



Michael Snyder, Ph.D.

Stanford W. Ascherman Professor of Genetics

CONTACT INFORMATION

- **Alternate Contact**

Shirley Ma - Executive Assistant

Email shirley.ma@stanford.edu

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, Wu Tsai Human Performance Alliance
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Medicine Children's Health Center for IBD and Celiac Disease
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Former Chair, Dept. of Genetics, (2009-2024)
- Director, Center for Genomics and Personalized Medicine, (2009- present)

HONORS AND AWARDS

- Pioneer Award, Precision Medicine World Conference (2025)
- George Beadle Award, GSA (2019)
- Elected Member, American Academy of Science (2015)
- Stanford B. Ascherman Professor, Stanford (2011)

- Pioneer Award, Human Proteome Organization (2009)
- CT Medal of Science, Connection Academy of Science (2007)
- Pew Scholar Award, Pew Foundation (1987-1991)

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
- The 28 Day Challenge, Not Recruiting

- The Lasting Change Study, Not Recruiting
- Understanding and Diagnosing Allergic Disease in Twins, Not Recruiting

Teaching

COURSES

2024-25

- AI for Beginners: GENE 231 (Spr)
- Cloud Computing for Biology and Healthcare: BIOMEDIN 222, CS 273C, GENE 222 (Spr)
- Genomics: GENE 211 (Win)
- Healthcare Entrepreneurship: GENE 134, GENE 234 (Aut)
- How We Age: GENE 229 (Win)

2023-24

- AI for Beginners: GENE 231 (Win)
- Aging: Science and Technology for Longevity: GENE 223 (Spr)
- Cloud Computing for Biology and Healthcare: BIOMEDIN 222, CS 273C, GENE 222 (Spr)
- Genomics: GENE 211 (Win)
- Healthcare Venture Capital: GENE 225 (Aut)

2022-23

- AI, Genes and Ethics: GENE 213 (Aut)
- Aging: Science and Technology for Longevity: GENE 223 (Win)
- Chronic Disease I: Applications of Novel Advances in Biology and Biotechnology: BIO 109A (Win)
- Chronic Disease II: Applications of Advances in Precision Medicine and Digital Health Technologies: BIO 109B (Spr)
- Cloud Computing for Biology and Healthcare: BIOMEDIN 222, CS 273C, GENE 222 (Spr)
- Engineering Wellness: BIOS 237 (Spr)
- Genomics: GENE 211 (Win)
- LONGEVITY VENTURE CAPITAL: GENE 226 (Spr)
- Stanford SKY Campus Happiness Retreat: BIOS 215 (Aut)

2021-22

- Cloud Computing for Biology and Healthcare: BIOMEDIN 222, CS 273C, GENE 222 (Spr)
- Genomics: GENE 211 (Win)
- Healthcare Venture Capital: GENE 225 (Spr)
- How We Age: GENE 229 (Win)
- LONGEVITY VENTURE CAPITAL: GENE 226 (Aut)
- Stanford SKY Campus Happiness Retreat: BIOS 215 (Aut, Spr)

STANFORD ADVISEES

Med Scholar Project Advisor

Isha Mehrotra

Doctoral Dissertation Reader (AC)

Elliot Hershberg, Michael Hittle, Eric Sun, Ronghao Zhou

Postdoctoral Faculty Sponsor

Abdalla Ahmed, Mohan Babu, Nasim Bararpour, John Cao, Varuna Chander, Faye Chleilat, Shubham Gupta, Brady Hislop, Linda Lan, Xiangping Lin, Caleb Mayer, Curtis McGinity, Pardis Miri, Daniel Panyard, Majid Rodgar, M. Reza Sailani, Mahasish Shome, Morgan Smith, Mingming Tong, Shannon White, Yue Wu, Yizhou Zhu

Doctoral Dissertation Advisor (AC)

Martin Acosta Parra, Siranush Babakhanova, Naomi Hunter, Jessica Kain, Ziv Lautman, Aubrey Roberts

Doctoral Dissertation Co-Advisor (AC)

Ben Ehlert

Doctoral (Program)

Alexander Johansen

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Data Science (Phd Program)
- Genetics (Phd Program)
- Immunology (Phd Program)

Publications

PUBLICATIONS

- **Short-chain fatty acid metabolites propionate and butyrate are unique epigenetic regulatory elements linking diet, metabolism and gene expression.** *Nature metabolism*
Nshanian, M., Gruber, J. J., Geller, B. S., Chleilat, F., Lancaster, S. M., White, S. M., Alexandrova, L., Camarillo, J. M., Kelleher, N. L., Zhao, Y., Snyder, M. P.
2025
- **Impact of digital health interventions on glycemic control and weight management.** *NPJ digital medicine*
Veluvali, A., Dehghani Zahedani, A., Hosseinian, A., Aghaeepour, N., McLaughlin, T., Woodward, M., DiTullio, A., Hashemi, N., Snyder, M. P.
2025; 8 (1): 20
- **Prediction of metabolic subphenotypes of type 2 diabetes via continuous glucose monitoring and machine learning.** *Nature biomedical engineering*
Metwally, A. A., Perelman, D., Park, H., Wu, Y., Jha, A., Sharp, S., Celli, A., Ayhan, E., Abbasi, F., Gloyn, A. L., McLaughlin, T., Snyder, M. P.
2024
- **Longitudinal urine metabolic profiling and gestational age prediction in human pregnancy.** *Briefings in bioinformatics*
Shen, X., Chen, S., Liang, L., Avina, M., Zackriah, H., Jelliffe-Pawlowski, L., Rand, L., Snyder, M. P.
2024; 26 (1)
- **Multomic analysis of familial adenomatous polyposis reveals molecular pathways associated with early tumorigenesis.** *Nature cancer*
Esplin, E. D., Hanson, C., Wu, S., Horning, A. M., Barapour, N., Nevins, S. A., Jiang, L., Contrepolis, K., Lee, H., Guha, T. K., Hu, Z., Laquindanum, R., Mills, et al
2024
- **Global loss of promoter-enhancer connectivity and rebalancing of gene expression during early colorectal cancer carcinogenesis.** *Nature cancer*
Zhu, Y., Lee, H., White, S., Weimer, A. K., Monte, E., Horning, A., Nevins, S. A., Esplin, E. D., Paul, K., Krieger, G., Shipony, Z., Chiu, R., Laquindanum, et al
2024
- **Nonlinear dynamics of multi-omics profiles during human aging.** *Nature aging*

Shen, X., Wang, C., Zhou, X., Zhou, W., Hornburg, D., Wu, S., Snyder, M. P.
2024

- **Post-GWAS multiomic functional investigation of the TNIP1 locus in Alzheimer's disease highlights a potential role for GPX3.** *Alzheimer's & dementia : the journal of the Alzheimer's Association*
Panyard, D. J., Reus, L. M., Ali, M., Liu, J., Deming, Y. K., Lu, Q., Kollmorgen, G., Carboni, M., Wild, N., Visser, P. J., Bertram, L., Zetterberg, H., Blennow, et al
2024
- **Temporal dynamics of the multi-omic response to endurance exercise training.** *Nature*
2024; 629 (8010): 174-183
- **Longitudinal profiling of the microbiome at four body sites reveals core stability and individualized dynamics during health and disease.** *Cell host & microbe*
Zhou, X., Shen, X., Johnson, J. S., Spakowicz, D. J., Agnello, M., Zhou, W., Avina, M., Honkala, A., Chleilat, F., Chen, S. J., Cha, K., Leopold, S., Zhu, et al
2024
- **The importance, challenges, and possible solutions for sharing proteomics data while safeguarding individuals' privacy.** *Molecular & cellular proteomics : MCP*
Shome, M., MacKenzie, T. M., Subbareddy, S. R., Snyder, M. P.
2024: 100731
- **Digital health application integrating wearable data and behavioral patterns improves metabolic health.** *NPJ digital medicine*
Zahedani, A. D., Veluvali, A., McLaughlin, T., Aghaeepour, N., Hosseini, A., Agarwal, S., Ruan, J., Tripathi, S., Woodward, M., Hashemi, N., Snyder, M.
2023; 6 (1): 216
- **Wearable Devices: Implications for Precision Medicine and the Future of Health Care.** *Annual review of medicine*
Babu, M., Lautman, Z., Lin, X., Sobota, M. H., Snyder, M. P.
2023
- **Dietary fiber deficiency in individuals with metabolic syndrome: a review.** *Current opinion in clinical nutrition and metabolic care*
Veluvali, A., Snyder, M.
2023
- **Dynamic lipidome alterations associated with human health, disease and ageing.** *Nature metabolism*
Hornburg, D., Wu, S., Moqri, M., Zhou, X., Contrepolis, K., Bararpour, N., Traber, G. M., Su, B., Metwally, A. A., Avina, M., Zhou, W., Ubellacker, J. M., Mishra, et al
2023
- **Biomarkers of aging for the identification and evaluation of longevity interventions.** *Cell*
Moqri, M., Herzog, C., Poganik, J. R., Biomarkers of Aging Consortium, Justice, J., Belsky, D. W., Higgins-Chen, A., Moskalev, A., Fuellen, G., Cohen, A. A., Bautmans, I., Widschwendter, M., Ding, J., et al
2023; 186 (18): 3758-3775
- **Advances and prospects for the Human BioMolecular Atlas Program (HuBMAP).** *Nature cell biology*
Jain, S., Pei, L., Spraggins, J. M., Angelo, M., Carson, J. P., Gehlenborg, N., Ginty, F., Gonçalves, J. P., Hagood, J. S., Hickey, J. W., Kelleher, N. L., Laurent, L. C., Lin, et al
2023
- **Organization of the human intestine at single-cell resolution.** *Nature*
Hickey, J. W., Becker, W. R., Nevins, S. A., Horning, A., Perez, A. E., Zhu, C., Zhu, B., Wei, B., Chiu, R., Chen, D. C., Cotter, D. L., Esplin, E. D., Weimer, et al
2023; 619 (7970): 572-584
- **Dynamic monitoring of thousands of biochemical analytes using microsampling** *NATURE BIOMEDICAL ENGINEERING*
Kellogg, R., Snyder, M.
2023
- **Multi-omics microsampling for the profiling of lifestyle-associated changes in health.** *Nature biomedical engineering*

Shen, X., Kellogg, R., Panyard, D. J., Bararpour, N., Castillo, K. E., Lee-McMullen, B., Delfarah, A., Ubellacker, J., Ahadi, S., Rosenberg-Hasson, Y., Ganz, A., Contrepolis, K., Michael, et al
2023

- **Recurrent repeat expansions in human cancer genomes.** *Nature*
Erwin, G. S., Gursoy, G., Al-Abri, R., Suriyaprakash, A., Dolzhenko, E., Zhu, K., Hoerner, C. R., White, S. M., Ramirez, L., Vadlakonda, A., Vadlakonda, A., von Kraut, K., Park, et al
2022
- **Distinct factors associated with short-term and long-term weight loss induced by low-fat or low-carbohydrate diet intervention.** *Cell reports. Medicine*
Li, X., Perelman, D., Leong, A. K., Fragiadakis, G., Gardner, C. D., Snyder, M. P.
2022: 100870
- **Longitudinally tracking personal physiomes for precision management of childhood epilepsy.** *PLOS digital health*
Jiang, P., Gao, F., Liu, S., Zhang, S., Zhang, X., Xia, Z., Zhang, W., Jiang, T., Zhu, J. L., Zhang, Z., Shu, Q., Snyder, M., Li, et al
2022; 1 (12): e0000161
- **Identification of non-coding silencer elements and their regulation of gene expression.** *Nature reviews. Molecular cell biology*
Pang, B., van Weerd, J. H., Hamoen, F. L., Snyder, M. P.
2022
- **Performance effectiveness of vital parameter combinations for early warning of sepsis-an exhaustive study using machine learning** *JAMIA OPEN*
Rangan, E., Pathinarupothi, R., Anand, K. S., Snyder, M. P.
2022; 5 (4): ooac080
- **Systems analysis of de novo mutations in congenital heart diseases identified a protein network in the hypoplastic left heart syndrome.** *Cell systems*
Wang, Y. J., Zhang, X., Lam, C. K., Guo, H., Wang, C., Zhang, S., Wu, J. C., Snyder, M., Li, J.
2022
- **Chimpanzee and pig-tailed macaque iPSCs: Improved culture and generation of primate cross-species embryos.** *Cell reports*
Roodgar, M., Suchy, F. P., Nguyen, L. H., Bajpai, V. K., Sinha, R., Vilches-Moure, J. G., Van Bortle, K., Bhadury, J., Metwally, A., Jiang, L., Jian, R., Chiang, R., Oikonomopoulos, et al
2022; 40 (9): 111264
- **massDatabase: utilities for the operation of the public compound and pathway database.** *Bioinformatics (Oxford, England)*
Shen, X., Wang, C., Snyder, M. P.
2022
- **TidyMass an object-oriented reproducible analysis framework for LC-MS data.** *Nature communications*
Shen, X., Yan, H., Wang, C., Gao, P., Johnson, C. H., Snyder, M. P.
2022; 13 (1): 4365
- **Single-cell analyses define a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer.** *Nature genetics*
Becker, W. R., Nevins, S. A., Chen, D. C., Chiu, R., Horning, A. M., Guha, T. K., Laquindanum, R., Mills, M., Chaib, H., Ladabaum, U., Longacre, T., Shen, J., Esplin, et al
2022
- **A genome-wide atlas of recurrent repeat expansions in human cancer genomes**
Erwin, G. S., Gursoy, G., Al-Abri, R., Hoerner, C., Dolzhenko, E., Eberle, M., Fan, A., Leppert, J., Gerstein, M., Snyder, M. P.
AMER ASSOC CANCER RESEARCH.2022
- **Precision environmental health monitoring by longitudinal exposome and multi-omics profiling.** *Genome research*
Gao, P., Shen, X., Zhang, X., Jiang, C., Zhang, S., Zhou, X., Schüssler-Fiorenza Rose, S. M., Snyder, M.
2022
- **Multomic analysis reveals cell-type-specific molecular determinants of COVID-19 severity.** *Cell systems*

- Zhang, S., Cooper-Knock, J., Weimer, A. K., Shi, M., Kozhaya, L., Unutmaz, D., Harvey, C., Julian, T. H., Furini, S., Frullanti, E., Fava, F., Renieri, A., Gao, et al
2022
- **Global, distinctive, and personal changes in molecular and microbial profiles by specific fibers in humans.** *Cell host & microbe*
Lancaster, S. M., Lee-McMullen, B., Abbott, C. W., Quijada, J. V., Hornburg, D., Park, H., Perelman, D., Peterson, D. J., Tang, M., Robinson, A., Ahadi, S., Contrepois, K., Hung, et al
2022
 - **Adverse childhood experiences, diabetes and associated conditions, preventive care practices and healthcare access: A population-based study.** *Preventive medicine*
Rose, S. M., Slavich, G. M., Snyder, M. P.
2022: 107044
 - **Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis.** *Neuron*
Zhang, S., Cooper-Knock, J., Weimer, A. K., Shi, M., Moll, T., Marshall, J. N., Harvey, C., Nezhad, H. G., Franklin, J., Souza, C. D., Ning, K., Wang, C., Li, et al
1800
 - **Phenotypic characteristics of peripheral immune cells of Myalgic encephalomyelitis/chronic fatigue syndrome via transmission electron microscopy: A pilot study.** *PloS one*
Jahanbani, F., Maynard, R. D., Sing, J. C., Jahanbani, S., Perrino, J. J., Spacek, D. V., Davis, R. W., Snyder, M. P.
2022; 17 (8): e0272703
 - **Real-time alerting system for COVID-19 and other stress events using wearable data.** *Nature medicine*
Alavi, A., Bogu, G. K., Wang, M., Rangan, E. S., Brooks, A. W., Wang, Q., Higgs, E., Celli, A., Mishra, T., Metwally, A. A., Cha, K., Knowles, P., Alavi, et al
2021
 - **A scalable, secure, and interoperable platform for deep data-driven health management.** *Nature communications*
Bahmani, A., Alavi, A., Buerger, T., Upadhyayula, S., Wang, Q., Ananthakrishnan, S. K., Alavi, A., Celis, D., Gillespie, D., Young, G., Xing, Z., Nguyen, M. H., Haque, et al
2021; 12 (1): 5757
 - **Chromatin accessibility associates with protein-RNA correlation in human cancer.** *Nature communications*
Sanghi, A., Gruber, J. J., Metwally, A., Jiang, L., Reynolds, W., Sunwoo, J., Orloff, L., Chang, H. Y., Kasowski, M., Snyder, M. P.
2021; 12 (1): 5732
 - **metID: a R package for automatable compound annotation for LC-MS-based data.** *Bioinformatics (Oxford, England)*
Shen, X., Wu, S., Liang, L., Chen, S., Contrepois, K., Zhu, Z., Snyder, M.
2021
 - **Five-year pediatric use of a digital wearable fitness device: lessons from a pilot case study.** *JAMIA open*
Butte, K. D., Bahmani, A., Butte, A. J., Li, X., Snyder, M. P.
2021; 4 (3): ooab054
 - **Wearable sensors enable personalized predictions of clinical laboratory measurements.** *Nature medicine*
Dunn, J., Kidzinski, L., Runge, R., Witt, D., Hicks, J. L., Schussler-Fiorenza Rose, S. M., Li, X., Bahmani, A., Delp, S. L., Hastie, T., Snyder, M. P.
2021
 - **Pre-symptomatic detection of COVID-19 from smartwatch data.** *Nature biomedical engineering*
Mishra, T., Wang, M., Metwally, A. A., Bogu, G. K., Brooks, A. W., Bahmani, A., Alavi, A., Celli, A., Higgs, E., Dagan-Rosenfeld, O., Fay, B., Kirkpatrick, S., Kellogg, et al
2020
 - **An integrative ENCODE resource for cancer genomics.** *Nature communications*
Zhang, J., Lee, D., Dhiman, V., Jiang, P., Xu, J., McGillivray, P., Yang, H., Liu, J., Meyerson, W., Clarke, D., Gu, M., Li, S., Lou, et al
2020; 11 (1): 3696
 - **Perspectives on ENCODE.** *Nature*

- ENCODE Project Consortium, Snyder, M. P., Gingeras, T. R., Moore, J. E., Weng, Z., Gerstein, M. B., Ren, B., Hardison, R. C., Stamatoyannopoulos, J. A., Graveley, B. R., Feingold, E. A., Pazin, M. J., Pagan, M., et al
2020; 583 (7818): 693–98
- **Metabolic Dynamics and Prediction of Gestational Age and Time to Delivery in Pregnant Women.** *Cell*
Liang, L., Rasmussen, M. H., Piening, B., Shen, X., Chen, S., Rost, H., Snyder, J. K., Tibshirani, R., Skotte, L., Lee, N. C., Contrepois, K., Feenstra, B., Zackriah, et al
2020; 181 (7): 1680
 - **Systematic identification of silencers in human cells.** *Nature genetics*
Pang, B., Snyder, M. P.
2020
 - **Deep Characterization of the Human Antibody Response to Natural Infection Using Longitudinal Immune Repertoire Sequencing.** *Molecular & cellular proteomics : MCP*
Mitsunaga, E. M., Snyder, M. P.
2020; 19 (2): 278-293
 - **Molecular Choreography of Acute Exercise.** *Cell*
Contrepois, K. n., Wu, S. n., Moneghetti, K. J., Hornburg, D. n., Ahadi, S. n., Tsai, M. S., Metwally, A. A., Wei, E. n., Lee-McMullen, B. n., Quijada, J. V., Chen, S. n., Christle, J. W., Ellenberger, et al
2020; 181 (5): 1112–30.e16
 - **Personal aging markers and ageotypes revealed by deep longitudinal profiling.** *Nature medicine*
Ahadi, S., Zhou, W., Schussler-Fiorenza Rose, S. M., Sailani, M. R., Contrepois, K., Avina, M., Ashland, M., Brunet, A., Snyder, M.
2020; 26 (1): 83–90
 - **A Quantitative Proteome Map of the Human Body.** *Cell*
Jiang, L. n., Wang, M. n., Lin, S. n., Jian, R. n., Li, X. n., Chan, J. n., Dong, G. n., Fang, H. n., Robinson, A. E., Snyder, M. P.
2020
 - **Candidate variants in TUB are associated with familial tremor.** *PLoS genetics*
Sailani, M. R., Jahanbani, F. n., Abbott, C. W., Lee, H. n., Zia, A. n., Rego, S. n., Winkelmann, J. n., Hopfner, F. n., Khan, T. N., Katsanis, N. n., Müller, S. H., Berg, D. n., Lyman, et al
2020; 16 (9): e1009010
 - **Landscape of cohesin-mediated chromatin loops in the human genome.** *Nature*
Grubert, F. n., Srivas, R. n., Spacek, D. V., Kasowski, M. n., Ruiz-Velasco, M. n., Sinnott-Armstrong, N. n., Greenside, P. n., Narasimha, A. n., Liu, Q. n., Geller, B. n., Sanghi, A. n., Kulik, M. n., Sa, et al
2020; 583 (7818): 737–43
 - **Expanded encyclopaedias of DNA elements in the human and mouse genomes.** *Nature*
Moore, J. E., Purcaro, M. J., Pratt, H. E., Epstein, C. B., Shores, N. n., Adrian, J. n., Kawli, T. n., Davis, C. A., Dobin, A. n., Kaul, R. n., Halow, J. n., Van Nostrand, E. L., Freese, et al
2020; 583 (7818): 699–710
 - **Deep longitudinal multiomics profiling reveals two biological seasonal patterns in California.** *Nature communications*
Sailani, M. R., Metwally, A. A., Zhou, W. n., Rose, S. M., Ahadi, S. n., Contrepois, K. n., Mishra, T. n., Zhang, M. J., Kidziński, Ł. n., Chu, T. J., Snyder, M. P.
2020; 11 (1): 4933
 - **The human body at cellular resolution: the NIH Human Biomolecular Atlas Program** *NATURE*
Snyder, M. P., Lin, S., Posgai, A., Atkinson, M., Regev, A., Rood, J., Rozenblatt-Rosen, O., Gaffney, L., Hupalowska, A., Satija, R., Gehlenborg, N., Shendure, J., Laskin, et al
2019; 574 (7777): 187–92
 - **Big data and health.** *The Lancet. Digital health*
Snyder, M., Zhou, W.
2019; 1 (6): e252-e254
 - **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., Contrepolis, 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., Contrepolis, 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., Contrepolis, K. n., Moneghetti, K. J., Zhou, W. n., Mishra, T. n., Mataraso, S. n., Dagan-Rosenfeld, O. n., Ganz, A. B., Dunn, J. n., Hornburg, D. n., Rego, S. n., Perelman, D. n., Ahadi, et al
2019; 25 (5): 792–804
 - **Chromatin Remodeling in Response to BRCA2-Crisis.** *Cell reports*
Gruber, J. J., Chen, J. n., Geller, B. n., Jäger, N. n., Lipchik, A. M., Wang, G. n., 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. n., Green, S. J., Gur, R. C., Lin, L. n., Macias, B. R., McKenna, M. J., Meydan, C. n., Mishra, T. n., Nasrini, J. n., 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. n., Haanpää, M. K., Gruber, J. J., Jäger, N. 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. n., Contrepolis, K. n., Röst, H. n., Gu Urban, G. J., Mishra, T. n., Hanson, B. M., Bautista, E. J., Leopold, S. n., Yeh, C. Y., Spakowicz, D. n., Banerjee, I. n., 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. n., Spacek, D. n., Hess, G. T., Shamim, M. S., Machol, I. n., 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
- **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
- **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
- **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., Ulrich, 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
- **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): 371-5
- **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-?
- **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., Fietze, 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 HugeSeq 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
- **Embracing Interpersonal Variability of Microbiome in Precision Medicine** *PHENOMICS*
Zhou, X., Chen, X., Davis, M. M., Snyder, M. P.
2025

- **Publisher Correction: The ENCODE Imputation Challenge: a critical assessment of methods for cross-cell type imputation of epigenomic profiles.** *Genome biology*
Schreiber, J. M., Boix, C. A., Wook Lee, J., Li, H., Guan, Y., Chang, C. C., Chang, J. C., Hawkins-Hooker, A., Schölkopf, B., Schweikert, G., Carulla, M. R., Canakoglu, A., Guzzo, et al
2025; 26 (1): 31
- **Exposomics: a review of methodologies, applications, and future directions in molecular medicine.** *EMBO molecular medicine*
Wan, M., Simonin, E. M., Johnson, M. M., Zhang, X., Lin, X., Gao, P., Patel, C. J., Yousuf, A., Snyder, M. P., Hong, X., Wang, X., Sampath, V., Nadeau, et al
2025
- **Author Correction: Global loss of promoter-enhancer connectivity and rebalancing of gene expression during early colorectal cancer carcinogenesis.** *Nature cancer*
Zhu, Y., Lee, H., White, S., Weimer, A. K., Monte, E., Horning, A., Nevins, S. A., Esplin, E. D., Paul, K., Krieger, G., Shipony, Z., Chiu, R., Laquindanum, et al
2025
- **The 40S ribosomal subunit recycling complex modulates mitochondrial dynamics and endoplasmic reticulum - mitochondria tethering at mitochondrial fission/fusion hotspots.** *Nature communications*
Tahmasebinia, F., Tang, Y., Tang, R., Zhang, Y., Bonderer, W., de Oliveira, M., Laboret, B., Chen, S., Jian, R., Jiang, L., Snyder, M., Chen, C. H., Shen, et al
2025; 16 (1): 1021
- **Author Correction: Considerations in the search for epistasis.** *Genome biology*
Balvert, M., Cooper-Knock, J., Stamp, J., Byrne, R. P., Mourragui, S., van Gils, J., Benonisdottir, S., Schlüter, J., Kenna, K., Abeln, S., Iacoangeli, A., Daub, J. T., Browning, et al
2025; 26 (1): 12
- **Evaluation of a biomarker for amyotrophic lateral sclerosis derived from a hypomethylated DNA signature of human motor neurons.** *BMC medical genomics*
Harvey, C., Nowak, A., Zhang, S., Moll, T., Weimer, A. K., Barcons, A. M., Souza, C. D., Ferraiuolo, L., Kenna, K., Zaitlen, N., Caggiano, C., Shaw, P. J., Snyder, et al
2025; 18 (1): 10
- **Prevalence of Adverse Childhood Experience Exposure by Disability Status.** *JAMA health forum*
Schussler-Fiorenza Rose, S. M., Rehkopf, D. H., Snyder, M. P., Slavich, G. M.
2025; 6 (1): e244881
- **Commentary: Molecular responses in pig heart to human xenotransplantation unveiled by longitudinal multi-omic profiling.** *Clinical and translational medicine*
Keating, B. J., Schmauch, E., Snyder, M. P., Motter, J. D., Piening, B. D.
2025; 15 (1): e70132
- **Dynamic human gut microbiome and immune shifts during an immersive psychosocial intervention program.** *Brain, behavior, and immunity*
Zhou, X., Ganz, A. B., Rayner, A., Cheng, T. Y., Oba, H., Rolnik, B., Lancaster, S., Lu, X., Li, Y., Johnson, J. S., Hoyd, R., Spakowicz, D. J., Slavich, et al
2024
- **Evaluation of a biomarker for amyotrophic lateral sclerosis derived from a hypomethylated DNA signature of human motor neurons.** *Research square*
Harvey, C., Nowak, A., Zhang, S., Moll, T., Weimer, A. K., Barcons, A. M., Dos Santos Souza, C., Ferraiuolo, L., Kenna, K., Zaitlen, N., Caggiano, C., Shaw, P. J., Snyder, et al
2024
- **Considerations in the search for epistasis.** *Genome biology*
Balvert, M., Cooper-Knock, J., Stamp, J., Byrne, R. P., Mourragui, S., van Gils, J., Benonisdottir, S., Schlüter, J., Kenna, K., Abeln, S., Iacoangeli, A., Daub, J. T., Browning, et al
2024; 25 (1): 296
- **Modeling gene interactions in polygenic prediction via geometric deep learning.** *Genome research*
Li, H., Zeng, J., Snyder, M. P., Zhang, S.

2024

- **IMPLICATION OF COMPLEX STRUCTURAL GENOME VARIATION IN THE GENETIC ARCHITECTURE OF NEUROPSYCHIATRIC DISORDERS: INSIGHTS FROM HUMAN POPULATION ANALYSIS AND FROM POSTMORTEM BRAINS OF INDIVIDUALS WITH PSYCHIATRIC DISORDERS**
Zhou, B., Arthur, J., Guo, H., Kim, T., Huang, Y., Pattni, R., Song, G., Palejev, D., Dohna, H., Roussos, P., Kundaje, A., Hallmayer, J., Snyder, et al
ELSEVIER.2024: 93
- **LONG-READ RNA ISOFORM MAP OF THE HUMAN BRAIN (ISOHUB)**
Lin, X., Hadas, Y., Hadjimichael, E., Li, L., Monte, E., Koornstra, E., Shieh, A., van Bakel, H., Snyder, M., Hallmayer, J., Wang, X., Liu, C., Urban, et al
ELSEVIER.2024: 86
- **Corrigendum to "Effects of an immersive psychosocial training program on depression and well-being: A randomized clinical trial" [J. Psychiatr. Res. 150 (2022) 292-299].** *Journal of psychiatric research*
Ganz, A. B., Rolnik, B., Chakraborty, M., Wilson, J., Tau, C., Sharp, M., Reber, D., Slavich, G. M., Snyder, M. P.
2024; 179: 163-166
- **Challenges and recommendations for the translation of biomarkers of aging.** *Nature aging*
Herzog, C. M., Goeminne, L. J., Poganik, J. R., Barzilai, N., Belsky, D. W., Betts-LaCroix, J., Chen, B. H., Chen, M., Cohen, A. A., Cummings, S. R., Fedichev, P. O., Ferrucci, L., Fleming, et al
2024
- **Interindividual Variability in Postprandial Plasma Fructose Patterns in Adults.** *Nutrients*
Gladding, M., Shen, X., Snyder, M. P., Havel, P. J., Adams, S. H.
2024; 16 (18)
- **Mapping spatial organization and genetic cell-state regulators to target immune evasion in ovarian cancer.** *Nature immunology*
Yeh, C. Y., Aguirre, K., Laveroni, O., Kim, S., Wang, A., Liang, B., Zhang, X., Han, L. M., Valbuena, R., Bassik, M. C., Kim, Y. M., Plevritis, S. K., Snyder, et al
2024
- **PRC2-AgeIndex as a universal biomarker of aging and rejuvenation.** *Nature communications*
Moqri, M., Cipriano, A., Simpson, D. J., Rasouli, S., Murty, T., de Jong, T. A., Nachun, D., de Sena Brandine, G., Ying, K., Tarkhov, A., Aberg, K. A., van den Oord, E., Zhou, et al
2024; 15 (1): 5956
- **Glycan clock of ageing-analytical precision and time-dependent inter- and i-individual variability.** *GeroScience*
Rapčan, B., Song, M., Frkatović-Hodžić, A., Pribić, T., Vuk, J., Beletić, A., Hanić, M., Jurić, J., Tominac, P., Milas, J., Ivić, V., Viland, S., Bonet, et al
2024
- **Psychogenic Aging: A Novel Prospect to Integrate Psychobiological Hallmarks of Aging.** *Translational psychiatry*
Faria, M., Ganz, A., Galkin, F., Zhavoronkov, A., Snyder, M.
2024; 14 (1): 226
- **Evolution of diapause in the African turquoise killifish by remodeling the ancient gene regulatory landscape.** *Cell*
Singh, P. P., Reeves, G. A., Contrepois, K., Papsdorf, K., Miklas, J. W., Ellenberger, M., Hu, C. K., Snyder, M. P., Brunet, A.
2024
- **Genome-wide Cas9-mediated screening of essential non-coding regulatory elements via libraries of paired single-guide RNAs.** *Nature biomedical engineering*
Li, Y., Tan, M., Akkari-Henic, A., Zhang, L., Kip, M., Sun, S., Sepers, J. J., Xu, N., Ariyurek, Y., Kloet, S. L., Davis, R. P., Mikkers, H., Gruber, et al
2024
- **Integrative multi-omics profiling in human decedents receiving pig heart xenografts.** *Nature medicine*
Schmauch, E., Piening, B., Mohebnasab, M., Xia, B., Zhu, C., Stern, J., Zhang, W., Dowdell, A. K., Kim, J. I., Andrijevic, D., Khalil, K., Jaffe, I. S., Loza, et al
2024
- **Deconvolution of polygenic risk score in single cells unravels cellular and molecular heterogeneity of complex human diseases.** *bioRxiv : the preprint server for biology*
Zhang, S., Shu, H., Zhou, J., Rubin-Sigler, J., Yang, X., Liu, Y., Cooper-Knock, J., Monte, E., Zhu, C., Tu, S., Li, H., Tong, M., Ecker, et al

2024

- **Personalized transcriptome signatures in a cardiomyopathy stem cell biobank.** *bioRxiv : the preprint server for biology*
Monte, E., Furihata, T., Wang, G., Perea-Gil, I., Wei, E., Chaib, H., Nair, R., Guevara, J. V., Mares, R., Cheng, X., Zhuge, Y., Black, K., Serrano, et al
2024
- **The impact of exercise on gene regulation in association with complex trait genetics.** *Nature communications*
Vetr, N. G., Gay, N. R., MoTrPAC Study Group, Montgomery, S. B., Adkins, J. N., Albertson, B. G., Amar, D., Amper, M. A., Armenteros, J. J., Ashley, E., Avila-Pacheco, J., Bae, D., Balci, A. T., et al
2024; 15 (1): 3346
- **Sexual dimorphism and the multi-omic response to exercise training in rat subcutaneous white adipose tissue.** *Nature metabolism*
Many, G. M., Sanford, J. A., Sagendorf, T. J., Hou, Z., Nigro, P., Whytock, K. L., Amar, D., Caputo, T., Gay, N. R., Gaul, D. A., Hirshman, M. F., Jimenez-Morales, D., Lindholm, et al
2024
- **Molecular adaptations in response to exercise training are associated with tissue-specific transcriptomic and epigenomic signatures.** *Cell genomics*
Nair, V. D., Pincas, H., Smith, G. R., Zaslavsky, E., Ge, Y., Amper, M. A., Vasoya, M., Chikina, M., Sun, Y., Raja, A. N., Mao, W., Gay, N. R., Esser, et al
2024: 100421
- **Molecular Transducers of Physical Activity Consortium (MoTrPAC): Human Studies Design and Protocol.** *Journal of applied physiology (Bethesda, Md. : 1985)*
Group, M. R., Jakicic, J. M., Kohrt, W. M., Houmard, J. A., Miller, M. E., Radom-Aizik, S., Rasmussen, B. B., Ravussin, E., Serra, M., Stowe, C. L., Trappe, S., AbouAssi, H., Adkins, et al
2024
- **The mitochondrial multi-omic response to exercise training across rat tissues.** *Cell metabolism*
Amar, D., Gay, N. R., Jimenez-Morales, D., Jean Beltran, P. M., Ramaker, M. E., Raja, A. N., Zhao, B., Sun, Y., Marwaha, S., Gaul, D. A., Hershman, S. G., Ferrasse, A., Xia, et al
2024
- **Vaginal microbiomes show ethnic evolutionary dynamics and positive selection of Lactobacillus adhesins driven by a long-term niche-specific process.** *Cell reports*
Wei, X., Tsai, M., Liang, L., Jiang, L., Hung, C., Jelliffe-Pawlowski, L., Rand, L., Snyder, M., Jiang, C.
2024; 43 (4): 114078
- **Longitudinal cytokine and multi-modal health data of an extremely severe ME/CFS patient with HSD reveals insights into immunopathology, and disease severity.** *Frontiers in immunology*
Jahanbani, F., Sing, J. C., Maynard, R. D., Jahanbani, S., Dafoe, J., Dafoe, W., Jones, N., Wallace, K. J., Rastan, A., Maecker, H. T., Röst, H. L., Snyder, M. P., Davis, et al
2024; 15: 1369295
- **Deep learning modeling of rare noncoding genetic variants in human motor neurons definesCCDC146as a therapeutic target for ALS.** *medRxiv : the preprint server for health sciences*
Zhang, S., Moll, T., Rubin-Sigler, J., Tu, S., Li, S., Yuan, E., Liu, M., Butt, A., Harvey, C., Gornall, S., Alhalthli, E., Shaw, A., Souza, et al
2024
- **Emerging therapeutic drug monitoring technologies: considerations and opportunities in precision medicine.** *Frontiers in pharmacology*
Liang, W. S., Beaulieu-Jones, B., Smalley, S., Snyder, M., Goetz, L. H., Schork, N. J.
2024; 15: 1348112
- **Immunotherapeutic IL-6R and targeting the MCT-1/IL-6/CXCL7/PD-L1 circuit prevent relapse and metastasis of triple-negative breast cancer.** *Theranostics*
Haq, A. T., Yang, P. P., Jin, C., Shih, J. H., Chen, L. M., Tseng, H. Y., Chen, Y. A., Weng, Y. S., Wang, L. H., Snyder, M. P., Hsu, H. L.
2024; 14 (5): 2167-2189
- **Author Correction: Advances and prospects for the Human BioMolecular Atlas Program (HuBMAP).** *Nature cell biology*
Jain, S., Pei, L., Spraggins, J. M., Angelo, M., Carson, J. P., Gehlenborg, N., Ginty, F., Goncalves, J. P., Hagoood, J. S., Hickey, J. W., Kelleher, N. L., Laurent, L. C., Lin, et al
2024

