




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, Adam He, Ruchir Rastogi, Isaac Vock, Lei Xiong

Doctoral Dissertation Advisor (AC)

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

Orals Evaluator

Sanket Gupte, Aman Patel

Doctoral Dissertation Co-Advisor (AC)

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

Master's Program Advisor

Matthew Lau, Rohan Mehrotra, Isabel Michel, Jessie Ou, Sarah Smale, Miro Swisher, Emmy Thamakaison, Feiyang Zhu

Undergraduate Major Advisor

Aaryan Shah

Postdoctoral Research Mentor

Danila Bredikhin, Selin Jessa

Doctoral (Program)

Ziwei Chen, Anvita Gupta, Chiho Im, Aman Patel, 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
 - **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., Fietze, S., Harrow, J., Kaul, R., Khatun, J., Lajoie, B. R., Landt, et al
2012; 489 (7414): 57-74
 - **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
 - **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
 - **Multomics 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., Contrepolis, 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., Contrepolis, 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
- **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., Gribbling-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.
2025
- **CXCL12 drives natural variation in coronary artery anatomy across diverse populations.** *Cell*
Rios Coronado, P. E., Zhou, J., Fan, X., Zanetti, D., Naftaly, J. A., Prabala, P., Martínez Jaimes, A. M., Farah, E. N., Kundu, S., Deshpande, S. S., Evergreen, I., Kho, P. F., Ma, et al
2025
- **Transfer learning reveals sequence determinants of the quantitative response to transcription factor dosage.** *Cell genomics*
Naqvi, S., Kim, S., Tabatabaee, S., Pampari, A., Kundaje, A., Pritchard, J. K., Wysocka, J.
2025: 100780
- **Mapping the regulatory effects of common and rare non-coding variants across cellular and developmental contexts in the brain and heart.** *bioRxiv : the preprint server for biology*
Marderstein, A. R., Kundu, S., Padhi, E. M., Deshpande, S., Wang, A., Robb, E., Sun, Y., Yun, C. M., Pomales-Matos, D., Xie, Y., Nachun, D., Jessa, S., Kundaje, et al
2025

- **Publisher Correction: The ENCODE Imputation Challenge: a critical assessment of methods for cross-cell type imputation of epigenomic profiles.** *Genome biology*
Schreiber, J. M., Boix, C. A., Wook Lee, J., Li, H., Guan, Y., Chang, C. C., Chang, J. C., Hawkins-Hooker, A., Schölkopf, B., Schweikert, G., Carulla, M. R., Canakoglu, A., Guzzo, et al
2025; 26 (1): 31
- **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
- **Author Correction: Global loss of promoter-enhancer connectivity and rebalancing of gene expression during early colorectal cancer carcinogenesis.** *Nature cancer*
Zhu, Y., Lee, H., White, S., Weimer, A. K., Monte, E., Horning, A., Nevins, S. A., Esplin, E. D., Paul, K., Krieger, G., Shipony, Z., Chiu, R., Laquindanum, et al
2025
- **Artificial intelligence in molecular biology** *MOLECULAR CELL*
Kundaje, A., Pollard, K. S., Ma, J., Chang, X., Chen, M., Rohs, R.
2025; 85 (2): 193-198
- **ChromBPNet: bias factorized, base-resolution deep learning models of chromatin accessibility reveal cis-regulatory sequence syntax, transcription factor footprints and regulatory variants.** *bioRxiv : the preprint server for biology*
Pampari, A., Shcherbina, A., Kvon, E. Z., Kosicki, M., Nair, S., Kundu, S., Kathiria, A. S., Risca, V. I., Kuningas, K., Alasoo, K., Greenleaf, W. J., Pennacchio, L. A., Kundaje, et al
2025
- **Somatic Hypermutation Informed Vocabulary Encoder Representations**
Im, C., Mikelov, A., Zhao, R., Kundaje, A., Boyd, S. D.
edited by Knowles, D. A., Koo, P. K.
JMLR-JOURNAL MACHINE LEARNING RESEARCH.2025
- **An Expanded Registry of Candidate cis-Regulatory Elements for Studying Transcriptional Regulation.** *bioRxiv : the preprint server for biology*
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., Ganna, et al
2024
- **Molecular convergence of risk variants for congenital heart defects leveraging a regulatory map of the human fetal heart.** *medRxiv : the preprint server for health sciences*
Ma, X. R., Conley, S. D., Kosicki, M., Bredikhin, D., Cui, R., Tran, S., Sheth, M. U., Qiu, W. L., Chen, S., Kundu, S., Kang, H. Y., Amgalan, D., Munger, et al
2024
- **The chromatin landscape of the histone-possessing Bacteriovorax bacteria.** *Genome research*
Marinov, G. K., Doughty, B., Kundaje, A., Greenleaf, W. J.
2024
- **GENCODE 2025: reference gene annotation for human and mouse.** *Nucleic acids research*
Mudge, J. M., Carbonell-Sala, S., Diekhans, M., Martinez, J. G., Hunt, T., Jungreis, I., Loveland, J. E., Arnan, C., Barnes, I., Bennett, R., Berry, A., Bignell, A., Cerdán-Vélez, et al
2024
- **Deep Learning the Cis-Regulatory Code of Epigenomic Rewiring By Fusion Transcription Factors in Pediatric Leukemia**
Mani, S., Grubert, F., Gratzinger, D., Kundaje, A., Kasowski, M.
ELSEVIER.2024: 4993
- **GENCODE: massively expanding the lncRNA catalog through capture long-read RNA sequencing.** *bioRxiv : the preprint server for biology*
Kaur, G., Perteghella, T., Carbonell-Sala, S., Gonzalez-Martinez, J., Hunt, T., Mađry, T., Jungreis, I., Arnan, C., Lagarde, J., Borsari, B., Sisu, C., Jiang, Y., Bennett, et al
2024

- **Multomic analysis of familial adenomatous polyposis reveals molecular pathways associated with early tumorigenesis.** *Nature cancer*
Esplin, E. D., Hanson, C., Wu, S., Horning, A. M., Barapour, N., Nevins, S. A., Jiang, L., Contrepois, K., Lee, H., Guha, T. K., Hu, Z., Laquindanum, R., Mills, et al
2024
- **Global loss of promoter-enhancer connectivity and rebalancing of gene expression during early colorectal cancer carcinogenesis.** *Nature cancer*
Zhu, Y., Lee, H., White, S., Weimer, A. K., Monte, E., Horning, A., Nevins, S. A., Esplin, E. D., Paul, K., Krieger, G., Shipony, Z., Chiu, R., Laquindanum, et al
2024
- **An SLC12A9-dependent ion transport mechanism maintains lysosomal osmolarity.** *Developmental cell*
Levin-Konigsberg, R., Mitra, K., Spees, K., Nigam, A., Liu, K., Januel, C., Hivare, P., Arana, S. M., Prolo, L. M., Kundaje, A., Leonetti, M. D., Krishnan, Y., Bassik, et al
2024
- **IMPLICATION OF COMPLEX STRUCTURAL GENOME VARIATION IN THE GENETIC ARCHITECTURE OF NEUROPSYCHIATRIC DISORDERS: INSIGHTS FROM HUMAN POPULATION ANALYSIS AND FROM POSTMORTEM BRAINS OF INDIVIDUALS WITH PSYCHIATRIC DISORDERS**
Zhou, B., Arthur, J., Guo, H., Kim, T., Huang, Y., Pattni, R., Song, G., Palejev, D., Dohna, H., Roussos, P., Kundaje, A., Hallmayer, J., Snyder, et al
ELSEVIER.2024: 93
- **Characterization of additive gene-environment interactions for colorectal cancer risk.** *Epidemiology (Cambridge, Mass.)*
Thomas, C. E., Lin, Y., Kim, M., Kawaguchi, E. S., Qu, C., Um, C. Y., Lynch, B. M., Van Guelpen, B., Tsilidis, K., Carreras-Torres, R., van Duijnhoven, F. J., Sakoda, L. C., Campbell, et al
2024
- **Prediction and functional interpretation of inter-chromosomal genome architecture from DNA sequence with TwinC.** *bioRxiv : the preprint server for biology*
Jha, A., Hristov, B., Wang, X., Wang, S., Greenleaf, W. J., Kundaje, A., Aiden, E. L., Bertero, A., Noble, W. S.
2024
- **Mutagenesis Sensitivity Mapping of Human Enhancers In Vivo.** *bioRxiv : the preprint server for biology*
Kosicki, M., Zhang, B., Pampari, A., Akiyama, J. A., Plajzer-Frick, I., Novak, C. S., Tran, S., Zhu, Y., Kato, M., Hunter, R. D., von Maydell, K., Barton, S., Beckman, et al
2024
- **Flexible use of conserved motif vocabularies constrains genome access in cell type evolution.** *bioRxiv : the preprint server for biology*
Chai, C., Gibson, J., Li, P., Pampari, A., Patel, A., Kundaje, A., Wang, B.
2024
- **Deciphering the impact of genomic variation on function.** *Nature*
2024; 633 (8028): 47-57
- **Multiplexed single-cell characterization of alternative polyadenylation regulators.** *Cell*
Kowalski, M. H., Wessels, H. H., Linder, J., Dalgarno, C., Mascio, I., Choudhary, S., Hartman, A., Hao, Y., Kundaje, A., Satija, R.
2024
- **An updated compendium and reevaluation of the evidence for nuclear transcription factor occupancy over the mitochondrial genome.** *bioRxiv : the preprint server for biology*
Marinov, G. K., Ramalingam, V., Greenleaf, W. J., Kundaje, A.
2024
- **Two genome-wide interaction loci modify the association of nonsteroidal anti-inflammatory drugs with colorectal cancer.** *Science advances*
Drew, D. A., Kim, A. E., Lin, Y., Qu, C., Morrison, J., Lewinger, J. P., Kawaguchi, E., Wang, J., Fu, Y., Zemlianskaia, N., Díez-Obrero, V., Bien, S. A., Dimou, et al
2024; 10 (22): eadk3121
- **Dissecting the cis-regulatory syntax of transcription initiation with deep learning.** *bioRxiv : the preprint server for biology*
Cochran, K., Yin, M., Mantripragada, A., Schreiber, J., Marinov, G. K., Kundaje, A.
2024

