

Resource Summary Report

Generated by [RRID](#) on Aug 14, 2026

Enformer

RRID:SCR_024805

Type: Tool

Proper Citation

Enformer (RRID:SCR_024805)

Resource Information

URL: <https://github.com/google-deepmind/deepmind-research/tree/master/enformer>

Proper Citation: Enformer (RRID:SCR_024805)

Description: Software package provides implementation of the Enformer model and examples on running the model.

Resource Type: software resource, source code

Keywords: implementation of Enformer model, examples on running the model,

Availability: Free, Available for download, Freely available

Resource Name: Enformer

Resource ID: SCR_024805

Record Creation Time: 20240103T212525+0000

Record Last Update: 20260813T055314+0000

Ratings and Alerts

No rating or validation information has been found for Enformer.

No alerts have been found for Enformer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Namba S, et al. (2026) A cross-population compendium of gene-environment interactions. *Nature*, 651(8106), 688.

Lv T, et al. (2026) Cross-species prediction of histone modifications in plants via deep learning. *Genome biology*, 27(1), 20.

Kempynck N, et al. (2026) CREsted: modeling genomic and synthetic cell-type-specific enhancers across tissues and species. *Nature methods*, 23(5), 946.

Zhang Q, et al. (2026) A scalable computational framework for predicting gene expression from candidate cis-regulatory elements. *Genome research*, 36(2), 361.

Mondragon-Estrada E, et al. (2025) Protocol to analyze deep-learning-predicted functional scores for noncoding de novo variants and their correlation with complex brain traits. *STAR protocols*, 6(2), 103738.

Ribeiro-Dos-Santos AM, et al. (2025) Iterative improvement of deep learning models using synthetic regulatory genomics. *bioRxiv : the preprint server for biology*.

Liu Z, et al. (2025) Epigenetic Impacts of Non-Coding Mutations Deciphered Through Pre-Trained DNA Language Model at Single-Cell Resolution. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(11), e2413571.

Mondragon-Estrada E, et al. (2025) Noncoding variants and sulcal patterns in congenital heart disease: Machine learning to predict functional impact. *iScience*, 28(2), 111707.

Ribeiro-Dos-Santos AM, et al. (2025) Iterative improvement of deep learning models using synthetic regulatory genomics. *Genome research*, 35(11), 2539.

Zhou JL, et al. (2024) Analysis of single-cell CRISPR perturbations indicates that enhancers predominantly act multiplicatively. *Cell genomics*, 4(11), 100672.

Taskiran II, et al. (2024) Cell-type-directed design of synthetic enhancers. *Nature*, 626(7997), 212.

Martyn GE, et al. (2023) Rewriting regulatory DNA to dissect and reprogram gene expression. *bioRxiv : the preprint server for biology*.