Toni Gabaldn

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

262	19,938	69	137
papers	citations	h-index	g-index
316	27,382	9.4	7.38
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
262	trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. *Bioinformatics*, **2009**, 25, 1972-3	7.2	4232
261	Whole-genome analyses resolve early branches in the tree of life of modern birds. *Science*, **2014**, 346, 1320-31	33.3	1182
260	Genome sequence of the pea aphid Acyrthosiphon pisum. *PLoS Biology*, **2010**, 8, e1000313	9.7	732
259	The genome of melon (Cucumis melo L.). *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 11872-7	11.5	462
258	eggNOG v4.0: nested orthology inference across 3686 organisms. *Nucleic Acids Research*, **2014**, 42, D231-9	20.1	387
257	Synonymous mutations frequently act as driver mutations in human cancers. *Cell*, **2014**, 156, 1324-1335	56.2	369
256	The genome of the recently domesticated crop plant sugar beet (Beta vulgaris). *Nature*, **2014**, 505, 546-9	50.4	365
255	Functional and evolutionary implications of gene orthology. *Nature Reviews Genetics*, **2013**, 14, 360-6	30.1	327
254	Immunity and other defenses in pea aphids, Acyrthosiphon pisum. *Genome Biology*, **2010**, 11, R21	18.3	304
253	ETE: a python Environment for Tree Exploration. *BMC Bioinformatics*, **2010**, 11, 24	3.6	290
252	Redundans: an assembly pipeline for highly heterozygous genomes. *Nucleic Acids Research*, **2016**, 44, e113	20.1	240
251	Genome structure and metabolic features in the red seaweed Chondrus crispus shed light on evolution of the Archaeplastida. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 5247-52	11.5	239
250	Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. *Science*, **2014**, 346, 1254449	33.3	231
249	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. *Genome Biology*, **2016**, 17, 184	18.3	218
248	An anaerobic mitochondrion that produces hydrogen. *Nature*, **2005**, 434, 74-9	50.4	213
247	Rapid transcriptional plasticity of duplicated gene clusters enables a clonally reproducing aphid to colonise diverse plant species. *Genome Biology*, **2017**, 18, 27	18.3	208
246	Tracing the evolution of a large protein complex in the eukaryotes, NADH:ubiquinone oxidoreductase (Complex I). *Journal of Molecular Biology*, **2005**, 348, 857-70	6.5	197

245	Beyond the Whole-Genome Duplication: Phylogenetic Evidence for an Ancient Interspecies Hybridization in the Baker's Yeast Lineage. *PLoS Biology*, **2015**, 13, e1002220	9.7	186
244	The first myriapod genome sequence reveals conservative arthropod gene content and genome organisation in the centipede Strigamia maritima. *PLoS Biology*, **2014**, 12, e1002005	9.7	182
243	Acquisition of prokaryotic genes by fungal genomes. *Trends in Genetics*, **2010**, 26, 5-8	8.5	181
242	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. *Nucleic Acids Research*, **2014**, 42, D897-902	20.1	171
241	Late acquisition of mitochondria by a host with chimaeric prokaryotic ancestry. *Nature*, **2016**, 531, 101-4	50.4	161
240	Genome sequence of the necrotrophic fungus Penicillium digitatum, the main postharvest pathogen of citrus. *BMC Genomics*, **2012**, 13, 646	4.5	158
239	Reconstruction of the proto-mitochondrial metabolism. *Science*, **2003**, 301, 609	33.3	144
238	Phylogenomics supports microsporidia as the earliest diverging clade of sequenced fungi. *BMC Biology*, **2012**, 10, 47	7.3	143
237	Genome, Transcriptome, and Functional Analyses of Penicillium expansum Provide New Insights Into Secondary Metabolism and Pathogenicity. *Molecular Plant-Microbe Interactions*, **2015**, 28, 232-48	3.6	140
236	High variability of mitochondrial gene order among fungi. *Genome Biology and Evolution*, **2014**, 6, 451-65	3.9	134
235	Large-scale assignment of orthology: back to phylogenetics?. *Genome Biology*, **2008**, 9, 235	18.3	134
234	Peroxisome diversity and evolution. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2010**, 365, 765-73	5.8	133
233	Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. *Nucleic Acids Research*, **2011**, 39, W470-4	20.1	133
232	Standardized benchmarking in the quest for orthologs. *Nature Methods*, **2016**, 13, 425-30	21.6	133
231	Origin and evolution of the peroxisomal proteome. *Biology Direct*, **2006**, 1, 8	7.2	132
230	Genome sequence of the olive tree, Olea europaea. *GigaScience*, **2016**, 5, 29	7.6	130
229	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, 13970-5	11.5	127
228	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, D556-60	20.1	125

