

# Marina Marcet-Houben

## List of Publications by Year in descending order

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Version: 2024-02-01

61  
papers

5,437  
citations

126708

33  
h-index

143772

57  
g-index

70  
all docs

70  
docs citations

70  
times ranked

8053  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	2.6	913
2	Beyond the Whole-Genome Duplication: Phylogenetic Evidence for an Ancient Interspecies Hybridization in the Baker's Yeast Lineage. <i>PLoS Biology</i> , 2015, 13, e1002220.	2.6	321
3	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. <i>Nucleic Acids Research</i> , 2014, 42, D897-D902.	6.5	264
4	Acquisition of prokaryotic genes by fungal genomes. <i>Trends in Genetics</i> , 2010, 26, 5-8.	2.9	219
5	Adaptation of <i>S. cerevisiae</i> to Fermented Food Environments Reveals Remarkable Genome Plasticity and the Footprints of Domestication. <i>Molecular Biology and Evolution</i> , 2018, 35, 1712-1727.	3.5	214
6	Genome sequence of the necrotrophic fungus <i>Penicillium digitatum</i> , the main postharvest pathogen of citrus. <i>BMC Genomics</i> , 2012, 13, 646.	1.2	205
7	Genome sequence of the olive tree, <i>Olea europaea</i> . <i>GigaScience</i> , 2016, 5, 29.	3.3	201
8	Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13970-13975.	3.3	192
9	Genome, Transcriptome, and Functional Analyses of <i>Penicillium expansum</i> Provide New Insights Into Secondary Metabolism and Pathogenicity. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 232-248.	1.4	183
10	Phylogenomics supports microsporidia as the earliest diverging clade of sequenced fungi. <i>BMC Biology</i> , 2012, 10, 47.	1.7	182
11	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	1.8	175
12	Comparative genomics of emerging pathogens in the <i>Candida glabrata</i> clade. <i>BMC Genomics</i> , 2013, 14, 623.	1.2	174
13	Systematic Phenotyping of a Large-Scale <i>Candida glabrata</i> Deletion Collection Reveals Novel Antifungal Tolerance Genes. <i>PLoS Pathogens</i> , 2014, 10, e1004211.	2.1	155
14	Whole genome sequencing of turbot ( <i>Scophthalmus maximus</i> ; Pleuronectiformes): a fish adapted to demersal life. <i>DNA Research</i> , 2016, 23, 181-192.	1.5	150
15	PhylomeDB v3.0: an expanding repository of genome-wide collections of trees, alignments and phylogeny-based orthology and paralogy predictions. <i>Nucleic Acids Research</i> , 2011, 39, D556-D560.	6.5	134
16	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , 2016, 17, 251.	3.8	131
17	Genetically encodable bioluminescent system from fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12728-12732.	3.3	130
18	The genome of wine yeast <i>Dekkera bruxellensis</i> provides a tool to explore its food-related properties. <i>International Journal of Food Microbiology</i> , 2012, 157, 202-209.	2.1	102

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19	Evolutionary genomics of yeast pathogens in the Saccharomycotina. FEMS Yeast Research, 2016, 16, fow064.	1.1	102
20	The Genome and Development-Dependent Transcriptomes of Pyronema confluens: A Window into Fungal Evolution. PLoS Genetics, 2013, 9, e1003820.	1.5	85
21	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.	1.5	80
22	The Tree versus the Forest: The Fungal Tree of Life and the Topological Diversity within the Yeast Phylome. PLoS ONE, 2009, 4, e4357.	1.1	77
23	Regulation of <i>Candida glabrata</i> oxidative stress resistance is adapted to host environment. FEBS Letters, 2011, 585, 319-327.	1.3	74
24	Phylogenomics of the oxidative phosphorylation in fungi reveals extensive gene duplication followed by functional divergence. BMC Evolutionary Biology, 2009, 9, 295.	3.2	73
25	Genome sequencing and secondary metabolism of the postharvest pathogen Penicillium griseofulvum. BMC Genomics, 2016, 17, 19.	1.2	70
26	Timing the origin of eukaryotic cellular complexity with ancient duplications. Nature Ecology and Evolution, 2021, 5, 92-100.	3.4	61
27	The complete genome of Blastobotrys (Arxula) adenivorans LS3 - a yeast of biotechnological interest. Biotechnology for Biofuels, 2014, 7, 66.	6.2	57
28	Differential gene retention as an evolutionary mechanism to generate biodiversity and adaptation in yeasts. Scientific Reports, 2015, 5, 11571.	1.6	50
29	TreeKO: a duplication-aware algorithm for the comparison of phylogenetic trees. Nucleic Acids Research, 2011, 39, e66-e66.	6.5	46
30	The pea aphid phylome: a complete catalogue of evolutionary histories and arthropod orthology and paralogy relationships for <i>Acyrtosiphon pisum</i> genes. Insect Molecular Biology, 2010, 19, 13-21.	1.0	45
31	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.	1.7	40
32	The transposable element-rich genome of the cereal pest Sitophilus oryzae. BMC Biology, 2021, 19, 241.	1.7	40
33	Complete DNA Sequence of Kuraishia capsulata Illustrates Novel Genomic Features among Budding Yeasts (Saccharomycotina). Genome Biology and Evolution, 2013, 5, 2524-2539.	1.1	39
34	A study of the <i>DNA</i> damage checkpoint in <i>Candida albicans</i> : uncoupling of the functions of <i>Rad53</i> in <i>DNA</i> repair, cell cycle regulation and genotoxic stress-induced polarized growth. Molecular Microbiology, 2014, 91, 452-471.	1.2	39
35	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.	1.1	37
36	Evolutionary and functional patterns of shared gene neighbourhood in fungi. Nature Microbiology, 2019, 4, 2383-2392.	5.9	35

