



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 3, 2021 – 01:20 AM EDT

PDB ID : 3LZB
Title : EGFR kinase domain complexed with an imidazo[2,1-b]thiazole inhibitor
Authors : Swinger, K.K.
Deposited on : 2010-03-01
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

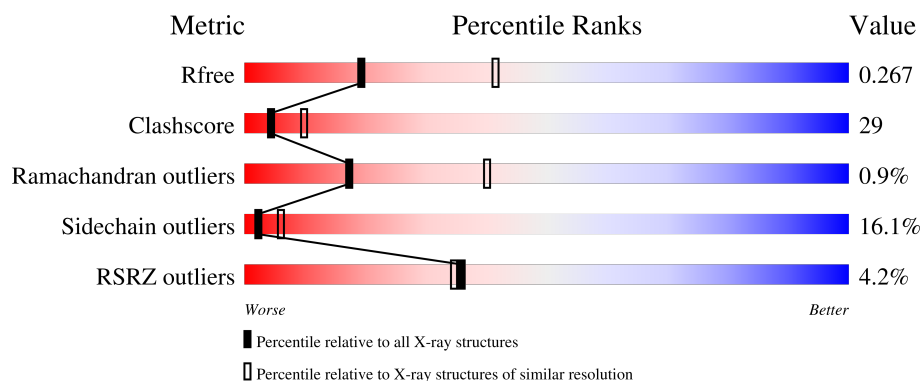
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	327	<div> <div>2%</div> <div> <div>46%</div> <div>28%</div> <div>7%</div> <div>19%</div> </div> </div>
1	B	327	<div> <div>%</div> <div> <div>46%</div> <div>28%</div> <div>6%</div> <div>19%</div> </div> </div>
1	C	327	<div> <div>5%</div> <div> <div>46%</div> <div>25%</div> <div>7%</div> <div>21%</div> </div> </div>
1	D	327	<div> <div>6%</div> <div> <div>43%</div> <div>28%</div> <div>9%</div> <div>20%</div> </div> </div>
1	E	327	<div> <div>..</div> <div>97%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	327	 98%
1	G	327	 98%
1	H	327	 97%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8885 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.

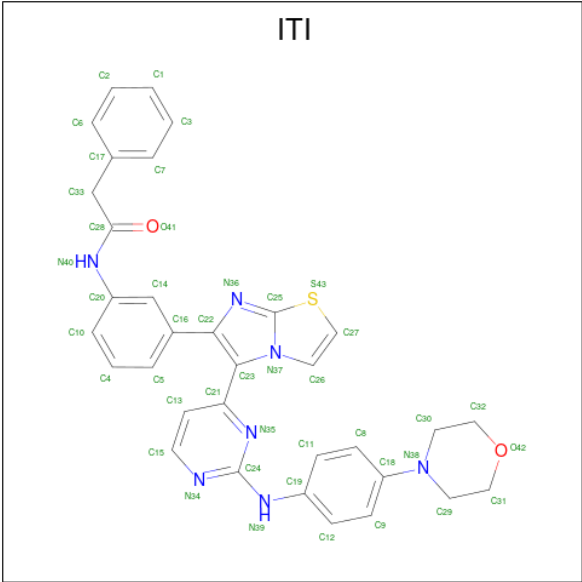
- Molecule 1 is a protein called Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	0	0
			2120	1370	360	375	15			
1	B	265	Total	C	N	O	S	0	0	0
			2116	1368	360	373	15			
1	C	259	Total	C	N	O	S	0	0	0
			2078	1343	354	366	15			
1	D	261	Total	C	N	O	S	0	0	0
			2087	1350	355	367	15			
1	E	9	Total	C	N	O		0	0	0
			45	27	9	9				
1	F	7	Total	C	N	O		0	0	0
			35	21	7	7				
1	G	7	Total	C	N	O		0	0	0
			35	21	7	7				
1	H	9	Total	C	N	O		0	0	0
			45	27	9	9				

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	924	ARG	VAL	engineered mutation	UNP P00533
B	924	ARG	VAL	engineered mutation	UNP P00533
C	924	ARG	VAL	engineered mutation	UNP P00533
D	924	ARG	VAL	engineered mutation	UNP P00533
E	-29	ARG	VAL	engineered mutation	UNP P00533
F	-28	ARG	VAL	engineered mutation	UNP P00533
G	-30	ARG	VAL	engineered mutation	UNP P00533
H	-31	ARG	VAL	engineered mutation	UNP P00533

- Molecule 2 is N-[3-(5-{2-[(4-morpholin-4-ylphenyl)amino]pyrimidin-4-yl}imidazo[2,1-b][1,3]thiazol-6-yl)phenyl]-2-phenylacetamide (three-letter code: ITI) (formula: C₃₃H₂₉N₇O₂S).



