

Bioinformatics Center - Bioknowledge Systems -

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BRINKAC, Lauren The Institute for Genomic Research July 2001–August 2001

Scope of Research

Owing to continuous developments of high throughput experimental technologies, ever increasing amounts of data are being generated in genomics and proteomics. We have been developing bioinformatics technologies for analyzing a large number of genes or proteins at a time, toward the understanding and utilization of higher order functional behaviors of the cell or the organism. The suite of databases and associated software that we develop is called KEGG and is made publicly available as part of the GenomeNet service (<http://www.genome.jp>).

Research Activities (Year 2002)

Grants

Kanehisa M, Deciphering genetic and molecular networks by comparative genomics and systematic interaction experiments. Genome Frontier Project, MEXT.

Kanehisa M, Biological systems database and genome information science. Research for the Future Program, JSPS.

Kanehisa M, BRITE: deductive database of the genome and the biological system based on binary relations. Bioinformatics Research and Development, JST.

Kanehisa M, Education and Research Organization

for Genome Information Science.

Goto S, Construction and retrieval of highly integrated biological databases. Grant-in-Aid for Scientific Research on Priority Areas "Genome Information Science", MEXT.

Nakaya A, Extraction of correlated gene clusters by parallel data mining, Grant-in-Aid for Scientific Research on Priority Areas "Genome Information Science", MEXT.

KEGG Orthology : a classification of all functional orthologs in gene universe

KEGG Orthology(KO), which is developed from the "Ortholog ID", an extension of the EC number in KEGG/PATHWAY database, is a new on-going project to identify and classify functional orthologs hierarchically among all species.

Using KEGG/SSDB database, we classify and annotate orthologs both automatically and manually. Namely, orthologs are classified by a computational clustering method according to the KEGG/SSDB scores (Fig. 1), and the function of each ortholog is further examined manually. In order to support this annotation process, GFIT(Gene Function Identification Tool) program is developed and is now available on WWW (Fig. 2).

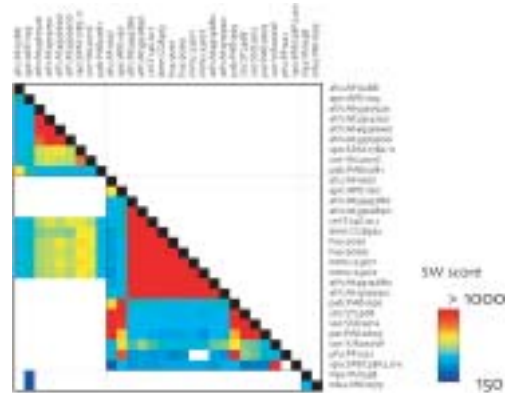


Fig. 1 All genes are clustered on the KEGG/SSDB scores.

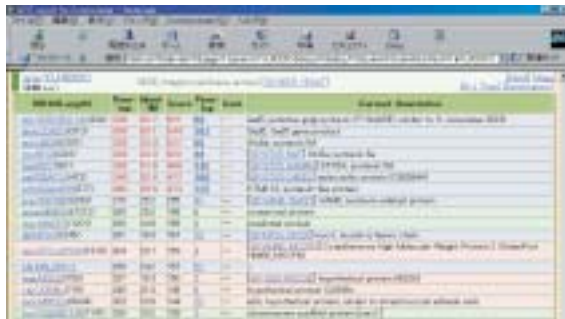


Fig. 2 GFIT is a supporting tool for the annotation of gene.

New sequence motifs : intracellular transport system

In eukaryotic cells, macromolecules like proteins and lipids are transferred between organelles by the vesicular transport system, and specific recognitions on the transport pathway are mediated by SNARE superfamily proteins. We collected candidates of SNARE proteins from KEGG/GENES database, and classified them by the hierarchical clustering method (Fig. 3). As the result, SNARE proteins were found to form clusters depending on their subfamilies and intracellular localization sites, and a new sequence motif was found for every cluster.

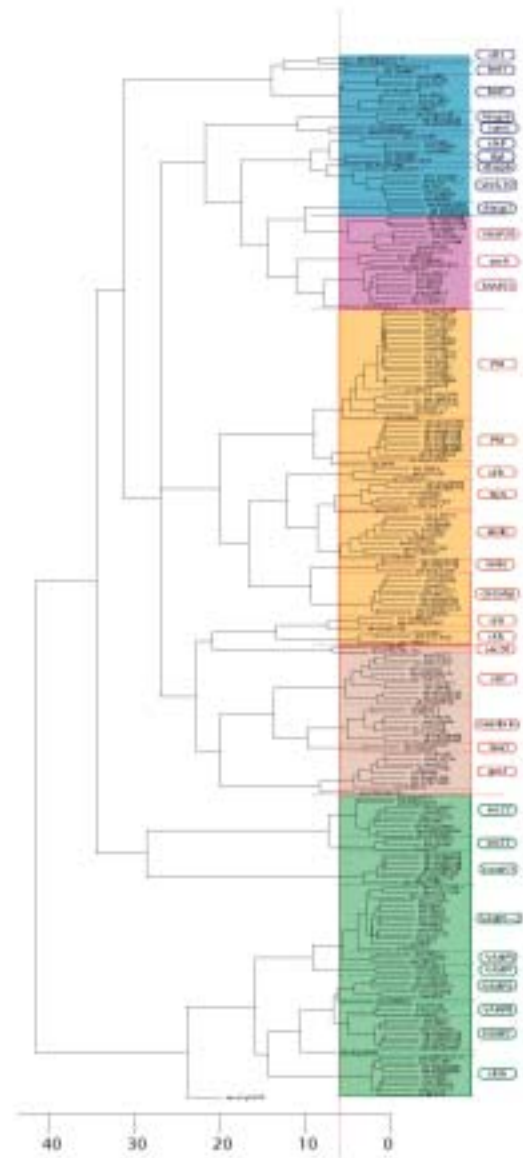


Fig. 3 SNARE proteins are clustered depending on their intracellular localization sites.

