

Mohammed El-Kebir

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

1,491
citations

566801

15
h-index

377514

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. | 3.2 | 207 |
| 2 | Reconstruction of clonal trees and tumor composition from multi-sample sequencing data. Bioinformatics, 2015, 31, i62-i70. | 1.8 | 194 |
| 3 | Multiscale Computational Modeling Reveals a Critical Role for TNF- α Receptor 1 Dynamics in Tuberculosis Granuloma Formation. Journal of Immunology, 2011, 186, 3472-3483. | 0.4 | 158 |
| 4 | Charge Group Partitioning in Biomolecular Simulation. Journal of Computational Biology, 2013, 20, 188-198. | 0.8 | 145 |
| 5 | Inferring the Mutational History of a Tumor Using Multi-state Perfect Phylogeny Mixtures. Cell Systems, 2016, 3, 43-53. | 2.9 | 140 |
| 6 | SPhyR: tumor phylogeny estimation from single-cell sequencing data under loss and error. Bioinformatics, 2018, 34, i671-i679. | 1.8 | 99 |
| 7 | Inferring parsimonious migration histories for metastatic cancers. Nature Genetics, 2018, 50, 718-726. | 9.4 | 93 |
| 8 | A hybrid multi-compartment model of granuloma formation and T cell priming in Tuberculosis. Journal of Theoretical Biology, 2011, 280, 50-62. | 0.8 | 81 |
| 9 | Lagrangian Relaxation Applied to Sparse Global Network Alignment. Lecture Notes in Computer Science, 2011, , 225-236. | 1.0 | 29 |
| 10 | Phylogenetic Copy-Number Factorization of Multiple Tumor Samples. Journal of Computational Biology, 2018, 25, 689-708. | 0.8 | 28 |
| 11 | Complexity and algorithms for copy-number evolution problems. Algorithms for Molecular Biology, 2017, 12, 13. | 0.3 | 27 |
| 12 | Summarizing the solution space in tumor phylogeny inference by multiple consensus trees. Bioinformatics, 2019, 35, i408-i416. | 1.8 | 24 |
| 13 | Natalie 2.0: Sparse Global Network Alignment as a Special Case of Quadratic Assignment. Algorithms, 2015, 8, 1035-1051. | 1.2 | 21 |
| 14 | metaModules identifies key functional subnetworks in microbiome-related disease. Bioinformatics, 2016, 32, 1678-1685. | 1.8 | 21 |
| 15 | Copy-Number Evolution Problems: Complexity and Algorithms. Lecture Notes in Computer Science, 2016, , 137-149. | 1.0 | 17 |
| 16 | eXamine: Exploring annotated modules in networks. BMC Bioinformatics, 2014, 15, 201. | 1.2 | 16 |
| 17 | Implications of non-uniqueness in phylogenetic deconvolution of bulk DNA samples of tumors. Algorithms for Molecular Biology, 2019, 14, 19. | 0.3 | 13 |
| 18 | doubletD: detecting doublets in single-cell DNA sequencing data. Bioinformatics, 2021, 37, i214-i221. | 1.8 | 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. | 2.9 | 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. | 1.4 | 12 |
| 21 | Detecting evolutionary patterns of cancers using consensus trees. <i>Bioinformatics</i> , 2020, 36, i684-i691. | 1.8 | 10 |
| 22 | On the Non-uniqueness of Solutions to the Perfect Phylogeny Mixture Problem. <i>Lecture Notes in Computer Science</i> , 2018, , 277-293. | 1.0 | 9 |
| 23 | Computational modeling of tuberculous meningitis reveals an important role for tumor necrosis. <i>Journal of Theoretical Biology</i> , 2013, 328, 43-53. | 0.8 | 8 |
| 24 | Charge Group Partitioning in Biomolecular Simulation. <i>Lecture Notes in Computer Science</i> , 2012, , 29-43. | 1.0 | 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. | 0.3 | 6 |
| 27 | A Mathematical Programming Approach to Marker-Assisted Gene Pyramiding. <i>Lecture Notes in Computer Science</i> , 2011, , 26-38. | 1.0 | 6 |
| 28 | Parsimonious Clone Tree Integration in cancer. <i>Algorithms for Molecular Biology</i> , 2022, 17, 3. | 0.3 | 6 |
| 29 | Mapping proteins in the presence of paralogs using units of coevolution. <i>BMC Bioinformatics</i> , 2013, 14, S18. | 1.2 | 4 |
| 30 | xHeinz: an algorithm for mining cross-species network modules under a flexible conservation model. <i>Bioinformatics</i> , 2015, 31, 3147-3155. | 1.8 | 4 |
| 31 | Jumper enables discontinuous transcript assembly in coronaviruses. <i>Nature Communications</i> , 2021, 12, 6728. | 5.8 | 4 |
| 32 | Sampling and summarizing transmission trees with multi-strain infections. <i>Bioinformatics</i> , 2020, 36, i362-i370. | 1.8 | 3 |
| 33 | Transcriptional Profiling of Porcine HCC Xenografts Provides Insights Into Tumor Cell Microenvironment Signaling. <i>Frontiers in Genetics</i> , 2021, 12, 657330. | 1.1 | 3 |
| 34 | eXamine: Visualizing annotated networks in Cytoscape. <i>F1000Research</i> , 2018, 7, 519. | 0.8 | 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. | 1.8 | 2 |

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|----|--|-----|-----------|
| 37 | eXamine: Visualizing annotated networks in Cytoscape. F1000Research, 2018, 7, 519. | 0.8 | 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, , . | 3.5 | 2 |
| 40 | PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. PLoS Computational Biology, 2020, 16, e1008240. | 1.5 | 1 |
| 41 | Moss enables high sensitivity single-nucleotide variant calling from multiple bulk DNA tumor samples. Nature Communications, 2021, 12, 2204. | 5.8 | 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 |