

Gerald Heckel

List of Publications by Year in descending order

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95
papers

4,006
citations

94433

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128289

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4834
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#	ARTICLE	IF	CITATIONS
1	Zoonotic pathogen screening of striped field mice (<i>Apodemus agrarius</i>) from Austria. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 886-890.	3.0	4
2	Host genetic factors associated with the range limit of a European hantavirus. <i>Molecular Ecology</i> , 2022, 31, 252-265.	3.9	6
3	Genetic and biological characteristics of species A rotaviruses detected in common shrews suggest a distinct evolutionary trajectory. <i>Virus Evolution</i> , 2022, 8, veac004.	4.9	7
4	Fitness, risk taking, and spatial behavior covary with boldness in experimental vole populations. <i>Ecology and Evolution</i> , 2022, 12, e8521.	1.9	6
5	Cocirculation of <i>Leptospira</i> spp. and multiple orthohantaviruses in rodents, Lithuania, Northern Europe. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	3.0	5
6	A Bocage Landscape Restricts the Gene Flow of Pest Vole Populations. <i>Life</i> , 2022, 12, 800.	2.4	3
7	Identification of a novel hantavirus strain in the root vole (<i>Microtus oeconomus</i>) in Lithuania, Eastern Europe. <i>Infection, Genetics and Evolution</i> , 2021, 90, 104520.	2.3	9
8	Hantavirus- <i>Leptospira</i> coinfections in small mammals from central Germany. <i>Epidemiology and Infection</i> , 2021, 149, e97.	2.1	19
9	Genomic insight into diet adaptation in the biological control agent <i>Cryptolaemus montrouzieri</i> . <i>BMC Genomics</i> , 2021, 22, 135.	2.8	7
10	A Putative Novel Hepatitis E Virus Genotype 3 Subtype Identified in Rabbit, Germany 2016. <i>Viruses</i> , 2021, 13, 1065.	3.3	6
11	Geographical Distribution and Genetic Diversity of Bank Vole Hepaciviruses in Europe. <i>Viruses</i> , 2021, 13, 1258.	3.3	2
12	Spatial and Temporal Dynamics and Molecular Evolution of Tula orthohantavirus in German Vole Populations. <i>Viruses</i> , 2021, 13, 1132.	3.3	6
13	Variation and Selection in the Putative Sperm-Binding Region of ZP3 in Muroid Rodents: A Comparison between Cricetids and Murines. <i>Genes</i> , 2021, 12, 1450.	2.4	0
14	FREQUENT LEPTOSPIRA SPP. DETECTION BUT ABSENCE OF TULA ORTHOHANTAVIRUS IN MICROTUS SPP. VOLES, NORTHWESTERN SPAIN. <i>Journal of Wildlife Diseases</i> , 2021, 57, 733-742.	0.8	3
15	Seasonal migration patterns and the maintenance of evolutionary diversity in a cryptic bird radiation. <i>Molecular Ecology</i> , 2021, , .	3.9	5
16	Spatial and Temporal Evolutionary Patterns in Puumala Orthohantavirus (PUUV) S Segment. <i>Pathogens</i> , 2020, 9, 548.	2.8	12
17	Assessing Genome-Wide Diversity in European Hantaviruses through Sequence Capture from Natural Host Samples. <i>Viruses</i> , 2020, 12, 749.	3.3	11
18	Genomic and spatial variability of a European common vole hepevirus. <i>Archives of Virology</i> , 2019, 164, 2671-2682.	2.1	15

