Toni GabaldÃ³n

List of Publications by Year
in descending order

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		7069	6113
260	31,741	78	159
papers	citations	h-index	g-index

316	316	316	38507
all docs	docs citations	times ranked	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.	6.5	30
2	Trends in yeast diversity discovery. Fungal Diversity, 2022, 114, 491-537.	4.7	31
3	Chromatin profiling reveals heterogeneity in clinical isolates of the human pathogen Aspergillus fumigatus. PLoS Genetics, 2022, 18, e1010001.	1.5	11
4	Candidemia Among Coronavirus Disease 2019 Patients in Turkey Admitted to Intensive Care Units: A Retrospective Multicenter Study. Open Forum Infectious Diseases, 2022, 9, ofac078.	0.4	13
5	Benzylic Dehydroxylation of Echinocandin Antifungal Drugs Restores Efficacy against Resistance Conferred by Mutated Glucan Synthase. Journal of the American Chemical Society, 2022, 144, 5965-5975.	6.6	8
6	Transcriptome and proteome profiling reveals complex adaptations of Candida parapsilosis cells assimilating hydroxyaromatic carbon sources. PLoS Genetics, 2022, 18, e1009815.	1.5	1
7	Multiple Hybridization Events Punctuate the Evolutionary Trajectory of<i>Malassezia furfur</i>. MBio, 2022, 13, e0385321.	1.8	9
8	Genome analysis of five recently described species of the CUG-Ser clade uncovers <i>Candida theae</i> as a new hybrid lineage with pathogenic potential in the <i>Candida parapsilosis</i> species complex. DNA Research, 2022, , .	1.5	4
9	The Quest for Orthologs orthology benchmark service in 2022. Nucleic Acids Research, 2022, 50, W623-W632.	6.5	29
10	Citizen-science reveals changes in the oral microbiome in Spain through age and lifestyle factors. Npj Biofilms and Microbiomes, 2022, 8, 38.	2.9	18
11	Chromosome-level assembly, annotation and phylome of <i>Pelobates cultripes</i>, the western spadefoot toad. DNA Research, 2022, 29, .	1.5	1
12	Using genomics to understand the mechanisms of virulence and drug resistance in fungal pathogens. Biochemical Society Transactions, 2022, 50, 1259-1268.	1.6	13
13			

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19	Structural characterization of NORAD reveals a stabilizing role of spacers and two new repeat units. Computational and Structural Biotechnology Journal, 2021, 19, 3245-3254.	1.9	9
20	A Mouse Model Suggests That Heart Failure and Its Common Comorbidity Sleep Fragmentation Have No Synergistic Impacts on the Gut Microbiome. Microorganisms, 2021, 9, 641.	1.6	4
21	Candida pathogens induce protective mitochondria-associated type I interferon signalling and a damage-driven response in vaginal epithelial cells. Nature Microbiology, 2021, 6, 643-657.	5.9	49
22	Shared evolutionary footprints suggest mitochondrial oxidative damage underlies multiple complex I losses in fungi. Open Biology, 2021, 11, 200362.	1.5	10
23	Comparative Genomics Used to Predict Virulence Factors and Metabolic Genes among Monilinia Species. Journal of Fungi (Basel, Switzerland), 2021, 7, 464.	1.5	11
24	OCT1 â€“ a yeast mitochondrial thiolase involved in the 3-oxoadipate pathway. FEMS Yeast Research, 2021, 21, .	1.1	2
25	The evolving species concepts used for yeasts: from phenotypes and genomes to speciation networks. Fungal Diversity, 2021, 109, 27-55.	4.7	37
26	Transient Mitochondria Dysfunction Confers Fungal Cross-Resistance against Phagocytic Killing and Fluconazole. MBio, 2021, 12, e0112821.	1.8	15
27	Genome analysis of <i>Candida subhashii</i> reveals its hybrid nature and dual mitochondrial genome conformations. DNA Research, 2021, 28, .	1.5	14
