

Kevin P Johnson

List of Publications by Year in descending order

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Version: 2024-02-01

117
papers

4,454
citations

94269

37
h-index

138251

58
g-index

126
all docs

126
docs citations

126
times ranked

3338
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenetics and host-specificity of the mega-diverse louse genus <i>Myrsidea</i> (Amblycera: Tj ETQq1 1 0.784314 rgBT /Overlock 1.7 Tf 50 622 Td (Ph	1.7	13
2	Long-distance dispersal of pigeons and doves generated new ecological opportunities for host-switching and adaptive radiation by their parasites. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20220042.	1.2	13
3	High levels of inbreeding with spatial and host-associated structure in lice of an endangered freshwater seal. <i>Molecular Ecology</i> , 2022, 31, 4593-4606.	2.0	10
4	Molecular phylogenetics of the avian feather louse <i>Philoaterus</i> -complex (Phthiraptera: Tj ETQq0 0 0 rgBT /Overlock 1.2 Tf 50 622 Td (Ph	1.2	10
5	Mining Ultraconserved Elements From Transcriptome and Genome Data to Explore the Phylogenomics of the Free-living Lice Suborder Psocomorpha (Insecta: Psocodea). <i>Insect Systematics and Diversity</i> , 2022, 6, .	0.7	2
6	Independent evolution of highly variable, fragmented mitogenomes of parasitic lice. <i>Communications Biology</i> , 2022, 5, .	2.0	8
7	Phylogenomics reveals the origin of mammal lice out of Afrotheria. <i>Nature Ecology and Evolution</i> , 2022, 6, 1205-1210.	3.4	12
8	Combining Nuclear and Mitochondrial Loci Provides Phylogenetic Information in the <i>Philoaterus</i> Complex of Lice (Psocodea: Ischnocera: Philoateridae). <i>Journal of Medical Entomology</i> , 2021, 58, 252-260.	0.9	8
9	Structure, gene order, and nucleotide composition of mitochondrial genomes in parasitic lice from Amblycera. <i>Gene</i> , 2021, 768, 145312.	1.0	13
10	Disentangling lousy relationships: Comparative phylogenomics of two sucking louse lineages parasitizing chipmunks. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106998.	1.2	3
11	Phylogenomics of the North American Plecoptera. <i>Systematic Entomology</i> , 2021, 46, 287-305.	1.7	19
12	The assembled and annotated genome of the pigeon louse <i>Columbicola columbae</i> , a model ectoparasite. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	18
13	Patterns of Microbiome Variation Among Infrapopulations of Permanent Bloodsucking Parasites. <i>Frontiers in Microbiology</i> , 2021, 12, 642543.	1.5	6
14	The reduced genome of a heritable symbiont from an ectoparasitic feather feeding louse. <i>Bmc Ecology and Evolution</i> , 2021, 21, 108.	0.7	7
15	Mitochondrial genomes within bark lice (Insecta: Psocodea: Psocomorpha) reveal novel gene rearrangements containing phylogenetic signal. <i>Systematic Entomology</i> , 2021, 46, 938-951.	1.7	10
16	Genome-Resolved Metagenomic Analyses Reveal the Presence of a Putative Bacterial Endosymbiont in an Avian Nasal Mite (Rhinonyssidae; Mesostigmata). <i>Microorganisms</i> , 2021, 9, 1734.	1.6	1
17	The interplay between host biogeography and phylogeny in structuring diversification of the feather louse genus <i>Penenirmus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 165, 107297.	1.2	14
18	Phylogenomics of Auchenorrhyncha (Insecta: Hemiptera) using transcriptomes: examining controversial relationships via degeneracy coding and interrogation of gene conflict. <i>Systematic Entomology</i> , 2020, 45, 85-113.	1.7	45

