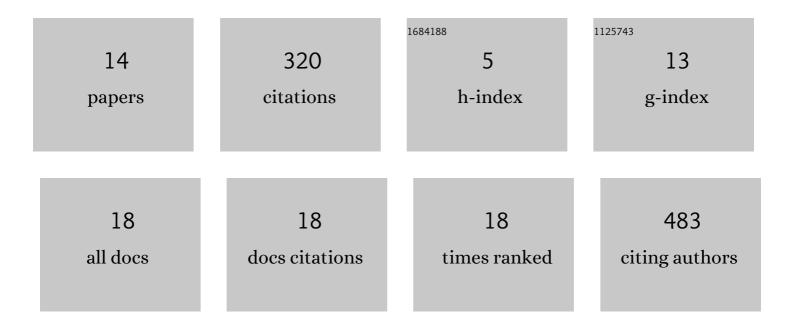
Toby Kenney

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4991328/publications.pdf Version: 2024-02-01



TORY KENNEY

#	Article	IF	CITATIONS
1	Discrepant gut microbiota markers for the classification of obesity-related metabolic abnormalities. Scientific Reports, 2019, 9, 13424.	3.3	235
2	Learning Microbial Community Structures with Supervised and Unsupervised Non-negative Matrix Factorization. Microbiome, 2017, 5, 110.	11.1	29
3	Improved inference of site-specific positive selection under a generalized parametric codon model when there are multinucleotide mutations and multiple nonsynonymous rates. BMC Evolutionary Biology, 2019, 19, 22.	3.2	11
4	Partial Generalized Additive Models: An Information-Theoretic Approach for Dealing With Concurvity and Selecting Variables. Journal of Computational and Graphical Statistics, 2010, 19, 531-551.	1.7	8
5	Association between metabolic status and gut microbiome in obese populations. Microbial Genomics, 2021, 7, .	2.0	8
6	Coxeter groups, Coxeter monoids and the Bruhat order. Journal of Algebraic Combinatorics, 2014, 39, 719-731.	0.8	6
7	Testing adequacy for DNA substitution models. BMC Bioinformatics, 2019, 20, 349.	2.6	6
8	Combining Distance Matrices on Identical Taxon Sets for Multi-Gene Analysis with Singular Value Decomposition. PLoS ONE, 2014, 9, e94279.	2.5	5
9	SuRF: A new method for sparse variable selection, with application in microbiome data analysis. Statistics in Medicine, 2021, 40, 897-919.	1.6	4
10	The path relation for directed planar graphs in rectangles, and its relation to the free diad. Discrete Mathematics, 2011, 311, 441-456.	0.7	3
11	Poisson PCA: Poisson measurement error corrected PCA, with application to microbiome data. Biometrics, 2021, 77, 1369-1384.	1.4	2
12	Diads and their Application to Topoi. Applied Categorical Structures, 2009, 17, 567-590.	0.5	1
13	The General Theory of Diads. Applied Categorical Structures, 2010, 18, 523-572.	0.5	1
14	Application of OU processes to modelling temporal dynamics of the human microbiome, and calculating optimal sampling schemes. BMC Bioinformatics, 2020, 21, 450.	2.6	1