- **Transfer learning reveals sequence determinants of the quantitative response to transcription factor dosage.** *bioRxiv : the preprint server for biology*
Naqvi, S., Kim, S., Tabatabaee, S., Pampari, A., Kundaje, A., Pritchard, J. K., Wysocka, J.
2024
- **Using a comprehensive atlas and predictive models to reveal the complexity and evolution of brain-active regulatory elements.** *Science advances*
Pratt, H. E., Andrews, G., Shedd, N., Phalke, N., Li, T., Pampari, A., Jensen, M., Wen, C., Consortium, P., Gandal, M. J., Geschwind, D. H., Gerstein, M., Moore, et al
2024; 10 (21): eadj4452
- **Application of established computational techniques to identify potential SARS-CoV-2 Nsp14-MTase inhibitors in low data regimes** *DIGITAL DISCOVERY*
Nigam, A., Hurley, M. F. D., Li, F., Konkolova, E., Klima, M., Trylcova, J., Pollice, R., Cinaroglu, S., Levin-Konigsberg, R., Handjaya, J., Schapira, M., Chau, I., Perveen, et al
2024
- **Genome-wide interaction study of dietary intake of fibre, fruits, and vegetables with risk of colorectal cancer.** *EBioMedicine*
Papadimitriou, N., Kim, A., Kawaguchi, E. S., Morrison, J., Diez-Obrero, V., Albanes, D., Berndt, S. I., Bézieau, S., Bien, S. A., Bishop, D. T., Bouras, E., Brenner, H., Buchanan, et al
2024; 104: 105146
- **Fine-mapping analysis including over 254,000 East Asian and European descendants identifies 136 putative colorectal cancer susceptibility genes.** *Nature communications*
Chen, Z., Guo, X., Tao, R., Huyghe, J. R., Law, P. J., Fernandez-Rozadilla, C., Ping, J., Jia, G., Long, J., Li, C., Shen, Q., Xie, Y., Timofeeva, et al
2024; 15 (1): 3557
- **Predicting chromatin conformation contact maps.** *bioRxiv : the preprint server for biology*
Min, A., Schreiber, J., Kundaje, A., Noble, W. S.
2024
- **Genetic risk impacts the association of menopausal hormone therapy with colorectal cancer risk.** *British journal of cancer*
Tian, Y., Lin, Y., Qu, C., Arndt, V., Baurley, J. W., Berndt, S. I., Bien, S. A., Bishop, D. T., Brenner, H., Buchanan, D. D., Budiarto, A., Campbell, P. T., Carreras-Torres, et al
2024
- **Multicenter integrated analysis of noncoding CRISPRi screens.** *Nature methods*
Yao, D., Tycko, J., Oh, J. W., Bounds, L. R., Gosai, S. J., Lataniotis, L., Mackay-Smith, A., Doughty, B. R., Gabdank, I., Schmidt, H., Guerrero-Altamirano, T., Siklenka, K., Guo, et al
2024
- **Protocol for mapping the three-dimensional organization of dinoflagellate genomes.** *STAR protocols*
Marinov, G. K., Kundaje, A., Greenleaf, W. J., Grossman, A. R.
2024; 5 (2): 102941
- **Author Correction: Advances and prospects for the Human BioMolecular Atlas Program (HuBMAP).** *Nature cell biology*
Jain, S., Pei, L., Spraggins, J. M., Angelo, M., Carson, J. P., Gehlenborg, N., Ginty, F., Goncalves, J. P., Hagood, J. S., Hickey, J. W., Kelleher, N. L., Laurent, L. C., Lin, et al
2024
- **CAGI, the Critical Assessment of Genome Interpretation, establishes progress and prospects for computational genetic variant interpretation methods** *GENOME BIOLOGY*
Jain, S., Bakolitsa, C., Brenner, S. E., Radivojac, P., Moul, J., Repo, S., Hoskins, R. A., Andreoletti, G., Barsky, D., Chellapan, A., Chu, H., Dabir, N., Kollipara, et al
2024; 25 (1): 53
- **Genome-wide interaction study with smoking for colorectal cancer risk identifies novel genetic loci related to tumor suppression, inflammation and immune response**
Carreras-Torres, R., Kim, A. E., Lin, Y., Diez-Obrero, V., Bien, S. A., Qu, C., Wang, J., Dimou, N., Aglago, E. K., Bouras, E., Campbell, P. T., Casey, G., Chang-Claude, et al
SPRINGER NATURE.2024: 772

- **DART-Eval: A Comprehensive DNA Language Model Evaluation Benchmark on Regulatory DNA**
Patel, A., Singhal, A., Wang, A., Pampari, A., Kasowski, M., Kundaje, A.
edited by Globerson, A., Mackey, L., Belgrave, D., Fan, A., Paquet, U., Tomczak, J., Zhang, C.
NEURAL INFORMATION PROCESSING SYSTEMS (NIPS).2024
- **Detection and analysis of complex structural variation in human genomes across populations and in brains of donors with psychiatric disorders** *Cell*
Zhou, B., Arthur, J. G., Guo, H., et al
2024; Published online September 30, 2024
- **Rewriting regulatory DNA to dissect and reprogram gene expression.** *bioRxiv : the preprint server for biology*
Martyn, G. E., Montgomery, M. T., Jones, H., Guo, K., Doughty, B. R., Linder, J., Chen, Z., Cochran, K., Lawrence, K. A., Munson, G., Pampari, A., Fulco, C. P., Kelley, et al
2023
- **Genome-wide gene-environment interaction analyses to understand the relationship between red meat and processed meat intake and colorectal cancer risk.** *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*
Stern, M. C., Sanchez Mendez, J., Kim, A. E., Obón-Santacana, M., Moratalla-Navarro, F., Martín, V., Moreno, V., Lin, Y., Bien, S. A., Qu, C., Su, Y. R., White, E., Harrison, et al
2023
- **Identification of constrained sequence elements across 239 primate genomes.** *Nature*
Kuderna, L. F., Ulirsch, J. C., Rashid, S., Ameen, M., Sundaram, L., Hickey, G., Cox, A. J., Gao, H., Kumar, A., Aguet, F., Christmas, M. J., Clawson, H., Haeussler, et al
2023
- **An encyclopedia of enhancer-gene regulatory interactions in the human genome.** *bioRxiv : the preprint server for biology*
Gschwind, A. R., Mualim, K. S., Karbalayghareh, A., Sheth, M. U., Dey, K. K., Jagoda, E., Nurtdinov, R. N., Xi, W., Tan, A. S., Jones, H., Ma, X. R., Yao, D., Nasser, et al
2023
- **Latent human herpesvirus 6 is reactivated in CAR T cells.** *Nature*
Lareau, C. A., Yin, Y., Maurer, K., Sandor, K. D., Daniel, B., Yagnik, G., Peña, J., Crawford, J. C., Spanjaart, A. M., Gutierrez, J. C., Haradhvala, N. J., Riberdy, J. M., Abay, et al
2023
- **The chromatin landscape of the euryarchaeon *Haloferax volcanii*.** *Genome biology*
Marinov, G. K., Bagdatli, S. T., Wu, T., He, C., Kundaje, A., Greenleaf, W. J.
2023; 24 (1): 253
- **Transcriptomics and chromatin accessibility in multiple African population samples.** *bioRxiv : the preprint server for biology*
DeGorter, M. K., Goddard, P. C., Karakoc, E., Kundu, S., Yan, S. M., Nachun, D., Abell, N., Aguirre, M., Carstensen, T., Chen, Z., Durrant, M., Dwaracherla, V. R., Feng, et al
2023
- **The landscape of the histone-organized chromatin of *Bdellovibrionota* bacteria.** *bioRxiv : the preprint server for biology*
Marinov, G. K., Doughty, B., Kundaje, A., Greenleaf, W. J.
2023
- **RNA polymerase II dynamics and mRNA stability feedback scale mRNA amounts with cell size.** *Cell*
Swaffer, M. P., Marinov, G. K., Zheng, H., Fuentes Valenzuela, L., Tsui, C. Y., Jones, A. W., Greenwood, J., Kundaje, A., Greenleaf, W. J., Reyes-Lamothe, R., Skotheim, J. M.
2023
- **CXCL12 regulates coronary artery dominance in diverse populations and links development to disease.** *medRxiv : the preprint server for health sciences*
Rios Coronado, P. E., Zanetti, D., Zhou, J., Naftaly, J. A., Prabala, P., Kho, P. F., Martínez Jaimes, A. M., Hilliard, A. T., Pyarajan, S., Dochtermann, D., Chang, K. M., Winn, V. D., Paşca, et al
2023

