

Dent Earl

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10498640/publications.pdf>

Version: 2024-02-01

12
papers

2,360
citations

840119

11
h-index

1199166

12
g-index

14
all docs

14
docs citations

14
times ranked

4887
citing authors

#	ARTICLE	IF	CITATIONS
1	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. <i>Nature Genetics</i> , 2018, 50, 1574-1583.	9.4	169
2	Comparative Annotation Toolkit (CAT)â€™ simultaneous clade and personal genome annotation. <i>Genome Research</i> , 2018, 28, 1029-1038.	2.4	86
3	Building a Pan-Genome Reference for a Population. <i>Journal of Computational Biology</i> , 2015, 22, 387-401.	0.8	48
4	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014, 24, 2077-2089.	2.4	102
5	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.	6.0	300
6	Building a Pangenome Reference for a Population. <i>Lecture Notes in Computer Science</i> , 2014, , 207-221.	1.0	6
7	Retrotransposition of gene transcripts leads to structural variation in mammalian genomes. <i>Genome Biology</i> , 2013, 14, R22.	13.9	102
8	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	3.3	582
9	HAL: a hierarchical format for storing and analyzing multiple genome alignments. <i>Bioinformatics</i> , 2013, 29, 1341-1342.	1.8	164
10	Cactus Graphs for Genome Comparisons. <i>Journal of Computational Biology</i> , 2011, 18, 469-481.	0.8	93
11	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443
12	Cactus: Algorithms for genome multiple sequence alignment. <i>Genome Research</i> , 2011, 21, 1512-1528.	2.4	245