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

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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
- 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)
- Founding Director, RNA Medicine Program, (2022-2024)

HONORS AND AWARDS

- Albany Prize in Medicine and Biomedical Research, for long noncoding RNAs (2024)
- Jonathan Kraft Prize for Excellence in Cancer Research, Massachusetts General Hospital (2024)
- King Faisal Prize in Science, for long noncoding RNAs and invention of epigenomic methods (2024)
- Lurie Prize in Biomedical Sciences, Foundation for NIH (2024)
- Stanley J. Korsmeyer Award, American Society for Clinical Investigation (2024)
- Member, National Academy of Sciences (2020)
- Member, American Academy of Arts and 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 lifetimeover 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 axesanterior-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 GESsingular 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 cellsthe cells that continually repopulate a tumor or its metastases.

Teaching

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Julie Lake, Lindsey Meservey

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

Publications

PUBLICATIONS

- **Somatic mutations reveal the ontogeny of microglia in human ageing.** *Nature*
  Belk, J. A., Zhang, Y., Reilly, E. E., Shi, Q., Liu, D. D., Womack-Gambrel, N., van der Linde, M., Ma, L., Paul, D., Enciso, A. M., Kalluru, R., Weiss, J., Li, et al
  2026
- **Autoantibody hotspots reveal the origin and impact of immunogenic XIST ribonucleoprotein complexes in autoimmune diseases.** *The Journal of clinical investigation*
  Yan, B., Lee, J., Srinivasan, S., Ambriz, P., Shi, Q., Dou, D. R., Davuluri, S., Nandyala, S., Woods, A., Leatherman, G., Zhao, Y., Reggiardo, R. E., Sawant, et al
  2026
- **Targeting extrachromosomal DNA in human cancers.** *Nature reviews. Drug discovery*
  Wong, I. T., Yi, H., Melillo, B., Cravatt, B. F., Chang, H. Y., Mischel, P. S.
  2026
- **EcDNA-borne structural variants drive oncogenic fusion transcript amplification.** *Cell*
  Yi, H., Zhang, S., Swinderman, J., Wang, Y., Kanakaveti, V., Hung, K. L., Tsz-Lo Wong, I., Srinivasan, S., Curtis, E. J., Bhargava-Shah, A., Li, R., Jones, M. G., Luebeck, et al
  2026
- **Genetic elements promote retention of extrachromosomal DNA in cancer cells.** *Nature*
  Sankar, V., Hung, K. L., Gnanasekar, A., Wong, I. T., Shi, Q., Kraft, K., Jones, M. G., He, B. J., Yan, X., Belk, J. A., Liu, K. J., Agarwal, S., Wang, et al
  2025
- **Enhancing transcription-replication conflict targets ecDNA-positive cancers.** *Nature*
  Tang, J., Weiser, N. E., Wang, G., Chowdhry, S., Curtis, E. J., Zhao, Y., Wong, I. T., Marinov, G. K., Li, R., Hanoian, P., Tse, E., Mojica, S. G., Hansen, et al
  2024; 635 (8037): 210-218
- **Coordinated inheritance of extrachromosomal DNAs in cancer cells.** *Nature*
  Hung, K. L., Jones, M. G., Wong, I. T., Curtis, E. J., Lange, J. T., He, B. J., Luebeck, J., Schmargon, R., Scanu, E., Bruckner, L., Yan, X., Li, R., Gnanasekar, et al
  2024; 635 (8037): 201-209
- **Single-cell chromatin accessibility reveals malignant regulatory programs in primary human cancers.** *Science (New York, N.Y.)*
  Sundaram, L., Kumar, A., Zatzman, M., Salcedo, A., Ravindra, N., Shams, S., Louie, B. H., Bagdatli, S. T., Myers, M. A., Sarmashghi, S., Choi, H. Y., Choi, W. Y., Yost, et al
  2024; 385 (6713): eadk9217
- **Bidirectional epigenetic editing reveals hierarchies in gene regulation.** *Nature biotechnology*

Pacalin, N. M., Steinhart, Z., Shi, Q., Belk, J. A., Dorovskyi, D., Kraft, K., Parker, K. R., Shy, B. R., Marson, A., Chang, H. Y.
2024

