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In bioinformatics, BLAST (basic local alignment search tool) is an algorithm for comparing primary biological sequence information, such as the amino-acid sequences of proteins or the nucleotides of DNA and/or RNA sequences. A BLAST search enables a researcher to compare a query sequence with a library or database of sequences, and identify library sequences that resemble the query sequence ...

BLAST - Wikipedia

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Scope of this Manual. This manual is intended for users who have a basic knowledge of the R environment, and would like to use R/Bioconductor to perform general or HT sequencing analysis.

NG Sequence - Manuals

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Structural dynamics - Wikipedia

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Fig. 1 illustrates a typical experimental workflow for protein identification and characterisation using MS/MS data. The starting point is a protein sample, which may be a single protein or a complex mixture of proteins. An enzyme, often trypsin, digests the proteins to peptides.

Protein identification using MS/MS data - ScienceDirect

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