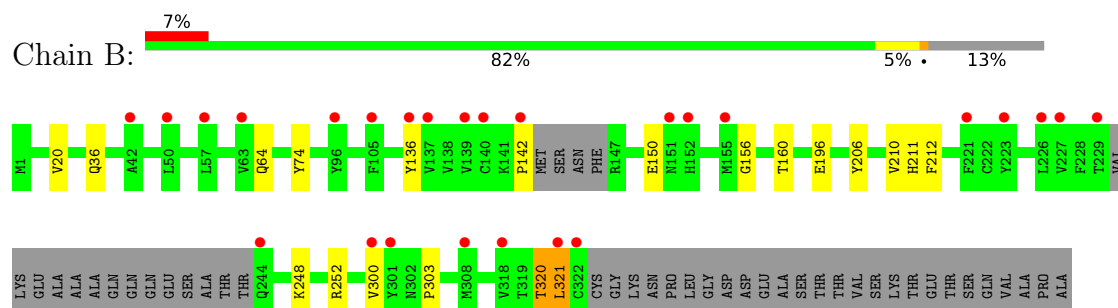
3 Residue-property plots

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.

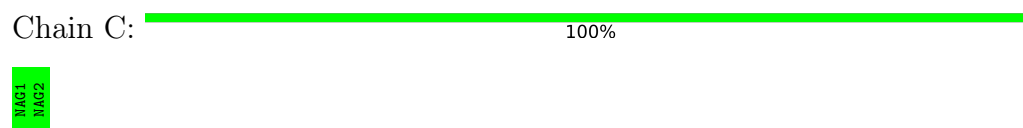
• Molecule 1: Rhodopsin



• 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	61.51Å 91.01Å 151.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	9.99 – 1.80 9.99 – 1.80	Depositor EDS
% Data completeness (in resolution range)	82.3 (9.99-1.80) 81.8 (9.99-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 1.80Å)	Xtriage
Refinement program	PHENIX 1.20_4459	Depositor
R, R_{free}	0.350 , 0.398 0.350 , 0.397	Depositor DCC
R_{free} test set	936 reflections (1.19%)	wwPDB-VP
Wilson B-factor (Å ²)	23.2	Xtriage
Anisotropy	0.441	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.49 , 95.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.58$, $\langle L^2 \rangle = 0.44$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5490	wwPDB-VP
Average B, all atoms (Å ²)	25.0	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 50.30 % 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 6.5949e-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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.17	0/2568	0.36	0/3507
1	B	0.17	0/2558	0.36	0/3493
All	All	0.17	0/5126	0.36	0/7000

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	2490	0	2453	5	0
1	B	2477	0	2436	16	0
2	C	28	0	25	0	0
2	D	28	0	25	1	0
3	A	3	0	3	0	0
3	B	3	0	3	0	0
4	A	20	0	27	1	0
4	B	20	0	27	2	0
5	A	14	0	13	0	0
5	B	14	0	13	0	0
6	A	13	0	18	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	119	0	176	2	0
7	B	71	0	100	2	0
8	A	12	0	18	0	0
8	B	7	0	8	0	0
9	A	88	0	0	0	0
9	B	83	0	0	0	0
All	All	5490	0	5345	25	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 2.

All (25) 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:74:TYR:OH	1:B:150:GLU:OE2	2.11	0.69
4:A:402:RET:H181	4:A:402:RET:H8	1.83	0.61
1:B:36:GLN:HE21	7:B:407:OLC:H4A	1.68	0.58
4:B:402:RET:H8	4:B:402:RET:H181	1.91	0.53
1:B:212:PHE:HE2	7:B:409:OLC:H11	1.75	0.51
1:A:156:GLY:O	1:A:160:THR:HG23	2.13	0.48
1:B:64:GLN:OE1	1:B:320:THR:OG1	2.28	0.46
1:B:248:LYS:HE3	1:B:252:ARG:CZ	2.46	0.46
1:B:206:TYR:CE1	1:B:210[B]:VAL:HG21	2.52	0.44
1:B:156:GLY:O	1:B:160:THR:HG23	2.17	0.44
1:B:248:LYS:HB3	1:B:248:LYS:HE2	1.77	0.43
1:B:206:TYR:O	1:B:210[B]:VAL:HG22	2.19	0.43
1:A:225:GLN:O	1:A:229:THR:HG23	2.17	0.43
1:B:20:VAL:HG12	2:D:1:NAG:H82	2.00	0.42
7:A:412:OLC:H2A	7:A:412:OLC:H21	1.74	0.42
1:B:321:LEU:HD12	1:B:321:LEU:HA	1.92	0.42
1:B:136:TYR:CZ	1:B:142:PRO:HG3	2.55	0.41
4:B:402:RET:H181	4:B:402:RET:C8	2.49	0.41
1:A:266:LEU:HD12	7:A:405:OLC:H16A	2.02	0.41
1:B:210[B]:VAL:HG23	1:B:211:HIS:CD2	2.55	0.41
1:B:136:TYR:CE2	1:B:142:PRO:HG3	2.55	0.41
1:A:189:ILE:HD13	1:A:189:ILE:HA	1.93	0.40
1:A:126:TRP:CH2	1:A:215:PRO:HG3	2.56	0.40
1:B:196:GLU:OE1	1:B:196:GLU:N	2.49	0.40
1:B:300:VAL:O	1:B:303:PRO:HD2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	309/348 (89%)	297 (96%)	12 (4%)	0	100	100
1	B	308/348 (88%)	298 (97%)	10 (3%)	0	100	100
All	All	617/696 (89%)	595 (96%)	22 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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%)	264 (100%)	1 (0%)	84	83
1	B	263/296 (89%)	261 (99%)	2 (1%)	73	70
All	All	528/592 (89%)	525 (99%)	3 (1%)	78	77

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

Mol	Chain	Res	Type
1	A	150	GLU
1	B	320	THR
1	B	321	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	HIS
1	B	302	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	0.45	0	17,19,21	0.50	0
2	NAG	C	2	2	14,14,15	0.28	0	17,19,21	0.47	0
2	NAG	D	1	1,2	14,14,15	0.50	0	17,19,21	0.47	0
2	NAG	D	2	2	14,14,15	0.26	0	17,19,21	0.48	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.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

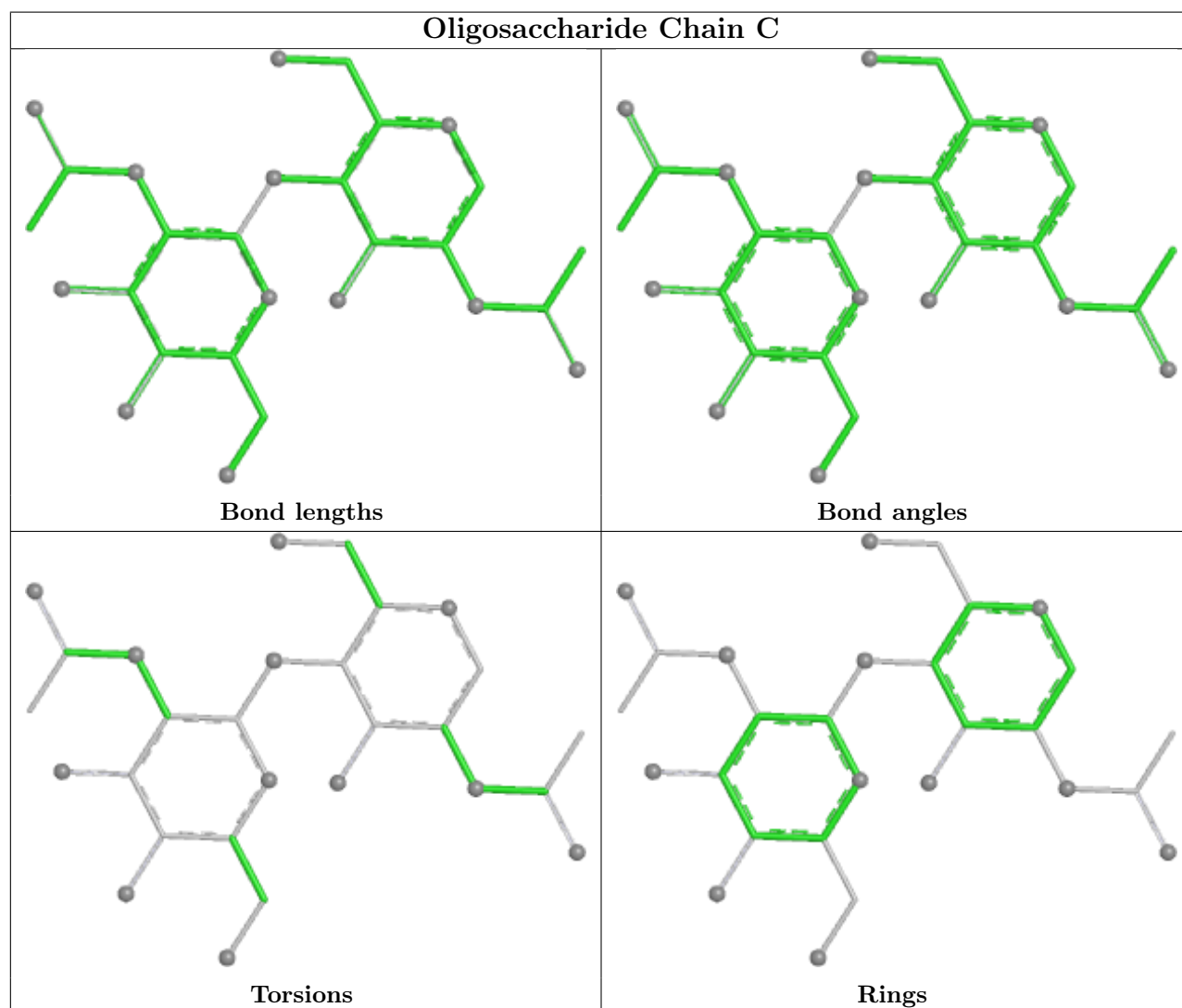
Mol	Chain	Res	Type	Atoms
2	D	2	NAG	C4-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6

