Stanford

# Michael Snyder

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

### CONTACT INFORMATION

- **Alternate Contact**

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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

- Understanding and Diagnosing Allergic Disease in Twins, Recruiting

# Teaching

## STANFORD ADVISEES

**Doctoral Dissertation Reader (AC)**

Thomas Ward

**Postdoctoral Faculty Sponsor**

Gireesh Bogu, Alessandra Breschi, Songjie Chen, Kai Fu, Takaaki Furihata, Ariel Ganz, Daniel Hornburg, Aaron Horning, Chao Jiang, Brian Johnson, Ryan Kellogg, Samuel Lancaster, Brittany Lee, Hayan Lee, Xiao Li, Liang Liang, Petra Mamic, David Marciano, Ahmed Metwally, Tejaswini Mishra, Emma Monte, Michael Nshanian, Jeniffer Quijada, Ashwin Ram, 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

### GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

## Publications

### PUBLICATIONS

- **Gene-Environment Interaction in the Era of Precision Medicine.** *Cell*
  Li, J., Li, X., Zhang, S., Snyder, M.
  2019; 177 (1): 38–44

- **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 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

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