

Jesse I Stombaugh

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

38
papers

34,995
citations

25
h-index

38
g-index

38
ext. papers

44,041
ext. citations

13.2
avg, IF

6.48
L-index

#	Paper	IF	Citations
38	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010 , 7, 335-6	21.6	22879
37	Diversity, stability and resilience of the human gut microbiota. <i>Nature</i> , 2012 , 489, 220-30	50.4	2919
36	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 Suppl 1, 4578-85	11.5	1674
35	UniFrac: an effective distance metric for microbial community comparison. <i>ISME Journal</i> , 2011 , 5, 169-72	11.9	1474
34	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011 , 12, R50	18.3	723
33	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 Suppl 1, 4592-8	11.5	679
32	The non-Watson-Crick base pairs and their associated isostericity matrices. <i>Nucleic Acids Research</i> , 2002 , 30, 3497-531	20.1	586
31	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. <i>GigaScience</i> , 2012 , 1, 7	7.6	484
30	Microbiota regulate intestinal absorption and metabolism of fatty acids in the zebrafish. <i>Cell Host and Microbe</i> , 2012 , 12, 277-88	23.4	477
29	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. <i>Nature Biotechnology</i> , 2011 , 29, 415-20	44.5	445
28	Using QIIME to analyze 16S rRNA gene sequences from microbial communities. <i>Current Protocols in Bioinformatics</i> , 2011 , Chapter 10, Unit 10.7.	24.2	381
27	Using QIIME to analyze 16S rRNA gene sequences from microbial communities. <i>Current Protocols in Microbiology</i> , 2012 , Chapter 1, Unit 1E.5.	7.1	312
26	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , 2013 , 23, 1704-14	9.7	289
25	Responses of gut microbiota to diet composition and weight loss in lean and obese mice. <i>Obesity</i> , 2012 , 20, 738-47	8	287
24	FR3D: finding local and composite recurrent structural motifs in RNA 3D structures. <i>Journal of Mathematical Biology</i> , 2008 , 56, 215-52	2	195
23	Microbial biogeography of public restroom surfaces. <i>PLoS ONE</i> , 2011 , 6, e28132	3.7	184
22	Frequency and isostericity of RNA base pairs. <i>Nucleic Acids Research</i> , 2009 , 37, 2294-312	20.1	146

21	Lake microbial communities are resilient after a whole-ecosystem disturbance. <i>ISME Journal</i> , 2012 , 6, 2153-67	11.9	143
20	Widespread colonization of the lung by <i>Tropheryma whippelii</i> in HIV infection. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013 , 187, 1110-7	10.2	140
19	Classification and energetics of the base-phosphate interactions in RNA. <i>Nucleic Acids Research</i> , 2009 , 37, 4898-918	20.1	126
18	Tertiary structure and function of an RNA motif required for plant vascular entry to initiate systemic trafficking. <i>EMBO Journal</i> , 2007 , 26, 3836-46	13	91
17	The mind-body-microbial continuum. <i>Dialogues in Clinical Neuroscience</i> , 2011 , 13, 55-62	5.7	85
16	Comprehensive survey and geometric classification of base triples in RNA structures. <i>Nucleic Acids Research</i> , 2012 , 40, 1407-23	20.1	64
15	The RNA structure alignment ontology. <i>Rna</i> , 2009 , 15, 1623-31	5.8	32
14	Sharing and archiving nucleic acid structure mapping data. <i>Rna</i> , 2011 , 17, 1204-12	5.8	27
13	Computer identification of snoRNA genes using a Mammalian Orthologous Intron Database. <i>Nucleic Acids Research</i> , 2005 , 33, 4578-83	20.1	25
12	Combined phylogenetic and genomic approaches for the high-throughput study of microbial habitat adaptation. <i>Trends in Microbiology</i> , 2011 , 19, 472-82	12.4	22
11	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. <i>Applied Ontology</i> , 2011 , 6, 53-89	1.4	20
10	RNASTAR: an RNA Structural Alignment Repository that provides insight into the evolution of natural and artificial RNAs. <i>Rna</i> , 2012 , 18, 1319-27	5.8	20
9	SitePainter: a tool for exploring biogeographical patterns. <i>Bioinformatics</i> , 2012 , 28, 436-8	7.2	18
8	TopiaryExplorer: visualizing large phylogenetic trees with environmental metadata. <i>Bioinformatics</i> , 2011 , 27, 3067-9	7.2	15
7	RNA 3D Structural Motifs: Definition, Identification, Annotation, and Database Searching. <i>Springer Series in Biophysics</i> , 2009 , 1-26		14
6	Boulder ALignment Editor (ALE): a web-based RNA alignment tool. <i>Bioinformatics</i> , 2011 , 27, 1706-7	7.2	8
5	Technology and data-intensive science in the beginning of the 21st century. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 203-7	3.8	5
4	The Power Decoder Simulator for the Evaluation of Pooled shRNA Screen Performance. <i>Journal of Biomolecular Screening</i> , 2015 , 20, 965-75		2

- 3 The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. *Nature Precedings*, **2009**, 2
- 2 Meeting report of the RNA Ontology Consortium January 8-9, 2011. *Standards in Genomic Sciences*, **2011**, 4, 252-6 1
- 1 Understanding Sequence Variability of RNA Motifs Using Geometric Search and IsoDiscrepancy Matrices **2009**, 1