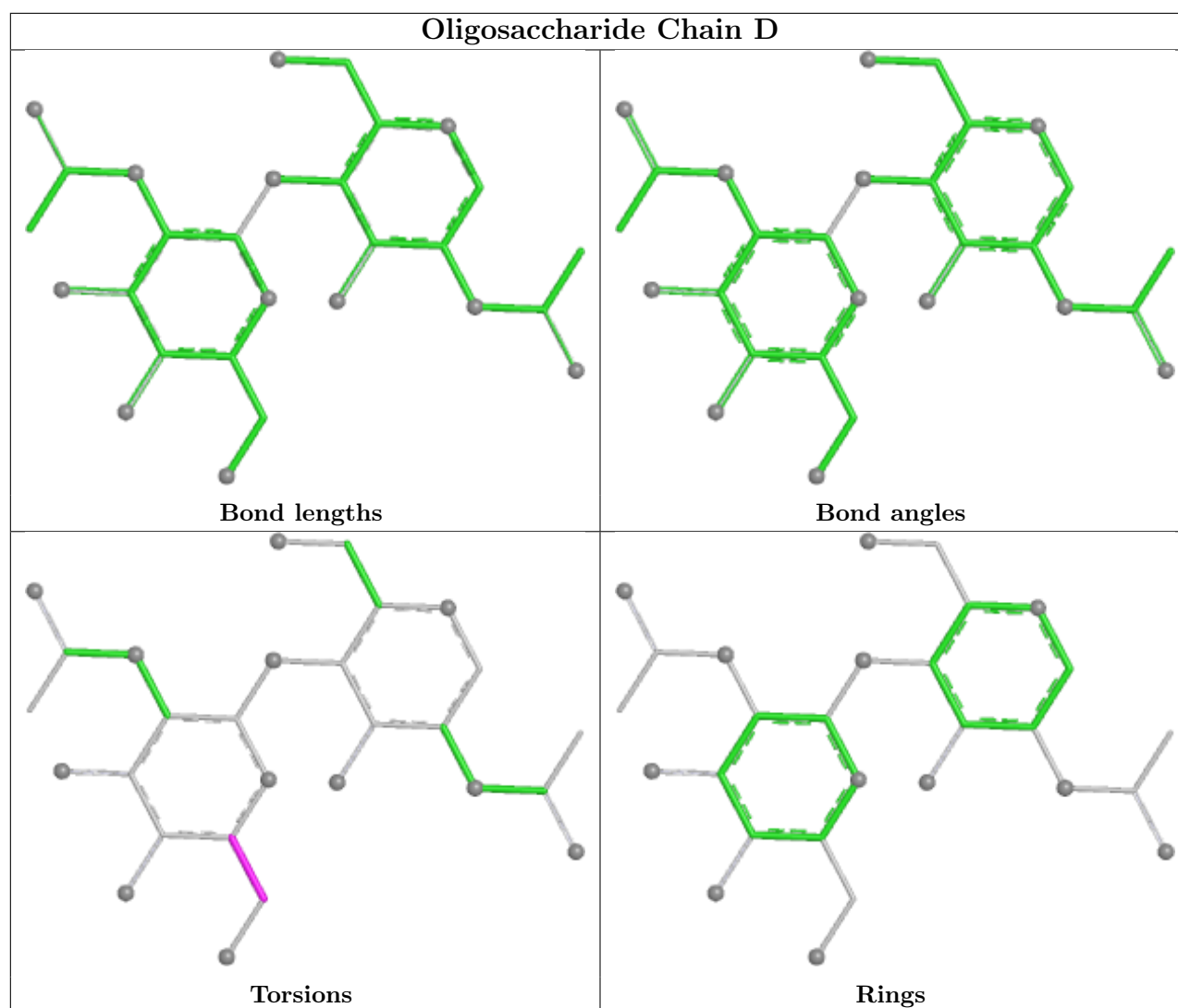
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1	NAG	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 oligosaccharide.





5.6 Ligand geometry [i](#)

22 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	$\# Z > 2$
8	PLM	B	408	1	5,6,17	0.67	0	4,5,17	0.61	0
8	PLM	A	410	1	10,11,17	0.54	0	9,10,17	0.41	0
7	OLC	A	405	-	24,24,24	0.27	0	25,25,25	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	A	403	1	14,14,15	0.25	0	17,19,21	0.55	0
7	OLC	A	407	-	6,6,24	0.17	0	5,5,25	0.16	0
7	OLC	B	405	-	9,9,24	1.53	2 (22%)	9,9,25	1.70	2 (22%)
7	OLC	A	413	-	12,12,24	0.24	0	11,11,25	0.09	0
3	ACE	A	401	1	1,2,2	0.82	0	0,1,1	-	-
7	OLC	B	404	-	18,18,24	0.33	0	18,18,25	0.21	0
3	ACE	B	401	1	1,2,2	0.78	0	0,1,1	-	-
7	OLC	B	409	-	6,6,24	0.18	0	5,5,25	0.13	0
7	OLC	A	411	-	9,9,24	1.56	2 (22%)	9,9,25	1.65	2 (22%)
7	OLC	A	409	-	11,11,24	0.22	0	10,10,25	0.15	0
7	OLC	B	406	-	17,17,24	0.27	0	18,18,25	0.34	0
7	OLC	A	408	-	9,9,24	0.26	0	8,8,25	0.22	0
7	OLC	A	412	-	24,24,24	0.24	0	25,25,25	0.26	0
5	NAG	B	403	1	14,14,15	0.29	0	17,19,21	0.56	0
4	RET	B	402	1	20,20,21	2.57	5 (25%)	27,27,28	1.18	2 (7%)
7	OLC	B	407	-	16,16,24	0.21	0	15,15,25	0.14	0
4	RET	A	402	1	20,20,21	2.45	5 (25%)	27,27,28	1.12	2 (7%)
7	OLC	A	406	-	16,16,24	0.34	0	16,16,25	0.28	0
6	DAO	A	404	-	12,12,13	0.74	0	12,12,13	0.64	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	PLM	B	408	1	-	0/4/4/15	-
8	PLM	A	410	1	-	1/9/9/15	-
7	OLC	A	405	-	-	5/24/24/24	-
5	NAG	A	403	1	-	0/6/23/26	0/1/1/1
7	OLC	A	407	-	-	0/4/4/24	-
7	OLC	B	405	-	-	2/7/7/24	-
7	OLC	A	413	-	-	2/10/10/24	-
7	OLC	B	404	-	-	5/17/17/24	-
7	OLC	B	409	-	-	1/4/4/24	-
7	OLC	A	411	-	-	2/7/7/24	-
7	OLC	A	409	-	-	2/9/9/24	-
7	OLC	B	406	-	-	4/17/17/24	-
7	OLC	A	408	-	-	1/7/7/24	-
7	OLC	A	412	-	-	7/24/24/24	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	B	403	1	-	0/6/23/26	0/1/1/1
4	RET	B	402	1	-	5/13/30/31	0/1/1/1
7	OLC	B	407	-	-	2/14/14/24	-
4	RET	A	402	1	-	5/13/30/31	0/1/1/1
7	OLC	A	406	-	-	4/14/14/24	-
6	DAO	A	404	-	-	5/10/10/11	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	402	RET	C14-C13	9.74	1.40	1.33
4	A	402	RET	C14-C13	9.08	1.39	1.33
7	A	411	OLC	O19-C1	3.49	1.33	1.22
7	B	405	OLC	O19-C1	3.39	1.33	1.22
7	A	411	OLC	O20-C1	-3.07	1.20	1.30
7	B	405	OLC	O20-C1	-3.02	1.20	1.30
4	B	402	RET	C8-C9	-2.84	1.39	1.46
4	A	402	RET	C8-C9	-2.83	1.39	1.46
4	A	402	RET	C15-C14	-2.69	1.39	1.49
4	B	402	RET	C15-C14	-2.62	1.39	1.49
4	B	402	RET	C10-C9	2.34	1.41	1.35
4	A	402	RET	C12-C13	-2.20	1.41	1.46
4	B	402	RET	C12-C13	-2.20	1.41	1.46
4	A	402	RET	C10-C9	2.18	1.40	1.35

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	405	OLC	O19-C1-C2	-3.65	111.52	123.09
7	A	411	OLC	O19-C1-C2	-3.53	111.88	123.09
7	B	405	OLC	O20-C1-C2	3.53	125.16	114.00
7	A	411	OLC	O20-C1-C2	3.44	124.86	114.00
4	B	402	RET	C19-C9-C10	-3.26	117.53	122.82
4	A	402	RET	C19-C9-C10	-3.21	117.61	122.82
4	B	402	RET	C19-C9-C8	2.66	122.16	118.09
4	A	402	RET	C19-C9-C8	2.35	121.68	118.09

There are no chirality outliers.

