Peter J Campbell

List of Publications by Citations

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	Signatures of mutational processes in human cancer. *Nature*, **2013**, 500, 415-21	50.4	5895
190	Patterns of somatic mutation in human cancer genomes. *Nature*, **2007**, 446, 153-8	50.4	2400
189	The cancer genome. *Nature*, **2009**, 458, 719-24	50.4	2272
188	Genomic Classification and Prognosis in Acute Myeloid Leukemia. *New England Journal of Medicine*, **2016**, 374, 2209-2221	59.2	1999
187	COSMIC: exploring the world's knowledge of somatic mutations in human cancer. *Nucleic Acids Research*, **2015**, 43, D805-11	20.1	1795
186	Massive genomic rearrangement acquired in a single catastrophic event during cancer development. *Cell*, **2011**, 144, 27-40	56.2	1628
185	COSMIC: the Catalogue Of Somatic Mutations In Cancer. *Nucleic Acids Research*, **2019**, 47, D941-D947	20.1	1497
184	A comprehensive catalogue of somatic mutations from a human cancer genome. *Nature*, **2010**, 463, 191-6	50.4	1303
183	COSMIC: somatic cancer genetics at high-resolution. *Nucleic Acids Research*, **2017**, 45, D777-D783	20.1	1279
182	Mutational processes molding the genomes of 21 breast cancers. *Cell*, **2012**, 149, 979-93	56.2	1279
181	The landscape of cancer genes and mutational processes in breast cancer. *Nature*, **2012**, 486, 400-4	50.4	1264
180	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. *Nature* , **2011**, 475, 101-5	50.4	1206
179	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. *Nature*, **2016**, 534, 47-54	50.4	1193
178	Clinical and biological implications of driver mutations in myelodysplastic syndromes. *Blood*, **2013**, 122, 3616-27; quiz 3699	2.2	1169
177	The patterns and dynamics of genomic instability in metastatic pancreatic cancer. *Nature*, **2010**, 467, 1109-13	50.4	1013
176	Tumor evolution. High burden and pervasive positive selection of somatic mutations in normal human skin. *Science*, **2015**, 348, 880-6	33.3	983
175	The life history of 21 breast cancers. *Cell*, **2012**, 149, 994-1007	56.2	979

174	Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. *Nature*, **2011**, 469, 539-42	50.4	943
173	The Human Cell Atlas. *ELife*, **2017**, 6,	8.9	937
172	Systematic sequencing of renal carcinoma reveals inactivation of histone modifying genes. *Nature*, **2010**, 463, 360-3	50.4	927
171	The evolutionary history of lethal metastatic prostate cancer. *Nature*, **2015**, 520, 353-357	50.4	857
170	A small-cell lung cancer genome with complex signatures of tobacco exposure. *Nature*, **2010**, 463, 184-90	50.4	852
169	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. *Science*, **2014**, 346, 251-6	33.3	752
168	Deciphering signatures of mutational processes operative in human cancer. *Cell Reports*, **2013**, 3, 246-59	10.6	725
167	Complex landscapes of somatic rearrangement in human breast cancer genomes. *Nature*, **2009**, 462, 1005-10	50.4	684
166	Identification of somatically acquired rearrangements in cancer using genome-wide massively parallel paired-end sequencing. *Nature Genetics*, **2008**, 40, 722-9	36.3	666
165	Somatic mutation in cancer and normal cells. *Science*, **2015**, 349, 1483-9	33.3	608
164	Universal Patterns of Selection in Cancer and Somatic Tissues. *Cell*, **2017**, 171, 1029-1041.e21	56.2	576
163	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. *Nature Communications*, **2014**, 5, 2997	17.4	564
162	Mutational signatures associated with tobacco smoking in human cancer. *Science*, **2016**, 354, 618-622	33.3	562
161	Clock-like mutational processes in human somatic cells. *Nature Genetics*, **2015**, 47, 1402-7	36.3	531
160	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. *Nature Medicine*, **2015**, 21, 751-9	50.5	521
159	The myeloproliferative disorders. *New England Journal of Medicine*, **2006**, 355, 2452-66	59.2	485
158	Somatic mutant clones colonize the human esophagus with age. *Science*, **2018**, 362, 911-917	33.3	465
157	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. *Nature Medicine*, **2017**, 23, 517-525	50.5	444

