Peter J Campbell

List of Publications by Year
in descending order

164 papers	79,256 citations	2215 99 h-index	5255 165 g-index
208 all docs	208 docs citations	208 times ranked	75259 citing authors

#	Article	IF	Citations
1	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
2	COSMIC: the Catalogue Of Somatic Mutations In Cancer. Nucleic Acids Research, 2019, 47, D941-D947.	14.5	3,196
3	Genomic Classification and Prognosis in Acute Myeloid Leukemia. New England Journal of Medicine, 2016, 374, 2209-2221.	27.0	3,067
4	The cancer genome. Nature, 2009, 458, 719-724.	27.8	2,904
5	Patterns of somatic mutation in human cancer genomes. Nature, 2007, 446, 153-158.	27.8	2,802
6	COSMIC: exploring the world's knowledge of somatic mutations in human cancer. Nucleic Acids Research, 2015, 43, D805-D811.	14.5	2,096
7	Massive Genomic Rearrangement Acquired in a Single Catastrophic Event during Cancer Development. Cell, 2011, 144, 27-40.	28.9	2,020
8	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	27.8	1,760
9	COSMIC: somatic cancer genetics at high-resolution. Nucleic Acids Research, 2017, 45, D777-D783.	14.5	1,692
10	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	28.9	1,673
11	Clinical and biological implications of driver mutations in myelodysplastic syndromes. Blood, 2013, 122, 3616-3627.	1.4	1,562
12	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
13	The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.	27.8	1,535
14	A comprehensive catalogue of somatic mutations from a human cancer genome. Nature, 2010, 463, 191-196.	27.8	1,519
15	High burden and pervasive positive selection of somatic mutations in normal human skin. Science, 2015, 348, 880-886.	12.6	1,431
16	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. Nature, 2011, 475, 101-105.	27.8	1,364
17	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	28.9	1,249
18	The patterns and dynamics of genomic instability in metastatic pancreatic cancer. Nature, 2010, 467, 1109-1113.	27.8	1,200

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19	The evolutionary history of lethal metastatic prostate cancer. Nature, 2015, 520, 353-357.	27.8	1,185
20	Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. Nature, 2011, 469, 539-542.	27.8	1,127
21	Deciphering Signatures of Mutational Processes Operative in Human Cancer. Cell Reports, 2013, 3, 246-259.	6.4	1,087
22	Universal Patterns of Selection in Cancer and Somatic Tissues. Cell, 2017, 171, 1029-1041.e21.	28.9	1,085
23	Systematic sequencing of renal carcinoma reveals inactivation of histone modifying genes. Nature, 2010, 463, 360-363.	27.8	1,062
24	Somatic mutation in cancer and normal cells. Science, 2015, 349, 1483-1489.	12.6	996
25	A small-cell lung cancer genome with complex signatures of tobacco exposure. Nature, 2010, 463, 184-190.	27.8	972
26	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. Science, 2014, 346, 251-256.	12.6	962
27	Mutational signatures associated with tobacco smoking in human cancer. Science, 2016, 354, 618-622.	12.6	842
28	Clock-like mutational processes in human somatic cells. Nature Genetics, 2015, 47, 1402-1407.	21.4	837
29	Somatic mutant clones colonize the human esophagus with age. Science, 2018, 362, 911-917.	12.6	805
30	Complex landscapes of somatic rearrangement in human breast cancer genomes. Nature, 2009, 462, 1005-1010.	27.8	776
31	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. Nature Medicine, 2017, 23, 517-525.	30.7	769
32	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. Nature Communications, 2014, 5, 2997.	12.8	741
33	Identification of somatically acquired rearrangements in cancer using genome-wide massively parallel paired-end sequencing. Nature Genetics, 2008, 40, 722-729.	21.4	736
34	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. Nature Medicine, 2015, 21, 751-759.	30.7	711
35	The Myeloproliferative Disorders. New England Journal of Medicine, 2006, 355, 2452-2466.	27.0	619
36	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	27.8	617

