



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:50 PM UTC

PDB ID : 5V1V / pdb_00005v1v
Title : TbiB1 in Complex with the TbiA(alpha) Leader Peptide
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Deposited on : 2017-03-02
Resolution : 1.35 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	:	NOT EXECUTED
Xtriage (Phenix)	:	2.0
EDS	:	NOT EXECUTED
Buster-report	:	NOT EXECUTED
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

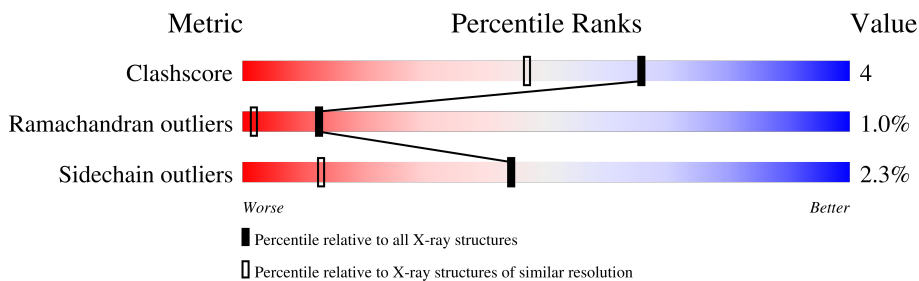
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.35 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	1232 (1.36-1.36)
Ramachandran outliers	187476	1220 (1.36-1.36)
Sidechain outliers	187428	1220 (1.36-1.36)

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 was not executed.

Mol	Chain	Length	Quality of chain
1	A	91	90% . . .
1	B	91	85% 8% . 7%
2	C	21	81% 19%
2	D	21	62% 14% 5% 19%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 1859 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 TbiB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	88	Total	C	N	O	S	0	4	0
			707	447	116	142	2			
1	B	85	Total	C	N	O	S	0	4	0
			688	435	114	137	2			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP D1CIZ5
A	-1	ASN	-	expression tag	UNP D1CIZ5
A	0	ALA	-	expression tag	UNP D1CIZ5
B	-2	SER	-	expression tag	UNP D1CIZ5
B	-1	ASN	-	expression tag	UNP D1CIZ5
B	0	ALA	-	expression tag	UNP D1CIZ5

- Molecule 2 is a protein called TbiA(alpha) Leader Peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	17	Total	C	N	O	S	0	0	0
			145	91	25	28	1			
2	D	17	Total	C	N	O	S	0	2	0
			157	99	25	32	1			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Zn	0	0
			3	3		
3	B	2	Total	Zn	0	0
			2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	67	Total 67	O 67	0	0
4	B	51	Total 51	O 51	0	0
4	C	15	Total 15	O 15	0	0
4	D	24	Total 24	O 24	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. 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 was not executed.

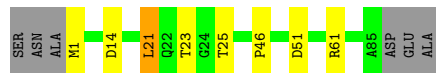
- Molecule 1: TbiB1

Chain A:  90% . . .



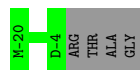
- Molecule 1: TbiB1

Chain B:  85% 8% • 7%



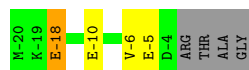
- Molecule 2: TbiA(alpha) Leader Peptide

Chain C:  81% 19%



- Molecule 2: TbiA(alpha) Leader Peptide

Chain D:  62% 14% 5% 19%



4 Data and refinement statistics

EDS was not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.11Å 60.23Å 62.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 1.35	Depositor
% Data completeness (in resolution range)	99.6 (25.00-1.35)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 1.35Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.192 , 0.227	Depositor
Wilson B-factor (Å ²)	14.8	Xtriage
Anisotropy	0.186	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.023 for -h,l,k	Xtriage
Total number of atoms	1859	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.28% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.43	0/729	0.63	0/988
1	B	0.40	0/710	0.72	0/962
2	C	0.32	0/147	0.59	0/194
2	D	0.30	0/165	0.54	0/218
All	All	0.40	0/1751	0.66	0/2362

There are no bond length outliers.

There are no bond angle outliers.

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	707	0	702	4	0
1	B	688	0	689	7	0
2	C	145	0	142	0	0
2	D	157	0	154	2	1
3	A	3	0	0	0	1
3	B	2	0	0	0	0
4	A	67	0	0	1	0
4	B	51	0	0	2	0
4	C	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	24	0	0	0	0
All	All	1859	0	1687	13	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 (13) 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)
4:B:208:HOH:O	2:D:-10[A]:GLU:HG3	1.49	1.08
1:B:51:ASP:OD1	1:B:61:ARG:NH1	1.97	0.96
1:B:21:LEU:H	1:B:21:LEU:HD23	1.39	0.85
1:B:21:LEU:HG	4:B:217:HOH:O	1.85	0.75
1:B:23:THR:OG1	1:B:25[A]:THR:HG22	1.96	0.64
1:B:21:LEU:HD23	1:B:21:LEU:N	2.18	0.54
1:B:21:LEU:H	1:B:21:LEU:CD2	2.07	0.51
1:A:13:ASP:O	1:A:14:ASP:HB3	2.15	0.47
1:A:73:ARG:NH2	4:A:201:HOH:O	2.46	0.47
1:A:12:ILE:O	1:A:13:ASP:C	2.62	0.42
1:B:1:MET:HE2	1:B:46:PRO:HD3	2.02	0.42
1:A:1:MET:HE3	1:A:40:LEU:CD2	2.51	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)
2:D:-5:GLU:OE2	3:A:101:ZN:ZN[2_554]	1.60	0.60

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	90/91 (99%)	87 (97%)	1 (1%)	2 (2%)	5	0
1	B	87/91 (96%)	85 (98%)	2 (2%)	0	100	100
2	C	15/21 (71%)	15 (100%)	0	0	100	100
2	D	17/21 (81%)	17 (100%)	0	0	100	100
All	All	209/224 (93%)	204 (98%)	3 (1%)	2 (1%)	12	2

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	ASP
1	A	14	ASP

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	77/76 (101%)	77 (100%)	0	100	100
1	B	76/76 (100%)	74 (97%)	2 (3%)	40	9
2	C	15/18 (83%)	15 (100%)	0	100	100
2	D	17/18 (94%)	14 (82%)	3 (18%)	2	0
All	All	185/188 (98%)	180 (97%)	5 (3%)	44	9

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	14	ASP
1	B	21	LEU
2	D	-18[A]	GLU
2	D	-18[B]	GLU
2	D	-6	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

Mogul was not executed - this section is therefore empty.

5.5 Carbohydrates [i](#)

Mogul was not executed - this section is therefore empty.

5.6 Ligand geometry [i](#)

Mogul was not executed - this section is therefore empty.

5.7 Other polymers [i](#)

Mogul was not executed - this section is therefore empty.

5.8 Polymer linkage issues [i](#)

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 is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.