

Stanford



Michael Snyder

Stanford W. Ascherman, MD, FACS, Professor in Genetics

CONTACT INFORMATION

- **Alternate Contact**

Lisa Stainton - Executive Assistant

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Bio

BIO

1977 B.A, Chemistry and Biology, University of Rochester, NY

1978-1982 Ph.D. California Institute of Technology, CA Advisor: Dr. Norman Davidson

1982-1986 Postdoctoral Research Stanford University School of Medicine, CA Advisor: Dr. Ronald Davis

1986-2009 Faculty Dept of Molecular, Cellular and Developmental Biology, Yale University, New Haven, CT

2009-present Dept of Genetics, Stanford University School of Medicine, Stanford, CA

ACADEMIC APPOINTMENTS

- Professor, Genetics
- Member, Bio-X
- Member, Cardiovascular Institute
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Chair, Dept. of Genetics, (2009- present)
- Director, Center for Genomics and Personalized Medicine, (2009- present)

LINKS

- Snyder Lab Website: <http://snyderlab.stanford.edu/>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

We are presently in an omics revolution in which genomes and other omes can be readily characterized. Our laboratory uses a variety of approaches to analyze genomes and regulatory networks. Our research focuses on yeast, an ideal model organism ideally suited to genetic analysis, and humans.

1) Transcriptomes

To annotate genomes, we developed RNA sequencing for annotation the yeast and human transcriptomes. We discovered that the eukaryotic transcriptome is much more complex than previously appreciated and that embryonic stem cells have more transcript isoforms than differentiated cells.

2) Transcription Factor Binding Networks

We have also developed methods for mapping transcription factor binding sites through the genome. We used this to develop regulatory maps and have been using this to help decipher the combinatorial regulatory code # which factors work together to regulate which genes. Using this approach we have mapped out pathways crucial for metabolism and inflammation.

3) Integrated Regulatory Networks

In addition to transcriptional factor binding networks we have also been mapping phosphorylation and metabolite-protein interaction networks. These studies have revealed novel global regulators and key points in integrated regulatory networks.

4) Variation

We have been analyzing differences between individuals and species at two levels: DNA sequence variation and regulatory information variations. We developed paired end sequencing for humans and found that humans have extensive structural variation (SV), i.e. deletions, insertions and inversions. This is likely to be a major cause of phenotypic variation and human disease. In addition, by mapping binding sites difference among different yeast strains and humans, we have found that individuals differ much more in their regulatory information than in coding sequence differences. We can correlate these differences with those in SNPS and SVs, thereby associating noncoding DNA differences with regulatory information.

5) Human Disease

Finally, we are applying omics approaches of genome sequencing, transcriptomics proteomics metabolomics, DNA methylation and microbiome assays to the analysis of human disease. These integrative omics approaches are being applied to help understand the molecular basis of disease and the development of diagnostics and therapeutics.

CLINICAL TRIALS

- Multiomic Signatures of Microbial Metabolites Following Prebiotic Fiber Supplementation, Recruiting
- Precision Diets for Diabetes Prevention, Recruiting
- Understanding and Diagnosing Allergic Disease in Twins, Recruiting
- The 28 Day Challenge, Not Recruiting

Teaching

STANFORD ADVISEES

Med Scholar Project Advisor

Akshay Sanghi

Doctoral Dissertation Reader (AC)

Nicole Gay, Michael Sikora

Postdoctoral Faculty Sponsor

Gireesh Bogu, Andrew Brooks, Matias Cabruja, Songjie Chen, Graham Erwin, Takaaki Furihata, Ariel Ganz, Peng Gao, Tuhin Guha, Casey Hanson, Aaron Horning, Brian Johnson, Ryan Kellogg, Samuel Lancaster, Brittany Lee, Hayan Lee, Tim MacKenzie, Petra Mamic, David Marciano, Ahmed Metwally, Emma Monte, Michael Nshanian, Heyjun Park, Jeniffer Quijada, Morteza Roodgar, M. Reza Sailani, Xiaotao Shen, Ming-Shian Tsai, Kevin Van Bortle, Meng Wang, Si Wu, Allison Zhang, Sai Zhang, Bingqing Zhao, Xin Zhou

