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Biomax Informatics AG
Launches Version 5.0 of the BioRS™ Integration and Retrieval System

MARTINSRIED, **Germany** — 17 October 2002 — Biomax Informatics AG today announces the release of version 5.0 of the BioRS Integration and Retrieval System, a powerful software tool for search and retrieval of biological information from flat-file and relational databases. Version 5.0 includes many new features expanding the capabilities of the software and making it easier to use for researchers, such as:

- Enhanced support for Extensible Markup Language (XML) databases, such as MEDLINE
- Increased accuracy and efficiency when searching hierarchical structures in databases
- Better general security and research efficiency through management tools for user accounts and databases
- Support for the AIX operating system on IBM platforms

These new developments are part of the ongoing Biomax commitment to providing the most effective and user-friendly bioinformatics systems available.

BioRS 5.0 now makes it much easier to integrate databases in XML format, such as the frequently used MEDLINE database, extending existing support for flat-file and relational databases.

Efficiency and accuracy of searches of hierarchically organized databases has been greatly improved in version 5.0 with the new nested database feature. Hierarchically structured parts of databases, such as feature keys in the GenBank and SWISS-PROT databases, can be integrated into nested databases, “databases within a database,” so that their structure is preserved.

Security and research efficiency have been improved in version 5.0 with a powerful system for the management of user accounts and databases. User accounts can be created and placed into groups and access to biological sources of information can be managed for users or for entire groups.

The BioRS system, first launched in 1998, is a high-speed, sophisticated search and retrieval system for biological information in public and proprietary databases. The speed and flexibility of the BioRS system greatly facilitates gene discovery projects, including genomics, proteomics and drug targeting and delivery. The system enables researchers to quickly and efficiently retrieve all known biological data on a given topic, independent of the size of the database or the complexity of the query. BioRS uses convenient web interfaces and standardizes data formats from different databases using XML for quick, easy access to data, independent of the source format. Both public and proprietary databases in flat-file or relational format are easily integrated.

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 Clustering and Assembly 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.

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