

Resource Summary Report

Generated by SPARC SAWG on Aug 8, 2026

betaVAEImputation

RRID:SCR_018730

Type: Tool

Proper Citation

betaVAEImputation (RRID:SCR_018730)

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: software resource, software application, data analysis software, data processing software

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: 20260808T190121+0000

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](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

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).