

Thierry Wirth

List of Publications by Year in descending order

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75
papers

8,846
citations

109321

35
h-index

91884

69
g-index

84
all docs

84
docs citations

84
times ranked

11225
citing authors

#	ARTICLE	IF	CITATIONS
1	Sex and virulence in <i>Escherichia coli</i> : an evolutionary perspective. <i>Molecular Microbiology</i> , 2006, 60, 1136-1151.	2.5	1,806
2	Traces of Human Migrations in <i>Helicobacter pylori</i> Populations. <i>Science</i> , 2003, 299, 1582-1585.	12.6	922
3	A New Perspective on <i>Listeria monocytogenes</i> Evolution. <i>PLoS Pathogens</i> , 2008, 4, e1000146.	4.7	518
4	<i>Yersinia pestis</i> genome sequencing identifies patterns of global phylogenetic diversity. <i>Nature Genetics</i> , 2010, 42, 1140-1143.	21.4	504
5	Evolutionary history and global spread of the <i>Mycobacterium tuberculosis</i> Beijing lineage. <i>Nature Genetics</i> , 2015, 47, 242-249.	21.4	466
6	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
7	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
8	Origin, Spread and Demography of the <i>Mycobacterium tuberculosis</i> Complex. <i>PLoS Pathogens</i> , 2008, 4, e1000160.	4.7	378
9	Genetic evidence against panmixia in the European eel. <i>Nature</i> , 2001, 409, 1037-1040.	27.8	217
10	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
11	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
12	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
13	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
14	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
15	Microsatellite analysis reveals genetic structure of <i>Leishmania tropica</i> . <i>International Journal for Parasitology</i> , 2006, 36, 237-246.	3.1	125
16	“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
17	Origin and Evolution of European Community-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2014, 5, e01044-14.	4.1	112
18	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

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19	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
20	Compensatory evolution drives multidrug-resistant tuberculosis in Central Asia. <i>ELife</i> , 2018, 7, .	6.0	93
21	Global genome diversity of the <i>Leishmania donovani</i> complex. <i>ELife</i> , 2020, 9, .	6.0	90
22	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
23	Deciphering host migrations and origins by means of their microbes. <i>Molecular Ecology</i> , 2005, 14, 3289-3306.	3.9	77
24	The rise and spread of a new pathogen: Seroresistant <i>Moraxella catarrhalis</i> . <i>Genome Research</i> , 2007, 17, 1647-1656.	5.5	73
25	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
26	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
27	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
28	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
29	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
30	Genome-wide mosaicism within <i>Mycobacterium abscessus</i> : evolutionary and epidemiological implications. <i>BMC Genomics</i> , 2016, 17, 118.	2.8	56
31	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
32	Conservatism and novelty in the genetic architecture of adaptation in <i>Heliconius</i> butterflies. <i>Heredity</i> , 2015, 114, 515-524.	2.6	50
33	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
34	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
35	Population Structure and Evidence for Both Clonality and Recombination among Brazilian Strains of the Subgenus <i>Leishmania</i> (Vianna). <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2490.	3.0	40
36	Niche specialization and spread of <i>Staphylococcus capitis</i> involved in neonatal sepsis. <i>Nature Microbiology</i> , 2020, 5, 735-745.	13.3	40

