

# François-Xavier Weill

## List of Publications by Year in descending order

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182  
papers

11,447  
citations

28190

55  
h-index

37111

96  
g-index

196  
all docs

196  
docs citations

196  
times ranked

9494  
citing authors

#	ARTICLE	IF	CITATIONS
1	Improved Molecular Diagnosis and Culture of the Emerging Heteropathotype Enterohemorrhagic <i>Escherichia coli</i> O80:H2 Using Its Non-Melibiose-Fermenting and Antibiotic-Resistance Properties. <i>Journal of Clinical Microbiology</i> , 2022, 60, JCM0153021.	1.8	2
2	Population structure analysis and laboratory monitoring of <i>Shigella</i> by core-genome multilocus sequence typing. <i>Nature Communications</i> , 2022, 13, 551.	5.8	17
3	Azithromycin Resistance in Shiga Toxin-Producing <i>Escherichia coli</i> in France between 2004 and 2020 and Detection of <i>mef</i> (C)- <i>mph</i> (G) Genes. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, AAC0194921.	1.4	3
4	<i>Salmonella enterica</i> subsp. <i>enterica</i> Welikade: guideline for phylogenetic analysis of serovars rarely involved in foodborne outbreaks. <i>BMC Genomics</i> , 2022, 23, 217.	1.2	4
5	Investigation of an international outbreak of multidrug-resistant monophasic <i>Salmonella</i> Typhimurium associated with chocolate products, EU/EEA and United Kingdom, February to April 2022. <i>Eurosurveillance</i> , 2022, 27, .	3.9	25
6	Contribution of microbial genomics to cholera epidemiology. <i>Comptes Rendus - Biologies</i> , 2022, 345, 37-56.	0.1	0
7	High prevalence of small intestine bacteria overgrowth and asymptomatic carriage of enteric pathogens in stunted children in Antananarivo, Madagascar. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0009849.	1.3	20
8	Outbreak of Imported Seventh Pandemic <i>Vibrio cholerae</i> O1 El Tor, Algeria, 2018. <i>Emerging Infectious Diseases</i> , 2022, 28, .	2.0	4
9	A retrospective and regional approach assessing the genomic diversity of <i>Salmonella</i> Dublin. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	1.5	5
10	Stepwise evolution of <i>Salmonella</i> Typhimurium ST313 causing bloodstream infection in Africa. <i>Nature Microbiology</i> , 2021, 6, 327-338.	5.9	68
11	Seventh Pandemic <i>Vibrio cholerae</i> O1 Sublineages, Central African Republic. <i>Emerging Infectious Diseases</i> , 2021, 27, 262-266.	2.0	6
12	Shiga Toxin-Associated Hemolytic Uremic Syndrome in Adults, France, 2009-2017. <i>Emerging Infectious Diseases</i> , 2021, 27, 1876-1885.	2.0	8
13	Endocannabinoids Attenuate the Virulence of Certain Enteropathogenic Bacteria. <i>Trends in Microbiology</i> , 2021, 29, 185-187.	3.5	0
14	Global population structure and genotyping framework for genomic surveillance of the major dysentery pathogen, <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2021, 12, 2684.	5.8	65
15	Contamination of street food with multidrug-resistant <i>Salmonella</i> , in Ouagadougou, Burkina Faso. <i>PLoS ONE</i> , 2021, 16, e0253312.	1.1	13
16	Comment on Tanmoy et al. CRISPR-Cas Diversity in Clinical <i>Salmonella enterica</i> Serovar Typhi Isolates from South Asian Countries. <i>Genes</i> 2020, 11, 1365. <i>Genes</i> , 2021, 12, 1142.	1.0	2
17	Emergence of New ST301 Shiga Toxin-Producing <i>Escherichia coli</i> Clones Harboring Extra-Intestinal Virulence Traits in Europe. <i>Toxins</i> , 2021, 13, 686.	1.5	4
18	Emergence of <i>Vibrio cholerae</i> O1 Sequence Type 75, South Africa, 2018-2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 2927-2931.	2.0	10

