Full wwPDB X-ray Structure Validation Report (i)

Jan 3, 2024 – 02:38 pm GMT

PDB ID	:	5FJG
Title	:	The crystal structure of light-driven chloride pump ClR in pH 4.5.
Authors	:	Kim, K.L.; Kwon, S.K.; Jun, S.H.; Cha, J.S.; Kim, H.Y.; Kim, J.H.; Cho, H.S.
Deposited on	:	2015-10-07
Resolution	:	2.00 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 (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:

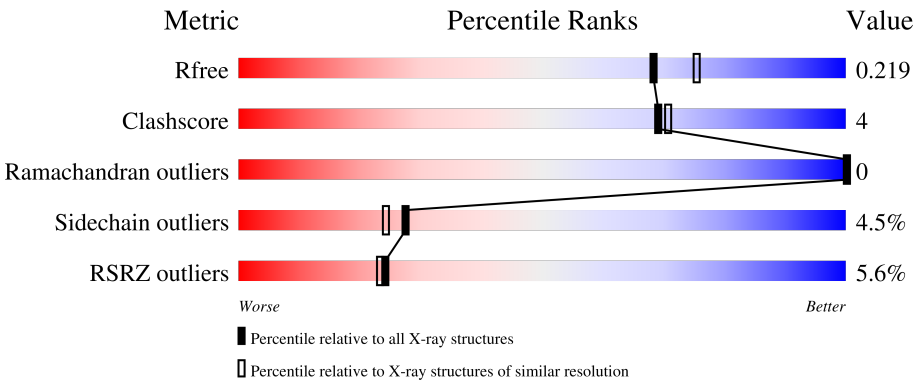
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
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 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	275	5% 88% 9% • •

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4578 atoms, of which 2265 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.

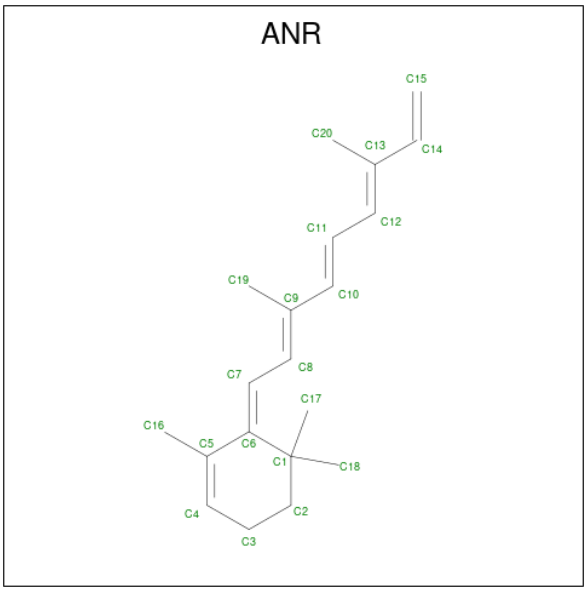
- Molecule 1 is a protein called CHLORIDE PUMPING RHODOPSIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	269	4242	1397	2137	327	366	15	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	PRO	-	expression tag	UNP W8VZW3
A	-1	ASN	-	expression tag	UNP W8VZW3
A	0	SER	-	expression tag	UNP W8VZW3

- Molecule 2 is ANHYDRORETINOL (three-letter code: ANR) (formula: $C_{20}H_{28}$).

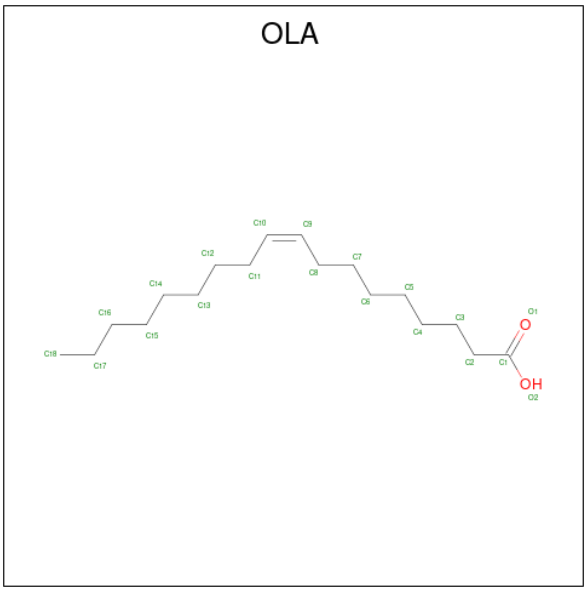


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	H		
2	A	1	49	20	29	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	3	Total Cl 3 3	0	0

- Molecule 4 is OLEIC ACID (three-letter code: OLA) (formula: $C_{18}H_{34}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C 9 9	0	0
4	A	1	Total C 9 9	0	0
4	A	1	Total C 9 9	0	0
4	A	1	Total C 9 9	0	0
4	A	1	Total C H O 31 11 18 2	0	0
4	A	1	Total C H O 37 13 22 2	0	0
4	A	1	Total C H O 53 18 33 2	0	0
4	A	1	Total C H O 43 15 26 2	0	0

- Molecule 5 is water.

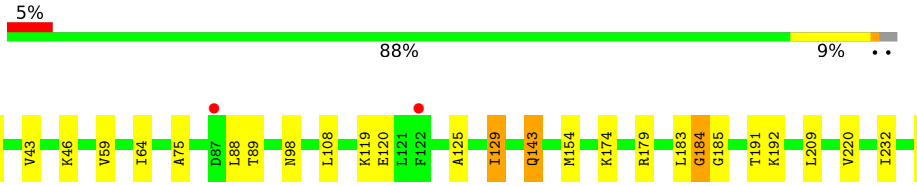
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	84	84	84	0	0

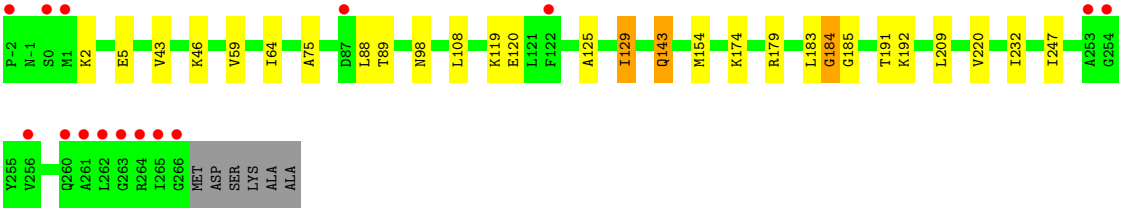
3 Residue-property plots (i)

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: CHLORIDE PUMPING RHODOPSIN

