

# Geoff Macintyre

## List of Publications by Year in descending order

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Version: 2024-02-01

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 Genomic Landscape of Early-Stage Ovarian High-Grade Serous Carcinoma. <i>Clinical Cancer Research</i> , 2022, 28, 2911-2922.	3.2	19
2	CNpare: matching DNA copy number profiles. <i>Bioinformatics</i> , 2022, 38, 3638-3641.	1.8	2
3	A pan-cancer compendium of chromosomal instability. <i>Nature</i> , 2022, 606, 976-983.	13.7	111
4	FrenchFISH: Poisson Models for Quantifying DNA Copy Number From Fluorescence In Situ Hybridization of Tissue Sections. <i>JCO Clinical Cancer Informatics</i> , 2021, 5, 176-186.	1.0	2
5	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021, 184, 2239-2254.e39.	13.5	260
6	Loss of <i>SNAI2</i> in Prostate Cancer Correlates With Clinical Response to Androgen Deprivation Therapy. <i>JCO Precision Oncology</i> , 2021, 5, 1048-1059.	1.5	9
7	MSH2-deficient prostate tumours have a distinct immune response and clinical outcome compared to MSH2-deficient colorectal or endometrial cancer. <i>Prostate Cancer and Prostatic Diseases</i> , 2021, 24, 1167-1180.	2.0	4
8	Genomic landscape of platinum resistant and sensitive testicular cancers. <i>Nature Communications</i> , 2020, 11, 2189.	5.8	43
9	Unraveling tumor immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. <i>Nature Genetics</i> , 2020, 52, 582-593.	9.4	136
10	Inferring structural variant cancer cell fraction. <i>Nature Communications</i> , 2020, 11, 730.	5.8	33
11	The evolutionary history of 2,658 cancers. <i>Nature</i> , 2020, 578, 122-128.	13.7	690
12	Periprostatic fat tissue transcriptome reveals a signature diagnostic for high-risk prostate cancer. <i>Endocrine-Related Cancer</i> , 2018, 25, 569-581.	1.6	19
13	Copy number signatures and mutational processes in ovarian carcinoma. <i>Nature Genetics</i> , 2018, 50, 1262-1270.	9.4	320
14	How Subclonal Modeling Is Changing the Metastatic Paradigm. <i>Clinical Cancer Research</i> , 2017, 23, 630-635.	3.2	34
15	Comparing nodal versus bony metastatic spread using tumour phylogenies. <i>Scientific Reports</i> , 2016, 6, 33918.	1.6	19
16	Sequencing Structural Variants in Cancer for Precision Therapeutics. <i>Trends in Genetics</i> , 2016, 32, 530-542.	2.9	86
17	Methanol-based fixation is superior to buffered formalin for next-generation sequencing of DNA from clinical cancer samples. <i>Annals of Oncology</i> , 2016, 27, 532-539.	0.6	34
18	A urinary microRNA signature can predict the presence of bladder urothelial carcinoma in patients undergoing surveillance. <i>British Journal of Cancer</i> , 2016, 114, 454-462.	2.9	78

#	ARTICLE	IF	CITATIONS
19	Reduction in expression of the benign AR transcriptome is a hallmark of localised prostate cancer progression. <i>Oncotarget</i> , 2016, 7, 31384-31392.	0.8	11
20	Tracking the origins and drivers of subclonal metastatic expansion in prostate cancer. <i>Nature Communications</i> , 2015, 6, 6605.	5.8	312
21	Curated MicroRNAs in Urine and Blood Fail to Validate as Predictive Biomarkers for High-Risk Prostate Cancer. <i>PLoS ONE</i> , 2014, 9, e91729.	1.1	43
22	Establishing and Managing a Global Student Network. <i>PLoS Computational Biology</i> , 2014, 10, e1003920.	1.5	1
23	Paving the Way Towards a Successful and Fulfilling Career in Computational Biology. <i>PLoS Computational Biology</i> , 2014, 10, e1003593.	1.5	4
24	Workshops: A Great Way to Enhance and Supplement a Degree. <i>PLoS Computational Biology</i> , 2014, 10, e1003497.	1.5	7
25	Reducing the risk of false discovery enabling identification of biologically significant genome-wide methylation status using the HumanMethylation450 array. <i>BMC Genomics</i> , 2014, 15, 51.	1.2	126
26	Socrates: identification of genomic rearrangements in tumour genomes by re-aligning soft clipped reads. <i>Bioinformatics</i> , 2014, 30, 1064-1072.	1.8	75
27	Percutaneous image-guided biopsy of prostate cancer metastases yields samples suitable for genomics and personalised oncology. <i>Clinical and Experimental Metastasis</i> , 2014, 31, 159-167.	1.7	8
28	Canonical Androstenedione Reduction Is the Predominant Source of Signaling Androgens in Hormone-Refractory Prostate Cancer. <i>Clinical Cancer Research</i> , 2014, 20, 5547-5557.	3.2	43
29	Associating disease-related genetic variants in intergenic regions to the genes they impact. <i>PeerJ</i> , 2014, 2, e639.	0.9	20
30	Molecular Profiling of Human Mammary Gland Links Breast Cancer Risk to a p27+ Cell Population with Progenitor Characteristics. <i>Cell Stem Cell</i> , 2013, 13, 117-130.	5.2	72
31	The Regional Student Group Program of the ISCB Student Council: Stories from the Road. <i>PLoS Computational Biology</i> , 2013, 9, e1003241.	1.5	13
32	ISCB Computational Biology Wikipedia Competition. <i>PLoS Computational Biology</i> , 2013, 9, e1003242.	1.5	8
33	Ten Simple Rules for Starting a Regional Student Group. <i>PLoS Computational Biology</i> , 2013, 9, e1003340.	1.5	10
34	The Young PI Buzz: Learning from the Organizers of the Junior Principal Investigator Meeting at ISMB-ECCB 2013. <i>PLoS Computational Biology</i> , 2013, 9, e1003350.	1.5	2
35	Breaking the Ice and Forging Links: The Importance of Socializing in Research. <i>PLoS Computational Biology</i> , 2013, 9, e1003355.	1.5	8
36	Highlights from the Eighth International Society for Computational Biology (ISCB) Student Council Symposium 2012. <i>BMC Bioinformatics</i> , 2012, 13, .	1.2	8

#	ARTICLE	IF	CITATIONS
37	Genome-wide analysis distinguishes hyperglycemia regulated epigenetic signatures of primary vascular cells. <i>Genome Research</i> , 2011, 21, 1601-1615.	2.4	198
38	Highlights from the Student Council Symposium 2011 at the International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology. <i>BMC Bioinformatics</i> , 2011, 12, .	1.2	11
39	Using Gene Ontology annotations in exploratory microarray clustering to understand cancer etiology. <i>Pattern Recognition Letters</i> , 2010, 31, 2138-2146.	2.6	16
40	A bi-ordering approach to linking gene expression with clinical annotations in gastric cancer. <i>BMC Bioinformatics</i> , 2010, 11, 477.	1.2	3
41	is-rSNP: a novel technique for in silico regulatory SNP detection. <i>BMC Bioinformatics</i> , 2010, 11, .	1.2	2
42	is-rSNP: a novel technique for <i>in silico</i> regulatory SNP detection. <i>Bioinformatics</i> , 2010, 26, i524-i530.	1.8	115
43	A voting approach to identify a small number of highly predictive genes using multiple classifiers. <i>BMC Bioinformatics</i> , 2009, 10, S19.	1.2	9
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. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0