Armanda Bastos

List of Publications by Year
in descending order

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		168829	145109
107	4,052	31	60
papers	citations	h-index	g-index

110	110	110	3233
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Risk assessment of urban yellow fever virus transmission in Kenya: is Aedes aegypti an efficient vector?. Emerging Microbes and Infections, 2022, , 1-26.	3.0	2
2	Editorial: Current Knowledge on Pathogenic and Endosymbiotic Tick-Borne Bacteria. Frontiers in Veterinary Science, 2022, 9, 900510.	0.9	0
3	Jingmen Tick Virus in Ticks from Kenya. Viruses, 2022, 14, 1041.	1.5	17
4	Tickâ€borne pathogens, including Crimeanâ€Congo haemorrhagic fever virus, at livestock markets and slaughterhouses in western Kenya. Transboundary and Emerging Diseases, 2021, 68, 2429-2445.	1.3	25
5	Sourcing Elephant Ivory from a Sixteenth-Century Portuguese Shipwreck. Current Biology, 2021, 31, 621-628.e4.	1.8	7
6	With or without a Vaccineâ€”A Review of Complementary and Alternative Approaches to Managing African Swine Fever in Resource-Constrained Smallholder Settings. Vaccines, 2021, 9, 116.	2.1	24
7	Molecular detection and characterization of novel haemotropic Mycoplasma in free-living mole rats from South Africa. Infection, Genetics and Evolution, 2021, 89, 104739.	1.0	3
8	A survey of mosquito-borne and insect-specific viruses in hospitals and livestock markets in western Kenya. PLoS ONE, 2021, 16, e0252369.	1.1	13
9	Molecular characterization of Trypanosoma vivax in tsetse flies confirms the presence of the virulent Tvv4 genotype in Kenya: Potential implications for the control of trypanosomiasis in Shimba Hills. Infection, Genetics and Evolution, 2021, 93, 104953.	1.0	2
10	Prevalence and Diversity of the Rat-bite Fever Agent, in Three Invasive, Commensal Species from South Africa. Yale Journal of Biology and Medicine, 2021, 94, 217-226.	0.2	2
11	Tsetse Bloodmeal Analyses Incriminate the Common Warthog Phacochoerus africanus as an Important Cryptic Host of Animal Trypanosomes in Smallholder Cattle Farming Communities in Shimba Hills, Kenya. Pathogens, 2021, 10, 1501.	1.2	4
12	Molecular prevalence and risk factors associated with tick-borne pathogens in cattle in western Kenya. BMC Veterinary Research, 2021, 17, 363.	0.7	10
13	A continent-wide high genetic load in African buffalo revealed by clines in the frequency of deleterious alleles, genetic hitchhiking and linkage disequilibrium. PLoS ONE, 2021, 16, e0259685.	1.1	2
14	Seroprevalence of Rift valley fever in South African domestic and wild suids (1999â€“2016). Transboundary and Emerging Diseases, 2020, 67, 811-821.	1.3	8
15	Multi-locus sequence analyses reveal a clonal L. borgpetersenii genotype in a heterogeneous invasive Rattus spp. community across the City of Johannesburg, South Africa. Parasites and Vectors, 2020, 13, 570.	1.0	5
16	Genome Sequences of Three African Swine Fever Viruses of Genotypes I, III, and XXII from South Africa and Zambia, Isolated from Ornithodoros Soft Ticks. Microbiology Resource Announcements, 2020, 9, .	0.3	11
17	Photoperiodic effects on the male gonads of the Namibian gerbil, Gerbilliscus cf. leucogaster from central Namibia. Mammalian Biology, 2020, 100, 165-171.	0.8	0
18	Mass Die-Off of African Elephants in Botswana: Pathogen, Poison or a Perfect Storm?. African Journal of Wildlife Research, 2020, 50, .	0.2	8

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19	Entomological assessment of dengue virus transmission risk in three urban areas of Kenya. PLoS Neglected Tropical Diseases, 2019, 13, e0007686.	1.3	18
20	A natural gene drive system influences bovine tuberculosis susceptibility in African buffalo: Possible implications for disease management. PLoS ONE, 2019, 14, e0221168.	1.1	1