Chain A:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	77.03Å 49.43Å 77.91Å 90.00° 96.94° 90.00°	Depositor
Resolution (Å)	38.67 – 2.00 38.67 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.2 (38.67-2.00) 96.2 (38.67-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.22 (at 2.00Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.167 , 0.219 0.171 , 0.219	Depositor DCC
R_{free} test set	1037 reflections (5.26%)	wwPDB-VP
Wilson B-factor (Å^2)	25.5	Xtriage
Anisotropy	0.160	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.42 , 63.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.014 for l,-k,h	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4578	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.11% 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: ANR, OLA, CL

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	0.59	1/2158 (0.0%)	0.67	1/2941 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	143	GLN	CB-CG	-5.70	1.37	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	184	GLY	N-CA-C	7.42	131.64	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	184	GLY	Peptide

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	2105	2137	2138	16	1
2	A	20	29	27	1	0
3	A	3	0	0	1	0
4	A	101	99	149	3	0
5	A	84	0	0	2	0
All	All	2313	2265	2314	17	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (17) 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:174:LYS:HE2	4:A:1269:OLA:H31	1.71	0.72
1:A:125:ALA:O	1:A:129:ILE:HG23	1.94	0.66
1:A:75:ALA:HB2	1:A:89:THR:HG22	1.78	0.65
1:A:43:VAL:HG22	1:A:247:ILE:HD13	1.80	0.63
2:A:1266:ANR:H182	2:A:1266:ANR:H8	1.80	0.63
1:A:75:ALA:HB2	1:A:89:THR:CG2	2.32	0.59
1:A:185:GLY:HA2	5:A:2079:HOH:O	2.03	0.58
1:A:43:VAL:HG22	1:A:247:ILE:CD1	2.34	0.58
1:A:120:GLU:HG3	4:A:1269:OLA:C8	2.39	0.51
1:A:120:GLU:HG3	4:A:1269:OLA:H81	1.92	0.51
1:A:179:ARG:HD3	1:A:191:THR:CG2	2.42	0.49
1:A:46:LYS:HB2	3:A:1268:CL:CL	2.55	0.44
1:A:2:LYS:NZ	5:A:2063:HOH:O	2.41	0.43
1:A:64:ILE:HG13	1:A:98:ASN:CG	2.39	0.42
1:A:179:ARG:HD3	1:A:191:THR:HG22	2.00	0.42
1:A:5:GLU:HG3	1:A:220:VAL:HG13	2.03	0.41
1:A:75:ALA:CB	1:A:89:THR:HG22	2.49	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:VAL:HG12	1:A:59:VAL:HG12[2_556]	1.34	0.26

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	267/275 (97%)	263 (98%)	4 (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	221/225 (98%)	211 (96%)	10 (4%)	27 24

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	LEU
1	A	108	LEU
1	A	119	LYS
1	A	129	ILE
1	A	143	GLN
1	A	154	MET
1	A	183	LEU
1	A	192	LYS

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Mol	Chain	Res	Type
1	A	209	LEU
1	A	232	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

Of 12 ligands modelled in this entry, 3 are monoatomic - leaving 9 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	OLA	A	1273	-	12,12,19	0.94	1 (8%)	12,12,19	1.18	1 (8%)
4	OLA	A	1275	-	19,19,19	0.78	1 (5%)	19,19,19	1.10	1 (5%)
4	OLA	A	1274	-	14,14,19	0.94	1 (7%)	14,14,19	0.95	2 (14%)
4	OLA	A	1272	-	8,8,19	0.29	0	7,7,19	0.42	0
4	OLA	A	1269	-	8,8,19	0.36	0	7,7,19	0.45	0
4	OLA	A	1276	-	16,16,19	0.90	1 (6%)	16,16,19	0.92	1 (6%)
2	ANR	A	1266	1	19,20,20	4.72	10 (52%)	21,27,27	2.18	6 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	OLA	A	1270	-	8,8,19	0.28	0	7,7,19	0.40	0
4	OLA	A	1271	-	8,8,19	0.29	0	7,7,19	0.37	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
4	OLA	A	1273	-	-	7/10/10/17	-
4	OLA	A	1275	-	-	10/17/17/17	-
4	OLA	A	1274	-	-	7/12/12/17	-
4	OLA	A	1272	-	-	1/6/6/17	-
4	OLA	A	1269	-	-	4/6/6/17	-
4	OLA	A	1276	-	-	7/14/14/17	-
2	ANR	A	1266	1	-	5/13/30/30	0/1/1/1
4	OLA	A	1270	-	-	4/6/6/17	-
4	OLA	A	1271	-	-	3/6/6/17	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1266	ANR	C4-C5	12.94	1.51	1.33
2	A	1266	ANR	C8-C9	8.22	1.46	1.35
2	A	1266	ANR	C12-C13	6.93	1.45	1.35
2	A	1266	ANR	C7-C6	5.98	1.47	1.36
2	A	1266	ANR	C14-C13	-5.97	1.35	1.46
2	A	1266	ANR	C10-C9	-4.84	1.35	1.45
2	A	1266	ANR	C15-C14	3.71	1.48	1.30
2	A	1266	ANR	C11-C10	3.38	1.43	1.34
2	A	1266	ANR	C11-C12	-3.35	1.33	1.43
4	A	1276	OLA	C10-C9	2.79	1.48	1.31
4	A	1274	OLA	C10-C9	2.74	1.47	1.31
4	A	1275	OLA	C10-C9	2.69	1.47	1.31
4	A	1273	OLA	C9-C10	2.40	1.47	1.29
2	A	1266	ANR	C7-C8	-2.06	1.34	1.42

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1266	ANR	C16-C5-C4	-4.90	114.87	123.03
2	A	1266	ANR	C19-C9-C10	4.26	124.79	118.08
2	A	1266	ANR	C15-C14-C13	-4.02	122.35	126.59
2	A	1266	ANR	C19-C9-C8	-3.51	118.00	122.92
4	A	1275	OLA	C3-C2-C1	-3.41	105.87	114.47
2	A	1266	ANR	C20-C13-C12	-3.20	118.44	122.92
4	A	1273	OLA	O2-C1-C2	2.44	121.86	114.03
4	A	1276	OLA	O2-C1-C2	2.38	121.68	114.03
4	A	1274	OLA	O2-C1-O1	-2.28	117.61	123.30
4	A	1274	OLA	O2-C1-C2	2.19	121.06	114.03
2	A	1266	ANR	C11-C12-C13	2.11	130.31	127.31

There are no chirality outliers.

