



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 25, 2026 – 09:34 PM UTC

PDB ID : 9KVM / pdb\_00009kvm  
Title : Neutron and X-ray joint refined structure of a copper-containing nitrite reductase (C135A mutant) in complex with formate  
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Deposited on : 2024-12-05  
Resolution : 1.20 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                     | : | 4-5-2 with Phenix2.0                                             |
| Mogul                          | : | 2022.3.0, CSD as543be (2022)                                     |
| Xtriage (Phenix)               | : | 2.0                                                              |
| EDS                            | : | <b>FAILED</b>                                                    |
| Buster-report                  | : | wwPDB partial adaption of 1.1.7 (2018)                           |
| 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                                                             |

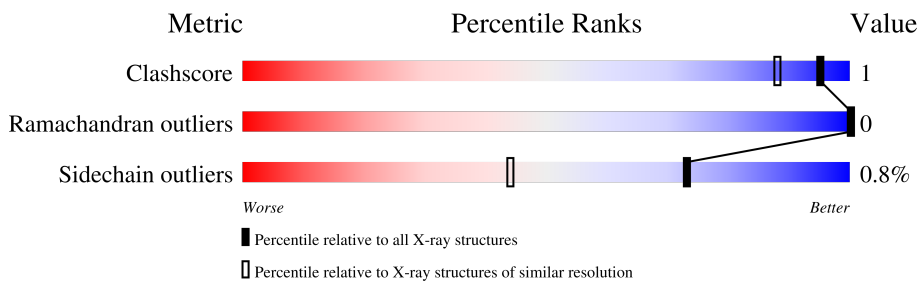
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION, NEUTRON DIFFRACTION*

The reported resolution of this entry is 1.20 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)) |
|-----------------------|-----------------------------|-------------------------------------------------------|
| Clashscore            | 190562                      | 1265 (1.20-1.20)                                      |
| Ramachandran outliers | 187476                      | 1226 (1.20-1.20)                                      |
| Sidechain outliers    | 187428                      | 1226 (1.20-1.20)                                      |

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  $\geq 3$ , 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  $\leq 5\%$ .

Note EDS failed to run properly.

| Mol | Chain | Length | Quality of chain                                                                                                                        |
|-----|-------|--------|-----------------------------------------------------------------------------------------------------------------------------------------|
| 1   | A     | 323    | <br>90% <span style="margin-left: 150px;">7%</span> |

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

| Mol | Type | Chain | Res    | Chirality | Geometry | Clashes | Electron density |
|-----|------|-------|--------|-----------|----------|---------|------------------|
| 3   | FMT  | A     | 405[A] | -         | -        | X       | -                |

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5631 atoms, of which 2159 are hydrogens and 701 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 Copper-containing nitrite reductase.

| Mol | Chain | Residues | Atoms |      |     |      |     |     |    | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|-----|-----|----|---------|---------|-------|
| 1   | A     | 301      | Total | C    | D   | H    | N   | O   | S  | 0       | 114     | 0     |
|     |       |          | 5033  | 1613 | 346 | 2159 | 430 | 469 | 16 |         |         |       |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| A     | 1       | MET      | -      | initiating methionine | UNP A4IL26 |
| A     | 135     | ALA      | CYS    | engineered mutation   | UNP A4IL26 |

- Molecule 2 is COPPER (II) ION (CCD ID: CU) (formula: Cu) (labeled as "Ligand of Interest" by depositor).

| Mol | Chain | Residues | Atoms |    | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---------|---------|
| 2   | A     | 4        | Total | Cu | 0       | 1       |
|     |       |          | 4     | 4  |         |         |

- Molecule 3 is FORMIC ACID (CCD ID: FMT) (formula: CH<sub>2</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



| Mol | Chain | Residues | Atoms |   |   |   | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---|---------|---------|
| 3   | A     | 1        | Total | C | D | O | 0       | 1       |
|     |       |          | 4     | 1 | 1 | 2 |         |         |

- Molecule 4 is water.

| Mol | Chain | Residues | Atoms |     |     | ZeroOcc | AltConf |
|-----|-------|----------|-------|-----|-----|---------|---------|
| 4   | A     | 227      | Total | D   | O   | 0       | 12      |
|     |       |          | 590   | 354 | 236 |         |         |

### 3 Residue-property plots [i](#)

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. 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. 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.

