

Zengyou He

List of Publications by Year in descending order

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77
papers

3,238
citations

257450

24
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149698

56
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78
all docs

78
docs citations

78
times ranked

3355
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Significance-Based Essential Protein Discovery. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 633-642. | 3.0 | 8 |
| 2 | Decision Tree for Sequences. IEEE Transactions on Knowledge and Data Engineering, 2021, , 1-1. | 5.7 | 7 |
| 3 | Instance-Based Classification Through Hypothesis Testing. IEEE Access, 2021, 9, 17485-17494. | 4.2 | 1 |
| 4 | Essential Protein Recognition via Community Significance. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2788-2794. | 3.0 | 4 |
| 5 | A graph-traversal approach to identify influential nodes in a network. Patterns, 2021, 2, 100321. | 5.9 | 9 |
| 6 | On the statistical significance of communities from weighted graphs. Scientific Reports, 2021, 11, 20304. | 3.3 | 1 |
| 7 | On the Statistical Significance of a Community Structure. IEEE Transactions on Knowledge and Data Engineering, 2021, , 1-1. | 5.7 | 0 |
| 8 | Protein Complexes Identification with Family-Wise Error Rate Control. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 2062-2073. | 3.0 | 6 |
| 9 | Detecting Statistically Significant Communities. IEEE Transactions on Knowledge and Data Engineering, 2020, , 1-1. | 5.7 | 4 |
| 10 | Reference-Based Sequence Classification. IEEE Access, 2020, 8, 218199-218214. | 4.2 | 1 |
| 11 | Computing exact P-values for community detection. Data Mining and Knowledge Discovery, 2020, 34, 833-869. | 3.7 | 7 |
| 12 | Significance-based discriminative sequential pattern mining. Expert Systems With Applications, 2019, 122, 54-64. | 7.6 | 22 |
| 13 | Mining conditional discriminative sequential patterns. Information Sciences, 2019, 478, 524-539. | 6.9 | 19 |
| 14 | Reinforce: An Ensemble Approach for Inferring PPI Network from AP-MS Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 365-376. | 3.0 | 2 |
| 15 | Protein complexes identification based on go attributed network embedding. BMC Bioinformatics, 2018, 19, 535. | 2.6 | 22 |
| 16 | On the statistical significance of protein complex. Quantitative Biology, 2018, 6, 313-320. | 0.5 | 3 |
| 17 | Reconstruction of the Protein-Protein Interaction Network for Protein Complexes Identification by Walking on the Protein Pair Fingerprints Similarity Network. Frontiers in Genetics, 2018, 9, 272. | 2.3 | 13 |
| 18 | RPML: A Learning-Based Approach for Reranking Protein-Spectrum Matches. Lecture Notes in Computer Science, 2018, , 559-564. | 1.3 | 0 |

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|----|--|-----|-----------|
| 19 | Conditional discriminative pattern mining: Concepts and algorithms. Information Sciences, 2017, 375, 1-15. | 6.9 | 21 |
| 20 | A two-step framework for inferring direct protein-protein interaction network from AP-MS data. BMC Systems Biology, 2017, 11, 82. | 3.0 | 8 |
| 21 | Protein Inference. Advances in Experimental Medicine and Biology, 2016, 919, 237-242. | 1.6 | 2 |
| 22 | Computing exact permutation p-values for association rules. Information Sciences, 2016, 346-347, 146-162. | 6.9 | 15 |
| 23 | Protein inference: A protein quantification perspective. Computational Biology and Chemistry, 2016, 63, 21-29. | 2.3 | 8 |
| 24 | BagReg: Protein inference through machine learning. Computational Biology and Chemistry, 2015, 57, 12-20. | 2.3 | 8 |
| 25 | Phosphorylation motif discovery. , 2015, , 19-27. | | 0 |
| 26 | Protein inference in shotgun proteomics. , 2015, , 39-49. | | 0 |
| 27 | Biomarker discovery. , 2015, , 69-78. | | 0 |
| 28 | Discriminative pattern mining and its applications in bioinformatics. Briefings in Bioinformatics, 2015, 16, 884-900. | 6.5 | 29 |
| 29 | Network inference from AP-MS data: computational challenges and solutions. Briefings in Bioinformatics, 2015, 16, 658-674. | 6.5 | 21 |
| 30 | Mining Conditional Phosphorylation Motifs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 915-927. | 3.0 | 9 |
| 31 | Decoy-free protein-level false discovery rate estimation. Bioinformatics, 2014, 30, 675-681. | 4.1 | 12 |
| 32 | Improved and Promising Identification of Human MicroRNAs by Incorporating a High-Quality Negative Set. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 192-201. | 3.0 | 207 |
| 33 | Data construction for phosphorylation site prediction. Briefings in Bioinformatics, 2014, 15, 839-855. | 6.5 | 12 |
| 34 | ProteinLasso: A Lasso regression approach to protein inference problem in shotgun proteomics. Computational Biology and Chemistry, 2013, 43, 46-54. | 2.3 | 18 |
| 35 | A Combinatorial Perspective of the Protein Inference Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1542-1547. | 3.0 | 3 |
| 36 | Comments on 'MMFPh: A Maximal Motif Finder for Phosphoproteomics Datasets'. Bioinformatics, 2012, 28, 2211-2212. | 4.1 | 1 |