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37	The Impact of Human Conflict on the Genetics of <i>Mastomys natalensis</i> and Lassa Virus in West Africa. PLoS ONE, 2012, 7, e37068.	2.5	39
38	MOLECULAR AND REPRODUCTIVE CHARACTERIZATION OF SIBLING SPECIES IN THE EUROPEAN EARWIG (<i>FORFICULA AURICULARIA</i>). Evolution; International Journal of Organic Evolution, 1998, 52, 260-265.	2.3	33
39	Molecular and Functional Characterization of Lymphoid Progenitor Subsets Reveals a Bipartite Architecture of Human Lymphopoiesis. Immunity, 2017, 47, 680-696.e8.	14.3	33
40	Emergence of enterovirus D68 clade D1, France, August to November 2018. Eurosurveillance, 2019, 24, .	7.0	32
41	Clonal Groupings in Serogroup X <i>Neisseria meningitidis</i> . Emerging Infectious Diseases, 2002, 8, 462-466.	4.3	31
42	The Evolutionary History, Demography, and Spread of the <i>Mycobacterium tuberculosis</i> Complex. Microbiology Spectrum, 2016, 4, .	3.0	30
43	Genetic variability in subpopulations of the asp viper (<i>Vipera aspis</i>) in the Swiss Jura mountains: implications for a conservation strategy. Biological Conservation, 2000, 94, 69-77.	4.1	28
44	Massive lineage replacements and cryptic outbreaks of <i>Salmonella</i> Typhi in eastern and southern Africa. Nature Genetics, 2015, 47, 565-567.	21.4	26
45	Molecular and Reproductive Characterization of Sibling Species in the European Earwig (<i>Forficula</i>) Tj ETQq1 1 0.784314 rgBT/Overlo	2.3	25
46	Mating System and Genetic Variability in the Simultaneously Hermaphroditic Terrestrial Gastropod <i>Balea Perversa</i> on the Baltic Island of Å-land, Sweden. Hereditas, 2004, 126, 199-209.	1.4	23
47	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. BMC Genomics, 2007, 8, 355.	2.8	23
48	Emergence and global spread of <i>Listeria monocytogenes</i> main clinical clonal complex. Science Advances, 2021, 7, eabj9805.	10.3	23
49	Using Gene-History and Expression Analyses to Assess the Involvement of LGI Genes in Human Disorders. Molecular Biology and Evolution, 2005, 22, 2209-2216.	8.9	19
50	Strain-specific estimation of epidemic success provides insights into the transmission dynamics of tuberculosis. Scientific Reports, 2017, 7, 45326.	3.3	19
51	The invasion biology of the invasive earwig, <i>Forficula auricularia</i> in Australasian ecosystems. Biological Invasions, 2018, 20, 1553-1565.	2.4	18
52	Presence of the neonatal <i>Staphylococcus capitis</i> outbreak clone (NRCS-A) in prosthetic joint infections. Scientific Reports, 2020, 10, 22389.	3.3	16
53	Introgressive hybridization and latitudinal admixture clines in North Atlantic eels. BMC Evolutionary Biology, 2014, 14, 61.	3.2	15
54	On the mutation rates of spoligotypes and variable numbers of tandem repeat loci of <i>Mycobacterium tuberculosis</i> . Infection, Genetics and Evolution, 2011, 11, 251-252.	2.3	11

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55	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
56	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
57	Applied phyloepidemiology: Detecting drivers of pathogen transmission from genomic signatures using density measures. <i>Evolutionary Applications</i> , 2020, 13, 1513-1525.	3.1	11
58	Exploring Semi-Quantitative Metagenomic Studies Using Oxford Nanopore Sequencing: A Computational and Experimental Protocol. <i>Genes</i> , 2021, 12, 1496.	2.4	11
59	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
60	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
61	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
62	Longitudinal Outbreak of Multidrug-Resistant Tuberculosis in a Hospital Setting, Serbia. <i>Emerging Infectious Diseases</i> , 2019, 25, 555-558.	4.3	8
63	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
64	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
65	Mice and Men: an Evolutionary History of Lassa Fever. , 2018, , 189-212.		6
66	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
67	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
68	Globalization and Infectious Diseases. , 2018, , 123-137.		3
69	Forecasting <i>Staphylococcus aureus</i> Infections Using Genome-Wide Association Studies, Machine Learning, and Transcriptomic Approaches. <i>MSystems</i> , 2022, 7, .	3.8	3
70	When specialized clones go global. <i>Nature Microbiology</i> , 2021, 6, 1215-1216.	13.3	2
71	Inferring Patterns of Migration. <i>Methods in Molecular Biology</i> , 2008, 452, 485-506.	0.9	2
72	Elucidating Human Migrations by Means of their Pathogens. , 2011, , 173-202.		1

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73	The Evolutionary History, Demography, and Spread of the Mycobacterium tuberculosis Complex. , 2017, , 453-473.		0
74	Microbes as Tracers of Past Human Demography and Migrations. , 2017, , 141-165.		0
75	Dispersion et d'Émographie de Mycobacterium tuberculosis dans un contexte de globalisation. , 2019, , 41-49.		0