

Piotr J Balwierz

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

4,972
citations

361413

20
h-index

642732

23
g-index

25
all docs

25
docs citations

25
times ranked

11996
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. <i>Nature Genetics</i> , 2022, 54, 1037-1050.	21.4	26
2	Germ cell differentiation requires Tdrd7-dependent chromatin and transcriptome reprogramming marked by germ plasm relocalization. <i>Developmental Cell</i> , 2021, 56, 641-656.e5.	7.0	18
3	Identification of downstream effectors of retinoic acid specifying the zebrafish pancreas by integrative genomics. <i>Scientific Reports</i> , 2021, 11, 22717.	3.3	6
4	Dual-initiation promoters with intertwined canonical and TCT/TOP transcription start sites diversify transcript processing. <i>Nature Communications</i> , 2020, 11, 168.	12.8	37
5	Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , 2018, 564, 64-70.	27.8	224
6	Embryonic stem cell-specific microRNAs contribute to pluripotency by inhibiting regulators of multiple differentiation pathways. <i>Nucleic Acids Research</i> , 2014, 42, 9313-9326.	14.5	32
7	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
8	An epigenetic profile of early T cell development from multipotent progenitors to committed T cell descendants. <i>European Journal of Immunology</i> , 2014, 44, 1181-1193.	2.9	21
9	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , 2014, 123, e68-e78.	1.4	77
10	ISMARA: automated modeling of genomic signals as a democracy of regulatory motifs. <i>Genome Research</i> , 2014, 24, 869-884.	5.5	278
11	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , 2014, 123, e90-e99.	1.4	157
12	Parity induces differentiation and reduces Wnt/Notch signaling ratio and proliferation potential of basal stem/progenitor cells isolated from mouse mammary epithelium. <i>Breast Cancer Research</i> , 2013, 15, R36.	5.0	82
13	Sox4 Is a Master Regulator of Epithelial-Mesenchymal Transition by Controlling Ezh2 Expression and Epigenetic Reprogramming. <i>Cancer Cell</i> , 2013, 23, 768-783.	16.8	415
14	Modeling of epigenome dynamics identifies transcription factors that mediate Polycomb targeting. <i>Genome Research</i> , 2013, 23, 60-73.	5.5	108
15	SwissRegulon, a database of genome-wide annotations of regulatory sites: recent updates. <i>Nucleic Acids Research</i> , 2012, 41, D214-D220.	14.5	137
16	The Corepressor NCoR1 Antagonizes PGC-1 and Estrogen-Related Receptor in the Regulation of Skeletal Muscle Function and Oxidative Metabolism. <i>Molecular and Cellular Biology</i> , 2012, 32, 4913-4924.	2.3	74
17	Adipose Tissue MicroRNAs as Regulators of CCL2 Production in Human Obesity. <i>Diabetes</i> , 2012, 61, 1986-1993.	0.6	263
18	Tyrosine phosphatase SHP2 promotes breast cancer progression and maintains tumor-initiating cells via activation of key transcription factors and a positive feedback signaling loop. <i>Nature Medicine</i> , 2012, 18, 529-537.	30.7	224

#	ARTICLE	IF	CITATIONS
19	The snoRNA MBII-52 (SNORD 115) is processed into smaller RNAs and regulates alternative splicing. <i>Human Molecular Genetics</i> , 2010, 19, 1153-1164.	2.9	259
20	Expression and Processing of a Small Nucleolar RNA from the Epstein-Barr Virus Genome. <i>PLoS Pathogens</i> , 2009, 5, e1000547.	4.7	84
21	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
22	Methods for analyzing deep sequencing expression data: constructing the human and mouse promoterome with deepCAGE data. <i>Genome Biology</i> , 2009, 10, R79.	9.6	131
23	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009, 10, R39.	9.6	67