Rob Willems

List of Publications by Year
in descending order

178 papers	13,911 citations	22548 61 h-index	27587 110 g-index
182 all docs	182 docs citations	182 times ranked	11847 citing authors

#	Article	IF	Citations
1	Comparative genomics of ESBL-producingEscherichia coli(ESBL-Ec) reveals a similar distribution of the 10 most prevalent ESBL-Ec clones and ESBL genes among human community faecal and extra-intestinal infection isolates in the Netherlands (2014â€“17). Journal of Antimicrobial Chemotherapy, 2021, 76, 901-908.	1.3	17
2	Recovering Escherichia coli Plasmids in the Absence of Long-Read Sequencing Data. Microorganisms, 2021, 9, 1613.	1.6	9
3	Functional characterization of a gene cluster responsible for inositol catabolism associated with hospital-adapted isolates of Enterococcus faecium. Microbiology (United Kingdom), 2021, 167, .	0.7	0
4	Microevolution of acquired colistin resistance in Enterobacteriaceae from ICU patients receiving selective decontamination of the digestive tract. Journal of Antimicrobial Chemotherapy, 2020, 75, 3135-3143.	1.3	18
5	Whole Genome Sequence Analysis of the First Vancomycin-Resistant Enterococcus faecium Isolates from a Libyan Hospital in Tripoli. Microbial Drug Resistance, 2020, 26, 1390-1398.	0.9	10
6	Mutational signature in colorectal cancer caused by genotoxic pks+ E. coli. Nature, 2020, 580, 269-273.	13.7	587
7	Low IgA Associated With Oropharyngeal Microbiota Changes and Lung Disease in Primary Antibody Deficiency. Frontiers in Immunology, 2020, 11, 1245.	2.2	25
8	Extended-spectrum beta-lactamase (ESBL)-producing and non-ESBL-producing Escherichia coli isolates causing bacteremia in the Netherlands (2014 â€“ 2016) differ in clonal distribution, antimicrobial resistance gene and virulence gene content. PLoS ONE, 2020, 15, e0227604.	1.1	31
9	Genomic rearrangements uncovered by genome-wide co-evolution analysis of a major nosocomial pathogen, Enterococcus faecium. Microbial Genomics, 2020, 6, .	1.0	9
10	Lowâ€calcium diet in mice leads to reduced gut colonization by Enterococcus faecium. MicrobiologyOpen, 2019, 8, e936.	1.2	3
11	In vivo acquisition of fosfomycin resistance in Escherichia coli by fosA transmission from commensal flora. Journal of Antimicrobial Chemotherapy, 2019, 74, 3630-3632.	1.3	18
12	Phylogenomics of Enterococcus faecalis from wild birds: new insights into hostâ€associated differences in core and accessory genomes of the species. Environmental Microbiology, 2019, 21, 3046-3062.	1.8	14
13	Prediction of the intestinal resistome by a three-dimensional structure-based method. Nature Microbiology, 2019, 4, 112-123.	5.9	129
14	Enterococcus faecium genome dynamics during long-term asymptomatic patient gut colonization. Microbial Genomics, 2019, 5, .	1.0	18
15	Primary murine mucosal response during cephalosporinâ€induced intestinal colonization by Enterococcus faecium. MicrobiologyOpen, 2018, 7, e00602.	1.2	5
16	Whole genome sequencing options for bacterial strain typing and epidemiologic analysis based on single nucleotide polymorphism versus gene-by-geneâ€“based approaches. Clinical Microbiology and Infection, 2018, 24, 350-354.	2.8	373
17	Intestinal carriage of ampicillin- and vancomycin-resistant Enterococcus faecium in humans, dogs and cats in the Netherlands. Journal of Antimicrobial Chemotherapy, 2018, 73, 607-614.	1.3	27
18	The Two-Component System ChtRS Contributes to Chlorhexidine Tolerance in Enterococcus faecium. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	33

