

Matthew T Webster

List of Publications by Year in descending order

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Version: 2024-02-01

73
papers

8,389
citations

81839

39
h-index

82499

72
g-index

81
all docs

81
docs citations

81
times ranked

10979
citing authors

#	ARTICLE	IF	CITATIONS
1	A genomic and morphometric analysis of alpine bumblebees: Ongoing reductions in tongue length but no clear genetic component. <i>Molecular Ecology</i> , 2022, 31, 1111-1127.	2.0	8
2	Massive genome inversion drives coexistence of divergent morphs in common quails. <i>Current Biology</i> , 2022, 32, 462-469.e6.	1.8	25
3	Genetic Barriers to Historical Gene Flow between Cryptic Species of Alpine Bumblebees Revealed by Comparative Population Genomics. <i>Molecular Biology and Evolution</i> , 2021, 38, 3126-3143.	3.5	25
4	Phylogenomics and evolutionary history of Oreobates (Anura: Craugastoridae) Neotropical frogs along elevational gradients. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107167.	1.2	1
5	Population Genomics: How Do Cape Honey Bees Do Without Sex?. <i>Current Biology</i> , 2020, 30, R820-R821.	1.8	0
6	Female-biased gene flow between two species of Darwin's finches. <i>Nature Ecology and Evolution</i> , 2020, 4, 979-986.	3.4	21
7	Substantial Heritable Variation in Recombination Rate on Multiple Scales in Honeybees and Bumblebees. <i>Genetics</i> , 2019, 212, 1101-1119.	1.2	17
8	<i>Apis mellifera</i> . <i>Trends in Genetics</i> , 2019, 35, 880-881.	2.9	2
9	Extreme Differences in Recombination Rate between the Genomes of a Solitary and a Social Bee. <i>Molecular Biology and Evolution</i> , 2019, 36, 2277-2291.	3.5	22
10	Social Parasitism in the Honeybee (<i>Apis mellifera</i>) Is Not Controlled by a Single SNP. <i>Molecular Biology and Evolution</i> , 2019, 36, 1764-1767.	3.5	7
11	A hybrid de novo genome assembly of the honeybee, <i>Apis mellifera</i> , with chromosome-length scaffolds. <i>BMC Genomics</i> , 2019, 20, 275.	1.2	171
12	The genomic basis of adaptation to high-altitude habitats in the eastern honey bee (<i>Apis cerana</i>). <i>Molecular Ecology</i> , 2019, 28, 746-760.	2.0	30
13	Chromosomal inversions associated with environmental adaptation in honeybees. <i>Molecular Ecology</i> , 2019, 28, 1358-1374.	2.0	50
14	Developing reduced SNP assays from whole-genome sequence data to estimate introgression in an organism with complex genetic patterns, the Iberian honeybee (<i>Apis mellifera</i>) Tj ETQq0 0 0 ngBT /Overdo 10 Tf		
15	Elevated Proportions of Deleterious Genetic Variation in Domestic Animals and Plants. <i>Genome Biology and Evolution</i> , 2018, 10, 276-290.	1.1	75
16	Rapid hybrid speciation in Darwin's finches. <i>Science</i> , 2018, 359, 224-228.	6.0	327
17	Multimodal surface matching with higher-order smoothness constraints. <i>NeuroImage</i> , 2018, 167, 453-465.	2.1	219
18	Whole genome SNP-associated signatures of local adaptation in honeybees of the Iberian Peninsula. <i>Scientific Reports</i> , 2018, 8, 11145.	1.6	24

