

# Anshul Kundaje

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

153 papers	31,700 citations	55 h-index	178 g-index
189 ext. papers	42,327 ext. citations	21.2 avg, IF	8.26 L-index

#	Paper	IF	Citations
153	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , <b>2012</b> , 489, 57-74	50.4	11449
152	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , <b>2015</b> , 518, 317-30	50.4	3849
151	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , <b>2012</b> , 22, 1813-31	9.7	1211
150	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , <b>2012</b> , 489, 91-100	50.4	1104
149	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , <b>2011</b> , 9, e1001046	9.7	1060
148	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , <b>2014</b> , 515, 355-64	50.4	1026
147	Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , <b>2018</b> , 15,	4.1	780
146	An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. <i>Nature Methods</i> , <b>2017</b> , 14, 959-962	21.6	727
145	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. <i>Genome Research</i> , <b>2012</b> , 22, 1798-812	9.7	596
144	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. <i>Nature Genetics</i> , <b>2016</b> , 48, 1193-203	36.3	555
143	Linking disease associations with regulatory information in the human genome. <i>Genome Research</i> , <b>2012</b> , 22, 1748-59	9.7	538
142	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 6131-8	11.5	490
141	Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers. <i>Nature Genetics</i> , <b>2015</b> , 47, 381-6	36.3	414
140	Conserved epigenomic signals in mice and humans reveal immune basis of Alzheimer's disease. <i>Nature</i> , <b>2015</b> , 518, 365-9	50.4	390
139	Integrative annotation of chromatin elements from ENCODE data. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 827-41	10.1	383
138	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , <b>2020</b> , 583, 699-710	50.4	360
137	The ENCODE Blacklist: Identification of Problematic Regions of the Genome. <i>Scientific Reports</i> , <b>2019</b> , 9, 9354	4.9	319

136	Long noncoding RNAs are rarely translated in two human cell lines. <i>Genome Research</i> , <b>2012</b> , 22, 1646-57	9.7	292
135	H3K4me3 breadth is linked to cell identity and transcriptional consistency. <i>Cell</i> , <b>2014</b> , 158, 673-88	56.2	278
134	Extensive variation in chromatin states across humans. <i>Science</i> , <b>2013</b> , 342, 750-2	33.3	276
133	Opportunities and challenges for transcriptome-wide association studies. <i>Nature Genetics</i> , <b>2019</b> , 51, 592-599	36.3	266
132	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , <b>2014</b> , 512, 449-52	50.4	265
131	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. <i>Nature Genetics</i> , <b>2017</b> , 49, 1602-1612	36.3	253
130	Mapping the Pairwise Choices Leading from Pluripotency to Human Bone, Heart, and Other Mesoderm Cell Types. <i>Cell</i> , <b>2016</b> , 166, 451-467	56.2	242
129	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , <b>2015</b> , 162, 1051-65	56.2	240
128	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , <b>2016</b> , 167, 1145-1149	56.2	232
127	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. <i>Genome Biology</i> , <b>2012</b> , 13, R48	18.3	194
126	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , <b>2014</b> , 515, 371-375	50.4	190
125	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , <b>2012</b> , 13, R53	18.3	182
124	Discovery of common and rare genetic risk variants for colorectal cancer. <i>Nature Genetics</i> , <b>2019</b> , 51, 76-83	36.3	177
123	Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation. <i>Nature Genetics</i> , <b>2017</b> , 49, 1522-1528	36.3	158
122	Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens. <i>Nature Communications</i> , <b>2017</b> , 8, 15178	17.4	148
121	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , <b>2020</b> , 181, 236-249	56.2	140
120	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , <b>2014</b> , 512, 453-6	50.4	135
119	Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. <i>Genome Research</i> , <b>2012</b> , 22, 1735-47	9.7	129

