

Jacques Ravel

List of Publications by Year in descending order

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300
papers

37,024
citations

3159

92
h-index

3650

180
g-index

332
all docs

332
docs citations

332
times ranked

35068
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Vaginal microbiome of reproductive-age women. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4680-4687. | 7.1 | 2,985 |
| 2 | An improved dual-indexing approach for multiplexed 16S rRNA gene sequencing on the Illumina MiSeq platform. Microbiome, 2014, 2, 6. | 11.1 | 1,454 |
| 3 | Temporal Dynamics of the Human Vaginal Microbiota. Science Translational Medicine, 2012, 4, 132ra52. | 12.4 | 1,168 |
| 4 | Insights on Evolution of Virulence and Resistance from the Complete Genome Analysis of an Early Methicillin-Resistant <i>Staphylococcus aureus</i> Strain and a Biofilm-Producing Methicillin-Resistant <i>Staphylococcus epidermidis</i> Strain. Journal of Bacteriology, 2005, 187, 2426-2438. | 2.2 | 940 |
| 5 | Moving pictures of the human microbiome. Genome Biology, 2011, 12, R50. | 9.6 | 934 |
| 6 | The vocabulary of microbiome research: a proposal. Microbiome, 2015, 3, 31. | 11.1 | 778 |
| 7 | The Pangenome Structure of <i>Escherichia coli</i> : Comparative Genomic Analysis of <i>E. coli</i> Commensal and Pathogenic Isolates. Journal of Bacteriology, 2008, 190, 6881-6893. | 2.2 | 763 |
| 8 | Predictive, structure-based model of amino acid recognition by nonribosomal peptide synthetase adenylation domains. Chemistry and Biology, 2000, 7, 211-224. | 6.0 | 746 |
| 9 | Complete genome sequence of the plant commensal <i>Pseudomonas fluorescens</i> Pf-5. Nature Biotechnology, 2005, 23, 873-878. | 17.5 | 615 |
| 10 | Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. Nature Biotechnology, 2011, 29, 415-420. | 17.5 | 608 |
| 11 | The composition and stability of the vaginal microbiota of normal pregnant women is different from that of non-pregnant women. Microbiome, 2014, 2, 4. | 11.1 | 607 |
| 12 | Vaginal Microbiome: Rethinking Health and Disease. Annual Review of Microbiology, 2012, 66, 371-389. | 7.3 | 584 |
| 13 | Patellamide A and C biosynthesis by a microcin-like pathway in <i>Prochloron didemni</i> , the cyanobacterial symbiont of <i>Lissoclinum patella</i> . Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7315-7320. | 7.1 | 553 |
| 14 | Human oral microbiome and prospective risk for pancreatic cancer: a population-based nested case-control study. Gut, 2018, 67, 120-127. | 12.1 | 536 |
| 15 | <i>Yersinia pestis</i> genome sequencing identifies patterns of global phylogenetic diversity. Nature Genetics, 2010, 42, 1140-1143. | 21.4 | 504 |
| 16 | Major Structural Differences and Novel Potential Virulence Mechanisms from the Genomes of Multiple <i>Campylobacter</i> Species. PLoS Biology, 2005, 3, e15. | 5.6 | 483 |
| 17 | Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen <i>Listeria monocytogenes</i> reveal new insights into the core genome components of this species. Nucleic Acids Research, 2004, 32, 2386-2395. | 14.5 | 460 |
| 18 | Identification of anthrax toxin genes in a <i>Bacillus cereus</i> associated with an illness resembling inhalation anthrax. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8449-8454. | 7.1 | 457 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Draft genome sequence of the oilseed species <i>Ricinus communis</i> . <i>Nature Biotechnology</i> , 2010, 28, 951-956. | 17.5 | 449 |
| 20 | Evaluation of Methods for the Extraction and Purification of DNA from the Human Microbiome. <i>PLoS ONE</i> , 2012, 7, e33865. | 2.5 | 425 |
| 21 | Genomics of the group of organisms. <i>FEMS Microbiology Reviews</i> , 2005, 29, 303-329. | 8.6 | 421 |
| 22 | Fecal microbial determinants of fecal and systemic estrogens and estrogen metabolites: a cross-sectional study. <i>Journal of Translational Medicine</i> , 2012, 10, 253. | 4.4 | 387 |
| 23 | The vaginal microbiota of pregnant women who subsequently have spontaneous preterm labor and delivery and those with a normal delivery at term. <i>Microbiome</i> , 2014, 2, 18. | 11.1 | 361 |
| 24 | Multiple Antimicrobial Resistance in Plague: An Emerging Public Health Risk. <i>PLoS ONE</i> , 2007, 2, e309. | 2.5 | 344 |
| 25 | Global Genetic Population Structure of <i>Bacillus anthracis</i> . <i>PLoS ONE</i> , 2007, 2, e461. | 2.5 | 317 |
| 26 | Chapter 8 Methods for In Silico Prediction of Microbial Polyketide and Nonribosomal Peptide Biosynthetic Pathways from DNA Sequence Data. <i>Methods in Enzymology</i> , 2009, 458, 181-217. | 1.0 | 312 |
| 27 | Association between the vaginal microbiota, menopause status, and signs of vulvovaginal atrophy. <i>Menopause</i> , 2014, 21, 450-458. | 2.0 | 296 |
| 28 | Metagenomics: Read Length Matters. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1453-1463. | 3.1 | 295 |
| 29 | Interplay Between the Temporal Dynamics of the Vaginal Microbiota and Human Papillomavirus Detection. <i>Journal of Infectious Diseases</i> , 2014, 210, 1723-1733. | 4.0 | 292 |
| 30 | Skewed genomic variability in strains of the toxigenic bacterial pathogen, <i>Clostridium perfringens</i> . <i>Genome Research</i> , 2006, 16, 1031-1040. | 5.5 | 281 |
| 31 | The vaginal microbiota, host defence and reproductive physiology. <i>Journal of Physiology</i> , 2017, 595, 451-463. | 2.9 | 279 |
| 32 | Genomic Insights into Methanotrophy: The Complete Genome Sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004, 2, e303. | 5.6 | 275 |
| 33 | The genome sequence of <i>Bacillus cereus</i> ATCC 10987 reveals metabolic adaptations and a large plasmid related to <i>Bacillus anthracis</i> pXO1. <i>Nucleic Acids Research</i> , 2004, 32, 977-988. | 14.5 | 273 |
| 34 | Characterizing human lung tissue microbiota and its relationship to epidemiological and clinical features. <i>Genome Biology</i> , 2016, 17, 163. | 8.8 | 264 |
| 35 | Uncovering effects of antibiotics on the host and microbiota using transkingdom gene networks. <i>Cut</i> , 2015, 64, 1732-1743. | 12.1 | 261 |
| 36 | Cervicovaginal microbiota and local immune response modulate the risk of spontaneous preterm delivery. <i>Nature Communications</i> , 2019, 10, 1305. | 12.8 | 260 |

