wwPDB X-ray Structure Validation Summary Report (i)

Aug 22, 2023 – 11:30 PM EDT

PDB ID	:	3DCT
Title	:	FXR with SRC1 and GW4064
Authors	:	Williams, S.P.; Madauss, K.P.
Deposited on	:	2008-06-04
Resolution	:	2.50 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

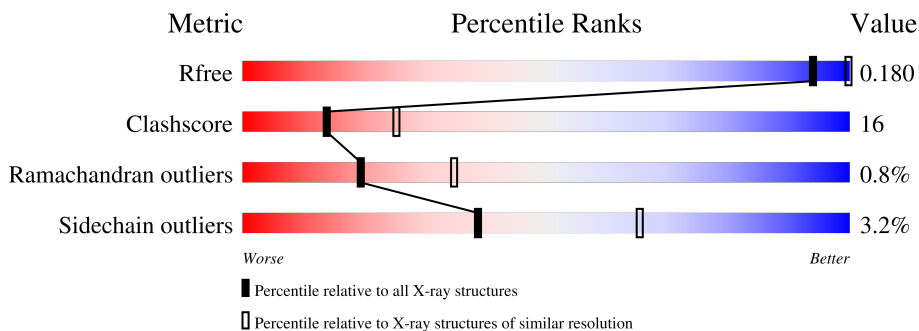|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh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

1 Overall quality at a glance ⓘ

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

The reported resolution of this entry is 2.50 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	Percentile Ranks	Value
Rfree		0.180
Clashscore		16
Ramachandran outliers		0.8%
Sidechain outliers		3.2%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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%

Mol	Chain	Length	Quality of chain
1	A	235	62% 34% • •
2	B	21	43% 10% 48%

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 1920 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 Bile acid receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	229	Total 1751	C 1119	N 292	O 329	S 11	0	0	0

- Molecule 2 is a protein called Nuclear receptor coactivator 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	11	Total 86	C 57	N 14	O 15	0	0	0

- Molecule 3 is 3-[(E)-2-(2-chloro-4-{[3-(2,6-dichlorophenyl)-5-(1-methylethyl)isoxazol-4-yl]methoxy}phenyl)ethenyl]benzoic acid (three-letter code: 064) (formula: $C_{28}H_{22}Cl_3NO_4$).
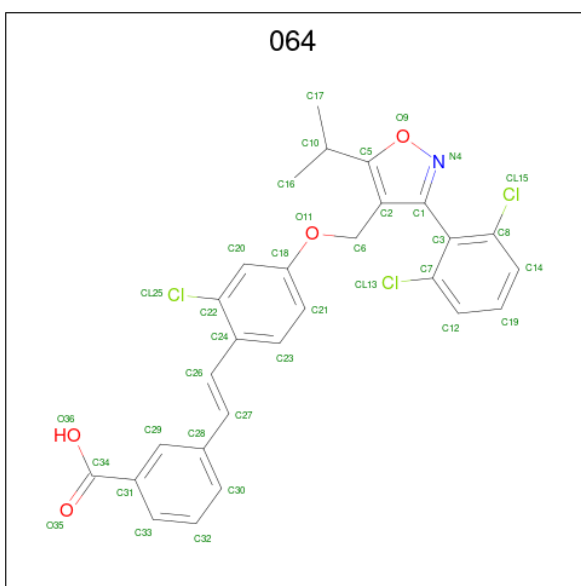
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 36	C 28	Cl 3	N 1	O 4	0	0

- Molecule 4 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	46	Total 46	O 46	0	0
4	B	1	Total 1	O 1	0	0

3 Residue-property plots ⓘ

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. 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. 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: Bile acid receptor