227	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	18.3	124
226	Comparative genomics of emerging pathogens in the Candida glabrata clade. *BMC Genomics*, **2013**, 14, 623	4.5	120
225	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. *Current Biology*, **2016**, 26, 1577-1584	6.3	119
224	Eukaryotic cold shock domain proteins: highly versatile regulators of gene expression. *BioEssays*, **2010**, 32, 109-18	4.1	117
223	Transcriptome analyses of primitively eusocial wasps reveal novel insights into the evolution of sociality and the origin of alternative phenotypes. *Genome Biology*, **2013**, 14, R20	18.3	114
222	The Solanum commersonii Genome Sequence Provides Insights into Adaptation to Stress Conditions and Genome Evolution of Wild Potato Relatives. *Plant Cell*, **2015**, 27, 954-68	11.6	112
221	Systematic phenotyping of a large-scale Candida glabrata deletion collection reveals novel antifungal tolerance genes. *PLoS Pathogens*, **2014**, 10, e1004211	7.6	111
220	The human phylome. *Genome Biology*, **2007**, 8, R109	18.3	111
219	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	8.3	105
218	Whole genome sequencing of turbot (Scophthalmus maximus; Pleuronectiformes): a fish adapted to demersal life. *DNA Research*, **2016**, 23, 181-92	4.5	103
217	Microbiome and colorectal cancer: Roles in carcinogenesis and clinical potential. *Molecular Aspects of Medicine*, **2019**, 69, 93-106	16.7	101
216	Shaping the mitochondrial proteome. *Biochimica Et Biophysica Acta - Bioenergetics*, **2004**, 1659, 212-20	4.6	101
215	Ancient dispersal of the human fungal pathogen Cryptococcus gattii from the Amazon rainforest. *PLoS ONE*, **2013**, 8, e71148	3.7	100
214	Fungal evolution: diversity, taxonomy and phylogeny of the Fungi. *Biological Reviews*, **2019**, 94, 2101-2137	13.5	99
213	The Human Oral Microbiome in Health and Disease: From Sequences to Ecosystems. *Microorganisms*, **2020**, 8,	4.9	94
212	From Saccharomyces cerevisiae to Candida glabratain a few easy steps: important adaptations for an opportunistic pathogen. *FEMS Microbiology Letters*, **2011**, 314, 1-9	2.9	94
211	MetaPhOrs: orthology and paralogy predictions from multiple phylogenetic evidence using a consistency-based confidence score. *Nucleic Acids Research*, **2011**, 39, e32	20.1	94
210	Candida parapsilosis: from Genes to the Bedside. *Clinical Microbiology Reviews*, **2019**, 32,	34	93

209	The genome of wine yeast Dekkera bruxellensis provides a tool to explore its food-related properties. *International Journal of Food Microbiology*, **2012**, 157, 202-9	5.8	85
208	From endosymbiont to host-controlled organelle: the hijacking of mitochondrial protein synthesis and metabolism. *PLoS Computational Biology*, **2007**, 3, e219	5	85
207	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. *Genome Biology*, **2016**, 17, 251	18.3	85
206	Fungal evolution: major ecological adaptations and evolutionary transitions. *Biological Reviews*, **2019**, 94, 1443-1476	13.5	82
205	PeroxisomeDB 2.0: an integrative view of the global peroxisomal metabolome. *Nucleic Acids Research*, **2010**, 38, D800-5	20.1	81
204	Evolutionary Emergence of Drug Resistance in Candida Opportunistic Pathogens. *Genes*, **2018**, 9,	4.2	81
203	Gene flow contributes to diversification of the major fungal pathogen Candida albicans. *Nature Communications*, **2018**, 9, 2253	17.4	80
202	Genomic history of the origin and domestication of common bean unveils its closest sister species. *Genome Biology*, **2017**, 18, 60	18.3	79
201	PhylomeDB: a database for genome-wide collections of gene phylogenies. *Nucleic Acids Research*, **2008**, 36, D491-6	20.1	79
200	Prediction of protein function and pathways in the genome era. *Cellular and Molecular Life Sciences*, **2004**, 61, 930-44	10.3	79
199	Genome comparison of Candida orthopsilosis clinical strains reveals the existence of hybrids between two distinct subspecies. *Genome Biology and Evolution*, **2014**, 6, 1069-78	3.9	77
198	Genetically encodable bioluminescent system from fungi. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 12728-12732	11.5	77
197	The Genomic Aftermath of Hybridization in the Opportunistic Pathogen Candida metapsilosis. *PLoS Genetics*, **2015**, 11, e1005626	6	72
196	A midzone-based ruler adjusts chromosome compaction to anaphase spindle length. *Science*, **2011**, 332, 465-8	33.3	70
195	The tree versus the forest: the fungal tree of life and the topological diversity within the yeast phylome. *PLoS ONE*, **2009**, 4, e4357	3.7	69
194	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. *Science Advances*, **2017**, 3, e1700299	14.3	67
193	Origin and evolution of metabolic sub-cellular compartmentalization in eukaryotes. *Biochimie*, **2015** , 119, 262-8	4.6	66
192	The genome and development-dependent transcriptomes of Pyronema confluens: a window into fungal evolution. *PLoS Genetics*, **2013**, 9, e1003820	6	65

