



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:15 AM GMT

PDB ID : 3A5K
Title : Crystal structure of protein-tyrosine phosphatase 1B
Authors : Ito, S.
Deposited on : 2009-08-08
Resolution : 1.85 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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

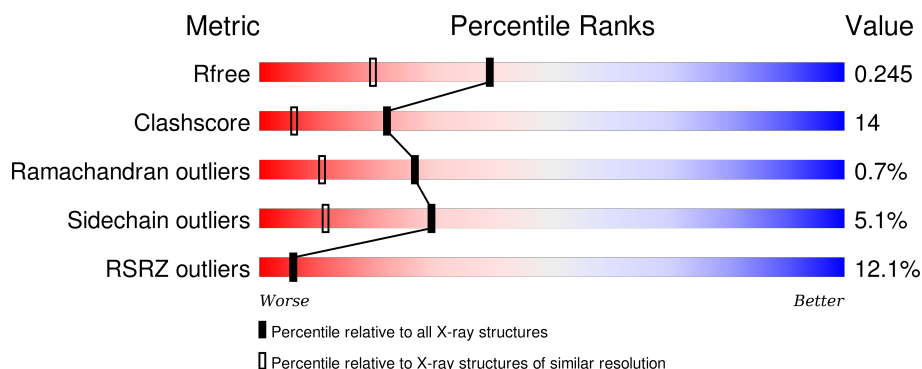
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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 $\leq 5\%$. 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	304	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2497 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 phosphatase non-receptor type 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	0	0	0
			2299	1463	397	424	15			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	EXPRESSION TAG	UNP P18031
A	-4	HIS	-	EXPRESSION TAG	UNP P18031
A	-3	HIS	-	EXPRESSION TAG	UNP P18031
A	-2	HIS	-	EXPRESSION TAG	UNP P18031
A	-1	HIS	-	EXPRESSION TAG	UNP P18031
A	0	HIS	-	EXPRESSION TAG	UNP P18031
A	1	HIS	-	EXPRESSION TAG	UNP P18031
A	121	TRP	CYS	ENGINEERED MUTATION	UNP P18031

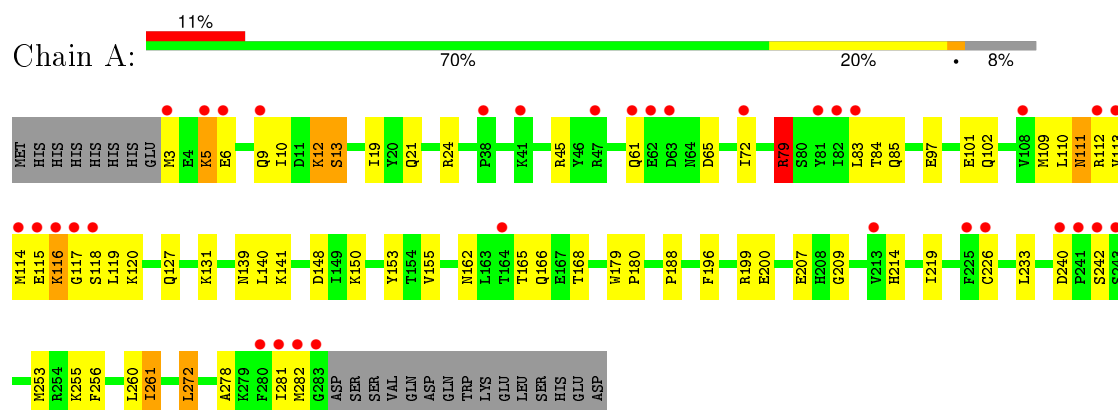
- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	197	Total	O	0	0
			197	197		

- Molecule 1: Tyrosine-protein phosphatase non-receptor type 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.09Å 60.76Å 87.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.51 – 1.85 30.51 – 1.85	Depositor EDS
% Data completeness (in resolution range)	98.5 (30.51-1.85) 98.5 (30.51-1.85)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.16 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.189 , 0.233 0.203 , 0.245	Depositor DCC
R_{free} test set	1382 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	27.1	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.4	EDS
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 27370 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2497	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.66% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: MG

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	1.08	2/2353 (0.1%)	1.02	5/3172 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	261	ILE	CB-CG2	5.52	1.70	1.52
1	A	255	LYS	CB-CG	5.08	1.66	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	79	ARG	NE-CZ-NH1	10.79	125.69	120.30
1	A	79	ARG	NE-CZ-NH2	-9.07	115.76	120.30
1	A	199	ARG	NE-CZ-NH2	-5.72	117.44	120.30
1	A	65	ASP	CB-CG-OD2	5.55	123.30	118.30
1	A	110	LEU	CA-CB-CG	-5.23	103.26	115.30

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	2299	0	2275	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1	0	0	0	0
3	A	197	0	0	13	0
All	All	2497	0	2275	64	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 14.

All (64) 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:5:LYS:HD3	1:A:6:GLU:N	1.56	1.19
1:A:114:MET:O	1:A:114:MET:HG2	1.49	1.10
1:A:240:ASP:OD1	1:A:242:SER:HB3	1.52	1.09
1:A:114:MET:HE2	1:A:117:GLY:HA2	1.31	1.09
1:A:5:LYS:HD3	1:A:5:LYS:C	1.71	1.07
1:A:114:MET:CE	1:A:117:GLY:HA2	1.91	1.01
1:A:21:GLN:HE22	1:A:24:ARG:HH11	1.17	0.90
1:A:153:TYR:HE1	1:A:155:VAL:CG2	1.88	0.86
1:A:153:TYR:CE1	1:A:155:VAL:HG23	2.13	0.83
1:A:119:LEU:HA	3:A:488:HOH:O	1.78	0.82
1:A:114:MET:O	1:A:114:MET:CG	2.28	0.82
1:A:5:LYS:CD	1:A:6:GLU:N	2.44	0.78
1:A:114:MET:HE2	1:A:117:GLY:CA	2.13	0.78
1:A:111:ASN:H	1:A:111:ASN:HD22	1.34	0.75
1:A:148:ASP:OD2	1:A:150:LYS:HE2	1.87	0.74
1:A:153:TYR:CE1	1:A:155:VAL:CG2	2.69	0.73
1:A:3:MET:CA	3:A:458:HOH:O	2.36	0.73
1:A:3:MET:N	3:A:458:HOH:O	2.22	0.73
1:A:3:MET:N	3:A:437:HOH:O	2.24	0.71
1:A:72:ILE:HD12	1:A:256:PHE:HB2	1.71	0.71
1:A:45:ARG:H	1:A:85:GLN:HE22	1.41	0.69
1:A:120:LYS:HE3	3:A:474:HOH:O	1.93	0.67
1:A:21:GLN:HE22	1:A:24:ARG:NH1	1.90	0.66
1:A:83:LEU:HD11	1:A:226:CYS:SG	2.35	0.65
1:A:240:ASP:OD1	1:A:242:SER:CB	2.40	0.65
1:A:114:MET:CE	1:A:117:GLY:CA	2.71	0.65
1:A:278:ALA:O	1:A:282:MET:HB2	1.97	0.65
1:A:21:GLN:NE2	1:A:24:ARG:HH11	1.93	0.63
1:A:61:GLN:C	3:A:436:HOH:O	2.38	0.60
1:A:45:ARG:H	1:A:85:GLN:NE2	2.02	0.58
1:A:141:LYS:CE	3:A:425:HOH:O	2.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:LYS:HE3	3:A:425:HOH:O	2.04	0.56
1:A:6:GLU:O	1:A:10:ILE:HG13	2.06	0.56
1:A:61:GLN:HB2	3:A:436:HOH:O	2.05	0.56
1:A:12:LYS:O	1:A:12:LYS:HD2	2.04	0.56
1:A:114:MET:HE3	1:A:117:GLY:HA2	1.85	0.52
1:A:219:ILE:O	1:A:260:LEU:HA	2.10	0.52
1:A:281:ILE:CG2	1:A:281:ILE:O	2.59	0.51
1:A:140:LEU:HD23	1:A:162:ASN:HA	1.93	0.51
1:A:72:ILE:HD12	1:A:256:PHE:CB	2.42	0.50
1:A:5:LYS:HD3	1:A:6:GLU:H	1.67	0.49
1:A:281:ILE:HG22	1:A:281:ILE:O	2.12	0.49
1:A:165:THR:O	1:A:166:GLN:HB2	2.12	0.49
1:A:61:GLN:CA	3:A:436:HOH:O	2.60	0.48
1:A:179:TRP:CD1	1:A:180:PRO:HD2	2.50	0.47
1:A:102:GLN:O	1:A:209:GLY:HA3	2.13	0.47
1:A:111:ASN:HD21	1:A:214:HIS:CE1	2.32	0.47
1:A:10:ILE:HD13	1:A:19:ILE:CD1	2.45	0.46
1:A:10:ILE:HD13	1:A:19:ILE:HD12	1.97	0.46
1:A:79:ARG:CZ	1:A:233:LEU:HD11	2.45	0.45
1:A:114:MET:O	1:A:115:GLU:C	2.54	0.45
1:A:3:MET:HA	3:A:458:HOH:O	2.13	0.45
1:A:111:ASN:ND2	1:A:111:ASN:H	2.09	0.44
1:A:253:MET:HB3	1:A:253:MET:HE2	1.62	0.44
1:A:112:ARG:HD2	1:A:112:ARG:HA	1.80	0.43
1:A:109:MET:CE	1:A:113:VAL:HG23	2.48	0.43
1:A:61:GLN:CB	3:A:436:HOH:O	2.66	0.43
1:A:278:ALA:O	1:A:282:MET:N	2.50	0.43
1:A:188:PRO:HD3	1:A:272:LEU:HD13	1.99	0.42
1:A:97:GLU:OE1	1:A:101:GLU:OE2	2.38	0.41
1:A:113:VAL:HB	3:A:303:HOH:O	2.20	0.41
1:A:9:GLN:O	1:A:13:SER:HB2	2.21	0.40
1:A:196:PHE:O	1:A:200:GLU:HG3	2.20	0.40
1:A:84:THR:O	1:A:214:HIS:HB2	2.20	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	279/304 (92%)	266 (95%)	11 (4%)	2 (1%)	26	11

