

# Patrice Francois

## List of Publications by Year in descending order

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Version: 2024-02-01

271  
papers

17,794  
citations

13827

67  
h-index

17546

121  
g-index

287  
all docs

287  
docs citations

287  
times ranked

18994  
citing authors

#	ARTICLE	IF	CITATIONS
1	Two-Component Systems of <i>S. aureus</i> : Signaling and Sensing Mechanisms. <i>Genes</i> , 2022, 13, 34.	1.0	29
2	Transcriptomic Analysis of <i>E. coli</i> after Exposure to a Sublethal Concentration of Hydrogen Peroxide Revealed a Coordinated Up-Regulation of the Cysteine Biosynthesis Pathway. <i>Antioxidants</i> , 2022, 11, 655.	2.2	12
3	Comparative genomics analysis of two <i>Helicobacterium</i> strains co-isolated with <i>Staphylococcus aureus</i> from diabetic foot ulcers. <i>Genomics</i> , 2022, 114, 110365.	1.3	3
4	Student characteristics associated with interpersonal skills in medical consultations. <i>BMC Medical Education</i> , 2022, 22, 338.	1.0	4
5	An interventional quasi-experimental study to evaluate the impact of a rapid screening strategy in improving control of nosocomial extended-spectrum beta-lactamase-producing Enterobacterales and carbapenemase-producing organisms in critically ill patients. <i>Critical Care</i> , 2022, 26, .	2.5	1
6	12/11phiA Prophage Domestication Is Associated with Autoaggregation and Increased Ability to Produce Biofilm in <i>Streptococcus agalactiae</i> . <i>Microorganisms</i> , 2021, 9, 1112.	1.6	2
7	Co-Carriage of Metal and Antibiotic Resistance Genes in Sewage Associated Staphylococci. <i>Genes</i> , 2021, 12, 1473.	1.0	6
8	Hydrogen Peroxide Affects Growth of <i>S. aureus</i> Through Downregulation of Genes Involved in Pyrimidine Biosynthesis. <i>Frontiers in Immunology</i> , 2021, 12, 673985.	2.2	10
9	<i>Staphylococcus aureus</i> Transcriptome Data and Metabolic Modelling Investigate the Interplay of Ser/Thr Kinase PknB, Its Phosphatase Stp, the glmR/yvck Regulon and the cdaA Operon for Metabolic Adaptation. <i>Microorganisms</i> , 2021, 9, 2148.	1.6	4
10	Epidemiology of ESBL-producing <i>Escherichia coli</i> from repeated prevalence studies over 11 years in a long-term-care facility. <i>Antimicrobial Resistance and Infection Control</i> , 2021, 10, 148.	1.5	16
11	The <i>Staphylococcus aureus</i> CC398 Lineage: An Evolution Driven by the Acquisition of Prophages and Other Mobile Genetic Elements. <i>Genes</i> , 2021, 12, 1752.	1.0	14
12	Phylogeographical Analysis Reveals the Historic Origin, Emergence, and Evolutionary Dynamics of Methicillin-Resistant <i>Staphylococcus aureus</i> ST228. <i>Frontiers in Microbiology</i> , 2020, 11, 2063.	1.5	6
13	The structure of the antimicrobial human cathelicidin LL-37 shows oligomerization and channel formation in the presence of membrane mimics. <i>Scientific Reports</i> , 2020, 10, 17356.	1.6	54
14	Impact of the Novel Prophage $\phi$ SA169 on Persistent Methicillin-Resistant <i>Staphylococcus aureus</i> Endovascular Infection. <i>MSystems</i> , 2020, 5, .	1.7	5
15	Comparative Transcriptomic and Functional Assessments of Linezolid-Responsive Small RNA Genes in <i>Staphylococcus aureus</i> . <i>MSystems</i> , 2020, 5, .	1.7	7
16	Influenza A viruses limit NLRP3 complex formation and pyroptosis in human macrophages. <i>EMBO Reports</i> , 2020, 21, e50421.	2.0	27
17	Respiratory tissue-associated commensal bacteria offer therapeutic potential against pneumococcal colonization. <i>ELife</i> , 2020, 9, .	2.8	22
18	fbl-Typing of <i>Staphylococcus lugdunensis</i> : A Frontline Tool for Epidemiological Studies, but Not Predictive of Fibrinogen Binding Ability. <i>Frontiers in Microbiology</i> , 2019, 10, 1109.	1.5	9