All (53) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	402	RET	C11-C10-C9-C8
4	A	402	RET	C11-C10-C9-C19
4	B	402	RET	C11-C10-C9-C8
4	B	402	RET	C11-C10-C9-C19
7	B	404	OLC	C2-C1-O20-C21
7	B	404	OLC	O19-C1-O20-C21
7	A	412	OLC	O19-C1-O20-C21
7	A	412	OLC	C2-C1-O20-C21
7	A	412	OLC	O20-C21-C22-O23
4	A	402	RET	C5-C6-C7-C8
4	B	402	RET	C5-C6-C7-C8
7	A	405	OLC	C2-C1-O20-C21
7	A	405	OLC	O19-C1-O20-C21
7	A	412	OLC	O20-C21-C22-C24
6	A	404	DAO	C2-C3-C4-C5
8	A	410	PLM	C6-C7-C8-C9
4	A	402	RET	C1-C6-C7-C8
4	B	402	RET	C1-C6-C7-C8
7	A	412	OLC	C3-C4-C5-C6
7	B	406	OLC	O20-C21-C22-O23
4	A	402	RET	C6-C7-C8-C9
7	B	404	OLC	C3-C4-C5-C6
7	A	408	OLC	C9-C10-C11-C12
7	B	404	OLC	C6-C7-C8-C9
7	B	406	OLC	O20-C21-C22-C24
7	A	405	OLC	C9-C10-C11-C12
7	A	406	OLC	C9-C10-C11-C12
7	A	413	OLC	C7-C8-C9-C10
7	B	404	OLC	C9-C10-C11-C12
7	B	409	OLC	C9-C10-C11-C12
7	A	406	OLC	C7-C8-C9-C10
7	B	406	OLC	O19-C1-O20-C21
7	A	405	OLC	C2-C3-C4-C5
7	B	406	OLC	C2-C1-O20-C21
6	A	404	DAO	O2-C1-C2-C3
7	A	413	OLC	C9-C10-C11-C12
7	A	406	OLC	O20-C1-C2-C3
7	A	409	OLC	C9-C10-C11-C12
7	A	409	OLC	C7-C8-C9-C10
6	A	404	DAO	O1-C1-C2-C3
7	A	406	OLC	O19-C1-C2-C3
7	B	405	OLC	O20-C1-C2-C3
7	A	412	OLC	C7-C8-C9-C10

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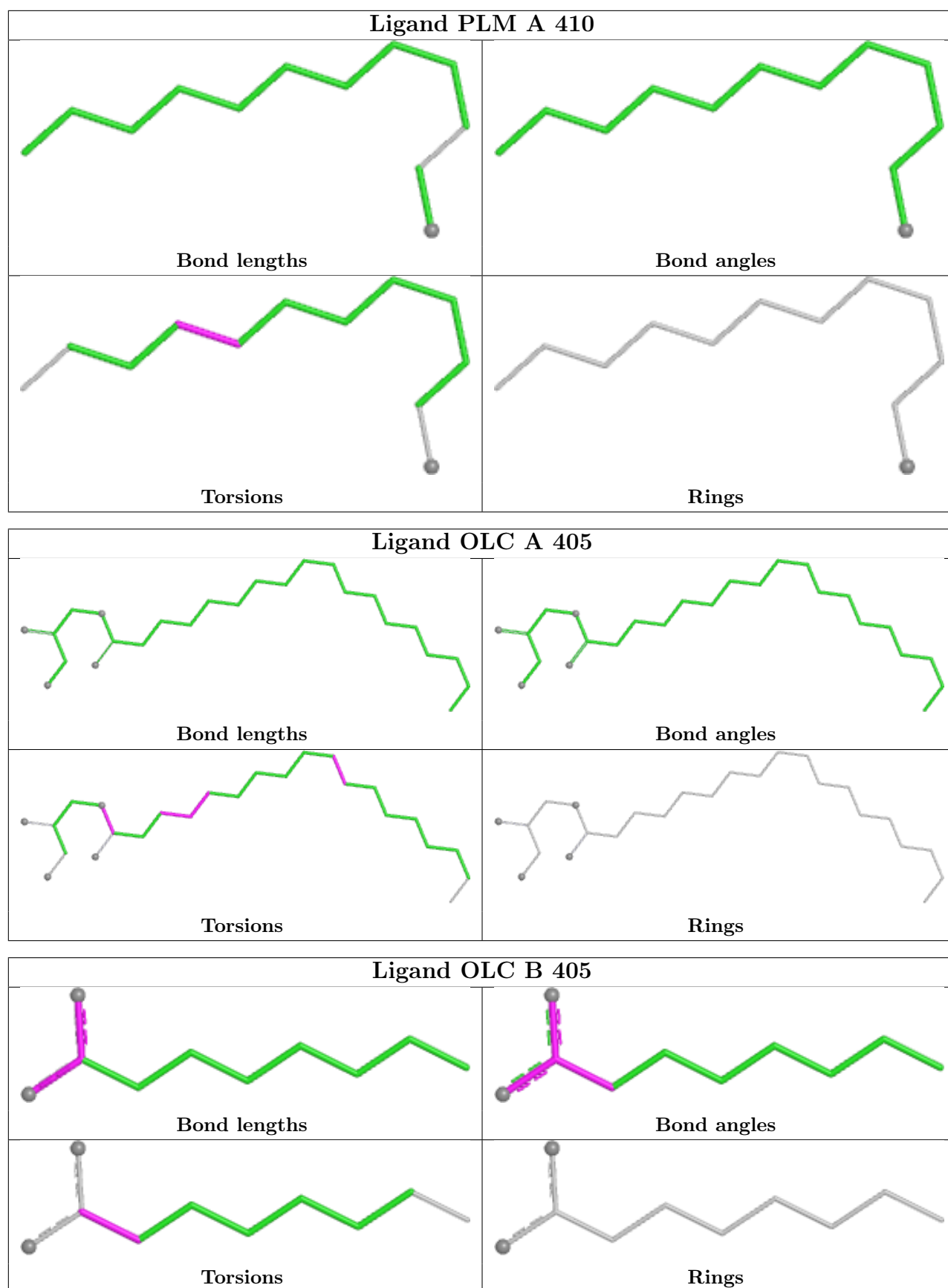
Mol	Chain	Res	Type	Atoms
7	B	407	OLC	C7-C8-C9-C10
7	A	411	OLC	O19-C1-C2-C3
7	A	411	OLC	O20-C1-C2-C3
4	B	402	RET	C10-C11-C12-C13
7	B	405	OLC	O19-C1-C2-C3
7	A	412	OLC	C5-C6-C7-C8
6	A	404	DAO	C11-C10-C9-C8
7	B	407	OLC	C5-C6-C7-C8
7	A	405	OLC	C3-C4-C5-C6
6	A	404	DAO	C3-C4-C5-C6

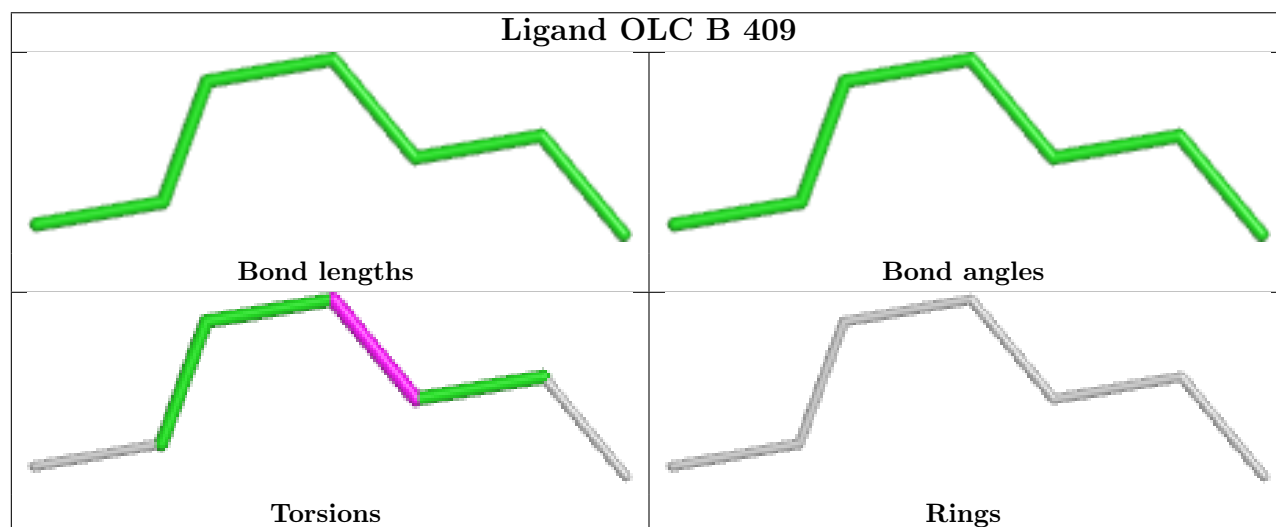
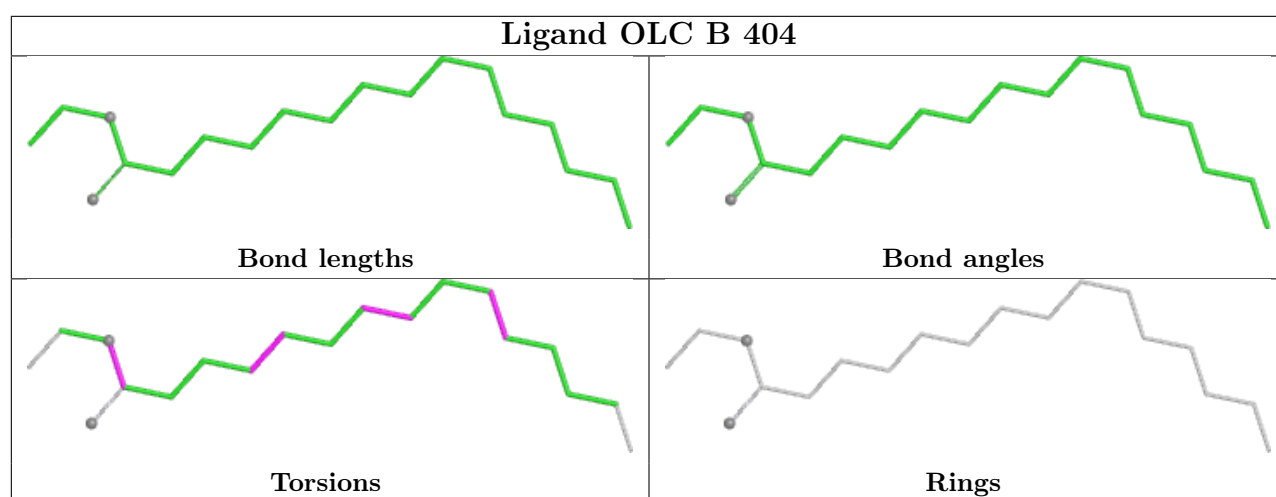
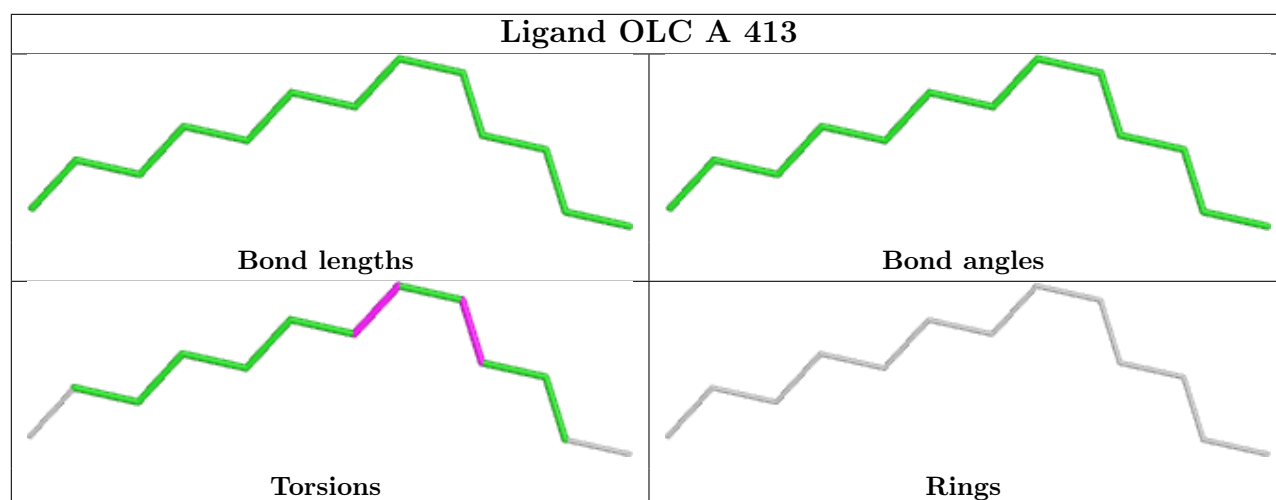
There are no ring outliers.

