John V Pearson

List of Publications by Year
in descending order

107	36,951	38742 50	28297 105
papers	citations	h-index	g-index

113	113	113	58492
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomic and Molecular Analyses Identify Molecular Subtypes of Pancreatic Cancer Recurrence. Gastroenterology, 2022, 162, 320-324.e4.	1.3	26
2	Patient-derived xenograft models capture genomic heterogeneity in endometrial cancer. Genome Medicine, 2022, 14, 3.	8.2	16
3	Multiomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance. Cancer Cell, 2022, 40, 88-102.e7.	16.8	64
4	qmotif: determination of telomere content from whole-genome sequence data. Bioinformatics Advances, 2022, 2, .	2.4	5
5	Anatomic position determines oncogenic specificity in melanoma. Nature, 2022, 604, 354-361.	27.8	44
6	Comprehensive genomic and tumour immune profiling reveals potential therapeutic targets in malignant pleural mesothelioma. Genome Medicine, 2022, 14, .	8.2	24
7	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. Gastroenterology, 2021, 160, 362-377.e13.	1.3	90
8	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. Communications Biology, 2021, 4, 155.	4.4	26
9	Considerations for using population frequency data in germline variant interpretation: Cancer syndrome genes as a model. Human Mutation, 2021, 42, 530-536.	2.5	8
10	Radiomics Biomarkers Correlate with CD8 Expression and Predict Immune Signatures in Melanoma Patients. Molecular Cancer Research, 2021, 19, 950-956.	3.4	19
11	Tumor Signature Analysis Implicates Hereditary Cancer Genes in Endometrial Cancer Development. Cancers, 2021, 13, 1762.	3.7	5
12	Deep learning in cancer diagnosis, prognosis and treatment selection. Genome Medicine, 2021, 13, 152.	8.2	274
13	Verifying explainability of a deep learning tissue classifier trained on RNA-seq data. Scientific Reports, 2021, 11, 2641.	3.3	32
14	Ask the people: developing guidelines for genomic research with Aboriginal and Torres Strait Islander peoples. BMJ Global Health, 2021, 6, e007259.	4.7	8
15	ROR1 and ROR2 expression in pancreatic cancer. BMC Cancer, 2021, 21, 1199.	2.6	4
16	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	12.8	102
17	Pathogenic germline variants are associated with poor survival in stage III/IV melanoma patients. Scientific Reports, 2020, 10, 17687.	3.3	14
18	Tumor Mutation Burden and Structural Chromosomal Aberrations Are Not Associated with T-cell Density or Patient Survival in Acral, Mucosal, and Cutaneous Melanomas. Cancer Immunology Research, 2020, 8, 1346-1353.	3.4	13

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19	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. Npj Breast Cancer, 2020, 6, 33.	5.2	19
20	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. Nature Communications, 2020, 11, 2408.	12.8	86
21	APC Mutation Marks an Aggressive Subtype of BRAF Mutant Colorectal Cancers. Cancers, 2020, 12, 1171.	3.7	28
22	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. Cell Reports, 2020, 31, 107625.	6.4	78
23	Alterations in signaling pathways that accompany spontaneous transition to malignancy in a mouse model of BRAF mutant microsatellite stable colorectal cancer. Neoplasia, 2020, 22, 120-128.	5.3	14
24	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	21.4	431
25	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	12.8	205
26	Integrative Genome-Scale DNA Methylation Analysis of a Large and Unselected Cohort Reveals 5 Distinct Subtypes of Colorectal Adenocarcinomas. Cellular and Molecular Gastroenterology and Hepatology, 2019, 8, 269-290.	4.5	42
27	Molecular Genomic Profiling of MelanocyticÂNevi. Journal of Investigative Dermatology, 2019, 139, 1762-1768.	0.7	55
28	Diff-Quik Cytology Smears from Endobronchial Ultrasound Transbronchial Needle Aspiration Lymph Node Specimens as a Source of DNA for Next-Generation Sequencing Instead of Cell Blocks. Respiration, 2019, 97, 525-539.	2.6	25
29	Complex structural rearrangements are present in high-grade dysplastic Barrettâ€™s oesophagus samples. BMC Medical Genomics, 2019, 12, 31.	1.5	19
30	Intratumoural Heterogeneity Underlies Distinct Therapy Responses and Treatment Resistance in Glioblastoma. Cancers, 2019, 11, 190.	3.7	39
31	Whole genome sequencing of melanomas in adolescent and young adults reveals distinct mutation landscapes and the potential role of germline variants in disease susceptibility. International Journal of Cancer, 2019, 144, 1049-1060.	5.1	54
32	Phenotypic and molecular dissection of metaplastic breast cancer and the prognostic implications. Journal of Pathology, 2019, 247, 214-227.	4.5	73
33	A SMART on FHIR Prototype for Genomic Test Ordering. Studies in Health Technology and Informatics, 2019, 266, 121-126.	0.3	4
34	Running Genomic Analyses in the Cloud. Studies in Health Technology and Informatics, 2019, 266, 149-155.	0.3	1
35	Mixed ductalâ€lobular carcinomas: evidence for progression from ductal to lobular morphology. Journal of Pathology, 2018, 244, 460-468.	4.5	31
36	Telomere sequence content can be used to determine ALT activity in tumours. Nucleic Acids Research, 2018, 46, 4903-4918.	14.5	40

