

# BS3560: Proteomics, Genomics And Bioinformatics

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1.  
Zvelebil, M. J. & Baum, J. O. Understanding Bioinformatics. (Garland Science, 2008).
  
  2.  
Zvelebil, M. J. & Baum, J. O. Protein Structure. in Understanding Bioinformatics (Garland Science, 2008).
  
  3.  
Zvelebil, M. J. & Baum, J. O. Dealing with Databases. in Understanding Bioinformatics (Garland Science, 2008).
  
  4.  
Zvelebil, M. J. & Baum, J. O. Revealing Genome Features. in Understanding Bioinformatics (Garland Science, 2008).
  
  5.  
Zvelebil, M. J. & Baum, J. O. Gene Detection and Genome Annotation. in Understanding Bioinformatics (Garland Science, 2008).
  
  6.  
Zvelebil, M. J. & Baum, J. O. Predicting Secondary Structures. in Understanding Bioinformatics (Garland Science, 2008).

7.

Zvelebil, M. J. & Baum, J. O. Analyzing Structure-Function Relationships. in *Understanding Bioinformatics* (Garland Science, 2008).

8.

Zvelebil, M. J. & Baum, J. O. Proteome and Gene Expression Analysis. in *Understanding Bioinformatics* (Garland Science, 2008).

9.

Zvelebil, M. J. & Baum, J. O. Systems Biology. in *Understanding Bioinformatics* (Garland Science, 2008).

10.

Baker, D. & Sali, A. Protein Structure Prediction and Structural Genomics. *Science* **294**, 93–96 (2001).

11.

Hughes, T. R. & Marton, M. J. Functional Discovery via a Compendium of Expression Profiles. *Cell* **102**, 109–126 (2000).

12.

Goldsmith-Fischman, S. & Honig, B. Structural Genomics: Computational Methods for Structure Analysis. *Protein Science* **12**, 1813–1821 (2003).

13.

Jung, J. W. & Lee, W. Structure-Based Functional Discovery of Proteins: Structural Proteomics. *Journal of Biochemistry and Molecular Biology* **37**, 28–34 (2004).

14.

Smith, R. S. & Gutierrez-Arcelus, M. Structural Diversity of the Human Genome and Disease Susceptibility. (2008) doi:10.1002/9780470015902.a0020764.

15.

Rockett, J. C. & Dix, D. J. Gene Expression Networks. (2006) doi:10.1038/npg.els.0005280.

16.

Stubbs, A. P., Van Yper, S. J. L. & van der Spek, P. J. Microarray Bioinformatics. (2008) doi:10.1002/9780470015902.a0005957.pub2.

17.

Rank, D. R. & Hanzel, D. K. Microarrays: Use in Gene Identification. (2006) doi:10.1038/npg.els.0005952.

18.

Brazma, A. & Sarkans, U. Gene Expression Databases. (2007) doi:10.1002/9780470015902.a0005248.pub2.

19.

Yates, J. R. & Link, A. J. Direct Analysis of Protein Complexes Using Mass Spectrometry. *Nature Biotechnology* **17**, 676–682 (1999).

20.

Makałowski, W., Shabardina, V. & Makałowska, I. Bioinformatics. in *Encyclopedia of Life Sciences 1–9* (Wiley Interscience, 2018). doi:10.1002/9780470015902.a0005247.pub3.

21.

Altschul, S. F., Boguski, M. S., Gish, W. & Wootton, J. C. Issues in Searching Molecular

Sequence Databases. *Nature Genetics* **6**, 119–129 (1994).

22.

Mathé, C. & Sagot, M.-F. Current Methods of Gene Prediction, Their Strengths and Weaknesses. *Nucleic Acids Research* **30**, 4103–4117 (2002).

23.

Sonnhammer, E. L. & Eddy, S. R. Pfam: Multiple Sequence Alignments and HMM-Profiles of Protein Domains. *Nucleic Acids Research* **26**, 320–322 (1998).

24.

Apweiler, R. & Attwood, T. K. The InterPro Database, an Integrated Documentation Resource for Protein Families, Domains and Functional Sites. *Nucleic Acids Research* **29**, 37–40 (2001).

25.

Pavy, N. & Leroy, P. Evaluation of Gene Prediction Software Using a Genomic Data Set: Application to Arabidopsis Thaliana Sequences. *Bioinformatics* **15**, 887–899 (1999).

26.

Katoh, M. & Kato, M. Comparative Genomics between Drosophila and Human [open access]. *Genome Informatics* **14**, 587–588 (2003).

27.

Tohge, T. & Fernie, A. R. Co-Expression and Co-Responses: Within and Beyond Transcription. *Frontiers in Plant Science* **3**, (2012).

