

SÃ¼ndÃ¼z KeleÅ

List of Publications by Year in descending order

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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	Gene by environment interaction mouse model reveals a functional role for 5-hydroxymethylcytosine in neurodevelopmental disorders. <i>Genome Research</i> , 2022, 32, 266-279.	5.5	6
2	scGAD: single-cell gene associating domain scores for exploratory analysis of scHi-C data. <i>Bioinformatics</i> , 2022, 38, 3642-3644.	4.1	3
3	FreeHi-C spike-in simulations for benchmarking differential chromatin interaction detection. <i>Methods</i> , 2021, 189, 3-11.	3.8	1
4	Transcriptome-wide transmission disequilibrium analysis identifies novel risk genes for autism spectrum disorder. <i>PLoS Genetics</i> , 2021, 17, e1009309.	3.5	14
5	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. <i>Frontiers in Immunology</i> , 2021, 12, 633654.	4.8	12
6	INFIMA leverages multi-omics model organism data to identify effector genes of human GWAS variants. <i>Genome Biology</i> , 2021, 22, 241.	8.8	3
7	PKM2â€™MEM33 axis regulates lipid homeostasis in cancer cells by controlling SCAP stability. <i>EMBO Journal</i> , 2021, 40, e108065.	7.8	24
8	Identification of direct transcriptional targets of NFATC2 that promote Î² cell proliferation. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	15
9	MLG: multilayer graph clustering for multi-condition scRNA-seq data. <i>Nucleic Acids Research</i> , 2021, 49, e127-e127.	14.5	2
10	FreeHi-C simulates high-fidelity Hi-C data for benchmarking and data augmentation. <i>Nature Methods</i> , 2020, 17, 37-40.	19.0	15
11	Ancestral Folate Promotes Neuronal Regeneration in Serial Generations of Progeny. <i>Molecular Neurobiology</i> , 2020, 57, 2048-2071.	4.0	8
12	Discovering How Heme Controls Genome Function Through Heme-omics. <i>Cell Reports</i> , 2020, 31, 107832.	6.4	21
13	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
14	Constructing and deconstructing GATA2-regulated cell fate programs to establish developmental trajectories. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	28
15	PRAM: a novel pooling approach for discovering intergenic transcripts from large-scale RNA sequencing experiments. <i>Genome Research</i> , 2020, 30, 1655-1666.	5.5	2
16	SURF: integrative analysis of a compendium of RNA-seq and CLIP-seq datasets highlights complex governing of alternative transcriptional regulation by RNA-binding proteins. <i>Genome Biology</i> , 2020, 21, 139.	8.8	5
17	CTCF loss mediates unique DNA hypermethylation landscapes in human cancers. <i>Clinical Epigenetics</i> , 2020, 12, 80.	4.1	32
18	Beta Cell Dedifferentiation Induced by IRE1Î± Deletion Prevents Type 1 Diabetes. <i>Cell Metabolism</i> , 2020, 31, 822-836.e5.	16.2	84

