Stanford

Howard Y. Chang, MD, PhD

Virginia and D. K. Ludwig Professor of Cancer Research, Professor of Genetics and, by courtesy, of Pathology

Dermatology

Curriculum Vitae available Online

CLINICAL OFFICE (PRIMARY)

- **Stanford Dermatology Clinic**

  450 Broadway St

  Pavilion B MC 5338

  Redwood City, CA 94063

  Tel (650) 723-6316 **Fax** (650) 721-3476

ACADEMIC CONTACT INFORMATION

- **Alternate Contact**

  Maxim Litvinov - Administrative Associate

  Email mlitv@stanford.edu

  Tel 650-723-4059

Bio

BIO

I am a physician-scientist who has trained in genome science. My research has focused on mechanisms that coordinate the activities of large number of genes in cell fate control. We made a series of discoveries that introduced the important and pervasive roles of long noncoding RNAs in biological regulation. My group has substantial experience in epigenetics and RNA biology, including invention of new methods for epigenomic profiling, map RNA occupancy on chromatin, and define RNA structures genome-wide. My group pioneered methods to identify key regulators of large-scale transcriptional programs; these methods have been highly fruitful for studies of development, cancer, and aging. The long term goal of my laboratory is to decipher the regulatory information in the human genome for disease diagnosis and therapy.

CLINICAL FOCUS

- Cancer > Cutaneous (Dermatologic) Oncology
- Dermatology
- General Dermatology

ACADEMIC APPOINTMENTS

- Professor, Dermatology
- Professor, Genetics
- Professor (By courtesy), Pathology
- Member, Bio-X
- Member, Wu Tsai Human Performance Alliance
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Director, NIH Center of Excellence in Genomic Science: Center for Personal Dynamic Regulome, (2014-2024)
- Member, Stanford Diabetes Research Center, (2018- present)

HONORS AND AWARDS

- Member, American Academy of Arts and Sciences (2020)
- Member, National Academy of Sciences (2020)
- Investigator, Howard Hughes Medical Institute (2018)
- NAS Award in Molecular Biology, National Academy of Science (2018)
- Member, National Academy of Medicine (2017)
- Outstanding Investigator Award, National Cancer Institute (2016)
- Paul Marks Prize for Cancer Research, Memorial Sloan Kettering Cancer Institute (2015)
- Judson Daland Prize, American Philosophical Society (2014)
- Montagna Lecture, Society for Investigative Dermatology (2012)
- Salvador E. Luria Lecture, Massachusetts Institute of Technology (2012)
- Alfred Marchionini Research Prize, Alfred Marchionini Foundation (2011)
- CE.R.I.E.S. Award, Chanel Research and Technology (2010)
- Early Career Scientist, Howard Hughes Medical Institute (2009-2015)
- Elected Member, American Society for Clinical Investigation (2009)
- Senior Scholar Award in Aging, Ellison Medical Foundation (2009)
- Vilcek Prize for Creative Promise, Vilcek Foundation (2009)
- New Faculty Award, California Institute for Regenerative Medicine (2008-2013)
- Research Scholar Award, American Cancer Society (2007-2010)
- Scholar Award, Damon Runyon Cancer Research Foundation (2006-2008)
- Clinical Scientist Career Development Award (K08), NIH (2004-2009)
- Physician-Scientist Career Development Award, Dermatology Foundation (2004)
- Young Investigator Award, American Academy of Dermatology (2003)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Editorial Board, Molecular Cell (2014 - present)

PROFESSIONAL EDUCATION

- Fellowship: Stanford University Dept of Dermatology (2004) CA
- Residency: Stanford University Dermatology Residency (2003) CA
- Internship: Santa Clara Valley Medical Center Dept of Medicine (2001) CA
- Board Certification: Dermatology, American Board of Dermatology (2004)
- Medical Education: Harvard Medical School (2000) MA
- Ph.D., MIT , Biology (1998)
- A.B., Harvard , Biochemistry (1994)

