WiesÅ‚aw Babik

List of Publications by Year
in descending order

93 papers	3,905 citations	117625 34 h-index	144013 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. Methods in Ecology and Evolution, 2022, 13, 22-41.	5.2	34
2	Next-generation phylogeography of the banded newts (Ommatotriton): A phylogenetic hypothesis for three ancient species with geographically restricted interspecific gene flow and deep intraspecific genetic structure. Molecular Phylogenetics and Evolution, 2022, 167, 107361.	2.7	7
3	Landscape genetics reveals contrasting patterns of connectivity in two newt species (<i>Lissotriton) Tj ETQq1 1 0.784314 rgBT /Ove	3.9	3
4	Genomic evidence that a sexually selected trait captures genome-wide variation and facilitates the purging of genetic load. Nature Ecology and Evolution, 2022, 6, 1330-1342.	7.8	8
5	Phylotranscriptomic evidence for pervasive ancient hybridization among Old World salamanders. Molecular Phylogenetics and Evolution, 2021, 155, 106967.	2.7	22
6	Balancing selection versus allele and supertype turnover in MHC class II genes in guppies. Heredity, 2021, 126, 548-560.	2.6	9
7	Coevolution between MHC Class I and Antigen-Processing Genes in Salamanders. Molecular Biology and Evolution, 2021, 38, 5092-5106.	8.9	5
8	Molecular Evolution of Antigen-Processing Genes in Salamanders: Do They Coevolve with MHC Class I Genes?. Genome Biology and Evolution, 2021, 13, .	2.5	2
9	Morphology is a poor predictor of interspecific admixtureÂâ€“ the case of two naturally hybridizing newts Lissotriton montandoni and Lissotriton vulgaris (Caudata: Salamandridae). Amphibia - Reptilia, 2020, 41, 489-500.	0.5	3
10	Evolutionary principles guiding amphibian conservation. Evolutionary Applications, 2020, 13, 857-878.	3.1	27
11	Advances in the Evolutionary Understanding of MHC Polymorphism. Trends in Genetics, 2020, 36, 298-311.	6.7	188
12	Massive introgression of major histocompatibility complex (MHC) genes in newt hybrid zones. Molecular Ecology, 2019, 28, 4798-4810.	3.9	34
13	Differential introgression across newt hybrid zones: Evidence from replicated transects. Molecular Ecology, 2019, 28, 4811-4824.	3.9	28
14	Vanishing benefits - The loss of actinobacterial symbionts at elevated temperatures. Journal of Thermal Biology, 2019, 82, 222-228.	2.5	16
15	MHC structuring and divergent allele advantage in a urodele amphibian: a hierarchical multi-scale approach. Heredity, 2019, 123, 593-607.	2.6	7
16	Genetic drift shaped MHC IIB diversity of an endangered anuran species within the Italian glacial refugium. Journal of Zoology, 2019, 307, 61-70.	1.7	12
17	Genomics of end-Pleistocene population replacement in a small mammal. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20172624.	2.6	26
18	The role of MHC supertypes in promoting trans-species polymorphism remains an open question. Nature Communications, 2018, 9, 4362.	12.8	13