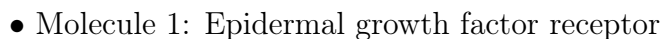
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			43	33	7	2	1		
2	B	1	Total	C	N	O	S	0	0
			43	33	7	2	1		
2	C	1	Total	C	N	O	S	0	0
			43	33	7	2	1		
2	D	1	Total	C	N	O	S	0	0
			43	33	7	2	1		

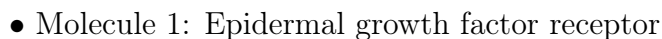
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	40	Total	O	0	0
			40	40		
3	B	45	Total	O	0	0
			45	45		
3	C	35	Total	O	0	0
			35	35		
3	D	21	Total	O	0	0
			21	21		
3	E	3	Total	O	0	0
			3	3		
3	F	4	Total	O	0	0
			4	4		
3	G	2	Total	O	0	0
			2	2		
3	H	2	Total	O	0	0
			2	2		

i

- Molecule 1: Epidermal growth factor receptor





[illegible]

- Molecule 1: Epidermal growth factor receptor

Chain F:

98%

VAL	PRO	PRO	ILE	LYS	TRP	MET	ALA	LEU	GLU	SER	SER	ILE	HIS	ARG	ILE	TYR	THR	HIS	GLN	SER	SER	ASP	VAL	TRP	SER	TYR	GLY	VAL	THR	THR	TRP	TRP	GLU	LEU	LEU	NET	THR	THR	PHE	GLY	SER	SER	LYS	PRO	PRO	TYR	ASP	GLY	ILE	ILE	PRO	ALA	SER	SER	ILE	LEU	GLU	LYS	GLY	GLU	ARG	ARG	LEU	LEU	PRO	PRO	TYR
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

[illegible]

- Molecule 1: Epidermal growth factor receptor


Chain G: ..

98%

	VAL	PRO	LYS	TRP	MET	ALA	LEU	GLY	SER	HIS	ARG	ILE	TYR	THR	HIS	GLN	SER	ASP	VAL	TRP	SER	TYR	GLY	THR	TRP	GLU	LEU	MET	PHE	GLY	SER	LYS	PRO	TYR	THR	ASP	GLY	ILE	PRO	ALA	SER	GLU	LEU	LYS	GLY	GLU	ARG	LEU	PRO	TYR
--	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

[illegible]

- Molecule 1: Epidermal growth factor receptor

Chain H:  ..

97%

[illegible]

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.59Å 70.87Å 115.18Å 90.00° 109.36° 90.00°	Depositor
Resolution (Å)	44.17 – 2.70 44.16 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (44.17-2.70) 99.7 (44.16-2.70)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 2.69Å)	Xtriage
Refinement program	BUSTER-TNT 2.5.1	Depositor
R, R_{free}	0.204 , 0.257 0.208 , 0.267	Depositor DCC
R_{free} test set	1801 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	49.4	Xtriage
Anisotropy	0.430	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 91.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8885	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 30.19 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.3626e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: ITI

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	0.70	0/2167	0.84	1/2935 (0.0%)
1	B	0.69	1/2163 (0.0%)	0.85	2/2930 (0.1%)
1	C	0.60	0/2123	0.75	1/2873 (0.0%)
1	D	0.55	0/2132	0.75	1/2886 (0.0%)
All	All	0.64	1/8585 (0.0%)	0.80	5/11624 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	750	VAL	CB-CG1	5.56	1.64	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	728	SER	C-N-CD	-14.71	88.23	120.60
1	A	728	SER	C-N-CD	-14.55	88.58	120.60
1	B	736	LEU	CA-CB-CG	5.62	128.21	115.30
1	C	704	LYS	N-CA-C	-5.17	97.03	111.00
1	D	704	LYS	N-CA-C	-5.09	97.26	111.00

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	2120	0	2169	113	0
1	B	2116	0	2165	119	0
1	C	2078	0	2122	115	0
1	D	2087	0	2129	136	0
1	E	45	0	11	6	0
1	F	35	0	10	4	0
1	G	35	0	11	8	0
1	H	45	0	11	6	0
2	A	43	0	29	16	0
2	B	43	0	29	11	0
2	C	43	0	29	13	0
2	D	43	0	29	19	0
3	A	40	0	0	2	0
3	B	45	0	0	8	0
3	C	35	0	0	1	0
3	D	21	0	0	0	0
3	E	3	0	0	1	0
3	F	4	0	0	0	0
3	G	2	0	0	0	0
3	H	2	0	0	0	0
All	All	8885	0	8744	505	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 29.

The worst 5 of 505 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:D:715:LYS:HE3	1:D:715:LYS:H	1.23	1.00
1:C:691:ILE:HG22	1:C:692:LYS:HG2	1.41	1.00
1:D:691:ILE:HG22	1:D:692:LYS:HG2	1.41	0.99
1:B:736:LEU:HD13	1:B:758:LEU:HD11	1.43	0.99
1:C:715:LYS:HE2	1:C:715:LYS:H	1.28	0.98

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	261/327 (80%)	245 (94%)	12 (5%)	4 (2%)	10	26
1	B	261/327 (80%)	247 (95%)	11 (4%)	3 (1%)	14	34
1	C	253/327 (77%)	243 (96%)	9 (4%)	1 (0%)	34	60
1	D	255/327 (78%)	240 (94%)	14 (6%)	1 (0%)	34	60
All	All	1030/1308 (79%)	975 (95%)	46 (4%)	9 (1%)	17	40

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	728	SER
1	A	729	PRO
1	B	728	SER
1	B	729	PRO
1	B	784	ASN