LINKS

- Chang Lab, Stanford University: http://changlab.stanford.edu

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

The same genetic blueprint gives rise to thousands of cell types that make up the human body. Intricate mechanisms govern the choice to make skin, heart, or brain cells. These different cell types must be correctly arranged in spatial patterns to make functioning tissues and organs. In many organisms with continual turnover of cells, the genome faces the additional challenge of ensuring the faithful transmission of information throughout a lifetime#over decades in the case of humans. Thus, how one genome encodes thousands of patterns in space and time is of central importance to biology and medicine. Inappropriate activation of genes can give rise to birth defects, premature aging, or cancer, among many other diseases. Restoration of proper organ function often requires restoring homeostatic gene regulation.

Long Noncoding RNAs and Positional Identity

As a practicing dermatologist, I am fascinated by what makes human skin from different parts of the body different, a fact that guides the diagnosis and treatment of many skin diseases. Why do long hairs grow on the scalp but not on our palms or soles? How do cells know where they are located in the body, and how do they remember this information?

We discovered that one class of skin cells, the fibroblasts, encode the positional identity of skin via specific markings on their chromatin, the DNA-protein complex where genes reside. Based on the chromatin configurations of specific genes, most notably the HOX genes, fibroblasts differentially activate hundreds of genes based on their the cell's location along three anatomic axes#anterior-posterior (head to tail), proximal-distal (close or far away from the trunk), and dermal-nondermal (surface or internal organ). This in effect creates a global positioning system for all cells to navigate.

These studies also revealed a surprising abundance of long intergenic long noncoding RNAs (also known as lincRNAs, a newly recognized type of genes that do not code forencode proteins) that are involved in programming chromatin states. We are particularly fascinated by HOTAIR, the first known lincRNA that can regulate the chromatin state of genes on distantly located chromosomes. We now appreciate that the genome is pervasively transcribed to give rise to thousands of lincRNAs, which are likely to play key roles in the gene regulation of diverse biological states and disease. We are interested in understanding how lincRNAs control gene activity, and in deciphering the rules that will allow the functions of thousands of lincRNAs to be predicted and studied.

Large-Scale Gene Regulatory Programs in Cancer Metastasis and Self-Renewal

In contrast to the orderly acquisition of positional identity, cancer progression is characterized by abrogation of normal positional boundaries, especially in metastasis, which is the leading cause of cancer death. We and many others have previously identified gene expression signatures (GES), composed of dozens to hundreds of genes, that distinguish indolent human cancers from those prone to metastasis; these signatures can provide improved prognostic prediction for cancer patients. Furthermore, we have developed methods to pinpoint master regulators of GES#singular control points that can toggle the activity of the entire genetic program. This allows complex gene programs observed in human cancers to be easily recapitulated in the laboratory as models for drug development. This has enabled the creation of faithful laboratory models of human cancer types, identified specific drugs that can target these cancers, and revealed the hierarchy of transcriptional programs involved in the generation of cancer stem cells#the cells that continually repopulate a tumor or its metastases.

Teaching

STANFORD ADVISEES

Med Scholar Project Advisor

Timothy Wu

Doctoral Dissertation Reader (AC)

Julisia Chau, Peter Du, Connor Duffy, Vincent Liu, Lindsey Meservey, Robin Meyers, Max Miao, Adele Xu, Xue Yang

Postdoctoral Faculty Sponsor

Sangya Agarwal, Julia Belk, Yonglu Che, Allison Daly, Yung-Hsin Huang, Matthew Jones, Sonia Nan Kim, Roman Reggiardo, Kseniia Vlasova, Guiping Wang, Bingyu Yan, Xiaowei Yan, Shu Zhang, Yanding Zhao, Yi Zhu

Doctoral Dissertation Advisor (AC)

King Hung, Christy Luong, Venkat Sankar

Doctoral Dissertation Co-Advisor (AC)

