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Clustering of protein families

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Abstract

The Protomap program classifies proteins into clusters according to sequence similarity.

Content

The Protomap program classifies proteins into clusters according to sequence similarity, using a combination of results from Smith-Waterman, FASTA and BLAST algorithms, and Blosum 50 and Blosum 62 similarity matrices. The clusters are taken at different levels of similarity and a hierarchy of clusters is built up. All proteins in [SWISS-PROT](#) have been classified in this manner. If not present in [SWISS-PROT](#), any new protein of interest can be incorporated into the classification using the server. The different levels of clustering can be browsed through a tree-like structure.

Navigation

Navigation is easy and the page design attractive. There is a guided tour and many help pages. When the search program runs, the different steps are clearly indicated on the screen. The results are easy to visualize and Java applets are provided to screen through the cluster tree organization or to see the alignment of two proteins.

Reporter's comments

Timeliness

The current version is Protomap 3.0, based on the latest release of [SWISS-PROT](#) (release 38).

Best feature

Close and distant homologies can be investigated in an organized and intuitive manner. There are also links to structural and sequence motif databases.

Worst feature

Alignments can only be performed in a pairwise fashion and are shown in a schematic form that is difficult to understand.

Wish list

Multiple alignments of the proteins in the different clusters would be welcome, at least for the ones that are highly related.

Related websites

Protein homologies can also be investigated at the [ProDom protein domain database](#) and the [Clusters of Orthologous Groups \(COG\)](#) site.

Table of links

[Protomap](#)

[SWISS-PROT](#)

[ProDom protein domain database](#)

[Clusters of Orthologous Groups](#)

References

1. [Protomap](#).