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19	Gene flow, ancient polymorphism, and ecological adaptation shape the genomic landscape of divergence among Darwin's finches. <i>Genome Research</i> , 2017, 27, 1004-1015.	2.4	152
20	Genomewide analysis of admixture and adaptation in the Africanized honeybee. <i>Molecular Ecology</i> , 2017, 26, 3603-3617.	2.0	44
21	Two extended haplotype blocks are associated with adaptation to high altitude habitats in East African honey bees. <i>PLoS Genetics</i> , 2017, 13, e1006792.	1.5	70
22	A practical guide to build <i>de-novo</i> assemblies for single tissues of non-model organisms: the example of a Neotropical frog. <i>PeerJ</i> , 2017, 5, e3702.	0.9	16
23	Identification of Multiple Loci Associated with Social Parasitism in Honeybees. <i>PLoS Genetics</i> , 2016, 12, e1006097.	1.5	31
24	Whole genome resequencing of a laboratory-adapted <i>Drosophila melanogaster</i> population sample. <i>F1000Research</i> , 2016, 5, 2644.	0.8	6
25	A beak size locus in Darwin's finches facilitated character displacement during a drought. <i>Science</i> , 2016, 352, 470-474.	6.0	206
26	Adaptive radiation of Darwin's finches revisited using whole genome sequencing. <i>BioEssays</i> , 2016, 38, 14-20.	1.2	30
27	Evolution of Darwin's finches and their beaks revealed by genome sequencing. <i>Nature</i> , 2015, 518, 371-375.	13.7	766
28	Germline Methylation Patterns Determine the Distribution of Recombination Events in the Dog Genome. <i>Genome Biology and Evolution</i> , 2015, 7, 522-530.	1.1	16
29	Extreme Recombination Frequencies Shape Genome Variation and Evolution in the Honeybee, <i>Apis mellifera</i> . <i>PLoS Genetics</i> , 2015, 11, e1005189.	1.5	98
30	Linked genetic variants on chromosome 10 control ear morphology and body mass among dog breeds. <i>BMC Genomics</i> , 2015, 16, 474.	1.2	32
31	A worldwide survey of genome sequence variation provides insight into the evolutionary history of the honeybee <i>Apis mellifera</i> . <i>Nature Genetics</i> , 2014, 46, 1081-1088.	9.4	273
32	Analysis of structural diversity in wolf-like canids reveals post-domestication variants. <i>BMC Genomics</i> , 2014, 15, 465.	1.2	16
33	Genome-wide copy number variant discovery in dogs using the CanineHD genotyping array. <i>BMC Genomics</i> , 2014, 15, 210.	1.2	35
34	Insights into the evolution of Darwin's finches from comparative analysis of the <i>Geospiza magnirostris</i> genome sequence. <i>BMC Genomics</i> , 2013, 14, 95.	1.2	38
35	The genomic signature of dog domestication reveals adaptation to a starch-rich diet. <i>Nature</i> , 2013, 495, 360-364.	13.7	805
36	Death of <i>PRDM9</i> coincides with stabilization of the recombination landscape in the dog genome. <i>Genome Research</i> , 2012, 22, 51-63.	2.4	116

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37	Rethinking dog domestication by integrating genetics, archeology, and biogeography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8878-8883.	3.3	412
38	Population-scale sequencing reveals genetic differentiation due to local adaptation in Atlantic herring. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19345-19350.	3.3	217
39	Novel origins of copy number variation in the dog genome. <i>Genome Biology</i> , 2012, 13, R73.	13.9	86
40	Two Loci on Chromosome 5 Are Associated with Serum IgE Levels in Labrador Retrievers. <i>PLoS ONE</i> , 2012, 7, e39176.	1.1	21
41	From where did the <i>Western honeybee</i> (<i>Apis mellifera</i>) originate?. <i>Ecology and Evolution</i> , 2012, 2, 1949-1957.	0.8	121
42	Direct and indirect consequences of meiotic recombination: implications for genome evolution. <i>Trends in Genetics</i> , 2012, 28, 101-109.	2.9	97
43	A Novel Unstable Duplication Upstream of HAS2 Predisposes to a Breed-Defining Skin Phenotype and a Periodic Fever Syndrome in Chinese Shar-Pei Dogs. <i>PLoS Genetics</i> , 2011, 7, e1001332.	1.5	118
44	A Locus on Chromosome 5 Is Associated with Dilated Cardiomyopathy in Doberman Pinschers. <i>PLoS ONE</i> , 2011, 6, e20042.	1.1	37
45	LGI2 Truncation Causes a Remitting Focal Epilepsy in Dogs. <i>PLoS Genetics</i> , 2011, 7, e1002194.	1.5	88
46	Identification of Genomic Regions Associated with Phenotypic Variation between Dog Breeds using Selection Mapping. <i>PLoS Genetics</i> , 2011, 7, e1002316.	1.5	339
47	Whole-genome resequencing reveals loci under selection during chicken domestication. <i>Nature</i> , 2010, 464, 587-591.	13.7	985
48	Localization of Canine Brachycephaly Using an Across Breed Mapping Approach. <i>PLoS ONE</i> , 2010, 5, e9632.	1.1	101
49	The recombination landscape of the zebra finch <i>Taeniopygia guttata</i> genome. <i>Genome Research</i> , 2010, 20, 485-495.	2.4	212
50	Detecting positive selection within genomes: the problem of biased gene conversion. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 2571-2580.	1.8	130
51	Hotspots of Biased Nucleotide Substitutions in Human Genes. <i>PLoS Biology</i> , 2009, 7, e1000026.	2.6	134
52	Patterns of autosomal divergence between the human and chimpanzee genomes support an allopatric model of speciation. <i>Gene</i> , 2009, 443, 70-75.	1.0	7
53	The Legacy of Domestication: Accumulation of Deleterious Mutations in the Dog Genome. <i>Molecular Biology and Evolution</i> , 2008, 25, 2331-2336.	3.5	129
54	Is There Evidence for Convergent Evolution around Human Microsatellites?. <i>Molecular Biology and Evolution</i> , 2007, 24, 1097-1100.	3.5	14

