

Stefan Bekiranov

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

9,811
citations

101496

36
h-index

66879

78
g-index

81
all docs

81
docs citations

81
times ranked

14209
citing authors

#	ARTICLE	IF	CITATIONS
1	Inhibition of DYRK1a Enhances Cardiomyocyte Cycling After Myocardial Infarction. <i>Circulation Research</i> , 2022, 130, 1345-1361.	2.0	12
2	Quantum computing at the frontiers of biological sciences. <i>Nature Methods</i> , 2021, 18, 701-709.	9.0	64
3	Genomic and evolutionary portraits of disease relapse in acute myeloid leukemia. <i>Leukemia</i> , 2021, 35, 2688-2692.	3.3	7
4	Upregulation of human endogenous retrovirus-K (HML-2) mRNAs in hepatoblastoma: Identification of potential new immunotherapeutic targets and biomarkers. <i>Journal of Pediatric Surgery</i> , 2021, 56, 286-292.	0.8	12
5	IGF1R and Src inhibition induce synergistic cytotoxicity in HNSCC through inhibition of FAK. <i>Scientific Reports</i> , 2021, 11, 10826.	1.6	9
6	Associations of immune cell homing gene signatures and infiltrates of lymphocyte subsets in human melanomas: discordance with CD163+ myeloid cell infiltrates. <i>Journal of Translational Medicine</i> , 2021, 19, 371.	1.8	9
7	Antitumor effect of insulin-like growth factor-1 receptor inhibition in head and neck squamous cell carcinoma. <i>Laryngoscope</i> , 2020, 130, 1470-1478.	1.1	5
8	Implementation of a Hamming distance-like genomic quantum classifier using inner products on ibmqx2 and ibmq_16_melbourne. <i>Quantum Machine Intelligence</i> , 2020, 2, 1-26.	2.7	16
9	Stem Cell Pluripotency Genes Klf4 and Oct4 Regulate Complex SMC Phenotypic Changes Critical in Late-Stage Atherosclerotic Lesion Pathogenesis. <i>Circulation</i> , 2020, 142, 2045-2059.	1.6	221
10	Human endogenous retrovirus-K mRNA expression and genomic alignment data in hepatoblastoma. <i>Data in Brief</i> , 2020, 31, 105895.	0.5	4
11	A Machine Learning Model Utilizing a Novel SNP Shows Enhanced Prediction of Coronary Artery Disease Severity. <i>Genes</i> , 2020, 11, 1446.	1.0	10
12	Pausing sites of RNA polymerase II on actively transcribed genes are enriched in DNA double-stranded breaks. <i>Journal of Biological Chemistry</i> , 2020, 295, 3990-4000.	1.6	21
13	Temporal and Spatial Epigenome Editing Allows Precise Gene Regulation in Mammalian Cells. <i>Journal of Molecular Biology</i> , 2019, 431, 111-121.	2.0	31
14	A Sir2-regulated locus control region in the recombination enhancer of <i>Saccharomyces cerevisiae</i> specifies chromosome III structure. <i>PLoS Genetics</i> , 2019, 15, e1008339.	1.5	8
15	Neurons with Complex Karyotypes Are Rare in Aged Human Neocortex. <i>Cell Reports</i> , 2019, 26, 825-835.e7.	2.9	60
16	NF- κ B upregulates glutamine-fructose-6-phosphate transaminase 2 to promote migration in non-small cell lung cancer. <i>Cell Communication and Signaling</i> , 2019, 17, 24.	2.7	33
17	Systems analysis of barrier molecule and ARNT-related gene expression regulation in melanoma. <i>Oncolmmunology</i> , 2019, 8, e1665978.	2.1	6
18	HIV-1 Rev interacts with HERV-K RcREs present in the human genome and promotes export of unspliced HERV-K proviral RNA. <i>Retrovirology</i> , 2019, 16, 40.	0.9	14

