

Carol A Stepien

List of Publications by Year in descending order

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Version: 2024-02-01

94
papers

3,306
citations

136740

32
h-index

174990

52
g-index

100
all docs

100
docs citations

100
times ranked

3260
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA Sequence Support for Reclassification of the Endemic Southern Caspian Sea Deepwater Goby as <i>Neogobius bathybius</i> (Formerly <i>Ponticola</i> ; Perciformes: Gobiidae) and Recent Population Expansion of a Continuous Population. <i>Ichthyology and Herpetology</i> , 2022, 110, .	0.3	2
2	Genetic trajectories of zebra and quagga mussel invasions across three decades: Lake Erie versus Hudson River populations. <i>Aquatic Invasions</i> , 2021, 16, 147-166.	0.6	2
3	Genomic and immunogenic changes of Piscine novirhabdovirus (Viral Hemorrhagic Septicemia Virus) over its evolutionary history in the Laurentian Great Lakes. <i>PLoS ONE</i> , 2021, 16, e0232923.	1.1	2
4	Strategic considerations for invasive species managers in the utilization of environmental DNA (eDNA): steps for incorporating this powerful surveillance tool. <i>Management of Biological Invasions</i> , 2021, 12, 747-775.	0.5	25
5	Macroinvertebrate community diversity and habitat quality relationships along a large river from targeted eDNA metabarcode assays. <i>Environmental DNA</i> , 2020, 2, 572-586.	3.1	18
6	Intra-Annual and Interannual Dynamics of Evaporation Over Western Lake Erie. <i>Earth and Space Science</i> , 2020, 7, e2020EA001091.	1.1	6
7	Evolutionary trajectory of fish <i>Piscine novirhabdovirus</i> (=Viral Hemorrhagic Septicemia Virus) across its Laurentian Great Lakes history: Spatial and temporal diversification. <i>Ecology and Evolution</i> , 2020, 10, 9740-9775.	0.8	5
8	Detecting aquatic invasive species in bait and pond stores with targeted environmental (e)DNA high-throughput sequencing metabarcode assays: Angler, retailer, and manager implications. <i>Biological Conservation</i> , 2020, 245, 108430.	1.9	13
9	SNP analyses highlight a unique, imperiled southern walleye (<i>Sander vitreus</i>) in the Mobile River Basin. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2020, 77, 1366-1378.	0.7	6
10	Rhabdovirus (viral haemorrhagic septicaemia virus).. , 2020, , 58-84.		3
11	Global Observational Needs and Resources for Marine Biodiversity. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	77
12	Invasion genetics from eDNA and thousands of larvae: A targeted metabarcoding assay that distinguishes species and population variation of zebra and quagga mussels. <i>Ecology and Evolution</i> , 2019, 9, 3515-3538.	0.8	42
13	Invasion genetics of the silver carp <i>Hypophthalmichthys molitrix</i> across North America: Differentiation of fronts, introgression, and eDNA metabarcode detection. <i>PLoS ONE</i> , 2019, 14, e0203012.	1.1	37
14	Effects of cortisol and lipopolysaccharide on expression of select growth-, stress- and immune-related genes in rainbow trout liver. <i>Fish and Shellfish Immunology</i> , 2018, 74, 410-418.	1.6	25
15	Genetic Divergence of Nearby Walleye Spawning Groups in Central Lake Erie: Implications for Management. <i>North American Journal of Fisheries Management</i> , 2018, 38, 783-793.	0.5	11
16	Genetic change versus stasis over the time course of invasions: trajectories of two concurrent, allopatric introductions of the Eurasian ruffe. <i>Aquatic Invasions</i> , 2018, 13, 537-552.	0.6	7
17	Population genetic structure and comparative diversity of smallmouth bass <i>Micropterus dolomieu</i> : congruent patterns from two genomes. <i>Journal of Fish Biology</i> , 2017, 90, 2125-2147.	0.7	11
18	Genetic patterns across an invasion's history: a test of change versus stasis for the Eurasian round goby in North America. <i>Molecular Ecology</i> , 2017, 26, 1075-1090.	2.0	18

