

Yi-Kuo Yu

List of Publications by Year in descending order

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96
papers

3,009
citations

304743

22
h-index

175258

52
g-index

112
all docs

112
docs citations

112
times ranked

4716
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein database searches using compositionally adjusted substitution matrices. FEBS Journal, 2005, 272, 5101-5109.	4.7	881
2	Composition-based statistics and translated nucleotide searches: Improving the TBLASTN module of BLAST. BMC Biology, 2006, 4, 41.	3.8	420
3	Heat Conduction Process on Community Networks as a Recommendation Model. Physical Review Letters, 2007, 99, 154301.	7.8	192
4	The construction of amino acid substitution matrices for the comparison of proteins with non-standard compositions. Bioinformatics, 2005, 21, 902-911.	4.1	86
5	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
6	Enhancing Peptide Identification Confidence by Combining Search Methods. Journal of Proteome Research, 2008, 7, 3102-3113.	3.7	66
7	The Construction and Use of Log-Odds Substitution Scores for Multiple Sequence Alignment. PLoS Computational Biology, 2010, 6, e1000852.	3.2	58
8	Statistical Significance of Probabilistic Sequence Alignment and Related Local Hidden Markov Models. Journal of Computational Biology, 2001, 8, 249-282.	1.6	55
9	Retrieval accuracy, statistical significance and compositional similarity in protein sequence database searches. Nucleic Acids Research, 2006, 34, 5966-5973.	14.5	53
10	Dimensional Crossover in the Purple BronzeLi _{0.9} Mo ₆ O ₁₇ . Physical Review Letters, 2007, 98, 266405.	7.8	53
11	Magnetic signatures of ferromagnetic polarons in $\langle \text{mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" display="inline"} \langle \text{mml:mrow} \langle \text{mml:msub} \langle \text{mml:mrow} \langle \text{mml:mtext} \text{La} \langle \text{mml:mtext} \rangle \langle \text{mml:mrow} \langle \text{mml:mrow} \langle \text{mml:mn} \rangle 0.7 \langle \text{mml:mtext} \rangle \text{La} \langle \text{mml:mtext} \rangle \rangle \rangle \rangle \rangle \rangle$ Colossal magnetoresistance is not a Griffiths singular. Physical Review B. 2008, 78, .	3.2	53
12	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
13	Information Flow in Interaction Networks. Journal of Computational Biology, 2007, 14, 1115-1143.	1.6	39
14	Decoding information from noisy, redundant, and intentionally distorted sources. Physica A: Statistical Mechanics and Its Applications, 2006, 371, 732-744.	2.6	37
15	Energy of an electrorheological solid calculated with inclusion of higher multipoles. Physical Review B, 1992, 46, 6582-6585.	3.2	30
16	Interfacial kinetic roughening with correlated noise. Physical Review E, 1995, 52, 3224-3227.	2.1	30
17	Electrostatics of charged dielectric spheres with application to biological systems. Physical Review E, 2006, 73, 061902.	2.1	27
18	RAId_DbS: Peptide Identification using Database Searches with Realistic Statistics. Biology Direct, 2007, 2, 25.	4.6	26