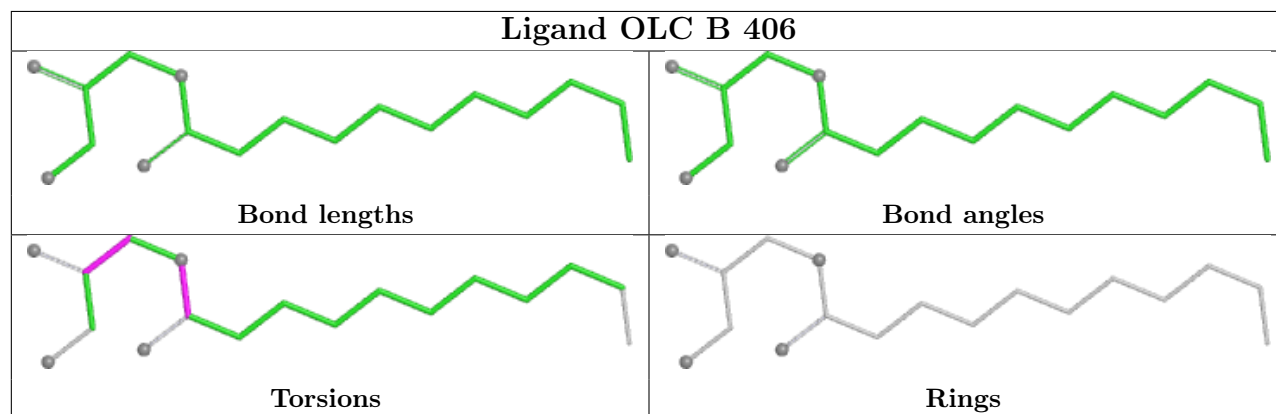
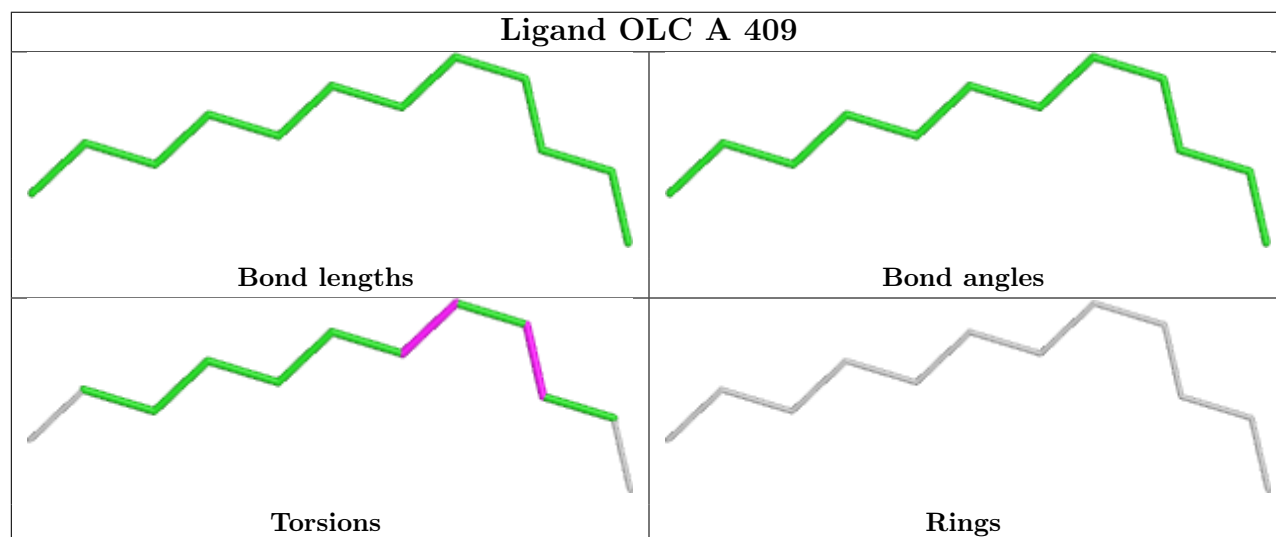
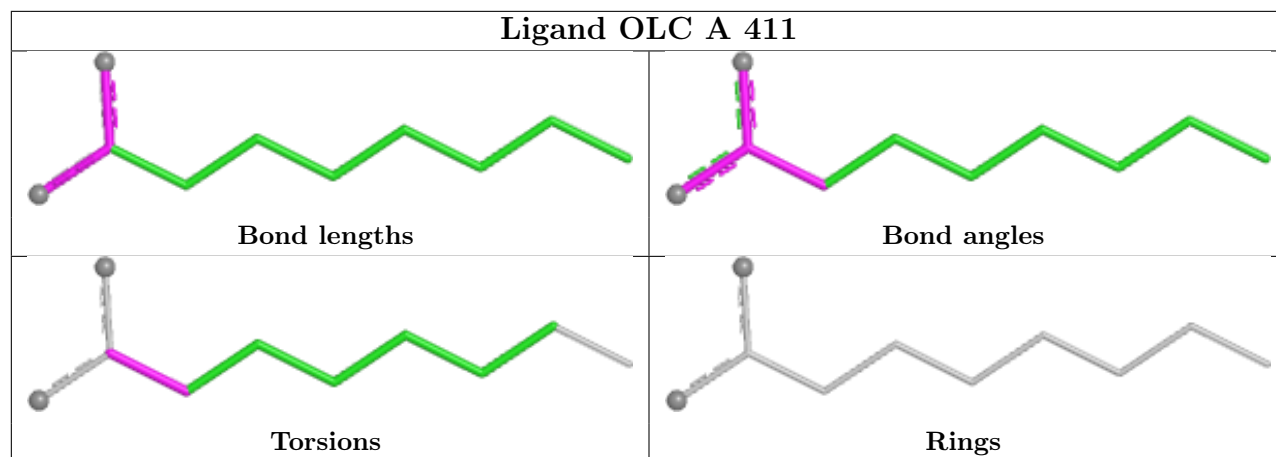
6 monomers are involved in 7 short contacts:

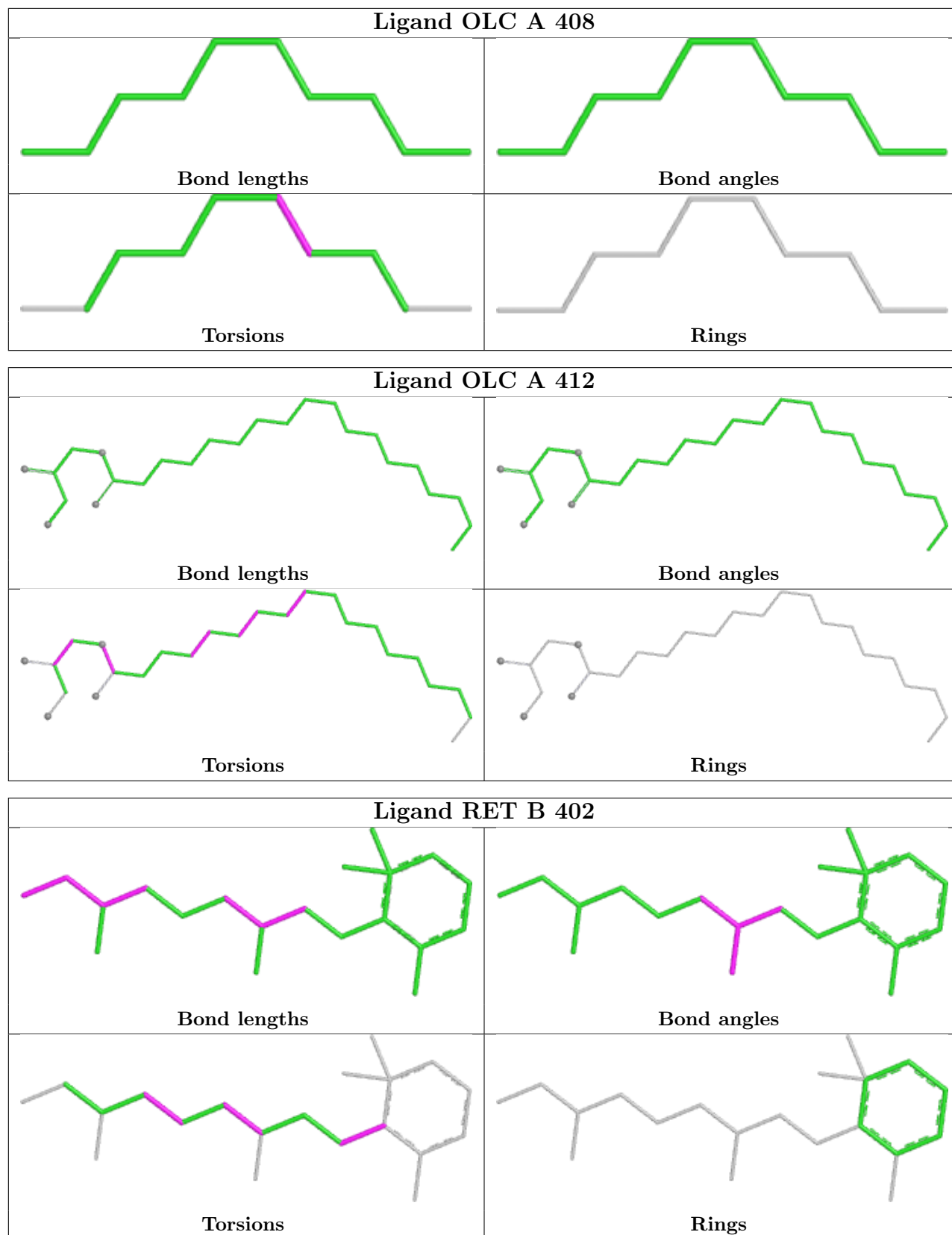
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	405	OLC	1	0
7	B	409	OLC	1	0
7	A	412	OLC	1	0
4	B	402	RET	2	0
7	B	407	OLC	1	0
4	A	402	RET	1	0

