Stanford

Anshul Kundaje

Associate Professor of Genetics and of Computer Science

NIH Biosketch available Online

Bio

BIO

Anshul Kundaje is Associate Professor of Genetics and Computer Science at Stanford University. The Kundaje lab develops machine learning models of gene regulation to decipher the genetic and molecular basis of disease. The lab has pioneered deep learning models and interpretation frameworks to decode the functional language encoded in DNA, RNA and proteins. Dr. Kundaje has led computational efforts of large genomics consortia including the ENCODE Project and the Roadmap Epigenomics Project. Dr. Kundaje is a recipient of the NIH Director's New Innovator Award, the Alfred Sloan Fellowship and the HUGO Chen Award of Excellence.

ACADEMIC APPOINTMENTS

- Associate Professor, Genetics
- Associate Professor, Computer Science
- Member, Bio-X
- 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

HONORS AND AWARDS

- HUGO Chen Award of Excellence, Human Genome Organization (2019)
- NIH Director's New Innovator Award, NIH (2016)
- Alfred Sloan Foundation Research Fellowship, Alfred Sloan Foundation (2014-2016)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Advisor, National Human Genome Research Institute Genomic Data Science Working Group (2021 - present)
- Editorial Board, Journal of Computational Biology (2021 - present)
- Editorial Board, Genome Research (2020 - present)
- Advisor, NIH Director's Advisory Committee for Artificial Intelligence in Biomedical Research (2019 - 2021)

LINKS

- My website: http://anshul.kundaje.net

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

My laboratory develops innovative machine learning methods to predict and decode biological sequences, molecular interactions, and genetic variation. We have pioneered deep learning models and interpretation frameworks that decode DNA and RNA sequence syntax governing context-specific transcription factor binding, RNA binding protein interactions, chromatin accessibility, histone modifications, transcription initiation, gene expression, alternative polyadenylation, and RNA editing. Using these approaches, we have built regulatory models across thousands of cellular contexts in humans and mice, elucidating dynamic regulation during differentiation and cellular reprogramming. Our methodological contributions span regulatory element mapping, deciphering the cis-regulatory code, long-range regulatory interaction modeling, and predictive regulatory network construction. We have adapted protein language models to predict and design transcription factor effector domains and developed machine learning frameworks leveraging T-cell and B-cell repertoire sequences for disease diagnostics.

I have extensive leadership experience in collaborative genomics consortia. As principal investigator, I led integrative analyses for the Encyclopedia of DNA Elements (ENCODE) consortium and the Roadmap Epigenomics Project. Currently, I serve as steering committee co-chair of the Impact of Genomic Variation on Function (IGVF) consortium and co-lead the Data Analysis and Coordination Center for the Multi-omics in Health and Disease (MOHD) consortium. My team has developed standardized processing and quality control pipelines for bulk and single-cell molecular profiling data across ENCODE, Roadmap, IGVF, and MOHD initiatives.

Translating our regulatory models to biomedical applications, we dissect functional genetic variation in rare and complex diseases using large biobanks and genome sequencing projects. Our disease-focused collaborations span colorectal cancer (GECCO and HTAN consortia), cardiometabolic disorders (AMP-CMD, CZI Seed networks), neurodegenerative diseases (ADSP consortium), and neuropsychiatric conditions (PsychENCODE consortium).

We have also developed widely-used software tools and web portals for mining and visualizing large-scale regulatory genomics data, facilitating community access to our resources and findings.

I have successfully mentored over 35 graduate students and postdocs who have gone on to leadership positions in academia (faculty at Carnegie Mellon, Michigan State, Memorial Sloan Kettering) and industry (Genentech, Illumina, NVIDIA), demonstrating our lab's commitment to training the next generation of computational biologists.

