Peter J Park

List of Publications by Citations

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	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *New England Journal of Medicine*, **2015**, 372, 2481-98	59.2	1828
150	ChIP-seq: advantages and challenges of a maturing technology. *Nature Reviews Genetics*, **2009**, 10, 669-80	30.1	1331
149	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. *Genome Research*, **2012**, 22, 1813-31	9.7	1211
148	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
147	Design and analysis of ChIP-seq experiments for DNA-binding proteins. *Nature Biotechnology*, **2008**, 26, 1351-9	44.5	662
146	Comprehensive analysis of the chromatin landscape in Drosophila melanogaster. *Nature*, **2011**, 471, 480-5	50.4	641
145	The somatic genomic landscape of chromophobe renal cell carcinoma. *Cancer Cell*, **2014**, 26, 319-330	24.3	521
144	Landscape of somatic retrotransposition in human cancers. *Science*, **2012**, 337, 967-71	33.3	507
143	Cumulative haploinsufficiency and triplosensitivity drive aneuploidy patterns and shape the cancer genome. *Cell*, **2013**, 155, 948-62	56.2	478
142	Single-neuron sequencing analysis of L1 retrotransposition and somatic mutation in the human brain. *Cell*, **2012**, 151, 483-96	56.2	404
141	Somatic mutation in single human neurons tracks developmental and transcriptional history. *Science*, **2015**, 350, 94-98	33.3	364
140	The 4D nucleome project. *Nature*, **2017**, 549, 219-226	50.4	332
139	Aging and neurodegeneration are associated with increased mutations in single human neurons. *Science*, **2018**, 359, 555-559	33.3	315
138	Comparative analysis of algorithms for identifying amplifications and deletions in array CGH data. *Bioinformatics*, **2005**, 21, 3763-70	7.2	310
137	A molecular portrait of microsatellite instability across multiple cancers. *Nature Communications*, **2017**, 8, 15180	17.4	288
136	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. *Cancer Cell*, **2017**, 31, 820-832.e3	24.3	286
135	Comparative analysis of metazoan chromatin organization. *Nature*, **2014**, 512, 449-52	50.4	265

134	Hallmarks of pluripotency. *Nature*, **2015**, 525, 469-78	50.4	253
133	A region of the human HOXD cluster that confers polycomb-group responsiveness. *Cell*, **2010**, 140, 99-110	36.2	250
132	The landscape of microsatellite instability in colorectal and endometrial cancer genomes. *Cell*, **2013**, 155, 858-68	56.2	247
131	HiGlass: web-based visual exploration and analysis of genome interaction maps. *Genome Biology*, **2018**, 19, 125	18.3	242
130	Diverse mechanisms of somatic structural variations in human cancer genomes. *Cell*, **2013**, 153, 919-29	56.2	238
129	Patient-Customized Oligonucleotide Therapy for a Rare Genetic Disease. *New England Journal of Medicine*, **2019**, 381, 1644-1652	59.2	232
128	Clonal History and Genetic Predictors of Transformation Into Small-Cell Carcinomas From Lung Adenocarcinomas. *Journal of Clinical Oncology*, **2017**, 35, 3065-3074	2.2	229
127	Characterization of HPV and host genome interactions in primary head and neck cancers. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 15544-9	11.5	229
126	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. *Cell Reports*, **2016**, 14, 2476-89	10.6	228
125	Intron retention is a widespread mechanism of tumor-suppressor inactivation. *Nature Genetics*, **2015**, 47, 1242-8	36.3	217
124	Ascorbic acid prevents loss of Dlk1-Dio3 imprinting and facilitates generation of all-iPS cell mice from terminally differentiated B cells. *Nature Genetics*, **2012**, 44, 398-405, S1-2	36.3	216
123	Comparative analysis of the transcriptome across distant species. *Nature*, **2014**, 512, 445-8	50.4	207
122	A comparison of genetically matched cell lines reveals the equivalence of human iPSCs and ESCs. *Nature Biotechnology*, **2015**, 33, 1173-81	44.5	192
121	The histone chaperone CAF-1 safeguards somatic cell identity. *Nature*, **2015**, 528, 218-24	50.4	183
120	Cell lineage analysis in human brain using endogenous retroelements. *Neuron*, **2015**, 85, 49-59	13.9	183
119	Spatiotemporal Evolution of the Primary Glioblastoma Genome. *Cancer Cell*, **2015**, 28, 318-28	24.3	180
118	ARID1A loss impairs enhancer-mediated gene regulation and drives colon cancer in mice. *Nature Genetics*, **2017**, 49, 296-302	36.3	178
117	SMARCB1-mediated SWI/SNF complex function is essential for enhancer regulation. *Nature Genetics*, **2017**, 49, 289-295	36.3	172

