Resource Summary Report

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InnateDB

RRID:SCR_006714
Type: Tool

Proper Citation

InnateDB (RRID:SCR_006714)

Resource Information

URL: 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, mouse and bovine 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

Synonyms: A Knowledge Resource for Innate Immunity Interactions and Pathways, InnateDB: Systems Biology of the Innate Immune Response, InnateDB - A Knowledge Resource for Innate Immunity Interactions and Pathways

Resource Type: data or information resource, database

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: Michael Smith Foundation for Health Research ;
AllerGen 12ASI1;
AllerGen 12B&B2;
Teagasc RMIS6018;
European Union PSIMEx project contract FP7-HEALTH-2007-223411

Availability: Free, Freely available

Resource Name: InnateDB

Resource ID: SCR_006714

Alternate IDs: nif-0000-20808, r3d100010676

Alternate URLs: https://doi.org/10.17616/R36S43

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260801T190315+0000

Ratings and Alerts

No rating or validation information has been found for InnateDB.

No alerts have been found for InnateDB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 496 mentions in open access literature.

Listed below are recent publications. The full list is available at ASWG .

Gou X, et al. (2026) Identification of a Two-Gene Biomarker Correlated with Sensitivity to Combined PARP7 Inhibition and AHR Activation in Cancer Cells. Cancer research communications, 6(1), 5.

Wu J, et al. (2025) Identification and validation of a novel signature based on immune?related genes from epithelial cells to predict prognosis and treatment response in patients with lung squamous cell cancer by integrated analysis of single?cell and bulk RNA sequencing. Oncology letters, 29(3), 158.

Vinette V, et al. (2025) PTPN2 Negatively Regulates Macrophage Immune Responses and Cellular Bioenergetics. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(9), e70536.

Beneker O, et al. (2025) Urbanization and genetic homogenization in the medieval Low Countries revealed through a ten-century paleogenomic study of the city of Sint-Truiden. Genome biology, 26(1), 127.

Zhang Y, et al. (2025) GATA1: A key biomarker for predicting the prognosis of patients with diffuse large B-cell lymphoma. Open medicine (Warsaw, Poland), 20(1), 20251185.

Kakavand N, et al. (2025) Atg16l1 and Xbp1 cooperatively protect from transcription-associated mutagenesis and small intestinal carcinogenesis. Oncogene, 44(45), 4413.

Li W, et al. (2025) Sphingolipid metabolism-related genes for the diagnosis of metabolic syndrome by integrated bioinformatics analysis and Mendelian randomization identification. Diabetology & metabolic syndrome, 17(1), 234.

Fernandes IG, et al. (2025) Heightened Innate Immune and Inflammatory Gene Expression in the Skin of Severe COVID-19 Cases. Journal of inflammation research, 18, 9119.

Zhang M, et al. (2025) Prognostic role of tumor microenvironment and immune- and autophagy-related genes in colorectal adenocarcinoma. Translational cancer research, 14(5), 2835.

Ma H, et al. (2025) Comprehensive characterization of NK cell-related genes in cutaneous melanoma identified a novel prognostic signature for predicting the prognosis, immunotherapy, and chemotherapy efficacy. Discover oncology, 16(1), 1243.

Bao Q, et al. (2025) Identification of immune-related cervical cancer prognostic biomarkers and construction of prognostic model based on tumor microenvironment. European journal of medical research, 30(1), 261.

Yan W, et al. (2025) Targeted editing of CCL5 with CRISPR-Cas9 nanoparticles enhances breast cancer immunotherapy. Apoptosis : an international journal on programmed cell death, 30(3-4), 912.

Liu G, et al. (2025) CD63-Mediated SARS-CoV-2 RBD Fusion Neoantigen DNA Vaccine Enhances Antitumor Immune Response in a Mouse Panc02 Model via EV-Targeted Delivery. Vaccines, 13(9).

Hu W, et al. (2025) Prognostic and therapeutic relevance of IL2RG-related LncRNAs in clear cell renal cell carcinoma. Scientific reports, 15(1), 29651.

Gray DT, et al. (2025) Midbrain extracellular matrix and microglia are associated with cognition in aging mice. Nature communications, 16(1), 11319.

Xu L, et al. (2025) Neuron-specific homologous coding genes and non-coding regulatory regions are the most conserved amongst amniotes despite neuron-specific cell size diversity. Scientific reports, 15(1), 43971.

Zhou W, et al. (2025) Integrated analysis of single?cell and bulk RNA sequencing data to construct a risk assessment model based on plasma cell immune?related genes for predicting patient prognosis and therapeutic response in lung adenocarcinoma. Oncology letters, 29(6), 271.

Wess M, et al. (2025) Versatile roles of annexin A4 in clear cell renal cell carcinoma: Impact on membrane repair, transcriptional signatures, and composition of the tumor microenvironment. iScience, 28(4), 112198.

Cui X, et al. (2025) Identification of biomarkers and target drugs for melanoma: a topological and deep learning approach. Frontiers in genetics, 16, 1471037.

Feng G, et al. (2025) Identification of UBE2N as a biomarker of Alzheimer's disease by combining WGCNA with machine learning algorithms. Scientific reports, 15(1), 6479.