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19	Inactivation of <i>farR</i> Causes High Rhodomyrtone Resistance and Increased Pathogenicity in <i>Staphylococcus aureus</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1157.	1.5	14
20	Temperate Prophages Increase Bacterial Adhesin Expression and Virulence in an Experimental Model of Endocarditis Due to <i>Staphylococcus aureus</i> From the CC398 Lineage. <i>Frontiers in Microbiology</i> , 2019, 10, 742.	1.5	22
21	Prevalence and characterization of <i>Staphylococcus aureus</i> in wastewater treatment plants by whole genomic sequencing. <i>Water Research</i> , 2019, 158, 193-202.	5.3	19
22	A multifaceted small <i>scp</i> RNA modulates gene expression upon glucose limitation in <i>Staphylococcus aureus</i> . <i>EMBO Journal</i> , 2019, 38, .	3.5	44
23	2142. Comparison of Molecular-Based vs. Conventional Culture-Based Screening Methods for Detection of Carriers of Extended-Spectrum $\beta$ -Lactamases (ESBL) and Carbapenemases-Producing Enterobacteriaceae (CPE). <i>Open Forum Infectious Diseases</i> , 2019, 6, S726-S726.	0.4	1
24	Comparative Genome Analysis of <i>Staphylococcus lugdunensis</i> Shows Clonal Complex-Dependent Diversity of the Putative Virulence Factor, <i>ess</i> /Type VII Locus. <i>Frontiers in Microbiology</i> , 2019, 10, 2479.	1.5	30
25	<i>YpdA</i> , a putative bacillithiol disulfide reductase, contributes to cellular redox homeostasis and virulence in <i>Staphylococcus aureus</i> . <i>Molecular Microbiology</i> , 2019, 111, 1039-1056.	1.2	29
26	The Polycyclic Polyprenylated Acylphloroglucinol Antibiotic PPAP 23 Targets the Membrane and Iron Metabolism in <i>Staphylococcus aureus</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 14.	1.5	22
27	Antibiotics Stimulate Formation of Vesicles in <i>Staphylococcus aureus</i> in both Phage-Dependent and -Independent Fashions and via Different Routes. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	86
28	Differential expression of hemoglobin receptor, <i>HmbR</i> , between carriage and invasive isolates of <i>Neisseria meningitidis</i> contributes to virulence: lessons from a clonal outbreak. <i>Virulence</i> , 2018, 9, 923-929.	1.8	9
29	Differential daptomycin resistance development in <i>Staphylococcus aureus</i> strains with active and mutated <i>gra</i> regulatory systems. <i>International Journal of Medical Microbiology</i> , 2018, 308, 335-348.	1.5	38
30	Analysis of the prophages carried by human infecting isolates provides new insight into the evolution of Group B <i>Streptococcus</i> species. <i>Clinical Microbiology and Infection</i> , 2018, 24, 514-521.	2.8	21
31	A Novel Mechanism of Inactivating Antibacterial Nitro Compounds in the Human Pathogen <i>Staphylococcus aureus</i> by Overexpression of a NADH-Dependent Flavin Nitroreductase. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	10
32	Small RNA <i>teg49</i> Is Derived from a <i>sarA</i> Transcript and Regulates Virulence Genes Independent of <i>SarA</i> in <i>Staphylococcus aureus</i> . <i>Infection and Immunity</i> , 2018, 86, .	1.0	31
33	Orbitofrontal pseudotumour in young adult. <i>Journal of Stomatology, Oral and Maxillofacial Surgery</i> , 2018, 119, 529-531.	0.5	0
34	Multiple-Locus Variable Number Tandem Repeat Analysis (MLVA) and Tandem Repeat Sequence Typing (TRST), helpful tools for subtyping <i>Staphylococcus lugdunensis</i> . <i>Scientific Reports</i> , 2018, 8, 11669.	1.6	20
35	Genetic Adaptation of a Mevalonate Pathway Deficient Mutant in <i>Staphylococcus aureus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1539.	1.5	7
36	Molecular characterization of fluoroquinolones, macrolides, and imipenem resistance in <i>Haemophilus influenzae</i> : analysis of the mutations in QRDRs and assessment of the extent of the <i>AcrAB-TolC</i> -mediated resistance. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2018, 37, 2201-2210.	1.3	18