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19	Assessing symbiont extinction risk using cophylogenetic data. <i>Biological Conservation</i> , 2020, 250, 108705.	1.9	9
20	Lousy grouse: Comparing evolutionary patterns in Alaska galliform lice to understand host evolution and host-parasite interactions. <i>Ecology and Evolution</i> , 2020, 10, 8379-8393.	0.8	11
21	Comparing rates of introgression in parasitic feather lice with differing dispersal capabilities. <i>Communications Biology</i> , 2020, 3, 610.	2.0	6
22	Extensive in situ radiation of feather lice on tinamous. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20193005.	1.2	5
23	Mitochondrial genomes of <i>Columbicola</i> feather lice are highly fragmented, indicating repeated evolution of minicircle-type genomes in parasitic lice. <i>PeerJ</i> , 2020, 8, e8759.	0.9	21
24	Two evolutionary units on the South American razor clam <i>Ensis macha</i> (Bivalvia: Pharidae): genetic and morphometric evidence. <i>Organisms Diversity and Evolution</i> , 2020, 20, 331-344.	0.7	1
25	Feather mites play a role in cleaning host feathers: New insights from DNA metabarcoding and microscopy. <i>Molecular Ecology</i> , 2019, 28, 203-218.	2.0	49
26	Putting the genome in insect phylogenomics. <i>Current Opinion in Insect Science</i> , 2019, 36, 111-117.	2.2	19
27	Deep Instability in the Phylogenetic Backbone of Heteroptera is Only Partly Overcome by Transcriptome-Based Phylogenomics. <i>Insect Systematics and Diversity</i> , 2019, 3, .	0.7	6
28	Nuclear Orthologs Derived from Whole Genome Sequencing Indicate Cryptic Diversity in the <i>Bemisia tabaci</i> (Insecta: Aleyrodidae) Complex of Whiteflies. <i>Diversity</i> , 2019, 11, 151.	0.7	39
29	Rapid experimental evolution of reproductive isolation from a single natural population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13440-13445.	3.3	33
30	Two lineages of kingfisher feather lice exhibit differing degrees of cospeciation with their hosts. <i>Parasitology</i> , 2019, 146, 1083-1095.	0.7	8
31	Phylogenomic analysis of seal lice reveals codivergence with their hosts. <i>Systematic Entomology</i> , 2019, 44, 699-708.	1.7	12
32	Host defense triggers rapid adaptive radiation in experimentally evolving parasites. <i>Evolution Letters</i> , 2019, 3, 120-128.	1.6	26
33	Dew-bathing in the Atlantic Forest endemic Robust Woodpecker <i>Campephilus robustus</i> (Lichtenstein.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	0.4	18
34	Extensive host-switching of avian feather lice following the Cretaceous-Paleogene mass extinction event. <i>Communications Biology</i> , 2019, 2, 445.	2.0	20
35	Persistence of single species of symbionts across multiple closely-related host species. <i>Scientific Reports</i> , 2019, 9, 17442.	1.6	8
36	Brochosomins and other novel proteins from brochosomes of leafhoppers (Insecta, Hemiptera.) <i>Tj ETQq0 0 0 rgBT /Overlock</i>	1.2	18

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37	Host and parasite morphology influence congruence between host and parasite phylogenies. <i>International Journal for Parasitology</i> , 2018, 48, 641-648.	1.3	12
38	Integrating phylogenomic and population genomic patterns in avian lice provides a more complete picture of parasite evolution. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 95-112.	1.1	22
39	Mitochondrial phylogenomics and genome rearrangements in the barklice (Insecta: Psocodea). <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 118-127.	1.2	44
40	Cophylogenetic analysis of lice in the <i>Colpocephalum</i> complex (Phthiraptera: Amblycera). <i>Zoologica Scripta</i> , 2018, 47, 72-83.	0.7	9
41	The role of parasite dispersal in shaping a host-parasite system at multiple evolutionary scales. <i>Molecular Ecology</i> , 2018, 27, 5104-5119.	2.0	32
42	Phylogenomics and the evolution of hemipteroid insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12775-12780.	3.3	275
43	Simultaneous radiation of bird and mammal lice following the K-Pg boundary. <i>Biology Letters</i> , 2018, 14, 20180141.	1.0	33
44	Introgression of regulatory alleles and a missense coding mutation drive plumage pattern diversity in the rock pigeon. <i>ELife</i> , 2018, 7, .	2.8	66
45	Phoretic dispersal influences parasite population genetic structure. <i>Molecular Ecology</i> , 2018, 27, 2770-2779.	2.0	27
46	aTRAM 2.0: An Improved, Flexible Locus Assembler for NGS Data. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431877454.	0.6	68
47	Composition and distribution of lice (Insecta: Phthiraptera) on Colombian and Peruvian birds: New data on louse-host association in the Neotropics. <i>Biodiversity Data Journal</i> , 2018, 6, e21635.	0.4	8
48	Comparative cophylogenetics of Australian phabine pigeons and doves (Aves: Columbidae) and their feather lice (Insecta: Phthiraptera). <i>International Journal for Parasitology</i> , 2017, 47, 347-356.	1.3	10
49	Primates, Lice and Bacteria: Speciation and Genome Evolution in the Symbionts of Hominid Lice. <i>Molecular Biology and Evolution</i> , 2017, 34, 1743-1757.	3.5	51
50	Phylogenomics from Whole Genome Sequences Using aTRAM. <i>Systematic Biology</i> , 2017, 66, syw105.	2.7	47
51	Phylogenomics using Target-restricted Assembly Resolves Intra-generic Relationships of Parasitic Lice (Phthiraptera: <i>Columbicola</i>). <i>Systematic Biology</i> , 2017, 66, syx027.	2.7	22
52	Cophylogenetic analyses reveal extensive host-shift speciation in a highly specialized and host-specific symbiont system. <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 190-196.	1.2	46
53	Multiple trans-Beringia dispersals of the barklouse genus <i>Trichadenotecnum</i> (Insecta: Psocodea: Tj ETQq1 1 0.784314 rgBT /Overlock	0.7	4
54	A complete molecular phylogeny of <i>Claravis</i> confirms its paraphyly within small New World ground-doves (Aves: Peristerinae) and implies multiple plumage state transitions. <i>Journal of Avian Biology</i> , 2017, 48, 459-464.	0.6	7

