Uri Keich

List of Publications by Year in Descending Order

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Version: 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

38 papers	812 citations	14 h-index	28 g-index
47 ext. papers	972 ext. citations	4 avg, IF	4.07 L-index

#	Paper	IF	Citations
38	Accurately Assigning Peptides to Spectra When Only a Subset of Peptides Are Relevant. *Journal of Proteome Research*, **2021**, 20, 4153-4164	5.6	2
37	Exactly Computing the Tail of the Poisson-Binomial Distribution. *ACM Transactions on Mathematical Software*, **2021**, 47, 1-19	2.3	1
36	Multiple Competition-Based FDR Control and Its Application to Peptide Detection. *Lecture Notes in Computer Science*, **2020**, 54-71	0.9	3
35	Averaging Strategy To Reduce Variability in Target-Decoy Estimates of False Discovery Rate. *Journal of Proteome Research*, **2019**, 18, 585-593	5.6	12
34	Controlling the FDR in imperfect matches to an incomplete database. *Journal of the American Statistical Association*, **2018**, 113, 973-982	2.8	5
33	Accurate Small Tail Probabilities of Sums of iid Lattice-Valued Random Variables via FFT. *Journal of Computational and Graphical Statistics*, **2017**, 26, 223-229	1.4	1
32	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	0.9	9
31	Response to "Mass spectrometrists should search for all peptides, but assess only the ones they care about". *Nature Methods*, **2017**, 14, 644	21.6	4
30	A Symmetric Length-Aware Enrichment Test. *Journal of Computational Biology*, **2016**, 23, 508-25	1.7	1
29	Accurate pairwise convolutions of non-negative vectors via FFT. *Computational Statistics and Data Analysis*, **2016**, 101, 300-315	1.6	3
28	Improved False Discovery Rate Estimation Procedure for Shotgun Proteomics. *Journal of Proteome Research*, **2015**, 14, 3148-61	5.6	39
27	Tandem Mass Spectrum Identification via Cascaded Search. *Journal of Proteome Research*, **2015**, 14, 3027-38	5.6	47
26	On the importance of well-calibrated scores for identifying shotgun proteomics spectra. *Journal of Proteome Research*, **2015**, 14, 1147-60	5.6	21
25	Improving MEME via a two-tiered significance analysis. *Bioinformatics*, **2014**, 30, 1965-73	7.2	15
24	High-resolution mapping, characterization, and optimization of autonomously replicating sequences in yeast. *Genome Research*, **2013**, 23, 698-704	9.7	38
23	Novel features of ARS selection in budding yeast Lachancea kluyveri. *BMC Genomics*, **2011**, 12, 633	4.5	16
22	Target-decoy approach and false discovery rate: when things may go wrong. *Journal of the American Society for Mass Spectrometry*, **2011**, 22, 1111-20	3.5	107

21	Alignment constrained sampling. *Journal of Computational Biology*, **2011**, 18, 155-68	1.7	
20	Improved similarity scores for comparing motifs. *Bioinformatics*, **2011**, 27, 1603-9	7.2	41
19	Confidently estimating the number of DNA replication origins. *Statistical Applications in Genetics and Molecular Biology*, **2010**, 9, Article28	1.2	3
18	A comprehensive genome-wide map of autonomously replicating sequences in a naive genome. *PLoS Genetics*, **2010**, 6, e1000946	6	41
17	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	4.5	145
16	Reliability and efficiency of algorithms for computing the significance of the Mann-Whitney test. *Computational Statistics*, **2009**, 24, 605-622	1	7
15	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	3.6	6
14	GIMSAN: a Gibbs motif finder with significance analysis. *Bioinformatics*, **2008**, 24, 2256-7	7.2	28
13	FAST: Fourier transform based algorithms for significance testing of ungapped multiple alignments. *Bioinformatics*, **2008**, 24, 577-8	7.2	6
12	Factoring local sequence composition in motif significance analysis. *Genome Informatics*, **2008**, 21, 15-26		2
11	Correcting base-assignment errors in repeat regions of shotgun assembly. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2007**, 4, 54-64	3	6
10	A conservative parametric approach to motif significance analysis. *Genome Informatics*, **2007**, 19, 61-72		2
9	Apples to apples: improving the performance of motif finders and their significance analysis in the Twilight Zone. *Bioinformatics*, **2006**, 22, e393-401	7.2	8
8	A Fast and Numerically Robust Method for Exact Multinomial Goodness-of-Fit Test. *Journal of Computational and Graphical Statistics*, **2006**, 15, 779-802	1.4	9
7	Designing seeds for similarity search in genomic DNA. *Journal of Computer and System Sciences*, **2005**, 70, 342-363	1	41
6	Computing the P-value of the information content from an alignment of multiple sequences. *Bioinformatics*, **2005**, 21 Suppl 1, i311-8	7.2	30
5	sFFT: a faster accurate computation of the p-value of the entropy score. *Journal of Computational Biology*, **2005**, 12, 416-30	1.7	9
4	On spaced seeds for similarity search. *Discrete Applied Mathematics*, **2004**, 138, 253-263	1	91

3	Optimal decompositions for the K-functional for a couple of Banach lattices. *Arkiv for Matematik*, **2001**, 39, 27-64	0.2	3
2	Kreinƶ strings, the symmetric moment problem, and extending a real positive definite function. *Communications on Pure and Applied Mathematics*, **1999**, 52, 1315-1334	2.5	4
1	A generalization of the Ahlswede-Daykin inequality. *Discrete Mathematics*, **1996**, 152, 1-12	0.7	4