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37	Clonal or not clonal? Investigating hospital outbreaks of KPC-producing <i>Klebsiella pneumoniae</i> with whole-genome sequencing. <i>Clinical Microbiology and Infection</i> , 2017, 23, 470-475.	2.8	35
38	Bypassing the Restriction System To Improve Transformation of <i>Staphylococcus epidermidis</i> . <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	22
39	Impact of Exposure of Methicillin-Resistant <i>Staphylococcus aureus</i> to Polyhexanide <i>In Vitro</i> and <i>In Vivo</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	33
40	Structural remodeling and oligomerization of human cathelicidin on membranes suggest fibril-like structures as active species. <i>Scientific Reports</i> , 2017, 7, 15371.	1.6	51
41	Prophages and adaptation of <i>Staphylococcus aureus</i> ST398 to the human clinic. <i>BMC Genomics</i> , 2017, 18, 133.	1.2	47
42	Rapid identification of ST131 <i>Escherichia coli</i> by a novel multiplex real-time allelic discrimination assay. <i>Journal of Microbiological Methods</i> , 2017, 140, 12-14.	0.7	2
43	Antimicrobial activity of ceftaroline against methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) isolates collected in 2013â€“2014 at the Geneva University Hospitals. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2017, 36, 343-350.	1.3	15
44	Imipenem heteroresistance in nontypeable <i>Haemophilus influenzae</i> is linked to a combination of altered PBP3, slow drug influx and direct efflux regulation. <i>Clinical Microbiology and Infection</i> , 2017, 23, 118.e9-118.e19.	2.8	26
45	Development of in vitro resistance to chitosan is related to changes in cell envelope structure of <i>Staphylococcus aureus</i> . <i>Carbohydrate Polymers</i> , 2017, 157, 146-155.	5.1	25
46	A Potential New Human Pathogen Belonging to <i>Helicobacter</i> Genus, Identified in a Bloodstream Infection. <i>Frontiers in Microbiology</i> , 2017, 8, 2533.	1.5	10
47	Emergence of <i>bla</i> <sub>NDM-7</sub> â€“Producing <i>Enterobacteriaceae</i> in Gabon, 2016. <i>Emerging Infectious Diseases</i> , 2017, 23, 356-358.	2.0	23
48	Management and investigation of a <i>Serratia marcescens</i> outbreak in a neonatal unit in Switzerland â€“ the role of hand hygiene and whole genome sequencing. <i>Antimicrobial Resistance and Infection Control</i> , 2017, 6, 125.	1.5	26
49	Transcriptional Modulation of Penicillin-Binding Protein 1b, Outer Membrane Protein P2 and Efflux Pump (AcrAB-TolC) during Heat Stress Is Correlated to Enhanced Bactericidal Action of Imipenem on Non-typeable <i>Haemophilus influenzae</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2676.	1.5	8
50	The TIR Homologue Lies near Resistance Genes in <i>Staphylococcus aureus</i> , Coupling Modulation of Virulence and Antimicrobial Susceptibility. <i>PLoS Pathogens</i> , 2017, 13, e1006092.	2.1	30
51	Determinants of Successful Methicillin-Resistant <i>Staphylococcus aureus</i> Decolonization. <i>Infection Control and Hospital Epidemiology</i> , 2016, 37, 732-736.	1.0	0
52	Enigmatic occurrence of NDM-7 enzyme in the community. <i>International Journal of Antimicrobial Agents</i> , 2016, 47, 505-507.	1.1	9
53	Gut microbiota analysis reveals a marked shift to bifidobacteria by a starter infant formula containing a synbiotic of bovine milkâ€“derived oligosaccharides and <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> â€“...CNCM Iâ€“3446. <i>Environmental Microbiology</i> , 2016, 18, 2185-2195.	1.8	68
54	Reply to Planet et al. <i>Journal of Infectious Diseases</i> , 2016, 214, 1610-1611.	1.9	0

