

Kevin P Johnson

List of Publications by Year in descending order

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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	Phylogenomics and the evolution of hemipteroid insects. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12775-12780.	3.3	275
2	Phylogeny and Biogeography of Dabbling Ducks (Genus: Anas): A Comparison of Molecular and Morphological Evidence. Auk, 1999, 116, 792-805.	0.7	165
3	When Do Parasites Fail to Speciate in Response to Host Speciation?. Systematic Biology, 2003, 52, 37-47.	2.7	134
4	The population genetics of host specificity: genetic differentiation in dove lice (Insecta: Phthiraptera). Molecular Ecology, 2002, 11, 25-38.	2.0	132
5	Phylogenetic Analysis of Partial Sequences of Elongation Factor 1 \pm Identifies Major Groups of Lice (Insecta: Phthiraptera). Molecular Phylogenetics and Evolution, 2001, 19, 202-215.	1.2	122
6	Multiple origins of parasitism in lice. Proceedings of the Royal Society B: Biological Sciences, 2004, 271, 1771-1776.	1.2	119
7	Host defense reinforces host-parasite cospeciation. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15694-15699.	3.3	117
8	Mitochondrial and Nuclear DNA Sequences Support a Cretaceous Origin of Columbiformes and a Dispersal-Driven Radiation in the Paleogene. Systematic Biology, 2007, 56, 656-672.	2.7	110
9	Anchored Hybrid Enrichment-Based Phylogenomics of Leafhoppers and Treehoppers (Hemiptera: Tj ETQq1 1 0.784314 rgBT /Overloc 0.7 110	0.7	110
10	Mitochondrial genome deletions and minicircles are common in lice (Insecta: Phthiraptera). BMC Genomics, 2011, 12, 394.	1.2	90
11	Dramatically elevated rate of mitochondrial substitution in lice (Insecta: Phthiraptera). Molecular Phylogenetics and Evolution, 2003, 26, 231-242.	1.2	89
12	LINKING COEVOLUTIONARY HISTORY TO ECOLOGICAL PROCESS: DOVES AND LICE. Evolution; International Journal of Organic Evolution, 2003, 57, 2335-2341.	1.1	89
13	Phylogenetic position of Phthiraptera (Insecta: Paraneoptera) and elevated rate of evolution in mitochondrial 12S and 16S rDNA. Molecular Phylogenetics and Evolution, 2003, 29, 102-114.	1.2	87
14	aTRAM - automated target restricted assembly method: a fast method for assembling loci across divergent taxa from next-generation sequencing data. BMC Bioinformatics, 2015, 16, 98.	1.2	78
15	CORRELATED EVOLUTION OF HOST AND PARASITE BODY SIZE: TESTS OF HARRISON'S RULE USING BIRDS AND LICE. Evolution; International Journal of Organic Evolution, 2005, 59, 1744-1753.	1.1	71
16	aTRAM 2.0: An Improved, Flexible Locus Assembler for NGS Data. Evolutionary Bioinformatics, 2018, 14, 117693431877454.	0.6	68
17	How stable is the "Polyphyly of Lice" hypothesis (Insecta: Psocodea)? A comparison of phylogenetic signal in multiple genes. Molecular Phylogenetics and Evolution, 2010, 55, 939-951.	1.2	67
18	Introgression of regulatory alleles and a missense coding mutation drive plumage pattern diversity in the rock pigeon. ELife, 2018, 7, .	2.8	66

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19	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
20	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
21	Unlocking the black box of feather louse diversity: A molecular phylogeny of the hyper-diverse genus <i>Bruelia</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 737-751.	1.2	62
22	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
23	Repeated adaptive divergence of microhabitat specialization in avian feather lice. <i>BMC Biology</i> , 2012, 10, 52.	1.7	60
24	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
25	Phylogeny of the lice (Insecta, Phthiraptera) inferred from small subunit rRNA. <i>Zoologica Scripta</i> , 2003, 32, 407-414.	0.7	52
26	Morphology of male genitalia in lice and their relatives and phylogenetic implications. <i>Systematic Entomology</i> , 2005, 31, 350-361.	1.7	51
27	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
28	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
29	Multiple lineages of lice pass through the P _g boundary. <i>Biology Letters</i> , 2011, 7, 782-785.	1.0	49
30	Feather mites play a role in cleaning host feathers: New insights from <i>scn</i> DNA metabarcoding and microscopy. <i>Molecular Ecology</i> , 2019, 28, 203-218.	2.0	49
31	Multiple Genes and the Monophyly of <i>Ischnocera</i> (Insecta: Phthiraptera). <i>Molecular Phylogenetics and Evolution</i> , 2002, 22, 101-110.	1.2	47
32	Phylogenomics from Whole Genome Sequences Using aTRAM. <i>Systematic Biology</i> , 2017, 66, syw105.	2.7	47
33	Molecular systematics of the suborder Trogiomorpha (Insecta: Psocodea: <i>Psocoptera</i>). <i>Zoological Journal of the Linnean Society</i> , 2006, 146, 287-299.	1.0	46
34	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
35	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
36	Evolutionary changes in color patches of blackbirds are associated with marsh nesting. <i>Behavioral Ecology</i> , 2000, 11, 515-519.	1.0	44

