Mitchell J Machiela

List of Publications by Year
in descending order

96 papers	6,622 citations	94433 37 h-index	76900 74 g-index
104 all docs	104 docs citations	104 times ranked	13982 citing authors

#	Article	IF	Citations
1	Different Pigmentation Risk Loci for High-Risk Monosomy 3 and Low-Risk Disomy 3 Uveal Melanomas. Journal of the National Cancer Institute, 2022, 114, 302-309.	6.3	5
2	Abstract PO-192: Comparing the association of self-reported race-ethnicity and genetic ancestry with all-cause mortality: A pan-cancer survivor analysis in the PLCO Screening Trial. , 2022, , .		0
3	The renal lineage factor PAX8 controls oncogenic signalling in kidney cancer. Nature, 2022, 606, 999-1006.	27.8	24
4	AuthorArranger automates formatting title pages and author affiliations for manuscript submissions. Communications Biology, 2022, 5, .	4.4	0
5	PCAmatchR: a flexible R package for optimal caseâ€“control matching using weighted principal components. Bioinformatics, 2021, 37, 1178-1181.	4.1	11
6	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	21.4	264
7	Detectable chromosome X mosaicism in males is rarely tolerated in peripheral leukocytes. Scientific Reports, 2021, 11, 1193.	3.3	13
8	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in the Childhood Cancer Survivor Study. JNCI Cancer Spectrum, 2021, 5, pkab007.	2.9	11
9	Genome-wide homozygosity and risk of four non-Hodgkin lymphoma subtypes. , 2021, 5, 200-217.		0
10	Genetically Inferred Telomere Length and Testicular Germ Cell Tumor Risk. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1275-1278.	2.5	2
11	In-utero exposure to zidovudine-containing antiretroviral therapy and clonal hematopoiesis in HIV-exposed uninfected newborns. Aids, 2021, 35, 1525-1535.	2.2	2
12	sparrpowR: a flexible R package to estimate statistical power to identify spatial clustering of two groups and its application. International Journal of Health Geographics, 2021, 20, 13.	2.5	4
13	Lack of transgenerational effects of ionizing radiation exposure from the Chernobyl accident. Science, 2021, 372, 725-729.	12.6	60
14	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. Science, 2021, 372, .	12.6	85
15	Comparative international incidence of Ewing sarcoma 1988 to 2012. International Journal of Cancer, 2021, 149, 1054-1066.	5.1	16
16	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. Nature Medicine, 2021, 27, 1012-1024.	30.7	109
17	Prognostic impact of pre-transplant chromosomal aberrations in peripheral blood of patients undergoing unrelated donor hematopoietic cell transplant for acute myeloid leukemia. Scientific Reports, 2021, 11, 15004.	3.3	4
18	Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. American Journal of Clinical Nutrition, 2021, 114, 1408-1417.	4.7	9

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19	Incident disease associations with mosaic chromosomal alterations on autosomes, X and Y chromosomes: insights from a phenome-wide association study in the UK Biobank. Cell and Bioscience, 2021, 11, 143.	4.8	14
20	Altered regulation of DPF3, a member of the SWI/SNF complexes, underlies the 14q24 renal cancer susceptibility locus. American Journal of Human Genetics, 2021, 108, 1590-1610.	6.2	9
21	Pre-HCT mosaicism increases relapse risk and lowers survival in acute lymphoblastic leukemia patients postâ€“unrelated HCT. Blood Advances, 2021, 5, 66-70.	5.2	6
22	Clonal hematopoiesis is associated with risk of severe Covid-19. Nature Communications, 2021, 12, 5975.	12.8	81
23	Germline Variation and Somatic Alterations in Ewing Sarcoma. Methods in Molecular Biology, 2021, 2226, 3-14.	0.9	2
24	Germline-Somatic Interactions in Myelofibrosis Susceptibility. Blood, 2021, 138, 313-313.	1.4	0
25	LDexpress: an online tool for integrating population-specific linkage disequilibrium patterns with tissue-specific expression data. BMC Bioinformatics, 2021, 22, 608.	2.6	6
26	Low-frequency variation near common germline susceptibility loci are associated with risk of Ewing sarcoma. PLoS ONE, 2020, 15, e0237792.	2.5	6
27	Field Study of the Possible Effect of Parental Irradiation on the Germline of Children Born to Cleanup Workers and Evacuees of the Chornobyl Nuclear Accident. American Journal of Epidemiology, 2020, 189, 1451-1460.	3.4	12
28	LDtrait: An Online Tool for Identifying Published Phenotype Associations in Linkage Disequilibrium. Cancer Research, 2020, 80, 3443-3446.	0.9	23
29	Coinherited genetics of multiple myeloma and its precursor, monoclonal gammopathy of undetermined significance. Blood Advances, 2020, 4, 2789-2797.	5.2	20
30	LDlinkR: An R Package for Rapidly Calculating Linkage Disequilibrium Statistics in Diverse Populations. Frontiers in Genetics, 2020, 11, 157.	2.3	185
31	Mosaic chromosome Y loss is associated with alterations in blood cell counts in UK Biobank men. Scientific Reports, 2020, 10, 3655.	3.3	31
32	Why Y? Downregulation of Chromosome Y Genes Potentially Contributes to Elevated Cancer Risk. Journal of the National Cancer Institute, 2020, 112, 871-872.	6.3	5
33	LDpop: an interactive online tool to calculate and visualize geographic LD patterns. BMC Bioinformatics, 2020, 21, 14.	2.6	45
34	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	21.4	138
35	Genetically predicted telomere length is associated with clonal somatic copy number alterations in peripheral leukocytes. PLoS Genetics, 2020, 16, e1009078.	3.5	14
36	Title is missing!. , 2020, 15, e0237792.		0

