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	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
2	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	27.8	7,209
3	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	27.8	2,700
4	Whole genomes redefine the mutational landscape of pancreatic cancer. Nature, 2015, 518, 495-501.	27.8	2,132
5	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
6	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	27.8	1,741
7	Wholeâ€“genome characterization of chemoresistant ovarian cancer. Nature, 2015, 521, 489-494.	27.8	1,206
8	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	27.8	1,068
9	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
10	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	27.8	716
11	A survey of genetic human cortical gene expression. Nature Genetics, 2007, 39, 1494-1499.	21.4	488
12	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
13	GAB2 Alleles Modify Alzheimer's Risk in APOE É›4 Carriers. Neuron, 2007, 54, 713-720.	8.1	451
14	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	21.4	431
15	Common Kibra Alleles Are Associated with Human Memory Performance. Science, 2006, 314, 475-478.	12.6	391
16	PINA v2.0: mining interactome modules. Nucleic Acids Research, 2012, 40, D862-D865.	14.5	321
17	Pathway and network analysis of cancer genomes. Nature Methods, 2015, 12, 615-621.	19.0	297
18	Genetic Control of Human Brain Transcript Expression in Alzheimer Disease. American Journal of Human Genetics, 2009, 84, 445-458.	6.2	290

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19	Identification of genetic variants using bar-coded multiplexed sequencing. Nature Methods, 2008, 5, 887-893.	19.0	285
20	Deep learning in cancer diagnosis, prognosis and treatment selection. Genome Medicine, 2021, 13, 152.	8.2	274
21	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
22	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	12.8	236
23	Whole-Genome Analysis of Sporadic Amyotrophic Lateral Sclerosis. New England Journal of Medicine, 2007, 357, 775-788.	27.0	234
24	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	12.8	205
25	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
26	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
27	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
28	GRM7 variants confer susceptibility to age-related hearing impairment. Human Molecular Genetics, 2009, 18, 785-796.	2.9	174
29	Hypermutation In Pancreatic Cancer. Gastroenterology, 2017, 152, 68-74.e2.	1.3	174
30	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	19.0	161
31	Compilation of somatic mutations of theCDKN2 gene in human cancers: Non-random distribution of base substitutions. , 1996, 15, 77-88.		155
32	Copy number and targeted mutational analysis reveals novel somatic events in metastatic prostate tumors. Genome Research, 2011, 21, 47-55.	5.5	148
33	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
34	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. Cell Reports, 2016, 14, 907-919.	6.4	107
35	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	12.8	102
36	Evidence for an association between KIBRA and late-onset Alzheimer's disease. Neurobiology of Aging, 2010, 31, 901-909.	3.1	100

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37	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
38	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. Genome Medicine, 2013, 5, 78.	8.2	97
39	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
40	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. PLoS ONE, 2012, 7, e45835.	2.5	92
41	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. Gastroenterology, 2021, 160, 362-377.e13.	1.3	90
42	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. Nature Communications, 2020, 11, 2408.	12.8	86
43	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
44	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. Cell Reports, 2020, 31, 107625.	6.4	78
45	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
46	<i>Sorl1</i> as an Alzheimerâ€™s Disease Predisposition Gene?. Neurodegenerative Diseases, 2008, 5, 60-64.	1.4	73
47	Phenotypic and molecular dissection of metaplastic breast cancer and the prognostic implications. Journal of Pathology, 2019, 247, 214-227.	4.5	73
48	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
49	Somatic Point Mutation Calling in Low Cellularity Tumors. PLoS ONE, 2013, 8, e74380.	2.5	67
50	Calmodulin-binding transcription activator 1 (CAMTA1) alleles predispose human episodic memory performance. Human Molecular Genetics, 2007, 16, 1469-1477.	2.9	66
51	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
52	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. PLoS ONE, 2018, 13, e0190264.	2.5	57
53	EIF1AX and NRAS Mutations Co-occur and Cooperate in Low-Grade Serous Ovarian Carcinomas. Cancer Research, 2017, 77, 4268-4278.	0.9	56
54	Molecular Genomic Profiling of MelanocyticÂNevi. Journal of Investigative Dermatology, 2019, 139, 1762-1768.	0.7	55

