

David A Relman

List of Publications by Citations

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

229
papers

38,467
citations

77
h-index

195
g-index

266
ext. papers

45,673
ext. citations

15
avg, IF

7.42
L-index

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 229 | Diversity of the human intestinal microbial flora. <i>Science</i> , 2005 , 308, 1635-8 | 33.3 | 5381 |
| 228 | Metagenomic analysis of the human distal gut microbiome. <i>Science</i> , 2006 , 312, 1355-9 | 33.3 | 3163 |
| 227 | Development of the human infant intestinal microbiota. <i>PLoS Biology</i> , 2007 , 5, e177 | 9.7 | 1931 |
| 226 | The pervasive effects of an antibiotic on the human gut microbiota, as revealed by deep 16S rRNA sequencing. <i>PLoS Biology</i> , 2008 , 6, e280 | 9.7 | 1660 |
| 225 | Incomplete recovery and individualized responses of the human distal gut microbiota to repeated antibiotic perturbation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108 Suppl 1, 4554-61 | 11.5 | 1480 |
| 224 | An ecological and evolutionary perspective on human-microbe mutualism and disease. <i>Nature</i> , 2007 , 449, 811-8 | 50.4 | 1172 |
| 223 | A new view of the tree of life. <i>Nature Microbiology</i> , 2016 , 1, 16048 | 26.6 | 1128 |
| 222 | Identification of the uncultured bacillus of Whipple's disease. <i>New England Journal of Medicine</i> , 1992 , 327, 293-301 | 59.2 | 989 |
| 221 | The application of ecological theory toward an understanding of the human microbiome. <i>Science</i> , 2012 , 336, 1255-62 | 33.3 | 910 |
| 220 | The agent of bacillary angiomatosis. An approach to the identification of uncultured pathogens. <i>New England Journal of Medicine</i> , 1990 , 323, 1573-80 | 59.2 | 799 |
| 219 | Gut immune maturation depends on colonization with a host-specific microbiota. <i>Cell</i> , 2012 , 149, 1578-936.2 | 36.2 | 778 |
| 218 | Molecular analysis of the bacterial microbiota in the human stomach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 732-7 | 11.5 | 733 |
| 217 | Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data. <i>Microbiome</i> , 2018 , 6, 226 | 16.6 | 680 |
| 216 | Exploring microbial diversity and taxonomy using SSU rRNA hypervariable tag sequencing. <i>PLoS Genetics</i> , 2008 , 4, e1000255 | 6 | 666 |
| 215 | Individuality and variation in gene expression patterns in human blood. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 1896-901 | 11.5 | 640 |
| 214 | Temporal and spatial variation of the human microbiota during pregnancy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 11060-5 | 11.5 | 581 |
| 213 | Microbial prevalence, diversity and abundance in amniotic fluid during preterm labor: a molecular and culture-based investigation. <i>PLoS ONE</i> , 2008 , 3, e3056 | 3.7 | 543 |