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37	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	27.8	560
38	Chromothripsis and Kataegis Induced by Telomere Crisis. Cell, 2015, 163, 1641-1654.	28.9	541
39	Genomic Evolution of Breast Cancer Metastasis and Relapse. Cancer Cell, 2017, 32, 169-184.e7.	16.8	534
40	Evolution of the cancer genome. Nature Reviews Genetics, 2012, 13, 795-806.	16.3	532
41	Deterministic Evolutionary Trajectories Influence Primary Tumor Growth: TRACERx Renal. Cell, 2018, 173, 595-610.e11.	28.9	472
42	The landscape of somatic mutation in normal colorectal epithelial cells. Nature, 2019, 574, 532-537.	27.8	468
43	Effect of Mutation Order on Myeloproliferative Neoplasms. New England Journal of Medicine, 2015, 372, 601-612.	27.0	467
44	Criteria for Inference of Chromothripsis in Cancer Genomes. Cell, 2013, 152, 1226-1236.	28.9	457
45	Classification and Personalized Prognosis in Myeloproliferative Neoplasms. New England Journal of Medicine, 2018, 379, 1416-1430.	27.0	442
46	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	21.4	431
47	Population dynamics of normal human blood inferred from somatic mutations. Nature, 2018, 561, 473-478.	27.8	427
48	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	27.8	424
49	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422
50	A renewed model of pancreatic cancer evolution based on genomic rearrangement patterns. Nature, 2016, 538, 378-382.	27.8	418
51	Intra-tumour diversification in colorectal cancer at the single-cell level. Nature, 2018, 556, 457-462.	27.8	406
52	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. Cell, 2018, 173, 611-623.e17.	28.9	398
53	Analysis of the genetic phylogeny of multifocal prostate cancer identifies multiple independent clonal expansions in neoplastic and morphologically normal prostate tissue. Nature Genetics, 2015, 47, 367-372.	21.4	380
54	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. Nature Genetics, 2020, 52, 231-240.	21.4	365

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55	Chromosomally unstable mouse tumours have genomic alterations similar to diverse human cancers. Nature, 2007, 447, 966-971.	27.8	355
56	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	12.6	348
57	The mutational landscape of normal human endometrial epithelium. Nature, 2020, 580, 640-646.	27.8	338
58	Tobacco smoking and somatic mutations in human bronchial epithelium. Nature, 2020, 578, 266-272.	27.8	336
59	Subclonal phylogenetic structures in cancer revealed by ultra-deep sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13081-13086.	7.1	320
60	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	6.0	318
61	Genome sequencing of normal cells reveals developmental lineages and mutational processes. Nature, 2014, 513, 422-425.	27.8	315
62	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. Nature Genetics, 2014, 46, 116-125.	21.4	313
63	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermutated cancers. Nature Genetics, 2015, 47, 257-262.	21.4	306
64	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. Cell, 2019, 176, 1282-1294.e20.	28.9	298
65	SvABA: genome-wide detection of structural variants and indels by local assembly. Genome Research, 2018, 28, 581-591.	5.5	288
66	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
67	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
68	Constitutional and somatic rearrangement of chromosome 21 in acute lymphoblastic leukaemia. Nature, 2014, 508, 98-102.	27.8	261
69	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	28.9	260
70	Comprehensive molecular characterization of mitochondrial genomes in human cancers. Nature Genetics, 2020, 52, 342-352.	21.4	256
71	Somatic mutation landscapes at single-molecule resolution. Nature, 2021, 593, 405-410.	27.8	254
72	Somatic mutations and clonal dynamics in healthy and cirrhotic human liver. Nature, 2019, 574, 538-542.	27.8	251

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73	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	12.8	236
74	The topography of mutational processes in breast cancer genomes. Nature Communications, 2016, 7, 11383.	12.8	235
75	Precision oncology for acute myeloid leukemia using a knowledge bank approach. Nature Genetics, 2017, 49, 332-340.	21.4	229
76	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	27.8	229
77	Chromothripsis drives the evolution of gene amplification in cancer. Nature, 2021, 591, 137-141.	27.8	228
78	Pervasive chromosomal instability and karyotype order in tumour evolution. Nature, 2020, 587, 126-132.	27.8	221
79	Mutational signatures of ionizing radiation in second malignancies. Nature Communications, 2016, 7, 12605.	12.8	214
80	Somatic mutation rates scale with lifespan across mammals. Nature, 2022, 604, 517-524.	27.8	211
81	Extensive heterogeneity in somatic mutation and selection in the human bladder. Science, 2020, 370, 75-82.	12.6	195
82	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. Nature Communications, 2019, 10, 3835.	12.8	183
83	Architectures of somatic genomic rearrangement in human cancer amplicons at sequence-level resolution. Genome Research, 2007, 17, 1296-1303.	5.5	180
84	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. Nature Genetics, 2020, 52, 294-305.	21.4	180
85	The mutational landscape of human somatic and germline cells. Nature, 2021, 597, 381-386.	27.8	180
86	Deciphering the genomic, epigenomic, and transcriptomic landscapes of pre-invasive lung cancer lesions. Nature Medicine, 2019, 25, 517-525.	30.7	178
87	Use of cancerâ€specific genomic rearrangements to quantify disease burden in plasma from patients with solid tumors. Genes Chromosomes and Cancer, 2010, 49, 1062-1069.	2.8	172
88	C. elegans whole-genome sequencing reveals mutational signatures related to carcinogens and DNA repair deficiency. Genome Research, 2014, 24, 1624-1636.	5.5	164
89	Genomic patterns of progression in smoldering multiple myeloma. Nature Communications, 2018, 9, 3363.	12.8	163
90	Clonal dynamics of haematopoiesis across the human lifespan. Nature, 2022, 606, 343-350.	27.8	160

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91	cgpCaVEManWrapper: Simple Execution of CaVEMan in Order to Detect Somatic Single Nucleotide Variants in NGS Data. Current Protocols in Bioinformatics, 2016, 56, 15.10.1-15.10.18.	25.8	155
92	A practical guide for mutational signature analysis in hematological malignancies. Nature Communications, 2019, 10, 2969.	12.8	145
93	Chromosome segregation errors generate a diverse spectrum of simple and complex genomic rearrangements. Nature Genetics, 2019, 51, 705-715.	21.4	145
94	Life histories of myeloproliferative neoplasms inferred from phylogenies. Nature, 2022, 602, 162-168.	27.8	140
95	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. Leukemia, 2018, 32, 2604-2616.	7.2	137
96	Mutational signatures are jointly shaped by DNA damage and repair. Nature Communications, 2020, 11, 2169.	12.8	137
97	The longitudinal dynamics and natural history of clonal haematopoiesis. Nature, 2022, 606, 335-342.	27.8	136
98	Inherent mosaicism and extensive mutation of human placentas. Nature, 2021, 592, 80-85.	27.8	126
99	Subclonal variant calling with multiple samples and prior knowledge. Bioinformatics, 2014, 30, 1198-1204.	4.1	122
100	Somatic Evolution in Non-neoplastic IBD-Affected Colon. Cell, 2020, 182, 672-684.e11.	28.9	122
101	Rearrangement bursts generate canonical gene fusions in bone and soft tissue tumors. Science, 2018, 361, .	12.6	121
102	Reticulin Accumulation in Essential Thrombocythemia: Prognostic Significance and Relationship to Therapy. Journal of Clinical Oncology, 2009, 27, 2991-2999.	1.6	116
103	The driver landscape of sporadic chordoma. Nature Communications, 2017, 8, 890.	12.8	115
104	Mutational signatures of DNA mismatch repair deficiency in C. elegans and human cancers. Genome Research, 2018, 28, 666-675.	5.5	112
105	Inactivating CUX1 mutations promote tumorigenesis. Nature Genetics, 2014, 46, 33-38.	21.4	111
106	ascatNgs: Identifying Somatically Acquired Copyâ€Number Alterations from Wholeâ€Genome Sequencing Data. Current Protocols in Bioinformatics, 2016, 56, 15.9.1-15.9.17.	25.8	111
107	Estimation of rearrangement phylogeny for cancer genomes. Genome Research, 2012, 22, 346-361.	5.5	108
108	APOBEC3-dependent kataegis and TREX1-driven chromothripsis during telomere crisis. Nature Genetics, 2020, 52, 884-890.	21.4	106

