

Artem Barski

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

13,995
citations

117453

34
h-index

118652

62
g-index

80
all docs

80
docs citations

80
times ranked

19227
citing authors

#	ARTICLE	IF	CITATIONS
1	Nuclear Vav3 is required for polycomb repression complex-1 activity in B-cell lymphoblastic leukemogenesis. <i>Nature Communications</i> , 2022, 13, .	5.8	3
2	FOXF1 is required for the oncogenic properties of PAX3-FOXO1 in rhabdomyosarcoma. <i>Oncogene</i> , 2021, 40, 2182-2199.	2.6	15
3	Methylation quantitative trait locus analysis of chronic postsurgical pain uncovers epigenetic mediators of genetic risk. <i>Epigenomics</i> , 2021, 13, 613-630.	1.0	5
4	Epigenetic Analysis of the Chromatin Landscape Identifies a Repertoire of Murine Eosinophil-Specific PU.1-Bound Enhancers. <i>Journal of Immunology</i> , 2021, 207, 1044-1054.	0.4	4
5	Runx Transcription Factors in T Cells—What Is Beyond Thymic Development?. <i>Frontiers in Immunology</i> , 2021, 12, 701924.	2.2	21
6	Aiolos regulates eosinophil migration into tissues. <i>Mucosal Immunology</i> , 2021, 14, 1271-1281.	2.7	10
7	Abstract PO-068: Cholesterol auxotrophy promotes the expansion of centroacinar cells giving rise to the basal subtype of pancreatic adenocarcinoma. , 2021, , .		1
8	Preparation of mouse pancreatic tumor for single-cell RNA sequencing and analysis of the data. <i>STAR Protocols</i> , 2021, 2, 100989.	0.5	1
9	AP-1 activity induced by co-stimulation is required for chromatin opening during T cell activation. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	80
10	Identification of anoctamin 1 (ANO1) as a key driver of esophageal epithelial proliferation in eosinophilic esophagitis. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 239-254.e2.	1.5	24
11	KMT2C/D COMPASS complex-associated diseases [KCDCOM-ADs]: an emerging class of congenital regulopathies. <i>Clinical Epigenetics</i> , 2020, 12, 10.	1.8	54
12	Abnormal Peyer patch development and B-cell gut homing drive IgA deficiency in Kabuki syndrome. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 982-992.	1.5	18
13	Endogenous retroviruses drive species-specific germline transcriptomes in mammals. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 967-977.	3.6	60
14	Super-enhancer switching drives a burst in gene expression at the mitosis-to-meiosis transition. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 978-988.	3.6	38
15	Mapping the epigenetic landscape of murine eosinophils. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, AB154.	1.5	0
16	KMT2D Haploinsufficiency in Kabuki Syndrome Impairs Differentiation of Neural Crest Cells. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.2	1
17	A rapidly evolved domain, the SCML2 DNA-binding repeats, contributes to chromatin binding of mouse SCML2. <i>Biology of Reproduction</i> , 2019, 100, 409-419.	1.2	5
18	CWL-Airflow: a lightweight pipeline manager supporting Common Workflow Language. <i>GigaScience</i> , 2019, 8, .	3.3	41

