Lars Steinmetz

Dieter Schwarz Foundation Endowed Professor

Genetics

Bio

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 2016-2022.

Associate Group Leader and Director of Life Science Alliance, EMBL 2023-present.

Professor of Genetics, Stanford University, 2013-present.

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

Dieter Schwarz Foundation Endowed Professor, Stanford University, 2023-present.

Chair, Department of Genetics, Stanford University, 2024-present

ACADEMIC APPOINTMENTS

- Professor, Genetics
- Member, Bio-X
- Member, Cardiovascular Institute
- Faculty Affiliate, Institute for Human-Centered Artificial Intelligence (HAI)
- Member, Wu Tsai Human Performance Alliance
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Chair, Department of Genetics, (2024- present)
- Co-Director, Stanford Genome Technology Center, (2013- present)
- Director of Life Science Alliance, a Stanford-EMBL collaboration, Stanford and EMBL, (2015- present)

- Director of Graduate Admissions, Department of Genetics, Stanford University, (2013- present)

HONORS AND AWARDS

- Dieter Schwarz Foundation Endowed Professorship, Stanford University (2023)
- 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 - 2023)
- EMBO Member, European Molecular Biology Organization (2013 - present)
- Scientific Advisory Board Member, Saccharomyces Genome Database (SGD, www.yeastgenome.org) (2013 - 2018)
- Associate Editor, G3: Genes | Genomes | Genetics (2011 - present)
- President, Scientific Advisory Board, Sophia Genetics (2011 - 2019)

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

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Current Research:

While technological advances have enabled the association of thousands of genetic variants to complex traits of health and disease, we lack a comprehensive understanding of how genetic variation governs phenotypic diversity and disease. This is largely due to the challenge of discovering the mechanisms through which genetic variation shape cellular phenotypes, as well as the complex interplay between variants and the impact of environmental factors. Our research is directed at developing genomics technologies and approaches to study the molecular processes that underlie complex genetic traits, gene regulation, and inherited diseases. Our approach has been to drive technology development together with biological application, in which we work across the broad axis of fundamental to translational research.

Our research is multi-faceted, including experimental and computational approaches:

Precision Health: We work with model organisms, ranging from induced pluripotent stem cells to mice and humans, to study genetic and cellular mechanisms in diseases and to assess potential treatments. We apply genome analysis and CRISPR editing to study human diseases, like dilated cardiomyopathy, immune disorders and mitochondria-related diseases. We are also developing biosensors for early diagnosis and intervention. The Steinmetz Cardiomyopathy Fund has been established to support this research.

Genome Regulation: We characterize and quantify transcriptome architecture using single-cell omics technologies. In particular, we are mapping enhancers to target genes in human cells using technologies developed in our lab. We are also interested in the function and regulation of splicing, non-coding RNAs, antisense transcription, and transcriptional heterogeneity.

Synthetic Biology: We are exploring the frontiers of DNA synthesis and synthetic biology. Using synthetic mitochondria or the first eukaryotic synthetic genome (Sc2.0), this work aims to enhance our understanding of genome architecture and transcriptional mechanisms, and to explore the potential of genome re-engineering.

Quantitative Genetics: We use functional genomics to study how genetics and environment interact and influence complex, polygenic traits. Our methods include genome-wide CRISPR editing screens and high-throughput analysis, aiding in understanding genetic diversity and developing predictive models linking genotype to phenotype. This also helps in identifying key genes for influencing phenotypic traits.

Genomics Technologies: As the basis for all our research, we are passionate about developing genomic technologies which increase the scale of biological questions that we can tackle. We’ve led innovations in therapeutic CRISPR genome editing, image-enabled cell sorting-based genetic screening, and single-cell multi-omics analyses, making them more efficient and suitable for complex eukaryotic genomes.

Future Goals
Our ultimate goal is to transform biomedical research to cure and prevent inherited diseases. We are dedicated to constant innovation in genomic technologies, which will help us achieve our goals more effectively. Our future plans include developing more precise genome editing tools, expanding functional genomics assays, mastering genome creation, and understanding disease causes. We aim for our work to have far-reaching implications, from advancing precision medicine to understanding the adaptability of natural populations to environmental changes.

