

David A Fitzpatrick

List of Publications by Year in descending order

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75
papers

4,385
citations

159525

30
h-index

114418

63
g-index

79
all docs

79
docs citations

79
times ranked

6134
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. <i>Nature</i> , 2009, 459, 657-662.	13.7	963
2	A fungal phylogeny based on 42 complete genomes derived from supertree and combined gene analysis. <i>BMC Evolutionary Biology</i> , 2006, 6, 99.	3.2	428
3	Genome of <i>Acanthamoeba castellanii</i> highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. <i>Genome Biology</i> , 2013, 14, R11.	13.9	296
4	Horizontal gene transfer in fungi. <i>FEMS Microbiology Letters</i> , 2012, 329, 1-8.	0.7	262
5	Genome expansion and lineage-specific genetic innovations in the forest pathogenic fungi <i>Armillaria</i> . <i>Nature Ecology and Evolution</i> , 2017, 1, 1931-1941.	3.4	145
6	Genome Phylogenies Indicate a Meaningful $\hat{\pm}$ -Proteobacterial Phylogeny and Support a Grouping of the Mitochondria with the Rickettsiales. <i>Molecular Biology and Evolution</i> , 2006, 23, 74-85.	3.5	133
7	Antibiotic resistance genes across a wide variety of metagenomes. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv168.	1.3	129
8	Fatty acid biosynthesis in <i>Mycobacterium tuberculosis</i> : Lateral gene transfer, adaptive evolution, and gene duplication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10320-10325.	3.3	119
9	Does a tree-like phylogeny only exist at the tips in the prokaryotes?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2004, 271, 2551-2558.	1.2	114
10	The copper regulon of the human fungal pathogen <i>Cryptococcus neoformans</i> H99. <i>Molecular Microbiology</i> , 2011, 81, 1560-1576.	1.2	105
11	Universally Distributed Single-Copy Genes Indicate a Constant Rate of Horizontal Transfer. <i>PLoS ONE</i> , 2011, 6, e22099.	1.1	99
12	Analysis of gene evolution and metabolic pathways using the <i>Candida</i> Gene Order Browser. <i>BMC Genomics</i> , 2010, 11, 290.	1.2	86
13	Genomic and Proteomic Dissection of the Ubiquitous Plant Pathogen, <i>Armillaria mellea</i> : Toward a New Infection Model System. <i>Journal of Proteome Research</i> , 2013, 12, 2552-2570.	1.8	85
14	Phylogenomic Reconstruction of the Oomycete Phylogeny Derived from 37 Genomes. <i>MSphere</i> , 2017, 2, .	1.3	84
15	Regulation of Nonribosomal Peptide Synthesis: bis-Thiomethylation Attenuates Gliotoxin Biosynthesis in <i>Aspergillus fumigatus</i> . <i>Chemistry and Biology</i> , 2014, 21, 999-1012.	6.2	79
16	Genomic, Network, and Phylogenetic Analysis of the Oomycete Effector Arsenal. <i>MSphere</i> , 2017, 2, .	1.3	64
17	The anhydrobiotic potential and molecular phylogenetics of species and strains of <i>Panagrolaimus</i> (Nematoda, Panagrolaimidae). <i>Journal of Experimental Biology</i> , 2005, 208, 2433-2445.	0.8	60
18	Pan-genome analyses of model fungal species. <i>Microbial Genomics</i> , 2019, 5, .	1.0	59

