Stefan Bekiranov

List of Publications by Year in descending order

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80 papers 9,811 citations

36 h-index 78 g-index

81 all docs

81 docs citations

81 times ranked 14209 citing authors

#	Article	IF	CITATIONS
1	Genomic Maps and Comparative Analysis of Histone Modifications in Human and Mouse. Cell, 2005, 120, 169-181.	28.9	1,348
2	Genome-wide analysis of estrogen receptor binding sites. Nature Genetics, 2006, 38, 1289-1297.	21.4	1,227
3	Transcriptional Maps of 10 Human Chromosomes at 5-Nucleotide Resolution. Science, 2005, 308, 1149-1154.	12.6	1,073
4	Unbiased Mapping of Transcription Factor Binding Sites along Human Chromosomes 21 and 22 Points to Widespread Regulation of Noncoding RNAs. Cell, 2004, 116, 499-509.	28.9	1,047
5	Large-Scale Transcriptional Activity in Chromosomes 21 and 22. Science, 2002, 296, 916-919.	12.6	793
6	Novel RNAs Identified From an In-Depth Analysis of the Transcriptome of Human Chromosomes 21 and 22. Genome Research, 2004, 14, 331-342.	5 . 5	460
7	Reprogramming of the Macrophage Transcriptome in Response to Interferon- \hat{I}^3 and Mycobacterium tuberculosis. Journal of Experimental Medicine, 2001, 194, 1123-1140.	8.5	437
8	Stem Cell Pluripotency Genes Klf4 and Oct4 Regulate Complex SMC Phenotypic Changes Critical in Late-Stage Atherosclerotic Lesion Pathogenesis. Circulation, 2020, 142, 2045-2059.	1.6	221
9	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. Science, 2017, 356, .	12.6	206
10	A Microarray-Based Genetic Screen for Yeast Chronological Aging Factors. PLoS Genetics, 2010, 6, e1000921.	3 . 5	198
11	Human Adipose-Derived Stromal Cells Accelerate Diabetic Wound Healing: Impact of Cell Formulation and Delivery. Tissue Engineering - Part A, 2010, 16, 1595-1606.	3.1	176
12	Activation of the pluripotency factor OCT4 in smooth muscle cells is atheroprotective. Nature Medicine, 2016, 22, 657-665.	30.7	165
13	Solution behavior of polyethylene oxide in water as a function of temperature and pressure. Physical Review E, 1997, 55, 577-585.	2.1	150
14	Diffusion in Inhomogeneous Media: Theory and Simulations Applied to Whole Cell Photobleach Recovery. Biophysical Journal, 2000, 79, 1761-1770.	0.5	121
15	Probe selection for high-density oligonucleotide arrays. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 11237-11242.	7.1	117
16	Temporal profile of replication of human chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 6419-6424.	7.1	105
17	NF-ÎB Regulates Mesenchymal Transition for the Induction of Non-Small Cell Lung Cancer Initiating Cells. PLoS ONE, 2013, 8, e68597.	2.5	95
18	Tolerogenic Properties of Lymphatic Endothelial Cells Are Controlled by the Lymph Node Microenvironment. PLoS ONE, 2014, 9, e87740.	2. 5	95

