

Thierry Wirth

List of Publications by Year in descending order

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75
papers

8,846
citations

109321

35
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91884

69
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84
docs citations

84
times ranked

11225
citing authors

#	ARTICLE	IF	CITATIONS
1	Forecasting <i>Staphylococcus aureus</i> Infections Using Genome-Wide Association Studies, Machine Learning, and Transcriptomic Approaches. <i>MSystems</i> , 2022, 7, .	3.8	3
2	When specialized clones go global. <i>Nature Microbiology</i> , 2021, 6, 1215-1216.	13.3	2
3	Exploring Semi-Quantitative Metagenomic Studies Using Oxford Nanopore Sequencing: A Computational and Experimental Protocol. <i>Genes</i> , 2021, 12, 1496.	2.4	11
4	Emergence and global spread of <i>Listeria monocytogenes</i> main clinical clonal complex. <i>Science Advances</i> , 2021, 7, eabj9805.	10.3	23
5	Applied phyloepidemiology: Detecting drivers of pathogen transmission from genomic signatures using density measures. <i>Evolutionary Applications</i> , 2020, 13, 1513-1525.	3.1	11
6	Population Structure of <i>Mycobacterium bovis</i> in Germany: a Long-Term Study Using Whole-Genome Sequencing Combined with Conventional Molecular Typing Methods. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	10
7	Niche specialization and spread of <i>Staphylococcus capitis</i> involved in neonatal sepsis. <i>Nature Microbiology</i> , 2020, 5, 735-745.	13.3	40
8	Global genome diversity of the <i>Leishmania donovani</i> complex. <i>ELife</i> , 2020, 9, .	6.0	90
9	Presence of the neonatal <i>Staphylococcus capitis</i> outbreak clone (NRCS-A) in prosthetic joint infections. <i>Scientific Reports</i> , 2020, 10, 22389.	3.3	16
10	Longitudinal Outbreak of Multidrug-Resistant Tuberculosis in a Hospital Setting, Serbia. <i>Emerging Infectious Diseases</i> , 2019, 25, 555-558.	4.3	8
11	Emergence of enterovirus D68 clade D1, France, August to November 2018. <i>Eurosurveillance</i> , 2019, 24, .	7.0	32
12	Dispersion et démographie de <i>Mycobacterium tuberculosis</i> dans un contexte de globalisation. , 2019, , 41-49.		0
13	Demographic fluctuation of community-acquired antibiotic-resistant <i>Staphylococcus aureus</i> lineages: potential role of flimsy antibiotic exposure. <i>ISME Journal</i> , 2018, 12, 1879-1894.	9.8	11
14	The invasion biology of the invasive earwig, <i>Forficula auricularia</i> in Australasian ecosystems. <i>Biological Invasions</i> , 2018, 20, 1553-1565.	2.4	18
15	Globalization and Infectious Diseases. , 2018, , 123-137.		3
16	Genes under positive selection in the core genome of pathogenic <i>Bacillus cereus</i> group members. <i>Infection, Genetics and Evolution</i> , 2018, 65, 55-64.	2.3	11
17	Changing patterns of human migrations shaped the global population structure of <i>Mycobacterium tuberculosis</i> in France. <i>Scientific Reports</i> , 2018, 8, 5855.	3.3	10
18	Mice and Men: an Evolutionary History of Lassa Fever. , 2018, , 189-212.		6

