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TITLE

BIOLOGICAL SEQUENCE PROCESSOR FOR COUNTING AND GROUPING BIOLOGICAL SEQUENCES

Abstract

[0089] The present invention is a method to allow rapid searches of biological sequences in a database by advantageously storing sub-sequences of said sequences. Each sequence that is to be stored in the database is sequentially shortened letter by letter and the remaining sub-sequences grouped with other identical sequences. This method uncovers any common shared sequences hidden within longer sequences. As the shortened sub-sequences are grouped with other identical sequences, the prevalence of any sequence may be really determined. The invention also relates to a system implementing this method of grouping biological sequences and the databases created therewith.

[0090] FIG. 1 accompanies the abstract.