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19	GATA factor-regulated solute carrier ensemble reveals a nucleoside transporter-dependent differentiation mechanism. <i>PLoS Genetics</i> , 2020, 16, e1009286.	3.5	13
20	iFunMed: Integrative functional mediation analysis of GWAS and eQTL studies. <i>Genetic Epidemiology</i> , 2019, 43, 742-760.	1.3	1
21	Epstein-Barr Virus Infection Promotes Epithelial Cell Growth by Attenuating Differentiation-Dependent Exit from the Cell Cycle. <i>MBio</i> , 2019, 10, .	4.1	25
22	Unbiased screen of RNA tailing activities reveals a poly(UG) polymerase. <i>Nature Methods</i> , 2019, 16, 437-445.	19.0	52
23	atSNP Search: a web resource for statistically evaluating influence of human genetic variation on transcription factor binding. <i>Bioinformatics</i> , 2019, 35, 2657-2659.	4.1	21
24	Single-nucleotide human disease mutation inactivates a blood-regenerative GATA2 enhancer. <i>Journal of Clinical Investigation</i> , 2019, 129, 1180-1192.	8.2	47
25	Generative modeling of multi-mapping reads with mHi-C advances analysis of Hi-C studies. <i>ELife</i> , 2019, 8, .	6.0	28
26	GATA2-Dependent Developmental and Regenerative Networks. <i>Blood</i> , 2019, 134, 1182-1182.	1.4	0
27	Mechanisms of erythrocyte development and regeneration: implications for regenerative medicine and beyond. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	107
28	An empirical Bayes test for allelic-imbalance detection in ChIP-seq. <i>Biostatistics</i> , 2018, 19, 546-561.	1.5	6
29	atSNPInfrastructure, a Case Study for Searching Billions of Records While Providing Significant Cost Savings over Cloud Providers. , 2018, 2018, 497-506.		2
30	GATA/Heme Multi-omics Reveals a Trace Metal-Dependent Cellular Differentiation Mechanism. <i>Developmental Cell</i> , 2018, 46, 581-594.e4.	7.0	31
31	GATA/Heme Multi-Omics Reveals a Trace Metal-Dependent Erythrocyte Developmental Mechanism. <i>Blood</i> , 2018, 132, 500-500.	1.4	0
32	Predicting gene expression in massively parallel reporter assays: A comparative study. <i>Human Mutation</i> , 2017, 38, 1240-1250.	2.5	39
33	RNA-Binding Protein IGF2BP1 in Cutaneous Squamous Cell Carcinoma. <i>Journal of Investigative Dermatology</i> , 2017, 137, 772-775.	0.7	10
34	GLANET: genomic loci annotation and enrichment tool. <i>Bioinformatics</i> , 2017, 33, 2818-2828.	4.1	15
35	O ₂ availability impacts iron homeostasis in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12261-12266.	7.1	72
36	Enhancer mechanisms governing developmental and regenerative hematopoietic programs. <i>Experimental Hematology</i> , 2017, 53, S28.	0.4	0

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37	Annotation Regression for Genome-Wide Association Studies with an Application to Psychiatric Genomic Consortium Data. <i>Statistics in Biosciences</i> , 2017, 9, 50-72.	1.2	2
38	GATA Factor-Regulated Samd14 Enhancer Confers Red Blood Cell Regeneration and Survival in Severe Anemia. <i>Developmental Cell</i> , 2017, 42, 213-225.e4.	7.0	29
39	A MAD-Bayes Algorithm for State-Space Inference and Clustering with Application to Querying Large Collections of ChIP-Seq Data Sets. <i>Journal of Computational Biology</i> , 2017, 24, 472-485.	1.6	0
40	Data exploration, quality control and statistical analysis of ChIP-exo/nexus experiments. <i>Nucleic Acids Research</i> , 2017, 45, e145-e145.	14.5	5
41	Misregulation of Alternative Splicing in a Mouse Model of Rett Syndrome. <i>PLoS Genetics</i> , 2016, 12, e1006129.	3.5	57
42	Integrative analysis with ChIP-seq advances the limits of transcript quantification from RNA-seq. <i>Genome Research</i> , 2016, 26, 1124-1133.	5.5	19
43	Regulation of WNT Signaling by VSX2 During Optic Vesicle Patterning in Human Induced Pluripotent Stem Cells. <i>Stem Cells</i> , 2016, 34, 2625-2634.	3.2	41
44	Sex-specific hippocampal 5-hydroxymethylcytosine is disrupted in response to acute stress. <i>Neurobiology of Disease</i> , 2016, 96, 54-66.	4.4	24
45	A hierarchical framework for state-space matrix inference and clustering. <i>Annals of Applied Statistics</i> , 2016, 10, 1348-1372.	1.1	3
46	Systematic evaluation of the impact of ChIP-seq read designs on genome coverage, peak identification, and allele-specific binding detection. <i>BMC Bioinformatics</i> , 2016, 17, 96.	2.6	6
47	Epstein-Barr Virus Nuclear Antigen 3 (EBNA3) Proteins Regulate EBNA2 Binding to Distinct RBPJ Genomic Sites. <i>Journal of Virology</i> , 2016, 90, 2906-2919.	3.4	35
48	Genome-wide alterations in hippocampal 5-hydroxymethylcytosine links plasticity genes to acute stress. <i>Neurobiology of Disease</i> , 2016, 86, 99-108.	4.4	48
49	A MAD-Bayes Algorithm for State-Space Inference and Clustering with Application to Querying Large Collections of ChIP-Seq Data Sets. <i>Lecture Notes in Computer Science</i> , 2016, , 19-36.	1.3	0
50	Differential Sox10 genomic occupancy in myelinating glia. <i>Glia</i> , 2015, 63, 1897-1914.	4.9	84
51	Fungal Morphology, Iron Homeostasis, and Lipid Metabolism Regulated by a GATA Transcription Factor in <i>Blastomyces dermatitidis</i> . <i>PLoS Pathogens</i> , 2015, 11, e1004959.	4.7	16
52	Impact of Anaerobiosis on Expression of the Iron-Responsive Fur and RyhB Regulons. <i>MBio</i> , 2015, 6, e01947-15.	4.1	67
53	Integromic Analysis of Genetic Variation and Gene Expression Identifies Networks for Cardiovascular Disease Phenotypes. <i>Circulation</i> , 2015, 131, 536-549.	1.6	65
54	Dynamic Regulation of Schwann Cell Enhancers after Peripheral Nerve Injury. <i>Journal of Biological Chemistry</i> , 2015, 290, 6937-6950.	3.4	98

