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Contact:

Shannon Frances
Biomax Informatics AG
Lochhamer Str. 9
D-82152 Martinsried
Germany
Tel: +49 89 895574-0
Fax: +49 89 895574-825
Website: www.biomax.com

New BioRS™ release from BIOMAX INFORMATICS AG combines database integration and retrieval with sequence search and alignment tools

MARTINSRIED, **Germany** — (2 October 2007) — Biomax releases today a new module for the BioRS™ Integration and Retrieval System, an application providing simultaneous searches in multiple biological and biomedical databases. The new module provides standard sequence similarity search and multiple alignment tools for querying nucleotide and protein sequences. With this module, the BioRS query form allows text fields to be searched while simultaneously using Basic Local Alignment Search Tool (BLAST) similarity and pattern searches with a sequence field. The integrated text and similarity search allows fast and specific results focusing on a topical area. Search results provide access to sequences in different formats as well as pair-wise and multiple sequence alignments. For more information about the BioRS Integration and Retrieval System, contact your Biomax representative or visit *www.biomax.com*.

About Biomax

Biomax Informatics AG (Martinsried, Germany), founded in 1997, is a leader in the development of customized bioinformatics solutions. Biomax developed the well-known Pedant-Pro™ Sequence Analysis Suite, the BioRS™ Integration and Retrieval System, the BioXM™ Knowledge Management Environment and other computational solutions for better decision making and knowledge management in the life science industry. Additional information about Biomax can be found at the company's site on the World Wide Web at *www.biomax.com*.

About the BioRS Integration and Retrieval System

The BioRS Integration and Retrieval System quickly and efficiently retrieves biological data from public and proprietary databases. Multiple databases can be searched simultaneously using convenient Web interfaces. Flat-file and relational databases (Oracle®, MySQL™) are easily integrated using Web or command-line interfaces and standardized data formats based on Extensible Markup Language (XML).