

Kelly A Brayton

List of Publications by Year in descending order

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111
papers

3,970
citations

136885

32
h-index

149623

56
g-index

112
all docs

112
docs citations

112
times ranked

2625
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Sequence of <i>Babesia bovis</i> and Comparative Analysis of Apicomplexan Hemoprotozoa. <i>PLoS Pathogens</i> , 2007, 3, e148.	2.1	335
2	Complete genome sequencing of <i>Anaplasma marginale</i> reveals that the surface is skewed to two superfamilies of outer membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 844-849.	3.3	238
3	The bacterial microbiome of <i>Dermacentor andersoni</i> ticks influences pathogen susceptibility. <i>ISME Journal</i> , 2016, 10, 1846-1855.	4.4	162
4	The genome of the heartwater agent <i>Ehrlichia ruminantium</i> contains multiple tandem repeats of actively variable copy number. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 838-843.	3.3	158
5	Polymorphisms in the prion precursor functional gene but not the pseudogene are associated with susceptibility to chronic wasting disease in white-tailed deer. <i>Journal of General Virology</i> , 2004, 85, 1339-1346.	1.3	152
6	Engineering of obligate intracellular bacteria: progress, challenges and paradigms. <i>Nature Reviews Microbiology</i> , 2017, 15, 544-558.	13.6	144
7	Antigenic variation of <i>Anaplasma marginale</i> msp2 occurs by combinatorial gene conversion. <i>Molecular Microbiology</i> , 2002, 43, 1151-1159.	1.2	124
8	Phylogenomics Reveals a Diverse <i>Rickettsiales</i> Type IV Secretion System. <i>Infection and Immunity</i> , 2010, 78, 1809-1823.	1.0	101
9	Identification of Novel Antigenic Proteins in a Complex <i>Anaplasma marginale</i> Outer Membrane Immunogen by Mass Spectrometry and Genomic Mapping. <i>Infection and Immunity</i> , 2005, 73, 8109-8118.	1.0	92
10	Superinfection as a driver of genomic diversification in antigenically variant pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2123-2127.	3.3	81
11	Proteomics informed by transcriptomics identifies novel secreted proteins in <i>Dermacentor andersoni</i> saliva. <i>International Journal for Parasitology</i> , 2014, 44, 1029-1037.	1.3	75
12	Composition of the Surface Proteome of <i>Anaplasma marginale</i> and Its Role in Protective Immunity Induced by Outer Membrane Immunization. <i>Infection and Immunity</i> , 2008, 76, 2219-2226.	1.0	70
13	The characterization and manipulation of the bacterial microbiome of the Rocky Mountain wood tick, <i>Dermacentor andersoni</i> . <i>Parasites and Vectors</i> , 2015, 8, 632.	1.0	68
14	Stochastic Transmission of Multiple Genotypically Distinct <i>Anaplasma marginale</i> Strains in a Herd with High Prevalence of <i>Anaplasma</i> Infection. <i>Journal of Clinical Microbiology</i> , 2004, 42, 5381-5384.	1.8	67
15	Immunogenicity of <i>Anaplasma marginale</i> Type IV Secretion System Proteins in a Protective Outer Membrane Vaccine. <i>Infection and Immunity</i> , 2007, 75, 2333-2342.	1.0	62
16	Gene conversion is a convergent strategy for pathogen antigenic variation. <i>Trends in Parasitology</i> , 2007, 23, 408-413.	1.5	60
17	Conservation in the face of diversity: multistrain analysis of an intracellular bacterium. <i>BMC Genomics</i> , 2009, 10, 16.	1.2	55
18	Conservation of a gene conversion mechanism in two distantly related paralogues of <i>Anaplasma marginale</i> . <i>Molecular Microbiology</i> , 2003, 47, 633-643.	1.2	53