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	233/251 (93%)	195 (84%)	38 (16%)	2	6
1	B	232/251 (92%)	199 (86%)	33 (14%)	3	8
1	C	228/251 (91%)	191 (84%)	37 (16%)	2	6
1	D	228/251 (91%)	188 (82%)	40 (18%)	2	4
All	All	921/1004 (92%)	773 (84%)	148 (16%)	2	6

5 of 148 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	715	LYS
1	D	921	MET
1	D	738	GLU
1	D	834	LEU
1	B	752	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	781	HIS
1	D	784	ASN
1	D	802	ASN
1	B	781	HIS
1	C	781	HIS

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 ⓘ

4 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	ITI	A	1	-	45,49,49	1.15	4 (8%)	53,68,68	1.70	13 (24%)
2	ITI	D	1	-	45,49,49	0.98	4 (8%)	53,68,68	1.23	3 (5%)
2	ITI	C	1	-	45,49,49	1.07	3 (6%)	53,68,68	1.57	8 (15%)
2	ITI	B	1	-	45,49,49	1.46	4 (8%)	53,68,68	1.63	10 (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
2	ITI	A	1	-	-	4/21/32/32	0/7/7/7
2	ITI	D	1	-	-	4/21/32/32	0/7/7/7
2	ITI	C	1	-	-	6/21/32/32	0/7/7/7
2	ITI	B	1	-	-	5/21/32/32	0/7/7/7

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	ITI	C16-C22	-6.99	1.41	1.49
2	B	1	ITI	C23-C21	-4.13	1.42	1.49
2	D	1	ITI	C16-C22	-3.91	1.44	1.49
2	A	1	ITI	C16-C22	-3.85	1.44	1.49
2	C	1	ITI	C16-C22	-3.66	1.44	1.49

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	ITI	C30-N38-C29	6.02	124.81	111.52
2	D	1	ITI	C30-N38-C29	5.23	123.06	111.52
2	C	1	ITI	C20-N40-C28	-4.91	118.90	127.50
2	A	1	ITI	C32-C30-N38	-4.47	101.77	110.02
2	A	1	ITI	C30-N38-C29	4.38	121.18	111.52

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1	ITI	C5-C16-C22-N36
2	A	1	ITI	C14-C16-C22-N36

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	B	1	ITI	C5-C16-C22-N36
2	B	1	ITI	C14-C16-C22-N36
2	C	1	ITI	C5-C16-C22-N36

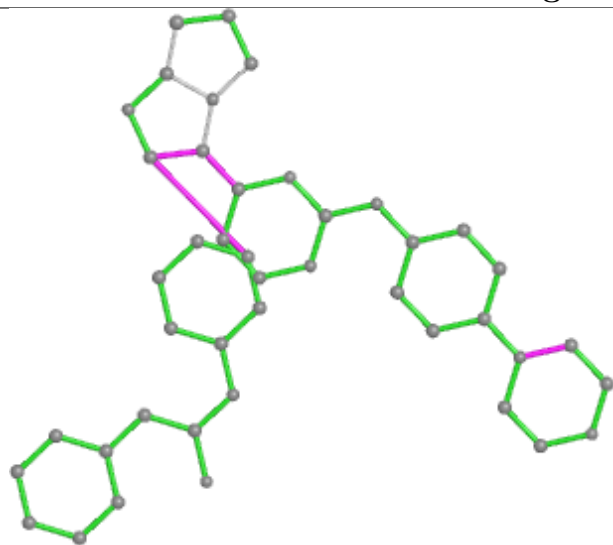
There are no ring outliers.

4 monomers are involved in 59 short contacts:

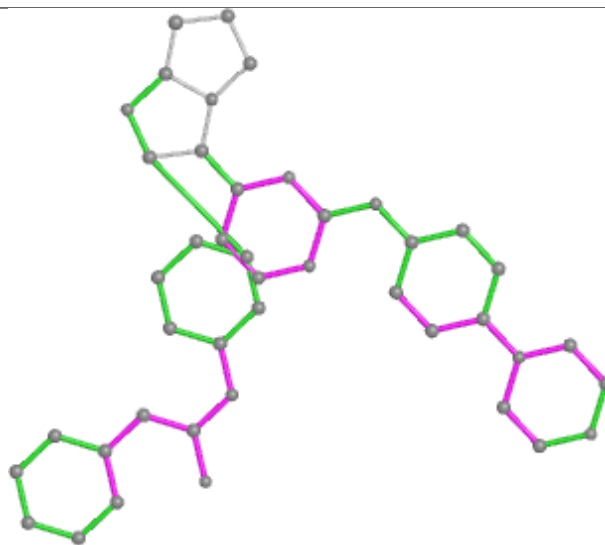
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	ITI	16	0
2	D	1	ITI	19	0
2	C	1	ITI	13	0
2	B	1	ITI	11	0

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.

