

# Alexander Mellmann

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

235 papers	9,792 citations	50 h-index	92 g-index
256 ext. papers	12,068 ext. citations	6.5 avg, IF	5.97 L-index

#	Paper	IF	Citations
235	Prospective genomic characterization of the German enterohemorrhagic <i>Escherichia coli</i> O104:H4 outbreak by rapid next generation sequencing technology. <i>PLoS ONE</i> , <b>2011</b> , 6, e22751	3.7	570
234	Characterisation of the <i>Escherichia coli</i> strain associated with an outbreak of haemolytic uraemic syndrome in Germany, 2011: a microbiological study. <i>Lancet Infectious Diseases</i> , <b>2011</b> , 11, 671-6	25.5	556
233	Multicenter evaluation of a sequence-based protocol for subtyping Shiga toxins and standardizing Stx nomenclature. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 2951-63	9.7	534
232	Evaluation of matrix-assisted laser desorption ionization-time-of-flight mass spectrometry in comparison to 16S rRNA gene sequencing for species identification of nonfermenting bacteria. <i>Journal of Clinical Microbiology</i> , <b>2008</b> , 46, 1946-54	9.7	300
231	Updating benchtop sequencing performance comparison. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 294-6	44.5	255
230	Analysis of collection of hemolytic uraemic syndrome-associated enterohemorrhagic <i>Escherichia coli</i> . <i>Emerging Infectious Diseases</i> , <b>2008</b> , 14, 1287-90	10.2	207
229	Defining and Evaluating a Core Genome Multilocus Sequence Typing Scheme for Whole-Genome Sequence-Based Typing of <i>Listeria monocytogenes</i> . <i>Journal of Clinical Microbiology</i> , <b>2015</b> , 53, 2869-76	9.7	182
228	Core Genome Multilocus Sequence Typing Scheme for High- Resolution Typing of <i>Enterococcus faecium</i> . <i>Journal of Clinical Microbiology</i> , <b>2015</b> , 53, 3788-97	9.7	173
227	Livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) as causes of human infection and colonization in Germany. <i>PLoS ONE</i> , <b>2013</b> , 8, e55040	3.7	172
226	Based Upon Repeat Pattern (BURP): an algorithm to characterize the long-term evolution of <i>Staphylococcus aureus</i> populations based on spa polymorphisms. <i>BMC Microbiology</i> , <b>2007</b> , 7, 98	4.5	172
225	Bacterial whole-genome sequencing revisited: portable, scalable, and standardized analysis for typing and detection of virulence and antibiotic resistance genes. <i>Journal of Clinical Microbiology</i> , <b>2014</b> , 52, 2365-70	9.7	168
224	High interlaboratory reproducibility of DNA sequence-based typing of bacteria in a multicenter study. <i>Journal of Clinical Microbiology</i> , <b>2006</b> , 44, 619-21	9.7	165
223	Shiga toxin gene loss and transfer in vitro and in vivo during enterohemorrhagic <i>Escherichia coli</i> O26 infection in humans. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 3144-50	4.8	159
222	Development and evaluation of a quality-controlled ribosomal sequence database for 16S ribosomal DNA-based identification of <i>Staphylococcus</i> species. <i>Journal of Clinical Microbiology</i> , <b>2004</b> , 42, 4988-95	9.7	154
221	High interlaboratory reproducibility of matrix-assisted laser desorption ionization-time of flight mass spectrometry-based species identification of nonfermenting bacteria. <i>Journal of Clinical Microbiology</i> , <b>2009</b> , 47, 3732-4	9.7	150
220	Effects of antibiotics on Shiga toxin 2 production and bacteriophage induction by epidemic <i>Escherichia coli</i> O104:H4 strain. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2012</b> , 56, 3277-82	5.9	135
219	Sequencing and staphylococci identification. <i>Emerging Infectious Diseases</i> , <b>2006</b> , 12, 333-6	10.2	134

