

Simon W Baxter

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/370158/publications.pdf>

Version: 2024-02-01

59
papers

6,200
citations

109137

35
h-index

133063

59
g-index

63
all docs

63
docs citations

63
times ranked

6508
citing authors

#	ARTICLE	IF	CITATIONS
1	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012, 487, 94-98.	13.7	1,086
2	Chromosomal rearrangements maintain a polymorphic supergene controlling butterfly mimicry. <i>Nature</i> , 2011, 477, 203-206.	13.7	509
3	A heterozygous moth genome provides insights into herbivory and detoxification. <i>Nature Genetics</i> , 2013, 45, 220-225.	9.4	472
4	Adaptive Introgression across Species Boundaries in <i>Heliconius</i> Butterflies. <i>PLoS Genetics</i> , 2012, 8, e1002752.	1.5	319
5	Genomic islands of divergence in hybridizing <i>Heliconius</i> butterflies identified by large-scale targeted sequencing. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 343-353.	1.8	294
6	Linkage Mapping and Comparative Genomics Using Next-Generation RAD Sequencing of a Non-Model Organism. <i>PLoS ONE</i> , 2011, 6, e19315.	1.1	270
7	A Conserved Supergene Locus Controls Colour Pattern Diversity in <i>Heliconius</i> Butterflies. <i>PLoS Biology</i> , 2006, 4, e303.	2.6	242
8	Parallel Evolution of <i>Bacillus thuringiensis</i> Toxin Resistance in Lepidoptera. <i>Genetics</i> , 2011, 189, 675-679.	1.2	239
9	MAPK Signaling Pathway Alters Expression of Midgut ALP and ABCC Genes and Causes Resistance to <i>Bacillus thuringiensis</i> Cry1Ac Toxin in Diamondback Moth. <i>PLoS Genetics</i> , 2015, 11, e1005124.	1.5	178
10	Genome-wide patterns of divergence and gene flow across a butterfly radiation. <i>Molecular Ecology</i> , 2013, 22, 814-826.	2.0	160
11	Major Improvements to the <i>Heliconius melpomene</i> Genome Assembly Used to Confirm 10 Chromosome Fusion Events in 6 Million Years of Butterfly Evolution. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 695-708.	0.8	149
12	Evolutionary Novelty in a Butterfly Wing Pattern through Enhancer Shuffling. <i>PLoS Biology</i> , 2016, 14, e1002353.	2.6	136
13	The diversity of Bt resistance genes in species of Lepidoptera. <i>Journal of Invertebrate Pathology</i> , 2007, 95, 192-197.	1.5	129
14	Mis-Spliced Transcripts of Nicotinic Acetylcholine Receptor $\alpha 6$ Are Associated with Field Evolved Spinosad Resistance in <i>Plutella xylostella</i> (L.). <i>PLoS Genetics</i> , 2010, 6, e1000802.	1.5	110
15	Synteny and Chromosome Evolution in the Lepidoptera: Evidence From Mapping in <i>Heliconius melpomene</i> . <i>Genetics</i> , 2007, 177, 417-426.	1.2	101
16	Genomic Hotspots for Adaptation: The Population Genetics of Alllerian Mimicry in <i>Heliconius erato</i> . <i>PLoS Genetics</i> , 2010, 6, e1000796.	1.5	99
17	Genomic Hotspots for Adaptation: The Population Genetics of Alllerian Mimicry in the <i>Heliconius melpomene</i> Clade. <i>PLoS Genetics</i> , 2010, 6, e1000794.	1.5	97
18	Genetic Evidence for Hybrid Trait Speciation in <i>Heliconius</i> Butterflies. <i>PLoS Genetics</i> , 2010, 6, e1000930.	1.5	90

