



# UAB CCC Mass Spectrometry & Proteomics (MSP) Shared Facility

Director: James A. Mobley, Ph.D., Web-site: <http://www.uab.edu/proteomics/bmsf>



## 1. Organization & Goal

The UAB CCC Mass Spectrometry/Proteomics Shared Facility (MSP-SF) offers access to capabilities that are not available in individual laboratories.

- The facility is organized into five modules
- (1) Administrative & Laboratory Management
  - (2) Experimental Design, Sample Preparation & Separations
  - (3) Discovery Proteomic Analysis
  - (4) Statistics, Bioinformatics, & Reporting
  - (5) Manuscripts, Grants, & Education.

Each module is supported by highly trained scientists who are experts in mass spectrometry, bioanalytical chemistry, statistics, systems biology, and information handling.

The goal of the MSP Shared Facility is to provide state-of-the-art capabilities in mass spectrometry, proteomics, and bioanalytical technologies to support the research needs of UAB internal and external researchers.

## 2. Facility Overview

- Research Team:**
  - James Mobley, Ph.D. (Facility Director)
  - Brandon Young, B.S. (Lab Manager)
  - Kyoko Kojima, Ph.D. (Operations Director, Applications Scientist)
  - Willis Hampton (IT Support and Programming)

- Instrumentation:**
  - Two Thermo Orbitrap Velos PROs with nanoLC-ESI/ CID/ PQD



- Bruker Ultraflex III MALDI ToF ToF with LC-MALDI-Spotter
  - Thermo Finnigan LTQ XL with nanoLC-ESI/CID/ ETD
  - Thermo Finnigan LTQ XL with LC-HESI/CID
  - GE Ettan™ Spot Picker
  - Beckman Optima MAX-XP Ultracentrifuge

- Computing**
  - Primary fileserver (44TB, 64GB RAM, AMD EPYC 7401P 24Core processor)
  - Unix application server powered by an Oracle Database (64GB RAM, 2- AMD 2.6GHz 12 Core processors)
  - Primary domain controller for our network (2GB RAM, 1-Intel 2.0GHZ Dual Core processor)
  - Secondary fileserver (30TB, 32GB RAM, 2-AMD 3.1GHz 8 Core processors)
  - Application server (64GB RAM, AMD EPYC 7401P 24Core processor 2.0GHZ, 44TB between 1.7 TB high speed SSD and 6 TB HDD in RAID 5 Array)
  - Backup Server (6Core Xeon Processor 1.9 GHz 8GB RAM 105TB Storage)
  - Virtual backup domain controller

- Software/ Licenses:**
  - SEQUEST & MASCOT (Search Engines)
  - Nonlinear SameSpots (2D-PAGE analysis)
  - ProteomeSoftware Scaffold PTM Q+/S (All-In-One Proteomic Analysis Tool)
  - Mascot Distiller Q+ (Quantitative & De Novo Sequencing Proteomic Analysis Tool)
  - Clarivate Analytics Metacore (Systems Biology & Pathway Analysis)

This Facility is supported by the UAB Office of VP of Research and UAB O'Neal Comprehensive Cancer Center.

