

Claire M Fraser

List of Publications by Year in descending order

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Version: 2024-02-01

241
papers

63,938
citations

4345

89
h-index

1311

230
g-index

254
all docs

254
docs citations

254
times ranked

56606
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamics of the infant gut microbiota in the first 18 months of life: the impact of maternal HIV infection and breastfeeding. <i>Microbiome</i> , 2022, 10, 61.	4.9	11
2	The evolution of synaptic and cognitive capacity: Insights from the nervous system transcriptome of <i>Aplysia</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	11
3	Comparative Analysis of Genome of <i>Ehrlichia</i> sp. HF, a Model Bacterium to Study Fatal Human Ehrlichiosis. <i>BMC Genomics</i> , 2021, 22, 11.	1.2	21
4	A genome to celebrate. <i>Science</i> , 2021, 371, 545-545.	6.0	1
5	FADU: a Quantification Tool for Prokaryotic Transcriptomic Analyses. <i>MSystems</i> , 2021, 6, .	1.7	8
6	Nasal Microbiota and Infectious Complications After Elective Surgical Procedures. <i>JAMA Network Open</i> , 2021, 4, e218386.	2.8	6
7	Changes in the Gut Microbiota Following Bariatric Surgery Are Associated with Increased Alcohol Intake in a Female Rat Model. <i>Alcohol and Alcoholism</i> , 2021, 56, 605-613.	0.9	7
8	<i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BB-12 Protects against Antibiotic-Induced Functional and Compositional Changes in Human Fecal Microbiome. <i>Nutrients</i> , 2021, 13, 2814.	1.7	22
9	Gut microbiome and metabolome in a non-human primate model of chronic excessive alcohol drinking. <i>Translational Psychiatry</i> , 2021, 11, 609.	2.4	12
10	Strains used in whole organism <i>Plasmodium falciparum</i> vaccine trials differ in genome structure, sequence, and immunogenic potential. <i>Genome Medicine</i> , 2020, 12, 6.	3.6	61
11	What influences practitioners' readiness to deliver psychological interventions by telephone? A qualitative study of behaviour change using the Theoretical Domains Framework. <i>BMC Psychiatry</i> , 2020, 20, 371.	1.1	16
12	Molecular mechanisms of probiotic prevention of antibiotic-associated diarrhea. <i>Current Opinion in Biotechnology</i> , 2020, 61, 226-234.	3.3	93
13	Cost effective, experimentally robust differential-expression analysis for human/mammalian, pathogen and dual-species transcriptomics. <i>Microbial Genomics</i> , 2020, 6, .	1.0	0
14	Establishing What Constitutes a Healthy Human Gut Microbiome: State of the Science, Regulatory Considerations, and Future Directions. <i>Journal of Nutrition</i> , 2019, 149, 1882-1895.	1.3	163
15	Telephone cognitive behavioural therapy to prevent the development of chronic widespread pain: a qualitative study of patient perspectives and treatment acceptability. <i>BMC Musculoskeletal Disorders</i> , 2019, 20, 198.	0.8	12
16	A Distinct Gut Microbiota Exists Within Crohn's Disease-Related Perianal Fistulae. <i>Journal of Surgical Research</i> , 2019, 242, 118-128.	0.8	18
17	Intratumor genetic heterogeneity in squamous cell carcinoma of the oral cavity. <i>Head and Neck</i> , 2019, 41, 2514-2524.	0.9	22
18	Metaproteomics reveals persistent and phylum-redundant metabolic functional stability in adult human gut microbiomes of Crohn's remission patients despite temporal variations in microbial taxa, genomes, and proteomes. <i>Microbiome</i> , 2019, 7, 18.	4.9	51