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19	Identification of <i>Anaplasma marginale</i> Type IV Secretion System Effector Proteins. <i>PLoS ONE</i> , 2011, 6, e27724.	1.1	53
20	Structural basis for segmental gene conversion in generation of <i>Anaplasma marginale</i> outer membrane protein variants. <i>Molecular Microbiology</i> , 2005, 57, 212-221.	1.2	52
21	Temporal characterisation of the organ-specific <i>Rhipicephalus microplus</i> transcriptional response to <i>Anaplasma marginale</i> infection. <i>International Journal of Parasitology</i> , 2011, 41, 851-860.	1.3	51
22	Distinctly different <i>msp2</i> pseudogene repertoires in <i>Anaplasma marginale</i> strains that are capable of superinfection. <i>Gene</i> , 2005, 361, 127-132.	1.0	50
23	Differential Expression and Sequence Conservation of the <i>Anaplasma marginale msp2</i> Gene Superfamily Outer Membrane Proteins. <i>Infection and Immunity</i> , 2006, 74, 3471-3479.	1.0	49
24	Expression of <i>Anaplasma marginale</i> Major Surface Protein 2 Operon-Associated Proteins during Mammalian and Arthropod Infection. <i>Infection and Immunity</i> , 2002, 70, 6005-6012.	1.0	48
25	A processed pseudogene contributes to apparent mule deer prion gene heterogeneity. <i>Gene</i> , 2004, 326, 167-173.	1.0	46
26	Identification of functional promoters in the <i>msp2</i> expression loci of <i>Anaplasma marginale</i> and <i>Anaplasma phagocytophilum</i> . <i>Gene</i> , 2005, 353, 89-97.	1.0	46
27	Complete Genome Sequence of <i>Anaplasma marginale</i> subsp. <i>centrale</i> . <i>Journal of Bacteriology</i> , 2010, 192, 379-380.	1.0	45
28	Characterization of a major outer membrane protein multigene family in <i>Ehrlichia ruminantium</i> . <i>Gene</i> , 2004, 330, 159-168.	1.0	43
29	Simultaneous Variation of the Immunodominant Outer Membrane Proteins, MSP2 and MSP3, during <i>Anaplasma marginale</i> Persistence In Vivo. <i>Infection and Immunity</i> , 2003, 71, 6627-6632.	1.0	41
30	<i>Anaplasma marginale</i> Type IV Secretion System Proteins VirB2, VirB7, VirB11, and VirD4 Are Immunogenic Components of a Protective Bacterial Membrane Vaccine. <i>Infection and Immunity</i> , 2010, 78, 1314-1325.	1.0	41
31	The Hypervariable Region of <i>Anaplasma marginale</i> Major Surface Protein 2 (MSP2) Contains Multiple Immunodominant CD4+T Lymphocyte Epitopes That Elicit Variant-Specific Proliferative and IFN- γ Responses in MSP2 Vaccinates. <i>Journal of Immunology</i> , 2003, 170, 3790-3798.	0.4	40
32	Gut transcriptome of replete adult female cattle ticks, <i>Rhipicephalus (Boophilus) microplus</i> , feeding upon a <i>Babesia bovis</i> -infected bovine host. <i>Parasitology Research</i> , 2013, 112, 3075-3090.	0.6	37
33	Genomic and proteomic approaches to vaccine candidate identification for <i>Anaplasma marginale</i> . <i>Expert Review of Vaccines</i> , 2006, 5, 95-101.	2.0	35
34	Expansion of Variant Diversity Associated with a High Prevalence of Pathogen Strain Superinfection under Conditions of Natural Transmission. <i>Infection and Immunity</i> , 2012, 80, 2354-2360.	1.0	35
35	Characterization of a Novel Microcin That Kills Enterohemorrhagic <i>Escherichia coli</i> O157:H7 and O26. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6592-6599.	1.4	35
36	Prediction of T4SS Effector Proteins for <i>Anaplasma phagocytophilum</i> Using OPT4e, A New Software Tool. <i>Frontiers in Microbiology</i> , 2019, 10, 1391.	1.5	32

