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**Gen 875**  
**Fall 2006 Reading List**

### **11/7 Intro to Proteomics & Course Set up**

#### **Systems Biology User Guide:**

Kersey P, Apweiler R. Linking publication, gene and protein data. *Nat Cell Biol.* 2006 Oct 22

#### **SMART: <http://smart.embl-heidelberg.de/>**

Schultz J, Milpetz F, Bork P, Ponting CP. SMART, a simple modular architecture research tool: identification of signaling domains. *Proc Natl Acad Sci U S A.* 1998 May 26;95(11):5857-64.

#### **PFAM: <http://www.sanger.ac.uk/Software/Pfam/>**

Sonnhammer EL, Eddy SR, Durbin R. Pfam: a comprehensive database of protein domain families based on seed alignments. *Proteins.* 1997 Jul;28(3):405-20.

#### **Review Predicting Protein Function:**

Watson JD, Laskowski RA, Thornton JM. Predicting protein function from sequence and structural data. *Curr Opin Struct Biol.* 2005 Jun;15(3):275-84. Review.

### **11/9 Discussion: Functional Genomics I & Chemical Genetics:**

1. Gonczy P, Echeverri C, Oegema K, Coulson A, Jones SJ, Copley RR, Duperon J, Oegema J, Brehm M, Cassin E, Hannak E, Kirkham M, Pichler S, Flohrs K, Goessen A, Leidel S, Alleaume AM, Martin C, Ozlu N, Bork P, Hyman AA. Functional genomic analysis of cell division in *C. elegans* using RNAi of genes on chromosome III. *Nature.* 2000 Nov 16;408(6810):331-6.
2. Eggert US, Kiger AA, Richter C, Perlman ZE, Perrimon N, Mitchison TJ, Field CM. Parallel chemical genetic and genome-wide RNAi screens identify cytokinesis inhibitors and targets. *PLoS Biol.* 2004 Dec;2(12):e379. Epub 2004 Oct 5.
3. Sonnichsen B, Koski LB, Walsh A, Marschall P, Neumann B, Brehm M, Alleaume AM, Artelt J, Bettencourt P, Cassin E, Hewitson M, Holz C, Khan M, Lazik S, Martin C, Nitzsche B, Ruer M, Stamford J, Winzi M, Heinkel R, Roder M, Finell J, Hantsch H, Jones SJ, Jones M, Piano F, Gunsalus KC, Oegema K, Gonczy P, Coulson A, Hyman AA, Echeverri CJ. Full-genome RNAi profiling of early embryogenesis in *Caenorhabditis elegans*. *Nature.* 2005 Mar 24;434(7032):462-9.

#### **Reviews:**

Sugimoto A. High-throughput RNAi in *Caenorhabditis elegans*: genome-wide screens and functional genomics. *Differentiation.* 2004 Mar;72(2-3):81-91. Review.

Bargmann CI. High-throughput reverse genetics: RNAi screens in *Caenorhabditis elegans*. *Genome Biol.* 2001;2(2):REVIEWS1005. Epub 2001 Jan 31. Review.

### **11/14 Discussion: Functional Genomics II: Global Analysis of Protein Localization**

1. Huh WK, Falvo JV, Gerke LC, Carroll AS, Howson RW, Weissman JS, O'Shea EK. Global analysis of protein localization in budding yeast. *Nature.* 2003 Oct 16;425(6959):686-91.

#### **\*Supporting paper:**

Matsuyama A, Arai R, Yashiroda Y, Shirai A, Kamata A, Sekido S, Kobayashi Y, Hashimoto A, Hamamoto M, Hiraoka Y, Horinouchi S, Yoshida M. ORFeome cloning and global analysis of protein localization in the fission yeast *Schizosaccharomyces pombe*. *Nat Biotechnol.* 2006 Jul;24(7):841-7. Epub 2006 Jun 25.

2. Morin X, Daneman R, Zavortink M, Chia W. A protein trap strategy to detect GFP-tagged proteins expressed from their endogenous loci in *Drosophila*. *Proc Natl Acad Sci U S A.* 2001 Dec 18;98(26):15050-5. Epub 2001 Dec 11.

