Integrated Database of Human Genes and Transcripts

H-InvDB hinv.jp

http://www.h-invitational.jp

Free!!

A comprehensive annotation resource for human genes and transcripts

Originality
High quality
Comprehensive
Freely available
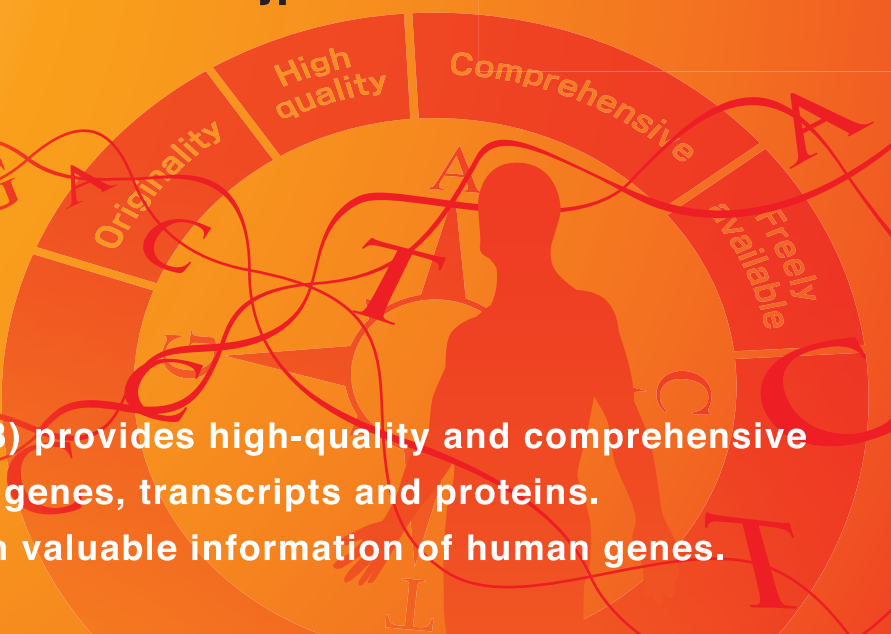
H-Invitational Database (H-InvDB) provides high-quality and comprehensive annotation for human genes, transcripts and proteins.
Users can search and obtain valuable information of human genes.

Searching H-InvDB

H-InvDB top page provides six different search interfaces;

1 Navi
search navigation for all search interfaces

2 BLAST
search by sequence similarity

3 Simple search
search by IDs or keywords

4 Advanced search
search by16 search contents

5 Chromosome map
search by the chromosomal location

6 Site search
search for web pages and documents

H-InvDB — Annotated Human Gene Database

5th Anniversary !! H-InvDB_7.0 released on February 16, 2010.

Search by Keyword for GO Advanced

Home Quick guide Navi BLAST Site map Download Contact us Help

[Japanese]

What is H-InvDB
About Projects
Publications
Presentation
Release Information
Web Service
Topic Annotation
Gene Families/Groups
News
Statistics
Mail magazine
Maintenance
FAQ

Site Search

What is H-InvDB [Sample view] RSS 1.0

An Integrated Database of Annotated Human Genes

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. [more]

News

16-Feb-10 H-InvDB 7.0 was released.
14-Jan-10 Update of H-InvDB Enrichment Analysis Tool (HEAT)
14-Jan-10 Renewal of FTP site (new FTP)
25-Dec-09 Closing of DDBJ mirror.
19-Oct-09 Publication related to H-InvDB (NAR database issue 2010)
30-Oct-08 Release of a new portal site (medals.jp)
28-Mar-08 New URL of H-InvDB
[more]

Human Chromosome Map

#Mirror BIRC | #Official site
Copyright (c) 2004-2010 JBIC and AIST All Rights Reserved.
AIST | JBiC | BIRC

http://hinv.jp/hinv/ahg-db/

H-InvDB is widely used in scientific researches and various applications in the related industries.

Key integrated DB in METI Database portal for Life Science (MEDALS)

METI Database portal for Life Science (MEDALS) is a portal site of databases and analysis tools for life science, that were developed by the research projects and institutions sponsored by METI. H-InvDB is presented as a key integrated database of human genes in MEDALS.

http://medals.jp/etop

MEDALS
METI database portal for life science

What is H-InvDB ?

By extensive analyses of all human transcripts, H-InvDB 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.

H-InvDB consists of three main views, six sub-databases and various related tools.

