List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Nucleocapsid-independent assembly of coronavirus-like particles by co-expression of viral envelope protein genes EMBO Journal, 1996, 15, 2020-2028.	7.8	435
2	Application of next generation sequencing in clinical microbiology and infection prevention. Journal of Biotechnology, 2017, 243, 16-24.	3.8	414
3	Variability and Diversity of Nasopharyngeal Microbiota in Children: A Metagenomic Analysis. PLoS ONE, 2011, 6, e17035.	2.5	399
4	The MUC family: an obituary. Trends in Biochemical Sciences, 2002, 27, 126-131.	7.5	335
5	Practical issues in implementing whole-genome-sequencing in routine diagnostic microbiology. Clinical Microbiology and Infection, 2018, 24, 355-360.	6.0	214
6	Innovative and rapid antimicrobial susceptibility testing systems. Nature Reviews Microbiology, 2020, 18, 299-311.	28.6	204
7	During Viral Infection of the Respiratory Tract, CD27, 4-1BB, and OX40 Collectively Determine Formation of CD8+ Memory T Cells and Their Capacity for Secondary Expansion. Journal of Immunology, 2005, 175, 1665-1676.	0.8	186
8	Associations between Pathogens in the Upper Respiratory Tract of Young Children: Interplay between Viruses and Bacteria. PLoS ONE, 2012, 7, e47711.	2.5	177
9	Dysbiosis of upper respiratory tract microbiota in elderly pneumonia patients. ISME Journal, 2016, 10, 97-108.	9.8	166
10	The dominance of human coronavirus OC43 and NL63 infections in infants. Journal of Clinical Virology, 2012, 53, 135-139.	3.1	161
11	Enterovirus and parechovirus infection in children: a brief overview. European Journal of Pediatrics, 2016, 175, 1023-1029.	2.7	139
12	Disease severity and viral load are correlated in infants with primary respiratory syncytial virus infection in the community. Journal of Medical Virology, 2010, 82, 1266-1271.	5.0	138
13	Diagnosis of bloodstream infections from positive blood cultures and directly from blood samples: recent developments in molecular approaches. Clinical Microbiology and Infection, 2018, 24, 944-955.	6.0	138
14	Use of whole-genome sequencing to trace, control and characterize the regional expansion of extended-spectrum β-lactamase producing ST15 Klebsiella pneumoniae. Scientific Reports, 2016, 6, 20840.	3.3	117
15	Increased Detection of Respiratory Syncytial Virus, Influenza Viruses, Parainfluenza Viruses, and Adenoviruses with Real-Time PCR in Samples from Patients with Respiratory Symptoms. Journal of Clinical Microbiology, 2007, 45, 2260-2262.	3.9	112
16	Targeted next-generation sequencing of the 16S-23S rRNA region for culture-independent bacterial identification - increased discrimination of closely related species. Scientific Reports, 2017, 7, 3434.	3.3	110
17	A Systemic Neutrophil Response Precedes Robust CD8 + T-Cell Activation during Natural Respiratory Syncytial Virus Infection in Infants. Journal of Virology, 2010, 84, 2374-2383.	3.4	109
18	Strong Association between Respiratory Viral Infection Early after Hematopoietic Stem Cell Transplantation and the Development of Life-Threatening Acute and Chronic Alloimmune Lung Syndromes. Biology of Blood and Marrow Transplantation, 2010, 16, 782-791.	2.0	100

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19	Whole-Genome Multilocus Sequence Typing of Extended-Spectrum-Beta-Lactamase-Producing Enterobacteriaceae. Journal of Clinical Microbiology, 2016, 54, 2919-2927.	3.9	97
20	Presence of mcr-1-positive Enterobacteriaceae in retail chicken meat but not in humans in the Netherlands since 2009. Eurosurveillance, 2016, 21, 30149.	7.0	93
