

# Stanford

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## Lars Steinmetz

Professor of Genetics

### CONTACT INFORMATION

- **Alternate Contact**

Michelle Nguyen - Executive Assistant

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### Bio

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#### BIO

B.S. 1994-1997, Molecular Biophysics and Biochemistry, Yale University.

Ph.D. 1997-2001, Genetics, Stanford University. Advisor: Ronald W. Davis.

Postdoctoral research at Stanford Genome Technology Center 2002 and visiting group leader 2003-2013.

Group leader at European Molecular Biology Laboratory (EMBL), 2003-present.

Founding Joint Head (chair) of Genome Biology Unit and Senior Scientist, EMBL 2009-2013.

Co-founder, Sophia Genetics 2011.

ERC Advanced Investigator (twice), 2012-present.

Associate Head of Genome Biology Unit and Senior Scientist, EMBL 2013-2016.

Senior Scientist and Director of Life Science Alliance, EMBL 2016-present.

Professor of Genetics, Stanford University, 2013-present.

Co-Director of the Stanford Genome Technology Center, 2013-present.

#### ACADEMIC APPOINTMENTS

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

#### ADMINISTRATIVE APPOINTMENTS

- Co-Director, Stanford Genome Technology Center, (2013- present)
- Senior Scientist and Director of Life Science Alliance, a Stanford-EMBL collaboration, European Molecular Biology Laboratory (EMBL), (2014- present)
- Director of Graduate Admissions, Department of Genetics, Stanford University, (2013- present)

## HONORS AND AWARDS

- Ira Herskowitz Award, Genetics Society of America (2016)
- Dr. V. Ramalingaswami Chair, Indian National Science Academy (2014-2015)
- EMBO Member, European Molecular Biology Organization (2013)
- Two times ERC Advanced Investigator, European Research Council (2012, 2017)
- Emmy Noether-Program Young Investigator, Deutsche Forschungsgemeinschaft (2004-2010)
- Howard Hughes Predoctoral Fellow, Howard Hughes Medical Institute (1998-2001)

## BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Advisory Editorial Board Member, Molecular Systems Biology (2014 - present)
- Associate Editor, Genetics (2014 - present)
- EMBO Member, European Molecular Biology Organization (2013 - present)
- Scientific Advisory Board Member, Saccharomyces Genome Database (SGD, [www.yeastgenome.org](http://www.yeastgenome.org)) (2013 - present)
- Associate Editor, G3: Genes | Genomes | Genetics (2011 - present)
- President, Scientific Advisory Board, Sophia Genetics (2011 - present)

## PROFESSIONAL EDUCATION

- Ph.D., Stanford University , Genetics (2001)
- Bachelor of Science, Yale University , Molecular Biophysics and Biochemistry (1997)

## LINKS

- Stanford Lab Website: <http://steinmetzlab.stanford.edu>
- EMBL Lab Website: <http://steinmetzlab.embl.de>
- Stanford Genome Technology Center: <http://med.stanford.edu/sgtc/>
- Stanford-EMBL Life Science Alliance: <http://lifesciencealliance.stanford.edu>
- Lars Steinmetz's Google Scholar Citations: <http://scholar.google.de/citations?user=eMs1ptMAAAAJ&hl=en>
- Lars Steinmetz's F1000 Recommendations: [http://f1000.com/prime/search/evaluations?query=steinmetz\\_lm&evaluations.queryField=author](http://f1000.com/prime/search/evaluations?query=steinmetz_lm&evaluations.queryField=author)

## Research & Scholarship

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### CURRENT RESEARCH AND SCHOLARLY INTERESTS

One of the most daunting challenges in medicine is the complex nature of most diseases (including cancer, diabetes, heart disease and some forms of rare disease) due to interactions between multiple genetic variants and environmental influences. Our research is directed at understanding such complex traits; to do so, we develop novel genomic approaches to investigate the molecular processes that link genotype to phenotype, identify the causal underlying factors, and quantify their contributions. We investigate variation at the level of the genome, transcriptome and proteome, which we integrate with higher-level phenotypes. We also use the resulting molecular networks to predict and evaluate intervention points that enable modulation of phenotype. In particular, our projects are in the following areas:

#### 1) Functions and mechanisms of gene regulation

We have developed several technologies to characterize and quantify pervasive transcription at the genome-wide level as well as its functional impact. In particular, we are interested in the function and regulation of non-coding RNAs, antisense transcription, and the molecular phenotypes that arise from transcriptome complexity.