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37	Title is missing!. , 2020, 15, e0237792.		0
38	Title is missing!. , 2020, 15, e0237792.		0
39	Title is missing!. , 2020, 15, e0237792.		0
40	Sex specific associations in genome wide association analysis of renal cell carcinoma. European Journal of Human Genetics, 2019, 27, 1589-1598.	2.8	27
41	Detectible mosaic truncating PPM1D mutations, age and breast cancer risk. Journal of Human Genetics, 2019, 64, 545-550.	2.3	6
42	Mosaicism, aging and cancer. Current Opinion in Oncology, 2019, 31, 108-113.	2.4	13
43	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	27.8	198
44	The influence of obesity-related factors in the etiology of renal cell carcinomaâ€"A mendelian randomization study. PLoS Medicine, 2019, 16, e1002724.	8.4	59
45	Telomere Length-Associated Genetic Variants and the Risk of Thyroid Cancer in Survivors of Childhood Cancer: A Report from the Childhood Cancer Survivor Study (CCSS). Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 417-419.	2.5	7
46	Reply to â€˜Mosaic loss of chromosome Y in leukocytes mattersâ€™. Nature Genetics, 2019, 51, 7-9.	21.4	7
47	Mosaic Y Loss Is Moderately Associated with Solid Tumor Risk. Cancer Research, 2019, 79, 461-466.	0.9	48
48	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. Frontiers in Oncology, 2019, 9, 1539.	2.8	6
49	De Novo and Therapy-Related Acute Myeloid Leukemia and Myelodysplastic Syndrome: Similarities and Differences in SNP-Array Detected Chromosomal Aberrations in Pre-Transplant Blood Samples. Blood, 2019, 134, 1430-1430.	1.4	2
50	Association between a Polygenic Risk Score for Multiple Myeloma Risk and Overall Survival. Blood, 2019, 134, 4366-4366.	1.4	0
51	LDassoc: an online tool for interactively exploring genome-wide association study results and prioritizing variants for functional investigation. Bioinformatics, 2018, 34, 887-889.	4.1	89
52	Predictors of mosaic chromosome Y loss and associations with mortality in the UK Biobank. Scientific Reports, 2018, 8, 12316.	3.3	105
53	Outdoor air pollution and mosaic loss of chromosome Y in older men from the Cardiovascular Health Study. Environment International, 2018, 116, 239-247.	10.0	32
54	Genome-wide association study identifies multiple new loci associated with Ewing sarcoma susceptibility. Nature Communications, 2018, 9, 3184.	12.8	50

