

Lin Zhu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2333372/publications.pdf>

Version: 2024-02-01

27
papers

846
citations

687363

13
h-index

752698

20
g-index

28
all docs

28
docs citations

28
times ranked

629
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of protein-protein interactions from amino acid sequences with ensemble extreme learning machines and principal component analysis. BMC Bioinformatics, 2013, 14, S10.	2.6	232
2	t-LSE: A Novel Robust Geometric Approach for Modeling Protein-Protein Interaction Networks. PLoS ONE, 2013, 8, e58368.	2.5	81
3	High-Order Convolutional Neural Network Architecture for Predicting DNA-Protein Binding Sites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1184-1192.	3.0	78
4	A Two-Stage Geometric Method for Pruning Unreliable Links in Protein-Protein Networks. IEEE Transactions on Nanobioscience, 2015, 14, 528-534.	3.3	62
5	ChIP-PIT: Enhancing the Analysis of ChIP-Seq Data Using Convex-Relaxed Pair-Wise Interaction Tensor Decomposition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 55-63.	3.0	61
6	Increasing the reliability of protein-protein interaction networks via non-convex semantic embedding. Neurocomputing, 2013, 121, 99-107.	5.9	51
7	Detecting Protein-Protein Interactions with a Novel Matrix-Based Protein Sequence Representation and Support Vector Machines. BioMed Research International, 2015, 2015, 1-9.	1.9	45
8	Identifying Spurious Interactions in the Protein-Protein Interaction Networks Using Local Similarity Preserving Embedding. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 345-352.	3.0	38
9	Weakly-Supervised Convolutional Neural Network Architecture for Predicting Protein-DNA Binding. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	38
10	Direct AUC optimization of regulatory motifs. Bioinformatics, 2017, 33, i243-i251.	4.1	30
11	DCDE: An Efficient Deep Convolutional Divergence Encoding Method for Human Promoter Recognition. IEEE Transactions on Nanobioscience, 2019, 18, 136-145.	3.3	26
12	DiscMLA: An Efficient Discriminative Motif Learning Algorithm over High-Throughput Datasets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1810-1820.	3.0	24
13	WSMD: weakly-supervised motif discovery in transcription factor ChIP-seq data. Scientific Reports, 2017, 7, 3217.	3.3	21
14	A Rayleigh-Ritz style method for large-scale discriminant analysis. Pattern Recognition, 2014, 47, 1698-1708.	8.1	15
15	LMMO: A Large Margin Approach for Refining Regulatory Motifs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 913-925.	3.0	12
16	Understanding tissue-specificity with human tissue-specific regulatory networks. Science China Information Sciences, 2016, 59, 1.	4.3	11
17	Learning regulatory motifs by direct optimization of Fisher Exact Test Score. , 2016, , .		8
18	Collaborative Completion of Transcription Factor Binding Profiles via Local Sensitive Unified Embedding. IEEE Transactions on Nanobioscience, 2016, 15, 1-1.	3.3	3

#	ARTICLE	IF	CITATIONS
19	Optimization of Gene Set Annotations Using Robust Trace-Norm Multitask Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1016-1021.	3.0	3
20	Editorial: Special Issue on Advanced Intelligent Computing: Theory and Applications. Neurocomputing, 2017, 228, 1-2.	5.9	2
21	A two-stage geometric method for detecting unreliable links in protein-protein networks. , 2014, , .		1
22	DiscMLA: AUC-based discriminative motif learning. , 2015, , .		1
23	Visual data completion via local sensitive low rank tensor learning. , 2016, , .		1
24	Convex local sensitive low rank matrix approximation. , 2017, , .		1
25	Imputation of ChIP-seq datasets via Low Rank Convex Co-Embedding. , 2015, , .		0
26	ILSES: Identification lysine succinylation-sites with ensemble classification. , 2016, , .		0
27	Cross-validated smooth multi-instance learning. , 2017, , .		0