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|----|---|------|-----------|
| 37 | Daily temporal dynamics of vaginal microbiota before, during and after episodes of bacterial vaginosis. <i>Microbiome</i> , 2013, 1, 29. | 11.1 | 258 |
| 38 | A global assembly line for cyanobactins. <i>Nature Chemical Biology</i> , 2008, 4, 341-343. | 8.0 | 257 |
| 39 | Investigation of the Association Between the Fecal Microbiota and Breast Cancer in Postmenopausal Women: a Population-Based Case-Control Pilot Study. <i>Journal of the National Cancer Institute</i> , 2015, 107, . | 6.3 | 257 |
| 40 | Phylogenetic discovery bias in <i>Bacillus anthracis</i> using single-nucleotide polymorphisms from whole-genome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13536-13541. | 7.1 | 243 |
| 41 | Natural combinatorial peptide libraries in cyanobacterial symbionts of marine ascidians. , 2006, 2, 729-735. | | 241 |
| 42 | Visualization of comparative genomic analyses by BLAST score ratio. <i>BMC Bioinformatics</i> , 2005, 6, 2. | 2.6 | 238 |
| 43 | Genomics of pyoverdine-mediated iron uptake in pseudomonads. <i>Trends in Microbiology</i> , 2003, 11, 195-200. | 7.7 | 225 |
| 44 | Associations of the Fecal Microbiome With Urinary Estrogens and Estrogen Metabolites in Postmenopausal Women. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014, 99, 4632-4640. | 3.6 | 222 |
| 45 | Proof of Concept of Microbiome-Metabolome Analysis and Delayed Gluten Exposure on Celiac Disease Autoimmunity in Genetically At-Risk Infants. <i>PLoS ONE</i> , 2012, 7, e33387. | 2.5 | 219 |
| 46 | The Effects of Circumcision on the Penis Microbiome. <i>PLoS ONE</i> , 2010, 5, e8422. | 2.5 | 216 |
| 47 | Genomic anatomy of <i>Escherichia coli</i> O157:H7 outbreaks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20142-20147. | 7.1 | 206 |
| 48 | Community Analysis of Chronic Wound Bacteria Using 16S rRNA Gene-Based Pyrosequencing: Impact of Diabetes and Antibiotics on Chronic Wound Microbiota. <i>PLoS ONE</i> , 2009, 4, e6462. | 2.5 | 199 |
| 49 | Comparative Genomics of the IncA/C Multidrug Resistance Plasmid Family. <i>Journal of Bacteriology</i> , 2009, 191, 4750-4757. | 2.2 | 199 |
| 50 | Understanding vaginal microbiome complexity from an ecological perspective. <i>Translational Research</i> , 2012, 160, 267-282. | 5.0 | 197 |
| 51 | The Evolving Facets of Bacterial Vaginosis: Implications for HIV Transmission. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 219-228. | 1.1 | 188 |
| 52 | Formation and Composition of the <i>Bacillus anthracis</i> Endospore. <i>Journal of Bacteriology</i> , 2004, 186, 164-178. | 2.2 | 187 |
| 53 | Coelichelin, a new peptide siderophore encoded by the <i>Streptomyces coelicolor</i> genome: structure prediction from the sequence of its non-ribosomal peptide synthetase. <i>FEMS Microbiology Letters</i> , 2000, 187, 111-114. | 1.8 | 186 |
| 54 | Free Glycogen in Vaginal Fluids Is Associated with <i>Lactobacillus</i> Colonization and Low Vaginal pH. <i>PLoS ONE</i> , 2014, 9, e102467. | 2.5 | 183 |

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|----|---|------|-----------|
| 55 | Population Dynamics of Chesapeake Bay Virioplankton: Total-Community Analysis by Pulsed-Field Gel Electrophoresis. <i>Applied and Environmental Microbiology</i> , 1999, 65, 231-240. | 3.1 | 181 |
| 56 | VALENCIA: a nearest centroid classification method for vaginal microbial communities based on composition. <i>Microbiome</i> , 2020, 8, 166. | 11.1 | 177 |
| 57 | Genomic diversity of 2010 Haitian cholera outbreak strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2010-7. | 7.1 | 173 |
| 58 | Cervicovaginal microbiota, women's health, and reproductive outcomes. <i>Fertility and Sterility</i> , 2018, 110, 327-336. | 1.0 | 165 |
| 59 | Differential immune responses and microbiota profiles in children with autism spectrum disorders and co-morbid gastrointestinal symptoms. <i>Brain, Behavior, and Immunity</i> , 2018, 70, 354-368. | 4.1 | 163 |
| 60 | Antimicrobial Resistance-Confering Plasmids with Similarity to Virulence Plasmids from Avian Pathogenic <i>Escherichia coli</i> Strains in <i>Salmonella enterica</i> Serovar Kentucky Isolates from Poultry. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5963-5971. | 3.1 | 160 |
| 61 | Comparative Genomics of 28 <i>Salmonella enterica</i> Isolates: Evidence for CRISPR-Mediated Adaptive Sublineage Evolution. <i>Journal of Bacteriology</i> , 2011, 193, 3556-3568. | 2.2 | 159 |
| 62 | Genome Sequences of the Biotechnologically Important <i>Bacillus megaterium</i> Strains QM B1551 and DSM319. <i>Journal of Bacteriology</i> , 2011, 193, 4199-4213. | 2.2 | 155 |
| 63 | <i>Bacillus anthracis</i> comparative genome analysis in support of the Amerithrax investigation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5027-5032. | 7.1 | 152 |
| 64 | Association of HPV infection and clearance with cervicovaginal immunology and the vaginal microbiota. <i>Mucosal Immunology</i> , 2017, 10, 1310-1319. | 6.0 | 148 |
| 65 | Complex microbiome underlying secondary and primary metabolism in the tunicate- <i>Prochloron</i> symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E1423-32. | 7.1 | 146 |
| 66 | Bacterial vaginosis and its association with infertility, endometritis, and pelvic inflammatory disease. <i>American Journal of Obstetrics and Gynecology</i> , 2021, 224, 251-257. | 1.3 | 146 |
| 67 | Enhanced Trapping of HIV-1 by Human Cervicovaginal Mucus Is Associated with <i>Lactobacillus crispatus</i> -Dominant Microbiota. <i>MBio</i> , 2015, 6, e01084-15. | 4.1 | 141 |
| 68 | The effect of cigarette smoking on the oral and nasal microbiota. <i>Microbiome</i> , 2017, 5, 3. | 11.1 | 141 |
| 69 | Complete Sequence Analysis of Novel Plasmids from Emetic and Periodontal <i>Bacillus cereus</i> Isolates Reveals a Common Evolutionary History among the <i>B. cereus</i> -Group Plasmids, Including <i>Bacillus anthracis</i> pXO1. <i>Journal of Bacteriology</i> , 2007, 189, 52-64. | 2.2 | 140 |
| 70 | Bacterial diversity in a glacier foreland of the high Arctic. <i>Molecular Ecology</i> , 2010, 19, 54-66. | 3.9 | 139 |
| 71 | Association Between <i>Trichomonas vaginalis</i> and Vaginal Bacterial Community Composition Among Reproductive-Age Women. <i>Sexually Transmitted Diseases</i> , 2012, 39, 807-812. | 1.7 | 138 |
| 72 | Rapid fluctuation of the vaginal microbiota measured by Gram stain analysis. <i>Sexually Transmitted Infections</i> , 2010, 86, 297-302. | 1.9 | 136 |

