



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2018 – 03:24 pm GMT

PDB ID : 4KBC
Title : CK1d in complex with {4-[3-(4-FLUOROPHENYL)-1H-PYRAZOL-4-YL]PYRIDIN-2-YL}METHANOL inhibitor
Authors : Liu, S.
Deposited on : 2013-04-23
Resolution : 1.98 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 : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

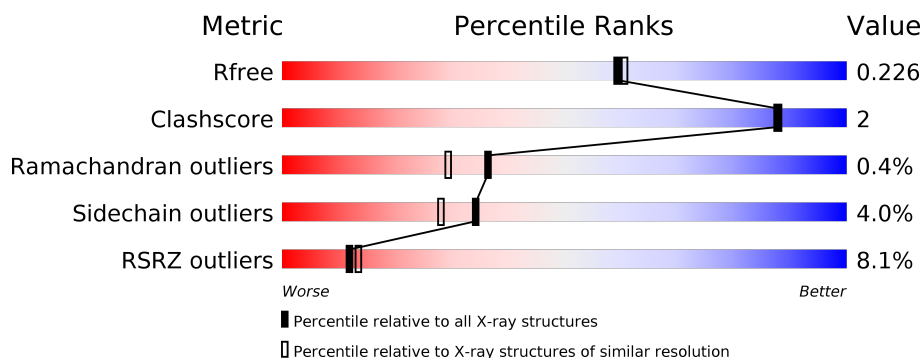
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.98 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}	111664	10189 (2.00-1.96)
Clashscore	122126	11405 (2.00-1.96)
Ramachandran outliers	120053	11281 (2.00-1.96)
Sidechain outliers	120020	11280 (2.00-1.96)
RSRZ outliers	108989	9953 (2.00-1.96)

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	317	<div> <div>5%</div> <div>83%</div> <div>8%</div> <div>9%</div> </div>
1	B	317	<div> <div>9%</div> <div>79%</div> <div>8%</div> <div>13%</div> </div>

2 Entry composition [i](#)

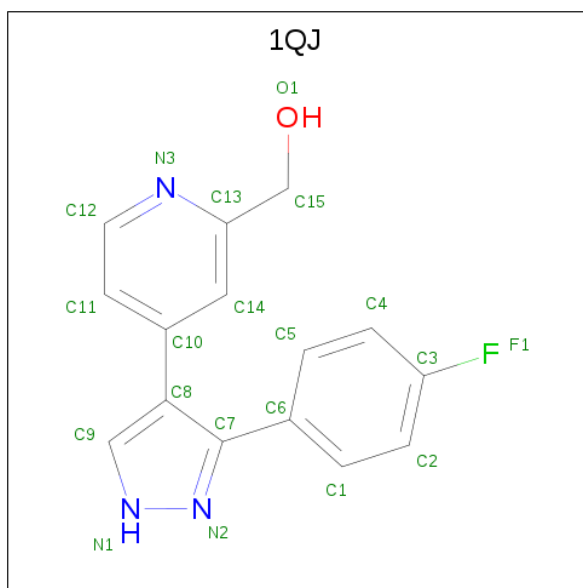
There are 5 unique types of molecules in this entry. The entry contains 5039 atoms, of which 30 are hydrogens and 0 are deuteriums.

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 Casein kinase I isoform delta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	0	1	0
			2367	1517	414	422	14			
1	B	277	Total	C	N	O	S	0	2	0
			2280	1466	392	409	13			

- Molecule 2 is {4-[3-(4-fluorophenyl)-1H-pyrazol-4-yl]pyridin-2-yl}methanol (three-letter code: 1QJ) (formula: C₁₅H₁₂FN₃O).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	H	N	O	12	0
			32	15	1	12	3	1		
2	B	1	Total	C	F	H	N	O	12	0
			32	15	1	12	3	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	148	Total	O	0	0
			148	148		
5	B	130	Total	O	0	0
			130	130		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.58Å 118.14Å 61.22Å 90.00° 109.23° 90.00°	Depositor
Resolution (Å)	19.96 – 1.98 19.81 – 1.98	Depositor EDS
% Data completeness (in resolution range)	93.8 (19.96-1.98) 94.4 (19.81-1.98)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 1.99Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.185 , 0.215 0.190 , 0.226	Depositor DCC
R_{free} test set	2546 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å ²)	36.5	Xtriage
Anisotropy	0.068	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5039	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.09% 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, 0.333 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: 1QJ, EDO, SO4

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	0.51	0/2423	0.64	1/3256 (0.0%)
1	B	0.50	0/2338	0.63	0/3140
All	All	0.51	0/4761	0.63	1/6396 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	173	LEU	CD1-CG-CD2	5.37	126.61	110.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2367	0	2371	12	0
1	B	2280	0	2266	9	0
2	A	20	12	12	0	0
2	B	20	12	12	0	0
3	A	10	0	0	0	0
3	B	30	0	0	0	0
4	A	4	6	6	0	0
5	A	148	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	130	0	0	0	0
All	All	5009	30	4667	21	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 2.

