**KEGG Mapper**

**Abstract :**

**KEGG** is a reference knowledge base for biological interpretation of molecular datasets, such as genome sequences. It accumulates experimental knowledge about high‐level functions of the cell and the organism represented in terms of KEGG molecular networks, including KEGG pathway maps, BRITE hierarchies, and KEGG modules. By the process called **KEGG mapping**, a set of protein coding genes in the genome, for example, can be converted to KEGG molecular networks enabling interpretation of cellular functions and other high‐level features. Here we report a new version of KEGG Mapper, a suite of KEGG mapping tools available at the KEGG website with the KOALA family tools for automatic assignment of KO (KEGG Orthology) identifiers used in the mapping.

**Introduction :**

The KEGG database resource has been developed for the purpose of uncovering cellular and organism‐level functions from large‐scale molecular‐level datasets. The three databases, PATHWAY, BRITE, and MODULE, contain experimental knowledge of such high‐level functions captured from published literature and represented in terms of KEGG pathway maps, BRITE hierarchies, and KEGG modules. **The BRITE hierarchy** is a classification system for various biological objects including genes and proteins . **The KEGG pathway** map is a manually drawn graphical diagram showing molecular reaction/interaction on network**. the PATHWAY** **database** is the most widely used as a reference knowledge base for biological interpretation of users' datasets through KEGG pathway mapping, a type of gene set enrichment analysis. KEGG PATHWAY can be compared with Gene Ontology (GO),2 a key database for gene set analysis**. GO** is a collection of controlled vocabularies for gene functions organized in three ontologies: biological process, cellular component, and molecular function. Many genomes are annotated with GO terms by community efforts, so that GO enrichment analysis can be performed on various gene sets. KEGG pathway mapping presents additional information about how genes or gene products interact in pathways, but the coverage of genes is less comprehensive than GO**. The BRITE database**, which is an ontology database, was introduced to supplement PATHWAY and to expand the coverage of genes for KEGG mapping**. The MODULE database** was added as an attempt to automate functional interpretation. these two databases have not been well utilized. In the new version of KEGG Mapper, the pathway mapping tools are redesigned to search by default the three databases, PATHWAY, BRITE, and MODULE, as well as other databases for human gene sets. Here we report these new developments.