**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.

**Related work :**

KEGG pathway could make compared with gene Ontol-ogy (GO),2a way database to gene set improvement Investigation. Try will be an accumulation from claiming controlled vocabularies for gene func-tions sorted out for three ontologies: living process, cellu-lar component, Furthermore atomic capacity. Large portions genomes are annotated with try terms Eventually Tom's perusing group keeping efforts, Along these lines that GO enrichment dissection camwood make performed around Different gene sets. For example, a improvement Investigation figures try terms that areover-represented to a provided for set about mankind's genes, empowering itsbiological elucidation. In contrast, KEGG pathway map-ping displays extra data over how genes orgene results cooperation done pathways, yet the scope o fgenes is lesquerella far reaching over try. The BRITE database, which is an metaphysics database, was introduced should supplement pathway and to extend the coverage for genes to KEGG mapping. The module data-base might have been included Similarly as a endeavor will computerize utilitarian inter-pretation. Unfortunately, however, these two databases have not been well utilized.

## KEGG MAPPER TOOLS:

KEGG Mapper is a collection of tools for KEGG mapping against PATHWAY, BRITE, and MODULE databases. Previously the tools were made available separately for separate databases, but in the new version released in July 2019, they are merged into three general mapping tools shown in Table 3. Each of them allows mapping against multiple databases at a time. “Reconstruct Pathway” is the tool for KO-based mapping against KEGG pathway maps, BRITE hierarchies, BRITE tables, and KEGG modules. It is linked from the KOALA family annotation tools and useful for analyzing genome and metagenome sequences. The analysis can be done for a single genome or multiple genomes, for example, to examine host-endosymbiont relationships.

## CONCLUSION

The pathway mapping tools in KEGG Mapper have been widely used for biological interpretation of genome sequences and other high-throughput data. The new release of KEGG Mapper integrates KEGG pathway mapping with BRITE enrichment analysis and module completeness check for genes and proteins