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19	Lipoteichoic acid synthesis inhibition in combination with antibiotics abrogates growth of multidrug-resistant Enterococcus faecium. International Journal of Antimicrobial Agents, 2017, 49, 355-363.	1.1	21
20	Multidrug-Resistant Enterococcal Infections: New Compounds, Novel Antimicrobial Therapies?. Trends in Microbiology, 2017, 25, 467-479.	3.5	98
21	De novo identification of lipid II binding lipopeptides with antibacterial activity against vancomycin-resistant bacteria. Chemical Science, 2017, 8, 7991-7997.	3.7	12
22	Characterization of Enterococcus Isolates Colonizing the Intestinal Tract of Intensive Care Unit Patients Receiving Selective Digestive Decontamination. Frontiers in Microbiology, 2017, 8, 1596.	1.5	18
23	Global Emergence and Dissemination of Enterococci as Nosocomial Pathogens: Attack of the Clones?. Frontiers in Microbiology, 2016, 7, 788.	1.5	248
24	The Effect of Strict Segregation on Pseudomonas aeruginosa in Cystic Fibrosis Patients. PLoS ONE, 2016, 11, e0157189.	1.1	11
25	Complete Genome Sequence of Enterococcus faecium Commensal Isolate E1002. Genome Announcements, 2016, 4, .	0.8	2
26	The N-terminal domain of the thermo-regulated surface protein PrpA of Enterococcus faecium binds to fibrinogen, fibronectin and platelets. Scientific Reports, 2016, 5, 18255.	1.6	12
27	Multilevel population genetic analysis ofvanAandvanB Enterococcus faeciumcausing nosocomial outbreaks in 27 countries (1986â€“2012). Journal of Antimicrobial Chemotherapy, 2016, 71, 3351-3366.	1.3	129
28	Whole-Genome Multilocus Sequence Typing of Extended-Spectrum-Beta-Lactamase-Producing Enterobacteriaceae. Journal of Clinical Microbiology, 2016, 54, 2919-2927.	1.8	97
29	Genome-wide Screening Identifies Phosphotransferase System Permease BepA to Be Involved inEnterococcus faeciumEndocarditis and Biofilm Formation. Journal of Infectious Diseases, 2016, 214, 189-195.	1.9	36
30	The impact of host metapopulation structure on the population genetics of colonizing bacteria. Journal of Theoretical Biology, 2016, 396, 53-62.	0.8	13
31	Molecular epidemiology of MRSA in 13 ICUs from eight European countries. Journal of Antimicrobial Chemotherapy, 2016, 71, 45-52.	1.3	43
32	Synergistic activity of a short lipidated antimicrobial peptide (lipoAMP) and colistin or tobramycin against Pseudomonas aeruginosa from cystic fibrosis patients. MedChemComm, 2016, 7, 148-156.	3.5	14
33	Within-Host Evolution of the Dutch High-Prevalent Pseudomonas aeruginosa Clone ST406 during Chronic Colonization of a Patient with Cystic Fibrosis. PLoS ONE, 2016, 11, e0158106.	1.1	23
34	The Association Between Colonization With Carbapenemase-Producing Enterobacteriaceae and Overall ICU Mortality. Critical Care Medicine, 2015, 43, 1170-1177.	0.4	77
35	Growth conditionâ€dependent cell surface proteome analysis of Enterococcus faecium. Proteomics, 2015, 15, 3806-3814.	1.3	3
36	What Is the Origin of Livestock-Associated Methicillin-Resistant Staphylococcus aureus Clonal Complex 398 Isolates from Humans without Livestock Contact? An Epidemiological and Genetic Analysis. Journal of Clinical Microbiology, 2015, 53, 1836-1841.	1.8	46

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37	Antibiotic-Driven Dysbiosis Mediates Intraluminal Agglutination and Alternative Segregation of Enterococcus faecium from the Intestinal Epithelium. MBio, 2015, 6, e01346-15.	1.8	52
38	Population Biology of Intestinal Enterococcus Isolates from Hospitalized and Nonhospitalized Individuals in Different Age Groups. Applied and Environmental Microbiology, 2015, 81, 1820-1831.	1.4	75
39	Comparison of an ST80 MRSA strain from the USA with European ST80 strains. Journal of Antimicrobial Chemotherapy, 2015, 70, 664-669.	1.3	14