218	Automated DNA sequence-based early warning system for the detection of methicillin-resistant <i>Staphylococcus aureus</i> outbreaks. <i>PLoS Medicine</i> , <b>2006</b> , 3, e33	11.6	132
217	Carbapenem-resistant Enterobacteriaceae in wildlife, food-producing, and companion animals: a systematic review. <i>Clinical Microbiology and Infection</i> , <b>2018</b> , 24, 1241-1250	9.5	125
216	Real-Time Genome Sequencing of Resistant Bacteria Provides Precision Infection Control in an Institutional Setting. <i>Journal of Clinical Microbiology</i> , <b>2016</b> , 54, 2874-2881	9.7	123
215	Shiga toxin-mediated hemolytic uremic syndrome: time to change the diagnostic paradigm?. <i>PLoS ONE</i> , <b>2007</b> , 2, e1024	3.7	116
214	Plasmid-Encoded Transferable mecB-Mediated Methicillin Resistance in <i>Staphylococcus aureus</i> . <i>Emerging Infectious Diseases</i> , <b>2018</b> , 24, 242-248	10.2	112
213	Point mutations in FimH adhesin of Crohn's disease-associated adherent-invasive <i>Escherichia coli</i> enhance intestinal inflammatory response. <i>PLoS Pathogens</i> , <b>2013</b> , 9, e1003141	7.6	108
212	Enterohemorrhagic <i>Escherichia coli</i> hemolysin employs outer membrane vesicles to target mitochondria and cause endothelial and epithelial apoptosis. <i>PLoS Pathogens</i> , <b>2013</b> , 9, e1003797	7.6	108
211	A precise reconstruction of the emergence and constrained radiations of <i>Escherichia coli</i> O157 portrayed by backbone concatenomic analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 8713-8	11.5	102
210	Enterohemorrhagic <i>Escherichia coli</i> in human infection: in vivo evolution of a bacterial pathogen. <i>Clinical Infectious Diseases</i> , <b>2005</b> , 41, 785-92	11.6	102
209	Prevalence, virulence profiles, and clinical significance of Shiga toxin-negative variants of enterohemorrhagic <i>Escherichia coli</i> O157 infection in humans. <i>Clinical Infectious Diseases</i> , <b>2007</b> , 45, 39-45	11.6	100
208	Enterohemorrhagic <i>Escherichia coli</i> O26:H11/H-: a new virulent clone emerges in Europe. <i>Clinical Infectious Diseases</i> , <b>2013</b> , 56, 1373-81	11.6	99
207	Host cell interactions of outer membrane vesicle-associated virulence factors of enterohemorrhagic <i>Escherichia coli</i> O157: Intracellular delivery, trafficking and mechanisms of cell injury. <i>PLoS Pathogens</i> , <b>2017</b> , 13, e1006159	7.6	99
206	Occurrence of ESBL-Producing <i>Escherichia coli</i> in Livestock and Farm Workers in Mecklenburg-Western Pomerania, Germany. <i>PLoS ONE</i> , <b>2015</b> , 10, e0143326	3.7	95
205	Population dynamics among methicillin-resistant <i>Staphylococcus aureus</i> isolates in Germany during a 6-year period. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 3186-92	9.7	93
204	Virulence from vesicles: Novel mechanisms of host cell injury by <i>Escherichia coli</i> O104:H4 outbreak strain. <i>Scientific Reports</i> , <b>2015</b> , 5, 13252	4.9	92
203	Characterization of <i>Escherichia coli</i> isolates from hospital inpatients or outpatients with urinary tract infection. <i>Journal of Clinical Microbiology</i> , <b>2014</b> , 52, 407-18	9.7	89
202	Whole genome sequencing as a tool to investigate a cluster of seven cases of listeriosis in Austria and Germany, 2011-2013. <i>Clinical Microbiology and Infection</i> , <b>2014</b> , 20, 431-6	9.5	88
201	Shiga toxin 2e-producing <i>Escherichia coli</i> isolates from humans and pigs differ in their virulence profiles and interactions with intestinal epithelial cells. <i>Applied and Environmental Microbiology</i> , <b>2005</b> , 71, 8855-63	4.8	88

