Guanghong Zuo

List of Publications by Year
in descending order

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27	1,356	566801 15	610482 24
papers	citations	h-index	g-index

28	28	28	1945
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	CVTree: A Parallel Alignment-free Phylogeny and Taxonomy Tool Based on Composition Vectors of Genomes. Genomics, Proteomics and Bioinformatics, 2021, 19, 662-667.	3.0	24
2	EspcTM: Kinetic Transition Network Based on Trajectory Mapping in Effective Energy Rescaling Space. Frontiers in Molecular Biosciences, 2020, 7, 589718.	1.6	0
3	Polyphyly in 16S rRNA-based LVTree Versus Monophyly in Whole-genome-based CVTree. Genomics, Proteomics and Bioinformatics, 2018, 16, 310-319.	3.0	8
4	On monospecific genera in prokaryotic taxonomy. Synthetic and Systems Biotechnology, 2017, 2, 226-235.	1.8	5
5	Whole-Genome-Based Phylogeny and Taxonomy for Prokaryotes. , 2017, , .		1
6	LVTree Viewer: An Interactive Display for the All-Species Living Tree Incorporating Automatic Comparison with Prokaryotic Systematics. Genomics, Proteomics and Bioinformatics, 2016, 14, 94-102.	3.0	3
7	Whole-genome-based phylogeny supports the objections against the reclassification of Eubacterium rectale to Agathobacter rectalis. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2451-2451.	0.8	6
8	CVTree3 Web Server for Whole-genome-based and Alignment-free Prokaryotic Phylogeny and Taxonomy. Genomics, Proteomics and Bioinformatics, 2015, 13, 321-331.	3.0	185
9	Phylogeny and Taxonomy of Archaea: A Comparison of the Whole-Genome-Based CVTree Approach with 16S rRNA Sequence Analysis. Life, 2015, 5, 949-968.	1.1	26
10	On K-peptide length in composition vector phylogeny of prokaryotes. Computational Biology and Chemistry, 2014, 53, 166-173.	1.1	16
11	Geographic divergence of â€œSulfolobus islandicusâ€•strains assessed by genomic analyses including electronic DNA hybridization confirms they are geovars. Antonie Van Leeuwenhoek, 2014, 105, 431-435.	0.7	6
12	Binding Preference of Carbon Nanotube Over Proline-Rich Motif Ligand on SH3-Domain: A Comparison with Different Force Fields. Journal of Physical Chemistry B, 2013, 117, 3541-3547.	1.2	14
13	Shigella Strains Are Not Clones of Escherichia Coli but Sister Species in the Genus Escherichia. Genomics, Proteomics and Bioinformatics, 2013, 11, 61-65.	3.0	52
14	Interactions Between Proteins and Carbonâ€Based Nanoparticles: Exploring the Origin of Nanotoxicity at the Molecular Level. Small, 2013, 9, 1546-1556.	5.2	132
15	Aggregated Gas Molecules: Toxic to Protein?. Scientific Reports, 2013, 3, 1660.	1.6	24
16	Conformational Changes of the Protein Domains Upon Binding with Carbon Nanotubes Studied by Molecular Dynamics Simulations. Current Physical Chemistry, 2012, 2, 12-22.	0.1	7
17	Carbon Nanotube Wins the Competitive Binding over Proline-Rich Motif Ligand on SH3 Domain. Journal of Physical Chemistry C, 2011, 115, 12322-12328.	1.5	56
18	Nanotoxicity: Exploring the Interactions Between Carbon Nanotubes and Proteins. , 2011, , .		2

#	Article	IF	Citations
19	Adsorption of Villin Headpiece onto Graphene, Carbon Nanotube, and C60: Effect of Contacting Surface Curvatures on Binding Affinity. Journal of Physical Chemistry C, 2011, 115, 23323-23328.	1.5	181
20	Effect of solvation-related interaction on the low-temperature dynamics of proteins. Physical Review E, 2010, 81, 031917.	0.8	5
21	Plugging into Proteins: Poisoning Protein Function by a Hydrophobic Nanoparticle. ACS Nano, 2010, 4, 7508-7514.	7.3	168
22	Folding of a Small RNA Hairpin Based on Simulation with Replica Exchange Molecular Dynamics. Journal of Physical Chemistry B, 2010, 114, 5835-5839.	1.2	26
23	Jackknife and Bootstrap Tests of the Composition Vector Trees. Genomics, Proteomics and Bioinformatics, 2010, 8, 262-267.	3.0	26
24	Stable Liquid Water Droplet on a Water Monolayer Formed at Room Temperature on Ionic Model Substrates. Physical Review Letters, 2009, 103, 137801.	2.9	238
25	Effect of the ordered water on protein folding: An off-lattice GÅ•like model study. Physical Review E, 2009, 79, 031925.	0.8	26
26	Protein folding simulations: From coarseâ€grained model to allâ€atom model. IUBMB Life, 2009, 61, 627-643.	1.5	55
27	Folding with downhill behavior and low cooperativity of proteins. Proteins: Structure, Function and Bioinformatics, 2006, 63, 165-173.	1.5	64