

Yi-Kuo Yu

List of Publications by Year in descending order

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96
papers

3,009
citations

304743

22
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175258

52
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112
all docs

112
docs citations

112
times ranked

4716
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Identification of Antibiotic Resistance Proteins via MiCId™s Augmented Workflow. A Mass Spectrometry-Based Proteomics Approach. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 917-931. | 2.8 | 3 |
| 2 | An 8-Gene Signature for Classifying Major Subtypes of Non-Small-Cell Lung Cancer. <i>Cancer Informatics</i> , 2022, 21, 117693512211007. | 1.9 | 5 |
| 3 | Novel Insights into Quantitative Proteomics from an Innovative Bottom-Up Simple Light Isotope Metabolic (bSLIM) Labeling Data Processing Strategy. <i>Journal of Proteome Research</i> , 2021, 20, 1476-1487. | 3.7 | 7 |
| 4 | Reply to the Comment on "Improving series convergence: the simple pendulum and beyond". <i>European Journal of Physics</i> , 2021, 42, 028006. | 0.6 | 0 |
| 5 | Mass Spectrometry Proteotyping-Based Detection and Identification of <i>Staphylococcus aureus</i> , <i>Escherichia coli</i> , and <i>Candida albicans</i> in Blood. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 634215. | 3.9 | 5 |
| 6 | Rigorous treatment of pairwise and many-body electrostatic interactions among dielectric spheres at the Debye-Hückel level. <i>European Physical Journal E</i> , 2021, 44, 129. | 1.6 | 5 |
| 7 | Electrostatics of charged dielectric spheres with application to biological systems. III. Rigorous ionic screening at the Debye-Hückel level. <i>Physical Review E</i> , 2020, 102, 052404. | 2.1 | 6 |
| 8 | Robust Accurate Identification and Biomass Estimates of Microorganisms via Tandem Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 85-102. | 2.8 | 6 |
| 9 | Exploring induced pluripotency in human fibroblasts via construction, validation, and application of a gene regulatory network. <i>PLoS ONE</i> , 2019, 14, e0220742. | 2.5 | 1 |
| 10 | Electrostatics of charged dielectric spheres with application to biological systems. II. A formalism bypassing Wigner rotation matrices. <i>Physical Review E</i> , 2019, 100, 012401. | 2.1 | 4 |
| 11 | Ultra-High-Frequency Reprogramming of Individual Long-Term Hematopoietic Stem Cells Yields Low Somatic Variant Induced Pluripotent Stem Cells. <i>Cell Reports</i> , 2019, 26, 2580-2592.e7. | 6.4 | 14 |
| 12 | RAId: Knowledge-Integrated Proteomics Web Service with Accurate Statistical Significance Assignment. <i>Proteomics</i> , 2019, 19, 1800367. | 2.2 | 1 |
| 13 | Surface charge method for molecular surfaces with curved areal elements I. Spherical triangles. <i>Journal of Physics Condensed Matter</i> , 2018, 30, 105003. | 1.8 | 3 |
| 14 | A graphical user interface for RAId, a knowledge integrated proteomics analysis suite with accurate statistics. <i>BMC Research Notes</i> , 2018, 11, 182. | 1.4 | 0 |
| 15 | Improving series convergence: the simple pendulum and beyond. <i>European Journal of Physics</i> , 2018, 39, 065802. | 0.6 | 3 |
| 16 | Thermal Expansion of Single-Crystal H ₂ O and D ₂ O Ice Ih. <i>Physical Review Letters</i> , 2018, 121, 185505. | 7.8 | 15 |
| 17 | Robust Hund rule without Coulomb repulsion and exclusion principle in quantum antiferromagnetic chains of composite half spins. <i>Journal of Physics Condensed Matter</i> , 2018, 30, 435801. | 1.8 | 0 |
| 18 | Rapid Classification and Identification of Multiple Microorganisms with Accurate Statistical Significance via High-Resolution Tandem Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 1721-1737. | 2.8 | 26 |

