

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	Characteristics associated with <i>Lactobacillus iners</i> -dominated vaginal microbiota. Sexually Transmitted Infections, 2022, 98, 353-359.	1.9	14
2	Vaginal Microbiome Components as Correlates of Cervical Human Papillomavirus Infection. Journal of Infectious Diseases, 2022, 226, 1084-1097.	4.0	7
3	Serum antibodies to surface proteins of <i>Chlamydia trachomatis</i> as candidate biomarkers of disease: results from the Baltimore Chlamydia Adolescent/Young Adult Reproductive Management (CHARM) cohort. FEMS Microbes, 2022, 3, .	2.1	3
4	Altered Gut Microbiome and Fecal Immune Phenotype in Early Preterm Infants With Leaky Gut. Frontiers in Immunology, 2022, 13, 815046.	4.8	10
5	Vaginal Microbiota and Mucosal Pharmacokinetics of Tenofovir in Healthy Women Using a 90-Day Tenofovir/Levonorgestrel Vaginal Ring. Frontiers in Cellular and Infection Microbiology, 2022, 12, 799501.	3.9	8
6	Insight into the ecology of vaginal bacteria through integrative analyses of metagenomic and metatranscriptomic data. Genome Biology, 2022, 23, 66.	8.8	40
7	Towards a deeper understanding of the vaginal microbiota. Nature Microbiology, 2022, 7, 367-378.	13.3	94
8	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
9	<i>Gardnerella vaginalis</i> induces matrix metalloproteinases in the cervicovaginal epithelium through TLR-2 activation. Journal of Reproductive Immunology, 2022, 152, 103648.	1.9	8
10	Comparison of two microscopic interpretations of vaginal microbiota with molecular profiling. Diagnostic Microbiology and Infectious Disease, 2022, 104, 115728.	1.8	1
11	HIV-associated vaginal microbiome and inflammation predict spontaneous preterm birth in Zambia. Scientific Reports, 2022, 12, .	3.3	7
12	Highly Specialized Carbohydrate Metabolism Capability in <i>Bifidobacterium</i> Strains Associated with Intestinal Barrier Maturation in Early Preterm Infants. MBio, 2022, 13, .	4.1	10
13	Bacterial vaginosis and its association with infertility, endometritis, and pelvic inflammatory disease. American Journal of Obstetrics and Gynecology, 2021, 224, 251-257.	1.3	146
14	Effect of a Nonoptimal Cervicovaginal Microbiota and Psychosocial Stress on Recurrent Spontaneous Preterm Birth. American Journal of Perinatology, 2021, 38, 407-413.	1.4	10
15	Vaginal host immune-microbiome interactions in a cohort of primarily African-American women who ultimately underwent spontaneous preterm birth or delivered at term. Cytokine, 2021, 137, 155316.	3.2	19
16	Microbiome or no microbiome: are we looking at the prenatal environment through the right lens?. Microbiome, 2021, 9, 9.	11.1	24
17	Protection and Risk: Male and Female Genital Microbiota and Sexually Transmitted Infections. Journal of Infectious Diseases, 2021, 223, S222-S235.	4.0	20
18	Biogenic Amines Increase the Odds of Bacterial Vaginosis and Affect the Growth of and Lactic Acid Production by Vaginal <i>Lactobacillus</i> spp.. Applied and Environmental Microbiology, 2021, 87, .	3.1	24

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19	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
20	Observational cohort study of the effect of a single lubricant exposure during transvaginal ultrasound on cell-shedding from the vaginal epithelium. <i>PLoS ONE</i> , 2021, 16, e0250153.	2.5	3
21	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
22	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
23	Supporting scale-up of COVID-19 RT-PCR testing processes with discrete event simulation. <i>PLoS ONE</i> , 2021, 16, e0255214.	2.5	9
24	Associations of public water system trihalomethane exposure during pregnancy with spontaneous preterm birth and the cervicovaginal microbial-immune state. <i>Environmental Research</i> , 2021, 199, 111288.	7.5	3
25	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. <i>Journal of Infectious Diseases</i> , 2021, 224, S145-S151.	4.0	2
26	Vaginal cytokine profile and microbiota before and after lubricant use compared with condomless vaginal sex: a preliminary observational study. <i>BMC Infectious Diseases</i> , 2021, 21, 973.	2.9	4
27	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
28	Association of E484K spike protein mutation with SARS-CoV-2 infection in vaccinated persons—Maryland, January 2021–May 2021. <i>Clinical Infectious Diseases</i> , 2021, , .	5.8	10
29	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
30	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
31	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
32	Sialidase Activity in the Cervicovaginal Fluid Is Associated With Changes in Bacterial Components of Lactobacillus-Deprived Microbiota. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 813520.	3.9	8
33	Vaginal microbiota of American Indian women and associations with measures of psychosocial stress. <i>PLoS ONE</i> , 2021, 16, e0260813.	2.5	8
34	The Impact of Human Immunodeficiency Virus Infection on Gut Microbiota \pm -Diversity: An Individual-level Meta-analysis. <i>Clinical Infectious Diseases</i> , 2020, 70, 615-627.	5.8	65
35	Nonoptimal Vaginal Microbiota After Azithromycin Treatment for Chlamydia trachomatis Infection. <i>Journal of Infectious Diseases</i> , 2020, 221, 627-635.	4.0	33
36	Cervicovaginal microbial communities deficient in Lactobacillus 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

