

Resource Summary Report

Generated by PRECISE-TBI on Aug 1, 2026

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: 20260801T190334+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 133 mentions in open access literature.

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

Li YY, et al. (2025) scImmOmics: 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.

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

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

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

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.

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

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.

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.

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

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.

Yang Z, et al. (2022) HPVMD-C: a disease-based mutation database of human papillomavirus in China. Database : the journal of biological databases and curation, 2022.

Shang L, et al. (2022) A super pan-genomic landscape of rice. Cell research, 32(10), 878.

Qian Z, et al. (2022) EfGD: the Erianthus fulvus genome database. Database : the journal of biological databases and curation, 2022.

Peng Z, et al. (2021) Development of an Online Tool for Pasteurella multocida Genotyping and Genotypes of Pasteurella multocida From Different Hosts. Frontiers in veterinary science, 8, 771157.

Liu D, et al. (2021) BnTIR: an online transcriptome platform for exploring RNA-seq libraries for oil crop Brassica napus. Plant biotechnology journal, 19(10), 1895.

Wang F, et al. (2021) ATACdb: a comprehensive human chromatin accessibility database. Nucleic acids research, 49(D1), D55.

Liu N, et al. (2021) The Rhododendron Plant Genome Database (RPGD): a comprehensive online omics database for Rhododendron. BMC genomics, 22(1), 376.