#### 2) Systems genetics

We have also piloted new technologies to dissect the genetic basis of complex, multifactorial phenotypes. We are interested in studying how genetic variation is inherited through recombination, the consequences of genetic variation, learning to predict phenotype from genotype, and integrating multiple layers of molecular data in order to define intervention points that can be targeted to modulate phenotypes of interest.

### 3) Disease models

We have used multiple model systems, primarily yeast and human cells, to characterize the genetic and cellular systems affected in particular diseases and assess potential therapeutic strategies. We are studying diseases in patient-derived cells using systematic, followed by mechanistic approaches, to unravel mechanisms and discover novel treatments.

Notably, we place a strong emphasis on the development of new technologies, leveraging the Stanford Genome Technology Center's strengths in this area. Some engineering applications we aim to develop include novel biosensors for detection of minute quantities of biological material and single-cell approaches to investigate genome and transcriptome complexity. Through developing such technologies, we will work with the Center to reduce the cost and increase the accuracy and throughput of biomedical research and health care. Ultimately, we strive to develop approaches that will enable personalized, preventive medicine.

## Teaching

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### STANFORD ADVISEES

#### Doctoral Dissertation Reader (AC)

Gun Woo Byeon

#### Postdoctoral Faculty Sponsor

Andreas Gschwind, Takeshi Matsui, Kevin Roy, Justin Smith, Han Sun, Jingyan Wu, Chenchen Zhu

#### Doctoral Dissertation Advisor (AC)

Michael Sikora, Kristen Wells

### GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Genetics (Phd Program)

## Publications

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### PUBLICATIONS

- **Thymic tuft cells promote an IL-4-enriched medulla and shape thymocyte development** *NATURE*  
Miller, C. N., Proekt, I., von Moltke, J., Wells, K. L., Rajpurkar, A. R., Wang, H., Rattay, K., Khan, I. S., Metzger, T. C., Pollack, J. L., Fries, A. C., Lwin, W. W., Wigton, et al  
2018; 559 (7715): 627+
- **Multiplexed precision genome editing with trackable genomic barcodes in yeast.** *Nature biotechnology*  
Roy, K. R., Smith, J. D., Vonesch, S. C., Lin, G., Tu, C. S., Lederer, A. R., Chu, A., Suresh, S., Nguyen, M., Horecka, J., Tripathi, A., Burnett, W. T., Morgan, et al  
2018
- **Large-Scale Low-Cost NGS Library Preparation Using a Robust Tn5 Purification and Tagmentation Protocol.** *G3 (Bethesda, Md.)*  
Hennig, B. P., Velten, L., Racke, I., Tu, C. S., Thoms, M., Rybin, V., Besir, H., Remans, K., Steinmetz, L. M.  
2018; 8 (1): 79–89
- **Human haematopoietic stem cell lineage commitment is a continuous process** *NATURE CELL BIOLOGY*  
Velten, L., Haas, S. F., Raffel, S., Blaszkiewicz, S., Islam, S., Hennig, B. P., Hirche, C., Lutz, C., Buss, E. C., Nowak, D., Boch, T., Hofmann, W., Ho, et al  
2017; 19 (4): 271-?
- **Single-cell transcriptome analysis reveals coordinated ectopic gene-expression patterns in medullary thymic epithelial cells** *NATURE IMMUNOLOGY*

