

Resource Summary Report

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InterProScan

RRID:SCR_005829

Type: Tool

Proper Citation

InterProScan (RRID:SCR_005829)

Resource Information

URL: <http://www.ebi.ac.uk/Tools/pfa/iprscan/>

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Description: Software package for functional analysis of sequences by classifying them into families and predicting presence of domains and sites. Scans sequences against InterPro's signatures. Characterizes nucleotide or protein function by matching it with models from several different databases. Used in large scale analysis of whole proteomes, genomes and metagenomes. Available as Web based version and standalone Perl version and SOAP Web Service.

Synonyms: InterProScan Sequence Search, InterProScan 2, InterProScan 3, InterProScan 4, InterProScan 5

Resource Type: software application, service resource, data analysis software, data analysis service, data access protocol, data processing software, software resource, production service resource, web service, analysis service resource

Defining Citation: [PMID:15980438](#), [PMID:17202162](#), [PMID:24451626](#)

Keywords: functional, analysis, sequence, protein, nucleotide, predict, presence, domain, site, proteome, genome, metagenome, bio.tools

Funding: European Union ;
Biotechnology and Biological Sciences Research Council ;
EMBL

Availability: Free, Available for download, Freely available

Resource Name: InterProScan

Resource ID: SCR_005829

Alternate IDs: OMICS_01479, biotools:interproscan_4, nlx_149337

Alternate URLs: <https://www.ebi.ac.uk/interpro/download.html>,
https://bio.tools/interproscan_4

License: Apache License version 2.0

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260729T044121+0000

Ratings and Alerts

No rating or validation information has been found for InterProScan.

No alerts have been found for InterProScan.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6936 mentions in open access literature.

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

Parnandi VA, et al. (2026) A small *Candida glabrata* protein promotes hyphal growth in *C. albicans* during mixed-species invasive candidiasis. *Current biology* : CB, 36(1), 1.

Maurstad MF, et al. (2026) The green lacewing venom system and the complex mechanisms underlying its evolution. *Molecular biology and evolution*, 43(1).

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.

García JF, et al. (2026) Intraspecies sequence-graph analysis of the *Phytophthora theobromicola* genome reveals a dynamic structure and variable effector repertoires. *G3* (Bethesda, Md.), 16(1).

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.

Kraege A, et al. (2026) Undermining the cry for help: the phytopathogenic fungus *Verticillium dahliae* secretes an antimicrobial effector protein to undermine host recruitment of antagonistic *Pseudomonas* bacteria. *The New phytologist*, 249(1), 406.

Gorman LM, et al. (2026) Coral Venom and Toxins as Protection Against Crown-of-Thorns Sea Star Attack. *Molecular ecology*, 35(1), e70202.

Marcianò D, et al. (2026) A Comparative Analysis of Receptor-Like Kinases in Chlorophyta Reveals the Presence of Putative Cell Wall Integrity Sensors. *Physiologia plantarum*, 178(1), e70703.

Hirase S, et al. (2026) Ancestral Origin and Structural Characteristics of Non-Syntenic Homologous Chromosomes in Abalones (*Haliotis*). *Molecular ecology resources*, 26(1), e70057.

Tagirdzhanova G, et al. (2026) Chromosome-level genome assembly of the photobiont microalga *Trebouxia* sp. 'A48' from the lichen *Xanthoria parietina*. *The New phytologist*, 249(2), 1036.

Contreras-Moreira B, et al. (2026) The PanOryza pangene catalog of Asian cultivated rice. *Genome research*, 36(1), 226.

Guang X, et al. (2025) Telomere-to-telomere African wild rice (*Oryza longistaminata*) reference genome reveals segmental and structural variation. *GigaScience*, 14.

Kumar V, et al. (2025) Whole genome sequencing and assembly of the house sparrow, *Passer domesticus*. *GigaByte (Hong Kong, China)*, 2025, gigabyte161.

Liang Y, et al. (2025) The molecular basis of octocoral calcification revealed by genome and skeletal proteome analyses. *GigaScience*, 14.

Chen M, et al. (2025) The genome of *Hippophae salicifolia* provides new insights into the sexual differentiation of sea buckthorn. *GigaScience*, 14.

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of Cypriniformes. *GigaScience*, 14.

Qin H, et al. (2025) The complete genome assembly of *Astragalus membranaceus*: enabling more accurate genetic research. *GigaScience*, 14.

Jiang M, et al. (2025) The telomere-to-telomere gap-free reference genome and taxonomic reassessment of *Siniperca roulei*. *GigaScience*, 14.

Galvis-Marín JC, et al. (2025) Characterisation of Antifungal Resistance to Azoles in Colombian Isolates of *Malassezia* spp. *Mycoses*, 68(9), e70112.

Javier MCF, et al. (2025) Draft genome of the endangered visayan spotted deer (*Rusa alfredi*), a Philippine endemic species. *GigaByte (Hong Kong, China)*, 2025, gigabyte150.