



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2021 – 06:34 PM EDT

PDB ID : 3D4S
Title : Cholesterol bound form of human beta2 adrenergic receptor.
Authors : Hanson, M.A.; Cherezov, V.; Roth, C.B.; Griffith, M.T.; Jaakola, V.-P.; Chien, E.Y.T.; Velasquez, J.; Kuhn, P.; Stevens, R.C.; Accelerated Technologies Center for Gene to 3D Structure (ATCG3D); GPCR Network (GPCR)
Deposited on : 2008-05-14
Resolution : 2.80 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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 : 2.23.2
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) : 2.23.2

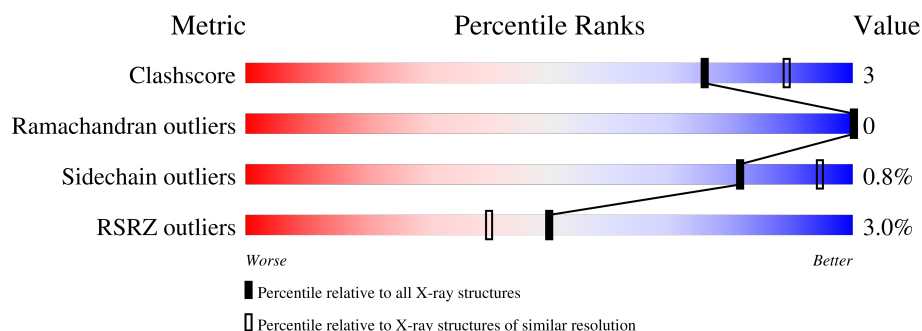
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	490	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3699 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.

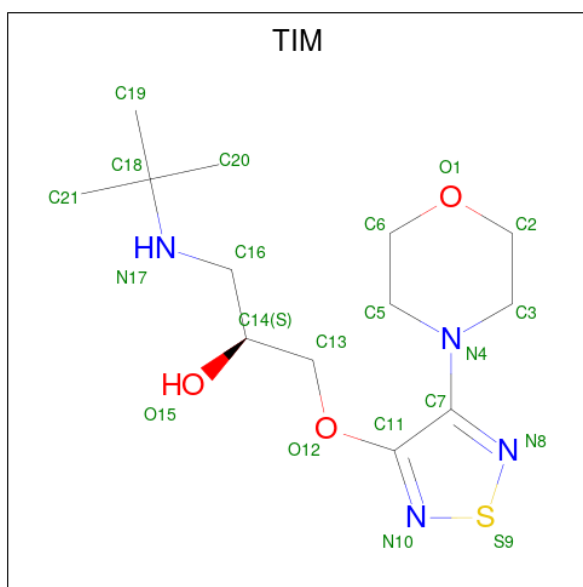
- Molecule 1 is a protein called Beta-2 adrenergic receptor/T4-lysozyme chimera.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	439	Total	C	N	O	S	0	0	0
			3527	2308	588	607	24			

There are 18 discrepancies between the modelled and reference sequences:

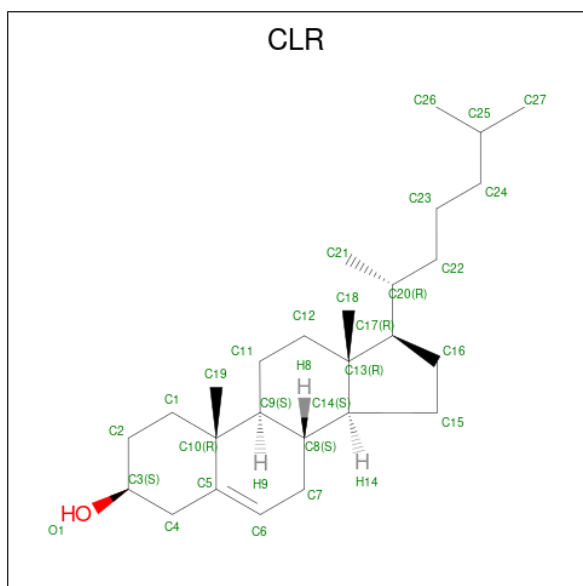
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	ASP	-	expression tag	UNP P07550
A	-6	TYR	-	expression tag	UNP P07550
A	-5	LYS	-	expression tag	UNP P07550
A	-4	ASP	-	expression tag	UNP P07550
A	-3	ASP	-	expression tag	UNP P07550
A	-2	ASP	-	expression tag	UNP P07550
A	-1	ASP	-	expression tag	UNP P07550
A	0	ALA	-	expression tag	UNP P07550
A	122	TRP	GLU	engineered mutation	UNP P07550
A	187	GLU	ASN	engineered mutation	UNP P07550
A	1054	THR	CYS	engineered mutation	UNP P00720
A	1097	ALA	CYS	engineered mutation	UNP P00720
A	349	HIS	-	expression tag	UNP P07550
A	350	HIS	-	expression tag	UNP P07550
A	351	HIS	-	expression tag	UNP P07550
A	352	HIS	-	expression tag	UNP P07550
A	353	HIS	-	expression tag	UNP P07550
A	354	HIS	-	expression tag	UNP P07550

- Molecule 2 is (2S)-1-(tert-butylamino)-3-[(4-morpholin-4-yl-1,2,5-thiadiazol-3-yl)oxy]propan-2-ol (three-letter code: TIM) (formula: C₁₃H₂₄N₄O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			21	13	4	3	1		