- **Drug Discovery in Low Data Regimes: Leveraging a Computational Pipeline for the Discovery of Novel SARS-CoV-2 Nsp14-MTase Inhibitors.** *bioRxiv : the preprint server for biology*
Nigam, A., Hurley, M. F., Li, F., Konkořová, E., Klíma, M., Trylčová, J., Pollice, R., Çinarođlu, S. S., Levin-Konigsberg, R., Handjaya, J., Schapira, M., Chau, I., Perveen, et al
2023
- **Short tandem repeats bind transcription factors to tune eukaryotic gene expression.** *Science (New York, N.Y.)*
Horton, C. A., Alexandari, A. M., Hayes, M. G., Marklund, E., Schaepe, J. M., Aditham, A. K., Shah, N., Suzuki, P. H., Shrikumar, A., Afek, A., Greenleaf, W. J., Gordân, R., Zeitlinger, et al
2023; 381 (6664): eadd1250
- **Genome-wide interaction analysis of folate for colorectal cancer risk.** *The American journal of clinical nutrition*
Bouras, E., Kim, A. E., Lin, Y., Morrison, J., Du, M., Albanes, D., Barry, E. L., Baurley, J. W., Berndt, S. I., Bien, S. A., Bishop, T. D., Brenner, H., Budiarto, et al
2023
- **Chromatin accessibility in the Drosophila embryo is determined by transcription factor pioneering and enhancer activation.** *Developmental cell*
Brennan, K. J., Weilert, M., Krueger, S., Pampari, A., Liu, H. Y., Yang, A. W., Morrison, J. A., Hughes, T. R., Rushlow, C. A., Kundaje, A., Zeitlinger, J.
2023
- **Advances and prospects for the Human BioMolecular Atlas Program (HuBMAP).** *Nature cell biology*
Jain, S., Pei, L., Spraggins, J. M., Angelo, M., Carson, J. P., Gehlenborg, N., Ginty, F., Gonçaves, J. P., Hagood, J. S., Hickey, J. W., Kelleher, N. L., Laurent, L. C., Lin, et al
2023
- **The ENCODE Uniform Analysis Pipelines.** *Research square*
Hitz, B. C., Lee, J. W., Jolanki, O., Kagda, M. S., Graham, K., Sud, P., Gabdank, I., Strattan, J. S., Sloan, C. A., Dreszer, T., Rowe, L. D., Podduturi, N. R., Malladi, et al
2023
- **Chromatin accessibility dynamics of neurogenic niche cells reveal defects in neural stem cell adhesion and migration during aging.** *Nature aging*
Yeo, R. W., Zhou, O. Y., Zhong, B. L., Sun, E. D., Navarro Negredo, P., Nair, S., Sharmin, M., Ruetz, T. J., Wilson, M., Kundaje, A., Dunn, A. R., Brunet, A.
2023
- **Single-cell multi-omics of mitochondrial DNA disorders reveals dynamics of purifying selection across human immune cells.** *Nature genetics*
Lareau, C. A., Dubois, S. M., Buquicchio, F. A., Hsieh, Y. H., Garg, K., Kautz, P., Nitsch, L., Praktijnjo, S. D., Maschmeyer, P., Verboon, J. M., Gutierrez, J. C., Yin, Y., Fiskin, et al
2023
- **Probing the diabetes and colorectal cancer relationship using gene - environment interaction analyses.** *British journal of cancer*
Dimou, N., Kim, A. E., Flanagan, O., Murphy, N., Diez-Obrero, V., Shcherbina, A., Aglago, E. K., Bouras, E., Campbell, P. T., Casey, G., Gallinger, S., Gruber, S. B., Jenkins, et al
2023
- **A genetic locus within the FMN1/GREM1 gene region interacts with body mass index in colorectal cancer risk.** *Cancer research*
Aglago, E. K., Kim, A. E., Lin, Y., Qu, C., Evangelou, M., Ren, Y., Morrison, J., Albanes, D., Arndt, V., Barry, E. L., Baurley, J. W., Berndt, S. I., Bien, et al
2023
- **De novo distillation of thermodynamic affinity from deep learning regulatory sequence models of in vivo protein-DNA binding.** *bioRxiv : the preprint server for biology*
Alexandari, A. M., Horton, C. A., Shrikumar, A., Shah, N., Li, E., Weilert, M., Pufall, M. A., Zeitlinger, J., Fordyce, P. M., Kundaje, A.
2023
- **CasKAS: direct profiling of genome-wide dCas9 and Cas9 specificity using ssDNA mapping.** *Genome biology*
Marinov, G. K., Kim, S. H., Bagdatli, S. T., Higashino, S. I., Trevino, A. E., Tycko, J., Wu, T., Bintu, L., Bassik, M. C., He, C., Kundaje, A., Greenleaf, W. J.

2023; 24 (1): 85

- **The ENCODE Imputation Challenge: a critical assessment of methods for cross-cell type imputation of epigenomic profiles.** *Genome biology*
Schreiber, J., Boix, C., Wook Lee, J., Li, H., Guan, Y., Chang, C. C., Chang, J. C., Hawkins-Hooker, A., Schölkopf, B., Schweikert, G., Carulla, M. R., Canakoglu, A., Guzzo, et al
2023; 24 (1): 79
- **The ENCODE Uniform Analysis Pipelines.** *bioRxiv : the preprint server for biology*
Hitz, B. C., Jin-Wook, L., Jolanki, O., Kagda, M. S., Graham, K., Sud, P., Gabdank, I., Strattan, J. S., Sloan, C. A., Dreszer, T., Rowe, L. D., Podduturi, N. R., Malladi, et al
2023
- **The polyclonal path to malignant transformation in familial adenomatous polyposis**
Schenck, R. O., Khan, A., Horning, A., Esplin, E. D., Monte, E., Wu, S., Hanson, C., Bararpour, N., Neves, S., Jiang, L., Contrepolis, K., Lee, H., Guha, et al
AMER ASSOC CANCER RESEARCH.2023
- **Genome-Wide Analyses Characterize Shared Heritability Among Cancers and Identify Novel Cancer Susceptibility Regions.** *Journal of the National Cancer Institute*
Lindström, S., Wang, L., Feng, H., Majumdar, A., Huo, S., Macdonald, J., Harrison, T., Turman, C., Chen, H., Mancuso, N., Bammler, T., Gallinger, S., Gruber, et al
2023
- **Aberrant phase separation is a common killing strategy of positively charged peptides in biology and human disease.** *bioRxiv : the preprint server for biology*
Boeynaems, S., Ma, X. R., Yeong, V., Ginell, G. M., Chen, J. H., Blum, J. A., Nakayama, L., Sanyal, A., Briner, A., Haver, D. V., Pauwels, J., Ekman, A., Schmidt, et al
2023
- **Author Correction: Deciphering colorectal cancer genetics through multi-omic analysis of 100,204 cases and 154,587 controls of European and east Asian ancestries.** *Nature genetics*
Fernandez-Rozadilla, C., Timofeeva, M., Chen, Z., Law, P., Thomas, M., Schmit, S., Diez-Obrero, V., Hsu, L., Fernandez-Tajes, J., Palles, C., Sherwood, K., Briggs, S., Svinti, et al
2023
- **CPA-Perturb-seq: Multiplexed single-cell characterization of alternative polyadenylation regulators.** *bioRxiv : the preprint server for biology*
Kowalski, M. H., Wessels, H., Linder, J., Choudhary, S., Hartman, A., Hao, Y., Mascio, I., Dalgarno, C., Kundaje, A., Satija, R.
2023
- **Single-Molecule Mapping of Chromatin Accessibility Using NOME-seq/dSMF.** *Methods in molecular biology (Clifton, N.J.)*
Hinks, M., Marinov, G. K., Kundaje, A., Bintu, L., Greenleaf, W. J.
2023; 2611: 101-119
- **TARTARUS: A Benchmarking Platform for Realistic And Practical Inverse Molecular Design**
Nigam, A., Pollice, R., Tom, G., Jorner, K., Willes, J., Thiede, L., Kundaje, A., Aspuru-Guzik, A.
edited by Oh, A., Neumann, T., Globerson, A., Saenko, K., Hardt, M., Levine, S.
NEURAL INFORMATION PROCESSING SYSTEMS (NIPS).2023
- **Simultaneous Single-Cell Profiling of the Transcriptome and Accessible Chromatin Using SHARE-seq.** *Methods in molecular biology (Clifton, N.J.)*
Kim, S. H., Marinov, G. K., Bagdatli, S. T., Higashino, S. I., Shipony, Z., Kundaje, A., Greenleaf, W. J.
2023; 2611: 187-230
- **Genome-Wide Mapping of Active Regulatory Elements Using ATAC-seq.** *Methods in molecular biology (Clifton, N.J.)*
Marinov, G. K., Shipony, Z., Kundaje, A., Greenleaf, W. J.
2023; 2611: 3-19
- **Genome-wide interaction study with smoking for colorectal cancer risk identifies novel genetic loci related to tumor suppression, inflammation and immune response.** *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*

