

# David A Relman

## List of Publications by Year in descending order

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236  
papers

50,456  
citations

5558

82  
h-index

1627

215  
g-index

266  
all docs

266  
docs citations

266  
times ranked

49688  
citing authors

#	ARTICLE	IF	CITATIONS
1	Diversity of the Human Intestinal Microbial Flora. <i>Science</i> , 2005, 308, 1635-1638.	6.0	6,617
2	Metagenomic Analysis of the Human Distal Gut Microbiome. <i>Science</i> , 2006, 312, 1355-1359.	6.0	3,964
3	Development of the Human Infant Intestinal Microbiota. <i>PLoS Biology</i> , 2007, 5, e177.	2.6	2,390
4	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.	2.6	2,013
5	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, 4554-4561.	3.3	1,912
6	A new view of the tree of life. <i>Nature Microbiology</i> , 2016, 1, 16048.	5.9	1,823
7	Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data. <i>Microbiome</i> , 2018, 6, 226.	4.9	1,729
8	An ecological and evolutionary perspective on human-microbe mutualism and disease. <i>Nature</i> , 2007, 449, 811-818.	13.7	1,430
9	The Application of Ecological Theory Toward an Understanding of the Human Microbiome. <i>Science</i> , 2012, 336, 1255-1262.	6.0	1,252
10	Identification of the Uncultured <i>Bacillus</i> of Whipple's Disease. <i>New England Journal of Medicine</i> , 1992, 327, 293-301.	13.9	1,196
11	Gut Immune Maturation Depends on Colonization with a Host-Specific Microbiota. <i>Cell</i> , 2012, 149, 1578-1593.	13.5	1,050
12	The Agent of Bacillary Angiomatosis. <i>New England Journal of Medicine</i> , 1990, 323, 1573-1580.	13.9	985
13	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, 732-737.	3.3	935
14	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, 11060-11065.	3.3	876
15	Exploring Microbial Diversity and Taxonomy Using SSU rRNA Hypervariable Tag Sequencing. <i>PLoS Genetics</i> , 2008, 4, e1000255.	1.5	779
16	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, 1896-1901.	3.3	723
17	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
18	Microbial Prevalence, Diversity and Abundance in Amniotic Fluid During Preterm Labor: A Molecular and Culture-Based Investigation. <i>PLoS ONE</i> , 2008, 3, e3056.	1.1	653

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19	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlxS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608
20	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, 11889-11894.	3.3	552
21	Bacterial diversity in the oral cavity of 10 healthy individuals. <i>ISME Journal</i> , 2010, 4, 962-974.	4.4	541
22	Antibiotics and the gut microbiota. <i>Journal of Clinical Investigation</i> , 2014, 124, 4212-4218.	3.9	529
23	Assembly of the human intestinal microbiota. <i>Trends in Ecology and Evolution</i> , 2006, 21, 517-523.	4.2	462
24	Recognition of a bacterial adhesin by an integrin: Macrophage CR3 ( $\alpha$ M $\beta$ 2, CD11bCD18) binds filamentous hemagglutinin of <i>Bordetella pertussis</i> . <i>Cell</i> , 1990, 61, 1375-1382.	13.5	438
25	Time series community genomics analysis reveals rapid shifts in bacterial species, strains, and phage during infant gut colonization. <i>Genome Research</i> , 2013, 23, 111-120.	2.4	409
26	Role of interleukin 6 in myocardial dysfunction of meningococcal septic shock. <i>Lancet</i> , The, 2004, 363, 203-209.	6.3	378
27	Methanogenic Archaea and human periodontal disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 6176-6181.	3.3	374
28	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, 972-977.	3.3	371
29	Type I Interferon Suppresses Type II Interferon-Triggered Human Anti-Mycobacterial Responses. <i>Science</i> , 2013, 339, 1448-1453.	6.0	359
30	Clades of huge phages from across Earth's ecosystems. <i>Nature</i> , 2020, 578, 425-431.	13.7	331
31	Microbiology in the post-genomic era. <i>Nature Reviews Microbiology</i> , 2008, 6, 419-430.	13.6	324
32	The human microbiome: ecosystem resilience and health. <i>Nutrition Reviews</i> , 2012, 70, S2-S9.	2.6	313
33	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.	3.3	297
34	Prevalence and Diversity of Microbes in the Amniotic Fluid, the Fetal Inflammatory Response, and Pregnancy Outcome in Women with Preterm Labor Rupture of Membranes. <i>American Journal of Reproductive Immunology</i> , 2010, 64, 38-57.	1.2	296
35	Evidence of a robust resident bacteriophage population revealed through analysis of the human salivary virome. <i>ISME Journal</i> , 2012, 6, 915-926.	4.4	295
36	Nasal Microenvironments and Interspecific Interactions Influence Nasal Microbiota Complexity and <i>S. Aureus</i> Carriage. <i>Cell Host and Microbe</i> , 2013, 14, 631-640.	5.1	294

