Full wwPDB X-ray Structure Validation Report (i)

May 28, 2020 – 04:29 am BST

PDB ID	:	3DCU
Title	:	FXR with SRC1 and GSK8062
Authors	:	Williams, S.P.; Madauss, K.P.
Deposited on	:	2008-06-04
Resolution	:	2.95 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 following versions of software and data (see references (i)) were used in the production of this report:

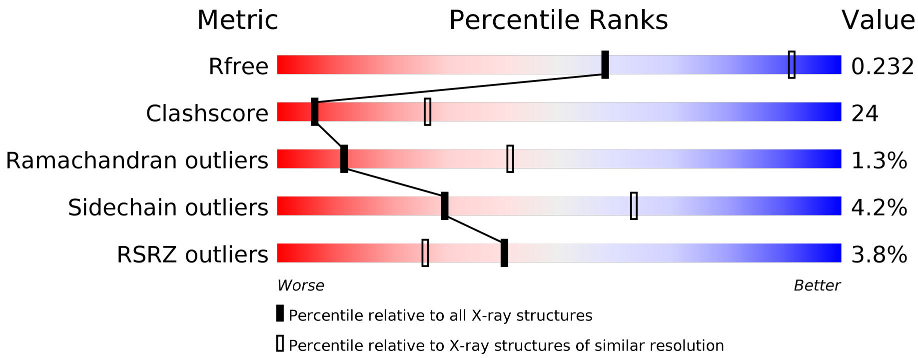
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.95 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	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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	235	4% 53% 42% • •
2	B	21	48% 5% 48%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1887 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.

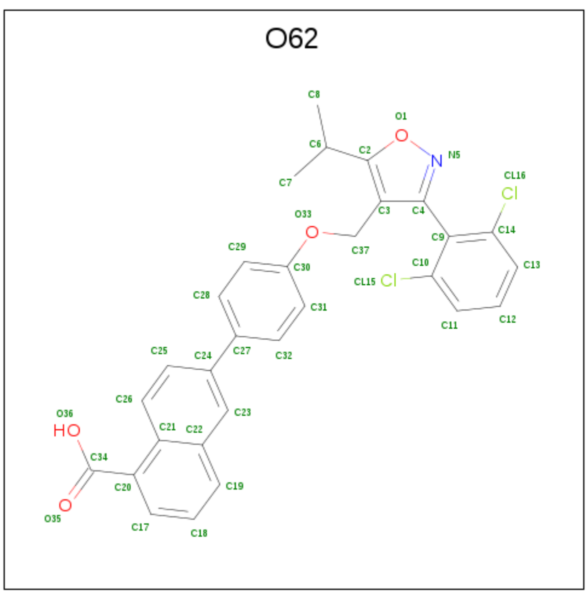
- Molecule 1 is a protein called Bile acid receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	229	1759	1126	295	327	11	0	0	0

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

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

- Molecule 3 is 6-(4-{[3-(2,6-dichlorophenyl)-5-(1-methylethyl)isoxazol-4-yl]methoxy}phenyl) naphthalene-1-carboxylic acid (three-letter code: O62) (formula: $C_{30}H_{23}Cl_2NO_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
3	A	1	37	30	2	1	4	0	0

