



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 11:07 pm BST

PDB ID : 3LJ1  
Title : IRE1 complexed with Cdk1/2 Inhibitor III  
Authors : Lee, K.P.K.; Sicheri, F.  
Deposited on : 2010-01-25  
Resolution : 3.33 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](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

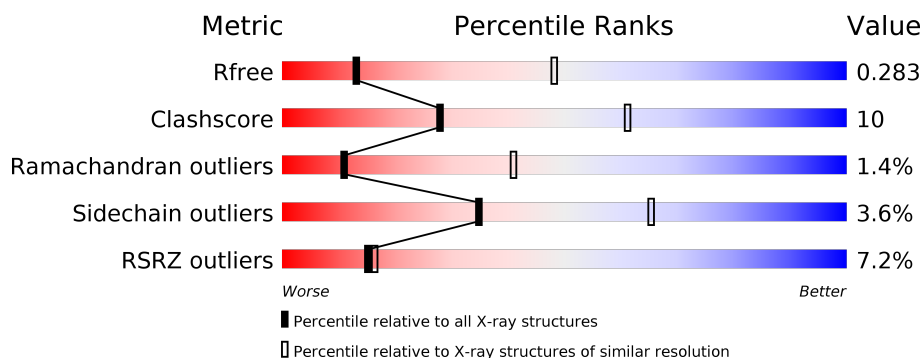
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.33 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	1060 (3.38-3.30)
Clashscore	141614	1111 (3.38-3.30)
Ramachandran outliers	138981	1090 (3.38-3.30)
Sidechain outliers	138945	1089 (3.38-3.30)
RSRZ outliers	127900	1028 (3.38-3.30)

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	434	
1	B	434	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 6348 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 Serine/threonine-protein kinase/endoribonuclease IRE1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	P	S	0	0	0
			3146	2012	535	582	3	14			
1	B	407	Total	C	N	O	P	S	0	0	0
			3146	2012	535	582	3	14			

There are 48 discrepancies between the modelled and reference sequences:

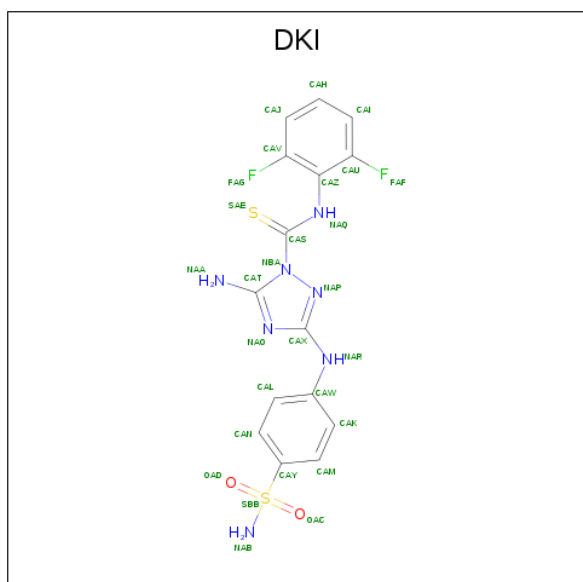
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	CYS	DELETION	UNP P32361
A	?	-	GLN	DELETION	UNP P32361
A	?	-	VAL	DELETION	UNP P32361
A	?	-	GLU	DELETION	UNP P32361
A	?	-	THR	DELETION	UNP P32361
A	?	-	GLU	DELETION	UNP P32361
A	?	-	HIS	DELETION	UNP P32361
A	?	-	SER	DELETION	UNP P32361
A	?	-	SER	DELETION	UNP P32361
A	?	-	SER	DELETION	UNP P32361
A	?	-	ARG	DELETION	UNP P32361
A	?	-	HIS	DELETION	UNP P32361
A	?	-	THR	DELETION	UNP P32361
A	?	-	VAL	DELETION	UNP P32361
A	?	-	VAL	DELETION	UNP P32361
A	?	-	SER	DELETION	UNP P32361
A	?	-	SER	DELETION	UNP P32361
A	?	-	ASP	DELETION	UNP P32361
A	?	-	SER	DELETION	UNP P32361
A	?	-	PHE	DELETION	UNP P32361
A	?	-	TYR	DELETION	UNP P32361
A	?	-	ASP	DELETION	UNP P32361
A	?	-	PRO	DELETION	UNP P32361
A	?	-	PHE	DELETION	UNP P32361
B	?	-	CYS	DELETION	UNP P32361

