

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 access protocol, data analysis service, software resource, web service, data or information resource, database, production service resource, analysis service 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, r3d100010798

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

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260731T042726+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 7000 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Sari E, et al. (2026) Gene duplication, horizontal gene transfer, and trait trade-offs drive evolution of postfire resource acquisition in pyrophilous fungi. Proceedings of the National Academy of Sciences of the United States of America, 123(1), e2519152123.

DiSanza BL, et al. (2026) Bi-allelic variants in BCAT1 impair mitochondrial function and are associated with a candidate neurometabolic disorder. HGG advances, 7(1), 100525.

- Ramasamy P, et al. (2026) Assessing the relation between protein phosphorylation, AlphaFold3 models, and conformational variability. *Protein science : a publication of the Protein Society*, 35(1), e70376.
- Wang YH, et al. (2026) Insights into dill (*Anethum graveolens*) flavor formation via integrative analysis of chromosomal-scale genome, metabolome and transcriptome. *Journal of advanced research*, 79, 847.
- Zhou Z, et al. (2026) Chromosome-level genome provides novel insights into the starch metabolism regulation and evolutionary history of *Tetraselmis helgolandica*. *Journal of advanced research*, 79, 251.
- Kamran Z, et al. (2026) In silico design of a matrix (M) protein-based vaccine candidate against Newcastle disease virus. *Poultry science*, 105(1), 106101.
- Contreras-Moreira B, et al. (2026) The PanOryza pangene catalog of Asian cultivated rice. *Genome research*, 36(1), 226.
- Ansari F, et al. (2026) Characterisation of a Novel Jumbo Lytic *Aeromonas dhakensis* Bacteriophage P19 and Its Endolysin. *Microbial biotechnology*, 19(1), e70289.
- Guest SL, et al. (2025) Myosin 2 drives actin contractility in fast-crawling species outside of the amorphean lineage. *Current biology : CB*, 35(23), 5696.
- De Coninck T, et al. (2025) OsAPSE modulates non-covalent interactions between arabinogalactan protein O-glycans and pectin in rice cell walls. *Frontiers in plant science*, 16, 1588802.
- Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.
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- Wang ZF, et al. (2025) Chromosome-scale assemblies of three *Ormosia* species: repetitive sequences distribution and structural rearrangement. *GigaScience*, 14.
- 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.
- 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.
- 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 silkworm, *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.