

Wiesław Babik

List of Publications by Year in descending order

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Version: 2024-02-01

93
papers

3,905
citations

117453

34
h-index

143772

57
g-index

98
all docs

98
docs citations

98
times ranked

4341
citing authors

#	ARTICLE	IF	CITATIONS
1	Navigating the temporal continuum of effective population size. <i>Methods in Ecology and Evolution</i> , 2022, 13, 22-41.	2.2	34
2	Next-generation phylogeography of the banded newts (<i>Ommatotriton</i>): A phylogenetic hypothesis for three ancient species with geographically restricted interspecific gene flow and deep intraspecific genetic structure. <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107361.	1.2	7
3	Landscape genetics reveals contrasting patterns of connectivity in two newt species (<i>Lissotriton</i>). <i>Trends in Ecology and Evolution</i> , 2020, 35, 1073-1083.	2.0	5
4	Genomic evidence that a sexually selected trait captures genome-wide variation and facilitates the purging of genetic load. <i>Nature Ecology and Evolution</i> , 2022, 6, 1330-1342.	3.4	8
5	Phylotranscriptomic evidence for pervasive ancient hybridization among Old World salamanders. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106967.	1.2	22
6	Balancing selection versus allele and supertype turnover in MHC class II genes in guppies. <i>Heredity</i> , 2021, 126, 548-560.	1.2	9
7	Coevolution between MHC Class I and Antigen-Processing Genes in Salamanders. <i>Molecular Biology and Evolution</i> , 2021, 38, 5092-5106.	3.5	5
8	Molecular Evolution of Antigen-Processing Genes in Salamanders: Do They Coevolve with MHC Class I Genes?. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	2
9	Morphology is a poor predictor of interspecific admixture – the case of two naturally hybridizing newts <i>Lissotriton montandoni</i> and <i>Lissotriton vulgaris</i> (Caudata: Salamandridae). <i>Amphibia - Reptilia</i> , 2020, 41, 489-500.	0.1	3
10	Evolutionary principles guiding amphibian conservation. <i>Evolutionary Applications</i> , 2020, 13, 857-878.	1.5	27
11	Advances in the Evolutionary Understanding of MHC Polymorphism. <i>Trends in Genetics</i> , 2020, 36, 298-311.	2.9	188
12	Massive introgression of major histocompatibility complex (MHC) genes in newt hybrid zones. <i>Molecular Ecology</i> , 2019, 28, 4798-4810.	2.0	34
13	Differential introgression across newt hybrid zones: Evidence from replicated transects. <i>Molecular Ecology</i> , 2019, 28, 4811-4824.	2.0	28
14	Vanishing benefits - The loss of actinobacterial symbionts at elevated temperatures. <i>Journal of Thermal Biology</i> , 2019, 82, 222-228.	1.1	16
15	MHC structuring and divergent allele advantage in a urodele amphibian: a hierarchical multi-scale approach. <i>Heredity</i> , 2019, 123, 593-607.	1.2	7
16	Genetic drift shaped MHC IIB diversity of an endangered anuran species within the Italian glacial refugium. <i>Journal of Zoology</i> , 2019, 307, 61-70.	0.8	12
17	Genomics of end-Pleistocene population replacement in a small mammal. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20172624.	1.2	26
18	The role of MHC supertypes in promoting trans-species polymorphism remains an open question. <i>Nature Communications</i> , 2018, 9, 4362.	5.8	13