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19	Evidence of recent interkingdom horizontal gene transfer between bacteria and <i>Candida parapsilosis</i> . <i>BMC Evolutionary Biology</i> , 2008, 8, 181.	3.2	57
20	Evolution of flower shape in <i>Plantago lanceolata</i> . <i>Plant Molecular Biology</i> , 2009, 71, 241-250.	2.0	49
21	The evolutionary history of the genes involved in the biosynthesis of the antioxidant ergothioneine. <i>Gene</i> , 2014, 549, 161-170.	1.0	48
22	Interplay between Gliotoxin Resistance, Secretion, and the Methyl/Methionine Cycle in <i>Aspergillus fumigatus</i> . <i>Eukaryotic Cell</i> , 2015, 14, 941-957.	3.4	48
23	RNA-seq reveals the pan-transcriptomic impact of attenuating the gliotoxin self-protection mechanism in <i>Aspergillus fumigatus</i> . <i>BMC Genomics</i> , 2014, 15, 894.	1.2	44
24	Reconstructing the Fungal Tree of Life Using Phylogenomics and a Preliminary Investigation of the Distribution of Yeast Prion-Like Proteins in the Fungal Kingdom. <i>Journal of Molecular Evolution</i> , 2011, 73, 116-133.	0.8	43
25	Multiple lineage specific expansions within the guanylyl cyclase gene family. <i>BMC Evolutionary Biology</i> , 2006, 6, 26.	3.2	42
26	Lines of Evidence for Horizontal Gene Transfer of a Phenazine Producing Operon into Multiple Bacterial Species. <i>Journal of Molecular Evolution</i> , 2009, 68, 171-185.	0.8	37
27	Epidemiological and virological investigations of equine influenza outbreaks in Ireland (2010–2012). <i>Influenza and Other Respiratory Viruses</i> , 2013, 7, 61-72.	1.5	37
28	A Pluralistic Account of Homology: Adapting the Models to the Data. <i>Molecular Biology and Evolution</i> , 2014, 31, 501-516.	3.5	37
29	Global transcript and phenotypic analysis of yeast cells expressing <i>Ssa1</i> , <i>Ssa2</i> , <i>Ssa3</i> or <i>Ssa4</i> as sole source of cytosolic Hsp70-Ssa chaperone activity. <i>BMC Genomics</i> , 2014, 15, 194.	1.2	36
30	Comparative Genomic and Proteomic Analyses of Three Widespread Phytophthora Species: <i>Phytophthora chlamydospora</i> , <i>Phytophthora gonapodyides</i> and <i>Phytophthora pseudosyringae</i> . <i>Microorganisms</i> , 2020, 8, 653.	1.6	36
31	Recent advances in oomycete genomics. <i>Advances in Genetics</i> , 2020, 105, 175-228.	0.8	36
32	Emergence and evolution of yeast prion and prion-like proteins. <i>BMC Evolutionary Biology</i> , 2016, 16, 24.	3.2	32
33	Different outcomes for the MYB floral symmetry genes <i>DIVARICATA</i> and <i>RADIALIS</i> during the evolution of derived actinomorphy in <i>Plantago</i> . <i>New Phytologist</i> , 2014, 202, 716-725.	3.5	28
34	Control of Development, Secondary Metabolism and Light-Dependent Carotenoid Biosynthesis by the Velvet Complex of <i>Neurospora crassa</i> . <i>Genetics</i> , 2019, 212, 691-710.	1.2	28
35	Cortical cartography revisited: a frequency perspective on the functional architecture of visual cortex. <i>Progress in Brain Research</i> , 2006, 154, 121-134.	0.9	26
36	The effect of entomopathogenic fungal culture filtrate on the immune response of the greater wax moth, <i>Galleria mellonella</i> . <i>Journal of Insect Physiology</i> , 2017, 100, 82-92.	0.9	26

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37	Proteome and allergenome of the European house dust mite <i>Dermatophagoides pteronyssinus</i> . PLoS ONE, 2019, 14, e0216171.	1.1	26
38	Systematic Search for Evidence of Interdomain Horizontal Gene Transfer from Prokaryotes to Oomycete Lineages. MSphere, 2016, 1, .	1.3	22
39	Multiple Approaches to Phylogenomic Reconstruction of the Fungal Kingdom. Advances in Genetics, 2017, 100, 211-266.	0.8	19
40	Towards understanding the gliotoxin detoxification mechanism: in vivo thiomethylation protects yeast from gliotoxin cytotoxicity. Microbial Cell, 2016, 3, 120-125.	1.4	19
41	Evidence of Positive Darwinian Selection in Omp85, a Highly Conserved Bacterial Outer Membrane Protein Essential for Cell Viability. Journal of Molecular Evolution, 2005, 60, 268-273.	0.8	18
42	The Molecular Phylogeny of a Nematode-Specific Clade of Heterotrimeric G-Protein β -Subunit Genes. Journal of Molecular Evolution, 2006, 63, 87-94.	0.8	18
43	Draft Genome Sequence of <i>Dermatophagoides pteronyssinus</i> , the European House Dust Mite. Genome Announcements, 2017, 5, .	0.8	18
44	Comparative Analysis of Oomycete Genome Evolution Using the Oomycete Gene Order Browser (OGOBS). Genome Biology and Evolution, 2019, 11, 189-206.	1.1	17
45	Insight into the Family of Na ⁺ /Ca ²⁺ Exchangers of <i>Caenorhabditis elegans</i> . Genetics, 2013, 195, 611-619.	1.2	16
46	Gene and genome trees conflict at many levels. Philosophical Transactions of the Royal Society B: Biological Sciences, 2009, 364, 2209-2219.	1.8	15
47	Evaluation of Whether Accelerated Protein Evolution in Chordates Has Occurred before, after, or Simultaneously with Gene Duplication. Molecular Biology and Evolution, 2006, 24, 315-323.	3.5	14
48	Pangloss: A Tool for Pan-Genome Analysis of Microbial Eukaryotes. Genes, 2019, 10, 521.	1.0	14
49	Assessment of Inactivating Stop Codon Mutations in Forty <i>Saccharomyces cerevisiae</i> Strains: Implications for [PSI ⁺] Prion-Mediated Phenotypes. PLoS ONE, 2011, 6, e28684.	1.1	13
50	Genome analysis of the yeast <i>Diutina catenulata</i> , a member of the Debaryomycetaceae/Metschnikowiaceae (CTG-Ser) clade. PLoS ONE, 2018, 13, e0198957.	1.1	13
51	Whole Genome Sequence of the Commercially Relevant Mushroom Strain <i>Agaricus bisporus</i> var. <i>bisporus</i> ARP23. G3: Genes, Genomes, Genetics, 2019, 9, 3057-3066.	0.8	13
52	Proteomic Characterization of <i>Armillaria mellea</i> Reveals Oxidative Stress Response Mechanisms and Altered Secondary Metabolism Profiles. Microorganisms, 2017, 5, 60.	1.6	12
53	Evolutionary, structural and functional analysis of the caleosin/peroxygenase gene family in the Fungi. BMC Genomics, 2018, 19, 976.	1.2	11
54	Transmission of mushroom virus X and the impact of virus infection on the transcriptomes and proteomes of different strains of <i>Agaricus bisporus</i> . Fungal Biology, 2021, 125, 704-717.	1.1	11

