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## NEWSLETTER

### For the scientific public:

The immune system has to fulfill the difficult task of discriminating pathogens (e.g. bacteria or viruses and cancerous cells) from cells of the own body. Foreign cells should be attacked and eliminated, whereas self-tissues should not be harmed. The main cell type involved in this decision is the T-cell. T-cell activation is a complex process relying on multiple layers of tightly controlled signaling molecules, which form an intricate and dynamic intracellular network. Defects in this network can cause inadequate immune responses and severe disorders such as type 1 diabetes or multiple sclerosis. In order to understand and predict the behaviour of this network it is therefore crucial to study it as a complete system and not only its isolated parts. Therefore, the European Union is funding the SYBILLA “Systems Biology of T-cell activation in health and disease” project for 5 years with 11.1 mio Euro in FP7. Dr. Wolfgang Schamel from the Max-Planck-Institute for Immunobiology in Freiburg, Germany, is the coordinator of this large collaborative project.

SYBILLA is a consortium of 17 scientific and industrial partners (14 are from Europe and 3 from the US and India). Through a multidisciplinary effort it aims to understand at systems level, how T-cells discriminate foreign- from self-peptides by activating quantitatively distinct signaling pathways. Data obtained in mouse models are extended to human T cells and to a mouse model of multiple sclerosis. SYBILLA develops new analytical and mathematical tools to generate and integrate high-density quantitative data describing T-cell activation. Proteomics, transcriptomics, imaging and biochemical techniques will be applied to obtain holistic maps of the T-cell signaling network and to achieve a quantitative and dynamic understanding of signaling networks and their regulation in response to different signal inputs. Building upon already existing schemes of the network connectivity, constant iteration between experiment and mathematical modelling will be used to develop robust and predictive models that describe the functioning of the T-cell signaling network. SYBILLA will allow the identification of new drug targets and the discovery of new biomarkers to refine prognosis of autoimmune diseases.

More information can be found at [www.SYBILLA-t-cell.de](http://www.SYBILLA-t-cell.de)