



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:01 PM UTC

PDB ID : 5VTG / pdb_00005vtg
Title : The structure of TamB963-1138 from Escherichia coli reveals a novel hydrophobic Beta-taco fold
Authors : Grinter, R.; Josts, I.
Deposited on : 2017-05-17
Resolution : 1.86 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
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

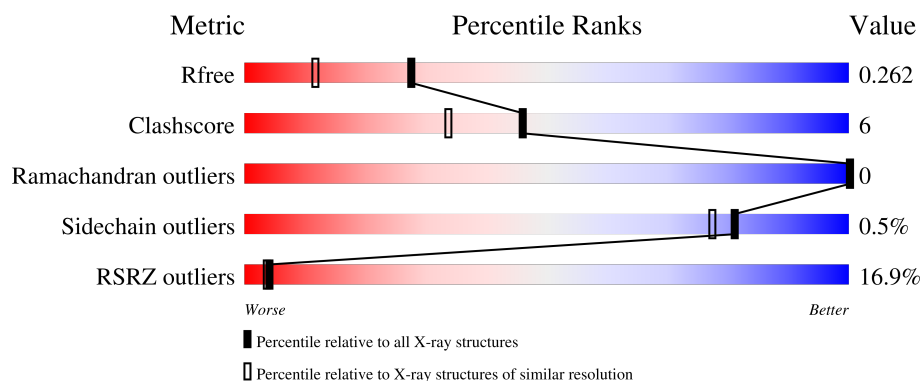
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.86 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}	180053	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	184	12% 65% 9% 26%
1	B	184	12% 62% 9% 29%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2222 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 Translocation and assembly module subunit TamB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	136	Total	C	N	O	S	0	4	0
			1079	682	193	203	1			
1	B	131	Total	C	N	O		0	0	0
			1012	640	180	192				

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1139	LEU	-	expression tag	UNP P39321
A	1140	GLU	-	expression tag	UNP P39321
A	1141	HIS	-	expression tag	UNP P39321
A	1142	HIS	-	expression tag	UNP P39321
A	1143	HIS	-	expression tag	UNP P39321
A	1144	HIS	-	expression tag	UNP P39321
A	1145	HIS	-	expression tag	UNP P39321
A	1146	HIS	-	expression tag	UNP P39321
B	1139	LEU	-	expression tag	UNP P39321
B	1140	GLU	-	expression tag	UNP P39321
B	1141	HIS	-	expression tag	UNP P39321
B	1142	HIS	-	expression tag	UNP P39321
B	1143	HIS	-	expression tag	UNP P39321
B	1144	HIS	-	expression tag	UNP P39321
B	1145	HIS	-	expression tag	UNP P39321
B	1146	HIS	-	expression tag	UNP P39321

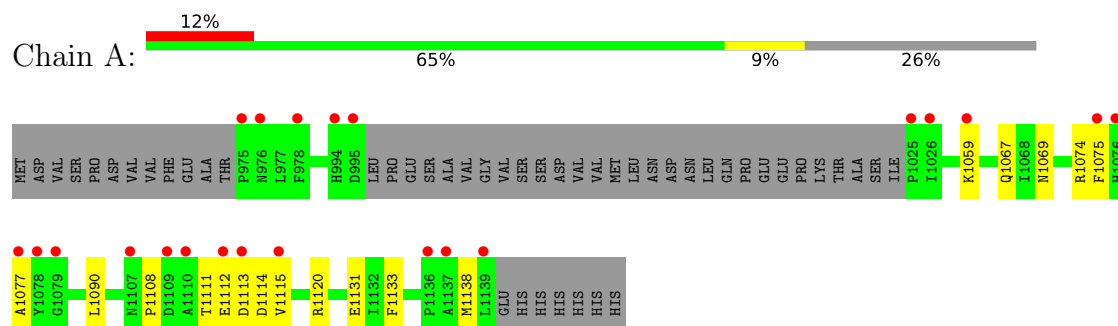
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	77	Total	O	0	0
			77	77		
2	B	54	Total	O	0	0
			54	54		