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19	Molecular diversity and biennial circulation of enterovirus D68: a systematic screening study in Lyon, France, 2010 to 2016. <i>Eurosurveillance</i> , 2018, 23, .	7.0	50
20	Compensatory evolution drives multidrug-resistant tuberculosis in Central Asia. <i>ELife</i> , 2018, 7, .	6.0	93
21	Strain-specific estimation of epidemic success provides insights into the transmission dynamics of tuberculosis. <i>Scientific Reports</i> , 2017, 7, 45326.	3.3	19
22	Molecular and Functional Characterization of Lymphoid Progenitor Subsets Reveals a Bipartite Architecture of Human Lymphopoiesis. <i>Immunity</i> , 2017, 47, 680-696.e8.	14.3	33
23	The Evolutionary History, Demography, and Spread of the <i>Mycobacterium tuberculosis</i> Complex. , 2017, , 453-473.		0
24	Microbes as Tracers of Past Human Demography and Migrations. , 2017, , 141-165.		0
25	Demography and Intercontinental Spread of the USA300 Community-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> Lineage. <i>MBio</i> , 2016, 7, e02183-15.	4.1	96
26	The Evolutionary History, Demography, and Spread of the <i>Mycobacterium tuberculosis</i> Complex. <i>Microbiology Spectrum</i> , 2016, 4, .	3.0	30
27	Genome-wide mosaicism within <i>Mycobacterium abscessus</i> : evolutionary and epidemiological implications. <i>BMC Genomics</i> , 2016, 17, 118.	2.8	56
28	Massive lineage replacements and cryptic outbreaks of <i>Salmonella</i> Typhi in eastern and southern Africa. <i>Nature Genetics</i> , 2015, 47, 565-567.	21.4	26
29	Evolutionary history and global spread of the <i>Mycobacterium tuberculosis</i> Beijing lineage. <i>Nature Genetics</i> , 2015, 47, 242-249.	21.4	466
30	Conservatism and novelty in the genetic architecture of adaptation in <i>Heliconius</i> butterflies. <i>Heredity</i> , 2015, 114, 515-524.	2.6	50
31	Origin and Evolution of European Community-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2014, 5, e01044-14.	4.1	112
32	Introgressive hybridization and latitudinal admixture clines in North Atlantic eels. <i>BMC Evolutionary Biology</i> , 2014, 14, 61.	3.2	15
33	Whole Genome Sequencing versus Traditional Genotyping for Investigation of a <i>Mycobacterium tuberculosis</i> Outbreak: A Longitudinal Molecular Epidemiological Study. <i>PLoS Medicine</i> , 2013, 10, e1001387.	8.4	425
34	Population Structure and Evidence for Both Clonality and Recombination among Brazilian Strains of the Subgenus <i>Leishmania</i> (Viannia). <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2490.	3.0	40
35	“Epidemic Clones” of <i>Listeria monocytogenes</i> Are Widespread and Ancient Clonal Groups. <i>Journal of Clinical Microbiology</i> , 2013, 51, 3770-3779.	3.9	121
36	The Impact of Human Conflict on the Genetics of <i>Mastomys natalensis</i> and Lassa Virus in West Africa. <i>PLoS ONE</i> , 2012, 7, e37068.	2.5	39

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37	Elucidating Human Migrations by Means of their Pathogens. , 2011, , 173-202.		1
38	Comparative Microsatellite Typing of New World <i>Leishmania infantum</i> Reveals Low Heterogeneity among Populations and Its Recent Old World Origin. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1155.	3.0	154
39	On the mutation rates of spoligotypes and variable numbers of tandem repeat loci of <i>Mycobacterium tuberculosis</i> . <i>Infection, Genetics and Evolution</i> , 2011, 11, 251-252.	2.3	11
40	On the mutation rates of spoligotypes and variable numbers of tandem repeat loci of <i>Mycobacterium tuberculosis</i> : Continued-When tuning matters. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1191.	2.3	4
41	Guns, germs and dogs: On the origin of <i>Leishmania chagasi</i> . <i>Infection, Genetics and Evolution</i> , 2011, 11, 1091-1095.	2.3	56
42	<i>Yersinia pestis</i> genome sequencing identifies patterns of global phylogenetic diversity. <i>Nature Genetics</i> , 2010, 42, 1140-1143.	21.4	504
43	Genetic signatures in an invasive parasite of <i>Anguilla anguilla</i> correlate with differential stock management. <i>Journal of Fish Biology</i> , 2010, 77, 191-210.	1.6	6
44	A Timescale for Evolution, Population Expansion, and Spatial Spread of an Emerging Clone of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>PLoS Pathogens</i> , 2010, 6, e1000855.	4.7	163
45	Pleistocene desiccation in East Africa bottlenecked but did not extirpate the adaptive radiation of Lake Victoria haplochromine cichlid fishes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13404-13409.	7.1	82
46	Population structure of the parasitic nematode <i>Anguillicola crassus</i> , an invader of declining North Atlantic eel stocks. <i>Molecular Ecology</i> , 2008, 17, 3478-3495.	3.9	55
47	Identification of geographically distributed sub-populations of <i>Leishmania (Leishmania) major</i> by microsatellite analysis. <i>BMC Evolutionary Biology</i> , 2008, 8, 183.	3.2	60
48	Origin, Spread and Demography of the <i>Mycobacterium tuberculosis</i> Complex. <i>PLoS Pathogens</i> , 2008, 4, e1000160.	4.7	378
49	Isolation and characterization of 12 dinucleotide microsatellites in the European eel, <i>Anguilla anguilla</i> L., and tests of amplification in other species of eels. <i>Molecular Ecology Resources</i> , 2008, 8, 1382-1385.	4.8	6
50	A New Perspective on <i>Listeria monocytogenes</i> Evolution. <i>PLoS Pathogens</i> , 2008, 4, e1000146.	4.7	518
51	Inferring Patterns of Migration. <i>Methods in Molecular Biology</i> , 2008, 452, 485-506.	0.9	2
52	The rise and spread of a new pathogen: Seroresistant <i>Moraxella catarrhalis</i> . <i>Genome Research</i> , 2007, 17, 1647-1656.	5.5	73
53	Isolation and characterization of short tandem repeats in an invasive swimbladder nematode, parasitic in Atlantic freshwater eels, <i>Anguillicola crassus</i> . <i>Molecular Ecology Notes</i> , 2007, 7, 1051-1053.	1.7	9
54	Genetic diversity of the obligate intracellular bacterium <i>Chlamydomonas pneumoniae</i> by genome-wide analysis of single nucleotide polymorphisms: evidence for highly clonal population structure. <i>BMC Genomics</i> , 2007, 8, 355.	2.8	23