All (48) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1266	ANR	C11-C10-C9-C19
2	A	1266	ANR	C1-C6-C7-C8
4	A	1274	OLA	C10-C11-C12-C13
4	A	1269	OLA	C4-C5-C6-C7
4	A	1273	OLA	C2-C3-C4-C5
4	A	1273	OLA	C1-C2-C3-C4
4	A	1276	OLA	C1-C2-C3-C4
4	A	1270	OLA	C3-C4-C5-C6
4	A	1275	OLA	C5-C6-C7-C8
4	A	1269	OLA	C3-C4-C5-C6
4	A	1276	OLA	C2-C3-C4-C5
4	A	1276	OLA	C5-C6-C7-C8
4	A	1272	OLA	C3-C4-C5-C6
4	A	1271	OLA	C6-C7-C8-C9
4	A	1275	OLA	C2-C3-C4-C5
4	A	1274	OLA	C2-C3-C4-C5
4	A	1276	OLA	C6-C7-C8-C9
4	A	1274	OLA	C11-C10-C9-C8
4	A	1270	OLA	C6-C7-C8-C9
4	A	1274	OLA	C6-C7-C8-C9
4	A	1275	OLA	C11-C12-C13-C14
4	A	1275	OLA	C11-C10-C9-C8
2	A	1266	ANR	C7-C8-C9-C10
4	A	1275	OLA	C13-C14-C15-C16
4	A	1276	OLA	C11-C10-C9-C8
4	A	1271	OLA	C4-C5-C6-C7
4	A	1269	OLA	C5-C6-C7-C8

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Mol	Chain	Res	Type	Atoms
2	A	1266	ANR	C11-C10-C9-C8
4	A	1274	OLA	C3-C4-C5-C6
2	A	1266	ANR	C7-C8-C9-C19
4	A	1269	OLA	C1-C2-C3-C4
4	A	1276	OLA	C12-C13-C14-C15
4	A	1270	OLA	C2-C3-C4-C5
4	A	1275	OLA	C14-C15-C16-C17
4	A	1271	OLA	C2-C3-C4-C5
4	A	1273	OLA	C5-C6-C7-C8
4	A	1275	OLA	O1-C1-C2-C3
4	A	1273	OLA	C7-C8-C9-C10
4	A	1274	OLA	C7-C8-C9-C10
4	A	1275	OLA	O2-C1-C2-C3
4	A	1274	OLA	C9-C10-C11-C12
4	A	1275	OLA	C7-C8-C9-C10
4	A	1275	OLA	C9-C10-C11-C12
4	A	1273	OLA	C4-C5-C6-C7
4	A	1276	OLA	C9-C10-C11-C12
4	A	1270	OLA	C5-C6-C7-C8
4	A	1273	OLA	O1-C1-C2-C3
4	A	1273	OLA	O2-C1-C2-C3

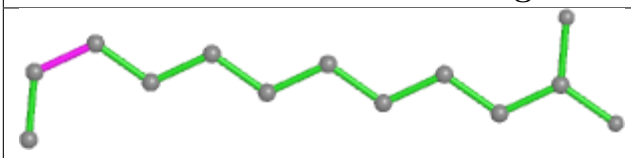
There are no ring outliers.

2 monomers are involved in 4 short contacts:

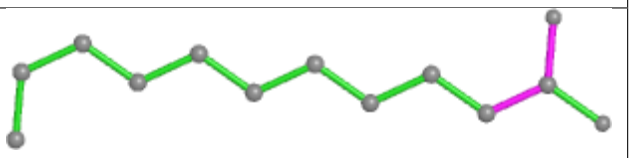
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1269	OLA	3	0
2	A	1266	ANR	1	0

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.