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19	An accessible, efficient and global approach for the large-scale sequencing of bacterial genomes. <i>Genome Biology</i> , 2021, 22, 349.	3.8	20
20	Highly Resistant Cholera Outbreak Strain in Zimbabwe. <i>New England Journal of Medicine</i> , 2020, 383, 687-689.	13.9	25
21	The seventh pandemic of cholera in Europe revisited by microbial genomics. <i>Nature Communications</i> , 2020, 11, 5347.	5.8	13
22	Antimicrobial Resistance in <i>Salmonella enterica</i> Serovar Paratyphi B Variant Java in Poultry from Europe and Latin America. <i>Emerging Infectious Diseases</i> , 2020, 26, 1164-1173.	2.0	11
23	Diagnostic challenge of gastrointestinal infection due to lactose-fermenting <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar 4,5:l:-. <i>Diagnostic Microbiology and Infectious Disease</i> , 2020, 98, 115105.	0.8	2
24	Genomic diversity of <i>Salmonella enterica</i> -The UoWUCC 10K genomes project. <i>Wellcome Open Research</i> , 2020, 5, 223.	0.9	43
25	Genomic diversity of <i>Salmonella enterica</i> -The UoWUCC 10K genomes project. <i>Wellcome Open Research</i> , 2020, 5, 223.	0.9	38
26	Endemic Cholera in India and Imported Cholera in Russia: What is Common?. <i>Problemy Osobo Opasnykh Infektsii</i> , 2020, , 17-26.	0.2	8
27	Source Attribution Study of Sporadic <i>Salmonella</i> Derby Cases in France. <i>Frontiers in Microbiology</i> , 2020, 11, 889.	1.5	27
28	<i>Salmonella enterica</i> Serovar Panama, an Understudied Serovar Responsible for Extraintestinal Salmonellosis Worldwide. <i>Infection and Immunity</i> , 2019, 87, .	1.0	6
29	Reptiles in Guadeloupe (French West Indies) are a reservoir of major human <i>Salmonella enterica</i> serovars. <i>PLoS ONE</i> , 2019, 14, e0220145.	1.1	10
30	Revisiting the Global Epidemiology of Cholera in Conjunction With the Genomics of <i>Vibrio cholerae</i> . <i>Frontiers in Public Health</i> , 2019, 7, 203.	1.3	56
31	Dissecting the molecular evolution of fluoroquinolone-resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2019, 10, 4828.	5.8	41
32	A Simple and Robust Statistical Method to Define Genetic Relatedness of Samples Related to Outbreaks at the Genomic Scale – Application to Retrospective <i>Salmonella</i> Foodborne Outbreak Investigations. <i>Frontiers in Microbiology</i> , 2019, 10, 2413.	1.5	17
33	Complement Gene Variants and Shiga Toxin–Producing <i>Escherichia coli</i> –Associated Hemolytic Uremic Syndrome. <i>Clinical Journal of the American Society of Nephrology: CJASN</i> , 2019, 14, 364-377.	2.2	33
34	Serotype distribution and antimicrobial resistance of human <i>Salmonella enterica</i> in Bangui, Central African Republic, from 2004 to 2013. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007917.	1.3	17
35	Genomic insights into the 2016–2017 cholera epidemic in Yemen. <i>Nature</i> , 2019, 565, 230-233.	13.7	129
36	Global phylogenomics of multidrug-resistant <i>Salmonella enterica</i> serotype Kentucky ST198. <i>Microbial Genomics</i> , 2019, 5, .	1.0	69

