

Peter J Park

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

151 papers	18,708 citations	59 h-index	136 g-index
165 ext. papers	24,401 ext. citations	20.3 avg, IF	6.69 L-index

#	Paper	IF	Citations
151	Pairs and Pairix: a file format and a tool for efficient storage and retrieval for Hi-C read pairs.. <i>Bioinformatics</i> , 2022 ,	7.2	2
150	Single-cell gene fusion detection by scFusion.. <i>Nature Communications</i> , 2022 , 13, 1084	17.4	1
149	Somatic mosaicism reveals clonal distributions of neocortical development.. <i>Nature</i> , 2022 ,	50.4	1
148	The 4D Nucleome Data Portal as a resource for searching and visualizing curated nucleomics data.. <i>Nature Communications</i> , 2022 , 13, 2365	17.4	3
147	Whole-genome analysis reveals the contribution of non-coding de novo transposon insertions to autism spectrum disorder. <i>Mobile DNA</i> , 2021 , 12, 28	4.4	2
146	Micro-Meta App: an interactive tool for collecting microscopy metadata based on community specifications. <i>Nature Methods</i> , 2021 , 18, 1489-1495	21.6	4
145	Landmarks of human embryonic development inscribed in somatic mutations. <i>Science</i> , 2021 , 371, 1249-1253	35.3	13
144	Comprehensive identification of somatic nucleotide variants in human brain tissue. <i>Genome Biology</i> , 2021 , 22, 92	18.3	3
143	The origins and genetic interactions of KRAS mutations are allele- and tissue-specific. <i>Nature Communications</i> , 2021 , 12, 1808	17.4	14
142	Negative elongation factor regulates muscle progenitor expansion for efficient myofiber repair and stem cell pool repopulation. <i>Developmental Cell</i> , 2021 , 56, 1014-1029.e7	10.2	5
141	Resources and challenges for integrative analysis of nuclear architecture data. <i>Current Opinion in Genetics and Development</i> , 2021 , 67, 103-110	4.9	1
140	Essential histone chaperones collaborate to regulate transcription and chromatin integrity. <i>Genes and Development</i> , 2021 , 35, 698-712	12.6	7
139	Comprehensive identification of transposable element insertions using multiple sequencing technologies. <i>Nature Communications</i> , 2021 , 12, 3836	17.4	7
138	Somatic mutation accumulation seen through a single-molecule lens. <i>Cell Research</i> , 2021 , 31, 949-950	24.7	
137	HiTea: a computational pipeline to identify non-reference transposable element insertions in Hi-C data. <i>Bioinformatics</i> , 2021 , 37, 1045-1051	7.2	2
136	Heterogeneity and Clonal Evolution of Acquired PARP Inhibitor Resistance in and -Deficient Cells. <i>Cancer Research</i> , 2021 , 81, 2774-2787	10.1	3
135	Large mosaic copy number variations confer autism risk. <i>Nature Neuroscience</i> , 2021 , 24, 197-203	25.5	10

134	Deletions in CWH43 cause idiopathic normal pressure hydrocephalus. <i>EMBO Molecular Medicine</i> , 2021 , 13, e13249	12	8
133	The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing. <i>Nature Neuroscience</i> , 2021 , 24, 176-185	25.5	19
132	Computational analysis of cancer genome sequencing data. <i>Nature Reviews Genetics</i> , 2021 ,	30.1	2
131	Parallel RNA and DNA analysis after deep sequencing (PRDD-seq) reveals cell type-specific lineage patterns in human brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 13886-13895	11.5	13
130	Immunogenomic profiling determines responses to combined PARP and PD-1 inhibition in ovarian cancer. <i>Nature Communications</i> , 2020 , 11, 1459	17.4	82
129	HiNT: a computational method for detecting copy number variations and translocations from Hi-C data. <i>Genome Biology</i> , 2020 , 21, 73	18.3	27
128	Dysregulation of cancer genes by recurrent intergenic fusions. <i>Genome Biology</i> , 2020 , 21, 166	18.3	8
127	A user guide for the online exploration and visualization of PCAWG data. <i>Nature Communications</i> , 2020 , 11, 3400	17.4	7
126	GiniQC: a measure for quantifying noise in single-cell Hi-C data. <i>Bioinformatics</i> , 2020 , 36, 2902-2904	7.2	2
125	Genomic footprints of activated telomere maintenance mechanisms in cancer. <i>Nature Communications</i> , 2020 , 11, 733	17.4	40
124	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020 , 52, 306-319	36.3	122
123	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020 , 52, 331-341	36.3	168
122	Accurate detection of mosaic variants in sequencing data without matched controls. <i>Nature Biotechnology</i> , 2020 , 38, 314-319	44.5	20
121	Genomic Determinants of De Novo Resistance to Immune Checkpoint Blockade in Mismatch Repair-Deficient Endometrial Cancer. <i>JCO Precision Oncology</i> , 2020 , 4, 492-497	3.6	2
120	Identification and Genotyping of Transposable Element Insertions From Genome Sequencing Data. <i>Current Protocols in Human Genetics</i> , 2020 , 107, e102	3.2	4
119	Epigenetic transcriptional reprogramming by WT1 mediates a repair response during podocyte injury. <i>Science Advances</i> , 2020 , 6, eabb5460	14.3	4
118	The conserved elongation factor Spn1 is required for normal transcription, histone modifications, and splicing in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2020 , 48, 10241-10258	20.1	6
117	Systematic Assessment of Tumor Purity and Its Clinical Implications. <i>JCO Precision Oncology</i> , 2020 , 4,	3.6	7

