Mario AlÃ- Fares

List of Publications by Year
in descending order

88	3,620	117453	149479
papers	citations	34	56
		h-index	g-index

111	111	111	4276
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	GroEL buffers against deleterious mutations. Nature, 2002, 417, 398-398.	13.7	241
2	Bioinformatic discovery and initial characterisation of nine novel antimicrobial peptide genes in the chicken. Immunogenetics, 2004, 56, 170-177.	1.2	197
3	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
4	A Novel Method for Detecting Intramolecular Coevolution: Adding a Further Dimension to Selective Constraints Analyses. Genetics, 2006, 173, 9-23.	1.2	149
5	CAPS: coevolution analysis using protein sequences. Bioinformatics, 2006, 22, 2821-2822.	1.8	120
6	A Revised Evolutionary History of Hepatitis B Virus (HBV). Journal of Molecular Evolution, 2002, 54, 807-814.	0.8	119
7	Chaperonin 60: a paradoxical, evolutionarily conserved protein family with multiple moonlighting functions. Biological Reviews, 2013, 88, 955-987.	4.7	107
8	Evidence from comparative genomics for a complete sexual cycle in the 'asexual' pathogenic yeast Candida glabrata. Genome Biology, 2003, 4, R10.	13.9	97
9	The Evolution of the Heat-Shock Protein GroEL from Buchnera, the Primary Endosymbiont of Aphids, Is Governed by Positive Selection. Molecular Biology and Evolution, 2002, 19, 1162-1170.	3.5	88
10	Evolutionary Dynamics and Functional Specialization of Plant Paralogs Formed by Whole and Small-Scale Genome Duplications. Molecular Biology and Evolution, 2012, 29, 3541-3551.	3.5	86
11	The Roles of Whole-Genome and Small-Scale Duplications in the Functional Specialization of Saccharomyces cerevisiae Genes. PLoS Genetics, 2013, 9, e1003176.	1.5	84
12	GroEL and the maintenance of bacterial endosymbiosis. Trends in Genetics, 2004, 20, 413-416.	2.9	76
13	The Effect of Chaperonin Buffering on Protein Evolution. Genome Biology and Evolution, 2010, 2, 609-619.	1.1	73
14	Rate Asymmetry After Genome Duplication Causes Substantial Long-Branch Attraction Artifacts in the Phylogeny of Saccharomyces Species. Molecular Biology and Evolution, 2006, 23, 245-253.	3.5	72
15	A Sliding Window-Based Method to Detect Selective Constraints in Protein-Coding Genes and Its Application to RNA Viruses. Journal of Molecular Evolution, 2002, 55, 509-521.	0.8	71
16	Evidence of Positively Selected Sites in Mammalian Î±-Defensins. Molecular Biology and Evolution, 2004, 21, 819-827.	3.5	67
17	Preservation of genetic and regulatory robustness in ancient gene duplicates of <i>Saccharomyces cerevisiae</i>. Genome Research, 2014, 24, 1830-1841.	2.4	66
18	Recent Positive Selection Has Acted on Genes Encoding Proteins with More Interactions within the Whole Human Interactome. Genome Biology and Evolution, 2015, 7, 1141-1154.	1.1	59

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19	Evidence for Positive Selection in the Capsid Protein-Coding Region of the Foot-and-Mouth Disease Virus (FMDV) Subjected to Experimental Passage Regimens. Molecular Biology and Evolution, 2001, 18, 10-21.	3.5	58
20	The Molecular Chaperone DnaK Is a Source of Mutational Robustness. Genome Biology and Evolution, 2016, 8, 2979-2991.	1.1	57
21	The origins of mutational robustness. Trends in Genetics, 2015, 31, 373-381.	2.9	56
22	The Evolution of the Flagellar Assembly Pathway in Endosymbiotic Bacterial Genomes. Molecular Biology and Evolution, 2008, 25, 2069-2076.	3.5	55
23	Evolutionary Rate and Duplicability in the Arabidopsis thaliana Protein–Protein Interaction Network. Genome Biology and Evolution, 2012, 4, 1263-1274.	1.1	52
24	Positive Selection and Subfunctionalization of Duplicated CCT Chaperonin Subunits. Molecular Biology and Evolution, 2003, 20, 1588-1597.	3.5	51
25	Functional Coevolutionary Networks of the Hsp70–Hop–Hsp90 System Revealed through Computational Analyses. Molecular Biology and Evolution, 2007, 24, 1032-1044.	3.5	50
26	The tale of a modern animal plague: Tracing the evolutionary history and determining the time-scale for foot and mouth disease virus. Virology, 2008, 382, 250-256.	1.1	50
27	Relationships of Gag-pol Diversity between Ty3/Gypsy and Retroviridae LTR retroelements and the three kings hypothesis. BMC Evolutionary Biology, 2008, 8, 276.	3.2	50
28	Evolution of flower shape in Plantago lanceolata. Plant Molecular Biology, 2009, 71, 241-250.	2.0	49
29	Why should we care about molecular coevolution?. Evolutionary Bioinformatics, 2008, 4, 29-38.	0.6	48
30	Group 1 LEA proteins, an ancestral plant protein group, are also present in other eukaryotes, and in the archeae and bacteria domains. Molecular Genetics and Genomics, 2013, 288, 503-517.	1.0	47
31	Fitness Trade-Offs Determine the Role of the Molecular Chaperonin GroEL in Buffering Mutations. Molecular Biology and Evolution, 2015, 32, 2681-2693.	3.5	43
32	A Study of the Coevolutionary Patterns Operating within the env Gene of the HIV-1 Group M Subtypes. Molecular Biology and Evolution, 2007, 24, 2787-2801.	3.5	41
33	Deconstruction of the beaten Path-Sidestep interaction network provides insights into neuromuscular system development. ELife, 2017, 6, .	2.8	41
34	Evolution by gene duplication of *Medicago truncatula PISTILLATA*-like transcription factors. Journal of Experimental Botany, 2016, 67, 1805-1817.	2.4	38
35	SWAPSC: sliding window analysis procedure to detect selective constraints. Bioinformatics, 2004, 20, 2867-2868.	1.8	36
36	Why Should We Care about Molecular Coevolution?. Evolutionary Bioinformatics, 2008, 4, 117693430800400.	0.6	36