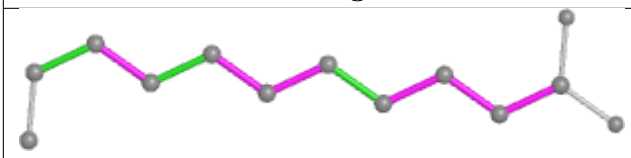
Ligand OLA A 1273



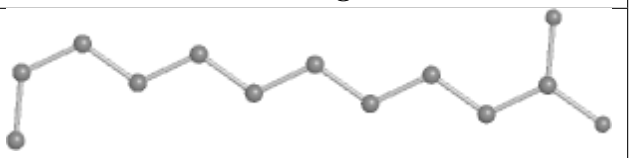
Bond lengths



Bond angles

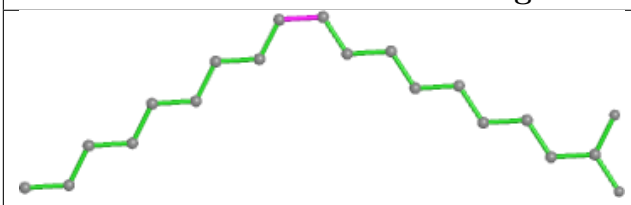


Torsions

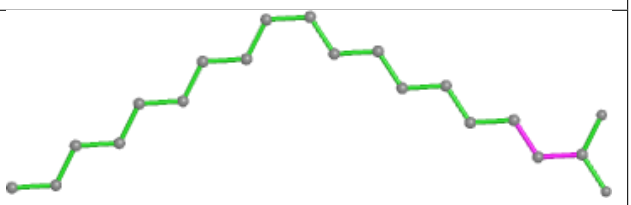


Rings

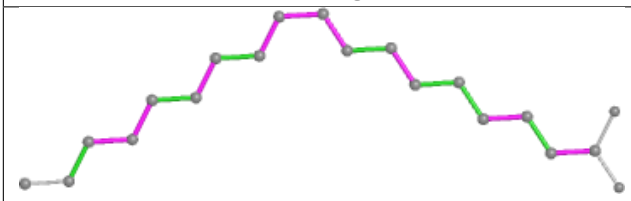
Ligand OLA A 1275



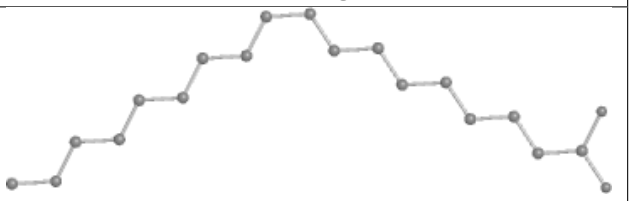
Bond lengths



Bond angles

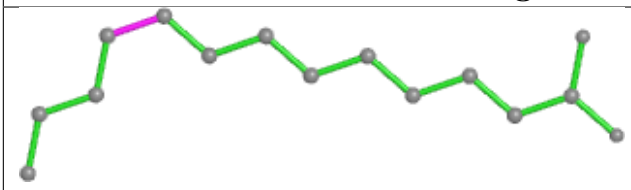


Torsions

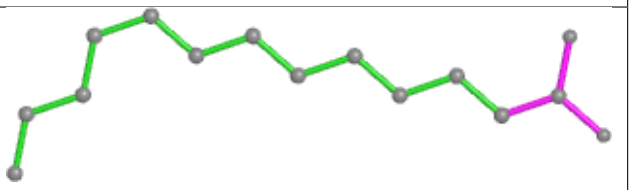


Rings

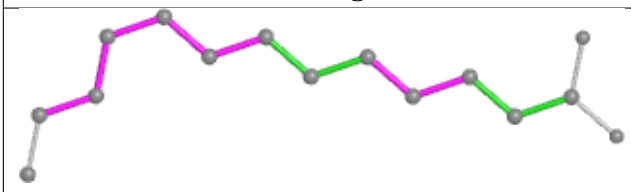
Ligand OLA A 1274



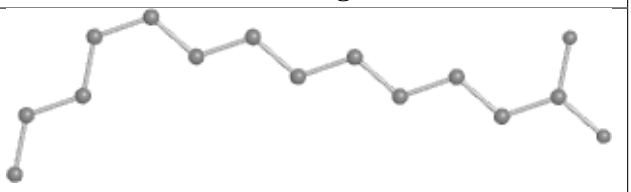
Bond lengths



Bond angles

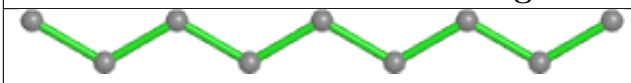


Torsions

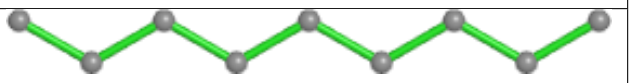


Rings

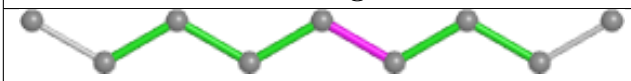
Ligand OLA A 1272



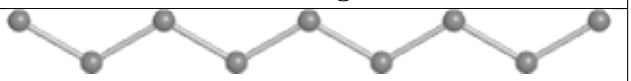
Bond lengths



Bond angles

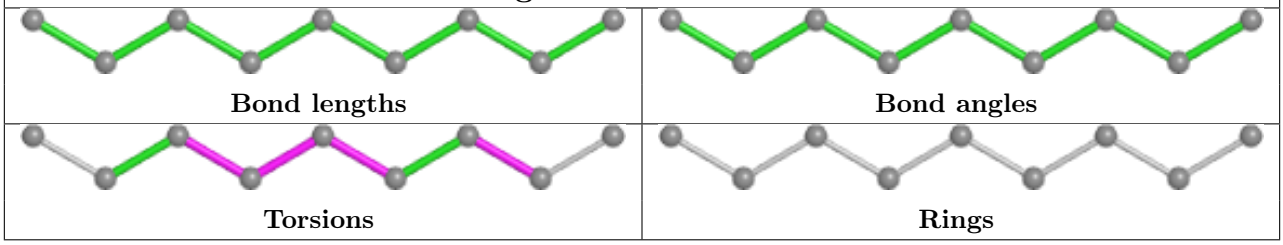


Torsions

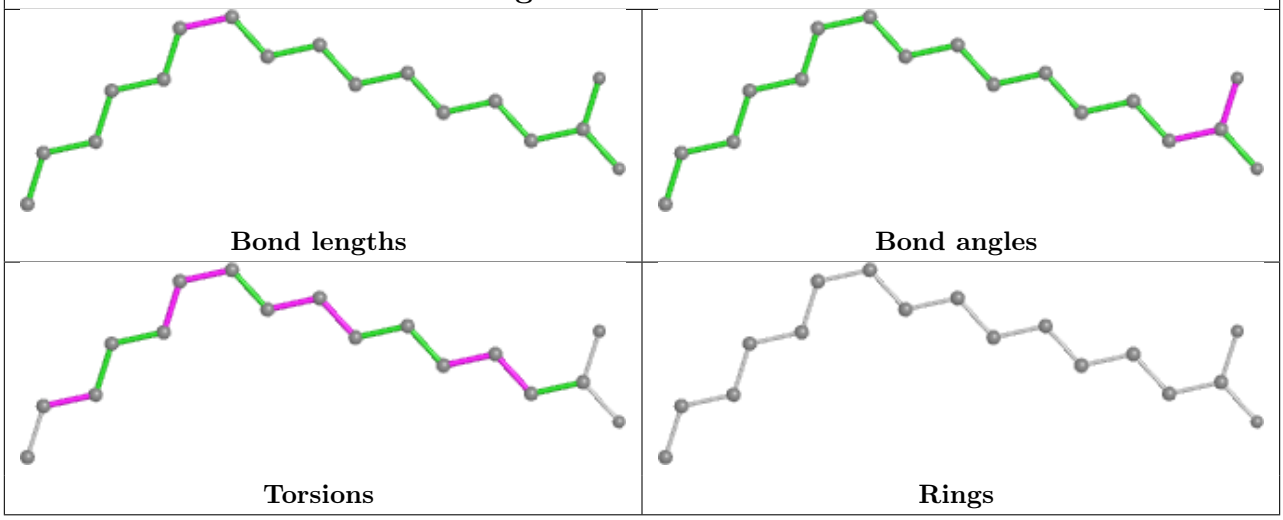


Rings

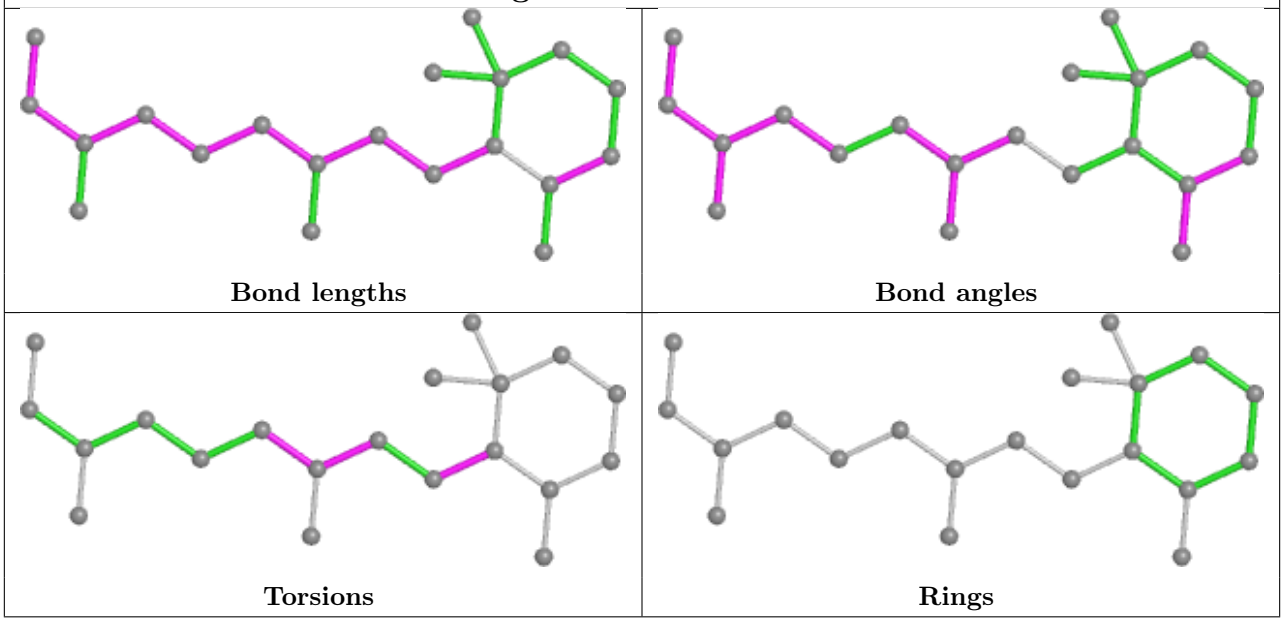
Ligand OLA A 1269



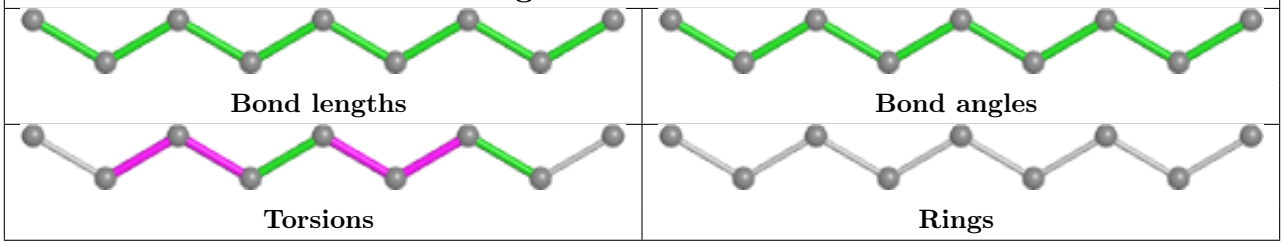
Ligand OLA A 1276

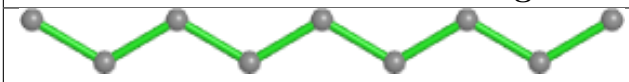
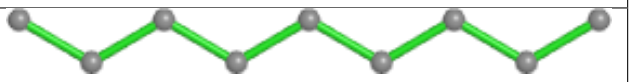
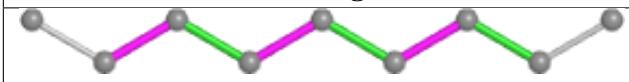
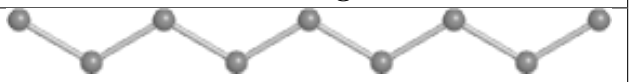