- Carreras-Torres, R., Kim, A. E., Lin, Y., Díez-Obrero, V., Bien, S. A., Qu, C., Wang, J., Dimou, N., Aglago, E. K., Albanes, D., Arndt, V., Baurley, J. W., Berndt, et al
2022
- **Deciphering colorectal cancer genetics through multi-omic analysis of 100,204 cases and 154,587 controls of European and east Asian ancestries.** *Nature genetics*
Fernandez-Rozadilla, C., Timofeeva, M., Chen, Z., Law, P., Thomas, M., Schmit, S., Díez-Obrero, V., Hsu, L., Fernandez-Tajes, J., Palles, C., Sherwood, K., Briggs, S., Svinti, et al
2022
 - **GENCODE: reference annotation for the human and mouse genomes in 2023.** *Nucleic acids research*
Frankish, A., Carbonell-Sala, S., Diekhans, M., Jungreis, I., Loveland, J. E., Mudge, J. M., Sisu, C., Wright, J. C., Arnan, C., Barnes, I., Banerjee, A., Bennett, R., Berry, et al
2022
 - **Deciphering the impact of genetic variation on human polyadenylation using APARENT2.** *Genome biology*
Linder, J., Koplik, S. E., Kundaje, A., Seelig, G.
2022; 23 (1): 232
 - **The dynseq browser track shows context-specific features at nucleotide resolution.** *Nature genetics*
Nair, S., Barrett, A., Li, D., Raney, B. J., Lee, B. T., Kerpedjiev, P., Ramalingam, V., Pampari, A., Lekschas, F., Wang, T., Haeussler, M., Kundaje, A.
2022
 - **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)
 - **Automated sequence-based annotation and interpretation of the human genome.** *Nature genetics*
Kundaje, A., Meuleman, W.
2022
 - **Author Correction: Single-nucleus chromatin accessibility profiling highlights regulatory mechanisms of coronary artery disease risk.** *Nature genetics*
Turner, A. W., Hu, S. S., Mosquera, J. V., Ma, W. F., Hodonsky, C. J., Wong, D., Auguste, G., Song, Y., Sol-Church, K., Farber, E., Kundu, S., Kundaje, A., Lopez, et al
2022
 - **Single-cell analyses define a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer.** *Nature genetics*
Becker, W. R., Nevins, S. A., Chen, D. C., Chiu, R., Horning, A. M., Guha, T. K., Laquindanum, R., Mills, M., Chaib, H., Ladabaum, U., Longacre, T., Shen, J., Esplin, et al
2022
 - **Accelerating in-silico saturation mutagenesis using compressed sensing.** *Bioinformatics (Oxford, England)*
Schreiber, J., Nair, S., Balsubramani, A., Kundaje, A.
2022
 - **Single-nucleus chromatin accessibility profiling highlights regulatory mechanisms of coronary artery disease risk.** *Nature genetics*
Turner, A. W., Hu, S. S., Mosquera, J. V., Ma, W. F., Hodonsky, C. J., Wong, D., Auguste, G., Song, Y., Sol-Church, K., Farber, E., Kundu, S., Kundaje, A., Lopez, et al
2022
 - **Genome-Wide Interaction Analysis of Genetic Variants with Menopausal Hormone Therapy for Colorectal Cancer Risk.** *Journal of the National Cancer Institute*
Tian, Y., Kim, A. E., Bien, S. A., Lin, Y., Qu, C., Harrison, T., Carreras-Torres, R., Díez-Obrero, V., Dimou, N., Drew, D. A., Hidaka, A., Huyghe, J. R., Jordahl, et al
2022
 - **Author Correction: Expanded encyclopaedias of DNA elements in the human and mouse genomes.** *Nature*
ENCODE Project Consortium, Moore, J. E., Purcaro, M. J., Pratt, H. E., Epstein, C. B., Shores, N., Adrian, J., Kawli, T., Davis, C. A., Dobin, A., Kaul, R., Halow, J., Van Nostrand, E. L., et al

2022

- **Author Correction: Perspectives on ENCODE.** *Nature*
ENCODE Project Consortium, Snyder, M. P., Gingeras, T. R., Moore, J. E., Weng, Z., Gerstein, M. B., Ren, B., Hardison, R. C., Stamatoyannopoulos, J. A., Graveley, B. R., Feingold, E. A., Pazin, M. J., Pagan, M., et al
2022
- **Beyond GWAS of Colorectal Cancer: Evidence of Interaction with Alcohol Consumption and Putative Causal Variant for the 10q24.2 Region.** *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*
Jordahl, K. M., Shcherbina, A., Kim, A. E., Su, Y. R., Lin, Y., Wang, J., Qu, C., Albanes, D., Arndt, V., Baurley, J. W., Berndt, S. I., Bien, S. A., Bishop, et al
2022: OF1-OF13
- **fastISM: Performant in-silico saturation mutagenesis for convolutional neural networks.** *Bioinformatics (Oxford, England)*
Nair, S., Shrikumar, A., Schreiber, J., Kundaje, A.
2022
- **The chromatin organization of a chlorarachniophyte nucleomorph genome.** *Genome biology*
Marinov, G. K., Chen, X., Wu, T., He, C., Grossman, A. R., Kundaje, A., Greenleaf, W. J.
2022; 23 (1): 65
- **Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network (vol 12, 3279, 2021) NATURE COMMUNICATIONS**
Grapotte, M., Saraswat, M., Bessiere, C., Menichelli, C., Ramilowski, J. A., Severin, J., Hayashizaki, Y., Itoh, M., Tagami, M., Murata, M., Kojima-Ishiyama, M., Noma, S., Noguchi, et al
2022; 13 (1): 1200
- **MITI minimum information guidelines for highly multiplexed tissue images.** *Nature methods*
Schapiro, D., Yapp, C., Sokolov, A., Reynolds, S. M., Chen, Y., Sudar, D., Xie, Y., Muhlich, J., Arias-Camison, R., Arena, S., Taylor, A. J., Nikolov, M., Tyler, et al
2022; 19 (3): 262-267
- **Short tandem repeats recruit transcription factors to tune eukaryotic gene expression**
Horton, C. A., Alexandari, A. M., Hayes, M. G., Schaepe, J. M., Marklund, E., Shah, N., Aditham, A. K., Shrikumar, A., Afek, A., Greenleaf, W. J., Gordan, R., Zeitlinger, J., Kundaje, et al
CELL PRESS.2022: 287A-288A
- **Domain adaptive neural networks improve cross-species prediction of transcription factor binding.** *Genome research*
Cochran, K., Srivastava, D., Shrikumar, A., Balsubramani, A., Hardison, R. C., Kundaje, A., Mahony, S.
1800
- **ZEB2 Shapes the Epigenetic Landscape of Atherosclerosis** *Circulation*
Cheng, P., Wirka, R. C., Clarke, L., Zhao, Q., Kundu, R., Nguyen, T., Nair, S., Sharma, D., Kim, H., Shi, H., Assimes, T., Kim, J., Kundaje, et al
2022; 145 (6): 469-485
- **ZEB2 Shapes the Epigenetic Landscape of Atherosclerosis.** *Circulation*
Cheng, P., Wirka, R. C., Clarke, L. S., Zhao, Q., Kundu, R., Nguyen, T., Nair, S., Sharma, D., Kim, H. J., Shi, H., Assimes, T., Kim, J. B., Kundaje, et al
2022
- **The epigenomic landscape of single vascular cells reflects developmental origin and identifies disease risk loci** *bioRxiv*
Weldy, C. S., Cheng, P. P., Pedroza, A. J., Dalal, A. R., Sharma, D., Kim, H., Shi, H., Nguyen, T., Kundu, R. K., Fischbein, M. P., Quertermous, T.
2022
- **Single-Molecule Multikilobase-Scale Profiling of Chromatin Accessibility Using m6A-SMAC-Seq and m6A-CpG-GpC-SMAC-Seq.** *Methods in molecular biology (Clifton, N.J.)*
Marinov, G. K., Shipony, Z., Kundaje, A., Greenleaf, W. J.
2022; 2458: 269-298
- **A Congenital Anemia Reveals Distinct Targeting Mechanisms for Master Transcription Factor GATA1.** *Blood*