PROJECTS

- The Encyclopedia of DNA Elements (ENCODE) Project - Stanford University, MIT
- The Roadmap Epigenomics Project - MIT (February 2012 - present)

Teaching

COURSES

2025-26

- Cloud Computing for Biology and Healthcare: BMDS 222, CS 273C, GENE 222 (Spr)
- Deep Learning in Genomics and Biomedicine: BMDS 273, CS 273B, GENE 236 (Spr)

2024-25

- Cloud Computing for Biology and Healthcare: BIOMEDIN 222, CS 273C, GENE 222 (Spr)

2023-24

- Cloud Computing for Biology and Healthcare: BIOMEDIN 222, CS 273C, GENE 222 (Spr)
- Deep Learning in Genomics and Biomedicine: BIODS 237, CS 273B (Spr)

2022-23

- Big Data for Biologists - Decoding Genomic Function: HUMBIO 51 (Win)
- Cloud Computing for Biology and Healthcare: BIOMEDIN 222, CS 273C, GENE 222 (Spr)
- Deep Learning in Genomics and Biomedicine: BIODS 237, BIOMEDIN 273B, CS 273B, GENE 236 (Spr)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

STANFORD ADVISEES

Arthur Deng

Doctoral Dissertation Reader (AC)

Shawn Cai, Meena Chakraborty, Benjamin Doughty, Tami Gjorgjieva, Michael Hayes, Maya Sheth, Elana Simon, Alp Tartici

Postdoctoral Faculty Sponsor

Pau Badia i Mompel, Seungbyn Baek, Mingze Dong, Adam He, Ruchir Rastogi, Isaac Vock, Lei Xiong

Doctoral Dissertation Advisor (AC)

Alejandro Buendia, Ziwei Chen, Salil Deshpande, Martin Kjellberg, Kamal Obbad, Valeh Valiollah Pour Amiri, Chang M. Yun, Chris Zou

Orals Evaluator

Minji Kang

Doctoral Dissertation Co-Advisor (AC)

Samuel Alber, Antony Chang, Nathaniel Diamant, Michal Gerasimiuk, Alexander Johansen, Minji Kang, Shouvik Mani, Owen Queen, Esther Robb, Jake Silberg, Arpita Singhal, Jason Tan, Nitya Thakkar, Zoe Wefers

Master's Program Advisor

Rohan Mehrotra, Isabel Michel, Sanjay Nagaraj, Jessie Ou, Emmy Thamakaison

Postdoctoral Research Mentor

Danila Bredikhin, Selin Jessa

Doctoral (Program)

Ziwei Chen, Anvita Gupta, Chiho Im, Riya Sinha

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Data Science (Masters Program)
- Biomedical Data Science (Phd Program)
- Genetics (Phd Program)

Publications

PUBLICATIONS

- **Disease diagnostics using machine learning of B cell and T cell receptor sequences.** *Science (New York, N.Y.)*
  Zaslavsky, M. E., Craig, E., Michuda, J. K., Sehgal, N., Ram-Mohan, N., Lee, J. Y., Nguyen, K. D., Hoh, R. A., Pham, T. D., Röltgen, K., Lam, B., Parsons, E. S., Macwana, et al

2025; 387 (6736): eadp2407

- **Transcription factor stoichiometry, motif affinity and syntax regulate single-cell chromatin dynamics during fibroblast reprogramming to pluripotency.** *bioRxiv : the preprint server for biology*
  Nair, S., Ameen, M., Sundaram, L., Pampari, A., Schreiber, J., Balsubramani, A., Wang, Y. X., Burns, D., Blau, H. M., Karakikes, I., Wang, K. C., Kundaje, A.
  2023

- **Integrative single-cell analysis of cardiogenesis identifies developmental trajectories and non-coding mutations in congenital heart disease.** *Cell*
  Ameen, M., Sundaram, L., Shen, M., Banerjee, A., Kundu, S., Nair, S., Shcherbina, A., Gu, M., Wilson, K. D., Varadarajan, A., Vadgama, N., Balsubramani, A., Wu, et al
  2022; 185 (26): 4937

- **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

- **A genome-wide atlas of co-essential modules assigns function to uncharacterized genes.** *Nature genetics*
  Wainberg, M., Kamber, R. A., Balsubramani, A., Meyers, R. M., Sinnott-Armstrong, N., Hornburg, D., Jiang, L., Chan, J., Jian, R., Gu, M., Shcherbina, A., Dubreuil, M. M., Spees, et al
  2021