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| 212 | Dissecting biological "dark matter" with single-cell genetic analysis of rare and uncultivated TM7 microbes from the human mouth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 11889-94 | 11.5 | 464 |
| 211 | 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 |
| 210 | Bacterial diversity in the oral cavity of 10 healthy individuals. <i>ISME Journal</i> , 2010 , 4, 962-74 | 11.9 | 428 |
| 209 | Assembly of the human intestinal microbiota. <i>Trends in Ecology and Evolution</i> , 2006 , 21, 517-23 | 10.9 | 400 |
| 208 | Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018 , 3, 8-16 | 26.6 | 387 |
| 207 | Antibiotics and the gut microbiota. <i>Journal of Clinical Investigation</i> , 2014 , 124, 4212-8 | 15.9 | 375 |
| 206 | Recognition of a bacterial adhesion by an integrin: macrophage CR3 (alpha M beta 2, CD11b/CD18) binds filamentous hemagglutinin of Bordetella pertussis. <i>Cell</i> , 1990 , 61, 1375-82 | 56.2 | 367 |
| 205 | Stereotyped and specific gene expression programs in human innate immune responses to bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 972-7 ^{11.5} | 11.5 | 337 |
| 204 | Time series community genomics analysis reveals rapid shifts in bacterial species, strains, and phage during infant gut colonization. <i>Genome Research</i> , 2013 , 23, 111-20 | 9.7 | 324 |
| 203 | Role of interleukin 6 in myocardial dysfunction of meningococcal septic shock. <i>Lancet, The</i> , 2004 , 363, 203-9 | 40 | 302 |
| 202 | Methanogenic Archaea and human periodontal disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 6176-81 | 11.5 | 293 |
| 201 | Type I interferon suppresses type II interferon-triggered human anti-mycobacterial responses. <i>Science</i> , 2013 , 339, 1448-53 | 33.3 | 283 |
| 200 | Microbiology in the post-genomic era. <i>Nature Reviews Microbiology</i> , 2008 , 6, 419-30 | 22.2 | 281 |
| 199 | Distinct distal gut microbiome diversity and composition in healthy children from Bangladesh and the United States. <i>PLoS ONE</i> , 2013 , 8, e53838 | 3.7 | 224 |
| 198 | Nasal microenvironments and interspecific interactions influence nasal microbiota complexity and <i>S. aureus</i> carriage. <i>Cell Host and Microbe</i> , 2013 , 14, 631-40 | 23.4 | 221 |
| 197 | <i>Bordetella pertussis</i> , the causative agent of whooping cough, evolved from a distinct, human-associated lineage of <i>B. bronchiseptica</i> . <i>PLoS Pathogens</i> , 2005 , 1, e45 | 7.6 | 214 |
| 196 | Evidence of a robust resident bacteriophage population revealed through analysis of the human salivary virome. <i>ISME Journal</i> , 2012 , 6, 915-26 | 11.9 | 211 |
| 195 | Prevalence and diversity of microbes in the amniotic fluid, the fetal inflammatory response, and pregnancy outcome in women with preterm pre-labor rupture of membranes. <i>American Journal of Reproductive Immunology</i> , 2010 , 64, 38-57 | 3.8 | 209 |

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|-----|--|------|-----|
| 194 | The human microbiome: ecosystem resilience and health. <i>Nutrition Reviews</i> , 2012 , 70 Suppl 1, S2-9 | 6.4 | 208 |
| 193 | Host transmission of <i>Salmonella enterica</i> serovar Typhimurium is controlled by virulence factors and indigenous intestinal microbiota. <i>Infection and Immunity</i> , 2008 , 76, 403-16 | 3.7 | 206 |
| 192 | Sequencing and analysis of the genome of the Whipple's disease bacterium <i>Tropheryma whippelii</i> . <i>Lancet, The</i> , 2003 , 361, 637-44 | 40 | 204 |
| 191 | Strain-resolved community genomic analysis of gut microbial colonization in a premature infant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 1128-33 | 11.5 | 201 |
| 190 | Linking microbial phylogeny to metabolic activity at the single-cell level by using enhanced element labeling-catalyzed reporter deposition fluorescence in situ hybridization (EL-FISH) and NanoSIMS. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 3143-50 | 4.8 | 200 |
| 189 | Replication and refinement of a vaginal microbial signature of preterm birth in two racially distinct cohorts of US women. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 9966-9971 | 11.5 | 182 |
| 188 | Genetically dictated change in host mucus carbohydrate landscape exerts a diet-dependent effect on the gut microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 17059-64 | 11.5 | 180 |
| 187 | Application of polymerase chain reaction to the diagnosis of infectious diseases. <i>Clinical Infectious Diseases</i> , 1999 , 29, 475-86; quiz 487-8 | 11.6 | 178 |
| 186 | A microbial perspective of human developmental biology. <i>Nature</i> , 2016 , 535, 48-55 | 50.4 | 172 |
| 185 | Microbiota-targeted therapies: an ecological perspective. <i>Science Translational Medicine</i> , 2012 , 4, 137rv517.5 | 17.1 | |
| 184 | Prevalence of bacteria of division TM7 in human subgingival plaque and their association with disease. <i>Applied and Environmental Microbiology</i> , 2003 , 69, 1687-94 | 4.8 | 171 |
| 183 | Does blood of healthy subjects contain bacterial ribosomal DNA?. <i>Journal of Clinical Microbiology</i> , 2001 , 39, 1956-9 | 9.7 | 170 |
| 182 | Acquired predisposition to mycobacterial disease due to autoantibodies to IFN-gamma. <i>Journal of Clinical Investigation</i> , 2005 , 115, 2480-8 | 15.9 | 159 |
| 181 | Improved amplification of microbial DNA from blood cultures by removal of the PCR inhibitor sodium polyanethanesulfonate. <i>Journal of Clinical Microbiology</i> , 1998 , 36, 2810-6 | 9.7 | 158 |
| 180 | Clades of huge phages from across Earth's ecosystems. <i>Nature</i> , 2020 , 578, 425-431 | 50.4 | 154 |
| 179 | The role of microbes in Crohn's disease. <i>Clinical Infectious Diseases</i> , 2007 , 44, 256-62 | 11.6 | 154 |
| 178 | Brief report: uveitis caused by <i>Tropheryma whippelii</i> (Whipple's bacillus). <i>New England Journal of Medicine</i> , 1995 , 332, 363-6 | 59.2 | 154 |
| 177 | Role of priority effects in the early-life assembly of the gut microbiota. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018 , 15, 197-205 | 24.2 | 153 |

