

# Sylvain Brisse

## List of Publications by Year in descending order

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228  
papers

22,761  
citations

7096

78  
h-index

10158

140  
g-index

274  
all docs

274  
docs citations

274  
times ranked

18345  
citing authors

#	ARTICLE	IF	CITATIONS
1	Effect of change in vaccine schedule on pertussis epidemiology in France: a modelling and serological study. <i>Lancet Infectious Diseases</i> , The, 2022, 22, 265-273.	9.1	12
2	Genomic evolution of the globally disseminated multidrug-resistant <i>Klebsiella pneumoniae</i> clonal group 147. <i>Microbial Genomics</i> , 2022, 8, .	2.0	22
3	Spontaneous and postsurgical/traumatic <i>Klebsiella pneumoniae</i> meningitis: two distinct clinico-microbiological entities. <i>International Journal of Infectious Diseases</i> , 2022, 114, 185-191.	3.3	3
4	Comparative phylogenomics of ESBL-, AmpC- and carbapenemase-producing <i>Klebsiella pneumoniae</i> originating from companion animals and humans. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 1263-1271.	3.0	18
5	High Prevalence of <i>Klebsiella pneumoniae</i> in European Food Products: a Multicentric Study Comparing Culture and Molecular Detection Methods. <i>Microbiology Spectrum</i> , 2022, 10, e0237621.	3.0	23
6	Multilateral benefit-sharing from digital sequence information will support both science and biodiversity conservation. <i>Nature Communications</i> , 2022, 13, 1086.	12.8	34
7	A curated collection of <i>Klebsiella</i> metabolic models reveals variable substrate usage and gene essentiality. <i>Genome Research</i> , 2022, , .	5.5	10
8	In vitro and in silico parameters for precise cgMLST typing of <i>Listeria monocytogenes</i> . <i>BMC Genomics</i> , 2022, 23, 235.	2.8	7
9	Pertussis surveillance results from a French general practitioner network, France, 2017 to 2020. <i>Eurosurveillance</i> , 2022, 27, .	7.0	5
10	Characterization of <i>Klebsiella pneumoniae</i> isolated from patients suspected of pulmonary or bubonic plague during the Madagascar epidemic in 2017. <i>Scientific Reports</i> , 2022, 12, 6871.	3.3	2
11	Global spatial dynamics and vaccine-induced fitness changes of <i>Bordetella pertussis</i> . <i>Science Translational Medicine</i> , 2022, 14, eabn3253.	12.4	22
12	Transmission of <i>Klebsiella</i> strains and plasmids within and between grey-headed flying fox colonies. <i>Environmental Microbiology</i> , 2022, 24, 4425-4436.	3.8	3
13	In Vitro and In Vivo Assessments of Two Newly Isolated Bacteriophages against an ST13 Urinary Tract Infection <i>Klebsiella pneumoniae</i> . <i>Viruses</i> , 2022, 14, 1079.	3.3	6
14	A Dual Barcoding Approach to Bacterial Strain Nomenclature: Genomic Taxonomy of <i>Klebsiella pneumoniae</i> Strains. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	31
15	Association between the COVID-19 pandemic and pertussis derived from multiple nationwide data sources, France, 2013 to 2020. <i>Eurosurveillance</i> , 2022, 27, .	7.0	11
16	A comprehensive resource for <i>Bordetella</i> genomic epidemiology and biodiversity studies. <i>Nature Communications</i> , 2022, 13, .	12.8	11
17	<i>Corynebacterium diphtheriae</i> Infection in Mahajanga, Madagascar: First Case Report. <i>Journal of Tropical Pediatrics</i> , 2021, 67, .	1.5	4
18	Rapid Genomic Characterization and Global Surveillance of <i>Klebsiella</i> Using Pathogenwatch. <i>Clinical Infectious Diseases</i> , 2021, 73, S325-S335.	5.8	47

