A HUMAN PROTEIN ATLAS FOR NORMAL AND CANCER TISSUES

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Antibody-based proteomics provides a powerful approach for the functional study of the human proteome involving the systematic generation of protein-specific affinity reagents. We have used this strategy to construct a comprehensive, antibody-based protein atlas for expression and localization profiles in 48 normal human tissues and 20 different cancers (1). The Human Protein Atlas is publicly available (www.proteinatlas.org) and contains, at present, approximately 1,2 million high-resolution images corresponding to more than 1500 antibodies towards human proteins. Each image has been annotated by certified pathologists to provide a knowledge base for functional studies and to allow queries about protein profiles in normal and disease tissues (2, 3). We have recently (4) used the antibody reagents for validation of potential biomarkers to Mantle Cell Lymphoma (MCL) as well as high-throughput biomarker analysis of thousands of serum samples using a reverse array format (5) and multiplex assays (6). Our results suggest it should be possible to extend this analysis to the majority of all human proteins thus providing a valuable tool for medical and biological research, in particular for biomarker analysis in various patient cohorts.

References:
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