21	Bartonella diversity and zoonotic potential in indigenous Tete Veld rats (Aethomys ineptus) from South Africa. Infection, Genetics and Evolution, 2019, 73, 44-48.	1.0	2
22	Evaluation of a Virus Neutralisation Test for Detection of Rift Valley Fever Antibodies in Suid Sera. Tropical Medicine and Infectious Disease, 2019, 4, 52.	0.9	10
23	Bartonellae of Synanthropic Four-Striped Mice (Rhabdomys pumilio) from the Western Cape Province, South Africa. Vector-Borne and Zoonotic Diseases, 2019, 19, 242-248.	0.6	1
24	Epidemiology of African swine fever in Africa today: Sylvatic cycle versus socioâ€economic imperatives. Transboundary and Emerging Diseases, 2019, 66, 672-686.	1.3	89
25	Multiâ€locus phylogeny of African pipits and longclaws (Aves: Motacillidae) highlights taxonomic inconsistencies. Ibis, 2019, 161, 781-792.	1.0	2
26	The reproductive pattern of the Gerbilliscus cf. leucogaster (Rodentia: Muridae) from Namibia. Canadian Journal of Zoology, 2019, 97, 57-62.	0.4	2
27	Genetic insights into dispersal distance and disperser fitness of African lions (Panthera leo) from the latitudinal extremes of the Kruger National Park, South Africa. BMC Genetics, 2018, 19, 21.	2.7	11
28	Attempted molecular detection of the thermally dimorphic human fungal pathogen Emergomyces africanus in terrestrial small mammals in South Africa. Medical Mycology, 2018, 56, 510-513.	0.3	15
29	Multi-locus sequence typing of African swine fever viruses from endemic regions of Kenya and Eastern Uganda (2011â€“2013) reveals rapid B602L central variable region evolution. Virus Genes, 2018, 54, 111-123.	0.7	29
30	Multi-locus phylogeny of southern African Acontias aurantiacus (Peters) subspecies (Scincidae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30 taxa. Zootaxa, 2018, 4442, 427-440.	0.2	4
31	Molecular assessment of Bartonella in Gerbillus nanus from Saudi Arabia reveals high levels of prevalence, diversity and co-infection. Infection, Genetics and Evolution, 2018, 65, 244-250.	1.0	6
32	Genetic responsiveness of African buffalo to environmental stressors: A role for epigenetics in balancing autosomal and sex chromosome interactions?. PLoS ONE, 2018, 13, e0191481.	1.1	6
33	The pattern of reproduction in the mole-ratHeliophobiusfrom Tanzania: do not refrain during the long rains!. Canadian Journal of Zoology, 2017, 95, 107-114.	0.4	10
34	Subterranean Mammals: Reservoirs of Infection or Overlooked Sentinels of Anthropogenic Environmental Soiling?. EcoHealth, 2017, 14, 662-674.	0.9	2
35	Pattern of ovulation in an ancient, solitary mole-rat lineage: Heliophobius argenteocinereus emini from Tanzania. Canadian Journal of Zoology, 2017, 95, 737-743.	0.4	2
36	Dengue and yellow fever virus vectors: seasonal abundance, diversity and resting preferences in three Kenyan cities. Parasites and Vectors, 2017, 10, 628.	1.0	33

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37	Assessment of risk of dengue and yellow fever virus transmission in three major Kenyan cities based on Stegomyia indices. PLoS Neglected Tropical Diseases, 2017, 11, e0005858.	1.3	30
38	Population differentiation in the context of Holocene climate change for a migratory marine species, the southern elephant seal. Journal of Evolutionary Biology, 2016, 29, 1667-1679.	0.8	19
39	Can Mathematics be Biologyâ€™s next microscope in disease research at the interface?. Biomath, 2016, 5, 1612237.	0.3	0
40	Evidence of a contact zone between twoRhabdomys dilectus(Rodentia: Muridae) mitotypes in Gauteng province, South Africa. African Zoology, 2015, 50, 63-68.	0.2	13
41	Molecular detection of novel Anaplasmataceae closely related to Anaplasma platys and Ehrlichia canis in the dromedary camel (Camelus dromedarius). Veterinary Microbiology, 2015, 179, 310-314.	0.8	64
