



# Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 07:06 pm BST

PDB ID : 6HVF  
Title : Kinase domain of cSrc in complex with compound 29B  
Authors : Keul, M.; Mueller, M.P.; Rauh, D.  
Deposited on : 2018-10-10  
Resolution : 2.10 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](mailto: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.

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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 : 2.11  
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

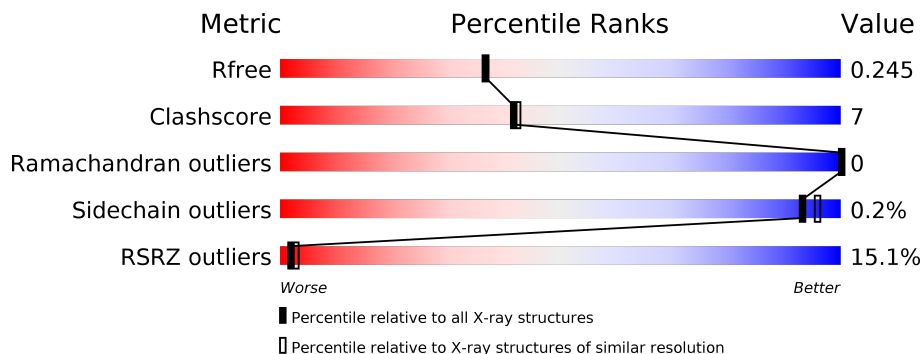
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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  $\geq 3$ , 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	286	
1	B	286	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4165 atoms, of which 6 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.

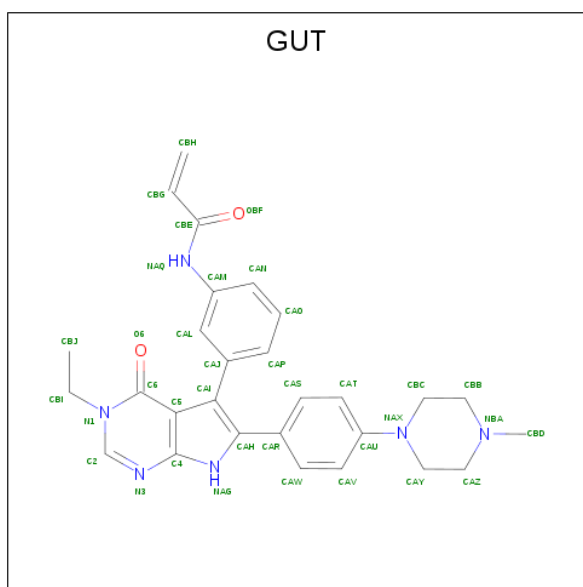
- Molecule 1 is a protein called Proto-oncogene tyrosine-protein kinase Src.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	246	1984	1275	329	362	18	0	6	0
1	B	244	1918	1225	317	359	17	0	1	0

There are 10 discrepancies between the modelled and reference sequences:

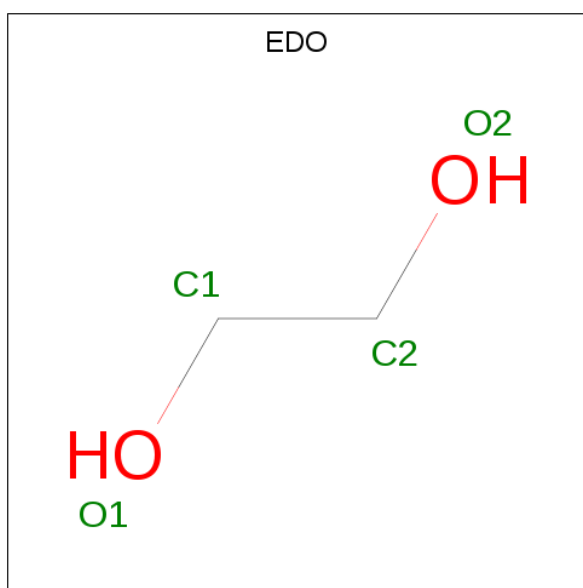
Chain	Residue	Modelled	Actual	Comment	Reference
A	248	GLY	-	expression tag	UNP P00523
A	249	HIS	-	expression tag	UNP P00523
A	250	MET	-	expression tag	UNP P00523
A	338	MET	THR	engineered mutation	UNP P00523
A	345	CYS	SER	engineered mutation	UNP P00523
B	248	GLY	-	expression tag	UNP P00523
B	249	HIS	-	expression tag	UNP P00523
B	250	MET	-	expression tag	UNP P00523
B	338	MET	THR	engineered mutation	UNP P00523
B	345	CYS	SER	engineered mutation	UNP P00523

