

**CURRICULUM VITAE:** Michael Snyder

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**Education**

1973-1977 B.A. University of Rochester, Rochester, New York  
Chemistry and Biology  
1978-1982 Ph.D. California Institute of Technology, Pasadena, California  
Department of Biology, Degree conferred 6/83

**Professional Experience**

1977-1978 Research Assistant, Department of Biology, University of  
Rochester, Rochester, New York  
1978-1982 Graduate Student with Dr. Norman Davidson, California Institute  
of Technology, Pasadena, California  
1982-1986 Postdoctoral Fellow with Dr. Ronald W. Davis, Department of  
Biochemistry, Stanford University School of Medicine,  
Stanford, California  
1986-1990 Assistant Professor, Department of Biology, Yale University,  
Connecticut  
1990-1997 Associate Professor, Department of Biology, Yale University,  
Connecticut (tenured 1994)  
1997-present Professor, Dept. of Biology (now Mol. Cell. Devel. Biol.), Yale Univ., CT  
1991-present Member Yale Comprehensive Cancer Center  
1992-present Associate Professor/Professor (Joint Appointment), Department of  
Molecular Biophysics and Biochemistry, Yale University  
1998-2004 Chair, Dept. of Molecular, Cellular and Developmental Biology, Yale Univ.  
(Dept. doubled in size and 3X in funds during my tenure).  
2002-present Director, Yale Center for Genomics and Proteomics  
2006-present Genetics Society of America Council Member (Elected)  
2006- 2008 President, US HUPO (Elected)

**Academic Honors/Fellowships**

1978-1982 NIH Predoctoral Training Fellowship  
1982-1985 Helen Hay Whitney Postdoctoral Fellowship  
1986 United Scleroderma Foundation Award  
1987-1991 Pew Scholar Award  
1989 Yale Junior Faculty Fellowship  
2000-2005 Burroughs Wellcome Scholar Award  
2002 Genome Technology Finalist in Microarray Masters  
2002-present Appointed Lewis B. Cullman Professor of MCDB  
2007 Connecticut Medal of Science

**Advisory Committees**

1989,90, 94-98, Member NIH Study Section- Ad hoc Reviewer

2000-07	
1993	Scientific Advisory Board Review Panel-American Cancer Society
1994-96	Howard Hughes Predoctoral Fellowship Review Committee
2002	Damon Runyan Walter Winchell Review Panel
1996-2002	March of Dimes Grant Review Panel
1997	ATCC Advisory Committee
1999	NSF Division Review Panel
2000, 2002	NIH Study Section Review Working Group
2000	Canadian Genome Center Review Panel
2001-present	Northeast Structural Genomics Consortium Scientific Advisory Committee
2001-present	Member, Institute of Genetics Advisory Council, CIHR Canada
2002-2007	Member, Ontario Genome Institute Scientific Advisory Board
2002-present	Member, Chinese National Human Genome Institute Advisory Board
2007-present	SAB, Integrated Genomics Project Univ. of Toronto
2008-present	SAB, Duke Univ. Systems Biology Center
2003-2006	SAB, Blueprint Initiative
2003	NIH Special Road Map Advisory Committee
2003	External Reviewer, Dept. of Medical Genetics, Univ. of Toronto
2003-present	Scientific Advisory Board, Gottenberg Univ. Genomics Meeting
2004-2007	Damon Runyan-Walter Winchell Review Panel
2007	NSF Plant Genomics Initiatives 5 Year Review
2008	External Review Committee, Gene Expression Unit, EMBL

### **Meeting Organizer**

1994	Coorganizer, Juan March Meeting on Signal Transduction & Morphogenesis
1996	Chair, FASEB Meeting: Yeast Chromosome Structure, Repl. & Segregation
2000	Yeast Genetics Meeting Program Committee
2004	CoOrganizer, ASBMB Genomics, Proteomics and Bioinformatics Meeting*
2004	CoOrganizer, GSA International Meeting on Yeast Molecular Genetics
2004	CoOrganizer, CSH Plant Genomes: From Sequence to Phenomes
2006	CoOrganizer, ASBMB Genomics, Proteomics and Bioinformatics Meeting
2006	Organizer, GSA International Meeting on Yeast Molecular Genetics*
2006	CoOrganizer, US HUPO
2007	CoOrganizer, CSH Plant Genomes: From Sequence to Phenomes
2007	CoOrganizer, Keystone Meeting on Functional Genomics

