Resource Summary Report

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Human Gene and Protein Database (HGPD)

RRID:SCR_002889
Type: Tool

Proper Citation

Human Gene and Protein Database (HGPD) (RRID:SCR_002889)

Resource Information

URL: http://www.HGPD.jp

Proper Citation: Human Gene and Protein Database (HGPD) (RRID:SCR_002889)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 4,2023.The Human Gene and Protein Database presents SDS-PAGE patterns and other informations of human genes and proteins. The HGPD was constructed from full-length cDNAs. For conversion to Gateway entry clones, we first determined an open reading frame (ORF) region in each cDNA meeting the criteria. Those ORF regions were PCR-amplified utilizing selected resource cDNAs as templates. All the details of the construction and utilization of entry clones will be published elsewhere. Amino acid and nucleotide sequences of an ORF for each cDNA and sequence differences of Gateway entry clones from source cDNAs are presented in the GW: Gateway Summary window. Utilizing those clones with a very efficient cell-free protein synthesis system featuring wheat germ, we have produced a large number of human proteins in vitro. Expressed proteins were detected in almost all cases. Proteins in both total and supernatant fractions are shown in the PE: Protein Expression window. In addition, we have also successfully expressed proteins in HeLa cells and determined subcellular localizations of human proteins. These biological data are presented on the frame of cDNA clusters in the Human Gene and Protein Database. To build the basic frame of HGPD, sequences of FLJ full-length cDNAs and others deposited in public databases (Human ESTs, RefSeq, Ensembl, MGC, etc.) are assembled onto the genome sequences (NCBI Build 35 (UCSC hg17)). The majority of analysis data for cDNA sequences in HGPD are shared with the FLJ Human cDNA Database (http://flj.hinv.jp/) constructed as a human cDNA sequence analysis database focusing on mRNA varieties caused by variations in transcription start site (TSS) and splicing.

Synonyms: HGPD

Resource Type: data or information resource, database

Defining Citation: PMID:22140100, PMID:19073703

Keywords: gene, cdna clusters, cdnas, cdna sequences, human, in vitro, mrna varieties, protein, sds-page

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Human Gene and Protein Database (HGPD)

Resource ID: SCR_002889

Alternate IDs: nif-0000-02956

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260904T000116+0000

Ratings and Alerts

No rating or validation information has been found for Human Gene and Protein Database (HGPD).

No alerts have been found for Human Gene and Protein Database (HGPD).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Inaba H, et al. (2016) Ndel1 suppresses ciliogenesis in proliferating cells by regulating the trichoplein-Aurora A pathway. The Journal of cell biology, 212(4), 409.

Motohashi T, et al. (2016) Gene array analysis of neural crest cells identifies transcription factors necessary for direct conversion of embryonic fibroblasts into neural crest cells. Biology open, 5(3), 311.

Hennig S, et al. (2015) Prion-like domains in RNA binding proteins are essential for building subnuclear paraspeckles. The Journal of cell biology, 210(4), 529.

Habibi N, et al. (2014) A review of machine learning methods to predict the solubility of overexpressed recombinant proteins in Escherichia coli. BMC bioinformatics, 15, 134.

Harbers M, et al. (2014) Wheat germ systems for cell-free protein expression. FEBS letters, 588(17), 2762.

Kasahara K, et al. (2014) Ubiquitin-proteasome system controls ciliogenesis at the initial step of axoneme extension. Nature communications, 5, 5081.