- Molecule 2 is {N}-[3-[3-ethyl-6-[4-(4-methylpiperazin-1-yl)phenyl]-4-oxidanylidene-7 {H}-pyrrolo[2,3-d]pyrimidin-5-yl]phenyl]prop-2-enamide (three-letter code: GUT) (formula: C<sub>28</sub>H<sub>30</sub>N<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	N			O
2	A	1	36	28	6	2	0	0
2	B	1	36	28	6	2	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	4	2	2	0	0
3	A	1	4	2	2	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
3	B	1	10	2	6	2	0	0

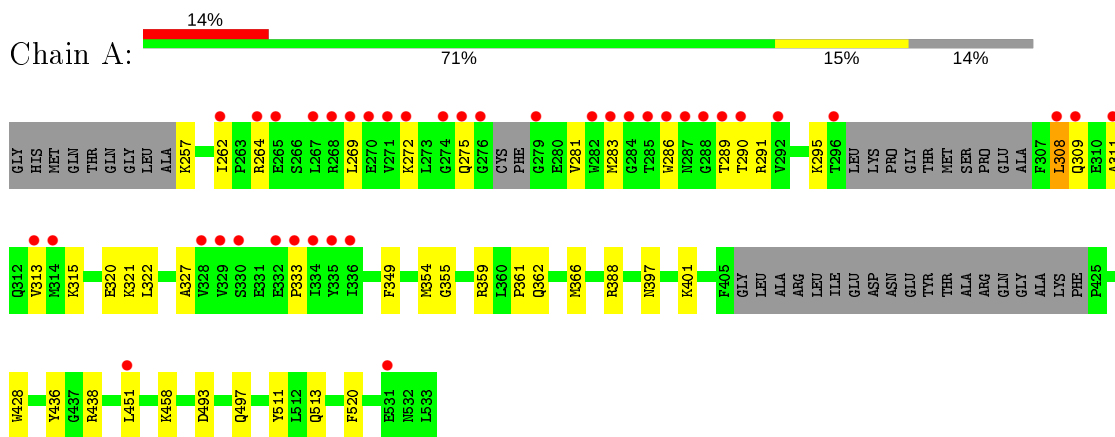
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	76	Total	O	0	0
			76	76		
4	B	97	Total	O	0	0
			97	97		

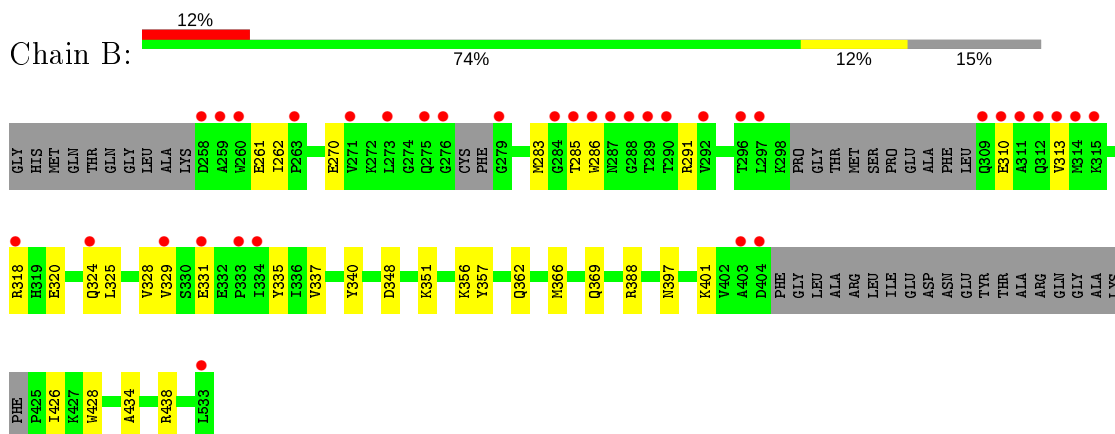
### 3 Residue-property plots [i](#)

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: Proto-oncogene tyrosine-protein kinase Src



- Molecule 1: Proto-oncogene tyrosine-protein kinase Src



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	42.17Å 62.97Å 74.54Å 100.23° 91.64° 90.03°	Depositor
Resolution (Å)	43.66 – 2.10 43.66 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.5 (43.66-2.10) 97.6 (43.66-2.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.68 (at 2.10Å)	Xtrriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, $R_{free}$	0.211 , 0.245 0.211 , 0.245	Depositor DCC
$R_{free}$ test set	2148 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.8	Xtrriage
Anisotropy	0.543	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 58.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.025 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4165	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.59% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical 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: EDO, GUT

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	0.27	0/2047	0.46	0/2770
1	B	0.26	0/1963	0.45	0/2662
All	All	0.27	0/4010	0.45	0/5432

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	1984	0	1958	32	2
1	B	1918	0	1851	23	1
2	A	36	0	0	0	0
2	B	36	0	0	1	0
3	A	8	0	12	0	0
3	B	4	6	6	1	0
4	A	76	0	0	1	0
4	B	97	0	0	1	0
All	All	4159	6	3827	55	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.