Main views in H-InvDB

Protein view **P**

Locus view **L**   **T** Transcript view

Sub-databases in H-InvDB

G-integra   Evola

H-ANGEL   PPI view

DiseaseInfo Viewer   Gene family/group

Applications of H-InvDB

L Obtain the detailed annotation for each gene locus
Locus view [Locus annotation view]

G Compare H-InvDB with RefSeq or Ensemble annotations
G-integra [Genome browser]

AS Examine alternative splicing pattern of each gene
H-DBAS [Database of the alternative splicing (AS)]

Examine gene expression profile of each gene
H-ANGEL [Human ANatomic Gene Expression Library]

Find the microarray probes mapped on each gene
DNAProbeLocator [Web tool to map and browse DNA array probes]

Examine polymorphism (SNP) information of each gene
VarySysDB [Database of annotated human polymorphism]

HG Find microsatellite markers of each human gene
H-GOLD (GDBS) [Gene Diversity DataBase System]

Find the disease related-genes located around each genes
DiseaseInfo Viewer [Disease information database]

Examine the gene-disease relationships using test-mining
LEGENDA [Literature-Extracted GENe-Disease Associations]

T Obtain the detailed annotation for each transcript (cDNA or mRNA)
Transcript view [Transcript annotation view]

P Obtain the detailed annotation for each protein
Protein view [Protein annotation view]

Find the interacting partners of each protein
PPI view [Human protein-protein interaction (PPI)]

GFA Investigate human gene family or groups
Gene family/group view [Annotation of gene families/groups]

Compare genes between human and model organisms
Evola [Evolutionary annotation database]

Find the conserved genomic regions between human and model organisms
G-compass [Comparative genome browser]

API Develop applications using H-InvDB data
H-InvDB web service [SOAP & REST APIs]

Predict function of mRNA or cDNA sequence as a protein
TACT [Transcriptome Auto-annotation Conducting Tool]

H Find features specific to a given human gene set
HEAT [H-InvDB Enrichment Analysis Tool]
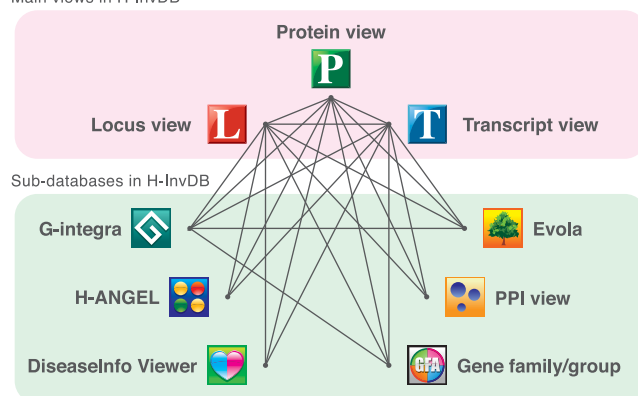
Please refer to "Quick guide" for description of H-InvDB databases and tools. **http://hinv.jp/hinv/ahg-db/tools.jsp**

NEW!!

Search Navi / New advanced search
http://www.h-invitational.jp/hinv/c-search/

Search navigation menu provides links to all searches available in H-InvDB and New advanced search is an extended search system that enables complicated searches by any combination of 16 different search contents.
The search contents: (1)Keyword or ID (2)Gene structure (3)Alternative splicing (4) Non-coding functional RNA (5) Protein functions (6)Functional domains (7)Subcellular localization (8)Metabolic pathway (9)Protein 3D structure (10)Genetic polymorphisms (11)Gene expression (12)Relation to diseases (13)Molecular evolution (14)Protein-protein interaction (PPI) (15)Gene family/groups (16)Transcript information

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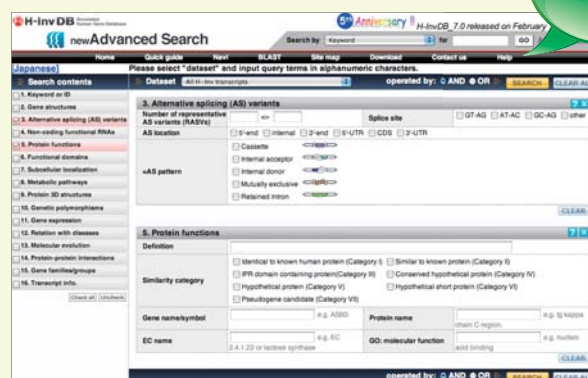
Let's join our mail magazine!!

H-InvDB mail magazine is to announce information useful to H-InvDB release announcements, introduction of tools, annotation data, etc.
Please join us!!

http://hinv.jp/hinv/mag/

JBiC Japan Biological Informatics Consortium

National Institute of Advanced Industrial Science and Technology
AIST

2010 April