

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, data access protocol, data analysis service, data or information resource, database, production service resource, service resource, software resource, web service

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, r3d100010798

Alternate URLs: <https://doi.org/10.17616/R3FS61>

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260903T234838+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 7722 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Withatanung P, et al. (2026) Genomic diversity and clade clustering of Burkholderia pseudomallei and B. thailandensis prophages with soil-derived phages. iScience, 29(2), 114658.

Bacher MC, et al. (2026) Divergent Rickettsia species exhibit distinct mechanisms of actin-based motility. The Journal of cell biology, 225(7).

Harris Snell P, et al. (2026) Coordinated regulation of mRNA translation and stability by ZC3H7A and ZC3H7B RNA-binding proteins. *Cell reports*, 45(6), 117511.

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. *PLoS biology*, 24(6), e3003855.

Hung HF, et al. (2026) Centrosome linker protein CEP68 modulates cellular stress responses via nuclear condensate formation and HSP27 interaction. *iScience*, 29(7), 116491.

Che W, et al. (2026) SARS-CoV-2 damages cardiomyocyte mitochondria and implicates long COVID-associated cardiovascular manifestations. *Journal of advanced research*, 80, 743.

Wu L, et al. (2026) Chromosome-level genome assembly of triploid *Cyperus rotundus* uncovers allelic expression patterns and herbicide resistance mechanisms. *Plant communications*, 7(2), 101624.

Shi F, et al. (2026) OsCPK9-mediated Thr105 phosphorylation activates OsCATC to enhance drought tolerance in rice. *Journal of advanced research*, 81, 57.

Kubo S, et al. (2026) Characterization of fucoxanthin-deficient strains in the haptophyte *Tisochrysis lutea* induced by heavy-ion beam irradiation. *Plant & cell physiology*, 67(3), 265.

HuangFu N, et al. (2026) Gut Microbe-Driven Resistance Mechanisms in *Propylea Japonica*: Insights from Horizontal Gene Transfer and Oxidative Phosphorylation. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(11), e20326.

Jian J, et al. (2026) The genome of *Pleurosigma* provides insights into the evolutionary adaptations of pelagic diatoms. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 33(1).

Crepin DM, et al. (2026) Staphylococcal internalization into osteoblasts: a partially conserved mechanism across the genus. *mBio*, 17(1), e0169725.

Trost K, et al. (2026) Oxygen reductase origin followed the great oxidation event and terminated the Lomagundi excursion. *Biochimica et biophysica acta. Bioenergetics*, 1867(2), 149575.

Passos GS, et al. (2026) Genomic and secondary metabolites of the marine cyanobacterium *Capilliphycus salinus* ALCB114379. *Journal of phycology*, 62(3), 904.

Ramelow J, et al. (2026) Disruption of the AgMOBP1-PfSyn5 interface abolishes malaria transmission. *bioRxiv : the preprint server for biology*.

Li Y, et al. (2026) Deciphering the ancestral mechanisms of neural regeneration through single-cell analyses of jellyfish rhopalium repair. *Science advances*, 12(21), eaeb8034.

Sun H, et al. (2026) The chromosome-level genome assembly and annotation of *Parabotia bimaculata* (Cypriniformes: Cobitidae: Botiinae). *Scientific data*, 13(1).

Carnielli JBT, et al. (2026) Chemical genetics reveals Leishmania KKT2 and CRK9 kinase activity is required for cell cycle progression. PLoS pathogens, 22(5), e1014194.

Guimar??es LO, et al. (2026) Wyeomyia confusa Lispivirus (WcLispV-SP): a novel neotropical mosquito virus in the Lispiviridae family. Archives of virology, 171(6).

Chen HX, et al. (2026) Plasma proteomics of extracellular vesicles identifies key proteins correlating to postoperative atrial fibrillation after coronary artery bypass surgery. Clinical proteomics, 23(1).