

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## betaVAEImputation

RRID:SCR\_018730

Type: Tool

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### Proper Citation

betaVAEImputation (RRID:SCR\_018730)

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### Resource Information

**URL:** <https://github.com/gevaertlab/BetaVAEImputation>

**Proper Citation:** betaVAEImputation (RRID:SCR\_018730)

**Description:** Software tool as deep learning framework based on variational autoencoder to impute missing values in transcriptome and methylome data analysis.

**Resource Type:** data analysis software, data processing software, software application, software resource

**Keywords:** Genomic data, handling missing data, deep learning framework, variational autoencoder, imputing missing values, transcriptome, methylome, data analysis, bio.tools

**Availability:** Free, Available for download, Freely available

**Resource Name:** betaVAEImputation

**Resource ID:** SCR\_018730

**Alternate IDs:** biotools:betavaeimputation

**Alternate URLs:** <https://bio.tools/betavaeimputation>

**License:** BSD 3-Clause

**Record Creation Time:** 20220129T080341+0000

**Record Last Update:** 20260905T132841+0000

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### Ratings and Alerts

No rating or validation information has been found for betaVAEImputation.

No alerts have been found for betaVAEImputation.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [Kravitz](#) .

Yassi M, et al. (2023) Application of deep learning in cancer epigenetics through DNA methylation analysis. Briefings in bioinformatics, 24(6).

Qiu YL, et al. (2020) Genomic data imputation with variational auto-encoders. GigaScience, 9(8).