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37	The speciation and hybridization history of the genus Salmonella. <i>Microbial Genomics</i> , 2019, 5, .	1.0	13
38	Outbreak of Salmonella enterica serotype Poona in infants linked to persistent Salmonella contamination in an infant formula manufacturing facility, France, August 2018 to February 2019. <i>Eurosurveillance</i> , 2019, 24, .	3.9	32
39	Outbreak of Shiga toxin-producing Escherichia coli (STEC) O26 paediatric haemolytic uraemic syndrome (HUS) cases associated with the consumption of soft raw cow's milk cheeses, France, March to May 2019. <i>Eurosurveillance</i> , 2019, 24, .	3.9	44
40	Paediatric haemolytic uraemic syndrome related to Shiga toxin-producing Escherichia coli, an overview of 10 years of surveillance in France, 2007 to 2016. <i>Eurosurveillance</i> , 2019, 24, .	3.9	44
41	Clinical Evaluation of a Multiplex PCR for the Detection of Salmonella enterica Serovars Typhi and Paratyphi A from Blood Specimens in a High-Endemic Setting. <i>American Journal of Tropical Medicine and Hygiene</i> , 2019, 101, 513-520.	0.6	15
42	Horizontal antimicrobial resistance transfer drives epidemics of multiple Shigella species. <i>Nature Communications</i> , 2018, 9, 1462.	5.8	121
43	Early transmissible ampicillin resistance in zoonotic Salmonella enterica serotype Typhimurium in the late 1950s: a retrospective, whole-genome sequencing study. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 207-214.	4.6	33
44	Genomic insights into the emergence and spread of antimicrobial-resistant bacterial pathogens. <i>Science</i> , 2018, 360, 733-738.	6.0	254
45	Pan-genome Analysis of Ancient and Modern Salmonella enterica Demonstrates Genomic Stability of the Invasive Para C Lineage for Millennia. <i>Current Biology</i> , 2018, 28, 2420-2428.e10.	1.8	65
46	Genomic epidemiology of Shigella in the United Kingdom shows transmission of pathogen sublineages and determinants of antimicrobial resistance. <i>Scientific Reports</i> , 2018, 8, 7389.	1.6	65
47	Serotype Distribution and Antimicrobial Resistance of Shigella Species in Bangui, Central African Republic, from 2002 to 2013. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 99, 283-286.	0.6	9
48	Salmonella enterica serovars Panama and Arechavaleta: Risk Factors for Invasive Non-Typhoidal Salmonella Disease in Guadeloupe, French West Indies. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 99, 584-589.	0.6	4
49	Genomic history of the seventh pandemic of cholera in Africa. <i>Science</i> , 2017, 358, 785-789.	6.0	255
50	Integrated view of <i>Vibrio cholerae</i> in the Americas. <i>Science</i> , 2017, 358, 789-793.	6.0	128
51	The clinical and microbiological characteristics of enteric fever in Cambodia, 2008-2015. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005964.	1.3	40
52	Multinational outbreak of travel-related Salmonella Chester infections in Europe, summers 2014 and 2015. <i>Eurosurveillance</i> , 2017, 22, .	3.9	31
53	Around the World in 1,475 Salmonella Geo-serotypes. <i>Emerging Infectious Diseases</i> , 2016, 22, 1298-1302.	2.0	8
54	Travel- and Community-Based Transmission of Multidrug-Resistant Shigella sonnei Lineage among International Orthodox Jewish Communities. <i>Emerging Infectious Diseases</i> , 2016, 22, 1545-1553.	2.0	23