- Brennecke, P., Reyes, A., Pinto, S., Rattay, K., Nguyen, M., Kuechler, R., Huber, W., Kyewski, B., Steinmetz, L. M.  
2015; 16 (9): 933-941
- **Widespread Co-translational RNA Decay Reveals Ribosome Dynamics.** *Cell*  
Pelechano, V., Wei, W., Steinmetz, L. M.  
2015; 161 (6): 1400-1412
  - **Genotype-environment interactions reveal causal pathways that mediate genetic effects on phenotype.** *PLoS genetics*  
Gagneur, J., Stegle, O., Zhu, C., Jakob, P., Tekkedil, M. M., Aiyar, R. S., Schuon, A., Pe'er, D., Steinmetz, L. M.  
2013; 9 (9)
  - **The Genomic and Transcriptomic Landscape of a HeLa Cell Line** *G3-GENES GENOMES GENETICS*  
Landry, J. J., Pyl, P. T., Rausch, T., Zichner, T., Tekkedil, M. M., Stuetz, A. M., Jauch, A., Aiyar, R. S., Pau, G., Delhomme, N., Gagneur, J., Korbel, J. O., Huber, et al  
2013; 3 (8): 1213-1224
  - **Extensive transcriptional heterogeneity revealed by isoform profiling.** *Nature*  
Pelechano, V., Wei, W., Steinmetz, L. M.  
2013; 497 (7447): 127-131
  - **Bidirectional promoters generate pervasive transcription in yeast** *NATURE*  
Xu, Z., Wei, W., Gagneur, J., Perocchi, F., Clauder-Muenster, S., Camblong, J., Guffanti, E., Stutz, F., Huber, W., Steinmetz, L. M.  
2009; 457 (7232): 1033-U7
  - **High-resolution mapping of meiotic crossovers and non-crossovers in yeast** *NATURE*  
Mancera, E., Bourgon, R., Brozzi, A., Huber, W., Steinmetz, L. M.  
2008; 454 (7203): 479-U1
  - **Genome sequencing and comparative analysis of *Saccharomyces cerevisiae* strain YJM789** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Wei, W., McCusker, J. H., Hyman, R. W., Jones, T., Ning, Y., Cao, Z., Gu, Z., Bruno, D., Miranda, M., Nguyen, M., Wilhelmy, J., Komp, C., Tamse, et al  
2007; 104 (31): 12825-12830
  - **A high-resolution map of transcription in the yeast genome** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
David, L., Huber, W., Granovskaia, M., Toedling, J., Palm, C. J., Bofkin, L., Jones, T., Davis, R. W., Steinmetz, L. M.  
2006; 103 (14): 5320-5325
  - **Select sequencing of clonally expanded CD8+ T cells reveals limits to clonal expansion.** *Proceedings of the National Academy of Sciences of the United States of America*  
Huang, H., Sikora, M. J., Islam, S., Chowdhury, R. R., Chien, Y., Scriba, T. J., Davis, M. M., Steinmetz, L. M.  
2019
  - **Regional Variation in RBM20 Causes a Highly Penetrant Arrhythmogenic Cardiomyopathy.** *Circulation. Heart failure*  
Parikh, V. N., Caleshu, C., Reuter, C., Lazzeroni, L. C., Ingles, J., Garcia, J., McCaleb, K., Adesiyun, T., Sedaghat-Hamedani, F., Kumar, S., Graw, S., Gigli, M., Stolfo, et al  
2019; 12 (3): e005371
  - **Evolthon: A community endeavor to evolve lab evolution** *PLOS BIOLOGY*  
Strauss, S., Schirman, D., Jona, G., Brooks, A. N., Kunjapur, A. M., Ba, A., Flint, A., Solt, A., Mershin, A., Dixit, A., Yona, A. H., Csorgo, B., Busby, et al  
2019; 17 (3): e3000182
  - **Cytosine base editor generates substantial off-target single-nucleotide variants in mouse embryos.** *Science (New York, N.Y.)*  
Zuo, E., Sun, Y., Wei, W., Yuan, T., Ying, W., Sun, H., Yuan, L., Steinmetz, L. M., Li, Y., Yang, H.  
2019
  - **Sensitive high-throughput single-cell RNA-seq reveals within-clonal transcript correlations in yeast populations.** *Nature microbiology*  
Nadal-Ribelles, M., Islam, S., Wei, W., Latorre, P., Nguyen, M., de Nadal, E., Posas, F., Steinmetz, L. M.  
2019
  - **Opposing T cell responses in experimental autoimmune encephalomyelitis.** *Nature*