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37	The vaginal metabolome and microbiota of cervical HPVâ€­positive and HPVâ€­negative women: a crossâ€­sectional analysis. BJOG: an International Journal of Obstetrics and Gynaecology, 2020, 127, 182-192.	2.3	86
38	Characterization of the Vaginal Microbiome in Women of Reproductive Age From 5 Regions in Brazil. Sexually Transmitted Diseases, 2020, 47, 562-569.	1.7	33
39	VALENCIA: a nearest centroid classification method for vaginal microbial communities based on composition. Microbiome, 2020, 8, 166.	11.1	177
40	Quantitative modeling predicts mechanistic links between pre-treatment microbiome composition and metronidazole efficacy in bacterial vaginosis. Nature Communications, 2020, 11, 6147.	12.8	24
41	Changes in the vaginal microbiota across a gradient of urbanization. Scientific Reports, 2020, 10, 12487.	3.3	25
42	Vaginal microbiota diversity and paucity of Lactobacillus species are associated with persistent hrHPV infection in HIV negative but not in HIV positive women. Scientific Reports, 2020, 10, 19095.	3.3	14
43	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
44	Complete Genome Sequences of Six Lactobacillus iners Strains Isolated from the Human Vagina. Microbiology Resource Announcements, 2020, 9, .	0.6	8
45	Intermittent Lactobacilli-containing Vaginal Probiotic or Metronidazole Use to Prevent Bacterial Vaginosis Recurrence: A Pilot Study Incorporating Microscopy and Sequencing. Scientific Reports, 2020, 10, 3884.	3.3	40
46	Authors' reply re: The vaginal metabolome and microbiota of cervical HPVâ€­positive and HPVâ€­negative women: a crossâ€­sectional analysis. BJOG: an International Journal of Obstetrics and Gynaecology, 2020, 127, 773-774.	2.3	5
47	Asymptomatic Bacterial Vaginosis Is Associated With Depletion of Mature Superficial Cells Shed From the Vaginal Epithelium. Frontiers in Cellular and Infection Microbiology, 2020, 10, 106.	3.9	17
48	A comprehensive non-redundant gene catalog reveals extensive within-community intraspecies diversity in the human vagina. Nature Communications, 2020, 11, 940.	12.8	86
49	The association of Chlamydia trachomatis and Mycoplasma genitalium infection with the vaginal metabolome. Scientific Reports, 2020, 10, 3420.	3.3	23
50	Dietary macronutrient intake and molecular-bacterial vaginosis: Role of fiber. Clinical Nutrition, 2020, 39, 3066-3071.	5.0	16
51	Comparative Metagenome-Assembled Genome Analysis of â€œCandidatus Lachnocurva vaginaeâ€­, Formerly Known as Bacterial Vaginosis-Associated Bacteriumâ€­1 (BVAB1). Frontiers in Cellular and Infection Microbiology, 2020, 10, 117.	3.9	49
52	A cross-sectional pilot study of birth mode and vaginal microbiota in reproductive-age women. PLoS ONE, 2020, 15, e0228574.	2.5	8
53	Meta-Pangenome: At the Crossroad of Pangenomics and Metagenomics. , 2020, , 205-218.		7
54	Association of Vaginal Microbiota With the Genitourinary Syndrome of Menopause Across Reproductive Stages. Innovation in Aging, 2020, 4, 171-171.	0.1	1