156	Evolution of the cancer genome. *Nature Reviews Genetics*, **2012**, 13, 795-806	30.1	424
155	Chromothripsis and Kataegis Induced by Telomere Crisis. *Cell*, **2015**, 163, 1641-54	56.2	371
154	Prediction of acute myeloid leukaemia risk in healthy individuals. *Nature*, **2018**, 559, 400-404	50.4	368
153	Genomic Evolution of Breast Cancer Metastasis and Relapse. *Cancer Cell*, **2017**, 32, 169-184.e7	24.3	346
152	Criteria for inference of chromothripsis in cancer genomes. *Cell*, **2013**, 152, 1226-36	56.2	342
151	Effect of mutation order on myeloproliferative neoplasms. *New England Journal of Medicine*, **2015**, 372, 601-612	59.2	334
150	Chromosomally unstable mouse tumours have genomic alterations similar to diverse human cancers. *Nature*, **2007**, 447, 966-71	50.4	327
149	A renewed model of pancreatic cancer evolution based on genomic rearrangement patterns. *Nature*, **2016**, 538, 378-382	50.4	304
148	Intra-tumour diversification in colorectal cancer at the single-cell level. *Nature*, **2018**, 556, 457-462	50.4	294
147	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	36.3	292
146	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, 13081-6	11.5	283
145	Deterministic Evolutionary Trajectories Influence Primary Tumor Growth: TRACERx Renal. *Cell*, **2018**, 173, 595-610.e11	56.2	268
144	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. *Cancer Discovery*, **2018**, 8, 1548-1565	24.4	258
143	Classification and Personalized Prognosis in Myeloproliferative Neoplasms. *New England Journal of Medicine*, **2018**, 379, 1416-1430	59.2	256
142	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermutated cancers. *Nature Genetics*, **2015**, 47, 257-62	36.3	253
141	Mobile DNA in cancer. Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. *Science*, **2014**, 345, 1251343	33.3	250
140	Genome sequencing of normal cells reveals developmental lineages and mutational processes. *Nature*, **2014**, 513, 422-425	50.4	249
139	Population dynamics of normal human blood inferred from somatic mutations. *Nature*, **2018**, 561, 473-478	50.4	245

138	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. *Nature Genetics*, **2014**, 46, 116-25	36.3	244
137	Patterns of somatic structural variation in human cancer genomes. *Nature*, **2020**, 578, 112-121	50.4	232
136	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. *ELife*, **2014**, 3,	8.9	229
135	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. *Cell*, **2018**, 173, 611-623.e17	56.2	228
134	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
133	The landscape of somatic mutation in normal colorectal epithelial cells. *Nature*, **2019**, 574, 532-537	50.4	217
132	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. *Nature Communications*, **2015**, 6, 10001	17.4	199
131	Constitutional and somatic rearrangement of chromosome 21 in acute lymphoblastic leukaemia. *Nature*, **2014**, 508, 98-102	50.4	192
130	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. *Nature Communications*, **2014**, 5, 5224	17.4	176
129	The topography of mutational processes in breast cancer genomes. *Nature Communications*, **2016**, 7, 11383	17.4	172
128	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. *Nature Genetics*, **2020**, 52, 331-341	36.3	168
127	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. *Cell*, **2019**, 176, 1282-1294.e20	56.2	165
126	Use of cancer-specific genomic rearrangements to quantify disease burden in plasma from patients with solid tumors. *Genes Chromosomes and Cancer*, **2010**, 49, 1062-9	5	161
125	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. *Nature*, **2017**, 543, 714-718	50.4	157
124	Precision oncology for acute myeloid leukemia using a knowledge bank approach. *Nature Genetics*, **2017**, 49, 332-340	36.3	155
123	Mutational signatures of ionizing radiation in second malignancies. *Nature Communications*, **2016**, 7, 12605	17.4	152
122	Architectures of somatic genomic rearrangement in human cancer amplicons at sequence-level resolution. *Genome Research*, **2007**, 17, 1296-303	9.7	152
121	Tobacco smoking and somatic mutations in human bronchial epithelium. *Nature*, **2020**, 578, 266-272	50.4	150

