Full wwPDB X-ray Structure Validation Report (i)

Sep 7, 2023 – 07:04 AM EDT

PDB ID	:	4GYC
Title	:	Structure of the SRII(D75N mutant)/HtrII Complex in I212121 space group ("U" shape)
Authors	:	Ishchenko, A.; Round, E.; Borshchevskiy, V.; Grudinin, S.; Gushchin, I.; Klare, J.; Remeeva, A.; Utrobin, P.; Balandin, T.; Engelhard, M.; Bueldt, G.; Gordeliy, V.
Deposited on	:	2012-09-05
Resolution	:	2.05 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:

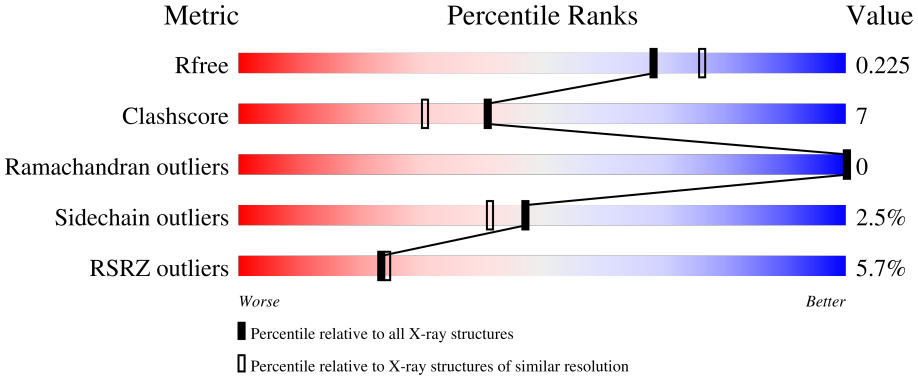
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.05 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	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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	245	6% 75% 14% • 10%
2	B	135	% 39% 7% 55%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2229 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 Sensory rhodopsin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	220	1662	1113	265	278	6	0	0	0

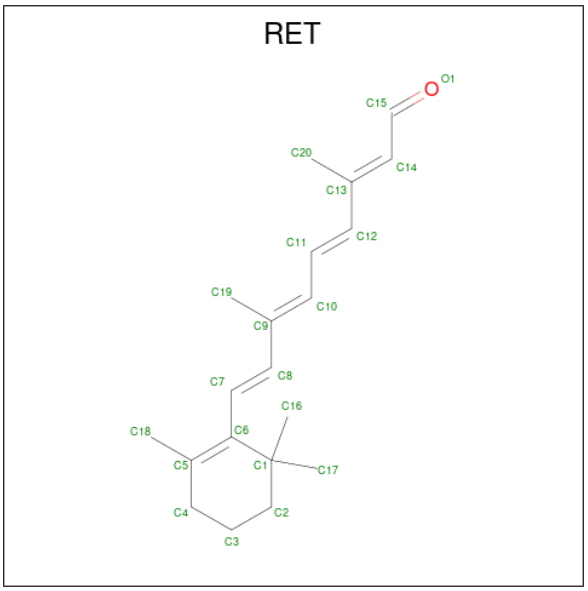
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	75	ASN	ASP	engineered mutation	UNP P42196
A	240	HIS	-	expression tag	UNP P42196
A	241	HIS	-	expression tag	UNP P42196
A	242	HIS	-	expression tag	UNP P42196
A	243	HIS	-	expression tag	UNP P42196
A	244	HIS	-	expression tag	UNP P42196
A	245	HIS	-	expression tag	UNP P42196

- Molecule 2 is a protein called Sensory rhodopsin II transducer.

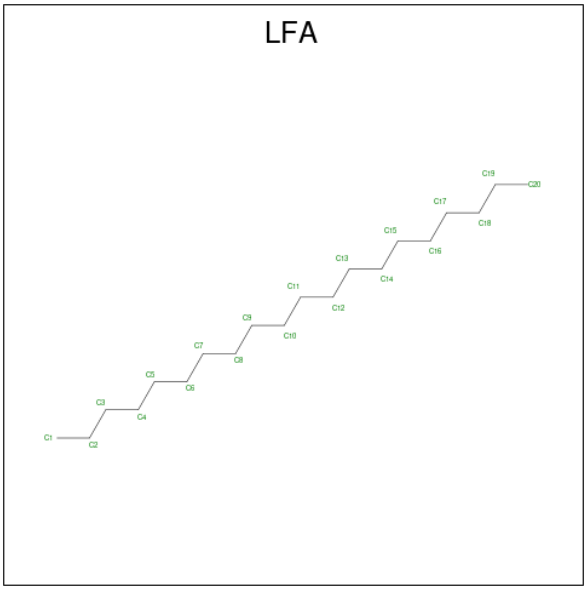
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	61	407	269	63	75	0	0	0

- Molecule 3 is RETINAL (three-letter code: RET) (formula: $C_{20}H_{28}O$).



