Sündüz Keleş

List of Publications by Year
in descending order

117 papers	4,918 citations	87888 38 h-index	110387 64 g-index
130 all docs	130 docs citations	130 times ranked	10525 citing authors

#	Article	IF	Citations
1	Discovering Hematopoietic Mechanisms through Genome-wide Analysis of GATA Factor Chromatin Occupancy. Molecular Cell, 2009, 36, 667-681.	9.7	314
2	GATA Switches as Developmental Drivers. Journal of Biological Chemistry, 2010, 285, 31087-31093.	3.4	235
3	Effects of Sleep and Wake on Oligodendrocytes and Their Precursors. Journal of Neuroscience, 2013, 33, 14288-14300.	3.6	213
4	Rho directs widespread termination of intragenic and stable RNA transcription. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15406-15411.	7.1	192
5	Cis-element mutated in GATA2-dependent immunodeficiency governs hematopoiesis and vascular integrity. Journal of Clinical Investigation, 2012, 122, 3692-3704.	8.2	162
6	Genome-scale Analysis of Escherichia coli FNR Reveals Complex Features of Transcription Factor Binding. PLoS Genetics, 2013, 9, e1003565.	3.5	158
7	Chemical-genomic dissection of the CTD code. Nature Structural and Molecular Biology, 2010, 17, 1154-1161.	8.2	130
8	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
9	Autophagy Driven by a Master Regulator of Hematopoiesis. Molecular and Cellular Biology, 2012, 32, 226-239.	2.3	119
10	Mechanisms of erythrocyte development and regeneration: implications for regenerative medicine and beyond. Development (Cambridge), 2018, 145, .	2.5	107
11	Detecting differential binding of transcription factors with ChIP-seq. Bioinformatics, 2012, 28, 121-122.	4.1	104
12	Expression Profiling of GABAergic Motor Neurons in Caenorhabditis elegans. Current Biology, 2005, 15, 340-346.	3.9	100
13	A Statistical Framework for the Analysis of ChIP-Seq Data. Journal of the American Statistical Association, 2011, 106, 891-903.	3.1	100
14	Dynamic Regulation of Schwann Cell Enhancers after Peripheral Nerve Injury. Journal of Biological Chemistry, 2015, 290, 6937-6950.	3.4	98
15	Transcription of histone gene cluster by differential core-promoter factors. Genes and Development, 2007, 21, 2936-2949.	5.9	96
16	Genetic framework for GATA factor function in vascular biology. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13641-13646.	7.1	96
17	Differential Sox10 genomic occupancy in myelinating glia. Glia, 2015, 63, 1897-1914.	4.9	84
18	Beta Cell Dedifferentiation Induced by IRE1α Deletion Prevents Type 1 Diabetes. Cell Metabolism, 2020, 31, 822-836.e5.	16.2	84

