

Weichuan Yu

List of Publications by Year in descending order

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87
papers

3,377
citations

279798

23
h-index

149698

56
g-index

93
all docs

93
docs citations

93
times ranked

4635
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Understanding the Limit of Open Search in the Identification of Peptides With Post-translational Modifications – A Simulation-Based Study. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2884-2890. | 3.0 | 0 |
| 2 | Development of genome-wide polygenic risk scores for lipid traits and clinical applications for dyslipidemia, subclinical atherosclerosis, and diabetes cardiovascular complications among East Asians. Genome Medicine, 2021, 13, 29. | 8.2 | 18 |
| 3 | Isotopically Dimethyl Labeling-Based Quantitative Proteomic Analysis of Phosphoproteomes of Soybean Cultivars. Biomolecules, 2021, 11, 1218. | 4.0 | 5 |
| 4 | Data imbalance in CRISPR off-target prediction. Briefings in Bioinformatics, 2020, 21, 1448-1454. | 6.5 | 24 |
| 5 | Xolik: finding cross-linked peptides with maximum paired scores in linear time. Bioinformatics, 2019, 35, 251-257. | 4.1 | 16 |
| 6 | Region-based interaction detection in genome-wide case-control studies. BMC Medical Genomics, 2019, 12, 133. | 1.5 | 7 |
| 7 | Progression of diabetic kidney disease and trajectory of kidney function decline in Chinese patients with Type 2 diabetes. Kidney International, 2019, 95, 178-187. | 5.2 | 105 |
| 8 | Establishment of Dimethyl Labeling-based Quantitative Acetylproteomics in Arabidopsis. Molecular and Cellular Proteomics, 2018, 17, 1010-1027. | 3.8 | 31 |
| 9 | A network approach to exploring the functional basis of gene-gene epistatic interactions in disease susceptibility. Bioinformatics, 2018, 34, 1741-1749. | 4.1 | 11 |
| 10 | Jointly determining significance levels of primary and replication studies by controlling the false discovery rate in two-stage genome-wide association studies. Statistical Methods in Medical Research, 2018, 27, 2795-2808. | 1.5 | 1 |
| 11 | Low-Rank Adaptive Clutter Filtering for Robust Ultrasound Vector Flow Imaging. , 2018, , . | | 2 |
| 12 | Development of in Planta Chemical Cross-Linking-Based Quantitative Interactomics in Arabidopsis. Journal of Proteome Research, 2018, 17, 3195-3213. | 3.7 | 20 |
| 13 | Controlling the joint local false discovery rate is more powerful than meta-analysis methods in joint analysis of summary statistics from multiple genome-wide association studies. Bioinformatics, 2017, 33, 500-507. | 4.1 | 21 |
| 14 | What is the probability of replicating a statistically significant association in genome-wide association studies?. Briefings in Bioinformatics, 2017, 18, bbw091. | 6.5 | 3 |
| 15 | Apical constriction is driven by a pulsatile apical myosin network in delaminating Drosophila neuroblasts. Development (Cambridge), 2017, 144, 2153-2164. | 2.5 | 47 |
| 16 | FPGA Implementation of the Coupled Filtering Method and the Affine Warping Method. IEEE Transactions on Nanobioscience, 2017, 16, 314-325. | 3.3 | 6 |
| 17 | Exhaustively Identifying Cross-Linked Peptides with a Linear Computational Complexity. Journal of Proteome Research, 2017, 16, 3942-3952. | 3.7 | 21 |
| 18 | In planta chemical cross-linking and mass spectrometry analysis of protein structure and interaction in Arabidopsis. Proteomics, 2016, 16, 1915-1927. | 2.2 | 18 |

