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FOR RELEASE ON 9 OCTOBER 2001

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BIOMAX INFORMATICS AG
releases the Biomax Gene Expression Analysis Suite, software for integrative
analysis of gene expression data

MARTINSRIED, Germany — 9 October 2001 — Biomax Informatics AG, a leader in custom-designed bioinformatics solutions, launches the Biomax Gene Expression Analysis Suite, an intelligent and innovative software for systematic analysis and visualization of gene expression data from different experiments. The software provides comprehensive and integrative analysis of complex data sets using available gene annotation. With the software suite, users can quickly find groups of tightly co-expressed genes, evaluate active metabolic pathways and predict interactions among the corresponding proteins.

Offering a sophisticated repertoire of functionalities, the Biomax Gene Expression Analysis Suite reduces complexity of data by clustering genes based on their experimental expression profiles, displays detailed expression information for any selected cluster and provides links to annotations for each gene using the hierarchical Biomax functional catalog to characterize protein function. The software displays the distribution of genes belonging to specified functional categories among the gene clusters and identifies groups of clusters containing co-expressed genes of selected functional categories and overlaps between such groups. Genes of interest are placed in a biochemical context by constructing both pathway models and protein interaction networks. The software suite answers questions such as the following:

- Which genes are differentially or co-expressed under a specific condition?
- To which functional categories do these genes belong?
- Do co-expressed genes form meaningful metabolic pathways?

- Are different functionalities reflected in differential gene expression?

The Biomax Gene Expression Analysis Suite is a client–server based system, which allows company-wide access for users with different operating systems and Web browsers. The server can run on Linux[®] or any other UNIX[®] operating system. The client can reside on any operating system (including Windows[®] and Macintosh[®]) supporting a commonly used browser.

The system is adaptable for various expression data formats and can be fully integrated with other Biomax software components to achieve comprehensive bioinformatics solutions fully optimized to meet any specific needs.

About Biomax

Biomax Informatics AG (Martinsried, Germany), a leader in the development of customized bioinformatics solutions, was founded in 1997 as a spin-off of the GSF-MIPS academic research group, now the German Research Center for Environment and Health-Institute for Bioinformatics (GSF-IBI). Founded by Dr. D. Frishman, Dr. K. Heumann and Prof. Dr. H. W. Mewes, Biomax developed the well-known Pedant-Pro™ Sequence Analysis Suite, the HarvESTer™ EST Assembly and Clustering System, and other bioinformatics tools used in metabolic pathway, proteomics, and gene expression analyses. Additional information about Biomax can be found at the company's site on the World Wide Web at www.biomax.de.

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