## Simona Kraberger

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5763982/publications.pdf

Version: 2024-02-01

147726 214721 3,211 128 31 47 citations g-index h-index papers 138 138 138 2844 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	The Ancient Evolutionary History of Polyomaviruses. PLoS Pathogens, 2016, 12, e1005574.	2.1	190
2	Diverse circular ssDNA viruses discovered in dragonflies (Odonata: Epiprocta). Journal of General Virology, 2012, 93, 2668-2681.	1.3	163
3	Dragonfly cyclovirus, a novel single-stranded DNA virus discovered in dragonflies (Odonata:) Tj ETQq1 1 0.78431	4 rgBT /Ov	verlock 10 Tf
4	High-throughput sequencing of SARS-CoV-2 in wastewater provides insights into circulating variants. Water Research, 2021, 205, 117710.	<b>5.</b> 3	93
5	Characterisation of a diverse range of circular replication-associated protein encoding DNA viruses recovered from a sewage treatment oxidation pond. Infection, Genetics and Evolution, 2015, 31, 73-86.	1.0	76
6	Ongoing geographical spread of Tomato yellow leaf curl virus. Virology, 2016, 498, 257-264.	1.1	76
7	Novel myco-like DNA viruses discovered in the faecal matter of various animals. Virus Research, 2013, 177, 209-216.	1.1	70
8	Diverse circular replication-associated protein encoding viruses circulating in invertebrates within a lake ecosystem. Infection, Genetics and Evolution, 2016, 39, 304-316.	1.0	66
9	Circular replication-associated protein encoding DNA viruses identified in the faecal matter of various animals in New Zealand. Infection, Genetics and Evolution, 2016, 43, 151-164.	1.0	65
10	Towards an ecoâ€phylogenetic framework for infectious disease ecology. Biological Reviews, 2018, 93, 950-970.	4.7	63
11	The global distribution of (i>Banana bunchy top virus (li>reveals little evidence for frequent recent, human-mediated long distance dispersal events. Virus Evolution, 2015, 1, vev009.	2.2	58
12	Feline Leukemia Virus (FeLV) Disease Outcomes in a Domestic Cat Breeding Colony: Relationship to Endogenous FeLV and Other Chronic Viral Infections. Journal of Virology, 2018, 92, .	1.5	56
13	Diverse and highly recombinant anelloviruses associated with Weddell seals in Antarctica. Virus Evolution, 2017, 3, vex017.	2,2	55
14	Taxonomic update for mammalian anelloviruses (family Anelloviridae). Archives of Virology, 2021, 166, 2943-2953.	0.9	55
15	Diverse small circular single-stranded DNA viruses identified in a freshwater pond on the McMurdo Ice Shelf (Antarctica). Infection, Genetics and Evolution, 2014, 26, 132-138.	1.0	53
16	Cycloviruses, gemycircularviruses and other novel replication-associated protein encoding circular viruses in Pacific flying fox (Pteropus tonganus) faeces. Infection, Genetics and Evolution, 2016, 39, 279-292.	1.0	53
17	Unique genome organization of non-mammalian papillomaviruses provides insights into the evolution of viral early proteins. Virus Evolution, 2017, 3, vex027.	2.2	51
18	A novel papillomavirus in Adélie penguin (Pygoscelis adeliae) faeces sampled at the Cape Crozier colony, Antarctica. Journal of General Virology, 2014, 95, 1352-1365.	1.3	50

