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**BIOMAX INFORMATICS AG
Launches the Biomax Human Genome Database**

MARTINSRIED, Germany — 1 August 2002 — Biomax Informatics AG today releases its manually annotated human genome database, the Biomax Human Genome Database, for licensing by life scientists. The database contains comprehensive automatic annotation as well as the results of extensive and consistent manual annotation performed by Biomax biologists. Used alone or as a unique content source for other applications, the database will facilitate data mining and bring increased efficiencies to research endeavors.

The Biomax Human Genome Database starts with publicly available sequence data. The genes are identified with the FGENESH++ gene modeling software exclusively licensed from Softberry, Inc. Automatic annotation (identification of putative protein structure and function, as well as additional key information) is then performed using the Pedant-Pro™ Sequence Analysis Suite from Biomax. Finally, each gene is verified by Biomax biologists using a systematic process of manual annotation, which includes refining functional information and adding literature references and other details not covered by the automatic annotation software.

Citing his opinion of the database, Dr. Marius Sudol of Mt Sinai School of Medicine said, "Without doubt, the Biomax Human Genome Database will bring increased efficiencies to our research. Tables of protein domains, including SH3 and WW modules, are superb and provide new information." Dr. Norbert Klugbauer of the Institute of Pharmacology and Toxicology of TU Munich, added "I no longer need to search dozens of databases since the Biomax database provides links to all other relevant databases as well as literature citations. The database offers information about human sequences and proteins – all in one place."

“It is rewarding to know that with the launch of this database, we are bringing to research projects everywhere a truly consistent, information-packed database that includes high-quality annotation,” stated Dr. Christine Schüller, Human Genome Project Leader at Biomax. “By capitalizing on our in-house bioinformatics expertise and scientific know-how, we have successfully produced a very useful database that will add measurable efficiencies to research projects.”

The Biomax Human Genome Database is being launched with a special, introductory low-price offer. Life scientists interested in previewing the database can view selected chromosomes by registering for a username and password at www.biomax.com. Interested subscribers can download a one year, one-user license for remote access via the Web. The introductory price offer is valid for the first 500 licenses submitted or until 31 October, 2002, whichever comes first.

The Biomax Human Genome Database is a client–server system available for easy and secure access via the Internet from Biomax servers or as a locally-installed, enterprise solution allowing organization-wide access. An easy-to-use graphical interface and powerful search tools have been developed specifically for working with the human genome, giving life scientists the ability to quickly find and analyze relevant data.

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 BioRS™ Integration and Retrieval System and other bioinformatics tools used in metabolic pathway, proteomics, and gene expression analyses. Additional information about Biomax and the Biomax Human Genome Database can be found at the company's site on the World Wide Web at www.biomax.com.

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