Resource Summary Report

Generated by RRID on Apr 8, 2025

Quantitative Enrichment of Sequence Tags

RRID:SCR_004065
Type: Tool

Proper Citation

Quantitative Enrichment of Sequence Tags (RRID:SCR_004065)

Resource Information

URL: http://mendel.stanford.edu/sidowlab/downloads/quest/

Proper Citation: Quantitative Enrichment of Sequence Tags (RRID:SCR_004065)

Description: A Kernel Density Estimator-based package for analysis of massively parallel sequencing data from chromatin immunoprecipitation (ChIP-seq) experiments.

Abbreviations: QuEST

Synonyms: Quantitative Enrichment of Sequence Tags: QuEST

Resource Type: software resource

Defining Citation: PMID:19160518

Keywords: genome-wide, transcription factor binding site, chip-seq, transcription factor, binding site, bio.tools

Funding:

Resource Name: Quantitative Enrichment of Sequence Tags

Resource ID: SCR_004065

Alternate IDs: OMICS_00458, biotools:quest

Alternate URLs: https://bio.tools/quest

Record Creation Time: 20220129T080222+0000

Record Last Update: 20250214T183016+0000

Ratings and Alerts

No rating or validation information has been found for Quantitative Enrichment of Sequence Tags.

No alerts have been found for Quantitative Enrichment of Sequence Tags.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 48 mentions in open access literature.

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

Mazzoni A, et al. (2024) Service Delivery Redesign for Noncommunicable Disease Management: Assessment of Needs and Solutions Through a Co-Creation Process in Argentina. Global health, science and practice, 12(6).

Arsenault C, et al. (2022) COVID-19 and resilience of healthcare systems in ten countries. Nature medicine, 28(6), 1314.

Lakey BD, et al. (2022) The essential Rhodobacter sphaeroides CenKR two-component system regulates cell division and envelope biosynthesis. PLoS genetics, 18(6), e1010270.

Gibson JA, et al. (2022) Sequestration of a dual function DNA-binding protein by Vibrio cholerae CRP. Proceedings of the National Academy of Sciences of the United States of America, 119(46), e2210115119.

Peña JM, et al. (2021) Control of a programmed cell death pathway in Pseudomonas aeruginosa by an antiterminator. Nature communications, 12(1), 1702.

Finn MB, et al. (2021) Identification of Group A Streptococcus Genes Directly Regulated by CsrRS and Novel Intermediate Regulators. mBio, 12(4), e0164221.

Balderas D, et al. (2021) Genome Scale Analysis Reveals IscR Directly and Indirectly Regulates Virulence Factor Genes in Pathogenic Yersinia. mBio, 12(3), e0063321.

Banerjee R, et al. (2020) Tailoring a Global Iron Regulon to a Uropathogen. mBio, 11(2).

Louis Sam Titus ASC, et al. (2019) The Bdnf and Npas4 genes are targets of HDAC3-mediated transcriptional repression. BMC neuroscience, 20(1), 65.

Kambara TK, et al. (2018) Pervasive Targeting of Nascent Transcripts by Hfq. Cell reports, 23(5), 1543.

O'Brien LL, et al. (2018) Transcriptional regulatory control of mammalian nephron progenitors revealed by multi-factor cistromic analysis and genetic studies. PLoS genetics, 14(1), e1007181.

Doidy J, et al. (2016) "Hit-and-Run" transcription: de novo transcription initiated by a transient bZIP1 "hit" persists after the "run". BMC genomics, 17, 92.

Kuosmanen SM, et al. (2016) The Effects of Sequence Variation on Genome-wide NRF2 Binding--New Target Genes and Regulatory SNPs. Nucleic acids research, 44(4), 1760.

Starmer J, et al. (2016) Detecting broad domains and narrow peaks in ChIP-seq data with hiddenDomains. BMC bioinformatics, 17, 144.

Peng JC, et al. (2016) Piwi maintains germline stem cells and oogenesis in Drosophila through negative regulation of Polycomb group proteins. Nature genetics, 48(3), 283.

Perdomo-Sabogal A, et al. (2016) Human Lineage-Specific Transcriptional Regulation through GA-Binding Protein Transcription Factor Alpha (GABPa). Molecular biology and evolution, 33(5), 1231.

Nettling M, et al. (2016) Detecting and correcting the binding-affinity bias in ChIP-seq data using inter-species information. BMC genomics, 17, 347.

Ramsey KM, et al. (2015) Ubiquitous promoter-localization of essential virulence regulators in Francisella tularensis. PLoS pathogens, 11(4), e1004793.

Su D, et al. (2015) Interactions of chromatin context, binding site sequence content, and sequence evolution in stress-induced p53 occupancy and transactivation. PLoS genetics, 11(1), e1004885.

Ayers S, et al. (2014) Genome-wide binding patterns of thyroid hormone receptor beta. PloS one, 9(2), e81186.