

# Sergios-orestis Kolokotronis

## List of Publications by Year in descending order

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84  
papers

3,959  
citations

132226

32  
h-index

128908

60  
g-index

100  
all docs

100  
docs citations

100  
times ranked

7831  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary. <i>BMC Evolutionary Biology</i> , 2008, 8, 220.	3.1	263
2	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. <i>Cell Systems</i> , 2015, 1, 72-87.	6.2	252
3	Concatenated Analysis Sheds Light on Early Metazoan Evolution and Fuels a Modern "Urmetazoon" Hypothesis. <i>PLoS Biology</i> , 2009, 7, e1000020.	5.4	238
4	Historical Mammal Extinction on Christmas Island (Indian Ocean) Correlates with Introduced Infectious Disease. <i>PLoS ONE</i> , 2008, 3, e3602.	2.5	201
5	Effects of male sterility on reproductive traits in gynodioecious plants: a meta-analysis. <i>Oecologia</i> , 2003, 135, 1-9.	2.1	162
6	The Real maccoyii: Identifying Tuna Sushi with DNA Barcodes – Contrasting Characteristic Attributes and Genetic Distances. <i>PLoS ONE</i> , 2009, 4, e7866.	2.5	149
7	Microbiome changes through ontogeny of a tick pathogen vector. <i>Molecular Ecology</i> , 2016, 25, 4963-4977.	3.6	145
8	A Functional Phylogenomic View of the Seed Plants. <i>PLoS Genetics</i> , 2011, 7, e1002411.	3.4	135
9	Zoonotic Viruses Associated with Illegally Imported Wildlife Products. <i>PLoS ONE</i> , 2012, 7, e29505.	2.5	126
10	Barcoding bushmeat: molecular identification of Central African and South American harvested vertebrates. <i>Conservation Genetics</i> , 2010, 11, 1389-1404.	1.5	118
11	Emergence of the Epidemic Methicillin-Resistant <i>Staphylococcus aureus</i> Strain USA300 Coincides with Horizontal Transfer of the Arginine Catabolic Mobile Element and <i>speG</i> -mediated Adaptations for Survival on Skin. <i>MBio</i> , 2013, 4, e00889-13.	4.4	116
12	Parallel Epidemics of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 Infection in North and South America. <i>Journal of Infectious Diseases</i> , 2015, 212, 1874-1882.	3.9	115
13	Evolution of hypervirulence by a <i>MRSA</i> clone through acquisition of a transposable element. <i>Molecular Microbiology</i> , 2014, 93, 664-681.	2.5	96
14	BS-Net: Learning COVID-19 pneumonia severity on a large chest X-ray dataset. <i>Medical Image Analysis</i> , 2021, 71, 102046.	11.8	96
15	Elevated substitution rates estimated from ancient DNA sequences. <i>Biology Letters</i> , 2007, 3, 702-705.	2.4	87
16	DNA barcodes reveal species-specific mercury levels in tuna sushi that pose a health risk to consumers. <i>Biology Letters</i> , 2010, 6, 692-695.	2.4	87
17	Genome assembly and geospatial phylogenomics of the bed bug <i>Cimex lectularius</i> . <i>Nature Communications</i> , 2016, 7, 10164.	13.2	83
18	Dynamically evolving novel overlapping gene as a factor in the SARS-CoV-2 pandemic. <i>ELife</i> , 2020, 9, .	5.9	82