All (55) 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:B:318:ARG:HA	1:B:324:GLN:HE22	1.29	0.96
1:A:283:MET:HE3	1:A:291:ARG:HD2	1.61	0.82
1:B:426:ILE:HD11	1:B:434:ALA:HB1	1.63	0.79
1:B:310:GLU:O	1:B:313:VAL:HG22	1.86	0.75
1:A:283:MET:CE	1:A:291:ARG:HD2	2.17	0.75
1:B:318:ARG:HG3	1:B:324:GLN:NE2	2.05	0.70
1:A:289:THR:HG23	1:A:290:THR:HG23	1.75	0.69
1:B:329:VAL:HG22	1:B:335:TYR:HB2	1.75	0.68
1:A:281:VAL:HG22	1:A:295:LYS:HG2	1.77	0.67
1:A:264:ARG:NH2	1:A:333:PRO:O	2.18	0.67
1:B:270:GLU:OE1	1:B:285:THR:HG23	1.98	0.62
1:B:388:ARG:HB3	1:B:428:TRP:CD1	2.36	0.60
1:B:362:GLN:O	1:B:366:MET:HG3	2.01	0.60
1:A:362:GLN:O	1:A:366:MET:HG3	2.03	0.59
1:A:513:GLN:OE1	4:A:701:HOH:O	2.17	0.59
1:A:355:GLY:O	1:A:458:LYS:HD3	2.04	0.58
1:A:308:LEU:HD22	1:A:309:GLN:N	2.21	0.56
1:A:272:LYS:HE2	1:A:275:GLN:HG3	1.90	0.54
1:B:318:ARG:CA	1:B:324:GLN:HE22	2.14	0.52
1:A:511:TYR:HE2	1:B:351:LYS:O	1.93	0.52
1:A:493[B]:ASP:OD2	1:A:497:GLN:NE2	2.43	0.52
1:A:272:LYS:NZ	1:A:275:GLN:OE1	2.27	0.52
1:B:329:VAL:CG2	1:B:335:TYR:HB2	2.41	0.50
1:A:272:LYS:HZ1	1:A:275:GLN:CD	2.09	0.50
1:B:348:ASP:OD1	4:B:701:HOH:O	2.20	0.49
2:B:601:GUT:CAS	2:B:601:GUT:CAL	2.91	0.49
1:A:308:LEU:H	1:A:308:LEU:CD1	2.26	0.48
1:A:388:ARG:HB3	1:A:428:TRP:CD1	2.48	0.48
1:A:309:GLN:O	1:A:313:VAL:HG23	2.13	0.48
1:B:283:MET:HG3	1:B:340:TYR:CZ	2.49	0.47
1:A:262:ILE:HG23	1:A:327:ALA:HB1	1.95	0.47
1:B:261:GLU:HA	1:B:328:VAL:O	2.15	0.47
1:B:320:GLU:O	1:B:401:LYS:HE2	2.15	0.46
1:A:311:ALA:O	1:A:315:LYS:HG3	2.16	0.45
1:B:356:LYS:HE2	1:B:357:TYR:CE2	2.51	0.45
1:A:286:TRP:HB3	1:A:290:THR:OG1	2.16	0.45
1:B:356:LYS:HE2	1:B:357:TYR:CZ	2.52	0.45
1:A:321:LYS:O	1:A:322:LEU:HD12	2.17	0.45
1:A:451:LEU:HD12	1:A:451:LEU:O	2.17	0.45
1:A:308:LEU:H	1:A:308:LEU:HD13	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:LYS:HE2	1:A:275:GLN:CG	2.47	0.44
1:B:369:GLN:HA	3:B:602:EDO:H12	1.99	0.44
1:B:325:LEU:HD12	1:B:337:VAL:O	2.18	0.44
1:A:262:ILE:CG2	1:A:327:ALA:HB1	2.48	0.43
1:B:331:GLU:HA	1:B:331:GLU:OE1	2.18	0.43
1:A:349:PHE:CZ	1:A:354:MET:HG3	2.54	0.42
1:A:269:LEU:HD12	1:A:269:LEU:N	2.34	0.42
1:A:257:LYS:HB2	1:A:257:LYS:HE3	1.83	0.42
1:A:320:GLU:O	1:A:401:LYS:HE2	2.19	0.42
1:B:291:ARG:HG2	1:B:340:TYR:CD2	2.55	0.42
1:A:361:PRO:HA	1:A:520:PHE:CE2	2.55	0.41
1:B:318:ARG:HG3	1:B:324:GLN:HE21	1.82	0.41
1:A:308:LEU:HD22	1:A:308:LEU:C	2.41	0.41
1:A:308:LEU:N	1:A:308:LEU:HD13	2.36	0.41
1:B:262:ILE:HG21	1:B:286:TRP:CZ2	2.57	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:397:ASN:OD1	1:B:438:ARG:NE[1_655]	2.00	0.20
1:A:397:ASN:OD1	1:A:438:ARG:NE[1_455]	2.07	0.13
1:A:359[A]:ARG:NH1	1:A:436:TYR:OH[1_455]	2.10	0.10

