

# Jens Reeder

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11956082/publications.pdf>

Version: 2024-02-01

16  
papers

41,948  
citations

586496

16  
h-index

1051228

16  
g-index

16  
all docs

16  
docs citations

16  
times ranked

60980  
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	Human gut microbiome viewed across age and geography. <i>Nature</i> , 2012, 486, 222-227.	13.7	6,247
3	Defining seasonal marine microbial community dynamics. <i>ISME Journal</i> , 2012, 6, 298-308.	4.4	928
4	Rapidly denoising pyrosequencing amplicon reads by exploiting rank-abundance distributions. <i>Nature Methods</i> , 2010, 7, 668-669.	9.0	647
5	A comprehensive transcriptional portrait of human cancer cell lines. <i>Nature Biotechnology</i> , 2015, 33, 306-312.	9.4	556
6	GMAP and GSNAP for Genomic Sequence Alignment: Enhancements to Speed, Accuracy, and Functionality. <i>Methods in Molecular Biology</i> , 2016, 1418, 283-334.	0.4	354
7	Spectrum of diverse genomic alterations define non-“clear cell renal carcinoma subtypes. <i>Nature Genetics</i> , 2015, 47, 13-21.	9.4	310
8	Design, implementation and evaluation of a practical pseudoknot folding algorithm based on thermodynamics. <i>BMC Bioinformatics</i> , 2004, 5, 104.	1.2	248
9	The 'rare biosphere': a reality check. <i>Nature Methods</i> , 2009, 6, 636-637.	9.0	231
10	Recurrent Loss of NFE2L2 Exon 2 Is a Mechanism for Nrf2 Pathway Activation in Human Cancers. <i>Cell Reports</i> , 2016, 16, 2605-2617.	2.9	155
11	Germline genetic polymorphisms influence tumor gene expression and immune cell infiltration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11701-E11710.	3.3	108
12	pKnotsRG: RNA pseudoknot folding including near-optimal structures and sliding windows. <i>Nucleic Acids Research</i> , 2007, 35, W320-W324.	6.5	102
13	Consensus shapes: an alternative to the Sankoff algorithm for RNA consensus structure prediction. <i>Bioinformatics</i> , 2005, 21, 3516-3523.	1.8	88
14	KnotInFrame: prediction of +1 ribosomal frameshift events. <i>Nucleic Acids Research</i> , 2008, 36, 6013-6020.	6.5	61
15	Beyond Mfold: Recent advances in RNA bioinformatics. <i>Journal of Biotechnology</i> , 2006, 124, 41-55.	1.9	59
16	Locomotif: from graphical motif description to RNA motif search. <i>Bioinformatics</i> , 2007, 23, i392-i400.	1.8	36