

Guanghong Zuo

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	CVTree: A Parallel Alignment-free Phylogeny and Taxonomy Tool Based on Composition Vectors of Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 662-667.	6.9	24
2	EspcTM: Kinetic Transition Network Based on Trajectory Mapping in Effective Energy Rescaling Space. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 589718.	3.5	0
3	Polyphyly in 16S rRNA-based LVTre Versus Monophyly in Whole-genome-based CVTree. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 310-319.	6.9	8
4	On monospecific genera in prokaryotic taxonomy. <i>Synthetic and Systems Biotechnology</i> , 2017, 2, 226-235.	3.7	5
5	Whole-Genome-Based Phylogeny and Taxonomy for Prokaryotes. , 2017, , .		1
6	LVTre Viewer: An Interactive Display for the All-Species Living Tree Incorporating Automatic Comparison with Prokaryotic Systematics. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 94-102.	6.9	3
7	Whole-genome-based phylogeny supports the objections against the reclassification of <i>Eubacterium rectale</i> to <i>Agathobacter rectalis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2451-2451.	1.7	6
8	CVTree3 Web Server for Whole-genome-based and Alignment-free Prokaryotic Phylogeny and Taxonomy. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 321-331.	6.9	185
9	Phylogeny and Taxonomy of Archaea: A Comparison of the Whole-Genome-Based CVTree Approach with 16S rRNA Sequence Analysis. <i>Life</i> , 2015, 5, 949-968.	2.4	26
10	On K-peptide length in composition vector phylogeny of prokaryotes. <i>Computational Biology and Chemistry</i> , 2014, 53, 166-173.	2.3	16
11	Geographic divergence of <i>Sulfolobus islandicus</i> strains assessed by genomic analyses including electronic DNA hybridization confirms they are geovars. <i>Antonie Van Leeuwenhoek</i> , 2014, 105, 431-435.	1.7	6
12	Binding Preference of Carbon Nanotube Over Proline-Rich Motif Ligand on SH3-Domain: A Comparison with Different Force Fields. <i>Journal of Physical Chemistry B</i> , 2013, 117, 3541-3547.	2.6	14
13	<i>Shigella</i> Strains Are Not Clones of <i>Escherichia Coli</i> but Sister Species in the Genus <i>Escherichia</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 61-65.	6.9	52
14	Interactions Between Proteins and Carbon-Based Nanoparticles: Exploring the Origin of Nanotoxicity at the Molecular Level. <i>Small</i> , 2013, 9, 1546-1556.	10.0	132
15	Aggregated Gas Molecules: Toxic to Protein?. <i>Scientific Reports</i> , 2013, 3, 1660.	3.3	24
16	Conformational Changes of the Protein Domains Upon Binding with Carbon Nanotubes Studied by Molecular Dynamics Simulations. <i>Current Physical Chemistry</i> , 2012, 2, 12-22.	0.2	7
17	Carbon Nanotube Wins the Competitive Binding over Proline-Rich Motif Ligand on SH3 Domain. <i>Journal of Physical Chemistry C</i> , 2011, 115, 12322-12328.	3.1	56
18	Nanotoxicity: Exploring the Interactions Between Carbon Nanotubes and Proteins. , 2011, , .		2

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19	Adsorption of Villin Headpiece onto Graphene, Carbon Nanotube, and C60: Effect of Contacting Surface Curvatures on Binding Affinity. <i>Journal of Physical Chemistry C</i> , 2011, 115, 23323-23328.	3.1	181
20	Effect of solvation-related interaction on the low-temperature dynamics of proteins. <i>Physical Review E</i> , 2010, 81, 031917.	2.1	5
21	Plugging into Proteins: Poisoning Protein Function by a Hydrophobic Nanoparticle. <i>ACS Nano</i> , 2010, 4, 7508-7514.	14.6	168
22	Folding of a Small RNA Hairpin Based on Simulation with Replica Exchange Molecular Dynamics. <i>Journal of Physical Chemistry B</i> , 2010, 114, 5835-5839.	2.6	26
23	Jackknife and Bootstrap Tests of the Composition Vector Trees. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 262-267.	6.9	26
24	Stable Liquid Water Droplet on a Water Monolayer Formed at Room Temperature on Ionic Model Substrates. <i>Physical Review Letters</i> , 2009, 103, 137801.	7.8	238
25	Effect of the ordered water on protein folding: An off-lattice GÅ-like model study. <i>Physical Review E</i> , 2009, 79, 031925.	2.1	26
26	Protein folding simulations: From coarse-grained model to all-atom model. <i>IUBMB Life</i> , 2009, 61, 627-643.	3.4	55
27	Folding with downhill behavior and low cooperativity of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 165-173.	2.6	64