



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 2FVZ  
Title : Human Inositol Monophosphatase 2  
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Deposited on : 2006-01-31  
Resolution : 2.40 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](mailto: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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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  
Xtriage (Phenix) : 1.20.1  
EDS : 2.37.1  
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)

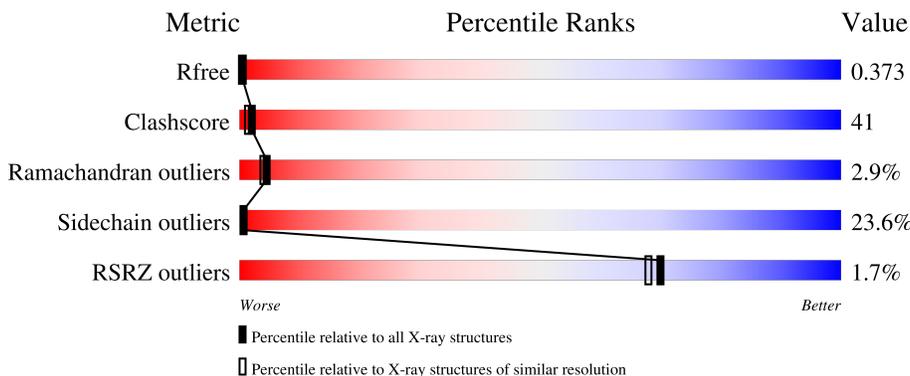
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
$R_{free}$	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	273	 3% 35% 44% 10% 11%
1	B	273	 35% 42% 12% 11%
1	C	273	 2% 30% 44% 15% 11%
1	D	273	 3% 33% 38% 15% 11%

Validation Pipeline (wwPDB-VP) : 2.37.1

## 2 Entry composition

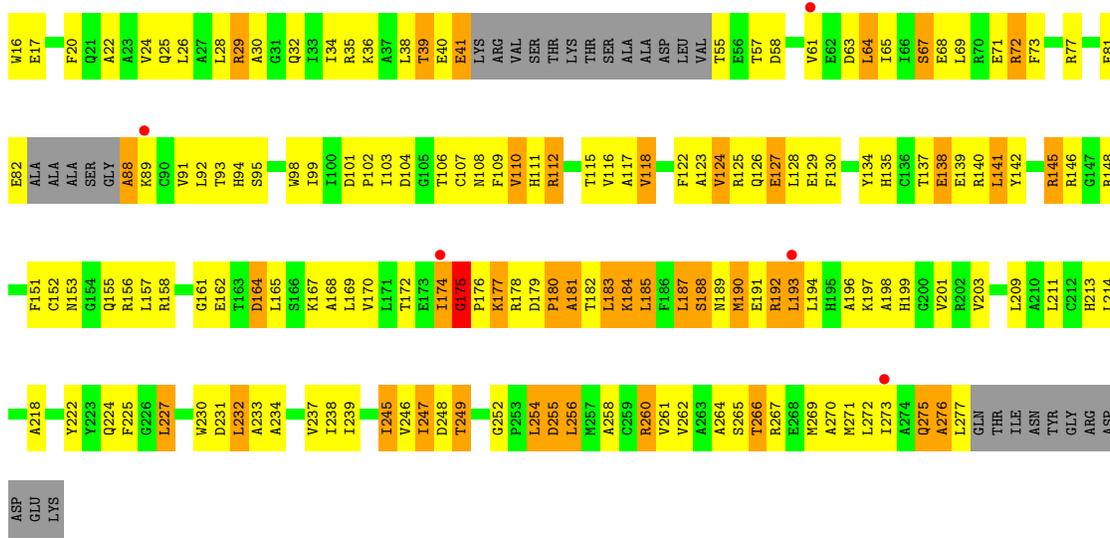
There is only 1 type of molecule in this entry. The entry contains 7516 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

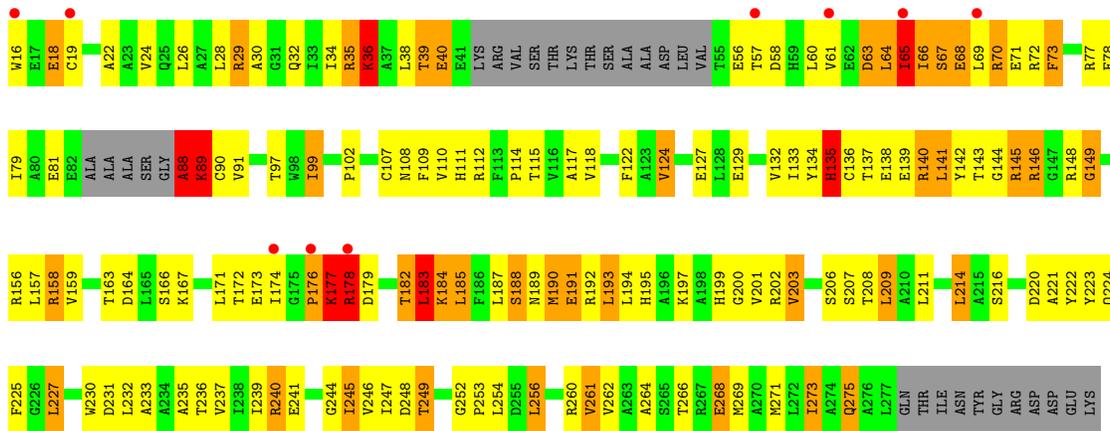
- Molecule 1 is a protein called Inositol monophosphatase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	244	Total 1878	C 1185	N 337	O 344	S 12	0	0	0
1	B	244	Total 1878	C 1185	N 337	O 344	S 12	0	0	0
1	C	244	Total 1882	C 1188	N 338	O 344	S 12	0	0	0
1	D	244	Total 1878	C 1185	N 337	O 344	S 12	0	0	0





