

David A Relman

List of Publications by Year in descending order

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Version: 2024-02-01

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	Characterizing the oral and distal gut microbiota of the threatened southern sea otter (<i>Enhydra</i>) Tj ETQq1 1 0.784314 rgBT /Overl	0.9	7
2	Optimization of the 16S rRNA sequencing analysis pipeline for studying inÂvitro communities of gut commensals. IScience, 2022, 25, 103907.	1.9	9
3	Cell types of origin of the cell-free transcriptome. Nature Biotechnology, 2022, 40, 855-861.	9.4	41
4	Cysteine dependence of <i>Lactobacillus iners</i> is a potential therapeutic target for vaginal microbiota modulation. Nature Microbiology, 2022, 7, 434-450.	5.9	32
5	Protocols and risks: when less is more. Nature Protocols, 2022, 17, 1-2.	5.5	6
6	Precise genotyping of circular mobile elements from metagenomic data uncovers human-associated plasmids with recent common ancestors. Genome Research, 2022, , gr.275894.121.	2.4	0
7	The Tabula Sapiens: A multiple-organ, single-cell transcriptomic atlas of humans. Science, 2022, 376, eabl4896.	6.0	289
8	Short-Term Dairy Product Elimination and Reintroduction Minimally Perturbs the Gut Microbiota in Self-Reported Lactose-Intolerant Adults. MBio, 2022, 13, .	1.8	3
9	Towards personalized medicine in maternal and child health: integrating biologic and social determinants. Pediatric Research, 2021, 89, 252-258.	1.1	19
10	Lessons learned from the prenatal microbiome controversy. Microbiome, 2021, 9, 8.	4.9	67
11	Understanding how biologic and social determinants affect disparities in preterm birth and outcomes of preterm infants in the NICU. Seminars in Perinatology, 2021, 45, 151408.	1.1	5
12	Investigate the origins of COVID-19. Science, 2021, 372, 694-694.	6.0	92
13	A BAFF/APRIL axis regulates obesogenic diet-driven weight gain. Nature Communications, 2021, 12, 2911.	5.8	17
14	Topical emollient therapy with sunflower seed oil alters the skin microbiota of young children with severe acute malnutrition in Bangladesh: A randomised, controlled study. Journal of Global Health, 2021, 11, 04047.	1.2	4
15	Tracking microbial evolution in the human gut using Hi-C reveals extensive horizontal gene transfer, persistence and adaptation. Nature Microbiology, 2020, 5, 343-353.	5.9	101
16	Microbial biogeography and ecology of the mouth and implications for periodontal diseases. Periodontology 2000, 2020, 82, 26-41.	6.3	50
17	Microbiota assembly, structure, and dynamics among Tsimane horticulturalists of the Bolivian Amazon. Nature Communications, 2020, 11, 3772.	5.8	29
18	The biosecurity benefits of genetic engineering attribution. Nature Communications, 2020, 11, 6294.	5.8	12

