



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 06:35 PM UTC

PDB ID : 8B5V / pdb_00008b5v
Title : Crystal Structure of Trypanosoma Cruzi phosphomannosemutase
Authors : Robinson, D.A.; Ferguson, M.A.J.
Deposited on : 2022-09-24
Resolution : 1.60 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 ⓘ 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	FAILED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

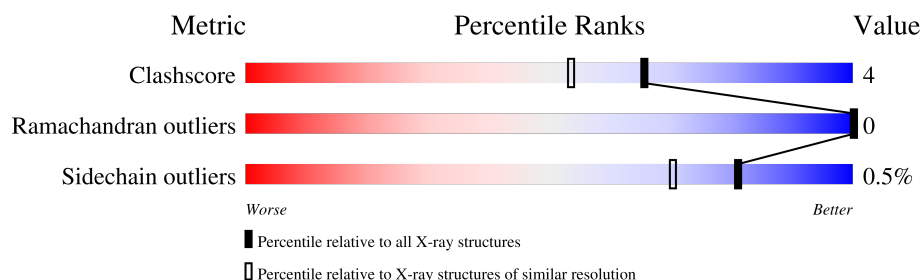
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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))
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)

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 $\leq 5\%$

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	245	
1	B	245	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4460 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 Phosphomannomutase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	244	Total	C	N	O	S	0	0	0
			1984	1261	345	373	5			
1	B	243	Total	C	N	O	S	0	0	0
			1972	1253	343	372	4			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	239	Total	O	0	0
			239	239		
4	B	253	Total	O	0	0
			253	253		

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. 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. 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.

Note EDS failed to run properly.

- Molecule 1: Phosphomannomutase

Chain A:  90% 9%



- Molecule 1: Phosphomannomutase

Chain B:  91% 8%



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	40.40Å 83.43Å 152.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.55 – 1.60	Depositor
% Data completeness (in resolution range)	92.1 (29.55-1.60)	Depositor
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.199 , 0.229	Depositor
Wilson B-factor (Å ²)	14.8	Xtriage
Anisotropy	0.223	Xtriage
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
Total number of atoms	4460	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 49.14 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.7819e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.03	1/2024 (0.0%)	1.31	5/2724 (0.2%)
1	B	1.05	2/2012 (0.1%)	1.25	5/2710 (0.2%)
All	All	1.04	3/4036 (0.1%)	1.28	10/5434 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	209	HIS	CE1-NE2	7.06	1.39	1.32
1	A	99	ARG	CD-NE	-5.49	1.38	1.46
1	B	85	LEU	C-O	-5.38	1.17	1.24

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	99	ARG	CG-CD-NE	-7.24	96.06	112.00
1	A	99	ARG	NE-CZ-NH2	-6.27	113.56	119.20
1	A	55	GLY	CA-C-O	-6.23	117.82	122.37
1	B	99	ARG	CG-CD-NE	-5.96	98.90	112.00
1	A	109	ASP	CA-CB-CG	5.66	118.26	112.60
1	B	93	ARG	CB-CG-CD	-5.59	98.45	111.30
1	A	111	PRO	CB-CA-C	-5.55	104.00	112.11
1	B	122	ASN	CB-CA-C	5.53	119.52	110.95
1	B	99	ARG	NE-CZ-NH2	-5.51	114.24	119.20
1	B	203	PHE	CA-CB-CG	-5.03	108.77	113.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	1984	0	1958	13	1
1	B	1972	0	1935	17	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	239	0	0	8	0
4	B	253	0	0	12	0
All	All	4460	0	3893	30	1

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 4.

All (30) 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:137:SER:OG	4:B:401:HOH:O	1.93	0.86
1:B:96:LYS:HE3	4:B:585:HOH:O	1.78	0.82
1:A:132:ARG:HD2	4:A:485:HOH:O	1.80	0.81
1:B:161:ASN:HB3	4:B:593:HOH:O	1.82	0.78
1:A:45:SER:HB2	4:A:596:HOH:O	1.87	0.75
1:A:27:GLU:OE1	4:A:401:HOH:O	2.07	0.72
1:B:96:LYS:CE	4:B:585:HOH:O	2.47	0.56
1:A:93:ARG:NH2	4:A:410:HOH:O	2.40	0.55
1:B:132:ARG:HD2	4:B:470:HOH:O	2.09	0.53
1:A:1:MET:HA	1:A:1:MET:HE2	1.91	0.52
1:A:132:ARG:CD	4:A:485:HOH:O	2.49	0.51
1:B:161:ASN:CB	4:B:593:HOH:O	2.49	0.50
1:A:92:GLU:OE2	1:A:96:LYS:HE2	2.10	0.50
1:A:208:THR:O	4:A:402:HOH:O	2.20	0.50
1:A:10:ILE:HD13	1:A:50:GLN:HG2	1.95	0.49
1:B:3:LYS:NZ	4:B:411:HOH:O	2.46	0.49
1:B:223:ILE:C	1:B:223:ILE:HD12	2.38	0.49
1:B:207:LYS:HD2	4:B:406:HOH:O	2.14	0.48
1:B:203:PHE:HB3	1:B:223:ILE:HD13	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:221:LYS:O	4:B:402:HOH:O	2.20	0.47
1:B:124:MET:HE1	4:B:538:HOH:O	2.15	0.44
1:A:79:GLU:OE2	4:A:403:HOH:O	2.21	0.44
1:A:78:LYS:NZ	4:A:414:HOH:O	2.42	0.44
1:B:161:ASN:HB3	4:B:619:HOH:O	2.17	0.44
1:A:25:VAL:O	1:A:28:VAL:HG12	2.19	0.42
1:B:116:THR:O	1:B:132:ARG:HG3	2.20	0.41
1:B:243:SER:O	1:B:244:SER:OG	2.29	0.41
1:B:121:ARG:NH1	4:B:424:HOH:O	2.54	0.41
1:A:191:LEU:HD21	1:A:223:ILE:HD11	2.04	0.40
1:B:223:ILE:HD12	1:B:224:ILE:C	2.47	0.40

All (1) 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:209:HIS:NE2	1:B:165:ASP:OD2[3_645]	2.10	0.10

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	242/245 (99%)	233 (96%)	9 (4%)	0	100	100
1	B	241/245 (98%)	232 (96%)	9 (4%)	0	100	100
All	All	483/490 (99%)	465 (96%)	18 (4%)	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	216/217 (100%)	214 (99%)	2 (1%)	70	55
1	B	214/217 (99%)	214 (100%)	0	100	100
All	All	430/434 (99%)	428 (100%)	2 (0%)	81	70

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	ARG
1	A	84	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	149	HIS
1	B	196	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	PO4	A	302	-	4,4,4	0.45	0	6,6,6	0.89	0
3	PO4	B	302	-	4,4,4	0.66	0	6,6,6	0.80	0

There are no bond length outliers.

There are no bond angle outliers.

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS failed to run properly - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS failed to run properly - this section is therefore empty.

6.4 Ligands [i](#)

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers [i](#)

EDS failed to run properly - this section is therefore empty.