Andrew W Mcpherson

List of Publications by Year
in descending order

33 papers	9,915 citations	186265 28 h-index	395702 33 g-index
48 all docs	48 docs citations	48 times ranked	19258 citing authors

#	Article	IF	Citations
1	A survey of best practices for RNA-seq data analysis. Genome Biology, 2016, 17, 13.	8.8	1,898
2	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	27.8	1,778
3	ARID1AMutations in Endometriosis-Associated Ovarian Carcinomas. New England Journal of Medicine, 2010, 363, 1532-1543.	27.0	1,460
4	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. Nature, 2015, 518, 422-426.	27.8	545
5	deFuse: An Algorithm for Gene Fusion Discovery in Tumor RNA-Seq Data. PLoS Computational Biology, 2011, 7, e1001138.	3.2	477
6	Spatial genomic heterogeneity within localized, multifocal prostate cancer. Nature Genetics, 2015, 47, 736-745.	21.4	395
7	TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data. Genome Research, 2014, 24, 1881-1893.	5.5	322
8	Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. Nature Genetics, 2016, 48, 758-767.	21.4	287
9	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. Cell, 2018, 173, 1755-1769.e22.	28.9	261
10	Probabilistic cell-type assignment of single-cell RNA-seq for tumor microenvironment profiling. Nature Methods, 2019, 16, 1007-1015.	19.0	241
11	14-3-3 fusion oncogenes in high-grade endometrial stromal sarcoma. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 929-934.	7.1	239
12	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. Nature Genetics, 2017, 49, 856-865.	21.4	220
13	Clonality inference in multiple tumor samples using phylogeny. Bioinformatics, 2015, 31, 1349-1356.	4.1	214
14	Histological Transformation and Progression in Follicular Lymphoma: A Clonal Evolution Study. PLoS Medicine, 2016, 13, e1002197.	8.4	185
15	Dissociation of solid tumor tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses. Genome Biology, 2019, 20, 210.	8.8	171
16	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. Cell, 2019, 179, 1207-1221.e22.	28.9	162
17	From sequence to molecular pathology, and a mechanism driving the neuroendocrine phenotype in prostate cancer. Journal of Pathology, 2012, 227, 286-297.	4.5	161
18	Clonal genotype and population structure inference from single-cell tumor sequencing. Nature Methods, 2016, 13, 573-576.	19.0	108

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19	Tim-4+ cavity-resident macrophages impair anti-tumor CD8+ TÂcell immunity. Cancer Cell, 2021, 39, 973-988.e9.	16.8	93
20	clonealign: statistical integration of independent single-cell RNA and DNA sequencing data from human cancers. Genome Biology, 2019, 20, 54.	8.8	92
21	Multimodal data integration using machine learning improves risk stratification of high-grade serous ovarian cancer. Nature Cancer, 2022, 3, 723-733.	13.2	82
22	Heterogeneity in the inter-tumor transcriptome of high risk prostate cancer. Genome Biology, 2014, 15, 426.	8.8	71
23	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. Nature, 2021, 595, 585-590.	27.8	71
24	nFuse: Discovery of complex genomic rearrangements in cancer using high-throughput sequencing. Genome Research, 2012, 22, 2250-2261.	5.5	67
25	Integrated genome and transcriptome sequencing identifies a novel form of hybrid and aggressive prostate cancer. Journal of Pathology, 2012, 227, 53-61.	4.5	63
26	Polyâ€gene fusion transcripts and chromothripsis in prostate cancer. Genes Chromosomes and Cancer, 2012, 51, 1144-1153.	2.8	46
27	E-scape: interactive visualization of single-cell phylogenetics and cancer evolution. Nature Methods, 2017, 14, 549-550.	19.0	46
28	Comrad: detection of expressed rearrangements by integrated analysis of RNA-Seq and low coverage genome sequence data. Bioinformatics, 2011, 27, 1481-1488.	4.1	39
29	ReMixT: clone-specific genomic structure estimation in cancer. Genome Biology, 2017, 18, 140.	8.8	29
30	Observing Clonal Dynamics across Spatiotemporal Axes: A Prelude to Quantitative Fitness Models for Cancer. Cold Spring Harbor Perspectives in Medicine, 2018, 8, a029603.	6.2	9
31	Computational identification of micro-structural variations and their proteogenomic consequences in cancer. Bioinformatics, 2018, 34, 1672-1681.	4.1	8
32	Genomic Rearrangements Involving Programmed Death Ligands Are Recurrent In Primary Mediastinal Large B-Cell Lymphoma. Blood, 2013, 122, 635-635.	1.4	3
33	Divergent Modes of Tumor Evolution Underlie Histological Transformation and Early Progression of Follicular Lymphoma. Blood, 2016, 128, 1091-1091.	1.4	0