Readings

Download a more detailed version of the Proteomics Unit Readings here.

T Sept 11 Incomplete or draft genome sequencing

Poinar HN, Schwarz C, Qi J, Shapiro B, Macphee RD, Buigues B, Tikhonov A, Huson DH, Tomsho LP, Auch A, Rampp M, Miller W, Schuster SC. Metagenomics to paleogenomics: large-scale sequencing of mammoth DNA.Science. 2006 Jan 20;311(5759):392-4 .

T Sept 18 Genome Alignment

DeBoy RT, Mongodin EF, Emerson JB, Nelson KE. Chromosome evolution in the Thermotogales: large-scale inversions and strain diversification of CRISPR sequences. J Bacteriol. 2006 Apr;188(7):2364-74 .

R Sept 20 Gene Prediction and HMMs (Recommended reading)

Eddy SR. What is a hidden Markov model? Nat Biotechnol. 2004 Oct;22(10):1315-6 .

T Sept 25 Under and Overprediction of Genes

Li J, Riehle MM, Zhang Y, Xu J, Oduol F, Gomez SM, Eiglmeier K, Ueberheide BM,
Shabanowitz J, Hunt DF, Ribeiro JM, Vernick KD. Anopheles gambiae genome reannotation through synthesis of ab initio and comparative gene prediction algorithms.
Genome Biol. 2006;7(3):R24 .

T Oct 2 Manual vs. automated annotation

Turnbaugh PJ, Ley RE, Mahowald MA, Magrini V, Mardis ER, Gordon JI. An obesity-associated gut microbiome with increased capacity for energy harvest. Nature. 2006 Dec 21;444(7122):1027-31.

R Oct 4 Orthology, Paralogy, Xenology (Recommended reading)

Fitch WM. Homology a personal view on some of the problems. Trends Genet. 2000 May;16(5):227-31.

T Oct 9 Orthologs and Function

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R Oct 18 Phylogenetic Profiling to infer Function

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T Oct 30 Functional Genomics using RNAi

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Review:

Mathey-Prevot B, Perrimon N. Drosophila genome-wide RNAi screens: are they delivering the promise? Cold Spring Harb Symp Quant Biol. 2006;71:141-8. Review.

R Nov 1 Chemical Genetics

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.

Review:
Stockwell BR. Exploring biology with small organic molecules. Nature. 2004 Dec 16;432(7019):846-54. Review.

T Nov 6 2D-Gel Analysis

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.

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.

R Nov 8 MuDPIT

Chu DS, Liu H, Nix P, Wu TF, Ralston EJ, Yates JR 3rd, Meyer BJ. Sperm chromatin proteomics identifies evolutionarily conserved fertility factors. Nature. 2006 Sep 7;443(7107):101-5. Epub 2006 Aug 30.

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Biological Networks: Y2H approaches

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.

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R Nov 15 Biological Networks: TAP tag approach

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

Review:

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

F Nov 16 LAB: Creating a Network using Osprey

Breitkreutz BJ, Stark C, Tyers M. Osprey: a network visualization system. Genome Biol. 2003;4(3):R22. Epub 2003 Feb 27.

Review:

Tucker CL, Gera JF, Uetz P. Towards an understanding of complex protein networks. Trends Cell Biol. 2001 Mar;11(3):102-6. ReviewT Nov 27 Microarray Analysis
Zhang Y, Laing C, Steele M, Ziebell K, Johnson R, Benson AK, Taboada E, Gannon VP. Genome evolution in major Escherichia coli O157:H7 lineages. BMC Genomics. 2007 May 16;8:121.

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