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19	Bubble-seq analysis of the human genome reveals distinct chromatin-mediated mechanisms for regulating early- and late-firing origins. Genome Research, 2013, 23, 1774-1788.	5.5	86
20	Measuring Chromatin Interaction Dynamics on the Second Time Scale at Single-Copy Genes. Science, 2013, 342, 369-372.	12.6	83
21	Bubble-chip analysis of human origin distributions demonstrates on a genomic scale significant clustering into zones and significant association with transcription. Genome Research, 2011, 21, 377-389.	5.5	78
22	Microenvironmental agonists generate de novo phenotypic resistance to combined ibrutinib plus venetoclax in CLL and MCL. Blood Advances, 2017, 1, 933-946.	5.2	75
23	Making the most of microarray data. Nature Genetics, 2000, 24, 204-206.	21.4	74
24	Application of machine learning methods to histone methylation ChIP-Seq data reveals H4R3me2 globally represses gene expression. BMC Bioinformatics, 2010, 11, 396.	2.6	74
25	Activin Upregulation by NF-κB Is Required to Maintain Mesenchymal Features of Cancer Stem–like Cells in Non–Small Cell Lung Cancer. Cancer Research, 2015, 75, 426-435.	0.9	73
26	Microarray-Based Analysis of Early Development in Xenopus laevis. Developmental Biology, 2001, 236, 64-75.	2.0	70
27	Thiamine Biosynthesis in <i>Saccharomyces cerevisiae</i> Is Regulated by the NAD ⁺ -Dependent Histone Deacetylase Hst1. Molecular and Cellular Biology, 2010, 30, 3329-3341.	2.3	64
28	Quantum computing at the frontiers of biological sciences. Nature Methods, 2021, 18, 701-709.	19.0	64
29	Compensatory Pathways Induced by MEK Inhibition Are Effective Drug Targets for Combination Therapy against Castration-Resistant Prostate Cancer. Molecular Cancer Therapeutics, 2011, 10, 1581-1590.	4.1	63
30	Neurons with Complex Karyotypes Are Rare in Aged Human Neocortex. Cell Reports, 2019, 26, 825-835.e7.	6.4	60
31	Homology-based annotation yields 1,042 new candidate genes in the Drosophila melanogaster genome. Nature Genetics, 2001, 27, 337-340.	21.4	58
32	Genome-wide analysis of functional sirtuin chromatin targets in yeast. Genome Biology, 2013, 14, R48.	9.6	53
33	Sexual differentiation in the developing mouse brain: contributions of sex chromosome genes. Genes, Brain and Behavior, 2013, 12, 166-180.	2.2	48
34	Alternative DNA secondary structure formation affects RNA polymerase II promoter-proximal pausing in human. Genome Biology, 2018, 19, 89.	8.8	44
35	Reelin is a target of polyglutamine expanded ataxin-7 in human spinocerebellar ataxia type 7 (SCA7) astrocytes. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21319-21324.	7.1	42
36	Epigenetic coordination of signaling pathways during the epithelial-mesenchymal transition. Epigenetics and Chromatin, 2013, 6, 28.	3.9	42

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37	The Modifier of Transcription 1 (Mot1) ATPase and Spt16 Histone Chaperone Co-regulate Transcription through Preinitiation Complex Assembly and Nucleosome Organization. Journal of Biological Chemistry, 2016, 291, 15307-15319.	3.4	33
38	NF-κB upregulates glutamine-fructose-6-phosphate transaminase 2 to promote migration in non-small cell lung cancer. Cell Communication and Signaling, 2019, 17, 24.	6.5	33
39	A pan-cancer analysis of prognostic genes. PeerJ, 2015, 3, e1499.	2.0	32
40	Temporal and Spatial Epigenome Editing Allows Precise Gene Regulation in Mammalian Cells. Journal of Molecular Biology, 2019, 431, 111-121.	4.2	31
41	Use of Yeast Chemigenomics and COXEN Informatics in Preclinical Evaluation of Anticancer Agents. Neoplasia, 2011, 13, 72-IN19.	5.3	27
42	An evolutionarily †young †lysine residue in histone H3 attenuates transcriptional output in <i>Saccharomyces cerevisiae i>. Genes and Development, 2011, 25, 1306-1319.</i>	5.9	27
43	The Snf1 kinase and proteasome-associated Rad23 regulate UV-responsive gene expression. EMBO Journal, 2009, 28, 2919-2931.	7.8	24
44	Amyloid \hat{l}^2 Precursor Protein Regulates Male Sexual Behavior. Journal of Neuroscience, 2010, 30, 9967-9972.	3.6	23
45	Histone H3 lysine 4 methylation signature associated with human undernutrition. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11264-E11273.	7.1	23
46	Pausing sites of RNA polymerase II on actively transcribed genes are enriched in DNA double-stranded breaks. Journal of Biological Chemistry, 2020, 295, 3990-4000.	3.4	21
47	High-content phenotypic assay for proliferation of human iPSC-derived cardiomyocytes identifies L-type calcium channels as targets. Journal of Molecular and Cellular Cardiology, 2019, 127, 204-214.	1.9	20
48	Combinatorial drug screening and molecular profiling reveal diverse mechanisms of intrinsic and adaptive resistance to BRAF inhibition in V600E BRAF mutant melanomas. Oncotarget, 2016, 7, 2734-2753.	1.8	19
49	Fluctuations in Electrolytes: The Lebowitz and Other Correlation Lengths. Physical Review Letters, 1998, 81, 5836-5839.	7.8	18
50	Diverging correlation lengths in electrolytes: Exact results at low densities. Physical Review E, 1999, 59, 492-511.	2.1	18
51	Combinatorial epigenetic patterns as quantitative predictors of chromatin biology. BMC Genomics, 2014, 15, 76.	2.8	18
52	Implementation of a Hamming distance–like genomic quantum classifier using inner products on ibmqx2 and ibmq_16_melbourne. Quantum Machine Intelligence, 2020, 2, 1-26.	4.8	16
53	Genome-wide predictors of NF-κB recruitment and transcriptional activity. BioData Mining, 2015, 8, 37.	4.0	14
54	HIV-1 Rev interacts with HERV-K RcREs present in the human genome and promotes export of unspliced HERV-K proviral RNA. Retrovirology, 2019, 16, 40.	2.0	14