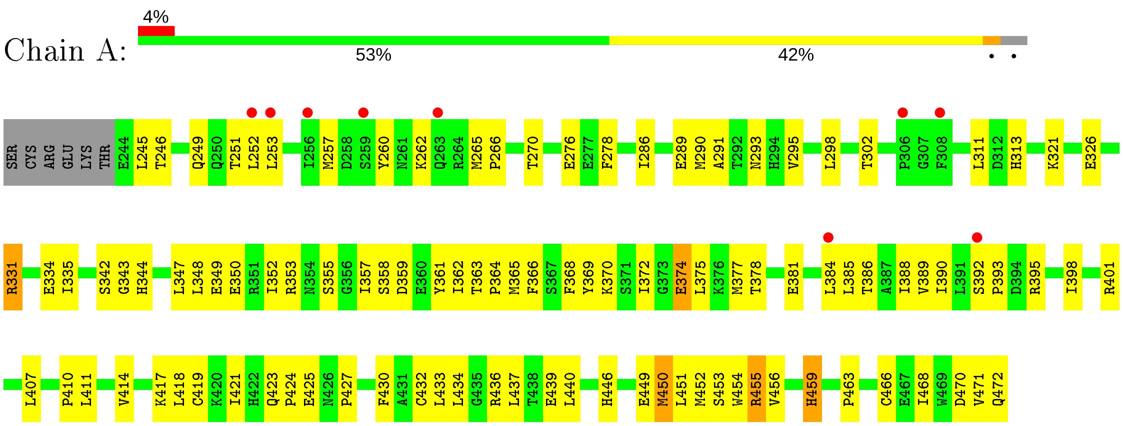
- Molecule 4 is water.

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

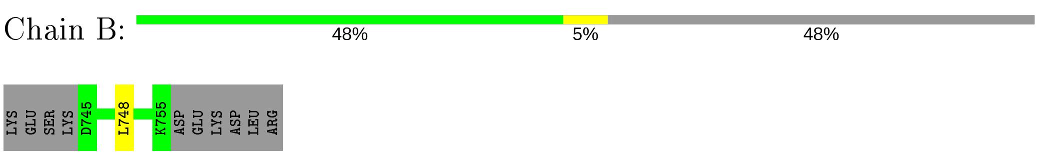
3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA 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: Bile acid receptor



• Molecule 2: Nuclear receptor coactivator 1



4 Data and refinement statistics

Property	Value	Source
Space group	F 2 3	Depositor
Cell constants a, b, c, α, β, γ	158.62Å 158.62Å 158.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.95 45.79 – 2.95	Depositor EDS
% Data completeness (in resolution range)	98.1 (30.00-2.95) 98.9 (45.79-2.95)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.88 (at 2.96Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.181 , 0.228 0.184 , 0.232	Depositor DCC
R_{free} test set	470 reflections (6.70%)	wwPDB-VP
Wilson B-factor (Å^2)	68.6	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 61.6	EDS
L-test for twinning[2]	$< \|L\| >$ = 0.42, $< L^2 >$ = 0.24	Xtriage
Estimated twinning fraction	0.228 for k,h,-l	Xtriage
Reported twinning fraction	0.177 for k,h,-l	Depositor
Outliers	0 of 7012 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	1887	wwPDB-VP
Average B, all atoms (Å^2)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.94% 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: O62

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	0.48	0/1796	0.74	0/2446
2	B	0.40	0/87	0.68	0/118
All	All	0.47	0/1883	0.73	0/2564

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	1759	0	1659	86	0
2	B	86	0	77	1	0
3	A	37	0	23	3	0
4	A	5	0	0	0	0
All	All	1887	0	1759	86	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 24.