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55	Assessment of the contribution of morbidity and mortality conferences to quality and safety improvement: a survey of participants'™ perceptions. BMC Health Services Research, 2016, 16, 176.	0.9	35
56	Randomized, placebo-controlled, double-blind clinical trial to evaluate the efficacy of polyhexanide for topical decolonization of MRSA carriers. Journal of Antimicrobial Chemotherapy, 2016, 71, 531-538.	1.3	19
57	Characterization of RNA Helicase CshA and Its Role in Protecting mRNAs and Small RNAs of Staphylococcus aureus Strain Newman. Infection and Immunity, 2016, 84, 833-844.	1.0	10
58	Daptomycin Tolerance in the Staphylococcus aureus pitA6 Mutant Is Due to Upregulation of the <i>hdt</i> Operon. Antimicrobial Agents and Chemotherapy, 2016, 60, 2684-2691.	1.4	32
59	Comparative Genomics of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Shows the Emergence of Clone ST8-USA300 in Geneva, Switzerland. Journal of Infectious Diseases, 2016, 213, 1370-1379.	1.9	43
60	Comparative Genomics Analysis of Streptococcus tigurinus Strains Identifies Genetic Elements Specifically and Uniquely Present in Highly Virulent Strains. PLoS ONE, 2016, 11, e0160554.	1.1	7
61	Randomized, placebo-controlled, double-blind clinical trial to evaluate the efficacy of polyhexanide for topical decolonization of methicillin-resistant Staphylococcus aureus (MRSA) carriers. Antimicrobial Resistance and Infection Control, 2015, 4, .	1.5	0
62	In vitro evidence for the anti-staphylococcal activity of a cationic polymer compound—preliminary results. Antimicrobial Resistance and Infection Control, 2015, 4, .	1.5	2
63	Characteristics of morbidity and mortality conferences associated with the implementation of patient safety improvement initiatives, an observational study. BMC Health Services Research, 2015, 16, 35.	0.9	23
64	Determinants of successful mrsa decolonization among patients included in a clinical trial of polyhexanide. Antimicrobial Resistance and Infection Control, 2015, 4, .	1.5	1
65	Comparative genomics to investigate the emergence of community-associated methicillin-resistant Staphylococcus aureus (CA-MRSA) USA300 clone in Geneva, Switzerland. Antimicrobial Resistance and Infection Control, 2015, 4, .	1.5	0
66	Bacterial contamination of the hands of intensive care unit staff during respiratory tract care: preliminary results. Antimicrobial Resistance and Infection Control, 2015, 4, .	1.5	0
67	Noma disease: 10 years of research in the quest of a microbial etiology. Antimicrobial Resistance and Infection Control, 2015, 4, .	1.5	0
68	Lactic Acid Bacteria Isolated from Bovine Mammary Microbiota: Potential Allies against Bovine Mastitis. PLoS ONE, 2015, 10, e0144831.	1.1	106
69	Modelling antibiotic and cytotoxic isoquinoline effects in Staphylococcus aureus, Staphylococcus epidermidis and mammalian cells. International Journal of Medical Microbiology, 2015, 305, 96-109.	1.5	30
70	Secular trends of methicillin-resistant Staphylococcus aureus (MRSA) at Geneva University Hospitals (HUG) over a 14-year period. Antimicrobial Resistance and Infection Control, 2015, 4, .	1.5	2
71	Breastfeeding Assessment Score: Systematic Review and Meta-analysis. Pediatrics, 2015, 135, e1276-e1285.	1.0	10
72	Staphylococcus epidermidis SrrAB Regulates Bacterial Growth and Biofilm Formation Differently under Oxidic and Microaerobic Conditions. Journal of Bacteriology, 2015, 197, 459-476.	1.0	52