21	Assembly of Spikes into Coronavirus Particles Is Mediated by the Carboxy-Terminal Domain of the Spike Protein. Journal of Virology, 2000, 74, 1566-1571.	3.4	89
22	Enterococcus faecium: from microbiological insights to practical recommendations for infection control and diagnostics. Antimicrobial Resistance and Infection Control, 2020, 9, 130.	4.1	87
23	An outbreak of colistin-resistant Klebsiella pneumoniae carbapenemase-producing Klebsiella pneumoniae in the Netherlands (July to December 2013), with inter-institutional spread. European Journal of Clinical Microbiology and Infectious Diseases, 2015, 34, 1647-1655.	2.9	84
24	The phylogenetic landscape and nosocomial spread of the multidrug-resistant opportunist Stenotrophomonas maltophilia. Nature Communications, 2020, 11, 2044.	12.8	76
25	High Interlaboratory Reproducibility and Accuracy of Next-Generation-Sequencing-Based Bacterial Genotyping in a Ring Trial. Journal of Clinical Microbiology, 2017, 55, 908-913.	3.9	75
26	Genotypic Diversity of Coxiella burnetii in the 2007-2010 Q Fever Outbreak Episodes in The Netherlands. Journal of Clinical Microbiology, 2012, 50, 1076-1078.	3.9	71
27	Critical steps in clinical shotgun metagenomics for the concomitant detection and typing of microbial pathogens. Scientific Reports, 2018, 8, 13767.	3.3	70
28	Is Shiga Toxin-Negative Escherichia coli O157:H7 Enteropathogenic or Enterohemorrhagic Escherichia coli? Comprehensive Molecular Analysis Using Whole-Genome Sequencing. Journal of Clinical Microbiology, 2015, 53, 3530-3538.	3.9	68
29	Virulence Factors of Enteric Pathogenic Escherichia coli: A Review. International Journal of Molecular Sciences, 2021, 22, 9922.	4.1	65
30	Prevalence of antimicrobial resistance genes in Bacteroides spp. and Prevotella spp. Dutch clinical isolates. Clinical Microbiology and Infection, 2019, 25, 1156.e9-1156.e13.	6.0	63
31	Inhibition of Cyclooxygenase Activity Reduces Rotavirus Infection at a Postbinding Step. Journal of Virology, 2004, 78, 9721-9730.	3.4	59
32	The value of signs and symptoms in differentiating between bacterial, viral and mixed aetiology in patients with community-acquired pneumonia. Journal of Medical Microbiology, 2014, 63, 441-452.	1.8	59
33	Performance Evaluation of the New Roche Cobas AmpliPrep/Cobas TaqMan HIV-1 Test Version 2.0 for Quantification of Human Immunodeficiency Virus Type 1 RNA. Journal of Clinical Microbiology, 2010, 48, 1195-1200.	3.9	58
34	Interaction of mouse hepatitis virus (MHV) spike glycoprotein with receptor glycoprotein MHVR is required for infection with an MHV strain that expresses the hemagglutinin-esterase glycoprotein. Journal of Virology, 1995, 69, 889-895.	3.4	58
35	Diagnostic value of real-time polymerase chain reaction to detect viruses in young children admitted to the paediatric intensive care unit with lower respiratory tract infection. Critical Care, 2006, 10, R61.	5.8	56
36	Typing and Species Identification of Clinical Klebsiella Isolates by Fourier Transform Infrared Spectroscopy and Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry. Journal of Clinical Microbiology, 2018, 56, .	3.9	56

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37	Absence of human metapneumovirus co-infection in cases of severe respiratory syncytial virus infection. Pediatric Pulmonology, 2006, 41, 872-874.	2.0	55
38	Genomic organization and expression of the 3′ end of the canine and feline enteric coronaviruses. Virology, 1992, 191, 134-140.	2.4	53
39	The tongue microbiome in healthy subjects and patients with intra-oral halitosis. Journal of Breath Research, 2017, 11, 036010.	3.0	53