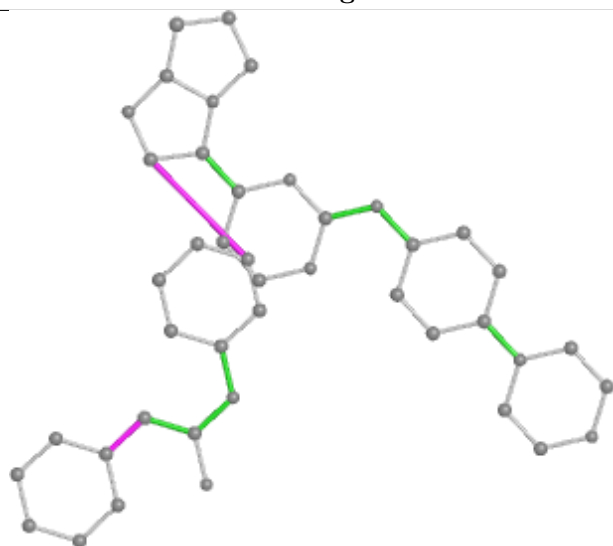
Ligand ITI A 1



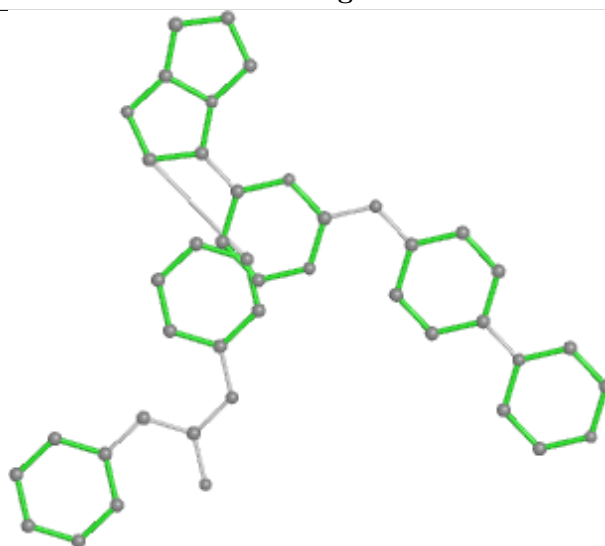
Bond lengths



Bond angles

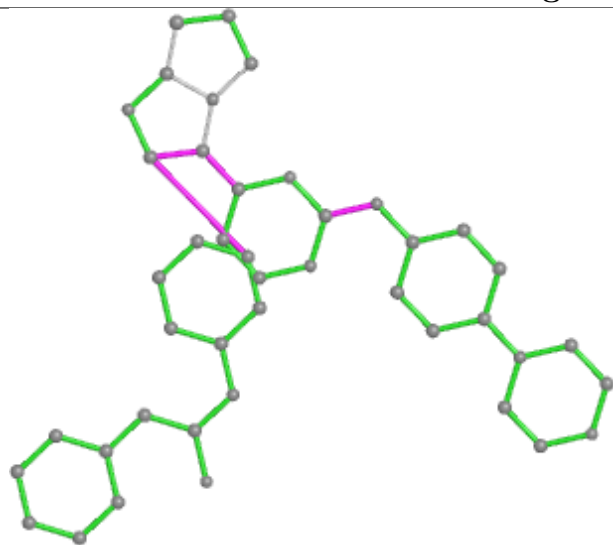


Torsions

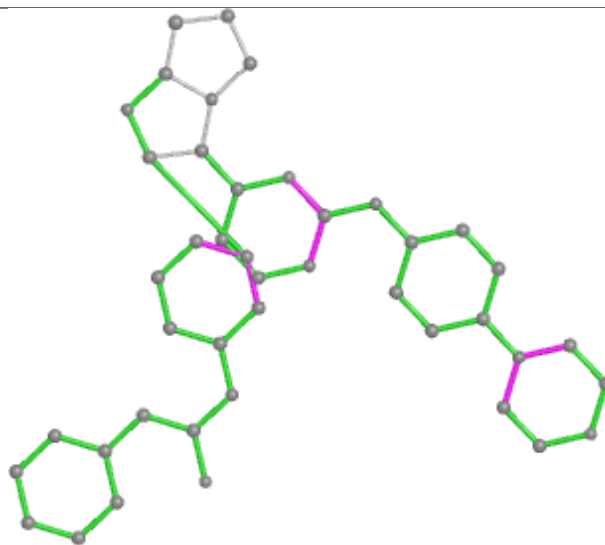


Rings

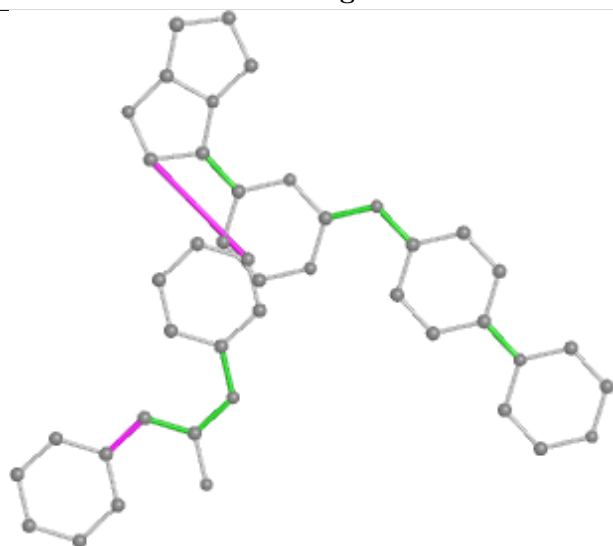
Ligand ITI D 1



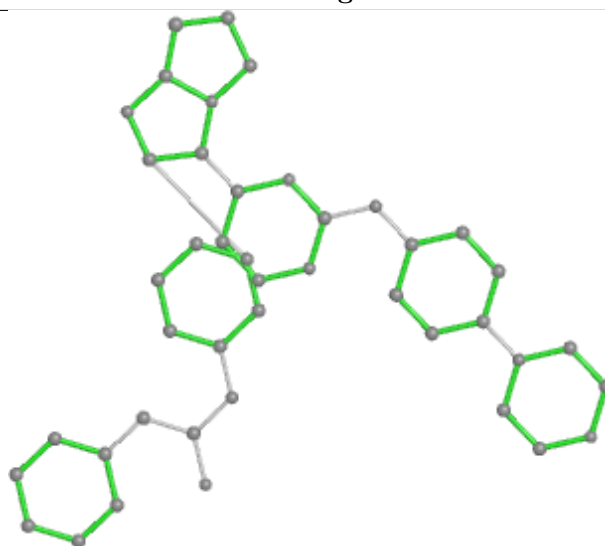
Bond lengths



Bond angles

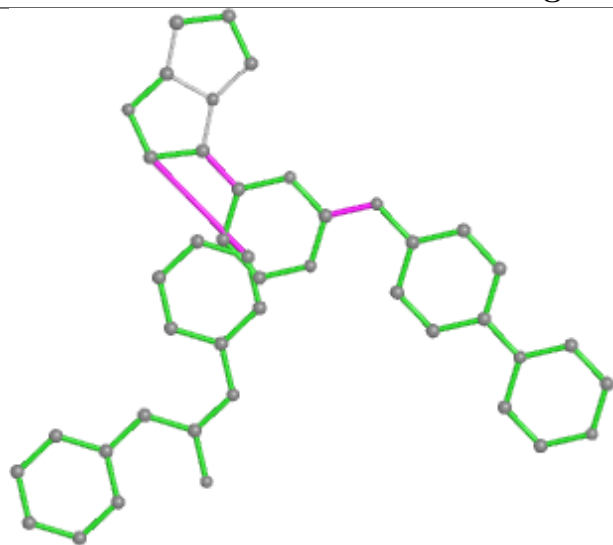


Torsions