- **Xist ribonucleoproteins promote female sex-biased autoimmunity.** *Cell*
  Dou, D. R., Zhao, Y., Belk, J. A., Zhao, Y., Casey, K. M., Chen, D. C., Li, R., Yu, B., Srinivasan, S., Abe, B. T., Kraft, K., Hellström, C., Sjöberg, et al
  2024; 187 (3): 733-749.e16

- **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

- **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

- **Spatiotemporal lineage tracing reveals the dynamic spatial architecture of tumor growth and metastasis.** *Nature genetics*
  Jones, M. G., Sun, D., Min, K. H., Colgan, W. N., Wang, H., Török, T., Ribeiro, J., Xue, J., Cardoso, E. C., Rong, Y., Tian, L., Weir, J. A., Chen, et al
  2026

- **RNA delivery to the corneal endothelium using charge-altering releasable transporters.** *Science advances*
  Wang, S. K., Li, Z., Shah, S. H., Edwards, Q. A., Bouffard, R., Hines, E. S., Imventarza, J. A., Korte, S., Lawrence, M. S., Song, E., Helmy, E., Amaya, L., Kang, et al
  2026; 12 (34): eady8161

- **Brain perivascular macrophages regulate endothelial cell function via a cMAF-dependent transcriptional program in mouse and human.** *Cell*
  Brioschi, S., Belk, J. A., Storck, S. E., Wu, Y., Wang, Z., Feng, Z., van Olst, L., Emery, J. L., Sudan, R., Wu, J., Du, S., Genua, M., La Terza, et al
  2026

- **scAmp enables focal gene amplification analysis from single-cell data.** *Nature communications*
  Jones, M. G., Weiser, N. E., Hung, K. L., Yan, X., Agarwal, S., Luebeck, J., Gnanasekar, A., Zhang, S., Wong, I. T., Tang, J., Howitt, B. E., Curtis, E. J., Yu, et al
  2026; 17 (1)

- **Epigenetic landscape, key transcriptional regulators, and in vivo identification of human Tr1 cells.** *Science advances*
  Cepika, A. M., Amaya, L., Waichler, C., Narula, M., Mantilla, M., Thomas, B. C., Chen, P. P., Freeborn, R. A., Pavel-Dinu, M., Nideffer, J., Porteus, M., Bacchetta, R., Müller, et al
  2026; 12 (28): eaec6358

- **XIST RNA-protein complex in female-biased autoimmunity: From molecular scaffolds to new clinical biomarkers.** *The Journal of investigative dermatology*
  Lee, J., Chang, H. Y.
  2026

- **Annotation of nuclear lncRNAs based on chromatin interactions (vol 19, e0295971, 2024)** *PLOS ONE*
  Agrawal, S., Buyan, A., Severin, J., Koido, M., Alam, T., Abugessaisa, I., Chang, H. Y., Dostie, J., Itoh, M., Kere, J., Kondo, N., Li, Y., Makeev, et al
  2026; 21 (4): e0339624

- **A recipe for chaos: Extrachromosomal DNA and the hallmarks of cancer.** *Cell*
  Wong, I. T., Bailey, C., Wu, S., Henssen, A. G., Cravatt, B. F., Chen, Z. J., Bafna, V., Jamal-Hanjani, M., Swanton, C., Chang, H. Y., Mischel, P. S.
  2026; 189 (8): 2307-2321

- **Accurate prediction of ecDNA in interphase cancer cells using deep neural networks.** *Communications biology*
  Prasad, G., Rajkumar, U., Curtis, E. J., Wong, I. T., Yan, X., Zhang, S., Brückner, L., Turner, K., Wiese, J., Wahl, J., Hemmati, H., Wu, S., Theissen, et al
  2026

- **RNA origin of sex-biased immunity** *MOLECULAR THERAPY NUCLEIC ACIDS*
  Chang, H. Y., Chung, L., Davis, M. M., Fiorentino, D., Lee, J., Lundberg, E., Utz, P. J.
  2026; 37 (1)

- **Fibroblasts of disparate developmental origins harbor anatomically variant scarring potential.** *Cell*
  Griffin, M. F., Li, D. J., Chen, K., Parker, J. B., Guo, J. L., Kim, S., Kraft, K., Downer, M., Morgan, A. G., Kuhnert, M. M., Jing, S. L., Yao, H., Valencia, et al
  2026