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

- Molecule 4 is EICOSANE (three-letter code: LFA) (formula: $C_{20}H_{42}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C 7 7	0	0
4	A	1	Total C 10 10	0	0
4	A	1	Total C 16 16	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	C		
4	A	1	10	10	0	0
			Total	C		
4	A	1	12	12	0	0
			Total	C		
4	A	1	12	12	0	0
			Total	C		
4	A	1	5	5	0	0
			Total	C		
4	A	1	5	5	0	0
			Total	C		
4	A	1	5	5	0	0

- Molecule 5 is water.

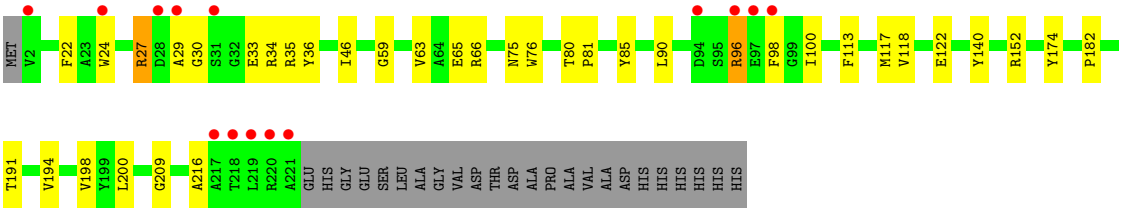
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	51	51	51	0	0
			Total	O		
5	B	7	7	7	0	0

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.

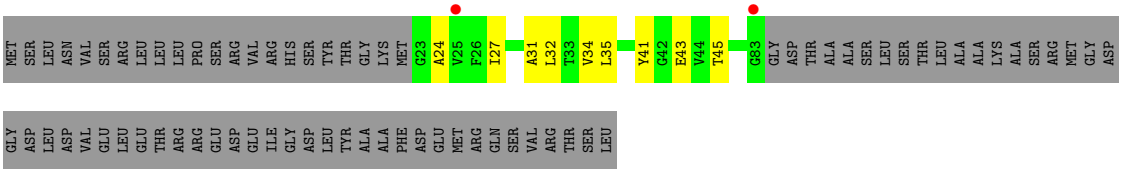
- Molecule 1: Sensory rhodopsin-2

Chain A:



- Molecule 2: Sensory rhodopsin II transducer

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	49.47Å 113.67Å 126.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.23 – 2.05 45.36 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.3 (42.23-2.05) 99.9 (45.36-2.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.80 (at 2.05Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.203 , 0.223 0.206 , 0.225	Depositor DCC
R_{free} test set	1136 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	31.2	Xtriage
Anisotropy	0.596	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 80.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	2229	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.29% 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: LFA, RET

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	0.45	0/1704	0.53	0/2333
2	B	0.34	0/410	0.46	0/561
All	All	0.43	0/2114	0.52	0/2894

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	1662	0	1735	25	0
2	B	407	0	433	6	0
3	A	20	0	27	3	0
4	A	82	0	155	6	0
5	A	51	0	0	0	0
5	B	7	0	0	0	0
All	All	2229	0	2350	32	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 7.

All (32) 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:59:GLY:HA2	4:A:304:LFA:H42	1.61	0.80
1:A:191:THR:HB	2:B:43:GLU:OE2	1.93	0.68
1:A:59:GLY:H	4:A:304:LFA:H13	1.60	0.67
1:A:24:TRP:O	1:A:27:ARG:HG3	1.96	0.65
2:B:24:ALA:O	2:B:27:ILE:HG13	2.04	0.58
1:A:63:VAL:O	1:A:66:ARG:HG2	2.04	0.57
1:A:66:ARG:HD2	1:A:182:PRO:O	2.03	0.57
2:B:31:ALA:O	2:B:34:VAL:HG22	2.06	0.56
1:A:76:TRP:CD1	3:A:301:RET:H14	2.43	0.54
1:A:36:TYR:CG	4:A:310:LFA:H22	2.44	0.53
1:A:216:ALA:HB2	4:A:310:LFA:H32	1.89	0.53
1:A:29:ALA:HB1	1:A:33:GLU:HB3	1.92	0.52
1:A:80:THR:N	1:A:81:PRO:HD2	2.25	0.51
1:A:46:ILE:HG23	4:A:304:LFA:H151	1.94	0.48
1:A:36:TYR:CD2	4:A:310:LFA:H22	2.49	0.48
3:A:301:RET:H7	3:A:301:RET:H181	1.74	0.46
1:A:85:TYR:HA	1:A:98:PHE:HE1	1.80	0.45
1:A:174:TYR:CE1	1:A:200:LEU:HG	2.51	0.45
3:A:301:RET:H8	3:A:301:RET:H161	1.97	0.45
1:A:113:PHE:O	1:A:117:MET:HG2	2.17	0.44
1:A:194:VAL:O	1:A:198:VAL:HG23	2.18	0.44
1:A:96:ARG:HA	1:A:96:ARG:HD2	1.62	0.43
2:B:35:LEU:HD23	2:B:35:LEU:O	2.18	0.43
1:A:65:GLU:HG3	1:A:65:GLU:O	2.18	0.43
1:A:90:LEU:O	1:A:152:ARG:HD3	2.19	0.43
1:A:30:GLY:O	1:A:34:ARG:HG3	2.19	0.42
1:A:100:ILE:HG21	1:A:140:TYR:CZ	2.54	0.42
2:B:41:TYR:O	2:B:45:THR:HG23	2.20	0.41
1:A:118:VAL:HG11	1:A:122:GLU:HG2	2.02	0.41
1:A:85:TYR:HA	1:A:98:PHE:CE1	2.55	0.41
1:A:22:PHE:CZ	1:A:209:GLY:HA3	2.56	0.41
2:B:35:LEU:HD23	2:B:35:LEU:C	2.41	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	218/245 (89%)	216 (99%)	2 (1%)	0	100	100
2	B	59/135 (44%)	59 (100%)	0	0	100	100
All	All	277/380 (73%)	275 (99%)	2 (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	167/186 (90%)	163 (98%)	4 (2%)	49	43
2	B	36/98 (37%)	35 (97%)	1 (3%)	43	37
All	All	203/284 (72%)	198 (98%)	5 (2%)	47	41

