

# Jesse I Stombaugh

## List of Publications by Year in descending order

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Version: 2024-02-01

38  
papers

48,277  
citations

270111

25  
h-index

371746

37  
g-index

38  
all docs

38  
docs citations

38  
times ranked

62787  
citing authors

#	ARTICLE	IF	CITATIONS
1	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	9.0	31,818
2	Diversity, stability and resilience of the human gut microbiota. <i>Nature</i> , 2012, 489, 220-230.	13.7	4,114
3	UniFrac: an effective distance metric for microbial community comparison. <i>ISME Journal</i> , 2011, 5, 169-172.	4.4	2,280
4	Succession of microbial consortia in the developing infant gut microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4578-4585.	3.3	2,108
5	Human oral, gut, and plaque microbiota in patients with atherosclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4592-4598.	3.3	943
6	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011, 12, R50.	13.9	934
7	Microbiota Regulate Intestinal Absorption and Metabolism of Fatty Acids in the Zebrafish. <i>Cell Host and Microbe</i> , 2012, 12, 277-288.	5.1	717
8	The non-Watson-Crick base pairs and their associated isostericity matrices. <i>Nucleic Acids Research</i> , 2002, 30, 3497-3531.	6.5	679
9	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. <i>GigaScience</i> , 2012, 1, 7.	3.3	671
10	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608
11	Using QIIME to Analyze 16S rRNA Gene Sequences from Microbial Communities. <i>Current Protocols in Bioinformatics</i> , 2011, 36, Unit 10.7..	25.8	507
12	Using QIIME to Analyze 16S rRNA Gene Sequences from Microbial Communities. <i>Current Protocols in Microbiology</i> , 2012, 27, Unit 1E.5..	6.5	486
13	Responses of Gut Microbiota to Diet Composition and Weight Loss in Lean and Obese Mice. <i>Obesity</i> , 2012, 20, 738-747.	1.5	352
14	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , 2013, 23, 1704-1714.	2.4	352
15	FR3D: finding local and composite recurrent structural motifs in RNA 3D structures. <i>Journal of Mathematical Biology</i> , 2007, 56, 215-252.	0.8	231
16	Microbial Biogeography of Public Restroom Surfaces. <i>PLoS ONE</i> , 2011, 6, e28132.	1.1	222
17	Lake microbial communities are resilient after a whole-ecosystem disturbance. <i>ISME Journal</i> , 2012, 6, 2153-2167.	4.4	198
18	Frequency and isostericity of RNA base pairs. <i>Nucleic Acids Research</i> , 2009, 37, 2294-2312.	6.5	190

#	ARTICLE	IF	CITATIONS
19	Widespread Colonization of the Lung by <i>Tropheryma whippelii</i> in HIV Infection. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 1110-1117.	2.5	175
20	Classification and energetics of the base-phosphate interactions in RNA. Nucleic Acids Research, 2009, 37, 4898-4918.	6.5	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.	3.5	111
22	The mind-body-microbial continuum. Dialogues in Clinical Neuroscience, 2011, 13, 55-62.	1.8	109
23	Comprehensive survey and geometric classification of base triples in RNA structures. Nucleic Acids Research, 2012, 40, 1407-1423.	6.5	79
24	The RNA structure alignment ontology. Rna, 2009, 15, 1623-1631.	1.6	34
25	RNASTAR: An RNA STRUCTURAL Alignment Repository that provides insight into the evolution of natural and artificial RNAs. Rna, 2012, 18, 1319-1327.	1.6	30
26	Sharing and archiving nucleic acid structure mapping data. Rna, 2011, 17, 1204-1212.	1.6	28
27	Computer identification of snoRNA genes using a Mammalian Orthologous Intron Database. Nucleic Acids Research, 2005, 33, 4578-4583.	6.5	26
28	Combined phylogenetic and genomic approaches for the high-throughput study of microbial habitat adaptation. Trends in Microbiology, 2011, 19, 472-482.	3.5	23
29	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. Applied Ontology, 2011, 6, 53-89.	1.0	23
30	SitePainter: a tool for exploring biogeographical patterns. Bioinformatics, 2012, 28, 436-438.	1.8	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.	1.8	15
33	Boulder ALIGNment Editor (ALE): a web-based RNA alignment tool. Bioinformatics, 2011, 27, 1706-1707.	1.8	8
34	Technology and Data-Intensive Science in the Beginning of the 21st Century. OMICS A Journal of Integrative Biology, 2011, 15, 203-207.	1.0	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