Note EDS failed to run properly.

- Molecule 1: Copper-containing nitrite reductase

Chain A:  90% 7%



## 4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

| Property                                                 | Value                                                       | Source    |
|----------------------------------------------------------|-------------------------------------------------------------|-----------|
| Space group                                              | H 3                                                         | Depositor |
| Cell constants<br>a, b, c, $\alpha$ , $\beta$ , $\gamma$ | 116.17Å 116.17Å 85.61Å<br>90.00° 90.00° 120.00°             | Depositor |
| Resolution (Å)                                           | 39.39 – 1.20                                                | Depositor |
| % Data completeness<br>(in resolution range)             | 100.0 (39.39-1.20)                                          | Depositor |
| $R_{merge}$                                              | 0.26                                                        | Depositor |
| $R_{sym}$                                                | (Not available)                                             | Depositor |
| $\langle I/\sigma(I) \rangle$ <sup>1</sup>               | 1.44 (at 1.20Å)                                             | Xtriage   |
| Refinement program                                       | PHENIX 1.19.2_4158                                          | Depositor |
| R, $R_{free}$                                            | 0.114 , 0.118                                               | Depositor |
| Wilson B-factor (Å <sup>2</sup> )                        | 11.8                                                        | Xtriage   |
| Anisotropy                                               | 0.361                                                       | Xtriage   |
| L-test for twinning <sup>2</sup>                         | $\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$ | Xtriage   |
| Estimated twinning fraction                              | 0.019 for h,-h-k,-l                                         | Xtriage   |
| Total number of atoms                                    | 5631                                                        | wwPDB-VP  |
| Average B, all atoms (Å <sup>2</sup> )                   | 31.0                                                        | wwPDB-VP  |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.60% of the height of the origin peak. No significant pseudotranslation is detected.*

<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.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CU, FMT

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     | 0.43         | 4/3334 (0.1%) | 0.60        | 0/4538      |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1   | A     | 0                   | 1                   |

All (4) bond length outliers are listed below:

| Mol | Chain | Res   | Type | Atoms  | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|-------|------|--------|-------|-------------|----------|
| 1   | A     | 34[A] | GLU  | CD-OE2 | -6.88 | 1.19        | 1.33     |
| 1   | A     | 34[B] | GLU  | CD-OE2 | -6.88 | 1.19        | 1.33     |
| 1   | A     | 34[A] | GLU  | CD-OE1 | 5.91  | 1.30        | 1.19     |
| 1   | A     | 34[B] | GLU  | CD-OE1 | 5.91  | 1.30        | 1.19     |

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group   |
|-----|-------|-----|------|---------|
| 1   | A     | 292 | VAL  | Peptide |

### 5.2 Too-close contacts

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     | 2874  | 2159     | 1810     | 3       | 1            |
| 2   | A     | 4     | 0        | 0        | 0       | 1            |
| 3   | A     | 4     | 0        | 1        | 2       | 0            |
| 4   | A     | 590   | 0        | 0        | 4       | 0            |
| All | All   | 3472  | 2159     | 1811     | 5       | 1            |

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 1.