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19	A case of misalignment: the perspectives of local and national decision-makers on the implementation of psychological treatment by telephone in the Improving Access to Psychological Therapies Service. <i>BMC Health Services Research</i> , 2019, 19, 997.	0.9	9
20	Ghrelin receptor deletion reduces binge-like alcohol drinking in rats. <i>Journal of Neuroendocrinology</i> , 2019, 31, e12663.	1.2	36
21	Implementing an intervention designed to enhance service user involvement in mental health care planning: a qualitative process evaluation. <i>Social Psychiatry and Psychiatric Epidemiology</i> , 2019, 54, 221-233.	1.6	15
22	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
23	Primordial origin and diversification of plasmids in Lyme disease agent bacteria. <i>BMC Genomics</i> , 2018, 19, 218.	1.2	46
24	Temporal Variability of <i>Escherichia coli</i> Diversity in the Gastrointestinal Tracts of Tanzanian Children with and without Exposure to Antibiotics. <i>MSphere</i> , 2018, 3, .	1.3	23
25	Embedding shared decision-making in the care of patients with severe and enduring mental health problems: The EQUIP pragmatic cluster randomised trial. <i>PLoS ONE</i> , 2018, 13, e0201533.	1.1	33
26	Targeted enrichment outperforms other enrichment techniques and enables more multi-species RNA-Seq analyses. <i>Scientific Reports</i> , 2018, 8, 13377.	1.6	17
27	Compositional and Functional Differences in the Human Gut Microbiome Correlate with Clinical Outcome following Infection with Wild-Type <i>Salmonella enterica</i> Serovar Typhi. <i>MBio</i> , 2018, 9, .	1.8	21
28	Analysis of complete genome sequence and major surface antigens of <i>Neorickettsia helminthoeca</i> , causative agent of salmon poisoning disease. <i>Microbial Biotechnology</i> , 2017, 10, 933-957.	2.0	11
29	Plasmid diversity and phylogenetic consistency in the Lyme disease agent <i>Borrelia burgdorferi</i> . <i>BMC Genomics</i> , 2017, 18, 165.	1.2	72
30	Systemic and Terminal Ileum Mucosal Immunity Elicited by Oral Immunization With the Ty21a Typhoid Vaccine in Humans. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2017, 4, 419-437.	2.3	21
31	New var reconstruction algorithm exposes high var sequence diversity in a single geographic location in Mali. <i>Genome Medicine</i> , 2017, 9, 30.	3.6	13
32	Whole-Genome Sequences of Bacteremia Isolates of <i>Bordetella holmesii</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	0
33	Aligner optimization increases accuracy and decreases compute times in multi-species sequence data. <i>Microbial Genomics</i> , 2017, 3, e000122.	1.0	13
34	Molecular Characterization of Autonomic and Neuropeptide Receptors. , 2017, , 225-250.		0
35	Efficient Enrichment of Bacterial mRNA from Host-Bacteria Total RNA Samples. <i>Scientific Reports</i> , 2016, 6, 34850.	1.6	32
36	An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. <i>Nature Communications</i> , 2016, 7, 12218.	5.8	103

