

Mario AlÃ- Fares

List of Publications by Year in descending order

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88
papers

3,620
citations

117453

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h-index

149479

56
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111
all docs

111
docs citations

111
times ranked

4276
citing authors

#	ARTICLE	IF	CITATIONS
1	The Role of Ancestral Duplicated Genes in Adaptation to Growth on Lactate, a Non-Fermentable Carbon Source for the Yeast <i>Saccharomyces cerevisiae</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 12293.	1.8	1
2	Transcriptional Rewiring, Adaptation, and the Role of Gene Duplication in the Metabolism of Ethanol of <i>Saccharomyces cerevisiae</i> . <i>MSystems</i> , 2020, 5, .	1.7	5
3	Exploring molecular evolution of Rubisco in C3 and CAM Orchidaceae and Bromeliaceae. <i>BMC Evolutionary Biology</i> , 2020, 20, 11.	3.2	16
4	Molecular Chaperones Accelerate the Evolution of Their Protein Clients in Yeast. <i>Genome Biology and Evolution</i> , 2019, 11, 2360-2375.	1.1	25
5	Chaperonin overproduction and metabolic erosion caused by mutation accumulation in <i>Escherichia coli</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	2
6	Intrinsic adaptive value and early fate of gene duplication revealed by a bottom-up approach. <i>ELife</i> , 2018, 7, .	2.8	30
7	Genome Mutational and Transcriptional Hotspots Are Traps for Duplicated Genes and Sources of Adaptations. <i>Genome Biology and Evolution</i> , 2017, 9, 1229-1240.	1.1	17
8	Expression properties exhibit correlated patterns with the fate of duplicated genes, their divergence, and transcriptional plasticity in <i>Saccharomycotina</i> . <i>DNA Research</i> , 2017, 24, 559-570.	1.5	23
9	Chance and necessity in the genome evolution of endosymbiotic bacteria of insects. <i>ISME Journal</i> , 2017, 11, 1291-1304.	4.4	35
10	The Phenotypic Plasticity of Duplicated Genes in <i>Saccharomyces cerevisiae</i> and the Origin of Adaptations. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 63-75.	0.8	32
11	Evolution of Multiple Chaperonins: Innovation of Evolutionary Capacitors. <i>Heat Shock Proteins</i> , 2017, , 149-170.	0.2	0
12	Glycerol stress in <i>Saccharomyces cerevisiae</i> : Cellular responses and evolved adaptations. <i>Environmental Microbiology</i> , 2017, 19, 990-1007.	1.8	24
13	Positively selected amino acid replacements within the RuBisCO enzyme of oak trees are associated with ecological adaptations. <i>PLoS ONE</i> , 2017, 12, e0183970.	1.1	11
14	Deconstruction of the beaten Path-Sidestep interaction network provides insights into neuromuscular system development. <i>ELife</i> , 2017, 6, .	2.8	41
15	The Molecular Chaperone DnaK Is a Source of Mutational Robustness. <i>Genome Biology and Evolution</i> , 2016, 8, 2979-2991.	1.1	57
16	Essentiality Is a Strong Determinant of Protein Rates of Evolution during Mutation Accumulation Experiments in <i>Escherichia coli</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 2914-2927.	1.1	25
17	Evolution by gene duplication of <i>Medicago truncatula</i> PISTILLATA-like transcription factors. <i>Journal of Experimental Botany</i> , 2016, 67, 1805-1817.	2.4	38
18	Functional conservation of an ancestral Pellino protein in helminth species. <i>Scientific Reports</i> , 2015, 5, 11687.	1.6	5

