Kevin J Olival

List of Publications by Year
in descending order

149 papers	27,077 citations	17440 63 h-index	10157 140 g-index
164 all docs	164 docs citations	164 times ranked	24494 citing authors

#	Article	IF	Citations
1	Global trends in emerging infectious diseases. Nature, 2008, 451, 990-993.	27.8	5,859
2	Bats Are Natural Reservoirs of SARS-Like Coronaviruses. Science, 2005, 310, 676-679.	12.6	2,130
3	Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. Nature, 2013, 503, 535-538.	27.8	1,439
4	Host and viral traits predict zoonotic spillover from mammals. Nature, 2017, 546, 646-650.	27.8	811
5	Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. PLoS Pathogens, 2017, 13, e1006698.	4.7	797
6	Prediction and prevention of the next pandemic zoonosis. Lancet, The, 2012, 380, 1956-1965.	13.7	744
7	Unhealthy Landscapes: Policy Recommendations on Land Use Change and Infectious Disease Emergence. Environmental Health Perspectives, 2004, 112, 1092-1098.	6.0	740
8	Cross-Species Virus Transmission and the Emergence of New Epidemic Diseases. Microbiology and Molecular Biology Reviews, 2008, 72, 457-470.	6.6	648
9	Global hotspots and correlates of emerging zoonotic diseases. Nature Communications, 2017, 8, 1124.	12.8	645
10	Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. Nature, 2018, 556, 255-258.	27.8	565
11	Middle East Respiratory Syndrome Coronavirus in Bats, Saudi Arabia. Emerging Infectious Diseases, 2013, 19, 1819-23.	4.3	562
12	Bushmeat Hunting, Deforestation, and Prediction of Zoonotic Disease. Emerging Infectious Diseases, 2005, 11, 1822-1827.	4.3	487
13	Ecology and economics for pandemic prevention. Science, 2020, 369, 379-381.	12.6	411
14	Climate change increases cross-species viral transmission risk. Nature, 2022, 607, 555-562.	27.8	361
15	Middle East Respiratory Syndrome Coronavirus Infection in Dromedary Camels in Saudi Arabia. MBio, 2014, 5, e00884-14.	4.1	359
16	Pteropid Bats are Confirmed as the Reservoir Hosts of Henipaviruses: A Comprehensive Experimental Study of Virus Transmission. American Journal of Tropical Medicine and Hygiene, 2011, 85, 946-951.	1.4	337
17	One Health, emerging infectious diseases and wildlife: two decades of progress?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160167.	4.0	334
18	The Global Virome Project. Science, 2018, 359, 872-874.	12.6	324

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19	A Strategy To Estimate Unknown Viral Diversity in Mammals. MBio, 2013, 4, e00598-13.	4.1	320
20	Global patterns in coronavirus diversity. Virus Evolution, 2017, 3, vex012.	4.9	310
21	Bat-borne virus diversity, spillover and emergence. Nature Reviews Microbiology, 2020, 18, 461-471.	28.6	298
22	Urban habituation, ecological connectivity and epidemic dampening: the emergence of Hendra virus from flying foxes (Pteropusspp.). Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 3703-3712.	2.6	274
23	Origin and cross-species transmission of bat coronaviruses in China. Nature Communications, 2020, 11, 4235.	12.8	264
24	Causal inference in disease ecology: investigating ecological drivers of disease emergence. Frontiers in Ecology and the Environment, 2008, 6, 420-429.	4.0	261
25	Bats are a major natural reservoir for hepaciviruses and pegiviruses. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8194-8199.	7.1	251
26	Filoviruses in Bats: Current Knowledge and Future Directions. Viruses, 2014, 6, 1759-1788.	3.3	247
27	Reproduction and nutritional stress are risk factors for Hendra virus infection in little red flying foxes (Pteropus scapulatus). Proceedings of the Royal Society B: Biological Sciences, 2008, 275, 861-869.	2.6	246
28	Agricultural intensification, priming for persistence and the emergence of Nipah virus: a lethal bat-borne zoonosis. Journal of the Royal Society Interface, 2012, 9, 89-101.	3.4	245
29	Reducing the Risks of the Wildlife Trade. Science, 2009, 324, 594-595.	12.6	242
30	Spillover and pandemic properties of zoonotic viruses with high host plasticity. Scientific Reports, 2015, 5, 14830.	3.3	238
31	Serological Evidence of Bat SARS-Related Coronavirus Infection in Humans, China. Virologica Sinica, 2018, 33, 104-107.	3.0	219
32	Correction to Middle East Respiratory Syndrome Coronavirus Infection in Dromedary Camels in Saudi Arabia. MBio, 2014, 5, .	4.1	209
33	Nipah virus: Impact, origins, and causes of emergence. Current Infectious Disease Reports, 2006, 8, 59-65.	3.0	182
34	Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. Microbiome, 2018, 6, 178.	11.1	150
35	Pteropus vampyrus, a hunted migratory species with a multinational homeâ€range and a need for regional management. Journal of Applied Ecology, 2009, 46, 991-1002.	4.0	145
36	Evidence for henipavirus spillover into human populations in Africa. Nature Communications, 2014, 5, 5342.	12.8	143

