Stanford

Anshul Kundaje

Assistant Professor of Genetics and of Computer Science

Bio

BIO

Anshul Kundaje is an Assistant 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

- Assistant Professor, Genetics
- Assistant Professor, Computer Science
- Member, Bio-X
- 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, NIH Director's Advisory Committee for Artificial Intelligence in Biomedical Research (2019 - present)

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 mechansisms 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

2019-20

- Big Data for Biologists - Decoding Genomic Function: HUMBIO 51 (Aut)
- 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)
- Statistical and Machine Learning Methods for Genomics: BIO 268 (Win)

2018-19

- Big Data for Biologists - Decoding Genomic Function: HUMBIO 51 (Aut)
- 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)

2017-18

- Advanced Genetics: GENE 205 (Win)
- Big Data for Biologists - Decoding Genomic Function: HUMBIO 51 (Aut)
- Deep Learning in Genomics and Biomedicine: BIODS 237, BIOMEDIN 273B, CS 273B, GENE 236 (Aut)

2016-17

- Advanced Genetics: GENE 205 (Win)
- Deep Learning in Genomics and Biomedicine: BIOMEDIN 273B, CS 273B (Aut)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)
- Statistical and Machine Learning Methods for Genomics: BIO 268, BIOMEDIN 245, CS 373, GENE 245, STATS 345 (Spr)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Matthew Buckley, Brayon Fremin, Naz Koska, Ragini Phansalkar, Tyler Shimko, Nate Stockham

Postdoctoral Faculty Sponsor

Akshay Balsubramani, Anthony Cesnik, Mahfuza Sharmin

Doctoral Dissertation Advisor (AC)

Abhimanyu Banerjee, Chris Probert, Anna Shcherbina, Avanti Shrikumar

Master's Program Advisor

Tom Jin, Santosh Murugan, Camilo Ruiz, Samir Sen, Ryan Tolsma, Yulian Zhou

Doctoral Dissertation Co-Advisor (AC)

Daniel Kim, Xin Zhou

Doctoral (Program)

Amr Alexandari, Soumya Kundu, Avanti Shrikumar, Alex Tseng

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

Publications

PUBLICATIONS

- **GkmExplain: fast and accurate interpretation of nonlinear gapped k-mer SVMs**
  Shrikumar, A., Prakash, E., Kundaje, A.
  OXFORD UNIV PRESS.2019: I173–I182
- **Integrating regulatory DNA sequence and gene expression to predict genome-wide chromatin accessibility across cellular contexts**
  Nair, S., Kim, D. S., Perricone, J., Kundaje, A.
  OXFORD UNIV PRESS.2019: 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
- **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

- **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
- **Measuring the reproducibility and quality of Hi-C data** *GENOME BIOLOGY*
  Yardimci, G., Ozadam, H., Sauria, M. G., Ursu, O., Yan, K., Yang, T., Chakraborty, A., Kaul, A., Lajoie, B. R., Song, F., Zhan, Y., Ay, F., Gerstein, et al
  2019; 20
- **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
- **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. P., Mahmoudi, S., Harel, I., Casey, K. M., Dulken, B. W., Kundaje, A., Brunet, A.
  2019
- **mtDNA Chromatin-like Organization Is Gradually Established during Mammalian Embryogenesis** *ISCIENCE*
  Marom, S., Blumberg, A., Kundaje, A., Mishmar, D.
  2019; 12: 141-+
- **mtDNA Chromatin-like Organization Is Gradually Established during Mammalian Embryogenesis.** *iScience*
  Marom, S., Blumberg, A., Kundaje, A., Mishmar, D.
  2019; 12: 141–51
- **Discovery of common and rare genetic risk variants for colorectal cancer** *NATURE GENETICS*
  Huyghe, J. R., Bien, S. A., Harrison, T. A., Kang, H., Chen, S., Schmit, S. L., Conti, D. V., Qu, C., Jeon, J., Edlund, C. K., Greenside, P., Wainberg, M., Schumacher, et al
  2019; 51 (1): 76-+
- **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
- **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
- **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., Björkegren, J. L., Im, H. K., Pasaniuc, et al
  2019; 51 (4): 592–99
- **Deciphering regulatory DNA sequences and noncoding genetic variants using neural network models of massively parallel reporter assays.** *PloS one*
  Movva, R., Greenside, P., Marinov, G. K., Nair, S., Shrikumar, A., Kundaje, A.
  2019; 14 (6): e0218073
- **Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements.** *Nature communications*
  Tycko, J., Wainberg, M., Marinov, G. K., Ursu, O., Hess, G. T., Ego, B. K., Li, A., Truong, A., Trevino, A. E., Spees, K., Yao, D., Kaplow, I. M., Greenside, 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

- **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. S., Kwok, S., Kong, C. S., Berghoff, A. S., Schmitt, et al

  2018

- **Discovering epistatic feature interactions from neural network models of regulatory DNA sequences**

  Greenside, P., Shimko, T., Fordyce, P., Kundaje, A.

  OXFORD UNIV PRESS.2018: 629–37

- **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

- **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)

- **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., Hillenmeyer, M., Kundaje, A.

  2018; 23: 20–31

- **Umap and Bismap: quantifying genome and methylome mappability.** *Nucleic acids research*

  Karimzadeh, M., Ernst, C., Kundaje, A., 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., Wang, Q., Moore, J. E., Purcaro, M. J., Pratt, H. E., Fan, K., Gu, C., Jiang, C., Zhu, R., Kundaje, A., Lu, A., Weng, Z.

  2018; 46 (21): 11184–201

- **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

- **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

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

- **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

- **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

- **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

- **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., Satpathy, A. T., Rubin, A. J., Montine, K. S., Wu, B., Kathiria, A., Cho, S. W., Mumbach, et al
  2017

- **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

- **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., Gowen, B. G., Cho, S. W., Nguyen, M. L., Rubin, A. J., Granja, J. M., Kazane, K. R., Wei, Y., Nguyen, T., Greenside, et al
  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., Lopez-Pajares, V., Mumbach, M. R., Howard, I., Kim, D. S., Boxer, L. D., Cairns, J., Spivakov, M., Wingett, S. W., Shi, M., Zhao, et al
  2017; 49 (10): 1522–28

- **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., Kundaje, A., 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

- **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

- **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., Lee, D. D., Sugiyama, M., Luxburg, U. V., Guyon, Garnett, R.
  NEURAL INFORMATION PROCESSING SYSTEMS (NIPS).2016

- **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

- **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

- **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

- **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

- **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-?

- **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

- **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*
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