

# Uri Keich

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Deep RNA sequencing of <i>L. monocytogenes</i> reveals overlapping and extensive stationary phase and sigma B-dependent transcriptomes, including multiple highly transcribed noncoding RNAs. <i>BMC Genomics</i> , 2009, 10, 641.	2.8	160
2	Target-Decoy Approach and False Discovery Rate: When Things May Go Wrong. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 1111-1120.	2.8	134
3	On spaced seeds for similarity search. <i>Discrete Applied Mathematics</i> , 2004, 138, 253-263.	0.9	110
4	Designing seeds for similarity search in genomic DNA. <i>Journal of Computer and System Sciences</i> , 2005, 70, 342-363.	1.2	64
5	Tandem Mass Spectrum Identification via Cascaded Search. <i>Journal of Proteome Research</i> , 2015, 14, 3027-3038.	3.7	63
6	Improved False Discovery Rate Estimation Procedure for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2015, 14, 3148-3161.	3.7	55
7	High-resolution mapping, characterization, and optimization of autonomously replicating sequences in yeast. <i>Genome Research</i> , 2013, 23, 698-704.	5.5	53
8	A Comprehensive Genome-Wide Map of Autonomously Replicating Sequences in a Naive Genome. <i>PLoS Genetics</i> , 2010, 6, e1000946.	3.5	51
9	Improved similarity scores for comparing motifs. <i>Bioinformatics</i> , 2011, 27, 1603-1609.	4.1	50
10	Computing the P-value of the information content from an alignment of multiple sequences. <i>Bioinformatics</i> , 2005, 21, i311-i318.	4.1	34
11	On the Importance of Well-Calibrated Scores for Identifying Shotgun Proteomics Spectra. <i>Journal of Proteome Research</i> , 2015, 14, 1147-1160.	3.7	30
12	GIMSAN: a Gibbs motif finder with significance analysis. <i>Bioinformatics</i> , 2008, 24, 2256-2257.	4.1	29
13	Averaging Strategy To Reduce Variability in Target-Decoy Estimates of False Discovery Rate. <i>Journal of Proteome Research</i> , 2019, 18, 585-593.	3.7	26
14	Improving MEME via a two-tiered significance analysis. <i>Bioinformatics</i> , 2014, 30, 1965-1973.	4.1	20
15	Novel features of ARS selection in budding yeast <i>Lachancea kluyveri</i> . <i>BMC Genomics</i> , 2011, 12, 633.	2.8	18
16	Multiple Competition-Based FDR Control and Its Application to Peptide Detection. <i>Lecture Notes in Computer Science</i> , 2020, , 54-71.	1.3	12
17	sFFT: A Faster Accurate Computation of the p-Value of the Entropy Score. <i>Journal of Computational Biology</i> , 2005, 12, 416-430.	1.6	11
18	A Fast and Numerically Robust Method for Exact Multinomial Goodness-of-Fit Test. <i>Journal of Computational and Graphical Statistics</i> , 2006, 15, 779-802.	1.7	11

#	ARTICLE	IF	CITATIONS
19	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
20	Reliability and efficiency of algorithms for computing the significance of the Mann-Whitney test. Computational Statistics, 2009, 24, 605-622.	1.5	10
21	Accurately Assigning Peptides to Spectra When Only a Subset of Peptides Are Relevant. Journal of Proteome Research, 2021, 20, 4153-4164.	3.7	10
22	A generalization of the Ahlswede-Daykin inequality. Discrete Mathematics, 1996, 152, 1-12.	0.7	9
23	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
24	Response to "Mass spectrometrists should search for all peptides, but assess only the ones they care about". Nature Methods, 2017, 14, 644-644.	19.0	9
25	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
26	FAST: Fourier transform based algorithms for significance testing of ungapped multiple alignments. Bioinformatics, 2008, 24, 577-578.	4.1	7
27	Controlling the FDR in Imperfect Matches to an Incomplete Database. Journal of the American Statistical Association, 2018, 113, 973-982.	3.1	7
28	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
29	Building Spectral Libraries from Narrow-Window Data-Independent Acquisition Mass Spectrometry Data. Journal of Proteome Research, 2022, 21, 1382-1391.	3.7	6
30	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
31	Optimal decompositions for the K-functional for a couple of Banach lattices. Arkiv for Matematik, 2001, 39, 27-64.	0.5	3
32	Confidently Estimating the Number of DNA Replication Origins. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article28.	0.6	3
33	Accurate pairwise convolutions of non-negative vectors via FFT. Computational Statistics and Data Analysis, 2016, 101, 300-315.	1.2	3
34	Factoring local sequence composition in motif significance analysis. Genome Informatics, 2008, 21, 15-26.	0.4	3
35	Exactly Computing the Tail of the Poisson-Binomial Distribution. ACM Transactions on Mathematical Software, 2021, 47, 1-19.	2.9	2
36	A conservative parametric approach to motif significance analysis. Genome Informatics, 2007, 19, 61-72.	0.4	2

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37	A Symmetric Length-Aware Enrichment Test. Journal of Computational Biology, 2016, 23, 508-525.	1.6	1
38	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
39	A conservative parametric approach to motif significance analysis. , 2007, , .		1
40	Alignment Constrained Sampling. Journal of Computational Biology, 2011, 18, 155-168.	1.6	0
41	Factoring local sequence composition in motif significance analysis. , 2008, , .		0