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37	Mitochondrial phylogenomics and genome rearrangements in the barklice (Insecta: Psocodea). <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 118-127.	1.2	44
38	Deletion Bias in Avian Introns over Evolutionary Timescales. <i>Molecular Biology and Evolution</i> , 2004, 21, 599-602.	3.5	41
39	Nuclear Orthologs Derived from Whole Genome Sequencing Indicate Cryptic Diversity in the Bemisia tabaci (Insecta: Aleyrodidae) Complex of Whiteflies. <i>Diversity</i> , 2019, 11, 151.	0.7	39
40	Molecular Systematics of Gonioididae (Insecta: Phthiraptera). <i>Journal of Parasitology</i> , 2001, 87, 862-869.	0.3	38
41	Phylogenetic analysis of nuclear and mitochondrial genes supports species groups for Columbicola (Insecta: Phthiraptera). <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 506-518.	1.2	38
42	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
43	Untangling Coevolutionary History. <i>Systematic Biology</i> , 2004, 53, 92-94.	2.7	36
44	Evolution of the assassin's arms: insights from a phylogeny of combined transcriptomic and ribosomal DNA data (Heteroptera: Reduvidae). <i>Scientific Reports</i> , 2016, 6, 22177.	1.6	36
45	Simultaneous radiation of bird and mammal lice following the K-Pg boundary. <i>Biology Letters</i> , 2018, 14, 20180141.	1.0	33
46	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
47	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
48	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
49	Data incongruence and the problem of avian louse phylogeny. <i>Zoologica Scripta</i> , 2004, 33, 239-259.	0.7	31
50	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
51	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
52	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
53	Next-generation phylogenomics using a Target Restricted Assembly Method. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 417-422.	1.2	28
54	Phoretic dispersal influences parasite population genetic structure. <i>Molecular Ecology</i> , 2018, 27, 2770-2779.	2.0	27

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55	Molecular systematics of Psocomorpha (Psocoptera). <i>Systematic Entomology</i> , 2003, 28, 409-416.	1.7	26
56	Host defense triggers rapid adaptive radiation in experimentally evolving parasites. <i>Evolution Letters</i> , 2019, 3, 120-128.	1.6	26
57	Phylogenetic relationships in the louse genus <i>Penenirmus</i> based on nuclear (EF-1 α) and mitochondrial (COI) DNA sequences. <i>Systematic Entomology</i> , 2001, 26, 491-497.	1.7	24
58	The importance of molecular dating analyses for inferring Hawaiian biogeographical history: a case study with bark lice (Psocidae: <i>Psocoptera</i>). <i>Journal of Biogeography</i> , 2014, 41, 158-167.	1.4	24
59	Phylogeny of the suborder Psocomorpha: congruence and incongruence between morphology and molecular data (Insecta: Psocodea: <i>Psocoptera</i>). <i>Zoological Journal of the Linnean Society</i> , 2014, 171, 716-731.	1.0	22
60	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
61	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
62	PATTERNS OF HOMOPLASY IN BEHAVIORAL EVOLUTION. , 1996, , 245-269.		21
63	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
64	Reinterpreting the origins of flamingo lice: cospeciation or host-switching?. <i>Biology Letters</i> , 2006, 2, 275-278.	1.0	20
65	Extensive host-switching of avian feather lice following the Cretaceous-Paleogene mass extinction event. <i>Communications Biology</i> , 2019, 2, 445.	2.0	20
66	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
67	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
68	Putting the genome in insect phylogenomics. <i>Current Opinion in Insect Science</i> , 2019, 36, 111-117.	2.2	19
69	Phylogenomics of the North American Plecoptera. <i>Systematic Entomology</i> , 2021, 46, 287-305.	1.7	19
70	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
71	Brochosomins and other novel proteins from brochosomes of leafhoppers (Insecta, Hemiptera,) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.2	18
72	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