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55	Anchored Hybrid Enrichment-Based Phylogenomics of Leafhoppers and Treehoppers (Hemiptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 702 Td (0.7	110
56	Comparative phylogeography of two codistributed subgenera of cave crickets (Orthoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 Td (1.4	11
57	Assessing genotype-phenotype associations in three dorsal colour morphs in the meadow spittlebug <i>Philaenus spumarius</i> (L.) (Hemiptera: Aphrophoridae) using genomic and transcriptomic resources. <i>BMC Genetics</i> , 2016, 17, 144.	2.7	14
58	Evolution of the assassinâ€™s arms: insights from a phylogeny of combined transcriptomic and ribosomal DNA data (Heteroptera: Reduviidae). <i>Scientific Reports</i> , 2016, 6, 22177.	1.6	36
59	Two Bacterial Genera, <i>Sodalis</i> and <i>Rickettsia</i> , Associated with the Seal Louse <i>Proechinophthirus fluctus</i> (Phthiraptera: Anoplura). <i>Applied and Environmental Microbiology</i> , 2016, 82, 3185-3197.	1.4	63
60	Cophylogenetic analysis of New World ground-doves (Aves: Columbidae) and their parasitic wing lice (Insecta: Phthiraptera: Columbicola). <i>Molecular Phylogenetics and Evolution</i> , 2016, 103, 122-132.	1.2	17
61	Cophylogenetic patterns are uncorrelated between two lineages of parasites on the same hosts. <i>Biological Journal of the Linnean Society</i> , 2016, 118, 813-828.	0.7	18
62	Unlocking the black box of feather louse diversity: A molecular phylogeny of the hyper-diverse genus <i>Brueelia</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 737-751.	1.2	62
63	Lineage sorting in multihost parasites: <i>Eidmanniella albescens</i> and <i>Fregatiella aurifasciata</i> on seabirds from the Galapagos Islands. <i>Ecology and Evolution</i> , 2015, 5, 3264-3271.	0.8	8
64	Data supporting a molecular phylogeny of the hyper-diverse genus <i>Brueelia</i> . <i>Data in Brief</i> , 2015, 5, 1078-1091.	0.5	6
65	Patterns of diversification in small New World ground doves are consistent with major geologic events. <i>Auk</i> , 2015, 132, 300-312.	0.7	19
66	aTRAM - automated target restricted assembly method: a fast method for assembling loci across divergent taxa from next-generation sequencing data. <i>BMC Bioinformatics</i> , 2015, 16, 98.	1.2	78
67	Independent origins of the feather lice (Insecta: <i>Degeeriella</i>) of raptors. <i>Biological Journal of the Linnean Society</i> , 2015, 114, 837-847.	0.7	12
68	Novel Primers From Informative Nuclear Loci for Louse Molecular Phylogenetics (Insecta: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 Td (0.9	11
69	The importance of molecular dating analyses for inferring Hawaiian biogeographical history: a case study with bark lice (Insecta: Psocoptera: <i>Ptyctocidae</i> : <i>Ptyctoc</i>). <i>Journal of Biogeography</i> , 2014, 41, 158-167.	1.4	24
70	Molecular systematics of the bark lice infraorder <i>Ceciliusetae</i> (Insecta: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4	1.7	4
71	Phylogeny of the suborder Psocomorpha: congruence and incongruence between morphology and molecular data (Insecta: Psocodea: <i>Psocoptera</i> â€™). <i>Zoological Journal of the Linnean Society</i> , 2014, 171, 716-731.	1.0	22
72	Population genetics of bisexual and unisexual populations of the scaly-winged bark louse <i>Echmepteryx hageni</i> (Insecta: Psocoptera). <i>Genetica</i> , 2014, 142, 405-418.	0.5	2