40	Distinct SagA from Hospital-Associated Clade A1 Enterococcus faecium Strains Contributes to Biofilm Formation. Applied and Environmental Microbiology, 2015, 81, 6873-6882.	1.4	35
41	Semisynthetic Lipopeptides Derived from Nisin Display Antibacterial Activity and Lipid II Binding on Par with That of the Parent Compound. Journal of the American Chemical Society, 2015, 137, 9382-9389.	6.6	70
42	Genetic relatedness and risk factor analysis of ampicillin-resistant and high-level gentamicin-resistant enterococci causing bloodstream infections in Tanzanian children. BMC Infectious Diseases, 2015, 15, 107.	1.3	15
43	A Genomic Virulence Reference Map of Enterococcus faecalis Reveals an Important Contribution of Phage03-Like Elements in Nosocomial Genetic Lineages to Pathogenicity in a Caenorhabditis elegans Infection Model. Infection and Immunity, 2015, 83, 2156-2167.	1.0	15
44	Core Genome Multilocus Sequence Typing Scheme for High-Resolution Typing of Enterococcus faecium. Journal of Clinical Microbiology, 2015, 53, 3788-3797.	1.8	240
45	Investigating the mobilome in clinically important lineages of Enterococcus faecium and Enterococcus faecalis. BMC Genomics, 2015, 16, 282.	1.2	82
46	Environmental survival of vancomycin-sensitive ampicillin-resistant Enterococcus faecium (AREfm). European Journal of Clinical Microbiology and Infectious Diseases, 2015, 34, 1901-1903.	1.3	11
47	Dissemination of Cephalosporin Resistance Genes between Escherichia coli Strains from Farm Animals and Humans by Specific Plasmid Lineages. PLoS Genetics, 2014, 10, e1004776.	1.5	276
48	Interventions to reduce colonisation and transmission of antimicrobial-resistant bacteria in intensive care units: an interrupted time series study and cluster randomised trial. Lancet Infectious Diseases, The, 2014, 14, 31-39.	4.6	297
49	Effects of selective digestive decontamination (SDD) on the gut resistome. Journal of Antimicrobial Chemotherapy, 2014, 69, 2215-2223.	1.3	90
50	Functional genomic analysis of bile salt resistance in Enterococcus faecium. BMC Genomics, 2013, 14, 299.	1.2	29
51	The cell wall architecture of Enterococcus faecium: from resistance to pathogenesis. Future Microbiology, 2013, 8, 993-1010.	1.0	33
52	Multiple-Locus Variable Number Tandem Repeat Analysis Typing of Vancomycin-Resistant Enterococcus faecium in Serbia. Infection Control and Hospital Epidemiology, 2013, 34, 1337-1339.	1.0	1
53	Identification of a Genetic Determinant in Clinical Enterococcus faecium Strains That Contributes to Intestinal Colonization During Antibiotic Treatment. Journal of Infectious Diseases, 2013, 207, 1780-1786.	1.9	79
54	Shared reservoir of ccrB gene sequences between coagulase-negative staphylococci and methicillin-resistant Staphylococcus aureus. Journal of Antimicrobial Chemotherapy, 2013, 68, 1707-1713.	1.3	29

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55	Recent Recombination Events in the Core Genome Are Associated with Adaptive Evolution in Enterococcus faecium. Genome Biology and Evolution, 2013, 5, 1524-1535.	1.1	87
56	Emergence of Epidemic Multidrug-Resistant Enterococcus faecium from Animal and Commensal Strains. MBio, 2013, 4, .	1.8	336
57	Pseudomonas aeruginosa Genotype Prevalence in Dutch Cystic Fibrosis Patients and Age Dependency of Colonization by Various P. aeruginosa Sequence Types. Journal of Clinical Microbiology, 2013, 51, 386-386.	1.8	0
58	Enterococcus faecium Biofilm Formation: Identification of Major Autolysin AtlA _{Efm} , Associated Acm Surface Localization, and AtlA _{Efm} -Independent Extracellular DNA Release. MBio, 2013, 4, e00154.	1.8	49
