Adrian W R Serohijos

List of Publications by Year
in descending order

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38 papers	1,826 citations	279798 23 h-index	315739 38 g-index
46 all docs	46 docs citations	46 times ranked	2065 citing authors

#	Article	IF	Citations
1	Phenylalanine-508 mediates a cytoplasmicâ€“membrane domain contact in the CFTR 3D structure crucial to assembly and channel function. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3256-3261.	7.1	354
2	Protein Quality Control Acts on Folding Intermediates to Shape the Effects of Mutations on Organismal Fitness. Molecular Cell, 2013, 49, 133-144.	9.7	145
3	Multiple Membrane-Cytoplasmic Domain Contacts in the Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) Mediate Regulation of Channel Gating. Journal of Biological Chemistry, 2008, 283, 26383-26390.	3.4	109
4	Protein Biophysics Explains Why Highly Abundant Proteins Evolve Slowly. Cell Reports, 2012, 2, 249-256.	6.4	108
5	Protein folding: Then and now. Archives of Biochemistry and Biophysics, 2008, 469, 4-19.	3.0	88
6	Merging molecular mechanism and evolution: theory and computation at the interface of biophysics and evolutionary population genetics. Current Opinion in Structural Biology, 2014, 26, 84-91.	5.7	88
7	Protein Homeostasis Imposes a Barrier on Functional Integration of Horizontally Transferred Genes in Bacteria. PLoS Genetics, 2015, 11, e1005612.	3.5	79
8	Bridging the physical scales in evolutionary biology: from protein sequence space to fitness of organisms and populations. Current Opinion in Structural Biology, 2017, 42, 31-40.	5.7	63
9	Computational Studies Reveal Phosphorylation-dependent Changes in the Unstructured R Domain of CFTR. Journal of Molecular Biology, 2008, 378, 1052-1063.	4.2	54
10	Identification and Rational Redesign of Peptide Ligands to CRIP1, A Novel Biomarker for Cancers. PLoS Computational Biology, 2008, 4, e1000138.	3.2	53
11	Positively Selected Sites in Cetacean Myoglobins Contribute to Protein Stability. PLoS Computational Biology, 2013, 9, e1002929.	3.2	52
12	Contribution of Selection for Protein Folding Stability in Shaping the Patterns of Polymorphisms in Coding Regions. Molecular Biology and Evolution, 2014, 31, 165-176.	8.9	51
13	The Influence of Selection for Protein Stability on dN/dS Estimations. Genome Biology and Evolution, 2014, 6, 2956-2967.	2.5	49
14	Diminished Self-Chaperoning Activity of the Î”F508 Mutant of CFTR Results in Protein Misfolding. PLoS Computational Biology, 2008, 4, e1000008.	3.2	46
15	Influenza A H1N1 Pandemic Strain Evolution â€“ Divergence and the Potential for Antigenic Drift Variants. PLoS ONE, 2014, 9, e93632.	2.5	45
16	Evolution on the Biophysical Fitness Landscape of an RNA Virus. Molecular Biology and Evolution, 2018, 35, 2390-2400.	8.9	45
17	Chromosomal barcoding of E. coli populations reveals lineage diversity dynamics at high resolution. Nature Ecology and Evolution, 2020, 4, 437-452.	7.8	44
18	A structural model reveals energy transduction in dynein. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18540-18545.	7.1	34

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19	Highly Abundant Proteins Favor More Stable 3D Structures in Yeast. Biophysical Journal, 2013, 104, L1-L3.	0.5	33
20	Isolation and Analysis of Rare Norovirus Recombinants from Coinfected Mice Using Drop-Based Microfluidics. Journal of Virology, 2015, 89, 7722-7734.	3.4	32
21	Stability of the Influenza Virus Hemagglutinin Protein Correlates with Evolutionary Dynamics. MSphere, 2018, 3, .	2.9	31
22	Structural Basis for Î¼-Opioid Receptor Binding and Activation. Structure, 2011, 19, 1683-1690.	3.3	30
23	A Structural Model of the Pore-Forming Region of the Skeletal Muscle Ryanodine Receptor (RyR1). PLoS Computational Biology, 2009, 5, e1000367.	3.2	25
24	Kinetic models for the coordinated stepping of cytoplasmic dynein. Journal of Chemical Physics, 2009, 130, 025101.	3.0	19
25	Minimalistic Predictor of Protein Binding Energy: Contribution of Solvation Factor to Protein Binding. Biophysical Journal, 2015, 108, 795-798.	0.5	17
26	Estimating the contribution of folding stability to nonspecific epistasis in protein evolution. Proteins: Structure, Function and Bioinformatics, 2018, 86, 1242-1250.	2.6	17
27	Multiscale approaches for studying energy transduction in dynein. Physical Chemistry Chemical Physics, 2009, 11, 4840.	2.8	14
28	Molecular basis of interactions between SH3 domain-containing proteins and the proline-rich region of the ubiquitin ligase Itch. Journal of Biological Chemistry, 2017, 292, 6325-6338.	3.4	13
29	Evolutionary dynamics of viral escape under antibodies stress: A biophysical model. Protein Science, 2016, 25, 1332-1340.	7.6	12
30	A Physical Model Reveals the Mechanochemistry Responsible for Dynein's Processive Motion. Biophysical Journal, 2011, 101, 144-150.	0.5	11
31	The Combination of IFN Î² and TNF Induces an Antiviral and Immunoregulatory Program via Non-Canonical Pathways Involving STAT2 and IRF9. Cells, 2019, 8, 919.	4.1	11
32	A functional substitution in the Lâ€aromatic amino acid decarboxylase enzyme worsens somatic symptoms via a serotonergic pathway. Annals of Neurology, 2019, 86, 168-180.	5.3	9
33	The Streptomyces-Produced Antibiotic Fosfomycin Is a Promiscuous Substrate for Archaeal Isopentenyl Phosphate Kinase. Biochemistry, 2012, 51, 917-925.	2.5	8
34	Mobile Gene Sequence Evolution within Individual Human Gut Microbiomes Is Better Explained by Gene-Specific Than Host-Specific Selective Pressures. Genome Biology and Evolution, 2021, 13, .	2.5	8
35	Avoidance of protein unfolding constrains protein stability in long-term evolution. Biophysical Journal, 2021, 120, 2413-2424.	0.5	7
36	SodaPop: a forward simulation suite for the evolutionary dynamics of asexual populations on protein fitness landscapes. Bioinformatics, 2019, 35, 4053-4062.	4.1	6

#	Article	IF	Citations
37	Highly expressed genes evolve under strong epistasis from a proteome-wide scan in E. coli. Scientific Reports, 2017, 7, 15844.	3.3	4
38	Molecular Modeling Tools and Approaches for CFTR and Cystic Fibrosis. Methods in Molecular Biology, 2011, 741, 347-363.	0.9	2