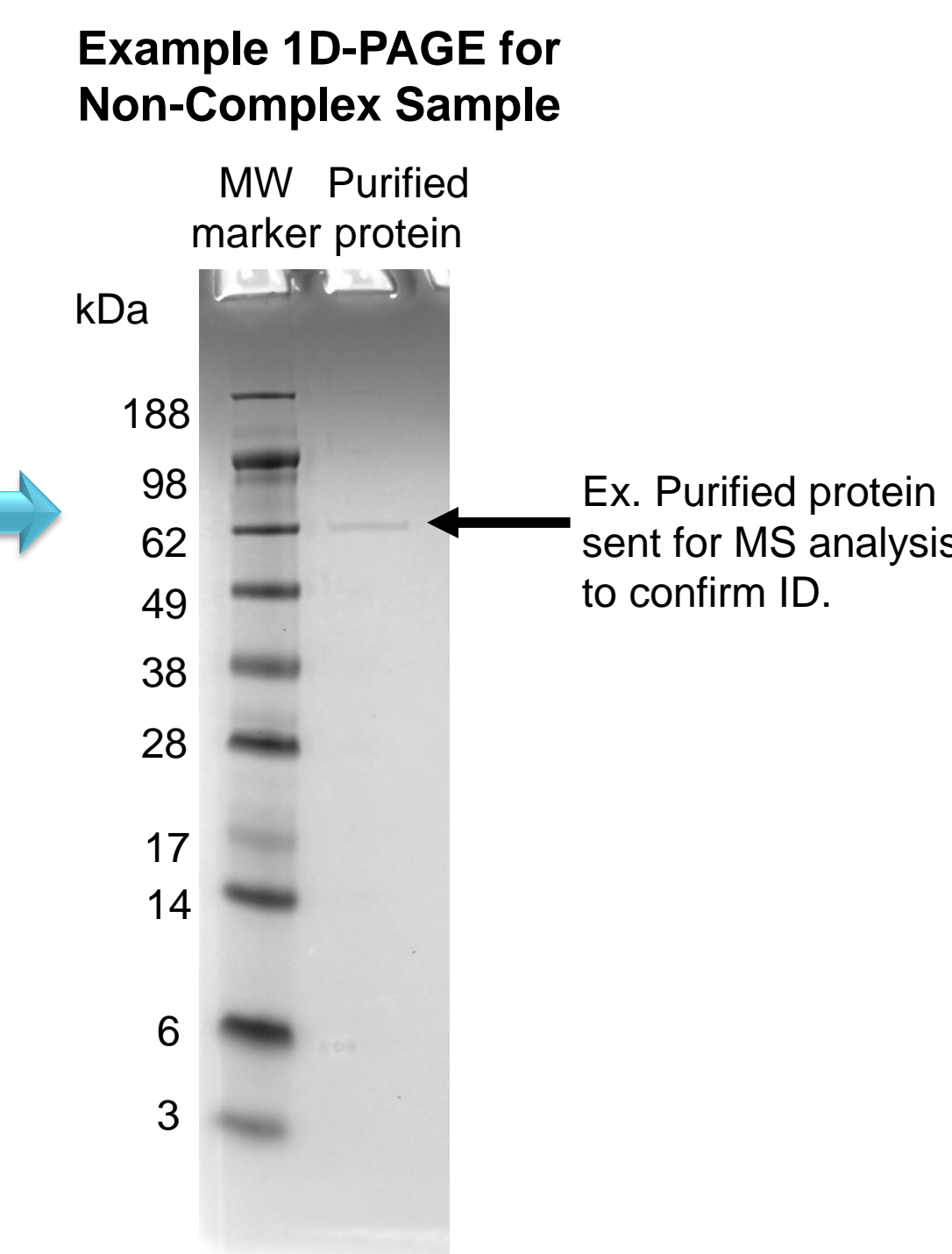
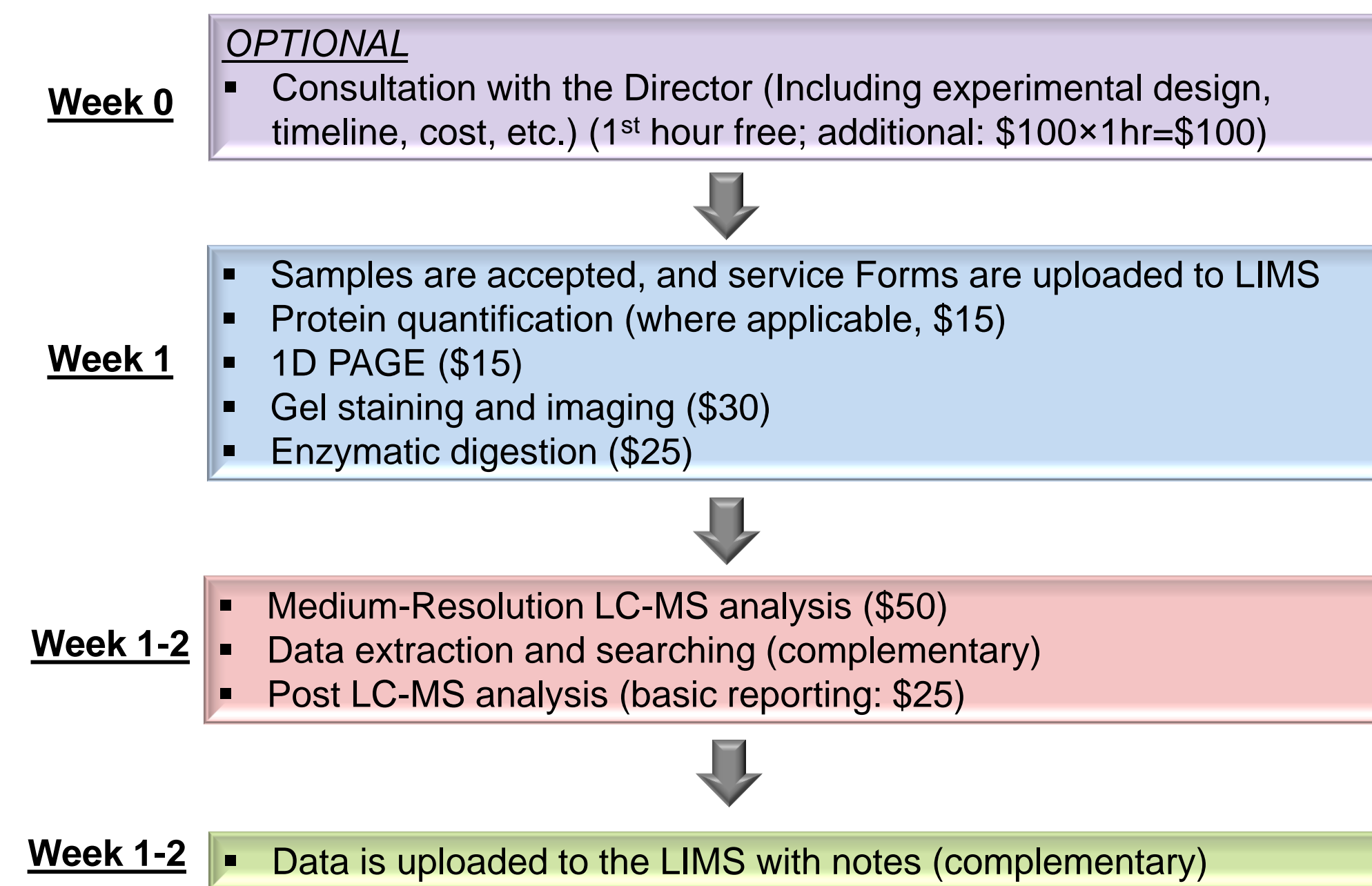
UAB CCC Mass Spectrometry/Proteomics Shared Facility