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55	A cross-sectional pilot study of birth mode and vaginal microbiota in reproductive-age women. , 2020, 15, e0228574.		0
56	A cross-sectional pilot study of birth mode and vaginal microbiota in reproductive-age women. , 2020, 15, e0228574.		0
57	A cross-sectional pilot study of birth mode and vaginal microbiota in reproductive-age women. , 2020, 15, e0228574.		0
58	A cross-sectional pilot study of birth mode and vaginal microbiota in reproductive-age women. , 2020, 15, e0228574.		0
59	Dynamics of Vaginal and Rectal Microbiota Over Several Menstrual Cycles in Female Cynomolgus Macaques. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 188.	3.9	24
60	The Cervicovaginal Microbiota-Host Interaction Modulates Chlamydia trachomatis Infection. <i>MBio</i> , 2019, 10, .	4.1	107
61	Crypt- and Mucosa-Associated Core Microbiotas in Humans and Their Alteration in Colon Cancer Patients. <i>MBio</i> , 2019, 10, .	4.1	94
62	Chlamydia in adolescent/adult reproductive management trial study (CHARM): Clinical core protocol. <i>Contemporary Clinical Trials Communications</i> , 2019, 16, 100414.	1.1	4
63	Associations between dietary micronutrient intake and molecular-Bacterial Vaginosis. <i>Reproductive Health</i> , 2019, 16, 151.	3.1	27
64	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
65	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
66	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
67	Cervicovaginal microbiota and local immune response modulate the risk of spontaneous preterm delivery. <i>Nature Communications</i> , 2019, 10, 1305.	12.8	260
68	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
69	Complete Genome Sequence of <i>Lactobacillus crispatus</i> CO3MRSI1. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
70	P591â€¦The effect of hormonal contraception on the vaginal microbiota over 2 years. , 2019, , .		2
71	P593â€¦A cross-sectional study of birth mode and vaginal microbiota in reproductive-age women. , 2019, , .		0
72	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

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73	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
74	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. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 267-275.	1.1	7
75	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
76	The Evolving Facets of Bacterial Vaginosis: Implications for HIV Transmission. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 219-228.	1.1	188
77	The authors reply. <i>Gut Microbes</i> , 2019, 10, 113-114.	9.8	1
78	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
79	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
80	Clinical Relevance of Gastrointestinal Microbiota During Pregnancy: A Primer for Nurses. <i>Biological Research for Nursing</i> , 2018, 20, 84-102.	1.9	9
81	Cigarette smoking is associated with an altered vaginal tract metabolomic profile. <i>Scientific Reports</i> , 2018, 8, 852.	3.3	84
82	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
83	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
84	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
85	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
86	Human oral microbiome and prospective risk for pancreatic cancer: a population-based nested case-control study. <i>Gut</i> , 2018, 67, 120-127.	12.1	536
87	<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
88	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
89	Microbial Biomarkers of Intestinal Barrier Maturation in Preterm Infants. <i>Frontiers in Microbiology</i> , 2018, 9, 2755.	3.5	40
90	Association between the vaginal microbiota, menopause status, and signs of vulvovaginal atrophy. <i>Menopause</i> , 2018, 25, 1321-1330.	2.0	63

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91	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
92	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
93	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
94	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
95	Anti-HIV-1 Activity of Lactic Acid in Human Cervicovaginal Fluid. <i>MSphere</i> , 2018, 3, .	2.9	66
96	“Available upon request” not good enough for microbiome data!. <i>Microbiome</i> , 2018, 6, 8.	11.1	35
97	The implausible “in vivo” role of hydrogen peroxide as an antimicrobial factor produced by vaginal microbiota. <i>Microbiome</i> , 2018, 6, 29.	11.1	81
98	Cervicovaginal microbiota, women's health, and reproductive outcomes. <i>Fertility and Sterility</i> , 2018, 110, 327-336.	1.0	165
99	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
100	The vaginal microbiota, host defence and reproductive physiology. <i>Journal of Physiology</i> , 2017, 595, 451-463.	2.9	279
101	The effect of cigarette smoking on the oral and nasal microbiota. <i>Microbiome</i> , 2017, 5, 3.	11.1	141
102	359: Integrating low and high risk cervicovaginal microbiota with antimicrobial peptides may identify those women at greatest risk for spontaneous preterm birth. <i>American Journal of Obstetrics and Gynecology</i> , 2017, 216, S218.	1.3	1
103	10: Distinct microbiota in the cervicovaginal space are associated with spontaneous preterm birth: findings from a large cohort and validation study. <i>American Journal of Obstetrics and Gynecology</i> , 2017, 216, S8-S9.	1.3	2
104	Association of HPV infection and clearance with cervicovaginal immunology and the vaginal microbiota. <i>Mucosal Immunology</i> , 2017, 10, 1310-1319.	6.0	148
105	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
106	Vaginal <i>Candida</i> spp. genomes from women with vulvovaginal candidiasis. <i>Pathogens and Disease</i> , 2017, 75, .	2.0	14
107	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
108	Rectal microbiota among HIV-uninfected, untreated HIV, and treated HIV-infected in Nigeria. <i>Aids</i> , 2017, 31, 857-862.	2.2	46

