

Son Pham

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11250074/publications.pdf>

Version: 2024-02-01

14
papers

21,578
citations

687363

13
h-index

940533

16
g-index

17
all docs

17
docs citations

17
times ranked

29244
citing authors

#	ARTICLE	IF	CITATIONS
1	Ultralow-input single-tube linked-read library method enables short-read second-generation sequencing systems to routinely generate highly accurate and economical long-range sequencing information. <i>Genome Research</i> , 2020, 30, 898-909.	5.5	68
2	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes. <i>Genome Research</i> , 2018, 28, 448-459.	5.5	99
3	Chromosome assembly of large and complex genomes using multiple references. <i>Genome Research</i> , 2018, 28, 1720-1732.	5.5	94
4	Mitochondrial Aging Defects Emerge in Directly Reprogrammed Human Neurons due to Their Metabolic Profile. <i>Cell Reports</i> , 2018, 23, 2550-2558.	6.4	93
5	Improved genome assembly of American alligator genome reveals conserved architecture of estrogen signaling. <i>Genome Research</i> , 2017, 27, 686-696.	5.5	38
6	The Pharmacogenomics of Bipolar Disorder study (PGBD): identification of genes for lithium response in a prospective sample. <i>BMC Psychiatry</i> , 2016, 16, 129.	2.6	61
7	Differential responses to lithium in hyperexcitable neurons from patients with bipolar disorder. <i>Nature</i> , 2015, 527, 95-99.	27.8	461
8	Ragout—a reference-assisted assembly tool for bacterial genomes. <i>Bioinformatics</i> , 2014, 30, i302-i309.	4.1	169
9	ExSPAnDer: a universal repeat resolver for DNA fragment assembly. <i>Bioinformatics</i> , 2014, 30, i293-i301.	4.1	103
10	Sibelia: A Scalable and Comprehensive Synteny Block Generation Tool for Closely Related Microbial Genomes. <i>Lecture Notes in Computer Science</i> , 2013, , 215-229.	1.3	74
11	C-Sibelia: an easy-to-use and highly accurate tool for bacterial genome comparison. <i>F1000Research</i> , 2013, 2, 258.	1.6	29
12	SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing. <i>Journal of Computational Biology</i> , 2012, 19, 455-477.	1.6	20,193
13	Paired de Bruijn Graphs: A Novel Approach for Incorporating Mate Pair Information into Genome Assemblers. <i>Journal of Computational Biology</i> , 2011, 18, 1625-1634.	1.6	60
14	Paired de Bruijn Graphs: A Novel Approach for Incorporating Mate Pair Information into Genome Assemblers. <i>Lecture Notes in Computer Science</i> , 2011, , 238-251.	1.3	13