

# Gareth A Palidwor

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

1,031  
citations

516215

16  
h-index

552369

26  
g-index

30  
all docs

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. <i>NAR Cancer</i> , 2021, 3, zcaa040.	1.6	2
2	Accuracy and reproducibility of somatic point mutation calling in clinical-type targeted sequencing data. <i>BMC Medical Genomics</i> , 2020, 13, 156.	0.7	8
3	An OTX2-PAX3 signaling axis regulates Group 3 medulloblastoma cell fate. <i>Nature Communications</i> , 2020, 11, 3627.	5.8	21
4	MEDU-04. AN OTX2-PAX GENE NETWORK REGULATES GROUP 3 MEDULLOBLASTOMA DIFFERENTIATION AND TUMOR GROWTH. <i>Neuro-Oncology</i> , 2019, 21, ii103-ii104.	0.6	0
5	PDTM-28. AN OTX2-PAX3 SIGNALLING AXIS REGULATES GROUP 3 MEDULLOBLASTOMA CELL FATE. <i>Neuro-Oncology</i> , 2019, 21, vi193-vi193.	0.6	0
6	Characterization of a novel OTX2-driven stem cell program in Group 3 and Group 4 medulloblastoma. <i>Molecular Oncology</i> , 2018, 12, 495-513.	2.1	16
7	Mtf2-PRC2 control of canonical Wnt signaling is required for definitive erythropoiesis. <i>Cell Discovery</i> , 2018, 4, 21.	3.1	37
8	A complex of C9ORF72 and p62 uses arginine methylation to eliminate stress granules by autophagy. <i>Nature Communications</i> , 2018, 9, 2794.	5.8	126
9	Cis-regulatory determinants of MyoD function. <i>Nucleic Acids Research</i> , 2018, 46, 7221-7235.	6.5	11
10	MEDU-14. OTX2 CONTROLS AN AXON GUIDANCE GENE EXPRESSION NETWORK TO REGULATE MEDULLOBLASTOMA SELF-RENEWAL. <i>Neuro-Oncology</i> , 2017, 19, iv40-iv40.	0.6	0
11	Reprogramming progeria fibroblasts reestablishes a normal epigenetic landscape. <i>Aging Cell</i> , 2017, 16, 870-887.	3.0	34
12	BIDCHIPS: bias decomposition and removal from ChIP-seq data clarifies true binding signal and its functional correlates. <i>Epigenetics and Chromatin</i> , 2015, 8, 33.	1.8	17
13	Chromatin tandem affinity purification sequencing. <i>Nature Protocols</i> , 2013, 8, 1525-1534.	5.5	13
14	MaSC: mappability-sensitive cross-correlation for estimating mean fragment length of single-end short-read sequencing data. <i>Bioinformatics</i> , 2013, 29, 444-450.	1.8	31
15	Functional and Genomic Analyses of Alpha-Solenoid Proteins. <i>PLoS ONE</i> , 2013, 8, e79894.	1.1	26
16	Transcriptional Dominance of Pax7 in Adult Myogenesis Is Due to High-Affinity Recognition of Homeodomain Motifs. <i>Developmental Cell</i> , 2012, 22, 1208-1220.	3.1	139
17	Peer2ref: a peer-reviewer finding web tool that uses author disambiguation. <i>BioData Mining</i> , 2012, 5, 14.	2.2	3
18	Acknowledging contributions to online expert assistance. <i>Nature Precedings</i> , 2011, , .	0.1	0

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19	Transcriptional profiling of skeletal muscle reveals factors that are necessary to maintain satellite cell integrity during ageing. <i>Mechanisms of Ageing and Development</i> , 2010, 131, 9-20.	2.2	37
20	A General Model of Codon Bias Due to GC Mutational Bias. <i>PLoS ONE</i> , 2010, 5, e13431.	1.1	144
21	MLTrends: Graphing MEDLINE term usage over time. <i>Journal of Biomedical Discovery and Collaboration</i> , 2010, 5, 1-6.	2.0	6
22	Detection of Alpha-Rod Protein Repeats Using a Neural Network and Application to Huntingtin. <i>PLoS Computational Biology</i> , 2009, 5, e1000304.	1.5	59
23	Recent developments in StemBase: a tool to study gene expression in human and murine stem cells. <i>BMC Research Notes</i> , 2009, 2, 39.	0.6	18
24	Towards completion of the Earth's proteome. <i>EMBO Reports</i> , 2007, 8, 1135-1141.	2.0	30
25	ChIP on SNP-chip for genome-wide analysis of human histone H4 hyperacetylation. <i>BMC Genomics</i> , 2007, 8, 322.	1.2	13
26	Gene function in early mouse embryonic stem cell differentiation. <i>BMC Genomics</i> , 2007, 8, 85.	1.2	123
27	StemBase. <i>Methods in Molecular Biology</i> , 2007, 407, 137-148.	0.4	24
28	Taxonomic colouring of phylogenetic trees of protein sequences. <i>BMC Bioinformatics</i> , 2006, 7, 79.	1.2	9
29	Study of stem cell function using microarray experiments. <i>FEBS Letters</i> , 2005, 579, 1795-1801.	1.3	66
30	Genomic Adaptation to Acidic Environment: Evidence from <i>Helicobacter pylori</i> . <i>American Naturalist</i> , 2005, 166, 776-784.	1.0	18