

Steve Paterson

List of Publications by Year in descending order

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113
papers

6,738
citations

81900

39
h-index

74163

75
g-index

126
all docs

126
docs citations

126
times ranked

8147
citing authors

#	ARTICLE	IF	CITATIONS
1	Antagonistic coevolution accelerates molecular evolution. <i>Nature</i> , 2010, 464, 275-278.	27.8	492
2	Species Interactions in a Parasite Community Drive Infection Risk in a Wildlife Population. <i>Science</i> , 2010, 330, 243-246.	12.6	461
3	Major histocompatibility complex variation associated with juvenile survival and parasite resistance in a large unmanaged ungulate population (<i>Ovis aries</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 3714-3719.	7.1	408
4	The diversity-generating benefits of a prokaryotic adaptive immune system. <i>Nature</i> , 2016, 532, 385-388.	27.8	236
5	<i>Pseudomonas aeruginosa</i> Population Diversity and Turnover in Cystic Fibrosis Chronic Infections. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011, 183, 1674-1679.	5.6	229
6	Running with the Red Queen: the role of biotic conflicts in evolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20141382.	2.6	225
7	Parallel Compensatory Evolution Stabilizes Plasmids across the Parasitism-Mutualism Continuum. <i>Current Biology</i> , 2015, 25, 2034-2039.	3.9	225
8	The <i>Fasciola hepatica</i> genome: gene duplication and polymorphism reveals adaptation to the host environment and the capacity for rapid evolution. <i>Genome Biology</i> , 2015, 16, 71.	8.8	224
9	The Extracellular Vesicles of the Helminth Pathogen, <i>Fasciola hepatica</i> : Biogenesis Pathways and Cargo Molecules Involved in Parasite Pathogenesis*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3258-3273.	3.8	194
10	The Genetic Basis of Inbreeding Avoidance in House Mice. <i>Current Biology</i> , 2007, 17, 2061-2066.	3.9	169
11	Rapid evolution of microbe-mediated protection against pathogens in a worm host. <i>ISME Journal</i> , 2016, 10, 1915-1924.	9.8	165
12	Divergent, Coexisting <i>Pseudomonas aeruginosa</i> Lineages in Chronic Cystic Fibrosis Lung Infections. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 191, 775-785.	5.6	148
13	Characterization and PCR multiplexing of novel highly variable tetranucleotide Atlantic salmon (<i>Salmo salar</i> L.) microsatellites. <i>Molecular Ecology Notes</i> , 2004, 4, 160-162.	1.7	146
14	No evidence for major histocompatibility complex-dependent mating patterns in a free-living ruminant population. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1997, 264, 1813-1819.	2.6	123
15	Mixed models: getting the best use of parasitological data. <i>Trends in Parasitology</i> , 2003, 19, 370-375.	3.3	122
16	Monitoring SARS-CoV-2 in municipal wastewater to evaluate the success of lockdown measures for controlling COVID-19 in the UK. <i>Water Research</i> , 2021, 200, 117214.	11.3	117
17	Parasite interactions in natural populations: insights from longitudinal data. <i>Parasitology</i> , 2008, 135, 767-781.	1.5	104
18	Temperate phages both mediate and drive adaptive evolution in pathogen biofilms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8266-8271.	7.1	102

