Anshul Kundaje

List of Publications by Year
in descending order

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129 papers	48,684 citations	20797 60 h-index	16636 123 g-index
189 all docs	189 docs citations	189 times ranked	65170 citing authors

#	Article	IF	Citations
1	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
2	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
3	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 2012, 22, 1813-1831.	2.4	1,708
4	An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. Nature Methods, 2017, 14, 959-962.	9.0	1,653
5	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
6	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	13.7	1,384
7	Opportunities and obstacles for deep learning in biology and medicine. Journal of the Royal Society Interface, 2018, 15, 20170387.	1.5	1,282
8	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	2.6	1,257
9	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
10	The ENCODE Blacklist: Identification of Problematic Regions of the Genome. Scientific Reports, 2019, 9, 9354.	1.6	1,010
11	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. Nature Genetics, 2016, 48, 1193-1203.	9.4	952
12	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. Genome Research, 2012, 22, 1798-1812.	2.4	762
13	Linking disease associations with regulatory information in the human genome. Genome Research, 2012, 22, 1748-1759.	2.4	657
14	Defining functional DNA elements in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6131-6138.	3.3	635
15	Opportunities and challenges for transcriptome-wide association studies. Nature Genetics, 2019, 51, 592-599.	9.4	592
16	Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers. Nature Genetics, 2015, 47, 381-386.	9.4	589
17	Conserved epigenomic signals in mice and humans reveal immune basis of Alzheimerâ€™s disease. Nature, 2015, 518, 365-369.	13.7	526
18	Integrative annotation of chromatin elements from ENCODE data. Nucleic Acids Research, 2013, 41, 827-841.	6.5	490

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19	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. Nature Genetics, 2017, 49, 1602-1612.	9.4	419
20	H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency. Cell, 2014, 158, 673-688.	13.5	404
21	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
22	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
23	Mapping the Pairwise Choices Leading from Pluripotency to Human Bone, Heart, and Other Mesoderm Cell Types. Cell, 2016, 166, 451-467.	13.5	367
24	Comparative analysis of metazoan chromatin organization. Nature, 2014, 512, 449-452.	13.7	363
25	Long noncoding RNAs are rarely translated in two human cell lines. Genome Research, 2012, 22, 1646-1657.	2.4	346
26	Extensive Variation in Chromatin States Across Humans. Science, 2013, 342, 750-752.	6.0	338
27	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	13.5	334
28	Genome-wide enhancer maps link risk variants to disease genes. Nature, 2021, 593, 238-243.	13.7	332
29	Base-resolution models of transcription-factor binding reveal soft motif syntax. Nature Genetics, 2021, 53, 354-366.	9.4	325
30	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. Cell, 2015, 162, 1051-1065.	13.5	304
31	Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens. Nature Communications, 2017, 8, 15178.	5.8	284
32	Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375.	13.7	259
33	Lineage-specific dynamic and pre-established enhancerâ€“promoter contacts cooperate in terminal differentiation. Nature Genetics, 2017, 49, 1522-1528.	9.4	255
34	Remodeling of epigenome and transcriptome landscapes with aging in mice reveals widespread induction of inflammatory responses. Genome Research, 2019, 29, 697-709.	2.4	234
35	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. Genome Biology, 2012, 13, R48.	13.9	233
36	Transparency and reproducibility in artificial intelligence. Nature, 2020, 586, E14-E16.	13.7	233

