Marina Marcet-Houben

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9497543/publications.pdf

Version: 2024-02-01

61 papers 5,437 citations

33 h-index 57 g-index

70 all docs 70 docs citations

70 times ranked

8053 citing authors

#	Article	IF	CITATIONS
1	PhylomeDB V5: an expanding repository for genome-wide catalogues of annotated gene phylogenies. Nucleic Acids Research, 2022, 50, D1062-D1068.	14.5	30
2	Chromatin profiling reveals heterogeneity in clinical isolates of the human pathogen Aspergillus fumigatus. PLoS Genetics, 2022, 18, e1010001.	3. 5	11
3	Evolutionary analyses of genes in Echinodermata offer insights towards the origin of metazoan phyla. Genomics, 2022, 114, 110431.	2.9	O
4	Timing the origin of eukaryotic cellular complexity with ancient duplications. Nature Ecology and Evolution, 2021, 5, 92-100.	7.8	61
5	Shared evolutionary footprints suggest mitochondrial oxidative damage underlies multiple complex I losses in fungi. Open Biology, 2021, 11, 200362.	3 . 6	10
6	Comparative Genomics Used to Predict Virulence Factors and Metabolic Genes among Monilinia Species. Journal of Fungi (Basel, Switzerland), 2021, 7, 464.	3 . 5	11
7	Human tRNAs with inosine 34 are essential to efficiently translate eukarya-specific low-complexity proteins. Nucleic Acids Research, 2021, 49, 7011-7034.	14.5	17
8	The transposable element-rich genome of the cereal pest Sitophilus oryzae. BMC Biology, 2021, 19, 241.	3.8	40
9	Phylogenomics Identifies an Ancestral Burst of Gene Duplications Predating the Diversification of Aphidomorpha. Molecular Biology and Evolution, 2020, 37, 730-756.	8.9	29
10	Parental origin of the allotetraploid tobacco <i>Nicotiana benthamiana</i> . Plant Journal, 2020, 102, 541-554.	5.7	31
11	The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. BMC Biology, 2020, 18, 90.	3 . 8	40
12	Differential Expression of Fungal Genes Determines the Lifestyle of Plectosphaerella Strains During Arabidopsis thaliana Colonization. Molecular Plant-Microbe Interactions, 2020, 33, 1299-1314.	2.6	9
13	Selection following Gene Duplication Shapes Recent Genome Evolution in the Pea Aphid Acyrthosiphon pisum. Molecular Biology and Evolution, 2020, 37, 2601-2615.	8.9	12
14	Evolutionary and functional patterns of shared gene neighbourhood in fungi. Nature Microbiology, 2019, 4, 2383-2392.	13.3	35
15	Genetically encodable bioluminescent system from fungi. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12728-12732.	7.1	130
16	Phylogenomics of the olive tree (Olea europaea) reveals the relative contribution of ancient allo- and autopolyploidization events. BMC Biology, 2018, 16, 15.	3.8	30
17	Adaptation of S. cerevisiae to Fermented Food Environments Reveals Remarkable Genome Plasticity and the Footprints of Domestication. Molecular Biology and Evolution, 2018, 35, 1712-1727.	8.9	214
18	Regulatory Mechanisms of a Highly Pectinolytic Mutant of Penicillium occitanis and Functional Analysis of a Candidate Gene in the Plant Pathogen Fusarium oxysporum. Frontiers in Microbiology, 2017, 8, 1627.	3 . 5	4

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19	The complete mitochondrial DNA of the silky shark (Carcharhinus falciformis). Mitochondrial DNA, 2016, 27, 157-158.	0.6	5
20	Widespread Inter- and Intra-Domain Horizontal Gene Transfer of d-Amino Acid Metabolism Enzymes in Eukaryotes. Frontiers in Microbiology, 2016, 7, 2001.	3 . 5	28
21	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	8.8	131
22	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. Current Biology, 2016, 26, 1577-1584.	3.9	175
23	Evolutionary genomics of yeast pathogens in the Saccharomycotina. FEMS Yeast Research, 2016, 16, fow064.	2.3	102
24	Whole genome sequencing of turbot (<i>Scophthalmus maximus</i> ; Pleuronectiformes): a fish adapted to demersal life. DNA Research, 2016, 23, 181-192.	3.4	150
25	Horizontal acquisition of toxic alkaloid synthesis in a clade of plant associated fungi. Fungal Genetics and Biology, 2016, 86, 71-80.	2.1	26
26	Genome sequencing and secondary metabolism of the postharvest pathogen Penicillium griseofulvum. BMC Genomics, 2016, 17, 19.	2.8	70
27	Genome sequence of the olive tree, Olea europaea. GigaScience, 2016, 5, 29.	6.4	201
28	Contrasting Genomic Diversity in Two Closely Related Postharvest Pathogens: <i>Penicillium digitatum </i> and <i>Penicillium expansum </i> Genome Biology and Evolution, 2016, 8, 218-227.	2.5	37
29	The complete mitogenome of the common dolphinfish (<i>Coryphaena hippurus</i>). Mitochondrial DNA, 2015, 26, 959-960.	0.6	1
30	Differential gene retention as an evolutionary mechanism to generate biodiversity and adaptation in yeasts. Scientific Reports, 2015, 5, 11571.	3.3	50
31	Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13970-13975.	7.1	192
32	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. Genome Biology and Evolution, 2015, 7, 1988-1999.	2.5	25
33	Genome, Transcriptome, and Functional Analyses of <i>Penicillium expansum</i> Provide New Insights Into Secondary Metabolism and Pathogenicity. Molecular Plant-Microbe Interactions, 2015, 28, 232-248.	2.6	183
34	The complete mitochondrial genome of the Giant Manta ray, Manta birostris. Mitochondrial DNA, 2015, 26, 787-788.	0.6	4
35	Beyond the Whole-Genome Duplication: Phylogenetic Evidence for an Ancient Interspecies Hybridization in the Baker's Yeast Lineage. PLoS Biology, 2015, 13, e1002220.	5.6	321
36	Gene Expansion Shapes Genome Architecture in the Human Pathogen Lichtheimia corymbifera: An Evolutionary Genomics Analysis in the Ancient Terrestrial Mucorales (Mucoromycotina). PLoS Genetics, 2014, 10, e1004496.	3.5	80

