

Mohammed El-Kebir

List of Publications by Year in descending order

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46
papers

1,491
citations

567281

15
h-index

377865

34
g-index

63
all docs

63
docs citations

63
times ranked

2113
citing authors

#	ARTICLE	IF	CITATIONS
1	Emerging Topics in Cancer Evolution. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2022, 27, 397-401.	0.7	0
2	Parsimonious Clone Tree Integration in cancer. Algorithms for Molecular Biology, 2022, 17, 3.	1.2	6
3	Design of SARS-CoV-2 Variant-Specific PCR Assays Considering Regional and Temporal Characteristics. Applied and Environmental Microbiology, 2022, 88, e0228921.	3.1	12
4	Moss enables high sensitivity single-nucleotide variant calling from multiple bulk DNA tumor samples. Nature Communications, 2021, 12, 2204.	12.8	1
5	Transcriptional Profiling of Porcine HCC Xenografts Provides Insights Into Tumor Cell Microenvironment Signaling. Frontiers in Genetics, 2021, 12, 657330.	2.3	3
6	Distinguishing linear and branched evolution given single-cell DNA sequencing data of tumors. Algorithms for Molecular Biology, 2021, 16, 14.	1.2	6
7	doubletD: detecting doublets in single-cell DNA sequencing data. Bioinformatics, 2021, 37, i214-i221.	4.1	13
8	DeCiFering the elusive cancer cell fraction in tumor heterogeneity and evolution. Cell Systems, 2021, 12, 1004-1018.e10.	6.2	12
9	Jumper enables discontinuous transcript assembly in coronaviruses. Nature Communications, 2021, 12, 6728.	12.8	4
10	Emerging Topics in Cancer Evolution. , 2021, , .		2
11	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. PLoS Computational Biology, 2020, 16, e1008240.	3.2	1
12	Sampling and summarizing transmission trees with multi-strain infections. Bioinformatics, 2020, 36, i362-i370.	4.1	3
13	ClonArch: visualizing the spatial clonal architecture of tumors. Bioinformatics, 2020, 36, i161-i168.	4.1	2
14	Detecting evolutionary patterns of cancers using consensus trees. Bioinformatics, 2020, 36, i684-i691.	4.1	10
15	PhySigs: Phylogenetic Inference of Mutational Signature Dynamics. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2020, 25, 226-237.	0.7	3
16	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0
17	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0
18	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0

#	ARTICLE	IF	CITATIONS
19	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0
20	Summarizing the solution space in tumor phylogeny inference by multiple consensus trees. Bioinformatics, 2019, 35, i408-i416.	4.1	24
21	Implications of non-uniqueness in phylogenetic deconvolution of bulk DNA samples of tumors. Algorithms for Molecular Biology, 2019, 14, 19.	1.2	13
22	Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089.	6.5	207
23	Phylogenetic Copy-Number Factorization of Multiple Tumor Samples. Journal of Computational Biology, 2018, 25, 689-708.	1.6	28
24	Inferring parsimonious migration histories for metastatic cancers. Nature Genetics, 2018, 50, 718-726.	21.4	93
25	SPhyR: tumor phylogeny estimation from single-cell sequencing data under loss and error. Bioinformatics, 2018, 34, i671-i679.	4.1	99
26	On the Non-uniqueness of Solutions to the Perfect Phylogeny Mixture Problem. Lecture Notes in Computer Science, 2018, , 277-293.	1.3	9
27	eXamine: Visualizing annotated networks in Cytoscape. F1000Research, 2018, 7, 519.	1.6	3
28	eXamine: Visualizing annotated networks in Cytoscape. F1000Research, 2018, 7, 519.	1.6	2
29	Complexity and algorithms for copy-number evolution problems. Algorithms for Molecular Biology, 2017, 12, 13.	1.2	27
30	Copy-Number Evolution Problems: Complexity and Algorithms. Lecture Notes in Computer Science, 2016, , 137-149.	1.3	17
31	Inferring the Mutational History of a Tumor Using Multi-state Perfect Phylogeny Mixtures. Cell Systems, 2016, 3, 43-53.	6.2	140
32	metaModules identifies key functional subnetworks in microbiome-related disease. Bioinformatics, 2016, 32, 1678-1685.	4.1	21
33	Natalie 2.0: Sparse Global Network Alignment as a Special Case of Quadratic Assignment. Algorithms, 2015, 8, 1035-1051.	2.1	21
34	xHeinz: an algorithm for mining cross-species network modules under a flexible conservation model. Bioinformatics, 2015, 31, 3147-3155.	4.1	4
35	Reconstruction of clonal trees and tumor composition from multi-sample sequencing data. Bioinformatics, 2015, 31, i62-i70.	4.1	194
36	eXamine: Exploring annotated modules in networks. BMC Bioinformatics, 2014, 15, 201.	2.6	16

#	ARTICLE	IF	CITATIONS
37	NatalieQ: A web server for protein-protein interaction network querying. BMC Systems Biology, 2014, 8, 40.	3.0	6
38	Computational modeling of tuberculous meningitis reveals an important role for tumor necrosis. Journal of Theoretical Biology, 2013, 328, 43-53.	1.7	8
39	Mapping proteins in the presence of paralogs using units of coevolution. BMC Bioinformatics, 2013, 14, S18.	2.6	4
40	Charge Group Partitioning in Biomolecular Simulation. Journal of Computational Biology, 2013, 20, 188-198.	1.6	145
41	Charge Group Partitioning in Biomolecular Simulation. Lecture Notes in Computer Science, 2012, , 29-43.	1.3	7
42	A hybrid multi-compartment model of granuloma formation and T cell priming in Tuberculosis. Journal of Theoretical Biology, 2011, 280, 50-62.	1.7	81
43	Multiscale Computational Modeling Reveals a Critical Role for TNF-Î± Receptor 1 Dynamics in Tuberculosis Granuloma Formation. Journal of Immunology, 2011, 186, 3472-3483.	0.8	158
44	A Mathematical Programming Approach to Marker-Assisted Gene Pyramiding. Lecture Notes in Computer Science, 2011, , 26-38.	1.3	6
45	Lagrangian Relaxation Applied to Sparse Global Network Alignment. Lecture Notes in Computer Science, 2011, , 225-236.	1.3	29
46	Accurate Identification of Transcription Regulatory Sequences and Genes in Coronaviruses. Molecular Biology and Evolution, 0, , .	8.9	2