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	ZEB2 Shapes the Epigenetic Landscape of Atherosclerosis. Circulation, 2022, 145, 469-485.	1.6	31
2	Domain-adaptive neural networks improve cross-species prediction of transcription factor binding. Genome Research, 2022, 32, 512-523.	2.4	16
3	Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. Blood, 2022, 139, 2534-2546.	0.6	14
4	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
5	fastISM: performantin silicosaturation mutagenesis for convolutional neural networks. Bioinformatics, 2022, 38, 2397-2403.	1.8	8
6	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	9.0	37
7	The chromatin organization of a chlorarachniophyte nucleomorph genome. Genome Biology, 2022, 23, 65.	3.8	4
8	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
9	OUP accepted manuscript. Journal of the National Cancer Institute, 2022, , .	3.0	0
10	Single-nucleus chromatin accessibility profiling highlights regulatory mechanisms of coronary artery disease risk. Nature Genetics, 2022, 54, 804-816.	9.4	51
11	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
12	Acceleratingin silicosaturation mutagenesis using compressed sensing. Bioinformatics, 2022, 38, 3557-3564.	1.8	5
13	Automated sequence-based annotation and interpretation of the human genome. Nature Genetics, 2022, 54, 916-917.	9.4	1
14	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
15	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	6.1	44
16	Base-resolution models of transcription-factor binding reveal soft motif syntax. Nature Genetics, 2021, 53, 354-366.	9.4	325
17	MTSplice predicts effects of genetic variants on tissue-specific splicing. Genome Biology, 2021, 22, 94.	3.8	23
18	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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19	Genome-wide enhancer maps link risk variants to disease genes. Nature, 2021, 593, 238-243.	13.7	332
20	A genome-wide atlas of co-essential modules assigns function to uncharacterized genes. Nature Genetics, 2021, 53, 638-649.	9.4	86
21	Transcription-dependent domain-scale three-dimensional genome organization in the dinoflagellate Breviolum minutum. Nature Genetics, 2021, 53, 613-617.	9.4	38
22	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
23	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	5.8	11
24	Chromatin and gene-regulatory dynamics of the developing human cerebral cortex at single-cell resolution. Cell, 2021, 184, 5053-5069.e23.	13.5	209
25	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation. Nature Genetics, 2021, 53, 1564-1576.	9.4	45
26	Transcriptional and chromatin-based partitioning mechanisms uncouple protein scaling from cell size. Molecular Cell, 2021, 81, 4861-4875.e7.	4.5	42
27	Transparency and reproducibility in artificial intelligence. Nature, 2020, 586, E14-E16.	13.7	233
28	Landscape of cohesin-mediated chromatin loops in the human genome. Nature, 2020, 583, 737-743.	13.7	134
29	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
30	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
31	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
32	High-Throughput Discovery and Characterization of Human Transcriptional Effectors. Cell, 2020, 183, 2020-2035.e16.	13.5	71
33	CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities. Nature, 2020, 580, 136-141.	13.7	203
34	Long-range single-molecule mapping of chromatin accessibility in eukaryotes. Nature Methods, 2020, 17, 319-327.	9.0	93
35	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	13.5	334
36	GkmExplain: fast and accurate interpretation of nonlinear gapped k-mer SVMs. Bioinformatics, 2019, 35, i173-i182.	1.8	41

