



Howard Y. Chang, MD, PhD

Virginia and D. K. Ludwig Professor of Cancer Genomics and of Genetics
Dermatology

 Curriculum Vitae available Online

CLINICAL OFFICES

- **Stanford Dermatology Clinic**

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ACADEMIC CONTACT INFORMATION

- **Alternate Contact**

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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
- Member, Bio-X
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute
- Faculty Fellow, Stanford ChEM-H
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Member, Stanford Diabetes Research Center, (2018- present)

- Director, NIH Center of Excellence in Genomic Science: Center for Personal Dynamic Regulome, (2014-2019)

HONORS AND AWARDS

- 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.

CLINICAL TRIALS

- A Pilot Study of Imatinib Mesylate in Steroid Refractory Chronic Graft Versus Host Disease, Not Recruiting

Teaching

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Maurice Youzong Lee

Postdoctoral Faculty Sponsor

Chun-Kan Chen, Diana Dou, Furqan Fazal, Katerina Kraft, Qing Ma, Bingfei Yu

Doctoral Dissertation Advisor (AC)

Laura Amaya, King Hung, Kevin Parker

Doctoral Dissertation Co-Advisor (AC)

Kevin Wu

Postdoctoral Research Mentor

Katerina Kraft, Jack Rose, Yuning Wei

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

Publications

PUBLICATIONS

- **Coupled Single-Cell CRISPR Screening and Epigenomic Profiling Reveals Causal Gene Regulatory Networks** *CELL*
Rubin, A. J., Parker, K. R., Satpathy, A. T., Qi, Y., Wu, B., Ong, A. J., Mumbach, M. R., Ji, A. L., Kim, D. S., Cho, S., Zarnegar, B. J., Greenleaf, W. J., Chang, et al
2019; 176 (1-2): 361-+
- **The novel lncRNA lnc-NR2F1 is pro-neurogenic and mutated in human neurodevelopmental disorders.** *eLife*
Ang, C. E., Ma, Q., Wapinski, O. L., Fan, S., Flynn, R. A., Lee, Q. Y., Coe, B., Onoguchi, M., Olmos, V. H., Do, B. T., Dukes-Rimsky, L., Xu, J., Tanabe, et al
2019; 8
- **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., Meschi, F., McDermott, G. P., Olsen, B. N., Mumbach, M. R., Pierce, S. E., Corces, M. R., Shah, P., Bell, J. C., Jhutti, et al
2019; 37 (8): 925-36
- **Atlas of Subcellular RNA Localization Revealed by APEX-Seq.** *Cell*
Fazal, F. M., Han, S., Parker, K. R., Kaewsapsak, P., Xu, J., 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., Wang, C., Kageyama, R., McNamara, K. L., Granja, J. M., Sarin, K. Y., Brown, R. A., Gupta, R. K., Curtis, C., 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
- **Transcript-indexed ATAC-seq for precision immune profiling.** *Nature medicine*
Satpathy, A. T., Saligrama, N., Buenrostro, J. D., Wei, Y., Wu, B., Rubin, A. J., Granja, J. M., Lareau, C. A., Li, R., Qi, Y., Parker, K. R., Mumbach, M. R., Serratelli, et al
2018
- **The chromatin accessibility landscape of primary human cancers.** *Science (New York, N.Y.)*
Corces, M. R., Granja, J. M., Shams, S., Louie, B. H., Seoane, J. A., Zhou, W., Silva, T. C., Groeneveld, C., Wong, C. K., Cho, S. W., Satpathy, A. T., Mumbach, M. R., Hoadley, et al

2018; 362 (6413)