191	Combining data from genomes, Y2H and 3D structure indicates that BolA is a reductase interacting with a glutaredoxin. *FEBS Letters*, **2005**, 579, 591-6	3.8	64
190	PeroxisomeDB: a database for the peroxisomal proteome, functional genomics and disease. *Nucleic Acids Research*, **2007**, 35, D815-22	20.1	63
189	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	6.3	61
188	A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. *Nature Genetics*, **2019**, 51, 1607-1615	36.3	59
187	spongeScan: A web for detecting microRNA binding elements in lncRNA sequences. *Nucleic Acids Research*, **2016**, 44, W176-80	20.1	59
186	Fine-scale evolution: genomic, phenotypic and ecological differentiation in two coexisting Salinibacter ruber strains. *ISME Journal*, **2010**, 4, 882-95	11.9	58
185	Phylogenomics of the oxidative phosphorylation in fungi reveals extensive gene duplication followed by functional divergence. *BMC Evolutionary Biology*, **2009**, 9, 295	3	58
184	Regulation of Candida glabrata oxidative stress resistance is adapted to host environment. *FEBS Letters*, **2011**, 585, 319-27	3.8	57
183	Evolutionary genomics of yeast pathogens in the Saccharomycotina. *FEMS Yeast Research*, **2016**, 16,	3.1	56
182	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	6	55
181	Genome sequencing and secondary metabolism of the postharvest pathogen Penicillium griseofulvum. *BMC Genomics*, **2016**, 17, 19	4.5	54
180	YibK is the 2RO-methyltransferase TrmL that modifies the wobble nucleotide in Escherichia coli tRNA(Leu) isoacceptors. *Rna*, **2010**, 16, 2131-43	5.8	53
179	The birth of a deadly yeast: tracing the evolutionary emergence of virulence traits in Candida glabrata. *FEMS Yeast Research*, **2016**, 16, fov110	3.1	52
178	Long Non-Coding RNAs As Potential Novel Prognostic Biomarkers in Colorectal Cancer. *Frontiers in Genetics*, **2016**, 7, 54	4.5	52
177	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	3.7	51
176	The complete genome of Blastobotrys (Arxula) adeninivorans LS3 - a yeast of biotechnological interest. *Biotechnology for Biofuels*, **2014**, 7, 66	7.8	50
175	The kinomes of apicomplexan parasites. *Microbes and Infection*, **2012**, 14, 796-810	9.3	48
174	Skin microbiome modulation induced by probiotic solutions. *Microbiome*, **2019**, 7, 95	16.6	46