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLN	DELETION	UNP P32361
B	?	-	VAL	DELETION	UNP P32361
B	?	-	GLU	DELETION	UNP P32361
B	?	-	THR	DELETION	UNP P32361
B	?	-	GLU	DELETION	UNP P32361
B	?	-	HIS	DELETION	UNP P32361
B	?	-	SER	DELETION	UNP P32361
B	?	-	SER	DELETION	UNP P32361
B	?	-	SER	DELETION	UNP P32361
B	?	-	ARG	DELETION	UNP P32361
B	?	-	HIS	DELETION	UNP P32361
B	?	-	THR	DELETION	UNP P32361
B	?	-	VAL	DELETION	UNP P32361
B	?	-	VAL	DELETION	UNP P32361
B	?	-	SER	DELETION	UNP P32361
B	?	-	SER	DELETION	UNP P32361
B	?	-	ASP	DELETION	UNP P32361
B	?	-	SER	DELETION	UNP P32361
B	?	-	PHE	DELETION	UNP P32361
B	?	-	TYR	DELETION	UNP P32361
B	?	-	ASP	DELETION	UNP P32361
B	?	-	PRO	DELETION	UNP P32361
B	?	-	PHE	DELETION	UNP P32361

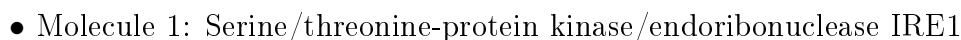
- Molecule 2 is 5-AMINO-3-{[4-(AMINOSULFONYL)PHENYL]AMINO}-N-(2,6-DIFLUOROPHENYL)-1H-1,2,4-TRIAZOLE-1-CARBOTHIOAMIDE (three-letter code: DKI) (formula: C<sub>15</sub>H<sub>13</sub>F<sub>2</sub>N<sub>7</sub>O<sub>2</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0	0
			28	15	2	7	2	2		
2	B	1	Total	C	F	N	O	S	0	0
			28	15	2	7	2	2		



- Molecule 1: Serine/threonine-protein kinase/endoribonuclease IRE1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 1 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	125.55Å 125.55Å 174.39Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	51.26 – 3.33 50.95 – 3.33	Depositor EDS
% Data completeness (in resolution range)	98.3 (51.26-3.33) 98.3 (50.95-3.33)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.60 (at 3.33Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, $R_{free}$	0.263 , 0.284 0.255 , 0.283	Depositor DCC
$R_{free}$ test set	1181 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	76.4	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 31.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.069 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	6348	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, DKI, SEP

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	0.35	0/3181	0.83	11/4309 (0.3%)
1	B	0.36	0/3181	0.57	2/4309 (0.0%)
All	All	0.36	0/6362	0.71	13/8618 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	1	2
All	All	1	4

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	862	GLU	C-N-CA	18.57	168.12	121.70
1	A	895	ARG	N-CA-CB	-16.45	80.99	110.60
1	A	863	GLU	N-CA-CB	15.94	139.28	110.60
1	A	843	ARG	N-CA-CB	15.06	137.71	110.60
1	A	897	LEU	N-CA-CB	-14.66	81.08	110.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	893	THR	CA

All (4) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	1003	ASP	Peptide
1	A	1076	VAL	Peptide
1	B	1003	ASP	Peptide
1	B	1076	VAL	Peptide

## 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	3146	0	3001	71	1
1	B	3146	0	3002	51	0
2	A	28	0	13	3	0
2	B	28	0	13	4	0
All	All	6348	0	6029	122	1

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 10.