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

Mol	Chain	Res	Type
1	A	27	ARG
1	A	35	ARG
1	A	75	ASN
1	A	96	ARG
2	B	32	LEU

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)

10 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	LFA	A	308	-	4,4,19	0.18	0	3,3,18	0.47	0
3	RET	A	301	1	20,20,21	2.08	6 (30%)	27,27,28	1.93	7 (25%)
4	LFA	A	304	-	15,15,19	0.27	0	14,14,18	0.79	0
4	LFA	A	306	-	11,11,19	0.30	0	10,10,18	0.73	0
4	LFA	A	309	-	4,4,19	0.17	0	3,3,18	0.45	0
4	LFA	A	303	-	9,9,19	0.26	0	8,8,18	0.73	0
4	LFA	A	302	-	6,6,19	0.21	0	5,5,18	0.55	0
4	LFA	A	310	-	4,4,19	0.19	0	3,3,18	0.41	0
4	LFA	A	305	-	9,9,19	0.25	0	8,8,18	0.67	0
4	LFA	A	307	-	11,11,19	0.28	0	10,10,18	0.75	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	LFA	A	308	-	-	0/2/2/17	-
3	RET	A	301	1	-	0/13/30/31	0/1/1/1
4	LFA	A	304	-	-	2/13/13/17	-
4	LFA	A	306	-	-	2/9/9/17	-
4	LFA	A	309	-	-	1/2/2/17	-
4	LFA	A	303	-	-	1/7/7/17	-
4	LFA	A	302	-	-	0/4/4/17	-
4	LFA	A	310	-	-	0/2/2/17	-
4	LFA	A	305	-	-	3/7/7/17	-
4	LFA	A	307	-	-	3/9/9/17	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	RET	C14-C13	5.26	1.37	1.33
3	A	301	RET	C16-C1	4.60	1.62	1.53
3	A	301	RET	C17-C1	3.20	1.60	1.53
3	A	301	RET	C11-C12	2.64	1.41	1.34
3	A	301	RET	C10-C9	2.15	1.38	1.35
3	A	301	RET	C1-C6	2.01	1.56	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	301	RET	C10-C11-C12	-3.95	110.89	123.22
3	A	301	RET	C11-C12-C13	-3.72	115.97	126.42
3	A	301	RET	C7-C6-C5	-3.23	113.65	121.46
3	A	301	RET	C20-C13-C12	3.17	123.07	118.08
3	A	301	RET	C18-C5-C6	3.15	128.06	124.53
3	A	301	RET	C11-C10-C9	-2.81	123.30	127.31
3	A	301	RET	C4-C5-C6	-2.38	119.27	122.73

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	305	LFA	C5-C6-C7-C8
4	A	306	LFA	C2-C3-C4-C5
4	A	304	LFA	C2-C3-C4-C5
4	A	304	LFA	C1-C2-C3-C4
4	A	307	LFA	C9-C10-C11-C12

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
4	A	307	LFA	C11-C10-C9-C8
4	A	306	LFA	C7-C8-C9-C10
4	A	305	LFA	C1-C2-C3-C4
4	A	307	LFA	C2-C3-C4-C5
4	A	309	LFA	C1-C2-C3-C4
4	A	303	LFA	C6-C7-C8-C9
4	A	305	LFA	C3-C4-C5-C6

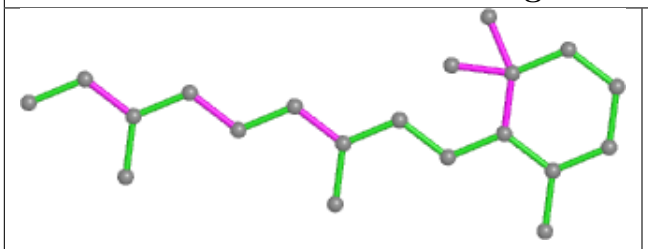
There are no ring outliers.

3 monomers are involved in 9 short contacts:

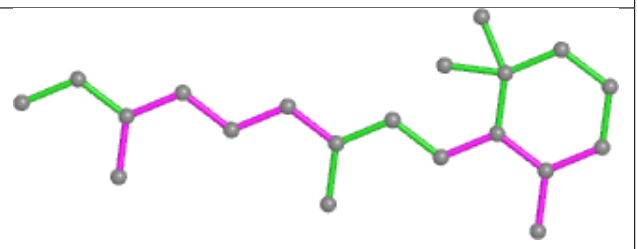
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	RET	3	0
4	A	304	LFA	3	0
4	A	310	LFA	3	0

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.