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37	Malignant cells from pleural fluids in malignant mesothelioma patients reveal novel mutations. Lung Cancer, 2018, 119, 64-70.	2.0	23
38	Homologous Recombination DNA Repair Pathway Disruption and Retinoblastoma Protein Loss Are Associated with Exceptional Survival in High-Grade Serous Ovarian Cancer. Clinical Cancer Research, 2018, 24, 569-580.	7.0	79
39	BRAF Mutations in Low-Grade Serous Ovarian Cancer and Response to BRAF Inhibition. JCO Precision Oncology, 2018, 2, 1-14.	3.0	19
40	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. PLoS ONE, 2018, 13, e0190264.	2.5	57
41	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	27.8	716
42	Unexpected UVR and non-UVR mutation burden in some acral and cutaneous melanomas. Laboratory Investigation, 2017, 97, 130-145.	3.7	40
43	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	27.8	1,068
44	Mitochondrial mutations and metabolic adaptation in pancreatic cancer. Cancer & Metabolism, 2017, 5, 2.	5.0	51
45	Mutation load in melanoma is affected by <scp>MC</scp>1R genotype. Pigment Cell and Melanoma Research, 2017, 30, 255-258.	3.3	19
46	Next-Generation Sequencing of Endobronchial Ultrasound Transbronchial Needle Aspiration Specimens in Lung Cancer. American Journal of Respiratory and Critical Care Medicine, 2017, 196, 388-391.	5.6	14
47	Long Noncoding RNAs CUPID1 and CUPID2 Mediate Breast Cancer Risk at 11q13 by Modulating the Response to DNA Damage. American Journal of Human Genetics, 2017, 101, 255-266.	6.2	77
48	EIF1AX and NRAS Mutations Co-occur and Cooperate in Low-Grade Serous Ovarian Carcinomas. Cancer Research, 2017, 77, 4268-4278.	0.9	56
49	Whole exome sequencing of an asbestos-induced wild-type murine model of malignant mesothelioma. BMC Cancer, 2017, 17, 396.	2.6	30
50	Lost in translation: returning germline genetic results in genome-scale cancer research. Genome Medicine, 2017, 9, 41.	8.2	27
51	Hypermutation In Pancreatic Cancer. Gastroenterology, 2017, 152, 68-74.e2.	1.3	174
52	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. American Journal of Human Genetics, 2016, 98, 830-842.	6.2	201
53	A Common Variant at the 14q32 Endometrial Cancer Risk Locus Activates AKT1 through YY1 Binding. American Journal of Human Genetics, 2016, 98, 1159-1169.	6.2	32
54	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. Cell Reports, 2016, 14, 907-919.	6.4	107

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55	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	27.8	2,700
56	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. Journal of Pathology, 2015, 237, 363-378.	4.5	98
57	Wholeâ€“genome characterization of chemoresistant ovarian cancer. Nature, 2015, 521, 489-494.	27.8	1,206
58	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
59	Whole genomes redefine the mutational landscape of pancreatic cancer. Nature, 2015, 518, 495-501.	27.8	2,132
60	Pathway and network analysis of cancer genomes. Nature Methods, 2015, 12, 615-621.	19.0	297
61	PGTools: A Software Suite for Proteogenomic Data Analysis and Visualization. Journal of Proteome Research, 2015, 14, 2255-2266.	3.7	52
62	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	1.8	0
63	Genomeâ€wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLITâ€ROBO, ITGA2 and MET signaling. International Journal of Cancer, 2014, 135, 1110-1118.	5.1	192
64	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	12.8	236
65	Returning individual research results for genome sequences of pancreatic cancer. Genome Medicine, 2014, 6, 42.	8.2	25
66	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	19.0	161
67	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
68	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. Genome Medicine, 2013, 5, 78.	8.2	97
69	Somatic Point Mutation Calling in Low Cellularity Tumors. PLoS ONE, 2013, 8, e74380.	2.5	67
70	PINA v2.0: mining interactome modules. Nucleic Acids Research, 2012, 40, D862-D865.	14.5	321
71	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	27.8	1,741
72	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. PLoS ONE, 2012, 7, e45835.	2.5	92

