David Alvarez-Ponce

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

43	papers
1,129	citations
17	h-index
33	g-index
47	ext. papers
1,462	ext. citations
5.9	avg, IF
4.5	L-index

#	Paper	IF	Citations
43	Mammals with Small Populations Do Not Exhibit Larger Genomes. *Molecular Biology and Evolution*, **2021**, 38, 3737-3741	8.3	1
42	Richard Dickerson, Molecular Clocks, and Rates of Protein Evolution. *Journal of Molecular Evolution*, **2021**, 89, 122-126	3.1	3
41	Myxosporea (Myxozoa, Cnidaria) Lack DNA Cytosine Methylation. *Molecular Biology and Evolution*, **2021**, 38, 393-404	8.3	8
40	Koala methylomes reveal divergent and conserved DNA methylation signatures of X chromosome regulation. *Proceedings of the Royal Society B: Biological Sciences*, **2021**, 288, 20202244	4.4	0
39	Mycoplasma agassizii, an opportunistic pathogen of tortoises, shows very little genetic variation across the Mojave and Sonoran Deserts. *PLoS ONE*, **2021**, 16, e0245895	3.7	1
38	Rates of protein evolution across the marsupial phylogeny: heterogeneity and link to life-history traits. *Genome Biology and Evolution*, **2021**,	3.9	2
37	Emerging Priorities for Microbiome Research. *Frontiers in Microbiology*, **2020**, 11, 136	5.7	50
36	N-glycoproteins exhibit a positive expression level-evolutionary rate correlation. *Journal of Evolutionary Biology*, **2019**, 32, 390-394	2.3	1
35	What lies beneath? Molecular evolution during the radiation of caecilian amphibians. *BMC Genomics* , **2019**, 20, 354	4.5	4
34	Codon Usage Differences among Genes Expressed in Different Tissues of Drosophila melanogaster. *Genome Biology and Evolution*, **2019**, 11, 1054-1065	3.9	6
33	Molecular Chaperones Accelerate the Evolution of Their Protein Clients in Yeast. *Genome Biology and Evolution*, **2019**, 11, 2360-2375	3.9	10
32	The avocado genome informs deep angiosperm phylogeny, highlights introgressive hybridization, and reveals pathogen-influenced gene space adaptation. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 17081-17089	11.5	66
31	Phylogenetic Distribution of CMP-Neu5Ac Hydroxylase (CMAH), the Enzyme Synthetizing the Proinflammatory Human Xenoantigen Neu5Gc. *Genome Biology and Evolution*, **2018**, 10, 207-219	3.9	41
30	High quality draft genome sequences of strains PS6 and 723 isolated from tortoises with upper respiratory tract disease. *Standards in Genomic Sciences*, **2018**, 13, 12		1
29	Molecular evolution of DNMT1 in vertebrates: Duplications in marsupials followed by positive selection. *PLoS ONE*, **2018**, 13, e0195162	3.7	12
28	High quality draft genome sequence of strain BH29, isolated from the respiratory tract of a desert tortoise. *Standards in Genomic Sciences*, **2018**, 13, 9		2
27	Higher Rates of Protein Evolution in the Self-Fertilizing Plant Arabidopsis thaliana than in the Out-Crossers Arabidopsis lyrata and Arabidopsis halleri. *Genome Biology and Evolution*, **2018**, 10, 895-900	3.9	4