- Ludwig, L., Lareau, C. A., Bao, E. L., Liu, N., Utsugisawa, T., Tseng, A. M., Myers, S. A., Verboon, J. M., Ulirsch, J. C., Luo, W., Muus, C., Fiorini, C., Olive, et al
2022
- **Transcriptional and chromatin-based partitioning mechanisms uncouple protein scaling from cell size.** *Molecular cell*
Swaffer, M. P., Kim, J., Chandler-Brown, D., Langhinrichs, M., Marinov, G. K., Greenleaf, W. J., Kundaje, A., Schmolter, K. M., Skotheim, J. M.
2021
 - **Cell-specific Chromatin Landscape Of Human Coronary Artery Resolves Mechanisms Of Disease Risk**
Turner, A. W., Hu, S., Mosquera, J., Ma, W., Hodonsky, C. J., Wong, D., Auguste, G. E., Sol-Church, K., Farber, E., Kundu, S., Kundaje, A. B., Lopez, N. G., Ma, et al
LIPPINCOTT WILLIAMS & WILKINS.2021
 - **Cell-free DNA fragments inform epigenomic mechanisms for early detection of breast cancer.**
Gafni, E., Harvey, A., Jaroszewicz, A., Solari, O., Landolin, J., Barbirou, M., Miller, A., Tonellato, P. J., Kundaje, A., Jeffrey, S. S., Curtis, C., Sledge, G. W., Giresi, et al
AMER ASSOC CANCER RESEARCH.2021
 - **AP-1 is a temporally regulated dual gatekeeper of reprogramming to pluripotency.** *Proceedings of the National Academy of Sciences of the United States of America*
Markov, G. J., Mai, T., Nair, S., Shcherbina, A., Wang, Y. X., Burns, D. M., Kundaje, A., Blau, H. M.
2021; 118 (23)
 - **Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network** *NATURE COMMUNICATIONS*
Grapotte, M., Saraswat, M., Bessiere, C., Menichelli, C., Ramilowski, J. A., Severin, J., Hayashizaki, Y., Itoh, M., Tagami, M., Murata, M., Kojima-Ishiyamas, M., Noma, S., Noguchi, et al
2021; 12 (1): 3297
 - **Transcription-dependent domain-scale three-dimensional genome organization in the dinoflagellate *Breviolum minutum*.** *Nature genetics*
Marinov, G. K., Trevino, A. E., Xiang, T., Kundaje, A., Grossman, A. R., Greenleaf, W. J.
2021
 - **Publisher Correction: MTSplice predicts effects of genetic variants on tissue-specific splicing.** *Genome biology*
Cheng, J., Celik, M. H., Kundaje, A., Gagneur, J.
2021; 22 (1): 107
 - **Genome-wide enhancer maps link risk variants to disease genes.** *Nature*
Nasser, J., Bergman, D. T., Fulco, C. P., Guckelberger, P., Doughty, B. R., Patwardhan, T. A., Jones, T. R., Nguyen, T. H., Ulirsch, J. C., Lekschas, F., Mualim, K., Natri, H. M., Weeks, et al
2021
 - **Genetic effects on transcriptome profiles in colon epithelium provide functional insights for genetic risk loci.** *Cellular and molecular gastroenterology and hepatology*
Díez-Obrero, V. n., Dampier, C. H., Moratalla-Navarro, F. n., Devall, M. n., Plummer, S. J., Díez-Villanueva, A. n., Peters, U. n., Bien, S. n., Huyghe, J. R., Kundaje, A. n., Ibáñez-Sanz, G. n., Guinó, E. n., Obón-Santacana, et al
2021
 - **WILDS: A Benchmark of in-the-Wild Distribution Shifts**
Koh, P., Sagawa, S., Marklund, H., Xie, S., Zhang, M., Balsubramani, A., Hu, W., Yasunaga, M., Phillips, R., Gao, I., Lee, T., David, E., Stavness, et al
edited by Meila, M., Zhang, T.
JMLR-JOURNAL MACHINE LEARNING RESEARCH.2021
 - **Chromatin and gene-regulatory dynamics of the developing human cerebral cortex at single-cell resolution.** *Cell*
Trevino, A. E., Müller, F., Andersen, J., Sundaram, L., Kathiria, A., Shcherbina, A., Farh, K., Chang, H. Y., Paşca, A. M., Kundaje, A., Paşca, S. P., Greenleaf, W. J.
2021
 - **Learning cis-regulatory principles of ADAR-based RNA editing from CRISPR-mediated mutagenesis.** *Nature communications*
Liu, X., Sun, T., Shcherbina, A., Li, Q., Jarmoskaite, I., Kappel, K., Ramaswami, G., Das, R., Kundaje, A., Li, J. B.

2021; 12 (1): 2165

- **MTSplice predicts effects of genetic variants on tissue-specific splicing.** *Genome biology*
Cheng, J. n., Çelik, M. H., Kundaje, A. n., Gagneur, J. n.
2021; 22 (1): 94
- **Genetic architectures of proximal and distal colorectal cancer are partly distinct.** *Gut*
Huyghe, J. R., Harrison, T. A., Bien, S. A., Hampel, H. n., Figueiredo, J. C., Schmit, S. L., Conti, D. V., Chen, S. n., Qu, C. n., Lin, Y. n., Barfield, R. n., Baron, J. A., Cross, et al
2021
- **Landscape of cohesin-mediated chromatin loops in the human genome**
Grubert, F., Srivas, R., Spacek, D., Kasowski, M., Ruiz-Velasco, M., Sinnott-Armstrong, N., Greenside, P., Narasimha, A., Liu, Q., Geller, B., Sanghi, A., Kulik, M., Sa, et al
SPRINGER NATURE.2020: 72
- **Transparency and reproducibility in artificial intelligence.** *Nature*
Haibe-Kains, B., Adam, G. A., Hosny, A., Khodakarami, F., Massive Analysis Quality Control (MAQC) Society Board of Directors, Waldron, L., Wang, B., McIntosh, C., Goldenberg, A., Kundaje, A., Greene, C. S., Broderick, T., Hoffman, M. M., et al
2020; 586 (7829): E14–E16
- **Perspectives on ENCODE.** *Nature*
ENCODE Project Consortium, Snyder, M. P., Gingeras, T. R., Moore, J. E., Weng, Z., Gerstein, M. B., Ren, B., Hardison, R. C., Stamatoyannopoulos, J. A., Graveley, B. R., Feingold, E. A., Pazin, M. J., Pagan, M., et al
2020; 583 (7818): 693–98
- **The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution.** *Cell*
Rozenblatt-Rosen, O., Regev, A., Oberdoerffer, P., Nawy, T., Hupalowska, A., Rood, J. E., Ashenberg, O., Cerami, E., Coffey, R. J., Demir, E., Ding, L., Esplin, E. D., Ford, et al
2020; 181 (2): 236–49
- **CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities.** *Nature*
Han, K., Pierce, S. E., Li, A., Spees, K., Anderson, G. R., Seoane, J. A., Lo, Y. H., Dubreuil, M., Olivas, M., Kamber, R. A., Wainberg, M., Kostyrko, K., Kelly, et al
2020; 580 (7801): 136–141
- **CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities** *NATURE*
Han, K., Pierce, S. E., Li, A., Spees, K., Anderson, G. R., Seoane, J. A., Lo, Y., Dubreuil, M., Olivas, M., Kamber, R. A., Wainberg, M., Kostyrko, K., Kelly, et al
2020
- **Long-range single-molecule mapping of chromatin accessibility in eukaryotes.** *Nature methods*
Shipony, Z., Marinov, G. K., Swaffler, M. P., Sinnott-Armstrong, N. A., Skotheim, J. M., Kundaje, A., Greenleaf, W. J.
2020
- **Expanded encyclopaedias of DNA elements in the human and mouse genomes.** *Nature*
Moore, J. E., Purcaro, M. J., Pratt, H. E., Epstein, C. B., Shores, N. n., Adrian, J. n., Kawli, T. n., Davis, C. A., Dobin, A. n., Kaul, R. n., Halow, J. n., Van Nostrand, E. L., Freese, et al
2020; 583 (7818): 699–710
- **Maximum Likelihood with Bias-Corrected Calibration is Hard-To-Beat at Label Shift Adaptation**
Alexandari, A. M., Kundaje, A., Shrikumar, A.
edited by Daume, H., Singh, A.
JMLR-JOURNAL MACHINE LEARNING RESEARCH.2020
- **High-Throughput Discovery and Characterization of Human Transcriptional Effectors.** *Cell*
Tycko, J. n., DelRosso, N. n., Hess, G. T., Aradhana, n. n., Banerjee, A. n., Mukund, A. n., Van, M. V., Ego, B. K., Yao, D. n., Spees, K. n., Suzuki, P. n., Marinov, G. K., Kundaje, et al
2020
- **Landscape of cohesin-mediated chromatin loops in the human genome.** *Nature*