#	Article	IF	CITATIONS
19	Evolutionary history of ssDNA bacilladnaviruses features horizontal acquisition of the capsid gene from ssRNA nodaviruses. Virology, 2017, 504, 114-121.	1.1	50
20	Discovery of a novel mastrevirus and alphasatellite-like circular DNA in dragonflies (Epiprocta) from Puerto Rico. Virus Research, 2013, 171, 231-237.	1.1	45
21	Evidence of inter-component recombination, intra-component recombination and reassortment in banana bunchy top virus. Journal of General Virology, 2012, 93, 1103-1119.	1.3	44
22	Identification of an avian polyomavirus associated with Adélie penguins (Pygoscelis adeliae). Journal of General Virology, 2015, 96, 851-857.	1.3	41
23	Discovery of Sclerotinia sclerotiorum Hypovirulence-Associated Virus-1 in Urban River Sediments of Heathcote and Styx Rivers in Christchurch City, New Zealand. Genome Announcements, 2013, 1, .	0.8	40
24	Begomovirus-Associated Satellite DNA Diversity Captured Through Vector-Enabled Metagenomic (VEM) Surveys Using Whiteflies (Aleyrodidae). Viruses, 2016, 8, 36.	1.5	40
25	Molecular characterization and prevalence of two capulaviruses: Alfalfa leaf curl virus from France and Euphorbia caput-medusae latent virus from South Africa. Virology, 2016, 493, 142-153.	1.1	40
26	Molecular characterisation of dicot-infecting mastreviruses from Australia. Virus Research, 2012, 166, 13-22.	1.1	39
27	Vector-Enabled Metagenomic (VEM) Surveys Using Whiteflies (Aleyrodidae) Reveal Novel Begomovirus Species in the New and OldWorlds. Viruses, 2015, 7, 5553-5570.	1.5	39
28	Genome sequences of a capulavirus infecting Plantago lanceolata in the $\tilde{A}$ land archipelago of Finland. Archives of Virology, 2017, 162, 2041-2045.	0.9	39
29	Multiple Introductions of Domestic Cat Feline Leukemia Virus in Endangered Florida Panthers 1. Emerging Infectious Diseases, 2019, 25, 92-101.	2.0	39
30	Evidence that dicot-infecting mastreviruses are particularly prone to inter-species recombination and have likely been circulating in Australia for longer than in Africa and the Middle East. Virology, 2013, 444, 282-291.	1.1	37
31	Identification of a polyomavirus in Weddell seal (Leptonychotes weddellii) from the Ross Sea (Antarctica). Archives of Virology, 2017, 162, 1403-1407.	0.9	36
32	From Spatial Metagenomics to Molecular Characterization of Plant Viruses: A Geminivirus Case Study. Advances in Virus Research, 2018, 101, 55-83.	0.9	34
33	Genetic Characterization of a Recombinant Myxoma Virus in the Iberian Hare (Lepus granatensis). Viruses, 2019, 11, 530.	1.5	33
34	Diverse single-stranded DNA viruses associated with honey bees (Apis mellifera). Infection, Genetics and Evolution, 2019, 71, 179-188.	1.0	31
35	Single-Stranded DNA Viruses in Antarctic Cryoconite Holes. Viruses, 2019, 11, 1022.	1.5	31
36	Identification of a Nanovirus-Alphasatellite Complex in Sophora alopecuroides. Virus Research, 2017, 235, 24-32.	1.1	30

#	Article	IF	CITATIONS
37	Identification of circular single-stranded DNA viruses in faecal samples of Canada lynx (Lynx) Tj ETQq1 1 0.784314 Juan Mountains. Infection, Genetics and Evolution, 2018, 64, 1-8.	4 rgBT /Ov 1.0	verlock 10 Tf 30
38	Diversity of Beet curly top Iran virus isolated from different hosts in Iran. Virus Genes, 2013, 46, 571-575.	0.7	29
39	Identification of novel Bromus- and Trifolium-associated circular DNA viruses. Archives of Virology, 2015, 160, 1303-1311.	0.9	28
40	Virus Discovery in Desert Tortoise Fecal Samples: Novel Circular Single-Stranded DNA Viruses. Viruses, 2020, 12, 143.	1.5	26
41	Nanovirus-alphasatellite complex identified in Vicia cracca in the RhÃ'ne delta region of France. Archives of Virology, 2018, 163, 695-700.	0.9	25
42	Genetic diversity and host range studies of turnip curly top virus. Virus Genes, 2013, 46, 345-353.	0.7	24
43	SYBR Green real-time quantitative PCR for the specific detection and quantification of  Candidatus Liberibacter solanacearum' in field samples from New Zealand. European Journal of Plant Pathology, 2013, 136, 203-215.	0.8	24
44	Unravelling the Single-Stranded DNA Virome of the New Zealand Blackfly. Viruses, 2019, 11, 532.	1.5	24
45	Australian monocot-infecting mastrevirus diversity rivals that in Africa. Virus Research, 2012, 169, 127-136.	1.1	23
46	Molecular characterisation of an avihepadnavirus isolated from Psittacula krameri (ring-necked) Tj ETQq0 0 0 rgB	T /Oyerloc	k 10 Tf 50 3
47	Urbanization impacts apex predator gene flow but not genetic diversity across an urbanâ€rural divide. Molecular Ecology, 2019, 28, 4926-4940.	2.0	23
48	Molecular diversity of turncurtoviruses in Iran. Archives of Virology, 2016, 161, 551-561.	0.9	22
49	Unveiling Crucivirus Diversity by Mining Metagenomic Data. MBio, 2020, 11, .	1.8	22
50	A high degree of African streak virus diversity within Nigerian maize fields includes a new mastrevirus from Axonopus compressus. Archives of Virology, 2014, 159, 2765-2770.	0.9	20
51	Molecular diversity of Chickpea chlorotic dwarf virus in Sudan: High rates of intra-species recombination $\hat{a} \in \mathbb{C}^n$ a driving force in the emergence of new strains. Infection, Genetics and Evolution, 2015, 29, 203-215.	1.0	20
52	Occurrence of a novel mastrevirus in sugarcane germplasm collections in Florida, Guadeloupe and RÃ@union. Virology Journal, 2017, 14, 146.	1.4	20
53	Host relatedness and landscape connectivity shape pathogen spread in the puma, a large secretive carnivore. Communications Biology, 2021, 4, 12.	2.0	20
54	Fish polyomaviruses belong to two distinct evolutionary lineages. Journal of General Virology, 2018, 99, 567-573.	1.3	19