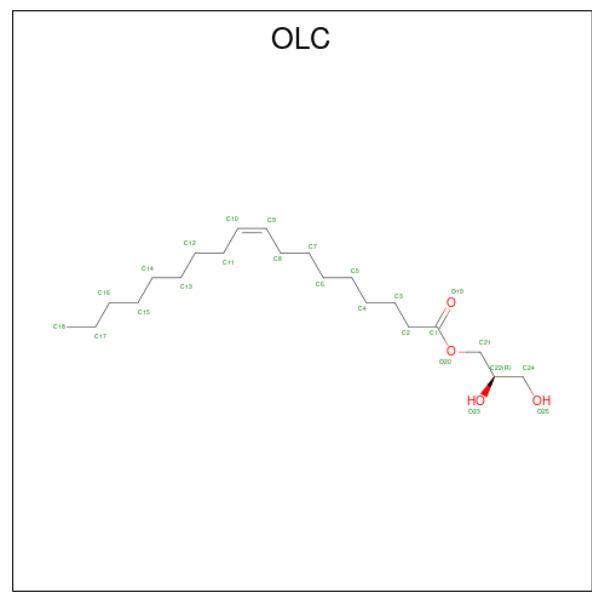
- Molecule 3 is CHOLESTEROL (three-letter code: CLR) (formula: C₂₇H₄₆O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			28	27	1		
3	A	1	Total	C	O	0	0
			28	27	1		

- Molecule 4 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLC)

(formula: C₂₁H₄₀O₄).



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

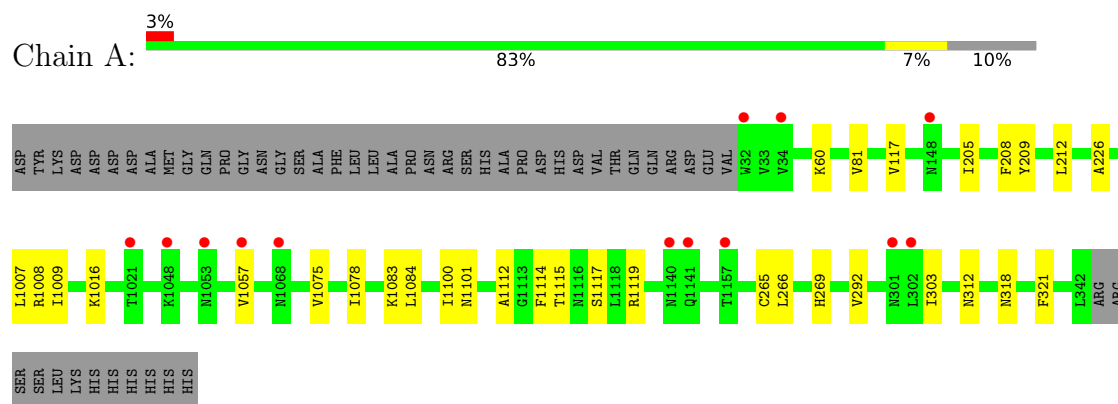
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	20	Total	O	0	0
			20	20		

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: Beta-2 adrenergic receptor/T4-lysozyme chimera



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	40.00Å 75.70Å 172.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80 19.88 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.80) 94.3 (19.88-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 2.79Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.230 , 0.273 0.230 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	57.6	Xtriage
Anisotropy	0.558	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3699	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.47% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.46	0/3610	0.62	0/4902

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3527	0	3599	19	0
2	A	21	0	24	1	0
3	A	56	0	90	6	0
4	A	75	0	120	0	0
5	A	20	0	0	0	0
All	All	3699	0	3833	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 3.

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:81:VAL:HG13	3:A:403:CLR:H263	1.85	0.57
1:A:1075:VAL:HG22	1:A:1100:ILE:HD13	1.87	0.57
1:A:1078:ILE:HG23	1:A:1084:LEU:HB3	1.91	0.52
1:A:318:ASN:HA	1:A:321:PHE:HD1	1.76	0.50
1:A:226:ALA:HB1	1:A:269:HIS:CE1	2.47	0.49
3:A:402:CLR:H3	3:A:403:CLR:H3	1.94	0.49
1:A:1009:ILE:HD13	1:A:265:CYS:HB2	1.95	0.49
1:A:1009:ILE:HD11	1:A:266:LEU:HB2	1.97	0.47
1:A:117:VAL:HG21	2:A:401:TIM:H13A	1.97	0.47
3:A:402:CLR:H212	3:A:402:CLR:H121	1.97	0.46
1:A:292:VAL:HG13	1:A:303:ILE:HG21	1.97	0.46
1:A:81:VAL:HG22	3:A:403:CLR:H221	1.97	0.46
1:A:1007:LEU:HD21	1:A:1101:ASN:HA	1.99	0.45
1:A:1016:LYS:HG2	1:A:1057:VAL:HG22	2.01	0.43
1:A:1083:LYS:HD2	1:A:1112:ALA:HB1	2.00	0.43
1:A:266:LEU:HB3	1:A:269:HIS:CD2	2.54	0.42
1:A:1114:PHE:HB3	1:A:1117:SER:HB2	2.01	0.42
1:A:1115:THR:HG22	1:A:1119:ARG:NH1	2.35	0.42
3:A:402:CLR:H273	3:A:402:CLR:H232	1.83	0.41
1:A:1075:VAL:HG22	1:A:1100:ILE:CD1	2.48	0.41
3:A:403:CLR:H212	3:A:403:CLR:H121	2.01	0.41
1:A:205:ILE:HA	1:A:209:TYR:HB2	2.04	0.40
1:A:208:PHE:CE2	1:A:212:LEU:HD22	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	437/490 (89%)	426 (98%)	11 (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	380/424 (90%)	377 (99%)	3 (1%)	81	94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	LYS
1	A	1008	ARG
1	A	312	ASN