200	Shiga toxin-negative attaching and effacing Escherichia coli: distinct clinical associations with bacterial phylogeny and virulence traits and inferred in-host pathogen evolution. <i>Clinical Infectious Diseases</i> , <b>2008</b> , 47, 208-17	11.6	86
199	Variation of the polymorphic region X of the protein A gene during persistent airway infection of cystic fibrosis patients reflects two independent mechanisms of genetic change in Staphylococcus aureus. <i>Journal of Clinical Microbiology</i> , <b>2005</b> , 43, 502-5	9.7	83
198	Origin, evolution, and global transmission of community-acquired ST8. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E10596-E10604	11.5	80
197	Characterization of clonal relatedness among the natural population of Staphylococcus aureus strains by using spa sequence typing and the BURP (based upon repeat patterns) algorithm. <i>Journal of Clinical Microbiology</i> , <b>2008</b> , 46, 2805-8	9.7	80
196	Virulence factors and genotypes of Staphylococcus aureus from infection and carriage in Gabon. <i>Clinical Microbiology and Infection</i> , <b>2011</b> , 17, 1507-13	9.5	76
195	First Reported Nosocomial Outbreak of Severe Acute Respiratory Syndrome Coronavirus 2 in a Pediatric Dialysis Unit. <i>Clinical Infectious Diseases</i> , <b>2021</b> , 72, 265-270	11.6	76
194	Cross-border comparison of the admission prevalence and clonal structure of methicillin-resistant Staphylococcus aureus. <i>Journal of Hospital Infection</i> , <b>2009</b> , 71, 320-6	6.9	68
193	A Pandemic in Times of Global Tourism: Superspreading and Exportation of COVID-19 Cases from a Ski Area in Austria. <i>Journal of Clinical Microbiology</i> , <b>2020</b> , 58,	9.7	64
192	High Interlaboratory Reproducibility and Accuracy of Next-Generation-Sequencing-Based Bacterial Genotyping in a Ring Trial. <i>Journal of Clinical Microbiology</i> , <b>2017</b> , 55, 908-913	9.7	59
191	Are cases of Methicillin-resistant Staphylococcus aureus clonal complex (CC) 398 among humans still livestock-associated?. <i>International Journal of Medical Microbiology</i> , <b>2015</b> , 305, 110-3	3.7	55
190	Phylogeny, clinical associations, and diagnostic utility of the pilin subunit gene (sfpA) of sorbitol-fermenting, enterohemorrhagic Escherichia coli O157:H-. <i>Journal of Clinical Microbiology</i> , <b>2004</b> , 42, 4697-701	9.7	55
189	Synergistic adaptive mutations in the hemagglutinin and polymerase acidic protein lead to increased virulence of pandemic 2009 H1N1 influenza A virus in mice. <i>Journal of Infectious Diseases</i> , <b>2012</b> , 205, 262-71	7	53
188	Recycling of Shiga toxin 2 genes in sorbitol-fermenting enterohemorrhagic Escherichia coli O157:NM. <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 67-72	4.8	53
187	Chromosomal dynamism in progeny of outbreak-related sorbitol-fermenting enterohemorrhagic Escherichia coli O157:NM. <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 1900-9	4.8	52
186	Inactivation of thyA in Staphylococcus aureus attenuates virulence and has a strong impact on metabolism and virulence gene expression. <i>MBio</i> , <b>2014</b> , 5, e01447-14	7.8	51
185	High burden of extended-spectrum $\beta$ -lactamase-producing Enterobacteriaceae in Gabon. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2013</b> , 68, 2140-3	5.1	49
184	Comparison of asymptomatic bacteriuria Escherichia coli isolates from healthy individuals versus those from hospital patients shows that long-term bladder colonization selects for attenuated virulence phenotypes. <i>Infection and Immunity</i> , <b>2012</b> , 80, 668-78	3.7	49
