Resource Summary Report

Generated by RRID on Apr 11, 2025

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.

Abbreviations: ProDom

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

Defining Citation: PMID:15608179, PMID:12230033

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

Funding: ‘Programme de Bio-Informatique InterOrganismes ;
Re´seau des Ge´nopoles ;
European Union

Availability: Free, Freely available

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

Record Last Update: 20250411T055133+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 332 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

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.

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.

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 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.

Ding K, et al. (2024) Chromosome-level genome provides insights into environmental adaptability and innate immunity in the common dolphin (delphinus delphis). BMC genomics, 25(1), 373.

C?rulis A, et al. (2024) Sex-limited experimental evolution drives transcriptomic divergence in a hermaphrodite. Genome biology and evolution, 16(1).

Ma J, et al. (2024) Combination of transcriptomic and proteomic approaches helps unravel the mechanisms of luteolin in inducing liver cancer cell death via targeting AKT1 and SRC. Frontiers in pharmacology, 15, 1450847.

Lin Q, et al. (2024) Plasma biomarkers in patients with age-related sarcopenia: a proteomic exploration and experimental validation. Aging clinical and experimental research, 37(1), 13.

Man X, et al. (2024) A chromosome-level genome assembly of the heteronomous hyperparasitoid wasp Encarsia sophia. Scientific data, 11(1), 1250.

Ali EW, et al. (2024) Exploring the Structural and Functional Consequences of Deleterious Missense Nonsynonymous SNPs in the EPOR Gene: A Computational Approach. Journal of personalized medicine, 14(11).

Liu Y, et al. (2024) A chromosome-level genome assembly of tropical purple sea urchin Heliocidaris crassispina. Scientific data, 11(1), 1382.

Lv F, et al. (2024) Cyclin-dependent kinases (CDKs) are key genes regulating early development of Neptunea arthritica cumingii: evidence from comparative transcriptome and proteome analyses. BMC genomics, 25(1), 1221.

Qiu H, et al. (2024) Lamin A/C deficiency-mediated ROS elevation contributes to pathogenic phenotypes of dilated cardiomyopathy in iPSC model. Nature communications, 15(1), 7000.

Shang H, et al. (2024) Genome assembly of Stephania longa provides insight into cepharanthine biosynthesis. Frontiers in plant science, 15, 1414636.

Wang J, et al. (2024) Metabolomics and proteomics insights into subacute ruminal acidosis etiology and inhibition of proliferation of yak rumen epithelial cells in vitro. BMC genomics, 25(1), 394.

Wu Q, et al. (2024) Chromosome-scale reference genome of broccoli (Brassica oleracea var. italica Plenck) provides insights into glucosinolate biosynthesis. Horticulture research, 11(5), uhae063.

He J, et al. (2024) Multiple Origins of Bioluminescence in Beetles and Evolution of Luciferase Function. Molecular biology and evolution, 41(1).

Shao L, et al. (2024) High-quality genomes of Bombax ceiba and Ceiba pentandra provide insights into the evolution of Malvaceae species and differences in their natural fiber development. Plant communications, 5(5), 100832.

Zhu F, et al. (2024) Polyploidization of Indotyphlops braminus: evidence from isoform-sequencing. BMC genomic data, 25(1), 23.

Xiong Z, et al. (2024) Chromosome-level genome assembly of navel orange cv. Gannanzao (Citrus sinensis Osbeck cv. Gannanzao). G3 (Bethesda, Md.), 14(2).