- **Single-cell multiome and enhancer connectome of human retinal pigment epithelium and choroid nominate causal variants in macular degeneration.** *Cell reports*
  Wang, S. K., Li, J., Nair, S., Kosaraju, R., Chen, Y., Zhang, Y., Kundaje, A., Liu, Y., Wang, N., Chang, H. Y.
  2026; 45 (1): 116814

- **Junction-targeting designs limit the application of CRISPR-Cas13d in circular RNA perturbation studies.** *Nucleic acids research*
  Lee-Yow, Y. C., Valbuena, R. C., Richter, C. S., Chang, H. Y., Engreitz, J. M.
  2026; 54 (1)

- **Fibroblasts of disparate developmental origins harbor anatomically variant scarring potential** *Cell*
  Griffin, M., Li, D., Chen, K., Parker, J., Guo, J., Kim, S., Kraft, K., Downer, M., Morgan, A., Kuhnert, M., Jing, S., Yao, H., Valencia, et al
  2026

- **Long noncoding RNA regulation of immunity.** *Nature immunology*
  Yu, B., Chang, H. Y.
  2026; 27 (1): 16-25

- **Reconstructing the three-dimensional architecture of extrachromosomal DNA with ec3D.** *Nature communications*
  Chowdhury, B., Zhu, K., Li, C., Alsing, J., Luebeck, J., Stefanova, M. E., Chapman, O. S., Kraft, K., Zhang, S., Lim, J. Y., Xie, Y., Kim, Y. J., Wu, et al
  2025

- **Escape from X inactivation is directly modulated by Xist noncoding RNA.** *Nature cell biology*
  Hauth, A., Panten, J., Kneuss, E., Picard, C., Servant, N., Rall, I., Pérez-Rico, Y. A., Clerquin, L., Servaas, N., Villacorta, L., Jung, F., Luong, C., Chang, et al
  2025

- **FOXP3 expression depends on cell-type-specific cis-regulatory elements and transcription factor circuitry.** *Immunity*
  Umhoefer, J. M., Arce, M. M., Kasinathan, S., Whalen, S., Dajani, R., Subramanya, S., Goudy, L., Belk, J. A., Zhou, R., Pham, M. T., Zhang, W., Hernandez, R., Tran, et al
  2025

- **Genetic and chromatin regulation of Pvt1 monoallelic expression.** *Cell reports*
  Luong, C., Chen, M., Belk, J. A., Kraft, K., Gendrel, A. V., Heard, E., Wysocka, J., Chang, H. Y.
  2025; 44 (11): 116554

- **Enhancer activation from transposable elements in extrachromosomal DNA.** *Nature cell biology*
  Kraft, K., Murphy, S. E., Jones, M. G., Shi, Q., Bhargava-Shah, A., Luong, C., Hung, K. L., He, B. J., Li, R., Park, S. K., Montgomery, M. T., Weiser, N. E., Wang, et al
  2025

- **Epigenomic profile of GBA1 in Parkinson's disease.** *Parkinsonism & related disorders*
  Berson, E., Zaghroun, R., Santoro, M., Bukhari, S., Seong, D., Shu, C. H., Perna, A., James, T., Montine, K. S., Serrano, G. E., Beach, T. G., Keene, C. D., Chang, et al
  2025; 140: 108066

- **Extrachromosomal DNA-Driven Oncogene Spatial Heterogeneity and Evolution in Glioblastoma.** *Cancer discovery*
  Noorani, I., Haughey, M., Luebeck, J., Rowan, A., Grönroos, E., Terenzi, F., Wong, I. T., Pradella, D., Lisi, M., Kittel, J., Sharma, N., Bailey, C., Weeden, et al
  2025: OF1-OF18

- **Multi-omic analysis reveals retinoic acid molecular drivers for dermal fibrosis and regenerative repair in the skin.** *Cell stem cell*
  Griffin, M., Guo, J. L., Parker, J. B., Kuhnert, M., Li, D. J., Valencia, C., Morgan, A., Downer, M., Cotterell, A. C., Lu, J. M., Dilorio, S., Bauer-Rowe Ramos, K. E., Januszyk, et al
  2025

- **Discrete Immolative Guanidinium Transporters deliver mRNA to specific organs and red blood cells.** *Nature communications*

Li, Z., Ee, A., Amaya, L., Hamad, J. L., Yadav, P. K., Wang, S. K., Chang, H. Y., Wender, P. A.
2025; 16 (1): 7055