All (86) 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:358:SER:H	1:A:450:MET:HE3	1.29	0.97
1:A:358:SER:H	1:A:450:MET:CE	1.85	0.90
1:A:466:CYS:HA	1:A:471:VAL:HG22	1.59	0.85
1:A:363:THR:HB	1:A:364:PRO:HD3	1.61	0.83
1:A:286:ILE:O	1:A:290:MET:HG2	1.80	0.81
1:A:414:VAL:O	1:A:418:LEU:HG	1.84	0.76
1:A:410:PRO:O	1:A:414:VAL:HG23	1.91	0.71
1:A:370:LYS:O	1:A:374:GLU:HG3	1.90	0.70
1:A:252:LEU:HD23	1:A:414:VAL:HG21	1.75	0.69
1:A:260:TYR:OH	1:A:334:GLU:OE2	2.11	0.68
1:A:349:GLU:HG3	1:A:366:PHE:CE2	2.29	0.67
1:A:466:CYS:HA	1:A:471:VAL:CG2	2.23	0.67
1:A:377:MET:HA	1:A:381:GLU:OE1	1.95	0.66
1:A:326:GLU:HG2	1:A:440:LEU:HB3	1.80	0.64
1:A:331:ARG:CZ	3:A:1:O62:O35	2.46	0.63
1:A:436:ARG:HD2	1:A:439:GLU:OE1	2.01	0.61
1:A:368:PHE:O	1:A:372:ILE:HG22	2.01	0.60
1:A:347:LEU:O	1:A:350:GLU:HB2	2.01	0.60
1:A:266:PRO:O	1:A:270:THR:HG23	2.03	0.58
1:A:452:MET:O	1:A:456:VAL:HG22	2.02	0.58
1:A:321:LYS:NZ	1:A:470:ASP:OD1	2.36	0.58
1:A:392:SER:O	1:A:395:ARG:HG2	2.04	0.58
1:A:466:CYS:CA	1:A:471:VAL:HG22	2.33	0.57
1:A:253:LEU:HD12	1:A:257:MET:HG2	1.86	0.57
1:A:291:ALA:O	1:A:295:VAL:HG23	2.04	0.57
1:A:378:THR:OG1	1:A:381:GLU:HG3	2.04	0.57
1:A:348:LEU:O	1:A:352:ILE:HG13	2.07	0.55
1:A:434:LEU:O	1:A:437:LEU:HB2	2.06	0.55
1:A:289:GLU:O	1:A:293:ASN:ND2	2.29	0.54
1:A:421:ILE:O	1:A:424:PRO:HD3	2.07	0.54
1:A:372:ILE:HG13	1:A:377:MET:HE3	1.91	0.53
1:A:425:GLU:O	1:A:427:PRO:HD3	2.09	0.52
1:A:454:TRP:O	1:A:459:HIS:HB2	2.09	0.52
1:A:311:LEU:HD11	1:A:407:LEU:CD1	2.39	0.52
1:A:375:LEU:HD12	1:A:377:MET:HE2	1.92	0.52
1:A:372:ILE:CG1	1:A:377:MET:HE3	2.40	0.52
1:A:252:LEU:HD21	1:A:411:LEU:HD23	1.91	0.51
1:A:245:LEU:HD12	1:A:249:GLN:OE1	2.10	0.51
1:A:446:HIS:O	1:A:449:GLU:HB2	2.11	0.51
1:A:453:SER:O	1:A:456:VAL:CG2	2.58	0.51
1:A:463:PRO:HB2	2:B:748:LEU:HD11	1.93	0.51
1:A:278:PHE:CZ	1:A:347:LEU:HD22	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:385:LEU:O	1:A:389:VAL:HG23	2.11	0.50
1:A:355:SER:OG	1:A:357:ILE:HG13	2.12	0.50