Chain A:
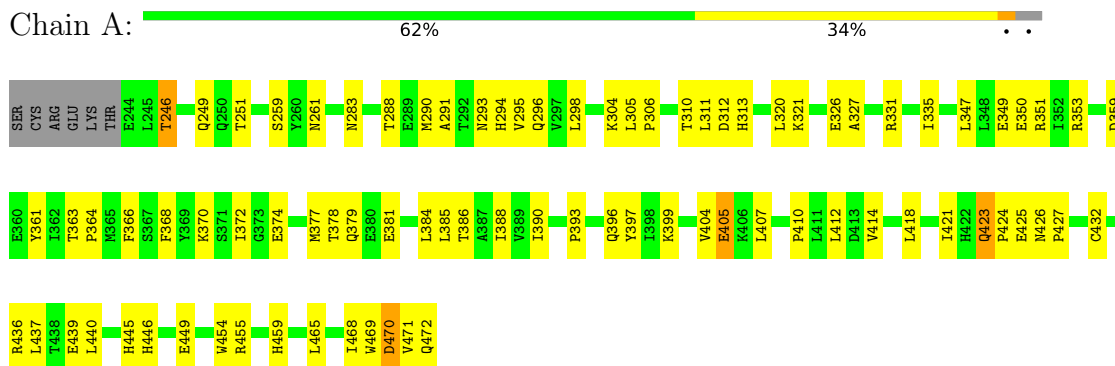
• Molecule 2: Nuclear receptor coactivator 1

Chain B:
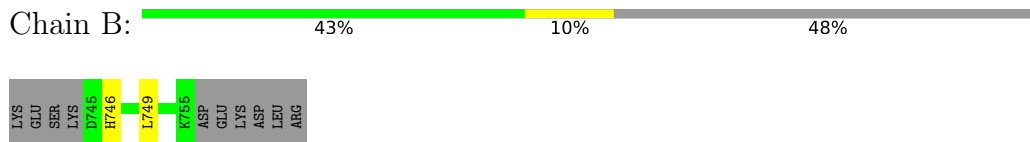
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	F 2 3	Depositor
Cell constants a, b, c, α, β, γ	159.45Å 159.45Å 159.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 48.08 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (20.00-2.50) 99.9 (48.08-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	2.93 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.230 , 0.240 0.182 , 0.180	Depositor DCC
R_{free} test set	879 reflections (7.48%)	wwPDB-VP
Wilson B-factor (Å^2)	46.8	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 37.5	EDS
L-test for twinning[2]	$< |L| > = 0.40, < L^2 > = 0.22$	Xtriage
Estimated twinning fraction	0.336 for k,h,-l	Xtriage
Reported twinning fraction	0.020 for k,h,-l	Depositor
Outliers	0 of 11745 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	1920	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.26% 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 ⓘ

5.1   Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 064

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	0.43	1/1788 (0.1%)	0.62	0/2436
2	B	0.40	0/87	0.65	0/118
All	All	0.43	1/1875 (0.1%)	0.62	0/2554

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	405	GLU	CA-CB	-6.05	1.40	1.53

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	1751	0	1634	57	0
2	B	86	0	77	2	0
3	A	36	0	21	4	0
4	A	46	0	0	7	0
4	B	1	0	0	0	0
All	All	1920	0	1732	57	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 16.

The worst 5 of 57 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:290:MET:HE2	3:A:1:064:H27	1.23	1.15
1:A:290:MET:CE	3:A:1:064:H27	1.92	1.00
1:A:405:GLU:CB	4:A:515:HOH:O	2.16	0.94
1:A:407:LEU:O	4:A:495:HOH:O	1.89	0.90
1:A:363:THR:HB	1:A:364:PRO:HD3	1.56	0.86

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	227/235 (97%)	212 (93%)	13 (6%)	2 (1%)	17	31
2	B	9/21 (43%)	9 (100%)	0	0	100	100
All	All	236/256 (92%)	221 (94%)	13 (6%)	2 (1%)	19	35

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	310	THR
1	A	470	ASP

5.3.2　Protein sidechains　ⓘ

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	179/218 (82%)	173 (97%)	6 (3%)	37	63
2	B	8/21 (38%)	8 (100%)	0	100	100
All	All	187/239 (78%)	181 (97%)	6 (3%)	39	65

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	423	GLN
1	A	432	CYS
1	A	455	ARG
1	A	251	THR
1	A	246	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	444	ASN
2	B	747	GLN
1	A	316	GLN
1	A	354	ASN
1	A	416	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	064	A	1	-	34,39,39	2.22	18 (52%)	43,55,55	1.99	8 (18%)