59	The Enterococcus faecium Enterococcal Biofilm Regulator, EbrB, Regulates the esp Operon and Is Implicated in Biofilm Formation and Intestinal Colonization. PLoS ONE, 2013, 8, e65224.	1.1	45
60	A LacI-Family Regulator Activates Maltodextrin Metabolism of Enterococcus faecium. PLoS ONE, 2013, 8, e72285.	1.1	8
61	Genome-Wide Identification of Ampicillin Resistance Determinants in Enterococcus faecium. PLoS Genetics, 2012, 8, e1002804.	1.5	83
62	AsrR Is an Oxidative Stress Sensing Regulator Modulating Enterococcus faecium Opportunistic Traits, Antimicrobial Resistance, and Pathogenicity. PLoS Pathogens, 2012, 8, e1002834.	2.1	70
63	Insight into antimicrobial susceptibility and population structure of contemporary human Enterococcus faecalis isolates from Europe. Journal of Antimicrobial Chemotherapy, 2012, 67, 551-558.	1.3	102
64	Restricted Gene Flow among Hospital Subpopulations of Enterococcus faecium. MBio, 2012, 3, e00151-12.	1.8	177
65	Optimizing future treatment of enterococcal infections: attacking the biofilm?. Trends in Microbiology, 2012, 20, 40-49.	3.5	92
66	Dynamics of ampicillin-resistant Enterococcus faecium clones colonizing hospitalized patients: data from a prospective observational study. BMC Infectious Diseases, 2012, 12, 68.	1.3	24
67	Hospital and Community Ampicillin-Resistant Enterococcus faecium Are Evolutionarily Closely Linked but Have Diversified through Niche Adaptation. PLoS ONE, 2012, 7, e30319.	1.1	45
68	High-density fecal Enterococcus faecium colonization in hospitalized patients is associated with the presence of the polyclonal subcluster CC17. European Journal of Clinical Microbiology and Infectious Diseases, 2012, 31, 519-522.	1.3	22
69	First outbreak of VIM-2 metallo-Î²-lactamase-producing Pseudomonas aeruginosa in The Netherlands: microbiology, epidemiology and clinical outcomes. International Journal of Antimicrobial Agents, 2011, 37, 513-518.	1.1	46
70	Contribution of the enterococcal surface protein Esp to pathogenesis of Enterococcus faecium endocarditis. Microbes and Infection, 2011, 13, 1185-1190.	1.0	63
71	Genetic Variation in Spatio-Temporal Confined USA300 Community-Associated MRSA Isolates: A Shift from Clonal Dispersion to Genetic Evolution?. PLoS ONE, 2011, 6, e16419.	1.1	15
72	Intra- and Interspecies Genomic Transfer of the Enterococcus faecalis Pathogenicity Island. PLoS ONE, 2011, 6, e16720.	1.1	54

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73	A genetic element present on megaplasmids allows Enterococcus faecium to use raffinose as carbon source. Environmental Microbiology, 2011, 13, 518-528.	1.8	48
74	Clinical impact of a highly prevalent Pseudomonas aeruginosa clone in Dutch cystic fibrosis patients. Clinical Microbiology and Infection, 2011, 17, 382-385.	2.8	12
75	Aspergillus fumigatus colonization in cystic fibrosis: implications for lung function?. Clinical Microbiology and Infection, 2011, 17, 1381-1386.	2.8	98
76	Population biology of Gram-positive pathogens: high-risk clones for dissemination of antibiotic resistance. FEMS Microbiology Reviews, 2011, 35, 872-900.	3.9	173
77	Environmental survival of vancomycin-resistant Enterococcus faecium. Journal of Hospital Infection, 2011, 77, 282-283.	1.4	50
78	Comparison of the identification of coagulase-negative staphylococci by matrix-assisted laser desorption ionization time-of-flight mass spectrometry and tuf sequencing. European Journal of Clinical Microbiology and Infectious Diseases, 2011, 30, 1169-1172.	1.3	44