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19	Balancing selection and introgression of newt immune-response genes. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20180819.	2.6	21
20	Linkage Map ofLissotritonNewts Provides Insight into the Genetic Basis of Reproductive Isolation. G3: Genes, Genomes, Genetics, 2017, 7, 2115-2124.	1.8	10
21	The Carpathians hosted extra-Mediterranean refugia-within-refugia during the Pleistocene Ice Age: genomic evidence from two newt genera. Biological Journal of the Linnean Society, 2017, 122, 605-613.	1.6	12
22	Isolation and gene flow in a speciation continuum in newts. Molecular Phylogenetics and Evolution, 2017, 116, 1-12.	2.7	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. Genome Biology and Evolution, 2016, 8, 2351-2357.	2.5	20
24	Divergence history of the Carpathian and smooth newts modelled in space and time. Molecular Ecology, 2016, 25, 3912-3928.	3.9	22
25	Genomic heterogeneity of historical gene flow between two species of newts inferred from transcriptome data. Ecology and Evolution, 2016, 6, 4513-4525.	1.9	21
26	Genomic Response to Selection for Predatory Behavior in a Mammalian Model of Adaptive Radiation. Molecular Biology and Evolution, 2016, 33, 2429-2440.	8.9	25
27	Selective Landscapes in newt Immune Genes Inferred from Patterns of Nucleotide Variation. Genome Biology and Evolution, 2016, 8, 3417-3432.	2.5	13
28	Genetic structure of the fire salamander Salamandra salamandra in the Polish Sudetes. Amphibia - Reptilia, 2016, 37, 405-415.	0.5	6
29	Biofilm feeding: Microbial colonization of food promotes the growth of a detritivorous arthropod. ZooKeys, 2016, 577, 25-41.	1.1	23
30	Plantâ€“herbivorous beetle networks: molecular characterization of trophic ecology within a threatened steppic environment. Molecular Ecology, 2015, 24, 4023-4038.	3.9	15
31	Genome-wide genetic diversity of rove beetle populations along a metal pollution gradient. Ecotoxicology and Environmental Safety, 2015, 119, 98-105.	6.0	19
32	Deeply divergent sympatric mitochondrial lineages of the earthworm Lumbricus rubellus are not reproductively isolated. BMC Evolutionary Biology, 2015, 15, 217.	3.2	50
33	Genetic structure and differentiation of the fire salamander Salamandra salamandra at the northern margin of its range in the Carpathians. Amphibia - Reptilia, 2015, 36, 301-311.	0.5	7
34	Effects of heterozygosity and MHC diversity on patterns of extra-pair paternity in the socially monogamous scarlet rosefinch. Behavioral Ecology and Sociobiology, 2015, 69, 459-469.	1.4	17
35	The crested newtTriturus cristatusrecolonized temperate Eurasia from an extra-Mediterranean glacial refugium. Biological Journal of the Linnean Society, 2015, 114, 574-587.	1.6	36
36	Constraint and Adaptation in newt Toll-Like Receptor Genes. Genome Biology and Evolution, 2015, 7, 81-95.	2.5	34

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37	Initial Molecular-Level Response to Artificial Selection for Increased Aerobic Metabolism Occurs Primarily through Changes in Gene Expression. Molecular Biology and Evolution, 2015, 32, 1461-1473.	8.9	26
38	Detecting balancing selection in genomes: limits and prospects. Molecular Ecology, 2015, 24, 3529-3545.	3.9	195
39	A three-marker DNA barcoding approach for ecological studies of xerothermic plants and herbivorous insects from central Europe. Botanical Journal of the Linnean Society, 2015, 177, 576-592.	1.6	12
40	The dissection of a Pleistocene refugium: phylogeography of the smooth newt, Lissotriton vulgaris, in the Balkans. Journal of Biogeography, 2015, 42, 671-683.	3.0	47
41	No Evidence for the Effect of MHC on Male Mating Success in the Brown Bear. PLoS ONE, 2014, 9, e113414.	2.5	8
42	Alternative reproductive tactics and sexâ€biased gene expression: the study of the bulb mite transcriptome. Ecology and Evolution, 2014, 4, 623-632.	1.9	50
43	Selective pressures on <scp>MHC</scp> class <scp>II</scp> genes in the guppy (<scp>P</scp>oecilia) Tj ETQq1 1 0.784314 rgBT /O Biology, 2014, 27, 2347-2359.	1.7	55
44	Parasite load and <scp>MHC</scp> diversity in undisturbed and agriculturally modified habitats of the ornate dragon lizard. Molecular Ecology, 2014, 23, 5966-5978.	3.9	32
45	Development, validation and highâ€throughput analysis of sequence markers in nonmodel species. Molecular Ecology Resources, 2014, 14, 352-360.	4.8	27
46	Low effective population sizes and limited connectivity in xerothermic beetles: implications for the conservation of an endangered habitat. Animal Conservation, 2014, 17, 454-466.	2.9	7
47	Accuracy of allele frequency estimation using pooled <scp>RNA</scp>â€Seq. Molecular Ecology Resources, 2014, 14, 381-392.	4.8	54
48	Population structure of guppies in north-eastern Venezuela, the area of putative incipient speciation. BMC Evolutionary Biology, 2014, 14, 28.	3.2	7
49	Admixture of two phylogeographic lineages of the Eurasian beaver in Poland. Mammalian Biology, 2014, 79, 287-296.	1.5	8
50	Evolutionary units of Coraebus elatus (Coleoptera: Buprestidae) in central and eastern Europe â€“ implications for origin and conservation. Insect Conservation and Diversity, 2014, 7, 41-54.	3.0	13
51	Single Nucleotide Polymorphisms Reveal Genetic Structuring of the Carpathian Newt and Provide Evidence of Interspecific Gene Flow in the Nuclear Genome. PLoS ONE, 2014, 9, e97431.	2.5	23
52	Data Concatenation, Bayesian Concordance and Coalescent-Based Analyses of the Species Tree for the Rapid Radiation of Triturus Newts. PLoS ONE, 2014, 9, e111011.	2.5	18
53	No evidence for nuclear introgression despite complete mt<scp>DNA</scp> replacement in the <scp>C</scp>arpathian newt (<scp>L</scp>issotriton montandoni). Molecular Ecology, 2013, 22, 1884-1903.	3.9	96
54	Low Major Histocompatibility Complex Class I (MHC I) Variation in the European Bison (Bison bonasus). Journal of Heredity, 2012, 103, 349-359.	2.4	18

