The Latest Information and Perspective of Human Gene and Protein Database (HGPD) as Human Proteome Study

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ABSTRACT

HGPD (<http://www.HGPD.jp/>) is a unique database that stores information on a set of human Gateway entry clones in addition to protein expression data. HGPD was launched in November 2008 and, since then, 33,275 human Gateway entry clones have been constructed from ORFs of full-length cDNAs, thus representing the largest collection in the world. Sequence information and protein expression of Gateway entry clones can also be retrieved from HGPD. The majority of analysis data for cDNA sequences in HGPD are shared with the FLJ Human cDNA Database (<http://flj.hinv.jp/v01/cgi/index.cgi>), which was constructed as human cDNA sequence analysis database focusing on mRNA varieties resulting from variations in transcription start site (TSS) and splicing.

DATA SET

- Approximately **43,000** kinds of Gateway entry clone are constructed (see following table). This construction is covered above 70% of human coding protein.

(Identified 2010/10/10)

Type of Gateway Entry Clones	Numbers
N (stop codon type of C-terminal)	17,802
F (fusion type of C-terminal)	25,447

- This human Gateway entry clone resource is named **HUPEX** (Human Proteome Expression-resource).

- 17,821** kinds of human proteins with a C-terminal V5 and His tag are expressed using SDS-PAGE.
- Sequence information of Gateway entry clone can be get from download site. The latest version is 2.0 (identified 2010/10/10). (http://riodb.ibase.aist.go.jp/hgpd/sys_info/download.html)
- Human protein expression data (SDS-PAGE) can be get from "Protein Expression" view of each Gateway entry clone.

WEB INTERFACE

(Following new design will be launched at end of 2010)

- ID search (DDBJ / EMBL / GenBank Accession, Gene symbol, etc.)
- Keyword search

(<http://www.HGPD.jp/>)

Information Overview: Link to other information from here

ORF alignment is displayed

(*2) Result of ESPRESSO search

HOW TO GET HUPEX

- HUPEX is distributed from NITE Biological Resource Center (NBRC) <http://www.nbrc.nite.go.jp/e/hgentry-e.html> (*1).

FUTURE WORKS

- HUPEX is categorized by protein function (protein kinase, protein phosphatase, transcription factor, GPCR, etc.).
- Linkage to ESPRESSO (<http://mbs.cbrc.jp/ESPRESSO/>) (*2) which is a sequence-based predictor for estimating protein expression and solubility is added.
- Subcellular localization image data of proteins with fluorescent proteins at the N- or C-terminal which are expressed in HeLa cells by using Gateway entry clones (*3) will be launched.

REFERENCES AND OTHERS

Goshima, N. *et al.* (2008), *Nature Methods* **5**, 1011-1017.
Maruyama, Y. *et al.* (2009), *Nucleic Acids Res.* **37**, D762-D766.
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