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37	Modeling gene expression using chromatin features in various cellular contexts. Genome Biology, 2012, 13, R53.	13.9	231
38	Single-cell epigenomic analyses implicate candidate causal variants at inherited risk loci for Alzheimerâ€™s and Parkinsonâ€™s diseases. Nature Genetics, 2020, 52, 1158-1168.	9.4	217
39	Chromatin and gene-regulatory dynamics of the developing human cerebral cortex at single-cell resolution. Cell, 2021, 184, 5053-5069.e23.	13.5	209
40	CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities. Nature, 2020, 580, 136-141.	13.7	203
41	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	13.7	184
42	Characterization of the direct targets of <scp>FOXO</scp> transcription factors throughout evolution. Aging Cell, 2016, 15, 673-685.	3.0	177
43	Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. Genome Research, 2012, 22, 1735-1747.	2.4	168
44	Chromatin accessibility dynamics reveal novel functional enhancers in C. elegans. Genome Research, 2017, 27, 2096-2107.	2.4	142
45	Matrix stiffness induces a tumorigenic phenotype in mammary epithelium through changes in chromatin accessibility. Nature Biomedical Engineering, 2019, 3, 1009-1019.	11.6	135
46	Landscape of cohesin-mediated chromatin loops in the human genome. Nature, 2020, 583, 737-743.	13.7	134
47	Molecular definition of a metastatic lung cancer state reveals a targetable CD109â€“Janus kinaseâ€“Stat axis. Nature Medicine, 2017, 23, 291-300.	15.2	126
48	Large-Scale Quality Analysis of Published ChIP-seq Data. G3: Genes, Genomes, Genetics, 2014, 4, 209-223.	0.8	125
49	Measuring the reproducibility and quality of Hi-C data. Genome Biology, 2019, 20, 57.	3.8	125
50	Intertumoral Heterogeneity in SCLC Is Influenced by the Cell Type of Origin. Cancer Discovery, 2018, 8, 1316-1331.	7.7	123
51	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
52	The Kipoi repository accelerates community exchange and reuse of predictive models for genomics. Nature Biotechnology, 2019, 37, 592-600.	9.4	118
53	Regulatory analysis of the C. elegans genome with spatiotemporal resolution. Nature, 2014, 512, 400-405.	13.7	115
54	Impact of regulatory variation across human iPSCs and differentiated cells. Genome Research, 2018, 28, 122-131.	2.4	114

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55	Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. Nature Communications, 2019, 10, 4063.	5.8	104
56	An Arntl2-Driven Secretome Enables Lung Adenocarcinoma Metastatic Self-Sufficiency. Cancer Cell, 2016, 29, 697-710.	7.7	99
57	Umap and Bismap: quantifying genome and methylome mappability. Nucleic Acids Research, 2018, 46, e120.	6.5	94
58	Long-range single-molecule mapping of chromatin accessibility in eukaryotes. Nature Methods, 2020, 17, 319-327.	9.0	93
59	GenomeDISCO: a concordance score for chromosome conformation capture experiments using random walks on contact map graphs. Bioinformatics, 2018, 34, 2701-2707.	1.8	90
60	Impact of the X Chromosome and sex on regulatory variation. Genome Research, 2016, 26, 768-777.	2.4	88
61	A genome-wide atlas of co-essential modules assigns function to uncharacterized genes. Nature Genetics, 2021, 53, 638-649.	9.4	86
62	Single-cell analyses define a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer. Nature Genetics, 2022, 54, 985-995.	9.4	77
63	Predicting genetic regulatory response using classification. Bioinformatics, 2004, 20, i232-i240.	1.8	72
64	High-Throughput Discovery and Characterization of Human Transcriptional Effectors. Cell, 2020, 183, 2020-2035.e16.	13.5	71
65	Discovering epistatic feature interactions from neural network models of regulatory DNA sequences. Bioinformatics, 2018, 34, i629-i637.	1.8	63
66	Deciphering regulatory DNA sequences and noncoding genetic variants using neural network models of massively parallel reporter assays. PLoS ONE, 2019, 14, e0218073.	1.1	61
67	Integrating regulatory DNA sequence and gene expression to predict genome-wide chromatin accessibility across cellular contexts. Bioinformatics, 2019, 35, i108-i116.	1.8	54
68	Single-nucleus chromatin accessibility profiling highlights regulatory mechanisms of coronary artery disease risk. Nature Genetics, 2022, 54, 804-816.	9.4	51
69	Spectrogram Analysis of Genomes. Eurasip Journal on Advances in Signal Processing, 2004, 2004, 1.	1.0	50
70	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, 2005, 102, 1402-1407.	3.3	50
71	Denoising genome-wide histone ChIP-seq with convolutional neural networks. Bioinformatics, 2017, 33, i225-i233.	1.8	48
72	Transcription Factors Bind Negatively Selected Sites within Human mtDNA Genes. Genome Biology and Evolution, 2014, 6, 2634-2646.	1.1	47

