

You have sequences from high-throughput analyses, e.g., entire genomes.

You need a fast and concise genome analysis.

We offer comprehensive automatic annotation of entire genomes (from €5000/prokaryotic genome\*). The results are presented with an easy-to-use graphical environment, which provides extensive overviews and detailed feature visualization.

**The situation**

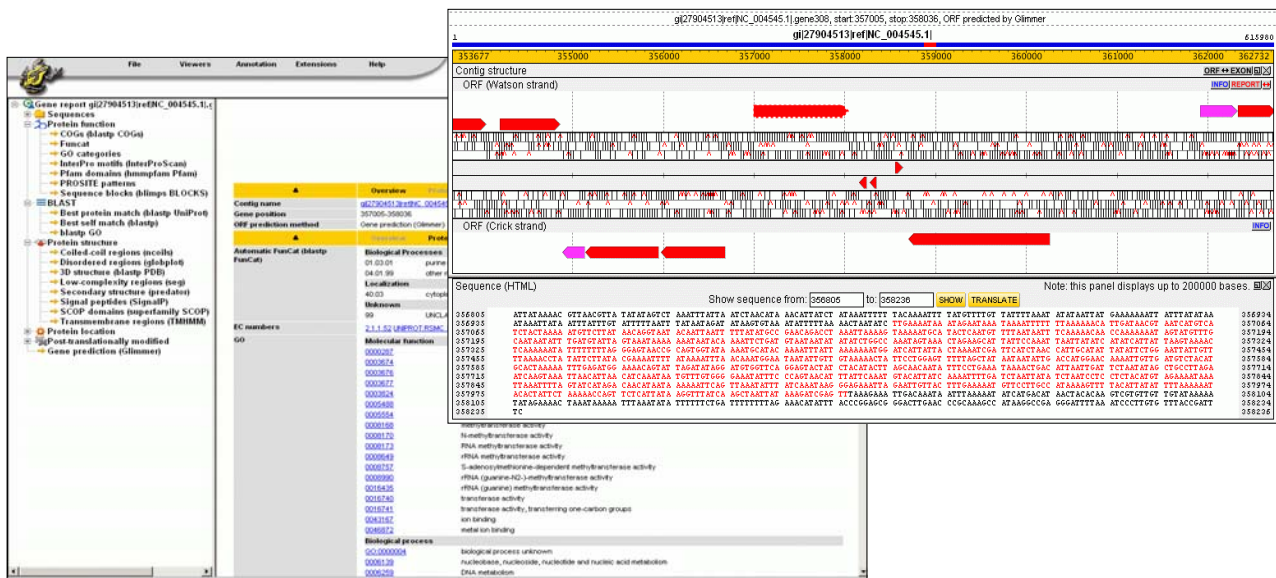
Recently, new sequencing techniques have revolutionized the genomics world — huge amounts of sequences are available in no time and almost for free. The number of completely sequenced genomes, which has increased immensely during the last decade, will increase at a dramatic pace in the future and the required annotation will "lag behind" more and more.

**The challenge**

The next step, the extraction of the full information hidden in the sequence data within reasonable time frame, is the bottleneck in the process. Often, the information extraction is too slow, not complete, and access and data exploration possibilities are not satisfying.

**The solution**

The Pedant-Pro™ Sequence Analysis Suite has a proven track record for providing fast, comprehensive and enterprise-scale automatic analysis of individual sequences and complete genomes. The Pedant-Pro suite finds genes and resulting proteins on a given sequence and predicts potential protein functions. In addition to the in-house installation, Biomax now offers the Pedant-Pro Genome Analysis On Demand, for which a genome is automatically annotated using the Biomax Pedant-Pro computing cluster. An intuitive graphical environment provides access to the data on all required levels.



**A Pedant-Pro gene report and the DNA Viewer**

\* The offer assumes assembled contigs as input sequences, a standard sequence quality and an intermediate GC content. Contact Biomax for further details of the analysis and of the mode of delivery.



The Pedant-Pro suite can be used to find answers the following questions, for example.

#### **Gene prediction and genome overview**

How many genes and non-coding elements are in the genome?

Where is the gene located? Is it part of an operon? What does the gene neighborhood look like?

Which types of RNA are found? Where are the RNA-genes located?

#### **Report about each gene**

What are the key facts — functional and structural — about each gene? Is the gene present in public or proprietary databases? Are there literature references about the gene?

#### **Function and pathways**

Which gene functions (determined by, e.g., GO categories or EC numbers) are found in the genome and, e.g., which genes code for acetyltransferases?

Are there strongly similar, presumably homologous, protein domains? Do the proteins in question consist of similar or different domains?

Which pathways are covered by the analyzed genome? Which enzymes of a pathway have been found? Are there expected enzymes missing?

How good is the evidence for the function prediction of a protein?

#### **Structure**

What kind of two-dimensional (2D) and three-dimensional (3D) structure does the protein have?

How many transmembrane proteins are there? With how many transmembrane domains?

#### **Localization**

Where are the proteins located within the cell?

**Analysis application built with expert biological know-how** Biomax is a proven provider of superior quality annotation for numerous global life science organizations. The Pedant-Pro suite was one of the first generation of bioinformatics applications. The current version 3.0 builds on years of experience and proven scientific knowledge and provides a concise sequence and protein repository for your company. The Pedant-Pro suite is used to annotate all publicly available genomes at the Munich Information Center for Protein Sequences (MIPS, now the Institute for Bioinformatics; <http://mips.gsf.de>).

**Contact Biomax Informatics today and get the most  
out of your genome sequences.**

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