Yannick Lee-Yow, Kevin Wu

Postdoctoral Research Mentor

Yung-Hsin Huang, Jack Rose, Guiping Wang, Xiaowei Yan

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Cancer Biology (Phd Program)
- Dermatology (Fellowship Program)

Publications

PUBLICATIONS

- **Reversing the Central Dogma: RNA-guided control of DNA in epigenetics and genome editing.** *Molecular cell*
  Chang, H. Y., Qi, L. S.
  2023; 83 (3): 442-451

- **Engineered cell entry links receptor biology with single-cell genomics.** *Cell*
  Yu, B., Shi, Q., Belk, J. A., Yost, K. E., Parker, K. R., Li, R., Liu, B. B., Huang, H., Lingwood, D., Greenleaf, W. J., Davis, M. M., Satpathy, A. T., Chang, et al
  2022

- **Targeted profiling of human extrachromosomal DNA by CRISPR-CATCH.** *Nature genetics*
  Hung, K. L., Luebeck, J., Dehkordi, S. R., Colon, C. I., Li, R., Wong, I. T., Coruh, C., Dharanipragada, P., Lomeli, S. H., Weiser, N. E., Moriceau, G., Zhang, X., Bailey, et al
  2022

- **Engineering circular RNA for enhanced protein production.** *Nature biotechnology*
  Chen, R., Wang, S. K., Belk, J. A., Amaya, L., Li, Z., Cardenas, A., Abe, B. T., Chen, C., Wender, P. A., Chang, H. Y.
  2022

- **ecDNA hubs drive cooperative intermolecular oncogene expression.** *Nature*
  Hung, K. L., Yost, K. E., Xie, L., Shi, Q., Helmsauer, K., Luebeck, J., Schopflin, R., Lange, J. T., Chamorro Gonzalez, R., Weiser, N. E., Chen, C., Valieva, M. E., Wong, et al
  2021

- **B cell-specific XIST complex enforces X-inactivation and restrains atypical B cells.** *Cell*
  Yu, B., Qi, Y., Li, R., Shi, Q., Satpathy, A. T., Chang, H. Y.
  2021

