

Jacques Ravel

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292
papers

27,002
citations

79
h-index

160
g-index

331
ext. papers

33,105
ext. citations

7.3
avg, IF

7.02
L-index

#	Paper	IF	Citations
292	Vaginal microbiome of reproductive-age women. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108 Suppl 1, 4680-7	11.5	2091
291	An improved dual-indexing approach for multiplexed 16S rRNA gene sequencing on the Illumina MiSeq platform. <i>Microbiome</i> , 2014 , 2, 6	16.6	930
290	Temporal dynamics of the human vaginal microbiota. <i>Science Translational Medicine</i> , 2012 , 4, 132ra52	17.5	835
289	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. <i>Journal of Bacteriology</i> , 2005 , 187, 2426-38	3.5	814
288	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011 , 12, R50	18.3	723
287	Predictive, structure-based model of amino acid recognition by nonribosomal peptide synthetase adenylation domains. <i>Chemistry and Biology</i> , 2000 , 7, 211-24		639
286	The pangenome structure of <i>Escherichia coli</i> : comparative genomic analysis of <i>E. coli</i> commensal and pathogenic isolates. <i>Journal of Bacteriology</i> , 2008 , 190, 6881-93	3.5	607
285	Complete genome sequence of the plant commensal <i>Pseudomonas fluorescens</i> Pf-5. <i>Nature Biotechnology</i> , 2005 , 23, 873-8	44.5	522
284	The vocabulary of microbiome research: a proposal. <i>Microbiome</i> , 2015 , 3, 31	16.6	500
283	Patellamide A and C biosynthesis by a microcin-like pathway in <i>Prochloron didemni</i> , the cyanobacterial symbiont of <i>Lissoclinum patella</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 7315-20	11.5	486
282	The composition and stability of the vaginal microbiota of normal pregnant women is different from that of non-pregnant women. <i>Microbiome</i> , 2014 , 2, 4	16.6	447
281	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. <i>Nature Biotechnology</i> , 2011 , 29, 415-20	44.5	445
280	Major structural differences and novel potential virulence mechanisms from the genomes of multiple campylobacter species. <i>PLoS Biology</i> , 2005 , 3, e15	9.7	440
279	Vaginal microbiome: rethinking health and disease. <i>Annual Review of Microbiology</i> , 2012 , 66, 371-89	17.5	424
278	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. <i>Nucleic Acids Research</i> , 2004 , 32, 2386-95	20.1	404
277	<i>Yersinia pestis</i> genome sequencing identifies patterns of global phylogenetic diversity. <i>Nature Genetics</i> , 2010 , 42, 1140-3	36.3	393
276	Draft genome sequence of the oilseed species <i>Ricinus communis</i> . <i>Nature Biotechnology</i> , 2010 , 28, 951-6	44.5	379

275	Identification of anthrax toxin genes in a <i>Bacillus cereus</i> associated with an illness resembling inhalation anthrax. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 8449-54	11.5	377
274	Genomics of the <i>Bacillus cereus</i> group of organisms. <i>FEMS Microbiology Reviews</i> , 2005 , 29, 303-29	15.1	362
273	Human oral microbiome and prospective risk for pancreatic cancer: a population-based nested case-control study. <i>Gut</i> , 2018 , 67, 120-127	19.2	342
272	Evaluation of methods for the extraction and purification of DNA from the human microbiome. <i>PLoS ONE</i> , 2012 , 7, e33865	3.7	326
271	Multiple antimicrobial resistance in plague: an emerging public health risk. <i>PLoS ONE</i> , 2007 , 2, e309	3.7	296
270	Global genetic population structure of <i>Bacillus anthracis</i> . <i>PLoS ONE</i> , 2007 , 2, e461	3.7	276
269	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	1.7	264
268	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, 977-88	20.1	253
267	Skewed genomic variability in strains of the toxigenic bacterial pathogen, <i>Clostridium perfringens</i> . <i>Genome Research</i> , 2006 , 16, 1031-40	9.7	250
266	Metagenomics: read length matters. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 1453-63	4.8	243
265	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	16.6	236
264	Genomic insights into methanotrophy: the complete genome sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004 , 2, e303	9.7	236
263	Fecal microbial determinants of fecal and systemic estrogens and estrogen metabolites: a cross-sectional study. <i>Journal of Translational Medicine</i> , 2012 , 10, 253	8.5	234
262	A global assembly line for cyanobactins. <i>Nature Chemical Biology</i> , 2008 , 4, 341-3	11.7	227
261	Natural combinatorial peptide libraries in cyanobacterial symbionts of marine ascidians 2006 , 2, 729-35		224
260	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, 13536-41	11.5	218
259	Genomics of pyoverdine-mediated iron uptake in pseudomonads. <i>Trends in Microbiology</i> , 2003 , 11, 195-200	10.4	202
258	Association between the vaginal microbiota, menopause status, and signs of vulvovaginal atrophy. <i>Menopause</i> , 2014 , 21, 450-8	2.5	198

