



NEWS RELEASE

Biomax™ Human Genome Database Integrated With AxCell's Protein Interaction Data

September 22, 2003, Savannah, GA. Biomax Solutions Inc. today announced the launch of the integrated Biomax™ Human Genome Database with AxCell's ProChart™ Protein Interaction Data at the GSAC XV Conference. The new combined product will provide researchers with a single information source to address a broad range of signal transduction and disease state experiments directly in the laboratory. This unique system provides a seamless bridge to laboratory experiments with a focus on AxCell's 12,000 binding reports of peptides associated with the WW, PDZ and SH3 domains.

"The Biomax Human Genome Database has proven to be very attractive to researchers in commercial and government labs," said Pat Blake, President of Biomax Solutions Inc. "Now the database is a unique entry point for additional experimental protein-protein interaction data from AxCell. It's our expectation that the system will save scientists considerable time and money"

Dr. Juan Herrero, Senior Director of Scientific Operations at AxCell, explained, "We invested significant time and resources to perform biochemical experiments in our wet-labs in order to identify and record the binding affinity and overall interaction of more than 4,000 proteins containing protein domains and ligands. One of our priorities was to focus on domains that are implicated in several important human diseases such as cancer, HIV, Alzheimer's and cardiovascular diseases. This unique linkage of the database information with wet-lab reagents is expected to save laboratory scientists time and resources ---- for example the set-up time for a Yeast-2-Hybrid or similar screen." said Dr. Herrero.

AxCell also provides wet-lab experiment kits to do follow-up experiments with the reagents derived from the domain and ligand interaction reports, as well as cost-effective, fully automated, high through-put, custom peptide synthesis. "Any of AxCell's peptide ligands found in the Biomax Human Genome Database are immediately available," Dr. Herrero continued. "In addition, we can synthesize custom peptides libraries of up to 25 amino acids that may incorporate unusual or chemically modified residues. Based on AxCell's experience of having made tens of thousands of peptides for our internal research, we are uniquely qualified to handle and provide customer-specific peptide sequence libraries for epitope mapping or other applications where large numbers of peptides are required."

The combined product launch coincides with the release of version 3.1 of the Biomax Human Genome Database developed in Munich, Germany at Biomax Informatics AG. "We are very excited about adding AxCell's ProChart data to our database," said Dr. Klaus Heumann, CEO of Biomax Informatics AG. "Our strategy is to collaborate with life science companies like AxCell to extend the rich content contained in our database. We envision a hub and spoke architecture that will allow the ongoing addition of new, valuable, genomic and proteomic information."

Version 3.1 of the Biomax Human Genome Database includes more extensive manual annotation of proteins, the integration of the entire mouse genome and comparison to the *Fugu rubripes* genome. The content of the database has been updated using genomic sequences from the *Homo sapiens* build 31 from the NCBI. Search capabilities using the BioRS™ Integration and Retrieval System version 5.2 have been extended and PubMed searches have been optimized to search all literature regarding any selected protein. Other new features include improved DNA Viewer and Protein Viewer interfaces, as well as enhanced protein report pages with convenient navigation to more external databases and genome viewers.

“Life scientists interested in previewing Version 3.1 can view a free demonstration of selected chromosomes at www.biomaxsolutionsinc.com. On this website, visitors can download a one year, single-user license for remote access via the website,” Pat Blake said. “This site also provides an easy process for scientists to order AxCell’s protein-to-protein domain or ligand interaction reports, wet-lab kits and custom peptides. All Biomax and AxCell products are available at very cost effective price points.” Mr. Blake concluded. For further information on Biomax and AxCell, contact Biomax Solutions Inc.

About Biomax Solutions Inc. – BSI is an integrator of bioinformatics software development companies. We sell, market, manage channels, implement and support the delivery of a broad range of software and services. Our alliance companies include Biomax Informatics AG and AxCell Biosciences. Our customers include pharmaceuticals, biotechs, academics and government research organizations in Europe and the U.S. Visit our website at www.biomaxsolutionsinc.com

Biomax Informatics AG Martinsried, Germany, a leader in providing customized bioinformatics solutions, 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 and the Biomax Human Genome Database can be found at the company's site on the World Wide Web at www.biomax.com.

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About AxCell Biosciences

AxCell Biosciences of Newtown, PA, a subsidiary of Cytogen Corporation, is engaged in the research and development of novel biopharmaceutical products using its growing portfolio of functional proteomics solutions and collection of proprietary signal transduction pathway information. For additional information on AxCell Biosciences, visit www.axcellbio.com., which is not part of this press release.

