



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 29, 2026 – 05:24 PM UTC

PDB ID : 4XKT / pdb\_00004xkt  
Title : E coli BFR variant Y149F  
Authors : Bradley, J.M.; Hemmings, A.M.; Le Brun, N.E.  
Deposited on : 2015-01-12  
Resolution : 1.82 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)               | : | 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                                                             |

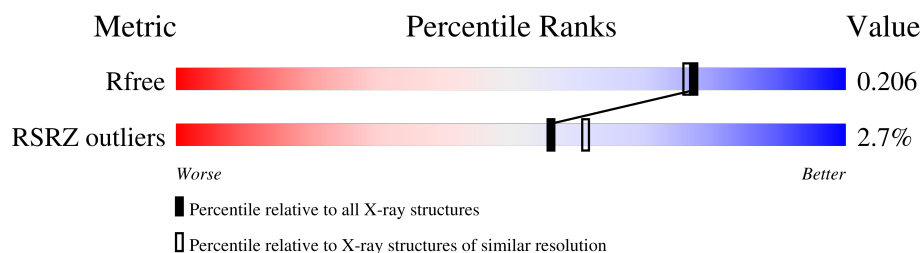
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.82 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<br>(#Entries) | Similar resolution<br>(#Entries, resolution range(Å)) |
|---------------|-----------------------------|-------------------------------------------------------|
| $R_{free}$    | 180053                      | 1112 (1.82-1.82)                                      |
| RSRZ outliers | 180081                      | 1112 (1.82-1.82)                                      |

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19321 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 Bacterioferritin.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 1   | A     | 158      | Total | C   | N   | O   | S | 0       | 15      | 1     |
|     |       |          | 1393  | 879 | 231 | 276 | 7 |         |         |       |
| 1   | B     | 158      | Total | C   | N   | O   | S | 0       | 16      | 1     |
|     |       |          | 1396  | 883 | 234 | 272 | 7 |         |         |       |
| 1   | C     | 158      | Total | C   | N   | O   | S | 0       | 14      | 1     |
|     |       |          | 1376  | 872 | 229 | 268 | 7 |         |         |       |
| 1   | D     | 158      | Total | C   | N   | O   | S | 0       | 12      | 1     |
|     |       |          | 1365  | 864 | 231 | 263 | 7 |         |         |       |
| 1   | E     | 158      | Total | C   | N   | O   | S | 0       | 13      | 1     |
|     |       |          | 1374  | 870 | 229 | 268 | 7 |         |         |       |
| 1   | F     | 158      | Total | C   | N   | O   | S | 0       | 15      | 1     |
|     |       |          | 1390  | 877 | 236 | 270 | 7 |         |         |       |
| 1   | G     | 158      | Total | C   | N   | O   | S | 0       | 16      | 1     |
|     |       |          | 1392  | 881 | 233 | 271 | 7 |         |         |       |
| 1   | H     | 158      | Total | C   | N   | O   | S | 0       | 13      | 1     |
|     |       |          | 1379  | 868 | 233 | 271 | 7 |         |         |       |
| 1   | I     | 158      | Total | C   | N   | O   | S | 0       | 14      | 1     |
|     |       |          | 1375  | 869 | 232 | 267 | 7 |         |         |       |
| 1   | J     | 158      | Total | C   | N   | O   | S | 0       | 8       | 1     |
|     |       |          | 1337  | 845 | 225 | 260 | 7 |         |         |       |
| 1   | K     | 158      | Total | C   | N   | O   | S | 0       | 10      | 1     |
|     |       |          | 1350  | 852 | 227 | 264 | 7 |         |         |       |
| 1   | L     | 158      | Total | C   | N   | O   | S | 0       | 11      | 1     |
|     |       |          | 1360  | 860 | 228 | 265 | 7 |         |         |       |

