

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

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

Funding Agency: European Union FP7 Scientific Data Repositories, BBSRC, NIGMS

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

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 5595 mentions in open access literature.

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

Lu Z, et al. (2024) Origin of eukaryotic-like Vps23 shapes an ancient functional interplay between ESCRT and ubiquitin system in Asgard archaea. Cell reports, 43(2), 113781.

Dong H, et al. (2024) The Toxoplasma monocarboxylate transporters are involved in the metabolism within the apicoplast and are linked to parasite survival. eLife, 12.

Haque B, et al. (2024) Estimating the proportion of nonsense variants undergoing the newly described phenomenon of manufactured splice rescue. European journal of human genetics : EJHG, 32(2), 238.

- Wang Z, et al. (2024) VarCards2: an integrated genetic and clinical database for ACMG-AMP variant-interpretation guidelines in the human whole genome. *Nucleic acids research*, 52(D1), D1478.
- Wang X, et al. (2024) Telomere-to-telomere and gap-free genome assembly of a susceptible grapevine species (Thompson Seedless) to facilitate grape functional genomics. *Horticulture research*, 11(1), uhad260.
- Xiong Y, et al. (2024) Generating detailed intercellular communication patterns in psoriasis at the single-cell level using social networking, pattern recognition, and manifold learning methods to optimize treatment strategies. *Aging*, 16(3), 2194.
- Zhao DR, et al. (2024) TMT-based quantitative proteomic analysis reveals eggshell matrix protein changes correlated with eggshell quality in Jing Tint 6 laying hens of different ages. *Poultry science*, 103(3), 103463.
- Lu J, et al. (2024) Genome-wide identification, expression and function analysis of the MTP gene family in tulip (*Tulipa gesneriana*). *Frontiers in plant science*, 15, 1346255.
- Özbilen A, et al. (2024) Identification and expression of strigolactone biosynthesis and signaling genes and the in vitro effects of strigolactones in olive (*Olea europaea* L.). *Plant direct*, 8(2), e568.
- Yan G, et al. (2024) A seven-sex species recognizes self and non-self mating-type via a novel protein complex. *eLife*, 13.
- Niu YG, et al. (2024) Surviving winter on the Qinghai-Xizang Plateau: Extensive reversible protein phosphorylation plays a dominant role in regulating hypometabolism in hibernating *Nanorana parkeri*. *Zoological research*, 45(1), 1.
- Wang W, et al. (2024) Exploring Corneal Neovascularization: An Integrated Approach Using Transcriptomics and Proteomics in an Alkali Burn Mouse Model. *Investigative ophthalmology & visual science*, 65(1), 21.
- Dodge AG, et al. (2024) Recombinant *Pseudomonas* growing on non-natural fluorinated substrates shows stress but overall tolerance to cytoplasmically released fluoride anion. *mBio*, 15(1), e0278523.
- Vijayakumar S, et al. (2024) Genomic investigation unveils colistin resistance mechanism in carbapenem-resistant *Acinetobacter baumannii* clinical isolates. *Microbiology spectrum*, 12(2), e0251123.
- Kennard AS, et al. (2024) An internally controlled system to study microtubule network diversification links tubulin evolution to the use of distinct microtubule regulators. *bioRxiv* : the preprint server for biology.

Yang L, et al. (2024) Oligoribonuclease mediates high adaptability of *P. aeruginosa* through metabolic conversion. *BMC microbiology*, 24(1), 25.

Gambelli L, et al. (2024) Structure of the two-component S-layer of the archaeon *Sulfolobus acidocaldarius*. *eLife*, 13.

Goher F, et al. (2024) The Calcium-Dependent Protein Kinase TaCDPK7 Positively Regulates Wheat Resistance to *Puccinia striiformis* f. sp. *tritici*. *International journal of molecular sciences*, 25(2).

Smolikova G, et al. (2024) Involvement of Abscissic Acid in Transition of Pea (*Pisum sativum* L.) Seeds from Germination to Post-Germination Stages. *Plants (Basel, Switzerland)*, 13(2).

Salehi-Najafabadi A, et al. (2024) Insights into additional lactone-based signaling circuits in *Streptomyces*: existence of acyl-homoserine lactones and LuxI/LuxR homologs in six *Streptomyces* species. *Frontiers in microbiology*, 15, 1342637.