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55	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	21.4	652
56	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	12.8	88
57	The ageing genome, clonal mosaicism and chronic disease. Current Opinion in Genetics and Development, 2017, 42, 8-13.	3.3	28
58	Mosaic chromosome Y loss and testicular germ cell tumor risk. Journal of Human Genetics, 2017, 62, 637-640.	2.3	34
59	Landscape of Combination Immunotherapy and Targeted Therapy to Improve Cancer Management. Cancer Research, 2017, 77, 3666-3671.	0.9	93
60	Genome-Wide Association Study to Identify Susceptibility Loci That Modify Radiation-Related Risk for Breast Cancer After Childhood Cancer. Journal of the National Cancer Institute, 2017, 109, .	6.3	66
61	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724.	12.8	106
62	Characterization of breakpoint regions of large structural autosomal mosaic events. Human Molecular Genetics, 2017, 26, 4388-4394.	2.9	2
63	Genetic Variants Related to Longer Telomere Length are Associated with Increased Risk of Renal Cell Carcinoma. European Urology, 2017, 72, 747-754.	1.9	39
64	Integrating Clinical and Multiple Omics Data for Prognostic Assessment across Human Cancers. Scientific Reports, 2017, 7, 16954.	3.3	79
65	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
66	Mosaic chromosome 20q deletions are more frequent in the aging population. Blood Advances, 2017, 1, 380-385.	5.2	15
67	Burden of Nonsynonymous Mutations among TCGA Cancers and Candidate Immune Checkpoint Inhibitor Responses. Cancer Research, 2016, 76, 3767-3772.	0.9	124
68	Mosaic loss of chromosome Y is associated with common variation near TCL1A. Nature Genetics, 2016, 48, 563-568.	21.4	134
69	An investigation of the association of genetic susceptibility risk with somatic mutation burden in breast cancer. British Journal of Cancer, 2016, 115, 752-760.	6.4	16
70	Functional characterization of the 12p12.1 renal cancer-susceptibility locus implicates BHLHE41. Nature Communications, 2016, 7, 12098.	12.8	30
71	Genomic characterization of viral integration sites in HPVâ€related cancers. International Journal of Cancer, 2016, 139, 2001-2011.	5.1	113
72	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86

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73	Mosaic 13q14 deletions in peripheral leukocytes of non-hematologic cancer cases and healthy controls. Journal of Human Genetics, 2016, 61, 411-418.	2.3	13
74	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676.	2.9	52
75	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
76	<scp>G</scp>enetic variants associated with longer telomere length are associated with increased lung cancer risk among neverâ€smoking women in Asia: a report from the female lung cancer consortium in Asia. International Journal of Cancer, 2015, 137, 311-319.	5.1	72
77	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
78	LDlink: a web-based application for exploring population-specific haplotype structure and linking correlated alleles of possible functional variants. Bioinformatics, 2015, 31, 3555-3557.	4.1	1,473
79	Chimeric EWSR1-FLI1 regulates the Ewing sarcoma susceptibility gene EGR2 via a GGAA microsatellite. Nature Genetics, 2015, 47, 1073-1078.	21.4	157
80	Deep sequencing of HPV16 genomes: A new high-throughput tool for exploring the carcinogenicity and natural history of HPV16 infection. Papillomavirus Research (Amsterdam, Netherlands), 2015, 1, 3-11.	4.5	75
81	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. Human Molecular Genetics, 2015, 24, 5603-5618.	2.9	50
82	A Genome-Wide Scan Identifies Variants in NFIB Associated with Metastasis in Patients with Osteosarcoma. Cancer Discovery, 2015, 5, 920-931.	9.4	88
83	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
84	Two susceptibility loci identified for prostate cancer aggressiveness. Nature Communications, 2015, 6, 6889.	12.8	88
85	Limited evidence that cancer susceptibility regions are preferential targets for somatic mutation. Genome Biology, 2015, 16, 193.	8.8	19
86	GWAS is going to the dogs. Genome Biology, 2014, 15, 105.	9.6	8
87	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	21.4	408
88	Detectable Clonal Mosaicism in the Human Genome. Seminars in Hematology, 2013, 50, 348-359.	3.4	32
89	One thousand genomes imputation in the national cancer institute breast and prostate cancer cohort consortium aggressive prostate cancer genomeâ€wide association study. Prostate, 2013, 73, 677-689.	2.3	6
90	Scanning for Clues to Better Use Selective Estrogen Receptor Modulators. Cancer Discovery, 2013, 3, 728-729.	9.4	0

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91	Re-Ranking Sequencing Variants in the Post-GWAS Era for Accurate Causal Variant Identification. PLoS Genetics, 2013, 9, e1003609.	3.5	36
92	Association of Type 2 Diabetes Susceptibility Variants With Advanced Prostate Cancer Risk in the Breast and Prostate Cancer Cohort Consortium. American Journal of Epidemiology, 2012, 176, 1121-1129.	3.4	67
93	Evaluation of polygenic risk scores for predicting breast and prostate cancer risk. Genetic Epidemiology, 2011, 35, n/a-n/a.	1.3	74
94	Chromosome 8q24 markers: Risk of early-onset and familial prostate cancer. International Journal of Cancer, 2008, 122, 2876-2879.	5.1	23
95	Chromosome 17q12 Variants Contribute to Risk of Early-Onset Prostate Cancer. Cancer Research, 2008, 68, 6492-6495.	0.9	40
96	Does a Multiple Myeloma Polygenic Risk Score Predict Overall Survival of Myeloma Patients?. Cancer Epidemiology Biomarkers and Prevention, 0, , .	2.5	2