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37	Annotated draft genome sequences of three species of <i>Cryptosporidium</i> : <i>Cryptosporidium meleagridis</i> isolate UKMEL1, <i>C. baileyi</i> isolate TAMU-09Q1 and <i>C. hominis</i> isolates TU502_2012 and UKH1. <i>Pathogens and Disease</i> , 2016, 74, ftw080.	0.8	33
38	Genome-wide diversity and gene expression profiling of <i>Babesia microti</i> isolates identify polymorphic genes that mediate host-pathogen interactions. <i>Scientific Reports</i> , 2016, 6, 35284.	1.6	74
39	The impact of advertising patient and public involvement on trial recruitment: embedded cluster randomised recruitment trial. <i>Trials</i> , 2016, 17, 586.	0.7	13
40	The revisited genome of <i>Pseudomonas putida</i> KT2440 enlightens its value as a robust metabolic chassis. <i>Environmental Microbiology</i> , 2016, 18, 3403-3424.	1.8	270
41	Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. <i>Nature Communications</i> , 2016, 7, 10507.	5.8	450
42	Evaluating and Quantifying User and Carer Involvement in Mental Health Care Planning (EQUIP): Co-Development of a New Patient-Reported Outcome Measure. <i>PLoS ONE</i> , 2016, 11, e0149973.	1.1	23
43	Carers' experiences of involvement in care planning: a qualitative exploration of the facilitators and barriers to engagement with mental health services. <i>BMC Psychiatry</i> , 2015, 15, 208.	1.1	66
44	A cluster randomised controlled trial and process evaluation of a training programme for mental health professionals to enhance user involvement in care planning in service users with severe mental health issues (EQUIP): study protocol for a randomised controlled trial. <i>Trials</i> , 2015, 16, 348.	0.7	20
45	Re-inventing care planning in mental health: stakeholder accounts of the imagined implementation of a user/carer involved intervention. <i>BMC Health Services Research</i> , 2015, 15, 490.	0.9	20
46	Gut Microbiota in Multiple Sclerosis: Possible Influence of Immunomodulators. <i>Journal of Investigative Medicine</i> , 2015, 63, 729-734.	0.7	309
47	Professional perspectives on service user and carer involvement in mental health care planning: A qualitative study. <i>International Journal of Nursing Studies</i> , 2015, 52, 1834-1845.	2.5	82
48	Defining the Phylogenomics of <i>Shigella</i> Species: a Pathway to Diagnostics. <i>Journal of Clinical Microbiology</i> , 2015, 53, 951-960.	1.8	82
49	Potential Influence of <i>Staphylococcus aureus</i> Clonal Complex 30 Genotype and Transcriptome on Hematogenous Infections. <i>Open Forum Infectious Diseases</i> , 2015, 2, ofv093.	0.4	28
50	Examination of the Enterotoxigenic <i>Escherichia coli</i> Population Structure during Human Infection. <i>MBio</i> , 2015, 6, e00501.	1.8	39
51	Functional Dynamics of the Gut Microbiome in Elderly People during Probiotic Consumption. <i>MBio</i> , 2015, 6, .	1.8	126
52	New signaling pathways govern the host response to <i>C. albicans</i> infection in various niches. <i>Genome Research</i> , 2015, 25, 679-689.	2.4	82
53	Phylogenomic Identification of Regulatory Sequences in Bacteria: an Analysis of Statistical Power and an Application to <i>Borrelia burgdorferi</i> Sensu Lato. <i>MBio</i> , 2015, 6, .	1.8	2
54	Transcriptional Attenuation Controls Macrolide Inducible Efflux and Resistance in <i>Streptococcus pneumoniae</i> and in Other Gram-Positive Bacteria Containing <i>mef/mel(msr(D))</i> Elements. <i>PLoS ONE</i> , 2015, 10, e0116254.	1.1	41

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55	The Oral Bacterial Communities of Children with Well-Controlled HIV Infection and without HIV Infection. PLoS ONE, 2015, 10, e0131615.	1.1	32
56	Aerosol Mycobacterium tuberculosis Infection Causes Rapid Loss of Diversity in Gut Microbiota. PLoS ONE, 2014, 9, e97048.	1.1	124
57	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. PLoS ONE, 2014, 9, e99979.	1.1	34
58	Hospice support and the transition to adult services and adulthood for young people with life-limiting conditions and their families: A qualitative study. Palliative Medicine, 2014, 28, 342-352.	1.3	29
59	Single molecule sequencing and genome assembly of a clinical specimen of Loa loa, the causative agent of loiasis. BMC Genomics, 2014, 15, 788.	1.2	32
60	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	2.6	190
61	Genomic Epidemiology of the Haitian Cholera Outbreak: a Single Introduction Followed by Rapid, Extensive, and Continued Spread Characterized the Onset of the Epidemic. MBio, 2014, 5, e01721.	1.8	112
62	High-level Relatedness among <i>Mycobacterium abscessus</i> subsp. <i>massiliense</i> Strains from Widely Separated Outbreaks. Emerging Infectious Diseases, 2014, 20, 364-371.	2.0	108
63	Genetic Variation <i>In Vitro</i> and <i>In Vivo</i> of an Attenuated Lassa Vaccine Candidate. Journal of Virology, 2014, 88, 3058-3066.	1.5	12
64	BorreliaBase: a phylogeny-centered browser of Borrelia genomes. BMC Bioinformatics, 2014, 15, 233.	1.2	40
65	“Is It Worth It?” A Qualitative Study of the Beliefs of Overweight and Obese Physically Active Children. Journal of Physical Activity and Health, 2014, 11, 1219-1224.	1.0	13
66	Culture-Independent Evaluation of the Appendix and Rectum Microbiomes in Children with and without Appendicitis. PLoS ONE, 2014, 9, e95414.	1.1	90
67	No Evidence of Harms of Probiotic Lactobacillus rhamnosus GG ATCC 53103 in Healthy Elderly—A Phase I Open Label Study to Assess Safety, Tolerability and Cytokine Responses. PLoS ONE, 2014, 9, e113456.	1.1	39
68	The microbiome explored: recent insights and future challenges. Nature Reviews Microbiology, 2013, 11, 213-217.	13.6	162
69	Genome sequences of 65 <i>Helicobacter pylori</i> strains isolated from asymptomatic individuals and patients with gastric cancer, peptic ulcer disease, or gastritis. Pathogens and Disease, 2013, 68, 39-43.	0.8	17
70	Refining the pathovar paradigm via phylogenomics of the attaching and effacing Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12810-12815.	3.3	103
71	Inter- and intra-specific pan-genomes of Borrelia burgdorferi sensu lato: genome stability and adaptive radiation. BMC Genomics, 2013, 14, 693.	1.2	74
72	Simultaneous Transcriptional Profiling of Bacteria and Their Host Cells. PLoS ONE, 2013, 8, e80597.	1.1	125