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19	Genetic, phenotypic and ecological differentiation suggests incipient speciation in two Charadrius plovers along the Chinese coast. BMC Evolutionary Biology, 2019, 19, 135.	3.2	30
20	Field vole-associated Traemmersee hantavirus from Germany represents a novel hantavirus species. Virus Genes, 2019, 55, 848-853.	1.6	12
21	Genomic changes in the biological control agent <i>Cryptolaemus montrouzieri</i> associated with introduction. Evolutionary Applications, 2019, 12, 989-1000.	3.1	9
22	Secondary contact between diverged host lineages entails ecological speciation in a European hantavirus. PLoS Biology, 2019, 17, e3000142.	5.6	26
23	Challenging the European southern refugium hypothesis: Species-specific structures versus general patterns of genetic diversity and differentiation among small mammals. Global Ecology and Biogeography, 2019, 28, 262-274.	5.8	20
24	Spatial and temporal genetic dynamics of the grasshopper <i>Oedaleus decorus</i> revealed by museum genomics. Ecology and Evolution, 2018, 8, 1480-1495.	1.9	13
25	Hepatitis E virus in feral rabbits along a rural-urban transect in Central Germany. Infection, Genetics and Evolution, 2018, 61, 155-159.	2.3	23
26	Effects of the Mitochondrial and Nuclear Genomes on Nonshivering Thermogenesis in a Wild Derived Rodent. Integrative and Comparative Biology, 2018, 58, 532-543.	2.0	5
27	Slimy invasion: Climatic niche and current and future biogeography of <i>Arion</i> slug invaders. Diversity and Distributions, 2018, 24, 1627-1640.	4.1	23
28	A highly divergent Puumala virus lineage in southern Poland. Archives of Virology, 2017, 162, 1177-1185.	2.1	5
29	Detection of rat hepatitis E virus in wild Norway rats (<i>Rattus norvegicus</i>) and Black rats (<i>Rattus</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 1.9 60	1.9	60
30	Revised time scales of RNA virus evolution based on spatial information. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170857.	2.6	23
31	Integrating genetic and stable isotope analyses to infer the population structure of the White-winged Snowfinch <i>Montifringilla nivalis</i> in Western Europe. Journal of Ornithology, 2017, 158, 395-405.	1.1	8
32	Introgressive replacement of natives by invading <i>Arion</i> pest slugs. Scientific Reports, 2017, 7, 14908.	3.3	31
33	Host-Associated Absence of Human Puumala Virus Infections in Northern and Eastern Germany. Emerging Infectious Diseases, 2017, 23, 83-86.	4.3	42
34	High genetic structuring of Tula hantavirus. Archives of Virology, 2016, 161, 1135-1149.	2.1	37
35	Phylogeographic past and invasive presence of <i>Arion</i> pest slugs in Europe. Molecular Ecology, 2016, 25, 5747-5764.	3.9	34
36	Olfactory receptors and behavioural isolation: a study on <i>Microtus</i> voles. Mammal Research, 2016, 61, 399-407.	1.3	1

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37	Spatiotemporal dynamics of Puumala hantavirus associated with its rodent host, <i>Myodes glareolus</i> . <i>Evolutionary Applications</i> , 2015, 8, 545-559.	3.1	41
38	Complete genome of a Puumala virus strain from Central Europe. <i>Virus Genes</i> , 2015, 50, 292-298.	1.6	16
39	Development and characterization of novel microsatellite markers for Arion slug species. <i>Conservation Genetics Resources</i> , 2015, 7, 501-503.	0.8	5
40	Tracing reinforcement through asymmetrical partner preference in the European common vole <i>Microtus arvalis</i> . <i>BMC Evolutionary Biology</i> , 2015, 15, 170.	3.2	19
41	Ignoring Heterozygous Sites Biases Phylogenomic Estimates of Divergence Times: Implications for the Evolutionary History of <i>Microtus Voles</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 817-831.	8.9	80
42	First Molecular Evidence for Puumala Hantavirus in Poland. <i>Viruses</i> , 2014, 6, 340-353.	3.3	17
43	Structure and dynamics of hybrid zones at different stages of speciation in the common vole (<i>Microtus arvalis</i>). <i>Molecular Ecology</i> , 2014, 23, 673-687.	3.9	52
44	Hepeviridae: An expanding family of vertebrate viruses. <i>Infection, Genetics and Evolution</i> , 2014, 27, 212-229.	2.3	122
45	Multiple Infections of Rodents with Zoonotic Pathogens in Austria. <i>Vector-Borne and Zoonotic Diseases</i> , 2014, 14, 467-475.	1.5	60
46	Continental-Scale Footprint of Balancing and Positive Selection in a Small Rodent (<i>Microtus arvalis</i>). <i>PLoS ONE</i> , 2014, 9, e112332.	2.5	16
47	Analysis of rotavirus species diversity and evolution including the newly determined full-length genome sequences of rotavirus F and G. <i>Infection, Genetics and Evolution</i> , 2013, 14, 58-67.	2.3	53
48	Divergent evolutionary processes associated with colonization of offshore islands. <i>Molecular Ecology</i> , 2013, 22, 5205-5220.	3.9	92
49	Sex-specific clines support incipient speciation in a common European mammal. <i>Heredity</i> , 2013, 110, 398-404.	2.6	22
50	Phylogeography of Silver Pheasant (<i>Lophura nycthemera</i> L.) across China: aggregate effects of refugia, introgression and riverine barriers. <i>Molecular Ecology</i> , 2013, 22, 3376-3390.	3.9	39
51	Adaptive evolution during an ongoing range expansion: the invasive bank vole (<i>Microtus yodensis</i>). <i>Trends in Ecology and Evolution</i> , 2013, 24, 145-149.	10.784314	145
52	Temporal genetic structure and relatedness in the Tufted Duck <i>Aythya fuligula</i> suggests limited kin association in winter. <i>Ibis</i> , 2013, 155, 499-507.	1.9	7
53	Source Attribution of Human <i>Campylobacter</i> Isolates by MLST and Fla-Typing and Association of Genotypes with Quinolone Resistance. <i>PLoS ONE</i> , 2013, 8, e81796.	2.5	105
54	Tula Virus Infections in the Eurasian Water Vole in Central Europe. <i>Vector-Borne and Zoonotic Diseases</i> , 2012, 12, 503-513.	1.5	52