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19	Early detection monitoring for aquatic non-indigenous species: Optimizing surveillance, incorporating advanced technologies, and identifying research needs. <i>Journal of Environmental Management</i> , 2017, 202, 299-310.	3.8	77
20	Role of Viral Hemorrhagic Septicemia Virus Matrix (M) Protein in Suppressing Host Transcription. <i>Journal of Virology</i> , 2017, 91, .	1.5	41
21	The Effect of Algal Blooms on Carbon Emissions in Western Lake Erie: An Integration of Remote Sensing and Eddy Covariance Measurements. <i>Remote Sensing</i> , 2017, 9, 44.	1.8	22
22	Environmental DNA (eDNA) metabarcoding assays to detect invasive invertebrate species in the Great Lakes. <i>PLoS ONE</i> , 2017, 12, e0177643.	1.1	121
23	Role of the invasive Chinese sleeper <i>Perccottus glenii</i> (Actinopterygii: Odontobutidae) in the distribution of fish parasites in Europe: New data and a review. <i>Biologia (Poland)</i> , 2016, 71, 941-951.	0.8	10
24	Two decades of genetic consistency in a reproductive population in the face of exploitation: patterns of adult and larval walleye (<i>Sander vitreus</i>) from Lake Erie's Maumee River. <i>Conservation Genetics</i> , 2016, 17, 1345-1362.	0.8	6
25	Diurnal to annual changes in latent, sensible heat, and CO ₂ fluxes over a Laurentian Great Lake: A case study in Western Lake Erie. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2015, 120, 1587-1604.	1.3	56
26	Temporal Population Genetic Structure of Yellow Perch Spawning Groups in the Lower Great Lakes. <i>Transactions of the American Fisheries Society</i> , 2015, 144, 211-226.	0.6	7
27	The parasite community of gobiid fishes (Actinopterygii: Gobiidae) from the Lower Volga River region. <i>Biologia (Poland)</i> , 2015, 70, 948-957.	0.8	20
28	Taxonomy, Distribution, and Evolution of the Percidae. , 2015, , 3-60.		15
29	Comparative Genetic Diversity, Population Structure, and Adaptations of Walleye and Yellow Perch Across North America. , 2015, , 643-689.		16
30	Evolutionary Relationships, Population Genetics, and Ecological and Genomic Adaptations of Perch (<i>Perca</i>). , 2015, , 7-46.		9
31	Gene Diversification of an Emerging Pathogen: A Decade of Mutation in a Novel Fish Viral Hemorrhagic Septicemia (VHS) Substrain since Its First Appearance in the Laurentian Great Lakes. <i>PLoS ONE</i> , 2015, 10, e0135146.	1.1	19
32	Genetic History of Walleyes Spawning in Lake Erie's Cattaraugus Creek: a Comparison of Pre- and Poststocking. <i>Transactions of the American Fisheries Society</i> , 2014, 143, 1295-1307.	0.6	9
33	A population genetic window into the past and future of the walleye <i>Sander vitreus</i> : relation to historic walleye and the extinct blue pike <i>S. v. glaucus</i> . <i>BMC Evolutionary Biology</i> , 2014, 14, 133.	3.2	17
34	Genetic diversity and divergence of yellow perch spawning populations across the Huron-Erie Corridor, from Lake Huron through western Lake Erie. <i>Journal of Great Lakes Research</i> , 2014, 40, 101-109.	0.8	14
35	Genetic connectivity and diversity of walleye (<i>Sander vitreus</i>) spawning groups in the Huron-Erie Corridor. <i>Journal of Great Lakes Research</i> , 2014, 40, 89-100.	0.8	15
36	A new StaRT-PCR approach to detect and quantify fish Viral Hemorrhagic Septicemia virus (VHSV): Enhanced quality control with internal standards. <i>Journal of Virological Methods</i> , 2013, 189, 129-142.	1.0	12