116	Mechanisms and therapeutic implications of hypermutation in gliomas. *Nature*, **2020**, 580, 517-523	50.4	172
115	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. *Nature Genetics*, **2020**, 52, 331-341	36.3	168
114	Copy number variation detection in whole-genome sequencing data using the Bayesian information criterion. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, E1128-36	11.5	163
113	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. *Science*, **2017**, 356,	33.3	152
112	The SWI/SNF chromatin remodelling complex is required for maintenance of lineage specific enhancers. *Nature Communications*, **2017**, 8, 14648	17.4	148
111	MNase titration reveals differences between nucleosome occupancy and chromatin accessibility. *Nature Communications*, **2016**, 7, 11485	17.4	132
110	Swi/Snf chromatin remodeling/tumor suppressor complex establishes nucleosome occupancy at target promoters. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 10165-70	11.5	127
109	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
108	Functional genomic analysis of chromosomal aberrations in a compendium of 8000 cancer genomes. *Genome Research*, **2013**, 23, 217-27	9.7	111
107	Resolving rates of mutation in the brain using single-neuron genomics. *ELife*, **2016**, 5,	8.9	109
106	Detecting the mutational signature of homologous recombination deficiency in clinical samples. *Nature Genetics*, **2019**, 51, 912-919	36.3	96
105	Prevalence and detection of low-allele-fraction variants in clinical cancer samples. *Nature Communications*, **2017**, 8, 1377	17.4	92
104	Pericentromeric satellite repeat expansions through RNA-derived DNA intermediates in cancer. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 15148-53	11.5	91
103	Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data. *Genome Research*, **2018**, 28, 1217-1227	9.7	90
102	Tracing Oncogene Rearrangements in the Mutational History of Lung Adenocarcinoma. *Cell*, **2019**, 177, 1842-1857.e21	56.2	84
101	Immunogenomic profiling determines responses to combined PARP and PD-1 inhibition in ovarian cancer. *Nature Communications*, **2020**, 11, 1459	17.4	82
100	Copy number analysis of whole-genome data using BIC-seq2 and its application to detection of cancer susceptibility variants. *Nucleic Acids Research*, **2016**, 44, 6274-86	20.1	82
99	Comparative analysis of H2A.Z nucleosome organization in the human and yeast genomes. *Genome Research*, **2009**, 19, 967-77	9.7	77

98	Mechanisms and Consequences of Cancer Genome Instability: Lessons from Genome Sequencing Studies. *Annual Review of Pathology: Mechanisms of Disease*, **2016**, 11, 283-312	34	72
97	Genome-Wide Analysis of WilmsUTumor 1-Controlled Gene Expression in Podocytes Reveals Key Regulatory Mechanisms. *Journal of the American Society of Nephrology: JASN*, **2015**, 26, 2097-104	12.7	72
96	Nucleosomal occupancy changes locally over key regulatory regions during cell differentiation and reprogramming. *Nature Communications*, **2014**, 5, 4719	17.4	67
95	A dynamic H3K27ac signature identifies VEGFA-stimulated endothelial enhancers and requires EP300 activity. *Genome Research*, **2013**, 23, 917-27	9.7	64
94	Spt5 Plays Vital Roles in the Control of Sense and Antisense Transcription Elongation. *Molecular Cell*, **2017**, 66, 77-88.e5	17.6	63
93	The BabySeq project: implementing genomic sequencing in newborns. *BMC Pediatrics*, **2018**, 18, 225	2.6	55
92	The Impact of Environmental and Endogenous Damage on Somatic Mutation Load in Human Skin Fibroblasts. *PLoS Genetics*, **2016**, 12, e1006385	6	55
91	Detecting Somatic Mutations in Normal Cells. *Trends in Genetics*, **2018**, 34, 545-557	8.5	53
90	BRD9 defines a SWI/SNF sub-complex and constitutes a specific vulnerability in malignant rhabdoid tumors. *Nature Communications*, **2019**, 10, 1881	17.4	51
89	A Pan-Cancer Compendium of Genes Deregulated by Somatic Genomic Rearrangement across More Than 1,400 Cases. *Cell Reports*, **2018**, 24, 515-527	10.6	49
88	Impact of sequencing depth in ChIP-seq experiments. *Nucleic Acids Research*, **2014**, 42, e74	20.1	49
87	VEGF amplifies transcription through ETS1 acetylation to enable angiogenesis. *Nature Communications*, **2017**, 8, 383	17.4	48
86	Sex comb on midleg (Scm) is a functional link between PcG-repressive complexes in Drosophila. *Genes and Development*, **2015**, 29, 1136-50	12.6	47
85	p53 prevents neurodegeneration by regulating synaptic genes. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 18055-60	11.5	47
84	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. *Cell Stem Cell*, **2017**, 20, 706-719.e7	18	43
83	NGSCheckMate: software for validating sample identity in next-generation sequencing studies within and across data types. *Nucleic Acids Research*, **2017**, 45, e103	20.1	43
82	Linked-read analysis identifies mutations in single-cell DNA-sequencing data. *Nature Genetics*, **2019**, 51, 749-754	36.3	42
81	Intravenous leiomyomatosis: an unusual intermediate between benign and malignant uterine smooth muscle tumors. *Modern Pathology*, **2016**, 29, 500-10	9.8	42

