wwPDB X-ray Structure Validation Summary Report (i)

Mar 13, 2024 – 02:12 PM JST

PDB ID	:	4U4W
Title	:	Structure of a nitrate/nitrite antiporter NarK in nitrate-bound occluded state
Authors	:	Fukuda, M.; Takeda, H.; Kato, H.E.; Doki, S.; Ito, K.; Maturana, A.D.; Ishitani, R.; Nureki, O.
Deposited on	:	2014-07-24
Resolution	:	2.40 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

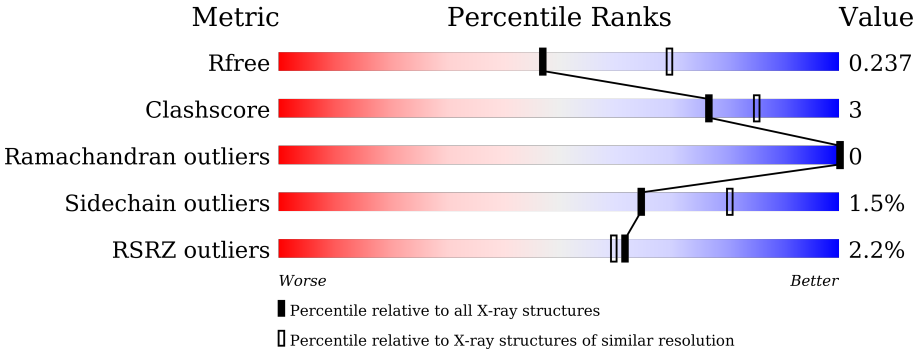
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 <=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	475	4% 81% 11% 8%
1	B	475	86% • 9%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6814 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.

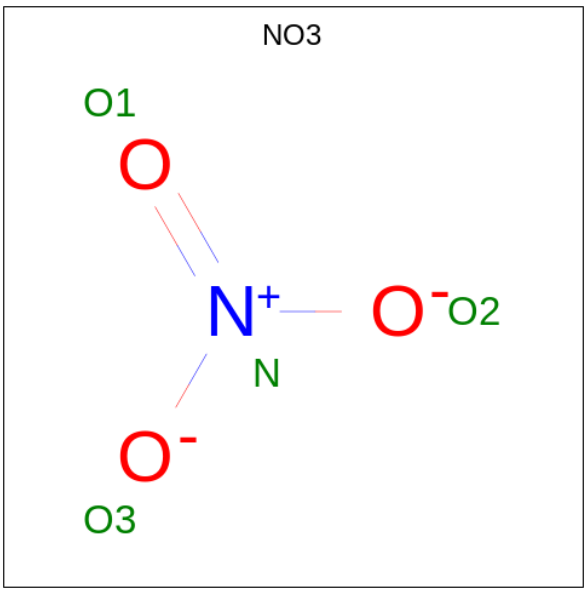
- Molecule 1 is a protein called Nitrate/nitrite transporter NarK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	438	3268	2173	522	554	19	0	0	0
1	B	430	3218	2142	512	544	20	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

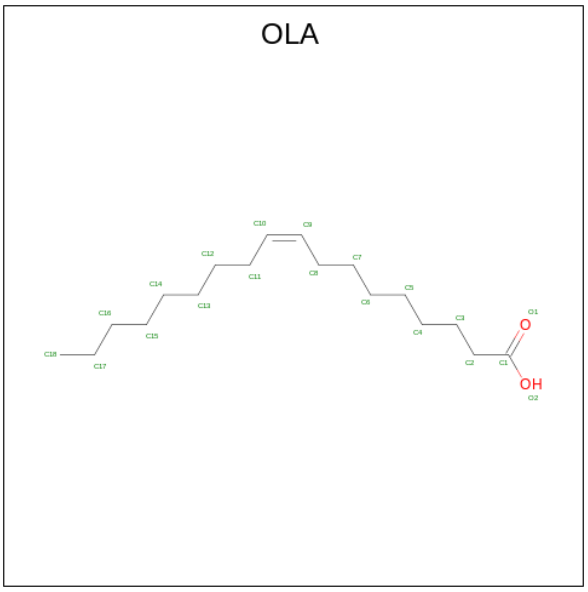
Chain	Residue	Modelled	Actual	Comment	Reference
A	464	LEU	-	expression tag	UNP P10903
A	465	GLU	-	expression tag	UNP P10903
A	466	SER	-	expression tag	UNP P10903
A	467	SER	-	expression tag	UNP P10903
A	468	GLY	-	expression tag	UNP P10903
A	469	GLU	-	expression tag	UNP P10903
A	470	ASN	-	expression tag	UNP P10903
A	471	LEU	-	expression tag	UNP P10903
A	472	TYR	-	expression tag	UNP P10903
A	473	PHE	-	expression tag	UNP P10903
A	474	GLN	-	expression tag	UNP P10903
A	475	GLY	-	expression tag	UNP P10903
B	464	LEU	-	expression tag	UNP P10903
B	465	GLU	-	expression tag	UNP P10903
B	466	SER	-	expression tag	UNP P10903
B	467	SER	-	expression tag	UNP P10903
B	468	GLY	-	expression tag	UNP P10903
B	469	GLU	-	expression tag	UNP P10903
B	470	ASN	-	expression tag	UNP P10903
B	471	LEU	-	expression tag	UNP P10903
B	472	TYR	-	expression tag	UNP P10903
B	473	PHE	-	expression tag	UNP P10903
B	474	GLN	-	expression tag	UNP P10903
B	475	GLY	-	expression tag	UNP P10903

- Molecule 2 is NITRATE ION (three-letter code: NO3) (formula: NO_3).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total N O 4 1 3	0	0
2	B	1	Total N O 4 1 3	0	0

- Molecule 3 is OLEIC ACID (three-letter code: OLA) (formula: $C_{18}H_{34}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C 12 12	0	0

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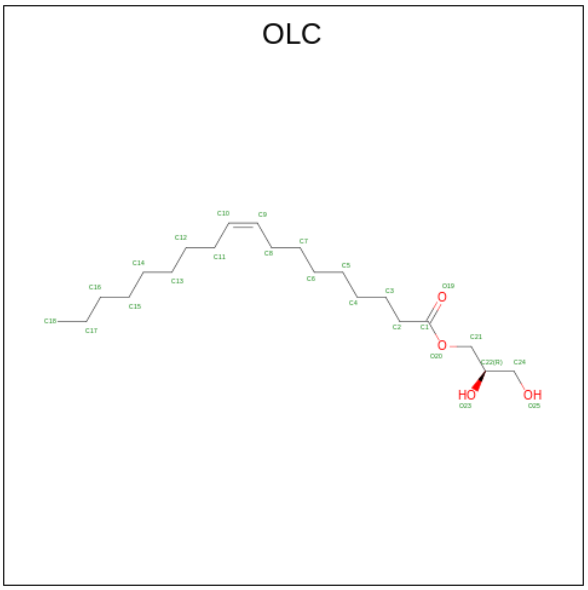
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C 12 12	0	0
3	A	1	Total C 8 8	0	0
3	A	1	Total C O 20 18 2	0	0
3	A	1	Total C 13 13	0	0
3	B	1	Total C 11 11	0	0
3	B	1	Total C 8 8	0	0
3	B	1	Total C 11 11	0	0
3	B	1	Total C 10 10	0	0
3	B	1	Total C O 17 15 2	0	0

- Molecule 4 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLC) (formula: $C_{21}H_{40}O_4$).



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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 20 18 2	0	0
4	B	1	Total C O 25 21 4	0	0
4	B	1	Total C 17 17	0	0

- Molecule 5 is water.

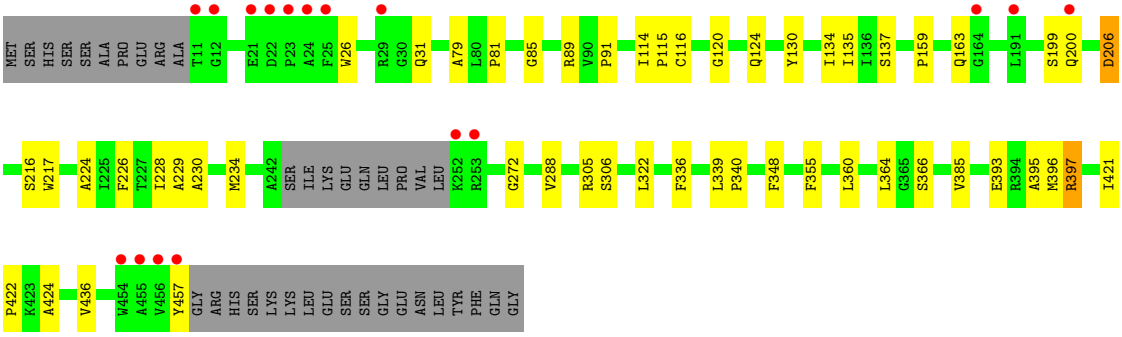
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	48	Total O 48 48	0	0
5	B	56	Total O 56 56	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

