Rene Sjå, gren Hendriksen

List of Publications by Year in descending order

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118 papers 8,406 citations

43973 48 h-index 87 g-index

123 all docs

123
docs citations

times ranked

123

9000 citing authors

#	Article	IF	CITATIONS
1	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. Nature Communications, 2019, 10, 1124.	5.8	612
2	Global Monitoring of <i>Salmonella</i> Serovar Distribution from the World Health Organization Global Foodborne Infections Network Country Data Bank: Results of Quality Assured Laboratories from 2001 to 2007. Foodborne Pathogens and Disease, 2011, 8, 887-900.	0.8	543
3	Identification of a novel transposon-associated phosphoethanolamine transferase gene, mcr-5, conferring colistin resistance in d-tartrate fermenting Salmonella enterica subsp. enterica serovar Paratyphi B. Journal of Antimicrobial Chemotherapy, 2017, 72, 3317-3324.	1.3	450
4	Multiplex PCR for detection of plasmid-mediated colistin resistance determinants, mcr-1, mcr-2, mcr-3, mcr-4 and mcr-5 for surveillance purposes. Eurosurveillance, 2018, 23, .	3.9	431
5	Detection of mcr-1 encoding plasmid-mediated colistin-resistant Escherichia coli isolates from human bloodstream infection and imported chicken meat, Denmark 2015. Eurosurveillance, 2015, 20, .	3.9	326
6	Population Genetics of Vibrio cholerae from Nepal in 2010: Evidence on the Origin of the Haitian Outbreak. MBio, 2011, 2, e00157-11.	1.8	268
7	Typhoid fever. Lancet, The, 2015, 385, 1136-1145.	6.3	265
8	Using Genomics to Track Global Antimicrobial Resistance. Frontiers in Public Health, 2019, 7, 242.	1.3	263
9	International Spread of an Epidemic Population of Salmonella enterica Serotype Kentucky ST198 Resistant to Ciprofloxacin. Journal of Infectious Diseases, 2011, 204, 675-684.	1.9	226
10	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. Nature Microbiology, 2019, 4, 1727-1736.	5.9	184
11	The Salmonella enterica Pan-genome. Microbial Ecology, 2011, 62, 487-504.	1.4	175
12	Emergence of a Clonal Lineage of Multidrug-Resistant ESBL-Producing Salmonella Infantis Transmitted from Broilers and Broiler Meat to Humans in Italy between 2011 and 2014. PLoS ONE, 2015, 10, e0144802.	1.1	171
13	<i>Salmonella</i> Serovars from Humans and Other Sources in Thailand, 1993–2002. Emerging Infectious Diseases, 2004, 10, 131-136.	2.0	169
14	Genomic Epidemiology: Whole-Genome-Sequencing–Powered Surveillance and Outbreak Investigation of Foodborne Bacterial Pathogens. Annual Review of Food Science and Technology, 2016, 7, 353-374.	5.1	152
15	Antimicrobial resistance of zoonotic and commensal bacteria in Europe: The missing link between consumption and resistance in veterinary medicine. Veterinary Microbiology, 2014, 170, 1-9.	0.8	144
16	Prevalence of antimicrobial resistance among bacterial pathogens isolated from cattle in different European countries: 2002–2004. Acta Veterinaria Scandinavica, 2008, 50, 28.	0.5	125
17	International Spread of Multidrug-resistant <i>Salmonella</i> Schwarzengrund in Food Products. Emerging Infectious Diseases, 2007, 13, 726-731.	2.0	117
18	The global establishment of a highly-fluoroquinolone resistant Salmonella enterica serotype Kentucky ST198 strain. Frontiers in Microbiology, 2013, 4, 395.	1.5	114

