

# 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	The Use and Limitations of the 16S rRNA Sequence for Species Classification of Anaplasma Samples. <i>Microorganisms</i> , 2022, 10, 605.	1.6	17
2	Iron Reduction in <i>Dermacentor andersoni</i> Tick Cells Inhibits <i>Anaplasma marginale</i> Replication. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3941.	1.8	1
3	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
4	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
5	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
6	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
7	PASS: Protein Annotation Surveillance Site for Protein Annotation Using Homologous Clusters, NLP, and Sequence Similarity Networks. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	0
8	Automated Confirmation of Protein Annotation Using NLP and the UniProtKB Database. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 24.	1.3	6
9	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
10	<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
11	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
12	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
13	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
14	<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
15	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
16	The <i>Anaplasma ovis</i> genome reveals a high proportion of pseudogenes. <i>BMC Genomics</i> , 2019, 20, 69.	1.2	13
17	Dynamics of repeat-associated plasticity in the aaap gene family in <i>Anaplasma marginale</i> . <i>Gene: X</i> , 2019, 721, 100010.	2.3	1
18	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

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19	<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
20	Segmental Variation in a Duplicated msp2 Pseudogene Generates <i>Anaplasma marginale</i> Antigenic Variants. <i>Infection and Immunity</i> , 2019, 87, .	1.0	4
21	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
22	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
23	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
24	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
25	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
26	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
27	Engineering of obligate intracellular bacteria: progress, challenges and paradigms. <i>Nature Reviews Microbiology</i> , 2017, 15, 544-558.	13.6	144
28	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
29	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
30	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
31	Comparative genomics reveals multiple pathways to mutualism for tick-borne pathogens. <i>BMC Genomics</i> , 2016, 17, 481.	1.2	11
32	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
33	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
34	RepeatAnalyzer: a tool for analysing and managing short-sequence repeat data. <i>BMC Genomics</i> , 2016, 17, 422.	1.2	30
35	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
36	The bacterial microbiome of <i>Dermacentor andersoni</i> ticks influences pathogen susceptibility. <i>ISME Journal</i> , 2016, 10, 1846-1855.	4.4	162

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37	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
38	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
39	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
40	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
41	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
42	Genetic Diversity of Tick-Borne Rickettsial Pathogens; Insights Gained from Distant Strains. <i>Pathogens</i> , 2014, 3, 57-72.	1.2	19
43	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
44	Growth of <i>Mannheimia haemolytica</i> : Inhibitory agents and putative mechanism of inhibition. <i>Veterinary Microbiology</i> , 2014, 174, 155-162.	0.8	4
45	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
46	Transcriptional pathways associated with the slow growth phenotype of transformed <i>Anaplasma marginale</i> . <i>BMC Genomics</i> , 2013, 14, 272.	1.2	13
47	Antigenic variation and transmission fitness as drivers of bacterial strain structure. <i>Cellular Microbiology</i> , 2013, 15, 1969-1975.	1.1	24
48	Protective immunity induced by immunization with a live, cultured <i>Anaplasma marginale</i> strain. <i>Vaccine</i> , 2013, 31, 3617-3622.	1.7	21
49	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
50	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
51	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
52	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
53	Comparative genomics and transcriptomics of trait-gene association. <i>BMC Genomics</i> , 2012, 13, 669.	1.2	16
54	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