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19	Balancing selection and introgression of newt immune-response genes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180819.	1.2	21
20	Linkage Map of <i>Lissotriton</i> Newts Provides Insight into the Genetic Basis of Reproductive Isolation. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2115-2124.	0.8	10
21	The Carpathians hosted extra-Mediterranean refugia-within-refugia during the Pleistocene Ice Age: genomic evidence from two newt genera. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 605-613.	0.7	12
22	Isolation and gene flow in a speciation continuum in newts. <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 1-12.	1.2	45
23	Transcriptomics of Intralocus Sexual Conflict: Gene Expression Patterns in Females Change in Response to Selection on a Male Secondary Sexual Trait in the Bulb Mite. <i>Genome Biology and Evolution</i> , 2016, 8, 2351-2357.	1.1	20
24	Divergence history of the Carpathian and smooth newts modelled in space and time. <i>Molecular Ecology</i> , 2016, 25, 3912-3928.	2.0	22
25	Genomic heterogeneity of historical gene flow between two species of newts inferred from transcriptome data. <i>Ecology and Evolution</i> , 2016, 6, 4513-4525.	0.8	21
26	Genomic Response to Selection for Predatory Behavior in a Mammalian Model of Adaptive Radiation. <i>Molecular Biology and Evolution</i> , 2016, 33, 2429-2440.	3.5	25
27	Selective Landscapes in newt Immune Genes Inferred from Patterns of Nucleotide Variation. <i>Genome Biology and Evolution</i> , 2016, 8, 3417-3432.	1.1	13
28	Genetic structure of the fire salamander <i>Salamandra salamandra</i> in the Polish Sudetes. <i>Amphibia - Reptilia</i> , 2016, 37, 405-415.	0.1	6
29	Biofilm feeding: Microbial colonization of food promotes the growth of a detritivorous arthropod. <i>ZooKeys</i> , 2016, 577, 25-41.	0.5	23
30	Plant-herbivorous beetle networks: molecular characterization of trophic ecology within a threatened steppic environment. <i>Molecular Ecology</i> , 2015, 24, 4023-4038.	2.0	15
31	Genome-wide genetic diversity of rove beetle populations along a metal pollution gradient. <i>Ecotoxicology and Environmental Safety</i> , 2015, 119, 98-105.	2.9	19
32	Deeply divergent sympatric mitochondrial lineages of the earthworm <i>Lumbricus rubellus</i> are not reproductively isolated. <i>BMC Evolutionary Biology</i> , 2015, 15, 217.	3.2	50
33	Genetic structure and differentiation of the fire salamander <i>Salamandra salamandra</i> at the northern margin of its range in the Carpathians. <i>Amphibia - Reptilia</i> , 2015, 36, 301-311.	0.1	7
34	Effects of heterozygosity and MHC diversity on patterns of extra-pair paternity in the socially monogamous scarlet rosefinch. <i>Behavioral Ecology and Sociobiology</i> , 2015, 69, 459-469.	0.6	17
35	The crested newt <i>Triturus cristatus</i> recolonized temperate Eurasia from an extra-Mediterranean glacial refugium. <i>Biological Journal of the Linnean Society</i> , 2015, 114, 574-587.	0.7	36
36	Constraint and Adaptation in newt Toll-Like Receptor Genes. <i>Genome Biology and Evolution</i> , 2015, 7, 81-95.	1.1	34

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37	Initial Molecular-Level Response to Artificial Selection for Increased Aerobic Metabolism Occurs Primarily through Changes in Gene Expression. <i>Molecular Biology and Evolution</i> , 2015, 32, 1461-1473.	3.5	26
38	Detecting balancing selection in genomes: limits and prospects. <i>Molecular Ecology</i> , 2015, 24, 3529-3545.	2.0	195
39	A three-marker DNA barcoding approach for ecological studies of xerothermic plants and herbivorous insects from central Europe. <i>Botanical Journal of the Linnean Society</i> , 2015, 177, 576-592.	0.8	12
40	The dissection of a Pleistocene refugium: phylogeography of the smooth newt, <i>Lissotriton vulgaris</i> , in the Balkans. <i>Journal of Biogeography</i> , 2015, 42, 671-683.	1.4	47
41	No Evidence for the Effect of MHC on Male Mating Success in the Brown Bear. <i>PLoS ONE</i> , 2014, 9, e113414.	1.1	8
42	Alternative reproductive tactics and sex-biased gene expression: the study of the bulb mite transcriptome. <i>Ecology and Evolution</i> , 2014, 4, 623-632.	0.8	50
43	Selective pressures on MHC class II genes in the guppy (<i>Poecilia reticulata</i>). <i>Evolutionary Biology</i> , 2014, 27, 2347-2359.	0.8	55
44	Parasite load and MHC diversity in undisturbed and agriculturally modified habitats of the ornate dragon lizard. <i>Molecular Ecology</i> , 2014, 23, 5966-5978.	2.0	32
45	Development, validation and high-throughput analysis of sequence markers in nonmodel species. <i>Molecular Ecology Resources</i> , 2014, 14, 352-360.	2.2	27
46	Low effective population sizes and limited connectivity in xerothermic beetles: implications for the conservation of an endangered habitat. <i>Animal Conservation</i> , 2014, 17, 454-466.	1.5	7
47	Accuracy of allele frequency estimation using pooled RNA-seq. <i>Molecular Ecology Resources</i> , 2014, 14, 381-392.	2.2	54
48	Population structure of guppies in north-eastern Venezuela, the area of putative incipient speciation. <i>BMC Evolutionary Biology</i> , 2014, 14, 28.	3.2	7
49	Admixture of two phylogeographic lineages of the Eurasian beaver in Poland. <i>Mammalian Biology</i> , 2014, 79, 287-296.	0.8	8
50	Evolutionary units of <i>Coraebus elatus</i> (Coleoptera: Buprestidae) in central and eastern Europe – implications for origin and conservation. <i>Insect Conservation and Diversity</i> , 2014, 7, 41-54.	1.4	13
51	Single Nucleotide Polymorphisms Reveal Genetic Structuring of the Carpathian Newt and Provide Evidence of Interspecific Gene Flow in the Nuclear Genome. <i>PLoS ONE</i> , 2014, 9, e97431.	1.1	23
52	Data Concatenation, Bayesian Concordance and Coalescent-Based Analyses of the Species Tree for the Rapid Radiation of Triturus Newts. <i>PLoS ONE</i> , 2014, 9, e111011.	1.1	18
53	No evidence for nuclear introgression despite complete mtDNA replacement in the Carpathian newt (<i>Lissotriton montandoni</i>). <i>Molecular Ecology</i> , 2013, 22, 1884-1903.	2.0	96
54	Low Major Histocompatibility Complex Class I (MHC I) Variation in the European Bison (<i>Bison bonasus</i>). <i>Journal of Heredity</i> , 2012, 103, 349-359.	1.0	18

