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: 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: 20250525T032416+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 65 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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

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.

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.

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

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

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.

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.

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.

Greenberg ZF, et al. (2024) Peptide-based capture-and-release purification of extracellular vesicles and statistical algorithm enabled quality assessment. bioRxiv : the preprint server for biology.

Tian J, et al. (2024) Hippocampal transcriptome-wide association study and pathway analysis of mitochondrial solute carriers in Alzheimer's disease. Translational psychiatry, 14(1), 250.

Chakraborty S, et al. (2024) Functional investigation suggests CNTNAP5 involvement in glaucomatous neurodegeneration obtained from a GWAS in primary angle closure glaucoma. PLoS genetics, 20(12), e1011502.

Arber C, et al. (2024) Microglia contribute to the production of the amyloidogenic ABri peptide in familial British dementia. Acta neuropathologica, 148(1), 65.

Escribano-Núñez A, et al. (2024) IGF1 drives Wnt-induced joint damage and is a potential therapeutic target for osteoarthritis. Nature communications, 15(1), 9170.

Schembri M, et al. (2024) Identification of osteoporosis genes using family studies. Frontiers in endocrinology, 15, 1455689.

Liu Z, et al. (2023) The Role of Ferroptosis and Cuproptosis in Curcumin against Hepatocellular Carcinoma. Molecules (Basel, Switzerland), 28(4).

Rajarajan S, et al. (2023) An androgen receptor regulated gene score is associated with epithelial to mesenchymal transition features in triple negative breast cancers. Translational oncology, 37, 101761.

Whitmore L, et al. (2023) Inadvertent human genomic bycatch and intentional capture raise beneficial applications and ethical concerns with environmental DNA. Nature ecology &

evolution, 7(6), 873.