

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

DAVID

RRID:SCR_001881

Type: Tool

Proper Citation

DAVID (RRID:SCR_001881)

Resource Information

URL: <https://david.ncifcrf.gov/>

Proper Citation: DAVID (RRID:SCR_001881)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16, 2025. Bioinformatics resource system including web server and web service for functional annotation and enrichment analyses of gene lists. Consists of comprehensive knowledgebase and set of functional analysis tools. Includes gene centered database integrating heterogeneous gene annotation resources to facilitate high throughput gene functional analysis.

Abbreviations: DAVID

Synonyms: DAVID Bioinformatics Resources, Visualization and Integrated Discovery Bioinformatics Resources, Database for Annotation Visualization and Integrated Discovery, The Database for Annotation, The Database for Annotation Visualization and Integrated Discovery Bioinformatics Resources

Resource Type: data or information resource, web service, software resource, data access protocol, database

Defining Citation: [PMID:19131956](#), [PMID:12734009](#), [PMID:35325185](#), [PMID:22543366](#), [PMID:17980028](#), [PMID:17576678](#)

Keywords: functional domain, annotation, motif, protein, ontology enrichment, gene, high-throughput, functional classification, functional annotation, clustering, genome, pathway, gene-disease association, interaction, functional domain, motif, visualization, FASEB list

Funding: NIAID NO1-CO-56000;
NCI

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: DAVID

Resource ID: SCR_001881

Alternate IDs: nif-0000-30408, nif-0000-10451, OMICS_02220, SCR_003033

Old URLs: <http://david.abcc.ncifcrf.gov/>

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260808T185745+0000

Ratings and Alerts

No rating or validation information has been found for DAVID.

No alerts have been found for DAVID.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20855 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Sun L, et al. (2026) Genomic Profile and Clinicopathologic Analyses of Wild-Type Gastrointestinal Stromal Tumors. *Molecular cancer research : MCR*, 24(4), 232.

Jeon H, et al. (2026) PGR-mediated transcriptome identifies SOX9 as a critical regulator of progesterone production in human ovulatory follicles. *iScience*, 29(6), 116044.

Wu N, et al. (2026) Arginine deprivation enhances ASS1-negative glioblastoma radiosensitivity via epigenetic silencing of DNA repair genes. *Cell death & disease*.

Tsakiri E, et al. (2026) RpS12-mediated induction of the Xrp1short isoform links ribosomal protein mutations to cell competition. *Cell reports*, 45(6), 117380.

Christenson JL, et al. (2026) Metastasis-Associated Wound Repair Promotes Reciprocal Lung Epithelium Activation and Breast Cancer Metastatic Outgrowth. *Cancer research communications*, 6(4), 750.

Sharma S, et al. (2026) MLC1 alteration in human iPSCs give rise to disease-like cellular vacuolation phenotype in the astrocyte lineage. *Orphanet journal of rare diseases*, 21(1).

Ulmke PA, et al. (2026) Identification of novel genes with enriched expression in human intermediate progenitors reveals a key role for CDKN3 in cortical development. *Stem cell reports*, 103012.

Gogoi A, et al. (2026) Proteomics of In Vivo models of ischemic stroke: A systematic review with a systems biological perspective. *Ageing research reviews*, 113, 102937.

Garcia FG, et al. (2026) The nBAF complex subunit CREST/SS18L1 regulates hippocampal memory processes via tyrosine 397 and histone acetyltransferase CBP. *Cell reports*, 45(4), 117158.

Zhu X, et al. (2026) Ferroptosis-STING co-activation drives GzmB+CD38+CD8+ T-cell expansion to overcome lymphoma immunosuppression. *Biomaterials*, 334, 124250.

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Blackmer-Raynolds L, et al. (2026) Indigenous gut microbes modulate neural cell state and neurodegenerative disease susceptibility. *Cell systems*, 17(2), 101481.

Kim DH, et al. (2026) Tumor Exosomal L1 Cell Adhesion Molecule Promotes Brain Metastasis of Lung Cancer. *Research (Washington, D.C.)*, 9, 1126.

Lohbihler M, et al. (2026) Human pluripotent stem cell-derived atrioventricular node-like pacemaker cells exhibit biological conduction bridge properties. *Cell stem cell*, 33(4), 571.

Kim J, et al. (2026) Electromagnetic field-inducible in vivo gene switch for remote spatiotemporal control of gene expression. *Cell*, 189(11), 3465.

Shen N, et al. (2026) A genome-wide in vivo CRISPR screen identifies neuroprotective strategies in the mouse and human retina. *Neuron*.

Li S, et al. (2026) PRECISE: A Prognostic Thyrocyte-Derived Gene Signature for Papillary Thyroid Carcinoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(13), 2667.

Nnyamah C, et al. (2026) Adipocyte-specific FFA2 deletion leads to increased adipose inflammation and is associated with altered intestinal lipid handling in mice. *Physiological reports*, 14(9), e70875.

Dong YP, et al. (2026) Early replication fragile sites are associated with cancer-related CNVs and SNVs in human embryonic stem cells. *Stem cell reports*, 21(7), 102968.

Li J, et al. (2026) FNDC4 Drives Metastasis and Immune Evasion in Pancreatic Cancer. *Cancer research*, 86(2), 349.