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37	Parental origin of the allotetraploid tobacco <i>Nicotiana benthamiana</i> . <i>Plant Journal</i> , 2020, 102, 541-554.	2.8	31
38	Phylogenomics of the olive tree ( <i>Olea europaea</i> ) reveals the relative contribution of ancient allo- and autopolyploidization events. <i>BMC Biology</i> , 2018, 16, 15.	1.7	30
39	PhylomeDB V5: an expanding repository for genome-wide catalogues of annotated gene phylogenies. <i>Nucleic Acids Research</i> , 2022, 50, D1062-D1068.	6.5	30
40	Phylogenomics Identifies an Ancestral Burst of Gene Duplications Predating the Diversification of Aphidomorpha. <i>Molecular Biology and Evolution</i> , 2020, 37, 730-756.	3.5	29
41	The <i>Schistosoma mansoni</i> phylome: using evolutionary genomics to gain insight into a parasite's biology. <i>BMC Genomics</i> , 2012, 13, 617.	1.2	28
42	Widespread Inter- and Intra-Domain Horizontal Gene Transfer of d-Amino Acid Metabolism Enzymes in Eukaryotes. <i>Frontiers in Microbiology</i> , 2016, 7, 2001.	1.5	28
43	Horizontal acquisition of toxic alkaloid synthesis in a clade of plant associated fungi. <i>Fungal Genetics and Biology</i> , 2016, 86, 71-80.	0.9	26
44	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. <i>Genome Biology and Evolution</i> , 2015, 7, 1988-1999.	1.1	25
45	Human tRNAs with inosine 34 are essential to efficiently translate eukarya-specific low-complexity proteins. <i>Nucleic Acids Research</i> , 2021, 49, 7011-7034.	6.5	17
46	Evolutionary histories of expanded peptidase families in <i>Schistosoma mansoni</i> . <i>Memorias Do Instituto Oswaldo Cruz</i> , 2011, 106, 864-877.	0.8	12
47	Selection following Gene Duplication Shapes Recent Genome Evolution in the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 2601-2615.	3.5	12
48	Comparative Genomics Used to Predict Virulence Factors and Metabolic Genes among <i>Monilinia</i> Species. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 464.	1.5	11
49	Chromatin profiling reveals heterogeneity in clinical isolates of the human pathogen <i>Aspergillus fumigatus</i> . <i>PLoS Genetics</i> , 2022, 18, e1010001.	1.5	11
50	Shared evolutionary footprints suggest mitochondrial oxidative damage underlies multiple complex I losses in fungi. <i>Open Biology</i> , 2021, 11, 200362.	1.5	10
51	Differential Expression of Fungal Genes Determines the Lifestyle of <i>Plectosphaerella</i> Strains During <i>Arabidopsis thaliana</i> Colonization. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1299-1314.	1.4	9
52	The complete mitochondrial DNA of the silky shark ( <i>Carcharhinus falciformis</i> ). <i>Mitochondrial DNA</i> , 2016, 27, 157-158.	0.6	5
53	The complete mitochondrial genome of the Giant Manta ray, <i>Manta birostris</i> . <i>Mitochondrial DNA</i> , 2015, 26, 787-788.	0.6	4
54	Regulatory Mechanisms of a Highly Pectinolytic Mutant of <i>Penicillium occitanis</i> and Functional Analysis of a Candidate Gene in the Plant Pathogen <i>Fusarium oxysporum</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1627.	1.5	4

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55	FUNGALOXPHOS: An integrated database for oxidative phosphorylation in fungi. <i>Mitochondrion</i> , 2013, 13, 357-359.	1.6	3
56	3 Phylogenomics for the Study of Fungal Biology. , 2014, , 61-79.		3
57	Towards reconstructing a metabolic tree of life. <i>Bioinformatics</i> , 2007, 2, 135-144.	0.2	3
58	Evolution of Fungi and Their Respiratory Metabolism. , 2011, , 257-272.		1
59	The complete mitogenome of the common dolphinfish ( <i>Coryphaena hippurus</i> ). <i>Mitochondrial DNA</i> , 2015, 26, 959-960.	0.6	1
60	Phylogenetic analysis of homologous fatty acid synthase and polyketide synthase involved in aflatoxin biosynthesis. <i>Bioinformatics</i> , 2008, 3, 33-40.	0.2	1
61	Evolutionary analyses of genes in Echinodermata offer insights towards the origin of metazoan phyla. <i>Genomics</i> , 2022, 114, 110431.	1.3	0