## 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	244/286 (85%)	240 (98%)	4 (2%)	0	100	100
1	B	237/286 (83%)	233 (98%)	4 (2%)	0	100	100
All	All	481/572 (84%)	473 (98%)	8 (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	212/245 (86%)	211 (100%)	1 (0%)	88	92
1	B	201/245 (82%)	201 (100%)	0	100	100
All	All	413/490 (84%)	412 (100%)	1 (0%)	93	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	308	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	324	GLN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry

5 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
2	GUT	B	601	1	40,40,40	3.44	13 (32%)	43,57,57	2.23	6 (13%)
3	EDO	A	603	-	3,3,3	0.49	0	2,2,2	0.33	0
3	EDO	B	602	-	3,3,3	0.47	0	2,2,2	0.28	0
2	GUT	A	601	1	40,40,40	3.41	12 (30%)	43,57,57	2.32	8 (18%)
3	EDO	A	602	-	3,3,3	0.46	0	2,2,2	0.35	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
2	GUT	B	601	1	-	6/20/30/30	0/5/5/5
3	EDO	A	603	-	-	0/1/1/1	-
3	EDO	B	602	-	-	1/1/1/1	-
2	GUT	A	601	1	-	4/20/30/30	0/5/5/5
3	EDO	A	602	-	-	1/1/1/1	-

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	GUT	CAR-CAH	-12.56	1.34	1.49
2	B	601	GUT	CAR-CAH	-12.34	1.35	1.49
2	B	601	GUT	CAI-CAJ	-11.93	1.35	1.49
2	A	601	GUT	CAI-CAJ	-11.55	1.35	1.49
2	A	601	GUT	CAI-CAH	-5.66	1.35	1.41
2	B	601	GUT	CAI-CAH	-5.43	1.35	1.41
2	B	601	GUT	CAI-C5	-5.15	1.35	1.42
2	B	601	GUT	C2-N3	4.90	1.39	1.30
2	A	601	GUT	C2-N3	4.87	1.39	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	GUT	CBH-CBG	4.81	1.54	1.30
2	B	601	GUT	CBH-CBG	4.80	1.54	1.30
2	A	601	GUT	CAI-C5	-4.69	1.35	1.42
2	B	601	GUT	C6-C5	-3.91	1.34	1.41
2	A	601	GUT	CBG-CBE	3.77	1.54	1.48
2	A	601	GUT	C6-C5	-3.63	1.35	1.41
2	B	601	GUT	CBG-CBE	3.58	1.54	1.48
2	B	601	GUT	CAM-NAQ	-3.34	1.34	1.41
2	A	601	GUT	CAM-NAQ	-3.22	1.35	1.41
2	A	601	GUT	C5-C4	-3.11	1.34	1.43
2	B	601	GUT	C5-C4	-3.11	1.34	1.43
2	A	601	GUT	CAH-NAG	-2.47	1.32	1.37
2	B	601	GUT	CAH-NAG	-2.37	1.33	1.37
2	B	601	GUT	C6-N1	-2.06	1.35	1.38
2	B	601	GUT	C4-N3	-2.03	1.34	1.37
2	A	601	GUT	C6-N1	-2.03	1.35	1.38

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	GUT	CBH-CBG-CBE	-9.60	111.30	122.27
2	B	601	GUT	CBH-CBG-CBE	-9.21	111.74	122.27
2	A	601	GUT	C5-C6-N1	7.87	121.52	116.15
2	B	601	GUT	C5-C6-N1	7.05	120.97	116.15
2	A	601	GUT	CAM-NAQ-CBE	-4.45	121.53	128.26
2	B	601	GUT	CBC-NAX-CAY	4.21	120.81	111.52
2	A	601	GUT	CBC-NAX-CAY	3.94	120.21	111.52
2	B	601	GUT	CAM-NAQ-CBE	-3.70	122.68	128.26
2	A	601	GUT	C2-N3-C4	2.81	120.10	116.58
2	B	601	GUT	C2-N3-C4	2.72	119.99	116.58
2	B	601	GUT	CAS-CAR-CAH	2.57	124.67	120.61
2	A	601	GUT	CAW-CAR-CAH	2.54	124.62	120.61
2	A	601	GUT	CAS-CAR-CAH	-2.20	117.11	120.61
2	A	601	GUT	N3-C2-N1	-2.01	117.18	125.33

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	GUT	CBJ-CBI-N1-C6
2	B	601	GUT	CBJ-CBI-N1-C2
2	B	601	GUT	NAQ-CBE-CBG-CBH