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|----|--|-----|-----------|
| 19 | Extending electrostatics of dielectric spheres to arbitrary charge distributions with applications to biosystems. <i>Physical Review E</i> , 2017, 96, 062414. | 2.1 | 7 |
| 20 | Can dielectric spheres accurately model atomic-scale interactions?. <i>Europhysics Letters</i> , 2016, 116, 24003. | 2.0 | 6 |
| 21 | Confidence assignment for mass spectrometry based peptide identifications via the extreme value distribution. <i>Bioinformatics</i> , 2016, 32, 2642-2649. | 4.1 | 4 |
| 22 | Identification of Microorganisms by High Resolution Tandem Mass Spectrometry with Accurate Statistical Significance. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 194-210. | 2.8 | 20 |
| 23 | Mechanism-based disease similarity. <i>Journal of Rare Diseases Research & Treatment</i> , 2016, 1, 1-4. | 1.1 | 3 |
| 24 | Analytical solution and scaling of fluctuations in complex networks traversed by damped, interacting random walkers. <i>Physical Review E</i> , 2015, 92, 052803. | 2.1 | 0 |
| 25 | A magnetic field tuned metal-insulator transition in unconventional metallic K-doped MoO. <i>Physica Status Solidi (B): Basic Research</i> , 2015, 252, 839-842. | 1.5 | 1 |
| 26 | DeCoaD: determining correlations among diseases using protein interaction networks. <i>BMC Research Notes</i> , 2015, 8, 226. | 1.4 | 16 |
| 27 | Log-odds sequence logos. <i>Bioinformatics</i> , 2015, 31, 324-331. | 4.1 | 14 |
| 28 | Mass spectrometry-based protein identification with accurate statistical significance assignment. <i>Bioinformatics</i> , 2015, 31, 699-706. | 4.1 | 17 |
| 29 | Accuracy Evaluation of the Unified P-Value from Combining Correlated P-Values. <i>PLoS ONE</i> , 2014, 9, e91225. | 2.5 | 23 |
| 30 | Molecular Isotopic Distribution Analysis (MIDAS) with Adjustable Mass Accuracy. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 57-70. | 2.8 | 16 |
| 31 | Electrical interactions in the cell: Asymmetric screening in a watery ϵ -antiverse. <i>American Journal of Physics</i> , 2014, 82, 460-465. | 0.7 | 6 |
| 32 | Relating Diseases by Integrating Gene Associations and Information Flow through Protein Interaction Network. <i>PLoS ONE</i> , 2014, 9, e110936. | 2.5 | 18 |
| 33 | Building a Hierarchical Organization of Protein Complexes Out of Protein Association Data. <i>PLoS ONE</i> , 2014, 9, e100098. | 2.5 | 0 |
| 34 | Using dissociation energies to predict observability of b- and y-peaks in mass spectra of short peptides. II. Results for hexapeptides with non-polar side chains. <i>Rapid Communications in Mass Spectrometry</i> , 2013, 27, 152-156. | 1.5 | 4 |
| 35 | Improving Peptide Identification Sensitivity in Shotgun Proteomics by Stratification of Search Space. <i>Journal of Proteome Research</i> , 2013, 12, 2571-2581. | 3.7 | 24 |
| 36 | CytoSaddleSum: a functional enrichment analysis plugin for Cytoscape based on sum-of-weights scores. <i>Bioinformatics</i> , 2012, 28, 893-894. | 4.1 | 4 |

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| 37 | Information Flow in Interaction Networks II: Channels, Path Lengths, and Potentials. <i>Journal of Computational Biology</i> , 2012, 19, 379-403. | 1.6 | 15 |
| 38 | CytoITMprobe: a network information flow plugin for Cytoscape. <i>BMC Research Notes</i> , 2012, 5, 237. | 1.4 | 3 |
| 39 | Using dissociation energies to predict observability of bàand yàpeaks in mass spectra of short peptides. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 915-920. | 1.5 | 10 |
| 40 | The Complexity of the Dirichlet Model for Multiple Alignment Data. <i>Journal of Computational Biology</i> , 2011, 18, 925-939. | 1.6 | 3 |
| 41 | Policy and Data-Intensive Scientific Discovery in the Beginning of the 21st Century. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 221-225. | 2.0 | 21 |
| 42 | Combining Independent, Weighted P-Values: Achieving Computational Stability by a Systematic Expansion with Controllable Accuracy. <i>PLoS ONE</i> , 2011, 6, e22647. | 2.5 | 14 |
| 43 | Assigning statistical significance to proteotypic peptides via database searches. <i>Journal of Proteomics</i> , 2011, 74, 199-211. | 2.4 | 12 |
| 44 | On the Inference of Dirichlet Mixture Priors for Protein Sequence Comparison. <i>Journal of Computational Biology</i> , 2011, 18, 941-954. | 1.6 | 5 |
| 45 | Challenges of Information Retrieval and Evaluation in Data-Centric Biology. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 239-240. | 2.0 | 0 |
| 46 | ppiTrim: constructing non-redundant and up-to-date interactomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar036. | 3.0 | 12 |
| 47 | Robust and accurate data enrichment statistics via distribution function of sum of weights. <i>Bioinformatics</i> , 2010, 26, 2752-2759. | 4.1 | 18 |
| 48 | Simple electrostatic model applicable to biomolecular recognition. <i>Physical Review E</i> , 2010, 81, 031925. | 2.1 | 6 |
| 49 | The Construction and Use of Log-Odds Substitution Scores for Multiple Sequence Alignment. <i>PLoS Computational Biology</i> , 2010, 6, e1000852. | 3.2 | 58 |
| 50 | Compositional Adjustment of Dirichlet Mixture Priors. <i>Journal of Computational Biology</i> , 2010, 17, 1607-1620. | 1.6 | 9 |
| 51 | RAld_aPS: MS/MS Analysis with Multiple Scoring Functions and Spectrum-Specific Statistics. <i>PLoS ONE</i> , 2010, 5, e15438. | 2.5 | 20 |
| 52 | Rigorous treatment of electrostatics for spatially varying dielectrics based on energy minimization. <i>Physical Review E</i> , 2009, 79, 041907. | 2.1 | 8 |
| 53 | Geometric Aspects of Biological Sequence Comparison. <i>Journal of Computational Biology</i> , 2009, 16, 579-610. | 1.6 | 10 |
| 54 | Statistical characterization of a 1D random potential problemàWith applications in score statistics of MS-based peptide sequencing. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2008, 387, 6538-6544. | 2.6 | 16 |