Doctoral Dissertation Advisor (AC)

Kevin Erazo, Stephanie Nevins, Akshay Sanghi

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Phd Program)
- Genetics (Phd Program)
- Immunology (Phd Program)

Publications

PUBLICATIONS

- **HAT1 Coordinates Histone Production and Acetylation via H4 Promoter Binding.** *Molecular cell*
Gruber, J. J., Geller, B., Lipchik, A. M., Chen, J., Salahudeen, A. A., Ram, A. N., Ford, J. M., Kuo, C. J., Snyder, M. P.
2019
- **The Integrative Human Microbiome Project** *NATURE*
Proctor, L. M., Creasy, H. H., Fettweis, J. M., Lloyd-Price, J., Mahurkar, A., Zhou, W., Buck, G. A., Snyder, M. P., Strauss, J. F., Weinstock, G. M., White, O., Huttenhower, C., Integrative HMP iHMP Res Network
2019; 569 (7758): 641–48
- **A longitudinal big data approach for precision health** *NATURE MEDICINE*
Rose, S., Contrepois, K., Moneghetti, K. J., Zhou, W., Mishra, T., Mataraso, S., Dagan-Rosenfeld, O., Ganz, A. B., Dunn, J., Hornburg, D., Rego, S., Perelman, D., Ahadi, et al
2019; 25 (5): 792+
- **Longitudinal multi-omics of host-microbe dynamics in prediabetes.** *Nature*
Zhou, W., Sailani, M. R., Contrepois, K., Zhou, Y., Ahadi, S., Leopold, S. R., Zhang, M. J., Rao, V., Avina, M., Mishra, T., Johnson, J., Lee-McMullen, B., Chen, et al
2019; 569 (7758): 663–71
- **The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight** *SCIENCE*
Garrett-Bakelman, F. E., Darshi, M., Green, S. J., Gur, R. C., Lin, L., Macias, B. R., McKenna, M. J., Meydan, C., Mishra, T., Nasrini, J., Piening, B. D., Rizzardi, L. F., Sharma, et al
2019; 364 (6436): 144+
- **Gene-Environment Interaction in the Era of Precision Medicine** *CELL*
Li, J., Li, X., Zhang, S., Snyder, M.
2019; 177 (1): 38–44
- **A longitudinal big data approach for precision health.** *Nature medicine*
Schüssler-Fiorenza Rose, S. M., Contrepois, K., Moneghetti, K. J., Zhou, W., Mishra, T., Mataraso, S., Dagan-Rosenfeld, O., Ganz, A. B., Dunn, J., Hornburg, D., Rego, S., Perelman, D., Ahadi, et al
2019; 25 (5): 792–804

