

Resource Summary Report

Generated by [NIF](#) on Aug 27, 2026

ProDom

RRID:SCR_006969

Type: Tool

Proper Citation

ProDom (RRID:SCR_006969)

Resource Information

URL: <http://prodom.prabi.fr/>

Proper Citation: ProDom (RRID:SCR_006969)

Description: Comprehensive set of protein domain families automatically generated from UniProt Knowledge Database. Automated clustering of homologous domains generated from global comparison of all available protein sequences., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: ProDom

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Defining Citation: [PMID:15608179](#), [PMID:12230033](#)

Keywords: set, protein, domain, family, automatically, generated, UniProt, database, homologous, sequence, compare, FASEB list

Funding: European Union ;
Réseau des Génoles ;
'Programme de Bio-Informatique InterOrganismes

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: ProDom

Resource ID: SCR_006969

Alternate IDs: OMICS_01698, nif-0000-03342

Alternate URLs: <http://prodom.prabi.fr/prodom/current/html/home.php>

Record Creation Time: 20220129T080239+0000

Ratings and Alerts

No rating or validation information has been found for ProDom.

No alerts have been found for ProDom.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 354 mentions in open access literature.

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

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia × blakeana* sheds light on the genetic basis of flower heterosis. *GigaScience*, 14.

He J, et al. (2025) Chromosome-level genome assembly of stem borer *Batocera rufomaculata* using PacBio HiFi and Hi-C sequencing. *Scientific data*, 12(1), 1099.

Chai J, et al. (2025) Multi-Omics Analysis of Chronic Heat Stress-Induced Biological Effects, Liver Injury, and Heat Tolerance Mechanisms via Oxidative and Anti-Inflammatory Pathways in Early-Pregnancy Sows. *Antioxidants (Basel, Switzerland)*, 14(6).

Santini S, et al. (2025) Pacmanvirus isolated from the Lost City hydrothermal field extends the concept of transpoviron beyond the family Mimiviridae. *The ISME journal*, 19(1).

Xu S, et al. (2025) Multi-omics analysis of yolk and allantoic fluid in chicken embryonic development and sexual differentiation. *Poultry science*, 104(8), 105349.

Chen F, et al. (2025) Data-independent acquisition-based blood proteomics unveils predictive biomarkers for neonatal necrotizing enterocolitis. *Analytical and bioanalytical chemistry*, 417(1), 199.

Chen Y, et al. (2025) An improved chromosomal-scale genome assembly of the Tanaka's snailfish (*Liparis tanakae*). *Scientific data*, 12(1), 965.

Qiu H-J, et al. (2025) In vitro and in vivo activity of quisinostat against *Toxoplasma gondii*. *Antimicrobial agents and chemotherapy*, 69(9), e0181924.

Sun YS, et al. (2025) Convergent musk biosynthesis across host and microbiota in musk deer and muskrat. *Zoological research*, 46(3), 505.

Li Y, et al. (2025) Fragment Autoantigens Stimulated T-Cell-Immunotherapy (FAST) as a Fast Autologous Cancer Vaccine. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(26), e2502937.

Chang H, et al. (2025) iTRAQ proteomic analysis of the anterior insula in morphine-induced conditioned place preference rats with high-frequency deep brain stimulation intervention. *Addiction biology*, 30(1), e70014.

Li Q, et al. (2025) Quantitative DIA-based proteomics unveils ribosomal biogenesis pathways associated with increased final size in three-year-old Chinese mitten crab (*Eriocheir sinensis*). *BMC genomics*, 26(1), 45.

Wang LZ, et al. (2025) Integration of transcriptomic and proteomic data uncovers the nutritional requirement of the immature development of an endoparasitoid wasp. *Scientific reports*, 15(1), 17744.

Xu QZ, et al. (2025) Chromosome-level genome assembly and single-cell analysis unveil molecular mechanisms of arm regeneration in the ophiuroid *Ophiura sarsii vadicola*. *Genome biology*, 26(1), 82.

Zhang Y, et al. (2025) A chromosome-level genome assembly of *Wurfbainia villosa* (Zingiberaceae). *Scientific data*, 12(1), 1490.

Li W, et al. (2025) Integrating proteomics and metabolomics to elucidate the regulatory mechanisms of pimpled egg production in chickens: Multi-omics analysis of the mechanism of pimpled egg formation. *Poultry science*, 104(2), 104818.

Jiang X, et al. (2025) A chromosome-level genome assembly of the aphid *Semiaphis heraclei* (Takahashi). *Scientific data*, 12(1), 770.

Zhang YJ, et al. (2025) A novel male accessory gland peptide reduces female post-mating receptivity in the brown planthopper. *PLoS genetics*, 21(5), e1011699.

Liang YY, et al. (2025) Pan-Genome Analysis Reveals Local Adaptation to Climate Driven by Introgression in Oak Species. *Molecular biology and evolution*, 42(5).