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55	Evolution of major histocompatibility complex class I and class II genes in the brown bear. BMC Evolutionary Biology, 2012, 12, 197.	3.2	63
56	The genomics of adaptation. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 5024-5028.	2.6	45
57	Development and characterization of microsatellite loci in the Centricnemus leucogrammus weevil. Molecular Biology Reports, 2012, 39, 11131-11136.	2.3	3
58	Evaluation of two approaches to genotyping major histocompatibility complex class I in a passerineâ€"CEâ€SSCP and 454 pyrosequencing. Molecular Ecology Resources, 2012, 12, 285-292.	4.8	42
59	Interspecific hybridization increases MHC class II diversity in two sister species of newts. Molecular Ecology, 2012, 21, 887-906.	3.9	69
60	MHC diversity, malaria and lifetime reproductive success in collared flycatchers. Molecular Ecology, 2012, 21, 2469-2479.	3.9	82
61	jMHC: software assistant for multilocus genotyping of gene families using nextâ€generation amplicon sequencing. Molecular Ecology Resources, 2011, 11, 739-742.	4.8	86
62	Nuclear and mitochondrial phylogeography of the European fireâ€bellied toadsBombina bombinaandBombina variegatasupports their independent histories. Molecular Ecology, 2011, 20, 3381-3398.	3.9	68
63	Strong genetic differentiation between Gymnadenia conopsea and G. densiflora despite morphological similarity. Plant Systematics and Evolution, 2011, 293, 213-226.	0.9	25
64	MHC allele frequency distributions under parasite-driven selection: A simulation model. BMC Evolutionary Biology, 2010, 10, 332.	3.2	31
65	Heart transcriptome of the bank vole (Myodes glareolus): towards understanding the evolutionary variation in metabolic rate. BMC Genomics, 2010, 11, 390.	2.8	22
66	Effects of an MHCâ€DRB genotype and allele number on the load of gut parasites in the bank vole Myodes glareolus. Molecular Ecology, 2010, 19, 255-265.	3.9	134
67	454 sequencing reveals extreme complexity of the class II Major Histocompatibility Complex in the collared flycatcher. BMC Evolutionary Biology, 2010, 10, 395.	3.2	106
68	Does reduced MHC diversity decrease viability of vertebrate populations?. Biological Conservation, 2010, 143, 537-544.	4.1	201
69	An evaluation of two potential risk factors, MHC diversity and host density, for infection by an invasive nematode Ashworthius sidemi in endangered European bison (Bison bonasus). Biological Conservation, 2010, 143, 2049-2053.	4.1	44
70	Methods for MHC genotyping in nonâ€model vertebrates. Molecular Ecology Resources, 2010, 10, 237-251.	4.8	125
71	Divergence in the Face of Gene Flow: The Case of Two Newts (Amphibia: Salamandridae). Molecular Biology and Evolution, 2009, 26, 829-841.	8.9	78
72	Fungi from the roots of the common terrestrial orchid Gymnadenia conopsea. Mycological Research, 2009, 113, 952-959.	2.5	87

