



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 3, 2016 – 01:54 PM EDT

PDB ID : 5L04  
Title : STRUCTURE OF INTERFERON LAMBDA 1 RECEPTOR WITH HUMAN KINASE JAK1  
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Deposited on : 2016-07-26  
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](mailto: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.

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

MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027939
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)	:	rb-20027939

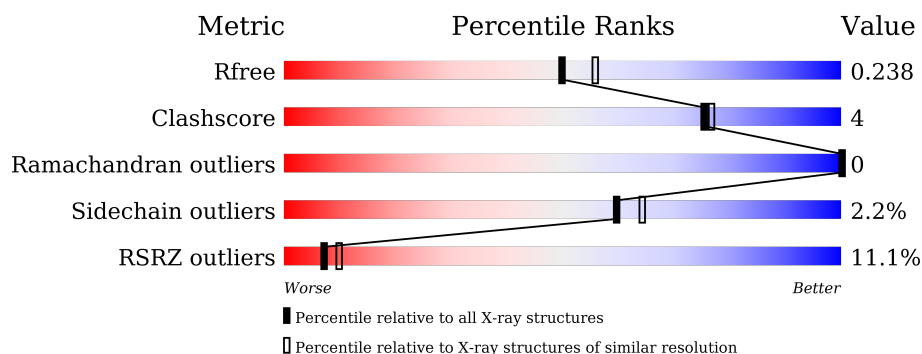
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	550	<div> <div>9%</div> <div>75%</div> <div>9%</div> <div>16%</div> </div>
2	B	48	<div> <div>15%</div> <div>73%</div> <div>23%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4221 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 Tyrosine-protein kinase JAK1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	460	Total	C	N	O	S	0	0	0
			3745	2377	647	694	27			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	GLY	-	expression tag	UNP P23458
A	578	SER	-	expression tag	UNP P23458
A	579	GLY	-	expression tag	UNP P23458

- Molecule 2 is a protein called Interferon lambda receptor 1.

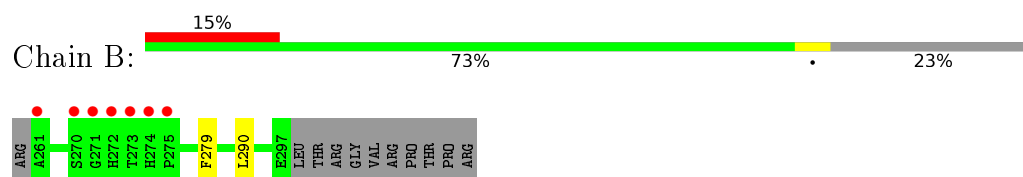
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	37	Total	C	N	O	S	0	0	0
			291	184	52	53	2			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	172	Total	O	0	0
			172	172		
3	B	13	Total	O	0	0
			13	13		



- Molecule 1: Tyrosine-protein kinase JAK1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	165.70 Å   53.80 Å   87.39 Å 90.00°   114.72°   90.00°	Depositor
Resolution (Å)	79.38 – 2.10 38.03 – 2.10	Depositor EDS
% Data completeness (in resolution range)	75.5 (79.38-2.10) 75.5 (38.03-2.10)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.04 (at 2.10 Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.169   ,   0.230 0.179   ,   0.238	Depositor DCC
$R_{free}$ test set	1080 reflections (3.59%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.9	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 53.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4221	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.73% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 ⓘ

### 5.1 Standard geometry ⓘ

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	0.89	1/3825 (0.0%)	0.97	7/5161 (0.1%)
2	B	0.73	0/300	0.86	0/407
All	All	0.88	1/4125 (0.0%)	0.96	7/5568 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	153	SER	CB-OG	-6.07	1.34	1.42

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	414	ARG	NE-CZ-NH2	-7.30	116.65	120.30
1	A	45	ARG	NE-CZ-NH1	7.24	123.92	120.30
1	A	421	HIS	CB-CA-C	5.95	122.29	110.40
1	A	174	ARG	NE-CZ-NH1	5.63	123.11	120.30
1	A	514	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	A	174	ARG	NE-CZ-NH2	-5.36	117.62	120.30
1	A	219	ARG	NE-CZ-NH1	5.25	122.93	120.30

There are no chirality outliers.

There are no planarity outliers.

### 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	3745	0	3701	31	1
2	B	291	0	281	2	0
3	A	172	0	0	3	0
3	B	13	0	0	0	0
All	All	4221	0	3982	31	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 4.

