

Resource Summary Report

Generated by [RRID](#) on Aug 6, 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: 20260806T054412+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 [RRID](#) .

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.

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.

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

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.