28.

Murray, D., Doran, P., MacMathuna, P. & Moss, A. C. In Silico Gene Expression Analysis – an Overview. *Molecular Cancer* **6**, (2007).

29.

Sakuma, Y. & Maruyama, K. Dual Function of an Arabidopsis Transcription Factor DREB2A in Water-Stress-Responsive and Heat-Stress-Responsive Gene Expression. *Proceedings of the National Academy of Sciences of the United States* **103**, 18822–18827 (2006).

30.

Zilberman, D. & Henikoff, S. Epigenetic Inheritance in Arabidopsis: Selective Silence. *Current Opinion in Genetics & Development* **15**, 557–562 (2005).

31.

Genetic Analysis of Genomic Methylation Patterns in Plants and Mammals. *Biological Chemistry Hoppe-Seyler* **377**, 605–618 (1996).

32.

Soppe, W. J. J., Jacobsen, S. E. & al, E. The Late Flowering Phenotype of Fwa Mutants Is Caused by Gain-of-Function Epigenetic Alleles of a Homeodomain Gene. *Molecular Cell* **6**, 791–802 (2000).

33.

Weigel, D. & Ahn, J. H. Activation Tagging in Arabidopsis. *Plant Physiology* **122**, 1003–1013 (2000).

34.

Mansouri, A. Knockout and Knock-in Animals. (2005) doi:10.1038/npg.els.0003840.

35.

Goljanek-Whysall, K. & Sweetman, D. MicroRNA Regulation of the Paired-Box Transcription Factor Pax3 Confers Robustness to Developmental Timing of Myogenesis (*Developmental Biology*). *Proceedings of the National Academy of Sciences of the United States* **108**, 11936–11941 (2011).

36.

Eamens, A. & Wang, M.-B. RNA Silencing in Plants: Yesterday, Today, and Tomorrow. *Plant Physiology* **147**, 456–468 (2008).

37.

E. Nicolas, F., Lopez-Gomollon, S., F. Lopez-Martinez, A. & Dalmay, T. Silencing Human Cancer: Identification and Uses of MicroRNAs. *Recent Patents on Anti-Cancer Drug Discovery* **6**, 94–105 (2011).

38.

Hannon, G. J. RNA Interference. *Nature* **418**, 244–251 (2002).

39.

Tuschl, T. Functional Genomics: RNA Sets the Standard. *Nature* **421**, 220–221 (2003).

40.

Silva, J. M., Hammond, S. M. & Hannon, G. J. RNA Interference: A Promising Approach to Antiviral Therapy? *Trends in Molecular Medicine* **8**, 505–508 (2002).

41.

Meyer, P. Gene Silencing in Plants. (2006) doi:10.1002/9780470015902.a0002022.pub2.

42.

Jacque, J.-M., Triques, K. & Stevenson, M. Modulation of HIV-1 Replication by RNA Interference. *Nature* **418**, 435–438 (2002).

43.

Latchman, D. S. Transcription Factors. (2007)  
doi:10.1002/9780470015902.a0005278.pub2.

44.

Mitchell, P. J. & Tjian, R. Transcriptional Regulation in Mammalian Cells by Sequence-Specific DNA Binding Proteins. *Science* **245**, 371–378 (1989).

45.

Semenza, G. L. Transcription Factors and Human Disorders. (2005)  
doi:10.1038/npg.els.0005504.

46.

Latchman, D. S. Transcriptional Gene Regulation in Eukaryotes. (2005)  
doi:10.1002/9780470015902.a0002322.pub2.

47.

Gehring, W. J. & Ikeo, K. Pax 6: Mastering Eye Morphogenesis and Eye Evolution. *Trends in Genetics* **15**, 371–377 (1999).

48.

Knight, H. & Knight, M. R. Abiotic Stress Signalling Pathways: Specificity and Cross-Talk. *Trends in Plant Science* **6**, 262–267 (2001).

49.

Zhu, J.-K. Salt and Drought Stress Signal Transduction in Plants. *Annual Review of Plant Biology* **53**, 247–273 (2002).

50.

Singh, K. Transcription Factors in Plant Defense and Stress Responses. *Current Opinion in Plant Biology* **5**, 430–436 (2002).

51.

Devoto, A. & Turner, J. G. Jasmonate-Regulated Arabidopsis Stress Signalling Network. *Physiologia Plantarum* **123**, 161–172 (2005).

52.

Matys, V. & Fricke, E. TRANSFAC: Transcriptional Regulation, From Patterns to Profiles. *Nucleic Acids Research* **31**, 374–378 (2003).

53.