116	Mechanisms and therapeutic implications of hypermutation in gliomas. <i>Nature</i> , 2020 , 580, 517-523	50.4	172
115	Genomics of MPNST (GeM) Consortium: Rationale and Study Design for Multi-Omic Characterization of NF1-Associated and Sporadic MPNSTs. <i>Genes</i> , 2020 , 11,	4.2	6
114	Small-Molecule and CRISPR Screening Converge to Reveal Receptor Tyrosine Kinase Dependencies in Pediatric Rhabdoid Tumors. <i>Cell Reports</i> , 2019 , 28, 2331-2344.e8	10.6	20
113	Identification of somatic mutations in single cell DNA-seq using a spatial model of allelic imbalance. <i>Nature Communications</i> , 2019 , 10, 3908	17.4	40
112	MicroRNA-29a activates a multi-component growth and invasion program in glioblastoma. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019 , 38, 36	12.8	12
111	A dynamic and integrated epigenetic program at distal regions orchestrates transcriptional responses to VEGFA. <i>Genome Research</i> , 2019 , 29, 193-207	9.7	5
110	Tracing Oncogene Rearrangements in the Mutational History of Lung Adenocarcinoma. <i>Cell</i> , 2019 , 177, 1842-1857.e21	56.2	84
109	Tibanna: software for scalable execution of portable pipelines on the cloud. <i>Bioinformatics</i> , 2019 , 35, 4424-4426	7.2	6
108	BRD9 defines a SWI/SNF sub-complex and constitutes a specific vulnerability in malignant rhabdoid tumors. <i>Nature Communications</i> , 2019 , 10, 1881	17.4	51
107	Linked-read analysis identifies mutations in single-cell DNA-sequencing data. <i>Nature Genetics</i> , 2019 , 51, 749-754	36.3	42
106	Detecting the mutational signature of homologous recombination deficiency in clinical samples. <i>Nature Genetics</i> , 2019 , 51, 912-919	36.3	96
105	MDM2 and MDM4 Are Therapeutic Vulnerabilities in Malignant Rhabdoid Tumors. <i>Cancer Research</i> , 2019 , 79, 2404-2414	10.1	24
104	An enhanced genetic model of colorectal cancer progression history. <i>Genome Biology</i> , 2019 , 20, 168	18.3	21
103	Global impact of somatic structural variation on the DNA methylome of human cancers. <i>Genome Biology</i> , 2019 , 20, 209	18.3	9
102	Patient-Customized Oligonucleotide Therapy for a Rare Genetic Disease. <i>New England Journal of Medicine</i> , 2019 , 381, 1644-1652	59.2	232
101	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
100	PaSD-qc: quality control for single cell whole-genome sequencing data using power spectral density estimation. <i>Nucleic Acids Research</i> , 2018 , 46, e20	20.1	11
99	Detecting Somatic Mutations in Normal Cells. <i>Trends in Genetics</i> , 2018 , 34, 545-557	8.5	53

