

Resource Summary Report

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InterPro

RRID:SCR_006695

Type: Tool

Proper Citation

InterPro (RRID:SCR_006695)

Resource Information

URL: <http://www.ebi.ac.uk/interpro>

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Description: Service providing functional analysis of proteins by classifying them into families and predicting domains and important sites. They combine protein signatures from a number of member databases into a single searchable resource, capitalizing on their individual strengths to produce a powerful integrated database and diagnostic tool. This integrated database of predictive protein signatures is used for the classification and automatic annotation of proteins and genomes. InterPro classifies sequences at superfamily, family and subfamily levels, predicting the occurrence of functional domains, repeats and important sites. InterPro adds in-depth annotation, including GO terms, to the protein signatures. You can access the data programmatically, via Web Services. The member databases use a number of approaches: # ProDom: provider of sequence-clusters built from UniProtKB using PSI-BLAST. # PROSITE patterns: provider of simple regular expressions. # PROSITE and HAMAP profiles: provide sequence matrices. # PRINTS provider of fingerprints, which are groups of aligned, un-weighted Position Specific Sequence Matrices (PSSMs). # PANTHER, PIRSF, Pfam, SMART, TIGRFAMs, Gene3D and SUPERFAMILY: are providers of hidden Markov models (HMMs). Your contributions are welcome. You are encouraged to use the ""Add your annotation"" button on InterPro entry pages to suggest updated or improved annotation for individual InterPro entries.

Abbreviations: InterPro

Synonyms: InterPro: protein sequence analysis & classification, InterPro protein sequence analysis and classification

Resource Type: analysis service resource, service resource, production service resource, database, software resource, web service, data analysis service, data access protocol, data

or information resource

Defining Citation: [PMID:22096229](#), [PMID:21082426](#), [PMID:18940856](#), [PMID:18428686](#), [PMID:18025686](#), [PMID:17202162](#), [PMID:16909843](#), [PMID:15608177](#), [PMID:12520011](#), [PMID:12230031](#), [PMID:11159333](#), [PMID:11119311](#), [PMID:11125043](#)

Keywords: protein, classify, prediction, protein domain, genome, protein family, functional site, protein sequence, protein function, analysis, nucleic acid, amino acid, amino acid sequence, gold standard

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Availability: Acknowledgement requested, Free, Public, The community can contribute to this resource

Resource Name: InterPro

Resource ID: SCR_006695

Alternate IDs: nif-0000-03035, OMICS_01694

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250501T080755+0000

Ratings and Alerts

No rating or validation information has been found for InterPro.

No alerts have been found for InterPro.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6281 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Tian Y, et al. (2025) Molecular and structural basis of a subfamily of PrfH rescuing both the damaged and intact ribosomes stalled in translation. bioRxiv : the preprint server for biology.

Zou X, et al. (2025) Chromosome-level genome assembly of the pine wood nematode carrier

Arhopalus unicolor. Scientific data, 12(1), 111.

Cerqueira de Araujo A, et al. (2025) Genome sequences of four Ixodes species expands understanding of tick evolution. BMC biology, 23(1), 17.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant Stylosanthes angustifolia: insights into genome evolution and drought adaptation. GigaScience, 14.

Kokoulin MS, et al. (2025) Structure of a Sulfated Capsular Polysaccharide from the Marine Bacterium Cobetia marina KMM 1449 and a Genomic Insight into Its Biosynthesis. Marine drugs, 23(1).

Debat H, et al. (2025) RNA Virus Discovery Sheds Light on the Virome of a Major Vineyard Pest, the European Grapevine Moth (Lobesia botrana). Viruses, 17(1).

Will I, et al. (2025) 'Re-Wilding' an Animal Model With Microbiota Shifts Immunity and Stress Gene Expression During Infection. Molecular ecology, 34(1), e17586.

Zhao W, et al. (2025) GoFCards: an integrated database and analytic platform for gain of function variants in humans. Nucleic acids research, 53(D1), D976.

Lee SY, et al. (2025) Exploring the importance of predicted camel NRAP exon 4 for environmental adaptation using a mouse model. Animal genetics, 56(1), e13490.

Shaikh MA, et al. (2025) StCDF1: A 'jack of all trades' clock output with a central role in regulating potato nitrate reduction activity. The New phytologist, 245(1), 282.

Castelo-Branco R, et al. (2025) Genome-informed Discovery of Monchicamides A-K: Cyanobactins from the Microcoleaceae Cyanobacterium LEGE 16532. Journal of natural products, 88(1), 86.

Petroll R, et al. (2025) Enhanced sensitivity of TAPscan v4 enables comprehensive analysis of streptophyte transcription factor evolution. The Plant journal : for cell and molecular biology, 121(1), e17184.

Namuunaa G, et al. (2025) Identification and functional analyses of drought stress resistance genes by transcriptomics of the Mongolian grassland plant Chloris virgata. BMC plant biology, 25(1), 44.

Liu Q, et al. (2025) Identification of EXPA4 as a key gene in cotton salt stress adaptation through transcriptomic and coexpression network analysis of root tip protoplasts. BMC plant biology, 25(1), 65.

Yum SJ, et al. (2025) Antibiotic Resistance Genes and Microbiota in Brassica oleracea var. acephala Cultivated in South Korea: Potential for Resistance Transmission. Journal of agricultural and food chemistry, 73(3), 2156.

Huang X, et al. (2025) Proteomic analysis of egg production peak and senescence in the ovaries of Taihe black-boned silky fowl (Gallus gallus domesticus Brisson). BMC genomics,

26(1), 17.

Lee J, et al. (2025) A chromosome-level genome assembly of wild silkmoth, *Bombyx mandarina*. *Scientific data*, 12(1), 27.

Albuquerque-Wendt A, et al. (2025) TransLeish: Identification of membrane transporters essential for survival of intracellular *Leishmania* parasites in a systematic gene deletion screen. *Nature communications*, 16(1), 299.

Wang GF, et al. (2025) Chromosome-level genome assembly of a destructive leaf-mining moth *Eriocrania semipurpurella alpina*. *Scientific data*, 12(1), 2.

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.