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73	Ampicillin-resistant <i>Haemophilus influenzae</i> isolates in Geneva: serotype, antimicrobial susceptibility, and $\beta$ -lactam resistance mechanisms. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2015, 34, 1937-1945.	1.3	15
74	Collateral damage from oral ciprofloxacin versus nitrofurantoin in outpatients with urinary tract infections: a culture-free analysis of gut microbiota. <i>Clinical Microbiology and Infection</i> , 2015, 21, 344.e1-344.e11.	2.8	110
75	Diagnosis of Whooping Cough in Switzerland: Differentiating <i>Bordetella pertussis</i> from <i>Bordetella holmesii</i> by Polymerase Chain Reaction. <i>PLoS ONE</i> , 2014, 9, e88936.	1.1	25
76	Importance of Bacillithiol in the Oxidative Stress Response of <i>Staphylococcus aureus</i> . <i>Infection and Immunity</i> , 2014, 82, 316-332.	1.0	70
77	Fine-tuned characterization of <i>Staphylococcus aureus</i> Newbould 305, a strain associated with mild and chronic mastitis in bovines. <i>Veterinary Research</i> , 2014, 45, 106.	1.1	34
78	Noma Affected Children from Niger Have Distinct Oral Microbial Communities Based on High-Throughput Sequencing of 16S rRNA Gene Fragments. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3240.	1.3	14
79	Emergence of a novel subpopulation of CC398 <i>Staphylococcus aureus</i> infecting animals is a serious hazard for humans. <i>Frontiers in Microbiology</i> , 2014, 5, 652.	1.5	28
80	Mupirocin-Induced Mutations in <i>ileS</i> in Various Genetic Backgrounds of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Journal of Clinical Microbiology</i> , 2014, 52, 3749-3754.	1.8	22
81	Genome Sequences of Sequence Type 45 (ST45) Persistent Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) Bacteremia Strain 300-169 and ST45 Resolving MRSA Bacteremia Strain 301-188. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
82	Microbiome of prebiotic-treated mice reveals novel targets involved in host response during obesity. <i>ISME Journal</i> , 2014, 8, 2116-2130.	4.4	491
83	GdpS contributes to <i>Staphylococcus aureus</i> biofilm formation by regulation of eDNA release. <i>International Journal of Medical Microbiology</i> , 2014, 304, 284-299.	1.5	23
84	<i>Pneumocystis jirovecii</i> (Pj) quantitative PCR to differentiate Pj pneumonia from Pj colonization in immunocompromised patients. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2014, 33, 331-336.	1.3	61
85	De novo finished 2.8 Mbp <i>Staphylococcus aureus</i> genome assembly from 100 bp short and long range paired-end reads. <i>Bioinformatics</i> , 2014, 30, 40-49.	1.8	50
86	Proteomic Approach to Investigate Pathogenicity and Metabolism of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Methods in Molecular Biology</i> , 2014, 1085, 231-250.	0.4	2
87	The importance of regulatory RNAs in <i>Staphylococcus aureus</i> . <i>Infection, Genetics and Evolution</i> , 2014, 21, 616-626.	1.0	41
88	Generation of a vancomycin-intermediate <i>Staphylococcus aureus</i> (VISA) strain by two amino acid exchanges in <i>VraS</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 3190-3198.	1.3	28
89	Contribution of <i>teg49</i> Small RNA in the 5' Upstream Transcriptional Region of <i>sarA</i> to Virulence in <i>Staphylococcus aureus</i> . <i>Infection and Immunity</i> , 2014, 82, 4369-4379.	1.0	36
90	A genomic perspective on a new bacterial genus and species from the <i>Alcaligenaceae</i> family, <i>Basilea psittacipulmonis</i> . <i>BMC Genomics</i> , 2014, 15, 169.	1.2	10