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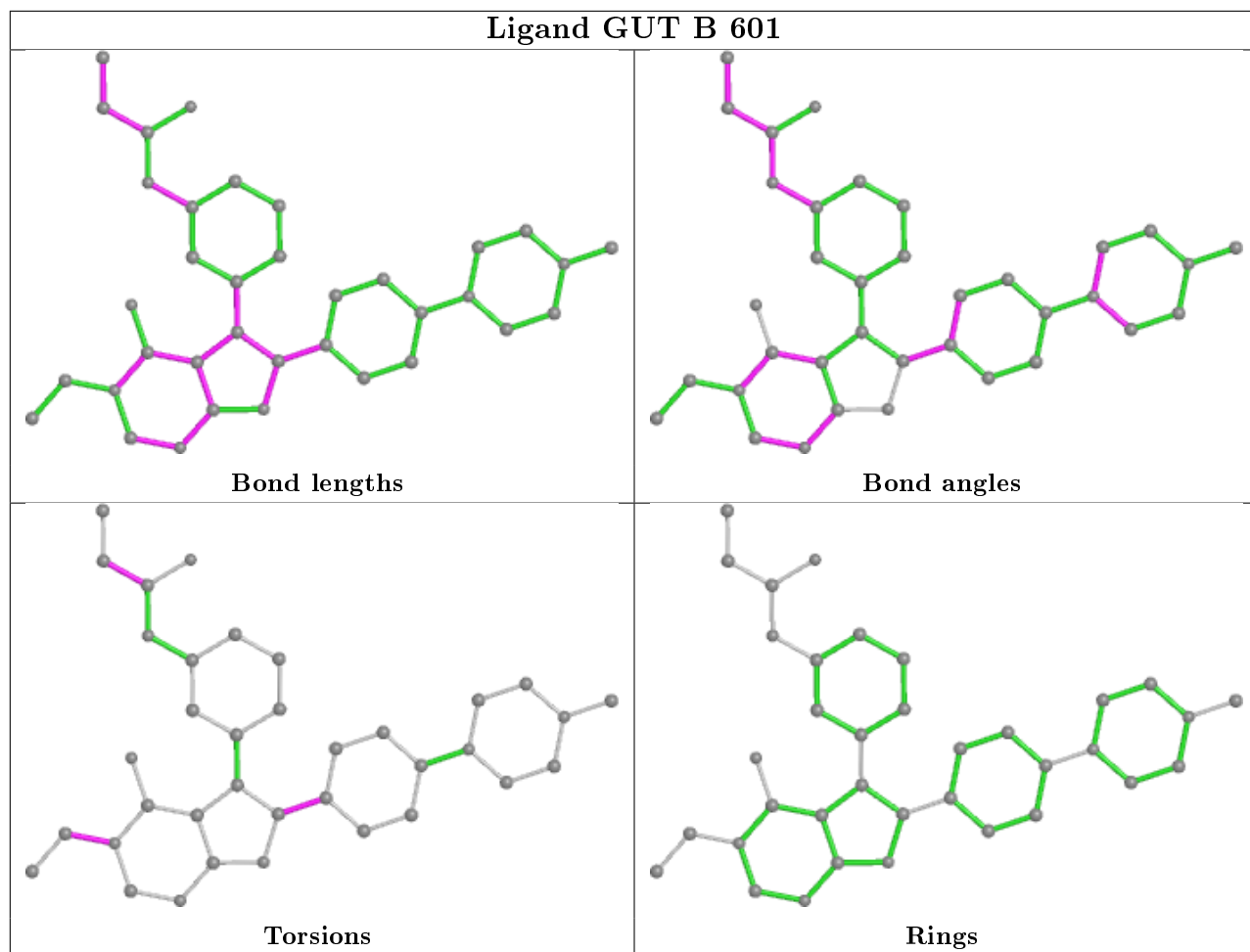
Mol	Chain	Res	Type	Atoms
2	B	601	GUT	OBF-CBE-CBG-CBH
2	B	601	GUT	CAI-CAH-CAR-CAW
2	B	601	GUT	CAI-CAH-CAR-CAS
2	A	601	GUT	CAI-CAH-CAR-CAW
2	A	601	GUT	CAI-CAH-CAR-CAS
2	A	601	GUT	CAL-CAM-NAQ-CBE
2	A	601	GUT	CAN-CAM-NAQ-CBE
3	B	602	EDO	O1-C1-C2-O2
3	A	602	EDO	O1-C1-C2-O2

