



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 10:08 pm GMT

PDB ID : 1MS9
Title : Triclinic form of Trypanosoma cruzi trans-sialidase, in complex with lactose
Authors : Buschiazzi, A.; Amaya, M.F.; Cremona, M.L.; Frasch, A.C.; Alzari, P.M.
Deposited on : 2002-09-19
Resolution : 1.58 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

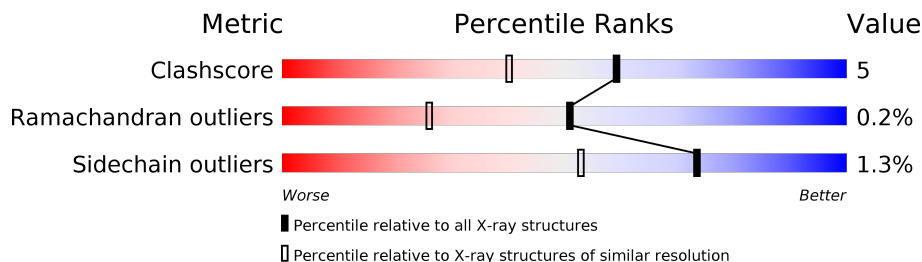
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 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	112137	4539 (1.60-1.56)
Ramachandran outliers	110173	4423 (1.60-1.56)
Sidechain outliers	110143	4420 (1.60-1.56)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	648	
1	B	648	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11115 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 trans-sialidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	622	Total	C	N	O	S	0	13	0
			4932	3118	861	936	17			
1	B	623	Total	C	N	O	S	0	12	0
			4937	3122	863	935	17			

There are 50 discrepancies between the modelled and reference sequences:

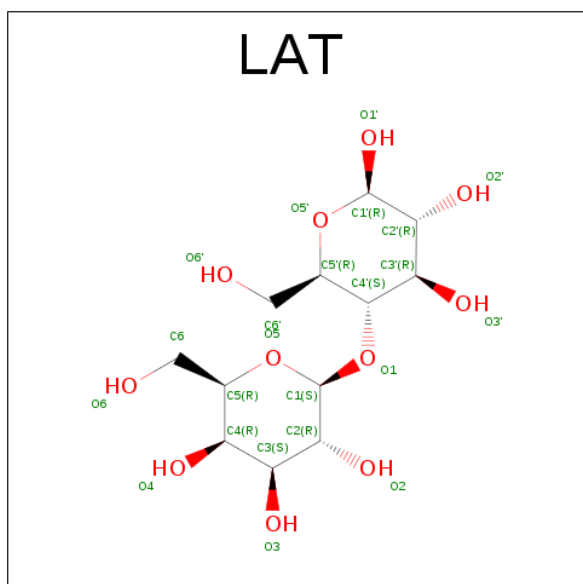
Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	EXPRESSION TAG	UNP Q26964
A	-12	GLY	-	EXPRESSION TAG	UNP Q26964
A	-11	GLY	-	EXPRESSION TAG	UNP Q26964
A	-10	SER	-	EXPRESSION TAG	UNP Q26964
A	-9	HIS	-	EXPRESSION TAG	UNP Q26964
A	-8	HIS	-	EXPRESSION TAG	UNP Q26964
A	-7	HIS	-	EXPRESSION TAG	UNP Q26964
A	-6	HIS	-	EXPRESSION TAG	UNP Q26964
A	-5	HIS	-	EXPRESSION TAG	UNP Q26964
A	-4	HIS	-	EXPRESSION TAG	UNP Q26964
A	-3	GLY	-	EXPRESSION TAG	UNP Q26964
A	-2	MET	-	EXPRESSION TAG	UNP Q26964
A	-1	ALA	-	EXPRESSION TAG	UNP Q26964
A	0	SER	-	EXPRESSION TAG	UNP Q26964
A	58	PHE	ASN	ENGINEERED	UNP Q26964
A	262	THR	SER	SEE REMARK 999	UNP Q26964
A	476	HIS	ARG	SEE REMARK 999	UNP Q26964
A	484	LEU	VAL	SEE REMARK 999	UNP Q26964
A	495	LYS	SER	ENGINEERED	UNP Q26964
A	496	GLY	VAL	ENGINEERED	UNP Q26964
A	520	LYS	GLU	ENGINEERED	UNP Q26964
A	558	VAL	GLU	SEE REMARK 999	UNP Q26964
A	593	GLY	ASP	ENGINEERED	UNP Q26964
A	597	ASP	ILE	ENGINEERED	UNP Q26964
A	599	ARG	HIS	ENGINEERED	UNP Q26964