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| 55 | RAId_DbS: mass-spectrometry based peptide identification web server with knowledge integration. BMC Genomics, 2008, 9, 505. | 2.8 | 19 |
| 56 | Detection of co-eluted peptides using database search methods. Biology Direct, 2008, 3, 27. | 4.6 | 22 |
| 57 | Magnetic signatures of ferromagnetic polarons in $\text{La}_{1-x}\text{Ca}_x\text{MnO}_3$. Colossal magnetoresistance is not a Griffiths singular. Physical Review B, 2008, 78, . | 3.2 | 53 |
| 58 | Enhancing Peptide Identification Confidence by Combining Search Methods. Journal of Proteome Research, 2008, 7, 3102-3113. | 3.7 | 66 |
| 59 | Electrical transport in single-crystalline $\text{Li}_{1-x}\text{La}_x\text{Ti}_2\text{O}_7$. A two-band Luttinger liquid exhibiting Bose metal behavior. Physical Review B, 2008, 77, . | 3.2 | 29 |
| 60 | Heat Conduction Process on Community Networks as a Recommendation Model. Physical Review Letters, 2007, 99, 154301. | 7.8 | 192 |
| 61 | Dimensional Crossover in the Purple Bronze $\text{Li}_{0.9}\text{Mo}_6\text{O}_{17}$. Physical Review Letters, 2007, 98, 266405. | 7.8 | 53 |
| 62 | Information Flow in Interaction Networks. Journal of Computational Biology, 2007, 14, 1115-1143. | 1.6 | 39 |
| 63 | RAId_DbS: Peptide Identification using Database Searches with Realistic Statistics. Biology Direct, 2007, 2, 25. | 4.6 | 26 |
| 64 | Calibrating E-values for MS2 database search methods. Biology Direct, 2007, 2, 26. | 4.6 | 24 |
| 65 | Cysteine-Cysteine Contact Preference Leads to Target-Focusing in Protein Folding. Biophysical Journal, 2007, 93, 938-951. | 0.5 | 12 |
| 66 | A metric measure for weight matrices of variable lengths with applications to clustering and classification of hidden Markov models. Physica A: Statistical Mechanics and Its Applications, 2007, 375, 212-220. | 2.6 | 1 |
| 67 | Composition-based statistics and translated nucleotide searches: Improving the TBLASTN module of BLAST. BMC Biology, 2006, 4, 41. | 3.8 | 420 |
| 68 | Decoding information from noisy, redundant, and intentionally distorted sources. Physica A: Statistical Mechanics and Its Applications, 2006, 371, 732-744. | 2.6 | 37 |
| 69 | Electrostatics of charged dielectric spheres with application to biological systems. Physical Review E, 2006, 73, 061902. | 2.1 | 27 |
| 70 | Retrieval accuracy, statistical significance and compositional similarity in protein sequence database searches. Nucleic Acids Research, 2006, 34, 5966-5973. | 14.5 | 53 |
| 71 | Thermodynamic nature of the antiferromagnetic transition in Na_xCoO_2 . Physical Review B, 2006, 74, . | 3.2 | 12 |
| 72 | Ranked solutions to a class of combinatorial optimizations with applications in mass spectrometry based peptide sequencing and a variant of directed paths in random media. Physica A: Statistical Mechanics and Its Applications, 2005, 354, 558-570. | 2.6 | 4 |

