

BIOGRAPHICAL SKETCH

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NAME Paul T Spellman	POSITION TITLE Computational Scientist		
eRA COMMONS USER NAME PAULSPELLMAN			
EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)			
INSTITUTION AND LOCATION	DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY
MIT, Cambridge, MA	S.B.	1995	Biology
Stanford University Medical School, Stanford, CA	Ph.D.	2000	Genetics

Positions

2000 – 2003 Post-doctoral Fellow, UC Berkeley, Department of Mol. and Cell.Biology
 2003 – 2007 Scientist, Lawrence Berkeley Lab, Life Science Division
 2007 – present Staff Scientist, Lawrence Berkeley Lab, Life Science Division

Awards and Other Professional Activities

2000 - 2001 NSF Biocomputing Post-doctoral Fellowship
 2002 Ad Hoc member, NSF, GEN-EN panel
 2002 - present Board member, Microarray Gene Expression Data Society
 2002 – 2006 Treasurer, Microarray Gene Expression Data Society
 2005 Ad Hoc member, EPA, Center for Bioinformatics Panel
 2006 Panel member, NIH/NHLBI, Exploratory Program in Systems Biology
 2007 Panel member, NIH/NHLBI, Exploratory Program in Systems Biology
 2007 – 2008 International Cancer Genomics Consortium, scientific planning committee
 2007 – 2008 International Cancer Genomics Consortium, working group on data analysis
 2008 NCI Intramural Program Reviewer
 2008 Welcome Trust Cancer Genome Sequencing Project External Advisory Board

Publications

P.T. Spellman, G. Sherlock, M. Q. Zhang, V. R. Iyer, K. Anders, M. B. Eisen, P. O. Brown, D. Botstein and B. Futcher. Comprehensive identification of cell cycle-regulated genes of the yeast *Saccharomyces cerevisiae* by microarray hybridization. *Molecular Biology of the Cell* 9: 3273-97, 1998.

M. B. Eisen, **P.T. Spellman**, P. O. Brown and D. Botstein. Cluster analysis and display of genome-wide expression patterns. *Proceedings of the National Academy of Sciences, U.S.A.* 95: 14863-8, 1998.

G. Zhu, **P.T. Spellman**, T. Volpe, P. O. Brown, D. Botstein, T. N. Davis and B. Futcher. Two yeast forkhead genes regulate the cell cycle and pseudohyphal growth. *Nature* 406: 90-4, 2000.

D. T. Ross, U. Scherf, M. B. Eisen, C. M. Perou, C. Rees, **P. Spellman**, V. Iyer, S. S. Jeffrey, M. Van de Rijn, M. Waltham, A. Pergamenschikov, J. C. Lee, D. Lashkari, D. Shalon, T. G. Myers, J. N. Weinstein, D. Botstein and P. O. Brown. Systematic variation in gene expression patterns in human cancer cell lines. *Nature Genetics* 24: 227-35, 2000.

A. P. Gasch, **P. T. Spellman**, C. M. Kao, O. Carmel-Harel, M. B. Eisen, G. Storz, D. Botstein and P. O. Brown. Genomic expression programs in the response of yeast cells to environmental changes. *Molecular Biology of the Cell* 11: 4241-57, 2000.