183	Subtypes of the plasmid-encoded serine protease EspP in Shiga toxin-producing Escherichia coli: distribution, secretion, and proteolytic activity. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 6351-9	4.8	49

182	The epidemiology of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) in Germany. <i>Deutsches A&amp;#x0308;rztblatt International</i> , <b>2011</b> , 108, 761-7	2.5	48
181	Structural and functional differences between disease-associated genes of enterohaemorrhagic <i>Escherichia coli</i> O111. <i>International Journal of Medical Microbiology</i> , <b>2007</b> , 297, 17-26	3.7	48
180	<i>Staphylococcus aureus</i> complex from animals and humans in three remote African regions. <i>Clinical Microbiology and Infection</i> , <b>2015</b> , 21, 345.e1-8	9.5	47
179	Shiga toxin, cytolethal distending toxin, and hemolysin repertoires in clinical <i>Escherichia coli</i> O91 isolates. <i>Journal of Clinical Microbiology</i> , <b>2009</b> , 47, 2061-6	9.7	46
178	Evidence for cost reduction based on pre-admission MRSA screening in general surgery. <i>International Journal of Hygiene and Environmental Health</i> , <b>2008</b> , 211, 205-12	6.9	44
177	Highly divergent <i>Staphylococcus aureus</i> isolates from African non-human primates. <i>Environmental Microbiology Reports</i> , <b>2012</b> , 4, 141-6	3.7	43
176	Phylogeny and disease association of Shiga toxin-producing <i>Escherichia coli</i> O91. <i>Emerging Infectious Diseases</i> , <b>2009</b> , 15, 1474-7	10.2	42
175	Simultaneous occurrence of MRSA and ESBL-producing Enterobacteriaceae on pig farms and in nasal and stool samples from farmers. <i>Veterinary Microbiology</i> , <b>2017</b> , 200, 107-113	3.3	40
174	Gut Colonization of Healthy Children and Their Mothers With Pathogenic Ciprofloxacin-Resistant <i>Escherichia coli</i> . <i>Journal of Infectious Diseases</i> , <b>2015</b> , 212, 1862-8	7	39
173	Heteropathogenic virulence and phylogeny reveal phased pathogenic metamorphosis in <i>Escherichia coli</i> O2:H6. <i>EMBO Molecular Medicine</i> , <b>2014</b> , 6, 347-57	12	39
172	Is Shiga Toxin-Negative <i>Escherichia coli</i> O157:H7 Enteropathogenic or Enterohemorrhagic <i>Escherichia coli</i> ? Comprehensive Molecular Analysis Using Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , <b>2015</b> , 53, 3530-8	9.7	38
171	Evaluation of RIDOM, MicroSeq, and Genbank services in the molecular identification of <i>Nocardia</i> species. <i>International Journal of Medical Microbiology</i> , <b>2003</b> , 293, 359-70	3.7	38
170	<i>Acinetobacter septicus</i> sp. nov. association with a nosocomial outbreak of bacteremia in a neonatal intensive care unit. <i>Journal of Clinical Microbiology</i> , <b>2008</b> , 46, 902-8	9.7	37
169	In the centre of an epidemic: Fifteen years of LA-MRSA CC398 at the University Hospital M&#x00dc;nster. <i>Veterinary Microbiology</i> , <b>2017</b> , 200, 19-24	3.3	36
168	Defining and Evaluating a Core Genome Multilocus Sequence Typing Scheme for Genome-Wide Typing of <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , <b>2018</b> , 56,	9.7	36
167	<i>Staphylococcus pettenkoferi</i> sp. nov., a novel coagulase-negative staphylococcal species isolated from human clinical specimens. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2007</b> , 57, 1543-1548	2.2	36
166	EUREGIO MRSA-net Twente/M&#x00dc;nsterland--a Dutch-German cross-border network for the prevention and control of infections caused by methicillin-resistant <i>Staphylococcus aureus</i> . <i>Eurosurveillance</i> , <b>2008</b> , 13,	19.8	36
165	Hemolytic uremic syndrome in a 65-Year-old male linked to a very unusual type of stx2e- and eae-harboring O51:H49 shiga toxin-producing <i>Escherichia coli</i> . <i>Journal of Clinical Microbiology</i> , <b>2014</b> , 52, 1301-3	9.7	35