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19	An Immunological Marker of Tolerance to Infection in Wild Rodents. <i>PLoS Biology</i> , 2014, 12, e1001901.	5.6	89
20	Predicting the Impact of Long-Term Temperature Changes on the Epidemiology and Control of Schistosomiasis: A Mechanistic Model. <i>PLoS ONE</i> , 2008, 3, e1438.	2.5	86
21	Host immune responses are necessary for density dependence in nematode infections. <i>Parasitology</i> , 2002, 125, 283-92.	1.5	84
22	Evidence for balancing selection at the major histocompatibility complex in a free-living ruminant. , 1998, 89, 289-294.		83
23	Genetic Diversity in Cytokines Associated with Immune Variation and Resistance to Multiple Pathogens in a Natural Rodent Population. <i>PLoS Genetics</i> , 2011, 7, e1002343.	3.5	83
24	Local adaptation of a bacterium is as important as its presence in structuring a natural microbial community. <i>Nature Communications</i> , 2016, 7, 12453.	12.8	79
25	Plasmid fitness costs are caused by specific genetic conflicts enabling resolution by compensatory mutation. <i>PLoS Biology</i> , 2021, 19, e3001225.	5.6	79
26	<i>Fasciola hepatica</i> demonstrates high levels of genetic diversity, a lack of population structure and high gene flow: possible implications for drug resistance. <i>International Journal for Parasitology</i> , 2017, 47, 11-20.	3.1	74
27	Baculum morphology predicts reproductive success of male house mice under sexual selection. <i>BMC Biology</i> , 2013, 11, 66.	3.8	70
28	Environmentally co-occurring mercury resistance plasmids are genetically and phenotypically diverse and confer variable context-dependent fitness effects. <i>Environmental Microbiology</i> , 2015, 17, 5008-5022.	3.8	68
29	The maintenance of genetic polymorphism in small island populations: large mammals in the Hebrides. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 1996, 351, 745-752.	4.0	65
30	Refugia and anthelmintic resistance: Concepts and challenges. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2019, 10, 51-57.	3.4	65
31	The Genetic Basis of Kin Recognition in a Cooperatively Breeding Mammal. <i>Current Biology</i> , 2015, 25, 2631-2641.	3.9	63
32	Positive selection inhibits gene mobilization and transfer in soil bacterial communities. <i>Nature Ecology and Evolution</i> , 2017, 1, 1348-1353.	7.8	63
33	Density-dependent immune responses against the gastrointestinal nematode <i>Strongyloides ratti</i> . <i>International Journal for Parasitology</i> , 2007, 37, 1501-1509.	3.1	59
34	The analysis of immunological profiles in wild animals: a case study on immunodynamics in the field vole, <i>Microtus agrestis</i> . <i>Molecular Ecology</i> , 2011, 20, 893-909.	3.9	57
35	Extensive diversification is a common feature of <i>Pseudomonas aeruginosa</i> populations during respiratory infections in cystic fibrosis. <i>Journal of Cystic Fibrosis</i> , 2013, 12, 790-793.	0.7	50
36	Rapid compensatory evolution promotes the survival of conjugative plasmids. <i>Mobile Genetic Elements</i> , 2016, 6, e1179074.	1.8	49

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37	The effect of the host immune response on the parasitic nematode <i>Strongyloides ratti</i> . <i>Parasitology</i> , 2004, 128, 661-669.	1.5	48
38	The effect of phage genetic diversity on bacterial resistance evolution. <i>ISME Journal</i> , 2020, 14, 828-836.	9.8	48
39	Adaptation to public goods cheats in <i>Pseudomonas aeruginosa</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171089.	2.6	48
40	A comparison of precipitation and filtration-based SARS-CoV-2 recovery methods and the influence of temperature, turbidity, and surfactant load in urban wastewater. <i>Science of the Total Environment</i> , 2022, 808, 151916.	8.0	47
41	Seasonal host dynamics drive the timing of recurrent epidemics in a wildlife population. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 1603-1610.	2.6	44
42	Evidence for selection at cytokine loci in a natural population of field voles (<i>Microtus</i>). <i>Evolution</i> , 2010, 64, 542-547.	3.9	44
43	High virulence sub-populations in <i>Pseudomonas aeruginosa</i> long-term cystic fibrosis airway infections. <i>BMC Microbiology</i> , 2017, 17, 30.	3.3	44
44	The immune response during a <i>Strongyloides ratti</i> infection of rats. <i>Parasite Immunology</i> , 2007, 29, 339-346.	1.5	43
45	Bacteriophages Limit the Existence Conditions for Conjugative Plasmids. <i>MBio</i> , 2015, 6, e00586.	4.1	41
46	Genomic diversity of the human intestinal parasite <i>Entamoeba histolytica</i> . <i>Genome Biology</i> , 2012, 13, R38.	9.6	39
47	Detecting genes for variation in parasite burden and immunological traits in a wild population: testing the candidate gene approach. <i>Molecular Ecology</i> , 2013, 22, 757-773.	3.9	39
48	HOST AVAILABILITY AND THE EVOLUTION OF PARASITE LIFE-HISTORY STRATEGIES. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 675-684.	2.3	38
49	Identification of putative markers of triclabendazole resistance by a genome-wide analysis of genetically recombinant <i>Fasciola hepatica</i> . <i>Parasitology</i> , 2013, 140, 1523-1533.	1.5	38
50	Coevolutionary dynamics between a defensive microbe and a pathogen driven by fluctuating selection. <i>Molecular Ecology</i> , 2017, 26, 1778-1789.	3.9	37
51	Experimental evolution of parasite life-history traits in <i>Strongyloides ratti</i> (Nematoda). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 1467-1474.	2.6	36
52	Sub-inhibitory concentrations of some antibiotics can drive diversification of <i>Pseudomonas aeruginosa</i> populations in artificial sputum medium. <i>BMC Microbiology</i> , 2013, 13, 170.	3.3	35
53	Proteomics and <i>In Silico</i> Approaches To Extend Understanding of the Glutathione Transferase Superfamily of the Tropical Liver Fluke <i>Fasciola gigantica</i> . <i>Journal of Proteome Research</i> , 2012, 11, 5876-5889.	3.7	34
54	Effects of abundance on infection in natural populations: Field voles and cowpox virus. <i>Epidemics</i> , 2009, 1, 35-46.	3.0	29

