

Resource Summary Report

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[inBio Map](#)

RRID:SCR_016147

Type: Tool

Proper Citation

inBio Map (RRID:SCR_016147)

Resource Information

URL: <https://www.intomics.com/inbio/map/#home>

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Description: Database for investigating and visualizing protein-protein interactions. It aims to maintain coverage, quality, convenience, and transparency in the field of PPI research.

Synonyms: inBio

Resource Type: data visualization software, data or information resource, database, software application, data processing software, software resource

Defining Citation: [PMID:27892958](#)

Keywords: ppi, protein, visualization

Funding: NICHD P01 HD068250;
Massachusetts General Hospital ;
Broad Institute of MIT and Harvard ;
NIMH R01 MH109903;
Lundbeck Foundation ;
Novo Nordisk Foundation NNF14CC0001

Availability: Freely available, Free, Available for download

Resource Name: inBio Map

Resource ID: SCR_016147

License: Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License

License URLs: https://www.intomics.com/inbio/map/#terms_of_use

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260801T042756+0000

Ratings and Alerts

No rating or validation information has been found for inBio Map.

No alerts have been found for inBio Map.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Campanelli L, et al. (2025) New insights into the molecular biology of Alzheimer's-like cerebral amyloidosis achieved through multi-omics approaches. PloS one, 20(9), e0330859.

Senatore E, et al. (2025) Praja2 controls P-body assembly and translation in glioblastoma by non-proteolytic ubiquitylation of DDX6. EMBO reports, 26(9), 2347.

Rinaldi L, et al. (2024) Downregulation of praja2 restrains endocytosis and boosts tyrosine kinase receptors in kidney cancer. Communications biology, 7(1), 208.

Cui Y, et al. (2023) Alternative polyadenylation transcriptome-wide association study identifies APA-linked susceptibility genes in brain disorders. Nature communications, 14(1), 583.

Modvig S, et al. (2022) High CD34 surface expression in BCP-ALL predicts poor induction therapy response and is associated with altered expression of genes related to cell migration and adhesion. Molecular oncology, 16(10), 2015.

Wang T, et al. (2022) Integrative analysis prioritised oxytocin-related biomarkers associated with the aetiology of autism spectrum disorder. EBioMedicine, 81, 104091.

Walakira A, et al. (2022) Detecting gene-gene interactions from GWAS using diffusion kernel principal components. BMC bioinformatics, 23(1), 57.

Huang M, et al. (2022) NRIP1 aggravates lung injury caused by Pseudomonas aeruginosa in mice by increasing PIAS1 ubiquitination. Aging, 14(8), 3529.

Chasapis CT, et al. (2022) The Human Myelin Proteome and Sub-Metalloproteome Interaction Map: Relevance to Myelin-Related Neurological Diseases. Brain sciences, 12(4).

Hu L, et al. (2021) The expression and clinical prognostic value of protein phosphatase 1 catalytic subunit beta in pancreatic cancer. *Bioengineered*, 12(1), 2763.

Sosnowska M, et al. (2021) Diamond Nanofilm Normalizes Proliferation and Metabolism in Liver Cancer Cells. *Nanotechnology, science and applications*, 14, 115.

Han Z, et al. (2021) Model-based analysis uncovers mutations altering autophagy selectivity in human cancer. *Nature communications*, 12(1), 3258.

Shi L, et al. (2021) AddictGene: An integrated knowledge base for differentially expressed genes associated with addictive substance. *Computational and structural biotechnology journal*, 19, 2416.

Colli ML, et al. (2020) An integrated multi-omics approach identifies the landscape of interferon- γ -mediated responses of human pancreatic beta cells. *Nature communications*, 11(1), 2584.

Zhang Z, et al. (2020) Determining the Clinical Value and Critical Pathway of GTPBP4 in Lung Adenocarcinoma Using a Bioinformatics Strategy: A Study Based on Datasets from The Cancer Genome Atlas. *BioMed research international*, 2020, 5171242.

Terkelsen T, et al. (2020) Secreted breast tumor interstitial fluid microRNAs and their target genes are associated with triple-negative breast cancer, tumor grade, and immune infiltration. *Breast cancer research : BCR*, 22(1), 73.

Zhang Q, et al. (2019) iTRAQ-based proteomic analysis of endotoxin tolerance induced by lipopolysaccharide. *Molecular medicine reports*, 20(1), 584.

Law PJ, et al. (2019) Association analyses identify 31 new risk loci for colorectal cancer susceptibility. *Nature communications*, 10(1), 2154.

Zhang W, et al. (2019) Predicting the survival of patients with lung adenocarcinoma using a four-gene prognosis risk model. *Oncology letters*, 18(1), 535.

Alexander-Dann B, et al. (2018) Developments in toxicogenomics: understanding and predicting compound-induced toxicity from gene expression data. *Molecular omics*, 14(4), 218.