



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:28 PM UTC

PDB ID : 8E7Z / pdb_00008e7z
Title : RsTSPO mutant -A138F
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Deposited on : 2022-08-25
Resolution : 2.60 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
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

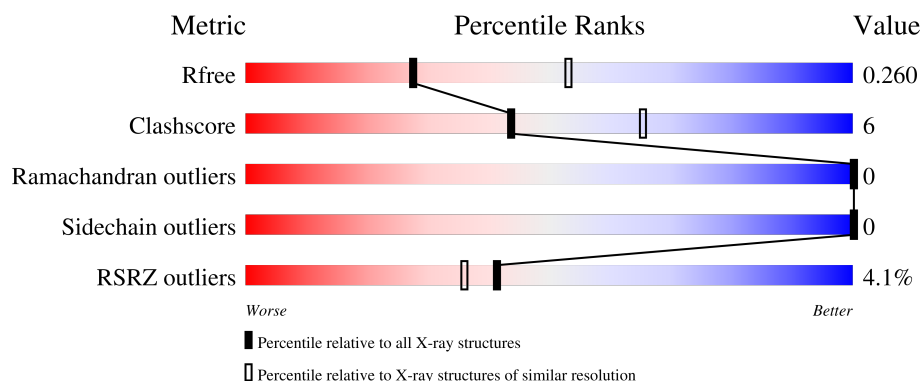
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

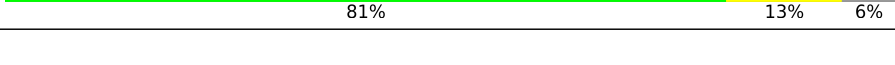
The reported resolution of this entry is 2.60 Å.

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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	158	 2% 85% 14% .
1	B	158	 4% 88% 10% .
1	C	158	 6% 81% 13% 6%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3981 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.

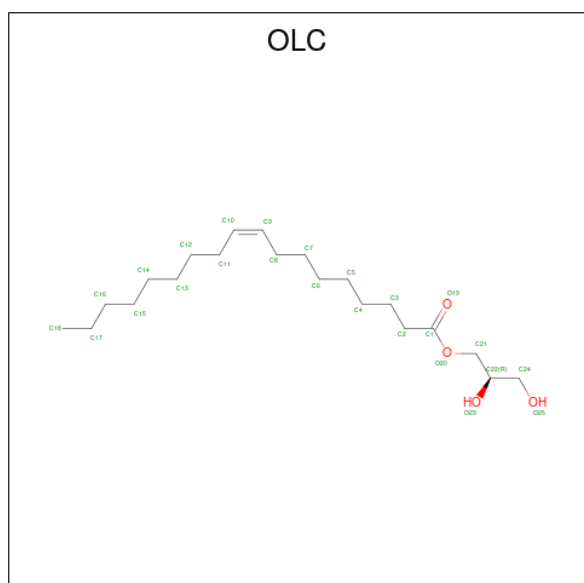
- Molecule 1 is a protein called Tryptophan-rich sensory protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	156	Total	C	N	O	S	0	0	0
			1243	840	194	198	11			
1	B	155	Total	C	N	O	S	0	0	0
			1231	833	194	194	10			
1	C	149	Total	C	N	O	S	5	0	0
			1165	791	178	186	10			

There are 3 discrepancies between the modelled and reference sequences:

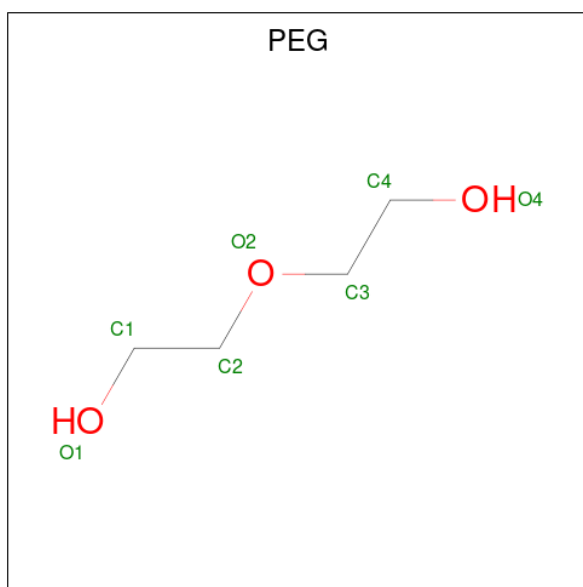
Chain	Residue	Modelled	Actual	Comment	Reference
A	138	PHE	ALA	engineered mutation	UNP Q9RFC8
B	138	PHE	ALA	engineered mutation	UNP Q9RFC8
C	138	PHE	ALA	engineered mutation	UNP Q9RFC8

- Molecule 2 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
2	A	1	Total C O 25 21 4	0	0
2	A	1	Total C O 25 21 4	0	0
2	A	1	Total C 12 12	0	0
2	A	1	Total C O 17 13 4	0	0
2	A	1	Total C 15 15	0	0
2	A	1	Total C O 18 14 4	0	0
2	B	1	Total C O 25 21 4	0	0
2	B	1	Total C O 25 21 4	0	0
2	B	1	Total C O 12 8 4	0	0
2	B	1	Total C O 25 21 4	0	0
2	C	1	Total C 17 17	0	0
2	C	1	Total C O 24 21 3	0	0
2	C	1	Total C O 25 21 4	0	0
2	C	1	Total C O 25 21 4	0	0

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			7	4	3		

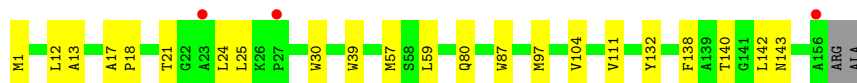
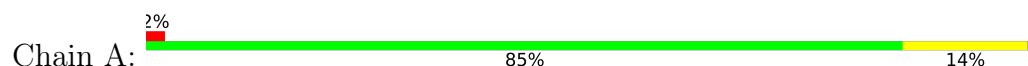
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	16	Total	O	0	0
			16	16		
4	B	12	Total	O	0	0
			12	12		
4	C	17	Total	O	0	0
			17	17		

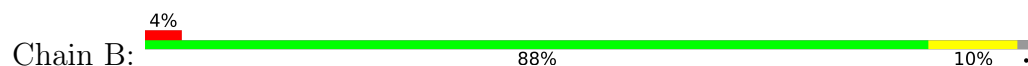
3 Residue-property plots [i](#)

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.

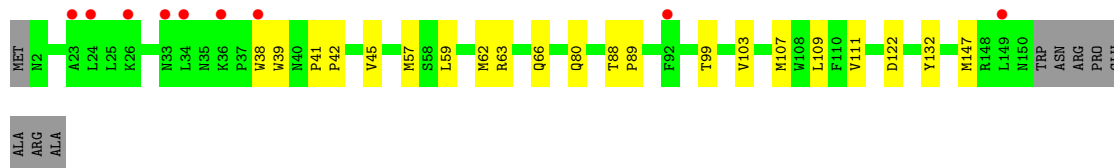
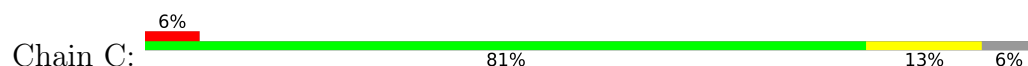
- Molecule 1: Tryptophan-rich sensory protein



- Molecule 1: Tryptophan-rich sensory protein



- Molecule 1: Tryptophan-rich sensory protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	58.55Å 99.53Å 95.48Å 90.00° 100.12° 90.00°	Depositor
Resolution (Å)	47.13 – 2.60 47.13 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.13-2.60) 95.6 (47.13-2.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.31 (at 1.92Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.204 , 0.263 0.204 , 0.260	Depositor DCC
R_{free} test set	1819 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	12.1	Xtriage
Anisotropy	0.571	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3981	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.79% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, OLC

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	0.13	0/1293	0.31	0/1778
1	B	0.20	0/1281	0.37	0/1763
1	C	0.16	0/1212	0.34	0/1670
All	All	0.17	0/3786	0.34	0/5211

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	1243	0	1202	18	0
1	B	1231	0	1184	16	0
1	C	1165	0	1106	15	0
2	A	112	0	167	7	0
2	B	87	0	133	6	0
2	C	91	0	149	1	0
3	C	7	0	10	1	0
4	A	16	0	0	1	0
4	B	12	0	0	0	0
4	C	17	0	0	0	0
All	All	3981	0	3951	48	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 6.