#	Article	IF	CITATIONS
55	Identification of a Novel Adélie Penguin Circovirus at Cape Crozier (Ross Island, Antarctica). Viruses, 2019, 11, 1088.	1.5	18
56	Immune protection is dependent on the gut microbiome in a lethal mouse gammaherpesviral infection. Scientific Reports, 2020, 10, 2371.	1.6	18
57	Taxonomic updates for the genus Gyrovirus (family Anelloviridae): recognition of several new members and establishment of species demarcation criteria. Archives of Virology, 2021, 166, 2937-2942.	0.9	18
58	Diverse papillomaviruses identified in Weddell seals. Journal of General Virology, 2018, 99, 549-557.	1.3	18
59	Frequent cross-species transmissions of foamy virus between domestic and wild felids. Virus Evolution, 2020, 6, vez058.	2.2	17
60	Molecular characterization of faba bean necrotic yellows viruses in Tunisia. Archives of Virology, 2018, 163, 687-694.	0.9	16
61	Genome Sequences of Poaceae-Associated Gemycircularviruses from the Pacific Ocean Island of Tonga. Genome Announcements, 2015, 3, .	0.8	15
62	Identification of an Australian-like dicot-infecting mastrevirus in Pakistan. Archives of Virology, 2015, 160, 825-830.	0.9	15
63	Novel anelloviruses identified in buccal swabs of Antarctic fur seals. Virus Genes, 2018, 54, 719-723.	0.7	15
64	Feline Leukemia Virus (FeLV) Endogenous and Exogenous Recombination Events Result in Multiple FeLV-B Subtypes during Natural Infection. Journal of Virology, 2021, 95, e0035321.	1.5	15
65	Recombinant Goose Circoviruses Circulating in Domesticated and Wild Geese in Poland. Viruses, 2018, 10, 107.	1.5	14
66	Preliminary surveillance for beak and feather disease virus in wild parrots of New Caledonia: implications of a reservoir species for Ouvea Parakeets. Emu, 2014, 114, 283-289.	0.2	13
67	Genome Sequences of <i>Beet curly top Iran virus</i> , <i>Oat dwarf virus</i> , <i>Turnip curly top virus</i> , and <i>Wheat dwarf virus</i> Identified in Leafhoppers. Genome Announcements, 2017, 5, .	0.8	13
68	Genomovirus Genomes Recovered from <i>Echinothrips americanus</i> Sampled in Florida, USA. Genome Announcements, 2017, 5, .	0.8	13
69	Novel mastreviruses identified in Australian wild rice. Virus Research, 2017, 238, 193-197.	1.1	13
70	Novel Circoviruses Detected in Feces of Sonoran Felids. Viruses, 2020, 12, 1027.	1.5	13
71	Diverse genomoviruses representing twenty-nine species identified associated with plants. Archives of Virology, 2020, 165, 2891-2901.	0.9	13
72	Complex evolutionary history of felid anelloviruses. Virology, 2021, 562, 176-189.	1.1	13