Latchman, D. S. *Transcription Factors*. (2007)  
doi:10.1002/9780470015902.a0005278.pub2.

54.

Mitchell, P. J. & Tjian, R. Transcriptional Regulation in Mammalian Cells by Sequence-Specific DNA Binding Proteins. *Science* **245**, 371–378 (1989).

55.

Semenza, G. L. *Transcription Factors and Human Disorders*. (2005)  
doi:10.1038/npg.els.0005504.

56.

Latchman, D. S. *Transcriptional Gene Regulation in Eukaryotes*. (2005)  
doi:10.1002/9780470015902.a0002322.pub2.

57.

Gehring, W. J. & Ikeo, K. Pax 6: Mastering Eye Morphogenesis and Eye Evolution. *Trends in Genetics* **15**, 371–377 (1999).



58.

Knight, H. & Knight, M. R. Abiotic Stress Signalling Pathways: Specificity and Cross-Talk. *Trends in Plant Science* **6**, 262–267 (2001).

59.

Zhu, J.-K. Salt and Drought Stress Signal Transduction in Plants. *Annual Review of Plant Biology* **53**, 247–273 (2002).

60.

Singh, K. Transcription Factors in Plant Defense and Stress Responses. *Current Opinion in Plant Biology* **5**, 430–436 (2002).

61.

Devoto, A. & Turner, J. G. Jasmonate-Regulated Arabidopsis Stress Signalling Network. *Physiologia Plantarum* **123**, 161–172 (2005).

62.

Matys, V. & Fricke, E. TRANSFAC: Transcriptional Regulation, From Patterns to Profiles. *Nucleic Acids Research* **31**, 374–378 (2003).

63.

Zerbino, D. R., Paten, B. & Haussler, D. Integrating Genomes. *Science* **336**, 179–182 (2012).

64.

Kitano, H. Computational Systems Biology. *Nature* **420**, 206–210 (2002).

65.

Ideker, T., Galitski, T. & Hood, L. A New Approach to Decoding Life: Systems Biology.

Annual Review of Genomics and Human Genetics **2**, 343–372 (2001).

66.

Tyson, J. J., Chen, K. & Novak, B. Milestones Network Dynamics and Cell Physiology. *Nature Reviews Molecular Cell Biology* **2**, 908–916 (2001).

67.

Bruggeman, F. J. & Westerhoff, H. V. The Nature of Systems Biology. *Trends in Microbiology* **15**, 45–50 (2007).

68.

Aloy, P. & Russell, R. B. Structure-Based Systems Biology: A Zoom Lens for the Cell. *FEBS Letters* **579**, 1854–1858 (2005).

69.

Harbison, C. T., Gordon, D. B. & Young, R. A. Transcriptional Regulatory Code of a Eukaryotic Genome. *Nature* **431**, 99–104 (2004).

70.

Jen, C.-H. & Manfield, I. W. The Arabidopsis Co-Expression Tool (Act): A WWW-Based Tool and Database for Microarray-Based Gene Expression Analysis. *The Plant Journal* **46**, 336–348 (2006).

71.

Oltvai, Z. N. & Barabási, A.-L. Systems Biology. Life's Complexity Pyramid. *Science (New York, N.Y.)* **298**, 763–764 (2002).

72.

Nemhauser, J. L., Hong, F. & Chory, J. Different Plant Hormones Regulate Similar Processes through Largely Nonoverlapping Transcriptional Responses. *Cell* **126**, 467–475 (2006).

73.

Legrain, P. Protein-Protein Interaction Maps. Encyclopedia of life sciences (2006)  
doi:10.1002/9780470015902.a0006205.

74.

Krogan, N. J. & Cagney, G. Global Landscape of Protein Complexes in the Yeast *Saccharomyces Cerevisiae*. *Nature* **440**, 637–643 (2006).

75.

Von Mering, C. & Jensen, L. J. STRING: Known and Predicted Protein-Protein Associations, Integrated and Transferred Across Organisms. *Nucleic Acids Research* **33**, D433–D437 (2005).

76.

Pieroni, E. & de la Fuente van Bentem, S. Protein Networking: Insights Into Global Functional Organization of Proteomes. *Proteomics* **8**, 799–816 (2008).

77.

Bork, P. & Jensen, L. J. Protein Interaction Networks From Yeast to Human. *Current Opinion in Structural Biology* **14**, 292–299 (2004).

78.

Jensen, L. J. & Kuhn, M. STRING 8--a Global View on Proteins and Their Functional Interactions in 630 Organisms. *Nucleic Acids Research* **37**, D412–D416 (2009).

79.