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|----|---|------|-----------|
| 73 | Molecular Characterization of the Human Stomach Microbiota in Gastric Cancer Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 302. | 3.9 | 136 |
| 74 | Male Circumcision Significantly Reduces Prevalence and Load of Genital Anaerobic Bacteria. <i>MBio</i> , 2013, 4, e00076. | 4.1 | 130 |
| 75 | Strain-Specific Single-Nucleotide Polymorphism Assays for the <i>Bacillus anthracis</i> Ames Strain. <i>Journal of Clinical Microbiology</i> , 2007, 45, 47-53. | 3.9 | 126 |
| 76 | Functional Dynamics of the Gut Microbiome in Elderly People during Probiotic Consumption. <i>MBio</i> , 2015, 6, . | 4.1 | 126 |
| 77 | The vaginal mycobiome: A contemporary perspective on fungi in women's health and diseases. <i>Virulence</i> , 2017, 8, 342-351. | 4.4 | 124 |
| 78 | Identification of new, conserved, non-ribosomal peptide synthetases from fluorescent pseudomonads involved in the biosynthesis of the siderophore pyoverdine. <i>Molecular Microbiology</i> , 2002, 45, 1673-1685. | 2.5 | 118 |
| 79 | Genome Sequence of the Deep-Rooted <i>Yersinia pestis</i> Strain Angola Reveals New Insights into the Evolution and Pangenome of the Plague Bacterium. <i>Journal of Bacteriology</i> , 2010, 192, 1685-1699. | 2.2 | 117 |
| 80 | Temperature-induced recovery of <i>Vibrio cholerae</i> from the viable but nonculturable state: growth or resuscitation?. <i>Microbiology (United Kingdom)</i> , 1995, 141, 377-383. | 1.8 | 114 |
| 81 | Vaginal biogenic amines: biomarkers of bacterial vaginosis or precursors to vaginal dysbiosis?. <i>Frontiers in Physiology</i> , 2015, 6, 253. | 2.8 | 114 |
| 82 | Genomic Epidemiology of the Haitian Cholera Outbreak: a Single Introduction Followed by Rapid, Extensive, and Continued Spread Characterized the Onset of the Epidemic. <i>MBio</i> , 2014, 5, e01721. | 4.1 | 112 |
| 83 | Microbiome, demystifying the role of microbial communities in the biosphere. <i>Microbiome</i> , 2013, 1, 1. | 11.1 | 108 |
| 84 | Microbial diversity and the presence of algae in halite endolithic communities are correlated to atmospheric moisture in the hyperarid zone of the Atacama Desert. <i>Environmental Microbiology</i> , 2015, 17, 299-315. | 3.8 | 108 |
| 85 | Association between cigarette smoking and the vaginal microbiota: a pilot study. <i>BMC Infectious Diseases</i> , 2014, 14, 471. | 2.9 | 107 |
| 86 | Functional interactions of archaea, bacteria and viruses in a hypersaline endolithic community. <i>Environmental Microbiology</i> , 2016, 18, 2064-2077. | 3.8 | 107 |
| 87 | The Cervicovaginal Microbiota-Host Interaction Modulates <i>Chlamydia trachomatis</i> Infection. <i>MBio</i> , 2019, 10, . | 4.1 | 107 |
| 88 | Repair of extensive ionizing-radiation DNA damage at 95 degrees C in the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> . <i>Journal of Bacteriology</i> , 1997, 179, 4643-4645. | 2.2 | 105 |
| 89 | Evidence that Human <i>Chlamydia pneumoniae</i> Was Zoonotically Acquired. <i>Journal of Bacteriology</i> , 2009, 191, 7225-7233. | 2.2 | 105 |
| 90 | Comparison of Self-Collected and Physician-Collected Vaginal Swabs for Microbiome Analysis. <i>Journal of Clinical Microbiology</i> , 2010, 48, 1741-1748. | 3.9 | 104 |

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|-----|--|------|-----------|
| 91 | Prevalent high-risk HPV infection and vaginal microbiota in Nigerian women. <i>Epidemiology and Infection</i> , 2016, 144, 123-137. | 2.1 | 104 |
| 92 | A retrospective pilot study to determine whether the reproductive tract microbiota differs between women with a history of infertility and fertile women. <i>Australian and New Zealand Journal of Obstetrics and Gynaecology</i> , 2018, 58, 341-348. | 1.0 | 104 |
| 93 | Ultrahigh-Throughput Multiplexing and Sequencing of >500-Base-Pair Amplicon Regions on the Illumina HiSeq 2500 Platform. <i>MSystems</i> , 2019, 4, . | 3.8 | 104 |
| 94 | Collection media and delayed freezing effects on microbial composition of human stool. <i>Microbiome</i> , 2015, 3, 33. | 11.1 | 103 |
| 95 | The vaginal microbiota and its association with human papillomavirus, <i>Chlamydia trachomatis</i> , <i>Neisseria gonorrhoeae</i> and <i>Mycoplasma genitalium</i> infections: a systematic review and meta-analysis. <i>Clinical Microbiology and Infection</i> , 2019, 25, 35-47. | 6.0 | 101 |
| 96 | The Complete Genome Sequence of <i>Yersinia pseudotuberculosis</i> IP31758, the Causative Agent of Far East Scarlet-Like Fever. <i>PLoS Genetics</i> , 2007, 3, e142. | 3.5 | 99 |
| 97 | Penile Microbiota and Female Partner Bacterial Vaginosis in Rakai, Uganda. <i>MBio</i> , 2015, 6, e00589. | 4.1 | 96 |
| 98 | Genomics of the <i>Bacillus cereus</i> group of organisms. <i>FEMS Microbiology Reviews</i> , 2005, 29, 303-329. | 8.6 | 95 |
| 99 | Single nucleotide polymorphisms for assessing genetic diversity in castor bean (<i>Ricinus communis</i>). <i>BMC Plant Biology</i> , 2010, 10, 13. | 3.6 | 95 |
| 100 | A proposal for the reclassification of <i>Bdellovibrio stolpii</i> and <i>Bdellovibrio starrii</i> into a new genus, <i>Bacteriovorax</i> gen. nov. as <i>Bacteriovorax stolpii</i> comb. nov. and <i>Bacteriovorax starrii</i> comb. nov., respectively.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2000, 50, 219-224. | 1.7 | 94 |
| 101 | Crypt- and Mucosa-Associated Core Microbiotas in Humans and Their Alteration in Colon Cancer Patients. <i>MBio</i> , 2019, 10, . | 4.1 | 94 |
| 102 | Towards a deeper understanding of the vaginal microbiota. <i>Nature Microbiology</i> , 2022, 7, 367-378. | 13.3 | 94 |
| 103 | Associations between sexual habits, menstrual hygiene practices, demographics and the vaginal microbiome as revealed by Bayesian network analysis. <i>PLoS ONE</i> , 2018, 13, e0191625. | 2.5 | 92 |
| 104 | Worldwide genotyping of castor bean germplasm (<i>Ricinus communis</i> L.) using AFLPs and SSRs. <i>Genetic Resources and Crop Evolution</i> , 2008, 55, 365-378. | 1.6 | 90 |
| 105 | <i>Lactobacillus crispatus</i> inhibits growth of <i>Gardnerella vaginalis</i> and <i>Neisseria gonorrhoeae</i> on a porcine vaginal mucosa model. <i>BMC Microbiology</i> , 2015, 15, 276. | 3.3 | 90 |
| 106 | Evaluation of a Transposase Protocol for Rapid Generation of Shotgun High-Throughput Sequencing Libraries from Nanogram Quantities of DNA. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8071-8079. | 3.1 | 89 |
| 107 | <i>Lactobacillus iners</i> -dominated vaginal microbiota is associated with increased susceptibility to <i>Chlamydia trachomatis</i> infection in Dutch women: a case-control study. <i>Sexually Transmitted Infections</i> , 2018, 94, 117-123. | 1.9 | 89 |
| 108 | The Complete Genome Sequence of <i>Bacillus anthracis</i> Ames Ancestor. <i>Journal of Bacteriology</i> , 2009, 191, 445-446. | 2.2 | 88 |