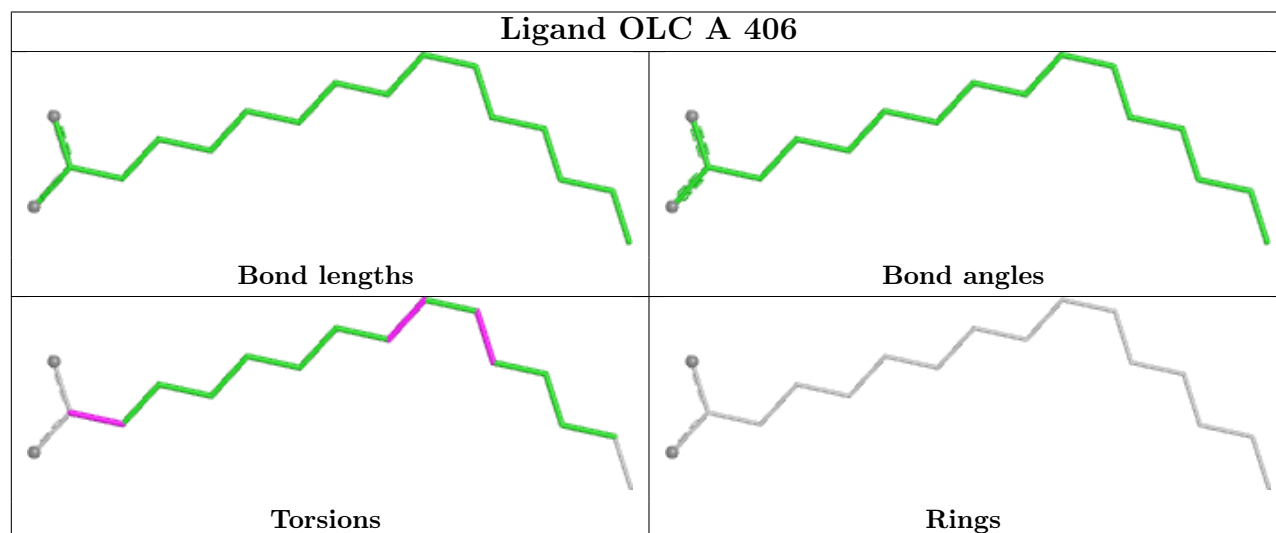
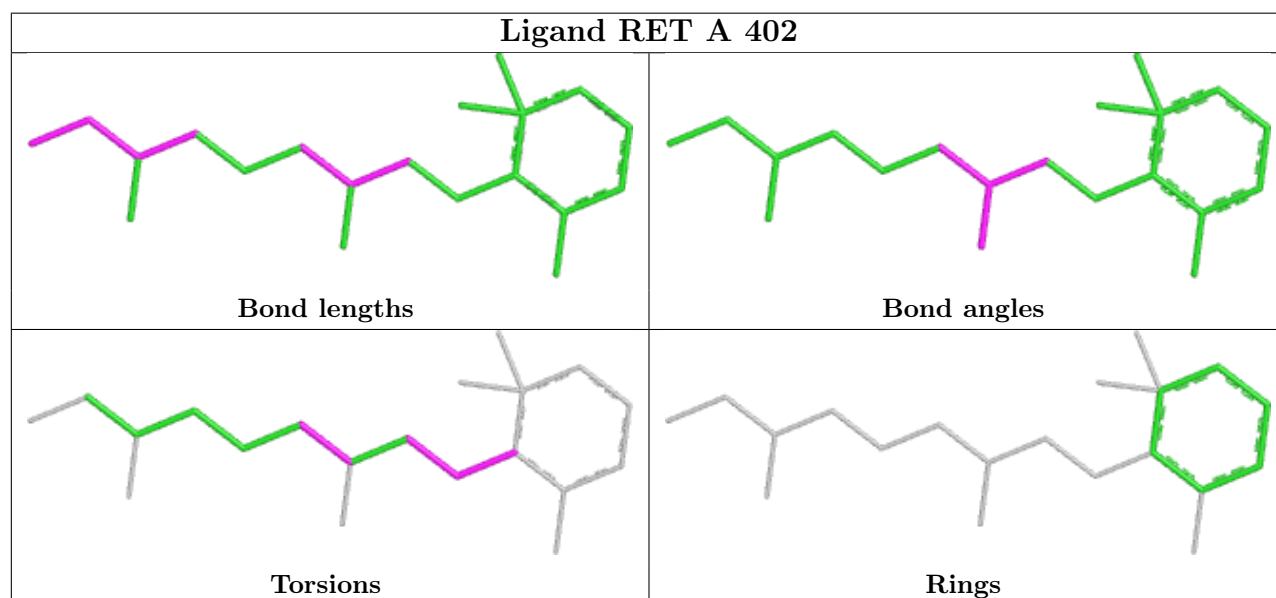
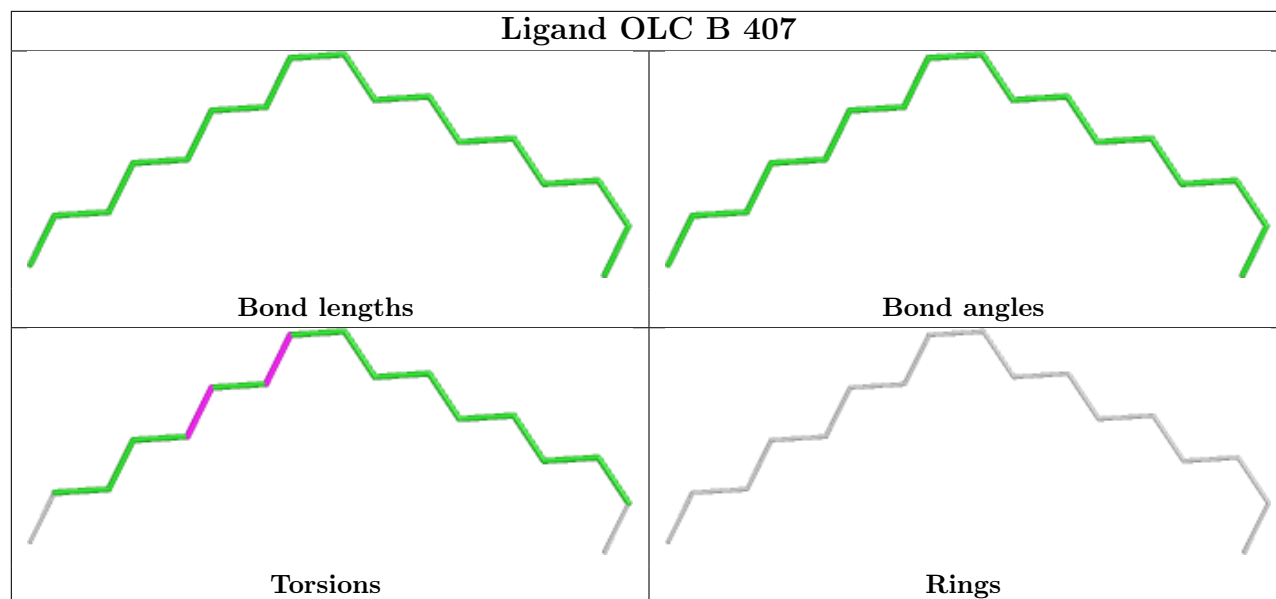
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	304/348 (87%)	1.06	51 (16%) 4 3	10, 23, 37, 60	11 (3%)
1	B	304/348 (87%)	0.89	26 (8%) 16 14	10, 23, 35, 63	10 (3%)
All	All	608/696 (87%)	0.97	77 (12%) 8 6	10, 23, 36, 63	21 (3%)