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19	Genomic Epidemiology of the Haitian Cholera Outbreak: a Single Introduction Followed by Rapid, Extensive, and Continued Spread Characterized the Onset of the Epidemic. MBio, 2014, 5, e01721.	1.8	112
20	Antimicrobial susceptibility and occurrence of resistance genes among Salmonella enterica serovar Weltevreden from different countries. Journal of Antimicrobial Chemotherapy, 2003, 52, 715-718.	1.3	111
21	Association Between Antimicrobial Resistance in <i>Escherichia coli</i> Isolates from Food Animals and Blood Stream Isolates from Humans in Europe: An Ecological Study. Foodborne Pathogens and Disease, 2011, 8, 1295-1301.	0.8	107
22	Molecular Characterization and Antimicrobial Susceptibility of <i>Salmonella</i> Isolates from Infections in Humans in Henan Province, China. Journal of Clinical Microbiology, 2009, 47, 401-409.	1.8	105
23	Global Genomic Epidemiology of Salmonella enterica Serovar Typhimurium DT104. Applied and Environmental Microbiology, 2016, 82, 2516-2526.	1.4	105
24	Molecular Characterization and Occurrence of Extended-Spectrum β-Lactamase Resistance Genes among Salmonella enterica Serovar Corvallis from Thailand, Bulgaria, and Denmark. Microbial Drug Resistance, 2006, 12, 192-198.	0.9	99
25	Antimicrobial susceptibility and serovars of Salmonella from chickens and humans in Ibadan, Nigeria. Journal of Infection in Developing Countries, 2010, 4, 484-494.	0.5	89
26	Characterization and Genetic Variation of Vibrio cholerae Isolated from Clinical and Environmental Sources in Thailand. PLoS ONE, 2017, 12, e0169324.	1.1	88
27	Genomic Epidemiology of Salmonella enterica Serotype Enteritidis based on Population Structure of Prevalent Lineages. Emerging Infectious Diseases, 2014, 20, 1481-1489.	2.0	87
28	Extended-Spectrum-Beta-Lactamases, AmpC Beta-Lactamases and Plasmid Mediated Quinolone Resistance in Klebsiella spp. from Companion Animals in Italy. PLoS ONE, 2014, 9, e90564.	1.1	86
29	Antimicrobial-resistant Shigella infections from Iran: an overlooked problem?. Journal of Antimicrobial Chemotherapy, 2012, 67, 1128-1133.	1.3	83
30	Genomic Signature of Multidrug-Resistant Salmonella enterica Serovar Typhi Isolates Related to a Massive Outbreak in Zambia between 2010 and 2012. Journal of Clinical Microbiology, 2015, 53, 262-272.	1.8	82
31	Is the Evolution of Salmonella enterica subsp. <i>enterica</i> Linked to Restriction-Modification Systems?. MSystems, 2016, 1, .	1.7	74
32	Molecular Epidemiology of mcr-Encoded Colistin Resistance in Enterobacteriaceae From Food-Producing Animals in Italy Revealed Through the EU Harmonized Antimicrobial Resistance Monitoring. Frontiers in Microbiology, 2018, 9, 1217.	1.5	74
33	Occurrence of antimicrobial resistance among bacterial pathogens and indicator bacteria in pigs in different European countries from year 2002 – 2004: the ARBAO-II study. Acta Veterinaria Scandinavica, 2008, 50, 19.	0.5	70
34	Population Genetic Structure of Listeria monocytogenes Strains as Determined by Pulsed-Field Gel Electrophoresis and Multilocus Sequence Typing. Applied and Environmental Microbiology, 2016, 82, 5720-5728.	1.4	69
35	Global phylogenomics of multidrug-resistant Salmonella enterica serotype Kentucky ST198. Microbial Genomics, 2019, 5, .	1.0	69
36	Molecular epidemiology of Salmonella Infantis in Europe: insights into the success of the bacterial host and its parasitic pESI-like megaplasmid. Microbial Genomics, 2020, 6, .	1.0	68