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55	Evidence of Gene Conversion in Genes Encoding the Gal/GalNac Lectin Complex of <i>Entamoeba</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1209.	3.0	27
56	Frontiers in host-parasite ecology and evolution. <i>Molecular Ecology</i> , 2011, 20, 869-871.	3.9	26
57	Draft Genome Assembly of the Poultry Red Mite, <i>Dermanyssus gallinae</i> . <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	26
58	Functional consequences of genetic diversity in <i>Strongyloides ratti</i> infections. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, 1023-1032.	2.6	24
59	How do insects react to novel inherited symbionts? A microarray analysis of <i>Drosophila melanogaster</i> response to the presence of natural and introduced <i>Spiroplasma</i> . <i>Molecular Ecology</i> , 2011, 20, 950-958.	3.9	24
60	Transcriptomic response of red grouse to gastrointestinal nematode parasites and testosterone: implications for population dynamics. <i>Molecular Ecology</i> , 2011, 20, 920-931.	3.9	23
61	Rapid evolution and gene expression: a rapidly evolving Mendelian trait that silences field crickets has widespread effects on mRNA and protein expression. <i>Journal of Evolutionary Biology</i> , 2016, 29, 1234-1246.	1.7	23
62	Resistance is futile: RNA-sequencing reveals differing responses to bat fungal pathogen in Nearctic <i>Myotis lucifugus</i> and Palearctic <i>Myotis myotis</i> . <i>Oecologia</i> , 2019, 191, 295-309.	2.0	23
63	Wild rodents as a model to discover genes and pathways underlying natural variation in infectious disease susceptibility. <i>Parasite Immunology</i> , 2013, 35, n/a-n/a.	1.5	22
64	Characterisation of a novel panel of polymorphic microsatellite loci for the liver fluke, <i>Fasciola hepatica</i> , using a next generation sequencing approach. <i>Infection, Genetics and Evolution</i> , 2015, 32, 298-304.	2.3	22
65	Conflicting selection alters the trajectory of molecular evolution in a tripartite bacteria-plasmid-phage interaction. <i>Molecular Ecology</i> , 2017, 26, 2757-2764.	3.9	22
66	Genetic Diversity and Gene Family Expansions in Members of the Genus <i>Entamoeba</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 688-705.	2.5	22
67	Profiling G protein-coupled receptors of <i>Fasciola hepatica</i> identifies orphan rhodopsins unique to phylum Platyhelminthes. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2018, 8, 87-103.	3.4	21
68	Identification of novel aspartic proteases from <i>Strongyloides ratti</i> and characterisation of their evolutionary relationships, stage-specific expression and molecular structure. <i>BMC Genomics</i> , 2009, 10, 611.	2.8	20
69	Exploring and Expanding the Fatty-Acid-Binding Protein Superfamily in <i>Fasciola</i> Species. <i>Journal of Proteome Research</i> , 2016, 15, 3308-3321.	3.7	20
70	Immunological Responses Elicited by Different Infection Regimes with <i>Strongyloides ratti</i> . <i>PLoS ONE</i> , 2008, 3, e2509.	2.5	19
71	Effects of Snail Density on Growth, Reproduction and Survival of <i>Biomphalaria alexandrina</i> Exposed to <i>Schistosoma mansoni</i> . <i>Journal of Parasitology Research</i> , 2010, 2010, 1-6.	1.2	19
72	HOW TO MEASURE MATURATION: A COMPARISON OF PROBABILISTIC METHODS USED TO TEST FOR GENOTYPIC VARIATION AND PLASTICITY IN THE DECISION TO MATURE. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 525-538.	2.3	19