All (48) 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:C:88:THR:HG23	1:C:89:PRO:HD3	1.69	0.74
1:B:148:ARG:HG2	2:B:202:OLC:H24A	1.71	0.70
2:A:206:OLC:H10	2:B:204:OLC:H12	1.72	0.70
1:A:24:LEU:HD11	1:B:99:THR:HG21	1.76	0.68
1:A:12:LEU:HG	2:A:206:OLC:H4A	1.76	0.66
1:C:80:GLN:NE2	1:C:132:TYR:OH	2.28	0.66
1:C:109:LEU:HD21	2:C:204:OLC:H8	1.79	0.64
1:A:138:PHE:HD1	2:A:202:OLC:H18A	1.62	0.64
1:B:116:TRP:HD1	2:B:201:OLC:H3A	1.68	0.59
1:B:154:PRO:HD2	1:B:155:GLU:OE1	2.04	0.57
1:A:140:THR:HG21	2:A:204:OLC:H6	1.87	0.56
1:A:39:TRP:H	1:A:39:TRP:CD1	2.27	0.53
1:C:57:MET:HE1	1:C:80:GLN:HE22	1.73	0.53
1:C:39:TRP:CD1	1:C:39:TRP:H	2.28	0.51
1:B:116:TRP:CD1	2:B:201:OLC:H3A	2.45	0.51
1:B:87:TRP:CD1	1:B:104:VAL:HB	2.45	0.50
1:B:155:GLU:H	1:B:155:GLU:CD	2.20	0.50
2:A:201:OLC:H18A	2:A:205:OLC:H12	1.94	0.49
1:C:107:MET:O	1:C:111:VAL:HG23	2.13	0.49
1:C:99:THR:O	1:C:103:VAL:HG23	2.12	0.48
1:A:25:LEU:O	1:C:38:TRP:NE1	2.47	0.48
1:B:152:ASN:H	1:B:152:ASN:HD22	1.61	0.47
1:A:80:GLN:HG3	1:A:111:VAL:HG22	1.97	0.47
1:A:59:LEU:HD13	2:A:201:OLC:H4A	1.97	0.46
1:A:87:TRP:CD1	1:A:104:VAL:HB	2.49	0.46
1:A:57:MET:HE2	1:A:132:TYR:CE2	2.50	0.46
1:C:41:PRO:HB2	1:C:45:VAL:HG11	1.98	0.46
1:A:138:PHE:CZ	1:A:142:LEU:HD11	2.51	0.45
1:C:42:PRO:O	1:C:45:VAL:HG12	2.17	0.45
1:C:147:MET:HE3	1:C:147:MET:HB3	1.76	0.45
1:A:24:LEU:HB3	1:B:94:MET:HE1	1.97	0.45
2:A:203:OLC:H4A	2:A:205:OLC:H6A	1.99	0.44
1:A:18:PRO:O	1:A:21:THR:OG1	2.28	0.44
1:B:115:MET:HE2	1:B:115:MET:HB3	1.86	0.44
1:A:30:TRP:HZ2	1:A:97:MET:HE2	1.82	0.43
1:A:13:ALA:HB1	2:B:204:OLC:H12A	2.00	0.43
1:C:62:MET:O	1:C:66:GLN:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MET:N	4:A:302:HOH:O	2.37	0.43
1:A:17:ALA:HA	1:B:86:LEU:HD22	2.01	0.43
1:C:88:THR:CG2	1:C:89:PRO:HD3	2.45	0.43
1:B:64:VAL:HG21	1:B:118:PHE:CD1	2.53	0.43
1:B:147:MET:HE2	2:B:202:OLC:H2	2.01	0.42
1:A:143:ASN:C	1:A:143:ASN:HD22	2.26	0.42
1:B:95:LYS:O	1:B:155:GLU:HB3	2.20	0.41
1:C:63:ARG:NH1	1:C:122:ASP:OD2	2.54	0.41
1:B:86:LEU:O	1:B:90:VAL:HG23	2.21	0.41
1:C:59:LEU:HD21	3:C:201:PEG:H22	2.02	0.41
1:B:94:MET:HE2	1:B:94:MET:HB3	1.84	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	154/158 (98%)	154 (100%)	0	0	100	100
1	B	153/158 (97%)	151 (99%)	2 (1%)	0	100	100
1	C	147/158 (93%)	146 (99%)	1 (1%)	0	100	100
All	All	454/474 (96%)	451 (99%)	3 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	119/124 (96%)	119 (100%)	0	100	100
1	B	116/124 (94%)	116 (100%)	0	100	100
1	C	108/124 (87%)	108 (100%)	0	100	100
All	All	343/372 (92%)	343 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	84	ASN
1	B	152	ASN
1	C	40	ASN
1	C	80	GLN
1	C	120	GLN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

15 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	$\# Z > 2$
2	OLC	C	203	-	23,23,24	0.66	1 (4%)	23,23,25	1.12	2 (8%)
2	OLC	B	203	-	11,11,24	1.01	1 (9%)	12,12,25	1.10	1 (8%)
2	OLC	A	206	-	17,17,24	0.82	1 (5%)	18,18,25	1.10	1 (5%)
2	OLC	A	204	-	16,16,24	0.87	1 (6%)	17,17,25	1.11	1 (5%)
2	OLC	A	203	-	11,11,24	0.26	0	10,10,25	0.79	0
2	OLC	A	202	-	24,24,24	0.70	1 (4%)	25,25,25	0.92	1 (4%)
2	OLC	C	202	-	16,16,24	0.21	0	15,15,25	0.77	0
3	PEG	C	201	-	6,6,6	0.13	0	5,5,5	0.07	0
2	OLC	B	202	-	24,24,24	0.69	1 (4%)	25,25,25	0.97	1 (4%)
2	OLC	B	201	-	24,24,24	0.69	1 (4%)	25,25,25	0.88	1 (4%)
2	OLC	A	205	-	14,14,24	0.23	0	13,13,25	0.73	0
2	OLC	A	201	-	24,24,24	0.71	1 (4%)	25,25,25	1.00	1 (4%)
2	OLC	C	205	-	24,24,24	0.68	1 (4%)	25,25,25	1.01	1 (4%)
2	OLC	B	204	-	24,24,24	0.68	1 (4%)	25,25,25	0.93	1 (4%)
2	OLC	C	204	-	24,24,24	0.71	1 (4%)	25,25,25	0.92	1 (4%)

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	OLC	C	203	-	-	5/22/22/24	-
2	OLC	B	203	-	-	0/11/11/24	-
2	OLC	A	206	-	-	7/17/17/24	-
2	OLC	A	204	-	-	5/16/16/24	-
2	OLC	A	203	-	-	4/9/9/24	-
2	OLC	A	202	-	-	11/24/24/24	-
2	OLC	C	202	-	-	10/14/14/24	-
3	PEG	C	201	-	-	0/4/4/4	-
2	OLC	B	202	-	-	9/24/24/24	-
2	OLC	B	201	-	-	12/24/24/24	-
2	OLC	A	205	-	-	4/12/12/24	-
2	OLC	A	201	-	-	9/24/24/24	-
2	OLC	C	205	-	-	13/24/24/24	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OLC	B	204	-	-	9/24/24/24	-
2	OLC	C	204	-	-	13/24/24/24	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	204	OLC	O20-C1	2.78	1.41	1.33
2	A	202	OLC	O20-C1	2.74	1.41	1.33
2	B	203	OLC	O20-C1	2.68	1.41	1.33
2	A	204	OLC	O20-C1	2.66	1.41	1.33
2	A	201	OLC	O20-C1	2.65	1.41	1.33
2	A	206	OLC	O20-C1	2.64	1.41	1.33
2	C	203	OLC	O20-C1	2.64	1.41	1.33
2	B	201	OLC	O20-C1	2.63	1.41	1.33
2	C	205	OLC	O20-C1	2.63	1.41	1.33
2	B	202	OLC	O20-C1	2.61	1.41	1.33
2	B	204	OLC	O20-C1	2.57	1.40	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	205	OLC	O20-C1-C2	2.96	120.86	111.83
2	A	201	OLC	O20-C1-C2	2.88	120.62	111.83
2	B	202	OLC	O20-C1-C2	2.82	120.44	111.83
2	C	203	OLC	O20-C1-C2	2.82	120.42	111.83
2	A	204	OLC	O20-C1-C2	2.74	120.20	111.83
2	B	203	OLC	O20-C1-C2	2.73	120.16	111.83
2	C	204	OLC	O20-C1-C2	2.71	120.11	111.83
2	A	206	OLC	O20-C1-C2	2.68	120.02	111.83
2	A	202	OLC	O20-C1-C2	2.60	119.78	111.83
2	B	204	OLC	O20-C1-C2	2.44	119.26	111.83
2	B	201	OLC	O20-C1-C2	2.40	119.14	111.83
2	C	203	OLC	C21-C22-C24	-2.10	109.40	113.55

There are no chirality outliers.