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37	Comparison of ovine herpesvirus 2 genomes isolated from domestic sheep (<i>Ovis aries</i>) and a clinically affected cow (<i>Bos bovis</i>). <i>Journal of General Virology</i> , 2007, 88, 40-45.	1.3	31
38	Expression of Major Surface Protein 2 Variants with Conserved T-Cell Epitopes in <i>Anaplasma centrale</i> Vaccinates. <i>Infection and Immunity</i> , 2002, 70, 642-648.	1.0	30
39	RepeatAnalyzer: a tool for analysing and managing short-sequence repeat data. <i>BMC Genomics</i> , 2016, 17, 422.	1.2	30
40	Analysis of <i>Babesia bovis</i> infection-induced gene expression changes in larvae from the cattle tick, <i>Rhipicephalus (Boophilus) microplus</i> . <i>Parasites and Vectors</i> , 2012, 5, 162.	1.0	29
41	Genome-wide screening and identification of antigens for rickettsial vaccine development: 1. <i>FEMS Immunology and Medical Microbiology</i> , 2012, 64, 115-119.	2.7	29
42	Laboratory colonization stabilizes the naturally dynamic microbiome composition of field collected <i>Dermacentor andersoni</i> ticks. <i>Microbiome</i> , 2017, 5, 133.	4.9	27
43	Maintenance of Antibody to Pathogen Epitopes Generated by Segmental Gene Conversion Is Highly Dynamic during Long-Term Persistent Infection. <i>Infection and Immunity</i> , 2007, 75, 5185-5190.	1.0	26
44	<i>Anaplasma marginale</i> Infection with Persistent High-Load Bacteremia Induces a Dysfunctional Memory CD4 ⁺ T Lymphocyte Response but Sustained High IgG Titers. <i>Vaccine Journal</i> , 2010, 17, 1881-1890.	3.2	26
45	Identification of <i>Anaplasma marginale</i> Proteins Specifically Upregulated during Colonization of the Tick Vector. <i>Infection and Immunity</i> , 2010, 78, 3047-3052.	1.0	26
46	Identification of <i>Anaplasma marginale</i> Outer Membrane Protein Antigens Conserved between <i>A. marginale</i> Sensu Stricto Strains and the Live <i>A. marginale</i> subsp. <i>centrale</i> Vaccine. <i>Infection and Immunity</i> , 2011, 79, 1311-1318.	1.0	26
47	Generation of Antigenic Variants via Gene Conversion: Evidence for Recombination Fitness Selection at the Locus Level in <i>Anaplasma marginale</i> . <i>Infection and Immunity</i> , 2009, 77, 3181-3187.	1.0	24
48	Stability and Tick Transmission Phenotype of <i>gfp</i> -Transformed <i>Anaplasma marginale</i> through a Complete <i>In Vivo</i> Infection Cycle. <i>Applied and Environmental Microbiology</i> , 2011, 77, 330-334.	1.4	24
49	Antigenic variation and transmission fitness as drivers of bacterial strain structure. <i>Cellular Microbiology</i> , 2013, 15, 1969-1975.	1.1	24
50	Expression Patterns of <i>Anaplasma marginale</i> msp2 Variants Change in Response to Growth in Cattle, and Tick Cells versus Mammalian Cells. <i>PLoS ONE</i> , 2012, 7, e36012.	1.1	24
51	Selection for Simple Major Surface Protein 2 Variants during <i>Anaplasma marginale</i> Transmission to Immunologically Naïve Animals. <i>Infection and Immunity</i> , 2007, 75, 1502-1506.	1.0	23
52	Subdominant Outer Membrane Antigens in <i>Anaplasma marginale</i> : Conservation, Antigenicity, and Protective Capacity Using Recombinant Protein. <i>PLoS ONE</i> , 2015, 10, e0129309.	1.1	23
53	Characterization of <i>Anaplasma marginale</i> subsp. <i>centrale</i> Strains by Use of msp1aS Genotyping Reveals a Wildlife Reservoir. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2503-2512.	1.8	23
54	An optimal set of features for predicting type IV secretion system effector proteins for a subset of species based on a multi-level feature selection approach. <i>PLoS ONE</i> , 2018, 13, e0197041.	1.1	23