- **Chromatin Remodeling in Response to BRCA2-Crisis.** *Cell reports*
Gruber, J. J., Chen, J., Geller, B., Jäger, N., Lipchik, A. M., Wang, G., Kurian, A. W., Ford, J. M., Snyder, M. P.
2019; 28 (8): 2182–93.e6
- **The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight.** *Science (New York, N.Y.)*
Garrett-Bakelman, F. E., Darshi, M., Green, S. J., Gur, R. C., Lin, L., Macias, B. R., McKenna, M. J., Meydan, C., Mishra, T., Nasrini, J., Piening, B. D., Rizzardi, L. F., Sharma, et al
2019; 364 (6436)
- **High-Resolution Bisulfite-Sequencing of Peripheral Blood DNA Methylation in Early-Onset and Familial Risk Breast Cancer Patients.** *Clinical cancer research : an official journal of the American Association for Cancer Research*
Chen, J., Haanpää, M. K., Gruber, J. J., Jäger, N., Ford, J. M., Snyder, M. P.
2019
- **Metformin Affects Heme Function as a Possible Mechanism of Action.** *G3 (Bethesda, Md.)*
Li, X., Wang, X., Snyder, M. P.
2018
- **High Frequency Actionable Pathogenic Exome Variants in an Average-Risk Cohort.** *Cold Spring Harbor molecular case studies*
Rego, S., Dagan-Rosenfeld, O., Zhou, W., Sailani, M. R., Limcaoco, P., Colbert, E., Avina, M., Wheeler, J., Craig, C., Salins, D., Rost, H. L., Dunn, J., McLaughlin, et al
2018
- **Longitudinal personal DNA methylome dynamics in a human with a chronic condition.** *Nature medicine*
Chen, R., Xia, L., Tu, K., Duan, M., Kukurba, K., Li-Pook-Than, J., Xie, D., Snyder, M.
2018
- **Dynamic Human Environmental Exposome Revealed by Longitudinal Personal Monitoring.** *Cell*
Jiang, C., Wang, X., Li, X., Inlora, J., Wang, T., Liu, Q., Snyder, M.
2018; 175 (1): 277
- **Decoding the Genomics of Abdominal Aortic Aneurysm.** *Cell*
Li, J., Pan, C., Zhang, S., Spin, J. M., Deng, A., Leung, L. L., Dalman, R. L., Tsao, P. S., Snyder, M.
2018; 174 (6): 1361
- **Glucotypes reveal new patterns of glucose dysregulation.** *PLoS biology*
Hall, H., Perelman, D., Breschi, A., Limcaoco, P., Kellogg, R., McLaughlin, T., Snyder, M.
2018; 16 (7): e2005143
- **Natural Selection Has Differentiated the Progesterone Receptor among Human Populations.** *American journal of human genetics*
Li, J., Hong, X., Mesiano, S., Muglia, L. J., Wang, X., Snyder, M., Stevenson, D. K., Shaw, G. M.
2018
- **Systematic Protein Prioritization for Targeted Proteomics Studies through Literature Mining** *JOURNAL OF PROTEOME RESEARCH*
Yu, K., Lee, T., Wan, C., Chen, Y., Re, C., Kou, S. C., Chiang, J., Kohane, I. S., Snyder, M.
2018; 17 (4): 1383–96
- **Microfluidic isoform sequencing shows widespread splicing coordination in the human transcriptome** *GENOME RESEARCH*
Tilgner, H., Jahanbani, F., Gupta, I., Collier, P., Wei, E., Rasmussen, M., Snyder, M.
2018; 28 (2): 231–42
- **A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth** *SCIENTIFIC REPORTS*
Rappoport, N., Toung, J., Hadley, D., Wong, R. J., Fujioka, K., Reuter, J., Abbott, C. W., Oh, S., Hu, D., Eng, C., Huntsman, S., Bodian, D. L., Niederhuber, et al
2018; 8: 226
- **Integrative Personal Omics Profiles during Periods of Weight Gain and Loss.** *Cell systems*
Piening, B. D., Zhou, W., Contrepois, K., Röst, H., Gu Urban, G. J., Mishra, T., Hanson, B. M., Bautista, E. J., Leopold, S., Yeh, C. Y., Spakowicz, D., Banerjee, I., Chen, et al
2018