Ligand ANR A 1266



Ligand OLA A 1270



Ligand OLA A 1271	
 Bond lengths	 Bond angles
 Torsions	 Rings

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	269/275 (97%)	0.10	15 (5%) 24 23	16, 24, 46, 79	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	265	ILE	7.3
1	A	266	GLY	7.0
1	A	263	GLY	6.9
1	A	264	ARG	6.1
1	A	262	LEU	4.3
1	A	260	GLN	3.6
1	A	122	PHE	3.2
1	A	261	ALA	2.8
1	A	254	GLY	2.6
1	A	1	MET	2.6
1	A	87	ASP	2.3
1	A	-2	PRO	2.2
1	A	0	SER	2.2
1	A	256	VAL	2.1
1	A	253	ALA	2.1

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

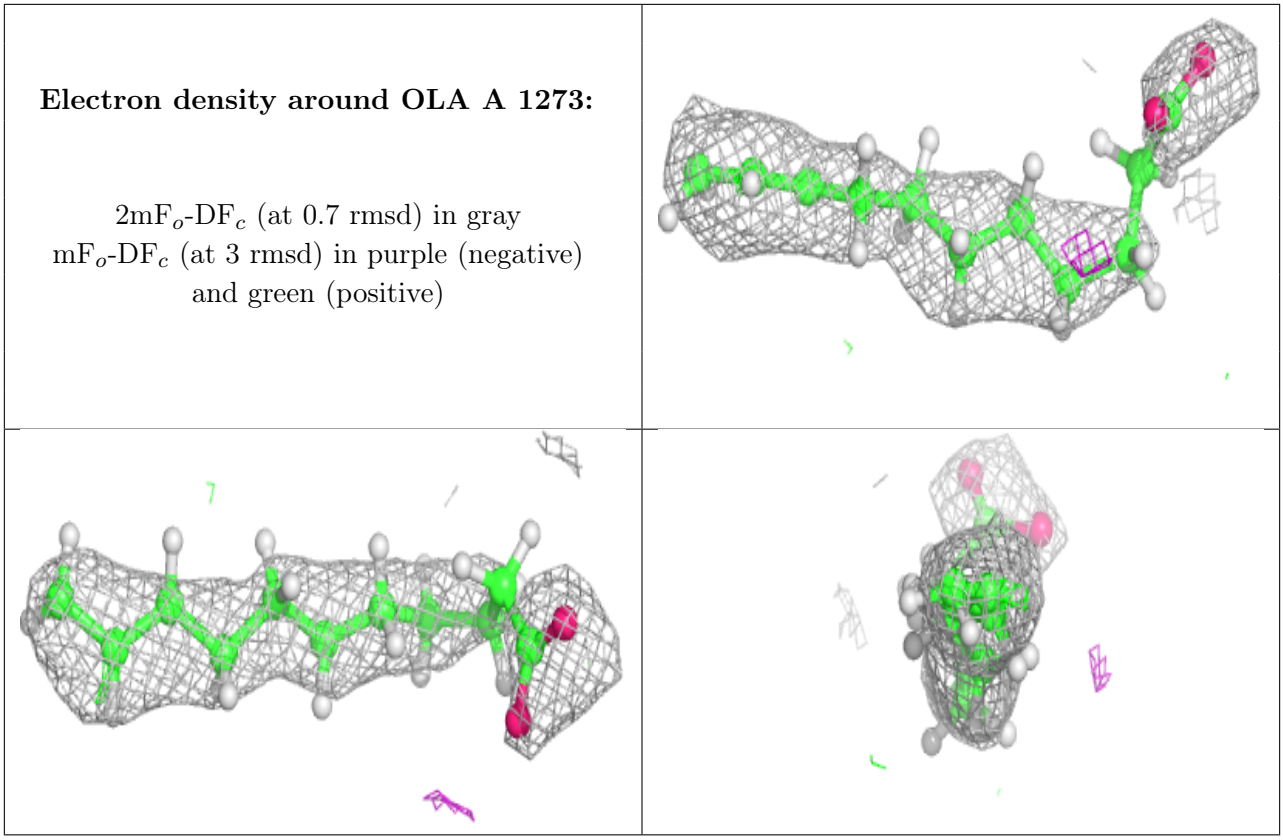
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	OLA	A	1273	13/20	0.67	0.22	49,61,75,82	0
4	OLA	A	1274	15/20	0.73	0.20	36,54,66,70	0
4	OLA	A	1272	9/20	0.76	0.20	44,50,52,53	0
4	OLA	A	1269	9/20	0.77	0.24	23,31,38,42	0
4	OLA	A	1270	9/20	0.83	0.15	41,47,55,59	0
4	OLA	A	1276	17/20	0.83	0.15	41,56,65,73	0
4	OLA	A	1275	20/20	0.84	0.17	34,48,64,72	0
4	OLA	A	1271	9/20	0.87	0.16	44,51,63,66	0
3	CL	A	1267	1/1	0.91	0.13	38,38,38,38	0
2	ANR	A	1266	20/20	0.94	0.14	12,19,26,35	0
3	CL	A	1268	1/1	0.96	0.15	42,42,42,42	0
3	CL	A	1277	1/1	0.96	0.05	44,44,44,44	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.