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55	Genome-scale rates of evolutionary change in bacteria. <i>Microbial Genomics</i> , 2016, 2, e000094.	1.0	224
56	Molecular Surveillance Identifies Multiple Transmissions of Typhoid in West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004781.	1.3	46
57	Genomic analysis of <i>Salmonella enterica</i> serotype Paratyphi A during an outbreak in Cambodia, 2013–2015. <i>Microbial Genomics</i> , 2016, 2, e000092.	1.0	24
58	Recurrent Hemolytic and Uremic Syndrome Induced by <i>Escherichia Coli</i> . <i>Medicine (United States)</i> , 2016, 95, e2050.	0.4	8
59	Global Genomic Epidemiology of <i>Salmonella enterica</i> Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2516-2526.	1.4	105
60	Distinct <i>Salmonella</i> Enteritidis lineages associated with enterocolitis in high-income settings and invasive disease in low-income settings. <i>Nature Genetics</i> , 2016, 48, 1211-1217.	9.4	191
61	What's in a Name? Species-Wide Whole-Genome Sequencing Resolves Invasive and Noninvasive Lineages of <i>Salmonella enterica</i> Serotype Paratyphi B. <i>MBio</i> , 2016, 7, .	1.8	29
62	Global phylogeography and evolutionary history of <i>Shigella dysenteriae</i> type 1. <i>Nature Microbiology</i> , 2016, 1, 16027.	5.9	65
63	Characterization of new <i>Salmonella</i> serovars by whole-genome sequencing and traditional typing techniques. <i>Journal of Medical Microbiology</i> , 2016, 65, 1074-1078.	0.7	21
64	A Phylogenetic and Phenotypic Analysis of <i>Salmonella enterica</i> Serovar Weltevreden, an Emerging Agent of Diarrheal Disease in Tropical Regions. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004446.	1.3	59
65	Travel- and Community-Based Transmission of Multidrug-Resistant <i>Shigella sonnei</i> Lineage among International Orthodox Jewish Communities. <i>Emerging Infectious Diseases</i> , 2016, 22, 1545-1553.	2.0	5
66	Allelic variation contributes to bacterial host specificity. <i>Nature Communications</i> , 2015, 6, 8754.	5.8	100
67	Species-wide whole genome sequencing reveals historical global spread and recent local persistence in <i>Shigella flexneri</i> . <i>ELife</i> , 2015, 4, e07335.	2.8	94
68	Prevalence of Shiga toxin-producing <i>Shigella</i> species isolated from French travellers returning from the Caribbean: an emerging pathogen with international implications. <i>Clinical Microbiology and Infection</i> , 2015, 21, 765.e9-765.e14.	2.8	29
69	Draft genomes of <i>Shigella</i> strains used by the STOPENTERICS consortium. <i>Gut Pathogens</i> , 2015, 7, 14.	1.6	7
70	Community Incidence of Campylobacteriosis and Nontyphoidal Salmonellosis, France, 2008–2013. <i>Foodborne Pathogens and Disease</i> , 2015, 12, 664-669.	0.8	23
71	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 913-921.	4.6	204
72	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of <i>Salmonella</i> Typhi identifies inter- and intracontinental transmission events. <i>Nature Genetics</i> , 2015, 47, 632-639.	9.4	403

