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Overview of KEGG applications to omics-related research

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Abstract:
KEGG (Kyoto Encyclopedia of Genes and Genomes) is a bioinformatics resource for analyzing cells and organisms from not only the genomic perspective but also a high-level perspective, integrating together genomic, chemical and network information. Accessible from http://www.genome.jp/, it basically consists of four databases: PATHWAY, GENES, LIGAND and BRITE. The KEGG PATHWAY database provides pathway diagrams, represented as networks of interactions that occur in the cell. These can be viewed according to organism or as generic “reference” maps. KEGG GENES is the collection of genes that are found in the complete genomes that are registered in KEGG. It serves as the repository of genes linked from the pathway diagrams. KEGG LIGAND is a database of compounds, glycans, reactions and enzymes. Finally, KEGG BRITE contains the KEGG Orthology, or KO, which is a manually curated identification system of gene orthologs. It also contains classifications of chemical compounds and enzymatic reactions. KO has become an indispensable tool for the functional annotation of new genomes, and it plays a key part in the KAAS (KEGG Automatic Annotation Server) tool.

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