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|-----|--|------|-----------|
| 109 | Castor Bean Organelle Genome Sequencing and Worldwide Genetic Diversity Analysis. <i>PLoS ONE</i> , 2011, 6, e21743. | 2.5 | 88 |
| 110 | Microbiome, sex hormones, and immune responses in the reproductive tract: Challenges for vaccine development against sexually transmitted infections. <i>Vaccine</i> , 2014, 32, 1543-1552. | 3.8 | 86 |
| 111 | The vaginal metabolome and microbiota of cervical HPVâ€positive and HPVâ€negative women: a crossâ€sectional analysis. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2020, 127, 182-192. | 2.3 | 86 |
| 112 | A comprehensive non-redundant gene catalog reveals extensive within-community intraspecies diversity in the human vagina. <i>Nature Communications</i> , 2020, 11, 940. | 12.8 | 86 |
| 113 | <i>Bacillus anthracis</i> in China and its relationship to worldwide lineages. <i>BMC Microbiology</i> , 2009, 9, 71. | 3.3 | 85 |
| 114 | Cigarette smoking is associated with an altered vaginal tract metabolomic profile. <i>Scientific Reports</i> , 2018, 8, 852. | 3.3 | 84 |
| 115 | Insights into the Environmental Resistance Gene Pool from the Genome Sequence of the Multidrug-Resistant Environmental Isolate <i>Escherichia coli</i> SMS-3-5. <i>Journal of Bacteriology</i> , 2008, 190, 6779-6794. | 2.2 | 82 |
| 116 | New signaling pathways govern the host response to <i>C. albicans</i> infection in various niches. <i>Genome Research</i> , 2015, 25, 679-689. | 5.5 | 82 |
| 117 | Postmenopausal breast cancer and oestrogen associations with the IgA-coated and IgA-noncoated faecal microbiota. <i>British Journal of Cancer</i> , 2018, 118, 471-479. | 6.4 | 82 |
| 118 | Translating the vaginal microbiome: gaps and challenges. <i>Genome Medicine</i> , 2016, 8, 35. | 8.2 | 81 |
| 119 | The implausible <i>in vivo</i> role of hydrogen peroxide as an antimicrobial factor produced by vaginal microbiota. <i>Microbiome</i> , 2018, 6, 29. | 11.1 | 81 |
| 120 | Phylogeography and Molecular Epidemiology of <i>Yersinia pestis</i> in Madagascar. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1319. | 3.0 | 80 |
| 121 | Impacts of Poultry House Environment on Poultry Litter Bacterial Community Composition. <i>PLoS ONE</i> , 2011, 6, e24785. | 2.5 | 79 |
| 122 | Hybridization Analysis of Chesapeake Bay Virioplankton. <i>Applied and Environmental Microbiology</i> , 1999, 65, 241-250. | 3.1 | 78 |
| 123 | Distinct Effects of the Cervicovaginal Microbiota and Herpes Simplex Type 2 Infection on Female Genital Tract Immunology. <i>Journal of Infectious Diseases</i> , 2017, 215, 1366-1375. | 4.0 | 74 |
| 124 | Engineering p-Hydroxyphenylpyruvate Dioxygenase to ap-Hydroxymandelate Synthase and Evidence for the Proposed Benzene Oxide Intermediate in Homogentisate Formationâ€. <i>Biochemistry</i> , 2004, 43, 663-674. | 2.5 | 71 |
| 125 | Origin and Variation of Tunicate Secondary Metabolites. <i>Journal of Natural Products</i> , 2012, 75, 295-304. | 3.0 | 71 |
| 126 | Toward a System of Microbial Forensics: from Sample Collection to Interpretation of Evidence. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2209-2213. | 3.1 | 70 |