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	MET	-	EXPRESSION TAG	UNP Q26964
B	-12	GLY	-	EXPRESSION TAG	UNP Q26964
B	-11	GLY	-	EXPRESSION TAG	UNP Q26964
B	-10	SER	-	EXPRESSION TAG	UNP Q26964
B	-9	HIS	-	EXPRESSION TAG	UNP Q26964
B	-8	HIS	-	EXPRESSION TAG	UNP Q26964
B	-7	HIS	-	EXPRESSION TAG	UNP Q26964
B	-6	HIS	-	EXPRESSION TAG	UNP Q26964
B	-5	HIS	-	EXPRESSION TAG	UNP Q26964
B	-4	HIS	-	EXPRESSION TAG	UNP Q26964
B	-3	GLY	-	EXPRESSION TAG	UNP Q26964
B	-2	MET	-	EXPRESSION TAG	UNP Q26964
B	-1	ALA	-	EXPRESSION TAG	UNP Q26964
B	0	SER	-	EXPRESSION TAG	UNP Q26964
B	58	PHE	ASN	ENGINEERED	UNP Q26964
B	262	THR	SER	SEE REMARK 999	UNP Q26964
B	476	HIS	ARG	SEE REMARK 999	UNP Q26964
B	484	LEU	VAL	SEE REMARK 999	UNP Q26964
B	495	LYS	SER	ENGINEERED	UNP Q26964
B	496	GLY	VAL	ENGINEERED	UNP Q26964
B	520	LYS	GLU	ENGINEERED	UNP Q26964
B	558	VAL	GLU	SEE REMARK 999	UNP Q26964
B	593	GLY	ASP	ENGINEERED	UNP Q26964
B	597	ASP	ILE	ENGINEERED	UNP Q26964
B	599	ARG	HIS	ENGINEERED	UNP Q26964

- Molecule 2 is lactose (three-letter code: LAT) (formula: C₁₂H₂₂O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			23	12	11		
2	B	1	Total	C	O	0	0
			23	12	11		

- Molecule 3 is water.

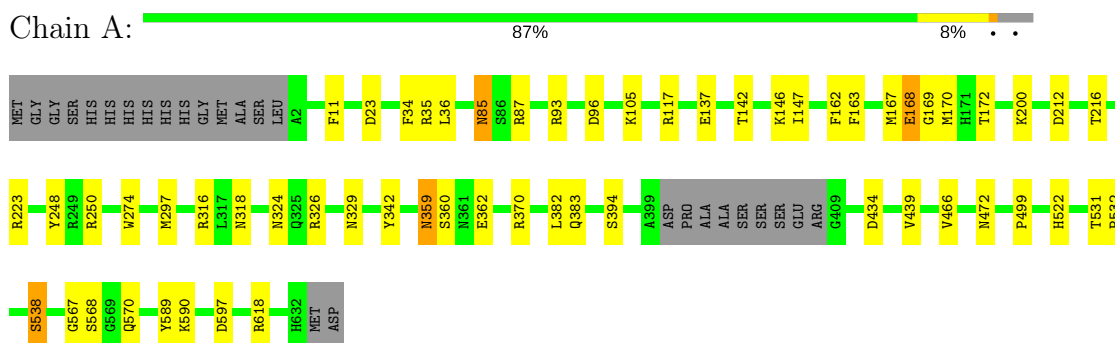
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	562	Total	O	0	0
			562	562		
3	B	638	Total	O	0	0
			638	638		

3 Residue-property plots

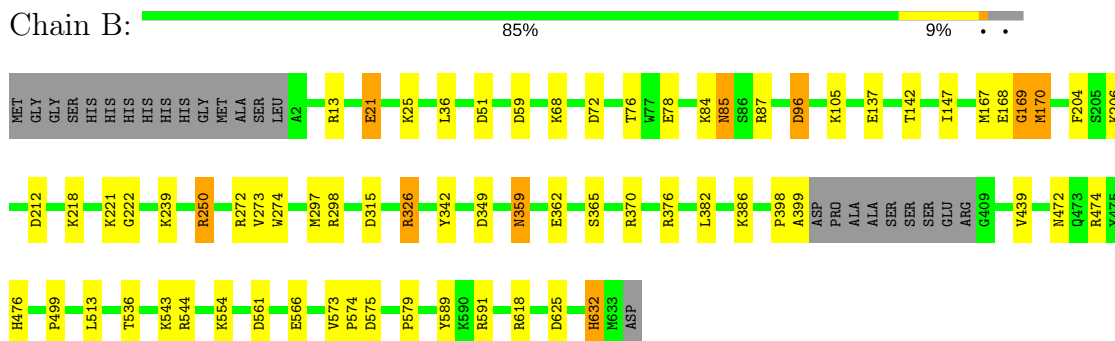
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS was not executed.