40	Prospective comparison of the detection rates of human enterovirus and parechovirus RT-qPCR and viral culture in different pediatric specimens. Journal of Clinical Virology, 2013, 58, 449-454.	3.1	52
41	Characterization of a CTX-M-15 Producing Klebsiella Pneumoniae Outbreak Strain Assigned to a Novel Sequence Type (1427). Frontiers in Microbiology, 2015, 6, 1250.	3.5	52
42	Interlaboratory Evaluation of Different Extraction and Real-Time PCR Methods for Detection of <i>Coxiella burnetii</i> DNA in Serum. Journal of Clinical Microbiology, 2010, 48, 3923-3927.	3.9	49
43	The peptidylarginine deiminase gene is a conserved feature of Porphyromonas gingivalis. Scientific Reports, 2015, 5, 13936.	3.3	49
44	The Viral Spike Protein Is Not Involved in the Polarized Sorting of Coronaviruses in Epithelial Cells. Journal of Virology, 1998, 72, 497-503.	3.4	47
45	Norovirus disease associated with excess mortality and use of statins: a retrospective cohort study of an outbreak following a pilgrimage to Lourdes. Epidemiology and Infection, 2011, 139, 453-463.	2.1	47
46	Metagenomic Characterization of the Human Intestinal Microbiota in Fecal Samples from STEC-Infected Patients. Frontiers in Cellular and Infection Microbiology, 2018, 8, 25.	3.9	47
47	Efficacy of Home Telemonitoring versus Conventional Follow-up: A Randomized Controlled Trial among Teenagers with Inflammatory Bowel Disease. Journal of Crohn's and Colitis, 2018, 12, 432-441.	1.3	46
48	Dynamics of Human Respiratory Virus-Specific CD8+ T Cell Responses in Blood and Airways during Episodes of Common Cold. Journal of Immunology, 2008, 181, 5551-5559.	0.8	44
49	September through October 2010 multi-centre study in the Netherlands examining laboratory ability to detect enterovirus 68, an emerging respiratory pathogen. Journal of Virological Methods, 2013, 190, 53-62.	2.1	44
50	Emerging infections—an increasingly important topic: review by the Emerging Infections Task Force. Clinical Microbiology and Infection, 2018, 24, 369-375.	6.0	44
51	Entry and release of transmissible gastroenteritis coronavirus are restricted to apical surfaces of polarized epithelial cells. Journal of Virology, 1994, 68, 7966-7973.	3.4	44
52	Diagnostic value of respiratory virus detection in symptomatic children using real-time PCR. Virology Journal, 2012, 9, 276.	3.4	42
53	Clinical Epidemiology of Bocavirus, Rhinovirus, Two Polyomaviruses and Four Coronaviruses in HIV-Infected and HIV-Uninfected South African Children. PLoS ONE, 2014, 9, e86448.	2.5	42
54	Comprehensive Molecular Characterization of Escherichia coli Isolates from Urine Samples of Hospitalized Patients in Rio de Janeiro, Brazil. Frontiers in Microbiology, 2018, 9, 243.	3.5	42

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55	A Comparison of Three Different Bioinformatics Analyses of the 16S–23S rRNA Encoding Region for Bacterial Identification. Frontiers in Microbiology, 2019, 10, 620.	3.5	42
56	Rotavirus Enterotoxin NSP4 Binds to the Extracellular Matrix Proteins Laminin-β3 and Fibronectin. Journal of Virology, 2004, 78, 10045-10053.	3.4	40
57	Increased risk of pneumonia in residents living near poultry farms: does the upper respiratory tract microbiota play a role?. Pneumonia (Nathan Qld), 2017, 9, 3.	6.1	40
58	Immunogenicity, Boostability, and Sustainability of the Immune Response after Vaccination against Influenza A Virus (H1N1) 2009 in a Healthy Population. Vaccine Journal, 2011, 18, 1401-1405.	3.1	39
59	Cyclooxygenase activity is important for efficient replication of mouse hepatitis virus at an early stage of infection. Virology Journal, 2007, 4, 55.	3.4	38