- Saligrama, N., Zhao, F., Sikora, M. J., Serratelli, W. S., Fernandes, R. A., Louis, D. M., Yao, W., Ji, X., Idoyaga, J., Mahajan, V. B., Steinmetz, L. M., Chien, Y. H., Hauser, et al  
2019
- **Biological plasticity rescues target activity in CRISPR knock outs.** *Nature methods*  
Smits, A. H., Ziebell, F., Joberty, G., Zinn, N., Mueller, W. F., Clauder-Münster, S., Eberhard, D., Fälth Savitski, M., Grandi, P., Jakob, P., Michon, A. M., Sun, H., Tessmer, et al  
2019
  - **Genetic analysis reveals functions of atypical polyubiquitin chains.** *eLife*  
Meza Gutierrez, F., Simsek, D., Mizrak, A., Deutschbauer, A., Braberg, H., Johnson, J., Xu, J., Shales, M., Nguyen, M., Tamse-Kuehn, R., Palm, C., Steinmetz, L. M., Krogan, et al  
2018; 7
  - **Conventional and Neo-antigenic Peptides Presented by beta Cells Are Targeted by Circulating Naive CD8+T Cells in Type 1 Diabetic and Healthy Donors** *CELL METABOLISM*  
Gonzalez-Duque, S., Azoury, M., Colli, M. L., Afonso, G., Turatsinze, J., Nigi, L., Lalanne, A., Sebastiani, G., Carre, A., Pinto, S., Culina, S., Corcos, N., Bugliani, et al  
2018; 28 (6): 946+
  - **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
  - **Gain of CTCF-Anchored Chromatin Loops Marks the Exit from Naive Pluripotency.** *Cell systems*  
Pekowska, A., Klaus, B., Xiang, W., Severino, J., Daigle, N., Klein, F. A., Oles, M., Casellas, R., Ellenberg, J., Steinmetz, L. M., Bertone, P., Huber, W.  
2018
  - **Rpd3L HDAC links H3K4me3 to transcriptional repression memory** *NUCLEIC ACIDS RESEARCH*  
Lee, B., Choi, A., Kim, J., Jun, Y., Woo, H., Ha, S., Yoon, C., Hwang, J., Steinmetz, L., Buratowski, S., Lee, S., Kim, H., Kim, et al  
2018; 46 (16): 8261–74
  - **NAD(P)HX repair deficiency causes central metabolic perturbations in yeast and human cells** *FEBS JOURNAL*  
Becker-Kettern, J., Paczia, N., Conrotte, J., Zhu, C., Fiehn, O., Jung, P. P., Steinmetz, L. M., Linster, C. L.  
2018; 285 (18): 3376–3401
  - **HEX: A heterologous expression platform for the discovery of fungal natural products** *SCIENCE ADVANCES*  
Harvey, C. B., Tang, M., Schlecht, U., Horecka, J., Fischer, C. R., Lin, H., Li, J., Naughton, B., Cherry, J., Miranda, M., Li, Y., Chu, A. M., Hennessy, et al  
2018; 4 (4): eaar5459
  - **Multiplexed ChIP-Seq Using Direct Nucleosome Barcoding: A Tool for High-Throughput Chromatin Analysis.** *Methods in molecular biology (Clifton, N.J.)*  
Chabbert, C. D., Adjalley, S. H., Steinmetz, L. M., Pelechano, V.  
2018; 1689: 177–94
  - **Evolutionary-like selection on-a-chip: Using microfluidics to isolate the fittest sperm**  
Chinnasamy, T., Kingsley, J., Durmus, N. G., Turek, P. J., Rosen, M. P., Behr, B., Steinmetz, L. M., Tuzel, E., Demirci, U.  
OXFORD UNIV PRESS.2017: 187–88
  - **A new fate mapping system reveals context-dependent random or clonal expansion of microglia.** *Nature neuroscience*  
Tay, T. L., Mai, D., Dautzenberg, J., Fernández-Klett, F., Lin, G., SAGAR, Datta, M., Drougard, A., Stempf, T., Ardura-Fabregat, A., Staszewski, O., Margineanu, A., Sporb, A., et al  
2017; 20 (6): 793-803
  - **Assembly of functionally integrated human forebrain spheroids** *NATURE*  
Birey, F., Andersen, J., Makinson, C. D., Islam, S., Wei, W., Huber, N., Fan, H. C., Metzler, K. R., Panagiotakos, G., Thom, N., O'Rourke, N. A., Steinmetz, L. M., Bernstein, et al  
2017; 545 (7652): 54-?
  - **Modulating Crossover Frequency and Interference for Obligate Crossovers in *Saccharomyces cerevisiae* Meiosis** *G3-GENES GENOMES GENETICS*  
Chakraborty, P., Pankajam, A. V., Lin, G., Dutta, A., Nandan, K. G., Tekkedil, M. M., Shinohara, A., Steinmetz, L. M., Thazath, N. K.

