



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:16 AM GMT

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
A user guide is available at
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

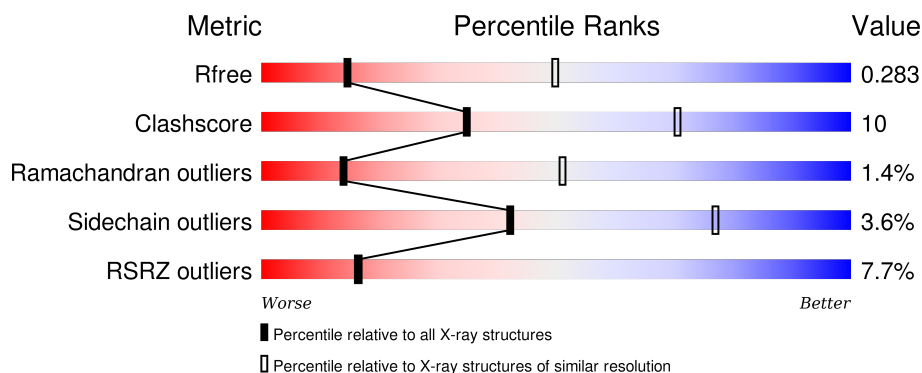
1 Overall quality at a glance ⓘ

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}	91344	1004 (3.40-3.28)
Clashscore	102246	1072 (3.40-3.28)
Ramachandran outliers	100387	1055 (3.40-3.28)
Sidechain outliers	100360	1054 (3.40-3.28)
RSRZ outliers	91569	1009 (3.40-3.28)

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. 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	<div> <div>8%</div> <div>76%</div> <div>14%</div> <div>• • 6%</div> </div>
1	B	434	<div> <div>6%</div> <div>77%</div> <div>15%</div> <div>• 6%</div> </div>

2 Entry composition

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:

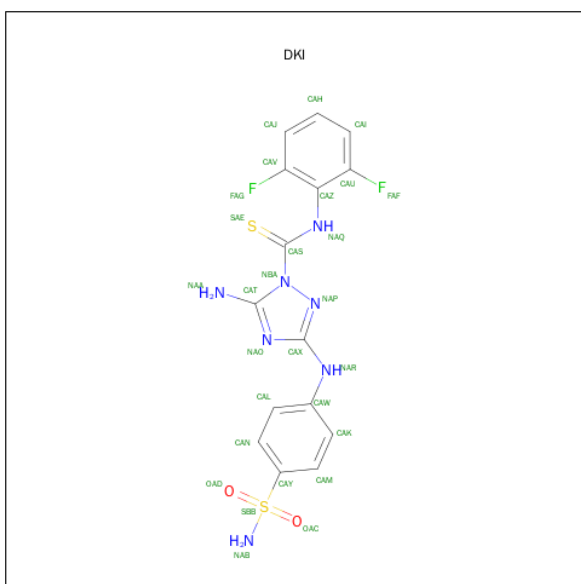
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	CYS	DELETION	UNP P32361
A	?	-	GLN	DELETION	UNP P32361
A	?	-	VAL	DELETION	UNP P32361
A	?	-	GLU	DELETION	UNP P32361
A	?	-	THR	DELETION	UNP P32361
A	?	-	GLU	DELETION	UNP P32361
A	?	-	HIS	DELETION	UNP P32361
A	?	-	SER	DELETION	UNP P32361
A	?	-	SER	DELETION	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

Continued on next page...

Continued from previous page...

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: C₁₅H₁₃F₂N₇O₂S₂).