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|-----|--|------|-----------|
| 127 | Recent Advances in Understanding the Microbiology of the Female Reproductive Tract and the Causes of Premature Birth. <i>Infectious Diseases in Obstetrics and Gynecology</i> , 2010, 2010, 1-10. | 1.5 | 70 |
| 128 | Anti-HIV-1 Activity of Lactic Acid in Human Cervicovaginal Fluid. <i>MSphere</i> , 2018, 3, . | 2.9 | 66 |
| 129 | Association of Fecal Microbial Diversity and Taxonomy with Selected Enzymatic Functions. <i>PLoS ONE</i> , 2012, 7, e39745. | 2.5 | 66 |
| 130 | Integration of Culture-Based and Molecular Analysis of a Complex Sponge-Associated Bacterial Community. <i>PLoS ONE</i> , 2014, 9, e90517. | 2.5 | 66 |
| 131 | Microbial colonisation of chasmoendolithic habitats in the hyper-arid zone of the Atacama Desert. <i>Biogeosciences</i> , 2013, 10, 2439-2450. | 3.3 | 65 |
| 132 | The Impact of Human Immunodeficiency Virus Infection on Gut Microbiota α -Diversity: An Individual-level Meta-analysis. <i>Clinical Infectious Diseases</i> , 2020, 70, 615-627. | 5.8 | 65 |
| 133 | Microarray-based resequencing of multiple <i>Bacillus anthracis</i> isolates. <i>Genome Biology</i> , 2004, 6, R10. | 9.6 | 64 |
| 134 | Advancing the Microbiome Research Community. <i>Cell</i> , 2014, 159, 227-230. | 28.9 | 64 |
| 135 | SINC, a type III secreted protein of <i>Chlamydia psittaci</i> , targets the inner nuclear membrane of infected cells and uninfected neighbors. <i>Molecular Biology of the Cell</i> , 2015, 26, 1918-1934. | 2.1 | 64 |
| 136 | The Biosynthetic Gene Cluster for a Monocyclic β -Lactam Antibiotic, Nocardicin A. <i>Chemistry and Biology</i> , 2004, 11, 927-938. | 6.0 | 63 |
| 137 | Anal microbiota profiles in HIV-positive and HIV-negative MSM. <i>Aids</i> , 2014, 28, 753-760. | 2.2 | 63 |
| 138 | Association between the vaginal microbiota, menopause status, and signs of vulvovaginal atrophy. <i>Menopause</i> , 2018, 25, 1321-1330. | 2.0 | 63 |
| 139 | Reclassification of salt-water <i>Bdellovibrio</i> sp. as <i>Bacteriovorax marinus</i> sp. nov. and <i>Bacteriovorax litoralis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 1011-1016. | 1.7 | 61 |
| 140 | Pre-Columbian Origins for North American Anthrax. <i>PLoS ONE</i> , 2009, 4, e4813. | 2.5 | 60 |
| 141 | Nested PCR Biases in Interpreting Microbial Community Structure in 16S rRNA Gene Sequence Datasets. <i>PLoS ONE</i> , 2015, 10, e0132253. | 2.5 | 60 |
| 142 | Phylogenetic and Functional Substrate Specificity for Endolithic Microbial Communities in Hyper-Arid Environments. <i>Frontiers in Microbiology</i> , 2016, 7, 301. | 3.5 | 60 |
| 143 | Variation in Tropical Reef Symbiont Metagenomes Defined by Secondary Metabolism. <i>PLoS ONE</i> , 2011, 6, e17897. | 2.5 | 59 |
| 144 | Comparison of Storage Conditions for Human Vaginal Microbiome Studies. <i>PLoS ONE</i> , 2012, 7, e36934. | 2.5 | 59 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 145 | Fecal Microbiota Characteristics of Patients with Colorectal Adenoma Detected by Screening: A Population-based Study. <i>EBioMedicine</i> , 2015, 2, 597-603. | 6.1 | 59 |
| 146 | Group B Streptococcus and the Vaginal Microbiota. <i>Journal of Infectious Diseases</i> , 2017, 216, 744-751. | 4.0 | 58 |
| 147 | <i>Mycoplasma hominis</i> and <i>Mycoplasma genitalium</i> in the Vaginal Microbiota and Persistent High-Risk Human Papillomavirus Infection. <i>Frontiers in Public Health</i> , 2017, 5, 140. | 2.7 | 55 |
| 148 | Genome Signatures of <i>Escherichia coli</i> O157:H7 Isolates from the Bovine Host Reservoir. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2916-2925. | 3.1 | 54 |
| 149 | Whole-Genome Sequences of <i>Bacillus subtilis</i> and Close Relatives. <i>Journal of Bacteriology</i> , 2012, 194, 2378-2379. | 2.2 | 52 |
| 150 | The Cervicovaginal Microbiota and Its Associations With Human Papillomavirus Detection in HIV-Infected and HIV-Uninfected Women. <i>Journal of Infectious Diseases</i> , 2016, 214, 1361-1369. | 4.0 | 51 |
| 151 | Intestinal Barrier Maturation in Very Low Birthweight Infants: Relationship to Feeding and Antibiotic Exposure. <i>Journal of Pediatrics</i> , 2017, 183, 31-36.e1. | 1.8 | 50 |
| 152 | Impact of Standard Bacterial Vaginosis Treatment on the Genital Microbiota, Immune Milieu, and Ex Vivo Human Immunodeficiency Virus Susceptibility. <i>Clinical Infectious Diseases</i> , 2019, 68, 1675-1683. | 5.8 | 50 |
| 153 | Macroscopic spatial variation in chronic wound microbiota: A cross-sectional study. <i>Wound Repair and Regeneration</i> , 2011, 19, 80-88. | 3.0 | 49 |
| 154 | Comparative Metagenome-Assembled Genome Analysis of <i>Candidatus Lachnocurva vaginae</i> , Formerly Known as Bacterial Vaginosis-Associated Bacterium 1 (BVAB1). <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 117. | 3.9 | 49 |
| 155 | Probiotics: Finding the Right Regulatory Balance. <i>Science</i> , 2013, 342, 314-315. | 12.6 | 46 |
| 156 | Intricacies of assessing the human microbiome in epidemiologic studies. <i>Annals of Epidemiology</i> , 2016, 26, 311-321. | 1.9 | 46 |
| 157 | Rectal microbiota among HIV-uninfected, untreated HIV, and treated HIV-infected in Nigeria. <i>Aids</i> , 2017, 31, 857-862. | 2.2 | 46 |
| 158 | Cervicovaginal microbial communities deficient in <i>Lactobacillus</i> species are associated with second-trimester short cervix. <i>American Journal of Obstetrics and Gynecology</i> , 2020, 222, 491.e1-491.e8. | 1.3 | 42 |
| 159 | Assessment of the human faecal microbiota: II. Reproducibility and associations of 16S rRNA pyrosequences. <i>European Journal of Clinical Investigation</i> , 2012, 42, 855-863. | 3.4 | 41 |
| 160 | Improving regulation of microbiota transplants. <i>Science</i> , 2017, 358, 1390-1391. | 12.6 | 41 |
| 161 | Early MicroRNA Expression Profile as a Prognostic Biomarker for the Development of Pelvic Inflammatory Disease in a Mouse Model of Chlamydial Genital Infection. <i>MBio</i> , 2014, 5, e01241-14. | 4.1 | 40 |
| 162 | A proposed definition of microbiota transplantation for regulatory purposes. <i>Gut Microbes</i> , 2017, 8, 208-213. | 9.8 | 40 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 163 | Host-targeted niclosamide inhibits <i>C. difficile</i> virulence and prevents disease in mice without disrupting the gut microbiota. <i>Nature Communications</i> , 2018, 9, 5233. | 12.8 | 40 |
| 164 | Microbial Biomarkers of Intestinal Barrier Maturation in Preterm Infants. <i>Frontiers in Microbiology</i> , 2018, 9, 2755. | 3.5 | 40 |
| 165 | Intermittent Lactobacilli-containing Vaginal Probiotic or Metronidazole Use to Prevent Bacterial Vaginosis Recurrence: A Pilot Study Incorporating Microscopy and Sequencing. <i>Scientific Reports</i> , 2020, 10, 3884. | 3.3 | 40 |
| 166 | Insight into the ecology of vaginal bacteria through integrative analyses of metagenomic and metatranscriptomic data. <i>Genome Biology</i> , 2022, 23, 66. | 8.8 | 40 |
| 167 | Phenotypic and functional characterization of <i>Bacillus anthracis</i> biofilms. <i>Microbiology (United Kingdom)</i> 10.1093/aeg/iaab114 | 1.8 | 38 |
| 168 | Twice-Daily Application of HIV Microbicides Alters the Vaginal Microbiota. <i>MBio</i> , 2012, 3, . | 4.1 | 38 |
| 169 | The composition of human vaginal microbiota transferred at birth affects offspring health in a mouse model. <i>Nature Communications</i> , 2021, 12, 6289. | 12.8 | 38 |
| 170 | Does Active Oral Sex Contribute to Female Infertility?. <i>Journal of Infectious Diseases</i> , 2017, 216, 932-935. | 4.0 | 36 |
| 171 | “Available upon request” not good enough for microbiome data!. <i>Microbiome</i> , 2018, 6, 8. | 11.1 | 35 |
| 172 | <i>Yersinia pestis</i> Evolution on a Small Timescale: Comparison of Whole Genome Sequences from North America. <i>PLoS ONE</i> , 2007, 2, e770. | 2.5 | 34 |