- **Corrigendum: Advances and potential of omics studies for understanding the development of food allergy.** *Frontiers in allergy*
Sindher, S. B., Chin, A. R., Aghaeepour, N., Prince, L., Maecker, H., Shaw, G. M., Stevenson, D., Nadeau, K. C., Snyder, M., Khatri, P., Boyd, S. D., Winn, V. D., Angst, et al
2024; 5: 1373485
- **CAGI, the Critical Assessment of Genome Interpretation, establishes progress and prospects for computational genetic variant interpretation methods** *GENOME BIOLOGY*
Jain, S., Bakolitsa, C., Brenner, S. E., Radivojac, P., Moul, J., Repo, S., Hoskins, R. A., Andreoletti, G., Barsky, D., Chellapan, A., Chu, H., Dabir, N., Kollipara, et al
2024; 25 (1): 53
- **Short-chain fatty acids propionate and butyrate control growth and differentiation linked to cellular metabolism.** *Research square*
Nshanian, M., Geller, B. S., Gruber, J. J., Chleilat, F., Camarillo, J. M., Kelleher, N. L., Zhao, Y., Snyder, M. P.
2024
- **Rare and common genetic determinants of mitochondrial function determine severity but not risk of amyotrophic lateral sclerosis.** *Heliyon*
Harvey, C., Weinreich, M., Lee, J. A., Shaw, A. C., Ferraiuolo, L., Mortiboys, H., Zhang, S., Hop, P. J., Zwamborn, R. A., van Eijk, K., Julian, T. H., Moll, T., Iacoangeli, et al
2024; 10 (3): e24975
- **Harnessing human genetics and stem cells for precision cardiovascular medicine.** *Cell genomics*
Caudal, A., Snyder, M. P., Wu, J. C.
2024; 4 (2): 100445
- **Validation of biomarkers of aging.** *Nature medicine*
Moqri, M., Herzog, C., Poganik, J. R., Ying, K., Justice, J. N., Belsky, D. W., Higgins-Chen, A. T., Chen, B. H., Cohen, A. A., Fuellen, G., Hägg, S., Marioni, R. E., Widschwendter, et al
2024
- **Miscarriage risk assessment: a bioinformatic approach to identifying candidate lethal genes and variants.** *Human genetics*
Aminbeidokhti, M., Qu, J., Belur, S., Cakmak, H., Jaswa, E., Lathi, R. B., Sirota, M., Snyder, M. P., Yatsenko, S. A., Rajkovic, A.
2024
- **Untargeted metabolomic profiling in children identifies novel pathways in asthma and atopy.** *The Journal of allergy and clinical immunology*
Lejeune, S., Kaushik, A., Parsons, E. S., Chinthrajah, S., Snyder, M., Desai, M., Manohar, M., Prunicki, M., Contrepolis, K., Gosset, P., Deschildre, A., Nadeau, K.
2024; 153 (2): 418-434
- **Correction: Digital health application integrating wearable data and behavioral patterns improves metabolic health.** *NPJ digital medicine*
Zahedani, A. D., McLaughlin, T., Veluvai, A., Aghaeepour, N., Hosseini, A., Agarwal, S., Ruan, J., Tripathi, S., Woodward, M., Hashemi, N., Snyder, M.
2024; 7 (1): 9
- **Semi-supervised Cooperative Learning for Multiomics Data Fusion**
Ding, D., Shen, X., Snyder, M., Tibshirani, R., Maier, A. K., Schnabel, J. A., Tiwari, P., Stegle, O.
SPRINGER INTERNATIONAL PUBLISHING AG.2024: 54-63
- **California Stress, Trauma, and Resilience Study (CalSTARS) protocol: A multiomics-based cross-sectional investigation and randomized controlled trial to elucidate the biology of ACEs and test a precision intervention for reducing stress and enhancing resilience.** *Stress (Amsterdam, Netherlands)*
Kim, L. Y., Schüssler-Fiorenza Rose, S. M., Mengelkoch, S., Moriarity, D. P., Gassen, J., Alley, J. C., Roos, L. G., Jiang, T., Alavi, A., Thota, D. D., Zhang, X., Perelman, D., Kodish, et al
2024; 27 (1): 2401788
- **Detection and analysis of complex structural variation in human genomes across populations and in brains of donors with psychiatric disorders** *Cell*
Zhou, B., Arthur, J. G., Guo, H., et al
2024; Published online September 30, 2024
- **Multi-omics in stress and health research: study designs that will drive the field forward.** *Stress (Amsterdam, Netherlands)*
Mengelkoch, S., Gassen, J., Lev-Ari, S., Alley, J. C., Schüssler-Fiorenza Rose, S. M., Snyder, M. P., Slavich, G. M.

2024; 27 (1): 2321610

- **Using Ecological Momentary Assessments to Study How Daily Fluctuations in Psychological States Impact Stress, Well-Being, and Health.** *Journal of clinical medicine*
Mengelkoch, S., Moriarity, D. P., Novak, A. M., Snyder, M. P., Slavich, G. M., Lev-Ari, S.
2023; 13 (1)
- **NGLY1 mutations cause protein aggregation in human neurons.** *Cell reports*
Manole, A., Wong, T., Rhee, A., Novak, S., Chin, S. M., Tsimring, K., Paucar, A., Williams, A., Newmeyer, T. F., Schafer, S. T., Rosh, I., Kaushik, S., Hoffman, et al
2023; 42 (12): 113466
- **Reduced FOXF1 links unrepaired DNA damage to pulmonary arterial hypertension.** *Nature communications*
Isobe, S., Nair, R. V., Kang, H. Y., Wang, L., Moonen, J. R., Shinohara, T., Cao, A., Taylor, S., Otsuki, S., Marciano, D. P., Harper, R. L., Adil, M. S., Zhang, et al
2023; 14 (1): 7578
- **Integrative multi-omic profiling of adult mouse brain endothelial cells and potential implications in Alzheimer's disease.** *Cell reports*
Yu, M., Nie, Y., Yang, J., Yang, S., Li, R., Rao, V., Hu, X., Fang, C., Li, S., Song, D., Guo, F., Snyder, M. P., Chang, et al
2023; 42 (11): 113392
- **Mental Health for All: The Case for Investing in Digital Mental Health to Improve Global Outcomes, Access, and Innovation in Low-Resource Settings.** *Journal of clinical medicine*
Faria, M., Zin, S. T., Chestnov, R., Novak, A. M., Lev-Ari, S., Snyder, M.
2023; 12 (21)
- **Relationship of Heterologous Virus Responses and Outcomes in Hospitalized COVID-19 Patients.** *Journal of immunology (Baltimore, Md. : 1950)*
Rosenberg-Hasson, Y., Holmes, T. H., Diray-Arce, J., Chen, J., Kellogg, R., Snyder, M., Becker, P. M., Ozonoff, A., Roupheal, N., Reed, E. F., Maecker, H. T.
2023; 211 (8): 1224-1231
- **Integrative omic profiling and analyses in two pig heart to human xenotransplants**
Keating, B., Schmauch, E., Piening, B., Xia, B., Zhu, C., Chang, B., Khalil, K., Kim, J., Weldon, E., Pass, H., Ayares, D., Griesemer, A., Mangiola, et al
LIPPINCOTT WILLIAMS & WILKINS.2023: 137
- **Integration of spatial and single-cell data across modalities with weakly linked features.** *Nature biotechnology*
Chen, S., Zhu, B., Huang, S., Hickey, J. W., Lin, K. Z., Snyder, M., Greenleaf, W. J., Nolan, G. P., Zhang, N. R., Ma, Z.
2023
- **Author Correction: Lipid droplets and peroxisomes are co-regulated to drive lifespan extension in response to mono-unsaturated fatty acids.** *Nature cell biology*
Papsdorf, K., Miklas, J. W., Hosseini, A., Cabruja, M., Morrow, C. S., Savini, M., Yu, Y., Silva-García, C. G., Haseley, N. R., Murphy, L. M., Yao, P., de Launoit, E., Dixon, et al
2023
- **Multi-omics approaches in psychoneuroimmunology and health research: Conceptual considerations and methodological recommendations.** *Brain, behavior, and immunity*
Mengelkoch, S., Lautman, Z., Alley, J. C., Roos, L. G., Ehlert, B., Moriarity, D. P., Lancaster, S., Miryam Schussler-Fiorenza Rose, S., Snyder, M. P., Slavich, G. M.
2023
- **Organ Mapping Antibody Panels: a community resource for standardized multiplexed tissue imaging.** *Nature methods*
Quardokus, E. M., Saunders, D. C., McDonough, E., Hickey, J. W., Werlein, C., Surette, C., Rajbhandari, P., Casals, A. M., Tian, H., Lowery, L., Neumann, E. K., Björklund, F., Neelakantan, et al
2023
- **Segmentation of human functional tissue units in support of a Human Reference Atlas.** *Communications biology*
Jain, Y., Godwin, L. L., Ju, Y., Sood, N., Quardokus, E. M., Bueckle, A., Longacre, T., Horning, A., Lin, Y., Esplin, E. D., Hickey, J. W., Snyder, M. P., Patterson, et al
2023; 6 (1): 717

- **Reverse-ChIP Techniques for Identifying Locus-Specific Proteomes: A Key Tool in Unlocking the Cancer Regulome.** *Cells*
MacKenzie, T. M., Cisneros, R., Maynard, R. D., Snyder, M. P.
2023; 12 (14)
- **Author Correction: Clonal haematopoiesis and risk of chronic liver disease.** *Nature*
Wong, W. J., Emdin, C., Bick, A. G., Zekavat, S. M., Niroula, A., Pirruccello, J. P., Dichtel, L., Griffin, G., Uddin, M. M., Gibson, C. J., Kovalcik, V., Lin, A. E., McConkey, et al
2023
- **A Roadmap for the Human Gut Cell Atlas.** *Nature reviews. Gastroenterology & hepatology*
Zilbauer, M., James, K. R., Kaur, M., Pott, S., Li, Z., Burger, A., Thiagarajah, J. R., Burclaff, J., Jahnsen, F. L., Perrone, F., Ross, A. D., Matteoli, G., Stakenborg, et al
2023
- **Multimic signals associated with maternal epidemiological factors contributing to preterm birth in low- and middle-income countries.** *Science advances*
Espinosa, C. A., Khan, W., Khanam, R., Das, S., Khalid, J., Pervin, J., Kasaro, M. P., Contrepolis, K., Chang, A. L., Phongpreecha, T., Michael, B., Ellenberger, M., Mehmood, et al
2023; 9 (21): eade7692
- **The ENCODE4 long-read RNA-seq collection reveals distinct classes of transcript structure diversity.** *bioRxiv : the preprint server for biology*
Reese, F., Williams, B., Balderrama-Gutierrez, G., Wyman, D., Çelik, M. H., Rebboah, E., Rezaie, N., Trout, D., Razavi-Mohseni, M., Jiang, Y., Borsari, B., Morabito, S., Liang, et al
2023
- **Organ-specific aging and the risk of chronic diseases.** *Nature medicine*
Moqri, M., Snyder, M.
2023
- **Gut Microbiome-Based Management of Patients With Heart Failure: JACC Review Topic of the Week.** *Journal of the American College of Cardiology*
Mamic, P., Snyder, M., Tang, W. H.
2023; 81 (17): 1729-1739
- **Association between the dynamics of the gut microbiota and responsiveness to mental health therapy**
Zhou, X., Ganz, A. B., Lu, X., Li, Y., Snyder, M.
AMER ASSOC IMMUNOLOGISTS.2023
- **Lipid droplets and peroxisomes are co-regulated to drive lifespan extension in response to mono-unsaturated fatty acids.** *Nature cell biology*
Papsdorf, K., Miklas, J. W., Hosseini, A., Cabruja, M., Morrow, C. S., Savini, M., Yu, Y., Silva-Garcia, C. G., Haseley, N. R., Murphy, L. M., Yao, P., de Launoit, E., Dixon, et al
2023
- **Organism-wide, cell-type-specific secretome mapping of exercise training in mice.** *Cell metabolism*
Wei, W., Riley, N. M., Lyu, X., Shen, X., Guo, J., Raun, S. H., Zhao, M., Moya-Garzon, M. D., Basu, H., Sheng-Hwa Tung, A., Li, V. L., Huang, W., Wiggernhorn, et al
2023
- **Leveraging Physiology and Artificial Intelligence to Deliver Advancements in Healthcare.** *Physiological reviews*
Zhang, A., Wu, Z., Wu, E., Wu, M., Snyder, M. P., Zou, J., Wu, J. C.
2023
- **Multi-omics profiling for health.** *Molecular & cellular proteomics : MCP*
Babu, M., Snyder, M.
2023: 100561
- **The ENCODE Imputation Challenge: a critical assessment of methods for cross-cell type imputation of epigenomic profiles.** *Genome biology*
Schreiber, J., Boix, C., Wook Lee, J., Li, H., Guan, Y., Chang, C. C., Chang, J. C., Hawkins-Hooker, A., Schölkopf, B., Schweikert, G., Carulla, M. R., Canakoglu, A., Guzzo, et al

2023; 24 (1): 79

- **Acetyl-Click Screening Platform Identifies Small-Molecule Inhibitors of Histone Acetyltransferase 1 (HAT1).** *Journal of medicinal chemistry*
Gaddameedi, J. D., Chou, T., Geller, B. S., Rangarajan, A., Swaminathan, T. A., Dixon, D., Long, K., Golder, C. J., Vuong, V. A., Banuelos, S., Greenhouse, R., Snyder, M. P., Lipchik, et al
2023
- **Withdrawal of 'Precision Neoantigen Discovery Using Large-scale Immunopeptidomes and Composite Modeling of MHC Peptide Presentation'.** *Molecular & cellular proteomics : MCP*
Pyke, R. M., Mellacheruvu, D., Dea, S., Abbott, C. W., Zhang, S. V., Phillips, N. A., Harris, J., Bartha, G., Desai, S., McClory, R., West, J., Snyder, M. P., Chen, et al
2023; 22 (4): 100511
- **Leveraging electronic health records to identify risk factors for recurrent pregnancy loss across two medical centers: a case-control study.** *Research square*
Roger, J., Xie, F., Costello, J., Tang, A., Liu, J., Oskotsky, T., Woldemariam, S., Kosti, I., Le, B., Snyder, M. P., Giudice, L. C., Torgerson, D., Shaw, et al
2023
- **The EN-TEx resource of multi-tissue personal epigenomes & variant-impact models.** *Cell*
Rozowsky, J., Gao, J., Borsari, B., Yang, Y. T., Galeev, T., Gürsoy, G., Epstein, C. B., Xiong, K., Xu, J., Li, T., Liu, J., Yu, K., Berthel, et al
2023; 186 (7): 1493-1511.e40
- **Advances and potential of omics studies for understanding the development of food allergy.** *Frontiers in allergy*
Sindher, S. B., Chin, A. R., Aghaeepour, N., Prince, L., Maecker, H., Shaw, G. M., Stevenson, D. K., Nadeau, K. C., Snyder, M., Khatri, P., Boyd, S. D., Winn, V. D., Angst, et al
2023; 4: 1149008
- **Proinflammatory polarization of monocytes by particulate air pollutants is mediated by induction of trained immunity in pediatric asthma.** *Allergy*
Movassagh, H., Prunicki, M., Kaushik, A., Zhou, X., Dunham, D., Smith, E. M., He, Z., Aleman Muench, G. R., Shi, M., Weimer, A. K., Cao, S., Andorf, S., Feizi, et al
2023
- **Simultaneous profiling of host expression and microbial abundance by spatial metatranscriptome sequencing** *GENOME RESEARCH*
Lyu, L., Li, X., Feng, R., Zhou, X., Guha, T. K., Yu, X., Chen, G., Yao, Y., Su, B., Zou, D., Snyder, M. P., Chen, L.
2023; 33 (3): 401-411
- **Biomonitoring and precision health in deep space supported by artificial intelligence** *NATURE MACHINE INTELLIGENCE*
Scott, R. T., Sanders, L. M., Antonsen, E. L., Hastings, J. A., Park, S., Mackintosh, G., Reynolds, R. J., Hoarfrost, A. L., Sawyer, A., Greene, C. S., Glicksberg, B. S., Theriot, C. A., Berrios, et al
2023; 5 (3): 196-207
- **Biological research and self-driving labs in deep space supported by artificial intelligence** *NATURE MACHINE INTELLIGENCE*
Sanders, L. M., Scott, R. T., Yang, J. H., Qutub, A., Garcia Martin, H., Berrios, D. C., Hastings, J. A., Rask, J., Mackintosh, G., Hoarfrost, A. L., Chalk, S., Kalantari, J., Khezeli, et al
2023; 5 (3): 208-219
- **Sensor-enabled Multilayer Artificial Intelligence Analysis for Predictive Wound Healing and Real-Time Patient Monitoring**
Trotsyuk, A. A., Jing, S., Chen, K., Henn, D., Jiang, Y., Niu, S., Sivaraj, D., Nag, R., Snyder, M., bao, Z., Gurtner, G. C.
WILEY.2023: 268-269
- **Simultaneous profiling of host expression and microbial abundance by spatial metatranscriptome sequencing.** *Genome research*
Lyu, L., Li, X., Feng, R., Zhou, X., Guha, T. K., Yu, X., Chen, G. Q., Yao, Y., Su, B., Zou, D., Snyder, M. P., Chen, L.
2023; 33 (3): 401-411
- **Precision neoantigen discovery using large-scale immunopeptidomes and composite modeling of MHC peptide presentation.** *Molecular & cellular proteomics : MCP*
Pyke, R. M., Mellacheruvu, D., Dea, S., Abbott, C., Zhang, S. V., Phillips, N. A., Harris, J., Bartha, G., Desai, S., McClory, R., West, J., Snyder, M. P., Chen, et al
2023: 100506

- **Challenging obesity and sex based differences in resting energy expenditure using allometric modeling, a sub-study of the DIETFITS clinical trial.** *Clinical nutrition ESPEN*
Haddad, F., Li, X., Perelman, D., Santana, E. J., Kuznetsova, T., Cauwenberghs, N., Busque, V., Contrepois, K., Snyder, M. P., Leonard, M. B., Gardner, C.
2023; 53: 43-52
- **Stem cell plasticity, acetylation of H3K14, and de novo gene activation rely on KAT7.** *Cell reports*
Kueh, A. J., Bergamasco, M. I., Quagliari, A., Phipson, B., Li-Wai-Suen, C. S., Lonnstedt, I. M., Hu, Y., Feng, Z., Woodruff, C., May, R. E., Wilcox, S., Garnham, A. L., Snyder, et al
2023; 42 (1): 111980
- **Multimic identification of key transcriptional regulatory programs during endurance exercise training.** *bioRxiv : the preprint server for biology*
Smith, G. R., Zhao, B., Lindholm, M. E., Raja, A., Viggars, M., Pincas, H., Gay, N. R., Sun, Y., Ge, Y., Nair, V. D., Sanford, J. A., S Amper, M. A., Vasoya, et al
2023
- **Low expression of EXOSC2 protects against clinical COVID-19 and impedes SARS-CoV-2 replication.** *Life science alliance*
Moll, T., Odon, V., Harvey, C., Collins, M. O., Peden, A., Franklin, J., Graves, E., Marshall, J. N., Dos Santos Souza, C., Zhang, S., Castelli, L., Hautbergue, G., Azzouz, et al
2023; 6 (1)
- **Harnessing human genetics and stem cells for precision cardiovascular medicine** *Cell Genomics*
Caudal, A., Snyder, M. P., Wu, J. C.
2023
- **Leveraging Mobile Technology for Public Health Promotion: A Multidisciplinary Perspective.** *Annual review of public health*
Hicks, J. L., Boswell, M. A., Althoff, T., Crum, A. J., Ku, J. P., Landay, J. A., Moya, P. M., Murnane, E. L., Snyder, M. P., King, A. C., Delp, S. L.
2022
- **Gut microbiota analyses of Saudi populations for type 2 diabetes-related phenotypes reveals significant association.** *BMC microbiology*
Al-Muhanna, F. A., Dowdell, A. K., Al Eleg, A. H., Albaker, W. I., Brooks, A. W., Al-Sultan, A. I., Al-Rubaish, A. M., Alkharsah, K. R., Sulaiman, R. M., Al-Quorain, A. A., Cyrus, C., Alali, R. A., Vatte, et al
2022; 22 (1): 301
- **Early prediction and longitudinal modeling of preeclampsia from multiomics.** *Patterns (New York, N.Y.)*
Maric, I., Contrepois, K., Moufarrej, M. N., Stelzer, I. A., Feyaerts, D., Han, X., Tang, A., Stanley, N., Wong, R. J., Traber, G. M., Ellenberger, M., Chang, A. L., Fallahzadeh, et al
2022; 3 (12): 100655
- **Wireless, closed-loop, smart bandage with integrated sensors and stimulators for advanced wound care and accelerated healing.** *Nature biotechnology*
Jiang, Y., Trotsyuk, A. A., Niu, S., Henn, D., Chen, K., Shih, C. C., Larson, M. R., Mermin-Bunnell, A. M., Mittal, S., Lai, J. C., Saberi, A., Beard, E., Jing, et al
2022
- **Author Correction: Prediction of gestational age using urinary metabolites in term and preterm pregnancies.** *Scientific reports*
Contrepois, K., Chen, S., Ghaemi, M. S., Wong, R. J., Jehan, F., Sazawal, S., Baqui, A. H., Stringer, J. S., Rahman, A., Nisar, M. I., Dhingra, U., Khanam, R., Ilyas, et al
2022; 12 (1): 19753
- **Annotation of spatially resolved single-cell data with STELLAR.** *Nature methods*
Brbic, M., Cao, K., Hickey, J. W., Tan, Y., Snyder, M. P., Nolan, G. P., Leskovec, J.
2022
- **The metabolomics of human aging: Advances, challenges, and opportunities.** *Science advances*
Panyard, D. J., Yu, B., Snyder, M. P.
2022; 8 (42): eadd6155
- **LEVERAGING ELECTRONIC HEALTH RECORD DATA TO IDENTIFY PHENOTYPES ASSOCIATED WITH PREGNANCY LOSS MAY LEAD TO IMPROVED UNDERSTANDING OF RECURRENT PREGNANCY LOSS**

Roger, J., Tang, A., Woldemariam, S., Oskotsky, T., Wen, T., Liu, J., Kosti, I., Le, B., Cakmak, H., Snyder, M., Aghaeepour, N., Shaw, G., Stevenson, et al
ELSEVIER SCIENCE INC.2022: E107

- **Precision Medicine Approaches to Mental Healthcare.** *Physiology (Bethesda, Md.)*
Scala, J. J., Ganz, A. B., Snyder, M. P.
2022
- **A method for intelligent allocation of diagnostic testing by leveraging data from commercial wearable devices: a case study on COVID-19.** *NPJ digital medicine*
Shandhi, M. M., Cho, P. J., Roghanizad, A. R., Singh, K., Wang, W., Enache, O. M., Stern, A., Sbahi, R., Tatar, B., Fiscus, S., Khoo, Q. X., Kuo, Y., Lu, et al
2022; 5 (1): 130
- **Deploying wearable sensors for pandemic mitigation: A counterfactual modelling study of Canada's second COVID-19 wave.** *PLOS digital health*
Duarte, N., Arora, R. K., Bennett, G., Wang, M., Snyder, M. P., Cooperstock, J. R., Wagner, C. E.
2022; 1 (9): e0000100
- **KLF4 recruits SWI/SNF to increase chromatin accessibility and reprogram the endothelial enhancer landscape under laminar shear stress.** *Nature communications*
Moonen, J. R., Chappell, J., Shi, M., Shinohara, T., Li, D., Mumbach, M. R., Zhang, F., Nair, R. V., Nasser, J., Mai, D. H., Taylor, S., Wang, L., Metzger, et al
2022; 13 (1): 4941
- **Deep learning-based pseudo-mass spectrometry imaging analysis for precision medicine.** *Briefings in bioinformatics*
Shen, X., Shao, W., Wang, C., Liang, L., Chen, S., Zhang, S., Rusu, M., Snyder, M. P.
2022
- **Transcriptome variation in human tissues revealed by long-read sequencing.** *Nature*
Gliinos, D. A., Garborcauskas, G., Hoffman, P., Ehsan, N., Jiang, L., Gokden, A., Dai, X., Aguet, F., Brown, K. L., Garimella, K., Bowers, T., Costello, M., Ardlie, et al
2022
- **Reply to 'Lactate as a major myokine and exerkine'.** *Nature reviews. Endocrinology*
Chow, L. S., Gerszten, R. E., Taylor, J. M., Pedersen, B. K., van Praag, H., Trappe, S., Febbraio, M. A., Galis, Z. S., Gao, Y., Haus, J. M., Lanza, I. R., Lavie, C. J., Lee, et al
2022
- **DSIF modulates RNA polymerase II occupancy according to template G plus C content** *NAR GENOMICS AND BIOINFORMATICS*
Deng, N., Zhang, Y., Ma, Z., Lin, R., Cheng, T., Tang, H., Snyder, M. P., Cohen, S. N.
2022; 4 (3)
- **Robust Identification of Temporal Biomarkers in Longitudinal Omics Studies.** *Bioinformatics (Oxford, England)*
Metwally, A. A., Zhang, T., Wu, S., Kellogg, R., Zhou, W., Contrepolis, K., Tang, H., Snyder, M.
2022
- **KMT2D-NOTCH Mediates Coronary Abnormalities in Hypoplastic Left Heart Syndrome.** *Circulation research*
Yu, Z., Zhou, X., Liu, Z., Pastrana-Gomez, V., Liu, Y., Guo, M., Tian, L., Nelson, T. J., Wang, N., Mital, S., Chitayat, D., Wu, J. C., Rabinovitch, et al
2022: 101161CIRCRESAHA122320783
- **Serine biosynthesis as a novel therapeutic target for dilated cardiomyopathy.** *European heart journal*
Perea-Gil, I., Seeger, T., Bruyneel, A. A., Termglinchan, V., Monte, E., Lim, E. W., Vadgama, N., Furihata, T., Gavidia, A. A., Arthur Ataam, J., Bharucha, N., Martinez-Amador, N., Ameen, et al
2022
- **An exercise-inducible metabolite that suppresses feeding and obesity.** *Nature*
Li, V. L., He, Y., Contrepolis, K., Liu, H., Kim, J. T., Wiggenhorn, A. L., Tanzo, J. T., Tung, A. S., Lyu, X., Zushin, P. H., Jansen, R. S., Michael, B., Loh, et al
2022

- **Ultra-Low Input High-Fidelity (ULI-HiFi) long-reads uncover variants in genomic dark matter from pre-cancer polyp and tumor samples**
Lee, H., Erwin, G., Horning, A., Kirtikar, R., Griffin-Baldwin, E., Rowell, W., Li, P., Kingan, S., Snyder, M. P.
AMER ASSOC CANCER RESEARCH.2022
- **Endogenous Retroviral Elements Generate Pathologic Neutrophils in Pulmonary Arterial Hypertension.** *American journal of respiratory and critical care medicine*
Taylor, S., Isobe, S., Cao, A., Contrepolis, K., Benayoun, B. A., Jiang, L., Wang, L., Melemenidis, S., Ozen, M. O., Otsuki, S., Shinohara, T., Sweatt, A. J., Kaplan, et al
2022
- **Wnt Signaling Interactor WTIP (Wilms Tumor Interacting Protein) Underlies Novel Mechanism for Cardiac Hypertrophy.** *Circulation. Genomic and precision medicine*
De Jong, H. N., Dewey, F. E., Cordero, P., Victorio, R. A., Kirillova, A., Huang, Y., Madhvani, R., Seo, K., Werdich, A. A., Lan, F., Orcholski, M., Robert Liu, W., Erbilgin, et al
2022: 101161CIRCGEN121003563
- **A cancer-associated RNA polymerase III identity drives robust transcription and expression of snR-A noncoding RNA.** *Nature communications*
Van Bortle, K., Marciano, D. P., Liu, Q., Chou, T., Lipchik, A. M., Gollapudi, S., Geller, B. S., Monte, E., Kamakaka, R. T., Snyder, M. P.
2022; 13 (1): 3007
- **Prediction of gestational age using urinary metabolites in term and preterm pregnancies.** *Scientific reports*
Contrepolis, K., Chen, S., Ghaemi, M. S., Wong, R. J., Alliance for Maternal and Newborn Health Improvement (AMANHI), Global Alliance to Prevent Prematurity and Stillbirth (GAPPS), Shaw, G., Stevenson, D. K., Aghaeepour, N., Snyder, M. P., Jehan, F., Sazawal, S., Baqui, A. H., Nisar, et al
2022; 12 (1): 8033
- **Author Correction: Expanded encyclopaedias of DNA elements in the human and mouse genomes.** *Nature*
ENCODE Project Consortium, Moore, J. E., Purcaro, M. J., Pratt, H. E., Epstein, C. B., Shores, N., Adrian, J., Kawli, T., Davis, C. A., Dobin, A., Kaul, R., Halow, J., Van Nostrand, E. L., et al
2022
- **Author Correction: Perspectives on ENCODE.** *Nature*
ENCODE Project Consortium, Snyder, M. P., Gingeras, T. R., Moore, J. E., Weng, Z., Gerstein, M. B., Ren, B., Hardison, R. C., Stamatoyannopoulos, J. A., Graveley, B. R., Feingold, E. A., Pazin, M. J., Pagan, M., et al
2022
- **A machine learning algorithm with subclonal sensitivity reveals widespread pan-cancer human leukocyte antigen loss of heterozygosity.** *Nature communications*
Pyke, R. M., Mellacheruvu, D., Dea, S., Abbott, C. W., McDaniel, L., Bhave, D. P., Zhang, S. V., Levy, E., Bartha, G., West, J., Snyder, M. P., Chen, R. O., Boyle, et al
2022; 13 (1): 1925
- **Exploring disease interrelationships in patients with lymphatic disorders: A single center retrospective experience.** *Clinical and translational medicine*
Rockson, S. G., Zhou, X., Zhao, L., Hosseini, D. K., Jiang, X., Sweatt, A. J., Kim, D., Tian, W., Snyder, M. P., Nicolls, M. R.
2022; 12 (4): e760
- **A Method for Intelligent Allocation of Diagnostic Testing by Leveraging Data from Commercial Wearable Devices: A Case Study on COVID-19.** *Research square*
Dunn, J., Shandhi, M. H., Cho, P., Roghanizad, A., Singh, K., Wang, W., Enache, O., Stern, A., Sbahi, R., Tatar, B., Fiscus, S., Khoo, Q. X., Kuo, et al
2022
- **Exerkines in health, resilience and disease.** *Nature reviews. Endocrinology*
Chow, L. S., Gerszten, R. E., Taylor, J. M., Pedersen, B. K., van Praag, H., Trappe, S., Febbraio, M. A., Galis, Z. S., Gao, Y., Haus, J. M., Lanza, I. R., Lavie, C. J., Lee, et al
2022
- **Effects of an immersive psychosocial training program on depression and well-being: A randomized clinical trial.** *Journal of psychiatric research*
Ganz, A. B., Rolnik, B., Chakraborty, M., Wilson, J., Tau, C., Sharp, M., Reber, D., Slavich, G. M., Snyder, M. P.
2022; 150: 292-299

- **Low expression of EXOSC2 protects against clinical COVID-19 and impedes SARS-CoV-2 replication.** *bioRxiv : the preprint server for biology*
Moll, T., Odon, V., Harvey, C., Collins, M. O., Peden, A., Franklin, J., Graves, E., Marshall, J. N., Souza, C. D., Zhang, S., Azzouz, M., Gordon, D., Krogan, et al
2022
- **MITI minimum information guidelines for highly multiplexed tissue images.** *Nature methods*
Schapiro, D., Yapp, C., Sokolov, A., Reynolds, S. M., Chen, Y., Sudar, D., Xie, Y., Muhlich, J., Arias-Camison, R., Arena, S., Taylor, A. J., Nikolov, M., Tyler, et al
2022; 19 (3): 262-267
- **Whole transcriptome profiling of prospective endomyocardial biopsies reveals prognostic and diagnostic signatures of cardiac allograft rejection.** *The Journal of heart and lung transplantation : the official publication of the International Society for Heart Transplantation*
Piening, B. D., Dowdell, A. K., Zhang, M., Loza, B., Walls, D., Gao, H., Mohebnasab, M., Li, Y. R., Elftmann, E., Wei, E., Gandla, D., Lad, H., Chaib, et al
2022
- **Dual isoform sequencing reveals complex transcriptomic and epitranscriptomic landscapes of a prototype baculovirus.** *Scientific reports*
Torma, G., Tombacz, D., Moldovan, N., Fulop, A., Prazsak, I., Csabai, Z., Snyder, M., Boldogkoi, Z.
1800; 12 (1): 1291
- **Unbiased metabolome screen leads to personalized medicine strategy for amyotrophic lateral sclerosis.** *Brain communications*
Boddy, S., Islam, M., Moll, T., Kurz, J., Burrows, D., McGown, A., Bhargava, A., Julian, T. H., Harvey, C., Marshall, J. N., Hall, B. P., Allen, S. P., Kenna, et al
2022; 4 (2): fcac069
- **Identification of end-stage renal disease metabolic signatures from human perspiration** *Natural Sciences*
Shankar, V., Michael, B., Celli, A., Zhou, Z., Ashland, M., Tibshirani, R., Snyder, M., Zare, R.
2022
- **Patient-derived gene and protein expression signatures of NGLY1 deficiency.** *Journal of biochemistry*
Rauscher, B., Mueller, W. F., Clauder-Munster, S., Jakob, P., Islam, M. S., Sun, H., Ghidelli-Disse, S., Boesche, M., Bantscheff, M., Pflaumer, H., Collier, P., Haase, B., Chen, et al
2021
- **Tet enzymes are essential for early embryogenesis and completion of embryonic genome activation.** *EMBO reports*
Arand, J., Chiang, H. R., Martin, D., Snyder, M. P., Sage, J., Reijo Pera, R. A., Wossidlo, M.
2021: e53968
- **Cross-Laboratory Standardization of Preclinical Lipidomics Using Differential Mobility Spectrometry and Multiple Reaction Monitoring.** *Analytical chemistry*
Ghorasaini, M., Mohammed, Y., Adamski, J., Bettcher, L., Bowden, J. A., Cabruja, M., Contrepois, K., Ellenberger, M., Gajera, B., Haid, M., Hornburg, D., Hunter, C., Jones, et al
2021
- **Human exposome assessment platform.** *Environmental epidemiology (Philadelphia, Pa.)*
Merino Martinez, R., Muller, H., Negru, S., Ormenisan, A., Arroyo Muhr, L. S., Zhang, X., Trier Moller, F., Clements, M. S., Kozlakidis, Z., Pimenoff, V. N., Wilkowski, B., Boeckhout, M., Ohman, et al
1800; 5 (6): e182
- **Design and Methods of the Validating Injury to the Renal Transplant Using Urinary Signatures (VIRTUUS) Study in Children.** *Transplantation direct*
Kumar, J., Contrepois, K., Snyder, M., Grimm, P. C., Moudgil, A., Smith, J. M., Bobrowski, A. E., Verghese, P. S., Hooper, D., Ingulli, E., Lestz, R., Weng, P., Reason, et al
2021; 7 (12): e791
- **Network biology bridges the gaps between quantitative genetics and multi-omics to map complex diseases.** *Current opinion in chemical biology*
Wu, S., Chen, D., Snyder, M. P.
2021; 66: 102101
- **Master lineage transcription factors anchor trans mega transcriptional complexes at highly accessible enhancer sites to promote long-range chromatin clustering and transcription of distal target genes.** *Nucleic acids research*