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73	Rates of genomic divergence in humans, chimpanzees and their lice. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132174.	1.2	29
74	Next-generation phylogenomics using a Target Restricted Assembly Method. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 417-422.	1.2	28
75	Changes in base composition bias of nuclear and mitochondrial genes in lice (Insecta: Psocodea). <i>Genetica</i> , 2013, 141, 491-499.	0.5	14
76	Repeated adaptive divergence of microhabitat specialization in avian feather lice. <i>BMC Biology</i> , 2012, 10, 52.	1.7	60
77	The evolution of host specificity in dove body lice. <i>Parasitology</i> , 2011, 138, 1730-1736.	0.7	16
78	The Central American land bridge as an engine of diversification in New World doves. <i>Journal of Biogeography</i> , 2011, 38, 1069-1076.	1.4	37
79	There and back again: switching between host orders by avian body lice (Ischnocera: Gonioididae). <i>Biological Journal of the Linnean Society</i> , 2011, 102, 614-625.	0.7	31
80	Mitochondrial genome deletions and minicircles are common in lice (Insecta: Phthiraptera). <i>BMC Genomics</i> , 2011, 12, 394.	1.2	90
81	Multiple lineages of lice pass through the μ -Pg boundary. <i>Biology Letters</i> , 2011, 7, 782-785.	1.0	49
82	Speciation, Subspecies Divergence, and Paraphyly in the Cinnamon Teal and Blue-winged Teal. <i>Condor</i> , 2011, 113, 747-761.	0.7	7
83	How stable is the μ -Polyphyly of Lice hypothesis (Insecta: Psocodea)? A comparison of phylogenetic signal in multiple genes. <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 939-951.	1.2	67
84	The flight of the Passenger Pigeon: Phylogenetics and biogeographic history of an extinct species. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 455-458.	1.2	30
85	A Target Restricted Assembly Method (TRAM) for Phylogenomics. <i>Nature Precedings</i> , 2010, , .	0.1	0
86	Competition promotes the evolution of host generalists in obligate parasites. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 3921-3926.	1.2	60
87	Mitochondrial and Nuclear DNA Sequences Support a Cretaceous Origin of Columbiformes and a Dispersal-Driven Radiation in the Paleogene. <i>Systematic Biology</i> , 2007, 56, 656-672.	2.7	110
88	Phylogenetic analysis of nuclear and mitochondrial genes supports species groups for <i>Columbicola</i> (Insecta: Phthiraptera). <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 506-518.	1.2	38
89	Reinterpreting the origins of flamingo lice: cospeciation or host-switching?. <i>Biology Letters</i> , 2006, 2, 275-278.	1.0	20
90	Molecular systematics of the suborder Trogiomorpha (Insecta: Psocodea: μ -Psocoptera μ TM). <i>Zoological Journal of the Linnean Society</i> , 2006, 146, 287-299.	1.0	46