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19	Genome of <i>Superficieibacter maynardsmithii</i> , a novel, antibiotic susceptible representative of Enterobacteriaceae. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	3
20	High-Resolution Typing of <i>Staphylococcus epidermidis</i> Based on Core Genome Multilocus Sequence Typing To Investigate the Hospital Spread of Multidrug-Resistant Clones. Journal of Clinical Microbiology, 2021, 59, .	3.9	4
21	Klebsiella MALDI TypeR: a web-based tool for Klebsiella identification based on MALDI-TOF mass spectrometry. Research in Microbiology, 2021, 172, 103835.	2.1	9
22	A Point Prevalence Survey of Antibiotic Resistance in the Irish Environment, 2018–2019. Environment International, 2021, 152, 106466.	10.0	26
23	Ongoing diphtheria outbreak in Yemen: a cross-sectional and genomic epidemiology study. Lancet Microbe, The, 2021, 2, e386-e396.	7.3	26
24	Genomic Epidemiology and Strain Taxonomy of <i>Corynebacterium diphtheriae</i> . Journal of Clinical Microbiology, 2021, 59, e0158121.	3.9	12
25	Evolution of <i>Bordetella pertussis</i> over a 23-year period in France, 1996 to 2018. Eurosurveillance, 2021, 26, .	7.0	15
26	Gastrointestinal carriage of <i>Klebsiella pneumoniae</i> in a general adult population: a cross-sectional study of risk factors and bacterial genomic diversity. Gut Microbes, 2021, 13, 1939599.	9.8	34
27	Cutaneous diphtheria: three case-reports to discuss determinants of re-emergence in resource-rich settings. Emerging Microbes and Infections, 2021, 10, 2300-2302.	6.5	5
28	Emergence and global spread of <i>Listeria monocytogenes</i> main clinical clonal complex. Science Advances, 2021, 7, eabj9805.	10.3	23
29	Population genomics and antimicrobial resistance in <i>Corynebacterium diphtheriae</i> . Genome Medicine, 2020, 12, 107.	8.2	47
30	Low Detection Rate of <i>Bordetella pertussis</i> Using the BioFire FilmArray Respiratory Panel 2plus. Open Forum Infectious Diseases, 2020, 7, ofaa267.	0.9	2
31	<i>Elizabethkingia anophelis meningitis</i> in a traveler returning from the Americas. MÃ©decine Et Maladies Infectieuses, 2020, 51, 503-505.	5.0	2
32	The ZKIR Assay, a Real-Time PCR Method for the Detection of <i>Klebsiella pneumoniae</i> and Closely Related Species in Environmental Samples. Applied and Environmental Microbiology, 2020, 86, .	3.1	15
33	<i>Klebsiella pneumoniae</i> carriage in low-income countries: antimicrobial resistance, genomic diversity and risk factors. Gut Microbes, 2020, 11, 1287-1299.	9.8	48
34	<i>Corynebacterium rouxii</i> sp. nov., a novel member of the diphtheriae species complex. Research in Microbiology, 2020, 171, 122-127.	2.1	45
35	The global meningitis genome partnership. Journal of Infection, 2020, 81, 510-520.	3.3	13
36	Determining Factors for Pertussis Vaccination Policy: A Study in Five EU Countries. Vaccines, 2020, 8, 46.	4.4	7