164	Highly Virulent Non-O157 Enterohemorrhagic Escherichia coli (EHEC) Serotypes Reflect Similar Phylogenetic Lineages, Providing New Insights into the Evolution of EHEC. <i>Applied and Environmental Microbiology</i> , <b>2015</b> , 81, 7041-7	4.8	33
163	Detecting Staphylococcus aureus Virulence and Resistance Genes: a Comparison of Whole-Genome Sequencing and DNA Microarray Technology. <i>Journal of Clinical Microbiology</i> , <b>2016</b> , 54, 1008-16	9.7	33
162	Phylogenetic and molecular analysis of food-borne shiga toxin-producing Escherichia coli. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 2731-40	4.8	33
161	Rapid high resolution genotyping of Francisella tularensis by whole genome sequence comparison of annotated genes ("MLST+"). <i>PLoS ONE</i> , <b>2015</b> , 10, e0123298	3.7	33
160	Intrahost genome alterations in enterohemorrhagic Escherichia coli. <i>Gastroenterology</i> , <b>2009</b> , 136, 1925-38	3.3	33
159	A nosocomial cluster of vancomycin resistant enterococci among COVID-19 patients in an intensive care unit. <i>Antimicrobial Resistance and Infection Control</i> , <b>2020</b> , 9, 154	6.2	31
158	Label-free imaging and spectroscopic analysis of intracellular bacterial infections. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 2137-42	7.8	30
157	Antibiotic-Mediated Modulations of Outer Membrane Vesicles in Enterohemorrhagic Escherichia coli O104:H4 and O157:H7. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2017</b> , 61,	5.9	29
156	Detection of mecA- and mecC-Positive Methicillin-Resistant Staphylococcus aureus (MRSA) Isolates by the New Xpert MRSA Gen 3 PCR Assay. <i>Journal of Clinical Microbiology</i> , <b>2016</b> , 54, 180-4	9.7	29
155	Sequence-based typing of flaB is a more stable screening tool than typing of flaA for monitoring of Campylobacter populations. <i>Journal of Clinical Microbiology</i> , <b>2004</b> , 42, 4840-2	9.7	28
154	Enterohemorrhagic Escherichia coli O26:H11-Associated Hemolytic Uremic Syndrome: Bacteriology and Clinical Presentation. <i>Seminars in Thrombosis and Hemostasis</i> , <b>2010</b> , 36, 586-93	5.3	27
153	Towards 3D modelling and imaging of infection scenarios at the single cell level using holographic optical tweezers and digital holographic microscopy. <i>Journal of Biophotonics</i> , <b>2013</b> , 6, 260-6	3.1	26
152	Semi-selective broth improves screening for methicillin-resistant Staphylococcus aureus. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2010</b> , 65, 717-20	5.1	26
151	Dynamic in vivo mutations within the ica operon during persistence of Staphylococcus aureus in the airways of cystic fibrosis patients. <i>PLoS Pathogens</i> , <b>2016</b> , 12, e1006024	7.6	26
150	Enterohemorrhagic Escherichia coli O157 outer membrane vesicles induce interleukin 8 production in human intestinal epithelial cells by signaling via Toll-like receptors TLR4 and TLR5 and activation of the nuclear factor NF- $\kappa$ B. <i>International Journal of Medical Microbiology</i> , <b>2018</b> , 308, 882-889	3.7	26
149	Whole-Genome Sequencing Elucidates Epidemiology of Nosocomial Clusters of Acinetobacter baumannii. <i>Journal of Clinical Microbiology</i> , <b>2016</b> , 54, 2391-4	9.7	25
148	Lability of the pAA Virulence Plasmid in Escherichia coli O104:H4: Implications for Virulence in Humans. <i>PLoS ONE</i> , <b>2013</b> , 8, e66717	3.7	25
147	Chromosomal instability in enterohaemorrhagic Escherichia coli O157:H7: impact on adherence, tellurite resistance and colony phenotype. <i>Molecular Microbiology</i> , <b>2011</b> , 79, 1024-44	4.1	25