- **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

- **N6-Methyladenosine Modification Controls Circular RNA Immunity.** *Molecular cell*
  Chen, Y. G., Chen, R., Ahmad, S., Verma, R., Kasturi, S. P., Amaya, L., Broughton, J. P., Kim, J., Cadena, C., Pulendran, B., Hur, S., Chang, H. Y.
  2019
- **Massively parallel single-cell chromatin landscapes of human immune cell development and intratumoral T cell exhaustion.** *Nature biotechnology*
  Satpathy, A. T., Granja, J. M., Yost, K. E., Qi, Y. n., Meschi, F. n., McDermott, G. P., Olsen, B. N., Mumbach, M. R., Pierce, S. E., Corces, M. R., Shah, P. n., Bell, J. C., Jhutty, et al
  2019; 37 (8): 925–36
- **Atlas of Subcellular RNA Localization Revealed by APEX-Seq.** *Cell*
  Fazal, F. M., Han, S. n., Parker, K. R., Kaewsapsak, P. n., Xu, J. n., Boettiger, A. N., Chang, H. Y., Ting, A. Y.
  2019
- **Clonal replacement of tumor-specific T cells following PD-1 blockade.** *Nature medicine*
  Yost, K. E., Satpathy, A. T., Wells, D. K., Qi, Y. n., Wang, C. n., Kageyama, R. n., McNamara, K. L., Granja, J. M., Sarin, K. Y., Brown, R. A., Gupta, R. K., Curtis, C. n., Bucktrout, et al
  2019
- **Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element.** *Cell*
  Cho, S. W., Xu, J., Sun, R., Mumbach, M. R., Carter, A. C., Chen, Y. G., Yost, K. E., Kim, J., He, J., Nevins, S. A., Chin, S., Caldas, C., Liu, et al
  2018; 173 (6): 1398
- **The chromatin accessibility landscape of primary human cancers.** *Science (New York, N.Y.)*
  Corces, M. R., Granja, J. M., Shams, S. n., Louie, B. H., Seoane, J. A., Zhou, W. n., Silva, T. C., Groeneveld, C. n., Wong, C. K., Cho, S. W., Satpathy, A. T., Mumbach, M. R., Hoadley, et al
  2018; 362 (6413)
- **Machine learning modeling of RNA structures: methods, challenges and future perspectives.** *Briefings in bioinformatics*
  Wu, K. E., Zou, J. Y., Chang, H.
  2023
- **Circular RNA vaccine induces potent T cell responses.** *Proceedings of the National Academy of Sciences of the United States of America*
  Amaya, L., Grigoryan, L., Li, Z., Lee, A., Wender, P. A., Pulendran, B., Chang, H. Y.
  2023; 120 (20): e2302191120
- **Parallel sequencing of extrachromosomal circular DNAs and transcriptomes in single cancer cells.** *Nature genetics*
  Chamorro González, R., Conrad, T., Stöber, M. C., Xu, R., Giurgiu, M., Rodriguez-Fos, E., Kasack, K., Brückner, L., van Leen, E., Helmsauer, K., Dorado Garcia, H., Stefanova, M. E., Hung, et al
  2023
- **The AAV capsid can influence the epigenetic marking of rAAV delivered episomal genomes in a species dependent manner.** *Nature communications*
  Gonzalez-Sandoval, A., Pekrun, K., Tsuji, S., Zhang, F., Hung, K. L., Chang, H. Y., Kay, M. A.
  2023; 14 (1): 2448
- **Extrachromosomal DNA in the cancerous transformation of Barrett's oesophagus.** *Nature*
  Luebeck, J., Ng, A. W., Galipeau, P. C., Li, X., Sanchez, C. A., Katz-Summercorn, A. C., Kim, H., Jammula, S., He, Y., Lippman, S. M., Verhaak, R. G., Maley, C. C., Alexandrov, et al
  2023
- **A guide to naming eukaryotic circular RNAs.** *Nature cell biology*
  Chen, L., Bindereif, A., Bozzoni, I., Chang, H. Y., Matera, A. G., Gorospe, M., Hansen, T. B., Kjems, J., Ma, X., Pek, J. W., Rajewsky, N., Salzman, J., Wilusz, et al
  2023
- **Long non-coding RNAs: definitions, functions, challenges and recommendations.** *Nature reviews. Molecular cell biology*
  Mattick, J. S., Amaral, P. P., Carninci, P., Carpenter, S., Chang, H. Y., Chen, L., Chen, R., Dean, C., Dinger, M. E., Fitzgerald, K. A., Gingeras, T. R., Guttman, M., Hirose, et al
  2023
- **Inducible lncRNA transgenic mice reveal continual role of HOTAIR in promoting breast cancer metastasis.** *eLife*
  Ma, Q., Yang, L., Tolentino, K., Wang, G., Zhao, Y., Litzenburger, U. M., Shi, Q., Zhu, L., Yang, C., Jiao, H., Zhang, F., Li, R., Tsai, et al