White, S. M., Snyder, M. P., Yi, C.
2021

- **Spatial mapping of protein composition and tissue organization: a primer for multiplexed antibody-based imaging.** *Nature methods*
Hickey, J. W., Neumann, E. K., Radtke, A. J., Camarillo, J. M., Beuschel, R. T., Albanese, A., McDonough, E., Hatler, J., Wiblin, A. E., Fisher, J., Croteau, J., Small, E. C., Sood, et al
2021
- **A review of Mendelian randomization in amyotrophic lateral sclerosis.** *Brain : a journal of neurology*
Julian, T. H., Boddy, S., Islam, M., Kurz, J., Whittaker, K. J., Moll, T., Harvey, C., Zhang, S., Snyder, M. P., McDermott, C., Cooper-Knock, J., Shaw, P. J.
2021
- **In-depth triacylglycerol profiling using MS3 Q-Trap mass spectrometry.** *Analytica chimica acta*
Cabruja, M., Priotti, J., Domizi, P., Papsdorf, K., Kroetz, D. L., Brunet, A., Contrepolis, K., Snyder, M. P.
2021; 1184: 339023
- **COVID-19-Induced New-Onset Diabetes: Trends and Technologies.** *Diabetes*
Metwally, A. A., Mehta, P., Johnson, B. S., Nagarjuna, A., Snyder, M. P.
2021
- **Altered Cardiac Energetics and Mitochondrial Dysfunction in Hypertrophic Cardiomyopathy.** *Circulation*
Ranjbarvaziri, S., Kooiker, K. B., Ellenberger, M., Fajardo, G., Zhao, M., Vander Roest, A. S., Woldeyes, R. A., Koyano, T. T., Fong, R., Ma, N., Tian, L., Traber, G. M., Chan, et al
2021
- **The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation.** *Nature genetics*
Kim, D. S., Risca, V. I., Reynolds, D. L., Chappell, J., Rubin, A. J., Jung, N., Donohue, L. K., Lopez-Pajares, V., Kathiria, A., Shi, M., Zhao, Z., Deep, H., Sharmin, et al
2021
- **Divergent patterns of selection on metabolite levels and gene expression.** *BMC ecology and evolution*
Kern, A. F., Yang, G. X., Khosla, N. M., Ang, R. M., Snyder, M. P., Fraser, H. B.
2021; 21 (1): 185
- **Statins Are Associated With Increased Insulin Resistance and Secretion.** *Arteriosclerosis, thrombosis, and vascular biology*
Abbasi, F., Lamendola, C., Harris, C. S., Harris, V., Tsai, M., Tripathi, P., Abbas, F., Reaven, G., Reaven, P., Snyder, M. P., Kim, S. H., Knowles, J. W.
2021: ATVBaha121316159
- **Temporal changes in soluble angiotensin-converting enzyme 2 associated with metabolic health, body composition, and proteome dynamics during a weight loss diet intervention: a randomized trial with implications for the COVID-19 pandemic.** *The American journal of clinical nutrition*
Cauwenberghs, N., Prunicki, M., Sabovcik, F., Perelman, D., Contrepolis, K., Li, X., Snyder, M. P., Nadeau, K. C., Kuznetsova, T., Haddad, F., Gardner, C. D.
2021
- **Prediction of Immunotherapy Response in Melanoma through Combined Modeling of Neoantigen Burden and Immune-Related Resistance Mechanisms.** *Clinical cancer research : an official journal of the American Association for Cancer Research*
Abbott, C. W., Boyle, S. M., Pyke, R. M., McDaniel, L. D., Levy, E., Navarro, F. C., Mellacheruvu, D., Zhang, S. V., Tan, M., Santiago, R., Rusan, Z. M., Milani, P., Bartha, et al
2021; 27 (15): 4265-4276
- **Longitudinal linked-read sequencing reveals ecological and evolutionary responses of a human gut microbiome during antibiotic treatment.** *Genome research*
Roodgar, M., Good, B. H., Garud, N. R., Martis, S., Avula, M., Zhou, W., Lancaster, S. M., Lee, H., Babveyh, A., Nesamoney, S., Pollard, K. S., Snyder, M. P.
2021
- **Time-Course Transcriptome Profiling of a Poxvirus Using Long-Read Full-Length Assay.** *Pathogens (Basel, Switzerland)*
Tombacz, D., Prazsak, I., Torma, G., Csabai, Z., Balazs, Z., Moldovan, N., Denes, B., Snyder, M., Boldogkoi, Z.
2021; 10 (8)

- **The Exposome in the Era of the Quantified Self.** *Annual review of biomedical data science*
Zhang, X., Gao, P., Snyder, M. P.
2021; 4: 255-277
- **Combined nanopore and single-molecule real-time sequencing survey of human betaherpesvirus 5 transcriptome.** *Scientific reports*
Kakuk, B., Tombacz, D., Balazs, Z., Moldovan, N., Csabai, Z., Torma, G., Megyeri, K., Snyder, M., Boldogkoi, Z.
2021; 11 (1): 14487
- **Multi-Omic, Longitudinal Profile of Third-Trimester Pregnancies Identifies a Molecular Switch That Predicts the Onset of Labor.**
Stelzer, I., Ghaemi, M., Han, X., Ando, K., Hedou, J., Feyaerts, D., Peterson, L., Ganio, E., Tsai, A., Tsai, E., Rumer, K., Stanley, N., Fallazadeh, et al
SPRINGER HEIDELBERG.2021: 233A-234A
- **Pan-cancer survey of HLA loss of heterozygosity using a robustly validated NGS-based machine learning algorithm.**
Pyke, R., Mellacheruvu, D., Abbott, C., Dea, S., Levy, E., Zhang, S. V., Bedi, N., Colevas, A., Bhav, D., Chinnappa, M., Bartha, G., Lyle, J., West, et al
AMER ASSOC CANCER RESEARCH.2021
- **Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices.** *Nature methods*
Aseekh, S., Aharoni, A., Brotman, Y., Contrepolis, K., D'Auria, J., Ewald, J., C Ewald, J., Fraser, P. D., Giavalisco, P., Hall, R. D., Heinemann, M., Link, H., Luo, et al
2021; 18 (7): 747-756
- **Time-course transcriptome analysis of host cell response to poxvirus infection using a dual long-read sequencing approach.** *BMC research notes*
Maroti, Z., Tombacz, D., Prazsak, I., Moldovan, N., Csabai, Z., Torma, G., Balazs, Z., Kalmar, T., Denes, B., Snyder, M., Boldogkoi, Z.
2021; 14 (1): 239
- **AdaTiSS: A Novel Data-Adaptive Robust Method for Identifying Tissue Specificity Scores.** *Bioinformatics (Oxford, England)*
Wang, M., Jiang, L., Snyder, M. P.
2021
- **Precision neoantigen discovery using large-scale immunopeptidomes and composite modeling of MHC peptide presentation.** *Molecular & cellular proteomics : MCP*
Pyke, R. M., Mellacheruvu, D., Dea, S., Abbott, C., Zhang, S. V., Phillips, N. A., Harris, J., Bartha, G., Desai, S., McClory, R., West, J., Snyder, M. P., Chen, et al
2021: 100111
- **Non-invasive wearables for remote monitoring of HbA1c and glucose variability: proof of concept.** *BMJ open diabetes research & care*
Bent, B., Cho, P. J., Wittmann, A., Thacker, C., Muppidi, S., Snyder, M., Crowley, M. J., Feinglos, M., Dunn, J. P.
2021; 9 (1)
- **Physical exercise is a risk factor for amyotrophic lateral sclerosis: Convergent evidence from Mendelian randomisation, transcriptomics and risk genotypes.** *EBioMedicine*
Julian, T. H., Glasgow, N., Barry, A. D., Moll, T., Harvey, C., Klimentidis, Y. C., Newell, M., Zhang, S., Snyder, M. P., Cooper-Knock, J., Shaw, P. J.
2021; 68: 103397
- **Association of HLA loss of heterozygosity with allele-specific neoantigen expansion in response to immunotherapy.**
Pyke, R., Abbott, C., Dea, S., Bedi, N., Colevas, A., Levy, E., Zhang, S. V., Snyder, M., Mellacheruvu, D., Sunwoo, J. B., Chen, R., Boyle, S.
LIPPINCOTT WILLIAMS & WILKINS.2021
- **Robust prediction of response to immunotherapy in a mixed cohort of previously treated and immunotherapy-naive melanoma patients.**
Abbott, C., McDaniel, L., Pyke, R., Levy, E., Navarro, F., Wang, S., McClory, R., Snyder, M., Jang, S., Boyle, S., Chen, R.
LIPPINCOTT WILLIAMS & WILKINS.2021
- **Integrated trajectories of the maternal metabolome, proteome, and immunome predict labor onset.** *Science translational medicine*
Stelzer, I. A., Ghaemi, M. S., Han, X., Ando, K., Hedou, J. J., Feyaerts, D., Peterson, L. S., Rumer, K. K., Tsai, E. S., Ganio, E. A., Gaudilliere, D. K., Tsai, A. S., Choisy, et al
2021; 13 (592)
- **A genome-wide atlas of co-essential modules assigns function to uncharacterized genes.** *Nature genetics*

Wainberg, M., Kamber, R. A., Balsubramani, A., Meyers, R. M., Sinnott-Armstrong, N., Hornburg, D., Jiang, L., Chan, J., Jian, R., Gu, M., Shcherbina, A., Dubreuil, M. M., Spees, et al
2021

- **Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease.** *Cell*
de Goede, O. M., Nachun, D. C., Ferraro, N. M., Gloudemans, M. J., Rao, A. S., Smail, C., Eulalio, T. Y., Aguet, F., Ng, B., Xu, J., Barbeira, A. N., Castel, S. E., Kim-Hellmuth, et al
2021
- **iNetModels 2.0: an interactive visualization and database of multi-omics data.** *Nucleic acids research*
Arif, M., Zhang, C., Li, X., Gungor, C., Cakmak, B., Arslanturk, M., Tebani, A., Ozcan, B., Subas, O., Zhou, W., Piening, B., Turkez, H., Fagerberg, et al
2021
- **Inherited causes of clonal haematopoiesis in 97,691 whole genomes (vol 586 , pg 763, 2020) NATURE**
Bick, A. G., Weinstock, J. S., Nandakumar, S. K., Fulco, C. P., Bao, E. L., Zekavat, S. M., Szeto, M. D., Liao, X., Leventhal, M. J., Nasser, J., Chang, K., Laurie, C., Burugula, et al
2021; 591 (7851): E27
- **ALDH1A3 Coordinates Metabolism with Gene Regulation in Pulmonary Arterial Hypertension.** *Circulation*
Li, D., Shao, N., Moonen, J., Zhao, Z., Shi, M., Otsuki, S., Wang, L., Nguyen, T., Yan, E., Marciano, D. P., Contrepolis, K., Li, C. G., Wu, et al
2021
- **Understanding how biologic and social determinants affect disparities in preterm birth and outcomes of preterm infants in the NICU.** *Seminars in perinatology*
Stevenson, D. K., Aghaeepour, N., Maric, I., Angst, M. S., Darmstadt, G. L., Druzin, M. L., Gaudilliere, B., Ling, X. B., Moufarrej, M. N., Peterson, L. S., Quake, S. R., Relman, D. A., Snyder, et al
2021: 151408
- **Early Detection of SARS-CoV-2 and other Infections in Solid Organ Transplant Recipients and Household Members using Wearable Devices.** *Transplant international : official journal of the European Society for Organ Transplantation*
Keating, B. J., Mukhtar, E. H., Eiftmann, E. D., Eweje, F. R., Gao, H., Ibrahim, L. I., Kathawate, R. G., Lee, A. C., Li, E. H., Moore, K. A., Nair, N., Chaluvadi, V., Reason, et al
2021
- **Hummingbird: Efficient Performance Prediction for Executing Genomic Applications in the Cloud.** *Bioinformatics (Oxford, England)*
Bahmani, A., Xing, Z., Krishnan, V., Ray, U., Mueller, F., Alavi, A., Tsao, P. S., Snyder, M. P., Pan, C.
2021
- **Response to Hulman and colleagues regarding "Glucotypes reveal new patterns of glucose dysregulation".** *PLoS biology*
Breschi, A., Perelman, D., Snyder, M. P.
2021; 19 (3): e3001092
- **Benchmarking workflows to assess performance and suitability of germline variant calling pipelines in clinical diagnostic assays.** *BMC bioinformatics*
Krishnan, V., Utiramerur, S., Ng, Z., Datta, S., Snyder, M. P., Ashley, E. A.
2021; 22 (1): 85
- **An Integrated Sequencing Approach for Updating the Pseudorabies Virus Transcriptome.** *Pathogens (Basel, Switzerland)*
Torma, G., Tombacz, D., Csabai, Z., Gobhardt, D., Deim, Z., Snyder, M., Boldogkoi, Z.
2021; 10 (2)
- **Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program.** *Nature*
Taliun, D., Harris, D. N., Kessler, M. D., Carlson, J., Szpiech, Z. A., Torres, R., Taliun, S. A., Corvelo, A., Gogarten, S. M., Kang, H. M., Pitsillides, A. N., LeFaive, J., Lee, et al
2021; 590 (7845): 290–99
- **Decoding personal biotic and abiotic airborne exposome.** *Nature protocols*
Jiang, C., Zhang, X., Gao, P., Chen, Q., Snyder, M.
2021

- **The gut microbiome: a key player in the complexity of amyotrophic lateral sclerosis (ALS).** *BMC medicine*
Boddy, S. L., Giovannelli, I. n., Sassani, M. n., Cooper-Knock, J. n., Snyder, M. P., Segal, E. n., Elinav, E. n., Barker, L. A., Shaw, P. J., McDermott, C. J.
2021; 19 (1): 13
- **The Exosome in the Era of the Quantified Self** *ANNUAL REVIEW OF BIOMEDICAL DATA SCIENCE, VOL 4*
Zhang, X., Gao, P., Snyder, M. P., Altman, R. B.
2021; 4: 255-277
- **Structured elements drive extensive circular RNA translation.** *Molecular cell*
Chen, C. K., Cheng, R., Demeter, J., Chen, J., Weingarten-Gabbay, S., Jiang, L., Snyder, M. P., Weissman, J. S., Segal, E., Jackson, P. K., Chang, H. Y.
2021
- **Non-invasive wearables for remote monitoring of HbA1c and glucose variability: proof of concept** *BMJ OPEN DIABETES RESEARCH & CARE*
Bent, B., Cho, P. J., Wittmann, A., Thacker, C., Muppidi, S., Snyder, M., Crowley, M. J., Feinglos, M., Dunn, J. P.
2021; 9 (1)
- **The X chromosome from telomere to telomere: key achievements and future opportunities.** *Faculty reviews*
Heard, E., Johnson, A. D., Korbel, J. O., Lee, C., Snyder, M. P., Sturgill, D.
1800; 10: 63
- **AdaReg: data adaptive robust estimation in linear regression with application in GTEx gene expressions.** *Statistical applications in genetics and molecular biology*
Wang, M., Jiang, L., Snyder, M. P.
2021
- **Exosome-wide Association Study for Metabolic Syndrome.** *Frontiers in genetics*
Gao, P., Snyder, M.
1800; 12: 783930
- **Adapting skills from genetic counseling to wearables technology research during the COVID-19 pandemic: Poised for the pivot.** *Journal of genetic counseling*
Higgs, E., Dagan-Rosenfeld, O., Snyder, M.
2021
- **Real-time Alerting System for COVID-19 Using Wearable Data.** *medRxiv : the preprint server for health sciences*
Alavi, A., Bogu, G. K., Wang, M., Rangan, E. S., Brooks, A. W., Wang, Q., Higgs, E., Celli, A., Mishra, T., Metwally, A. A., Cha, K., Knowles, P., Alavi, et al
2021
- **A DMS Shotgun Lipidomics Workflow Application to Facilitate High-Throughput, Comprehensive Lipidomics.** *Journal of the American Society for Mass Spectrometry*
Su, B., Bettcher, L. F., Hsieh, W. Y., Hornburg, D., Pearson, M. J., Blomberg, N., Giera, M., Snyder, M. P., Raftery, D., Bensinger, S. J., Williams, K. J.
2021
- **Swarm: A federated cloud framework for large-scale variant analysis.** *PLoS computational biology*
Bahmani, A. n., Ferriter, K. n., Krishnan, V. n., Alavi, A. n., Alavi, A. n., Tsao, P. S., Snyder, M. P., Pan, C. n.
2021; 17 (5): e1008977
- **Precision medicine in women with epilepsy: The challenge, systematic review, and future direction.** *Epilepsy & behavior : E&B*
Li, Y. n., Zhang, S. n., Snyder, M. P., Meador, K. J.
2021; 118: 107928
- **CTLA-4 expression by B-1a B cells is essential for immune tolerance.** *Nature communications*
Yang, Y. n., Li, X. n., Ma, Z. n., Wang, C. n., Yang, Q. n., Byrne-Steele, M. n., Hong, R. n., Min, Q. n., Zhou, G. n., Cheng, Y. n., Qin, G. n., Youngyupipatkul, J. V., Wing, et al
2021; 12 (1): 525
- **Cell-free DNA (cfDNA) and Exosome Profiling from a Year-Long Human Spaceflight Reveals Circulating Biomarkers.** *iScience*

- Bezdan, D., Grigorev, K., Meydan, C., Pelissier Vatter, F. A., Cioffi, M., Rao, V., MacKay, M., Nakahira, K., Burnham, P., Afshinnekoo, E., Westover, C., Butler, D., Mozsary, et al
2020; 23 (12): 101844
- **Rare Variant Burden Analysis within Enhancers Identifies CAV1 as an ALS Risk Gene.** *Cell reports*
Cooper-Knock, J., Zhang, S., Kenna, K. P., Moll, T., Franklin, J. P., Allen, S., Nezhad, H. G., Iacoangeli, A., Yacovzada, N. Y., Eitan, C., Hornstein, E., Ehilak, E., Celadova, et al
2020; 33 (9): 108456
 - **A Customizable Analysis Flow in Integrative Multi-Omics.** *Biomolecules*
Lancaster, S. M., Sanghi, A., Wu, S., Snyder, M. P.
2020; 10 (12)
 - **Metabolic Dynamics and Prediction of Gestational Age and Time to Delivery in Pregnant Women** *OBSTETRICAL & GYNECOLOGICAL SURVEY*
Liang, L., Rasmussen, M., Piening, B., Shen, X., Chen, S., Rost, H., Snyder, J. K., Tibshirani, R., Skotte, L., Lee, N. Y., Contrepolis, K., Feenstra, B., Zackriah, et al
2020; 75 (11): 649–51
 - **Inherited causes of clonal haematopoiesis in 97,691 whole genomes.** *Nature*
Bick, A. G., Weinstock, J. S., Nandakumar, S. K., Fulco, C. P., Bao, E. L., Zekavat, S. M., Szeto, M. D., Liao, X., Leventhal, M. J., Nasser, J., Chang, K., Laurie, C., Burugula, et al
2020
 - **Quality-control mechanisms targeting translationally stalled and C-terminally extended poly(GR) associated with ALS/FTD.** *Proceedings of the National Academy of Sciences of the United States of America*
Li, S., Wu, Z., Tantray, I., Li, Y., Chen, S., Dong, J., Glynn, S., Vogel, H., Snyder, M., Lu, B.
2020
 - **The GTEx Consortium atlas of genetic regulatory effects across human tissues** *SCIENCE*
Aguet, F., Barbeira, A. N., Bonazzola, R., Brown, A., Castel, S. E., Jo, B., Kasela, S., Kim-Hellmuth, S., Liang, Y., Parsana, P., Flynn, E., Fresard, L., Gamazon, et al
2020; 369 (6509): 1318+
 - **Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale.** *Nature genetics*
Li, X., Li, Z., Zhou, H., Gaynor, S. M., Liu, Y., Chen, H., Sun, R., Dey, R., Arnett, D. K., Aslibekyan, S., Ballantyne, C. M., Bielak, L. F., Blangero, et al
2020
 - **Multi-faceted epigenetic dysregulation of gene expression promotes esophageal squamous cell carcinoma.** *Nature communications*
Cao, W., Lee, H., Wu, W., Zaman, A., McCorkle, S., Yan, M., Chen, J., Xing, Q., Sinnott-Armstrong, N., Xu, H., Sailani, M. R., Tang, W., Cui, et al
2020; 11 (1): 3675
 - **Prevention of Severe Intestinal Barrier Dysfunction Through a Single-Species Probiotics Is Associated With the Activation of Microbiome-Mediated Glutamate-Glutamine Biosynthesis.** *Shock (Augusta, Ga.)*
Leng, Y., Jiang, C., Xing, X., Tsai, M., Snyder, M., Zhai, A., Yao, G.
2020
 - **Physiological blood-brain transport is impaired with age by a shift in transcytosis.** *Nature*
Yang, A. C., Stevens, M. Y., Chen, M. B., Lee, D. P., Stahli, D., Gate, D., Contrepolis, K., Chen, W., Iram, T., Zhang, L., Vest, R. T., Chaney, A., Lehallier, et al
2020
 - **Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise.** *Cell*
Sanford, J. A., Nogiec, C. D., Lindholm, M. E., Adkins, J. N., Amar, D., Dasari, S., Drugan, J. K., Fernandez, F. M., Radom-Aizik, S., Schenk, S., Snyder, M. P., Tracy, R. P., Vanderboom, et al
2020; 181 (7): 1464–74
 - **Towards personalized medicine in maternal and child health: integrating biologic and social determinants.** *Pediatric research*
Stevenson, D. K., Wong, R. J., Aghaeepour, N., Maric, I., Angst, M. S., Contrepolis, K., Darmstadt, G. L., Druzin, M. L., Eisenberg, M. L., Gaudilliere, B., Gibbs, R. S., Gotlib, I. H., Gould, et al

2020

- **The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution.** *Cell*
Rozenblatt-Rosen, O., Regev, A., Oberdoerffer, P., Nawy, T., Hupalowska, A., Rood, J. E., Ashenberg, O., Cerami, E., Coffey, R. J., Demir, E., Ding, L., Esplin, E. D., Ford, et al
2020; 181 (2): 236–49
- **Humans Are Selectively Exposed to *Pneumocystis jirovecii*.** *mBio*
Cisse, O. H., Ma, L., Jiang, C., Snyder, M., Kovacs, J. A.
2020; 11 (2)
- **Systematic Identification of Regulators of Oxidative Stress Reveals Non-canonical Roles for Peroxisomal Import and the Pentose Phosphate Pathway.** *Cell reports*
Dubreuil, M. M., Morgens, D. W., Okumoto, K., Honsho, M., Contrepolis, K., Lee-McMullen, B., Traber, G. M., Sood, R. S., Dixon, S. J., Snyder, M. P., Fujiki, Y., Bassik, M. C.
2020; 30 (5): 1417
- **The MEK5-ERK5 kinase axis controls lipid metabolism in small cell lung cancer.** *Cancer research*
Cristea, S., Coles, G. L., Hornburg, D., Gershkovitz, M., Arand, J., Cao, S., Sen, T., Williamson, S. C., Kim, J. W., Drinas, A. P., He, A., Le Cam, L., Byers, et al
2020
- **Multiomic immune clockworks of pregnancy.** *Seminars in immunopathology*
Peterson, L. S., Stelzer, I. A., Tsai, A. S., Ghaemi, M. S., Han, X. n., Ando, K. n., Winn, V. D., Martinez, N. R., Contrepolis, K. n., Moufarrej, M. N., Quake, S. n., Relman, D. A., Snyder, et al
2020
- **Cumulative Lifetime Burden of Cardiovascular Disease From Early Exposure to Air Pollution.** *Journal of the American Heart Association*
Kim, J. B., Prunicki, M. n., Haddad, F. n., Dant, C. n., Sampath, V. n., Patel, R. n., Smith, E. n., Akdis, C. n., Balmes, J. n., Snyder, M. P., Wu, J. C., Nadeau, K. C.
2020; 9 (6): e014944
- **A limited set of transcriptional programs define major cell types.** *Genome research*
Breschi, A. n., Muñoz-Aguirre, M. n., Wucher, V. n., Davis, C. A., Garrido-Martín, D. n., Djebali, S. n., Gillis, J. n., Pervouchine, D. D., Vlasova, A. n., Dobin, A. n., Zaleski, C. n., Drenkow, J. n., Danyko, et al
2020; 30 (7): 1047–59
- **Multiomics Characterization of Preterm Birth in Low- and Middle-Income Countries.** *JAMA network open*
Jehan, F. n., Sazawal, S. n., Baqui, A. H., Nisar, M. I., Dhingra, U. n., Khanam, R. n., Ilyas, M. n., Dutta, A. n., Mitra, D. K., Mehmood, U. n., Deb, S. n., Mahmud, A. n., Hotwani, et al
2020; 3 (12): e2029655
- **Remodeling of active endothelial enhancers is associated with aberrant gene-regulatory networks in pulmonary arterial hypertension.** *Nature communications*
Reyes-Palomares, A. n., Gu, M. n., Grubert, F. n., Berest, I. n., Sa, S. n., Kasowski, M. n., Arnold, C. n., Shuai, M. n., Srivas, R. n., Miao, S. n., Li, D. n., Snyder, M. P., Rabinovitch, et al
2020; 11 (1): 1673
- **Classifying non-small cell lung cancer types and transcriptomic subtypes using convolutional neural networks.** *Journal of the American Medical Informatics Association : JAMIA*
Yu, K. H., Wang, F. n., Berry, G. J., Ré, C. n., Altman, R. B., Snyder, M. n., Kohane, I. S.
2020; 27 (5): 757–69
- **Long-read assays shed new light on the transcriptome complexity of a viral pathogen.** *Scientific reports*
Tombácz, D. n., Prazsák, I. n., Csabai, Z. n., Moldován, N. n., Dénes, B. n., Snyder, M. n., Boldogkői, Z. n.
2020; 10 (1): 13822
- **Research on the Human Proteome Reaches a Major Milestone: >90% of Predicted Human Proteins Now Credibly Detected, According to the HUPO Human Proteome Project.** *Journal of proteome research*
Omenn, G. S., Lane, L. n., Overall, C. M., Cristea, I. M., Corrales, F. J., Lindskog, C. n., Paik, Y. K., Van Eyk, J. E., Liu, S. n., Pennington, S. R., Snyder, M. P., Baker, M. S., Bandeira, et al
2020

- **A high-stringency blueprint of the human proteome.** *Nature communications*
Adhikari, S., Nice, E. C., Deutsch, E. W., Lane, L., Omenn, G. S., Pennington, S. R., Paik, Y., Overall, C. M., Corrales, F. J., Cristea, I. M., Van Eyk, J. E., Uhlen, M., Lindskog, et al
2020; 11 (1): 5301
- **iPSC Modeling of RBM20-Deficient DCM Identifies Upregulation of RBM20 as a Therapeutic Strategy.** *Cell reports*
Briganti, F. n., Sun, H. n., Wei, W. n., Wu, J. n., Zhu, C. n., Liss, M. n., Karakikes, I. n., Rego, S. n., Cipriano, A. n., Snyder, M. n., Meder, B. n., Xu, Z. n., Millat, et al
2020; 32 (10): 108117
- **RobNorm: Model-Based Robust Normalization Method for Labeled Quantitative Mass Spectrometry Proteomics Data.** *Bioinformatics (Oxford, England)*
Wang, M. n., Jiang, L. n., Jian, R. n., Chan, J. Y., Liu, Q. n., Snyder, M. P., Tang, H. n.
2020
- **Longitudinal Analysis of Serum Cytokine Levels and Gut Microbial Abundance Links IL-17/IL-22 with Clostridia and Insulin Sensitivity in Humans.** *Diabetes*
Zhou, X. n., Johnson, J. S., Spakowicz, D. n., Zhou, W. n., Zhou, Y. n., Sodergren, E. n., Snyder, M. n., Weinstock, G. M.
2020
- **Immunologic effects of forest fire exposure show increases in IL-1 β and CRP.** *Allergy*
Prunicki, M. M., Dant, C. C., Cao, S. n., Maecker, H. n., Haddad, F. n., Kim, J. B., Snyder, M. n., Wu, J. n., Nadeau, K. n.
2020
- **Human-engineered Treg-like cells suppress FOXP3-deficient T cells but preserve adaptive immune responses in vivo.** *Clinical & translational immunology*
Sato, Y. n., Passerini, L. n., Piening, B. D., Uyeda, M. J., Goodwin, M. n., Gregori, S. n., Snyder, M. P., Bertaina, A. n., Roncarolo, M. G., Bacchetta, R. n.
2020; 9 (11): e1214
- **Meta-analytic approach for transcriptome profiling of herpes simplex virus type 1.** *Scientific data*
Tombácz, D. n., Torma, G. n., Gulyás, G. n., Moldován, N. n., Snyder, M. n., Boldogkői, Z. n.
2020; 7 (1): 223
- **Chromosome-level de novo assembly of the pig-tailed macaque genome using linked-read sequencing and HiC proximity scaffolding.** *GigaScience*
Roodgar, M. n., Babveyh, A. n., Nguyen, L. H., Zhou, W. n., Sinha, R. n., Lee, H. n., Hanks, J. B., Avula, M. n., Jiang, L. n., Jian, R. n., Lee, H. n., Song, G. n., Chaib, et al
2020; 9 (7)
- **PPAR γ -p53-Mediated Vasculoregenerative Program to Reverse Pulmonary Hypertension.** *Circulation research*
Hennigs, J. K., Cao, A. n., Li, C. G., Shi, M. n., Mienert, J. n., Miyagawa, K. n., Körbelin, J. n., Marciano, D. P., Chen, P. I., Roughley, M. n., Elliott, M. V., Harper, R. L., Bill, et al
2020
- **Obesity Drives Delayed Infarct Expansion, Inflammation, and Distinct Gene Networks in a Mouse Stroke Model.** *Translational stroke research*
Peterson, T. C., Lechtenberg, K. J., Piening, B. D., Lucas, T. A., Wei, E. n., Chaib, H. n., Dowdell, A. K., Snyder, M. n., Buckwalter, M. S.
2020
- **Template-switching artifacts resemble alternative polyadenylation.** *BMC genomics*
Balazs, Z., Tombacz, D., Csabai, Z., Moldovan, N., Snyder, M., Boldogkoi, Z.
2019; 20 (1): 824
- **Big data and health** *LANCET DIGITAL HEALTH*
Snyder, M., Zhou, W.
2019; 1 (6): E252–E254
- **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
2019; 8
- **Engineering Genetic Predisposition in Human Neuroepithelial Stem Cells Recapitulates Medulloblastoma Tumorigenesis.** *Cell stem cell*
Huang, M., Taylor, J., Zhen, Q., Gillmor, A. H., Miller, M. L., Weishaupt, H., Chen, J., Zheng, T., Nash, E. K., McHenry, L. K., An, Z., Ye, F., Takashima, et al
2019
- **Novel mutations in PIEZO1 cause an autosomal recessive generalized lymphatic dysplasia with non-immune hydrops fetalis (vol 6, 8035, 2015) NATURE COMMUNICATIONS**
Fotiou, E., Martin-Almedina, S., Simpson, M. A., Lin, S., Gordon, K., Brice, G., Atton, G., Jeffery, I., Rees, D. C., Mignot, C., Vogt, J., Homfray, T., Snyder, et al
2019; 10
- **Analysis of the Complete Genome Sequence of a Novel, Pseudorabies Virus Strain Isolated in Southeast Europe** *CANADIAN JOURNAL OF INFECTIOUS DISEASES & MEDICAL MICROBIOLOGY*
Csabai, Z., Tombacz, D., Deim, Z., Snyder, M., Boldogkoi, Z.
2019; 2019
- **Much ado about nothing: A qualitative study of the experiences of an average-risk population receiving results of exome sequencing** *JOURNAL OF GENETIC COUNSELING*
Rego, S., Dagan-Rosenfeld, O., Bivona, S. A., Snyder, M. P., Ormond, K. E.
2019; 28 (2): 428–37
- **Much ado about nothing: A qualitative study of the experiences of an average-risk population receiving results of exome sequencing.** *Journal of genetic counseling*
Rego, S., Dagan-Rosenfeld, O., Bivona, S. A., Snyder, M. P., Ormond, K. E.
2019
- **Multi-Omics Profiling, Microscopic Cervical Remodeling, and Parturition: Insights from the Smart Diaphragm Study.**
Liang, L., Dunn, J. P., Chen, S., Tsai, M., Hornburg, D., Newmann, S., Avina, M., Leng, Y., Holman, R., Lee, T. H., Qureshi, S., Montelongo, E., Zhao, et al