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19	The origins of mutational robustness. <i>Trends in Genetics</i> , 2015, 31, 373-381.	2.9	56
20	Recent Positive Selection Has Acted on Genes Encoding Proteins with More Interactions within the Whole Human Interactome. <i>Genome Biology and Evolution</i> , 2015, 7, 1141-1154.	1.1	59
21	Experimental Evolution and Next Generation Sequencing Illuminate the Evolutionary Trajectories of Microbes. , 2015, , 101-113.		1
22	Fitness Trade-Offs Determine the Role of the Molecular Chaperonin GroEL in Buffering Mutations. <i>Molecular Biology and Evolution</i> , 2015, 32, 2681-2693.	3.5	43
23	Survival and innovation: The role of mutational robustness in evolution. <i>Biochimie</i> , 2015, 119, 254-261.	1.3	11
24	The evolution of protein moonlighting: adaptive traps and promiscuity in the chaperonins. <i>Biochemical Society Transactions</i> , 2014, 42, 1709-1714.	1.6	19
25	Molecular Evolution of Viral Multifunctional Proteins: The Case of Potyvirus HC-Pro. <i>Journal of Molecular Evolution</i> , 2014, 78, 75-86.	0.8	23
26	Preservation of genetic and regulatory robustness in ancient gene duplicates of <i>Saccharomyces cerevisiae</i> . <i>Genome Research</i> , 2014, 24, 1830-1841.	2.4	66
27	Coevolution analyses illuminate the dependencies between amino acid sites in the chaperonin system GroES-L. <i>BMC Evolutionary Biology</i> , 2013, 13, 156.	3.2	13
28	Group 1 LEA proteins, an ancestral plant protein group, are also present in other eukaryotes, and in the archaea and bacteria domains. <i>Molecular Genetics and Genomics</i> , 2013, 288, 503-517.	1.0	47
29	Chaperonin 60: a paradoxical, evolutionarily conserved protein family with multiple moonlighting functions. <i>Biological Reviews</i> , 2013, 88, 955-987.	4.7	107
30	The Roles of Whole-Genome and Small-Scale Duplications in the Functional Specialization of <i>Saccharomyces cerevisiae</i> Genes. <i>PLoS Genetics</i> , 2013, 9, e1003176.	1.5	84
31	ChloroMitoSSRDB: Open Source Repository of Perfect and Imperfect Repeats in Organelle Genomes for Evolutionary Genomics. <i>DNA Research</i> , 2013, 20, 127-133.	1.5	24
32	Molecular Evolutionary Mechanisms Driving Functional Diversification of the HSP90A Family of Heat Shock Proteins in Eukaryotes. <i>Molecular Biology and Evolution</i> , 2013, 30, 2035-2043.	3.5	27
33	Evolutionary Rate and Duplicability in the <i>Arabidopsis thaliana</i> Protein-Protein Interaction Network. <i>Genome Biology and Evolution</i> , 2012, 4, 1263-1274.	1.1	52
34	Molecular evolution of psbA gene in ferns: unraveling selective pressure and co-evolutionary pattern. <i>BMC Evolutionary Biology</i> , 2012, 12, 145.	3.2	7
35	Describing the structural robustness landscape of bacterial small RNAs. <i>BMC Evolutionary Biology</i> , 2012, 12, 52.	3.2	6
36	Evolutionary Dynamics and Functional Specialization of Plant Paralogs Formed by Whole and Small-Scale Genome Duplications. <i>Molecular Biology and Evolution</i> , 2012, 29, 3541-3551.	3.5	86

