## David O Odongo

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Phylogenetic analysis of the microbial populations in the wild herbivore gastrointestinal tract: insights into an unexplored niche. Environmental Microbiology, 2003, 5, 1212-1220.	3.8	95
2	A panel of microsatellite and minisatellite markers for the characterisation of field isolates of Theileria parva. International Journal for Parasitology, 2003, 33, 1641-1653.	3.1	77
3	Vaccination of cattle with TickGARD induces cross-reactive antibodies binding to conserved linear peptides of Bm86 homologues in Boophilus decoloratus. Vaccine, 2007, 25, 1287-1296.	3.8	62
4	Two Theileria parva CD8 T Cell Antigen Genes Are More Variable in Buffalo than Cattle Parasites, but Differ in Pattern of Sequence Diversity. PLoS ONE, 2011, 6, e19015.	2.5	62
5	Discovery of a novel species, Theileria haneyi n. sp., infective to equids, highlights exceptional genomic diversity within the genus Theileria: implications for apicomplexan parasite surveillance. International Journal for Parasitology, 2018, 48, 679-690.	3.1	61
6	A nested PCR assay exhibits enhanced sensitivity for detection of Theileria parva infections in bovine blood samples from carrier animals. Parasitology Research, 2010, 106, 357-365.	1.6	59
7	Subunit vaccine based on the p67 major surface protein of Theileria parva sporozoites reduces severity of infection derived from field tick challenge. Vaccine, 2005, 23, 3084-3095.	3.8	57
8	Novel Rickettsia and emergent tick-borne pathogens: A molecular survey of ticks and tick-borne pathogens in Shimba Hills National Reserve, Kenya. Ticks and Tick-borne Diseases, 2017, 8, 208-218.	2.7	44
9	Characterization of Tannin-tolerant Bacterial Isolates from East African Ruminants. Anaerobe, 2001, 7, 5-15.	2.1	40
10	The African buffalo parasite Theileria. sp. (buffalo) can infect and immortalize cattle leukocytes and encodes divergent orthologues ofÂTheileria parva antigen genes. International Journal for Parasitology: Parasites and Wildlife, 2015, 4, 333-342.	1.5	32
11	Prevalence of livestock diseases and their impact on livelihoods in Central Equatoria State, southern Sudan. Preventive Veterinary Medicine, 2012, 104, 216-223.	1.9	31
12	The genomes of three stocks comprising the most widely utilized live sporozoite Theileria parva vaccine exhibit very different degrees and patterns of sequence divergence. BMC Genomics, 2015, 16, 729.	2.8	31
13	Linkage disequilibrium between alleles at highly polymorphic mini- and micro-satellite loci of Theileria parva isolated from cattle in three regions of Kenya. International Journal for Parasitology, 2006, 36, 937-946.	3.1	30
14	A review of recent research on <i>Theileria parva</i> : Implications for the infection and treatment vaccination method for control of East Coast fever. Transboundary and Emerging Diseases, 2020, 67, 56-67.	3.0	28
15	Identification and sequence characterization of novel Theileria genotypes from the waterbuck (Kobus) Tj ETQq1	1 0.7843 1.8	14 rgBT /Ove
16	Molecular characterization of Echinococcus species in dogs from four regions of Kenya. Veterinary Parasitology, 2018, 255, 49-57.	1.8	27
17	Induction of humoral immune response to multiple recombinant Rhipicephalus appendiculatus antigens and their effect on tick feeding success and pathogen transmission. Parasites and Vectors, 2016, 9, 484.	2.5	25
18	Quantification of <i>Theileria parva</i> in <i>Rhipicephalus appendiculatus</i> (Acari: Ixodidae) Confirms Differences in Infection Between Selected Tick Strains. Journal of Medical Entomology, 2009, 46, 888-894.	1.8	23

