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INOH pathway data ontologies



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Short Abstract: INOH is a manually curated database of signal transduction pathways. While conventional pathway data are highly structured, they use open vocabularies to annotate their pathway components. To resolve the problem of data integration or mapping between data from different sources, INOH pathway objects are annotated by our pathway annotation ontologies.

Long Abstract:

INOH is a manually curated biological database of mammal signal transduction pathways. The aim of INOH project is to provide pathway knowledge in a machine-accessible form that resides in the scientific literature. In INOH, a pathway has a hierarchical and recursive structure. This means a pathway consists from a set of pathways (sub-pathways) and a physical entity in these pathways may consist from multiple components (sub-units). A sub-pathway is defined by a process or reaction and its input/output/controller material, e.g., a protein and its phosphorylated form and an enzyme. Those sub-pathways are connected to each other to form a bigger pathway. In INOH, a pathway is called “event” and each event consists of other events (subpathways) or a process, input/output materials and controllers.

While conventional pathway data are highly structured, they use open vocabularies to annotate their pathway components. As this hampers data integration or mapping between data from different sources, we are developing a set of annotation ontologies for pathways. For example, the MoleculeRole ontology categorizes proteins as they appear in the scientific literature. It captures the relations among molecule functions, generic molecules, concrete molecules, sequence accession numbers and complexes and their subunits. The Event Ontology manages the relations between pathways and sub-pathways and biological phenomena of molecular, cellular and organism levels. Both ontologies are available from the OBO (Open Biomedical Ontologies) site and the INOH project site (<http://www.inoh.org>). Other annotation ontologies include Location Ontology. Every pathway object such as physical-entity or biological-event is annotated by these ontologies.

The INOH data release 1.0 includes 1379 interactions, 1743 biological events, 6921 physical-entities and is available in our INOH graph format and the BioPAX data exchange format. The MoleculeRole Ontology version 2.11 has 7236 terms including more than 7149 protein terms with 4619 UniProt accession numbers and the Event Ontology version 1.59 has more than 2665 terms with GO IDs, KEGG PATHWAY IDs, Reactome IDs and PSI-MI interaction type IDs.

The following is a list of pathways curated in the INOH project:

B cell receptor signaling, CD4 T cell receptor signaling (ERK/JNK/NF-kb cascade), CD4 T cell receptor signaling, GPCR Dopamine D1like receptor, GPCR GroupI metabotropic glutamate receptor, GPCR signaling (G alpha i/q/s, Epac and ERK, PKA and ERK, cholera toxin, pertussis toxin), IL-1 signaling pathway (through JNK cascade, through NF-kappaB, through p38 cascade), Toll-like receptor signaling pathway (through ECSIT, MEKK1, MKKs, JNK cascade, through ECSIT, MEKK1, MKKs, p38 cascade, through JNK cascade, through NF-kappaB, p38 cascade), Notch signaling pathway Diagram, BMP2 signaling(through TAK1), BMP2 signaling (TGF-beta_signaling MolecularVariation), Drosophila IMD pathway, Drosophila, EGF signaling pathway, FGF signaling pathway, Growth hormone signaling (JAK2 STAT5), HGF signaling pathway, IFN alpha signaling (JAK1 TYK2 STAT1 STAT2/3), IFN gamma signaling (JAK1 JAK2 STAT1), IL-10 signaling (JAK1 TYK2 STAT3), IL-12 signaling (JAK2 TYK2 STAT4), IL-2 signaling (JAK1 JAK3 STAT5), IL-3 signaling (JAK2 STAT5), IL-4 signaling (JAK1 JAK3 STAT6), IL-6 signaling (JAK1 JAK2 STAT3), IL-7 signaling (JAK1 JAK3 STAT5), Integrin signaling pathway, JAK-STAT pathway and regulation pathway, LIF signaling (JAK1 JAK2 STAT3), NGF signaling pathway, PDGF signaling pathway, TGF-beta signaling (through TAK1), TGF-beta_super_family_signaling_pathway (canonical), TPO signaling (JAK2 STAT3), VEGF signaling pathway, C. elegans endoderm induction Wnt signaling pathway Diagram, Canonical Wnt signaling pathway Diagram, Drosophila Wingless/Wnt signaling pathway Diagram, Mammalian Wnt signaling pathway Diagram, Xenopus axis formation Wnt signaling pathway Diagram

[Reference]

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- [2] Tatsuya Kushida, Toshihisa Takagi and Ken Ichiro Fukuda, Event ontology: a pathway-centric ontology for biological processes, Pacific Symposium on Biocomputing 11:152-163(2006).