120	SvABA: genome-wide detection of structural variants and indels by local assembly. *Genome Research*, **2018**, 28, 581-591	9.7	149
119	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. *Nature Genetics*, **2020**, 52, 231-240	36.3	148
118	The mutational landscape of normal human endometrial epithelium. *Nature*, **2020**, 580, 640-646	50.4	148
117	C. elegans whole-genome sequencing reveals mutational signatures related to carcinogens and DNA repair deficiency. *Genome Research*, **2014**, 24, 1624-36	9.7	125
116	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
115	Somatic mutations and clonal dynamics in healthy and cirrhotic human liver. *Nature*, **2019**, 574, 538-542	50.4	120
114	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	24.2	107
113	Comprehensive molecular characterization of mitochondrial genomes in human cancers. *Nature Genetics*, **2020**, 52, 342-352	36.3	105
112	Deciphering the genomic, epigenomic, and transcriptomic landscapes of pre-invasive lung cancer lesions. *Nature Medicine*, **2019**, 25, 517-525	50.5	101
111	Genomic patterns of progression in smoldering multiple myeloma. *Nature Communications*, **2018**, 9, 3363	17.4	99
110	Reticulin accumulation in essential thrombocythemia: prognostic significance and relationship to therapy. *Journal of Clinical Oncology*, **2009**, 27, 2991-9	2.2	99
109	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. *Nature Communications*, **2019**, 10, 3835	17.4	94
108	Estimation of rearrangement phylogeny for cancer genomes. *Genome Research*, **2012**, 22, 346-61	9.7	94
107	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. *Leukemia*, **2018**, 32, 2604-2616	10.7	90
106	Inactivating CUX1 mutations promote tumorigenesis. *Nature Genetics*, **2014**, 46, 33-8	36.3	89
105	Subclonal variant calling with multiple samples and prior knowledge. *Bioinformatics*, **2014**, 30, 1198-204	7.2	86
104	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. *Nature Genetics*, **2020**, 52, 294-305	36.3	81
103	JAK2V617F homozygosity arises commonly and recurrently in PV and ET, but PV is characterized by expansion of a dominant homozygous subclone. *Blood*, **2012**, 120, 2704-7	2.2	81

102	The JAK2 46/1 haplotype predisposes to MPL-mutated myeloproliferative neoplasms. *Blood*, **2010**, 115, 4517-23	2.2	80
101	cgpPindel: Identifying Somatically Acquired Insertion and Deletion Events from Paired End Sequencing. *Current Protocols in Bioinformatics*, **2015**, 52, 15.7.1-15.7.12	24.2	74
100	A practical guide for mutational signature analysis in hematological malignancies. *Nature Communications*, **2019**, 10, 2969	17.4	73
99	Integrative Genomics Identifies the Molecular Basis of Resistance to Azacitidine Therapy in Myelodysplastic Syndromes. *Cell Reports*, **2017**, 20, 572-585	10.6	72
98	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. *Journal of Pathology*, **2012**, 227, 446-55	9.4	72
97	Rearrangement bursts generate canonical gene fusions in bone and soft tissue tumors. *Science*, **2018**, 361,	33.3	72
96	Chromosome segregation errors generate a diverse spectrum of simple and complex genomic rearrangements. *Nature Genetics*, **2019**, 51, 705-715	36.3	70
95	Mutational signatures are jointly shaped by DNA damage and repair. *Nature Communications*, **2020**, 11, 2169	17.4	70
94	DNMT3A mutations occur early or late in patients with myeloproliferative neoplasms and mutation order influences phenotype. *Haematologica*, **2015**, 100, e438-42	6.6	70
93	Pan-cancer analysis of whole genomes		70
92	Processed pseudogenes acquired somatically during cancer development. *Nature Communications*, **2014**, 5, 3644	17.4	68
91	Extensive heterogeneity in somatic mutation and selection in the human bladder. *Science*, **2020**, 370, 75-82	33.3	67
90	Pervasive chromosomal instability and karyotype order in tumour evolution. *Nature*, **2020**, 587, 126-132	50.4	67
89	Chromothripsis drives the evolution of gene amplification in cancer. *Nature*, **2021**, 591, 137-141	50.4	65
88	The driver landscape of sporadic chordoma. *Nature Communications*, **2017**, 8, 890	17.4	64
87	Next-generation sequencing in breast cancer: first take home messages. *Current Opinion in Oncology*, **2012**, 24, 597-604	4.2	62
86	Mutational signatures of DNA mismatch repair deficiency in and human cancers. *Genome Research*, **2018**, 28, 666-675	9.7	61
85	ascatNgs: Identifying Somatically Acquired Copy-Number Alterations from Whole-Genome Sequencing Data. *Current Protocols in Bioinformatics*, **2016**, 56, 15.9.1-15.9.17	24.2	60