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73	Copy number and targeted mutational analysis reveals novel somatic events in metastatic prostate tumors. Genome Research, 2011, 21, 47-55.	5.5	148
74	Microarray-Based Genome-Wide Association Studies Using Pooled DNA. Methods in Molecular Biology, 2011, 700, 49-60.	0.9	12
75	Next-Generation Sequencing ofCoccidioides immitisIsolated during Cluster Investigation. Emerging Infectious Diseases, 2011, 17, 227-232.	4.3	48
76	X-MATE: a flexible system for mapping short read data. Bioinformatics, 2011, 27, 580-581.	4.1	11
77	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
78	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	27.8	7,209
79	Evidence for an association between KIBRA and late-onset Alzheimer's disease. Neurobiology of Aging, 2010, 31, 901-909.	3.1	100
80	Whole genome association analysis shows that ACE is a risk factor for Alzheimer's disease and fails to replicate most candidates from Meta-analysis. International Journal of Molecular Epidemiology and Genetics, 2010, 1, 19-30.	0.4	4
81	Statistical Comparison Framework and Visualization Scheme for Ranking-Based Algorithms in High-Throughput Genome-Wide Studies. Journal of Computational Biology, 2009, 16, 565-577.	1.6	0
82	GRM7 variants confer susceptibility to age-related hearing impairment. Human Molecular Genetics, 2009, 18, 785-796.	2.9	174
83	Genetic Control of Human Brain Transcript Expression in Alzheimer Disease. American Journal of Human Genetics, 2009, 84, 445-458.	6.2	290
84	Neuronal gene expression correlates of Parkinson's disease with dementia. Movement Disorders, 2008, 23, 1588-1595.	3.9	45
85	Identification of genetic variants using bar-coded multiplexed sequencing. Nature Methods, 2008, 5, 887-893.	19.0	285
86	<i>Sorl1</i> as an Alzheimerâ€™s Disease Predisposition Gene?. Neurodegenerative Diseases, 2008, 5, 60-64.	1.4	73
87	Gene expression profiling-based identification of cell-surface targets for developing multimeric ligands in pancreatic cancer. Molecular Cancer Therapeutics, 2008, 7, 3071-3080.	4.1	25
88	Multimarker analysis and imputation of multiple platform pooling-based genome-wide association studies. Bioinformatics, 2008, 24, 1896-1902.	4.1	18
89	Resolving Individuals Contributing Trace Amounts of DNA to Highly Complex Mixtures Using High-Density SNP Genotyping Microarrays. PLoS Genetics, 2008, 4, e1000167.	3.5	892
90	Whole-Genome Analysis of Sporadic Amyotrophic Lateral Sclerosis. New England Journal of Medicine, 2007, 357, 775-788.	27.0	234

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91	GAB2 Alleles Modify Alzheimer's Risk in APOE É›4 Carriers. Neuron, 2007, 54, 713-720.	8.1	451
92	Identification of the Genetic Basis for Complex Disorders by Use of Pooling-Based Genomewide Single-Nucleotideâ€“Polymorphism Association Studies. American Journal of Human Genetics, 2007, 80, 126-139.	6.2	139
93	Identification of a Novel Risk Locus for Progressive Supranuclear Palsy by a Pooled Genomewide Scan of 500,288 Single-Nucleotide Polymorphisms. American Journal of Human Genetics, 2007, 80, 769-778.	6.2	68
94	Calmodulin-binding transcription activator 1 (CAMTA1) alleles predispose human episodic memory performance. Human Molecular Genetics, 2007, 16, 1469-1477.	2.9	66
95	Identification of PVT1 as a Candidate Gene for End-Stage Renal Disease in Type 2 Diabetes Using a Pooling-Based Genome-Wide Single Nucleotide Polymorphism Association Study. Diabetes, 2007, 56, 975-983.	0.6	184
96	A survey of genetic human cortical gene expression. Nature Genetics, 2007, 39, 1494-1499.	21.4	488
97	Complete Genomic Characterization of a Pathogenic A.II Strain of Francisella tularensis Subspecies tularensis. PLoS ONE, 2007, 2, e947.	2.5	46
98	A High-Density Whole-Genome Association Study Reveals That APOE Is the Major Susceptibility Gene for Sporadic Late-Onset Alzheimer's Disease. Journal of Clinical Psychiatry, 2007, 68, 613-618.	2.2	484
99	Common Kibra Alleles Are Associated with Human Memory Performance. Science, 2006, 314, 475-478.	12.6	391
100	The Value of Molecular Haplotypes in a Family-Based Linkage Study. American Journal of Human Genetics, 2006, 79, 458-468.	6.2	10
101	Quantitation of heteroplasmy of mtDNA sequence variants identified in a population of AD patients and controls by array-based resequencing. Mitochondrion, 2006, 6, 194-210.	3.4	41
102	SNiPer: Improved SNP genotype calling for Affymetrix 10K GeneChip microarray data. BMC Genomics, 2005, 6, 149.	2.8	26
103	Genetic and environmental contributions to size, color, shape, and other characteristics of melanocytic naevi in a sample of adolescent twins. , 1999, 16, 40-53.		96
104	Compilation of somatic mutations of theCDKN2 gene in human cancers: Non-random distribution of base substitutions. , 1996, 15, 77-88.		155
105	Control of ion transport in the thyroid: prostaglandin E2 activates cation transport on the basal membrane of cultured porcine thyroid cell monolayers. Journal of Endocrinology, 1990, 127, 197-202.	2.6	8
106	Inhibitory effects of amiloride and its analogues on prostaglandin E2-stimulated fluid transport by cultured porcine thyroid cells: evidence for apical membrane Na+ channels. Journal of Endocrinology, 1989, 123, 93-97.	2.6	6
107	Electrophysiological correlates of fluid transport in cultured porcine thyroid cells. Journal of Endocrinology, 1988, 119, 309-314.	2.6	17