- Grubert, F. n., Srivas, R. n., Spacek, D. V., Kasowski, M. n., Ruiz-Velasco, M. n., Sinnott-Armstrong, N. n., Greenside, P. n., Narasimha, A. n., Liu, Q. n., Geller, B. n., Sanghi, A. n., Kulik, M. n., Sa, et al
2020; 583 (7818): 737–43
- **Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study.** *PLoS medicine*
Wainberg, M., Mahajan, A., Kundaje, A., McCarthy, M. I., Ingelsson, E., Sinnott-Armstrong, N., Rivas, M. A.
2019; 16 (12): e1002982
 - **NETWORK MODELLING OF TOPOLOGICAL DOMAINS USING HI-C DATA** *ANNALS OF APPLIED STATISTICS*
Wang, Y., Sarkar, P., Ursu, O., Kundaje, A., Bickel, P. J.
2019; 13 (3): 1511–36
 - **NETWORK MODELLING OF TOPOLOGICAL DOMAINS USING HI-C DATA.** *The annals of applied statistics*
Wang, Y. X., Sarkar, P., Ursu, O., Kundaje, A., Bickel, P. J.
2019; 13 (3): 1511-1536
 - **GkmExplain: fast and accurate interpretation of nonlinear gapped k-mer SVMs.** *Bioinformatics (Oxford, England)*
Shrikumar, A., Prakash, E., Kundaje, A.
2019; 35 (14): i173-i182
 - **Integrating regulatory DNA sequence and gene expression to predict genome-wide chromatin accessibility across cellular contexts.** *Bioinformatics (Oxford, England)*
Nair, S., Kim, D. S., Perricone, J., Kundaje, A.
2019; 35 (14): i108-i116
 - **Matrix stiffness induces a tumorigenic phenotype in mammary epithelium through changes in chromatin accessibility.** *Nature biomedical engineering*
Stowers, R. S., Shcherbina, A., Israeli, J., Gruber, J. J., Chang, J., Nam, S., Rabiee, A., Teruel, M. N., Snyder, M. P., Kundaje, A., Chaudhuri, O.
2019
 - **Predicting gene expression from plasma cell-free DNA using both the fragment length and fragment position**
St John, J. A., Gafni, E., White, B., Kannan, A., Hansen, L., Jaroszewicz, A., Kundaje, A., Boley, N.
AMER ASSOC CANCER RESEARCH.2019
 - **The ENCODE Blacklist: Identification of Problematic Regions of the Genome.** *Scientific reports*
Amemiya, H. M., Kundaje, A., Boyle, A. P.
2019; 9 (1): 9354
 - **The Kipoi repository accelerates community exchange and reuse of predictive models for genomics.** *Nature biotechnology*
Avsec, Z., Kreuzhuber, R., Israeli, J., Xu, N., Cheng, J., Shrikumar, A., Banerjee, A., Kim, D. S., Beier, T., Urban, L., Kundaje, A., Stegle, O., Gagneur, et al
2019
 - **Cell cycle dynamics of human pluripotent stem cells primed for differentiation.** *Stem cells (Dayton, Ohio)*
Shcherbina, A., Li, J., Narayanan, C., Greenleaf, W., Kundaje, A., Chetty, S.
2019
 - **Remodeling of epigenome and transcriptome landscapes with aging in mice reveals widespread induction of inflammatory responses** *GENOME RESEARCH*
Benayoun, B. A., Pollina, E. A., Singh, P., Mahmoudi, S., Harel, I., Casey, K. M., Dulken, B. W., Kundaje, A., Brunet, A.
2019; 29 (4): 697–709
 - **Initiation of mtDNA transcription is followed by pausing, and diverges across human cell types and during evolution (vol 27, pg 362, 2017)** *GENOME RESEARCH*
Blumberg, A., Rice, E. J., Kundaje, A., Danko, C. G., Mishmar, D.
2019; 29 (4): 710
 - **Measuring the reproducibility and quality of Hi-C data.** *Genome biology*
Yardimci, G. G., Ozadam, H., Sauria, M. E., Ursu, O., Yan, K., Yang, T., Chakraborty, A., Kaul, A., Lajoie, B. R., Song, F., Zhan, Y., Ay, F., Gerstein, et al

2019; 20 (1): 57

- **mtDNA Chromatin-like Organization Is Gradually Established during Mammalian Embryogenesis.** *iScience*
Marom, S., Blumberg, A., Kundaje, A., Mishmar, D.
2019; 12: 141–51
- **Deciphering regulatory DNA sequences and noncoding genetic variants using neural network models of massively parallel reporter assays.** *PLoS one*
Movva, R. n., Greenside, P. n., Marinov, G. K., Nair, S. n., Shrikumar, A. n., Kundaje, A. n.
2019; 14 (6): e0218073
- **Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements.** *Nature communications*
Tycko, J. n., Wainberg, M. n., Marinov, G. K., Ursu, O. n., Hess, G. T., Ego, B. K., Aradhana, n. n., Li, A. n., Truong, A. n., Trevino, A. E., Spees, K. n., Yao, D. n., Kaplow, et al
2019; 10 (1): 4063
- **Discovery of common and rare genetic risk variants for colorectal cancer.** *Nature genetics*
Huyghe, J. R., Bien, S. A., Harrison, T. A., Kang, H. M., Chen, S., Schmit, S. L., Conti, D. V., Qu, C., Jeon, J., Edlund, C. K., Greenside, P., Wainberg, M., Schumacher, et al
2018
- **Intertumoral Heterogeneity in SCLC Is Influenced by the Cell Type of Origin** *CANCER DISCOVERY*
Yang, D., Denny, S. K., Greenside, P. G., Chaikovsky, A. C., Brady, J. J., Ouadah, Y., Granja, J. M., Jahchan, N. S., Lim, J., Kwok, S., Kong, C. S., Berghoff, A. S., Schmitt, et al
2018; 8 (10): 1316–31
- **GenomeDISCO: a concordance score for chromosome conformation capture experiments using random walks on contact map graphs** *BIOINFORMATICS*
Ursu, O., Boley, N., Taranova, M., Wang, Y., Yardimci, G., Noble, W., Kundaje, A.
2018; 34 (16): 2701–7
- **A common pattern of DNase I footprinting throughout the human mtDNA unveils clues for a chromatin-like organization** *GENOME RESEARCH*
Blumberg, A., Danko, C. G., Kundaje, A., Mishmar, D.
2018; 28 (8): 1158–68
- **Decoding regulatory sequence across skin differentiation with deep learning**
Kim, D., Risca, V., Chappell, J., Shi, M., Zhao, Z., Jung, N., Chang, H., Snyder, M., Greenleaf, W., Kundaje, A., Khavari, P.
ELSEVIER SCIENCE INC.2018: S135
- **GenomeDISCO: A concordance score for chromosome conformation capture experiments using random walks on contact map graphs.** *Bioinformatics (Oxford, England)*
Ursu, O., Boley, N., Taranova, M., Wang, Y. X., Yardimci, G. G., Noble, W. S., Kundaje, A.
2018
- **ChIP-ping the branches of the tree: functional genomics and the evolution of eukaryotic gene regulation** *BRIEFINGS IN FUNCTIONAL GENOMICS*
Marinov, G. K., Kundaje, A.
2018; 17 (2): 116–37
- **Impact of regulatory variation across human iPSCs and differentiated cells** *GENOME RESEARCH*
Banovich, N. E., Li, Y. I., Raj, A., Ward, M. C., Greenside, P., Calderon, D., Tung, P., Burnett, J. E., Myrthil, M., Thomas, S. M., Burrows, C. K., Romero, I., Pavlovic, et al
2018; 28 (1): 122–31
- **Prediction of protein-ligand interactions from paired protein sequence motifs and ligand substructures.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
Greenside, P. n., Hillenmeyer, M. n., Kundaje, A. n.
2018; 23: 20–31
- **Umap and Bimap: quantifying genome and methylome mappability.** *Nucleic acids research*
Karimzadeh, M. n., Ernst, C. n., Kundaje, A. n., Hoffman, M. M.

2018; 46 (20): e120

- **Differential analysis of chromatin accessibility and histone modifications for predicting mouse developmental enhancers.** *Nucleic acids research*
Fu, S. n., Wang, Q. n., Moore, J. E., Purcaro, M. J., Pratt, H. E., Fan, K. n., Gu, C. n., Jiang, C. n., Zhu, R. n., Kundaje, A. n., Lu, A. n., Weng, Z. n.
2018; 46 (21): 11184–201
- **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
- **Chromatin accessibility dynamics reveal novel functional enhancers in *C. elegans*** *GENOME RESEARCH*
Daugherty, A. C., Yeo, R. W., Buenrostro, J. D., Greenleaf, W. J., Kundaje, A., Brunet, A.
2017; 27 (12): 2096–2107
- **Enrichment of colorectal cancer associations in functional regions: Insight for using epigenomics data in the analysis of whole genome sequence-imputed GWAS data** *PLOS ONE*
Bien, S. A., Auer, P. L., Harrison, T. A., Qu, C., Connolly, C. M., Greenside, P. G., Chen, S., Berndt, S. I., Bezieau, S., Kang, H. M., Huyghe, J., Brenner, H., Casey, et al
2017; 12 (11): e0186518
- **Vicus: Exploiting local structures to improve network-based analysis of biological data** *PLOS COMPUTATIONAL BIOLOGY*
Wang, B., Huang, L., Zhu, Y., Kundaje, A., Batzoglou, S., Goldenberg, A.
2017; 13 (10): e1005621
- **Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens** *NATURE COMMUNICATIONS*
Morgens, D. W., Wainberg, M., Boyle, E. A., Ursu, O., Araya, C. L., Tsui, C. K., Haney, M. S., Hess, G. T., Han, K., Jeng, E. E., Li, A., Snyder, M. P., Greenleaf, et al
2017; 8
- **Dynamic and stable enhancer-promoter contacts regulate epidermal terminal differentiation**
Lopez-Pajares, V., Rubin, A., Barajas, B., Furlan-Magaril, M., Mumbach, M., Greenleaf, W., Kundaje, A., Snyder, M., Chang, H., Fraser, P., Khavari, P. A.
ELSEVIER SCIENCE INC.2017: S80
- **Molecular definition of a metastatic lung cancer state reveals a targetable CD109-Janus kinase-Stat axis.** *Nature medicine*
Chuang, C., Greenside, P. G., Rogers, Z. N., Brady, J. J., Yang, D., Ma, R. K., Caswell, D. R., Chiou, S., Winters, A. F., Grüner, B. M., Ramaswami, G., Spencley, A. L., Kopecky, et al
2017; 23 (3): 291-300
- **Initiation of mtDNA transcription is followed by pausing, and diverges across human cell types and during evolution.** *Genome research*
Blumberg, A., Rice, E. J., Kundaje, A., Danko, C. G., Mishmar, D.
2017; 27 (3): 362-373
- **Predicting gene expression in massively parallel reporter assays: a comparative study.** *Human mutation*
Kreimer, A., Zeng, H., Edwards, M. D., Guo, Y., Tian, K., Shin, S., Welch, R., Wainberg, M., Mohan, R., Sinnott-Armstrong, N. A., Li, Y., Eraslan, G., Amin, et al
2017
- **An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues.** *Nature methods*
Corces, M. R., Trevino, A. E., Hamilton, E. G., Greenside, P. G., Sinnott-Armstrong, N. A., Vesuna, S. n., Satpathy, A. T., Rubin, A. J., Montine, K. S., Wu, B. n., Kathiria, A. n., Cho, S. W., Mumbach, et al
2017
- **Learning Important Features Through Propagating Activation Differences**
Shrikumar, A., Greenside, P., Kundaje, A.
edited by Precup, D., Teh, Y. W.
JMLR-JOURNAL MACHINE LEARNING RESEARCH.2017
- **Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation.** *Nature genetics*

