

## **How To Uncover the Secrets of Disease-Relevant Proteins**

Cancer researchers have developed a guide for piecing together the jigsaw puzzle of genome research

To elucidate cellular mechanisms that lead to diseases such as cancer is a big challenge of biomedicine. Scientists of the Division of Molecular Genome Analysis headed by Professor Annemarie Poustka, German Cancer Research Center (DKFZ), have tackled this complex task and developed a unique guide which enables researchers to identify the function of proteins swiftly and efficiently. In a recently published article in the journal *Genome Research*<sup>\*</sup>, Dr. Stefan Wiemann and his colleagues have presented this "Functional Pipeline". In this pipeline, the scientists have compiled a host of data from genome research and show examples of how genes and their proteins work in cellular systems. This comprehensive collection of numerous data leads to concrete information such as whether a protein is involved in the cell cycle and, thus, may also be associated with cancer. The project was funded by the Research Ministry (BMBF) within the framework of the National Genome Research Network.

Deciphering the human genome was only the beginning. Researchers are now faced with the task of identifying the existing genes and their RNA copies which serve as blueprints for producing proteins. In a next step they need to find out where these proteins work and analyze their actions and interactions with other cellular components. Understanding these complex biological processes will eventually make it possible to distinguish healthy from sick organisms. Therefore, these findings are a prerequisite for developing novel diagnostic and prognostic approaches and new treatments.

Stefan Wiemann and his colleagues are using methods of bioinformatics and genomic databases to compile and evaluate research results and to link these with a variety of data obtained by high-throughput methods. In combination with results from experimental research, such as about the localization of proteins within the cell or activation patterns of genes, so-called expression profiles, this yields a comprehensive collection of currently available information. By providing this knowledge in a public Internet platform at [www.dkfz.de/LIFEdb](http://www.dkfz.de/LIFEdb), Wiemann and his colleagues have made a major contribution to our understanding of biological processes in the post genome sequencing era.

<sup>\*</sup>"From ORFeome to Biology: A Functional Genomics Pipeline", Stefan Wiemann et. al., *Genome Research*, October 2004; 14(10B):2136-44.

The task of the Deutsches Krebsforschungszentrum in Heidelberg (German Cancer Research Center, DKFZ) is to systematically investigate the mechanisms of cancer development and to identify cancer risk factors. The results of this basic research are expected to lead to new approaches in the prevention, diagnosis and treatment of cancer. The Center is financed to 90 percent by the Federal Ministry of Education and Research and to 10 percent by the State of Baden-Wuerttemberg. It is a member of the Helmholtz Association of National Research Centers (Helmholtz-Gemeinschaft Deutscher Forschungszentren e.V.).

This press release is available at [www.dkfz.de/pressemitteilungen](http://www.dkfz.de/pressemitteilungen)

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