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	116	LYS
1	A	261	ILE

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	254/277 (92%)	241 (95%)	13 (5%)	29	11

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LYS
1	A	12	LYS
1	A	13	SER
1	A	79	ARG
1	A	111	ASN
1	A	116	LYS
1	A	118	SER
1	A	127	GLN
1	A	131	LYS

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Mol	Chain	Res	Type
1	A	139	ASN
1	A	168	THR
1	A	207	GLU
1	A	272	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	85	GLN
1	A	111	ASN
1	A	139	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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 ⓘ

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, 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	281/304 (92%)	0.48	34 (12%) 6 6	19, 28, 60, 81	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	113	VAL	9.3
1	A	118	SER	8.7
1	A	117	GLY	8.2
1	A	282	MET	7.8
1	A	116	LYS	6.0
1	A	62	GLU	5.0
1	A	283	GLY	4.8
1	A	280	PHE	4.8
1	A	114	MET	4.2
1	A	5	LYS	3.9
1	A	281	ILE	3.4
1	A	63	ASP	2.9
1	A	226	CYS	2.9
1	A	38	PRO	2.8
1	A	243	SER	2.8
1	A	83	LEU	2.7
1	A	164	THR	2.7
1	A	47	ARG	2.6
1	A	112	ARG	2.5
1	A	81	TYR	2.5
1	A	9	GLN	2.4
1	A	115	GLU	2.4
1	A	41	LYS	2.4
1	A	225	PHE	2.4
1	A	242	SER	2.3
1	A	72	ILE	2.3
1	A	3	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	61	GLN	2.2
1	A	240	ASP	2.2
1	A	241	PRO	2.1
1	A	213	VAL	2.1
1	A	108	VAL	2.1
1	A	6	GLU	2.0
1	A	82	ILE	2.0

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. 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	MG	A	300	1/1	0.76	0.06	-	40,40,40,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.