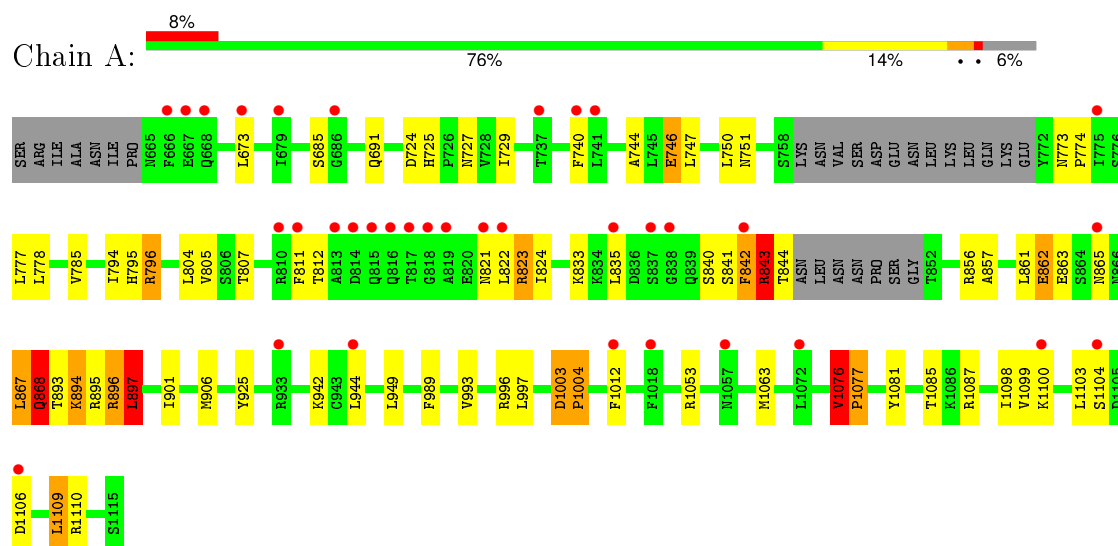


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0	0
			28	15	2	7	2	2		
2	B	1	Total	C	F	N	O	S	0	0
			28	15	2	7	2	2		

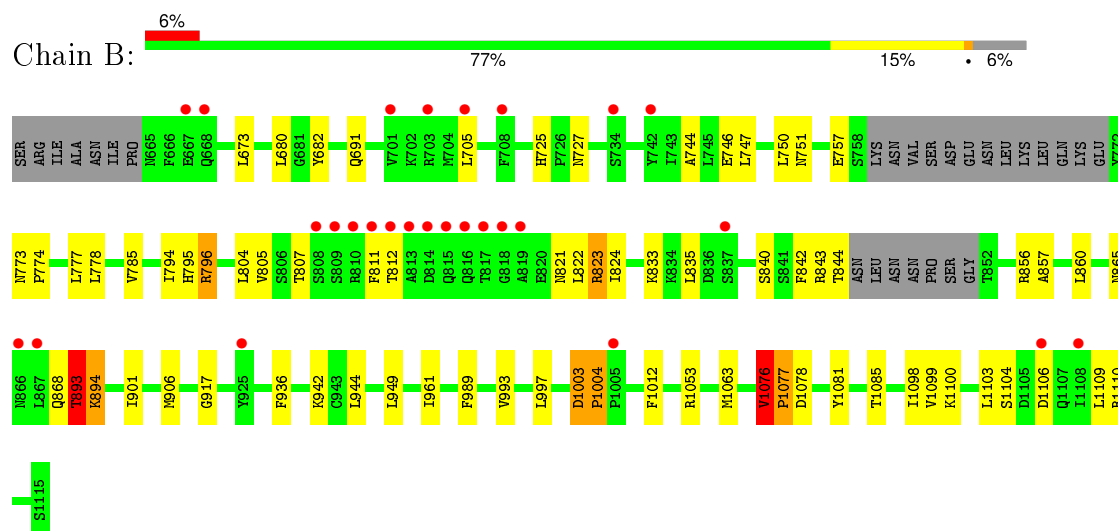
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Serine/threonine-protein kinase/endoribonuclease IRE1



- 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, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	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 (5.44%)	DCC
Wilson B-factor (Å ²)	76.4	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 31.9	EDS
Estimated twinning fraction	0.069 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 22876 reflections	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	6348	wwPDB-VP
Average B, all atoms (Å ²)	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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: 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 [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	399/434 (92%)	371 (93%)	22 (6%)	6 (2%)	13	50
1	B	399/434 (92%)	370 (93%)	24 (6%)	5 (1%)	15	53
All	All	798/868 (92%)	741 (93%)	46 (6%)	11 (1%)	14	51

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 [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	323/395 (82%)	309 (96%)	14 (4%)	35	73
1	B	323/395 (82%)	314 (97%)	9 (3%)	51	82
All	All	646/790 (82%)	623 (96%)	23 (4%)	42	77

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

Mol	Chain	Res	Type
1	A	1053	ARG

Continued on next page...

Continued from previous page...