Teaching

COURSES

2024-25

- The Emergence of Digital Biology and Precision Health: BIO 109A (Aut)

2022-23

- Biology and Applications of CRISPR/Cas9: Genome Editing and Epigenome Modifications: BIOS 268, GENE 268 (Spr)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Kristle Garcia, Lorenzo Magni

Postdoctoral Faculty Sponsor

Chris Mathy, Marta Seczynska, Simon Sretenovic, Han Sun, Jielin Yan

Doctoral Dissertation Advisor (AC)

Julia Bauman, Jon Bezney

Doctoral Dissertation Co-Advisor (AC)

Bianca Edozie

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Genetics (Phd Program)

Publications

PUBLICATIONS

- **A scalable and cGMP-compatible autologous organotypic cell therapy for Dystrophic Epidermolysis Bullosa.** *Nature communications*
  Neumayer, G., Torkelson, J. L., Li, S., McCarthy, K., Zhen, H. H., Vangipuram, M., Mader, M. M., Gebeyehu, G., Jaouni, T. M., Jacków-Malinowska, J., Rami, A., Hansen, C., Guo, et al
  2024; 15 (1): 5834
- **Genome-scale analysis of interactions between genetic perturbations and natural variation.** *Nature communications*
  Hale, J. J., Matsui, T., Goldstein, I., Mullis, M. N., Roy, K. R., Ville, C. N., Miller, D., Wang, C., Reynolds, T., Steinmetz, L. M., Levy, S. F., Ehrenreich, I. M.
  2024; 15 (1): 4234
- **Size-exclusion chromatography combined with DIA-MS enables deep proteome profiling of extracellular vesicles from melanoma plasma and serum.** *Cellular and molecular life sciences : CMLS*
  Lattmann, E., Rass, L., Tognetti, M., Gomez, J. M., Lapaire, V., Bruderer, R., Reiter, L., Feng, Y., Steinmetz, L. M., Levesque, M. P.
  2024; 81 (1): 90
- **Dissecting quantitative trait nucleotides by saturation genome editing.** *bioRxiv : the preprint server for biology*
  Roy, K. R., Smith, J. D., Li, S., Vonesch, S. C., Nguyen, M., Burnett, W. T., Orsley, K. M., Lee, C. S., Haber, J. E., St Onge, R. P., Steinmetz, L. M.
  2024
- **Genome-scale analysis of interactions between genetic perturbations and natural variation.** *bioRxiv : the preprint server for biology*
  Hale, J. J., Matsui, T., Goldstein, I., Mullis, M. N., Roy, K. R., Ville, C. N., Miller, D., Wang, C., Reynolds, T., Steinmetz, L. M., Levy, S. F., Ehrenreich, I. M.
  2024
- **Uterine injury during diestrus leads to placental and embryonic defects in future pregnancies in mice.** *Biology of reproduction*
  Zhang, E. T., Wells, K. L., Bergman, A. J., Ryan, E. E., Steinmetz, L. M., Baker, J. C.
  2024
- **An encyclopedia of enhancer-gene regulatory interactions in the human genome.** *bioRxiv : the preprint server for biology*
  Gschwind, A. R., Mualim, K. S., Karbalayghareh, A., Sheth, M. U., Dey, K. K., Jagoda, E., Nurtdinov, R. N., Xi, W., Tan, A. S., Jones, H., Ma, X. R., Yao, D., Nasser, et al
  2023
- **Consequences of a telomerase-related fitness defect and chromosome substitution technology in yeast synIX strains.** *Cell genomics*
  McCulloch, L. H., Sambasivam, V., Hughes, A. L., Annaluru, N., Ramalingam, S., Fanfani, V., Lobzaev, E., Mitchell, L. A., Cai, J., Jiang, H., LaCava, J., Taylor, M. S., Bishai, et al
  2023; 3 (11): 100419
- **Design, construction, and functional characterization of a tRNA neochromosome in yeast.** *Cell*
  Schindler, D., Walker, R. S., Jiang, S., Brooks, A. N., Wang, Y., Muller, C. A., Cockram, C., Luo, Y., Garcia, A., Schraivogel, D., Mozziconacci, J., Pena, N., Assari, et al
  2023
- **Debugging and consolidating multiple synthetic chromosomes reveals combinatorial genetic interactions.** *Cell*
  Zhao, Y., Coelho, C., Hughes, A. L., Lazar-Stefanita, L., Yang, S., Brooks, A. N., Walker, R. S., Zhang, W., Lauer, S., Hernandez, C., Cai, J., Mitchell, L. A., Agmon, et al