2017; 7 (5): 1511-1524

- **INO80 represses osmostress induced gene expression by resetting promoter proximal nucleosomes** *NUCLEIC ACIDS RESEARCH*  
Klopf, E., Schmidt, H. A., Clauder-Muenster, S., Steinmetz, L. M., Schueller, C.  
2017; 45 (7): 3752-3766
- **Myt1l safeguards neuronal identity by actively repressing many non-neuronal fates** *NATURE*  
Mall, M., Kareta, M. S., Chanda, S., Ahlenius, H., Perotti, N., Zhou, B., Grieder, S. D., Ge, X., Drake, S., Ang, C. E., Walker, B. M., Vierbuchen, T., Fuentes, et al  
2017; 544 (7649): 245-?
- **A method for high-throughput production of sequence-verified DNA libraries and strain collections.** *Molecular systems biology*  
Smith, J. D., Schlecht, U., Xu, W., Suresh, S., Horecka, J., Proctor, M. J., Aiyar, R. S., Bennett, R. A., Chu, A., Li, Y. F., Roy, K., Davis, R. W., Steinmetz, et al  
2017; 13 (2): 913-?
- **Inhibition of NGLY1 Inactivates the Transcription Factor Nrfl and Potentiates Proteasome Inhibitor Cytotoxicity.** *ACS central science*  
Tomlin, F. M., Gerling-Driessen, U. I., Liu, Y. C., Flynn, R. A., Vangala, J. R., Lentz, C. S., Clauder-Muenster, S., Jakob, P., Mueller, W. F., Ordoñez-Rueda, D., Paulsen, M., Matsui, N., Foley, et al  
2017; 3 (11): 1143-55
- **The State of Systems Genetics in 2017.** *Cell systems*  
Baliga, N. S., Björkegren, J. L., Boeke, J. D., Boutros, M., Crawford, N. P., Dudley, A. M., Farber, C. R., Jones, A., Levey, A. I., Lusic, A. J., Mak, H. C., Nadeau, J. H., Noyes, et al  
2017; 4 (1): 7-15
- **Genome Dynamics of Hybrid Saccharomyces cerevisiae During Vegetative and Meiotic Divisions.** *G3 (Bethesda, Md.)*  
Dutta, A., Lin, G., Pankajam, A. V., Chakraborty, P., Bhat, N., Steinmetz, L. M., Nishant, K. T.  
2017; 7 (11): 3669-79
- **Modulation of mRNA and lncRNA expression dynamics by the Set2-Rpd3S pathway** *NATURE COMMUNICATIONS*  
Kim, J. H., Lee, B. B., Oh, Y. M., Zhu, C., Steinmetz, L. M., Lee, Y., Kim, W. K., Lee, S. B., Buratowski, S., Kim, T.  