28	Roles of the human microbiome in cancer. Hepatobiliary Surgery and Nutrition, 2021, 10, 558-560.	0.7	4
29	Origin and Early Evolution of the Eukaryotic Cell. Annual Review of Microbiology, 2021, 75, 631-647.	2.9	28
30	Profiling of RNA Structure at Single-Nucleotide Resolution Using nextPARS. Methods in Molecular Biology, 2021, 2284, 51-62.	0.4	6
31	Factors enforcing the species boundary between the human pathogens Cryptococcus neoformans and Cryptococcus deneoformans. PLoS Genetics, 2021, 17, e1008871.	1.5	13
32	Oral microbiome in down syndrome and its implications on oral health. Journal of Oral Microbiology, 2021, 13, 1865690.	1.2	15
33	Extreme diversification driven by parallel events of massive loss of heterozygosity in the hybrid lineage of <i>Candida albicans</i>. Genetics, 2021, 217, .	1.2	16
34	Narrow mutational signatures drive acquisition of multidrug resistance in the fungal pathogen Candida glabrata. Current Biology, 2021, 31, 5314-5326.e10.	1.8	47
35	Human albumin enhances the pathogenic potential of Candida glabrata on vaginal epithelial cells. PLoS Pathogens, 2021, 17, e1010037.	2.1	5
36	The transposable element-rich genome of the cereal pest Sitophilus oryzae. BMC Biology, 2021, 19, 241.	1.7	40

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37	The long non-coding RNA landscape of Candida yeast pathogens. Nature Communications, 2021, 12, 7317.	5.8	10
38	Molecular Typing of Candida glabrata. Mycopathologia, 2020, 185, 755-764.	1.3	14
39	EvolClust: automated inference of evolutionary conserved gene clusters in eukaryotes. Bioinformatics, 2020, 36, 1265-1266.	1.8	10
40	CROSSMAPPER: estimating cross-mapping rates and optimizing experimental design in multi-species sequencing studies. Bioinformatics, 2020, 36, 925-927.	1.8	34
41	Phylogenomics Identifies an Ancestral Burst of Gene Duplications Predating the Diversification of Aphidomorpha. Molecular Biology and Evolution, 2020, 37, 730-756.	3.5	29
42	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. Plant Journal, 2020, 101, 455-472.	2.8	94
43	HaploTypo: a variant-calling pipeline for phased genomes. Bioinformatics, 2020, 36, 2569-2571.	1.8	14
44	Parental origin of the allotetraploid tobacco <i>Nicotiana benthamiana</i>. Plant Journal, 2020, 102, 541-554.	2.8	31
45	Phenotypic Variability in a Coinfection With Three Independent Candida parapsilosis Lineages. Frontiers in Microbiology, 2020, 11, 1994.	1.5	10
46	Target Enrichment Enables the Discovery of lncRNAs with Somatic Mutations or Altered Expression in Paraffin-Embedded Colorectal Cancer Samples. Cancers, 2020, 12, 2844.	1.7	7
47	Hybridization and the origin of new yeast lineages. FEMS Yeast Research, 2020, 20, .	1.1	46
48	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. Genome Biology, 2020, 21, 275.	3.8	105
49	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
50	Discovery of EMRE in fungi resolves the true evolutionary history of the mitochondrial calcium uniporter. Nature Communications, 2020, 11, 4031.	5.8	18
51	Triazole Evolution of Candida parapsilosis Results in Cross-Resistance to Other Antifungal Drugs, Influences Stress Responses, and Alters Virulence in an Antifungal Drug-Dependent Manner. MSphere, 2020, 5, .	1.3	23
52	Genomic evidence for recurrent genetic admixture during the domestication of Mediterranean olive trees (Olea europaea L.). BMC Biology, 2020, 18, 148.	1.7	39
53	Patterns and impacts of nonvertical evolution in eukaryotes: a paradigm shift. Annals of the New York Academy of Sciences, 2020, 1476, 78-92.	1.8	21