80	Transcriptional control of a whole chromosome: emerging models for dosage compensation. *Nature Structural and Molecular Biology*, **2014**, 21, 118-25	17.6	42
79	Normalization and experimental design for ChIP-chip data. *BMC Bioinformatics*, **2007**, 8, 219	3.6	41
78	Identification of somatic mutations in single cell DNA-seq using a spatial model of allelic imbalance. *Nature Communications*, **2019**, 10, 3908	17.4	40
77	Genomic footprints of activated telomere maintenance mechanisms in cancer. *Nature Communications*, **2020**, 11, 733	17.4	40
76	Htt CAG repeat expansion confers pleiotropic gains of mutant huntingtin function in chromatin regulation. *Human Molecular Genetics*, **2015**, 24, 2442-57	5.6	38
75	Evaluation of somatic copy number estimation tools for whole-exome sequencing data. *Briefings in Bioinformatics*, **2016**, 17, 185-92	13.4	35
74	Comprehensive analysis of promoter-proximal RNA polymerase II pausing across mammalian cell types. *Genome Biology*, **2016**, 17, 120	18.3	35
73	Failure to replicate the STAP cell phenomenon. *Nature*, **2015**, 525, E6-9	50.4	34
72	Epigenetics meets next-generation sequencing. *Epigenetics*, **2008**, 3, 318-21	5.7	34
71	HiNT: a computational method for detecting copy number variations and translocations from Hi-C data. *Genome Biology*, **2020**, 21, 73	18.3	27
70	Analyzing Somatic Genome Rearrangements in Human Cancers by Using Whole-Exome Sequencing. *American Journal of Human Genetics*, **2016**, 98, 843-856	11	27
69	Identification of rare germline copy number variations over-represented in five human cancer types. *Molecular Cancer*, **2015**, 14, 25	42.1	26
68	MDM2 and MDM4 Are Therapeutic Vulnerabilities in Malignant Rhabdoid Tumors. *Cancer Research*, **2019**, 79, 2404-2414	10.1	24
67	Engineering and Functional Characterization of Fusion Genes Identifies Novel Oncogenic Drivers of Cancer. *Cancer Research*, **2017**, 77, 3502-3512	10.1	22
66	An enhanced genetic model of colorectal cancer progression history. *Genome Biology*, **2019**, 20, 168	18.3	21
65	Small-Molecule and CRISPR Screening Converge to Reveal Receptor Tyrosine Kinase Dependencies in Pediatric Rhabdoid Tumors. *Cell Reports*, **2019**, 28, 2331-2344.e8	10.6	20
64	Accurate detection of mosaic variants in sequencing data without matched controls. *Nature Biotechnology*, **2020**, 38, 314-319	44.5	20
63	The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing. *Nature Neuroscience*, **2021**, 24, 176-185	25.5	19

