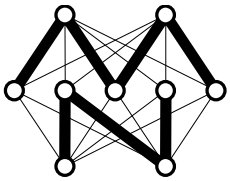

Molecular Networks

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For immediate release

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BIOMAX INFORMATICS AG and MOLECULAR NETWORKS, GmbH ANNOUNCE PRODUCT DEVELOPMENT ALLIANCE

MARTINSRIED and ERLANGEN, Germany — July 9, 2001 — Biomax Informatics and Molecular Networks announce today the formation of a strategic partnership that will effectively join bioinformatics and chemoinformatics into one stream of research. Molecular Networks, which specializes in the development of software for drug design, combinatorial chemistry, and data-mining, and Biomax, with its expertise in DNA and protein sequence analysis used in drug-target design and database integration, will collaborate in the development of software tools for optimized drug-target lead generation and validation.

By sharing proprietary technology, Biomax and Molecular Networks create a cooperative platform for developing the next generation of drug discovery tools. Resulting products from the collaboration will be jointly marketed by both companies. The processes in the drug discovery pipeline – such as gene sequencing, combinatorial molecule synthesis, high-throughput screening, lead discovering and optimization, and finally molecule design – are increasingly being automated. The challenges in drug discovery today involve using computational power and data-mining techniques to quickly extract useful information from the available data. Up-to-date information is critical for decision-making in downstream steps and accelerating the whole process. The companies believe the cooperative environment the agreement creates will allow these challenges to be addressed.

“Although the two companies have been sharing resources for quite some time, this formal agreement, complete with milestones, will give better focus and direction to new product development,” said Prof. Dr. Johann Gasteiger, CEO of Molecular Networks. “As a leading provider of customized bioinformatics solutions, Biomax has correctly recognized their customers’ need for an integrated product incorporating chemoinformatics tools, which we can provide, into Biomax software solutions. Thus, a ‘comprehensive’ solution, dealing with the entire drug discovery pipeline, will be achieved. The signing of this agreement is a logical step in driving the process.”

“Molecular Networks developed CORINA, which automatically generates three-dimensional atomic coordinates using the composition of a molecule,” explained Dr. Klaus Heumann, CEO of Biomax. “This powerful software and other tools from Molecular Networks combined with Biomax tools such as the Pedant-Pro™ Sequence Analysis Suite will take the drug discovery process to the next level. Processes that used to require many steps will become streamlined, seamlessly integrating and optimizing target identification and small molecule validation. Until now, bioinformatics and chemoinformatics have been treated as separate entities. Our customers have already started asking for such software integration and this arrangement with Molecular Networks was an obvious and natural next step in our product development process.”

About Molecular Networks

Molecular Networks (Erlangen, Germany) was founded in 1997 as a spin-off of the Computer-Chemie-Centrum of the Universität Erlangen-Nürnberg and specializes in the development of software tools for solving a host of chemical problems including automatic generation of three-dimensional molecular models (CORINA), conversion of databases into three-dimensional structures, comparison of commercially available libraries of compounds, designing of organic syntheses and combinatorial libraries, lead discovery and optimization, quantitative structure-activity relationships, and simulation of chemical reactions and metabolic pathways. Molecular Networks has more than 80 placements of CORINA worldwide and since January 2001, MDL Information Systems is exclusively using CORINA for new 3D structure databases. Additional information about Molecular Networks can be found at the company’s web site www.mol-net.de.

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.de.

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