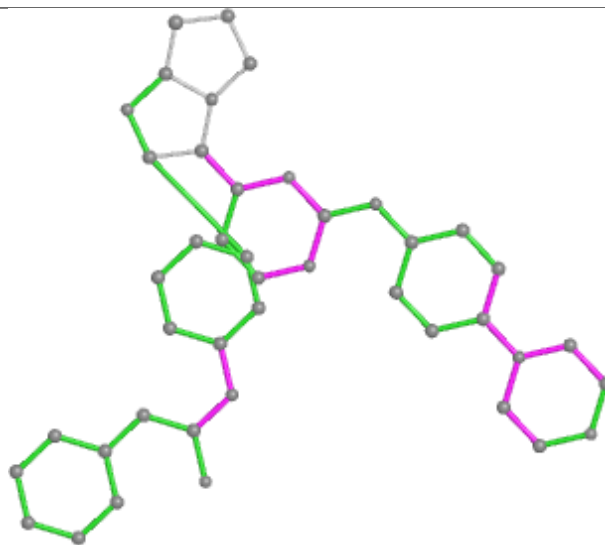


Rings

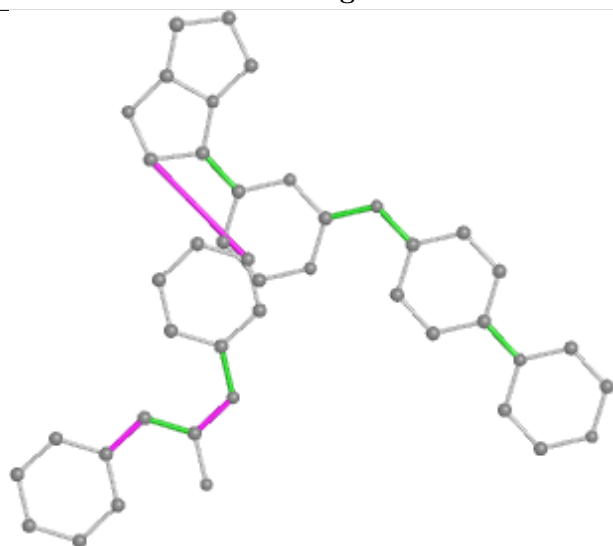
Ligand ITI C 1



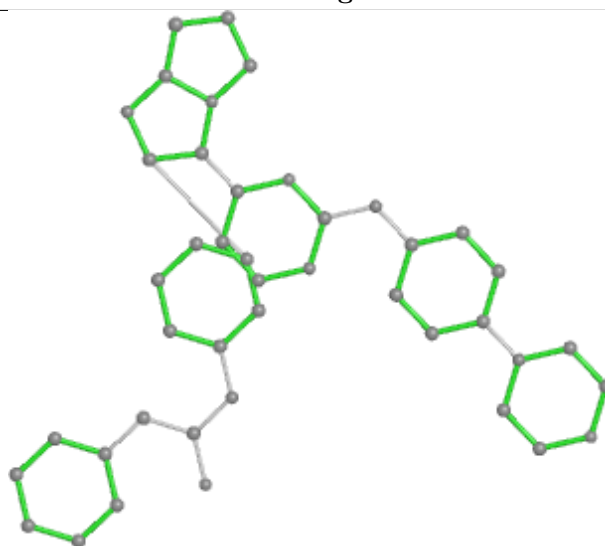
Bond lengths



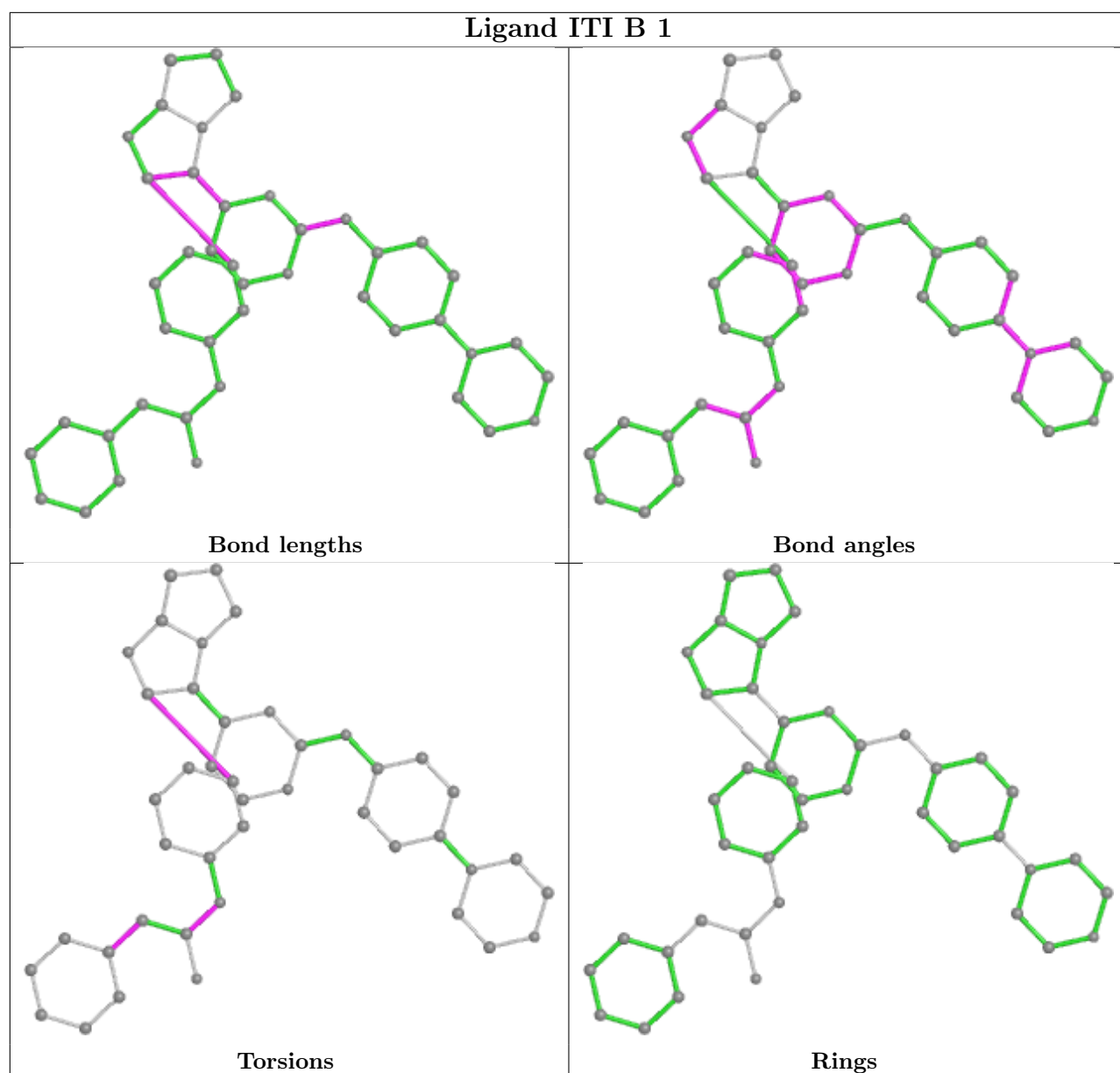
Bond angles



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 [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	265/327 (81%)	-0.03	6 (2%) 60 62	27, 47, 80, 117	0
1	B	265/327 (81%)	-0.11	2 (0%) 86 87	27, 45, 79, 112	0
1	C	259/327 (79%)	0.23	16 (6%) 20 19	39, 60, 93, 130	0
1	D	261/327 (79%)	0.36	20 (7%) 13 11	41, 64, 97, 136	0
1	E	0/327	-	-	-	-
1	F	0/327	-	-	-	-
1	G	0/327	-	-	-	-
1	H	0/327	-	-	-	-
All	All	1050/2616 (40%)	0.11	44 (4%) 36 35	27, 56, 92, 136	0

The worst 5 of 44 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	728	SER	6.3
1	B	727	THR	5.7
1	C	735	ILE	5.6
1	A	699	PHE	5.5
1	A	726	ALA	5.4

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](#)