98	A Pan-Cancer Compendium of Genes Deregulated by Somatic Genomic Rearrangement across More Than 1,400 Cases. <i>Cell Reports</i> , 2018 , 24, 515-527	10.6	49
97	The BabySeq project: implementing genomic sequencing in newborns. <i>BMC Pediatrics</i> , 2018 , 18, 225	2.6	55
96	HiGlass: web-based visual exploration and analysis of genome interaction maps. <i>Genome Biology</i> , 2018 , 19, 125	18.3	242
95	Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data. <i>Genome Research</i> , 2018 , 28, 1217-1227	9.7	90
94	Aging and neurodegeneration are associated with increased mutations in single human neurons. <i>Science</i> , 2018 , 359, 555-559	33.3	315
93	EED, a member of the polycomb group, is required for nephron differentiation and the maintenance of nephron progenitor cells. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	10
92	The SWI/SNF chromatin remodelling complex is required for maintenance of lineage specific enhancers. <i>Nature Communications</i> , 2017 , 8, 14648	17.4	148
91	Engineering and Functional Characterization of Fusion Genes Identifies Novel Oncogenic Drivers of Cancer. <i>Cancer Research</i> , 2017 , 77, 3502-3512	10.1	22
90	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. <i>Science</i> , 2017 , 356,	33.3	152
89	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. <i>Cancer Cell</i> , 2017 , 31, 820-832.e3	24.3	286
88	A molecular portrait of microsatellite instability across multiple cancers. <i>Nature Communications</i> , 2017 , 8, 15180	17.4	288
87	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2017 , 20, 706-719.e7	18	43
86	Spt5 Plays Vital Roles in the Control of Sense and Antisense Transcription Elongation. <i>Molecular Cell</i> , 2017 , 66, 77-88.e5	17.6	63
85	ARID1A loss impairs enhancer-mediated gene regulation and drives colon cancer in mice. <i>Nature Genetics</i> , 2017 , 49, 296-302	36.3	178
84	SMARCB1-mediated SWI/SNF complex function is essential for enhancer regulation. <i>Nature Genetics</i> , 2017 , 49, 289-295	36.3	172
83	Bivalent complexes of PRC1 with orthologs of BRD4 and MOZ/MORF target developmental genes in. <i>Genes and Development</i> , 2017 , 31, 1988-2002	12.6	14
82	NGSCheckMate: software for validating sample identity in next-generation sequencing studies within and across data types. <i>Nucleic Acids Research</i> , 2017 , 45, e103	20.1	43
81	Clonal History and Genetic Predictors of Transformation Into Small-Cell Carcinomas From Lung Adenocarcinomas. <i>Journal of Clinical Oncology</i> , 2017 , 35, 3065-3074	2.2	229

80	The 4D nucleome project. <i>Nature</i> , 2017 , 549, 219-226	50.4	332
79	VEGF amplifies transcription through ETS1 acetylation to enable angiogenesis. <i>Nature Communications</i> , 2017 , 8, 383	17.4	48
78	Clinical Application of Targeted Deep Sequencing in Solid-Cancer Patients and Utility for Biomarker-Selected Clinical Trials. <i>Oncologist</i> , 2017 , 22, 1169-1177	5.7	10
77	Prevalence and detection of low-allele-fraction variants in clinical cancer samples. <i>Nature Communications</i> , 2017 , 8, 1377	17.4	92
76	, the homologue of SET3, Is Required for Viability and the Proper Balance of Active and Repressive Chromatin Marks. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 625-635	3.2	8
75	Evaluation of somatic copy number estimation tools for whole-exome sequencing data. <i>Briefings in Bioinformatics</i> , 2016 , 17, 185-92	13.4	35
74	Copy number analysis of whole-genome data using BIC-seq2 and its application to detection of cancer susceptibility variants. <i>Nucleic Acids Research</i> , 2016 , 44, 6274-86	20.1	82
73	Next-generation sequencing-based detection of germline L1-mediated transductions. <i>BMC Genomics</i> , 2016 , 17, 342	4.5	7
72	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. <i>Cell Reports</i> , 2016 , 14, 2476-89	10.6	228
71	Intravenous leiomyomatosis: an unusual intermediate between benign and malignant uterine smooth muscle tumors. <i>Modern Pathology</i> , 2016 , 29, 500-10	9.8	42
70	Mechanisms and Consequences of Cancer Genome Instability: Lessons from Genome Sequencing Studies. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2016 , 11, 283-312	34	72
69	The Impact of Environmental and Endogenous Damage on Somatic Mutation Load in Human Skin Fibroblasts. <i>PLoS Genetics</i> , 2016 , 12, e1006385	6	55
68	Resolving rates of mutation in the brain using single-neuron genomics. <i>ELife</i> , 2016 , 5,	8.9	109
67	Comprehensive analysis of promoter-proximal RNA polymerase II pausing across mammalian cell types. <i>Genome Biology</i> , 2016 , 17, 120	18.3	35
66	MNase titration reveals differences between nucleosome occupancy and chromatin accessibility. <i>Nature Communications</i> , 2016 , 7, 11485	17.4	132
65	Analyzing Somatic Genome Rearrangements in Human Cancers by Using Whole-Exome Sequencing. <i>American Journal of Human Genetics</i> , 2016 , 98, 843-856	11	27
64	Sex comb on midleg (Scm) is a functional link between PcG-repressive complexes in Drosophila. <i>Genes and Development</i> , 2015 , 29, 1136-50	12.6	47
63	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828

