Thomas Zichner

List of Publications by Year
in descending order

27 papers	9,223 citations	331670 21 h-index	526287 27 g-index
29 all docs	29 docs citations	29 times ranked	17265 citing authors

#	Article	IF	Citations
1	DELLY: structural variant discovery by integrated paired-end and split-read analysis. Bioinformatics, 2012, 28, i333-i339.	4.1	1,785
2	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
3	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	27.8	765
4	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	27.8	761
5	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. Cell, 2012, 148, 59-71.	28.9	743
6	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. Nature Genetics, 2013, 45, 927-932.	21.4	674
7	Natural variation in genome architecture among 205 *Drosophila melanogaster* Genetic Reference Panel lines. Genome Research, 2014, 24, 1193-1208.	5.5	565
8	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. Nature, 2014, 506, 445-450.	27.8	521
9	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. Nature, 2014, 511, 428-434.	27.8	520
10	The Genomic and Transcriptomic Landscape of a HeLa Cell Line. G3: Genes, Genomes, Genetics, 2013, 3, 1213-1224.	1.8	355
11	Pan-cancer analysis of somatic copy-number alterations implicates IRS4 and IGF2 in enhancer hijacking. Nature Genetics, 2017, 49, 65-74.	21.4	326
12	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. Cancer Cell, 2013, 23, 159-170.	16.8	292
13	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. Lancet Oncology, The, 2018, 19, 785-798.	10.7	268
14	Shadow Enhancers Are Pervasive Features of Developmental Regulatory Networks. Current Biology, 2016, 26, 38-51.	3.9	212
15	Genomics and drug profiling of fatal TCF3-HLFâˆ'positive acute lymphoblastic leukemia identifies recurrent mutation patterns and therapeutic options. Nature Genetics, 2015, 47, 1020-1029.	21.4	190
16	Identifying the Unknowns by Aligning Fragmentation Trees. Analytical Chemistry, 2012, 84, 3417-3426.	6.5	104
17	Impact of genomic structural variation in *Drosophila melanogaster* based on population-scale sequencing. Genome Research, 2013, 23, 568-579.	5.5	72
18	PD-1 and LAG-3 Dominate Checkpoint Receptorâ€"Mediated T-cell Inhibition in Renal Cell Carcinoma. Cancer Immunology Research, 2019, 7, 1891-1899.	3.4	66

#	Article	IF	Citations
19	Algorithm Engineering for Color-Coding with Applications to Signaling Pathway Detection. Algorithmica, 2008, 52, 114-132.	1.3	58
20	Systematic Inference of Copy-Number Genotypes from Personal Genome Sequencing Data Reveals Extensive Olfactory Receptor Gene Content Diversity. PLoS Computational Biology, 2010, 6, e1000988.	3.2	56
21	SMARCA2-deficiency confers sensitivity to targeted inhibition of SMARCA4 in esophageal squamous cell carcinoma cell lines. Scientific Reports, 2019, 9, 11661.	3.3	25
22	Taggle: Combining overview and details in tabular data visualizations. Information Visualization, 2020, 19, 114-136.	1.9	25
23	SPAG7 is a candidate gene for the periodic fever, aphthous stomatitis, pharyngitis and adenopathy (PFAPA) syndrome. Genes and Immunity, 2014, 15, 190-194.	4.1	18
24	Faspad: fast signaling pathway detection. Bioinformatics, 2007, 23, 1708-1709.	4.1	16
25	Ordino: a visual cancer analysis tool for ranking and exploring genes, cell lines and tissue samples. Bioinformatics, 2019, 35, 3140-3142.	4.1	13
26	Coral: a web-based visual analysis tool for creating and characterizing cohorts. Bioinformatics, 2021, 37, 4559-4561.	4.1	3
27	ICGC PedBrain - dissecting the genomic complexity underlying medulloblastoma using whole-genome sequencing. BMC Proceedings, 2012, 6, .	1.6	1