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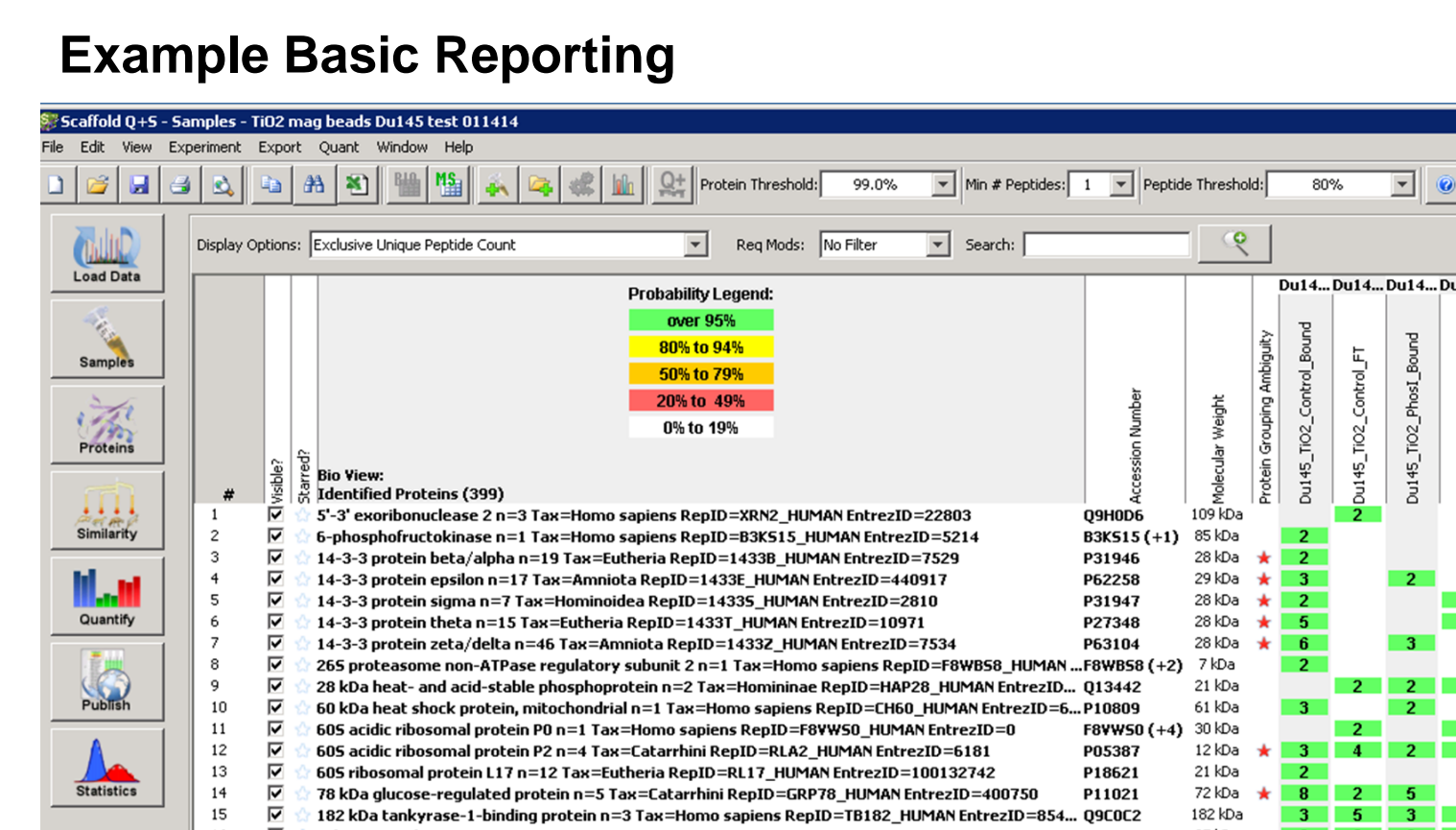
## 3. Workflow and Pricing for Non-Complex Samples