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19	To stop the next pandemic, we need to unravel the origins of COVID-19. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29246-29248.	3.3	38
20	Complete Genome Sequences of Six Lactobacillus iners Strains Isolated from the Human Vagina. Microbiology Resource Announcements, 2020, 9, .	0.3	8
21	Multiomeric immune clockworks of pregnancy. Seminars in Immunopathology, 2020, 42, 397-412.	2.8	47
22	Thinking about the microbiome as a causal factor in human health and disease: philosophical and experimental considerations. Current Opinion in Microbiology, 2020, 54, 119-126.	2.3	5
23	Clades of huge phages from across Earth's ecosystems. Nature, 2020, 578, 425-431.	13.7	331
24	Competitors versus Collaborators: Micronutrient Processing by Pathogenic and Commensal Human-Associated Gut Bacteria. Molecular Cell, 2020, 78, 570-576.	4.5	25
25	Unraveling the Role of the Gut Microbiome in Iron-Deficiency Anemia During Pregnancy. FASEB Journal, 2020, 34, 1-1.	0.2	1
26	Multimomics modeling of the immunome, transcriptome, microbiome, proteome and metabolome adaptations during human pregnancy. Bioinformatics, 2019, 35, 95-103.	1.8	162
27	Treatment-Specific Composition of the Gut Microbiota Is Associated With Disease Remission in a Pediatric Crohn's Disease Cohort. Inflammatory Bowel Diseases, 2019, 25, 1927-1938.	0.9	20
28	Reduced Gut Microbiome Diversity and Metabolome Differences in Rhinoceros Species at Risk for Iron Overload Disorder. Frontiers in Microbiology, 2019, 10, 2291.	1.5	26
29	Maternal IgA: Matchmaking in Early Childhood. Immunity, 2019, 51, 211-213.	6.6	2
30	Understanding health disparities. Journal of Perinatology, 2019, 39, 354-358.	0.9	14
31	A spatial gradient of bacterial diversity in the human oral cavity shaped by salivary flow. Nature Communications, 2018, 9, 681.	5.8	87
32	Role of priority effects in the early-life assembly of the gut microbiota. Nature Reviews Gastroenterology and Hepatology, 2018, 15, 197-205.	8.2	258
33	Enterotypes in the landscape of gut microbial community composition. Nature Microbiology, 2018, 3, 8-16.	5.9	717
34	Clostridium difficile, Aging, and the Gut: Can Microbiome Rejuvenation Keep Us Young and Healthy?. Journal of Infectious Diseases, 2018, 217, 174-176.	1.9	11
35	Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data. Microbiome, 2018, 6, 226.	4.9	1,729
36	Microbiome as a tool and a target in the effort to address antimicrobial resistance. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12902-12910.	3.3	72

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37	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
38	Early Transcriptional Responses After Dengue Vaccination Mirror the Response to Natural Infection and Predict Neutralizing Antibody Titers. <i>Journal of Infectious Diseases</i> , 2018, 218, 1911-1921.	1.9	13
39	Poverty and Community-Acquired Antimicrobial Resistance with Extended-Spectrum β -Lactamase-Producing Organisms, Hyderabad, India. <i>Emerging Infectious Diseases</i> , 2018, 24, 1490-1496.	2.0	19
40	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
41	A geographically-diverse collection of 418 human gut microbiome pathway genome databases. <i>Scientific Data</i> , 2017, 4, 170035.	2.4	8
42	Candidatus <i>Mycoplasma girerdii</i> replicates, diversifies, and co-occurs with <i>Trichomonas vaginalis</i> in the oral cavity of a premature infant. <i>Scientific Reports</i> , 2017, 7, 3764.	1.6	17
43	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
44	The Human Virome: Implications for Clinical Practice in Transplantation Medicine. <i>Journal of Clinical Microbiology</i> , 2017, 55, 2884-2893.	1.8	15
45	Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. <i>Current Biology</i> , 2017, 27, 3752-3762.e6.	1.8	82
46	A high-pressure situation for bacteria. <i>Nature</i> , 2017, 551, 571-572.	13.7	13
47	Risky Business: Meeting the Structural Needs of Transdisciplinary Science. <i>Journal of Pediatrics</i> , 2017, 191, 255-258.	0.9	11
48	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.	0.4	0
49	Multidomain analyses of a longitudinal human microbiome intestinal cleanout perturbation experiment. <i>PLoS Computational Biology</i> , 2017, 13, e1005706.	1.5	64
50	On Defining Global Catastrophic Biological Risks. <i>Health Security</i> , 2017, 15, 347-348.	0.9	6
51	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
52	Childhood tuberculosis is associated with decreased abundance of T cell gene transcripts and impaired T cell function. <i>PLoS ONE</i> , 2017, 12, e0185973.	1.1	15
53	Early Transcriptional Signatures of the Immune Response to a Live Attenuated Tetravalent Dengue Vaccine Candidate in Non-human Primates. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004731.	1.3	12
54	A microbial perspective of human developmental biology. <i>Nature</i> , 2016, 535, 48-55.	13.7	215