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55	Transcriptomes of six mutants in the Sen1 pathway reveal combinatorial control of transcription termination across the Saccharomyces cerevisiae genome. PLoS Genetics, 2017, 13, e1006863.	3.5	14
56	Epigenetic methodologies for behavioral scientists. Hormones and Behavior, 2011, 59, 407-416.	2.1	13
57	Second-generation method for analysis of chromatin binding with formaldehyde–cross-linking kinetics. Journal of Biological Chemistry, 2017, 292, 19338-19355.	3.4	13
58	Yeast genome analysis identifies chromosomal translocation, gene conversion events and several sites of Ty element insertion. Nucleic Acids Research, 2009, 37, 6454-6465.	14.5	12
59	RNA synthesis precision is regulated by preinitiation complex turnover. Genome Research, 2010, 20, 1679-1688.	5.5	12
60	Upregulation of human endogenous retrovirus-K (HML-2) mRNAs in hepatoblastoma: Identification of potential new immunotherapeutic targets and biomarkers. Journal of Pediatric Surgery, 2021, 56, 286-292.	1.6	12
61	Inhibition of DYRK1a Enhances Cardiomyocyte Cycling After Myocardial Infarction. Circulation Research, 2022, 130, 1345-1361.	4.5	12
62	Quantification of histone modification ChIP-seq enrichment for data mining and machine learning applications. BMC Research Notes, 2011, 4, 288.	1.4	10
63	The Network Architecture of the Saccharomyces cerevisiae Genome. PLoS ONE, 2013, 8, e81972.	2.5	10
64	A Machine Learning Model Utilizing a Novel SNP Shows Enhanced Prediction of Coronary Artery Disease Severity. Genes, 2020, 11, 1446.	2.4	10
65	Functional genomic analysis reveals overlapping and distinct features of chronologically long-lived yeast populations. Aging, 2015, 7, 177-194.	3.1	10
66	Analysis of chromatin binding dynamics using the crosslinking kinetics (CLK) method. Methods, 2014, 70, 97-107.	3.8	9
67	Systems Analysis of Adaptive Responses to MAP Kinase Pathway Blockade in BRAF Mutant Melanoma. PLoS ONE, 2015, 10, e0138210.	2.5	9
68	IGF1R and Src inhibition induce synergistic cytotoxicity in HNSCC through inhibition of FAK. Scientific Reports, 2021, 11, 10826.	3.3	9
69	Associations of immune cell homing gene signatures and infiltrates of lymphocyte subsets in human melanomas: discordance with CD163+ myeloid cell infiltrates. Journal of Translational Medicine, 2021, 19, 371.	4.4	9
70	Error-pooling-based statistical methods for identifying novel temporal replication profiles of human chromosomes observed by DNA tiling arrays. Nucleic Acids Research, 2007, 35, e69.	14.5	8
71	A Sir2-regulated locus control region in the recombination enhancer of Saccharomyces cerevisiae specifies chromosome III structure. PLoS Genetics, 2019, 15, e1008339.	3.5	8
72	RNA synthesis is associated with multiple TBP-chromatin binding events. Scientific Reports, 2017, 7, 39631.	3.3	7

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73	Genomic and evolutionary portraits of disease relapse in acute myeloid leukemia. Leukemia, 2021, 35, 2688-2692.	7.2	7
74	Systems analysis of barrier molecule and ARNT-related gene expression regulation in melanoma. Oncolmmunology, 2019, 8, e1665978.	4.6	6
75	Charge and density fluctuations in electrolytes: The Lebowitz and other correlation lengths. Physica A: Statistical Mechanics and Its Applications, 1999, 263, 466-476.	2.6	5
76	Antitumor effect of insulinâ€like growth factorâ€1 receptor inhibition in head and neck squamous cell carcinoma. Laryngoscope, 2020, 130, 1470-1478.	2.0	5
77	Human endogenous retrovirus-K mRNA expression and genomic alignment data in hepatoblastoma. Data in Brief, 2020, 31, 105895.	1.0	4
78	An Improved Method for Measuring Chromatin-binding Dynamics Using Time-dependent Formaldehyde Crosslinking. Bio-protocol, 2018, 8, .	0.4	1
79	Extrinsic Factors in the In Vivo Macroenvironment Generate Phenotypic Resistance to BTK/Bcl-2 Targeted Therapies in Chronic Lymphocytic Leukemia and Mantle Cell Lymphoma. Blood, 2016, 128, 754-754.	1.4	0
80	Elucidating Epigenetic Readers of H3T45ph in S. cerevisiae. FASEB Journal, 2018, 32, 524.14.	0.5	0