

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/>

Proper Citation: InterProScan (RRID:SCR_005829)

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

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

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

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

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: 20260905T132542+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 7512 mentions in open access literature.

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

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. *GigaScience*, 15.

Wu X, et al. (2026) Locus-Specific Human Endogenous Retrovirus ERVK18 Expression Indicates an Inflamed Microenvironment and Favorable Immunotherapy Outcome in Small Cell Lung Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(11), 2214.

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Kim DH, et al. (2026) Tumor Exosomal L1 Cell Adhesion Molecule Promotes Brain Metastasis of Lung Cancer. *Research (Washington, D.C.)*, 9, 1126.

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.

Plasil M, et al. (2026) A chromosome-level genome assembly of the snow leopard, *Panthera uncia*. *The Journal of heredity*, 117(2), 272.

Yan L, et al. (2026) A NACHT domain-containing protein Ncp is required for appendage-associated unconventional protein secretion in the fungus *Penicillium herquei*. *iScience*, 29(7), 116464.

Nickles GR, et al. (2026) Tracing the origins of crmA megasynthase through lichen genomes. *Current biology : CB*, 36(13), 3354.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

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

Puccetti G, et al. (2026) A large European diversity panel reveals complex azole fungicide resistance gains of a major wheat pathogen. *mBio*, 17(1), e0276625.

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

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.

Huang Y, et al. (2026) RIFinder reveals widespread adaptive remote introgression in grass genomes. *Plant communications*, 7(2), 101658.

Zou R, et al. (2026) A chromosome-level genome assembly of *Cistanche deserticola* provides insights into its evolution and molecular mechanisms of parasitism. *Plant communications*, 7(1), 101581.

Boulay A, et al. (2026) PhaLP 2.0: extending the community-oriented phage lysin database with a SUBLYME pipeline for metagenomic discovery. *Database : the journal of biological databases and curation*, 2026.

Saado I, et al. (2026) Engineering an Exo70 integrated domain of a barley NLR for improved blast resistance. *The Plant cell*, 38(6).

Wan Y, et al. (2026) Genomic and molecular characterisation of a KPC-producing *Klebsiella pneumoniae* clinical isolate resistant to meropenem-vaborbactam, imipenem-relebactam, and ceftazidime-avibactam. *BMC genomic data*, 27(1).

Hamm JN, et al. (2026) New lineages provide insights into the convergent evolution of extreme salt adaptation within symbiotic Archaea. *Molecular biology and evolution*, 43(5).