

GMS-BI-793 Final paper instructions, Spring, 2013

The final paper is due May 10, 2013

Select a primary paper from the list below. If you have a paper that you wish to use that is not on the list, please send it to one of the instructors. If the instructor approves, you may use that as your primary paper.

Claim this paper by emailing Joe Zaia (jzaia@bu.edu). Each student must select a different primary paper.

Choose two other related papers from the recent literature.

Write a paper using the following format:

Written commentary. Describe each of the three papers, pointing out the major features of the research, important novel results and provide criticism of any flaws you see in either the methods or the conclusions.

Proposed research project. Describe a project that would extend the observations made in these three papers. Include the following:

- i. Rationale for the proposed work
- ii. Proposed experiments
- iii. Expected results and significance
- iv. Description of possible pitfalls/difficulties that may be encountered and alternative strategies.

The project should be one that a graduate student could accomplish in about one year.

Total paper length should be 10-12 pages, double-spaced. It should be delivered to 670 Albany St, 5th floor (CEC, CL, MM or JZ) on or before May 9, 2012.

Include copies of the three papers chosen for discussion.

Reminder: You must write the entire paper in your own words. To copy any text from any source and use it in your paper without making proper bibliographic reference is plagiarism.

<http://en.wikipedia.org/wiki/Plagiarism>

List of primary papers:

[1-62]

1. Cooks, R.G., et al., *Ambient Mass Spectrometry*. Science, 2006. **311**(5767): p. 1566-1570.
2. Jackson, S.N., et al., *MALDI-ion mobility-TOFMS imaging of lipids in rat brain tissue*. J Mass Spectrom, 2007. **42**(8): p. 1093-8.
3. Kaji, H., et al., *Proteomics Reveals N-Linked Glycoprotein Diversity in Caenorhabditis elegans and Suggests an Atypical Translocation Mechanism for Integral Membrane Proteins*. Mol Cell Proteomics, 2007. **6**(12): p. 2100-2109.
4. Mueller, L.N., et al., *SuperHirn - a novel tool for high resolution LC-MS-based peptide/protein profiling*. Proteomics, 2007. **7**(19): p. 3470-80.
5. Puchades, M., et al., *Proteomic investigation of glioblastoma cell lines treated with wild-type p53 and cytotoxic chemotherapy demonstrates an association between galectin-1 and p53 expression*. J Proteome Res, 2007. **6**(2): p. 869-75.
6. Renfrow, M.B., et al., *Analysis of O-glycan heterogeneity in IgA1 myeloma proteins by Fourier transform ion cyclotron resonance mass spectrometry: implications for IgA nephropathy*. Anal Bioanal Chem, 2007. **389**(5): p. 1397-407.
7. Yamada, K., et al., *Rapid and sensitive analysis of mucin-type glycans using an in-line flow glycan-releasing apparatus*. Anal Biochem, 2007. **371**(1): p. 52-61.
8. Burnum, K.E., et al., *Imaging Mass Spectrometry Reveals Unique Protein Profiles During Embryo Implantation*. Endocrinology, 2008.
9. Ceroni, A., et al., *GlycoWorkbench: A Tool for the Computer-Assisted Annotation of Mass Spectra of Glycans*. J Proteome Res, 2008.
10. Distler, U., et al., *Matching IR-MALDI-o-TOF mass spectrometry with the TLC overlay binding assay and its clinical application for tracing tumor-associated glycosphingolipids in hepatocellular and pancreatic cancer*. Anal Chem, 2008. **80**(6): p. 1835-46.
11. Isailovic, D., et al., *Profiling of Human Serum Glycans Associated with Liver Cancer and Cirrhosis by IMS-MS*. J Proteome Res, 2008. **7**(3): p. 1109-17.
12. Joenvaara, S., et al., *N-glycoproteomics - an automated workflow approach*. Glycobiology, 2008. **18**(4): p. 339-49.
13. Jones, S.P., et al., *Cardioprotection by N-acetylglucosamine linkage to cellular proteins*. Circulation, 2008. **117**(9): p. 1172-82.
14. Kang, P., Y. Mechref, and M.V. Novotny, *High-throughput solid-phase permethylation of glycans prior to mass spectrometry*. Rapid Commun Mass Spectrom, 2008. **22**(5): p. 721-34.
15. Kruger, M., et al., *Dissection of the insulin signaling pathway via quantitative phosphoproteomics*. Proc Natl Acad Sci U S A, 2008. **105**(7): p. 2451-6.
16. Kweon, H.K. and K. Hakansson, *Metal Oxide-Based Enrichment Combined with Gas-Phase Ion-Electron Reactions for Improved Mass Spectrometric Characterization of Protein Phosphorylation*. J Proteome Res, 2008.
17. Liu, Z. and K.L. Schey, *Fragmentation of multiply-charged intact protein ions using MALDI TOF-TOF mass spectrometry*. J Am Soc Mass Spectrom, 2008. **19**(2): p. 231-8.
18. Oberg, A.L., et al., *Statistical Analysis of Relative Labeled Mass Spectrometry Data from Complex Samples Using ANOVA*. J Proteome Res, 2008. **7**(1): p. 225-233.