All (111) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	202	OLC	O20-C21-C22-O23
2	B	201	OLC	O20-C21-C22-O23
2	B	202	OLC	C21-C22-C24-O25

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Mol	Chain	Res	Type	Atoms
2	B	204	OLC	O19-C1-O20-C21
2	C	205	OLC	C21-C22-C24-O25
2	A	206	OLC	O19-C1-O20-C21
2	B	204	OLC	C2-C1-O20-C21
2	A	206	OLC	C2-C1-O20-C21
2	B	201	OLC	C2-C1-O20-C21
2	B	202	OLC	C2-C1-O20-C21
2	A	201	OLC	O20-C21-C22-C24
2	A	201	OLC	O20-C21-C22-O23
2	A	204	OLC	O20-C21-C22-O23
2	B	201	OLC	C1-C2-C3-C4
2	B	204	OLC	C1-C2-C3-C4
2	B	201	OLC	O19-C1-O20-C21
2	B	202	OLC	O23-C22-C24-O25
2	C	204	OLC	C1-C2-C3-C4
2	A	201	OLC	C1-C2-C3-C4
2	A	202	OLC	C1-C2-C3-C4
2	A	206	OLC	C1-C2-C3-C4
2	B	202	OLC	O19-C1-O20-C21
2	C	204	OLC	O20-C21-C22-O23
2	C	204	OLC	C2-C1-O20-C21
2	B	201	OLC	O20-C21-C22-C24
2	C	204	OLC	O20-C21-C22-C24
2	A	201	OLC	C21-C22-C24-O25
2	B	204	OLC	C4-C5-C6-C7
2	C	204	OLC	C14-C15-C16-C17
2	A	202	OLC	C2-C3-C4-C5
2	A	201	OLC	O23-C22-C24-O25
2	C	202	OLC	C5-C6-C7-C8
2	C	203	OLC	C1-C2-C3-C4
2	A	205	OLC	C6-C7-C8-C9
2	B	201	OLC	C4-C5-C6-C7
2	C	205	OLC	C1-C2-C3-C4
2	A	201	OLC	C2-C1-O20-C21
2	C	205	OLC	C12-C13-C14-C15
2	A	202	OLC	C3-C4-C5-C6
2	C	204	OLC	C5-C6-C7-C8
2	C	204	OLC	O19-C1-O20-C21
2	A	204	OLC	C4-C5-C6-C7
2	C	205	OLC	C2-C3-C4-C5
2	C	204	OLC	C13-C14-C15-C16
2	A	202	OLC	C12-C13-C14-C15

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Mol	Chain	Res	Type	Atoms
2	A	206	OLC	C4-C5-C6-C7
2	C	204	OLC	C11-C12-C13-C14
2	A	203	OLC	C9-C10-C11-C12
2	B	204	OLC	C10-C11-C12-C13
2	A	201	OLC	O19-C1-O20-C21
2	C	205	OLC	C14-C15-C16-C17
2	B	201	OLC	C3-C4-C5-C6
2	A	205	OLC	C10-C11-C12-C13
2	A	206	OLC	C2-C3-C4-C5
2	B	204	OLC	C2-C3-C4-C5
2	B	202	OLC	C13-C14-C15-C16
2	C	205	OLC	O23-C22-C24-O25
2	B	204	OLC	C3-C4-C5-C6
2	B	202	OLC	C5-C6-C7-C8
2	A	202	OLC	C6-C7-C8-C9
2	B	201	OLC	C2-C3-C4-C5
2	B	204	OLC	C13-C14-C15-C16
2	C	202	OLC	C4-C5-C6-C7
2	A	206	OLC	C6-C7-C8-C9
2	A	202	OLC	C11-C12-C13-C14
2	A	206	OLC	C5-C6-C7-C8
2	B	201	OLC	C13-C14-C15-C16
2	A	202	OLC	O20-C21-C22-C24
2	C	204	OLC	C12-C13-C14-C15
2	A	205	OLC	C5-C6-C7-C8
2	C	202	OLC	C13-C14-C15-C16
2	B	202	OLC	C1-C2-C3-C4
2	C	205	OLC	C2-C1-O20-C21
2	C	205	OLC	C13-C14-C15-C16
2	C	203	OLC	C2-C3-C4-C5
2	C	205	OLC	C6-C7-C8-C9
2	C	205	OLC	C5-C6-C7-C8
2	A	203	OLC	C1-C2-C3-C4
2	C	205	OLC	O19-C1-O20-C21
2	A	204	OLC	C6-C7-C8-C9
2	A	202	OLC	C13-C14-C15-C16
2	C	204	OLC	C9-C10-C11-C12
2	A	205	OLC	C1-C2-C3-C4
2	A	201	OLC	C15-C16-C17-C18
2	B	202	OLC	C9-C10-C11-C12
2	C	202	OLC	C10-C11-C12-C13
2	C	203	OLC	O20-C21-C22-C24

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Mol	Chain	Res	Type	Atoms
2	B	201	OLC	C6-C7-C8-C9
2	C	202	OLC	C9-C10-C11-C12
2	B	204	OLC	C7-C8-C9-C10
2	C	202	OLC	C15-C16-C17-C18
2	A	203	OLC	C5-C6-C7-C8
2	C	205	OLC	C9-C10-C11-C12
2	C	204	OLC	C6-C7-C8-C9
2	A	202	OLC	C7-C8-C9-C10
2	C	203	OLC	C5-C6-C7-C8
2	C	204	OLC	C3-C4-C5-C6
2	A	201	OLC	C9-C10-C11-C12
2	A	203	OLC	C7-C8-C9-C10
2	A	204	OLC	O20-C21-C22-C24
2	C	203	OLC	C9-C10-C11-C12
2	C	205	OLC	C7-C8-C9-C10
2	C	202	OLC	C2-C3-C4-C5
2	B	202	OLC	C7-C8-C9-C10
2	B	201	OLC	O20-C1-C2-C3
2	C	202	OLC	C14-C15-C16-C17
2	A	202	OLC	C14-C15-C16-C17
2	C	202	OLC	C7-C8-C9-C10
2	A	204	OLC	C2-C3-C4-C5
2	B	201	OLC	O19-C1-C2-C3
2	C	202	OLC	C12-C13-C14-C15