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37	Ranking the risk of animal-to-human spillover for newly discovered viruses. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	140
38	Human ecology in pathogenic landscapes: two hypotheses on how land use change drives viral emergence. Current Opinion in Virology, 2013, 3, 79-83.	5.4	137
39	Ebola Virus Antibodies in Fruit Bats, Bangladesh. Emerging Infectious Diseases, 2013, 19, 270-273.	4.3	129
40	Interdisciplinary approaches to understanding disease emergence: The past, present, and future drivers of Nipah virus emergence. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3681-3688.	7.1	128
41	Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: A case study of bats. PLoS Pathogens, 2020, 16, e1008758.	4.7	127
42	Evolutionary Relationships between Bat Coronaviruses and Their Hosts. Emerging Infectious Diseases, 2007, 13, 1526-1532.	4.3	123
43	HenipavirusInfection in Fruit Bats (Pteropus giganteus), India. Emerging Infectious Diseases, 2008, 14, 1309-1311.	4.3	121
44	Targeting Transmission Pathways for Emerging Zoonotic Disease Surveillance and Control. Vector-Borne and Zoonotic Diseases, 2015, 15, 432-437.	1.5	119
45	Nipah virus dynamics in bats and implications for spillover to humans. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29190-29201.	7.1	119
46	Transmission of Nipah Virus â€" 14 Years of Investigations in Bangladesh. New England Journal of Medicine, 2019, 380, 1804-1814.	27.0	114
47	Characterization of Nipah Virus from Naturally InfectedPteropus vampyrusBats, Malaysia. Emerging Infectious Diseases, 2010, 16, 1990-1993.	4.3	113
48	Henipavirus susceptibility to environmental variables. Virus Research, 2008, 132, 140-144.	2.2	112
49	Global distribution and genetic diversity of Bartonella in bat flies (Hippoboscoidea, Streblidae,) Tj ETQq1 1 0.784314 rgBT /Overlock 1	2.3	111
50	Nipah Virus Transmission from Bats to Humans Associated with Drinking Traditional Liquor Made from Date Palm Sap, Bangladesh, 2011â€"2014. Emerging Infectious Diseases, 2016, 22, 664-670.	4.3	104
51	A strategy to prevent future epidemics similar to the 2019-nCoV outbreak. Biosafety and Health, 2020, 2, 6-8.	2.7	102
52	Pandemic COVID-19 Joins Historyâ€™s Pandemic Legion. MBio, 2020, 11, .	4.1	100
53	The costs and benefits of primary prevention of zoonotic pandemics. Science Advances, 2022, 8, eabl4183.	10.3	99
54	The ecology of emerging neurotropic viruses. Journal of NeuroVirology, 2005, 11, 441-446.	2.1	97

