Keiran M Raine

List of Publications by Citations

67 papers	32,553 citations	51 h-index	73 g-index
73 ext. papers	39,181 ext. citations	29.1 avg, IF	5.63 L-index

#	Paper	IF	Citations
67	Signatures of mutational processes in human cancer. *Nature*, **2013**, 500, 415-21	50.4	5895
66	Intratumor heterogeneity and branched evolution revealed by multiregion sequencing. *New England Journal of Medicine*, **2012**, 366, 883-892	59.2	5559
65	Patterns of somatic mutation in human cancer genomes. *Nature*, **2007**, 446, 153-8	50.4	2400
64	Genomic Classification and Prognosis in Acute Myeloid Leukemia. *New England Journal of Medicine*, **2016**, 374, 2209-2221	59.2	1999
63	Mutational processes molding the genomes of 21 breast cancers. *Cell*, **2012**, 149, 979-93	56.2	1279
62	The landscape of cancer genes and mutational processes in breast cancer. *Nature*, **2012**, 486, 400-4	50.4	1264
61	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. *Nature* , **2011**, 475, 101-5	50.4	1206
60	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. *Nature*, **2016**, 534, 47-54	50.4	1193
59	Clinical and biological implications of driver mutations in myelodysplastic syndromes. *Blood*, **2013**, 122, 3616-27; quiz 3699	2.2	1169
58	The life history of 21 breast cancers. *Cell*, **2012**, 149, 994-1007	56.2	979
57	Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. *Nature*, **2011**, 469, 539-42	50.4	943
56	Lung cancer: intragenic ERBB2 kinase mutations in tumours. *Nature*, **2004**, 431, 525-6	50.4	655
55	Universal Patterns of Selection in Cancer and Somatic Tissues. *Cell*, **2017**, 171, 1029-1041.e21	56.2	576
54	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. *Nature Medicine*, **2015**, 21, 751-9	50.5	521
53	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. *Nature Medicine*, **2017**, 23, 517-525	50.5	444
52	Somatic mutations of the protein kinase gene family in human lung cancer. *Cancer Research*, **2005**, 65, 7591-5	10.1	392
51	Prediction of acute myeloid leukaemia risk in healthy individuals. *Nature*, **2018**, 559, 400-404	50.4	368

50	Genomic Evolution of Breast Cancer Metastasis and Relapse. *Cancer Cell*, **2017**, 32, 169-184.e7	24.3	346
49	A hypermutation phenotype and somatic MSH6 mutations in recurrent human malignant gliomas after alkylator chemotherapy. *Cancer Research*, **2006**, 66, 3987-91	10.1	328
48	Mutation analysis of 24 known cancer genes in the NCI-60 cell line set. *Molecular Cancer Therapeutics*, **2006**, 5, 2606-12	6.1	322
47	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
46	A screen of the complete protein kinase gene family identifies diverse patterns of somatic mutations in human breast cancer. *Nature Genetics*, **2005**, 37, 590-2	36.3	289
45	Genome sequencing and analysis of the Tasmanian devil and its transmissible cancer. *Cell*, **2012**, 148, 780-91	56.2	251
44	Mobile DNA in cancer. Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. *Science*, **2014**, 345, 1251343	33.3	250
43	DNA deaminases induce break-associated mutation showers with implication of APOBEC3B and 3A in breast cancer kataegis. *ELife*, **2013**, 2, e00534	8.9	246
42	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
41	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. *Cell*, **2018**, 173, 611-623.e17	56.2	228
40	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. *Nature Communications*, **2015**, 6, 10001	17.4	199
39	Mutations in UPF3B, a member of the nonsense-mediated mRNA decay complex, cause syndromic and nonsyndromic mental retardation. *Nature Genetics*, **2007**, 39, 1127-33	36.3	189
38	Whole exome sequencing of adenoid cystic carcinoma. *Journal of Clinical Investigation*, **2013**, 123, 2965-8	15.9	188
37	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. *Cell*, **2019**, 176, 1282-1294.e20	56.2	165
36	Mutations in CUL4B, which encodes a ubiquitin E3 ligase subunit, cause an X-linked mental retardation syndrome associated with aggressive outbursts, seizures, relative macrocephaly, central obesity, hypogonadism, pes cavus, and tremor. *American Journal of Human Genetics*, **2007**, 80, 345-52	11	163
35	Mutational signatures of ionizing radiation in second malignancies. *Nature Communications*, **2016**, 7, 12605	17.4	152
34	Frequent mutation of the major cartilage collagen gene COL2A1 in chondrosarcoma. *Nature Genetics*, **2013**, 45, 923-6	36.3	138
33	Single-cell paired-end genome sequencing reveals structural variation per cell cycle. *Nucleic Acids Research*, **2013**, 41, 6119-38	20.1	125