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37	Characterization of <i>Klebsiella pneumoniae</i> isolates from a mother–child cohort in Madagascar. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1736-1746.	3.0	9
38	Community-acquired infection caused by the uncommon hypervirulent <i>Klebsiella pneumoniae</i> ST66-K2 lineage. <i>Microbial Genomics</i> , 2020, 6, .	2.0	16
39	Detection of OXA-48-like-producing Enterobacterales in Irish recreational water. <i>Science of the Total Environment</i> , 2019, 690, 1-6.	8.0	25
40	Gene Composition as a Potential Barrier to Large Recombinations in the Bacterial Pathogen <i>Klebsiella pneumoniae</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 3240-3251.	2.5	18
41	Description of <i>Klebsiella spallanzanii</i> sp. nov. and of <i>Klebsiella pasteurii</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2019, 10, 2360.	3.5	49
42	Whole genome sequencing reveals resemblance between ESBL-producing and carbapenem resistant <i>Klebsiella pneumoniae</i> isolates from Austrian rivers and clinical isolates from hospitals. <i>Science of the Total Environment</i> , 2019, 662, 227-235.	8.0	60
43	Hypervirulent <i>Listeria monocytogenes</i> clones™ adaption to mammalian gut accounts for their association with dairy products. <i>Nature Communications</i> , 2019, 10, 2488.	12.8	157
44	New Bacteriophages against Emerging Lineages ST23 and ST258 of <i>Klebsiella pneumoniae</i> and Efficacy Assessment in <i>Galleria mellonella</i> Larvae. <i>Viruses</i> , 2019, 11, 411.	3.3	36
45	Comparative Analysis of the Two <i>Acinetobacter baumannii</i> Multilocus Sequence Typing (MLST) Schemes. <i>Frontiers in Microbiology</i> , 2019, 10, 930.	3.5	133
46	An MLST approach to support tracking of plasmids carrying OXA-48-like carbapenemase. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1856-1862.	3.0	16
47	Genus-wide <i>Leptospira</i> core genome multilocus sequence typing for strain taxonomy and global surveillance. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007374.	3.0	98
48	Carriage of a Single Strain of Nontoxigenic <i>Corynebacterium diphtheriae</i> bv. Belfanti () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 <i>Microbiology</i> , 2019, 57, .	3.9	10
49	Hospital effluent: A reservoir for carbapenemase-producing Enterobacterales?. <i>Science of the Total Environment</i> , 2019, 672, 618-624.	8.0	83
50	<i>Bordetella parapertussis</i> Bacteremia: Clinical Expression and Bacterial Genomics. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz122.	0.9	10
51	Description of <i>Klebsiella africanensis</i> sp. nov., <i>Klebsiella variicola</i> subsp. <i>atropicalensis</i> subsp. nov. and <i>Klebsiella variicola</i> subsp. <i>variicola</i> subsp. nov.. <i>Research in Microbiology</i> , 2019, 170, 165-170.	2.1	92
52	Re-emergence of <i>Corynebacterium diphtheriae</i> . <i>Médecine Et Maladies Infectieuses</i> , 2019, 49, 463-466.	5.0	16
53	Core/Whole Genome Multilocus Sequence Typing and Core Genome SNP-Based Typing of OXA-48-Producing <i>Klebsiella pneumoniae</i> Clinical Isolates From Spain. <i>Frontiers in Microbiology</i> , 2019, 10, 2961.	3.5	35
54	Application of whole genome sequencing to query a potential outbreak of <i>Elizabethkingia anophelis</i> in Ontario, Canada. <i>Access Microbiology</i> , 2019, 1, e000017.	0.5	7

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55	Pertussis epidemiology in Tunisian infants and children and characterization of <i>Bordetella pertussis</i> isolates: results of a 9-year surveillance study, 2007 to 2016. <i>Journal of Medical Microbiology</i> , 2019, 68, 241-247.	1.8	14
56	Improved quadruplex real-time PCR assay for the diagnosis of diphtheria. <i>Journal of Medical Microbiology</i> , 2019, 68, 1455-1465.	1.8	32
57	LiSEQ “whole-genome sequencing of a cross-sectional survey of <i>Listeria monocytogenes</i> in ready-to-eat foods and human clinical cases in Europe. <i>Microbial Genomics</i> , 2019, 5, .	2.0	64
58	The speciation and hybridization history of the genus <i>Salmonella</i> . <i>Microbial Genomics</i> , 2019, 5, .	2.0	13
59	Genus-wide <i>Yersinia</i> core-genome multilocus sequence typing for species identification and strain characterization. <i>Microbial Genomics</i> , 2019, 5, .	2.0	31
60	Genome characteristics of <i>Bordetella pertussis</i> isolates from Tunisia. <i>Journal of Medical Microbiology</i> , 2019, 68, 1320-1323.	1.8	2
61	Revisiting the taxonomy of the genus <i>Elizabethkingia</i> using whole-genome sequencing, optical mapping, and MALDI-TOF, along with proposal of three novel <i>Elizabethkingia</i> species: <i>Elizabethkingia bruuniana</i> sp. nov., <i>Elizabethkingia ursingii</i> sp. nov., and <i>Elizabethkingia occulta</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 55-72.	1.7	91
62	Genetic diversity, mobilisation and spread of the yersiniabactin-encoding mobile element ICEKp in <i>Klebsiella pneumoniae</i> populations. <i>Microbial Genomics</i> , 2018, 4, .	2.0	197
63	Complete Genome Sequences of <i>Bordetella pertussis</i> Clinical Isolate FR5810 and Reference Strain Tohama from Combined Oxford Nanopore and Illumina Sequencing. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	11
64	Identification of <i>Klebsiella pneumoniae</i> , <i>Klebsiella quasipneumoniae</i> , <i>Klebsiella variicola</i> and Related Phylogroups by MALDI-TOF Mass Spectrometry. <i>Frontiers in Microbiology</i> , 2018, 9, 3000.	3.5	96
65	Tracking key virulence loci encoding aerobactin and salmochelin siderophore synthesis in <i>Klebsiella pneumoniae</i> . <i>Genome Medicine</i> , 2018, 10, 77.	8.2	153
66	Outbreak of Invasive Wound Mucormycosis in a Burn Unit Due to Multiple Strains of <i>Mucor circinelloides</i> f. <i>circinelloides</i> Resolved by Whole-Genome Sequencing. <i>MBio</i> , 2018, 9, .	4.1	54
67	Population genomics of hypervirulent <i>Klebsiella pneumoniae</i> clonal-group 23 reveals early emergence and rapid global dissemination. <i>Nature Communications</i> , 2018, 9, 2703.	12.8	205
68	Genomic Sequencing of <i>Bordetella pertussis</i> for Epidemiology and Global Surveillance of Whooping Cough. <i>Emerging Infectious Diseases</i> , 2018, 24, 988-994.	4.3	29
69	Rhinoscleroma pathogenesis: The type K3 capsule of <i>Klebsiella rhinoscleromatis</i> is a virulence factor not involved in Mikulicz cells formation. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006201.	3.0	9
70	Description of <i>Klebsiella grimontii</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 377-381.	1.7	51
71	Taxonomic status of <i>Corynebacterium diphtheriae</i> biovar Belfanti and proposal of <i>Corynebacterium belfantii</i> sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3826-3831.	1.7	56
72	Rare <i>Elizabethkingia anophelis</i> meningitis case in a Danish male. <i>JMM Case Reports</i> , 2018, 5, e005163.	1.3	14