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55	Emerging Viruses: Coming in on a Wrinkled Wing and a Prayer. Clinical Infectious Diseases, 2007, 44, 711-717.	5.8	94
56	Human-animal interactions and bat coronavirus spillover potential among rural residents in Southern China. Biosafety and Health, 2019, 1, 84-90.	2.7	94
57	Contrasting Patterns in Mammalâ€“Bacteria Coevolution: Bartonella and Leptospira in Bats and Rodents. PLoS Neglected Tropical Diseases, 2014, 8, e2738.	3.0	84
58	Predicting the global mammalian viral sharing network using phylogeography. Nature Communications, 2020, 11, 2260.	12.8	78
59	Correlates of Viral Richness in Bats (Order Chiroptera). EcoHealth, 2009, 6, 522-539.	2.0	76
60	Convergence of Humans, Bats, Trees, and Culture in Nipah Virus Transmission, Bangladesh. Emerging Infectious Diseases, 2017, 23, 1446-1453.	4.3	76
61	Molecular evidence of Ebola Reston virus infection in Philippine bats. Virology Journal, 2015, 12, 107.	3.4	71
62	Diversity of coronavirus in bats from Eastern Thailand. Virology Journal, 2015, 12, 57.	3.4	70
63	Identification of GBV-D, a Novel GB-like Flavivirus from Old World Frugivorous Bats (Pteropus) Tj ETQq1 1 0.784314 rgBT /Overlock 10	4.3	69
64	Quantitative Risk Assessment of the Pathways by Which West Nile Virus Could Reach Hawaii. EcoHealth, 2004, 1, 205-209.	2.0	65
65	Group C Betacoronavirus in Bat Guano Fertilizer, Thailand. Emerging Infectious Diseases, 2013, 19, 1349-51.	4.3	65
66	Non-random patterns in viral diversity. Nature Communications, 2015, 6, 8147.	12.8	65
67	Genetically Diverse Filoviruses in Rousettus and Eonycteris spp. Bats, China, 2009 and 2015. Emerging Infectious Diseases, 2017, 23, 482-486.	4.3	64
68	Parasite and viral species richness of Southeast Asian bats: Fragmentation of area distribution matters. International Journal for Parasitology: Parasites and Wildlife, 2014, 3, 161-170.	1.5	63
69	The Role of Landscape Composition and Configuration on Pteropus giganteus Roosting Ecology and Nipah Virus Spillover Risk in Bangladesh. American Journal of Tropical Medicine and Hygiene, 2014, 90, 247-255.	1.4	62
70	Roosting behaviour and habitat selection of Pteropus giganteus reveal potential links to Nipah virus epidemiology. Journal of Applied Ecology, 2014, 51, 376-387.	4.0	58
71	Does the impact of biodiversity differ between emerging and endemic pathogens? The need to separate the concepts of hazard and risk. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160129.	4.0	58
72	Serological Evidence of Henipavirus Exposure in Cattle, Goats and Pigs in Bangladesh. PLoS Neglected Tropical Diseases, 2014, 8, e3302.	3.0	57