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55	How to build healthy growth-promoting gut communities. Nature Reviews Gastroenterology and Hepatology, 2016, 13, 379-380.	8.2	4
56	A new view of the tree of life. Nature Microbiology, 2016, 1, 16048.	5.9	1,823
57	How likely is it that biological agents will be used deliberately to cause widespread harm?. EMBO Reports, 2016, 17, 127-130.	2.0	4
58	Infectious Diseases Society of America and Gain-of-Function Experiments With Pathogens Having Pandemic Potential. Journal of Infectious Diseases, 2016, 213, 1359-1361.	1.9	5
59	Marine mammals harbor unique microbiotas shaped by and yet distinct from the sea. Nature Communications, 2016, 7, 10516.	5.8	196
60	Cathelicidin Insufficiency in Patients with Fatal Leptospirosis. PLoS Pathogens, 2016, 12, e1005943.	2.1	22
61	REPRODUCIBLE RESEARCH WORKFLOW IN R FOR THE ANALYSIS OF PERSONALIZED HUMAN MICROBIOME DATA. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 183-94.	0.7	12
62	A Molecular Perspective of Microbial Pathogenicity. , 2015, , 1-10.e2.		6
63	Variation in Taxonomic Composition of the Fecal Microbiota in an Inbred Mouse Strain across Individuals and Time. PLoS ONE, 2015, 10, e0142825.	1.1	84
64	A more systematic approach to biological risk. Science, 2015, 350, 1471-1473.	6.0	20
65	Reply to Keelan and Payne: Microbiota-related pathways for preterm birth. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6415.	3.3	5
66	Temporal and spatial variation of the human microbiota during pregnancy. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11060-11065.	3.3	876
67	The Human Microbiome and the Future Practice of Medicine. JAMA - Journal of the American Medical Association, 2015, 314, 1127.	3.8	58
68	Gain-of-function experiments: time for a real debate. Nature Reviews Microbiology, 2015, 13, 58-64.	13.6	49
69	Actionable Sequence Data on Infectious Diseases in the Clinical Workplace. Clinical Chemistry, 2015, 61, 38-40.	1.5	6
70	Redaction of Sensitive Data in the Publication of Dual Use Research of Concern. MBio, 2014, 5, e00991-13.	1.8	12
71	"Inconvenient Truths" in the Pursuit of Scientific Knowledge and Public Health. Journal of Infectious Diseases, 2014, 209, 170-172.	1.9	20
72	Biological Engineering, Risk, and Uncertainty. Hastings Center Report, 2014, 44, S36-S37.	0.7	0

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73	The Importance of Influenza Vaccination. JAMA Internal Medicine, 2014, 174, 644.	2.6	0
74	Editorial Overview: Insights into Molecular Mechanisms of Microbiota. Journal of Molecular Biology, 2014, 426, 3827-3829.	2.0	1
75	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. Microbiome, 2014, 2, .	4.9	25
76	Immaturity in the gut microbial community. Nature, 2014, 510, 344-345.	13.7	8
77	Antibiotics and the gut microbiota. Journal of Clinical Investigation, 2014, 124, 4212-4218.	3.9	529
78	Unrest at home: diarrheal disease and microbiota disturbance. Genome Biology, 2014, 15, 120.	13.9	5
79	Identification of <i>Lactobacillus</i> strains with probiotic features from the bottlenose dolphin (<i>Tursiops truncatus</i>). Journal of Applied Microbiology, 2013, 115, 1037-1051.	1.4	21
80	Metagenomics, Infectious Disease Diagnostics, and Outbreak Investigations. JAMA - Journal of the American Medical Association, 2013, 309, 1531.	3.8	19
81	Probiotics, prebiotics, and the host microbiome: the science of translation. Annals of the New York Academy of Sciences, 2013, 1306, 1-17.	1.8	98
82	Genetically dictated change in host mucus carbohydrate landscape exerts a diet-dependent effect on the gut microbiota. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17059-17064.	3.3	237
83	Nasal Microenvironments and Interspecific Interactions Influence Nasal Microbiota Complexity and <i>S. Aureus</i> Carriage. Cell Host and Microbe, 2013, 14, 631-640.	5.1	294
84	Microbiota's 'little helpers': bacteriophages and antibiotic-associated responses in the gut microbiome. Genome Biology, 2013, 14, 127.	13.9	14
85	Type I Interferon Suppresses Type II Interferon-Triggered Human Anti-Mycobacterial Responses. Science, 2013, 339, 1448-1453.	6.0	359
86	Time series community genomics analysis reveals rapid shifts in bacterial species, strains, and phage during infant gut colonization. Genome Research, 2013, 23, 111-120.	2.4	409
87	Distinct Distal Gut Microbiome Diversity and Composition in Healthy Children from Bangladesh and the United States. PLoS ONE, 2013, 8, e53838.	1.1	278
88	The Increasingly Compelling Moral Responsibilities of Life Scientists. Hastings Center Report, 2013, 43, 34-35.	0.7	10
89	Undernutrition-Looking Within for Answers. Science, 2013, 339, 530-532.	6.0	4
90	Restoration of the gut microbial habitat as a disease therapy. Nature Biotechnology, 2013, 31, 35-37.	9.4	9