The worst 5 of 21 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:1:MET:HG3	1:B:2:GLU:H	1.45	0.80
1:A:168:ARG:HD2	1:A:171:LYS:HD3	1.69	0.74
1:A:59:MET:HE1	1:A:119:ILE:HA	1.81	0.62
1:A:222:ARG:HG3	1:A:222:ARG:HH11	1.67	0.58
1:B:237:ILE:HD12	1:B:252:LEU:HB3	1.88	0.54

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	285/317 (90%)	280 (98%)	3 (1%)	2 (1%)	24	16
1	B	271/317 (86%)	266 (98%)	4 (2%)	1 (0%)	36	29
All	All	556/634 (88%)	546 (98%)	7 (1%)	3 (0%)	36	23

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	149	ASP
1	A	149[A]	ASP
1	A	149[B]	ASP

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	255/276 (92%)	246 (96%)	9 (4%)	39	34
1	B	246/276 (89%)	235 (96%)	11 (4%)	30	23
All	All	501/552 (91%)	481 (96%)	20 (4%)	34	28

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	4	ARG
1	B	17	SER
1	B	168	ARG
1	A	168	ARG
1	A	221	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	48	GLN
1	B	291	ASN
1	B	271	GLN
1	A	275	ASN
1	B	78	ASN

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 [i](#)

11 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	1QJ	A	401	-	21,22,22	1.98	5 (23%)	24,30,30	1.72	2 (8%)
3	SO4	A	402	-	4,4,4	0.40	0	6,6,6	0.32	0
3	SO4	A	403	-	4,4,4	0.30	0	6,6,6	0.40	0
4	EDO	A	404	-	3,3,3	0.59	0	2,2,2	0.25	0
2	1QJ	B	401	-	21,22,22	1.96	5 (23%)	24,30,30	1.51	2 (8%)
3	SO4	B	402	-	4,4,4	0.53	0	6,6,6	0.25	0
3	SO4	B	403	-	4,4,4	0.15	0	6,6,6	0.26	0
3	SO4	B	404	-	4,4,4	0.26	0	6,6,6	0.28	0
3	SO4	B	405	-	4,4,4	0.20	0	6,6,6	0.08	0
3	SO4	B	406	-	4,4,4	0.26	0	6,6,6	0.54	0
3	SO4	B	407	-	4,4,4	0.31	0	6,6,6	0.19	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	1QJ	A	401	-	-	0/10/10/10	0/3/3/3
3	SO4	A	402	-	-	0/0/0/0	0/0/0/0
3	SO4	A	403	-	-	0/0/0/0	0/0/0/0
4	EDO	A	404	-	-	0/1/1/1	0/0/0/0
2	1QJ	B	401	-	-	0/10/10/10	0/3/3/3
3	SO4	B	402	-	-	0/0/0/0	0/0/0/0
3	SO4	B	403	-	-	0/0/0/0	0/0/0/0
3	SO4	B	404	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	B	405	-	-	0/0/0/0	0/0/0/0
3	SO4	B	406	-	-	0/0/0/0	0/0/0/0
3	SO4	B	407	-	-	0/0/0/0	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)
2	A	401	1QJ	C6-C7	-3.24	1.45	1.49
2	B	401	1QJ	C6-C7	-3.07	1.45	1.49
2	B	401	1QJ	C8-C10	-3.00	1.44	1.49
2	A	401	1QJ	C8-C10	-3.00	1.44	1.49
2	B	401	1QJ	C8-C7	2.06	1.43	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	1QJ	C8-C9-N1	-6.69	105.73	108.15
2	B	401	1QJ	C8-C9-N1	-5.83	106.04	108.15
2	A	401	1QJ	C15-C13-C14	-2.47	118.80	122.33
2	B	401	1QJ	C8-C7-N2	-2.01	109.81	111.80

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	288/317 (90%)	0.21	16 (5%) 24 27	24, 40, 69, 101	0
1	B	277/317 (87%)	0.45	30 (10%) 6 7	26, 44, 89, 120	0
All	All	565/634 (89%)	0.33	46 (8%) 12 13	24, 42, 80, 120	0

The worst 5 of 46 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	76	ASP	6.2
1	B	30	ALA	5.9
1	B	46	HIS	5.8
1	A	46	HIS	5.6
1	B	224	LYS	5.3

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, 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
3	SO4	B	402	5/5	0.79	0.22	74,75,79,81	0
2	1QJ	A	401	20/20	0.87	0.12	36,41,50,54	12
2	1QJ	B	401	20/20	0.92	0.14	46,55,61,61	12
4	EDO	A	404	4/4	0.93	0.07	54,57,60,60	0
3	SO4	A	403	5/5	0.97	0.08	63,65,65,68	0
3	SO4	B	407	5/5	0.97	0.10	62,63,67,68	0
3	SO4	B	404	5/5	0.97	0.07	57,62,65,65	0
3	SO4	B	406	5/5	0.97	0.10	60,61,65,65	0
3	SO4	B	405	5/5	0.97	0.19	80,80,81,83	0
3	SO4	B	403	5/5	0.98	0.09	48,50,54,56	0
3	SO4	A	402	5/5	0.99	0.06	38,43,44,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.