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91	Antibiotic susceptibility and molecular epidemiology of Pantona€“Valentine leukocidin-positive methicillin-resistant <i>Staphylococcus aureus</i> : An international survey. <i>Journal of Global Antimicrobial Resistance</i> , 2014, 2, 43-47.	0.9	6
92	Characterization of <i>Streptococcus tigurinus</i> Small-Colony Variants Causing Prosthetic Joint Infection by Comparative Whole-Genome Analyses. <i>Journal of Clinical Microbiology</i> , 2014, 52, 467-474.	1.8	23
93	Antibacterial Efficacy of Accelerated Photoactivated Chromophore for Keratitisa€“Corneal Collagen Cross-linking (PACK-CXL). <i>Journal of Refractive Surgery</i> , 2014, 30, 850-854.	1.1	53
94	Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> bv. <i>diacetylactis</i> LD61. <i>Genome Announcements</i> , 2014, 2, .	0.8	10
95	P053: Secular trends of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) at Geneva University Hospitals (HUG) over a 12-year period. <i>Antimicrobial Resistance and Infection Control</i> , 2013, 2, .	1.5	0
96	CC9 Livestock-Associated <i>Staphylococcus aureus</i> Emerges in Bloodstream Infections in French Patients Unconnected With Animal Farming. <i>Clinical Infectious Diseases</i> , 2013, 56, e83-e86.	2.9	9
97	Analysis of prophages harbored by the human-adapted subpopulation of <i>Staphylococcus aureus</i> CC398. <i>Infection, Genetics and Evolution</i> , 2013, 18, 299-308.	1.0	42
98	A <i>de novo</i> designed antimicrobial peptide with activity against multiresistant <i>Staphylococcus aureus</i> acting on RsbW kinase. <i>FASEB Journal</i> , 2013, 27, 4476-4488.	0.2	21
99	Analysis of the Small RNA Transcriptional Response in Multidrug-Resistant <i>Staphylococcus aureus</i> after Antimicrobial Exposure. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3864-3874.	1.4	84
100	Rapid Screening and Identification of Methicillin-Resistant <i>Staphylococcus aureus</i> . , 2013, , 587-603.		1
101	Risk factors for noma disease: a 6-year, prospective, matched case-control study in Niger. <i>The Lancet Global Health</i> , 2013, 1, e87-e96.	2.9	58
102	Bacterial genome evolution within a clonal population: from <i>in vitro</i> investigations to <i>in vivo</i> observations. <i>Future Microbiology</i> , 2013, 8, 661-674.	1.0	4
103	A correlative analysis of epidemiologic and molecular characteristics of methicillin-resistant <i>Staphylococcus aureus</i> clones from diverse geographic locations with virulence measured by a <i>Caenorhabditis elegans</i> host model. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2013, 32, 33-42.	1.3	8
104	Functional genomics of microbial pathogens. <i>Briefings in Functional Genomics</i> , 2013, 12, 289-290.	1.3	3
105	Whole-Genome Sequences of <i>Streptococcus tigurinus</i> Type Strain AZ_3a and <i>S. tigurinus</i> 1366, a Strain Causing Prosthetic Joint Infection. <i>Genome Announcements</i> , 2013, 1, .	0.8	12
106	Whole-Genome Sequences of <i>Staphylococcus aureus</i> ST398 Strains of Animal Origin. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
107	Whole-Genome Sequence of the Ancestral Animal-Borne ST398 <i>Staphylococcus aureus</i> Strain S123. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
108	The CshA DEAD-box RNA helicase is important for quorum sensing control in <i>Staphylococcus aureus</i> . <i>RNA Biology</i> , 2013, 10, 157-165.	1.5	60

