Keiran M Raine

List of Publications by Year
in descending order

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61 papers	43,311 citations	34105 52 h-index	98798 67 g-index
73 all docs	73 docs citations	73 times ranked	54481 citing authors

#	Article	IF	Citations
1	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
2	Intratumor Heterogeneity and Branched Evolution Revealed by Multiregion Sequencing. New England Journal of Medicine, 2012, 366, 883-892.	27.0	6,769
3	Genomic Classification and Prognosis in Acute Myeloid Leukemia. New England Journal of Medicine, 2016, 374, 2209-2221.	27.0	3,067
4	Patterns of somatic mutation in human cancer genomes. Nature, 2007, 446, 153-158.	27.8	2,802
5	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	27.8	1,760
6	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	28.9	1,673
7	Clinical and biological implications of driver mutations in myelodysplastic syndromes. Blood, 2013, 122, 3616-3627.	1.4	1,562
8	The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.	27.8	1,535
9	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. Nature, 2011, 475, 101-105.	27.8	1,364
10	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	28.9	1,249
11	Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. Nature, 2011, 469, 539-542.	27.8	1,127
12	Universal Patterns of Selection in Cancer and Somatic Tissues. Cell, 2017, 171, 1029-1041.e21.	28.9	1,085
13	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. Nature Medicine, 2017, 23, 517-525.	30.7	769
14	Intragenic ERBB2 kinase mutations in tumours. Nature, 2004, 431, 525-526.	27.8	757
15	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. Nature Medicine, 2015, 21, 751-759.	30.7	711
16	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	27.8	617
17	Genomic Evolution of Breast Cancer Metastasis and Relapse. Cancer Cell, 2017, 32, 169-184.e7.	16.8	534
18	Somatic Mutations of the Protein Kinase Gene Family in Human Lung Cancer. Cancer Research, 2005, 65, 7591-7595.	0.9	429

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19	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. Cell, 2018, 173, 611-623.e17.	28.9	398
20	A Hypermutation Phenotype and Somatic MSH6 Mutations in Recurrent Human Malignant Gliomas after Alkylator Chemotherapy. Cancer Research, 2006, 66, 3987-3991.	0.9	383
21	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
22	Mutation analysis of 24 known cancer genes in the NCI-60 cell line set. Molecular Cancer Therapeutics, 2006, 5, 2606-2612.	4.1	374
23	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	12.6	348
24	DNA deaminases induce break-associated mutation showers with implication of APOBEC3B and 3A in breast cancer kataegis. ELife, 2013, 2, e00534.	6.0	322
25	A screen of the complete protein kinase gene family identifies diverse patterns of somatic mutations in human breast cancer. Nature Genetics, 2005, 37, 590-592.	21.4	318
26	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
27	Genome Sequencing and Analysis of the Tasmanian Devil and Its Transmissible Cancer. Cell, 2012, 148, 780-791.	28.9	300
28	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. Cell, 2019, 176, 1282-1294.e20.	28.9	298
29	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
30	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
31	Whole exome sequencing of adenoid cystic carcinoma. Journal of Clinical Investigation, 2013, 123, 2965-2968.	8.2	233
32	Mutations in UPF3B, a member of the nonsense-mediated mRNA decay complex, cause syndromic and nonsyndromic mental retardation. Nature Genetics, 2007, 39, 1127-1133.	21.4	228
33	Mutational signatures of ionizing radiation in second malignancies. Nature Communications, 2016, 7, 12605.	12.8	214
34	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, 345-352.	6.2	197
35	Extensive heterogeneity in somatic mutation and selection in the human bladder. Science, 2020, 370, 75-82.	12.6	195
36	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. Nature Genetics, 2018, 50, 682-692.	21.4	182

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37	Frequent mutation of the major cartilage collagen gene COL2A1 in chondrosarcoma. Nature Genetics, 2013, 45, 923-926.	21.4	180
38	C. elegans whole-genome sequencing reveals mutational signatures related to carcinogens and DNA repair deficiency. Genome Research, 2014, 24, 1624-1636.	5.5	164
39	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
40	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, 982-987.	6.2	150
41	Single-cell paired-end genome sequencing reveals structural variation per cell cycle. Nucleic Acids Research, 2013, 41, 6119-6138.	14.5	142
42	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. Leukemia, 2018, 32, 2604-2616.	7.2	137
43	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
44	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
45	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, 1119-1124.	6.2	102
46	Sequence analysis of the protein kinase gene family in human testicular germâ€cell tumors of adolescents and adults. Genes Chromosomes and Cancer, 2006, 45, 42-46.	2.8	96
47	Convergent somatic mutations in metabolism genes in chronic liver disease. Nature, 2021, 598, 473-478.	27.8	87
48	Processed pseudogenes acquired somatically during cancer development. Nature Communications, 2014, 5, 3644.	12.8	86
49	Mutations in the BRWD3 Gene Cause X-Linked Mental Retardation Associated with Macrocephaly. American Journal of Human Genetics, 2007, 81, 367-374.	6.2	85
50	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. Journal of Pathology, 2012, 227, 446-455.	4.5	81
51	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
52	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, 1026-1032.	0.6	40
53	The genetic heterogeneity and mutational burden of engineered melanomas in zebrafish models. Genome Biology, 2013, 14, R113.	9.6	40
54	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. Cell Reports, 2016, 16, 2032-2046.	6.4	36

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55	Appraising the relevance of DNA copy number loss and gain in prostate cancer using whole genome DNA sequence data. PLoS Genetics, 2017, 13, e1007001.	3.5	34
56	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	12.8	27
57	Aberrant integration of Hepatitis B virus DNA promotes major restructuring of human hepatocellular carcinoma genome architecture. Nature Communications, 2021, 12, 6910.	12.8	27
58	Split-Read Indel and Structural Variant Calling Using PINDEL. Methods in Molecular Biology, 2018, 1833, 95-105.	0.9	20
59	Butler enables rapid cloud-based analysis of thousands of human genomes. Nature Biotechnology, 2020, 38, 288-292.	17.5	11
60	Framework for quality assessment of whole genome cancer sequences. Nature Communications, 2020, 11, 5040.	12.8	5
61	Polygenic in vivovalidation of cancer mutations using transposons. Genome Biology, 2014, 15, 455.	8.8	3