257	Uncovering effects of antibiotics on the host and microbiota using transkingdom gene networks. <i>Gut</i> , 2015 , 64, 1732-43	19.2	183
256	Visualization of comparative genomic analyses by BLAST score ratio. <i>BMC Bioinformatics</i> , 2005 , 6, 2	3.6	183
255	Interplay between the temporal dynamics of the vaginal microbiota and human papillomavirus detection. <i>Journal of Infectious Diseases</i> , 2014 , 210, 1723-33	7	174
254	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	3.7	171
253	Formation and composition of the Bacillus anthracis endospore. <i>Journal of Bacteriology</i> , 2004 , 186, 164-78	3.8	170
252	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	3.7	169
251	The effects of circumcision on the penis microbiome. <i>PLoS ONE</i> , 2010 , 5, e8422	3.7	165
250	The vaginal microbiota, host defence and reproductive physiology. <i>Journal of Physiology</i> , 2017 , 595, 451-63	3.6	164
249	Comparative genomics of the IncA/C multidrug resistance plasmid family. <i>Journal of Bacteriology</i> , 2009 , 191, 4750-7	3.5	164
248	Characterizing human lung tissue microbiota and its relationship to epidemiological and clinical features. <i>Genome Biology</i> , 2016 , 17, 163	18.3	163
247	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,	9.7	161
246	Coelichelin, a new peptide siderophore encoded by the Streptomyces coelicolor genome: structure prediction from the sequence of its non-ribosomal peptide synthetase. <i>FEMS Microbiology Letters</i> , 2000 , 187, 111-4	2.9	157
245	Daily temporal dynamics of vaginal microbiota before, during and after episodes of bacterial vaginosis. <i>Microbiome</i> , 2013 , 1, 29	16.6	156
244	Genomic anatomy of Escherichia coli O157:H7 outbreaks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 20142-7	11.5	148
243	Population dynamics of Chesapeake Bay virioplankton: total-community analysis by pulsed-field gel electrophoresis. <i>Applied and Environmental Microbiology</i> , 1999 , 65, 231-40	4.8	146
242	Understanding vaginal microbiome complexity from an ecological perspective. <i>Translational Research</i> , 2012 , 160, 267-82	11	145
241	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	11.5	143
240	Associations of the fecal microbiome with urinary estrogens and estrogen metabolites in postmenopausal women. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014 , 99, 4632-40	5.6	141

239	Cervicovaginal microbiota and local immune response modulate the risk of spontaneous preterm delivery. <i>Nature Communications</i> , 2019 , 10, 1305	17.4	130
238	Bacillus anthracis 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, 5027-32	11.5	130
237	Genome sequences of the biotechnologically important Bacillus megaterium strains QM B1551 and DSM319. <i>Journal of Bacteriology</i> , 2011 , 193, 4199-213	3.5	128
236	Comparative genomics of 28 Salmonella enterica isolates: evidence for CRISPR-mediated adaptive sublineage evolution. <i>Journal of Bacteriology</i> , 2011 , 193, 3556-68	3.5	127
235	Antimicrobial resistance-conferring plasmids with similarity to virulence plasmids from avian pathogenic Escherichia coli strains in Salmonella enterica serovar Kentucky isolates from poultry. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 5963-71	4.8	126
234	Complex microbiome underlying secondary and primary metabolism in the tunicate-Prochloron symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E1423-32	11.5	117
233	Complete sequence analysis of novel plasmids from emetic and periodontal Bacillus cereus isolates reveals a common evolutionary history among the B. cereus-group plasmids, including Bacillus anthracis pXO1. <i>Journal of Bacteriology</i> , 2007 , 189, 52-64	3.5	114
232	Free glycogen in vaginal fluids is associated with Lactobacillus colonization and low vaginal pH. <i>PLoS ONE</i> , 2014 , 9, e102467	3.7	113
231	Strain-specific single-nucleotide polymorphism assays for the Bacillus anthracis Ames strain. <i>Journal of Clinical Microbiology</i> , 2007 , 45, 47-53	9.7	112
230	Rapid fluctuation of the vaginal microbiota measured by Gram stain analysis. <i>Sexually Transmitted Infections</i> , 2010 , 86, 297-302	2.8	109
229	Association between Trichomonas vaginalis and vaginal bacterial community composition among reproductive-age women. <i>Sexually Transmitted Diseases</i> , 2012 , 39, 807-12	2.4	105
228	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, 1673-85	4.1	105
227	Functional dynamics of the gut microbiome in elderly people during probiotic consumption. <i>MBio</i> , 2015 , 6,	7.8	102
226	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	16.6	102
225	Bacterial diversity in a glacier foreland of the high Arctic. <i>Molecular Ecology</i> , 2010 , 19 Suppl 1, 54-66	5.7	99
224	Cervicovaginal microbiota, women's health, and reproductive outcomes. <i>Fertility and Sterility</i> , 2018 , 110, 327-336	4.8	98
223	The Evolving Facets of Bacterial Vaginosis: Implications for HIV Transmission. <i>AIDS Research and Human Retroviruses</i> , 2019 , 35, 219-228	1.6	98
222	Repair of extensive ionizing-radiation DNA damage at 95 degrees C in the hyperthermophilic archaeon Pyrococcus furiosus. <i>Journal of Bacteriology</i> , 1997 , 179, 4643-5	3.5	96