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55	Comparative analysis of gene expression between <i>Babesia bovis</i> blood stages and kinetes allowed by improved genome annotation. <i>International Journal for Parasitology</i> , 2021, 51, 123-136.	1.3	23
56	<i>Anaplasma phagocytophilum</i> and Other <i>Anaplasma</i> spp. in Various Hosts in the Mnisi Community, Mpumalanga Province, South Africa. <i>Microorganisms</i> , 2020, 8, 1812.	1.6	22
57	Protective immunity induced by immunization with a live, cultured <i>Anaplasma marginale</i> strain. <i>Vaccine</i> , 2013, 31, 3617-3622.	1.7	21
58	Preparation of <i>Ehrlichia ruminantium</i> challenge material for quantifiable and reproducible challenge in mice and sheep. <i>Veterinary Parasitology</i> , 2003, 112, 63-73.	0.7	20
59	The <i>Babesia bovis</i> Merozoite Surface Antigen 1 Hypervariable Region Induces Surface-Reactive Antibodies That Block Merozoite Invasion. <i>Infection and Immunity</i> , 2006, 74, 3663-3667.	1.0	19
60	Tick-Borne Transmission of Two Genetically Distinct <i>Anaplasma marginale</i> Strains following Superinfection of the Mammalian Reservoir Host. <i>Infection and Immunity</i> , 2008, 76, 4066-4070.	1.0	19
61	Independence of <i>Anaplasma marginale</i> Strains with High and Low Transmission Efficiencies in the Tick Vector following Simultaneous Acquisition by Feeding on a Superinfected Mammalian Reservoir Host. <i>Infection and Immunity</i> , 2009, 77, 1459-1464.	1.0	19
62	Expression and strain variation of the novel <i>smorf</i> multigene family in <i>Babesia bovis</i> . <i>International Journal for Parasitology</i> , 2012, 42, 131-138.	1.3	19
63	Genetic Diversity of Tick-Borne Rickettsial Pathogens; Insights Gained from Distant Strains. <i>Pathogens</i> , 2014, 3, 57-72.	1.2	19
64	Reduced Infectivity in Cattle for an Outer Membrane Protein Mutant of <i>Anaplasma marginale</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 2206-2214.	1.4	19
65	Detection and Characterisation of <i>Anaplasma marginale</i> and <i>A. centrale</i> in South Africa. <i>Veterinary Sciences</i> , 2018, 5, 26.	0.6	19
66	Identification of a Novel <i>Anaplasma marginale</i> Appendage-Associated Protein That Localizes with Actin Filaments during Intraerythrocytic Infection. <i>Infection and Immunity</i> , 2004, 72, 7257-7264.	1.0	18
67	The immunization-induced antibody response to the <i>Anaplasma marginale</i> major surface protein 2 and its association with protective immunity. <i>Vaccine</i> , 2010, 28, 3741-3747.	1.7	18
68	Using an optimal set of features with a machine learning-based approach to predict effector proteins for <i>Legionella pneumophila</i> . <i>PLoS ONE</i> , 2019, 14, e0202312.	1.1	18
69	Co-infections with multiple genotypes of <i>Anaplasma marginale</i> in cattle indicate pathogen diversity. <i>Parasites and Vectors</i> , 2018, 11, 5.	1.0	17
70	The Use and Limitations of the 16S rRNA Sequence for Species Classification of <i>Anaplasma</i> Samples. <i>Microorganisms</i> , 2022, 10, 605.	1.6	17
71	Insights into Mechanisms of Bacterial Antigenic Variation Derived from the Complete Genome Sequence of <i>Anaplasma marginale</i> . <i>Annals of the New York Academy of Sciences</i> , 2006, 1078, 15-25.	1.8	16
72	Comparative genomics and transcriptomics of trait-gene association. <i>BMC Genomics</i> , 2012, 13, 669.	1.2	16