60	Characteristics of pediatric patients with enterovirus meningitis and no cerebral fluid pleocytosis. European Journal of Pediatrics, 2012, 171, 795-800.	2.7	37
61	Sputum microbiome profiling in COPD: beyond singular pathogen detection. Thorax, 2020, 75, 338-344.	5.6	37
62	Expansion of KPC-producing Klebsiella pneumoniae with various mgrB mutations giving rise to colistin resistance: the role of IS L3 on plasmids. International Journal of Antimicrobial Agents, 2018, 51, 260-265.	2.5	35
63	Core/Whole Genome Multilocus Sequence Typing and Core Genome SNP-Based Typing of OXA-48-Producing Klebsiella pneumoniae Clinical Isolates From Spain. Frontiers in Microbiology, 2019, 10, 2961.	3.5	35
64	Assessing the Public Health Risk of Shiga Toxin-Producing Escherichia coli by Use of a Rapid Diagnostic Screening Algorithm. Journal of Clinical Microbiology, 2015, 53, 1588-1598.	3.9	34
65	Reprint of "Application of next generation sequencing in clinical microbiology and infection prevention― Journal of Biotechnology, 2017, 250, 2-10.	3.8	34
66	Human Rhinovirus and Wheezing. Pediatric Infectious Disease Journal, 2013, 32, 827-833.	2.0	34
67	Isolation of an NDM-5-producing ST16 Klebsiella pneumoniae from a Dutch patient without travel history abroad, August 2015. Eurosurveillance, 2015, 20, .	7.0	33
68	Laboratory-based surveillance in the molecular era: the TYPENED model, a joint data-sharing platform for clinical and public health laboratories. Eurosurveillance, 2013, 18, 20387.	7.0	33
69	Emergence of pan-resistance in KPC-2 carbapenemase-producing <i>Klebsiella pneumoniae</i> in Crete, Greece: a close call. Journal of Antimicrobial Chemotherapy, 2016, 71, 1207-1212.	3.0	32
70	MRSA Prevalence and Associated Risk Factors among Health-Care Workers in Non-outbreak Situations in the Dutch-German EUREGIO. Frontiers in Microbiology, 2016, 7, 1273.	3.5	31
71	There's no place like OM: Vesicular sorting and secretion of the peptidylarginine deiminase of <i>Porphyromonas gingivalis</i> . Virulence, 2018, 9, 459-467.	4.4	31
72	The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. F1000Research, 2018, 7, 459.	1.6	31

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73	Contact precautions in single-bed or multiple-bed rooms for patients with extended-spectrum β-lactamase-producing Enterobacteriaceae in Dutch hospitals: a cluster-randomised, crossover, non-inferiority study. Lancet Infectious Diseases, The, 2019, 19, 1069-1079.	9.1	31
74	Epidemiology of Extended-Spectrum β-Lactamase-Producing E. coli and Vancomycin-Resistant Enterococci in the Northern Dutch–German Cross-Border Region. Frontiers in Microbiology, 2017, 8, 1914.	3.5	30
75	Characterization of the population structure, drug resistance mechanisms and plasmids of the community-associated Enterobacter cloacae complex in China. Journal of Antimicrobial Chemotherapy, 2018, 73, 66-76.	3.0	30
76	Human Bocavirus and KI/WU Polyomaviruses in Pediatric Intensive Care Patients. Emerging Infectious Diseases, 2009, 15, 454-457.	4.3	28
77	Profiling of Humoral Response to Influenza A(H1N1)pdm09 Infection and Vaccination Measured by a Protein Microarray in Persons with and without History of Seasonal Vaccination. PLoS ONE, 2013, 8, e54890.	2.5	28
78	Genetic characterization of Shiga toxin-producing Escherichia coli O26:H11 strains isolated from animal, food, and clinical samples. Frontiers in Cellular and Infection Microbiology, 2015, 5, 74.	3.9	28
79	Prospective assessment of clinical symptoms associated with enterovirus and parechovirus genotypes in a multicenter study in Dutch children. Journal of Clinical Virology, 2016, 77, 15-20.	3.1	28
