



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 06:53 AM GMT

PDB ID : 1MS9  
Title : Triclinic form of Trypanosoma cruzi trans-sialidase, in complex with lactose  
Authors : Buschiazzo, 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 full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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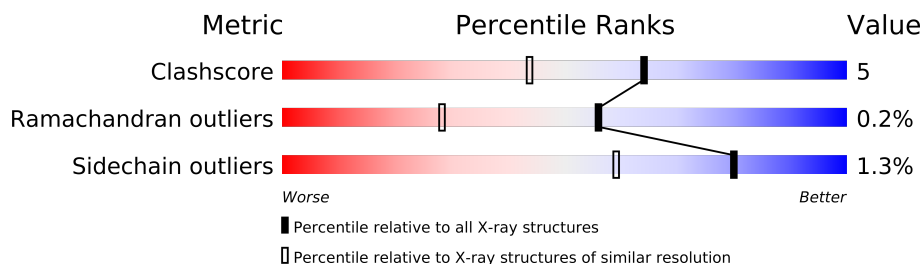
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

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	79885	3207 (1.60-1.56)
Ramachandran outliers	78287	3107 (1.60-1.56)
Sidechain outliers	78261	3104 (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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

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 hydrogen and 0 are deuterium.

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:

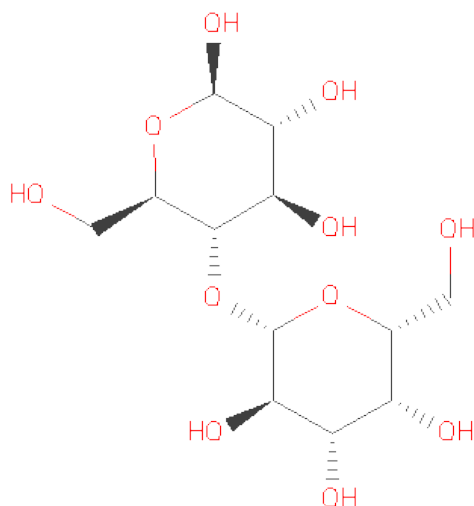
Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	EXPRESSION TAG	UNP Q26964
A	-12	GLY	-	EXPRESSION TAG	UNP Q26964
A	-11	GLY	-	EXPRESSION TAG	UNP Q26964
A	-10	SER	-	EXPRESSION TAG	UNP Q26964
A	-9	HIS	-	EXPRESSION TAG	UNP Q26964
A	-8	HIS	-	EXPRESSION TAG	UNP Q26964
A	-7	HIS	-	EXPRESSION TAG	UNP 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: C<sub>12</sub>H<sub>22</sub>O<sub>11</sub>).



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

- Molecule 3 is water.

