Joshua L Phillips

List of Publications by Year
in descending order

30	722	1307594 7	1372567 10
papers	citations	h-index	g-index

31	31	31	1363
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Computational Electrostatics Predict Variations in SARS-CoV-2 Spike and Human ACE2 Interactions. , 2021, , .		0
2	pH Dependent Binding Energies of Broadly Neutralizing Antibodies. , 2021, , .		0
3	Accelerated Protein Folding Using Greedy-Proximal A*. Journal of Chemical Information and Modeling, 2020, 60, 3093-3104.	5.4	3
4	The Molecular Basis of pH-Modulated HIV gp120 Binding Revealed. Evolutionary Bioinformatics, 2019, 15, 117693431983130.	1.2	4
5	Creation of a Curated Aquatic Toxicology Database: EnviroTox. Environmental Toxicology and Chemistry, 2019, 38, 1062-1073.	4.3	73
6	Sub-Class Differences of PH-Dependent HIV GP120-CD4 Interactions. , 2018, , .		3
7	Hybrid Spectral/Subspace Clustering of Molecular Dynamics Simulations. , 2018, , .		2
8	Dimensionality Estimation of Protein Dynamics Using Polymer Models. , 2018, , .		1
9	Computational Modeling of pH Sensitivity in the Critical HIV gp120-CD4 Interaction. Biophysical Journal, 2017, 112, 294a.	0.5	0
10	Switch Loop Flexibility Affects Substrate Transport of the AcrB Efflux Pump. Journal of Molecular Biology, 2017, 429, 3863-3874.	4.2	33
11	High-throughput structural modeling of the HIV transmission bottleneck. , 2017, , .		3
12	Computational Modeling of pH-dependent gp120-CD4 Interactions in Founder and Chronic HIV Strains. , 2017, , .		4
13	Mechanistic Details of Drug Translocation in MexAB-OprM Efflux Pump. Biophysical Journal, 2015, 108, 310a.	0.5	0
14	A dataâ€driven approach to modeling the tripartite structure of multidrug resistance efflux pumps. Proteins: Structure, Function and Bioinformatics, 2015, 83, 46-65.	2.6	31
15	Systems Level Study of Bacterial Multi-Drug Resistance from Efflux Machinery. Biophysical Journal, 2014, 106, 791a.	0.5	0
16	Comparison of Metrics of Inter-Structure Distance When Applied to Molecular Dynamics Simulations of Intrinsically Disordered Proteins. Biophysical Journal, 2014, 106, 610a-611a.	0.5	0
17	Dynamic electrophoretic fingerprinting of the HIV-1 envelope glycoprotein. Retrovirology, 2013, 10, 33.	2.0	14
18	Coarse-Grained Simulations of the MexAB-OprM Multidrug Resistance Efflux Pump. Biophysical Journal, 2013, 104, 286a.	0.5	0

#	Article	IF	Citations
19	Measuring Disorder and Dynamical Properties of FG-Nucleoporins. Biophysical Journal, 2013, 104, 233a-234a.	0.5	0
20	Plasma IgG to Linear Epitopes in the V2 and V3 Regions of HIV-1 gp120 Correlate with a Reduced Risk of Infection in the RV144 Vaccine Efficacy Trial. PLoS ONE, 2013, 8, e75665.	2.5	214
21	Conformational Sampling of FG-Nucleoporins using Extended Molecular Dynamics Simulations. Biophysical Journal, 2012, 102, 632a.	0.5	0
22	Dimensionality Estimation of Disordered Protein Dynamics. Biophysical Journal, 2012, 102, 451a.	0.5	0
23	Sorting with Disorder at Nuclear Pores. Biophysical Journal, 2012, 102, 2a.	0.5	0
24	Probing the Conformation Landscape of the Unfolded State: Do Disordered and Unfolded Dynamics Differ?. Biophysical Journal, 2011, 100, 185a.	0.5	0
25	Validating clustering of molecular dynamics simulations using polymer models. BMC Bioinformatics, 2011, 12, 445.	2.6	32
26	A Bimodal Distribution of Two Distinct Categories of Intrinsically Disordered Structures with Separate Functions in FG Nucleoporins. Molecular and Cellular Proteomics, 2010, 9, 2205-2224.	3.8	289
27	Metric Scaling for Dimensionality Reduction of Disordered Protein Dynamics. Biophysical Journal, 2010, 98, 631a.	0.5	0
28	Analytic Parameter Fitting in Stochastic Stem Cell Models. Biophysical Journal, 2010, 98, 739a.	0.5	0
29	Molecular dynamics simulations of highly charged green fluorescent proteins. Molecular Physics, 2009, 107, 1233-1241.	1.7	4
30	Analyzing dynamical simulations of intrinsically disordered proteins using spectral clustering. , 2008, , .		7