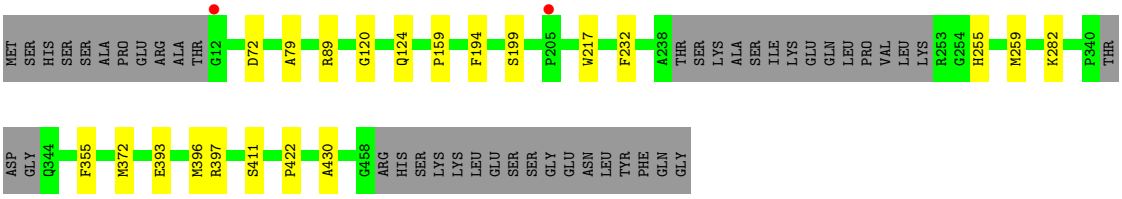
• Molecule 1: Nitrate/nitrite transporter NarK

Chain A: 4% 81% 11% 8%



• Molecule 1: Nitrate/nitrite transporter NarK

Chain B: 86% • 9%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	68.78Å 86.10Å 221.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.35 – 2.40 48.35 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.2 (48.35-2.40) 81.8 (48.35-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.12 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.3_1479)	Depositor
R, R_{free}	0.219 , 0.237 0.221 , 0.237	Depositor DCC
R_{free} test set	2000 reflections (3.47%)	wwPDB-VP
Wilson B-factor (Å^2)	32.0	Xtriage
Anisotropy	0.747	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 51.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6814	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.06% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: OLC, OLA, NO3

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	0.23	0/3359	0.38	0/4572
1	B	0.22	0/3307	0.36	0/4496
All	All	0.23	0/6666	0.37	0/9068

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	3268	0	3265	26	0
1	B	3218	0	3226	13	0
2	A	4	0	0	0	0
2	B	4	0	0	1	0
3	A	65	0	107	2	0
3	B	57	0	85	4	0
4	A	52	0	83	1	0
4	B	42	0	71	1	0
5	A	48	0	0	0	0
5	B	56	0	0	0	0
All	All	6814	0	6837	40	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.

The worst 5 of 40 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:A:124:GLN:HE22	1:A:199:SER:HA	1.52	0.75
1:B:124:GLN:HE22	1:B:199:SER:HA	1.58	0.68
1:A:91:PRO:HB3	3:A:502:OLA:H171	1.77	0.66
1:A:159:PRO:HB2	1:A:396:MET:HB3	1.77	0.65
1:A:385:VAL:HG11	1:A:395:ALA:HA	1.87	0.57

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	434/475 (91%)	426 (98%)	8 (2%)	0	100	100
1	B	424/475 (89%)	414 (98%)	10 (2%)	0	100	100
All	All	858/950 (90%)	840 (98%)	18 (2%)	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	326/372 (88%)	318 (98%)	8 (2%)	47	67
1	B	322/372 (87%)	320 (99%)	2 (1%)	86	94
All	All	648/744 (87%)	638 (98%)	10 (2%)	65	80

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	457	TYR
1	B	355	PHE
1	B	372	MET
1	A	355	PHE
1	A	360	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	284	GLN
1	B	124	GLN
1	B	170	ASN
1	A	146	ASN
1	A	124	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

17 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	$\#\|Z\| > 2$
4	OLC	B	507	-	24,24,24	1.08	2 (8%)	25,25,25	0.92	1 (4%)
4	OLC	B	508	-	16,16,24	0.84	1 (6%)	15,15,25	0.75	0
3	OLA	B	503	-	7,7,19	0.27	0	6,6,19	0.47	0
3	OLA	A	503	-	11,11,19	0.87	1 (9%)	9,10,19	0.61	0
3	OLA	A	502	-	11,11,19	0.88	1 (9%)	9,10,19	0.55	0
3	OLA	B	502	-	10,10,19	0.91	1 (10%)	8,9,19	0.61	0
3	OLA	B	506	-	16,16,19	0.86	1 (6%)	16,16,19	0.95	1 (6%)
3	OLA	B	505	-	9,9,19	0.95	1 (11%)	8,8,19	0.47	0
3	OLA	B	504	-	10,10,19	0.90	1 (10%)	9,9,19	0.51	0
3	OLA	A	504	-	7,7,19	0.36	0	6,6,19	0.66	0
2	NO3	B	501	-	1,3,3	3.57	1 (100%)	0,3,3	-	-
2	NO3	A	501	-	1,3,3	3.58	1 (100%)	0,3,3	-	-
3	OLA	A	505	-	19,19,19	0.79	1 (5%)	19,19,19	0.93	0
4	OLC	A	507	-	6,6,24	0.27	0	5,5,25	0.68	0
4	OLC	A	509	-	19,19,24	0.94	2 (10%)	19,19,25	1.04	0
3	OLA	A	506	-	12,12,19	0.81	1 (8%)	11,11,19	0.58	0
4	OLC	A	508	-	24,24,24	1.08	2 (8%)	25,25,25	1.00	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
4	OLC	B	507	-	-	8/24/24/24	-
4	OLC	B	508	-	-	5/14/14/24	-
3	OLA	B	503	-	-	4/5/5/17	-
3	OLA	A	503	-	-	4/9/9/17	-
3	OLA	A	502	-	-	5/9/9/17	-
3	OLA	B	502	-	-	6/8/8/17	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OLA	B	506	-	-	7/14/14/17	-
3	OLA	B	505	-	-	5/7/7/17	-
3	OLA	B	504	-	-	5/8/8/17	-
3	OLA	A	504	-	-	3/5/5/17	-
3	OLA	A	505	-	-	6/17/17/17	-
4	OLC	A	507	-	-	0/4/4/24	-
4	OLC	A	509	-	-	2/17/17/24	-
3	OLA	A	506	-	-	5/10/10/17	-
4	OLC	A	508	-	-	11/24/24/24	-

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	NO3	O1-N	3.58	1.40	1.24
2	B	501	NO3	O1-N	3.57	1.40	1.24
4	B	507	OLC	C9-C10	3.09	1.49	1.31
4	B	508	OLC	C9-C10	3.08	1.49	1.31
4	A	509	OLC	C9-C10	3.07	1.49	1.31

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	508	OLC	O20-C1-C2	2.54	119.88	111.91
4	B	507	OLC	O20-C1-C2	2.40	119.43	111.91
3	B	506	OLA	O2-C1-C2	2.05	120.63	114.03

There are no chirality outliers.

5 of 76 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	503	OLA	C7-C8-C9-C10
4	A	508	OLC	C2-C1-O20-C21
4	A	508	OLC	O19-C1-O20-C21
4	B	507	OLC	O20-C21-C22-O23
4	B	507	OLC	O20-C21-C22-C24

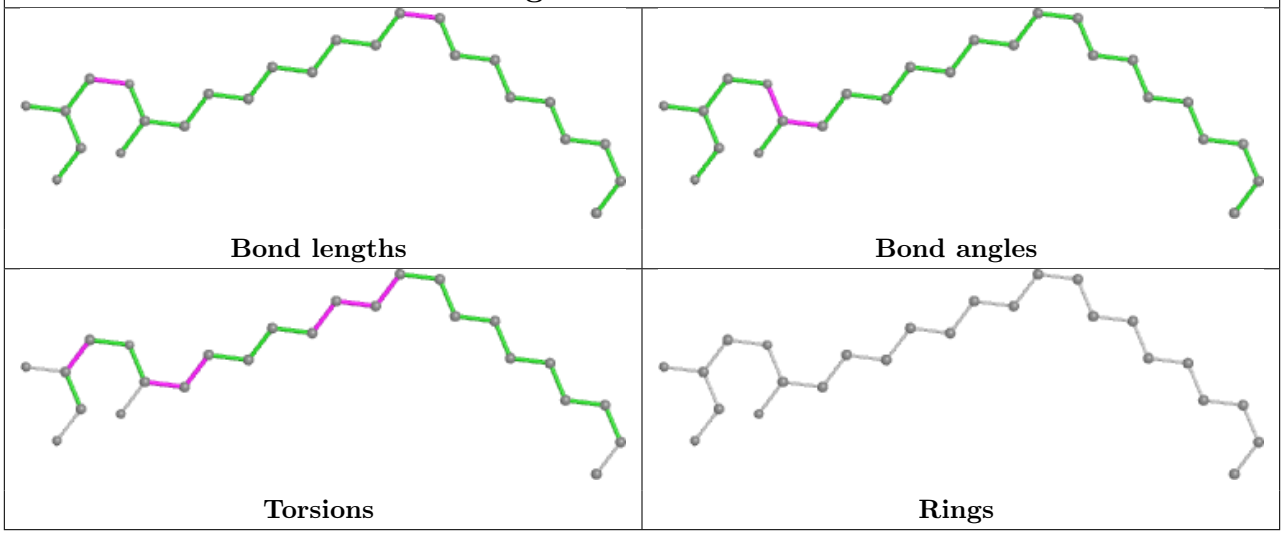
There are no ring outliers.