80	Integrated Stewardship Model Comprising Antimicrobial, Infection Prevention, and Diagnostic Stewardship (AID Stewardship). Journal of Clinical Microbiology, 2017, 55, 3306-3307.	3.9	28
81	Viral and bacterial aetiology of communityâ€acquired pneumonia in adults. Influenza and Other Respiratory Viruses, 2013, 7, 567-573.	3.4	27
82	DETECTION OFGIARDIA LAMBLIA, CRYPTOSPORIDIUMSPP. ANDENTAMOEBA HISTOLYTICAIN CLINICAL STOOL SAMPLES BY USING MULTIPLEX REAL-TIME PCR AFTER AUTOMATED DNA ISOLATION. Acta Clinica Belgica, 2013, 68, 188-192.	1.2	27
83	Molecular Typing of Enterobacteriaceae from Pig Holdings in North-Western Germany Reveals Extended- Spectrum and AmpC β-Lactamases Producing but no Carbapenem Resistant Ones. PLoS ONE, 2015, 10, e0134533.	2.5	27
84	Unusual severe case of hemolytic uremic syndrome due to Shiga toxin 2d-producing E. coli O80:H2. Pediatric Nephrology, 2017, 32, 1263-1268.	1.7	27
85	Elucidating vancomycin-resistant Enterococcus faecium outbreaks: the role of clonal spread and movement of mobile genetic elements. Journal of Antimicrobial Chemotherapy, 2018, 73, 3259-3267.	3.0	27
86	Preparing the outbreak assistance laboratory network in the Netherlands for the detection of the influenza virus A(H1N1) variant. Journal of Clinical Virology, 2009, 45, 179-184.	3.1	26
87	Coronavirus infection of polarized epithelial cells. Trends in Microbiology, 1995, 3, 486-490.	7.7	25
88	Coronavirus Escape from Heptad Repeat 2 (HR2)-Derived Peptide Entry Inhibition as a Result of Mutations in the HR1 Domain of the Spike Fusion Protein. Journal of Virology, 2008, 82, 2580-2585.	3.4	25
89	Performance of cobas® 4800 and m2000 real-timeâ,,¢ assays for detection of Chlamydia trachomatis and Neisseria gonorrhoeae in rectal and self-collected vaginal specimen. Diagnostic Microbiology and Infectious Disease, 2013, 77, 101-105.	1.8	25
90	Cross-border comparison of the Dutch and German guidelines on multidrug-resistant Gram-negative microorganisms. Antimicrobial Resistance and Infection Control, 2015, 4, 7.	4.1	25

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91	Silent transmission of an IS 1294b -deactivated mcr-1 gene with inducible colistin resistance. International Journal of Antimicrobial Agents, 2018, 51, 822-828.	2.5	25
92	Epidemiology of Staphylococcus aureus in a burn unit of a tertiary care center in Ghana. PLoS ONE, 2017, 12, e0181072.	2.5	25
93	MHV-A59 Enters Polarized Murine Epithelial Cells through the Apical Surface but Is Released Basolaterally. Virology, 1995, 210, 54-66.	2.4	24
94	Molecular Quantification of Respiratory Syncytial Virus in Respiratory Samples: Reliable Detection during the Initial Phase of Infection. Journal of Clinical Microbiology, 2010, 48, 3569-3574.	3.9	24
95	Genetic loci of Staphylococcus aureus associated with anti-neutrophil cytoplasmic autoantibody (ANCA)-associated vasculitides. Scientific Reports, 2017, 7, 12211.	3.3	24
96	Revealing the Virulence Potential of Clinical and Environmental Aspergillus fumigatus Isolates Using Whole-Genome Sequencing. Frontiers in Microbiology, 2019, 10, 1970.	3.5	24
97	The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. F1000Research, 2018, 7, 459.	1.6	24
98	Detection of enterovirus RNA in cerebrospinal fluid: Comparison of two molecular assays. Journal of Virological Methods, 2012, 179, 104-107.	2.1	23
99	Contribution of AcrAB-TolC to multidrug resistance in an Escherichia coli sequence type 131 isolate. International Journal of Antimicrobial Agents, 2017, 50, 477-481.	2.5	23
