

# Mohammed El-Kebir

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3098320/publications.pdf>

Version: 2024-02-01

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	Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089.	6.5	207
2	Reconstruction of clonal trees and tumor composition from multi-sample sequencing data. Bioinformatics, 2015, 31, i62-i70.	4.1	194
3	Multiscale Computational Modeling Reveals a Critical Role for TNF- $\alpha$ Receptor 1 Dynamics in Tuberculosis Granuloma Formation. Journal of Immunology, 2011, 186, 3472-3483.	0.8	158
4	Charge Group Partitioning in Biomolecular Simulation. Journal of Computational Biology, 2013, 20, 188-198.	1.6	145
5	Inferring the Mutational History of a Tumor Using Multi-state Perfect Phylogeny Mixtures. Cell Systems, 2016, 3, 43-53.	6.2	140
6	SPhyR: tumor phylogeny estimation from single-cell sequencing data under loss and error. Bioinformatics, 2018, 34, i671-i679.	4.1	99
7	Inferring parsimonious migration histories for metastatic cancers. Nature Genetics, 2018, 50, 718-726.	21.4	93
8	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
9	Lagrangian Relaxation Applied to Sparse Global Network Alignment. Lecture Notes in Computer Science, 2011, , 225-236.	1.3	29
10	Phylogenetic Copy-Number Factorization of Multiple Tumor Samples. Journal of Computational Biology, 2018, 25, 689-708.	1.6	28
11	Complexity and algorithms for copy-number evolution problems. Algorithms for Molecular Biology, 2017, 12, 13.	1.2	27
12	Summarizing the solution space in tumor phylogeny inference by multiple consensus trees. Bioinformatics, 2019, 35, i408-i416.	4.1	24
13	Natalie 2.0: Sparse Global Network Alignment as a Special Case of Quadratic Assignment. Algorithms, 2015, 8, 1035-1051.	2.1	21
14	metaModules identifies key functional subnetworks in microbiome-related disease. Bioinformatics, 2016, 32, 1678-1685.	4.1	21
15	Copy-Number Evolution Problems: Complexity and Algorithms. Lecture Notes in Computer Science, 2016, , 137-149.	1.3	17
16	eXamine: Exploring annotated modules in networks. BMC Bioinformatics, 2014, 15, 201.	2.6	16
17	Implications of non-uniqueness in phylogenetic deconvolution of bulk DNA samples of tumors. Algorithms for Molecular Biology, 2019, 14, 19.	1.2	13
18	doubletD: detecting doublets in single-cell DNA sequencing data. Bioinformatics, 2021, 37, i214-i221.	4.1	13

#	ARTICLE	IF	CITATIONS
19	DeCiFering the elusive cancer cell fraction in tumor heterogeneity and evolution. <i>Cell Systems</i> , 2021, 12, 1004-1018.e10.	6.2	12
20	Design of SARS-CoV-2 Variant-Specific PCR Assays Considering Regional and Temporal Characteristics. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0228921.	3.1	12
21	Detecting evolutionary patterns of cancers using consensus trees. <i>Bioinformatics</i> , 2020, 36, i684-i691.	4.1	10
22	On the Non-uniqueness of Solutions to the Perfect Phylogeny Mixture Problem. <i>Lecture Notes in Computer Science</i> , 2018, , 277-293.	1.3	9
23	Computational modeling of tuberculous meningitis reveals an important role for tumor necrosis. <i>Journal of Theoretical Biology</i> , 2013, 328, 43-53.	1.7	8
24	Charge Group Partitioning in Biomolecular Simulation. <i>Lecture Notes in Computer Science</i> , 2012, , 29-43.	1.3	7
25	NatalieQ: A web server for protein-protein interaction network querying. <i>BMC Systems Biology</i> , 2014, 8, 40.	3.0	6
26	Distinguishing linear and branched evolution given single-cell DNA sequencing data of tumors. <i>Algorithms for Molecular Biology</i> , 2021, 16, 14.	1.2	6
27	A Mathematical Programming Approach to Marker-Assisted Gene Pyramiding. <i>Lecture Notes in Computer Science</i> , 2011, , 26-38.	1.3	6
28	Parsimonious Clone Tree Integration in cancer. <i>Algorithms for Molecular Biology</i> , 2022, 17, 3.	1.2	6
29	Mapping proteins in the presence of paralogs using units of coevolution. <i>BMC Bioinformatics</i> , 2013, 14, S18.	2.6	4
30	xHeinz: an algorithm for mining cross-species network modules under a flexible conservation model. <i>Bioinformatics</i> , 2015, 31, 3147-3155.	4.1	4
31	Jumper enables discontinuous transcript assembly in coronaviruses. <i>Nature Communications</i> , 2021, 12, 6728.	12.8	4
32	Sampling and summarizing transmission trees with multi-strain infections. <i>Bioinformatics</i> , 2020, 36, i362-i370.	4.1	3
33	Transcriptional Profiling of Porcine HCC Xenografts Provides Insights Into Tumor Cell Microenvironment Signaling. <i>Frontiers in Genetics</i> , 2021, 12, 657330.	2.3	3
34	eXamine: Visualizing annotated networks in Cytoscape. <i>F1000Research</i> , 2018, 7, 519.	1.6	3
35	PhySigs: Phylogenetic Inference of Mutational Signature Dynamics. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2020, 25, 226-237.	0.7	3
36	ClonArch: visualizing the spatial clonal architecture of tumors. <i>Bioinformatics</i> , 2020, 36, i161-i168.	4.1	2

#	ARTICLE	IF	CITATIONS
37	eXamine: Visualizing annotated networks in Cytoscape. F1000Research, 2018, 7, 519.	1.6	2
38	Emerging Topics in Cancer Evolution. , 2021, , .		2
39	Accurate Identification of Transcription Regulatory Sequences and Genes in Coronaviruses. Molecular Biology and Evolution, 0, , .	8.9	2
40	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. PLoS Computational Biology, 2020, 16, e1008240.	3.2	1
41	Moss enables high sensitivity single-nucleotide variant calling from multiple bulk DNA tumor samples. Nature Communications, 2021, 12, 2204.	12.8	1
42	Emerging Topics in Cancer Evolution. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2022, 27, 397-401.	0.7	0
43	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0
44	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0
45	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0
46	PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. , 2020, 16, e1008240.		0