2023

- **Identification and quantification of small exon-containing isoforms in long-read RNA sequencing data.** *Nucleic acids research*
  Liu, Z., Zhu, C., Steinmetz, L. M., Wei, W.
  2023
- **Gut barrier defects, intestinal immune hyperactivation and enhanced lipid catabolism drive lethality in NGLY1-deficient Drosophila.** *Nature communications*
  Pandey, A., Galeone, A., Han, S. Y., Story, B. A., Consonni, G., Mueller, W. F., Steinmetz, L. M., Vaccari, T., Jafar-Nejad, H.
  2023; 14 (1): 5667
- **Digital assay for rapid electronic quantification of clinical pathogens using DNA nanoballs.** *Science advances*
  Tayyab, M., Barrett, D., van Riel, G., Liu, S., Reinius, B., Scharfe, C., Griffin, P., Steinmetz, L. M., Javanmard, M., Pelechano, V.
  2023; 9 (36): eadi4997
- **Pooled Genome-Scale CRISPR Screens in Single Cells.** *Annual review of genetics*
  Schraivogel, D., Steinmetz, L. M., Parts, L.
  2023
- **Large scale microfluidic CRISPR screening for increased amylase secretion in yeast.** *Lab on a chip*
  Johansson, S. A., Dulermo, T., Jann, C., Smith, J. D., Pryszlak, A., Pignede, G., Schraivogel, D., Colavizza, D., Desfougères, T., Rave, C., Farwick, A., Merten, C. A., Roy, et al
  2023
- **Mislocalization of pathogenic RBM20 variants in dilated cardiomyopathy is caused by loss-of-interaction with Transportin-3.** *Nature communications*
  Kornienko, J., Rodríguez-Martínez, M., Fenzl, K., Hinze, F., Schraivogel, D., Grosch, M., Tunaj, B., Lindenhofer, D., Schraft, L., Kueblbeck, M., Smith, E., Mao, C., Brown, et al
  2023; 14 (1): 4312
- **Striated muscle-specific base editing enables correction of mutations causing dilated cardiomyopathy.** *Nature communications*
  Grosch, M., Schraft, L., Chan, A., Kuchenhoff, L., Rapti, K., Ferreira, A., Kornienko, J., Li, S., Radke, M. H., Kramer, C., Clauder-Munster, S., Perlas, E., Backs, et al
  2023; 14 (1): 3714
- **Atlas of mRNA translation and decay for bacteria.** *Nature microbiology*
  Huch, S., Nersisyan, L., Ropat, M., Barrett, D., Wu, M., Wang, J., Valeriano, V. D., Vardazaryan, N., Huerta-Cepas, J., Wei, W., Du, J., Steinmetz, L. M., Engstrand, et al
  2023
- **A scalable, GMP-compatible, autologous organotypic cell therapy for Dystrophic Epidermolysis Bullosa.** *bioRxiv : the preprint server for biology*
  Neumayer, G., Torkelson, J. L., Li, S., McCarthy, K., Zhen, H. H., Vangipuram, M., Jackow, J., Rami, A., Hansen, C., Guo, Z., Gaddam, S., Pappalardo, A., Li, et al
  2023
- **Differential regulation of mRNA stability modulates transcriptional memory and facilitates environmental adaptation.** *Nature communications*
  Li, B., Zeis, P., Zhang, Y., Alekseenko, A., Fürst, E., Sanchez, Y. P., Lin, G., Tekkedil, M. M., Piazza, I., Steinmetz, L. M., Pelechano, V.
  2023; 14 (1): 910
- **Ehf and Fezf2 regulate late medullary thymic epithelial cell and thymic tuft cell development.** *Frontiers in immunology*
  Lammers, S., Barrera, V., Brennecke, P., Miller, C., Yoon, J., Balolong, J., Anderson, M. S., Ho Sui, S., Steinmetz, L. M., von Andrian, U. H., Rattay, K.
  2023; 14: 1277365
- **Cell sorters see things more clearly now.** *Molecular systems biology*
  Schraivogel, D., Steinmetz, L. M.
  2023: e11254
- **Cardiac splicing as a diagnostic and therapeutic target.** *Nature reviews. Cardiology*

Gotthardt, M., Badillo-Lisakowski, V., Parikh, V. N., Ashley, E., Furtado, M., Carmo-Fonseca, M., Schudy, S., Meder, B., Grosch, M., Steinmetz, L., Crocini, C., Leinwand, L.