### **Editorial Boards**

1996-2000	Editorial Board, The Dynamic Cell
2001-2004	Editorial Board, Chemistry and Biology
2000-2006	Editorial Board, FEMS Yeast Research
2000-present	Editor-in-Chief (until 2002; now Editor) Functional and Integrative Genomics
2001-present	Editorial Board, Molecular and Cellular Proteomics
2002-present	Editorial Board, Drug Discovery Today
2004- present	Editorial Board, PloS Genetics
2005-present	Editorial Board, Genes and Development
2005-present	Editorial Board, Molecular Systems Biology

### **Named/Distinguished Lectureships (starting 2004)**

2004	California Institute of Technology, Norman Davidson Lecture
2004	University of Chicago, Fredrick Setiz Lecture

2004 Tulane University, Gerber Lecture  
2004 University of Iowa, Raymond Fung Lecture  
2006 Northeastern University, Hoehn Lecture  
2007 EBI Distinguished Lecturer  
2008 Northwestern University Distinguished Lectureship  
2008 Fred Sherman Lecture, Univ. of Rochester

### **Keynote/Featured Speaker**

2000 University of Sherbrooke Graduate Symposium\*  
2001 CHI: Functional Genomics  
2002 Yale University Pathology Retreat  
2002 Georgia Bioinformatics Symposium  
2003 University of Texas Medical Faculty Symposium  
2003 Structural and Functional Genomics, Singapore  
2004 International Meeting On Arabidopsis\*  
2004 Pennsylvania State Graduate Student Symposium  
2005 Keystone Conference on Plant Signaling  
2005 New York University: Genomics Symposium—Genomes in Action  
2005 Chip to Hits  
2005 Systems Biology Meeting  
2006 AGCT Genomics Meeting  
2006 Genomes to Biology Meeting, Manchester, UK  
2006 Keystone Conference on Plant Abiotic Stress  
2006 CHI Genes to Targets  
2006 AUHUPO\*  
2007 ABRF\*  
2007 Pan American and Brazilian Biochemistry and Molecular Biology Meeting\*  
2007 Uppsala Neuroscience Center Launch  
2007 IBC Diagnostics 2 Discovery  
2007 DREAM 2 Conference  
2008 CHI Mining the Plasma Proteome  
2008 Student Invited Speaker, Vanderbilt Genetics Retreat  
2008 Genetics Day, Univ. of Rochester

\*Meetings attended by over 900 people

### **Commercial Activity**

Topogenetics/Exelexis 1990-1991 Partial Founder  
Genaissance 1999-2001 Scientific Advisory Board (SAB)  
Mycota 1996-2000 SAB  
Protometrix 2001-2004 (now subsidiary of Invitrogen) Founder and Chair of SAB  
RxGen 2003-present SAB  
Affomix 2006- Present Founder and Chair of SAB

### **Publications**

1. Kung LA\*, Tao S-C\*, Qian J, **Snyder M**, Zhu H. Global analysis of the glycoproteome in *S. cerevisiae* reveals new roles for protein glycosylation in eukaryotes. Submitted.
2. Korbel JO, Kim PM, Chen X, Urban AE, Weissman S, **Snyder M**, Gerstein MB. The current excitement about copy-number variation: how it relates to gene duplications and protein families. *Curr Opin Struct Biol.* 2008. [Epub ahead of print] PMID: 18511261