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73	Rapid Genotyping of <i>Shigella sonnei</i> by Use of Multiplex High-Resolution Melting. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2389-2391.	1.8	8
74	Carbapenemase-producing <i>Salmonella enterica</i> serotype Kentucky ST198, North Africa: Table 1. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, dkv276.	1.3	10
75	One-Step Identification of Five Prominent Chicken <i>Salmonella</i> Serovars and Biotypes. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3881-3883.	1.8	44
76	High-Throughput CRISPR Typing of <i>Mycobacterium tuberculosis</i> Complex and <i>Salmonella enterica</i> Serotype Typhimurium. <i>Methods in Molecular Biology</i> , 2015, 1311, 91-109.	0.4	15
77	Multidrug-Resistant <i>Salmonella enterica</i> Serotype Typhi, Gulf of Guinea Region, Africa. <i>Emerging Infectious Diseases</i> , 2015, 21, 655-659.	2.0	16
78	<i>Salmonella enterica</i> Serotype Enteritidis in French Polynesia, South Pacific, 2008–2013. <i>Emerging Infectious Diseases</i> , 2015, 21, 1045-1048.	2.0	6
79	Enteric Bacterial Pathogens in Children with Diarrhea in Niger: Diversity and Antimicrobial Resistance. <i>PLoS ONE</i> , 2015, 10, e0120275.	1.1	66
80	Lack of efflux mediated quinolone resistance in <i>Salmonella enterica</i> serovars Typhi and Paratyphi A. <i>Frontiers in Microbiology</i> , 2014, 5, 12.	1.5	15
81	CRISPR Is an Optimal Target for the Design of Specific PCR Assays for <i>Salmonella enterica</i> Serotypes Typhi and Paratyphi A. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2671.	1.3	25
82	Invasive <i>Salmonella enterica</i> Serotype Typhimurium Infections, Democratic Republic of the Congo, 2007–2011. <i>Emerging Infectious Diseases</i> , 2014, 20, 701-704.	2.0	20
83	Transient Darwinian selection in <i>Salmonella enterica</i> serovar Paratyphi A during 450 years of global spread of enteric fever. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12199-12204.	3.3	122
84	Targeting relaxase genes for classification of the predominant plasmids in Enterobacteriaceae. <i>International Journal of Medical Microbiology</i> , 2014, 304, 236-242.	1.5	43
85	Prevalence and characterization of extended-spectrum $\beta$ -lactamase-producing clinical <i>Salmonella enterica</i> isolates in Dakar, Senegal, from 1999 to 2009. <i>Clinical Microbiology and Infection</i> , 2014, 20, O109-O116.	2.8	46
86	Supplement 2008–2010 (no. 48) to the White–Kauffmann–Le Minor scheme. <i>Research in Microbiology</i> , 2014, 165, 526-530.	1.0	309
87	Foodborne transmission of sorbitol-fermenting <i>Escherichia coli</i> O157:[H7] via ground beef: an outbreak in northern France, 2011. <i>Clinical Microbiology and Infection</i> , 2014, 20, O1136-O1144.	2.8	29
88	<i>Salmonella</i> serotypes in reptiles and humans, French Guiana. <i>Veterinary Microbiology</i> , 2014, 170, 167-171.	0.8	24
89	Highly drug-resistant <i>Salmonella enterica</i> serotype Kentucky ST198-X1: a microbiological study. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 672-679.	4.6	149
90	Attribution of the French human Salmonellosis cases to the main food-sources according to the type of surveillance data. <i>Preventive Veterinary Medicine</i> , 2013, 110, 12-27.	0.7	30

