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Human protein atlas enabled neuroproteomic profiling of body fluids

The Human Protein Atlas currently contains more than 24,000 validated antibodies targeting 17000 proteins corresponding to approximately 83% of the encoded human proteins. The publicly available portal contains several million high-resolution images generated by immunohistochemistry on tissue microarrays and confocal microscopy for subcellular localization. The antibodies are antigen-purified and the long-term objective is to generate paired antibodies towards all human protein targets. A systematic biomarker discovery approach has been implemented utilizing array-based platforms and the massive antigen and antibody production pipeline as well as whole proteome ultra-high-density peptide microarrays. Proteomic profiling of serum, plasma and CSF in multi-disease cohorts are performed with large number of peptides and antigens on planar microarrays for the analysis of autoimmunity repertoires with subsequent verifications with on suspension bead arrays. Furthermore, large set of samples are also profiled with massive numbers of antibodies to generate protein profiles from labeled samples for biomarker discovery. The results from both autoimmunity and antibody-based neuroproteomic profiling utilizing both platforms will be presented within the context of multiple sclerosis, ALS, Alzheimer's disease, Parkinson's disease, Narcolepsy as well as various psychiatric disorders.

Biography

Peter Nilsson is a professor in proteomics at the SciLifeLab Stockholm, KTH-Royal Institute of Technology. Since 2002, he has been heading the Protein Microarray Technology group within the Human Protein Atlas project. He is the executive platform director of affinity proteomics at SciLifeLab and the site director of the Human Protein Atlas at SciLifeLab Stockholm. He is also the Vice Dean of the School of Biotechnology at KTH. The main research focus is within development and utilization of various protein microarray technologies for peptide, antigen and antibody based proteomic profiling and biomarker discovery.

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