

Looking for needles in haystacks. Application of proteomic techniques in the study of diseases

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The human genome contains more than 20,000 protein-coding genes. The number of different proteins encoded from this relatively small number of genes is probably approaching one million through transcriptional, translational and posttranslational processes. Proteomics deals with the qualitative and quantitative analyses of these proteins, although the techniques available at present are much less suited for such large-scale analyses than genomic and transcriptomic methods. Generally, a variety of techniques need to be combined in order to reach a reasonable depth of the proteome. Our current effort is directed towards the study of pathogenic changes in a number of diseases by performing proteomic analyses on tissues from patients as well as from laboratory animals. The long-term goal is to stratify patients with different risk profiles, to identify protein disease biomarkers as well as to discover molecular treatment targets. Our focus is on cancers, especially lymphomas and cardiovascular diseases as well as eye diseases. Examples from these studies will be presented.