Simone Zaccaria

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.

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

List of Publications

3	Single-cell tumor phylogeny inference with copy-number constrained mutation losses		1
2	DeCiFering the Elusive Cancer Cell Fraction in Tumor Heterogeneity and Evolution		1
1	Parsimonious Clone Tree Integration in cancer.. *Algorithms for Molecular Biology*, **2022**, 17, 3	1.8	0