8 monomers are involved in 8 short contacts:

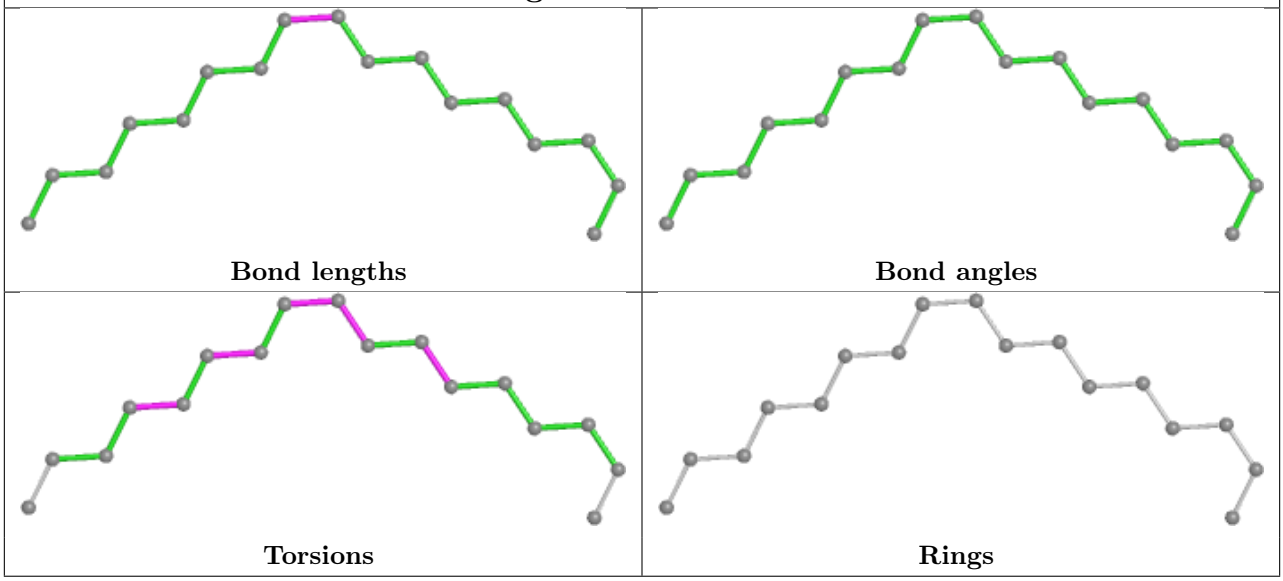
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	508	OLC	1	0
3	B	503	OLA	1	0
3	A	502	OLA	1	0
3	B	502	OLA	1	0
3	B	504	OLA	2	0
2	B	501	NO3	1	0
3	A	506	OLA	1	0
4	A	508	OLC	1	0

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 then 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.

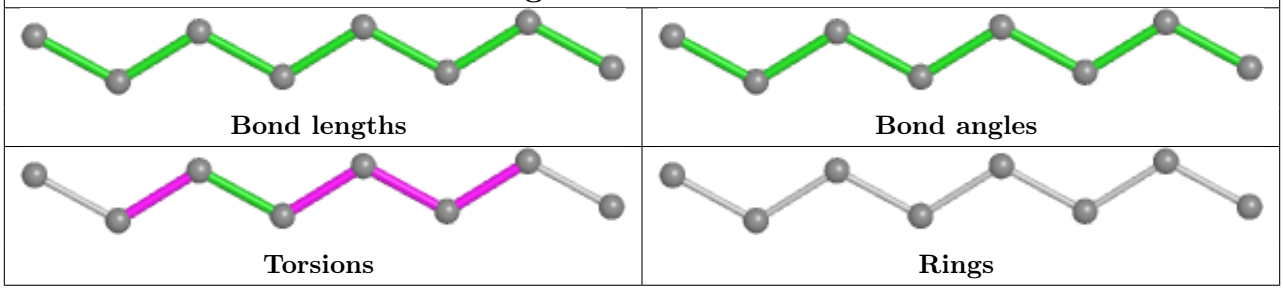
Ligand OLC B 507



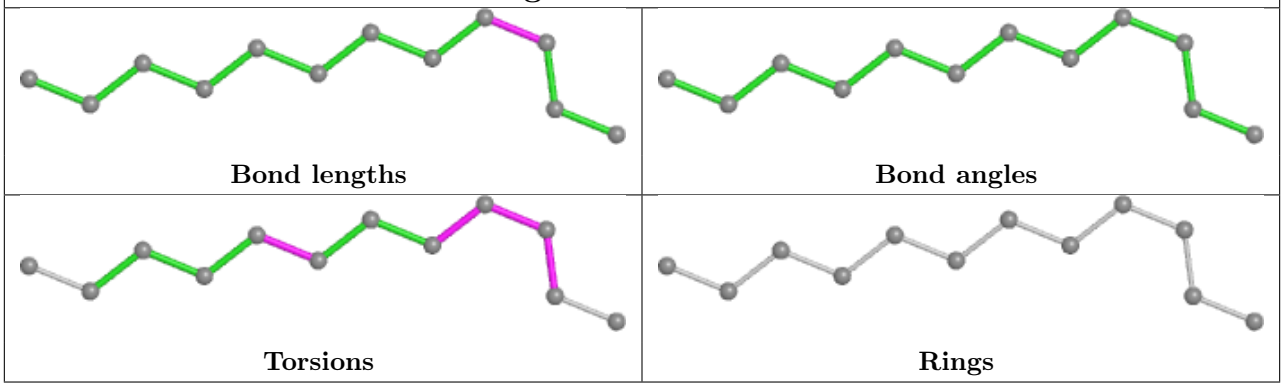
Ligand OLC B 508

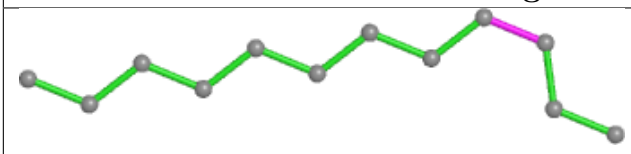
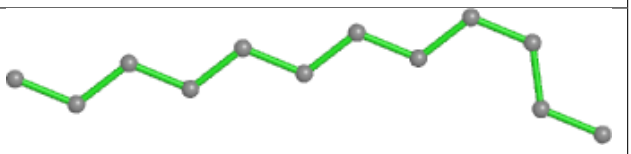
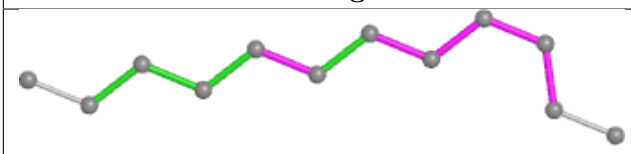
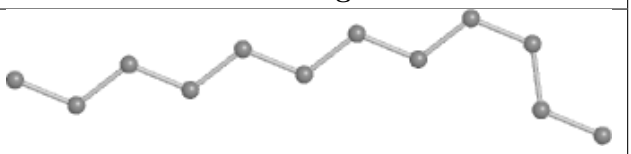


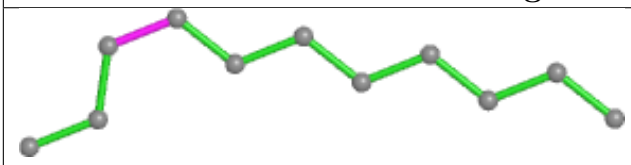
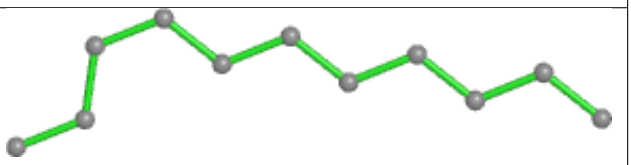
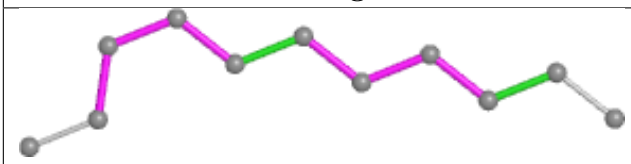
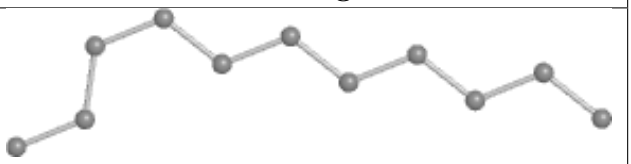
Ligand OLA B 503



Ligand OLA A 503



Ligand OLA A 502	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand OLA B 502	
 Bond lengths	 Bond angles
 Torsions	 Rings

