

Resource Summary Report

Generated by ASWG on Aug 10, 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: 20260808T185904+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 [ASWG](#).

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.

Sahbou AE, et al. (2022) BuscoPhylo: a webserver for Busco-based phylogenomic analysis for non-specialists. *Scientific reports*, 12(1), 17352.

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.