- **RNA Duplex Map in Living Cells Reveals Higher-Order Transcriptome Structure** *CELL*
Lu, Z., Zhang, Q. C., Lee, B., Flynn, R. A., Smith, M. A., Robinson, J. T., Davidovich, C., Gooding, A. R., Goodrich, K. J., Mattick, J. S., Mesirov, J. P., Cech, T. R., Chang, et al
2016; 165 (5): 1267-1279
- **Long Noncoding RNAs in Cancer Pathways.** *Cancer cell*
Schmitt, A. M., Chang, H. Y.
2016; 29 (4): 452-463
- **HiChIRP reveals RNA-associated chromosome conformation.** *Nature methods*
Mumbach, M. R., Granja, J. M., Flynn, R. A., Roake, C. M., Satpathy, A. T., Rubin, A. J., Qi, Y., Jiang, Z., Shams, S., Louie, B. H., Guo, J. K., Gennert, D. G., Corces, et al
2019
- **Single-cell lineage tracing by endogenous mutations enriched in transposase accessible mitochondrial DNA** *ELIFE*
Xu, J., Nuno, K., Litzenburger, U. M., Qi, Y., Corces, M., Majeti, R., Chang, H. Y.
2019; 8
- **Single-cell lineage tracing by endogenous mutations enriched in transposase accessible mitochondrial DNA.** *eLife*
Xu, J., Nuno, K., Litzenburger, U. M., Qi, Y., Corces, M. R., Majeti, R., Chang, H. Y.
2019; 8
- **RNA structure maps across mammalian cellular compartments** *NATURE STRUCTURAL & MOLECULAR BIOLOGY*
Sun, L., Fazal, F. M., Li, P., Broughton, J. P., Lee, B., Tang, L., Huang, W., Kool, E. T., Chang, H. Y., Zhang, Q.
2019; 26 (4): 322-+
- **RNA structure maps across mammalian cellular compartments.** *Nature structural & molecular biology*
Sun, L., Fazal, F. M., Li, P., Broughton, J. P., Lee, B., Tang, L., Huang, W., Kool, E. T., Chang, H. Y., Zhang, Q. C.
2019
- **Enhancer Connectome Nominates Target Genes of Inherited Risk Variants from Inflammatory Skin Disorders** *JOURNAL OF INVESTIGATIVE DERMATOLOGY*
Jeng, M. Y., Mumbach, M. R., Granja, J. M., Satpathy, A. T., Chang, H. Y., Chang, A. S.
2019; 139 (3): 605-14
- **A Mutation in the Transcription Factor Foxp3 Drives T Helper 2 Effector Function in Regulatory T Cells** *IMMUNITY*
Van Gool, F., Nguyen, M. T., Mumbach, M. R., Satpathy, A. T., Rosenthal, W. L., Giacometti, S., Le, D. T., Liu, W., Brusko, T. M., Anderson, M. S., Rudensky, A. Y., Marson, A., Chang, et al
2019; 50 (2): 362-+
- **TFAP2C-and p63-Dependent Networks Sequentially Rearrange Chromatin Landscapes to Drive Human Epidermal Lineage Commitment** *CELL STEM CELL*
Li, L., Wang, Y., Torkelson, J. L., Shankar, G., Pattison, J. M., Zhen, H. H., Fang, F., Duren, Z., Xin, J., Gaddam, S., Melo, S. P., Piekos, S. N., Li, et al
2019; 24 (2): 271-+
- **Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons** *ELIFE*
Luo, C., Lee, Q., Wapinski, O., Castanon, R., Nery, J. R., Malin, M., Kareta, M. S., Cullen, S. M., Goodell, M. A., Chang, H. Y., Wernig, M., Ecker, J. R.
2019; 8
- **TFAP2C- and p63-Dependent Networks Sequentially Rearrange Chromatin Landscapes to Drive Human Epidermal Lineage Commitment.** *Cell stem cell*
Li, L., Wang, Y., Torkelson, J. L., Shankar, G., Pattison, J. M., Zhen, H. H., Fang, F., Duren, Z., Xin, J., Gaddam, S., Melo, S. P., Piekos, S. N., Li, et al
2019
- **The novel lncRNA Inc-NR2F1 is proneurogenic and mutated in human neurodevelopmental disorders** *ELIFE*
Ang, C., Ma, Q., Wapinski, O. L., Fan, S., Flynn, R. A., Lee, Q., Coe, B., Onoguchi, M., Olmos, V., Do, B. T., Dukes-Rimsky, L., Xu, J., Tanabe, et al
2019; 8
- **Activation of PDGF pathway links LMNA mutation to dilated cardiomyopathy.** *Nature*
Lee, J., Termglinchan, V., Diecke, S., Itzhaki, I., Lam, C. K., Garg, P., Lau, E., Greenhaw, M., Seeger, T., Wu, H., Zhang, J. Z., Chen, X., Gil, et al