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37	What's in a name? Taxonomy and nomenclature of invasive gobies in the Great Lakes and beyond. <i>Journal of Great Lakes Research</i> , 2013, 39, 555-559.	0.8	4
38	Phylogenetic and biogeographical relationships of the <i>Sander</i> pikeperches (Percidae). <i>Journal of Great Lakes Research</i> , 2013, 39, 156-179.	0.7	32
39	Genetic and morphometric differences demonstrate fine-scale population substructure of the yellow perch <i>Perca flavescens</i> : need for redefined management units. <i>Journal of Fish Biology</i> , 2013, 82, 2015-2030.	0.7	24
40	Accurate Detection and Quantification of the Fish Viral Hemorrhagic Septicemia virus (VHSV) with a Two-Color Fluorometric Real-Time PCR Assay. <i>PLoS ONE</i> , 2013, 8, e71851.	1.1	14
41	Temporal and Spatial Genetic Consistency of Walleye Spawning Groups. <i>Transactions of the American Fisheries Society</i> , 2012, 141, 660-672.	0.6	23
42	Evolution and biogeography of an emerging quasispecies: Diversity patterns of the fish Viral Hemorrhagic Septicemia virus (VHSV). <i>Molecular Phylogenetics and Evolution</i> , 2012, 63, 327-341.	1.2	73
43	Salinity tolerance of the invasive round goby: Experimental implications for seawater ballast exchange and spread to North American estuaries. <i>Journal of Great Lakes Research</i> , 2012, 38, 121-128.	0.8	27
44	Waterscape genetics of the yellow perch (<i>Perca flavescens</i>): patterns across large connected ecosystems and isolated relict populations. <i>Molecular Ecology</i> , 2012, 21, 5795-5826.	2.0	28
45	Fine-scale population genetic structure of the yellow perch <i>Perca flavescens</i> in Lake Erie. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2011, 68, 1435-1453.	0.7	36
46	Microsatellite loci for dreissenid mussels (Mollusca: Bivalvia: Dreissenidae) and relatives: markers for assessing exotic and native populations. <i>Molecular Ecology Resources</i> , 2011, 11, 725-732.	2.2	13
47	Historic speciation and recent colonization of Eurasian monkey gobies (<i>Neogobius fluviatilis</i>) Distributions, 2011, 17, 688-702.	1.9	29
48	Expansion of tubenose gobies <i>Proterorhinus semilunaris</i> into western Lake Erie and potential effects on native species. <i>Biological Invasions</i> , 2011, 13, 2775-2784.	1.2	46
49	Population genetic history of the dreissenid mussel invasions: expansion patterns across North America. <i>Biological Invasions</i> , 2010, 12, 3687-3710.	1.2	45
50	Systematics of the greenside darter <i>Etheostoma blennioides</i> complex: Consensus from nuclear and mitochondrial DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 434-447.	1.2	2
51	Genetic Variation of 17 Wild Yellow Perch Populations from the Midwest and East Coast Analyzed via Microsatellites. <i>Transactions of the American Fisheries Society</i> , 2010, 139, 270-287.	0.6	18
52	Invasion genetics of the Eurasian round goby in North America: tracing sources and spread patterns. <i>Molecular Ecology</i> , 2009, 18, 64-79.	2.0	102
53	Microsatellite loci for Ponto-Caspian gobies: markers for assessing exotic invasions. <i>Molecular Ecology Resources</i> , 2009, 9, 639-644.	2.2	11
54	The Interplay of Morphology, Habitat, Resource Use, and Genetic Relationships in Young Yellow Perch. <i>Transactions of the American Fisheries Society</i> , 2009, 138, 899-914.	0.6	30