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|----|--|-----|-----------|
| 37 | A linear programming model for protein inference problem in shotgun proteomics. <i>Bioinformatics</i> , 2012, 28, 2956-2962. | 4.1 | 22 |
| 38 | Protein inference: a review. <i>Briefings in Bioinformatics</i> , 2012, 13, 586-614. | 6.5 | 96 |
| 39 | Peptide Reranking with Protein-Peptide Correspondence and Precursor Peak Intensity Information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1212-1219. | 3.0 | 1 |
| 40 | Bioinformatic Analysis of Data Generated from MALDI Mass Spectrometry for Biomarker Discovery. <i>Topics in Current Chemistry</i> , 2012, 331, 193-209. | 4.0 | 6 |
| 41 | Permutation methods for testing the significance of phosphorylation motifs. <i>Statistics and Its Interface</i> , 2012, 5, 61-73. | 0.3 | 5 |
| 42 | Score regularization for peptide identification. <i>BMC Bioinformatics</i> , 2011, 12, S2. | 2.6 | 9 |
| 43 | Clustering categorical data streams. <i>Journal of Computational Methods in Sciences and Engineering</i> , 2011, 11, 185-192. | 0.2 | 4 |
| 44 | Attribute value weighting in k-modes clustering. <i>Expert Systems With Applications</i> , 2011, 38, 15365-15369. | 7.6 | 27 |
| 45 | Motif-All: discovering all phosphorylation motifs. <i>BMC Bioinformatics</i> , 2011, 12, S22. | 2.6 | 32 |
| 46 | The choice of null distributions for detecting gene-gene interactions in genome-wide association studies. <i>BMC Bioinformatics</i> , 2011, 12, S26. | 2.6 | 6 |
| 47 | A Partial Set Covering Model for Protein Mixture Identification Using Mass Spectrometry Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 368-380. | 3.0 | 13 |
| 48 | G-ANMI: A mutual information based genetic clustering algorithm for categorical data. <i>Knowledge-Based Systems</i> , 2010, 23, 144-149. | 7.1 | 44 |
| 49 | Stable feature selection for biomarker discovery. <i>Computational Biology and Chemistry</i> , 2010, 34, 215-225. | 2.3 | 251 |
| 50 | Optimization-Based Peptide Mass Fingerprinting for Protein Mixture Identification. <i>Journal of Computational Biology</i> , 2010, 17, 221-235. | 1.6 | 10 |
| 51 | SNPHarvester: a filtering-based approach for detecting epistatic interactions in genome-wide association studies. <i>Bioinformatics</i> , 2009, 25, 504-511. | 4.1 | 182 |
| 52 | Improving peptide identification with single-stage mass spectrum peaks. <i>Bioinformatics</i> , 2009, 25, 2969-2974. | 4.1 | 6 |
| 53 | Comparison of public peak detection algorithms for MALDI mass spectrometry data analysis. <i>BMC Bioinformatics</i> , 2009, 10, 4. | 2.6 | 220 |
| 54 | Dynamic Self-configuration of User QoS for Next Generation Network. , 2009, , . | | 1 |

