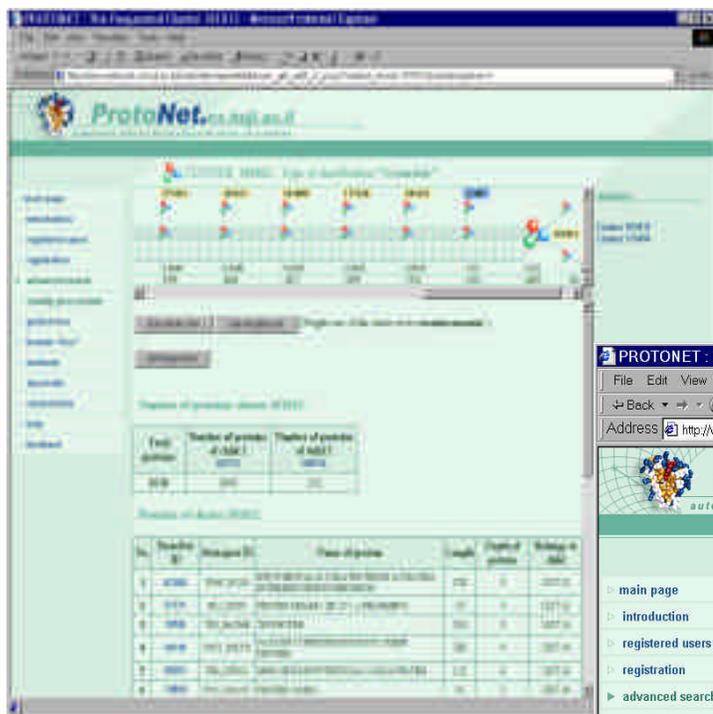# ProtoNet: Automatic Classification of Protein Families
Version 1.3 (July 2002)

ProtoNet is being developed jointly by biologists and computer scientists at the Hebrew University of Jerusalem, Israel. The ProtoNet development group consists of faculty members from Life Science and Computer Science, as well as a group of students.

ProtoNet provides an automatic hierarchical classification of proteins to their families, sub-familes and superfamilies. It provides the user with the necessary tools to browse the hierarchy of clusters in several ways, and to apply comparative analyses based on classification by other systems (e.g. InterPro, Prosite, PDB). Clusters may be retrieved according to combinations of keywords associated with them.
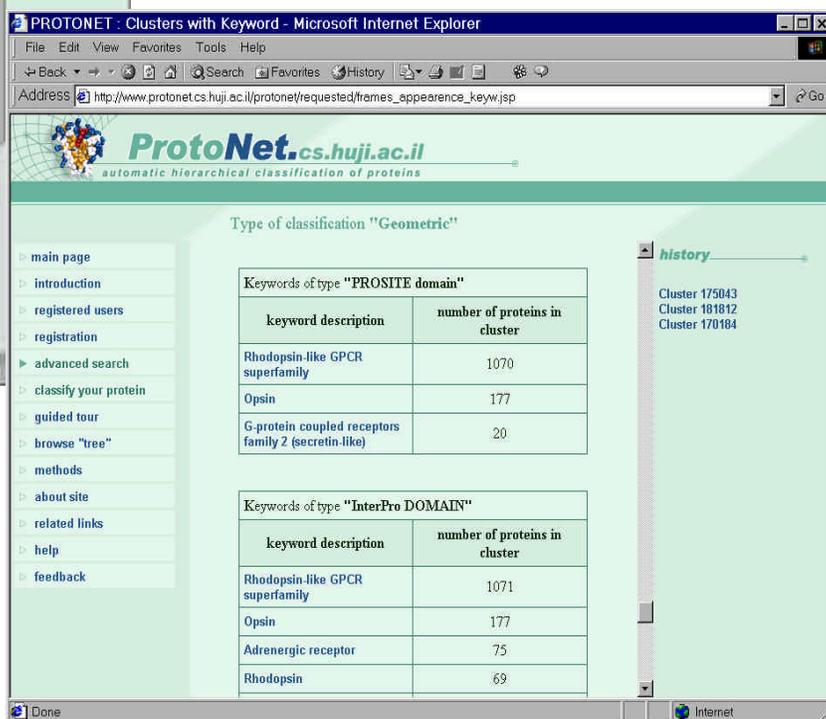
ProtoNet is based on a multiple clustering algorithms that have been extensively cross-validated.

ProtoNet (version 1.3, July 2002) provides a friendly and an easy-to-use interface and is implemented using Java 2 Enterprise Edition (J2EE) technology.

http://www.protonet.cs.huji.ac.il

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What you can do with ProtoNet version 1.3
Details on new and improved options are in 'ProtoNet News'

- ❖ Search for ANY protein in the Swissprot database (~100,000 proteins) to detect closely related and remote homologues (by name, by ID, by accession..)

- ❖ Search a NEW sequence (your protein) for its relationship with all known proteins. Resulting the optimal merge in ProtNet tree.

- ❖ View your protein using advance graphic tools indicating size and location of all domains and motifs (InterPro & as in Pfam, SMART, Prosite, ProDom etc).

- ❖ Obtain statistical and biological features of any cluster (and at any level of resolution) including average size of proteins, annotation by InterPro, biological keywords associated with the proteins within, taxonomy partition, PDB, and much more.

 A rich set of tools to navigate ProtoNet is provided

- ❖ Find the minimal cluster that includes both proteins A and B.
- ❖ Display statistical significance value for pairs within a cluster and pairs in any two clusters.
- ❖ Search all solved 3D structures within a cluster
- ❖ Compare the properties of a cluster that was constructed using alternative algorithms
- ❖ Search clusters that have proteins associated with specific keywords (i.e., kinase, antibiotic biosynthesis, postsynaptic membrane..)
- ❖ Retrieve clusters based on InterPro or Swissprot Kewords and get a statistical estimation of the cluster purity
- ❖ Navigate ProtoNet horizontally - using *ProtoLevel*
- ❖ BLAST any 2 proteins

 For the beginners

- ❖ Guided tour helps you to learn 'how to use ProtoNet'.
- ❖ Introduction briefly describes 'how we constructed ProtoNet'.
- ❖ In Methods we included recent publications describing ProtoNet.
- ❖ Related links provides a list of other major servers and protein DB.

ProtoNet version 2.1 (October 2002) will include latest Swissprot release and will provide features such as personalization tools and storage of your ProtoNet