Abstract: Proteomics is a relatively new vocabulary word to most scientists, although its precise meaning remains unclear. To most scientists, proteomics is the corollary of 'genomics' as applied to proteins instead of genes, and implies the study of the changes in protein expression in a cell or system relative to some control, i.e., 'quantitative proteomics'. However, this definition is much too limiting and a larger more expansive definition of proteomics needs to be put forward. Such as definition should encompass other aspects of protein chemistry as applied to the study of large assemblies of proteins. In this talks, I will present data from our laboratory on several on-going proteomic-based studies whose goals range from the determination of the total set of proteins associated with human heart mitochondria (i.e., defining the 'mitochondrial proteome') to a novel method for high throughput determination of a protein's three-dimensional structure ('ms3d').