New version of the Human Protein Atlas

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Today, the 15th version of the Human Protein Atlas is launched. The new version includes data from different sources, which makes comparisons between tissue profiles on both the RNA and protein level possible.

Looking closely at healthy and sick conditions in the human tissues or cells makes it possible to learn more and thereby improve healthcare. To do this comparisons the researchers first need to know how the human body is built. One way is to analyze the transcriptome. This means looking into which genes are activated to create a protein in the tissue or cell sample.

The human biology is constructed in three steps; from DNA to RNA and then to protein. The DNA code needs to be copied to the RNA, and then read to make a protein. To detect and count protein molecules is very complicated and the scientists need different methods to make sure the data is valid. One way is to analyze the transcriptome to count the amount of RNA molecules being copied from the DNA of a certain gene, creating a picture of what proteins to expect from the sample. Counting RNA molecules is easier than counting protein molecules.

The Human Protein Atlas includes proteome analysis based on more than 25 000 antibodies targeting more than 17 000 unique proteins, combined with transcriptome analysis covering all 20 000 human protein coding genes. The new atlas launched on April 11 also includes primary data from several sources, which allows for comparisons.
– The new version of the Human Protein Atlas is significantly advancing

in terms of mapping the transcriptome in different human tissues. These data have been the basis for much of the metabolic modelling we are doing here at Chalmers. I am therefore very excited about the progress, and the Human Protein Atlas will certainly be an important resources in our aims to advance towards better diagnostics and precision medicine, says Professor Jens Nielsen at the Department of Biology and Biological Engineering.

The launch is accompanied by an article in *Molecular Systems Biology* describing transcriptome resources with a focus on the comparison between the datasets generated from the Broad Institute, Boston, US (GTEx) and the Human Protein Atlas. The GTEx dataset includes more than 1600 samples from mostly overlapping, but in some cases unique, tissues compared to the Human Protein Atlas. RNA-seq data from 28 of the GTEx tissues with a corresponding tissue in Human Protein Atlas have been included to allow for direct comparisons between the Human Protein Atlas and GTEx data sets.
– The inclusion of the GTEx dataset to the Human Protein Atlas database makes it even more comprehensive and it is reassuring that there is a significant overlap in the tissue classification of the genes based on the two independent datasets, says Professor Mathias Uhlén, program director for the Human Protein Atlas project.

The article published in *Molecular Systems Biology* discusses publicly available human transcriptome resources and the possible use of these databases for various applications, such as building genome-scale metabolic models used for analyzing cell and tissue functions both in health an disease contexts.

More information: M. Uhlen et al. Transcriptomics resources of human tissues and organs, *Molecular Systems Biology* (2016). DOI: 10.15252/msb.20155865

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