221	Enhanced Trapping of HIV-1 by Human Cervicovaginal Mucus Is Associated with Lactobacillus crispatus-Dominant Microbiota. <i>MBio</i> , 2015 , 6, e01084-15	7.8	95
220	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	6	88
219	Temperature-induced recovery of <i>Vibrio cholerae</i> from the viable but nonculturable state: growth or resuscitation?. <i>Microbiology (United Kingdom)</i> , 1995 , 141 (Pt 2), 377-83	2.9	88
218	Collection media and delayed freezing effects on microbial composition of human stool. <i>Microbiome</i> , 2015 , 3, 33	16.6	87
217	The vaginal mycobiome: A contemporary perspective on fungi in women's health and diseases. <i>Virulence</i> , 2017 , 8, 342-351	4.7	83
216	Male circumcision significantly reduces prevalence and load of genital anaerobic bacteria. <i>MBio</i> , 2013 , 4, e00076	7.8	81
215	The complete genome sequence of <i>Bacillus anthracis</i> Ames "Ancestor". <i>Journal of Bacteriology</i> , 2009 , 191, 445-6	3.5	81
214	Comparison of self-collected and physician-collected vaginal swabs for microbiome analysis. <i>Journal of Clinical Microbiology</i> , 2010 , 48, 1741-8	9.7	80
213	Prevalent high-risk HPV infection and vaginal microbiota in Nigerian women. <i>Epidemiology and Infection</i> , 2016 , 144, 123-37	4.3	79
212	The effect of cigarette smoking on the oral and nasal microbiota. <i>Microbiome</i> , 2017 , 5, 3	16.6	78
211	Association of HPV infection and clearance with cervicovaginal immunology and the vaginal microbiota. <i>Mucosal Immunology</i> , 2017 , 10, 1310-1319	9.2	78
210	Microbial diversity and the presence of algae in halite endolithic communities are correlated to atmospheric moisture in the hyper-arid zone of the Atacama Desert. <i>Environmental Microbiology</i> , 2015 , 17, 299-315	5.2	78
209	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. <i>MBio</i> , 2014 , 5,	7.8	78
208	Single nucleotide polymorphisms for assessing genetic diversity in castor bean (<i>Ricinus communis</i>). <i>BMC Plant Biology</i> , 2010 , 10, 13	5.3	78
207	Molecular Characterization of the Human Stomach Microbiota in Gastric Cancer Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017 , 7, 302	5.9	77
206	Castor bean organelle genome sequencing and worldwide genetic diversity analysis. <i>PLoS ONE</i> , 2011 , 6, e21743	3.7	77
205	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	2	77
204	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, 8071-9	4.8	76