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91	Microbiome Assembly across Multiple Body Sites in Low-Birthweight Infants. <i>MBio</i> , 2013, 4, e00782-13.	1.8	147
92	Superorganisms and Holobionts. <i>Microbe Magazine</i> , 2013, 8, 152-153.	0.4	64
93	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
94	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
95	Adaptations of avian flu virus are a cause for concern. <i>Nature</i> , 2012, 482, 153-154.	13.7	30
96	Adaptations of Avian Flu Virus Are a Cause for Concern. <i>Science</i> , 2012, 335, 660-661.	6.0	88
97	Presumed Guilt in the Anthrax Case—Response. <i>Science</i> , 2012, 336, 669-670.	6.0	0
98	The human microbiome: ecosystem resilience and health. <i>Nutrition Reviews</i> , 2012, 70, S2-S9.	2.6	313
99	Gut Immune Maturation Depends on Colonization with a Host-Specific Microbiota. <i>Cell</i> , 2012, 149, 1578-1593.	13.5	1,050
100	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
101	The Application of Ecological Theory Toward an Understanding of the Human Microbiome. <i>Science</i> , 2012, 336, 1255-1262.	6.0	1,252
102	Creating a Mammalian-Transmissible A/H5N1 Influenza Virus: Social Contracts, Prudence, and Alternative Perspectives. <i>Journal of Infectious Diseases</i> , 2012, 205, 1636-1638.	1.9	13
103	Microbiota-Targeted Therapies: An Ecological Perspective. <i>Science Translational Medicine</i> , 2012, 4, 137rv5.	5.8	217
104	Learning about who we are. <i>Nature</i> , 2012, 486, 194-195.	13.7	75
105	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
106	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
107	Transforming Growth Factor- β 2 Signaling Pathway in Patients With Kawasaki Disease. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 16-25.	5.1	127
108	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

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109	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
110	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
111	Modulation of the Host Interferon Response and ISGylation Pathway by B. pertussis Filamentous Hemagglutinin. <i>PLoS ONE</i> , 2011, 6, e27535.	1.1	20
112	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
113	Postnatal assembly of microbial communities across multiple body habitats in low birthweight infants. <i>Journal of the American College of Surgeons</i> , 2011, 213, S83-S84.	0.2	0
114	Microbial Genomics and Infectious Diseases. <i>New England Journal of Medicine</i> , 2011, 365, 347-357.	13.9	156
115	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
116	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
117	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
118	Stunned Silence: Gene Expression Programs in Human Cells Infected with Monkeypox or Vaccinia Virus. <i>PLoS ONE</i> , 2011, 6, e15615.	1.1	73
119	Pox. <i>Journal of Clinical Investigation</i> , 2011, 121, 4571-4571.	3.9	0
120	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.	1.2	296
121	Bacterial diversity in the oral cavity of 10 healthy individuals. <i>ISME Journal</i> , 2010, 4, 962-974.	4.4	541
122	2020 visions. <i>Nature</i> , 2010, 463, 26-32.	13.7	75
123	The biological century: coming to terms with risk in the life sciences. <i>Nature Immunology</i> , 2010, 11, 275-278.	7.0	9
124	Microbial threat lists: obstacles in the quest for biosecurity?. <i>Nature Reviews Microbiology</i> , 2010, 8, 149-154.	13.6	43
125	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
126	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