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	064	A	1	-	-	3/14/22/22	0/4/4/4

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1	064	O35-C34	4.88	1.37	1.22
3	A	1	064	C21-C18	3.67	1.46	1.38
3	A	1	064	C6-C2	3.26	1.55	1.51
3	A	1	064	C30-C28	3.25	1.45	1.39
3	A	1	064	C23-C24	3.09	1.46	1.41

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1	064	C22-C24-C26	-8.71	115.21	121.86
3	A	1	064	C23-C24-C22	3.99	120.33	116.69
3	A	1	064	O11-C6-C2	3.62	114.08	107.20
3	A	1	064	C21-C23-C24	-2.88	117.84	121.74
3	A	1	064	C7-C3-C8	-2.86	118.87	125.49

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1	064	C26-C27-C28-C29

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WORLD WIDE PDB
PROTEIN DATA BANK

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Mol	Chain	Res	Type	Atoms
3	A	1	064	C26-C27-C28-C30
3	A	1	064	C22-C24-C26-C27

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1	064	4	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 064 A 1 — Bond lengths, Bond angles, Torsions, Rings
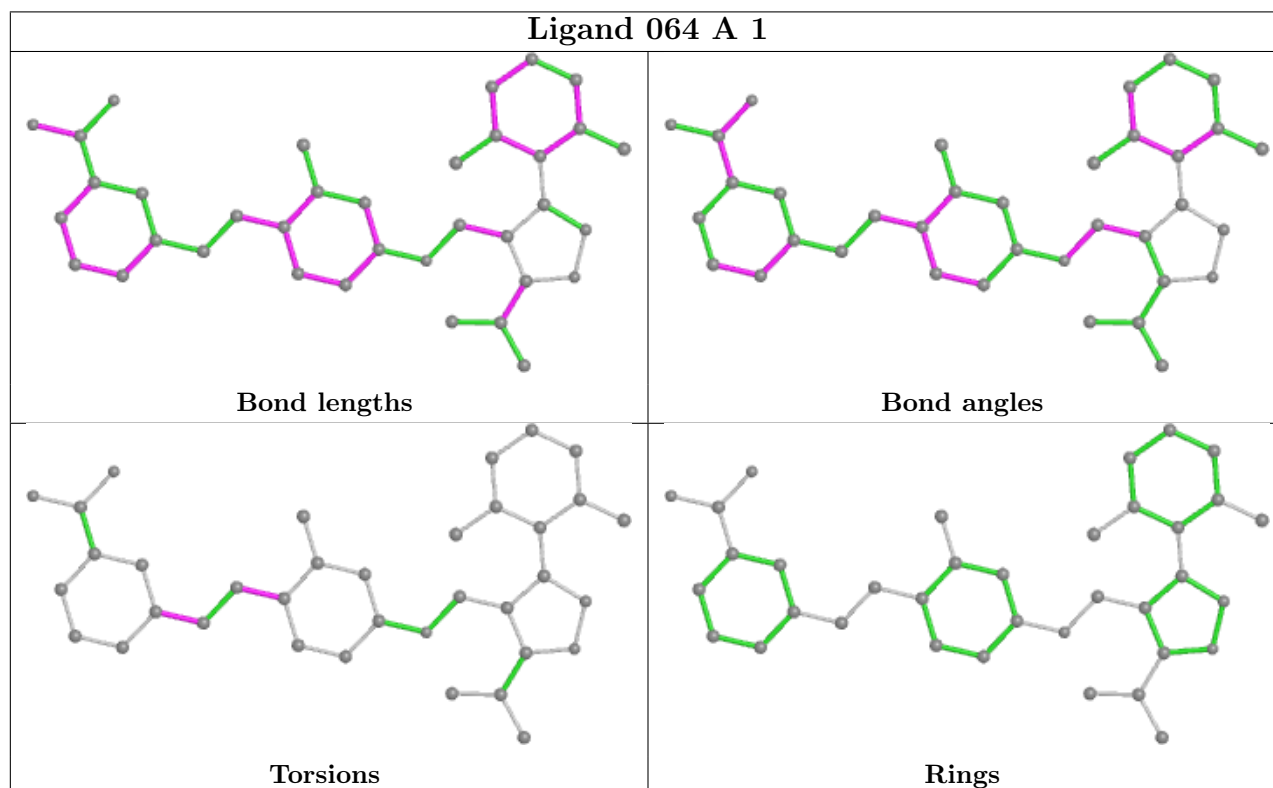
5.7 Other polymers (i)