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

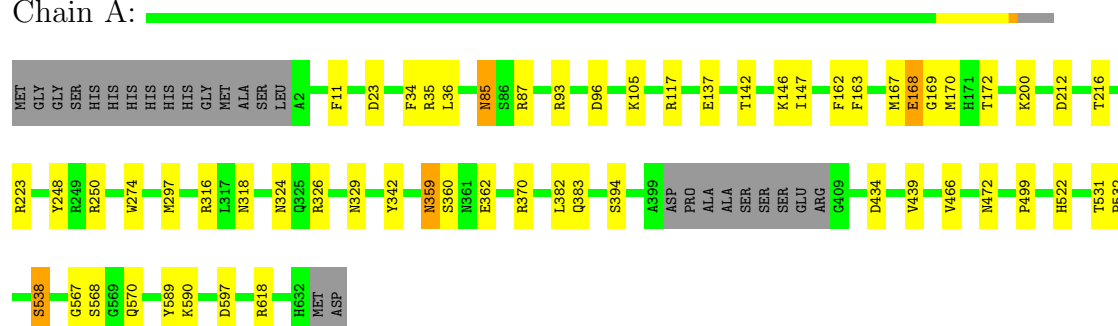
### 3 Residue-property plots i

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

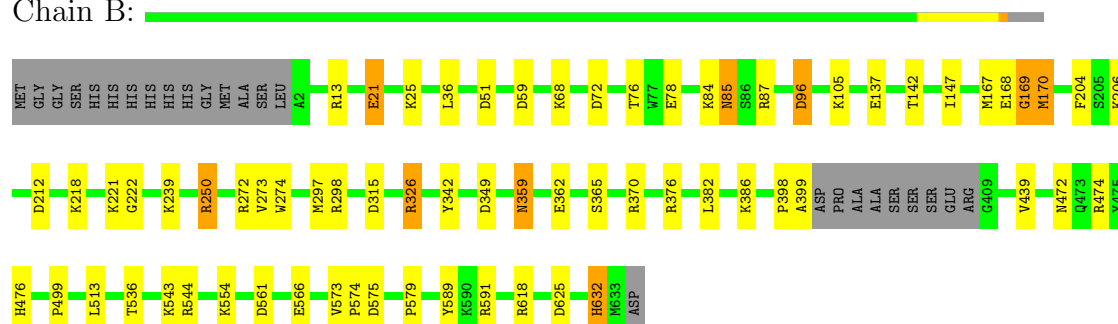
- Molecule 1: trans-sialidase

Chain A:



- Molecule 1: trans-sialidase

Chain B:



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	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 <sup>2</sup> )	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

All (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
1	B	370	ARG	NE-CZ-NH2	-7.44	116.58	120.30
1	B	51	ASP	CB-CG-OD1	7.44	124.99	118.30
1	A	212	ASP	CB-CG-OD2	6.83	124.44	118.30
1	B	298	ARG	NE-CZ-NH1	-6.81	116.89	120.30
1	B	315	ASP	CB-CG-OD2	6.51	124.16	118.30
1	B	376	ARG	NE-CZ-NH2	6.47	123.53	120.30
1	A	316	ARG	NE-CZ-NH2	-6.40	117.10	120.30
1	B	250	ARG	NE-CZ-NH2	-6.36	117.12	120.30
1	B	376	ARG	NE-CZ-NH1	-6.27	117.16	120.30
1	B	212	ASP	CB-CG-OD2	6.25	123.92	118.30
1	B	575	ASP	CB-CG-OD2	6.12	123.81	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	223	ARG	NE-CZ-NH2	-5.94	117.33	120.30
1	A	23	ASP	CB-CG-OD2	5.88	123.60	118.30
1	A	96	ASP	CB-CG-OD2	5.82	123.54	118.30
1	B	326	ARG	NE-CZ-NH2	-5.75	117.42	120.30
1	B	349	ASP	CB-CG-OD2	5.75	123.47	118.30
1	B	591	ARG	NE-CZ-NH2	-5.54	117.53	120.30
1	A	93	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	B	96	ASP	CB-CG-OD2	5.31	123.08	118.30
1	B	59	ASP	CB-CG-OD2	5.27	123.05	118.30
1	B	561	ASP	CB-CG-OD2	5.17	122.96	118.30
1	B	169	GLY	O-C-N	5.12	130.90	122.70
1	A	597	ASP	CB-CG-OD1	5.04	122.83	118.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

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

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (106) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(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