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19	Genome-wide analysis of EGR2/SOX10 binding in myelinating peripheral nerve. Nucleic Acids Research, 2012, 40, 6449-6460.	14.5	81
20	atSNP: transcription factor binding affinity testing for regulatory SNP detection. Bioinformatics, 2015, 31, 3353-3355.	4.1	81
21	Expression Quantitative Trait Loci Mapping With Multivariate Sparse Partial Least Squares Regression. Genetics, 2009, 182, 79-90.	2.9	79
22	Discovering Transcription Factor Binding Sites in Highly Repetitive Regions of Genomes with Multi-Read Analysis of ChIP-Seq Data. PLoS Computational Biology, 2011, 7, e1002111.	3.2	73
23	O_2 availability impacts iron homeostasis in *Escherichia coli*. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12261-12266.	7.1	72
24	Impact of Anaerobiosis on Expression of the Iron-Responsive Fur and RyhB Regulons. MBio, 2015, 6, e01947-15.	4.1	67
25	Integromic Analysis of Genetic Variation and Gene Expression Identifies Networks for Cardiovascular Disease Phenotypes. Circulation, 2015, 131, 536-549.	1.6	65
26	Identification of Estrogen Receptor Dimer Selective Ligands Reveals Growth-Inhibitory Effects on Cells That Co-Express ERα and ERβ. PLoS ONE, 2012, 7, e30993.	2.5	62
27	Molecular Hallmarks of Endogenous Chromatin Complexes Containing Master Regulators of Hematopoiesis. Molecular and Cellular Biology, 2008, 28, 6681-6694.	2.3	57
28	Dynamic Changes in Nucleosome Occupancy Are Not Predictive of Gene Expression Dynamics but Are Linked to Transcription and Chromatin Regulators. Molecular and Cellular Biology, 2012, 32, 1645-1653.	2.3	57
29	Misregulation of Alternative Splicing in a Mouse Model of Rett Syndrome. PLoS Genetics, 2016, 12, e1006129.	3.5	57
30	Research Resource: Global Identification of Estrogen Receptor β Target Genes in Triple Negative Breast Cancer Cells. Molecular Endocrinology, 2013, 27, 1762-1775.	3.7	52
31	Unbiased screen of RNA tailing activities reveals a poly(UG) polymerase. Nature Methods, 2019, 16, 437-445.	19.0	52
32	Genome-wide alterations in hippocampal 5-hydroxymethylcytosine links plasticity genes to acute stress. Neurobiology of Disease, 2016, 86, 99-108.	4.4	48
33	Single-nucleotide human disease mutation inactivates a blood-regenerative GATA2 enhancer. Journal of Clinical Investigation, 2019, 129, 1180-1192.	8.2	47
34	Residual-based tree-structured survival analysis. Statistics in Medicine, 2002, 21, 313-326.	1.6	44
35	Multiple Testing Methods For ChIP–Chip High Density Oligonucleotide Array Data. Journal of Computational Biology, 2006, 13, 579-613.	1.6	44
36	Exploratory and Confirmatory Gene Expression Profiling of mac1Δ. Journal of Biological Chemistry, 2004, 279, 4450-4458.	3.4	43

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37	A single <i>C. elegans</i> PUF protein binds RNA in multiple modes. Rna, 2009, 15, 1090-1099.	3.5	42
38	Increases in Central Aortic Impedance Precede Alterations in Arterial Stiffness Measures in Type 1 Diabetes. Diabetes Care, 2007, 30, 2886-2891.	8.6	41
39	Novel TRF1/BRF target genes revealed by genome-wide analysis of Drosophila Pol III transcription. EMBO Journal, 2007, 26, 79-89.	7.8	41
40	Differentially Methylated Plasticity Genes in the Amygdala of Young Primates Are Linked to Anxious Temperament, an at Risk Phenotype for Anxiety and Depressive Disorders. Journal of Neuroscience, 2014, 34, 15548-15556.	3.6	41
41	Regulation of WNT Signaling by VSX2 During Optic Vesicle Patterning in Human Induced Pluripotent Stem Cells. Stem Cells, 2016, 34, 2625-2634.	3.2	41
42	Hematopoietic Signaling Mechanism Revealed from a Stem/Progenitor Cell Cistrome. Molecular Cell, 2015, 59, 62-74.	9.7	40
43	Predicting gene expression in massively parallel reporter assays: A comparative study. Human Mutation, 2017, 38, 1240-1250.	2.5	39
44	Mixture Modeling for Genome-Wide Localization of Transcription Factors. Biometrics, 2007, 63, 10-21.	1.4	38
45	A study of the relationships between oligonucleotide properties and hybridization signal intensities from NimbleGen microarray datasets. Nucleic Acids Research, 2008, 36, 2926-2938.	14.5	38
46	Locus‑wide identification of Egr2/Krox20 regulatory targets in myelin genes. Journal of Neurochemistry, 2010, 115, 1409-1420.	3.9	38
47	Genome-wide disruption of 5-hydroxymethylcytosine in a mouse model of autism. Human Molecular Genetics, 2015, 24, ddv411.	2.9	38
48	Divergence of Pumilio/fem-3 mRNA Binding Factor (PUF) Protein Specificity through Variations in an RNA-binding Pocket. Journal of Biological Chemistry, 2012, 287, 6949-6957.	3.4	37
49	Framework for kernel regularization with application to protein clustering. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12332-12337.	7.1	36
50	Epstein-Barr Virus Nuclear Antigen 3 (EBNA3) Proteins Regulate EBNA2 Binding to Distinct RBPJ Genomic Sites. Journal of Virology, 2016, 90, 2906-2919.	3.4	35
51	Distal enhancers upstream of the Charcot-Marie-Tooth type 1A disease gene PMP22. Human Molecular Genetics, 2012, 21, 1581-1591.	2.9	32
52	CTCF loss mediates unique DNA hypermethylation landscapes in human cancers. Clinical Epigenetics, 2020, 12, 80.	4.1	32
53	GATA/Heme Multi-omics Reveals a Trace Metal-Dependent Cellular Differentiation Mechanism. Developmental Cell, 2018, 46, 581-594.e4.	7.0	31
54	GATA Factor-Regulated Samd14 Enhancer Confers Red Blood Cell Regeneration and Survival in Severe Anemia. Developmental Cell, 2017, 42, 213-225.e4.	7.0	29