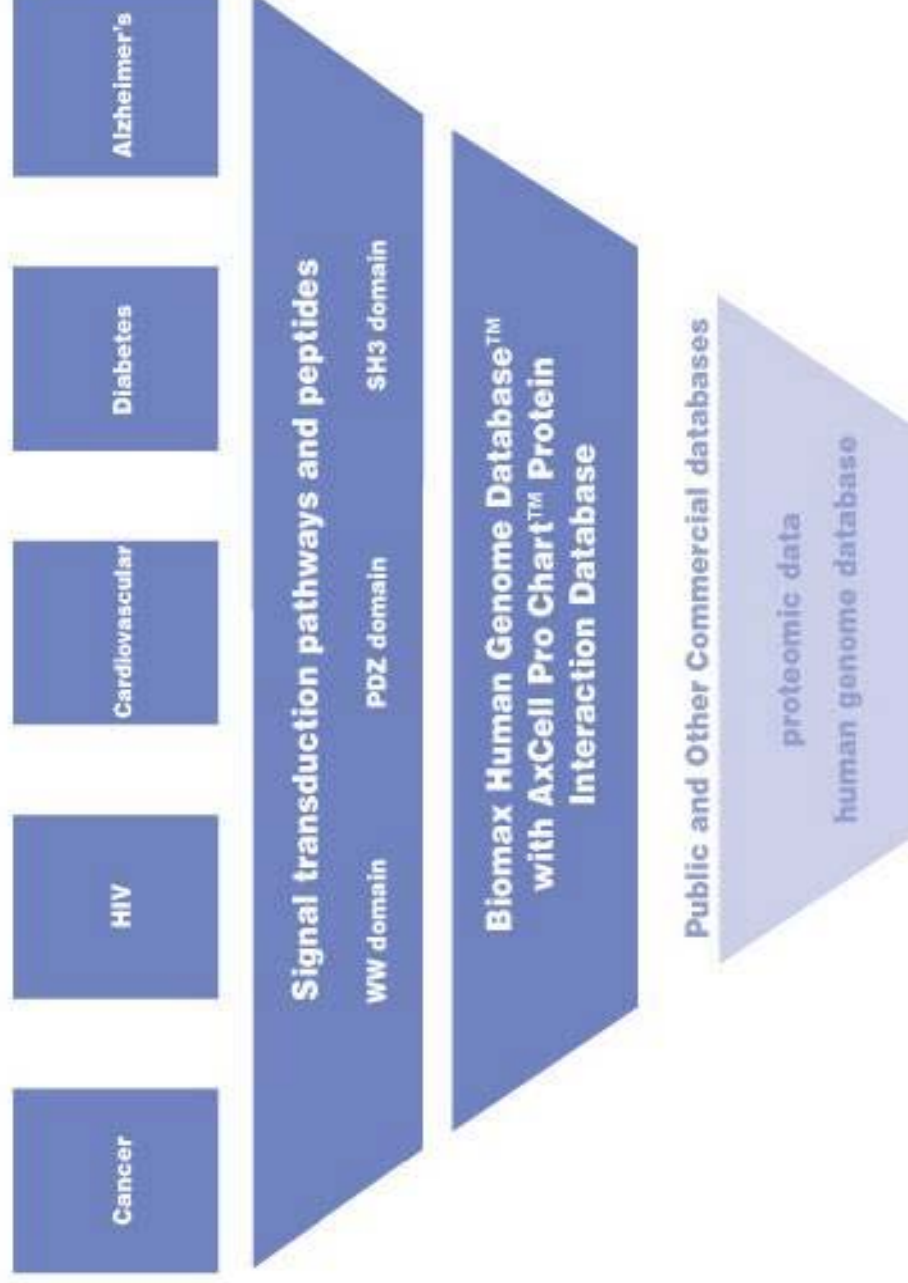
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Biomax™ Human Genome Database (BHGDB) with AxCell ProChart™ Protein Interaction

Greater flexibility to unleash your research creativity



Biomax™ Human Genome Database (BHGDB) with AxCell ProChart™ provides validated protein-protein interaction information for three major domains, so researchers can focus on the proteins that play a role in key diseases.

Typical human genome databases stop at a catalog description of genes, gene function, and limited curated protein data.