100	Latent introduction to the Netherlands of multiple antibiotic resistance including NDM-1 after hospitalisation in Egypt, August 2013. Eurosurveillance, 2013, 18, .	7.0	23
101	Three metronidazole-resistant Prevotella bivia strains harbour a mobile element, encoding a novel nim gene, nimK, and an efflux small MDR transporter. Journal of Antimicrobial Chemotherapy, 2018, 73, 2687-2690.	3.0	22
102	Campylobacter blaseri sp. nov., isolated from common seals (Phoca vitulina). International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1787-1794.	1.7	22
103	Prevalence and Pathogenicity of WU and KI Polyomaviruses in Children, the Netherlands. Emerging Infectious Diseases, 2008, 14, 1787-1789.	4.3	21
104	OXY-2-15, a novel variant showing increased ceftazidime hydrolytic activity. Journal of Antimicrobial Chemotherapy, 2015, 70, 1429-1433.	3.0	21
105	Genetic Diversity of Staphylococcus aureus in Buruli Ulcer. PLoS Neglected Tropical Diseases, 2015, 9, e0003421.	3.0	21
106	Comparative genomics reveals a lack of evidence for pigeons as a main source of stx2f-carrying Escherichia coli causing disease in humans and the common existence of hybrid Shiga toxin-producing and enteropathogenic E. coli pathotypes. BMC Genomics, 2019, 20, 271.	2.8	21
107	Proof of an Outer Membrane Target of the Efflux Inhibitor Phe-Arg-Î ² -Naphthylamide from Random Mutagenesis. Molecules, 2019, 24, 470.	3.8	21
108	Whole-Genome Characterization and Genotyping of Global WU Polyomavirus Strains. Journal of Virology, 2010, 84, 6229-6234.	3.4	20

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109	Evaluation of the Xpert <i>vanA</i> / <i>vanB</i> Assay Using Enriched Inoculated Broths for Direct Detection of <i>vanB</i> Vancomycin-Resistant Enterococci. Journal of Clinical Microbiology, 2014, 52, 4293-4297.	3.9	20
110	Low anti-staphylococcal IgG responses in granulomatosis with polyangiitis patients despite long-term Staphylococcus aureus exposure. Scientific Reports, 2015, 5, 8188.	3.3	20
111	A novel Tn1696-like composite transposon (Tn6404) harboring bla IMP-4 in a Klebsiella pneumoniae isolate carrying a rare ESBL gene bla SFO-1. Scientific Reports, 2017, 7, 17321.	3.3	20
112	Antibiotic Resistance Plasmids Cointegrated into a Megaplasmid Harboring the <i>bla</i> _{OXA-427} Carbapenemase Gene. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	20
113	Comparison of 14 Molecular Assays for Detection of Mycobacterium tuberculosis Complex in Bronchoalveolar Lavage Fluid. Journal of Clinical Microbiology, 2013, 51, 3505-3511.	3.9	19
114	Evaluation of yield of currently available diagnostics by sample type to optimize detection of respiratory pathogens in patients with a communityâ€acquired pneumonia. Influenza and Other Respiratory Viruses, 2014, 8, 243-249.	3.4	19
115	Prevalence, risk factors and molecular epidemiology of highly resistant gram negative rods in hospitalized patients in the Dutch region Kennemerland. Antimicrobial Resistance and Infection Control, 2016, 5, 8.	4.1	19
116	No evidence for cross-protection of the HPV-16/18 vaccine against HPV-6/11 positivity in female STI clinic visitors. Journal of Infection, 2017, 74, 393-400.	3.3	19
117	Conserved Citrullinating Exoenzymes in <i>Porphyromonas</i> Species. Journal of Dental Research, 2018, 97, 556-562.	5.2	19
118	Incidence, clinical implications and impact on public health of infections with Shigella spp. and entero-invasive Escherichia coli (EIEC): results of a multicenter cross-sectional study in the Netherlands during 2016–2017. BMC Infectious Diseases, 2019, 19, 1037.	2.9	19