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|-----|---|------|-----|
| 176 | Archaea and their potential role in human disease. <i>Infection and Immunity</i> , 2003 , 71, 591-6 | 3.7 | 146 |
| 175 | Rapid quantitative profiling of complex microbial populations. <i>Nucleic Acids Research</i> , 2006 , 34, e5 | 20.1 | 145 |
| 174 | Microbial genomics and infectious diseases. <i>New England Journal of Medicine</i> , 2011 , 365, 347-57 | 59.2 | 135 |
| 173 | Patterns of host genome-wide gene transcript abundance in the peripheral blood of patients with acute dengue hemorrhagic fever. <i>Journal of Infectious Diseases</i> , 2007 , 195, 1097-107 | 7 | 135 |
| 172 | Exploring the potentials of variola virus infection of cynomolgus macaques as a model for human smallpox. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 15196-200 | 11.5 | 134 |
| 171 | Marine mammals harbor unique microbiotas shaped by and yet distinct from the sea. <i>Nature Communications</i> , 2016 , 7, 10516 | 17.4 | 129 |
| 170 | Filamentous hemagglutinin of <i>Bordetella bronchiseptica</i> is required for efficient establishment of tracheal colonization. <i>Infection and Immunity</i> , 1998 , 66, 5921-9 | 3.7 | 123 |
| 169 | Dissecting interferon-induced transcriptional programs in human peripheral blood cells. <i>PLoS ONE</i> , 2010 , 5, e9753 | 3.7 | 123 |
| 168 | Species- and strain-specific control of a complex, flexible regulon by <i>Bordetella BvgAS</i> . <i>Journal of Bacteriology</i> , 2006 , 188, 1775-85 | 3.5 | 119 |
| 167 | How the host 'sees' pathogens: global gene expression responses to infection. <i>Current Opinion in Immunology</i> , 2000 , 12, 215-8 | 7.8 | 107 |
| 166 | Microbiome assembly across multiple body sites in low-birthweight infants. <i>MBio</i> , 2013 , 4, e00782-13 | 7.8 | 103 |
| 165 | Metagenomic detection of phage-encoded platelet-binding factors in the human oral cavity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108 Suppl 1, 4547-53 | 11.5 | 103 |
| 164 | Genomewide analysis of the host response to malaria in Kenyan children. <i>Journal of Infectious Diseases</i> , 2005 , 191, 1599-611 | 7 | 100 |
| 163 | The Landscape Ecology and Microbiota of the Human Nose, Mouth, and Throat. <i>Cell Host and Microbe</i> , 2017 , 21, 421-432 | 23.4 | 98 |
| 162 | Transforming growth factor-beta signaling pathway in patients with Kawasaki disease. <i>Circulation: Cardiovascular Genetics</i> , 2011 , 4, 16-25 | | 96 |
| 161 | The host response to smallpox: analysis of the gene expression program in peripheral blood cells in a nonhuman primate model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 15190-5 | 11.5 | 93 |
| 160 | Analysis of streptococcal CRISPRs from human saliva reveals substantial sequence diversity within and between subjects over time. <i>Genome Research</i> , 2011 , 21, 126-36 | 9.7 | 90 |
| 159 | Single-cell sequencing provides clues about the host interactions of segmented filamentous bacteria (SFB). <i>Genome Research</i> , 2012 , 22, 1107-19 | 9.7 | 90 |