- **Association of Omics Features with Histopathology Patterns in Lung Adenocarcinoma** *CELL SYSTEMS*
Yu, K., Berry, G. J., Rubin, D. L., Re, C., Altman, R. B., Snyder, M.
2017; 5 (6): 620-+
- **Plasma sterols and depressive symptom severity in a population-based cohort** *PLOS ONE*
Cenik, B., Cenik, C., Snyder, M. P., Brown, E.
2017; 12 (9): e0184382
- **Fetal de novo mutations and preterm birth.** *PLoS genetics*
Li, J., Oehlert, J., Snyder, M., Stevenson, D. K., Shaw, G. M.
2017; 13 (4)
- **De novo and rare mutations in the HSPA1L heat shock gene associated with inflammatory bowel disease** *GENOME MEDICINE*
Takahashi, S., Andreoletti, G., Chen, R., Munehira, Y., Batra, A., Afzal, N. A., Beattie, R. M., Bernstein, J. A., Ennis, S., Snyder, M.
2017; 9
- **Digital Health: Tracking Physiomes and Activity Using Wearable Biosensors Reveals Useful Health-Related Information.** *PLoS biology*
Li, X., Dunn, J., Salins, D., Zhou, G., Zhou, W., Schüssler-Fiorenza Rose, S. M., Perelman, D., Colbert, E., Runge, R., Rego, S., Sonecha, R., Datta, S., McLaughlin, et al
2017; 15 (1)
- **Static and Dynamic DNA Loops form AP-1-Bound Activation Hubs during Macrophage Development.** *Molecular cell*
Phanstiel, D. H., Van Bortle, K., Spacek, D., Hess, G. T., Shamim, M. S., Machol, I., Love, M. I., Aiden, E. L., Bassik, M. C., Snyder, M. P.
2017; 67 (6): 1037-48.e6
- **Patient-Specific iPSC-Derived Endothelial Cells Uncover Pathways that Protect against Pulmonary Hypertension in BMPR2 Mutation Carriers.** *Cell stem cell*
Gu, M., Shao, N., Sa, S., Li, D., Termglinchan, V., Ameen, M., Karakikes, I., Sosa, G., Grubert, F., Lee, J., Cao, A., Taylor, S., Ma, et al
2016
- **Simul-seq: combined DNA and RNA sequencing for whole-genome and transcriptome profiling.** *Nature methods*
Reuter, J. A., Spacek, D. V., Pai, R. K., Snyder, M. P.
2016; 13 (11): 953-958
- **Identification of significantly mutated regions across cancer types highlights a rich landscape of functional molecular alterations** *NATURE GENETICS*
Araya, C. L., Cenik, C., Reuters, J. A., Kiss, G., Pande, V. S., Snyder, M. P., Greenleaf, W. J.
2016; 48 (2): 117-125
- **Synthetic long-read sequencing reveals intraspecies diversity in the human microbiome.** *Nature biotechnology*
Kuleshov, V., Jiang, C., Zhou, W., Jahanbani, F., Batzoglou, S., Snyder, M.
2016; 34 (1): 64-69
- **Yeast longevity promoted by reversing aging-associated decline in heavy isotope content.** *NPJ aging and mechanisms of disease*
Li, X., Snyder, M. P.
2016; 2: 16004
- **Predicting non-small cell lung cancer prognosis by fully automated microscopic pathology image features.** *Nature communications*
Yu, K., Zhang, C., Berry, G. J., Altman, R. B., Ré, C., Rubin, D. L., Snyder, M.
2016; 7: 12474-?
- **Identification of Human Neuronal Protein Complexes Reveals Biochemical Activities and Convergent Mechanisms of Action in Autism Spectrum Disorders** *CELL SYSTEMS*
Li, J., Ma, Z., Shi, M., Maly, R. H., Aoki, H., Minic, Z., Phanse, S., Jin, K., Wall, D. P., Zhang, Z., Urban, A. E., Hallmayer, J., Babu, et al
2015; 1 (5): 361-374
- **Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions** *CELL*
Grubert, F., Zaugg, J. B., Kasowski, M., Ursu, O., Spacek, D. V., Martin, A. R., Greenside, P., Srivas, R., Phanstiel, D. H., Pekowska, A., Heidari, N., Euskirchen, G., Huber, et al
2015; 162 (5): 1051-1065