3. Lian Z, Karpikov A, Lian J, Mahajan MC, Hartman S, Gerstein M, **Snyder M**, Weissman SM. A Genomics Analysis of RNA polymerase II modification and chromatin architecture related to 3' end RNA polyadenylation. *Genome Res.* 2008 May 16. [Epub ahead of print] PMID: 18487515.
4. Nagalakshmi U, Wang Z, Waern K, Shou C, Raha D, Gerstein M, **Snyder M**. The Transcriptional Landscape of the Yeast Genome Defined by RNA Sequencing. *Science.* 2008 May 1. [Epub ahead of print] PMID: 18451266
5. Wu JQ, **Snyder M**. RNA polymerase II stalling: loading at the start prepares genes for a sprint. *Genome Biol.* 2008 May 2;9:220. PMID: 18466645
6. Wu JQ, Du J, Rozowsky J, Zhang Z, Urban AE, Euskirchen G, Weissman S, Gerstein M, **Snyder M**. Systematic analysis of transcribed loci in ENCODE regions using RACE sequencing reveals extensive transcription in the human genome. *Genome Biol.* 2008;9: R3.
7. Nath AK, Brown RM, Michaud M, Sierra-Honigmann MR, **Snyder M**, Madri JA. Leptin affects endocardial cushion formation by modulating EMT and migration via Akt signaling cascades. *J. Cell Biol.* 2008 181:367-80. Epub 2008 Apr 14. PMID: 18411306
8. Johnson DS, Li W, Gordon DB, Bhattacharjee A, Curry B, Ghosh J, Brizuela L, Carroll JS, Brown M, Flicek P, Koch CM, Dunham I, Bieda M, Xu X, Farnham PJ, Kapranov P, Nix DA, Gingeras TR, Zhang X, Holster H, Jiang N, Green R, Song JS, McCuine SA, Anton E, Nguyen L, Trinklein ND, Ye Z, Ching K, Hawkins D, Ren B, Scacheri PC, Rozowsky J, Karpikov A, Euskirchen G, Weissman S, Gerstein M, **Snyder M**, Yang A, Moqtaderi Z, Hirsch H, Shulha HP, Fu Y, Weng Z, Struhl K, Myers RM, Lieb JD, Liu XS. Systematic evaluation of variability in CHIP-chip experiments using predefined DNA targets. *Genome Res.* 2008, in press.
9. Chang W, Zaarour RF, Reck-Peterson S, Rinn J, Singer RH, **Snyder M**, Novick P, Mooseker MS. Myo2p, a class V myosin in budding yeast, associates with a large ribonucleic acid-protein complex that contains mRNAs and subunits of the RNA-processing body. *RNA.* 491-502.
10. Hudson ME, Pozdnyakova I, Haines K, Mor G, **Snyder M**. Identification of differentially expressed proteins in ovarian cancer using high-density protein microarrays. *Proc Natl Acad Sci USA.* 2007;104: 17494-9.
11. ENCODE Project Consortium. Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature.* 2007;447: 799-816.
12. Korbel JO,\* Urban AE,\* Affourtit J,\* Godwin B, Grubert F, Simons JF, Kim PK, Palejev D, Carriero N, Du L, Taillon B, Tanzer A, Chi J, Yang F, Carter N, Hurles ME, Weissman S, Harkins T, Gerstein M, Egholm M, **Snyder M**. Paired-end mapping reveals extensive structural variation in the human genome. *Science.* 2007;318: 420-6.
13. Robertson G, Hirst M, Bainbridge M, Bilenky M, Zhao Y, Zeng T, Euskirchen G, Bernier B, Varhol R, Delaney A, Thiessen N, Griffith OL, He A, Marra M, **Snyder M**, Jones S. Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. *Nat Methods.* 2007;4: 651-7.
14. Zhu X, Gerstein M, **Snyder M**. Getting connected: analysis and principles of biological networks. *Genes Dev.* 2007;21: 1010-24.