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19	Evolution of the indoor biome. <i>Trends in Ecology and Evolution</i> , 2015, 30, 223-232.	8.8	80
20	In the Wake of Invasion: Tracing the Historical Biogeography of the South American Cricetid Radiation (Rodentia, Sigmodontinae). <i>PLoS ONE</i> , 2014, 9, e100687.	2.5	76
21	Bayesian Estimation of Substitution Rates from Ancient DNA Sequences with Low Information Content. <i>Systematic Biology</i> , 2011, 60, 366-375.	6.0	75
22	Integrating multiple lines of evidence to better understand the evolutionary divergence of humpback dolphins along their entire distribution range: a new dolphin species in Australian waters?. <i>Molecular Ecology</i> , 2013, 22, 5936-5948.	3.6	67
23	The Impact of Outgroup Choice and Missing Data on Major Seed Plant Phylogenetics Using Genome-Wide EST Data. <i>PLoS ONE</i> , 2009, 4, e5764.	2.5	57
24	Testing the Effectiveness of an International Conservation Agreement: Marketplace Forensics and CITES Caviar Trade Regulation. <i>PLoS ONE</i> , 2012, 7, e40907.	2.5	48
25	Reconciling Apparent Conflicts between Mitochondrial and Nuclear Phylogenies in African Elephants. <i>PLoS ONE</i> , 2011, 6, e20642.	2.5	46
26	To beat or not to beat a tick: comparison of DNA extraction methods for ticks ( <i>Ixodes</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 Td (	2.0	45
27	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. <i>Cell Systems</i> , 2015, 1, 97-97.e3.	6.2	43
28	Transient influence of blood meal and natural environment on blacklegged tick bacterial communities. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 563-572.	2.8	43
29	Genomic Epidemiology of Vancomycin-Resistant <i>Enterococcus faecium</i> (VREfm) in Latin America: Revisiting The Global VRE Population Structure. <i>Scientific Reports</i> , 2020, 10, 5636.	3.4	42
30	Outer surface protein polymorphisms linked to host- <i>Spirochete</i> association in Lyme borreliae. <i>Molecular Microbiology</i> , 2019, 111, 868-882.	2.5	39
31	Evolutionary dynamics of endogenous feline leukemia virus proliferation among species of the domestic cat lineage. <i>Virology</i> , 2010, 405, 397-407.	2.5	38
32	Random Addition Concatenation Analysis: A Novel Approach to the Exploration of Phylogenomic Signal Reveals Strong Agreement between Core and Shell Genomic Partitions in the Cyanobacteria. <i>Genome Biology and Evolution</i> , 2012, 4, 30-43.	2.6	35
33	Bats, Primates, and the Evolutionary Origins and Diversification of Mammalian Gammaherpesviruses. <i>MBio</i> , 2016, 7, .	4.4	34
34	Phylogenetic and evolutionary analyses of St. Louis encephalitis virus genomes. <i>Molecular Phylogenetics and Evolution</i> , 2008, 47, 717-728.	2.9	33
35	Molecular Surveillance of Low Pathogenic Avian Influenza Viruses in Wild Birds across the United States: Inferences from the Hemagglutinin Gene. <i>PLoS ONE</i> , 2012, 7, e50834.	2.5	30
36	Whole genome sequencing identifies bacterial factors affecting transmission of multidrug-resistant tuberculosis in a high-prevalence setting. <i>Scientific Reports</i> , 2019, 9, 5602.	3.4	28