79	Comparative genomic analysis reveals significant enrichment of mobile genetic elements and genes encoding surface structure-proteins in hospital-associated clonal complex 2 Enterococcus faecalis. BMC Microbiology, 2011, 11, 3.	1.3	43
80	The Recombinase IntA Is Required for Excision of esp -Containing ICE Efm1 in Enterococcus faecium. Journal of Bacteriology, 2011, 193, 1003-1006.	1.0	22
81	Wide Dispersion of ST175 Clone despite High Genetic Diversity of Carbapenem-Nonsusceptible Pseudomonas aeruginosa Clinical Strains in 16 Spanish Hospitals. Journal of Clinical Microbiology, 2011, 49, 2905-2910.	1.8	76
82	Molecular analysis of ciprofloxacin resistance and clonal relatedness of clinical Escherichia coli isolates from haematology patients receiving ciprofloxacin prophylaxis. Journal of Antimicrobial Chemotherapy, 2011, 66, 1739-1744.	1.3	7
83	Host range of enterococcal vanA plasmids among Gram-positive intestinal bacteria. Journal of Antimicrobial Chemotherapy, 2011, 66, 273-282.	1.3	55
84	Rhesus Macaques (Macaca mulatta) Are Natural Hosts of Specific Staphylococcus aureus Lineages. PLoS ONE, 2011, 6, e26170.	1.1	31
85	Pyrosequencing-based comparative genome analysis of the nosocomial pathogen Enterococcus faecium and identification of a large transferable pathogenicity island. BMC Genomics, 2010, 11, 239.	1.2	190
86	Effects of reducing beta-lactam antibiotic pressure on intestinal colonization of antibiotic-resistant gram-negative bacteria. Intensive Care Medicine, 2010, 36, 512-519.	3.9	41
87	Genome-based insights into the evolution of enterococci. Clinical Microbiology and Infection, 2010, 16, 527-532.	2.8	72
88	Enterococcus research: recent developments and clinical challenges. Clinical Microbiology and Infection, 2010, 16, 525-526.	2.8	12
89	The Complement System Facilitates Clearance ofEnterococcus faeciumduring Murine Peritonitis. Journal of Infectious Diseases, 2010, 201, 544-552.	1.9	17
90	Enterococcal surface protein contributes to persistence in the host but is not a target of opsonic and protective antibodies in Enterococcus faecium infection. Journal of Medical Microbiology, 2010, 59, 1001-1004.	0.7	21

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91	Effects of Probiotics on Acquisition and Spread of Multiresistant Enterococci. Antimicrobial Agents and Chemotherapy, 2010, 54, 2801-2805.	1.4	24
92	Differential PilA pilus assembly by a hospital-acquired and a community-derived Enterococcus faecium isolate. Microbiology (United Kingdom), 2010, 156, 2649-2659.	0.7	17
93	Insights into the biofilm lifestyle of enterococci. Virulence, 2010, 1, 219-221.	1.8	15
94	ccrAB Ent serine recombinase genes are widely distributed in the Enterococcus faecium and Enterococcus casseliflavus species groups and are expressed in E. faecium. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	0.7	2
95	The Population Genetics of Pseudomonas aeruginosa Isolates from Different Patient Populations Exhibits High-Level Host Specificity. PLoS ONE, 2010, 5, e13482.	1.1	43
96	Intestinal Colonization with Enterococcus faecium Does Not Influence Pulmonary Defense against Pseudomonas aeruginosa in Mice. PLoS ONE, 2009, 4, e6775.	1.1	0
97	SgrA, a Nidogen-Binding LPXTG Surface Adhesin Implicated in Biofilm Formation, and EcbA, a Collagen Binding MSCRAMM, Are Two Novel Adhesins of Hospital-Acquired Enterococcus faecium. Infection and Immunity, 2009, 77, 5097-5106.	1.0	78
98	Genetic Variation and Evolution of the Pathogenicity Island of Enterococcus faecalis. Journal of Bacteriology, 2009, 191, 3392-3402.	1.0	64
99	Occurrence, Population Structure, and Antimicrobial Resistance of Enterococci in Marginal and Apical Periodontitis. Journal of Clinical Microbiology, 2009, 47, 2218-2225.	1.8	44