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73	Quantifying Global Drivers of Zoonotic Bat Viruses: A Process-Based Perspective. American Naturalist, 2016, 187, E53-E64.	2.1	56
74	The Conflict Between Pteropodid Bats and Fruit Growers: Species, Legislation and Mitigation. , 2016, , 377-426.		56
75	No Evidence of Coronaviruses or Other Potentially Zoonotic Viruses in Sunda pangolins (Manis) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.0	53
76	A Comparative Analysis of Viral Richness and Viral Sharing in Cave-Roosting Bats. Diversity, 2017, 9, 35.	1.7	52
77	Infectious Disease Threats: A Rebound To Resilience. Health Affairs, 2021, 40, 204-211.	5.2	50
78	The future of zoonotic risk prediction. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20200358.	4.0	47
79	The emergence of Nipah and Hendra virus: pathogen dynamics across a wildlife-livestock-human continuum. , 2006, , 186-201.		47
80	Microbicidal actives with virucidal efficacy against SARS-CoV-2 and other beta- and alpha-coronaviruses and implications for future emerging coronaviruses and other enveloped viruses. Scientific Reports, 2021, 11, 5626.	3.3	45
81	Risk Factors for Nipah Virus Infection among Pteropid Bats, Peninsular Malaysia. Emerging Infectious Diseases, 2013, 19, 51-60.	4.3	44
82	Emerging henipaviruses and flying foxes â€“ Conservation and management perspectives. Biological Conservation, 2006, 131, 211-220.	4.1	43
83	Decoding the RNA viromes in rodent lungs provides new insight into the origin and evolutionary patterns of rodent-borne pathogens in Mainland Southeast Asia. Microbiome, 2021, 9, 18.	11.1	43
84	Beyond Ebola: lessons to mitigate future pandemics. The Lancet Global Health, 2015, 3, e354-e355.	6.3	42
85	Make science evolve into a One Health approach to improve health and security: a white paper. One Health Outlook, 2020, 2, 6.	3.4	42
86	Building a global atlas of zoonotic viruses. Bulletin of the World Health Organization, 2018, 96, 292-294.	3.3	42
87	Investigating Rare Risk Factors for Nipah Virus in Bangladesh: 2001â€“2012. EcoHealth, 2016, 13, 720-728.	2.0	41
88	Cross-sectional surveillance of Middle East respiratory syndrome coronavirus (MERS-CoV) in dromedary camels and other mammals in Egypt, August 2015 to January 2016. Eurosurveillance, 2017, 22, .	7.0	41
89	Lack of population genetic structure and host specificity in the bat fly, Cyclopodia horsfieldi, across species of Pteropus bats in Southeast Asia. Parasites and Vectors, 2013, 6, 231.	2.5	37
90	Targeting Surveillance for Zoonotic Virus Discovery. Emerging Infectious Diseases, 2013, 19, 743-747.	4.3	37

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91	Viral Diversity, Prey Preference, and Bartonella Prevalence in Desmodus rotundus in Guatemala. EcoHealth, 2016, 13, 761-774.	2.0	37
92	Duration of Maternal Antibodies against Canine Distemper Virus and Hendra Virus in Pteropid Bats. PLoS ONE, 2013, 8, e67584.	2.5	37
93	Optimizing Viral Discovery in Bats. PLoS ONE, 2016, 11, e0149237.	2.5	36
94	A viral metagenomic survey identifies known and novel mammalian viruses in bats from Saudi Arabia. PLoS ONE, 2019, 14, e0214227.	2.5	36
95	Nycteria parasites of Afrotropical insectivorous bats. International Journal for Parasitology, 2015, 45, 375-384.	3.1	33
96	Climate Change and Health: Transcending Silos to Find Solutions. Annals of Global Health, 2018, 81, 445.	2.0	32
97	Isolation and Full-Genome Characterization of Nipah Viruses from Bats, Bangladesh. Emerging Infectious Diseases, 2019, 25, 166-170.	4.3	32
98	Synergistic Chinaâ€“US Ecological Research is Essential for Global Emerging Infectious Disease Preparedness. EcoHealth, 2020, 17, 160-173.	2.0	30
99	Detection of Hepatocystis sp. in Southeast Asian Flying Foxes (Pteropodidae) Using Microscopic and Molecular Methods. Journal of Parasitology, 2007, 93, 1538-1540.	0.7	29
100	Bat Research Networks and Viral Surveillance: Gaps and Opportunities in Western Asia. Viruses, 2019, 11, 240.	3.3	29
101	To Cull, or Not To Cull, Bat is the Question. EcoHealth, 2016, 13, 6-8.	2.0	28
102	Was the COVIDâ€19 pandemic avoidable? A call for a â€œsolutionâ€orientedâ€•approach in pathogen evolutionary ecology to prevent future outbreaks. Ecology Letters, 2020, 23, 1557-1560.	6.4	27
103	A qualitative study of zoonotic risk factors among rural communities in southern China. International Health, 2020, 12, 77-85.	2.0	27
104	Bartonella spp. in a Puerto Rican Bat Community. Journal of Wildlife Diseases, 2015, 51, 274-278.	0.8	26
105	Population genetics of fruit bat reservoir informs the dynamics, distribution and diversity of Nipah virus. Molecular Ecology, 2020, 29, 970-985.	3.9	24
106	Satellite Telemetry and Long-Range Bat Movements. PLoS ONE, 2011, 6, e14696.	2.5	24
107	Horizontal Transfers and Gene Losses in the Phospholipid Pathway of Bartonella Reveal Clues about Early Ecological Niches. Genome Biology and Evolution, 2014, 6, 2156-2169.	2.5	23
108	Determinants of Pseudogymnoascus destructans within bat hibernacula: Implications for surveillance and management of whiteâ€nose syndrome. Journal of Applied Ecology, 2018, 55, 820-829.	4.0	23

