

# THE HUMAN PROTEIN ATLAS

## **New Pathology Atlas maps the genes involved in cancer to accelerate progress in personalized cancer medicine**

**Stockholm August 17, 2017**

*A new Pathology Atlas is launched today with an analysis of all human genes in all major cancers showing the consequence of their corresponding protein levels for overall patient survival. The difference in expression patterns of individual cancers observed in the study strongly reinforces the need for personalized cancer treatment based on precision medicine. In addition, the systems level approach used to construct the Pathology Atlas demonstrates the power of “big data” to change how medical research is performed.*

The dream of personalized treatment for cancer patients takes a major step forward today with the launch by Swedish researchers of the Human Pathology Atlas. Published in *Science*<sup>1</sup>, the Atlas is based on the analysis of 17 main cancer types using data from 8,000 patients. In addition, a new concept for showing patient survival data is introduced, called Interactive Survival Scatter plots, and the atlas includes more than 400,000 such plots. A national supercomputer center was used to analyze more than 2.5 petabytes of underlying publicly available data from the Cancer Genome Atlas (TCGA) to generate more than 900,000 survival plots describing the consequence of RNA and protein levels on clinical survival. The Pathology Atlas also contains 5 million pathology-based images generated by the Human Protein Atlas consortium.

Professor Mathias Uhlen, Director of the Human Protein Atlas consortium and leader of the Pathology Atlas effort says: “This study differs from earlier cancer investigations, since it is not focused on the mutations in cancers, but the downstream effects of such mutations across all protein-coding genes. We show, for the first time, the influence of the gene expression levels demonstrating the power of “big data” to change how medical research is performed. It also shows the advantage of open access policies in science in which researchers share data with each other to allow integration of huge amounts of data from different sources.”

The Research Article in *Science*<sup>1</sup> reports several important findings related to cancer biology and treatment. Firstly, a large fraction of genes is differentially expressed in cancers - and in many cases - have an impact on overall patient survival. The research also showed that gene expression patterns of individual tumors varied considerably, and could exceed the variation observed between different cancer types. Shorter patient survival was generally associated with up-regulation of genes involved in mitosis and cell growth, and down-regulation of genes involved in cellular differentiation. The data allowed the researchers to generate personalized genome-scale metabolic models for cancer patients to identify key genes involved in tumor growth.

The work depends heavily on the supercomputing power available to the Human Protein Atlas consortium through the Science for Life Laboratory (SciLifeLab). According to Dr Adil Mardinoglu, SciLifeLab Fellow and leader of the systems biology effort in the project: "We are now in possession of incredibly powerful systems biology tools for medical research, allowing, for the first time, genome-wide analysis of individual patients with regards to the consequence of their expression profiles for clinical survival."

The Pathology Atlas team also looked to demonstrate the utility of the new tool in two particular cancers. "For lung and colorectal cancer, a selection of prognostic genes identified in the Atlas were also analyzed in independent, prospective cancer cohorts using immunohistochemistry to validate the gene expression patterns at the protein level," says Fredrik Ponten, Professor in Pathology of Uppsala University. "We are pleased to provide a stand-alone open-access resource for cancer researchers worldwide, which we hope will help accelerate their efforts to find the biomarkers needed to develop personalized cancer treatments."

The Pathology Atlas is available via an interactive open-access database ([www.proteinatlas.org/pathology](http://www.proteinatlas.org/pathology)).

### **Reference list**

<sup>1</sup> Uhlen et al "A Pathology Atlas of human cancer transcriptomes" *Science* (August 17, 2017) accessed on-line at:  
<http://dx.doi.org/10.1126/science.aan2507>

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## **About**

### **Human Protein Atlas**

The Human Protein Atlas (HPA) is a Swedish-based program started in 2003 with the aim to map of all the human proteins in cells, tissues and organs using integration of various omics technologies, including antibody-based imaging, mass spectrometry-based proteomics, transcriptomics and systems biology. All the data in the knowledge resource is open access to allow scientists both in academia and industry to freely access the data for exploration of the human proteome. The version 17 (launched August 17, 2017) consists of three separate parts, each focusing on a particular aspect of the genome-wide analysis of the human proteins; the Tissue Atlas showing the distribution of the proteins across all major tissues and organs in the human body, the Cell Atlas showing the subcellular localization of proteins in single cells, and finally the new Pathology Atlas showing the impact of protein levels for survival of patients with cancer. The Human Protein Atlas program has already contributed to several thousands of publications in the field of human biology and disease and it was recently (July 25, 2017) selected by the organization ELIXIR ([www.elixir-europe.org](http://www.elixir-europe.org)) as a European core resource due to its fundamental importance for a wider life science community. The HPA consortium is funded by the Knut and Alice Wallenberg Foundation. For more information, see: [www.proteinatlas.org](http://www.proteinatlas.org).

### **The Cancer Genome Atlas**

The Cancer Genome Atlas (TCGA) is a collaboration between the National Cancer Institute (NCI) and National Human Genome Research Institute (NHGRI). The program has generated comprehensive, multi-dimensional maps of the key genomic changes in large number of cancers. The TCGA dataset consists of 2.5 petabytes of data describing tumor tissue and matched normal tissues from more than 11,000 patients. The data is publically available and has contributed to more than a thousand studies of cancer by independent researchers. For more information, see: <https://cancergenome.nih.gov>.

### **Science for Life Laboratory**

Science for Life Laboratory (SciLifeLab) is a national center for molecular biosciences in Sweden with state-of-the-art infrastructures for life science with focus on health and environmental research. Technical platforms within the center include genomics, proteomics, metabolomics, bioimaging, structural biology, bioinformatics, systems biology and drug development. There are approximately 1200 persons affiliated with the center divided between two nodes in Stockholm and Uppsala. The center is a collaboration between four universities: Karolinska Institute, KTH Royal Institute of Technology, Stockholm University and Uppsala University. For more information, see: [www.scilifelab.se](http://www.scilifelab.se).

### **Knut and Alice Wallenberg Foundation**

The Knut and Alice Wallenberg Foundation is the largest private financier of research in Sweden and also one of Europe's largest. The Foundation's aim is to benefit Sweden by supporting basic research and education, mainly in medicine, technology, and the natural sciences. The Foundation can also initiate grants to strategic projects and scholarship programs. For more information, see: <https://kaw.wallenberg.org/en>.