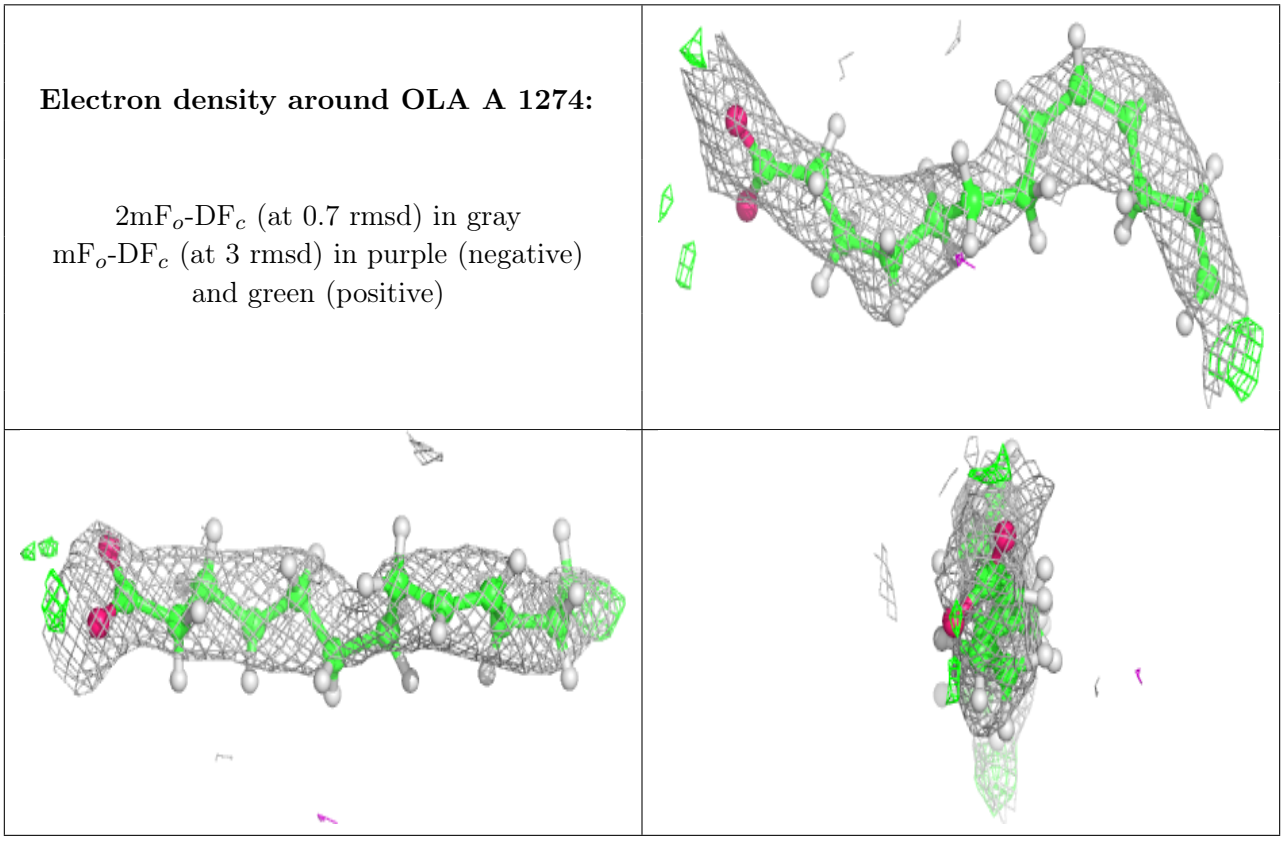
Electron density around OLA A 1273:

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



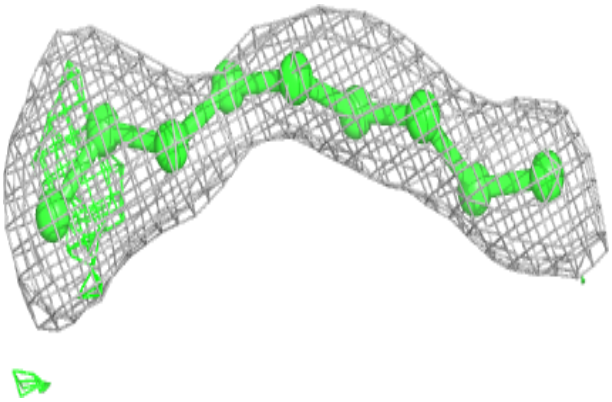
Electron density around OLA A 1274:

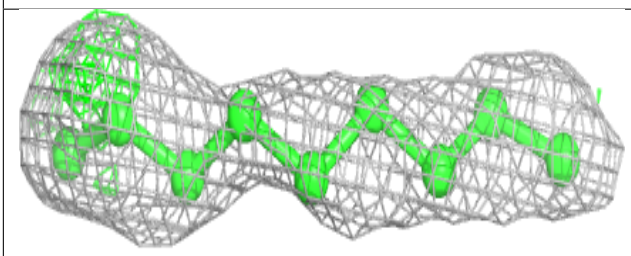
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

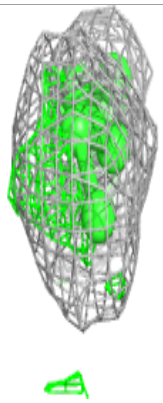


Electron density around OLA A 1272:

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

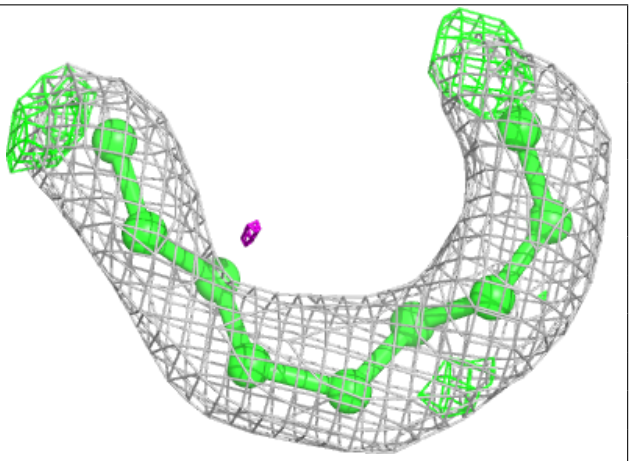


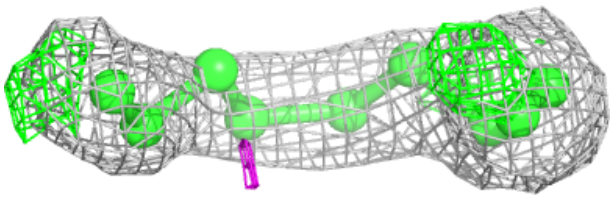


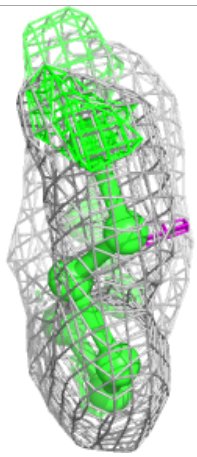


Electron density around OLA A 1269:

