

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

#### Dec 3, 2023 - 10:26 pm GMT

PDB ID	:	2IWP
Title	:	12th PDZ domain of Multiple PDZ Domain Protein MPDZ
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Deposited on	:	2006-07-03
Resolution	:	2.15  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 (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	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 2.15 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	$\begin{array}{c} {\rm Whole \ archive} \\ {\rm (\#Entries)} \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$		
R <sub>free</sub>	130704	1479 (2.16-2.16)		
Clashscore	141614	1585 (2.16-2.16)		
RSRZ outliers	127900	1456 (2.16-2.16)		

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				
1	А	120	9%	63%	13%	23%	
1	В	120	24%	74%		13% • 12%	



#### 2IWP

## 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1401 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Δ	02	Total	С	Ν	0	$\mathbf{S}$	0	0	0
	A	92	643	397	110	130	6	0	0	0
1	Р	106	Total	С	Ν	0	S	0	0	0
	D	100	734	454	127	146	7		0	U

• Molecule 1 is a protein called MULTIPLE PDZ DOMAIN PROTEIN.

• Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	15	Total         O           15         15	0	0
2	В	9	Total O 9 9	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: MULTIPLE PDZ DOMAIN PROTEIN



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	76.71Å 88.10Å 73.15Å	Deperitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Bosolution(A)	57.83 - 2.15	Depositor
Resolution (A)	38.35 - 2.15	EDS
% Data completeness	99.3 (57.83-2.15)	Depositor
(in resolution range)	99.3 (38.35-2.15)	EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.27 (at 2.16 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
P. P.	0.221 , $0.270$	Depositor
$n, n_{free}$	0.228 , $0.264$	DCC
$R_{free}$ test set	687 reflections $(5.01%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	42.4	Xtriage
Anisotropy	0.701	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.36 , 74.6	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.48, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	1401	wwPDB-VP
Average B, all atoms $(Å^2)$	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.95% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality (i)

## 5.1 Standard geometry (i)

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	Bo	nd lengths	Bond angles		
Moi Chain		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.77	1/647~(0.2%)	0.78	0/874	
1	В	0.69	0/742	0.81	1/1006~(0.1%)	
All	All	0.73	1/1389~(0.1%)	0.80	1/1880~(0.1%)	

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	В	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	1913	GLU	CG-CD	5.12	1.59	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	1883	ASP	CB-CG-OD1	5.89	123.60	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Chain Res Type		Group
1	В	1830	MET	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	А	643	0	650	10	0
1	В	734	0	717	15	0
2	А	15	0	0	0	0
2	В	9	0	0	0	0
All	All	1401	0	1367	23	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 8.

All (23) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:1847:ILE:HG22	1:A:1867:MET:HG2	1.82	0.60	
1:B:1851:GLY:C	1:B:1862:ILE:HD13	2.24	0.58	
1:B:1852:GLY:HA3	1:B:1862:ILE:HD11	1.85	0.57	
1:B:1873:ALA:HB1	1:B:1879:LEU:HD23	1.89	0.53	
1:B:1851:GLY:O	1:B:1862:ILE:HD13	2.09	0.53	
1:A:1867:MET:HE3	1:A:1874:ALA:HB2	1.89	0.52	
1:B:1852:GLY:CA	1:B:1862:ILE:HD11	2.39	0.52	
1:B:1835:VAL:HG11	1:B:1876:THR:HG21	1.92	0.51	
1:B:1845:LEU:HD21	1:B:1912:ILE:HD12	1.91	0.51	
1:B:1842:THR:O	1:B:1842:THR:HG22	2.10	0.51	
1:A:1924:GLU:OE2	1:B:1866:MET:SD	2.68	0.50	
1:B:1835:VAL:CG1	1:B:1876:THR:HG21	2.40	0.50	
1:B:1852:GLY:CA	1:B:1862:ILE:CD1	2.90	0.48	
1:B:1876:THR:HG22	1:B:1878:LYS:H	1.79	0.47	
1:B:1864:ILE:HD12	1:B:1883:ASP:HB2	1.97	0.47	
1:A:1862:ILE:CD1	1:A:1901:ALA:HB2	2.46	0.46	
1:A:1862:ILE:HD13	1:A:1901:ALA:CB	2.45	0.46	
1:A:1881:VAL:HG12	1:B:1866:MET:HE3	1.97	0.45	
1:A:1860:VAL:O	1:A:1861:PRO:C	2.53	0.45	
1:B:1881:VAL:HG11	1:B:1924:GLU:HG2	1.99	0.44	
1:A:1873:ALA:HB1	1:A:1879:LEU:HD12	2.02	0.42	
1:A:1849:ILE:O	1:A:1898:HIS:HE1	2.03	0.41	
1:A:1896:MET:HE1	1:A:1904:LEU:HD23	2.03	0.41	



There are no symmetry-related clashes.

## 5.3 Torsion angles (i)

#### 5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

#### 5.3.2 Protein sidechains (i)

There are no protein residues with a non-rotameric sidechain to report in this entry.

#### 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)

There are no ligands in this entry.

## 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 $>$	# <b>RSRZ</b> >2	2	$OWAB(Å^2)$	Q<0.9
1	А	92/120~(76%)	0.73	11 (11%) 4	6	42, 55, 64, 71	0
1	В	106/120~(88%)	1.24	29~(27%) 0	0	48, 56, 65, 68	0
All	All	198/240~(82%)	1.01	40 (20%) 1	1	42, 56, 66, 71	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	1822	THR	7.2
1	В	1841	PRO	6.8
1	А	1855	SER	4.2
1	В	1922	VAL	4.0
1	В	1920	GLY	4.0
1	В	1921	ASP	3.8
1	В	1840	GLY	3.8
1	В	1919	GLY	3.7
1	В	1885	ILE	3.4
1	В	1874	ALA	3.2
1	А	1877	GLN	3.1
1	В	1888	ILE	3.1
1	В	1891	THR	3.0
1	А	1927	VAL	2.9
1	В	1899	THR	2.9
1	В	1890	GLY	2.9
1	А	1868	HIS	2.8
1	А	1867	MET	2.8
1	В	1900	GLN	2.8
1	В	1824	ASN	2.7
1	А	1891	THR	2.7
1	В	1896	MET	2.6
1	В	1897	THR	2.6
1	В	1876	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	В	1849	ILE	2.5
1	В	1901	ALA	2.5
1	А	1854	GLY	2.4
1	А	1890	GLY	2.4
1	А	1857	LEU	2.4
1	В	1886	VAL	2.4
1	В	1875	GLN	2.4
1	В	1902	VAL	2.3
1	В	1862	ILE	2.3
1	В	1823	GLU	2.3
1	А	1872	VAL	2.3
1	А	1876	THR	2.3
1	В	1927	VAL	2.2
1	В	1826	TYR	2.2
1	В	1887	THR	2.1
1	В	1905	LEU	2.0

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### 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)

There are no ligands in this entry.

### 6.5 Other polymers (i)

There are no such residues in this entry.