100	Pseudomonas aeruginosa Genotype Prevalence in Dutch Cystic Fibrosis Patients and Age Dependency of Colonization by Various P. aeruginosa Sequence Types. Journal of Clinical Microbiology, 2009, 47, 4096-4101.	1.8	51
101	Dogs Are a Reservoir of Ampicillin-Resistant Enterococcus faecium Lineages Associated with Human Infections. Applied and Environmental Microbiology, 2009, 75, 2360-2365.	1.4	81
102	A Trilocus Sequence Typing Scheme for Hospital Epidemiology and Subspecies Differentiation of an Important Nosocomial Pathogen, Enterococcus faecalis. Journal of Clinical Microbiology, 2009, 47, 2713-2719.	1.8	19
103	Enterococcal Surface Protein Transiently AggravatesEnterococcus faeciumâ€“Induced Urinary Tract Infection in Mice. Journal of Infectious Diseases, 2009, 200, 1162-1165.	1.9	47
104	Longer Intestinal Persistence of Enterococcus faecalis Compared to Enterococcus faecium Clones in Intensive-Care-Unit Patients. Journal of Clinical Microbiology, 2009, 47, 345-351.	1.8	13
105	Neutrophils Are Essential for Rapid Clearance ofEnterococcus faeciumin Mice. Infection and Immunity, 2009, 77, 485-491.	1.0	59
106	IntestinalEnterococcus faeciumColonization Improves Host Defense during Polymicrobial Peritonitis. Journal of Infectious Diseases, 2009, 200, 735-744.	1.9	12
107	Molecular characterisation of outbreak-related strains of vancomycin-resistant Enterococcus faecium from an intensive care unit in Beijing, China. Journal of Hospital Infection, 2009, 72, 147-154.	1.4	37
108	New methods to analyse microarray data that partially lack a reference signal. BMC Genomics, 2009, 10, 522.	1.2	3

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109	Enterococcal surface protein Esp is not essential for cell adhesion and intestinal colonization of Enterococcus faecium in mice. BMC Microbiology, 2009, 9, 19.	1.3	32
110	Cecal ligation and puncture induced sepsis impairs host defense against Enterococcus faecium peritonitis. Intensive Care Medicine, 2009, 35, 924-932.	3.9	6
111	The acuteâ€phase response impairs host defence against Enterococcus faecium peritonitis. Immunology, 2009, 128, e335-42.	2.0	7
112	LPxTG surface proteins of enterococci. Trends in Microbiology, 2009, 17, 423-430.	3.5	106
113	Transition of Enterococcus faecium from commensal organism to nosocomial pathogen. Future Microbiology, 2009, 4, 1125-1135.	1.0	151
114	Peritoneal macrophages are important for the early containment of Enterococcus faecium peritonitis in mice. Innate Immunity, 2009, 15, 3-12.	1.1	35
115	Emergence of CC17Enterococcus faecium: from commensal to hospital-adapted pathogen. FEMS Immunology and Medical Microbiology, 2008, 52, 297-308.	2.7	206
116	Comparison of multiple-locus variable-number tandem repeat analysis and pulsed-field gel electrophoresis in a setting of polyclonal endemicity of vancomycin-resistant Enterococcus faecium. Clinical Microbiology and Infection, 2008, 14, 363-369.	2.8	18
117	Molecular characterization of vancomycin-resistant Enterococcus spp. clinical isolates from Hungary and Serbia. Scandinavian Journal of Infectious Diseases, 2008, 40, 778-784.	1.5	13
118	Identification of a Novel Genomic Island Specific to Hospital-Acquired Clonal Complex 17 Enterococcus faecium Isolates. Applied and Environmental Microbiology, 2008, 74, 7094-7097.	1.4	41
119	Expression of two distinct types of pili by a hospital-acquired Enterococcus faecium isolate. Microbiology (United Kingdom), 2008, 154, 3212-3223.	0.7	87
