

Manuel E Lladser

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9575486/publications.pdf>

Version: 2024-02-01

23
papers

2,783
citations

933447

10
h-index

888059

17
g-index

25
all docs

25
docs citations

25
times ranked

5540
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Truncated metric dimension for finite graphs. <i>Discrete Applied Mathematics</i> , 2022, 320, 150-169. | 0.9 | 4 |
| 2 | Stochastic Analysis of Minimal Automata Growth for Generalized Strings. <i>Methodology and Computing in Applied Probability</i> , 2020, 22, 329-347. | 1.2 | 0 |
| 3 | Resolvability of Hamming Graphs. <i>SIAM Journal on Discrete Mathematics</i> , 2020, 34, 2063-2081. | 0.8 | 6 |
| 4 | Low-dimensional representation of genomic sequences. <i>Journal of Mathematical Biology</i> , 2019, 79, 1-29. | 1.9 | 21 |
| 5 | An Annotation Agnostic Algorithm for Detecting Nascent RNA Transcripts in GRO-Seq. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1070-1081. | 3.0 | 19 |
| 6 | RNA Pol II transcription model and interpretation of GRO-seq data. <i>Journal of Mathematical Biology</i> , 2017, 74, 77-97. | 1.9 | 9 |
| 7 | Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017, 2, . | 3.8 | 284 |
| 8 | Metric-space Positioning Systems (MPS) for Machine Learning. , 2016, , . | | 0 |
| 9 | FStitch. , 2014, , . | | 8 |
| 10 | Approximation of sojourn-times via maximal couplings: motif frequency distributions. <i>Journal of Mathematical Biology</i> , 2014, 69, 147-182. | 1.9 | 5 |
| 11 | Estimation of Distribution Overlap of Urn Models. <i>PLoS ONE</i> , 2012, 7, e42368. | 2.5 | 7 |
| 12 | UniFrac: an effective distance metric for microbial community comparison. <i>ISME Journal</i> , 2011, 5, 169-172. | 9.8 | 2,280 |
| 13 | Extrapolation of Urn Models via Poissonization: Accurate Measurements of the Microbial Unknown. <i>PLoS ONE</i> , 2011, 6, e21105. | 2.5 | 19 |
| 14 | Natural and artificial RNAs occupy the same restricted region of sequence space. <i>Rna</i> , 2010, 16, 280-289. | 3.5 | 21 |
| 15 | Chiral histidine selection by D-ribose RNA. <i>Rna</i> , 2010, 16, 2370-2383. | 3.5 | 12 |
| 16 | Prediction of unseen proportions in urn models with restricted sampling. , 2009, , . | | 2 |
| 17 | Comparison of methods for estimating the nucleotide substitution matrix. <i>BMC Bioinformatics</i> , 2008, 9, 511. | 2.6 | 8 |
| 18 | Information, probability, and the abundance of the simplest RNA active sites. <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 6060. | 3.0 | 11 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Markovian embeddings of general random strings. , 2008, , . | | 5 |
| 20 | Minimal Markov chain embeddings of pattern problems. , 2007, , . | | 13 |
| 21 | Multiple pattern matching: a Markov chain approach. Journal of Mathematical Biology, 2007, 56, 51-92. | 1.9 | 27 |
| 22 | Uniform Formulae for Coefficients of Meromorphic Functions in Two Variables. Part I. SIAM Journal on Discrete Mathematics, 2006, 20, 811-828. | 0.8 | 8 |
| 23 | Domain of attraction of the quasi-stationary distributions for the Ornstein-Uhlenbeck process. Journal of Applied Probability, 2000, 37, 511-520. | 0.7 | 11 |