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| 73 | Protein database searches using compositionally adjusted substitution matrices. FEBS Journal, 2005, 272, 5101-5109. | 4.7 | 881 |
| 74 | Toward an accurate statistics of gapped alignments. Bulletin of Mathematical Biology, 2005, 67, 169-191. | 1.9 | 20 |
| 75 | The construction of amino acid substitution matrices for the comparison of proteins with non-standard compositions. Bioinformatics, 2005, 21, 902-911. | 4.1 | 86 |
| 76 | Method for Analyzing Second-Order Phase Transitions: Application to the Ferromagnetic Transition of a Polaronic System. Physical Review Letters, 2005, 94, 207209. | 7.8 | 48 |
| 77 | Robust accurate identification of peptides (RAld): deciphering MS2 data using a structured library search with de novo based statistics. Bioinformatics, 2005, 21, 3726-3732. | 4.1 | 22 |
| 78 | Replica model for an unusual directed polymer in 1+1 dimensions and prediction of the extremal parameter of gapped sequence alignment statistics. Physical Review E, 2004, 69, 061904. | 2.1 | 3 |
| 79 | Scale-free networks versus evolutionary drift. Computational Biology and Chemistry, 2004, 28, 257-264. | 2.3 | 16 |
| 80 | Electrostatics in the presence of dielectrics: The benefits of treating the induced surface charge density directly. American Journal of Physics, 2004, 72, 190-196. | 0.7 | 25 |
| 81 | On a class of integrals of Legendre polynomials with complicated arguments with applications in electrostatics and biomolecular modeling. Physica A: Statistical Mechanics and Its Applications, 2003, 326, 522-533. | 2.6 | 8 |
| 82 | The compositional adjustment of amino acid substitution matrices. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15688-15693. | 7.1 | 79 |
| 83 | Hybrid alignment: high-performance with universal statistics. Bioinformatics, 2002, 18, 864-872. | 4.1 | 24 |
| 84 | On the Anti-Wishart distribution. Physica A: Statistical Mechanics and Its Applications, 2002, 312, 1-22. | 2.6 | 9 |
| 85 | Buyer feedback as a filtering mechanism for reputable sellers. Physica A: Statistical Mechanics and Its Applications, 2002, 316, 413-429. | 2.6 | 10 |
| 86 | Statistical Significance of Probabilistic Sequence Alignment and Related Local Hidden Markov Models. Journal of Computational Biology, 2001, 8, 249-282. | 1.6 | 55 |
| 87 | Effect of Noise on a Quantum Bound State. Physical Review Letters, 2000, 85, 4199-4202. | 7.8 | 1 |
| 88 | Self-Consistent Approach to a Strongly Disordered Planar Model with Application to 2D Nematic Elastomers. Physical Review Letters, 1999, 83, 5515-5518. | 7.8 | 3 |
| 89 | Are Directed Waves Multifractal?. Physical Review Letters, 1998, 81, 3924-3927. | 7.8 | 5 |
| 90 | Preliminary communication Nematic-substrate repulsion in the nematic-isotropic phase coexistence region. Liquid Crystals, 1998, 24, 891-894. | 2.2 | 0 |

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| 91 | Cell Thickness-Induced Ferrielectric Phases in Antiferroelectric/Ferrielectric Liquid Crystals. Japanese Journal of Applied Physics, 1996, 35, L1608-L1610. | 1.5 | 15 |
| 92 | Interfacial kinetic roughening with correlated noise. Physical Review E, 1995, 52, 3224-3227. | 2.1 | 30 |
| 93 | Concise calculation of the scaling function, exponents, and probability functional of the Edwards-Wilkinson equation with correlated noise. Physical Review E, 1994, 50, 5111-5114. | 2.1 | 19 |
| 94 | Replica model at low integer N for directed polymers in $(1+1)$ dimensions. Physical Review E, 1994, 49, 4157-4166. | 2.1 | 4 |
| 95 | Directed waves in random media: An analytical calculation. Physical Review E, 1994, 49, 5755-5762. | 2.1 | 6 |
| 96 | Energy of an electrorheological solid calculated with inclusion of higher multipoles. Physical Review B, 1992, 46, 6582-6585. | 3.2 | 30 |