

Austin Burt

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

9,565
citations

87888

38
h-index

106344

65
g-index

73
all docs

73
docs citations

73
times ranked

7869
citing authors

#	ARTICLE	IF	CITATIONS
1	Indices of multilocus linkage disequilibrium. <i>Molecular Ecology Notes</i> , 2001, 1, 101-102.	1.7	1,073
2	A CRISPR-Cas9 gene drive system targeting female reproduction in the malaria mosquito vector <i>Anopheles gambiae</i> . <i>Nature Biotechnology</i> , 2016, 34, 78-83.	17.5	985
3	A CRISPR-Cas9 gene drive targeting doublesex causes complete population suppression in caged <i>Anopheles gambiae</i> mosquitoes. <i>Nature Biotechnology</i> , 2018, 36, 1062-1066.	17.5	648
4	Site-specific selfish genes as tools for the control and genetic engineering of natural populations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, 921-928.	2.6	567
5	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258-1262.	12.6	492
6	The Evolutionary Biology and Population Genetics Underlying Fungal Strain Typing. <i>Clinical Microbiology Reviews</i> , 1999, 12, 126-146.	13.6	320
7	A synthetic homing endonuclease-based gene drive system in the human malaria mosquito. <i>Nature</i> , 2011, 473, 212-215.	27.8	303
8	A synthetic sex ratio distortion system for the control of the human malaria mosquito. <i>Nature Communications</i> , 2014, 5, 3977.	12.8	258
9	PERSPECTIVE: SEX, RECOMBINATION, AND THE EFFICACY OF SELECTION? WAS WEISMANN RIGHT?. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 337-351.	2.3	256
10	Safeguarding gene drive experiments in the laboratory. <i>Science</i> , 2015, 349, 927-929.	12.6	254
11	The Population Genetics of Using Homing Endonuclease Genes in Vector and Pest Management. <i>Genetics</i> , 2008, 179, 2013-2026.	2.9	236
12	Mammalian chiasma frequencies as a test of two theories of recombination. <i>Nature</i> , 1987, 326, 803-805.	27.8	213
13	Requirements for effective malaria control with homing endonuclease genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E874-80.	7.1	189
14	Heritable strategies for controlling insect vectors of disease. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130432.	4.0	184
15	Homing endonuclease genes: the rise and fall and rise again of a selfish element. <i>Current Opinion in Genetics and Development</i> , 2004, 14, 609-615.	3.3	169
16	Impact of mosquito gene drive on malaria elimination in a computational model with explicit spatial and temporal dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E255-E264.	7.1	158
17	A male-biased sex-distorter gene drive for the human malaria vector <i>Anopheles gambiae</i> . <i>Nature Biotechnology</i> , 2020, 38, 1054-1060.	17.5	153
18	Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage. <i>Science</i> , 2014, 343, 437-440.	12.6	144

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19	Population Genetics of the Wild Yeast <i>Saccharomyces paradoxus</i> . <i>Genetics</i> , 2004, 166, 43-52.	2.9	143
20	Sex differences in recombination. <i>Journal of Evolutionary Biology</i> , 1991, 4, 259-277.	1.7	135
21	ORIGINS AND EVOLUTION OF A TRANSMISSIBLE CANCER. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 2340-2349.	2.3	113
22	The Comparative Biology of Parasite Species Diversity: Internal Helminths of Freshwater Fish. <i>Journal of Animal Ecology</i> , 1991, 60, 1047.	2.8	107
23	Mitochondrial Capture by a Transmissible Cancer. <i>Science</i> , 2011, 331, 303-303.	12.6	105
24	Modelling the potential of genetic control of malaria mosquitoes at national scale. <i>BMC Biology</i> , 2019, 17, 26.	3.8	94
25	Adaptation for Horizontal Transfer in a Homing Endonuclease. <i>Molecular Biology and Evolution</i> , 2002, 19, 239-246.	8.9	91
26	The tempo of reproduction in <i>Hyphessobrycon pulchripinnis</i> (Characidae), with a discussion on the biology of "multiple spawning"™ in fishes. <i>Journal of Applied Phycology</i> , 1988, 22, 15-27.	2.8	89
27	Modelling the spatial spread of a homing endonuclease gene in a mosquito population. <i>Journal of Applied Ecology</i> , 2013, 50, 1216-1225.	4.0	88
28	The spatial scale of genetic differentiation in a model organism: the wild yeast <i>Saccharomyces paradoxus</i> . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 1941-1946.	4.0	81
29	The vasa regulatory region mediates germline expression and maternal transmission of proteins in the malaria mosquito <i>Anopheles gambiae</i> : a versatile tool for genetic control strategies. <i>BMC Molecular Biology</i> , 2009, 10, 65.	3.0	80
30	Regulating the expression of gene drives is key to increasing their invasive potential and the mitigation of resistance. <i>PLoS Genetics</i> , 2021, 17, e1009321.	3.5	72
31	Modelling the suppression of a malaria vector using a CRISPR-Cas9 gene drive to reduce female fertility. <i>BMC Biology</i> , 2020, 18, 98.	3.8	70
32	Gene Drive: Evolved and Synthetic. <i>ACS Chemical Biology</i> , 2018, 13, 343-346.	3.4	68
33	Gene drive through a landscape: Reaction-diffusion models of population suppression and elimination by a sex ratio distorter. <i>Theoretical Population Biology</i> , 2016, 108, 51-69.	1.1	67
34	How driving endonuclease genes can be used to combat pests and disease vectors. <i>BMC Biology</i> , 2017, 15, 81.	3.8	66
35	Genetic conflicts in genomic imprinting. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1998, 265, 2393-2397.	2.6	65
36	Requirements for Driving Antipathogen Effector Genes into Populations of Disease Vectors by Homing. <i>Genetics</i> , 2017, 205, 1587-1596.	2.9	62

