

Dragnet Investigation of Proteins

German physicist Matthias Mann to receive the Körber European Science Prize 2012

The physicist and bioinformatician Matthias Mann set himself the goal of cracking the code of the »proteome«. Amongst other things, he hopes that this will lead to new insights in the fight against diabetes and cancer.

The Körber Prize 2012, endowed with 750,000 euros, goes to Matthias Mann. The interdisciplinary scientist is to receive the award for his ground-breaking work on the proteome, the entirety of all the proteins of a living organism. The Körber Prize honours scientists working on particularly innovative research projects. An international Trustee Committee chaired by Professor Peter Gruss, President of the Max Planck Society, selects the prizewinner.

The 52-year-old »protein detective«, as his staff call him, studied mathematics and physics in Göttingen and subsequently at Yale University in the Department of Chemical Engineering. As a Ph.D. student in Yale he concentrated on protein research and developed the electrospray technique with his Ph.D. supervisor John Fenn. This makes it possible to charge proteins electrically, transfer them into the atmosphere and measure them using mass spectrometry methods. Fenn received the Nobel Prize in Chemistry in 2002 for this development.

Mass spectrometers were used in the past mainly by physicists and chemists. The electrospray technique now also allows the use of this high-precision measuring technique in the world of biology. In 2005, while working as a staff member at the Max Planck Institute of Biochemistry in Martinsried, of which he has been the director since 2007, Mann further refined the technique: »We have developed the best technology. Hundreds of research teams worldwide now work with it.«

The sequencing of the proteome complements and expands on the already completed »Human Genome Project« with which the human genome was sequenced. The genome is the entirety of all the hereditary factors (genes) and the proteome the entirety of all proteins. While the genes (DNA) slumber passively in the cell nuclei and usually remain unchanged

Kehrwieder 12
 20457 Hamburg
 Telefon +49 · 40 · 80 81 92 - 181
 Telefax +49 · 40 · 80 81 92 - 303
 E-Mail wissenschaft@koerber-stiftung.de
www.koerberforum.de

Further information:
 Matthias Mayer M.A.

The **KörberForum – Kehrwieder 12** is the location of the Körber Foundation in Hamburg's HafenCity district. Its programme focuses on results and impetus' from the foundations activities in the fields of International Affairs, Education, Science, Civil Society and Young Culture. It offers citizens who are not content with merely upholding the status quo the opportunity to participate actively, and provides them with ideas for their own initiatives.

throughout their existence, the proteins, which are created from DNA by the cell machinery, change constantly. The proteome therefore provides only a kind of »snapshot«. Yet it is precisely this which opens up completely new perspectives for research scientists. A comparison of the proteome of healthy and diseased cells, for example, reveals which proteins benefit or hinder the emergence of diseases such as cancer.

What is remarkable about the mass spectrometry technique developed by Matthias Mann is that all the proteins in a cell can be analysed at once, while researchers traditionally concern themselves only with the effects of one or a few proteins. A human cell contains up to well in excess of 100,000 different proteins, but only 20,000 genes that encode for them. In fact, up to 100 different proteins can originate from a single gene sequence: partly due to the fact that the cell machinery divides the copied DNA sequences as required and combines them to form new amino acid chains; on the other hand, the proteins are given modifications such as »on and off switches«. The sequencing of the proteome is therefore far more difficult than that of the genome, and research is still in its infancy.

In 2010, Mann and his team were the first to successfully sequence the complete proteome of a living organism – a yeast cell, which contains more than 4,000 proteins at once. In the meantime, researchers all over the world are working frantically on analysing the complete human proteome. The »Human Proteome Project« promises a race as exciting as the »Human Genome Project« at the turn of the millennium.

Matthias Mann has already received numerous prestigious awards, including the Leibniz Prize at the beginning of 2012. The 28th presentation of the Körber European Science Prize will take place on 7 September 2012 in the Great Ceremonial Hall of Hamburg's City Hall.

You will find photos of the prizewinner at www.koerber-preis.de.

Hamburg, 13.06.2012