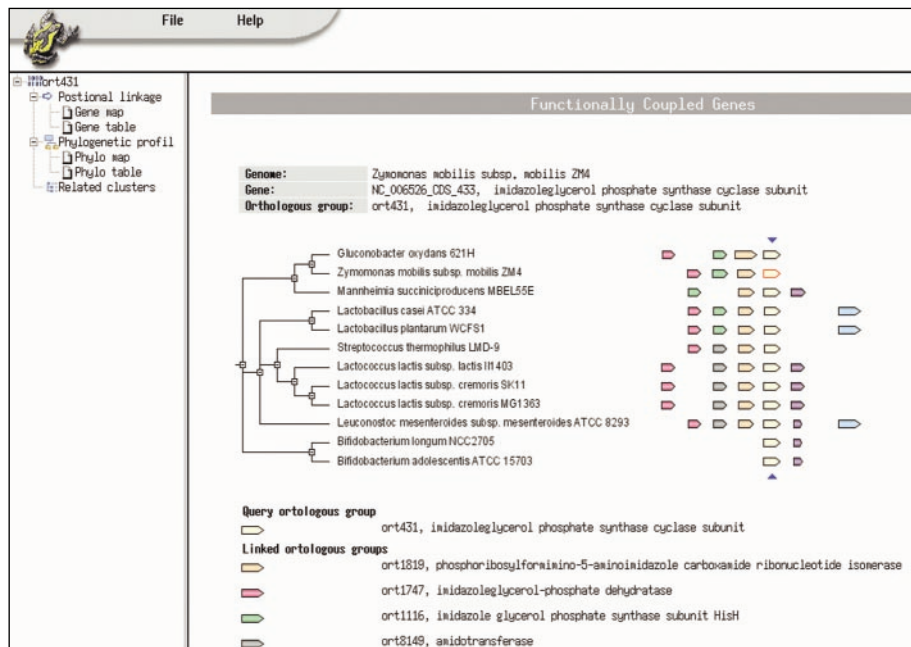


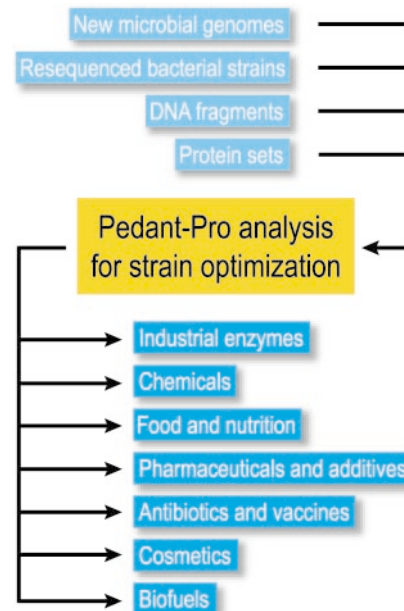
Product: Pedant-Pro Sequence Analysis Suite

Applications: high-throughput enterprise system for automatic and manual annotation, configurable sequence and genome analysis, comparative genomics (synteny, pathways, gene co-occurrence)

Contact: pedantpro@biomax.com



Comparison of microbial genomes (here: positional linkage) in Pedant-Pro suite



Highly efficient microbial genome analysis

Quick high-throughput automated sequence annotation and comparison of microbial genomes as the basis for the R&D pipeline in white biotechnology

The gap between the increasing amount of raw sequence data and qualified biological information is widening: it is not possible to provide qualified annotation for new genomes with the same speed at which sequences are generated — especially with next generation sequencing technologies. Additionally, managing the huge number of available bioinformatics algorithms represents a challenge of its own. Thus, a system which provides maximum annotation quality with approved methods in a minimum of time is absolutely critical as the basis for the R&D pipeline in industrial biotechnology.

The Pedant-Pro™ suite provides high-quality, industrial-scale genome annotation with respect to data volume and processing time. Genome comparison is an indispensable tool for strain improvement in markets such as enzyme production or the use of microorganisms in the food and pharmaceutical industries. The Pedant-Pro suite offers several aspects of comparative genomics, such as positional linkage (figure above), which can be applied to proprietary and public genomes.

An intuitive user interface, including tools for manual annotation, permits efficient work for the lab biologist as well as for the bioinformatician from the first minute on.

Extend IP portfolio with new enzymes:

- Scrutinize newly sequenced microbial genomes
- Facilitate protein engineering and gene shuffling
- Understand metabolic pathways for metabolic engineering and to find new design oportunites
- Streamline IP management

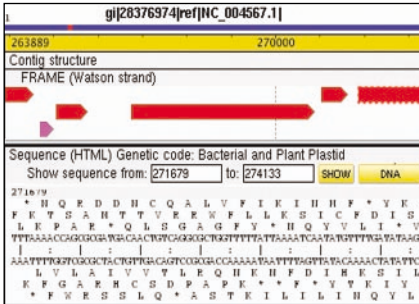
Increase production rates:

- Enhance expression of known enzymes
- Reveal and remove pathway bottlenecks

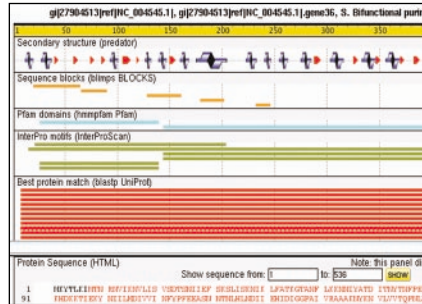
Optimize culture conditions:

- Reduce production costs
- Find new fermentation processes
- Improve stability for industrial conditions

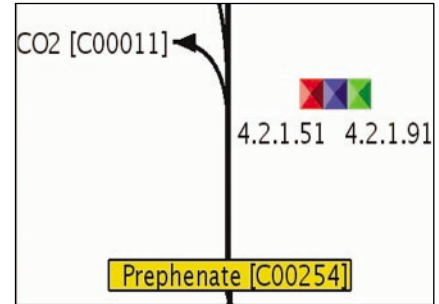




Detail of the Pedant-Pro DNA Viewer



Detail of the Pedant-Pro Protein Viewer



Detail of the Biomax Pathway Viewer

Gene finding

Pedant-Pro gene prediction uses the GLIMMER (prokaryotes) and GenEID (eukaryotes) algorithms. Additional algorithms can be integrated as required. Using a proprietary Biomax™ database with over 1.2 million entries, many non-coding elements, including more than ten types of non-translated RNAs, are predicted.

Explore the contig structure

The DNA Viewer allows operon structures, reading frames and alternative gene predictions to be viewed at optimal zoom levels. Quality scores and detailed information are available for each gene. When comparing DNA sets (e.g., bacterial strains), the number of polymorphisms in each gene is indicated.

Refine your results

Automatically predicted data can easily be extended manually. The Apollo module is integrated to provide a comfortable graphical tool for modeling genes. The Pedant-Pro manual annotation module allows additional notes, such as protein domains, literature references and general remarks, to be attached.

Viewing proteins and pathways

A number of viewers provide a graphical summary of protein information.

- Protein — comprehensive overview of features facilitate prediction of function
- Cluster — protein families reveal candidates for alternative gene products
- Pathway — places protein in relevant pathway context, including cross-genome comparison

Compare genomes

Genome comparison can be performed with your proprietary genomes. Additionally, genomes from the PEDANT™ Genome Database, comprised of more than 500 pre-calculated data sets, can be included to ensure the comparison covers a specific taxonomic range.

- Positional linkage (see figure on front page) compares orthologous genes in different genomes
- Phylogenetic profiling reveals the presence of orthologous gene groups over a specified taxonomic range
- Synteny analysis allows gene order comparison for two microbial genomes

Calculate with exactly the methods you need

The Pedant-Pro system is delivered with standard workflows which have been designed by Biomax scientists. In addition, new workflows can easily be defined with the new Pedant-Pro Workflow Manager by selecting standard and custom algorithms. This allows, for example, BLAST searches of proprietary databases to be included in an analysis.

Add your own data for each gene or protein

As an additional service, Biomax constructs a database from non-annotation data and integrate this information for each gene and protein. Experimental data, such as expression analysis results, can be accessed from the gene report. The Pedant-Pro system thus provides a single point of access to your gene and protein repository.

Biomax also offers expert genome annotation to deliver manually annotated genomes as PEDANT databases.

"Long term success story": Biomax is a proven provider of superior quality annotation for numerous global life science organizations. Pedant-Pro version 3 continues the successful track-record of the application. It builds on years of experience, close collaboration with customers and proven scientific knowledge. Please see the Pedant-Pro success story on the Biomax product page for a list of selected Pedant-Pro projects: <http://www.biomax.com/pedantpro>. 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>).

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Biomax Informatics AG

Lochhamer Str. 9, 82152 Martinsried, Germany, +49 89 895574-0

www.biomax.com