15. Zhang ZD, Rozowsky J, Lam HY, Du J, **Snyder M**, Gerstein M. Telescope: online analysis pipeline for high-density tiling microarray data. *Genome Biol.* 2007;8: R81.
16. Korbel JO, Urban AE, Grubert F, Du J, Royce TE, Starr P, Zhong G, Emanuel BS, Weissman SM, **Snyder M**, Gerstein MB. Systematic prediction and validation of breakpoints associated with copy-number variants in the human genome. *Proc Natl Acad Sci USA.* 2007;104: 10110-5.
17. Gerstein MB, Bruce C, Rozowsky JS, Zheng D, Du J, Korbel JO, Emanuelsson O, Zhang ZD, Weissman S, **Snyder M**. What is a gene, post-ENCODE? History and updated definition. *Genome Res.* 2007;17: 669-81.
18. Trinklein ND, Karaoz U, Wu J, Halees A, Force Aldred S, Collins PJ, Zheng D, Zhang ZD, Gerstein MB, **Snyder M**, Myers RM, Weng Z. Integrated analysis of experimental data sets reveals many novel promoters in 1% of the human genome. *Genome Res.* 2007;17: 720-31.
19. Rozowsky JS, Newburger D, Sayward F, Wu J, Jordan G, Korbel JO, Nagalakshmi U, Yang J, Zheng D, Guigo R, Gingeras TR, Weissman S, Miller P, **Snyder M**, Gerstein MB. The DART classification of unannotated transcription within the ENCODE regions: associating transcription with known and novel loci. *Genome Res.* 2007;17: 732-45.
20. Zhang ZD, Paccanaro A, Fu Y, Weissman S, Weng Z, Chang J, **Snyder M**, Gerstein MB. Statistical analysis of the genomic distribution and correlation of regulatory elements in the ENCODE regions. *Genome Res.* 2007;17: 787-97.
21. Zheng D, Frankish A, Baertsch R, Kapranov P, Reymond A, Choo SW, Lu Y, Denoeud F, Antonarakis SE, **Snyder M**, Ruan Y, Wei CL, Gingeras TR, Guigo R, Harrow J, Gerstein MB. Pseudogenes in the ENCODE regions: consensus annotation, analysis of transcription, and evolution. *Genome Res.* 2007;17: 839-51.
22. Washietl S, Pedersen JS, Korbel JO, Stocsits C, Gruber AR, Hackermuller J, Hertel J, Lindemeyer M, Reiche K, Tanzer A, Ucla C, Wyss C, Antonarakis SE, Denoeud F, Lagarde J, Drenkow J, Kapranov P, Gingeras TR, Guigo R, **Snyder M**, Gerstein MB, Reymond A, Hofacker IL, Stadler PF. Structured RNAs in the ENCODE selected regions of the human genome. *Genome Res.* 2007;17: 852-64.
23. Bhinge AA, Kim J, Euskirchen GM, **Snyder M**, Iyer VR. Mapping the chromosomal targets of STAT1 by Sequence Tag Analysis of Genomic Enrichment (STAGE). *Genome Res.* 2007;17: 910-6.
24. Borneman AR, Zhang ZD, Rozowsky J, Seringhaus MR, Gerstein M, **Snyder M**. Transcription factor binding site identification in yeast: a comparison of high-density oligonucleotide and PCR-based microarray platforms. *Funct Integr Genomics.* 2007;7: 335-45.
25. Borneman AR, Gianoulis TA, Zhang ZD, Yu H, Rozowsky J, Seringhaus MR, Wang LY, Gerstein M, **Snyder M**. Divergence of transcription factor binding sites across related yeast species. *Science.* 2007;317: 815-19.
26. Devgan G, **Snyder M**. Kinase substrate identification using yeast protein micorarrays. In: Functional Microarrays in Drug Discovery. P Predki, ed. 2007. CRC Press 351-360.
27. Popescu SC, Popescu GV, Bachan S, Zhang Z, Seay M, Gerstein M, **Snyder M**, Dinesh-