54	Elevated Vacuolar Uptake of Fluorescently Labeled Antifungal Drug Caspofungin Predicts Echinocandin Resistance in Pathogenic Yeast. ACS Central Science, 2020, 6, 1698-1712.	5.3	15

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55	The Quiet and Underappreciated Rise of Drug-Resistant Invasive Fungal Pathogens. Journal of Fungi (Basel, Switzerland), 2020, 6, 138.	1.5	84
56	Grand Challenges in Fungal Genomics and Evolution. Frontiers in Fungal Biology, 2020, 1, .	0.9	4
57	Drug-Resistant Fungi: An Emerging Challenge Threatening Our Limited Antifungal Armamentarium. Antibiotics, 2020, 9, 877.	1.5	125
58	Selection following Gene Duplication Shapes Recent Genome Evolution in the Pea Aphid Acyrthosiphon pisum. Molecular Biology and Evolution, 2020, 37, 2601-2615.	3.5	12
59	Bacillus firmus Strain I-1582, a Nematode Antagonist by Itself and Through the Plant. Frontiers in Plant Science, 2020, 11, 796.	1.7	37
60	The Transcriptional Aftermath in Two Independently Formed Hybrids of the Opportunistic Pathogen Candida orthopsilosis. MSphere, 2020, 5, .	1.3	7
61	Genomic evidence for a hybrid origin of the yeast opportunistic pathogen Candida albicans. BMC Biology, 2020, 18, 48.	1.7	46
62	Coronavirus Disease 2019 (COVID-19): Emerging and Future Challenges for Dental and Oral Medicine. Journal of Dental Research, 2020, 99, 1113-1113.	2.5	33
63	Integrative Omics Analysis Reveals a Limited Transcriptional Shock After Yeast Interspecies Hybridization. Frontiers in Genetics, 2020, 11, 404.	1.1	22
64	The Human Oral Microbiome in Health and Disease: From Sequences to Ecosystems. Microorganisms, 2020, 8, 308.	1.6	231
65	Soybean aphid biotype 1 genome: Insights into the invasive biology and adaptive evolution of a major agricultural pest. Insect Biochemistry and Molecular Biology, 2020, 120, 103334.	1.2	15
66	Gene gain and loss across the metazoan tree of life. Nature Ecology and Evolution, 2020, 4, 524-533.	3.4	116
67	MetaPhOrs 2.0: integrative, phylogeny-based inference of orthology and paralogy across the tree of life. Nucleic Acids Research, 2020, 48, W553-W557.	6.5	27
68	Fungal evolution: cellular, genomic and metabolic complexity. Biological Reviews, 2020, 95, 1198-1232.	4.7	71
69	Genomes shed light on the secret life of Candida glabrata: not so asexual, not so commensal. Current Genetics, 2019, 65, 93-98.	0.8	49
70	Pochonia chlamydosporia Induces Plant-Dependent Systemic Resistance to Meloidogyne incognita. Frontiers in Plant Science, 2019, 10, 945.	1.7	59
71	Post-exercise hypotension and skeletal muscle oxygenation is regulated by nitrate-reducing activity of oral bacteria. Free Radical Biology and Medicine, 2019, 143, 252-259.	1.3	22
72	Fungal evolution: diversity, taxonomy and phylogeny of the Fungi. Biological Reviews, 2019, 94, 2101-2137.	4.7	191

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73	A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. Nature Genetics, 2019, 51, 1607-1615.	9.4	153
74	Evolutionary and functional patterns of shared gene neighbourhood in fungi. Nature Microbiology, 2019, 4, 2383-2392.	5.9	35
75	Impact of Homologous Recombination on the Evolution of Prokaryotic Core Genomes. MBio, 2019, 10, .	1.8	60
76	Transcriptomic analyses reveal groups of co-expressed, syntenic lncRNAs in four species of the genus <i>Caenorhabditis</i>. RNA Biology, 2019, 16, 320-329.	1.5	16
77	Microbiome and colorectal cancer: Roles in carcinogenesis and clinical potential. Molecular Aspects of Medicine, 2019, 69, 93-106.	2.7	212
78	Skin microbiome modulation induced by probiotic solutions. Microbiome, 2019, 7, 95.	4.9	74