All (31) 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:229:ILE:HD12	1:A:240:ILE:HD13	1.69	0.74
1:A:56:THR:HG22	1:A:58:GLU:H	1.55	0.72
1:A:368:TYR:OH	1:A:558:THR:HG21	1.90	0.71
1:A:197:ILE:HD11	1:A:220:TYR:CE2	2.28	0.69
1:A:483:GLU:HG2	1:A:484:LYS:N	2.15	0.62
1:A:414:ARG:HD2	3:A:747:HOH:O	2.00	0.61
1:A:483:GLU:HG2	1:A:484:LYS:H	1.66	0.60
1:A:285:ILE:HD11	1:A:316:MET:CE	2.31	0.60
1:A:280:HIS:HB2	3:A:718:HOH:O	2.01	0.60
1:A:232:ARG:O	1:A:237:ARG:NH1	2.35	0.58
1:A:532:ARG:HG3	1:A:533:THR:N	2.17	0.58
1:A:56:THR:HG22	1:A:58:GLU:N	2.19	0.56
1:A:73:LEU:HD11	1:A:128:ARG:NE	2.20	0.55
1:A:481:CYS:HB3	1:A:536:ILE:HG21	1.88	0.55
1:A:73:LEU:HD11	1:A:128:ARG:CZ	2.36	0.55
1:A:285:ILE:CG1	1:A:316:MET:HE3	2.39	0.52
1:A:285:ILE:HG12	1:A:316:MET:HE3	1.92	0.52
1:A:156:GLU:OE1	1:A:267:LYS:HE2	2.10	0.51
1:A:197:ILE:HD11	1:A:220:TYR:CD2	2.47	0.50
1:A:151:ASP:HB3	2:B:279:PHE:CZ	2.47	0.49
1:A:558:THR:HG23	1:A:561:ALA:H	1.80	0.46
1:A:509:LEU:HD13	2:B:290:LEU:HD23	2.00	0.44
1:A:208:LEU:HD12	1:A:208:LEU:O	2.18	0.43
1:A:69:ARG:NH1	3:A:609:HOH:O	2.52	0.43
1:A:217:TYR:C	1:A:217:TYR:CD1	2.92	0.42
1:A:127:TRP:CE3	1:A:148:PRO:HA	2.55	0.42
1:A:229:ILE:HD13	1:A:232:ARG:CZ	2.50	0.42
1:A:73:LEU:CD1	1:A:128:ARG:CZ	2.98	0.41
1:A:285:ILE:HD11	1:A:316:MET:HE3	2.01	0.41
1:A:193:ALA:O	1:A:197:ILE:HG12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:369:PHE:N	1:A:370:PRO:CD	2.84	0.40

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:535:ASN:OD1	1:A:535:ASN:OD1[2_556]	1.81	0.39

## 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	448/550 (82%)	429 (96%)	19 (4%)	0	100	100
2	B	35/48 (73%)	35 (100%)	0	0	100	100
All	All	483/598 (81%)	464 (96%)	19 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	419/502 (84%)	409 (98%)	10 (2%)	57	61
2	B	33/43 (77%)	33 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	452/545 (83%)	442 (98%)	10 (2%)	60	64

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	ARG
1	A	102	SER
1	A	121	ASP
1	A	206	MET
1	A	210	GLU
1	A	235	LEU
1	A	258	ASP
1	A	290	MET
1	A	536	ILE
1	A	541	LYS

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

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	460/550 (83%)	0.31	48 (10%) 8 12	23, 43, 88, 120	0
2	B	37/48 (77%)	0.64	7 (18%) 2 2	32, 59, 117, 131	0
All	All	497/598 (83%)	0.33	55 (11%) 7 10	23, 45, 93, 131	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	272	HIS	6.0
2	B	273	THR	5.7
1	A	100	LYS	5.2
1	A	310	VAL	5.0
2	B	271	GLY	4.9
1	A	309	ASN	4.2
1	A	77	LEU	3.9
1	A	158	LEU	3.9
1	A	563	GLU	3.8
1	A	257	CYS	3.7
1	A	99	ASP	3.5
1	A	296	GLU	3.4
1	A	98	ASP	3.4
1	A	209	PRO	3.3
1	A	102	SER	3.2
1	A	101	MET	3.2
1	A	78	PHE	3.2
2	B	261	ALA	3.2
1	A	112	TYR	3.1
1	A	207	GLN	3.1
1	A	51	GLY	3.0
1	A	254	LYS	3.0
1	A	109	MET	3.0
1	A	562	GLN	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	111	PHE	2.9
1	A	208	LEU	2.9
1	A	274	LEU	2.8
1	A	35	GLY	2.7
1	A	252	ASN	2.6
1	A	415	LEU	2.6
1	A	97	VAL	2.5
1	A	258	ASP	2.5
1	A	260	SER	2.5
1	A	149	LEU	2.4
1	A	150	LEU	2.4
1	A	74	CYS	2.4
1	A	271	LEU	2.4
1	A	205	LYS	2.4
1	A	52	SER	2.4
1	A	311	LEU	2.4
1	A	116	TRP	2.3
1	A	457	GLY	2.3
1	A	55	TYR	2.2
2	B	275	PRO	2.2
1	A	179	GLU	2.2
1	A	155	LEU	2.2
1	A	412	TYR	2.2
1	A	259	SER	2.2
1	A	253	ASN	2.1
1	A	408	LEU	2.1
2	B	274	HIS	2.1
2	B	270	SER	2.0
1	A	492	GLN	2.0
1	A	206	MET	2.0
1	A	50	LEU	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.