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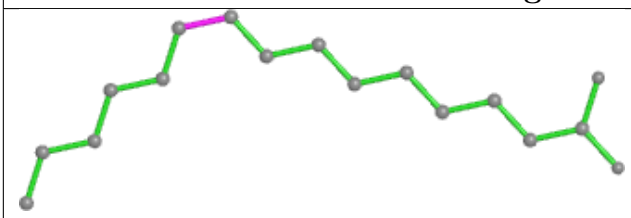
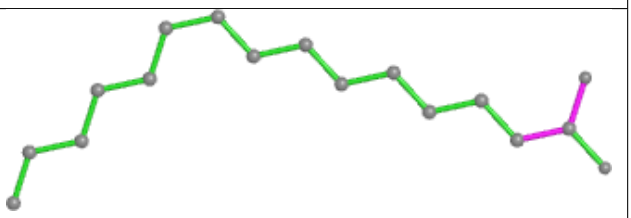
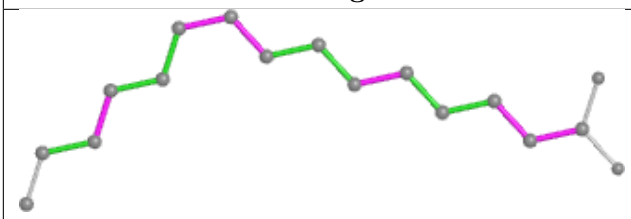
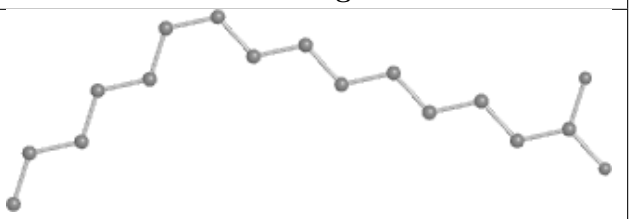
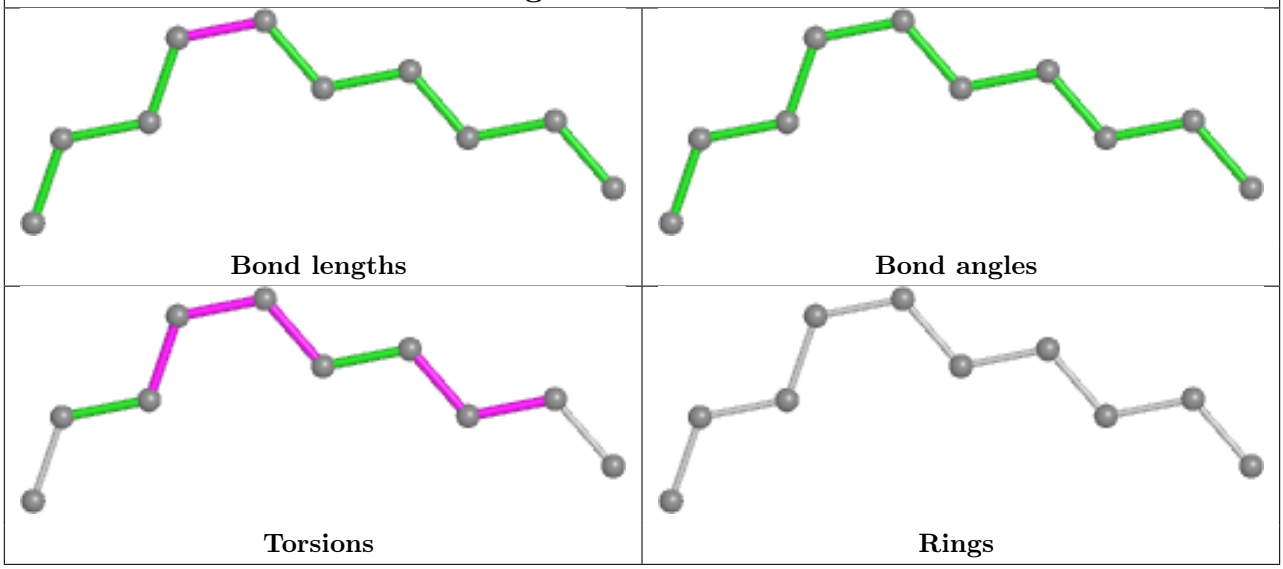
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand OLA B 505



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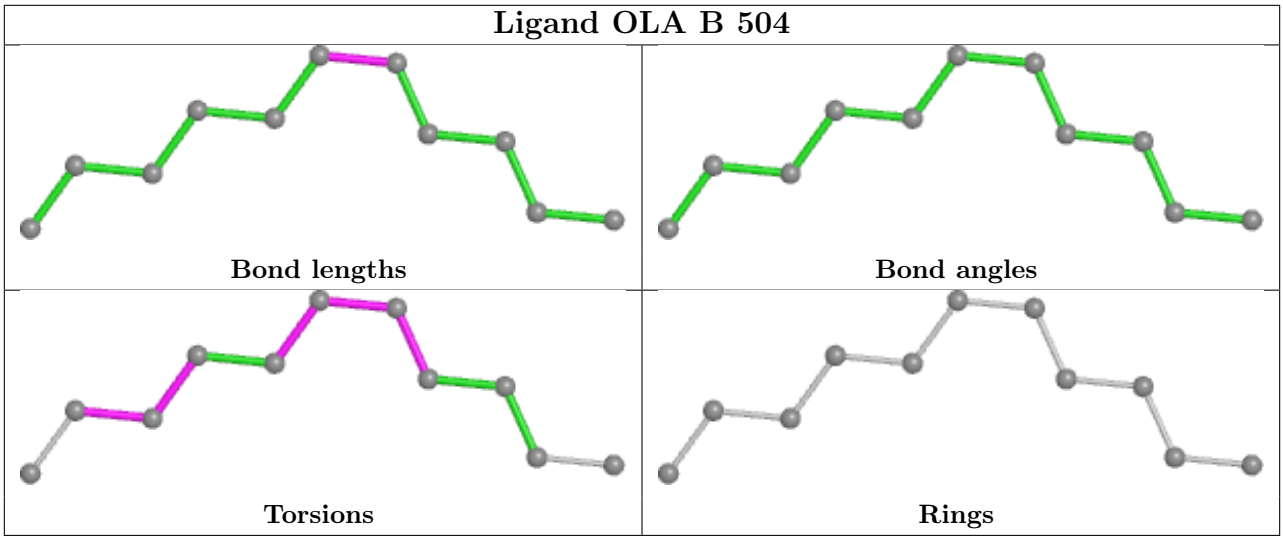
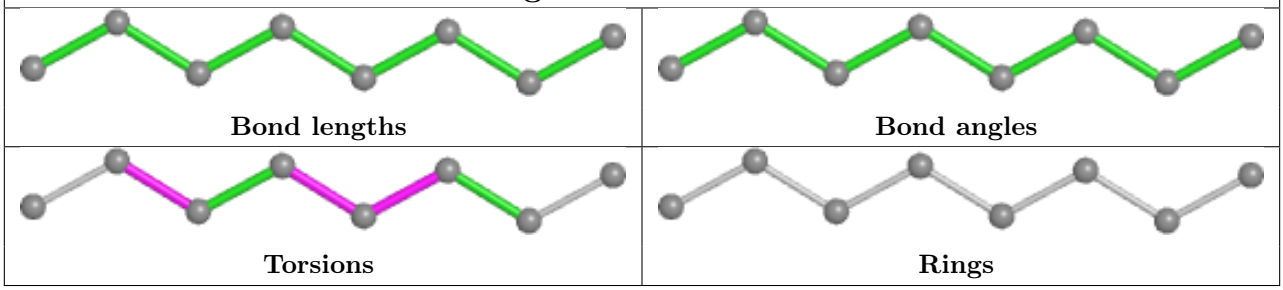
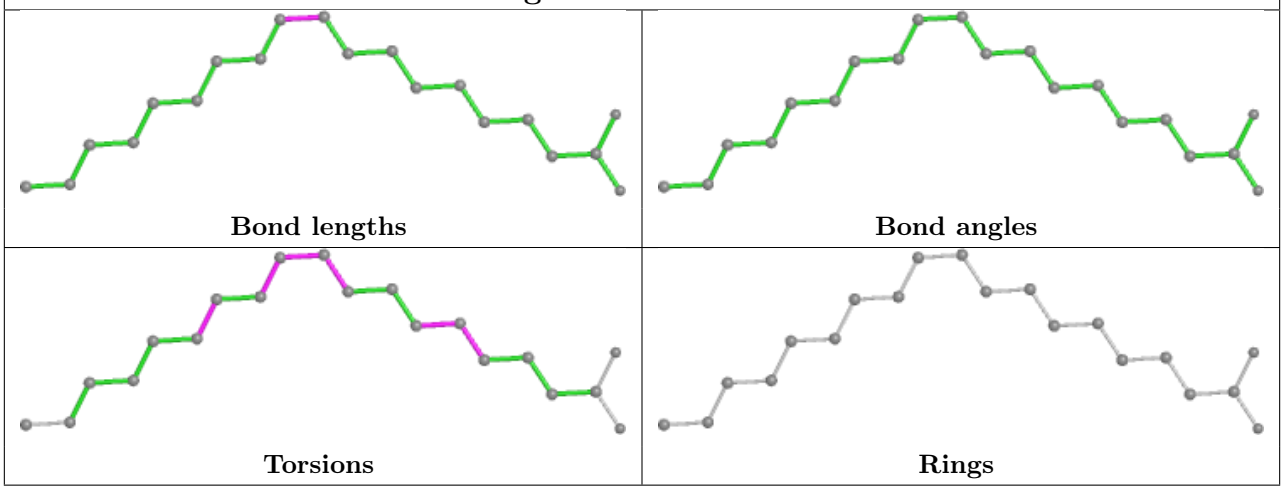