| 173 | Vaginal microbiota composition and association with prevalent <i>Chlamydia trachomatis</i> infection: a cross-sectional study of young women attending a STI clinic in France. <i>Sexually Transmitted Infections</i> , 2018, 94, 616-618. | 1.9 | 33 |
| 174 | Nonoptimal Vaginal Microbiota After Azithromycin Treatment for <i>Chlamydia trachomatis</i> Infection. <i>Journal of Infectious Diseases</i> , 2020, 221, 627-635. | 4.0 | 33 |
| 175 | Characterization of the Vaginal Microbiome in Women of Reproductive Age From 5 Regions in Brazil. <i>Sexually Transmitted Diseases</i> , 2020, 47, 562-569. | 1.7 | 33 |
| 176 | The Vaginal Microbiota over an 8- to 10-Year Period in a Cohort of HIV-Infected and HIV-Uninfected Women. <i>PLoS ONE</i> , 2015, 10, e0116894. | 2.5 | 32 |
| 177 | Whole-Genome Draft Sequences of 26 Enterohemorrhagic <i>Escherichia coli</i> O157:H7 Strains. <i>Genome Announcements</i> , 2013, 1, e0013412. | 0.8 | 31 |
| 178 | Paired-End Sequence Mapping Detects Extensive Genomic Rearrangement and Translocation during Divergence of <i>Francisella tularensis</i> subsp. <i>tularensis</i> and <i>Francisella tularensis</i> subsp. <i>holarctica</i> Populations. <i>Journal of Bacteriology</i> , 2006, 188, 5904-5914. | 2.2 | 29 |
| 179 | Biosynthesis of the apoptolidins in <i>Nocardopsis</i> sp. FU 40. <i>Tetrahedron</i> , 2011, 67, 6568-6575. | 1.9 | 29 |
| 180 | Gastric microbiota features associated with cancer risk factors and clinical outcomes: A pilot study in gastric cardia cancer patients from Shanxi, China. <i>International Journal of Cancer</i> , 2017, 141, 45-51. | 5.1 | 29 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 181 | Herpes simplex virus-binding IgG traps HSV in human cervicovaginal mucus across the menstrual cycle and diverse vaginal microbial composition. <i>Mucosal Immunology</i> , 2018, 11, 1477-1486. | 6.0 | 29 |
| 182 | The Vaginal Microbiota and Behavioral Factors Associated With Genital <i>Candida albicans</i> Detection in Reproductive-Age Women. <i>Sexually Transmitted Diseases</i> , 2019, 46, 753-758. | 1.7 | 29 |
| 183 | Exploring a Road Map to Counter Misconceptions About the Cervicovaginal Microbiome and Disease. <i>Reproductive Sciences</i> , 2012, 19, 1154-1162. | 2.5 | 28 |
| 184 | Genome sequence alterations detected upon passage of <i>Burkholderia mallei</i> ATCC 23344 in culture and in mammalian hosts. <i>BMC Genomics</i> , 2006, 7, 228. | 2.8 | 27 |
| 185 | Evaluation of Buccal Cell Samples for Studies of Oral Microbiota. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 249-253. | 2.5 | 27 |
| 186 | Impact of the griffithsin anti-HIV microbicide and placebo gels on the rectal mucosal proteome and microbiome in non-human primates. <i>Scientific Reports</i> , 2018, 8, 8059. | 3.3 | 27 |
| 187 | Associations between dietary micronutrient intake and molecular-Bacterial Vaginosis. <i>Reproductive Health</i> , 2019, 16, 151. | 3.1 | 27 |
| 188 | Probiotics: achieving a better regulatory fit. <i>Food and Drug Law Journal</i> , 2014, 69, 237-72, ii. | 0.4 | 26 |
| 189 | Genomics at the genus scale. <i>Trends in Microbiology</i> , 2005, 13, 95-97. | 7.7 | 25 |
| 190 | Genome Sequence of <i>Escherichia coli</i> O157:H7 Strain 2886-75, Associated with the First Reported Case of Human Infection in the United States. <i>Genome Announcements</i> , 2014, 2, . | 0.8 | 25 |
| 191 | Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. <i>Microbiome</i> , 2014, 2, . | 11.1 | 25 |
| 192 | Changes in the vaginal microbiota across a gradient of urbanization. <i>Scientific Reports</i> , 2020, 10, 12487. | 3.3 | 25 |
| 193 | Association of Vaginal Microbiota With Signs and Symptoms of the Genitourinary Syndrome of Menopause Across Reproductive Stages. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, 76, 1542-1550. | 3.6 | 25 |
| 194 | Temporal Changes in Vaginal Microbiota and Genital Tract Cytokines Among South African Women Treated for Bacterial Vaginosis. <i>Frontiers in Immunology</i> , 2021, 12, 730986. | 4.8 | 25 |
| 195 | Integrated Microbial Survey Analysis of Prokaryotic Communities for the PhyloChip Microarray. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5636-5638. | 3.1 | 24 |
| 196 | Phylogenetic Diversity of <i>Vibrio cholerae</i> Associated with Endemic Cholera in Mexico from 1991 to 2008. <i>MBio</i> , 2016, 7, e02160. | 4.1 | 24 |
| 197 | Dynamics of Vaginal and Rectal Microbiota Over Several Menstrual Cycles in Female <i>Cynomolgus</i> Macaques. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 188. | 3.9 | 24 |
| 198 | Quantitative modeling predicts mechanistic links between pre-treatment microbiome composition and metronidazole efficacy in bacterial vaginosis. <i>Nature Communications</i> , 2020, 11, 6147. | 12.8 | 24 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 199 | Microbiome or no microbiome: are we looking at the prenatal environment through the right lens? <i>Microbiome</i> , 2021, 9, 9. | 11.1 | 24 |
| 200 | Biogenic Amines Increase the Odds of Bacterial Vaginosis and Affect the Growth of and Lactic Acid Production by Vaginal <i>Lactobacillus</i> spp.. <i>Applied and Environmental Microbiology</i> , 2021, 87, . | 3.1 | 24 |
| 201 | The Role of Genomics in the Identification, Prediction, and Prevention of Biological Threats. <i>PLoS Biology</i> , 2009, 7, e1000217. | 5.6 | 23 |
| 202 | Assessment of the human faecal microbiota: I. Measurement and reproducibility of selected enzymatic activities. <i>European Journal of Clinical Investigation</i> , 2012, 42, 848-854. | 3.4 | 23 |
| 203 | The association of <i>Chlamydia trachomatis</i> and <i>Mycoplasma genitalium</i> infection with the vaginal metabolome. <i>Scientific Reports</i> , 2020, 10, 3420. | 3.3 | 23 |
| 204 | Feasibility of self-collection of fecal specimens by randomly sampled women for health-related studies of the gut microbiome. <i>BMC Research Notes</i> , 2014, 7, 204. | 1.4 | 22 |
| 205 | Genus-optimized strategy for the identification of chlamydial type III secretion substrates. <i>Pathogens and Disease</i> , 2013, 69, 213-222. | 2.0 | 21 |
| 206 | <i>Chlamydia caviae</i> infection alters abundance but not composition of the guinea pig vaginal microbiota. <i>Pathogens and Disease</i> , 2015, 73, . | 2.0 | 21 |
| 207 | A high-throughput sequencing assay to comprehensively detect and characterize unicellular eukaryotes and helminths from biological and environmental samples. <i>Microbiome</i> , 2018, 6, 195. | 11.1 | 21 |
| 208 | Vaginal microbiota and mucosal pharmacokinetics of tenofovir in healthy women using tenofovir and tenofovir/levonorgestrel vaginal rings. <i>PLoS ONE</i> , 2019, 14, e0217229. | 2.5 | 21 |
| 209 | Higher Levels of a Cytotoxic Protein, Vaginolysin, in <i>Lactobacillus</i> -Deficient Community State Types at the Vaginal Mucosa. <i>Sexually Transmitted Diseases</i> , 2018, 45, e14-e17. | 1.7 | 20 |
| 210 | Protection and Risk: Male and Female Genital Microbiota and Sexually Transmitted Infections. <i>Journal of Infectious Diseases</i> , 2021, 223, S222-S235. | 4.0 | 20 |
| 211 | Phylogeography of <i>Bacillus anthracis</i> in the Country of Georgia Shows Evidence of Population Structuring and Is Dissimilar to Other Regional Genotypes. <i>PLoS ONE</i> , 2014, 9, e102651. | 2.5 | 20 |
| 212 | All hail reproducibility in microbiome research. <i>Microbiome</i> , 2014, 2, 8. | 11.1 | 19 |
| 213 | Draft Genome Sequence of Biocontrol Agent <i>Bacillus cereus</i> UW85. <i>Genome Announcements</i> , 2016, 4, . | 0.8 | 19 |
| 214 | Vaginal host immune-microbiome interactions in a cohort of primarily African-American women who ultimately underwent spontaneous preterm birth or delivered at term. <i>Cytokine</i> , 2021, 137, 155316. | 3.2 | 19 |
| 215 | <i>Editorial Commentary:</i> Ready or Not: The Molecular Diagnosis of Bacterial Vaginosis. <i>Clinical Infectious Diseases</i> , 2008, 47, 44-46. | 5.8 | 17 |