There are 12 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment             | Reference  |
|-------|---------|----------|--------|---------------------|------------|
| A     | 149     | PHE      | TYR    | engineered mutation | UNP E2QFJ1 |
| B     | 149     | PHE      | TYR    | engineered mutation | UNP E2QFJ1 |
| C     | 149     | PHE      | TYR    | engineered mutation | UNP E2QFJ1 |
| D     | 149     | PHE      | TYR    | engineered mutation | UNP E2QFJ1 |
| E     | 149     | PHE      | TYR    | engineered mutation | UNP E2QFJ1 |

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| Chain | Residue | Modelled | Actual | Comment             | Reference  |
|-------|---------|----------|--------|---------------------|------------|
| F     | 149     | PHE      | TYR    | engineered mutation | UNP E2QFJ1 |
| G     | 149     | PHE      | TYR    | engineered mutation | UNP E2QFJ1 |
| H     | 149     | PHE      | TYR    | engineered mutation | UNP E2QFJ1 |
| I     | 149     | PHE      | TYR    | engineered mutation | UNP E2QFJ1 |
| J     | 149     | PHE      | TYR    | engineered mutation | UNP E2QFJ1 |
| K     | 149     | PHE      | TYR    | engineered mutation | UNP E2QFJ1 |
| L     | 149     | PHE      | TYR    | engineered mutation | UNP E2QFJ1 |

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



| Mol | Chain | Residues | Atoms |   |   | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---------|---------|
| 2   | B     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |
| 2   | C     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |
| 2   | C     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |
| 2   | C     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |
| 2   | D     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |
| 2   | E     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |
| 2   | F     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |
| 2   | G     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |

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| Mol | Chain | Residues | Atoms |   |   | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---------|---------|
| 2   | H     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |
| 2   | H     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |
| 2   | J     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |
| 2   | K     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |
| 2   | L     | 1        | Total | O | S | 0       | 0       |
|     |       |          | 5     | 4 | 1 |         |         |

- Molecule 3 is water.

| Mol | Chain | Residues | Atoms |     | ZeroOcc | AltConf |
|-----|-------|----------|-------|-----|---------|---------|
| 3   | A     | 233      | Total | O   | 0       | 0       |
|     |       |          | 233   | 233 |         |         |
| 3   | B     | 234      | Total | O   | 0       | 0       |
|     |       |          | 234   | 234 |         |         |
| 3   | C     | 246      | Total | O   | 0       | 0       |
|     |       |          | 246   | 246 |         |         |
| 3   | D     | 231      | Total | O   | 0       | 0       |
|     |       |          | 231   | 231 |         |         |
| 3   | E     | 228      | Total | O   | 0       | 0       |
|     |       |          | 228   | 228 |         |         |
| 3   | F     | 232      | Total | O   | 0       | 0       |
|     |       |          | 232   | 232 |         |         |
| 3   | G     | 236      | Total | O   | 0       | 0       |
|     |       |          | 236   | 236 |         |         |
| 3   | H     | 220      | Total | O   | 0       | 0       |
|     |       |          | 220   | 220 |         |         |
| 3   | I     | 219      | Total | O   | 0       | 0       |
|     |       |          | 219   | 219 |         |         |
| 3   | J     | 229      | Total | O   | 0       | 0       |
|     |       |          | 229   | 229 |         |         |
| 3   | K     | 230      | Total | O   | 0       | 0       |
|     |       |          | 230   | 230 |         |         |
| 3   | L     | 231      | Total | O   | 0       | 0       |
|     |       |          | 231   | 231 |         |         |

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### 3 Data and refinement statistics

