Gareth A Palidwor

List of Publications by Year
in descending order

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30
papers

1,031
citations

516710
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552781
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30
docs citations

30
times ranked

2509
citing authors

#	ARTICLE	IF	CITATIONS
1	A genome-wide strategy to identify causes and consequences of retrotransposon expression finds activation by BRCA1 in ovarian cancer. NAR Cancer, 2021, 3, zcaa040.	3.1	2
2	Accuracy and reproducibility of somatic point mutation calling in clinical-type targeted sequencing data. BMC Medical Genomics, 2020, 13, 156.	1.5	8
3	An OTX2-PAX3 signaling axis regulates Group 3 medulloblastoma cell fate. Nature Communications, 2020, 11, 3627.	12.8	21
4	MEDU-04. AN OTX2-PAX GENE NETWORK REGULATES GROUP 3 MEDULLOBLASTOMA DIFFERENTIATION AND TUMOR GROWTH. Neuro-Oncology, 2019, 21, ii103-ii104.	1.2	0
5	PDTM-28. AN OTX2-PAX3 SIGNALLING AXIS REGULATES GROUP 3 MEDULLOBLASTOMA CELL FATE. Neuro-Oncology, 2019, 21, vi193-vi193.	1.2	0
6	Characterization of a novel <scp>OTX</scp>2â€driven stem cell program in Group 3 and Group 4 medulloblastoma. Molecular Oncology, 2018, 12, 495-513.	4.6	16
7	Mtf2-PRC2 control of canonical Wnt signaling is required for definitive erythropoiesis. Cell Discovery, 2018, 4, 21.	6.7	37
8	A complex of C9ORF72 and p62 uses arginine methylation to eliminate stress granules by autophagy. Nature Communications, 2018, 9, 2794.	12.8	126
9	Cis-regulatory determinants of MyoD function. Nucleic Acids Research, 2018, 46, 7221-7235.	14.5	11
10	MEDU-14. OTX2 CONTROLS AN AXON GUIDANCE GENE EXPRESSION NETWORK TO REGULATE MEDULLOBLASTOMA SELF-RENEWAL. Neuro-Oncology, 2017, 19, iv40-iv40.	1.2	0
11	Reprogramming progeria fibroblasts reâ€establishes a normal epigenetic landscape. Aging Cell, 2017, 16, 870-887.	6.7	34
12	BIDCHIPS: bias decomposition and removal from ChIP-seq data clarifies true binding signal and its functional correlates. Epigenetics and Chromatin, 2015, 8, 33.	3.9	17
13	Chromatin tandem affinity purification sequencing. Nature Protocols, 2013, 8, 1525-1534.	12.0	13
14	MaSC: mappability-sensitive cross-correlation for estimating mean fragment length of single-end short-read sequencing data. Bioinformatics, 2013, 29, 444-450.	4.1	31
15	Functional and Genomic Analyses of Alpha-Solenoid Proteins. PLoS ONE, 2013, 8, e79894.	2.5	26
16	Transcriptional Dominance of Pax7 in Adult Myogenesis Is Due to High-Affinity Recognition of Homeodomain Motifs. Developmental Cell, 2012, 22, 1208-1220.	7.0	139
17	Peer2ref: a peer-reviewer finding web tool that uses author disambiguation. BioData Mining, 2012, 5, 14.	4.0	3
18	Acknowledging contributions to online expert assistance. Nature Precedings, 2011, , .	0.1	0

#	ARTICLE	IF	CITATIONS
19	Transcriptional profiling of skeletal muscle reveals factors that are necessary to maintain satellite cell integrity during ageing. Mechanisms of Ageing and Development, 2010, 131, 9-20.	4.6	37
20	A General Model of Codon Bias Due to GC Mutational Bias. PLoS ONE, 2010, 5, e13431.	2.5	144
21	MLTrends: Graphing MEDLINE term usage over time. Journal of Biomedical Discovery and Collaboration, 2010, 5, 1-6.	2.0	6
22	Detection of Alpha-Rod Protein Repeats Using a Neural Network and Application to Huntingtin. PLoS Computational Biology, 2009, 5, e1000304.	3.2	59
23	Recent developments in StemBase: a tool to study gene expression in human and murine stem cells. BMC Research Notes, 2009, 2, 39.	1.4	18
24	Towards completion of the Earth's proteome. EMBO Reports, 2007, 8, 1135-1141.	4.5	30
25	ChIP on SNP-chip for genome-wide analysis of human histone H4 hyperacetylation. BMC Genomics, 2007, 8, 322.	2.8	13
26	Gene function in early mouse embryonic stem cell differentiation. BMC Genomics, 2007, 8, 85.	2.8	123
27	StemBase. Methods in Molecular Biology, 2007, 407, 137-148.	0.9	24
28	Taxonomic colouring of phylogenetic trees of protein sequences. BMC Bioinformatics, 2006, 7, 79.	2.6	9
29	Study of stem cell function using microarray experiments. FEBS Letters, 2005, 579, 1795-1801.	2.8	66
30	Genomic Adaptation to Acidic Environment: Evidence fromHelicobacter pylori. American Naturalist, 2005, 166, 776-784.	2.1	18