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

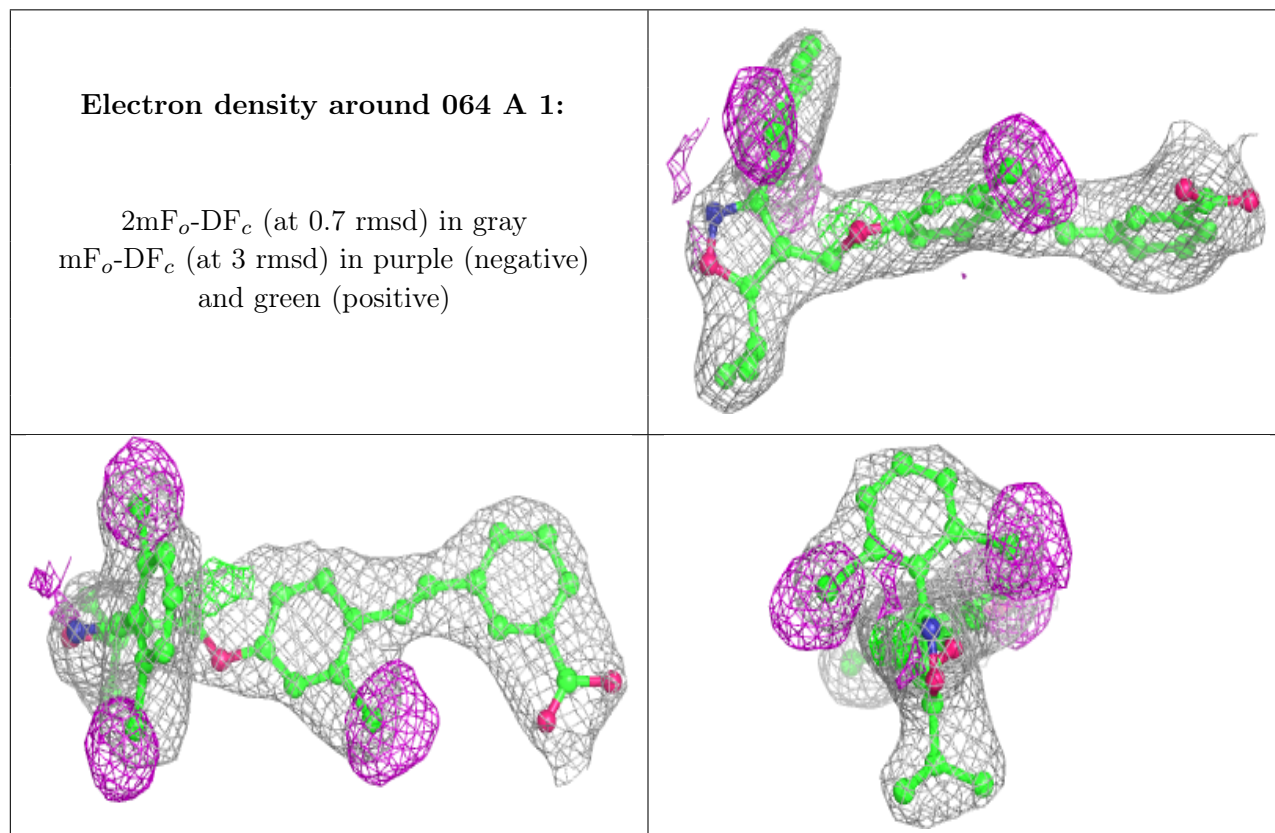Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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 064 A 1:

$2mF_o$-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 ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.