42	Virus genome dynamics under different propagation pressures: reconstruction of whole genome haplotypes of west nile viruses from NGS data. BMC Genomics, 2015, 16, 118.	1.2	16
43	New insights into the role of ticks in African swine fever epidemiology. OIE Revue Scientifique Et Technique, 2015, 34, 503-511.	0.5	43
44	First molecular assessment of the African swine fever virus status of Ornithodoros ticks from Swaziland. Onderstepoort Journal of Veterinary Research, 2014, 81, E1-5.	0.6	7
45	Population Genetics of Two Key Mosquito Vectors of Rift Valley Fever Virus Reveals New Insights into the Changing Disease Outbreak Patterns in Kenya. PLoS Neglected Tropical Diseases, 2014, 8, e3364.	1.3	31
46	Drivers and risk factors for circulating African swine fever virus in Uganda, 2012â€“2013. Research in Veterinary Science, 2014, 97, 218-225.	0.9	25
47	Diversity of novel arenaviruses in South Africa. International Journal of Infectious Diseases, 2014, 21, 185.	1.5	0
48	African Swine Fever Virus. , 2014, , 579-588.		1
49	Positive Selection of Deleterious Alleles through Interaction with a Sex-Ratio Suppressor Gene in African Buffalo: A Plausible New Mechanism for a High Frequency Anomaly. PLoS ONE, 2014, 9, e111778.	1.1	4
50	Phytochemical analysis and in-vitro anti-African swine fever virus activity of extracts and fractions of Ancistrocladus uncinatus, Hutch and Dalziel (Ancistrocladaceae). BMC Veterinary Research, 2013, 9, 120.	0.7	4
51	Eastern rock sengis as reservoir hosts of Anaplasma bovis in South Africa. Ticks and Tick-borne Diseases, 2013, 4, 503-505.	1.1	13
52	African swine fever virus eradication in Africa. Virus Research, 2013, 173, 228-246.	1.1	152
53	Retrospective genetic characterisation of Encephalomyocarditis viruses from African elephant and swine recovers two distinct lineages in South Africa. Veterinary Microbiology, 2013, 162, 23-31.	0.8	9
54	Common Host-Derived Chemicals Increase Catches of Disease-Transmitting Mosquitoes and Can Improve Early Warning Systems for Rift Valley Fever Virus. PLoS Neglected Tropical Diseases, 2013, 7, e2007.	1.3	43

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55	Sheep Skin Odor Improves Trap Captures of Mosquito Vectors of Rift Valley Fever. PLoS Neglected Tropical Diseases, 2012, 6, e1879.	1.3	18
56	A mathematical epidemiological model of gram-negativeBartonellabacteria: does differential ectoparasite load fully explain the differences in infection prevalence ofRattus rattusandRattus norvegicus?. Journal of Biological Dynamics, 2012, 6, 763-781.	0.8	6
57	Risk factors for farm-level African swine fever infection in major pig-producing areas in Nigeria, 1997â€“2011. Preventive Veterinary Medicine, 2012, 107, 65-75.	0.7	56
58	Trapping of Rift Valley Fever (RVF) vectors using Light Emitting Diode (LED) CDC traps in two arboviral disease hot spots in Kenya. Parasites and Vectors, 2012, 5, 94.	1.0	18
59	Cost Implications of African Swine Fever in Smallholder Farrow-to-Finish Units: Economic Benefits of Disease Prevention Through Biosecurity. Transboundary and Emerging Diseases, 2012, 59, 244-255.	1.3	48
60	Bartonellae of the Namaqua rock mouse, Micaelamys namaquensis (Rodentia: Muridae) from South Africa. Veterinary Microbiology, 2012, 157, 132-136.	0.8	13
61	Multiple Geographic Origins of Commensalism and Complex Dispersal History of Black Rats. PLoS ONE, 2011, 6, e26357.	1.1	250
62	Cryptic species, biogeographic complexity and the evolutionary history of theEctemnorhinusgroup in the sub-Antarctic, including a description ofBothrometopus huntleyi, n. sp.. Antarctic Science, 2011, 23, 211-224.	0.5	15
63	Inter-island dispersal of flightless Bothrometopus huntleyi (Coleoptera: Curculionidae) from the sub-Antarctic Prince Edward Island archipelago. Antarctic Science, 2011, 23, 225-234.	0.5	9
