A TRANSOMICS PLATFORM FOR DISCOVERY RESEARCH





A Common Platform for Metabolite & Protein Profiling in Unbiased Discovery

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Complementary metabolomic and proteomic studies can provide a three dimensional view of biological processes at the molecular level. Endogenous metabolite profiling and bottom-up protein profiling are conventionally performed with highly specific analytical systems.

We describe a novel discovery platform enabling a common workflow for bottom-up protein profiling or endogenous metabolite/lipid profiling in unbiased discovery research. This unique strategy is based on Ultra Performance Liquid Chromatography (UPLC), High Definition Mass Spectrometry (HDMS) and a coherent bioinformatics environment. Data Independent UPLC/HDMS acquisition provides unprecedented duty cycle, peak capacity and dynamic range to profile either metabolites/lipids or proteins in complex biological extracts. Progenisis QI, a novel bioinformatics software, developed in collaboration with Nonlinear Dynamics (Newcastle, UK), provides statistically powerful co-detection and intuitive data visualization for large studies and a common workflow for integrative TransOmics analysis. The utility of this platform will be demonstrated with a study of drug-mitigated obesity.