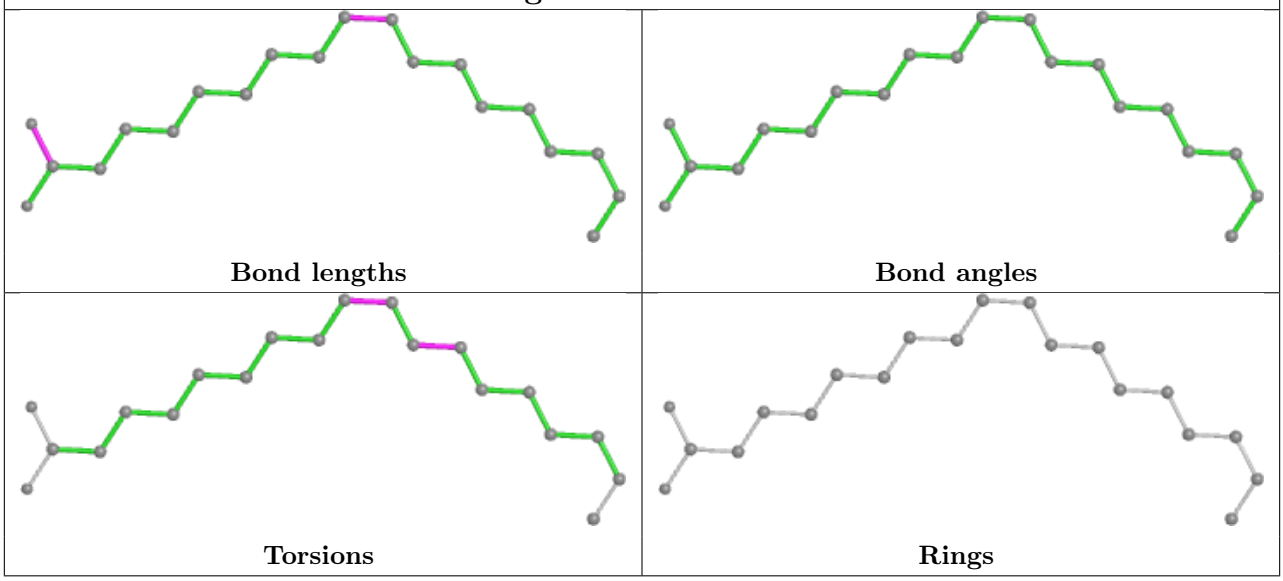
Ligand OLA A 504



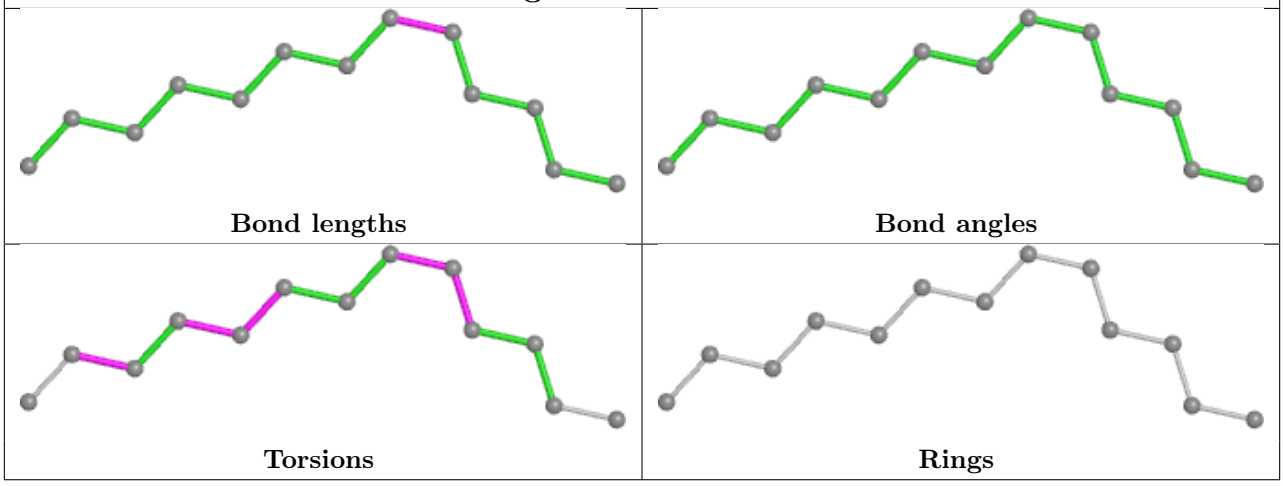
Ligand OLA A 505

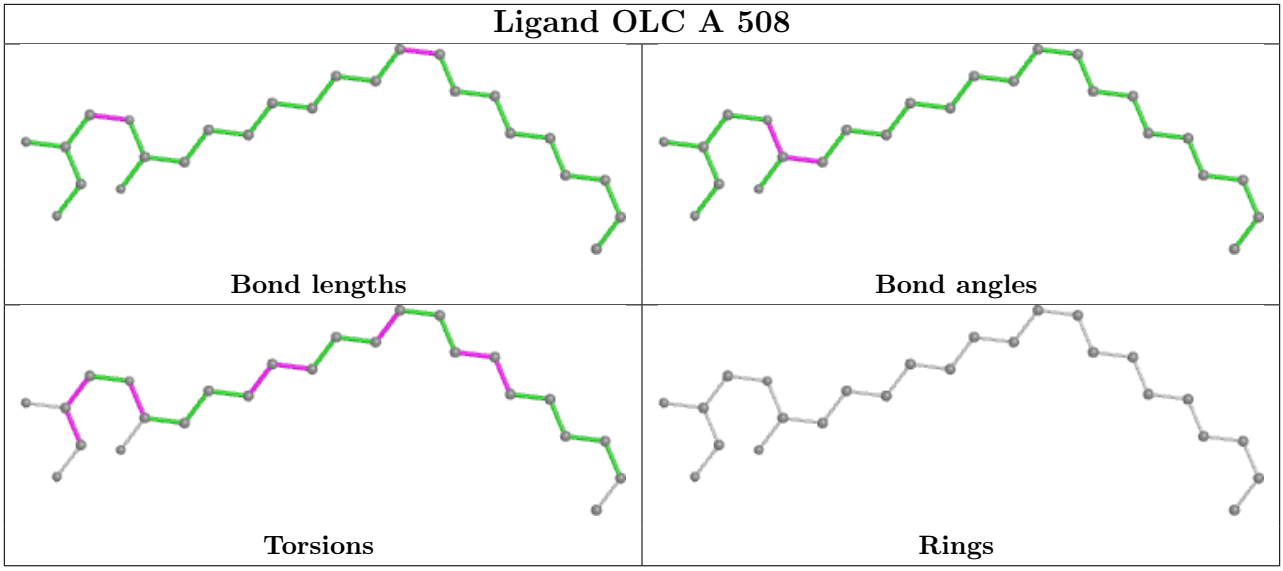


Ligand OLC A 509



Ligand OLA A 506





5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	438/475 (92%)	-0.12	17 (3%)	39	38	37, 47, 77, 115	0
1	B	430/475 (90%)	-0.12	2 (0%)	91	89	36, 51, 75, 101	0
All	All	868/950 (91%)	-0.12	19 (2%)	62	60	36, 49, 76, 115	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	164	GLY	5.4
1	A	457	TYR	4.8
1	A	454	TRP	4.1
1	A	456	VAL	4.1
1	A	24	ALA	3.8

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

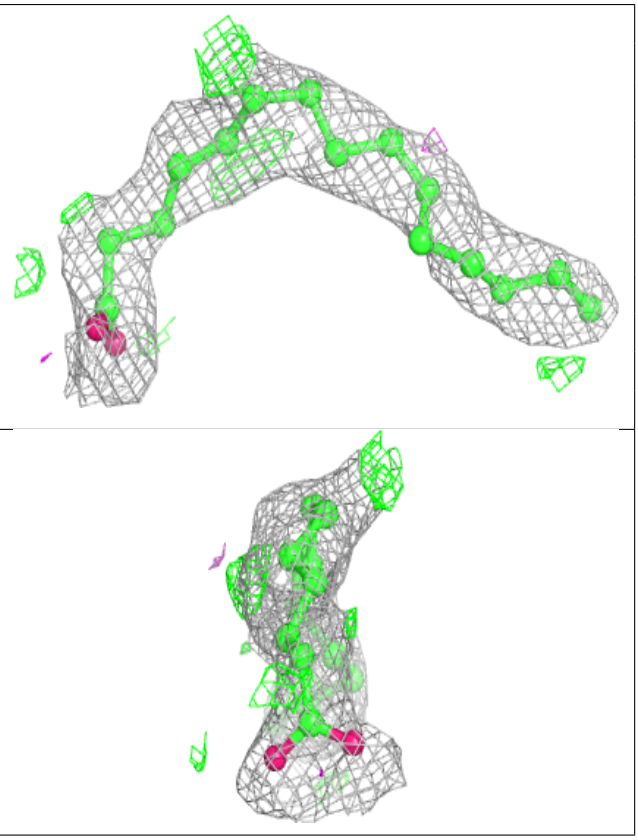
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	OLC	A	507	7/25	0.60	0.28	63,64,66,67	0
3	OLA	B	506	17/20	0.74	0.30	59,66,83,84	0
3	OLA	B	505	10/20	0.75	0.29	67,73,75,75	0
4	OLC	B	507	25/25	0.75	0.25	48,62,86,88	0
4	OLC	B	508	17/25	0.78	0.29	61,69,75,75	0
3	OLA	A	506	13/20	0.80	0.20	55,58,63,63	0
3	OLA	A	505	20/20	0.80	0.23	40,54,69,75	0
4	OLC	A	508	25/25	0.81	0.21	56,66,80,81	0
3	OLA	A	503	12/20	0.84	0.26	61,63,66,69	0
3	OLA	A	502	12/20	0.85	0.31	54,60,65,68	0
3	OLA	A	504	8/20	0.85	0.19	53,56,59,60	0
2	NO3	B	501	4/4	0.86	0.26	42,43,44,47	4
3	OLA	B	504	11/20	0.87	0.17	45,54,60,60	0
3	OLA	B	502	11/20	0.88	0.24	59,61,65,66	0
3	OLA	B	503	8/20	0.90	0.32	67,70,71,71	0
2	NO3	A	501	4/4	0.92	0.21	44,44,44,46	4
4	OLC	A	509	20/25	0.92	0.22	38,47,73,73	0

