

# Stefan Prost

## List of Publications by Year in descending order

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Version: 2024-02-01

58  
papers

2,043  
citations

257450

24  
h-index

289244

40  
g-index

76  
all docs

76  
docs citations

76  
times ranked

3782  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide diversity loss in reintroduced Eurasian lynx populations urges immediate conservation management. <i>Biological Conservation</i> , 2022, 266, 109442.	4.1	18
2	Rapid in situ identification of biological specimens via DNA amplicon sequencing using miniaturized laboratory equipment. <i>Nature Protocols</i> , 2022, 17, 1415-1443.	12.0	23
3	Climate change leads to higher NPP at the end of the century in the Antarctic Tundra: Response patterns through the lens of lichens. <i>Science of the Total Environment</i> , 2022, 835, 155495.	8.0	6
4	Genomic analyses show extremely perilous conservation status of African and Asiatic cheetahs ( <i>Acinonyx jubatus</i> ). <i>Molecular Ecology</i> , 2022, 31, 4208-4223.	3.9	21
5	Unlocking the potential of a validated single nucleotide polymorphism array for genomic monitoring of trade in cheetahs ( <i>Acinonyx jubatus</i> ). <i>Molecular Biology Reports</i> , 2021, 48, 171-181.	2.3	6
6	NGSpeciesID: DNA barcode and amplicon consensus generation from long-read sequencing data. <i>Ecology and Evolution</i> , 2021, 11, 1392-1398.	1.9	30
7	Recent Evolutionary History of Tigers Highlights Contrasting Roles of Genetic Drift and Selection. <i>Molecular Biology and Evolution</i> , 2021, 38, 2366-2379.	8.9	35
8	Ecological Specialization and Evolutionary Reticulation in Extant Hyaenidae. <i>Molecular Biology and Evolution</i> , 2021, 38, 3884-3897.	8.9	15
9	Genomic insights into the conservation status of the world's last remaining Sumatran rhinoceros populations. <i>Nature Communications</i> , 2021, 12, 2393.	12.8	39
10	Nanopore sequencing in non-human forensic genetics. <i>Emerging Topics in Life Sciences</i> , 2021, 5, 465-473.	2.6	5
11	Developmental validation of Oxford Nanopore Technology MinION sequence data and the NGSpeciesID bioinformatic pipeline for forensic genetic species identification. <i>Forensic Science International: Genetics</i> , 2021, 53, 102493.	3.1	31
12	Chromosome-level reference genome of the European wasp spider <i>Argiope bruennichi</i> : a resource for studies on range expansion and evolutionary adaptation. <i>GigaScience</i> , 2021, 10, .	6.4	35
13	Evidence of two deeply divergent co-existing mitochondrial genomes in the Tuatara reveals an extremely complex genomic organization. <i>Communications Biology</i> , 2021, 4, 116.	4.4	16
14	Rhinoceros genomes uncover family secrets. <i>Nature</i> , 2021, 599, 209-210.	27.8	0
15	The <i>Tetragnatha kauaiensis</i> Genome Sheds Light on the Origins of Genomic Novelty in Spiders. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	16
16	Functional analysis of natural PCSK9 mutants in modern and archaic humans. <i>FEBS Journal</i> , 2020, 287, 515-528.	4.7	8
17	Tissue- and Population-Level Microbiome Analysis of the Wasp Spider <i>Argiope bruennichi</i> Identified a Novel Dominant Bacterial Symbiont. <i>Microorganisms</i> , 2020, 8, 8.	3.6	26
18	Chromosome-level de novo assembly of the pig-tailed macaque genome using linked-read sequencing and HiC proximity scaffolding. <i>GigaScience</i> , 2020, 9, .	6.4	6

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19	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020, 584, 403-409.	27.8	105
20	Pre-extinction Demographic Stability and Genomic Signatures of Adaptation in the Woolly Rhinoceros. <i>Current Biology</i> , 2020, 30, 3871-3879.e7.	3.9	41
21	Improving the Chromosome-Level Genome Assembly of the Siamese Fighting Fish ( <i>Betta</i> ) Tj ETQq1 1 0.784314 <sup>1.8</sup> / <sup>15</sup> Overlock 10	1.8	15
22	Education in the genomics era: Generating high-quality genome assemblies in university courses. <i>GigaScience</i> , 2020, 9, .	6.4	9
23	Interspecific Gene Flow and the Evolution of Specialization in Black and White Rhinoceros. <i>Molecular Biology and Evolution</i> , 2020, 37, 3105-3117.	8.9	20
24	Rigorous wildlife disease surveillance. <i>Science</i> , 2020, 369, 145-147.	12.6	78
25	High-throughput sequencing for community analysis: the promise of DNA barcoding to uncover diversity, relatedness, abundances and interactions in spider communities. <i>Development Genes and Evolution</i> , 2020, 230, 185-201.	0.9	39
26	MinION-Based DNA Barcoding of Preserved and Non-Invasively Collected Wildlife Samples. <i>Genes</i> , 2020, 11, 445.	2.4	30
27	Portable sequencing as a teaching tool in conservation and biodiversity research. <i>PLoS Biology</i> , 2020, 18, e3000667.	5.6	37
28	Host and geography together drive early adaptive radiation of Hawaiian planthoppers. <i>Molecular Ecology</i> , 2019, 28, 4513-4528.	3.9	6
29	Genetic Biomonitoring and Biodiversity Assessment Using Portable Sequencing Technologies: Current Uses and Future Directions. <i>Genes</i> , 2019, 10, 858.	2.4	69
30	Comparative analyses identify genomic features potentially involved in the evolution of birds-of-paradise. <i>GigaScience</i> , 2019, 8, .	6.4	22
31	Nanopore sequencing of long ribosomal DNA amplicons enables portable and simple biodiversity assessments with high phylogenetic resolution across broad taxonomic scale. <i>GigaScience</i> , 2019, 8, .	6.4	126
32	The Genome and mRNA Transcriptome of the Cosmopolitan Calanoid Copepod <i>Acartia tonsa</i> Dana Improve the Understanding of Copepod Genome Size Evolution. <i>Genome Biology and Evolution</i> , 2019, 11, 1440-1450.	2.5	26
33	Dynamic evolutionary history and gene content of sex chromosomes across diverse songbirds. <i>Nature Ecology and Evolution</i> , 2019, 3, 834-844.	7.8	68
34	Mitogenomic evidence of close relationships between New Zealand's extinct giant raptors and small-sized Australian sister-taxa. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 122-128.	2.7	17
35	Annotated Draft Genomes of Two Caddisfly Species <i>Plectrocnemia conspersa</i> CURTIS and <i>Hydropsyche tenuis</i> NAVAS (Insecta: Trichoptera). <i>Genome Biology and Evolution</i> , 2019, 11, 3445-3451.	2.5	21
36	Cost-effective assembly of the African wild dog ( <i>Lycaon pictus</i> ) genome using linked reads. <i>GigaScience</i> , 2019, 8, .	6.4	22

