Resource Summary Report

Generated by ASWG on Aug 4, 2026

H-InvDB

RRID:SCR_013265
Type: Tool

Proper Citation

H-InvDB (RRID:SCR_013265)

Resource Information

URL: http://www.h-invitational.jp/

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Description: H-Invitational Database (H-InvDB) is an integrated database of human genes and transcripts. By extensive analyses of all human transcripts, we provide curated annotations of human genes and transcripts that include gene structures, alternative splicing isoforms, non-coding functional RNAs, protein functions, functional domains, sub-cellular localizations, metabolic pathways, protein 3D structure, genetic polymorphisms (SNPs, indels and microsatellite repeats) , relation with diseases, gene expression profiling, and molecular evolutionary features , protein-protein interactions (PPIs) and gene families/groups. This database is produced by the Genome Information Integration Project (2005-) based upon the annotation technology established in the H-Invitational Project for annotation of human full-length cDNAs.

Abbreviations: H-InvDB, H-InvDB cDNA, H-InvDB locus

Synonyms: H-Invitational Database, H-InvDB cDNA, H-InvDB locus, H-InvDB: Annotated Human Gene Database

Resource Type: data or information resource, database

Keywords: human gene, human genome, transcripts, bio.tools

Resource Name: H-InvDB

Resource ID: SCR_013265

Alternate IDs: nif-0000-02936, biotools:h-invdb

Alternate URLs: https://bio.tools/h-invdb

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260804T043521+0000

Ratings and Alerts

No rating or validation information has been found for H-InvDB.

No alerts have been found for H-InvDB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Hameed BMZ, et al. (2021) Big Data Analytics in urology: the story so far and the road ahead. Therapeutic advances in urology, 13, 1756287221998134.

Lee YW, et al. (2021) lncExplore: a database of pan-cancer analysis and systematic functional annotation for lncRNAs from RNA-sequencing data. Database : the journal of biological databases and curation, 2021.

Gao L, et al. (2020) Comprehensive Transcriptomic Analysis Reveals Dysregulated Competing Endogenous RNA Network in Endocrine Resistant Breast Cancer Cells. Frontiers in oncology, 10, 600487.

Kim Y, et al. (2019) A Mutation in ZNF143 as a Novel Candidate Gene for Endothelial Corneal Dystrophy. Journal of clinical medicine, 8(8).

Chang AY, et al. (2017) Recruitment of histone modifications to assist mRNA dosage maintenance after degeneration of cytosine DNA methylation during animal evolution. Genome research, 27(9), 1513.

Nakashima H, et al. (2016) R-spondin 2 promotes acetylcholine receptor clustering at the neuromuscular junction via Lgr5. Scientific reports, 6, 28512.

Yuan J, et al. (2016) Transcriptional profiling analysis and functional prediction of long noncoding RNAs in cancer. Oncotarget, 7(7), 8131.

Shen Z, et al. (2014) Long non-coding RNA profiling in laryngeal squamous cell carcinoma and its clinical significance: potential biomarkers for LSCC. PloS one, 9(9), e108237.

Yi Z, et al. (2014) Identifcation of differentially expressed long non-coding RNAs in CD4+ T cells response to latent tuberculosis infection. The Journal of infection, 69(6), 558.

Takeda J, et al. (2013) H-InvDB in 2013: an omics study platform for human functional gene and transcript discovery. Nucleic acids research, 41(Database issue), D915.

Da Sacco L, et al. (2012) Bioinformatics tools and novel challenges in long non-coding RNAs (lncRNAs) functional analysis. International journal of molecular sciences, 13(1), 97.

Kikugawa S, et al. (2012) PCDq: human protein complex database with quality index which summarizes different levels of evidences of protein complexes predicted from h-invitational protein-protein interactions integrative dataset. BMC systems biology, 6 Suppl 2(Suppl 2), S7.

Satoh J, et al. (2012) Molecular network analysis of human microRNA targetome: from cancers to Alzheimer's disease. BioData mining, 5(1), 17.

Michelhaugh SK, et al. (2011) Mining Affymetrix microarray data for long non-coding RNAs: altered expression in the nucleus accumbens of heroin abusers. Journal of neurochemistry, 116(3), 459.

Boucher P, et al. (2010) Unusual duplication of the insulin-like receptor in the crustacean Daphnia pulex. BMC evolutionary biology, 10, 305.

Yamasaki C, et al. (2010) H-InvDB in 2009: extended database and data mining resources for human genes and transcripts. Nucleic acids research, 38(Database issue), D626.

Khachane AN, et al. (2010) Mining mammalian transcript data for functional long non-coding RNAs. PloS one, 5(4), e10316.

Yamaguchi-Kabata Y, et al. (2008) Distribution and effects of nonsense polymorphisms in human genes. PloS one, 3(10), e3393.

Takeda J, et al. (2008) Low conservation and species-specific evolution of alternative splicing in humans and mice: comparative genomics analysis using well-annotated full-length cDNAs. Nucleic acids research, 36(20), 6386.

Chern TM, et al. (2008) Computational analysis of full-length cDNAs reveals frequent coupling between transcriptional and splicing programs. DNA research : an international journal for rapid publication of reports on genes and genomes, 15(2), 63.