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73	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
74	Are ducks impressed by drakes' display?. <i>Nature</i> , 2001, 413, 128-128.	13.7	16
75	The evolution of host specificity in dove body lice. <i>Parasitology</i> , 2011, 138, 1730-1736.	0.7	16
76	Changes in base composition bias of nuclear and mitochondrial genes in lice (Insecta: Psocodea). <i>Genetica</i> , 2013, 141, 491-499.	0.5	14
77	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
78	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
79	Structure, gene order, and nucleotide composition of mitochondrial genomes in parasitic lice from <i>Amblycera</i> . <i>Gene</i> , 2021, 768, 145312.	1.0	13
80	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
81	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
82	Host and parasite morphology influence congruence between host and parasite phylogenies. <i>International Journal for Parasitology</i> , 2018, 48, 641-648.	1.3	12
83	Phylogenomic analysis of seal lice reveals codivergence with their hosts. <i>Systematic Entomology</i> , 2019, 44, 699-708.	1.7	12
84	Phylogenomics reveals the origin of mammal lice out of Afrotheria. <i>Nature Ecology and Evolution</i> , 2022, 6, 1205-1210.	3.4	12
85	Novel Primers From Informative Nuclear Loci for Louse Molecular Phylogenetics (Insecta: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	0.9	11
86	Comparative phylogeography of two codistributed subgenera of cave crickets (Orthoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 T	1.4	11
87	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
88	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
89	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
90	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

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91	Cophylogenetic analysis of lice in the Colpocephalum complex (Phthiraptera: Amblycera). <i>Zoologica Scripta</i> , 2018, 47, 72-83.	0.7	9
92	Assessing symbiont extinction risk using cophylogenetic data. <i>Biological Conservation</i> , 2020, 250, 108705.	1.9	9
93	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
94	Two lineages of kingfisher feather lice exhibit differing degrees of cospeciation with their hosts. <i>Parasitology</i> , 2019, 146, 1083-1095.	0.7	8
95	Persistence of single species of symbionts across multiple closely-related host species. <i>Scientific Reports</i> , 2019, 9, 17442.	1.6	8
96	Combining Nuclear and Mitochondrial Loci Provides Phylogenetic Information in the Philopterus Complex of Lice (Psocodea: Ischnocera: Philopteridae). <i>Journal of Medical Entomology</i> , 2021, 58, 252-260.	0.9	8
97	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
98	Independent evolution of highly variable, fragmented mitogenomes of parasitic lice. <i>Communications Biology</i> , 2022, 5, .	2.0	8
99	Speciation, Subspecies Divergence, and Paraphyly in the Cinnamon Teal and Blue-winged Teal. <i>Condor</i> , 2011, 113, 747-761.	0.7	7
100	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
101	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
102	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
103	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
104	Comparing rates of introgression in parasitic feather lice with differing dispersal capabilities. <i>Communications Biology</i> , 2020, 3, 610.	2.0	6
105	Patterns of Microbiome Variation Among Infrapopulations of Permanent Bloodsucking Parasites. <i>Frontiers in Microbiology</i> , 2021, 12, 642543.	1.5	6
106	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
107	Phylogenetics and host-specificity of the mega-diverse louse genus <i>Myrsidea</i> (Amblycera: Tj ETQq1 1 0.784314 rgBT /Overlock 1.7 5	1.7	5
108	Molecular systematics of the bark lice infraorder <i>C</i> (<i>aciliusetae</i> (Insecta: Tj ETQq0 0 0 rgBT /Overlock 1.7 4 Tf 50	1.7	4

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109	Multiple trans-Beringia dispersals of the barklouse genus <i>Trichadenotecnum</i> (Insecta: Psocodea: Tj ETQq1 1 0.784314 rgBT /Overlock	0.7	4
110	Disentangling lousy relationships: Comparative phylogenomics of two sucking louse lineages parasitizing chipmunks. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106998.	1.2	3
111	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
112	Molecular phylogenetics of the avian feather louse <i>Phthirus</i> -complex (Phthiraptera: Tj ETQq0 0 0 rgBT /Overlock 1.2 Tf 50 622 Td (Ph	1.2	2
113	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
114	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
115	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
116	A Target Restricted Assembly Method (TRAM) for Phylogenomics. <i>Nature Precedings</i> , 2010, , .	0.1	0
117	Dew-bathing in the Atlantic Forest endemic Robust Woodpecker <i>Campephilus robustus</i> (Lichtenstein,) Tj ETQq1 1 0.784314 rgBT /Ove	0.4	1