- **Recurrent somatic mutations in regulatory regions of human cancer genomes.** *Nature genetics*
Melton, C., Reuter, J. A., Spacek, D. V., Snyder, M.
2015; 47 (7): 710-716
- **Comprehensive transcriptome analysis using synthetic long-read sequencing reveals molecular co-association of distant splicing events** *NATURE BIOTECHNOLOGY*
Tilgner, H., Jahanbani, F., Blauwkamp, T., Moshrefi, A., Jaeger, E., Chen, F., Harel, I., Bustamante, C. D., Rasmussen, M., Snyder, M. P.
2015; 33 (7): 736-742
- **Comprehensive transcriptome analysis using synthetic long-read sequencing reveals molecular co-association of distant splicing events.** *Nature biotechnology*
Tilgner, H., Jahanbani, F., Blauwkamp, T., Moshrefi, A., Jaeger, E., Chen, F., Harel, I., Bustamante, C. D., Rasmussen, M., Snyder, M. P.
2015
- **Comparison of the transcriptional landscapes between human and mouse tissues** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Lin, S., Lin, Y., Nery, J. R., Urich, M. A., Breschi, A., Davis, C. A., Dobin, A., Zaleski, C., Beer, M. A., Chapman, W. C., Gingeras, T. R., Ecker, J. R., Snyder, et al
2014; 111 (48): 17224-17229
- **Regulatory analysis of the C. elegans genome with spatiotemporal resolution.** *Nature*
Araya, C. L., Kawli, T., Kundaje, A., Jiang, L., Wu, B., Vafeados, D., Terrell, R., Weissdepp, P., Gevirtzman, L., Mace, D., Niu, W., Boyle, A. P., Xie, et al
2014; 512 (7515): 400-405
- **Comparative analysis of regulatory information and circuits across distant species.** *Nature*
Boyle, A. P., Araya, C. L., Brdlik, C., Cayting, P., Cheng, C., Cheng, Y., Gardner, K., Hillier, L. W., Janette, J., Jiang, L., Kasper, D., Kawli, T., Kheradpour, et al
2014; 512 (7515): 453-456
- **Defining a personal, allele-specific, and single-molecule long-read transcriptome** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Tilgner, H., Grubert, F., Sharon, D., Snyder, M. P.
2014; 111 (27): 9869-9874
- **Clinical interpretation and implications of whole-genome sequencing.** *JAMA : the journal of the American Medical Association*
Dewey, F. E., Grove, M. E., Pan, C., Goldstein, B. A., Bernstein, J. A., Chaib, H., Merker, J. D., Goldfeder, R. L., Enns, G. M., David, S. P., Pakdaman, N., Ormond, K. E., Caleshu, et al
2014; 311 (10): 1035-1045
- **Divergence in a master variator generates distinct phenotypes and transcriptional responses** *GENES & DEVELOPMENT*
Gallagher, J. E., Zheng, W., Rong, X., Miranda, N., Lin, Z., Dunn, B., Zhao, H., Snyder, M. P.
2014; 28 (4): 409-421
- **Integrated systems analysis reveals a molecular network underlying autism spectrum disorders.** *Molecular systems biology*
Li, J., Shi, M., Ma, Z., Zhao, S., Euskirchen, G., Ziskin, J., Urban, A., Hallmayer, J., Snyder, M.
2014; 10: 774-?
- **Principles of regulatory information conservation between mouse and human.** *Nature*
Cheng, Y., Ma, Z., Kim, B. H., Wu, W., Cayting, P., Boyle, A. P., Sundaram, V., Xing, X., Dogan, N., Li, J., Euskirchen, G., Lin, S., Lin, et al
2014; 515 (7527): 371-75
- **Integrated systems analysis reveals a molecular network underlying autism spectrum disorders.** *Molecular systems biology*
Li, J., Shi, M., Ma, Z., Zhao, S., Euskirchen, G., Ziskin, J., Urban, A., Hallmayer, J., Snyder, M.
2014; 10 (12): 774-?
- **Extensive Variation in Chromatin States Across Humans** *SCIENCE*
Kasowski, M., Kyriazopoulou-Panagiotopoulou, S., Grubert, F., Zaugg, J. B., Kundaje, A., Liu, Y., Boyle, A. P., Zhang, Q. C., Zakharia, F., Spacek, D. V., Li, J., Xie, D., Olarerin-George, et al
2013; 342 (6159): 750-752
- **A single-molecule long-read survey of the human transcriptome.** *Nature biotechnology*
Sharon, D., Tilgner, H., Grubert, F., Snyder, M.