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55	Genome-wide screening and identification of antigens for rickettsial vaccine development: 1. FEMS Immunology and Medical Microbiology, 2012, 64, 115-119.	2.7	29
56	Expression and strain variation of the novel <i>smorf</i> multigene family in <i>Babesia bovis</i> . International Journal for Parasitology, 2012, 42, 131-138.	1.3	19
57	Expression Patterns of <i>Anaplasma marginale</i> msp2 Variants Change in Response to Growth in Cattle, and Tick Cells versus Mammalian Cells. PLoS ONE, 2012, 7, e36012.	1.1	24
58	Identification of <i>Anaplasma marginale</i> Type IV Secretion System Effector Proteins. PLoS ONE, 2011, 6, e27724.	1.1	53
59	Temporal characterisation of the organ-specific <i>Rhipicephalus microplus</i> transcriptional response to <i>Anaplasma marginale</i> infection. International Journal for Parasitology, 2011, 41, 851-860.	1.3	51
60	Expression of <i>Anaplasma marginale</i> Ankyrin Repeat-Containing Proteins during Infection of the Mammalian Host and Tick Vector. Infection and Immunity, 2011, 79, 2847-2855.	1.0	8
61	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. Infection and Immunity, 2011, 79, 1311-1318.	1.0	26
62	Stability and Tick Transmission Phenotype of <i>gfp</i> -Transformed <i>Anaplasma marginale</i> through a Complete <i>In Vivo</i> Infection Cycle. Applied and Environmental Microbiology, 2011, 77, 330-334.	1.4	24
63	Association of Pathogen Strain-Specific Gene Transcription and Transmission Efficiency Phenotype of <i>Anaplasma marginale</i> . Infection and Immunity, 2010, 78, 2446-2453.	1.0	7
64	<i>Anaplasma marginale</i> Infection with Persistent High-Load Bacteremia Induces a Dysfunctional Memory CD4 <sup>+</sup> T Lymphocyte Response but Sustained High IgG Titers. Vaccine Journal, 2010, 17, 1881-1890.	3.2	26
65	<i>Anaplasma marginale</i> Type IV Secretion System Proteins VirB2, VirB7, VirB11, and VirD4 Are Immunogenic Components of a Protective Bacterial Membrane Vaccine. Infection and Immunity, 2010, 78, 1314-1325.	1.0	41
66	Identification of <i>Anaplasma marginale</i> Proteins Specifically Upregulated during Colonization of the Tick Vector. Infection and Immunity, 2010, 78, 3047-3052.	1.0	26
67	Complete Genome Sequence of <i>Anaplasma marginale</i> subsp. <i>centrale</i> . Journal of Bacteriology, 2010, 192, 379-380.	1.0	45
68	Phylogenomics Reveals a Diverse <i>Rickettsiales</i> Type IV Secretion System. Infection and Immunity, 2010, 78, 1809-1823.	1.0	101
69	The immunization-induced antibody response to the <i>Anaplasma marginale</i> major surface protein 2 and its association with protective immunity. Vaccine, 2010, 28, 3741-3747.	1.7	18
70	Generation of Antigenic Variants via Gene Conversion: Evidence for Recombination Fitness Selection at the Locus Level in <i>Anaplasma marginale</i> . Infection and Immunity, 2009, 77, 3181-3187.	1.0	24
71	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. Infection and Immunity, 2009, 77, 1459-1464.	1.0	19
72	Conservation in the face of diversity: multistrain analysis of an intracellular bacterium. BMC Genomics, 2009, 10, 16.	1.2	55

