

Proteomics – an important pillar of biomedical research

by Albert Sickmann

Protein molecules play a prominent role in the body. Not only do they have transport, supportive, and metabolic functions; they are also the most important regulators of all of the processes essential for life. Therefore, most lifestyle diseases such as cardiovascular diseases, diabetes, obesity, cancer, and allergies are attributable to protein malfunctioning. For this reason, they have been the most important objects of research for a long time, even 100 years before the gene era. However, classical protein biochemistry has hit several snags and can be used only to a limited extent to investigate important mechanisms. Therefore, a decade ago, triggered by new technical developments, proteomic research emerged. It attempts to understand the closely integrated and biochemically optimally regulated processes of entire signaling pathways.

Our research focuses on investigating the/these protein networks, which, when impaired, can lead to the development of a disease. If the majority of the components of these networks and their regulatory mechanisms can be understood, then our results can serve as a basis for modeling these networks. With such a model, various types of cellular processes can be better understood and new therapeutic approaches in medicine can be developed. We focus predominantly on cellular components that have essential functions in the body, such as mitochondria, the powerhouses of the cell, and simple cells with enormous significance, such as platelets, which are responsible for blood coagulation. In addition to the global identification of protein networks in the cell, we have a special interest in rare proteins that have important regulatory properties. Many of these proteins are posttranslationally modified; i.e., after they are synthesized in the cell, they are provided with molecular switches that can turn their regulatory functions on or off.

In recent years, we conducted the first comprehensive inventory of the powerhouse of the cell and, by nationally and internationally networking with other scientists, have been able to provide critical new findings in order to understand the functioning of this "mini-powerhouse". Many of the findings that were obtained in the yeast model system are directly transferable to humans and are currently the focus of additional studies.

In the area of platelets, we are currently in the process of identifying as many network components as possible in order to understand the regulation of these cells. Disorders can lead to too rapid clotting of platelets, which causes thromboses, the main cause of heart attack and stroke. If this reaction occurs too slowly, life-threatening blood losses can occur. Thus, platelets represent a very finely balanced system, which we would like to understand better in the future. With the latest technology and sophisticated analytical methods, we are in search of the molecular switches that can cause an imbalance in the platelets and can cause disease. If these can be recognized, the path is clear for developing new therapeutic approaches. One of the next goals is the successive modeling of networks that ultimately lead to "e-Platelet," the virtual platelet, in order to better understand these cells.