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55	Deep mitochondrial introgression and hybridization among ecologically divergent vole species. <i>Molecular Ecology</i> , 2012, 21, 5309-5323.	3.9	33
56	Range expansion in an invasive small mammal: influence of life-history and habitat quality. <i>Biological Invasions</i> , 2012, 14, 2203-2215.	2.4	30
57	Deep phylogeographic divergence and cytonuclear discordance in the grasshopper <i>Oedaleus decorus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 695-704.	2.7	26
58	Breeding site fidelity and winter admixture in a long-distance migrant, the tufted duck (<i>Aythya tjingensis</i>). <i>Journal of Ornithology</i> , 2012, 153, 107-115.	2.6	31
59	Asymmetric and differential gene introgression at a contact zone between two highly divergent lineages of field voles (<i>Microtus agrestis</i>). <i>Journal of Evolutionary Biology</i> , 2012, 25, 400-408.	1.7	54
60	Rat hepatitis E virus: Geographical clustering within Germany and serological detection in wild Norway rats (<i>Rattus norvegicus</i>). <i>Infection, Genetics and Evolution</i> , 2012, 12, 947-956.	2.3	73
61	Life-stage specific environments in a cichlid fish: implications for inducible maternal effects. <i>Evolutionary Ecology</i> , 2012, 26, 123-137.	1.2	17
62	Enhanced AFLP genome scans detect local adaptation in high-altitude populations of a small rodent (<i>Microtus arvalis</i>). <i>Molecular Ecology</i> , 2011, 20, 1450-1462.	3.9	126
63	Establishment success and resulting fitness consequences for vole dispersers. <i>Oikos</i> , 2011, 120, 95-105.	2.7	24
64	Range-wide genetic population structure of common pochard (<i>Aythya ferina</i>): a potentially important vector of highly pathogenic avian influenza viruses. <i>Ecology and Evolution</i> , 2011, 1, 529-545.	1.9	18
65	Phylogenetic analysis of Puumala virus subtype Bavaria, characterization and diagnostic use of its recombinant nucleocapsid protein. <i>Virus Genes</i> , 2011, 43, 177-191.	1.6	35
66	Development of microsatellite markers for a diving duck, the common pochard (<i>Aythya ferina</i>). <i>Conservation Genetics Resources</i> , 2011, 3, 573-576.	0.8	3
67	Novel Hepatitis E Virus Genotype in Norway Rats, Germany. <i>Emerging Infectious Diseases</i> , 2011, 17, 1982-1983.	4.3	2
68	Estimating population structure from AFLP amplification intensity. <i>Molecular Ecology</i> , 2010, 19, 4638-4647.	3.9	66
69	Extensive Host Sharing of Central European Tula Virus. <i>Journal of Virology</i> , 2010, 84, 459-474.	3.4	84
70	Whole-genome characterization of a novel polyomavirus detected in fatally diseased canary birds. <i>Journal of General Virology</i> , 2010, 91, 3016-3022.	2.9	35
71	Genomic Scans Support Repetitive Continental Colonization Events during the Rapid Radiation of Voles (Rodentia: <i>Microtus</i>): the Utility of AFLPs versus Mitochondrial and Nuclear Sequence Markers. <i>Systematic Biology</i> , 2010, 59, 548-572.	5.6	59
72	Novel Hepatitis E Virus Genotype in Norway Rats, Germany. <i>Emerging Infectious Diseases</i> , 2010, 16, 1452-1455.	4.3	181

