Christina Beryl McCarthy

List of Publications by Year in descending order

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1307594 1125743 14 252 13 7 citations h-index g-index papers 15 15 15 333 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	AcMNPV ac143 (odv-e18) is essential for mediating budded virus production and is the 30th baculovirus core gene. Virology, 2008, 375, 277-291.	2.4	62
2	Autographa californica multiple nucleopolyhedrovirus ac142, a core gene that is essential for BV production and ODV envelopment. Virology, 2008, 372, 325-339.	2.4	61
3	Metagenomic Analysis of Taxa Associated with Lutzomyia longipalpis, Vector of Visceral Leishmaniasis, Using an Unbiased High-Throughput Approach. PLoS Neglected Tropical Diseases, 2011, 5, e1304.	3.0	55
4	Gut microbiota of <i>Spodoptera frugiperda</i> (J.E. Smith) larvae as revealed by metatranscriptomic analysis. Journal of Applied Entomology, 2020, 144, 351-363.	1.8	21
5	First Comparative Transcriptomic Analysis of Wild Adult Male and Female Lutzomyia longipalpis, Vector of Visceral Leishmaniasis. PLoS ONE, 2013, 8, e58645.	2.5	17
6	Development of a Recombination System for the Generation of Occlusion Positive Genetically Modified Anticarsia Gemmatalis Multiple Nucleopolyhedrovirus. Viruses, 2015, 7, 1599-1612.	3.3	9
7	A simplified method for the extraction of baculoviral DNA for PCR analysis: A practical application. Journal of Virological Methods, 2008, 148, 286-290.	2.1	8
8	Optimization of DNA Extraction from Individual Sand Flies for PCR Amplification. Methods and Protocols, 2019, 2, 36.	2.0	6
9	Metatranscriptomic Analysis of Larval Guts from Field-Collected and Laboratory-Reared Spodoptera frugiperda from the South American Subtropical Region. Genome Announcements, 2015, 3, .	0.8	4
10	Polymerase chain reaction-based assay for the detection and identification of sand fly gregarines inLutzomyia longipalpis, a vector of visceral leishmaniasis. Journal of Vector Ecology, 2014, 39, 83-93.	1.0	3
11	Noise Minimisation in Gene Expression Switches. PLoS ONE, 2013, 8, e84020.	2.5	3
12	Digestion of I-Ppol Recognition Sites in Unfavorable Sequence Contexts Achieved by Changing the Reaction Conditions. Biochemical Genetics, 2006, 44, 58-65.	1.7	2
13	Soil Metagenomes from Different Pristine Environments of Northwest Argentina. Genome Announcements, 2015, 3, .	0.8	1
14	HoSeln: A Workflow for Integrating Various Homology Search Results from Metagenomic and Metatranscriptomic Sequence Datasets. Bio-protocol, 2020, 10, e3679.	0.4	0