2016; 7
- **A privacy-preserving solution for compressed storage and selective retrieval of genomic data.** *Genome research*  
Huang, Z., Ayday, E., Lin, H., Aiyar, R. S., Molyneaux, A., Xu, Z., Fellay, J., Steinmetz, L. M., Hubaux, J.  
2016
- **A global genetic interaction network maps a wiring diagram of cellular function** *SCIENCE*  
Costanzo, M., VanderSluis, B., Koch, E. N., Baryshnikova, A., Pons, C., Tan, G., Wang, W., Usaj, M., Hanchard, J., Lee, S. D., Pelechano, V., Styles, E. B., Billmann, et al  
2016; 353 (6306): 1381-?
- **Principles for RNA metabolism and alternative transcription initiation within closely spaced promoters** *NATURE GENETICS*  
Chen, Y., Pai, A. A., Herudek, J., Lubas, M., Meola, N., Jaervelin, A. I., Andersson, R., Pelechano, V., Steinmetz, L. M., Jensen, T. H., Sandelin, A.  
2016; 48 (9): 984-?
- **Meiotic Interactors of a Mitotic Gene TAO3 Revealed by Functional Analysis of its Rare Variant** *G3-GENES GENOMES GENETICS*  
Gupta, S., Radhakrishnan, A., Nitin, R., Raharja-Liu, P., Lin, G., Steinmetz, L. M., Gagneur, J., Sinha, H.  
2016; 6 (8): 2255-2263
- **Protein Abundance Control by Non-coding Antisense Transcription** *CELL REPORTS*  
Huber, F., Bunina, D., Gupta, I., Khmelinskii, A., Meurer, M., Theer, P., Steinmetz, L. M., Knop, M.  
2016; 15 (12): 2625-2636
- **Functional interplay between MSL1 and CDK7 controls RNA polymerase II Ser5 phosphorylation** *NATURE STRUCTURAL & MOLECULAR BIOLOGY*  
Chlamydas, S., Holz, H., Samata, M., Chelmicki, T., Georgiev, P., Pelechano, V., Dundar, F., Dasmeh, P., Mittler, G., Cadete, F. T., Ramirez, F., Conrad, T., Wei, et al  
2016; 23 (6): 580-589
- **Translational Capacity of a Cell Is Determined during Transcription Elongation via the Ccr4-Not Complex** *CELL REPORTS*  
Gupta, I., Villanyi, Z., Kassem, S., Hughes, C., Panasenko, O. O., Steinmetz, L. M., Collart, M. A.  
2016; 15 (8): 1782-1794