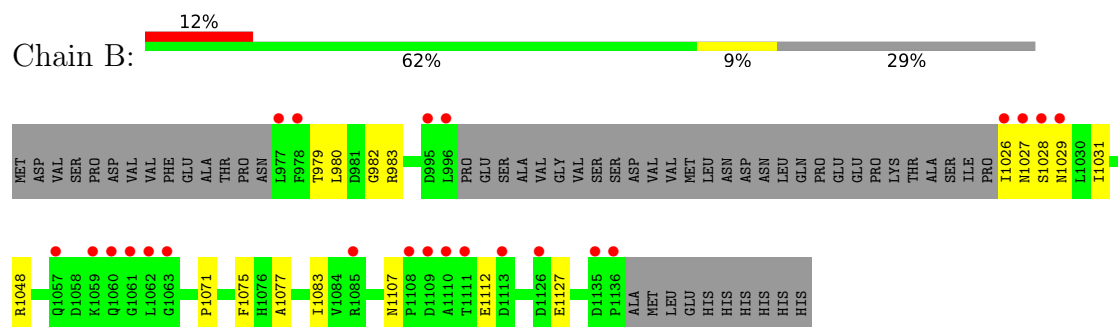
3 Residue-property plots

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 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.

- Molecule 1: Translocation and assembly module subunit TamB



- Molecule 1: Translocation and assembly module subunit TamB



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	57.24Å 57.24Å 220.71Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.57 – 1.86 49.57 – 1.86	Depositor EDS
% Data completeness (in resolution range)	66.2 (49.57-1.86) 66.3 (49.57-1.86)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.61 (at 1.86Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.208 , 0.251 0.214 , 0.262	Depositor DCC
R_{free} test set	1218 reflections (3.29%)	wwPDB-VP
Wilson B-factor (Å ²)	24.2	Xtriage
Anisotropy	0.209	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 52.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.042 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2222	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.43% 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	0.51	0/1100	0.74	0/1495
1	B	0.50	0/1030	0.77	2/1401 (0.1%)
All	All	0.51	0/2130	0.75	2/2896 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	982	GLY	N-CA-C	5.38	118.33	110.63
1	B	1127	GLU	CA-CB-CG	5.04	124.18	114.10

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	1079	0	1064	14	1
1	B	1012	0	1005	10	0
2	A	77	0	0	3	2
2	B	54	0	0	3	0
All	All	2222	0	2069	24	2

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 6.

All (24) 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:A:1067:GLN:HE21	1:A:1069:ASN:HD21	1.26	0.82
1:A:1111:THR:O	2:A:1201:HOH:O	2.09	0.70
1:A:1067:GLN:NE2	1:A:1069:ASN:HD21	1.95	0.62
1:B:979:THR:HG22	1:B:1027:ASN:HB2	1.83	0.60
1:B:983:ARG:HD2	1:B:1031:ILE:HB	1.83	0.59
1:A:1067:GLN:HG3	1:A:1090:LEU:HD12	1.92	0.52
1:A:1067:GLN:HE21	1:A:1069:ASN:ND2	2.01	0.49
1:B:980:LEU:O	1:B:1028:SER:HA	2.14	0.47
1:B:1026:ILE:HG22	1:B:1027:ASN:OD1	2.14	0.47
1:A:1133:PHE:CD1	1:A:1138:MET:HE2	2.51	0.46
1:B:1048:ARG:O	1:B:1071:PRO:HD2	2.15	0.46
1:B:1075:PHE:CZ	1:B:1077:ALA:HB3	2.52	0.45
1:A:1108:PRO:O	1:A:1114:ASP:HB3	2.17	0.44
1:A:1075:PHE:CE2	1:A:1077:ALA:HB2	2.52	0.44
1:B:983:ARG:NE	2:B:1201:HOH:O	2.29	0.44
1:A:1059:LYS:HD3	1:A:1059:LYS:H	1.81	0.44
1:A:1120:ARG:HD2	1:A:1131:GLU:OE2	2.18	0.44
1:A:1113:ASP:O	1:A:1115:VAL:HG23	2.19	0.43
1:B:1112:GLU:HG3	2:B:1250:HOH:O	2.19	0.42
1:B:1083:ILE:HD11	1:B:1107:ASN:ND2	2.34	0.41
1:B:1029:ASN:ND2	2:B:1207:HOH:O	2.53	0.41
1:A:1120:ARG:NH1	1:A:1133:PHE:HZ	2.19	0.41
1:A:1074[A]:ARG:NH1	2:A:1210:HOH:O	2.54	0.40
1:A:1113:ASP:HB2	2:A:1206:HOH:O	2.21	0.40