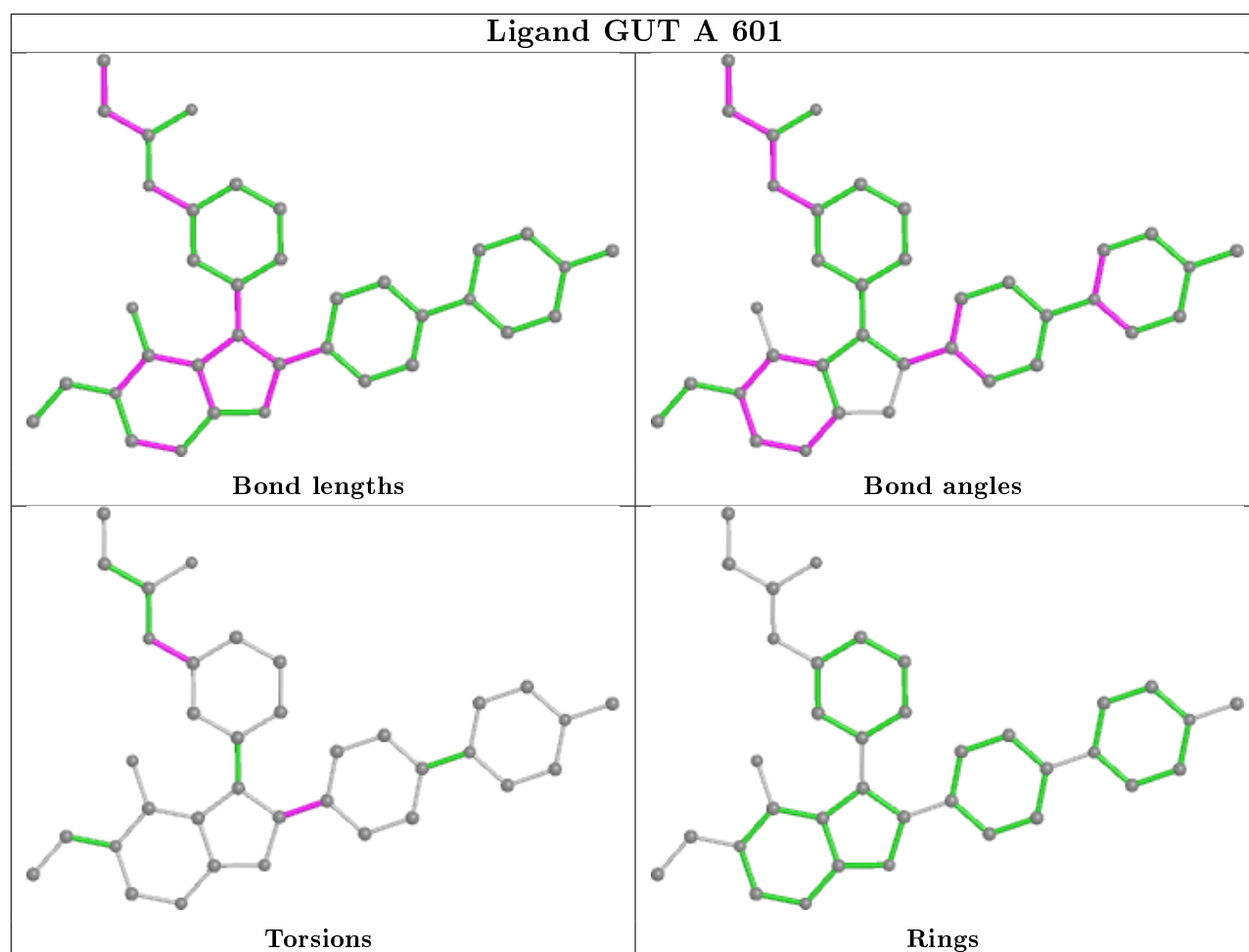
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	GUT	1	0
3	B	602	EDO	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	246/286 (86%)	1.13	39 (15%) <b>1</b> <b>2</b>	24, 41, 100, 119	0
1	B	244/286 (85%)	1.05	35 (14%) <b>2</b> <b>3</b>	25, 41, 94, 111	0
All	All	490/572 (85%)	1.09	74 (15%) <b>2</b> <b>3</b>	24, 41, 96, 119	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	334	ILE	8.5
1	B	313	VAL	7.5
1	A	329	VAL	7.5
1	A	333	PRO	5.9
1	B	311	ALA	5.8
1	B	329	VAL	5.8
1	B	259	ALA	5.4
1	B	260	TRP	5.3
1	A	271	VAL	5.2
1	A	285	THR	5.1
1	A	328	VAL	5.1
1	A	313	VAL	5.0
1	A	309	GLN	4.8
1	B	403	ALA	4.6
1	A	275	GLN	4.6
1	B	285	THR	4.6
1	A	314[A]	MET	4.4
1	B	310	GLU	4.4
1	A	332	GLU	4.4
1	A	284	GLY	4.4
1	A	288	GLY	4.3
1	A	282	TRP	4.2
1	A	287	ASN	4.1
1	A	267	LEU	4.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	334	ILE	3.9
1	A	269	LEU	3.9
1	A	262	ILE	3.9
1	B	271	VAL	3.8
1	B	287	ASN	3.6
1	B	333	PRO	3.6
1	A	308	LEU	3.6
1	B	263	PRO	3.5
1	A	296	THR	3.4
1	A	279	GLY	3.4
1	A	335	TYR	3.3
1	A	311	ALA	3.3
1	B	284	GLY	3.3
1	B	258	ASP	3.3
1	A	289	THR	3.3
1	B	292	VAL	3.3
1	B	331	GLU	3.2
1	A	272	LYS	2.9
1	B	289	THR	2.9
1	B	312	GLN	2.9
1	A	290	THR	2.9
1	B	288	GLY	2.8
1	A	274	GLY	2.8
1	B	309	GLN	2.7
1	B	404	ASP	2.7
1	A	268	ARG	2.7
1	A	265	GLU	2.7
1	A	283	MET	2.4
1	A	292	VAL	2.4
1	B	315	LYS	2.4
1	B	318	ARG	2.4
1	B	296	THR	2.3
1	B	286	TRP	2.3
1	B	297	LEU	2.3
1	A	330	SER	2.3
1	A	451	LEU	2.2
1	B	290	THR	2.2
1	A	286	TRP	2.2
1	A	531	GLU	2.2
1	A	270	GLU	2.2
1	B	314	MET	2.2
1	A	264	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	324	GLN	2.1
1	A	336	ILE	2.1
1	A	276	GLY	2.1
1	B	275	GLN	2.1
1	B	273	LEU	2.0
1	B	533	LEU	2.0
1	B	279	GLY	2.0
1	B	276	GLY	2.0

