

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

STRING

RRID:SCR_005223

Type: Tool

Proper Citation

STRING (RRID:SCR_005223)

Resource Information

URL: <http://string.embl.de/>

Proper Citation: STRING (RRID:SCR_005223)

Description: Database of known and predicted protein interactions. The interactions include direct (physical) and indirect (functional) associations and are derived from four sources: Genomic Context, High-throughput experiments, (Conserved) Coexpression, and previous knowledge. STRING quantitatively integrates interaction data from these sources for a large number of organisms, and transfers information between these organisms where applicable. The database currently covers 5"214"234 proteins from 1133 organisms. (2013)

Abbreviations: STRING

Synonyms: Search Tool for the Retrieval of Interacting Genes/Proteins, STRING - Known and Predicted Protein-Protein Interactions

Resource Type: data or information resource, database

Defining Citation: [PMID:23203871](#), [PMID:21045058](#), [PMID:18940858](#), [PMID:17098935](#), [PMID:15608232](#), [PMID:12519996](#)

Keywords: protein association, protein functional association, protein interaction, protein-protein interaction, protein, sequence, protein sequence, interaction, gene, FASEB list

Funding: BMBF ;
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Resource Name: STRING

Resource ID: SCR_005223

Alternate IDs: nif-0000-03503, r3d100010604

Alternate URLs: <https://doi.org/10.17616/R3VS40>

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260729T044118+0000

Ratings and Alerts

No rating or validation information has been found for STRING.

No alerts have been found for STRING.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 29246 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Martedì R, et al. (2026) De novo cysteine biosynthesis in *Pseudomonas aeruginosa*: Characterization of the two main cysteine synthase isoforms. *iScience*, 29(1), 114304.

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.

Ferreira JV, et al. (2026) LAMP2A regulates endosomal protein composition and membrane identity in exosome biogenesis. *iScience*, 29(1), 114305.

Yesupatham SK, et al. (2026) Transcriptome profiling suggests molecular sexual dimorphism in lumbosacral dorsal root ganglia and sex-specific mechanisms underlying visceral pain. *Physiological genomics*, 58(1), 12.

Yamada S, et al. (2026) Long-Term Biobanked Dental Pulp Stem Cells Retain Angiogenic Potential for Vascularised Tissue Engineering-Laboratory Investigation. *International endodontic journal*, 59(1), 105.

Li X, et al. (2026) Dynamic transcriptomic landscape of myogenesis in Muscovy ducks (*Cairina moschata*): integrative analysis of hub genes post-hatching. *Animal bioscience*, 39(1), 250159.

Cai S, et al. (2026) Identification and validation of novel inflammatory response-related diagnostic biomarkers in diabetic foot ulcers. *Journal of diabetes investigation*, 17(1), 103.

Xiang X, et al. (2026) Herbal treatment of IBV-E. coli salpingitis establishment of a salpingitis model of layer chickens caused by co-infection of infectious bronchitis virus and Escherichia coli for the curative efficacy assessment of three Chinese herbal compounds. Poultry science, 105(1), 106093.

Zhou P, et al. (2026) Exploring the role of cytochrome P450 family 1 subfamily B member 1 and quercetin in modulating neuropathic pain after spinal cord injury. Molecular medicine reports, 33(1).

Matsunuma R, et al. (2026) CD44 knockdown and TGF β inhibition modulate cell proliferation and invasion in claudin-low breast cancer cells. Oncology reports, 55(1).

Xu L, et al. (2026) Identification of cuproptosis-related subtypes, construction of a prognosis model, and tumor microenvironment landscape in multiple myeloma. Translational oncology, 63, 102601.

Martins R, et al. (2026) Homeostatic control of energy metabolism by monocyte-derived macrophages. The EMBO journal, 45(1), 106.

Castro RC, et al. (2026) Extracellular Vesicles Favor Early Peripheral Immunosenescence Through Modulation of the Senescence-Associated Secretory Phenotype in HIV Infection. Aging cell, 25(1), e70320.

Mu Q, et al. (2026) Temporal Dynamics of the Milk Proteome in Women with Gestational Diabetes Mellitus. Journal of proteome research, 25(1), 131.

Ji D, et al. (2026) KRAS-Driven Hypertranscription and Metastatic Dissemination in Colorectal Cancer Could be Overcome by Targeting the NMHC IIA/ PLK1 Signaling Axis with a Novel Acridine Derivative. International journal of biological sciences, 22(1), 500.

Jiang M, et al. (2026) SIRT6-Mediated Regulation of TFAM: A Central Mechanism Connecting Nuclear and Mitochondrial Transcriptional Processes and Mitophagy. International journal of biological sciences, 22(1), 178.

Dey S, et al. (2026) Serial proteomic analysis identifies small extracellular vesicle-MASP2 as an early biomarker of chemotherapy response in advanced pancreatic cancer. Translational oncology, 64, 102636.

Yang R, et al. (2026) Exploring and Validating the Molecular Mechanisms Linking Fatty Acid Metabolism and Sarcopenia. IET systems biology, 20(1), e70052.

Gulbey O, et al. (2026) Integrated Bioinformatics and Experimental Analysis of Argonaute Family Members in Pancreatic Adenocarcinoma. In vivo (Athens, Greece), 40(1), 123.

Chen Z, et al. (2026) Bone marrow-derived mesenchymal stem cells alleviate hepatic lipid metabolism disorders after scald injury: integrating liver transcriptome and metabolome. Stem cell research & therapy, 17(1), 1.