Resource Summary Report

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HumanCyc: Encyclopedia of Homo sapiens Genes and Metabolism

RRID:SCR_007050
Type: Tool

Proper Citation

HumanCyc: Encyclopedia of Homo sapiens Genes and Metabolism (RRID:SCR_007050)

Resource Information

URL: http://humancyc.org/

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Description: The HumanCyc database describes human metabolic pathways and the human genome. By presenting metabolic pathways as an organizing framework for the human genome, HumanCyc provides the user with an extended dimension for functional analysis of Homo sapiens at the genomic level. A computational pathway analysis of the human genome assigned human enzymes to predicted metabolic pathways. Pathway assignments place genes in their larger biological context, and are a necessary step toward quantitative modeling of metabolism. HumanCyc contains the complete genome sequence of Homo sapiens, as presented in Build 31. Data on the human genome from Ensembl, LocusLink and GenBank were carefully merged to create a minimally redundant human gene set to serve as an input to SRI''s PathoLogic software, which generated the database and predicted Homo sapiens metabolic pathways from functional information contained in the genome''s annotation. SRI did not re-annotate the genome, but worked with the gene function assignments in Ensembl, LocusLink, and GenBank. The resulting pathway/genome database (PGDB) includes information on 28,783 genes, their products and the metabolic reactions and pathways they catalyze. Also included are many links to other databases and publications. The Pathway Tools software/database bundle includes HumanCyc and the Pathway Tools software suite and is available under license. This form of HumanCyc is faster and more powerful than the Web version.

Abbreviations: HumanCyc

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

Defining Citation: PMID:15642094

Keywords: enzyme, function, functional, gene, genome, genomic, human, human genome, metabolic, metabolism, mitochondrion, nucleotide, pathway, position, reaction, sequence, metabolomics, gene expression, bioreaction, metabolic pathway, nutrition, FASEB list

Funding: Pharmaceutical company ;
NIGMS GM092729

Availability: Public

Resource Name: HumanCyc: Encyclopedia of Homo sapiens Genes and Metabolism

Resource ID: SCR_007050

Alternate IDs: nif-0000-21206

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250421T053611+0000

Ratings and Alerts

No rating or validation information has been found for HumanCyc: Encyclopedia of Homo sapiens Genes and Metabolism.

No alerts have been found for HumanCyc: Encyclopedia of Homo sapiens Genes and Metabolism.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 59 mentions in open access literature.

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

Li GX, et al. (2024) Comprehensive proteogenomic characterization of rare kidney tumors. Cell reports. Medicine, 5(5), 101547.

Lisowski P, et al. (2024) Mutant huntingtin impairs neurodevelopment in human brain organoids through CHCHD2-mediated neurometabolic failure. Nature communications, 15(1), 7027.

Nazemi M, et al. (2024) The extracellular matrix supports breast cancer cell growth under amino acid starvation by promoting tyrosine catabolism. PLoS biology, 22(1), e3002406.

Costantini C, et al. (2024) Harnessing inter-kingdom metabolic disparities at the human-fungal interface for novel therapeutic approaches. Frontiers in molecular biosciences, 11, 1386598.

Liska O, et al. (2023) Principles of metabolome conservation in animals. Proceedings of the National Academy of Sciences of the United States of America, 120(35), e2302147120.

Soussi S, et al. (2023) IPSC derived cardiac fibroblasts of DMD patients show compromised actin microfilaments, metabolic shift and pro-fibrotic phenotype. Biology direct, 18(1), 41.

Leitner BP, et al. (2023) Tissue-specific reprogramming of glutamine metabolism maintains tolerance to sepsis. PloS one, 18(7), e0286525.

Tran TTV, et al. (2023) Artificial Intelligence in Drug Metabolism and Excretion Prediction: Recent Advances, Challenges, and Future Perspectives. Pharmaceutics, 15(4).

Zolotovskaia M, et al. (2023) Algorithmically Reconstructed Molecular Pathways as the New Generation of Prognostic Molecular Biomarkers in Human Solid Cancers. Proteomes, 11(3).

Villalba GC, et al. (2021) Fantastic databases and where to find them: Web applications for researchers in a rush. Genetics and molecular biology, 44(2), e20200203.

Ruberto AA, et al. (2021) KLF10 integrates circadian timing and sugar signaling to coordinate hepatic metabolism. eLife, 10.

Shao J, et al. (2021) Integrated Proteomics and Metabolomics Analysis of Perirenal Adipose Tissue in Obese Rabbits Treated with a Restricted Diet. Biology, 10(4).

Emri E, et al. (2020) A Multi-Omics Approach Identifies Key Regulatory Pathways Induced by Long-Term Zinc Supplementation in Human Primary Retinal Pigment Epithelium. Nutrients, 12(10).

Kang HJ, et al. (2020) Genetic Markers for Later Remission in Response to Early Improvement of Antidepressants. International journal of molecular sciences, 21(14).

Li H, et al. (2020) CaMeRe: A Novel Tool for Inference of Cancer Metabolic Reprogramming. Frontiers in oncology, 10, 207.

Rahman MH, et al. (2020) A Network-Based Bioinformatics Approach to Identify Molecular Biomarkers for Type 2 Diabetes that Are Linked to the Progression of Neurological Diseases. International journal of environmental research and public health, 17(3).

Winnard PT, et al. (2020) Divergent organ-specific isogenic metastatic cell lines identified using multi-omics exhibit differential drug sensitivity. PloS one, 15(11), e0242384.

Rmaileh AA, et al. (2020) Large-Scale Differential Gene Expression Transcriptomic Analysis Identifies a Metabolic Signature Shared by All Cancer Cells. Biomolecules, 10(5).

Islam ABMMK, et al. (2020) Lung transcriptome of a COVID-19 patient and systems biology predictions suggest impaired surfactant production which may be druggable by surfactant therapy. Scientific reports, 10(1), 19395.

White R, et al. (2019) Quantitative mass spectrometry to identify protein markers for diagnosis of malignant pleural mesothelioma. Journal of proteomics, 192, 374.