

Mohammad Shahrokh Esfahani

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

1,791
citations

687363

13
h-index

752698

20
g-index

26
all docs

26
docs citations

26
times ranked

2780
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Inferring gene expression from cell-free DNA fragmentation profiles. <i>Nature Biotechnology</i> , 2022, 40, 585-597. | 17.5 | 63 |
| 2 | Short Diagnosis-to-Treatment Interval Is Associated With Higher Circulating Tumor DNA Levels in Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2021, 39, 2605-2616. | 1.6 | 37 |
| 3 | Profiling of Circulating Tumor DNA for Noninvasive Disease Detection, Risk Stratification, and MRD Monitoring in Patients with CNS Lymphoma. <i>Blood</i> , 2021, 138, 6-6. | 1.4 | 15 |
| 4 | Noninvasive Cell-of-Origin Classification of Diffuse Large B-Cell Lymphoma Using Inferred Gene Expression from Cell-Free DNA Sequencing. <i>Blood</i> , 2021, 138, 37-37. | 1.4 | 0 |
| 5 | Evaluating upfront high-dose consolidation after R-CHOP for follicular lymphoma by clinical and genetic risk models. <i>Blood Advances</i> , 2020, 4, 4451-4462. | 5.2 | 8 |
| 6 | Circulating DNA for Molecular Response Prediction, Characterization of Resistance Mechanisms and Quantification of CAR T-Cells during Axicabtagene Ciloleucef Therapy. <i>Blood</i> , 2019, 134, 550-550. | 1.4 | 13 |
| 7 | An Atlas of Clinically-Distinct Tumor Cellular Ecosystems in Diffuse Large B Cell Lymphoma. <i>Blood</i> , 2019, 134, 655-655. | 1.4 | 4 |
| 8 | Towards Non-Invasive Classification of DLBCL Genetic Subtypes By Ctdna Profiling. <i>Blood</i> , 2019, 134, 551-551. | 1.4 | 9 |
| 9 | Short Diagnosis-to-Treatment Interval Is Associated with Higher Levels of Circulating Tumor DNA in Aggressive B-Cell Non-Hodgkin Lymphoma. <i>Blood</i> , 2019, 134, 491-491. | 1.4 | 0 |
| 10 | Optimal Bayesian Kalman Filtering With Prior Update. <i>IEEE Transactions on Signal Processing</i> , 2018, 66, 1982-1996. | 5.3 | 26 |
| 11 | Circulating Tumor DNA Measurements As Early Outcome Predictors in Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2018, 36, 2845-2853. | 1.6 | 313 |
| 12 | An experimental design framework for Markovian gene regulatory networks under stationary control policy. <i>BMC Systems Biology</i> , 2018, 12, 137. | 3.0 | 3 |
| 13 | Intrinsically Bayesian Robust Kalman Filter: An Innovation Process Approach. <i>IEEE Transactions on Signal Processing</i> , 2017, 65, 2531-2546. | 5.3 | 43 |
| 14 | Early Detection of Molecular Residual Disease in Localized Lung Cancer by Circulating Tumor DNA Profiling. <i>Cancer Discovery</i> , 2017, 7, 1394-1403. | 9.4 | 701 |
| 15 | Bayesian Kalman filtering in the presence of unknown noise statistics using factor graphs. , 2017, , . | | 1 |
| 16 | Incorporating biological prior knowledge for Bayesian learning via maximal knowledge-driven information priors. <i>BMC Bioinformatics</i> , 2017, 18, 552. | 2.6 | 32 |
| 17 | A Bayesian framework for robust Kalman filtering under uncertain noise statistics. , 2016, , . | | 3 |
| 18 | Distinct biological subtypes and patterns of genome evolution in lymphoma revealed by circulating tumor DNA. <i>Science Translational Medicine</i> , 2016, 8, 364ra155. | 12.4 | 348 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Inference of Nonlinear ODE-Based Gene Regulatory Networks via Intrinsically Bayesian Robust Kalman Filtering. , 2016, , . | | 1 |
| 20 | An Optimization-Based Framework for the Transformation of Incomplete Biological Knowledge into a Probabilistic Structure and Its Application to the Utilization of Gene/Protein Signaling Pathways in Discrete Phenotype Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1304-1321. | 3.0 | 15 |
| 21 | Discrete optimal Bayesian classification with error-conditioned sequential sampling. Pattern Recognition, 2015, 48, 3766-3782. | 8.1 | 22 |
| 22 | Effect of separate sampling on classification accuracy. Bioinformatics, 2014, 30, 242-250. | 4.1 | 77 |
| 23 | Incorporation of Biological Pathway Knowledge in the Construction of Priors for Optimal Bayesian Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 202-218. | 3.0 | 38 |
| 24 | Classifier design given an uncertainty class of feature distributions via regularized maximum likelihood and the incorporation of biological pathway knowledge in steady-state phenotype classification. Pattern Recognition, 2013, 46, 2783-2797. | 8.1 | 9 |
| 25 | Probabilistic reconstruction of the tumor progression process in gene regulatory networks in the presence of uncertainty. BMC Bioinformatics, 2011, 12, S9. | 2.6 | 10 |
| 26 | Designing enhanced classifiers using prior process knowledge: Regularized maximum-likelihood. , 2011, , . | | 0 |