

wwPDB X-ray Structure Validation Summary Report (i)

Aug 17, 2022 – 09:24 PM EDT

PDB ID	:	4PTK
Title	:	Crystal structure of Staphylococcal IMPase-I complex with $3Mg2+$ and Phos-
		phate
Authors	:	Dutta, A.; Bhattacharyya, S.; Dutta, D.; Das, A.K.
Deposited on		
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 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:

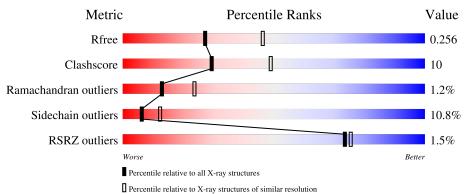
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.29
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.29

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

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	$egin{array}{c} \mathbf{Whole \ archive} \ (\#\mathbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 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	271	% 76%	17%	•
1	В	271	% 7 7%	17%	••••



4PTK

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4291 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	Λ	262	Total	С	N	0	S	0	0	0
1	1 A	202	2098	1352	346	386	14	0	0	U
1	В	261	Total	С	Ν	0	S	0	0	0
	I B	201	2093	1348	344	387	14	U	0	0

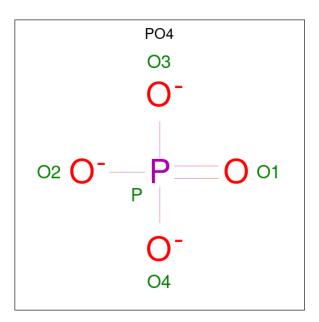
• Molecule 1 is a protein called Inositol monophosphatase family protein.

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	expression tag	UNP Q6G709
А	-4	HIS	-	expression tag	UNP Q6G709
A	-3	HIS	-	expression tag	UNP Q6G709
A	-2	HIS	-	expression tag	UNP Q6G709
А	-1	HIS	-	expression tag	UNP Q6G709
А	0	HIS	-	expression tag	UNP Q6G709
В	-5	HIS	-	expression tag	UNP Q6G709
В	-4	HIS	-	expression tag	UNP Q6G709
В	-3	HIS	-	expression tag	UNP Q6G709
В	-2	HIS	-	expression tag	UNP Q6G709
В	-1	HIS	-	expression tag	UNP Q6G709
В	0	HIS	-	expression tag	UNP Q6G709

There are 12 discrepancies between the modelled and reference sequences:

• Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



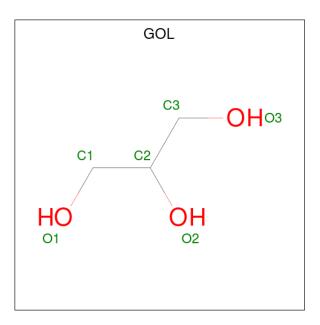


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{P} \\ 5 & 4 & 1 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{P} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	3	Total Mg 3 3	0	0
3	В	3	Total Mg 3 3	0	0





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
4	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	42	$\begin{array}{cc} \text{Total} & \text{O} \\ 42 & 42 \end{array}$	0	0
5	В	30	Total O 30 30	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: Inositol monophosphatase family protein
Chain A: 76% 17%

 11.16
 HIS

 11.26
 HIS

 11.33
 HIS

 11.33
 HIS

 11.66
 HIS

 11.76
 HIS

 11.76
 11.12

 11.77
 11.12

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 11.13

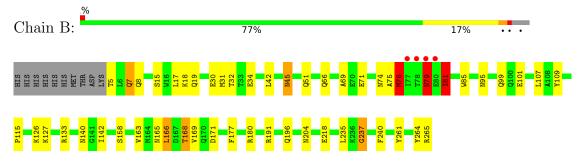
 11.82
 11.13

 11.81
 11.14

 11.82
 11.14

 <

• Molecule 1: Inositol monophosphatase family protein





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants	60.43Å 62.45 Å 140.50 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.72 - 2.50	Depositor
	46.68 - 2.50	EDS
% Data completeness	96.8 (46.72-2.50)	Depositor
(in resolution range)	$96.8 \ (46.68-2.50)$	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$< I/\sigma(I) > 1$	$2.85 (at 2.51 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.177 , 0.257	Depositor
It, Itfree	0.184 , 0.256	DCC
R_{free} test set	953 reflections (5.18%)	wwPDB-VP
Wilson B-factor $(Å^2)$	29.1	Xtriage
Anisotropy	0.331	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38, 41.3	EDS
L-test for twinning ²	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.027 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4291	wwPDB-VP
Average B, all atoms $(Å^2)$	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.81% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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: PO4, GOL, 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		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.71	0/2144	0.92	4/2899~(0.1%)	
1	В	0.65	0/2139	0.86	4/2893~(0.1%)	
All	All	0.68	0/4283	0.89	8/5792~(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