#### **Review:**

Phizicky E, Bastiaens PI, Zhu H, Snyder M, Fields S. Protein analysis on a proteomic scale. *Nature.* 2003 Mar 13;422(6928):208-15. Review

**11/16 Discussion: Mass Spec I: 2D gel analysis & MuDPIT****2D Gel Analysis:**

1. Oh J, Pyo JH, Jo EH, Hwang SI, Kang SC, Jung JH, Park EK, Kim SY, Choi JY, Lim J. Establishment of a near-standard two-dimensional human urine proteomic map. *Proteomics*. 2004 Nov;4(11):3485-97.

**2D Gels Review:**

Van den Bergh G, Arckens L.

Recent advances in 2D electrophoresis: an array of possibilities. *Expert Rev Proteomics*. 2005 Apr;2(2):243-52. Review.

**MuDPIT analysis:**

2. Ru QC, Katenhusen RA, Zhu LA, Silberman J, Yang S, Orchard TJ, Brzeski H, Liebman M, Ellsworth DL. Proteomic profiling of human urine using multi-dimensional protein identification technology. *J Chromatogr A*. 2006 Apr 14;1111(2):166-74. Epub 2005 Jul 25.

**MuDPIT Review:**

\*Lin D, Tabb DL, Yates JR 3rd.

Large-scale protein identification using mass spectrometry. *Biochim Biophys Acta*. 2003 Mar 21;1646(1-2):1-10. Review.

**REVIEW of Topic:** Aebersold R, Mann M.

Mass spectrometry-based proteomics. *Nature*. 2003 Mar 13;422(6928):198-207. Review.

**11/21 Discussion: Quantitative Proteomics-ICAT**

1. Marelli M, Smith JJ, Jung S, Yi E, Nesvizhskii AI, Christmas RH, Saleem RA, Tam YY, Fagarasanu A, Goodlett DR, Aebersold R, Rachubinski RA, Aitchison JD. Quantitative mass spectrometry reveals a role for the GTPase Rho1p in actin organization on the peroxisome membrane. *J Cell Biol*. 2004 Dec 20;167(6):1099-112. Epub 2004 Dec 13.

**ICAT BACKGROUND:**

Gygi SP, Rist B, Gerber SA, Turecek F, Gelb MH, Aebersold R. Quantitative analysis of complex protein mixtures using isotope-coded affinity tags. *Nat Biotechnol*. 1999 Oct;17(10):994-9.

2. de Hoog CL, Foster LJ, Mann M.

RNA and RNA binding proteins participate in early stages of cell spreading through spreading initiation centers. *Cell*. 2004 May 28;117(5):649-62.

**SILAC BACKGROUND:**

Ong SE, Blagoev B, Kratchmarova I, Kristensen DB, Steen H, Pandey A, Mann M. Stable isotope labeling by amino acids in cell culture, SILAC, as a simple and accurate approach to expression proteomics. *Mol Cell Proteomics*. 2002 May;1(5):376-86.

**REVIEW of topics:**

Ong SE, Mann M. Mass spectrometry-based proteomics turns quantitative. *Nat Chem Biol*. 2005 Oct;1(5):252-62. Review.

**11/23 NO CLASS Thanksgiving****11/28 Discussion: Organelle Proteomics**

1. Wigge PA, Jensen ON, Holmes S, Soues S, Mann M, Kilmartin JV. Analysis of the *Saccharomyces* spindle pole by matrix-assisted laser desorption/ionization (MALDI) mass spectrometry. *J Cell Biol*. 1998 May 18;141(4):967-77.

2. Andersen JS, Wilkinson CJ, Mayor T, Mortensen P, Nigg EA, Mann M. Proteomic characterization of the human centrosome by protein correlation profiling. *Nature*. 2003 Dec 4;426(6966):570-4.

3. Schirmer EC, Florens L, Guan T, Yates JR 3rd, Gerace L. Nuclear membrane proteins with potential disease links found by subtractive proteomics. *Science*. 2003 Sep 5;301(5638):1380-2.

**REVIEW of Topic:**

Yates JR 3rd, Gilchrist A, Howell KE, Bergeron JJ. Proteomics of organelles and large cellular structures. *Nat Rev Mol Cell Biol*. 2005 Sep;6(9):702-14. Review.