84	Somatic mutation landscapes at single-molecule resolution. *Nature*, **2021**, 593, 405-410	50.4	57
83	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. *Cell*, **2021**, 184, 2239-2254.e39	56.2	57
82	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. *Nature Genetics*, **2017**, 49, 341-348	36.3	54
81	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. *Genome Research*, **2015**, 25, 814-24	9.7	52
80	Recurrent intragenic rearrangements of EGFR and BRAF in soft tissue tumors of infants. *Nature Communications*, **2018**, 9, 2378	17.4	50
79	Somatic Evolution in Non-neoplastic IBD-Affected Colon. *Cell*, **2020**, 182, 672-684.e11	56.2	50
78	Somatic and germline genetics at the JAK2 locus. *Nature Genetics*, **2009**, 41, 385-6	36.3	44
77	Inherent mosaicism and extensive mutation of human placentas. *Nature*, **2021**, 592, 80-85	50.4	44
76	APOBEC3-dependent kataegis and TREX1-driven chromothripsis during telomere crisis. *Nature Genetics*, **2020**, 52, 884-890	36.3	43
75	Differential and limited expression of mutant alleles in multiple myeloma. *Blood*, **2014**, 124, 3110-7	2.2	42
74	The Human Cell Atlas **2017**,		41
73	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. *Nature Communications*, **2017**, 8, 1221	17.4	40
72	Embryonal precursors of Wilms tumor. *Science*, **2019**, 366, 1247-1251	33.3	40
71	The whole-genome panorama of cancer drivers		38
70	Timing the initiation of multiple myeloma. *Nature Communications*, **2020**, 11, 1917	17.4	36
69	Undifferentiated Sarcomas Develop through Distinct Evolutionary Pathways. *Cancer Cell*, **2019**, 35, 441-456.e8	23.3	35
68	Management of polycythemia vera and essential thrombocythemia. *Hematology American Society of Hematology Education Program*, **2005**, 2005, 201-8	3.1	35
67	Genome Sequencing during a Patient's Journey through Cancer. *New England Journal of Medicine*, **2019**, 381, 2145-2156	59.2	35

66	The mutational signature profile of known and suspected human carcinogens in mice. *Nature Genetics*, **2020**, 52, 1189-1197	36.3	34
65	Reliable detection of somatic mutations in solid tissues by laser-capture microdissection and low-input DNA sequencing. *Nature Protocols*, **2021**, 16, 841-871	18.8	34
64	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	2.2	32
63	The mutational landscape of human somatic and germline cells. *Nature*, **2021**, 597, 381-386	50.4	32
62	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. *Cell Reports*, **2016**, 16, 2032-2046	6.6	30
61	Revealing the impact of structural variants in multiple myeloma. *Blood Cancer Discovery*, **2020**, 1, 258-273	7	28
60	Patterns of structural variation in human cancer		26
59	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. *Nature Genetics*, **2020**, 52, 1178-1188	36.3	25
58	Immune Surveillance in Clinical Regression of Preinvasive Squamous Cell Lung Cancer. *Cancer Discovery*, **2020**, 10, 1489-1499	24.4	25
57	A Distinct Class of Genome Rearrangements Driven by Heterologous Recombination. *Molecular Cell* , **2018**, 69, 292-305.e6	17.6	23
56	Telomeres and cancer: from crisis to stability to crisis to stability. *Cell*, **2012**, 148, 633-5	56.2	21
55	Extensive phylogenies of human development inferred from somatic mutations. *Nature*, **2021**, 597, 387-392	50.4	21
54	Phylogenetic reconstruction of myeloproliferative neoplasm reveals very early origins and lifelong evolution		19
53	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	11.5	18
52	Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities. *Nature Communications*, **2021**, 12, 1861	17.4	16
51	Lineage tracing of human development through somatic mutations. *Nature*, **2021**, 595, 85-90	50.4	15
50	The landscape of somatic mutation in normal colorectal epithelial cells		14
49	Life histories of myeloproliferative neoplasms inferred from phylogenies.. *Nature*, **2022**,	50.4	13