146	Distribution of capsular and surface polysaccharide serotypes of <i>Staphylococcus aureus</i> . <i>Diagnostic Microbiology and Infectious Disease</i> , <b>2007</b> , 58, 297-302	2.9	25
145	State-wide surveillance of antibiotic resistance patterns and spa types of methicillin-resistant <i>Staphylococcus aureus</i> from blood cultures in North Rhine-Westphalia, 2011-2013. <i>Clinical Microbiology and Infection</i> , <b>2015</b> , 21, 750-7	9.5	24
144	Social structure and <i>Escherichia coli</i> sharing in a group-living wild primate, Verreaux's sifaka. <i>BMC Ecology</i> , <b>2016</b> , 16, 6	2.7	24
143	Acquisition and colonization dynamics of antimicrobial-resistant bacteria during international travel: a prospective cohort study. <i>Clinical Microbiology and Infection</i> , <b>2019</b> , 25, 1287.e1-1287.e7	9.5	24
142	Detection and characterization of the fimbrial sfp cluster in enterohemorrhagic <i>Escherichia coli</i> O165:H25/NM isolates from humans and cattle. <i>Applied and Environmental Microbiology</i> , <b>2009</b> , 75, 64-71	4.8	24
141	Staphylococcal chromosomal cassette mec type I, spa type, and expression of PIs are determinants of reduced cellular invasiveness of methicillin-resistant <i>Staphylococcus aureus</i> isolates. <i>Journal of Infectious Diseases</i> , <b>2007</b> , 195, 1678-85	7	24
140	Phosphorylation of influenza A virus NS1 protein at threonine 49 suppresses its interferon antagonistic activity. <i>Cellular Microbiology</i> , <b>2016</b> , 18, 784-91	3.9	23
139	Development and evaluation of a novel universal $\beta$ -lactamase gene subtyping assay for blaSHV, blaTEM and blaCTX-M using clinical and livestock-associated <i>Escherichia coli</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>2015</b> , 70, 710-5	5.1	23
138	Intrahost milieu modulates production of outer membrane vesicles, vesicle-associated Shiga toxin 2a and cytotoxicity in <i>Escherichia coli</i> O157:H7 and O104:H4. <i>Environmental Microbiology Reports</i> , <b>2017</b> , 9, 626-634	3.7	22
137	The risk to import ESBL-producing Enterobacteriaceae and <i>Staphylococcus aureus</i> through chicken meat trade in Gabon. <i>BMC Microbiology</i> , <b>2014</b> , 14, 286	4.5	22
136	Evolution of enterohemorrhagic <i>Escherichia coli</i> O26 based on single-nucleotide polymorphisms. <i>Genome Biology and Evolution</i> , <b>2013</b> , 5, 1807-16	3.9	22
135	Weekly screening supports terminating nosocomial transmissions of vancomycin-resistant enterococci on an oncologic ward - a retrospective analysis. <i>Antimicrobial Resistance and Infection Control</i> , <b>2017</b> , 6, 48	6.2	21
134	Microbiologic contamination and time efficiency of use of automatic MDCT injectors with prefilled syringes: Results of a clinical investigation. <i>American Journal of Roentgenology</i> , <b>2010</b> , 194, 299-303	5.4	21
133	Enterohaemorrhagic <i>Escherichia coli</i> O26:H11/H-: a human pathogen in emergence. <i>Berliner Und Munchener Tierarztliche Wochenschrift</i> , <b>2007</b> , 120, 279-87		21
132	Community-Associated <i>Staphylococcus aureus</i> from Sub-Saharan Africa and Germany: A Cross-Sectional Geographic Correlation Study. <i>Scientific Reports</i> , <b>2017</b> , 7, 154	4.9	20
131	Control of Multidrug-Resistant <i>Pseudomonas aeruginosa</i> in Allogeneic Hematopoietic Stem Cell Transplant Recipients by a Novel Bundle Including Remodeling of Sanitary and Water Supply Systems. <i>Clinical Infectious Diseases</i> , <b>2017</b> , 65, 935-942	11.6	20
130	Ensuring backwards compatibility: traditional genotyping efforts in the era of whole genome sequencing. <i>Clinical Microbiology and Infection</i> , <b>2015</b> , 21, 347.e1-4	9.5	20