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109	Characterizing and quantifying the wildlife trade network in Sulawesi, Indonesia. Global Ecology and Conservation, 2020, 21, e00887.	2.1	23
110	Taxonomic patterns in the zoonotic potential of mammalian viruses. PeerJ, 2018, 6, e5979.	2.0	22
111	Using healthcare-seeking behaviour to estimate the number of Nipah outbreaks missed by hospital-based surveillance in Bangladesh. International Journal of Epidemiology, 2019, 48, 1219-1227.	1.9	21
112	Characterization of the Spatial and Temporal Distribution of Nipah Virus Spillover Events in Bangladesh, 2007â€“2013. Journal of Infectious Diseases, 2018, 217, 1390-1394.	4.0	20
113	De-urbanization and Zoonotic Disease Risk. EcoHealth, 2018, 15, 707-712.	2.0	20
114	A Call for â€œSmart Surveillanceâ€: A Lesson Learned from H1N1. EcoHealth, 2009, 6, 1-2.	2.0	19
115	Quantifying Trends in Disease Impact to Produce a Consistent and Reproducible Definition of an Emerging Infectious Disease. PLoS ONE, 2013, 8, e69951.	2.5	19
116	Middle East Respiratory Syndrome Coronavirus Antibodies in Dromedary Camels, Bangladesh, 2015. Emerging Infectious Diseases, 2018, 24, 926-928.	4.3	19
117	Science, not speculation, is essential to determine how SARS-CoV-2 reached humans. Lancet, The, 2021, 398, 209-211.	13.7	18
118	Wild animal and zoonotic disease risk management and regulation in China: Examining gaps and One Health opportunities in scope, mandates, and monitoring systems. One Health, 2021, 13, 100301.	3.4	18
119	Two Tickets to Paradise: Multiple Dispersal Events in the Founding of Hoary Bat Populations in Hawai'i. PLoS ONE, 2015, 10, e0127912.	2.5	17
120	A Novel Potentially Recombinant Rodent Coronavirus with a Polybasic Cleavage Site in the Spike Protein. Journal of Virology, 2021, 95, e0117321.	3.4	16
121	Foraging Behaviour and Landscape Utilisation by the Endangered Golden-Crowned Flying Fox (Acerodon jubatus), The Philippines. PLoS ONE, 2013, 8, e79665.	2.5	15
122	Wildlife hosts for OIE â€Listed diseases: considerations regarding global wildlife trade and hostâ€“pathogen relationships. Veterinary Medicine and Science, 2017, 3, 71-81.	1.6	14
123	Contributions of Ex Situ Propagation and Molecular Genetics to Conservation of Hawaiian Tree Snails. , 2004, , 16-34.		14
124	Prioritizing the â€˜Dormantâ€™ Flaviviruses. EcoHealth, 2017, 14, 1-2.	2.0	12
125	Emerging Viral Zoonoses from Wildlife Associated with Animal-Based Food Systems: Risks and Opportunities. , 2016, , 31-57.		11
126	Comparison of Intravenous Medetomidine and Medetomidine/Ketamine for Immobilization of Free-Ranging Variable Flying Foxes (Pteropus hypomelanus). PLoS ONE, 2011, 6, e25361.	2.5	11

