

BLAST2SEQUENCES

[BIO316] Database analysis are of two categories, these are;
Genomic analysis and Proteomics analysis

[BIO316] A sequence-based database program that performs, one-by-one, a heuristic local alignment of the query sequence is the
BLAST

[BIO316] The version of BLAST that inputs a protein sequence and a regular expression pattern in it is called the
PHI-BLAST

[BIO316] Structural classification of proteins in which the proteins are classified into hierarchy such as classes, folds, super-families is obtained in the
SCOP

[BIO316] A text-based search engine for bioinformatics databases, at NCBI is
ENTREZ

[BIO316] The statistical method used to access the robustness of phylogenetic trees produced by various tree-building methods is the
BOOTSTRAP

[BIO316] Searching human genome, chromosomes, genes, genomic sequences similar to a given protein sequence, all are activities that can be done in
ENSEMBL

[BIO316] The two main databases that are widely used for novel gene discovery are
High-throughput genomic and Expressed sequence tag databases

[BIO316] Meta PredictProtein section is a program for predicting protein
secondary structure

Whatsapp: 08089722160 or click here for TMA assistance

Practice E-exams & Chat with course mates on noungeeks.net