Mark J Dunning

List of Publications by Year
in descending order

40 papers	14,917 citations	212478 28 h-index	312153 41 g-index
44 all docs	44 docs citations	44 times ranked	33633 citing authors

#	Article	IF	Citations
1	Fostering accessible online education using Galaxy as an e-learning platform. PLoS Computational Biology, 2021, 17, e1008923.	1.5	15
2	Biological heterogeneity in idiopathic pulmonary arterial hypertension identified through unsupervised transcriptomic profiling of whole blood. Nature Communications, 2021, 12, 7104.	5.8	21
3	Consensus Genomic Subtypes of Muscle-invasive Bladder Cancer: A Step in the Right Direction but Still a Long Way To Go. European Urology, 2020, 77, 434-435.	0.9	3
4	Whole-Blood RNA Profiles Associated with Pulmonary Arterial Hypertension and Clinical Outcome. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 586-594.	2.5	45
5	The failure of microglia to digest developmental apoptotic cells contributes to the pathology of RNASET2â€"deficient leukoencephalopathy. Glia, 2020, 68, 1531-1545.	2.5	35
6	Identification and validation of DOCK4 as a potential biomarker for risk of bone metastasis development in patients with early breast cancer. Journal of Pathology, 2019, 247, 381-391.	2.1	33
7	Neuroendocrine differentiation of prostate cancer leads to PSMA suppression. Endocrine-Related Cancer, 2019, 26, 131-146.	1.6	98
8	Identification of potential therapeutic targets in prostate cancer through a crossâ€"species approach. EMBO Molecular Medicine, 2018, 10, .	3.3	46
9	Mining Human Prostate Cancer Datasets: The â€œcamcAPPâ€•Shiny App. EBioMedicine, 2017, 17, 5-6.	2.7	31
10	Translating a Prognostic DNA Genomic Classifier into the Clinic: Retrospective Validation in 563 Localized Prostate Tumors. European Urology, 2017, 72, 22-31.	0.9	37
11	Gene regulatory mechanisms underpinning prostate cancer susceptibility. Nature Genetics, 2016, 48, 387-397.	9.4	119
12	The Early Effects of Rapid Androgen Deprivation on Human Prostate Cancer. European Urology, 2016, 70, 214-218.	0.9	56
13	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. Molecular Oncology, 2015, 9, 115-127.	2.1	38
14	5-hydroxymethylcytosine marks promoters in colon that resist DNA hypermethylation in cancer. Genome Biology, 2015, 16, 69.	3.8	60
15	HES5 silencing is an early and recurrent change in prostate tumourigenesis. Endocrine-Related Cancer, 2015, 22, 131-144.	1.6	10
16	Integration of copy number and transcriptomics provides risk stratification in prostate cancer: A discovery and validation cohort study. EBioMedicine, 2015, 2, 1133-1144.	2.7	260
17	Tumour genomic and microenvironmental heterogeneity for integrated prediction of 5-year biochemical recurrence of prostate cancer: a retrospective cohort study. Lancet Oncology, The, 2014, 15, 1521-1532.	5.1	291
18	Genome-driven integrated classification of breast cancer validated in over 7,500 samples. Genome Biology, 2014, 15, 431.	3.8	178

#	ARTICLE	IF	CITATIONS
19	Ordering of mutations in preinvasive disease stages of esophageal carcinogenesis. Nature Genetics, 2014, 46, 837-843.	9.4	302
20	Analysis of Circulating Tumor DNA to Monitor Metastatic Breast Cancer. New England Journal of Medicine, 2013, 368, 1199-1209.	13.9	1,884
21	Loss of centrioles causes chromosomal instability in vertebrate somatic cells. Journal of Cell Biology, 2013, 203, 747-756.	2.3	114
22	Quantitative Image Analysis of Cellular Heterogeneity in Breast Tumors Complements Genomic Profiling. Science Translational Medicine, 2012, 4, 157ra143.	5.8	356
23	Effects of BRCA2 cis-regulation in normal breast and cancer risk amongst BRCA2 mutation carriers. Breast Cancer Research, 2012, 14, R63.	2.2	22
24	Differential oestrogen receptor binding is associated with clinical outcome in breast cancer. Nature, 2012, 481, 389-393.	13.7	1,655
25	Calling Sample Mix-Ups in Cancer Population Studies. PLoS ONE, 2012, 7, e41815.	1.1	6
26	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352.	13.7	4,708
27	*ZNF703* is a common Luminal B breast cancer oncogene that differentially regulates luminal and basal progenitors in human mammary epithelium. EMBO Molecular Medicine, 2011, 3, 167-180.	3.3	119
28	BeadArray Expression Analysis Using Bioconductor. PLoS Computational Biology, 2011, 7, e1002276.	1.5	49
29	Identification and correction of previously unreported spatial phenomena using raw Illumina BeadArray data. BMC Bioinformatics, 2010, 11, 208.	1.2	8
30	The cost of reducing starting RNA quantity for Illumina BeadArrays: A bead-level dilution experiment. BMC Genomics, 2010, 11, 540.	1.2	4
31	A re-annotation pipeline for Illumina BeadArrays: improving the interpretation of gene expression data. Nucleic Acids Research, 2010, 38, e17-e17.	6.5	200
32	The importance of platform annotation in interpreting microarray data. Lancet Oncology, The, 2010, 11, 717.	5.1	14
33	The pitfalls of platform comparison: DNA copy number array technologies assessed. BMC Genomics, 2009, 10, 588.	1.2	80
34	Statistical issues in the analysis of Illumina data. BMC Bioinformatics, 2008, 9, 85.	1.2	90
35	Spike-in validation of an Illumina-specific variance-stabilizing transformation. BMC Research Notes, 2008, 1, 18.	0.6	13
36	PMC42, a breast progenitor cancer cell line, has normal-like mRNA and microRNA transcriptomes. Breast Cancer Research, 2008, 10, R54.	2.2	22

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37	beadarray: R classes and methods for Illumina bead-based data. Bioinformatics, 2007, 23, 2183-2184.	1.8	443
38	MicroRNA expression profiling of human breast cancer identifies new markers of tumor subtype. Genome Biology, 2007, 8, R214.	13.9	828
39	Relative Impact of Nucleotide and Copy Number Variation on Gene Expression Phenotypes. Science, 2007, 315, 848-853.	6.0	1,546
40	Population genomics of human gene expression. Nature Genetics, 2007, 39, 1217-1224.	9.4	1,072