118	Characterization of the direct targets of FOXO transcription factors throughout evolution. <i>Aging Cell</i> , <b>2016</b> , 15, 673-85	9.9	116
117	Remodeling of epigenome and transcriptome landscapes with aging in mice reveals widespread induction of inflammatory responses. <i>Genome Research</i> , <b>2019</b> , 29, 697-709	9.7	104
116	CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities. <i>Nature</i> , <b>2020</b> , 580, 136-141	9.4	96
115	Large-scale quality analysis of published ChIP-seq data. <i>G3: Genes, Genomes, Genetics</i> , <b>2014</b> , 4, 209-23	3.2	90
114	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , <b>2020</b> , 586, E14-E16	50.4	85
113	Regulatory analysis of the <i>C. elegans</i> genome with spatiotemporal resolution. <i>Nature</i> , <b>2014</b> , 512, 400-5	50.4	81
112	Chromatin accessibility dynamics reveal novel functional enhancers in. <i>Genome Research</i> , <b>2017</b> , 27, 2096-2107	21.07	79
111	Molecular definition of a metastatic lung cancer state reveals a targetable CD109-Janus kinase-Stat axis. <i>Nature Medicine</i> , <b>2017</b> , 23, 291-300	50.5	77
110	Impact of regulatory variation across human iPSCs and differentiated cells. <i>Genome Research</i> , <b>2018</b> , 28, 122-131	9.7	70
109	The Kipoi repository accelerates community exchange and reuse of predictive models for genomics. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 592-600	44.5	69
108	Intertumoral Heterogeneity in SCLC Is Influenced by the Cell Type of Origin. <i>Cancer Discovery</i> , <b>2018</b> , 8, 1316-1331	24.4	65
107	Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , <b>2019</b> , 20, 57	18.3	62
106	Perspectives on ENCODE. <i>Nature</i> , <b>2020</b> , 583, 693-698	50.4	61
105	Matrix stiffness induces a tumorigenic phenotype in mammary epithelium through changes in chromatin accessibility. <i>Nature Biomedical Engineering</i> , <b>2019</b> , 3, 1009-1019	19	60
104	Base-resolution models of transcription-factor binding reveal soft motif syntax. <i>Nature Genetics</i> , <b>2021</b> , 53, 354-366	36.3	60
103	Impact of the X Chromosome and sex on regulatory variation. <i>Genome Research</i> , <b>2016</b> , 26, 768-77	9.7	59
102	Predicting genetic regulatory response using classification. <i>Bioinformatics</i> , <b>2004</b> , 20 Suppl 1, i232-40	7.2	58
101	Single-cell epigenomic analyses implicate candidate causal variants at inherited risk loci for Alzheimer's and Parkinson's diseases. <i>Nature Genetics</i> , <b>2020</b> , 52, 1158-1168	36.3	58

