Yongwook Choi

List of Publications by Year
in descending order

25	5,258	623734	794594
25 papers	**5,258** citations	**14** h-index	**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.	2.5	2,465
2	PROVEAN web server: a tool to predict the functional effect of amino acid substitutions and indels. Bioinformatics, 2015, 31, 2745-2747.	4.1	2,033
3	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.	9.6	122
4	Comparison of phasing strategies for whole human genomes. PLoS Genetics, 2018, 14, e1007308.	3.5	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.	2.4	74
7	Mechanism-of-Action Classification of Antibiotics by Global Transcriptome Profiling. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	56
8	Electrochemical detection of *Pseudomonas* in wound exudate samples from patients with chronic wounds. Wound Repair and Regeneration, 2016, 24, 366-372.	3.0	49
9	Conserved Genomic Terminals of SARS-CoV-2 as Coevolving Functional Elements and Potential Therapeutic Targets. MSphere, 2020, 5, .	2.9	41
10	Co-occurrence of Anaerobes in Human Chronic Wounds. Microbial Ecology, 2019, 77, 808-820.	2.8	40
11	Dominance and Sexual Dimorphism Pervade the Salix purpurea L. Transcriptome. Genome Biology and Evolution, 2017, 9, 2377-2394.	2.5	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.	3.1	29
13	Multidrug resistant pathogens respond differently to the presence of co-pathogen, commensal, probiotic and host cells. Scientific Reports, 2018, 8, 8656.	3.3	19
14	AbGRI4, a novel antibiotic resistance island in multiply antibiotic-resistant Acinetobacter baumannii clinical isolates. Journal of Antimicrobial Chemotherapy, 2020, 75, 2760-2768.	3.0	18
15	Energy-Optimal Distributed Algorithms for Minimum Spanning Trees. IEEE Journal on Selected Areas in Communications, 2009, 27, 1297-1304.	14.0	16
16	Predicting antimicrobial mechanism-of-action from transcriptomes: A generalizable explainable artificial intelligence approach. PLoS Computational Biology, 2021, 17, e1008857.	3.2	16
17	Identification of microRNAs and their targets in four Gossypium species using RNA sequencing. Current Plant Biology, 2018, 14, 30-40.	4.7	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.	2.1	4
21	Constrained pattern matching. ACM Transactions on Algorithms, 2011, 7, 1-19.	1.0	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, .	1.8	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