

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: database, data or information resource

Defining Citation: [PMID:25915600](#)

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

Funding: NIGMS R01 GM071966;
NHGRI R01 HG005998;
NHLBI U54 HL117798;
NIGMS P20 GM103534;
NHGRI T32 HG003284;
NCI T32 CA009528;
NIGMS P50 GM071508;
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: 20260805T044350+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 74 mentions in open access literature.

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

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.

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.

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.

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).

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

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.

Wakasugi D, et al. (2024) A rare olive compound oleacein functions as a TrkB agonist and mitigates neuroinflammation both in vitro and in vivo. *Cell communication and signaling : CCS*, 22(1), 309.

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

Pividori M, et al. (2024) An efficient, not-only-linear correlation coefficient based on clustering. *Cell systems*, 15(9), 854.

Kars ME, et al. (2024) The landscape of rare genetic variation associated with inflammatory bowel disease and Parkinson's disease comorbidity. *Genome medicine*, 16(1), 66.

Zhao Y, et al. (2024) MDDOmics: multi-omics resource of major depressive disorder. *Database : the journal of biological databases and curation*, 2024.

Uchida Y, et al. (2024) Comprehensive Transcriptome Profiling of Antioxidant Activities by Glutathione in Human HepG2 Cells. *Molecules (Basel, Switzerland)*, 29(5).

Iijima H, et al. (2024) Network-based cytokine inference implicates Oncostatin M as a driver of an inflammation phenotype in knee osteoarthritis. *Aging cell*, 23(2), e14043.

Murthy M, et al. (2024) DNA methylation patterns in the frontal lobe white matter of multiple system atrophy, Parkinson's disease, and progressive supranuclear palsy: a cross-comparative investigation. *Acta neuropathologica*, 148(1), 4.

Tshilenge KT, et al. (2024) Proteomic analysis of X-linked dystonia parkinsonism disease striatal neurons reveals altered RNA metabolism and splicing. *Neurobiology of disease*, 190, 106367.

Santos-Rebouças CB, et al. (2024) Immune response stability to the SARS-CoV-2 mRNA vaccine booster is influenced by differential splicing of HLA genes. *Scientific reports*, 14(1), 8982.

Matoba K, et al. (2024) Deletion of podocyte Rho-associated, coiled-coil-containing protein kinase 2 protects mice from focal segmental glomerulosclerosis. *Communications biology*, 7(1), 402.