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	229	THR	7.4
1	A	205[A]	ILE	5.7
1	A	1	MET	5.6
1	A	228	PHE	5.0
1	A	229	THR	4.5
1	B	318	VAL	4.4
1	B	151	ASN	4.0
1	A	319	THR	3.9
1	A	218	VAL	3.9
1	A	139	VAL	3.6
1	A	140	CYS	3.5
1	A	320	THR	3.4
1	B	322	CYS	3.4
1	B	227	VAL	3.4
1	A	148	PHE	3.3
1	A	269	ALA	3.3
1	A	45	PHE	3.2
1	A	322	CYS	3.2
1	B	57[A]	LEU	3.2
1	A	57[A]	LEU	3.0
1	B	226	LEU	3.0
1	B	63	VAL	2.9
1	A	246	ALA	2.9
1	A	141	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	214[A]	ILE	2.9
1	B	308[A]	MET	2.8
1	B	137	VAL	2.8
1	A	2	ASN	2.8
1	A	244	GLN	2.8
1	A	102	TYR	2.7
1	A	156	GLY	2.7
1	A	142	PRO	2.7
1	B	155	MET	2.7
1	A	147	ARG	2.6
1	A	151	ASN	2.6
1	A	137	VAL	2.6
1	B	244	GLN	2.6
1	B	321	LEU	2.6
1	A	105	PHE	2.5
1	A	272	ALA	2.5
1	A	308	MET	2.5
1	B	300	VAL	2.5
1	A	155	MET	2.4
1	B	105	PHE	2.4
1	A	59	LEU	2.3
1	B	50	LEU	2.3
1	A	60	TYR	2.3
1	B	223	TYR	2.3
1	A	149	GLY	2.3
1	A	224	GLY	2.3
1	A	63	VAL	2.3
1	A	56	PHE	2.3
1	A	318	VAL	2.3
1	B	139	VAL	2.3
1	A	33	GLU	2.2
1	A	178	TYR	2.2
1	A	276	PHE	2.2
1	A	37	PHE	2.2
1	B	42	ALA	2.2
1	A	301	TYR	2.2
1	A	226	LEU	2.2
1	A	43	TYR	2.1
1	A	307	ILE	2.1
1	A	35	TRP	2.1
1	A	227	VAL	2.1
1	B	142	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	225	GLN	2.1
1	B	221	PHE	2.1
1	B	140	CYS	2.1
1	A	286	ILE	2.1
1	B	152	HIS	2.1
1	B	136	TYR	2.0
1	B	301	TYR	2.0
1	A	138	VAL	2.0
1	A	153	ALA	2.0
1	A	223	TYR	2.0
1	B	96	TYR	2.0

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

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

6.3 Carbohydrates [i](#)

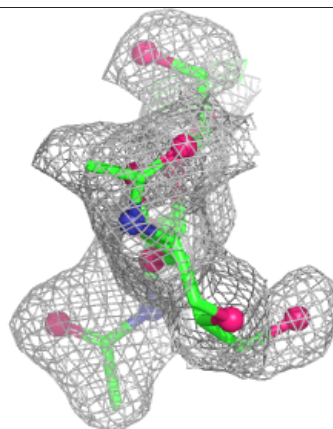
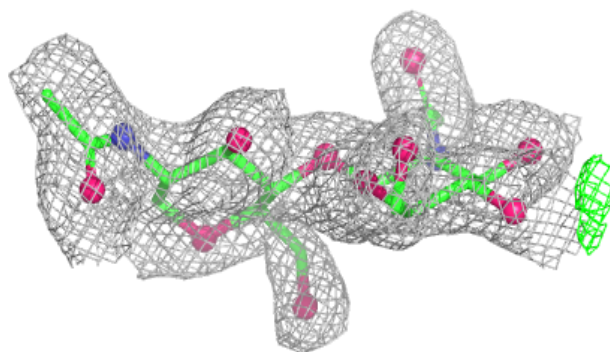
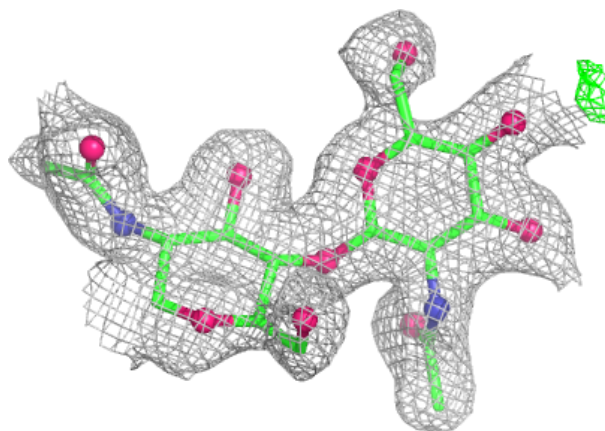
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

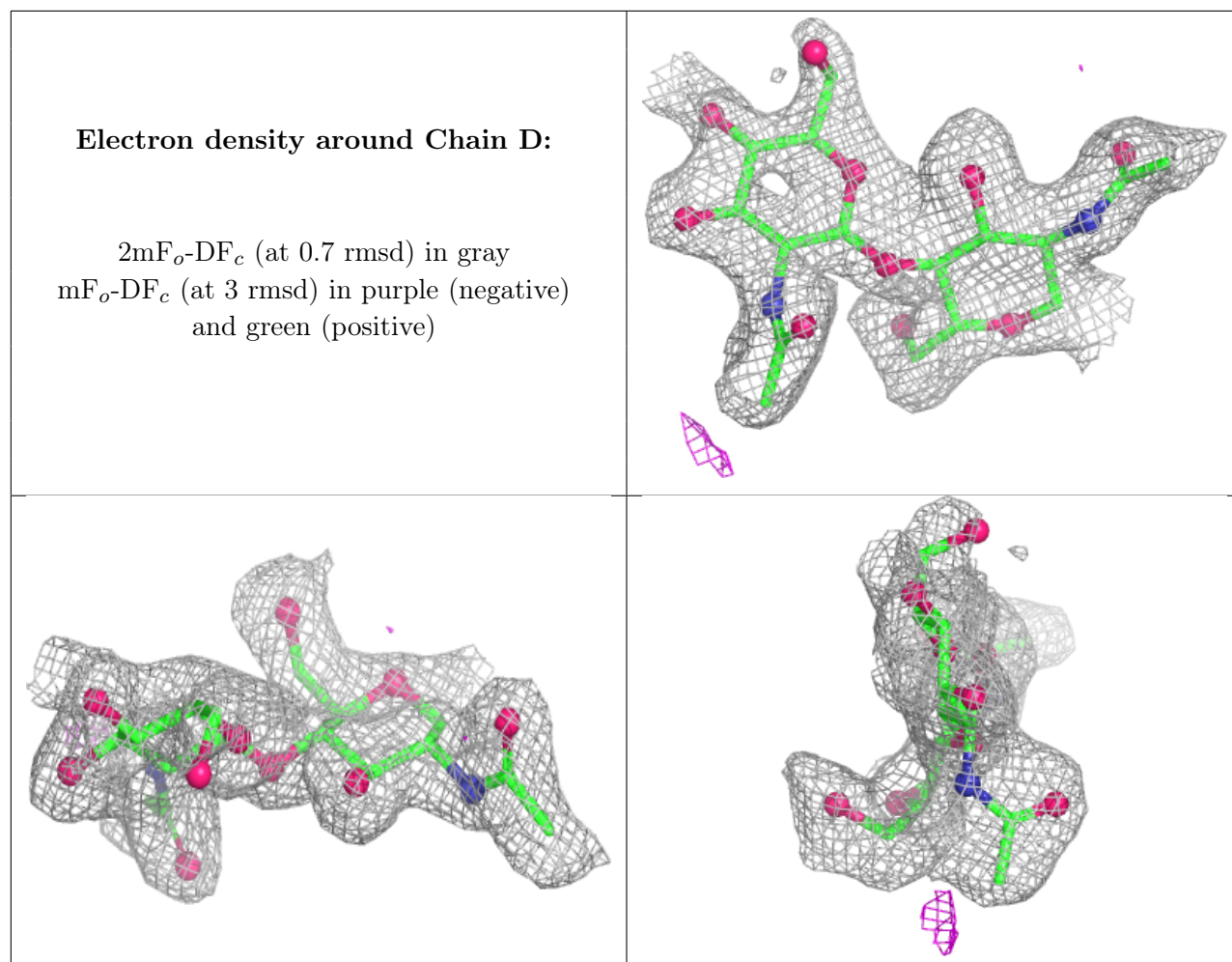
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	D	2	14/15	0.71	0.14	40,45,54,57	0
2	NAG	D	1	14/15	0.78	0.12	28,32,36,36	0
2	NAG	C	2	14/15	0.84	0.11	28,32,38,43	0
2	NAG	C	1	14/15	0.87	0.10	24,26,30,33	0

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.