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	SEP	A	840	1	8,9,10	1.62	2 (25%)	8,12,14	1.85	2 (25%)
1	SEP	A	841	1	8,9,10	1.57	2 (25%)	8,12,14	1.49	1 (12%)
1	TPO	A	844	1	8,10,11	0.68	0	7,14,16	1.53	1 (14%)
1	SEP	B	840	1	8,9,10	1.69	3 (37%)	8,12,14	1.79	2 (25%)
1	SEP	B	841	1	8,9,10	1.63	3 (37%)	8,12,14	1.68	2 (25%)
1	TPO	B	844	1	8,10,11	0.63	0	7,14,16	1.55	1 (14%)

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	SEP	A	840	1	-	0/6/8/10	0/0/0/0
1	SEP	A	841	1	-	0/6/8/10	0/0/0/0
1	TPO	A	844	1	-	1/8/11/13	0/0/0/0
1	SEP	B	840	1	-	0/6/8/10	0/0/0/0
1	SEP	B	841	1	-	0/6/8/10	0/0/0/0
1	TPO	B	844	1	-	1/8/11/13	0/0/0/0

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	841	SEP	P-O2P	2.01	1.61	1.54
1	B	841	SEP	P-O2P	2.01	1.61	1.54
1	A	840	SEP	P-O3P	2.04	1.62	1.54
1	B	840	SEP	P-O2P	2.06	1.62	1.54
1	B	841	SEP	P-O3P	2.10	1.62	1.54

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	840	SEP	O-C-CA	-2.28	119.56	125.49
1	A	840	SEP	O-C-CA	-2.24	119.67	125.49
1	B	841	SEP	O-C-CA	-2.00	120.27	125.49
1	A	844	TPO	C-CA-N	2.61	115.29	109.83
1	B	844	TPO	C-CA-N	2.62	115.31	109.83

There are no chirality outliers.

All (2) torsion outliers are listed below:

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

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	840	SEP	1	0
1	A	841	SEP	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	844	TPO	4	0
1	B	840	SEP	1	0
1	B	844	TPO	4	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	-	27,30,30	3.86	6 (22%)	32,44,44	2.82	10 (31%)
2	DKI	B	1	-	27,30,30	3.62	6 (22%)	32,44,44	2.40	8 (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	-	-	0/12/18/18	0/3/3/3
2	DKI	B	1	-	-	0/12/18/18	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	-11.18	1.60	1.77
2	B	1	DKI	CAY-SBB	-10.64	1.61	1.77
2	A	1	DKI	CAS-SAE	-7.47	1.55	1.67
2	B	1	DKI	CAS-SAE	-6.02	1.58	1.67

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	DKI	CAZ-NAQ	-4.79	1.34	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	DKI	OAD-SBB-OAC	-7.11	108.80	118.80
2	A	1	DKI	CAU-CAZ-NAQ	-6.83	115.21	122.12
2	B	1	DKI	OAD-SBB-OAC	-6.69	109.40	118.80
2	B	1	DKI	CAV-CAZ-NAQ	-4.61	117.45	122.12
2	B	1	DKI	CAZ-NAQ-CAS	-4.57	115.87	122.54

There are no chirality outliers.

There are no torsion outliers.

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

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	404/434 (93%)	0.89	35 (8%) 13 12	48, 69, 101, 159	0
1	B	404/434 (93%)	0.80	27 (6%) 21 21	35, 54, 82, 103	0
All	All	808/868 (93%)	0.85	62 (7%) 16 16	35, 62, 96, 159	0

The worst 5 of 62 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	818	GLY	6.0
1	B	816	GLN	5.1
1	B	813	ALA	4.7
1	B	819	ALA	4.3
1	B	817	THR	4.3

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	TPO	A	844	11/12	0.71	0.35	-	82,87,92,94	0
1	SEP	B	840	10/11	0.82	0.22	-	56,60,64,65	0
1	SEP	A	840	10/11	0.71	0.33	-	81,88,93,97	0
1	TPO	B	844	11/12	0.85	0.19	-	61,62,64,65	0
1	SEP	B	841	10/11	0.83	0.25	-	59,63,69,70	0
1	SEP	A	841	10/11	0.79	0.35	-	87,91,103,106	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	DKI	A	1	28/28	0.93	0.31	0.06	53,56,66,67	0
2	DKI	B	1	28/28	0.95	0.26	-0.65	42,43,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.