wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 10:27 AM GMT

PDB ID	:	3LXN
Title	:	Structural and Thermodynamic Characterization of the TYK2 and JAK3 Kinase Domains in Complex with CP-690550 and CMP-6
Authors	:	Chrencik, J.E.; Benson, T.E.
Deposited on	:	2010-02-25
Resolution	:	2.50 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
http://wwpdb.org/validation/2016/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:

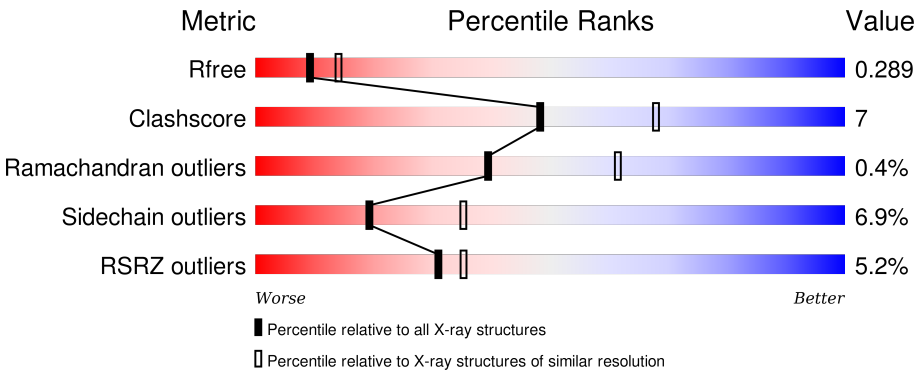
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 <=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	318	5% 71% 17% • • 9%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2349 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 Non-receptor tyrosine-protein kinase TYK2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	288	2238	1454	370	400	1	13	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	865	MET	-	EXPRESSION TAG	UNP P29597
A	866	ALA	-	EXPRESSION TAG	UNP P29597
A	867	HIS	-	EXPRESSION TAG	UNP P29597
A	868	HIS	-	EXPRESSION TAG	UNP P29597
A	869	HIS	-	EXPRESSION TAG	UNP P29597
A	870	HIS	-	EXPRESSION TAG	UNP P29597
A	871	HIS	-	EXPRESSION TAG	UNP P29597
A	872	HIS	-	EXPRESSION TAG	UNP P29597
A	873	HIS	-	EXPRESSION TAG	UNP P29597
A	874	HIS	-	EXPRESSION TAG	UNP P29597
A	875	HIS	-	EXPRESSION TAG	UNP P29597
A	876	HIS	-	EXPRESSION TAG	UNP P29597
A	877	GLY	-	EXPRESSION TAG	UNP P29597
A	878	ALA	-	EXPRESSION TAG	UNP P29597
A	879	LEU	-	EXPRESSION TAG	UNP P29597
A	880	GLU	-	EXPRESSION TAG	UNP P29597
A	881	VAL	-	EXPRESSION TAG	UNP P29597
A	882	LEU	-	EXPRESSION TAG	UNP P29597
A	883	PHE	-	EXPRESSION TAG	UNP P29597
A	884	GLN	-	EXPRESSION TAG	UNP P29597
A	885	GLY	-	EXPRESSION TAG	UNP P29597
A	886	PRO	-	EXPRESSION TAG	UNP P29597
A	887	GLY	-	EXPRESSION TAG	UNP P29597
A	936	ALA	CYS	ENGINEERED	UNP P29597
A	969	ALA	GLN	ENGINEERED	UNP P29597
A	971	ALA	GLU	ENGINEERED	UNP P29597
A	972	ALA	LYS	ENGINEERED	UNP P29597

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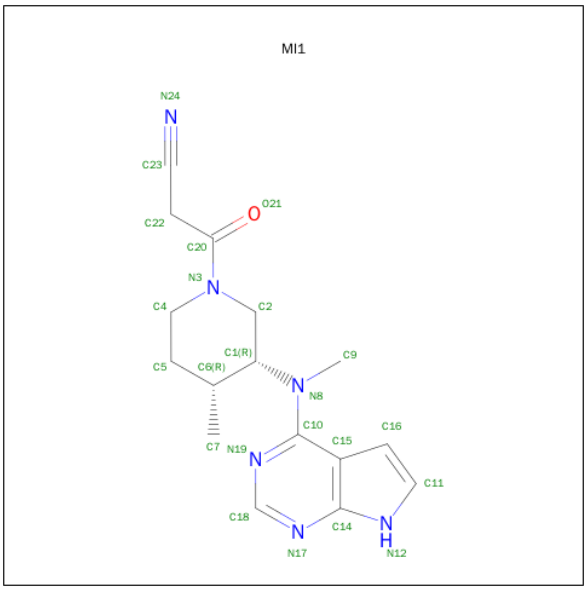
Chain	Residue	Modelled	Actual	Comment	Reference
A	1142	ALA	CYS	ENGINEERED	UNP P29597

- Molecule 2 is 3-{(3R,4R)-4-METHYL-3-[METHYL(7H-PYRROLO[2,3-D]PYRIMIDIN-4-YL)AMINO]PIPERIDIN-1-YL}-3-OXOPROPANENITRILE (three-letter code: MI1) (formula: $C_{16}H_{20}N_6O$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	23	16	6	1	0	0

- Molecule 3 is water.