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127	Classification of new morbillivirus and jeilongvirus sequences from bats sampled in Brazil and Malaysia. Archives of Virology, 2022, 167, 1977-1987.	2.1	11
128	Increased Morbidity and Mortality in Domestic Animals Eating Dropped and Bitten Fruit in Bangladeshi Villages: Implications for Zoonotic Disease Transmission. EcoHealth, 2016, 13, 39-48.	2.0	10
129	Evolutionary and ecological correlates of population genetic structure in bats. , 0, , 267-316.		9
130	Epidemiology and Molecular Characterization of Rotavirus A in Fruit Bats in Bangladesh. EcoHealth, 2020, 17, 398-405.	2.0	9
131	First Complete Genome Sequence of Human Coronavirus HKU1 from a Nonill Bat Guano Miner in Thailand. Microbiology Resource Announcements, 2019, 8, .	0.6	8
132	Two decades of one health surveillance of Nipah virus in Thailand. One Health Outlook, 2021, 3, 12.	3.4	8
133	Surveillance for Ebola Virus in Wildlife, Thailand. Emerging Infectious Diseases, 2015, 21, 2271-2273.	4.3	7
134	Incorporating Health Outcomes into Land-Use Planning. EcoHealth, 2019, 16, 627-637.	2.0	7
135	Molecular Identification of Host Feeding Patterns of Snow-Melt Mosquitoes (Diptera: Culicidae): Potential Implications for the Transmission Ecology of Jamestown Canyon Virus. Journal of Medical Entomology, 2010, 47, 226-229.	1.8	5
136	Linking the Historical Roots of Environmental Conservation with Human and Wildlife Health. EcoHealth, 2013, 10, 224-227.	2.0	3
137	Genetic diversity and relationships among Lyle's flying fox colonies in Thailand. Agriculture and Natural Resources, 2018, 52, 607-611.	0.1	3
138	Detection of influenza virus in rectal swabs of patients admitted in hospital for febrile illnesses in Thailand. SAGE Open Medicine, 2021, 9, 205031212198963.	1.8	3
139	Knowledge, attitudes, and practices associated with zoonotic disease transmission risk in North Sulawesi, Indonesia. One Health Outlook, 2022, 4, .	3.4	3
140	Knowledge, perceptions, and attitudes by residents in Punjab and Khyber Pakhtunkhwa, Pakistan in connection with bats. Journal of Ethnobiology and Ethnomedicine, 2022, 18, .	2.6	3
141	Nipah Virus Detection at Bat Roosts after Spillover Events, Bangladesh, 2012â€“2019. Emerging Infectious Diseases, 2022, 28, 1384-1392.	4.3	3
142	Seasonality of Date Palm Sap Feeding Behavior by Bats in Bangladesh. EcoHealth, 2021, 18, 359-371.	2.0	2
143	Lessons from COVID-19 to Help Prevent Future Pandemics. China CDC Weekly, 2021, 3, 132-133.	2.3	1
144	Genetically Diverse Filoviruses in Rousettus and Eonycteris spp. Bats, China, 2009 and 2015. Emerging Infectious Diseases, 2017, 23, 482-486.	4.3	1

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145	Mapping Risk of Nipah Virus Transmission from Bats to Humans in Thailand. EcoHealth, 0, , .	2.0	1
146	Corrigendum to â€œGlobal correlates of emerging zoonoses: Anthropogenic, environmental, and biodiversity risk factorsâ€•[Int. J. Infect. Dis. 53 (Supplement) (December 2016) 21]. International Journal of Infectious Diseases, 2017, 58, 68.	3.3	0
147	Incubus. EcoHealth, 2017, 14, 189-192.	2.0	0
148	Surveillance for Ebola Virus in Wildlife, Thailand. Emerging Infectious Diseases, 2015, 21, .	4.3	0
149	Behavioralâ€“biological surveillance of emerging infectious diseases among a dynamic cohort in Thailand. BMC Infectious Diseases, 2022, 22, 472.	2.9	0