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19	Genetic, Inflammatory, and Epithelial Cell Differentiation Factors Control Expression of Human Calpain-14. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 729-736.	0.8	16
20	Attenuated chromatin compartmentalization in meiosis and its maturation in sperm development. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 175-184.	3.6	92
21	Polycomb protein SCML2 facilitates H3K27me3 to establish bivalent domains in the male germline. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4957-4962.	3.3	57
22	Transcription factors operate across disease loci, with EBNA2 implicated in autoimmunity. <i>Nature Genetics</i> , 2018, 50, 699-707.	9.4	286
23	Dynamic reorganization of open chromatin underlies diverse transcriptomes during spermatogenesis. <i>Nucleic Acids Research</i> , 2018, 46, 593-608.	6.5	100
24	TSLP signaling in CD4 ⁺ T cells programs a pathogenic T helper 2 cell state. <i>Science Signaling</i> , 2018, 11, .	1.6	72
25	GG-09...A role for EBNA2 in mechanisms that are responsible for lupus and other autoimmune diseases. , 2018, , .		0
26	Microbiota-sensitive epigenetic signature predicts inflammation in Crohn's disease. <i>JCI Insight</i> , 2018, 3, .	2.3	54
27	Analysis of ChIP-Seq and RNA-Seq Data with BioWardrobe. <i>Methods in Molecular Biology</i> , 2018, 1783, 343-360.	0.4	11
28	Reuse of public, genome-wide, murine eosinophil expression data for hypotheses development. <i>Journal of Leukocyte Biology</i> , 2018, 104, 185-193.	1.5	8
29	635 - Intestinal Microbiota Direct an Epithelial Epigenetic Signature of Pediatric Crohn's Disease. <i>Gastroenterology</i> , 2018, 154, S-133-S-134.	0.6	0
30	RNF8 and SCML2 cooperate to regulate ubiquitination and H3K27 acetylation for escape gene activation on the sex chromosomes. <i>PLoS Genetics</i> , 2018, 14, e1007233.	1.5	45
31	Chromatin Preparation from Murine Eosinophils for Genome-Wide Analyses. <i>Methods in Molecular Biology</i> , 2018, 1799, 265-274.	0.4	0
32	SCML2 promotes heterochromatin organization in late spermatogenesis. <i>Journal of Cell Science</i> , 2018, 131, .	1.2	20
33	Rapid Recall Ability of Memory T cells is Encoded in their Epigenome. <i>Scientific Reports</i> , 2017, 7, 39785.	1.6	39
34	Genomic integration of Wnt/ β -catenin and BMP/Smad1 signaling coordinates foregut and hindgut transcriptional program. <i>Development (Cambridge)</i> , 2017, 144, 1283-1295.	1.2	39
35	The Effect Of SLC9A3 On Esophageal Epithelium In Eosinophilic Esophagitis (EoE). <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, AB87.	1.5	0
36	FOXF1 transcription factor promotes lung regeneration after partial pneumonectomy. <i>Scientific Reports</i> , 2017, 7, 10690.	1.6	46

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37	Polycomb directs timely activation of germline genes in spermatogenesis. <i>Genes and Development</i> , 2017, 31, 1693-1703.	2.7	52
38	Xist RNA repeat E is essential for ASH2L recruitment to the inactive X and regulates histone modifications and escape gene expression. <i>PLoS Genetics</i> , 2017, 13, e1006890.	1.5	25
39	Nuclear Factor κ B1/RelA Mediates Inflammation in Human Lung Epithelial Cells at Atmospheric Oxygen Levels. <i>Journal of Cellular Physiology</i> , 2016, 231, 1611-1620.	2.0	9
40	Polycomb repressive complex 1 controls uterine decidualization. <i>Scientific Reports</i> , 2016, 6, 26061.	1.6	18
41	Global Expression and Epigenetic Analyses of Eosinophil Development Reveal Potential Novel Regulators. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, AB161.	1.5	0
42	SCML2 Establishes the Male Germline Epigenome through Regulation of Histone H2A Ubiquitination. <i>Developmental Cell</i> , 2015, 32, 574-588.	3.1	109
43	Su1104 Dysregulation of SLC9A3 Function in Eosinophilic Esophagitis. <i>Gastroenterology</i> , 2015, 148, S-409.	0.6	0
44	Su1110 IL-13-Induced Dilated Intracellular Space (DIS) Formation in Esophageal Epithelial Cells Is Dependent on SLC9A3 Function. <i>Gastroenterology</i> , 2015, 148, S-410.	0.6	0
45	Induction of Interleukin-9-Producing Mucosal Mast Cells Promotes Susceptibility to IgE-Mediated Experimental Food Allergy. <i>Immunity</i> , 2015, 43, 788-802.	6.6	178
46	BioWardrobe: an integrated platform for analysis of epigenomics and transcriptomics data. <i>Genome Biology</i> , 2015, 16, 158.	3.8	74
47	Poised chromatin and bivalent domains facilitate the mitosis-to-meiosis transition in the male germline. <i>BMC Biology</i> , 2015, 13, 53.	1.7	64
48	Transcription Factor Repertoire of Homeostatic Eosinophilopoiesis. <i>Journal of Immunology</i> , 2015, 195, 2683-2695.	0.4	43
49	Neurotrophic tyrosine kinase receptor 1 is a direct transcriptional and epigenetic target of IL-13 involved in allergic inflammation. <i>Mucosal Immunology</i> , 2015, 8, 785-798.	2.7	40
50	Functional Characterization of Human T Cell Hyporesponsiveness Induced by CTLA4-Ig. <i>PLoS ONE</i> , 2015, 10, e0122198.	1.1	27
51	Epigenetic regulation of gene expression and cellular differentiation. <i>Molecular Pain</i> , 2014, 10, O20.	1.0	0
52	IL-33 Markedly Activates Murine Eosinophils by an NF- κ B-Dependent Mechanism Differentially Dependent upon an IL-4-Driven Autoinflammatory Loop. <i>Journal of Immunology</i> , 2013, 191, 4317-4325.	0.4	85
53	The ATP-dependent Chromatin Remodeling Enzyme Fun30 Represses Transcription by Sliding Promoter-proximal Nucleosomes. <i>Journal of Biological Chemistry</i> , 2013, 288, 23182-23193.	1.6	31
54	RNF8 regulates active epigenetic modifications and escape gene activation from inactive sex chromosomes in post-meiotic spermatids. <i>Genes and Development</i> , 2012, 26, 2737-2748.	2.7	108

