

## Media Release

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Swiss Institute of Bioinformatics celebrates 10<sup>th</sup> birthday by presenting major gifts to human health

### Highlights

#### **The Swiss Institute of Bioinformatics (SIB): “A Swiss success story”**

Ten years old. The SIB is a Swiss success story at the frontier of biology and computer science. It brings together 300 scientists, organised into 25 working groups, one of which has just made a major scientific breakthrough in the field of human proteins.

The SIB is backed by some of the best universities and research centres in Switzerland and the world. Funded by the Swiss government as well as international agencies, the EU, UK and US. The SIB's resources such as its Web server ExPASy are accessed more than one million times a day by life science researchers worldwide.

#### **SIB announces first mapping of all human proteins**

The Swiss Institute of Bioinformatics has produced a groundbreaking encyclopaedic knowledge that captures all that is known about the functions and interaction of the full set of human proteins.

Proteins are the physical expression of our genetic code. They are the essence of life itself, providing the basic building blocks of all cells. In short, proteins are minute “machines” that transport material, run chemical reactions and recognize other vital molecules within our body. Studying them is not only crucial to understanding how life functions, but to fighting genetic-based diseases as well. The results are available free to the world over the Web.

#### **SIB inaugurates annual award to recognise talented young scientists**

The first winner is Zoltán Kutalik, 29, a Hungarian national who has been working with the SIB at the University of Lausanne for two years. The award is for the “Ping Pong” code, published earlier in the journal *Nature Biotechnology* (May 2008), which allows scientists to check human cell lines for their sensitivity to thousands of drugs.

#### **Major breakthrough in biological science – first protein encyclopaedia**

Speaking at the 10<sup>th</sup> anniversary conference of the Swiss Institute of Bioinformatics in Berne, Switzerland, its director Professor Ron Appel described his institute as a “Swiss success story”. He said that he was proud that as pioneers at the heart of science one of the SIB's 25 working groups was today able to announce the completion of the annotation of human proteins.

Professor Amos Bairoch, head of the SIB's Swiss-Prot group said: “If human DNA is the script of life, proteins are its actors, its living embodiment.”

He added that the human genome-sequencing project produced a dictionary. This new encyclopaedia takes one major step further by looking at life as it is really organised in our body at the molecular level. The results will speed up the scientific work which aims to improve our quality of life. Particularly when it comes to understanding what life is, and how we can combat genetic-based diseases.

While proteins are the essence of life, when they become defective they can cause much suffering and often early death. Man's knowledge of proteins such as insulin and haemoglobins is crucial to combating diseases such as cancer, Alzheimer's, cystic fibrosis and haemophilia.

Professor Bairoch said, "The general public would understand some of the entries in our protein encyclopaedia. Insulin, for instance, is a small protein that controls glucose levels in our blood. The performance-booster EPO is the protein used illegally by some cyclists. In the human body it takes many forms. But we detect its use in sport because competitors use a manufactured form which is not natural."

The new protein encyclopaedia, which will evolve further as our knowledge is refined, now informs a major part of the work of thousands of health researchers around the world. The data covers 20,325 human proteins. The information could ultimately be used for developing exact treatments for individual patients based on an understanding of their specific protein set.

The breakthrough can be seen as one of the 21<sup>st</sup> century's major life science outcomes. It can help improve our chances of defeating a variety of diseases, by enabling researchers to model the interaction between individual patients, diseases and drugs.

Progress on the Human Protein Initiative (HPI) project has been rapid. Ten years ago, we had good data on less than 1000 proteins. Two years ago, we had good entries for 15,000, now the collection is complete. But one of the remaining challenges, though, is still to complete the same encyclopaedia of proteins for other animals.

Professor Bairoch said, "More than 45,000 scientific papers were read. We examined databases that were out there to get a picture of the knowledge which existed. We had to go out and find the material."

This new protein encyclopaedia is published online and available for free to users. In printed form, it would correspond to 57 volumes of about 1,000 pages each.

### **New Award for drug code breakthrough**

The Swiss Institute of Bioinformatics also inaugurated the annual SIB Young Bioinformatician Award during the Institute's 10th anniversary celebrations in Berne, Switzerland.

The winner of the 2008 SIB Young Bioinformatician Award was Zoltán Kutalik, 29, a Hungarian national who has been working with the SIB in the Computational Biology Group of Prof. Sven Bergmann at the University of Lausanne for two years. Dr Kutalik and colleagues at the University of Lausanne devised a computational tool which may eventually allow scientists to predict the sensitivity of different patients to a range of drugs.

"We call it the Ping-Pong algorithm", said Dr Kutalik. "It pulls out relevant information on gene expression and drug sensitivity. Based on 60 cell-lines the algorithm reveals hidden links between our genes and thousands of drugs. These genetic links help us to predict how other cell lines – other tissue – will react to the drugs."

Having a powerful predictive tool to explore these relationships opens new perspectives for the creation and use of medicines.

"So far, we can't validate this work in real patients. But our results can be checked against databases of results from work with hundreds of thousands of tests with mostly real tissues in Petri dishes rather than actual patients."

Out of 15 excellent applications for the Award, the jury, composed of SIB group leaders, chose this work entitled "A modular approach for integrative analysis of large-scale gene-expression and drug-response data," published in May 2008 in the prestigious journal "Nature Biotechnology."

As a "bioinformatician" Dr Kutalik describes himself as mathematician who became something of a

statistician and then a computer programmer. “I would say I have about the biological knowledge of an undergraduate, but of course I have learned quite a lot about some parts of biology.”

The 2008 SIB Young Bioinformatician Award, funded by the Swiss National Science Foundation (NSF) was presented during a gala dinner celebrating the 10th anniversary of the SIB, in Berne.

### **SIB director praise donors, scientists and working groups**

The Swiss Institute of Bioinformatics director Professor Ron Appel closed the press conference praising the collaboration between five universities and two institutes of technology across the length and breadth of Switzerland.

He said: “Their collective success shows what can be achieved when experts pool their knowledge and vision.

“The SIB is a pioneering institute. More successes can be expected in future. These will add to what is already an impressive track record in all the fields of bio-informatics technology research we work in.”

He also emphasised that without the support of the Swiss government and international partners, none of this would be possible, “so we owe a big thanks to them”, he added.

In addition, Professor Bairoch thanked the Swiss government, international funding agencies and all the scientists who contributed to their recent breakthrough. He said, “ours is just one of the 25 SIB groups working at the frontiers of scientific knowledge for the benefit of mankind”.

### **About the SIB**

The Swiss Institute of Bioinformatics is an academic not-for-profit foundation federating bioinformatics activities throughout Switzerland. Its mission is to provide essential services and support to the national and international life science community, through databases, software, Web servers and core facilities, as well as teaching and research activities in the field of bioinformatics. It has a long-standing tradition of producing state-of-the-art software for the life science research community, as well as carefully annotated databases including UniProtKB/Swiss-Prot, the world’s most widely used source of information about proteins. The SIB includes world-class research and service groups in the fields of proteomics, transcriptomics, genomics, systems biology, structural bioinformatics, evolutionary bioinformatics, modelling, imaging, biophysics, and population genetics in Geneva, Lausanne, Berne, Basel and Zurich. The SIB expertise is widely appreciated and its services are used worldwide by researchers in life sciences.

For more information about the SIB, please visit: <http://www.isb-sib.ch/>

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