

# Resource Summary Report

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## HumanCyc: Encyclopedia of Homo sapiens Genes and Metabolism

RRID:SCR\_007050

Type: Tool

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### Proper Citation

HumanCyc: Encyclopedia of Homo sapiens Genes and Metabolism (RRID:SCR\_007050)

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### Resource Information

**URL:** <http://humancyc.org/>

**Proper Citation:** HumanCyc: Encyclopedia of Homo sapiens Genes and Metabolism (RRID:SCR\_007050)

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

**Defining Citation:** [PMID:15642094](https://pubmed.ncbi.nlm.nih.gov/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:** r3d100011286, nif-0000-21206

**Alternate URLs:** <https://doi.org/10.17616/R3ZS72>

**Record Creation Time:** 20220129T080239+0000

**Record Last Update:** 20260731T042733+0000

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## 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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 60 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Cavanagh M, et al. (2025) Vaginal host immune-microbiome-metabolite interactions associated with spontaneous preterm birth in a predominantly white cohort. NPJ biofilms and microbiomes, 11(1), 52.

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.

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

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.

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).

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

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.

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.