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37	An Assessment of Different Genomic Approaches for Inferring Phylogeny of Listeria monocytogenes. Frontiers in Microbiology, 2017, 8, 2351.	1.5	66
38	Antimicrobial Resistance and Molecular Epidemiology of <i>Salmonella </i> Rissen from Animals, Food Products, and Patients in Thailand and Denmark. Foodborne Pathogens and Disease, 2008, 5, 605-619.	0.8	65
39	Occurrence and Characterization of mcr-1-Positive Escherichia coli Isolated From Food-Producing Animals in Poland, 2011–2016. Frontiers in Microbiology, 2019, 10, 1753.	1.5	65
40	Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. Emerging Infectious Diseases, 2012, 18, e1-e1.	2.0	64
41	Risk Factors and Epidemiology of the Ten Most Common <i>Salmonella</i> Serovars from Patients in Thailand: 2002–2007. Foodborne Pathogens and Disease, 2009, 6, 1009-1019.	0.8	63
42	Emergence of Multidrug-Resistant Salmonella Concord Infections in Europe and the United States in Children Adopted From Ethiopia, 2003–2007. Pediatric Infectious Disease Journal, 2009, 28, 814-818.	1.1	62
43	Proficiency testing for bacterial whole genome sequencing: an end-user survey of current capabilities, requirements and priorities. BMC Infectious Diseases, 2015, 15, 174.	1.3	62
44	Genetic relatedness of multidrug resistant Escherichia coli isolated from humans, chickens and poultry environments. Antimicrobial Resistance and Infection Control, 2021, 10, 58.	1.5	61
45	Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. Emerging Infectious Diseases, 2012, 18, e1-e1.	2.0	61
46	Prevalence and Characterization of Human <i>Shigella</i> Infections in Henan Province, China, in 2006. Journal of Clinical Microbiology, 2011, 49, 232-242.	1.8	54
47	Molecular clonality and antimicrobial resistance in Salmonella entericaserovars Enteritidis and Infantis from broilers in three Northern regions of Iran. BMC Veterinary Research, 2013, 9, 66.	0.7	53
48	Molecular Characterization of Extended-Spectrum Cephalosporinase-Producing Salmonella enterica Serovar Choleraesuis Isolates from Patients in Thailand and Denmark. Journal of Clinical Microbiology, 2010, 48, 883-888.	1.8	52
49	Carbapenemase VCC-1–Producing <i>Vibrio cholerae</i> in Coastal Waters of Germany. Emerging Infectious Diseases, 2017, 23, 1735-1737.	2.0	52
50	WHO Global Salm-Surv External Quality Assurance System for Serotyping of <i>Salmonella</i> Isolates from 2000 to 2007. Journal of Clinical Microbiology, 2009, 47, 2729-2736.	1.8	49
51	The Role of the st313-td Gene in Virulence of Salmonella Typhimurium ST313. PLoS ONE, 2014, 9, e84566.	1.1	48
52	<i>Shigella</i> from Humans in Thailand During 1993 to 2006: Spatial-Time Trends in Species and Serotype Distribution. Foodborne Pathogens and Disease, 2008, 5, 773-784.	0.8	39
53	CHROMagar COL-APSE: a selective bacterial culture medium for the isolation and differentiation of colistin-resistant Gram-negative pathogens. Journal of Medical Microbiology, 2017, 66, 1554-1561.	0.7	39
54	Microbiologic and Clinical Features of Salmonella Species Isolated From Bacteremic Children in Eastern Democratic Republic of Congo. Pediatric Infectious Disease Journal, 2010, 29, 504-510.	1.1	37