1:A:393:PRO:O	1:A:401:ARG:HG2	2.12	0.50
1:A:331:ARG:O	1:A:335:ILE:HG12	2.13	0.48
1:A:372:ILE:HG13	1:A:377:MET:CE	2.43	0.48
1:A:375:LEU:HD23	1:A:375:LEU:HA	1.71	0.48
1:A:386:THR:O	1:A:390:ILE:HG13	2.14	0.48
1:A:361:TYR:O	1:A:365:MET:HB2	2.14	0.47
1:A:436:ARG:CD	1:A:439:GLU:OE1	2.61	0.47
1:A:453:SER:O	1:A:456:VAL:HG22	2.15	0.47
1:A:419:CYS:O	1:A:423:GLN:HB2	2.14	0.46
1:A:358:SER:N	1:A:450:MET:CE	2.68	0.46
1:A:471:VAL:HG23	1:A:471:VAL:O	2.16	0.45
1:A:423:GLN:HA	1:A:423:GLN:HE21	1.81	0.45
1:A:349:GLU:O	1:A:353:ARG:HG2	2.17	0.45
1:A:358:SER:H	1:A:450:MET:HE1	1.77	0.44
1:A:455:ARG:NH2	1:A:472:GLN:O	2.47	0.44
1:A:253:LEU:CD1	1:A:257:MET:HG2	2.48	0.44
1:A:342:SER:O	3:A:1:O62:H18	2.18	0.44
1:A:321:LYS:HG2	1:A:468:ILE:HD12	1.99	0.44
1:A:385:LEU:HA	1:A:385:LEU:HD23	1.81	0.44
1:A:343:GLY:O	1:A:344:HIS:C	2.56	0.43
1:A:384:LEU:O	1:A:388:ILE:HG13	2.19	0.43
1:A:331:ARG:HG2	3:A:1:O62:H26	2.01	0.42
1:A:347:LEU:HD23	1:A:347:LEU:HA	1.74	0.42
1:A:375:LEU:CD1	1:A:377:MET:HE2	2.49	0.42
1:A:313:HIS:CD2	1:A:313:HIS:H	2.37	0.42
1:A:417:LYS:O	1:A:421:ILE:HG13	2.19	0.42
1:A:451:LEU:O	1:A:455:ARG:HB2	2.19	0.42
1:A:302:THR:HG23	1:A:390:ILE:HG21	2.01	0.42
1:A:298:LEU:HD23	1:A:298:LEU:HA	1.86	0.42
1:A:372:ILE:O	1:A:375:LEU:HB2	2.19	0.42
1:A:362:ILE:O	1:A:366:PHE:HD1	2.03	0.41
1:A:466:CYS:CA	1:A:471:VAL:CG2	2.96	0.41
1:A:453:SER:O	1:A:456:VAL:HG23	2.21	0.41
1:A:265:MET:HE3	1:A:265:MET:HB3	1.99	0.41
1:A:466:CYS:SG	1:A:471:VAL:CG2	3.09	0.41
1:A:375:LEU:HD13	1:A:433:LEU:HD23	2.02	0.41
1:A:366:PHE:HA	1:A:369:TYR:HD2	1.86	0.41
1:A:423:GLN:N	1:A:424:PRO:CD	2.84	0.41
1:A:398:ILE:HG22	1:A:401:ARG:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:395:ARG:HB2	1:A:398:ILE:HG13	2.02	0.40
1:A:349:GLU:HG3	1:A:366:PHE:CZ	2.56	0.40
1:A:430:PHE:O	1:A:434:LEU:HG	2.21	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	227/235 (97%)	204 (90%)	20 (9%)	3 (1%)	12	41
2	B	9/21 (43%)	9 (100%)	0	0	100	100
All	All	236/256 (92%)	213 (90%)	20 (8%)	3 (1%)	12	41