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55	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
56	PGTools: A Software Suite for Proteogenomic Data Analysis and Visualization. Journal of Proteome Research, 2015, 14, 2255-2266.	3.7	52
57	Mitochondrial mutations and metabolic adaptation in pancreatic cancer. Cancer & Metabolism, 2017, 5, 2.	5.0	51
58	Next-Generation Sequencing ofCoccidioides immitisIsolated during Cluster Investigation. Emerging Infectious Diseases, 2011, 17, 227-232.	4.3	48
59	Complete Genomic Characterization of a Pathogenic A.II Strain of Francisella tularensis Subspecies tularensis. PLoS ONE, 2007, 2, e947.	2.5	46
60	Neuronal gene expression correlates of Parkinson's disease with dementia. Movement Disorders, 2008, 23, 1588-1595.	3.9	45
61	Anatomic position determines oncogenic specificity in melanoma. Nature, 2022, 604, 354-361.	27.8	44
62	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
63	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
64	Unexpected UVR and non-UVR mutation burden in some acral and cutaneous melanomas. Laboratory Investigation, 2017, 97, 130-145.	3.7	40
65	Telomere sequence content can be used to determine ALT activity in tumours. Nucleic Acids Research, 2018, 46, 4903-4918.	14.5	40
66	Intratumoural Heterogeneity Underlies Distinct Therapy Responses and Treatment Resistance in Glioblastoma. Cancers, 2019, 11, 190.	3.7	39
67	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
68	Verifying explainability of a deep learning tissue classifier trained on RNA-seq data. Scientific Reports, 2021, 11, 2641.	3.3	32
69	Mixed ductalâ€lobular carcinomas: evidence for progression from ductal to lobular morphology. Journal of Pathology, 2018, 244, 460-468.	4.5	31
70	Whole exome sequencing of an asbestos-induced wild-type murine model of malignant mesothelioma. BMC Cancer, 2017, 17, 396.	2.6	30
71	APC Mutation Marks an Aggressive Subtype of BRAF Mutant Colorectal Cancers. Cancers, 2020, 12, 1171.	3.7	28
72	Lost in translation: returning germline genetic results in genome-scale cancer research. Genome Medicine, 2017, 9, 41.	8.2	27

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73	SNiPer: Improved SNP genotype calling for Affymetrix 10K GeneChip microarray data. BMC Genomics, 2005, 6, 149.	2.8	26
74	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. Communications Biology, 2021, 4, 155.	4.4	26
75	Genomic and Molecular Analyses Identify Molecular Subtypes of Pancreatic Cancer Recurrence. Gastroenterology, 2022, 162, 320-324.e4.	1.3	26
76	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
77	Returning individual research results for genome sequences of pancreatic cancer. Genome Medicine, 2014, 6, 42.	8.2	25
78	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
79	Comprehensive genomic and tumour immune profiling reveals potential therapeutic targets in malignant pleural mesothelioma. Genome Medicine, 2022, 14, .	8.2	24
80	Malignant cells from pleural fluids in malignant mesothelioma patients reveal novel mutations. Lung Cancer, 2018, 119, 64-70.	2.0	23
81	Mutation load in melanoma is affected by <scp>MC</scp>1R genotype. Pigment Cell and Melanoma Research, 2017, 30, 255-258.	3.3	19
82	BRAF Mutations in Low-Grade Serous Ovarian Cancer and Response to BRAF Inhibition. JCO Precision Oncology, 2018, 2, 1-14.	3.0	19
83	Complex structural rearrangements are present in high-grade dysplastic Barrettâ€™s oesophagus samples. BMC Medical Genomics, 2019, 12, 31.	1.5	19
84	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. Npj Breast Cancer, 2020, 6, 33.	5.2	19
85	Radiomics Biomarkers Correlate with CD8 Expression and Predict Immune Signatures in Melanoma Patients. Molecular Cancer Research, 2021, 19, 950-956.	3.4	19
86	Multimarker analysis and imputation of multiple platform pooling-based genome-wide association studies. Bioinformatics, 2008, 24, 1896-1902.	4.1	18
87	Electrophysiological correlates of fluid transport in cultured porcine thyroid cells. Journal of Endocrinology, 1988, 119, 309-314.	2.6	17
88	Patient-derived xenograft models capture genomic heterogeneity in endometrial cancer. Genome Medicine, 2022, 14, 3.	8.2	16
89	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
90	Pathogenic germline variants are associated with poor survival in stage III/IV melanoma patients. Scientific Reports, 2020, 10, 17687.	3.3	14

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91	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
92	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
93	Microarray-Based Genome-Wide Association Studies Using Pooled DNA. Methods in Molecular Biology, 2011, 700, 49-60.	0.9	12
94	X-MATE: a flexible system for mapping short read data. Bioinformatics, 2011, 27, 580-581.	4.1	11
95	The Value of Molecular Haplotypes in a Family-Based Linkage Study. American Journal of Human Genetics, 2006, 79, 458-468.	6.2	10
96	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
97	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
98	Ask the people: developing guidelines for genomic research with Aboriginal and Torres Strait Islander peoples. BMJ Global Health, 2021, 6, e007259.	4.7	8
99	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
100	Tumor Signature Analysis Implicates Hereditary Cancer Genes in Endometrial Cancer Development. Cancers, 2021, 13, 1762.	3.7	5
101	qmotif: determination of telomere content from whole-genome sequence data. Bioinformatics Advances, 2022, 2, .	2.4	5
102	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
103	ROR1 and ROR2 expression in pancreatic cancer. BMC Cancer, 2021, 21, 1199.	2.6	4
104	A SMART on FHIR Prototype for Genomic Test Ordering. Studies in Health Technology and Informatics, 2019, 266, 121-126.	0.3	4
105	Running Genomic Analyses in the Cloud. Studies in Health Technology and Informatics, 2019, 266, 149-155.	0.3	1
106	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
107	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	1.8	0