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19	High-content phenotypic assay for proliferation of human iPSC-derived cardiomyocytes identifies L-type calcium channels as targets. <i>Journal of Molecular and Cellular Cardiology</i> , 2019, 127, 204-214.	0.9	20
20	Histone H3 lysine 4 methylation signature associated with human undernutrition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11264-E11273.	3.3	23
21	Alternative DNA secondary structure formation affects RNA polymerase II promoter-proximal pausing in human. <i>Genome Biology</i> , 2018, 19, 89.	3.8	44
22	An Improved Method for Measuring Chromatin-binding Dynamics Using Time-dependent Formaldehyde Crosslinking. <i>Bio-protocol</i> , 2018, 8, .	0.2	1
23	Elucidating Epigenetic Readers of H3T45ph in <i>S. cerevisiae</i> . <i>FASEB Journal</i> , 2018, 32, 524.14.	0.2	0
24	RNA synthesis is associated with multiple TBP-chromatin binding events. <i>Scientific Reports</i> , 2017, 7, 39631.	1.6	7
25	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. <i>Science</i> , 2017, 356, .	6.0	206
26	Second-generation method for analysis of chromatin binding with formaldehydeâ€“cross-linking kinetics. <i>Journal of Biological Chemistry</i> , 2017, 292, 19338-19355.	1.6	13
27	Microenvironmental agonists generate de novo phenotypic resistance to combined ibrutinib plus venetoclax in CLL and MCL. <i>Blood Advances</i> , 2017, 1, 933-946.	2.5	75
28	Transcriptomes of six mutants in the Sen1 pathway reveal combinatorial control of transcription termination across the <i>Saccharomyces cerevisiae</i> genome. <i>PLoS Genetics</i> , 2017, 13, e1006863.	1.5	14
29	The Modifier of Transcription 1 (Mot1) ATPase and Spt16 Histone Chaperone Co-regulate Transcription through Preinitiation Complex Assembly and Nucleosome Organization. <i>Journal of Biological Chemistry</i> , 2016, 291, 15307-15319.	1.6	33
30	Activation of the pluripotency factor OCT4 in smooth muscle cells is atheroprotective. <i>Nature Medicine</i> , 2016, 22, 657-665.	15.2	165
31	Combinatorial drug screening and molecular profiling reveal diverse mechanisms of intrinsic and adaptive resistance to BRAF inhibition in V600E BRAF mutant melanomas. <i>Oncotarget</i> , 2016, 7, 2734-2753.	0.8	19
32	Extrinsic Factors in the In Vivo Macroenvironment Generate Phenotypic Resistance to BTK/Bcl-2 Targeted Therapies in Chronic Lymphocytic Leukemia and Mantle Cell Lymphoma. <i>Blood</i> , 2016, 128, 754-754.	0.6	0
33	Genome-wide predictors of NF- κ B recruitment and transcriptional activity. <i>BioData Mining</i> , 2015, 8, 37.	2.2	14
34	Systems Analysis of Adaptive Responses to MAP Kinase Pathway Blockade in BRAF Mutant Melanoma. <i>PLoS ONE</i> , 2015, 10, e0138210.	1.1	9
35	Activin Upregulation by NF- κ B Is Required to Maintain Mesenchymal Features of Cancer Stemâ€“like Cells in Nonâ€“Small Cell Lung Cancer. <i>Cancer Research</i> , 2015, 75, 426-435.	0.4	73
36	Functional genomic analysis reveals overlapping and distinct features of chronologically long-lived yeast populations. <i>Aging</i> , 2015, 7, 177-194.	1.4	10

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37	A pan-cancer analysis of prognostic genes. PeerJ, 2015, 3, e1499.	0.9	32
38	Analysis of chromatin binding dynamics using the crosslinking kinetics (CLK) method. Methods, 2014, 70, 97-107.	1.9	9
39	Combinatorial epigenetic patterns as quantitative predictors of chromatin biology. BMC Genomics, 2014, 15, 76.	1.2	18
40	Tolerogenic Properties of Lymphatic Endothelial Cells Are Controlled by the Lymph Node Microenvironment. PLoS ONE, 2014, 9, e87740.	1.1	95
41	Genome-wide analysis of functional sirtuin chromatin targets in yeast. Genome Biology, 2013, 14, R48.	13.9	53
42	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.	2.4	86
43	Epigenetic coordination of signaling pathways during the epithelial-mesenchymal transition. Epigenetics and Chromatin, 2013, 6, 28.	1.8	42
44	Sexual differentiation in the developing mouse brain: contributions of sex chromosome genes. Genes, Brain and Behavior, 2013, 12, 166-180.	1.1	48
45	Measuring Chromatin Interaction Dynamics on the Second Time Scale at Single-Copy Genes. Science, 2013, 342, 369-372.	6.0	83
46	NF- κ B Regulates Mesenchymal Transition for the Induction of Non-Small Cell Lung Cancer Initiating Cells. PLoS ONE, 2013, 8, e68597.	1.1	95
47	The Network Architecture of the Saccharomyces cerevisiae Genome. PLoS ONE, 2013, 8, e81972.	1.1	10
48	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.	3.3	42
49	Use of Yeast Chemigenomics and COXEN Informatics in Preclinical Evaluation of Anticancer Agents. Neoplasia, 2011, 13, 72-IN19.	2.3	27
50	Epigenetic methodologies for behavioral scientists. Hormones and Behavior, 2011, 59, 407-416.	1.0	13
51	Quantification of histone modification ChIP-seq enrichment for data mining and machine learning applications. BMC Research Notes, 2011, 4, 288.	0.6	10
52	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.	2.4	78
53	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.	1.9	63
54	An evolutionarily $\hat{\epsilon}$ young $\hat{\epsilon}$ ™ lysine residue in histone H3 attenuates transcriptional output in <i>Saccharomyces cerevisiae</i> . Genes and Development, 2011, 25, 1306-1319.	2.7	27

