

Resource Summary Report

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ProtParam Tool

RRID:SCR_018087

Type: Tool

Proper Citation

ProtParam Tool (RRID:SCR_018087)

Resource Information

URL: <https://web.expasy.org/protparam/>

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Description: Software tool to calculate various physicochemical parameters for given protein stored in Swiss-Prot or TrEMBL or for user entered protein sequence. Protein can either be specified as Swiss-Prot/TrEMBL accession number or ID, or in form of raw sequence. Computed parameters include molecular weight, theoretical pI, amino acid composition, atomic composition, extinction coefficient, estimated half-life, instability index, aliphatic index and grand average of hydropathicity.

Synonyms: ProtParam

Resource Type: analysis service resource, data analysis software, data processing software, production service resource, sequence analysis software, service resource, software application, software resource

Defining Citation: [PMID:10027275](#)

Keywords: Calculate physicochemical parameter, protein, Swiss-Prot, TrEMBL, protein sequence, molecular weight, theoretical pI, amino acid composition, atomic composition, extinction coefficient, bio.tools

Funding: NHGRI U01 HG02712;
Swiss Federal Government through Federal Office of Education and Science

Availability: Free, Freely available

Resource Name: ProtParam Tool

Resource ID: SCR_018087

Alternate IDs: biotools:protparam

Alternate URLs: <https://bio.tools/protparam>

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260912T195857+0000

Ratings and Alerts

No rating or validation information has been found for ProtParam Tool.

No alerts have been found for ProtParam Tool.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7206 mentions in open access literature.

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

Ding XW, et al. (2027) Evolution of alcohol oxidase for improved methanol bioconversion and formaldehyde tolerance. *Synthetic and systems biotechnology*, 15, 22.

Zhang L, et al. (2027) Discovery of leucine analogues of tyrocidines and tryptocidines from *Brevibacillus brevis* B011 through genome mining and in vitro biosynthesis. *Synthetic and systems biotechnology*, 15, 58.

Barajas JM, et al. (2026) Tandem Duplications in UBTF Create XPO1-Dependent Nuclear Export Signals that Reveal a Leukemic Therapeutic Dependency. *Blood cancer discovery*, 7(1), 51.

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

Wang Y, et al. (2026) Characterization of the YCjN ABC Transporter in *Escherichia coli*: Role in Maltose and Ethidium Bromide Transport. *Molecular biotechnology*, 68(4), 1940.

Zeng J, et al. (2026) Construction of mitochondrial-targeted ferritin carrier: subunit-terminal fused mitochondrial presequences facilitate efficient delivery. *Journal of advanced research*, 81, 1023.

Tang LX, et al. (2026) Biochemical characterization of a thermostable uricase from Tengchong hot spring and its urate-lowering therapeutic potential. *AMB Express*, 16(1), 12.

Zhang C, et al. (2026) RpNACs transcription factors coordinate leaf margin development in *Rosa persica*. *BMC genomics*, 27(1), 132.

- Gong Y, et al. (2026) Design of B-Cell Multi-Epitope Subunit Vaccines Against *Glaesserella parasuis* by Reverse Vaccinology: An In Silico and In Vivo Study. *Transboundary and emerging diseases*, 2026, 5696948.
- Reid EK, et al. (2026) Electrochemical Insight into the Copper Redox Chemistry and H₂O₂ and O₂ Reducing Capability of Two AA10 Lytic Polysaccharide Monooxygenases. *ACS electrochemistry*, 2(2), 239.
- Liu X, et al. (2026) Evolutionary and functional characterization of BBX genes in the barley pangenome. *BMC plant biology*, 26(1).
- Li H, et al. (2026) Genome-wide phylogenetic analysis and expression profiling of F-box gene family in *Verbena bonariensis* under cold stress. *BMC plant biology*, 26(1).
- Garg S, et al. (2026) Mustard derived compounds as insecticides and modulators of human metabolism. *Scientific reports*, 16(1), 5783.
- Khanzada H, et al. (2026) Comprehensive Genome-Wide Identification and Expression Analysis of the N⁶-Methyladenosine (m⁶A) Regulatory Network Influences Rapid Stress Adaptation With Exogenous Melatonin in Rice. *Journal of pineal research*, 78(1), e70109.
- Naveed M, et al. (2026) In silico design and immunoinformatics assessment of a multiepitope vaccine targeting borealpox virus. *Scientific reports*, 16(1), 3885.
- Li H, et al. (2026) Genome-wide identification of the GLK gene family in wheat (*Triticum aestivum* L.) and analysis of expression responses in different environments. *BMC genomics*, 27(1), 78.
- Zhang X, et al. (2026) Evolutionary history and functional diversification of WOX genes in *Annona Atemoya*. *BMC plant biology*, 26(1), 312.
- Liu R, et al. (2026) The mitigation mechanism of exogenous pyridoxal-5-phosphate on Pb stress damage in *Polygonatum Cyrtonema* Hua by multi-omics combined analysis. *BMC genomics*, 27(1), 195.
- Ma B, et al. (2026) Protection of goose adiponectin-derived peptide gADP3 on LPS-induced thymus and spleen injury in goose. *Poultry science*, 105(3), 106454.
- Xue T, et al. (2026) Genome-wide analysis of the Cesa gene family in *Brassica napus* under abiotic stress and functional study of in root growth. *BMC plant biology*, 26(1), 269.