119	The Equine Faecal Microbiota of Healthy Horses and Ponies in The Netherlands: Impact of Host and Environmental Factors. Animals, 2021, 11, 1762.	2.3	19
120	Structural characterisation of Toll-like receptor 1 (TLR1) and Toll-like receptor 6 (TLR6) in elephant and harbor seals. Veterinary Immunology and Immunopathology, 2016, 169, 10-14.	1.2	18
121	Clinical sensitivity and specificity of the Check-Points Check-Direct ESBL Screen for BD MAX, a real-time PCR for direct ESBL detection from rectal swabs. Journal of Antimicrobial Chemotherapy, 2017, 72, 2512-2518.	3.0	18
122	Extensive colonization with carbapenemase-producing microorganisms in Romanian burn patients: infectious consequences from the Colectiv fire disaster. European Journal of Clinical Microbiology and Infectious Diseases, 2018, 37, 175-183.	2.9	18
123	Description of Citrobacter cronae sp. nov., isolated from human rectal swabs and stool samples. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2998-3003.	1.7	18
124	Antibiotic Resistance and Molecular Characterization of Cronobacter sakazakii Strains Isolated from Powdered Infant Formula Milk. Foods, 2022, 11, 1093.	4.3	18
125	A Murine and a Porcine Coronavirus Are Released from Opposite Surfaces of the Same Epithelial Cells. Virology, 1996, 224, 345-351.	2.4	17
126	First report of invasive liver abscess syndrome with endophthalmitis caused by a K2 serotype ST2398 hypervirulent Klebsiella pneumoniae in Germany, 2016. New Microbes and New Infections, 2017, 17, 77-80.	1.6	17

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127	Antimicrobial Resistance in Class 1 Integron-Positive Shiga Toxin-Producing Escherichia coli Isolated from Cattle, Pigs, Food and Farm Environment. Microorganisms, 2018, 6, 99.	3.6	17
128	Admission prevalence and acquisition of nasal carriage of meticillin-resistant Staphylococcus aureus (MRSA) in German rehabilitation centres. Journal of Hospital Infection, 2014, 87, 115-118.	2.9	16
129	Comprehensive Characterization of Escherichia coli O104:H4 Isolated from Patients in the Netherlands. Frontiers in Microbiology, 2015, 6, 1348.	3.5	16
130	Identification of a Novel Genomic Island Associated with <i>vanD</i> -Type Vancomycin Resistance in Six Dutch Vancomycin-Resistant Enterococcus faecium Isolates. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	16
131	Detection of Legionella anisa in Water from Hospital Dental Chair Units and Molecular Characterization by Whole-Genome Sequencing. Microorganisms, 2018, 6, 71.	3.6	16
132	Virulence potential of Staphylococcus aureus isolates from Buruli ulcer patients. International Journal of Medical Microbiology, 2017, 307, 223-232.	3.6	15
133	Real-time genomic investigation underlying the public health response to a Shiga toxin-producingEscherichia coliO26:H11 outbreak in a nursery. Epidemiology and Infection, 2017, 145, 2998-3006.	2.1	15
134	Fosfomycin Etest for Enterobacteriaceae: Interobserver and interlaboratory agreement. International Journal of Antimicrobial Agents, 2018, 52, 678-681.	2.5	15
135	Surveillance-embedded genomic outbreak resolution of methicillin-susceptible Staphylococcus aureus in a neonatal intensive care unit. Scientific Reports, 2020, 10, 2619.	3.3	15
136	First detection of porcine respirovirus 1 in Germany and the Netherlands. Transboundary and Emerging Diseases, 2021, 68, 3120-3125.	3.0	15
137	Mouse hepatitis virus strain A59 is released from opposite sides of different epithelial cell types Journal of General Virology, 1997, 78, 61-69.	2.9	15
