Yongwook Choi

List of Publications by Year
in descending order

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	Nonadditive gene expression is correlated with nonadditive phenotypic expression in interspecific triploid hybrids of willow (*Salix* spp.). G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	3
2	Predicting antimicrobial mechanism-of-action from transcriptomes: A generalizable explainable artificial intelligence approach. PLoS Computational Biology, 2021, 17, e1008857.	1.5	16
3	AbGRI4, a novel antibiotic resistance island in multiply antibiotic-resistant Acinetobacter baumannii clinical isolates. Journal of Antimicrobial Chemotherapy, 2020, 75, 2760-2768.	1.3	18
4	Conserved Genomic Terminals of SARS-CoV-2 as Coevolving Functional Elements and Potential Therapeutic Targets. MSphere, 2020, 5, .	1.3	41
5	Mechanism-of-Action Classification of Antibiotics by Global Transcriptome Profiling. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	56
6	Co-occurrence of Anaerobes in Human Chronic Wounds. Microbial Ecology, 2019, 77, 808-820.	1.4	40
7	Identification of microRNAs and their targets in four Gossypium species using RNA sequencing. Current Plant Biology, 2018, 14, 30-40.	2.3	8
8	Comparison of phasing strategies for whole human genomes. PLoS Genetics, 2018, 14, e1007308.	1.5	118
9	Multidrug resistant pathogens respond differently to the presence of co-pathogen, commensal, probiotic and host cells. Scientific Reports, 2018, 8, 8656.	1.6	19
10	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
11	Dominance and Sexual Dimorphism Pervade the Salix purpurea L. Transcriptome. Genome Biology and Evolution, 2017, 9, 2377-2394.	1.1	35
12	Electrochemical detection of *Pseudomonas* in wound exudate samples from patients with chronic wounds. Wound Repair and Regeneration, 2016, 24, 366-372.	1.5	49
13	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
14	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
15	A novel method of consensus pan-chromosome assembly and large-scale comparative analysis reveal the highly flexible pan-genome of Acinetobacter baumannii. Genome Biology, 2015, 16, 143.	13.9	122
16	A fast computation of pairwise sequence alignment scores between a protein and a set of single-locus variants of another protein. , 2012, , .		91
17	Predicting the Functional Effect of Amino Acid Substitutions and Indels. PLoS ONE, 2012, 7, e46688.	1.1	2,465
18	Compression of Graphical Structures: Fundamental Limits, Algorithms, and Experiments. IEEE Transactions on Information Theory, 2012, 58, 620-638.	1.5	74

#	Article	IF	Citations
19	Constrained pattern matching. ACM Transactions on Algorithms, 2011, 7, 1-19.	0.9	3
20	Fast Algorithm for Optimal Compression of Graphs. , 2010, , .		1
21	Compression of graphical structures. , 2009, , .		4
22	Energy-Optimal Distributed Algorithms for Minimum Spanning Trees. IEEE Journal on Selected Areas in Communications, 2009, 27, 1297-1304.	9.7	16
23	Large deviations for constrained pattern matching. , 2008, , .		0
24	Energy-optimal distributed algorithms for minimum spanning trees. , 2008, , .		1
25	Pattern Matching in Constrained Sequences. , 2007, , .		5