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

Mol	Chain	Res	Type
1	A	142	GLN
1	A	172	HIS
1	A	197	GLN
1	A	224	GLN
1	A	1055	ASN

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

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	OLC	A	405	-	24,24,24	0.41	0	25,25,25	0.60	0
4	OLC	A	406	-	24,24,24	0.41	0	25,25,25	0.64	1 (4%)
3	CLR	A	402	-	31,31,31	0.56	0	48,48,48	1.51	8 (16%)
3	CLR	A	403	-	31,31,31	0.59	0	48,48,48	1.59	6 (12%)
2	TIM	A	401	-	20,22,22	1.02	1 (5%)	22,30,30	2.69	5 (22%)
4	OLC	A	404	-	24,24,24	0.41	0	25,25,25	0.59	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	OLC	A	405	-	-	9/24/24/24	-
4	OLC	A	406	-	-	10/24/24/24	-
3	CLR	A	402	-	-	3/10/68/68	0/4/4/4
3	CLR	A	403	-	-	5/10/68/68	0/4/4/4
2	TIM	A	401	-	-	5/9/23/23	0/2/2/2
4	OLC	A	404	-	-	15/24/24/24	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	TIM	C7-C11	2.35	1.52	1.45

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	TIM	C16-N17-C18	-8.85	107.10	116.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	TIM	C14-C16-N17	6.24	119.30	110.74
3	A	403	CLR	C19-C10-C9	-4.75	106.02	111.68
3	A	403	CLR	C15-C14-C8	4.51	126.51	119.08
3	A	402	CLR	C3-C4-C5	-4.11	105.05	112.03
3	A	402	CLR	C19-C10-C9	-3.88	107.06	111.68
2	A	401	TIM	O12-C13-C14	-3.78	100.57	107.63
3	A	403	CLR	C12-C13-C17	-3.63	111.14	116.57
3	A	403	CLR	C15-C14-C13	3.48	108.04	103.84
2	A	401	TIM	C3-N4-C5	3.28	118.76	111.52
3	A	402	CLR	C15-C14-C8	3.23	124.40	119.08
3	A	403	CLR	C1-C10-C9	3.10	113.06	108.73
3	A	403	CLR	C13-C14-C8	2.79	118.51	114.38
2	A	401	TIM	C2-C3-N4	2.61	114.83	110.02
3	A	402	CLR	C19-C10-C1	-2.54	105.41	109.43
3	A	402	CLR	C15-C14-C13	2.53	106.89	103.84
3	A	402	CLR	C1-C10-C9	2.46	112.16	108.73
3	A	402	CLR	C13-C14-C8	2.26	117.73	114.38
4	A	406	OLC	O20-C1-O19	-2.03	118.46	123.59
3	A	402	CLR	C12-C13-C17	-2.03	113.53	116.57

There are no chirality outliers.

All (47) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	406	OLC	C2-C1-O20-C21
4	A	406	OLC	O19-C1-O20-C21
3	A	403	CLR	C17-C20-C22-C23
4	A	406	OLC	C1-C2-C3-C4
3	A	403	CLR	C22-C23-C24-C25
4	A	404	OLC	O19-C1-O20-C21
3	A	402	CLR	C22-C23-C24-C25
3	A	403	CLR	C21-C20-C22-C23
4	A	405	OLC	C5-C6-C7-C8
4	A	406	OLC	C4-C5-C6-C7
3	A	402	CLR	C23-C24-C25-C26
4	A	406	OLC	C12-C13-C14-C15
2	A	401	TIM	O12-C13-C14-O15
4	A	404	OLC	C2-C1-O20-C21
4	A	406	OLC	C5-C6-C7-C8
4	A	404	OLC	C10-C11-C12-C13
4	A	406	OLC	C10-C11-C12-C13
4	A	404	OLC	C15-C16-C17-C18

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Mol	Chain	Res	Type	Atoms
4	A	406	OLC	C3-C4-C5-C6
4	A	404	OLC	C3-C4-C5-C6
4	A	404	OLC	C12-C13-C14-C15
4	A	405	OLC	C15-C16-C17-C18
2	A	401	TIM	O12-C13-C14-C16
4	A	404	OLC	C13-C14-C15-C16
4	A	406	OLC	C14-C15-C16-C17
3	A	402	CLR	C23-C24-C25-C27
4	A	405	OLC	C10-C11-C12-C13
4	A	404	OLC	C4-C5-C6-C7
4	A	405	OLC	O19-C1-O20-C21
4	A	405	OLC	C11-C12-C13-C14
4	A	404	OLC	C1-C2-C3-C4
4	A	405	OLC	C12-C13-C14-C15
4	A	404	OLC	C9-C10-C11-C12
4	A	404	OLC	C2-C3-C4-C5
4	A	404	OLC	C11-C12-C13-C14
4	A	404	OLC	C6-C7-C8-C9
2	A	401	TIM	C19-C18-N17-C16
3	A	403	CLR	C23-C24-C25-C27
2	A	401	TIM	O15-C14-C16-N17
2	A	401	TIM	C20-C18-N17-C16
4	A	404	OLC	C5-C6-C7-C8
4	A	404	OLC	O20-C1-C2-C3
4	A	405	OLC	C9-C10-C11-C12
3	A	403	CLR	C23-C24-C25-C26
4	A	406	OLC	C13-C14-C15-C16
4	A	405	OLC	O19-C1-C2-C3
4	A	405	OLC	O20-C1-C2-C3