120	Novel Multiple-Locus Variable-Number Tandem-Repeat Analysis Method for Rapid Molecular Typing of Human Staphylococcus aureus. Journal of Clinical Microbiology, 2008, 46, 3147-3151.	1.8	22
121	Emergence of Clonal Complex 17 Enterococcus faecium in The Netherlands. Journal of Clinical Microbiology, 2008, 46, 214-219.	1.8	91
122	TLR2-Dependent MyD88 Signaling Contributes to Early Host Defense in MurineEnterococcus faeciumPeritonitis. Journal of Immunology, 2008, 180, 4865-4874.	0.4	53
123	High acquisition and environmental contamination rates of CC17 ampicillin-resistant Enterococcus faecium in a Dutch hospital. Journal of Antimicrobial Chemotherapy, 2008, 62, 1401-1406.	1.3	45
124	Enterococcal Surface Protein Esp Is Important for Biofilm Formation of Enterococcus faecium E1162. Journal of Bacteriology, 2007, 189, 8233-8240.	1.0	175
125	Insertion Sequenceâ€“Driven Diversification Creates a Globally Dispersed Emerging Multiresistant Subspecies of E. faecium. PLoS Pathogens, 2007, 3, e7.	2.1	180
126	Clonal Structure of Enterococcus faecalis Isolated from Polish Hospitals: Characterization of Epidemic Clones. Journal of Clinical Microbiology, 2007, 45, 147-153.	1.8	86

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127	Five Genes Encoding Surface-Exposed LPXTG Proteins Are Enriched in Hospital-Adapted Enterococcus faecium Clonal Complex 17 Isolates. Journal of Bacteriology, 2007, 189, 8321-8332.	1.0	73
128	Growth Condition-Dependent Esp Expression by Enterococcus faecium Affects Initial Adherence and Biofilm Formation. Infection and Immunity, 2007, 75, 924-931.	1.0	73
129	Glycopeptide-resistant enterococci: deciphering virulence, resistance and epidemicity. Current Opinion in Infectious Diseases, 2007, 20, 384-390.	1.3	79
130	Ecological replacement of Enterococcus faecalis by multiresistant clonal complex 17 Enterococcus faecium. Clinical Microbiology and Infection, 2007, 13, 316-319.	2.8	96
131	Identification of high-risk enterococcal clonal complexes: global dispersion and antibiotic resistance. Current Opinion in Microbiology, 2006, 9, 454-460.	2.3	288
132	Genetic and phenotypic differences among Enterococcus faecalis clones from intestinal colonisation and invasive disease. Clinical Microbiology and Infection, 2006, 12, 1193-1198.	2.8	24
133	Presence of Pathogenicity Island Genes in Enterococcus faecalis Isolates from Pigs in Denmark. Journal of Clinical Microbiology, 2006, 44, 4200-4203.	1.8	37
134	Genotyping and Preemptive Isolation to Control an Outbreak of Vancomycin-Resistant Enterococcus faecium. Clinical Infectious Diseases, 2006, 42, 739-746.	2.9	56
135	Multilocus Sequence Typing of Hospital-Associated Enterococcus faecium from Brazil Reveals Their Unique Evolutionary History. Microbial Drug Resistance, 2006, 12, 121.	0.9	16
136	Multilocus Sequence Typing Scheme for Enterococcus faecalis Reveals Hospital-Adapted Genetic Complexes in a Background of High Rates of Recombination. Journal of Clinical Microbiology, 2006, 44, 2220-2228.	1.8	321
137	High-Level Ciprofloxacin Resistance from Point Mutations in gyrA and parC Confined to Global Hospital-Adapted Clonal Lineage CC17 of Enterococcus faecium. Journal of Clinical Microbiology, 2006, 44, 1059-1064.	1.8	93
138	Emergence of Virulent Methicillin-Resistant Staphylococcus aureus Strains Carrying Panton-Valentine Leucocidin Genes in The Netherlands. Journal of Clinical Microbiology, 2005, 43, 3341-3345.	1.8	103
139	Unnoticed Spread of Integron-Carrying Enterobacteriaceae in Intensive Care Units. Clinical Infectious Diseases, 2005, 41, 1-9.	2.9	53
