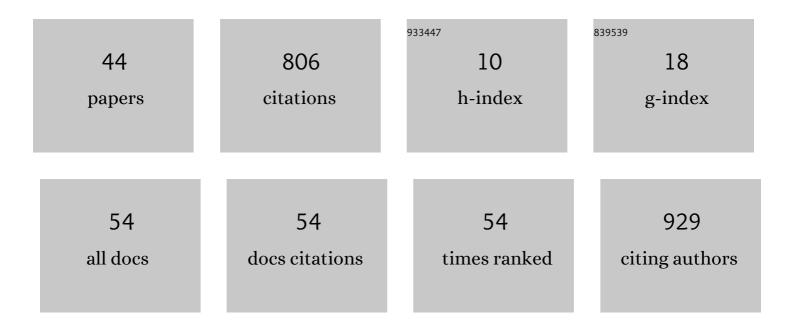
Rui Fa

List of Publications by Year in descending order

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Ριμ Ελ

#	Article	IF	CITATIONS
1	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
2	Reduced-Rank STAP Schemes for Airborne Radar Based on Switched Joint Interpolation, Decimation and Filtering Algorithm. IEEE Transactions on Signal Processing, 2010, 58, 4182-4194.	5.3	125
3	Predicting human protein function with multi-task deep neural networks. PLoS ONE, 2018, 13, e0198216.	2.5	58
4	Paradigm of Tunable Clustering Using Binarization of Consensus Partition Matrices (Bi-CoPaM) for Gene Discovery. PLoS ONE, 2013, 8, e56432.	2.5	48
5	Knowledgeâ€aided STAP with sparseâ€recovery by exploiting spatioâ€temporal sparsity. IET Signal Processing, 2016, 10, 150-161.	1.5	39
6	Yeast gene CMR1/YDL156W is consistently co-expressed with genes participating in DNA-metabolic processes in a variety of stringent clustering experiments. Journal of the Royal Society Interface, 2013, 10, 20120990.	3.4	30
7	Switched Interleaving Techniques with Limited Feedback for Interference Mitigation in DS-CDMA Systems. IEEE Transactions on Communications, 2011, 59, 1946-1956.	7.8	22
8	Distinct gene expression program dynamics during erythropoiesis from human induced pluripotent stem cells compared with adult and cord blood progenitors. BMC Genomics, 2016, 17, 817.	2.8	21
9	UNCLES: method for the identification of genes differentially consistently co-expressed in a specific subset of datasets. BMC Bioinformatics, 2015, 16, 184.	2.6	18
10	Comprehensive analysis of forty yeast microarray datasets reveals a novel subset of genes (APha-RiB) consistently negatively associated with ribosome biogenesis. BMC Bioinformatics, 2014, 15, 322.	2.6	12
11	Using deep maxout neural networks to improve the accuracy of function prediction from protein interaction networks. PLoS ONE, 2019, 14, e0209958.	2.5	11
12	Reduced-rank STAP algorithm for adaptive radar based on joint iterative optimization of adaptive filters. , 2008, , .		8
13	Direct Data Domain Sparsity-Based STAP Utilizing Subaperture Smoothing Techniques. International Journal of Antennas and Propagation, 2015, 2015, 1-10.	1.2	7
14	Reduced-rank STAP for MIMO radar based on joint iterative optimization of knowledge-aided adaptive filters. , 2009, , .		6
15	Clustering analysis for gene expression data: A methodological review. , 2012, , .		6
16	Generalised grouped minimum meanâ€squared errorâ€based multiâ€stage interference cancellation scheme for orthogonal frequency division multiple access uplink systems with carrier frequency offsets. IET Communications, 2013, 7, 685-695.	2.2	6
17	SMART: Unique Splitting-While-Merging Framework for Gene Clustering. PLoS ONE, 2014, 9, e94141.	2.5	6
18	Knowledge-aided reduced-rank STAP for MIMO radar based on joint iterative constrained optimization		5

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#	Article	IF	CITATIONS
19	Multiple feedback successive interference cancellation with shadow area constraints for MIMO systems. , 2010, , .		5
20	Reduced-Rank Linear Interference Suppression for DS-UWB Systems Based on Switched Approximations of Adaptive Basis Functions. IEEE Transactions on Vehicular Technology, 2011, 60, 485-497.	6.3	5
21	Multi-Branch Successive Interference Cancellation for MIMO Spatial Multiplexing Systems. , 2009, , .		4
22	Joint data detection and phase recovery for downlink MC-2D-CDMA systems. IEEE Transactions on Communications, 2009, 57, 2782-2789.	7.8	4
23	Generalized Phase Spatial Shift Keying Modulation for MIMO Channels. , 2011, , .		4
24	Enhanced SMART framework for gene clustering using successive processing. , 2013, , .		4
25	An enhanced splitting-while-merging algorithm with finite mixture models. , 2013, , .		4
26	Noise Resistant Generalized Parametric Validity Index of Clustering for Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 741-752.	3.0	4
27	Application of the Bi-CoPaM Method to Five Escherichia Coli Datasets Generated under Various Biological Conditions. Journal of Signal Processing Systems, 2015, 79, 159-166.	2.1	4
28	Parametric validity index of clustering for microarray gene expression data. , 2011, , .		3
29	Method for the identification of the subsets of genes specifically consistently co-expressed in a set of datasets. , 2013, , .		3
30	Identification of genes consistently co-expressed in multiple microarray datasets by a genome-wide Bi-CoPaM approach. , 2013, , .		3
31	Linear Interference Suppression for Spread Spectrum Systems with Switched Interleaving and Limited Feedback. , 2009, , .		2
32	Design of adaptive multi-branch SIC receivers for MIMO spatial multiplexing systems. , 2009, , .		2
33	Comprehensive analysis of multiple microarray datasets by binarization of consensus partition matrix. , 2012, , .		2
34	M-N scatter plots technique for evaluating varying-size clusters and setting the parameters of Bi-CoPaM and Uncles methods. , 2014, , .		2
35	Reduced-rank interference suppression for GPS systems based on adaptive basis-function approximation. , 2008, , .		1
36	Performance Analysis for MC-CDMA System in Impulsive Noise. , 2009, , .		1

Performance Analysis for MC-CDMA System in Impulsive Noise. , 2009, , . 36

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#	Article	IF	CITATIONS
37	Reduced-rank STAP algorithm for adaptive radar based on basis-functions approximation. , 2009, , .		1
38	An adaptive LCMV beamforming algorithm based on dynamic selection of constraints. , 2010, , .		1
39	Kernel-based parametric validity index for assessing clusters from microarray gene expression data. , 2012, , .		1
40	Splitting-while-merging framework for clustering high-dimension data with component-wise expectation conditional maximisation. , 2014, , .		1
41	Scalable clustering based on enhanced-SMART for large-scale FMRI datasets. , 2015, , .		1
42	CoCE-SMART: Consensus clustering based on enhanced splitting-merging awareness tactics. , 2015, , .		1
43	Switched interleaving turbo codes with transmission of side information for short blocks. , 2010, , .		0
44	Network community degree based fast community detection algorithm for fMRI data. , 2016, , .		0