100	An Arntl2-Driven Secretome Enables Lung Adenocarcinoma Metastatic Self-Sufficiency. <i>Cancer Cell</i> , <b>2016</b> , 29, 697-710	24.3	57
99	Umap and Bimap: quantifying genome and methylome mappability. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e120	20.1	57
98	Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. <i>Nature Communications</i> , <b>2019</b> , 10, 4063	17.4	49
97	Statistical analysis of MPSS measurements: application to the study of LPS-activated macrophage gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 1402-7	11.5	46
96	Opportunities and obstacles for deep learning in biology and medicine		45
95	Genome-wide enhancer maps link risk variants to disease genes. <i>Nature</i> , <b>2021</b> , 593, 238-243	50.4	45
94	GenomeDISCO: a concordance score for chromosome conformation capture experiments using random walks on contact map graphs. <i>Bioinformatics</i> , <b>2018</b> , 34, 2701-2707	7.2	38
93	Discovering epistatic feature interactions from neural network models of regulatory DNA sequences. <i>Bioinformatics</i> , <b>2018</b> , 34, i629-i637	7.2	38
92	Landscape of cohesin-mediated chromatin loops in the human genome. <i>Nature</i> , <b>2020</b> , 583, 737-743	50.4	37
91	Characterization of TCF21 Downstream Target Regions Identifies a Transcriptional Network Linking Multiple Independent Coronary Artery Disease Loci. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005202	6	36
90	Long-range single-molecule mapping of chromatin accessibility in eukaryotes. <i>Nature Methods</i> , <b>2020</b> , 17, 319-327	21.6	36
89	Transcription factors bind negatively selected sites within human mtDNA genes. <i>Genome Biology and Evolution</i> , <b>2014</b> , 6, 2634-46	3.9	36
88	A predictive model of the oxygen and heme regulatory network in yeast. <i>PLoS Computational Biology</i> , <b>2008</b> , 4, e1000224	5	36
87	Denoising genome-wide histone ChIP-seq with convolutional neural networks. <i>Bioinformatics</i> , <b>2017</b> , 33, i225-i233	7.2	34
86	Spectrogram Analysis of Genomes. <i>Eurasip Journal on Advances in Signal Processing</i> , <b>2004</b> , 2004, 1	1.9	32
85	Deciphering regulatory DNA sequences and noncoding genetic variants using neural network models of massively parallel reporter assays. <i>PLoS ONE</i> , <b>2019</b> , 14, e0218073	3.7	27
84	Diverse patterns of genomic targeting by transcriptional regulators in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , <b>2014</b> , 24, 1224-35	9.7	27
83	An atlas of transcriptional, chromatin accessibility, and surface marker changes in human mesoderm development. <i>Scientific Data</i> , <b>2016</b> , 3, 160109	8.2	27

82	Reverse-complement parameter sharing improves deep learning models for genomics		26
81	Chromatin and gene-regulatory dynamics of the developing human cerebral cortex at single-cell resolution. <i>Cell</i> , <b>2021</b> , 184, 5053-5069.e23	56.2	26
80	Integrating regulatory DNA sequence and gene expression to predict genome-wide chromatin accessibility across cellular contexts. <i>Bioinformatics</i> , <b>2019</b> , 35, i108-i116	7.2	24
79	STAT3 targets suggest mechanisms of aggressive tumorigenesis in diffuse large B-cell lymphoma. <i>G3: Genes, Genomes, Genetics</i> , <b>2013</b> , 3, 2173-85	3.2	24
78	Predicting gene expression in massively parallel reporter assays: A comparative study. <i>Human Mutation</i> , <b>2017</b> , 38, 1240-1250	4.7	23
77	Initiation of mtDNA transcription is followed by pausing, and diverges across human cell types and during evolution. <i>Genome Research</i> , <b>2017</b> , 27, 362-373	9.7	22
76	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E3366	11.5	22
75	A genome-wide atlas of co-essential modules assigns function to uncharacterized genes. <i>Nature Genetics</i> , <b>2021</b> , 53, 638-649	36.3	20
74	Differential analysis of chromatin accessibility and histone modifications for predicting mouse developmental enhancers. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 11184-11201	20.1	18
73	High-Throughput Characterization of Cascade type I-E CRISPR Guide Efficacy Reveals Unexpected PAM Diversity and Target Sequence Preferences. <i>Genetics</i> , <b>2017</b> , 206, 1727-1738	4	16
72	GkmExplain: fast and accurate interpretation of nonlinear gapped k-mer SVMs. <i>Bioinformatics</i> , <b>2019</b> , 35, i173-i182	7.2	16
71	Challenges and recommendations for epigenomics in precision health. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 1128-1132	44.5	16
70	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study. <i>PLoS Medicine</i> , <b>2019</b> , 16, e1002982	11.6	15
69	High-Throughput Discovery and Characterization of Human Transcriptional Effectors. <i>Cell</i> , <b>2020</b> , 183, 2020-2035.e16	56.2	14
68	Combining sequence and time series expression data to learn transcriptional modules. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2005</b> , 2, 194-202	3	14
67	Base-resolution models of transcription factor binding reveal soft motif syntax		14
66	Kipoi: accelerating the community exchange and reuse of predictive models for genomics		13
65	A classification-based framework for predicting and analyzing gene regulatory response. <i>BMC Bioinformatics</i> , <b>2006</b> , 7 Suppl 1, S5	3.6	12