2022; 11

- **The autism risk factor CHD8 is a chromatin activator in human neurons and functionally dependent on the ERK-MAPK pathway effector ELK1.** *Scientific reports*
  Haddad Derafshi, B., Danko, T., Chanda, S., Batista, P. J., Litzenburger, U., Lee, Q. Y., Ng, Y. H., Sebin, A., Chang, H. Y., Sudhof, T. C., Wernig, M.
  2022; 12 (1): 22425
- **Macrophage inflammatory and regenerative response periodicity is programmed by cell cycle and chromatin state.** *Molecular cell*
  Daniel, B., Belk, J. A., Meier, S. L., Chen, A. Y., Sandor, K., Czimmerer, Z., Varga, Z., Bene, K., Buquicchio, F. A., Qi, Y., Kitano, H., Wheeler, J. R., Foster, et al
  2022
- **Reading and writing extrachromosomal DNA.**
  Chang, H. Y.
  AMER ASSOC CANCER RESEARCH.2022
- **Enhanced T cell effector activity by targeting the Mediator kinase module.** *Science (New York, N.Y.)*
  Freitas, K. A., Belk, J. A., Sotillo, E., Quinn, P. J., Ramello, M. C., Malipatlolla, M., Daniel, B., Sandor, K., Klysz, D., Bjelajac, J., Xu, P., Burdsall, K. A., Tieu, et al
  2022; 378 (6620): eabn5647
- **Profiling oncogenic extra-chromosomal DNA in cancer** *NATURE GENETICS*
  Hung, K. L., Chang, H. Y.
  2022: 1591-1592
- **Divergent clonal differentiation trajectories of T cell exhaustion.** *Nature immunology*
  Daniel, B., Yost, K. E., Hsiung, S., Sandor, K., Xia, Y., Qi, Y., Hiam-Galvez, K. J., Black, M., J Raposo, C., Shi, Q., Meier, S. L., Belk, J. A., Giles, et al
  2022
- **Multiomic analysis reveals conservation of cancer-associated fibroblast phenotypes across species and tissue of origin.** *Cancer cell*
  Foster, D. S., Januszyk, M., Delitto, D., Yost, K. E., Griffin, M., Guo, J., Guardino, N., Delitto, A. E., Chinta, M., Burcham, A. R., Nguyen, A. T., Bauer-Rowe, K. E., Titan, et al
  2022
- **The evolutionary dynamics of extrachromosomal DNA in human cancers.** *Nature genetics*
  Lange, J. T., Rose, J. C., Chen, C. Y., Pichugin, Y., Xie, L., Tang, J., Hung, K. L., Yost, K. E., Shi, Q., Erb, M. L., Rajkumar, U., Wu, S., Taschner-Mandl, et al
  2022
- **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
- **Single-cell multiome of the human retina and deep learning nominate causal variants in complex eye diseases.** *Cell genomics*
  Wang, S. K., Nair, S., Li, R., Kraft, K., Pampari, A., Patel, A., Kang, J. B., Luong, C., Kundaje, A., Chang, H. Y.
  2022; 2 (8)
- **Gene regulation on extrachromosomal DNA.** *Nature structural & molecular biology*
  Hung, K. L., Mischel, P. S., Chang, H. Y.
  2022
- **Enhanced effector activity of mediator CDK8 kinase module deficient CAR-T Cells**
  Freitas, K. A., Belk, J. A., Sotillo, E., Daniel, B., Sandor, K., Klysz, D., Duong, V. T., Xu, P., Malipatlolla, M., Weber, E. W., Majzner, R. G., Chang, H. Y., Satpathy, et al
  AMER ASSOC CANCER RESEARCH.2022
- **RNA-binding proteins direct myogenic cell fate decisions.** *eLife*
  Wheeler, J. R., Whitney, O. N., Vogler, T. O., Nguyen, E. D., Pawlikowski, B., Lester, E., Cutler, A., Elston, T., Dalla Betta, N., Parker, K. R., Yost, K. E., Vogel, H., Rando, et al
  2022; 11
- **Polycomb-mediated genome architecture enables long-range spreading of H3K27 methylation.** *Proceedings of the National Academy of Sciences of the United States of America*

Kraft, K., Yost, K. E., Murphy, S. E., Magg, A., Long, Y., Corces, M. R., Granja, J. M., Wittler, L., Mundlos, S., Cech, T. R., Boettiger, A. N., Chang, H. Y.
2022; 119 (22): e2201883119

- **A genetic bottleneck of mitochondrial DNA during human lymphocyte development.** *Molecular biology and evolution*
  Tang, Z., Lu, Z., Chen, B., Zhang, W., Chang, H. Y., Hu, Z., Xu, J.
  2022