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55	Constructing and deconstructing GATA2-regulated cell fate programs to establish developmental trajectories. Journal of Experimental Medicine, 2020, 217, .	8.5	28
56	Generative modeling of multi-mapping reads with mHi-C advances analysis of Hi-C studies. ELife, 2019, 8, .	6.0	28
57	CMARRT: a tool for the analysis of ChIP-chip data from tiling arrays by incorporating the correlation structure. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 515-26.	0.7	26
58	Epstein-Barr Virus Infection Promotes Epithelial Cell Growth by Attenuating Differentiation-Dependent Exit from the Cell Cycle. MBio, 2019, 10, .	4.1	25
59	Mixture models with multiple levels, with application to the analysis of multifactor gene expression data. Biostatistics, 2008, 9, 540-554.	1.5	24
60	Sex-specific hippocampal 5-hydroxymethylcytosine is disrupted in response to acute stress. Neurobiology of Disease, 2016, 96, 54-66.	4.4	24
61	PKM2–TMEM33 axis regulates lipid homeostasis in cancer cells by controlling SCAP stability. EMBO Journal, 2021, 40, e108065.	7.8	24
62	Angiogenesis Induced by Signal Transducer and Activator of Transcription 5A (STAT5A) Is Dependent on Autocrine Activity of Proliferin. Journal of Biological Chemistry, 2012, 287, 6490-6502.	3.4	23
63	Statistical Analysis of ChIP-seq Data with MOSAiCS. Methods in Molecular Biology, 2013, 1038, 193-212.	0.9	22
64	atSNP Search: a web resource for statistically evaluating influence of human genetic variation on transcription factor binding. Bioinformatics, 2019, 35, 2657-2659.	4.1	21
65	Discovering How Heme Controls Genome Function Through Heme-omics. Cell Reports, 2020, 31, 107832.	6.4	21
66	Hematopoietic transcriptional mechanisms: From locus-specific to genome-wide vantage points. Experimental Hematology, 2014, 42, 618-629.	0.4	19
67	Integrative analysis with ChIP-seq advances the limits of transcript quantification from RNA-seq. Genome Research, 2016, 26, 1124-1133.	5.5	19
68	Transient Genotype-by-Environment Interactions Following Environmental Shock Provide a Source of Expression Variation for Essential Genes. Genetics, 2010, 184, 587-593.	2.9	18
69	Fungal Morphology, Iron Homeostasis, and Lipid Metabolism Regulated by a GATA Transcription Factor in Blastomyces dermatitidis. PLoS Pathogens, 2015, 11, e1004959.	4.7	16
70	Supervised Detection of Regulatory Motifs in DNA Sequences. Statistical Applications in Genetics and Molecular Biology, 2003, 2, Article5.	0.6	15
71	dPeak: High Resolution Identification of Transcription Factor Binding Sites from PET and SET ChIP-Seq Data. PLoS Computational Biology, 2013, 9, e1003246.	3.2	15
72	GLANET: genomic loci annotation and enrichment tool. Bioinformatics, 2017, 33, 2818-2828.	4.1	15