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19	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
20	Electrostatics in the presence of dielectrics: The benefits of treating the induced surface charge density directly. <i>American Journal of Physics</i> , 2004, 72, 190-196.	0.7	25
21	Hybrid alignment: high-performance with universal statistics. <i>Bioinformatics</i> , 2002, 18, 864-872.	4.1	24
22	Calibrating E-values for MS2 database search methods. <i>Biology Direct</i> , 2007, 2, 26.	4.6	24
23	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
24	Accuracy Evaluation of the Unified P-Value from Combining Correlated P-Values. <i>PLoS ONE</i> , 2014, 9, e91225.	2.5	23
25	Robust accurate identification of peptides (RAId): deciphering MS2 data using a structured library search with de novo based statistics. <i>Bioinformatics</i> , 2005, 21, 3726-3732.	4.1	22
26	Detection of co-eluted peptides using database search methods. <i>Biology Direct</i> , 2008, 3, 27.	4.6	22
27	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
28	Toward an accurate statistics of gapped alignments. <i>Bulletin of Mathematical Biology</i> , 2005, 67, 169-191.	1.9	20
29	Electrical transport in single-crystalline Li . A two-band Luttinger liquid exhibiting Bose metal behavior. <i>Physical Review B</i> . 2008. 77, .	3.2	20
30	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
31	RAId_aPS: MS/MS Analysis with Multiple Scoring Functions and Spectrum-Specific Statistics. <i>PLoS ONE</i> , 2010, 5, e15438.	2.5	20
32	Concise calculation of the scaling function, exponents, and probability functional of the Edwards-Wilkinson equation with correlated noise. <i>Physical Review E</i> , 1994, 50, 5111-5114.	2.1	19
33	RAId_DbS: mass-spectrometry based peptide identification web server with knowledge integration. <i>BMC Genomics</i> , 2008, 9, 505.	2.8	19
34	Robust and accurate data enrichment statistics via distribution function of sum of weights. <i>Bioinformatics</i> , 2010, 26, 2752-2759.	4.1	18
35	Relating Diseases by Integrating Gene Associations and Information Flow through Protein Interaction Network. <i>PLoS ONE</i> , 2014, 9, e110936.	2.5	18
36	Mass spectrometry-based protein identification with accurate statistical significance assignment. <i>Bioinformatics</i> , 2015, 31, 699-706.	4.1	17

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37	Scale-free networks versus evolutionary drift. <i>Computational Biology and Chemistry</i> , 2004, 28, 257-264.	2.3	16
38	Statistical characterization of a 1D random potential problem—With 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
39	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
40	DeCoaD: determining correlations among diseases using protein interaction networks. <i>BMC Research Notes</i> , 2015, 8, 226.	1.4	16
41	Cell Thickness-Induced Ferrielectric Phases in Antiferroelectric/Ferrielectric Liquid Crystals. <i>Japanese Journal of Applied Physics</i> , 1996, 35, L1608-L1610.	1.5	15
42	Information Flow in Interaction Networks II: Channels, Path Lengths, and Potentials. <i>Journal of Computational Biology</i> , 2012, 19, 379-403.	1.6	15
43	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
44	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
45	Log-odds sequence logos. <i>Bioinformatics</i> , 2015, 31, 324-331.	4.1	14
46	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
47	Thermodynamic nature of the antiferromagnetic transition in Na _x CoO ₂ . <i>Physical Review B</i> , 2006, 74, .	3.2	12
48	Cysteine-Cysteine Contact Preference Leads to Target-Focusing in Protein Folding. <i>Biophysical Journal</i> , 2007, 93, 938-951.	0.5	12
49	Assigning statistical significance to proteotypic peptides via database searches. <i>Journal of Proteomics</i> , 2011, 74, 199-211.	2.4	12
50	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
51	Buyer feedback as a filtering mechanism for reputable sellers. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2002, 316, 413-429.	2.6	10
52	Geometric Aspects of Biological Sequence Comparison. <i>Journal of Computational Biology</i> , 2009, 16, 579-610.	1.6	10
53	Using dissociation energies to predict observability of b ⁺ - and y ⁺ -peaks in mass spectra of short peptides. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 915-920.	1.5	10
54	On the Anti-Wishart distribution. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2002, 312, 1-22.	2.6	9