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73	Metabolic diversity of the emerging pathogenic lineages of <i>Klebsiella pneumoniae</i> . Environmental Microbiology, 2017, 19, 1881-1898.	3.8	79
74	Evolutionary dynamics and genomic features of the Elizabethkingia anophelis 2015 to 2016 Wisconsin outbreak strain. Nature Communications, 2017, 8, 15483.	12.8	132
75	Metagenomic assessment of the interplay between the environment and the genetic diversification of <i>Acinetobacter</i> . Environmental Microbiology, 2017, 19, 5010-5024.	3.8	24
76	In-vivo loss of carbapenem resistance by extensively drug-resistant <i>Klebsiella pneumoniae</i> during treatment via porin expression modification. Scientific Reports, 2017, 7, 6722.	3.3	25
77	Whole genome-based population biology and epidemiological surveillance of <i>Listeria monocytogenes</i> . Nature Microbiology, 2017, 2, 16185.	13.3	562
78	Enterobacteriaceae. , 2017, , 1565-1578.e2.		10
79	Real-Time Whole-Genome Sequencing for Surveillance of <i>Listeria monocytogenes</i> , France. Emerging Infectious Diseases, 2017, 23, 1462-1470.	4.3	154
80	Diagnosis in France of a Non-Toxigenic tox Gene-Bearing Strain of <i>Corynebacterium diphtheriae</i> in a Young Male Back From Senegal. Open Forum Infectious Diseases, 2017, 4, ofw271.	0.9	11
81	Molecular and epidemiological characterization of carbapenemase-producing Enterobacteriaceae in Norway, 2007 to 2014. PLoS ONE, 2017, 12, e0187832.	2.5	53
82	Comparative genomic analysis of <i>Acinetobacter</i> strains isolated from murine colonic crypts. BMC Genomics, 2017, 18, 525.	2.8	14
83	Genomic analysis of endemic clones of toxigenic and non-toxigenic <i>Corynebacterium diphtheriae</i> in Belarus during and after the major epidemic in 1990s. BMC Genomics, 2017, 18, 873.	2.8	41
84	Diversity, virulence, and antimicrobial resistance of the KPC-producing <i>Klebsiella pneumoniae</i> ST307 clone. Microbial Genomics, 2017, 3, e000110.	2.0	122
85	<i>Citrobacter europaeus</i> sp. nov., isolated from water and human faecal samples. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 170-173.	1.7	30
86	<i>Psychrobacter pasteurii</i> and <i>Psychrobacter piechaudii</i> sp. nov., two novel species within the genus <i>Psychrobacter</i> . International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3192-3197.	1.7	13
87	Liver Abscess Caused by Infection with Community-Acquired <i>Klebsiella quasipneumoniae</i> subsp. <i>quasipneumoniae</i> . Emerging Infectious Diseases, 2016, 22, 529-531.	4.3	46
88	Global phylogeography and evolutionary history of <i>Shigella dysenteriae</i> type 1. Nature Microbiology, 2016, 1, 16027.	13.3	65
89	Molecular Epidemiology of Colonizing and Infecting Isolates of <i>Klebsiella pneumoniae</i> . MSphere, 2016, 1, .	2.9	204
90	Genomic epidemiology and global diversity of the emerging bacterial pathogen <i>Elizabethkingia anophelis</i> . Scientific Reports, 2016, 6, 30379.	3.3	65