140	Population Structure of Enterococcus faecium Causing Bacteremia in a Spanish University Hospital: Setting the Scene for a Future Increase in Vancomycin Resistance?. Antimicrobial Agents and Chemotherapy, 2005, 49, 2693-2700.	1.4	79
141	Molecular Analysis of Human, Porcine, and Poultry Enterococcus faecium Isolates and Their erm (B) Genes. Applied and Environmental Microbiology, 2005, 71, 2766-2770.	1.4	39
142	Streptococcal toxic shock syndrome by an iMLS resistant M type 77 Streptococcus pyogenes in the Netherlands. Scandinavian Journal of Infectious Diseases, 2005, 37, 85-89.	1.5	7
143	Global Spread of Vancomycin-resistantEnterococcus faeciumfrom Distinct Nosocomial Genetic Complex. Emerging Infectious Diseases, 2005, 11, 821-828.	2.0	491
144	A Novel Putative Enterococcal Pathogenicity Island Linked to the esp Virulence Gene of Enterococcus faecium and Associated with Epidemicity. Journal of Bacteriology, 2004, 186, 672-682.	1.0	185

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145	Duplex Real-Time PCR Assay for Rapid Detection of Ampicillin-Resistant Enterococcus faecium. Antimicrobial Agents and Chemotherapy, 2004, 48, 556-560.	1.4	18
146	Multiple-Locus Variable-Number Tandem Repeat Analysis, a Novel Typing Scheme To Study the Genetic Relatedness and Epidemiology of Enterococcus faecium Isolates. Journal of Clinical Microbiology, 2004, 42, 4503-4511.	1.8	125
147	Multilocus Variable-Number Tandem-Repeat Polymorphism among Brazilian Enterococcus faecalis Strains. Journal of Clinical Microbiology, 2004, 42, 4879-4881.	1.8	33
148	Widespread Dissemination in The Netherlands of the Epidemic Berlin Methicillin-Resistant Staphylococcus aureus Clone with Low-Level Resistance to Oxacillin. Journal of Clinical Microbiology, 2004, 42, 3077-3082.	1.8	56
149	Comparative analysis of amplified fragment length polymorphism and pulsed field gel electrophoresis in a hospital outbreak and subsequent endemicity of ampicillin-resistantEnterococcus faecium. FEMS Immunology and Medical Microbiology, 2004, 40, 33-39.	2.7	9
150	Genetic characterization of glycopeptide-resistant enterococci of human and animal origin from mixed pig and poultry farms. Apmis, 2003, 111, 669-672.	0.9	10
151	Comparative Genotyping of Campylobacter jejuni by Amplified Fragment Length Polymorphism, Multilocus Sequence Typing, and Short Repeat Sequencing: Strain Diversity, Host Range, and Recombination. Journal of Clinical Microbiology, 2003, 41, 15-26.	1.8	242
152	Molecular epidemiology of Enterococcus faecalis in liver transplant patients at University Hospital Groningen. Journal of Hospital Infection, 2003, 55, 53-60.	1.4	7
153	Influence of Transferable Genetic Determinants on the Outcome of Typing Methods Commonly Used for Enterococcus faecium. Journal of Clinical Microbiology, 2003, 41, 1499-1506.	1.8	56
154	Molecular Characterization of Ampicillin-Resistant Enterococcus faecium Isolates from Hospitalized Patients in Norway. Journal of Clinical Microbiology, 2003, 41, 2330-2336.	1.8	50
155	Mutations in the DNA Mismatch Repair Proteins MutS and MutL of Oxazolidinone-Resistant or -Susceptible Enterococcus faecium. Antimicrobial Agents and Chemotherapy, 2003, 47, 3061-3066.	1.4	34
156	Detection of Enterococcal Surface Protein Gene (esp) and Amplified Fragment Length Polymorphism Typing of Glycopeptide-Resistant Enterococcus faecium during Its Emergence in a Greek Intensive Care Unit. Journal of Clinical Microbiology, 2003, 41, 5742-5746.	1.8	10
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158	Multilocus Sequence Typing Scheme for Enterococcus faecium. Journal of Clinical Microbiology, 2002, 40, 1963-1971.	1.8	458
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