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37	The Diploblast-Bilateria sister hypothesis. <i>Communicative and Integrative Biology</i> , 2009, 2, 403-405.	1.5	24
38	Changes in the Mitogenome Announcement manuscript category. <i>Mitochondrial DNA</i> , 2015, 26, 1-1.	0.8	24
39	Pre-detection history of extensively drug-resistant tuberculosis in KwaZulu-Natal, South Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23284-23291.	7.6	24
40	Modern Methods for Delineating Metagenomic Complexity. <i>Cell Systems</i> , 2015, 1, 6-7.	6.2	22
41	Local Diversification of Methicillin-Resistant <i>Staphylococcus aureus</i> ST239 in South America After Its Rapid Worldwide Dissemination. <i>Frontiers in Microbiology</i> , 2019, 10, 82.	3.6	22
42	Path integral for particles of spin zero and 1/2 in the field of an electromagnetic plane wave. <i>Physica Scripta</i> , 1992, 46, 289-294.	2.5	21
43	Molecular data from contemporary and historical collections reveal a complex story of cryptic diversification in the <i>Varanus (Polydaedalus) niloticus</i> Species Group. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 591-604.	2.9	21
44	Host tropism determination by convergent evolution of immunological evasion in the Lyme disease system. <i>PLoS Pathogens</i> , 2021, 17, e1009801.	4.1	21
45	Detection of mitochondrial insertions in the nucleus (NuMts) of Pleistocene and modern muskoxen. <i>BMC Evolutionary Biology</i> , 2007, 7, 67.	3.1	20
46	Genetic variation at hair length candidate genes in elephants and the extinct woolly mammoth. <i>BMC Evolutionary Biology</i> , 2009, 9, 232.	3.1	18
47	No Observed Effect of Landscape Fragmentation on Pathogen Infection Prevalence in Blacklegged Ticks ( <i>Ixodes scapularis</i> ) in the Northeastern United States. <i>PLoS ONE</i> , 2015, 10, e0139473.	2.5	18
48	Historical mitochondrial diversity in African leopards ( <i>Panthera pardus</i> ) revealed by archival museum specimens. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 455-473.	0.6	18
49	Drought legacy effects on root morphological traits and plant biomass via soil biota feedback. <i>New Phytologist</i> , 2022, 236, 222-234.	7.8	18
50	Mycobacterial Phylogenomics: An Enhanced Method for Gene Turnover Analysis Reveals Uneven Levels of Gene Gain and Loss among Species and Gene Families. <i>Genome Biology and Evolution</i> , 2014, 6, 1454-1465.	2.6	15
51	Genetic identification of mammalian meal source in dung beetle gut contents. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 612-615.	0.6	14
52	The Fish Barcode of Life (FISH-BOL) special issue. <i>Mitochondrial DNA</i> , 2011, 22, 1-2.	0.8	13
53	Evolutionary Analyses and Natural Selection of Betaine-Homocysteine S-Methyltransferase (BHMT) and BHMT2 Genes. <i>PLoS ONE</i> , 2015, 10, e0134084.	2.5	13
54	Genomic epidemiology of Lineage 4 <i>Mycobacterium tuberculosis</i> subpopulations in New York City and New Jersey, 1999-2009. <i>BMC Genomics</i> , 2016, 17, 947.	2.9	13