2023

- **RBM20 mislocalisation in dilated cardiomyopathy**

  Kornienko, J., Martinez, M., Fenzl, K., Schraft, L., Clauder-Muenster, S., Grosch, M., Steinmetz, L.

  ELSEVIER SCI LTD.2022: S102

- **Deep phenotyping of two pre-clinical mouse models and a cohort of RBM20 mutation carriers reveals no sex-dependent disease severity in RBM20 cardiomyopathy.** *American journal of physiology. Heart and circulatory physiology*

  Lennermann, D. C., Pepin, M. E., Grosch, M., Konrad, L., Kemmling, E., Hartmann, J., Nolte, J. L., Clauder-Munster, S., Kayvanpour, E., Sedaghat-Hamedani, F., Haas, J., Meder, B., van den Boogaard, et al

  2022

- **Hyperactive innate immune response and altered metabolism in a Drosophila model of NGLY1 deficiency**

  Pandey, A., Han, S., Galeone, A., Storey, B. A., Consonni, G., Mueller, W. F., Steinmetz, L., Vaccari, T., Jafar-Nejad, H.

  OXFORD UNIV PRESS INC.2022: 1039

- **NIMA-related kinase 9 regulates the phosphorylation of the essential myosin light chain in the heart.** *Nature communications*

  Muller, M., Eghbalian, R., Boeckel, J., Frese, K. S., Haas, J., Kayvanpour, E., Sedaghat-Hamedani, F., Lackner, M. K., Tugrul, O. F., Ruppert, T., Tappu, R., Martins Bordalo, D., Kneuer, et al

  2022; 13 (1): 6209

- **Genotype Complements the Phenotype: Identification of the Pathogenicity of an LMNA Splice Variant by Nanopore Long-Read Sequencing in a Large DCM Family.** *International journal of molecular sciences*

  Sedaghat-Hamedani, F., Rebs, S., Kayvanpour, E., Zhu, C., Amr, A., Müller, M., Haas, J., Wu, J., Steinmetz, L. M., Ehlermann, P., Streckfuss-Bömeke, K., Frey, N., Meder, et al

  2022; 23 (20)

- **A new mechanism of ATP synthase subunit 6 and 9 translation regulation by their assembly in yeast mitochondria**

  Kabala, A., Binko, K., Godard, F., Dautant, A., Baranowska, E., Skoczen, N., Gombeau, K., Bouhier, M., Becker, H., Ackerman, S., Steinmetz, L., Tribouillard-Tanvier, D., Kucharczyk, et al

  ELSEVIER.2022: 65

- **Transcription Factor GATA4 Regulates Cell Type-Specific Splicing Through Direct Interaction With RNA in Human Induced Pluripotent Stem Cell-Derived Cardiac Progenitors.** *Circulation*

  Zhu, L., Choudhary, K., Gonzalez-Teran, B., Ang, Y., Thomas, R., Stone, N. R., Liu, L., Zhou, P., Zhu, C., Ruan, H., Huang, Y., Jin, S., Pelonero, et al

  2022: CIRCULATIONAHA121057620

- **Transcriptomic diversity in human medullary thymic epithelial cells.** *Nature communications*

  Carter, J. A., Stromich, L., Peacey, M., Chapin, S. R., Velten, L., Steinmetz, L. M., Brors, B., Pinto, S., Meyer, H. V.

  2022; 13 (1): 4296

- **KIR+CD8+ T cells suppress pathogenic T cells and are active in autoimmune diseases and COVID-19.** *Science (New York, N.Y.)*

  Li, J., Zaslavsky, M., Su, Y., Guo, J., Sikora, M. J., van Unen, V., Christophersen, A., Chiou, S., Chen, L., Li, J., Ji, X., Wilhelmy, J., McSween, et al

  2022: eabi9591

- **Transcriptional neighborhoods regulate transcript isoform lengths and expression levels.** *Science (New York, N.Y.)*

  Brooks, A. N., Hughes, A. L., Clauder-Munster, S., Mitchell, L. A., Boeke, J. D., Steinmetz, L. M.