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55	SCCmec Type IX Element in Methicillin Resistant Staphylococcusaureusspa Type t337 (CC9) Isolated from Pigs and Pork in Thailand. Frontiers in Microbiology, 2012, 3, 103.	1.5	35
56	Proficiency Testing of Virus Diagnostics Based on Bioinformatics Analysis of Simulated <i>In Silico</i> High-Throughput Sequencing Data Sets. Journal of Clinical Microbiology, 2019, 57, .	1.8	34
57	ST131 <i>fimH</i> 22 <i>Escherichia coli</i> isolate with a <i>bla</i> CMY-2/IncI1/ST12 plasmid obtained from a patient with bloodstream infection: highly similar to <i>E. coli</i> isolates of broiler origin. Journal of Antimicrobial Chemotherapy, 2019, 74, 557-560.	1.3	34
58	Serotypes and antimicrobial resistance of Salmonella enterica ssp in central Thailand, 2001-2006. Southeast Asian Journal of Tropical Medicine and Public Health, 2010, 41, 1405-15.	1.0	34
59	Machine Learning Methods as a Tool for Predicting Risk of Illness Applying Nextâ€Generation Sequencing Data. Risk Analysis, 2019, 39, 1397-1413.	1.5	33
60	Incl1 ST3 and Incl1 ST7 plasmids from CTX-M-1-producing Escherichia coli obtained from patients with bloodstream infections are closely related to plasmids from E. coli of animal origin. Journal of Antimicrobial Chemotherapy, 2019, 74, 2171-2175.	1.3	33
61	Characterization of Isolates of Salmonella enterica Serovar Stanley, a Serovar Endemic to Asia and Associated with Travel. Journal of Clinical Microbiology, 2012, 50, 709-720.	1.8	32
62	Reappearance of Salmonella serovar Choleraesuis var. Kunzendorf in Danish pig herds. Veterinary Microbiology, 2015, 176, 282-291.	0.8	32
63	Extended-spectrum ß-lactamase-producing Escherichia coli among humans, chickens and poultry environments in Abuja, Nigeria. One Health Outlook, 2020, 2, 8.	1.4	32
64	Genomics of an emerging clone of Salmonella serovar Typhimurium ST313 from Nigeria and the Democratic Republic of Congo. Journal of Infection in Developing Countries, 2013, 7, 696-706.	0.5	30
65	A metagenomic glimpse into the gut of wild and domestic animals: Quantification of antimicrobial resistance and more. PLoS ONE, 2020, 15, e0242987.	1.1	30
66	Prevalence and Antibiotic Resistance of <i>Salmonella</i> Isolated from a Poultry Farm and Processing Plant Environment in the State of Kuwait. Foodborne Pathogens and Disease, 2007, 4, 367-373.	0.8	29
67	Characterization of Salmonella Occurring at High Prevalence in a Population of the Land Iguana Conolophus subcristatus in $Gal ilde{A}_i$ pagos Islands, Ecuador. PLoS ONE, 2011, 6, e23147.	1.1	27
68	Establishing Streptomycin Epidemiological Cut-Off Values for <i>Salmonella</i> and <i>Escherichia coli</i> . Microbial Drug Resistance, 2012, 18, 88-93.	0.9	27
69	Results of Use of WHO Global Salm-Surv External Quality Assurance System for Antimicrobial Susceptibility Testing of <i>Salmonella</i> Isolates from 2000 to 2007. Journal of Clinical Microbiology, 2009, 47, 79-85.	1.8	26
70	Antimicrobial resistance in Salmonella spp. recovered from patients admitted to six different hospitals in Tehran, Iran from 2007 to 2008. Folia Microbiologica, 2012, 57, 91-97.	1.1	26
71	Extremely Drug-Resistant Salmonella enterica Serovar Senftenberg Infections in Patients in Zambia. Journal of Clinical Microbiology, 2013, 51, 284-286.	1.8	26
72	Genomic Dissection of Travel-Associated Extended-Spectrum-Beta-Lactamase-Producing Salmonella enterica Serovar Typhi Isolates Originating from the Philippines: a One-Off Occurrence or a Threat to Effective Treatment of Typhoid Fever?. Journal of Clinical Microbiology, 2015, 53, 677-680.	1.8	25