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91	<i>Listeria monocytogenes</i> sequence type 1 is predominant in ruminant rhombencephalitis. <i>Scientific Reports</i> , 2016, 6, 36419.	3.3	105
92	Community-acquired meningitis caused by a CG86 hypervirulent <i>Klebsiella pneumoniae</i> strain: first case report in the Caribbean. <i>BMC Infectious Diseases</i> , 2016, 16, 736.	2.9	24
93	Genome-wide mosaicism within <i>Mycobacterium abscessus</i> : evolutionary and epidemiological implications. <i>BMC Genomics</i> , 2016, 17, 118.	2.8	56
94	Emergence of Antimicrobial-Resistant <i>Escherichia coli</i> of Animal Origin Spreading in Humans. <i>Molecular Biology and Evolution</i> , 2016, 33, 898-914.	8.9	65
95	Uncovering <i>Listeria monocytogenes</i> hypervirulence by harnessing its biodiversity. <i>Nature Genetics</i> , 2016, 48, 308-313.	21.4	541
96	Multilocus sequence analysis of the genus <i>Citrobacter</i> and description of <i>Citrobacter pasteurii</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1486-1490.	1.7	50
97	In Silico Analysis of Usher Encoding Genes in <i>Klebsiella pneumoniae</i> and Characterization of Their Role in Adhesion and Colonization. <i>PLoS ONE</i> , 2015, 10, e0116215.	2.5	37
98	Exploring the Diversity of <i>Listeria monocytogenes</i> Biofilm Architecture by High-Throughput Confocal Laser Scanning Microscopy and the Predominance of the Honeycomb-Like Morphotype. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1813-1819.	3.1	129
99	Association of Tellurite Resistance with Hypervirulent Clonal Groups of <i>Klebsiella pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 1380-1382.	3.9	49
100	<i>Acinetobacter seifertii</i> sp. nov., a member of the <i>Acinetobacter calcoaceticus</i> "Acinetobacter baumannii" complex isolated from human clinical specimens. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 934-942.	1.7	137
101	Clonogrouping, a Rapid Multiplex PCR Method for Identification of Major Clones of <i>Listeria monocytogenes</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 3355-3358.	3.9	11
102	Tracking Nosocomial <i>Klebsiella pneumoniae</i> Infections and Outbreaks by Whole-Genome Analysis: Small-Scale Italian Scenario within a Single Hospital. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2861-2868.	3.9	71
103	Genomic analysis of diversity, population structure, virulence, and antimicrobial resistance in <i>Klebsiella pneumoniae</i> , an urgent threat to public health. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3574-81.	7.1	942
104	Phenotypic and genotypic characteristics of <i>Listeria monocytogenes</i> strains isolated during 2011-2014 from different food matrices in Switzerland. <i>Food Control</i> , 2015, 57, 321-326.	5.5	110
105	Phylogenetic lineages, clones and $\beta$ -lactamases in an international collection of <i>Klebsiella oxytoca</i> isolates non-susceptible to expanded-spectrum cephalosporins. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, dkv273.	3.0	24
106	Differential contribution of AcrAB and OqxAB efflux pumps to multidrug resistance and virulence in <i>Klebsiella pneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 81-88.	3.0	93
107	AlienTrimmer removes adapter oligonucleotides with high sensitivity in short-insert paired-end reads. Commentary on Turner (2014) Assessment of insert sizes and adapter content in FASTQ data from NexteraXT libraries. <i>Frontiers in Genetics</i> , 2014, 5, 130.	2.3	36
108	Draft Genome Sequence of <i>Campylobacter coli</i> Strain IPSID-1 Isolated from a Patient with Immunoproliferative Small Intestinal Disease. <i>Genome Announcements</i> , 2014, 2, .	0.8	4



