



Press Release

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MeITec collaborates with Proteome Center Rostock in Rheumatoid Arthritis

Magdeburg, Germany, **February 6, 2003** – MeITec GmbH and the Proteome Center Rostock announced a collaboration in the field of Rheumatoid Arthritis (RA). In a feasibility study the partners will apply MELK technology for the first time to tissue samples collected from inflamed human joints. Dependent on these results, the collaboration will then expand to utilize topological proteomics (or toponomics) for the discovery of biomarkers and targets in RA. The Proteome Center Rostock is an integral part of the Proteome Alliance, a research network of more than 20 industrial and academic groups supported by the German Ministry for Education and Research (*Bundesministerium für Bildung und Forschung*, BMBF). The consortium has already identified a large group of potential targets. MeITec will apply its toponomics technology platform to decipher cellular function and dysfunction in RA patients by determining the situation of protein networks in time and space in every intact cell in situ.

Hans-Jürgen Thiesen, M.D., Director of the Institute of Immunology and Michael O. Glocker, Ph.D., Director of the Proteome Center Rostock explained, "One significant challenge in understanding the molecular situation in RA is accurately identifying and comparing protein networks in situ within diseased and control cells and tissues. MeITec's proprietary MELK technology provides a novel and sophisticated method that may prove important for the discovery of new diagnostic biomarkers and drug development targets for this disease."

Walter Schubert, M.D., Founder and Chief Executive Officer of MeITec added, "The Proteome Center Rostock has conducted significant preliminary integrated proteomics and genomics research on RA, providing an ideal basis for applying our core technology MELK."

RA is a chronic, systemic, inflammatory disease that chiefly affects the synovial membranes of multiple joints in the body. In most cases of RA, the patient has remissions and exacerbations of the symptoms. The prevalence of the disease is 1-2 percent of the general population and is found world-wide. Females with RA outnumber males by a 3:1 margin. Onset of the disease in adults is usually between the ages of 40 to 60 years, although it can occur at any age. The worldwide health and economic impact of RA is significant with 2.1 million people suffering from the condition in the U.S. alone.

Financial terms of the deal were not disclosed.

About MelTec

MelTec GmbH is a privately held biotechnology company specializing in using topological proteomics to identify mechanisms underlying disease pathology, drug targets and to prioritize lead compounds focused on immune-mediated disease, neurological disorders, cancer, and arteriosclerosis. MelTec's proprietary robotic imaging technology, MELK (Multi-Epitope-Ligand-Kartographie), performs completely automated proteomic characterization of single cells, for hundreds of proteins simultaneously, thus identifying the proteomic fingerprint, or the topology, of individual cells, such as lymphocytes. Using its technology, MelTec believes that it can greatly accelerate pre-clinical research in the drug development process, and has already identified new targets and lead compounds in amyotrophic lateral sclerosis (ALS, Lou Gehrig's Disease) and cancer.

About Proteome Center Rostock

The Proteome Center Rostock was founded in late 1999 as a department of the Institute of Immunology at the University of Rostock and currently employs 30 specialized scientists and highly trained technicians. It provides a cutting edge scientific methodology and technology platform for improving speed and sensitivity of clinical transcriptome and proteome analysis. Samples from patients suffering from multigenic diseases are investigated at the Proteome Center Rostock by a) high-performance proteome analysis, including modern sample work-up and pre-fractionation, b) state-of-the-art 2D-gel electrophoresis and visualization combined with in-depth mass spectrometry, c) RNA-expression profiling via global microarrays and high-sensitivity custom-made chips, d) protein-protein-interaction monitoring by using surface plasmon resonance spectroscopy, e) detailed mass spectrometric protein structure characterization and peptide sequencing (MSⁿ), and f) structural and functional genomics-oriented bioinformatics on top of the in-house LIM-System (ProteoBase).