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 and classification, InterPro: protein sequence analysis & classification

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

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 5133 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Herrera S, et al. (2023) Genome assembly of the deep-sea coral Lophelia pertusa. GigaByte (Hong Kong, China), 2023, gigabyte78.


Figueroa W, et al. (2023) Distribution and molecular evolution of the anti-CRISPR family


Rashid RSM, et al. (2023) Drug Repurposing of FDA Compounds against ?-Glucosidase for the Treatment of Type 2 Diabetes: Insights from Molecular Docking and Molecular Dynamics Simulations. Pharmaceuticals (Basel, Switzerland), 16(4).


Chino de la Cruz CM, et al. (2023) Complete genome sequence and characterization of a novel Enterococcus faecium with probiotic potential isolated from the gut of Litopenaeus vannamei. Microbial genomics, 9(3).

Lê-Bury P, et al. (2023) Yersiniomics, a Multi-Omics Interactive Database for Yersinia Species. Microbiology spectrum, 11(2), e0382622.


Lin H, et al. (2023) Haplotype-resolved genomes of two buckwheat crops provide insights into their contrasted rutin concentrations and reproductive systems. BMC biology, 21(1), 87.