**11/30 Discussion: Protein Complex Identification—Y2H & TAP TAGS****Protein-protein interaction – Yeast two-hybrid**

1. Uetz P, Giot L, Cagney G, Mansfield TA, Judson RS, Knight JR, Lockshon D, Narayan V, Srinivasan M, Pochart P, Qureshi-Emili A, Li Y, Godwin B, Conover D, Kalbfleisch T, Vijayadamodar G, Yang M, Johnston M, Fields S, Rothberg JM. A comprehensive analysis of protein-protein interactions in *Saccharomyces cerevisiae*. *Nature*. 2000 Feb 10;403(6770):623-7.

**Y2H REVIEW:**

Ito T, Ota K, Kubota H, Yamaguchi Y, Chiba T, Sakuraba K, Yoshida M.

Roles for the two-hybrid system in exploration of the yeast protein interactome. *Mol Cell Proteomics*. 2002 Aug;1(8):561-6. Review.

**Protein-protein interaction – tandem affinity purification method**

2. Gavin et al. (2002) Functional organization of the yeast proteome by systematic analysis of protein complexes. *Nature* 415: 141-147.

**TAP Tag Review:**

Puig et al. (2001) The tandem affinity purification (TAP) method: a general procedure of protein complex purification. *Methods* 24: 218-229.

**12/5 Discussion: Protein Chips & MicroArrays—SELDI-TOF****Protein-protein interaction – protein chip array**

1. Zhu, H. et al. (2001) Global analysis of protein activities using proteome chips. *Science* 293: 2101-2105.

**Protein-protein interaction – protein chips using antibodies**

2. Haab, BB et al.(2001) Protein microarrays for highly parallel detection and quantitation of specific proteins and antibodies in complex solutions. *Genome Biology* 2:1465-6906.

**Protein MicroArrays Review:**

Gavin MacBeath and Stuart L. Schreiber (8 September 2000) "Printing Proteins as Microarrays for High-Throughput Function Determination". *Science* 289 (5485), 1760-1763

**12/7 Discussion: Biological Networks**

1. Li S, Armstrong CM, Bertin N, Ge H, Milstein S, Boxem M, Vidalain PO, Han JD, Chesneau A, Hao T, Goldberg DS, Li N, Martinez M, Rual JF, Lamesch P, Xu L, Tewari M, Wong SL, Zhang LV, Berriz GF, Jacotot L, Vaglio P, Reboul J, Hirozane-Kishikawa T, Li Q, Gabel HW, Elewa A, Baumgartner B, Rose DJ, Yu H, Bosak S, Sequerra R, Fraser A, Mango SE, Saxton WM, Strome S, Van Den Heuvel S, Piano F, Vandenhaute J, Sardet C, Gerstein M, Doucette-Stamm L, Gunsalus KC, Harper JW, Cusick ME, Roth FP, Hill DE, Vidal M. A map of the interactome network of the metazoan *C. elegans*. *Science*. 2004 Jan 23;303(5657):540-3. Epub 2004 Jan 2.

2. Gunsalus KC, Ge H, Schetter AJ, Goldberg DS, Han JD, Hao T, Berriz GF, Bertin N, Huang J, Chuang LS, Li N, Mani R, Hyman AA, Sonnichsen B, Echeverri CJ, Roth FP, Vidal M, Piano F. Predictive models of molecular machines involved in *Caenorhabditis elegans* early embryogenesis. *Nature*. 2005 Aug 11;436(7052):861-5.

**REVIEWS:** Sharan R, Ideker T.

Modeling cellular machinery through biological network comparison. *Nat Biotechnol*. 2006 Apr;24(4):427-33. Review

Tucker CL, Gera JF, Uetz P.

Towards an understanding of complex protein networks. *Trends Cell Biol*. 2001 Mar;11(3):102-6. Review.

**LAB: CYTOSCAPE & Creating Protein Interaction Networks**

Shannon P, Markiel A, Ozier O, Baliga NS, Wang JT, Ramage D, Amin N, Schwikowski B, Ideker T. Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Res*. 2003 Nov;13(11):2498-504.