

Der Rat für die Verleihung des Otto Naegeli-Preises  
hat am 25. November 2009 beschlossen,  
den Otto Naegeli-Preis  
zur Förderung der medizinischen Forschung 2010

PROF. DR.  
RUEDI AEBERSOLD

zu verleihen.  
Dieser Beschluss wurde aufgrund folgender  
Laudatio gefasst:

## PROF. RUEDI AEBERSOLD

has made outstanding contributions to the development of analytical methods for the identification of proteins and to the promotion of systems biology as a new multidisciplinary approach in biology. As a postdoctoral fellow at the California Institute of Technology, he improved methods to determine the sequence of proteins from small samples. Recognizing the sensitivity of mass spectrometry to identify proteins from complex cellular mixtures, he developed new techniques such as the Isotope-Coded Affinity Tag (ICAT) method that permits the comparison of the concentration of specific proteins in different samples. The technique of Selected Reaction Monitoring (SRM), the most recent development, allows, for the first time, the targeted identification of proteins. With this technique, proteomics has moved from the random sampling of peptides in a mixture to the directed identification of proteins and their concentration like it is the case for mRNAs in transcriptomics. The selectivity and high sensitivity of this method offers new opportunities for the identification of diagnostic markers for diseases and to use proteomics as a standard method in the early diagnosis of diseases such as cancer and metabolic diseases. His outstanding contributions to the field of proteomics over the past 25 years have resulted in more than 39'000 citations of his scientific articles and have been recognized by numerous international awards.

As a co-founder of the Institute of Systems Biology in Seattle, the first of its kind worldwide, he has been one of the advocates of a new approach to biology that goes beyond the classical single gene approach. Biological information is encoded not only in individual genes but also in the resulting dynamic protein networks in the cell. Decoding this information requires new quantitative methods derived from physics, mathematics and Computer science, thus necessitating a novel multidisciplinary approach to these problems. After his return to Switzerland, he was instrumental in establishing this new approach in biology and medicine by initiating the national initiative in systems biology, SystemsX.ch and the foundation of the new Institute of Molecular Systems Biology at the ETH Zurich.

ZÜRICH, 29. April 2010

DER PRÄSIDENT DES PREISRATES: