

# Peter J Campbell

## 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.

191  
papers

54,734  
citations

86  
h-index

208  
g-index

208  
ext. papers

69,540  
ext. citations

30.1  
avg, IF

7.18  
L-index

#	Paper	IF	Citations
191	Life histories of myeloproliferative neoplasms inferred from phylogenies.. <i>Nature</i> , <b>2022</b> ,	50.4	13
190	The eternal quest for self-improvement of somatic cells. <i>Cell Genomics</i> , <b>2022</b> , 2, 100094		
189	Bayesian networks elucidate complex genomic landscapes in cancer.. <i>Communications Biology</i> , <b>2022</b> , 5, 306	6.7	1
188	Somatic mutation rates scale with lifespan across mammals.. <i>Nature</i> , <b>2022</b> ,	50.4	9
187	Mutational landscape of normal epithelial cells in Lynch Syndrome patients.. <i>Nature Communications</i> , <b>2022</b> , 13, 2710	17.4	1
186	Aberrant integration of Hepatitis B virus DNA promotes major restructuring of human hepatocellular carcinoma genome architecture. <i>Nature Communications</i> , <b>2021</b> , 12, 6910	17.4	6
185	CDKN2A deletion is a frequent event associated with poor outcome in patients with peripheral T-cell lymphoma not otherwise specified (PTCL-NOS). <i>Haematologica</i> , <b>2021</b> , 106, 2918-2926	6.6	3
184	Convergent somatic mutations in metabolism genes in chronic liver disease. <i>Nature</i> , <b>2021</b> , 598, 473-478	50.4	10
183	C. elegans genome-wide analysis reveals DNA repair pathways that act cooperatively to preserve genome integrity upon ionizing radiation. <i>PLoS ONE</i> , <b>2021</b> , 16, e0258269	3.7	
182	Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities. <i>Nature Communications</i> , <b>2021</b> , 12, 1861	17.4	16
181	Inherent mosaicism and extensive mutation of human placentas. <i>Nature</i> , <b>2021</b> , 592, 80-85	50.4	44
180	Somatic mutation landscapes at single-molecule resolution. <i>Nature</i> , <b>2021</b> , 593, 405-410	50.4	57
179	Protection of the C. elegans germ cell genome depends on diverse DNA repair pathways during normal proliferation. <i>PLoS ONE</i> , <b>2021</b> , 16, e0250291	3.7	3
178	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , <b>2021</b> , 184, 2239-2254.e39	56.2	57
177	Lineage tracing of human development through somatic mutations. <i>Nature</i> , <b>2021</b> , 595, 85-90	50.4	15
176	Reliable detection of somatic mutations in solid tissues by laser-capture microdissection and low-input DNA sequencing. <i>Nature Protocols</i> , <b>2021</b> , 16, 841-871	18.8	34
175	Chromothripsis drives the evolution of gene amplification in cancer. <i>Nature</i> , <b>2021</b> , 591, 137-141	50.4	65

174	Development, maturation, and maintenance of human prostate inferred from somatic mutations. <i>Cell Stem Cell</i> , <b>2021</b> , 28, 1262-1274.e5	18	7
173	Extensive phylogenies of human development inferred from somatic mutations. <i>Nature</i> , <b>2021</b> , 597, 387-394	30.4	21
172	The mutational landscape of human somatic and germline cells. <i>Nature</i> , <b>2021</b> , 597, 381-386	50.4	32
171	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. <i>Nature Genetics</i> , <b>2021</b> , 53, 1434-1442	36.3	13
170	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. <i>Nature Communications</i> , <b>2020</b> , 11, 3390	17.4	8
169	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. <i>Nature Genetics</i> , <b>2020</b> , 52, 231-240	36.3	148
168	Tobacco smoking and somatic mutations in human bronchial epithelium. <i>Nature</i> , <b>2020</b> , 578, 266-272	50.4	150
167	Patterns of somatic structural variation in human cancer genomes. <i>Nature</i> , <b>2020</b> , 578, 112-121	50.4	232
166	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , <b>2020</b> , 578, 102-111	50.4	220
165	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , <b>2020</b> , 52, 306-319	36.3	122
164	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. <i>Nature Genetics</i> , <b>2020</b> , 52, 294-305	36.3	81
163	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , <b>2020</b> , 52, 331-341	36.3	168
162	Mutational signatures are jointly shaped by DNA damage and repair. <i>Nature Communications</i> , <b>2020</b> , 11, 2169	17.4	70
161	Timing the initiation of multiple myeloma. <i>Nature Communications</i> , <b>2020</b> , 11, 1917	17.4	36
160	Extensive heterogeneity in somatic mutation and selection in the human bladder. <i>Science</i> , <b>2020</b> , 370, 75-82	33.3	67
159	Comprehensive molecular characterization of mitochondrial genomes in human cancers. <i>Nature Genetics</i> , <b>2020</b> , 52, 342-352	36.3	105
158	The mutational signature profile of known and suspected human carcinogens in mice. <i>Nature Genetics</i> , <b>2020</b> , 52, 1189-1197	36.3	34
157	Framework for quality assessment of whole genome cancer sequences. <i>Nature Communications</i> , <b>2020</b> , 11, 5040	17.4	1

156	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. <i>Nature Genetics</i> , <b>2020</b> , 52, 1178-1188	36.3	25
155	Somatic Evolution in Non-neoplastic IBD-Affected Colon. <i>Cell</i> , <b>2020</b> , 182, 672-684.e11	56.2	50
154	Tissue-Biased Expansion of DNMT3A-Mutant Clones in a Mosaic Individual Is Associated with Conserved Epigenetic Erosion. <i>Cell Stem Cell</i> , <b>2020</b> , 27, 326-335.e4	18	11
153	Immune Surveillance in Clinical Regression of Preinvasive Squamous Cell Lung Cancer. <i>Cancer Discovery</i> , <b>2020</b> , 10, 1489-1499	24.4	25
152	APOBEC3-dependent kataegis and TREX1-driven chromothripsis during telomere crisis. <i>Nature Genetics</i> , <b>2020</b> , 52, 884-890	36.3	43
151	Pervasive chromosomal instability and karyotype order in tumour evolution. <i>Nature</i> , <b>2020</b> , 587, 126-132	50.4	67
150	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. <i>Nature Communications</i> , <b>2020</b> , 11, 4306	17.4	12
149	Revealing the impact of structural variants in multiple myeloma. <i>Blood Cancer Discovery</i> , <b>2020</b> , 1, 258-273		28
148	The mutational landscape of normal human endometrial epithelium. <i>Nature</i> , <b>2020</b> , 580, 640-646	50.4	148
147	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. <i>Nature Communications</i> , <b>2019</b> , 10, 3835	17.4	94
146	Deciphering the genomic, epigenomic, and transcriptomic landscapes of pre-invasive lung cancer lesions. <i>Nature Medicine</i> , <b>2019</b> , 25, 517-525	50.5	101
145	Undifferentiated Sarcomas Develop through Distinct Evolutionary Pathways. <i>Cancer Cell</i> , <b>2019</b> , 35, 441-453.e8	45.3	35
144	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. <i>Cell</i> , <b>2019</b> , 176, 1282-1294.e20	56.2	165
143	Chromosome segregation errors generate a diverse spectrum of simple and complex genomic rearrangements. <i>Nature Genetics</i> , <b>2019</b> , 51, 705-715	36.3	70
142	A practical guide for mutational signature analysis in hematological malignancies. <i>Nature Communications</i> , <b>2019</b> , 10, 2969	17.4	73
141	Embryonal precursors of Wilms tumor. <i>Science</i> , <b>2019</b> , 366, 1247-1251	33.3	40
140	Somatic mutations and clonal dynamics in healthy and cirrhotic human liver. <i>Nature</i> , <b>2019</b> , 574, 538-542	50.4	120
139	The landscape of somatic mutation in normal colorectal epithelial cells. <i>Nature</i> , <b>2019</b> , 574, 532-537	50.4	217

138	Genome Sequencing during a Patient's Journey through Cancer. <i>New England Journal of Medicine</i> , <b>2019</b> , 381, 2145-2156	59.2	35
137	COSMIC: the Catalogue Of Somatic Mutations In Cancer. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D941-D947	20.1	1497
136	Recurrent histone mutations in T-cell acute lymphoblastic leukaemia. <i>British Journal of Haematology</i> , <b>2019</b> , 184, 676-679	4.5	6
135	Mutational signatures of DNA mismatch repair deficiency in and human cancers. <i>Genome Research</i> , <b>2018</b> , 28, 666-675	9.7	61
134	Intra-tumour diversification in colorectal cancer at the single-cell level. <i>Nature</i> , <b>2018</b> , 556, 457-462	50.4	294
133	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. <i>Cell</i> , <b>2018</b> , 173, 611-623.e17	56.2	228
132	Deterministic Evolutionary Trajectories Influence Primary Tumor Growth: TRACERx Renal. <i>Cell</i> , <b>2018</b> , 173, 595-610.e11	56.2	268
131	A Distinct Class of Genome Rearrangements Driven by Heterologous Recombination. <i>Molecular Cell</i> , <b>2018</b> , 69, 292-305.e6	17.6	23
130	SvABA: genome-wide detection of structural variants and indels by local assembly. <i>Genome Research</i> , <b>2018</b> , 28, 581-591	9.7	149
129	Prediction of acute myeloid leukaemia risk in healthy individuals. <i>Nature</i> , <b>2018</b> , 559, 400-404	50.4	368
128	Genomic patterns of progression in smoldering multiple myeloma. <i>Nature Communications</i> , <b>2018</b> , 9, 3363	7.4	99
127	Recurrent intragenic rearrangements of EGFR and BRAF in soft tissue tumors of infants. <i>Nature Communications</i> , <b>2018</b> , 9, 2378	17.4	50
126	Hydroxycarbamide Plus Aspirin Versus Aspirin Alone in Patients With Essential Thrombocythemia Age 40 to 59 Years Without High-Risk Features. <i>Journal of Clinical Oncology</i> , <b>2018</b> , 36, 3361-3369	2.2	32
125	Classification and Personalized Prognosis in Myeloproliferative Neoplasms. <i>New England Journal of Medicine</i> , <b>2018</b> , 379, 1416-1430	59.2	256
124	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , <b>2018</b> , 8, 1548-1565	24.4	258
123	Somatic mutant clones colonize the human esophagus with age. <i>Science</i> , <b>2018</b> , 362, 911-917	33.3	465
122	Population dynamics of normal human blood inferred from somatic mutations. <i>Nature</i> , <b>2018</b> , 561, 473-478	58.4	245
121	Rearrangement bursts generate canonical gene fusions in bone and soft tissue tumors. <i>Science</i> , <b>2018</b> , 361,	33.3	72

120	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. <i>Leukemia</i> , <b>2018</b> , 32, 2604-2616	10.7	90
119	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. <i>Nature Genetics</i> , <b>2017</b> , 49, 341-348	36.3	54
118	COSMIC: somatic cancer genetics at high-resolution. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D777-D783	20.1	1279
117	Precision oncology for acute myeloid leukemia using a knowledge bank approach. <i>Nature Genetics</i> , <b>2017</b> , 49, 332-340	36.3	155
116	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. <i>Nature Medicine</i> , <b>2017</b> , 23, 517-525	50.5	444
115	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. <i>Nature</i> , <b>2017</b> , 543, 714-718	50.4	157
114	The Human Cell Atlas <b>2017</b> ,		41
113	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. <i>Nature Communications</i> , <b>2017</b> , 8, 1221	17.4	40
112	The driver landscape of sporadic chordoma. <i>Nature Communications</i> , <b>2017</b> , 8, 890	17.4	64
111	Universal Patterns of Selection in Cancer and Somatic Tissues. <i>Cell</i> , <b>2017</b> , 171, 1029-1041.e21	56.2	576
110	Integrative Genomics Identifies the Molecular Basis of Resistance to Azacitidine Therapy in Myelodysplastic Syndromes. <i>Cell Reports</i> , <b>2017</b> , 20, 572-585	10.6	72
109	Genomic Evolution of Breast Cancer Metastasis and Relapse. <i>Cancer Cell</i> , <b>2017</b> , 32, 169-184.e7	24.3	346
108	Cliques and Schisms of Cancer Genes. <i>Cancer Cell</i> , <b>2017</b> , 32, 129-130	24.3	3
107	The Human Cell Atlas. <i>ELife</i> , <b>2017</b> , 6,	8.9	937
106	The topography of mutational processes in breast cancer genomes. <i>Nature Communications</i> , <b>2016</b> , 7, 11383	17.4	172
105	Mutational signatures of ionizing radiation in second malignancies. <i>Nature Communications</i> , <b>2016</b> , 7, 12605	17.4	152
104	Mutational signatures associated with tobacco smoking in human cancer. <i>Science</i> , <b>2016</b> , 354, 618-622	33.3	562
103	Genomic Classification and Prognosis in Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , <b>2016</b> , 374, 2209-2221	59.2	1999

102	Constrained positive selection on cancer mutations in normal skin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E1128-9	11.5	18
101	cgpCaVEManWrapper: Simple Execution of CaVEMan in Order to Detect Somatic Single Nucleotide Variants in NGS Data. <i>Current Protocols in Bioinformatics</i> , <b>2016</b> , 56, 15.10.1-15.10.18	24.2	107
100	ascats: Identifying Somatic Copy-Number Alterations from Whole-Genome Sequencing Data. <i>Current Protocols in Bioinformatics</i> , <b>2016</b> , 56, 15.9.1-15.9.17	24.2	60
99	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , <b>2016</b> , 534, 47-54	50.4	1193
98	A renewed model of pancreatic cancer evolution based on genomic rearrangement patterns. <i>Nature</i> , <b>2016</b> , 538, 378-382	50.4	304
97	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. <i>Cell Reports</i> , <b>2016</b> , 16, 2032-46	46.6	30
96	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. <i>Nature Medicine</i> , <b>2015</b> , 21, 751-9	50.5	521
95	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. <i>Genome Research</i> , <b>2015</b> , 25, 814-24	9.7	52
94	Analysis of the genetic phylogeny of multifocal prostate cancer identifies multiple independent clonal expansions in neoplastic and morphologically normal prostate tissue. <i>Nature Genetics</i> , <b>2015</b> , 47, 367-372	36.3	292
93	The evolutionary history of lethal metastatic prostate cancer. <i>Nature</i> , <b>2015</b> , 520, 353-357	50.4	857
92	Somatic mutation in cancer and normal cells. <i>Science</i> , <b>2015</b> , 349, 1483-9	33.3	608
91	COSMIC: exploring the world's knowledge of somatic mutations in human cancer. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D805-11	20.1	1795
90	Clock-like mutational processes in human somatic cells. <i>Nature Genetics</i> , <b>2015</b> , 47, 1402-7	36.3	531
89	DNMT3A mutations occur early or late in patients with myeloproliferative neoplasms and mutation order influences phenotype. <i>Haematologica</i> , <b>2015</b> , 100, e438-42	6.6	70
88	cgpPindel: Identifying Somatic Insertion and Deletion Events from Paired End Sequencing. <i>Current Protocols in Bioinformatics</i> , <b>2015</b> , 52, 15.7.1-15.7.12	24.2	74
87	VAGrENT: Variation Annotation Generator. <i>Current Protocols in Bioinformatics</i> , <b>2015</b> , 52, 15.8.1-15.8.11	24.2	12
86	Tumor evolution. High burden and pervasive positive selection of somatic mutations in normal human skin. <i>Science</i> , <b>2015</b> , 348, 880-6	33.3	983
85	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , <b>2015</b> , 6, 10001	17.4	199

84	Chromothripsis and Kataegis Induced by Telomere Crisis. <i>Cell</i> , <b>2015</b> , 163, 1641-54	56.2	371
83	Effect of mutation order on myeloproliferative neoplasms. <i>New England Journal of Medicine</i> , <b>2015</b> , 372, 601-612	59.2	334
82	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermuted cancers. <i>Nature Genetics</i> , <b>2015</b> , 47, 257-62	36.3	253
81	Constitutional and somatic rearrangement of chromosome 21 in acute lymphoblastic leukaemia. <i>Nature</i> , <b>2014</b> , 508, 98-102	50.4	192
80	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. <i>Nature Communications</i> , <b>2014</b> , 5, 2997	17.4	564
79	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. <i>Nature Genetics</i> , <b>2014</b> , 46, 116-25	36.3	244
78	Inactivating CUX1 mutations promote tumorigenesis. <i>Nature Genetics</i> , <b>2014</b> , 46, 33-8	36.3	89
77	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. <i>Nature Communications</i> , <b>2014</b> , 5, 5224	17.4	176
76	Mobile DNA in cancer. Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , <b>2014</b> , 345, 1251343	33.3	250
75	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. <i>Science</i> , <b>2014</b> , 346, 251-6	33.3	752
74	Genome sequencing of normal cells reveals developmental lineages and mutational processes. <i>Nature</i> , <b>2014</b> , 513, 422-425	50.4	249
73	Differential and limited expression of mutant alleles in multiple myeloma. <i>Blood</i> , <b>2014</b> , 124, 3110-7	2.2	42
72	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. <i>ELife</i> , <b>2014</b> , 3,	8.9	229
71	Processed pseudogenes acquired somatically during cancer development. <i>Nature Communications</i> , <b>2014</b> , 5, 3644	17.4	68
70	C. elegans whole-genome sequencing reveals mutational signatures related to carcinogens and DNA repair deficiency. <i>Genome Research</i> , <b>2014</b> , 24, 1624-36	9.7	125
69	Subclonal variant calling with multiple samples and prior knowledge. <i>Bioinformatics</i> , <b>2014</b> , 30, 1198-204	7.2	86
68	Signatures of mutational processes in human cancer. <i>Nature</i> , <b>2013</b> , 500, 415-21	50.4	5895
67	Deciphering signatures of mutational processes operative in human cancer. <i>Cell Reports</i> , <b>2013</b> , 3, 246-59	10.6	725



66	Clinical and biological implications of driver mutations in myelodysplastic syndromes. <i>Blood</i> , <b>2013</b> , 122, 3616-27; quiz 3699	2.2	1169
65	Criteria for inference of chromothripsis in cancer genomes. <i>Cell</i> , <b>2013</b> , 152, 1226-36	56.2	342
64	The Genomic Landscape of Myeloproliferative Neoplasms: Somatic Calr Mutations in the Majority of JAK2-Wildtype Patients. <i>Blood</i> , <b>2013</b> , 122, LBA-2-LBA-2	2.2	1
63	Estimation of rearrangement phylogeny for cancer genomes. <i>Genome Research</i> , <b>2012</b> , 22, 346-61	9.7	94
62	JAK2V617F homozygosity arises commonly and recurrently in PV and ET, but PV is characterized by expansion of a dominant homozygous subclone. <i>Blood</i> , <b>2012</b> , 120, 2704-7	2.2	81
61	Telomeres and cancer: from crisis to stability to crisis to stability. <i>Cell</i> , <b>2012</b> , 148, 633-5	56.2	21
60	Evolution of the cancer genome. <i>Nature Reviews Genetics</i> , <b>2012</b> , 13, 795-806	30.1	424
59	Circulating DNA and next-generation sequencing. <i>Recent Results in Cancer Research</i> , <b>2012</b> , 195, 143-9	1.5	8
58	The landscape of cancer genes and mutational processes in breast cancer. <i>Nature</i> , <b>2012</b> , 486, 400-4	50.4	1264
57	Mutational processes molding the genomes of 21 breast cancers. <i>Cell</i> , <b>2012</b> , 149, 979-93	56.2	1279
56	The life history of 21 breast cancers. <i>Cell</i> , <b>2012</b> , 149, 994-1007	56.2	979
55	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. <i>Journal of Pathology</i> , <b>2012</b> , 227, 446-55	9.4	72
54	Next-generation sequencing in breast cancer: first take home messages. <i>Current Opinion in Oncology</i> , <b>2012</b> , 24, 597-604	4.2	62
53	Massive genomic rearrangement acquired in a single catastrophic event during cancer development. <i>Cell</i> , <b>2011</b> , 144, 27-40	56.2	1628
52	Response: essential thrombocythemia: seeing the wood for the trees. <i>Blood</i> , <b>2011</b> , 118, 1180-1181	2.2	
51	Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. <i>Nature</i> , <b>2011</b> , 469, 539-42	50.4	943
50	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , <b>2011</b> , 475, 101-5	50.4	1206
49	A small-cell lung cancer genome with complex signatures of tobacco exposure. <i>Nature</i> , <b>2010</b> , 463, 184-90	50.4	852

48	A comprehensive catalogue of somatic mutations from a human cancer genome. <i>Nature</i> , <b>2010</b> , 463, 191-504	50.4	1303
47	Systematic sequencing of renal carcinoma reveals inactivation of histone modifying genes. <i>Nature</i> , <b>2010</b> , 463, 360-3	50.4	927
46	The patterns and dynamics of genomic instability in metastatic pancreatic cancer. <i>Nature</i> , <b>2010</b> , 467, 1109-13	50.4	1013
45	The JAK2 46/1 haplotype predisposes to MPL-mutated myeloproliferative neoplasms. <i>Blood</i> , <b>2010</b> , 115, 4517-23	2.2	80
44	Use of cancer-specific genomic rearrangements to quantify disease burden in plasma from patients with solid tumors. <i>Genes Chromosomes and Cancer</i> , <b>2010</b> , 49, 1062-9	5	161
43	Reticulin accumulation in essential thrombocythemia: prognostic significance and relationship to therapy. <i>Journal of Clinical Oncology</i> , <b>2009</b> , 27, 2991-9	2.2	99
42	The cancer genome. <i>Nature</i> , <b>2009</b> , 458, 719-24	50.4	2272
41	Complex landscapes of somatic rearrangement in human breast cancer genomes. <i>Nature</i> , <b>2009</b> , 462, 1005-10	50.4	684
40	Somatic and germline genetics at the JAK2 locus. <i>Nature Genetics</i> , <b>2009</b> , 41, 385-6	36.3	44
39	Identification of somatically acquired rearrangements in cancer using genome-wide massively parallel paired-end sequencing. <i>Nature Genetics</i> , <b>2008</b> , 40, 722-9	36.3	666
38	Subclonal phylogenetic structures in cancer revealed by ultra-deep sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 13081-6	11.5	283
37	Patterns of somatic mutation in human cancer genomes. <i>Nature</i> , <b>2007</b> , 446, 153-8	50.4	2400
36	Chromosomally unstable mouse tumours have genomic alterations similar to diverse human cancers. <i>Nature</i> , <b>2007</b> , 447, 966-71	50.4	327
35	Architectures of somatic genomic rearrangement in human cancer amplicons at sequence-level resolution. <i>Genome Research</i> , <b>2007</b> , 17, 1296-303	9.7	152
34	The myeloproliferative disorders. <i>New England Journal of Medicine</i> , <b>2006</b> , 355, 2452-66	59.2	485
33	Management of polycythemia vera and essential thrombocythemia. <i>Hematology American Society of Hematology Education Program</i> , <b>2005</b> , 2005, 201-8	3.1	35
32	Clonal diversification and histogenesis of malignant germ cell tumours		1
31	Inherited MUTYH mutations cause elevated somatic mutation rates and distinctive mutational signatures in normal human cells		1

30	Mutational signatures are jointly shaped by DNA damage and repair	3
29	Universal patterns of selection in cancer and somatic tissues	7
28	Pan-cancer analysis of whole genomes	70
27	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours	10
26	Patterns of structural variation in human cancer	26
25	The whole-genome panorama of cancer drivers	38
24	Revealing the impact of recurrent and rare structural variants in multiple myeloma	1
23	Lineage tracing of human embryonic development and foetal haematopoiesis through somatic mutations	4
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