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55	Signatures of vicariance, postglacial dispersal and spawning philopatry: population genetics of the walleye <i>Sander vitreus</i> . <i>Molecular Ecology</i> , 2009, 18, 3411-3428.	2.0	77
56	Evolution and phylogeography of the tubenose goby genus <i>Proterorhinus</i> (Gobiidae: Teleostei): evidence for new cryptic species. <i>Biological Journal of the Linnean Society</i> , 2009, 96, 664-684.	0.7	62
57	Evolution and phylogeography of the tubenose goby genus <i>Proterorhinus</i> (Gobiidae: Teleostei): evidence for new cryptic species. <i>Biological Journal of the Linnean Society</i> , 2009, 97, 708-708.	0.7	2
58	Landscape genetic patterns of the rainbow darter <i>Etheostoma caeruleum</i> : a catchment analysis of mitochondrial DNA sequences and nuclear microsatellites. <i>Journal of Fish Biology</i> , 2009, 75, 2244-2268.	0.7	26
59	Escape from the Ponto-Caspian: Evolution and biogeography of an endemic goby species flock (Benthophilinae: Gobiidae: Teleostei). <i>Molecular Phylogenetics and Evolution</i> , 2009, 52, 84-102.	1.2	104
60	Population genetic diversity and phylogeographic divergence patterns of the yellow perch (<i>Perca</i>)	0.8	34
61	Molecular, morphological, and biogeographic resolution of cryptic taxa in the Greenside Darter <i>Etheostoma blennioides</i> complex. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 69-83.	1.2	20
62	The invasive round goby <i>Apollonia melanostoma</i> (Actinopterygii: Gobiidae) - a new intermediate host of the trematode <i>Neochasmus umbellus</i> (Trematoda: Cryptogonimidae) in Lake Erie, Ohio, USA. <i>Journal of Applied Ichthyology</i> , 2008, 24, 103-105.	0.3	5
63	Ancient divisions, recent expansions: phylogeography and population genetics of the round goby <i>Apollonia melanostoma</i> . <i>Molecular Ecology</i> , 2008, 17, 2598-2615.	2.0	75
64	Metazoan Parasites of Introduced Round and Tubenose Gobies in the Great Lakes: Support for the "Enemy Release Hypothesis". <i>Journal of Great Lakes Research</i> , 2008, 34, 23-35.	0.8	50
65	Occurrence of the Quagga Mussel (<i>Dreissena bugensis</i>) and the Zebra Mussel (<i>Dreissena</i>)	0.5	15
66	Genetic divergence and connectivity among river and reef spawning groups of walleye (<i>Sander vitreus</i>)	0.7	66
67	Genetic Divergence across a Low-head Dam: A Preliminary Analysis using Logperch and Greenside Darters. <i>Journal of Great Lakes Research</i> , 2007, 33, 117-126.	0.8	21
68	Genetic and biogeographic relationships of the racer goby <i>Neogobius gymnotrachelus</i> (Gobiidae)	0.7	15
69	Broad- to fine-scale population genetic patterning in the smallmouth bass <i>Micropterus dolomieu</i> across the Laurentian Great Lakes and beyond: an interplay of behaviour and geography. <i>Molecular Ecology</i> , 2007, 16, 1605-1624.	2.0	53
70	Discordant Population Genetic Structuring of Smallmouth Bass, <i>Micropterus dolomieu</i> Lacepède, in Lake Erie Based on Mitochondrial DNA Sequences and Nuclear DNA Microsatellites. <i>Journal of Great Lakes Research</i> , 2006, 32, 242-257.	0.8	17
71	Invasion Genetics of Ponto-Caspian Gobies in the Great Lakes: A "Cryptic" Species, Absence of Founder Effects, and Comparative Risk Analysis. <i>Biological Invasions</i> , 2006, 8, 61-78.	1.2	117
72	Genetic Diversity of Invasive Species in the Great Lakes Versus Their Eurasian Source Populations: Insights for Risk Analysis. <i>Risk Analysis</i> , 2005, 25, 1043-1060.	1.5	126

