



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2025 – 03:35 PM EDT

PDB ID : 3DEW  
Title : The structure of a putative TetR family transcriptional regulator from *Geobacter sulfurreducens* PCA.  
Authors : Cuff, M.E.; Bigelow, L.; Abdullah, J.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)  
Deposited on : 2008-06-10  
Resolution : 1.75 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                     | : | 4.02b-467  |
| Mogul                          | : | 2022.3.0, CSD as543be (2022)                                       |
| Xtriage (Phenix)               | : | 1.21   |
| EDS                            | : | 3.0  |
| Percentile statistics          | : | 20231227.v01 (using entries in the PDB archive December 27th 2023) |
| CCP4                           | : | 9.0.004 (Gargrove)   |
| Density-Fitness                | : | 1.0.11   |
| Ideal geometry (proteins)      | : | Engh & Huber (2001)  |
| Ideal geometry (DNA, RNA)      | : | Parkinson et al. (1996)  |
| Validation Pipeline (wwPDB-VP) | : | 2.41.4   |



















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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|----------|-------|
| 4   | EDO  | A     | 206 | -    | -       | 1/1/1/1  | -     |
| 4   | EDO  | A     | 208 | -    | -       | 1/1/1/1  | -     |
| 4   | EDO  | A     | 207 | -    | -       | 1/1/1/1  | -     |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms       |
|-----|-------|-----|------|-------------|
| 4   | A     | 207 | EDO  | O1-C1-C2-O2 |
| 4   | A     | 208 | EDO  | O1-C1-C2-O2 |
| 4   | A     | 206 | EDO  | O1-C1-C2-O2 |

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.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.