- **Base-resolution models of transcription-factor binding reveal soft motif syntax.** *Nature genetics*
  Avsec, Ž. n., Weilert, M. n., Shrikumar, A. n., Krueger, S. n., Alexandari, A. n., Dalal, K. n., Fropf, R. n., McAnany, C. n., Gagneur, J. n., Kundaje, A. n., Zeitlinger, J. n.
  2021

- **Single-cell epigenomic analyses implicate candidate causal variants at inherited risk loci for Alzheimer's and Parkinson's diseases.** *Nature genetics*
  Corces, M. R., Shcherbina, A., Kundu, S., Gloudemans, M. J., Fresard, L., Granja, J. M., Louie, B. H., Eulalio, T., Shams, S., Bagdatli, S. T., Mumbach, M. R., Liu, B., Montine, et al
  2020

- **Opportunities and challenges for transcriptome-wide association studies** *NATURE GENETICS*
  Wainberg, M., Sinnott-Armstrong, N., Mancuso, N., Barbeira, A. N., Knowles, D. A., Golan, D., Ermel, R., Ruusalepp, A., Quertermous, T., Hao, K., Bjorkegren, J. L. M., Im, H., Pasaniuc, et al
  2019; 51 (4): 592–99

- **Discovering epistatic feature interactions from neural network models of regulatory DNA sequences.** *Bioinformatics (Oxford, England)*
  Greenside, P., Shimko, T., Fordyce, P., Kundaje, A.
  2018; 34 (17): i629-i637

- **Opportunities and obstacles for deep learning in biology and medicine** *JOURNAL OF THE ROYAL SOCIETY INTERFACE*
  Ching, T., Himmelstein, D. S., Beaulieu-Jones, B. K., Kalinin, A. A., Do, B. T., Way, G. P., Ferrero, E., Agapow, P., Zietz, M., Hoffman, M. M., Xie, W., Rosen, G. L., Lengerich, et al
  2018; 15 (141)

- **Denoising genome-wide histone ChIP-seq with convolutional neural networks** *BIOINFORMATICS*
  Koh, P., Pierson, E., Kundaje, A.
  2017; 33 (14): I225–I233

- **Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions** *CELL*
  Grubert, F., Zaugg, J. B., Kasowski, M., Ursu, O., Spacek, D. V., Martin, A. R., Greenside, P., Srivas, R., Phanstiel, D. H., Pekowska, A., Heidari, N., Euskirchen, G., Huber, et al
  2015; 162 (5): 1051-1065

- **Conserved epigenomic signals in mice and humans reveal immune basis of Alzheimer's disease.** *Nature*
  Gjoneska, E., Pfenning, A. R., Mathys, H., Quon, G., Kundaje, A., Tsai, L., Kellis, M.
  2015; 518 (7539): 365-369

- **Integrative analysis of 111 reference human epigenomes.** *Nature*
  Kundaje, A., Meuleman, W., Ernst, J., Bilenky, M., Yen, A., Heravi-Moussavi, A., Kheradpour, P., Zhang, Z., Wang, J., Ziller, M. J., Amin, V., Whitaker, J. W., Schultz, et al
  2015; 518 (7539): 317-330

- **Architecture of the human regulatory network derived from ENCODE data** *NATURE*
  Gerstein, M. B., Kundaje, A., Hariharan, M., Landt, S. G., Yan, K., Cheng, C., Mu, X. J., Khurana, E., Rozowsky, J., Alexander, R., Min, R., Alves, P., Abyzov, et al
  2012; 489 (7414): 91-100

- **An integrated encyclopedia of DNA elements in the human genome** *NATURE*
  Dunham, I., Kundaje, A., Aldred, S. F., Collins, P. J., Davis, C., Doyle, F., Epstein, C. B., Frietze, S., Harrow, J., Kaul, R., Khatun, J., Lajoie, B. R., Landt, et al
  2012; 489 (7414): 57-74