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

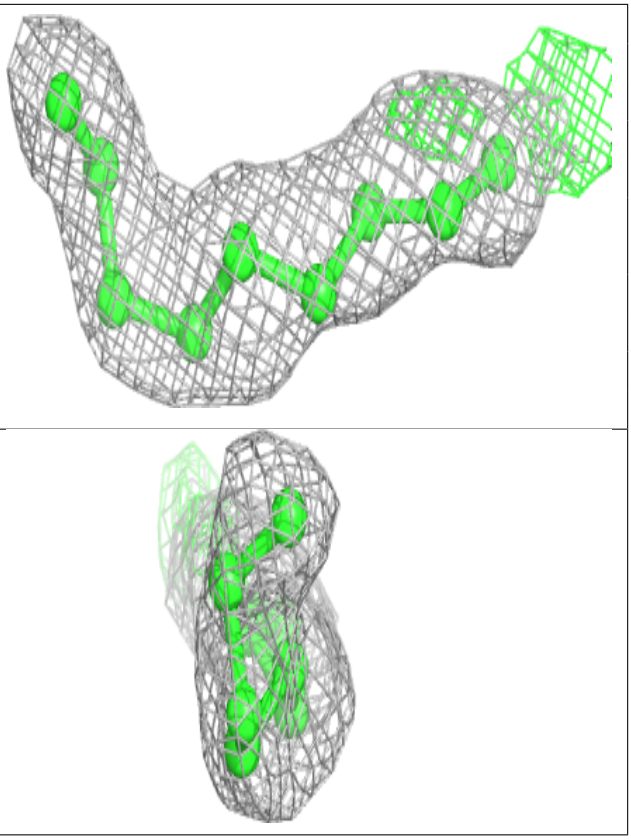


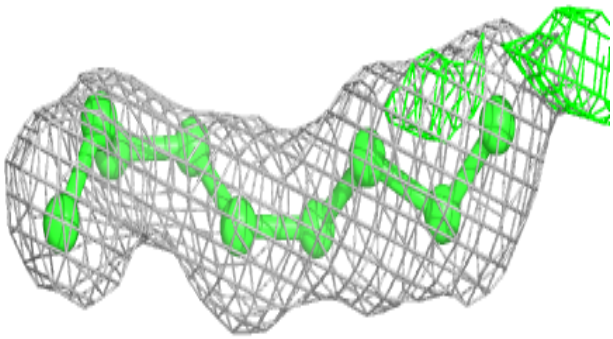




Electron density around OLA A 1270:

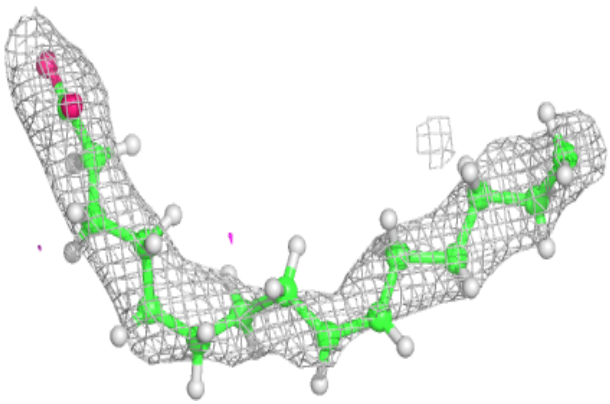
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

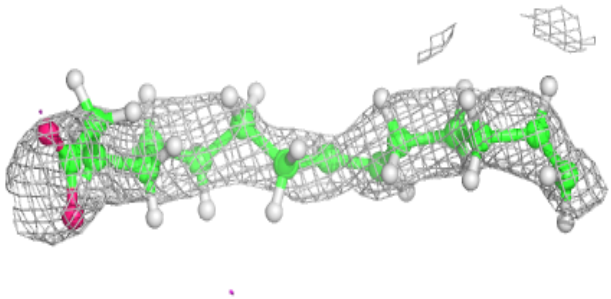


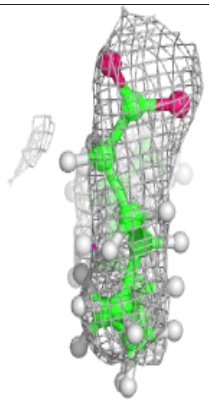


Electron density around OLA A 1276:

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

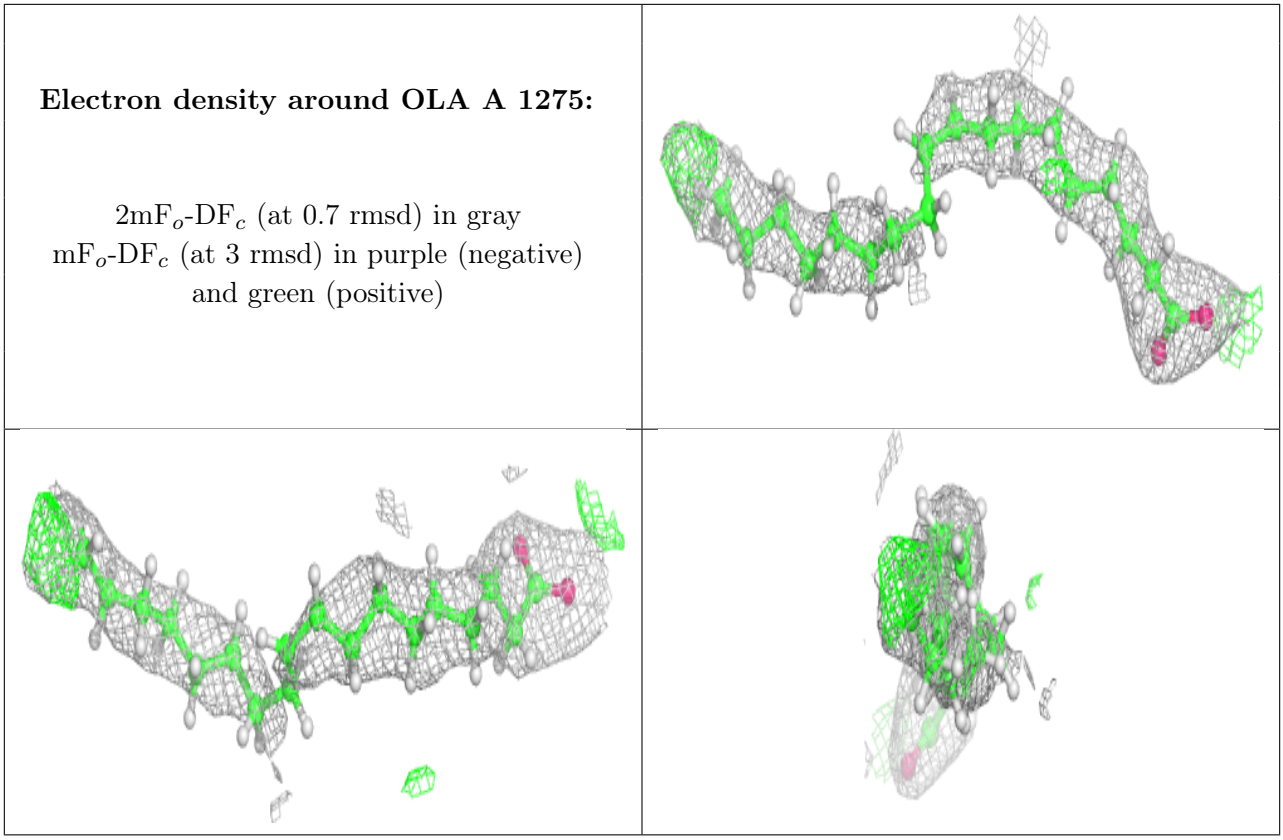






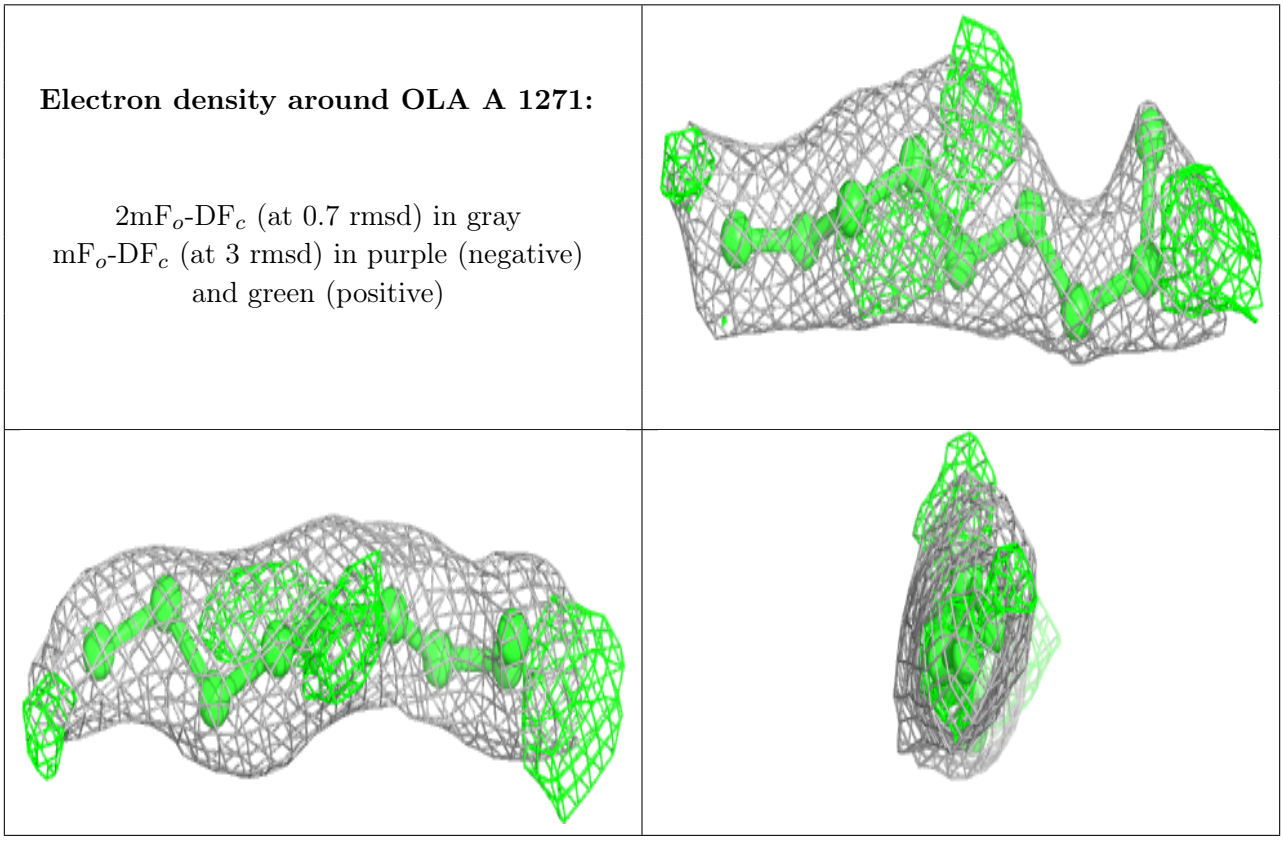
Electron density around OLA A 1275:

$2mF_o$-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 1271:

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



Electron density around ANR A 1266:

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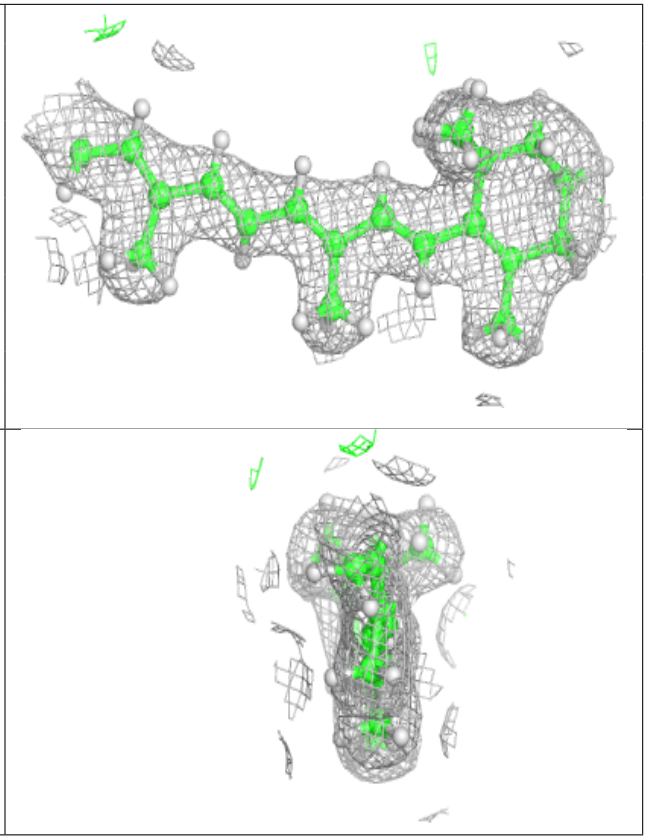
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.