



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 08:20 PM UTC

PDB ID : 4DDV / pdb_00004ddv
Title : Thermotoga maritima reverse gyrase, triclinic form
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Deposited on : 2012-01-19
Resolution : 3.46 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

<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
Xtrriage (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

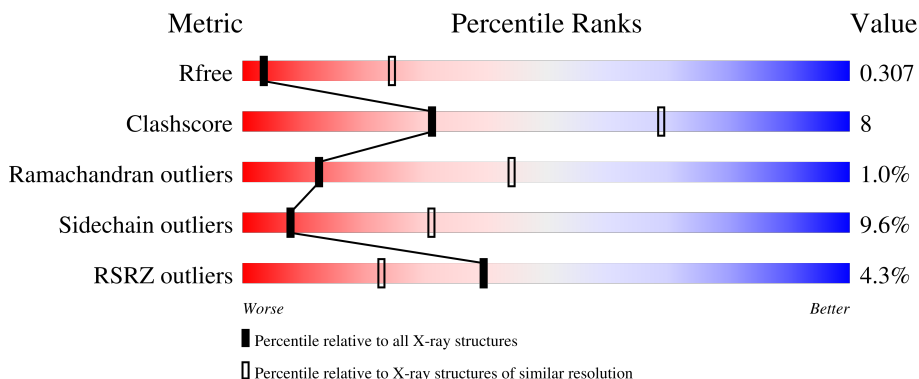
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.46 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	1070 (3.50-3.42)
Clashscore	190562	1128 (3.50-3.42)
Ramachandran outliers	187476	1101 (3.50-3.42)
Sidechain outliers	187428	1102 (3.50-3.42)
RSRZ outliers	180081	1070 (3.50-3.42)

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	1104	
1	B	1104	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18064 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.

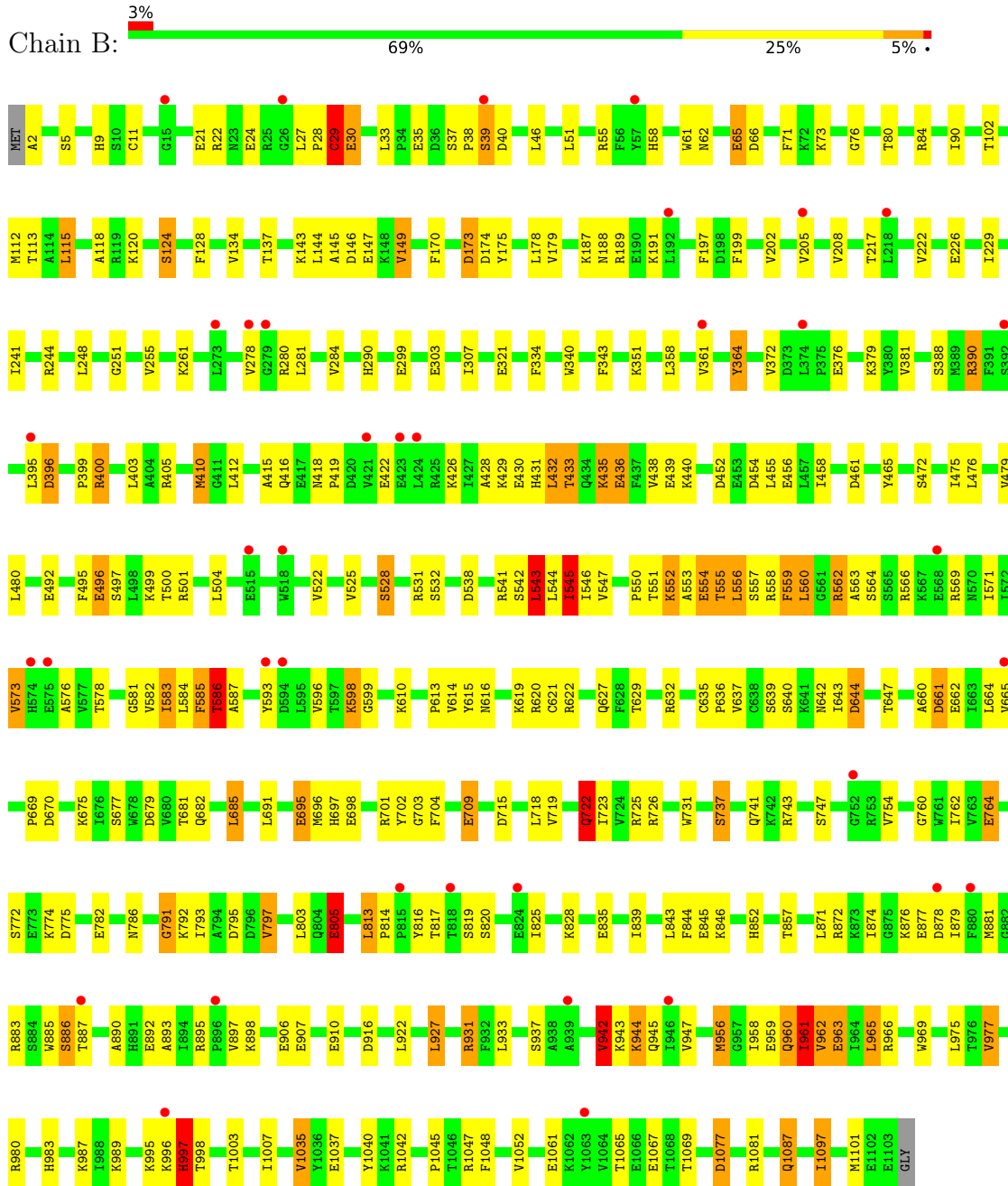
- Molecule 1 is a protein called Reverse gyrase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1102	9030	5759	1563	1682	26	0	0	0
1	B	1102	9030	5759	1563	1682	26	0	0	0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