The worst 5 of 122 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:842:PHE:CE2	1:A:897:LEU:HD13	1.34	1.56
1:A:842:PHE:CE2	1:A:897:LEU:CD1	1.85	1.56
1:A:842:PHE:CD2	1:A:897:LEU:CD1	2.14	1.31
1:A:842:PHE:CD2	1:A:897:LEU:HD12	1.66	1.29
1:A:843:ARG:H	1:A:896:ARG:HA	1.05	1.14

All (1) 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:A:865:ASN:ND2	1:A:996:ARG:NH2[6_555]	2.00	0.20

## 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	399/434 (92%)	371 (93%)	22 (6%)	6 (2%)	10	40
1	B	399/434 (92%)	370 (93%)	24 (6%)	5 (1%)	12	43
All	All	798/868 (92%)	741 (93%)	46 (6%)	11 (1%)	11	41

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	843	ARG
1	A	868	GLN
1	A	1076	VAL
1	A	1077	PRO
1	B	893	THR

### 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	323/395 (82%)	309 (96%)	14 (4%)	29	62
1	B	323/395 (82%)	314 (97%)	9 (3%)	43	71
All	All	646/790 (82%)	623 (96%)	23 (4%)	35	65

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1053	ARG

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Mol	Chain	Res	Type
1	A	1087	ARG
1	B	1063	MET
1	A	1063	MET
1	A	1109	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1090	ASN
1	B	725	HIS
1	B	787	HIS
1	A	1057	ASN
1	B	773	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	TPO	A	844	1	8,10,11	0.94	1 (12%)	10,14,16	0.94	0
1	SEP	B	840	1	8,9,10	1.72	2 (25%)	8,12,14	1.97	2 (25%)
1	SEP	A	840	1	8,9,10	1.65	1 (12%)	8,12,14	2.01	2 (25%)
1	TPO	B	844	1	8,10,11	0.86	0	10,14,16	0.99	0
1	SEP	B	841	1	8,9,10	1.66	1 (12%)	8,12,14	1.60	2 (25%)
1	SEP	A	841	1	8,9,10	1.60	1 (12%)	8,12,14	1.36	1 (12%)

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
1	TPO	A	844	1	-	4/9/11/13	-
1	SEP	B	840	1	-	0/5/8/10	-
1	SEP	A	840	1	-	1/5/8/10	-
1	TPO	B	844	1	-	4/9/11/13	-
1	SEP	B	841	1	-	3/5/8/10	-
1	SEP	A	841	1	-	3/5/8/10	-

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	840	SEP	P-O1P	3.70	1.62	1.50
1	B	841	SEP	P-O1P	3.63	1.62	1.50
1	A	840	SEP	P-O1P	3.58	1.62	1.50
1	A	841	SEP	P-O1P	3.52	1.61	1.50
1	A	844	TPO	P-OG1	2.04	1.63	1.59

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	840	SEP	OG-CB-CA	3.99	112.02	108.14
1	B	840	SEP	OG-CB-CA	3.82	111.87	108.14
1	B	840	SEP	P-OG-CB	-3.64	108.26	118.30
1	A	840	SEP	P-OG-CB	-3.62	108.31	118.30
1	B	841	SEP	OG-CB-CA	3.35	111.40	108.14

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	844	TPO	N-CA-CB-CG2
1	A	844	TPO	N-CA-CB-OG1
1	A	844	TPO	C-CA-CB-CG2
1	B	844	TPO	N-CA-CB-CG2
1	B	844	TPO	N-CA-CB-OG1

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	844	TPO	4	0
1	B	840	SEP	1	0
1	A	840	SEP	1	0
1	B	844	TPO	4	0
1	A	841	SEP	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

2 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	DKI	A	1	-	28,30,30	3.72	6 (21%)	35,44,44	2.50	10 (28%)
2	DKI	B	1	-	28,30,30	3.48	6 (21%)	35,44,44	2.25	9 (25%)

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	DKI	A	1	-	-	4/12/18/18	0/3/3/3
2	DKI	B	1	-	-	4/12/18/18	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	DKI	CAY-SBB	-10.82	1.60	1.77
2	B	1	DKI	CAY-SBB	-10.30	1.61	1.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	DKI	CAZ-CAU	9.20	1.48	1.38
2	A	1	DKI	CAZ-CAV	9.14	1.48	1.38
2	A	1	DKI	CAZ-CAU	9.02	1.48	1.38

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	DKI	OAD-SBB-OAC	-6.06	108.80	118.76
2	B	1	DKI	OAD-SBB-OAC	-5.69	109.40	118.76
2	A	1	DKI	CAU-CAZ-NAQ	-5.52	115.21	122.12
2	A	1	DKI	CAZ-NAQ-CAS	5.24	130.68	122.99
2	B	1	DKI	SAE-CAS-NAQ	5.17	128.10	119.22