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73	FreeHi-C simulates high-fidelity Hi-C data for benchmarking and data augmentation. Nature Methods, 2020, 17, 37-40.	19.0	15
74	Identification of direct transcriptional targets of NFATC2 that promote Î² cell proliferation. Journal of Clinical Investigation, 2021, 131, .	8.2	15
75	CSI-Tree: a regression tree approach for modeling binding properties of DNA-binding molecules based on cognate site identification (CSI) data. Nucleic Acids Research, 2008, 36, 3171-3184.	14.5	14
76	A statistical framework for power calculations in ChIP-seq experiments. Bioinformatics, 2014, 30, 753-760.	4.1	14
77	Transcriptome-wide transmission disequilibrium analysis identifies novel risk genes for autism spectrum disorder. PLoS Genetics, 2021, 17, e1009309.	3.5	14
78	Comments on: Augmenting the bootstrap to analyze high dimensional genomic data. Test, 2008, 17, 36-39.	1.1	13
79	A Phylogenetic Mixture Model for the Evolution of Gene Expression. Molecular Biology and Evolution, 2009, 26, 2363-2372.	8.9	13
80	GATA factor-regulated solute carrier ensemble reveals a nucleoside transporter-dependent differentiation mechanism. PLoS Genetics, 2020, 16, e1009286.	3.5	13
81	The SWI/SNF-Related, Matrix Associated, Actin-Dependent Regulator of Chromatin A4 Core Complex Represses Respiratory Syncytial Virus-Induced Syncytia Formation and Subepithelial Myofibroblast Transition. Frontiers in Immunology, 2021, 12, 633654.	4.8	12
82	Perm-seq: Mapping Protein-DNA Interactions in Segmental Duplication and Highly Repetitive Regions of Genomes with Prior-Enhanced Read Mapping. PLoS Computational Biology, 2015, 11, e1004491.	3.2	11
83	Asymptotically optimal model selection method with right censored outcomes. Bernoulli, 2004, 10, 1011.	1.3	10
84	Epigenetic and genetic mechanisms in red cell biology. Current Opinion in Hematology, 2014, 21, 155-164.	2.5	10
85	CNV-guided multi-read allocation for ChIP-seq. Bioinformatics, 2014, 30, 2860-2867.	4.1	10
86	RNA-Binding Protein IGF2BP1 in Cutaneous Squamous Cell Carcinoma. Journal of Investigative Dermatology, 2017, 137, 772-775.	0.7	10
87	Loss-based estimation with cross-validation. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2003, 5, 56-68.	4.0	9
88	Ancestral Folate Promotes Neuronal Regeneration in Serial Generations of Progeny. Molecular Neurobiology, 2020, 57, 2048-2071.	4.0	8
89	Integrating quantitative information from ChIP-chip experiments into motif finding. Biostatistics, 2008, 9, 51-65.	1.5	6
90	Systematic evaluation of the impact of ChIP-seq read designs on genome coverage, peak identification, and allele-specific binding detection. BMC Bioinformatics, 2016, 17, 96.	2.6	6

