

wwPDB X-ray Structure Validation Summary Report (i)

Feb 5, 2024 – 08:33 PM EST

PDB ID : 1YXV

Title: Crystal Structure of Kinase Pim1 in complex with 3,4-Dihydroxy-1-methylqu

inolin-2(1H)-one

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Deposited on : 2005-02-22

Resolution : 2.00 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 (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) 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 : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

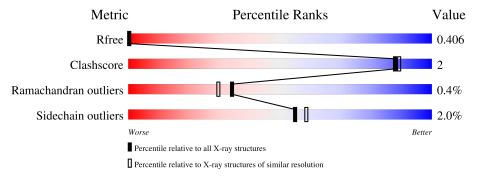
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 2.00 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	Similar resolution
Wietrie	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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 <=5%

Mol	Chain	Length	Quality of chain	
1	A	293	84%	8% • 6%



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2436 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.

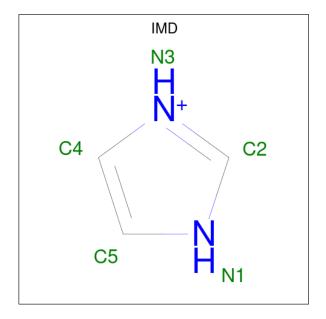
• Molecule 1 is a protein called Proto-oncogene serine/threonine-protein kinase Pim-1.

Mol	Chain	Residues		\mathbf{At}	oms			ZeroOcc	AltConf	Trace
1	Δ	274	Total	С	N	О	S	0	9	0
1	Λ	214	2247	1435	393	411	8		2	

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	314	VAL	-	expression tag	UNP P11309
A	315	ASP	-	expression tag	UNP P11309
A	316	HIS	-	expression tag	UNP P11309
A	317	HIS	-	expression tag	UNP P11309
A	318	HIS	-	expression tag	UNP P11309
A	319	HIS	-	expression tag	UNP P11309
A	320	HIS	-	expression tag	UNP P11309
A	321	HIS	=	expression tag	UNP P11309

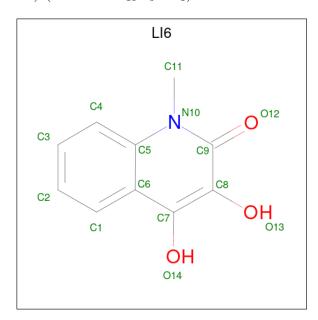
• Molecule 2 is IMIDAZOLE (three-letter code: IMD) (formula: $C_3H_5N_2$).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total C I 5 3 5	N 2	0	0

• Molecule 3 is 3,4-DIHYDROXY-1-METHYLQUINOLIN-2(1H)-ONE (three-letter code: LI6) (formula: $C_{10}H_9NO_3$).



Mol	Chain	Residues	A	Lton	ns		ZeroOcc	AltConf
2	Λ	1	Total	С	N	О	0	0
3	Α	1	14	10	1	3	U	0

• Molecule 4 is water.

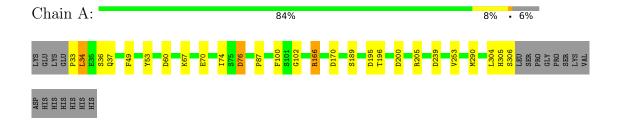
\mathbf{Mol}	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	170	Total O 170 170	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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. 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. 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 serine/threonine-protein kinase Pim-1





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants	96.59Å 96.59Å 80.56Å	Domositon
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	84.51 - 2.00	Depositor
Resolution (A)	48.30 - 1.98	EDS
% Data completeness	99.5 (84.51-2.00)	Depositor
(in resolution range)	98.6 (48.30-1.98)	EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) > 1$	1.82 (at 1.98Å)	Xtriage
Refinement program	REFMAC 5.1.25	Depositor
D D	0.188 , 0.211	Depositor
R, R_{free}	0.410 , 0.406	DCC
R_{free} test set	1495 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	33.5	Xtriage
Anisotropy	0.187	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.33, 28.5	EDS
L-test for twinning ²	$< L >=0.48, < L^2>=0.31$	Xtriage
Estimated twinning fraction	0.049 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.79	EDS
Total number of atoms	2436	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.77% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: LI6, IMD

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).

Mal	Chain	Bond	lengths	Bo	nd angles
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.44	0/2307	0.79	8/3131 (0.3%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	195	ASP	CB-CG-OD2	5.98	123.68	118.30
1	A	76	ASP	CB-CG-OD2	5.82	123.54	118.30
1	A	166	ARG	NE-CZ-NH2	-5.79	117.41	120.30
1	A	60	ASP	CB-CG-OD2	5.69	123.42	118.30
1	A	200	ASP	CB-CG-OD2	5.66	123.40	118.30

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	2247	0	2185	9	2
2	A	5	0	5	0	0
3	A	14	0	7	0	0
4	A	170	0	0	2	1
All	All	2436	0	2197	9	2



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 9 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ (\rm \mathring{A}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap (Å)} \end{array}$
1:A:33:PRO:HA	1:A:37:GLN:HE21	1.38	0.89
1:A:166:ARG:HD3	1:A:189:SER:O	2.04	0.57
1:A:33:PRO:O	1:A:34:LEU:CB	2.60	0.49
1:A:100:PHE:CZ	1:A:102:GLY:HA3	2.48	0.49
1:A:253:VAL:HG23	4:A:489:HOH:O	2.15	0.46

All (2) 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	$egin{aligned} & ext{Interatomic} \ & ext{distance} \ & ext{(Å)} \end{aligned}$	Clash overlap (Å)	
1:A:70:GLU:OE2	1:A:196:THR:OG1[5_665]	1.94	0.26	
1:A:53:TYR:OH	4:A:457:HOH:O[5_665]	1.96	0.24	

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	274/293 (94%)	265 (97%)	8 (3%)	1 (0%)	34 30	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	LEU



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	247/263 (94%)	242 (98%)	5 (2%)	55 58	

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	SER
1	A	76	ASP
1	A	290	MET
1	A	304	LEU
1	A	306	SER

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

Mol	Chain	Res	Type
1	A	37	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 monosaccharides 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	Tuna	Chain	Res Link		Des	T inle	Bond lengths			В	ond ang	les
MOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2		
3	LI6	A	323	-	14,15,15	1.97	4 (28%)	13,22,22	0.92	0		
2	IMD	A	322	-	3,5,5	0.42	0	4,5,5	0.62	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
3	LI6	A	323	-	-	-	0/2/2/2
2	IMD	A	322	-	-	-	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
3	A	323	LI6	C6-C5	4.11	1.49	1.42
3	A	323	LI6	C8-C9	3.77	1.49	1.40
3	A	323	LI6	C9-N10	2.98	1.42	1.38
3	A	323	LI6	C7-C6	2.36	1.48	1.43

There are no bond angle outliers.

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)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