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55	Strong Regional Biases in Nucleotide Substitution in the Chicken Genome. <i>Molecular Biology and Evolution</i> , 2006, 23, 1203-1216.	3.5	91
56	Relaxation of selective constraint on dog mitochondrial DNA following domestication. <i>Genome Research</i> , 2006, 16, 990-994.	2.4	163
57	Why Are Young and Old Repetitive Elements Distributed Differently in the Human Genome?. <i>Journal of Molecular Evolution</i> , 2005, 60, 290-296.	0.8	9
58	Male-Driven Biased Gene Conversion Governs the Evolution of Base Composition in Human Alu Repeats. <i>Molecular Biology and Evolution</i> , 2005, 22, 1468-1474.	3.5	64
59	Contrasting Patterns of Polymorphism and Divergence on the Z Chromosome and Autosomes in Two <i>Ficedula</i> Flycatcher Species. <i>Genetics</i> , 2005, 171, 1861-1873.	1.2	99
60	Comparison of the chicken and turkey genomes reveals a higher rate of nucleotide divergence on microchromosomes than macrochromosomes. <i>Genome Research</i> , 2005, 15, 120-125.	2.4	138
61	Reduced Variation on the Chicken Z Chromosome. <i>Genetics</i> , 2004, 167, 377-385.	1.2	66
62	Gene Expression, Synteny, and Local Similarity in Human Noncoding Mutation Rates. <i>Molecular Biology and Evolution</i> , 2004, 21, 1820-1830.	3.5	35
63	Fixation biases affecting human SNPs. <i>Trends in Genetics</i> , 2004, 20, 122-126.	2.9	50
64	Common 5' β -globin RFLP haplotypes harbour a surprising level of ancestral sequence mosaicism. <i>Human Genetics</i> , 2003, 113, 123-139.	1.8	12
65	Mutation rate variation in the mammalian genome. <i>Current Opinion in Genetics and Development</i> , 2003, 13, 562-568.	1.5	135
66	A Low Rate of Simultaneous Double-Nucleotide Mutations in Primates. <i>Molecular Biology and Evolution</i> , 2003, 20, 47-53.	3.5	38
67	Compositional Evolution of Noncoding DNA in the Human and Chimpanzee Genomes. <i>Molecular Biology and Evolution</i> , 2003, 20, 278-286.	3.5	75
68	Is the Rate of Insertion and Deletion Mutation Male Biased?: Molecular Evolutionary Analysis of Avian and Primate Sex Chromosome Sequences. <i>Genetics</i> , 2003, 164, 259-268.	1.2	21
69	Microsatellite evolution inferred from human- chimpanzee genomic sequence alignments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8748-8753.	3.3	118
70	Deterministic Mutation Rate Variation in the Human Genome. <i>Genome Research</i> , 2002, 12, 1350-1356.	2.4	108
71	Analysis of variation in the human β -globin gene cluster using a novel DHPLC technique. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2002, 501, 99-103.	0.4	13
72	Born to clot: the European burden. <i>British Journal of Haematology</i> , 1999, 105, 564-566.	1.2	100

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73	Born to clot: the European burden. <i>British Journal of Haematology</i> , 1999, 105, 564-566.	1.2	2