WORLDWIDE wwPDB PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Aug 21, 2020 – 10:53 PM BST

PDB ID	:	6TK6
Title	:	Femtosecond to millisecond structural changes in a light-driven sodium pump: Dark structure in neutral conditions with attached light datasets at 800fs, 2ps, 100ps, 1ns, 16ns, 1us, 30us, 150us, 1ms and 20ms
Authors	:	Skopintsev, P.; Ehrenberg, D.; Weinert, T.; James, D.; Kar, R.; Johnson, P.; Ozerov, D.; Furrer, A.; Martiel, I.; Dworkowski, F.; Nass, K.; Knopp, G.; Cirelli, C.; Gashi, D.; Mous, S.; Wranik, M.; Gruhl, T.; Kekilli, D.; Bruenle, S.; Deupi, X.; Schertler, G.F.X.; Benoit, R.; Panneels, V.; Nogly, P.; Schapiro, I.; Milne, C.; Heberle, J.; Standfuss, J.
Deposited on	:	2019-11-28
Resolution	:	1.60 Å(reported)

The following versions of software and data (see references (1)) were used in the production of this report:
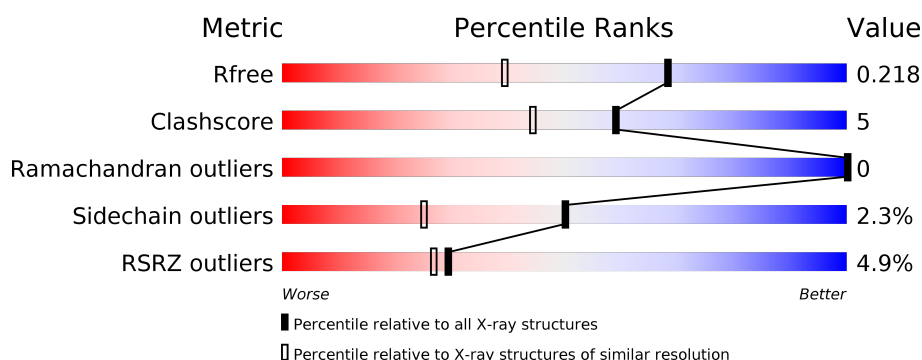
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.60 Å.

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

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on 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	290	4% / 86% / 5% · / 9%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	LFA	A	315	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2407 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 Sodium pumping rhodopsin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	4	0
			2105	1405	321	370	9			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	276	GLU	-	expression tag	UNP N0DKS8
A	277	ASN	-	expression tag	UNP N0DKS8
A	278	LEU	-	expression tag	UNP N0DKS8
A	279	TYR	-	expression tag	UNP N0DKS8
A	280	PHE	-	expression tag	UNP N0DKS8
A	281	GLN	-	expression tag	UNP N0DKS8
A	282	SER	-	expression tag	UNP N0DKS8
A	283	GLY	-	expression tag	UNP N0DKS8
A	284	SER	-	expression tag	UNP N0DKS8
A	285	HIS	-	expression tag	UNP N0DKS8
A	286	HIS	-	expression tag	UNP N0DKS8
A	287	HIS	-	expression tag	UNP N0DKS8
A	288	HIS	-	expression tag	UNP N0DKS8
A	289	HIS	-	expression tag	UNP N0DKS8
A	290	HIS	-	expression tag	UNP N0DKS8

- Molecule 2 is RETINAL (three-letter code: RET) (formula: $C_{20}H_{28}O$) (labeled as "Ligand of Interest" by author).

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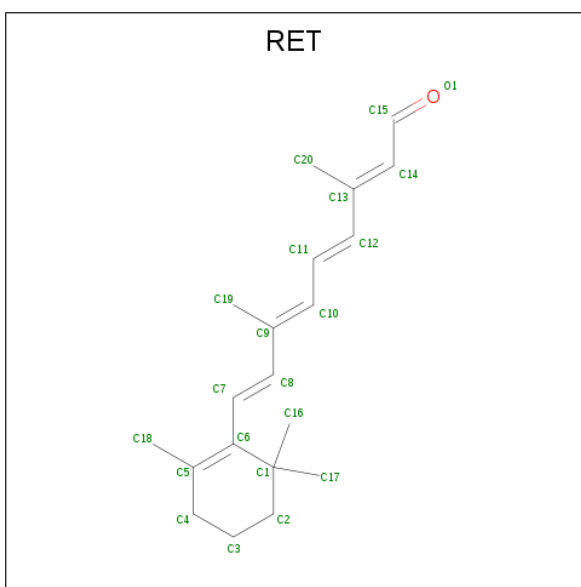
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 20	C 20	0	0

- Molecule 3 is EICOSANE (three-letter code: LFA) (formula: $C_{20}H_{42}$).

LFA

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 16	C 16	0	0
3	A	1	Total 8	C 8	0	0
3	A	1	Total 6	C 6	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 6	C 6	0	0
3	A	1	Total 5	C 5	0	0
3	A	1	Total 13	C 13	0	0
3	A	1	Total 10	C 10	0	0
3	A	1	Total 8	C 8	0	0
3	A	1	Total 8	C 8	0	0
3	A	1	Total 12	C 12	0	0
3	A	1	Total 16	C 16	0	0
3	A	1	Total 5	C 5	0	0
3	A	1	Total 10	C 10	0	0
3	A	1	Total 5	C 5	0	0
3	A	1	Total 11	C 11	0	0
3	A	1	Total 9	C 9	0	0
3	A	1	Total 9	C 9	0	0
3	A	1	Total 6	C 6	0	0
3	A	1	Total 5	C 5	0	0
3	A	1	Total 4	C 4	0	0
3	A	1	Total 6	C 6	0	0
3	A	1	Total 10	C 10	0	0
3	A	1	Total 3	C 3	0	0
3	A	1	Total 9	C 9	0	0

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	60	Total 60	O 60	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: Sodium pumping rhodopsin
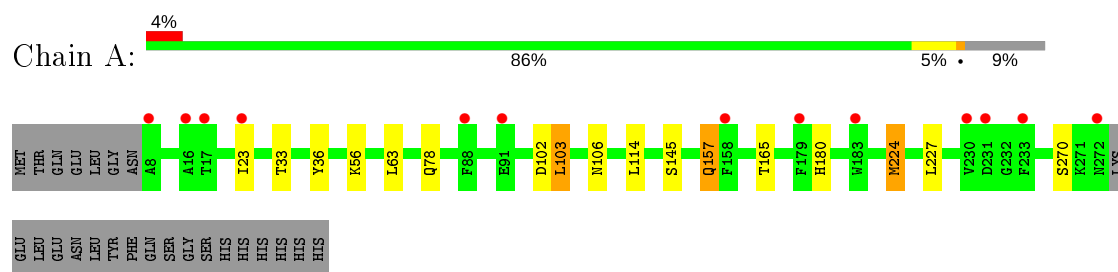
4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	41.54Å 84.48Å 235.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.43 – 1.60 12.43 – 1.60	Depositor EDS
% Data completeness (in resolution range)	57.5 (12.43-1.60) 57.5 (12.43-1.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	2.66 (at 1.60Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.188 , 0.217 0.188 , 0.218	Depositor DCC
R_{free} test set	2078 reflections (6.55%)	wwPDB-VP
Wilson B-factor (Å^2)	29.2	Xtriage
Anisotropy	0.626	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 108.7	EDS
L-test for twinning[2]	$<|L|> = 0.49$, $<L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	2407	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.84% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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	0.36	0/2172	0.49	0/2958

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	2105	0	2075	14	0
2	A	20	0	27	2	0
3	A	222	0	403	9	0
4	A	60	0	0	5	0
All	All	2407	0	2505	23	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 5.

