

Resource Summary Report

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ExPASy Bioinformatics Resource Portal

RRID:SCR_012880

Type: Tool

Proper Citation

ExPASy Bioinformatics Resource Portal (RRID:SCR_012880)

Resource Information

URL: <http://expasy.org/>

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Description: Portal which provides access to scientific databases and software tools (i.e., resources) in different areas of life sciences including proteomics, genomics, phylogeny, systems biology, population genetics, transcriptomics etc. It contains resources from many different SIB groups as well as external institutions.

Abbreviations: ExPASy

Synonyms: Bioinformatics Resource Portal, SIB Bioinformatics Resource Portal, Expert Protein Analysis System

Resource Type: data or information resource, portal

Defining Citation: [PMID:22661580](#), [PMID:12824418](#), [PMID:8073505](#)

Keywords: proteomics, genomics, structural bioinformatics, systems biology, phylogeny, evolution, population genetics, transcriptomics, biophysics, imaging, it infrastructure, drug design, protein, resource, portal

Funding: Swiss State Secretariat for Education and Research

Availability: Free, Public

Resource Name: ExPASy Bioinformatics Resource Portal

Resource ID: SCR_012880

Alternate IDs: SCR_015894

License URLs: <http://expasy.org/disclaimer.html>

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260912T200101+0000

Ratings and Alerts

No rating or validation information has been found for ExPASy Bioinformatics Resource Portal.

No alerts have been found for ExPASy Bioinformatics Resource Portal.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7119 mentions in open access literature.

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

Pohto A, et al. (2026) Uncovering Sequence and Structural Characteristics of Fungal Expansin-Related Proteins With Potential to Drive Substrate Targeting. *Proteins*, 94(2), 547.

Lian Q, et al. (2026) A chromosome-level genome assembly of *Hemibarbus maculatus*. *Scientific data*, 13(1).

Xia L, et al. (2026) Genome-wide analysis of BAHD gene family and in vivo characterization of HQT-like genes involved in chlorogenic acid synthesis in tobacco (*Nicotiana tabacum* L.). *BMC plant biology*, 26(1).

Han L, et al. (2026) Genome-Wide Identification and Characterization of Stress-Responsive SNARE Genes in Quinoa (*Chenopodium quinoa* Willd.). *Biology*, 15(5).

Wang G, et al. (2026) Genome-Wide Identification of Ovarian Tumor Proteases Gene Family and Knockout of TaOTU6 Increases Grain Width and Weight in Wheat. *Plants (Basel, Switzerland)*, 15(5).

Liu K, et al. (2026) Characterization of histone acetyltransferase and histone deacetylase genes under abiotic and hormone stresses in soybean. *Frontiers in plant science*, 17, 1753615.

Long X, et al. (2026) Identification of the NLP Gene Family in *Populus euphratica* and Its Expression Analysis Under Drought Stress. *International journal of molecular sciences*, 27(7).

Luo W, et al. (2026) Genome-wide identification and expression analysis of the expansin gene family in *Brassica napus* L. *Scientific reports*, 16(1).

- Guo W, et al. (2026) Genome-Wide Identification and Expression Analysis of m6A Regulators in *Bursaphelenchus xylophilus* Across Developmental and Stress Conditions. *Biology*, 15(10).
- Du T, et al. (2026) Genome-wide analysis of DC1 domain proteins in *Ipomoea* species reveals IbCHR10 as a positive regulator of salt tolerance in sweet potato. *Frontiers in plant science*, 17, 1780326.
- Huang J, et al. (2026) Comprehensive Analysis of the Polygalacturonase Gene Family and Transcriptome Screening for Candidate Genes Associated with Postharvest Softening in *Atemoya*. *Plants (Basel, Switzerland)*, 15(12).
- Lin Z, et al. (2026) Genome-wide analysis of HSP70 gene superfamily in kelp (*Saccharina japonica*): identification, characterization, and heat stress-responsive expression profiles. *PeerJ*, 14, e21451.
- Tang Y, et al. (2026) Genome-Wide Analysis of the TIFY Gene Family in Litchi (*Litchi chinensis* Sonn.): Identification and Expression Profiling. *Biology*, 15(5).
- Zhao X, et al. (2026) Genome-wide analysis and characterization of the rice OsFBA family provides insights into its responses to ABA and cold stress. *BMC plant biology*, 26(1).
- Bai G, et al. (2026) LARS promotes osteosarcoma proliferation through leucine-dependent PRIM2 translation and DNA replication activation. *Journal of experimental & clinical cancer research : CR*, 45(1).
- Li J, et al. (2026) Identification of the phosphate transporter 1 family genes in the *Eucalyptus grandis* genome and their expression under different phosphate regimes. *BMC genomics*, 27(1), 148.
- Zhang S, et al. (2026) Bioengineered ferritin-based lysosome-targeting chimera platform for tumor-targeted therapy. *Nature communications*, 17(1).
- Luan X, et al. (2026) Identification and Expression Analysis of MADS-Box Gene Family in *Pinus koraiensis* and Overexpression of PkMADS9 Promoting Early Flowering in Transgenic *Arabidopsis*. *Plants (Basel, Switzerland)*, 15(4).
- Singh CM, et al. (2026) Genome-wide identification and characterization of polygalacturonase gene family in linseed (*Linum usitatissimum* L.) and comparative expression in its wild relative (*Linum bienne*) upon bud fly infestation. *BMC plant biology*, 26(1), 231.
- Yang L, et al. (2026) Functional characterization of 2,3-oxidosqualene cyclase8 in *Taraxacum mongolicum*: overexpression enhances taraxasterol biosynthesis and antioxidant capacity. *BMC genomics*, 27(1), 221.