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109	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
110	A proposed definition of microbiota transplantation for regulatory purposes. <i>Gut Microbes</i> , 2017, 8, 208-213.	9.8	40
111	O10.4â€¦Concordance between random catch urine and mid-vaginal microbiota. , 2017, , .		0
112	P1.27â€¦Hpv is associated with an altered metabolomic profile in the vaginal tract. , 2017, , .		0
113	Role of Molecular Biology in Diagnosis and Characterization of Vulvo-Vaginitis in Clinical Practice. <i>Gynecologic and Obstetric Investigation</i> , 2017, 82, 607-616.	1.6	7
114	Does Active Oral Sex Contribute to Female Infertility?. <i>Journal of Infectious Diseases</i> , 2017, 216, 932-935.	4.0	36
115	Group B Streptococcus and the Vaginal Microbiota. <i>Journal of Infectious Diseases</i> , 2017, 216, 744-751.	4.0	58
116	Improving regulation of microbiota transplants. <i>Science</i> , 2017, 358, 1390-1391.	12.6	41
117	Evaluation of Buccal Cell Samples for Studies of Oral Microbiota. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 249-253.	2.5	27
118	The vaginal mycobiome: A contemporary perspective on fungi in women's health and diseases. <i>Virulence</i> , 2017, 8, 342-351.	4.4	124
119	P1.21â€¦Comparison of shipped versus freshly frozen self-collected vaginal samples for microbiota assessment. , 2017, , .		0
120	Mycoplasma hominis and Mycoplasma genitalium in the Vaginal Microbiota and Persistent High-Risk Human Papillomavirus Infection. <i>Frontiers in Public Health</i> , 2017, 5, 140.	2.7	55
121	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
122	Early screening for Chlamydia trachomatis 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
123	Phylogenetic and Functional Substrate Specificity for Endolithic Microbial Communities in Hyper-Arid Environments. <i>Frontiers in Microbiology</i> , 2016, 7, 301.	3.5	60
124	Functional interactions of archaea, bacteria and viruses in a hypersaline endolithic community. <i>Environmental Microbiology</i> , 2016, 18, 2064-2077.	3.8	107
125	Draft Genome Sequence of Biocontrol Agent Bacillus cereus UW85. <i>Genome Announcements</i> , 2016, 4, .	0.8	19
126	Characterizing human lung tissue microbiota and its relationship to epidemiological and clinical features. <i>Genome Biology</i> , 2016, 17, 163.	8.8	264

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127	Prevalent high-risk HPV infection and vaginal microbiota in Nigerian women. <i>Epidemiology and Infection</i> , 2016, 144, 123-137.	2.1	104
128	Translating the vaginal microbiome: gaps and challenges. <i>Genome Medicine</i> , 2016, 8, 35.	8.2	81
129	Intricacies of assessing the human microbiome in epidemiologic studies. <i>Annals of Epidemiology</i> , 2016, 26, 311-321.	1.9	46
130	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
131	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
132	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
133	O13.5â€¦Association between dietary intake and dysbiotic vaginal microbiota. <i>Sexually Transmitted Infections</i> , 2015, 91, A54.2-A55.	1.9	0
134	The vocabulary of microbiome research: a proposal. <i>Microbiome</i> , 2015, 3, 31.	11.1	778
135	<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
136	P06.09â€¦<i>Lactobacillus</i> <i>crispatus</i> inhibits growth of <i>gardnerella vaginalis</i> and <i>neisseria gonorrhoeae</i> on a porcine vaginal mucosa model. <i>Sexually Transmitted Infections</i> , 2015, 91, A117.2-A117.	1.9	0
137	O13.2â€¦Hormonal contraception is associated with stability and <i>lactobacillus</i>-dominance of the vaginal microbiota in a two-year observational study. <i>Sexually Transmitted Infections</i> , 2015, 91, A53.2-A53.	1.9	1
138	O13.6â€¦Cigarette smoking is associated with an altered metabolic profile in the vaginal tract. <i>Sexually Transmitted Infections</i> , 2015, 91, A55.1-A55.	1.9	0
139	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
140	Nested PCR Biases in Interpreting Microbial Community Structure in 16S rRNA Gene Sequence Datasets. <i>PLoS ONE</i> , 2015, 10, e0132253.	2.5	60
141	Vaginal biogenic amines: biomarkers of bacterial vaginosis or precursors to vaginal dysbiosis?. <i>Frontiers in Physiology</i> , 2015, 6, 253.	2.8	114
142	<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
143	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
144	Uncovering effects of antibiotics on the host and microbiota using transkingdom gene networks. <i>Gut</i> , 2015, 64, 1732-1743.	12.1	261

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145	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
146	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
147	Functional Dynamics of the Gut Microbiome in Elderly People during Probiotic Consumption. <i>MBio</i> , 2015, 6, .	4.1	126
148	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
149	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
150	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
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300	Complete Genome Sequences of <i>Ezakiella coagulans</i> C0061C1 and <i>Fenollaria massiliensis</i> C0061C2. <i>Microbiology Resource Announcements</i> , 0, , .	0.6	1