All (23) 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:106[B]:ASN:ND2	4:A:488:HOH:O	2.19	0.68
2:A:301:RET:H161	2:A:301:RET:H8	1.79	0.65
1:A:78[A]:GLN:NE2	4:A:487:HOH:O	2.11	0.60
3:A:302:LFA:H141	3:A:316:LFA:H111	1.83	0.59
1:A:106[B]:ASN:OD1	4:A:489:HOH:O	2.16	0.57
3:A:312:LFA:H61	3:A:323:LFA:H61	1.90	0.54
3:A:302:LFA:H132	3:A:312:LFA:H141	1.89	0.54
1:A:145:SER:OG	1:A:180:HIS:HD2	1.91	0.53
1:A:102:ASP:O	1:A:103:LEU:HB2	2.09	0.51
1:A:270:SER:OG	4:A:420:HOH:O	2.11	0.50
1:A:224:MET:HE3	1:A:227:LEU:HD12	1.96	0.47
1:A:106[A]:ASN:ND2	1:A:157:GLN:OE1	2.46	0.47
1:A:33:THR:HA	1:A:36:TYR:CE2	2.50	0.46
1:A:224:MET:CE	1:A:227:LEU:HD12	2.46	0.46
1:A:157:GLN:HB3	1:A:157:GLN:HE21	1.57	0.45
3:A:307:LFA:H51	3:A:307:LFA:H22	1.65	0.45
1:A:114:LEU:HD22	3:A:307:LFA:H31	1.97	0.45
3:A:312:LFA:H21	3:A:323:LFA:H21	1.98	0.44
1:A:63:LEU:HD21	3:A:320:LFA:H12	1.99	0.44
2:A:301:RET:H181	2:A:301:RET:H7	1.81	0.43
3:A:302:LFA:H122	3:A:316:LFA:H102	2.02	0.42
1:A:56:LYS:NZ	4:A:464:HOH:O	2.51	0.41
3:A:310:LFA:H71	3:A:310:LFA:H41	1.90	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	267/290 (92%)	261 (98%)	6 (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	222/250 (89%)	217 (98%)	5 (2%)	50 25

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

Mol	Chain	Res	Type
1	A	23	ILE
1	A	103	LEU
1	A	157	GLN
1	A	165	THR
1	A	224	MET

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

Mol	Chain	Res	Type
1	A	61	ASN
1	A	180	HIS

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)

27 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	$\#|Z| > 2$
3	LFA	A	312	-	15,15,19	0.33	0	14,14,18	0.79	0
3	LFA	A	305	-	5,5,19	0.34	0	4,4,18	0.51	0
3	LFA	A	325	-	8,8,19	0.34	0	7,7,18	0.70	0
3	LFA	A	317	-	8,8,19	0.32	0	7,7,18	0.74	0
3	LFA	A	323	-	9,9,19	0.33	0	8,8,18	0.67	0
3	LFA	A	303	-	7,7,19	0.29	0	6,6,18	0.73	0
3	LFA	A	309	-	7,7,19	0.37	0	6,6,18	0.58	0
3	LFA	A	307	-	12,12,19	0.32	0	11,11,18	0.76	0
3	LFA	A	320	-	4,4,19	0.32	0	3,3,18	0.50	0
3	LFA	A	321	-	3,3,19	0.42	0	2,2,18	0.71	0
3	LFA	A	302	-	15,15,19	0.32	0	14,14,18	0.83	0
3	LFA	A	306	-	4,4,19	0.33	0	3,3,18	0.54	0
3	LFA	A	322	-	5,5,19	0.34	0	4,4,18	0.55	0
3	LFA	A	319	-	5,5,19	0.33	0	4,4,18	0.57	0
3	LFA	A	318	-	8,8,19	0.37	0	7,7,18	0.57	0
3	LFA	A	326	-	9,9,19	0.34	0	8,8,18	0.71	0
3	LFA	A	316	-	10,10,19	0.34	0	9,9,18	0.75	0
3	LFA	A	304	-	5,5,19	0.33	0	4,4,18	0.57	0
3	LFA	A	308	-	9,9,19	0.31	0	8,8,18	0.77	0
3	LFA	A	324	-	2,2,19	0.34	0	0,1,18	0.00	-
3	LFA	A	310	-	7,7,19	0.33	0	6,6,18	0.71	0
3	LFA	A	327	-	11,11,19	0.33	0	10,10,18	0.81	0
3	LFA	A	313	-	4,4,19	0.34	0	3,3,18	0.57	0
3	LFA	A	314	-	9,9,19	0.36	0	8,8,18	0.71	0
2	RET	A	301	1	20,20,21	0.90	`1 (5%)`	27,27,28	0.51	0
3	LFA	A	311	-	11,11,19	0.36	0	10,10,18	0.75	0
3	LFA	A	315	-	4,4,19	0.37	0	3,3,18	0.45	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
3	LFA	A	312	-	-	5/13/13/17	-
3	LFA	A	305	-	-	2/3/3/17	-
3	LFA	A	325	-	-	3/6/6/17	-
3	LFA	A	317	-	-	3/6/6/17	-
3	LFA	A	323	-	-	2/7/7/17	-
3	LFA	A	303	-	-	2/5/5/17	-
3	LFA	A	309	-	-	1/5/5/17	-
3	LFA	A	307	-	-	5/10/10/17	-
3	LFA	A	320	-	-	0/2/2/17	-
3	LFA	A	321	-	-	1/1/1/17	-
3	LFA	A	302	-	-	5/13/13/17	-
3	LFA	A	306	-	-	2/2/2/17	-
3	LFA	A	322	-	-	0/3/3/17	-
3	LFA	A	319	-	-	1/3/3/17	-
3	LFA	A	318	-	-	3/6/6/17	-
3	LFA	A	326	-	-	4/7/7/17	-
3	LFA	A	316	-	-	4/8/8/17	-
3	LFA	A	304	-	-	0/3/3/17	-
3	LFA	A	308	-	-	4/7/7/17	-
3	LFA	A	310	-	-	2/5/5/17	-
3	LFA	A	327	-	-	3/9/9/17	-
3	LFA	A	313	-	-	1/2/2/17	-
3	LFA	A	314	-	-	1/7/7/17	-
2	RET	A	301	1	-	0/13/30/31	0/1/1/1
3	LFA	A	311	-	-	2/9/9/17	-
3	LFA	A	315	-	-	0/2/2/17	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	RET	C14-C13	3.27	1.36	1.33

There are no bond angle outliers.

There are no chirality outliers.

All (56) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	321	LFA	C3-C4-C5-C6

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Mol	Chain	Res	Type	Atoms
3	A	318	LFA	C3-C4-C5-C6
3	A	312	LFA	C5-C6-C7-C8
3	A	317	LFA	C6-C7-C8-C9
3	A	310	LFA	C4-C5-C6-C7
3	A	312	LFA	C11-C10-C9-C8
3	A	302	LFA	C2-C3-C4-C5
3	A	302	LFA	C9-C10-C11-C12
3	A	317	LFA	C11-C10-C9-C8
3	A	312	LFA	C11-C12-C13-C14
3	A	308	LFA	C5-C6-C7-C8
3	A	319	LFA	C2-C3-C4-C5
3	A	316	LFA	C3-C4-C5-C6
3	A	325	LFA	C4-C5-C6-C7
3	A	318	LFA	C4-C5-C6-C7
3	A	314	LFA	C4-C5-C6-C7
3	A	311	LFA	C5-C6-C7-C8
3	A	317	LFA	C7-C8-C9-C10
3	A	325	LFA	C6-C7-C8-C9
3	A	308	LFA	C1-C2-C3-C4
3	A	308	LFA	C4-C5-C6-C7
3	A	318	LFA	C1-C2-C3-C4
3	A	327	LFA	C9-C10-C11-C12
3	A	302	LFA	C7-C8-C9-C10
3	A	323	LFA	C3-C4-C5-C6
3	A	325	LFA	C1-C2-C3-C4
3	A	326	LFA	C6-C7-C8-C9
3	A	302	LFA	C13-C14-C15-C16
3	A	303	LFA	C4-C5-C6-C7
3	A	306	LFA	C1-C2-C3-C4
3	A	326	LFA	C3-C4-C5-C6
3	A	311	LFA	C6-C7-C8-C9
3	A	307	LFA	C6-C7-C8-C9
3	A	312	LFA	C9-C10-C11-C12
3	A	327	LFA	C6-C7-C8-C9
3	A	307	LFA	C2-C3-C4-C5
3	A	316	LFA	C4-C5-C6-C7
3	A	307	LFA	C11-C10-C9-C8
3	A	326	LFA	C5-C6-C7-C8
3	A	310	LFA	C3-C4-C5-C6
3	A	305	LFA	C2-C3-C4-C5
3	A	326	LFA	C4-C5-C6-C7
3	A	316	LFA	C11-C10-C9-C8

