

Andrew W Mcpherson

List of Publications by Year in descending order

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Version: 2024-02-01

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	Multimodal data integration using machine learning improves risk stratification of high-grade serous ovarian cancer. <i>Nature Cancer</i> , 2022, 3, 723-733.	13.2	82
2	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. <i>Nature</i> , 2021, 595, 585-590.	27.8	71
3	Tim-4+ cavity-resident macrophages impair anti-tumor CD8+ T cell immunity. <i>Cancer Cell</i> , 2021, 39, 973-988.e9.	16.8	93
4	Dissociation of solid tumor tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses. <i>Genome Biology</i> , 2019, 20, 210.	8.8	171
5	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. <i>Cell</i> , 2019, 179, 1207-1221.e22.	28.9	162
6	Probabilistic cell-type assignment of single-cell RNA-seq for tumor microenvironment profiling. <i>Nature Methods</i> , 2019, 16, 1007-1015.	19.0	241
7	clonealign: statistical integration of independent single-cell RNA and DNA sequencing data from human cancers. <i>Genome Biology</i> , 2019, 20, 54.	8.8	92
8	Computational identification of micro-structural variations and their proteogenomic consequences in cancer. <i>Bioinformatics</i> , 2018, 34, 1672-1681.	4.1	8
9	Observing Clonal Dynamics across Spatiotemporal Axes: A Prelude to Quantitative Fitness Models for Cancer. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2018, 8, a029603.	6.2	9
10	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. <i>Cell</i> , 2018, 173, 1755-1769.e22.	28.9	261
11	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. <i>Nature Genetics</i> , 2017, 49, 856-865.	21.4	220
12	E-scape: interactive visualization of single-cell phylogenetics and cancer evolution. <i>Nature Methods</i> , 2017, 14, 549-550.	19.0	46
13	ReMixT: clone-specific genomic structure estimation in cancer. <i>Genome Biology</i> , 2017, 18, 140.	8.8	29
14	Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. <i>Nature Genetics</i> , 2016, 48, 758-767.	21.4	287
15	Clonal genotype and population structure inference from single-cell tumor sequencing. <i>Nature Methods</i> , 2016, 13, 573-576.	19.0	108
16	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016, 17, 13.	8.8	1,898
17	Histological Transformation and Progression in Follicular Lymphoma: A Clonal Evolution Study. <i>PLoS Medicine</i> , 2016, 13, e1002197.	8.4	185
18	Divergent Modes of Tumor Evolution Underlie Histological Transformation and Early Progression of Follicular Lymphoma. <i>Blood</i> , 2016, 128, 1091-1091.	1.4	0

#	ARTICLE	IF	CITATIONS
19	Spatial genomic heterogeneity within localized, multifocal prostate cancer. <i>Nature Genetics</i> , 2015, 47, 736-745.	21.4	395
20	Clonality inference in multiple tumor samples using phylogeny. <i>Bioinformatics</i> , 2015, 31, 1349-1356.	4.1	214
21	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. <i>Nature</i> , 2015, 518, 422-426.	27.8	545
22	Heterogeneity in the inter-tumor transcriptome of high risk prostate cancer. <i>Genome Biology</i> , 2014, 15, 426.	8.8	71
23	TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data. <i>Genome Research</i> , 2014, 24, 1881-1893.	5.5	322
24	Genomic Rearrangements Involving Programmed Death Ligands Are Recurrent In Primary Mediastinal Large B-Cell Lymphoma. <i>Blood</i> , 2013, 122, 635-635.	1.4	3
25	nFuse: Discovery of complex genomic rearrangements in cancer using high-throughput sequencing. <i>Genome Research</i> , 2012, 22, 2250-2261.	5.5	67
26	14-3-3 fusion oncogenes in high-grade endometrial stromal sarcoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 929-934.	7.1	239
27	Polygene fusion transcripts and chromothripsis in prostate cancer. <i>Genes Chromosomes and Cancer</i> , 2012, 51, 1144-1153.	2.8	46
28	Integrated genome and transcriptome sequencing identifies a novel form of hybrid and aggressive prostate cancer. <i>Journal of Pathology</i> , 2012, 227, 53-61.	4.5	63
29	From sequence to molecular pathology, and a mechanism driving the neuroendocrine phenotype in prostate cancer. <i>Journal of Pathology</i> , 2012, 227, 286-297.	4.5	161
30	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. <i>Nature</i> , 2012, 486, 395-399.	27.8	1,778
31	Comrad: detection of expressed rearrangements by integrated analysis of RNA-Seq and low coverage genome sequence data. <i>Bioinformatics</i> , 2011, 27, 1481-1488.	4.1	39
32	deFuse: An Algorithm for Gene Fusion Discovery in Tumor RNA-Seq Data. <i>PLoS Computational Biology</i> , 2011, 7, e1001138.	3.2	477
33	<i>ARID1A</i> Mutations in Endometriosis-Associated Ovarian Carcinomas. <i>New England Journal of Medicine</i> , 2010, 363, 1532-1543.	27.0	1,460