- **Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements** *GENOME RESEARCH*
  Kundaje, A., Kyriazopoulou-Panagiotopoulou, S., Libbrecht, M., Smith, C. L., Raha, D., Winters, E. E., Johnson, S. M., Snyder, M., Batzoglou, S., Sidow, A.
  2012; 22 (9): 1735-1747

- **ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia** *GENOME RESEARCH*
  Landt, S. G., Marinov, G. K., Kundaje, A., Kheradpour, P., Pauli, F., Batzoglou, S., Bernstein, B. E., Bickel, P., Brown, J. B., Cayting, P., Chen, Y., DeSalvo, G., Epstein, et al
  2012; 22 (9): 1813-1831

- **Linking disease associations with regulatory information in the human genome** *GENOME RESEARCH*
  Schaub, M. A., Boyle, A. P., Kundaje, A., Batzoglou, S., Snyder, M.
  2012; 22 (9): 1748-1759

- **A Predictive Model of the Oxygen and Heme Regulatory Network in Yeast** *PLOS COMPUTATIONAL BIOLOGY*
  Kundaje, A., Xin, X., Lan, C., Lianoglou, S., Zhou, M., Zhang, L., Leslie, C.
  2008; 4 (11)

- **Learning regulatory programs that accurately predict differential expression with MEDUSA** *Workshop on Dialogue on Reverse Engineering Assessment and Methods*
  Kundaje, A., Lianoglou, S., Li, X., Quigley, D., Arias, M., Wiggins, C. H., Zhang, L., Leslie, C.
  WILEY-BLACKWELL.2007: 178–202

- **Combining sequence and time series expression data to learn transcriptional modules** *IEEE-ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS*
  Kundaje, A., Middendorf, M., Gao, F., Wiggins, C., Leslie, C.
  2005; 2 (3): 194-202

- **Learning Important Features Through Propagating Activation Differences** *Proceedings of the 34th International Conference on Machine Learning, 70:3145-3153, 2017*
  Shrikumar, A., Greenside, P., Kundaje, A.
  2017

- **Decoding common and rare noncoding variant effects across cellular and developmental contexts.** *Nature genetics*
  Marderstein, A. R., Kundu, S., Padhi, E. M., Deshpande, S., Wang, A., Robb, E., Sun, Y., Yun, C. M., Pomales-Matos, D., Xie, Y., Chang, S. H., Chin, I. M., Shah, et al
  2026

- **Ribo-Tweezer: Rapid removal of ribosomal proteins reveals additional layers of post-transcriptional gene regulation.** *Molecular cell*
  Chen, Y., Cheng, C. P., Cates, K., Marinov, G. K., Lantz, T. C., Yang, H., Liu, I., Genuth, N. R., Andronescu, C., Hung, V., Bermudez, A., Rothschild, D., Georgeson, et al
  2026

- **Bio-BLIP: A Multimodal Architecture for Transferable Reasoning in Genomic Variant Interpretation.** *bioRxiv : the preprint server for biology*
  Gupta, A., Kundaje, A., Buendia, A., Leskovec, J.
  2026

- **Prediction and functional interpretation of inter-chromosomal genome architecture from DNA sequence with TwinC.** *Nature communications*
  Jha, A., Hristov, B., Wang, X., Wang, S., Greenleaf, W. J., Kundaje, A., Aiden, E. L., Bertero, A., Noble, W. S.
  2026

- **Multiomics and deep learning dissect regulatory syntax in human development.** *Nature*
  Liu, B. B., Jessa, S., Kim, S. H., Ng, Y. T., Higashino, S. I., Marinov, G. K., Chen, D. C., Parks, B. E., Li, L., Nguyen, T. C., Wang, A. T., Wang, S. K., Tan, et al
  2026

- **TGF-β-pathway-based polygenic risk score modifies the association between red meat intake and colorectal cancer risk: Application of a novel pathway-based PRS method.** *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*
  Sanchez Mendez, J., Queme, B., Fu, Y., Morrison, J. L., Lewinger, J. P., Kawaguchi, E. S., Mi, H., Obón-Santacana, M., Moratalla-Navarro, F., Martín, V., Moreno, V., Qu, C., Huyghe, et al
  2026