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91	Phylogenetic relationships of the Papuan Swiftlet <i>Aerodramus papuensis</i> and implications for the evolution of avian echolocation. <i>Ibis</i> , 2005, 147, 790-796.	1.0	19
92	CORRELATED EVOLUTION OF HOST AND PARASITE BODY SIZE: TESTS OF HARRISON'S RULE USING BIRDS AND LICE. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 1744-1753.	1.1	71
93	Morphology of male genitalia in lice and their relatives and phylogenetic implications. <i>Systematic Entomology</i> , 2005, 31, 350-361.	1.7	51
94	Correlated evolution of host and parasite body size: tests of Harrison's rule using birds and lice. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 1744-53.	1.1	58
95	Untangling Coevolutionary History. <i>Systematic Biology</i> , 2004, 53, 92-94.	2.7	36
96	Deletion Bias in Avian Introns over Evolutionary Timescales. <i>Molecular Biology and Evolution</i> , 2004, 21, 599-602.	3.5	41
97	Differences in straggling rates between two genera of dove lice (Insecta: Phthiraptera) reinforce population genetic and cophylogenetic patterns. <i>International Journal for Parasitology</i> , 2004, 34, 1113-1119.	1.3	63
98	Multiple origins of parasitism in lice. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2004, 271, 1771-1776.	1.2	119
99	Data incongruence and the problem of avian louse phylogeny. <i>Zoologica Scripta</i> , 2004, 33, 239-259.	0.7	31
100	Molecular systematics of Psocomorpha (Psocoptera). <i>Systematic Entomology</i> , 2003, 28, 409-416.	1.7	26
101	Dramatically elevated rate of mitochondrial substitution in lice (Insecta: Phthiraptera). <i>Molecular Phylogenetics and Evolution</i> , 2003, 26, 231-242.	1.2	89
102	Phylogenetic position of Phthiraptera (Insecta: Paraneoptera) and elevated rate of evolution in mitochondrial 12S and 16S rDNA. <i>Molecular Phylogenetics and Evolution</i> , 2003, 29, 102-114.	1.2	87
103	Phylogeny of the lice (Insecta, Phthiraptera) inferred from small subunit rRNA. <i>Zoologica Scripta</i> , 2003, 32, 407-414.	0.7	52
104	LINKING COEVOLUTIONARY HISTORY TO ECOLOGICAL PROCESS: DOVES AND LICE. <i>Evolution; International Journal of Organic Evolution</i> , 2003, 57, 2335-2341.	1.1	89
105	When Do Parasites Fail to Speciate in Response to Host Speciation?. <i>Systematic Biology</i> , 2003, 52, 37-47.	2.7	134
106	Host defense reinforces host-parasite cospeciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15694-15699.	3.3	117
107	Multiple Genes and the Monophyly of Ischnocera (Insecta: Phthiraptera). <i>Molecular Phylogenetics and Evolution</i> , 2002, 22, 101-110.	1.2	47
108	The perils of using host relationships in parasite taxonomy: phylogeny of the <i>Degeeriella</i> complex. <i>Molecular Phylogenetics and Evolution</i> , 2002, 23, 150-157.	1.2	49

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109	The population genetics of host specificity: genetic differentiation in dove lice (Insecta: Phthiraptera). <i>Molecular Ecology</i> , 2002, 11, 25-38.	2.0	132
110	Phylogenetic Analysis of Partial Sequences of Elongation Factor 1 $\hat{\pm}$ Identifies Major Groups of Lice (Insecta: Phthiraptera). <i>Molecular Phylogenetics and Evolution</i> , 2001, 19, 202-215.	1.2	122
111	Are ducks impressed by drakes' display?. <i>Nature</i> , 2001, 413, 128-128.	13.7	16
112	Phylogenetic relationships in the louse genus <i>Penenirmus</i> based on nuclear (EF-1 $\hat{\pm}$) and mitochondrial (COI) DNA sequences. <i>Systematic Entomology</i> , 2001, 26, 491-497.	1.7	24
113	Molecular Systematics of Gonioididae (Insecta: Phthiraptera). <i>Journal of Parasitology</i> , 2001, 87, 862-869.	0.3	38
114	Evolutionary changes in color patches of blackbirds are associated with marsh nesting. <i>Behavioral Ecology</i> , 2000, 11, 515-519.	1.0	44
115	The evolution of bill coloration and plumage dimorphism supports the transference hypothesis in dabbling ducks. <i>Behavioral Ecology</i> , 1999, 10, 63-67.	1.0	32
116	Phylogeny and Biogeography of Dabbling Ducks (Genus: <i>Anas</i>): A Comparison of Molecular and Morphological Evidence. <i>Auk</i> , 1999, 116, 792-805.	0.7	165
117	PATTERNS OF HOMOPLASY IN BEHAVIORAL EVOLUTION. , 1996, , 245-269.		21