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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
1:B:105:LYS:NZ	1:B:137[A]:GLU:OE2	2.04	0.90
1:B:36[A]:LEU:HD23	1:B:342[A]:TYR:CD2	2.09	0.88
1:B:36[A]:LEU:CD2	1:B:342[A]:TYR:CE2	2.57	0.88
1:A:146:LYS:CE	3:A:3465:HOH:O	2.24	0.80
1:B:168:GLU:O	3:B:3560:HOH:O	1.97	0.80
1:B:36[A]:LEU:HD23	1:B:342[A]:TYR:HD2	1.47	0.79
1:B:13[B]:ARG:CD	3:B:3499:HOH:O	2.32	0.78
1:B:543:LYS:HE3	3:B:3384:HOH:O	1.84	0.76
1:A:394:SER:OG	3:A:3479:HOH:O	2.04	0.75
1:B:36[A]:LEU:CD2	1:B:342[A]:TYR:HE2	1.93	0.75
1:B:85:ASN:HD22	1:B:87:ARG:H	1.38	0.69
1:B:36[A]:LEU:CD2	1:B:342[A]:TYR:CD2	2.74	0.69
1:B:218:LYS:NZ	3:B:3501:HOH:O	2.26	0.68
1:B:36[B]:LEU:HD23	1:B:96:ASP:HA	1.76	0.67
1:A:168:GLU:CD	1:A:168:GLU:H	1.98	0.67
1:A:85:ASN:HD22	1:A:87:ARG:H	1.41	0.67
1:B:169:GLY:CA	3:B:3529:HOH:O	2.42	0.66
1:B:25:LYS:HD3	3:B:3449:HOH:O	1.94	0.66
1:B:386:LYS:NZ	3:B:3369:HOH:O	2.30	0.64
1:B:169:GLY:N	3:B:3529:HOH:O	2.30	0.64
1:B:632:HIS:ND1	1:B:632:HIS:C	2.50	0.64
1:B:221:LYS:HE3	3:B:3418:HOH:O	1.97	0.64
1:A:105:LYS:NZ	1:A:137[A]:GLU:OE2	2.31	0.63
1:B:574:PRO:HB2	3:B:3547:HOH:O	1.99	0.61
1:B:21:GLU:OE2	1:B:84:LYS:NZ	2.28	0.60
1:A:170[A]:MET:N	3:A:3484:HOH:O	2.34	0.60
1:A:170[B]:MET:N	3:A:3484:HOH:O	2.34	0.60
1:A:359:ASN:HD21	1:A:362:GLU:H	1.49	0.60
1:A:170[A]:MET:HG2	3:A:3484:HOH:O	2.03	0.59
1:B:13[B]:ARG:N	1:B:13[B]:ARG:HD2	2.17	0.59
1:B:566:GLU:HG2	3:B:3250:HOH:O	2.02	0.58
1:A:318[A]:ASN:ND2	1:A:329:ASN:OD1	2.26	0.58
1:B:72:ASP:OD2	1:B:76:THR:HG23	2.04	0.58
1:B:13[B]:ARG:NE	3:B:3499:HOH:O	2.37	0.57
1:B:13[B]:ARG:O	1:B:13[B]:ARG:HD2	2.05	0.57
1:B:206:LYS:HE3	3:B:3445:HOH:O	2.04	0.56
1:B:476:HIS:ND1	1:B:476:HIS:O	2.39	0.56
1:B:573:VAL:HG21	1:B:579:PRO:HG3	1.87	0.56
1:A:142:THR:HG22	1:A:147:ILE:HD13	1.88	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:169:GLY:HA3	3:B:3560:HOH:O	2.06	0.55
1:A:167:MET:O	1:A:168:GLU:C	2.44	0.55
1:A:167:MET:O	1:A:169:GLY:N	2.40	0.54
1:A:146:LYS:NZ	3:A:3465:HOH:O	2.42	0.52
1:B:632:HIS:ND1	1:B:632:HIS:O	2.42	0.52
1:A:567:GLY:O	1:A:570:GLN:NE2	2.39	0.52
1:B:36[B]:LEU:HD21	1:B:96:ASP:OD2	2.10	0.51
1:B:167:MET:O	1:B:170:MET:HG2	2.10	0.51
1:A:35:ARG:HB3	1:A:36[A]:LEU:CD1	2.41	0.51
1:A:35:ARG:HB3	1:A:36[A]:LEU:HD12	1.94	0.50
1:B:85:ASN:ND2	1:B:87:ARG:H	2.10	0.49
1:A:168:GLU:CD	1:A:168:GLU:N	2.64	0.49
1:A:163:PHE:CZ	1:A:172:THR:HB	2.49	0.48
1:B:13[B]:ARG:HG3	1:B:365:SER:OG	2.13	0.48
1:B:137[A]:GLU:CG	3:B:3389:HOH:O	2.62	0.47
1:B:554:LYS:HD3	1:B:573:VAL:HG12	1.97	0.47
1:A:342[B]:TYR:CD1	1:A:342[B]:TYR:N	2.80	0.47
1:A:499:PRO:HG3	1:A:589:TYR:CE1	2.50	0.47
1:B:170:MET:SD	1:B:204:PHE:CZ	3.09	0.46
1:B:250:ARG:NH2	1:B:273:VAL:O	2.48	0.46
1:B:573:VAL:CG2	1:B:579:PRO:HG3	2.46	0.46
1:B:398:PRO:O	1:B:399:ALA:C	2.54	0.46
1:B:297[A]:MET:SD	1:B:382:LEU:HD22	2.56	0.46
1:B:513:LEU:HD11	1:B:573:VAL:HG23	1.98	0.46
1:B:167:MET:O	1:B:168:GLU:C	2.52	0.45
1:A:142:THR:HG22	1:A:147:ILE:CD1	2.46	0.45
1:B:36[A]:LEU:HD23	1:B:342[A]:TYR:CE2	2.34	0.45
1:A:85:ASN:ND2	1:A:87:ARG:H	2.12	0.45
1:A:36[A]:LEU:N	1:A:36[A]:LEU:HD12	2.32	0.44
1:B:536:THR:OG1	1:B:566:GLU:CG	2.65	0.44
1:B:142:THR:HG22	1:B:147:ILE:HD13	1.98	0.44
1:B:499:PRO:HG3	1:B:589:TYR:CE1	2.52	0.44
1:B:13[B]:ARG:O	1:B:13[B]:ARG:CD	2.66	0.43
1:A:359:ASN:ND2	1:A:359:ASN:C	2.71	0.43
1:B:13[B]:ARG:CZ	3:B:3499:HOH:O	2.67	0.43
1:B:13[B]:ARG:HD3	3:B:3499:HOH:O	2.10	0.43
1:B:536:THR:OG1	1:B:566:GLU:HG2	2.19	0.43
1:B:544:ARG:NH1	3:B:3295:HOH:O	2.30	0.43
1:A:200:LYS:HE3	3:A:3378:HOH:O	2.18	0.43
1:B:499:PRO:HG3	1:B:589:TYR:CD1	2.54	0.42
1:A:274:TRP:HA	1:A:472:ASN:HD22	1.83	0.42
1:B:272:ARG:HD2	1:B:476:HIS:CE1	2.53	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:170[A]:MET:CG	3:A:3484:HOH:O	2.63	0.42
1:A:383:GLN:HG2	3:A:3269:HOH:O	2.19	0.42
1:B:359:ASN:HD21	1:B:362:GLU:N	2.16	0.42
1:A:531:THR:CG2	1:A:532:PRO:HD2	2.50	0.42
1:A:162:PHE:CZ	1:A:216:THR:HA	2.55	0.42
1:A:11:PHE:HB3	1:A:34:PHE:CG	2.55	0.41
1:B:168:GLU:N	1:B:168:GLU:CD	2.72	0.41
1:B:169:GLY:N	3:B:3552:HOH:O	2.13	0.41
1:B:206:LYS:HE2	1:B:222:GLY:O	2.20	0.41
1:A:522:HIS:O	1:A:538:SER:HA	2.20	0.41
1:B:274:TRP:HA	1:B:472:ASN:HD22	1.86	0.41
1:B:21:GLU:CD	1:B:84:LYS:HZ1	2.18	0.41
1:B:439:VAL:CG2	1:B:474:ARG:HD2	2.51	0.41
1:A:297[A]:MET:SD	1:A:382:LEU:HD22	2.61	0.40
1:A:434:ASP:HB2	1:A:439:VAL:O	2.22	0.40
1:B:68:LYS:HA	1:B:78:GLU:O	2.22	0.40
1:A:170[A]:MET:HG3	1:A:170[A]:MET:H	1.61	0.40
1:A:359:ASN:HD22	1:A:360:SER:N	2.19	0.40