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73	Impact of Oral Typhoid Vaccination on the Human Gut Microbiota and Correlations with S. Typhi-Specific Immunological Responses. PLoS ONE, 2013, 8, e62026.	1.1	82
74	Differential Response of the Cynomolgus Macaque Gut Microbiota to Shigella Infection. PLoS ONE, 2013, 8, e64212.	1.1	52
75	Increased Gut Microbiome Diversity Following a High Fiber Mediterranean Style Diet. FASEB Journal, 2013, 27, 1056.3.	0.2	4
76	Genomic Insights into the Emerging Human Pathogen Mycobacterium massiliense. Journal of Bacteriology, 2012, 194, 5450-5450.	1.0	22
77	Comparative Genomics and stx Phage Characterization of LEE-Negative Shiga Toxin-Producing Escherichia coli. Frontiers in Cellular and Infection Microbiology, 2012, 2, 133.	1.8	84
78	Defining a Healthy Human Gut Microbiome: Current Concepts, Future Directions, and Clinical Applications. Cell Host and Microbe, 2012, 12, 611-622.	5.1	615
79	Working with Fathers around Domestic Violence: Contemporary Debates. Child Abuse Review, 2012, 21, 255-263.	0.4	34
80	Analysis of the Gut Microbiota in the Old Order Amish and Its Relation to the Metabolic Syndrome. PLoS ONE, 2012, 7, e43052.	1.1	183
81	Integrated Metagenomics/Metaproteomics Reveals Human Host-Microbiota Signatures of Crohn's Disease. PLoS ONE, 2012, 7, e49138.	1.1	374
82	Steps in the Right Direction, Against the Odds, An Evaluation of a Community-Based Programme Aiming to Reduce Inactivity and Improve Health and Morale in Overweight and Obese School-Age Children. Children and Society, 2012, 26, 124-137.	1.0	4
83	"I'm just a mother. I'm nothing special, they're all professionals": parental advocacy as an aid to parental engagement. Child and Family Social Work, 2012, 17, 244-253.	0.6	22
84	Genome Stability of Lyme Disease Spirochetes: Comparative Genomics of Borrelia burgdorferi Plasmids. PLoS ONE, 2012, 7, e33280.	1.1	146
85	Advocacy for parents and carers involved with children's services: making a difference to working in partnership?. Child and Family Social Work, 2011, 16, 266-275.	0.6	21
86	Human Microbiome Project "paving the way to a better understanding of ourselves and our microbes. Drug Discovery Today, 2009, 14, 331-333.	3.2	25
87	Microbial Genome Sequencing: New Insights into Physiology and Evolution. Novartis Foundation Symposium, 2008, , 54-62.	1.2	3
88	Strain-Specific Single-Nucleotide Polymorphism Assays for the Bacillus anthracis Ames Strain. Journal of Clinical Microbiology, 2007, 45, 47-53.	1.8	126
89	Genomics. Current Opinion in Microbiology, 2007, 10, 479-480.	2.3	0
90	Theileria parva candidate vaccine antigens recognized by immune bovine cytotoxic T lymphocytes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3286-3291.	3.3	129