- Kumar SP. Differential binding of calmodulin related proteins to their targets revealed using high density Arabidopsis protein microarrays. *Proc Natl Acad Sci USA*. 2007;104: 4730-5.
28. Rozowsky J, Wu J, Lian Z, Nagalakshmi U, Korbel JO, Kapranov PD, Zheng D, Dyke S, Newburger P, Miller P, Gingeras T, Weissman S, Gerstein M, **Snyder M**. Novel transcribed regions in the human genome. *Cold Spring Harb Symp Quant Biol*. 2007;71: 111-116.
  29. Euskirchen GM, Rozowsky J, Wei CL, Lee WH, Zhang ZD, Hartman S, Emanuelsson O, Stolc V, Weissman S, Gerstein M, Ruan Y, **Snyder M**. Mapping of transcription factor binding regions in mammalian cells by ChIP: comparison of array- and sequencing-based technologies. *Genome Res*. 2007;17: 898-909.
  30. Smith MG, Gianoulis TA, Pukatzki S, Mekalanos J, Ornston LN, Gerstein M, **Snyder M**. New insights into *Acinetobacter baumannii* pathogenesis revealed by high-density pyrosequencing and transposon mutagenesis. *Genes Dev*. 2007;21: 601-14.
  31. Hall DA, Ptacek J, **Snyder M**. Protein microarray technology. *Mech Aging Dev*. 2007;128: 161-7.
  32. Emanuelsson O, Nagalakshmi U, Zheng D, Rozowsky JS, Urban AE, Du J, Lian Z, Stolc V, Weissman S, **Snyder M**, Gerstein M. Assessing the performance of different high-density tiling microarray strategies for mapping transcribed regions of the human genome. *Genome Res*. 2007;17: 886-97.
  33. Yu H, Nguyen K, Royce T, Qian J, Nelson K, **Snyder M**, Gerstein M. Positional artifacts in microarrays: experimental verification and construction of COP, an automated detection tool. *Nucleic Acids Res*. 2007;35.e8.
  34. **Snyder M**. Yeast is still the beast. *GSA Newsletter*. Fall 2006.
  35. Dewan A, Liu M, Hartman S, Zhang SS, Liu DT, Zhao C, Tam PO, Chan WM, Lam DS, **Snyder M**, Barnstable C, Pang CP, Hoh J. HTRA1 promoter polymorphism in wet age-related macular degeneration. *Science*. 2006;314: 989-92.
  36. Wang LY, **Snyder M**, Gerstein M. BoCaTFBS: a boosted cascade learner to refine the binding sites suggested by ChIP-chip experiments. *Genome Biol*. 2006;7:R102.
  37. Zhu X, Gerstein M, **Snyder M**. ProCAT: a data analysis approach for protein microarrays. *Genome Biol*. 2006;7: R110.
  38. Hudson ME, **Snyder M**. High-throughput methods of regulatory element discovery. *Biotechniques*. 2006;41: 673-677.
  39. Du J, Rozowsky JS, Korbel JO, Zhang ZD, Royce TE, Schultz MH, **Snyder M**, Gerstein M. A supervised hidden markov model framework for efficiently segmenting tiling array data in transcriptional and ChIP-chip experiments: systematically incorporating validated biological knowledge. *Bioinformatics*. 2006;22: 3016-24.
  40. Seringhaus M, Pacanaro A, Borneman A, **Snyder M**, Gerstein M. Predicting essential genes in fungal genomes. *Genome Res*. 2006;16: 1126-35.
  41. Ptacek J, **Snyder M**. Charging it up: global analysis of protein phosphorylation. *Trends Genet*. 2006;22: 545-54