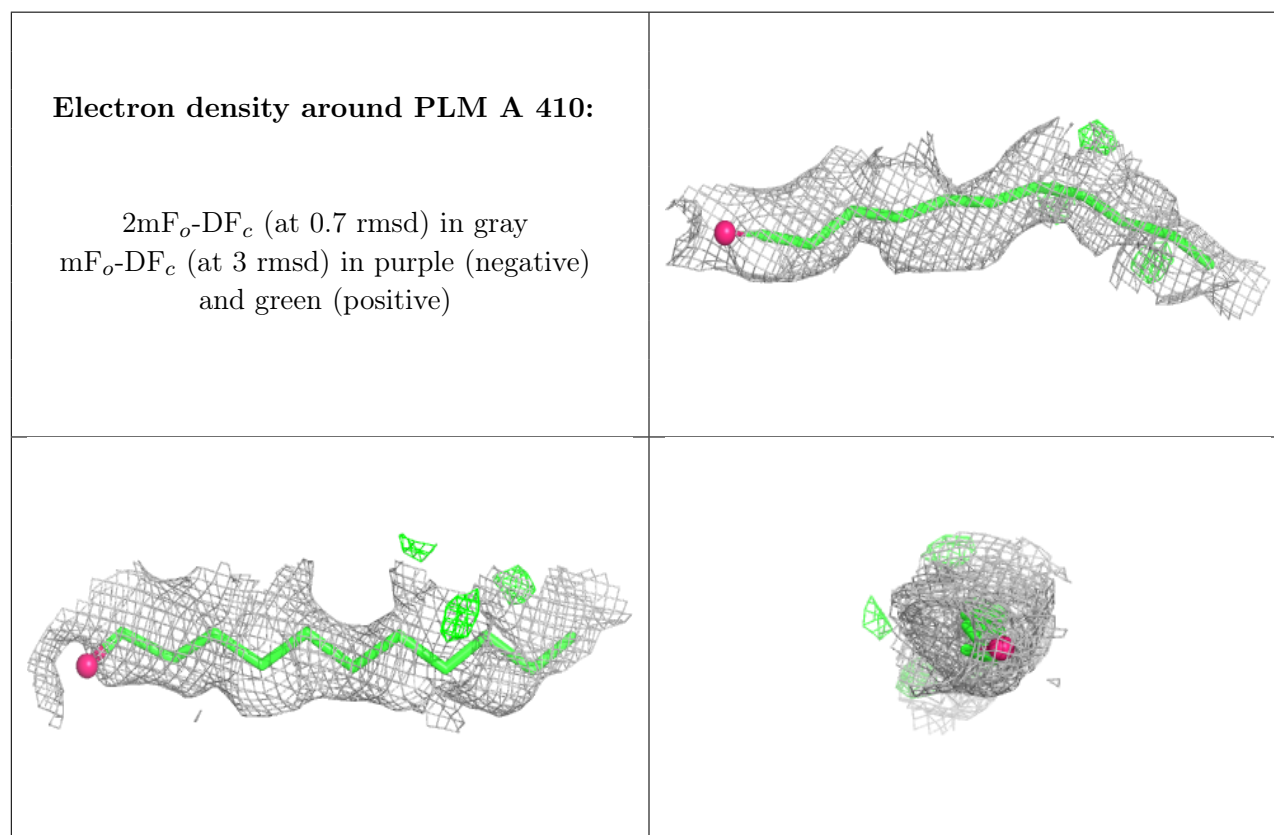
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	PLM	A	410	12/18	0.45	0.20	49,55,60,63	0
7	OLC	B	409	7/25	0.48	0.22	57,61,64,67	0
7	OLC	A	411	10/25	0.52	0.21	42,46,53,57	0
3	ACE	A	401	3/3	0.53	0.25	44,44,44,45	0
8	PLM	B	408	7/18	0.56	0.16	47,49,54,54	0
7	OLC	B	404	19/25	0.60	0.20	39,44,56,57	0
7	OLC	B	405	10/25	0.61	0.18	36,40,46,50	0
7	OLC	A	406	17/25	0.62	0.18	48,51,70,74	0
7	OLC	A	405	25/25	0.62	0.16	40,46,50,52	0
7	OLC	B	407	17/25	0.62	0.17	38,42,57,60	0

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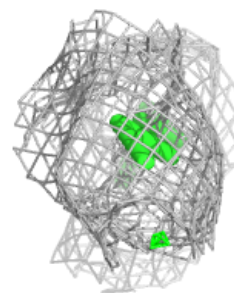
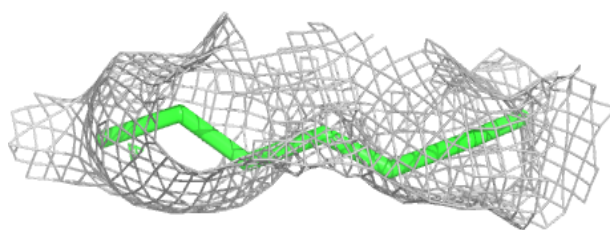
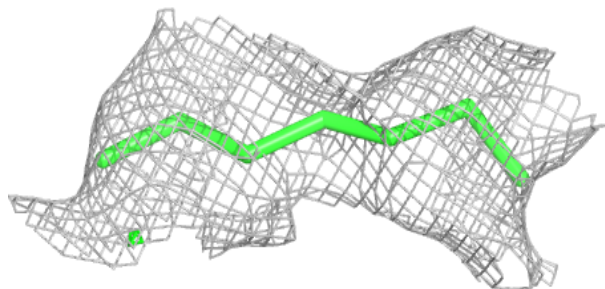
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	OLC	A	412	25/25	0.63	0.17	40,45,50,54	0
7	OLC	A	408	10/25	0.66	0.17	37,42,45,46	0
7	OLC	B	406	18/25	0.66	0.18	36,41,52,52	0
5	NAG	A	403	14/15	0.66	0.16	35,45,49,51	0
6	DAO	A	404	13/14	0.72	0.15	28,35,41,42	0
7	OLC	A	409	12/25	0.74	0.12	18,30,39,41	0
7	OLC	A	413	13/25	0.75	0.12	30,33,39,39	0
4	RET	A	402	20/21	0.80	0.11	17,23,25,32	0
3	ACE	B	401	3/3	0.81	0.13	29,29,30,36	0
5	NAG	B	403	14/15	0.82	0.11	28,34,39,40	0
7	OLC	A	407	7/25	0.82	0.10	23,25,29,33	0
4	RET	B	402	20/21	0.83	0.09	19,24,29,31	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.

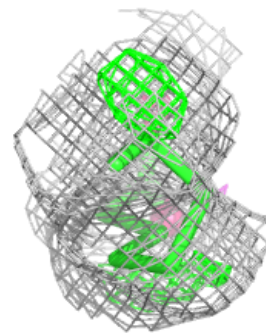
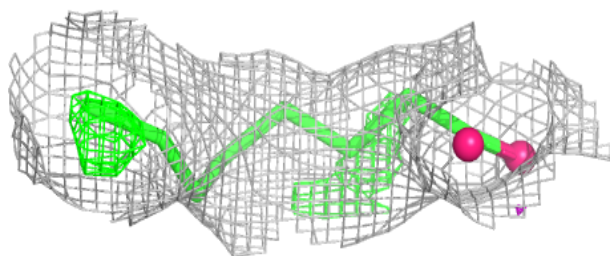
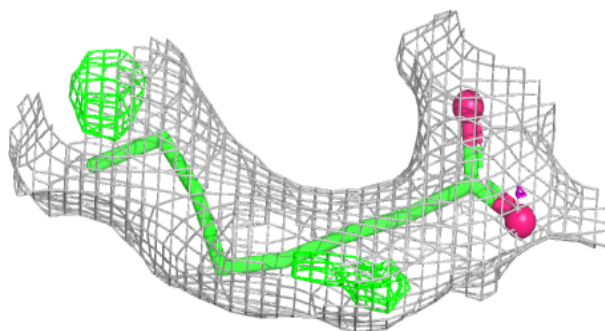


Electron density around OLC B 409:

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

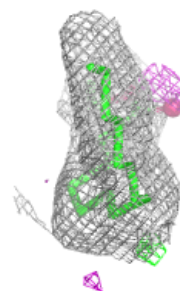
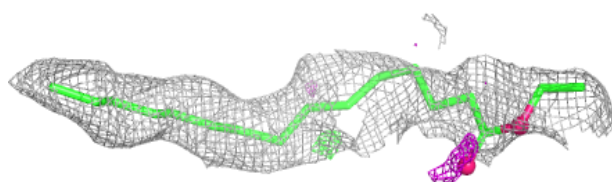
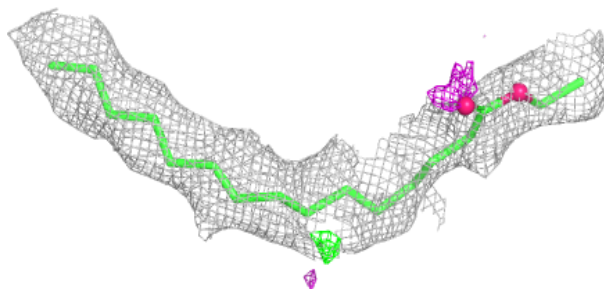
**Electron density around OLC A 411:**

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

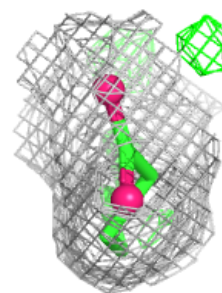
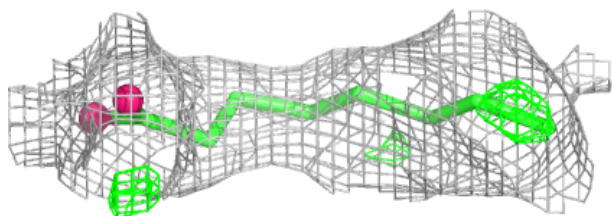
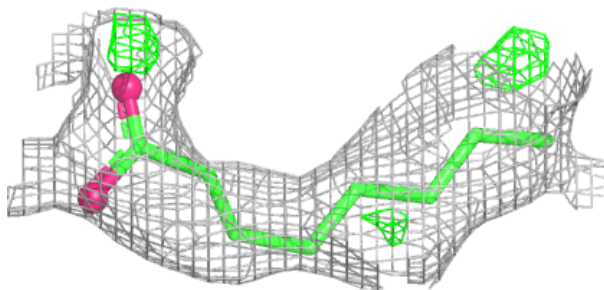


Electron density around OLC B 404:

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

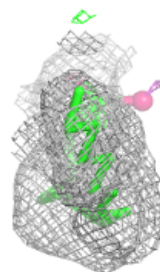
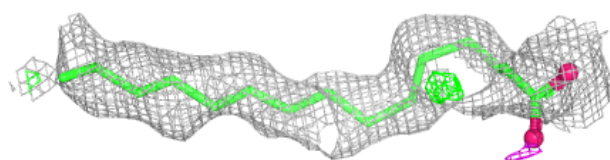
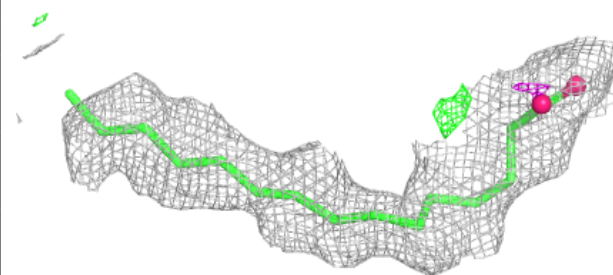
**Electron density around OLC B 405:**