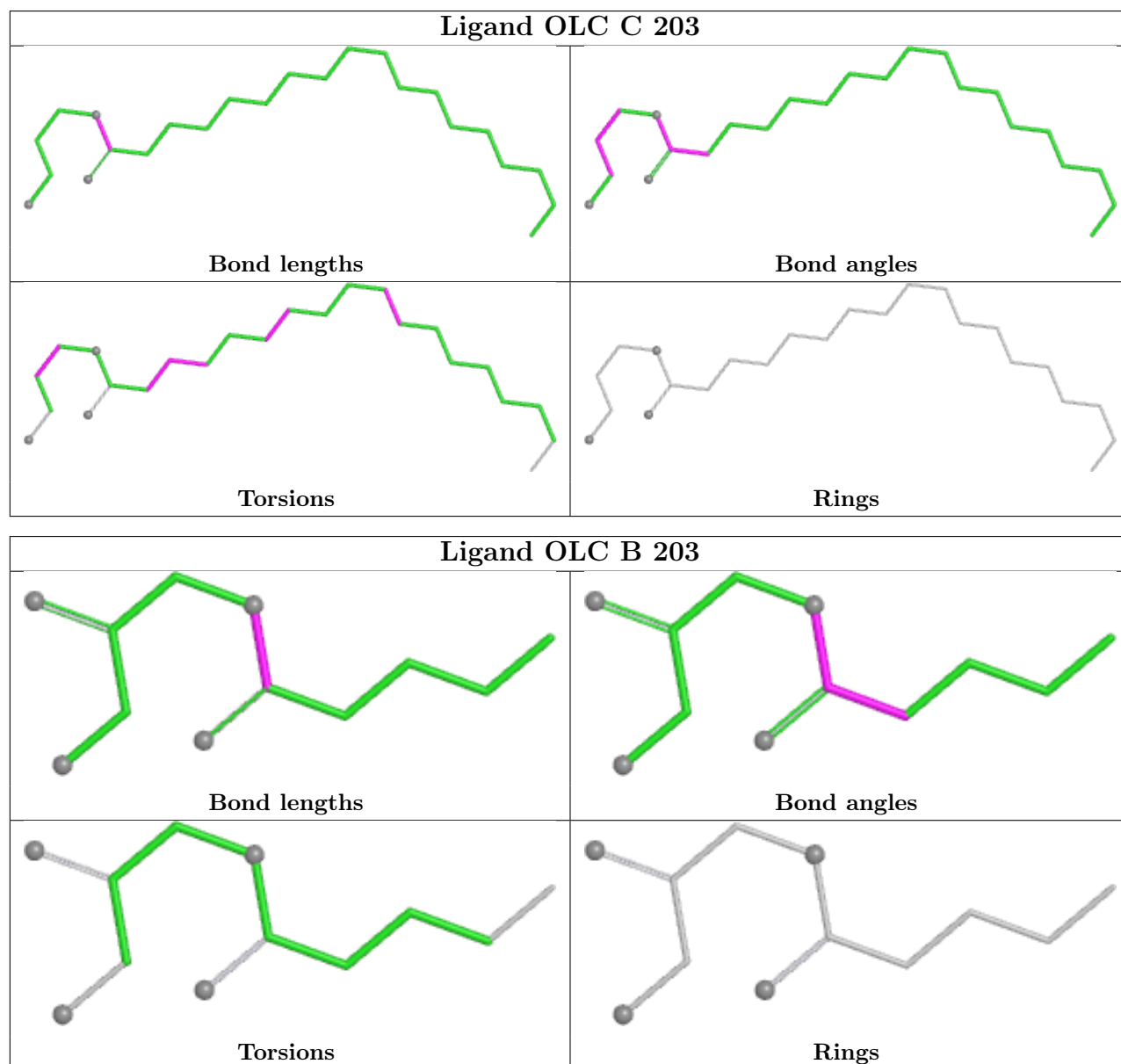
There are no ring outliers.

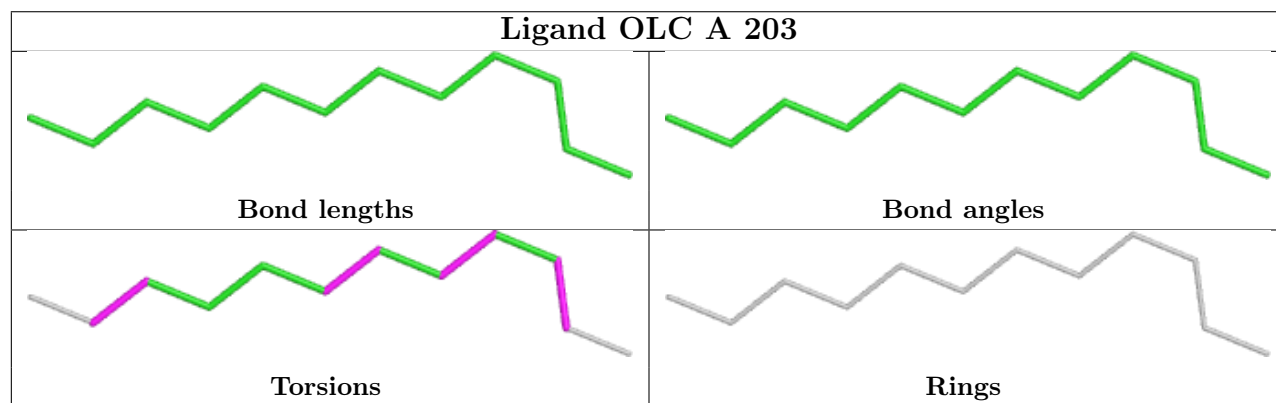
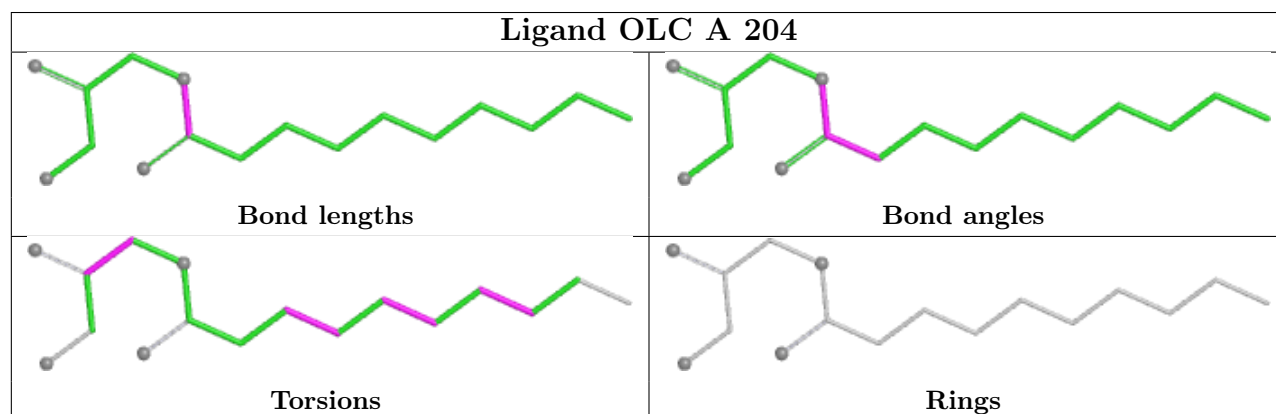
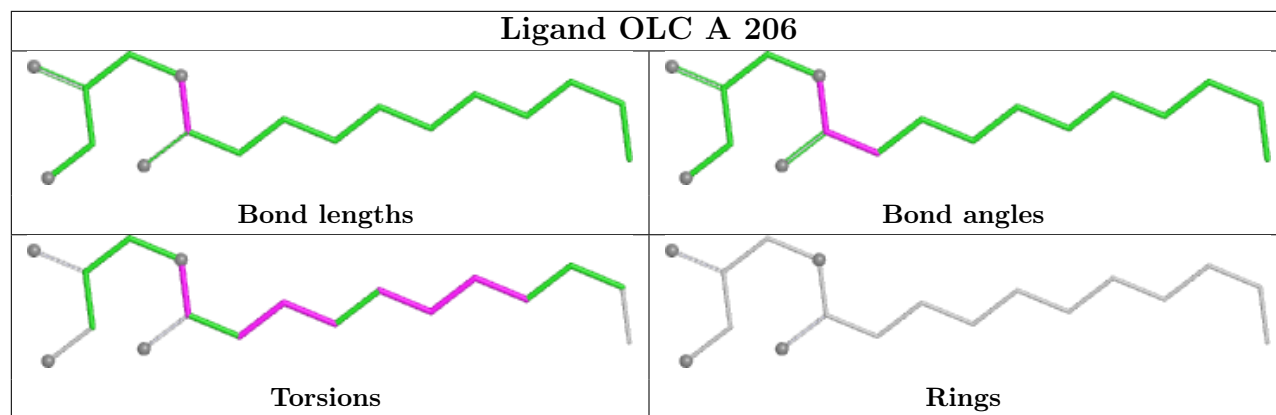
11 monomers are involved in 14 short contacts:

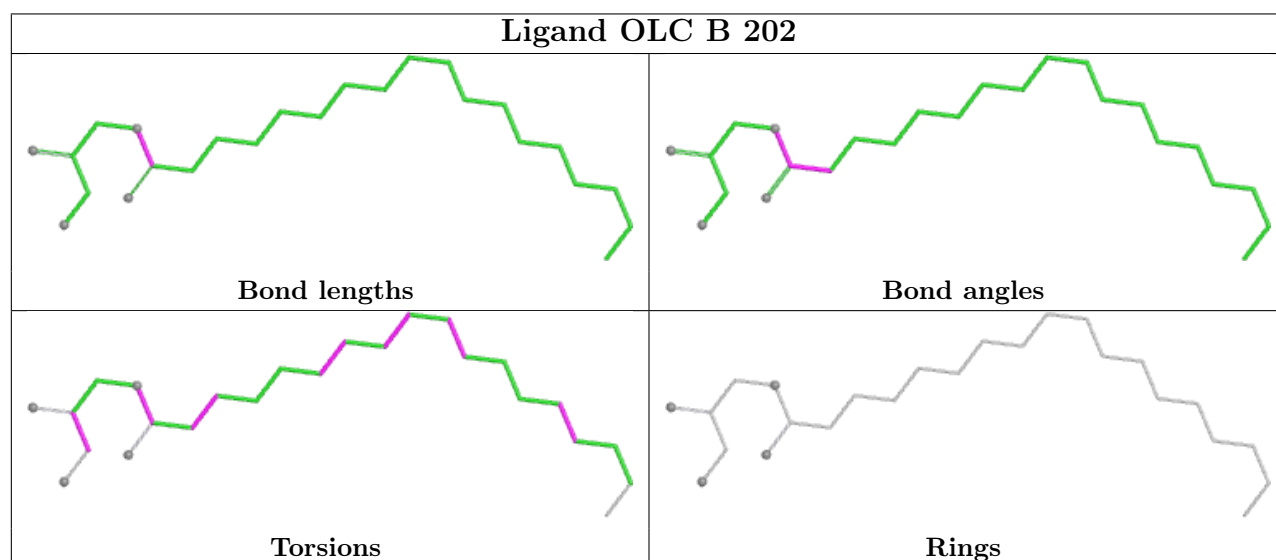
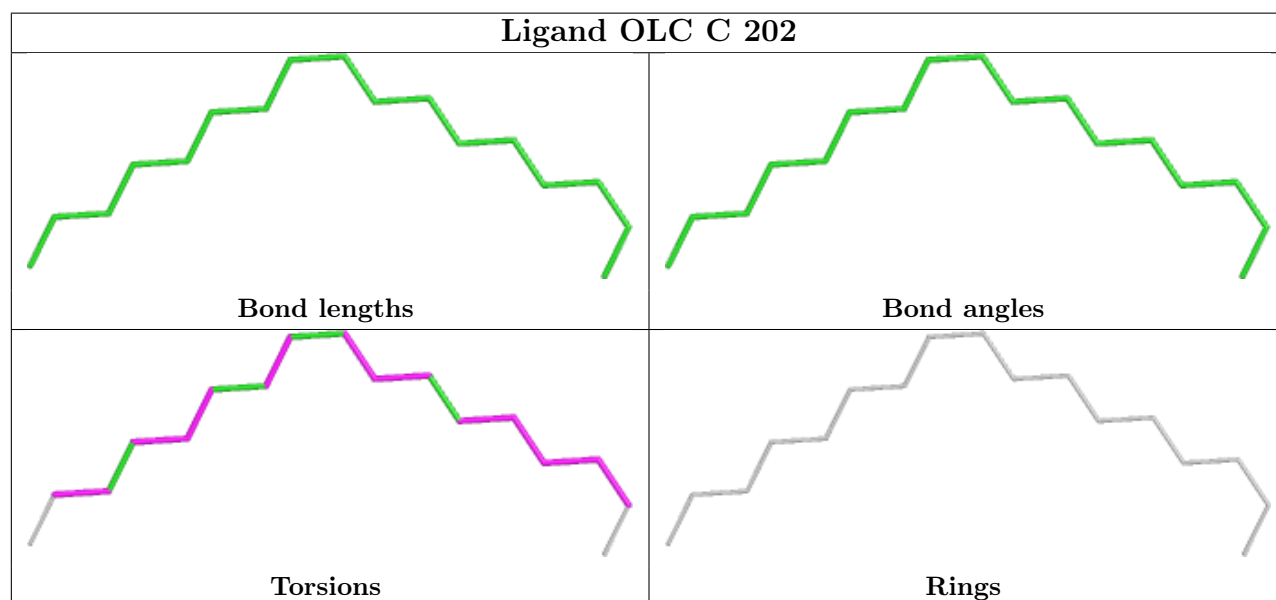
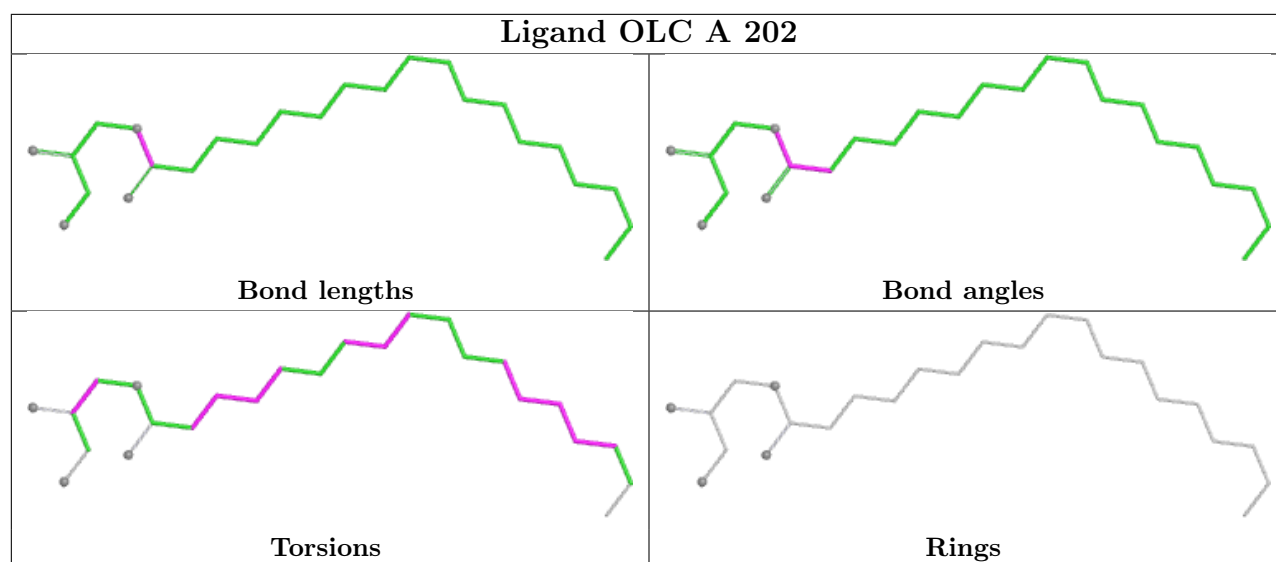
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	206	OLC	2	0
2	A	204	OLC	1	0
2	A	203	OLC	1	0
2	A	202	OLC	1	0
3	C	201	PEG	1	0
2	B	202	OLC	2	0
2	B	201	OLC	2	0
2	A	205	OLC	2	0
2	A	201	OLC	2	0
2	B	204	OLC	2	0
2	C	204	OLC	1	0