2019

- **A Mutation in the Transcription Factor Foxp3 Drives T Helper 2 Effector Function in Regulatory T Cells.** *Immunity*
Van Gool, F., Nguyen, M. L., Mumbach, M. R., Satpathy, A. T., Rosenthal, W. L., Giacometti, S., Le, D. T., Liu, W., Brusko, T. M., Anderson, M. S., Rudensky, A. Y., Marson, A., Chang, et al
2019
- **Satb1 integrates DNA binding site geometry and torsional stress to differentially target nucleosome-dense regions.** *Nature communications*
Ghosh, R. P., Shi, Q., Yang, L., Reddick, M. P., Nikitina, T., Zhurkin, V. B., Fordyce, P., Stasevich, T. J., Chang, H. Y., Greenleaf, W. J., Liphardt, J. T.
2019; 10 (1): 3221
- **Retinoic acid and BMP4 cooperate with p63 to alter chromatin dynamics during surface epithelial commitment** *NATURE GENETICS*
Pattison, J. M., Melo, S. P., Piekos, S. N., Torkelson, J. L., Bashkirova, E., Mumbach, M. R., Rajasingh, C., Zhen, H., Li, L., Liaw, E., Alber, D., Rubin, A. J., Shankar, et al
2018; 50 (12): 1658-+
- **The RNA Base-Pairing Problem and Base-Pairing Solutions** *COLD SPRING HARBOR PERSPECTIVES IN BIOLOGY*
Lu, Z., Chang, H. Y.
2018; 10 (12)
- **Mechanoresponsive stem cells acquire neural crest fate in jaw regeneration** *NATURE*
Ransom, R. C., Carter, A. C., Salhotra, A., Leavitt, T., Marecic, O., Murphy, M. P., Lopez, M. L., Wei, Y., Marshall, C. D., Shen, E. Z., Jones, R., Sharir, A., Klein, et al
2018; 563 (7732): 514-+
- **Retinoic acid and BMP4 cooperate with p63 to alter chromatin dynamics during surface epithelial commitment.** *Nature genetics*
Pattison, J. M., Melo, S. P., Piekos, S. N., Torkelson, J. L., Bashkirova, E., Mumbach, M. R., Rajasingh, C., Zhen, H. H., Li, L., Liaw, E., Alber, D., Rubin, A. J., Shankar, et al
2018
- **Joint single-cell DNA accessibility and protein epitope profiling reveals environmental regulation of epigenomic heterogeneity** *NATURE COMMUNICATIONS*
Chen, X., Litzenburger, U. M., Wei, Y., Schep, A. N., LaGory, E. L., Choudhry, H., Giaccia, A. J., Greenleaf, W. J., Chang, H. Y.
2018; 9
- **Joint single-cell DNA accessibility and protein epitope profiling reveals environmental regulation of epigenomic heterogeneity.** *Nature communications*
Chen, X., Litzenburger, U. M., Wei, Y., Schep, A. N., LaGory, E. L., Choudhry, H., Giaccia, A. J., Greenleaf, W. J., Chang, H. Y.
2018; 9 (1): 4590
- **Mechanoresponsive stem cells acquire neural crest fate in jaw regeneration.** *Nature*
Ransom, R. C., Carter, A. C., Salhotra, A., Leavitt, T., Marecic, O., Murphy, M. P., Lopez, M. L., Wei, Y., Marshall, C. D., Shen, E. Z., Jones, R. E., Sharir, A., Klein, et al
2018
- **Enhancer connectome nominates target genes of inherited risk variants from inflammatory skin disorders.** *The Journal of investigative dermatology*
Jeng, M. Y., Mumbach, M. R., Granja, J. M., Satpathy, A. T., Chang, H. Y., Chang, A. L.
2018
- **A Chromatin Basis for Cell Lineage and Disease Risk in the Human Pancreas** *CELL SYSTEMS*
Arda, H., Tsai, J., Rosli, Y. R., Giresi, P., Bottino, R., Greenleaf, W. J., Chang, H. Y., Kim, S. K.
2018; 7 (3): 310-+
- **Identification of the Human Skeletal Stem Cell** *CELL*
Chan, C. F., Gulati, G. S., Sinha, R., Tompkins, J., Lopez, M., Carter, A. C., Ransom, R. C., Reinisch, A., Wearda, T., Murphy, M., Brewer, R. E., Koepke, L. S., Marecic, et al
2018; 175 (1): 43-+
- **Identification of the Human Skeletal Stem Cell.** *Cell*
Chan, C. K., Gulati, G. S., Sinha, R., Tompkins, J. V., Lopez, M., Carter, A. C., Ransom, R. C., Reinisch, A., Wearda, T., Murphy, M., Brewer, R. E., Koepke, L. S., Marecic, et al
2018; 175 (1): 43

