

Austin Burt

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

9,565
citations

87723

38
h-index

106150

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. | 9.4 | 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. | 9.4 | 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. | 1.2 | 567 |
| 5 | Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258-1262. | 6.0 | 492 |
| 6 | The Evolutionary Biology and Population Genetics Underlying Fungal Strain Typing. <i>Clinical Microbiology Reviews</i> , 1999, 12, 126-146. | 5.7 | 320 |
| 7 | A synthetic homing endonuclease-based gene drive system in the human malaria mosquito. <i>Nature</i> , 2011, 473, 212-215. | 13.7 | 303 |
| 8 | A synthetic sex ratio distortion system for the control of the human malaria mosquito. <i>Nature Communications</i> , 2014, 5, 3977. | 5.8 | 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. | 1.1 | 256 |
| 10 | Safeguarding gene drive experiments in the laboratory. <i>Science</i> , 2015, 349, 927-929. | 6.0 | 254 |
| 11 | The Population Genetics of Using Homing Endonuclease Genes in Vector and Pest Management. <i>Genetics</i> , 2008, 179, 2013-2026. | 1.2 | 236 |
| 12 | Mammalian chiasma frequencies as a test of two theories of recombination. <i>Nature</i> , 1987, 326, 803-805. | 13.7 | 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. | 3.3 | 189 |
| 14 | Heritable strategies for controlling insect vectors of disease. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130432. | 1.8 | 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. | 1.5 | 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. | 3.3 | 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. | 9.4 | 153 |
| 18 | Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage. <i>Science</i> , 2014, 343, 437-440. | 6.0 | 144 |

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|----|--|-----|-----------|
| 19 | Population Genetics of the Wild Yeast <i>Saccharomyces paradoxus</i> . <i>Genetics</i> , 2004, 166, 43-52. | 1.2 | 143 |
| 20 | Sex differences in recombination. <i>Journal of Evolutionary Biology</i> , 1991, 4, 259-277. | 0.8 | 135 |
| 21 | ORIGINS AND EVOLUTION OF A TRANSMISSIBLE CANCER. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 2340-2349. | 1.1 | 113 |
| 22 | The Comparative Biology of Parasite Species Diversity: Internal Helminths of Freshwater Fish. <i>Journal of Animal Ecology</i> , 1991, 60, 1047. | 1.3 | 107 |
| 23 | Mitochondrial Capture by a Transmissible Cancer. <i>Science</i> , 2011, 331, 303-303. | 6.0 | 105 |
| 24 | Modelling the potential of genetic control of malaria mosquitoes at national scale. <i>BMC Biology</i> , 2019, 17, 26. | 1.7 | 94 |
| 25 | Adaptation for Horizontal Transfer in a Homing Endonuclease. <i>Molecular Biology and Evolution</i> , 2002, 19, 239-246. | 3.5 | 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. | 1.5 | 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. | 1.9 | 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. | 1.8 | 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. | 1.5 | 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. | 1.7 | 70 |
| 32 | Gene Drive: Evolved and Synthetic. <i>ACS Chemical Biology</i> , 2018, 13, 343-346. | 1.6 | 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. | 0.5 | 67 |
| 34 | How driving endonuclease genes can be used to combat pests and disease vectors. <i>BMC Biology</i> , 2017, 15, 81. | 1.7 | 66 |
| 35 | Genetic conflicts in genomic imprinting. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1998, 265, 2393-2397. | 1.2 | 65 |
| 36 | Requirements for Driving Antipathogen Effector Genes into Populations of Disease Vectors by Homing. <i>Genetics</i> , 2017, 205, 1587-1596. | 1.2 | 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. | 1.2 | 52 |
| 38 | Gene drive to reduce malaria transmission in sub-Saharan Africa. <i>Journal of Responsible Innovation</i> , 2018, 5, S66-S80. | 2.3 | 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. | 6.5 | 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. | 1.2 | 39 |
| 41 | Vector control with driving Y chromosomes: modelling the evolution of resistance. <i>Malaria Journal</i> , 2017, 16, 286. | 0.8 | 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. | 3.5 | 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. | 1.2 | 32 |
| 44 | The mutational structure of metabolism in <i>Caenorhabditis elegans</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 2239-2246. | 1.1 | 30 |
| 45 | Estimating Effective Population Size from Temporally Spaced Samples with a Novel, Efficient Maximum-Likelihood Algorithm. <i>Genetics</i> , 2015, 200, 285-293. | 1.2 | 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. | 0.8 | 26 |
| 47 | Double drives and private alleles for localised population genetic control. <i>PLoS Genetics</i> , 2021, 17, e1009333. | 1.5 | 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. | 0.8 | 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. | 1.5 | 21 |
| 50 | Seed Reproduction Is Associated with a Transient Escape from Parasite Damage in American Beech. <i>Oikos</i> , 1991, 61, 145. | 1.2 | 20 |
| 51 | Metabolic variation in natural populations of wild yeast. <i>Ecology and Evolution</i> , 2015, 5, 722-732. | 0.8 | 16 |
| 52 | Red Queen versus Tangled Bank models. <i>Nature</i> , 1987, 330, 118-118. | 13.7 | 15 |
| 53 | Genomic signatures of population decline in the malaria mosquito <i>Anopheles gambiae</i> . <i>Malaria Journal</i> , 2016, 15, 182. | 0.8 | 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. | 3.5 | 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. | 0.8 | 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. | 1.1 | 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. | 1.1 | 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. | 0.5 | 8 |
| 60 | Sources of variance in protein heterozygosity: the importance of the species-protein interaction. <i>Heredity</i> , 1992, 68, 241-252. | 1.2 | 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. | 1.1 | 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, . | 0.8 | 3 |
| 63 | Identifying the time scale of temporal association. <i>Canadian Journal of Zoology</i> , 1988, 66, 2090-2092. | 0.4 | 2 |
| 64 | Partitioning the contributions of alternative malaria vector species. <i>Malaria Journal</i> , 2016, 15, 60. | 0.8 | 2 |
| 65 | Editorial: gene drive for vector control. <i>Pathogens and Global Health</i> , 2017, 111, 397-398. | 1.0 | 0 |
| 66 | Contemporary N_e estimation using temporally spaced data with linked loci. <i>Molecular Ecology Resources</i> , 2021, 21, 2221-2230. | 2.2 | 0 |