P. T. Spellman. The future of publishing microarray data. *Briefings in Bioinformatics* 2: 316-8, 2001.

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- E. De Gregorio, **P. T. Spellman**, G. M. Rubin and B. Lemaitre. Genome-wide analysis of the Drosophila immune response by using oligonucleotide microarrays. *Proceedings of the National Academy of Sciences, U.S.A.* 98: 12590-5, 2001.
- A. Brazma, P. Hingamp, J. Quackenbush, G. Sherlock, **P. Spellman**, C. Stoeckert, J. Aach, W. Ansorge, C. A. Ball, H. C. Causton, T. Gaasterland, P. Glenisson, F. C. Holstege, I. F. Kim, V. Markowitz, J. C. Matese, H. Parkinson, A. Robinson, U. Sarkans, S. Schulze-Kremer, J. Stewart, R. Taylor, J. Vilo and M. Vingron. Minimum information about a microarray experiment (MIAME)-toward standards for microarray data. *Nature Genetics* 29: 365-71, 2001.
- P. T. Spellman** and G. M. Rubin. Evidence for large domains of similarly expressed genes in the Drosophila genome. *Journal of Biology* 1: 5, 2002.
- P. T. Spellman**, M. Miller, J. Stewart, C. Troup, U. Sarkans, S. Chervitz, D. Bernhart, G. Sherlock, C. Ball, M. Lepage, M. Swiatek, W. L. Marks, J. Goncalves, S. Markel, D. Jordan, M. Shojatalab, A. Pizarro, J. White, R. Hubley, E. Deutsch, M. Senger, B. J. Aronow, A. Robinson, D. Bassett, C. J. Stoeckert, Jr. and A. Brazma. Design and implementation of microarray gene expression markup language (MAGE-ML). *Genome Biology* 3: RESEARCH0046, 2002.
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- E. De Gregorio, **P. T. Spellman**, P. Tzou, G. M. Rubin and B. Lemaitre. The Toll and Imd pathways are the major regulators of the immune response in Drosophila. *Embo Journal* 21: 2568-79, 2002.
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- L. A. Pile, **P. T. Spellman**, R. J. Katzenberger and D. A. Wassarman. The SIN3 deacetylase complex represses genes encoding mitochondrial proteins: implications for the regulation of energy metabolism. *J Biol Chem* 278: 37840-8, 2003.
- C. A. Ball, A. Brazma, H. Causton, S. Chervitz, R. Edgar, P. Hingamp, John C. Matese, H. Parkinson, J. Quackenbush, M. Ringwald, S. Sansone, G. Sherlock, **P. Spellman**, C. Stoeckert, Y. Tateno, R. Taylor, J. White, N. Winegarden. Submission of Microarray Data to Public Repositories. *PLOS Biology* 2: e317
- P. T. Spellman** and G. Sherlock. Final words: cell age and cell cycle are unlinked. *Trends Biotechnology*. 6: 270-3, 2004.
- P. T. Spellman** and G. Sherlock. Reply: whole-culture synchronization – effective tools for cell cycle studies. *Trends Biotechnology*. 6: 277-8, 2004.
- N. Vodovar, M. Vinal, P. Liehl, A. Basset, J. Degrouard, **P. Spellman**, F. Boccard, B. Lemaitre. Drosophila host defense after oral infection by an entomopathogenic Pseudomonas species. *PNAS* 102:11414-9, 2005
- P. Spellman**. A status report on MAGE. *Bioinformatics* 21:3459-60, 2005.
- S. Brun, S. Vidal, **P. Spellman**, K. Takahashi, H. Tricoire, B. Lemaitre. The MAPKKK Mekk1 regulates the expression of Turandot stress genes in response to septic injury in Drosophila. *Genes Cells* 11:397-407, 2006
- A.R. Jones, A. Pizarro, **P. Spellman**, M. Miller. FuGE: Functional Genomics Object Model. *Omics* 10:179-84. 2006

Principal Investigator/Program Director (Last, First, Middle):

- K. Chin K, S. DeVries, J. Fridlyand, **P.T. Spellman**, R. Roydasgupta, W.L. Kuo, A. Lapuk, R.M. Neve, Z. Qian, T. Ryder, F. Chen, H. Feiler, T. Tokuyasu, C. Kingsley, S. Daikree, Z. Meng, K. Chew, D. Pinkel, A. Jain, B.M. Ljung, L. Esserman, D.G. Albertson, F.M. Waldman, J.W. Gray. Genomic and transcriptional aberrations linked to breast cancer pathophysiologies. *Cancer Cell* 6:529-41. 2006
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- T.F. Rayner, P. Rocca-Serra, **P.T. Spellman**, H.C. Causton, A. Farne, E. Holloway, R.A. Irizarry, J. Liu, D.S. Maier, M. Miller, K. Petersen, J. Quackenbush, G. Sherlock, C.J. Stoeckert, J. White, P.L. Whetzel, F. Wymore, H. Parkinson, U. Sarkans, C.A. Ball, A. Brazma. A simple spreadsheet-based, MIAME-supportive format for microarray data: MAGE-TAB. *BMC Bioinformatics*. 7:489. 2006
- A.R. Jones, M. Miller, R. Aebersold, R. Apweiler, C.A. Ball, A. Brazma, J. Degreef, N. Hardy, H. Hermjakob, S.J. Hubbard, P. Hussey, M. Igra, H. Jenkins, R.K. Julian, K. Laursen, S.G. Oliver, N.W. Paton, S.A. Sansone, U. Sarkans, C.J. Stoeckert, C.F. Taylor, P.L. Whetzel, J.A. White, **P. Spellman**, A. Pizarro. The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. *Nat. Biotechnology*. 25:1127-33. 2007
- Y. Wang, M. Moorhead, G. Karlin-Neumann, N. Wang, J. Ireland, S. Lin, C. Chen, L.M. Heiser, K. Chin, L. Esserman, J.W. Gray, **P.T. Spellman**, M. Faham. Performance of Molecular Inversion Probes (MIP) in Allele Copy Number Determination. *Genome Biology*. 8:R246. 2007
- P.T. Spellman**, J.F. Costello, J.W. Gray. *Molecular Basis of Cancer, Mendelsohn J., Ed.*, Elsevier. 2008
- L.A. Brown, S.E. Kalloger, M.A. Miller, I.M. Shih, S.E. McKinney, J.L. Santos, K. Swenerton, **P.T. Spellman**, J. Gray, C.B. Gilks, D.G. Huntsman. Amplification of 11q13 in ovarian carcinoma. *Genes Chromosomes Cancer*. 47:481-9. 2008
- J.Z. Press, A. De Luca, N. Boyd, S. Young, A. Troussard, Y. Ridge, P. Kaurah, S.E. Kalloger, K.A. Blood, M. Smith, **P.T. Spellman**, Y. Yang, D.M. Miller, D. Horsman, M. Faham, C.B. Gilks, J. Gray, D.G. Huntsman. Ovarian carcinomas with genetic and epigenetic BRCA1 loss have distinct molecular abnormalities. *BMC Cancer*. 22:17. 2008

C. Ongoing Research Support