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Mol	Chain	Res	Type	Atoms
3	A	307	LFA	C9-C10-C11-C12
3	A	323	LFA	C6-C7-C8-C9
3	A	305	LFA	C1-C2-C3-C4
3	A	309	LFA	C2-C3-C4-C5
3	A	306	LFA	C2-C3-C4-C5
3	A	307	LFA	C4-C5-C6-C7
3	A	316	LFA	C9-C10-C11-C12
3	A	302	LFA	C11-C10-C9-C8
3	A	303	LFA	C3-C4-C5-C6
3	A	313	LFA	C1-C2-C3-C4
3	A	312	LFA	C7-C8-C9-C10
3	A	308	LFA	C3-C4-C5-C6
3	A	327	LFA	C1-C2-C3-C4

There are no ring outliers.

8 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	312	LFA	3	0
3	A	323	LFA	2	0
3	A	307	LFA	2	0
3	A	320	LFA	1	0
3	A	302	LFA	3	0
3	A	316	LFA	2	0
3	A	310	LFA	1	0
2	A	301	RET	2	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 LFA A 312

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 305

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 325

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 317

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 323

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 303

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 309

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 307

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 321

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 302

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 306

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 319

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 318

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 326

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 316

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 308

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 310

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 327

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 313

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 314

Bond lengths

Bond angles

Torsions

Rings

Ligand RET A 301

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 311

Bond lengths

Bond angles

Torsions

Rings

Ligand LFA A 315

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	265/290 (91%)	-0.01	13 (4%)	29	27	19, 34, 60, 87	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	272	ASN	5.9