  2022; 375 (6584): 1000-1005

- **High-speed fluorescence image-enabled cell sorting.** *Science (New York, N.Y.)*

  Schraivogel, D., Kuhn, T. M., Rauscher, B., Rodríguez-Martínez, M., Paulsen, M., Owsley, K., Middlebrook, A., Tischer, C., Ramasz, B., Ordoñez-Rueda, D., Dees, M., Cuylen-Haering, S., Diebold, et al

  2022; 375 (6578): 315-320

- **Assembly-dependent translation of subunits 6 (Atp6) and 9 (Atp9) of ATP synthase in yeast mitochondria.** *Genetics*

  Kabala, A. M., Binko, K., Godard, F., Charles, C., Dautant, A., Baranowska, E., Skoczen, N., Gombeau, K., Bouhier, M., Becker, H. D., Ackerman, S. H., Steinmetz, L. M., Tribouillard-Tanvier, et al

  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

- **Evidence for hyperactivation of innate immunity in a Drosophila model of NGLY1 deficiency**

  Pandey, A., Han, S., Mueller, W. F., Story, B. A., Galeone, A., Steinmetz, L., Jafar-Nejad, H.

  OXFORD UNIV PRESS INC.2021: 1715-1716

- **High-throughput functional characterization of protein phosphorylation sites in yeast.** *Nature biotechnology*

  Vieitez, C., Busby, B. P., Ochoa, D., Mateus, A., Memon, D., Galardini, M., Yildiz, U., Trovato, M., Jawed, A., Geiger, A. G., Oborska-Oplova, M., Potel, C. M., Vonesch, et al

  2021

- **Regulation of Msh4-Msh5 association with meiotic chromosomes in budding yeast.** *Genetics*

  Nandanan, K. G., Salim, S., Pankajam, A. V., Shinohara, M., Lin, G., Chakraborty, P., Farnaz, A., Steinmetz, L. M., Shinohara, A., Nishant, K. T.

  2021; 219 (2)

- **Regulation of Msh4-Msh5 association with meiotic chromosomes in budding yeast** *GENETICS*

  Nandanan, K. G., Salim, S., Pankajam, A., Shinohara, M., Lin, G., Chakraborty, P., Farnaz, A., Steinmetz, L. M., Shinohara, A., Nishant, K. T.

  2021; 219 (2)

- **High-Throughput Nucleotide Resolution Predictions of Assay Limitations Increase the Reliability and Concordance of Clinical Tests.** *JCO clinical cancer informatics*

  Bieler, J., Pozzorini, C., Garcia, J., Tuck, A. C., Macheret, M., Willig, A., Couraud, S., Xing, X., Menu, P., Steinmetz, L. M., Payen, L., Xu, Z.

  2021; 5: 1085-1095

- **Case-control study evaluating risk factors for SARS-CoV-2 outbreak amongst healthcare personnel at a tertiary care center.** *American journal of infection control*

  Rosser, J. I., Tayyar, R., Giardina, R., Kolonoski, P., Kenski, D., Shen, P., Steinmetz, L. M., Hung, L., Xiao, W., Bains, K., Morrison, T., Madison, A., Chang, et al

  2021

- **Dysregulated ribonucleoprotein granules promote cardiomyopathy in RBM20 gene-edited pigs (vol 26, pg 1788, 2020)** *NATURE MEDICINE*

  Schneider, J. W., Oommen, S., Qureshi, M. Y., Goetsch, S. C., Pease, D. R., Sundsbak, R. S., Guo, W., Sun, M., Sun, H., Kuroyanagi, H., Webster, D. A., Coutts, A. W., Holst, et al

  2021

- **The chaperone-binding activity of the mitochondrial surface receptor Tom70 protects the cytosol against mitoprotein-induced stress.** *Cell reports*

  Backes, S., Bykov, Y. S., Flohr, T., Raschle, M., Zhou, J., Lenhard, S., Kramer, L., Muhlhaus, T., Bibi, C., Jann, C., Smith, J. D., Steinmetz, L. M., Rapaport, et al

  2021; 35 (1): 108936

- **Recommendations for accurate genotyping of SARS-CoV-2 using amplicon-based sequencing of clinical samples.** *Clinical microbiology and infection : the official publication of the European Society of Clinical Microbiology and Infectious Diseases*

  Kubik, S., Marques, A. C., Xing, X., Silvery, J., Bertelli, C., De Maio, F., Pournaras, S., Burr, T., Duffourd, Y., Siemens, H., Alloui, C., Song, L., Wenger, et al