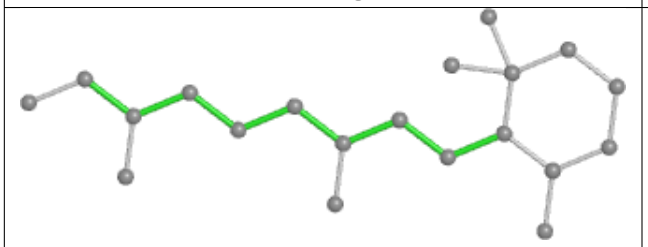
Ligand RET A 301



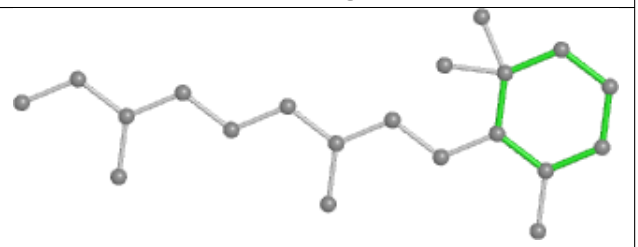
Bond lengths



Bond angles

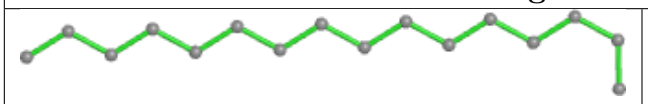


Torsions

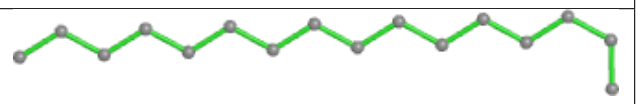


Rings

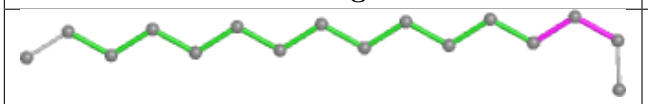
Ligand LFA A 304



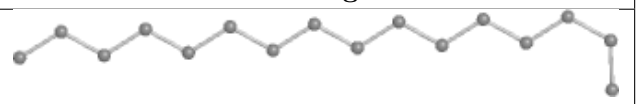
Bond lengths



Bond angles

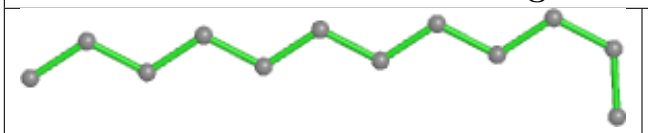


Torsions

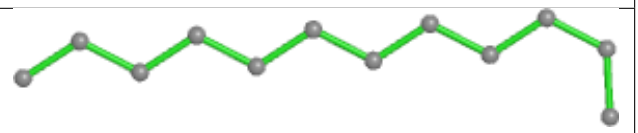


Rings

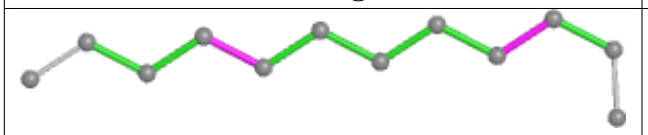
Ligand LFA A 306



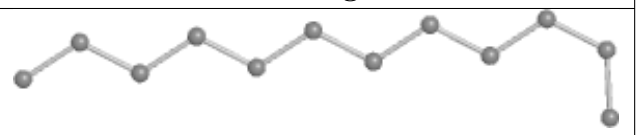
Bond lengths



Bond angles

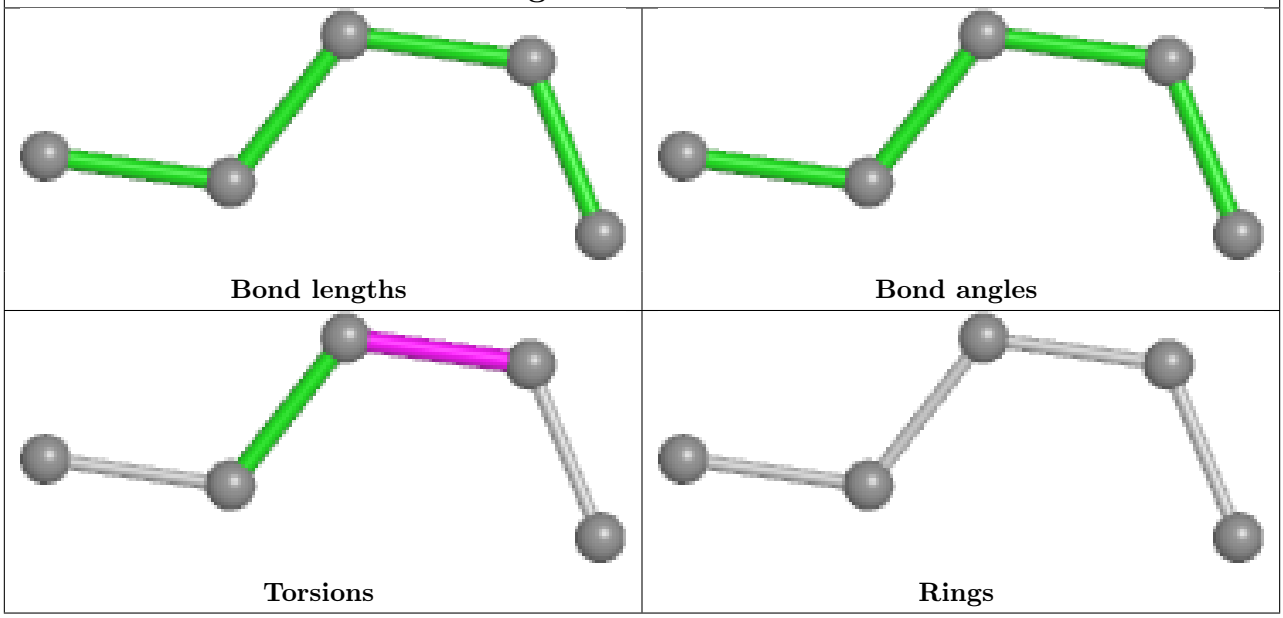


Torsions

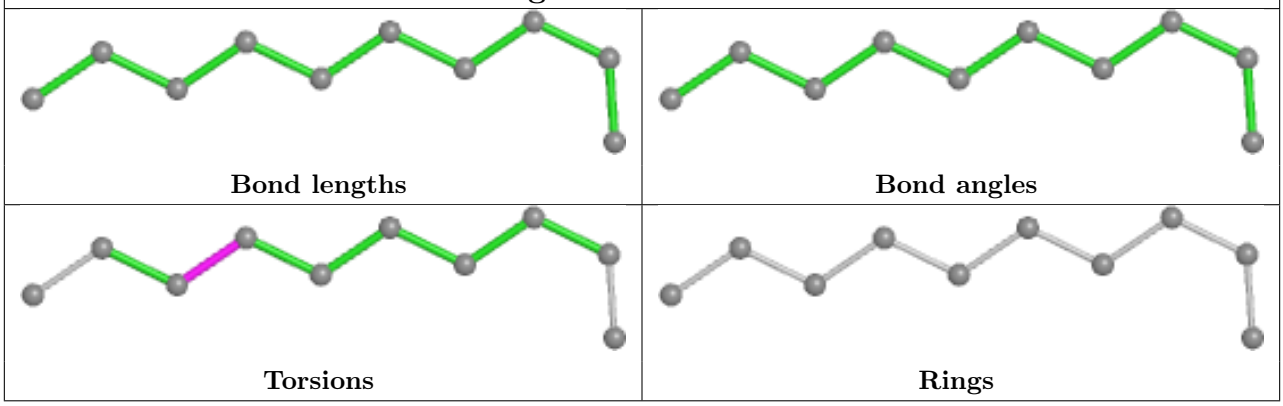


Rings