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37	Real-time DNA barcoding in a rainforest using nanopore sequencing: opportunities for rapid biodiversity assessments and local capacity building. <i>GigaScience</i> , 2018, 7, .	6.4	176
38	Rapid divergence of mussel populations despite incomplete barriers to dispersal. <i>Molecular Ecology</i> , 2018, 27, 1556-1571.	3.9	29
39	Draft Genome Sequence and Annotation of the Lichen-Forming Fungus <i>Arthonia radiata</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	12
40	Co-occurrence of ecologically similar species of Hawaiian spiders reveals critical early phase of adaptive radiation. <i>BMC Evolutionary Biology</i> , 2018, 18, 100.	3.2	20
41	Ancient mitogenomes of Phoenicians from Sardinia and Lebanon: A story of settlement, integration, and female mobility. <i>PLoS ONE</i> , 2018, 13, e0190169.	2.5	40
42	The Proprotein Convertases in Hypercholesterolemia and Cardiovascular Diseases: Emphasis on Proprotein Convertase Subtilisin/Kexin 9. <i>Pharmacological Reviews</i> , 2017, 69, 33-52.	16.0	90
43	Synchronous genetic turnovers across Western Eurasia in Late Pleistocene collared lemmings. <i>Global Change Biology</i> , 2016, 22, 1710-1721.	9.5	45
44	First complete mitochondrial genome data from ancient South American camelids - The mystery of the chilihueques from Isla Mocha (Chile). <i>Scientific Reports</i> , 2016, 6, 38708.	3.3	9
45	Geographically contrasting biodiversity reductions in a widespread New Zealand seabird. <i>Molecular Ecology</i> , 2015, 24, 4605-4616.	3.9	22
46	Complete Mitochondrial Genomes of New Zealand's First Dogs. <i>PLoS ONE</i> , 2015, 10, e0138536.	2.5	26
47	From cheek swabs to consensus sequences: an A to Z protocol for high-throughput DNA sequencing of complete human mitochondrial genomes. <i>BMC Genomics</i> , 2014, 15, 68.	2.8	27
48	Integrating multiple lines of evidence into historical biogeography hypothesis testing: a <i>Bison bison</i> case study. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132782.	2.6	41
49	Extinction and recolonization of coastal megafauna following human arrival in New Zealand. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140097.	2.6	53
50	Ancient mitochondrial DNA and the genetic history of Eurasian beaver ( <i>Castor fiber</i> ) in Europe. <i>Molecular Ecology</i> , 2014, 23, 1717-1729.	3.9	24
51	Effects of late quaternary climate change on Palearctic shrews. <i>Global Change Biology</i> , 2013, 19, 1865-1874.	9.5	24
52	Losing ground: past history and future fate of Arctic small mammals in a changing climate. <i>Global Change Biology</i> , 2013, 19, 1854-1864.	9.5	46
53	The Genetic Diversity of the Nguni Breed of African Cattle ( <i>Bos</i> spp.): Complete Mitochondrial Genomes of Haplogroup T1. <i>PLoS ONE</i> , 2013, 8, e71956.	2.5	36
54	Complete mitochondrial DNA genome sequences from the first New Zealanders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18350-18354.	7.1	51

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55	TempNet: a method to display statistical parsimony networks for heterochronous DNA sequence data. <i>Methods in Ecology and Evolution</i> , 2011, 2, 663-667.	5.2	98
56	Influence of Climate Warming on Arctic Mammals? New Insights from Ancient DNA Studies of the Collared Lemming <i>Dicrostonyx torquatus</i> . <i>PLoS ONE</i> , 2010, 5, e10447.	2.5	48
57	A population history of Tokelau's genetic variation and change in atoll populations. <i>Journal of Island and Coastal Archaeology</i> , 0, , 1-18.	1.4	0
58	Chromosome-level genome assembly of a benthic associated Syngnathiformes species: the common dragonet, <i>Callionymus lyra</i> . <i>GigaByte</i> , 0, 2020, 1-10.	0.0	7