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37	Proteome-Wide Analysis of Functional Divergence in Bacteria: Exploring a Host of Ecological Adaptations. PLoS ONE, 2012, 7, e35659.	1.1	16
38	Molecular evolution of <i>rbcl</i> in three gymnosperm families: identifying adaptive and coevolutionary patterns. Biology Direct, 2011, 6, 29.	1.9	29
39	Protein coadaptation and the design of novel approaches to identify proteinâ€“protein interactions. IUBMB Life, 2011, 63, 264-271.	1.5	11
40	Functional Diversification of the Twin-Arginine Translocation Pathway Mediates the Emergence of Novel Ecological Adaptations. Molecular Biology and Evolution, 2011, 28, 3183-3193.	3.5	4
41	The Effect of Chaperonin Buffering on Protein Evolution. Genome Biology and Evolution, 2010, 2, 609-619.	1.1	73
42	Two chaperonin systems in bacterial genomes with distinct ecological roles. Trends in Genetics, 2010, 26, 47-51.	2.9	27
43	Mutational dynamics of murine angiogenin duplicates. BMC Evolutionary Biology, 2010, 10, 310.	3.2	6
44	Pivotal Advance: Avian colony-stimulating factor 1 (<i>CSF-1</i>), interleukin-34 (<i>IL-34</i>), and <i>CSF-1</i> receptor genes and gene products. Journal of Leukocyte Biology, 2010, 87, 753-764.	1.5	173
45	Structural Calibration of the Rates of Amino Acid Evolution in a Search for Darwin in Drifting Biological Systems. Molecular Biology and Evolution, 2010, 27, 2375-2385.	3.5	9
46	Selection for Translational Robustness in <i>Buchnera aphidicola</i> , Endosymbiotic Bacteria of Aphids. Molecular Biology and Evolution, 2009, 26, 743-751.	3.5	14
47	No Rosetta Stone for a Senseâ€“Antisense Origin of Aminoacyl tRNA Synthetase Classes. Molecular Biology and Evolution, 2009, 26, 445-450.	3.5	14
48	Genome-Wide Functional Divergence after the Symbiosis of Proteobacteria with Insects Unraveled through a Novel Computational Approach. PLoS Computational Biology, 2009, 5, e1000344.	1.5	23
49	Phylogenomic inference of functional divergence. BMC Bioinformatics, 2009, 10, .	1.2	1
50	Evolution of flower shape in <i>Plantago lanceolata</i> . Plant Molecular Biology, 2009, 71, 241-250.	2.0	49
51	Computational Biology Methods and Their Application to the Comparative Genomics of Endocellular Symbiotic Bacteria of Insects. Biological Procedures Online, 2009, 11, 52-78.	1.4	6
52	IDENTIFYING COEVOLUTIONARY PATTERNS IN HUMAN LEUKOCYTE ANTIGEN (HLA) MOLECULES. Evolution; International Journal of Organic Evolution, 2009, 64, 1429-45.	1.1	3
53	Shifts in the Selection-Drift Balance Drive the Evolution and Epidemiology of Foot-and-Mouth Disease Virus. Journal of Virology, 2009, 83, 781-790.	1.5	23
54	Molecular Coevolution and the Three-Dimensionality of Natural Selection. , 2009, , 237-251.		0

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55	The tale of a modern animal plague: Tracing the evolutionary history and determining the time-scale for foot and mouth disease virus. <i>Virology</i> , 2008, 382, 250-256.	1.1	50
56	Reducing the false positive rate in the non-parametric analysis of molecular coevolution. <i>BMC Evolutionary Biology</i> , 2008, 8, 106.	3.2	10
57	Relationships of Gag-pol Diversity between Ty3/Gypsy and Retroviridae LTR retroelements and the three kings hypothesis. <i>BMC Evolutionary Biology</i> , 2008, 8, 276.	3.2	50
58	The Evolution of the Flagellar Assembly Pathway in Endosymbiotic Bacterial Genomes. <i>Molecular Biology and Evolution</i> , 2008, 25, 2069-2076.	3.5	55
59	Why Should We Care about Molecular Coevolution?. <i>Evolutionary Bioinformatics</i> , 2008, 4, 117693430800400.	0.6	36
60	Why should we care about molecular coevolution?. <i>Evolutionary Bioinformatics</i> , 2008, 4, 29-38.	0.6	48
61	A Study of the Coevolutionary Patterns Operating within the env Gene of the HIV-1 Group M Subtypes. <i>Molecular Biology and Evolution</i> , 2007, 24, 2787-2801.	3.5	41
62	Artifactual Phylogenies Caused by Correlated Distribution of Substitution Rates among Sites and Lineages: The Good, the Bad, and the Ugly. <i>Systematic Biology</i> , 2007, 56, 68-82.	2.7	24
63	Comparative genomic analysis of a mammalian Î²-defensin gene cluster. <i>Physiological Genomics</i> , 2007, 30, 213-222.	1.0	19
64	Testing the Neutral Fixation of Hetero-Oligomerism in the Archaeal Chaperonin CCT. <i>Molecular Biology and Evolution</i> , 2007, 24, 1384-1396.	3.5	13
65	Functional Coevolutionary Networks of the Hsp70â€“Hopâ€“Hsp90 System Revealed through Computational Analyses. <i>Molecular Biology and Evolution</i> , 2007, 24, 1032-1044.	3.5	50
66	In silico identification of functional divergence between the multiple groEL gene paralogs in Chlamydiae. <i>BMC Evolutionary Biology</i> , 2007, 7, 81.	3.2	29
67	Unravelling selection shifts among foot-and-mouth disease virus (FMDV) serotypes. <i>Evolutionary Bioinformatics</i> , 2007, 2, 211-25.	0.6	10
68	Unravelling Selection Shifts among Foot-and-Mouth Disease virus (FMDV) Serotypes. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	0.6	15
69	CAPS: coevolution analysis using protein sequences. <i>Bioinformatics</i> , 2006, 22, 2821-2822.	1.8	120
70	GRAST: a new way of genome reduction analysis using comparative genomics. <i>Bioinformatics</i> , 2006, 22, 1551-1561.	1.8	3
71	Adaptive Covariation between the Coat and Movement Proteins of Prunus Necrotic Ringspot Virus. <i>Journal of Virology</i> , 2006, 80, 5833-5840.	1.5	24
72	Rate Asymmetry After Genome Duplication Causes Substantial Long-Branch Attraction Artifacts in the Phylogeny of Saccharomyces Species. <i>Molecular Biology and Evolution</i> , 2006, 23, 245-253.	3.5	72