SAGE PUBLICATIONS INC.2019: 216A

- **Applying circulating tumor DNA methylation in the diagnosis of lung cancer.** *Precision clinical medicine*
Li, L., Fu, K., Zhou, W., Snyder, M.
2019; 2 (1): 45-56
- **Windows Into Human Health Through Wearables Data Analytics.** *Current opinion in biomedical engineering*
Witt, D., Kellogg, R., Snyder, M., Dunn, J.
2019; 9: 28-46
- **Lifelong physical activity is associated with promoter hypomethylation of genes involved in metabolism, myogenesis, contractile properties and oxidative stress resistance in aged human skeletal muscle.** *Scientific reports*
Sailani, M. R., Halling, J. F., Moller, H. D., Lee, H., Plomgaard, P., Pilegaard, H., Snyder, M. P., Regenberg, B.
2019; 9 (1): 3272
- **Long-Read Sequencing - A Powerful Tool in Viral Transcriptome Research.** *Trends in microbiology*
Boldogkoi, Z., Moldovan, N., Balazs, Z., Snyder, M., Tombacz, D.
2019
- **2017 NIH-wide workshop report on "The Human Microbiome: Emerging Themes at the Horizon of the 21st Century"** *MICROBIOME*
Alm, E., Borenstein, E., Britton, R. A., Bultman, S. J., Chang, E. B., Cho, M., Dantas, G., Dominguez-Bello, M., Donovan, S. M., Dorrestein, P., Douglas, A. E., Gewirtz, A., Ghannoum, et al
2019; 7: 32
- **Whole-exome sequencing data of suicide victims who had suffered from major depressive disorder.** *Scientific data*
Tombacz, D., Maroti, Z., Kalmar, T., Palkovits, M., Snyder, M., Boldogkoi, Z.
2019; 6: 190010
- **Whole-exome sequencing data of suicide victims who had suffered from major depressive disorder** *SCIENTIFIC DATA*
Tombacz, D., Maroti, Z., Kalmar, T., Palkovits, M., Snyder, M., Boldogkoi, Z.
2019; 6
- **Smooth Muscle Contact Drives Endothelial Regeneration by BMPR2-Notch1-Mediated Metabolic and Epigenetic Changes** *CIRCULATION RESEARCH*
Miyagawa, K., Shi, M., Chen, P., Hennigs, J. K., Zhao, Z., Wang, M., Li, C. G., Saito, T., Taylor, S., Sa, S., Cao, A., Wang, L., Snyder, et al
2019; 124 (2): 211-24
- **Activation of PDGF pathway links LMNA mutation to dilated cardiomyopathy.** *Nature*
Lee, J. n., Termglinchan, V. n., Diecke, S. n., Itzhaki, I. n., Lam, C. K., Garg, P. n., Lau, E. n., Greenhaw, M. n., Seeger, T. n., Wu, H. n., Zhang, J. Z., Chen, X. n., Gil, et al
2019
- **Phenotypically-Silent Bone Morphogenetic Protein Receptor 2 (Bmpr2) Mutations Predispose Rats to Inflammation-Induced Pulmonary Arterial Hypertension by Enhancing The Risk for Neointimal Transformation.** *Circulation*
Tian, W. n., Jiang, X. n., Sung, Y. K., Shuffle, E. n., Wu, T. H., Kao, P. N., Tu, A. B., Dorfmueller, P. n., Cao, A. n., Wang, L. n., Peng, G. n., Kim, Y. n., Zhang, et al
2019
- **Macrophage de novo NAD(+) synthesis specifies immune function in aging and inflammation** *NATURE IMMUNOLOGY*
Minhas, P. S., Liu, L., Moon, P. K., Joshi, A. U., Dove, C., Mhatre, S., Contrepois, K., Wang, Q., Lee, B. A., Coronado, M., Bernstein, D., Snyder, M. P., Migaud, et al
2019; 20 (1): 50-+
- **Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project.** *Journal of proteome research*
Omenn, G. S., Lane, L. n., Overall, C. M., Corrales, F. J., Schwenk, J. M., Paik, Y. K., Van Eyk, J. E., Liu, S. n., Pennington, S. n., Snyder, M. P., Baker, M. S., Deutsch, E. W.
2019
- **MACHINE LEARNING ANALYSIS OF ULTRA-DEEP WHOLE-GENOME SEQUENCING IN HUMAN BRAIN REVEALS SOMATIC GENOMIC RETROTRANSPOSITION IN GLIA AS WELL AS IN NEURONS**

Urban, A., Zhu, X., Zhou, B., Sloan, S., Pattni, R., Fiston-Lavier, A., Snyder, M., Petrov, D., Abyzov, A., Vaccarino, F., Barres, B., Vogel, H., Tammimga, et al
ELSEVIER.2019: 1240

- **Global metabolic profiling to model biological processes of aging in twins.** *Aging cell*
Bunning, B. J., Contrepois, K. n., Lee-McMullen, B. n., Dhondalay, G. K., Zhang, W. n., Tupa, D. n., Raeber, O. n., Desai, M. n., Nadeau, K. C., Snyder, M. P., Andorf, S. n.
2019: e13073
- **Smart Diaphragm Study: Multi-omics profiling and cervical device measurements during pregnancy**
Liang, L., Dunn, J. P., Chen, S., Tsai, M., Hornburg, D., Newmann, S., Chung, P., Avina, M., Leng, Y., Holman, R., Lee, T. H., Berrios, S., Qureshi, et al
MOSBY-ELSEVIER.2019: S649
- **Personalized Metabolomics.** *Methods in molecular biology (Clifton, N.J.)*
Marciano, D. P., Snyder, M. P.
2019; 1978: 447–56
- **Analysis of the Complete Genome Sequence of a Novel, Pseudorabies Virus Strain Isolated in Southeast Europe.** *The Canadian journal of infectious diseases & medical microbiology = Journal canadien des maladies infectieuses et de la microbiologie medicale*
Csabai, Z. n., Tombác, D. n., Deim, Z. n., Snyder, M. n., Boldogkői, Z. n.
2019; 2019: 1806842
- **Heterogeneity in old fibroblasts is linked to variability in reprogramming and wound healing.** *Nature*
Mahmoudi, S. n., Mancini, E. n., Xu, L. n., Moore, A. n., Jahanbani, F. n., Hebestreit, K. n., Srinivasan, R. n., Li, X. n., Devarajan, K. n., Prélôt, L. n., Ang, C. E., Shibuya, Y. n., Benayoun, et al
2019; 574 (7779): 553–58
- **Multomics modeling of the immunome, transcriptome, microbiome, proteome and metabolome adaptations during human pregnancy** *BIOINFORMATICS*
Ghaemi, M., DiGiulio, D. B., Contrepois, K., Callahan, B., Ngo, T. M., Lee-McMullen, B., Lehallier, B., Robaczewska, A., Mcilwain, D., Rosenberg-Hasson, Y., Wong, R. J., Quaintance, C., Culos, et al
2019; 35 (1): 95–103
- **Multomics modeling of the immunome, transcriptome, microbiome, proteome and metabolome adaptations during human pregnancy.** *Bioinformatics (Oxford, England)*
Ghaemi, M. S., DiGiulio, D. B., Contrepois, K., Callahan, B., Ngo, T. T., Lee-McMullen, B., Lehallier, B., Robaczewska, A., Mcilwain, D., Rosenberg-Hasson, Y., Wong, R. J., Quaintance, C., Culos, et al
2019; 35 (1): 95–103
- **A machine-compiled database of genome-wide association studies.** *Nature communications*
Kuleshov, V. n., Ding, J. n., Vo, C. n., Hancock, B. n., Ratner, A. n., Li, Y. n., Ré, C. n., Batzoglou, S. n., Snyder, M. n.
2019; 10 (1): 3341
- **Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements.** *Nature communications*
Tycko, J. n., Wainberg, M. n., Marinov, G. K., Ursu, O. n., Hess, G. T., Ego, B. K., Aradhana, n. n., Li, A. n., Truong, A. n., Trevino, A. E., Spees, K. n., Yao, D. n., Kaplow, et al
2019; 10 (1): 4063
- **Understanding health disparities.** *Journal of perinatology : official journal of the California Perinatal Association*
Stevenson, D. K., Wong, R. J., Aghaeepour, N., Angst, M. S., Darmstadt, G. L., DiGiulio, D. B., Druzin, M. L., Gaudilliere, B., Gibbs, R. S., B Gould, J., Katz, M., Li, J., Moufarrej, et al
2018
- **Cross-Platform Comparison of Untargeted and Targeted Lipidomics Approaches on Aging Mouse Plasma.** *Scientific reports*
Contrepois, K., Mahmoudi, S., Ubhi, B. K., Papsdorf, K., Hornburg, D., Brunet, A., Snyder, M.
2018; 8 (1): 17747
- **Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project** *JOURNAL OF PROTEOME RESEARCH*
Omenn, G. S., Lane, L., Overall, C. M., Corrales, F. J., Schwenk, J. M., Paik, Y., Van Eyk, J. E., Liu, S., Snyder, M., Baker, M. S., Deutsch, E. W.

2018; 17 (12): 4031–41

- **Transcriptomic study of Herpes simplex virus type-1 using full-length sequencing techniques.** *Scientific data*
Boldogkoi, Z., Szucs, A., Balazs, Z., Sharon, D., Snyder, M., Tombacz, D.
2018; 5: 180266
- **Transcriptomic study of Herpes simplex virus type-1 using full-length sequencing techniques** *SCIENTIFIC DATA*
Boldogkoi, Z., Szucs, A., Balazs, Z., Sharon, D., Snyder, M., Tombacz, D.
2018; 5
- **Macrophage de novo NAD⁺ synthesis specifies immune function in aging and inflammation.** *Nature immunology*
Minhas, P. S., Liu, L., Moon, P. K., Joshi, A. U., Dove, C., Mhatre, S., Contrepois, K., Wang, Q., Lee, B. A., Coronado, M., Bernstein, D., Snyder, M. P., Migaud, et al
2018
- **Dynamic Transcriptome Profiling Dataset of Vaccinia Virus Obtained from Long-read Sequencing Techniques.** *GigaScience*
Tombacz, D., Prazsak, I., Szucs, A., Denes, B., Snyder, M., Boldogkoi, Z.
2018
- **Smooth Muscle Contact Drives Endothelial Regeneration by BMPR2-Notch1 Mediated Metabolic and Epigenetic Changes.** *Circulation research*
Miyagawa, K., Shi, M., Chen, P., Hennigs, J. K., Zhao, Z., Wang, M., Li, C. G., Saito, T., Taylor, S., Sa, S., Cao, A., Wang, L., Snyder, et al
2018
- **Identification of phagocytosis regulators using magnetic genome-wide CRISPR screens.** *Nature genetics*
Haney, M. S., Bohlen, C. J., Morgens, D. W., Ousey, J. A., Barkal, A. A., Tsui, C. K., Ego, B. K., Levin, R., Kamber, R. A., Collins, H., Tucker, A., Li, A., Vorselen, et al
2018
- **Systematic Screening For Environmental And Behavioral Determinants Identifies Factors Detrimental to Skeletal Health**
Oei, L., Wu, J., Oei, E., Rivadeneira, F., Uitterlinden, A., Ioannidis, J., Snyder, M., Patel, C.
WILEY.2018: 279
- **Evaluation of whole exome sequencing as an alternative to BeadChip and whole genome sequencing in human population genetic analysis.** *BMC genomics*
Maroti, Z., Boldogkoi, Z., Tombacz, D., Snyder, M., Kalmar, T.
2018; 19 (1): 778
- **Precision Medicine: Role of Proteomics in Changing Clinical Management and Care.** *Journal of proteome research*
Van Eyk, J. E., Snyder, M. P.
2018
- **Wearables and the medical revolution.** *Personalized medicine*
Dunn, J., Runge, R., Snyder, M.
2018
- **Dual Platform Long-Read RNA-Sequencing Dataset of the Human Cytomegalovirus Lytic Transcriptome** *FRONTIERS IN GENETICS*
Balazs, Z., Tombacz, D., Szucs, A., Snyder, M., Boldogkoi, Z.
2018; 9
- **Dual Platform Long-Read RNA-Sequencing Dataset of the Human Cytomegalovirus Lytic Transcriptome.** *Frontiers in genetics*
Balázs, Z., Tombác, D., Szúcs, A., Snyder, M., Boldogkői, Z.
2018; 9: 432
- **Disruption of mesoderm formation during cardiac differentiation due to developmental exposure to 13-cis-retinoic acid.** *Scientific reports*
Liu, Q., Van Bortle, K., Zhang, Y., Zhao, M., Zhang, J. Z., Geller, B. S., Gruber, J. J., Jiang, C., Wu, J. C., Snyder, M. P.
2018; 8 (1): 12960
- **A Cloud-Based Metabolite and Chemical Prioritization System for the Biology/Disease-Driven Human Proteome Project.** *Journal of proteome research*
Yu, K., Lee, T. M., Chen, Y., Re, C., Kou, S. C., Chiang, J., Snyder, M., Kohane, I. S.

2018

- **Long-Read Sequencing Revealed an Extensive Transcript Complexity in Herpesviruses** *FRONTIERS IN GENETICS*
Tombacz, D., Balazs, Z., Csabai, Z., Snyder, M., Boldogkoi, Z.
2018; 9
- **Long-Read Sequencing Revealed an Extensive Transcript Complexity in Herpesviruses.** *Frontiers in genetics*
Tombacz, D., Balázs, Z., Csabai, Z., Snyder, M., Boldogkői, Z.
2018; 9: 259
- **An integrated global regulatory network of hematopoietic precursor cell self-renewal and differentiation** *INTEGRATIVE BIOLOGY*
You, Y., Duran, R., Jiang, L., Dong, X., Zong, S., Snyder, M., Wu, J.
2018; 10 (7): 390–405
- **High Throughput Sequencing and Assessing Disease Risk.** *Cold Spring Harbor perspectives in medicine*
Rego, S. M., Snyder, M. P.
2018
- **Transcriptome-wide survey of pseudorabies virus using next- and third-generation sequencing platforms** *SCIENTIFIC DATA*
Tombacz, D., Sharon, D., Szucs, A., Moldovan, N., Snyder, M., Boldogkoi, Z.
2018; 5: 180119
- **Integrative omics for health and disease** *NATURE REVIEWS GENETICS*
Karczewski, K. J., Snyder, M. P.
2018; 19 (5): 299–310
- **Personal Omics for Precision Health** *CIRCULATION RESEARCH*
Kellogg, R. A., Dunn, J., Snyder, M. P.
2018; 122 (9): 1169–71
- **Fast Metagenomic Binning via Hashing and Bayesian Clustering** *JOURNAL OF COMPUTATIONAL BIOLOGY*
Popic, V., Kuleshov, V., Snyder, M., Batzoglou, S.
2018
- **Distinct transcriptomic and exomic abnormalities within myelodysplastic syndrome marrow cells.** *Leukemia & lymphoma*
Im, H., Rao, V., Sridhar, K., Bentley, J., Mishra, T., Chen, R., Hall, J., Graber, A., Zhang, Y., Li, X., Mias, G. I., Snyder, M. P., Greenberg, et al
2018: 1-11
- **A global transcriptional network connecting noncoding mutations to changes in tumor gene expression** *NATURE GENETICS*
Zhang, W., Bojorquez-Gomez, A., Velez, D., Xu, G., Sanchez, K. S., Shen, J., Chen, K., Licon, K., Melton, C., Olson, K. M., Yu, M., Huang, J. K., Carter, et al
2018; 50 (4): 613–+
- **NF90/ILF3 is a transcription factor that promotes proliferation over differentiation by hierarchical regulation in K562 erythroleukemia cells** *PLOS ONE*
Wu, T., Shi, L., Adrian, J., Shi, M., Nair, R. V., Snyder, M. P., Kao, P. N.
2018; 13 (3): e0193126
- **Circular DNA elements of chromosomal origin are common in healthy human somatic tissue** *NATURE COMMUNICATIONS*
Moller, H., Mohiyuddin, M., Prada-Luengo, I., Sailani, M., Halling, J., Plomgaard, P., Maretty, L., Hansen, A., Snyder, M. P., Pilegaard, H., Lam, H. K., Regenber, B.
2018; 9: 1069
- **An Integrated Understanding of the Rapid Metabolic Benefits of a Carbohydrate-Restricted Diet on Hepatic Steatosis in Humans** *CELL METABOLISM*
Mardinoglu, A., Wu, H., Bjornson, E., Zhang, C., Hakkarainen, A., Rasanen, S. M., Lee, S., Mancina, R. M., Bergentall, M., Pietilainen, K. H., Soderlund, S., Matikainen, N., Stahlman, et al
2018; 27 (3): 559–+
- **Biallelic Mutations in ATP5F1D, which Encodes a Subunit of ATP Synthase, Cause a Metabolic Disorder** *AMERICAN JOURNAL OF HUMAN GENETICS*

- Olahova, M., Yoon, W., Thompson, K., Jangam, S., Fernandez, L., Davidson, J. M., Kyle, J. E., Grove, M. E., Fisk, D. G., Kohler, J. N., Holmes, M., Dries, A. M., Huang, et al
2018; 102 (3): 494–504
- **Full Genome Sequence of the Western Reserve Strain of Vaccinia Virus Determined by Third-Generation Sequencing** *MICROBIOLOGY RESOURCE ANNOUNCEMENTS*
Prazsak, I., Tombacz, D., Szucs, A., Denes, B., Snyder, M., Boldogkoi, Z.
2018; 6 (11)
 - **Applying genomics in heart transplantation** *TRANSPLANT INTERNATIONAL*
Keating, B. J., Pereira, A. C., Snyder, M., Piening, B. D.
2018; 31 (3): 278–90
 - **Multiplatform next-generation sequencing identifies novel RNA molecules and transcript isoforms of the endogenous retrovirus isolated from cultured cells** *FEMS MICROBIOLOGY LETTERS*
Moldovan, N., Szucs, A., Tombacz, D., Balazs, Z., Csabai, Z., Snyder, M., Boldogkoi, Z.
2018; 365 (5)
 - **Multi-Platform Sequencing Approach Reveals a Novel Transcriptome Profile in Pseudorabies Virus** *FRONTIERS IN MICROBIOLOGY*
Moldovan, N., Tombacz, D., Szucs, A., Csabai, Z., Snyder, M., Boldogkoi, Z.
2018; 8
 - **Omics AnalySis System for PRrecision Oncology (OASISPRO): a web-based omics analysis tool for clinical phenotype prediction** *BIOINFORMATICS*
Yu, K., Fitzpatrick, M. R., Pappas, L., Chan, W., Kung, J., Snyder, M.
2018; 34 (2): 319–20
 - **How many human proteoforms are there?** *Nature chemical biology*
Aebersold, R. n., Agar, J. N., Amster, I. J., Baker, M. S., Bertozzi, C. R., Boja, E. S., Costello, C. E., Cravatt, B. F., Fenselau, C. n., Garcia, B. A., Ge, Y. n., Gunawardena, J. n., Hendrickson, et al
2018; 14 (3): 206–14
 - **Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus.** *PLoS genetics*
Nanda, V. n., Wang, T. n., Pjanic, M. n., Liu, B. n., Nguyen, T. n., Matic, L. P., Hedin, U. n., Koplev, S. n., Ma, L. n., Franzén, O. n., Ruusalepp, A. n., Schadt, E. E., Björkegren, et al
2018; 14 (11): e1007755
 - **Distinct Transcriptomic and Exomic Abnormalities Within Myelodysplastic Syndrome Marrow Cells** *Leukemia & Lymphoma*
Im, H., Rao, V., Sridhar, K., Bentley, J., Mishra, T., Chen, R., Hall, J., Graber, A., Zhang, Y., Xiao, L., Mias, G., Snyder, M. P., Greenberg, et al
2018: 1-11
 - **SETD7 Drives Cardiac Lineage Commitment through Stage-Specific Transcriptional Activation.** *Cell stem cell*
Lee, J. n., Shao, N. Y., Paik, D. T., Wu, H. n., Guo, H. n., Termglinchan, V. n., Churko, J. M., Kim, Y. n., Kitani, T. n., Zhao, M. T., Zhang, Y. n., Wilson, K. D., Karakikes, et al
2018; 22 (3): 428–44.e5
 - **Value of Circulating Cytokine Profiling During Submaximal Exercise Testing in Myalgic Encephalomyelitis/Chronic Fatigue Syndrome.** *Scientific reports*
Moneghetti, K. J., Skhiri, M. n., Contrepolis, K. n., Kobayashi, Y. n., Maecker, H. n., Davis, M. n., Snyder, M. n., Haddad, F. n., Montoya, J. G.
2018; 8 (1): 2779
 - **Long-read sequencing of the human cytomegalovirus transcriptome with the Pacific Biosciences RSII platform** *SCIENTIFIC DATA*
Balazs, Z., Tombacz, D., Szucs, A., Snyder, M., Boldogkoi, Z.
2017; 4: 170194
 - **Challenges and recommendations for epigenomics in precision health** *NATURE BIOTECHNOLOGY*
Carter, A. C., Chang, H. Y., Church, G., Dombkowski, A., Ecker, J. R., Gil, E., Giresi, P. G., Greely, H., Greenleaf, W. J., Hacohen, N., He, C., Hill, D., Ko, et al
2017; 35 (12): 1128–32
 - **Cloud-based interactive analytics for terabytes of genomic variants data.** *Bioinformatics (Oxford, England)*

- Pan, C., McInnes, G., Deflaux, N., Snyder, M., Bingham, J., Datta, S., Tsao, P. S.
2017; 33 (23): 3709-3715
- **Long-Read Sequencing of Human Cytomegalovirus Transcriptome Reveals RNA Isoforms Carrying Distinct Coding Potentials** *SCIENTIFIC REPORTS*
Balazs, Z., Tombacz, D., Szucs, A., Csabai, Z., Megyeri, K., Petrov, A. N., Snyder, M., Boldogkoi, Z.
2017; 7: 15989
 - **Transcriptomic and epigenomic differences in human induced pluripotent stem cells generated from six reprogramming methods** *NATURE BIOMEDICAL ENGINEERING*
Churko, J. M., Lee, J., Ameen, M., Gu, M., Venkatasubramanian, M., Diecke, S., Sallam, K., Im, H., Wang, G., Gold, J. D., Salomonis, N., Snyder, M. P., Wu, et al
2017; 1 (10): 826–37
 - **Transcriptomic and epigenomic differences in human induced pluripotent stem cells generated from six reprogramming methods.** *Nature biomedical engineering*
Churko, J. M., Lee, J., Ameen, M., Gu, M., Venkatasubramanian, M., Diecke, S., Sallam, K., Im, H., Wang, G., Gold, J. D., Salomonis, N., Snyder, M. P., Wu, et al
2017; 1 (10): 826-837
 - **Long-Read Sequencing Reveals a GC Pressure during the Evolution of Porcine Endogenous Retrovirus** *MICROBIOLOGY RESOURCE ANNOUNCEMENTS*
Szucs, A., Moldovan, N., Tombacz, D., Csabai, Z., Snyder, M., Boldogkoi, Z.
2017; 5 (40)
 - **Novel nonsense gain-of-function NFKB2 mutations associated with a combined immunodeficiency phenotype** *BLOOD*
Kuehn, H., Niemela, J. E., Sreedhara, K., Stoddard, J. L., Grossman, J., Wysocki, C. A., de la Morena, M., Garofalo, M., Inlora, J., Snyder, M. P., Lewis, D. B., Stratakis, C. A., Fleisher, et al
2017; 130 (13): 1553–64
 - **Evaluation of the impact of ul54 gene-deletion on the global transcription and DNA replication of pseudorabies virus** *ARCHIVES OF VIROLOGY*
Csabai, Z., Takacs, I. F., Snyder, M., Boldogkoi, Z., Tombacz, D.
2017; 162 (9): 2679–94
 - **High-Coverage Whole-Exome Sequencing Identifies Candidate Genes for Suicide in Victims with Major Depressive Disorder** *SCIENTIFIC REPORTS*
Tombacz, D., Maroti, Z., Kalmar, T., Csabai, Z., Balazs, Z., Takahashi, S., Palkovits, M., Snyder, M., Boldogkoi, Z.
2017; 7: 7106
 - **Network analyses identify liver-specific targets for treating liver diseases** *MOLECULAR SYSTEMS BIOLOGY*
Lee, S., Zhang, C., Liu, Z., Klevstig, M., Mukhopadhyay, B., Bergentall, M., Cinar, R., Stahlman, M., Sikanic, N., Park, J. K., Deshmukh, S., Harzandi, A. M., Kuijpers, et al
2017; 13 (8): 938
 - **A Droplet Microfluidics Based Platform for Mining Metagenomic Libraries for Natural Compounds** *MICROMACHINES*
Theodorou, E., Scanga, R., Twardowski, M., Snyder, M. P., Brouzes, E.
2017; 8 (8)
 - **Discovery of Novel Human Gene Regulatory Modules from Gene Co-expression and Promoter Motif Analysis** *SCIENTIFIC REPORTS*
Ma, S., Snyder, M., Dinesh-Kumar, S. P.
2017; 7: 5557
 - **Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis** *NATURE COMMUNICATIONS*
Sahraeian, S., Mohiyuddin, M., Sebra, R., Tilgner, H., Afshar, P. T., Au, K., Asadi, N., Gerstein, M. B., Wong, W., Snyder, M. P., Schadt, E., Lam, H. K.
2017; 8: 59
 - **Long-Read Isoform Sequencing Reveals a Hidden Complexity of the Transcriptional Landscape of Herpes Simplex Virus Type 1** *FRONTIERS IN MICROBIOLOGY*
Tombacz, D., Csabai, Z., Szuca, A., Balazs, Z., Moldovan, N., Sharon, D., Snyder, M., Boldogkoi, Z.

2017; 8: 1079

- **Bisulfite-independent analysis of CpG island methylation enables genome-scale stratification of single cells** *NUCLEIC ACIDS RESEARCH*
Han, L., Wu, H., Zhu, H., Kim, K., Marjani, S. L., Riester, M., Euskirchen, G., Zi, X., Yang, J., Han, J., Snyder, M., Park, I., Irizarry, et al
2017; 45 (10): e77
- **Isolated Congenital Anosmia and CNGA2 Mutation.** *Scientific reports*
Sailani, M. R., Jingga, I., MirMazlomi, S. H., Bitarafan, F., Bernstein, J. A., Snyder, M. P., Garshasbi, M.
2017; 7 (1): 2667-?
- **Succinate and its G-protein-coupled receptor stimulates osteoclastogenesis.** *Nature communications*
Guo, Y., Xie, C., Li, X., Yang, J., Yu, T., Zhang, R., Zhang, T., Saxena, D., Snyder, M., Wu, Y., Li, X.
2017; 8: 15621-?
- **Multi-platform analysis reveals a complex transcriptome architecture of a circovirus.** *Virus research*
Moldován, N., Balázs, Z., Tombácz, D., Csabai, Z., Szucs, A., Snyder, M., Boldogkoi, Z.
2017; 237: 37-46
- **Non-equivalence of Wnt and R-spondin ligands during Lgr5(+) intestinal stem-cell self-renewal** *NATURE*
Yan, K. S., Janda, C. Y., Chang, J., Zheng, G. X., Larkin, K. A., Luca, V. C., Chia, L. A., Mah, A. T., Han, A., Terry, J. M., Ootani, A., Roelf, K., Lee, et al
2017; 545 (7653): 238-?
- **intestinal stem-cell self-renewal.** *Nature*
Yan, K. S., Janda, C. Y., Chang, J., Zheng, G. X., Larkin, K. A., Luca, V. C., Chia, L. A., Mah, A. T., Han, A., Terry, J. M., Ootani, A., Roelf, K., Lee, et al
2017; 545 (7653): 238-242
- **Histone variant H2A.J accumulates in senescent cells and promotes inflammatory gene expression** *NATURE COMMUNICATIONS*
Contrepolis, K., Coudereau, C., Benayoun, B. A., Schuler, N., Roux, P., Bischof, O., Courbeyrette, R., Carvalho, C., Thuret, J., Ma, Z., Derbois, C., Nevers, M., Volland, et al
2017; 8
- **Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens** *NATURE COMMUNICATIONS*
Morgens, D. W., Wainberg, M., Boyle, E. A., Ursu, O., Araya, C. L., Tsui, C. K., Haney, M. S., Hess, G. T., Han, K., Jeng, E. E., Li, A., Snyder, M. P., Greenleaf, et al
2017; 8
- **A Case Report of Hypoglycemia and Hypogammaglobulinemia: DAVID syndrome in a patient with a novel NFKB2 mutation.** *journal of clinical endocrinology and metabolism*
Lal, R. A., Bachrach, L. K., Hoffman, A. R., Inlora, J., Rego, S., Snyder, M. P., Lewis, D. B.
2017
- **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
2017; 20 (4): 490-?
- **Gpr124 is essential for blood-brain barrier integrity in central nervous system disease** *NATURE MEDICINE*
Chang, J., Mancuso, M. R., Maier, C., Liang, X., Yuki, K., Yang, L., Kwong, J. W., Wang, J., Rao, V., Vallon, M., Kosinski, C., Zhang, J. J., Mah, et al
2017; 23 (4): 450-?
- **Induced Pluripotent Stem Cell Model of Pulmonary Arterial Hypertension Reveals Novel Gene Expression and Patient Specificity** *AMERICAN JOURNAL OF RESPIRATORY AND CRITICAL CARE MEDICINE*
Sa, S., Gu, M., Chappe, J., Shao, N., Ameen, M., Elliott, K. A., Li, D., Grubert, F., Li, C. G., Taylor, S., Cao, A., Ma, Y., Fong, et al
2017; 195 (7): 930-941
- **Characterization of the Dynamic Transcriptome of a Herpesvirus with Long-read Single Molecule Real-Time Sequencing.** *Scientific reports*
Tombácz, D., Balázs, Z., Csabai, Z., Moldován, N., Szucs, A., Sharon, D., Snyder, M., Boldogkoi, Z.
2017; 7: 43751-?

- **Association of AHSG with alopecia and mental retardation (APMR) syndrome.** *Human genetics*
Reza Sailani, M., Jahanbani, F., Nasiri, J., Behnam, M., Salehi, M., Sedghi, M., Hoseinzadeh, M., Takahashi, S., Zia, A., Gruber, J., Lynch, J. L., Lam, D., Winkelmann, et al
2017; 136 (3): 287-296
- **A common class of transcripts with 5'-intron depletion, distinct early coding sequence features, and N-1-methyladenosine modification** *RNA*
Cenik, C., Chua, H. N., Singh, G., Akef, A., Snyder, M. P., Palazzo, A. F., Moore, M. J., Roth, F. P.
2017; 23 (3): 270-283
- **-methyladenosine modification.** *RNA (New York, N.Y.)*
Cenik, C., Chua, H. N., Singh, G., Akef, A., Snyder, M. P., Palazzo, A. F., Moore, M. J., Roth, F. P.
2017; 23 (3): 270-283
- **Single cell transcriptomics reveals unanticipated features of early hematopoietic precursors.** *Nucleic acids research*
Yang, J., Tanaka, Y., Seay, M., Li, Z., Jin, J., Garmire, L. X., Zhu, X., Taylor, A., Li, W., Euskirchen, G., Halene, S., Kluger, Y., Snyder, et al
2017; 45 (3): 1281-1296
- **Single cell transcriptomics reveals unanticipated features of early hematopoietic precursors** *NUCLEIC ACIDS RESEARCH*
Yang, J., Tanaka, Y., Seay, M., Li, Z., Jin, J., Garmire, L. X., Zhu, X., Taylor, A., Li, W., Euskirchen, G., Halene, S., Kluger, Y., Snyder, et al
2017; 45 (3): 1281-1296
- **Genetic Adaptation of Porcine Circovirus Type 1 to Cultured Porcine Kidney Cells Revealed by Single-Molecule Long-Read Sequencing Technology** *MICROBIOLOGY RESOURCE ANNOUNCEMENTS*
Tombacz, D., Moldovan, N., Balazs, Z., Csabai, Z., Snyder, M., Boldogkői, Z.
2017; 5 (5)
- **Multi-Platform Sequencing Approach Reveals a Novel Transcriptome Profile in Pseudorabies Virus.** *Frontiers in microbiology*
Moldován, N., Tombácz, D., Szűcs, A., Csabai, Z., Snyder, M., Boldogkői, Z.
2017; 8: 2708
- **Pharmacological rescue of diabetic skeletal stem cell niches.** *Science translational medicine*
Tevlin, R., Seo, E. Y., Marecic, O., McArdle, A., Tong, X., Zimdahl, B., Malkovskiy, A., Sinha, R., Gulati, G., Li, X., Wearda, T., Morganti, R., Lopez, et al
2017; 9 (372)
- **ChIA-PET2: a versatile and flexible pipeline for ChIA-PET data analysis.** *Nucleic acids research*
Li, G., Chen, Y., Snyder, M. P., Zhang, M. Q.
2017; 45 (1)
- **Identification of a novel mutation in APTX gene associated with Ataxia-oculomotor apraxia.** *Cold Spring Harbor molecular case studies*
Inlora, J. n., Sailani, M. R., Khodadadi, H. n., Teymurinezhad, A. n., Takahashi, S. n., Bernstein, J. A., Garshasbi, M. n., Snyder, M. P.
2017
- **Genome-Wide Temporal Profiling of Transcriptome and Open Chromatin of Early Cardiomyocyte Differentiation Derived From hiPSCs and hESCs.** *Circulation research*
Liu, Q. n., Jiang, C. n., Xu, J. n., Zhao, M. T., Van Bortle, K. n., Cheng, X. n., Wang, G. n., Chang, H. Y., Wu, J. C., Snyder, M. P.
2017; 121 (4): 376–91
- **WISP3 mutation associated with Pseudorheumatoid Dysplasia.** *Cold Spring Harbor molecular case studies*
Sailani, M. R., Chappell, J. n., Inlora, J. n., Lynch, L. n., Narasimha, A. n., Mazroui, S. n., Zia, A. n., Bernstein, J. n., Aryani, O. n., Snyder, M. P.
2017
- **Topological organization and dynamic regulation of human tRNA genes during macrophage differentiation.** *Genome biology*
Van Bortle, K. n., Phanstiel, D. H., Snyder, M. P.
2017; 18 (1): 180
- **GATTACA: Lightweight Metagenomic Binning Using Kmer Counting**
Popic, V., Kuleshov, V., Snyder, M., Batzoglou, S., Sahinalp, S. C.
SPRINGER-VERLAG BERLIN.2017: 391–92

- **Cell Type-Specific Chromatin Signatures Underline Regulatory DNA Elements in Human Induced Pluripotent Stem Cells and Somatic Cells.** *Circulation research*
Zhao, M. T., Shao, N. Y., Hu, S. n., Ma, N. n., Srinivasan, R. n., Jahanbani, F. n., Lee, J. n., Zhang, S. L., Snyder, M. P., Wu, J. C.
2017; 121 (11): 1237–50
- **Dynamic landscape and regulation of RNA editing in mammals.** *Nature*
Tan, M. H., Li, Q. n., Shanmugam, R. n., Piskol, R. n., Kohler, J. n., Young, A. N., Liu, K. I., Zhang, R. n., Ramaswami, G. n., Ariyoshi, K. n., Gupte, A. n., Keegan, L. P., George, et al
2017; 550 (7675): 249–54
- **Landscape of X chromosome inactivation across human tissues.** *Nature*
Tukiainen, T. n., Villani, A. C., Yen, A. n., Rivas, M. A., Marshall, J. L., Satija, R. n., Aguirre, M. n., Gauthier, L. n., Fleharty, M. n., Kirby, A. n., Cummings, B. B., Castel, S. E., Karczewski, et al
2017; 550 (7675): 244–48
- **Molecular and functional resemblance of differentiated cells derived from isogenic human iPSCs and SCNT-derived ESCs.** *Proceedings of the National Academy of Sciences of the United States of America*
Zhao, M. T., Chen, H. n., Liu, Q. n., Shao, N. Y., Sayed, N. n., Wo, H. T., Zhang, J. Z., Ong, S. G., Liu, C. n., Kim, Y. n., Yang, H. n., Chour, T. n., Ma, et al
2017
- **Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease.** *Nature genetics*
2017; 49 (12): 1664–70
- **The impact of rare variation on gene expression across tissues.** *Nature*
Li, X. n., Kim, Y. n., Tsang, E. K., Davis, J. R., Damani, F. N., Chiang, C. n., Hess, G. T., Zappala, Z. n., Strober, B. J., Scott, A. J., Li, A. n., Ganna, A. n., Bassik, et al
2017; 550 (7675): 239–43
- **Genetic effects on gene expression across human tissues.** *Nature*
Battle, A. n., Brown, C. D., Engelhardt, B. E., Montgomery, S. B.
2017; 550 (7675): 204–13
- **Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation.** *Nature genetics*
Rubin, A. J., Barajas, B. C., Furlan-Magaril, M. n., Lopez-Pajares, V. n., Mumbach, M. R., Howard, I. n., Kim, D. S., Boxer, L. D., Cairns, J. n., Spivakov, M. n., Wingett, S. W., Shi, M. n., Zhao, et al
2017; 49 (10): 1522–28
- **Cloud-based Interactive Analytics for Terabytes of Genomic Variants Data** *Bioinformatics*
Pan, C., McInnes, G., Deflaux, N., Snyder, M. P., Bingham, J., Datta, S., Tsao, P. S.
2017: 3709–15
- **Disease Model of GATA4 Mutation Reveals Transcription Factor Cooperativity in Human Cardiogenesis** *CELL*
Ang, Y., Rivas, R. N., Ribeiro, A. J., Srivas, R., Rivera, J., Stone, N. R., Pratt, K., Mohamed, T. M., Fu, J., Spencer, C. I., Tippens, N. D., Li, M., Narasimha, et al
2016; 167 (7): 1734-?
- **Can heavy isotopes increase lifespan? Studies of relative abundance in various organisms reveal chemical perspectives on aging.** *BioEssays*
Li, X., Snyder, M. P.
2016; 38 (11): 1093-1101
- **iPSC Model of Pulmonary Arterial Hypertension Reveals Novel Gene Expression and Patient Specificity.** *American journal of respiratory and critical care medicine*
Sa, S., Gu, M., Chappell, J., Shao, N., Ameen, M., Elliott, K. A., Li, D., Grubert, F., Li, C. G., Taylor, S., Cao, A., Ma, Y., Fong, et al
2016: -?
- **Nat1 Deficiency Is Associated with Mitochondrial Dysfunction and Exercise Intolerance in Mice** *CELL REPORTS*
Chennamsetty, I., Coronado, M., Contrepolis, K., Keller, M. P., Carcamo-Orive, I., Sandin, J., Fajardo, G., Whittle, A. J., Fathzadeh, M., Snyder, M., Reaven, G., Attie, A. D., Bernstein, et al
2016; 17 (2): 527-540