64	Genetic monitoring detects an overlooked cryptic species and reveals the diversity and distribution of three invasive Rattus congeners in south Africa. BMC Genetics, 2011, 12, 26.	2.7	78
65	Trophic interrelationships between the exotic Nile tilapia, Oreochromis niloticus and indigenous tilapiine cichlids in a subtropical African river system (Limpopo River, South Africa). Environmental Biology of Fishes, 2011, 92, 479-489.	0.4	40
66	Molecular characterisation of African swine fever viruses from Nigeria (2003â€“2006) recovers multiple virus variants and reaffirms CVR epidemiological utility. Virus Genes, 2010, 41, 361-368.	0.7	34
67	Rainfall-driven sex-ratio genes in African buffalo suggested by correlations between Y-chromosomal haplotype frequencies and foetal sex ratio. BMC Evolutionary Biology, 2010, 10, 106.	3.2	15
68	A Case of Multi-vector and Multi-host Epidemiological Model: Bartonella Infection. , 2010, , .		0
69	Molecular monitoring of African swine fever virus using surveys targeted at adult Ornithodoros ticks : a re-evaluation of Mkuze Game Reserve, South Africa. Onderstepoort Journal of Veterinary Research, 2009, 76, 385-92.	0.6	17
70	The tusked king cricket, Libanasidus vittatus (Kirby, 1899) (Anostostomatidae), from South Africa: morphological and molecular evidence suggest two cryptic species. Insect Systematics and Evolution, 2009, 40, 85-103.	0.2	2
71	Role of Wild Suids in the Epidemiology of African Swine Fever. EcoHealth, 2009, 6, 296-310.	0.9	149
72	Genetic clues from olfactory cues: brown hyaena scent marks provide a non-invasive source of DNA for genetic profiling. Conservation Genetics, 2009, 10, 759-762.	0.8	4

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73	A host speciesâ€informative internal control for molecular assessment of African swine fever virus infection rates in the African sylvatic cycle Ornithodoros vector. Medical and Veterinary Entomology, 2009, 23, 399-409.	0.7	24
74	Intraspecific Patterns of Mitochondrial Variation in Natural Population Fragments of a Localized Desert Dung Beetle Species, Pachysoma gariepinum (Coleoptera: Scarabaeidae). Journal of Heredity, 2008, 99, 464-475.	1.0	4
75	Mass Mortality of Adult Male Subantarctic Fur Seals: Are Alien Mice the Culprits?. PLoS ONE, 2008, 3, e3757.	1.1	12
76	Do individual and combined data analyses of molecules and morphology reveal the generic status of 'Pachysoma' MacLeay (Coleoptera: Scarabaeidae)?. Insect Systematics and Evolution, 2007, 38, 311-330.	0.2	2
77	Selection at the Y Chromosome of the African Buffalo Driven by Rainfall. PLoS ONE, 2007, 2, e1086.	1.1	13
78	Genetic characterisation of African swine fever viruses from outbreaks in southern Africa (1973â€“1999). Veterinary Microbiology, 2007, 121, 45-55.	0.8	151
79	Intra-genotypic resolution of African swine fever viruses from an East African domestic pig cycle: a combined p72-CVR approach. Virus Genes, 2007, 35, 729-735.	0.7	56
80	Molecular and morphometric assessment of the taxonomic status of Ectemnorhinus weevil species (Coleoptera: Curculionidae, Entiminae) from the sub-Antarctic Prince Edward Islands. Journal of Zoological Systematics and Evolutionary Research, 2006, 44, 200-211.	0.6	19
81	Retrospective genetic analysis of SAT-1 type foot-and-mouth disease outbreaks in southern Africa. Archives of Virology, 2006, 151, 285-298.	0.9	32
82	Molecular epidemiology of African swine fever in East Africa. Archives of Virology, 2005, 150, 2439-2452.	0.9	135
83	Intra- and Inter-Genotypic Size Variation in the Central Variable Region of the 9RL Open Reading Frame of Diverse African Swine Fever Viruses. Virus Genes, 2005, 31, 357-360.	0.7	33
84	Phylogeography of the Namib Desert dung beetles Scarabaeus (Pachysoma) MacLeay (Coleoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.4	32
