

# Proteome Analyst

<http://www.cs.ualberta.ca/~bioinfo/PA/>

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## What is Proteome Analyst?

Proteome Analyst is a publicly available, high-throughput, web-based system for automatically predicting the **function** and **properties** of proteins. Its unique use of sequence analysis tools and machine learning gives it high accuracy and broad coverage for both **molecular function** and **subcellular localization** predictions and ranks it among the best predictors of its kind in the world.

## What Does Proteome Analyst Do?

Proteome Analyst provides two main services: **Protein Analysis** and **Custom Classifier Creation**.

For **Protein Analysis**, a user uploads one or more unannotated sequences, or sequences the biologist wish to study further, into Proteome Analyst. The tool then uses a machine-learned **classifier** to predict the classification of the sequence.

A key component to accurate prediction results is the built in classifier which was trained on many examples of proteins that have been annotated with the function (or localization) of interest.

However, with the **Custom Classifier Creation** component of the tool, a user can supply their own annotated sample sequences and create their own custom classifier. This new classifier can then be used to classify unannotated sequences in the same manner as the built in classifier.

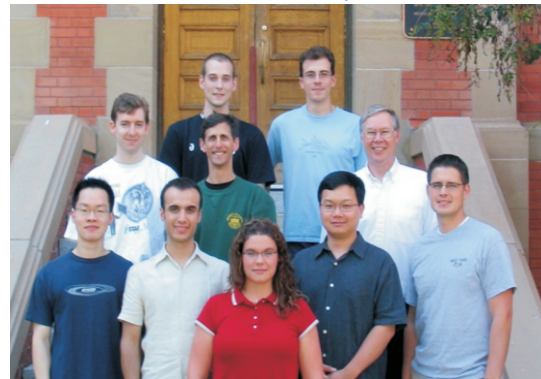
## Who Uses Proteome Analyst?

Proteome Analyst is used by bioscientists around the world at an ever-increasing rate. Multiple papers on Proteome Analyst have appeared in the high-profile scientific journals Bioinformatics and Nucleic Acids Research.

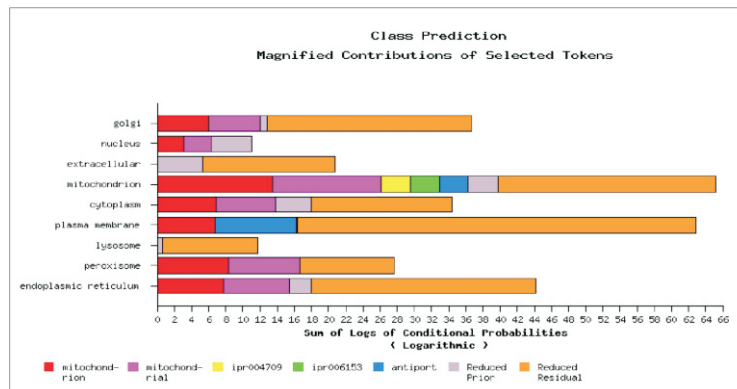
## What's Next?

We are currently extending this system to predict metabolic pathways, crucial cell processes that involve interactions between proteins.

The Proteome Analyst Team



from left to right  
 Back: Brandon Pearcy, Roman Eisner  
 Center: Nicholas Lamb, Russell Greiner, Duane Szafron  
 Front: Danny Ngo, Luca Pireddu, Alona Fyshe, Paul Lu, Brett Poulin  
 Not Present: David Wishart



A sophisticated feature of the Proteome Analyst tool is its *Explanation Graph*. It is a graphical representation that shows the user why one prediction is chosen over another. By allowing users to see why a particular prediction is made, user confidence in the prediction is increased.

For the latest information about the Proteome Analyst Project please visit us at

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