- **Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution.** *Nature genetics*
Corces, M. R., Buenrostro, J. D., Wu, B., Greenside, P. G., Chan, S. M., Koenig, J. L., Snyder, M. P., Pritchard, J. K., Kundaje, A., Greenleaf, W. J., Majeti, R., Chang, H. Y.
2016; 48 (10): 1193-1203
- **A proposal for validation of antibodies** *NATURE METHODS*
Uhlen, M., Bandrowski, A., Carr, S., Edwards, A., Ellenberg, J., Lundberg, E., Rimm, D. L., Rodriguez, H., Hiltke, T., Snyder, M., Yamamoto, T.
2016; 13 (10): 823-?
- **Multiple Pairwise Analysis of Non-homologous Centromere Coupling Reveals Preferential Chromosome Size-Dependent Interactions and a Role for Bouquet Formation in Establishing the Interaction Pattern** *PLOS GENETICS*
Lefrancois, P., Rockmill, B., Xie, P., Roeder, G. S., Snyder, M.
2016; 12 (10)
- **iPSC-derived cardiomyocytes reveal abnormal TGF- β signalling in left ventricular non-compaction cardiomyopathy.** *Nature cell biology*
Kodo, K., Ong, S., Jahanbani, F., Termglinchan, V., Hirono, K., Inanloorahatloo, K., Ebert, A. D., Shukla, P., Abilez, O. J., Churko, J. M., Karakikes, I., Jung, G., Ichida, et al
2016; 18 (10): 1031-1042
- **Full-Length Isoform Sequencing Reveals Novel Transcripts and Substantial Transcriptional Overlaps in a Herpesvirus** *PLOS ONE*
Tombacz, D., Csabai, Z., Olah, P., Balazs, Z., Liko, I., Zsigmond, L., Sharon, D., Snyder, M., Boldogkoi, Z.
2016; 11 (9)
- **Transcriptome Profiling of Patient-Specific Human iPSC-Cardiomyocytes Predicts Individual Drug Safety and Efficacy Responses In Vitro.** *Cell stem cell*
Matsa, E., BurrIDGE, P. W., Yu, K., Ahrens, J. H., Termglinchan, V., Wu, H., Liu, C., Shukla, P., Sayed, N., Churko, J. M., Shao, N., Woo, N. A., Chao, et al
2016; 19 (3): 311-325
- **Predicting Ovarian Cancer Patients' Clinical Response to Platinum-Based Chemotherapy by Their Tumor Proteomic Signatures** *JOURNAL OF PROTEOME RESEARCH*
Yu, K., Levine, D. A., Zhang, H., Chan, D. W., Zhang, Z., Snyder, M.
2016; 15 (8): 2455-2465
- **EPHB4 kinase-inactivating mutations cause autosomal dominant lymphatic-related hydrops fetalis.** *journal of clinical investigation*
Martin-Almedina, S., Martinez-Corral, I., Holdhus, R., Vicente, A., Fotiou, E., Lin, S., Petersen, K., Simpson, M. A., Hoischen, A., Gilissen, C., Jeffery, H., Atton, G., Karapouliou, et al
2016; 126 (8): 3080-3088
- **Omics Profiling in Precision Oncology.** *Molecular & cellular proteomics*
Yu, K., Snyder, M.
2016; 15 (8): 2525-2536
- **Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer.** *Cell*
Zhang, H., Liu, T., Zhang, Z., Payne, S. H., Zhang, B., McDermott, J. E., Zhou, J., Petyuk, V. A., Chen, L., Ray, D., Sun, S., Yang, F., Chen, et al
2016; 166 (3): 755-765
- **Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance** *CELL METABOLISM*
Lee, S., Zhang, C., Kilicarslan, M., Piening, B. D., Bjornson, E., Hallstrom, B. M., Groen, A. K., Ferrannini, E., Laakso, M., Snyder, M., Bluher, M., Uhlen, M., Nielsen, et al
2016; 24 (1): 172-184
- **Using Mass Spectrometry to Quantify Rituximab and Perform Individualized Immunoglobulin Phenotyping in ANCA-Associated Vasculitis** *ANALYTICAL CHEMISTRY*
Mills, J. R., Cornec, D., Dasari, S., Ladwig, P. M., Hummel, A. M., Cheu, M., Murray, D. L., Willrich, M. A., Snyder, M. R., Hoffman, G. S., Kallenberg, C. G., Langford, C. A., Merkel, et al
2016; 88 (12): 6317-6325
- **Genome assembly from synthetic long read clouds** *BIOINFORMATICS*
Kuleshov, V., Snyder, M. P., Batzoglou, S.
2016; 32 (12): 216-224

- **Genome assembly from synthetic long read clouds.** *Bioinformatics*
Kuleshov, V., Snyder, M. P., Batzoglou, S.
2016; 32 (12): i216-i224
- **Effects of cellular origin on differentiation of human induced pluripotent stem cell-derived endothelial cells.** *JCI insight*
Hu, S., Zhao, M., Jahanbani, F., Shao, N., Lee, W. H., Chen, H., Snyder, M. P., Wu, J. C.
2016; 1 (8)
- **Effects of cellular origin on differentiation of human induced pluripotent stem cell-derived endothelial cells** *JCI INSIGHT*
Hu, S., Zhao, M., Jahanbani, F., Shao, N., Lee, W., Chen, H., Snyder, M. P., Wu, J. C.
2016; 1 (8)
- **The genetic predisposition to bronchopulmonary dysplasia** *CURRENT OPINION IN PEDIATRICS*
Yu, K., Li, J., Snyder, M., Shaw, G. M., O'Brodovich, H. M.
2016; 28 (3): 318-323
- **Concerted genomic targeting of H3K27 demethylase REF6 and chromatin-remodeling ATPase BRM in Arabidopsis** *NATURE GENETICS*
Li, C., Gu, L., Gao, L., Chen, C., Wei, C., Qiu, Q., Chien, C., Wang, S., Jiang, L., Ai, L., Chen, C., Yang, S., Nguyen, et al
2016; 48 (6): 687-?
- **Age-Dependent Pancreatic Gene Regulation Reveals Mechanisms Governing Human beta Cell Function** *CELL METABOLISM*
Arda, H. E., Li, L., Tsai, J., Torre, E. A., Rosli, Y., Peiris, H., Spitale, R. C., Dai, C., Gu, X., Qu, K., Wang, P., Wang, J., Grompe, et al
2016; 23 (5): 909-920
- **Can Metabolic Profiles Be Used as a Phenotypic Readout of the Genome to Enhance Precision Medicine?** *CLINICAL CHEMISTRY*
Contrepolis, K., Liang, L., Snyder, M.
2016; 62 (5): 676-78
- **Systematic evaluation of the impact of ChIP-seq read designs on genome coverage, peak identification, and allele-specific binding detection** *BMC BIOINFORMATICS*
Zhang, Q., Zeng, X., Younkin, S., Kawli, T., Snyder, M. P., Keles, S.
2016; 17
- **Identification of significantly mutated regions across cancer types highlights a rich landscape of functional molecular alterations.** *Nature genetics*
Araya, C. L., Cenik, C., Reuter, J. A., Kiss, G., Pande, V. S., Snyder, M. P., Greenleaf, W. J.
2016; 48 (2): 117-125
- **Protein substrates of the arginine methyltransferase Hmt1 identified by proteome arrays** *PROTEOMICS*
Low, J. K., Im, H., Erce, M. A., Hart-Smith, G., Snyder, M. P., Wilkins, M. R.
2016; 16 (3): 465-76
- **Effects of Formalin Fixation Variables on DNA Integrity for Genomic Applications in Cancer**
Lefterova, M., Clark, M. J., Alla, R. K., Luo, S., Morra, M., Helman, E., Boyle, S. M., Kirk, S., Sripakdeevong, P., Karbelashvili, M., Church, D. M., Snyder, M. P., West, et al
NATURE PUBLISHING GROUP.2016: 516A-517A
- **Proteome-wide survey of the autoimmune target repertoire in autoimmune polyendocrine syndrome type 1** *SCIENTIFIC REPORTS*
Landegren, N., Sharon, D., Freyhult, E., Hallgren, A., Eriksson, D., Edqvist, P., Bensing, S., Wahlberg, J., Nelson, L. M., Gustafsson, J., Husebye, E. S., Anderson, M. S., Snyder, et al
2016; 6
- **Distance from sub-Saharan Africa predicts mutational load in diverse human genomes** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Henn, B. M., Botigue, L. R., Peischl, S., Dupanloup, I., Lipatov, M., Maples, B. K., Martin, A. R., Musharoff, S., Cann, H., Snyder, M. P., Excoffier, L., Kidd, J. M., Bustamante, et al
2016; 113 (4): E440-E449
- **Distance from sub-Saharan Africa predicts mutational load in diverse human genomes.** *Proceedings of the National Academy of Sciences of the United States of America*

- Henn, B. M., Botigué, L. R., Peischl, S., Dupanloup, I., Lipatov, M., Maples, B. K., Martin, A. R., Musharoff, S., Cann, H., Snyder, M. P., Excoffier, L., Kidd, J. M., Bustamante, et al
2016; 113 (4): E440-9
- **Disease Variant Landscape of a Large Multiethnic Population of Moyamoya Patients by Exome Sequencing** *G3-GENES GENOMES GENETICS*
Shoemaker, L. D., Clark, M. J., Patwardhan, A., Chandratillake, G., Garcia, S., Chen, R., Morgan, A. A., Leng, N., Kirk, S., Chen, R., Cook, D. J., Snyder, M., Steinberg, et al
2016; 6 (1): 41-49
 - **Secure cloud computing for genomic data** *Nature Biotechnology*
Somalee, D., Keith, B., Michael, S.
2016; 34 (6): 588-91
 - **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): 16004
 - **HARNESSING BIG DATA FOR PRECISION MEDICINE: INFRASTRUCTURES AND APPLICATIONS.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
Yu, K., Hart, S. N., Goldfeder, R., Zhang, Q. C., Parker, S. C., Snyder, M.
2016; 22: 635-639
 - **NIH working group report-using genomic information to guide weight management: From universal to precision treatment** *OBESITY*
Bray, M. S., Loos, R. J., McCaffery, J. M., Ling, C., Franks, P. W., Weinstock, G. M., Snyder, M. P., Vassy, J. L., Agurs-Collins, T.
2016; 24 (1): 14-22
 - **Metformin Improves Diabetic Bone Health by Re-Balancing Catabolism and Nitrogen Disposal** *PLOS ONE*
Li, X., Guo, Y., Yan, W., Snyder, M. P., Li, X.
2015; 10 (12)
 - **Integrated Proteomic and Genomic Analysis of Gastric Cancer Patient Tissues** *JOURNAL OF PROTEOME RESEARCH*
Yan, J. F., Kim, H., Jeong, S., Lee, H., Sethi, M. K., Lee, L. Y., Beavis, R. C., Im, H., Snyder, M. P., Hofree, M., Ideker, T., Wu, S., Paik, et al
2015; 14 (12): 4995-5006
 - **Integrative analysis of RNA, translation, and protein levels reveals distinct regulatory variation across humans** *GENOME RESEARCH*
Cenik, C., Cenik, E. S., Byeon, G. W., Grubert, F., Candille, S. I., Spacek, D., Alsallakh, B., Tilgner, H., Araya, C. L., Tang, H., Ricci, E., Snyder, M. P.
2015; 25 (11): 1610-1621
 - **Design and Implementation of the International Genetics and Translational Research in Transplantation Network** *TRANSPLANTATION*
Keating, B. J., van Setten, J., Jacobson, P. A., Holmes, M. V., Verma, S. S., Chandrupatla, H. R., Nair, N., Gao, H., Li, Y. R., Chang, B., Wong, C., Phillips, R., Cole, et al
2015; 99 (11): 2401-2412
 - **Sequence to Medical Phenotypes: A Framework for Interpretation of Human Whole Genome DNA Sequence Data** *PLOS GENETICS*
Dewey, F. E., Grove, M. E., Priest, J. R., Waggott, D., Batra, P., Miller, C. L., Wheeler, M., Zia, A., Pan, C., Karzcewski, K. J., Miyake, C., Whirl-Carrillo, M., Klein, et al
2015; 11 (10)
 - **Mango: a bias-correcting ChIA-PET analysis pipeline.** *Bioinformatics*
Phanstiel, D. H., Boyle, A. P., Heidari, N., Snyder, M. P.
2015; 31 (19): 3092-3098
 - **Sequence to Medical Phenotypes: A Framework for Interpretation of Human Whole Genome DNA Sequence Data.** *PLoS genetics*
Dewey, F. E., Grove, M. E., Priest, J. R., Waggott, D., Batra, P., Miller, C. L., Wheeler, M., Zia, A., Pan, C., Karzcewski, K. J., Miyake, C., Whirl-Carrillo, M., Klein, et al
2015; 11 (10)
 - **Exome Sequencing of Neonatal Blood Spots and the Identification of Genes Implicated in Bronchopulmonary Dysplasia.** *American journal of respiratory and critical care medicine*
Li, J., Yu, K., Oehlert, J., Jelliffe-Pawlowski, L. L., Gould, J. B., Stevenson, D. K., Snyder, M., Shaw, G. M., O'Brodovich, H. M.

2015; 192 (5): 589-596

- **Genomic analysis of mycosis fungoides and Sézary syndrome identifies recurrent alterations in TNFR2.** *Nature genetics*
Ungewickell, A., Bhaduri, A., Rios, E., Reuter, J., Lee, C. S., Mah, A., Zehnder, A., Ohgami, R., Kulkarni, S., Armstrong, R., Weng, W., Gratzinger, D., Tavallae, et al
2015; 47 (9): 1056-1060
- **Evaluating Common Humoral Responses against Fungal Infections with Yeast Protein Microarrays** *JOURNAL OF PROTEOME RESEARCH*
Coelho, P. S., Im, H., Clemons, K. V., Snyder, M. P., Stevens, D. A.
2015; 14 (9): 3924-3931
- **RNA Sequencing Analysis Detection of a Novel Pathway of Endothelial Dysfunction in Pulmonary Arterial Hypertension** *AMERICAN JOURNAL OF RESPIRATORY AND CRITICAL CARE MEDICINE*
Rhodes, C. J., Im, H., Cao, A., Hennigs, J. K., Wang, L., Sa, S., Chen, P., Nickel, N. P., Miyagawa, K., Hopper, R. K., Tojais, N. F., Li, C. G., Gu, et al
2015; 192 (3): 356-366
- **Probing High-density Functional Protein Microarrays to Detect Protein-protein Interactions** *JOVE-JOURNAL OF VISUALIZED EXPERIMENTS*
Fasolo, J., Im, H., Snyder, M. P.
2015
- **Single-cell chromatin accessibility reveals principles of regulatory variation** *NATURE*
Buenostro, J. D., Wu, B., Litzenburger, U. M., Ruff, D., Gonzales, M. L., Snyder, M. P., Chang, H. Y., Greenleaf, W. J.
2015; 523 (7561): 486-U264
- **Single-cell chromatin accessibility reveals principles of regulatory variation.** *Nature*
Buenostro, J. D., Wu, B., Litzenburger, U. M., Ruff, D., Gonzales, M. L., Snyder, M. P., Chang, H. Y., Greenleaf, W. J.
2015; 523 (7561): 486-490
- **Achieving high-sensitivity for clinical applications using augmented exome sequencing** *GENOME MEDICINE*
Patwardhan, A., Harris, J., Leng, N., Bartha, G., Church, D. M., Luo, S., Haudenschild, C., Pratt, M., Zook, J., Salit, M., Tirch, J., Morra, M., Chervitz, et al
2015; 7
- **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-?
- **Where Next for Genetics and Genomics?** *PLoS biology*
Tyler-Smith, C., Yang, H., Landweber, L. F., Dunham, I., Knoppers, B. M., Donnelly, P., Mardis, E. R., Snyder, M., McVean, G.
2015; 13 (7): e1002216
- **Where Next for Genetics and Genomics?** *PLOS BIOLOGY*
Tyler-Smith, C., Yang, H., Landweber, L. F., Dunham, I., Knoppers, B. M., Donnelly, P., Mardis, E. R., Snyder, M., McVean, G.
2015; 13 (7)
- **Metabolome progression during early gut microbial colonization of gnotobiotic mice** *SCIENTIFIC REPORTS*
Marcobal, A., Yusufaly, T., Higginbottom, S., Snyder, M., Sonnenburg, J. L., Mias, G. I.
2015; 5
- **Transglutaminase 4 as a prostate autoantigen in male subfertility** *SCIENCE TRANSLATIONAL MEDICINE*
Landegren, N., Sharon, D., Shum, A. K., Khan, I. S., Fasano, K. J., Hallgren, A., Kampf, C., Freyhult, E., Ardesjo-Lundgren, B., Alimohammadi, M., Rathsmann, S., Ludvigsson, J. F., Lundh, et al
2015; 7 (292)
- **Transcriptome Signature and Regulation in Human Somatic Cell Reprogramming** *STEM CELL REPORTS*
Tanaka, Y., Hysolli, E., Su, J., Xiang, Y., Kim, K., Zhong, M., Li, Y., Heydari, K., Euskirchen, G., Snyder, M. P., Pan, X., Weissman, S. M., Park, et al
2015; 4 (6): 1125-1139
- **Optimized Analytical Procedures for the Untargeted Metabolomic Profiling of Human Urine and Plasma by Combining Hydrophilic Interaction (HILIC) and Reverse-Phase Liquid Chromatography (RPLC)-Mass Spectrometry** *MOLECULAR & CELLULAR PROTEOMICS*

- Contrepois, K., Jiang, L., Snyder, M.
2015; 14 (6): 1684-1695
- **AGAPE (Automated Genome Analysis PipelinE) for Pan-Genome Analysis of *Saccharomyces cerevisiae* (vol 10, e0120671, 2015) *PLOS ONE***
Song, G., Dickins, B. A., Demeter, J., Engel, S., Gallagher, J., Choe, K., Dunn, B., Snyder, M., Cherry, J.
2015; 10 (5): e0129184
 - **High-Throughput Sequencing Technologies *MOLECULAR CELL***
Reuter, J. A., Spacek, D. V., Snyder, M. P.
2015; 58 (4): 586-597
 - **High-throughput sequencing technologies. *Molecular cell***
Reuter, J. A., Spacek, D. V., Snyder, M. P.
2015; 58 (4): 586-597
 - **Characterization of Novel Transcripts in Pseudorabies Virus *VIRUSES-BASEL***
Tombacz, D., Csabai, Z., Olah, P., Havelda, Z., Sharon, D., Snyder, M., Boldogkoi, Z.
2015; 7 (5): 2727-2744
 - **Impact of allele-specific peptides in proteome quantification *PROTEOMICS CLINICAL APPLICATIONS***
Wu, L., Snyder, M.
2015; 9 (3-4): 432-436
 - **Reassessment of Piwi Binding to the Genome and Piwi Impact on RNA Polymerase II Distribution *DEVELOPMENTAL CELL***
Lin, H., Chen, M., Kundaje, A., Valouev, A., Yin, H., Liu, N., Neuenkirchen, N., Zhong, M., Snyder, M.
2015; 32 (6): 772-774
 - **The conserved histone deacetylase Rpd3 and its DNA binding subunit Ume6 control dynamic transcript architecture during mitotic growth and meiotic development *NUCLEIC ACIDS RESEARCH***
Lardenois, A., Stuparevic, I., Liu, Y., Law, M. J., Becker, E., Smagulova, F., Waern, K., Guilleux, M., Horecka, J., Chu, A., Kervarrec, C., Strich, R., Snyder, et al
2015; 43 (1): 115-128
 - **Disease Variant Landscape of a Large Multiethnic Population of Moyamoya Patients by Exome Sequencing. *G3 (Bethesda, Md.)***
Shoemaker, L. D., Clark, M. J., Patwardhan, A., Chandratillake, G., Garcia, S., Chen, R., Morgan, A. A., Leng, N., Kirk, S., Chen, R., Cook, D. J., Snyder, M., Steinberg, et al
2015; 6 (1): 41-49
 - **AGAPE (Automated Genome Analysis PipelinE) for pan-genome analysis of *Saccharomyces cerevisiae*. *PloS one***
Song, G., Dickins, B. J., Demeter, J., Engel, S., Gallagher, J., Choe, K., Dunn, B., Snyder, M., Cherry, J. M.
2015; 10 (3)
 - **Metformin Improves Diabetic Bone Health by Re-Balancing Catabolism and Nitrogen Disposal. *PloS one***
Li, X., Guo, Y., Yan, W., Snyder, M. P., Li, X.
2015; 10 (12)
 - **Achieving high-sensitivity for clinical applications using augmented exome sequencing. *Genome medicine***
Patwardhan, A., Harris, J., Leng, N., Bartha, G., Church, D. M., Luo, S., Haudenschild, C., Pratt, M., Zook, J., Salit, M., Tirch, J., Morra, M., Chervitz, et al
2015; 7 (1): 71-?
 - **Novel mutations in *PIEZO1* cause an autosomal recessive generalized lymphatic dysplasia with non-immune hydrops fetalis. *Nature communications***
Fotiou, E., Martin-Almedina, S., Simpson, M. A., Lin, S., Gordon, K., Brice, G., Atton, G., Jeffery, I., Rees, D. C., Mignot, C., Vogt, J., Homfray, T., Snyder, et al
2015; 6: 8085-?
 - **Novel mutations in *PIEZO1* cause an autosomal recessive generalized lymphatic dysplasia with non-immune hydrops fetalis. *Nature communications***

- Fotiou, E., Martin-Almedina, S., Simpson, M. A., Lin, S., Gordon, K., Brice, G., Atton, G., Jeffery, I., Rees, D. C., Mignot, C., Vogt, J., Homfray, T., Snyder, et al
2015; 6: 8085-?
- **Whole-Exome Enrichment with the Agilent SureSelect Human All Exon Platform.** *Cold Spring Harbor protocols*
Chen, R., Im, H., Snyder, M.
2015; 2015 (7): pdb prot083659-?
 - **Metabolome progression during early gut microbial colonization of gnotobiotic mice.** *Scientific reports*
Marcobal, A., Yusufaly, T., Higginbottom, S., Snyder, M., Sonnenburg, J. L., Mias, G. I.
2015; 5: 11589-?
 - **Genomic analysis of fibrolamellar hepatocellular carcinoma.** *Human molecular genetics*
Xu, L., Hazard, F. K., Zmoos, A., Jahchan, N., Chaib, H., Garfin, P. M., Rangaswami, A., Snyder, M. P., Sage, J.
2015; 24 (1): 50-63
 - **Exome sequencing and genome-wide copy number variant mapping reveal novel associations with sensorineural hereditary hearing loss** *BMC GENOMICS*
Haraksingh, R. R., Jahanbani, F., Rodriguez-Paris, J., Gelernter, J., Nadeau, K. C., Oghalai, J. S., Schrijver, I., Snyder, M. P.
2014; 15
 - **Genomic era diagnosis and management of hereditary and sporadic colon cancer.** *World journal of clinical oncology*
Esplin, E. D., Snyder, M. P.
2014; 5 (5): 1036-1047
 - **Widespread contribution of transposable elements to the innovation of gene regulatory networks** *GENOME RESEARCH*
Sundaram, V., Cheng, Y., Ma, Z., Li, D., Xing, X., Edge, P., Snyder, M. P., Wang, T.
2014; 24 (12): 1963-1976
 - **Genome-wide map of regulatory interactions in the human genome** *GENOME RESEARCH*
Heidari, N., Phanstiel, D. H., He, C., Grubert, F., Jahanbani, F., Kasowski, M., Zhang, M. Q., Snyder, M. P.
2014; 24 (12): 1905-1917
 - **A comparative encyclopedia of DNA elements in the mouse genome** *NATURE*
Yue, F., Cheng, Y., Breschi, A., Vierstra, J., Wu, W., Ryba, T., Sandstrom, R., Ma, Z., Davis, C., Pope, B. D., Shen, Y., Pervouchine, D. D., Djebali, et al
2014; 515 (7527): 355-?
 - **A comparative encyclopedia of DNA elements in the mouse genome.** *Nature*
Yue, F., Cheng, Y., Breschi, A., Vierstra, J., Wu, W., Ryba, T., Sandstrom, R., Ma, Z., Davis, C., Pope, B. D., Shen, Y., Pervouchine, D. D., Djebali, et al
2014; 515 (7527): 355-364
 - **Topologically associating domains are stable units of replication-timing regulation.** *Nature*
Pope, B. D., Ryba, T., Dileep, V., Yue, F., Wu, W., Denas, O., Vera, D. L., Wang, Y., Hansen, R. S., Canfield, T. K., Thurman, R. E., Cheng, Y., Gülsöy, et al
2014; 515 (7527): 402-405
 - **Principles of regulatory information conservation between mouse and human** *NATURE*
Cheng, Y., Ma, Z., Kim, B., 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-?
 - **Topologically associating domains are stable units of replication-timing regulation** *NATURE*
Pope, B. D., Ryba, T., Dileep, V., Yue, F., Wu, W., Denas, O., Vera, D. L., Wang, Y., Hansen, R. S., Canfield, T. K., Thurman, R. E., Cheng, Y., Guelsoy, et al
2014; 515 (7527): 402-?
 - **Personalized sequencing and the future of medicine: discovery, diagnosis and defeat of disease.** *Pharmacogenomics*
Esplin, E. D., Oei, L., Snyder, M. P.
2014; 15 (14): 1771-1790

- **Mutations in NGLY1 cause an inherited disorder of the endoplasmic reticulum-associated degradation pathway** *GENETICS IN MEDICINE*
Enns, G. M., Shashi, V., Bainbridge, M., Gambello, M. J., Zahir, F. R., Bast, T., Crimian, R., Schoch, K., Platt, J., Cox, R., Bernstein, J. A., Scavina, M., Walter, et al
2014; 16 (10): 751-758
- **Mutations in NGLY1 cause an inherited disorder of the endoplasmic reticulum-associated degradation pathway.** *Genetics in medicine*
Enns, G. M., Shashi, V., Bainbridge, M., Gambello, M. J., Zahir, F. R., Bast, T., Crimian, R., Schoch, K., Platt, J., Cox, R., Bernstein, J. A., Scavina, M., Walter, et al
2014; 16 (10): 751-758
- **Sushi.R: flexible, quantitative and integrative genomic visualizations for publication-quality multi-panel figures.** *Bioinformatics*
Phanstiel, D. H., Boyle, A. P., Araya, C. L., Snyder, M. P.
2014; 30 (19): 2808-2810
- **Sushi.R: flexible, quantitative and integrative genomic visualizations for publication-quality multi-panel figures** *BIOINFORMATICS*
Phanstiel, D. H., Boyle, A. P., Araya, C. L., Snyder, M. P.
2014; 30 (19): 2808-2810
- **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
- **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
- **Shared functions of plant and mammalian StAR-related lipid transfer (START) domains in modulating transcription factor activity** *BMC BIOLOGY*
Schrick, K., Bruno, M., Khosla, A., Cox, P. N., Marlatt, S. A., Roque, R. A., Nguyen, H. C., He, C., Snyder, M. P., Singh, D., Yadav, G.
2014; 12
- **Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Kellis, M., Wold, B., Snyder, M. P., Bernstein, B. E., Kundaje, A., Marinov, G. K., Ward, L. D., Birney, E., Crawford, G. E., Dekker, J., Dunham, I., Elnitski, L. L., Farnham, et al
2014; 111 (33): E3366-E3366
- **Transcriptome sequencing from diverse human populations reveals differentiated regulatory architecture.** *PLoS genetics*
Martin, A. R., Costa, H. A., Lappalainen, T., Henn, B. M., Kidd, J. M., Yee, M., Grubert, F., Cann, H. M., Snyder, M., Montgomery, S. B., Bustamante, C. D.
2014; 10 (8)
- **Transcriptome sequencing from diverse human populations reveals differentiated regulatory architecture.** *PLoS genetics*
Martin, A. R., Costa, H. A., Lappalainen, T., Henn, B. M., Kidd, J. M., Yee, M., Grubert, F., Cann, H. M., Snyder, M., Montgomery, S. B., Bustamante, C. D.
2014; 10 (8)
- **H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency.** *Cell*
Benayoun, B. A., Pollina, E. A., Ucar, D., Mahmoudi, S., Karra, K., Wong, E. D., Devarajan, K., Daugherty, A. C., Kundaje, A. B., Mancini, E., Hitz, B. C., Gupta, R., Rando, et al
2014; 158 (3): 673-688
- **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
- **Mutations in NGLY1 cause an inherited disorder of the endoplasmic reticulum-associated degradation pathway (vol 111, pg 236, 2014)** *GENETICS IN MEDICINE*

- Enns, G. M., Shashi, V., Bainbridge, M., Gambello, M. J., Zahir, F. R., Bast, T., Crimian, R., Schoch, K., Platt, J., Cox, R., Bernstein, J. A., Scavina, M., Walter, et al
2014; 16 (7): 568
- **Quantitative analysis of RNA-protein interactions on a massively parallel array reveals biophysical and evolutionary landscapes.** *Nature biotechnology*
Buenrostro, J. D., Araya, C. L., Chircus, L. M., Layton, C. J., Chang, H. Y., Snyder, M. P., Greenleaf, W. J.
2014; 32 (6): 562-568
 - **Quantitative analysis of RNA-protein interactions on a massively parallel array reveals biophysical and evolutionary landscapes.** *Nature biotechnology*
Buenrostro, J. D., Araya, C. L., Chircus, L. M., Layton, C. J., Chang, H. Y., Snyder, M. P., Greenleaf, W. J.
2014; 32 (6): 562-568
 - **Reconstructing lineage hierarchies of the distal lung epithelium using single-cell RNA-seq.** *Nature*
Treutlein, B., Brownfield, D. G., Wu, A. R., Neff, N. F., Mantalas, G. L., Espinoza, F. H., Desai, T. J., Krasnow, M. A., Quake, S. R.
2014; 509 (7500): 371-375
 - **Allelic Expression of Deleterious Protein-Coding Variants across Human Tissues** *PLOS GENETICS*
Kukurba, K. R., Zhang, R., Li, X., Smith, K. S., Knowles, D. A., Tan, M. H., Piskol, R., Lek, M., Snyder, M., MacArthur, D. G., Li, J. B., Montgomery, S. B.
2014; 10 (5)
 - **Allelic Expression of Deleterious Protein-Coding Variants across Human Tissues.** *PLoS genetics*
Kukurba, K. R., Zhang, R., Li, X., Smith, K. S., Knowles, D. A., How Tan, M., Piskol, R., Lek, M., Snyder, M., MacArthur, D. G., Li, J. B., Montgomery, S. B.
2014; 10 (5)
 - **Defining functional DNA elements in the human genome** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Kellis, M., Wold, B., Snyder, M. P., Bernstein, B. E., Kundaje, A., Marinov, G. K., Ward, L. D., Birney, E., Crawford, G. E., Dekker, J., Dunham, I., Elnitski, L. L., Farnham, et al
2014; 111 (17): 6131-6138
 - **Extended lifespan and reduced adiposity in mice lacking the FAT10 gene.** *Proceedings of the National Academy of Sciences of the United States of America*
Canaan, A., DeFuria, J., Perelman, E., Schultz, V., Seay, M., Tuck, D., Flavell, R. A., Snyder, M. P., Obin, M. S., Weissman, S. M.
2014; 111 (14): 5313-5318
 - **Haplotype structure and positive selection at TLR1** *EUROPEAN JOURNAL OF HUMAN GENETICS*
Heffelfinger, C., Pakstis, A. J., Speed, W. C., Clark, A. P., Haigh, E., Fang, R., Furtado, M. R., Kidd, K. K., Snyder, M. P.
2014; 22 (4): 551-557
 - **Clinical interpretation and implications of whole-genome sequencing.** *JAMA*
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
 - **Erratum: A single-molecule long-read survey of the human transcriptome.** *Nature biotechnology*
Sharon, D., Tilgner, H., Grubert, F., Snyder, M.
2014; 32 (3): 291-?
 - **Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci.** *American journal of human genetics*
Tragante, V., Barnes, M. R., Ganesh, S. K., Lanktree, M. B., Guo, W., Franceschini, N., Smith, E. N., Johnson, T., Holmes, M. V., Padmanabhan, S., Karczewski, K. J., Almqvera, B., Barnard, et al
2014; 94 (3): 349-360
 - **Whole-genome haplotyping using long reads and statistical methods** *NATURE BIOTECHNOLOGY*
Kuleshov, V., Xie, D., Chen, R., Pushkarev, D., Ma, Z., Blauwkamp, T., Kertesz, M., Snyder, M.
2014; 32 (3): 261-266

- **Ordering and dynamical properties of superbright C-60 molecules on Ag(111)** *PHYSICAL REVIEW B*
Li, H. I., Abreu, G. J., Shukla, A. K., Fournée, V., Ledieu, J., Loli, L. N., Rauterkus, S. E., Snyder, M. V., Su, S. Y., Marino, K. E., Diehl, R. D.
2014; 89 (8)
- **Coherent functional modules improve transcription factor target identification, cooperativity prediction, and disease association.** *PLoS genetics*
Karczewski, K. J., Snyder, M., Altman, R. B., Tatonetti, N. P.
2014; 10 (2)
- **Coherent functional modules improve transcription factor target identification, cooperativity prediction, and disease association.** *PLoS genetics*
Karczewski, K. J., Snyder, M., Altman, R. B., Tatonetti, N. P.
2014; 10 (2)
- **Landscape and variation of RNA secondary structure across the human transcriptome.** *Nature*
Wan, Y., Qu, K., Zhang, Q. C., Flynn, R. A., Manor, O., Ouyang, Z., Zhang, J., Spitale, R. C., Snyder, M. P., Segal, E., Chang, H. Y.
2014; 505 (7485): 706-709
- **Landscape and variation of RNA secondary structure across the human transcriptome.** *Nature*
Wan, Y., Qu, K., Zhang, Q. C., Flynn, R. A., Manor, O., Ouyang, Z., Zhang, J., Spitale, R. C., Snyder, M. P., Segal, E., Chang, H. Y.
2014; 505 (7485): 706-709
- **iPOP and its role in participatory medicine** *GENOME MEDICINE*
Snyder, M.
2014; 6
- **Identification of STAT5A and STAT5B Target Genes in Human T Cells.** *PloS one*
Kanai, T., Seki, S., Jenks, J. A., Kohli, A., Kawli, T., Martin, D. P., Snyder, M., Bacchetta, R., Nadeau, K. C.
2014; 9 (1)
- **Path-scan: a reporting tool for identifying clinically actionable variants.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
Daneshjou, R., Zappala, Z., Kukurba, K., Boyle, S. M., Ormond, K. E., Klein, T. E., Snyder, M., Bustamante, C. D., Altman, R. B., Montgomery, S. B.
2014; 19: 229-240
- **Toward More Transparent and Reproducible Omics Studies Through a Common Metadata Checklist and Data Publications** *OMICS-A JOURNAL OF INTEGRATIVE BIOLOGY*
Kolker, E., Ozdemir, V., Martens, L., Hancock, W., Anderson, G., Anderson, N., Aynacioglu, S., Baranova, A., Campagna, S. R., Chen, R., Choiniere, J., Dearth, S. P., Feng, et al
2014; 18 (1): 10-14
- **Metadata Checklist for the Integrated Personal OMICS Study: Proteomics and Metabolomics Experiments** *OMICS-A JOURNAL OF INTEGRATIVE BIOLOGY*
Snyder, M., Mias, G., Stanberry, L., Kolker, E.
2014; 18 (1): 81-85
- **Identification of STAT5A and STAT5B target genes in human T cells.** *PloS one*
Kanai, T., Seki, S., Jenks, J. A., Kohli, A., Kawli, T., Martin, D. P., Snyder, M., Bacchetta, R., Nadeau, K. C.
2014; 9 (1)
- **Exome sequencing and genome-wide copy number variant mapping reveal novel associations with sensorineural hereditary hearing loss.** *BMC genomics*
Haraksingh, R. R., Jahanbani, F., Rodriguez-Paris, J., Gelernter, J., Nadeau, K. C., Oghalai, J. S., Schrijver, I., Snyder, M. P.
2014; 15: 1155-?
- **Global analysis of transcription factor-binding sites in yeast using ChIP-Seq.** *Methods in molecular biology (Clifton, N.J.)*
Lefrançois, P., Gallagher, J. E., Snyder, M.
2014; 1205: 231-255
- **Strain Kaplan of Pseudorabies Virus Genome Sequenced by PacBio Single-Molecule Real-Time Sequencing Technology.** *Genome announcements*