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73	Genetic variability and phylogeographical patterns of a nonindigenous species invasion: a comparison of exotic vs. native zebra and quagga mussel populations. <i>Journal of Evolutionary Biology</i> , 2002, 15, 314-328.	0.8	82
74	Genetic and Biogeographic Relationships of the Invasive Round (Neogobius melanostomus) and Tubenose (Proterorhinus marmoratus) Gobies in the Great Lakes Versus Eurasian Populations. <i>Journal of Great Lakes Research</i> , 2001, 27, 267-280.	0.8	41
75	PHYLOGEOGRAPHY OF THE SPOTTED SAND BASS, PARALABRAX MACULATOFASCIATUS: DIVERGENCE OF GULF OF CALIFORNIA AND PACIFIC COAST POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 1852.	1.1	3
76	Genetic diversity and evolutionary relationships of the troglodytic "living fossil" <i>Congerius kusceri</i> (Bivalvia: Dreissenidae). <i>Molecular Ecology</i> , 2001, 10, 1873-1879.	2.0	36
77	PHYLOGEOGRAPHY OF THE SPOTTED SAND BASS, PARALABRAX MACULATOFASCIATUS: DIVERGENCE OF GULF OF CALIFORNIA AND PACIFIC COAST POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 1852-1862.	1.1	59
78	PHYLOGEOGRAPHY OF OPHIOBLENNIUS: THE ROLE OF OCEAN CURRENTS AND GEOGRAPHY IN REEF FISH EVOLUTION. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 561.	1.1	182
79	PHYLOGEOGRAPHY OF OPHIOBLENNIUS: THE ROLE OF OCEAN CURRENTS AND GEOGRAPHY IN REEF FISH EVOLUTION. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 561-572.	1.1	24
80	Population genetics, phylogeography, and systematics of the thornyhead rockfishes (<i>Sebastes</i>) along the deep continental slopes of the North Pacific Ocean. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2000, 57, 1701-1717.	0.7	25
81	Phylogeographical structure of the Dover sole <i>Microstomus pacificus</i> : the larval retention hypothesis and genetic divergence along the deep continental slope of the northeastern Pacific Ocean. <i>Molecular Ecology</i> , 1999, 8, 923-939.	2.0	56
82	Diagnostic Genetic Markers and Evolutionary Relationships among Invasive Dreissenoid and Corbiculoid Bivalves in North America: Phylogenetic Signal from Mitochondrial 16S rDNA. <i>Molecular Phylogenetics and Evolution</i> , 1999, 13, 31-49.	1.2	72
83	Tandemly Repeated Sequences in the Mitochondrial DNA Control Region and Phylogeography of the Pike-Perches <i>Stizostedion</i> . <i>Molecular Phylogenetics and Evolution</i> , 1998, 10, 310-322.	1.2	73
84	Population genetic structure, phylogeography and spawning philopatry in walleye (<i>Stizostedion</i>) <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 3</i>	2.0	115
85	Genetic Identity, Phylogeography, and Systematics of Ruffe <i>Gymnocephalus</i> in the North American Great Lakes and Eurasia. <i>Journal of Great Lakes Research</i> , 1998, 24, 361-378.	0.8	43
86	Molecules and Morphology in Studies of Fish Evolution. , 1997, , 1-11.		57
87	The Utility of Mitochondrial DNA Control Region Sequences for Analyzing Phylogenetic Relationships among Populations, Species, and Genera of the Percidae. , 1997, , 129-143.		34
88	The Evolution of Blennioid Fishes Based on an Analysis of Mitochondrial 12S rDNA. , 1997, , 245-270.		35
89	Genetic Divergence in Antitropical Pelagic Marine Fishes (<i>Trachurus</i> , <i>Merluccius</i> , and <i>Scomber</i>) between North and South America. <i>Copeia</i> , 1996, 1996, 586.	1.4	53
90	Evolution and Biogeography of the Clinidae (Teleostei: Blennioidei). <i>Copeia</i> , 1992, 1992, 375.	1.4	19

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91	Patterns of Gene Flow and Genetic Divergence in the Northeastern Pacific Clinidae (Teleostei: Tj ETQq1 1 0.784314 rgBT /Overlock 101	1.48	29
92	Regulation of color morphic patterns in the giant kelpfish, <i>Heterostichus rostratus</i> Girard: genetic versus environmental factors. <i>Journal of Experimental Marine Biology and Ecology</i> , 1986, 100, 181-208.	0.7	11
93	Addressing the "Paradox of the Plankton": Using Metabarcoding to Explore Zooplankton Diversity Patterns Across Chemical Conditions in the Salish Sea. <i>ARPHA Conference Abstracts</i> , 0, 4, .	0.0	0
94	Increasing confidence for discerning species and population compositions from metabarcoding assays of environmental samples: case studies of fishes in the Laurentian Great Lakes and Wabash River. <i>Metabarcoding and Metagenomics</i> , 0, 4, .	0.0	5