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55	Hematopoietic Signaling Mechanism Revealed from a Stem/Progenitor Cell Cistrome. <i>Molecular Cell</i> , 2015, 59, 62-74.	9.7	40
56	atSNP: transcription factor binding affinity testing for regulatory SNP detection. <i>Bioinformatics</i> , 2015, 31, 3353-3355.	4.1	81
57	Genome-wide disruption of 5-hydroxymethylcytosine in a mouse model of autism. <i>Human Molecular Genetics</i> , 2015, 24, ddv411.	2.9	38
58	Perm-seq: Mapping Protein-DNA Interactions in Segmental Duplication and Highly Repetitive Regions of Genomes with Prior-Enhanced Read Mapping. <i>PLoS Computational Biology</i> , 2015, 11, e1004491.	3.2	11
59	Cistrome Control of Hematopoietic Stem/Progenitor Cell Function. <i>Blood</i> , 2015, 126, 43-43.	1.4	0
60	In Silico Pooling of ChIP-seq Control Experiments. <i>PLoS ONE</i> , 2014, 9, e109691.	2.5	2
61	Epigenetic and genetic mechanisms in red cell biology. <i>Current Opinion in Hematology</i> , 2014, 21, 155-164.	2.5	10
62	CNV-guided multi-read allocation for ChIP-seq. <i>Bioinformatics</i> , 2014, 30, 2860-2867.	4.1	10
63	Differentially Methylated Plasticity Genes in the Amygdala of Young Primates Are Linked to Anxious Temperament, an at Risk Phenotype for Anxiety and Depressive Disorders. <i>Journal of Neuroscience</i> , 2014, 34, 15548-15556.	3.6	41
64	A statistical framework for power calculations in ChIP-seq experiments. <i>Bioinformatics</i> , 2014, 30, 753-760.	4.1	14
65	Hematopoietic transcriptional mechanisms: From locus-specific to genome-wide vantage points. <i>Experimental Hematology</i> , 2014, 42, 618-629.	0.4	19
66	Multivariate Boosting for Integrative Analysis of High-Dimensional Cancer Genomic Data. <i>Cancer Informatics</i> , 2014, 13s7, CIN.S16353.	1.9	2
67	MOSAIcs-HMM: A Model-Based Approach for Detecting Regions of Histone Modifications from ChIP-Seq Data. , 2014, , 277-295.		3
68	Effects of Sleep and Wake on Oligodendrocytes and Their Precursors. <i>Journal of Neuroscience</i> , 2013, 33, 14288-14300.	3.6	213
69	Research Resource: Global Identification of Estrogen Receptor $\hat{1}^2$ Target Genes in Triple Negative Breast Cancer Cells. <i>Molecular Endocrinology</i> , 2013, 27, 1762-1775.	3.7	52
70	dPeak: High Resolution Identification of Transcription Factor Binding Sites from PET and SET ChIP-Seq Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003246.	3.2	15
71	Genome-scale Analysis of Escherichia coli FNR Reveals Complex Features of Transcription Factor Binding. <i>PLoS Genetics</i> , 2013, 9, e1003565.	3.5	158
72	Statistical Analysis of ChIP-seq Data with MOSAIcs. <i>Methods in Molecular Biology</i> , 2013, 1038, 193-212.	0.9	22

