Resource Summary Report

Generated by NIF on Apr 26, 2025

AnnotationHub

RRID:SCR_024227

Type: Tool

Proper Citation

AnnotationHub (RRID:SCR_024227)

Resource Information

URL: https://bioconductor.org/packages/release/bioc/html/AnnotationHub.html

Proper Citation: AnnotationHub (RRID:SCR_024227)

Description: Software R package to provide a client for the Bioconductor AnnotationHub web resource. AnnotationHub web resource provides a central location where genomic files (e.g., VCF, bed, wig) and other resources from standard locations (e.g., UCSC, Ensembl) can be discovered.

Resource Type: software toolkit, software resource

Keywords: client, Bioconductor AnnotationHub web resource,

Funding:

Availability: Free, Available for download, Freely available,

Resource Name: AnnotationHub

Resource ID: SCR 024227

Alternate IDs: OMICS_29380

Alternate URLs: https://sources.debian.org/src/r-bioc-annotationhub/

Record Creation Time: 20230830T050216+0000

Record Last Update: 20250425T060559+0000

Ratings and Alerts

No rating or validation information has been found for AnnotationHub.

No alerts have been found for AnnotationHub.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Großkinsky DK, et al. (2025) Structure-function relation of cytokinins determines their differential efficiency in mediating tobacco resistance against Pseudomonas syringae. Physiologia plantarum, 177(1), e70028.

López-García I, et al. (2024) Epithelial tubule interconnection driven by HGF-Met signaling in the kidney. bioRxiv: the preprint server for biology.

Deng S, et al. (2024) An RNA-Seq analysis of coronavirus in the skin of the Pangolin. Scientific reports, 14(1), 910.

Wang Q, et al. (2024) Weighted gene co-expression network analysis reveals genes related to growth performance in Hu sheep. Scientific reports, 14(1), 13043.

Lin TY, et al. (2024) The molecular basis of tRNA selectivity by human pseudouridine synthase 3. Molecular cell, 84(13), 2472.

Tsuyuzaki K, et al. (2023) Sctensor detects many-to-many cell-cell interactions from single cell RNA-sequencing data. BMC bioinformatics, 24(1), 420.

Sharma A, et al. (2023) ELONGATED HYPOCOTYL5 (HY5) and HY5 HOMOLOGUE (HYH) maintain shade avoidance suppression in UV-B. The Plant journal: for cell and molecular biology, 115(5), 1394.

Noviello TMR, et al. (2023) Guadecitabine plus ipilimumab in unresectable melanoma: five-year follow-up and integrated multi-omic analysis in the phase 1b NIBIT-M4 trial. Nature communications, 14(1), 5914.

Paris JR, et al. (2022) A large and diverse autosomal haplotype is associated with sex-linked colour polymorphism in the guppy. Nature communications, 13(1), 1233.

Rizzardi LF, et al. (2021) Human brain region-specific variably methylated regions are enriched for heritability of distinct neuropsychiatric traits. Genome biology, 22(1), 116.

Muzzi JCD, et al. (2021) Adrenocortical Carcinoma Steroid Profiles: In Silico Pan-Cancer Analysis of TCGA Data Uncovers Immunotherapy Targets for Potential Improved Outcomes. Frontiers in endocrinology, 12, 672319.

Ko?odziej-Wojnar P, et al. (2020) Alterations in the Genomic Distribution of 5hmC in In Vivo Aged Human Skin Fibroblasts. International journal of molecular sciences, 22(1).

Price AJ, et al. (2019) Divergent neuronal DNA methylation patterns across human cortical development reveal critical periods and a unique role of CpH methylation. Genome biology, 20(1), 196.

Marzi SJ, et al. (2016) Tissue-specific patterns of allelically-skewed DNA methylation. Epigenetics, 11(1), 24.