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55	Sex and virulence in <i>Escherichia coli</i> : an evolutionary perspective. <i>Molecular Microbiology</i> , 2006, 60, 1136-1151.	2.5	1,806
56	Population genetics of microbial pathogens estimated from multilocus sequence typing (MLST) data. <i>Infection, Genetics and Evolution</i> , 2006, 6, 97-112.	2.3	135
57	Microsatellite analysis reveals genetic structure of <i>Leishmania tropica</i> . <i>International Journal for Parasitology</i> , 2006, 36, 237-246.	3.1	125
58	Deciphering host migrations and origins by means of their microbes. <i>Molecular Ecology</i> , 2005, 14, 3289-3306.	3.9	77
59	Using Gene-History and Expression Analyses to Assess the Involvement of LGI Genes in Human Disorders. <i>Molecular Biology and Evolution</i> , 2005, 22, 2209-2216.	8.9	19
60	Distinguishing human ethnic groups by means of sequences from <i>Helicobacter pylori</i> : Lessons from Ladakh. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 4746-4751.	7.1	146
61	Mating System and Genetic Variability in the Simultaneously Hermaphroditic Terrestrial Gastropod <i>Balea Perversa</i> on the Baltic Island of Å–land, Sweden. <i>Hereditas</i> , 2004, 126, 199-209.	1.4	23
62	Microevolution and history of the plague bacillus, <i>Yersinia pestis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 17837-17842.	7.1	463
63	Mitochondrial differentiation in a polymorphic land snail: evidence for Pleistocene survival within the boundaries of permafrost. <i>Journal of Evolutionary Biology</i> , 2003, 16, 415-428.	1.7	63
64	Traces of Human Migrations in <i>Helicobacter pylori</i> Populations. <i>Science</i> , 2003, 299, 1582-1585.	12.6	922
65	Decline of North Atlantic eels: a fatal synergy?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, 681-688.	2.6	125
66	Prospective Study of a Serogroup X <i>Neisseria meningitidis</i> Outbreak in Northern Ghana. <i>Journal of Infectious Diseases</i> , 2002, 185, 618-626.	4.0	106
67	Clonal Groupings in Serogroup X <i>Neisseria meningitidis</i> . <i>Emerging Infectious Diseases</i> , 2002, 8, 462-466.	4.3	31
68	Genetic evidence against panmixia in the European eel. <i>Nature</i> , 2001, 409, 1037-1040.	27.8	217
69	Isolation and characterization of microsatellite loci in the yellow perch (<i>Perca flavescens</i>), and cross-species amplification within the family Percidae. <i>Molecular Ecology</i> , 2000, 9, 995-997.	3.9	56
70	Isolation and characterization of microsatellite loci in the land snail <i>Helicella itala</i> , and cross-species amplification within the family Helicidae. <i>Molecular Ecology</i> , 2000, 9, 501-502.	3.9	4
71	Genetic variability in subpopulations of the asp viper (<i>Vipera aspis</i>) in the Swiss Jura mountains: implications for a conservation strategy. <i>Biological Conservation</i> , 2000, 94, 69-77.	4.1	28
72	Directional substitution and evolution of nucleotide content in the cytochrome oxidase II gene in earwigs (dermapteran insects) [Citation]. <i>Molecular Biology and Evolution</i> , 1999, 16, 1645-1653.	8.9	43

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73	Isolation and characterization of microsatellite loci in the walleye (<i>Stizostedion vitreum</i>), and cross-species amplification within the family Percidae. <i>Molecular Ecology</i> , 1999, 8, 1960-1962.	3.9	68
74	Molecular and Reproductive Characterization of Sibling Species in the European Earwig (<i>Forficula</i>) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50	2.3	25
75	MOLECULAR AND REPRODUCTIVE CHARACTERIZATION OF SIBLING SPECIES IN THE EUROPEAN EARWIG (<i>FORFICULA AURICULARIA</i>). <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 260-265.	2.3	33