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91	An empirical Bayes test for allelic-imbalance detection in ChIP-seq. Biostatistics, 2018, 19, 546-561.	1.5	6
92	Gene by environment interaction mouse model reveals a functional role for 5-hydroxymethylcytosine in neurodevelopmental disorders. Genome Research, 2022, 32, 266-279.	5.5	6
93	Data exploration, quality control and statistical analysis of ChIP-exo/nexus experiments. Nucleic Acids Research, 2017, 45, e145-e145.	14.5	5
94	SURF: integrative analysis of a compendium of RNA-seq and CLIP-seq datasets highlights complex governing of alternative transcriptional regulation by RNA-binding proteins. Genome Biology, 2020, 21, 139.	8.8	5
95	Bioinformatic analysis of neural stem cell differentiation. Journal of Biomolecular Techniques, 2007, 18, 205-12.	1.5	5
96	CMARRT: A TOOL FOR THE ANALYSIS OF CHIP-CHIP DATA FROM TILING ARRAYS BY INCORPORATING THE CORRELATION STRUCTURE. , 2007, , .		4
97	Regulatory Architecture of the RCA Gene Cluster Captures an Intragenic TAD Boundary, CTCF-Mediated Chromatin Looping and a Long-Range Intergenic Enhancer. Frontiers in Immunology, 0, 13, .	4.8	4
98	A hierarchical framework for state-space matrix inference and clustering. Annals of Applied Statistics, 2016, 10, 1348-1372.	1.1	3
99	INFIMA leverages multi-omics model organism data to identify effector genes of human GWAS variants. Genome Biology, 2021, 22, 241.	8.8	3
100	MOSAiCS-HMM: A Model-Based Approach for Detecting Regions of Histone Modifications from ChIP-Seq Data. , 2014, , 277-295.		3
101	scGAD: single-cell gene associating domain scores for exploratory analysis of scHi-C data. Bioinformatics, 2022, 38, 3642-3644.	4.1	3
102	In Silico Pooling of ChIP-seq Control Experiments. PLoS ONE, 2014, 9, e109691.	2.5	2
103	Multivariate Boosting for Integrative Analysis of High-Dimensional Cancer Genomic Data. Cancer Informatics, 2014, 13s7, CIN.S16353.	1.9	2
104	Annotation Regression for Genome-Wide Association Studies with an Application to Psychiatric Genomic Consortium Data. Statistics in Biosciences, 2017, 9, 50-72.	1.2	2
105	atSNPInfrastructure, a Case Study for Searching Billions of Records While Providing Significant Cost Savings over Cloud Providers. , 2018, 2018, 497-506.		2
106	PRAM: a novel pooling approach for discovering intergenic transcripts from large-scale RNA sequencing experiments. Genome Research, 2020, 30, 1655-1666.	5.5	2
107	MLG: multilayer graph clustering for multi-condition scRNA-seq data. Nucleic Acids Research, 2021, 49, e127-e127.	14.5	2
108	Estimation of the Bivariate Survival Function with Generalized Bivariate Right Censored Data Structures. Handbook of Statistics, 2003, 23, 143-173.	0.6	1

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109	iFunMed: Integrative functional mediation analysis of GWAS and eQTL studies. Genetic Epidemiology, 2019, 43, 742-760.	1.3	1
110	FreeHi-C spike-in simulations for benchmarking differential chromatin interaction detection. Methods, 2021, 189, 3-11.	3.8	1
111	Enhancer mechanisms governing developmental and regenerative hematopoietic programs. Experimental Hematology, 2017, 53, S28.	0.4	0
112	A MAD-Bayes Algorithm for State-Space Inference and Clustering with Application to Querying Large Collections of ChIP-Seq Data Sets. Journal of Computational Biology, 2017, 24, 472-485.	1.6	0
113	Genetic Determinants of the Definitive Hematopoietic Stem/Progenitor Cell Compartment. Blood, 2012, 120, 1226-1226.	1.4	0
114	Cistrome Control of Hematopoieitic Stem/Progenitor Cell Function. Blood, 2015, 126, 43-43.	1.4	0
115	A MAD-Bayes Algorithm for State-Space Inference and Clustering with Application to Querying Large Collections of ChIP-Seq Data Sets. Lecture Notes in Computer Science, 2016, , 19-36.	1.3	0
116	GATA/Heme Multi-Omics Reveals a Trace Metal-Dependent Erythrocyte Developmental Mechanism. Blood, 2018, 132, 500-500.	1.4	0
117	GATA2-Dependent Developmental and Regenerative Networks. Blood, 2019, 134, 1182-1182.	1.4	0