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55	Application of machine learning methods to histone methylation ChIP-Seq data reveals H4R3me2 globally represses gene expression. <i>BMC Bioinformatics</i> , 2010, 11, 396.	1.2	74
56	Amyloid β Precursor Protein Regulates Male Sexual Behavior. <i>Journal of Neuroscience</i> , 2010, 30, 9967-9972.	1.7	23
57	Thiamine Biosynthesis in <i>Saccharomyces cerevisiae</i> Is Regulated by the NAD ⁺ -Dependent Histone Deacetylase Hst1. <i>Molecular and Cellular Biology</i> , 2010, 30, 3329-3341.	1.1	64
58	RNA synthesis precision is regulated by preinitiation complex turnover. <i>Genome Research</i> , 2010, 20, 1679-1688.	2.4	12
59	Human Adipose-Derived Stromal Cells Accelerate Diabetic Wound Healing: Impact of Cell Formulation and Delivery. <i>Tissue Engineering - Part A</i> , 2010, 16, 1595-1606.	1.6	176
60	A Microarray-Based Genetic Screen for Yeast Chronological Aging Factors. <i>PLoS Genetics</i> , 2010, 6, e1000921.	1.5	198
61	Yeast genome analysis identifies chromosomal translocation, gene conversion events and several sites of Ty element insertion. <i>Nucleic Acids Research</i> , 2009, 37, 6454-6465.	6.5	12
62	The Snf1 kinase and proteasome-associated Rad23 regulate UV-responsive gene expression. <i>EMBO Journal</i> , 2009, 28, 2919-2931.	3.5	24
63	Error-pooling-based statistical methods for identifying novel temporal replication profiles of human chromosomes observed by DNA tiling arrays. <i>Nucleic Acids Research</i> , 2007, 35, e69.	6.5	8
64	Genome-wide analysis of estrogen receptor binding sites. <i>Nature Genetics</i> , 2006, 38, 1289-1297.	9.4	1,227
65	Temporal profile of replication of human chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 6419-6424.	3.3	105
66	Genomic Maps and Comparative Analysis of Histone Modifications in Human and Mouse. <i>Cell</i> , 2005, 120, 169-181.	13.5	1,348
67	Transcriptional Maps of 10 Human Chromosomes at 5-Nucleotide Resolution. <i>Science</i> , 2005, 308, 1149-1154.	6.0	1,073
68	Novel RNAs Identified From an In-Depth Analysis of the Transcriptome of Human Chromosomes 21 and 22. <i>Genome Research</i> , 2004, 14, 331-342.	2.4	460
69	Unbiased Mapping of Transcription Factor Binding Sites along Human Chromosomes 21 and 22 Points to Widespread Regulation of Noncoding RNAs. <i>Cell</i> , 2004, 116, 499-509.	13.5	1,047
70	Probe selection for high-density oligonucleotide arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 11237-11242.	3.3	117
71	Large-Scale Transcriptional Activity in Chromosomes 21 and 22. <i>Science</i> , 2002, 296, 916-919.	6.0	793
72	Microarray-Based Analysis of Early Development in <i>Xenopus laevis</i> . <i>Developmental Biology</i> , 2001, 236, 64-75.	0.9	70

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73	Homology-based annotation yields 1,042 new candidate genes in the <i>Drosophila melanogaster</i> genome. <i>Nature Genetics</i> , 2001, 27, 337-340.	9.4	58
74	Reprogramming of the Macrophage Transcriptome in Response to Interferon- β and <i>Mycobacterium tuberculosis</i> . <i>Journal of Experimental Medicine</i> , 2001, 194, 1123-1140.	4.2	437
75	Making the most of microarray data. <i>Nature Genetics</i> , 2000, 24, 204-206.	9.4	74
76	Diffusion in Inhomogeneous Media: Theory and Simulations Applied to Whole Cell Photobleach Recovery. <i>Biophysical Journal</i> , 2000, 79, 1761-1770.	0.2	121
77	Diverging correlation lengths in electrolytes: Exact results at low densities. <i>Physical Review E</i> , 1999, 59, 492-511.	0.8	18
78	Charge and density fluctuations in electrolytes: The Lebowitz and other correlation lengths. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1999, 263, 466-476.	1.2	5
79	Fluctuations in Electrolytes: The Lebowitz and Other Correlation Lengths. <i>Physical Review Letters</i> , 1998, 81, 5836-5839.	2.9	18
80	Solution behavior of polyethylene oxide in water as a function of temperature and pressure. <i>Physical Review E</i> , 1997, 55, 577-585.	0.8	150