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55	Compositional Adjustment of Dirichlet Mixture Priors. <i>Journal of Computational Biology</i> , 2010, 17, 1607-1620.	1.6	9
56	On a class of integrals of Legendre polynomials with complicated arguments with applications in electrostatics and biomolecular modeling. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2003, 326, 522-533.	2.6	8
57	Rigorous treatment of electrostatics for spatially varying dielectrics based on energy minimization. <i>Physical Review E</i> , 2009, 79, 041907.	2.1	8
58	Extending electrostatics of dielectric spheres to arbitrary charge distributions with applications to biosystems. <i>Physical Review E</i> , 2017, 96, 062414.	2.1	7
59	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
60	Directed waves in random media: An analytical calculation. <i>Physical Review E</i> , 1994, 49, 5755-5762.	2.1	6
61	Simple electrostatic model applicable to biomolecular recognition. <i>Physical Review E</i> , 2010, 81, 031925.	2.1	6
62	Electrical interactions in the cell: Asymmetric screening in a watery environment. <i>American Journal of Physics</i> , 2014, 82, 460-465.	0.7	6
63	Can dielectric spheres accurately model atomic-scale interactions?. <i>Europhysics Letters</i> , 2016, 116, 24003.	2.0	6
64	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
65	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
66	Are Directed Waves Multifractal?. <i>Physical Review Letters</i> , 1998, 81, 3924-3927.	7.8	5
67	On the Inference of Dirichlet Mixture Priors for Protein Sequence Comparison. <i>Journal of Computational Biology</i> , 2011, 18, 941-954.	1.6	5
68	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
69	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
70	An 8-Gene Signature for Classifying Major Subtypes of Non-Small-Cell Lung Cancer. <i>Cancer Informatics</i> , 2022, 21, 117693512211007.	1.9	5
71	Replica model at low integer N for directed polymers in $(1+1)$ dimensions. <i>Physical Review E</i> , 1994, 49, 4157-4166.	2.1	4
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. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2005, 354, 558-570.	2.6	4

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73	CytoSaddleSum: a functional enrichment analysis plugin for Cytoscape based on sum-of-weights scores. <i>Bioinformatics</i> , 2012, 28, 893-894.	4.1	4
74	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
75	Confidence assignment for mass spectrometry based peptide identifications via the extreme value distribution. <i>Bioinformatics</i> , 2016, 32, 2642-2649.	4.1	4
76	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
77	Self-Consistent Approach to a Strongly Disordered Planar Model with Application to 2D Nematic Elastomers. <i>Physical Review Letters</i> , 1999, 83, 5515-5518.	7.8	3
78	Replica model for an unusual directed polymer in 1+1 dimensions and prediction of the extremal parameter of gapped sequence alignment statistics. <i>Physical Review E</i> , 2004, 69, 061904.	2.1	3
79	The Complexity of the Dirichlet Model for Multiple Alignment Data. <i>Journal of Computational Biology</i> , 2011, 18, 925-939.	1.6	3
80	CytoITMprobe: a network information flow plugin for Cytoscape. <i>BMC Research Notes</i> , 2012, 5, 237.	1.4	3
81	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
82	Improving series convergence: the simple pendulum and beyond. <i>European Journal of Physics</i> , 2018, 39, 065802.	0.6	3
83	Mechanism-based disease similarity. <i>Journal of Rare Diseases Research & Treatment</i> , 2016, 1, 1-4.	1.1	3
84	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
85	Effect of Noise on a Quantum Bound State. <i>Physical Review Letters</i> , 2000, 85, 4199-4202.	7.8	1
86	A metric measure for weight matrices of variable lengths ⁺ with applications to clustering and classification of hidden Markov models. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007, 375, 212-220.	2.6	1
87	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
88	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
89	RAId: Knowledge ⁺ Integrated Proteomics Web Service with Accurate Statistical Significance Assignment. <i>Proteomics</i> , 2019, 19, 1800367.	2.2	1
90	Preliminary communication Nematic-substrate repulsion in the nematic-isotropic phase coexistence region. <i>Liquid Crystals</i> , 1998, 24, 891-894.	2.2	0

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91	Challenges of Information Retrieval and Evaluation in Data-Centric Biology. OMICS A Journal of Integrative Biology, 2011, 15, 239-240.	2.0	0
92	Analytical solution and scaling of fluctuations in complex networks traversed by damped, interacting random walkers. Physical Review E, 2015, 92, 052803.	2.1	0
93	A graphical user interface for RAId, a knowledge integrated proteomics analysis suite with accurate statistics. BMC Research Notes, 2018, 11, 182.	1.4	0
94	Robust Hund rule without Coulomb repulsion and exclusion principle in quantum antiferromagnetic chains of composite half spins. Journal of Physics Condensed Matter, 2018, 30, 435801.	1.8	0
95	Reply to the Comment on "Improving series convergence: the simple pendulum and beyond". European Journal of Physics, 2021, 42, 028006.	0.6	0
96	Building a Hierarchical Organization of Protein Complexes Out of Protein Association Data. PLoS ONE, 2014, 9, e100098.	2.5	0