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127	Synthetic "Life," Ethics, National Security, and Public Discourse. <i>Science</i> , 2010, 329, 38-39.	6.0	29
128	SmashCell: a software framework for the analysis of single-cell amplified genome sequences. <i>Bioinformatics</i> , 2010, 26, 2979-2980.	1.8	24
129	A Molecular Perspective of Microbial Pathogenicity. , 2010, , 1-13.		3
130	Whipple's Disease. , 2010, , 1833-1842.e3.		2
131	Dissecting Interferon-Induced Transcriptional Programs in Human Peripheral Blood Cells. <i>PLoS ONE</i> , 2010, 5, e9753.	1.1	134
132	Majority Rules? Tallying the Microbial Census in an Abscess by Means of Molecular Methods. <i>Clinical Infectious Diseases</i> , 2009, 48, 1179-1181.	2.9	8
133	Gene Transcript Abundance Profiles Distinguish Kawasaki Disease from Adenovirus Infection. <i>Journal of Infectious Diseases</i> , 2009, 200, 657-666.	1.9	46
134	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
135	Microbiology in the post-genomic era. <i>Nature Reviews Microbiology</i> , 2008, 6, 419-430.	13.6	324
136	'Til death do us part': coming to terms with symbiotic relationships. <i>Nature Reviews Microbiology</i> , 2008, 6, 721-724.	13.6	47
137	Exploring Microbial Diversity and Taxonomy Using SSU rRNA Hypervariable Tag Sequencing. <i>PLoS Genetics</i> , 2008, 4, e1000255.	1.5	779
138	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
139	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
140	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
141	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
142	Learning to Appreciate Our Differences. <i>Journal of Infectious Diseases</i> , 2008, 198, 4-5.	1.9	5
143	Modulation of the NF- κ B Pathway by <i>Bordetella pertussis</i> Filamentous Hemagglutinin. <i>PLoS ONE</i> , 2008, 3, e3825.	1.1	25
144	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

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145	Patterns of Host Genomeâ€“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
146	The Role of Microbes in Crohn's Disease. <i>Clinical Infectious Diseases</i> , 2007, 44, 256-262.	2.9	190
147	Gene-expression patterns reveal underlying biological processes in Kawasaki disease. <i>Genome Biology</i> , 2007, 8, R261.	13.9	89
148	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
149	Dissecting biological â€œdark matterâ€•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
150	Development of the Human Infant Intestinal Microbiota. <i>PLoS Biology</i> , 2007, 5, e177.	2.6	2,390
151	An ecological and evolutionary perspective on humanâ€“microbe mutualism and disease. <i>Nature</i> , 2007, 449, 811-818.	13.7	1,430
152	The importance of individuals and scale: moving towards single cell microbiology. <i>Environmental Microbiology</i> , 2007, 9, 8-10.	1.8	14
153	Phase variation and microevolution at homopolymeric tracts in <i>Bordetella pertussis</i> . <i>BMC Genomics</i> , 2007, 8, 122.	1.2	26
154	Differential NF-kappaB Responses Induced by <i>Bordetella Pertussis</i> Filamentous-Hemagglutinin (FHA) in Macrophages and Bronchial Epithelial Cells. <i>Clinical Immunology</i> , 2007, 123, S37.	1.4	0
155	Building a better virus trap. <i>Trends in Biotechnology</i> , 2007, 25, 535-538.	4.9	0
156	Genomic features of <i>Bordetella parapertussis</i> clades with distinct host species specificity. <i>Genome Biology</i> , 2006, 7, R81.	13.9	24
157	Rapid quantitative profiling of complex microbial populations. <i>Nucleic Acids Research</i> , 2006, 34, e5-e5.	6.5	158
158	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
159	Early days: genomics and human responses to infection. <i>Current Opinion in Microbiology</i> , 2006, 9, 312-319.	2.3	18
160	Assembly of the human intestinal microbiota. <i>Trends in Ecology and Evolution</i> , 2006, 21, 517-523.	4.2	462
161	Metagenomic Analysis of the Human Distal Gut Microbiome. <i>Science</i> , 2006, 312, 1355-1359.	6.0	3,964
162	In Search of Biosecurity. <i>Science</i> , 2006, 311, 1835-1835.	6.0	10