- **The Mettl3 epitranscriptomic writer amplifies p53 stress responses.** *Molecular cell*
  Raj, N., Wang, M., Seoane, J. A., Zhao, R. L., Kaiser, A. M., Moonie, N. A., Demeter, J., Boutelle, A. M., Kerr, C. H., Mulligan, A. S., Moffatt, C., Zeng, S. X., Lu, et al
  2022

- **Enhanced safety and efficacy of protease-regulated CAR-T cell receptors.** *Cell*
  Labanieh, L., Majzner, R. G., Klysz, D., Sotillo, E., Fisher, C. J., Vilches-Moure, J. G., Pacheco, K. Z., Malipatlolla, M., Xu, P., Hui, J. H., Murty, T., Theruvath, J., Mehta, et al
  2022

- **BRD2 compartmentalizes the accessible genome.** *Nature genetics*
  Xie, L., Dong, P., Qi, Y., Hsieh, T. S., English, B. P., Jung, S., Chen, X., De Marzio, M., Casellas, R., Chang, H. Y., Zhang, B., Tjian, R., Liu, et al
  2022

- **Oncogene Convergence in Extrachromosomal DNA Hubs.** *Cancer discovery*
  Weiser, N. E., Hung, K. L., Chang, H. Y.
  2022: OF1-OF4

- **Circular RNA migration in agarose gel electrophoresis.** *Molecular cell*
  Abe, B. T., Wesselhoeft, R. A., Chen, R., Anderson, D. G., Chang, H. Y.
  2022

- **Epigenomic priming of immune genes implicates oligodendroglia in multiple sclerosis susceptibility.** *Neuron*
  Meijer, M., Agirre, E., Kabbe, M., van Tuijn, C. A., Heskol, A., Zheng, C., Mendanha Falcao, A., Bartosovic, M., Kirby, L., Calini, D., Johnson, M. R., Corces, M. R., Montine, et al
  1800

- **GPC2-CAR T cells tuned for low antigen density mediate potent activity against neuroblastoma without toxicity** *CANCER CELL*
  Heitzeneder, S., Bosse, K. R., Zhu, Z., Zhelev, D., Majzner, R. G., Radosevich, M. T., Dhingra, S., Sotillo, E., Buongervino, S., Pascual-Pasto, G., Garrigan, E., Xu, P., Huang, et al
  2022; 40 (1): 53-+

- **Identification of Protein-RNA Interactions in Mouse Testis Tissue Using fRIP.** *Bio-protocol*
  Bailey, A. S., Batista, P. J., Chang, H. Y., Fuller, M. T.
  2022; 12 (1): e4286

- **Identification of Protein-RNA Interactions in Mouse Testis Tissue Using fRIP** *BIO-PROTOCOL*
  Bailey, A., Batista, P., Chang, H., Fuller, M.
  2022; 12 (01)

- **GPC2-CAR Tcells tuned for low antigen density mediate potent activity against neuroblastoma without toxicity.** *Cancer cell*
  Heitzeneder, S., Bosse, K. R., Zhu, Z., Zhelev, D., Majzner, R. G., Radosevich, M. T., Dhingra, S., Sotillo, E., Buongervino, S., Pascual-Pasto, G., Garrigan, E., Xu, P., Huang, et al
  1800

- **Toward a better understanding of T cells in cancer** *CANCER CELL*
  Oh, D. Y., Fong, L., Newell, E. W., Turk, M., Chi, H., Chang, H. Y., Satpathy, A. T., Fairfax, B., Silva-Santos, B., Lantz, O.
  2021; 39 (12): 1549-1552

- **PEPATAC: an optimized pipeline for ATAC-seq data analysis with serial alignments.** *NAR genomics and bioinformatics*
  Smith, J. P., Corces, M. R., Xu, J., Reuter, V. P., Chang, H. Y., Sheffield, N. C.
  2021; 3 (4): lqab101

- **Extrachromosomal DNA: An Emerging Hallmark in Human Cancer.** *Annual review of pathology*
  Wu, S., Bafna, V., Chang, H. Y., Mischel, P. S.
  2021

