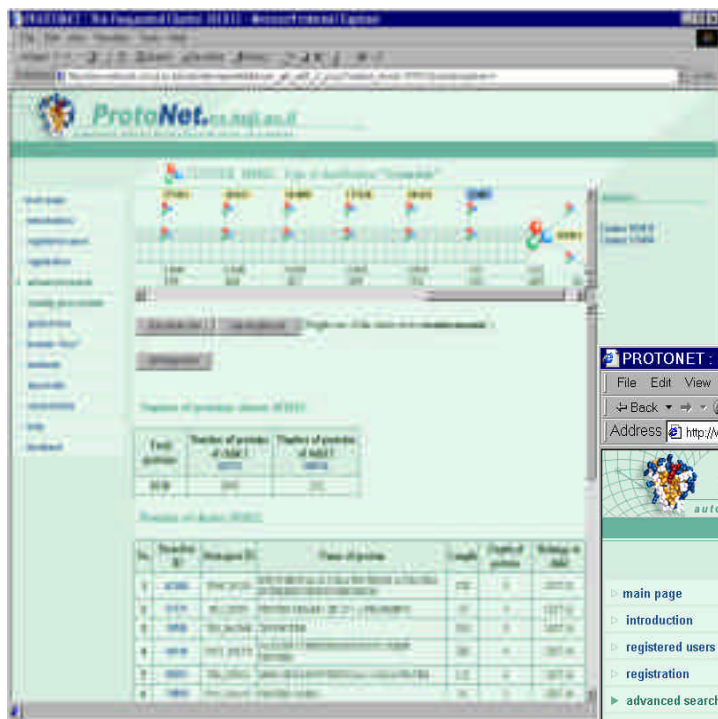


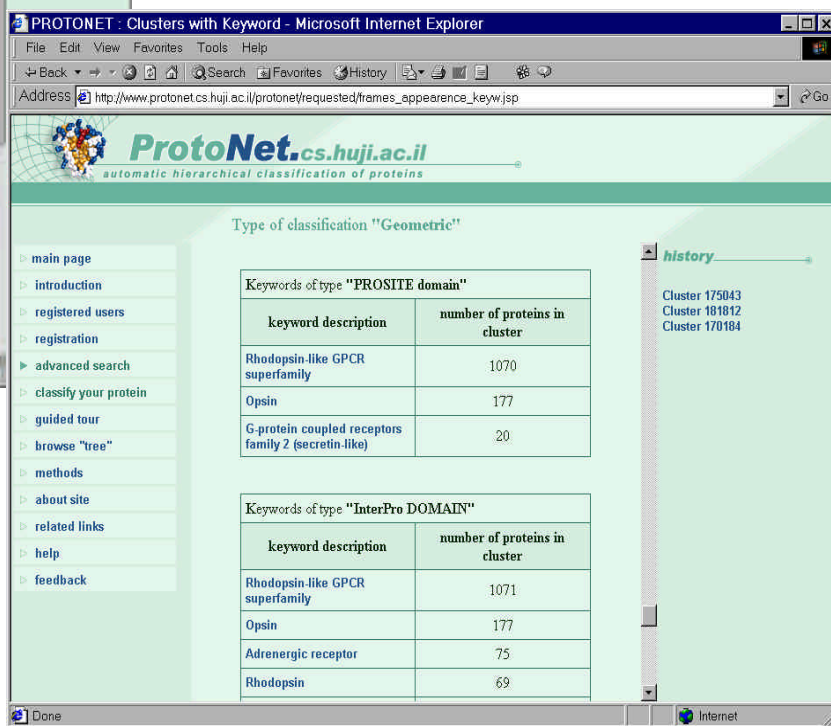
ProtoNet: Automatic Classification of Protein Families

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-families 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>

Contact information:

Michal Linial
Dept. of Biological Chemistry
The Hebrew University
Jerusalem, 91904
Israel

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 Keywords 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