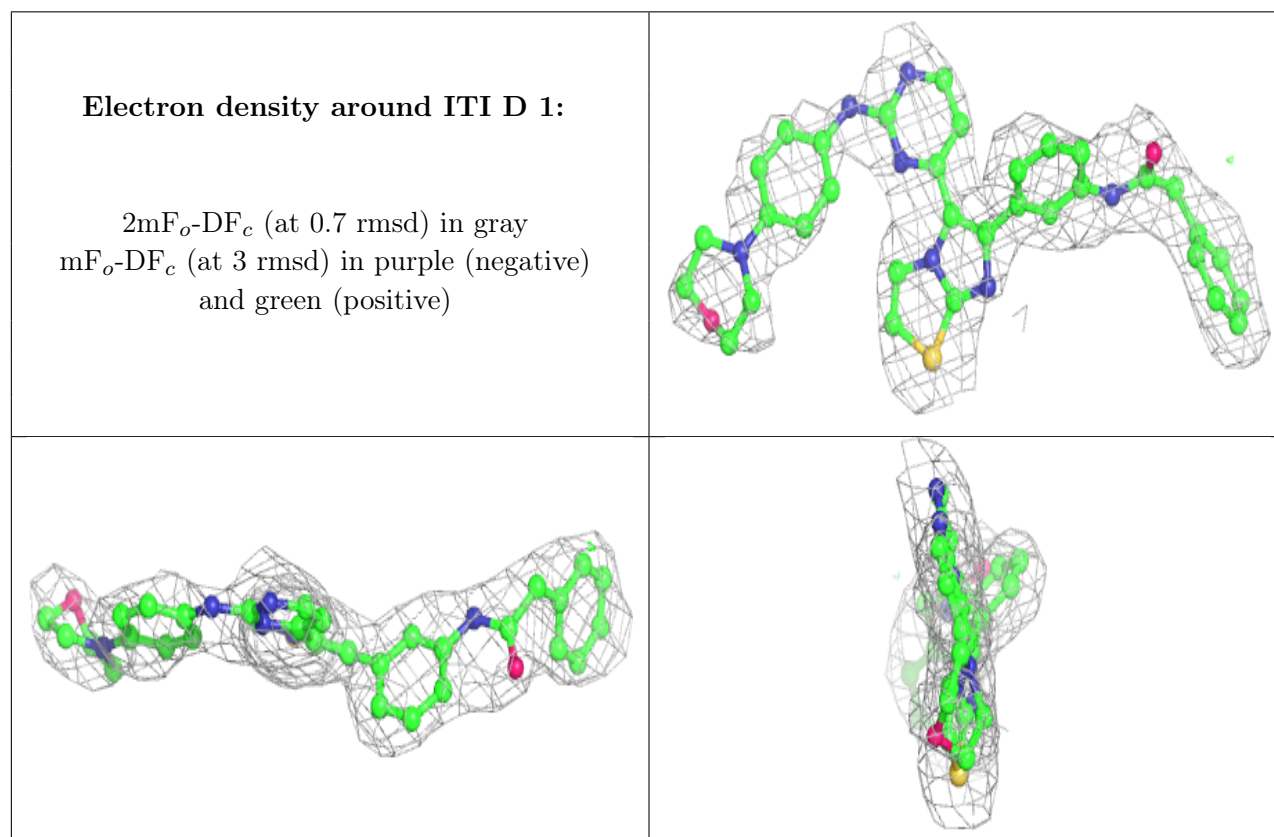
There are no monosaccharides in this entry.

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.

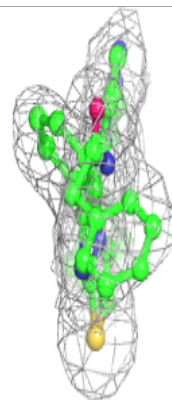
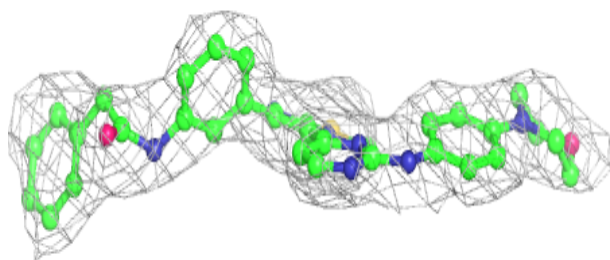
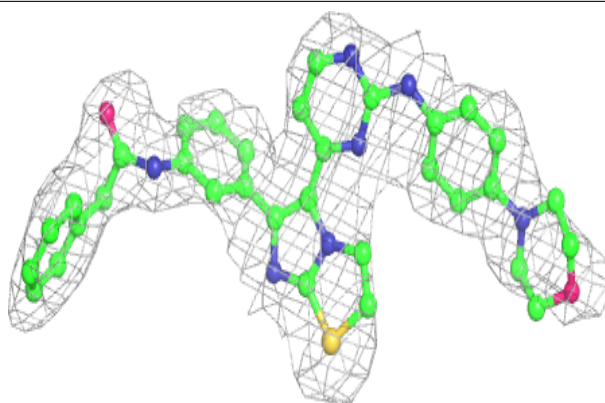
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	ITI	D	1	43/43	0.94	0.18	14,57,195,300	0
2	ITI	C	1	43/43	0.96	0.15	23,56,210,300	0
2	ITI	A	1	43/43	0.97	0.16	11,36,81,106	0
2	ITI	B	1	43/43	0.98	0.14	6,33,79,236	0

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.

