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

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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 75 mentions in open access literature.

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

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.

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

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

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.

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.

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

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

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

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

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

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.

Sekiya M, et al. (2023) Loss of CtBP2 may be a mechanistic link between metabolic derangements and progressive impairment of pancreatic ? cell function. Cell reports, 42(8), 112914.

Oger F, et al. (2023) Pharmacological HDAC inhibition impairs pancreatic ?-cell function through an epigenome-wide reprogramming. iScience, 26(7), 107231.

Kitt MM, et al. (2022) An adult-stage transcriptional program for survival of serotonergic connectivity. Cell reports, 39(3), 110711.

Lawler AJ, et al. (2022) Machine learning sequence prioritization for cell type-specific enhancer design. eLife, 11.

Li J, et al. (2022) Limb development genes underlie variation in human fingerprint patterns. Cell, 185(1), 95.

Tsai JW, et al. (2022) FOXR2 Is an Epigenetically Regulated Pan-Cancer Oncogene That Activates ETS Transcriptional Circuits. Cancer research, 82(17), 2980.

Xiong L, et al. (2022) Oct4 differentially regulates chromatin opening and enhancer transcription in pluripotent stem cells. eLife, 11.

Janas JA, et al. (2022) Tip60-mediated H2A.Z acetylation promotes neuronal fate specification and bivalent gene activation. Molecular cell, 82(24), 4627.