

# D Allan Drummond

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/965985/publications.pdf>

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	Using fluorescence anisotropy to monitor chaperone dispersal of RNA-binding protein condensates. STAR Protocols, 2022, 3, 101409.	1.2	1
2	Stressful steps: Progress and challenges in understanding stress-induced mRNA condensation and accumulation in stress granules. Molecular Cell, 2022, 82, 2544-2556.	9.7	54
3	Reversible amyloids of pyruvate kinase couple cell metabolism and stress granule disassembly. Nature Cell Biology, 2021, 23, 1085-1094.	10.3	33
4	Transient intracellular acidification regulates the core transcriptional heat shock response. ELife, 2020, 9, .	6.0	52
5	Cellular sensing by phase separation: Using the process, not just the products. Journal of Biological Chemistry, 2019, 294, 7151-7159.	3.4	152
6	Stress-Triggered Phase Separation Is an Adaptive, Evolutionarily Tuned Response. Cell, 2017, 168, 1028-1040.e19.	28.9	674
7	Dying mRNA Tells a Story of Its Life. Cell, 2015, 161, 1246-1248.	28.9	3
8	Accounting for Experimental Noise Reveals That mRNA Levels, Amplified by Post-Transcriptional Processes, Largely Determine Steady-State Protein Levels in Yeast. PLoS Genetics, 2015, 11, e1005206.	3.5	164
9	Reversible, Specific, Active Aggregates of Endogenous Proteins Assemble upon Heat Stress. Cell, 2015, 162, 1286-1298.	28.9	395
10	A Nutrient-Driven tRNA Modification Alters Translational Fidelity and Genome-wide Protein Coding across an Animal Genus. PLoS Biology, 2014, 12, e1002015.	5.6	93
11	Good Codons, Bad Transcript: Large Reductions in Gene Expression and Fitness Arising from Synonymous Mutations in a Key Enzyme. Molecular Biology and Evolution, 2013, 30, 549-560.	8.9	120
12	Estimating Selection on Synonymous Codon Usage from Noisy Experimental Data. Molecular Biology and Evolution, 2013, 30, 1438-1453.	8.9	44
13	Quantifying Condition-Dependent Intracellular Protein Levels Enables High-Precision Fitness Estimates. PLoS ONE, 2013, 8, e75320.	2.5	8
14	How Infidelity Creates a Sticky Situation. Molecular Cell, 2012, 48, 663-664.	9.7	3
15	Misfolded proteins impose a dosage-dependent fitness cost and trigger a cytosolic unfolded protein response in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 680-685.	7.1	264
16	Signatures of protein biophysics in coding sequence evolution. Current Opinion in Structural Biology, 2010, 20, 385-389.	5.7	42
17	Protein Evolution: Innovative Chaps. Current Biology, 2009, 19, R740-R742.	3.9	5
18	The evolutionary consequences of erroneous protein synthesis. Nature Reviews Genetics, 2009, 10, 715-724.	16.3	437

#	ARTICLE	IF	CITATIONS
19	Contact Density Affects Protein Evolutionary Rate from Bacteria to Animals. <i>Journal of Molecular Evolution</i> , 2008, 66, 395-404.	1.8	53
20	Mistranslation-Induced Protein Misfolding as a Dominant Constraint on Coding-Sequence Evolution. <i>Cell</i> , 2008, 134, 341-352.	28.9	949
21	A diverse family of thermostable cytochrome P450s created by recombination of stabilizing fragments. <i>Nature Biotechnology</i> , 2007, 25, 1051-1056.	17.5	144
22	Structural Determinants of the Rate of Protein Evolution in Yeast. <i>Molecular Biology and Evolution</i> , 2006, 23, 1751-1761.	8.9	162
23	Population Genetics of Translational Robustness. <i>Genetics</i> , 2006, 173, 473-481.	2.9	50
24	A Single Determinant Dominates the Rate of Yeast Protein Evolution. <i>Molecular Biology and Evolution</i> , 2006, 23, 327-337.	8.9	373
25	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
26	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
27	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
28	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
29	Predicting the Tolerance of Proteins to Random Amino Acid Substitution. <i>Biophysical Journal</i> , 2005, 89, 3714-3720.	0.5	40