(ex: purified protein, overexpressed/ enriched, etc.)

Example: non-complex sample (one sample)



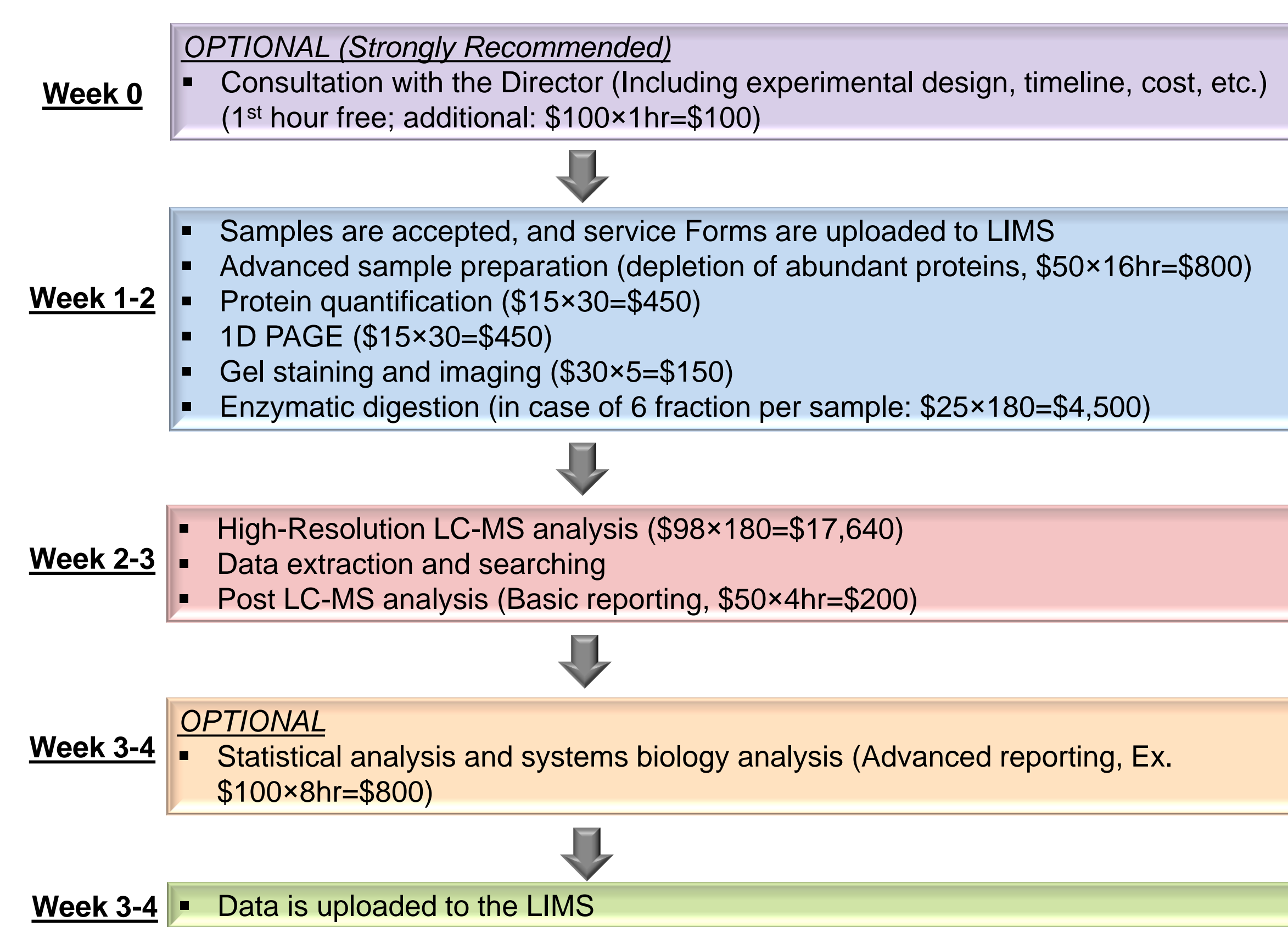
Total Price: \$160 (bulk discounted for more than 5-10 samples to ~\$100/ sample)