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

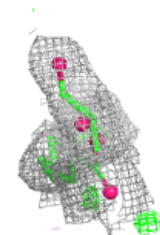
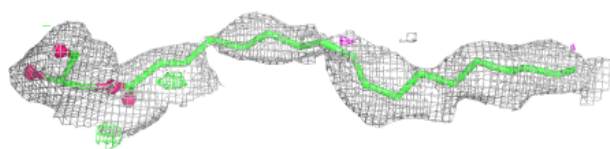
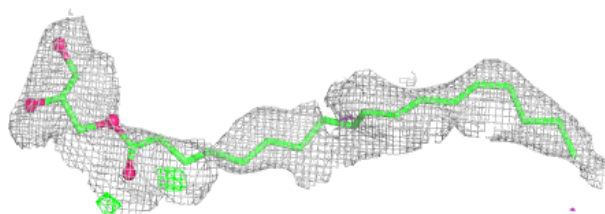


Electron density around OLC A 406:

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

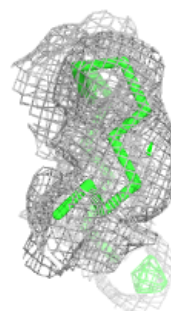
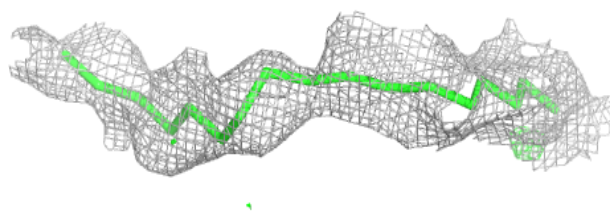
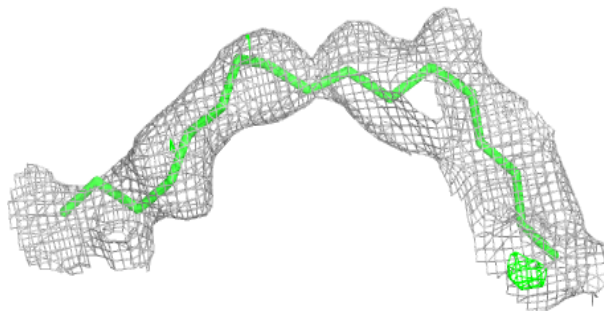
**Electron density around OLC A 405:**

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

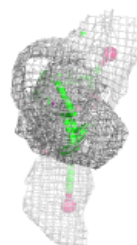
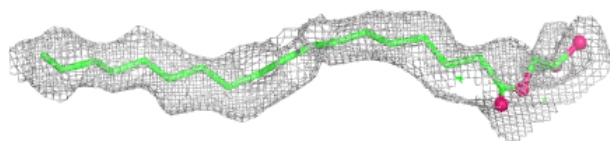
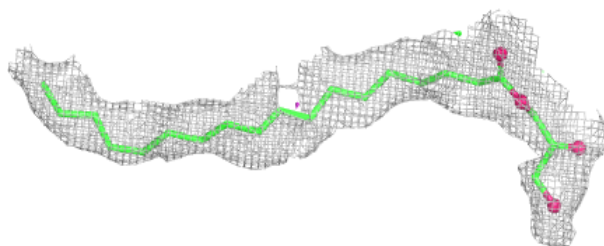


Electron density around OLC B 407:

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

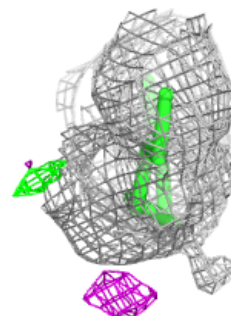
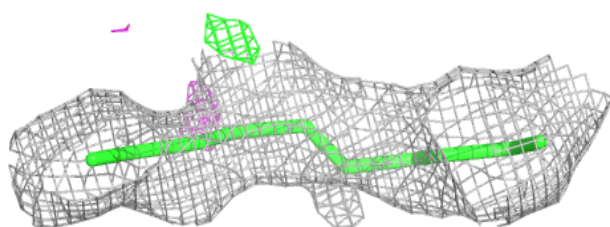
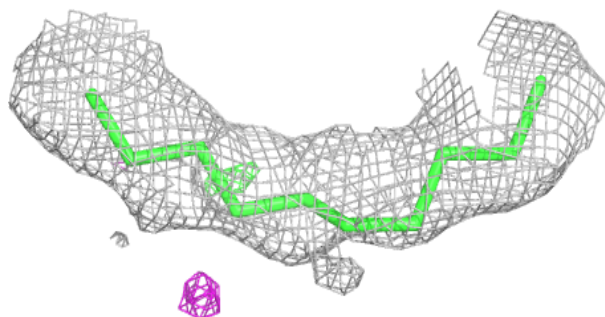
**Electron density around OLC A 412:**

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

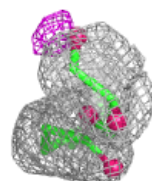
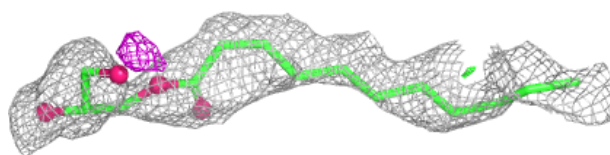


Electron density around OLC A 408:

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

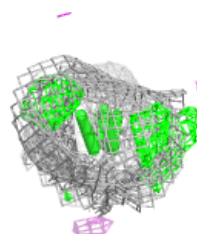
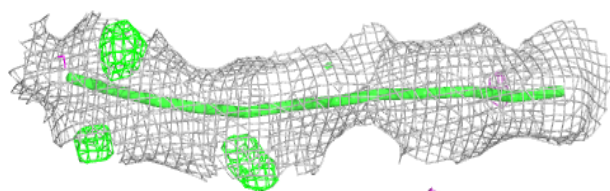
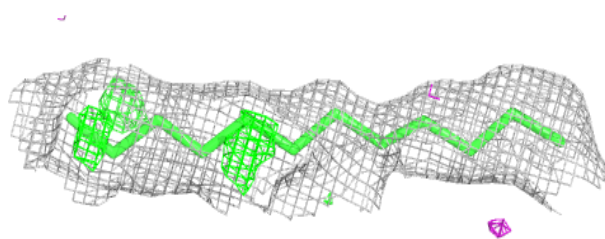
**Electron density around OLC B 406:**

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

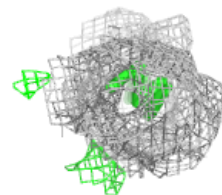
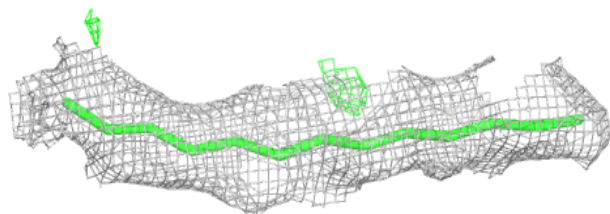
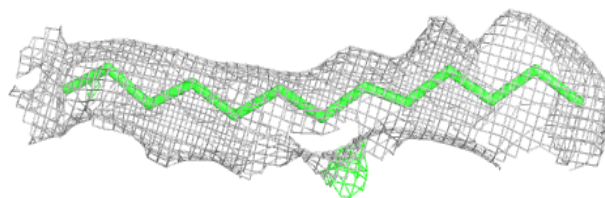


Electron density around OLC A 409:

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

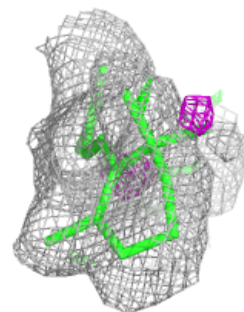
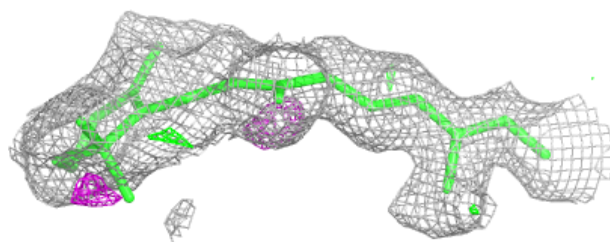
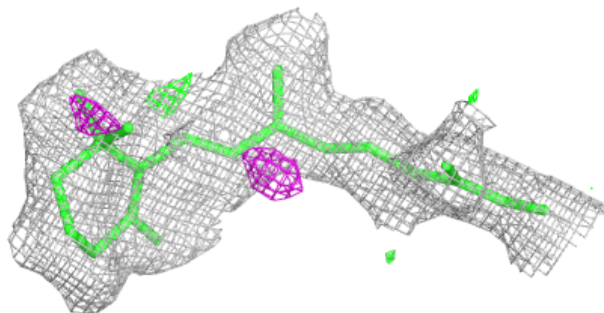
**Electron density around OLC A 413:**

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

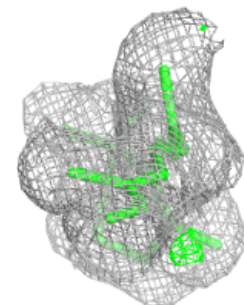
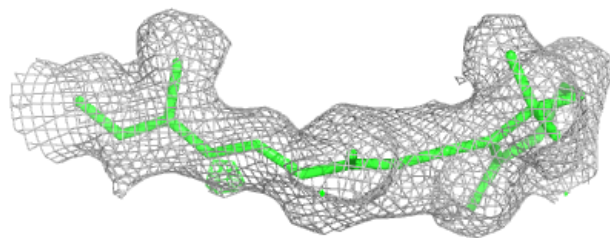
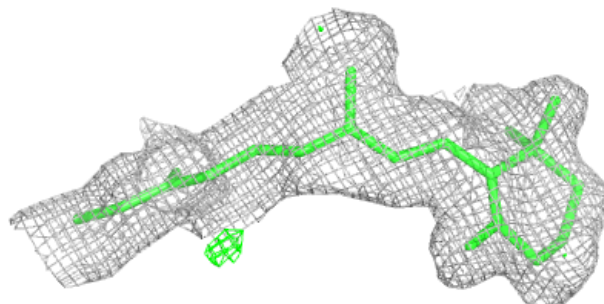


Electron density around RET A 402:

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

**Electron density around RET B 402:**

$2mF_o-DF_c$ (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.