1	A	23	ILE	5.0
1	A	158	PHE	4.3
1	A	8	ALA	4.2
1	A	88	PHE	3.9
1	A	230	VAL	3.7
1	A	231	ASP	3.3
1	A	233	PHE	3.2
1	A	183	TRP	3.1
1	A	91	GLU	2.3
1	A	179	PHE	2.2
1	A	16	ALA	2.1
1	A	17	THR	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
3	LFA	A	311	12/20	0.13	0.22	54,65,70,72	0
3	LFA	A	309	8/20	0.44	0.23	69,75,80,82	0
3	LFA	A	314	10/20	0.51	0.29	59,68,83,85	0
3	LFA	A	306	5/20	0.58	0.24	77,79,89,91	0
3	LFA	A	315	5/20	0.60	0.45	56,58,69,70	0
3	LFA	A	327	12/20	0.64	0.22	48,56,64,65	0
3	LFA	A	316	11/20	0.66	0.35	63,77,89,91	0
3	LFA	A	323	10/20	0.68	0.26	64,72,73,74	0
3	LFA	A	322	6/20	0.69	0.23	54,59,71,72	0
3	LFA	A	302	16/20	0.69	0.14	48,62,74,77	0
3	LFA	A	318	9/20	0.72	0.26	56,66,74,76	0
3	LFA	A	307	13/20	0.76	0.14	49,54,61,62	0
3	LFA	A	305	6/20	0.76	0.16	59,62,65,69	0
3	LFA	A	321	4/20	0.77	0.30	57,66,68,69	0
3	LFA	A	312	16/20	0.78	0.13	57,66,72,73	0
3	LFA	A	325	9/20	0.82	0.32	63,68,75,77	0
3	LFA	A	320	5/20	0.82	0.09	56,57,63,65	0
3	LFA	A	317	9/20	0.83	0.23	68,70,72,73	0
3	LFA	A	324	3/20	0.85	0.12	61,61,64,67	0
3	LFA	A	310	8/20	0.85	0.16	48,56,63,63	0
3	LFA	A	326	10/20	0.85	0.21	55,59,68,70	0
3	LFA	A	304	6/20	0.87	0.20	65,70,74,75	0
3	LFA	A	308	10/20	0.88	0.19	52,60,65,71	0
3	LFA	A	319	6/20	0.89	0.10	53,56,62,62	0
3	LFA	A	303	8/20	0.91	0.14	39,41,44,45	8
3	LFA	A	313	5/20	0.92	0.18	58,59,66,69	0
2	RET	A	301	20/21	0.94	0.07	21,27,31,32	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 311:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
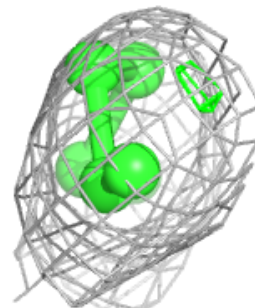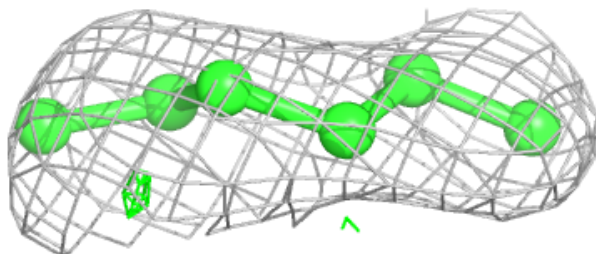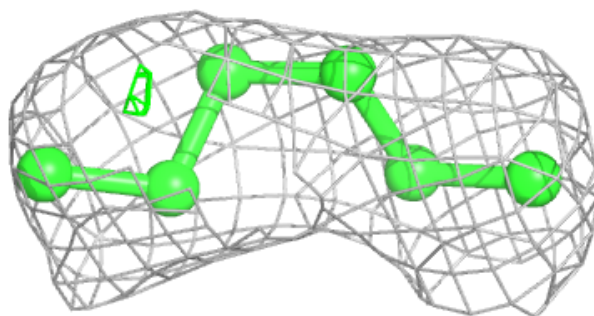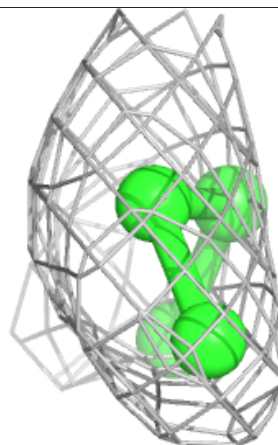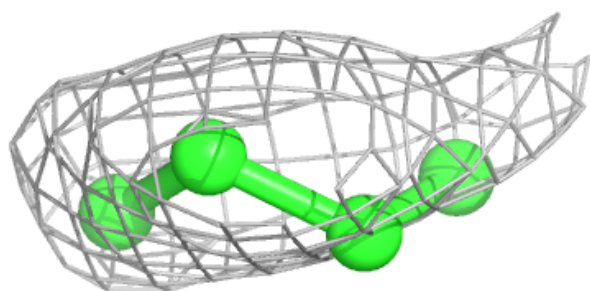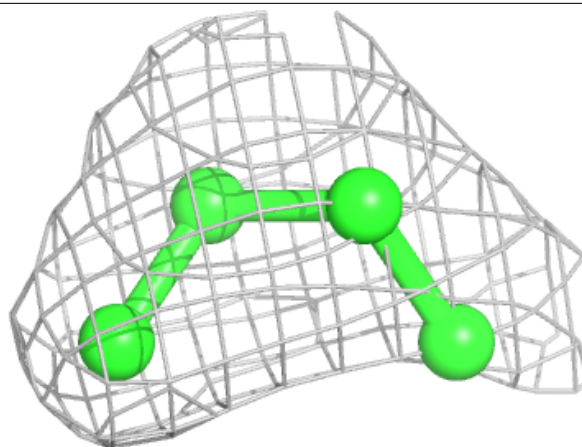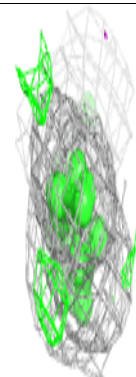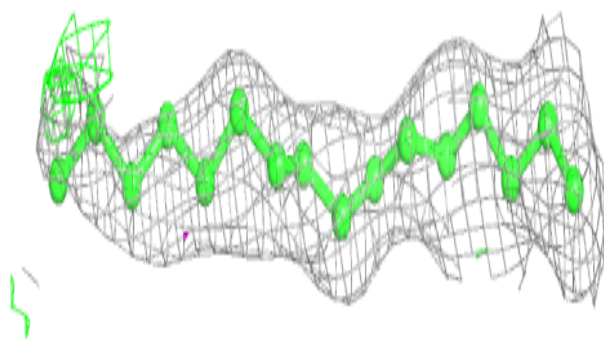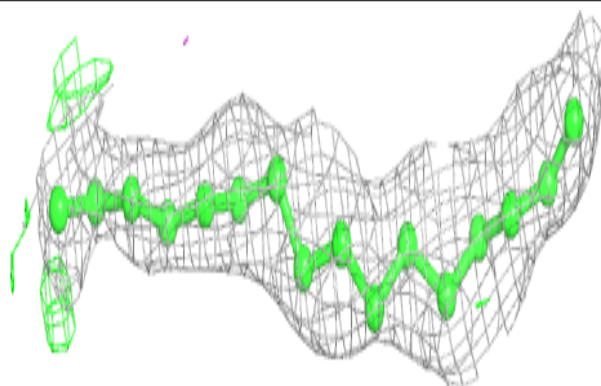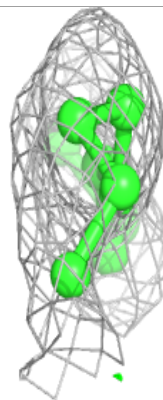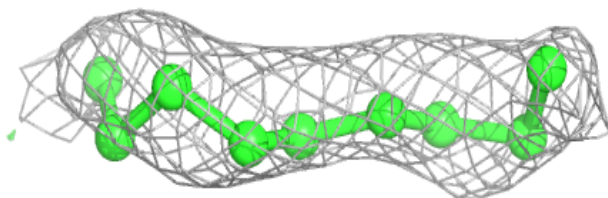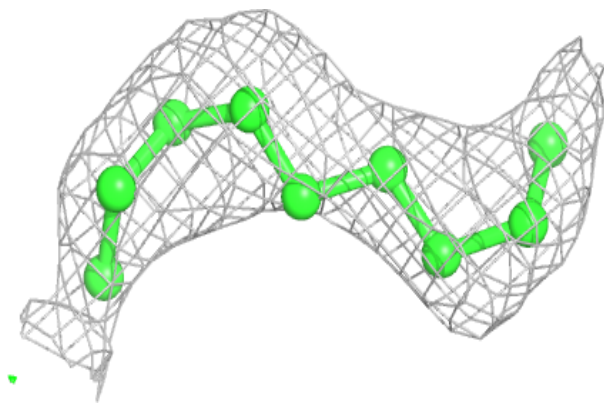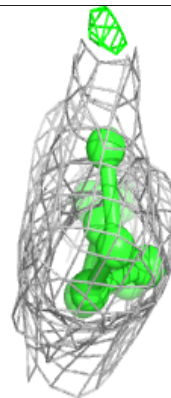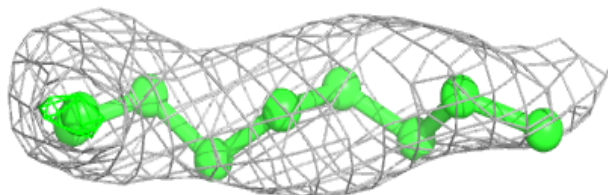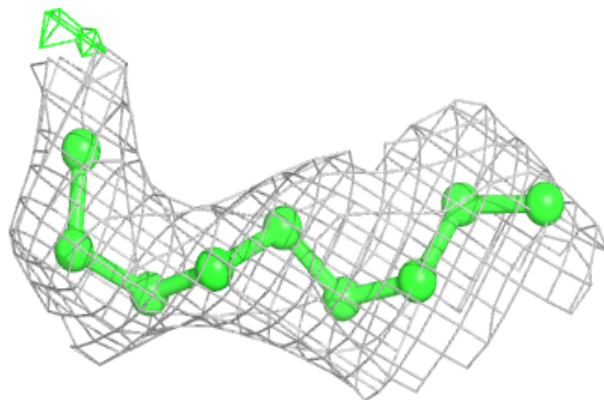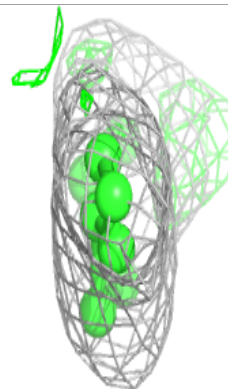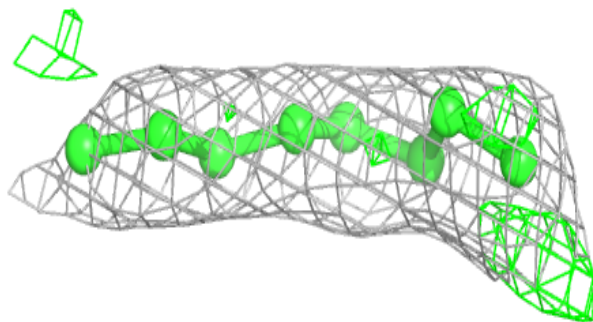mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
