

# Adrian W R Serohijos

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Mobile Gene Sequence Evolution within Individual Human Gut Microbiomes Is Better Explained by Gene-Specific Than Host-Specific Selective Pressures. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	8
2	Avoidance of protein unfolding constrains protein stability in long-term evolution. <i>Biophysical Journal</i> , 2021, 120, 2413-2424.	0.5	7
3	Chromosomal barcoding of <i>E. coli</i> populations reveals lineage diversity dynamics at high resolution. <i>Nature Ecology and Evolution</i> , 2020, 4, 437-452.	7.8	44
4	The Combination of IFN $\hat{I}^2$ and TNF Induces an Antiviral and Immunoregulatory Program via Non-Canonical Pathways Involving STAT2 and IRF9. <i>Cells</i> , 2019, 8, 919.	4.1	11
5	A functional substitution in the Lâ€aromatic amino acid decarboxylase enzyme worsens somatic symptoms via a serotonergic pathway. <i>Annals of Neurology</i> , 2019, 86, 168-180.	5.3	9
6	SodaPop: a forward simulation suite for the evolutionary dynamics of asexual populations on protein fitness landscapes. <i>Bioinformatics</i> , 2019, 35, 4053-4062.	4.1	6
7	Stability of the Influenza Virus Hemagglutinin Protein Correlates with Evolutionary Dynamics. <i>MSphere</i> , 2018, 3, .	2.9	31
8	Evolution on the Biophysical Fitness Landscape of an RNA Virus. <i>Molecular Biology and Evolution</i> , 2018, 35, 2390-2400.	8.9	45
9	Estimating the contribution of folding stability to nonspecific epistasis in protein evolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 1242-1250.	2.6	17
10	Molecular basis of interactions between SH3 domain-containing proteins and the proline-rich region of the ubiquitin ligase Itch. <i>Journal of Biological Chemistry</i> , 2017, 292, 6325-6338.	3.4	13
11	Highly expressed genes evolve under strong epistasis from a proteome-wide scan in <i>E. coli</i> . <i>Scientific Reports</i> , 2017, 7, 15844.	3.3	4
12	Bridging the physical scales in evolutionary biology: from protein sequence space to fitness of organisms and populations. <i>Current Opinion in Structural Biology</i> , 2017, 42, 31-40.	5.7	63
13	Evolutionary dynamics of viral escape under antibodies stress: A biophysical model. <i>Protein Science</i> , 2016, 25, 1332-1340.	7.6	12
14	Isolation and Analysis of Rare Norovirus Recombinants from Coinfected Mice Using Drop-Based Microfluidics. <i>Journal of Virology</i> , 2015, 89, 7722-7734.	3.4	32
15	Minimalistic Predictor of Protein Binding Energy: Contribution of Solvation Factor to Protein Binding. <i>Biophysical Journal</i> , 2015, 108, 795-798.	0.5	17
16	Protein Homeostasis Imposes a Barrier on Functional Integration of Horizontally Transferred Genes in Bacteria. <i>PLoS Genetics</i> , 2015, 11, e1005612.	3.5	79
17	Influenza A H1N1 Pandemic Strain Evolution â€“ Divergence and the Potential for Antigenic Drift Variants. <i>PLoS ONE</i> , 2014, 9, e93632.	2.5	45
18	Contribution of Selection for Protein Folding Stability in Shaping the Patterns of Polymorphisms in Coding Regions. <i>Molecular Biology and Evolution</i> , 2014, 31, 165-176.	8.9	51

#	ARTICLE	IF	CITATIONS
19	The Influence of Selection for Protein Stability on dN/dS Estimations. <i>Genome Biology and Evolution</i> , 2014, 6, 2956-2967.	2.5	49
20	Merging molecular mechanism and evolution: theory and computation at the interface of biophysics and evolutionary population genetics. <i>Current Opinion in Structural Biology</i> , 2014, 26, 84-91.	5.7	88
21	Protein Quality Control Acts on Folding Intermediates to Shape the Effects of Mutations on Organismal Fitness. <i>Molecular Cell</i> , 2013, 49, 133-144.	9.7	145
22	Highly Abundant Proteins Favor More Stable 3D Structures in Yeast. <i>Biophysical Journal</i> , 2013, 104, L1-L3.	0.5	33
23	Positively Selected Sites in Cetacean Myoglobins Contribute to Protein Stability. <i>PLoS Computational Biology</i> , 2013, 9, e1002929.	3.2	52
24	Protein Biophysics Explains Why Highly Abundant Proteins Evolve Slowly. <i>Cell Reports</i> , 2012, 2, 249-256.	6.4	108
25	The <i>Streptomyces</i> -Produced Antibiotic Fosfomycin Is a Promiscuous Substrate for Archaeal Isopentenyl Phosphate Kinase. <i>Biochemistry</i> , 2012, 51, 917-925.	2.5	8
26	A Physical Model Reveals the Mechanochemistry Responsible for Dynein's Processive Motion. <i>Biophysical Journal</i> , 2011, 101, 144-150.	0.5	11
27	Structural Basis for $\mu$ -Opioid Receptor Binding and Activation. <i>Structure</i> , 2011, 19, 1683-1690.	3.3	30
28	Molecular Modeling Tools and Approaches for CFTR and Cystic Fibrosis. <i>Methods in Molecular Biology</i> , 2011, 741, 347-363.	0.9	2
29	Kinetic models for the coordinated stepping of cytoplasmic dynein. <i>Journal of Chemical Physics</i> , 2009, 130, 025101.	3.0	19
30	A Structural Model of the Pore-Forming Region of the Skeletal Muscle Ryanodine Receptor (RyR1). <i>PLoS Computational Biology</i> , 2009, 5, e1000367.	3.2	25
31	Multiscale approaches for studying energy transduction in dynein. <i>Physical Chemistry Chemical Physics</i> , 2009, 11, 4840.	2.8	14
32	Computational Studies Reveal Phosphorylation-dependent Changes in the Unstructured R Domain of CFTR. <i>Journal of Molecular Biology</i> , 2008, 378, 1052-1063.	4.2	54
33	Protein folding: Then and now. <i>Archives of Biochemistry and Biophysics</i> , 2008, 469, 4-19.	3.0	88
34	Multiple Membrane-Cytoplasmic Domain Contacts in the Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) Mediate Regulation of Channel Gating. <i>Journal of Biological Chemistry</i> , 2008, 283, 26383-26390.	3.4	109
35	Identification and Rational Redesign of Peptide Ligands to CRIP1, A Novel Biomarker for Cancers. <i>PLoS Computational Biology</i> , 2008, 4, e1000138.	3.2	53
36	Phenylalanine-508 mediates a cytoplasmicâ€”membrane domain contact in the CFTR 3D structure crucial to assembly and channel function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3256-3261.	7.1	354

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37	Diminished Self-Chaperoning Activity of the $\Delta$ F508 Mutant of CFTR Results in Protein Misfolding. PLoS Computational Biology, 2008, 4, e1000008.	3.2	46
38	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