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109	Genomic Definition of Hypervirulent and Multidrug-Resistant <i>Klebsiella pneumoniae</i> Clonal Groups. <i>Emerging Infectious Diseases</i> , 2014, 20, 1812-1820.	4.3	409
110	Multicenter Outbreak of Infections by <i>Saprochaete clavata</i> , an Unrecognized Opportunistic Fungal Pathogen. <i>MBio</i> , 2014, 5, .	4.1	75
111	Comparison of Widely Used <i>Listeria monocytogenes</i> Strains EGD, 10403S, and EGD-e Highlights Genomic Differences Underlying Variations in Pathogenicity. <i>MBio</i> , 2014, 5, e00969-14.	4.1	201
112	Characterization of <i>Listeria monocytogenes</i> Strains Isolated During 2011–2013 from Human Infections in Switzerland. <i>Foodborne Pathogens and Disease</i> , 2014, 11, 753-758.	1.8	92
113	Comparative analysis of <i>Klebsiella pneumoniae</i> genomes identifies a phospholipase D family protein as a novel virulence factor. <i>BMC Biology</i> , 2014, 12, 41.	3.8	132
114	Patterns of selection on <i>Plasmodium falciparum</i> erythrocyte-binding antigens after the colonization of the New World. <i>Molecular Ecology</i> , 2014, 23, 1979-1993.	3.9	8
115	Multilocus sequence typing scheme for the <i>Mycobacterium abscessus</i> complex. <i>Research in Microbiology</i> , 2014, 165, 82-90.	2.1	49
116	Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Exhibit Variability in Capsular Polysaccharide and Capsule Associated Virulence Traits. <i>Journal of Infectious Diseases</i> , 2014, 210, 803-813.	4.0	123
117	<i>Leptospira mayottensis</i> sp. nov., a pathogenic species of the genus <i>Leptospira</i> isolated from humans. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 4061-4067.	1.7	112
118	Description of <i>Klebsiella quasipneumoniae</i> sp. nov., isolated from human infections, with two subspecies, <i>Klebsiella quasipneumoniae</i> subsp. <i>quasipneumoniae</i> subsp. nov. and <i>Klebsiella quasipneumoniae</i> subsp. <i>similipneumoniae</i> subsp. nov., and demonstration that <i>Klebsiella singaporensis</i> is a junior heterotypic synonym of <i>Klebsiella variicola</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 3146-3152.	1.7	188
119	Multiplex PCR for Detection of Seven Virulence Factors and K1/K2 Capsular Serotypes of <i>Klebsiella pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2014, 52, 4377-4380.	3.9	188
120	Development of a multiplex PCR assay for identification of <i>Klebsiella pneumoniae</i> hypervirulent clones of capsular serotype K2. <i>Journal of Medical Microbiology</i> , 2014, 63, 1608-1614.	1.8	46
121	Complete Nucleotide Sequence of Two Multidrug-Resistant IncR Plasmids from <i>Klebsiella pneumoniae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4207-4210.	3.2	54
122	Resequencing Microarray Technology for Genotyping Human Papillomavirus in Cervical Smears. <i>PLoS ONE</i> , 2014, 9, e109301.	2.5	3
123	<i>Klebsiella variicola</i> Is a Frequent Cause of Bloodstream Infection in the Stockholm Area, and Associated with Higher Mortality Compared to <i>K. pneumoniae</i> . <i>PLoS ONE</i> , 2014, 9, e113539.	2.5	143
124	Molecular Epidemiology of Carbapenem Non-Susceptible <i>Acinetobacter baumannii</i> in France. <i>PLoS ONE</i> , 2014, 9, e115452.	2.5	31
125	AlienTrimmer: A tool to quickly and accurately trim off multiple short contaminant sequences from high-throughput sequencing reads. <i>Genomics</i> , 2013, 102, 500-506.	2.9	195
126	<i>wzi</i> Gene Sequencing, a Rapid Method for Determination of Capsular Type for <i>Klebsiella</i> Strains. <i>Journal of Clinical Microbiology</i> , 2013, 51, 4073-4078.	3.9	292



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127	Development of variable number of tandem repeats typing schemes for <i>Ralstonia solanacearum</i> , the agent of bacterial wilt, banana Moko disease and potato brown rot. <i>Journal of Microbiological Methods</i> , 2013, 92, 366-374.	1.6	50
128	Genomic analysis of smooth tubercle bacilli provides insights into ancestry and pathoadaptation of <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2013, 45, 172-179.	21.4	264
129	Complete Nucleotide Sequence of the First KPC-2- and SHV-12-Encoding IncX Plasmid, pKpS90, from <i>Klebsiella pneumoniae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 618-620.	3.2	41
130	<i>Klebsiella pneumoniae</i> resistant to third-generation cephalosporins in five African and two Vietnamese major towns: multiclonal population structure with two major international clonal groups, CG15 and CG258. <i>Clinical Microbiology and Infection</i> , 2013, 19, 349-355.	6.0	106
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