64	Transcriptome-wide association studies: opportunities and challenges		12
63	A common pattern of DNase I footprinting throughout the human mtDNA unveils clues for a chromatin-like organization. <i>Genome Research</i> , <b>2018</b> , 28, 1158-1168	9.7	11
62	Vicus: Exploiting local structures to improve network-based analysis of biological data. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005621	5	10
61	Omni-ATAC-seq: Improved ATAC-seq protocol. <i>Protocol Exchange</i> ,		10
60	Transcription-dependent domain-scale three-dimensional genome organization in the dinoflagellate <i>Breviolum minutum</i> . <i>Nature Genetics</i> , <b>2021</b> , 53, 613-617	36.3	10
59	Single-cell epigenomic identification of inherited risk loci in Alzheimer's and Parkinson's disease		9
58	A genome-wide almanac of co-essential modules assigns function to uncharacterized genes		9
57	Learning regulatory programs that accurately predict differential expression with MEDUSA. <i>Annals of the New York Academy of Sciences</i> , <b>2007</b> , 1115, 178-202	6.5	8
56	Motif Discovery Through Predictive Modeling of Gene Regulation. <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 538-552	0.9	8
55	mtDNA Chromatin-like Organization Is Gradually Established during Mammalian Embryogenesis. <i>iScience</i> , <b>2019</b> , 12, 141-151	6.1	7
54	Brief Report: Cell Cycle Dynamics of Human Pluripotent Stem Cells Primed for Differentiation. <i>Stem Cells</i> , <b>2019</b> , 37, 1151-1157	5.8	7
53	Reassessment of Piwi binding to the genome and Piwi impact on RNA polymerase II distribution. <i>Developmental Cell</i> , <b>2015</b> , 32, 772-4	10.2	7
52	Enrichment of colorectal cancer associations in functional regions: Insight for using epigenomics data in the analysis of whole genome sequence-imputed GWAS data. <i>PLoS ONE</i> , <b>2017</b> , 12, e0186518	3.7	7
51	Genome-wide maps of enhancer regulation connect risk variants to disease genes		7
50	Genetic architectures of proximal and distal colorectal cancer are partly distinct. <i>Gut</i> , <b>2021</b> , 70, 1325-1334	19.2	7
49	Transcriptional and chromatin-based partitioning mechanisms uncouple protein scaling from cell size. <i>Molecular Cell</i> , <b>2021</b> , 81, 4861-4875.e7	17.6	6
48	Denoising Genome-wide Histone ChIP-seq with Convolutional Neural Networks		6
47	Impact of regulatory variation across human iPSCs and differentiated cells		6

46	Measuring the reproducibility and quality of Hi-C data		6
45	Separable Fully Connected Layers Improve Deep Learning Models For Genomics		5
44	ChIP-ping the branches of the tree: functional genomics and the evolution of eukaryotic gene regulation. <i>Briefings in Functional Genomics</i> , <b>2018</b> , 17, 116-137	4.9	4
43	Prediction of protein-ligand interactions from paired protein sequence motifs and ligand substructures. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2018</b> , 23, 20-31	1.3	4
42	Umap and Bimap: quantifying genome and methylome mappability		4
41	Fourier-transform-based attribution priors improve the interpretability and stability of deep learning models for genomics		4
40	Long-range single-molecule mapping of chromatin accessibility in eukaryotes		4
39	Genetic Effects on Transcriptome Profiles in Colon Epithelium Provide Functional Insights for Genetic Risk Loci. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , <b>2021</b> , 12, 181-197	7.9	4
38	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation		3
37	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation. <i>Nature Genetics</i> , <b>2021</b> , 53, 1564-1576	36.3	3
36	Size-independent mRNA synthesis and chromatin-based partitioning mechanisms generate and maintain constant amounts of protein per cell		3
35	Targeted optimization of regulatory DNA sequences with neural editing architectures		3
34	AP-1 is a temporally regulated dual gatekeeper of reprogramming to pluripotency. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	3
33	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , <b>2021</b> , 12, 3297	17.4	3
32	Prediction of protein-ligand interactions from paired protein sequence motifs and ligand substructures <b>2018</b> ,		2
31	ZEB2 Shapes the Epigenetic Landscape of Atherosclerosis.. <i>Circulation</i> , <b>2022</b> ,	16.7	2
30	A Congenital Anemia Reveals Distinct Targeting Mechanisms for Master Transcription Factor GATA1.. <i>Blood</i> , <b>2022</b> ,	2.2	2
29	NETWORK MODELLING OF TOPOLOGICAL DOMAINS USING HI-C DATA. <i>Annals of Applied Statistics</i> , <b>2019</b> , 13, 1511-1536	2.1	2