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73	The Lake Chad Basin, an Isolated and Persistent Reservoir of Vibrio cholerae O1: A Genomic Insight into the Outbreak in Cameroon, 2010. PLoS ONE, 2016, 11, e0155691.	1.1	25
74	Using next generation sequencing to tackle non-typhoidal Salmonella infections. Journal of Infection in Developing Countries, 2013, 7, 001-005.	0.5	25
75	Pathogen surveillance in the informal settlement, Kibera, Kenya, using a metagenomics approach. PLoS ONE, 2019, 14, e0222531.	1.1	24
76	Occurrence and Characterization of <i>Salmonella </i> Hiduddify from Chickens and Poultry Meat in Nigeria. Foodborne Pathogens and Disease, 2009, 6, 425-430.	0.8	23
77	Persistence of fluoroquinolone-resistant Salmonella enterica serovar Kentucky from poultry and poultry sources in Nigeria. Journal of Infection in Developing Countries, 2014, 8, 384-388.	0.5	23
78	Genomic insights into Vibrio cholerae O1 responsible for cholera epidemics in Tanzania between 1993 and 2017. PLoS Neglected Tropical Diseases, 2019, 13, e0007934.	1.3	21
79	Surveillance and Genomics of Toxigenic Vibrio cholerae O1 From Fish, Phytoplankton and Water in Lake Victoria, Tanzania. Frontiers in Microbiology, 2019, 10, 901.	1.5	20
80	Emergence and Clonal Spread of CTX-M-65-Producing Escherichia coli From Retail Meat in Portugal. Frontiers in Microbiology, 2021, 12, 653595.	1.5	19
81	Apramycin treatment affects selection and spread of a multidrug-resistant Escherichia coli strain able to colonize the human gut in the intestinal microbiota of pigs. Veterinary Research, 2016, 47, 12.	1.1	18
82	Characterization of Salmonella enterica serovar Enteritidis isolates recovered from blood and stool specimens in Thailand. BMC Microbiology, 2012, 12, 92.	1.3	17
83	Proficiency of WHO Global Foodborne Infections Network External Quality Assurance System Participants in Identification and Susceptibility Testing of Thermotolerant Campylobacter spp. from 2003 to 2012. Journal of Clinical Microbiology, 2018, 56, .	1.8	17
84	Cross-Border Transmission of Salmonella Choleraesuis var. Kunzendorf in European Pigs and Wild Boar: Infection, Genetics, and Evolution. Frontiers in Microbiology, 2019, 10, 179.	1.5	17
85	Whole-Genome Sequencing Analysis of Nontyphoidal Salmonella enterica of Chicken Meat and Human Origin Under Surveillance in Sri Lanka. Foodborne Pathogens and Disease, 2019, 16, 531-537.	0.8	16
86	Molecular Characteristics and Zoonotic Potential of Salmonella Weltevreden From Cultured Shrimp and Tilapia in Vietnam and China. Frontiers in Microbiology, 2020, 11, 1985.	1.5	15
87	Reply to "South Asia Instead of Nepal May Be the Origin of the Haitian Cholera Outbreak Strain― MBio, 2011, 2, e00245-11.	1.8	14
88	Final report of ENGAGE ―Establishing Next Generation sequencing Ability for Genomic analysis in Europe. EFSA Supporting Publications, 2018, 15, 1431E.	0.3	14
89	Diversity and antimicrobial susceptibility of Salmonella enterica serovars isolated from pig farms in Ibadan, Nigeria. Folia Microbiologica, 2014, 59, 69-77.	1.1	13
90	Quantitative Microbial Risk Assessment Based on Whole Genome Sequencing Data: Case of Listeria monocytogenes. Microorganisms, 2020, 8, 1772.	1.6	13

