

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	Germline genetic polymorphisms influence tumor gene expression and immune cell infiltration. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11701-E11710.	3.3	108
2	Recurrent Loss of NFE2L2 Exon 2 Is a Mechanism for Nrf2 Pathway Activation in Human Cancers. Cell Reports, 2016, 16, 2605-2617.	2.9	155
3	GMAP and GSNAP for Genomic Sequence Alignment: Enhancements to Speed, Accuracy, and Functionality. Methods in Molecular Biology, 2016, 1418, 283-334.	0.4	354
4	A comprehensive transcriptional portrait of human cancer cell lines. Nature Biotechnology, 2015, 33, 306-312.	9.4	556
5	Spectrum of diverse genomic alterations define non-“clear cell renal carcinoma subtypes. Nature Genetics, 2015, 47, 13-21.	9.4	310
6	Defining seasonal marine microbial community dynamics. ISME Journal, 2012, 6, 298-308.	4.4	928
7	Human gut microbiome viewed across age and geography. Nature, 2012, 486, 222-227.	13.7	6,247
8	QIIME allows analysis of high-throughput community sequencing data. Nature Methods, 2010, 7, 335-336.	9.0	31,818
9	Rapidly denoising pyrosequencing amplicon reads by exploiting rank-abundance distributions. Nature Methods, 2010, 7, 668-669.	9.0	647
10	The 'rare biosphere': a reality check. Nature Methods, 2009, 6, 636-637.	9.0	231
11	KnotInFrame: prediction of +1 ribosomal frameshift events. Nucleic Acids Research, 2008, 36, 6013-6020.	6.5	61
12	Locomotif: from graphical motif description to RNA motif search. Bioinformatics, 2007, 23, i392-i400.	1.8	36
13	pknotsRG: RNA pseudoknot folding including near-optimal structures and sliding windows. Nucleic Acids Research, 2007, 35, W320-W324.	6.5	102
14	Beyond Mfold: Recent advances in RNA bioinformatics. Journal of Biotechnology, 2006, 124, 41-55.	1.9	59
15	Consensus shapes: an alternative to the Sankoff algorithm for RNA consensus structure prediction. Bioinformatics, 2005, 21, 3516-3523.	1.8	88
16	Design, implementation and evaluation of a practical pseudoknot folding algorithm based on thermodynamics. BMC Bioinformatics, 2004, 5, 104.	1.2	248