Jen, C.-H. & Manfield, I. W. The Arabidopsis Co-Expression Tool (Act): A WWW-Based Tool and Database for Microarray-Based Gene Expression Analysis. *The Plant Journal* **46**, 336–348 (2006).

80.

Oltvai, Z. N. Systems Biology: Life's Complexity Pyramid. *Science* **298**, 763–764 (2002).

81.

Nemhauser, J. L., Hong, F. & Chory, J. Different Plant Hormones Regulate Similar Processes through Largely Nonoverlapping Transcriptional Responses. *Cell* **126**, 467–475 (2006).

82.

Legrain, P. Protein-Protein Interaction Maps. *eLS* (2006).

83.

Krogan, N. J. & Cagney, G. Global Landscape of Protein Complexes in the Yeast *Saccharomyces Cerevisiae*. *Nature* **440**, 637–643 (2006).

84.

Von Mering, C. & Jensen, L. J. STRING: Known and Predicted Protein-Protein Associations, Integrated and Transferred Across Organisms. *Nucleic Acids Research* **33**, D433–D437 (2005).

85.

Pieroni, E. & de la Fuente van Bentem, S. Protein Networking: Insights Into Global Functional Organization of Proteomes. *Proteomics* **8**, 799–816 (2008).

86.

Bork, P. & Jensen, L. J. Protein Interaction Networks From Yeast to Human. *Current Opinion in Structural Biology* **14**, 292–299 (2004).

87.

Jensen, L. J. & Kuhn, M. STRING 8--a Global View on Proteins and Their Functional Interactions in 630 Organisms. *Nucleic Acids Research* **37**, D412–D416 (2009).

88.

Massie, C. E. & Mills, I. G. ChIPping Away at Gene Regulation. *EMBO Reports* **9**, 337–343 (2008).

89.

Harbison, C. T., Gordon, D. B. & Young, R. A. Transcriptional Regulatory Code of a Eukaryotic Genome. *Nature* **431**, 99–104 (2004).

90.

Ren, B. & Dynlacht, B. D. Use of Chromatin Immunoprecipitation Assays in Genome-Wide Location Analysis of Mammalian Transcription Factors. *Chromatin and Chromatin Remodeling Enzymes, Part B* **376**, 304–315 (2003).

91.

Ren, B. & Robert, F. Genome-Wide Location and Function of DNA Binding Proteins. *Science* **290**, 2306–2309 (2000).

92.

Mardis, E. R. ChIP-Seq: Welcome to the New Frontier. *Nature Methods* **4**, 613–614 (2007).

93.

Johnson, D. S., Mortazavi, A., Myers, R. M. & Wold, B. Genome-Wide Mapping of in Vivo Protein-DNA Interactions. *Science (New York, N.Y.)* **316**, 1497–1502 (2007).

94.

Mardis, E. R. Next-Generation DNA Sequencing Methods. *Annual Review of Genomics and*

Human Genetics **9**, 387–402 (2008).

95.

Metzker, M. L. Emerging Technologies in DNA Sequencing. *Genome Research* **15**, 1767–1776 (2005).

96.

Amaral, A. J. & Megens, H.-J. Application of Massive Parallel Sequencing to Whole Genome SNP Discovery in the Porcine Genome. *BMC Genomics* **10**, (2009).

97.

Mardis, E. R. The Impact of Next-Generation Sequencing Technology on Genetics. *Trends in Genetics* **24**, 133–141 (2008).

98.

Ideker, T., Galitski, T. & Hood, L. A New Approach to Decoding Life: Systems Biology. *Annual Review of Genomics and Human Genetics* **2**, 343–372 (2001).

99.

Tyson, J. J., Chen, K. & Novak, B. Milestones Network Dynamics and Cell Physiology. *Nature Reviews Molecular Cell Biology* **2**, 908–916 (2001).

100.

Bruggeman, F. J. & Westerhoff, H. V. The Nature of Systems Biology. *Trends in Microbiology* **15**, 45–50 (2007).

101.

Aloy, P. & Russell, R. B. Structure-Based Systems Biology: A Zoom Lens for the Cell. *FEBS Letters* **579**, 1854–1858 (2005).

102.

Cravatt, B. F., Simon, G. M. & Yates III, J. R. The Biological Impact of Mass-Spectrometry-Based Proteomics. *Nature* **450**, 991–1000 (2007).

103.

Choudhary, C. & Mann, M. Decoding Signalling Networks by Mass Spectrometry-Based Proteomics. *Nature Reviews Molecular Cell Biology* **11**, 427–439 (2010).

104.

Domon, B. & Aebersold, R. Options and Considerations When Selecting a Quantitative Proteomics Strategy. *Nature Biotechnology* **28**, 710–721 (2010).

105.

