Resource Summary Report

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HumanBase

RRID:SCR_016145
Type: Tool

Proper Citation

HumanBase (RRID:SCR_016145)

Resource Information

URL: http://hb.flatironinstitute.org/

Proper Citation: HumanBase (RRID:SCR_016145)

Description: Formerly known as GIANT (Genome-scale Integrated Analysis of gene Networks in Tissues), HumanBase applies machine learning algorithms to learn biological associations from massive genomic data collections. These integrative analyses reach beyond existing "biological knowledge" represented in the literature to identify novel, data-driven associations.

Synonyms: GIANT (Genome-scale Integrated Analysis of gene Networks in Tissues), GIANT

Resource Type: data or information resource, database

Defining Citation: PMID:25915600

Keywords: genome, analysis, tissue, network, gene, machine, learning, biology

Funding: NCI T32 CA009528;
NHGRI R01 HG005998;
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NHLBI U54 HL117798;
NIGMS P20 GM103534;
NIGMS P50 GM071508;
NIGMS R01 GM071966;
US Department Of Health And Human Services HHSN272201000054C

Availability: Free, Public

Resource Name: HumanBase

Resource ID: SCR_016145

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260905T133213+0000

Ratings and Alerts

No rating or validation information has been found for HumanBase.

No alerts have been found for HumanBase.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 95 mentions in open access literature.

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

Ju W, et al. (2026) Urinary clusterin as a biomarker of human kidney disease progression and response to the endothelin receptor antagonist atrasentan: An exploratory analysis from the SONAR trial. Nature communications, 17(1).

Reed TJ, et al. (2026) Exploring How Workflow Variations in Denaturation-Based Assays Impact Global Protein-Protein Interaction Predictions. Molecular & cellular proteomics : MCP, 25(2), 101479.

Azad T, et al. (2026) Predictive modeling of molecular activity underlying physical cell-cell interactions. Cell reports methods, 6(2), 101301.

Lodi MK, et al. (2026) Narrow Versus Broad Phenotype Definitions Affect Genetic Analysis of Language More than Other Broad Autism Phenotype Traits. Genes, 17(2).

Song J, et al. (2026) Human multi-tissue transcriptomics identifies galectin-1 and follistatin-like 1 as exerkines with distinct transcript-to-serum coupling after exercise. The Journal of physiology, 604(12), 4815.

Nayar G, et al. (2026) GATSBI: Improving context-aware protein embeddings through biologically motivated data splits. bioRxiv : the preprint server for biology.

Marvin T, et al. (2026) Single-cell profiling reveals epithelial and immune responses in BK polyomavirus-infected human kidney biopsies. JCI insight, 11(8).

Erkizan HV, et al. (2026) Preliminary examination of noncoding mutations of esophageal squamous cell carcinoma in African Americans. Frontiers in genetics, 17, 1779147.

Huang X, et al. (2025) Revealing age-related changes in the intraocular microenvironment and senescence modulators using aqueous humor proteomics and machine learning. Frontiers in cell and developmental biology, 13, 1583330.

Srivastava R, et al. (2025) Advancing precision oncology with AI-powered genomic analysis. Frontiers in pharmacology, 16, 1591696.

Metzger PJ, et al. (2025) Sequestration of ribosome biogenesis factors in HSV-1 nuclear aggregates revealed by spatially resolved thermal profiling. Science advances, 11(26), eadw6814.

Yu JE, et al. (2025) CHI3L1 promotes cell division through activation of RhoA in lung cancer cells. Cell communication and signaling : CCS, 24(1), 48.

Dominguez-Alonso S, et al. (2025) Alternative splicing analysis in a Spanish ASD (Autism Spectrum Disorders) cohort: in silico prediction and characterization. Scientific reports, 15(1), 10730.

Lai H, et al. (2025) Novel estrogen-related gene variants identified by whole-exome sequencing in pregnancy-associated intrahepatic cholestasis. Frontiers in genetics, 16, 1626890.

Greenberg ZF, et al. (2025) Urinary extracellular vesicles for high-precision bladder cancer subtyping and prognosis. medRxiv : the preprint server for health sciences.

Ravichandran P, et al. (2025) Aggregation of recount3 RNA-seq data improves inference of consensus and tissue-specific gene coexpression networks. Genome research, 35(9), 2087.

Smith LA, et al. (2025) Equitable machine learning counteracts ancestral bias in precision medicine. Nature communications, 16(1), 2144.

Junyent M, et al. (2025) Unravelling Convergent Signaling Mechanisms Underlying the Aging-Disease Nexus Using Computational Language Analysis. Current issues in molecular biology, 47(3).

Lara MK, et al. (2024) Network-based analysis predicts interacting genetic modifiers from a meta-mapping study of spike-wave discharge in mice. Genes, brain, and behavior, 23(2), e12879.

Chakraborty S, et al. (2024) Post-GWAS functional analyses of CNTNAP5 suggests its role in glaucomatous neurodegeneration. bioRxiv : the preprint server for biology.