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73	An atlas of transcriptional, chromatin accessibility, and surface marker changes in human mesoderm development. Scientific Data, 2016, 3, 160109.	2.4	47
74	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation. Nature Genetics, 2021, 53, 1564-1576.	9.4	45
75	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	6.1	44
76	Transcriptional and chromatin-based partitioning mechanisms uncouple protein scaling from cell size. Molecular Cell, 2021, 81, 4861-4875.e7.	4.5	42
77	Characterization of TCF21 Downstream Target Regions Identifies a Transcriptional Network Linking Multiple Independent Coronary Artery Disease Loci. PLoS Genetics, 2015, 11, e1005202.	1.5	41
78	Initiation of mtDNA transcription is followed by pausing, and diverges across human cell types and during evolution. Genome Research, 2017, 27, 362-373.	2.4	41
79	GkmExplain: fast and accurate interpretation of nonlinear gapped k-mer SVMs. Bioinformatics, 2019, 35, i173-i182.	1.8	41
80	A Predictive Model of the Oxygen and Heme Regulatory Network in Yeast. PLoS Computational Biology, 2008, 4, e1000224.	1.5	40
81	Predicting gene expression in massively parallel reporter assays: A comparative study. Human Mutation, 2017, 38, 1240-1250.	1.1	39
82	Transcription-dependent domain-scale three-dimensional genome organization in the dinoflagellate Breviolum minutum. Nature Genetics, 2021, 53, 613-617.	9.4	38
83	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	9.0	37
84	Differential analysis of chromatin accessibility and histone modifications for predicting mouse developmental enhancers. Nucleic Acids Research, 2018, 46, 11184-11201.	6.5	36
85	STAT3 Targets Suggest Mechanisms of Aggressive Tumorigenesis in Diffuse Large B-Cell Lymphoma. G3: Genes, Genomes, Genetics, 2013, 3, 2173-2185.	0.8	34
86	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study. PLoS Medicine, 2019, 16, e1002982.	3.9	34
87	Diverse patterns of genomic targeting by transcriptional regulators in Drosophila melanogaster. Genome Research, 2014, 24, 1224-1235.	2.4	31
88	ZEB2 Shapes the Epigenetic Landscape of Atherosclerosis. Circulation, 2022, 145, 469-485.	1.6	31
89	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, 2014, 111, E3366.	3.3	25
90	High-Throughput Characterization of Cascade type I-E CRISPR Guide Efficacy Reveals Unexpected PAM Diversity and Target Sequence Preferences. Genetics, 2017, 206, 1727-1738.	1.2	23