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19	Secondary bacterial infections and antibiotic resistance among tungiasis patients in Western, Kenya. PLoS Neglected Tropical Diseases, 2017, 11, e0005901.	3.0	22
20	Identification of a synthetic peptide inducing cross-reactive antibodies binding to Rhipicephalus (Boophilus) decoloratus, Rhipicephalus (Boophilus) microplus, Hyalomma anatolicum anatolicum and Rhipicephalus appendiculatus BM86 homologues. Vaccine, 2009, 28, 261-269.	3.8	21
21	Zoonotic Pathogen Seroprevalence in Cattle in a Wildlife–Livestock Interface, Kenya. EcoHealth, 2019, 16, 712-725.	2.0	20
22	A participatory epidemiological study of major cattle diseases amongst Maasai pastoralists living in wildlife-livestock interfaces in Maasai Mara, Kenya. Tropical Animal Health and Production, 2019, 51, 1097-1103.	1.4	20
23	Equid infective Theileria cluster in distinct 18S rRNA gene clades comprising multiple taxa with unusually broad mammalian host ranges. Parasites and Vectors, 2020, 13, 261.	2.5	19
24	Spatial distribution, prevalence and potential risk factors of Tungiasis in Vihiga County, Kenya. PLoS Neglected Tropical Diseases, 2019, 13, e0007244.	3.0	17
25	Molecular evolution of a central region containing B cell epitopes in the gene encoding the p67 sporozoite antigen within a field population of Theileria parva. Parasitology Research, 2015, 114, 1729-1737.	1.6	15
26	Differential response to plant- and human-derived odorants in field surveillance of the dengue vector, Aedes aegypti. Acta Tropica, 2019, 200, 105163.	2.0	15
27	Differential transcription of two highly divergent gutâ€expressed Bm86 antigen gene homologues in the tick <i>Rhipicephalus appendiculatus</i> (Acari: Ixodida). Insect Molecular Biology, 2011, 20, 105-114.	2.0	14
28	Immunization of cattle with Ra86 impedes Rhipicephalus appendiculatus nymphal-to-adult molting. Ticks and Tick-borne Diseases, 2012, 3, 170-178.	2.7	12
29	Prevalence and genotyping of Echinococcus granulosus in sheep in Narok County, Kenya. Parasitology Research, 2018, 117, 2065-2073.	1.6	12
30	Genetic diversity and population structure of Theileria parva in South Sudan. Ticks and Tick-borne Diseases, 2018, 9, 806-813.	2.7	11
31	Genetic and antigenic variation of the bovine tick-borne pathogen Theileria parva in the Great Lakes region of Central Africa. Parasites and Vectors, 2019, 12, 588.	2.5	11
32	First detection of <i>Theileria parva</i> in cattle from Cameroon in the absence of the main tick vector <i>Rhipicephalus appendiculatus</i> . Transboundary and Emerging Diseases, 2020, 67, 68-78.	3.0	11
33	Genomic Polymorphism, Sexual Recombination and Molecular Epidemiology of Theileria Parva. World Class Parasites, 2002, , 23-39.	0.3	10
34	Theileria. , 2009, , 191-231.		10
35	Prevalence of tick-transmitted pathogens in cattle reveals that Theileria parva, Babesia bigemina and Anaplasma marginale are endemic in Burundi. Parasites and Vectors, 2021, 14, 6.	2.5	9
36	<i>Trypanosoma</i> Infection Rates in <i>Glossina</i> Species in Mtito Andei Division, Makueni County, Kenya. Journal of Parasitology Research, 2015, 2015, 1-8.	1.2	7

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37	Analysis of p67 allelic sequences reveals a subtype of allele type 1 unique to buffalo-derived Theileria parva parasites from southern Africa. PLoS ONE, 2020, 15, e0231434.	2.5	7
38	Diversity of Taenia and Hydatigera (Cestoda: Taeniidae) in domestic dogs in Kenya. Parasitology Research, 2020, 119, 2863-2875.	1.6	5
39	Seroprevalence of foot-and-mouth disease virus in cattle herds raised in Maasai Mara ecosystem in Kenya. Preventive Veterinary Medicine, 2020, 176, 104929.	1.9	5
40	Specific PCR Assay for a Tannin-Tolerant Selenomonas ruminantium Isolate, Derived from Helicase Coding Sequences. Applied and Environmental Microbiology, 2004, 70, 3180-3182.	3.1	4
41	Baseline analysis of Mycoplasma mycoides subsp. mycoides antigens as targets for a DIVA assay for use with a subunit vaccine for contagious bovine pleuropneumonia. BMC Veterinary Research, 2020, 16, 236.	1.9	4
42	Multilocus genotyping of Theileria parva isolates associated with a live vaccination trial in Kenya provides evidence for transmission of immunizing parasites into local tick and cattle populations. Transboundary and Emerging Diseases, 2020, 67, 88-98.	3.0	4
43	Bioactivity and toxicity of Bridelia micrantha, Chenopodium ambrosoides and Ocimum americanum plant extracts. International Journal of Basic and Clinical Pharmacology, 2016, 6, 5.	0.1	4
44	Variant analysis of the sporozoite surface antigen gene reveals that asymptomatic cattle from wildlife-livestock interface areas in northern Tanzania harbour buffalo-derived T. parva. Parasitology Research, 2020, 119, 3817-3828.	1.6	3
45	Microsatellite and minisatellite genotyping of Theileria parva population from southern Africa reveals possible discriminatory allele profiles with parasites from eastern Africa. Ticks and Tick-borne Diseases, 2020, 11, 101539.	2.7	3
46	Unique Mitochondrial Single Nucleotide Polymorphisms Demonstrate Resolution Potential to Discriminate Theileria parva Vaccine and Buffalo-Derived Strains. Life, 2020, 10, 334.	2.4	3
47	THEILERIOSIS IN MOUNTAIN BONGO REPATRIATED TO KENYA: A CLINICAL AND MOLECULAR INVESTIGATION. Journal of Zoo and Wildlife Medicine, 2019, 50, 342.	0.6	3
48	Antigen gene and variable number tandem repeat ( VNTR ) diversity in Theileria parva parasites from Ankole cattle in southâ€western Uganda: Evidence for conservation in antigen gene sequences combined with extensive polymorphism at VNTR loci. Transboundary and Emerging Diseases, 2020, 67, 99-107.	3.0	1
49	Preliminary Findings of Lipoprotein B in Detecting Cattle Chronically Infected with Contagious Bovine Pleuropneumonia. Journal of Veterinary Science & Medical Diagnosis, 2018, 07, .	0.0	1
50	A Simple Method for Storing Mosquito Bloodmeals for Human DNA Profiling. International Journal of Tropical Insect Science, 2002, 22, 155-158.	1.0	0
51	Limited diversity in the CD8+ antigen-coding loci in Theileria parva parasites from cattle from southern and eastern Africa. Veterinary Parasitology, 2021, 291, 109371.	1.8	0