  2021

- **Single-cell analyses reveal SARS-CoV-2 interference with intrinsic immune response in the human gut.** *Molecular systems biology*

  Triana, S., Metz-Zumaran, C., Ramirez, C., Kee, C., Doldan, P., Shahraz, M., Schraivogel, D., Gschwind, A. R., Sharma, A. K., Steinmetz, L. M., Herrmann, C., Alexandrov, T., Boulant, et al

  2021; 17 (4): e10232

- **CRISPRi screens reveal genes modulating yeast growth in lignocellulose hydrolysate.** *Biotechnology for biofuels*

  Gutmann, F., Jann, C., Pereira, F., Johansson, A., Steinmetz, L. M., Patil, K. R.

  2021; 14 (1): 41

- **Fast and inexpensive whole-genome sequencing library preparation from intact yeast cells.** *G3 (Bethesda, Md.)*

  Vonesch, S. C., Li, S., Szu Tu, C., Hennig, B. P., Dobrev, N., Steinmetz, L. M.

2021; 11 (1)

- **Identification of leukemic and pre-leukemic stem cells by clonal tracking from single-cell transcriptomics.** *Nature communications*
  Velten, L., Story, B. A., Hernandez-Malmierca, P., Raffel, S., Leonce, D. R., Milbank, J., Paulsen, M., Demir, A., Szu-Tu, C., Fromel, R., Lutz, C., Nowak, D., Jann, et al
  2021; 12 (1): 1366
- **Single-molecule, full-length transcript isoform sequencing reveals disease-associated RNA isoforms in cardiomyocytes.** *Nature communications*
  Zhu, C., Wu, J., Sun, H., Briganti, F., Meder, B., Wei, W., Steinmetz, L. M.
  2021; 12 (1): 4203
- **RBM20-Related Cardiomyopathy: Current Understanding and Future Options.** *Journal of clinical medicine*
  Koelemen, J., Gotthardt, M., Steinmetz, L. M., Meder, B.
  2021; 10 (18)
- **Single-molecule, full-length transcript isoform sequencing reveals disease-associated RNA isoforms in cardiomyocytes.** *Nature communications*
  Zhu, C., Wu, J., Sun, H., Briganti, F., Meder, B., Wei, W., Steinmetz, L. M.
  2021; 12 (1): 4203
- **A functional connection between translation elongation and protein folding at the ribosome exit tunnel in Saccharomyces cerevisiae.** *Nucleic acids research*
  Rodriguez-Galan, O., Garcia-Gomez, J. J., Rosado, I. V., Wei, W., Mendez-Godoy, A., Pillet, B., Alekseenko, A., Steinmetz, L. M., Pelechano, V., Kressler, D., de la Cruz, J.
  2020
- **Exploring the mechanisms underlying the NGLY1 loss-of-function phenotypes in Drosophila**
  Pandey, A., Han, S., Mueller, W. F., Story, B. A., Moore, T., Galeone, A., Cowan, T. M., Steinmetz, L.
  OXFORD UNIV PRESS INC.2020: 1026
- **Combined transient ablation and single cell RNA sequencing reveals the development of medullary thymic epithelial cells.** *eLife*
  Wells, K. L., Miller, C. N., Gschwind, A. R., Wei, W., Phipps, J. D., Anderson, M. S., Steinmetz, L. M.
  2020; 9
- **Rpb4 and Puf3 imprint and post-transcriptionally control the stability of a common set of mRNAs in yeast.** *RNA biology*
  Garrido-Godino, A. I., Gupta, I., Gutierrez-Santiago, F., Martinez-Padilla, A. B., Alekseenko, A., Steinmetz, L. M., Perez-Ortin, J. E., Pelechano, V., Navarro, F.
  2020
- **MULTI-LAYERED SINGLE-CELL TRANSCRIPTIONAL PROFILING OF ALL BONE AND BONE MARROW POPULATIONS PROVIDES A SYSTEMS VIEW OF THE MESENCHYMALAND HEMATOPOIETIC STEM CELL NICHE**
  Haas, S., Velten, L., Al-Sabah, J., Baccin, C., Steinmetz, L., Trumpp, A.
  ELSEVIER SCIENCE INC.2018: S47-S48
- **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
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