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| 158 | New technologies, human-microbe interactions, and the search for previously unrecognized pathogens. <i>Journal of Infectious Diseases</i> , 2002 , 186 Suppl 2, S254-8 | 7 | 90 |
| 157 | Phylogenetic relationships among the agent of bacillary angiomatosis, <i>Bartonella bacilliformis</i> , and other alpha-proteobacteria. <i>Molecular Microbiology</i> , 1992 , 6, 1801-7 | 4.1 | 88 |
| 156 | Probiotics, prebiotics, and the host microbiome: the science of translation. <i>Annals of the New York Academy of Sciences</i> , 2013 , 1306, 1-17 | 6.5 | 80 |
| 155 | Integration of Next-Generation Sequencing, Viral Sequencing, and Host-Response Profiling for the Diagnosis of Acute Infections. <i>Open Forum Infectious Diseases</i> , 2017 , 4, S71-S71 | 1 | 78 |
| 154 | Pox. <i>Journal of Clinical Investigation</i> , 2011 , 121, 4571-4571 | 15.9 | 78 |
| 153 | Gene-expression patterns reveal underlying biological processes in Kawasaki disease. <i>Genome Biology</i> , 2007 , 8, R261 | 18.3 | 76 |
| 152 | Broad-range bacterial detection and the analysis of unexplained death and critical illness. <i>Emerging Infectious Diseases</i> , 2002 , 8, 188-94 | 10.2 | 75 |
| 151 | Genomics and microbiology. Microbial forensics--"cross-examining pathogens". <i>Science</i> , 2002 , 296, 1976-9 | 35.3 | 73 |
| 150 | Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. <i>Genome Research</i> , 2018 , 28, 1467-1480 | 9.7 | 73 |
| 149 | The temporal program of peripheral blood gene expression in the response of nonhuman primates to Ebola hemorrhagic fever. <i>Genome Biology</i> , 2007 , 8, R174 | 18.3 | 72 |
| 148 | <i>Tropheryma whippelii</i> DNA is rare in the intestinal mucosa of patients without other evidence of Whipple disease. <i>Annals of Internal Medicine</i> , 2001 , 134, 115-9 | 8 | 72 |
| 147 | A spatial gradient of bacterial diversity in the human oral cavity shaped by salivary flow. <i>Nature Communications</i> , 2018 , 9, 681 | 17.4 | 64 |
| 146 | Significant gene order and expression differences in <i>Bordetella pertussis</i> despite limited gene content variation. <i>Journal of Bacteriology</i> , 2006 , 188, 2375-82 | 3.5 | 63 |
| 145 | 2020 visions. <i>Nature</i> , 2010 , 463, 26-32 | 50.4 | 61 |
| 144 | Detection and identification of previously unrecognized microbial pathogens. <i>Emerging Infectious Diseases</i> , 1998 , 4, 382-9 | 10.2 | 60 |
| 143 | Microbial invasion of the amniotic cavity in preeclampsia as assessed by cultivation and sequence-based methods. <i>Journal of Perinatal Medicine</i> , 2010 , 38, 503-13 | 2.7 | 59 |
| 142 | Microbial invasion of the amniotic cavity in pregnancies with small-for-gestational-age fetuses. <i>Journal of Perinatal Medicine</i> , 2010 , 38, 495-502 | 2.7 | 58 |
| 141 | Invasion of human respiratory epithelial cells by <i>Bordetella pertussis</i> : possible role for a filamentous hemagglutinin Arg-Gly-Asp sequence and alpha5beta1 integrin. <i>Microbial Pathogenesis</i> , 2001 , 30, 279-88 | 3.8 | 58 |

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| 140 | Comparing functional genomic datasets: lessons from DNA microarray analyses of host-pathogen interactions. <i>Current Opinion in Microbiology</i> , 2001 , 4, 95-101 | 7.9 | 56 |
| 139 | Phylogenetic identification of uncultured pathogens using ribosomal RNA sequences. <i>Methods in Enzymology</i> , 1994 , 235, 205-22 | 1.7 | 56 |
| 138 | Smallpox research activities: U.S. interagency collaboration, 2001. <i>Emerging Infectious Diseases</i> , 2002 , 8, 743-5 | 10.2 | 55 |
| 137 | Multimomics modeling of the immunome, transcriptome, microbiome, proteome and metabolome adaptations during human pregnancy. <i>Bioinformatics</i> , 2019 , 35, 95-103 | 7.2 | 54 |
| 136 | Sequence variability in the first internal transcribed spacer region within and among <i>Cyclospora</i> species is consistent with polyparasitism. <i>International Journal for Parasitology</i> , 2001 , 31, 1475-87 | 4.3 | 54 |
| 135 | Paraffin removal from tissue sections for digestion and PCR analysis. <i>BioTechniques</i> , 1999 , 26, 198-200 | 2.5 | 54 |
| 134 | Proinflammatory and proapoptotic activities associated with <i>Bordetella pertussis</i> filamentous hemagglutinin. <i>Infection and Immunity</i> , 2001 , 69, 2650-8 | 3.7 | 53 |
| 133 | Molecular identification of cyanobacteria associated with stromatolites from distinct geographical locations. <i>Astrobiology</i> , 2002 , 2, 271-80 | 3.7 | 52 |
| 132 | Comparisons of clustered regularly interspaced short palindromic repeats and viromes in human saliva reveal bacterial adaptations to salivary viruses. <i>Environmental Microbiology</i> , 2012 , 14, 2564-76 | 5.2 | 51 |
| 131 | Myocardial depressant effects of interleukin 6 in meningococcal sepsis are regulated by p38 mitogen-activated protein kinase. <i>Critical Care Medicine</i> , 2011 , 39, 1692-711 | 1.4 | 51 |
| 130 | Superorganisms and Holobionts. <i>Microbe Magazine</i> , 2013 , 8, 152-153 | | 51 |
| 129 | Public health and biosecurity. Adaptations of avian flu virus are a cause for concern. <i>Science</i> , 2012 , 335, 660-1 | 33.3 | 50 |
| 128 | Variation in Taxonomic Composition of the Fecal Microbiota in an Inbred Mouse Strain across Individuals and Time. <i>PLoS ONE</i> , 2015 , 10, e0142825 | 3.7 | 49 |
| 127 | Whipple's disease and <i>Tropheryma whippelii</i> : secrets slowly revealed. <i>Clinical Infectious Diseases</i> , 2001 , 32, 457-63 | 11.6 | 49 |
| 126 | Transcriptional profiling of the iron starvation response in <i>Bordetella pertussis</i> provides new insights into siderophore utilization and virulence gene expression. <i>Journal of Bacteriology</i> , 2011 , 193, 4798-812 | 3.5 | 48 |
| 125 | Single-cell enumeration of an uncultivated TM7 subgroup in the human subgingival crevice. <i>Applied and Environmental Microbiology</i> , 2003 , 69, 6294-8 | 4.8 | 48 |
| 124 | Tracking microbial evolution in the human gut using Hi-C reveals extensive horizontal gene transfer, persistence and adaptation. <i>Nature Microbiology</i> , 2020 , 5, 343-353 | 26.6 | 48 |
| 123 | Search for highly conserved viral and bacterial nucleic acid sequences corresponding to an etiologic agent of Kawasaki disease. <i>Pediatric Research</i> , 1994 , 36, 567-71 | 3.2 | 46 |