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73	Anaplasma. , 2009, , 85-116.		8
74	Succinate dehydrogenase gene arrangement and expression in Anaplasma phagocytophilum. Gene, 2008, 414, 41-48.	1.0	5
75	Superinfection as a driver of genomic diversification in antigenically variant pathogens. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2123-2127.	3.3	81
76	Tick-Borne Transmission of Two Genetically Distinct <i>Anaplasma marginale</i> Strains following Superinfection of the Mammalian Reservoir Host. Infection and Immunity, 2008, 76, 4066-4070.	1.0	19
77	Composition of the Surface Proteome of <i>Anaplasma marginale</i> and Its Role in Protective Immunity Induced by Outer Membrane Immunization. Infection and Immunity, 2008, 76, 2219-2226.	1.0	70
78	Genome Sequence of Babesia bovis and Comparative Analysis of Apicomplexan Hemoprotozoa. PLoS Pathogens, 2007, 3, e148.	2.1	335
79	Immunogenicity of Anaplasma marginale Type IV Secretion System Proteins in a Protective Outer Membrane Vaccine. Infection and Immunity, 2007, 75, 2333-2342.	1.0	62
80	Selection for Simple Major Surface Protein 2 Variants during Anaplasma marginale Transmission to Immunologically Naïve Animals. Infection and Immunity, 2007, 75, 1502-1506.	1.0	23
81	Comparison of ovine herpesvirus 2 genomes isolated from domestic sheep (Ovis aries) and a clinically affected cow (Bos bovis). Journal of General Virology, 2007, 88, 40-45.	1.3	31
82	Maintenance of Antibody to Pathogen Epitopes Generated by Segmental Gene Conversion Is Highly Dynamic during Long-Term Persistent Infection. Infection and Immunity, 2007, 75, 5185-5190.	1.0	26
83	Gene conversion is a convergent strategy for pathogen antigenic variation. Trends in Parasitology, 2007, 23, 408-413.	1.5	60
84	Genomic and proteomic approaches to vaccine candidate identification for Anaplasma marginale. Expert Review of Vaccines, 2006, 5, 95-101.	2.0	35
85	Insights into Mechanisms of Bacterial Antigenic Variation Derived from the Complete Genome Sequence of Anaplasma marginale. Annals of the New York Academy of Sciences, 2006, 1078, 15-25.	1.8	16
86	The Babesia bovis Merozoite Surface Antigen 1 Hypervariable Region Induces Surface-Reactive Antibodies That Block Merozoite Invasion. Infection and Immunity, 2006, 74, 3663-3667.	1.0	19
87	Analysis of the Anaplasma marginale Major Surface Protein 1 Complex Protein Composition by Tandem Mass Spectrometry. Journal of Bacteriology, 2006, 188, 4983-4991.	1.0	15
88	Differential Expression and Sequence Conservation of the Anaplasma marginale msp2 Gene Superfamily Outer Membrane Proteins. Infection and Immunity, 2006, 74, 3471-3479.	1.0	49
89	Structural basis for segmental gene conversion in generation of Anaplasma marginale outer membrane protein variants. Molecular Microbiology, 2005, 57, 212-221.	1.2	52
90	Complete genome sequencing of Anaplasma marginale reveals that the surface is skewed to two superfamilies of outer membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 844-849.	3.3	238

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91	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
92	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
93	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
94	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
95	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
96	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
97	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
98	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
99	Characterization of the <i>Anaplasma marginale msp2</i> locus and its synteny with the <i>omp1/p30</i> loci of <i>Ehrlichia chaffeensis</i> and <i>E. canis</i> . <i>Gene</i> , 2004, 325, 115-121.	1.0	13
100	A processed pseudogene contributes to apparent mule deer prion gene heterogeneity. <i>Gene</i> , 2004, 326, 167-173.	1.0	46
101	Characterization of a major outer membrane protein multigene family in <i>Ehrlichia ruminantium</i> . <i>Gene</i> , 2004, 330, 159-168.	1.0	43
102	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
103	Development of Improved Vaccines for Heartwater. <i>Annals of the New York Academy of Sciences</i> , 2003, 990, 474-484.	1.8	15
104	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
105	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
106	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- $\gamma$ Responses in MSP2 Vaccinees. <i>Journal of Immunology</i> , 2003, 170, 3790-3798.	0.4	40
107	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
108	Expression of Major Surface Protein 2 Variants with Conserved T-Cell Epitopes in <i>Anaplasma centrale</i> Vaccinees. <i>Infection and Immunity</i> , 2002, 70, 642-648.	1.0	30

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109	Antigenic variation of <i>Anaplasma marginale</i> msp2 occurs by combinatorial gene conversion. <i>Molecular Microbiology</i> , 2002, 43, 1151-1159.	1.2	124
110	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
111	Persistence and Antigenic Variation. , 0, , 366-390.		0