28	Gkmexplain: Fast and Accurate Interpretation of Nonlinear Gapped k-mer SVMs Using Integrated Gradients	2
27	Initiation of mtDNA transcription is followed by pausing, and diverge across human cell types and during evolution	2
26	GenomeDISCO: A concordance score for chromosome conformation capture experiments using random walks on contact map graphs	2
25	Discovering epistatic feature interactions from neural network models of regulatory DNA sequences	2
24	Integrating regulatory DNA sequence and gene expression to predict genome-wide chromatin accessibility across cellular contexts	2
23	Enhancer connectome in primary human cells reveals target genes of disease-associated DNA elements	2
22	MTSplice predicts effects of genetic variants on tissue-specific splicing. <i>Genome Biology</i> , <b>2021</b> , 22, 94	18.3 2
21	Domain adaptive neural networks improve cross-species prediction of transcription factor binding	2
20	MITI minimum information guidelines for highly multiplexed tissue images.. <i>Nature Methods</i> , <b>2022</b> , 19, 262-267	21.6 2
19	Predicting Genetic Regulatory Response Using Classification: Yeast Stress Response. <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 1-13	0.9 1
18	Identification and mitigation of pervasive off-target activity in CRISPR-Cas9 screens for essential non-coding elements	1
17	Chromatin accessibility dynamics reveal novel functional enhancers in <i>C. elegans</i>	1
16	MTSplice predicts effects of genetic variants on tissue-specific splicing	1
15	High-throughput discovery and characterization of human transcriptional effectors	1
14	Deciphering regulatory DNA sequences and noncoding genetic variants using neural network models of massively parallel reporter assays	1
13	Semi-automated genome annotation using epigenomic data and Segway	1
12	Single-cell analyses reveal a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer	1
11	Cell-specific chromatin landscape of human coronary artery resolves regulatory mechanisms of disease risk	1

10	fastISM: Performant in-silico saturation mutagenesis for convolutional neural networks.. <i>Bioinformatics</i> , <b>2022</b> ,	7.2	1
9	The chromatin organization of a chlorarachniophyte nucleomorph genome.. <i>Genome Biology</i> , <b>2022</b> , 23, 65	18.3	1
8	Learning cis-regulatory principles of ADAR-based RNA editing from CRISPR-mediated mutagenesis. <i>Nature Communications</i> , <b>2021</b> , 12, 2165	17.4	0
7	Beyond GWAS of Colorectal Cancer: Evidence of Interaction with Alcohol Consumption and Putative Causal Variant for the 10q24.2 Region.. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2022</b> , OF1-OF13	4	0
6	Single-Molecule Multikilobase-Scale Profiling of Chromatin Accessibility Using m6A-SMAC-Seq and m6A-CpG-GpC-SMAC-Seq.. <i>Methods in Molecular Biology</i> , <b>2022</b> , 2458, 269-298	1.4	
5	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study <b>2019</b> , 16, e1002982		
4	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study <b>2019</b> , 16, e1002982		
3	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study <b>2019</b> , 16, e1002982		
2	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study <b>2019</b> , 16, e1002982		
1	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study <b>2019</b> , 16, e1002982		