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91	MTSplice predicts effects of genetic variants on tissue-specific splicing. Genome Biology, 2021, 22, 94.	3.8	23
92	Omni-ATAC-seq: Improved ATAC-seq protocol. Protocol Exchange, 0, , .	0.3	21
93	Combining Sequence and Time Series Expression Data to Learn Transcriptional Modules. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 194-202.	1.9	20
94	Challenges and recommendations for epigenomics in precision health. Nature Biotechnology, 2017, 35, 1128-1132.	9.4	19
95	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, 2021, 118, .	3.3	19
96	Genetic Effects on Transcriptome Profiles in Colon Epithelium Provide Functional Insights for Genetic Risk Loci. Cellular and Molecular Gastroenterology and Hepatology, 2021, 12, 181-197.	2.3	18
97	Network modelling of topological domains using Hi-C data. Annals of Applied Statistics, 2019, 13, 1511-1536.	0.5	17
98	Domain-adaptive neural networks improve cross-species prediction of transcription factor binding. Genome Research, 2022, 32, 512-523.	2.4	16
99	A classification-based framework for predicting and analyzing gene regulatory response. BMC Bioinformatics, 2006, 7, S5.	1.2	15
100	A common pattern of DNase I footprinting throughout the human mtDNA unveils clues for a chromatin-like organization. Genome Research, 2018, 28, 1158-1168.	2.4	15
101	Vicus: Exploiting local structures to improve network-based analysis of biological data. PLoS Computational Biology, 2017, 13, e1005621.	1.5	15
102	Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. Blood, 2022, 139, 2534-2546.	0.6	14
103	Learning Regulatory Programs That Accurately Predict Differential Expression with MEDUSA. Annals of the New York Academy of Sciences, 2007, 1115, 178-202.	1.8	13
104	Motif Discovery Through Predictive Modeling of Gene Regulation. Lecture Notes in Computer Science, 2005, , 538-552.	1.0	12
105	mtDNA Chromatin-like Organization Is Gradually Established during Mammalian Embryogenesis. IScience, 2019, 12, 141-151.	1.9	12
106	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	5.8	11
107	Reassessment of Piwi Binding to the Genome and Piwi Impact on RNA Polymerase II Distribution. Developmental Cell, 2015, 32, 772-774.	3.1	9
108	Learning cis-regulatory principles of ADAR-based RNA editing from CRISPR-mediated mutagenesis. Nature Communications, 2021, 12, 2165.	5.8	9

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109	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, 2017, 12, e0186518.	1.1	8
110	fastISM: performantin silicosaturation mutagenesis for convolutional neural networks. Bioinformatics, 2022, 38, 2397-2403.	1.8	8
111	Brief Report: Cell Cycle Dynamics of Human Pluripotent Stem Cells Primed for Differentiation. Stem Cells, 2019, 37, 1151-1157.	1.4	7
112	Prediction of protein-ligand interactions from paired protein sequence motifs and ligand substructures. , 2018, , .		6
113	Beyond GWAS of Colorectal Cancer: Evidence of Interaction with Alcohol Consumption and Putative Causal Variant for the 10q24.2 Region. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1077-1089.	1.1	6
114	ChIP-ping the branches of the tree: functional genomics and the evolution of eukaryotic gene regulation. Briefings in Functional Genomics, 2018, 17, 116-137.	1.3	5
115	Acceleratingin silicosaturation mutagenesis using compressed sensing. Bioinformatics, 2022, 38, 3557-3564.	1.8	5
116	Prediction of protein-ligand interactions from paired protein sequence motifs and ligand substructures. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 20-31.	0.7	4
117	The chromatin organization of a chlorarachniophyte nucleomorph genome. Genome Biology, 2022, 23, 65.	3.8	4
118	Predicting Genetic Regulatory Response Using Classification: Yeast Stress Response. Lecture Notes in Computer Science, 2005, , 1-13.	1.0	2
119	464 Dynamic and stable enhancer-promoter contacts regulate epidermal terminal differentiation. Journal of Investigative Dermatology, 2017, 137, S80.	0.3	2
120	Single-Molecule Multikilobase-Scale Profiling of Chromatin Using m6A-SMAC-Seq and m6A-CpG-GpC-SMAC-Seq. Methods in Molecular Biology, 2022, 2458, 269-298.	0.4	1
121	Automated sequence-based annotation and interpretation of the human genome. Nature Genetics, 2022, 54, 916-917.	9.4	1
122	Abstract 4489: Using functional data from Roadmap Epigenomics to inform analysis of rare variants linked to gene expression in a large colorectal cancer study. , 2016, , .		0
123	Abstract 4349: Predicting gene expression from plasma cell-free DNA using both the fragment length and fragment position. , 2019, , .		0
124	Title is missing!. , 2019, 16, e1002982.		0
125	Title is missing!. , 2019, 16, e1002982.		0
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127	Title is missing!. , 2019, 16, e1002982.		0
128	Title is missing!. , 2019, 16, e1002982.		0
129	OUP accepted manuscript. Journal of the National Cancer Institute, 2022, , .	3.0	0