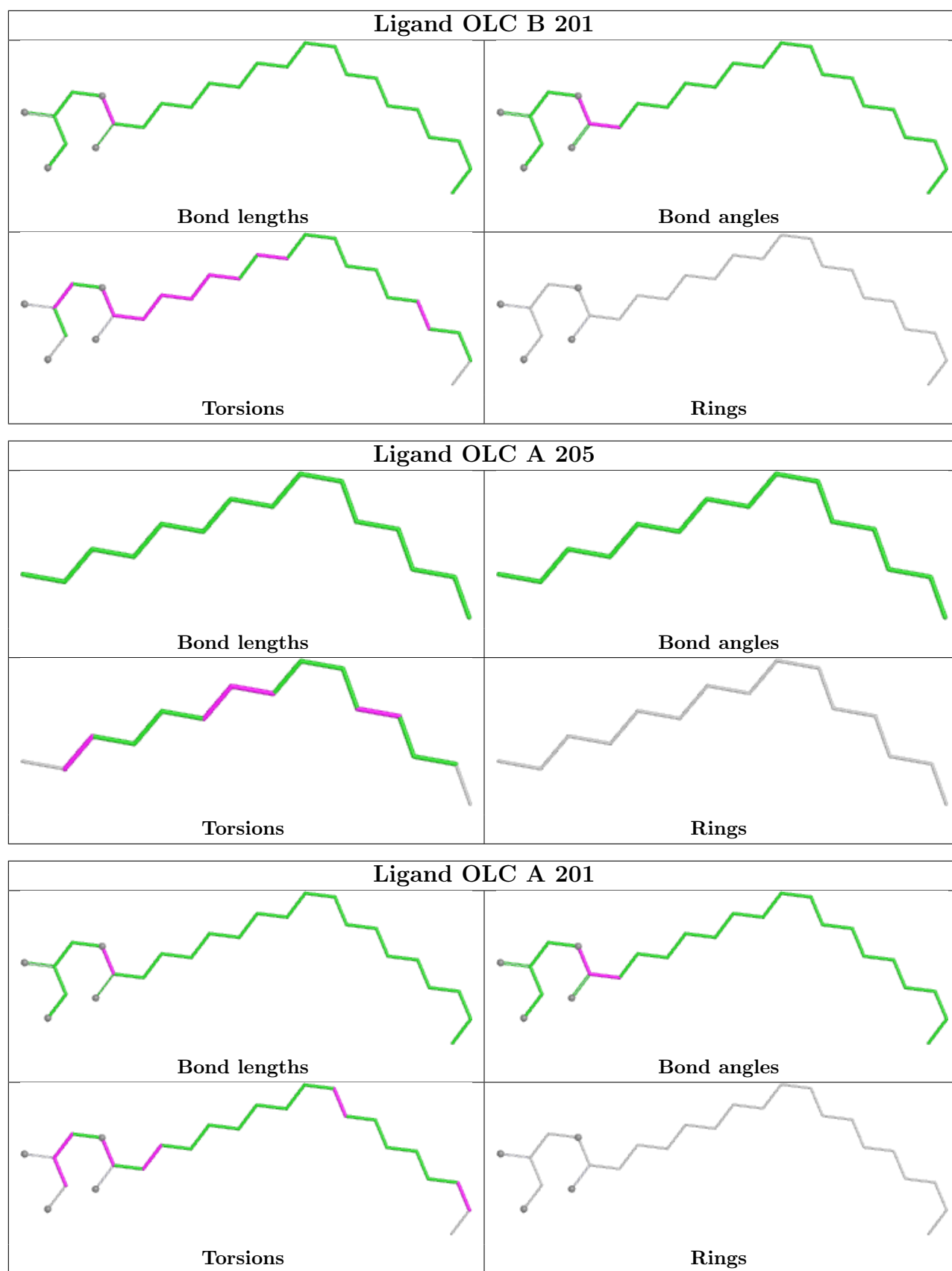
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

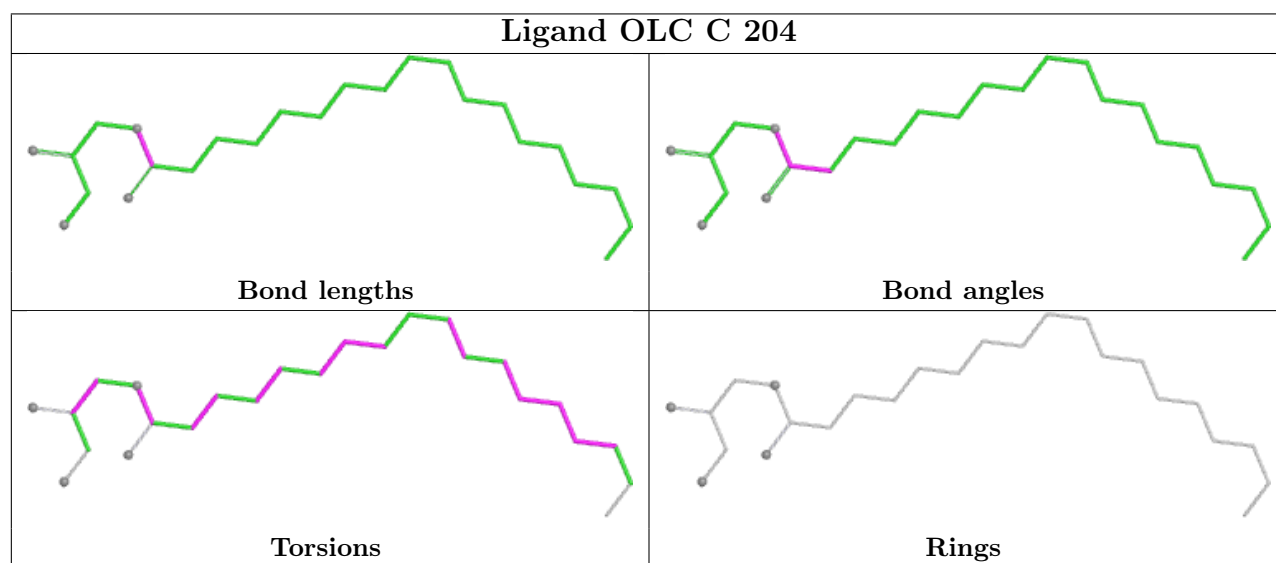
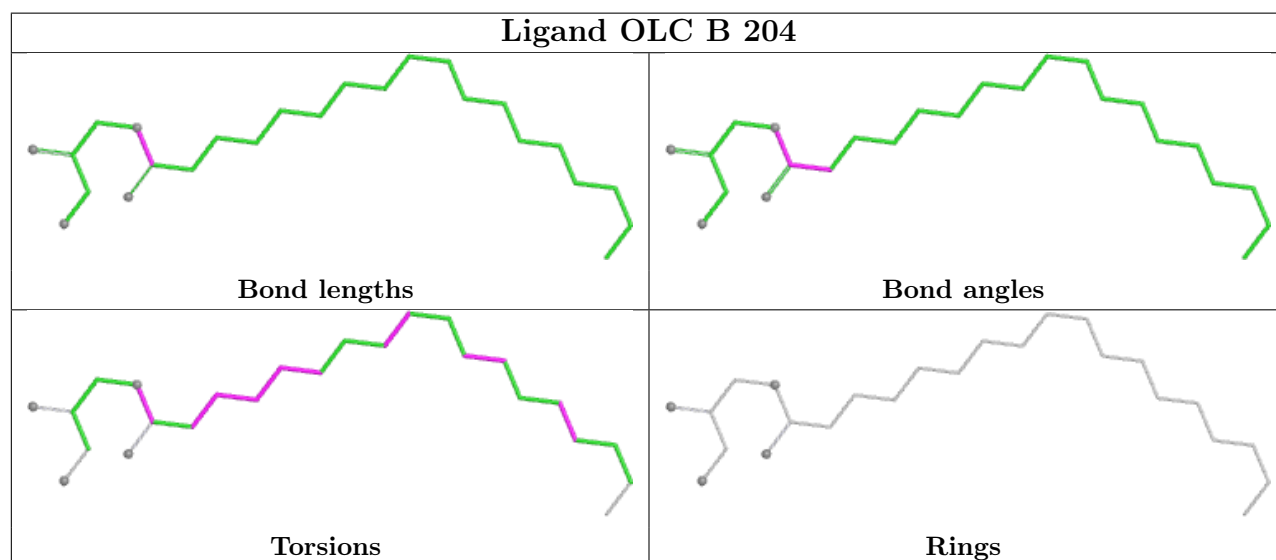
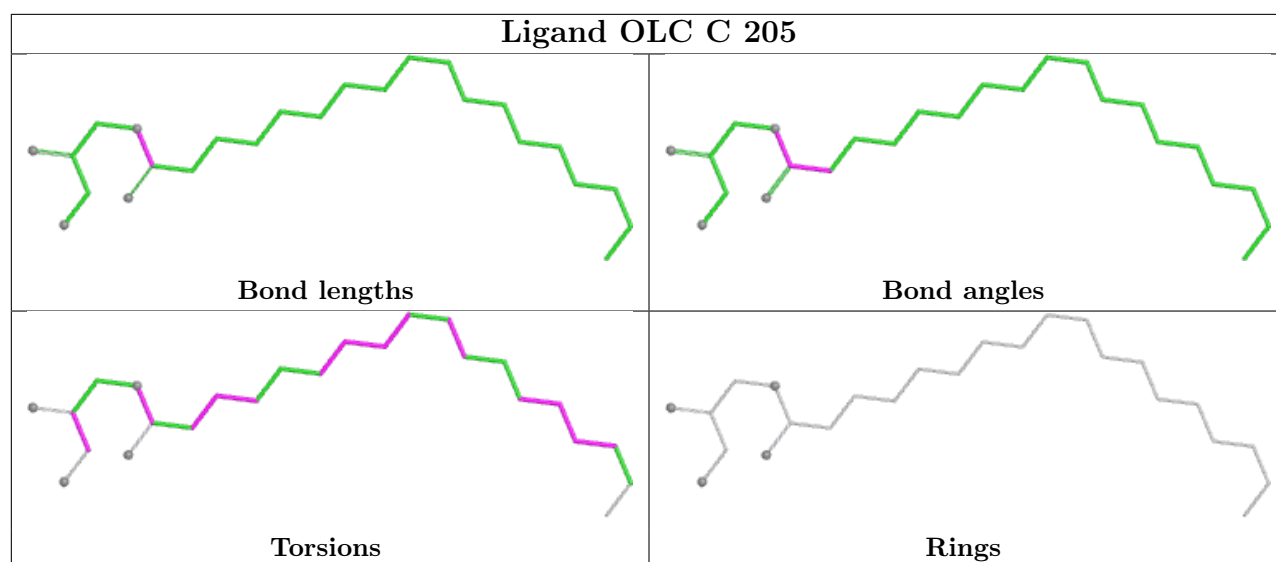
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 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	156/158 (98%)	0.09	3 (1%) 66 61	20, 29, 47, 66	0
1	B	155/158 (98%)	0.34	7 (4%) 38 32	19, 31, 50, 63	0
1	C	148/158 (93%)	0.32	9 (6%) 27 22	17, 29, 61, 75	0
All	All	459/474 (96%)	0.25	19 (4%) 41 36	17, 30, 55, 75	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	28	ASP	4.0
1	C	38	TRP	3.5
1	A	23	ALA	3.1
1	C	34	LEU	2.9
1	C	33	ASN	2.8
1	C	149	LEU	2.8
1	C	92	PHE	2.7
1	B	27	PRO	2.7
1	B	32	ASP	2.7
1	B	30	TRP	2.6
1	A	27	PRO	2.5
1	B	46	PHE	2.5
1	B	29	GLU	2.5
1	C	26	LYS	2.4
1	C	23	ALA	2.2
1	B	33	ASN	2.2
1	A	156	ALA	2.1
1	C	36	LYS	2.0
1	C	24	LEU	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](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