All (5) 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:122[B]:THR:HG21 | 4:A:651:HOH:O     | 1.96                     | 0.60              |
| 3:A:405[A]:FMT:O2   | 4:A:501[A]:HOH:O  | 2.20                     | 0.58              |
| 1:A:17:VAL:HG23     | 1:A:180[B]:TYR:OH | 2.01                     | 0.56              |
| 3:A:405[A]:FMT:O1   | 4:A:502[A]:HOH:O  | 2.25                     | 0.43              |
| 1:A:198[B]:SER:OG   | 4:A:539[B]:HOH:O  | 2.26                     | 0.41              |

All (1) 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) |
|--------------------|-------------------------|--------------------------|-------------------|
| 1:A:244[A]:HIS:NE2 | 2:A:404[B]:CU:CU[3_555] | 1.70                     | 0.50              |

## 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     | 415/323 (128%) | 403 (97%) | 12 (3%) | 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     | 362/276 (131%) | 359 (99%) | 3 (1%)   | 73 44       |

All (3) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res    | Type |
|-----|-------|--------|------|
| 1   | A     | 22     | LYS  |
| 1   | A     | 123[A] | TYR  |
| 1   | A     | 123[B] | TYR  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | A     | 16  | ASN  |
| 1   | A     | 233 | ASN  |
| 1   | A     | 295 | GLN  |

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

Of 5 ligands modelled in this entry, 4 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 | $\# Z  > 2$ |
| 3   | FMT  | A     | 405[A] | 2    | 2,2,2        | 0.86 | 0           | 1,1,1       | 0.45 | 0           |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

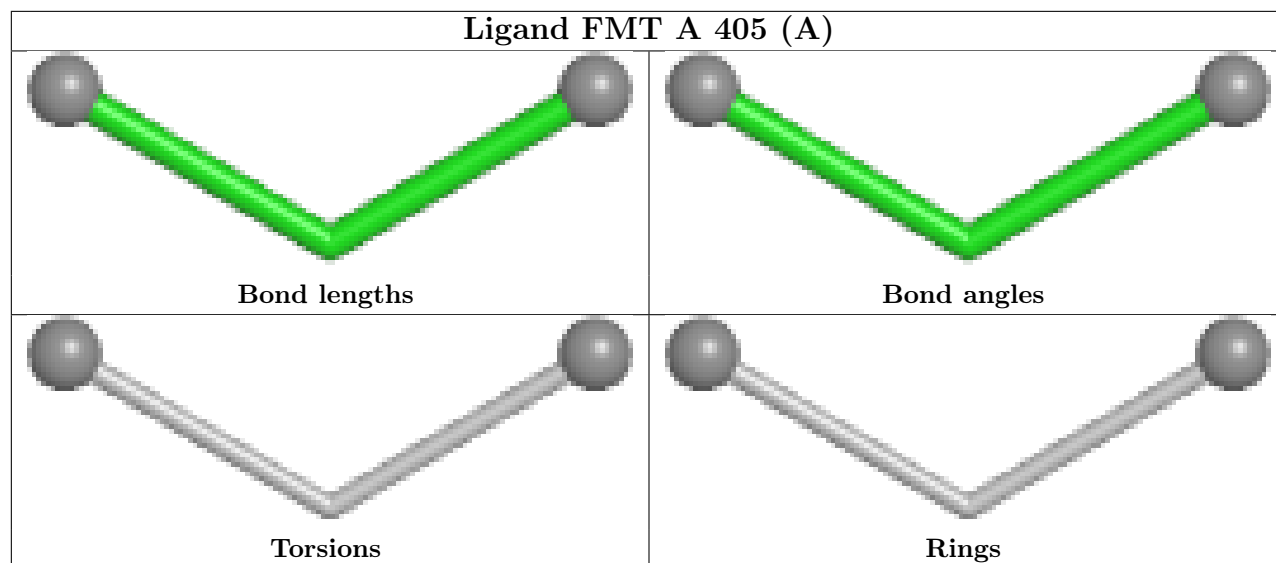
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

| Mol | Chain | Res    | Type | Clashes | Symm-Clashes |
|-----|-------|--------|------|---------|--------------|
| 3   | A     | 405[A] | FMT  | 2       | 0            |

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight  $> 250$  and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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](#)

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

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

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

### 6.3 Carbohydrates [i](#)

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

### 6.4 Ligands [i](#)

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

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

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