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91	Salmonella enterica serovar Typhi H58 clone has been endemic in Zimbabwe from 2012 to 2019. Journal of Antimicrobial Chemotherapy, 2021, 76, 1160-1167.	1.3	13
92	Phenotypic and genotypic characterization of mcr-1-positive multidrug-resistant Escherichia coli ST93, ST117, ST156, ST10, and ST744 isolated from poultry in Poland. Brazilian Journal of Microbiology, 2021, 52, 1597-1609.	0.8	13
93	Global Microbial Identifier. , 2017, , 13-31.		13
94	Application of different DNA extraction procedures, library preparation protocols and sequencing platforms: impact on sequencing results. Heliyon, 2019, 5, e02745.	1.4	12
95	Epidemiological Investigation of <i>Salmonella enterica</i> Serovar Kedougou in Thailand. Foodborne Pathogens and Disease, 2011, 8, 203-211.	0.8	11
96	Comparative genomics of quinoloneâ€resistant and susceptible Campylobacter jejuni of poultry origin from major poultry producing European countries (GENCAMP). EFSA Supporting Publications, 2018, 15, 1398E.	0.3	11
97	Salmonella enterica Serovar Typhimurium in Mauritius Linked to Consumption of Marlin Mousse. Foodborne Pathogens and Disease, 2009, 6, 739-741.	0.8	10
98	Audouin's gull, a potential vehicle of an extended spectrum \hat{I}^2 -lactamase producing Salmonella Agona. FEMS Microbiology Letters, 2015, 362, 1-4.	0.7	10
99	Co-localization of carbapenem (<i>bla</i> OXA-162) and colistin (<i>mcr-1</i>) resistance genes on a transferable IncHI2 plasmid in <i>Escherichia coli</i> of chicken origin. Journal of Antimicrobial Chemotherapy, 2021, 76, 3063-3065.	1.3	10
100	External quality assurance system for antibiotic resistance in bacteria of animal origin in Europe (ARBAO-II), 2003. Veterinary Microbiology, 2006, 115, 128-139.	0.8	8
101	Antimicrobial Susceptibilities, Phage Types, and Molecular Characterization of Salmonella enterica Serovar Enteritidis from Chickens and Chicken Meat in Turkey. Foodborne Pathogens and Disease, 2009, 6, 265-271.	0.8	8
102	Prevalence and risk factors for faecal carriage of multidrug resistant Escherichia coli among slaughterhouse workers. Scientific Reports, 2021, 11, 13362.	1.6	8
103	Investigating Salmonella Eko from Various Sources in Nigeria by Whole Genome Sequencing to Identify the Source of Human Infections. PLoS ONE, 2016, 11, e0156212.	1.1	8
104	Analysis of the contribution of bacteriophage ST64B to in vitro virulence traits of Salmonella enterica serovar Typhimurium. Journal of Medical Microbiology, 2014, 63, 331-342.	0.7	7
105	Proficiency Testing of Metagenomics-Based Detection of Food-Borne Pathogens Using a Complex Artificial Sequencing Dataset. Frontiers in Microbiology, 2020, 11, 575377.	1.5	7
106	Metaphylogenetic analysis of global sewage reveals that bacterial strains associated with human disease show less degree of geographic clustering. Scientific Reports, 2020, 10, 3033.	1.6	7
107	Extended-Spectrum ß-Lactamase-Producing Escherichia coli Among Humans, Beef Cattle, and Abattoir Environments in Nigeria. Frontiers in Cellular and Infection Microbiology, 2022, 12, 869314.	1.8	6
108	Emergence and clonal dissemination of Salmonella enterica serovar Enteritidis causing salmonellosis in Mauritius. Journal of Infection in Developing Countries, 2014, 8, 454-460.	0.5	5

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109	Evaluation of temocillin for phenotypic carbapenemase screening of Escherichia coli and Salmonella enterica isolates in relation to the presence of genes encoding ESBLs and carbapenemase production. Journal of Antimicrobial Chemotherapy, 2019, 74, 639-644.	1.3	5
110	Accelerating surveillance and research of antimicrobial resistance $\hat{a} \in ``an online repository for sharing of antimicrobial susceptibility data associated with whole-genome sequences. Microbial Genomics, 2020, 6, .$	1.0	5
111	Metagenomics-Based Proficiency Test of Smoked Salmon Spiked with a Mock Community. Microorganisms, 2020, 8, 1861.	1.6	4
112	Mapping the coverage, availability and uptake of External Quality Assessment programmes across One Health sectors in Asia. Journal of Antimicrobial Chemotherapy, 2021, , .	1.3	4
113	Dissemination of Clonal <i>Salmonella enterica < i>Serovar Typhimurium Isolates Causing Salmonellosis in Mauritius. Foodborne Pathogens and Disease, 2013, 10, 618-623.</i>	0.8	3
114	New Brucella variant isolated from Croatian cattle. BMC Veterinary Research, 2021, 17, 126.	0.7	3
115	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serotype Typhimurium Sequence Type 313, Isolated from India. Microbiology Resource Announcements, 2018, 7, .	0.3	1
116	Antimicrobial and Genomic Characterization of Salmonella Nigeria from Pigs and Poultry in Ilorin, North-central, Nigeria. Journal of Infection in Developing Countries, 2021, 15, 1899-1909.	0.5	1
117	Rapid risk assessment framework to assess public health risk of antimicrobial resistance found in foods. Food Control, 2022, 137, 108852.	2.8	1
118	Human skin bacterial flora differ with altitudes in different ethnic groups of Nepal. Asian Journal of Medical Sciences, 2019, 10, 11-17.	0.0	0