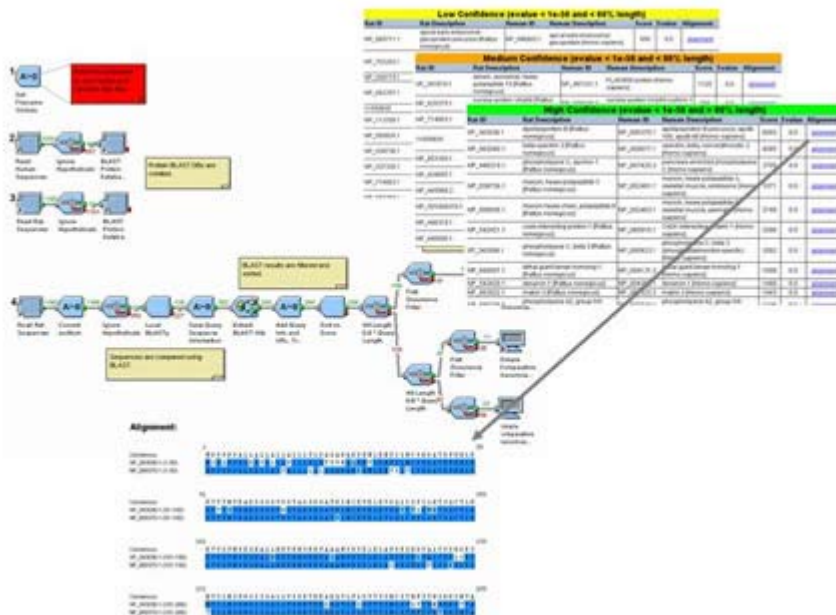




Ortholog Comparison

Sequencing a genome from an organism has become rather common place, and this approach has resulted in new genomes being published almost monthly. Several research groups are using ortholog comparison to facilitate the finding of potential targets by detecting genomic correlations among several organisms.



The example above shows you how you can use the Sequence Analysis and Reporting components to generate interactive reports. In this example, a few proteins from the human RefSeq database and the rat RefSeq database are compared using BLASTp.

Next, the results are filtered and sorted, and three reports are generated with respect to a user-specified "confidence score".

Next, a hidden alignment protocol (which includes ClustalW) can be launched from each table report, and an alignment report is created dynamically.

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