#	Article	IF	CITATIONS
73	Diverse single-stranded DNA viruses identified in New Zealand (Aotearoa) South Island robin (Petroica) Tj ETQq1	l 0.784314 1:1	1 rgBT /Ove
74	The role of Kenya in the trans-African spread of maize streak virus strain A. Virus Research, 2017, 232, 69-76.	1.1	12
75	Novel circular DNA viruses associated with Apiaceae and Poaceae from South Africa and New Zealand. Archives of Virology, 2019, 164, 237-242.	0.9	12
76	MrIML: Multiâ€response interpretable machine learning to model genomic landscapes. Molecular Ecology Resources, 2021, 21, 2766-2781.	2.2	12
77	A novel maize-infecting mastrevirus from La Réunion Island. Archives of Virology, 2012, 157, 1617-1621.	0.9	11
78	Molecular diversity, geographic distribution and host range of monocot-infecting mastreviruses in Africa and surrounding islands. Virus Research, 2017, 238, 171-178.	1.1	11
79	Genomoviruses associated with mountain and western pine beetles. Virus Research, 2018, 256, 17-20.	1.1	11
80	Identification of Circovirus Genome in a Chinstrap Penguin (Pygoscelis antarcticus) and Adélie Penguin (Pygoscelis adeliae) on the Antarctic Peninsula. Viruses, 2020, 12, 858.	1.5	11
81	Diverse cressdnaviruses and an anellovirus identified in the fecal samples of yellow-bellied marmots. Virology, 2021, 554, 89-96.	1.1	11
82	Agricultural practices drive biological loads, seasonal patterns and potential pathogens in the aerobiome of a mixed-land-use dryland. Science of the Total Environment, 2021, 798, 149239.	3.9	11
83	Genome Sequences of Two Single-Stranded DNA Viruses Identified in <i>Varroa destructor</i> Genome Announcements, 2018, 6, .	0.8	10
84	Feline Foamy Virus is Highly Prevalent in Free-Ranging Puma concolor from Colorado, Florida and Southern California. Viruses, 2019, 11, 359.	1.5	10
85	Identification and Distribution of Novel Cressdnaviruses and Circular Molecules in Four Penguin Species in South Georgia and the Antarctic Peninsula. Viruses, 2020, 12, 1029.	1.5	10
86	A Novel Divergent Geminivirus Identified in Asymptomatic New World Cactaceae Plants. Viruses, 2020, 12, 398.	1.5	10
87	Discovery of novel fish papillomaviruses: From the Antarctic to the commercial fish market. Virology, 2022, 565, 65-72.	1.1	10
88	Extensive Wastewater-Based Epidemiology as a Resourceful Tool for SARS-CoV-2 Surveillance in a Low-to-Middle-Income Country through a Successful Collaborative Quest: WBE, Mobility, and Clinical Tests. Water (Switzerland), 2022, 14, 1842.	1.2	10
89	Bromus catharticus striate mosaic virus: a new mastrevirus infecting Bromus catharticus from Australia. Archives of Virology, 2011, 156, 335-341.	0.9	9
90	The Expectations and Challenges of Wildlife Disease Research in the Era of Genomics: Forecasting with a Horizon Scan-like Exercise. Journal of Heredity, 2019, 110, 261-274.	1.0	9

#	Article	IF	CITATIONS
91	Viruses representing two new genomovirus species identified in citrus from Tunisia. Archives of Virology, 2020, 165, 1225-1229.	0.9	9
92	Identification of novel circovirus and anelloviruses from wolverines using a non-invasive faecal sampling approach. Infection, Genetics and Evolution, 2021, 93, 104914.	1.0	9
93	A novel lineage of polyomaviruses identified in bark scorpions. Virology, 2021, 563, 58-63.	1.1	9
94	Genome Sequence of a Gyrovirus Associated with Ashy Storm-Petrel. Microbiology Resource Announcements, 2018, $7$ , .	0.3	8
95	Diagnostic Uncertainty and the Epidemiology of Feline Foamy Virus in Pumas (Puma concolor). Scientific Reports, 2020, 10, 1587.	1.6	8
96	Identification of a Novel Myxoma Virus C7-Like Host Range Factor That Enabled a Species Leap from Rabbits to Hares. MBio, 2022, 13, e0346121.	1.8	8
97	Genome Sequences of Microviruses Associated with <i>Coptotermes formosanus</i> . Microbiology Resource Announcements, 2019, 8, .	0.3	7
98	Novel nanovirus and associated alphasatellites identified in milk vetch plants with chlorotic dwarf disease in Iran. Virus Research, 2020, 276, 197830.	1.1	7
99	Does the virus cross the road? Viral phylogeographic patterns among bobcat populations reflect a history of urban development. Evolutionary Applications, 2020, 13, 1806-1817.	1.5	7
100	Genome characterization of parsley severe stunt-associated virus in Iran. Virus Genes, 2021, 57, 293-301.	0.7	7
101	A Pilot Study Investigating the Dynamics of Pigeon Circovirus Recombination in Domesticated Pigeons Housed in a Single Loft. Viruses, 2021, 13, 964.	1.5	7
102	Circoviruses and cycloviruses identified in Weddell seal fecal samples from McMurdo Sound, Antarctica. Infection, Genetics and Evolution, 2021, 95, 105070.	1.0	7
103	Virion-Associated Nucleic Acid-Based Metagenomics: A Decade of Advances in Molecular Characterization of Plant Viruses. Phytopathology, 2022, 112, 2253-2272.	1.1	7
104	Coinfections of Novel Polyomavirus, Anelloviruses and a Recombinant Strain of Myxoma Virus-MYXV-Tol Identified in Iberian Hares. Viruses, 2020, 12, 340.	1.5	6
105	Genome Sequences of Microviruses Identified in Gila Monster Feces. Microbiology Resource Announcements, 2021, 10, .	0.3	6
106	Identification of the Begomoviruses Squash Leaf Curl Virus and Watermelon Chlorotic Stunt Virus in Various Plant Samples in North America. Viruses, 2021, 13, 810.	1.5	6
107	Diverse Single-Stranded DNA Viruses Identified in Chicken Buccal Swabs. Microorganisms, 2021, 9, 2602.	1.6	6
108	Novel Single-Stranded DNA Virus Genomes Recovered from Chimpanzee Feces Sampled from the Mambilla Plateau in Nigeria. Genome Announcements, 2017, 5, .	0.8	5