Foster, L. J. & de Hoog, C. L. A Mammalian Organelle Map by Protein Correlation Profiling. *Cell* **125**, 187–199 (2006).

106.

Olsen, J. V., Blagoev, B. & al, E. Global, In Vivo, and Site-Specific Phosphorylation Dynamics in Signaling Networks. *Cell* **127**, 635–648 (2006).

107.

Oppermann, F. S., Gnad, F. & al, E. Large-Scale Proteomics Analysis of the Human Kinome. *Molecular & Cellular Proteomics* **8**, 1751–1764 (2009).

108.

Pan, C., Olsen, J. V., Daub, H. & Mann, M. Global Effects of Kinase Inhibitors on Signaling Networks Revealed by Quantitative Phosphoproteomics. *Molecular & Cellular Proteomics* **8**, 2796–2808 (2009).

109.

Olsen, J. V., Vermeulen, M. & al, E. Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. *Science Signalling* **3**, (2010).

110.

Matsuoka, S. & Ballif, B. A. ATM and ATR Substrate Analysis Reveals Extensive Protein Networks Responsive to DNA Damage. *Science (New York, N.Y.)* **316**, 1160–1166 (2007).

111.

Danial, N. N., Gramm, C. F. & al, E. BAD and Glucokinase Reside in a Mitochondrial Complex That Integrates Glycolysis and Apoptosis. *Nature* **424**, 952–956 (2003).

112.

Gstaiger, M. & Aebersold, R. Applying Mass Spectrometry-Based Proteomics to Genetics, Genomics and Network Biology. *Nature Reviews Genetics* **10**, 617–627 (2009).

113.

Aebersold, R. *Quantitative Proteomics*. (2008).

114.

Aebersold, R. & Mann, M. Mass Spectrometry-Based Proteomics. *Nature* **422**, 198–207 (2003).

115.

Domon, B. & Aebersold, R. Mass Spectrometry and Protein Analysis. *Science* **312**, 212–217 (2006).

116.



Canas, B. Mass Spectrometry Technologies for Proteomics. Briefings in Functional Genomics and Proteomics **4**, 295–320 (2006).

117.

Gary Siuzdak. The Expanding Role of Mass Spectrometry in Biotechnology. (Mcc Pr, 2003).

118.

Proteomics Analysis Step by Step Tutorial Educative File.

119.

Balog, J. & Sasi-Szabo, L. Intraoperative Tissue Identification Using Rapid Evaporative Ionization Mass Spectrometry. Science Translational Medicine **5**, 194ra93-194ra93 (2013).

120.

Boersema, P. J., Kahraman, A. & Picotti, P. Proteomics Beyond Large-Scale Protein Expression Analysis. Current Opinion in Biotechnology **34**, 162–170 (2015).

121.

Aebersold, R. & Mann, M. Mass Spectrometry-Based Proteomics. Nature **422**, 198–207 (2003).

122.

Canas, B. Mass Spectrometry Technologies for Proteomics. Briefings in Functional Genomics and Proteomics **4**, 295–320 (2006).

123.

Cox, J. & Mann, M. Quantitative, High-Resolution Proteomics for Data-Driven Systems Biology. Annual Review of Biochemistry **80**, 273–299 (2011).

124.

Geiger, T. & Wehner, A. Comparative Proteomic Analysis of Eleven Common Cell Lines Reveals Ubiquitous but Varying Expression of Most Proteins. *Molecular & Cellular Proteomics* **11**, (2012).

125.

Domon, B. & Aebersold, R. Mass Spectrometry and Protein Analysis. *Science* **312**, 212–217 (2006).

126.

Ahn, N. G., Shabb, J. B., Old, W. M. & Resing, K. A. Achieving In-Depth Proteomics Profiling by Mass Spectrometry. *ACS Chemical Biology* **2**, 39–52 (2007).

127.

Chen, X. & Sun, L. Amino Acid-Coded Tagging Approaches in Quantitative Proteomics. *Expert Review of Proteomics* **4**, 25–37 (2007).

128.

Cravatt, B. F., Simon, G. M. & Yates III, J. R. The Biological Impact of Mass-Spectrometry-Based Proteomics. *Nature* **450**, 991–1000 (2007).

129.

Han, X., Aslanian, A. & Yates, J. R. Mass Spectrometry for Proteomics. *Current Opinion in Chemical Biology* **12**, 483–490 (2008).

130.

Ansong, C. & Purvine, S. O. Proteogenomics: Needs and Roles to Be Filled by Proteomics in Genome Annotation. *Briefings in Functional Genomics and Proteomics* **7**, 50–62 (2008).

131.

