

Yongwook Choi

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

5,258
citations

623574

14
h-index

794469

19
g-index

26
all docs

26
docs citations

26
times ranked

13385
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting the Functional Effect of Amino Acid Substitutions and Indels. PLoS ONE, 2012, 7, e46688.	1.1	2,465
2	PROVEAN web server: a tool to predict the functional effect of amino acid substitutions and indels. Bioinformatics, 2015, 31, 2745-2747.	1.8	2,033
3	A novel method of consensus pan-chromosome assembly and large-scale comparative analysis reveal the highly flexible pan-genome of <i>Acinetobacter baumannii</i> . Genome Biology, 2015, 16, 143.	13.9	122
4	Comparison of phasing strategies for whole human genomes. PLoS Genetics, 2018, 14, e1007308.	1.5	118
5	A fast computation of pairwise sequence alignment scores between a protein and a set of single-locus variants of another protein. , 2012, , .		91
6	Compression of Graphical Structures: Fundamental Limits, Algorithms, and Experiments. IEEE Transactions on Information Theory, 2012, 58, 620-638.	1.5	74
7	Mechanism-of-Action Classification of Antibiotics by Global Transcriptome Profiling. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	56
8	Electrochemical detection of <i>Pseudomonas</i> in wound exudate samples from patients with chronic wounds. Wound Repair and Regeneration, 2016, 24, 366-372.	1.5	49
9	Conserved Genomic Terminals of SARS-CoV-2 as Coevolving Functional Elements and Potential Therapeutic Targets. MSphere, 2020, 5, .	1.3	41
10	Co-occurrence of Anaerobes in Human Chronic Wounds. Microbial Ecology, 2019, 77, 808-820.	1.4	40
11	Dominance and Sexual Dimorphism Pervade the <i>Salix purpurea</i> L. Transcriptome. Genome Biology and Evolution, 2017, 9, 2377-2394.	1.1	35
12	A Maize Database Resource that Captures Tissue-Specific and Subcellular-Localized Gene Expression, via Fluorescent Tags and Confocal Imaging (Maize Cell Genomics Database). Plant and Cell Physiology, 2015, 56, e12-e12.	1.5	29
13	Multidrug resistant pathogens respond differently to the presence of co-pathogen, commensal, probiotic and host cells. Scientific Reports, 2018, 8, 8656.	1.6	19
14	AbGRI4, a novel antibiotic resistance island in multiply antibiotic-resistant <i>Acinetobacter baumannii</i> clinical isolates. Journal of Antimicrobial Chemotherapy, 2020, 75, 2760-2768.	1.3	18
15	Energy-Optimal Distributed Algorithms for Minimum Spanning Trees. IEEE Journal on Selected Areas in Communications, 2009, 27, 1297-1304.	9.7	16
16	Predicting antimicrobial mechanism-of-action from transcriptomes: A generalizable explainable artificial intelligence approach. PLoS Computational Biology, 2021, 17, e1008857.	1.5	16
17	Identification of microRNAs and their targets in four <i>Gossypium</i> species using RNA sequencing. Current Plant Biology, 2018, 14, 30-40.	2.3	8
18	Pattern Matching in Constrained Sequences. , 2007, , .		5

#	ARTICLE	IF	CITATIONS
19	Compression of graphical structures. , 2009, , .		4
20	HSV-1 clinical isolates with unique in vivo and in vitro phenotypes and insight into genomic differences. Journal of NeuroVirology, 2017, 23, 171-185.	1.0	4
21	Constrained pattern matching. ACM Transactions on Algorithms, 2011, 7, 1-19.	0.9	3
22	Nonadditive gene expression is correlated with nonadditive phenotypic expression in interspecific triploid hybrids of willow (<i>Salix</i> spp.). G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	3
23	Energy-optimal distributed algorithms for minimum spanning trees. , 2008, , .		1
24	Fast Algorithm for Optimal Compression of Graphs. , 2010, , .		1
25	Large deviations for constrained pattern matching. , 2008, , .		0