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37	The Tabula Sapiens: A multiple-organ, single-cell transcriptomic atlas of humans. <i>Science</i> , 2022, 376, eabl4896.	6.0	289
38	Distinct Distal Gut Microbiome Diversity and Composition in Healthy Children from Bangladesh and the United States. <i>PLoS ONE</i> , 2013, 8, e53838.	1.1	278
39	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, 403-416.	1.0	263
40	Role of priority effects in the early-life assembly of the gut microbiota. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018, 15, 197-205.	8.2	258
41	<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.	2.1	252
42	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, 17059-17064.	3.3	237
43	Sequencing and analysis of the genome of the Whipple's disease bacterium <i>Tropheryma whippelii</i> . <i>Lancet</i> , The, 2003, 361, 637-644.	6.3	232
44	Does Blood of Healthy Subjects Contain Bacterial Ribosomal DNA?. <i>Journal of Clinical Microbiology</i> , 2001, 39, 1956-1959.	1.8	231
45	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, 1128-1133.	3.3	224
46	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, 3143-3150.	1.4	223
47	Microbiota-Targeted Therapies: An Ecological Perspective. <i>Science Translational Medicine</i> , 2012, 4, 137rv5.	5.8	217
48	A microbial perspective of human developmental biology. <i>Nature</i> , 2016, 535, 48-55.	13.7	215
49	Acquired predisposition to mycobacterial disease due to autoantibodies to IFN- $\beta$ . <i>Journal of Clinical Investigation</i> , 2005, 115, 2480-2488.	3.9	206
50	Application of Polymerase Chain Reaction to the Diagnosis of Infectious Diseases. <i>Clinical Infectious Diseases</i> , 1999, 29, 475-486.	2.9	201
51	Prevalence of Bacteria of Division TM7 in Human Subgingival Plaque and Their Association with Disease. <i>Applied and Environmental Microbiology</i> , 2003, 69, 1687-1694.	1.4	200
52	Uveitis Caused by <i>Tropheryma whippelii</i> (Whipple's Bacillus). <i>New England Journal of Medicine</i> , 1995, 332, 363-366.	13.9	197
53	Marine mammals harbor unique microbiotas shaped by and yet distinct from the sea. <i>Nature Communications</i> , 2016, 7, 10516.	5.8	196
54	Improved Amplification of Microbial DNA from Blood Cultures by Removal of the PCR Inhibitor Sodium Polyanetholesulfonate. <i>Journal of Clinical Microbiology</i> , 1998, 36, 2810-2816.	1.8	196

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55	The Role of Microbes in Crohn's Disease. <i>Clinical Infectious Diseases</i> , 2007, 44, 256-262.	2.9	190
56	Archaea and Their Potential Role in Human Disease. <i>Infection and Immunity</i> , 2003, 71, 591-596.	1.0	169
57	From The Cover: Exploring the potential 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, 15196-15200.	3.3	163
58	Multimomics modeling of the immunome, transcriptome, microbiome, proteome and metabolome adaptations during human pregnancy. <i>Bioinformatics</i> , 2019, 35, 95-103.	1.8	162
59	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, 1097-1107.	1.9	159
60	Rapid quantitative profiling of complex microbial populations. <i>Nucleic Acids Research</i> , 2006, 34, e5-e5.	6.5	158
61	Microbial Genomics and Infectious Diseases. <i>New England Journal of Medicine</i> , 2011, 365, 347-357.	13.9	156
62	The Landscape Ecology and Microbiota of the Human Nose, Mouth, and Throat. <i>Cell Host and Microbe</i> , 2017, 21, 421-432.	5.1	151
63	Microbiome Assembly across Multiple Body Sites in Low-Birthweight Infants. <i>MBio</i> , 2013, 4, e00782-13.	1.8	147
64	Filamentous Hemagglutinin of <i>Bordetella bronchiseptica</i> Is Required for Efficient Establishment of Tracheal Colonization. <i>Infection and Immunity</i> , 1998, 66, 5921-5929.	1.0	141
65	Dissecting Interferon-Induced Transcriptional Programs in Human Peripheral Blood Cells. <i>PLoS ONE</i> , 2010, 5, e9753.	1.1	134
66	Species- and Strain-Specific Control of a Complex, Flexible Regulon by <i>Bordetella BvgAS</i> . <i>Journal of Bacteriology</i> , 2006, 188, 1775-1785.	1.0	129
67	Transforming Growth Factor- $\beta^2$ Signaling Pathway in Patients With Kawasaki Disease. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 16-25.	5.1	127
68	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, 4547-4553.	3.3	123
69	How the host "sees" pathogens: global gene expression responses to infection. <i>Current Opinion in Immunology</i> , 2000, 12, 215-218.	2.4	118
70	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. <i>Genome Research</i> , 2018, 28, 1467-1480.	2.4	117
71	Phylogenetic relationships among the agent of bacillary angiomatosis, <i>Bartonella bacilliformis</i> , and other alpha-proteobacteria. <i>Molecular Microbiology</i> , 1992, 6, 1801-1807.	1.2	111
72	From The Cover: 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, 15190-15195.	3.3	111