## 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](#)

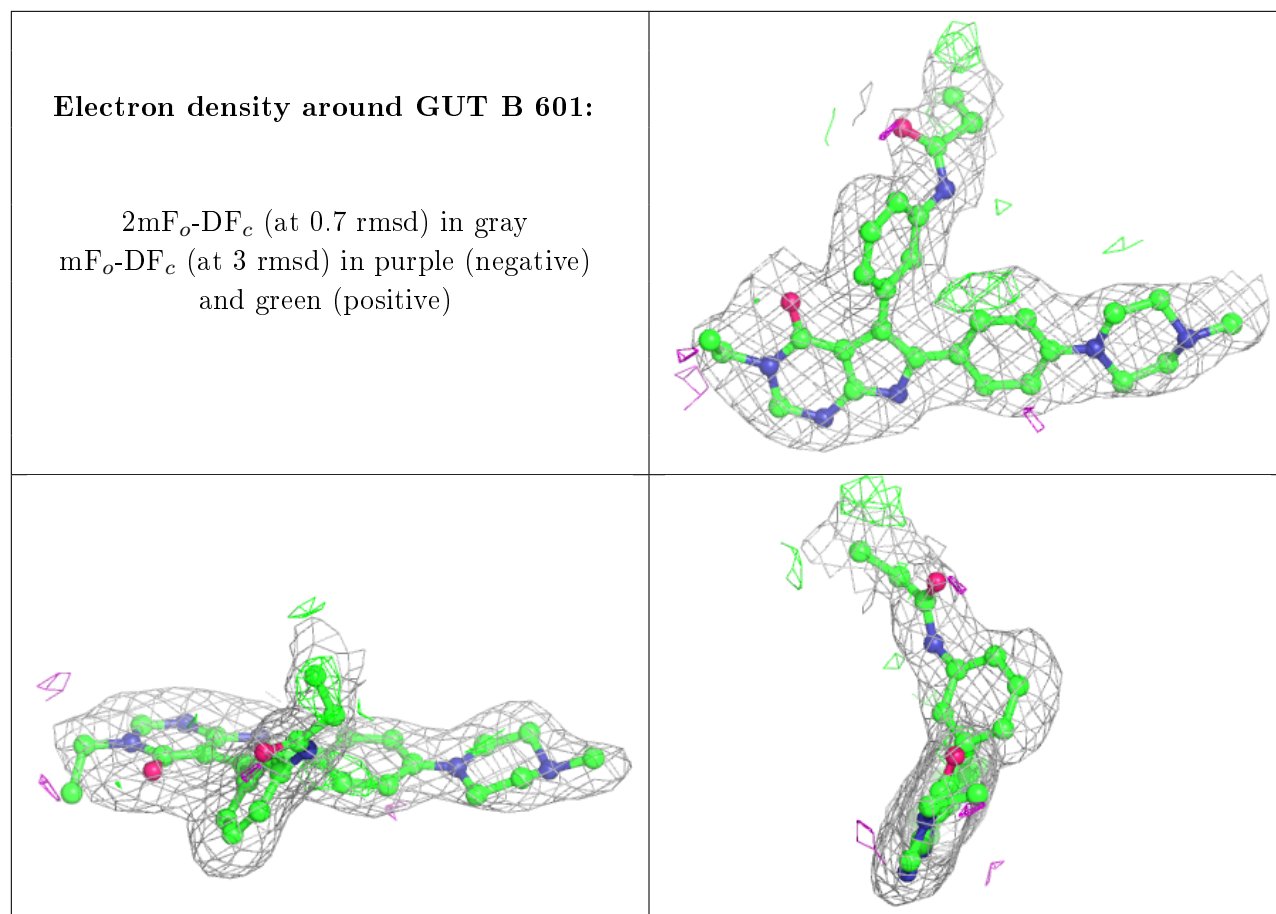
There are no carbohydrates in this entry.