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73	A Novel Method for Detecting Intramolecular Coevolution: Adding a Further Dimension to Selective Constraints Analyses. <i>Genetics</i> , 2006, 173, 9-23.	1.2	149
74	Computational and Statistical Methods to Explore the Various Dimensions of Protein Evolution. <i>Current Bioinformatics</i> , 2006, 1, 207-217.	0.7	15
75	Adaptive evolution in GroEL from distantly related endosymbiotic bacteria of insects. <i>Journal of Evolutionary Biology</i> , 2005, 18, 651-660.	0.8	31
76	SWAPSC: sliding window analysis procedure to detect selective constraints. <i>Bioinformatics</i> , 2004, 20, 2867-2868.	1.8	36
77	Evidence of Positively Selected Sites in Mammalian Î±-Defensins. <i>Molecular Biology and Evolution</i> , 2004, 21, 819-827.	3.5	67
78	GroEL and the maintenance of bacterial endosymbiosis. <i>Trends in Genetics</i> , 2004, 20, 413-416.	2.9	76
79	Bioinformatic discovery and initial characterisation of nine novel antimicrobial peptide genes in the chicken. <i>Immunogenetics</i> , 2004, 56, 170-177.	1.2	197
80	Evidence from comparative genomics for a complete sexual cycle in the 'asexual' pathogenic yeast <i>Candida glabrata</i> . <i>Genome Biology</i> , 2003, 4, R10.	13.9	97
81	Positive Selection and Subfunctionalization of Duplicated CCT Chaperonin Subunits. <i>Molecular Biology and Evolution</i> , 2003, 20, 1588-1597.	3.5	51
82	Selection on Coding Regions Determined Hox7 Genes Evolution. <i>Molecular Biology and Evolution</i> , 2003, 20, 2104-2112.	3.5	29
83	The Evolution of the Heat-Shock Protein GroEL from Buchnera, the Primary Endosymbiont of Aphids, Is Governed by Positive Selection. <i>Molecular Biology and Evolution</i> , 2002, 19, 1162-1170.	3.5	88
84	A Revised Evolutionary History of Hepatitis B Virus (HBV). <i>Journal of Molecular Evolution</i> , 2002, 54, 807-814.	0.8	119
85	A Sliding Window-Based Method to Detect Selective Constraints in Protein-Coding Genes and Its Application to RNA Viruses. <i>Journal of Molecular Evolution</i> , 2002, 55, 509-521.	0.8	71
86	GroEL buffers against deleterious mutations. <i>Nature</i> , 2002, 417, 398-398.	13.7	241
87	Evidence for Positive Selection in the Capsid Protein-Coding Region of the Foot-and-Mouth Disease Virus (FMDV) Subjected to Experimental Passage Regimens. <i>Molecular Biology and Evolution</i> , 2001, 18, 10-21.	3.5	58
88	Detecting Changes in the Functional Constraints of Paralogous Genes. <i>Journal of Molecular Evolution</i> , 2001, 52, 17-28.	0.8	15