- Rubin, A. J., Barajas, B. C., Furlan-Magaril, M. n., Lopez-Pajares, V. n., Mumbach, M. R., Howard, I. n., Kim, D. S., Boxer, L. D., Cairns, J. n., Spivakov, M. n., Wingett, S. W., Shi, M. n., Zhao, et al
2017; 49 (10): 1522–28
- **Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements.** *Nature genetics*
Mumbach, M. R., Satpathy, A. T., Boyle, E. A., Dai, C. n., Gowen, B. G., Cho, S. W., Nguyen, M. L., Rubin, A. J., Granja, J. M., Kazane, K. R., Wei, Y. n., Nguyen, T. n., Greenside, et al
2017
 - **High-Throughput Characterization of Cascade type I-E CRISPR Guide Efficacy Reveals Unexpected PAM Diversity and Target Sequence Preferences.** *Genetics*
Fu, B. X., Wainberg, M. n., Kundaje, A. n., Fire, A. Z.
2017; 206 (4): 1727–38
 - **An atlas of transcriptional, chromatin accessibility, and surface marker changes in human mesoderm development** *SCIENTIFIC DATA*
Koh, P. W., Sinha, R., Barkal, A. A., Morganti, R. M., Chen, A., Weissman, I. L., Ang, L. T., Kundaje, A., Loh, K. M.
2016; 3
 - **The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery** *CELL*
Stunnenberg, H. G., Hirst, M., Int Human Epigenome Consortium
2016; 167 (5): 1145-1149
 - **Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution.** *Nature genetics*
Corces, M. R., Buenrostro, J. D., Wu, B., Greenside, P. G., Chan, S. M., Koenig, J. L., Snyder, M. P., Pritchard, J. K., Kundaje, A., Greenleaf, W. J., Majeti, R., Chang, H. Y.
2016; 48 (10): 1193-1203
 - **Characterization of the direct targets of FOXO transcription factors throughout evolution.** *Aging cell*
Webb, A. E., Kundaje, A., Brunet, A.
2016; 15 (4): 673-685
 - **Mapping the Pairwise Choices Leading from Pluripotency to Human Bone, Heart, and Other Mesoderm Cell Types** *CELL*
Loh, K. M., Chen, A., Koh, P. W., Deng, T. Z., Sinha, R., Tsai, J. M., Barkal, A. A., Shen, K. Y., Jain, R., Morganti, R. M., Shyh-Chang, N., Fernhoff, N. B., George, et al
2016; 166 (2): 451-467
 - **Using functional data from Roadmap Epigenomics to inform analysis of rare variants linked to gene expression in a large colorectal cancer study**
Bien, S. A., Harrison, T. A., Auer, P. L., Qu, F., Huyghe, J., Banbury, B., Greenside, P., Abecasis, G. R., Berndt, S. I., Bezieau, S., Brenner, H., Casey, G., Chan, et al
AMER ASSOC CANCER RESEARCH.2016
 - **Impact of the X Chromosome and sex on regulatory variation** *GENOME RESEARCH*
Kukurba, K. R., Parsana, P., Balliu, B., Smith, K. S., Zappala, Z., Knowles, D. A., Fave, M., Davis, J. R., Li, X., Zhu, X., Potash, J. B., Weissman, M. M., Shi, et al
2016; 26 (6): 768-777
 - **An Arntl2-Driven Secretome Enables Lung Adenocarcinoma Metastatic Self-Sufficiency** *CANCER CELL*
Brady, J. J., Chuang, C., Greenside, P. G., Rogers, Z. N., Murray, C. W., Caswell, D. R., Hartmann, U., Connolly, A. J., Sweet-Cordero, E. A., Kundaje, A., Winslow, M. M.
2016; 29 (5): 697-710
 - **Unsupervised Learning from Noisy Networks with Applications to Hi-C Data**
Wang, B., Zhu, J., Ursu, O., Pourshafeie, A., Batzoglou, S., Kundaje, A.
edited by Lee, D. D., Sugiyama, M., Luxburg, U. V., Guyon, Garnett, R.
NEURAL INFORMATION PROCESSING SYSTEMS (NIPS).2016
 - **Regulatory analysis of the C. elegans genome with spatiotemporal resolution (vol 512, pg 400, 2014)** *NATURE*
Araya, C. L., Kawli, T., Kundaje, A., Jiang, L., Wu, B., Vafeados, D., Terrell, R., Weissdepp, P., Gevirtzman, L., Mace, D., Niu, W., Boyle, A. P., Xie, et al
2015; 528 (7580): 152

- **H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency (vol 158, pg 673, 2014) CELL**
Benayoun, B. A., Pollina, E. A., Ucar, D., Mahmoudi, S., Karra, K., Wong, E. D., Devarajan, K., Daugherty, A. C., Kundaje, A. B., Mancini, E., Hitz, B. C., Gupta, R., Rando, et al
2015; 163 (5): 1281-U264
- **Characterization of TCF21 Downstream Target Regions Identifies a Transcriptional Network Linking Multiple Independent Coronary Artery Disease Loci. PLoS genetics**
Sazonova, O., Zhao, Y., Nürnberg, S., Miller, C., Pjanic, M., Castano, V. G., Kim, J. B., Salfati, E. L., Kundaje, A. B., Bejerano, G., Assimes, T., Yang, X., Quertermous, et al
2015; 11 (5)
- **Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers. Nature genetics**
Onengut-Gumuscu, S., Chen, W., Burren, O., Cooper, N. J., Quinlan, A. R., Mychaleckyj, J. C., Farber, E., Bonnie, J. K., Szpak, M., Schofield, E., Achuthan, P., Guo, H., Fortune, et al
2015; 47 (4): 381-386
- **Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers NATURE GENETICS**
Onengut-Gumuscu, S., Chen, W., Burren, O., Cooper, N. J., Quinlan, A. R., Mychaleckyj, J. C., Farber, E., Bonnie, J. K., Szpak, M., Schofield, E., Achuthan, P., Guo, H., Fortune, et al
2015; 47 (4): 381-U199
- **Reassessment of Piwi Binding to the Genome and Piwi Impact on RNA Polymerase II Distribution DEVELOPMENTAL CELL**
Lin, H., Chen, M., Kundaje, A., Valouev, A., Yin, H., Liu, N., Neuenkirchen, N., Zhong, M., Snyder, M.
2015; 32 (6): 772-774
- **A comparative encyclopedia of DNA elements in the mouse genome NATURE**
Yue, F., Cheng, Y., Breschi, A., Vierstra, J., Wu, W., Ryba, T., Sandstrom, R., Ma, Z., Davis, C., Pope, B. D., Shen, Y., Pervouchine, D. D., Djebali, et al
2014; 515 (7527): 355-?
- **Principles of regulatory information conservation between mouse and human. Nature**
Cheng, Y., Ma, Z., Kim, B. H., Wu, W., Cayting, P., Boyle, A. P., Sundaram, V., Xing, X., Dogan, N., Li, J., Euskirchen, G., Lin, S., Lin, et al
2014; 515 (7527): 371-5
- **A comparative encyclopedia of DNA elements in the mouse genome. Nature**
Yue, F., Cheng, Y., Breschi, A., Vierstra, J., Wu, W., Ryba, T., Sandstrom, R., Ma, Z., Davis, C., Pope, B. D., Shen, Y., Pervouchine, D. D., Djebali, et al
2014; 515 (7527): 355-364
- **Principles of regulatory information conservation between mouse and human NATURE**
Cheng, Y., Ma, Z., Kim, B., Wu, W., Cayting, P., Boyle, A. P., Sundaram, V., Xing, X., Dogan, N., Li, J., Euskirchen, G., Lin, S., Lin, et al
2014; 515 (7527): 371-?
- **Transcription Factors Bind Negatively Selected Sites within Human mtDNA Genes GENOME BIOLOGY AND EVOLUTION**
Blumberg, A., Sailaja, B. S., Kundaje, A., Levin, L., Dadon, S., Shmorak, S., Shaulian, E., Meshorer, E., Mishmar, D.
2014; 6 (10): 2634-2646
- **Comparative analysis of regulatory information and circuits across distant species. Nature**
Boyle, A. P., Araya, C. L., Brdlik, C., Cayting, P., Cheng, C., Cheng, Y., Gardner, K., Hillier, L. W., Janette, J., Jiang, L., Kasper, D., Kawli, T., Kheradpour, et al
2014; 512 (7515): 453-456
- **Regulatory analysis of the C. elegans genome with spatiotemporal resolution. Nature**
Araya, C. L., Kawli, T., Kundaje, A., Jiang, L., Wu, B., Vafeados, D., Terrell, R., Weissdepp, P., Gevitzman, L., Mace, D., Niu, W., Boyle, A. P., Xie, et al
2014; 512 (7515): 400-405
- **Comparative analysis of metazoan chromatin organization. Nature**