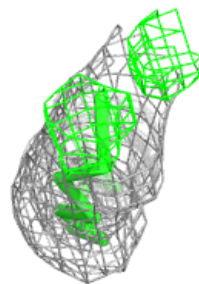
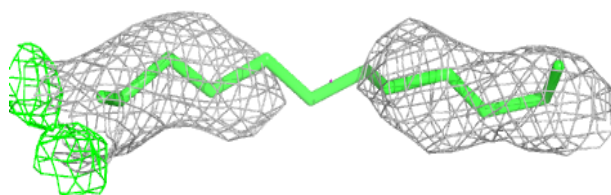
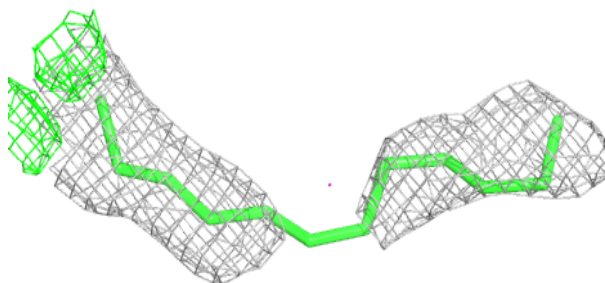
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	OLC	A	203	12/25	0.68	0.22	39,47,52,55	0
2	OLC	B	203	12/25	0.68	0.19	43,59,64,64	0
2	OLC	B	201	25/25	0.71	0.19	30,47,52,54	0
2	OLC	A	205	15/25	0.74	0.21	38,47,53,54	0
2	OLC	C	205	25/25	0.75	0.17	37,46,56,58	0
2	OLC	B	202	25/25	0.76	0.17	35,48,56,60	0
2	OLC	A	202	25/25	0.77	0.17	28,45,55,61	0
2	OLC	A	204	17/25	0.80	0.14	31,39,58,64	0
2	OLC	C	204	25/25	0.81	0.17	29,42,55,58	0
2	OLC	B	204	25/25	0.83	0.16	32,42,53,61	0
2	OLC	A	206	18/25	0.84	0.14	32,41,55,58	0
2	OLC	C	202	17/25	0.84	0.16	28,37,44,48	0
2	OLC	A	201	25/25	0.85	0.15	27,40,52,53	0
2	OLC	C	203	24/25	0.87	0.12	29,39,51,53	0
3	PEG	C	201	7/7	0.89	0.11	41,45,49,56	0

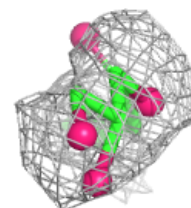
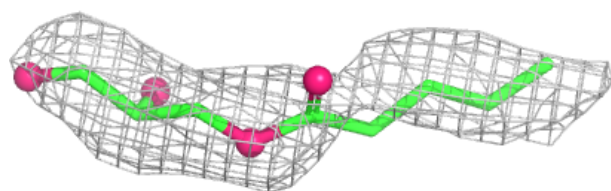
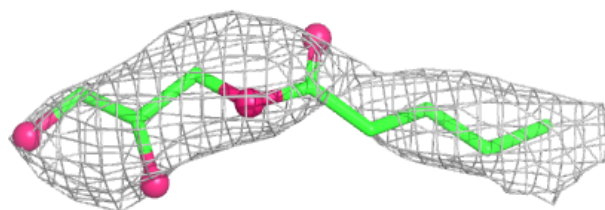
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around OLC A 203:

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

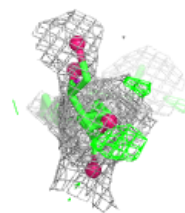
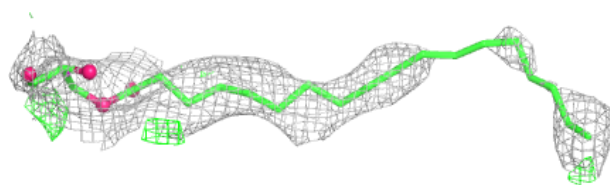
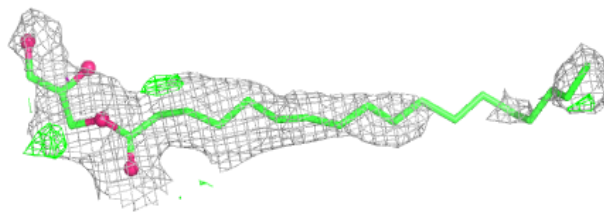
**Electron density around OLC B 203:**

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

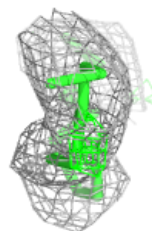
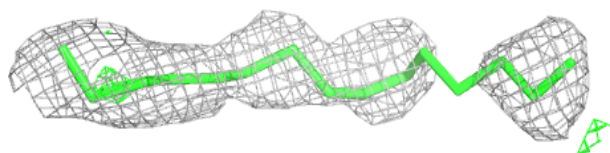
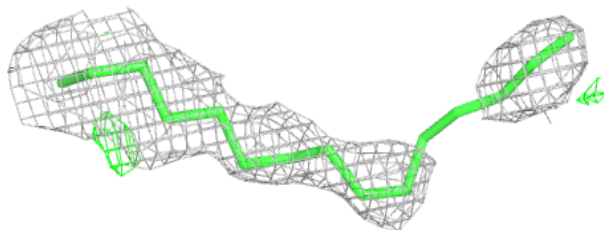


Electron density around OLC B 201:

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

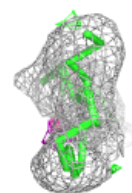
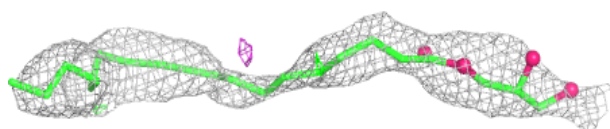
**Electron density around OLC A 205:**