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55	Evolution of major histocompatibility complex class I and class II genes in the brown bear. <i>BMC Evolutionary Biology</i> , 2012, 12, 197.	3.2	63
56	The genomics of adaptation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 5024-5028.	1.2	45
57	Development and characterization of microsatellite loci in the <i>Centricnemus leucogrammus</i> weevil. <i>Molecular Biology Reports</i> , 2012, 39, 11131-11136.	1.0	3
58	Evaluation of two approaches to genotyping major histocompatibility complex class I in a passerineâ€”CEâ€”SSCP and 454 pyrosequencing. <i>Molecular Ecology Resources</i> , 2012, 12, 285-292.	2.2	42
59	Interspecific hybridization increases MHC class II diversity in two sister species of newts. <i>Molecular Ecology</i> , 2012, 21, 887-906.	2.0	69
60	MHC diversity, malaria and lifetime reproductive success in collared flycatchers. <i>Molecular Ecology</i> , 2012, 21, 2469-2479.	2.0	82
61	jMHC: software assistant for multilocus genotyping of gene families using nextâ€”generation amplicon sequencing. <i>Molecular Ecology Resources</i> , 2011, 11, 739-742.	2.2	86
62	Nuclear and mitochondrial phylogeography of the European fireâ€”bellied toads <i>Bombina bombina</i> and <i>Bombina variegata</i> supports their independent histories. <i>Molecular Ecology</i> , 2011, 20, 3381-3398.	2.0	68
63	Strong genetic differentiation between <i>Gymnadenia conopsea</i> and <i>G. densiflora</i> despite morphological similarity. <i>Plant Systematics and Evolution</i> , 2011, 293, 213-226.	0.3	25
64	MHC allele frequency distributions under parasite-driven selection: A simulation model. <i>BMC Evolutionary Biology</i> , 2010, 10, 332.	3.2	31
65	Heart transcriptome of the bank vole (<i>Myodes glareolus</i>): towards understanding the evolutionary variation in metabolic rate. <i>BMC Genomics</i> , 2010, 11, 390.	1.2	22
66	Effects of an MHCâ€”DRB genotype and allele number on the load of gut parasites in the bank vole <i>Myodes glareolus</i> . <i>Molecular Ecology</i> , 2010, 19, 255-265.	2.0	134
67	454 sequencing reveals extreme complexity of the class II Major Histocompatibility Complex in the collared flycatcher. <i>BMC Evolutionary Biology</i> , 2010, 10, 395.	3.2	106
68	Does reduced MHC diversity decrease viability of vertebrate populations?. <i>Biological Conservation</i> , 2010, 143, 537-544.	1.9	201
69	An evaluation of two potential risk factors, MHC diversity and host density, for infection by an invasive nematode <i>Ashworthius sidemi</i> in endangered European bison (<i>Bison bonasus</i>). <i>Biological Conservation</i> , 2010, 143, 2049-2053.	1.9	44
70	Methods for MHC genotyping in nonâ€”model vertebrates. <i>Molecular Ecology Resources</i> , 2010, 10, 237-251.	2.2	125
71	Divergence in the Face of Gene Flow: The Case of Two Newts (Amphibia: Salamandridae). <i>Molecular Biology and Evolution</i> , 2009, 26, 829-841.	3.5	78
72	Fungi from the roots of the common terrestrial orchid <i>Gymnadenia conopsea</i> . <i>Mycological Research</i> , 2009, 113, 952-959.	2.5	87