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91	Serological Cross-Reaction Between O-Antigens of <i>Shigella dysenteriae</i> Type 4 and an Environmental <i>Escherichia albertii</i> Isolate. <i>Current Microbiology</i> , 2013, 67, 590-595.	1.0	12
92	Les <i>Escherichia coli</i> entérohémorragiques : des bactéries d'actualité. <i>Revue Francophone Des Laboratoires</i> , 2013, 2013, 44-49.	0.0	0
93	Genetic Diversity and Antimicrobial Resistance Profiles of <i>Salmonella enterica</i> Serotype Derby Isolated from Pigs, Pork, and Humans in France. <i>Foodborne Pathogens and Disease</i> , 2013, 10, 977-984.	0.8	43
94	The Bayesian Microbial Subtyping Attribution Model: Robustness to Prior Information and a Proposition. <i>Risk Analysis</i> , 2013, 33, 397-408.	1.5	15
95	Comparative Genomics of Recent Shiga Toxin-Producing <i>Escherichia coli</i> O104:H4: Short-Term Evolution of an Emerging Pathogen. <i>MBio</i> , 2013, 4, e00452-12.	1.8	68
96	Community-acquired infectious diarrhoea in children under 5 years of age in Dakar, Senegal. <i>Paediatrics and International Child Health</i> , 2013, 33, 139-144.	0.3	35
97	Evaluation of CHROMagar STEC and STEC O104 Chromogenic Agar Media for Detection of Shiga Toxin-Producing <i>Escherichia coli</i> in Stool Specimens. <i>Journal of Clinical Microbiology</i> , 2013, 51, 894-900.	1.8	42
98	Global Phylogeny of <i>Shigella sonnei</i> Strains from Limited Single Nucleotide Polymorphisms (SNPs) and Development of a Rapid and Cost-Effective SNP-Typing Scheme for Strain Identification by High-Resolution Melting Analysis. <i>Journal of Clinical Microbiology</i> , 2013, 51, 303-305.	1.8	20
99	ramR mutations affecting fluoroquinolone susceptibility in epidemic multidrug-resistant <i>Salmonella enterica</i> serovar Kentucky ST198. <i>Frontiers in Microbiology</i> , 2013, 4, 213.	1.5	26
100	The global establishment of a highly-fluoroquinolone resistant <i>Salmonella enterica</i> serotype Kentucky ST198 strain. <i>Frontiers in Microbiology</i> , 2013, 4, 395.	1.5	114
101	Use of multilocus variable-number tandem repeat analysis (MLVA) in eight European countries, 2012. <i>Eurosurveillance</i> , 2013, 18, 20385.	3.9	63
102	Multilocus Sequence Typing as a Replacement for Serotyping in <i>Salmonella enterica</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002776.	2.1	574
103	Characterization of Isolates of <i>Salmonella enterica</i> Serovar Stanley, a Serovar Endemic to Asia and Associated with Travel. <i>Journal of Clinical Microbiology</i> , 2012, 50, 709-720.	1.8	32
104	Genomic epidemiology of the <i>Escherichia coli</i> O104:H4 outbreaks in Europe, 2011. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3065-3070.	3.3	262
105	Outbreak of Shiga Toxin-Producing <i>Escherichia coli</i> O104:H4 Associated With Organic Fenugreek Sprouts, France, June 2011. <i>Clinical Infectious Diseases</i> , 2012, 54, 1588-1594.	2.9	154
106	Reply to Guy et al.: Support for a bottleneck in the 2011 <i>Escherichia coli</i> O104:H4 outbreak in Germany. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3629-E3630.	3.3	2
107	Population Genetic Structure of 4,12:a:â” Salmonella enterica Strains from Harbor Porpoises. <i>Applied and Environmental Microbiology</i> , 2012, 78, 8829-8833.	1.4	6
108	Characterization of Extended-Spectrum Beta-Lactamase-Producing <i>Salmonella enterica</i> Serotype Brunei and Heidelberg at the Hussein Dey Hospital in Algiers (Algeria). <i>Foodborne Pathogens and Disease</i> , 2012, 9, 803-808.	0.8	15