- **Expression of the transcription factor ZBTB46 distinguishes human histiocytic disorders of classical dendritic cell origin** *MODERN PATHOLOGY*
Satpathy, A. T., Brown, R. A., Gomulia, E., Briseno, C. G., Mumbach, M. R., Pan, Z., Murphy, K. M., Natkunam, Y., Chang, H. Y., Kim, J.
2018; 31 (9): 1479–86
- **A Chromatin Basis for Cell Lineage and Disease Risk in the Human Pancreas.** *Cell systems*
Arda, H. E., Tsai, J., Rosli, Y. R., Giresi, P., Bottino, R., Greenleaf, W. J., Chang, H. Y., Kim, S. K.
2018
- **Genetic determinants of co-accessible chromatin regions in activated T cells across humans** *NATURE GENETICS*
Gate, R. E., Cheng, C. S., Aiden, A. P., Siba, A., Tabaka, M., Lituiev, D., Machol, I., Gordon, M., Subramaniam, M., Shamim, M., Hougen, K. L., Wortman, I., Huang, et al
2018; 50 (8): 1140+
- **Discovery of stimulation-responsive immune enhancers with CRISPR activation (vol 549, pg 111, 2017)** *NATURE*
Simeonov, D. R., Gowen, B. G., Boontanart, M., Roth, T. L., Gagnon, J. D., Mumbach, M. R., Satpathy, A. T., Lee, Y., Bray, N. L., Chan, A. Y., Lituiev, D. S., Nguyen, M. L., Gate, et al
2018; 559 (7715): E13
- **Integrative analysis of single-cell genomics data by coupled nonnegative matrix factorizations** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Duren, Z., Chen, X., Zamanighomi, M., Zeng, W., Satpathy, A. T., Chang, H. Y., Wang, Y., Wong, W.
2018; 115 (30): 7723–28
- **Integrative analysis of single-cell genomics data by coupled nonnegative matrix factorizations.** *Proceedings of the National Academy of Sciences of the United States of America*
Duren, Z., Chen, X., Zamanighomi, M., Zeng, W., Satpathy, A. T., Chang, H. Y., Wang, Y., Wong, W. H.
2018
- **An Activity Switch in Human Telomerase Based on RNA Conformation and Shaped by TCAB1** *CELL*
Chen, L., Roake, C. M., Freund, A., Batista, P. J., Tian, S., Yin, Y. A., Gajera, C. R., Lin, S., Lee, B., Pech, M. F., Venteicher, A. S., Das, R., Chang, et al
2018; 174 (1): 218+
- **Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element** *CELL*
Cho, S., Xu, J., Sun, R., Mumbach, M. R., Carter, A. C., Chen, Y., Yost, K. E., Kim, J., He, J., Nevins, S. A., Chin, S., Caldas, C., Liu, et al
2018; 173 (6): 1398+
- **Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation** *CELL*
Buenrostro, J. D., Corces, M., Lareau, C. A., Wu, B., Schep, A. N., Aryee, M. J., Majeti, R., Chang, H. Y., Greenleaf, W. J.
2018; 173 (6): 1535+
- **ATAC Primer Tool for targeted analysis of accessible chromatin** *NATURE METHODS*
Yost, K. E., Carter, A. C., Xu, J., Litzgenburger, U., Chang, H. Y.
2018; 15 (5): 304–5
- **Epigenomics: Technologies and Applications.** *Circulation research*
Wang, K. C., Chang, H. Y.
2018; 122 (9): 1191–99
- **Epigenomics Technologies and Applications** *CIRCULATION RESEARCH*
Wang, K. C., Chang, H. Y.
2018; 122 (9): 1191–99
- **Tissue-selective effects of nucleolar stress and rDNA damage in developmental disorders** *NATURE*
Calo, E., Gu, B., Bowen, M. E., Aryan, F., Zalc, A., Liang, J., Flynn, R. A., Swigut, T., Chang, H. Y., Attardi, L. D., Wysocka, J.
2018; 554 (7690): 112+
- **m(6A) mRNA methylation sustains Treg suppressive functions** *CELL RESEARCH*
Tong, J., Cao, G., Zhang, T., Sefik, E., Vesely, M., Broughton, J. P., Zhu, S., Li, H., Li, B., Chen, L., Chang, H. Y., Su, B., Flavell, et al
2018; 28 (2): 253–56