- **Vascular smooth muscle cell state trajectories mediate molecular mechanisms of coronary disease risk.** *Nature communications*
  Li, D. Y., Kundu, S., Cheng, P., Gu, W., Worssam, M. D., Jackson, W. R., Zhao, Q., Nguyen, T., Yu, A. M., Monteiro, J. P., Caceres, R. D., Dale, S., Palmisano, et al
  2026

- **Short-Context Regulatory DNA Language Models with Motif-Discovery Regularization.** *bioRxiv : the preprint server for biology*
  Patel, A., Kundaje, A.
  2026

- **Genetic risk factors modulate the association between physical activity and colorectal cancer.** *BMC medicine*
  Peoples, A. R., Obón-Santacana, M., Kim, A. E., Kawaguchi, E. S., Fu, Y., Qu, C., Moratalla-Navarro, F., Morrison, J., Lin, Y., Arndt, V., Berndt, S. I., Bien, S. A., Bishop, et al
  2026

- **Deep learning-guided design of cell type-specific AAV promoters.** *bioRxiv : the preprint server for biology*
  Wang, S. K., Deng, B., Nair, S., Ren, X., Li, J., Tijerina, J., Prakhar, P., Luo, Z., Nnebe, C., Kim, S. H., Zhou, Y., Shah, S. H., Davis, 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

- **An expanded registry of candidate cis-regulatory elements.** *Nature*
  Moore, J. E., Pratt, H. E., Fan, K., Phalke, N., Fisher, J., Elhajjajy, S. I., Andrews, G., Gao, M., Shedd, N., Fu, Y., Lacadie, M. C., Meza, J., Khandpekar, et al
  2026

- **JASPAR 2026: expansion of transcription factor binding profiles and integration of deep learning models.** *Nucleic acids research*
  Ovek Baydar, D., Rauluseviciute, I., Aronsen, D. R., Blanc-Mathieu, R., Bonthuis, I., de Beukelaer, H., Ferenc, K., Jegou, A., Kumar, V., Lemma, R. B., Lucas, J., Pochon, M., Yun, et al
  2025

- **Polyclonal origins of human premalignant colorectal lesions.** *Nature*
  Van Egeren, D., Schenck, R. O., Khan, A., Horning, A. M., Mo, S., Weiß, C. L., Esplin, E. D., Becker, W. R., Wu, S., Hanson, C., Barapour, N., Jiang, L., Contrepois, et al
  2025

- **Polyclonal origins of human premalignant colorectal lesions.** *bioRxiv : the preprint server for biology*
  Van Egeren, D., Schenck, R. O., Khan, A., Horning, A. M., Mo, S., Weiß, C. L., Esplin, E. D., Becker, W. R., Wu, S., Hanson, C., Barapour, N., Jiang, L., Contrepois, et al
  2025

- **Vascular smooth muscle cell atherosclerosis trajectories characterized at single cell resolution identify causal transcriptomic and epigenomic mechanisms of disease risk**

Li, D., Kundu, S., Cheng, P., Gu, W., Jackson, W., Zhao, Q., Nguyen, T., Worssam, M., Monteiro, J., Palmisano, B., Weldy, C., Kundu, R., Kundaje, et al

LIPPINCOTT WILLIAMS & WILKINS.2025

- **The epigenomic landscape of single vascular cells reflects developmental origin and identifies disease risk loci**

  Weldy, C., Kundu, S., Monteiro, J., Gu, W., Pedroza, A., Dalal, A., Worssam, M., Li, D., Palmisano, B., Zhao, Q., Sharma, D., Nguyen, T., Kundu, et al

  LIPPINCOTT WILLIAMS & WILKINS.2025

- **GREGoR: accelerating genomics for rare diseases.** *Nature*

  Dawood, M., Heavner, B., Wheeler, M. M., Ungar, R. A., LoTempio, J., Wiel, L., Berger, S., Bernstein, J. A., Chong, J. X., Délot, E. C., Eichler, E. E., Lupski, J. R., Shojaie, et al

