Resource Summary Report

Generated by dkNET on Apr 16, 2025

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: database, data analysis service, data or information resource, service resource, analysis service resource, production service resource

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

Resource Name: InnateDB

Resource ID: SCR_006714

Alternate IDs: nif-0000-20808

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250416T063444+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 460 mentions in open access literature.

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

Song W, et al. (2025) Role of immune cell homeostasis in research and treatment response in hepatocellular carcinoma. Clinical and experimental medicine, 25(1), 42.

Mahmud MS, et al. (2025) Computational network analysis of two popular skin cancers provides insights into the molecular mechanisms and reveals common therapeutic targets. Heliyon, 11(1), e41688.

Evans DJ, et al. (2024) Transcriptomic analysis of primary nasal epithelial cells reveals altered interferon signalling in preterm birth survivors at one year of age. Frontiers in cell and developmental biology, 12, 1399005.

Yang X, et al. (2024) Comparative analysis of dynamic transcriptomes reveals specific COVID-19 features and pathogenesis of immunocompromised populations. mSystems, 9(6), e0138523.

Mei H, et al. (2024) Multi-omics and pathway analyses of genome-wide associations implicate regulation and immunity in verbal declarative memory performance. Alzheimer's research & therapy, 16(1), 14.

Herrera-Rivero M, et al. (2024) Immunogenetics of lithium response and psychiatric phenotypes in patients with bipolar disorder. Translational psychiatry, 14(1), 174.

Wang K, et al. (2024) Comprehensive analysis of PPP4C's impact on prognosis, immune microenvironment, and immunotherapy response in lung adenocarcinoma using single-cell sequencing and multi-omics. Frontiers in immunology, 15, 1416632.

Ab Rajab NS, et al. (2024) Schizophrenia and Rheumatoid Arthritis Genetic Scenery: Potential Non-HLA Genes Involved in Both Diseases Relationship. The Yale journal of biology and medicine, 97(3), 281.

Wahl V, et al. (2024) Variola Virus and Clade I Mpox Virus Differentially Modulate Cellular Responses Longitudinally in Monocytes During Infection. The Journal of infectious diseases, 229(Supplement_2), S265.

Wang W, et al. (2024) Integrating single-cell and bulk RNA sequencing data unveils antigen presentation and process-related CAFS and establishes a predictive signature in prostate cancer. Journal of translational medicine, 22(1), 57.

Gladow N, et al. (2024) Role of CD4+ T-cells for regulating splenic myelopoiesis and monocyte differentiation after experimental myocardial infarction. Basic research in cardiology.

Yang B, et al. (2024) Identification of ferroptosis-related gene signature for tuberculosis diagnosis and therapy efficacy. iScience, 27(7), 110182.

Li Q, et al. (2024) Multi-omic validation of the cuproptosis-sphingolipid metabolism network: modulating the immune landscape in osteosarcoma. Frontiers in immunology, 15, 1424806.

Wang L, et al. (2024) Identification of immune-associated biomarkers of diabetes nephropathy tubulointerstitial injury based on machine learning: a bioinformatics multi-chip integrated analysis. BioData mining, 17(1), 20.

Wan Y, et al. (2024) Deciphering COPS5 influence on immune infiltration and prognosis in head and neck squamous cell carcinoma. Heliyon, 10(13), e33553.

Gu Y, et al. (2024) Immune- and metabolism-related gene signature analysis uncovers the prognostic and immune microenvironments of hepatocellular carcinoma. Journal of cancer research and clinical oncology, 150(6), 311.

Moeed A, et al. (2024) The Caspase-Activated DNase drives inflammation and contributes to defense against viral infection. Cell death and differentiation, 31(7), 924.

Xiao Y, et al. (2024) A novel immune-related gene signature for diagnosis and potential immunotherapy of microsatellite stable endometrial carcinoma. Scientific reports, 14(1), 3738.

Wu S, et al. (2024) Integrated analysis of single-cell RNA-seq and bulk RNA-seq unravels the molecular feature of M2 macrophages of head and neck squamous cell carcinoma. Journal of cellular and molecular medicine, 28(5), e18083.

He X, et al. (2024) A novel sphingolipid metabolism-related long noncoding RNA signature predicts the prognosis, immune landscape and therapeutic response in pancreatic adenocarcinoma. Heliyon, 10(1), e23659.