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|----|---|------|-----------|
| 55 | Technical, bioinformatical and statistical aspects of liquid chromatographyâ€“mass spectrometry (LCâ€“MS) and capillary electrophoresis-mass spectrometry (CE-MS) based clinical proteomics: A critical assessmentâ€“†. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2009, 877, 1250-1258. | 2.3 | 80 |
| 56 | k-ANMI: A mutual information based clustering algorithm for categorical data. <i>Information Fusion</i> , 2008, 9, 223-233. | 19.1 | 58 |
| 57 | Improving Mass Spectrometry Peak Detection Using Multiple Peak Alignment Results. <i>Journal of Proteome Research</i> , 2008, 7, 123-129. | 3.7 | 21 |
| 58 | Peak bagging for peptide mass fingerprinting. <i>Bioinformatics</i> , 2008, 24, 1293-1299. | 4.1 | 8 |
| 59 | Optimization-Based Peptide Mass Fingerprinting for Protein Mixture Identification. <i>Nature Precedings</i> , 2008, , . | 0.1 | 0 |
| 60 | On the Impact of Dissimilarity Measure in k-Modes Clustering Algorithm. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2007, 29, 503-507. | 13.9 | 172 |
| 61 | Mining top-k strongly correlated item pairs without minimum correlation threshold. <i>International Journal of Knowledge-Based and Intelligent Engineering Systems</i> , 2006, 10, 105-112. | 1.0 | 8 |
| 62 | A Fast Greedy Algorithm for Outlier Mining. <i>Lecture Notes in Computer Science</i> , 2006, , 567-576. | 1.3 | 47 |
| 63 | Improving categorical data clustering algorithm by weighting uncommon attribute value matches. <i>Computer Science and Information Systems</i> , 2006, 3, 23-32. | 1.0 | 2 |
| 64 | Mining action rules from scratch. <i>Expert Systems With Applications</i> , 2005, 29, 691-699. | 7.6 | 64 |
| 65 | Scalable algorithms for clustering large datasets with mixed type attributes. <i>International Journal of Intelligent Systems</i> , 2005, 20, 1077-1089. | 5.7 | 55 |
| 66 | A cluster ensemble method for clustering categorical data. <i>Information Fusion</i> , 2005, 6, 143-151. | 19.1 | 63 |
| 67 | TCSOM: Clustering Transactions Using Self-Organizing Map. <i>Neural Processing Letters</i> , 2005, 22, 249-262. | 3.2 | 19 |
| 68 | An FP-Tree Based Approach for Mining All Strongly Correlated Item Pairs. <i>Lecture Notes in Computer Science</i> , 2005, , 735-740. | 1.3 | 7 |
| 69 | An Optimization Model for Outlier Detection in Categorical Data. <i>Lecture Notes in Computer Science</i> , 2005, , 400-409. | 1.3 | 70 |
| 70 | A Unified Subspace Outlier Ensemble Framework for Outlier Detection. <i>Lecture Notes in Computer Science</i> , 2005, , 632-637. | 1.3 | 15 |
| 71 | FP-outlier: Frequent pattern based outlier detection. <i>Computer Science and Information Systems</i> , 2005, 2, 103-118. | 1.0 | 130 |
| 72 | A Frequent Pattern Discovery Method for Outlier Detection. <i>Lecture Notes in Computer Science</i> , 2004, , 726-732. | 1.3 | 35 |

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| 73 | Mining class outliers: concepts, algorithms and applications in CRM. Expert Systems With Applications, 2004, 27, 681-697. | 7.6 | 62 |
| 74 | Mining Class Outliers: Concepts, Algorithms and Applications. Lecture Notes in Computer Science, 2004, , 589-599. | 1.3 | 10 |
| 75 | Discovering cluster-based local outliers. Pattern Recognition Letters, 2003, 24, 1641-1650. | 4.2 | 689 |
| 76 | Outlier Detection Integrating Semantic Knowledge. Lecture Notes in Computer Science, 2002, , 126-131. | 1.3 | 27 |
| 77 | Squeezer: An efficient algorithm for clustering categorical data. Journal of Computer Science and Technology, 2002, 17, 611-624. | 1.5 | 120 |