● Molecule 1: Inositol monophosphatase 2



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.03Å 96.95Å 106.97Å 90.00° 90.03° 90.00°	Depositor
Resolution (Å)	10.00 – 2.40 28.94 – 2.35	Depositor EDS
% Data completeness (in resolution range)	98.2 (10.00-2.40) 97.6 (28.94-2.35)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.88 (at 2.36Å)	Xtrriage
Refinement program	SHELX, SHELXL-97	Depositor
R, $R_{free}$	0.211 , 0.297 0.210 , 0.373	Depositor DCC
$R_{free}$ test set	34 reflections (0.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.6	Xtrriage
Anisotropy	0.262	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 66.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.447 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	7516	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.19% 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 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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.39	0/1911	0.53	0/2587
1	B	0.64	4/1911 (0.2%)	0.56	1/2587 (0.0%)
1	C	0.48	1/1915 (0.1%)	0.53	0/2591
1	D	1.42	5/1911 (0.3%)	0.86	5/2587 (0.2%)
All	All	0.84	10/7648 (0.1%)	0.64	6/10352 (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	C	0	1
1	D	0	3
All	All	0	4

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	89	LYS	C-O	50.90	2.20	1.23
1	D	88	ALA	C-N	-25.68	0.74	1.34
1	B	71	GLU	CD-OE2	16.85	1.44	1.25
1	D	178	ARG	C-N	-10.74	1.09	1.34
1	B	71	GLU	CD-OE1	10.71	1.37	1.25

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	89	LYS	O-C-N	-26.75	79.89	122.70
1	D	88	ALA	O-C-N	-13.42	101.22	122.70
1	D	88	ALA	C-N-CA	12.65	153.34	121.70
1	D	178	ARG	O-C-N	-9.19	108.00	122.70
1	D	88	ALA	CA-C-N	6.40	131.28	117.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	88	ALA	Peptide
1	D	178	ARG	Mainchain
1	D	88	ALA	Mainchain
1	D	89	LYS	Mainchain

## 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	1878	0	1871	141	0
1	B	1878	0	1871	158	0
1	C	1882	0	1882	176	0
1	D	1878	0	1869	163	0
All	All	7516	0	7493	611	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 41.

The worst 5 of 611 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:D:65:ILE:CD1	1:D:65:ILE:CG1	2.01	1.37
1:D:89:LYS:O	1:D:91:VAL:N	1.69	1.26
1:C:88:ALA:HA	1:C:89:LYS:HB3	1.32	1.11
1:C:88:ALA:HB1	1:C:89:LYS:HG2	1.07	1.06
1:A:74:PRO:HB2	1:C:39:THR:HG21	1.39	1.04

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	238/273 (87%)	210 (88%)	20 (8%)	8 (3%)	3	3
1	B	238/273 (87%)	208 (87%)	23 (10%)	7 (3%)	4	4
1	C	238/273 (87%)	208 (87%)	25 (10%)	5 (2%)	7	8
1	D	238/273 (87%)	206 (87%)	24 (10%)	8 (3%)	3	3
All	All	952/1092 (87%)	832 (87%)	92 (10%)	28 (3%)	4	4

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	176	PRO
1	B	229	CYS
1	C	175	GLY
1	D	40	GLU
1	D	89	LYS

### 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	195/219 (89%)	157 (80%)	38 (20%)	1	1
1	B	195/219 (89%)	152 (78%)	43 (22%)	1	1
1	C	196/219 (90%)	146 (74%)	50 (26%)	0	0
1	D	195/219 (89%)	142 (73%)	53 (27%)	0	0
All	All	781/876 (89%)	597 (76%)	184 (24%)	1	1

5 of 184 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	191	GLU
1	D	68	GLU
1	C	214	LEU
1	C	275	GLN
1	D	124	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	94	HIS
1	C	153	ASN
1	C	135	HIS
1	C	199	HIS
1	B	153	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 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	178:ARG	C	179:ASP	N	1.09
1	D	88:ALA	C	89:LYS	N	0.75

## 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<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	244/273 (89%)	-0.29	2 (0%) 86 84	22, 46, 90, 118	0
1	B	244/273 (89%)	-0.24	1 (0%) 92 91	25, 49, 98, 138	0
1	C	244/273 (89%)	-0.26	5 (2%) 65 63	23, 52, 94, 124	0
1	D	244/273 (89%)	-0.15	9 (3%) 41 41	22, 56, 109, 139	0
All	All	976/1092 (89%)	-0.24	17 (1%) 70 68	22, 51, 100, 139	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	16	TRP	5.1
1	B	38	LEU	4.9
1	D	178	ARG	3.8
1	C	174	ILE	3.3
1	C	89	LYS	3.2

### 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.