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

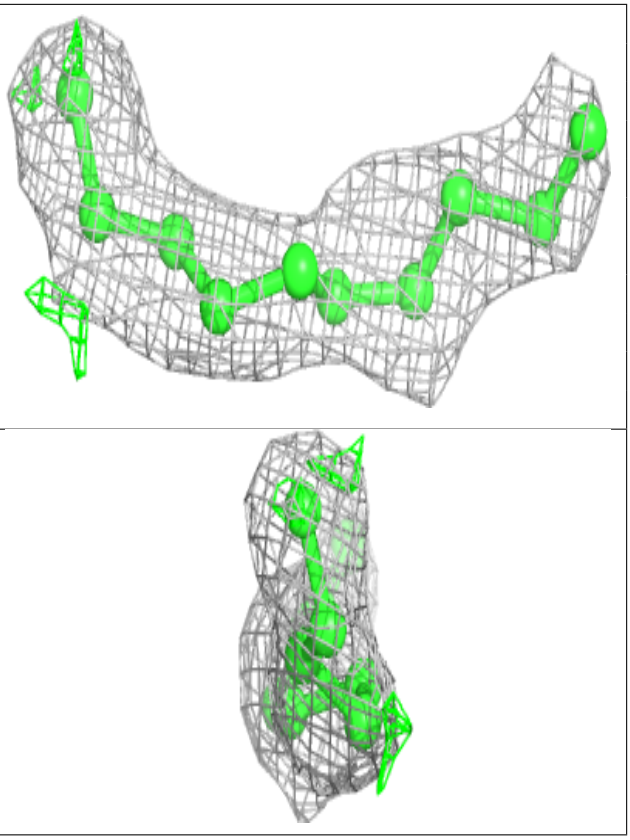
Electron density around OLA B 506:

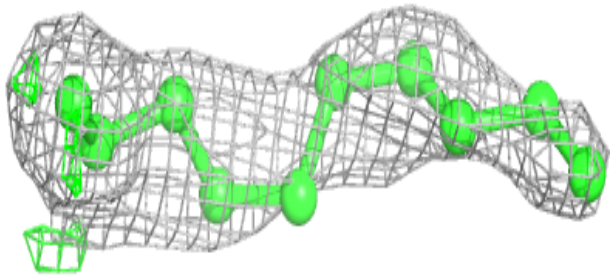
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)



Electron density around OLA B 505:

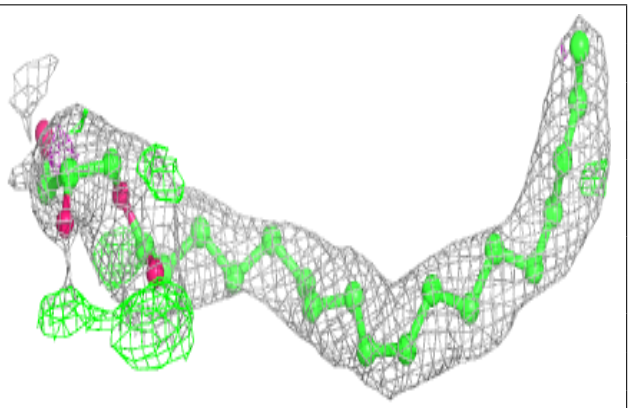
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

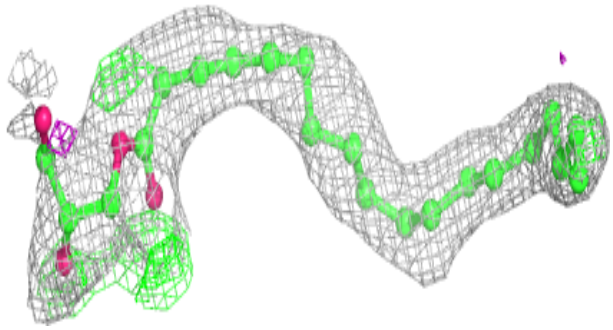


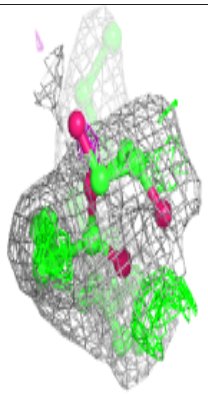


Electron density around OLC B 507:

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

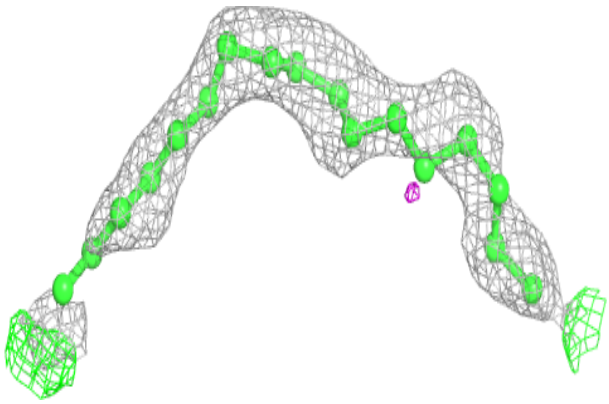


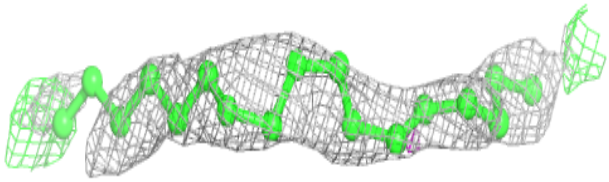


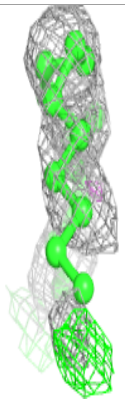


Electron density around OLC B 508:

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

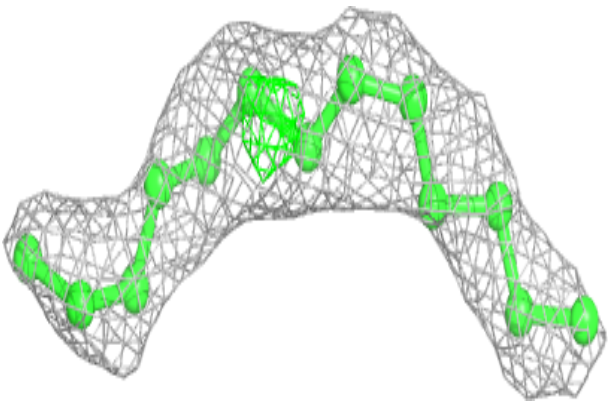


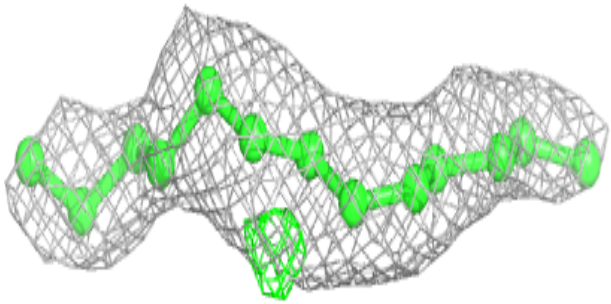


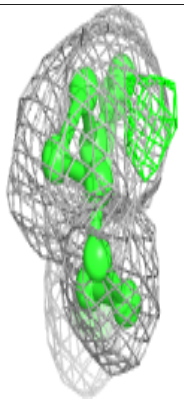


Electron density around OLA A 506:

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

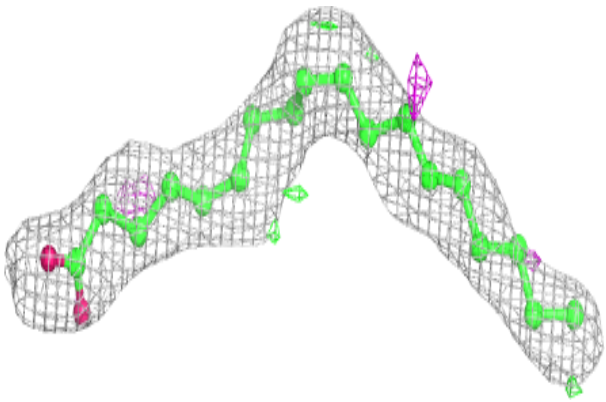


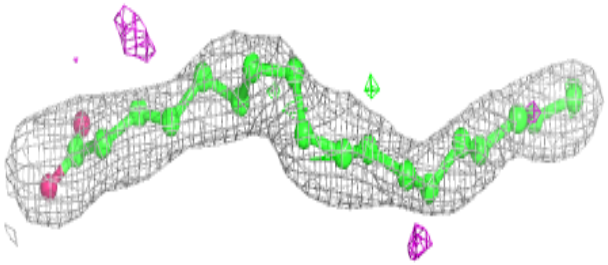


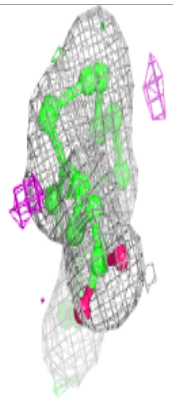


Electron density around OLA A 505:

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

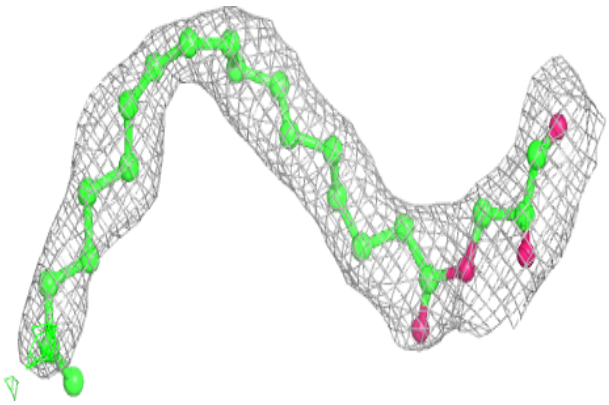


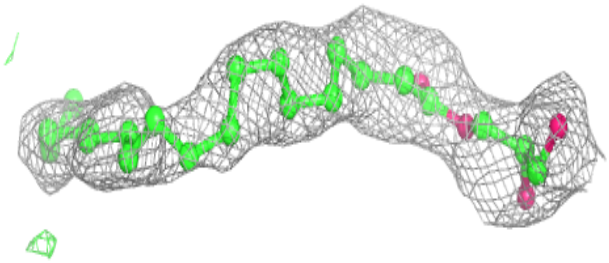


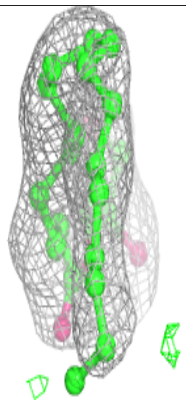


Electron density around OLC A 508:

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







Electron density around OLA A 503:

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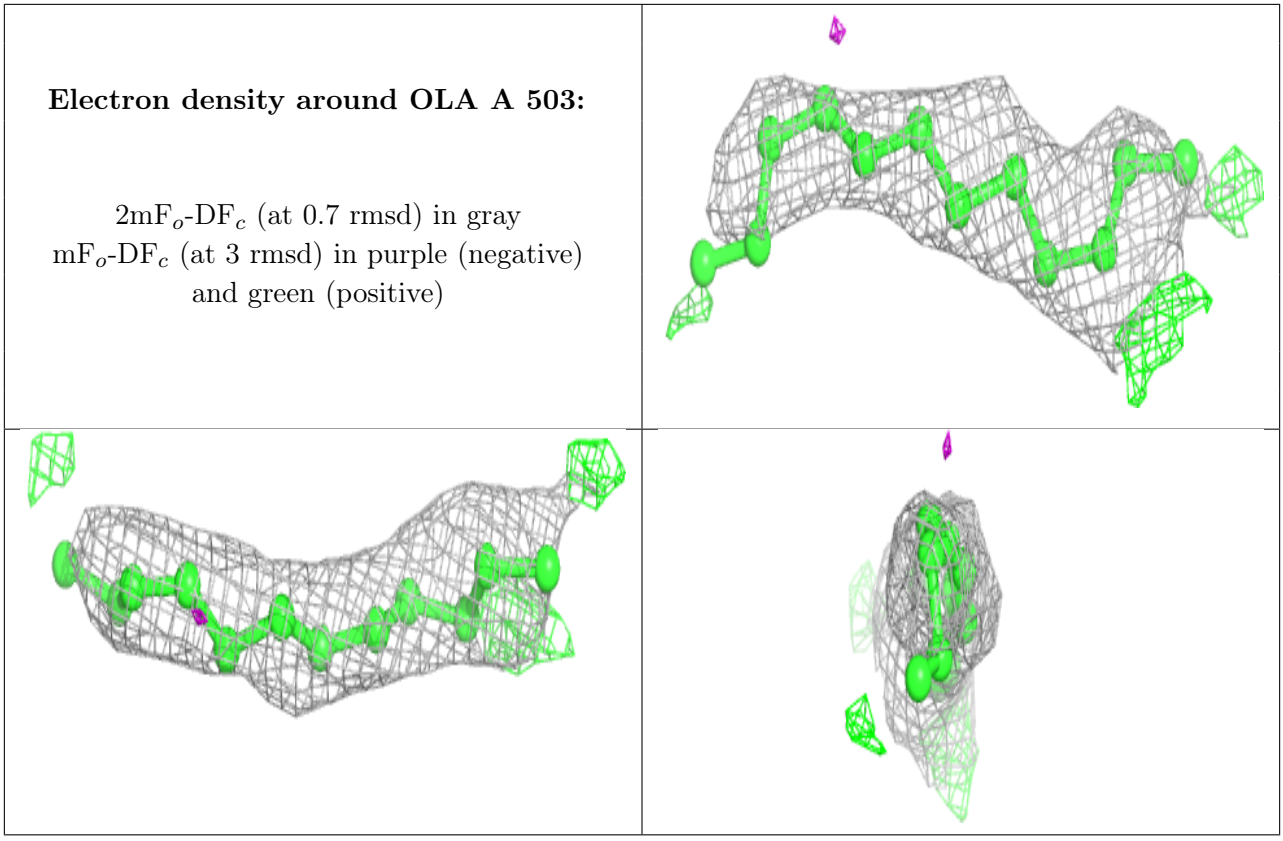
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around OLA A 502:

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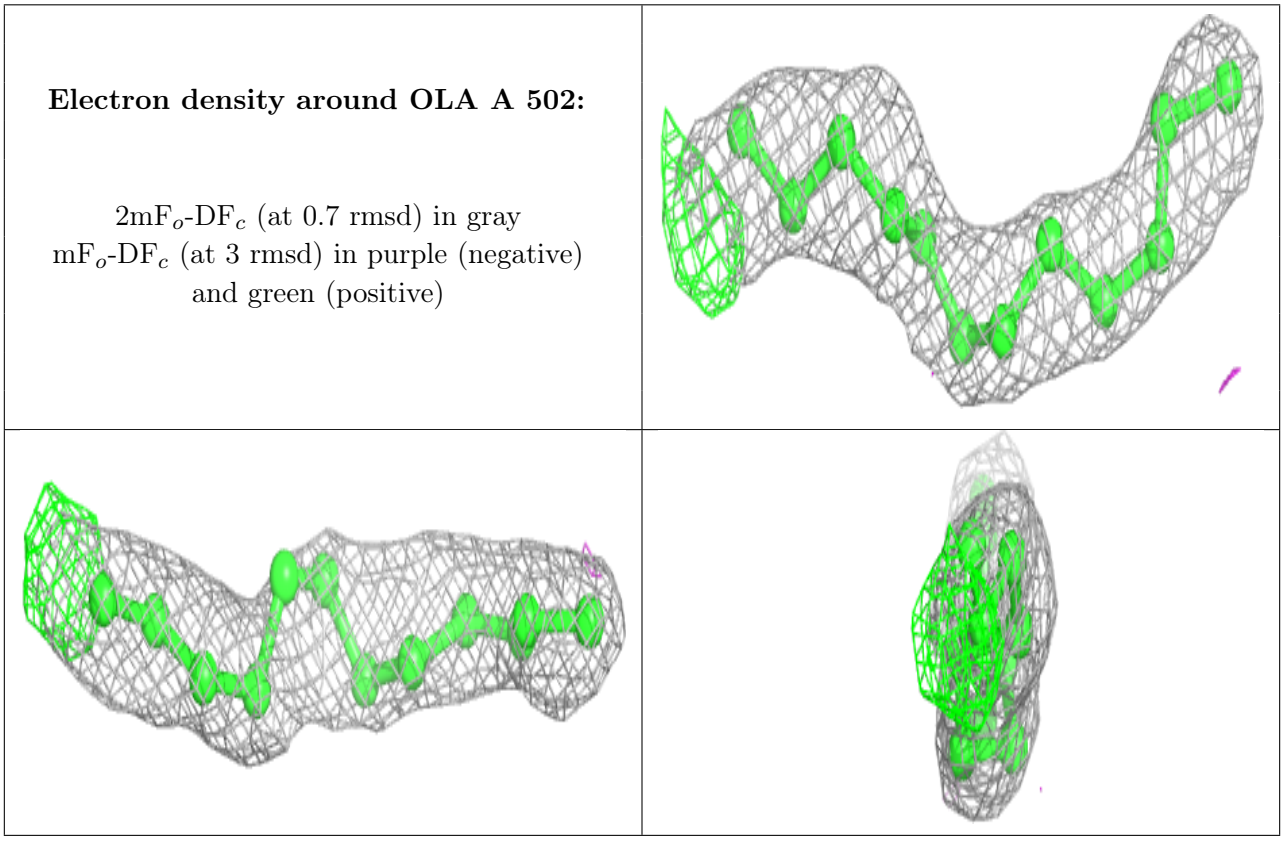
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around OLA A 504:

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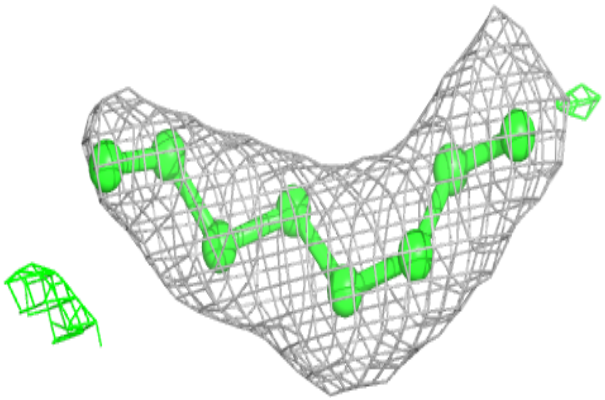
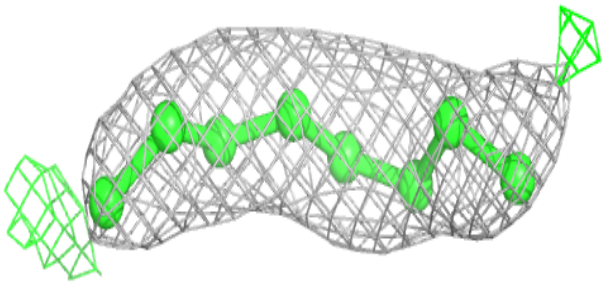
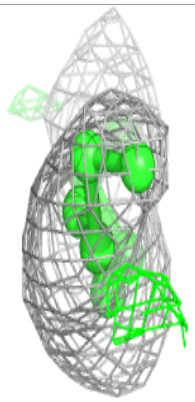
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