79	Recent trends in molecular diagnostics of yeast infections: from PCR to NGS. FEMS Microbiology Reviews, 2019, 43, 517-547.	3.9	77
80	Whole-Genome Sequencing of the Opportunistic Yeast Pathogen Candida inconspicua Uncovers Its Hybrid Origin. Frontiers in Genetics, 2019, 10, 383.	1.1	63
81	Fungal evolution: major ecological adaptations and evolutionary transitions. Biological Reviews, 2019, 94, 1443-1476.	4.7	181
82	Utilization of selenocysteine in early-branching fungal phyla. Nature Microbiology, 2019, 4, 759-765.	5.9	41
83	Candida parapsilosis: from Genes to the Bedside. Clinical Microbiology Reviews, 2019, 32, .	5.7	182
84	Genome Comparisons of Candida glabrata Serial Clinical Isolates Reveal Patterns of Genetic Variation in Infecting Clonal Populations. Frontiers in Microbiology, 2019, 10, 112.	1.5	40
85	Genome Assemblies of Two Rare Opportunistic Yeast Pathogens:<i>Diutina rugosa</i>(syn.<i>Candida) Tj ETQq1 1 0.784314 rgBT /Ove Genetics, 2019, 9, 3921-3927.	0.8	6
86	Genome Sequencing and Transcriptome Analysis Reveal Recent Species-Specific Gene Duplications in the Plastic Gilthead Sea Bream (Sparus aurata). Frontiers in Marine Science, 2019, 6, .	1.2	26
87	Comparative Genomics and Transcriptomics To Analyze Fruiting Body Development in Filamentous Ascomycetes. Genetics, 2019, 213, 1545-1563.	1.2	14
88	Commercial Formulates of Trichoderma Induce Systemic Plant Resistance to Meloidogyne incognita in Tomato and the Effect Is Additive to That of the Mi-1.2 Resistance Gene. Frontiers in Microbiology, 2019, 10, 3042.	1.5	41
89	Investigation of Candida parapsilosis virulence regulatory factors during host-pathogen interaction. Scientific Reports, 2018, 8, 1346.	1.6	21
90	Patterns of Genomic Variation in the Opportunistic Pathogen Candida glabrata Suggest the Existence of Mating and a Secondary Association with Humans. Current Biology, 2018, 28, 15-27.e7.	1.8	114

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91	Misidentification of genome assemblies in public databases: The case of <i>Naumovozyma dairenensis</i> and proposal of a protocol to correct misidentifications. Yeast, 2018, 35, 425-429.	0.8	30
92	nextPARS: parallel probing of RNA structures in Illumina. Rna, 2018, 24, 609-619.	1.6	23
93	Characterization of ecologically diverse viruses infecting co-occurring strains of cosmopolitan hyperhalophilic <i>Bacteroidetes</i>. ISME Journal, 2018, 12, 424-437.	4.4	29
94	Hybridization and emergence of virulence in opportunistic human yeast pathogens. Yeast, 2018, 35, 5-20.	0.8	104
95	Genetically encodable bioluminescent system from fungi. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12728-12732.	3.3	130
96	Echinocandin-Induced Microevolution of Candida parapsilosis Influences Virulence and Abiotic Stress Tolerance. MSphere, 2018, 3, .	1.3	29
97	MICU1 Confers Protection from MCU-Dependent Manganese Toxicity. Cell Reports, 2018, 25, 1425-1435.e7.	2.9	26
98	Citizen science charts two major â€œstomatotypesâ€•in the oral microbiome of adolescents and reveals links with habits and drinking water composition. Microbiome, 2018, 6, 218.	4.9	86
99	Evolutionary Emergence of Drug Resistance in Candida Opportunistic Pathogens. Genes, 2018, 9, 461.	1.0	161
100	Relative timing of mitochondrial endosymbiosis and the â€œpreâ€•mitochondrial symbiosesâ€•hypothesis. IUBMB Life, 2018, 70, 1188-1196.	1.5	36
101	Evolution of the Peroxisomal Proteome. Sub-Cellular Biochemistry, 2018, 89, 221-233.	1.0	11
102	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	1.8	36
