

# Artem Barski

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

66  
papers

11,447  
citations

29  
h-index

80  
g-index

80  
ext. papers

13,138  
ext. citations

12  
avg, IF

5.82  
L-index

#	Paper	IF	Citations
66	Preparation of mouse pancreatic tumor for single-cell RNA sequencing and analysis of the data.. <i>STAR Protocols</i> , <b>2021</b> , 2, 100989	1.4	0
65	Methylation quantitative trait locus analysis of chronic postsurgical pain uncovers epigenetic mediators of genetic risk. <i>Epigenomics</i> , <b>2021</b> , 13, 613-630	4.4	3
64	Epigenetic Analysis of the Chromatin Landscape Identifies a Repertoire of Murine Eosinophil-Specific PU.1-Bound Enhancers. <i>Journal of Immunology</i> , <b>2021</b> , 207, 1044-1054	5.3	2
63	FOXF1 is required for the oncogenic properties of PAX3-FOXO1 in rhabdomyosarcoma. <i>Oncogene</i> , <b>2021</b> , 40, 2182-2199	9.2	4
62	Runx Transcription Factors in T Cells-What Is Beyond Thymic Development?. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 701924	8.4	3
61	Aiolos regulates eosinophil migration into tissues. <i>Mucosal Immunology</i> , <b>2021</b> , 14, 1271-1281	9.2	2
60	KMT2D Haploinsufficiency in Kabuki Syndrome Impairs Differentiation of Neural Crest Cells. <i>FASEB Journal</i> , <b>2020</b> , 34, 1-1	0.9	1
59	Identification of anoctamin 1 (ANO1) as a key driver of esophageal epithelial proliferation in eosinophilic esophagitis. <i>Journal of Allergy and Clinical Immunology</i> , <b>2020</b> , 145, 239-254.e2	11.5	9
58	KMT2C/D COMPASS complex-associated diseases [KCOM-ADs]: an emerging class of congenital regulopathies. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 10	7.7	14
57	Abnormal Peyer patch development and B-cell gut homing drive IgA deficiency in Kabuki syndrome. <i>Journal of Allergy and Clinical Immunology</i> , <b>2020</b> , 145, 982-992	11.5	4
56	Endogenous retroviruses drive species-specific germline transcriptomes in mammals. <i>Nature Structural and Molecular Biology</i> , <b>2020</b> , 27, 967-977	17.6	15
55	Super-enhancer switching drives a burst in gene expression at the mitosis-to-meiosis transition. <i>Nature Structural and Molecular Biology</i> , <b>2020</b> , 27, 978-988	17.6	15
54	AP-1 activity induced by co-stimulation is required for chromatin opening during T cell activation. <i>Journal of Experimental Medicine</i> , <b>2020</b> , 217,	16.6	23
53	Genetic, Inflammatory, and Epithelial Cell Differentiation Factors Control Expression of Human Calpain-14. <i>G3: Genes, Genomes, Genetics</i> , <b>2019</b> , 9, 729-736	3.2	9
52	A rapidly evolved domain, the SCML2 DNA-binding repeats, contributes to chromatin binding of mouse SCML2. <i>Biology of Reproduction</i> , <b>2019</b> , 100, 409-419	3.9	2
51	CWL-Airflow: a lightweight pipeline manager supporting Common Workflow Language. <i>GigaScience</i> , <b>2019</b> , 8,	7.6	20
50	Attenuated chromatin compartmentalization in meiosis and its maturation in sperm development. <i>Nature Structural and Molecular Biology</i> , <b>2019</b> , 26, 175-184	17.6	50

49	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> , <b>2018</b> , 115, 4957-4962	11.5	23
48	Transcription factors operate across disease loci, with EBNA2 implicated in autoimmunity. <i>Nature Genetics</i> , <b>2018</b> , 50, 699-707	36.3	169
47	Dynamic reorganization of open chromatin underlies diverse transcriptomes during spermatogenesis. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 593-608	20.1	51
46	TSLP signaling in CD4 T cells programs a pathogenic T helper 2 cell state. <i>Science Signaling</i> , <b>2018</b> , 11,	8.8	48
45	Chromatin Preparation from Murine Eosinophils for Genome-Wide Analyses. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1799, 265-274	1.4	
44	SCML2 promotes heterochromatin organization in late spermatogenesis. <i>Journal of Cell Science</i> , <b>2018</b> , 131,	5.3	10
43	Microbiota-sensitive epigenetic signature predicts inflammation in Crohn's disease. <i>JCI Insight</i> , <b>2018</b> , 3,	9.9	33
42	Analysis of CHIP-Seq and RNA-Seq Data with BioWardrobe. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1783, 343-360	1.4	8
41	Reuse of public, genome-wide, murine eosinophil expression data for hypotheses development. <i>Journal of Leukocyte Biology</i> , <b>2018</b> , 104, 185-193	6.5	7
40	RNF8 and SCML2 cooperate to regulate ubiquitination and H3K27 acetylation for escape gene activation on the sex chromosomes. <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007233	6	28
39	Rapid Recall Ability of Memory T cells is Encoded in their Epigenome. <i>Scientific Reports</i> , <b>2017</b> , 7, 39785	4.9	26
38	Genomic integration of Wnt/ $\beta$ -catenin and BMP/Smad1 signaling coordinates foregut and hindgut transcriptional programs. <i>Development (Cambridge)</i> , <b>2017</b> , 144, 1283-1295	6.6	22
37	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> , <b>2017</b> , 13, e1006890	6	19
36	FOXF1 transcription factor promotes lung regeneration after partial pneumonectomy. <i>Scientific Reports</i> , <b>2017</b> , 7, 10690	4.9	31
35	Polycomb directs timely activation of germline genes in spermatogenesis. <i>Genes and Development</i> , <b>2017</b> , 31, 1693-1703	12.6	31
34	Polycomb repressive complex 1 controls uterine decidualization. <i>Scientific Reports</i> , <b>2016</b> , 6, 26061	4.9	12
33	Nuclear Factor $\kappa$ B1/RelA Mediates Inflammation in Human Lung Epithelial Cells at Atmospheric Oxygen Levels. <i>Journal of Cellular Physiology</i> , <b>2016</b> , 231, 1611-20	7	5
32	SCML2 establishes the male germline epigenome through regulation of histone H2A ubiquitination. <i>Developmental Cell</i> , <b>2015</b> , 32, 574-88	10.2	59

