

# Mark Kon

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11182328/publications.pdf>

Version: 2024-02-01

21  
papers

296  
citations

1163117

8  
h-index

1125743

13  
g-index

21  
all docs

21  
docs citations

21  
times ranked

445  
citing authors

#	ARTICLE	IF	CITATIONS
1	Analytic regularity and stochastic collocation of high-dimensional Newton iterates. <i>Advances in Computational Mathematics</i> , 2020, 46, 1.	1.6	0
2	Identifying factors associated with opioid cessation in a biracial sample using machine learning. , 2020, 1, 27-41.		1
3	Optimizing decision tree structures for spectral histopathology (SHP). <i>Analyst, The</i> , 2018, 143, 5935-5939.	3.5	3
4	Absorption probabilities of quantum walks. <i>Quantum Information Processing</i> , 2018, 17, 1.	2.2	6
5	Multimodal Learning and Intelligent Prediction of Symptom Development in Individual Parkinsonâ€™s Patients. <i>Sensors</i> , 2016, 16, 1498.	3.8	30
6	Some comparisons of gene expression classifiers. , 2016, , .		0
7	Differentiation and Integration of Machine Learning Feature Vectors. , 2016, , .		0
8	A Method for Generating New Datasets Based on Copy Number for Cancer Analysis. <i>BioMed Research International</i> , 2015, 2015, 1-8.	1.9	3
9	Statistical analysis of a lung cancer spectral histopathology (SHP) data set. <i>Analyst, The</i> , 2015, 140, 2449-2464.	3.5	29
10	Unique recovery from edge information. , 2015, , .		1
11	Class Discovery via Bimodal Feature Selection in Unsupervised Settings. , 2015, , .		1
12	Cancer survival classification using integrated data sets and intermediate information. <i>Artificial Intelligence in Medicine</i> , 2014, 62, 23-31.	6.5	19
13	Infrared spectral histopathology (SHP): a novel diagnostic tool for the accurate classification of lung cancer. <i>Laboratory Investigation</i> , 2012, 92, 1358-1373.	3.7	114
14	Smoothing Gene Expression Using Biological Networks. , 2010, , .		1
15	Classifying transcription factor targets and discovering relevant biological features. <i>Biology Direct</i> , 2008, 3, 22.	4.6	9
16	In silico regulatory analysis for exploring human disease progression. <i>Biology Direct</i> , 2008, 3, 24.	4.6	6
17	Learning Methods for DNA Binding in Computational Biology. <i>Neural Networks (IJCNN), International Joint Conference on</i> , 2007, , .	0.0	0
18	Machine learning for regulatory analysis and transcription factor target prediction in yeast. <i>Systems and Synthetic Biology</i> , 2007, 1, 25-46.	1.0	21

#	ARTICLE	IF	CITATIONS
19	Information-based nonlinear approximation: an average case setting. <i>Journal of Complexity</i> , 2005, 21, 211-229.	1.3	13
20	Integrating genomic data to predict transcription factor binding. <i>Genome Informatics</i> , 2005, 16, 83-94.	0.4	31
21	Complexity of Neural Network Approximation with Limited Information: A Worst Case Approach. <i>Journal of Complexity</i> , 2001, 17, 345-365.	1.3	8