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55	The effect of entomopathogenic fungal culture filtrate on the immune response and haemolymph proteome of the large pine weevil, <i>Hylobius abietis</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2018, 101, 1-13.	1.2	10
56	Evidence of Positive Darwinian Selection in Putative Meningococcal Vaccine Antigens. <i>Journal of Molecular Evolution</i> , 2005, 61, 90-98.	0.8	9
57	A role for the Parkinson's disease protein DJ-1 as a chaperone and antioxidant in the anhydrobiotic nematode <i>Panagrolaimus superbus</i> . <i>Cell Stress and Chaperones</i> , 2015, 20, 121-137.	1.2	9
58	The involvement of the low-oxygen-activated locus of <i>Burkholderia cenocepacia</i> in adaptation during cystic fibrosis infection. <i>Scientific Reports</i> , 2018, 8, 13386.	1.6	7
59	Analysis of the effect of <i>Bacillus velezensis</i> culture filtrate on the growth and proteome of <i>Cladobotryum mycophilum</i> . <i>Fungal Biology</i> , 2022, 126, 11-19.	1.1	7
60	Estimation of phylogenetic divergence times in Panagrolaimidae and other nematodes using relaxed molecular clocks calibrated with insect and crustacean fossils. <i>Nematology</i> , 2017, 19, 899-913.	0.2	6
61	Characterisation of three novel β -1,3 glucanases from the medically important house dust mite <i>Dermatophagoides pteronyssinus</i> (airmid). <i>Insect Biochemistry and Molecular Biology</i> , 2019, 115, 103242.	1.2	6
62	Molecular characterization of an adaptive response to alkylating agents in the opportunistic pathogen <i>Aspergillus fumigatus</i> . <i>Nucleic Acids Research</i> , 2012, 40, 7806-7820.	6.5	5
63	Insights into the transcriptomic response of the plant engineering bacterium <i>Ensifer adhaerens</i> OV14 during transformation. <i>Scientific Reports</i> , 2019, 9, 10344.	1.6	5
64	Characterising the proteomic response of mushroom pathogen <i>Lecanicillium fungicola</i> to <i>Bacillus velezensis</i> QST 713 and <i>Kos</i> biocontrol agents. <i>European Journal of Plant Pathology</i> , 2022, 163, 369-379.	0.8	5
65	Proteomic investigation of interhyphal interactions between strains of <i>Agaricus bisporus</i> . <i>Fungal Biology</i> , 2020, 124, 579-591.	1.1	4
66	FISHing in fungi: Visualisation of mushroom virus X in the mycelium of <i>Agaricus bisporus</i> by fluorescence in situ hybridisation. <i>Journal of Microbiological Methods</i> , 2020, 173, 105913.	0.7	4
67	Metabolic responses of two pioneer wood decay fungi to diurnally cycling temperature. <i>Journal of Ecology</i> , 2022, 110, 68-79.	1.9	4
68	Comparative Genomic Analysis of Pathogenic Yeasts and the Evolution of Virulence. , 2010, , 1-18.		3
69	Generation and characterisation of a semi-synthetic siderophore-immunogen conjugate and a derivative recombinant triacetylfusarinine C-specific monoclonal antibody with fungal diagnostic application. <i>Analytical Biochemistry</i> , 2021, 632, 114384.	1.1	3
70	Investigating the Relationship between Topology and Evolution in a Dynamic Nematode Odor Genetic Network. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-8.	1.0	2
71	A comparative study of the molecular evolution of signalling pathway members across olfactory, gustatory and photosensory modalities. <i>Journal of Genetics</i> , 2013, 92, 327-334.	0.4	2
72	Genomic diversity, chromosomal rearrangements, and interspecies hybridization in the <i>Ogataea polymorpha</i> species complex. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	2

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73	Characterisation of the complete mitochondrial genome of the insect-parasitic nematode <i>Heterorhabditis bacteriophora</i> : an idiosyncratic gene order and the presence of multiple long non-coding regions. <i>Nematology</i> , 2021, -1, 1-18.	0.2	0
74	Proteomic analysis of three ubiquitous phytophthora species threatening global forest ecosystems. <i>Access Microbiology</i> , 2019, 1, .	0.2	0
75	Investigating the pangenomes of microbial eukaryotes. <i>Access Microbiology</i> , 2019, 1, .	0.2	0