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|-----|--|------|----|
| 122 | The Human Microbiome and the Future Practice of Medicine. <i>JAMA - Journal of the American Medical Association</i> , 2015 , 314, 1127-8 | 27.4 | 45 |
| 121 | Multidomain analyses of a longitudinal human microbiome intestinal cleanout perturbation experiment. <i>PLoS Computational Biology</i> , 2017 , 13, e1005706 | 5 | 45 |
| 120 | Surveillance for unexplained deaths and critical illnesses due to possibly infectious causes, United States, 1995-1998. <i>Emerging Infectious Diseases</i> , 2002 , 8, 145-53 | 10.2 | 45 |
| 119 | Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. <i>Current Biology</i> , 2017 , 27, 3752-3762.e6 | 6.3 | 44 |
| 118 | Long-term taxonomic and functional divergence from donor bacterial strains following fecal microbiota transplantation in immunocompromised patients. <i>PLoS ONE</i> , 2017 , 12, e0182585 | 3.7 | 44 |
| 117 | Temporal dynamics of the transcriptional response to dengue virus infection in Nicaraguan children. <i>PLoS Neglected Tropical Diseases</i> , 2012 , 6, e1966 | 4.8 | 42 |
| 116 | 'Til death do us part': coming to terms with symbiotic relationships. Forward. <i>Nature Reviews Microbiology</i> , 2008 , 6, 721-4 | 22.2 | 42 |
| 115 | Growth phase- and nutrient limitation-associated transcript abundance regulation in <i>Bordetella pertussis</i> . <i>Infection and Immunity</i> , 2006 , 74, 5537-48 | 3.7 | 42 |
| 114 | Microbiome as a tool and a target in the effort to address antimicrobial resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 12902-12910 | 11.5 | 42 |
| 113 | Comparative analysis of viral gene expression programs during poxvirus infection: a transcriptional map of the vaccinia and monkeypox genomes. <i>PLoS ONE</i> , 2008 , 3, e2628 | 3.7 | 39 |
| 112 | Investigate the origins of COVID-19. <i>Science</i> , 2021 , 372, 694 | 33.3 | 39 |
| 111 | Gene transcript abundance profiles distinguish Kawasaki disease from adenovirus infection. <i>Journal of Infectious Diseases</i> , 2009 , 200, 657-66 | 7 | 38 |
| 110 | Natural-host animal models indicate functional interchangeability between the filamentous haemagglutinins of <i>Bordetella pertussis</i> and <i>Bordetella bronchiseptica</i> and reveal a role for the mature C-terminal domain, but not the RGD motif, during infection. <i>Molecular Microbiology</i> , 2009 , 71, 1574-90 | 4.1 | 38 |
| 109 | Molecular characterization of <i>Bordetella bronchiseptica</i> filamentous haemagglutinin and its secretion machinery. <i>Microbiology (United Kingdom)</i> , 2000 , 146 (Pt 5), 1211-1221 | 2.9 | 38 |
| 108 | Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data | | 37 |
| 107 | Culture-negative endocarditis caused by <i>Bartonella henselae</i> . <i>Journal of Pediatrics</i> , 1998 , 132, 1051-4 | 3.6 | 36 |
| 106 | Stunned silence: gene expression programs in human cells infected with monkeypox or vaccinia virus. <i>PLoS ONE</i> , 2011 , 6, e15615 | 3.7 | 36 |
| 105 | Cultivation of <i>Tropheryma whipplei</i> from cerebrospinal fluid. <i>Journal of Infectious Diseases</i> , 2003 , 188, 801-8 | 7 | 35 |