26	Arabidopsis Heat Stress-Induced Proteins Are Enriched in Electrostatically Charged Amino Acids and Intrinsically Disordered Regions. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	6
25	Proteins of generalist and specialist pathogens differ in their amino acid composition. *Life Science Alliance*, **2018**, 1, e201800017	5.8	3
24	Genome of the pitcher plant Cephalotus reveals genetic changes associated with carnivory. *Nature Ecology and Evolution*, **2017**, 1, 59	12.3	61
23	Intrinsic protein disorder reduces small-scale gene duplicability. *DNA Research*, **2017**, 24, 435-444	4.5	3
22	Disulfide Bonds Enable Accelerated Protein Evolution. *Molecular Biology and Evolution*, **2017**, 34, 1833-1837	8.3	11
21	Chance and necessity in the genome evolution of endosymbiotic bacteria of insects. *ISME Journal*, **2017**, 11, 1291-1304	11.9	20
20	Recording negative results of protein-protein interaction assays: an easy way to deal with the biases and errors of interactomic data sets. *Briefings in Bioinformatics*, **2017**, 18, 1017-1020	13.4	3
19	Position Matters: Network Centrality Considerably Impacts Rates of Protein Evolution in the Human Protein-Protein Interaction Network. *Genome Biology and Evolution*, **2017**, 9, 1742-1756	3.9	24
18	Secreted Proteins Defy the Expression Level-Evolutionary Rate Anticorrelation. *Molecular Biology and Evolution*, **2017**, 34, 692-706	8.3	9
17	Essentiality Is a Strong Determinant of Protein Rates of Evolution during Mutation Accumulation Experiments in Escherichia coli. *Genome Biology and Evolution*, **2016**, 8, 2914-2927	3.9	16
16	Positive Selection and Centrality in the Yeast and Fly Protein-Protein Interaction Networks. *BioMed Research International*, **2016**, 2016, 4658506	3	11
15	The Molecular Chaperone DnaK Is a Source of Mutational Robustness. *Genome Biology and Evolution*, **2016**, 8, 2979-2991	3.9	34
14	Recent positive selection has acted on genes encoding proteins with more interactions within the whole human interactome. *Genome Biology and Evolution*, **2015**, 7, 1141-54	3.9	36
13	Integration of two ancestral chaperone systems into one: the evolution of eukaryotic molecular chaperones in light of eukaryogenesis. *Molecular Biology and Evolution*, **2014**, 31, 410-8	8.3	14
12	Why Proteins Evolve at Different Rates: The Determinants of Proteins Rates of Evolution **2014**, 126-178		9
11	Gene similarity networks provide tools for understanding eukaryote origins and evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, E1594-603	11.5	46
10	Comment on "The Molecular Evolutionary Patterns of the Insulin/FOXO Signaling Pathway". *Evolutionary Bioinformatics*, **2013**, 9, 229-34	1.9	2
9	Evolutionary rate and duplicability in the Arabidopsis thaliana protein-protein interaction network. *Genome Biology and Evolution*, **2012**, 4, 1263-74	3.9	40

8	The relationship between the hierarchical position of proteins in the human signal transduction network and their rate of evolution. *BMC Evolutionary Biology*, **2012**, 12, 192	3	21
7	Molecular population genetics of the insulin/TOR signal transduction pathway: a network-level analysis in Drosophila melanogaster. *Molecular Biology and Evolution*, **2012**, 29, 123-32	8.3	17
6	Increased genome sampling reveals a dynamic relationship between gene duplicability and the structure of the primate protein-protein interaction network. *Molecular Biology and Evolution*, **2012** , 29, 3563-73	8.3	6
5	Network-level and population genetics analysis of the insulin/TOR signal transduction pathway across human populations. *Molecular Biology and Evolution*, **2012**, 29, 1379-92	8.3	22
4	The human genome retains relics of its prokaryotic ancestry: human genes of archaebacterial and eubacterial origin exhibit remarkable differences. *Genome Biology and Evolution*, **2011**, 3, 782-90	3.9	18
3	Comparative genomics of the vertebrate insulin/TOR signal transduction pathway: a network-level analysis of selective pressures. *Genome Biology and Evolution*, **2011**, 3, 87-101	3.9	38
2	Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 12168-73	11.5	383
1	Network-level molecular evolutionary analysis of the insulin/TOR signal transduction pathway across 12 Drosophila genomes. *Genome Research*, **2009**, 19, 234-42	9.7	64