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PL01: OPENING PLENARY SESSION

Population Proteomics: Embracing Genomic Variability

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Abstract:
The presentation will discuss the development of highly reproducible and high throughput proteomics techniques to do comparative analyses on a large number of samples. It will also discuss the use for these techniques to quantify the proteome of populations of cell, or animals with defined genomes to determine how genotypic variation is translated into the proteome and how proteome variation affects phenotypes. Examples from yeast strains, flies and medically relevant examples from mouse strain collections will be presented.