Brock A Harpur

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1783486/publications.pdf

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38 papers

1,090 citations

18 h-index 433756 31 g-index

44 all docs

44 docs citations

times ranked

44

1404 citing authors

#	Article	IF	Citations
1	Haploid and Sexual Selection Shape the Rate of Evolution of Genes across the Honey Bee (<i>Apis) Tj ETQq1</i>	1 0.784314 1.1	rgBŢ/Overlock
2	Genetic past, present, and future of the honey bee (Apis mellifera) in the United States of America. Apidologie, 2021, 52, 63-79.	0.9	21
3	Connecting social polymorphism to single nucleotide polymorphism: population genomics of the small carpenter bee, Ceratina australensis. Biological Journal of the Linnean Society, 2021, 132, 945-954.	0.7	5
4	Improved <i>Apis mellifera</i> reference genome based on the alternative long-read-based assemblies. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	2
5	Prospects in Connecting Genetic Variation to Variation in Fertility in Male Bees. Genes, 2021, 12, 1251.	1.0	5
6	A gene drive does not spread easily in populations of the honey bee parasite Varroa destructor. Apidologie, 2021, 52, 1112-1127.	0.9	10
7	Eusociality influences the strength of negative selection on insect genomes. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201512.	1.2	8
8	Developmental plasticity shapes social traits and selection in a facultatively eusocial bee. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13615-13625.	3.3	37
9	Defense Response in Brazilian Honey Bees (Apis mellifera scutellata × spp.) Is Underpinned by Complex Patterns of Admixture. Genome Biology and Evolution, 2020, 12, 1367-1377.	1.1	13
10	Paternallyâ€biased gene expression follows kinâ€selected predictions in female honey bee embryos. Molecular Ecology, 2020, 29, 1523-1533.	2.0	16
11	Honey Bee: Management. , 2020, , 5281-5283.		O
12	Integrative Genomics Reveals the Genetics and Evolution of the Honey Bee's Social Immune System. Genome Biology and Evolution, 2019, 11, 937-948.	1.1	33
13	Strikingly high levels of heterozygosity despite 20 years of inbreeding in a clonal honey bee. Journal of Evolutionary Biology, 2019, 32, 144-152.	0.8	19
14	Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee (Halictidae: <i>Nomia melanderi</i>). G3: Genes, Genomes, Genetics, 2019, 9, 625-634.	0.8	19
15	Genetic origins of honey bees (Apis mellifera) on Kangaroo Island and Norfolk Island (Australia) and the Kingdom of Tonga. Apidologie, 2019, 50, 28-39.	0.9	5
16	Genomic footprint of evolution of eusociality in bees: floral food use and CYPome "blooms― Insectes Sociaux, 2018, 65, 445-454.	0.7	29
17	Conservation Genomics of the Declining North American Bumblebee Bombus terricola Reveals Inbreeding and Selection on Immune Genes. Frontiers in Genetics, 2018, 9, 316.	1.1	31
18	Insects with similar social complexity show convergent patterns of adaptive molecular evolution. Scientific Reports, 2018, 8, 10388.	1.6	20

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19	Honey Bee: Management., 2018,, 1-3.		О
20	Adaptive maintenance of European alleles in the Brazilian Africanized honeybee. Molecular Ecology, 2017, 26, 3591-3593.	2.0	0
21	An abbreviated SNP panel for ancestry assignment of honeybees (Apis mellifera). Apidologie, 2017, 48, 776-783.	0.9	10
22	Queens and Workers Contribute Differently to Adaptive Evolution in Bumble Bees and Honey Bees. Genome Biology and Evolution, 2017, 9, 2395-2402.	1.1	25
23	A variant reference data set for the Africanized honeybee, Apis mellifera. Scientific Data, 2016, 3, 160097.	2.4	13
24	Toward an Upgraded Honey Bee (<i>Apis mellifera</i> L.) Genome Annotation Using Proteogenomics. Journal of Proteome Research, 2016, 15, 411-421.	1.8	22
25	Hybrid origins of Australian honeybees (Apis mellifera). Apidologie, 2016, 47, 26-34.	0.9	21
26	The transcriptomic and evolutionary signature of social interactions regulating honey bee caste development. Ecology and Evolution, 2015, 5, 4795-4807.	0.8	36
27	A <scp>SNP</scp> test to identify Africanized honeybees via proportion of â€~African' ancestry. Molecular Ecology Resources, 2015, 15, 1346-1355.	2.2	39
28	Assessing patterns of admixture and ancestry in Canadian honey bees. Insectes Sociaux, 2015, 62, 479-489.	0.7	31
29	Population genomics of the honey bee reveals strong signatures of positive selection on worker traits. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2614-2619.	3.3	177
30	Pleiotropy constrains the evolution of protein but not regulatory sequences in a transcription regulatory network influencing complex social behaviors. Frontiers in Genetics, 2014, 5, 431.	1.1	30
31	No Genetic Tradeoffs between Hygienic Behaviour and Individual Innate Immunity in the Honey Bee, Apis mellifera. PLoS ONE, 2014, 9, e104214.	1.1	28
32	A review of the consequences of complementary sex determination and diploid male production on mating failures in the <scp>H</scp> ymenoptera. Entomologia Experimentalis Et Applicata, 2013, 146, 156-164.	0.7	59
33	Accelerated Evolution of Innate Immunity Proteins in Social Insects: Adaptive Evolution or Relaxed Constraint?. Molecular Biology and Evolution, 2013, 30, 1665-1674.	3.5	59
34	Admixture increases diversity in managed honey bees: Reply to De la Rúa <i>etÂal</i> . (2013). Molecular Ecology, 2013, 22, 3211-3215.	2.0	28
35	Reply to Hunt et al.: Worker-biased genes have high guanine-cytosine content and rates of nucleotide diversity in the honey bee. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E447-E447.	3.3	0
36	Recombination is associated with the evolution of genome structure and worker behavior in honey bees. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18012-18017.	3.3	82

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37	Management increases genetic diversity of honey bees via admixture. Molecular Ecology, 2012, 21, 4414-4421.	2.0	128
38	Effective stimulation of growth in MCF-7 human breast cancer cells by inhibition of syntaxin18 by external guide sequence and ribonuclease P. Cancer Letters, 2008, 272, 167-175.	3.2	18