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73	Genome-wide analysis of EGR2/SOX10 binding in myelinating peripheral nerve. <i>Nucleic Acids Research</i> , 2012, 40, 6449-6460.	14.5	81
74	Divergence of Pumilio/fem-3 mRNA Binding Factor (PUF) Protein Specificity through Variations in an RNA-binding Pocket. <i>Journal of Biological Chemistry</i> , 2012, 287, 6949-6957.	3.4	37
75	Dynamic Changes in Nucleosome Occupancy Are Not Predictive of Gene Expression Dynamics but Are Linked to Transcription and Chromatin Regulators. <i>Molecular and Cellular Biology</i> , 2012, 32, 1645-1653.	2.3	57
76	Distal enhancers upstream of the Charcot-Marie-Tooth type 1A disease gene PMP22. <i>Human Molecular Genetics</i> , 2012, 21, 1581-1591.	2.9	32
77	Autophagy Driven by a Master Regulator of Hematopoiesis. <i>Molecular and Cellular Biology</i> , 2012, 32, 226-239.	2.3	119
78	Detecting differential binding of transcription factors with ChIP-seq. <i>Bioinformatics</i> , 2012, 28, 121-122.	4.1	104
79	Angiogenesis Induced by Signal Transducer and Activator of Transcription 5A (STAT5A) Is Dependent on Autocrine Activity of Proliferin. <i>Journal of Biological Chemistry</i> , 2012, 287, 6490-6502.	3.4	23
80	Cis-element mutated in GATA2-dependent immunodeficiency governs hematopoiesis and vascular integrity. <i>Journal of Clinical Investigation</i> , 2012, 122, 3692-3704.	8.2	162
81	Identification of Estrogen Receptor Dimer Selective Ligands Reveals Growth-Inhibitory Effects on Cells That Co-Express ER α and ER β . <i>PLoS ONE</i> , 2012, 7, e30993.	2.5	62
82	Genetic Determinants of the Definitive Hematopoietic Stem/Progenitor Cell Compartment. <i>Blood</i> , 2012, 120, 1226-1226.	1.4	0
83	A Statistical Framework for the Analysis of ChIP-Seq Data. <i>Journal of the American Statistical Association</i> , 2011, 106, 891-903.	3.1	100
84	Genetic framework for GATA factor function in vascular biology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13641-13646.	7.1	96
85	Discovering Transcription Factor Binding Sites in Highly Repetitive Regions of Genomes with Multi-Read Analysis of ChIP-Seq Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002111.	3.2	73
86	Locus-wide identification of Egr2/Krox20 regulatory targets in myelin genes. <i>Journal of Neurochemistry</i> , 2010, 115, 1409-1420.	3.9	38
87	Chemical-genomic dissection of the CTD code. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1154-1161.	8.2	130
88	Transient Genotype-by-Environment Interactions Following Environmental Shock Provide a Source of Expression Variation for Essential Genes. <i>Genetics</i> , 2010, 184, 587-593.	2.9	18
89	GATA Switches as Developmental Drivers. <i>Journal of Biological Chemistry</i> , 2010, 285, 31087-31093.	3.4	235
90	Rho directs widespread termination of intragenic and stable RNA transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15406-15411.	7.1	192

