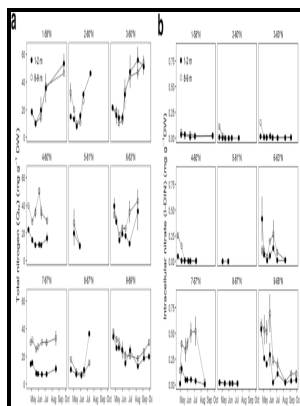# Serratus - protein sequence database and analysis tools : users guide : [version 1.1].

Oxford Molecular - Alignment

Description: -
-Serratus - protein sequence database and analysis tools : users guide
: [version 1.1].
-Serratus - protein sequence database and analysis tools : users guide
: [version 1.1].
Notes: Looseleaf in ringbinder.
This edition was published in 1992

Filesize: 58.31 MB

Tags: #MUSCLE #User #Guide

MESSA: MEta

The Ectocarpus genome and the independent evolution of multicellularity in brown algae. What are the next steps? Every residue in one sequence is compared to every residue in the other and a score is calculated. Availabilty of supporting data The SeqTools programs are designed to be generic viewers of certain text file formats, such as GFF, FASTA and Stockholm.

MESSA: MEta

A message will be written to the log file when muscle starts and stops.

Protein BLAST: search protein databases using a protein query

Only loci with clear GO identifications were retained from the two lists.

High

Since reliable prediction is usually based on the consensus of many computer programs, meta-severs have been developed to fit such needs. This gave a list of 2,710 genes among which, 1,156 had associated GO terms.

Training & Tutorials

Also available as a Java tool. In addition to simple consensus, other evidence provided by MESSA was essential to ensure reliable predictions.

MUSCLE User Guide

Iteration continues as long as the number of conserved columns increases. Johnston CA, Temple BR, Chen JG, Gao Y, Moriyama EN, Jones

AM, Siderovski DP, Willard FS: Comment on 'A G protein coupled receptor is a plasma membrane receptor for the plant hormone abscisic acid'.

Training & Tutorials

Ashburner M, Ball CA, Blake JA, Botstein D, Butler H, Cherry JM, Davis AP, Dolinski K, Dwight SS, Eppig JT, Harris MA, Hill DP, Issel-Tarver L, Kasarskis A, Lewis S, Matese JC, Richardson JE, Ringwald M, Rubin GM, Sherlock G: Gene ontology: tool for the unification of biology. Step 6: Perform optional refinement by determining a new set of constraints and iterating from Step 4 as long as the number of constraints keeps increasing.

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