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|-----|--|------|----|
| 104 | Gain-of-function experiments: time for a real debate. <i>Nature Reviews Microbiology</i> , 2015 , 13, 58-64 | 22.2 | 33 |
| 103 | Characterization of a highly conserved island in the otherwise divergent <i>Bordetella holmesii</i> and <i>Bordetella pertussis</i> genomes. <i>Journal of Bacteriology</i> , 2006 , 188, 8385-94 | 3.5 | 33 |
| 102 | Organization, structure, and variability of the rRNA operon of the Whipple's disease bacterium (<i>Tropheryma whippelii</i>). <i>Journal of Bacteriology</i> , 2000 , 182, 3292-7 | 3.5 | 33 |
| 101 | Microbial biogeography and ecology of the mouth and implications for periodontal diseases. <i>Periodontology 2000</i> , 2020 , 82, 26-41 | 12.9 | 32 |
| 100 | Has trench fever returned?. <i>New England Journal of Medicine</i> , 1995 , 332, 463-4 | 59.2 | 30 |
| 99 | <i>Bordetella pertussis</i> infection of primary human monocytes alters HLA-DR expression. <i>Infection and Immunity</i> , 2004 , 72, 1450-62 | 3.7 | 27 |
| 98 | Lessons learned from the prenatal microbiome controversy. <i>Microbiome</i> , 2021 , 9, 8 | 16.6 | 25 |
| 97 | Multiomeric immune clockworks of pregnancy. <i>Seminars in Immunopathology</i> , 2020 , 42, 397-412 | 12 | 24 |
| 96 | Phase variation and microevolution at homopolymeric tracts in <i>Bordetella pertussis</i> . <i>BMC Genomics</i> , 2007 , 8, 122 | 4.5 | 24 |
| 95 | Bioterrorism--preparing to fight the next war. <i>New England Journal of Medicine</i> , 2006 , 354, 113-5 | 59.2 | 24 |
| 94 | Policy: Adaptations of avian flu virus are a cause for concern. <i>Nature</i> , 2012 , 482, 153-4 | 50.4 | 23 |
| 93 | Limited role for PCR-based diagnosis of Whipple's disease from peripheral blood mononuclear cells. <i>Lancet, The</i> , 1996 , 348, 66-7 | 40 | 23 |
| 92 | Identification of <i>Cardiobacterium hominis</i> by broad-range bacterial polymerase chain reaction analysis in a case of culture-negative endocarditis. <i>Archives of Internal Medicine</i> , 2002 , 162, 477-9 | | 22 |
| 91 | Comparisons of distance methods for combining covariates and abundances in microbiome studies. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012 , 213-24 | 1.3 | 22 |
| 90 | SmashCell: a software framework for the analysis of single-cell amplified genome sequences. <i>Bioinformatics</i> , 2010 , 26, 2979-80 | 7.2 | 21 |
| 89 | Modulation of the NF-kappaB pathway by <i>Bordetella pertussis</i> filamentous hemagglutinin. <i>PLoS ONE</i> , 2008 , 3, e3825 | 3.7 | 21 |
| 88 | Genetic technologies. Synthetic "life," ethics, national security, and public discourse. <i>Science</i> , 2010 , 329, 38-9 | 33.3 | 20 |
| 87 | Genomic features of <i>Bordetella parapertussis</i> clades with distinct host species specificity. <i>Genome Biology</i> , 2006 , 7, R81 | 18.3 | 20 |

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|----|--|------|----|
| 86 | Opinion: To stop the next pandemic, we need to unravel the origins of COVID-19. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 29246-29248 | 11.5 | 19 |
| 85 | Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. <i>Microbiome</i> , 2014 , 2, | 16.6 | 18 |
| 84 | Early days: genomics and human responses to infection. <i>Current Opinion in Microbiology</i> , 2006 , 9, 312-9 | 7.9 | 18 |
| 83 | Identification of Lactobacillus strains with probiotic features from the bottlenose dolphin (<i>Tursiops truncatus</i>). <i>Journal of Applied Microbiology</i> , 2013 , 115, 1037-51 | 4.7 | 17 |
| 82 | Modulation of the host interferon response and ISGylation pathway by B. pertussis filamentous hemagglutinin. <i>PLoS ONE</i> , 2011 , 6, e27535 | 3.7 | 17 |
| 81 | Molecular approaches for identification of infectious agents in Wegener's granulomatosis and other vasculitides. <i>Current Opinion in Rheumatology</i> , 1999 , 11, 11-6 | 5.3 | 17 |
| 80 | Role of phosphatidylinositol 3-kinase in the binding of Bordetella pertussis to human monocytes. <i>Cellular Microbiology</i> , 2002 , 4, 825-33 | 3.9 | 16 |
| 79 | Analysis of conserved non-rRNA genes of <i>Tropheryma whippelii</i> . <i>Systematic and Applied Microbiology</i> , 2003 , 26, 3-12 | 4.2 | 16 |
| 78 | Cathelicidin Insufficiency in Patients with Fatal Leptospirosis. <i>PLoS Pathogens</i> , 2016 , 12, e1005943 | 7.6 | 16 |
| 77 | SCIENCE GOVERNANCE. A more systematic approach to biological risk. <i>Science</i> , 2015 , 350, 1471-3 | 33.3 | 15 |
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