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

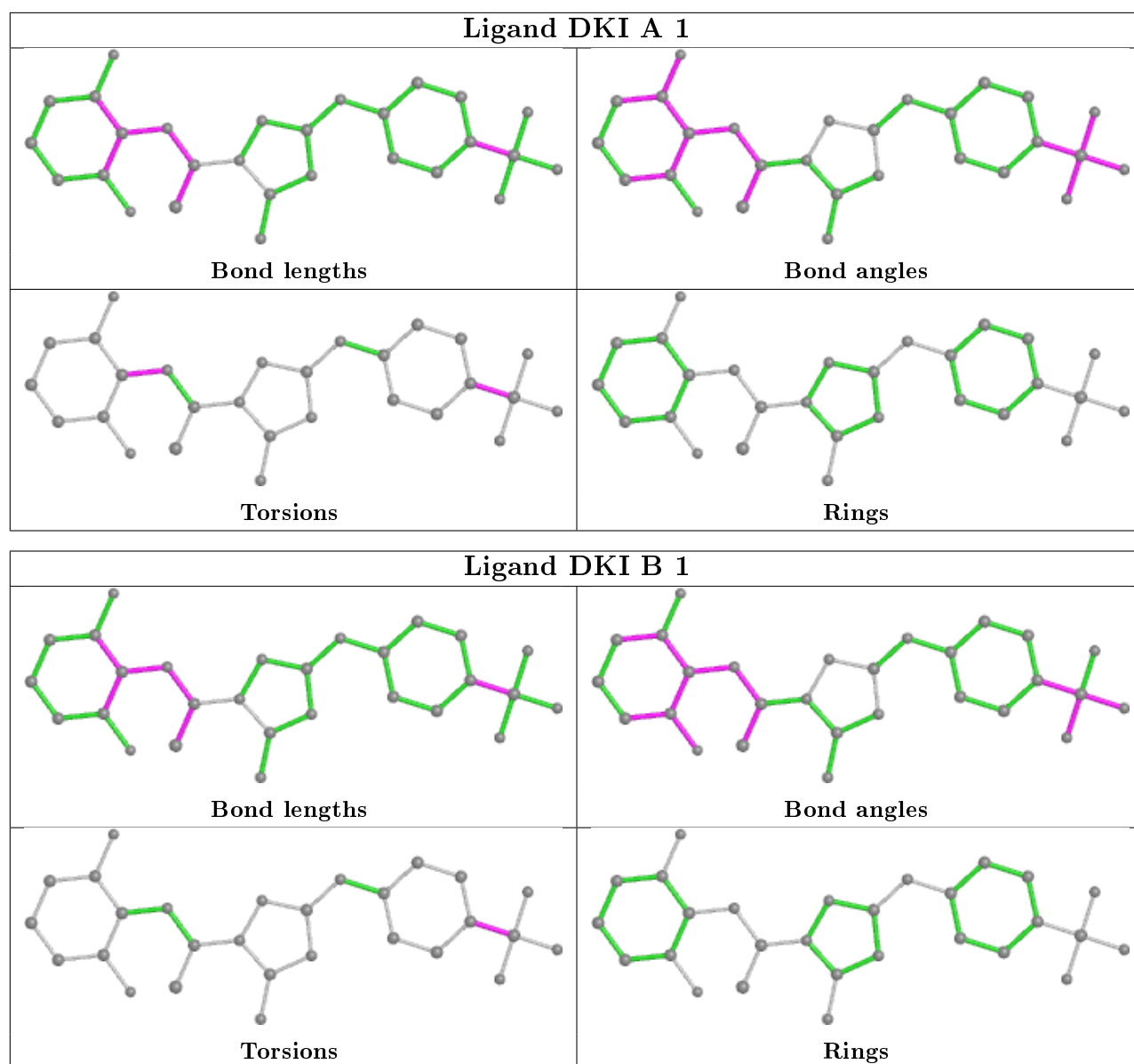
Mol	Chain	Res	Type	Atoms
2	A	1	DKI	CAU-CAZ-NAQ-CAS
2	A	1	DKI	CAV-CAZ-NAQ-CAS
2	B	1	DKI	CAN-CAY-SBB-OAC
2	B	1	DKI	CAM-CAY-SBB-NAB
2	B	1	DKI	CAN-CAY-SBB-NAB