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37	Integrating regulatory DNA sequence and gene expression to predict genome-wide chromatin accessibility across cellular contexts. Bioinformatics, 2019, 35, i108-i116.	1.8	54
38	The ENCODE Blacklist: Identification of Problematic Regions of the Genome. Scientific Reports, 2019, 9, 9354.	1.6	1,010
39	Matrix stiffness induces a tumorigenic phenotype in mammary epithelium through changes in chromatin accessibility. Nature Biomedical Engineering, 2019, 3, 1009-1019.	11.6	135
40	Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. Nature Communications, 2019, 10, 4063.	5.8	104
41	mtDNA Chromatin-like Organization Is Gradually Established during Mammalian Embryogenesis. IScience, 2019, 12, 141-151.	1.9	12
42	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
43	Brief Report: Cell Cycle Dynamics of Human Pluripotent Stem Cells Primed for Differentiation. Stem Cells, 2019, 37, 1151-1157.	1.4	7
44	The Kipoi repository accelerates community exchange and reuse of predictive models for genomics. Nature Biotechnology, 2019, 37, 592-600.	9.4	118
45	Measuring the reproducibility and quality of Hi-C data. Genome Biology, 2019, 20, 57.	3.8	125
46	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
47	Opportunities and challenges for transcriptome-wide association studies. Nature Genetics, 2019, 51, 592-599.	9.4	592
48	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
49	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
50	Network modelling of topological domains using Hi-C data. Annals of Applied Statistics, 2019, 13, 1511-1536.	0.5	17
51	Abstract 4349: Predicting gene expression from plasma cell-free DNA using both the fragment length and fragment position. , 2019, , .		0
52	Title is missing!. , 2019, 16, e1002982.		0
53	Title is missing!. , 2019, 16, e1002982.		0
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55	Title is missing!. , 2019, 16, e1002982.		0
56	Title is missing!. , 2019, 16, e1002982.		0
57	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
58	Prediction of protein-ligand interactions from paired protein sequence motifs and ligand substructures. , 2018, , .		6
59	Opportunities and obstacles for deep learning in biology and medicine. Journal of the Royal Society Interface, 2018, 15, 20170387.	1.5	1,282
60	GenomeDISCO: a concordance score for chromosome conformation capture experiments using random walks on contact map graphs. Bioinformatics, 2018, 34, 2701-2707.	1.8	90
61	Impact of regulatory variation across human iPSCs and differentiated cells. Genome Research, 2018, 28, 122-131.	2.4	114
62	Discovering epistatic feature interactions from neural network models of regulatory DNA sequences. Bioinformatics, 2018, 34, i629-i637.	1.8	63
63	Intertumoral Heterogeneity in SCLC Is Influenced by the Cell Type of Origin. Cancer Discovery, 2018, 8, 1316-1331.	7.7	123
64	Umap and Bismap: quantifying genome and methylome mappability. Nucleic Acids Research, 2018, 46, e120.	6.5	94
65	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
66	Differential analysis of chromatin accessibility and histone modifications for predicting mouse developmental enhancers. Nucleic Acids Research, 2018, 46, 11184-11201.	6.5	36
67	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
68	Predicting gene expression in massively parallel reporter assays: A comparative study. Human Mutation, 2017, 38, 1240-1250.	1.1	39
69	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
70	Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens. Nature Communications, 2017, 8, 15178.	5.8	284
71	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
72	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

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73	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. Nature Genetics, 2017, 49, 1602-1612.	9.4	419
74	464 Dynamic and stable enhancer-promoter contacts regulate epidermal terminal differentiation. Journal of Investigative Dermatology, 2017, 137, S80.	0.3	2
75	Lineage-specific dynamic and pre-established enhancerâ€“promoter contacts cooperate in terminal differentiation. Nature Genetics, 2017, 49, 1522-1528.	9.4	255
76	Challenges and recommendations for epigenomics in precision health. Nature Biotechnology, 2017, 35, 1128-1132.	9.4	19
77	Chromatin accessibility dynamics reveal novel functional enhancers in C. elegans. Genome Research, 2017, 27, 2096-2107.	2.4	142
78	Denoising genome-wide histone ChIP-seq with convolutional neural networks. Bioinformatics, 2017, 33, i225-i233.	1.8	48
79	An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. Nature Methods, 2017, 14, 959-962.	9.0	1,653
80	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
81	Vicus: Exploiting local structures to improve network-based analysis of biological data. PLoS Computational Biology, 2017, 13, e1005621.	1.5	15
82	Impact of the X Chromosome and sex on regulatory variation. Genome Research, 2016, 26, 768-777.	2.4	88
83	An atlas of transcriptional, chromatin accessibility, and surface marker changes in human mesoderm development. Scientific Data, 2016, 3, 160109.	2.4	47
84	An Arntl2-Driven Secretome Enables Lung Adenocarcinoma Metastatic Self-Sufficiency. Cancer Cell, 2016, 29, 697-710.	7.7	99
85	Characterization of the direct targets of <scp>FOXO</scp> transcription factors throughout evolution. Aging Cell, 2016, 15, 673-685.	3.0	177
86	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. Nature Genetics, 2016, 48, 1193-1203.	9.4	952
87	Mapping the Pairwise Choices Leading from Pluripotency to Human Bone, Heart, and Other Mesoderm Cell Types. Cell, 2016, 166, 451-467.	13.5	367
88	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
89	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
90	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