103	Genome Sequence of the Brown Rot Fungal Pathogen Monilinia laxa. Genome Announcements, 2018, 6, .	0.8	17
104	Biological Processes Modulating Longevity across Primates: A Phylogenetic Genome-Phenome Analysis. Molecular Biology and Evolution, 2018, 35, 1990-2004.	3.5	58
105	Eicosanoid biosynthesis influences the virulence of <i>Candida parapsilosis</i>. Virulence, 2018, 9, 1019-1035.	1.8	18
106	Phylogenomics of the olive tree (Olea europaea) reveals the relative contribution of ancient allo- and autopolyploidization events. BMC Biology, 2018, 16, 15.	1.7	30
107	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.	3.5	214
108	Genome Variation in the Model Halophilic Bacterium Salinibacter ruber. Frontiers in Microbiology, 2018, 9, 1499.	1.5	12

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109	Transcriptome Sequencing Approaches to Elucidate Hostâ€“Microbe Interactions in Opportunistic Human Fungal Pathogens. Current Topics in Microbiology and Immunology, 2018, 422, 193-235.	0.7	8
110	Gene flow contributes to diversification of the major fungal pathogen Candida albicans. Nature Communications, 2018, 9, 2253.	5.8	131
111	Dating nodes in a phylogeny using inferred horizontal gene transfers. Peer Community in Evolutionary Biology, 2018, , 100037.	0.0	0
112	Rapid transcriptional plasticity of duplicated gene clusters enables a clonally reproducing aphid to colonise diverse plant species. Genome Biology, 2017, 18, 27.	3.8	624
113	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. Science Advances, 2017, 3, e1700299.	4.7	142
114	Distinct roles of the polarity factors Boi1 and Boi2 in the control of exocytosis and abscission in budding yeast. Molecular Biology of the Cell, 2017, 28, 3082-3094.	0.9	19
115	Eukaryotic transporters for hydroxyderivatives of benzoic acid. Scientific Reports, 2017, 7, 8998.	1.6	8
116	Genomic history of the origin and domestication of common bean unveils its closest sister species. Genome Biology, 2017, 18, 60.	3.8	142
117	Phylogenomics: The Evolution of Common Bean as Seen from the Perspective of All of Its Genes. Compendium of Plant Genomes, 2017, , 263-287.	0.3	0
118	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.	1.5	4
119	Lack of the PGA exopolysaccharide in Salmonella as an adaptive trait for survival in the host. PLoS Genetics, 2017, 13, e1006816.	1.5	16
120	Long Non-Coding RNAs As Potential Novel Prognostic Biomarkers in Colorectal Cancer. Frontiers in Genetics, 2016, 7, 54.	1.1	64
121	Widespread Inter- and Intra-Domain Horizontal Gene Transfer of d-Amino Acid Metabolism Enzymes in Eukaryotes. Frontiers in Microbiology, 2016, 7, 2001.	1.5	28
122	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	3.8	131
123	Secondary structure impacts patterns of selection in human lncRNAs. BMC Biology, 2016, 14, 60.	1.7	43
124	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	9.0	198
125	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. Current Biology, 2016, 26, 1577-1584.	1.8	175
126	spongeScan: A web for detecting microRNA binding elements in lncRNA sequences. Nucleic Acids Research, 2016, 44, W176-W180.	6.5	92

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127	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. Genome Biology, 2016, 17, 32.	3.8	166
128	Redundans: an assembly pipeline for highly heterozygous genomes. Nucleic Acids Research, 2016, 44, e113-e113.	6.5	429
129	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
130	Evolutionary genomics of yeast pathogens in the Saccharomycotina. FEMS Yeast Research, 2016, 16, fow064.	1.1	102
