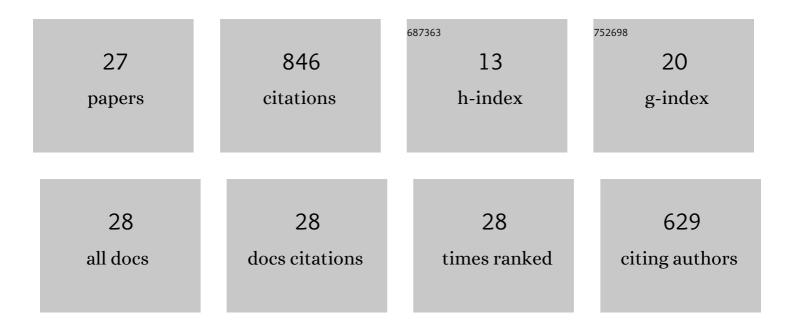
Lin Zhu

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	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
2	DCDE: An Efficient Deep Convolutional Divergence Encoding Method for Human Promoter Recognition. IEEE Transactions on Nanobioscience, 2019, 18, 136-145.	3.3	26
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	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
5	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
6	LMMO: A Large Margin Approach for Refining Regulatory Motifs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 913-925.	3.0	12
7	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
8	Cross-validated smooth multi-instance learning. , 2017, , .		0
9	WSMD: weakly-supervised motif discovery in transcription factor ChIP-seq data. Scientific Reports, 2017, 7, 3217.	3.3	21
10	Convex local sensitive low rank matrix approximation. , 2017, , .		1
11	Editorial: Special Issue on Advanced Intelligent Computing: Theory and Applications. Neurocomputing, 2017, 228, 1-2.	5.9	2
12	Direct AUC optimization of regulatory motifs. Bioinformatics, 2017, 33, i243-i251.	4.1	30
13	Collaborative Completion of Transcription Factor Binding Profiles via Local Sensitive Unified Embedding. IEEE Transactions on Nanobioscience, 2016, 15, 1-1.	3.3	3
14	Learning regulatory motifs by direct optimization of Fisher Exact Test Score. , 2016, , .		8
15	Visual data completion via local sensitive low rank tensor learning. , 2016, , .		1
16	ILSES: Identification lysine succinylation-sites with ensemble classification. , 2016, , .		0
17	Understanding tissue-specificity with human tissue-specific regulatory networks. Science China Information Sciences, 2016, 59, 1.	4.3	11
18	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

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#	Article	IF	CITATIONS
19	Imputation of ChIP-seq datasets via Low Rank Convex Co-Embedding. , 2015, , .		0
20	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
21	DiscMLA: AUC-based discriminative motif learning. , 2015, , .		1
22	A Two-Stage Geometric Method for Pruning Unreliable Links in Protein-Protein Networks. IEEE Transactions on Nanobioscience, 2015, 14, 528-534.	3.3	62
23	A two-stage geometric method for detecting unreliable links in protein-protein networks. , 2014, , .		1
24	A Rayleigh–Ritz style method for large-scale discriminant analysis. Pattern Recognition, 2014, 47, 1698-1708.	8.1	15
25	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
26	Increasing the reliability of protein–protein interaction networks via non-convex semantic embedding. Neurocomputing, 2013, 121, 99-107.	5.9	51
27	t-LSE: A Novel Robust Geometric Approach for Modeling Protein-Protein Interaction Networks. PLoS ONE, 2013, 8, e58368.	2.5	81