● Molecule 1: Reverse gyrase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	95.71Å 101.25Å 104.43Å 113.61° 97.50° 110.42°	Depositor
Resolution (Å)	49.11 – 3.46 49.11 – 3.46	Depositor EDS
% Data completeness (in resolution range)	98.3 (49.11-3.46) 98.3 (49.11-3.46)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 3.48Å)	Xtrriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.235 , 0.278 0.260 , 0.307	Depositor DCC
R_{free} test set	2069 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	82.1	Xtrriage
Anisotropy	0.566	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 112.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	18064	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.41 % 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 4.6894e-03. 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 [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	0.75	3/9191 (0.0%)	1.20	34/12356 (0.3%)
1	B	0.94	11/9191 (0.1%)	1.40	70/12356 (0.6%)
All	All	0.85	14/18382 (0.1%)	1.30	104/24712 (0.4%)

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	958	ILE	CG1-CD1	6.48	1.77	1.51
1	B	560	LEU	CA-C	6.35	1.60	1.52
1	B	704	PHE	CA-C	6.23	1.60	1.52
1	B	585	PHE	CA-C	-6.23	1.45	1.52
1	B	563	ALA	C-N	6.18	1.42	1.33

The worst 5 of 104 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	670	ASP	CA-CB-CG	9.64	122.24	112.60
1	A	1048	PHE	CA-CB-CG	9.19	122.99	113.80
1	B	660	ALA	CA-C-N	8.67	132.77	120.28
1	B	660	ALA	C-N-CA	8.67	132.77	120.28
1	B	977	VAL	N-CA-CB	8.57	120.77	111.00

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	9030	0	9187	136	0
1	B	9030	0	9187	165	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
All	All	18064	0	18374	298	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 8.

The worst 5 of 298 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:958:ILE:CD1	1:A:958:ILE:CG1	1.77	1.57
1:B:961:ILE:CD1	1:B:961:ILE:CG1	1.74	1.56
1:B:544:LEU:HD12	1:B:584:LEU:O	1.67	0.95
1:A:14:CYS:HB3	1:A:32:CYS:SG	2.10	0.91
1:A:722:GLN:HE22	1:A:726:ARG:HB2	1.37	0.89

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	1100/1104 (100%)	997 (91%)	95 (9%)	8 (1%)	18	51
1	B	1100/1104 (100%)	988 (90%)	99 (9%)	13 (1%)	10	41
All	All	2200/2208 (100%)	1985 (90%)	194 (9%)	21 (1%)	12	44

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	417	GLU
1	A	792	LYS
1	A	791	GLY
1	B	39	SER
1	B	562	ARG

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	992/993 (100%)	914 (92%)	78 (8%)	11 37
1	B	992/993 (100%)	879 (89%)	113 (11%)	5 25
All	All	1984/1986 (100%)	1793 (90%)	191 (10%)	8 31

5 of 191 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	416	GLN
1	B	647	THR
1	B	432	LEU
1	B	542	SER
1	B	709	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	23	ASN
1	B	346	ASN
1	B	865	ASN
1	B	335	ASN
1	B	431	HIS

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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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 [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 [i](#)

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

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	1102/1104 (99%)	0.56	57 (5%) 33 20	48, 100, 169, 216	0
1	B	1102/1104 (99%)	0.43	37 (3%) 48 29	25, 90, 175, 224	0
All	All	2204/2208 (99%)	0.49	94 (4%) 40 23	25, 96, 174, 224	0

The worst 5 of 94 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	594	ASP	4.8
1	B	15	GLY	4.3
1	A	896	PRO	4.1
1	A	748	ASN	4.1
1	A	851	TYR	3.9

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	ZN	A	2001	1/1	0.98	0.05	137,137,137,137	0
2	ZN	B	2001	1/1	0.98	0.05	137,137,137,137	0
2	ZN	A	2002	1/1	0.99	0.04	75,75,75,75	0
2	ZN	B	2002	1/1	0.99	0.03	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.