31	Induction of Interleukin-9-Producing Mucosal Mast Cells Promotes Susceptibility to IgE-Mediated Experimental Food Allergy. <i>Immunity</i> , <b>2015</b> , 43, 788-802	32.3	133
30	BioWardrobe: an integrated platform for analysis of epigenomics and transcriptomics data. <i>Genome Biology</i> , <b>2015</b> , 16, 158	18.3	60
29	Poised chromatin and bivalent domains facilitate the mitosis-to-meiosis transition in the male germline. <i>BMC Biology</i> , <b>2015</b> , 13, 53	7.3	37
28	Transcription Factor Repertoire of Homeostatic Eosinophiloipoiesis. <i>Journal of Immunology</i> , <b>2015</b> , 195, 2683-95	5.3	34
27	Neurotrophic tyrosine kinase receptor 1 is a direct transcriptional and epigenetic target of IL-13 involved in allergic inflammation. <i>Mucosal Immunology</i> , <b>2015</b> , 8, 785-98	9.2	29
26	Functional characterization of human T cell hyporesponsiveness induced by CTLA4-Ig. <i>PLoS ONE</i> , <b>2015</b> , 10, e0122198	3.7	18
25	Epigenetic regulation of gene expression and cellular differentiation. <i>Molecular Pain</i> , <b>2014</b> , 10, O20	3.4	78
24	IL-33 markedly activates murine eosinophils by an NF- $\kappa$ B-dependent mechanism differentially dependent upon an IL-4-driven autoinflammatory loop. <i>Journal of Immunology</i> , <b>2013</b> , 191, 4317-25	5.3	66
23	The ATP-dependent chromatin remodeling enzyme Fun30 represses transcription by sliding promoter-proximal nucleosomes. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 23182-93	5.4	24
22	RNF8 regulates active epigenetic modifications and escape gene activation from inactive sex chromosomes in post-meiotic spermatids. <i>Genes and Development</i> , <b>2012</b> , 26, 2737-48	12.6	75
21	Genomic profiling of HMGN1 reveals an association with chromatin at regulatory regions. <i>Molecular and Cellular Biology</i> , <b>2011</b> , 31, 700-9	4.8	37
20	Pol II and its associated epigenetic marks are present at Pol III-transcribed noncoding RNA genes. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 629-34	17.6	132
19	Epigenomics of T cell activation, differentiation, and memory. <i>Current Opinion in Immunology</i> , <b>2010</b> , 22, 341-7	7.8	77
18	Native chromatin preparation and Illumina/Solexa library construction. <i>Cold Spring Harbor Protocols</i> , <b>2009</b> , 2009, pdb.prot5237	1.2	24
17	Chromatin poises miRNA- and protein-coding genes for expression. <i>Genome Research</i> , <b>2009</b> , 19, 1742-51	9.7	128
16	Genomic location analysis by ChIP-Seq. <i>Journal of Cellular Biochemistry</i> , <b>2009</b> , 107, 11-8	4.7	130
15	Genome-wide mapping of HATs and HDACs reveals distinct functions in active and inactive genes. <i>Cell</i> , <b>2009</b> , 138, 1019-31	56.2	997
14	Combinatorial patterns of histone acetylations and methylations in the human genome. <i>Nature Genetics</i> , <b>2008</b> , 40, 897-903	36.3	1745

13	Genome-wide identification of in vivo protein-DNA binding sites from ChIP-Seq data. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, 5221-31	20.1	442
12	Dynamic regulation of nucleosome positioning in the human genome. <i>Cell</i> , <b>2008</b> , 132, 887-98	56.2	1053
11	Identification of transcription factor target genes by ChIP display. <i>Methods in Molecular Biology</i> , <b>2008</b> , 455, 177-90	1.4	4
10	Identification of novel androgen receptor target genes in prostate cancer. <i>Molecular Cancer</i> , <b>2007</b> , 6, 39	42.1	71
9	Identification of novel Runx2 targets in osteoblasts: cell type-specific BMP-dependent regulation of Tram2. <i>Journal of Cellular Biochemistry</i> , <b>2007</b> , 102, 1458-71	4.7	17
8	Androgen receptor-mediated repression of novel target genes. <i>Prostate</i> , <b>2007</b> , 67, 1371-83	4.2	32
7	High-resolution profiling of histone methylations in the human genome. <i>Cell</i> , <b>2007</b> , 129, 823-37	56.2	5134
6	Response: Mapping Nucleosome Positions Using ChIP-Seq Data. <i>Cell</i> , <b>2007</b> , 131, 832-833	56.2	28
5	ChIP Display: novel method for identification of genomic targets of transcription factors. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, e104	20.1	24
4	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> , <b>2003</b> , 278, 44995-5003	5.4	50
3	BioWardrobe: an integrated platform for analysis of epigenomics and transcriptomics data		4
2	CWL-Airflow: a lightweight pipeline manager supporting Common Workflow Language		2
1	Co-Stimulation-Induced AP-1 Activity is Required for Chromatin Opening During T Cell Activation		2