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	DKI	3	0
2	B	1	DKI	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 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	404/434 (93%)	0.85	34 (8%) 11 11	48, 69, 101, 159	0
1	B	404/434 (93%)	0.76	24 (5%) 22 23	35, 54, 82, 103	0
All	All	808/868 (93%)	0.80	58 (7%) 15 16	35, 62, 96, 159	0

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	818	GLY	5.8
1	B	816	GLN	5.0
1	B	813	ALA	4.6
1	B	819	ALA	4.2
1	B	817	THR	4.2

### 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	TPO	A	844	11/12	0.71	0.35	82,87,92,94	0
1	SEP	A	840	10/11	0.71	0.33	81,88,93,97	0
1	SEP	A	841	10/11	0.79	0.35	87,91,103,106	0
1	SEP	B	840	10/11	0.82	0.22	56,60,64,65	0
1	SEP	B	841	10/11	0.83	0.25	59,63,69,70	0
1	TPO	B	844	11/12	0.85	0.19	61,62,64,65	0



## 6.3 Carbohydrates [i](#)

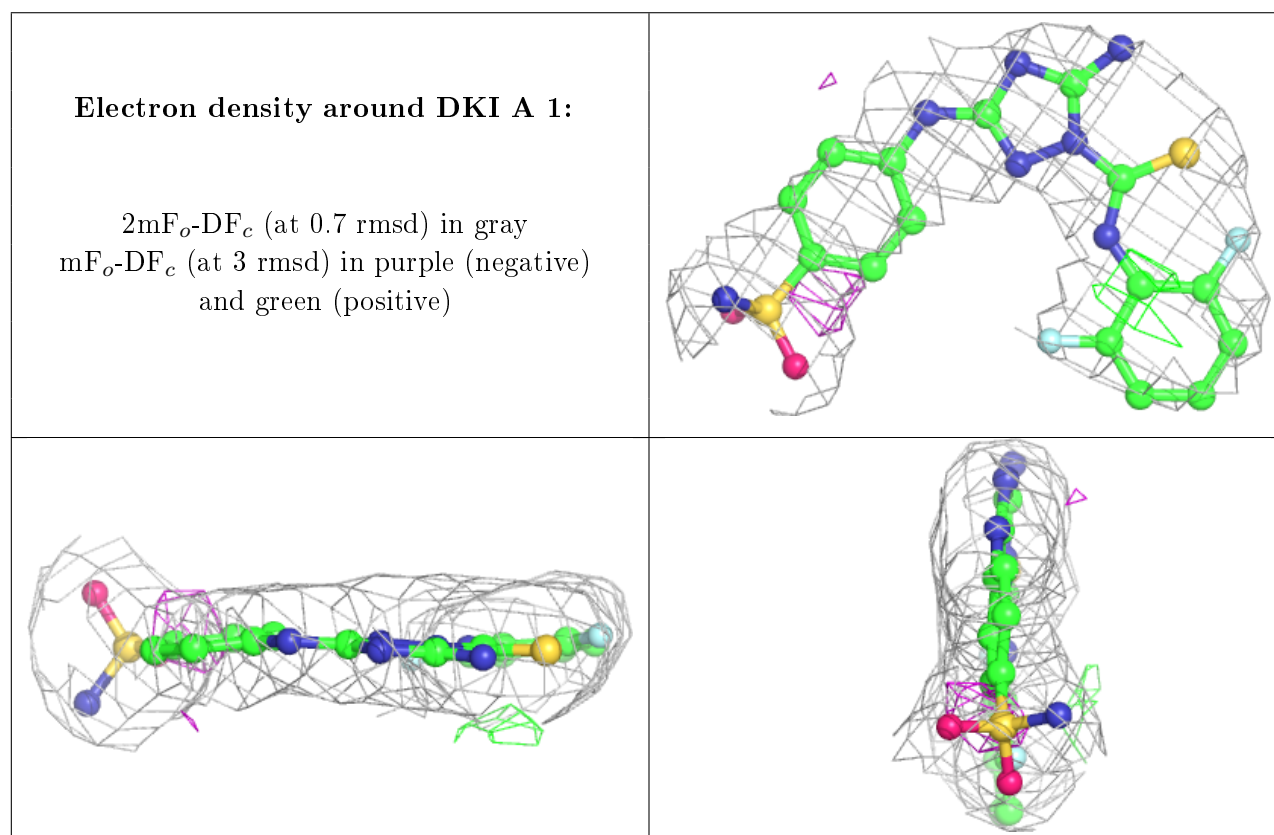
There are no carbohydrates in this entry.

