

Patome : Patented Biological Sequences and an Analysis Database Server

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ABSTRACT

Patent biosequences (PAT division) account for 5% of GenBank, the third largest division in entries. However, they have attracted relatively little attention compared to other major sequence resources. We have built a database server called Patome which contains the annotation and analysis information for patent biosequences from GenBank, the European Molecular Biology Laboratory (EMBL), and the DNA Database of Japan (DDBJ). The aims of the Patome are to assign biological functions to the patented biosequences and to provide information on the patent relationship of a particular gene or disease. The patented biosequences were annotated with RefSeq. Two kinds of analysis maps were built from the annotated data and gene information of major model organisms. They are gene- and disease-patent maps. We also present a classification of genes associated with patent biosequences according to the hierarchical structure of the Gene Ontology (GO). Map information can be used to determine whether a particular gene, a disease, or GO terms are patented or patent-related. Patome is available at <http://www.patome.org/> the information is updated bimonthly.