| Property                                                                | Value                                                       | Source           |
|-------------------------------------------------------------------------|-------------------------------------------------------------|------------------|
| Space group                                                             | P 42 21 2                                                   | Depositor        |
| Cell constants<br>a, b, c, $\alpha$ , $\beta$ , $\gamma$                | 208.47Å 208.47Å 142.94Å<br>90.00° 90.00° 90.00°             | Depositor        |
| Resolution (Å)                                                          | 31.75 – 1.82<br>31.75 – 1.82                                | Depositor<br>EDS |
| % Data completeness<br>(in resolution range)                            | 99.5 (31.75-1.82)<br>99.8 (31.75-1.82)                      | Depositor<br>EDS |
| $R_{merge}$                                                             | 0.13                                                        | Depositor        |
| $R_{sym}$                                                               | (Not available)                                             | Depositor        |
| $\langle I/\sigma(I) \rangle$ <sup>1</sup>                              | 5.64 (at 1.82Å)                                             | Xtriage          |
| Refinement program                                                      | PHENIX (phenix.refine: 1.8.2_1309)                          | Depositor        |
| R, $R_{free}$                                                           | 0.167 , 0.206<br>0.170 , 0.206                              | Depositor<br>DCC |
| $R_{free}$ test set                                                     | 13933 reflections (5.02%)                                   | wwPDB-VP         |
| Wilson B-factor (Å <sup>2</sup> )                                       | 14.8                                                        | Xtriage          |
| Anisotropy                                                              | 0.069                                                       | Xtriage          |
| Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> ) | 0.37 , 55.0                                                 | EDS              |
| L-test for twinning <sup>2</sup>                                        | $\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$ | Xtriage          |
| Estimated twinning fraction                                             | No twinning to report.                                      | Xtriage          |
| $F_o, F_c$ correlation                                                  | 0.97                                                        | EDS              |
| Total number of atoms                                                   | 19321                                                       | wwPDB-VP         |
| Average B, all atoms (Å <sup>2</sup> )                                  | 14.0                                                        | wwPDB-VP         |

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 49.41 % 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 7.4915e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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.

## 4 Model quality [i](#)

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

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

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

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

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#### 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](#)

There are no oligosaccharides in this entry.

### 4.6 Ligand geometry [i](#)

13 ligands 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   | SO4  | C     | 201 | -    | 4,4,4        | 0.20 | 0           | 6,6,6       | 0.18 | 0           |
| 2   | SO4  | E     | 201 | -    | 4,4,4        | 0.21 | 0           | 6,6,6       | 0.23 | 0           |
| 2   | SO4  | H     | 201 | -    | 4,4,4        | 0.23 | 0           | 6,6,6       | 0.13 | 0           |
| 2   | SO4  | H     | 202 | -    | 4,4,4        | 0.28 | 0           | 6,6,6       | 0.10 | 0           |
| 2   | SO4  | K     | 201 | -    | 4,4,4        | 0.25 | 0           | 6,6,6       | 0.13 | 0           |
| 2   | SO4  | C     | 203 | -    | 4,4,4        | 0.26 | 0           | 6,6,6       | 0.14 | 0           |
| 2   | SO4  | L     | 201 | -    | 4,4,4        | 0.26 | 0           | 6,6,6       | 0.10 | 0           |
| 2   | SO4  | G     | 201 | -    | 4,4,4        | 0.20 | 0           | 6,6,6       | 0.09 | 0           |
| 2   | SO4  | J     | 201 | -    | 4,4,4        | 0.28 | 0           | 6,6,6       | 0.11 | 0           |
| 2   | SO4  | D     | 201 | -    | 4,4,4        | 0.26 | 0           | 6,6,6       | 0.09 | 0           |
| 2   | SO4  | B     | 201 | -    | 4,4,4        | 0.23 | 0           | 6,6,6       | 0.08 | 0           |
| 2   | SO4  | C     | 202 | -    | 4,4,4        | 0.22 | 0           | 6,6,6       | 0.08 | 0           |
| 2   | SO4  | F     | 201 | -    | 4,4,4        | 0.21 | 0           | 6,6,6       | 0.09 | 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 [i](#)