- **Massively parallel immunopeptidome by DNA sequencing provides insights into cancer antigen presentation.** *Nature genetics*
  Shi, Q., Simon, E. P., Cimen Bozkus, C., Kaminska, A., Velazquez, L., Saxena, M., Zhang, Z., Belk, J. A., Wang, S., Yang, N., Zhang, Y., Kwong, A., Che, et al
  2025
- **Accurate Prediction of ecDNA in Interphase Cancer Cells using Deep Neural Networks.** *bioRxiv : the preprint server for biology*
  Rajkumar, U., Prasad, G., Curtis, E. J., Wong, I. T., Yan, X., Zhang, S., Brückner, L., Turner, K., Wiese, J., Wahl, J., Wu, S., Theissen, J., Fischer, et al
  2025
- **Three-dimensional genome landscape of primary human cancers.** *Nature genetics*
  Yost, K. E., Zhao, Y., Hung, K. L., Zhu, K., Xu, D., Corces, M. R., Shams, S., Louie, B. H., Sarmashghi, S., Sundaram, L., Luebeck, J., Clarke, S., Doane, et al
  2025
- **Induced B cell receptor diversity predicts PD-1 blockade immunotherapy response.** *Proceedings of the National Academy of Sciences of the United States of America*
  Che, Y., Lee, J., Abou-Taleb, F., Rieger, K. E., Satpathy, A. T., Chang, A. L., Chang, H. Y.
  2025; 122 (18): e2501269122
- **A Guide to Extrachromosomal DNA: Cancer's Dynamic Circular Genome.** *Cancer discovery*
  Weiser, N. E., Watkins, T. B., Chang, H. Y., Mischel, P. S.
  2025: OF1-OF10
- **Unified molecular approach for spatial epigenome, transcriptome, and cell lineages.** *Proceedings of the National Academy of Sciences of the United States of America*
  Huang, Y. H., Belk, J. A., Zhang, R., Weiser, N. E., Chiang, Z., Jones, M. G., Mischel, P. S., Buenrostro, J. D., Chang, H. Y.
  2025; 122 (16): e2424070122
- **Histological signatures map anti-fibrotic factors in mouse and human lungs.** *Nature*
  Guo, J. L., Griffin, M., Yoon, J. K., Lopez, D. M., Zhu, Y., Lu, J. M., Mikos, G., Parker, J. B., Mascharak, S., Brenac, C., Guardino, N. J., Abbas, D. B., Li, et al
  2025
- **Breakage fusion bridge cycles drive high oncogene number with moderate intratumoural heterogeneity.** *Nature communications*
  Raeisi Dehkordi, S., Wong, I. T., Ni, J., Luebeck, J., Zhu, K., Prasad, G., Krockenberger, L., Xu, G., Chowdhury, B., Rajkumar, U., Caplin, A., Muliaditan, D., Gnanasekar, et al
  2025; 16 (1): 1497
- **MorPhiC Consortium: towards functional characterization of all human genes.** *Nature*
  Adli, M., Przybyla, L., Burdett, T., Burridge, P. W., Cacheiro, P., Chang, H. Y., Engreitz, J. M., Gilbert, L. A., Greenleaf, W. J., Hsu, L., Huangfu, D., Hung, L. H., Kundaje, et al
  2025; 638 (8050): 351-359
- **A STAG2-PAXIP1/PAGR1 axis suppresses lung tumorigenesis.** *The Journal of experimental medicine*
  Ashkin, E. L., Tang, Y. J., Xu, H., Hung, K. L., Belk, J. A., Cai, H., Lopez, S. S., Dolcen, D. N., Hebert, J. D., Li, R., Ruiz, P. A., Keal, T., Andrejka, et al
  2025; 222 (1)
- **Engineered extrachromosomal oncogene amplifications promote tumorigenesis.** *Nature*
  Pradella, D., Zhang, M., Gao, R., Yao, M. A., Gluchowska, K. M., Cendon-Florez, Y., Mishra, T., La Rocca, G., Weigl, M., Jiao, Z., Nguyen, H. H., Lisi, M., Ozimek, et al
  2024
- **Origins and impact of extrachromosomal DNA.** *Nature*
  Bailey, C., Pich, O., Thol, K., Watkins, T. B., Luebeck, J., Rowan, A., Stavrou, G., Weiser, N. E., Dameracharla, B., Bentham, R., Lu, W., Kittel, J., Yang, et al
  2024; 635 (8037): 193-200