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73	Genomewide Analysis of the Host Response to Malaria in Kenyan Children. <i>Journal of Infectious Diseases</i> , 2005, 191, 1599-1611.	1.9	111
74	Single-cell sequencing provides clues about the host interactions of segmented filamentous bacteria (SFB). <i>Genome Research</i> , 2012, 22, 1107-1119.	2.4	108
75	New Technologies, Human-Microbe Interactions, and the Search for Previously Unrecognized Pathogens. <i>Journal of Infectious Diseases</i> , 2002, 186, S254-S258.	1.9	106
76	Analysis of streptococcal CRISPRs from human saliva reveals substantial sequence diversity within and between subjects over time. <i>Genome Research</i> , 2011, 21, 126-136.	2.4	104
77	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.	5.9	101
78	Probiotics, prebiotics, and the host microbiome: the science of translation. <i>Annals of the New York Academy of Sciences</i> , 2013, 1306, 1-17.	1.8	98
79	Investigate the origins of COVID-19. <i>Science</i> , 2021, 372, 694-694.	6.0	92
80	Gene-expression patterns reveal underlying biological processes in Kawasaki disease. <i>Genome Biology</i> , 2007, 8, R261.	13.9	89
81	<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.	2.0	88
82	Adaptations of Avian Flu Virus Are a Cause for Concern. <i>Science</i> , 2012, 335, 660-661.	6.0	88
83	A spatial gradient of bacterial diversity in the human oral cavity shaped by salivary flow. <i>Nature Communications</i> , 2018, 9, 681.	5.8	87
84	GENOMICS AND MICROBIOLOGY: Enhanced: Microbial Forensics--"Cross-Examining Pathogens". <i>Science</i> , 2002, 296, 1976-1979.	6.0	85
85	Broad-Range Bacterial Detection and the Analysis of Unexplained Death and Critical Illness. <i>Emerging Infectious Diseases</i> , 2002, 8, 188-194.	2.0	85
86	Variation in Taxonomic Composition of the Fecal Microbiota in an Inbred Mouse Strain across Individuals and Time. <i>PLoS ONE</i> , 2015, 10, e0142825.	1.1	84
87	Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. <i>Current Biology</i> , 2017, 27, 3752-3762.e6.	1.8	82
88	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.	13.9	80
89	Detection and Identification of Previously Unrecognized Microbial Pathogens. <i>Emerging Infectious Diseases</i> , 1998, 4, 382-389.	2.0	77
90	2020 visions. <i>Nature</i> , 2010, 463, 26-32.	13.7	75

