



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 15, 2026 – 10:27 AM UTC

PDB ID : 1R87 / pdb\_00001r87  
Title : Crystal structure of the extracellular xylanase from *Geobacillus stearothermophilus* T-6 (XT6, monoclinic form): The complex of the WT enzyme with xylopentaose at 1.67Å resolution  
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Deposited on : 2003-10-23  
Resolution : 1.67 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](mailto: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>.

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

|                                |   |                                                                  |
|--------------------------------|---|------------------------------------------------------------------|
| MolProbity                     | : | <b>FAILED</b>                                                    |
| Mogul                          | : | 2022.3.0, CSD as543be (2022)                                     |
| Xtriage (Phenix)               | : | <b>NOT EXECUTED</b>                                              |
| EDS                            | : | <b>NOT EXECUTED</b>                                              |
| 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 1.67 Å.

There are no overall percentile quality scores available for this entry.

MolProbity failed to run properly; EDS was not executed - the sequence quality summary graphics cannot be shown.

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 3451 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 Endo-1,4-beta-xylanase.

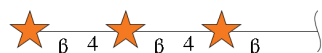
| Mol | Chain | Residues | Atoms |      |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 1   | A     | 371      | Total | C    | N   | O   | S | 0       | 9       | 0     |
|     |       |          | 3087  | 1983 | 526 | 571 | 7 |         |         |       |

- Molecule 2 is an oligosaccharide called beta-D-xylopyranose-(1-4)-beta-D-xylopyranose.



| Mol | Chain | Residues | Atoms |    |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|----|---|---------|---------|-------|
| 2   | B     | 2        | Total | C  | O | 0       | 0       | 0     |
|     |       |          | 19    | 10 | 9 |         |         |       |

- Molecule 3 is an oligosaccharide called beta-D-xylopyranose-(1-4)-beta-D-xylopyranose-(1-4)-beta-D-xylopyranose.



| Mol | Chain | Residues | Atoms |    |    | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|----|----|---------|---------|-------|
| 3   | C     | 3        | Total | C  | O  | 0       | 0       | 0     |
|     |       |          | 28    | 15 | 13 |         |         |       |

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms |    | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---------|---------|
| 4   | A     | 7        | Total | Zn | 0       | 0       |
|     |       |          | 7     | 7  |         |         |

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

| Mol | Chain | Residues | Atoms |    | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---------|---------|
| 5   | A     | 2        | Total | Cl | 0       | 0       |
|     |       |          | 2     | 2  |         |         |

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



| Mol | Chain | Residues | Atoms |   |   | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---------|---------|
| 6   | A     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |

- Molecule 7 is water.

| Mol | Chain | Residues | Atoms |     | ZeroOcc | AltConf |
|-----|-------|----------|-------|-----|---------|---------|
| 7   | A     | 303      | Total | O   | 0       | 0       |
|     |       |          | 303   | 303 |         |         |

MolProbity failed to run properly; EDS was not executed - this section is therefore empty.

### 3 Data and refinement statistics

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

| Property                                                 | Value                                          | Source    |
|----------------------------------------------------------|------------------------------------------------|-----------|
| Space group                                              | C 1 2 1                                        | Depositor |
| Cell constants<br>a, b, c, $\alpha$ , $\beta$ , $\gamma$ | 120.42Å 61.22Å 89.58Å<br>90.00° 119.50° 90.00° | Depositor |
| Resolution (Å)                                           | 25.00 – 1.67                                   | Depositor |
| % Data completeness<br>(in resolution range)             | 97.2 (25.00-1.67)                              | Depositor |
| $R_{merge}$                                              | 0.07                                           | Depositor |
| $R_{sym}$                                                | (Not available)                                | Depositor |
| Refinement program                                       | CNS 1.0                                        | Depositor |
| R, $R_{free}$                                            | 0.169 , 0.186                                  | Depositor |
| Estimated twinning fraction                              | No twinning to report.                         | Xtriage   |
| Total number of atoms                                    | 3451                                           | wwPDB-VP  |
| Average B, all atoms (Å <sup>2</sup> )                   | 25.0                                           | wwPDB-VP  |

## 4 Model quality [i](#)

### 4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 4.3 Torsion angles [i](#)

#### 4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

### 4.5 Carbohydrates [i](#)

5 monosaccharides 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   | XYP  | B     | 1   | 2    | 10,10,10     | 0.70 | 0        | 14,14,14    | 0.64 | 0        |
| 2   | XYP  | B     | 2   | 2    | 9,9,10       | 0.83 | 0        | 10,12,14    | 0.74 | 0        |
| 3   | XYP  | C     | 1   | 3    | 10,10,10     | 0.90 | 0        | 14,14,14    | 0.94 | 1 (7%)   |
| 3   | XYP  | C     | 2   | 3    | 9,9,10       | 1.03 | 0        | 10,12,14    | 0.89 | 0        |
| 3   | XYP  | C     | 3   | 3    | 9,9,10       | 0.86 | 0        | 10,12,14    | 0.61 | 0        |

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   | XYP  | B     | 1   | 2    | -       | -        | 0/1/1/1 |
| 2   | XYP  | B     | 2   | 2    | -       | -        | 0/1/1/1 |
| 3   | XYP  | C     | 1   | 3    | -       | -        | 0/1/1/1 |
| 3   | XYP  | C     | 2   | 3    | -       | -        | 0/1/1/1 |
| 3   | XYP  | C     | 3   | 3    | -       | -        | 0/1/1/1 |

There are no bond length outliers.