- **Rapid chromatin repression by Aire provides precise control of immune tolerance** *NATURE IMMUNOLOGY*
Koh, A. S., Miller, E. L., Buenrostro, J. D., Moskowitz, D. M., Wang, J., Greenleaf, W. J., Chang, H. Y., Crabtree, G. R.
2018; 19 (2): 162-+
- **ChIRP-MS: RNA-Directed Proteomic Discovery** *X-CHROMOSOME INACTIVATION: METHODS AND PROTOCOLS*
Chu, C., Chang, H. Y., Sado, T.
2018; 1861: 37-45
- **ChIRP-MS: RNA-Directed Proteomic Discovery.** *Methods in molecular biology (Clifton, N.J.)*
Chu, C., Chang, H. Y.
2018; 1861: 37-45
- **An Activity Switch in Human Telomerase Based on RNA Conformation and Shaped by TCAB1.** *Cell*
Chen, L., Roake, C. M., Freund, A., Batista, P. J., Tian, S., Yin, Y. A., Gajera, C. R., Lin, S., Lee, B., Pech, M. F., Venteicher, A. S., Das, R., Chang, et al
2018
- **Expression of the transcription factor ZBTB46 distinguishes human histiocytic disorders of classical dendritic cell origin.** *Modern pathology : an official journal of the United States and Canadian Academy of Pathology, Inc*
Satpathy, A. T., Brown, R. A., Gomulia, E., Briseño, C. G., Mumbach, M. R., Pan, Z., Murphy, K. M., Natkunam, Y., Chang, H. Y., Kim, J.
2018
- **LncRNA Seduction of GOT2 Goes Viral** *IMMUNITY*
Chen, Y., Chang, H. Y.
2017; 47 (6): 1021-23
- **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
- **Mechanistic insights in X-chromosome inactivation.** *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*
Lu, Z., Carter, A. C., Chang, H. Y.
2017; 372 (1733)
- **The conserved RNA helicase YTHDC2 regulates the transition from proliferation to differentiation in the germline** *ELIFE*
Bailey, A. S., Batista, P. J., Gold, R. S., Chen, Y., de Rooij, D. G., Chang, H. Y., Fuller, M. T.
2017; 6
- **m(6A) mRNA methylation controls T cell homeostasis by targeting the IL-7/STAT5/SOCS pathways** *NATURE*
Li, H., Tong, J., Zhu, S., Batista, P. J., Duffy, E. E., Zhao, J., Bailis, W., Cao, G., Kroehling, L., Chen, Y., Wang, G., Broughton, J. P., Chen, et al
2017; 548 (7667): 338+
- **Long Noncoding RNAs: At the Intersection of Cancer and Chromatin Biology** *COLD SPRING HARBOR PERSPECTIVES IN MEDICINE*
Schmitt, A. M., Chang, H. Y.
2017; 7 (7)
- **The Mammalian Ribo-interactome Reveals Ribosome Functional Diversity and Heterogeneity.** *Cell*
Simsek, D., Tiu, G. C., Flynn, R. A., Byeon, G. W., Leppke, K., Xu, A. F., Chang, H. Y., Barna, M.
2017; 169 (6): 1051-1065 e18
- **Transcription coactivator and lncRNA duet evoke Hox genes** *PLOS GENETICS*
Wang, K. C., Chang, H. Y.
2017; 13 (6): e1006797
- **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-?
- **Landscape of monoallelic DNA accessibility in mouse embryonic stem cells and neural progenitor cells.** *Nature genetics*
Xu, J., Carter, A. C., Gendrel, A., Attia, M., Loftus, J., Greenleaf, W. J., Tibshirani, R., Heard, E., Chang, H. Y.
2017; 49 (3): 377-386

- **Comparison of SHAPE reagents for mapping RNA structures inside living cells** *RNA*
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