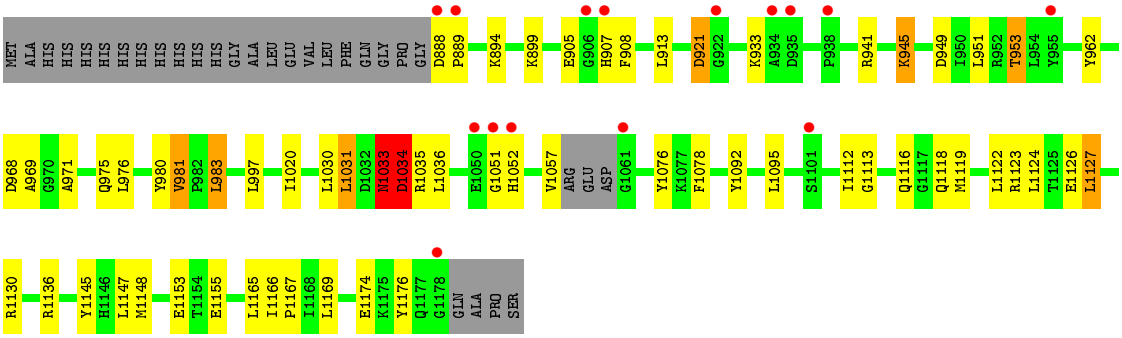
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	88	88	88	0	0

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 errors 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: Non-receptor tyrosine-protein kinase TYK2

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	36.31Å 74.26Å 106.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	18.58 – 2.50 18.57 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (18.58-2.50) 99.6 (18.57-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	7.28 (at 2.49Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.220 , 0.286 0.221 , 0.289	Depositor DCC
R_{free} test set	497 reflections (5.00%)	DCC
Wilson B-factor (Å^2)	24.6	Xtriage
Anisotropy	0.146	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 40.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 10504 reflections	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	2349	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.24% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: MI1, PTR

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	0.82	7/2280 (0.3%)	0.77	5/3097 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	2	3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1153	GLU	CB-CG	-8.29	1.36	1.52
1	A	1153	GLU	CG-CD	-6.06	1.42	1.51
1	A	1153	GLU	CD-OE2	-5.96	1.19	1.25
1	A	1034	ASP	CB-CG	-5.74	1.39	1.51
1	A	905	GLU	CB-CG	-5.36	1.42	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1034	ASP	CB-CG-OD2	-9.73	109.54	118.30
1	A	921	ASP	N-CA-C	6.51	128.57	111.00
1	A	907	HIS	N-CA-CB	6.18	121.73	110.60
1	A	1033	ASN	CB-CA-C	-6.12	98.16	110.40
1	A	1034	ASP	N-CA-CB	5.60	120.69	110.60

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	907	HIS	CA
1	A	921	ASP	CA

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1033	ASN	Peptide
1	A	888	ASP	Peptide
1	A	969	ALA	Peptide

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	2238	0	2132	30	0
2	A	23	0	20	3	0
3	A	88	0	0	0	0
All	All	2349	0	2152	32	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 7.

The worst 5 of 32 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:983:LEU:HD23	1:A:1031:LEU:HD13	1.78	0.66
1:A:951:LEU:HD23	1:A:976:LEU:HD21	1.82	0.60
2:A:1:MI1:H16	2:A:1:MI1:H1	1.86	0.58
1:A:1119:MET:O	1:A:1123:ARG:HB2	2.05	0.56
1:A:1112:ILE:HD11	1:A:1124:LEU:HB2	1.88	0.55

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	283/318 (89%)	268 (95%)	14 (5%)	1 (0%)	39 61

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	889	PRO

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	217/270 (80%)	202 (93%)	15 (7%)	19 35

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1031	LEU
1	A	1034	ASP
1	A	1127	LEU
1	A	983	LEU
1	A	1122	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1097	HIS
1	A	1116	GLN
1	A	1146	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	PTR	A	1054	1	14,16,17	2.28	1 (7%)	18,22,24	1.19	2 (11%)

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
1	PTR	A	1054	1	-	0/9/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1054	PTR	OH-CZ	-7.59	1.22	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1054	PTR	O-C-CA	-2.94	117.82	125.49
1	A	1054	PTR	O2P-P-OH	3.21	116.75	105.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	MI1	A	1	-	22,25,25	1.52	4 (18%)	21,35,35	2.08	5 (23%)

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	MI1	A	1	-	-	0/14/28/28	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	MI1	C14-N17	-2.46	1.33	1.37
2	A	1	MI1	C2-N3	-2.28	1.44	1.46
2	A	1	MI1	C10-C15	-2.10	1.39	1.43
2	A	1	MI1	C9-N8	4.88	1.61	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1	MI1	C10-N8-C1	-3.69	117.08	121.16
2	A	1	MI1	C15-C10-N19	-2.81	116.96	123.47
2	A	1	MI1	C18-N19-C10	3.89	119.70	111.43
2	A	1	MI1	C4-N3-C2	4.22	121.27	112.76
2	A	1	MI1	C9-N8-C1	4.87	126.36	118.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	MI1	3	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)

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	287/318 (90%)	0.06	15 (5%) 31 35	4, 18, 35, 39	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	934	ALA	12.1
1	A	906	GLY	6.0
1	A	1178	GLY	5.3
1	A	1051	GLY	4.3
1	A	922	GLY	4.0

6.2 Non-standard residues in protein, DNA, RNA chains (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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å^2)	Q<0.9
1	PTR	A	1054	16/17	0.63	0.27	-	37,39,45,45	0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å^2)	Q<0.9
2	MI1	A	1	23/23	0.86	0.19	0.19	18,19,21,22	0

6.5 Other polymers (i)

There are no such residues in this entry.