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91	Myocardial depressant effects of interleukin 6 in meningococcal sepsis are regulated by p38 mitogen-activated protein kinase*. <i>Critical Care Medicine</i> , 2011, 39, 1692-1711.	0.4	75
92	Learning about who we are. <i>Nature</i> , 2012, 486, 194-195.	13.7	75
93	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.	0.6	74
94	Stunned Silence: Gene Expression Programs in Human Cells Infected with Monkeypox or Vaccinia Virus. <i>PLoS ONE</i> , 2011, 6, e15615.	1.1	73
95	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.	3.3	72
96	[16] Phylogenetic identification of uncultured pathogens using ribosomal RNA sequences. <i>Methods in Enzymology</i> , 1994, 235, 205-222.	0.4	71
97	Microbial invasion of the amniotic cavity in pregnancies with small-for-gestational-age fetuses. <i>Journal of Perinatal Medicine</i> , 2010, 38, 495-502.	0.6	71
98	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, 4798-4812.	1.0	68
99	Significant Gene Order and Expression Differences in <i>Bordetella pertussis</i> Despite Limited Gene Content Variation. <i>Journal of Bacteriology</i> , 2006, 188, 2375-2382.	1.0	67
100	Lessons learned from the prenatal microbiome controversy. <i>Microbiome</i> , 2021, 9, 8.	4.9	67
101	Smallpox Research Activities: U.S. Interagency Collaboration, 2001. <i>Emerging Infectious Diseases</i> , 2002, 8, 743-745.	2.0	65
102	Multidomain analyses of a longitudinal human microbiome intestinal cleanout perturbation experiment. <i>PLoS Computational Biology</i> , 2017, 13, e1005706.	1.5	64
103	Superorganisms and Holobionts. <i>Microbe Magazine</i> , 2013, 8, 152-153.	0.4	64
104	Invasion of human respiratory epithelial cells by <i>Bordetella pertussis</i> : Possible role for a filamentous hemagglutinin Arg-Gly-Asp sequence and $\alpha 5 \beta 1$ integrin. <i>Microbial Pathogenesis</i> , 2001, 30, 279-288.	1.3	62
105	Paraffin Removal from Tissue Sections for Digestion and PCR Analysis. <i>BioTechniques</i> , 1999, 26, 198-200.	0.8	60
106	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, 1475-1487.	1.3	60
107	Proinflammatory and Proapoptotic Activities Associated with <i>Bordetella pertussis</i> Filamentous Hemagglutinin. <i>Infection and Immunity</i> , 2001, 69, 2650-2658.	1.0	60
108	Comparing functional genomic datasets: lessons from DNA microarray analyses of host-pathogen interactions. <i>Current Opinion in Microbiology</i> , 2001, 4, 95-101.	2.3	59

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109	Molecular Identification of Cyanobacteria Associated with Stromatolites from Distinct Geographical Locations. <i>Astrobiology</i> , 2002, 2, 271-280.	1.5	59
110	Long-term taxonomic and functional divergence from donor bacterial strains following fecal microbiota transplantation in immunocompromised patients. <i>PLoS ONE</i> , 2017, 12, e0182585.	1.1	59
111	The Human Microbiome and the Future Practice of Medicine. <i>JAMA - Journal of the American Medical Association</i> , 2015, 314, 1127.	3.8	58
112	Search for Highly Conserved Viral and Bacterial Nucleic Acid Sequences Corresponding to an Etiologic Agent of Kawasaki Disease. <i>Pediatric Research</i> , 1994, 36, 567-570.	1.1	57
113	Single-Cell Enumeration of an Uncultivated TM7 Subgroup in the Human Subgingival Crevice. <i>Applied and Environmental Microbiology</i> , 2003, 69, 6294-6298.	1.4	57
114	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, 2564-2576.	1.8	57
115	Growth Phase- and Nutrient Limitation-Associated Transcript Abundance Regulation in <i>Bordetella pertussis</i> . <i>Infection and Immunity</i> , 2006, 74, 5537-5548.	1.0	55
116	Surveillance for Unexplained Deaths and Critical Illnesses Due to Possibly Infectious Causes, United States, 1995-1998. <i>Emerging Infectious Diseases</i> , 2002, 8, 145-153.	2.0	55
117	Whipple's Disease and <i>Tropheryma whippelii</i> : Secrets Slowly Revealed. <i>Clinical Infectious Diseases</i> , 2001, 32, 457-463.	2.9	54
118	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.	1.1	54
119	Temporal Dynamics of the Transcriptional Response to Dengue Virus Infection in Nicaraguan Children. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1966.	1.3	52
120	Microbial biogeography and ecology of the mouth and implications for periodontal diseases. <i>Periodontology 2000</i> , 2020, 82, 26-41.	6.3	50
121	Cultivation of <i>Tropheryma whippelii</i> from Cerebrospinal Fluid. <i>Journal of Infectious Diseases</i> , 2003, 188, 801-808.	1.9	49
122	Gain-of-function experiments: time for a real debate. <i>Nature Reviews Microbiology</i> , 2015, 13, 58-64.	13.6	49
123	Culture-negative endocarditis caused by <i>Bartonella henselae</i> . <i>Journal of Pediatrics</i> , 1998, 132, 1051-1054.	0.9	47
124	'Til death do us part': coming to terms with symbiotic relationships. <i>Nature Reviews Microbiology</i> , 2008, 6, 721-724.	13.6	47
125	Multimic immune clockworks of pregnancy. <i>Seminars in Immunopathology</i> , 2020, 42, 397-412.	2.8	47
126	Gene Transcript Abundance Profiles Distinguish Kawasaki Disease from Adenovirus Infection. <i>Journal of Infectious Diseases</i> , 2009, 200, 657-666.	1.9	46



