

Resource Summary Report

Generated by [nidm-terms](#) on Sep 23, 2026

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>

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

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, production service resource, service resource, software resource, source code

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

Funding: Bio-X ;
Howard Hughes Medical Institute ;

Stanford University; California; USA ;
Packard ;
Searle Scholar ;
Microsoft Research ;
Alfred P. Sloan Foundation ;
Edward Mallinckrodt Jr. Foundation ;
NIH ;
Human Frontier Science Program fellowship LT000896/2009-I;
NICHD 1R01HD059862;
NHGRI R01HG005058;
NSF CCF-0939370;
DFG Hi 1423/2-1

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: 20260919T195100+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 89 mentions in open access literature.

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

Nanayakkara J, et al. (2026) YAP and TEAD Are Transcriptional Regulators of Neuroendocrine Differentiation and Growth in Carcinoid Cells. The American journal of pathology, 196(2), 345.

L??pez-Fuentes E, et al. (2026) Epigenetic and Transcriptional Programs Define Osteosarcoma Subtypes and Establish Targetable Vulnerabilities. Cancer discovery, 16(2), 296.

- Camp SY, et al. (2026) Single-cell epigenetic profiling reveals a tumor-intrinsic interferon response program in ccRCC tied to poor prognosis and BAP1 loss. *Science advances*, 12(8), eadv5457.
- Rodriguez A, et al. (2026) An epigenomic investigation of atrial fibrillation in a matched left and right atrial human cohort. *Clinical epigenetics*, 18(1).
- Sato K, et al. (2026) Aberrant Hippo-YAP/TEAD Signaling Drives Malignant Transcriptional Reprogramming in External Auditory Canal Squamous Cell Carcinoma. *Cancer research communications*, 6(2), 260.
- Maeda M, et al. (2026) CRISPR screen of human pancreatic cancer xenografts identifies a KLF5 proliferation vulnerability through epigenetic modifiers NCAPD2 and MTHFD1. *Molecular cancer*, 25(1).
- Huang K, et al. (2026) Exploring a genetic basis for the metabolic perturbations in ME/CFS using UK biobank. *iScience*, 29(1), 114316.
- 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.
- Liksitwatanakul P, et al. (2025) Chemical Perturbations Impacting Histone Acetylation Govern Colorectal Cancer Differentiation. *Gastroenterology*.
- Liksitwatanakul P, et al. (2024) Chemical perturbations impacting histone acetylation govern colorectal cancer differentiation. *bioRxiv : the preprint server for biology*.
- 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*.

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

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.