173	Recent trends in molecular diagnostics of yeast infections: from PCR to NGS. *FEMS Microbiology Reviews*, **2019**, 43, 517-547	15.1	45
172	Phylemon: a suite of web tools for molecular evolution, phylogenetics and phylogenomics. *Nucleic Acids Research*, **2007**, 35, W38-42	20.1	45
171	Hybridization and emergence of virulence in opportunistic human yeast pathogens. *Yeast*, **2018**, 35, 5-20	3.4	45
170	Sex and parasites: genomic and transcriptomic analysis of Microbotryum lychnidis-dioicae, the biotrophic and plant-castrating anther smut fungus. *BMC Genomics*, **2015**, 16, 461	4.5	44
169	2x genomes--depth does matter. *Genome Biology*, **2010**, 11, R16	18.3	44
168	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. *Genome Biology*, **2020**, 21, 275	18.3	42
167	Biological Processes Modulating Longevity across Primates: A Phylogenetic Genome-Phenome Analysis. *Molecular Biology and Evolution*, **2018**, 35, 1990-2004	8.3	42
166	Assigning duplication events to relative temporal scales in genome-wide studies. *Bioinformatics*, **2011**, 27, 38-45	7.2	41
165	Citizen science charts two major "stomatotypes" in the oral microbiome of adolescents and reveals links with habits and drinking water composition. *Microbiome*, **2018**, 6, 218	16.6	41
164	Evolution of selenophosphate synthetases: emergence and relocation of function through independent duplications and recurrent subfunctionalization. *Genome Research*, **2015**, 25, 1256-67	9.7	39
163	Peroxisomes in parasitic protists. *Molecular and Biochemical Parasitology*, **2016**, 209, 35-45	1.9	39
162	Origin, diversification and substrate specificity in the family of NCS1/FUR transporters. *Molecular Microbiology*, **2015**, 96, 927-50	4.1	39
161	Unexpected genomic variability in clinical and environmental strains of the pathogenic yeast Candida parapsilosis. *Genome Biology and Evolution*, **2013**, 5, 2382-92	3.9	38
160	Structural analyses of a hypothetical minimal metabolism. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2007**, 362, 1751-62	5.8	38
159	From community approaches to single-cell genomics: the discovery of ubiquitous hyperhalophilic Bacteroidetes generalists. *ISME Journal*, **2015**, 9, 16-31	11.9	37
158	Inferring gene function from evolutionary change in signatures of translation efficiency. *Genome Biology*, **2014**, 15, R44	18.3	37
157	Differential gene retention as an evolutionary mechanism to generate biodiversity and adaptation in yeasts. *Scientific Reports*, **2015**, 5, 11571	4.9	36
156	Comparative transcriptomics of early dipteran development. *BMC Genomics*, **2013**, 14, 123	4.5	35

155	Evidence for short-time divergence and long-time conservation of tissue-specific expression after gene duplication. *Briefings in Bioinformatics*, **2011**, 12, 442-8	13.4	35
154	The Quiet and Underappreciated Rise of Drug-Resistant Invasive Fungal Pathogens. *Journal of Fungi (Basel, Switzerland)*, **2020**, 6,	5.6	35
153	Secondary structure impacts patterns of selection in human lncRNAs. *BMC Biology*, **2016**, 14, 60	7.3	35
152	Gene gain and loss across the metazoan tree of life. *Nature Ecology and Evolution*, **2020**, 4, 524-533	12.3	34
151	High-Throughput Proteomics Reveals the Unicellular Roots of Animal Phosphosignaling and Cell Differentiation. *Developmental Cell*, **2016**, 39, 186-197	10.2	34
150	TreeKO: a duplication-aware algorithm for the comparison of phylogenetic trees. *Nucleic Acids Research*, **2011**, 39, e66	20.1	34
149	Complete DNA sequence of Kuraishia capsulata illustrates novel genomic features among budding yeasts (Saccharomycotina). *Genome Biology and Evolution*, **2013**, 5, 2524-39	3.9	33
148	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	6.9	33
147	Genomes shed light on the secret life of Candida glabrata: not so asexual, not so commensal. *Current Genetics*, **2019**, 65, 93-98	2.9	32
146	A phylogenomics approach for selecting robust sets of phylogenetic markers. *Nucleic Acids Research*, **2014**, 42, e54	20.1	32
145	Lokiarchaeota Marks the Transition between the Archaeal and Eukaryotic Selenocysteine Encoding Systems. *Molecular Biology and Evolution*, **2016**, 33, 2441-53	8.3	31
144	Contrasting Genomic Diversity in Two Closely Related Postharvest Pathogens: Penicillium digitatum and Penicillium expansum. *Genome Biology and Evolution*, **2015**, 8, 218-27	3.9	31
143	TACC3-TSC2 maintains nuclear envelope structure and controls cell division. *Cell Cycle*, **2010**, 9, 1143-55	4.7	30
142	Impact of Homologous Recombination on the Evolution of Prokaryotic Core Genomes. *MBio*, **2019**, 10,	7.8	29
141	Pathogenic mutations in the 5Runtranslated region of BCS1L mRNA in mitochondrial complex III deficiency. *Mitochondrion*, **2009**, 9, 299-305	4.9	29
140	Utilization of selenocysteine in early-branching fungal phyla. *Nature Microbiology*, **2019**, 4, 759-765	26.6	28
139	Drug-Resistant Fungi: An Emerging Challenge Threatening Our Limited Antifungal Armamentarium. *Antibiotics*, **2020**, 9,	4.9	28
138	Induces Plant-Dependent Systemic Resistance to. *Frontiers in Plant Science*, **2019**, 10, 945	6.2	28

