Jesse I Stombaugh

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2217801/publications.pdf Version: 2024-02-01



IESSE | STOMBALICH

#	Article	IF	CITATIONS
1	QIIME allows analysis of high-throughput community sequencing data. Nature Methods, 2010, 7, 335-336.	19.0	31,818
2	Diversity, stability and resilience of the human gut microbiota. Nature, 2012, 489, 220-230.	27.8	4,114
3	UniFrac: an effective distance metric for microbial community comparison. ISME Journal, 2011, 5, 169-172.	9.8	2,280
4	Succession of microbial consortia in the developing infant gut microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4578-4585.	7.1	2,108
5	Human oral, gut, and plaque microbiota in patients with atherosclerosis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4592-4598.	7.1	943
6	Moving pictures of the human microbiome. Genome Biology, 2011, 12, R50.	9.6	934
7	Microbiota Regulate Intestinal Absorption and Metabolism of Fatty Acids in the Zebrafish. Cell Host and Microbe, 2012, 12, 277-288.	11.0	717
8	The non-Watson-Crick base pairs and their associated isostericity matrices. Nucleic Acids Research, 2002, 30, 3497-3531.	14.5	679
9	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. GigaScience, 2012, 1, 7.	6.4	671
10	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	17.5	608
11	Using QIIME to Analyze 16S rRNA Gene Sequences from Microbial Communities. Current Protocols in Bioinformatics, 2011, 36, Unit 10.7	25.8	507
12	Using QIIME to Analyze 16S rRNA Gene Sequences from Microbial Communities. Current Protocols in Microbiology, 2012, 27, Unit 1E.5	6.5	486
13	Responses of Gut Microbiota to Diet Composition and Weight Loss in Lean and Obese Mice. Obesity, 2012, 20, 738-747.	3.0	352
14	Meta-analyses of studies of the human microbiota. Genome Research, 2013, 23, 1704-1714.	5.5	352
15	FR3D: finding local and composite recurrent structural motifs in RNA 3D structures. Journal of Mathematical Biology, 2007, 56, 215-252.	1.9	231
16	Microbial Biogeography of Public Restroom Surfaces. PLoS ONE, 2011, 6, e28132.	2.5	222
17	Lake microbial communities are resilient after a whole-ecosystem disturbance. ISME Journal, 2012, 6, 2153-2167.	9.8	198
18	Frequency and isostericity of RNA base pairs. Nucleic Acids Research, 2009, 37, 2294-2312.	14.5	190

JESSE I STOMBAUGH

#	Article	IF	CITATIONS
19	Widespread Colonization of the Lung by <i>Tropheryma whipplei</i> in HIV Infection. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 1110-1117.	5.6	175
20	Classification and energetics of the base-phosphate interactions in RNA. Nucleic Acids Research, 2009, 37, 4898-4918.	14.5	156
21	Tertiary structure and function of an RNA motif required for plant vascular entry to initiate systemic trafficking. EMBO Journal, 2007, 26, 3836-3846.	7.8	111
22	The mind-body-microbial continuum. Dialogues in Clinical Neuroscience, 2011, 13, 55-62.	3.7	109
23	Comprehensive survey and geometric classification of base triples in RNA structures. Nucleic Acids Research, 2012, 40, 1407-1423.	14.5	79
24	The RNA structure alignment ontology. Rna, 2009, 15, 1623-1631.	3.5	34
25	RNASTAR: An RNA STructural Alignment Repository that provides insight into the evolution of natural and artificial RNAs. Rna, 2012, 18, 1319-1327.	3.5	30
26	Sharing and archiving nucleic acid structure mapping data. Rna, 2011, 17, 1204-1212.	3.5	28
27	Computer identification of snoRNA genes using a Mammalian Orthologous Intron Database. Nucleic Acids Research, 2005, 33, 4578-4583.	14.5	26
28	Combined phylogenetic and genomic approaches for the high-throughput study of microbial habitat adaptation. Trends in Microbiology, 2011, 19, 472-482.	7.7	23
29	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. Applied Ontology, 2011, 6, 53-89.	2.0	23
30	SitePainter: a tool for exploring biogeographical patterns. Bioinformatics, 2012, 28, 436-438.	4.1	22
31	RNA 3D Structural Motifs: Definition, Identification, Annotation, and Database Searching. Springer Series in Biophysics, 2009, , 1-26.	0.4	15
32	TopiaryExplorer: visualizing large phylogenetic trees with environmental metadata. Bioinformatics, 2011, 27, 3067-3069.	4.1	15
33	Boulder ALignment Editor (ALE): a web-based RNA alignment tool. Bioinformatics, 2011, 27, 1706-1707.	4.1	8
34	Technology and Data-Intensive Science in the Beginning of the 21st Century. OMICS A Journal of Integrative Biology, 2011, 15, 203-207.	2.0	5
35	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. Nature Precedings, 2009, , .	0.1	3
36	The Power Decoder Simulator for the Evaluation of Pooled shRNA Screen Performance. Journal of Biomolecular Screening, 2015, 20, 965-975.	2.6	3

#	Article	IF	CITATIONS
37	Understanding Sequence Variability of RNA Motifs Using Geometric Search and IsoDiscrepancy Matrices. , 2009, , .		1
38	Meeting report of the RNA Ontology Consortium January 8-9, 2011. Standards in Genomic Sciences, 2011, 4, 252-256.	1.5	1