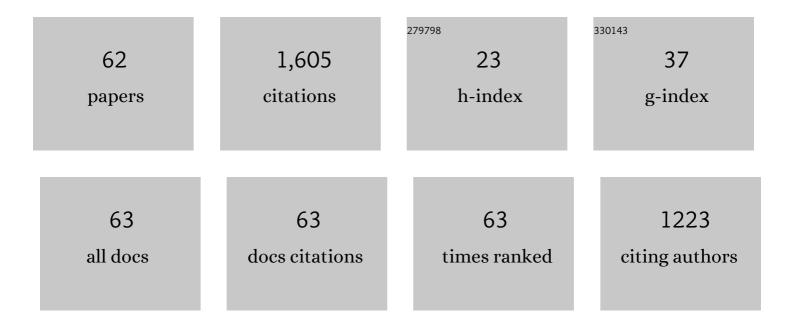
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Engineering of obligate intracellular bacteria: progress, challenges and paradigms. Nature Reviews Microbiology, 2017, 15, 544-558.	28.6	144
2	Current and Future Distribution of the Lone Star Tick, Amblyomma americanum (L.) (Acari: Ixodidae) in North America. PLoS ONE, 2019, 14, e0209082.	2.5	137
3	Persistent Ehrlichia chaffeensis Infection Occurs in the Absence of Functional Major Histocompatibility Complex Class II Genes. Infection and Immunity, 2002, 70, 380-388.	2.2	77
4	Multiplex Detection of Ehrlichia and Anaplasma Species Pathogens in Peripheral Blood by Real-Time Reverse Transcriptase-Polymerase Chain Reaction. Journal of Molecular Diagnostics, 2005, 7, 308-316.	2.8	72
5	Targeted and Random Mutagenesis of Ehrlichia chaffeensis for the Identification of Genes Required for In vivo Infection. PLoS Pathogens, 2013, 9, e1003171.	4.7	66
6	Ehrlichia chaffeensis Expresses Macrophage- and Tick Cell-Specific 28-Kilodalton Outer Membrane Proteins. Infection and Immunity, 2005, 73, 79-87.	2.2	63
7	Unique macrophage and tick cell-specific protein expression from the p28/p30-outer membrane protein multigene locus in Ehrlichia chaffeensis and Ehrlichia canis. Cellular Microbiology, 2006, 8, 1475-1487.	2.1	63
8	High prevalence of "Candidatus Rickettsia andeanae―and apparent exclusion of Rickettsia parkeri in adult Amblyomma maculatum (Acari: Ixodidae) from Kansas and Oklahoma. Ticks and Tick-borne Diseases, 2015, 6, 297-302.	2.7	49
9	Comparative Experimental Infection Study in Dogs with Ehrlichia canis, E. chaffeensis, Anaplasma platys and A. phagocytophilum. PLoS ONE, 2016, 11, e0148239.	2.5	48
10	Total, Membrane, and Immunogenic Proteomes of Macrophage- and Tick Cell-Derived <i>Ehrlichia chaffeensis</i> Evaluated by Liquid Chromatography-Tandem Mass Spectrometry and MALDI-TOF Methods. Infection and Immunity, 2008, 76, 4823-4832.	2.2	45
11	Differential Clearance and Immune Responses to Tick Cell-Derived versus Macrophage Culture-Derived Ehrlichia chaffeensis in Mice. Infection and Immunity, 2007, 75, 135-145.	2.2	43
12	Maximum Entropy-Based Ecological Niche Model and Bio-Climatic Determinants of Lone Star Tick (<i>Amblyomma americanum</i>) Niche. Vector-Borne and Zoonotic Diseases, 2016, 16, 205-211.	1.5	40
13	Delayed Clearance of Ehrlichia chaffeensis Infection in CD4 + T-Cell Knockout Miceâ€. Infection and Immunity, 2004, 72, 159-167.	2.2	39
14	Comparison of iatrogenic transmission of Anaplasma marginale in Holstein steers via needle and needle-free injection techniques. American Journal of Veterinary Research, 2010, 71, 1178-1188.	0.6	38
15	Aggregate-Reactivation Activity of the Molecular Chaperone ClpB from Ehrlichia chaffeensis. PLoS ONE, 2013, 8, e62454.	2.5	37
16	Assessing the current and future potential geographic distribution of the American dog tick, Dermacentor variabilis (Say) (Acari: Ixodidae) in North America. PLoS ONE, 2020, 15, e0237191.	2.5	36
17	Detection of <i>Anaplasma marginale</i> and <i>A. phagocytophilum</i> in Bovine Peripheral Blood Samples by Duplex Real-Time Reverse Transcriptase PCR Assay. Journal of Clinical Microbiology, 2010, 48, 2424-2432.	3.9	32
18	Transmission Electron Microscopy Reveals Distinct Macrophage- and Tick Cell-Specific Morphological Stages of Ehrlichia chaffeensis. PLoS ONE, 2012, 7, e36749.	2.5	30

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19	Attenuated Mutants of Ehrlichia chaffeensis Induce Protection against Wild-Type Infection Challenge in the Reservoir Host and in an Incidental Host. Infection and Immunity, 2015, 83, 2827-2835.	2.2	30
20	Ehrlichia chaffeensis Infection in the Reservoir Host (White-Tailed Deer) and in an Incidental Host (Dog) Is Impacted by Its Prior Growth in Macrophage and Tick Cell Environments. PLoS ONE, 2014, 9, e109056.	2.5	29