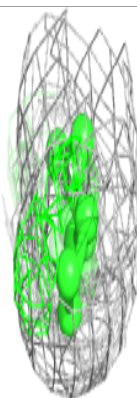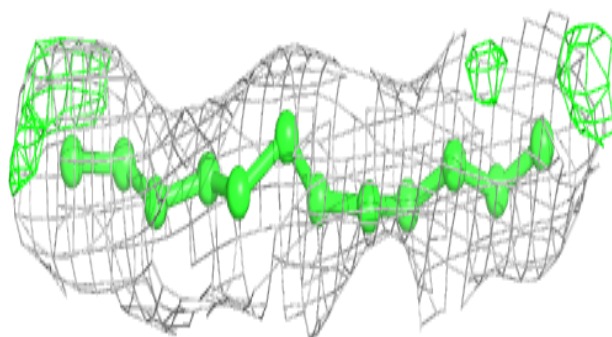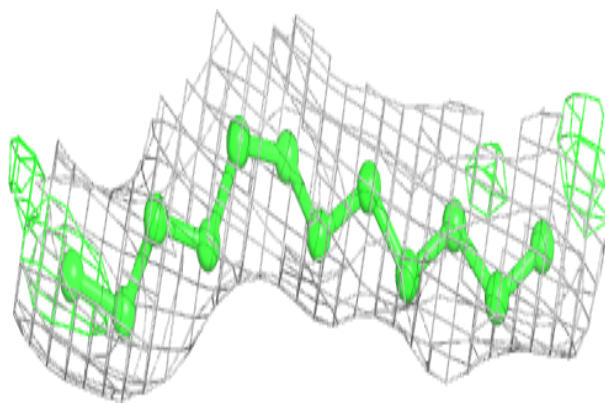
Electron density around LFA A 309:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
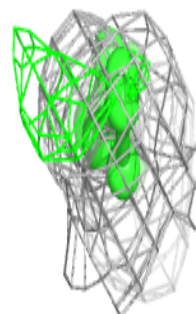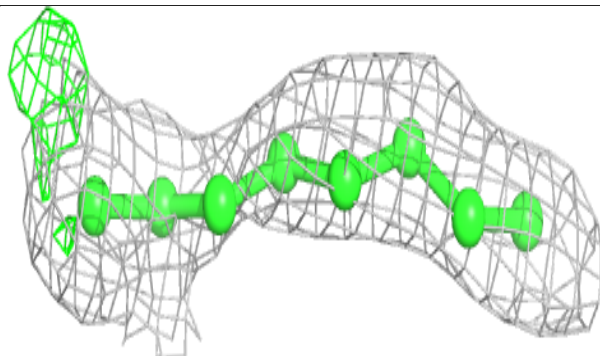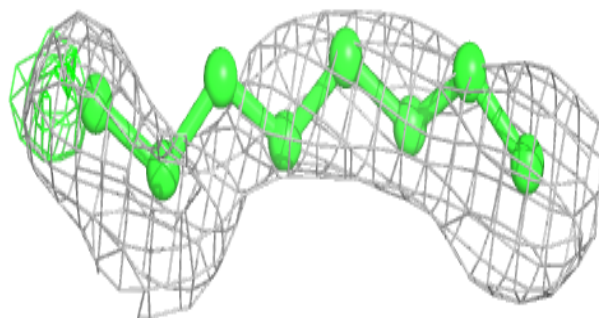
Electron density around LFA A 314:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
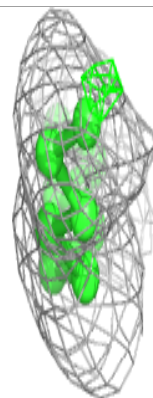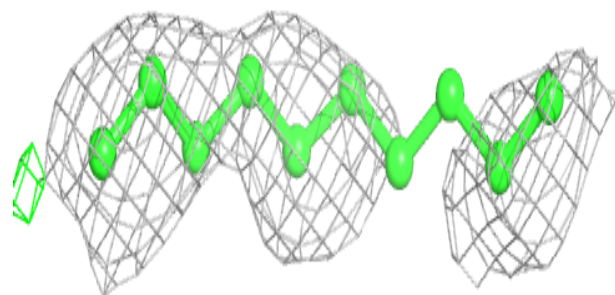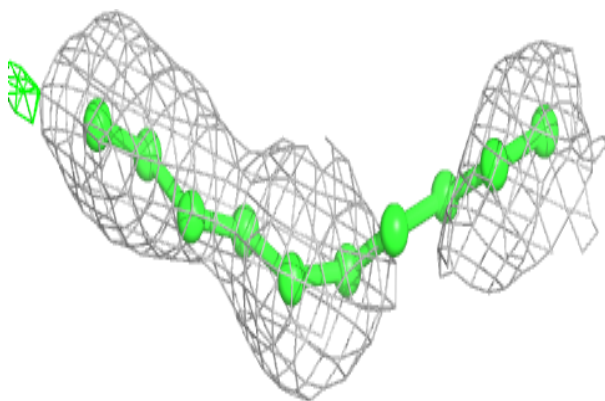
Electron density around LFA A 306:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
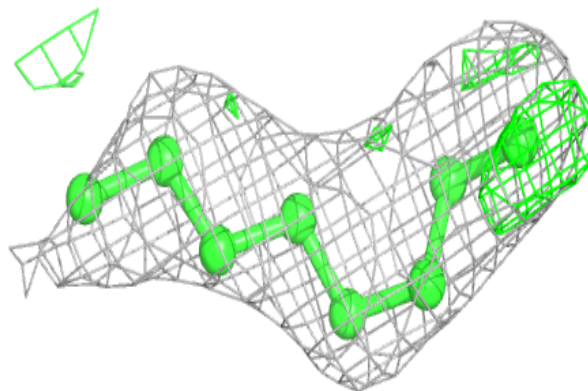$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
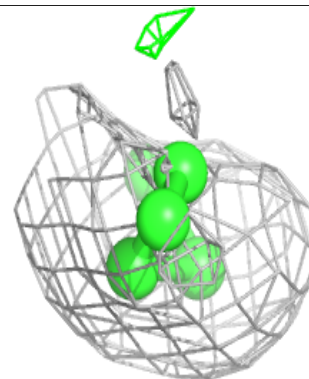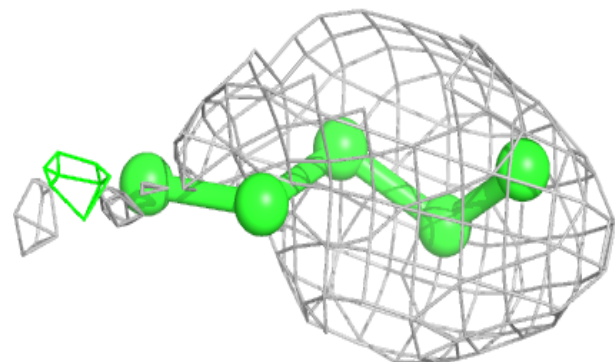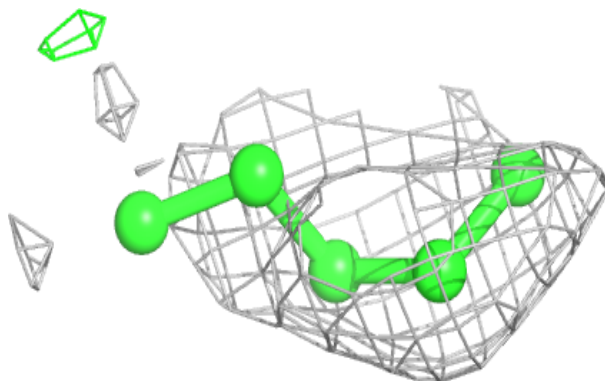
Electron density around LFA A 315:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
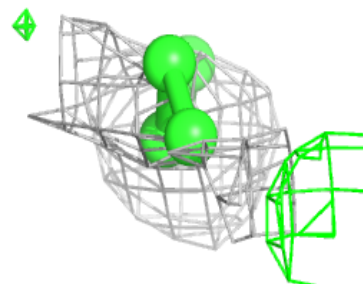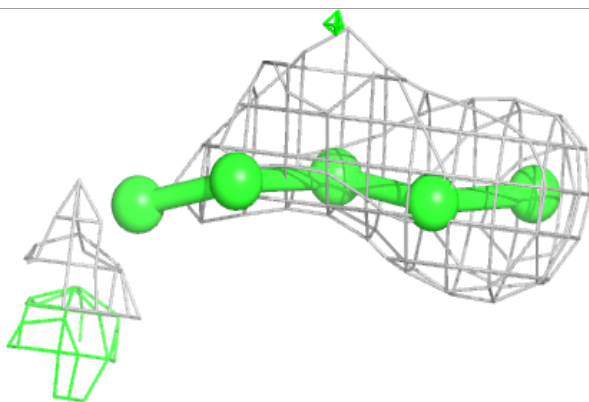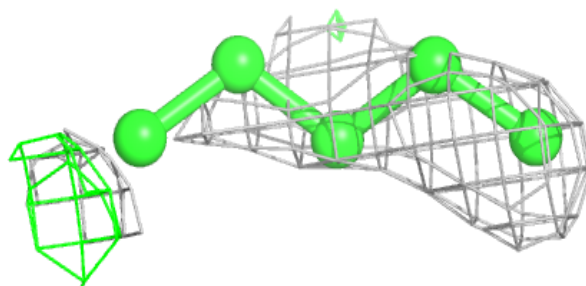
Electron density around LFA A 327:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
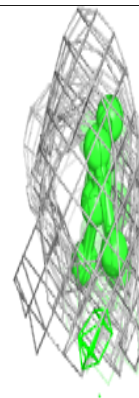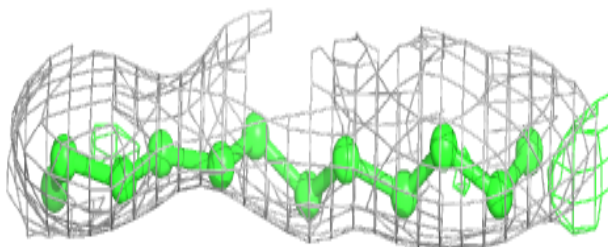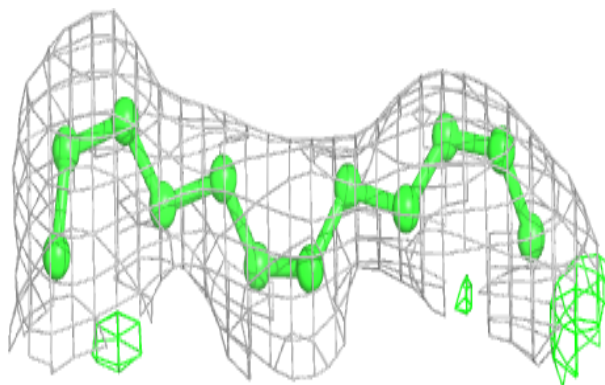
Electron density around LFA A 316:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
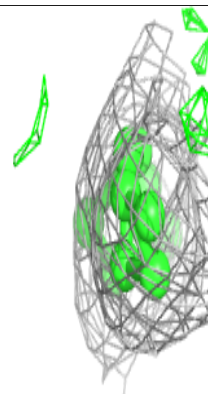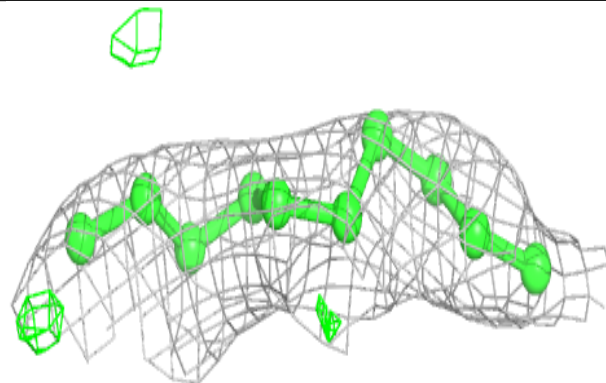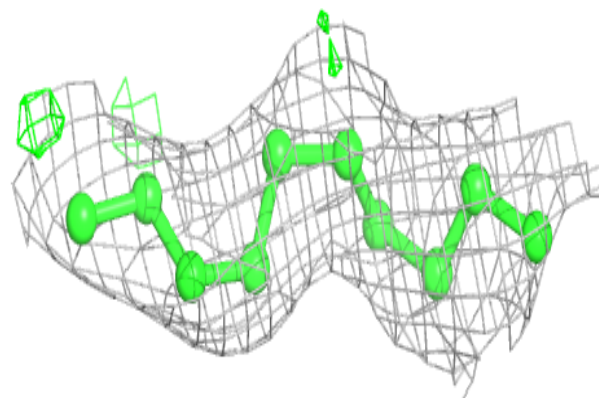mF_o-DF_c (at 3 rmsd) in purple (negative)
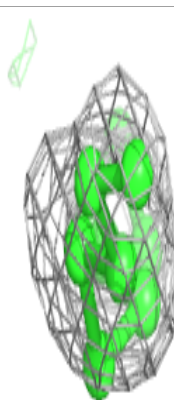and green (positive)
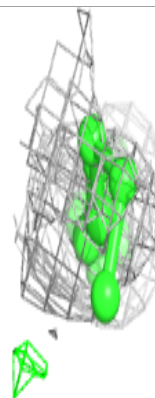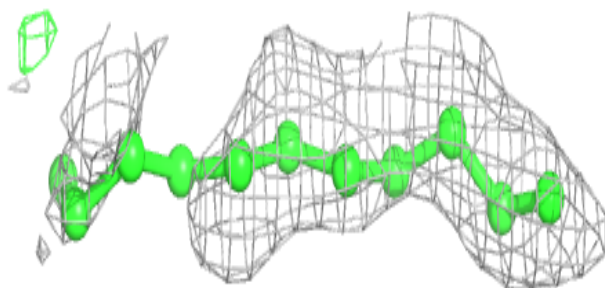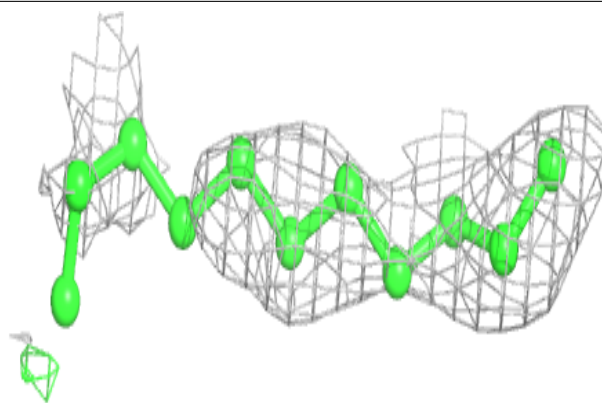
Electron density around LFA A 323:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
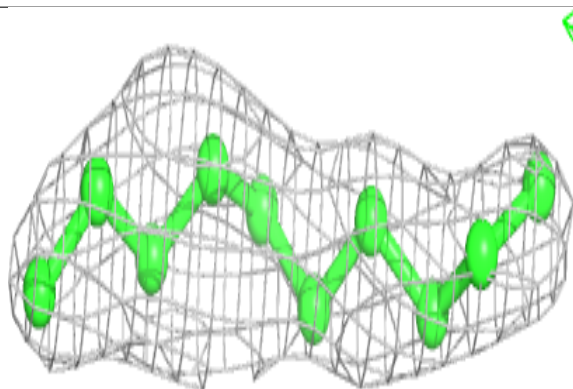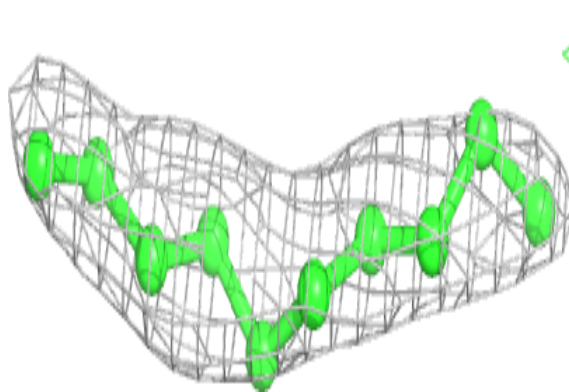and green (positive)
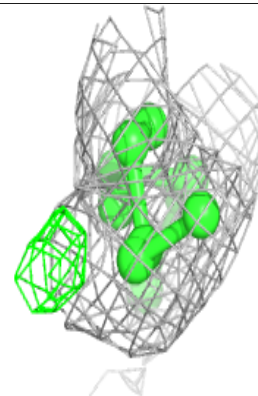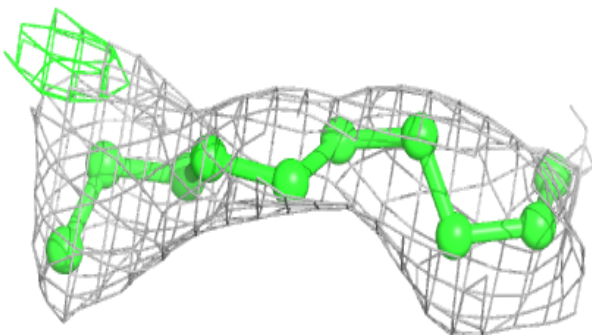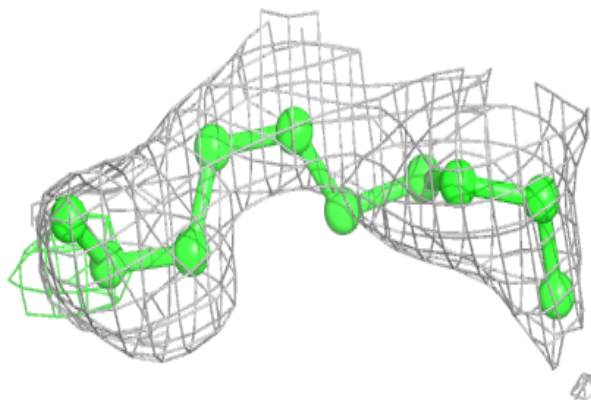
Electron density around LFA A 302:

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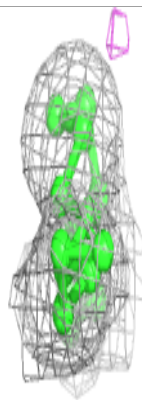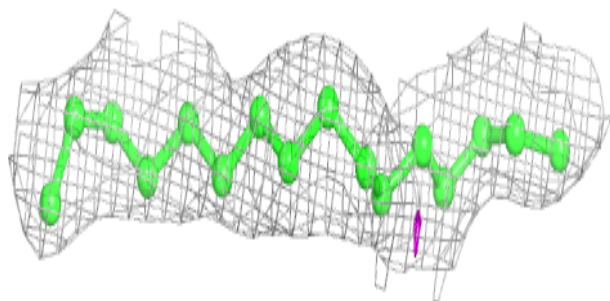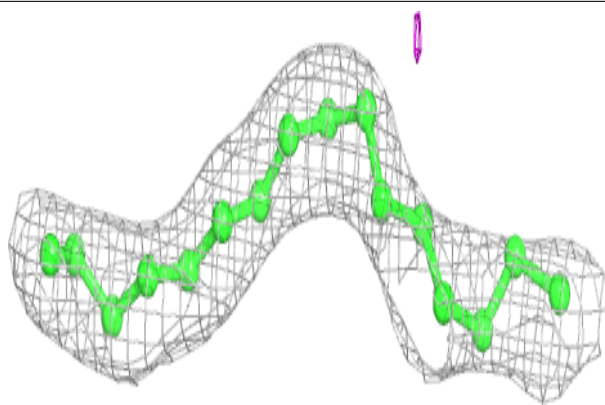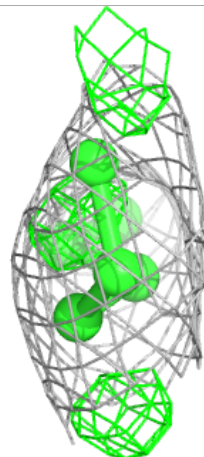