42. Srikantha T, Borneman AR, Daniels KJ, Pujol C, Wu W, Seringhaus MR, Gerstein M, Yi S, **Snyder M**, Soll DR. TOS9 regulates white-opaque switching in *Candida albicans*. *Eukaryot Cell*. 2006;5: 1674-87.
43. Kastenmayer JP,\* Ni L,\* Chu A, Kitchen LE, Au WC, Yang H, Carter CD, Wheeler D, Davis RW, Boeke JD, **Snyder MA**, Basrai MA. Functional genomics of genes with small open reading frames (sORFs) in *S. cerevisiae*. *Genome Res*. 2006;16: 365-73.
44. Seringhaus M, Kumar A, Hartigan J, **Snyder M**, Gerstein M. Genomic analysis of insertion behavior and target specificity of mini-Tn7 and Tn3 transposons in *Saccharomyces cerevisiae*. *Nucleic Acids Res*. 2006;34: e57.
45. Kung LA, **Snyder M**. Proteome chips for whole-organism assays. *Nat Rev Mol Cell Biol*. 2006;7: 617-22.
46. Sopko R, Huang D, Preston N, Chua G, Papp B, Kafadar K, **Snyder M**, Oliver SG, Cyert M, Hughes TR, Boone C, Andrews B. Mapping pathways and phenotypes by systematic gene overexpression. *Mol Cell*. 2006;21: 319-30.
47. **Snyder M**, Gelperin D. Community resources for *Saccharomyces cerevisiae*. 2006, Jan/Feb 9.
48. Lu J, Hou R, Booth CJ, Yang S-H, **Snyder M**. Defined culture of human embryonic stem cells. *Proc Natl Acad Sci USA*. 2006;103: 5688-93.
49. Royce TE, Rozowsky JS, Luscombe NM, Emanuelsson O, Yu H, Zhu X, **Snyder M**, Gerstein M. Extrapolating traditional DNA microarray statistics to the tiling and protein microarray technologies. *Meth Enzymol*. 2006;411: 282-311.
50. Ho S, Jona G, Johnston M, **Snyder M**. Linking DNA-binding proteins to their recognition sequences using protein microarrays. *Proc Natl Acad Sci USA*. 2006;103: 9940-45.
51. Smith MG, **Snyder M**. Yeast as a model for human disease. *Current Protocols in Human Genetics*. 2006;15.6.1-15.6.8.
52. Urban AE, Korbel J, Selzer R, Popescu GV, Richmond T, Cubells JF, Green R, Emanuel BS, Gerstein M, Weissman SM, **Snyder M**. High resolution mapping of DNA copy alterations using high density tiling oligonucleotide arrays. *Proc Natl Acad Sci USA*. 2006;103: 4534-9.
53. Borneman R, Leigh-Bell J, Yu H, Bertone P, Gerstein M, **Snyder M**. Target hub proteins serve as master regulators of the complex transcriptional network controlling yeast pseudohyphal growth. *Genes Devel*. 2006;20: 435-448.
54. Zhu H, Hu S, Jona G, Zhu X, Kreiswirth N, Willey BM, Mazzulli T, Liu G, Song Q, Chen P, Cameron M, Tyler A, Wang J, Wen J, Chen W, Compton S, **Snyder M**. SARS diagnostics using a coronavirus protein chip. *Proc Nat Acad Sci USA*. 2006;103: 4011-16.
55. Bertone P, Trifonov V, Rozowsky JS, Schubert F, Emanuelsson O, Karro J, Kao M-Y, **Snyder M**, Gerstein M. Design optimization methods for genomic DNA tiling arrays. *Genome Res*. 2006;16: 271-81.
56. Stolc V, Li L, Wang X, Li X, Su N, Tongprasit W, Han B, Xue Y, Li J, **Snyder M**, Gerstein M, Wang J, Deng XW. A pilot study of transcription unit analysis in rice using oligonucleotide tiling-path microarray. *Plant Mol Biol*. 2005;59: 137-49.

