

# Full wwPDB X-ray Structure Validation Report (i)

#### May 14, 2020 – 06:04 pm BST

PDB ID : 5N4Z

Title : Crystal structure of human Pim-1 kinase in complex with a consensus peptide

and fragment like molecule (E)-4-(4-hydroxyphenyl)but-3-en-2-one

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Deposited on : 2017-02-11

Resolution : 2.26 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 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 : 2.11

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

Refmac: 5.8.0158

CCP4 : 7.0.044 (Gargrove) roteins) : Engh & Huber (2001)

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

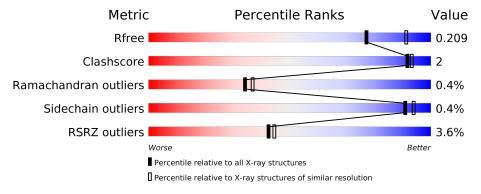
Validation Pipeline (wwPDB-VP) : 2.11

## 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.26 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
$R_{free}$	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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 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% 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	313	82%	• 13%				
2	В	14	7% 64%	36%				



## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2375 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 pim-1.

Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf	Trace		
1	Λ	272	Total	С	N	О	S	0	2	0
1	1 A		2184	1405	380	391	8	U	3	0

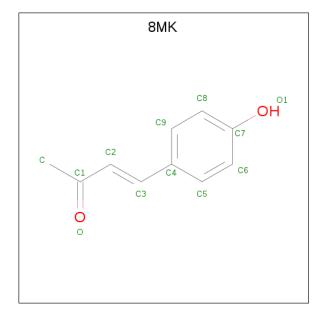
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Α	250	GLY	ARG	engineered mutation	UNP P11309

• Molecule 2 is a protein called Pimtide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	В	9	Total 72	C 42	N 21	O 9	0	0	0

• Molecule 3 is ( $\{E\}$ )-4-(4-hydroxyphenyl)but-3-en-2-one (three-letter code: 8MK) (formula:  $C_{10}H_{10}O_2$ ).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 12	C 10	O 2	0	0

## • Molecule 4 is water.

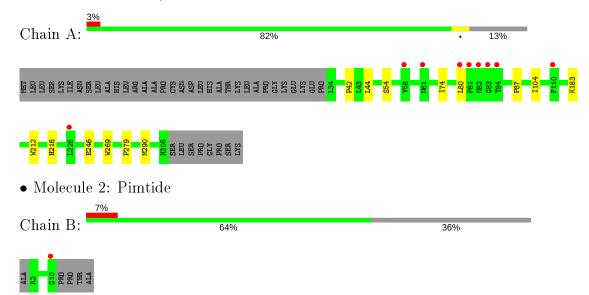
Mol	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
4	A	104	Total O 105 105	0	1
4	В	2	Total O 2 2	0	0



# 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 the various outlier classes 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 pim-1





# 4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 65	Depositor	
Cell constants	98.55Å 98.55Å 80.94Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor	
Resolution (Å)	37.75 - 2.26	Depositor	
resolution (A)	37.75 - 2.26	EDS	
% Data completeness	97.1 (37.75-2.26)	Depositor	
(in resolution range)	97.1 (37.75-2.26)	EDS	
$R_{merge}$	(Not available)	Depositor	
$R_{sym}$	(Not available)	Depositor	
$< I/\sigma(I) > 1$	$1.91~({\rm at}~2.27{\rm \AA})$	Xtriage	
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor	
$R, R_{free}$	0.179 , $0.208$	Depositor	
$\Pi, \Pi free$	0.180 , $0.209$	DCC	
$R_{free}$ test set	1025  reflections  (5.00%)	wwPDB-VP	
Wilson B-factor (Å <sup>2</sup> )	37.6	Xtriage	
Anisotropy	0.199	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	$0.32\;,30.9$	EDS	
L-test for twinning <sup>2</sup>	$< L >=0.48, < L^2>=0.32$	Xtriage	
Estimated twinning fraction	0.055 for h,-h-k,-l	Xtriage	
$F_o, F_c$ correlation	0.96	EDS	
Total number of atoms	2375	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.70% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: 8MK

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	0.43	0/2242	0.53	0/3045	
	2	В	0.37	0/73	0.52	0/94	
Ī	All	All	0.43	0/2315	0.53	0/3139	

There are no bond length outliers.

There are no bond angle outliers.

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	$\mathbf{H}(\mathbf{model})$	H(added)	Clashes	Symm-Clashes
1	A	2184	0	2082	7	0
2	В	72	0	70	0	0
3	A	12	0	0	0	0
4	A	105	0	0	0	0
4	В	2	0	0	0	0
All	All	2375	0	2152	7	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.

All (7) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	$egin{array}{l}  ext{Interatomic} \  ext{distance } ( ext{Å}) \end{array}$	$egin{array}{c} { m Clash} \\ { m overlap} \ ({ m \AA}) \end{array}$
1:A:74:ILE:HD13	1:A:87:PRO:HG3	1.83	0.60
1:A:104:ILE:HG12	1:A:183:LYS:HB3	1.87	0.56
1:A:42:PRO:HD2	1:A:54:SER:HB3	1.91	0.52
1:A:212:TRP:CE3	1:A:216:HIS:HA	2.45	0.51
1:A:269:TRP:CD1	1:A:279:PRO:HD3	2.46	0.51
1:A:44:LEU:HD21	1:A:54:SER:HB2	1.93	0.50
1:A:246:GLU:H	1:A:246:GLU:CD	2.24	0.41

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	${f Analysed}$	Favoured	Allowed	Outliers	Percentile	$\mathbf{s}$
1	A	$273/313 \ (87\%)$	267 (98%)	5 (2%)	1 (0%)	34 37	
2	В	7/14~(50%)	7 (100%)	0	0	100 100	
All	All	280/327~(86%)	274 (98%)	5 (2%)	1 (0%)	34 37	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	80	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	Perce	ntiles
1	A	225/276~(82%)	224 (100%)	1 (0%)	91	94
2	В	6/11 (54%)	6 (100%)	0	100	100
All	All	$231/287 \; (80\%)$	230 (100%)	1 (0%)	91	94

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Α	290	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 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)

1 ligand is 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 Re		Chain Res	Link	Bond lengths			Bond angles		
10101	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	8MK	A	401	-	12,12,12	0.19	0	15,15,15	0.42	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	8MK	A	401	_	-	0/5/5/5	0/1/1/1

There are no bond length outliers.

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)

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,  $95^{th}$  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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(\AA^2)$	Q < 0.9
1	A	272/313 (86%)	-0.04	9 (3%) 46 48	24, 37, 71, 108	0
2	В	9/14 (64%)	-0.05	1 (11%) 5 5	37, 40, 55, 55	1 (11%)
All	All	281/327 (85%)	-0.04	10 (3%) 42 44	24, 37, 69, 108	1 (0%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	81	PRO	7.6
1	A	80	LEU	4.9
1	A	61	ASN	3.3
1	A	84	THR	3.1
1	A	58	VAL	2.9
1	A	83	GLY	2.7
1	A	82	ASN	2.5
1	A	110	PHE	2.3
2	В	10	GLY	2.1
1	A	228	LEU	2.1

## 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,  $95^{th}$  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	${f B\text{-factors}}({f \AA}^2)$	Q<0.9
3	8MK	A	401	12/12	0.94	0.08	28,38,48,51	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

