

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

Jan 30, 2024 – 10:39 PM EST

PDB ID : 1IRK

Title : CRYSTAL STRUCTURE OF THE TYROSINE KINASE DOMAIN OF THE

HUMAN INSULIN RECEPTOR

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Deposited on : 1995-01-02

Resolution : 2.10 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : NOT EXECUTED EDS : NOT EXECUTED

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

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

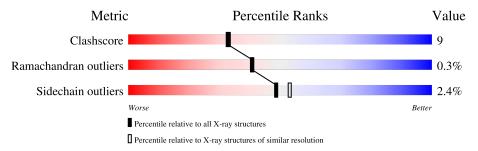
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.10 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	
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$	
Clashscore	141614	5710 (2.10-2.10)	
Ramachandran outliers	138981	5647 (2.10-2.10)	
Sidechain outliers	138945	5648 (2.10-2.10)	

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain			
1	A	306	82%	16%		



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2585 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.

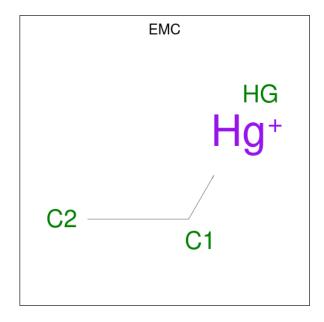
• Molecule 1 is a protein called INSULIN RECEPTOR TYROSINE KINASE DOMAIN.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Δ	303	Total	С	N	О	S	0	3	0
1	11	303	2380	1509	410	441	20			U

There are 2 discrepancies between the modelled and reference sequences:

Chain Residue		Modelled Actual		Comment	Reference	
A	981	SER	CYS conflict		UNP P06213	
A	A 984 PHE		TYR	conflict	UNP P06213	

• Molecule 2 is ETHYL MERCURY ION (three-letter code: EMC) (formula: C<sub>2</sub>H<sub>5</sub>Hg).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C Hg 3 2 1	0	0
2	A	1	Total C Hg 3 2 1	0	0



## • Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	199	Total O 199 199	0	0

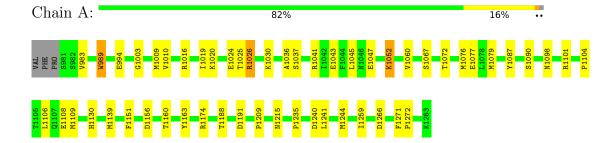


# 3 Residue-property plots (i)

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.

Note EDS was not executed.

• Molecule 1: INSULIN RECEPTOR TYROSINE KINASE DOMAIN





# 4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	54.03Å 72.99Å 89.18Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	6.00 - 2.10	Depositor	
% Data completeness	91.2 (6.00-2.10)	Depositor	
(in resolution range)	31.2 (0.00 2.10)	Depositor	
$R_{merge}$	(Not available)	Depositor	
$R_{sym}$	(Not available)	Depositor	
Refinement program	X-PLOR	Depositor	
$R, R_{free}$	0.196 , 0.232	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	2585	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP	



# 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: EMC

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		
IVIOI		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.51	0/2450	0.72	0/3313	

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	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2380	0	2320	41	0
2	A	6	0	0	1	0
3	A	199	0	0	2	0
All	All	2585	0	2320	41	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 9.

All (41) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:1030:LYS:HE2	1:A:1076[B]:MET:SD	2.23	0.78

