Jesse I Stombaugh

List of Publications by Year in Descending Order

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	The Power Decoder Simulator for the Evaluation of Pooled shRNA Screen Performance. *Journal of Biomolecular Screening*, **2015**, 20, 965-75		2
37	Meta-analyses of studies of the human microbiota. *Genome Research*, **2013**, 23, 1704-14	9.7	289
36	Widespread colonization of the lung by Tropheryma whipplei in HIV infection. *American Journal of Respiratory and Critical Care Medicine*, **2013**, 187, 1110-7	10.2	140
35	Microbiota regulate intestinal absorption and metabolism of fatty acids in the zebrafish. *Cell Host and Microbe*, **2012**, 12, 277-88	23.4	477
34	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. *GigaScience*, **2012**, 1, 7	7.6	484
33	Using QIIME to analyze 16S rRNA gene sequences from microbial communities. *Current Protocols in Microbiology*, **2012**, Chapter 1, Unit 1E.5.	7.1	312
32	Diversity, stability and resilience of the human gut microbiota. *Nature*, **2012**, 489, 220-30	50.4	2919
31	Responses of gut microbiota to diet composition and weight loss in lean and obese mice. *Obesity*, **2012**, 20, 738-47	8	287
30	Comprehensive survey and geometric classification of base triples in RNA structures. *Nucleic Acids Research*, **2012**, 40, 1407-23	20.1	64
29	Lake microbial communities are resilient after a whole-ecosystem disturbance. *ISME Journal*, **2012**, 6, 2153-67	11.9	143
28	SitePainter: a tool for exploring biogeographical patterns. *Bioinformatics*, **2012**, 28, 436-8	7.2	18
27	RNASTAR: an RNA STructural Alignment Repository that provides insight into the evolution of natural and artificial RNAs. *Rna*, **2012**, 18, 1319-27	5.8	20
26	Using QIIME to analyze 16S rRNA gene sequences from microbial communities. *Current Protocols in Bioinformatics*, **2011**, Chapter 10, Unit 10.7.	24.2	381
25	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. *Nature Biotechnology*, **2011**, 29, 415-20	44.5	445
24	Moving pictures of the human microbiome. *Genome Biology*, **2011**, 12, R50	18.3	723
23	Combined phylogenetic and genomic approaches for the high-throughput study of microbial habitat adaptation. *Trends in Microbiology*, **2011**, 19, 472-82	12.4	22
22	Meeting report of the RNA Ontology Consortium January 8-9, 2011. *Standards in Genomic Sciences*, **2011**, 4, 252-6		1

#	Citation		
21	UniFrac: an effective distance metric for microbial community comparison. *ISME Journal*, **2011**, 5, 169-72	11.9	1474
20	Technology and data-intensive science in the beginning of the 21st century. *OMICS A Journal of Integrative Biology*, **2011**, 15, 203-7	3.8	5
19	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 Suppl 1, 4592-8	11.5	679
18	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. *Applied Ontology*, **2011**, 6, 53-89	1.4	20
17	Boulder ALignment Editor (ALE): a web-based RNA alignment tool. *Bioinformatics*, **2011**, 27, 1706-7	7.2	8
16	Sharing and archiving nucleic acid structure mapping data. *Rna*, **2011**, 17, 1204-12	5.8	27
15	TopiaryExplorer: visualizing large phylogenetic trees with environmental metadata. *Bioinformatics*, **2011**, 27, 3067-9	7.2	15
14	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 Suppl 1, 4578-85	11.5	1674
13	Microbial biogeography of public restroom surfaces. *PLoS ONE*, **2011**, 6, e28132	3.7	184
12	The mind-body-microbial continuum. *Dialogues in Clinical Neuroscience*, **2011**, 13, 55-62	5.7	85
11	QIIME allows analysis of high-throughput community sequencing data. *Nature Methods*, **2010**, 7, 335-6	21.6	22879
10	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. *Nature Precedings*, **2009**,		2
9	Classification and energetics of the base-phosphate interactions in RNA. *Nucleic Acids Research*, **2009**, 37, 4898-918	20.1	126
8	RNA 3D Structural Motifs: Definition, Identification, Annotation, and Database Searching. *Springer Series in Biophysics*, **2009**, 1-26		14
7	The RNA structure alignment ontology. *Rna*, **2009**, 15, 1623-31	5.8	32
6	Frequency and isostericity of RNA base pairs. *Nucleic Acids Research*, **2009**, 37, 2294-312	20.1	146
5	Understanding Sequence Variability of RNA Motifs Using Geometric Search and IsoDiscrepancy Matrices **2009**,		1
4	FR3D: finding local and composite recurrent structural motifs in RNA 3D structures. *Journal of Mathematical Biology*, **2008**, 56, 215-52	2	195

3	Tertiary structure and function of an RNA motif required for plant vascular entry to initiate systemic trafficking. *EMBO Journal*, **2007**, 26, 3836-46	13	91
2	Computer identification of snoRNA genes using a Mammalian Orthologous Intron Database. *Nucleic Acids Research*, **2005**, 33, 4578-83	20.1	25
1	The non-Watson-Crick base pairs and their associated isostericity matrices. *Nucleic Acids Research*, **2002**, 30, 3497-531	20.1	586