- Tombácz, D., Sharon, D., Oláh, P., Csabai, Z., Snyder, M., Boldogkoi, Z.
2014; 2 (4)
- **Serum profiling using protein microarrays to identify disease related antigens.** *Methods in molecular biology (Clifton, N.J.)*
Sharon, D., Snyder, M.
2014; 1176: 169-178
 - **Personalized sequencing and the future of medicine: discovery, diagnosis and defeat of disease** *PHARMACOGENOMICS*
Esplin, E. D., Oei, L., Snyder, M. P.
2014; 15 (14): 1771-1790
 - **STORMSeq: an open-source, user-friendly pipeline for processing personal genomics data in the cloud.** *PloS one*
Karczewski, K. J., Fernald, G. H., Martin, A. R., Snyder, M., Tatonetti, N. P., Dudley, J. T.
2014; 9 (1)
 - **Distinct Splice Variants and Pathway Enrichment in the Cell-Line Models of Aggressive Human Breast Cancer Subtypes** *JOURNAL OF PROTEOME RESEARCH*
Menon, R., Im, H., Zhang, E. (. Wu, S., Chen, R., Snyder, M., Hancock, W. S., Omenn, G. S.
2014; 13 (1): 212-227
 - **Chromatin immunoprecipitation and multiplex sequencing (ChIP-Seq) to identify global transcription factor binding sites in the nematode *Caenorhabditis elegans*.** *Methods in enzymology*
Brdlik, C. M., Niu, W., Snyder, M.
2014; 539: 89-111
 - **STAT3 Targets Suggest Mechanisms of Aggressive Tumorigenesis in Diffuse Large B-Cell Lymphoma** *G3-GENES GENOMES GENETICS*
Hardee, J., Ouyang, Z., Zhang, Y., Kundaje, A., Lacroute, P., Snyder, M.
2013; 3 (12): 2173-2185
 - **Toward More Transparent and Reproducible Omics Studies Through a Common Metadata Checklist and Data Publications.** *Big data*
Kolker, E., Özdemir, V., Martens, L., Hancock, W., Anderson, G., Anderson, N., Aynacioglu, S., Baranova, A., Campagna, S. R., Chen, R., Choiniere, J., Dearth, S. P., Feng, et al
2013; 1 (4): 196-201
 - **Metadata Checklist for the Integrated Personal Omics Study: Proteomics and Metabolomics Experiments.** *Big data*
Snyder, M., Mias, G., Stanberry, L., Kolker, E.
2013; 1 (4): 202-206
 - **METADATA CHECKLIST FOR THE INTEGRATED PERSONAL OMICS STUDY: Proteomics and Metabolomics Experiments** *BIG DATA*
Snyder, M., Mias, G., Stanberry, L., Kolker, E.
2013; 1 (4): BD202-U81
 - **TOWARD MORE TRANSPARENT AND REPRODUCIBLE OMICS STUDIES THROUGH A COMMON METADATA CHECKLIST AND DATA PUBLICATIONS** *BIG DATA*
Kolker, E., Oezdemir, V., Martens, L., Hancock, W., Anderson, G., Anderson, N., Aynacioglu, S., Baranova, A., Campagna, S. R., Chen, R., Choiniere, J., Dearth, S. P., Feng, et al
2013; 1 (4): BD196-?
 - **Impacts of variation in the human genome on gene regulation.** *Journal of molecular biology*
Haraksingh, R. R., Snyder, M. P.
2013; 425 (21): 3970-3977
 - **Defective sphingosine 1-phosphate receptor 1 (S1P1) phosphorylation exacerbates TH17-mediated autoimmune neuroinflammation.** *Nature immunology*
Garris, C. S., Wu, L., Acharya, S., Arac, A., Blaho, V. A., Huang, Y., Moon, B. S., Axtell, R. C., Ho, P. P., Steinberg, G. K., Lewis, D. B., Sobel, R. A., Han, et al
2013; 14 (11): 1166-1172
 - **Defective sphingosine 1-phosphate receptor 1 (S1P1) phosphorylation exacerbates TH17-mediated autoimmune neuroinflammation.** *Nature immunology*

- Garris, C. S., Wu, L., Acharya, S., Arac, A., Blaho, V. A., Huang, Y., Moon, B. S., Axtell, R. C., Ho, P. P., Steinberg, G. K., Lewis, D. B., Sobel, R. A., Han, et al
2013; 14 (11): 1166-1172
- **Comprehensive whole-genome sequencing of an early-stage primary myelofibrosis patient defines low mutational burden and non-recurrent candidate genes.** *Haematologica*
Merker, J. D., Roskin, K. M., Ng, D., Pan, C., Fisk, D. G., King, J. J., Hoh, R., Stadler, M., Okumoto, L. M., Abidi, P., Hewitt, R., Jones, C. D., Gojenola, et al
2013; 98 (11): 1689-1696
 - **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
 - **Incorporating Motif Analysis into Gene Co-expression Networks Reveals Novel Modular Expression Pattern and New Signaling Pathways** *PLOS GENETICS*
Ma, S., Shah, S., Bohnert, H. J., Snyder, M., Dinesh-Kumar, S. P.
2013; 9 (10)
 - **Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations** *AMERICAN JOURNAL OF HUMAN GENETICS*
Franceschini, N., Fox, E., Zhang, Z., Edwards, T. L., Nalls, M. A., Sung, Y. J., Tayo, B. O., Sun, Y. V., Gottesman, O., Adeyemo, A., Johnson, A. D., Young, J. H., Rice, et al
2013; 93 (3): 545-554
 - **Sequencing Y Chromosomes Resolves Discrepancy in Time to Common Ancestor of Males Versus Females** *SCIENCE*
Poznik, G. D., Henn, B. M., Yee, M., Sliwerska, E., Euskirchen, G. M., Lin, A. A., Snyder, M., Quintana-Murci, L., Kidd, J. M., Underhill, P. A., Bustamante, C. D.
2013; 341 (6145): 562-565
 - **Genome-wide profiling of human cap-independent translation-enhancing elements.** *Nature methods*
Wellensiek, B. P., Larsen, A. C., Stephens, B., Kukurba, K., Waern, K., Briones, N., Liu, L., Snyder, M., Jacobs, B. L., Kumar, S., Chaput, J. C.
2013; 10 (8): 747-750
 - **Genome-wide profiling of human cap-independent translation-enhancing elements** *NATURE METHODS*
Wellensiek, B. P., Larsen, A. C., Stephens, B., Kukurba, K., Waern, K., Briones, N., Liu, L., Snyder, M., Jacobs, B. L., Kumar, S., Chaput, J. C.
2013; 10 (8): 747-?
 - **Functional genomic screen of human stem cell differentiation reveals pathways involved in neurodevelopment and neurodegeneration** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Zhang, Y., Schulz, V. P., Reed, B. D., Wang, Z., Pan, X., Mariani, J., Euskirchen, G., Snyder, M. P., Vaccarino, F. M., Ivanova, N., Weissman, S. M., Szekely, A. M.
2013; 110 (30): 12361-12366
 - **Variation and genetic control of protein abundance in humans** *NATURE*
Wu, L., Candille, S. I., Choi, Y., Xie, D., Jiang, L., Li-Pook-Than, J., Tang, H., Snyder, M.
2013; 499 (7456): 79-82
 - **Identification of Genes Critical for Resistance to Infection by West Nile Virus Using RNA-Seq Analysis** *VIRUSES-BASEL*
Qian, F., Chung, L., Zheng, W., Bruno, V., Alexander, R. P., Wang, Z., Wang, X., Kurscheid, S., Zhao, H., Fikrig, E., Gerstein, M., Snyder, M., Montgomery, et al
2013; 5 (7): 1664-1681
 - **Genome Wide Proteomics of ERBB2 and EGFR and Other Oncogenic Pathways in Inflammatory Breast Cancer.** *Journal of proteome research*
Zhang, E. Y., Cristofanilli, M., Robertson, F., Reuben, J. M., Mu, Z., Beavis, R. C., Im, H., Snyder, M., Hofree, M., Ideker, T., Omenn, G. S., Fanayan, S., Jeong, et al
2013; 12 (6): 2805-2817
 - **Overview of high throughput sequencing technologies to elucidate molecular pathways in cardiovascular diseases.** *Circulation research*
Churko, J. M., Mantalas, G. L., Snyder, M. P., Wu, J. C.

2013; 112 (12): 1613-1623

- **Metabolomics as a robust tool in systems biology and personalized medicine: an open letter to the metabolomics community** *METABOLOMICS*
Snyder, M., Li, X.
2013; 9 (3): 532-534
- **iPOP Goes the World: Integrated Personalized Omics Profiling and the Road toward Improved Health Care.** *Chemistry & biology*
Li-Pook-Than, J., Snyder, M.
2013; 20 (5): 660-666
- **Identification of Potential Glycan Cancer Markers with Sialic Acid Attached to Sialic Acid and Up-regulated Fucosylated Galactose Structures in Epidermal Growth Factor Receptor Secreted from A431 Cell Line.** *Molecular & cellular proteomics*
Wu, S., Taylor, A. D., Lu, Q., Hanash, S. M., Im, H., Snyder, M., Hancock, W. S.
2013; 12 (5): 1239-1249
- **Preparation of recombinant protein spotted arrays for proteome-wide identification of kinase targets.** *Current protocols in protein science / editorial board, John E. Coligan ... [et al.]*
Im, H., Snyder, M.
2013; Chapter 27: Unit 27 4-?
- **Proteogenomic Analysis of Human Colon Carcinoma Cell Lines LIM1215, LIM1899, and LIM2405** *JOURNAL OF PROTEOME RESEARCH*
Fanayan, S., Smith, J. T., Lee, L. Y., Yan, F., Snyder, M., Hancock, W. S., Nice, E.
2013; 12 (4): 1732-1742
- **Comparative annotation of functional regions in the human genome using epigenomic data** *NUCLEIC ACIDS RESEARCH*
Won, K., Zhang, X., Wang, T., Ding, B., Raha, D., Snyder, M., Ren, B., Wang, W.
2013; 41 (8): 4423-4432
- **Proteogenomic Analysis of Human Colon Carcinoma Cell Lines LIM1215, LIM1899, and LIM2405.** *Journal of proteome research*
Fanayan, S., Smith, J. T., Lee, L. Y., Yan, F., Snyder, M., Hancock, W. S., Nice, E.
2013
- **A Major Epigenetic Programming Mechanism Guided by piRNAs** *DEVELOPMENTAL CELL*
Huang, X. A., Yin, H., Sweeney, S., Raha, D., Snyder, M., Lin, H.
2013; 24 (5): 502-516
- **Accurate Identification and Analysis of Human mRNA Isoforms Using Deep Long Read Sequencing** *G3-GENES GENOMES GENETICS*
Tilgner, H., Raha, D., Habegger, L., Mohiuddin, M., Gerstein, M., Snyder, M.
2013; 3 (3): 387-397
- **Personal genomes, quantitative dynamic omics and personalized medicine.** *Quantitative biology (Beijing, China)*
Mias, G. I., Snyder, M.
2013; 1 (1): 71-90
- **Extensive Transcript Diversity and Novel Upstream Open Reading Frame Regulation in Yeast** *G3-GENES GENOMES GENETICS*
Waern, K., Snyder, M.
2013; 3 (2): 343-352
- **SeqFold: Genome-scale reconstruction of RNA secondary structure integrating high-throughput sequencing data** *GENOME RESEARCH*
Ouyang, Z., Snyder, M. P., Chang, H. Y.
2013; 23 (2): 377-387
- **Tissue-specific direct targets of Caenorhabditis elegans Rb/E2F dictate distinct somatic and germline programs.** *Genome biology*
Kudron, M., Niu, W., Lu, Z., Wang, G., Gerstein, M., Snyder, M., Reinke, V.
2013; 14 (1): R5
- **Two methods for full-length RNA sequencing for low quantities of cells and single cells** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Pan, X., Durrett, R. E., Zhu, H., Tanaka, Y., Li, Y., Zi, X., Marjani, S. L., Euskirchen, G., Ma, C., LaMotte, R. H., Park, I., Snyder, M. P., Mason, et al
2013; 110 (2): 594-599

- **Multimodal Dynamic Profiling of Healthy and Diseased States for Future Personalized Health Care** *CLINICAL PHARMACOLOGY & THERAPEUTICS*
Mias, G. I., Snyder, M.
2013; 93 (1): 29-32
- **Integrative analysis of longitudinal metabolomics data from a personal multi-omics profile.** *Metabolites*
Stanberry, L., Mias, G. I., Haynes, W., Higdon, R., Snyder, M., Kolker, E.
2013; 3 (3): 741-760
- **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-?
- **Tissue-specific direct targets of *Caenorhabditis elegans* Rb/E2F dictate distinct somatic and germline programs** *GENOME BIOLOGY*
Kudron, M., Niu, W., Lu, Z., Wang, G., Gerstein, M., Snyder, M., Reinke, V.
2013; 14 (1)
- **High-throughput sequencing for biology and medicine** *MOLECULAR SYSTEMS BIOLOGY*
Soon, W. W., Hariharan, M., Snyder, M. P.
2013; 9
- **Systematic investigation of protein-small molecule interactions** *IUBMB LIFE*
Li, X., Wang, X., Snyder, M.
2013; 65 (1): 2-8
- **A Chromosome-centric Human Proteome Project (C-HPP) to Characterize the Sets of Proteins Encoded in Chromosome 17** *JOURNAL OF PROTEOME RESEARCH*
Liu, S., Im, H., Bairoch, A., Cristofanilli, M., Chen, R., Deutsch, E. W., Dalton, S., Fenyo, D., Fanayan, S., Gates, C., Gaudet, P., Hincapie, M., Hanash, et al
2013; 12 (1): 45-57
- **Exome sequencing by targeted enrichment.** *Current protocols in molecular biology / edited by Frederick M. Ausubel ... [et al.]*
Clark, M. J., Chen, R., Snyder, M.
2013; Chapter 7: Unit7 12-?
- **The variable somatic genome.** *Cell cycle*
O'Huallachain, M., Weissman, S. M., Snyder, M. P.
2013; 12 (1): 5-6
- **Promise of personalized omics to precision medicine** *WILEY INTERDISCIPLINARY REVIEWS-SYSTEMS BIOLOGY AND MEDICINE*
Chen, R., Snyder, M.
2013; 5 (1): 73-82
- **Centromere-Like Regions in the Budding Yeast Genome** *PLOS GENETICS*
Lefrancois, P., Auerbach, R. K., Yellman, C. M., Roeder, G. S., Snyder, M.
2013; 9 (1)
- **Copy Number Variation detection from 1000 Genomes project exon capture sequencing data** *BMC BIOINFORMATICS*
Wu, J., Grzeda, K. R., Stewart, C., Grubert, F., Urban, A. E., Snyder, M. P., Marth, G. T.
2012; 13
- **Whole Genome Sequence Analysis of Primary Myelofibrosis.** *54th Annual Meeting and Exposition of the American-Society-of-Hematology (ASH)*
Merker, J. D., Roskin, K., Ng, D., Pan, C., Fisk, D. G., Jones, C. D., Gojenola, L., Clark, M. J., Zhang, B., Cherry, M., Snyder, M., Boyd, S. D., Zehnder, et al
AMER SOC HEMATOLOGY.2012
- **Genome interpretation and assembly-recent progress and next steps.** *Nature biotechnology*
Baker, S., Joecker, A., Church, G., Snyder, M., West, J., Salzberg, S., Worthey, E., Smith, T., Wang, J., Reid, J. G.
2012; 30 (11): 1081-1083

- **Michael Snyder. Interview by Asher Mullard.** *Nature reviews. Drug discovery*
Snyder, M.
2012; 11 (10): 744-?
- **Systems biology: personalized medicine for the future?** *CURRENT OPINION IN PHARMACOLOGY*
Chen, R., Snyder, M.
2012; 12 (5): 623-628
- **SWI/SNF Chromatin-remodeling Factors: Multiscale Analyses and Diverse Functions** *JOURNAL OF BIOLOGICAL CHEMISTRY*
Euskirchen, G., Auerbach, R. K., Snyder, M.
2012; 287 (37): 30897-30905
- **Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements** *GENOME RESEARCH*
Kundaje, A., Kyriazopoulou-Panagiotopoulou, S., Libbrecht, M., Smith, C. L., Raha, D., Winters, E. E., Johnson, S. M., Snyder, M., Batzoglu, S., Sidow, A.
2012; 22 (9): 1735-1747
- **A highly integrated and complex PPARGC1A transcription factor binding network in HepG2 cells** *GENOME RESEARCH*
Charos, A. E., Reed, B. D., Raha, D., Szekely, A. M., Weissman, S. M., Snyder, M.
2012; 22 (9): 1668-1679
- **Deep sequencing of subcellular RNA fractions shows splicing to be predominantly co-transcriptional in the human genome but inefficient for lncRNAs** *GENOME RESEARCH*
Tilgner, H., Knowles, D. G., Johnson, R., Davis, C. A., Chakraborty, S., Djebali, S., Curado, J., Snyder, M., Gingeras, T. R., Guigo, R.
2012; 22 (9): 1616-1625
- **VAT: a computational framework to functionally annotate variants in personal genomes within a cloud-computing environment** *BIOINFORMATICS*
Habegger, L., Balasubramanian, S., Chen, D. Z., Khurana, E., Sboner, A., Harmanci, A., Rozowsky, J., Clarke, D., Snyder, M., Gerstein, M.
2012; 28 (17): 2267-2269
- **Understanding transcriptional regulation by integrative analysis of transcription factor binding data** *GENOME RESEARCH*
Cheng, C., Alexander, R., Min, R., Leng, J., Yip, K. Y., Rozowsky, J., Yan, K., Dong, X., Djebali, S., Ruan, Y., Davis, C. A., Carninci, P., Lassman, et al
2012; 22 (9): 1658-1667
- **Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors** *GENOME RESEARCH*
Wang, J., Zhuang, J., Iyer, S., Lin, X., Whitfield, T. W., Greven, M. C., Pierce, B. G., Dong, X., Kundaje, A., Cheng, Y., Rando, O. J., Birney, E., Myers, et al
2012; 22 (9): 1798-1812
- **A Genome-Scale Resource for In Vivo Tag-Based Protein Function Exploration in C. elegans** *CELL*
Sarov, M., Murray, J. I., Schanze, K., Pozniakovski, A., Niu, W., Angermann, K., Hasse, S., Rupprecht, M., Vinis, E., Tinney, M., Preston, E., Zinke, A., Enst, et al
2012; 150 (4): 855-866
- **Discovery of Stress Responsive DNA Regulatory Motifs in Arabidopsis** *PLOS ONE*
Ma, S., Bachan, S., Porto, M., Bohnert, H. J., Snyder, M., Dinesh-Kumar, S. P.
2012; 7 (8)
- **An encyclopedia of mouse DNA elements (Mouse ENCODE).** *Genome biology*
Stamatoyannopoulos, J. A., Snyder, M., Hardison, R., Ren, B., Gingeras, T., Gilbert, D. M., Groudine, M., Bender, M., Kaul, R., Canfield, T., Giste, E., Johnson, A., Zhang, et al
2012; 13 (8): 418
- **Investigating metabolite-protein interactions: An overview of available techniques** *METHODS*
Yang, G. X., Li, X., Snyder, M.
2012; 57 (4): 459-466
- **Patient-Specific Induced Pluripotent Stem Cells as a Model for Familial Dilated Cardiomyopathy** *SCIENCE TRANSLATIONAL MEDICINE*
Sun, N., Yazawa, M., Liu, J., Han, L., Sanchez-Freire, V., Abilez, O. J., Navarrete, E. G., Hu, S., Wang, L., Lee, A., Pavlovic, A., Lin, S., Chen, et al

2012; 4 (130)

- **Extensive In vivo Metabolite-Protein Interactions Revealed by Large-Scale Systematic Analyses** *Experimental Biology Meeting 2012*
Snyder, M., Li, X., Gianoulis, T., Yip, K., Gerstein, M.
FEDERATION AMER SOC EXP BIOL.2012
- **A core erythroid transcriptional network is repressed by a master regulator of myelo-lymphoid differentiation** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Wontakal, S. N., Guo, X., Smith, C., MacCarthy, T., Bresnick, E. H., Bergman, A., Snyder, M. P., Weissman, S. M., Zheng, D., Skoultchi, A. I.
2012; 109 (10): 3832-3837
- **Tcf7 Is an Important Regulator of the Switch of Self-Renewal and Differentiation in a Multipotential Hematopoietic Cell Line** *PLOS GENETICS*
Wu, J. Q., Seay, M., Schulz, V. P., Hariharan, M., Tuck, D., Lian, J., Du, J., Shi, M., Ye, Z., Gerstein, M., Snyder, M. P., Weissman, S.
2012; 8 (3)
- **The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome** *NATURE BIOTECHNOLOGY*
Paik, Y., Jeong, S., Omenn, G. S., Uhlen, M., Hanash, S., Cho, S. Y., Lee, H., Na, K., Choi, E., Yan, F., Zhang, F., Zhang, Y., Snyder, et al
2012; 30 (3): 221-223
- **Correlation of Global MicroRNA Expression With Basal Cell Carcinoma Subtype** *G3-GENES GENOMES GENETICS*
Heffelfinger, C., Ouyang, Z., Engberg, A., Leffell, D. J., Hanlon, A. M., Gordon, P. B., Zheng, W., Zhao, H., Snyder, M. P., Bale, A. E.
2012; 2 (2): 279-286
- **Characterization of Enhancer Function from Genome-Wide Analyses** *ANNUAL REVIEW OF GENOMICS AND HUMAN GENETICS, VOL 13*
Maston, G. A., Landt, S. G., Snyder, M., Green, M. R.
2012; 13: 29-57
- **Deciphering DNA Sequence Information** *GENOME ORGANIZATION AND FUNCTION IN THE CELL NUCLEUS*
Kaganovich, M., Snyder, M., Rippe, K.
2012: 1-20
- **An encyclopedia of mouse DNA elements (Mouse ENCODE)** *GENOME BIOLOGY*
Stamatoyannopoulos, J. A., Snyder, M., Hardison, R., Ren, B., Gingeras, T., Gilbert, D. M., Groudine, M., Bender, M., Kaul, R., Canfield, T., Giste, E., Johnson, A., Zhang, et al
2012; 13 (8)
- **Q & A: the Snyderome** *GENOME BIOLOGY*
Snyder, M.
2012; 13 (3)
- **Phosphorylation of Yeast Transcription Factors Correlates with the Evolution of Novel Sequence and Function** *JOURNAL OF PROTEOME RESEARCH*
Kaganovich, M., Snyder, M.
2012; 11 (1): 261-268
- **Interpretome: a freely available, modular, and secure personal genome interpretation engine.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
Karczewski, K. J., Tirrell, R. P., Cordero, P., Tatonetti, N. P., Dudley, J. T., Salari, K., Snyder, M., Altman, R. B., Kim, S. K.
2012: 339-350
- **Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors** *GENOME BIOLOGY*
Yip, K. Y., Cheng, C., Bhardwaj, N., Brown, J. B., Leng, J., Kundaje, A., Rozowsky, J., Birney, E., Bickel, P., Snyder, M., Gerstein, M.
2012; 13 (9)
- **A High-Resolution Whole-Genome Map of Key Chromatin Modifications in the Adult *Drosophila melanogaster*** *PLOS GENETICS*
Yin, H., Sweeney, S., Raha, D., Snyder, M., Lin, H.
2011; 7 (12)
- **Genome-Wide Mapping of Copy Number Variation in Humans: Comparative Analysis of High Resolution Array Platforms** *PLOS ONE*

- Haraksingh, R. R., Abyzov, A., Gerstein, M., Urban, A. E., Snyder, M.
2011; 6 (11)
- **Construction and Analysis of an Integrated Regulatory Network Derived from High-Throughput Sequencing Data** *PLOS COMPUTATIONAL BIOLOGY*
Cheng, C., Yan, K., Hwang, W., Qian, J., Bhardwaj, N., Rozowsky, J., Lu, Z. J., Niu, W., Alves, P., Kato, M., Snyder, M., Gerstein, M.
2011; 7 (11)
 - **Performance comparison of exome DNA sequencing technologies** *NATURE BIOTECHNOLOGY*
Clark, M. J., Chen, R., Lam, H. Y., Karczewski, K. J., Chen, R., Euskirchen, G., Butte, A. J., Snyder, M.
2011; 29 (10): 908-U206
 - **Phased Whole-Genome Genetic Risk in a Family Quartet Using a Major Allele Reference Sequence** *PLOS GENETICS*
Dewey, F. E., Chen, R., Cordero, S. P., Ormond, K. E., Caleshu, C., Karczewski, K. J., Whirl-Carrillo, M., Wheeler, M. T., Dudley, J. T., Byrnes, J. K., Cornejo, O. E., Knowles, J. W., Woon, et al
2011; 7 (9)
 - **Arabidopsis RTNLB1 and RTNLB2 Reticulon-Like Proteins Regulate Intracellular Trafficking and Activity of the FLS2 Immune Receptor** *PLANT CELL*
Lee, H. Y., Bowen, C. H., Popescu, G. V., Kang, H., Kato, N., Ma, S., Dinesh-Kumar, S., Snyder, M., Popescu, S. C.
2011; 23 (9): 3374-3391
 - **Cooperative transcription factor associations discovered using regulatory variation** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Karczewski, K. J., Tatonetti, N. P., Landt, S. G., Yang, X., Slifer, T., Altman, R. B., Snyder, M.
2011; 108 (32): 13353-13358
 - **A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans** *PLOS GENETICS*
Stewart, C., Kural, D., Stroemberg, M. P., Walker, J. A., Konkel, M. K., Stuetz, A. M., Urban, A. E., Grubert, F., Lam, H. Y., Lee, W., Busby, M., Indap, A. R., Garrison, et al
2011; 7 (8)
 - **AlleleSeq: analysis of allele-specific expression and binding in a network framework** *MOLECULAR SYSTEMS BIOLOGY*
Rozowsky, J., Abyzov, A., Wang, J., Alves, P., Raha, D., Harmanci, A., Leng, J., Bjornson, R., Kong, Y., Kitabayashi, N., Bhardwaj, N., Rubin, M., Snyder, et al
2011; 7
 - **Identification of genomic indels and structural variations using split reads** *BMC GENOMICS*
Zhang, Z. D., Du, J., Lam, H., Abyzov, A., Urban, A. E., Snyder, M., Gerstein, M.
2011; 12
 - **Metabolites as global regulators: A new view of protein regulation** *BIOESSAYS*
Li, X., Snyder, M.
2011; 33 (7): 485-489
 - **The Human Proteome Project: Current State and Future Direction** *MOLECULAR & CELLULAR PROTEOMICS*
Legrain, P., Aebersold, R., Archakov, A., Bairoch, A., Bala, K., Beretta, L., Bergeron, J., Borchers, C. H., Corthals, G. L., Costello, C. E., Deutsch, E. W., Domon, B., Hancock, et al
2011; 10 (7)
 - **Landscape of Next-Generation Sequencing Technologies** *ANALYTICAL CHEMISTRY*
Niedringhaus, T. P., Milanova, D., Kerby, M. B., Snyder, M. P., Barron, A. E.
2011; 83 (12): 4327-4341
 - **A Large Gene Network in Immature Erythroid Cells Is Controlled by the Myeloid and B Cell Transcriptional Regulator PU.1** *PLOS GENETICS*
Wontakal, S. N., Guo, X., Will, B., Shi, M., Raha, D., Mahajan, M. C., Weissman, S., Snyder, M., Steidl, U., Zheng, D., Skoutlchi, A. I.
2011; 7 (6)
 - **CNVnator: An approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing** *GENOME RESEARCH*

- Abyzov, A., Urban, A. E., Snyder, M., Gerstein, M.
2011; 21 (6): 974-984
- **Genome-wide chromatin occupancy analysis reveals a role for ASH2 in transcriptional pausing** *NUCLEIC ACIDS RESEARCH*
Perez-Lluch, S., Blanco, E., Carbonell, A., Raha, D., Snyder, M., Serras, F., Corominas, M.
2011; 39 (11): 4628-4639
 - **The human proteome project: Current state and future direction.** *Molecular & cellular proteomics : MCP*
Legrain, P., Aebersold, R., Archakov, A., Bairoch, A., Bala, K., Beretta, L., Bergeron, J., Borchers, C., Corthals, G. L., Costello, C. E., Deutsch, E. W., Domon, B., Hancock, et al
2011
 - **Diverse protein kinase interactions identified by protein microarrays reveal novel connections between cellular processes** *GENES & DEVELOPMENT*
Fasolo, J., Sboner, A., Sun, M. G., Yu, H., Chen, R., Sharon, D., Kim, P. M., Gerstein, M., Snyder, M.
2011; 25 (7): 767-778
 - **A User's Guide to the Encyclopedia of DNA Elements (ENCODE)** *PLOS BIOLOGY*
Myers, R. M., Stamatoyannopoulos, J., Snyder, M., Dunham, I., Hardison, R. C., Bernstein, B. E., Gingeras, T. R., Kent, W. J., Birney, E., Wold, B., Crawford, G. E., Bernstein, B. E., Epstein, et al
2011; 9 (4)
 - **Diverse Roles and Interactions of the SWI/SNF Chromatin Remodeling Complex Revealed Using Global Approaches** *PLOS GENETICS*
Euskirchen, G. M., Auerbach, R. K., Davidov, E., Gianoulis, T. A., Zhong, G., Rozowsky, J., Bhardwaj, N., Gerstein, M. B., Snyder, M.
2011; 7 (3)
 - **Mapping copy number variation by population-scale genome sequencing** *NATURE*
Mills, R. E., Walter, K., Stewart, C., Handsaker, R. E., Chen, K., Alkan, C., Abyzov, A., Yoon, S. C., Ye, K., Cheetham, R. K., Chinwalla, A., Conrad, D. F., Fu, et al
2011; 470 (7332): 59-65
 - **Prediction and characterization of noncoding RNAs in C. elegans by integrating conservation, secondary structure, and high-throughput sequencing and array data** *GENOME RESEARCH*
Lu, Z. J., Yip, K. Y., Wang, G., Shou, C., Hillier, L. W., Khurana, E., Agarwal, A., Auerbach, R., Rozowsky, J., Cheng, C., Kato, M., Miller, D. M., Slack, et al
2011; 21 (2): 276-285
 - **Diverse transcription factor binding features revealed by genome-wide ChIP-seq in C. elegans** *GENOME RESEARCH*
Niu, W., Lu, Z. J., Zhong, M., Sarov, M., Murray, J. I., Brdlik, C. M., Janette, J., Chen, C., Alves, P., Preston, E., Slightham, C., Jiang, L., Hyman, et al
2011; 21 (2): 245-254
 - **RSEQtools: a modular framework to analyze RNA-Seq data using compact, anonymized data summaries** *BIOINFORMATICS*
Habegger, L., Sboner, A., Gianoulis, T. A., Rozowsky, J., Agarwal, A., Snyder, M., Gerstein, M.
2011; 27 (2): 281-283
 - **Stat3 is essential for neuronal differentiation through direct transcriptional regulation of the Sox6 gene** *FEBS LETTERS*
Snyder, M., Huang, X., Zhang, J. J.
2011; 585 (1): 148-152
 - **RNA sequencing.** *Methods in molecular biology (Clifton, N.J.)*
Waern, K., Nagalakshmi, U., Snyder, M.
2011; 759: 125-132
 - **Embryonic Stem Cells: Discovery, Development, and Current Trends** *STEM CELLS AND REGENERATIVE MEDICINE: FROM MOLECULAR EMBRYOLOGY TO TISSUE ENGINEERING*
Theodorou, E., Snyder, M., Appasani, K., Appasani, R. K.
2011: 19-43
 - **Analyzing In Vivo Metabolite-Protein Interactions By Large-Scale Systematic Analyses.** *Current protocols in chemical biology*
Li, X., Snyder, M.
2011; 3 (4): 181-196

- **The CRIT framework for identifying cross patterns in systems biology and application to chemogenomics** *GENOME BIOLOGY*
Gianoulis, T. A., Agarwal, A., Snyder, M., Gerstein, M. B.
2011; 12 (3)
- **Regulatory Variation Within Between Species** *ANNUAL REVIEW OF GENOMICS AND HUMAN GENETICS, VOL 12*
Zheng, W., Gianoulis, T. A., Karczewski, K. J., Zhao, H., Snyder, M.
2011; 12: 327-346
- **Kinase substrate interactions.** *Methods in molecular biology (Clifton, N.J.)*
Smith, M. G., Ptacek, J., Snyder, M.
2011; 723: 201-212
- **Measuring the Evolutionary Rewiring of Biological Networks** *PLOS COMPUTATIONAL BIOLOGY*
Shou, C., Bhardwaj, N., Lam, H. Y., Yan, K., Kim, P. M., Snyder, M., Gerstein, M. B.
2011; 7 (1)
- **Integrative Analysis of the Caenorhabditis elegans Genome by the modENCODE Project** *SCIENCE*
Gerstein, M. B., Lu, Z. J., Van Nostrand, E. L., Cheng, C., Arshinoff, B. I., Liu, T., Yip, K. Y., Robilotto, R., Rechtsteiner, A., Ikegami, K., Alves, P., Chateigner, A., Perry, et al
2010; 330 (6012): 1775-1787
- **Statistical Issues in Mapping QTLs for RNA-seq Data** *19th Annual Meeting of the International-Genetic-Epidemiology-Society*
Zheng, W., Raha, D., Snyder, M., Zhao, H.
WILEY-BLACKWELL.2010: 942-42
- **Exploring successful community pharmacist-physician collaborative working relationships using mixed methods** *RESEARCH IN SOCIAL & ADMINISTRATIVE PHARMACY*
Snyder, M. E., Zillich, A. J., Primack, B. A., Rice, K. R., McGivney, M. A., Pringle, J. L., Smith, R. B.
2010; 6 (4): 307-323
- **Transformation of Candida albicans with a synthetic hygromycin B resistance gene** *YEAST*
Basso, L. R., Bartiss, A., Mao, Y., Gast, C. E., Coelho, P. S., Snyder, M., Wong, B.
2010; 27 (12): 1039-1048
- **Rnnotator: an automated de novo transcriptome assembly pipeline from stranded RNA-Seq reads** *BMC GENOMICS*
Martin, J., Bruno, V. M., Fang, Z., Meng, X., Blow, M., Zhang, T., Sherlock, G., Snyder, M., Wang, Z.
2010; 11
- **Extensive In Vivo Metabolite-Protein Interactions Revealed by Large-Scale Systematic Analyses** *CELL*
Li, X., Gianoulis, T. A., Yip, K. Y., Gerstein, M., Snyder, M.
2010; 143 (4): 639-650
- **A map of human genome variation from population-scale sequencing** *NATURE*
Altshuler, D., Durbin, R. M., Abecasis, G. R., Bentley, D. R., Chakravarti, A., Clark, A. G., Collins, F. S., De La Vega, F. M., Donnelly, P., Egholm, M., Flicek, P., Gabriel, S. B., Gibbs, et al
2010; 467 (7319): 1061-1073
- **Yeast proteomics and protein microarrays** *JOURNAL OF PROTEOMICS*
Chen, R., Snyder, M.
2010; 73 (11): 2147-2157
- **Comprehensive annotation of the transcriptome of the human fungal pathogen Candida albicans using RNA-seq** *GENOME RESEARCH*
Bruno, V. M., Wang, Z., Marjani, S. L., Euskirchen, G. M., Martin, J., Sherlock, G., Snyder, M.
2010; 20 (10): 1451-1458
- **Annotating non-coding regions of the genome** *NATURE REVIEWS GENETICS*
Alexander, R. P., Fang, G., Rozowsky, J., Snyder, M., Gerstein, M. B.
2010; 11 (8): 559-571
- **Minimum information about a protein affinity reagent (MIAPAR)** *NATURE BIOTECHNOLOGY*

