

Aaron M Berlin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10804526/publications.pdf>

Version: 2024-02-01

13
papers

4,902
citations

686830

13
h-index

996533

15
g-index

15
all docs

15
docs citations

15
times ranked

11833
citing authors

#	ARTICLE	IF	CITATIONS
1	High-quality draft assemblies of mammalian genomes from massively parallel sequence data. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1513-1518.	3.3	1,476
2	A Catalog of Reference Genomes from the Human Microbiome. Science, 2010, 328, 994-999.	6.0	621
3	The African coelacanth genome provides insights into tetrapod evolution. Nature, 2013, 496, 311-316.	13.7	612
4	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. Nature Genetics, 2016, 48, 427-437.	9.4	545
5	Comparative analysis of RNA sequencing methods for degraded or low-input samples. Nature Methods, 2013, 10, 623-629.	9.0	419
6	Genomic analysis of oceanic cyanobacterial myoviruses compared with T4-like myoviruses from diverse hosts and environments. Environmental Microbiology, 2010, 12, 3035-3056.	1.8	318
7	Whole Genome Deep Sequencing of HIV-1 Reveals the Impact of Early Minor Variants Upon Immune Recognition During Acute Infection. PLoS Pathogens, 2012, 8, e1002529.	2.1	306
8	Finished bacterial genomes from shotgun sequence data. Genome Research, 2012, 22, 2270-2277.	2.4	205
9	The draft genome sequence of the ferret (<i>Mustela putorius furo</i>) facilitates study of human respiratory disease. Nature Biotechnology, 2014, 32, 1250-1255.	9.4	110
10	Analysis of High-Throughput Sequencing and Annotation Strategies for Phage Genomes. PLoS ONE, 2010, 5, e9083.	1.1	76
11	Complete viral RNA genome sequencing of ultra-low copy samples by sequence-independent amplification. Nucleic Acids Research, 2013, 41, e13-e13.	6.5	75
12	The Naked Mole Rat Genome Resource: facilitating analyses of cancer and longevity-related adaptations. Bioinformatics, 2014, 30, 3558-3560.	1.8	71
13	Paired-end sequencing of Fosmid libraries by Illumina. Genome Research, 2012, 22, 2241-2249.	2.4	52