Yutaka Akiyama

List of Publications by Year
in descending order

17	193	1306789 7	1125271 13
papers	citations	h-index	g-index

18	18	18	241
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Plasma protein binding prediction focusing on residue-level features and circularity of cyclic peptides by deep learning. Bioinformatics, 2022, 38, 1110-1117.	1.8	5
2	Solving Generalized Polyomino Puzzles Using the Ising Model. Entropy, 2022, 24, 354.	1.1	6
3	Taxonomic and Gene Category Analyses of Subgingival Plaques from a Group of Japanese Individuals with and without Periodontitis. International Journal of Molecular Sciences, 2021, 22, 5298.	1.8	3
4	Large-Scale Membrane Permeability Prediction of Cyclic Peptides Crossing a Lipid Bilayer Based on Enhanced Sampling Molecular Dynamics Simulations. Journal of Chemical Information and Modeling, 2021, 61, 3681-3695.	2.5	50
5	Improved Large-Scale Homology Search by Two-Step Seed Search Using Multiple Reduced Amino Acid Alphabets. Genes, 2021, 12, 1455.	1.0	1
6	Comprehensive Fungal Community Analysis of House Dust Using Next-Generation Sequencing. International Journal of Environmental Research and Public Health, 2020, 17, 5842.	1.2	8
7	Multiple HPC Environments-Aware Container Image Configuration Workflow for Large-Scale All-to-All Proteinâ€“Protein Docking Calculations. Lecture Notes in Computer Science, 2020, , 23-39.	1.0	3
8	QEX: target-specific druglikeness filter enhances ligand-based virtual screening. Molecular Diversity, 2019, 23, 11-18.	2.1	9
9	Learning-to-rank technique based on ignoring meaningless ranking orders between compounds. Journal of Molecular Graphics and Modelling, 2019, 92, 192-200.	1.3	1
10	A prospective compound screening contest identified broader inhibitors for Sirtuin 1. Scientific Reports, 2019, 9, 19585.	1.6	15
11	Multiple grid arrangement improves ligand docking with unknown binding sites: Application to the inverse docking problem. Computational Biology and Chemistry, 2018, 73, 139-146.	1.1	30
12	Optimization of memory use of fragment extension-based proteinâ€“ligand docking with an original fast minimum cost flow algorithm. Computational Biology and Chemistry, 2018, 74, 399-406.	1.1	2
13	Computational prediction of plasma protein binding of cyclic peptides from small molecule experimental data using sparse modeling techniques. BMC Bioinformatics, 2018, 19, 527.	1.2	9
14	PKRank: a novel learning-to-rank method for ligand-based virtual screening using pairwise kernel and RankSVM. Artificial Life and Robotics, 2018, 23, 205-212.	0.7	6
15	MEGADOCK-Web: an integrated database of high-throughput structure-based protein-protein interaction predictions. BMC Bioinformatics, 2018, 19, 62.	1.2	25
16	GHOSTX: A Fast Sequence Homology Search Tool for Functional Annotation of Metagenomic Data. Methods in Molecular Biology, 2017, 1611, 15-25.	0.4	8
17	A Massively Parallel Sequence Similarity Search for Metagenomic Sequencing Data. International Journal of Molecular Sciences, 2017, 18, 2124.	1.8	4