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73	Development of Improved Vaccines for Heartwater. <i>Annals of the New York Academy of Sciences</i> , 2003, 990, 474-484.	1.8	15
74	Analysis of the <i>Anaplasma marginale</i> Major Surface Protein 1 Complex Protein Composition by Tandem Mass Spectrometry. <i>Journal of Bacteriology</i> , 2006, 188, 4983-4991.	1.0	15
75	Conservation of the unique rickettsial rRNA gene arrangement in <i>Anaplasma</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 1405-1409.	0.8	14
76	Characterization of the <i>Anaplasma marginale</i> msp2 locus and its synteny with the omp1/p30 loci of <i>Ehrlichia chaffeensis</i> and <i>E. canis</i> . <i>Gene</i> , 2004, 325, 115-121.	1.0	13
77	Transcriptional pathways associated with the slow growth phenotype of transformed <i>Anaplasma marginale</i> . <i>BMC Genomics</i> , 2013, 14, 272.	1.2	13
78	The <i>Anaplasma ovis</i> genome reveals a high proportion of pseudogenes. <i>BMC Genomics</i> , 2019, 20, 69.	1.2	13
79	Transcriptome dataset of <i>Babesia bovis</i> life stages within vertebrate and invertebrate hosts. <i>Data in Brief</i> , 2020, 33, 106533.	0.5	13
80	Evidence confirming the phylogenetic position of <i>Anaplasma centrale</i> (ex Theiler 1911) Ristic and Kreier 1984. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2682-2691.	0.8	13
81	CD4 + T Lymphocytes from <i>Anaplasma marginale</i> Major Surface Protein 2 (MSP2) Vaccinees Recognize Naturally Processed Epitopes Conserved in MSP3. <i>Infection and Immunity</i> , 2004, 72, 3688-3692.	1.0	12
82	Global transcriptional analysis reveals surface remodeling of <i>Anaplasma marginale</i> in the tick vector. <i>Parasites and Vectors</i> , 2014, 7, 193.	1.0	11
83	Comparative genomics reveals multiple pathways to mutualism for tick-borne pathogens. <i>BMC Genomics</i> , 2016, 17, 481.	1.2	11
84	Quantitative analysis of <i>Anaplasma marginale</i> acquisition and transmission by <i>Dermacentor andersoni</i> fed in vitro. <i>Scientific Reports</i> , 2020, 10, 470.	1.6	11
85	Comparison of three nucleic acid-based tests for detecting <i>Anaplasma marginale</i> and <i>Anaplasma centrale</i> in cattle. <i>Onderstepoort Journal of Veterinary Research</i> , 2017, 84, e1-e9.	0.6	10
86	A Systematic Approach to Bacterial Phylogeny Using Order Level Sampling and Identification of HGT Using Network Science. <i>Microorganisms</i> , 2020, 8, 312.	1.6	9
87	Expression of <i>Anaplasma marginale</i> Ankyrin Repeat-Containing Proteins during Infection of the Mammalian Host and Tick Vector. <i>Infection and Immunity</i> , 2011, 79, 2847-2855.	1.0	8
88	<i>Anaplasma</i> . , 2009, , 85-116.		8
89	Association of Pathogen Strain-Specific Gene Transcription and Transmission Efficiency Phenotype of <i>Anaplasma marginale</i> . <i>Infection and Immunity</i> , 2010, 78, 2446-2453.	1.0	7
90	Superinfection Exclusion of the Ruminant Pathogen <i>Anaplasma marginale</i> in Its Tick Vector Is Dependent on the Time between Exposures to the Strains. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3217-3224.	1.4	7