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163	How Bacterial Communities Expand Functional Repertoires. <i>PLoS Biology</i> , 2006, 4, e430.	2.6	11
164	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
165	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
166	Bioterrorism "Preparing to Fight the Next War. <i>New England Journal of Medicine</i> , 2006, 354, 113-115.	13.9	31
167	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
168	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
169	A brave new world in the life sciences. <i>Bulletin of the Atomic Scientists</i> , 2006, 62, 26-33.	0.2	4
170	The infectious aetiology of disease: the search for new agents. <i>Medicine</i> , 2005, 33, 37-38.	0.2	1
171	<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
172	Genomewide Analysis of the Host Response to Malaria in Kenyan Children. <i>Journal of Infectious Diseases</i> , 2005, 191, 1599-1611.	1.9	111
173	Diversity of the Human Intestinal Microbial Flora. <i>Science</i> , 2005, 308, 1635-1638.	6.0	6,617
174	Acquired predisposition to mycobacterial disease due to autoantibodies to IFN- γ . <i>Journal of Clinical Investigation</i> , 2005, 115, 2480-2488.	3.9	206
175	<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
176	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
177	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
178	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
179	Role of interleukin 6 in myocardial dysfunction of meningococcal septic shock. <i>Lancet, The</i> , 2004, 363, 203-209.	6.3	378
180	Analysis of Conserved Non-rRNA Genes of <i>Tropheryma whippelii</i> . <i>Systematic and Applied Microbiology</i> , 2003, 26, 3-12.	1.2	18

#	ARTICLE	IF	CITATIONS
181	Archaea and Their Potential Role in Human Disease. <i>Infection and Immunity</i> , 2003, 71, 591-596.	1.0	169
182	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
183	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
184	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
185	PUBLIC HEALTH: Understanding Threats to Scientific Openness. <i>Science</i> , 2003, 302, 1898-1898.	6.0	15
186	Cultivation of <i>Tropheryma whippelii</i> from Cerebrospinal Fluid. <i>Journal of Infectious Diseases</i> , 2003, 188, 801-808.	1.9	49
187	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
188	Shedding Light on Microbial Detection. <i>New England Journal of Medicine</i> , 2003, 349, 2162-2163.	13.9	14
189	Progression of the Lesion at the Site of Inoculation after Smallpox Vaccination. <i>New England Journal of Medicine</i> , 2003, 348, 414-414.	13.9	3
190	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
191	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
192	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
193	Human Herpesvirus 8 and Sarcoidosis. <i>Clinical Infectious Diseases</i> , 2002, 34, 559-560.	2.9	10
194	GENOMICS AND MICROBIOLOGY: Enhanced: Microbial Forensics--"Cross-Examining Pathogens". <i>Science</i> , 2002, 296, 1976-1979.	6.0	85
195	Molecular Identification of Cyanobacteria Associated with Stromatolites from Distinct Geographical Locations. <i>Astrobiology</i> , 2002, 2, 271-280.	1.5	59
196	Smallpox Research Activities: U.S. Interagency Collaboration, 2001. <i>Emerging Infectious Diseases</i> , 2002, 8, 743-745.	2.0	65
197	Role of phosphatidylinositol 3-kinase in the binding of <i>Bordetella pertussis</i> to human monocytes. <i>Cellular Microbiology</i> , 2002, 4, 825-833.	1.1	18
198	The human body as microbial observatory. <i>Nature Genetics</i> , 2002, 30, 131-133.	9.4	22

#	ARTICLE	IF	CITATIONS
199	Genome-wide responses of a pathogenic bacterium to its host. <i>Journal of Clinical Investigation</i> , 2002, 110, 1071-1073.	3.9	9
200	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
201	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
202	Mining the natural world for new pathogens.. <i>American Journal of Tropical Medicine and Hygiene</i> , 2002, 67, 133-134.	0.6	8
203	Genome-wide responses of a pathogenic bacterium to its host. <i>Journal of Clinical Investigation</i> , 2002, 110, 1071-1073.	3.9	3
204	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
205	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
206	<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
207	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
208	Whipple's Disease and <i>Tropheryma whippelii</i> : Secrets Slowly Revealed. <i>Clinical Infectious Diseases</i> , 2001, 32, 457-463.	2.9	54
209	Proinflammatory and Proapoptotic Activities Associated with <i>Bordetella pertussis</i> Filamentous Hemagglutinin. <i>Infection and Immunity</i> , 2001, 69, 2650-2658.	1.0	60
210	Does Blood of Healthy Subjects Contain Bacterial Ribosomal DNA?. <i>Journal of Clinical Microbiology</i> , 2001, 39, 1956-1959.	1.8	231
211	How the host "sees" pathogens: global gene expression responses to infection. <i>Current Opinion in Immunology</i> , 2000, 12, 215-218.	2.4	118
212	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
213	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
214	Paraffin Removal from Tissue Sections for Digestion and PCR Analysis. <i>BioTechniques</i> , 1999, 26, 198-200.	0.8	60
215	Application of Polymerase Chain Reaction to the Diagnosis of Infectious Diseases. <i>Clinical Infectious Diseases</i> , 1999, 29, 475-486.	2.9	201
216	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

