

Resource Summary Report

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H-Invitational Database: Protein-Protein Interaction Viewer

RRID:SCR_008054

Type: Tool

Proper Citation

H-Invitational Database: Protein-Protein Interaction Viewer (RRID:SCR_008054)

Resource Information

URL: <http://jbirc.jbic.or.jp/hinv/ppi/>

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Description: The PPI view displays H-InvDB human protein-protein interaction (PPI) information. It is constructed by assigning interaction data to H-InvDB proteins which were originally predicted from transcriptional products generated by the H-Invitational project. The PPI view is now providing 32,198 human PPIs comprised of 9,268 H-InvDB proteins. 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, molecular evolutionary features, protein-protein interactions (PPIs) and gene families/groups. Sponsors: This research is financially supported by the Ministry of Economy, Trade and Industry of Japan (METI), the Ministry of Education, Culture, Sports, Science and Technology of Japan (MEXT) and the Japan Biological Informatics Consortium (JBIC). Also, this work is partly supported by the Research Grant for the RIKEN Genome Exploration Research Project from MEXT to Y.H. and the Grant for the RIKEN Frontier Research System, Functional RNA research program.

Synonyms: H0InvDB PPI View

Resource Type: database, data or information resource

Keywords: evolutionary, expression, function, gene, genetic, 3-dimensional, alternative splicing, disease, domain, human, interaction, isoform, localization, metabolic, microsatellite, molecular, non-coding, pathway, polymorphism, protein, rna, snps, structure, sub-cellular, transcript

Resource Name: H-Invitational Database: Protein-Protein Interaction Viewer

Resource ID: SCR_008054

Alternate IDs: nif-0000-10401

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260805T044202+0000

Ratings and Alerts

No rating or validation information has been found for H-Invitational Database: Protein-Protein Interaction Viewer.

No alerts have been found for H-Invitational Database: Protein-Protein Interaction Viewer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.