**InnateDB**

**RRID:** SCR_006714  
**Type:** Tool

**Proper Citation**

InnateDB (RRID:SCR_006714)

**Resource Information**

**URL:** [http://www.innatedb.com](http://www.innatedb.com)

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**Description:** Publicly available database of the genes, proteins, experimentally-verified interactions and signaling pathways involved in the innate immune response of humans, mice and bovines to microbial infection. The database captures coverage of the innate immunity interactome by integrating known interactions and pathways from major public databases together with manually-curated data into a centralized resource. The database can be mined as a knowledgebase or used with the integrated bioinformatics and visualization tools for the systems level analysis of the innate immune response. Although InnateDB curation focuses on innate immunity-relevant interactions and pathways, it also incorporates detailed annotation on the entire human, mouse and bovine interactomes by integrating data (178,000+ interactions & 3,900+ pathways) from several of the major public interaction and pathway databases. InnateDB also has integrated human and mouse orthology predictions generated using Ortholgue software. Ortholgue uses a phylogenetic distance-based method to identify possible paralogs in high-throughput orthology predictions. Integrated human and mouse conserved gene order and synteny information has also been determined to provide further support for orthology predictions. InnateDB Capabilities:  
* View statistics for manually-curated innate immunity relevant molecular interactions. New manually curated interactions are submitted weekly.  
* Search for genes and proteins of interest.  
* Search for experimentally-verified molecular interactions by gene/protein name, interaction type, cell type, etc.  
* Search genes/interactions belonging to 3,900 pathways.  
* Visualize interactions using an intuitive subcellular localization-based layout in Cerebral.  
* Upload your own list of genes along with associated gene expression data (from up to 10 experimental conditions) to interactively analyze this data in a molecular interaction network context. Once you have uploaded your data, you will be able to interactively visualize interaction networks with expression data overlaid; carry out Pathway, Gene Ontology and Transcription Factor Binding Site over-representation analyses; construct orthologous
interaction networks in other species; and much more. * Access curated interaction data via a dedicated PSICQUIC webservice.

**Abbreviations:** InnateDB


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

**Defining Citation:** PMID:23180781, PMID:18766178

**Keywords:** gene, immune response, pathway, protein, signaling pathway, interaction, immune, signaling response, gene, orthology prediction, orthology, ortholg, annotation, interactome, gene expression, molecule, protein-protein interaction, molecular interaction, visualization, nucleic acid-protein, nucleic acid, network, web service, transcription factor binding site, software resource, FASEB list

**Related Condition:** Microbial infection, Allergy, Asthma

**Funding Agency:** Michael Smith Foundation for Health Research, AllerGen, AllerGen, Teagasc, European Union

**Availability:** Public, Acknowledgement requested, Curated interactions are licensed under the, Design Science License, All other data is licensed under the terms of the originating database.

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**Alternate IDs:** nif-0000-20808

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**Ratings and Alerts**

No rating or validation information has been found for InnateDB.

No alerts have been found for InnateDB.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**
We found 384 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [RRID](https://rrid.org).


Welz L, et al. (2022) Epithelial X-Box Binding Protein 1 Coordinates Tumor Protein p53-Driven DNA Damage Responses and Suppression of Intestinal Carcinogenesis. Gastroenterology, 162(1), 223.

Chung AW, et al. (2022) Tocilizumab overcomes chemotherapy resistance in mesenchymal stem-like breast cancer by negating autocrine IL-1A induction of IL-6. NPJ breast cancer, 8(1), 30.


Cooke M, et al. (2022) PROTEIN KINASE C ALPHA IS A CENTRAL NODE FOR TUMORIGENIC TRANSCRIPTIONAL NETWORKS IN HUMAN PROSTATE CANCER. Cancer research communications, 2(11), 1372.


Ashley SE, et al. (2022) Remission of peanut allergy is associated with rewiring of allergen-driven T helper 2-related gene networks. Allergy, 77(10), 3015.