- **Cancer-Associated Fibroblasts Share Highly Conserved Phenotypes and Functions Across Tumor Types and Species**
  Foster, D. S., Januszyk, M., Yost, K. E., Chinta, M., Titan, A. L., Wapnir, I. L., Gurtner, G. C., Chang, H. Y., Norton, J. A., Longaker, M. T.
  ELSEVIER SCIENCE INC.2021: S243-S244

- **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

- **Integrated spatial multiomics reveals fibroblast fate during tissue repair.** *Proceedings of the National Academy of Sciences of the United States of America*
  Foster, D. S., Januszyk, M., Yost, K. E., Chinta, M. S., Gulati, G. S., Nguyen, A. T., Burcham, A. R., Salhotra, A., Ransom, R. C., Henn, D., Chen, K., Mascharak, S., Tolentino, et al
  2021; 118 (41)

- **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

- **fSHAPE, fSHAPE-eCLIP, and SHAPE-eCLIP probe transcript regions that interact with specific proteins.** *STAR protocols*
  Corley, M., Flynn, R. A., Blue, S. M., Yee, B. A., Chang, H. Y., Yeo, G. W.
  2021; 2 (3): 100762

- **JUN promotes hypertrophic skin scarring via CD36 in preclinical in vitro and in vivo models.** *Science translational medicine*
  Griffin, M. F., Borrelli, M. R., Garcia, J. T., Januszyk, M., King, M., Lerbs, T., Cui, L., Moore, A. L., Shen, A. H., Mascharak, S., Diaz Deleon, N. M., Adem, S., Taylor, et al
  2021; 13 (609): eabb3312

- **LKB1 inactivation modulates chromatin accessibility to drive metastatic progression.** *Nature cell biology*
  Pierce, S. E., Granja, J. M., Corces, M. R., Brady, J. J., Tsai, M. K., Pierce, A. B., Tang, R., Chu, P., Feldser, D. M., Chang, H. Y., Bassik, M. C., Greenleaf, W. J., Winslow, et al
  2021

- **Dynamic chromatin regulatory landscape of human CAR T cell exhaustion.** *Proceedings of the National Academy of Sciences of the United States of America*
  Gennert, D. G., Lynn, R. C., Granja, J. M., Weber, E. W., Mumbach, M. R., Zhao, Y., Duren, Z., Sotillo, E., Greenleaf, W. J., Wong, W. H., Satpathy, A. T., Mackall, C. L., Chang, et al
  2021; 118 (30)

- **Personal regulome navigation of cancer.** *Nature reviews. Cancer*
  Chang, H. Y.
  2021

- **Invariant Natural Killer T Cell Subsets Have Diverse Graft-Versus-Host-Disease-Preventing and Anti-Tumor Effects.** *Blood*
  Maas-Bauer, K., Lohmeyer, J. K., Hirai, T., Lopes Ramos, T., Fazal, F. M., Litzenburger, U. M., Yost, K. E., Ribado, J. V., Kambham, N., Wenokur, A., Lin, P., Alvarez, M., Mavers, et al
  2021

- **BABEL enables cross-modality translation between multiomic profiles at single-cell resolution.** *Proceedings of the National Academy of Sciences of the United States of America*
  Wu, K. E., Yost, K. E., Chang, H. Y., Zou, J.
  2021; 118 (15)

- **Recruiting T cells in cancer immunotherapy.** *Science (New York, N.Y.)*
  Yost, K. E., Chang, H. Y., Satpathy, A. T.
  2021; 372 (6538): 130–31

- **Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing.** *Cell*

Nunez, J. K., Chen, J., Pommier, G. C., Cogan, J. Z., Replogle, J. M., Adriaens, C., Ramadoss, G. N., Shi, Q., Hung, K. L., Samelson, A. J., Pogson, A. N., Kim, J. Y., Chung, et al
2021

- **Transient rest restores functionality in exhausted CAR-T cells through epigenetic remodeling.** *Science (New York, N.Y.)*
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