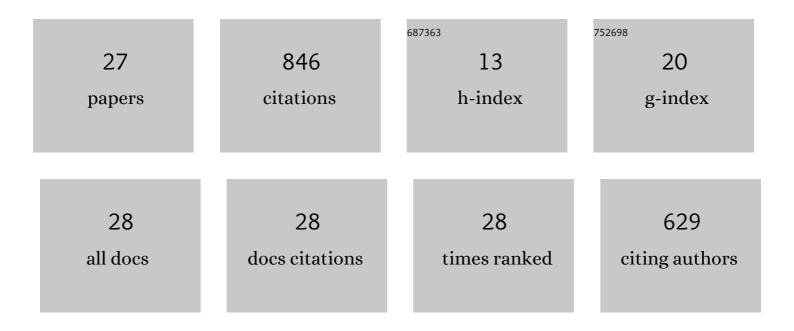
## Lin Zhu

## 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.<br>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.<br>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.<br>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<br>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<br>Preserving Embedding. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14,<br>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<br>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<br>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<br>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,<br>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<br>embedding. Neurocomputing, 2013, 121, 99-107.                                       | 5.9 | 51        |
| 27 | t-LSE: A Novel Robust Geometric Approach for Modeling Protein-Protein Interaction Networks. PLoS<br>ONE, 2013, 8, e58368.   | 2.5 | 81        |