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109	DNMT3A mutations occur early or late in patients with myeloproliferative neoplasms and mutation order influences phenotype. Haematologica, 2015, 100, e438-e442.	3.5	105
110	cgpPindel: Identifying Somatically Acquired Insertion and Deletion Events from Paired End Sequencing. Current Protocols in Bioinformatics, 2015, 52, 15.7.1-15.7.12.	25.8	104
111	Embryonal precursors of Wilms tumor. Science, 2019, 366, 1247-1251.	12.6	101
112	Integrative Genomics Identifies the Molecular Basis of Resistance to Azacitidine Therapy in Myelodysplastic Syndromes. Cell Reports, 2017, 20, 572-585.	6.4	99
113	Timing the initiation of multiple myeloma. Nature Communications, 2020, 11, 1917.	12.8	99
114	JAK2V617F homozygosity arises commonly and recurrently in PV and ET, but PV is characterized by expansion of a dominant homozygous subclone. Blood, 2012, 120, 2704-2707.	1.4	94
115	The JAK2 46/1 haplotype predisposes to MPL-mutated myeloproliferative neoplasms. Blood, 2010, 115, 4517-4523.	1.4	93
116	Extensive phylogenies of human development inferred from somatic mutations. Nature, 2021, 597, 387-392.	27.8	87
117	Convergent somatic mutations in metabolism genes in chronic liver disease. Nature, 2021, 598, 473-478.	27.8	87
118	Processed pseudogenes acquired somatically during cancer development. Nature Communications, 2014, 5, 3644.	12.8	86
119	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. Nature Genetics, 2021, 53, 1434-1442.	21.4	85
120	The mutational signature profile of known and suspected human carcinogens in mice. Nature Genetics, 2020, 52, 1189-1197.	21.4	84
121	Undifferentiated Sarcomas Develop through Distinct Evolutionary Pathways. Cancer Cell, 2019, 35, 441-456.e8.	16.8	82
122	Reliable detection of somatic mutations in solid tissues by laser-capture microdissection and low-input DNA sequencing. Nature Protocols, 2021, 16, 841-871.	12.0	82
123	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. Journal of Pathology, 2012, 227, 446-455.	4.5	81
124	Revealing the Impact of Structural Variants in Multiple Myeloma. Blood Cancer Discovery, 2020, 1, 258-273.	5.0	81
125	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. Nature Genetics, 2020, 52, 1178-1188.	21.4	79
126	Lineage tracing of human development through somatic mutations. Nature, 2021, 595, 85-90.	27.8	79

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127	Next-generation sequencing in breast cancer. Current Opinion in Oncology, 2012, 24, 597-604.	2.4	76
128	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. Nature Genetics, 2017, 49, 341-348.	21.4	75
129	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. Nature Communications, 2017, 8, 1221.	12.8	75
130	Recurrent intragenic rearrangements of EGFR and BRAF in soft tissue tumors of infants. Nature Communications, 2018, 9, 2378.	12.8	72
131	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	5.5	69
132	Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities. Nature Communications, 2021, 12, 1861.	12.8	68
133	Immune Surveillance in Clinical Regression of Preinvasive Squamous Cell Lung Cancer. Cancer Discovery, 2020, 10, 1489-1499.	9.4	60
134	Differential and limited expression of mutant alleles in multiple myeloma. Blood, 2014, 124, 3110-3117.	1.4	54
135	Hydroxycarbamide Plus Aspirin Versus Aspirin Alone in Patients With Essential Thrombocythemia Age 40 to 59 Years Without High-Risk Features. Journal of Clinical Oncology, 2018, 36, 3361-3369.	1.6	54
136	Somatic and germline genetics at the JAK2 locus. Nature Genetics, 2009, 41, 385-386.	21.4	52
137	Genome Sequencing during a Patientâ€™s Journey through Cancer. New England Journal of Medicine, 2019, 381, 2145-2156.	27.0	50
138	Management of Polycythemia Vera and Essential Thrombocythemia. Hematology American Society of Hematology Education Program, 2005, 2005, 201-208.	2.5	45
139	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. Cell Reports, 2016, 16, 2032-2046.	6.4	36
140	A Distinct Class of Genome Rearrangements Driven by Heterologous Recombination. Molecular Cell, 2018, 69, 292-305.e6.	9.7	33
141	Estimation of tumor cell total mRNA expression in 15 cancer types predicts disease progression. Nature Biotechnology, 2022, 40, 1624-1633.	17.5	31
142	Inherited MUTYH mutations cause elevated somatic mutation rates and distinctive mutational signatures in normal human cells. Nature Communications, 2022, 13, .	12.8	30
143	Development, maturation, and maintenance of human prostate inferred from somatic mutations. Cell Stem Cell, 2021, 28, 1262-1274.e5.	11.1	29
144	Aberrant integration of Hepatitis B virus DNA promotes major restructuring of human hepatocellular carcinoma genome architecture. Nature Communications, 2021, 12, 6910.	12.8	27

