

# Benjamin Raeder

## 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.

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