#	ARTICLE	IF	CITATIONS
217	The 'emergence' of Bartonella and the development of molecular discovery methods for microbial pathogens. Netherlands Journal of Medicine, 1998, 52, 249-255.	0.6	3
218	Techniques Molecular and cellular microbiology: new tools of the trade. Current Opinion in Microbiology, 1998, 1, 337-339.	2.3	2
219	Culture-negative endocarditis caused by Bartonella henselae. Journal of Pediatrics, 1998, 132, 1051-1054.	0.9	47
220	PCR Analysis of T. Whippelii DNA in a Case of Whipple's Disease: Effect of Antibiotics and Correlation With Histology. American Journal of Gastroenterology, 1998, 93, 1579-1582.	0.2	21
221	Diagnostic Utility of the Polymerase Chain Reaction in 2 Cases of Suspected Whipple Disease. Archives of Internal Medicine, 1998, 158, 801.	4.3	9
222	Detection and Identification of Previously Unrecognized Microbial Pathogens. Emerging Infectious Diseases, 1998, 4, 382-389.	2.0	77
223	Filamentous Hemagglutinin of <i>Bordetella bronchiseptica</i> Is Required for Efficient Establishment of Tracheal Colonization. Infection and Immunity, 1998, 66, 5921-5929.	1.0	141
224	Improved Amplification of Microbial DNA from Blood Cultures by Removal of the PCR Inhibitor Sodium Polyanetholesulfonate. Journal of Clinical Microbiology, 1998, 36, 2810-2816.	1.8	196
225	Cultivation of Whipple bacillus: the irony and the ecstasy. Lancet, The, 1997, 350, 1262-1263.	6.3	10
226	Limited role for PCR-based diagnosis of Whipple's disease from peripheral blood mononuclear cells. Lancet, The, 1996, 348, 66-67.	6.3	27
227	Uveitis Caused by Tropheryma whippelii (Whipple's Bacillus). New England Journal of Medicine, 1995, 332, 363-366.	13.9	197
228	Has Trench Fever Returned?. New England Journal of Medicine, 1995, 332, 463-464.	13.9	34
229	[16] Phylogenetic identification of uncultured pathogens using ribosomal RNA sequences. Methods in Enzymology, 1994, 235, 205-222.	0.4	71
230	Search for Highly Conserved Viral and Bacterial Nucleic Acid Sequences Corresponding to an Etiologic Agent of Kawasaki Disease. Pediatric Research, 1994, 36, 567-570.	1.1	57
231	Identification of the Uncultured Bacillus of Whipple's Disease. New England Journal of Medicine, 1992, 327, 293-301.	13.9	1,196
232	Phylogenetic relationships among the agent of bacillary angiomatosis, Bartonella bacilliformis, and other alpha-proteobacteria. Molecular Microbiology, 1992, 6, 1801-1807.	1.2	111
233	The Agent of Bacillary Angiomatosis. New England Journal of Medicine, 1990, 323, 1573-1580.	13.9	985
234	Recognition of a bacterial adhesin by an integrin: Macrophage CR3 (α M β 2, CD11bCD18) binds filamentous hemagglutinin of Bordetella pertussis. Cell, 1990, 61, 1375-1382.	13.5	438

#	ARTICLE	IF	CITATIONS
235	Sequence-Based Methods for Pathogen Discovery: the Complex Associations of Microbes, Microbial Sequences, and Host. , 0, , 69-81.		1
236	Phylogenetic Diversity of Microbial Pathogens. , 0, , 507-517.		2