57. Mah AS, Elia AE, Devgan G, Ptacek J, Schutkowski M, **Snyder M**, Yaffe MB, Deshaies RJ. Substrate specificity analysis of protein kinase complex Dbf2-Mob1 by peptide library and proteome array screening. *BMC Biochem.* 2005;6: 22.
58. Hartman SE, Bertone P, Nath A, Royce TE, Gerstein M, Weissman S, **Snyder M**. Global changes in STAT target selection and transcription regulation upon interferon treatments. *Genes Devel.* 2005;19: 2953-68.
59. Royce TE, Rozowsky JS, Bertone P, Samantac M, Stolc V, Weissman S, **Snyder M**, Gerstein M. Issues in the analysis of oligonucleotide tiling microarrays for transcript mapping. *Trends Genet.* 2005;21: 466-75.
60. Bertone P, **Snyder M**. Advances in functional protein microarrays. *FEBS J.* 2005;272: 5400-5411.
61. Ptacek J, Devgan G, Michaud G, Zhu H, Zhu X, Fasolo J, Guo H, Jona G, Breitkreutz A, Sopko R, Lee S, McCartney RR, Schmidt MC, Rachidi N, Stark MJR, Stern DF, Tyers M, de Virgilio C, Andrews B, Gerstein M, Schweitzer B, Predki P, **Snyder M**. Global analysis of protein phosphorylation in yeast. *Nature.* 2005;438: 679-84.
62. Gelperin DM, White MA, Wilkinson ML, Kon Y, Li A, Kung LA, Wise KJ, Lopez-Hoyo N, Jiang L, Piccirillo S, Yu H, Gerstein M, Dumont ME, Phizicky EM, **Snyder M**,\* Grayhack EJ.\* Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. *Genes Devel.* 2005;19: 2816-26. \*Co-Senior Authors
63. Pot I, Knockleby J, Aneliunas V, Nguyen T, Ah-Kye S, Liszt G, **Snyder M**, Hieter P, Vogel J. Spindle checkpoint maintenance requires Ame1 and Okp1. *Cell Cycle.* 2005;4: 1448-56.
64. Oh SW, Moon JD, Lim HJ, Park SY, Kim T, Park J, Han MH, **Snyder M**, Choi EY. Calixarene derivative as a tool for highly sensitive detection and oriented immobilization of proteins in a microarray format through noncovalent molecular interaction. *FASEB J.* 2005;19: 1335-7.
65. Bertone P, **Snyder M**. Prospects and challenges in proteomics. *Plant Physiol.* 2005;138: 560-2.
66. Bertone P, Gerstein M, **Snyder M**. Applications of DNA tiling arrays to experimental genome annotation and regulatory pathway discovery. *Chromosome Res.* 2005;13: 259-74.
67. Martone R, **Snyder M**. Mapping transcription factor binding sites using chIP Chip - general considerations. *DNA Microarrays.* 2005, in press.
68. Rinn JL, **Snyder M**. Sexual dimorphism in mammalian gene expression. *Trends Genet.* 2005;21: 298-305.
69. Smith MG, Jona G, Ptacek J, Devgan G, Zhu H, Zhu X, **Snyder M**. Global analysis of protein function using protein microarrays. *Mechanisms Ageing Devel.* 2005;126: 171-175.
70. ENCODE Project Consortium. The ENCODE (EnCyclopedia Of DNA Elements) Project. *Science.* 2004;306: 636-640.
71. Bertone P, Stolc V, Royce TE, Rozowsky JS, Urban AE, Zhu X, Rinn JL, Tongprasit W, Samanta M, Weissman S, Gerstein M, **Snyder M**. Global identification of human transcribed sequences with genome tiling arrays. *Science.* 2004;306: 2242-6.