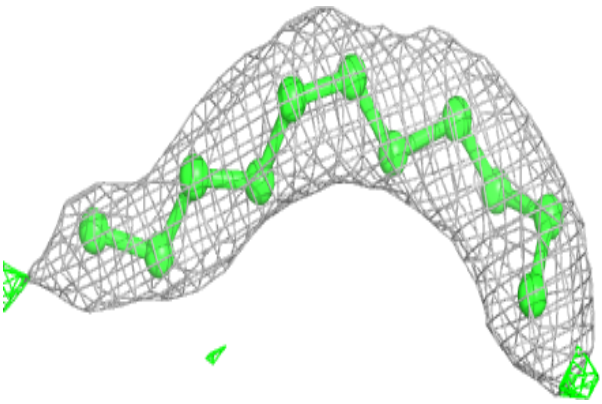


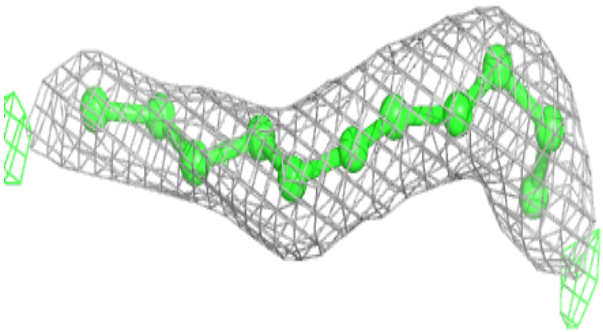


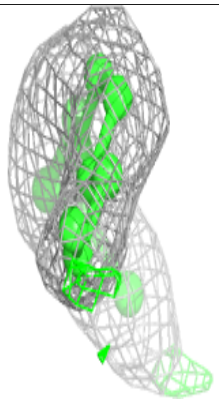


Electron density around OLA B 504:

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

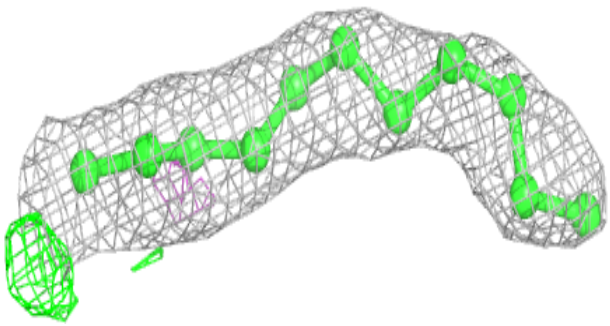


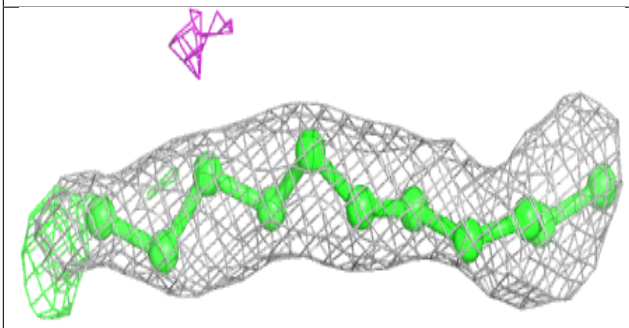


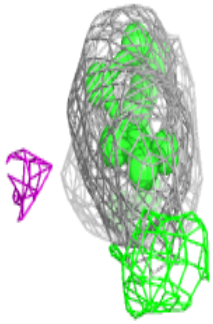


Electron density around OLA B 502:

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

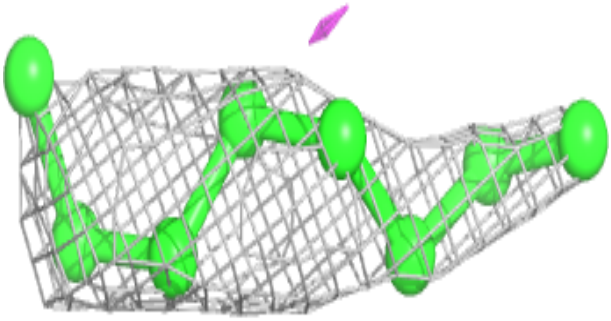


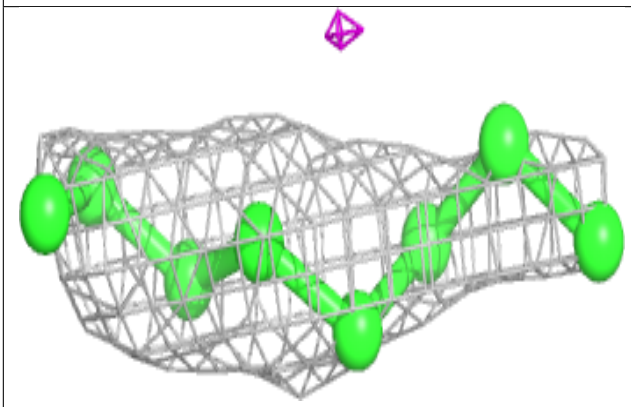


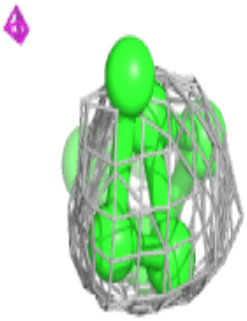


Electron density around OLA B 503:

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

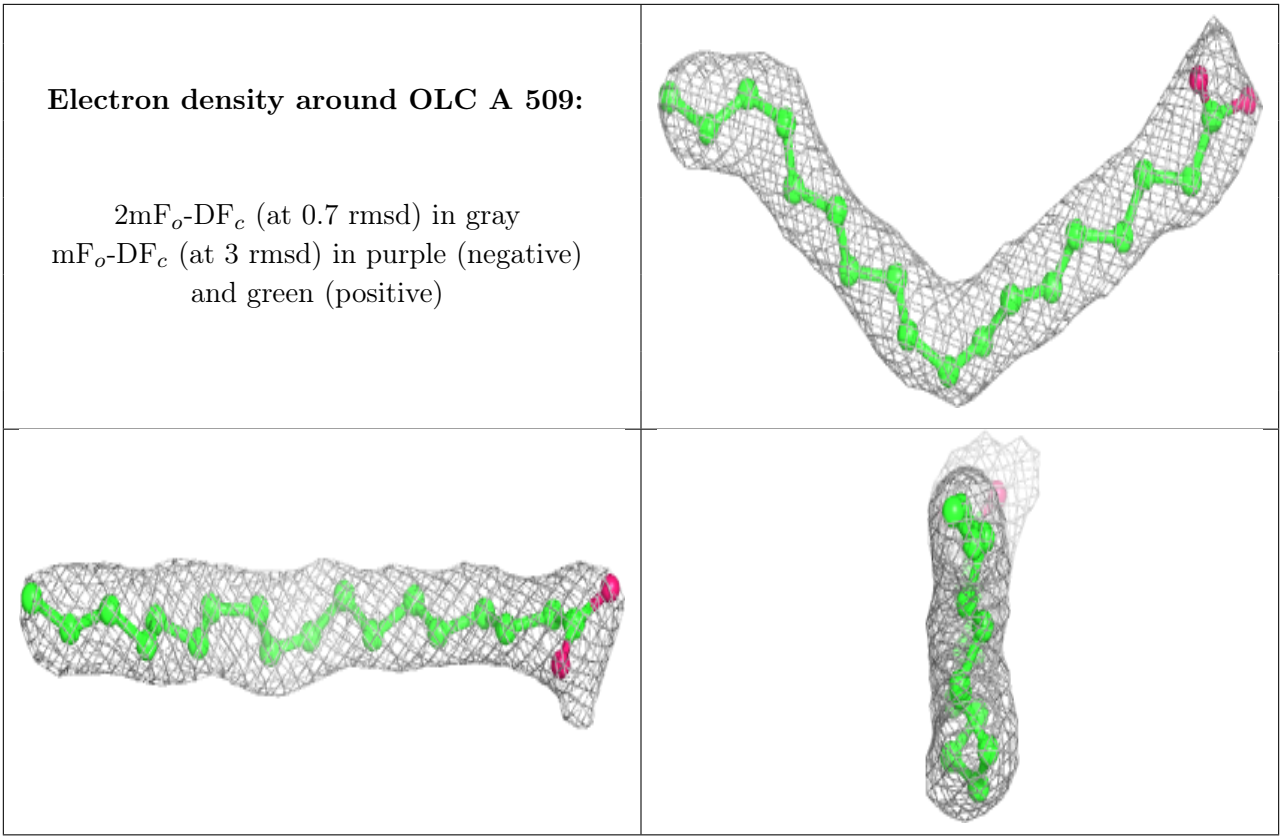






Electron density around OLC A 509:

$2mF_o$-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.