Geoff Macintyre

List of Publications by Year
in descending order

44 papers	3,125 citations	393982 19 h-index	253896 43 g-index
52 all docs	52 docs citations	52 times ranked	7214 citing authors

#	Article	IF	Citations
1	The evolutionary history of 2,658 cancers. Nature, 2020, 578, 122-128.	13.7	690
2	Copy number signatures and mutational processes in ovarian carcinoma. Nature Genetics, 2018, 50, 1262-1270.	9.4	320
3	Tracking the origins and drivers of subclonal metastatic expansion in prostate cancer. Nature Communications, 2015, 6, 6605.	5.8	312
4	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	13.5	260
5	Genome-wide analysis distinguishes hyperglycemia regulated epigenetic signatures of primary vascular cells. Genome Research, 2011, 21, 1601-1615.	2.4	198
6	Unraveling tumor–immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. Nature Genetics, 2020, 52, 582-593.	9.4	136
7	Reducing the risk of false discovery enabling identification of biologically significant genome-wide methylation status using the HumanMethylation450 array. BMC Genomics, 2014, 15, 51.	1.2	126
8	is-rSNP: a novel technique for *in silico* regulatory SNP detection. Bioinformatics, 2010, 26, i524-i530.	1.8	115
9	A pan-cancer compendium of chromosomal instability. Nature, 2022, 606, 976-983.	13.7	111
10	Sequencing Structural Variants in Cancer for Precision Therapeutics. Trends in Genetics, 2016, 32, 530-542.	2.9	86
11	A urinary microRNA signature can predict the presence of bladder urothelial carcinoma in patients undergoing surveillance. British Journal of Cancer, 2016, 114, 454-462.	2.9	78
12	Socrates: identification of genomic rearrangements in tumour genomes by re-aligning soft clipped reads. Bioinformatics, 2014, 30, 1064-1072.	1.8	75
13	Molecular Profiling of Human Mammary Gland Links Breast Cancer Risk to a p27+ Cell Population with Progenitor Characteristics. Cell Stem Cell, 2013, 13, 117-130.	5.2	72
14	Curated MicroRNAs in Urine and Blood Fail to Validate as Predictive Biomarkers for High-Risk Prostate Cancer. PLoS ONE, 2014, 9, e91729.	1.1	43
15	Canonical Androstenedione Reduction Is the Predominant Source of Signaling Androgens in Hormone-Refractory Prostate Cancer. Clinical Cancer Research, 2014, 20, 5547-5557.	3.2	43
16	Genomic landscape of platinum resistant and sensitive testicular cancers. Nature Communications, 2020, 11, 2189.	5.8	43
17	Methanol-based fixation is superior to buffered formalin for next-generation sequencing of DNA from clinical cancer samples. Annals of Oncology, 2016, 27, 532-539.	0.6	34
18	How Subclonal Modeling Is Changing the Metastatic Paradigm. Clinical Cancer Research, 2017, 23, 630-635.	3.2	34

#	Article	IF	Citations
19	Inferring structural variant cancer cell fraction. Nature Communications, 2020, 11, 730.	5.8	33
20	Associating disease-related genetic variants in intergenic regions to the genes they impact. PeerJ, 2014, 2, e639.	0.9	20
21	Comparing nodal versus bony metastatic spread using tumour phylogenies. Scientific Reports, 2016, 6, 33918.	1.6	19
22	Periprostatic fat tissue transcriptome reveals a signature diagnostic for high-risk prostate cancer. Endocrine-Related Cancer, 2018, 25, 569-581.	1.6	19
23	The Genomic Landscape of Early-Stage Ovarian High-Grade Serous Carcinoma. Clinical Cancer Research, 2022, 28, 2911-2922.	3.2	19
24	Using Gene Ontology annotations in exploratory microarray clustering to understand cancer etiology. Pattern Recognition Letters, 2010, 31, 2138-2146.	2.6	16
25	The Regional Student Group Program of the ISCB Student Council: Stories from the Road. PLoS Computational Biology, 2013, 9, e1003241.	1.5	13
26	Highlights from the Student Council Symposium 2011 at the International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology. BMC Bioinformatics, 2011, 12, .	1.2	11
27	Reduction in expression of the benign AR transcriptome is a hallmark of localised prostate cancer progression. Oncotarget, 2016, 7, 31384-31392.	0.8	11
28	Ten Simple Rules for Starting a Regional Student Group. PLoS Computational Biology, 2013, 9, e1003340.	1.5	10
29	A voting approach to identify a small number of highly predictive genes using multiple classifiers. BMC Bioinformatics, 2009, 10, S19.	1.2	9
30	Loss of *SNAI2* in Prostate Cancer Correlates With Clinical Response to Androgen Deprivation Therapy. JCO Precision Oncology, 2021, 5, 1048-1059.	1.5	9
31	Highlights from the Eighth International Society for Computational Biology (ISCB) Student Council Symposium 2012. BMC Bioinformatics, 2012, 13, .	1.2	8
32	ISCB Computational Biology Wikipedia Competition. PLoS Computational Biology, 2013, 9, e1003242.	1.5	8
33	Breaking the Ice and Forging Links: The Importance of Socializing in Research. PLoS Computational Biology, 2013, 9, e1003355.	1.5	8
34	Percutaneous image-guided biopsy of prostate cancer metastases yields samples suitable for genomics and personalised oncology. Clinical and Experimental Metastasis, 2014, 31, 159-167.	1.7	8
35	Workshops: A Great Way to Enhance and Supplement a Degree. PLoS Computational Biology, 2014, 10, e1003497.	1.5	7
36	Paving the Way Towards a Successful and Fulfilling Career in Computational Biology. PLoS Computational Biology, 2014, 10, e1003593.	1.5	4

#	Article	IF	Citations
37	MSH2-deficient prostate tumours have a distinct immune response and clinical outcome compared to MSH2-deficient colorectal or endometrial cancer. Prostate Cancer and Prostatic Diseases, 2021, 24, 1167-1180.	2.0	4
38	A bi-ordering approach to linking gene expression with clinical annotations in gastric cancer. BMC Bioinformatics, 2010, 11, 477.	1.2	3
39	is-rSNP: a novel technique for in silico regulatory SNP detection. BMC Bioinformatics, 2010, 11, .	1.2	2
40	The Young PI Buzz: Learning from the Organizers of the Junior Principal Investigator Meeting at ISMB-ECCB 2013. PLoS Computational Biology, 2013, 9, e1003350.	1.5	2
41	FrenchFISH: Poisson Models for Quantifying DNA Copy Number From Fluorescence In Situ Hybridization of Tissue Sections. JCO Clinical Cancer Informatics, 2021, 5, 176-186.	1.0	2
42	CNpare: matching DNA copy number profiles. Bioinformatics, 2022, 38, 3638-3641.	1.8	2
43	Establishing and Managing a Global Student Network. PLoS Computational Biology, 2014, 10, e1003920.	1.5	1
44	MSH2 is Inactivated by Multiple Mechanisms in Prostate Tumors, Leading to a Distinct Immune Response and Clinical Outcome Compared to MSH2 Deficient Colorectal Cancer. SSRN Electronic Journal, 0, , .	0.4	0