| 216 | An Effective Intervention to Reduce Intravaginal Practices Among HIV-1 Uninfected Kenyan Women. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, 1046-1057. | 1.1 | 17 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 217 | Comparative phase I randomized open-label pilot clinical trial of Gynophilus® (Lcr regenerans®) immediate release capsules versus slow release muco-adhesive tablets. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2018, 37, 1869-1880. | 2.9 | 17 |
| 218 | Natural history, dynamics, and ecology of human papillomaviruses in genital infections of young women: protocol of the PAPCLEAR cohort study. <i>BMJ Open</i> , 2019, 9, e025129. | 1.9 | 17 |
| 219 | Asymptomatic Bacterial Vaginosis Is Associated With Depletion of Mature Superficial Cells Shed From the Vaginal Epithelium. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 106. | 3.9 | 17 |
| 220 | Draft Genome Sequences of <i>Yersinia pestis</i> Isolates from Natural Foci of Endemic Plague in China. <i>Journal of Bacteriology</i> , 2009, 191, 7628-7629. | 2.2 | 16 |
| 221 | Novel Plasmids and Resistance Phenotypes in <i>Yersinia pestis</i> : Unique Plasmid Inventory of Strain Java 9 Mediates High Levels of Arsenic Resistance. <i>PLoS ONE</i> , 2012, 7, e32911. | 2.5 | 16 |
| 222 | Draft Genome Sequence of <i>Synechococcus</i> sp. Strain CB0101, Isolated From the Chesapeake Bay Estuary. <i>Genome Announcements</i> , 2014, 2, . | 0.8 | 16 |
| 223 | Fine-scale analysis of 16S rRNA sequences reveals a high level of taxonomic diversity among vaginal <i>Atopobium</i> spp.. <i>Pathogens and Disease</i> , 2015, 73, . | 2.0 | 16 |
| 224 | Dietary macronutrient intake and molecular-bacterial vaginosis: Role of fiber. <i>Clinical Nutrition</i> , 2020, 39, 3066-3071. | 5.0 | 16 |
| 225 | Microbial Forensic Investigation of the Anthrax-Letter Attacks. , 2011, , 15-25. | | 14 |
| 226 | Vaginal <i>Candida</i> spp. genomes from women with vulvovaginal candidiasis. <i>Pathogens and Disease</i> , 2017, 75, . | 2.0 | 14 |
| 227 | Vaginal microbiota diversity and paucity of <i>Lactobacillus</i> species are associated with persistent hrHPV infection in HIV negative but not in HIV positive women. <i>Scientific Reports</i> , 2020, 10, 19095. | 3.3 | 14 |
| 228 | Characteristics associated with <i>Lactobacillus iners</i> -dominated vaginal microbiota. <i>Sexually Transmitted Infections</i> , 2022, 98, 353-359. | 1.9 | 14 |
| 229 | Characterization of Clinically-Attenuated <i>Burkholderia mallei</i> by Whole Genome Sequencing: Candidate Strain for Exclusion from Select Agent Lists. <i>PLoS ONE</i> , 2008, 3, e2058. | 2.5 | 13 |
| 230 | Genome Sequence of <i>Ruegeria</i> sp. Strain KLH11, an <i>N</i> -Acylhomoserine Lactone-Producing Bacterium Isolated from the Marine Sponge <i>Mycale laxissima</i> . <i>Journal of Bacteriology</i> , 2011, 193, 5011-5012. | 2.2 | 13 |
| 231 | Understanding Vulvovaginal Candidiasis Through a Community Genomics Approach. <i>Current Fungal Infection Reports</i> , 2013, 7, 126-131. | 2.6 | 13 |
| 232 | Multiple-Ascending-Dose Phase 1 Clinical Study of the Safety, Tolerability, and Pharmacokinetics of CRS3123, a Narrow-Spectrum Agent with Minimal Disruption of Normal Gut Microbiota. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 64, . | 3.2 | 13 |
| 233 | Early screening for <i>Chlamydia trachomatis</i> in young women for primary prevention of pelvic inflammatory disease (i-Predict): study protocol for a randomised controlled trial. <i>Trials</i> , 2017, 18, 534. | 1.6 | 12 |
| 234 | Mammographic breast density and its association with urinary estrogens and the fecal microbiota in postmenopausal women. <i>PLoS ONE</i> , 2019, 14, e0216114. | 2.5 | 12 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 235 | The Effect of Gender-Affirming Medical Care on the Vaginal and Neovaginal Microbiomes of Transgender and Gender-Diverse People. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 769950. | 3.9 | 12 |
| 236 | Preparation of DNA extracted from environmental water samples for PCR amplification. <i>Journal of Microbiological Methods</i> , 1998, 31, 193-199. | 1.6 | 10 |
| 237 | No Resistance Plasmid in <i>Yersinia pestis</i> , North America. <i>Emerging Infectious Diseases</i> , 2010, 16, 885-887. | 4.3 | 10 |
| 238 | Effect of a Nonoptimal Cervicovaginal Microbiota and Psychosocial Stress on Recurrent Spontaneous Preterm Birth. <i>American Journal of Perinatology</i> , 2021, 38, 407-413. | 1.4 | 10 |
| 239 | Association of E484K spike protein mutation with SARS-CoV-2 infection in vaccinated persons—Maryland, January–May 2021. <i>Clinical Infectious Diseases</i> , 2021, . . | 5.8 | 10 |
| 240 | Analysis of Polymorphic Membrane Protein Expression in Cultured Cells Identifies PmpA and PmpH of <i>Chlamydia psittaci</i> as Candidate Factors in Pathogenesis and Immunity to Infection. <i>PLoS ONE</i> , 2016, 11, e0162392. | 2.5 | 10 |
| 241 | Altered Gut Microbiome and Fecal Immune Phenotype in Early Preterm Infants With Leaky Gut. <i>Frontiers in Immunology</i> , 2022, 13, 815046. | 4.8 | 10 |
| 242 | Highly Specialized Carbohydrate Metabolism Capability in <i>Bifidobacterium</i> Strains Associated with Intestinal Barrier Maturation in Early Preterm Infants. <i>MBio</i> , 2022, 13, . | 4.1 | 10 |
| 243 | Clinical Relevance of Gastrointestinal Microbiota During Pregnancy: A Primer for Nurses. <i>Biological Research for Nursing</i> , 2018, 20, 84-102. | 1.9 | 9 |
| 244 | Assessing the Concordance Between Urogenital and Vaginal Microbiota: Can Urine Specimens Be Used as a Proxy for Vaginal Samples?. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 671413. | 3.9 | 9 |
| 245 | Supporting scale-up of COVID-19 RT-PCR testing processes with discrete event simulation. <i>PLoS ONE</i> , 2021, 16, e0255214. | 2.5 | 9 |
| 246 | Complete Genome Sequences of Six <i>Lactobacillus iners</i> Strains Isolated from the Human Vagina. <i>Microbiology Resource Announcements</i> , 2020, 9, . | 0.6 | 8 |
| 247 | A cross-sectional pilot study of birth mode and vaginal microbiota in reproductive-age women. <i>PLoS ONE</i> , 2020, 15, e0228574. | 2.5 | 8 |
| 248 | Perceived Stress and Molecular Bacterial Vaginosis in the National Institutes of Health Longitudinal Study of Vaginal Flora. <i>American Journal of Epidemiology</i> , 2021, 190, 2374-2383. | 3.4 | 8 |
| 249 | A non-optimal cervicovaginal microbiota in pregnancy is associated with a distinct metabolomic signature among non-Hispanic Black individuals. <i>Scientific Reports</i> , 2021, 11, 22794. | 3.3 | 8 |
| 250 | Sialidase Activity in the Cervicovaginal Fluid Is Associated With Changes in Bacterial Components of <i>Lactobacillus</i> -Deprived Microbiota. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 813520. | 3.9 | 8 |
| 251 | Vaginal Microbiota and Mucosal Pharmacokinetics of Tenofovir in Healthy Women Using a 90-Day Tenofovir/Levonorgestrel Vaginal Ring. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 799501. | 3.9 | 8 |
| 252 | Vaginal microbiota of American Indian women and associations with measures of psychosocial stress. <i>PLoS ONE</i> , 2021, 16, e0260813. | 2.5 | 8 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 253 | Gardnerella vaginalis induces matrix metalloproteinases in the cervicovaginal epithelium through TLR-2 activation. Journal of Reproductive Immunology, 2022, 152, 103648. | 1.9 | 8 |
| 254 | Are Changes to the Common Rule Necessary to Address Evolving Areas of Research?. Journal of Law, Medicine and Ethics, 2013, 41, 454-469. | 0.9 | 7 |
| 255 | Role of Molecular Biology in Diagnosis and Characterization of Vulvo-Vaginitis in Clinical Practice. Gynecologic and Obstetric Investigation, 2017, 82, 607-616. | 1.6 | 7 |