131	<i>Lokiarchaeota</i>Marks the Transition between the Archaeal and Eukaryotic Selenocysteine Encoding Systems. Molecular Biology and Evolution, 2016, 33, 2441-2453.	3.5	39
132	High-Throughput Proteomics Reveals the Unicellular Roots of Animal Phosphosignaling and Cell Differentiation. Developmental Cell, 2016, 39, 186-197.	3.1	51
133	The Case of the Missing Ancient Fungal Polyploids. American Naturalist, 2016, 188, 602-614.	1.0	38
134	ArthropodaCyc: a CycADS powered collection of BioCyc databases to analyse and compare metabolism of arthropods. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw081.	1.4	22
135	Mitochondrial Carriers Link the Catabolism of Hydroxyaromatic Compounds to the Central Metabolism in Candida parapsilosis. G3: Genes, Genomes, Genetics, 2016, 6, 4047-4058.	0.8	7
136	Whole genome sequencing of turbot (<i>Scophthalmus maximus</i>; Pleuronectiformes): a fish adapted to demersal life. DNA Research, 2016, 23, 181-192.	1.5	150
137	Horizontal acquisition of toxic alkaloid synthesis in a clade of plant associated fungi. Fungal Genetics and Biology, 2016, 86, 71-80.	0.9	26
138	Genome sequencing and secondary metabolism of the postharvest pathogen Penicillium griseofulvum. BMC Genomics, 2016, 17, 19.	1.2	70
139	Genome sequence of the olive tree, Olea europaea. GigaScience, 2016, 5, 29.	3.3	201
140	The birth of a deadly yeast: tracing the evolutionary emergence of virulence traits in<i>Candida glabrata</i>. FEMS Yeast Research, 2016, 16, fov110.	1.1	123
141	Contrasting patterns of evolutionary diversification in the olfactory repertoires of reptile and bird genomes. Genome Biology and Evolution, 2016, 8, evw013.	1.1	28
142	Peroxisomes in parasitic protists. Molecular and Biochemical Parasitology, 2016, 209, 35-45.	0.5	47
143	Late acquisition of mitochondria by a host with chimaeric prokaryotic ancestry. Nature, 2016, 531, 101-104.	13.7	204
144	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

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145	The Leishmania metaphylome: a comprehensive survey of Leishmania protein phylogenetic relationships. BMC Genomics, 2015, 16, 887.	1.2	21
146	Origin, diversification and substrate specificity in the family of <scp>NCS</scp>1/<scp>FUR</scp> transporters. Molecular Microbiology, 2015, 96, 927-950.	1.2	56
147	Differential gene retention as an evolutionary mechanism to generate biodiversity and adaptation in yeasts. Scientific Reports, 2015, 5, 11571.	1.6	50
148	The <i>Solanum commersonii</i> Genome Sequence Provides Insights into Adaptation to Stress Conditions and Genome Evolution of Wild Potato Relatives. Plant Cell, 2015, 27, 954-968.	3.1	149
149	Metabolic gene clusters encoding the enzymes of two branches of the 3-oxoadipate pathway in the pathogenic yeast Candida albicans. FEMS Yeast Research, 2015, 15, .	1.1	20
150	Origin and evolution of metabolic sub-cellular compartmentalization in eukaryotes. Biochimie, 2015, 119, 262-268.	1.3	101
151	Sex and parasites: genomic and transcriptomic analysis of Microbotryum lychnidis-dioicae, the biotrophic and plant-castrating anther smut fungus. BMC Genomics, 2015, 16, 461.	1.2	58
152	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.	3.3	192
153	Interactions between Closely Related Bacterial Strains Are Revealed by Deep Transcriptome Sequencing. Applied and Environmental Microbiology, 2015, 81, 8445-8456.	1.4	40
154	Evolution of selenophosphate synthetases: emergence and relocation of function through independent duplications and recurrent subfunctionalization. Genome Research, 2015, 25, 1256-1267.	2.4	46