2013; 31 (11): 1009-1014

- **Dynamic trans-Acting Factor Colocalization in Human Cells** *CELL*
Xie, D., Boyle, A. P., Wu, L., Zhai, J., Kawli, T., Snyder, M.
2013; 155 (3): 713-724
- **Whole-exome sequencing identifies tetratricopeptide repeat domain 7A (TTC7A) mutations for combined immunodeficiency with intestinal atresias.** *journal of allergy and clinical immunology*
Chen, R., Giliani, S., Lanzi, G., Mias, G. I., Lonardi, S., Dobbs, K., Manis, J., Im, H., Gallagher, J. E., Phanstiel, D. H., Euskirchen, G., Lacroute, P., Bettinger, et al
2013; 132 (3): 656-664 e17
- **Whole-exome sequencing identifies tetratricopeptide repeat domain 7A (TTC7A) mutations for combined immunodeficiency with intestinal atresias** *JOURNAL OF ALLERGY AND CLINICAL IMMUNOLOGY*
Chen, R., Giliani, S., Lanzi, G., Mias, G. I., Lonardi, S., Dobbs, K., Manis, J., Im, H., Gallagher, J. E., Phanstiel, D. H., Euskirchen, G., Lacroute, P., Bettinger, et al
2013; 132 (3): 656-?
- **Systematic functional regulatory assessment of disease-associated variants.** *Proceedings of the National Academy of Sciences of the United States of America*
Karczewski, K. J., Dudley, J. T., Kukurba, K. R., Chen, R., Butte, A. J., Montgomery, S. B., Snyder, M.
2013; 110 (23): 9607-9612
- **Specific plasma autoantibody reactivity in myelodysplastic syndromes.** *Scientific reports*
Mias, G. I., Chen, R., Zhang, Y., Sridhar, K., Sharon, D., Xiao, L., Im, H., Snyder, M. P., Greenberg, P. L.
2013; 3: 3311-?
- **Extensive genetic variation in somatic human tissues** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
O'Huallachain, M., Karczewski, K. J., Weissman, S. M., Urban, A. E., Snyder, M. P.
2012; 109 (44): 18018-18023
- **An integrated encyclopedia of DNA elements in the human genome** *NATURE*
Dunham, I., Kundaje, A., Aldred, S. F., Collins, P. J., Davis, C., Doyle, F., Epstein, C. B., Frietze, S., Harrow, J., Kaul, R., Khatun, J., Lajoie, B. R., Landt, et al
2012; 489 (7414): 57-74
- **Architecture of the human regulatory network derived from ENCODE data** *NATURE*
Gerstein, M. B., Kundaje, A., Hariharan, M., Landt, S. G., Yan, K., Cheng, C., Mu, X. J., Khurana, E., Rozowsky, J., Alexander, R., Min, R., Alves, P., Abyzov, et al
2012; 489 (7414): 91-100
- **Linking disease associations with regulatory information in the human genome** *GENOME RESEARCH*
Schaub, M. A., Boyle, A. P., Kundaje, A., Batzoglou, S., Snyder, M.
2012; 22 (9): 1748-1759
- **Annotation of functional variation in personal genomes using RegulomeDB** *GENOME RESEARCH*
Boyle, A. P., Hong, E. L., Hariharan, M., Cheng, Y., Schaub, M. A., Kasowski, M., Karczewski, K. J., Park, J., Hitz, B. C., Weng, S., Cherry, J. M., Snyder, M.
2012; 22 (9): 1790-1797
- **ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia** *GENOME RESEARCH*
Landt, S. G., Marinov, G. K., Kundaje, A., Kheradpour, P., Pauli, F., Batzoglou, S., Bernstein, B. E., Bickel, P., Brown, J. B., Cayting, P., Chen, Y., DeSalvo, G., Epstein, et al
2012; 22 (9): 1813-1831
- **Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes** *CELL*
Chen, R., Mias, G. I., Li-Pook-Than, J., Jiang, L., Lam, H. Y., Chen, R., Miriami, E., Karczewski, K. J., Hariharan, M., Dewey, F. E., Cheng, Y., Clark, M. J., Im, et al
2012; 148 (6): 1293-1307
- **Detecting and annotating genetic variations using the HugerSeq pipeline** *NATURE BIOTECHNOLOGY*
Lam, H. Y., Pan, C., Clark, M. J., Lacroute, P., Chen, R., Haraksingh, R., O'Huallachain, M., Gerstein, M. B., Kidd, J. M., Bustamante, C. D., Snyder, M.
2012; 30 (3): 226-229
- **Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation** *CELL*