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73	Long-term survival of a urodele amphibian despite depleted major histocompatibility complex variation. <i>Molecular Ecology</i> , 2009, 18, 769-781.	2.0	58
74	How sympatric is speciation in the <i>Howea</i> palms of Lord Howe Island?. <i>Molecular Ecology</i> , 2009, 18, 3629-3638.	2.0	33
75	A combination of techniques proves useful in the development of nuclear markers in the newt genus <i>Triturus</i> . <i>Molecular Ecology Resources</i> , 2009, 9, 1160-1162.	2.2	4
76	New generation sequencers as a tool for genotyping of highly polymorphic multilocus MHC system. <i>Molecular Ecology Resources</i> , 2009, 9, 713-719.	2.2	133
77	Contrasting patterns of variation in MHC loci in the Alpine newt. <i>Molecular Ecology</i> , 2008, 17, 2339-2355.	2.0	59
78	in the Abdominal Glands of the Smooth Newt (<i>Lissotriton vulgaris</i>) and Montandon's Newt (<i>L. montandoni</i>). <i>Journal of Herpetology</i> , 2008, 42, 101-110.	0.3	11
79	Phylogeography of the fire-bellied toads <i>Bombina</i> : independent Pleistocene histories inferred from mitochondrial genomes. <i>Molecular Ecology</i> , 2007, 16, 2301-2316.	2.0	77
80	Sequence diversity of MHC class II DRB genes in the bank vole <i>Myodes glareolus</i> . <i>Acta Theriologica</i> , 2007, 52, 227-235.	1.1	10
81	Genetic structure in northeastern populations of the Alpine newt (<i>Triturus alpestris</i>): evidence for post-Pleistocene differentiation. <i>Molecular Ecology</i> , 2006, 15, 2397-2407.	2.0	28
82	MHC-DRB3 variation in a free-living population of the European bison, <i>Bison bonasus</i> . <i>Molecular Ecology</i> , 2006, 16, 531-540.	2.0	61
83	Phylogeography of two European newt species - discordance between mtDNA and morphology. <i>Molecular Ecology</i> , 2005, 14, 2475-2491.	2.0	173
84	Mitochondrial phylogeography of the Eurasian beaver <i>Castor fiber</i> L.. <i>Molecular Ecology</i> , 2005, 14, 3843-3856.	2.0	51
85	Sequence diversity of the MHC DRB gene in the Eurasian beaver (<i>Castor fiber</i>). <i>Molecular Ecology</i> , 2005, 14, 4249-4257.	2.0	80
86	Conservation units in north-eastern populations of the Alpine newt (<i>Triturus alpestris</i>). <i>Conservation Genetics</i> , 2005, 6, 307-312.	0.8	13
87	Mitochondrial phylogeography of the moor frog, <i>Rana arvalis</i> . <i>Molecular Ecology</i> , 2004, 13, 1469-1480.	2.0	108
88	Relationship between morphometric and genetic variation in pure and hybrid populations of the smooth and Montandon's newt (<i>Triturus vulgaris</i> and <i>T. montandoni</i>). <i>Journal of Zoology</i> , 2004, 262, 135-143.	0.8	15
89	Nuclear markers, mitochondrial DNA and male secondary sexual traits variation in a newt hybrid zone (<i>Triturus vulgaris</i> and <i>T. montandoni</i>). <i>Molecular Ecology</i> , 2003, 12, 1913-1930.	2.0	67
90	Genetic differentiation among northern and southern populations of the moor frog <i>Rana arvalis</i> Nilsson in central Europe. <i>Heredity</i> , 2000, 84, 610-618.	1.2	25

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91	Morphometric differentiation of the moor frog (<i>Rana arvalis</i> Nilss.) in Central Europe. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2000, 38, 239-247.	0.6	16
92	Knowledge Representation in Map Collections for Information Retrieval Systems. <i>LIBER Quarterly</i> , 1999, 9, 172-179.	0.6	1
93	Intrageneric predation in larval newts (<i>Triturus</i> , Salamandridae, Urodela). <i>Amphibia - Reptilia</i> , 1998, 19, 446-451.	0.1	5