

# Justin Kuczynski

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12195530/publications.pdf>

Version: 2024-02-01

16  
papers

44,715  
citations

567281

15  
h-index

940533

16  
g-index

16  
all docs

16  
docs citations

16  
times ranked

54667  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identifying qualitative effects of different grazing types on below-ground communities and function in a long-term field experiment. <i>Environmental Microbiology</i> , 2015, 17, 841-854.	3.8	21
2	An <i>in vitro</i> culture model to study the dynamics of colonic microbiota in Syrian golden hamsters and their susceptibility to infection with <i>Clostridium difficile</i> . <i>ISME Journal</i> , 2015, 9, 321-332.	9.8	17
3	Changes in Abundance of Oral Microbiota Associated with Oral Cancer. <i>PLoS ONE</i> , 2014, 9, e98741.	2.5	295
4	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. <i>GigaScience</i> , 2012, 1, 7.	6.4	671
5	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
6	Human gut microbiome viewed across age and geography. <i>Nature</i> , 2012, 486, 222-227.	27.8	6,247
7	Experimental and analytical tools for studying the human microbiome. <i>Nature Reviews Genetics</i> , 2012, 13, 47-58.	16.3	601
8	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
9	Diet Drives Convergence in Gut Microbiome Functions Across Mammalian Phylogeny and Within Humans. <i>Science</i> , 2011, 332, 970-974.	12.6	1,712
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.	17.5	608
11	Combined phylogenetic and genomic approaches for the high-throughput study of microbial habitat adaptation. <i>Trends in Microbiology</i> , 2011, 19, 472-482.	7.7	23
12	Supervised classification of microbiota mitigates mislabeling errors. <i>ISME Journal</i> , 2011, 5, 570-573.	9.8	42
13	Bayesian community-wide culture-independent microbial source tracking. <i>Nature Methods</i> , 2011, 8, 761-763.	19.0	1,284
14	Microbial community resemblance methods differ in their ability to detect biologically relevant patterns. <i>Nature Methods</i> , 2010, 7, 813-819.	19.0	249
15	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	19.0	31,818
16	Direct sequencing of the human microbiome readily reveals community differences. <i>Genome Biology</i> , 2010, 11, 210.	9.6	134