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37	Chance and necessity in the genome evolution of endosymbiotic bacteria of insects. ISME Journal, 2017, 11, 1291-1304.	4.4	35
38	The Phenotypic Plasticity of Duplicated Genes in<i>Saccharomyces cerevisiae</i>and the Origin of Adaptations. G3: Genes, Genomes, Genetics, 2017, 7, 63-75.	0.8	32
39	Adaptive evolution in GroEL from distantly related endosymbiotic bacteria of insects. Journal of Evolutionary Biology, 2005, 18, 651-660.	0.8	31
40	Intrinsic adaptive value and early fate of gene duplication revealed by a bottom-up approach. ELife, 2018, 7, .	2.8	30
41	Selection on Coding Regions Determined Hox7 Genes Evolution. Molecular Biology and Evolution, 2003, 20, 2104-2112.	3.5	29
42	In silico identification of functional divergence between the multiple groEL gene paralogs in Chlamydiae. BMC Evolutionary Biology, 2007, 7, 81.	3.2	29
43	Molecular evolution of rbcL in three gymnosperm families: identifying adaptive and coevolutionary patterns. Biology Direct, 2011, 6, 29.	1.9	29
44	Two chaperonin systems in bacterial genomes with distinct ecological roles. Trends in Genetics, 2010, 26, 47-51.	2.9	27
45	Molecular Evolutionary Mechanisms Driving Functional Diversification of the HSP90A Family of Heat Shock Proteins in Eukaryotes. Molecular Biology and Evolution, 2013, 30, 2035-2043.	3.5	27
46	Essentiality Is a Strong Determinant of Protein Rates of Evolution during Mutation Accumulation Experiments in<i>Escherichia coli</i>. Genome Biology and Evolution, 2016, 8, 2914-2927.	1.1	25
47	Molecular Chaperones Accelerate the Evolution of Their Protein Clients in Yeast. Genome Biology and Evolution, 2019, 11, 2360-2375.	1.1	25
48	Adaptive Covariation between the Coat and Movement Proteins of Prunus Necrotic Ringspot Virus. Journal of Virology, 2006, 80, 5833-5840.	1.5	24
49	Artifactual Phylogenies Caused by Correlated Distribution of Substitution Rates among Sites and Lineages: The Good, the Bad, and the Ugly. Systematic Biology, 2007, 56, 68-82.	2.7	24
50	ChloroMitoSSRDB: Open Source Repository of Perfect and Imperfect Repeats in Organelle Genomes for Evolutionary Genomics. DNA Research, 2013, 20, 127-133.	1.5	24
51	Glycerol stress in <scp><i>S</i></scp><i>accharomyces cerevisiae</i>: Cellular responses and evolved adaptations. Environmental Microbiology, 2017, 19, 990-1007.	1.8	24
52	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
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 Evolution of Viral Multifunctional Proteins: The Case of Potyvirus HC-Pro. Journal of Molecular Evolution, 2014, 78, 75-86.	0.8	23

