Title: **LOI3-RT-02-C Proteomic Assessment of NCS Plasma Quality and Plasma Protein Normals in Pregnancy to 1 year of age**

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Introduction: In the field of proteomics children are orphans. For example, a major multinational effort, the Human Proteome Organization (HUPO) has undertaken to identify the circulating plasma proteins in only normal-adults. Therefore we lack the fundamental data to establish what's normal in the developing child. Therefore it is nearly impossible to identify disease biomarkers in children when normative data does not exist. This lack of data hinders both population based research and clinical drug development in children.

Methods and Results: Our optimized approach detailed schematically in Figure 1 requires only 250 uL of plasma. Briefly, with this pipeline, tandem LC/MS/MS spectra of the tryptic peptides are obtained with a LTQ Orbitrap Hybrid LC/Mass Spectrometer and the proteins identified using the Xtandem! protein database search engine and the Uniprot human protein database. At least a two peptide coverage is required for confident protein identification. Using this combination of methods allows us to routinely identify 1,500-2,500 even low abundant cellular and secreted proteins/plasma sample.

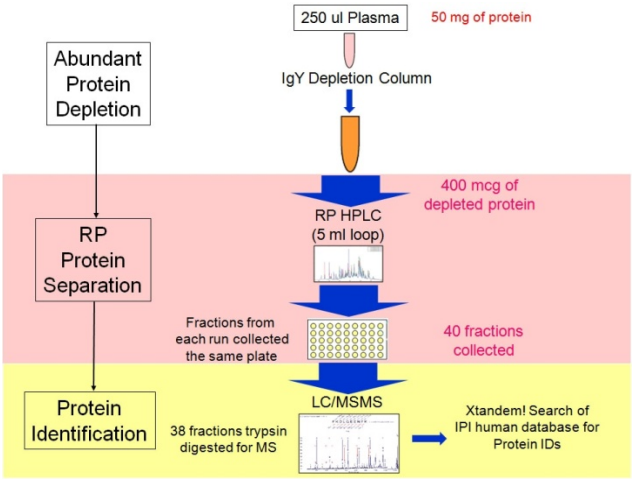

Figure 1. Proteomic Pipeline Workflow

Conclusion: As no data exists on the normal circulating proteome during pregnancy and in children, we will use the structure of the NCS to define the normal circulating proteome ultimately from conception to adult using non-biased mass spectroscopy based proteomics. These data will inform the NCS on sample quality for proteomic studies and other more focused analytics, establish normal values, and provide data to further focus NCS protocol development on potential prenatal influences on fetal and child development and fetal patterning of adult disease.

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