

Resource Summary Report

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Integrating Network Objects with Hierarchies

RRID:SCR_002084

Type: Tool

Proper Citation

Integrating Network Objects with Hierarchies (RRID:SCR_002084)

Resource Information

URL: <http://www.inoh.org>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on October 28, 2025. INOH (Integrating Network Objects with Hierarchies) is a pathway database of model organisms including human, mouse, rat and others. In INOH, the term pathway refers to higher order functional knowledge such as relationships among multiple bio-molecules that constitute signal transduction pathways or biological events in general. As most part of this knowledge resides in scientific articles, the database focuses on curating and encoding textual knowledge into a machine-processable form. The system provides pathway information as a composite of biological events, since functional knowledge is usually described as a set of fragmented processes. Each event is annotated with entries of a event ontology, which also has links to GO.

Synonyms: INOH

Resource Type: data or information resource, ontology, controlled vocabulary, database

Defining Citation: [PMID:22120663](#)

Keywords: biomolecule, human, mouse, pathway, rat, transduction

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Integrating Network Objects with Hierarchies

Resource ID: SCR_002084

Alternate IDs: nif-0000-20859

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260731T042626+0000

Ratings and Alerts

No rating or validation information has been found for Integrating Network Objects with Hierarchies.

No alerts have been found for Integrating Network Objects with Hierarchies.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Yun JW, et al. (2019) Elucidation of Novel Therapeutic Targets for Acute Myeloid Leukemias with RUNX1-RUNX1T1 Fusion. International journal of molecular sciences, 20(7).

Rohfritsch A, et al. (2018) Preliminary insights into the genetics of bank vole tolerance to Puumala hantavirus in Sweden. Ecology and evolution, 8(22), 11273.

Wathieu H, et al. (2017) Differential prioritization of therapies to subtypes of triple negative breast cancer using a systems medicine method. Oncotarget, 8(54), 92926.

Blohmke CJ, et al. (2016) Interferon-driven alterations of the host's amino acid metabolism in the pathogenesis of typhoid fever. The Journal of experimental medicine, 213(6), 1061.

Gupta SK, et al. (2015) Scrutinizing the immune defence inventory of Camponotus floridanus applying total transcriptome sequencing. BMC genomics, 16(1), 540.

Raju R, et al. (2014) A Network Map of FGF-1/FGFR Signaling System. Journal of signal transduction, 2014, 962962.

Telikicherla D, et al. (2011) A comprehensive curated resource for follicle stimulating hormone signaling. BMC research notes, 4, 408.

Yamamoto S, et al. (2011) INOH: ontology-based highly structured database of signal transduction pathways. Database : the journal of biological databases and curation, 2011, bar052.

Cavalieri D, et al. (2010) DC-ATLAS: a systems biology resource to dissect receptor specific signal transduction in dendritic cells. Immunome research, 6, 10.

Isserlin R, et al. (2010) Pathway analysis of dilated cardiomyopathy using global proteomic profiling and enrichment maps. Proteomics, 10(6), 1316.

Wu G, et al. (2010) A human functional protein interaction network and its application to cancer data analysis. Genome biology, 11(5), R53.

Demir E, et al. (2010) The BioPAX community standard for pathway data sharing. *Nature biotechnology*, 28(9), 935.

Kandasamy K, et al. (2010) NetPath: a public resource of curated signal transduction pathways. *Genome biology*, 11(1), R3.

Lynn DJ, et al. (2008) InnateDB: facilitating systems-level analyses of the mammalian innate immune response. *Molecular systems biology*, 4, 218.

Tsui IF, et al. (2007) Public databases and software for the pathway analysis of cancer genomes. *Cancer informatics*, 3, 379.