

# Aryn P Wilder

## List of Publications by Year in descending order

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Version: 2024-02-01

15  
papers

917  
citations

840776

11  
h-index

996975

15  
g-index

20  
all docs

20  
docs citations

20  
times ranked

947  
citing authors

#	ARTICLE	IF	CITATIONS
1	Early-phase transmission of <i>Yersinia pestis</i> by unblocked fleas as a mechanism explaining rapidly spreading plague epizootics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15380-15385.	7.1	203
2	Contrasting genomic shifts underlie parallel phenotypic evolution in response to fishing. <i>Science</i> , 2019, 365, 487-490.	12.6	123
3	A beginner's guide to low-coverage whole genome sequencing for population genomics. <i>Molecular Ecology</i> , 2021, 30, 5966-5993.	3.9	119
4	Early-phase Transmission of <i>Yersinia pestis</i> by Cat Fleas ( <i>Ctenocephalides felis</i> ) and Their Potential Role as Vectors in a Plague-endemic Region of Uganda. <i>American Journal of Tropical Medicine and Hygiene</i> , 2008, 78, 949-956.	1.4	83
5	Transmission Efficiency of Two Flea Species ( <i>Oropsylla tuberculata cynomuris</i> and <i>Oropsylla hirsuta</i> ) Involved in Plague Epizootics among Prairie Dogs. <i>EcoHealth</i> , 2008, 5, 205-212.	2.0	77
6	Early-Phase Transmission of <i>Yersinia pestis</i> by Unblocked <i>Xenopsylla cheopis</i> (Siphonaptera: Tj ETQq0 0 0 rgBT /Overlock 10 678-682.	1.8	73
7	Risk factors associated with mortality from white-nose syndrome among hibernating bat colonies. <i>Biology Letters</i> , 2011, 7, 950-953.	2.3	62
8	Population genetic structure of a common host predicts the spread of white-nose syndrome, an emerging infectious disease in bats. <i>Molecular Ecology</i> , 2015, 24, 5495-5506.	3.9	37
9	Footprints of local adaptation span hundreds of linked genes in the Atlantic silverside genome. <i>Evolution Letters</i> , 2020, 4, 430-443.	3.3	36
10	THE POTENTIAL ROLE OF SWIFT FOXES ( <i>VULPES VELOX</i> ) AND THEIR FLEAS IN PLAGUE OUTBREAKS IN PRAIRIE DOGS. <i>Journal of Wildlife Diseases</i> , 2007, 43, 425-431.	0.8	28
11	Chromosome-Level Assembly of the Atlantic Silverside Genome Reveals Extreme Levels of Sequence Diversity and Structural Genetic Variation. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	20
12	Fitness costs associated with ancestry to isolated populations of an endangered species. <i>Conservation Genetics</i> , 2020, 21, 589-601.	1.5	18
13	Full mitochondrial genome sequences reveal new insights about post-glacial expansion and regional phylogeographic structure in the Atlantic silverside ( <i>Menidia menidia</i> ). <i>Marine Biology</i> , 2018, 165, 1.	1.5	16
14	Comparative linkage mapping uncovers recombination suppression across massive chromosomal inversions associated with local adaptation in Atlantic silversides. <i>Molecular Ecology</i> , 2022, 31, 3323-3341.	3.9	11
15	Patterns of genetic partitioning and gene flow in the endangered San Bernardino kangaroo rat ( <i>Dipodomys merriami parvus</i> ) and implications for conservation management. <i>Conservation Genetics</i> , 2020, 21, 819-833.	1.5	5