  2025; 647 (8089): 331-342

- **Deep learning the dynamic regulatory sequence code of cardiac organoid differentiation.** *bioRxiv : the preprint server for biology*

  Metzl-Raz, E., Zhao, R., Deshpande, S., Powell, J., Porter, E. G., Zouaghi, Y., Liu, B. B., Kim, S. H., Abdi, I., Evergreen, I., Agarwal, M., Sheth, M. U., Rico, et al

  2025

- **A cell and transcriptome atlas of human arterial vasculature.** *Cell genomics*

  Zhao, Q., Pedroza, A., Sharma, D., Gu, W., Dalal, A., Weldy, C., Jackson, W., Li, D. Y., Ryan, Y., Nguyen, T., Shad, R., Palmisano, B. T., Monteiro, et al

  2025: 101034

- **Using gene-environment interactions to explore pathways for colorectal cancer risk.** *EBioMedicine*

  Bouras, E., Yu, R., Kim, A. E., Markozannes, G., Murphy, N., Albanes, D., Anderson, L. N., Barry, E. L., Berndt, S. I., Bishop, D. T., Brenner, H., Burnett-Hartman, A., Campbell, et al

  2025; 121: 105964

- **Predicting chromatin conformation contact maps.** *PloS one*

  Min, A., Schreiber, J., Kundaje, A., Noble, W. S.

  2025; 20 (9): e0331124

- **The regulatory landscape of nascent transcription in human health and disease.** *bioRxiv : the preprint server for biology*

  Shah, S. R., Chen, Y., Leung, A. K., Navarro, P. V., Paramo, M. I., Gupta, J., Gurumurthy, A., Fite, R. F., Weimer, A. K., Du, Q., Mohyeldin, A. M., Egli, D., Creusot, et al

  2025

- **Sensitive, direct detection of non-coding off-target base editor unwinding and editing in primary cells.** *bioRxiv : the preprint server for biology*

  Wang, T., Jessa, S., Marinov, G. K., Klemm, S., Kundaje, A., Greenleaf, W. J.

  2025

- **Epigenomic landscape of single vascular cells reflects developmental origin and disease risk loci.** *Molecular systems biology*

  Weldy, C. S., Kundu, S., Monteiro, J., Gu, W., Pedroza, A. J., Dalal, A. R., Worssam, M. D., Li, D., Palmisano, B., Zhao, Q., Sharma, D., Nguyen, T., Kundu, et al

  2025

- **Enhancer-targeting CRISPR screens at coronary artery disease loci suggest shared mechanisms of disease risk.** *medRxiv : the preprint server for health sciences*

  Ramste, M., Weldy, C., Kundu, S., Zhao, Q., Li, D., Brand, K., Sharma, D., Ramste, A., Jagoda, E., Ray, J., Caceres, R. D., Galante, J., Gschwind, et al

  2025

- **Genetic risk factors modulate the association between physical activity and colorectal cancer.** *Research square*

  Peoples, A. R., Obón-Santacana, M., Kim, A. E., Kawaguchi, E. S., Fu, Y., Qu, C., Moratalla-Navarro, F., Morrison, J., Lin, Y., Arndt, V., Berndt, S. I., Bien, S. A., Bishop, et al

  2025

- **Achieving inclusive healthcare through integrating education and research with AI and personalized curricula.** *Communications medicine*

  Bahmani, A., Cha, K., Alavi, A., Dixit, A., Ross, A., Park, R., Goncalves, F., Ma, S., Saxman, P., Nair, R., Akhavan-Sarraf, R., Zhou, X., Wang, et al

