Mehmet Eren Ahsen

List of Publications by Year
in descending order

37 papers	1,648 citations	623734 14 h-index	434195 31 g-index
42 all docs	42 docs citations	42 times ranked	2988 citing authors

#	Article	IF	Citations
1	Unannotated small RNA clusters associated with circulating extracellular vesicles detect early stage liver cancer. Gut, 2022, 71, 2069-2080.	12.1	24
2	The Societal Impact of Sharing Economy Platform Self-Regulations—An Empirical Investigation. Information Systems Research, 2022, 33, 1303-1323.	3.7	9
3	COSIFER: a Python package for the consensus inference of molecular interaction networks. Bioinformatics, 2021, 37, 2070-2072.	4.1	4
4	Evaluation of artificial intelligence systems for assisting neurologists with fast and accurate annotations of scalp electroencephalography data. EBioMedicine, 2021, 66, 103275.	6.1	15
5	Effect of AI Explanations on Human Perceptions of Patient-Facing AI-Powered Healthcare Systems. Journal of Medical Systems, 2021, 45, 64.	3.6	26
6	Transcriptomic characterization of cancer-testis antigens identifies MAGEA3 as a driver of tumor progression in hepatocellular carcinoma. PLoS Genetics, 2021, 17, e1009589.	3.5	15
7	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. Cell Systems, 2021, 12, 827-838.e5.	6.2	15
8	The Fermi–Dirac distribution provides a calibrated probabilistic output for binary classifiers. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	4
9	Radiogenomics Consortium Genome-Wide Association Study Meta-Analysis of Late Toxicity After Prostate Cancer Radiotherapy. Journal of the National Cancer Institute, 2020, 112, 179-190.	6.3	71
10	R/PY-SUMMA: An R/Python Package for Unsupervised Ensemble Learning for Binary Classification Problems in Bioinformatics. Journal of Computational Biology, 2020, 27, 1337-1340.	1.6	0
11	Evaluation of Combined Artificial Intelligence and Radiologist Assessment to Interpret Screening Mammograms. JAMA Network Open, 2020, 3, e200265.	5.9	236
12	Intratumoral heterogeneity and clonal evolution in liver cancer. Nature Communications, 2020, 11, 291.	12.8	230
13	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. Life Science Alliance, 2020, 3, e202000867.	2.8	20
14	The transcriptomic response of cells to a drug combination is more than the sum of the responses to the monotherapies. ELife, 2020, 9, .	6.0	21
15	Assessment of network module identification across complex diseases. Nature Methods, 2019, 16, 843-852.	19.0	213
16	NeTFactor, a framework for identifying transcriptional regulators of gene expression-based biomarkers. Scientific Reports, 2019, 9, 12970.	3.3	12
17	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
18	exRNA Atlas Analysis Reveals Distinct Extracellular RNA Cargo Types and Their Carriers Present across Human Biofluids. Cell, 2019, 177, 463-477.e15.	28.9	228

#	Article	IF	Citations
19	When Algorithmic Predictions Use Human-Generated Data: A Bias-Aware Classification Algorithm for Breast Cancer Diagnosis. Information Systems Research, 2019, 30, 97-116.	3.7	41
20	Preferenceâ€Sensitive Management of Postâ€Mammography Decisions in Breast Cancer Diagnosis. Production and Operations Management, 2018, 27, 2313-2338.	3.8	10
21	Inferring Genome-Wide Interaction Networks Using the Phi-Mixing Coefficient, and Applications to Lung and Breast Cancer. IEEE Transactions on Molecular, Biological, and Multi-Scale Communications, 2018, 4, 123-139.	2.1	6
22	A crowdsourced analysis to identify ab initio molecular signatures predictive of susceptibility to viral infection. Nature Communications, 2018, 9, 4418.	12.8	14
23	A Nasal Brush-based Classifier of Asthma Identified by Machine Learning Analysis of Nasal RNA Sequence Data. Scientific Reports, 2018, 8, 8826.	3.3	51
24	Error bounds for compressed sensing algorithms with group sparsity: A unified approach. Applied and Computational Harmonic Analysis, 2017, 43, 212-232.	2.2	55
25	Two new approaches to compressed sensing exhibiting both robust sparse recovery and the grouping effect. , 2017, , .		5
26	Sparse feature selection for classification and prediction of metastasis in endometrial cancer. BMC Genomics, 2017, 18, 233.	2.8	19
27	Stability and Robustness Analysis of a Class of Cyclic Biological Systems. Advances in Delays and Dynamics, 2017, , 155-168.	0.4	0
28	Timing the Use of Breast Cancer Risk Information in Biopsy Decisionâ€Making. Production and Operations Management, 2017, 26, 1333-1358.	3.8	11
29	Analysis of a Gene Regulatory Network Model With Time Delay Using the Secant Condition. IEEE Life Sciences Letters, 2016, 2, 5-8.	1.2	5
30	Sparse Feature Selection for Classification and Prediction of Metastasis in Endometrial Cancer. , 2016, , .		0
31	A Secant Condition for Cyclic Systems with Time Delays and its Application to Gene Regulatory Networks. IFAC-PapersOnLine, 2015, 48, 171-176.	0.9	2
32	Gene Regulatory Networks Under Positive Feedback. Springer Briefs in Electrical and Computer Engineering, 2015, , 73-85.	0.5	0
33	Opportunistic wireless charging for mobile social and sensor networks. , 2014, , .		17
34	Mixing Coefficients Between Discrete and Real Random Variables: Computation and Properties. IEEE Transactions on Automatic Control, 2014, 59, 34-47.	5.7	8
35	Analysis of Gene Regulatory Networks under Positive Feedback. Advances in Delays and Dynamics, 2014, , 127-140.	0.4	4
36	Inferring weighted and directed gene interaction networks from gene expression data using the phi-mixing coefficient. , 2012, , .		3

#	Article	IF	Citations
37	Stability Analysis of a Dynamical Model Representing Gene Regulatory Networks. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2012, 45, 191-196.	0.4	2