### 5.1 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, 95<sup>th</sup> 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 <sup>2</sup> ) | Q < 0.9  |
|-----|-------|------------------|--------|-----------|----|----|-----------------------|----------|
| 1   | A     | 158/158 (100%)   | -0.53  | 5 (3%)    | 50 | 57 | 3, 9, 19, 77          | 15 (9%)  |
| 1   | B     | 158/158 (100%)   | -0.59  | 4 (2%)    | 58 | 64 | 4, 9, 21, 78          | 16 (10%) |
| 1   | C     | 158/158 (100%)   | -0.60  | 4 (2%)    | 58 | 64 | 4, 9, 20, 77          | 14 (8%)  |
| 1   | D     | 158/158 (100%)   | -0.54  | 4 (2%)    | 58 | 64 | 4, 9, 22, 86          | 12 (7%)  |
| 1   | E     | 158/158 (100%)   | -0.57  | 6 (3%)    | 44 | 50 | 4, 9, 22, 83          | 13 (8%)  |
| 1   | F     | 158/158 (100%)   | -0.62  | 3 (1%)    | 66 | 72 | 3, 9, 19, 81          | 15 (9%)  |
| 1   | G     | 158/158 (100%)   | -0.59  | 5 (3%)    | 50 | 57 | 4, 8, 20, 79          | 16 (10%) |
| 1   | H     | 158/158 (100%)   | -0.58  | 5 (3%)    | 50 | 57 | 4, 9, 20, 82          | 13 (8%)  |
| 1   | I     | 158/158 (100%)   | -0.64  | 3 (1%)    | 66 | 72 | 4, 9, 21, 76          | 14 (8%)  |
| 1   | J     | 158/158 (100%)   | -0.58  | 5 (3%)    | 50 | 57 | 4, 9, 22, 80          | 8 (5%)   |
| 1   | K     | 158/158 (100%)   | -0.57  | 4 (2%)    | 58 | 64 | 4, 9, 19, 80          | 10 (6%)  |
| 1   | L     | 158/158 (100%)   | -0.61  | 4 (2%)    | 58 | 64 | 4, 9, 21, 80          | 11 (6%)  |
| All | All   | 1896/1896 (100%) | -0.59  | 52 (2%)   | 56 | 61 | 3, 9, 21, 86          | 157 (8%) |

The worst 5 of 52 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1   | H     | 158 | GLY  | 7.3  |
| 1   | A     | 158 | GLY  | 7.0  |
| 1   | D     | 158 | GLY  | 6.2  |
| 1   | F     | 158 | GLY  | 6.0  |
| 1   | E     | 158 | GLY  | 5.9  |

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

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

### 5.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.4 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, 95<sup>th</sup> 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( $\text{\AA}^2$ ) | Q<0.9 |
|-----|------|-------|-----|-------|------|------|-----------------------------|-------|
| 2   | SO4  | J     | 201 | 5/5   | 0.77 | 0.34 | 38,44,48,51                 | 0     |
| 2   | SO4  | C     | 202 | 5/5   | 0.81 | 0.23 | 72,76,77,81                 | 0     |
| 2   | SO4  | D     | 201 | 5/5   | 0.92 | 0.12 | 40,45,48,54                 | 0     |
| 2   | SO4  | C     | 203 | 5/5   | 0.92 | 0.15 | 45,46,47,51                 | 0     |
| 2   | SO4  | F     | 201 | 5/5   | 0.93 | 0.10 | 46,52,53,58                 | 0     |
| 2   | SO4  | H     | 202 | 5/5   | 0.94 | 0.10 | 44,47,52,52                 | 0     |
| 2   | SO4  | K     | 201 | 5/5   | 0.94 | 0.18 | 39,40,45,50                 | 0     |
| 2   | SO4  | L     | 201 | 5/5   | 0.94 | 0.15 | 41,43,46,48                 | 0     |
| 2   | SO4  | G     | 201 | 5/5   | 0.96 | 0.08 | 44,49,56,61                 | 0     |
| 2   | SO4  | C     | 201 | 5/5   | 0.99 | 0.03 | 10,11,11,12                 | 0     |
| 2   | SO4  | E     | 201 | 5/5   | 0.99 | 0.04 | 11,12,14,16                 | 0     |
| 2   | SO4  | B     | 201 | 5/5   | 1.00 | 0.02 | 8,10,12,13                  | 0     |
| 2   | SO4  | H     | 201 | 5/5   | 1.00 | 0.02 | 10,10,11,12                 | 0     |

### 5.5 Other polymers [i](#)

There are no such residues in this entry.