137	Impact of the mitochondrial genetic background in complex III deficiency. *PLoS ONE*, **2010**, 5, e12801	3.7	27
136	Fungal evolution: cellular, genomic and metabolic complexity. *Biological Reviews*, **2020**, 95, 1198-1232	13.5	27
135	Lineage-specific gene loss following mitochondrial endosymbiosis and its potential for function prediction in eukaryotes. *Bioinformatics*, **2005**, 21 Suppl 2, ii144-50	7.2	25
134	Gearing up to handle the mosaic nature of life in the quest for orthologs. *Bioinformatics*, **2018**, 34, 323-329	7.2	25
133	Whole-Genome Sequencing of the Opportunistic Yeast Pathogen Uncovers Its Hybrid Origin. *Frontiers in Genetics*, **2019**, 10, 383	4.5	24
132	The Case of the Missing Ancient Fungal Polyploids. *American Naturalist*, **2016**, 188, 602-614	3.7	23
131	The Schistosoma mansoni phylome: using evolutionary genomics to gain insight into a parasite's biology. *BMC Genomics*, **2012**, 13, 617	4.5	23
130	Comparison of gene repertoires and patterns of evolutionary rates in eight aphid species that differ by reproductive mode. *Genome Biology and Evolution*, **2012**, 4, 155-67	3.9	22
129	Interactions between closely related bacterial strains are revealed by deep transcriptome sequencing. *Applied and Environmental Microbiology*, **2015**, 81, 8445-56	4.8	21
128	Genomic evidence for a hybrid origin of the yeast opportunistic pathogen Candida albicans. *BMC Biology*, **2020**, 18, 48	7.3	21
127	Horizontal acquisition of toxic alkaloid synthesis in a clade of plant associated fungi. *Fungal Genetics and Biology*, **2016**, 86, 71-80	3.9	21
126	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	4.5	21
125	Evolution of spliceosomal introns following endosymbiotic gene transfer. *BMC Evolutionary Biology*, **2010**, 10, 57	3	21
124	Relative timing of mitochondrial endosymbiosis and the "pre-mitochondrial symbioses" hypothesis. *IUBMB Life*, **2018**, 70, 1188-1196	4.7	20
123	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. *Genome Biology and Evolution*, **2015**, 7, 1988-99	3.9	19
122	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	7.3	19
121	Genome Comparisons of Serial Clinical Isolates Reveal Patterns of Genetic Variation in Infecting Clonal Populations. *Frontiers in Microbiology*, **2019**, 10, 112	5.7	19
120	Commercial Formulates of Induce Systemic Plant Resistance to in Tomato and the Effect Is Additive to That of the Resistance Gene. *Frontiers in Microbiology*, **2019**, 10, 3042	5.7	18