There are no symmetry-related clashes.

## 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	631/648 (97%)	603 (96%)	26 (4%)	2 (0%)	50	23
1	B	631/648 (97%)	607 (96%)	23 (4%)	1 (0%)	56	28
All	All	1262/1296 (97%)	1210 (96%)	49 (4%)	3 (0%)	56	28

All (3) Ramachandran outliers are listed below:

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

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Mol	Chain	Res	Type
1	A	466	VAL

### 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	538/547 (98%)	530 (98%)	8 (2%)	76	52
1	B	538/547 (98%)	532 (99%)	6 (1%)	84	66
All	All	1076/1094 (98%)	1062 (99%)	14 (1%)	80	59

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	ASN
1	A	324	ASN
1	A	326	ARG
1	A	359	ASN
1	A	538	SER
1	A	568	SER
1	A	590	LYS
1	A	618	ARG
1	B	85	ASN
1	B	326	ARG
1	B	359	ASN
1	B	618	ARG
1	B	625	ASP
1	B	632	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	ASN
1	A	123	HIS
1	A	174	GLN
1	A	359	ASN
1	A	472	ASN

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Mol	Chain	Res	Type
1	A	603	ASN
1	A	604	ASN
1	A	611	GLN
1	B	85	ASN
1	B	123	HIS
1	B	174	GLN
1	B	359	ASN
1	B	472	ASN
1	B	603	ASN
1	B	604	ASN
1	B	611	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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	0.43	0	35,35,35	1.18	3 (8%)
2	LAT	B	2923	-	24,24,24	0.47	0	35,35,35	1.32	3 (8%)

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.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2922	LAT	C1-O5-C5	-2.99	107.92	113.73
2	B	2923	LAT	O1-C4'-C3'	2.41	113.35	107.16
2	B	2923	LAT	C1-O5-C5	-2.30	109.26	113.73
2	A	2922	LAT	C1-C2-C3	2.28	114.43	110.00
2	A	2922	LAT	O4-C4-C5	2.19	115.06	109.28
2	B	2923	LAT	C1-C2-C3	2.01	113.90	110.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.