James B Anderson

List of Publications by Year
in descending order

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43 papers	3,696 citations	201674 27 h-index	254184 43 g-index
48 all docs	48 docs citations	48 times ranked	3378 citing authors

#	Article	IF	Citations
1	Mobile genetic elements explain size variation in the mitochondrial genomes of four closely-related Armillaria species. BMC Genomics, 2019, 20, 351.	2.8	49
2	Hybridization is a recurrent evolutionary stimulus in wild yeast speciation. Nature Communications, 2019, 10, 923.	12.8	62
3	Armillaria. Current Biology, 2018, 28, R297-R298.	3.9	29
4	Clonal evolution and genome stability in a 2500-year-old fungal individual. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20182233.	2.6	39
5	Persistence of Resident and Transplanted Genotypes of the Undomesticated Yeast Saccharomyces paradoxus in Forest Soil. MSphere, 2018, 3, .	2.9	9
6	Population genomics reveals structure at the individual, hostâ€tree scale and persistence of genotypic variants of the undomesticated yeast Saccharomyces paradoxus in a natural woodland. Molecular Ecology, 2017, 26, 995-1007.	3.9	21
7	Genome expansion and lineage-specific genetic innovations in the forest pathogenic fungi Armillaria. Nature Ecology and Evolution, 2017, 1, 1931-1941.	7.8	145
8	Fungus Causing White-Nose Syndrome in Bats Accumulates Genetic Variability in North America with No Sign of Recombination. MSphere, 2017, 2, .	2.9	24
9	A Genetic Incompatibility Accelerates Adaptation in Yeast. PLoS Genetics, 2015, 11, e1005407.	3.5	22
10	The Underlying Structure of Adaptation under Strong Selection in 12 Experimental Yeast Populations. Eukaryotic Cell, 2014, 13, 1200-1206.	3.4	16
11	Genomewide mutation dynamic within a long-lived individual ofArmillaria gallica. Mycologia, 2014, 106, 642-648.	1.9	28
12	Cellular Effects and Epistasis among Three Determinants of Adaptation in Experimental Populations of Saccharomyces cerevisiae. Eukaryotic Cell, 2011, 10, 1348-1356.	3.4	15
13	Determinants of Divergent Adaptation and Dobzhansky-Muller Interaction in Experimental Yeast Populations. Current Biology, 2010, 20, 1383-1388.	3.9	68
14	Gene Expression and Evolution of Antifungal Drug Resistance. Antimicrobial Agents and Chemotherapy, 2009, 53, 1931-1936.	3.2	22
15	Acquisition of Aneuploidy Provides Increased Fitness during the Evolution of Antifungal Drug Resistance. PLoS Genetics, 2009, 5, e1000705.	3.5	293
16	Incipient speciation by divergent adaptation and antagonistic epistasis in yeast. Nature, 2007, 447, 585-588.	27.8	185
17	Antagonism between Two Mechanisms of Antifungal Drug Resistance. Eukaryotic Cell, 2006, 5, 1243-1251.	3.4	17
18	Evolution of antifungal-drug resistance: mechanisms and pathogen fitness. Nature Reviews Microbiology, 2005, 3, 547-556.	28.6	298

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19	Dikaryons of the Basidiomycete FungusSchizophyllum commune. Genetics, 2004, 167, 1663-1675.	2.9	82
20	Haploidy, Diploidy and Evolution of Antifungal Drug Resistance in Saccharomyces cerevisiae. Genetics, 2004, 168, 1915-1923.	2.9	80
21	Mode of Selection and Experimental Evolution of Antifungal Drug Resistance in Saccharomyces cerevisiae. Genetics, 2003, 163, 1287-1298.	2.9	134
22	Population genomics of drug resistance in Candida albicans. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9284-9289.	7.1	133
23	Multilocus Genotyping Indicates that the Ability To Invade the Bloodstream Is Widespread among Candida albicans Isolates. Journal of Clinical Microbiology, 2001, 39, 1657-1660.	3.9	32
24	Infrequent Genetic Exchange and Recombination in the Mitochondrial Genome of Candida albicans. Journal of Bacteriology, 2001, 183, 865-872.	2.2	91
25	Genomic stability of two individuals of Armillaria gallica. Mycologia, 2000, 92, 894-899.	1.9	14
26	Genomic Stability of Two Individuals of Armillaria gallica. Mycologia, 2000, 92, 894.	1.9	10
27	PATTERNS OF DESCENT IN CLONAL LINEAGES AND THEIR MULTILOCUS FINGERPRINTS ARE RESOLVED WITH COMBINED GENE GENEALOGIES. Evolution; International Journal of Organic Evolution, 1999, 53, 11-21.	2.3	82
28	Mitochondrial DNA variation in natural populations of the mushroomAgaricus bisporus. Molecular Ecology, 1998, 7, 19-33.	3.9	32
29	A comparison of different methods for the identification of genets ofArmillariaspp.. New Phytologist, 1996, 133, 333-343.	7.3	54
30	Molecular Phylogeny of Northern Hemisphere Species ofArmillaria. Mycologia, 1992, 84, 505-516.	1.9	215
31	Strategies for the Efficient Recovery ofAgaricus BisporusHomokaryons. Mycologia, 1992, 84, 575-579.	1.9	27
32	The fungus Armillaria bulbosa is among the largest and oldest living organisms. Nature, 1992, 356, 428-431.	27.8	612
33	VARIATION IN RIBOSOMAL DNA AMONG BIOLOGICAL SPECIES OF ARMILLARIA , A GENUS OF ROOTâ€INFECTING FUNGI. Evolution; International Journal of Organic Evolution, 1989, 43, 1652-1662.	2.3	71
34	Physical mapping of the mitochondrial genome of the cultivated mushroom Agaricus brunnescens (=) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.9	46
35	Restriction Fragment Polymorphisms in Biological Species of Armillaria Mellea. Mycologia, 1987, 79, 69-76.	1.9	92
36	Restriction Fragment Length Polymorphisms in the Mushrooms Agaricus brunnescens and Agaricus bitorquis. Applied and Environmental Microbiology, 1987, 53, 816-822.	3.1	93

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37	Biological Species of Armillaria in North America: Redesignation of Groups IV and VIII and Enumeration of Voucher Strains for Other Groups. Mycologia, 1986, 78, 837-839.	1.9	43
38	Bifactorial Heterothallism and Vegetative Diploidy in Clitocybe Tabescens. Mycologia, 1982, 74, 911-916.	1.9	18
39	Biological Species ofArmillaria Melleain North America. Mycologia, 1979, 71, 402-414.	1.9	186
40	Random Assortment In Armillaria Mellea. Mycologia, 1979, 71, 1278-1279.	1.9	2
41	Genetic Identification of Clones ofArmillaria melleain Coniferous Forests in Washington. Phytopathology, 1979, 69, 1109.	2.2	44
42	Sex and diploidy in Armillaria mellea. Experimental Mycology, 1978, 2, 119-129.	1.6	132
43	Dikaryons, Diploids, and Evolution. , 0, , 333-348.		25