

Resource Summary Report

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Information Hyperlinked Over Proteins

RRID:SCR_004829

Type: Tool

Proper Citation

Information Hyperlinked Over Proteins (RRID:SCR_004829)

Resource Information

URL: <http://www.ihop-net.org/UniPub/iHOP/>

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Description: Information system that provides a network of concurring genes and proteins extends through the scientific literature touching on phenotypes, pathologies and gene function. It provides this network as a natural way of accessing millions of PubMed abstracts. By using genes and proteins as hyperlinks between sentences and abstracts, the information in PubMed can be converted into one navigable resource, bringing all advantages of the internet to scientific literature research. Moreover, this literature network can be superimposed on experimental interaction data (e.g., yeast-two hybrid data from *Drosophila melanogaster* and *Caenorhabditis elegans*) to make possible a simultaneous analysis of new and existing knowledge. The network contains half a million sentences and 30,000 different genes from humans, mice, *D. melanogaster*, *C. elegans*, zebrafish, *Arabidopsis thaliana*, yeast and *Escherichia coli*.

Abbreviations: iHOP

Synonyms: iHOP - Information Hyperlinked over Proteins

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

Defining Citation: [PMID:15226743](#)

Keywords: phenotype, gene, protein, interaction, pathology, physiology, gene network, network, literature, gene function, text-mining, bio.tools

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Availability: Creative Commons Attribution-NoDerivs License, Works v3

Resource Name: Information Hyperlinked Over Proteins

Resource ID: SCR_004829

Alternate IDs: biotools:ihop, nif-0000-00232, OMICS_01185

Alternate URLs: <https://bio.tools/ihop>

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260905T133126+0000

Ratings and Alerts

No rating or validation information has been found for Information Hyperlinked Over Proteins.

No alerts have been found for Information Hyperlinked Over Proteins.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Heinrich F, et al. (2017) Morphologic, phenotypic, and transcriptomic characterization of classically and alternatively activated canine blood-derived macrophages in vitro. PloS one, 12(8), e0183572.

Pfankuche VM, et al. (2017) Reduced angiogenic gene expression in morbillivirus-triggered oncolysis in a translational model for histiocytic sarcoma. Journal of cellular and molecular medicine, 21(4), 816.

Dulcis D, et al. (2017) Neurotransmitter Switching Regulated by miRNAs Controls Changes in Social Preference. Neuron, 95(6), 1319.

Loviglio MN, et al. (2016) Identification of a RAI1-associated disease network through integration of exome sequencing, transcriptomics, and 3D genomics. Genome medicine, 8(1), 105.

Spitzbarth I, et al. (2016) Immunohistochemical and transcriptome analyses indicate complex breakdown of axonal transport mechanisms in canine distemper leukoencephalitis. Brain and behavior, 6(7), e00472.

Seehusen F, et al. (2016) Accumulation of Extracellular Matrix in Advanced Lesions of Canine Distemper Demyelinating Encephalitis. PloS one, 11(7), e0159752.

Ahmed Z, et al. (2016) Mining biomedical images towards valuable information retrieval in biomedical and life sciences. Database : the journal of biological databases and curation, 2016.

Venkatesan A, et al. (2016) SciLite: a platform for displaying text-mined annotations as a means to link research articles with biological data. Wellcome open research, 1, 25.

Wang J, et al. (2015) Pathway and network approaches for identification of cancer signature markers from omics data. Journal of Cancer, 6(1), 54.

Tripathi S, et al. (2015) The gastrin and cholecystokinin receptors mediated signaling network: a scaffold for data analysis and new hypotheses on regulatory mechanisms. BMC systems biology, 9, 40.

Choi M, et al. (2014) Overexpression of human GATA-1 and GATA-2 interferes with spine formation and produces depressive behavior in rats. PloS one, 9(10), e109253.

Lim JM, et al. (2014) Quantitative secretome and glycome of primary human adipocytes during insulin resistance. Clinical proteomics, 11(1), 20.

Patnala R, et al. (2013) Candidate gene association studies: a comprehensive guide to useful in silico tools. BMC genetics, 14, 39.

Feltes BC, et al. (2013) Toxicological effects of the different substances in tobacco smoke on human embryonic development by a systems chemo-biology approach. PloS one, 8(4), e61743.

Zaman N, et al. (2013) Signaling network assessment of mutations and copy number variations predict breast cancer subtype-specific drug targets. Cell reports, 5(1), 216.

Li SC, et al. (2012) The somatostatin analogue octreotide inhibits growth of small intestine neuroendocrine tumour cells. PloS one, 7(10), e48411.

S??hngen C, et al. (2011) Development of a classification scheme for disease-related enzyme information. BMC bioinformatics, 12, 329.

Seo SM, et al. (2011) Deoxyribonucleic Acid copy number aberrations in vasospastic angina patients using an array comparative genomic hybridization. Korean circulation journal, 41(7), 385.

Bay-Jensen AC, et al. (2011) A microarray analysis of full depth knee cartilage of ovariectomized rats. BMC research notes, 4, 63.

Berretta R, et al. (2010) Cancer biomarker discovery: the entropic hallmark. PloS one, 5(8), e12262.