

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 Orthologue software. Orthologue 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: 20260905T132559+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 571 mentions in open access literature.

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

Ng MY, et al. (2026) A druggable redox switch on SHP1 controls macrophage inflammation. *bioRxiv : the preprint server for biology*.

Mishra D, et al. (2026) Glyphosate-Induced Metabolic and Immune Modulation in Hepatoma Cells: Identification of Key Genes as Diagnostic and Therapeutic Targets Using an In Silico Systems Biology Approach. *Journal of xenobiotics*, 16(2).

Thambiraja M, et al. (2026) Genetic basis of immunity in Indian cattle as revealed by comparative analysis of Bos genome. *Scientific reports*, 16(1).

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.

Zhang X, et al. (2026) Evolutionary Complexity of Primate Immune System Uncovered by the Extensive Phylogenomic Sampling. *Genome biology and evolution*, 18(4).

Mou L, et al. (2026) Advancing lupus nephritis research through multi-omics and predictive modeling. *Innate immunity*, 32, 17534259261426818.

Piroozmand S, et al. (2026) Suboptimal Responses to Anti-VEGF in Retinal Neurovascular Diseases: Linking Aging and Alternative Angioinflammatory Pathways. *Investigative ophthalmology & visual science*, 67(5), 4.

Kotlyar M, et al. (2026) IID 2025: Physical protein interaction data with detection types, co-purified protein sets, molecular docking, and immune cell networks. *Nucleic acids research*, 54(D1), D593.

Saaoud F, et al. (2026) Chronic obstructive pulmonary disease reprograms the lung into an immune organ through trained immunity, cell death networks, and immune checkpoint dysregulation. *Frontiers in medicine*, 13, 1721780.

Koo KM, et al. (2026) Rapid Decentralized Prostate Cancer Risk Stratification by Portable Liquid Biopsy Analysis within a Clinical Biosensor Validation Framework. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(13), e12126.

Li M, et al. (2026) ITPG: an immune-related transcriptomic predictive model for gastric cancer prognosis. *Translational cancer research*, 15(2), 125.

Guo L, et al. (2026) CRISPR-Cas9 Screening and Simulated Infection Transcriptomic Identify Key Drivers of Innate Immunity in Bactrian Camels. *Animals : an open access journal from MDPI*, 16(4).

Ng MY, et al. (2026) A druggable redox switch on SHP1 controls macrophage inflammation. *Nature chemical biology*, 22(7), 1187.

Li N, et al. (2026) Exploration of m7G-related immune genes and construction of a prognostic risk model in gastric cancer. *Scientific reports*, 16(1).

Liu C, et al. (2026) Multi-omics profiling of fungal balls in chronic pulmonary aspergillosis patients reveals microbiome dynamics and metabolic adaptations. *mBio*, 17(6), e0034826.

McHugo GP, et al. (2026) Integrative Genomics Identifies Candidate Genes Underlying Trypanotolerance in Hybrid African Cattle. *Evolutionary applications*, 19(6), e70274.

Li J, et al. (2026) Deciphering the Heterogeneous Microenvironment of Head and Neck Squamous Cell Carcinoma Through an Integrated Immune Inflammation Framework. *International journal of genomics*, 2026, 8714244.

Yang Y, et al. (2026) Identification of prognostic immune-related genes and evaluation of chemotherapy and immunotherapy responses in pancreatic cancer. *Translational cancer research*, 15(5), 396.

Mokhashi O, et al. (2025) Obesity-related microbial dysbiosis as a potential modulator of tumour progression. *Access microbiology*, 7(10).

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