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For immediate release

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BIOMAX INFORMATICS AG and SOFTBERRY, INC., ANNOUNCE STRATEGIC ALLIANCE
Biomax gains exlusive license to Softberry human genome database

MARTINSRIED, Germany, and WHITE PLAINS, New York, USA – April 3, 2001 –Biomax Informatics AG and Softberry, Inc., announce a strategic agreement granting Biomax an exclusive worldwide license to Softberry's complete human genome database. The Softberry™ database includes predicted gene sequences which were automatically generated using Softberry's exclusive software, Fgenesh™++ and other computational tools. Biomax will further develop and annotate the database using the proprietary Biomax™ Pedant-Pro™ Sequence Analysis Suite to create the PEDANT™ Human Genome Database. ***This database will be the most complete and accurate source of systematically annotated data for the human genome available and will be distributed by Biomax and its partners***.

Soon the enormous amount of raw human genome data will be transformed into useful and formatted information which will be made available to researchers worldwide to enhance their gene-discovery projects. Using publicly available sequence, Softberry identified the potential location of genes using exclusive Softberry software. Now, Biomax will bring additional information as well as provide optimal visualization using the sophisticated Pedant-Pro software. The companies will release database updates each quarter or as often as improved versions of human genome sequence become available.

"Biomax is the logical partner for Softberry to bring this valuable database to the marketplace, not only because of their proprietary Pedant-Pro system, but because Biomax is a globally recognized leader in providing customized bioinformatics solutions," says Dr. Valery Sagitov,

president of Softberry. "We are confident that the synergy of combining our analysis tool, Fgenesh++, and the Biomax Pedant-Pro system will result in the most accurate and biologically significant human genome database."

"Instead of seeing long strings of As, Cs, Gs, and Ts when looking at the genome, researchers will see transmembrane proteins, tRNAs, the 3D structure of their favorite protein and a multitude of other biologically relevant information," explains Dr. Klaus Heumann, CEO of Biomax. "The exclusive Fgenesh++ Softberry software is one of the most powerful systems for gene prediction available and gives substantially more accurate predictions than other commonly used approaches, such as *ab initio*. By combining this first-class gene prediction with fine tuning and easy-to-understand visual representation using the Pedant-Pro software, the PEDANT Human Genome Database will, without a doubt, be the most comprehensive, accurate and useful source for human gene information," said Dr. Heumann.

The Softberry and PEDANT databases (including updates) use the publicly available human genome sequences assembled at the University of California at Santa Cruz. The raw data is analyzed to generate a set of coordinates for the location of predicted genes. The Fgenesh++ script uses repeat masked sequences of human chromosomes, alignment software, such as DBScan™ or BLAST, and Softberry's well-known gene prediction programs, Fgenesh and Fgenesh+, as well as the complete set of protein sequences in the NR protein database for improved identification of human genes. Softberry gene prediction programs can produce *ab initio* annotation of the whole human genome in several hours, which is important for producing updated versions of the database when improved sequences of human genome become available.

The database prepared for Biomax will consist of several data sets: locations of predicted coding regions and the corresponding protein sequences in FASTA format as well as relevant sequence information for predicted exons. Biomax will analyze this data using the Pedant-Pro Sequence Analysis Suite to identify other genetic elements, such as centromeres and various species of RNA. The Pedant-Pro system displays primary information such as sequence similarity, multiple sequence alignments and sequence domains, as well the results of analysis including three-dimensional models based on predicted secondary structure of putative proteins. The agreement grants Biomax exclusive rights to modify, sell, or redistribute the new PEDANT Database. The PEDANT Human Genome Database will complement the PEDANT Genome Database which contains 90 sequenced and fully annotated genomes, also distributed by Biomax.

About Softberry

Headquartered in White Plains, New York, Softberry, Inc., is a leading developer of software tools for genomic research. Its list of commercial products includes family of leading gene prediction programs (Fgenesh, Fgenesh+, Fgenesh2), genome comparison tools DBScan and Scan2, protein sub-cellular localization predictor ProtComp™, expression analysis program Seltarget™, RNAmap and Oligomap programs for fast RNA/EST/oligo mapping to chromosome sequences, Genome Information Viewer and many others. Some programs developed by Softberry use well-know algorithms developed in academia. For example, the gene finder program FGENESH, developed originally at Sanger Center, was completely rewritten to improve its speed (~50 times) and analyze long chromosome sequences. The company is privately held by its management and research staff, which include programmers and bioinformatics professionals mostly from USA and Russia. Additional information about Softberry can be found at the company's web site www.softberry.com.

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 GFS-MIPS academic research group of the German Research Center for Environment and Health (Neuherberg) and the Munich Information Center for Protein Sequences (Max Planck Institute for Biochemistry, Martinsried). 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 can be found at the company's web site www.biomax.de.

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