

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

#### Jan 22, 2024 – 04:14 PM EST

PDB ID : 7GU5

Title: PanDDA analysis group deposition of ground-state model of PTP1B, using

pre-clustering, cluster12

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Deposited on : 2024-01-05

Resolution : 1.52 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.orgA 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 (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 : 2.36

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

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

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

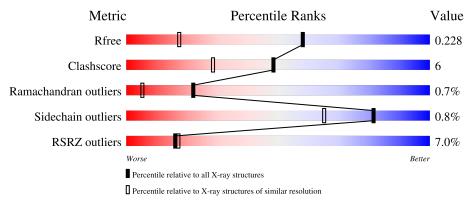
Validation Pipeline (wwPDB-VP) : 2.36

## 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 1.52 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 $(\# \text{Entries})$	Similar resolution $(\#\text{Entries, resolution range}(\text{\AA}))$
$R_{free}$	130704	4009 (1.54-1.50)
Clashscore	141614	4249 (1.54-1.50)
Ramachandran outliers	138981	4148 (1.54-1.50)
Sidechain outliers	138945	4146 (1.54-1.50)
RSRZ outliers	127900	3943 (1.54-1.50)

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 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% 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			
			6%			
1	A	321	79%	9%	•	12%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	$\operatorname{Res}$	Chirality	Geometry	Clashes	Electron density
2	TRS	A	500	-	-	-	X



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4920 atoms, of which 2308 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.

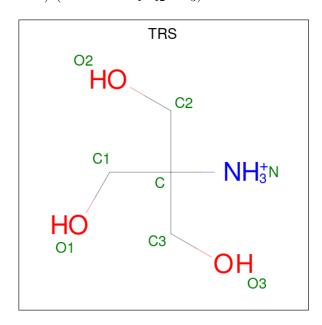
• Molecule 1 is a protein called Tyrosine-protein phosphatase non-receptor type 1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
1	A	284	Total 4613	C 1471	H 2296	N 399	O 432	S 15	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue Modelled A		Actual	Comment	Reference
A	32	SER	CYS	engineered mutation	UNP P18031
A	92	VAL	CYS	engineered mutation	UNP P18031

• Molecule 2 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C<sub>4</sub>H<sub>12</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
2	٨	1	Total	С	Н	N	О	0	0
2	A	1	20	4	12	1	3	0	U

• Molecule 3 is water.



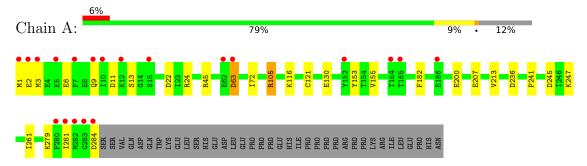
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	287	Total O 287 287	0	0



# 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 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: Tyrosine-protein phosphatase non-receptor type 1





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	89.91Å 89.91Å 106.52Å	Danagitan
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	44.96 - 1.52	Depositor
resolution (A)	44.96 - 1.52	EDS
% Data completeness	99.9 (44.96-1.52)	Depositor
(in resolution range)	99.9 (44.96-1.52)	EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.40  (at  1.52Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
$R, R_{free}$	0.200 , $0.227$	Depositor
it, it free	0.199 , $0.228$	DCC
$R_{free}$ test set	3005  reflections  (3.93%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.3	Xtriage
Anisotropy	0.266	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.37, 45.2	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.49, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	0.022 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4920	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.41% 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: TRS

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).

Mal	Chain	Bond	lengths	Bond angles		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.51	0/2369	0.73	$2/3192 \ (0.1\%)$	

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
1	A	213	VAL	CA-CB-CG2	5.44	119.06	110.90
1	A	72	ILE	CG1-CB-CG2	-5.00	100.39	111.40

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	2317	2296	2296	28	1
2	A	8	12	12	0	1
3	A	287	0	0	19	0
All	All	2612	2308	2308	28	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 6.

All (28) close contacts within the same asymmetric unit are listed below, sorted by their clash



magnitude.