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91	Conserved epigenomic signals in mice and humans reveal immune basis of Alzheimerâ€™s disease. Nature, 2015, 518, 365-369.	13.7	526
92	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
93	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
94	Reassessment of Piwi Binding to the Genome and Piwi Impact on RNA Polymerase II Distribution. Developmental Cell, 2015, 32, 772-774.	3.1	9
95	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. Cell, 2015, 162, 1051-1065.	13.5	304
96	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
97	Diverse patterns of genomic targeting by transcriptional regulators in Drosophila melanogaster. Genome Research, 2014, 24, 1224-1235.	2.4	31
98	Transcription Factors Bind Negatively Selected Sites within Human mtDNA Genes. Genome Biology and Evolution, 2014, 6, 2634-2646.	1.1	47
99	Large-Scale Quality Analysis of Published ChIP-seq Data. G3: Genes, Genomes, Genetics, 2014, 4, 209-223.	0.8	125
100	Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375.	13.7	259
101	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
102	Regulatory analysis of the C. elegans genome with spatiotemporal resolution. Nature, 2014, 512, 400-405.	13.7	115
103	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	13.7	184
104	Comparative analysis of metazoan chromatin organization. Nature, 2014, 512, 449-452.	13.7	363
105	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
106	H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency. Cell, 2014, 158, 673-688.	13.5	404
107	Extensive Variation in Chromatin States Across Humans. Science, 2013, 342, 750-752.	6.0	338
108	Integrative annotation of chromatin elements from ENCODE data. Nucleic Acids Research, 2013, 41, 827-841.	6.5	490

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109	STAT3 Targets Suggest Mechanisms of Aggressive Tumorigenesis in Diffuse Large B-Cell Lymphoma. G3: Genes, Genomes, Genetics, 2013, 3, 2173-2185.	0.8	34
110	Linking disease associations with regulatory information in the human genome. Genome Research, 2012, 22, 1748-1759.	2.4	657
111	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. Genome Research, 2012, 22, 1798-1812.	2.4	762
112	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
113	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
114	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 2012, 22, 1813-1831.	2.4	1,708
115	Long noncoding RNAs are rarely translated in two human cell lines. Genome Research, 2012, 22, 1646-1657.	2.4	346
116	Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. Genome Research, 2012, 22, 1735-1747.	2.4	168
117	Modeling gene expression using chromatin features in various cellular contexts. Genome Biology, 2012, 13, R53.	13.9	231
118	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	13.7	1,384
119	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	2.6	1,257
120	A Predictive Model of the Oxygen and Heme Regulatory Network in Yeast. PLoS Computational Biology, 2008, 4, e1000224.	1.5	40
121	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
122	A classification-based framework for predicting and analyzing gene regulatory response. BMC Bioinformatics, 2006, 7, S5.	1.2	15
123	Motif Discovery Through Predictive Modeling of Gene Regulation. Lecture Notes in Computer Science, 2005, , 538-552.	1.0	12
124	Predicting Genetic Regulatory Response Using Classification: Yeast Stress Response. Lecture Notes in Computer Science, 2005, , 1-13.	1.0	2
125	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
126	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

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127	Predicting genetic regulatory response using classification. Bioinformatics, 2004, 20, i232-i240.	1.8	72
128	Spectrogram Analysis of Genomes. Eurasip Journal on Advances in Signal Processing, 2004, 2004, 1.	1.0	50
129	Omni-ATAC-seq: Improved ATAC-seq protocol. Protocol Exchange, 0, , .	0.3	21