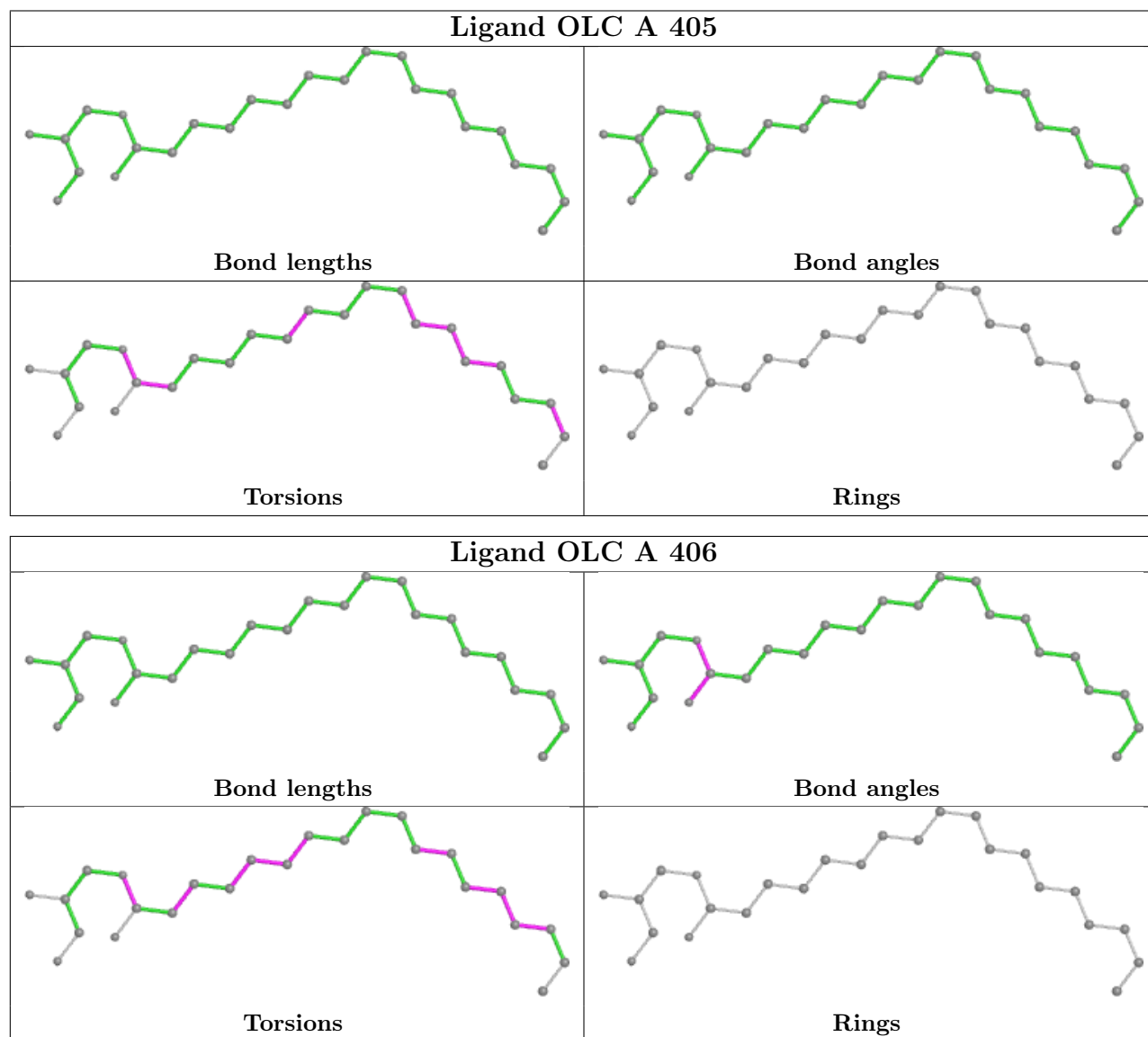
There are no ring outliers.