- Ho, J. W., Jung, Y. L., Liu, T., Alver, B. H., Lee, S., Ikegami, K., Sohn, K., Minoda, A., Tolstorukov, M. Y., Appert, A., Parker, S. C., Gu, T., Kundaje, et al
2014; 512 (7515): 449-452
- **Regulatory analysis of the *C. elegans* genome with spatiotemporal resolution.** *Nature*
Araya, C. L., Kawli, T., Kundaje, A., Jiang, L., Wu, B., Vafeados, D., Terrell, R., Weissdepp, P., Gevirtzman, L., Mace, D., Niu, W., Boyle, A. P., Xie, et al
2014; 512 (7515): 400-405
 - **Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Kellis, M., Wold, B., Snyder, M. P., Bernstein, B. E., Kundaje, A., Marinov, G. K., Ward, L. D., Birney, E., Crawford, G. E., Dekker, J., Dunham, I., Elnitski, L. L., Farnham, et al
2014; 111 (33): E3366-E3366
 - **H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency.** *Cell*
Benayoun, B. A., Pollina, E. A., Ucar, D., Mahmoudi, S., Karra, K., Wong, E. D., Devarajan, K., Daugherty, A. C., Kundaje, A. B., Mancini, E., Hitz, B. C., Gupta, R., Rando, et al
2014; 158 (3): 673-688
 - **Diverse patterns of genomic targeting by transcriptional regulators in *Drosophila melanogaster*** *GENOME RESEARCH*
Slattery, M., Ma, L., Spokony, R. F., Arthur, R. K., Kheradpour, P., Kundaje, A., Negre, N., Crofts, A., Ptashkin, R., Zieba, J., Ostapenko, A., Suchy, S., Victorsen, et al
2014; 24 (7): 1224-1235
 - **Defining functional DNA elements in the human genome** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Kellis, M., Wold, B., Snyder, M. P., Bernstein, B. E., Kundaje, A., Marinov, G. K., Ward, L. D., Birney, E., Crawford, G. E., Dekker, J., Dunham, I., Elnitski, L. L., Farnham, et al
2014; 111 (17): 6131-6138
 - **Large-Scale Quality Analysis of Published ChIP-seq Data.** *G3 (Bethesda, Md.)*
Marinov, G. K., Kundaje, A., Park, P. J., Wold, B. J.
2014; 4 (2): 209-223
 - **STAT3 Targets Suggest Mechanisms of Aggressive Tumorigenesis in Diffuse Large B-Cell Lymphoma** *G3-GENES GENOMES GENETICS*
Hardee, J., Ouyang, Z., Zhang, Y., Kundaje, A., Lacroute, P., Snyder, M.
2013; 3 (12): 2173-2185
 - **Extensive Variation in Chromatin States Across Humans** *SCIENCE*
Kasowski, M., Kyriazopoulou-Panagiotopoulou, S., Grubert, F., Zaugg, J. B., Kundaje, A., Liu, Y., Boyle, A. P., Zhang, Q. C., Zakharia, F., Spacek, D. V., Li, J., Xie, D., Olarerin-George, et al
2013; 342 (6159): 750-752
 - **Integrative annotation of chromatin elements from ENCODE data** *NUCLEIC ACIDS RESEARCH*
Hoffman, M. M., Ernst, J., Wilder, S. P., Kundaje, A., Harris, R. S., Libbrecht, M., Giardine, B., Ellenbogen, P. M., Bilmes, J. A., Birney, E., Hardison, R. C., Dunham, I., Kellis, et al
2013; 41 (2): 827-841
 - **Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors**
Wang, J., Zhuang, J., Iyer, S., Lin, X., Whitfield, T. W., Greven, M. C., Pierce, B. G., Dong, X., Kundaje, A., Cheng, Y., Rando, O. J., Birney, E., Myers, et al
TAYLOR & FRANCIS INC.2013: 49-50
 - **Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors** *GENOME RESEARCH*
Wang, J., Zhuang, J., Iyer, S., Lin, X., Whitfield, T. W., Greven, M. C., Pierce, B. G., Dong, X., Kundaje, A., Cheng, Y., Rando, O. J., Birney, E., Myers, et al
2012; 22 (9): 1798-1812
 - **Long noncoding RNAs are rarely translated in two human cell lines** *GENOME RESEARCH*
Banfai, B., Jia, H., Khatun, J., Wood, E., Risk, B., Gundling, W. E., Kundaje, A., Gunawardena, H. P., Yu, Y., Xie, L., Krajewski, K., Strahl, B. D., Chen, et al

2012; 22 (9): 1646-1657

- **Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors** *GENOME BIOLOGY*
Yip, K. Y., Cheng, C., Bhardwaj, N., Brown, J. B., Leng, J., Kundaje, A., Rozowsky, J., Birney, E., Bickel, P., Snyder, M., Gerstein, M.
2012; 13 (9)
- **Modeling gene expression using chromatin features in various cellular contexts** *GENOME BIOLOGY*
Dong, X., Greven, M. C., Kundaje, A., Djebali, S., Brown, J. B., Cheng, C., Gingeras, T. R., Gerstein, M., Guigo, R., Birney, E., Weng, Z.
2012; 13 (9)
- **A User's Guide to the Encyclopedia of DNA Elements (ENCODE)** *PLOS BIOLOGY*
Myers, R. M., Stamatoyannopoulos, J., Snyder, M., Dunham, I., Hardison, R. C., Bernstein, B. E., Gingeras, T. R., Kent, W. J., Birney, E., Wold, B., Crawford, G. E., Bernstein, B. E., Epstein, et al
2011; 9 (4)
- **CP motifs, Hap1 and heme signaling**
Zhang, L., Leslie, C., Lee, H. C., Kundaje, A., Ie, E., Xin, X., Freund, Y., MEDIMOND
MEDIMOND S R L.2007: 45-+
- **A classification-based framework for predicting and analyzing gene regulatory response** *NIPS Workshop on New Problems and Methods in Computational Biology*
Kundaje, A., Middendorf, M., Shah, M., Wiggins, C. H., Freund, Y., Leslie, C.
BIOMED CENTRAL LTD.2006
- **Statistical analysis of MPSS measurements: Application to the study of LPS-activated macrophage gene expression** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Stolovitzky, G. A., Kundaje, A., Held, G. A., Duggar, K. H., Haudenschild, C. D., Zhou, D., Vasicek, T. J., Smith, K. D., Aderem, A., Roach, J. C.
2005; 102 (5): 1402-1407
- **Motif discovery through predictive modeling of gene regulation** *9th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2005)*
Middendorf, M., Kundaje, A., Shah, M., Freund, Y., Wiggins, C. H., Leslie, C.
SPRINGER-VERLAG BERLIN.2005: 538-552
- **Predicting genetic regulatory response using classification: Yeast stress response** *1st Annual RECOMB Satellite Workshop on Regulatory Genomics*
Middendorf, M., Kundaje, A., Wiggins, C., Freund, Y., Leslie, C.
SPRINGER-VERLAG BERLIN.2005: 1-13
- **Predicting genetic regulatory response using classification** *BIOINFORMATICS*
Middendorf, M., Kundaje, A., Wiggins, C., Freund, Y., Leslie, C.
2004; 20: 232-240
- **Support vector machine (SVM) classification of multifocal visual evoked potential responses (mfVEP) from Glaucoma patients.**
Baroumand, F., Kundaje, A. B., Zhang, Leslie, C., Hood, D. C.
ASSOC RESEARCH VISION OPHTHALMOLOGY INC.2004: U106
- **Spectrogram analysis of genomes** *EURASIP JOURNAL ON APPLIED SIGNAL PROCESSING*
Sussillo, D., Kundaje, A., Anastassiou, D.
2004; 2004 (1): 29-42