

Layla Oesper

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/502493/publications.pdf>

Version: 2024-02-01

14
papers

856
citations

1307594

7
h-index

1372567

10
g-index

14
all docs

14
docs citations

14
times ranked

1413
citing authors

#	ARTICLE	IF	CITATIONS
1	Reconstruction of clonal trees and tumor composition from multi-sample sequencing data. <i>Bioinformatics</i> , 2015, 31, i62-i70.	4.1	194
2	Identifying driver mutations in sequenced cancer genomes: computational approaches to enable precision medicine. <i>Genome Medicine</i> , 2014, 6, 5.	8.2	186
3	Inferring the Mutational History of a Tumor Using Multi-state Perfect Phylogeny Mixtures. <i>Cell Systems</i> , 2016, 3, 43-53.	6.2	140
4	WordCloud: a Cytoscape plugin to create a visual semantic summary of networks. <i>Source Code for Biology and Medicine</i> , 2011, 6, 7.	1.7	120
5	Quantifying tumor heterogeneity in whole-genome and whole-exome sequencing data. <i>Bioinformatics</i> , 2014, 30, 3532-3540.	4.1	115
6	Reconstructing cancer genomes from paired-end sequencing data. <i>BMC Bioinformatics</i> , 2012, 13, S10.	2.6	36
7	Distance measures for tumor evolutionary trees. <i>Bioinformatics</i> , 2020, 36, 2090-2097.	4.1	26
8	A Consensus Approach to Infer Tumor Evolutionary Histories. , 2018, , .		24
9	GraPhyC: Using Consensus to Infer Tumor Evolution. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 465-478.	3.0	5
10	Identifying simultaneous rearrangements in cancer genomes. <i>Bioinformatics</i> , 2018, 34, 346-352.	4.1	4
11	Examining Tumor Phylogeny Inference in Noisy Sequencing Data. , 2018, , .		2
12	Parameter, noise, and tree topology effects in tumor phylogeny inference. <i>BMC Medical Genomics</i> , 2019, 12, 184.	1.5	2
13	Emerging Topics in Cancer Evolution. , 2021, , .		2
14	Workshop: Reconstructing the organization of cancer genomes. , 2013, , .		0