203	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, 1685-99	3.5	75
202	Association between cigarette smoking and the vaginal microbiota: a pilot study. <i>BMC Infectious Diseases</i> , 2014 , 14, 471	4	74
201	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 Pt 1, 219-224	2.2	73
200	Penile Microbiota and Female Partner Bacterial Vaginosis in Rakai, Uganda. <i>MBio</i> , 2015 , 6, e00589	7.8	70
199	Vaginal biogenic amines: biomarkers of bacterial vaginosis or precursors to vaginal dysbiosis?. <i>Frontiers in Physiology</i> , 2015 , 6, 253	4.6	70
198	<i>Bacillus anthracis</i> in China and its relationship to worldwide lineages. <i>BMC Microbiology</i> , 2009 , 9, 71	4.5	70
197	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, 6779-94	3.5	70
196	Phylogeography and molecular epidemiology of <i>Yersinia pestis</i> in Madagascar. <i>PLoS Neglected Tropical Diseases</i> , 2011 , 5, e1319	4.8	68
195	<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	4.5	67
194	Engineering p-hydroxyphenylpyruvate dioxygenase to a p-hydroxymandelate synthase and evidence for the proposed benzene oxide intermediate in homogentisate formation. <i>Biochemistry</i> , 2004 , 43, 663-74	3.2	66
193	Functional interactions of archaea, bacteria and viruses in a hypersaline endolithic community. <i>Environmental Microbiology</i> , 2016 , 18, 2064-77	5.2	66
192	Origin and variation of tunicate secondary metabolites. <i>Journal of Natural Products</i> , 2012 , 75, 295-304	4.9	65
191	Microbiome, sex hormones, and immune responses in the reproductive tract: challenges for vaccine development against sexually transmitted infections. <i>Vaccine</i> , 2014 , 32, 1543-52	4.1	63
190	Evidence that human <i>Chlamydia pneumoniae</i> was zoonotically acquired. <i>Journal of Bacteriology</i> , 2009 , 191, 7225-33	3.5	62
189	Genomics of the <i>Bacillus cereus</i> group of organisms. <i>FEMS Microbiology Reviews</i> , 2005 , 29, 303-329	15.1	62
188	The biosynthetic gene cluster for a monocyclic beta-lactam antibiotic, nocardicin A. <i>Chemistry and Biology</i> , 2004 , 11, 927-38		59
187	Hybridization analysis of Chesapeake Bay viroplankton. <i>Applied and Environmental Microbiology</i> , 1999 , 65, 241-50	4.8	59
186	-dominated vaginal microbiota is associated with increased susceptibility to infection in Dutch women: a case-control study. <i>Sexually Transmitted Infections</i> , 2018 , 94, 117-123	2.8	58

185	Microarray-based resequencing of multiple <i>Bacillus anthracis</i> isolates. <i>Genome Biology</i> , 2005 , 6, R10	18.3	58
184	Toward a system of microbial forensics: from sample collection to interpretation of evidence. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 2209-13	4.8	58
183	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	9.5	58
182	New signaling pathways govern the host response to <i>C. albicans</i> infection in various niches. <i>Genome Research</i> , 2015 , 25, 679-89	9.7	57
181	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	7.8	57
180	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, 737425	2.4	57
179	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	1.7	56
178	The implausible "in vivo" role of hydrogen peroxide as an antimicrobial factor produced by vaginal microbiota. <i>Microbiome</i> , 2018 , 6, 29	16.6	55
177	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	3.7	55
176	Variation in tropical reef symbiont metagenomes defined by secondary metabolism. <i>PLoS ONE</i> , 2011 , 6, e17897	3.7	55
175	Ultrahigh-Throughput Multiplexing and Sequencing of >500-Base-Pair Amplicon Regions on the Illumina HiSeq 2500 Platform. <i>MSystems</i> , 2019 , 4,	7.6	54
174	Anal microbiota profiles in HIV-positive and HIV-negative MSM. <i>Aids</i> , 2014 , 28, 753-60	3.5	54
173	Impacts of poultry house environment on poultry litter bacterial community composition. <i>PLoS ONE</i> , 2011 , 6, e24785	3.7	54
172	Microbial colonisation of chasmoendolithic habitats in the hyper-arid zone of the Atacama Desert. <i>Biogeosciences</i> , 2013 , 10, 2439-2450	4.6	52
171	Cigarette smoking is associated with an altered vaginal tract metabolomic profile. <i>Scientific Reports</i> , 2018 , 8, 852	4.9	51
170	The Cervicovaginal Microbiota-Host Interaction Modulates <i>Chlamydia trachomatis</i> Infection. <i>MBio</i> , 2019 , 10,	7.8	51
169	Pre-Columbian origins for North American anthrax. <i>PLoS ONE</i> , 2009 , 4, e4813	3.7	51
168	Crypt- and Mucosa-Associated Core Microbiotas in Humans and Their Alteration in Colon Cancer Patients. <i>MBio</i> , 2019 , 10,	7.8	50