Atom-1	Atom-2	Interatomic	Clash
		distance (Å)	overlap (Å)
1:A:2:GLU:OE2	3:A:601:HOH:O	1.82	0.97
1:A:2:GLU:O	3:A:602:HOH:O	1.96	0.84
1:A:22:ASP:OD1	3:A:603:HOH:O	2.00	0.80
1:A:2:GLU:C	3:A:602:HOH:O	2.21	0.77
1:A:207:GLU:OE2	3:A:604:HOH:O	2.00	0.77
1:A:236:ASP:OD1	1:A:281:ILE:HG23	1.87	0.75
1:A:245:ASP:OD1	3:A:605:HOH:O	2.05	0.74
1:A:2:GLU:HG2	3:A:601:HOH:O	1.93	0.67
1:A:105:ARG:HH11	1:A:105:ARG:HG2	1.62	0.65
1:A:1:MET:O	3:A:602:HOH:O	2.15	0.64
1:A:105:ARG:NE	3:A:606:HOH:O	2.09	0.62
1:A:6:GLU:HB2	3:A:602:HOH:O	2.04	0.57
1:A:105:ARG:NH2	3:A:606:HOH:O	2.36	0.56
1:A:247:LYS:HE2	3:A:605:HOH:O	2.05	0.55
1:A:2:GLU:CG	3:A:601:HOH:O	2.53	0.54
1:A:200:GLU:OE1	3:A:607:HOH:O	2.19	0.53
1:A:2:GLU:CD	3:A:601:HOH:O	2.39	0.53
1:A:116:LYS:HE2	1:A:182:PHE:CE1	2.46	0.51
1:A:3:MET:HA	3:A:602:HOH:O	2.10	0.51
1:A:116:LYS:HE2	1:A:182:PHE:CZ	2.47	0.49
1:A:105:ARG:HH11	1:A:105:ARG:CG	2.27	0.46
1:A:9:GLN:O	1:A:13:SER:OG	2.29	0.45
1:A:279:LYS:O	1:A:284:ASP:HB3	2.18	0.44
1:A:153:TYR:CE2	1:A:155:VAL:HG23	2.52	0.43
1:A:63:ASP:OD2	3:A:608:HOH:O	2.21	0.43
1:A:24:ARG:NH1	3:A:619:HOH:O	2.52	0.42
1:A:241:PRO:HG3	3:A:680:HOH:O	2.18	0.41
1:A:45:ARG:NH2	1:A:121:CYS:HA	2.35	0.41

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	$egin{array}{c}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{array}$	Clash overlap (Å)
1:A:130:GLU:OE2	2:A:500:TRS:O2[4_565]	2.18	0.02



## 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	282/321 (88%)	272 (96%)	8 (3%)	2 (1%)	22 5

#### All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	63	ASP
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	257/294 (87%)	255 (99%)	2 (1%)	81 65	

#### All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ASP
1	A	105	ARG

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	139	ASN
1	A	157	GLN



#### 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)

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	B	ond leng	gths	В	ond ang	gles
MIOI	Type		nes	Lilik	Counts	RMSZ	# Z  > 2	RMSZ	# Z  > 2	
2	TRS	A	500	-	7,7,7	1.12	1 (14%)	9,9,9	0.81	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
2	TRS	A	500	-	-	3/9/9/9	-

#### All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\textup{\AA})$	$\operatorname{Ideal}(\text{\AA})$
2	A	500	TRS	C-N	2.87	1.59	1.49

There are no bond angle outliers.



There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	TRS	C1-C-C2-O2
2	A	500	TRS	N-C-C2-O2
2	A	500	TRS	C3-C-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	TRS	0	1

## 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 $>$	# RSRZ > 2	$OWAB(A^2)$	Q < 0.9
1	A	284/321 (88%)	0.58	20 (7%) 16 17	20, 31, 65, 89	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	281	ILE	15.3
1	A	280	PHE	9.5
1	A	282	MET	8.3
1	A	1	MET	7.3
1	A	284	ASP	5.9
1	A	152	TYR	4.8
1	A	63	ASP	4.3
1	A	283	GLY	4.1
1	A	9	GLN	3.7
1	A	62	GLU	3.7
1	A	5	LYS	3.6
1	A	12	LYS	3.6
1	A	10	ILE	3.6
1	A	2	GLU	3.4
1	A	15	SER	2.9
1	A	7	PHE	2.7
1	A	3	MET	2.5
1	A	165	THR	2.5
1	A	186	GLU	2.4
1	A	164	THR	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 monosaccharides 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	TRS	A	500	8/8	0.32	0.47	30,36,41,41	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

