

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: 20260919T195116+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 [nidm-terms](#) .

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.

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.

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.

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.

Zhong Z, et al. (2026) Phylogenomic analysis of Cervidae provides insights into antler origin and evolution. *Zoological research*, 47(1), 289.

Tachibana K, et al. (2026) Identification and intracellular functional characterization of myosin XI and VIII in the lycophyte *Selaginella moellendorffii*. *Planta*, 263(3), 66.

Horikawa S, et al. (2026) Gene expression profiling to elucidate the promotive effects of the volatile organic compound 3-octanone on the mycelial growth of *Ganoderma lucidum*. *Biotechnology letters*, 48(1), 32.

Chen Y, et al. (2026) Identification and expression analysis of the Xyloglucan Transglycosylase/Hydrolase (XTH) gene family under salt stress in cowpea (*Vigna unguiculata* L.). *BMC genomics*, 27(1), 187.

Bai Y, et al. (2026) Evolutionary innovation within conserved gene regulatory networks underlying biomineralized skeletons in Bilateria. *Molecular biology and evolution*, 43(2).

Omelchenko O, et al. (2026) Evolved populations of *Listeria monocytogenes* related to biofilm formation and biocide stress in the context of food production environment niches. *Microbial genomics*, 12(1).

Dos Santos MJM, et al. (2026) In Silico Analysis and Expression Profiling of Adhesin-Like Flocculins in *Trichosporon asahii*. *Mycopathologia*, 191(1), 28.

Habib I, et al. (2026) Viral metagenome characterization reveals species-specific virome profiles in Triatominae populations from the southern United States. *PLoS neglected tropical diseases*, 20(2), e0013576.

Lin A, et al. (2026) Chromosome-level genome assembly of the stonefly *Rhopalopsale triangulispina* Mo and Li, 2025 (Plecoptera: Leuctridae). *Scientific data*, 13(1).

Candeliere F, et al. (2026) Altered abundance in cancer patients gut of diadenylate cyclase-encoding bacteria. *Scientific reports*, 16(1), 6070.

Wang Y, et al. (2026) Haplotype-resolved genome assembly of the colored calla lily (*Zantedeschia elliottiana*) provides new insights into the evolution of the family Araceae. *Molecular horticulture*, 6(1), 12.

Gao H, et al. (2026) Genomic landscape and genetic manipulation of an ectoparasitoid wasp, *Gregopimpla kuwanae*. *Communications biology*, 9(1).