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	262	LYS
1	A	374	GLU
1	A	276	GLU

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	181/218 (83%)	173 (96%)	8 (4%)	28	62
2	B	8/21 (38%)	8 (100%)	0	100	100
All	All	189/239 (79%)	181 (96%)	8 (4%)	30	63

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	246	THR
1	A	251	THR
1	A	331	ARG
1	A	359	ASP
1	A	432	CYS
1	A	450	MET
1	A	455	ARG
1	A	459	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	261	ASN
1	A	294	HIS
1	A	313	HIS
1	A	337	ASN
1	A	354	ASN
1	A	396	GLN
1	A	416	GLN
1	A	423	GLN
1	A	447	HIS
2	B	747	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 (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

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	O62	A	1	-	35,41,41	1.78	6 (17%)	45,59,59	1.73	8 (17%)

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	O62	A	1	-	-	2/11/21/21	0/5/5/5

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1	O62	C9-C4	-4.21	1.45	1.50
3	A	1	O62	C9-C14	4.15	1.44	1.40
3	A	1	O62	C26-C25	3.28	1.43	1.36
3	A	1	O62	C29-C28	3.26	1.44	1.38
3	A	1	O62	C17-C20	2.92	1.43	1.38
3	A	1	O62	C9-C10	2.92	1.42	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1	O62	C37-O33-C30	5.42	131.04	117.65
3	A	1	O62	C9-C10-CL15	4.68	125.72	119.74
3	A	1	O62	C14-C9-C10	3.98	120.24	116.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1	O62	C9-C14-CL16	3.23	123.87	119.74
3	A	1	O62	C11-C10-C9	-3.10	119.05	122.35
3	A	1	O62	C17-C20-C34	-2.79	116.05	120.20
3	A	1	O62	C19-C22-C23	-2.71	117.24	122.02
3	A	1	O62	C13-C14-C9	-2.54	119.65	122.35

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1	O62	C31-C30-O33-C37
3	A	1	O62	C29-C30-O33-C37

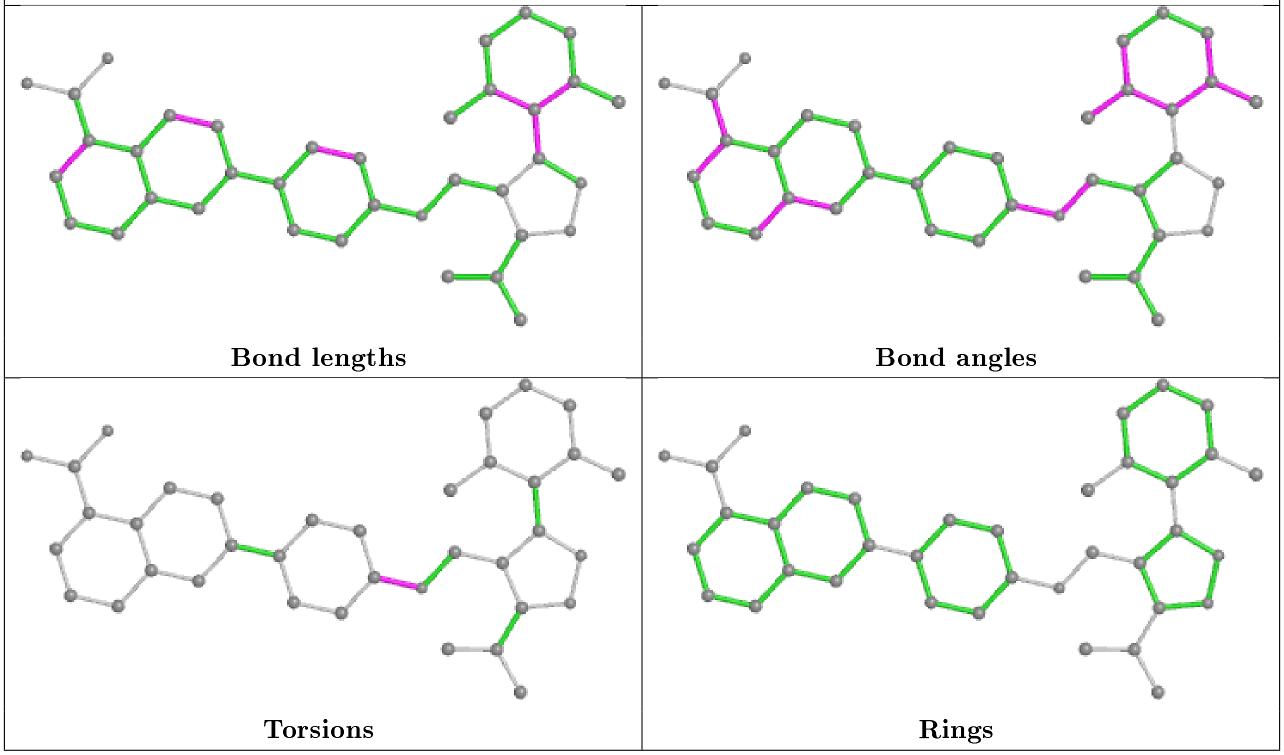
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1	O62	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 O62 A 1



