Uri Keich

List of Publications by Year
in descending order

41 papers	1,051 citations	567281 15 h-index	434195 31 g-index
47 all docs	47 docs citations	47 times ranked	1405 citing authors

#	Article	IF	Citations
1	Building Spectral Libraries from Narrow-Window Data-Independent Acquisition Mass Spectrometry Data. Journal of Proteome Research, 2022, 21, 1382-1391.	3.7	6
2	Accurately Assigning Peptides to Spectra When Only a Subset of Peptides Are Relevant. Journal of Proteome Research, 2021, 20, 4153-4164.	3.7	10
3	Exactly Computing the Tail of the Poisson-Binomial Distribution. ACM Transactions on Mathematical Software, 2021, 47, 1-19.	2.9	2
4	Multiple Competition-Based FDR Control and Its Application to Peptide Detection. Lecture Notes in Computer Science, 2020, , 54-71.	1.3	12
5	Averaging Strategy To Reduce Variability in Target-Decoy Estimates of False Discovery Rate. Journal of Proteome Research, 2019, 18, 585-593.	3.7	26
6	Controlling the FDR in Imperfect Matches to an Incomplete Database. Journal of the American Statistical Association, 2018, 113, 973-982.	3.1	7
7	Accurate Small Tail Probabilities of Sums of iid Lattice-Valued Random Variables via FFT. Journal of Computational and Graphical Statistics, 2017, 26, 223-229.	1.7	1
8	Progressive Calibration and Averaging for Tandem Mass Spectrometry Statistical Confidence Estimation: Why Settle for a Single Decoy?. Lecture Notes in Computer Science, 2017, 10229, 99-116.	1.3	11
9	Response to â€œMass spectrometrists should search for all peptides, but assess only the ones they care aboutâ€. Nature Methods, 2017, 14, 644-644.	19.0	9
10	Accurate pairwise convolutions of non-negative vectors via FFT. Computational Statistics and Data Analysis, 2016, 101, 300-315.	1.2	3
11	A Symmetric Length-Aware Enrichment Test. Journal of Computational Biology, 2016, 23, 508-525.	1.6	1
12	Improved False Discovery Rate Estimation Procedure for Shotgun Proteomics. Journal of Proteome Research, 2015, 14, 3148-3161.	3.7	55
13	Tandem Mass Spectrum Identification via Cascaded Search. Journal of Proteome Research, 2015, 14, 3027-3038.	3.7	63
14	On the Importance of Well-Calibrated Scores for Identifying Shotgun Proteomics Spectra. Journal of Proteome Research, 2015, 14, 1147-1160.	3.7	30
15	Improving MEME via a two-tiered significance analysis. Bioinformatics, 2014, 30, 1965-1973.	4.1	20
16	High-resolution mapping, characterization, and optimization of autonomously replicating sequences in yeast. Genome Research, 2013, 23, 698-704.	5.5	53
17	Novel features of ARS selection in budding yeast Lachancea kluyveri. BMC Genomics, 2011, 12, 633.	2.8	18
18	Target-Decoy Approach and False Discovery Rate: When Things May Go Wrong. Journal of the American Society for Mass Spectrometry, 2011, 22, 1111-1120.	2.8	134

#	ARTICLE	IF	CITATIONS
19	Alignment Constrained Sampling. Journal of Computational Biology, 2011, 18, 155-168.	1.6	0
20	Improved similarity scores for comparing motifs. Bioinformatics, 2011, 27, 1603-1609.	4.1	50
21	Confidently Estimating the Number of DNA Replication Origins. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article28.	0.6	3
22	A Comprehensive Genome-Wide Map of Autonomously Replicating Sequences in a Naive Genome. PLoS Genetics, 2010, 6, e1000946.	3.5	51
23	Deep RNA sequencing of L. monocytogenes reveals overlapping and extensive stationary phase and sigma B-dependent transcriptomes, including multiple highly transcribed noncoding RNAs. BMC Genomics, 2009, 10, 641.	2.8	160
24	Reliability and efficiency of algorithms for computing the significance of the Mannâ€"Whitney test. Computational Statistics, 2009, 24, 605-622.	1.5	10
25	Computational detection of significant variation in binding affinity across two sets of sequences with application to the analysis of replication origins in yeast. BMC Bioinformatics, 2008, 9, 372.	2.6	6
26	GIMSAN: a Gibbs motif finder with significance analysis. Bioinformatics, 2008, 24, 2256-2257.	4.1	29
27	FAST: Fourier transform based algorithms for significance testing of ungapped multiple alignments. Bioinformatics, 2008, 24, 577-578.	4.1	7
28	Factoring local sequence composition in motif significance analysis. , 2008, , .		0
29	Factoring local sequence composition in motif significance analysis. Genome Informatics, 2008, 21, 15-26.	0.4	3
30	Correcting Base-Assignment Errors in Repeat Regions of Shotgun Assembly. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 54-64.	3.0	9
31	A conservative parametric approach to motif significance analysis. , 2007, , .		1
32	A conservative parametric approach to motif significance analysis. Genome Informatics, 2007, 19, 61-72.	0.4	2
33	Apples to apples: improving the performance of motif finders and their significance analysis in the Twilight Zone. Bioinformatics, 2006, 22, e393-e401.	4.1	8
34	A Fast and Numerically Robust Method for Exact Multinomial Goodness-of-Fit Test. Journal of Computational and Graphical Statistics, 2006, 15, 779-802.	1.7	11
35	Designing seeds for similarity search in genomic DNA. Journal of Computer and System Sciences, 2005, 70, 342-363.	1.2	64
36	Computing the P-value of the information content from an alignment of multiple sequences. Bioinformatics, 2005, 21, i311-i318.	4.1	34

#	Article	IF	Citations
37	sFFT: A Faster Accurate Computation of the p-Value of the Entropy Score. Journal of Computational Biology, 2005, 12, 416-430.	1.6	11
38	On spaced seeds for similarity search. Discrete Applied Mathematics, 2004, 138, 253-263.	0.9	110
39	Optimal decompositions for the K-functional for a couple of Banach lattices. Arkiv for Matematik, 2001, 39, 27-64.	0.5	3
40	Krein's strings, the symmetric moment problem, and extending a real positive definite function. Communications on Pure and Applied Mathematics, 1999, 52, 1315-1334.	3.1	4
41	A generalization of the Ahlswede-Daykin inequality. Discrete Mathematics, 1996, 152, 1-12.	0.7	9