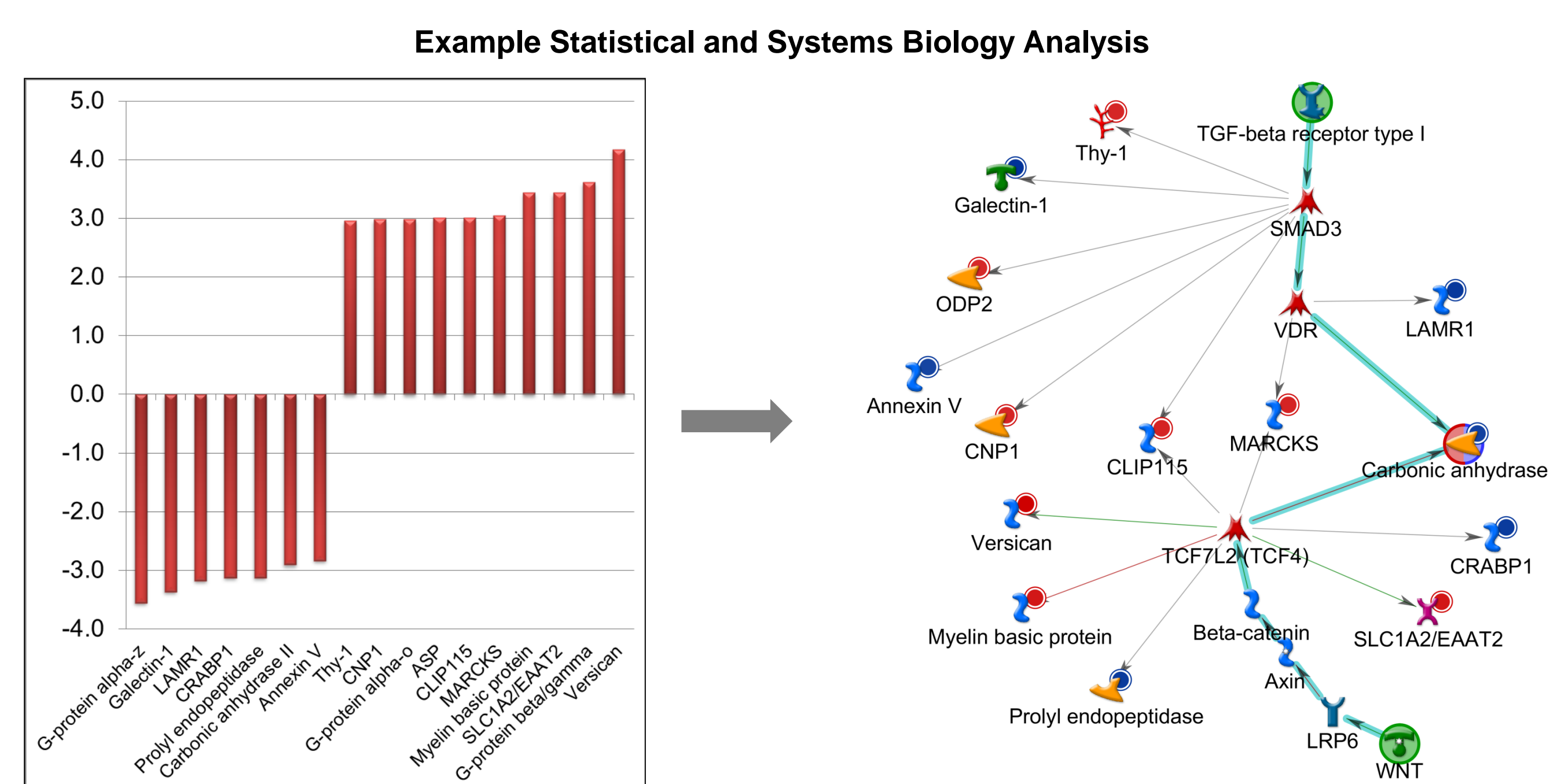
## 4. Workflow and Pricing for Label-Free Biomarker Studies

(ex: animal models & clinical specimens such as serum, urine, tissues)

Example: 30 serum samples



Total Price: \$25,090 (Optional items included)