- **Disparate pathways for extrachromosomal DNA biogenesis and genomic DNA repair.** *Cancer discovery*
  Rose, J. C., Belk, J. A., Wong, I. T., Luebeck, J., Horn, H. T., Daniel, B., Jones, M. G., Yost, K. E., Hung, K. L., Kolahi, K. S., Curtis, E. J., Kuo, C. J., Bafna, et al
  2024

- **A human autoimmune organoid model reveals IL-7 function in coeliac disease.** *Nature*
  Santos, A. J., van Unen, V., Lin, Z., Chirieleison, S. M., Ha, N., Batish, A., Chan, J. E., Cedano, J., Zhang, E. T., Mu, Q., Guh-Siesel, A., Tomaske, M., Colburg, et al
  2024

- **Cohesin prevents cross-domain gene coactivation.** *Nature genetics*
  Dong, P., Zhang, S., Gandin, V., Xie, L., Wang, L., Lemire, A. L., Li, W., Otsuna, H., Kawase, T., Lander, A. D., Chang, H. Y., Liu, Z. J.
  2024

- **Clonal inactivation of TERT impairs stem cell competition.** *Nature*
  Hasegawa, K., Zhao, Y., Garbuzov, A., Corces, M. R., Neuhöfer, P., Gillespie, V. M., Cheung, P., Belk, J. A., Huang, Y. H., Wei, Y., Chen, L., Chang, H. Y., Artandi, et al
  2024

- **CoRAL accurately resolves extrachromosomal DNA genome structures with long-read sequencing.** *Genome research*
  Zhu, K., Jones, M. G., Luebeck, J., Bu, X., Yi, H., Huang, K. L., Wong, I. T., Zhang, S., Mischel, P. S., Chang, H., Bafna, V.
  2024

- **Transcriptional immune suppression and up-regulation of double-stranded DNA damage and repair repertoires in ecDNA-containing tumors.** *eLife*
  Lin, M. S., Jo, S. Y., Luebeck, J., Chang, H. Y., Wu, S., Mischel, P. S., Bafna, V.
  2024; 12

- **hnRNPM protects against the dsRNA-mediated interferon response by repressing LINE-associated cryptic splicing.** *Molecular cell*
  Zheng, R., Dunlap, M., Bobkov, G. O., Gonzalez-Figueroa, C., Patel, K. J., Lyu, J., Harvey, S. E., Chan, T. W., Quinones-Valdez, G., Choudhury, M., Le Roux, C. A., Bartels, M. D., Vuong, et al
  2024

- **The CD8+Tcell tolerance checkpoint triggers a distinct differentiation state defined by protein translation defects.** *Immunity*
  Van Der Byl, W., Nussing, S., Peters, T. J., Ahn, A., Li, H., Ledergor, G., David, E., Koh, A. S., Wagle, M. V., Deguit, C. D., de Menezes, M. N., Travers, A., Sampurno, et al
  2024

- **Organ- and Cell-Selective Delivery of mRNA In Vivo Using Guanidinylated Serinol Charge-Altering Releasable Transporters.** *Journal of the American Chemical Society*
  Li, Z., Amaya, L., Ee, A., Wang, S. K., Ranjan, A., Waymouth, R. M., Chang, H. Y., Wender, P. A.
  2024

- **Pathways for macrophage uptake of cell-free circular RNAs.** *Molecular cell*
  Amaya, L., Abe, B., Liu, J., Zhao, F., Zhang, W. L., Chen, R., Li, R., Wang, S., Kamber, R. A., Tsai, M. C., Bassik, M. C., Majeti, R., Chang, et al
  2024

- **Annotation of nuclear lncRNAs based on chromatin interactions.** *PloS one*
  Agrawal, S., Buyan, A., Severin, J., Koido, M., Alam, T., Abugessaisa, I., Chang, H. Y., Dostie, J., Itoh, M., Kere, J., Kondo, N., Li, Y., Makeev, et al
  2024; 19 (5): e0295971

- **Escape from X inactivation is directly modulated by levels of Xist non-coding RNA.** *bioRxiv : the preprint server for biology*
  Hauth, A., Panten, J., Kneuss, E., Picard, C., Servant, N., Rall, I., Perez-Rico, Y. A., Clerquin, L., Servaas, N., Villacorta, L., Jung, F., Luong, C., Chang, et al
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