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109	Microarray Analysis of Microbiota of Gingival Lesions in Noma Patients. PLoS Neglected Tropical Diseases, 2013, 7, e2453.	1.3	28
110	Functional genomics of microbial pathogens. Briefings in Functional Genomics, 2013, 12, 548-548.	1.3	0
111	Effects of amoxicillin treatment on the salivary microbiota in children with acute otitis media. Clinical Microbiology and Infection, 2013, 19, e335-e342.	2.8	36
112	Whole-Genome Sequences of Two Staphylococcus aureus ST398 Strains of Human Origin, S94 and S100. Genome Announcements, 2013, 1, .	0.8	7
113	Human-to-Bovine Jump of Staphylococcus aureus CC8 Is Associated with the Loss of a $\hat{I}^2$ -Hemolysin Converting Prophage and the Acquisition of a New Staphylococcal Cassette Chromosome. PLoS ONE, 2013, 8, e58187.	1.1	63
114	Comparison of DNA Extraction Methods in Analysis of Salivary Bacterial Communities. PLoS ONE, 2013, 8, e67699.	1.1	76
115	Impact of Fluorescein on the Antimicrobial Efficacy of Photoactivated Riboflavin in Corneal Collagen Cross-linking. Journal of Refractive Surgery, 2013, 29, 842-845.	1.1	22
116	The Stringent Response of Staphylococcus aureus and Its Impact on Survival after Phagocytosis through the Induction of Intracellular PSMs Expression. PLoS Pathogens, 2012, 8, e1003016.	2.1	209
117	Global Analysis of the Staphylococcus aureus Response to Mupirocin. Antimicrobial Agents and Chemotherapy, 2012, 56, 787-804.	1.4	88
118	Genome Sequence of Staphylococcus aureus Newbould 305, a Strain Associated with Mild Bovine Mastitis. Journal of Bacteriology, 2012, 194, 6292-6293.	1.0	29
119	High Prevalence of Isolates with Reduced Glycopeptide Susceptibility in Persistent or Recurrent Bloodstream Infections Due to Methicillin-Resistant Staphylococcus aureus. Antimicrobial Agents and Chemotherapy, 2012, 56, 1258-1264.	1.4	21
120	Core genome conservation of Staphylococcus haemolyticus limits sequence based population structure analysis. Journal of Microbiological Methods, 2012, 89, 159-166.	0.7	32
121	Prevalence of isolates with reduced glycopeptide susceptibility in orthopedic device-related infections due to methicillin-resistant Staphylococcus aureus. European Journal of Clinical Microbiology and Infectious Diseases, 2012, 31, 3367-3374.	1.3	13
122	Infant gut microbial colonization and health: recent findings from metagenomics studies. Journal of Integrated OMICS, 2012, 2, .	0.5	4
123	Analysis of the salivary microbiome using culture-independent techniques. Journal of Clinical Bioinformatics, 2012, 2, 4.	1.2	54
124	Orientation and expression of methicillin-resistant Staphylococcus aureus small RNAs by direct multiplexed measurements using the nCounter of NanoString technology. Journal of Microbiological Methods, 2011, 84, 327-334.	0.7	32
125	<i>Staphylococcus aureus</i> virulence and metabolism are dramatically affected by <i>Lactococcus lactis</i> in cheese matrix. Environmental Microbiology Reports, 2011, 3, 340-351.	1.0	56
126	Epidemiology and virulence insights from MRSA and MSSA genome analysis. Future Microbiology, 2011, 6, 513-532.	1.0	9



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127	The salivary microbiome, assessed by a high-throughput and culture-independent approach. <i>Journal of Integrated OMICS</i> , 2011, 1, .	0.5	11
128	Methicillin-Susceptible ST398 <i>Staphylococcus aureus</i> Responsible for Bloodstream Infections: An Emerging Human-Adapted Subclone?. <i>PLoS ONE</i> , 2011, 6, e28369.	1.1	86
129	Differentiating Osteoarticular Infections Caused By <i>Kingella Kingae</i> From Those Due to Typical Pathogens in Young Children. <i>Pediatric Infectious Disease Journal</i> , 2011, 30, 906-909.	1.1	81
130	Histone deacetylase inhibitors impair innate immune responses to Toll-like receptor agonists and to infection. <i>Blood</i> , 2011, 117, 1205-1217.	0.6	311
131	Intrapartum Group B streptococcus detection by rapid polymerase chain reaction assay for the prevention of neonatal sepsis. <i>Clinical Microbiology and Infection</i> , 2011, 17, 1786-1791.	2.8	39
132	Robustness of a loop-mediated isothermal amplification reaction for diagnostic applications. <i>FEMS Immunology and Medical Microbiology</i> , 2011, 62, 41-48.	2.7	378
133	The CodY pleiotropic repressor controls virulence in gram-positive pathogens. <i>FEMS Immunology and Medical Microbiology</i> , 2011, 62, 123-139.	2.7	94
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