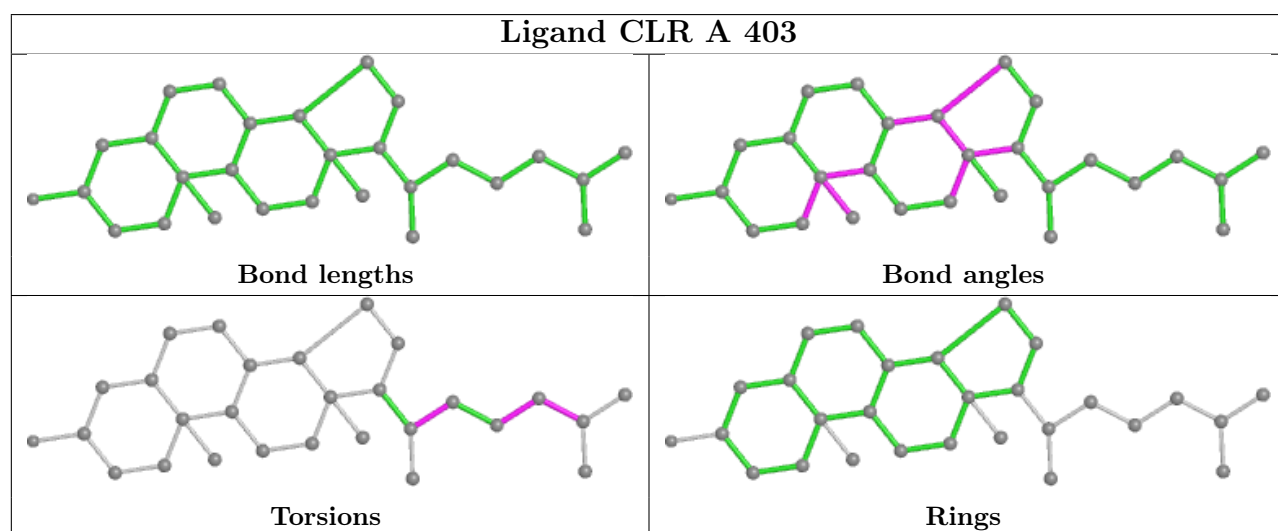
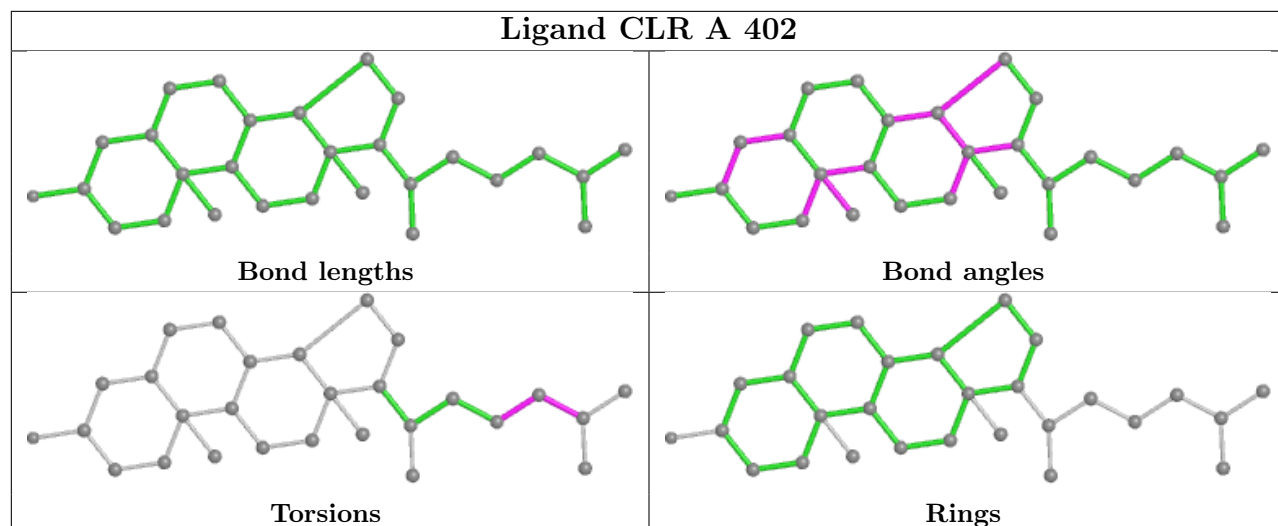
3 monomers are involved in 7 short contacts:

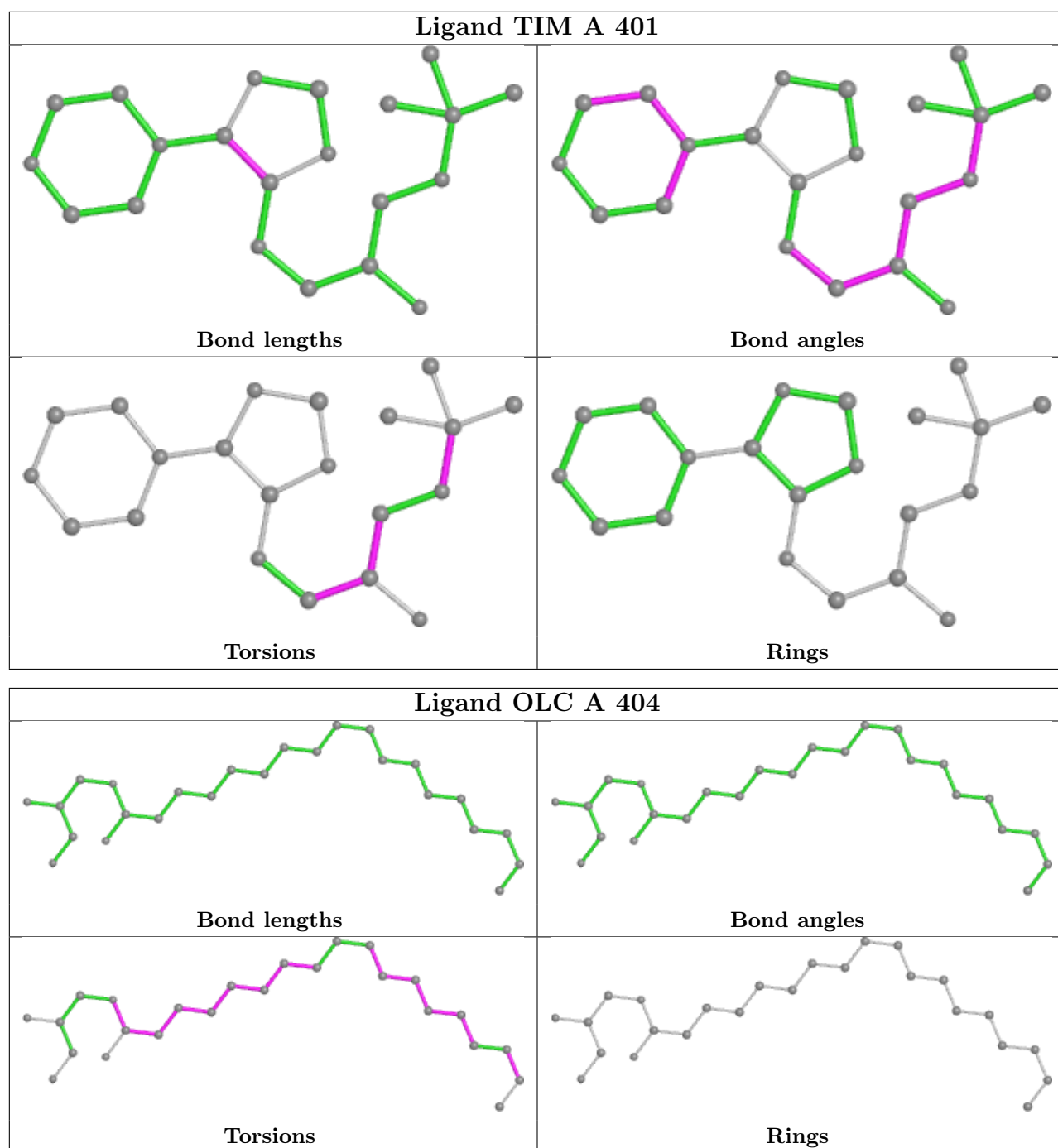
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	CLR	3	0
3	A	403	CLR	4	0
2	A	401	TIM	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	439/490 (89%)	0.06	13 (2%)	50 40	39, 66, 99, 131	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1053	ASN	4.3
1	A	32	TRP	4.1
1	A	1048	LYS	3.6
1	A	302	LEU	3.3
1	A	1141	GLN	3.1
1	A	148	ASN	2.7
1	A	1021	THR	2.7
1	A	1068	ASN	2.6
1	A	34	VAL	2.5
1	A	1140	ASN	2.2
1	A	1157	THR	2.2
1	A	301	ASN	2.1
1	A	1057	VAL	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](#)

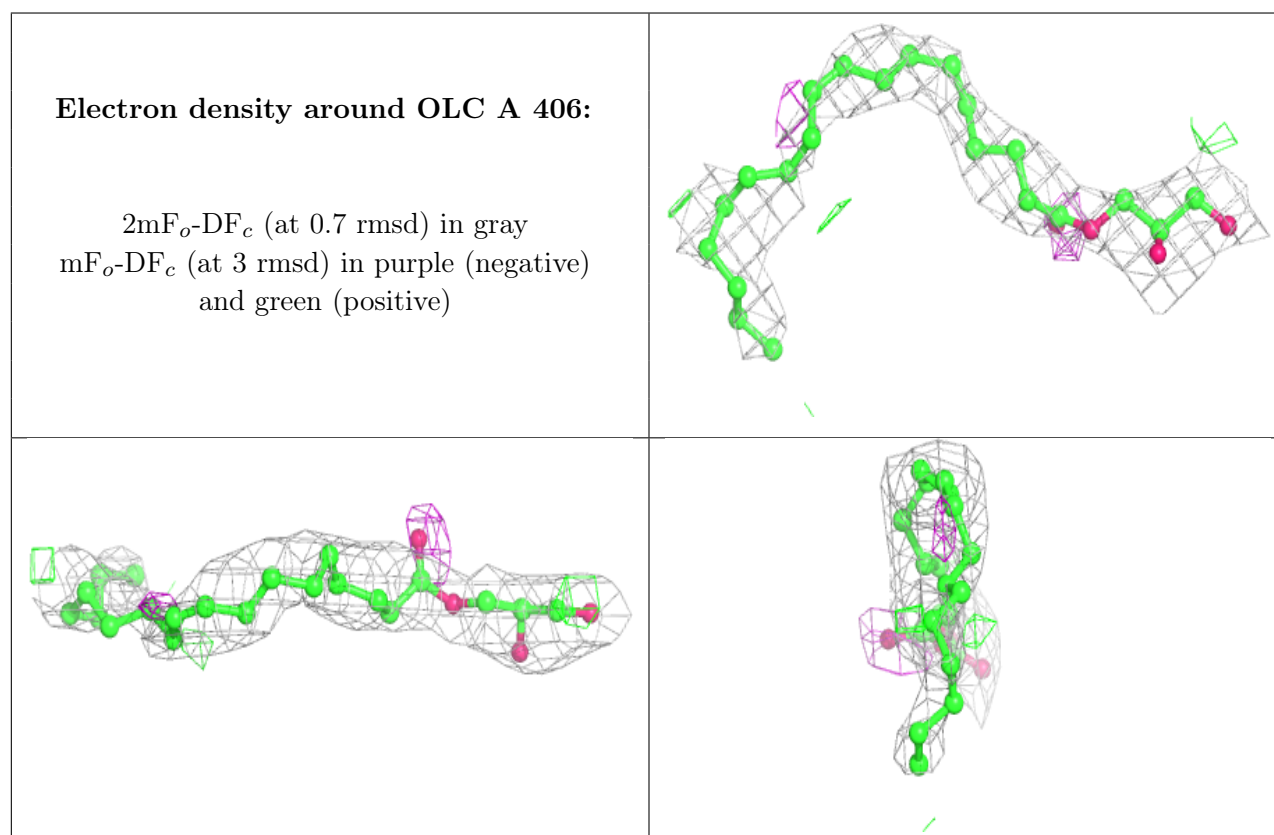
There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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

