



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 1, 2017 – 08:36 PM EDT

PDB ID : 1NS2
Title : Crystal structure of galactose mutarotase from *Lactococcus lactis* mutant E304A complexed with galactose
Authors : Holden, H.M.; Thoden, J.B.
Deposited on : unknown
Resolution : 1.95 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : **FAILED**
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

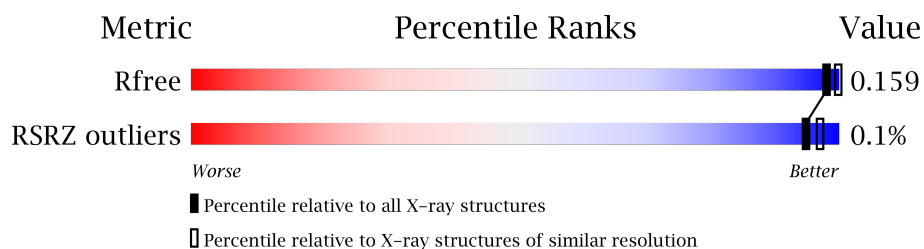
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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} | 100719 | 2004 (1.96-1.96) |
| RSRZ outliers | 101464 | 2018 (1.96-1.96) |

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

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5787 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 GALACTOSE MUTAROTASE.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 1 | A | 339 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 2645 | 1669 | 447 | 526 | 3 | | | |
| 1 | B | 346 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2713 | 1709 | 466 | 535 | 3 | | | |

There are 20 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|------------------|------------|
| A | 2 | SER | GLU | CLONING ARTIFACT | UNP Q9ZB17 |
| A | 304 | ALA | GLU | ENGINEERED | UNP Q9ZB17 |
| A | 340 | LEU | - | EXPRESSION TAG | UNP Q9ZB17 |
| A | 341 | GLU | - | EXPRESSION TAG | UNP Q9ZB17 |
| A | 342 | HIS | - | EXPRESSION TAG | UNP Q9ZB17 |
| A | 343 | HIS | - | EXPRESSION TAG | UNP Q9ZB17 |
| A | 344 | HIS | - | EXPRESSION TAG | UNP Q9ZB17 |
| A | 345 | HIS | - | EXPRESSION TAG | UNP Q9ZB17 |
| A | 346 | HIS | - | EXPRESSION TAG | UNP Q9ZB17 |
| A | 347 | HIS | - | EXPRESSION TAG | UNP Q9ZB17 |
| B | 2 | SER | GLU | CLONING ARTIFACT | UNP Q9ZB17 |
| B | 304 | ALA | GLU | ENGINEERED | UNP Q9ZB17 |
| B | 340 | LEU | - | EXPRESSION TAG | UNP Q9ZB17 |
| B | 341 | GLU | - | EXPRESSION TAG | UNP Q9ZB17 |
| B | 342 | HIS | - | EXPRESSION TAG | UNP Q9ZB17 |
| B | 343 | HIS | - | EXPRESSION TAG | UNP Q9ZB17 |
| B | 344 | HIS | - | EXPRESSION TAG | UNP Q9ZB17 |
| B | 345 | HIS | - | EXPRESSION TAG | UNP Q9ZB17 |
| B | 346 | HIS | - | EXPRESSION TAG | UNP Q9ZB17 |
| B | 347 | HIS | - | EXPRESSION TAG | UNP Q9ZB17 |

- Molecule 2 is BETA-D-GALACTOSE (three-letter code: GAL) (formula: C₆H₁₂O₆).



| Mol | Chain | Residues | Atoms | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---------|---------|
| 2 | A | 1 | Total | C | O | 0 | 1 |
| | | | 13 | 6 | 7 | | |
| 2 | B | 1 | Total | C | O | 0 | 1 |
| | | | 13 | 6 | 7 | | |

- Molecule 3 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---------|---------|
| 3 | A | 1 | Total | Ni | 0 | 0 |
| | | | 1 | 1 | | |

- Molecule 4 is water.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|-----|---------|---------|
| 4 | A | 178 | Total | O | 0 | 0 |
| | | | 178 | 178 | | |
| 4 | B | 224 | Total | O | 0 | 0 |
| | | | 224 | 224 | | |

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3 Data and refinement statistics

| Property | Value | Source |
|---|---|------------------|
| Space group | P 21 21 21 | Depositor |
| Cell constants a, b, c, α , β , γ | 44.80 Å 76.40 Å 211.40 Å 90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 30.00 – 1.95 61.92 – 1.91 | Depositor EDS |
| % Data completeness (in resolution range) | 94.1 (30.00-1.95) 92.5 (61.92-1.91) | Depositor EDS |
| R_{merge} | (Not available) | Depositor |
| R_{sym} | 0.07 | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 1.68 (at 1.91 Å) | Xtriage |
| Refinement program | TNT | Depositor |
| R, R_{free} | 0.163 , 0.229 0.160 , 0.159 | Depositor DCC |
| R_{free} test set | 5088 reflections (11.12%) | DCC |
| Wilson B-factor (Å ²) | 20.8 | Xtriage |
| Anisotropy | 0.180 | Xtriage |
| Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²) | 0.31 , 103.0 | EDS |
| L-test for twinning ² | $\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| F_o, F_c correlation | 0.97 | EDS |
| Total number of atoms | 5787 | wwPDB-VP |
| Average B, all atoms (Å ²) | 29.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% of the height of the origin peak. No significant pseudotranslation is detected.*

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.

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](#)

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4.3.3 RNA [i](#)

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

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4.5 Carbohydrates [i](#)

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4.6 Ligand geometry [i](#)

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4.7 Other polymers [i](#)

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4.8 Polymer linkage issues ⓘ

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, 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 | 339/347 (97%) | -0.53 | 1 (0%) 93 96 | 15, 26, 58, 91 | 0 |
| 1 | B | 346/347 (99%) | -0.63 | 0 100 100 | 15, 23, 50, 60 | 0 |
| All | All | 685/694 (98%) | -0.58 | 1 (0%) 95 97 | 15, 24, 54, 91 | 0 |

All (1) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | A | 340 | LEU | 3.6 |

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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 | LLDF | B-factors(Å ²) | Q<0.9 |
|-----|------|-------|---------|-------|------|------|------|----------------------------|-------|
| 2 | GAL | A | 1400[A] | 12/12 | 0.95 | 0.09 | 1.18 | 16,22,37,45 | 1 |
| 2 | GAL | A | 1400[B] | 12/12 | 0.95 | 0.09 | 1.01 | 16,22,37,45 | 1 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | LLDF | B-factors(\AA^2) | Q<0.9 |
|-----|------|-------|---------|-------|------|------|-------|-----------------------------|-------|
| 2 | GAL | B | 2400[A] | 12/12 | 0.98 | 0.08 | -0.15 | 19,25,31,39 | 1 |
| 2 | GAL | B | 2400[B] | 12/12 | 0.98 | 0.08 | -0.35 | 19,22,28,31 | 1 |
| 3 | NI | A | 1401 | 1/1 | 0.99 | 0.05 | -2.45 | 28,28,28,28 | 0 |

5.5 Other polymers [i](#)

There are no such residues in this entry.