Electron density around LFA A 318:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
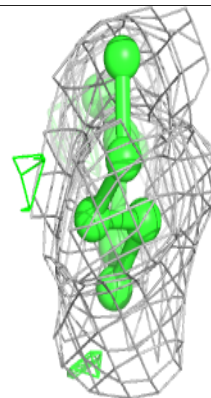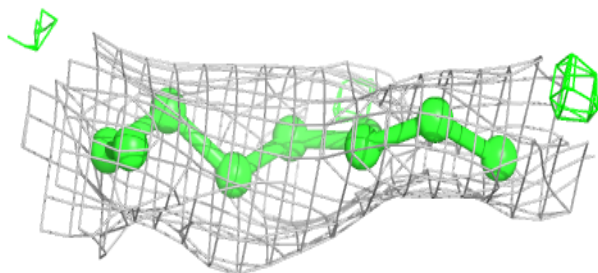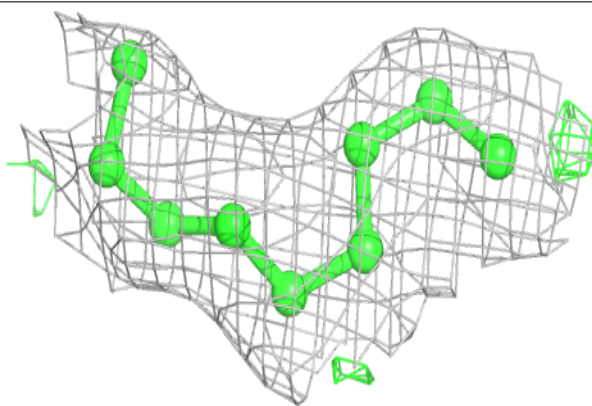
Electron density around LFA A 307:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
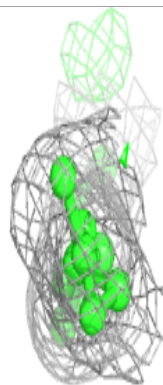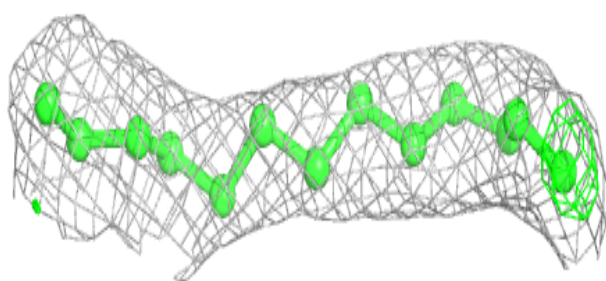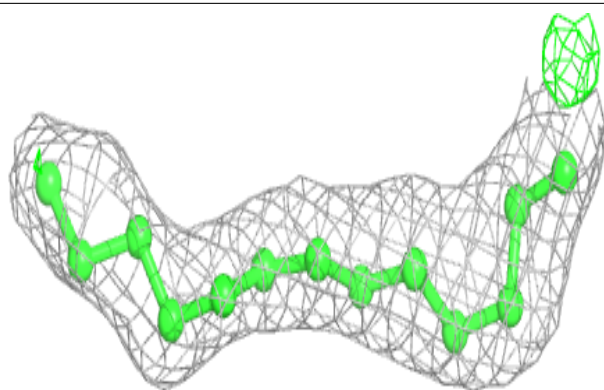
Electron density around LFA A 305:

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

Electron density around LFA A 321:

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

Electron density around LFA A 312:

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

Electron density around LFA A 325:

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

Electron density around LFA A 317:

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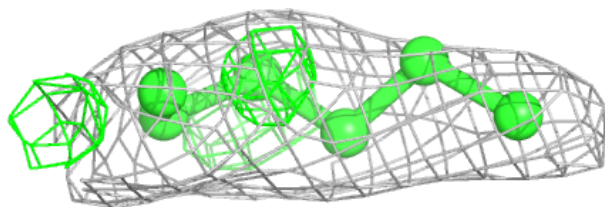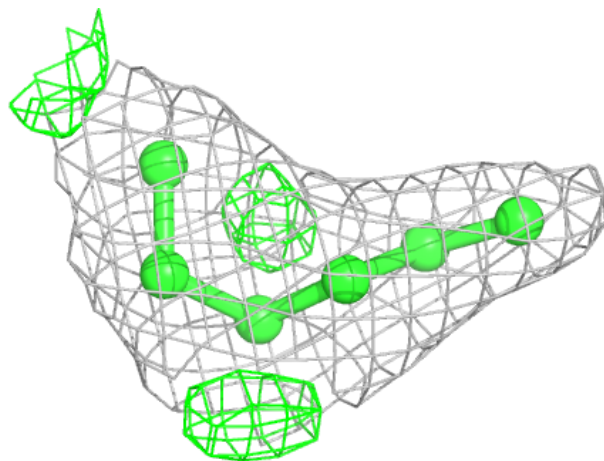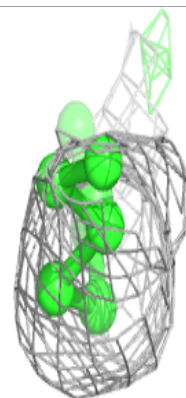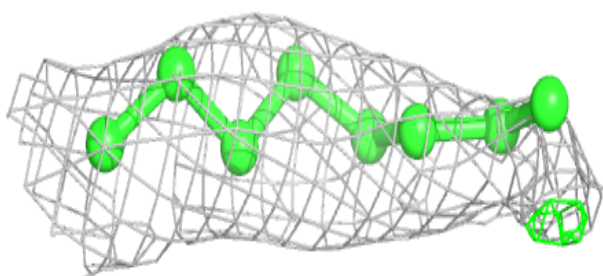$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
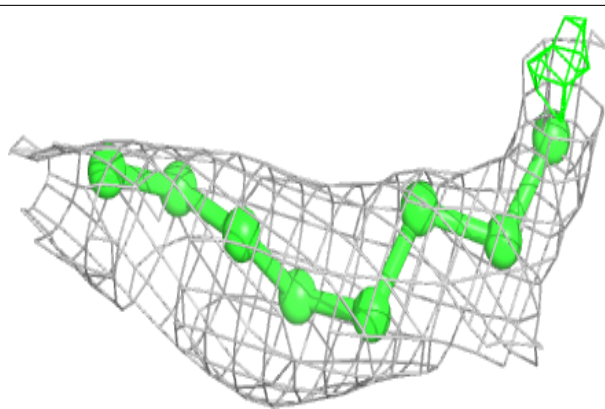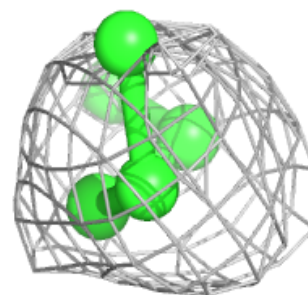and green (positive)

Electron density around LFA A 310:

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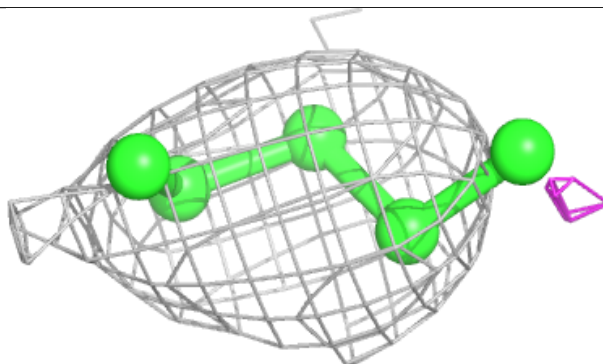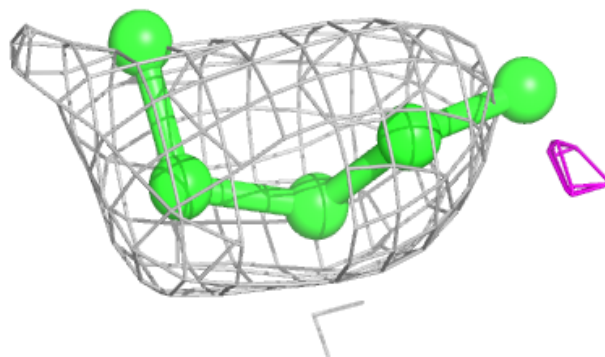and green (positive)

Electron density around LFA A 326:

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

Electron density around LFA A 308:

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

Electron density around LFA A 319:

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

Electron density around LFA A 303:

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

Electron density around LFA A 313:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (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
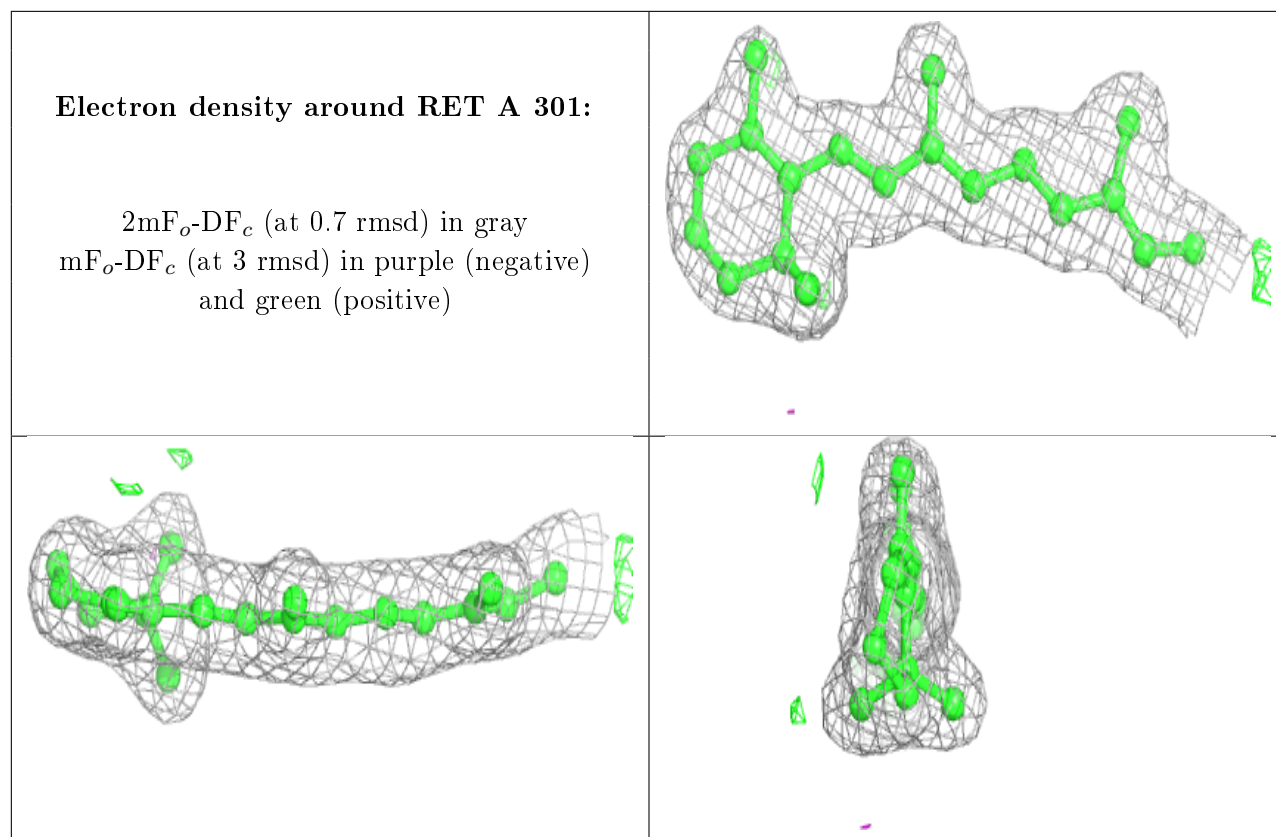mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

6.5 Other polymers (i)

There are no such residues in this entry.