62	A survey of copy-number variation detection tools based on high-throughput sequencing data. *Current Protocols in Human Genetics*, **2012**, Chapter 7, Unit7.19	3.2	18
61	Guided visual exploration of genomic stratifications in cancer. *Nature Methods*, **2014**, 11, 884-885	21.6	17
60	Integration of heterogeneous expression data sets extends the role of the retinol pathway in diabetes and insulin resistance. *Bioinformatics*, **2009**, 25, 3121-7	7.2	17
59	A genome-wide view of microsatellite instability: old stories of cancer mutations revisited with new sequencing technologies. *Cancer Research*, **2014**, 74, 6377-82	10.1	15
58	Nozzle: a report generation toolkit for data analysis pipelines. *Bioinformatics*, **2013**, 29, 1089-91	7.2	15
57	Bivalent complexes of PRC1 with orthologs of BRD4 and MOZ/MORF target developmental genes in. *Genes and Development*, **2017**, 31, 1988-2002	12.6	14
56	The origins and genetic interactions of KRAS mutations are allele- and tissue-specific. *Nature Communications*, **2021**, 12, 1808	17.4	14
55	Parallel RNA and DNA analysis after deep sequencing (PRDD-seq) reveals cell type-specific lineage patterns in human brain. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 13886-13895	11.5	13
54	Landmarks of human embryonic development inscribed in somatic mutations. *Science*, **2021**, 371, 1249-1253	3.3	13
53	MicroRNA-29a activates a multi-component growth and invasion program in glioblastoma. *Journal of Experimental and Clinical Cancer Research*, **2019**, 38, 36	12.8	12
52	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing		12
51	PaSD-qc: quality control for single cell whole-genome sequencing data using power spectral density estimation. *Nucleic Acids Research*, **2018**, 46, e20	20.1	11
50	EMSAR: estimation of transcript abundance from RNA-seq data by mappability-based segmentation and reclustering. *BMC Bioinformatics*, **2015**, 16, 278	3.6	11
49	HiGlass: Web-based Visual Exploration and Analysis of Genome Interaction Maps		11
48	Clinical Application of Targeted Deep Sequencing in Solid-Cancer Patients and Utility for Biomarker-Selected Clinical Trials. *Oncologist*, **2017**, 22, 1169-1177	5.7	10
47	Analysis of primary structure of chromatin with next-generation sequencing. *Epigenomics*, **2010**, 2, 187-197	4.4	10
46	Large mosaic copy number variations confer autism risk. *Nature Neuroscience*, **2021**, 24, 197-203	25.5	10
45	EED, a member of the polycomb group, is required for nephron differentiation and the maintenance of nephron progenitor cells. *Development (Cambridge)*, **2018**, 145,	6.6	10

44	Global impact of somatic structural variation on the DNA methylome of human cancers. *Genome Biology*, **2019**, 20, 209	18.3	9
43	Dysregulation of cancer genes by recurrent intergenic fusions. *Genome Biology*, **2020**, 21, 166	18.3	8
42	, the homologue of SET3, Is Required for Viability and the Proper Balance of Active and Repressive Chromatin Marks. *G3: Genes, Genomes, Genetics*, **2017**, 7, 625-635	3.2	8
41	Deletions in CWH43 cause idiopathic normal pressure hydrocephalus. *EMBO Molecular Medicine*, **2021**, 13, e13249	12	8
40	A user guide for the online exploration and visualization of PCAWG data. *Nature Communications*, **2020**, 11, 3400	17.4	7
39	Next-generation sequencing-based detection of germline L1-mediated transductions. *BMC Genomics*, **2016**, 17, 342	4.5	7
38	Systematic Assessment of Tumor Purity and Its Clinical Implications. *JCO Precision Oncology*, **2020**, 4,	3.6	7
37	Essential histone chaperones collaborate to regulate transcription and chromatin integrity. *Genes and Development*, **2021**, 35, 698-712	12.6	7
36	Comprehensive identification of transposable element insertions using multiple sequencing technologies. *Nature Communications*, **2021**, 12, 3836	17.4	7
35	Tibanna: software for scalable execution of portable pipelines on the cloud. *Bioinformatics*, **2019**, 35, 4424-4426	7.2	6
34	The conserved elongation factor Spn1 is required for normal transcription, histone modifications, and splicing in Saccharomyces cerevisiae. *Nucleic Acids Research*, **2020**, 48, 10241-10258	20.1	6
33	Micro-Meta App: an interactive software tool to facilitate the collection of microscopy metadata based on community-driven specifications		6
32	Genomics of MPNST (GeM) Consortium: Rationale and Study Design for Multi-Omic Characterization of NF1-Associated and Sporadic MPNSTs. *Genes*, **2020**, 11,	4.2	6
31	A dynamic and integrated epigenetic program at distal regions orchestrates transcriptional responses to VEGFA. *Genome Research*, **2019**, 29, 193-207	9.7	5
30	The Landscape of Mutational Mosaicism in Autistic and Normal Human Cerebral Cortex		5
29	Linked-read analysis identifies mutations in single cell DNA sequencing data		5
28	Negative elongation factor regulates muscle progenitor expansion for efficient myofiber repair and stem cell pool repopulation. *Developmental Cell*, **2021**, 56, 1014-1029.e7	10.2	5
27	Response to Brosch et al. *Cell Metabolism*, **2012**, 15, 267-269	24.6	4