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73	Longâ€term survival of a urodele amphibian despite depleted major histocompatibility complex variation. Molecular Ecology, 2009, 18, 769-781.	3.9	58
74	How sympatric is speciation in the Howea palms of Lord Howe Island?. Molecular Ecology, 2009, 18, 3629-3638.	3.9	33
75	A combination of techniques proves useful in the development of nuclear markers in the newt genus Triturus. Molecular Ecology Resources, 2009, 9, 1160-1162.	4.8	4
76	New generation sequencers as a tool for genotyping of highly polymorphic multilocus MHC system. Molecular Ecology Resources, 2009, 9, 713-719.	4.8	133
77	Contrasting patterns of variation in MHC loci in the Alpine newt. Molecular Ecology, 2008, 17, 2339-2355.	3.9	59
78	in the Abdominal Glands of the Smooth Newt (Lissotriton vulgaris) and Montandonâ€™s Newt (L.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.7	11
79	Phylogeography of the fire-bellied toads Bombina: independent Pleistocene histories inferred from mitochondrial genomes. Molecular Ecology, 2007, 16, 2301-2316.	3.9	77
80	Sequence diversity of MHC class II DRB genes in the bank voleMyodes glareolus. Acta Theriologica, 2007, 52, 227-235.	1.1	10
81	Genetic structure in northeastern populations of the Alpine newt (Triturus alpestris): evidence for post-Pleistocene differentiation. Molecular Ecology, 2006, 15, 2397-2407.	3.9	28
82	MHC-DRB3 variation in a free-living population of the European bison, Bison bonasus. Molecular Ecology, 2006, 16, 531-540.	3.9	61
83	Phylogeography of two European newt species - discordance between mtDNA and morphology. Molecular Ecology, 2005, 14, 2475-2491.	3.9	173
84	Mitochondrial phylogeography of the Eurasian beaver Castor fiber L.. Molecular Ecology, 2005, 14, 3843-3856.	3.9	51
85	Sequence diversity of the MHC DRB gene in the Eurasian beaver (Castor fiber). Molecular Ecology, 2005, 14, 4249-4257.	3.9	80
86	Conservation units in north-eastern populations of the Alpine newt (Triturus alpestris). Conservation Genetics, 2005, 6, 307-312.	1.5	13
87	Mitochondrial phylogeography of the moor frog, Rana arvalis. Molecular Ecology, 2004, 13, 1469-1480.	3.9	108
88	Relationship between morphometric and genetic variation in pure and hybrid populations of the smooth and Montandons newt (Triturus vulgaris and T. montandoni). Journal of Zoology, 2004, 262, 135-143.	1.7	15
89	Nuclear markers, mitochondrial DNA and male secondary sexual traits variation in a newt hybrid zone (Triturus vulgaris ÂÃ—Â T. montandoni). Molecular Ecology, 2003, 12, 1913-1930.	3.9	67
90	Genetic differentiation among northern and southern populations of the moor frog Rana arvalis Nilsson in central Europe. Heredity, 2000, 84, 610-618.	2.6	25

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91	Morphometric differentiation of the moor frog (Rana arvalis Nilss.) in Central Europe. Journal of Zoological Systematics and Evolutionary Research, 2000, 38, 239-247.	1.4	16
92	Knowledge Representation in Map Collections for Information Retrieval Systems. LIBER Quarterly, 1999, 9, 172-179.	0.7	1
93	Intrageneric predation in larval newts (Triturus, Salamandridae, Urodela). Amphibia - Reptilia, 1998, 19, 446-451.	0.5	5