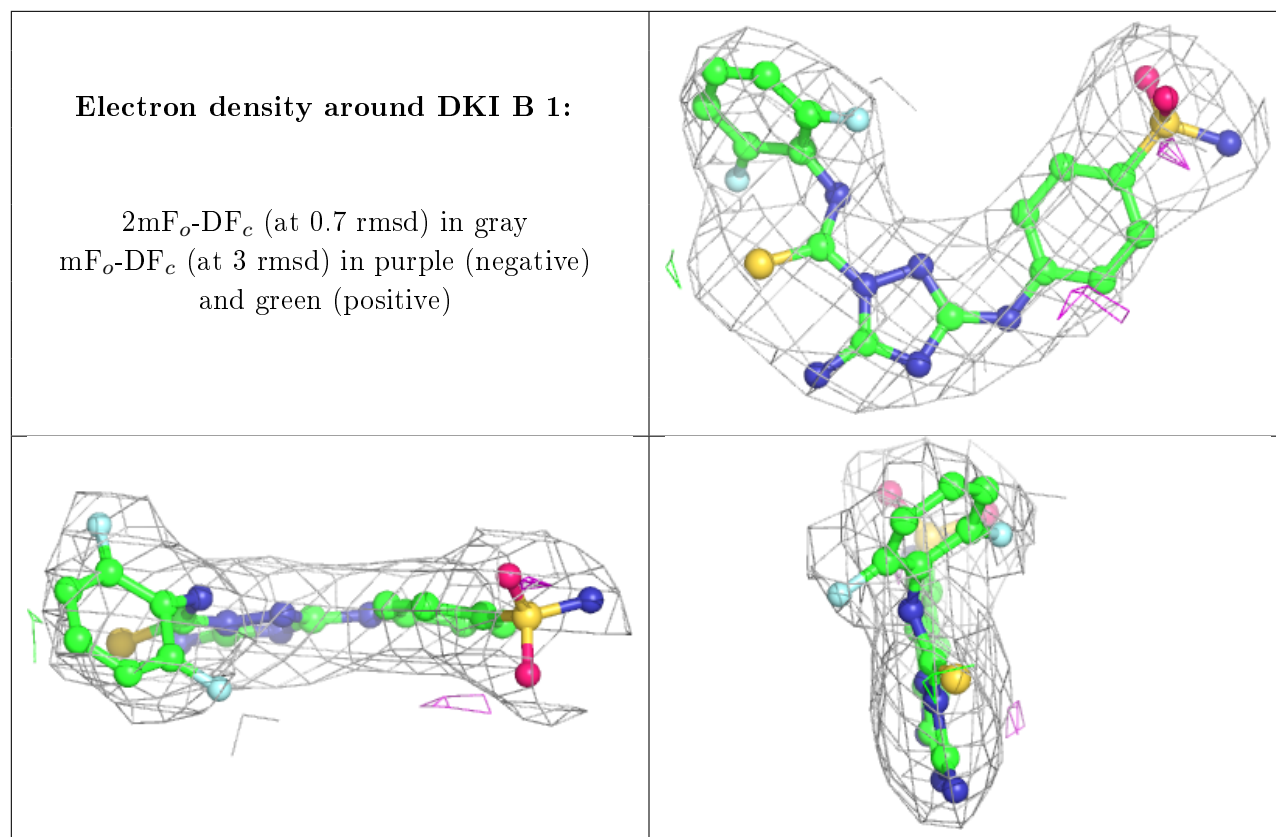
## 6.4 Ligands [i](#)

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( $\text{\AA}^2$ )	Q<0.9
2	DKI	A	1	28/28	0.93	0.31	53,56,66,67	0
2	DKI	B	1	28/28	0.95	0.26	42,43,48,48	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.