- **The cellular growth rate controls overall mRNA turnover, and modulates either transcription or degradation rates of particular gene regulons** *NUCLEIC ACIDS RESEARCH*  
Garcia-Martinez, J., Delgado-Ramos, L., Ayala, G., Pelechano, V., Medina, D. A., Carrasco, F., Gonzalez, R., Andres-Leon, E., Steinmetz, L., Warringer, J., Chavez, S., Perez-Ortin, J. E.  
2016; 44 (8): 3643-3658
- **DChIPRep, an R/Bioconductor package for differential enrichment analysis in chromatin studies** *PEERJ*  
Chabbert, C. D., Steinmetz, L. M., Klaus, B.  
2016; 4
- **Landscape and Dynamics of Transcription Initiation in the Malaria Parasite *Plasmodium falciparum*** *CELL REPORTS*  
Adjalley, S. H., Chabbert, C. D., Klaus, B., Pelechano, V., Steinmetz, L. M.  
2016; 14 (10): 2463-2475
- **Integrating Cell Phone Imaging with Magnetic Levitation (i-LEV) for Label-Free Blood Analysis at the Point-of-Living.** *Small*  
Baday, M., Calamak, S., Durmus, N. G., Davis, R. W., Steinmetz, L. M., Demirci, U.  
2016; 12 (9): 1222-1229
- **Genome-wide quantification of 5'-phosphorylated mRNA degradation intermediates for analysis of ribosome dynamics.** *Nature protocols*  
Pelechano, V., Wei, W., Steinmetz, L. M.  
2016; 11 (2): 359-376
- **Comprehensive Identification of RNA-Binding Proteins by RNA Interactome Capture.** *Methods in molecular biology (Clifton, N.J.)*  
Castello, A., Horos, R., Strein, C., Fischer, B., Eichelbaum, K., Steinmetz, L. M., Krijgsveld, J., Hentze, M. W.  
2016; 1358: 131-139
- **Sensing a revolution.** *Molecular systems biology*  
Steinmetz, L. M., Jones, A.  
2016; 12 (4): 867
- **SYGNALing a Red Light for Glioblastoma.** *Cell systems*  
Brooks, A. N., Mueller, W. F., Steinmetz, L. M.  
2016; 3 (2): 118-20
- **Quantitative CRISPR interference screens in yeast identify chemical-genetic interactions and new rules for guide RNA design.** *Genome biology*  
Smith, J. D., Suresh, S., Schlecht, U., Wu, M., Wagih, O., Peltz, G., Davis, R. W., Steinmetz, L. M., Parts, L., St Onge, R. P.  
2016; 17 (1): 45-?
- **Genome-Wide Identification of Alternative Polyadenylation Events Using 3'T-Fill.** *Methods in molecular biology (Clifton, N.J.)*  
Wilkening, S., Pelechano, V., Steinmetz, L. M.  
2016; 1358: 295-302
- **Loss of the Yeast SR Protein Npl3 Alters Gene Expression Due to Transcription Readthrough** *PLOS GENETICS*  
Holmes, R. K., Tuck, A. C., Zhu, C., Dunn-Davies, H. R., Kudla, G., Clauder-Munster, S., Granneman, S., Steinmetz, L. M., Guthrie, C., Tollervey, D.  
2015; 11 (12)
- **Chromatin Dynamics and the RNA Exosome Function in Concert to Regulate Transcriptional Homeostasis** *CELL REPORTS*  
Rege, M., Subramanian, V., Zhu, C., Hsieh, T. S., Weiner, A., Friedman, N., Clauder-Muenster, S., Steinmetz, L. M., Rando, O. J., Boyer, L. A., Peterson, C. L.  
2015; 13 (8): 1610-1622
- **Inflammation-Induced Emergency Megakaryopoiesis Driven by Hematopoietic Stem Cell-like Megakaryocyte Progenitors** *CELL STEM CELL*  
Haas, S., Hansson, J., Klimmeck, D., Loeffler, D., Velten, L., Uckelmann, H., Wurzer, S., Prendergast, A. M., Schnell, A., Hexel, K., Santarella-Mellwig, R., Blaszkiewicz, S., Kuck, et al  
2015; 17 (4): 422-434
- **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

- **Multitarget, quantitative nanoplasmonic electrical field-enhanced resonating device (NE2RD) for diagnostics.** *Proceedings of the National Academy of Sciences of the United States of America*  
Inci, F., Filippini, C., Baday, M., Ozen, M. O., Calamak, S., Durmus, N. G., Wang, S., Hanhauser, E., Hobbs, K. S., Juillard, F., Kuang, P. P., Vetter, M. L., Carocci, et al  
2015; 112 (32): E4354-63
- **Multitarget, quantitative nanoplasmonic electrical field-enhanced resonating device ((NERD)-R-2) for diagnostics** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Inci, F., Filippini, C., Baday, M., Ozen, M. O., Calamak, S., Durmus, N. G., Wang, S., Hanhauser, E., Hobbs, K. S., Juillard, F., Kuang, P. P., Vetter, M. L., Carocci, et al  
2015; 112 (32): E4354-E4363
- **Magnetic levitation of single cells.** *Proceedings of the National Academy of Sciences of the United States of America*  
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