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

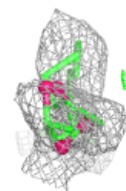
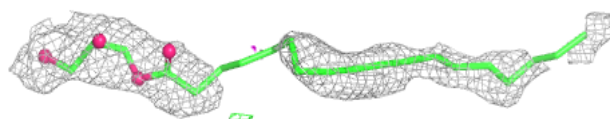
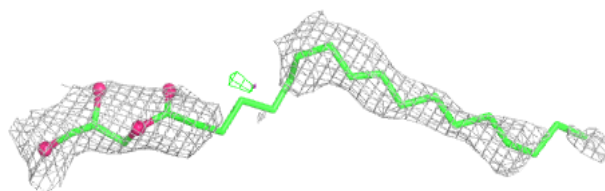


Electron density around OLC C 205:

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

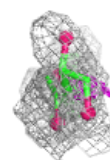
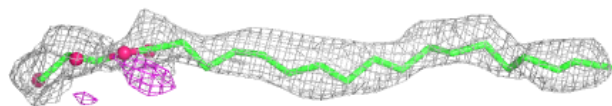
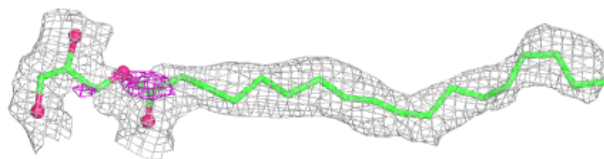
**Electron density around OLC B 202:**

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

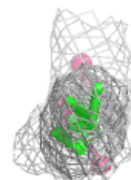
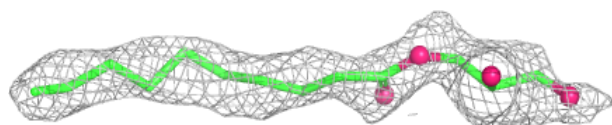
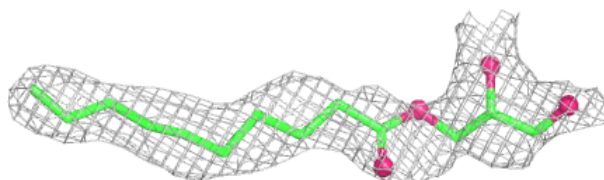


Electron density around OLC A 202:

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

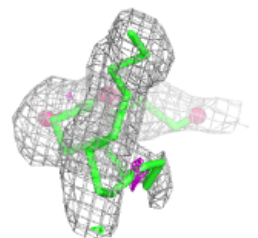
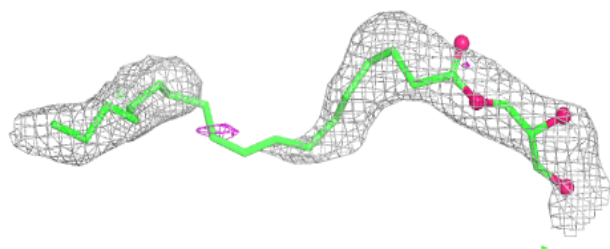
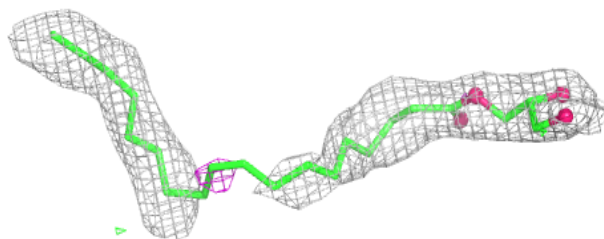
**Electron density around OLC A 204:**

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

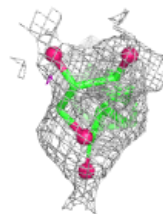
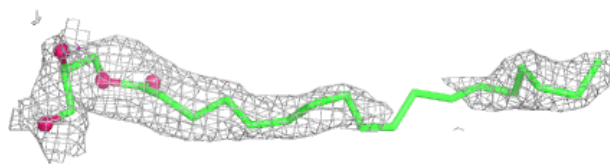
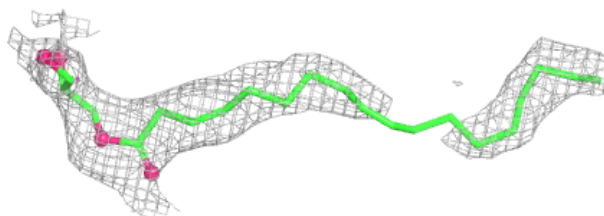


Electron density around OLC C 204:

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

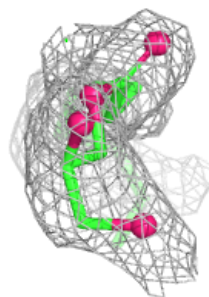
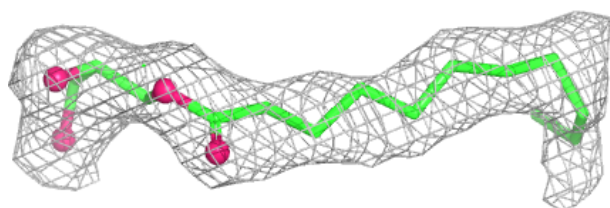
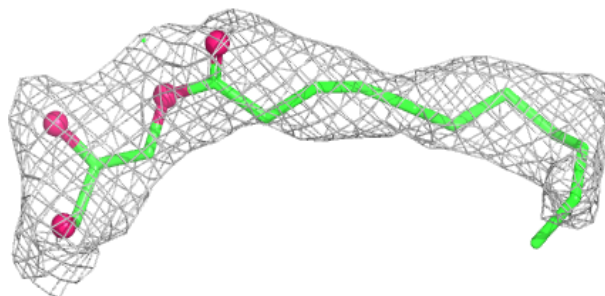
**Electron density around OLC B 204:**

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

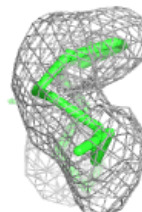
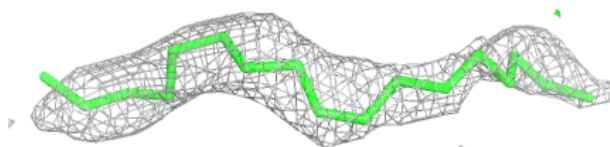
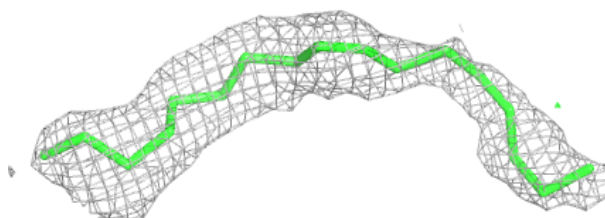


Electron density around OLC A 206:

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

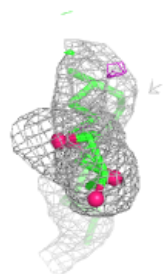
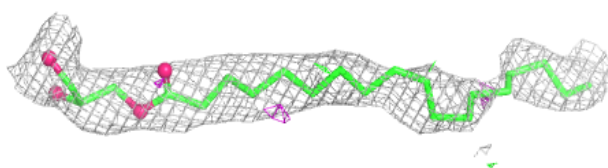
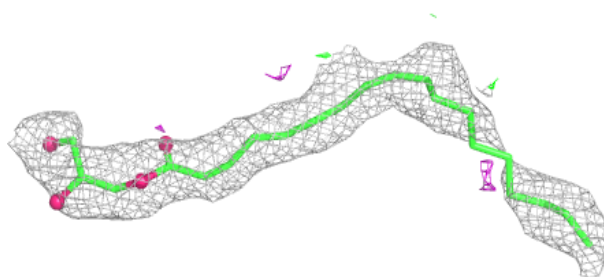
**Electron density around OLC C 202:**

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

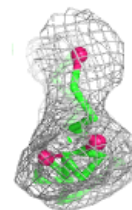
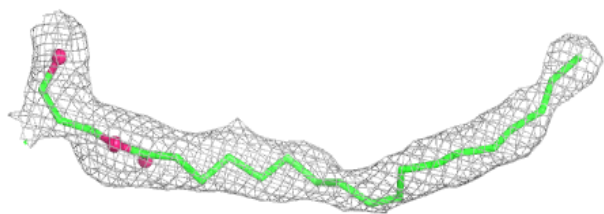


Electron density around OLC A 201:

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

**Electron density around OLC C 203:**

$2mF_o-DF_c$ (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.