Center for Metabolomics and Mass Spectrometry | Scripps Research.  
<https://www.scripps.edu/science-and-medicine/cores-and-services/mass-spec-and-metabolomics/index.html>.

132.

Mass Spectrometry Facility. <http://www.chm.bris.ac.uk/ms/mshome.xhtml>.

133.

Ashcroft, D. A. E. An Introduction to Mass Spectrometry.  
<http://www.astbury.leeds.ac.uk/facil/MStut/mstutorial.htm>.

134.

Peptide Mass Fingerprinting an IonSource Tutorial. <http://www.ionsource.com/tutorial/>.

135.

Mass Spectrometry Proteomics - Wikipedia, the Free Encyclopedia.  
[https://en.wikipedia.org/wiki/Mass\\_spectrometry\\_proteomics](https://en.wikipedia.org/wiki/Mass_spectrometry_proteomics).

136.

About Mass Spec. <https://www.asms.org/about-mass-spectrometry>.

137.

Mass Spectrometry - FTICR. (2006).

138.

Aebersold, R. & Mann, M. Mass Spectrometry-Based Proteomics. *Nature* **422**, 198–207 (2003).

139.

Domon, B. & Aebersold, R. Mass Spectrometry and Protein Analysis. *Science* **312**, 212–217 (2006).

140.

Canas, B. Mass Spectrometry Technologies for Proteomics. *Briefings in Functional Genomics and Proteomics* **4**, 295–320 (2006).

141.

Cravatt, B. F., Simon, G. M. & Yates III, J. R. The Biological Impact of Mass-Spectrometry-Based Proteomics. *Nature* **450**, 991–1000 (2007).

142.

Bantscheff, M., Schirle, M. & al, E. Quantitative Mass Spectrometry in Proteomics: A Critical Review. *Analytical and Bioanalytical Chemistry* **389**, 1017–1031 (2007).

143.

Coombs, K. M. & Berard, A. Quantitative Proteomic Analyses of Influenza Virus-Infected Cultured Human Lung Cells. *Journal Of Virology* **84**, 10888–10906 (2010).

144.

Domon, B. & Aebersold, R. Options and Considerations When Selecting a Quantitative Proteomics Strategy. *Nature Biotechnology* **28**, 710–721 (2010).

145.

Geiger, T. & Cox, J. Super-SILAC Mix for Quantitative Proteomics of Human Tumor Tissue. *Nature Methods* **7**, 383–385 (2010).

146.

Bindschedler, L. V. & Cramer, R. Quantitative Plant Proteomics. *Proteomics* **11**, 756–775 (2011).

147.

Nikolov, M., Schmidt, C. & Urlaub, H. Quantitative Mass Spectrometry-Based Proteomics: An Overview. in *Quantitative Methods in Proteomics* vol. *Methods in molecular biology* 85–100 (Humana Press, 2012).

148.

Lesur, A. & Domon, B. Advances in High-Resolution Accurate Mass Spectrometry Application to Targeted Proteomics. *Proteomics* **15**, 880–890 (2015).

149.

Larance, M. & Lamond, A. I. Multidimensional Proteomics for Cell Biology. *Nature Reviews Molecular Cell Biology* **16**, 269–280 (2015).

150.

Canas, B. Mass Spectrometry Technologies for Proteomics. *Briefings in Functional Genomics and Proteomics* **4**, 295–320 (2006).

151.

Cox, J. & Mann, M. Quantitative, High-Resolution Proteomics for Data-Driven Systems Biology. *Annual Review of Biochemistry* **80**, 273–299 (2011).

152.

Bindschedler, L. V. & Cramer, R. Quantitative Plant Proteomics. *Proteomics* **11**, 756–775 (2011).

153.

Nikolov, M., Schmidt, C. & Urlaub, H. Quantitative Mass Spectrometry-Based Proteomics: An Overview. in *Quantitative Methods in Proteomics* vol. *Methods in molecular biology* 85–100 (Humana Press, 2012).

154.

Geiger, T. & Wehner, A. Comparative Proteomic Analysis of Eleven Common Cell Lines Reveals Ubiquitous but Varying Expression of Most Proteins. *Molecular & Cellular Proteomics* **11**, (2012).

155.

Chen, X. & Sun, L. Amino Acid-Coded Tagging Approaches in Quantitative Proteomics. *Expert Review of Proteomics* **4**, 25–37 (2007).

156.

Han, X., Aslanian, A. & Yates, J. R. Mass Spectrometry for Proteomics. *Current Opinion in Chemical Biology* **12**, 483–490 (2008).

157.

Ansong, C. & Purvine, S. O. Proteogenomics: Needs and Roles to Be Filled by Proteomics in Genome Annotation. *Briefings in Functional Genomics and Proteomics* **7**, 50–62 (2008).