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127	Molecular characterization of <i>Bordetella bronchiseptica</i> filamentous haemagglutinin and its secretion machinery The GenBank accession numbers for the sequences reported in this paper are AF111794, AF111796, AF111797 and AF111798.. <i>Microbiology (United Kingdom)</i> , 2000, 146, 1211-1221.	0.7	46
128	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, 1574-1590.	1.2	45
129	Microbial threat lists: obstacles in the quest for biosecurity?. <i>Nature Reviews Microbiology</i> , 2010, 8, 149-154.	13.6	43
130	Cell types of origin of the cell-free transcriptome. <i>Nature Biotechnology</i> , 2022, 40, 855-861.	9.4	41
131	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.	3.3	38
132	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, 3292-3297.	1.0	35
133	Has Trench Fever Returned?. <i>New England Journal of Medicine</i> , 1995, 332, 463-464.	13.9	34
134	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, 8385-8394.	1.0	34
135	Cysteine dependence of <i>Lactobacillus iners</i> is a potential therapeutic target for vaginal microbiota modulation. <i>Nature Microbiology</i> , 2022, 7, 434-450.	5.9	32
136	Bioterrorism "Preparing to Fight the Next War. <i>New England Journal of Medicine</i> , 2006, 354, 113-115.	13.9	31
137	Adaptations of avian flu virus are a cause for concern. <i>Nature</i> , 2012, 482, 153-154.	13.7	30
138	Synthetic "Life," Ethics, National Security, and Public Discourse. <i>Science</i> , 2010, 329, 38-39.	6.0	29
139	Microbiota assembly, structure, and dynamics among Tsimane horticulturalists of the Bolivian Amazon. <i>Nature Communications</i> , 2020, 11, 3772.	5.8	29
140	<i>Bordetella pertussis</i> Infection of Primary Human Monocytes Alters HLA-DR Expression. <i>Infection and Immunity</i> , 2004, 72, 1450-1462.	1.0	28
141	Limited role for PCR-based diagnosis of Whipple's disease from peripheral blood mononuclear cells. <i>Lancet, The</i> , 1996, 348, 66-67.	6.3	27
142	Phase variation and microevolution at homopolymeric tracts in <i>Bordetella pertussis</i> . <i>BMC Genomics</i> , 2007, 8, 122.	1.2	26
143	Reduced Gut Microbiome Diversity and Metabolome Differences in Rhinoceros Species at Risk for Iron Overload Disorder. <i>Frontiers in Microbiology</i> , 2019, 10, 2291.	1.5	26
144	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.	4.3	25

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145	Modulation of the NF- $\kappa$ B Pathway by <i>Bordetella pertussis</i> Filamentous Hemagglutinin. <i>PLoS ONE</i> , 2008, 3, e3825.	1.1	25
146	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. <i>Microbiome</i> , 2014, 2, .	4.9	25
147	Competitors versus Collaborators: Micronutrient Processing by Pathogenic and Commensal Human-Associated Gut Bacteria. <i>Molecular Cell</i> , 2020, 78, 570-576.	4.5	25
148	Genomic features of <i>Bordetella parapertussis</i> clades with distinct host species specificity. <i>Genome Biology</i> , 2006, 7, R81.	13.9	24
149	SmashCell: a software framework for the analysis of single-cell amplified genome sequences. <i>Bioinformatics</i> , 2010, 26, 2979-2980.	1.8	24
150	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.	0.7	24
151	Molecular approaches for identification of infectious agents in Wegener's granulomatosis and other vasculitides. <i>Current Opinion in Rheumatology</i> , 1999, 11, 11-16.	2.0	22
152	The human body as microbial observatory. <i>Nature Genetics</i> , 2002, 30, 131-133.	9.4	22
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