

Development of Quantitative MRM Assays for the Measurement of 3,000 Proteins across 20 Mouse Tissues



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Project Overview



- Develop MRM assays for 3,000 mouse proteins in 20 tissues
- Establish strain and tissue-specific protein concentrations
- Enable proteomic phenotyping of mouse models







- 1-2 proteotypic surrogate peptides per protein
- Synthesize ¹³C/¹⁵N-labelled and unlabeled peptide standards





- precursor charge
- best product ion
- collision energy









Assay development follows the CPTAC (Clinical Proteomic Tumor Analysis Consortium) guidelines

1) Response curve in tissue sample

2) Assay variability





Intra-day variability for LQAVEVVITHLAPGTK





- Assays developed for >1800 unique proteins in 11 tissues to date
- Protein measured in multiple tissues based expression

Plasma	730	Liver	554
Red Blood Cells	260	Eye	138
Lung	501	Heart	386
Spleen	265	Testes	259
Brain	609	Skin	141
Kidney	302	TOTAL UNIQUE	1803







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Establishing Normal Tissue Protein Concentrations

- Samples from 3 mouse strains, C57BL/6N, NOD SCID, BALB/c
- n=6 females and n=6 males



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Alpha-1B-glycoprotein

Knockout Strain Analysis Pilot Study #1 Example Knockout Profile: C8a



- C57BL/6NCrl_F - C57BL/6NCrl_M - C8a_tm1b_F01_F - C8a_tm1b_F01_M



 All 3 chains of the C8 heterotrimer, C8α, C8β, and C8γ, are decreased in knockout mice vs control mice.

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Project Team

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