- Bourbeillon, J., Orchard, S., Benhar, I., Borrebaeck, C., de Daruvar, A., Duebel, S., Frank, R., Gibson, F., Gloriam, D., Haslam, N., Hiltker, T., Humphrey-Smith, I., Hust, et al
2010; 28 (7): 650–53
- **Initiation of the TORC1-Regulated G(0) Program Requires Igo1/2, which License Specific mRNAs to Evade Degradation via the 5'-3' mRNA Decay Pathway** *MOLECULAR CELL*
Talarek, N., Cameroni, E., Jaquenoud, M., Luo, X., Bontron, S., Lippman, S., Devgan, G., Snyder, M., Broach, J. R., De Virgilio, C.
2010; 38 (3): 345-355
 - **MOTIPS: Automated Motif Analysis for Predicting Targets of Modular Protein Domains** *BMC BIOINFORMATICS*
Lam, H. Y., Kim, P. M., Mok, J., Tonikian, R., Sidhu, S. S., Turk, B. E., Snyder, M., Gerstein, M. B.
2010; 11
 - **Genomic binding profiles of functionally distinct RNA polymerase III transcription complexes in human cells** *NATURE STRUCTURAL & MOLECULAR BIOLOGY*
Moqtaderi, Z., Wang, J., Raha, D., White, R. J., Snyder, M., Weng, Z., Struhl, K.
2010; 17 (5): 635-U139
 - **Genetic analysis of variation in transcription factor binding in yeast** *NATURE*
Zheng, W., Zhao, H., Mancera, E., Steinmetz, L. M., Snyder, M.
2010; 464 (7292): 1187-U106
 - **Variation in Transcription Factor Binding Among Humans** *SCIENCE*
Kasowski, M., Grubert, F., Heffelfinger, C., Hariharan, M., Asabere, A., Waszak, S. M., Habegger, L., Rozowsky, J., Shi, M., Urban, A. E., Hong, M., Karczewski, K. J., Huber, et al
2010; 328 (5975): 232-235
 - **Molecular Mechanisms of Ethanol-Induced Pathogenesis Revealed by RNA-Sequencing** *PLOS PATHOGENS*
Camarena, L., Bruno, V., Euskirchen, G., Poggio, S., Snyder, M.
2010; 6 (4)
 - **Dynamic transcriptomes during neural differentiation of human embryonic stem cells revealed by short, long, and paired-end sequencing** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Wu, J. Q., Habegger, L., Noisa, P., Szekeley, A., Qiu, C., Hutchison, S., Raha, D., Egholm, M., Lin, H., Weissman, S., Cui, W., Gerstein, M., Snyder, et al
2010; 107 (11): 5254-5259
 - **Personal genome sequencing: current approaches and challenges** *GENES & DEVELOPMENT*
Snyder, M., Du, J., Gerstein, M.
2010; 24 (5): 423-431
 - **X chromosome-wide analyses of genomic DNA methylation states and gene expression in male and female neutrophils** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Yasukochi, Y., Maruyama, O., Mahajan, M. C., Padden, C., Euskirchen, G. M., Schulz, V., Hirakawa, H., Kuhara, S., Pan, X., Newburger, P. E., Snyder, M., Weissman, S. M.
2010; 107 (8): 3704-3709
 - **Close association of RNA polymerase II and many transcription factors with Pol III genes** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Raha, D., Wang, Z., Moqtaderi, Z., Wu, L., Zhong, G., Gerstein, M., Struhl, K., Snyder, M.
2010; 107 (8): 3639-3644
 - **Deciphering Protein Kinase Specificity Through Large-Scale Analysis of Yeast Phosphorylation Site Motifs** *SCIENCE SIGNALING*
Mok, J., Kim, P. M., Lam, H. Y., Piccirillo, S., Zhou, X., Jeschke, G. R., Sheridan, D. L., Parker, S. A., Desai, V., Jwa, M., Cameroni, E., Niu, H., Good, et al
2010; 3 (109)
 - **Genome-Wide Identification of Binding Sites Defines Distinct Functions for Caenorhabditis elegans PHA-4/FOXA in Development and Environmental Response** *PLOS GENETICS*
Zhong, M., Niu, W., Lu, Z. J., Sarov, M., Murray, J. I., Janette, J., Raha, D., Sheaffer, K. L., Lam, H. Y., Preston, E., Slightham, C., Hillier, L. W., Brock, et al

2010; 6 (2)

- **Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library** *NATURE BIOTECHNOLOGY*
Lam, H. Y., Mu, X. J., Stuetz, A. M., Tanzer, A., Cayting, P. D., Snyder, M., Kim, P. M., Korb, J. O., Gerstein, M. B.
2010; 28 (1): 47-U76
- **CHIP-SEQ: USING HIGH-THROUGHPUT DNA SEQUENCING FOR GENOME-WIDE IDENTIFICATION OF TRANSCRIPTION FACTOR BINDING SITES** *METHODS IN ENZYMOLOGY, VOL 470: GUIDE TO YEAST GENETICS:*
Lefrancois, P., Zheng, W., Snyder, M.
2010; 470: 77-104
- **RNA-Seq: a method for comprehensive transcriptome analysis.** *Current protocols in molecular biology / edited by Frederick M. Ausubel ... [et al.]*
Nagalakshmi, U., Waern, K., Snyder, M.
2010; Chapter 4: Unit 4 11 1-13
- **Systems biology approaches to disease marker discovery** *DISEASE MARKERS*
Sharon, D., Chen, R., Snyder, M.
2010; 28 (4): 209-224
- **EBNA1 regulates cellular gene expression by binding cellular promoters** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Canaan, A., Haviv, I., Urban, A. E., Schulz, V. P., Hartman, S., Zhang, Z., Palejev, D., Deisseroth, A. B., Lacy, J., Snyder, M., Gerstein, M., Weissman, S. M.
2009; 106 (52): 22421-22426
- **Mapping accessible chromatin regions using Sono-Seq** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Auerbach, R. K., Euskirchen, G., Rozowsky, J., Lamarre-Vincent, N., Moqtaderi, Z., Lefrancois, P., Struhl, K., Gerstein, M., Snyder, M.
2009; 106 (35): 14926-14931
- **Global analysis of the glycoproteome in *Saccharomyces cerevisiae* reveals new roles for protein glycosylation in eukaryotes** *MOLECULAR SYSTEMS BIOLOGY*
Kung, L. A., Tao, S., Qian, J., Smith, M. G., Snyder, M., Zhu, H.
2009; 5
- **Impact of Chromatin Structures on DNA Processing for Genomic Analyses** *PLOS ONE*
Teytelman, L., Oezaydin, B., Zill, O., Lefrancois, P., Snyder, M., Rine, J., Eisen, M. B.
2009; 4 (8)
- **Intrinsic histone-DNA interactions are not the major determinant of nucleosome positions in vivo** *NATURE STRUCTURAL & MOLECULAR BIOLOGY*
Zhang, Y., Moqtaderi, Z., Rattner, B. P., Euskirchen, G., Snyder, M., Kadonaga, J. T., Liu, X. S., Struhl, K.
2009; 16 (8): 847-U70
- **The genetic architecture of Down syndrome phenotypes revealed by high-resolution analysis of human segmental trisomies** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Korb, J. O., Tirosh-Wagner, T., Urban, A. E., Chen, X., Kasowski, M., Dai, L., Grubert, F., Erdman, C., Gao, M. C., Lange, K., Sobel, E. M., Barlow, G. M., Aylsworth, et al
2009; 106 (29): 12031-12036
- **Integrating Sequencing Technologies in Personal Genomics: Optimal Low Cost Reconstruction of Structural Variants** *PLOS COMPUTATIONAL BIOLOGY*
Du, J., Bjornson, R. D., Zhang, Z. D., Kong, Y., Snyder, M., Gerstein, M. B.
2009; 5 (7)
- **Recommendations from the 2008 International Summit on Proteomics Data Release and Sharing Policy: The Amsterdam Principles** *JOURNAL OF PROTEOME RESEARCH*
Rodriguez, H., Snyder, M., Uhlen, M., Andrews, P., Beavis, R., Borchers, C., Chalkley, R. J., Cho, S. Y., Cottingham, K., Dunn, M., Dylag, T., Edgar, R., Hare, et al
2009; 8 (7): 3689-3692

- **Unlocking the secrets of the genome** *NATURE*
Celniker, S. E., Dillon, L. A., Gerstein, M. B., Gunsalus, K. C., Henikoff, S., Karpen, G. H., Kellis, M., Lai, E. C., Lieb, J. D., MacAlpine, D. M., Micklem, G., Piano, F., Snyder, et al
2009; 459 (7249): 927-930
- **Dynamic and complex transcription factor binding during an inducible response in yeast** *GENES & DEVELOPMENT*
Ni, L., Bruce, C., Hart, C., Leigh-Bell, J., Gelperin, D., Umansky, L., Gerstein, M. B., Snyder, M.
2009; 23 (11): 1351-1363
- **Integrated analysis of co-expressed MAP kinase substrates in Arabidopsis thaliana.** *Plant signaling & behavior*
Popescu, S. C., Popescu, G. V., Snyder, M., Dinesh-Kumar, S. P.
2009; 4 (6): 524-527
- **Distinct Genomic Aberrations Associated with ERG Rearranged Prostate Cancer** *GENES CHROMOSOMES & CANCER*
Demichelis, F., Setlur, S. R., Beroukhim, R., Perner, S., Korbelt, J. O., LaFargue, C. J., Pflueger, D., Pina, C., Hofer, M. D., Sboner, A., Svensson, M. A., Rickman, D. S., Urban, et al
2009; 48 (4): 366-380
- **A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster** *BLOOD*
Zhang, X., Lian, Z., Padden, C., Gerstein, M. B., Rozowsky, J., Snyder, M., Gingeras, T. R., Kapranov, P., Weissman, S. M., Newburger, P. E.
2009; 113 (11): 2526-2534
- **A high throughput embryonic stem cell screen identifies Oct-2 as a bifunctional regulator of neuronal differentiation** *GENES & DEVELOPMENT*
Theodorou, E., Dalembert, G., Heffelfinger, C., White, E., Weissman, S., Corcoran, L., Snyder, M.
2009; 23 (5): 575-588
- **Quantifying environmental adaptation of metabolic pathways in metagenomics** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Gianoulis, T. A., Raes, J., Patel, P. V., Bjornson, R., Korbelt, J. O., Letunic, I., Yamada, T., Paccanaro, A., Jensen, L. J., Snyder, M., Bork, P., Gerstein, M. B.
2009; 106 (5): 1374-1379
- **Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing** *BMC GENOMICS*
Lefrancois, P., Euskirchen, G. M., Auerbach, R. K., Rozowsky, J., Gibson, T., Yellman, C. M., Gerstein, M., Snyder, M.
2009; 10
- **Proteomic-Based Detection of a Protein Cluster Dysregulated during Cardiovascular Development Identifies Biomarkers of Congenital Heart Defects** *PLOS ONE*
Nath, A. K., Krauthammer, M., Li, P., Davidov, E., Butler, L. C., Copel, J., Katajamaa, M., Oresic, M., Buhimschi, I., Buhimschi, C., Snyder, M., Madri, J. A.
2009; 4 (1)
- **Three Distinct Condensin Complexes Control C. elegans Chromosome Dynamics** *CURRENT BIOLOGY*
Csankovszki, G., Collette, K., Spahl, K., Carey, J., Snyder, M., Petty, E., Patel, U., Tabuchi, T., Liu, H., Mcleod, I., Thompson, J., Sarkesik, A., Yates, et al
2009; 19 (1): 9-19
- **PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data** *GENOME BIOLOGY*
Korbelt, J. O., Abyzov, A., Mu, X. J., Carriero, N., Cayting, P., Zhang, Z., Snyder, M., Gerstein, M. B.
2009; 10 (2)
- **RNA-Seq: a revolutionary tool for transcriptomics** *NATURE REVIEWS GENETICS*
Wang, Z., Gerstein, M., Snyder, M.
2009; 10 (1): 57-63
- **MAPK target networks in Arabidopsis thaliana revealed using functional protein microarrays** *GENES & DEVELOPMENT*
Popescu, S. C., Popescu, G. V., Bachan, S., Zhang, Z., Gerstein, M., Snyder, M., Dinesh-Kumar, S. P.
2009; 23 (1): 80-92

- **PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls** *NATURE BIOTECHNOLOGY*
Rozowsky, J., Euskirchen, G., Auerbach, R. K., Zhang, Z. D., Gibson, T., Bjornson, R., Carriero, N., Snyder, M., Gerstein, M. B.
2009; 27 (1): 66-75
- **Protein microarrays.** *Methods in molecular biology (Clifton, N.J.)*
Fasolo, J., Snyder, M.
2009; 548: 209-222
- **Global identification of protein kinase substrates by protein microarray analysis** *NATURE PROTOCOLS*
Mok, J., Im, H., Snyder, M.
2009; 4 (12): 1820-1827
- **MSB: A mean-shift-based approach for the analysis of structural variation in the genome** *GENOME RESEARCH*
Wang, L., Abyzov, A., Korb, J. O., Snyder, M., Gerstein, M.
2009; 19 (1): 106-117
- **Mismatch oligonucleotides in human and yeast: guidelines for probe design on tiling microarrays** *BMC GENOMICS*
Serinhaus, M., Rozowsky, J., Royce, T., Nagalakshmi, U., Jee, J., Snyder, M., Gerstein, M.
2008; 9
- **Analysis of copy number variants and segmental duplications in the human genome: Evidence for a change in the process of formation in recent evolutionary history** *GENOME RESEARCH*
Kim, P. M., Lam, H. Y., Urban, A. E., Korb, J. O., Affourtit, J., Grubert, F., Chen, X., Weissman, S., Snyder, M., Gerstein, M. B.
2008; 18 (12): 1865-1874
- **Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding** *GENOME RESEARCH*
Robertson, A. G., Bilenky, M., Tam, A., Zhao, Y., Zeng, T., Thiessen, N., Cezard, T., Fejes, A. P., Wederell, E. D., Cullum, R., Euskirchen, G., Krzywinski, M., Birol, et al
2008; 18 (12): 1906-1917
- **High-Resolution Copy-Number Variation Map Reflects Human Olfactory Receptor Diversity and Evolution** *PLOS GENETICS*
Hasin, Y., Olender, T., Khen, M., Gonzaga-Jauregui, C., Kim, P. M., Urban, A. E., Snyder, M., Gerstein, M. B., Lancet, D., Korb, J. O.
2008; 4 (11)
- **A procedure for highly specific, sensitive, and unbiased whole-genome amplification** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Pan, X., Urban, A. E., Palejev, D., Schulz, V., Grubert, F., Hu, Y., Snyder, M., Weissman, S. M.
2008; 105 (40): 15499-15504
- **High-quality binary protein interaction map of the yeast interactome network** *SCIENCE*
Yu, H., Braun, P., Yildirim, M. A., Lemmens, I., Venkatesan, K., Sahalie, J., Hirozane-Kishikawa, T., Gebreab, F., Li, N., Simonis, N., Hao, T., Rual, J., Dricot, et al
2008; 322 (5898): 104-110
- **Modeling ChIP Sequencing In Silico with Applications** *PLOS COMPUTATIONAL BIOLOGY*
Zhang, Z. D., Rozowsky, J., Snyder, M., Chang, J., Gerstein, M.
2008; 4 (8)
- **A genomic analysis of RNA polymerase II modification and chromatin architecture related to 3' end RNA polyadenylation** *GENOME RESEARCH*
Lian, Z., Karpikov, A., Lian, J., Mahajan, M. C., Hartman, S., Gerstein, M., Snyder, M., Weissman, S. M.
2008; 18 (8): 1224-1237
- **Genome-Wide Occupancy of SREBP1 and Its Partners NFY and SP1 Reveals Novel Functional Roles and Combinatorial Regulation of Distinct Classes of Genes** *PLOS GENETICS*
Reed, B. D., Charos, A. E., Szekely, A. M., Weissman, S. M., Snyder, M.
2008; 4 (7)
- **The transcriptional landscape of the yeast genome defined by RNA sequencing** *SCIENCE*
Nagalakshmi, U., Wang, Z., Waern, K., Shou, C., Raha, D., Gerstein, M., Snyder, M.

2008; 320 (5881): 1344-1349

- **The current excitement about copy-number variation: how it relates to gene duplications and protein families** *CURRENT OPINION IN STRUCTURAL BIOLOGY*
Korbel, J. O., Kim, P. M., Chen, X., Urban, A. E., Weissman, S., Snyder, M., Gerstein, M. B.
2008; 18 (3): 366-374
- **Leptin affects endocardial cushion formation by modulating EMT and migration via Akt signaling cascades** *JOURNAL OF CELL BIOLOGY*
Nath, A. K., Brown, R. M., Michaud, M., Sierra-Honigmann, M. R., Snyder, M., Madri, J. A.
2008; 181 (2): 367-380
- **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-A PUBLICATION OF THE RNA SOCIETY*
Chang, W., Zaarour, R. F., Reck-Peterson, S., Rinn, J., Singer, R. H., Snyder, M., Novick, P., Mooseker, M. S.
2008; 14 (3): 491-502
- **Systematic analysis of transcribed loci in ENCODE regions using RACE sequencing reveals extensive transcription in the human genome** *GENOME BIOLOGY*
QianWu, J., Du, J., Rozowsky, J., Zhang, Z., Urban, A. E., Euskirchen, G., Weissman, S., Gerstein, M., Snyder, M.
2008; 9 (1)
- **The development of protein microarrays and their applications in DNA-protein and protein-protein interaction analyses of Arabidopsis transcription factors** *MOLECULAR PLANT*
Gong, W., He, K., Covington, M., Dinesh-Kumar, S. P., Snyder, M., Harmer, S. L., Zhu, Y., Deng, X. W.
2008; 1 (1): 27-41
- **RNA polymerase II stalling: loading at the start prepares genes for a sprint** *GENOME BIOLOGY*
Wu, J. Q., Snyder, M.
2008; 9 (5)
- **Identification of differentially expressed proteins in ovarian cancer using high-density protein microarrays** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Hudson, M. E., Pozdnyakova, I., Haines, K., Mor, G., Snyder, M.
2007; 104 (44): 17494-17499
- **Paired-end mapping reveals extensive structural variation in the human genome** *SCIENCE*
Korbel, J. O., Urban, A. E., Affourtit, J. P., Godwin, B., Grubert, F., Simons, J. F., Kim, P. M., Palejev, D., Carriero, N. J., Du, L., Taillon, B. E., Chen, Z., Tanzer, et al
2007; 318 (5849): 420-426
- **Transcription factor binding site identification in yeast: a comparison of high-density oligonucleotide and PCR-based microarray platforms** *FUNCTIONAL & INTEGRATIVE GENOMICS*
Borneman, A. R., Zhang, Z. D., Rozowsky, J., Seringhaus, M. R., Gerstein, M., Snyder, M.
2007; 7 (4): 335-345
- **Arabidopsis protein microarrays for the high-throughput identification of protein-protein interactions.** *Plant signaling & behavior*
Popescu, S. C., Snyder, M., Dinesh-Kumar, S.
2007; 2 (5): 416-420
- **Divergence of transcription factor binding sites across related yeast species** *SCIENCE*
Borneman, A. R., Gianoulis, T. A., Zhang, Z. D., Yu, H., Rozowsky, J., Seringhaus, M. R., Wang, L. Y., Gerstein, M., Snyder, M.
2007; 317 (5839): 815-819
- **Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project** *NATURE*
Birney, E., Stamatoyannopoulos, J. A., Dutta, A., Guigo, R., Gingeras, T. R., Margulies, E. H., Weng, Z., Snyder, M., Dermitzakis, E. T., Stamatoyannopoulos, J. A., Thurman, R. E., Kuehn, M. S., Taylor, et al
2007; 447 (7146): 799-816
- **Systematic prediction and validation of breakpoints associated with copy-number variants in the human genome** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Korbel, J. O., Urban, A. E., Grubert, F., Du, J., Royce, T. E., Starr, P., Zhong, G., Emanuel, B. S., Weissman, S. M., Snyder, M., Gerstein, M. B.

2007; 104 (24): 10110-10115

- **Assessing the performance of different high-density tiling microarray strategies for mapping transcribed regions of the human genome** *GENOME RESEARCH*
Emanuelsson, O., Nagalakshmi, U., Zheng, D., Rozowsky, J. S., Urban, A. E., Du, J., Lian, Z., Stolc, V., Weissman, S., Snyder, M., Gerstein, M. B.
2007; 17 (6): 886-897
- **Mapping the chromosomal targets of STAT1 by Sequence Tag Analysis of Genomic Enrichment (STAGE)** *GENOME RESEARCH*
Bhinge, A. A., Kim, J., Euskirchen, G. M., Snyder, M., Iyer, V. R.
2007; 17 (6): 910-916
- **Structured RNAs in the ENCODE selected regions of the human genome** *GENOME RESEARCH*
Washietl, S., Pedersen, J. S., Korbil, J. O., Stocsits, C., Gruber, A. R., Hackermueller, J., Hertel, J., Lindemeyer, M., Reiche, K., Tanzer, A., Ucla, C., Wyss, C., Antonarakis, et al
2007; 17 (6): 852-864
- **Mapping of transcription factor binding regions in mammalian cells by ChIP: Comparison of array- and sequencing-based technologies** *GENOME RESEARCH*
Euskirchen, G. M., Rozowsky, J. S., Wei, C., Lee, W. H., Zhang, Z. D., Hartman, S., Emanuelsson, O., Stolc, V., Weissman, S., Gerstein, M. B., Ruan, Y., Snyder, M.
2007; 17 (6): 898-909
- **Integrated analysis of experimental data sets reveals many novel promoters in 1% of the human genome** *GENOME RESEARCH*
Trinklein, N. D., Karaoz, U., Wu, J., Halees, A., Aldred, S. F., Collins, P. J., Zheng, D., Zhang, Z. D., Gerstein, M. B., Snyder, M., Myers, R. M., Weng, Z.
2007; 17 (6): 720-731
- **Statistical analysis of the genomic distribution and correlation of regulatory elements in the ENCODE regions** *GENOME RESEARCH*
Zhang, Z. D., Paccanaro, A., Fu, Y., Weissman, S., Weng, Z., Chang, J., Snyder, M., Gerstein, M. B.
2007; 17 (6): 787-797
- **The DART classification of unannotated transcription within the ENCODE regions: Associating transcription with known and novel loci** *GENOME RESEARCH*
Rozowsky, J. S., Newburger, D., Sayward, F., Wu, J., Jordan, G., Korbil, J. O., Nagalakshmi, U., Yang, J., Zheng, D., Guigo, R., Gingeras, T. R., Weissman, S., Miller, et al
2007; 17 (6): 732-745
- **What is a gene, post-ENCODE? History and updated definition** *GENOME RESEARCH*
Gerstein, M. B., Bruce, C., Rozowsky, J. S., Zheng, D., Du, J., Korbil, J. O., Emanuelsson, O., Zhang, Z. D., Weissman, S., Snyder, M.
2007; 17 (6): 669-681
- **Pseudogenes in the ENCODE regions: Consensus annotation, analysis of transcription, and evolution** *GENOME RESEARCH*
Zheng, D., Frankish, A., Baertsch, R., Kapranov, P., Reymond, A., Choo, S. W., Lu, Y., Denoeud, F., Antonarakis, S. E., Snyder, M., Ruan, Y., Wei, C., Gingeras, et al
2007; 17 (6): 839-851
- **Getting connected: analysis and principles of biological networks** *GENES & DEVELOPMENT*
Zhu, X., Gerstein, M., Snyder, M.
2007; 21 (9): 1010-1024
- **Differential binding of calmodulin-related proteins to their targets revealed through high-density Arabidopsis protein microarrays** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Popescu, S. C., Popescu, G. V., Bachan, S., Zhang, Z., Seay, M., Gerstein, M., Snyder, M., Dinesh-Kumar, S. P.
2007; 104 (11): 4730-4735
- **New insights into Acinetobacter baumannii pathogenesis revealed by high-density pyrosequencing and transposon mutagenesis** *GENES & DEVELOPMENT*
Smith, M. G., Gianoulis, T. A., Pukatzki, S., Mekalanos, J. J., Ornston, L. N., Gerstein, M., Snyder, M.
2007; 21 (5): 601-614
- **Positional artifacts in microarrays: experimental verification and construction of COP, an automated detection tool** *NUCLEIC ACIDS RESEARCH*

- Yu, H., Nguyen, K., Royce, T., Qian, J., Nelson, K., Snyder, M., Gerstein, M.
2007; 35 (2)
- **Yeast protein microarrays** *YEAST GENE ANALYSIS, SECOND EDITION*
Ptacek, J., Snyder, M.
2007; 36: 303-?
 - **Protein microarray technology** *3rd International Conference on Functional Genomics of Ageing*
Hall, D. A., Ptacek, J., Snyder, M.
ELSEVIER IRELAND LTD.2007: 161-67
 - **Telescope: online analysis pipeline for high-density tiling microarray data** *GENOME BIOLOGY*
Zhang, Z. D., Rozowsky, J., Lam, H. Y., Du, J., Snyder, M., Gerstein, M.
2007; 8 (5)
 - **A supervised hidden markov model framework for efficiently segmenting tiling array data in transcriptional and chIP-chip experiments: systematically incorporating validated biological knowledge** *BIOINFORMATICS*
Du, J., Rozowsky, J. S., Korbelt, J. O., Zhang, Z. D., Royce, T. E., Schultz, M. H., Snyder, M., Gerstein, M.
2006; 22 (24): 3016-3024
 - **High-throughput methods of regulatory element discovery** *BIOTECHNIQUES*
Hudson, M. E., Snyder, M.
2006; 41 (6): 673-?
 - **HTRA1 promoter polymorphism in wet age-related macular degeneration** *SCIENCE*
DeWan, A., Liu, M., Hartman, S., Zhang, S. S., Liu, D. T., Zhao, C., Tam, P. O., Chan, W. M., Lam, D. S., Snyder, M., Barnstable, C., Pang, C. P., Hoh, et al
2006; 314 (5801): 989-992
 - **Charging it up: global analysis of protein phosphorylation** *TRENDS IN GENETICS*
Ptacek, J., Snyder, M.
2006; 22 (10): 545-554
 - **TOS9 regulates white-opaque switching in Candida albicans** *EUKARYOTIC CELL*
Srikantha, T., Borneman, A. R., Daniels, K. J., Pujol, C., Wu, W., Seringhaus, M. R., Gerstein, M., Yi, S., Snyder, M., Soll, D. R.
2006; 5 (10): 1674-1687
 - **Predicting essential genes in fungal genomes** *GENOME RESEARCH*
Seringhaus, M., Paccanaro, A., Borneman, A., Snyder, M., Gerstein, M.
2006; 16 (9): 1126-1135
 - **Proteome chips for whole-organism assays** *NATURE REVIEWS MOLECULAR CELL BIOLOGY*
Kung, L. A., Snyder, M.
2006; 7 (8): 617-622
 - **Linking DNA-binding proteins to their recognition sequences by using protein microarrays** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Ho, S., Jona, G., Chen, C. T., Johnston, M., Snyder, M.
2006; 103 (26): 9940-9945
 - **Defined culture conditions of human embryonic stem cells** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Lu, J., Hou, R. H., Booth, C. J., Yang, S. H., Snyder, M.
2006; 103 (15): 5688-5693
 - **High-resolution mapping of DNA copy alterations in human chromosome 22 using high-density tiling oligonucleotide arrays** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Urban, A. E., Korbelt, J. O., Selzer, R., Richmond, T., Hacker, A., Popescu, G. V., Clubbells, J. F., Green, R., Emanuel, B. S., Gerstein, M. B., Weissman, S. M., Snyder, M.
2006; 103 (12): 4534-4539

- **Severe acute respiratory syndrome diagnostics using a coronavirus protein microarray** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Zhu, H., Hu, S. H., Jona, G., Zhu, X. W., Kreiswirth, N., Willey, B. M., Mazzulli, T., Liu, G. Z., Song, Q. F., Chen, P., Cameron, M., Tyler, A., Wang, et al
2006; 103 (11): 4011-4016
- **Target hub proteins serve as master regulators of development in yeast** *GENES & DEVELOPMENT*
Borneman, A. R., Leigh-Bell, J. A., Yu, H. Y., Bertone, P., Gerstein, M., Snyder, M.
2006; 20 (4): 435-448
- **Mapping pathways and phenotypes by systematic gene overexpression** *MOLECULAR CELL*
Sopko, R., Huang, D. Q., Preston, N., Chua, G., Papp, B., Kafadar, K., Snyder, M., Oliver, S. G., Cyert, M., Hughes, T. R., Boone, C., Andrews, B.
2006; 21 (3): 319-330
- **Yeast as a model for human disease.** *Current protocols in human genetics / editorial board, Jonathan L. Haines ... [et al.]*
Smith, M. G., Snyder, M.
2006; Chapter 15: Unit 15 6-?
- **Design optimization methods for genomic DNA tiling arrays** *GENOME RESEARCH*
Bertone, P., Trifonov, V., Rozowsky, J. S., Schubert, F., Emanuelsson, O., Karro, J., Kao, M. Y., Snyder, M., Gerstein, M.
2006; 16 (2): 271-281
- **ProCAT: a data analysis approach for protein microarrays** *GENOME BIOLOGY*
Zhu, X., Gerstein, M., Snyder, M.
2006; 7 (11)
- **BoCaTFBS: a boosted cascade learner to refine the binding sites suggested by ChIP-chip experiments** *GENOME BIOLOGY*
Wang, L., Snyder, M., Gerstein, M.
2006; 7 (11)
- **Extrapolating traditional DNA microarray statistics to tiling and protein microarray technologies** *DNA MICROARRAYS, PART B: DATABASES AND STATISTICS*
Royce, T. E., Rozowsky, J. S., Luscombe, N. M., Emanuelsson, O., Yu, H., Zhu, X., Snyder, M., Gerstein, M. B.
2006; 411: 282-311
- **Genomic analysis of insertion behavior and target specificity of mini-Tn7 and Tn3 transposons in *Saccharomyces cerevisiae*** *NUCLEIC ACIDS RESEARCH*
Seringshaus, M., Kumar, A., Hartigan, J., Snyder, M., Gerstein, M.
2006; 34 (8)
- **Novel transcribed regions in the human genome** *71st Cold Spring Harbor Symposium on Quantitative Biology*
Rozowsky, J., Wu, J., Lian, Z., Nagalakshmi, U., Korbil, J. O., Kapranov, P., Zheng, D., Dyke, S., Newburger, P., Miller, P., Gingeras, T. R., Weissman, S., Gerstein, et al
COLD SPRING HARBOR LAB PRESS, PUBLICATIONS DEPT.2006: 111-116
- **Global changes in STAT target selection and transcription regulation upon interferon treatments** *GENES & DEVELOPMENT*
Hartman, S. E., Bertone, P., Nath, A. K., Royce, T. E., Gerstein, M., Weissman, S., Snyder, M.
2005; 19 (24): 2953-2968
- **Global analysis of protein phosphorylation in yeast** *NATURE*
Ptacek, J., Devgan, G., Michaud, G., Zhu, H., Zhu, X. W., Fasolo, J., Guo, H., Jona, G., Breitkreutz, A., Sopko, R., McCartney, R. R., Schmidt, M. C., Rachidi, et al
2005; 438 (7068): 679-684
- **Biochemical and genetic analysis of the yeast proteome with a movable ORF collection** *GENES & DEVELOPMENT*
Gelperin, D. M., White, M. A., Wilkinson, M. L., Kon, Y., Kung, L. A., Wise, K. J., Lopez-Hoyo, N., Jiang, L. X., Piccirillo, S., Yu, H. Y., Gerstein, M., Dumont, M. E., Phizicky, et al
2005; 19 (23): 2816-2826
- **Advances in functional protein microarray technology** *15th Biennial Conference on Methods in Protein Structure Analysis*
Bertone, P., Snyder, M.