158.

Schreiber, T. B. & Mausbacher, N. An Integrated Phosphoproteomics Work Flow Reveals Extensive Network Regulation in Early Lysophosphatidic Acid Signaling. *Molecular & Cellular Proteomics* **9**, 1047–1062 (2010).

159.

Macek, B., Mann, M. & Olsen, J. V. Global and Site-Specific Quantitative Phosphoproteomics: Principles and Applications. *Annual Review of Pharmacology and Toxicology* **49**, 199–221 (2009).

160.

Engholm-Keller, K. & Birck, P. TiSH — a Robust and Sensitive Global Phosphoproteomics Strategy Employing a Combination of TiO<sub>2</sub>, SIMAC, and HILIC. *Journal of Proteomics* **75**, 5749–5761 (2012).

161.

Engholm-Keller, K. & Larsen, M. R. Technologies and Challenges in Large-Scale Phosphoproteomics. *Proteomics* **13**, 910–931 (2013).

162.

Palumbo, A. M. & Smith, S. A. Tandem Mass Spectrometry Strategies for Phosphoproteome Analysis. *Mass Spectrometry Reviews* **30**, 600–625 (2011).

163.

Nilsson, C. L. Advances in Quantitative Phosphoproteomics. *Analytical Chemistry* **84**, 735–746 (2012).

164.

Coombs, K. M. & Berard, A. Quantitative Proteomic Analyses of Influenza Virus-Infected Cultured Human Lung Cells. *Journal Of Virology* **84**, 10888–10906 (2010).

165.

Suter, B., Kittanakom, S. & Stagljar, I. Two-Hybrid Technologies in Proteomics Research. *Current Opinion in Biotechnology* **19**, 316–323 (2008).

166.

Rajagopala, S. V., Sikorski, P., Caufield, J. H., Tovchigrechko, A. & Uetz, P. Studying Protein Complexes by the Yeast Two-Hybrid System. *Methods* **58**, 392–399 (2012).

167.

Petschnigg, J., Snider, J. & Stagljar, I. Interactive Proteomics Research Technologies: Recent

Applications and Advances. *Current Opinion in Biotechnology* **22**, 50–58 (2011).

168.

Rual, J.-F. & Venkatesan, K. Towards a Proteome-Scale Map of the Human Protein–protein Interaction Network. *Nature* **437**, 1173–1178 (2005).

169.

Steckelberg, A.-L., Boehm, V., Gromadzka, A. M. & Gehring, N. H. CWC22 Connects Pre-mRNA Splicing and Exon Junction Complex Assembly. *Cell Reports* **2**, 454–461 (2012).

170.

Puig, O. & Caspary, F. The Tandem Affinity Purification (TAP) Method: A General Procedure of Protein Complex Purification. *Methods* **24**, 218–229 (2001).

171.

Thingholm, T. E. & Jensen, O. N. SIMAC (Sequential Elution From IMAC), a Phosphoproteomics Strategy for the Rapid Separation of Monophosphorylated From Multiply Phosphorylated Peptides. *Molecular & Cellular Proteomics: Mcp* **7**, 661–671 (2008).

172.

Benschop, J. J. & Mohammed, S. Quantitative Phosphoproteomics of Early Elicitor Signaling in Arabidopsis. *Molecular & Cellular Proteomics : Mcp* **6**, 1198–1214 (2007).

173.

Ummanni, R., Mundt, F. & Balabanov, S. Identification of Clinically Relevant Protein Targets in Prostate Cancer with 2D-DIGE Coupled Mass Spectrometry and Systems Biology Network Platform. *PLoS ONE* **6**, (2011).

174.



Foster, L. J., De Hoog, C. L. & Mann, M. Unbiased Quantitative Proteomics of Lipid Rafts Reveals High Specificity for Signaling Factors. *Proceedings Of The National Academy Of Sciences Of The United States Of America* **100**, 5813–5818 (2003).

175.

Rajagopala, S. V., Sikorski, P., Caufield, J. H., Tovchigrechko, A. & Uetz, P. Studying Protein Complexes by the Yeast Two-Hybrid System. *Methods* **58**, 392–399 (2012).

176.

Petschnigg, J., Snider, J. & Stagljar, I. Interactive Proteomics Research Technologies: Recent Applications and Advances. *Current Opinion in Biotechnology* **22**, 50–58 (2011).

177.

Steckelberg, A.-L., Boehm, V., Gromadzka, A. M. & Gehring, N. H. CWC22 Connects Pre-mRNA Splicing and Exon Junction Complex Assembly. *Cell Reports* **2**, 454–461 (2012).