26	Micro-Meta App: an interactive tool for collecting microscopy metadata based on community specifications. *Nature Methods*, **2021**, 18, 1489-1495	21.6	4
25	Identification and Genotyping of Transposable Element Insertions From Genome Sequencing Data. *Current Protocols in Human Genetics*, **2020**, 107, e102	3.2	4
24	Epigenetic transcriptional reprogramming by WT1 mediates a repair response during podocyte injury. *Science Advances*, **2020**, 6, eabb5460	14.3	4
23	The 4D Nucleome Data Portal: a resource for searching and visualizing curated nucleomics data		3
22	Aging and neurodegeneration are associated with increased mutations in single human neurons		3
21	Comprehensive identification of somatic nucleotide variants in human brain tissue. *Genome Biology*, **2021**, 22, 92	18.3	3
20	Heterogeneity and Clonal Evolution of Acquired PARP Inhibitor Resistance in and -Deficient Cells. *Cancer Research*, **2021**, 81, 2774-2787	10.1	3
19	The 4D Nucleome Data Portal as a resource for searching and visualizing curated nucleomics data.. *Nature Communications*, **2022**, 13, 2365	17.4	3
18	GiniQC: a measure for quantifying noise in single-cell Hi-C data. *Bioinformatics*, **2020**, 36, 2902-2904	7.2	2
17	Whole-genome analysis reveals the contribution of non-coding de novo transposon insertions to autism spectrum disorder. *Mobile DNA*, **2021**, 12, 28	4.4	2
16	Pairs and Pairix: a file format and a tool for efficient storage and retrieval for Hi-C read pairs.. *Bioinformatics*, **2022**,	7.2	2
15	PaSD-qc: Quality control for single cell whole-genome sequencing data using power spectral density estimation		2
14	HiNT: a computational method for detecting copy number variations and translocations from Hi-C data		2
13	Genomic Determinants of De Novo Resistance to Immune Checkpoint Blockade in Mismatch Repair-Deficient Endometrial Cancer. *JCO Precision Oncology*, **2020**, 4, 492-497	3.6	2
12	Ultraspecific somatic SNV and indel detection in single neurons using primary template-directed amplification		2
11	HiTea: a computational pipeline to identify non-reference transposable element insertions in Hi-C data. *Bioinformatics*, **2021**, 37, 1045-1051	7.2	2
10	Pairs and Pairix: a file format and a tool for efficient storage and retrieval for Hi-C read pairs		2
9	Computational analysis of cancer genome sequencing data. *Nature Reviews Genetics*, **2021**,	30.1	2

8	Correspondence of Drosophila polycomb group proteins with broad H3K27me3 silent domains. *Fly*, **2015**, 9, 178-82	1.3	1
7	Genome-Wide Mapping of ProteinDNA Interactions by ChIP-Seq **2012**, 139-151		1
6	Resources and challenges for integrative analysis of nuclear architecture data. *Current Opinion in Genetics and Development*, **2021**, 67, 103-110	4.9	1
5	Whole-genome analysis ofde novoand polymorphic retrotransposon insertions in Autism Spectrum Disorder		1
4	Single-cell gene fusion detection by scFusion.. *Nature Communications*, **2022**, 13, 1084	17.4	1
3	Somatic mosaicism reveals clonal distributions of neocortical development.. *Nature*, **2022**,	50.4	1
2	Dosage compensation in drosophila: Sequence-specific initiation and sequence-independent spreading of MSL complex to the active genes on the male X chromosome. *Russian Journal of Genetics*, **2010**, 46, 1263-1266	0.6	
1	Somatic mutation accumulation seen through a single-molecule lens. *Cell Research*, **2021**, 31, 949-950	24.7	