



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. His primary research area is large-scale computational regulatory genomics. The Kundaje lab specializes in developing statistical and machine learning methods for large-scale integrative analysis of heterogeneous, high-throughput functional genomic and genetic data to decipher regulatory elements and long-range regulatory interactions, learn predictive regulatory network models across individuals, cell-types and species and improve detection and interpretation of natural and disease-associated genetic variation. Previously as a postdoc at Stanford and Research Scientist at MIT, Anshul was the lead computational analyst of the ENCODE Project and the Roadmap Epigenomics Project. Anshul is also a recipient of the 2016 NIH Director's New Innovator Award and the 2014 Alfred Sloan Fellowship.

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

Our research focusses on development of statistical and machine learning methods for integrative analysis of diverse functional genomic and genetic data to learn models of gene regulation. We have led the analysis efforts of the Encyclopedia of DNA Elements (ENCODE) and The Roadmap Epigenomics Projects with the development of novel methods for

1. Adaptive thresholding and normalization of massive collections of functional genomic data (e.g. ChIP-seq and DNase-seq)
2. Dissecting combinatorial transcription factor co-occupancy within and across cell-types
3. Predicting cell-type specific enhancers from chromatin state profiles
4. Exploiting expression and chromatin co-dynamics with to predict enhancer-target gene links
5. Jointly modeling sequence grammars at regulatory elements and their chromatin state dynamics, expression changes of regulators and functional interaction data to learn unified multi-scale gene regulation programs
6. Elucidating the heterogeneity of chromatin architecture at regulatory elements
7. Improving the detection and interpretation of potentially causal disease-associated variants from Genome-wide association studies

More recently, we have also been developing methods to

1. Decipher the functional heterogeneity of transcription factor binding
2. Learn long-range, three-dimensional regulatory interactions
3. Infer causal regulatory mechanisms by integrating diverse functional genomic data from temporal (e.g. differentiation/reprogramming) and perturbation (e.g. drug response, knockdown, genome-editing) experiments
4. Model the complex relationships between genetic variation, regulatory chromatin variation and expression variation in healthy and diseased individuals
5. Deep learning frameworks for genomics

PROJECTS

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

Teaching

COURSES

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)

2021-22

- Cloud Computing for Biology and Healthcare: BIOMEDIN 222, CS 273C, GENE 222 (Spr)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

2020-21

- Big Data for Biologists - Decoding Genomic Function: HUMBIO 51 (Sum)
- 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 (Aut)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Chew Chai, Meena Chakraborty, Benjamin Doughty, Jesse Gibson, Tami Gjorgjieva, Renee Hastings, Michael Hayes, Naz Koska, Robin Meyers, Michael Montgomery, Adi Xiyal Mukund, Eun Sun Song, Nate Stockham, Peter Suzuki, Alp Tartici, Raeline Valbuena, Kevin Wu

Postdoctoral Faculty Sponsor

Jacob Schreiber, Lei Xiong, Boyang Zhang

Doctoral Dissertation Advisor (AC)

Akshat Nigam, Chang M. Yun, Maxim Zaslavsky

Orals Evaluator

Maxim Zaslavsky

Master's Program Advisor

Kaushal Alate, Rohan Mehrotra, Isabel Michel, Nikesh Mishra, Sanjay Nagaraj, Rashon Poole, Eva Prakash, Sarah Smale, Jessica Yang

Doctoral Dissertation Co-Advisor (AC)

Sanket Gupte, Minji Kang, Shouvik Mani, Esther Robb, Arpita Singhal, Kyle Swanson, Jason Tan, Xikun Zhang

Postdoctoral Research Mentor

Danila Bredikhin, Selin Jessa

Doctoral (Program)

Ziwei Chen, Kelly Cochran, Chiho Im, Soumya Kundu, Akshat Nigam, Anusri Pampari, Aman Patel, Austin Wang, Maxim Zaslavsky

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Masters Program)
- Biomedical Informatics (Phd Program)
- Genetics (Phd Program)

Publications

PUBLICATIONS

- **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. 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
 - **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. 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
SPRINGERNATURE.2024: 772
 - **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
 - **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., Konko#ová, E., Klíma, M., Tryl#ová, J., Pollice, R., Çınaro#lu, 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., Gordán, 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
 - **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
 - **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., Gonçalves, J. P., Hagood, J. S., Hickey, J. W., Kelleher, N. L., Laurent, L. C., Lin, 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
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