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109	<i>Shigella sonnei</i> genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. <i>Nature Genetics</i> , 2012, 44, 1056-1059.	9.4	278
110	Early Strains of Multidrug-Resistant <i>Salmonella enterica</i> Serovar Kentucky Sequence Type 198 from Southeast Asia Harbor <i>Salmonella</i> Genomic Island 1-J Variants with a Novel Insertion Sequence. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 5096-5102.	1.4	36
111	CRISPR Typing and Subtyping for Improved Laboratory Surveillance of <i>Salmonella</i> Infections. <i>PLoS ONE</i> , 2012, 7, e36995.	1.1	198
112	Heterogeneity of Persistence of <i>Salmonella enterica</i> Serotype Senftenberg Strains Could Explain the Emergence of this Serotype in Poultry Flocks. <i>PLoS ONE</i> , 2012, 7, e35782.	1.1	19
113	Foodborne Outbreak and Nonmotile <i>Salmonella enterica</i> Variant, France. <i>Emerging Infectious Diseases</i> , 2012, 18, 132-134.	2.0	15
114	<i>Escherichia coli</i> O104:H4 south-west France, June 2011. <i>Lancet Infectious Diseases</i> , The, 2011, 11, 732-733.	4.6	38
115	Nationwide pseudo-outbreak of <i>Salmonella enterica</i> ssp. <i>diarizonae</i> , France. <i>Clinical Microbiology and Infection</i> , 2011, 17, 915-918.	2.8	4
116	A multiplex real-time PCR assay targeting virulence and resistance genes in <i>Salmonella enterica</i> serotype Typhimurium. <i>BMC Microbiology</i> , 2011, 11, 151.	1.3	26
117	<i>Salmonella enterica</i> Serotype Typhi with Nonclassical Quinolone Resistance Phenotype. <i>Emerging Infectious Diseases</i> , 2011, 17, 1091-1094.	2.0	16
118	International Spread of an Epidemic Population of <i>Salmonella enterica</i> Serotype Kentucky ST198 Resistant to Ciprofloxacin. <i>Journal of Infectious Diseases</i> , 2011, 204, 675-684.	1.9	226
119	Presence of Enterohemorrhagic <i>Escherichia coli</i> ST678/O104:H4 in France Prior to 2011. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8784-8786.	1.4	34
120	<i>Salmonella enterica</i> Serotype Gambia with CTX-M-3 and <i>armA</i> Resistance Markers: Nosocomial Infections with a Fatal Outcome. <i>Journal of Clinical Microbiology</i> , 2011, 49, 1676-1678.	1.8	5
121	Prevalence and Characterization of Extended-Spectrum Beta-lactamases-Producing <i>Salmonella enterica</i> isolates in Saragossa, Spain (2001-2008). <i>Microbial Drug Resistance</i> , 2011, 17, 207-213.	0.9	17
122	Emergence of a Globally Dominant IncHI1 Plasmid Type Associated with Multiple Drug Resistant Typhoid. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1245.	1.3	114
123	<i>Salmonella enterica</i> Serotype Typhi with Nonclassical Quinolone Resistance Phenotype. <i>Emerging Infectious Diseases</i> , 2011, 17, 1091-1094.	2.0	26
124	Molecular epidemiology of extended-spectrum $\beta$ -lactamase-producing <i>Klebsiella pneumoniae</i> strains in a university hospital in Tunis, Tunisia, 1999-2005. <i>Clinical Microbiology and Infection</i> , 2010, 16, 157-164.	2.8	56
125	Inc11 Plasmid Carrying Extended-Spectrum $\beta$ -Lactamase Gene bla CTX-M-1 in <i>Salmonella enterica</i> Isolates from Poultry and Humans in France, 2003 to 2008. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 4484-4486.	1.4	52
126	Evolution and Population Structure of <i>Salmonella enterica</i> Serovar Newport. <i>Journal of Bacteriology</i> , 2010, 192, 6465-6476.	1.0	109



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127	A multiplex single nucleotide polymorphism typing assay for detecting mutations that result in decreased fluoroquinolone susceptibility in <i>Salmonella enterica</i> serovars Typhi and Paratyphi A. <i>Journal of Antimicrobial Chemotherapy</i> , 2010, 65, 1631-1641.	1.3	36
128	Serological reactivity and bacterial genotypes in <i>Chlamydia trachomatis</i> urogenital infections in Guadeloupe, French West Indies. <i>Sexually Transmitted Infections</i> , 2010, 86, 101-105.	0.8	11
129	Molecular Epidemiology of Ampicillin Resistance in <i>Salmonella</i> spp. and <i>Escherichia coli</i> from Wastewater and Clinical Specimens. <i>Foodborne Pathogens and Disease</i> , 2010, 7, 945-951.	0.8	16
130	Supplement 2003–2007 (No. 47) to the White-Kauffmann-Le Minor scheme. <i>Research in Microbiology</i> , 2010, 161, 26-29.	1.0	389
131	Molecular and Biochemical Characterization of the Natural Chromosome-Encoded Class A $\beta$ -Lactamase from <i>Pseudomonas luteola</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 45-51.	1.4	14
132	WHO Global Salm-Surv External Quality Assurance System for Serotyping of <i>Salmonella</i> Isolates from 2000 to 2007. <i>Journal of Clinical Microbiology</i> , 2009, 47, 2729-2736.	1.8	49
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