

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

DeepAnnotation

RRID:SCR_026630

Type: Tool

Proper Citation

DeepAnnotation (RRID:SCR_026630)

Resource Information

URL: <https://github.com/mawenlong2016/DeepAnnotation>

Proper Citation: DeepAnnotation (RRID:SCR_026630)

Description: Software Python package to perform genomic selection. Predicts phenotypes from comprehensive multi-omics functional annotations with interpretable deep learning framework. Novel interpretable DL-based genomic prediction model that integrates comprehensive species- and tissue-level transcriptional regulatory functional annotations to predict phenotypes.

Resource Type: software toolkit, source code, software resource

Keywords: Predict phenotype, perform genomic selection, multi-omics functional annotations,

Availability: Free, Available for download, Freely available

Resource Name: DeepAnnotation

Resource ID: SCR_026630

Alternate URLs: <https://doi.org/10.5281/zenodo.8410693>

License: GNU GPL v3

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Ratings and Alerts

No rating or validation information has been found for DeepAnnotation.

No alerts have been found for DeepAnnotation.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Ma W, et al. (2025) DeepAnnotation: A novel interpretable deep learning-based genomic selection model that integrates comprehensive functional annotations. GigaScience, 14.