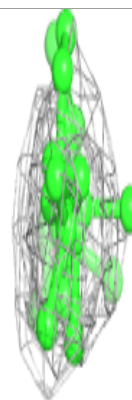
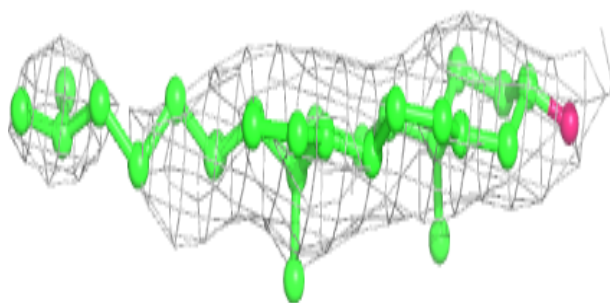
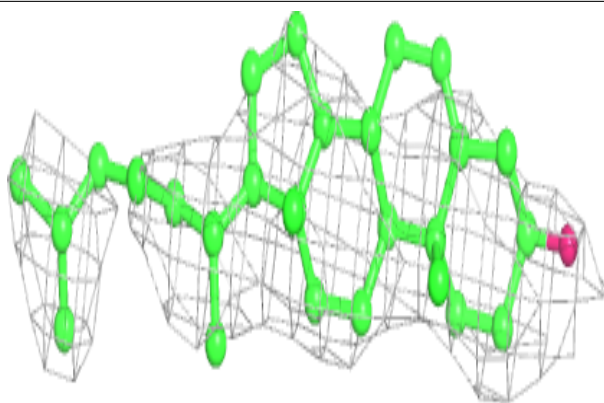
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	OLC	A	406	25/25	0.74	0.35	54,68,79,83	0
3	CLR	A	403	28/28	0.76	0.40	71,97,104,105	0
4	OLC	A	404	25/25	0.81	0.27	51,62,76,77	0
4	OLC	A	405	25/25	0.85	0.26	52,63,72,72	0
3	CLR	A	402	28/28	0.85	0.26	56,81,93,96	0
2	TIM	A	401	21/21	0.95	0.22	36,48,57,58	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.

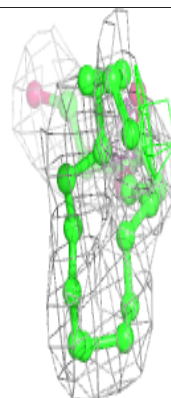
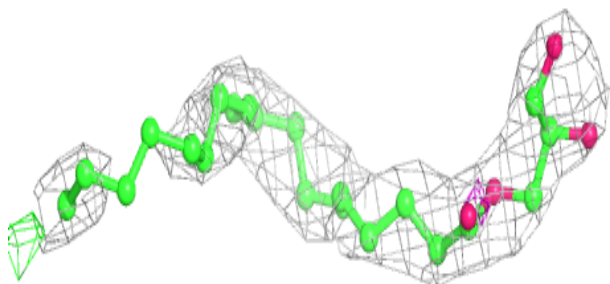
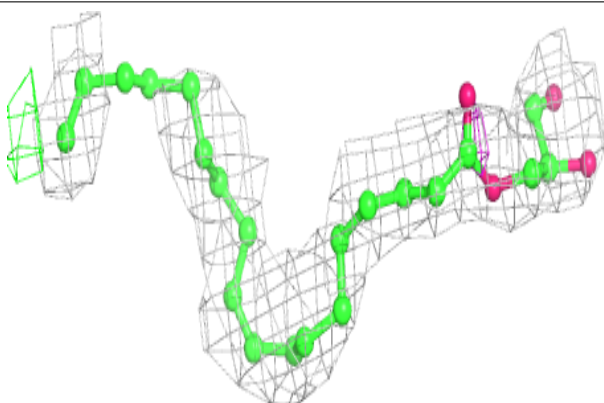


Electron density around CLR A 403:

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

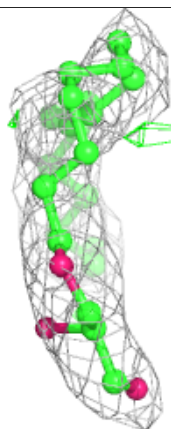
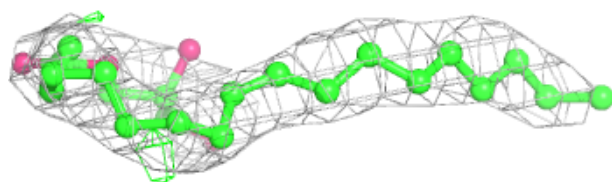
**Electron density around OLC A 404:**