138	Feline and canine coronaviruses are released from the basolateral side of polarized epithelial LLC-PK1 cells expressing the recombinant feline aminopeptidase-N cDNA. Archives of Virology, 2001, 146, 791-799.	2.1	14
139	Commonality of Multidrug-Resistant Klebsiella pneumoniae ST348 Isolates in Horses and Humans in Portugal. Frontiers in Microbiology, 2019, 10, 1657.	3.5	14
140	Sonication of heart valves detects more bacteria in infective endocarditis. Scientific Reports, 2018, 8, 12967.	3.3	13
141	Association between rectal colonization with Highly Resistant Gram-negative Rods (HR-GNRs) and subsequent infection with HR-GNRs in clinical patients: A one year historical cohort study. PLoS ONE, 2019, 14, e0211016.	2.5	13
142	A Multifactorial Approach for Surveillance of Shigella spp. and Entero-Invasive Escherichia coli Is Important for Detecting (Inter)national Clusters. Frontiers in Microbiology, 2020, 11, 564103.	3.5	13
143	Assessment of Viral Targeted Sequence Capture Using Nanopore Sequencing Directly from Clinical Samples. Viruses, 2020, 12, 1358.	3.3	13
144	Within-patient plasmid dynamics in Klebsiella pneumoniae during an outbreak of a carbapenemase-producing Klebsiella pneumoniae. PLoS ONE, 2020, 15, e0233313.	2.5	13

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145	Evaluation of whole-genome sequence data analysis approaches for short- and long-read sequencing of Mycobacterium tuberculosis. Microbial Genomics, 2021, 7, .	2.0	13
146	Molecular Characterization of Staphylococcus aureus Isolates Transmitted between Patients with Buruli Ulcer. PLoS Neglected Tropical Diseases, 2015, 9, e0004049.	3.0	12
147	Extended-spectrum beta-lactamase producing Enterobacteriaceae (ESBL-E) isolated from bean sprouts in the Netherlands. PLoS ONE, 2018, 13, e0203338.	2.5	12
148	Evaluation of a Culture-Dependent Algorithm and a Molecular Algorithm for Identification of Shigella spp., Escherichia coli, and Enteroinvasive E. coli. Journal of Clinical Microbiology, 2018, 56, .	3.9	12
149	Proportion of asylum seekers carrying multi-drug resistant microorganisms is persistently increased after arrival in the Netherlands. Antimicrobial Resistance and Infection Control, 2019, 8, 6.	4.1	12
150	Limited Multidrug Resistance Efflux Pump Overexpression among Multidrug-Resistant Escherichia coli Strains of ST131. Antimicrobial Agents and Chemotherapy, 2021, 65, .	3.2	12
151	Strengthening the diagnostic capacity to detect Bio Safety Level 3 organisms in unusual respiratory viral outbreaks. Journal of Clinical Virology, 2009, 45, 185-190.	3.1	11
152	Impact of PCR for respiratory viruses on antibiotic use: Theory and practice. Pediatric Pulmonology, 2011, 46, 428-434.	2.0	11
153	Changes in oral microflora after fullâ€mouth tooth extraction: a prospective cohort study. Journal of Clinical Periodontology, 2014, 41, 981-989.	4.9	11
154	Virulence, Antimicrobial Resistance Properties and Phylogenetic Background of Non-H7 Enteropathogenic Escherichia coli O157. Frontiers in Microbiology, 2016, 7, 1540.	3.5	11
155	Methicillin Resistant Staphylococcus aureus Transmission in a Ghanaian Burn Unit: The Importance of Active Surveillance in Resource-Limited Settings. Frontiers in Microbiology, 2017, 8, 1906.	3.5	11
156	ArgO145, a Stx2a prophage of a bovine O145:H- STEC strain, is closely related to phages of virulent human strains. Infection, Genetics and Evolution, 2018, 60, 126-132.	2.3	11
157	Detection of a novel mcr-5.4 gene variant in hospital tap water by shotgun metagenomic sequencing. Journal of Antimicrobial Chemotherapy, 2019, 74, 3626-3628.	3.0	11
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