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145	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. Nature Communications, 2020, 11, 4306.	12.8	26
146	Telomeres and Cancer: From Crisis to Stability to Crisis to Stability. Cell, 2012, 148, 633-635.	28.9	25
147	Tissue-Biased Expansion of DNMT3A-Mutant Clones in a Mosaic Individual Is Associated with Conserved Epigenetic Erosion. Cell Stem Cell, 2020, 27, 326-335.e4.	11.1	25
148	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. Nature Communications, 2020, 11, 3390.	12.8	24
149	Constrained positive selection on cancer mutations in normal skin. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1128-9.	7.1	23
150	Mutational landscape of normal epithelial cells in Lynch Syndrome patients. Nature Communications, 2022, 13, 2710.	12.8	19
151	Protection of the C. elegans germ cell genome depends on diverse DNA repair pathways during normal proliferation. PLoS ONE, 2021, 16, e0250291.	2.5	18
152	<i>CDKN2A</i> deletion is a frequent event associated with poor outcome in patients with peripheral T-cell lymphoma not otherwise specified (PTCL-NOS). Haematologica, 2021, 106, 2918-2926.	3.5	18
153	VAGrENT: Variation Annotation Generator. Current Protocols in Bioinformatics, 2015, 52, 15.8.1-15.8.11.	25.8	15
154	Acetyl-CoA metabolism drives epigenome change and contributes to carcinogenesis risk in fatty liver disease. Genome Medicine, 2022, 14, .	8.2	12
155	Circulating DNA and Next-Generation Sequencing. Recent Results in Cancer Research, 2012, 195, 143-149.	1.8	11
156	Interrogating breast cancer heterogeneity using single and pooled circulating tumor cell analysis. Npj Breast Cancer, 2022, 8, .	5.2	8
157	Recurrent histone mutations in Tâ€cell acute lymphoblastic leukaemia. British Journal of Haematology, 2019, 184, 676-679.	2.5	7
158	Cliques and Schisms of Cancer Genes. Cancer Cell, 2017, 32, 129-130.	16.8	6
159	Framework for quality assessment of whole genome cancer sequences. Nature Communications, 2020, 11, 5040.	12.8	5
160	Bayesian networks elucidate complex genomic landscapes in cancer. Communications Biology, 2022, 5, 306.	4.4	5
161	The Genomic Landscape of Myeloproliferative Neoplasms: Somatic Calr Mutations in the Majority of JAK2-Wildtype Patients. Blood, 2013, 122, LBA-2-LBA-2.	1.4	1
162	Response: essential thrombocythemia: seeing the wood for the trees. Blood, 2011, 118, 1180-1181.	1.4	0

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163	C. elegans genome-wide analysis reveals DNA repair pathways that act cooperatively to preserve genome integrity upon ionizing radiation. PLoS ONE, 2021, 16, e0258269.	2.5	0
164	The eternal quest for self-improvement of somatic cells. Cell Genomics, 2022, 2, 100094.	6.5	0