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
1	А	133	ARG	NE-CZ-NH2	-8.73	115.94	120.30
1	В	180	ARG	NE-CZ-NH2	-8.23	116.18	120.30
1	А	133	ARG	NE-CZ-NH1	8.22	124.41	120.30
1	В	180	ARG	NE-CZ-NH1	7.37	123.99	120.30
1	А	180	ARG	NE-CZ-NH2	-7.12	116.74	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	В	237	GLY	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	2098	0	2091	57	0
1	В	2093	0	2082	32	0
2	А	5	0	0	0	0
2	В	5	0	0	0	0
3	А	3	0	0	0	0
3	В	3	0	0	0	0
4	А	6	0	8	0	0
4	В	6	0	8	0	0
5	А	42	0	0	1	0
5	В	30	0	0	0	0
All	All	4291	0	4189	80	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 10.

The worst 5 of 80 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:57:PHE:O	1:A:61:TYR:HD2	1.55	0.89
1:A:79:ASN:H	1:A:80:GLU:CA	1.85	0.88
1:A:79:ASN:H	1:A:80:GLU:CB	1.92	0.82
1:A:168:THR:HG21	1:A:261:TYR:HA	1.63	0.80
1:B:165:ASN:OD1	1:B:264:TYR:CE2	2.35	0.79

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



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
1	А	260/271~(96%)	250~(96%)	8(3%)	2(1%)	19	35
1	В	259/271~(96%)	249 (96%)	6(2%)	4 (2%)	10	18
All	All	519/542~(96%)	499 (96%)	14 (3%)	6 (1%)	13	24

analysed, and the total number of residues.

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	79	ASN
1	В	79	ASN
1	В	76	MET
1	В	237	GLY
1	А	76	MET

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	P	erce	entiles
1	А	226/238~(95%)	202~(89%)	24 (11%)		6	13
1	В	226/238~(95%)	201 (89%)	25 (11%)		6	11
All	All	452/476~(95%)	403 (89%)	49 (11%)		6	12

5 of 49 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	В	18	LYS
1	В	76	MET
1	В	19	GLN
1	В	34	GLU
1	В	81	ILE

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such side chains are listed below:



Mol	Chain	Res	Type
1	В	82	ASN
1	В	165	ASN
1	А	165	ASN
1	А	170	GLN
1	А	204	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)

Of 10 ligands modelled in this entry, 6 are monoatomic - leaving 4 for Mogul analysis.

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	Turne	ype Chain	Res	Link	Bond lengths			Bond angles		
	Type	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
2	PO4	А	301	3	4,4,4	0.71	0	6,6,6	1.31	0
2	PO4	В	303	3	4,4,4	0.77	0	6,6,6	1.01	0
4	GOL	А	305	3	$5,\!5,\!5$	0.44	0	$5,\!5,\!5$	0.87	0
4	GOL	В	305	3	$5,\!5,\!5$	0.34	0	$5,\!5,\!5$	0.61	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
4	GOL	В	305	3	-	4/4/4/4	-
4	GOL	А	305	3	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	В	305	GOL	O1-C1-C2-C3
4	А	305	GOL	O1-C1-C2-C3
4	В	305	GOL	C1-C2-C3-O3
4	В	305	GOL	O1-C1-C2-O2
4	В	305	GOL	O2-C2-C3-O3

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 (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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q < 0.9
1	А	262/271~(96%)	-0.37	4 (1%) 73 75	13, 24, 43, 75	0
1	В	261/271 (96%)	-0.33	4 (1%) 73 75	14, 26, 44, 81	0
All	All	523/542~(96%)	-0.35	8 (1%) 73 75	13, 25, 44, 81	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	78	THR	5.0
1	А	78	THR	3.6
1	А	79	ASN	3.4
1	В	77	ILE	3.3
1	В	79	ASN	3.1

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	B-factors(Å ²)	Q<0.9
4	GOL	А	305	6/6	0.87	0.18	$30,\!35,\!36,\!37$	0
3	MG	А	304	1/1	0.94	0.07	$25,\!25,\!25,\!25$	0
4	GOL	В	305	6/6	0.95	0.15	33,37,40,45	0
3	MG	А	302	1/1	0.96	0.08	19,19,19,19	0
3	MG	В	301	1/1	0.96	0.06	$25,\!25,\!25,\!25$	0
3	MG	В	304	1/1	0.97	0.08	32,32,32,32	0
3	MG	В	302	1/1	0.98	0.04	27,27,27,27	0
3	MG	А	303	1/1	0.98	0.06	18,18,18,18	0
2	PO4	А	301	5/5	0.99	0.12	23,24,25,26	0
2	PO4	В	303	5/5	0.99	0.10	21,23,25,26	0

6.5 Other polymers (i)

There are no such residues in this entry.

