Resource Summary Report

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GREAT: Genomic Regions Enrichment of Annotations Tool

RRID:SCR_005807
Type: Tool

Proper Citation

GREAT: Genomic Regions Enrichment of Annotations Tool (RRID:SCR_005807)

Resource Information

URL: http://great.stanford.edu/public/html/splash.php

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Description: Data analysis service that predicts functions of cis-regulatory regions identified by localized measurements of DNA binding events across an entire genome. Whereas previous methods took into account only binding proximal to genes, GREAT is able to properly incorporate distal binding sites and control for false positives using a binomial test over the input genomic regions. GREAT incorporates annotations from 20 ontologies and is available as a web application. The utility of GREAT extends to data generated for transcription-associated factors, open chromatin, localized epigenomic markers and similar functional data sets, and comparative genomics sets. Platform: Online tool

Abbreviations: GREAT

Synonyms: Genomic Regions Enrichment of Annotations Tool (GREAT), Genomic Regions Enrichment of Annotations Tool

Resource Type: production service resource, data analysis service, source code, analysis service resource, service resource, software resource

Defining Citation: PMID:20436461, PMID:23814184

Keywords: term enrichment, cis-regulatory region, function, gene, genomic, annotation, ontology, chromatin immunoprecipitation, sequencing, chip-seq, comparative genomics, transcription factor binding

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Availability: Free for academic use, Acknowledgement requested

Resource Name: GREAT: Genomic Regions Enrichment of Annotations Tool

Resource ID: SCR_005807

Alternate IDs: nlx_149295, OMICS_00635

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260804T043256+0000

Ratings and Alerts

No rating or validation information has been found for GREAT: Genomic Regions Enrichment of Annotations Tool.

No alerts have been found for GREAT: Genomic Regions Enrichment of Annotations Tool.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 82 mentions in open access literature.

Listed below are recent publications. The full list is available at ASWG .

Seasock MJ, et al. (2025) Let-7 restrains an epigenetic circuit in AT2 cells to prevent fibrogenic intermediates in pulmonary fibrosis. Nature communications, 16(1), 4353.

Chatterjee S, et al. (2025) Age-Dependent Histone Deacetylase 3 Regulation by ??A3/A1-Crystallin and Inositol Hexaphosphate in Retinal Pigmented Epithelial Cells Reveals a Novel Pathway in Age-Related Macular Degeneration. Aging cell, 24(9), e70163.

Hu M, et al. (2025) Myogenic enhancer snatching promotes adipogenic differentiation during epigenetic reprogramming mediated by lineage-specific transcription factors. Cellular and molecular life sciences : CMLS, 82(1), 412.

Mogol AN, et al. (2025) ACSS2-Mediated Metabolic-Epigenetic Crosstalk Drives Fulvestrant Resistance and Represents a Novel Therapeutic Target. bioRxiv : the preprint server for biology.

Moore JL, et al. (2025) The impact of air pollution on sperm DNA methylation. Reproductive toxicology (Elmsford, N.Y.), 132, 108850.

Tingvall-Gustafsson J, et al. (2025) Chromatin interaction-based annotation of regulatory elements reveals dynamic promoter-enhancer interactions in lymphocyte development. iScience, 28(7), 112855.

Likasitwatanakul P, et al. (2025) Chemical Perturbations Impacting Histone Acetylation Govern Colorectal Cancer Differentiation. Gastroenterology.

Zhou Y, et al. (2024) Utilizing multimodal AI to improve genetic analyses of cardiovascular traits. medRxiv : the preprint server for health sciences.

Dansu DK, et al. (2024) Histone H4 acetylation differentially modulates proliferation in adult oligodendrocyte progenitors. The Journal of cell biology, 223(11).

Laub V, et al. (2024) Integrated multi-omics analysis of PBX1 in mouse adult neural stem- and progenitor cells identifies a transcriptional module that functionally links PBX1 to TCF3/4. Nucleic acids research, 52(20), 12262.

Likasitwatanakul P, et al. (2024) Chemical perturbations impacting histone acetylation govern colorectal cancer differentiation. bioRxiv : the preprint server for biology.

Heath H, et al. (2024) The Effect of Exposure to Neighborhood Violence on Glucocorticoid Receptor Signaling in Lung Tumors. Cancer research communications, 4(7), 1643.

Short AK, et al. (2024) Individual longitudinal changes in DNA-methylome identify signatures of early-life adversity and correlate with later outcome. Neurobiology of stress, 31, 100652.

Zhang J, et al. (2024) Osr2 functions as a biomechanical checkpoint to aggravate CD8+ T??cell exhaustion in tumor. Cell, 187(13), 3409.

Tanaka M, et al. (2023) HEY1-NCOA2 expression modulates chondrogenic differentiation and induces mesenchymal chondrosarcoma in mice. JCI insight, 8(10).

Preiss NK, et al. (2023) Characterizing control of memory CD8 T cell differentiation by BTB-ZF transcription factor Zbtb20. Life science alliance, 6(9).

Tanaka M, et al. (2023) ASPSCR1::TFE3 orchestrates the angiogenic program of alveolar soft part sarcoma. Nature communications, 14(1), 1957.

Perez-Garcia J, et al. (2023) Epigenomic response to albuterol treatment in asthma-relevant airway epithelial cells. Clinical epigenetics, 15(1), 156.

Short AK, et al. (2023) Within-subject changes in methylome profile identify individual signatures of early-life adversity, with a potential to predict neuropsychiatric outcome. bioRxiv : the preprint server for biology.

Cho YW, et al. (2023) Thyroid hormone-regulated chromatin landscape and transcriptional sensitivity of the pituitary gland. Communications biology, 6(1), 1253.