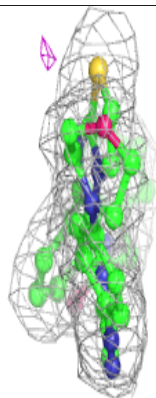
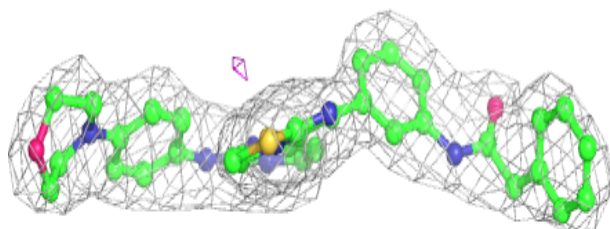
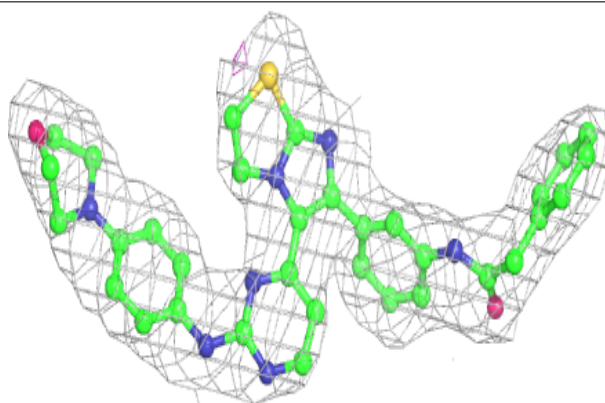


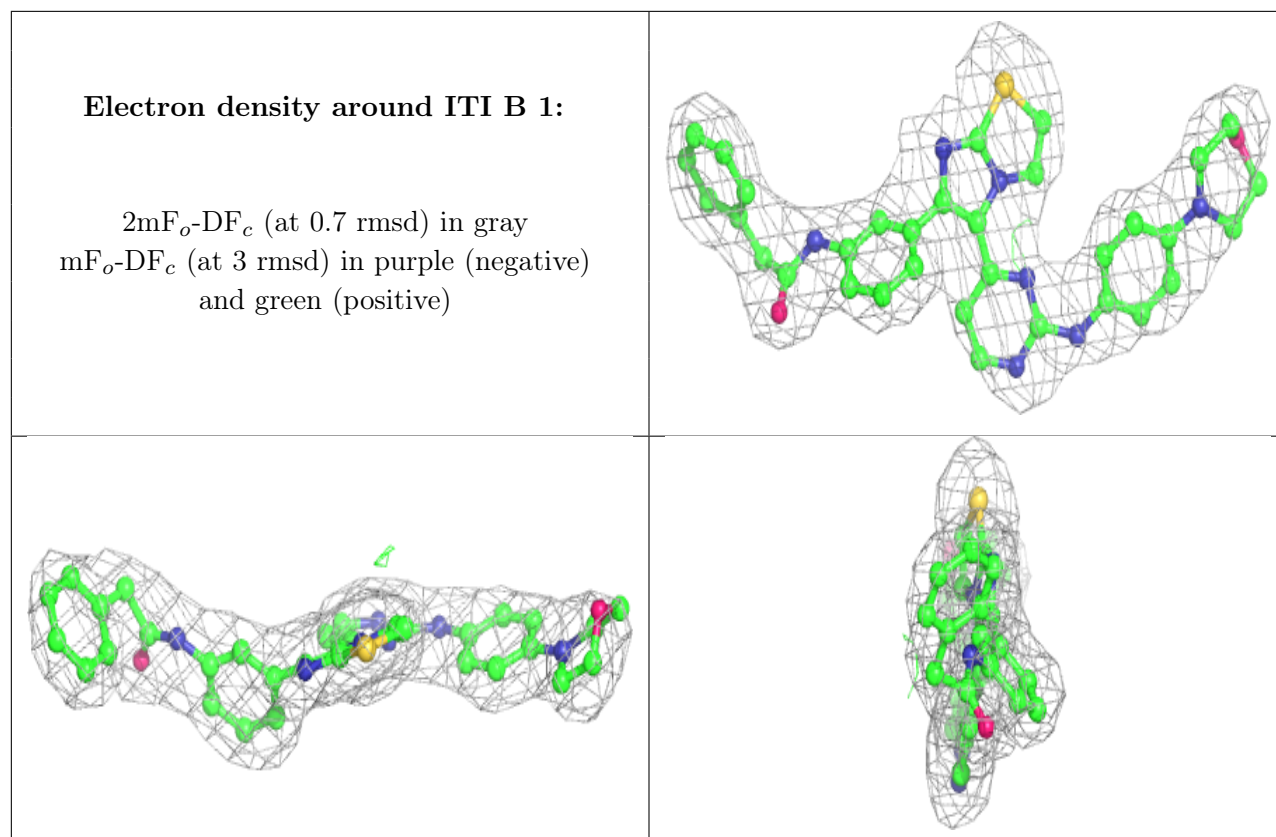
Electron density around ITI C 1:

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

**Electron density around ITI 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.