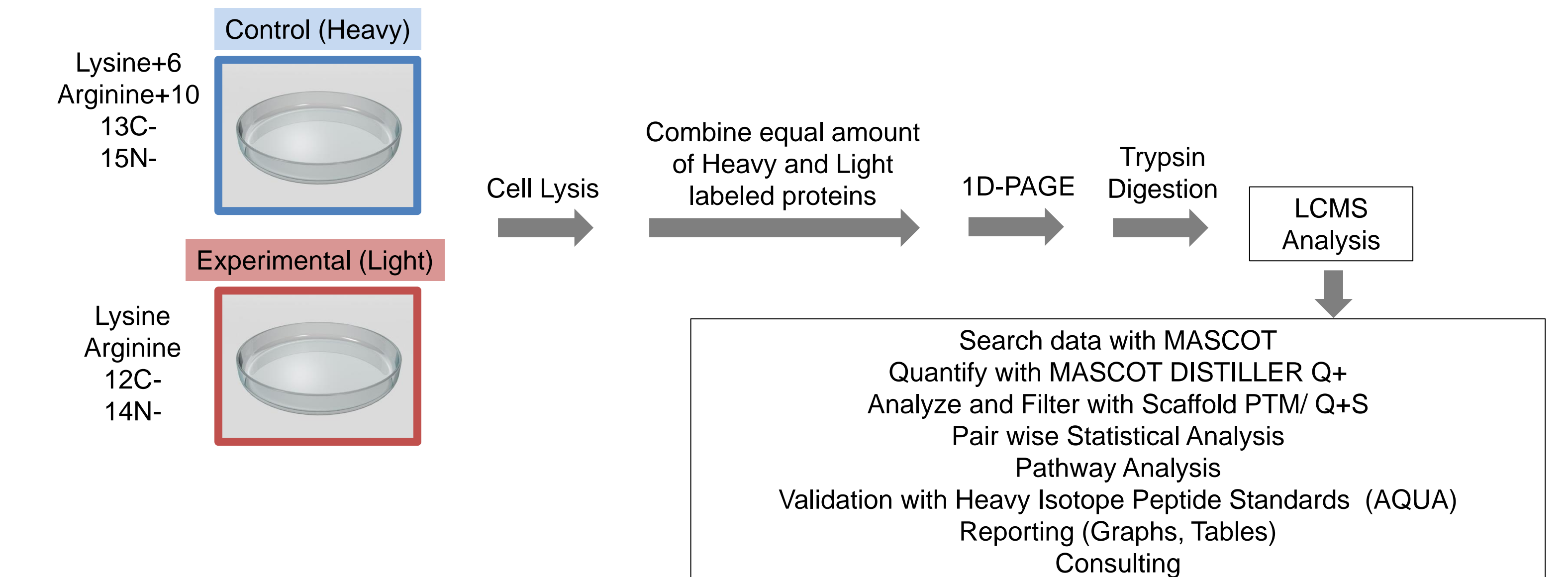


## 5. Labeled - Quantitative Proteomics Studies

Including SILAC, SILAM, AQUA, etc. (pricing varies based on application)

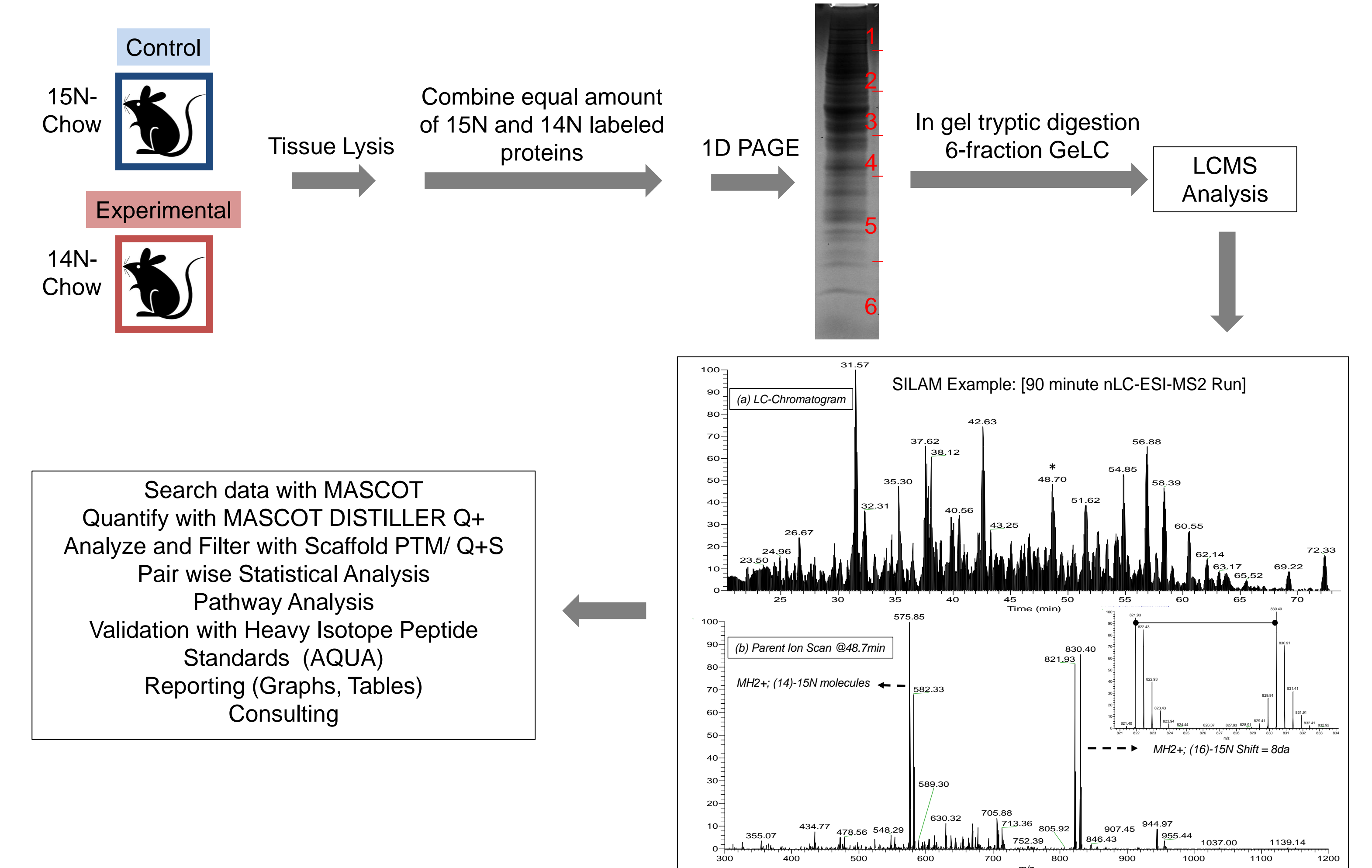
Example: Stable Isotope Labeling with Amino Acid in Cell Culture (SILAC)