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91	Biostatistical prediction of genes essential for growth of <i>Anaplasma phagocytophilum</i> in a human promyelocytic cell line using a random transposon mutant library. <i>Pathogens and Disease</i> , 2021, 79, .	0.8	7
92	Whole Proteome Clustering of 2,307 Proteobacterial Genomes Reveals Conserved Proteins and Significant Annotation Issues. <i>Frontiers in Microbiology</i> , 2019, 10, 383.	1.5	6
93	A conserved coccidian gene is involved in <i>Toxoplasma</i> sensitivity to the anti-apicomplexan compound, tartrolon E. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2020, 14, 1-7.	1.4	6
94	Automated Confirmation of Protein Annotation Using NLP and the UniProtKB Database. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 24.	1.3	6
95	Succinate dehydrogenase gene arrangement and expression in <i>Anaplasma phagocytophilum</i> . <i>Gene</i> , 2008, 414, 41-48.	1.0	5
96	Identification of Multilocus Genetic Heterogeneity in <i>Anaplasma marginale</i> subsp. <i>centrale</i> and Its Restriction following Tick-Borne Transmission. <i>Infection and Immunity</i> , 2013, 81, 1852-1858.	1.0	5
97	Identification of <i>Anaplasma ovis</i> appendage-associated protein (AAP) for development of an indirect ELISA and its application. <i>Parasites and Vectors</i> , 2017, 10, 359.	1.0	5
98	<i>Anaplasma ovis</i> as the suspected cause of mortality in a neonatal elk calf. <i>Journal of Veterinary Diagnostic Investigation</i> , 2019, 31, 267-270.	0.5	5
99	Predicted iron metabolism genes in hard ticks and their response to iron reduction in <i>Dermacentor andersoni</i> cells. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101584.	1.1	5
100	Growth of <i>Mannheimia haemolytica</i> : Inhibitory agents and putative mechanism of inhibition. <i>Veterinary Microbiology</i> , 2014, 174, 155-162.	0.8	4
101	Segmental Variation in a Duplicated <i>msp2</i> Pseudogene Generates <i>Anaplasma marginale</i> Antigenic Variants. <i>Infection and Immunity</i> , 2019, 87, .	1.0	4
102	Both co-infection and superinfection drive complex <i>Anaplasma marginale</i> strain structure in a natural transmission setting. <i>Infection and Immunity</i> , 2021, 89, e0016621.	1.0	4
103	A nearest-neighbors network model for sequence data reveals new insight into genotype distribution of a pathogen. <i>BMC Bioinformatics</i> , 2018, 19, 475.	1.2	3
104	<i>Anaplasma marginale</i> outer membrane protein vaccine candidates are conserved in North American and South African strains. <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101444.	1.1	3
105	Transcriptional Profiling of a Cross-Protective <i>Salmonella enterica</i> serovar Typhimurium UK-1 dam Mutant Identifies a Set of Genes More Transcriptionally Active Compared to Wild-Type, and Stably Transcribed across Biologically Relevant Microenvironments. <i>Pathogens</i> , 2014, 3, 417-436.	1.2	2
106	Genome Sequence of <i>Bibersteinia trehalosi</i> Strain Y31 Isolated from the Pneumonic Lung of a Bighorn Sheep. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
107	Identification of <i>Rhipicephalus microplus</i> Genes That Modulate the Infection Rate of the <i>Rickettsia Anaplasma marginale</i> . <i>PLoS ONE</i> , 2014, 9, e91062.	1.1	1
108	Dynamics of repeat-associated plasticity in the <i>aaap</i> gene family in <i>Anaplasma marginale</i> . <i>Gene: X</i> , 2019, 721, 100010.	2.3	1

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109	Iron Reduction in Dermacentor andersoni Tick Cells Inhibits Anaplasma marginale Replication. International Journal of Molecular Sciences, 2022, 23, 3941.	1.8	1
110	PASS: Protein Annotation Surveillance Site for Protein Annotation Using Homologous Clusters, NLP, and Sequence Similarity Networks. Frontiers in Bioinformatics, 2021, 1, .	1.0	0
111	Persistence and Antigenic Variation. , 0, , 366-390.		0