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91	A single <i>C. elegans</i> PUF protein binds RNA in multiple modes. <i>Rna</i> , 2009, 15, 1090-1099.	3.5	42
92	Expression Quantitative Trait Loci Mapping With Multivariate Sparse Partial Least Squares Regression. <i>Genetics</i> , 2009, 182, 79-90.	2.9	79
93	A Phylogenetic Mixture Model for the Evolution of Gene Expression. <i>Molecular Biology and Evolution</i> , 2009, 26, 2363-2372.	8.9	13
94	Discovering Hematopoietic Mechanisms through Genome-wide Analysis of GATA Factor Chromatin Occupancy. <i>Molecular Cell</i> , 2009, 36, 667-681.	9.7	314
95	Comments on: Augmenting the bootstrap to analyze high dimensional genomic data. <i>Test</i> , 2008, 17, 36-39.	1.1	13
96	Integrating quantitative information from ChIP-chip experiments into motif finding. <i>Biostatistics</i> , 2008, 9, 51-65.	1.5	6
97	Molecular Hallmarks of Endogenous Chromatin Complexes Containing Master Regulators of Hematopoiesis. <i>Molecular and Cellular Biology</i> , 2008, 28, 6681-6694.	2.3	57
98	A study of the relationships between oligonucleotide properties and hybridization signal intensities from NimbleGen microarray datasets. <i>Nucleic Acids Research</i> , 2008, 36, 2926-2938.	14.5	38
99	CSI-Tree: a regression tree approach for modeling binding properties of DNA-binding molecules based on cognate site identification (CSI) data. <i>Nucleic Acids Research</i> , 2008, 36, 3171-3184.	14.5	14
100	Mixture models with multiple levels, with application to the analysis of multifactor gene expression data. <i>Biostatistics</i> , 2008, 9, 540-554.	1.5	24
101	CMARRT: a tool for the analysis of ChIP-chip data from tiling arrays by incorporating the correlation structure. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2008, , 515-26.	0.7	26
102	Transcription of histone gene cluster by differential core-promoter factors. <i>Genes and Development</i> , 2007, 21, 2936-2949.	5.9	96
103	Increases in Central Aortic Impedance Precede Alterations in Arterial Stiffness Measures in Type 1 Diabetes. <i>Diabetes Care</i> , 2007, 30, 2886-2891.	8.6	41
104	Novel TRF1/BRF target genes revealed by genome-wide analysis of Drosophila Pol III transcription. <i>EMBO Journal</i> , 2007, 26, 79-89.	7.8	41
105	Mixture Modeling for Genome-Wide Localization of Transcription Factors. <i>Biometrics</i> , 2007, 63, 10-21.	1.4	38
106	CMARRT: A TOOL FOR THE ANALYSIS OF CHIP-CHIP DATA FROM TILING ARRAYS BY INCORPORATING THE CORRELATION STRUCTURE. , 2007, , .		4
107	Bioinformatic analysis of neural stem cell differentiation. <i>Journal of Biomolecular Techniques</i> , 2007, 18, 205-12.	1.5	5
108	Multiple Testing Methods For ChIPâ€“Chip High Density Oligonucleotide Array Data. <i>Journal of Computational Biology</i> , 2006, 13, 579-613.	1.6	44

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109	Expression Profiling of GABAergic Motor Neurons in <i>Caenorhabditis elegans</i> . <i>Current Biology</i> , 2005, 15, 340-346.	3.9	100
110	Framework for kernel regularization with application to protein clustering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12332-12337.	7.1	36
111	Exploratory and Confirmatory Gene Expression Profiling of <i>mac1</i> ⁺ . <i>Journal of Biological Chemistry</i> , 2004, 279, 4450-4458.	3.4	43
112	Asymptotically optimal model selection method with right censored outcomes. <i>Bernoulli</i> , 2004, 10, 1011.	1.3	10
113	Supervised Detection of Regulatory Motifs in DNA Sequences. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2003, 2, Article5.	0.6	15
114	Estimation of the Bivariate Survival Function with Generalized Bivariate Right Censored Data Structures. <i>Handbook of Statistics</i> , 2003, 23, 143-173.	0.6	1
115	Loss-based estimation with cross-validation. <i>SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining</i> , 2003, 5, 56-68.	4.0	9
116	Residual-based tree-structured survival analysis. <i>Statistics in Medicine</i> , 2002, 21, 313-326.	1.6	44
117	Regulatory Architecture of the RCA Gene Cluster Captures an Intragenic TAD Boundary, CTCF-Mediated Chromatin Looping and a Long-Range Intergenic Enhancer. <i>Frontiers in Immunology</i> , 0, 13, .	4.8	4