All (2) 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:A:1210:HOH:O	2:A:1236:HOH:O[5_547]	2.16	0.04
1:A:1059:LYS:NZ	2:A:1275:HOH:O[5_447]	2.19	0.01

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	136/184 (74%)	130 (96%)	6 (4%)	0	100	100
1	B	127/184 (69%)	120 (94%)	7 (6%)	0	100	100
All	All	263/368 (72%)	250 (95%)	13 (5%)	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	116/157 (74%)	115 (99%)	1 (1%)	70	64
1	B	109/157 (69%)	109 (100%)	0	100	100
All	All	225/314 (72%)	224 (100%)	1 (0%)	81	82

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1112	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	976	ASN
1	A	1027	ASN
1	A	1037	ASN
1	A	1054	ASN
1	A	1067	GLN
1	A	1069	ASN
1	A	1101	ASN
1	B	1060	GLN
1	B	1065	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 [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

6.1 Protein, DNA and RNA chains

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	136/184 (73%)	0.52	22 (16%) 4 4	9, 29, 79, 113	4 (2%)
1	B	131/184 (71%)	0.77	23 (17%) 4 3	19, 35, 82, 118	0
All	All	267/368 (72%)	0.64	45 (16%) 4 4	9, 32, 82, 118	4 (1%)

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	977	LEU	8.3
1	B	1026	ILE	8.0
1	A	1139	LEU	7.1
1	A	1025	PRO	6.3
1	A	975	PRO	6.2
1	A	1078	TYR	6.1
1	A	1026	ILE	5.1
1	B	996	LEU	4.8
1	B	1059	LYS	4.5
1	B	1136	PRO	4.4
1	A	1112	GLU	4.3
1	A	995	ASP	4.2
1	A	1136	PRO	4.0
1	B	1109	ASP	4.0
1	B	1062	LEU	3.9
1	A	1079	GLY	3.9
1	B	1060	GLN	3.6
1	B	1110	ALA	3.5
1	B	978	PHE	3.5
1	B	1028	SER	3.5
1	A	1110	ALA	3.5
1	A	976	ASN	3.3
1	A	1109	ASP	3.3
1	B	1027	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	1077	ALA	2.9
1	A	1059	LYS	2.9
1	B	1135	ASP	2.8
1	B	1108	PRO	2.8
1	A	994	HIS	2.7
1	A	1113	ASP	2.6
1	B	1113	ASP	2.6
1	A	1137	ALA	2.5
1	B	1057	GLN	2.5
1	B	995	ASP	2.5
1	A	978[A]	PHE	2.4
1	B	1126	ASP	2.4
1	A	1076	HIS	2.4
1	A	1107	ASN	2.4
1	B	1085	ARG	2.3
1	B	1111	THR	2.2
1	B	1063	GLY	2.2
1	B	1061	GLY	2.2
1	A	1115	VAL	2.1
1	A	1075	PHE	2.0
1	B	1029	ASN	2.0

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 oligosaccharides 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.