  2025; 5 (1): 356

- **DART-Eval: A Comprehensive DNA Language Model Evaluation Benchmark on Regulatory DNA.** *ArXiv*
  Patel, A., Singhal, A., Wang, A., Pampari, A., Kasowski, M., Kundaje, A.
  2025
- **DART-Eval: A Comprehensive DNA Language Model Evaluation Benchmark on Regulatory DNA.** *ArXiv*
  Patel, A., Singhal, A., Wang, A., Pampari, A., Kasowski, M., Kundaje, A.
  2025
- **Cell type-specific purifying selection of synonymous mitochondrial DNA variation.** *Proceedings of the National Academy of Sciences of the United States of America*
  Lareau, C. A., Maschmeyer, P., Yin, Y., Gutierrez, J. C., Dhindsa, R. S., Gribling-Burrer, A. S., Zielinski, S., Hsieh, Y. H., Nitsch, L., Dimitrova, V., Nalbant, B., Buquicchio, F. A., Abay, et al
  2025; 122 (30): e2505704122
- **In vivo mapping of mutagenesis sensitivity of human enhancers.** *Nature*
  Kosicki, M., Zhang, B., Hecht, V., Pampari, A., Cook, L. E., Slaven, N., Akiyama, J. A., Plajzer-Frick, I., Novak, C. S., Kato, M., Tran, S., Hunter, R. D., von Maydell, et al
  2025
- **Red meat intake interacts with a TGF-β-pathway-based polygenic risk score to impact colorectal cancer risk: Application of a novel approach for polygenic risk score construction.** *medRxiv : the preprint server for health sciences*
  Mendez, J. S., Queme, B., Fu, Y., Morrison, J., Lewinger, J. P., Kawaguchi, E., Mi, H., Obón-Santacana, M., Moratalla-Navarro, F., Martín, V., Moreno, V., Lin, Y., Bien, et al
  2025
- **Multiomic profiling reveals that prostaglandin E2 reverses aged muscle stem cell dysfunction, leading to increased regeneration and strength.** *Cell stem cell*
  Wang, Y. X., Palla, A. R., Ho, A. T., Robinson, D. C., Ravichandran, M., Markov, G. J., Mai, T., Still, C. 2., Balsubramani, A., Nair, S., Holbrook, C. A., Yang, A. V., Kraft, et al
  2025
- **Deep learning guided design of cell type-specific AAV promoters**
  Wang, S. K., Nair, S., Deng, B., Ren, X., Shah, S., Kundaje, A., Chang, H. Y., Wang, S.
  ASSOC RESEARCH VISION OPHTHALMOLOGY INC.2025
- **Predicting expression-altering promoter mutations with deep learning.** *Science (New York, N.Y.)*
  Jaganathan, K., Ersaro, N., Novakovsky, G., Wang, Y., James, T., Schwartzentruber, J., Fiziev, P., Kassam, I., Cao, F., Hawe, J., Cavanagh, H., Lim, A., Png, et al
  2025: eads7373
- **The epigenomic landscape of single vascular cells reflects developmental origin and identifies disease risk loci.** *bioRxiv : the preprint server for biology*
  Weldy, C. S., Kundu, S., Monteiro, J., Gu, W., Pedroza, A. J., Dalal, A. R., Worssam, M. D., Li, D., Palmisano, B., Zhao, Q., Sharma, D., Nguyen, T., Kundu, et al
  2025
- **Rewriting regulatory DNA to dissect and reprogram gene expression.** *Cell*
  Martyn, G. E., Montgomery, M. T., Jones, H., Guo, K., Doughty, B. R., Linder, J., Bisht, D., Xia, F., Cai, X. S., Chen, Z., Cochran, K., Lawrence, K. A., Munson, et al
  2025
- **An updated compendium and reevaluation of the evidence for nuclear transcription factor occupancy over the mitochondrial genome.** *PloS one*
  Marinov, G. K., Ramalingam, V., Greenleaf, W. J., Kundaje, A.
  2025; 20 (3): e0318796
- **Single-cell multiome and enhancer connectome of human retinal pigment epithelium and choroid nominate pathogenic variants in age-related macular degeneration.** *bioRxiv : the preprint server for biology*
  Wang, S. K., Li, J., Nair, S., Korasaju, R., Chen, Y., Zhang, Y., Kundaje, A., Liu, Y., Wang, N., Chang, H. Y.
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