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91	Involving Children in Health and Social Research. <i>Childhood</i> , 2006, 13, 29-48.	0.6	118
92	Transcriptional profiling of the hyperthermophilic methanarchaeon <i>Methanococcus jannaschii</i> in response to lethal heat and non-lethal cold shock. <i>Environmental Microbiology</i> , 2005, 7, 789-797.	1.8	56
93	Facilitating genome navigation: survey sequencing and dense radiation-hybrid gene mapping. <i>Nature Reviews Genetics</i> , 2005, 6, 643-648.	7.7	69
94	The genome of the protist parasite <i>Entamoeba histolytica</i> . <i>Nature</i> , 2005, 433, 865-868.	13.7	783
95	Large-scale sequencing of human influenza reveals the dynamic nature of viral genome evolution. <i>Nature</i> , 2005, 437, 1162-1166.	13.7	419
96	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	13.7	1,272
97	Immune responses to <i>Plasmodium vivax</i> pre-erythrocytic stage antigens in naturally exposed Duffy-negative humans: a potential model for identification of liver-stage antigens. <i>European Journal of Immunology</i> , 2005, 35, 1859-1868.	1.6	25
98	Genome sequencing of microbial species. , 2005, , .		0
99	Toward a System of Microbial Forensics: from Sample Collection to Interpretation of Evidence. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2209-2213.	1.4	70
100	Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. <i>Genome Research</i> , 2005, 15, 1284-1291.	2.4	73
101	Gene Transfer and Genome Plasticity in <i>Thermotoga maritima</i> , a Model Hyperthermophilic Species. <i>Journal of Bacteriology</i> , 2005, 187, 4935-4944.	1.0	43
102	Whole-Genome Sequence Analysis of <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A Reveals Divergence among Pathovars in Genes Involved in Virulence and Transposition. <i>Journal of Bacteriology</i> , 2005, 187, 6488-6498.	1.0	301
103	The psychrophilic lifestyle as revealed by the genome sequence of <i>Colwellia psychrerythraea</i> 34H through genomic and proteomic analyses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10913-10918.	3.3	529
104	Genome Sequence of the PCE-Dechlorinating Bacterium <i>Dehalococcoides ethenogenes</i> . <i>Science</i> , 2005, 307, 105-108.	6.0	402
105	Whole-Genome Analysis of Human Influenza A Virus Reveals Multiple Persistent Lineages and Reassortment among Recent H3N2 Viruses. <i>PLoS Biology</i> , 2005, 3, e300.	2.6	340
106	Genome analysis of multiple pathogenic isolates of <i>Streptococcus agalactiae</i> : Implications for the microbial "pan-genome". <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13950-13955.	3.3	2,161
107	The Genome Sequence of <i>Trypanosoma cruzi</i> , Etiologic Agent of Chagas Disease. <i>Science</i> , 2005, 309, 409-415.	6.0	1,273
108	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005, 307, 1321-1324.	6.0	664

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109	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	6.0	309
110	Identification of a Universal Group B <i>Streptococcus</i> Vaccine by Multiple Genome Screen. <i>Science</i> , 2005, 309, 148-150.	6.0	497
111	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, 2426-2438.	1.0	940
112	How genomics has affected the concept of microbiology. <i>Current Opinion in Microbiology</i> , 2005, 8, 564-571.	2.3	40
113	Genomes and evolution. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 569-571.	1.5	9
114	A virus with big ambitions. <i>Trends in Microbiology</i> , 2005, 13, 56-57.	3.5	11
115	Genomics at the genus scale. <i>Trends in Microbiology</i> , 2005, 13, 95-97.	3.5	25
116	The Genome of the African Trypanosome <i>Trypanosoma brucei</i> . <i>Science</i> , 2005, 309, 416-422.	6.0	1,496
117	Major Structural Differences and Novel Potential Virulence Mechanisms from the Genomes of Multiple <i>Campylobacter</i> Species. <i>PLoS Biology</i> , 2005, 3, e15.	2.6	483
118	Application of Microbial Genomic Science to Advanced Therapeutics. <i>Annual Review of Medicine</i> , 2005, 56, 459-474.	5.0	39
119	Genetic Analysis and Attribution of Microbial Forensics Evidence. <i>Critical Reviews in Microbiology</i> , 2005, 31, 233-254.	2.7	66
120	Human, Mouse, and Rat Genome Large-Scale Rearrangements: Stability Versus Speciation. <i>Genome Research</i> , 2004, 14, 1851-1860.	2.4	130
121	Comparison of the genome of the oral pathogen <i>Treponema denticola</i> with other spirochete genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5646-5651.	3.3	251
122	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, 13536-13541.	3.3	243
123	An Uncertain Call to Arms. <i>Science</i> , 2004, 304, 359-359.	6.0	2
124	Genetic exchange and plasmid transfers in <i>Borrelia burgdorferi sensu stricto</i> revealed by three-way genome comparisons and multilocus sequence typing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14150-14155.	3.3	125
125	Genomic Insights into Methanotrophy: The Complete Genome Sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004, 2, e303.	2.6	275
126	The genome sequence of the anaerobic, sulfate-reducing bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Nature Biotechnology</i> , 2004, 22, 554-559.	9.4	559

