

Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

I2D

RRID:SCR_002957

Type: Tool

Proper Citation

I2D (RRID:SCR_002957)

Resource Information

URL: <http://ophid.utoronto.ca/i2d>

Proper Citation: I2D (RRID:SCR_002957)

Description: Database of known and predicted mammalian and eukaryotic protein-protein interactions, it is designed to be both a resource for the laboratory scientist to explore known and predicted protein-protein interactions, and to facilitate bioinformatics initiatives exploring protein interaction networks. It has been built by mapping high-throughput (HTP) data between species. Thus, until experimentally verified, these interactions should be considered predictions. It remains one of the most comprehensive sources of known and predicted eukaryotic PPI. It contains 490,600 Source Interactions, 370,002 Predicted Interactions, for a total of 846,116 interactions, and continues to expand as new protein-protein interaction data becomes available.

Abbreviations: I2D

Synonyms: Interologous Interaction Database, OPHID, I2D - Interologous Interaction Database

Resource Type: data analysis service, data or information resource, database, service resource, production service resource, analysis service resource

Defining Citation: [PMID:17535438](#), [PMID:15657099](#)

Keywords: interaction, prediction, protein-protein interaction, high-throughput, model organism, mammal, eukaryote, visualization, interolog, protein

Funding: National Science and Engineering Research Council RGPIN 203833-02; NIGMS P50-GM62413

Availability: Free, Available for download, Freely available

Resource Name: I2D

Resource ID: SCR_002957

Alternate IDs: nif-0000-03005, r3d100010675

Alternate URLs: <https://doi.org/10.17616/R3BG8R>

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260801T190222+0000

Ratings and Alerts

No rating or validation information has been found for I2D.

No alerts have been found for I2D.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Ma F, et al. (2021) Applications and analytical tools of cell communication based on ligand-receptor interactions at single cell level. Cell & bioscience, 11(1), 121.

Glaus Garzon JF, et al. (2020) Tumor cell endogenous HIF-1?? activity induces aberrant angiogenesis and interacts with TRAF6 pathway required for colorectal cancer development. Neoplasia (New York, N.Y.), 22(12), 745.

Mao Y, et al. (2020) A network analysis revealed the essential and common downstream proteins related to inguinal hernia. PloS one, 15(1), e0226885.

Kuasne H, et al. (2017) Integrative miRNA and mRNA analysis in penile carcinomas reveals markers and pathways with potential clinical impact. Oncotarget, 8(9), 15294.

Stojanova A, et al. (2016) MYC interaction with the tumor suppressive SWI/SNF complex member INI1 regulates transcription and cellular transformation. Cell cycle (Georgetown, Tex.), 15(13), 1693.

Cervigne NK, et al. (2014) Recurrent genomic alterations in sequential progressive leukoplakia and oral cancer: drivers of oral tumorigenesis? Human molecular genetics, 23(10), 2618.

Pastrello C, et al. (2014) Integration, visualization and analysis of human interactome. Biochemical and biophysical research communications, 445(4), 757.

- Lapin V, et al. (2014) Kinome-wide screening of HER2+ breast cancer cells for molecules that mediate cell proliferation or sensitize cells to trastuzumab therapy. *Oncogenesis*, 3(12), e133.
- Feng M, et al. (2014) Hemolymph proteome changes during worker brood development match the biological divergences between western honey bees (*Apis mellifera*) and eastern honey bees (*Apis cerana*). *BMC genomics*, 15(1), 563.
- Cirilo PD, et al. (2013) An integrative genomic and transcriptomic analysis reveals potential targets associated with cell proliferation in uterine leiomyomas. *PloS one*, 8(3), e57901.
- Yakhini Z, et al. (2011) Cancer computational biology. *BMC bioinformatics*, 12, 120.
- Osei-Kumah A, et al. (2011) Sex-specific differences in placental global gene expression in pregnancies complicated by asthma. *Placenta*, 32(8), 570.
- Fortney K, et al. (2011) Integrative computational biology for cancer research. *Human genetics*, 130(4), 465.
- Radulovich N, et al. (2010) Differential roles of cyclin D1 and D3 in pancreatic ductal adenocarcinoma. *Molecular cancer*, 9, 24.
- Reis PP, et al. (2010) Programmed cell death 4 loss increases tumor cell invasion and is regulated by miR-21 in oral squamous cell carcinoma. *Molecular cancer*, 9, 238.
- Makridakis M, et al. (2010) Secretome proteomics for discovery of cancer biomarkers. *Journal of proteomics*, 73(12), 2291.
- Li MX, et al. (2010) A knowledge-based weighting framework to boost the power of genome-wide association studies. *PloS one*, 5(12), e14480.
- Wu G, et al. (2010) A human functional protein interaction network and its application to cancer data analysis. *Genome biology*, 11(5), R53.
- Agarwal R, et al. (2009) The emerging role of the RAB25 small GTPase in cancer. *Traffic (Copenhagen, Denmark)*, 10(11), 1561.
- Cox B, et al. (2009) Comparative systems biology of human and mouse as a tool to guide the modeling of human placental pathology. *Molecular systems biology*, 5, 279.