21	Vaccination with an Attenuated Mutant of Ehrlichia chaffeensis Induces Pathogen-Specific CD4+ T Cell Immunity and Protection from Tick-Transmitted Wild-Type Challenge in the Canine Host. PLoS ONE, 2016, 11, e0148229.	2.5	28
22	Laboratory Maintenance of <i>Ehrlichia chaffeensis</i> and <i>Ehrlichia canis</i> and Recovery of Organisms for Molecular Biology and Proteomics Studies. Current Protocols in Microbiology, 2008, 9, Unit 3A.1.	6.5	28
23	Mutations in Ehrlichia chaffeensis Causing Polar Effects in Gene Expression and Differential Host Specificities. PLoS ONE, 2015, 10, e0132657.	2.5	28
24	Rickettsia rickettsii Whole-Cell Antigens Offer Protection against Rocky Mountain Spotted Fever in the Canine Host. Infection and Immunity, 2019, 87, .	2.2	27
25	Identification of Critical Host Mitochondrion-Associated Genes during Ehrlichia chaffeensis Infections. Infection and Immunity, 2012, 80, 3576-3586.	2.2	23
26	The efficacy of three chlortetracycline regimens in the treatment of persistent Anaplasma marginale infection. Veterinary Microbiology, 2010, 145, 69-75.	1.9	22
27	Hierarchical Bayesian Spatio–Temporal Analysis of Climatic and Socio–Economic Determinants of Rocky Mountain Spotted Fever. PLoS ONE, 2016, 11, e0150180.	2.5	21
28	AMPâ€activated protein kinase (AMPK) regulates autophagy, inflammation and immunity and contributes to osteoclast differentiation and functionabs. Biology of the Cell, 2020, 112, 251-264.	2.0	21
29	Bayesian Space-Time Patterns and Climatic Determinants of Bovine Anaplasmosis. PLoS ONE, 2016, 11, e0151924.	2.5	21
30	A genetic system for targeted mutations to disrupt and restore genes in the obligate bacterium, Ehrlichia chaffeensis. Scientific Reports, 2017, 7, 15801.	3.3	17
31	Bayesian Spatio-Temporal Analysis and Geospatial Risk Factors of Human Monocytic Ehrlichiosis. PLoS ONE, 2014, 9, e100850.	2.5	17
32	Use of Drosophila S2 Cells as a Model for Studying Ehrlichia chaffeensis Infections. Applied and Environmental Microbiology, 2008, 74, 1886-1891.	3.1	15
33	Amblyomma americanum ticks infected with in vitro cultured wild-type and mutants of Ehrlichia chaffeensis are competent to produce infection in naÃ-ve deer and dogs. Ticks and Tick-borne Diseases, 2017, 8, 60-64.	2.7	15
34	Transcription of Ehrlichia chaffeensis Genes Is Accomplished by RNA Polymerase Holoenzyme Containing either Sigma 32 or Sigma 70. PLoS ONE, 2013, 8, e81780.	2.5	14
35	Promoter analysis of macrophage- and tick cell-specific differentially expressed Ehrlichia chaffeensis p28-Omp genes. BMC Microbiology, 2009, 9, 99.	3.3	13
36	Molecular detection and characterization of Anaplasma platys and Ehrlichia canis in dogs from the Caribbean. Ticks and Tick-borne Diseases, 2021, 12, 101727.	2.7	13

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37	Defining the immune response to Ehrlichia species using murine models. Veterinary Parasitology, 2008, 158, 344-359.	1.8	11
38	Isolation and characterization of Ehrlichia chaffeensis RNA polymerase and its use in evaluating p28 outer membrane protein gene promoters. BMC Microbiology, 2011, 11, 83.	3.3	11
39	Heterogeneous Associations of Ecological Attributes with Tick-Borne Rickettsial Pathogens in a Periurban Landscape. Vector-Borne and Zoonotic Diseases, 2016, 16, 569-576.	1.5	11
40	Antigen-Specific CD4+CD8+ Double-Positive T Cells Are Increased in the Blood and Spleen During Ehrlichia chaffeensis Infection in the Canine Host. Frontiers in Immunology, 2018, 9, 1585.	4.8	11
41	Genetic characterization of extraintestinal Escherichia coli isolates from chicken, cow and swine. AMB Express, 2018, 8, 117.	3.0	10