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73	Gene flow in admixed populations and implications for the conservation of the Western honeybee, <i>Apis mellifera</i> . <i>Journal of Insect Conservation</i> , 2009, 13, 317-328.	1.4	56
74	Transalpine colonisation and partial phylogeographic erosion by dispersal in the common vole (<i>Microtus arvalis</i>). <i>Molecular Ecology</i> , 2009, 18, 2518-2531.	3.9	58
75	Microsatellite markers for the common vole (<i>Microtus arvalis</i>) and their cross-species utility. <i>Conservation Genetics</i> , 2008, 9, 479-481.	1.5	20
76	Italy as a major Ice Age refuge area for the bat <i>Myotis myotis</i> (Chiroptera: Vespertilionidae) in Europe. <i>Molecular Ecology</i> , 2008, 17, 1801-1814.	3.9	60
77	Evolution of the arginine vasopressin 1a receptor and implications for mammalian social behaviour. <i>Progress in Brain Research</i> , 2008, 170, 321-330.	1.4	12
78	Molecular Analysis of Varicella-Zoster Virus Strains Circulating in Tanzania Demonstrating the Presence of Genotype M1. <i>Journal of Clinical Microbiology</i> , 2008, 46, 3530-3533.	3.9	12
79	Novel Approach for Genotyping Varicella-Zoster Virus Strains from Germany. <i>Journal of Clinical Microbiology</i> , 2007, 45, 3540-3545.	3.9	16
80	Female-biased dispersal and patrilocal kin groups in a mammal with resource-defence polygyny. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 3019-3025.	2.6	83
81	Fine-scale genetic structure and dispersal in the common vole (<i>Microtus arvalis</i>). <i>Molecular Ecology</i> , 2007, 16, 2463-2473.	3.9	90
82	Territorial songs indicate male quality in the sac-winged bat <i>Saccopteryx bilineata</i> (Chiroptera, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 38	2.2	72
83	Computer programs for population genetics data analysis: a survival guide. <i>Nature Reviews Genetics</i> , 2006, 7, 745-758.	16.3	316
84	Cichlids do not adjust reproductive skew to the availability of independent breeding options. <i>Behavioral Ecology</i> , 2006, 17, 419-429.	2.2	74
85	Mammalian monogamy is not controlled by a single gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10956-10960.	7.1	121
86	GENETIC STRUCTURE AND COLONIZATION PROCESSES IN EUROPEAN POPULATIONS OF THE COMMON VOLE, <i>MICROTUS ARVALIS</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2231-2242.	2.3	121
87	Sexual selection favours small and symmetric males in the polygynous greater sac-winged bat <i>Saccopteryx bilineata</i> (Emballonuridae, Chiroptera). <i>Behavioral Ecology and Sociobiology</i> , 2005, 57, 457-464.	1.4	43
88	Bayesian Estimation of Recent Migration Rates After a Spatial Expansion. <i>Genetics</i> , 2005, 170, 409-417.	2.9	112
89	Genetic structure and colonization processes in European populations of the common vole, <i>Microtus arvalis</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2231-42.	2.3	38
90	Mitochondrial gene diversity in the common vole <i>Microtus arvalis</i> shaped by historical divergence and local adaptations. <i>Molecular Ecology</i> , 2004, 13, 3501-3514.	3.9	90

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91	Male tactics and reproductive success in the harem polygynous bat <i>Saccopteryx bilineata</i> . Behavioral Ecology, 2002, 13, 750-756.	2.2	61
92	Genetic mating system and the significance of harem associations in the bat <i>Saccopteryx bilineata</i> . Molecular Ecology, 2002, 12, 219-227.	3.9	62
93	Title is missing!. Conservation Genetics, 2002, 3, 77-79.	1.5	28
94	Highly polymorphic microsatellite markers in the white-lined bat (<i>Saccopteryx bilineata</i>). Molecular Ecology, 2000, 9, 242-244.	3.9	14
95	EXTRA-HAREM PATERNITY IN THE WHITE-LINED BAT <i>SACCOPTERYX BILINEATA</i> (EMBALLONURIDAE). Behaviour, 1999, 136, 1173-1185.	0.8	65