BIOMAX INFORMATICS AG and SOFTBERRY, Inc.,
extend collaboration to provide an integrated bioinformatics environment
that combines data management and retrieval of biological information with
the most comprehensive array of sequence and structure analysis
programs

MARTINSRIED, **Germany and Mount Kisco, NY, USA** — 23 May 2005 — Biomax Informatics AG and Softberry, Inc., announce the integration of a wide array of genome analysis programs from Softberry into the Biomax Pedant-Pro™ Sequence Analysis Suite and BioRS™ Integration and Retrieval System, creating a powerful and flexible environment for management, access and analysis of biological data. The system provides a comprehensive database and software package that can accommodate user-specific preferences to include approximately a hundred software modules addressing specific research needs related to sequence analysis, protein modeling and visualization.

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.com*.

About Softberry
Softberry, Inc., (Mount Kisco, NY, USA) is a leading developer of software tools for genomic and proteomic research. Its list of commercial products includes a family of gene, promoter and functional site prediction, new genome annotation, genomes comparison and sequence mapping programs, RNA and protein structure modeling tools, protein sub-cellular location and epitope prediction, database of regulatory motifs and many others. Softberry customers include over 50 leading pharmaceutical, biotech and agribusiness companies, as well as academic research institutions worldwide. Additional information is available at *www.softberry.com*.

About Softberry sequence and structure analysis software
Softberry FGENESH family of gene prediction and genome annotation programs is being used for annotating vast majority of newly sequenced genomes. Its functional site prediction programs, TSSW/TSSG/TSSP, NSITE and PromH, and genome mapping and comparison programs, Prot_Map, FMAP, EST_MAP, GenomesMatch and others, are widely acclaimed as fastest and most accurate. Other widely used programs include protein sub-cellular localization prediction program ProtComp and an array of protein modeling tools.