19. Ressom, H.W., et al., *Analysis of MALDI-TOF mass spectrometry data for discovery of peptide and glycan biomarkers of hepatocellular carcinoma*. J Proteome Res, 2008. 7(2): p. 603-10.
20. Rinner, O., et al., *Identification of cross-linked peptides from large sequence databases*. Nat Methods, 2008. 5(4): p. 315-8.
21. Alkass, K., et al., *Age estimation in forensic sciences: Application of combined aspartic acid racemization and radiocarbon analysis*. Mol Cell Proteomics, 2009: p. M900525-MCP200.
22. Guan, S. and A.L. Burlingame, *Data processing algorithms for analysis of high resolution MSMS spectra of peptides with complex patterns of posttranslational modifications*. Mol Cell Proteomics, 2009: p. M900431-MCP200.
23. Knezevic, A., et al., *Variability, heritability and environmental determinants of human plasma N-glycome*. J Proteome Res, 2009. 8(2): p. 694-701.
24. Pflieger, D., et al., *Analysis of human C1q by combined bottom-up and top-down mass spectrometry: Detailed mapping of post-translational modifications and insights into the C1r/C1s binding sites*. Mol Cell Proteomics, 2009: p. M900350-MCP200.
25. Schenauer, M.R., et al., *Heparan Sulfate Separation, Sequencing, and Isomeric Differentiation: Ion Mobility Spectrometry Reveals Specific Iduronic and Glucuronic Acid-Containing Hexasaccharides*. Anal Chem, 2009. 81(24): p. 10179-10185.
26. Wang, Z., et al., *Enrichment and site-mapping of O-Linked N-Acetylglucosamine by a combination of chemical/enzymatic tagging, photochemical cleavage, and electron transfer dissociation (ETD) mass spectrometry*. Mol Cell Proteomics, 2009.
27. Zhang, Y., et al., *A robust error model for iTRAQ quantification reveals divergent signaling between oncogenic FLT3 mutants in acute myeloid leukemia*. Mol Cell Proteomics, 2009: p. M900452-MCP200.
28. Ambatipudi, K.S., et al., *Human common salivary protein 1 (CSP-1) promotes binding of Streptococcus mutans to experimental salivary pellicle and glucans formed on hydroxyapatite surface*. Journal of Proteome Research, 2010. 9(12): p. 6605-14.
29. Balog, C.I.A., et al., *Mass spectrometric identification of aberrantly glycosylated human apolipoprotein C-III peptides in urine from Schistosoma mansoni-infected individuals*. Mol Cell Proteomics, 2010: p. M900537-MCP200.
30. Castellana, N.E., et al., *Template proteogenomics: sequencing whole proteins using an imperfect database*. Mol Cell Proteomics, 2010: p. M900504-MCP200.
31. Helbig, A.O., et al., *Profiling of N-acetylated protein termini provides in-depth insights into the N-terminal nature of the proteome*. Mol Cell Proteomics, 2010: p. M900463-MCP200.
32. Houde, D., et al., *Post-translational modifications differentially affect IgG1 conformation and receptor binding*. Mol Cell Proteomics, 2010: p. M900540-MCP200.
33. Jami, M.-S., et al., *Proteome analysis of the penicillin producer Penicillium chrysogenum: Characterization of protein changes during the industrial strain improvement*. Mol Cell Proteomics, 2010: p. M900327-MCP200.