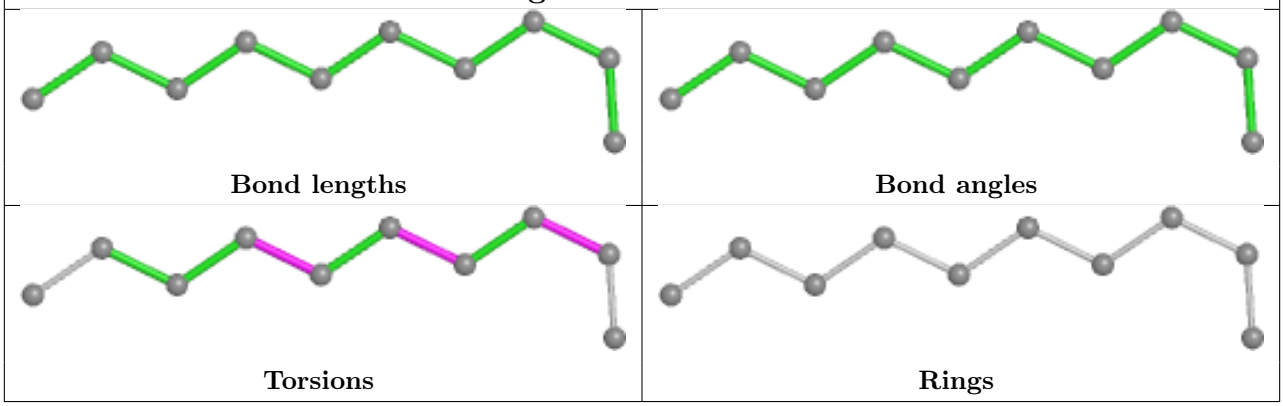
Ligand LFA A 309



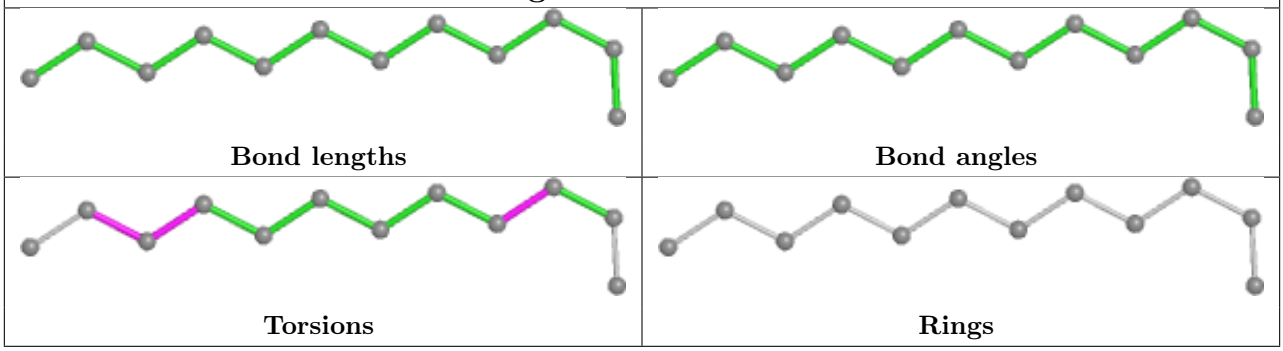
Ligand LFA A 303



Ligand LFA A 305



Ligand LFA A 307



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	220/245 (89%)	0.03	14 (6%)	19	19	9, 21, 53, 78	4 (1%)
2	B	61/135 (45%)	0.02	2 (3%)	46	49	13, 32, 53, 56	0
All	All	281/380 (73%)	0.03	16 (5%)	23	24	9, 22, 53, 78	4 (1%)

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	221	ALA	5.2
1	A	31	SER	5.0
1	A	96	ARG	4.7
1	A	219	LEU	4.0
1	A	24	TRP	4.0
1	A	28	ASP	3.8
1	A	220	ARG	3.3
1	A	98	PHE	3.1
1	A	2	VAL	3.0
2	B	83	GLY	3.0
1	A	94	ASP	2.9
1	A	218	THR	2.7
1	A	217	ALA	2.6
1	A	29	ALA	2.6
1	A	97	GLU	2.4
2	B	25	VAL	2.2

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)