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|----|--|------|-----------|
| 19 | ECL: an exhaustive search tool for the identification of cross-linked peptides using whole database. BMC Bioinformatics, 2016, 17, 217. | 2.6 | 16 |
| 20 | FPGA implementation of the coupled filtering method. , 2016, , . | | 0 |
| 21 | PIPI: PTM-Invariant Peptide Identification Using Coding Method. Journal of Proteome Research, 2016, 15, 4423-4435. | 3.7 | 28 |
| 22 | Power estimation and sample size determination for replication studies of genome-wide association studies. BMC Genomics, 2016, 17, 3. | 2.8 | 17 |
| 23 | Low-Rank Modeling and Its Applications in Image Analysis. ACM Computing Surveys, 2015, 47, 1-33. | 23.0 | 102 |
| 24 | PBOOST: a GPU-based tool for parallel permutation tests in genome-wide association studies. Bioinformatics, 2015, 31, 1460-1462. | 4.1 | 11 |
| 25 | Piecewise-constant and low-rank approximation for identification of recurrent copy number variations. Bioinformatics, 2014, 30, 1943-1949. | 4.1 | 29 |
| 26 | Moving Object Detection by Detecting Contiguous Outliers in the Low-Rank Representation. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2013, 35, 597-610. | 13.9 | 623 |
| 27 | The complete compositional epistasis detection in genome-wide association studies. BMC Genetics, 2013, 14, 7. | 2.7 | 18 |
| 28 | Low-rank modeling and its applications in medical image analysis. Proceedings of SPIE, 2013, , . | 0.8 | 9 |
| 29 | On Feature Motion Decorrelation in Ultrasound Speckle Tracking. IEEE Transactions on Medical Imaging, 2013, 32, 435-448. | 8.9 | 22 |
| 30 | Multisample aCGH Data Analysis via Total Variation and Spectral Regularization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 230-235. | 3.0 | 23 |
| 31 | HapBoost: A Fast Approach to Boosting Haplotype Association Analyses in Genome-Wide Association Studies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 207-212. | 3.0 | 2 |
| 32 | A Combinatorial Perspective of the Protein Inference Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1542-1547. | 3.0 | 3 |
| 33 | Ultrasound bio-microscopic image segmentation for evaluation of zebrafish cardiac function. IEEE Transactions on Ultrasonics, Ferroelectrics, and Frequency Control, 2013, 60, 718-726. | 3.0 | 6 |
| 34 | Active Contours with Group Similarity. , 2013, , . | | 24 |
| 35 | Using MicroPET Imaging in Quantitative Verification of the Acupuncture Effect in Ischemia Stroke Treatment. Scientific Reports, 2013, 3, 1070. | 3.3 | 31 |
| 36 | Protein inference: a review. Briefings in Bioinformatics, 2012, 13, 586-614. | 6.5 | 96 |

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| 37 | Peptide Reranking with Protein-Peptide Correspondence and Precursor Peak Intensity Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1212-1219. | 3.0 | 1 |
| 38 | Bioinformatic Analysis of Data Generated from MALDI Mass Spectrometry for Biomarker Discovery. Topics in Current Chemistry, 2012, 331, 193-209. | 4.0 | 6 |
| 39 | Automatic mitral leaflet tracking in echocardiography by outlier detection in the low-rank representation. , 2012, , . | | 7 |
| 40 | Comments on "An empirical comparison of several recent epistatic interaction detection methods". Bioinformatics, 2012, 28, 145-146. | 4.1 | 3 |
| 41 | Guest Editors' Introduction to the Special Issue on "New Trends in Signal Processing and Biomedical Engineering". Computers and Electrical Engineering, 2012, 38, 1-2. | 4.8 | 2 |
| 42 | A brief review of signal processing issues in mass spectrometry-based proteomics studies. , 2011, , . | | 0 |
| 43 | Score regularization for peptide identification. BMC Bioinformatics, 2011, 12, S2. | 2.6 | 9 |
| 44 | A hidden two-locus disease association pattern in genome-wide association studies. BMC Bioinformatics, 2011, 12, 156. | 2.6 | 2 |
| 45 | Motif-All: discovering all phosphorylation motifs. BMC Bioinformatics, 2011, 12, S22. | 2.6 | 32 |
| 46 | The choice of null distributions for detecting gene-gene interactions in genome-wide association studies. BMC Bioinformatics, 2011, 12, S26. | 2.6 | 6 |
| 47 | A Partial Set Covering Model for Protein Mixture Identification Using Mass Spectrometry Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 368-380. | 3.0 | 13 |
| 48 | GBOOST: a GPU-based tool for detecting gene-gene interactions in genome-wide case control studies. Bioinformatics, 2011, 27, 1309-1310. | 4.1 | 137 |
| 49 | Identifying disease-associated SNP clusters via contiguous outlier detection. Bioinformatics, 2011, 27, 2578-2585. | 4.1 | 6 |
| 50 | BOOST: A Fast Approach to Detecting Gene-Gene Interactions in Genome-wide Case-Control Studies. American Journal of Human Genetics, 2010, 87, 325-340. | 6.2 | 452 |
| 51 | Identifying main effects and epistatic interactions from large-scale SNP data via adaptive group Lasso. BMC Bioinformatics, 2010, 11, S18. | 2.6 | 33 |
| 52 | Stable feature selection for biomarker discovery. Computational Biology and Chemistry, 2010, 34, 215-225. | 2.3 | 251 |
| 53 | Using MicroPET Imaging in Quantitative Verification of Acupuncture Effect in Ischemia Stroke Treatment. Nature Precedings, 2010, , . | 0.1 | 1 |
| 54 | A Recombination Hotspot in a Schizophrenia-Associated Region of GABRB2. PLoS ONE, 2010, 5, e9547. | 2.5 | 28 |