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37	Systematic Phenotyping of a Large-Scale Candida glabrata Deletion Collection Reveals Novel Antifungal Tolerance Genes. PLoS Pathogens, 2014, 10, e1004211.	4.7	155
38	A study of the <scp>DNA</scp> damage checkpoint in <i><scp>C</scp>andida albicans</i> : uncoupling of the functions of <scp>Rad</scp> 53 in <scp>DNA</scp> repair, cell cycle regulation and genotoxic stressâ€induced polarized growth. Molecular Microbiology, 2014, 91, 452-471.	2.5	39
39	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. Nucleic Acids Research, 2014, 42, D897-D902.	14.5	264
40	The complete genome of Blastobotrys (Arxula) adeninivorans LS3 - a yeast of biotechnological interest. Biotechnology for Biofuels, 2014, 7, 66.	6.2	57
41	3 Phylogenomics for the Study of Fungal Biology. , 2014, , 61-79.		3
42	FUNGALOXPHOS: An integrated database for oxidative phosphorylation in fungi. Mitochondrion, 2013, 13, 357-359.	3.4	3
43	Comparative genomics of emerging pathogens in the Candida glabrata clade. BMC Genomics, 2013, 14, 623.	2.8	174
44	The Genome and Development-Dependent Transcriptomes of Pyronema confluens: A Window into Fungal Evolution. PLoS Genetics, 2013, 9, e1003820.	3.5	85
45	Complete DNA Sequence of Kuraishia capsulata Illustrates Novel Genomic Features among Budding Yeasts (Saccharomycotina). Genome Biology and Evolution, 2013, 5, 2524-2539.	2.5	39
46	The Schistosoma mansoni phylome: using evolutionary genomics to gain insight into a parasite's biology. BMC Genomics, 2012, 13, 617.	2.8	28
47	Phylogenomics supports microsporidia as the earliest diverging clade of sequenced fungi. BMC Biology, 2012, 10, 47.	3.8	182
48	Genome sequence of the necrotrophic fungus Penicillium digitatum, the main postharvest pathogen of citrus. BMC Genomics, 2012, 13, 646.	2.8	205
49	The genome of wine yeast Dekkera bruxellensis provides a tool to explore its food-related properties. International Journal of Food Microbiology, 2012, 157, 202-209.	4.7	102
50	Evolution of Fungi and Their Respiratory Metabolism. , 2011, , 257-272.		1
51	Evolutionary histories of expanded peptidase families in Schistosoma mansoni. Memorias Do Instituto Oswaldo Cruz, 2011, 106, 864-877.	1.6	12
52	Regulation of <i>Candida glabrata </i> oxidative stress resistance is adapted to host environment. FEBS Letters, 2011, 585, 319-327.	2.8	74
53	TreeKO: a duplication-aware algorithm for the comparison of phylogenetic trees. Nucleic Acids Research, 2011, 39, e66-e66.	14.5	46
54	PhylomeDB v3.0: an expanding repository of genome-wide collections of trees, alignments and phylogeny-based orthology and paralogy predictions. Nucleic Acids Research, 2011, 39, D556-D560.	14.5	134

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55	Acquisition of prokaryotic genes by fungal genomes. Trends in Genetics, 2010, 26, 5-8.	6.7	219
56	The pea aphid phylome: a complete catalogue of evolutionary histories and arthropod orthology and paralogy relationships for <i>Acyrthosiphon pisum</i> genes. Insect Molecular Biology, 2010, 19, 13-21.	2.0	45
57	Genome Sequence of the Pea Aphid Acyrthosiphon pisum. PLoS Biology, 2010, 8, e1000313.	5.6	913
58	The Tree versus the Forest: The Fungal Tree of Life and the Topological Diversity within the Yeast Phylome. PLoS ONE, 2009, 4, e4357.	2.5	77
59	Phylogenomics of the oxidative phosphorylation in fungi reveals extensive gene duplication followed by functional divergence. BMC Evolutionary Biology, 2009, 9, 295.	3.2	73
60	Phylogenetic analysis of homologous fatty acid synthase and polyketide synthase involved in aflatoxin biosynthesis. Bioinformation, 2008, 3, 33-40.	0.5	1
61	Towards reconstructing a metabolic tree of life. Bioinformation, 2007, 2, 135-144.	0.5	3