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55	Expression properties exhibit correlated patterns with the fate of duplicated genes, their divergence, and transcriptional plasticity in Saccharomycotina. DNA Research, 2017, 24, 559-570.	1.5	23
56	Comparative genomic analysis of a mammalian Î²-defensin gene cluster. Physiological Genomics, 2007, 30, 213-222.	1.0	19
57	The evolution of protein moonlighting: adaptive traps and promiscuity in the chaperonins. Biochemical Society Transactions, 2014, 42, 1709-1714.	1.6	19
58	Genome Mutational and Transcriptional Hotspots Are Traps for Duplicated Genes and Sources of Adaptations. Genome Biology and Evolution, 2017, 9, 1229-1240.	1.1	17
59	Exploring molecular evolution of Rubisco in C3 and CAM Orchidaceae and Bromeliaceae. BMC Evolutionary Biology, 2020, 20, 11.	3.2	16
60	Proteome-Wide Analysis of Functional Divergence in Bacteria: Exploring a Host of Ecological Adaptations. PLoS ONE, 2012, 7, e35659.	1.1	16
61	Detecting Changes in the Functional Constraints of Paralogous Genes. Journal of Molecular Evolution, 2001, 52, 17-28.	0.8	15
62	Unravelling Selection Shifts among Foot-and-Mouth Disease virus (FMDV) Serotypes. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	0.6	15
63	Computational and Statistical Methods to Explore the Various Dimensions of Protein Evolution. Current Bioinformatics, 2006, 1, 207-217.	0.7	15
64	Selection for Translational Robustness in Buchnera aphidicola, Endosymbiotic Bacteria of Aphids. Molecular Biology and Evolution, 2009, 26, 743-751.	3.5	14
65	No Rosetta Stone for a Senseâ€"Antisense Origin of Aminoacyl tRNA Synthetase Classes. Molecular Biology and Evolution, 2009, 26, 445-450.	3.5	14
66	Testing the Neutral Fixation of Hetero-Oligomerism in the Archaeal Chaperonin CCT. Molecular Biology and Evolution, 2007, 24, 1384-1396.	3.5	13
67	Coevolution analyses illuminate the dependencies between amino acid sites in the chaperonin system GroES-L. BMC Evolutionary Biology, 2013, 13, 156.	3.2	13
68	Protein coadaptation and the design of novel approaches to identify proteinâ€"protein interactions. IUBMB Life, 2011, 63, 264-271.	1.5	11
69	Survival and innovation: The role of mutational robustness in evolution. Biochimie, 2015, 119, 254-261.	1.3	11
70	Positively selected amino acid replacements within the RuBisCO enzyme of oak trees are associated with ecological adaptations. PLoS ONE, 2017, 12, e0183970.	1.1	11
71	Reducing the false positive rate in the non-parametric analysis of molecular coevolution. BMC Evolutionary Biology, 2008, 8, 106.	3.2	10
72	Unravelling selection shifts among foot-and-mouth disease virus (FMDV) serotypes. Evolutionary Bioinformatics, 2007, 2, 211-25.	0.6	10

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73	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
74	Molecular evolution of psbA gene in ferns: unraveling selective pressure and co-evolutionary pattern. BMC Evolutionary Biology, 2012, 12, 145.	3.2	7
75	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
76	Mutational dynamics of murine angiogenin duplicates. BMC Evolutionary Biology, 2010, 10, 310.	3.2	6
77	Describing the structural robustness landscape of bacterial small RNAs. BMC Evolutionary Biology, 2012, 12, 52.	3.2	6
78	Functional conservation of an ancestral Pellino protein in helminth species. Scientific Reports, 2015, 5, 11687.	1.6	5
79	Transcriptional Rewiring, Adaptation, and the Role of Gene Duplication in the Metabolism of Ethanol of Saccharomyces cerevisiae. MSystems, 2020, 5, .	1.7	5
80	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
81	GRAST: a new way of genome reduction analysis using comparative genomics. Bioinformatics, 2006, 22, 1551-1561.	1.8	3
82	IDENTIFYING COEVOLUTIONARY PATTERNS IN HUMAN LEUKOCYTE ANTIGEN (HLA) MOLECULES. Evolution; International Journal of Organic Evolution, 2009, 64, 1429-45.	1.1	3
83	Chaperonin overproduction and metabolic erosion caused by mutation accumulation in Escherichia coli. FEMS Microbiology Letters, 2019, 366, .	0.7	2
84	Phylogenomic inference of functional divergence. BMC Bioinformatics, 2009, 10, .	1.2	1
85	Experimental Evolution and Next Generation Sequencing Illuminate the Evolutionary Trajectories of Microbes. , 2015, , 101-113.		1
86	The Role of Ancestral Duplicated Genes in Adaptation to Growth on Lactate, a Non-Fermentable Carbon Source for the Yeast Saccharomyces cerevisiae. International Journal of Molecular Sciences, 2021, 22, 12293.	1.8	1
87	Evolution of Multiple Chaperonins: Innovation of Evolutionary Capacitors. Heat Shock Proteins, 2017, , 149-170.	0.2	0
88	Molecular Coevolution and the Three-Dimensionality of Natural Selection. , 2009, , 237-251.		0