32	C. elegans whole-genome sequencing reveals mutational signatures related to carcinogens and DNA repair deficiency. *Genome Research*, **2014**, 24, 1624-36	9.7	125
31	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
30	Mutations in ZDHHC9, which encodes a palmitoyltransferase of NRAS and HRAS, cause X-linked mental retardation associated with a Marfanoid habitus. *American Journal of Human Genetics*, **2007**, 80, 982-7	11	120
29	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. *Nature Genetics*, **2018**, 50, 682-692	36.3	112
28	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
27	Mutations in the gene encoding the Sigma 2 subunit of the adaptor protein 1 complex, AP1S2, cause X-linked mental retardation. *American Journal of Human Genetics*, **2006**, 79, 1119-24	11	92
26	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. *Leukemia*, **2018**, 32, 2604-2616	10.7	90
25	Sequence analysis of the protein kinase gene family in human testicular germ-cell tumors of adolescents and adults. *Genes Chromosomes and Cancer*, **2006**, 45, 42-6	5	88
24	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
23	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. *Journal of Pathology*, **2012**, 227, 446-55	9.4	72
22	Processed pseudogenes acquired somatically during cancer development. *Nature Communications*, **2014**, 5, 3644	17.4	68
21	Extensive heterogeneity in somatic mutation and selection in the human bladder. *Science*, **2020**, 370, 75-82	33.3	67
20	Mutations in the BRWD3 gene cause X-linked mental retardation associated with macrocephaly. *American Journal of Human Genetics*, **2007**, 81, 367-74	11	66
19	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
18	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
17	The genetic heterogeneity and mutational burden of engineered melanomas in zebrafish models. *Genome Biology*, **2013**, 14, R113	18.3	33
16	Aging as accelerated accumulation of somatic variants: whole-genome sequencing of centenarian and middle-aged monozygotic twin pairs. *Twin Research and Human Genetics*, **2013**, 16, 1026-32	2.2	30
15	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. *Cell Reports*, **2016**, 16, 2032-**46**.6		30

14	Appraising the relevance of DNA copy number loss and gain in prostate cancer using whole genome DNA sequence data. *PLoS Genetics*, **2017**, 13, e1007001	6	20
13	Large-Scale Uniform Analysis of Cancer Whole Genomes in Multiple Computing Environments		14
12	Convergent somatic mutations in metabolism genes in chronic liver disease. *Nature*, **2021**, 598, 473-478	50.4	10
11	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10
10	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nature Communications*, **2020**, 11, 4748	17.4	10
9	Butler enables rapid cloud-based analysis of thousands of human genomes. *Nature Biotechnology*, **2020**, 38, 288-292	44.5	9
8	Split-Read Indel and Structural Variant Calling Using PINDEL. *Methods in Molecular Biology*, **2018**, 1833, 95-105	1.4	8
7	The Life History of 21 Breast Cancers. *Cell*, **2015**, 162, 924	56.2	7
6	Universal patterns of selection in cancer and somatic tissues		7
5	Aberrant integration of Hepatitis B virus DNA promotes major restructuring of human hepatocellular carcinoma genome architecture. *Nature Communications*, **2021**, 12, 6910	17.4	6
4	Framework for quality assessment of whole genome, cancer sequences		6
3	Polygenic in vivo validation of cancer mutations using transposons. *Genome Biology*, **2014**, 15, 455	18.3	3
2	Author response: DNA deaminases induce break-associated mutation showers with implication of APOBEC3B and 3A in breast cancer kataegis **2013**,		2
1	Framework for quality assessment of whole genome cancer sequences. *Nature Communications*, **2020**, 11, 5040	17.4	1