155	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. Genome Biology and Evolution, 2015, 7, 1988-1999.	1.1	25
156	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.	1.4	183
157	The complete mitochondrial genome of the Giant Manta ray,Manta birostris. Mitochondrial DNA, 2015, 26, 787-788.	0.6	4
158	From community approaches to single-cell genomics: the discovery of ubiquitous hyperhalophilic <i>Bacteroidetes</i> generalists. ISME Journal, 2015, 9, 16-31.	4.4	51
159	Beyond the Whole-Genome Duplication: Phylogenetic Evidence for an Ancient Interspecies Hybridization in the Baker's Yeast Lineage. PLoS Biology, 2015, 13, e1002220.	2.6	321
160	The Genomic Aftermath of Hybridization in the Opportunistic Pathogen Candida metapsilosis. PLoS Genetics, 2015, 11, e1005626.	1.5	139
161	The Genome of the Generalist Plant Pathogen Fusarium avenaceum Is Enriched with Genes Involved in Redox, Signaling and Secondary Metabolism. PLoS ONE, 2014, 9, e112703.	1.1	78
162	Highly expressed captured genes and cross-kingdom domains present in Helitrons create novel diversity in Pleurotus ostreatus and other fungi. BMC Genomics, 2014, 15, 1071.	1.2	20

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163	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede Strigamia maritima. PLoS Biology, 2014, 12, e1002005.	2.6	221
164	Big data and other challenges in the quest for orthologs. Bioinformatics, 2014, 30, 2993-2998.	1.8	109
165	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
166	Systematic Phenotyping of a Large-Scale Candida glabrata Deletion Collection Reveals Novel Antifungal Tolerance Genes. PLoS Pathogens, 2014, 10, e1004211.	2.1	155
167	Transcriptomic analysis of a psammophyte food crop, sand rice (Agriophyllum squarrosum) and identification of candidate genes essential for sand dune adaptation. BMC Genomics, 2014, 15, 872.	1.2	27
168	Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. Science, 2014, 346, 1254449.	6.0	300
169	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	6.0	1,583
170	A phylogenomics approach for selecting robust sets of phylogenetic markers. Nucleic Acids Research, 2014, 42, e54-e54.	6.5	45
171	Inferring gene function from evolutionary change in signatures of translation efficiency. Genome Biology, 2014, 15, R44.	13.9	53
172	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. Nucleic Acids Research, 2014, 42, D897-D902.	6.5	264
173	eggNOG v4.0: nested orthology inference across 3686 organisms. Nucleic Acids Research, 2014, 42, D231-D239.	6.5	526
174	Genome Comparison of Candida orthopsilosis Clinical Strains Reveals the Existence of Hybrids between Two Distinct Subspecies. Genome Biology and Evolution, 2014, 6, 1069-1078.	1.1	138
175	A metabolic scenario for the evolutionary origin of peroxisomes from the endomembranous system. Cellular and Molecular Life Sciences, 2014, 71, 2373-2376.	2.4	19
176	Synonymous Mutations Frequently Act as Driver Mutations in Human Cancers. Cell, 2014, 156, 1324-1335.	13.5	482
177	The genome of the recently domesticated crop plant sugar beet (Beta vulgaris). Nature, 2014, 505, 546-549.	13.7	569
178	High Variability of Mitochondrial Gene Order among Fungi. Genome Biology and Evolution, 2014, 6, 451-465.	1.1	223
179	Evolutionary considerations on the origin of peroxisomes from the endoplasmic reticulum, and their relationships with mitochondria. Cellular and Molecular Life Sciences, 2014, 71, 2379-2382.	2.4	13
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