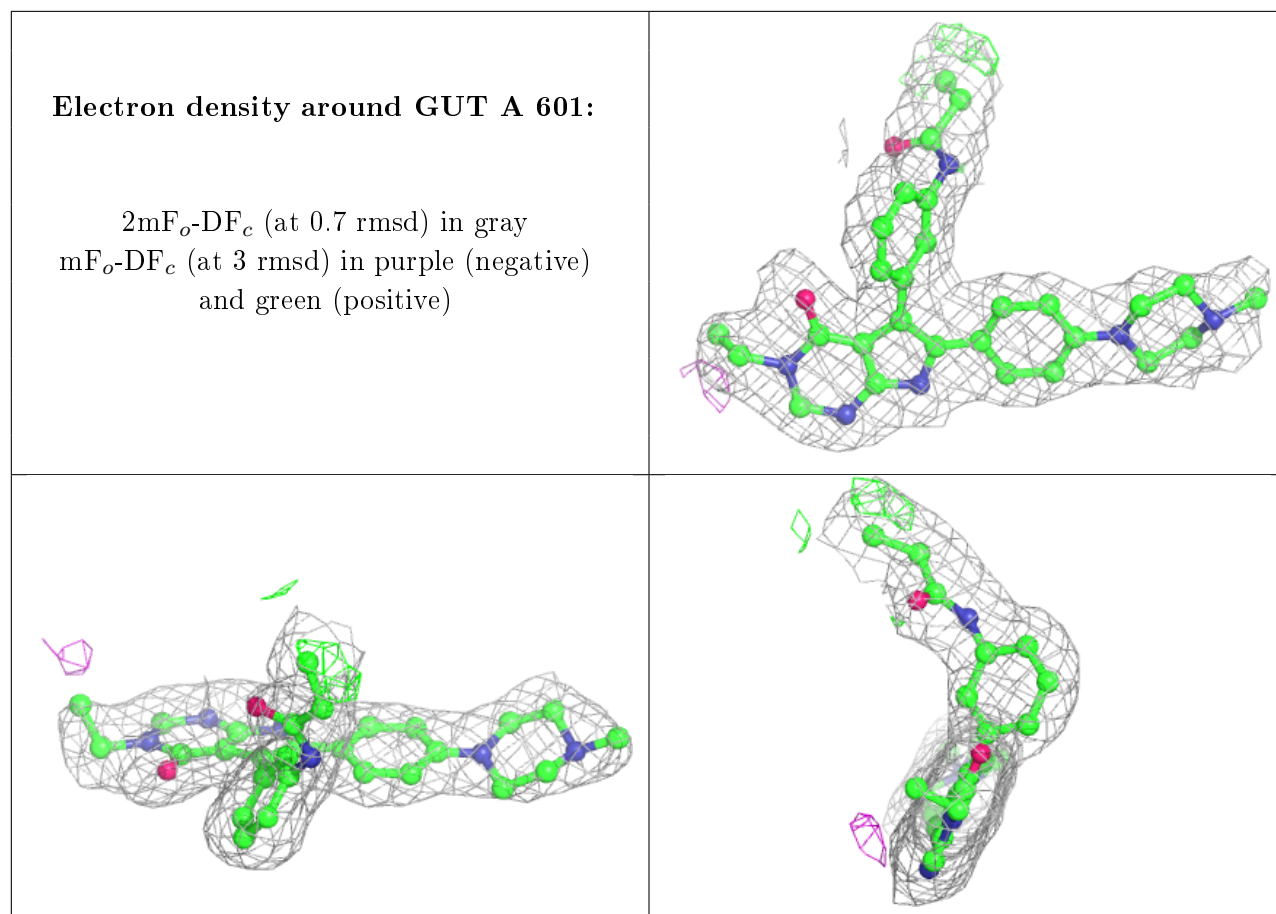
## 6.4 Ligands [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	EDO	A	603	4/4	0.74	0.27	44,46,49,50	0
3	EDO	B	602	4/4	0.84	0.25	65,78,79,82	0
2	GUT	B	601	36/36	0.86	0.17	38,49,62,65	0
2	GUT	A	601	36/36	0.88	0.15	33,50,68,70	0
3	EDO	A	602	4/4	0.88	0.27	57,58,60,61	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.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.