72. Mukherjee S, Berger MF, Jona G, Wang XS, Muzzey D, **Snyder M**, Young RA, Bulyk ML. Rapid analysis of the DNA-binding specificities of transcription factors with DNA microarrays. *Nat Genet.* 2004;36: 1331-9.
73. White EJ, Emanuelsson O, Scalzo D, Royce T, Kosak S, Weissman S, Gerstein M, Groudine M, **Snyder M**, Schubeler D. High resolution DNA replication analysis of human chromosome 22 reveals cell type specific differences in DNA replication timing. *Proc Natl Acad Sci USA.* 2004;101: 17771-6.
74. Kumar A, Seringhaus M, Biery MC, Sarnovsky RJ, Umansky L, Piccirillo S, Matson S, Heidtman M, Cheung KH, Dobry CJ, Gerstein M, Craig NL, **Snyder M**. Large-scale mutagenesis of the yeast genome using a Tn7-derived multipurpose transposon. *Genome Res.* 2004;14: 1975-86.
75. Luscombe NM, Babu MM, Yu H, **Snyder M**, Teichmann SA, Gerstein M. Genome analysis of regulatory network dynamics reveals large topological changes. *Nature.* 2004;431: 308-12.
76. Hall DA, Zhu H, Royce T, Gerstein M, **Snyder M**. Regulation of gene expression by a metabolic enzyme. *Science.* 2004;306: 482-484.
77. Berman P, Bertone P, DasGupta B, Gerstein M, Ming-Yang Kao M-Y, **Snyder M**. Fast optimal genome tiling with applications to microarray design and homology search. *J. Computational Biol.* 2004;11: 766-785.
78. Euskirchen G, **Snyder M**. A plethora of sites. *Nat Genet.* 2004;36: 325-326.
79. Rinn JL, Rozowsky JS, Laurenz IJ, Petersen PH, Zou K, Zhong W, Gerstein M, **Snyder M**. Major molecular differences between mammalian sexes are involved in drug metabolism and renal function. *Dev Cell.* 2004;6: 791-800.
80. Euskirchen G, Royce TE, Bertone P, Martone R, Rinn JL, Nelson FK, Sayward F, Luscombe NM, Miller P, Gerstein M, Weissman S, **Snyder M**. CREB binds to multiple loci on chromosome 22. *Mol Cell Biol.* 2004;24: 3804-3814.
81. Smith M, des Etages S, **Snyder M**. Microbial synergy via an ethanol triggered pathway. *Mol Cell Biol.* 2004;24: 3874-3884.
82. Bidlingmaier S, **Snyder M**. Regulation of polarized growth initiation and termination cycles by the polarisome and Cdc42 regulators. *J Cell Biol.* 2004;164: 201-18. (Featured on cover).
83. Huang J, Zhu H, Haggarty SJ, Spring DR, **Snyder M**, Schreiber S. Finding new components of the TOR signaling pathway using chemical genetics and proteome chips. *Proc Natl Acad Sci USA.* 2004;101: 16594-9.
84. Lian Z, Euskirchen G, Rinn J, Martone R, Bertone P, Hartman S, Royce T, Nelson K, Sayward F, Luscombe N, Yang J, Li JL, Miller P, Urban AE, Gerstein M, Weissman S, **Snyder M**. Identification of novel functional elements in the human genome. *Cold Spring Harb Symp Quant Biol.* 2003;68: 317-322.
85. Jansen R, Yu H, Greenbaum D, Kluger Y, Krogan NJ, Chung S, Emili A, **Snyder M**, Greenblatt JF, Gerstein M. A Bayesian networks approach for predicting protein-protein interactions from genomic data. *Science.* 2003;302: 449-53.

86. Michaud GA, Salcius M, Zhou F, Bangham R, Bonin J, Guo H, **Snyder M**, Predki PF, Schweitzer BI. Analyzing antibody specificity with whole proteome microarrays. *Nat Biotechnol.* 2003;21: 1509-12.
87. Kafadar KA, Zhu H, **Snyder M**, Cyert M. Negative regulation of calcineurin signaling by Hrr25p, a yeast homolog of casein kinase I. *Genes Devel.* 2003;17: 2698-708.
88. Martone R, Euskirchen G, Bertone P, Hartman S, Royce TE, Luscombe NL, Rinn JL, Nelson FK, Miller P, Gerstein M, Weissman S, **Snyder M**. Distribution of NF- $\kappa$ B binding sites across human chromosome 22. *Proc Natl Acad Sci USA.* 2003;100: 12247-12252.
89. Schweitzer B, Predki P, **Snyder M**. Microarrays to characterize protein interactions on a whole-proteome scale. *Proteomics.* 2003;3: 2190-9.
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91. Phizicky E, Bastiaens PI, Zhu H, **Snyder M**, Fields S. Protein analysis on a proteomic scale. *Nature.* 2003;422: 208-15.
92. Hanrahan J, **Snyder M**. Cytoskeletal activation of a checkpoint kinase. *Mol Cell.* 2003;12: 663-73. (Featured on cover)
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