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73	Transmission and lineage displacement drive rapid population genomic flux in cystic fibrosis airway infections of a <i>Pseudomonas aeruginosa</i> epidemic strain. <i>Microbial Genomics</i> , 2018, 4, .	2.0	19
74	Microarray analysis of gender- and parasite-specific gene transcription in <i>Strongyloides ratti</i> . <i>International Journal for Parasitology</i> , 2008, 38, 1329-1341.	3.1	17
75	Plasmid carriage can limit bacteria-phage coevolution. <i>Biology Letters</i> , 2015, 11, 20150361.	2.3	17
76	From the animal house to the field: Are there consistent individual differences in immunological profile in wild populations of field voles (<i>Microtus agrestis</i>)?. <i>PLoS ONE</i> , 2017, 12, e0183450.	2.5	17
77	DETERMINING THE OPTIMAL DEVELOPMENTAL ROUTE OF <i>STRONGYLOIDES RATTI</i> : AN EVOLUTIONARILY STABLE STRATEGY APPROACH. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 989-1008.	2.3	16
78	Identification of genes responding to nematode infection in red grouse. <i>Molecular Ecology Resources</i> , 2011, 11, 305-313.	4.8	16
79	The Interface Between Epidemiology and Population Genetics. <i>Parasitology Today</i> , 2000, 16, 528-532.	3.0	15
80	Ovine IgA-reactive proteins from <i>Teladorsagia circumcincta</i> infective larvae. <i>International Journal for Parasitology</i> , 2014, 44, 743-750.	3.1	15
81	Inferring infection processes of a parasitic nematode using population genetics. <i>Parasitology</i> , 2000, 120, 185-194.	1.5	14
82	Response of the <i>Strongyloides ratti</i> transcriptome to host immunological environment. <i>International Journal for Parasitology</i> , 2010, 40, 1609-1617.	3.1	14
83	Endemic Hantavirus in Field Voles, Northern England. <i>Emerging Infectious Diseases</i> , 2017, 23, 1033-1035.	4.3	13
84	A candidate tolerance gene identified in a natural population of field voles (<i>Microtus agrestis</i>). <i>Molecular Ecology</i> , 2018, 27, 1044-1052.	3.9	13
85	Transposable temperate phages promote the evolution of divergent social strategies in <i>Pseudomonas aeruginosa</i> populations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191794.	2.6	13
86	Heterogeneity in the distribution of <i>Strongyloides ratti</i> infective stages among the faecal pellets of rats. <i>Parasitology</i> , 1999, 119, 227-235.	1.5	12
87	Genomic Signatures of Historical Allopatry and Ecological Divergence in an Island Lizard. <i>Genome Biology and Evolution</i> , 2016, 8, 3618-3626.	2.5	12
88	Physiological, but not fitness, effects of two interacting haemoparasitic infections in a wild rodent. <i>International Journal for Parasitology</i> , 2018, 48, 463-471.	3.1	12
89	Transmission, adaptation and geographical spread of the <i>Pseudomonas aeruginosa</i> Liverpool epidemic strain. <i>Microbial Genomics</i> , 2021, 7, .	2.0	12
90	Transcriptome analysis of a parasitic clade V nematode: Comparative analysis of potential molecular anthelmintic targets in <i>Cylicostephanus goldi</i> . <i>International Journal for Parasitology</i> , 2013, 43, 917-927.	3.1	11