85	Co-circulation of two genetically distinct viruses in an outbreak of African swine fever in Mozambique: no evidence for individual co-infection. Veterinary Microbiology, 2004, 103, 169-182.	0.8	72
86	Low linkage disequilibrium indicative of recombination in foot-and-mouth disease virus gene sequence alignments. Journal of General Virology, 2004, 85, 1095-1100.	1.3	28
87	A first molecular epidemiological study of SAT-2 type foot-and-mouth disease viruses in West Africa. Epidemiology and Infection, 2004, 132, 525-532.	1.0	25
88	An investigation into the source and spread of foot and mouth disease virus from a wildlife conservancy in Zimbabwe. OIE Revue Scientifique Et Technique, 2004, 23, 783-790.	0.5	50
89	Foot and mouth disease in Mali: the current situation and proposed control strategies. OIE Revue Scientifique Et Technique, 2004, 23, 863-872.	0.5	8
90	An investigation into natural resistance to African swine fever in domestic pigs from an endemic area in southern Africa. OIE Revue Scientifique Et Technique, 2004, 23, 965-977.	0.5	77

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91	Molecular epidemiology of SAT3-type foot-and-mouth disease. Virus Genes, 2003, 27, 283-290.	0.7	41
92	Morphometric measurement selection: an invertebrate case study based on weevils from sub-Antarctic Marion Island. Polar Biology, 2003, 27, 38-49.	0.5	1
93	Genotyping field strains of African swine fever virus by partial p72 gene characterisation. Archives of Virology, 2003, 148, 693-706.	0.9	347
94	Retrospective genetic analysis of SAT-1 type foot-and-mouth disease outbreaks in West Africa (1975â€“1981). Veterinary Microbiology, 2003, 93, 279-289.	0.8	28
95	Development of a TaqManÂ® PCR assay with internal amplification control for the detection of African swine fever virus. Journal of Virological Methods, 2003, 107, 53-61.	1.0	392
96	Foot and mouth disease in wildlife. Virus Research, 2003, 91, 145-161.	1.1	216
97	The implications of virus diversity within the SAT 2 serotype for control of foot-and-mouth disease in sub-Saharan Africa. Journal of General Virology, 2003, 84, 1595-1606.	1.3	96
98	Genetic heterogeneity in the foot-and-mouth disease virus Leader and 3C proteinases. Gene, 2002, 289, 19-29.	1.0	49
99	The Possible Role That Buffalo Played in the Recent Outbreaks of Footâ€andâ€Mouth Disease in South Africa. Annals of the New York Academy of Sciences, 2002, 969, 187-190.	1.8	49
100	Isolation of a non-haemadsorbing, non-cytopathic strain of African swine fever virus in Madagascar. Epidemiology and Infection, 2001, 126, 453-459.	1.0	30
101	Genetic heterogeneity of SAT-1 type foot-and-mouth disease viruses in southern Africa. Archives of Virology, 2001, 146, 1537-1551.	0.9	82
102	Molecular epidemiology of serotype O foot-and-mouth disease virus with emphasis on West and South Africa. Virus Genes, 2001, 22, 345-351.	0.7	40
103	Natural transmission of foot-and-mouth disease virus between African buffalo (Syncerus caffer) and impala (Aepyceros melampus) in the Kruger National Park, South Africa. Epidemiology and Infection, 2000, 124, 591-598.	1.0	112
104	Possibility of sexual transmission of footâ€andâ€•mouth disease from African buffalo to cattle. Veterinary Record, 1999, 145, 77-79.	0.2	43
105	Persistent infection of African buffalo (Syncerus caffer) with SAT-type foot-and-mouth disease viruses: rate of fixation of mutations, antigenic change and interspecies transmission. Journal of General Virology, 1996, 77, 1457-1467.	1.3	104
106	Mitochondrial DNA Sequence Relationships of the Extinct Blue Antelope Hippotragus leucophaeus. Die Naturwissenschaften, 1996, 83, 178-182.	0.6	11
107	Dynamics of Rodent-Borne Zoonotic Diseases and Their Reservoir Hosts: Invasive Rattus in South Africa. Proceedings of the Vertebrate Pest Conference, 0, 25, .	0.1	5