

THE HUMAN PROTEIN ATLAS

New version of the human proteins atlas with extensive transcriptomics data

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Today, the Human Protein Atlas consortium launched version 15 of the database including extensive transcriptomics data and a new display view to allow comparisons of human tissue profiles on both the RNA and protein level. The launch is accompanied with 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 consortium at Science for Life Laboratory, Sweden.

The Human Protein Atlas, a major multinational research project supported by the Knut and Alice Wallenberg Foundation, 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. In the new version it is now possible to do comparisons of primary data from several sources, including external efforts.

The GTEx dataset includes more than 1600 postmortem samples from mostly overlapping, but in some cases unique, tissues compared to the Human Protein Atlas consortium. 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 Uhlen, 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 and in disease contexts.

Read the article in Molecular Systems Biology:

<http://msb.embopress.org/content/msb/12/4/862.full.pdf>

About the Human Protein Atlas project

The Human Protein Atlas project, funded by the Knut and Alice Wallenberg Foundation, has been set up to allow for a systematic exploration of the human proteome using antibody-based proteomics. This is accomplished by combining high-throughput generation of affinity-purified antibodies with protein profiling in a multitude of tissues and cells assembled in tissue microarrays. Confocal microscopy analysis using human cell lines is performed for more detailed protein localization. The program hosts the Human Protein Atlas portal with expression profiles of human genes and proteins in a multitude of tissues and cells. The main sites are located at AlbaNova and SciLifeLab, KTH - Royal Institute of Technology, Stockholm, Sweden, and the Rudbeck Laboratory, Uppsala University, Uppsala, Sweden. For more information on the Human Protein Atlas, visit our website at www.proteinatlas.org