All (1) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms    | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|-------|-------------|----------|
| 3   | C     | 1   | XYP  | C4-C3-C2 | -2.02 | 107.31      | 110.86   |

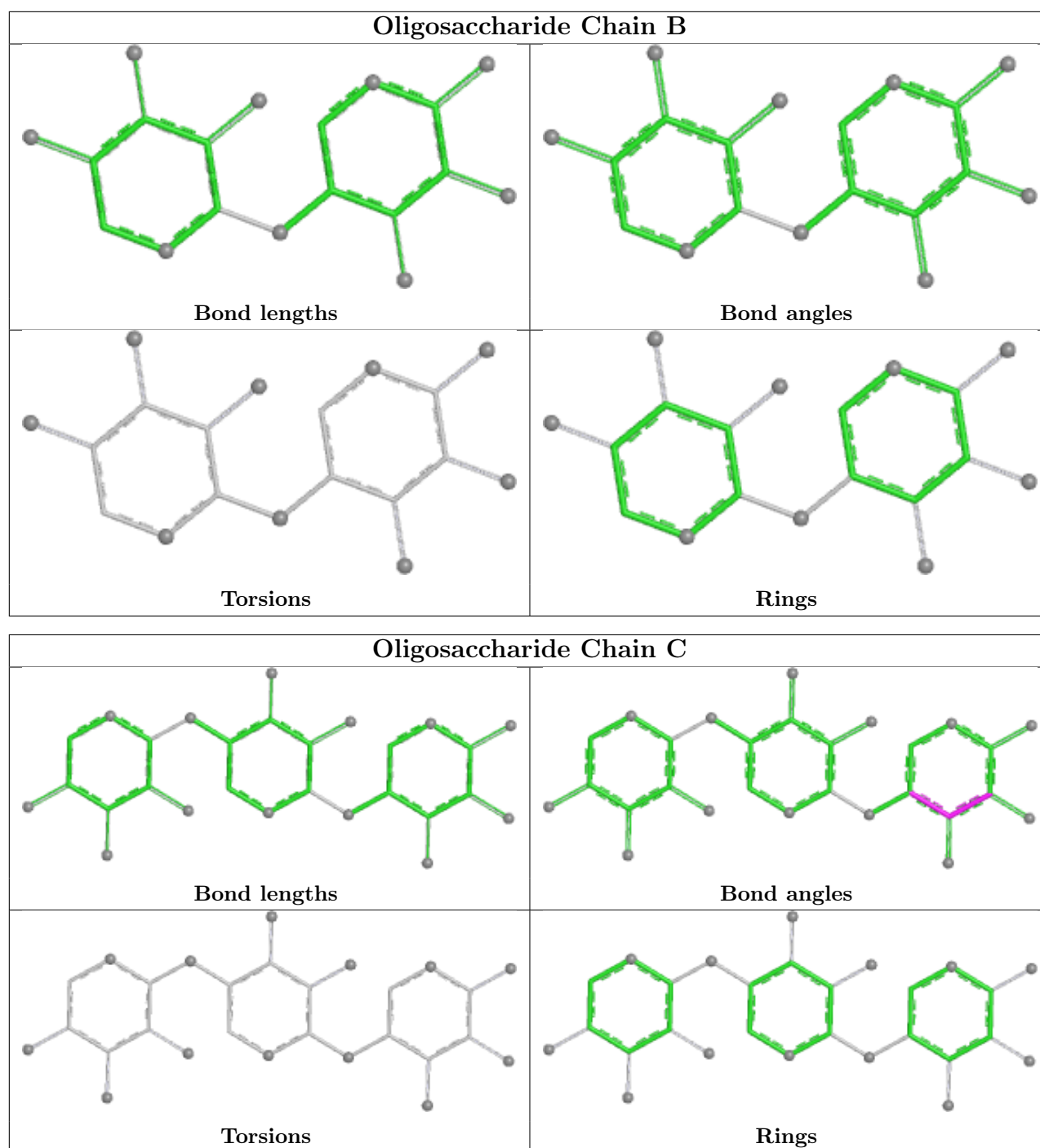
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



## 4.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 9 are monoatomic - leaving 1 for Mogul analysis.

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 | $\# Z  > 2$ |
| 6   | SO4  | A     | 801 | 4    | 4,4,4        | 0.64 | 0           | 6,6,6       | 0.31 | 0           |

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.

## 4.7 Other polymers [i](#)

There are no such residues in this entry.

## 4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 5 Fit of model and data

### 5.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

### 5.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

### 5.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 5.4 Ligands

EDS was not executed - this section is therefore empty.

### 5.5 Other polymers

EDS was not executed - this section is therefore empty.