- Molecule 1: trans-sialidase



- Molecule 1: trans-sialidase



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	51.05Å 74.20Å 87.50Å 86.02° 84.17° 88.31°	Depositor
Resolution (Å)	20.00 – 1.58	Depositor
% Data completeness (in resolution range)	94.4 (20.00-1.58)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
Refinement program	REFMAC 5	Depositor
R, R_{free}	0.163 , 0.198	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11115	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

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: LAT

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	0.94	2/5046 (0.0%)	1.00	11/6849 (0.2%)
1	B	0.99	1/5051 (0.0%)	1.04	17/6855 (0.2%)
All	All	0.97	3/10097 (0.0%)	1.02	28/13704 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	117	ARG	CZ-NH1	-5.65	1.25	1.33
1	A	248	TYR	CE1-CZ	-5.43	1.31	1.38
1	B	21	GLU	CD-OE1	5.38	1.31	1.25

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	370	ARG	NE-CZ-NH1	10.33	125.47	120.30
1	A	370	ARG	NE-CZ-NH1	9.48	125.04	120.30
1	A	250	ARG	NE-CZ-NH2	-9.03	115.79	120.30
1	A	250	ARG	NE-CZ-NH1	8.22	124.41	120.30
1	A	370	ARG	NE-CZ-NH2	-7.64	116.48	120.30

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	4932	0	4837	38	0
1	B	4937	0	4848	68	0
2	A	23	0	22	0	0
2	B	23	0	22	0	0
3	A	562	0	0	10	0
3	B	638	0	0	21	0
All	All	11115	0	9729	106	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 5.

The worst 5 of 106 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:36[A]:LEU:HD21	1:B:342[A]:TYR:HE2	1.18	1.03
1:B:239:LYS:HE3	3:B:3542:HOH:O	1.57	1.02
1:B:206:LYS:NZ	3:B:3551:HOH:O	1.96	0.99
1:B:36[A]:LEU:HD21	1:B:342[A]:TYR:CE2	1.99	0.97
1:A:146:LYS:HE3	3:A:3465:HOH:O	1.69	0.91

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	631/648 (97%)	603 (96%)	26 (4%)	2 (0%)	44	21
1	B	631/648 (97%)	607 (96%)	23 (4%)	1 (0%)	51	26
All	All	1262/1296 (97%)	1210 (96%)	49 (4%)	3 (0%)	51	26

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	168	GLU
1	B	170	MET
1	A	466	VAL

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	538/547 (98%)	530 (98%)	8 (2%)	70	46
1	B	538/547 (98%)	532 (99%)	6 (1%)	78	60
All	All	1076/1094 (98%)	1062 (99%)	14 (1%)	73	53

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	590	LYS
1	A	618	ARG
1	B	618	ARG
1	A	568	SER
1	B	359	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	611	GLN
1	B	85	ASN
1	B	472	ASN
1	A	604	ASN
1	B	603	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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	$\# Z > 2$
2	LAT	A	2922	-	24,24,24	0.46	0	35,35,35	1.22	3 (8%)
2	LAT	B	2923	-	24,24,24	0.48	0	35,35,35	1.35	4 (11%)

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
2	LAT	A	2922	-	-	0/8/48/48	0/2/2/2
2	LAT	B	2923	-	-	0/8/48/48	0/2/2/2

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2922	LAT	C1-O5-C5	-3.08	107.92	113.72
2	B	2923	LAT	C1-O5-C5	-2.37	109.26	113.72
2	B	2923	LAT	O4-C4-C5	2.02	114.37	109.28
2	B	2923	LAT	C1-C2-C3	2.11	113.90	109.98
2	A	2922	LAT	O4-C4-C5	2.29	115.06	109.28

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 was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.