#	ARTICLE	IF	CITATIONS
19	Methylenetetrahydrofolate reductase polymorphism and susceptibility to breast cancer. <i>Breast Cancer Research</i> , 2002, 4, R14.	2.2	89
20	Novel genetic basis of field-evolved resistance to Bt toxins in <i>Plutella xylostella</i> . <i>Insect Molecular Biology</i> , 2005, 14, 327-334.	1.0	86
21	Convergent Evolution in the Genetic Basis of Müllerian Mimicry in <i>Heliconius</i> Butterflies. <i>Genetics</i> , 2008, 180, 1567-1577.	1.2	79
22	Characterization and expression of the cytochrome P450 gene family in diamondback moth, <i>Plutella xylostella</i> (L.). <i>Scientific Reports</i> , 2015, 5, 8952.	1.6	77
23	Mutation analysis of EP300 in colon, breast and ovarian carcinomas. <i>International Journal of Cancer</i> , 2002, 102, 137-141.	2.3	75
24	Characterization of a hotspot for mimicry: assembly of a butterfly wing transcriptome to genomic sequence at the <i>HmYb/Sb</i> locus. <i>Molecular Ecology</i> , 2010, 19, 240-254.	2.0	70
25	DBM-DB: the diamondback moth genome database. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bat087-bat087.	1.4	69
26	Genome-wide characterization and expression profiling of immune genes in the diamondback moth, <i>Plutella xylostella</i> (L.). <i>Scientific Reports</i> , 2015, 5, 9877.	1.6	69
27	Polymorphic variation in CYP19 and the risk of breast cancer. <i>Carcinogenesis</i> , 2001, 22, 347-349.	1.3	67
28	Microsomal epoxide hydrolase polymorphism and susceptibility to ovarian cancer. <i>Cancer Letters</i> , 2002, 177, 75-81.	3.2	59
29	Conservatism and novelty in the genetic architecture of adaptation in <i>Heliconius</i> butterflies. <i>Heredity</i> , 2015, 114, 515-524.	1.2	50
30	Resistance to <i>Bacillus thuringiensis</i> Cry1Ac toxin requires mutations in two <i>Plutella xylostella</i> ATP-binding cassette transporter paralogs. <i>PLoS Pathogens</i> , 2020, 16, e1008697.	2.1	49
31	CRISPR/Cas9-mediated mutagenesis of the <i>white</i> gene in the tephritid pest <i>Bactrocera tryoni</i> . <i>Journal of Applied Entomology</i> , 2018, 142, 52-58.	0.8	48
32	Variation among 532 genomes unveils the origin and evolutionary history of a global insect herbivore. <i>Nature Communications</i> , 2020, 11, 2321.	5.8	47
33	Butterfly speciation and the distribution of gene effect sizes fixed during adaptation. <i>Heredity</i> , 2009, 102, 57-65.	1.2	46
34	Expressing a moth <i>abcc2</i> gene in transgenic <i>Drosophila</i> causes susceptibility to Bt Cry1Ac without requiring a cadherin-like protein receptor. <i>Insect Biochemistry and Molecular Biology</i> , 2017, 80, 61-70.	1.2	44
35	Genetic mapping of Bt-toxin binding proteins in a Cry1A-toxin resistant strain of diamondback moth <i>Plutella xylostella</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 125-135.	1.2	41
36	An Insect Counteradaptation against Host Plant Defenses Evolved through Concerted Neofunctionalization. <i>Molecular Biology and Evolution</i> , 2019, 36, 930-941.	3.5	41