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127	A genomics-based approach to biodefence preparedness. <i>Nature Reviews Genetics</i> , 2004, 5, 23-33.	7.7	27
128	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
129	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 183-191.	0.5	92
130	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, 977-988.	6.5	273
131	An integrated 4249 marker FISH/RH map of the canine genome. <i>BMC Genomics</i> , 2004, 5, 65.	1.2	107
132	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, 2386-2395.	6.5	460
133	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, 8449-8454.	3.3	457
134	Structural flexibility in the <i>Burkholderia mallei</i> genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14246-14251.	3.3	366
135	All things great and small. <i>Trends in Microbiology</i> , 2004, 12, 7-8.	3.5	4
136	The power in comparisons. <i>Trends in Microbiology</i> , 2004, 12, 62-63.	3.5	6
137	Champions of versatility. <i>Trends in Microbiology</i> , 2004, 12, 111-112.	3.5	5
138	Bugs N the 'hood. <i>Trends in Microbiology</i> , 2004, 12, 155-156.	3.5	0
139	Non-pathogenic bacteria take center stage: a lesson in contrasts. <i>Trends in Microbiology</i> , 2004, 12, 303-305.	3.5	1
140	Exploring the boundaries of life. <i>Trends in Microbiology</i> , 2004, 12, 404-405.	3.5	0
141	Roll with the flow: microbial masters of redox chemistry. <i>Trends in Microbiology</i> , 2004, 12, 439-441.	3.5	3
142	Insights into the evolution of phytopathogens. <i>Trends in Microbiology</i> , 2004, 12, 482-483.	3.5	2
143	It's a cold world out there (but the prospects are hot). <i>Trends in Microbiology</i> , 2004, 12, 532-534.	3.5	4
144	Complete genome sequence of the Q-fever pathogen <i>Coxiella burnetii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5455-5460.	3.3	506

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145	The Dog Genome: Survey Sequencing and Comparative Analysis. <i>Science</i> , 2003, 301, 1898-1903.	6.0	482
146	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , 2003, 423, 81-86.	13.7	760
147	The complete genome sequence of the <i>Arabidopsis</i> and tomato pathogen <i>Pseudomonas syringae</i> pv. tomato DC3000. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10181-10186.	3.3	785
148	Phylogenomics: Intersection of Evolution and Genomics. <i>Science</i> , 2003, 300, 1706-1707.	6.0	286
149	The sequence and analysis of <i>Trypanosoma brucei</i> chromosome II. <i>Nucleic Acids Research</i> , 2003, 31, 4856-4863.	6.5	59
150	Complete Genome Sequence of the Broad-Host-Range Vibriophage KVP40: Comparative Genomics of a T4-Related Bacteriophage. <i>Journal of Bacteriology</i> , 2003, 185, 5220-5233.	1.0	214
151	Functional Selection of Vaccine Candidate Peptides from <i>Staphylococcus aureus</i> Whole-Genome Expression Libraries In Vitro. <i>Infection and Immunity</i> , 2003, 71, 4633-4641.	1.0	62
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