Macarena Toll-Riera

List of Publications by Year
in descending order

23 papers	1,053 citations	516710 16 h-index	713466 21 g-index
25 all docs	25 docs citations	25 times ranked	1686 citing authors

#	Article	IF	Citations
1	Origin of Primate Orphan Genes: A Comparative Genomics Approach. Molecular Biology and Evolution, 2008, 26, 603-612.	8.9	201
2	Interactions between horizontally acquired genes create a fitness cost in Pseudomonas aeruginosa. Nature Communications, 2015, 6, 6845.	12.8	147
3	Role of Low-Complexity Sequences in the Formation of Novel Protein Coding Sequences. Molecular Biology and Evolution, 2012, 29, 883-886.	8.9	93
4	Natural selection drives the accumulation of amino acid tandem repeats in human proteins. Genome Research, 2010, 20, 745-754.	5.5	88
5	Integrative analysis of fitness and metabolic effects of plasmids in Pseudomonas aeruginosa PAO1. ISME Journal, 2018, 12, 3014-3024.	9.8	80
6	Fitness Is Strongly Influenced by Rare Mutations of Large Effect in a Microbial Mutation Accumulation Experiment. Genetics, 2014, 197, 981-990.	2.9	59
7	Genetic dominance governs the evolution and spread of mobile genetic elements in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15755-15762.	7.1	41
8	Lineage-Specific Variation in Intensity of Natural Selection in Mammals. Molecular Biology and Evolution, 2011, 28, 383-398.	8.9	38
9	Emergence of novel domains in proteins. BMC Evolutionary Biology, 2013, 13, 47.	3.2	36
10	Sequencing of plasmids pAMBL1 and pAMBL2 fromPseudomonas aeruginosareveals abla_{VIM-1}amplification causing high-level carbapenem resistance. Journal of Antimicrobial Chemotherapy, 2015, 70, 3000-3003.	3.0	35
11	The Genomic Basis of Evolutionary Innovation in Pseudomonas aeruginosa. PLoS Genetics, 2016, 12, e1006005.	3.5	35
12	Evolution of primate orphan proteins. Biochemical Society Transactions, 2009, 37, 778-782.	3.4	31
13	Mistranslation can enhance fitness through purging of deleterious mutations. Nature Communications, 2017, 8, 15410.	12.8	28
14	Staphylococcal phages and pathogenicity islands drive plasmid evolution. Nature Communications, 2021, 12, 5845.	12.8	26
15	The genomic basis of adaptation to the fitness cost of rifampicin resistance inPseudomonas aeruginosa. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20152452.	2.6	25
16	Sequence shortening in the rodent ancestor. Genome Research, 2012, 22, 478-485.	5.5	19
17	Structure and Age Jointly Influence Rates of Protein Evolution. PLoS Computational Biology, 2012, 8, e1002542.	3.2	18
18	Epistatic interactions between ancestral genotype and beneficial mutations shape evolvability inPseudomonas aeruginosa. Evolution; International Journal of Organic Evolution, 2016, 70, 1659-1666.	2.3	18

#	Article	IF	Citations
19	New insights on Pseudoalteromonas haloplanktis TAC125 genome organization and benchmarks of genome assembly applications using next and third generation sequencing technologies. Scientific Reports, 2019, 9, 16444.	3.3	14
20	Partial Gene Duplication and the Formation of Novel Genes. , 2011, , .		4
21	Accelerated Evolution of Genes of Recent Origin. , 2008, , 45-59.		4
22	A limit on the evolutionary rescue of an Antarctic bacterium from rising temperatures. Science Advances, 2022, 8, .	10.3	4
23	Hereâ€™s to the Losers: Evolvable Residents Accelerate the Evolution of High-Fitness Invaders. American Naturalist, 2015, 186, 41-49.	2.1	2