

Full wwPDB X-ray Structure Validation Report (i)

Aug 20, 2023 – 07:14 PM EDT

PDB ID : 2IK4

Title: Yeast inorganic pyrophosphatase variant D117E with magnesium and phos-

phate

Authors: Oksanen, E.; Ahonen, A.K.; Tuominen, H.; Tuominen, V.; Lahti, R.; Goldman,

A.; Heikinheimo, P.

Deposited on : 2006-10-02

Resolution : 1.80 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:

 $Mol Probity \quad : \quad 4.02b\text{--}467$

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.35

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)

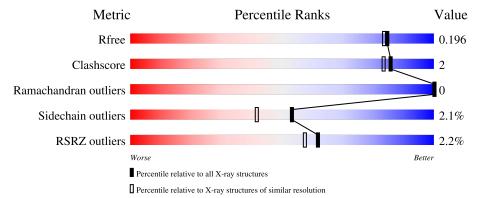
Validation Pipeline (wwPDB-VP) : 2.35

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 1.80 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{\rm A})}) \end{array}$
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	A	286	88%	7%	5%
1	В	286	90%	8%	, ··



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4868 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 Inorganic pyrophosphatase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	273	Total 2167	C 1397	N 354	O 413	S 3	0	0	0
1	В	284	Total 2254	_	N 370	O 433	S 3	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

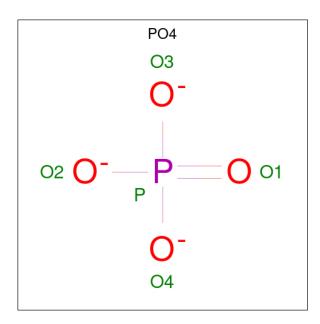
Chain	Residue	Modelled	Actual	Comment	Reference
A	117	GLU	ASP	engineered mutation	UNP P00817
В	117	GLU	ASP	engineered mutation	UNP P00817

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mg 2 2	0	0
2	В	3	Total Mg 3 3	0	0

• Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
3	В	1	Total 5	O 4	P 1	0	0

• Molecule 4 is water.

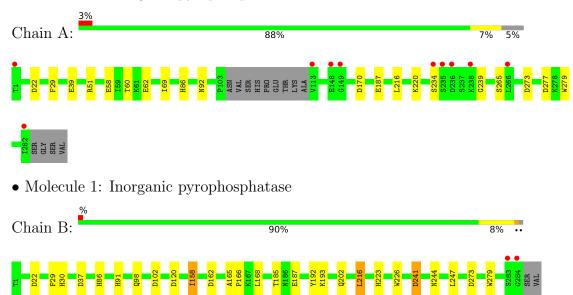
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	171	Total O 171 171	0	0
4	В	266	Total O 266 266	0	0



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: Inorganic pyrophosphatase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	51.76Å 93.23Å 69.22Å	Donositor
a, b, c, α , β , γ	90.00° 99.58° 90.00°	Depositor
Resolution (Å)	19.88 - 1.80	Depositor
rtesolution (A)	19.86 - 1.80	EDS
% Data completeness	100.0 (19.88-1.80)	Depositor
(in resolution range)	99.2 (19.86-1.80)	EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) > 1$	3.00 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
D D.	0.162 , 0.190	Depositor
R, R_{free}	0.173 , 0.196	DCC
R_{free} test set	3002 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	21.2	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34, 44.1	EDS
L-test for twinning ²	$ < L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4868	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.61% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



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: MG, PO4

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		nd lengths	Bond angles		
Mol Chain		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.63	$1/2222 \ (0.0\%)$	0.78	$4/3021 \ (0.1\%)$	
1	В	0.64	0/2312	0.83	8/3145 (0.3%)	
All	All	0.64	1/4534 (0.0%)	0.80	$12/6166 \ (0.2\%)$	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(Å)	Ideal(A)
1	A	39	GLU	CB-CG	-5.24	1.42	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^{o})$	$\mathbf{Ideal}(^{o})$
1	В	102	ASP	CB-CG-OD2	7.20	124.78	118.30
1	В	162	ASP	CB-CG-OD2	6.47	124.12	118.30
1	В	37	ASP	CB-CG-OD2	5.95	123.66	118.30
1	В	22	ASP	CB-CG-OD2	5.86	123.58	118.30
1	A	277	ASP	CB-CG-OD1	5.56	123.31	118.30
1	A	170	ASP	CB-CG-OD2	5.43	123.19	118.30
1	В	216	LEU	CB-CG-CD1	5.27	119.96	111.00
1	В	273	ASP	CB-CG-OD2	5.26	123.03	118.30
1	A	273	ASP	CB-CG-OD2	5.22	122.99	118.30
1	В	241	ASP	CB-CG-OD2	5.17	122.95	118.30
1	В	120	ASP	CB-CG-OD2	5.13	122.92	118.30
1	A	22	ASP	CB-CG-OD2	5.05	122.84	118.30

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	2167	0	2128	7	0
1	В	2254	0	2218	12	0
2	A	2	0	0	0	0
2	В	3	0	0	0	0
3	В	5	0	0	0	0
4	A	171	0	0	1	0
4	В	266	0	0	1	0
All	All	4868	0	4346	19	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 2.