#	Article	IF	Citations
109	Novel smacoviruses identified in the faeces of two wild felids: North American bobcat and African lion. Archives of Virology, 2019, 164, 2395-2399.	0.9	5
110	Complete Genome Sequence of a Phapecoctavirus Isolated from a Pigeon Cloacal Swab Sample. Microbiology Resource Announcements, 2021, 10, .	0.3	5
111	Hunting alters viral transmission and evolution in a large carnivore. Nature Ecology and Evolution, 2022, 6, 174-182.	3.4	5
112	Coevolutionary Analysis Implicates Toll-Like Receptor 9 in Papillomavirus Restriction. MBio, 2022, 13, e0005422.	1.8	5
113	Genome Sequence of a Single-Stranded DNA Virus Identified in Gila Monster Feces. Microbiology Resource Announcements, 2018, 7, .	0.3	4
114	Feline foamy virus seroprevalence and demographic risk factors in stray domestic cat populations in Colorado, Southern California and Florida, USA. Journal of Feline Medicine and Surgery Open Reports, 2019, 5, 205511691987373.	0.1	4
115	Genome Sequences of Microviruses Identified in a Sample from a Sewage Treatment Oxidation Pond. Microbiology Resource Announcements, 2021, 10, .	0.3	4
116	Circular DNA viruses identified in short-finned pilot whale and orca tissue samples. Virology, 2021, 559, 156-164.	1.1	4
117	Poxvirus infection in house finches ( <i>Haemorhous mexicanus</i> ): Genome sequence analysis and patterns of infection in wild birds. Transboundary and Emerging Diseases, 2022, 69, .	1.3	4
118	Altered lentiviral infection dynamics follow genetic rescue of the Florida panther. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191689.	1.2	3
119	Genome Sequences of Novel Torque Teno Viruses Identified in Human Brain Tissue. Microbiology Resource Announcements, 2020, 9, .	0.3	3
120	Genomes of Bacteriophages Belonging to the Orders <i>Caudovirales</i> and <i>Petitvirales</i> Identified in Fecal Samples from Pacific Flying Fox ( <i>Pteropus tonganus</i> ) from the Kingdom of Tonga. Microbiology Resource Announcements, 2022, 11, e0003822.	0.3	3
121	RNA Virus Gene Signatures Detected in Patients With Cardiomyopathy After Chemotherapy; A Pilot Study. Frontiers in Cardiovascular Medicine, 2022, 9, 821162.	1.1	3
122	A parasite outbreak in notothenioid fish in an Antarctic fjord. IScience, 2022, 25, 104588.	1.9	3
123	Novel viruses belonging to the family Circoviridae identified in wild American wigeon samples. Archives of Virology, 2021, 166, 3437-3441.	0.9	2
124	Novel adenovirus associated with common tern (Sterna hirundo) chicks. Archives of Virology, 2022, 167, 659-663.	0.9	2
125	Geometric morphometrics and molecular systematics of Xanthocnemis sobrina (McLachlan, 1873) (Odonata: Coenagrionidae) and comparison to its congeners. Zootaxa, 2016, 4078, 84-120.	0.2	1
126	Novel circular DNA virus identified in Opuntia discolor (Cactaceae) that codes for proteins with similarity to those of geminiviruses. Journal of General Virology, 2021, 102, .	1.3	1

#	ŧ	Article	IF	CITATIONS
1	.27	Viral Sequences Recovered From Puma Tooth DNA Reconstruct Statewide Viral Phylogenies. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	0
1	.28	Microvirus Genomes Identified in Fecal Samples from Yellow-Bellied Marmots. Microbiology Resource Announcements, 2022, , e0121821.	0.3	0