WILEY-BLACKWELL.2005: 5400-5411

- **Checkpoint maintenance requires Ame1 and Okp1** *CELL CYCLE*
Pot, I., Knockleby, J., Aneliunas, V., Nguyen, T., Ah-Kye, S., Liszt, G., Snyder, M., Hieter, P., Vogel, J.
2005; 4 (10): 1448-1456
- **A pilot study of transcription unit analysis in rice using oligonucleotide tiling-path microarray** *PLANT MOLECULAR BIOLOGY*
Stolc, V., Li, L., Wang, X. F., Li, X. Y., Su, N., Tongprasit, W., Han, B., Xue, Y. B., Li, J. Y., Snyder, M., Gerstein, M., Wang, J., Deng, et al
2005; 59 (1): 137-149
- **Issues in the analysis of oligonucleotide tiling microarrays for transcript mapping** *TRENDS IN GENETICS*
Royce, T. E., Rozowsky, J. S., Bertone, P., Samanta, M., Stolc, V., Weissman, S., Snyder, M., Gerstein, M.
2005; 21 (8): 466-475
- **Prospects and challenges in proteomics** *PLANT PHYSIOLOGY*
Bertone, P., Snyder, M.
2005; 138 (2): 560-562
- **Sexual dimorphism in mammalian gene expression** *TRENDS IN GENETICS*
Rinn, J. L., Snyder, M.
2005; 21 (5): 298-305
- **Applications of DNA tiling arrays to experimental genome annotation and regulatory pathway discovery** *CHROMOSOME RESEARCH*
Bertone, P., Gerstein, M., Snyder, M.
2005; 13 (3): 259-274
- **Substrate specificity analysis of protein kinase complex Dbf2-Mob1 by peptide library and proteome array screening.** *BMC biochemistry*
Mah, A. S., Elia, A. E., Devgan, G., Ptacek, J., Schutkowski, M., Snyder, M., Yaffe, M. B., Deshaies, R. J.
2005; 6: 22-?
- **Global analysis of protein function using protein microarrays** *2nd International Conference on Functional Genomics of Ageing*
Smith, M. G., Jona, G., Ptacek, J., Devgan, G., Zhu, H., Zhu, X. W., Snyder, M.
ELSEVIER IRELAND LTD.2005: 171-75
- **Global identification of human transcribed sequences with genome tiling arrays** *SCIENCE*
Bertone, P., Stolc, V., Royce, T. E., Rozowsky, J. S., Urban, A. E., Zhu, X. W., Rinn, J. L., Tongprasit, W., Samanta, M., Weissman, S., Gerstein, M., Snyder, M.
2004; 306 (5705): 2242-2246
- **DNA replication-timing analysis of human chromosome 22 at high resolution and different developmental states** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
White, E. J., Emanuelsson, O., Scalzo, D., Royce, T., Kosak, S., Oakeley, E. J., Weissman, S., Gerstein, M., Groudine, M., Snyder, M., Schubeler, D.
2004; 101 (51): 17771-17776
- **Regulation of gene expression by a metabolic enzyme** *SCIENCE*
Hall, D. A., Zhu, H., Zhu, X. W., Royce, T., Gerstein, M., Snyder, M.
2004; 306 (5695): 482-484
- **Large-scale mutagenesis of the yeast genome using a Tn7-derived multipurpose transposon** *GENOME RESEARCH*
Kumar, A., Seringhaus, M., Biery, M. C., Sarnovsky, R. J., Umansky, L., Piccirillo, S., Heidtman, M., Cheung, K. H., Dobry, C. J., Gerstein, M. B., Craig, N. L., Snyder, M.
2004; 14 (10A): 1975-1986
- **Genomic analysis of regulatory network dynamics reveals large topological changes** *NATURE*
Luscombe, N. M., Babu, M. M., Yu, H. Y., Snyder, M., Teichmann, S. A., Gerstein, M.
2004; 431 (7006): 308-312
- **Major molecular differences between mammalian sexes are involved in drug metabolism and renal function** *DEVELOPMENTAL CELL*
Rinn, J. L., Rozowsky, J. S., Laurenzi, I. J., Petersen, P. H., Zou, K. Y., Zhong, W. M., Gerstein, M., Snyder, M.
2004; 6 (6): 791-800

- **CREB binds to multiple loci on human chromosome 22** *MOLECULAR AND CELLULAR BIOLOGY*
Euskirchen, G., Royce, T. E., Bertone, P., Martone, R., Rinn, J. L., Nelson, F. K., Sayward, F., Luscombe, N. M., Miller, P., Gerstein, M., Weissman, S., Snyder, M.
2004; 24 (9): 3804-3814
- **Microbial synergy via an ethanol-triggered pathway** *MOLECULAR AND CELLULAR BIOLOGY*
Smith, M. G., Des Etages, S. G., Snyder, M.
2004; 24 (9): 3874-3884
- **Regulation of polarized growth initiation and termination cycles by the polarisome and Cdc42 regulators** *JOURNAL OF CELL BIOLOGY*
Bidlingmaier, S., Snyder, M.
2004; 164 (2): 207-218
- **Fast optimal genome tiling with applications to microarray design and homology search** *JOURNAL OF COMPUTATIONAL BIOLOGY*
Berman, P., Bertone, P., DasGupta, B., Gerstein, M., Kao, M. Y., Snyder, M.
2004; 11 (4): 766-785
- **Analyzing antibody specificity with whole proteome microarrays** *NATURE BIOTECHNOLOGY*
Michaud, G. A., Salcius, M., Zhou, F., Bangham, R., Bonin, J., Guo, H., Snyder, M., Predki, P. F., Schweitzer, B. I.
2003; 21 (12): 1509-1512
- **Changes in the nutrient content of school lunches: results from the Pathways study** *PREVENTIVE MEDICINE*
Story, M., Snyder, M. P., Anliker, J., Weber, J. L., Cunningham-Sabo, L., Stone, E. J., Chamberlain, A., Ethelbah, B., Suchindran, C., Ring, K.
2003; 37 (6): S35-S45
- **Negative regulation of calcineurin signaling by Hrr25p, a yeast homolog of casein kinase I** *GENES & DEVELOPMENT*
Kafadar, K. A., Zhu, H., Snyder, M., Cyert, M. S.
2003; 17 (21): 2698-2708
- **Microarrays to characterize protein interactions on a whole-proteome scale** *PROTEOMICS*
Schweitzer, B., Predki, P., Snyder, M.
2003; 3 (11): 2190-2199
- **A Bayesian networks approach for predicting protein-protein interactions from genomic data** *SCIENCE*
Jansen, R., Yu, H. Y., Greenbaum, D., Kluger, Y., Krogan, N. J., Chung, S. B., Emili, A., Snyder, M., Greenblatt, J. F., Gerstein, M.
2003; 302 (5644): 449-453
- **Distribution of NF-kappa B-binding sites across human chromosome 22** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Martone, R., Euskirchen, G., Bertone, P., Hartman, S., Royce, T. E., Luscombe, N. M., Rinn, J. L., Nelson, F. K., Miller, P., Gerstein, M., Weissman, S., Snyder, M.
2003; 100 (21): 12247-12252
- **Cytoskeletal activation of a checkpoint kinase** *MOLECULAR CELL*
Hanrahan, J., Snyder, M.
2003; 12 (3): 663-673
- **Specific protein targeting during cell differentiation: Polarized localization of Fus1p during mating depends on Chs5p in *Saccharomyces cerevisiae*** *EUKARYOTIC CELL*
Santos, B., Snyder, M.
2003; 2 (4): 821-825
- **ExpressYourself: a modular platform for processing and visualizing microarray data** *NUCLEIC ACIDS RESEARCH*
Luscombe, N. M., Royce, T. E., Bertone, P., Echols, N., Horak, C. E., Chang, J. T., Snyder, M., Gerstein, M.
2003; 31 (13): 3477-3482
- **Recent developments in analytical and functional protein microarrays** *CURRENT OPINION IN MOLECULAR THERAPEUTICS*
Jona, G., Snyder, M.
2003; 5 (3): 271-277

- **Genomics - Defining genes in the genomics era** *SCIENCE*
Snyder, M., Gerstein, M.
2003; 300 (5617): 258-260
- **Molecular dissection of a yeast septin: Distinct domains are required for septin interaction, localization, and function** *MOLECULAR AND CELLULAR BIOLOGY*
Casamayor, A., Snyder, M.
2003; 23 (8): 2762-2777
- **Protein analysis on a proteomic scale** *NATURE*
Phizicky, E., Bastiaens, P. I., Zhu, H., Snyder, M., Fields, S.
2003; 422 (6928): 208-215
- **The transcriptional activity of human Chromosome 22** *GENES & DEVELOPMENT*
Rinn, J. L., Euskirchen, G., Bertone, P., Martone, R., Luscombe, N. M., Hartman, S., Harrison, P. M., Nelson, F. K., Miller, P., Gerstein, M., Weissman, S., Snyder, M.
2003; 17 (4): 529-540
- **Protein chip technology** *CURRENT OPINION IN CHEMICAL BIOLOGY*
Zhu, H., Snyder, M.
2003; 7 (1): 55-63
- **Identification of novel functional elements in the human genome** *67th Cold Spring Harbor Symposium on Quantitative Biology*
Lian, Z., Euskirchen, G., Rinn, J., Martone, R., Bertone, P., Hartman, S., Royce, T., Nelson, K., Sayward, F., Luscombe, N., Yang, J., Li, J. L., Miller, et al
COLD SPRING HARBOR LAB PRESS, PUBLICATIONS DEPT.2003: 317-322
- **Proteomics** *ANNUAL REVIEW OF BIOCHEMISTRY*
Zhu, H., Bilgin, M., Snyder, M.
2003; 72: 783-812
- **Proteomic approaches for the global analysis of proteins** *BIOTECHNIQUES*
Michaud, G. A., Snyder, M.
2002; 33 (6): 1308-1316
- **Complex transcriptional circuitry at the G1/S transition in *Saccharomyces cerevisiae*** *GENES & DEVELOPMENT*
Horak, C. E., Luscombe, N. M., Qian, J. A., Bertone, P., Piccirillo, S., Gerstein, M., Snyder, M.
2002; 16 (23): 3017-3033
- **The alpha-factor receptor C-terminus is important for mating projection formation and orientation in *Saccharomyces cerevisiae*** *CELL MOTILITY AND THE CYTOSKELETON*
Vallier, L. G., Segall, J. E., Snyder, M.
2002; 53 (4): 251-266
- **A novel mitochondrial protein, Tar1p, is encoded on the antisense strand of the nuclear 25S rDNA** *GENES & DEVELOPMENT*
Coelho, P. S., Bryan, A. C., Kumar, A., Shadel, G. S., Snyder, M.
2002; 16 (21): 2755-2760
- **A dynamic approach to mapping coordinates between microplates and microarrays** *JOURNAL OF BIOMEDICAL INFORMATICS*
Cheung, K. H., Hager, J., Nelson, K., White, K., Li, Y. L., Snyder, M., Williams, K., Miller, P.
2002; 35 (5-6): 306-312
- **Global analysis of gene expression in yeast. *Functional & integrative genomics***
Horak, C. E., Snyder, M.
2002; 2 (4-5): 171-180
- **Functional profiling of the *Saccharomyces cerevisiae* genome** *NATURE*
Giaever, G., Chu, A. M., Ni, L., CONNELLY, C., Riles, L., Veronneau, S., Dow, S., Lucau-Danila, A., Anderson, K., Andre, B., Arkin, A. P., Astromoff, A., El Bakkoury, et al
2002; 418 (6896): 387-391

- **Microtubule capture by the cleavage apparatus is required for proper spindle positioning in yeast** *GENES & DEVELOPMENT*
Kusch, J., Meyer, A., Snyder, M. P., Barral, Y.
2002; 16 (13): 1627-1639
- **Large-scale identification of genes important for apical growth in *Saccharomyces cerevisiae* by directed allele replacement technology (DART) screening.** *Functional & integrative genomics*
Bidlingmaier, S., Snyder, M.
2002; 1 (6): 345-356
- **Bud-site selection and cell polarity in budding yeast** *CURRENT OPINION IN MICROBIOLOGY*
Casamayor, A., Snyder, M.
2002; 5 (2): 179-186
- **'Omic' approaches for unraveling signaling networks** *CURRENT OPINION IN CELL BIOLOGY*
Zhu, H., Snyder, M.
2002; 14 (2): 173-179
- **Carbohydrate analysis prepares to enter the "omics" era** *CHEMISTRY & BIOLOGY*
Bidlingmaier, S., Snyder, M.
2002; 9 (4): 400-401
- **Subcellular localization of the yeast proteome** *GENES & DEVELOPMENT*
Kumar, A., Agarwal, S., Heyman, J. A., Matson, S., Heidtman, M., Piccirillo, S., Umansky, L., Drawid, A., Jansen, R., Liu, Y., Cheung, K. H., Miller, P., Gerstein, et al
2002; 16 (6): 707-719
- **GATA-1 binding sites mapped in the beta-globin locus by using mammalian chlp-chip analysis** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Horak, C. E., Mahajan, M. C., Luscombe, N. M., Gerstein, M., Weissman, S. M., Snyder, M.
2002; 99 (5): 2924-2929
- **A question of size: the eukaryotic proteome and the problems in defining it** *NUCLEIC ACIDS RESEARCH*
Harrison, P. M., Kumar, A., Lang, N., Snyder, M., Gerstein, M.
2002; 30 (5): 1083-1090
- **A small reservoir of disabled ORFs in the yeast genome and its implications for the dynamics of proteome evolution** *JOURNAL OF MOLECULAR BIOLOGY*
Harrison, P., Kumar, A., Lan, N., Echols, N., Snyder, M., Gerstein, M.
2002; 316 (3): 409-419
- **An integrated approach for finding overlooked genes in yeast** *NATURE BIOTECHNOLOGY*
Kumar, A., Harrison, P. M., Cheung, K. H., Lan, N., Echols, N., Bertone, P., Miller, P., Gerstein, M. B., Snyder, M.
2002; 20 (1): 58-63
- **Insertional mutagenesis: Transposon-insertion libraries as mutagens in yeast** *GUIDE TO YEAST GENETICS AND MOLECULAR AND CELL BIOLOGY, PT B*
Kumar, A., Vidan, S., Snyder, M.
2002; 350: 219-229
- **ChIP-chip: A genomic approach for identifying transcription factor binding sites** *GUIDE TO YEAST GENETICS AND MOLECULAR AND CELL BIOLOGY, PT B*
Horak, C. E., Snyder, M.
2002; 350: 469-483
- **The TRIPLES database: a community resource for yeast molecular biology** *NUCLEIC ACIDS RESEARCH*
Kumar, A., Cheung, K. H., Tosches, N., Masiar, P., Liu, Y., Miller, P., Snyder, M.
2002; 30 (1): 73-75
- **YMD: A microarray database for large-scale gene expression analysis** *Annual Symposium of the American-Medical-Informatics-Association*
Cheung, K. H., White, K., Hager, J., Gerstein, M., Reinke, V., Nelson, K., Masiar, P., Srivastava, R., Li, Y. L., Li, J., Zhao, H. Y., Li, J. M., Allison, et al

HANLEY & BELFUS INC MED PUBLISHERS.2002: 140–144

- **Phosphorylation of gamma-tubulin regulates microtubule organization in budding yeast** *DEVELOPMENTAL CELL*
Vogel, J., Drapkin, B., Oomen, J., Beach, D., Bloom, K., Snyder, M.
2001; 1 (5): 621-631
- **A filamentous growth response mediated by the yeast mating pathway** *GENETICS*
Erdman, S., Snyder, M.
2001; 159 (3): 919-928
- **Global analysis of protein activities using proteome chips** *SCIENCE*
Zhu, H., Bilgin, M., Bangham, R., Hall, D., Casamayor, A., Bertone, P., Lan, N., Jansen, R., Bidlingmaier, S., Houfek, T., Mitchell, T., Miller, P., Dean, et al
2001; 293 (5537): 2101-2105
- **A genomic study of the bipolar bud site selection pattern in *Saccharomyces cerevisiae*** *MOLECULAR BIOLOGY OF THE CELL*
Ni, L., Snyder, M.
2001; 12 (7): 2147-2170
- **Genome-wide transposon mutagenesis in yeast.** *Current protocols in molecular biology / edited by Frederick M. Ausubel ... [et al.]*
Kumar, A., Snyder, M.
2001; Chapter 13: Unit13 3-?
- **Emerging technologies in yeast genomics** *NATURE REVIEWS GENETICS*
Kumar, A., Snyder, M.
2001; 2 (4): 302-312
- **The Cbk1p pathway is important for polarized cell growth and cell separation in *Saccharomyces cerevisiae*** *MOLECULAR AND CELLULAR BIOLOGY*
Bidlingmaier, S., Weiss, E. L., Seidel, C., Drubin, D. G., Snyder, M.
2001; 21 (7): 2449-2462
- **Protein arrays and microarrays** *CURRENT OPINION IN CHEMICAL BIOLOGY*
Zhu, H., Snyder, M.
2001; 5 (1): 40-45
- **Large-scale mutagenesis: yeast genetics in the genome era** *CURRENT OPINION IN BIOTECHNOLOGY*
Vidan, S., Snyder, M.
2001; 12 (1): 28-34
- **A metadata framework for interoperating heterogeneous genome data using XML** *Annual Symposium of the American-Medical-Informatics-Association (AMIA 2001)*
Cheung, K. H., Deshpande, A. M., Tosches, N., Nath, S., Agrawal, A., Miller, P., Kumar, A., Snyder, M.
BMJ PUBLISHING GROUP.2001: 110–114
- **The carboxy terminus of Tub4p is required for gamma-tubulin function in budding yeast** *JOURNAL OF CELL SCIENCE*
Vogel, J., Snyder, M.
2000; 113 (21): 3871-3882
- **Analysis of yeast protein kinases using protein chips** *NATURE GENETICS*
Zhu, H., Klemic, J. F., Chang, S., Bertone, P., Casamayor, A., Klemic, K. G., Smith, D., Gerstein, M., Reed, M. A., Snyder, M.
2000; 26 (3): 283-289
- **New antimicrobial flavanones from *Physena madagascariensis*** *JOURNAL OF NATURAL PRODUCTS*
Deng, Y. H., Lee, J. P., Tianasoa-Ramamonjy, M., Snyder, J. K., Des Etages, S. A., Kanada, D., Snyder, M. P., Turner, C. J.
2000; 63 (8): 1082-1089
- **Polarized growth controls cell shape and bipolar bud site selection in *Saccharomyces cerevisiae*** *MOLECULAR AND CELLULAR BIOLOGY*
Sheu, Y. J., Barral, Y., Snyder, M.
2000; 20 (14): 5235-5247

- **The Kar3p kinesin-related protein forms a novel heterodimeric structure with its associated protein Cik1p** *MOLECULAR BIOLOGY OF THE CELL*
Barrett, J. G., Manning, B. D., Snyder, M.
2000; 11 (7): 2373-2385
- **Drivers and passengers wanted! The role of kinesin-associated proteins** *TRENDS IN CELL BIOLOGY*
Manning, B. D., Snyder, M.
2000; 10 (7): 281-289
- **Genome-wide mutant collections: toolboxes for functional genomics** *CURRENT OPINION IN MICROBIOLOGY*
Coelho, P. S., Kumar, A., Snyder, M.
2000; 3 (3): 309-315
- **An integrated web interface for large-scale characterization of sequence data.** *Functional & integrative genomics*
Cheung, K. H., Kumar, A., Snyder, M., Miller, P.
2000; 1 (1): 70-75
- **Compartmentalization of the cell cortex by septins is required for maintenance of cell polarity in yeast** *MOLECULAR CELL*
Barral, Y., Mermall, V., Mooseker, M. S., Snyder, M.
2000; 5 (5): 841-851
- **Regulation of cytokinesis by the Elm1 protein kinase in *Saccharomyces cerevisiae*** *JOURNAL OF CELL SCIENCE*
BOUQUIN, N., Barral, Y., Courbeyrette, R., Blondel, M., Snyder, M., Mann, C.
2000; 113 (8): 1435-1445
- **Sbe2p and Sbe22p, two homologous Golgi proteins involved in yeast cell wall formation** *MOLECULAR BIOLOGY OF THE CELL*
Santos, B., Snyder, M.
2000; 11 (2): 435-452
- **Mutagenesis of murine cytomegalovirus using a Tn3-based transposon** *VIROLOGY*
Zhan, X. Y., Lee, M., Abenes, G., Von Reis, I., Kittinunvorakoon, C., Ross-Macdonald, P., Snyder, M., Liu, F. Y.
2000; 266 (2): 264-274
- **Graphically-enabled integration of bioinformatics tools allowing parallel execution** *Annual Symposium of the American-Medical-Informatics-Association*
Cheung, K. H., Miller, P., Sherman, A., Weston, S., Stratmann, E., Schultz, M., Snyder, M., Kumar, A.
HANLEY & BELFUS INC.2000: 141-145
- **TRIPLES: a database of gene function in *Saccharomyces cerevisiae*** *NUCLEIC ACIDS RESEARCH*
Kumar, A., Cheung, K. H., Ross-Macdonald, P., Coelho, P. S., Miller, P., Snyder, M.
2000; 28 (1): 81-84
- **gamma-tubulin of budding yeast** *CENTROSOME IN CELL REPLICATION AND EARLY DEVELOPMENT*
Vogel, J., Snyder, M.
2000; 49: 75-104
- **High-throughput methods for the large-scale analysis of gene function by transposon tagging** *APPLICATIONS OF CHIMERIC GENES AND HYBRID PROTEINS, PT C*
Kumar, A., Des Etages, S. A., Coelho, P. S., Roeder, G. S., Snyder, M.
2000; 328: 550-574
- **Large-scale analysis of the yeast genome by transposon tagging and gene disruption** *NATURE*
Ross-Macdonald, P., Coelho, P. S., Roemer, T., Agarwal, S., Kumar, A., Jansen, R., Cheung, K. H., Sheehan, A., Symoniatis, D., Umansky, L., Heldtman, M., Nelson, F. K., Iwasaki, et al
1999; 402 (6760): 413-418
- **Rationale and design of the National Emphysema Treatment Trial (NETT): A prospective randomized trial of lung volume reduction surgery** *JOURNAL OF THORACIC AND CARDIOVASCULAR SURGERY*
Rodarte, J., Miller, C., Barnard, P., Carter, J., DuBose, K., Flanigan, T., Fox, P., Haddad, J., Hale, K., Hood, E., Jahn, A., King, K., Nguyen, et al
1999; 118 (3): 518-528

- **Functional characterization of the S-cerevisiae genome by gene deletion and parallel analysis** *SCIENCE*
Winzeler, E. A., Shoemaker, D. D., Astromoff, A., Liang, H., Anderson, K., Andre, B., Bangham, R., Benito, R., Boeke, J. D., Bussey, H., Chu, A. M., CONNELLY, C., Davis, et al
1999; 285 (5429): 901-906
- **Differential regulation of the Kar3p kinesin-related protein by two associated proteins, Cik1p and Vik1p** *JOURNAL OF CELL BIOLOGY*
Manning, B. D., Barrett, J. G., Wallace, J. A., Granok, H., Snyder, M.
1999; 144 (6): 1219-1233
- **SHC1, a high pH inducible gene required for growth at alkaline pH in Saccharomyces cerevisiae** *BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS*
Hong, S. K., Han, S. B., Snyder, M., Choi, E. Y.
1999; 255 (1): 116-122
- **Nim1-related kinases coordinate cell cycle progression with the organization of the peripheral cytoskeleton in yeast** *GENES & DEVELOPMENT*
Barral, Y., Parra, M., Bidlingmaier, S., Snyder, M.
1999; 13 (2): 176-187
- **Transposon mutagenesis for the analysis of protein production, function, and localization** *CDNA PREPARATION AND CHARACTERIZATION*
Ross-Macdonald, P., Sheehan, A., Friddle, C., Roeder, G. S., Snyder, M.
1999; 303: 512-532
- **Spa2p interacts with cell polarity proteins and signaling components involved in yeast cell morphogenesis** *MOLECULAR AND CELLULAR BIOLOGY*
Sheu, Y. J., Santos, B., Fortin, N., Costigan, C., Snyder, M.
1998; 18 (7): 4053-4069
- **Ursodiol prophylaxis against hepatic complications of allogeneic bone marrow transplantation - A randomized, double-blind, placebo-controlled trial** *ANNALS OF INTERNAL MEDICINE*
Essell, J. H., Schroeder, M. T., Harman, G. S., Halvorson, R., Lew, V., Callander, N., Snyder, M., Lewis, S. K., Allerton, J. P., Thompson, J. M.
1998; 128 (12): 975-?
- **Pheromone-regulated genes required for yeast mating differentiation** *JOURNAL OF CELL BIOLOGY*
Erdman, S., Lin, L., Malczynski, M., Snyder, M.
1998; 140 (3): 461-483
- **The Spa2-related protein, Sph1p, is important for polarized growth in yeast** *JOURNAL OF CELL SCIENCE*
Roemer, T., Vallier, L., Sheu, Y. J., Snyder, M.
1998; 111: 479-494
- **Transposon tagging I: A novel system for monitoring protein production, function and localization** *YEAST GENE ANALYSIS*
Ross-Macdonald, P., Sheehan, A., Friddle, C., Roeder, G. S., Snyder, M.
1998; 26: 161-179
- **Cell polarity and morphogenesis in budding yeast** *ANNUAL REVIEW OF MICROBIOLOGY*
Madden, K., Snyder, M.
1998; 52: 687-744
- **The Rho-GEF Rom2p localizes to sites of polarized cell growth and participates in cytoskeletal functions in Saccharomyces cerevisiae** *MOLECULAR BIOLOGY OF THE CELL*
Manning, B. D., Padmanabha, R., Snyder, M.
1997; 8 (10): 1829-1844
- **Human dishevelled genes constitute a DHR-containing multigene family** *GENOMICS*
Semenov, M. V., Snyder, M.
1997; 42 (2): 302-310
- **SBF cell cycle regulator as a target of the yeast PKC-MAP kinase pathway** *SCIENCE*
Madden, K., Sheu, Y. J., Baetz, K., Andrews, B., Snyder, M.

1997; 275 (5307): 1781-1784

- **Targeting of chitin synthase 3 to polarized growth sites in yeast requires Chs5p and Myo2p** *JOURNAL OF CELL BIOLOGY*
Santos, B., Snyder, M.
1997; 136 (1): 95-110
- **A multipurpose transposon system for analyzing protein production, localization, and function in *Saccharomyces cerevisiae*** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
ROSSMACDONALD, P., Sheehan, A., Roeder, G. S., Snyder, M.
1997; 94 (1): 190-195
- **Selection of polarized growth sites in yeast** *TRENDS IN CELL BIOLOGY*
Roemer, T., Vallier, L. G., Snyder, M.
1996; 6 (11): 434-441
- **DNA gyrase and topoisomerase IV on the bacterial chromosome: Quinolone-induced DNA cleavage** *JOURNAL OF MOLECULAR BIOLOGY*
Chen, C. R., Malik, M., Snyder, M., Drica, K.
1996; 258 (4): 627-637
- **Selection of axial growth sites in yeast requires Axl2p, a novel plasma membrane glycoprotein** *GENES & DEVELOPMENT*
Roemer, T., Madden, K., Chang, J. T., Snyder, M.
1996; 10 (7): 777-793
- **Target gene identification: Target specific transcriptional activation by three murine homeodomain VP16 hybrid proteins in *Saccharomyces cerevisiae*** *JOURNAL OF EXPERIMENTAL ZOOLOGY*
FriedmanEinat, M., Einat, P., Snyder, M., Ruddle, F.
1996; 274 (3): 145-156
- **Highly divergent gamma-tubulin gene is essential for cell growth and proper microtubule organization in *Saccharomyces cerevisiae*** *JOURNAL OF CELL BIOLOGY*
Sobel, S. G., Snyder, M.
1995; 131 (6): 1775-1788
- **Nuclear pore complex clustering and nuclear accumulation of poly(A)(+) RNA associated with mutation of the *Saccharomyces cerevisiae* RAT2/NUP120 gene** *JOURNAL OF CELL BIOLOGY*
Heath, C. V., Copeland, C. S., Amberg, D. C., DELPRIORE, V., Snyder, M., Cole, C. N.
1995; 131 (6): 1677-1697
- **MOLECULAR-BASIS OF CELL INTEGRITY AND MORPHOGENESIS IN SACCHAROMYCES-CEREVISIAE** *MICROBIOLOGICAL REVIEWS*
Cid, V. J., Duran, A., DELREY, F., Snyder, M. P., Nombela, C., Sanchez, M.
1995; 59 (3): 345-386
- **MUTATION OR DELETION OF THE SACCHAROMYCES-CEREVISIAE RAT3/NUP133 GENE CAUSES TEMPERATURE-DEPENDENT NUCLEAR ACCUMULATION OF POLY(A)(+) RNA AND CONSTITUTIVE CLUSTERING OF NUCLEAR-PORE COMPLEXES** *MOLECULAR BIOLOGY OF THE CELL*
Li, O., Heath, C. V., Amberg, D. C., Dockendorff, T. C., Copeland, C. S., Snyder, M., Cole, C. N.
1995; 6 (4): 401-417
- **2 SHORT AUTOEPITOPES ON THE NUCLEAR DOT ANTIGEN ARE SIMILAR TO EPITOPES ENCODED BY THE EPSTEIN-BARR-VIRUS** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
XIE, K. W., Snyder, M.
1995; 92 (5): 1639-1643
- **Methods for large-scale analysis of gene expression, protein localization, and disruption phenotypes in *Saccharomyces cerevisiae*** *METHODS IN MOLECULAR AND CELLULAR BIOLOGY*
ROSSMACDONALD, P., Burns, N., Malczynski, M., Sheehan, A., Roeder, S., Snyder, M.
1995; 5 (5): 298-308
- **THE SPINDLE POLE BODY OF YEAST** *CHROMOSOMA*
Snyder, M.
1994; 103 (6): 369-380

- **SLK1, A YEAST HOMOLOG OF MAP KINASE ACTIVATORS, HAS A RAS/CAMP INDEPENDENT ROLE IN NUTRIENT SENSING** *MOLECULAR & GENERAL GENETICS*
Costigan, C., Snyder, M.
1994; 243 (3): 286-296
- **LARGE-SCALE ANALYSIS OF GENE-EXPRESSION, PROTEIN LOCALIZATION, AND GENE DISRUPTION SACCHAROMYCES-CEREVISIAE** *GENES & DEVELOPMENT*
Burns, N., Grimwade, B., ROSSMACDONALD, P. B., Choi, E. Y., Finberg, K., Roeder, G. S., Snyder, M.
1994; 8 (9): 1087-1105
- **NHP6A AND NHP6B, WHICH ENCODE HMG1-LIKE PROTEINS, ARE CANDIDATES FOR DOWNSTREAM COMPONENTS OF THE YEAST SLT2 MITOGEN-ACTIVATED PROTEIN-KINASE PATHWAY** *MOLECULAR AND CELLULAR BIOLOGY*
Costigan, C., Kolodrubetz, D., Snyder, M.
1994; 14 (4): 2391-2403
- **MUTATIONS IN PRG1, A YEAST PROTEASOME-RELATED GENE, CAUSE DEFECTS IN NUCLEAR DIVISION AND ARE SUPPRESSED BY DELETION OF A MITOTIC CYCLIN GENE** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Friedman, H., Snyder, M.
1994; 91 (6): 2031-2035
- **LOCALIZATION OF THE KAR3 KINESIN HEAVY CHAIN-RELATED PROTEIN REQUIRES THE CIK1 INTERACTING PROTEIN** *JOURNAL OF CELL BIOLOGY*
Page, B. D., Satterwhite, L. L., Rose, M. D., Snyder, M.
1994; 124 (4): 507-519
- **NUCLEAR DOT ANTIGENS MAY SPECIFY TRANSCRIPTIONAL DOMAINS IN THE NUCLEUS** *MOLECULAR AND CELLULAR BIOLOGY*
XIE, K. W., Lambie, E. J., Snyder, M.
1993; 13 (10): 6170-6179
- **COMPONENTS REQUIRED FOR CYTOKINESIS ARE IMPORTANT FOR BUD SITE SELECTION IN YEAST** *JOURNAL OF CELL BIOLOGY*
FLESCHER, E. G., Madden, K., Snyder, M.
1993; 122 (2): 373-386
- **CARBON SOURCE INDUCES GROWTH OF STATIONARY PHASE YEAST-CELLS, INDEPENDENT OF CARBON SOURCE METABOLISM** *YEAST*
Granot, D., Snyder, M.
1993; 9 (5): 465-479
- **NUCLEAR-PORE COMPLEX ANTIGENS DELINEATE NUCLEAR-ENVELOPE DYNAMICS IN VEGETATIVE AND CONJUGATING SACCHAROMYCES-CEREVISIAE** *YEAST*
Copeland, C. S., Snyder, M.
1993; 9 (3): 235-249
- **CHROMOSOME SEGREGATION IN YEAST** *ANNUAL REVIEW OF MICROBIOLOGY*
Page, B. D., Snyder, M.
1993; 47: 231-261
- **A HOMOLOG OF THE PROTEASOME-RELATED RING10 GENE IS ESSENTIAL FOR YEAST-CELL GROWTH** *GENE*
Friedman, H., Goebel, M., Snyder, M.
1992; 122 (1): 203-206
- **THE NUCLEAR-MITOTIC APPARATUS PROTEIN IS IMPORTANT IN THE ESTABLISHMENT AND MAINTENANCE OF THE BIPOLAR MITOTIC SPINDLE APPARATUS** *MOLECULAR BIOLOGY OF THE CELL*
Yang, C. H., Snyder, M.
1992; 3 (11): 1259-1267
- **SPECIFICATION OF SITES FOR POLARIZED GROWTH IN SACCHAROMYCES-CEREVISIAE AND THE INFLUENCE OF EXTERNAL FACTORS ON SITE SELECTION** *MOLECULAR BIOLOGY OF THE CELL*
Madden, K., Snyder, M.
1992; 3 (9): 1025-1035

- **CIK1 - A DEVELOPMENTALLY REGULATED SPINDLE POLE BODY-ASSOCIATED PROTEIN IMPORTANT FOR MICROTUBULE FUNCTIONS IN SACCHAROMYCES-CEREVISIAE** *GENES & DEVELOPMENT*
Page, B. D., Snyder, M.
1992; 6 (8): 1414-1429
- **NUMA - AN UNUSUALLY LONG COILED-COIL RELATED PROTEIN IN THE MAMMALIAN NUCLEUS** *JOURNAL OF CELL BIOLOGY*
Yang, C. H., Lambie, E. J., Snyder, M.
1992; 116 (6): 1303-1317
- **A SYNTHETIC LETHAL SCREEN IDENTIFIES SLK1, A NOVEL PROTEIN-KINASE HOMOLOG IMPLICATED IN YEAST-CELL MORPHOGENESIS AND CELL-GROWTH** *MOLECULAR AND CELLULAR BIOLOGY*
Costigan, C., GEHRUNG, S., Snyder, M.
1992; 12 (3): 1162-1178
- **THE NUF1 GENE ENCODES AN ESSENTIAL COILED-COIL RELATED PROTEIN THAT IS A POTENTIAL COMPONENT OF THE YEAST NUCLEOSKELETON** *JOURNAL OF CELL BIOLOGY*
Mirzayan, C., Copeland, C. S., Snyder, M.
1992; 116 (6): 1319-1332
- **Cell polarity and morphogenesis in *Saccharomyces cerevisiae*.** *Trends in cell biology*
Madden, K., Costigan, C., Snyder, M.
1992; 2 (1): 22-29
- **THE KNS1 GENE OF SACCHAROMYCES-CEREVISIAE ENCODES A NONESSENTIAL PROTEIN-KINASE HOMOLOG THAT IS DISTANTLY RELATED TO MEMBERS OF THE CDC28/CDC2 GENE FAMILY** *MOLECULAR & GENERAL GENETICS*
Padmanabha, R., GEHRUNG, S., Snyder, M.
1991; 229 (1): 1-9
- **STUDIES CONCERNING THE TEMPORAL AND GENETIC-CONTROL OF CELL POLARITY IN SACCHAROMYCES-CEREVISIAE** *JOURNAL OF CELL BIOLOGY*
Snyder, M., GEHRUNG, S., Page, B. D.
1991; 114 (3): 515-532
- **GLUCOSE INDUCES CAMP-INDEPENDENT GROWTH-RELATED CHANGES IN STATIONARY-PHASE CELLS OF SACCHAROMYCES-CEREVISIAE** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Granot, D., Snyder, M.
1991; 88 (13): 5724-5728
- **SEGREGATION OF THE NUCLEOLUS DURING MITOSIS IN BUDDING AND FISSION YEAST** *CELL MOTILITY AND THE CYTOSKELETON*
Granot, D., Snyder, M.
1991; 20 (1): 47-54
- **THE SPA2 GENE OF SACCHAROMYCES-CEREVISIAE IS IMPORTANT FOR PHEROMONE-INDUCED MORPHOGENESIS AND EFFICIENT MATING** *JOURNAL OF CELL BIOLOGY*
GEHRUNG, S., Snyder, M.
1990; 111 (4): 1451-1464
- **HIGHER-ORDER STRUCTURE IS PRESENT IN THE YEAST NUCLEUS - AUTOANTIBODY PROBES DEMONSTRATE THAT THE NUCLEOLUS LIES OPPOSITE THE SPINDLE POLE BODY** *CHROMOSOMA*
Yang, C. H., Lambie, E. J., Hardin, J., Craft, J., Snyder, M.
1989; 98 (2): 123-128
- **THE SPA2 PROTEIN OF YEAST LOCALIZES TO SITES OF CELL-GROWTH** *JOURNAL OF CELL BIOLOGY*
Snyder, M.
1989; 108 (4): 1419-1429
- **GENOMIC ORGANIZATION OF TRANSFER-RNA AND AMINOACYL-TRNA SYNTHETASE GENES FOR 2 AMINO-ACIDS IN SACCHAROMYCES-CEREVISIAE** *GENOMICS*
Kolman, C. J., Snyder, M., Soll, D.
1988; 3 (3): 201-206

- **DNA GYRASE ON THE BACTERIAL CHROMOSOME - DNA CLEAVAGE INDUCED BY OXOLINIC ACID** *JOURNAL OF MOLECULAR BIOLOGY*
Snyder, M., Drlaca, K.
1979; 131 (2): 287-302
- **SUPERHELICAL ESCHERICHIA-COLI DNA - RELAXATION BY COUMERMYCIN** *JOURNAL OF MOLECULAR BIOLOGY*
Drlaca, K., Snyder, M.
1978; 120 (2): 145-154