All (19) 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:B:30:HIS:HD2	1:B:226:TRP:HE1	1.33	0.74
1:A:60:THR:OG1	1:A:69:ILE:HG12	2.00	0.60
1:B:98:GLN:O	1:B:223:HIS:HD2	1.86	0.57
1:A:86:HIS:HE1	1:A:187:GLU:OE1	1.88	0.57
1:B:86:HIS:HE1	1:B:187:GLU:OE1	1.88	0.56
1:A:216:LEU:O	1:A:220:LYS:HD3	2.06	0.55
1:A:86:HIS:HD2	4:B:525:HOH:O	1.92	0.53
1:B:158:ILE:HD13	1:B:168:LEU:HD12	1.92	0.52
1:B:158:ILE:HD13	1:B:168:LEU:CD1	2.41	0.51
1:B:30:HIS:HE1	1:B:241:ASP:O	1.96	0.47
1:A:62:GLU:HG3	1:A:239:GLY:O	2.15	0.46
1:B:30:HIS:CD2	1:B:226:TRP:HE1	2.21	0.45
1:A:51:ARG:H	1:A:92:ASN:HD22	1.64	0.45
1:B:91:HIS:HE1	1:B:185:THR:OG1	1.99	0.45
1:B:165:ALA:HB3	1:B:166:PRO:HD3	1.98	0.44
4:A:445:HOH:O	1:B:86:HIS:HD2	1.99	0.43
1:B:192:TYR:CZ	1:B:193:LYS:HE2	2.55	0.42
1:B:244:ASN:ND2	1:B:247:LEU:H	2.18	0.41
1:A:51:ARG:H	1:A:92:ASN:ND2	2.19	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	Perce	ntiles
1	A	$269/286 \ (94\%)$	266 (99%)	3 (1%)	0	100	100
1	В	282/286 (99%)	276 (98%)	6 (2%)	0	100	100
All	All	551/572 (96%)	542 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	231/248 (93%)	226 (98%)	5 (2%)	52 39		
1	В	243/248 (98%)	238 (98%)	5 (2%)	53 42		
All	All	474/496 (96%)	464 (98%)	10 (2%)	53 42		

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	PHE
1	A	58	GLU
1	A	234	SER
1	A	265	SER
1	A	279	TRP

Continued on next page...



Continued from previous page...

Mol	Chain	Res	Type
1	В	29	PHE
1	В	158	ILE
1	В	202	GLN
1	В	216	LEU
1	В	279	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	66	ASN
1	A	86	HIS
1	A	92	ASN
1	A	201	ASN
1	В	30	HIS
1	В	54	ASN
1	В	86	HIS
1	В	91	HIS
1	В	223	HIS
1	В	244	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 6 ligands modelled in this entry, 5 are monoatomic - leaving 1 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	Type	Chain	Res	Link		ond leng	,		ond ang	,
IVIOI	туре	Chain	nes	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PO4	В	290	2	4,4,4	0.67	0	6,6,6	1.67	2 (33%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$Ideal(^{o})$
3	В	290	PO4	O4-P-O3	2.31	115.39	107.97
3	В	290	PO4	O3-P-O1	-2.06	103.37	110.89

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 (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 $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q < 0.9
1	A	273/286 (95%)	0.04	10 (3%) 41 36	17, 28, 41, 51	0
1	В	284/286~(99%)	-0.26	2 (0%) 87 86	18, 23, 33, 43	0
All	All	557/572 (97%)	-0.12	12 (2%) 62 57	17, 25, 38, 51	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	266	LEU	5.3
1	A	149	GLY	4.0
1	A	235	SER	3.3
1	В	283	SER	3.1
1	A	236	ASP	3.0
1	A	113	VAL	2.9
1	A	148	GLU	2.8
1	В	284	GLY	2.5
1	A	234	SER	2.4
1	A	282	ILE	2.3
1	A	238	LYS	2.2
1	A	1	THR	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 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	MG	A	288	1/1	0.96	0.12	28,28,28,28	0
2	MG	A	287	1/1	0.97	0.07	30,30,30,30	0
2	MG	В	288	1/1	0.97	0.04	21,21,21,21	0
2	MG	В	287	1/1	0.99	0.03	17,17,17,17	0
2	MG	В	289	1/1	0.99	0.05	23,23,23,23	0
3	PO4	В	290	5/5	0.99	0.08	21,23,25,28	0

6.5 Other polymers (i)

There are no such residues in this entry.

