

# David Plotkin

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3515646/publications.pdf>

Version: 2024-02-01

11  
papers

498  
citations

1477746

6  
h-index

1372195

10  
g-index

13  
all docs

13  
docs citations

13  
times ranked

575  
citing authors

#	ARTICLE	IF	CITATIONS
1	Anti-bat ultrasound production in moths is globally and phylogenetically widespread. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	13
2	Revisiting the evolution of <i>Ostrinia</i> moths with phylogenomics (Pyraloidea: Crambidae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702	1.7	9
3	First Annotated Genome of a Mandibulate Moth, <i>Neomicropteryx cornuta</i> , Generated Using PacBio HiFi Sequencing. Genome Biology and Evolution, 2021, 13, .	1.1	7
4	Review of recent taxonomic changes to the emerald moths (Lepidoptera: Geometridae: Geometrinae). Biodiversity Data Journal, 2020, 8, e52190.	0.4	2
5	Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22657-22663.	3.3	291
6	Developing a vocabulary and ontology for modeling insect natural history data: example data, use cases, and competency questions. Biodiversity Data Journal, 2019, 7, e33303.	0.4	3
7	Diel behavior in moths and butterflies: a synthesis of data illuminates the evolution of temporal activity. Organisms Diversity and Evolution, 2018, 18, 13-27.	0.7	37
8	Phylogenetics of moth-like butterflies (Papilionoidea: Hedyllidae) based on a new 13-locus target capture probe set. Molecular Phylogenetics and Evolution, 2018, 127, 600-605.	1.2	33
9	A molecular phylogeny and revised higher-level classification for the leaf-mining moth family <i>racillariidae</i> and its implications for larval host-use evolution. Systematic Entomology, 2017, 42, 60-81.	1.7	61
10	Preserving and vouchering butterflies and moths for large-scale museum-based molecular research. PeerJ, 2016, 4, e2160.	0.9	22
11	Long-read HiFi sequencing correctly assembles repetitive heavy fibroin silk genes in new moth and caddisfly genomes. GigaByte, 0, 2022, 1-14.	0.0	17