62	Identification of rare germline copy number variations over-represented in five human cancer types. <i>Molecular Cancer</i> , 2015 , 14, 25	42.1	26
61	Somatic mutation in single human neurons tracks developmental and transcriptional history. <i>Science</i> , 2015 , 350, 94-98	33.3	364
60	Intron retention is a widespread mechanism of tumor-suppressor inactivation. <i>Nature Genetics</i> , 2015 , 47, 1242-8	36.3	217
59	Failure to replicate the STAP cell phenomenon. <i>Nature</i> , 2015 , 525, E6-9	50.4	34
58	Hallmarks of pluripotency. <i>Nature</i> , 2015 , 525, 469-78	50.4	253
57	Pericentromeric satellite repeat expansions through RNA-derived DNA intermediates in cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 15148-53	11.5	91
56	A comparison of genetically matched cell lines reveals the equivalence of human iPSCs and ESCs. <i>Nature Biotechnology</i> , 2015 , 33, 1173-81	44.5	192
55	Spatiotemporal Evolution of the Primary Glioblastoma Genome. <i>Cancer Cell</i> , 2015 , 28, 318-28	24.3	180
54	EMSAR: estimation of transcript abundance from RNA-seq data by mappability-based segmentation and reclustering. <i>BMC Bioinformatics</i> , 2015 , 16, 278	3.6	11
53	The histone chaperone CAF-1 safeguards somatic cell identity. <i>Nature</i> , 2015 , 528, 218-24	50.4	183
52	Correspondence of Drosophila polycomb group proteins with broad H3K27me3 silent domains. <i>Fly</i> , 2015 , 9, 178-82	1.3	1
51	Genome-Wide Analysis of WilmsTumor 1-Controlled Gene Expression in Podocytes Reveals Key Regulatory Mechanisms. <i>Journal of the American Society of Nephrology: JASN</i> , 2015 , 26, 2097-104	12.7	72
50	Htt CAG repeat expansion confers pleiotropic gains of mutant huntingtin function in chromatin regulation. <i>Human Molecular Genetics</i> , 2015 , 24, 2442-57	5.6	38
49	Cell lineage analysis in human brain using endogenous retroelements. <i>Neuron</i> , 2015 , 85, 49-59	13.9	183
48	Transcriptional control of a whole chromosome: emerging models for dosage compensation. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 118-25	17.6	42
47	A genome-wide view of microsatellite instability: old stories of cancer mutations revisited with new sequencing technologies. <i>Cancer Research</i> , 2014 , 74, 6377-82	10.1	15
46	Characterization of HPV and host genome interactions in primary head and neck cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 15544-9	11.5	229
45	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014 , 512, 445-8	50.4	207

44	Guided visual exploration of genomic stratifications in cancer. <i>Nature Methods</i> , 2014 , 11, 884-885	21.6	17
43	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , 2014 , 512, 449-52	50.4	265
42	The somatic genomic landscape of chromophobe renal cell carcinoma. <i>Cancer Cell</i> , 2014 , 26, 319-330	24.3	521
41	Nucleosomal occupancy changes locally over key regulatory regions during cell differentiation and reprogramming. <i>Nature Communications</i> , 2014 , 5, 4719	17.4	67
40	p53 prevents neurodegeneration by regulating synaptic genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 18055-60	11.5	47
39	Impact of sequencing depth in ChIP-seq experiments. <i>Nucleic Acids Research</i> , 2014 , 42, e74	20.1	49
38	Cumulative haploinsufficiency and triplosensitivity drive aneuploidy patterns and shape the cancer genome. <i>Cell</i> , 2013 , 155, 948-62	56.2	478
37	The landscape of microsatellite instability in colorectal and endometrial cancer genomes. <i>Cell</i> , 2013 , 155, 858-68	56.2	247
36	Nozzle: a report generation toolkit for data analysis pipelines. <i>Bioinformatics</i> , 2013 , 29, 1089-91	7.2	15
35	Functional genomic analysis of chromosomal aberrations in a compendium of 8000 cancer genomes. <i>Genome Research</i> , 2013 , 23, 217-27	9.7	111
34	Diverse mechanisms of somatic structural variations in human cancer genomes. <i>Cell</i> , 2013 , 153, 919-29	56.2	238
33	A dynamic H3K27ac signature identifies VEGFA-stimulated endothelial enhancers and requires EP300 activity. <i>Genome Research</i> , 2013 , 23, 917-27	9.7	64
32	Swi/Snf chromatin remodeling/tumor suppressor complex establishes nucleosome occupancy at target promoters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 10165-70	11.5	127
31	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012 , 22, 1813-31	9.7	1211
30	Response to Brosch et al. <i>Cell Metabolism</i> , 2012 , 15, 267-269	24.6	4
29	Single-neuron sequencing analysis of L1 retrotransposition and somatic mutation in the human brain. <i>Cell</i> , 2012 , 151, 483-96	56.2	404
28	A survey of copy-number variation detection tools based on high-throughput sequencing data. <i>Current Protocols in Human Genetics</i> , 2012 , Chapter 7, Unit 7.19	3.2	18
27	Genome-Wide Mapping of Protein-DNA Interactions by ChIP-Seq 2012 , 139-151		1

