## Integration and web-based representation of heterogeneous metabolic databases

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As the number of completely sequenced genomes increases, more and more biological data generated from the analysis of the genomes are becoming available. Through the annotation and molecular analysis of these sequenced genomes, numerous genes that encode enzymes catalyzing various metabolic reactions have been identified. Quantitative as well as qualitative analyses of metabolic pathways involving various metabolic reactions are important for the elucidation of the metabolic and physiological characteristics of organisms. We have developed a web-based database system that facilitates the search and analysis of metabolic pathways. The system allows efficient retrieval of all available information on enzymes, biochemical compounds and biological reactions and pathways by integrating the heterogeneous metabolic databases including BioCyc, LIGAND and ENZYME. It generates well-designed view pages showing retrieved data in a systematic way. All the source data and compiled modules have been installed on the IBM server system running IBM AIX 4.3 operating system. BIOSILICO uses the IBM DB2 UDB and the MySQL as DBMS.

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