

D Allan Drummond

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

5,606
citations

257450

24
h-index

454955

30
g-index

32
all docs

32
docs citations

32
times ranked

6345
citing authors

#	ARTICLE	IF	CITATIONS
1	Mistranslation-Induced Protein Misfolding as a Dominant Constraint on Coding-Sequence Evolution. <i>Cell</i> , 2008, 134, 341-352.	28.9	949
2	Why highly expressed proteins evolve slowly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14338-14343.	7.1	738
3	Stress-Triggered Phase Separation Is an Adaptive, Evolutionarily Tuned Response. <i>Cell</i> , 2017, 168, 1028-1040.e19.	28.9	674
4	The evolutionary consequences of erroneous protein synthesis. <i>Nature Reviews Genetics</i> , 2009, 10, 715-724.	16.3	437
5	Reversible, Specific, Active Aggregates of Endogenous Proteins Assemble upon Heat Stress. <i>Cell</i> , 2015, 162, 1286-1298.	28.9	395
6	A Single Determinant Dominates the Rate of Yeast Protein Evolution. <i>Molecular Biology and Evolution</i> , 2006, 23, 327-337.	8.9	373
7	Thermodynamic prediction of protein neutrality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 606-611.	7.1	320
8	Misfolded proteins impose a dosage-dependent fitness cost and trigger a cytosolic unfolded protein response in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 680-685.	7.1	264
9	Accounting for Experimental Noise Reveals That mRNA Levels, Amplified by Post-Transcriptional Processes, Largely Determine Steady-State Protein Levels in Yeast. <i>PLoS Genetics</i> , 2015, 11, e1005206.	3.5	164
10	Structural Determinants of the Rate of Protein Evolution in Yeast. <i>Molecular Biology and Evolution</i> , 2006, 23, 1751-1761.	8.9	162
11	Cellular sensing by phase separation: Using the process, not just the products. <i>Journal of Biological Chemistry</i> , 2019, 294, 7151-7159.	3.4	152
12	A diverse family of thermostable cytochrome P450s created by recombination of stabilizing fragments. <i>Nature Biotechnology</i> , 2007, 25, 1051-1056.	17.5	144
13	Why High-error-rate Random Mutagenesis Libraries are Enriched in Functional and Improved Proteins. <i>Journal of Molecular Biology</i> , 2005, 350, 806-816.	4.2	130
14	Good Codons, Bad Transcript: Large Reductions in Gene Expression and Fitness Arising from Synonymous Mutations in a Key Enzyme. <i>Molecular Biology and Evolution</i> , 2013, 30, 549-560.	8.9	120
15	On the conservative nature of intragenic recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5380-5385.	7.1	95
16	A Nutrient-Driven tRNA Modification Alters Translational Fidelity and Genome-wide Protein Coding across an Animal Genus. <i>PLoS Biology</i> , 2014, 12, e1002015.	5.6	93
17	Stressful steps: Progress and challenges in understanding stress-induced mRNA condensation and accumulation in stress granules. <i>Molecular Cell</i> , 2022, 82, 2544-2556.	9.7	54
18	Contact Density Affects Protein Evolutionary Rate from Bacteria to Animals. <i>Journal of Molecular Evolution</i> , 2008, 66, 395-404.	1.8	53

#	ARTICLE	IF	CITATIONS
19	Transient intracellular acidification regulates the core transcriptional heat shock response. <i>ELife</i> , 2020, 9, .	6.0	52
20	Population Genetics of Translational Robustness. <i>Genetics</i> , 2006, 173, 473-481.	2.9	50
21	Estimating Selection on Synonymous Codon Usage from Noisy Experimental Data. <i>Molecular Biology and Evolution</i> , 2013, 30, 1438-1453.	8.9	44
22	Signatures of protein biophysics in coding sequence evolution. <i>Current Opinion in Structural Biology</i> , 2010, 20, 385-389.	5.7	42
23	Predicting the Tolerance of Proteins to Random Amino Acid Substitution. <i>Biophysical Journal</i> , 2005, 89, 3714-3720.	0.5	40
24	Reversible amyloids of pyruvate kinase couple cell metabolism and stress granule disassembly. <i>Nature Cell Biology</i> , 2021, 23, 1085-1094.	10.3	33
25	Quantifying Condition-Dependent Intracellular Protein Levels Enables High-Precision Fitness Estimates. <i>PLoS ONE</i> , 2013, 8, e75320.	2.5	8
26	Protein Evolution: Innovative Chaps. <i>Current Biology</i> , 2009, 19, R740-R742.	3.9	5
27	How Infidelity Creates a Sticky Situation. <i>Molecular Cell</i> , 2012, 48, 663-664.	9.7	3
28	Dying mRNA Tells a Story of Its Life. <i>Cell</i> , 2015, 161, 1246-1248.	28.9	3
29	Using fluorescence anisotropy to monitor chaperone dispersal of RNA-binding protein condensates. <i>STAR Protocols</i> , 2022, 3, 101409.	1.2	1