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91	Offspring development and life-history variation in a water flea depends upon clone-specific integration of genetic, non-genetic and environmental cues. <i>Functional Ecology</i> , 2017, 31, 1996-2007.	3.6	11
92	Refined analyses suggest that recombination is a minor source of genomic diversity in <i>Pseudomonas aeruginosa</i> chronic cystic fibrosis infections. <i>Microbial Genomics</i> , 2016, 2, e000051.	2.0	11
93	No evidence for specificity between host and parasite genotypes in experimental (Nematoda) infections. <i>International Journal for Parasitology</i> , 2005, 35, 1539-1545.	3.1	10
94	Genome-Wide Changes in Genetic Diversity in a Population of <i>Myotis lucifugus</i> Affected by White-Nose Syndrome. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2007-2020.	1.8	10
95	Pollution induces epigenetic effects that are stably transmitted across multiple generations. <i>Evolution Letters</i> , 2022, 6, 118-135.	3.3	10
96	Polymicrobial infections can select against <i>Pseudomonas aeruginosa</i> mutators because of quorum-sensing trade-offs. <i>Nature Ecology and Evolution</i> , 2022, 6, 979-988.	7.8	10
97	How effective is recognition of siblings on the basis of genotype?. <i>Journal of Evolutionary Biology</i> , 2009, 22, 1875-1881.	1.7	9
98	A transcriptomic investigation of handicap models in sexual selection. <i>Behavioral Ecology and Sociobiology</i> , 2013, 67, 221-234.	1.4	9
99	Evolution of diversity explains the impact of pre-adaptation of a focal species on the structure of a natural microbial community. <i>ISME Journal</i> , 2020, 14, 2877-2889.	9.8	9
100	Resource quality determines the evolution of resistance and its genetic basis. <i>Molecular Ecology</i> , 2020, 29, 4128-4142.	3.9	8
101	The effect of infection history on the fitness of the gastrointestinal nematode <i>Strongyloides ratti</i> . <i>Parasitology</i> , 2009, 136, 567-577.	1.5	6
102	Transcriptional changes during <i>Aphnia pulex</i> development indicate that the maturation decision resembles a rate more than a threshold. <i>Journal of Evolutionary Biology</i> , 2015, 28, 944-958.	1.7	6
103	Rapid decline of adaptation of <i>Pseudomonas fluorescens</i> to soil biotic environment. <i>Biology Letters</i> , 2022, 18, 20210593.	2.3	6
104	Compost spatial heterogeneity promotes evolutionary diversification of a bacterium. <i>Journal of Evolutionary Biology</i> , 2021, 34, 246-255.	1.7	5
105	USE OF REPEATED MEASURE LINEAR MODELING TO ANALYZE LONGITUDINAL DATA FROM EXPERIMENTAL PARASITE INFECTIONS. <i>Journal of Parasitology</i> , 2001, 87, 969-971.	0.7	4
106	The effect of host heterogeneity and parasite intragenomic interactions on parasite population structure. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005, 272, 1647-1653.	2.6	4
107	Microbe Interactions Undermine Predictions of Response. <i>Science</i> , 2011, 331, 145-147.	12.6	4
108	The immunology and ecology of co-infection. <i>Molecular Ecology</i> , 2013, 22, 2603-2604.	3.9	4

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109	Transcriptome and Secretome Analysis of Intra-Mammalian Life-Stages of <i>Calicophoron daubneyi</i> Reveals Adaptation to a Unique Host Environment. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100055.	3.8	4
110	Identification and characterisation of 17 polymorphic candidate genes for response to parasitic nematode (<i>Trichostrongylus tenuis</i>) infection in red grouse (<i>Lagopus lagopus scotica</i>). <i>Conservation Genetics Resources</i> , 2015, 7, 23-28.	0.8	3
111	Transcriptome-wide analysis reveals different categories of response to a standardised immune challenge in a wild rodent. <i>Scientific Reports</i> , 2020, 10, 7444.	3.3	3
112	Use of Repeated Measure Linear Modeling to Analyze Longitudinal Data from Experimental Parasite Infections. <i>Journal of Parasitology</i> , 2001, 87, 969.	0.7	0
113	DETERMINING THE OPTIMAL DEVELOPMENTAL ROUTE OF <i>STRONGYLOIDES RATTI</i> : AN EVOLUTIONARILY STABLE STRATEGY APPROACH. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 989.	2.3	0