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55	Genomic Profiling of HMG1 Reveals an Association with Chromatin at Regulatory Regions. <i>Molecular and Cellular Biology</i> , 2011, 31, 700-709.	1.1	44
56	Epigenomics of T cell activation, differentiation, and memory. <i>Current Opinion in Immunology</i> , 2010, 22, 341-347.	2.4	91
57	Pol II and its associated epigenetic marks are present at Pol III-transcribed noncoding RNA genes. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 629-634.	3.6	161
58	Native Chromatin Preparation and Illumina/Solexa Library Construction. <i>Cold Spring Harbor Protocols</i> , 2009, 2009, pdb.prot5237.	0.2	26
59	Chromatin poises miRNA- and protein-coding genes for expression. <i>Genome Research</i> , 2009, 19, 1742-1751.	2.4	135
60	Genomic location analysis by ChIP-seq. <i>Journal of Cellular Biochemistry</i> , 2009, 107, 11-18.	1.2	153
61	Genome-wide Mapping of HATs and HDACs Reveals Distinct Functions in Active and Inactive Genes. <i>Cell</i> , 2009, 138, 1019-1031.	13.5	1,174
62	Combinatorial patterns of histone acetylations and methylations in the human genome. <i>Nature Genetics</i> , 2008, 40, 897-903.	9.4	2,034
63	Genome-wide identification of <i>in vivo</i> protein-DNA binding sites from ChIP-Seq data. <i>Nucleic Acids Research</i> , 2008, 36, 5221-5231.	6.5	500
64	Dynamic Regulation of Nucleosome Positioning in the Human Genome. <i>Cell</i> , 2008, 132, 887-898.	13.5	1,211
65	Identification of Transcription Factor Target Genes by ChIP Display. <i>Methods in Molecular Biology</i> , 2008, 455, 177-190.	0.4	4
66	High-Resolution Profiling of Histone Methylations in the Human Genome. <i>Cell</i> , 2007, 129, 823-837.	13.5	6,036
67	Response: Mapping Nucleosome Positions Using ChIP-Seq Data. <i>Cell</i> , 2007, 131, 832-833.	13.5	32
68	Identification of novel androgen receptor target genes in prostate cancer. <i>Molecular Cancer</i> , 2007, 6, 39.	7.9	88
69	Identification of novel Runx2 targets in osteoblasts: Cell type-specific BMP-dependent regulation of <i>Tram2</i> . <i>Journal of Cellular Biochemistry</i> , 2007, 102, 1458-1471.	1.2	25
70	Androgen receptor-mediated repression of novel target genes. <i>Prostate</i> , 2007, 67, 1371-1383.	1.2	49
71	ChIP Display: novel method for identification of genomic targets of transcription factors. <i>Nucleic Acids Research</i> , 2004, 32, e104-e104.	6.5	28
72	Brief Bone Morphogenetic Protein 2 Treatment of Glucocorticoid-inhibited MC3T3-E1 Osteoblasts Rescues Commitment-associated Cell Cycle and Mineralization without Alteration of Runx2. <i>Journal of Biological Chemistry</i> , 2003, 278, 44995-45003.	1.6	57