



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 5NZH
Title : Crystal structure of UDP-glucose pyrophosphorylase V402W mutant from Leishmania major
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Deposited on : 2017-05-14
Resolution : 2.90 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
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)
Validation Pipeline (wwPDB-VP)	:	2.37.1

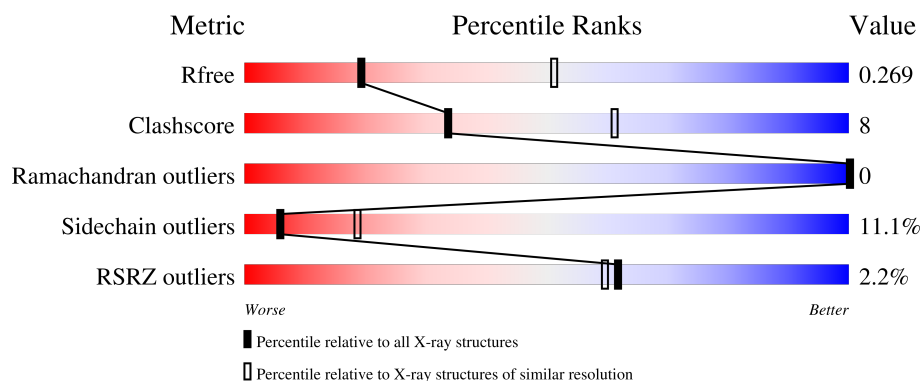
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 $\leq 5\%$. 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	505	 73% 18% • •
1	B	505	 4% 72% 19% • 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7820 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 UDP-glucose pyrophosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	483	Total	C	N	O	S	0	0	0
			3737	2357	637	717	26			
1	B	482	Total	C	N	O	S	0	0	0
			3728	2351	635	716	26			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	402	TRP	VAL	engineered mutation	UNP Q4QDU3
A	495	MET	-	expression tag	UNP Q4QDU3
A	496	ARG	-	expression tag	UNP Q4QDU3
A	497	PRO	-	expression tag	UNP Q4QDU3
A	498	LEU	-	expression tag	UNP Q4QDU3
A	499	GLU	-	expression tag	UNP Q4QDU3
A	500	HIS	-	expression tag	UNP Q4QDU3
A	501	HIS	-	expression tag	UNP Q4QDU3
A	502	HIS	-	expression tag	UNP Q4QDU3
A	503	HIS	-	expression tag	UNP Q4QDU3
A	504	HIS	-	expression tag	UNP Q4QDU3
A	505	HIS	-	expression tag	UNP Q4QDU3
B	402	TRP	VAL	engineered mutation	UNP Q4QDU3
B	495	MET	-	expression tag	UNP Q4QDU3
B	496	ARG	-	expression tag	UNP Q4QDU3
B	497	PRO	-	expression tag	UNP Q4QDU3
B	498	LEU	-	expression tag	UNP Q4QDU3
B	499	GLU	-	expression tag	UNP Q4QDU3
B	500	HIS	-	expression tag	UNP Q4QDU3
B	501	HIS	-	expression tag	UNP Q4QDU3
B	502	HIS	-	expression tag	UNP Q4QDU3
B	503	HIS	-	expression tag	UNP Q4QDU3
B	504	HIS	-	expression tag	UNP Q4QDU3
B	505	HIS	-	expression tag	UNP Q4QDU3

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	175	Total 175	O 175	0	0
2	B	180	Total 180	O 180	0	0

- Molecule 1: UDP-glucose pyrophosphorylase

- Molecule 1: UDP-glucose pyrophosphorylase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	179.56Å 70.89Å 112.29Å 90.00° 123.54° 90.00°	Depositor
Resolution (Å)	47.85 – 2.90 47.85 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (47.85-2.90) 99.7 (47.85-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.02	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 2.91Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.226 , 0.269 0.225 , 0.269	Depositor DCC
R_{free} test set	1399 reflections (5.31%)	wwPDB-VP
Wilson B-factor (Å ²)	43.6	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 7.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	7820	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.95% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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	0.42	0/3809	0.57	1/5160 (0.0%)
1	B	0.43	0/3800	0.58	2/5149 (0.0%)
All	All	0.42	0/7609	0.57	3/10309 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	471	SER	N-CA-C	-8.39	88.35	111.00
1	A	272	GLN	N-CA-C	6.78	129.30	111.00
1	B	8	LEU	CA-CB-CG	5.09	127.01	115.30

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	3737	0	3720	65	3
1	B	3728	0	3707	62	0
2	A	175	0	0	5	0
2	B	180	0	0	5	0
All	All	7820	0	7427	126	3

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.

The worst 5 of 126 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:449:LEU:HB3	1:B:472:ALA:HB2	1.41	1.02
1:A:417:ASP:OD2	1:A:447:LYS:O	1.78	1.02
1:B:465:GLU:O	1:B:466:ASN:OD1	1.77	1.01
1:B:449:LEU:HD22	1:B:472:ALA:H	1.33	0.93
1:A:451:GLN:HG3	1:A:474:VAL:HG12	1.55	0.87

All (3) 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:271:GLY:CA	1:A:405:ASP:OD2[4_758]	1.83	0.37
1:A:271:GLY:N	1:A:405:ASP:OD2[4_758]	1.96	0.24
1:A:271:GLY:C	1:A:405:ASP:OD2[4_758]	2.04	0.16

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	481/505 (95%)	466 (97%)	15 (3%)	0	100	100
1	B	480/505 (95%)	455 (95%)	25 (5%)	0	100	100
All	All	961/1010 (95%)	921 (96%)	40 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	410/432 (95%)	360 (88%)	50 (12%)	5	15
1	B	409/432 (95%)	368 (90%)	41 (10%)	7	23
All	All	819/864 (95%)	728 (89%)	91 (11%)	6	19

5 of 91 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	146	ARG
1	B	344	SER
1	B	194	ILE
1	B	281	LEU
1	B	403	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	272	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](#)

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, 95th 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 ²)	Q<0.9
1	A	483/505 (95%)	-0.27	2 (0%) 92 93	10, 26, 64, 115	0
1	B	482/505 (95%)	-0.12	19 (3%) 39 35	10, 27, 85, 120	0
All	All	965/1010 (95%)	-0.19	21 (2%) 62 59	10, 26, 79, 120	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	464	ILE	4.1
1	B	454	ALA	3.9
1	B	465	GLU	3.6
1	B	471	SER	3.6
1	B	445	THR	3.5

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.