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

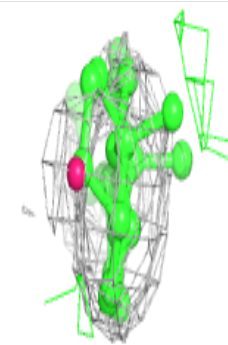
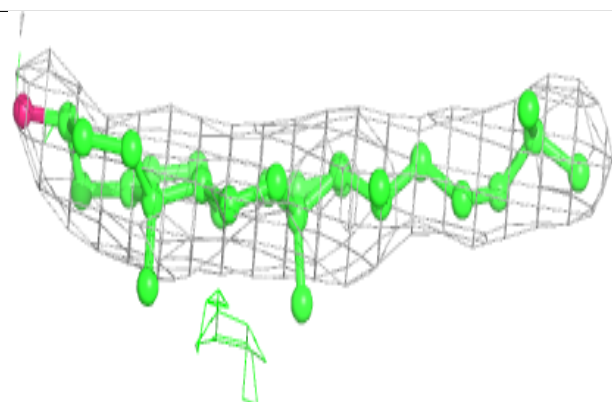
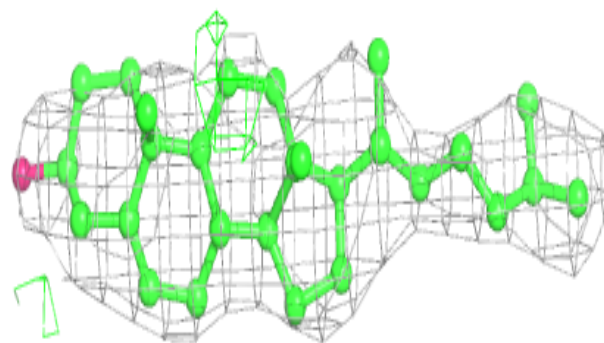


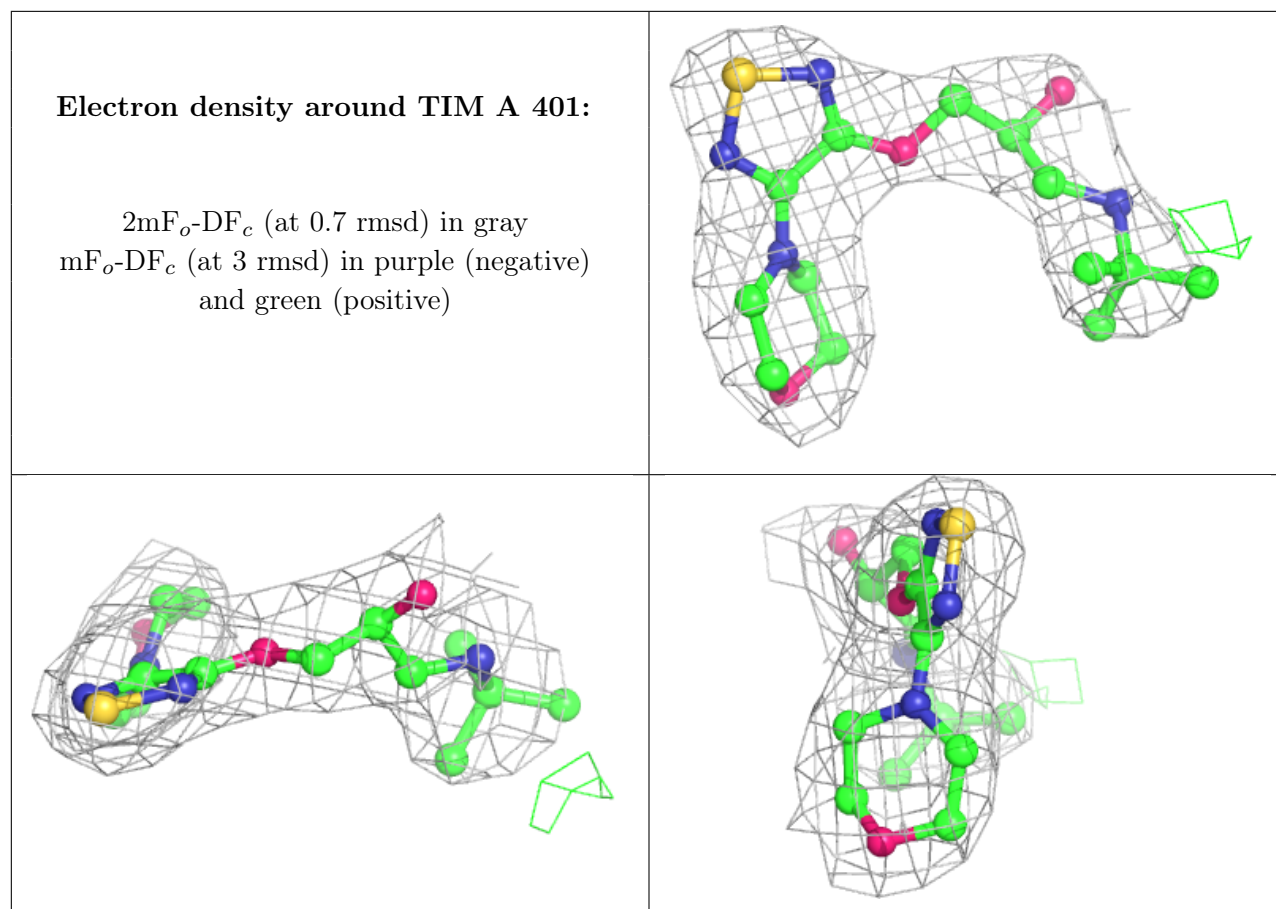
Electron density around OLC A 405:

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

**Electron density around CLR A 402:**

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





6.5 Other polymers ⓘ

There are no such residues in this entry.