

Resource Summary Report

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ABC-Enhancer-Gene-Prediction

RRID:SCR_027918

Type: Tool

Proper Citation

ABC-Enhancer-Gene-Prediction (RRID:SCR_027918)

Resource Information

URL: <https://github.com/broadinstitute/ABC-Enhancer-Gene-Prediction>

Proper Citation: ABC-Enhancer-Gene-Prediction (RRID:SCR_027918)

Description: Software tool for cell type specific enhancer-gene predictions using ABC model.

Resource Type: source code, software application, software resource

Defining Citation: [DOI:s41588-019-0538-0](#)

Keywords: cell type specific enhancer-gene predictions, ABC model,

Availability: Free, Available for download, Freely available,

Resource Name: ABC-Enhancer-Gene-Prediction

Resource ID: SCR_027918

License: MIT license

Record Creation Time: 20260204T060344+0000

Record Last Update: 20260815T183304+0000

Ratings and Alerts

No rating or validation information has been found for ABC-Enhancer-Gene-Prediction.

No alerts have been found for ABC-Enhancer-Gene-Prediction.

Data and Source Information

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Lin J, et al. (2026) EPInformer: scalable and integrative prediction of gene expression from promoter-enhancer sequences with multimodal epigenomic profiles. *Nature communications*, 17(1).

Berico P, et al. (2026) A Targetable Developmental Program Coregulates Angiogenesis and Immune Evasion in Melanoma. *Cancer discovery*, 16(6), 1200.

Berico P, et al. (2026) Chromatin architecture and physical constriction cooperate in phenotype switching and cancer cell dissemination. *bioRxiv : the preprint server for biology*.

Ding W, et al. (2026) A Multimodal Single-Cell Epigenomic and 3D Genome Atlas of the Human Basal Ganglia. *bioRxiv : the preprint server for biology*.

Sokolowski DJ, et al. (2024) An updated reference genome sequence and annotation reveals gene losses and gains underlying naked mole-rat biology. *bioRxiv : the preprint server for biology*.

Pettie KP, et al. (2024) Chromatin activity identifies differential gene regulation across human ancestries. *Genome biology*, 25(1), 21.

Harvey C, et al. (2024) Evaluation of a biomarker for amyotrophic lateral sclerosis derived from a hypomethylated DNA signature of human motor neurons. *Research square*.

Barnett KR, et al. (2023) Epigenomic mapping reveals distinct B cell acute lymphoblastic leukemia chromatin architectures and regulators. *Cell genomics*, 3(12), 100442.

Hoellinger T, et al. (2023) Enhancer/gene relationships: Need for more reliable genome-wide reference sets. *Frontiers in bioinformatics*, 3, 1092853.

Xie F, et al. (2023) Robust enhancer-gene regulation identified by single-cell transcriptomes and epigenomes. *Cell genomics*, 3(7), 100342.

Mahmood SR, et al. (2023) ??-actin mediated H3K27ac changes demonstrate the link between compartment switching and enhancer-dependent transcriptional regulation. *Genome biology*, 24(1), 18.

Moonen JR, et al. (2022) KLF4 recruits SWI/SNF to increase chromatin accessibility and reprogram the endothelial enhancer landscape under laminar shear stress. *Nature communications*, 13(1), 4941.

Wang C, et al. (2022) Lineage-selective super enhancers mediate core regulatory circuitry during adipogenic and osteogenic differentiation of human mesenchymal stem cells. *Cell*

death & disease, 13(10), 866.

Chen Q, et al. (2022) Integration of 3D genome topology and local chromatin features uncovers enhancers underlying craniofacial-specific cartilage defects. Science advances, 8(47), eabo3648.