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37	Self-limiting population genetic control with sex-linked genome editors. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180776.	2.6	52
38	Gene drive to reduce malaria transmission in sub-Saharan Africa. <i>Journal of Responsible Innovation</i> , 2018, 5, S66-S80.	4.9	49
39	Evolution of divergent DNA recognition specificities in VDE homing endonucleases from two yeast species. <i>Nucleic Acids Research</i> , 2004, 32, 3947-3956.	14.5	40
40	Gene drive for population genetic control: non-functional resistance and parental effects. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191586.	2.6	39
41	Vector control with driving Y chromosomes: modelling the evolution of resistance. <i>Malaria Journal</i> , 2017, 16, 286.	2.3	38
42	Degeneration and Domestication of a Selfish Gene in Yeast: Molecular Evolution Versus Site-Directed Mutagenesis. <i>Molecular Biology and Evolution</i> , 2005, 22, 1535-1538.	8.9	37
43	Outcrossed sex allows a selfish gene to invade yeast populations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2001, 268, 2537-2542.	2.6	32
44	The mutational structure of metabolism in <i>Caenorhabditis elegans</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 2239-2246.	2.3	30
45	Estimating Effective Population Size from Temporally Spaced Samples with a Novel, Efficient Maximum-Likelihood Algorithm. <i>Genetics</i> , 2015, 200, 285-293.	2.9	27
46	Systematic identification of plausible pathways to potential harm via problem formulation for investigational releases of a population suppression gene drive to control the human malaria vector <i>Anopheles gambiae</i> in West Africa. <i>Malaria Journal</i> , 2021, 20, 170.	2.3	26
47	Double drives and private alleles for localised population genetic control. <i>PLoS Genetics</i> , 2021, 17, e1009333.	3.5	24
48	The use of driving endonuclease genes to suppress mosquito vectors of malaria in temporally variable environments. <i>Malaria Journal</i> , 2018, 17, 154.	2.3	22
49	Resistance to a CRISPR-based gene drive at an evolutionarily conserved site is revealed by mimicking genotype fixation. <i>PLoS Genetics</i> , 2021, 17, e1009740.	3.5	21
50	Seed Reproduction Is Associated with a Transient Escape from Parasite Damage in American Beech. <i>Oikos</i> , 1991, 61, 145.	2.7	20
51	Metabolic variation in natural populations of wild yeast. <i>Ecology and Evolution</i> , 2015, 5, 722-732.	1.9	16
52	Red Queen versus Tangled Bank models. <i>Nature</i> , 1987, 330, 118-118.	27.8	15
53	Genomic signatures of population decline in the malaria mosquito <i>Anopheles gambiae</i> . <i>Malaria Journal</i> , 2016, 15, 182.	2.3	14
54	Robust Estimation of Recent Effective Population Size from Number of Independent Origins in Soft Sweeps. <i>Molecular Biology and Evolution</i> , 2019, 36, 2040-2052.	8.9	13

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55	Tests of sib diversification theories of outcrossing in <i>Impatiens capensis</i> : Effects of inbreeding and neighbour relatedness on production and infestation. <i>Journal of Evolutionary Biology</i> , 1992, 5, 575-588.	1.7	12
56	Estimating the fitness effects of new mutations in the wild yeast <i>Saccharomyces paradoxus</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 1887-95.	2.5	12
57	Estimating linkage disequilibrium from genotypes under Hardy-Weinberg equilibrium. <i>BMC Genetics</i> , 2020, 21, 21.	2.7	11
58	80 questions for UK biological security. <i>PLoS ONE</i> , 2021, 16, e0241190.	2.5	8
59	Gene drives and population persistence vs elimination: The impact of spatial structure and inbreeding at low density. <i>Theoretical Population Biology</i> , 2022, 145, 109-125.	1.1	8
60	Sources of variance in protein heterozygosity: the importance of the species-protein interaction. <i>Heredity</i> , 1992, 68, 241-252.	2.6	7
61	Population Size, Sex and Purifying Selection: Comparative Genomics of Two Sister Taxa of the Wild Yeast <i>Saccharomyces paradoxus</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 1636-1645.	2.5	7
62	Ultra-conserved sequences in the genomes of highly diverse <i>Anopheles</i> mosquitoes, with implications for malaria vector control. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	3
63	Identifying the time scale of temporal association. <i>Canadian Journal of Zoology</i> , 1988, 66, 2090-2092.	1.0	2
64	Partitioning the contributions of alternative malaria vector species. <i>Malaria Journal</i> , 2016, 15, 60.	2.3	2
65	Editorial: gene drive for vector control. <i>Pathogens and Global Health</i> , 2017, 111, 397-398.	2.3	0
66	Contemporary N_e estimation using temporally spaced data with linked loci. <i>Molecular Ecology Resources</i> , 2021, 21, 2221-2230.	4.8	0