| 256 | Anal Microbial Patterns and Oncogenic Human Papillomavirus in a Pilot Study of Nigerian Men Who Have Sex with Men at Risk for or Living with HIV. AIDS Research and Human Retroviruses, 2019, 35, 267-275. | 1.1 | 7 |
| 257 | Meta-Pangenome: At the Crossroad of Pangenomics and Metagenomics. , 2020, , 205-218. | | 7 |
| 258 | Vaginal Microbiome Components as Correlates of Cervical Human Papillomavirus Infection. Journal of Infectious Diseases, 2022, 226, 1084-1097. | 4.0 | 7 |
| 259 | HIV-associated vaginal microbiome and inflammation predict spontaneous preterm birth in Zambia. Scientific Reports, 2022, 12, . | 3.3 | 7 |
| 260 | Coelichelin, a new peptide siderophore encoded by the Streptomyces coelicolor genome: structure prediction from the sequence of its non-ribosomal peptide synthetase. FEMS Microbiology Letters, 2000, 187, 111-114. | 1.8 | 6 |
| 261 | Second trimester short cervix is associated with decreased abundance of cervicovaginal lipid metabolites. American Journal of Obstetrics and Gynecology, 2022, 227, 273.e1-273.e18. | 1.3 | 6 |
| 262 | Genome Sequence of the Human Abscess Isolate Streptococcus intermedius BA1. Genome Announcements, 2013, 1, . | 0.8 | 5 |
| 263 | Authors' reply re: The vaginal metabolome and microbiota of cervical HPV-positive and HPV-negative women: a cross-sectional analysis. BJOG: an International Journal of Obstetrics and Gynaecology, 2020, 127, 773-774. | 2.3 | 5 |
| 264 | Chlamydia in adolescent/adult reproductive management trial study (CHARM): Clinical core protocol. Contemporary Clinical Trials Communications, 2019, 16, 100414. | 1.1 | 4 |
| 265 | Vaginal cytokine profile and microbiota before and after lubricant use compared with condomless vaginal sex: a preliminary observational study. BMC Infectious Diseases, 2021, 21, 973. | 2.9 | 4 |
| 266 | 26: The cervicovaginal microbiota is different in women destined to have a preterm birth. American Journal of Obstetrics and Gynecology, 2014, 210, S16-S17. | 1.3 | 3 |
| 267 | Complete Genome Sequence of Lactobacillus crispatus CO3MRSI1. Microbiology Resource Announcements, 2019, 8, . | 0.6 | 3 |
| 268 | Observational cohort study of the effect of a single lubricant exposure during transvaginal ultrasound on cell-shedding from the vaginal epithelium. PLoS ONE, 2021, 16, e0250153. | 2.5 | 3 |
| 269 | Associations of public water system trihalomethane exposure during pregnancy with spontaneous preterm birth and the cervicovaginal microbial-immune state. Environmental Research, 2021, 199, 111288. | 7.5 | 3 |
| 270 | Serum antibodies to surface proteins of Chlamydia trachomatis as candidate biomarkers of disease: results from the Baltimore Chlamydia Adolescent/Young Adult Reproductive Management (CHARM) cohort. FEMS Microbes, 2022, 3, . | 2.1 | 3 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 271 | 10: Distinct microbiota in the cervicovaginal space are associated with spontaneous preterm birth: findings from a large cohort and validation study. American Journal of Obstetrics and Gynecology, 2017, 216, S8-S9. | 1.3 | 2 |
| 272 | P591â€¦The effect of hormonal contraception on the vaginal microbiota over 2 years. , 2019, , . | | 2 |
| 273 | High-Risk Human Papillomavirus Persistence and Anal Microbiota Among Nigerian Men Who Have Sex With Men Living With or At Risk for HIV. JCO Global Oncology, 2020, 6, 26-27. | 1.8 | 2 |
| 274 | Using Innovation to Address Adolescent and Young Adult Health Disparities in Pelvic Inflammatory Disease: Design of the Technology Enhanced Community Health Precision Nursing (TECH-PN) Trial. Journal of Infectious Diseases, 2021, 224, S145-S151. | 4.0 | 2 |
| 275 | The Impact of Over-The-Counter Lactic Acid Containing Vaginal Gels on the Integrity and Inflammatory State of the Vaginal Epithelium in vitro. Frontiers in Reproductive Health, 0, 4, . | 1.9 | 2 |
| 276 | The Microbial Ecology of Bacterial Vaginosis: A Fine Scale Resolution Metagenomic Analysis. Nature Precedings, 2010, , . | 0.1 | 1 |
| 277 | O13.2â€¦Hormonal contraception is associated with stability and<i>lactobacillus</i>-dominance of the vaginal microbiota in a two-year observational study. Sexually Transmitted Infections, 2015, 91, A53.2-A53. | 1.9 | 1 |
| 278 | 359: Integrating low and high risk cervicovaginal microbiota with antimicrobial peptides may identify those women at greatest risk for spontaneous preterm birth. American Journal of Obstetrics and Gynecology, 2017, 216, S218. | 1.3 | 1 |
| 279 | The authors reply. Gut Microbes, 2019, 10, 113-114. | 9.8 | 1 |
| 280 | Association of Vaginal Microbiota With the Genitourinary Syndrome of Menopause Across Reproductive Stages. Innovation in Aging, 2020, 4, 171-171. | 0.1 | 1 |
| 281 | Comparison of two microscopic interpretations of vaginal microbiota with molecular profiling. Diagnostic Microbiology and Infectious Disease, 2022, 104, 115728. | 1.8 | 1 |
| 282 | Complete Genome Sequences of Ezakiella coagulans C0061C1 and Fenollaria massiliensis C0061C2. Microbiology Resource Announcements, 0, , . | 0.6 | 1 |
| 283 | P4-S3.07 Population genomics of Trichomonas vaginalis reveals a globally distributed two-phylo-type population structure. Sexually Transmitted Infections, 2011, 87, A314-A315. | 1.9 | 0 |
| 284 | P4-S4.04 Temporal dynamics of vaginal bacterial communities. Sexually Transmitted Infections, 2011, 87, A316-A317. | 1.9 | 0 |
| 285 | P1.034â€¦Biomarkers of Cigarette Smoking and Association with the Vaginal Microbiota. Sexually Transmitted Infections, 2013, 89, A84.2-A84. | 1.9 | 0 |
| 286 | O05.5â€¦A Longitudinal Study of the Vaginal Microbiota and HPV Detection. Sexually Transmitted Infections, 2013, 89, A36.1-A36. | 1.9 | 0 |
| 287 | P1.030â€¦A Molecular Study of Vaginal Bacterial Communities and Candida Albicans Detection. Sexually Transmitted Infections, 2013, 89, A83.1-A83. | 1.9 | 0 |
| 288 | Erratum for Yeruva et al., Early MicroRNA Expression Profile as a Prognostic Biomarker for the Development of Pelvic Inflammatory Disease in a Mouse Model of Chlamydial Genital Infection. MBio, 2014, 5, . | 4.1 | 0 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 289 | O13.5â€¦Association between dietary intake and dysbiotic vaginal microbiota. Sexually Transmitted Infections, 2015, 91, A54.2-A55. | 1.9 | 0 |
| 290 | P06.09â€¦<i>Lactobacillus</i> crispatus inhibits growth of<i>gardnerella vaginalis</i> and<i>neisseria gonorrhoeae</i> on a porcine vaginal mucosa model. Sexually Transmitted Infections, 2015, 91, A117.2-A117. | 1.9 | 0 |
| 291 | O13.6â€¦Cigarette smoking is associated with an altered metabolic profile in the vaginal tract. Sexually Transmitted Infections, 2015, 91, A55.1-A55. | 1.9 | 0 |
| 292 | O10.4â€¦Concordance between random catch urine and mid-vaginal microbiota. , 2017, , . | | 0 |
| 293 | P1.27â€¦Hpv is associated with an altered metabolomic profile in the vaginal tract. , 2017, , . | | 0 |
| 294 | P1.21â€¦Comparison of shipped versus freshly frozen self-collected vaginal samples for microbiota assessment. , 2017, , . | | 0 |
| 295 | P593â€¦A cross-sectional study of birth mode and vaginal microbiota in reproductive-age women. , 2019, , . | | 0 |
| 296 | A cross-sectional pilot study of birth mode and vaginal microbiota in reproductive-age women. , 2020, 15, e0228574. | | 0 |
| 297 | A cross-sectional pilot study of birth mode and vaginal microbiota in reproductive-age women. , 2020, 15, e0228574. | | 0 |
| 298 | A cross-sectional pilot study of birth mode and vaginal microbiota in reproductive-age women. , 2020, 15, e0228574. | | 0 |
| 299 | A cross-sectional pilot study of birth mode and vaginal microbiota in reproductive-age women. , 2020, 15, e0228574. | | 0 |
| 300 | Douching cessation and molecular bacterial vaginosis: a reanalysis of archived specimens. Sexually Transmitted Infections, 0, , sextrans-2022-055459. | 1.9 | 0 |