129	A geospatial analysis of flies and the spread of antimicrobial resistant bacteria. <i>International Journal of Medical Microbiology</i> , <b>2016</b> , 306, 566-571	3.7	20

128	Molecular Typing of Enterobacteriaceae from Pig Holdings in North-Western Germany Reveals Extended-Spectrum and AmpC $\beta$ -Lactamases Producing but no Carbapenem Resistant Ones. <i>PLoS ONE</i> , <b>2015</b> , 10, e0134533	3.7	19
127	Evolutionary analysis and distribution of type III effector genes in pathogenic <i>Escherichia coli</i> from human, animal and food sources. <i>Environmental Microbiology</i> , <b>2011</b> , 13, 439-52	5.2	19
126	Unveiling the molecular basis of antimicrobial resistance in <i>Staphylococcus aureus</i> from the Democratic Republic of the Congo using whole genome sequencing. <i>Clinical Microbiology and Infection</i> , <b>2016</b> , 22, 644.e1-5	9.5	19
125	Co-detection of Panton-Valentine leukocidin encoding genes and cotrimoxazole resistance in <i>Staphylococcus aureus</i> in Gabon: implications for HIV-patients' care. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 60	5.7	18
124	A Nosocomial Foodborne Outbreak of a VIM Carbapenemase-Expressing <i>Citrobacter freundii</i> . <i>Clinical Infectious Diseases</i> , <b>2018</b> , 67, 58-64	11.6	18
123	Detection of a phylogenetically distinct IMP-type metallo- $\beta$ -lactamase, IMP-35, in a CC235 <i>Pseudomonas aeruginosa</i> from the Dutch-German border region (Euregio). <i>Journal of Antimicrobial Chemotherapy</i> , <b>2013</b> , 68, 1271-6	5.1	18
122	Phylogenetic analysis of enterohemorrhagic <i>Escherichia coli</i> O157, Germany, 1987-2008. <i>Emerging Infectious Diseases</i> , <b>2010</b> , 16, 610-6	10.2	18
121	Real-time multiplex PCR for detecting Shiga toxin 2-producing <i>Escherichia coli</i> O104:H4 in human stools. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 1752-4	9.7	18
120	Outbreak of complex infections associated with contaminated octenidine mouthwash solution, Germany, August to September 2018. <i>Eurosurveillance</i> , <b>2018</b> , 23,	19.8	18
119	Susceptibility of MDR <i>Pseudomonas aeruginosa</i> to ceftolozane/tazobactam and comparison of different susceptibility testing methods. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2017</b> , 72, 3079-3084	5.1	17
118	Transcriptional adaptations during long-term persistence of <i>Staphylococcus aureus</i> in the airways of a cystic fibrosis patient. <i>International Journal of Medical Microbiology</i> , <b>2015</b> , 305, 38-46	3.7	17
117	Distribution and phylogeny of immunoglobulin-binding protein G in Shiga toxin-producing <i>Escherichia coli</i> and its association with adherence phenotypes. <i>Infection and Immunity</i> , <b>2010</b> , 78, 3625-36	3.7	17
116	Microbiologic contamination of automatic injectors at MDCT: experimental and clinical investigations. <i>American Journal of Roentgenology</i> , <b>2008</b> , 191, W283-7	5.4	17
115	Carriage of Shiga toxin phage profoundly affects <i>Escherichia coli</i> gene expression and carbon source utilization. <i>BMC Genomics</i> , <b>2019</b> , 20, 504	4.5	16
114	High Nuclease Activity of Long Persisting Isolates Within the Airways of Cystic Fibrosis Patients Protects Against NET-Mediated Killing. <i>Frontiers in Immunology</i> , <b>2019</b> , 10, 2552	8.4	16
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- 2 Phenotypic Variants of Bacterial Colonies in Microbiological Diagnostics: How Often Are They Indicative of Differing Antimicrobial Susceptibility Patterns?. *Microbiology Spectrum*, **2021**, 9, e0055521 8.9
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