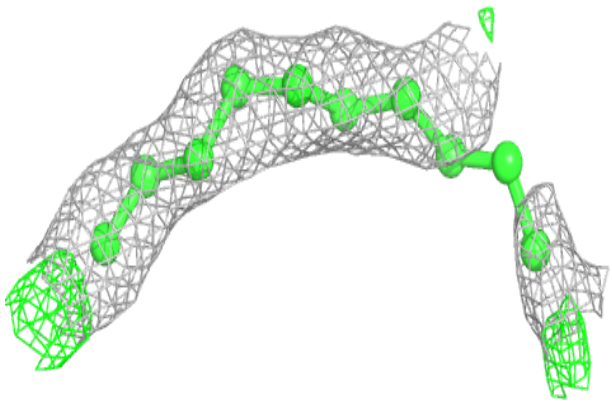
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

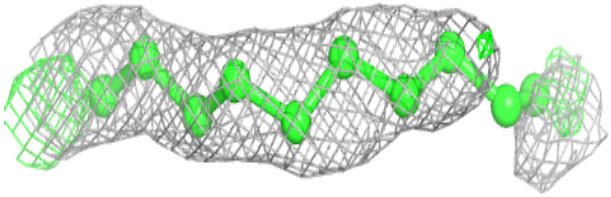
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	LFA	A	308	5/20	0.46	0.22	52,52,56,56	0
4	LFA	A	305	10/20	0.58	0.25	28,41,56,57	0
4	LFA	A	302	7/20	0.65	0.40	41,46,49,50	0
4	LFA	A	304	16/20	0.66	0.33	28,36,46,46	0
4	LFA	A	309	5/20	0.69	0.26	41,42,42,43	0
4	LFA	A	303	10/20	0.70	0.19	45,49,58,59	0
4	LFA	A	307	12/20	0.79	0.17	43,49,55,55	0
4	LFA	A	310	5/20	0.85	0.18	29,33,39,43	0
4	LFA	A	306	12/20	0.89	0.20	37,42,48,49	0
3	RET	A	301	20/21	0.96	0.12	3,10,18,18	0

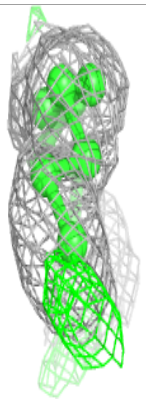
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around LFA A 305:

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

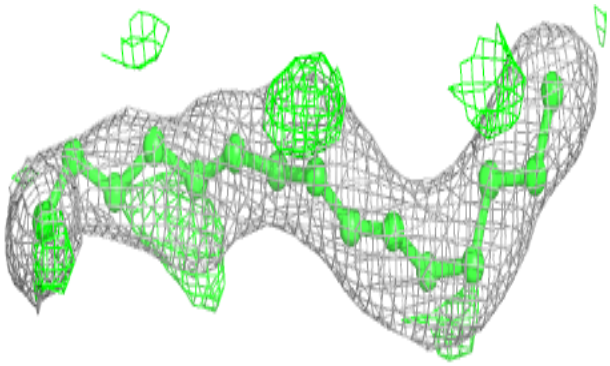


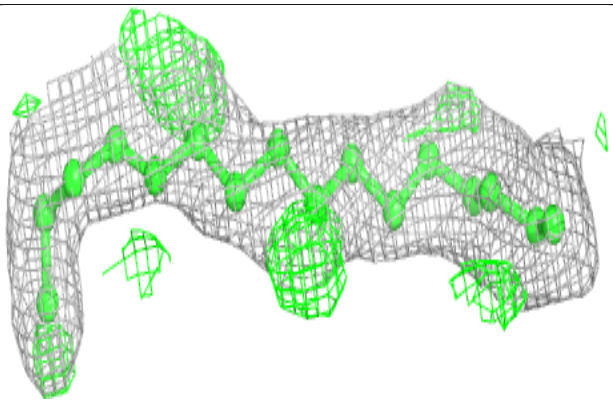


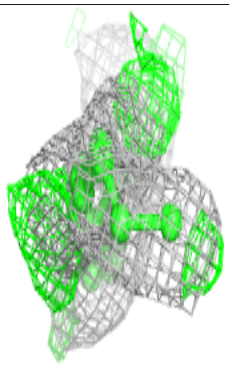


Electron density around LFA A 304:

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

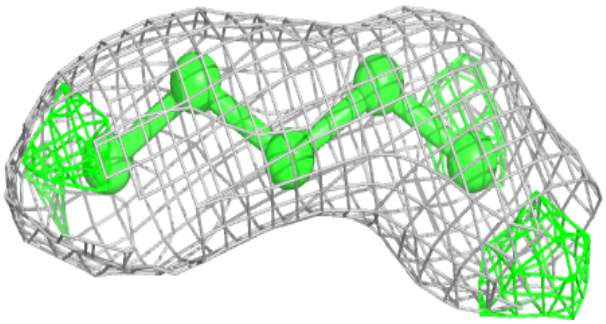


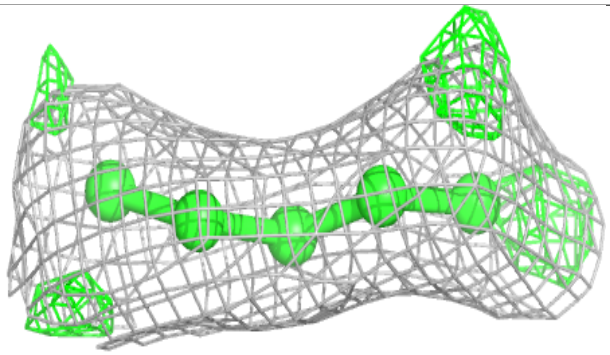


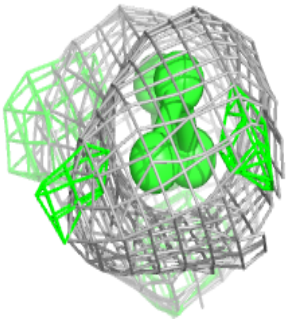


Electron density around LFA A 309:

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

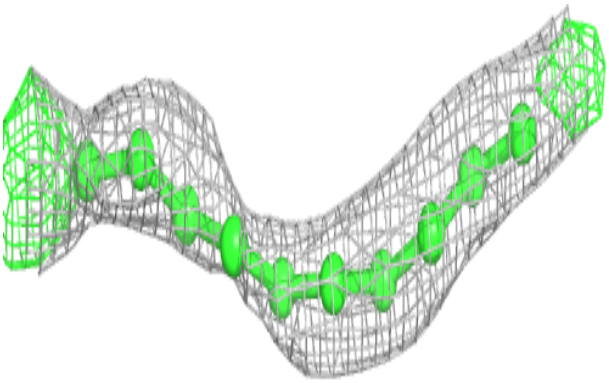


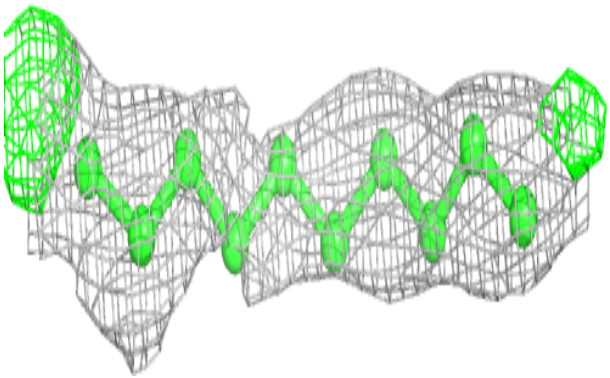


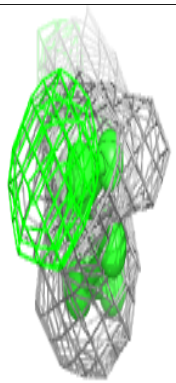


Electron density around LFA A 303:

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

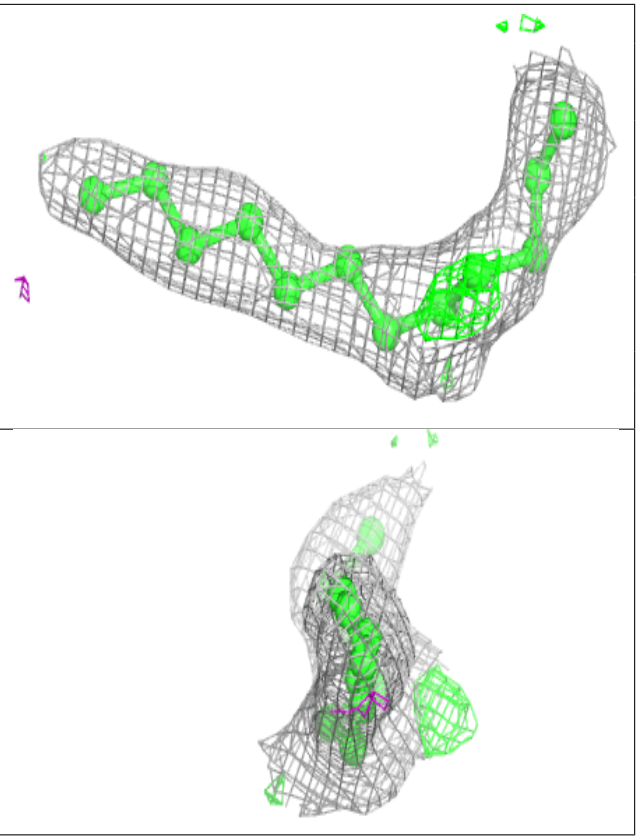






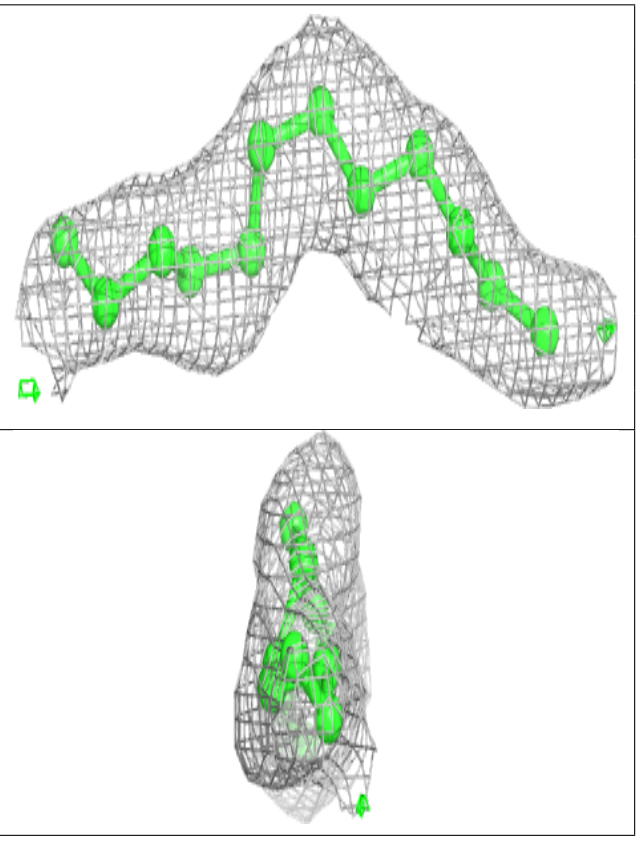
Electron density around LFA A 307:

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



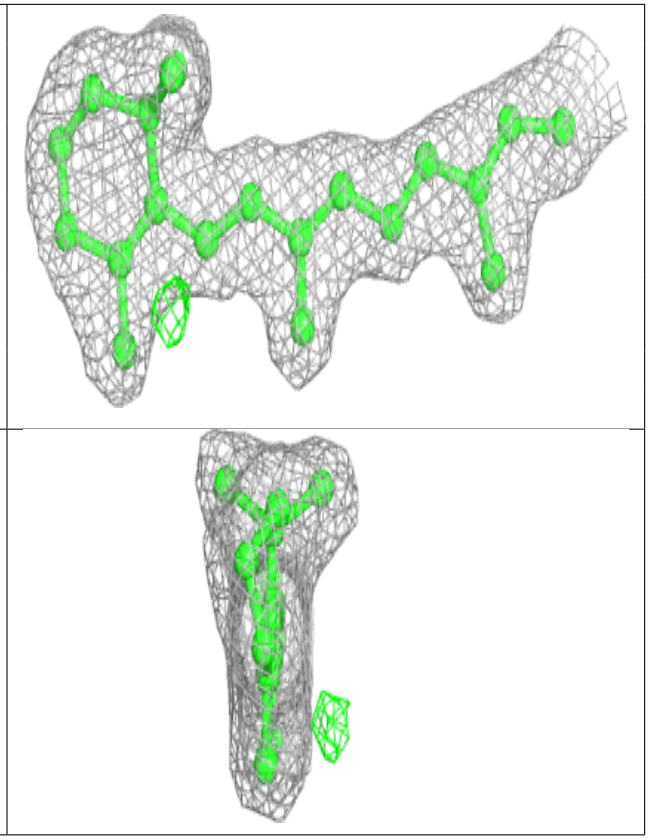
Electron density around LFA A 306:

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



Electron density around RET A 301:

$2mF_o$-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.