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|----|---|-----|-----------|
| 55 | A coupled filtering method to solve feature-motion decorrelation in speckle tracking. , 2010, , . | | 1 |
| 56 | Optimization-Based Peptide Mass Fingerprinting for Protein Mixture Identification. Journal of Computational Biology, 2010, 17, 221-235. | 1.6 | 10 |
| 57 | Detecting two-locus associations allowing for interactions in genome-wide association studies. Bioinformatics, 2010, 26, 2517-2525. | 4.1 | 23 |
| 58 | A Regularized Method for Peptide Quantification. Journal of Proteome Research, 2010, 9, 2705-2712. | 3.7 | 8 |
| 59 | Accurate segmentation of ultrasound images using the motion cue. , 2010, , . | | 0 |
| 60 | SyncPro : A synchronized visualization tool for differential analysis of proteomics data sets. , 2010, , . | | 1 |
| 61 | SNPHarvester: a filtering-based approach for detecting epistatic interactions in genome-wide association studies. Bioinformatics, 2009, 25, 504-511. | 4.1 | 182 |
| 62 | Improving peptide identification with single-stage mass spectrum peaks. Bioinformatics, 2009, 25, 2969-2974. | 4.1 | 6 |
| 63 | MegaSNPHunter: a learning approach to detect disease predisposition SNPs and high level interactions in genome wide association study. BMC Bioinformatics, 2009, 10, 13. | 2.6 | 86 |
| 64 | Comparison of public peak detection algorithms for MALDI mass spectrometry data analysis. BMC Bioinformatics, 2009, 10, 4. | 2.6 | 220 |
| 65 | Semi-supervised protein subcellular localization. BMC Bioinformatics, 2009, 10, S47. | 2.6 | 26 |
| 66 | 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€“t. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2009, 877, 1250-1258. | 2.3 | 80 |
| 67 | Optimization-Based Peptide Mass Fingerprinting for Protein Mixture Identification. Lecture Notes in Computer Science, 2009, , 16-30. | 1.3 | 6 |
| 68 | Peak bagging for peptide mass fingerprinting. Bioinformatics, 2008, 24, 1293-1299. | 4.1 | 8 |
| 69 | Bayesian Mass Spectra Peak Alignment from Mass Charge Ratios. Cancer Informatics, 2008, 6, 117693510800600. | 1.9 | 0 |
| 70 | Optimization-Based Peptide Mass Fingerprinting for Protein Mixture Identification. Nature Precedings, 2008, , . | 0.1 | 0 |
| 71 | Bayesian mass spectra peak alignment from mass charge ratios. Cancer Informatics, 2008, 6, 217-41. | 1.9 | 0 |
| 72 | A new protocol of analyzing isotope-coded affinity tag data from high-resolution LCâ€“MS spectrometry. Computational Biology and Chemistry, 2007, 31, 215-221. | 2.3 | 5 |

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| 73 | Multiple Peak Alignment in Sequential Data Analysis: A Scale-Space-Based Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 208-219. | 3.0 | 24 |
| 74 | Detecting and aligning peaks in mass spectrometry data with applications to MALDI. Computational Biology and Chemistry, 2006, 30, 27-38. | 2.3 | 45 |
| 75 | Towards pointwise motion tracking in echocardiographic image sequences – Comparing the reliability of different features for speckle tracking. Medical Image Analysis, 2006, 10, 495-508. | 11.6 | 58 |
| 76 | MALDI-MS Data Analysis for Disease Biomarker Discovery. , 2006, 328, 199-216. | | 4 |
| 77 | Statistical Methods in Proteomics. , 2006, , 623-638. | | 9 |
| 78 | Using skew Gabor filter in source signal separation and local spectral orientation analysis. Image and Vision Computing, 2005, 23, 377-392. | 4.5 | 5 |
| 79 | LEFT VENTRICULAR BOUNDARY SEGMENTATION FROM ECHOCARDIOGRAPHY. , 2005, , 89-108. | | 1 |
| 80 | Three dimensional orientation signatures with conic kernel filtering for multiple motion analysis. Image and Vision Computing, 2003, 21, 447-458. | 4.5 | 10 |
| 81 | Multiple motion analysis: in spatial or in spectral domain?. Computer Vision and Image Understanding, 2003, 90, 129-152. | 4.7 | 14 |
| 82 | Combinative multi-scale level set framework for echocardiographic image segmentation. Medical Image Analysis, 2003, 7, 529-537. | 11.6 | 121 |
| 83 | Oriented structure of the occlusion distortion: is it reliable?. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2002, 24, 1286-1290. | 13.9 | 8 |
| 84 | Rotated wedge averaging method for junction characterization. , 0, , . | | 7 |
| 85 | 3D-orientation signatures with conic kernel filtering for multiple motion analysis. , 0, , . | | 2 |
| 86 | Using skew gabor filter in source signal separation and local spectral multi-orientation analysis. , 0, , . | | 0 |
| 87 | Aligning Peaks Across Multiple Mass Spectrometry Data Sets Using A Scale-Space Based Approach. , 0, , . | | 0 |