

Simone Zaccaria

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.

20
papers

222
citations

10
h-index

14
g-index

25
ext. papers

384
ext. citations

7.5
avg, IF

4.17
L-index

#	Paper	IF	Citations
20	Parsimonious Clone Tree Integration in cancer.. <i>Algorithms for Molecular Biology</i> , 2022 , 17, 3	1.8	0
19	Characterizing allele- and haplotype-specific copy numbers in single cells with CHISEL. <i>Nature Biotechnology</i> , 2021 , 39, 207-214	44.5	24
18	Comprehensive characterization of 536 patient-derived xenograft models prioritizes candidates for targeted treatment. <i>Nature Communications</i> , 2021 , 12, 5086	17.4	6
17	DeCiFering the elusive cancer cell fraction in tumor heterogeneity and evolution. <i>Cell Systems</i> , 2021 , 12, 1004-1018.e10	10.6	3
16	SCARLET: Single-cell tumor phylogeny inference with copy-number constrained mutation losses. <i>Cell Systems</i> , 2020 , 10, 323-332.e8	10.6	21
15	Identifying tumor clones in sparse single-cell mutation data. <i>Bioinformatics</i> , 2020 , 36, i186-i193	7.2	5
14	Accurate quantification of copy-number aberrations and whole-genome duplications in multi-sample tumor sequencing data. <i>Nature Communications</i> , 2020 , 11, 4301	17.4	21
13	Phylogenetic Copy-Number Factorization of Multiple Tumor Samples. <i>Journal of Computational Biology</i> , 2018 , 25, 689-708	1.7	17
12	HapCHAT: adaptive haplotype assembly for efficiently leveraging high coverage in long reads. <i>BMC Bioinformatics</i> , 2018 , 19, 252	3.6	3
11	The Copy-Number Tree Mixture Deconvolution Problem and Applications to Multi-sample Bulk Sequencing Tumor Data. <i>Lecture Notes in Computer Science</i> , 2017 , 318-335	0.9	8
10	Complexity and algorithms for copy-number evolution problems. <i>Algorithms for Molecular Biology</i> , 2017 , 12, 13	1.8	19
9	On the Minimum Error Correction Problem for Haplotype Assembly in Diploid and Polyploid Genomes. <i>Journal of Computational Biology</i> , 2016 , 23, 718-36	1.7	17
8	HapCol: accurate and memory-efficient haplotype assembly from long reads. <i>Bioinformatics</i> , 2016 , 32, 1610-7	7.2	30
7	Copy-Number Evolution Problems: Complexity and Algorithms. <i>Lecture Notes in Computer Science</i> , 2016 , 137-149	0.9	12
6	On the Fixed Parameter Tractability and Approximability of the Minimum Error Correction Problem. <i>Lecture Notes in Computer Science</i> , 2015 , 100-113	0.9	6
5	On the inversion-indel distance. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 15, S3	3.6	12
4	Accurate quantification of copy-number aberrations and whole-genome duplications in multi-sample tumor sequencing data		10

3	Characterizing the allele- and haplotype-specific copy number landscape of cancer genomes at single-cell resolution with CHISEL	5
2	Single-cell tumor phylogeny inference with copy-number constrained mutation losses	1
1	DeCiFering the Elusive Cancer Cell Fraction in Tumor Heterogeneity and Evolution	1