- Li, G., Ruan, X., Auerbach, R. K., Sandhu, K. S., Zheng, M., Wang, P., Poh, H. M., Goh, Y., Lim, J., Zhang, J., Sim, H. S., Peh, S. Q., Mulawadi, et al
2012; 148 (1-2): 84-98
- **Performance comparison of whole-genome sequencing platforms** *NATURE BIOTECHNOLOGY*
Lam, H. Y., Clark, M. J., Chen, R., Chen, R., Natsoulis, G., O'Huallachain, M., Dewey, F. E., Habegger, L., Ashley, E. A., Gerstein, M. B., Butte, A. J., Ji, H. P., Snyder, et al
2012; 30 (1): 78-U118
 - **Dissecting phosphorylation networks: lessons learned from yeast** *EXPERT REVIEW OF PROTEOMICS*
Mok, J., Zhu, X., Snyder, M.
2011; 8 (6): 775-786
 - **Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF** *NATURE*
Iyer, V. R., Horak, C. E., Scafe, C. S., Botstein, D., Snyder, M., Brown, P. O.
2001; 409 (6819): 533-538
 - **Genome-wide effects of social status on DNA methylation in the brain of a cichlid fish, *Astatotilapia burtoni***. *BMC genomics*
Hilliard, A. T., Xie, D., Ma, Z., Snyder, M. P., Fernald, R. D.
2019; 20 (1): 699
 - **Systematic Identification of Host Cell Regulators of *Legionella pneumophila* Pathogenesis Using a Genome-wide CRISPR Screen**. *Cell host & microbe*
Jeng, E. E., Bhadkamkar, V., Ibe, N. U., Gause, H., Jiang, L., Chan, J., Jian, R., Jimenez-Morales, D., Stevenson, E., Krogan, N. J., Swaney, D. L., Snyder, M. P., Mukherjee, et al
2019
 - **Large-Scale Analyses of Human Microbiomes Reveal Thousands of Small, Novel Genes**. *Cell*
Sberro, H., Fremin, B. J., Zlitni, S., Edfors, F., Greenfield, N., Snyder, M. P., Pavlopoulos, G. A., Kyrpides, N. C., Bhatt, A. S.
2019
 - **Simultaneous RNA purification and size selection using on-chip isotachopheresis with an ionic spacer**. *Lab on a chip*
Han, C. M., Catoe, D., Munro, S. A., Khnouf, R., Snyder, M. P., Santiago, J. G., Salit, M. L., Cenik, C.
2019
 - **MISTERMINATE Mechanistically Links Mitochondrial Dysfunction with Proteostasis Failure**. *Molecular cell*
Wu, Z., Tantray, I., Lim, J., Chen, S., Li, Y., Davis, Z., Sitron, C., Dong, J., Gispert, S., Auburger, G., Brandman, O., Bi, X., Snyder, et al
2019
 - **Matrix stiffness induces a tumorigenic phenotype in mammary epithelium through changes in chromatin accessibility**. *Nature biomedical engineering*
Stowers, R. S., Shcherbina, A., Israeli, J., Gruber, J. J., Chang, J., Nam, S., Rabiee, A., Teruel, M. N., Snyder, M. P., Kundaje, A., Chaudhuri, O.
2019
 - **Long-Read Sequencing - A Powerful Toll in Viral Transcriptome Research** *TRENDS IN MICROBIOLOGY*
Boldogkoi, Z., Moldovan, N., Balazs, Z., Snyder, M., Tombacz, D.
2019; 27 (7): 578-92
 - **Comment on 'AIRE-deficient patients harbor unique high-affinity disease-ameliorating autoantibodies'**. *eLife*
Landegren, N., Rosen, L. B., Freyhult, E., Eriksson, D., Fall, T., Smith, G., Ferre, E. M., Brodin, P., Sharon, D., Snyder, M., Lionakis, M., Anderson, M., Kampe, et al
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