

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

NCBI Protein Database

RRID:SCR_003257

Type: Tool

Proper Citation

NCBI Protein Database (RRID:SCR_003257)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/protein>

Proper Citation: NCBI Protein Database (RRID:SCR_003257)

Description: Databases of protein sequences and 3D structures of proteins. Collection of sequences from several sources, including translations from annotated coding regions in GenBank, RefSeq and TPA, as well as records from SwissProt, PIR, PRF, and PDB.

Abbreviations: NCBI_GP, NCBI Protein, NCBI GP

Synonyms: Entrez Protein, Protein Database, NCBI Protein Database, Protein sequence database, Entrez Protein Database

Resource Type: database, data or information resource

Keywords: amino acid sequence, nucleotide, dna sequence, protein, sequence, sequence data, structure, function, dna, nucleotide sequence, genomics, protein binding, gold standard

Availability: Free, Freely available

Resource Name: NCBI Protein Database

Resource ID: SCR_003257

Alternate IDs: SCR_017486, r3d100011331, nif-0000-03178

Alternate URLs: <http://www.ncbi.nlm.nih.gov/sites/entrez?db=protein>,
<https://doi.org/10.17616/R3JH0X>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260805T044051+0000

Ratings and Alerts

No rating or validation information has been found for NCBI Protein Database.

No alerts have been found for NCBI Protein Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 963 mentions in open access literature.

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

Minesso S, et al. (2026) Generation, characterization, and application of caprine herpesvirus 1 secreted glycoprotein D. *Microbiology spectrum*, 14(1), e0237325.

Laureano F, et al. (2025) Biochemical features and biotechnological potential of a proteolytic extract from a psychrophilic Antarctic bacterium. *Brazilian journal of microbiology* : [publication of the Brazilian Society for Microbiology], 56(2), 767.

Dündar T, et al. (2025) Antimicrobial resistance in coagulase negative staphylococci: Genome analysis and role of horizontal gene transfer. *Research in microbiology*, 176(5-6), 104298.

Liu Z, et al. (2025) Enhanced multistress tolerance of *Saccharomyces cerevisiae* with the sugar transporter-like protein Stt1F427L mutation in the presence of glycerol. *Microbiology spectrum*, 13(2), e0008924.

Ramirez P, et al. (2025) Diverse toxin repertoire but limited metabolic capacities inferred from the draft genome assemblies of three *Spiroplasma* (Citri clade) strains associated with *Drosophila*. *Microbial genomics*, 11(6).

Wang L, et al. (2025) Integrative Transcriptome and Metabolome Analysis Reveals Candidate Genes Related to Terpenoid Synthesis in *Amylostereum areolatum* (Russulales: Amylostereaceae). *Journal of fungi* (Basel, Switzerland), 11(5).

Kelly ETR, et al. (2025) Crystal structure of the fungal mannosyltransferase Och1 reveals active site primed for N-glycan binding. *PloS one*, 20(7), e0329259.

Simoncek AM, et al. (2025) Tissue-specific I-Smad mechanisms revealed by structure-function analysis in *Drosophila*. *bioRxiv* : the preprint server for biology.

Shahraki PK, et al. (2025) Design of a multi-epitope vaccine against *Staphylococcus Aureus* leukotoxin ED using in silico approaches. *Scientific reports*, 15(1), 14517.

Basu K, et al. (2025) The truncated isoform of the receptor for hyaluronan-mediated motility (RHAMM^Δ163) modulates shelterin and telomerase reverse transcriptase transcription affecting telomerase activity. *Frontiers in aging*, 6, 1604051.

Mikami K, et al. (2025) N-acetylchitohexaose confers resistance to *Pseudomonas aeruginosa* infection in the silkworm, *Bombyx mori*. *Infection and immunity*, 93(12), e0038525.

Khan F, et al. (2025) Functional Division of Insect Blood Cells by Single-Cell RNA-Sequencing and Cell-Type-Specific FISH Markers. *Cells*, 14(23).

Chen L, et al. (2025) Chemical cross-linking facilitates antigen uptake and presentation and provides improved protection from Mpox with a dual-antigen subunit vaccine. *MedComm*, 6(1), e70045.

Yoshimi Y, et al. (2025) Glucomannan engineering highlights roles of galactosyl modification in fine-tuning cellulose-glucomannan interaction in *Arabidopsis* cell walls. *Nature communications*, 16(1), 1235.

Wang J, et al. (2025) Comparative functional analysis of a new CDR1-like ABC transporter gene in multidrug resistance and virulence between *Magnaporthe oryzae* and *Trichophyton mentagrophytes*. *Cell communication and signaling : CCS*, 23(1), 69.

Adeleke MA, et al. (2025) Computational Development of Transmission-Blocking Vaccine Candidates Based on Fused Antigens of Pre- and Post-fertilization Gametocytes Against *Plasmodium falciparum*. *Bioinformatics and biology insights*, 19, 11779322241306215.

Jantarawong S, et al. (2025) Prediction of ADMET profile and anti-inflammatory potential of chamuangone. *Scientific reports*, 15(1), 2963.

Wei Y, et al. (2025) VviWRKY24 promotes γ -damascenone biosynthesis by targeting VviNCED1 to increase abscisic acid in grape berries. *Horticulture research*, 12(5), uhaf017.

Chen Y, et al. (2025) Integrated Analysis of Survival, Physiological-Biochemical, and Transcriptomic Changes Reveals the Impact of Saline Stress on the Freshwater Snail *Pomacea canaliculata*. *Ecology and evolution*, 15(7), e71581.

Pan H, et al. (2025) Genome-wide identification and expression analysis of the ADH gene family in *Artemisia annua* L. under UV-B stress. *Frontiers in plant science*, 16, 1533225.