

Resource Summary Report

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Apache Software Foundation

RRID:SCR_008588

Type: Tool

Proper Citation

Apache Software Foundation (RRID:SCR_008588)

Resource Information

URL: <http://www.apache.org/>

Proper Citation: Apache Software Foundation (RRID:SCR_008588)

Description: Provides support for the Apache community of open-source software projects. The Apache projects are characterized by a collaborative, consensus based development process, open and pragmatic software license, and a desire to create high quality software that leads the way in its field.

Abbreviations: ASF

Synonyms: ApacheCon, The Apache Software Foundation, The Apache Software Foundation

Resource Type: software resource

Keywords: open-source software projects, open and pragmatic software license,

Resource Name: Apache Software Foundation

Resource ID: SCR_008588

Alternate IDs: nif-0000-31892

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260919T195142+0000

Ratings and Alerts

No rating or validation information has been found for Apache Software Foundation.

No alerts have been found for Apache Software Foundation.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 142 mentions in open access literature.

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

Nahm M, et al. (2026) Prediction of Posterior Communicating Artery Aneurysm Rupture Risk: A Multivariate Analysis of Aneurysm and Surrounding Arterial Morphological Factors. *Journal of clinical medicine*, 15(10).

Li YY, et al. (2025) sclmmOmics: a manually curated resource of single-cell multi-omics immune data. *Nucleic acids research*, 53(D1), D1162.

Zou X, et al. (2025) Impact of rare non-coding variants on human diseases through alternative polyadenylation outliers. *Nature communications*, 16(1), 682.

Zhang G, et al. (2025) TRAPT: a multi-stage fused deep learning framework for predicting transcriptional regulators based on large-scale epigenomic data. *Nature communications*, 16(1), 3611.

Manske F, et al. (2025) Development of a new data management system for the study of the gut microbiome of children who are small for their gestational age. *Computational and structural biotechnology journal*, 27, 221.

Zhao J, et al. (2024) SCInter: A comprehensive single-cell transcriptome integration database for human and mouse. *Computational and structural biotechnology journal*, 23, 77.

Wu H, et al. (2024) ESKtides: a comprehensive database and mining method for ESKAPE phage-derived antimicrobial peptides. *Database : the journal of biological databases and curation*, 2024.

Wang X, et al. (2024) RCDdb: A manually curated database and analysis platform for regulated cell death. *Computational and structural biotechnology journal*, 23, 3211.

Yang P, et al. (2024) AlliumDB: a central portal for comparative and functional genomics in Allium. *Horticulture research*, 11(2), uhad285.

Zhang Q, et al. (2024) GETdb: A comprehensive database for genetic and evolutionary features of drug targets. *Computational and structural biotechnology journal*, 23, 1429.

Zeng W, et al. (2023) HiChIPdb: a comprehensive database of HiChIP regulatory interactions. *Nucleic acids research*, 51(D1), D159.

Li G, et al. (2023) IMOPAC: A web server for interactive multiomics and pharmacological analyses of patient-derived cancer cell lines. *Computational and structural biotechnology journal*, 21, 3705.

Jain A, et al. (2023) AFRbase: a database of protein mutations responsible for antifungal resistance. *Bioinformatics* (Oxford, England), 39(11).

Ma X, et al. (2023) ipaQTL-atlas: an atlas of intronic polyadenylation quantitative trait loci across human tissues. *Nucleic acids research*, 51(D1), D1046.

de Sainte Agathe JM, et al. (2023) SpliceAI-visual: a free online tool to improve SpliceAI splicing variant interpretation. *Human genomics*, 17(1), 7.

Ma X, et al. (2022) PlantGSAD: a comprehensive gene set annotation database for plant species. *Nucleic acids research*, 50(D1), D1456.

Cui Y, et al. (2022) 3'aQTL-atlas: an atlas of 3'UTR alternative polyadenylation quantitative trait loci across human normal tissues. *Nucleic acids research*, 50(D1), D39.

Jin H, et al. (2022) mBodyMap: a curated database for microbes across human body and their associations with health and diseases. *Nucleic acids research*, 50(D1), D808.

Ni P, et al. (2022) PCRMS: a database of predicted cis-regulatory modules and constituent transcription factor binding sites in genomes. *Database : the journal of biological databases and curation*, 2022.

Newman PM, et al. (2022) Integration of visual landmark cues in spatial memory. *Psychological research*, 86(5), 1636.