#	ARTICLE	IF	CITATIONS
37	Comparative genomics of the mimicry switch in <i>Papilio dardanus</i> . Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20140465.	1.2	40
38	Widespread pyrethroid resistance in Australian diamondback moth, <i>Plutella xylostella</i> (L.), is related to multiple mutations in the <i>para</i> sodium channel gene. Bulletin of Entomological Research, 2011, 101, 393-405.	0.5	37
39	Construction and characterisation of near-isogenic <i>Plutella xylostella</i> (Lepidoptera:) Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 50	1.7	36
40	A flavin-dependent monooxygenase confers resistance to chlorantraniliprole in the diamondback moth, <i>Plutella xylostella</i> . Insect Biochemistry and Molecular Biology, 2019, 115, 103247.	1.2	29
41	Microsatellites isolated from diamondback moth, <i>Plutella xylostella</i> (L.), for studies of dispersal in Australian populations. Molecular Ecology Notes, 2005, 5, 51-53.	1.7	27
42	Genetic analysis of benign ovarian tumors. International Journal of Cancer, 2003, 105, 499-505.	2.3	26
43	Cryptic <i>Plutella</i> species show deep divergence despite the capacity to hybridize. BMC Evolutionary Biology, 2018, 18, 77.	3.2	26
44	Transforming growth factor beta receptor 1 polyalanine polymorphism and exon 5 mutation analysis in breast and ovarian cancer. Cancer Epidemiology Biomarkers and Prevention, 2002, 11, 211-4.	1.1	26
45	White pupae phenotype of tephritids is caused by parallel mutations of a MFS transporter. Nature Communications, 2021, 12, 491.	5.8	25
46	Deep mitochondrial divergence within a <i>Heliconius</i> butterfly species is not explained by cryptic speciation or endosymbiotic bacteria. BMC Evolutionary Biology, 2011, 11, 358.	3.2	23
47	A haploid diamondback moth (<i>Plutella xylostella</i> L.) genome assembly resolves 31 chromosomes and identifies a diamide resistance mutation. Insect Biochemistry and Molecular Biology, 2021, 138, 103622.	1.2	19
48	Lessons from <i>Drosophila</i> : Engineering Genetic Sexing Strains with Temperature-Sensitive Lethality for Sterile Insect Technique Applications. Insects, 2021, 12, 243.	1.0	14
49	Comparative population genetics of a mimicry locus among hybridizing <i>Heliconius</i> butterfly species. Heredity, 2011, 107, 200-204.	1.2	13
50	Precise single base substitution in the <i>shibire</i> gene by CRISPR/Cas9-mediated homology directed repair in <i>Bactrocera tryoni</i> . BMC Genetics, 2020, 21, 127.	2.7	12
51	Genome-wide analysis of diamondback moth, <i>Plutella xylostella</i> L., from Brassica crops and wild host plants reveals no genetic structure in Australia. Scientific Reports, 2020, 10, 12047.	1.6	11
52	Identification of Y-chromosome scaffolds of the Queensland fruit fly reveals a duplicated <i>gyf</i> gene paralogue common to many <i>Bactrocera</i> pest species. Insect Molecular Biology, 2019, 28, 873-886.	1.0	10
53	Structure and expression of sulfatase and sulfatase modifying factor genes in the diamondback moth, <i>Plutella xylostella</i> . Insect Science, 2018, 25, 946-958.	1.5	8
54	Draft Genome Assembly of a <i>Wolbachia</i> Endosymbiont of <i>Plutella australiana</i> . Genome Announcements, 2017, 5, .	0.8	6

#	ARTICLE	IF	CITATIONS
55	EB Ford revisited: assessing the long-term stability of wing-spot patterns and population genetic structure of the meadow brown butterfly on the Isles of Scilly. <i>Heredity</i> , 2017, 118, 322-329.	1.2	5
56	Assessing genomic admixture between cryptic <i>Plutella</i> moth species following secondary contact. <i>Genome Biology and Evolution</i> , 2018, 10, 2973-2985.	1.1	5
57	Disruption of duplicated yellow genes in <i>Bactrocera tryoni</i> modifies pigmentation colouration and impacts behaviour. <i>Journal of Pest Science</i> , 2021, 94, 917-932.	1.9	5
58	De Novo Genome Assembly of the Meadow Brown Butterfly, <i>Maniola jurtina</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1477-1484.	0.8	4
59	Genomic Libraries: I. Construction and Screening of Fosmid Genomic Libraries. <i>Methods in Molecular Biology</i> , 2012, 772, 37-58.	0.4	2