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

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, 95^{th} 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	229/235 (97%)	0.46	9 (3%)	39	25	40, 59, 89, 92	0
2	B	11/21 (52%)	0.37	0	100	100	60, 65, 80, 80	0
All	All	240/256 (93%)	0.45	9 (3%)	40	26	40, 60, 89, 92	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	256	ILE	3.8
1	A	384	LEU	2.9
1	A	253	LEU	2.6
1	A	252	LEU	2.6
1	A	308	PHE	2.3
1	A	259	SER	2.3
1	A	392	SER	2.2
1	A	306	PRO	2.0
1	A	263	GLN	2.0

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

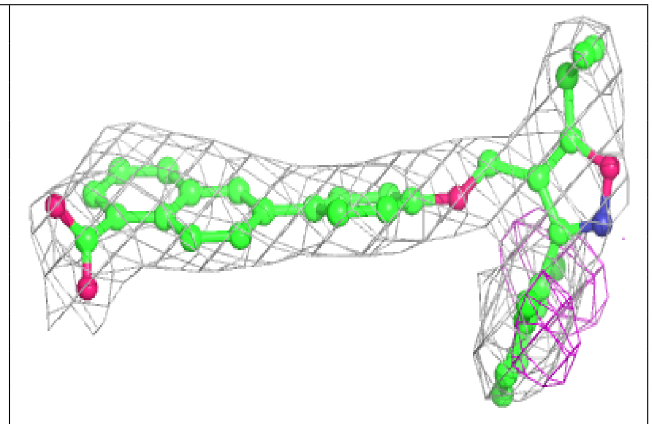
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

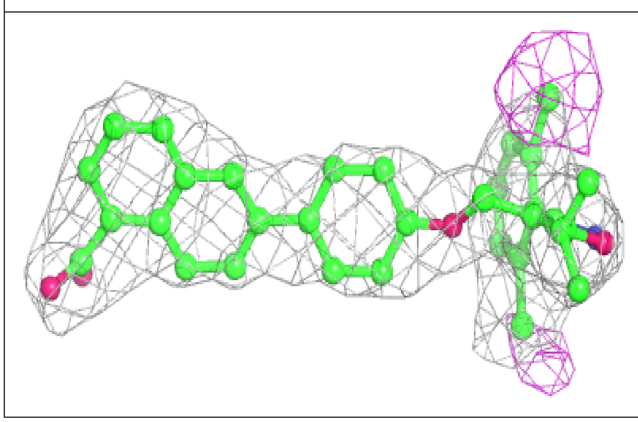
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($Å^2$)	Q<0.9
3	O62	A	1	37/37	0.90	0.30	48,53,56,57	0

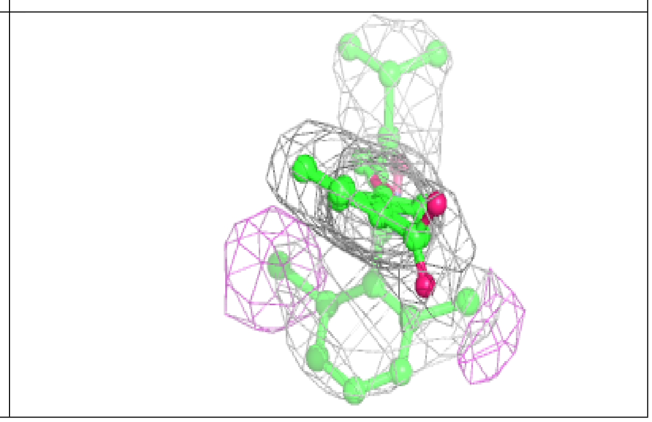
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around O62 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 (i)

There are no such residues in this entry.