

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: 20260919T195100+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 [T1D](#).

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

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.

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

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.

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.

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.

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

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.

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.

Wu B, et al. (2026) A chromosome-level genome assembly of *Coryphaenoides armatus*. *Scientific data*, 13(1).

Ringeval A, et al. (2026) Multi-omics characterization of toxin expression and producing organs in the predatory gastropods *Monoplex corrugatus* and *Stramonita haemastoma*. *BMC genomics*, 27(1).

Pfeifer K, et al. (2026) Chemical capture of diazo metabolites reveals biosynthetic hydrazone oxidation. *Nature*, 652(8109), 517.

Selleri E, et al. (2026) Assessment of genome evolution in *Bifidobacterium adolescentis* indicates genetic adaptation to the human gut. *mSystems*, 11(3), e0117325.

Sasidharan V, et al. (2026) Extracellular vesicles mediate stem cell signaling and systemic RNAi in planarians. *Science advances*, 12(6), eady1461.

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

Usmani SF, et al. (2026) Genome-wide identification of ADK gene family associated with heat stress tolerance in chili (*Capsicum annuum* L.). *BMC genomic data*, 27(1).

Stilwell PA, et al. (2026) The genome of *Istocheta aldrichi* (Diptera: Tachinidae), a parasitoid of the Japanese beetle, *Popillia japonica* (Coleoptera: Scarabaeidae). *G3 (Bethesda, Md.)*, 16(4).

Nguyen TNG, et al. (2026) Splicing regulation and intron evolution in the short-intron ciliate model of endosymbiosis *Paramecium bursaria*. *Nucleic acids research*, 54(3).