34. Jung, H.R., et al., *Quantitative mass spectrometry of histone H3.2 and H3.3 in Suz12 deficient mouse ES cells reveals distinct, dynamic post-translational modifications at K27 and K36*. Mol Cell Proteomics, 2010: p. M900489-MCP200.
35. Lee, A., et al., *Liver membrane proteome glycosylation changes in mice bearing an extra-hepatic tumour*. Mol Cell Proteomics, 2010: p. M900538-MCP200.
36. Lee, J.E., et al., *Endogenous peptide discovery of the rat circadian clock: a focused study of the suprachiasmatic nucleus by ultrahigh performance tandem mass spectrometry*. Mol Cell Proteomics, 2010. **9**(2): p. 285-97.
37. Ong, E.S., et al., *Metabolic profiling in colorectal cancer reveals signature metabolic shifts during tumorigenesis*. Mol Cell Proteomics, 2010: p. M900551-MCP200.
38. Park, J.E., et al., *Hypoxia modulates tumor microenvironment to enhance angiogenic and metastatic potential by secretion of proteins and exosomes*. Mol Cell Proteomics, 2010: p. M900381-MCP200.
39. Ryan, C.M., et al., *Post-translational modifications of integral membrane proteins resolved by top-down Fourier-transform mass spectrometry with collisionally activated dissociation*. Mol Cell Proteomics, 2010: p. M900516-MCP200.
40. Schroder, C., et al., *Dual-color proteomic profiling of complex samples with a microarray of 810 cancer-related antibodies*. Mol Cell Proteomics, 2010: p. M900419-MCP200.
41. Stengel, F., et al., *Quaternary dynamics and plasticity underlie small heat shock protein chaperone function*. Proc Natl Acad Sci U S A, 2010. **107**(5): p. 2007-12.
42. Vellaichamy, A., et al., *Size-Sorting Combined with Improved Nanocapillary Liquid Chromatography-Mass Spectrometry for Identification of Intact Proteins up to 80 kDa*. Anal Chem, 2010. **82**(4): p. 1234-44.
43. Wada, Y., et al., *Comparison of Methods for Profiling O-glycosylation: HUPO Human Disease Glycomics/Proteome Initiative Multi-Institutional Study of IgA1*. Mol Cell Proteomics, 2010: p. M900450-MCP200.
44. Wenger, C.D., et al., *Sub-part-per-million precursor and product mass accuracy for high-throughput proteomics on an ETD-enabled orbitrap mass spectrometer*. Mol Cell Proteomics, 2010: p. M900541-MCP200.
45. Zhang, H., et al., *Simultaneous characterization of glyco- and phospho-proteomes of mouse brain membrane proteome with electrostatic repulsion hydrophilic interaction chromatography (ERLIC)*. Mol Cell Proteomics, 2010: p. M900314-MCP200.
46. Zhang, X., et al., *Endogenous DOPA and dopaquinone modifications on protein tyrosine: Links to mitochondrially-derived oxidative stress via hydroxyl radical*. Mol Cell Proteomics, 2010: p. M900321-MCP200.
47. Bonner, M.K., et al., *Mitotic spindle proteomics in Chinese hamster ovary cells*. PLoS ONE, 2011. **6**(5): p. e20489.
48. Cox, J. and M. Mann, *Quantitative, high-resolution proteomics for data-driven systems biology*. Annual Review of Biochemistry, 2011. **80**: p. 273-99.

49. de Saldanha da Gama Fischer, J., et al., *Chemo-resistant protein expression pattern of glioblastoma cells (A172) to perillyl alcohol*. Journal of Proteome Research, 2011. **10**(1): p. 153-60.
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51. Fonslow, B.R., et al., *Improvements in proteomic metrics of low abundance proteins through proteome equalization using ProteoMiner prior to MudPIT*. Journal of Proteome Research, 2011. **10**(8): p. 3690-700.
52. Geiger, T., et al., *Use of stable isotope labeling by amino acids in cell culture as a spike-in standard in quantitative proteomics*. Nature protocols, 2011. **6**(2): p. 147-57.
53. Michalski, A., J. Cox, and M. Mann, *More than 100,000 detectable peptide species elute in single shotgun proteomics runs but the majority is inaccessible to data-dependent LC-MS/MS*. Journal of Proteome Research, 2011. **10**(4): p. 1785-93.
54. Michalski, A., et al., *Mass spectrometry-based proteomics using Q Exactive, a high-performance benchtop quadrupole Orbitrap mass spectrometer*. Molecular & cellular proteomics : MCP, 2011. **10**(9): p. M111 011015.
55. Rhee, E.P., et al., *Lipid profiling identifies a triacylglycerol signature of insulin resistance and improves diabetes prediction in humans*. The Journal of clinical investigation, 2011. **121**(4): p. 1402-11.
56. Sartain, M.J., et al., *Lipidomic analyses of Mycobacterium tuberculosis based on accurate mass measurements and the novel "Mtb LipidDB"*. Journal of lipid research, 2011. **52**(5): p. 861-72.
57. Gillet, L.C., et al., *Targeted data extraction of the MS/MS spectra generated by data independent acquisition: a new concept for consistent and accurate proteome analysis*. Molecular & cellular proteomics : MCP, 2012.
58. Lasker, K., et al., *Molecular architecture of the 26S proteasome holocomplex determined by an integrative approach*. Proceedings of the National Academy of Sciences of the United States of America, 2012. **109**(5): p. 1380-7.
59. Malmstrom, L., et al., *Automated workflow for large-scale selected reaction monitoring experiments*. Journal of Proteome Research, 2012. **11**(3): p. 1644-53.
60. Sabido, E., et al., *Targeted proteomics of the eicosanoid biosynthetic pathway completes an integrated genomics-proteomics-metabolomics picture of cellular metabolism*. Molecular & cellular proteomics : MCP, 2012.
61. Zanivan, S., M. Krueger, and M. Mann, *In vivo quantitative proteomics: the SILAC mouse*. Methods in molecular biology, 2012. **757**: p. 435-50.
62. Zhang, J.I., et al., *Direct analysis of steviol glycosides from Stevia leaves by ambient ionization mass spectrometry performed on whole leaves*. The Analyst, 2012. **137**(13): p. 3091-8.