

# Sean W J Prosser

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2587710/publications.pdf>

Version: 2024-02-01

27  
papers

1,118  
citations

759055

12  
h-index

713332

21  
g-index

27  
all docs

27  
docs citations

27  
times ranked

1562  
citing authors

#	ARTICLE	IF	CITATIONS
1	Message in a Bottle“Metabarcoding enables biodiversity comparisons across ecoregions. <i>GigaScience</i> , 2022, 11, .	3.3	14
2	Culicoides species community composition and feeding preferences in two aquatic ecosystems in northern Spain. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	5
3	A SMRT approach for targeted amplicon sequencing of museum specimens (Lepidoptera)“patterns of nucleotide misincorporation. <i>PeerJ</i> , 2021, 9, e10420.	0.9	11
4	Drought at a coastal wetland affects refuelling and migration strategies of shorebirds. <i>Oecologia</i> , 2021, 197, 661-674.	0.9	13
5	Phylogenetic reassignment of basal cyclostome braconid parasitoid wasps (Hymenoptera) with description of a new, enigmatic Afrotropical tribe with a highly anomalous 28S D2 secondary structure. <i>Zoological Journal of the Linnean Society</i> , 2020, 190, 1002-1019.	1.0	15
6	Dynamics of a host“parasitoid interaction clarified by modelling and DNA sequencing. <i>Ecology Letters</i> , 2020, 23, 851-859.	3.0	4
7	An Integrated Molecular Approach to Untangling Host“Vector“Pathogen Interactions in Mosquitoes (Diptera: Culicidae) From Sylvan Communities in Mexico. <i>Frontiers in Veterinary Science</i> , 2020, 7, 564791.	0.9	8
8	Vertebrate-Aedes aegypti and Culex quinquefasciatus (Diptera)-arbovirus transmission networks: Non-human feeding revealed by meta-barcoding and next-generation sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008867.	1.3	20
9	Title is missing!. , 2020, 14, e0008867.		0
10	Title is missing!. , 2020, 14, e0008867.		0
11	Title is missing!. , 2020, 14, e0008867.		0
12	Title is missing!. , 2020, 14, e0008867.		0
13	Title is missing!. , 2020, 14, e0008867.		0
14	Title is missing!. , 2020, 14, e0008867.		0
15	DNA metabarcoding allows non-invasive identification of arthropod prey provisioned to nestling Rufous hummingbirds ( <i>Selasphorus rufus</i> ). <i>PeerJ</i> , 2019, 7, e6596.	0.9	27
16	Metabarcoding a diverse arthropod mock community. <i>Molecular Ecology Resources</i> , 2019, 19, 711-727.	2.2	107
17	A reference library for Canadian invertebrates with 1.5 million barcodes, voucher specimens, and DNA samples. <i>Scientific Data</i> , 2019, 6, 308.	2.4	39
18	Validation of COI metabarcoding primers for terrestrial arthropods. <i>PeerJ</i> , 2019, 7, e7745.	0.9	161

#	ARTICLE	IF	CITATIONS
19	Rapid identification of the botanical and entomological sources of honey using DNA metabarcoding. Food Chemistry, 2017, 214, 183-191.	4.2	106
20	Century-Old DNA Barcodes Reveal Phylogenetic Placement of the Extinct Jamaican Sunset Moth, <i>Urania sloanus</i> Cramer (Lepidoptera: Uraniidae). PLoS ONE, 2016, 11, e0164405.	1.1	10
21	DNA barcodes from century-old type specimens using next-generation sequencing. Molecular Ecology Resources, 2016, 16, 487-497.	2.2	118
22	Taxonomy 2.0: Sequencing of old type specimens supports the description of two new species of the <i>Lasiocampa decolorata</i> group from Morocco (Lepidoptera). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 617 Td (La	1.1	10
23	DNA barcoding of Neotropical black flies (Diptera: Simuliidae): Species identification and discovery of cryptic diversity in Mesoamerica. Zootaxa, 2015, 3936, 93.	0.2	31
24	One species in eight: DNA barcodes from type specimens resolve a taxonomic quagmire. Molecular Ecology Resources, 2015, 15, 967-984.	2.2	56
25	Advancing nematode barcoding: A primer cocktail for the cytochrome <i>c</i> oxidase subunit I gene from vertebrate parasitic nematodes. Molecular Ecology Resources, 2013, 13, 1108-1115.	2.2	103
26	A new set of primers for COI amplification from freshwater microcrustaceans. Molecular Ecology Resources, 2013, 13, 1151-1155.	2.2	73
27	A DNA Barcode Blitz™: Rapid Digitization and Sequencing of a Natural History Collection. PLoS ONE, 2013, 8, e68535.	1.1	184