42	Multiple Ehrlichia chaffeensis Genes Critical for Its Persistent Infection in a Vertebrate Host Are Identified by Random Mutagenesis Coupled with <i>In Vivo</i> Infection Assessment. Infection and Immunity, 2020, 88, .	2.2	10
43	Protein aggregation in Ehrlichia chaffeensis during infection of mammalian cells. FEMS Microbiology Letters, 2017, 364, .	1.8	9
44	Sequence determinants spanning -35 motif and AT-rich spacer region impactingEhrlichia chaffeensisSigma 70-dependent promoter activity of two differentially expressed p28 outer membrane protein genes. DNA Research, 2016, 23, 495-505.	3.4	9
45	Experimental infection of Rhipicephalus sanguineus with Ehrlichia chaffeensis. Veterinary Microbiology, 2014, 172, 334-338.	1.9	8
46	Impact of Three Different Mutations in Ehrlichia chaffeensis in Altering the Global Gene Expression Patterns. Scientific Reports, 2018, 8, 6162.	3.3	8
47	Bovine anaplasmosis herd prevalence and management practices as risk-factors associated with herd disease status. Veterinary Parasitology: X, 2020, 277, 100021.	2.7	8
48	Initial development and preliminary evaluation of a multiplex bead assay to detect antibodies to Ehrlichia canis, Anaplasma platys, and Ehrlichia chaffeensis outer membrane peptides in naturally infected dogs from Grenada, West Indies. Journal of Veterinary Diagnostic Investigation, 2017, 29, 109-114.	1.1	7
49	Protein and DNA synthesis demonstrated in cell-free Ehrlichia chaffeensis organisms in axenic medium. Scientific Reports, 2018, 8, 9293.	3.3	7
50	Development of a Multiplex PCR and Magnetic DNA Capture Assay for Detecting Six Species Pathogens of the Genera Anaplasma and Ehrlichia in Canine, Bovine, Caprine and Ovine Blood Samples from Grenada, West Indies. Pathogens, 2021, 10, 192.	2.8	7
51	Proteome Analysis Revealed Changes in Protein Expression Patterns Caused by Mutations in Ehrlichia chaffeensis. Frontiers in Cellular and Infection Microbiology, 2019, 9, 58.	3.9	6
52	Unexpected winter questing activity of ticks in the Central Midwestern United States. PLoS ONE, 2021, 16, e0259769.	2.5	6
53	The transcriptome of the lone star tick, Amblyomma americanum, reveals molecular changes in response to infection with the pathogen, Ehrlichia chaffeensis. Journal of Asia-Pacific Entomology, 2018, 21, 852-863.	0.9	5
54	Protein and DNA Biosynthesis Demonstrated in Host Cell-Free Phagosomes Containing Anaplasma phagocytophilum or Ehrlichia chaffeensis in Axenic Media. Infection and Immunity, 2021, 89, .	2.2	4

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55	Targeted mutagenesis in Anaplasma marginale to define virulence and vaccine development against bovine anaplasmosis. PLoS Pathogens, 2022, 18, e1010540.	4.7	4
56	Mutations in Ehrlichia chaffeensis Genes ECH_0660 and ECH_0665 Cause Transcriptional Changes in Response to Zinc or Iron Limitation. Journal of Bacteriology, 2021, 203, e0002721.	2.2	3
57	Sequence Determinants Spanning â^10 Motif and Spacer Region Implicated in Unique Ehrlichia chaffeensis Sigma 32-Dependent Promoter Activity of dnaK Gene. Frontiers in Microbiology, 2019, 10, 1772.	3.5	2
58	Experimental Infection of North American Sheep with Ehrlichia ruminantium. Pathogens, 2021, 10, 451.	2.8	2
59	Functional Characterization of Multiple Ehrlichia chaffeensis Sodium (Cation)/Proton Antiporter Genes Involved in the Bacterial pH Homeostasis. International Journal of Molecular Sciences, 2021, 22, 8420.	4.1	2
60	Isolation and Molecular Detection of <i>Ehrlichia</i> from Vertebrate Animals. Current Protocols in Microbiology, 2008, 9, Unit 3A.3.	6.5	2
61	Identification of T-Cell Epitopes in the Murine Host Response to Ehrlichia chaffeensis. , 2016, , 197-214.		1
62	Mutagenesis in Ehrlichia and Anaplasma Species: Its Application for Studies Focused on Understanding the Pathogenesis and Vaccine Development. , 2016, , 215-224.		0