26	Ascorbic acid prevents loss of Dlk1-Dio3 imprinting and facilitates generation of all-iPS cell mice from terminally differentiated B cells. <i>Nature Genetics</i> , 2012 , 44, 398-405, S1-2	36.3	216
25	Landscape of somatic retrotransposition in human cancers. <i>Science</i> , 2012 , 337, 967-71	33.3	507
24	Comprehensive analysis of the chromatin landscape in <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011 , 471, 480-5	50.4	641
23	Copy number variation detection in whole-genome sequencing data using the Bayesian information criterion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E1128-36	11.5	163
22	A region of the human HOXD cluster that confers polycomb-group responsiveness. <i>Cell</i> , 2010 , 140, 99-110	10.2	250
21	Dosage compensation in drosophila: Sequence-specific initiation and sequence-independent spreading of MSL complex to the active genes on the male X chromosome. <i>Russian Journal of Genetics</i> , 2010 , 46, 1263-1266	0.6	
20	Analysis of primary structure of chromatin with next-generation sequencing. <i>Epigenomics</i> , 2010 , 2, 187-197	1.4	10
19	Comparative analysis of H2A.Z nucleosome organization in the human and yeast genomes. <i>Genome Research</i> , 2009 , 19, 967-77	9.7	77
18	Integration of heterogeneous expression data sets extends the role of the retinol pathway in diabetes and insulin resistance. <i>Bioinformatics</i> , 2009 , 25, 3121-7	7.2	17
17	ChIP-seq: advantages and challenges of a maturing technology. <i>Nature Reviews Genetics</i> , 2009 , 10, 669-89	30.1	1331
16	Design and analysis of ChIP-seq experiments for DNA-binding proteins. <i>Nature Biotechnology</i> , 2008 , 26, 1351-9	44.5	662
15	Epigenetics meets next-generation sequencing. <i>Epigenetics</i> , 2008 , 3, 318-21	5.7	34
14	Normalization and experimental design for ChIP-chip data. <i>BMC Bioinformatics</i> , 2007 , 8, 219	3.6	41
13	Comparative analysis of algorithms for identifying amplifications and deletions in array CGH data. <i>Bioinformatics</i> , 2005 , 21, 3763-70	7.2	310
12	The 4D Nucleome Data Portal: a resource for searching and visualizing curated nucleomics data		3
11	HiGlass: Web-based Visual Exploration and Analysis of Genome Interaction Maps		11
10	PaSD-qc: Quality control for single cell whole-genome sequencing data using power spectral density estimation		2
9	The Landscape of Mutational Mosaicism in Autistic and Normal Human Cerebral Cortex		5

8	Linked-read analysis identifies mutations in single cell DNA sequencing data	5
7	Aging and neurodegeneration are associated with increased mutations in single human neurons	3
6	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing	12
5	HiNT: a computational method for detecting copy number variations and translocations from Hi-C data	2
4	Micro-Meta App: an interactive software tool to facilitate the collection of microscopy metadata based on community-driven specifications	6
3	Ultraspecific somatic SNV and indel detection in single neurons using primary template-directed amplification	2
2	Pairs and Pairix: a file format and a tool for efficient storage and retrieval for Hi-C read pairs	2
1	Whole-genome analysis of de novo and polymorphic retrotransposon insertions in Autism Spectrum Disorder	1