167	Advancing the microbiome research community. <i>Cell</i> , 2014 , 159, 227-30	56.2	50
166	Comparison of storage conditions for human vaginal microbiome studies. <i>PLoS ONE</i> , 2012 , 7, e36934	3.7	50
165	Translating the vaginal microbiome: gaps and challenges. <i>Genome Medicine</i> , 2016 , 8, 35	14.4	50
164	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	2.2	48
163	VALENCIA: a nearest centroid classification method for vaginal microbial communities based on composition. <i>Microbiome</i> , 2020 , 8, 166	16.6	45
162	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	7	44
161	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, 1918-34	3.5	44
160	Microbiome, demystifying the role of microbial communities in the biosphere. <i>Microbiome</i> , 2013 , 1, 1	16.6	44
159	Nested PCR Biases in Interpreting Microbial Community Structure in 16S rRNA Gene Sequence Datasets. <i>PLoS ONE</i> , 2015 , 10, e0132253	3.7	44
158	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	8.7	43
157	Integration of culture-based and molecular analysis of a complex sponge-associated bacterial community. <i>PLoS ONE</i> , 2014 , 9, e90517	3.7	41
156	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	7	39
155	Anti-HIV-1 Activity of Lactic Acid in Human Cervicovaginal Fluid. <i>MSphere</i> , 2018 , 3,	5	39
154	Group B Streptococcus and the Vaginal Microbiota. <i>Journal of Infectious Diseases</i> , 2017 , 216, 744-751	7	39
153	Whole-genome sequences of <i>Bacillus subtilis</i> and close relatives. <i>Journal of Bacteriology</i> , 2012 , 194, 2378-9	38	38
152	The vaginal metabolome and microbiota of cervical HPV-positive and HPV-negative women: a cross-sectional analysis. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2020 , 127, 182-192	3.7	38
151	Phylogenetic and Functional Substrate Specificity for Endolithic Microbial Communities in Hyper-Arid Environments. <i>Frontiers in Microbiology</i> , 2016 , 7, 301	5.7	38
150	Science and regulation. Probiotics: finding the right regulatory balance. <i>Science</i> , 2013 , 342, 314-5	33.3	37

149	Fecal Microbiota Characteristics of Patients with Colorectal Adenoma Detected by Screening: A Population-based Study. <i>EBioMedicine</i> , 2015 , 2, 597-603	8.8	37
148	Bacterial vaginosis and its association with infertility, endometritis, and pelvic inflammatory disease. <i>American Journal of Obstetrics and Gynecology</i> , 2021 , 224, 251-257	6.4	37
147	A comprehensive non-redundant gene catalog reveals extensive within-community intraspecies diversity in the human vagina. <i>Nature Communications</i> , 2020 , 11, 940	17.4	35
146	Improving regulation of microbiota transplants. <i>Science</i> , 2017 , 358, 1390-1391	33.3	35
145	Association between the vaginal microbiota, menopause status, and signs of vulvovaginal atrophy. <i>Menopause</i> , 2018 , 25, 1321-1330	2.5	35
144	Intestinal Barrier Maturation in Very Low Birthweight Infants: Relationship to Feeding and Antibiotic Exposure. <i>Journal of Pediatrics</i> , 2017 , 183, 31-36.e1	3.6	34
143	Macroscale spatial variation in chronic wound microbiota: a cross-sectional study. <i>Wound Repair and Regeneration</i> , 2011 , 19, 80-8	3.6	34
142	Twice-daily application of HIV microbicides alter the vaginal microbiota. <i>MBio</i> , 2012 , 3,	7.8	34
141	Assessment of the human faecal microbiota: II. Reproducibility and associations of 16S rRNA pyrosequences. <i>European Journal of Clinical Investigation</i> , 2012 , 42, 855-63	4.6	33
140	Phenotypic and functional characterization of Bacillus anthracis biofilms. <i>Microbiology (United Kingdom)</i> , 2007 , 153, 1693-1701	2.9	33
139	The Impact of Human Immunodeficiency Virus Infection on Gut Microbiota Diversity: An Individual-level Meta-analysis. <i>Clinical Infectious Diseases</i> , 2020 , 70, 615-627	11.6	33
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- 2 A cross-sectional pilot study of birth mode and vaginal microbiota in reproductive-age women **2020**, 15, e0228574
- 1 A cross-sectional pilot study of birth mode and vaginal microbiota in reproductive-age women **2020**, 15, e0228574