178.

Suter, B., Kittanakom, S. & Stagljar, I. Two-Hybrid Technologies in Proteomics Research. *Current Opinion in Biotechnology* **19**, 316–323 (2008).

179.

Rual, J.-F. & Venkatesan, K. Towards a Proteome-Scale Map of the Human Protein–protein Interaction Network. *Nature* **437**, 1173–1178 (2005).

180.

Zhang, W.-J., Pedersen, C. & al, E. Interaction of Barley Powdery Mildew Effector Candidate CSEP0055 With the Defence Protein PR17c. *Molecular Plant Pathology* **13**, 1110–1119 (2012).

181.

Ahrens, C. H., Brunner, E. & al, E. Generating and Navigating Proteome Maps Using Mass Spectrometry. *Nature Reviews Molecular Cell Biology* **11**, 789–801 (2010).

182.

Cox, J. & Mann, M. Is Proteomics the New Genomics? *Cell* **130**, 395–398 (2007).

183.

Cravatt, B. F., Simon, G. M. & Yates III, J. R. The Biological Impact of Mass-Spectrometry-Based Proteomics. *Nature* **450**, 991–1000 (2007).

184.

Choudhary, C. & Mann, M. Decoding Signalling Networks by Mass Spectrometry-Based Proteomics. *Nature Reviews Molecular Cell Biology* **11**, 427–439 (2010).

185.

Domon, B. & Aebersold, R. Options and Considerations When Selecting a Quantitative Proteomics Strategy. *Nature Biotechnology* **28**, 710–721 (2010).

186.

Foster, L. J. & de Hoog, C. L. A Mammalian Organelle Map by Protein Correlation Profiling. *Cell* **125**, 187–199 (2006).

187.

Olsen, J. V., Vermeulen, M. & al, E. Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. *Science Signalling* **3**, (2010).

188.

Keck, J. M. & Jones, M. H. A Cell Cycle Phosphoproteome of the Yeast Centrosome. *Science* **332**, 1557–1561 (2011).

189.

Santamaria, A. & Wang, B. The Plk1-dependent Phosphoproteome of the Early Mitotic Spindle. *Molecular & Cellular Proteomics* **10**, M110.004457-M110.004457 (2011).

190.

Pan, C., Olsen, J. V., Daub, H. & Mann, M. Global Effects of Kinase Inhibitors on Signaling Networks Revealed by Quantitative Phosphoproteomics. *Molecular & Cellular Proteomics* **8**, 2796–2808 (2009).

191.

Bisson, N. & James, D. A. Selected Reaction Monitoring Mass Spectrometry Reveals the Dynamics of Signaling Through the GRB2 Adaptor. *Nature Biotechnology* **29**, 653–658 (2011).

192.

Liu, Y. & Aebersold, R. The Interdependence of Transcript and Protein Abundance: New Data-New Complexities. *Molecular Systems Biology* **12**, 856–856 (2016).

193.

Leitner, A., Faini, M., Stengel, F. & Aebersold, R. Crosslinking and Mass Spectrometry: An Integrated Technology to Understand the Structure and Function of Molecular Machines. *Trends in Biochemical Sciences* **41**, 20–32 (2016).

194.

Ebhardt, H. A., Root, A., Sander, C. & Aebersold, R. Applications of Targeted Proteomics in Systems Biology and Translational Medicine. *Proteomics* **15**, 3193–3208 (2015).

195.

Aebersold, R. & Mann, M. Mass Spectrometry-Based Proteomics. *Nature* **422**, 198–207 (2003).

196.

Cox, J. & Mann, M. Is Proteomics the New Genomics? *Cell* **130**, 395–398 (2007).

197.

Cravatt, B. F., Simon, G. M. & Yates III, J. R. The Biological Impact of Mass-Spectrometry-Based Proteomics. *Nature* **450**, 991–1000 (2007).

198.

Gstaiger, M. & Aebersold, R. Applying Mass Spectrometry-Based Proteomics to Genetics, Genomics and Network Biology. *Nature Reviews Genetics* **10**, 617–627 (2009).

199.

Steen, H. & Mann, M. The ABC's (And XYZ's) of Peptide Sequencing. *Nature Reviews Molecular Cell Biology* **5**, 699–711 (2004).

200.

Gary Siuzdak. *The Expanding Role of Mass Spectrometry in Biotechnology*. (Mcc Pr, 2003).

201.

What is Mass Spectrometry?

[https://masspec.scripps.edu/landing\\_page.php?pgcontent=whatIsMassSpec](https://masspec.scripps.edu/landing_page.php?pgcontent=whatIsMassSpec).