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Atom-1	Atom-2	Interatomic	Clash	
		$\operatorname{distance}\ ( ext{\AA})$	overlap (Å)	
1:A:1041:ARG:HG2	1:A:1041:ARG:HH11	1.49	0.77	
1:A:1036:ALA:HB3	1:A:1041:ARG:NH1	2.05	0.70	
1:A:1016:ARG:HG2	1:A:1024:GLU:HG2	1.81	0.62	
1:A:1043:GLU:O	1:A:1047:GLU:HG3	2.03	0.58	
1:A:1060:VAL:HG13	1:A:1077:GLU:HG2	1.86	0.56	
1:A:1019:ILE:HD12	1:A:1025:THR:HG21	1.87	0.56	
1:A:1041:ARG:HD3	3:A:170:HOH:O	2.04	0.56	
1:A:1052:LYS:O	1:A:1052:LYS:HD2	2.05	0.56	
1:A:1174:ARG:HB3	1:A:1209:PRO:HB2	1.88	0.56	
1:A:1041:ARG:HH11	1:A:1041:ARG:CG	2.17	0.55	
1:A:1090:SER:O	1:A:1098:ASN:HA	2.07	0.54	
1:A:1010:VAL:HG21	1:A:1151:PHE:HB3	1.91	0.52	
1:A:1106:LEU:HD21	1:A:1235:PRO:HG2	1.91	0.52	
1:A:1240:ASP:O	1:A:1244:MET:HG3	2.11	0.50	
1:A:1241:LEU:HD21	1:A:1259:ILE:HD12	1.95	0.48	
1:A:1163:TYR:CD2	1:A:1215:ASN:HB3	2.49	0.47	
1:A:1036:ALA:HB3	1:A:1041:ARG:HH12	1.78	0.47	
1:A:989:TRP:CH2	1:A:1052:LYS:HD3	2.50	0.46	
1:A:1045:LEU:HD11	1:A:1072:THR:HG21	1.96	0.46	
1:A:1060:VAL:HG21	1:A:1139:MET:HE2	1.98	0.46	
1:A:1026:ARG:H	1:A:1026:ARG:CZ	2.30	0.45	
1:A:1151:PHE:HE1	3:A:90:HOH:O	1.97	0.45	
1:A:1160:THR:O	1:A:1160:THR:HG22	2.17	0.44	
1:A:1079:MET:HA	1:A:1079:MET:CE	2.48	0.43	
1:A:983:VAL:O	1:A:983:VAL:HG23	2.18	0.43	
1:A:1041:ARG:NH1	1:A:1041:ARG:CG	2.82	0.43	
1:A:1271:PHE:HB3	1:A:1272:PRO:HD3	2.01	0.43	
1:A:1104:PRO:HA	1:A:1108:GLU:OE1	2.19	0.42	
1:A:1188:THR:O	1:A:1191:ASP:HB2	2.19	0.42	
1:A:1087:TYR:HE1	1:A:1101:ARG:NH1	2.16	0.42	
1:A:1109:MET:SD	2:A:501:EMC:C2	3.07	0.42	
1:A:1079:MET:HA	1:A:1079:MET:HE2	2.01	0.42	
1:A:1076[B]:MET:HE1	1:A:1151:PHE:HD1	1.85	0.42	
1:A:1087:TYR:CE1	1:A:1101:ARG:NH1	2.88	0.41	
1:A:1037:SER:O	1:A:1041:ARG:HG3	2.20	0.41	
1:A:1020:LYS:HE2	1:A:1020:LYS:HB3	1.81	0.40	
1:A:1003:GLY:O	1:A:1009:MET:SD	2.79	0.40	
1:A:1076[B]:MET:HE1	1:A:1151:PHE:CD1	2.56	0.40	
1:A:1045:LEU:HD23	1:A:1045:LEU:HA	1.86	0.40	

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	304/306 (99%)	296 (97%)	7 (2%)	1 (0%)	41 41

#### All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1156	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	Analysed Rotameric Out		Percentiles
1	A	257/268 (96%)	251 (98%)	6 (2%)	50 55

#### All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	989	TRP
1	A	994	GLU
1	A	1026	ARG
1	A	1052	LYS
1	A	1067	SER
1	A	1266	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:



Mol	Chain	Res	Type
1	A	1014	ASN
1	A	1124	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 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	Trens	Chain	Res	Link	Bond lengths			Bond angles	
MIOI	Type				Counts	RMSZ	# Z  > 2	Counts	$\mid \text{RMSZ} \mid \# Z  > 2$
2	EMC	A	500	1	1,2,2	0.49	0	-	
2	EMC	A	501	1	1,2,2	0.67	0	-	

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.

1 monomer is involved in 1 short contact:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	EMC	1	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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

## 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

## 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

## 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