- Control cells are cultured in heavy stable isotope 15N, 13C lysine (K+6) and heavy stable isotope 15N, 13C arginine (R+10) supplemented media, without any treatment. Experimental cells are cultured in standard lysine (K) and arginine (R) supplemented media, with the treatment of interest.
- Cells are lysed, protein is quantified, the control and treated protein lysates are combined, and digested in-gel with trypsin.



Example: Stable Isotope Labeling with Amino Acids in Mammals (SILAM)

- Tissues obtained from 15N-labeled control and N14-labeled experimental animals are analyzed. Following lysis of tissue, equal amount of protein from experimental mice are mixed with 15N-labeled standard control lysate and analyzed by 1D-PAGE. Each gel lane are excised in 6 MW fractions and digested with trypsin, and each fraction is analyzed via LCMS.



## 6. Recent Selected Publications

(we support grant submission and publications)

- Martinez, E.; Cosnahan, R. K.; Wu, M.; Gadila, S. K.; Quick, E. B.; **Mobley, J. A.**; Campos-Gomez, J., Oxylipins mediate cell-to-cell communication in *Pseudomonas aeruginosa*. *Commun Biol* **2019**, *2*, 66.
- Eustace, N. J.; Anderson, J. C.; Langford, C. P.; Trummell, H. Q.; Hicks, P. H.; Jarboe, J. S.; Bonner, J. A.; Willey, C. D., Myristoylated alanine-rich C-kinase substrate effector domain phosphorylation regulates the growth and radiation sensitization of glioblastoma. *Int J Oncol* **2019**, *54* (6), 2039-2053.
- Chanda, D.; Otupalova, E.; Hough, K. P.; Locy, M. L.; Bernard, K.; Deshane, J. S.; Sanderson, R. D.; **Mobley, J. A.**; Thannickal, V. J., Fibronectin on the Surface of Extracellular Vesicles Mediates Fibroblast Invasion. *Am J Respir Cell Mol Biol* **2019**, *60* (3), 279-288.
- Carnes, R. M.; **Mobley, J. A.**; Crossman, D. K.; Liu, H.; Korf, B. R.; Kesterson, R. A.; Wallis, D., Multi-Omics Profiling for NF1 Target Discovery in Neurofibromin (NF1) Deficient Cells. *Proteomics* **2019**, *19* (11), e1800334.
- Chou, C. F.; Hsieh, Y. H.; Grubbs, C. J.; Atigadda, V. R.; **Mobley, J. A.**; Dummer, R.; Muccio, D. D.; Eto, I.; Elmets, C. A.; Garvey, W. T.; Chang, P. L., The retinoid X receptor agonist, 9-cis UAB30, inhibits cutaneous T-cell lymphoma proliferation through the SKP2-p27kip1 axis. *J Dermatol Sci* **2018**, *90* (3), 343-356.
- Bandari, S. K.; Purushothaman, A.; Ramani, V. C.; Brinkley, G. J.; Chandrashekar, D. S.; Varambally, S.; **Mobley, J. A.**; Zhang, Y.; Brown, E. E.; Vlodavsky, I.; Sanderson, R. D., Chemotherapy induces secretion of exosomes loaded with heparanase that degrades extracellular matrix and impacts tumor and host cell behavior. *Matrix Biol* **2018**, *65*, 104-118.