48	Germline determinants of the somatic mutation landscape in 2,642 cancer genomes		13
47	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. *Nature Genetics*, **2021**, 53, 1434-1442	36.3	13
46	VAGrENT: Variation Annotation Generator. *Current Protocols in Bioinformatics*, **2015**, 52, 15.8.1-15.8.11	24.2	12
45	Discovery and characterization of coding and non-coding driver mutations in more than 2,500 whole cancer genomes		12
44	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. *Nature Communications*, **2020**, 11, 4306	17.4	12
43	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	18	11
42	Convergent somatic mutations in metabolism genes in chronic liver disease. *Nature*, **2021**, 598, 473-478	50.4	10
41	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10
40	Elevated somatic mutation burdens in normal human cells due to defective DNA polymerases		10
39	The mutational landscape of normal human endometrial epithelium		9
38	APOBEC3B-dependent kataegis and TREX1-driven chromothripsis in telomere crisis		9
37	Somatic mutation rates scale with lifespan across mammals.. *Nature*, **2022**,	50.4	9
36	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. *Nature Communications*, **2020**, 11, 3390	17.4	8
35	Circulating DNA and next-generation sequencing. *Recent Results in Cancer Research*, **2012**, 195, 143-9	1.5	8
34	Universal patterns of selection in cancer and somatic tissues		7
33	Development, maturation, and maintenance of human prostate inferred from somatic mutations. *Cell Stem Cell*, **2021**, 28, 1262-1274.e5	18	7
32	Clonal dynamics of haematopoiesis across the human lifespan. *Nature*,	50.4	7
31	Aberrant integration of Hepatitis B virus DNA promotes major restructuring of human hepatocellular carcinoma genome architecture. *Nature Communications*, **2021**, 12, 6910	17.4	6

30	Genomic landscape and chronological reconstruction of driver events in multiple myeloma		6
29	Life without mismatch repair		6
28	Recurrent histone mutations in T-cell acute lymphoblastic leukaemia. *British Journal of Haematology*, **2019**, 184, 676-679	4.5	6
27	The mutational landscape of human somatic and germline cells		5
26	Spatial genomics maps the structure, character and evolution of cancer clones		5
25	Lineage tracing of human embryonic development and foetal haematopoiesis through somatic mutations		4
24	Somatic mutation rates scale with lifespan across mammals		4
23	Cliques and Schisms of Cancer Genes. *Cancer Cell*, **2017**, 32, 129-130	24.3	3
22	CDKN2A 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	6.6	3
21	Mutational signatures are jointly shaped by DNA damage and repair		3
20	Protection of the C. elegans germ cell genome depends on diverse DNA repair pathways during normal proliferation. *PLoS ONE*, **2021**, 16, e0250291	3.7	3
19	The longitudinal dynamics and natural history of clonal haematopoiesis. *Nature*,	50.4	3
18	Tumor cell total mRNA expression shapes the molecular and clinical phenotype of cancer		2
17	Multi-site clonality analyses uncovers pervasive subclonal heterogeneity and branching evolution across melanoma metastases		2
16	Fanconi Anemia Pathway Deficiency Drives Copy Number Variation in Squamous Cell Carcinomas		2
15	The longitudinal dynamics and natural history of clonal haematopoiesis		2
14	Clonal dynamics of haematopoiesis across the human lifespan		2
13	Clonal diversification and histogenesis of malignant germ cell tumours		1

12	The Genomic Landscape of Myeloproliferative Neoplasms: Somatic Calr Mutations in the Majority of JAK2-Wildtype Patients. *Blood*, **2013**, 122, LBA-2-LBA-2	2.2	1
11	Inherited MUTYH mutations cause elevated somatic mutation rates and distinctive mutational signatures in normal human cells		1
10	Revealing the impact of recurrent and rare structural variants in multiple myeloma		1
9	Whole genome sequencing provides evidence of two biologically and clinically distinct entities of asymptomatic monoclonal gammopathies: progressive versus stable myeloma precursor condition		1
8	Extensive phylogenies of human development reveal variable embryonic patterns		1
7	Framework for quality assessment of whole genome cancer sequences. *Nature Communications*, **2020**, 11, 5040	17.4	1
6	Genome-wide mutational signatures of immunological diversification in normal lymphocytes		1
5	Bayesian networks elucidate complex genomic landscapes in cancer.. *Communications Biology*, **2022**, 5, 306	6.7	1
4	Mutational landscape of normal epithelial cells in Lynch Syndrome patients.. *Nature Communications*, **2022**, 13, 2710	17.4	1
3	Response: essential thrombocythemia: seeing the wood for the trees. *Blood*, **2011**, 118, 1180-1181	2.2	
2	The eternal quest for self-improvement of somatic cells. *Cell Genomics*, **2022**, 2, 100094		
1	C. elegans genome-wide analysis reveals DNA repair pathways that act cooperatively to preserve genome integrity upon ionizing radiation. *PLoS ONE*, **2021**, 16, e0258269	3.7	