

Benjamin Raeder

List of Publications by Citations

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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.

13
papers

3,833
citations

11
h-index

14
g-index

14
ext. papers

4,868
ext. citations

32.7
avg, IF

3.3
L-index

#	Paper	IF	Citations
13	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015 , 526, 75-81	50.4	1368
12	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , 2012 , 488, 100-5	50.4	623
11	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. <i>Nature Genetics</i> , 2013 , 45, 927-32	36.3	550
10	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. <i>Nature</i> , 2014 , 511, 428-34	50.4	377
9	Integrative genomic analyses reveal an androgen-driven somatic alteration landscape in early-onset prostate cancer. <i>Cancer Cell</i> , 2013 , 23, 159-70	24.3	259
8	Pan-cancer analysis of somatic copy-number alterations implicates IRS4 and IGF2 in enhancer hijacking. <i>Nature Genetics</i> , 2017 , 49, 65-74	36.3	220
7	Genomics and drug profiling of fatal TCF3-HLF-positive acute lymphoblastic leukemia identifies recurrent mutation patterns and therapeutic options. <i>Nature Genetics</i> , 2015 , 47, 1020-1029	36.3	127
6	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. <i>Science</i> , 2021 , 372,	33.3	100
5	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. <i>Cancer Cell</i> , 2018 , 34, 996-1011.e8	24.3	89
4	A cell-based model system links chromothripsis with hyperploidy. <i>Molecular Systems Biology</i> , 2015 , 11, 828	12.2	88
3	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. <i>Nature Biotechnology</i> , 2020 , 38, 343-354	44.5	17
2	Genome-wide Screens Implicate Loss of Cullin Ring Ligase 3 in Persistent Proliferation and Genome Instability in TP53-Deficient Cells. <i>Cell Reports</i> , 2020 , 31, 107465	10.6	11
1	De novo assembly of 64 haplotype-resolved human genomes of diverse ancestry and integrated analysis of structural variation		3