119	Misidentification of genome assemblies in public databases: The case of Naumovozyma dairenensis and proposal of a protocol to correct misidentifications. *Yeast*, **2018**, 35, 425-429	3.4	18
118	Investigation of Candida parapsilosis virulence regulatory factors during host-pathogen interaction. *Scientific Reports*, **2018**, 8, 1346	4.9	17
117	Phylogenomics of the olive tree (Olea europaea) reveals the relative contribution of ancient allo- and autopolyploidization events. *BMC Biology*, **2018**, 16, 15	7.3	17
116	Mitochondrial genome variability within the Candida parapsilosis species complex. *Mitochondrion*, **2012**, 12, 514-9	4.9	17
115	Comparative genomics-based prediction of protein function. *Methods in Molecular Biology*, **2008**, 439, 387-401	1.4	17
114	Hybridization and the origin of new yeast lineages. *FEMS Yeast Research*, **2020**, 20,	3.1	17
113	Timing the origin of eukaryotic cellular complexity with ancient duplications. *Nature Ecology and Evolution*, **2021**, 5, 92-100	12.3	17
112	A metabolic scenario for the evolutionary origin of peroxisomes from the endomembranous system. *Cellular and Molecular Life Sciences*, **2014**, 71, 2373-6	10.3	16
111	Evolution of Proteins and Proteomes: A Phylogenetics Approach. *Evolutionary Bioinformatics*, **2005**, 1, 117693430500100	1.9	16
110	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	26.6	16
109	MICU1 Confers Protection from MCU-Dependent Manganese Toxicity. *Cell Reports*, **2018**, 25, 1425-1435.e7	10.6	16
108	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,	3.1	15
107	Coronavirus Disease 2019 (COVID-19): Emerging and Future Challenges for Dental and Oral Medicine. *Journal of Dental Research*, **2020**, 99, 1113	8.1	15
106	Computational approaches for the prediction of protein function in the mitochondrion. *American Journal of Physiology - Cell Physiology*, **2006**, 291, C1121-8	5.4	15
105	Evolution of proteins and proteomes: a phylogenetics approach. *Evolutionary Bioinformatics*, **2007**, 1, 51-61	1.9	15
104	Evolutionary and functional patterns of shared gene neighbourhood in fungi. *Nature Microbiology*, **2019**, 4, 2383-2392	26.6	14
103	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	7.8	14
102	PTP-central: a comprehensive resource of protein tyrosine phosphatases in eukaryotic genomes. *Methods*, **2014**, 65, 156-64	4.6	14

101	Genomic evidence for recurrent genetic admixture during the domestication of Mediterranean olive trees (Olea europaea L.). *BMC Biology*, **2020**, 18, 148	7.3	14
100	Widespread Inter- and Intra-Domain Horizontal Gene Transfer of d-Amino Acid Metabolism Enzymes in Eukaryotes. *Frontiers in Microbiology*, **2016**, 7, 2001	5.7	14
99	Lack of the PGA exopolysaccharide in Salmonella as an adaptive trait for survival in the host. *PLoS Genetics*, **2017**, 13, e1006816	6	13
98	Contrasting Patterns of Evolutionary Diversification in the Olfactory Repertoires of Reptile and Bird Genomes. *Genome Biology and Evolution*, **2016**, 8, 470-80	3.9	13
97	Evolutionary considerations on the origin of peroxisomes from the endoplasmic reticulum, and their relationships with mitochondria. *Cellular and Molecular Life Sciences*, **2014**, 71, 2379-82	10.3	13
96	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	4.5	13
95	CycADS: an annotation database system to ease the development and update of BioCyc databases. *Database: the Journal of Biological Databases and Curation*, **2011**, 2011, bar008	5	13
94	Genome Sequence of the Brown Rot Fungal Pathogen Monilinia laxa. *Genome Announcements*, **2018** , 6,		13
93	nextPARS: parallel probing of RNA structures in Illumina. *Rna*, **2018**, 24, 609-619	5.8	12
92	Eicosanoid biosynthesis influences the virulence of Candida parapsilosis. *Virulence*, **2018**, 9, 1019-1035	4.7	12
91	Measuring guide-tree dependency of inferred gaps in progressive aligners. *Bioinformatics*, **2013**, 29, 1011-7	7.2	12
90	Lack of phylogenetic support for a supposed actinobacterial origin of peroxisomes. *Gene*, **2010**, 465, 61-5	3.8	12
89	Variation and evolution of biomolecular systems: searching for functional relevance. *FEBS Letters*, **2005**, 579, 1839-45	3.8	12
88	The Leishmania metaphylome: a comprehensive survey of Leishmania protein phylogenetic relationships. *BMC Genomics*, **2015**, 16, 887	4.5	11
87	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	3.5	11
86	Evolutionary histories of expanded peptidase families in Schistosoma mansoni. *Memorias Do Instituto Oswaldo Cruz*, **2011**, 106, 864-77	2.6	11
85	Massive gene presence/absence variation in the mussel genome as an adaptive strategy: first evidence of a pan-genome in Metazoa		11
84	Strain I-1582, a Nematode Antagonist by Itself and Through the Plant. *Frontiers in Plant Science*, **2020**, 11, 796	6.2	10

83	Integrative Omics Analysis Reveals a Limited Transcriptional Shock After Yeast Interspecies Hybridization. *Frontiers in Genetics*, **2020**, 11, 404	4.5	10
82	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,	5	10
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