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55	Selective constraint and adaptive potential of West Nile virus within and among naturally infected avian hosts and mosquito vectors. <i>Virus Evolution</i> , 2018, 4, vey013.	4.9	13
56	Cellular and immunological mechanisms influence host-adapted phenotypes in a vector-borne microparasite. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20212087.	2.8	11
57	Population trends for humpback whales ( <i>Megaptera novaeangliae</i> ) foraging in the Francisco Coloane Coastal Marine Protected Area, Magellan Strait, Chile. <i>Marine Mammal Science</i> , 2019, 35, 1212-1231.	1.7	9
58	Using fisherâ€™s contributed secondary fins to fill critical sharkâ€™s fisheries data gaps. <i>Conservation Biology</i> , 2021, 35, 991-1001.	4.7	9
59	Host adaptation drives genetic diversity in a vector-borne disease system. <i>PNAS Nexus</i> , 2023, 2, .	2.6	9
60	Genetic variation in avocado stem weevils ( <i>Copturus aguacatae</i> ) (Coleoptera: Curculionidae) in Mexico. <i>Mitochondrial DNA</i> , 2010, 21, 38-43.	0.8	8
61	Episodic Diversifying Selection Shaped the Genomes of Gibbon Ape Leukemia Virus and Related Gammaretroviruses. <i>Journal of Virology</i> , 2016, 90, 1757-1772.	3.5	8
62	Clusterflock: a flocking algorithm for isolating congruent phylogenomic datasets. <i>GigaScience</i> , 2016, 5, 44.	6.8	7
63	Modeling the eradication of invasive mammals using the sterile male technique. <i>Biological Invasions</i> , 2010, 12, 751-759.	2.4	6
64	Negative Purifying Selection Drives Prion and Doppel Protein Evolution. <i>Journal of Molecular Evolution</i> , 2014, 79, 12-20.	1.9	6
65	Phylogenomic Diversity Elucidates Mechanistic Insights into Lyme Borreliae-Host Association. <i>MSystems</i> , 2022, 7, .	4.1	6
66	Structural evolution of an immune evasion determinant shapes pathogen host tropism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.6	6
67	Combining genetic and distributional approaches to sourcing introduced species: a case study on the Nile monitor ( <i>Varanus niloticus</i> ) in Florida. <i>Royal Society Open Science</i> , 2016, 3, 150619.	2.5	5
68	Biodegradability study of <i>Egeria densa</i> biomass using acid and basic pre-treatments for use in bioprocessing of energy products. <i>Bioresource Technology Reports</i> , 2019, 6, 279-284.	2.8	5
69	Decisions about restorative dental treatment among dentists attending a postgraduate continuing professional development course. <i>British Dental Journal</i> , 2010, 209, 455-459.	1.0	4
70	High-quality YIG films preparation by metallo-organic decomposition and their use to fabricate spintronics nanostructures by focused ion beam. <i>Applied Nanoscience (Switzerland)</i> , 2022, 12, 2389-2396.	3.1	3
71	Wild Birdâ€™s-eye View of Influenza Virus A(H1N1) Phylogenetic Evolution. <i>EcoHealth</i> , 2009, 6, 346-350.	2.0	2
72	The MexBOL initiative. <i>Mitochondrial DNA</i> , 2010, 21, 1-2.	0.8	2

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73	Within-trial cost-effectiveness of lifestyle intervention using a 3-tier shared care approach for pregnancy outcomes in Chinese women with gestational diabetes. PLoS ONE, 2020, 15, e0237738.	2.5	2
74	MTT assay as a viability test of homograft valves. Indian Journal of Thoracic and Cardiovascular Surgery, 1995, 11, 38-41.	0.6	1
75	Building surveying: an introduction. , 2021, , 1-10.		1
76	Zusanli (ST36) Acupoint Injection With Dexamethasone for Chemotherapy-Induced Myelosuppression: A Systematic Review and Meta-Analysis. Frontiers in Oncology, 2021, 11, 684129.	2.9	1
77	Material balance of melts in the Consteel 120-t arc furnace at OAO Ashinskii Metallurgicheskii Zavod. Steel in Translation, 2013, 43, 374-378.	0.3	0
78	1232. Phylogenomics of Enterococcus faecium From South America: Revisiting Worldwide VRE Population Structure. Open Forum Infectious Diseases, 2018, 5, S374-S374.	0.9	0
79	Non-commutative analogues of weak compactness criteria in symmetric spaces. Advances in Operator Theory, 2021, 6, 1.	0.6	0
80	Case Report: Long-Term Survival of a Pediatric Patient With an Intra-Abdominal Undifferentiated Carcinoma of Unknown Primary. Frontiers in Oncology, 2021, 11, 590913.	2.9	0
81	Association between Influenza-like Illnesses and Social Determinants of Health by Census Tract in Houston/Harris County. Online Journal of Public Health Informatics, 2014, 6, .	0.8	0
82	Learning how a tree branches out: A statistical modeling approach. PLoS ONE, 2022, 17, e0274168.	2.5	0
83	Knowledge, Attitudes and Practices About Zika Virus Infection Among Women of Reproductive Age in Central Brooklyn, New York City, USA. Journal of Community Health, 2024, 49, 78-85.	3.9	0
84	Zika Virus Infection Knowledge and Communication Preferences Among Women of Reproductive Age in Central Brooklyn, New York: A Thematic Analysis. Journal of Community Health, 0, , .	3.9	0