

Claire M Fraser

List of Publications by Year in Descending Order

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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.

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|--------------------|--------------------------|-----------------|-----------------|
| 232 papers | 54,242 citations | 86 h-index | 232 g-index |
| 254 ext. papers | 59,721 ext. citations | 13.7 avg, IF | 6.12 L-index |

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 232 | 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 | 16.6 | 0 |
| 231 | Gut microbiome and metabolome in a non-human primate model of chronic excessive alcohol drinking. <i>Translational Psychiatry</i> , 2021 , 11, 609 | 8.6 | 2 |
| 230 | Nasal Microbiota and Infectious Complications After Elective Surgical Procedures. <i>JAMA Network Open</i> , 2021 , 4, e218386 | 10.4 | 3 |
| 229 | 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 | 3.5 | 2 |
| 228 | Comparative Analysis of Genome of Ehrlichia sp. HF, a Model Bacterium to Study Fatal Human Ehrlichiosis. <i>BMC Genomics</i> , 2021 , 22, 11 | 4.5 | 1 |
| 227 | FADU: a Quantification Tool for Prokaryotic Transcriptomic Analyses. <i>MSystems</i> , 2021 , 6, | 7.6 | 2 |
| 226 | subsp. BB-12 Protects against Antibiotic-Induced Functional and Compositional Changes in Human Fecal Microbiome. <i>Nutrients</i> , 2021 , 13, | 6.7 | 6 |
| 225 | Molecular mechanisms of probiotic prevention of antibiotic-associated diarrhea. <i>Current Opinion in Biotechnology</i> , 2020 , 61, 226-234 | 11.4 | 38 |
| 224 | Strains used in whole organism Plasmodium falciparum vaccine trials differ in genome structure, sequence, and immunogenic potential. <i>Genome Medicine</i> , 2020 , 12, 6 | 14.4 | 27 |
| 223 | 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 | 4.2 | 4 |
| 222 | 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 | 2.8 | 6 |
| 221 | A Distinct Gut Microbiota Exists Within Crohn's Disease-Related Perianal Fistulae. <i>Journal of Surgical Research</i> , 2019 , 242, 118-128 | 2.5 | 4 |
| 220 | Intratumor genetic heterogeneity in squamous cell carcinoma of the oral cavity. <i>Head and Neck</i> , 2019 , 41, 2514-2524 | 4.2 | 10 |
| 219 | 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 | 16.6 | 37 |
| 218 | 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 | 4.1 | 91 |
| 217 | 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 | 2.9 | 4 |
| 216 | Ghrelin receptor deletion reduces binge-like alcohol drinking in rats. <i>Journal of Neuroendocrinology</i> , 2019 , 31, e12663 | 3.8 | 20 |

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|-----|--|------|-----|
| 215 | 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 | 4.5 | 9 |
| 214 | Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018 , 3, 8-16 | 26.6 | 387 |
| 213 | Primordial origin and diversification of plasmids in Lyme disease agent bacteria. <i>BMC Genomics</i> , 2018 , 19, 218 | 4.5 | 24 |
| 212 | Compositional and Functional Differences in the Human Gut Microbiome Correlate with Clinical Outcome Following Infection with Wild-Type Salmonella enterica Serovar Typhi. <i>MBio</i> , 2018 , 9, | 7.8 | 16 |
| 211 | Temporal Variability of Diversity in the Gastrointestinal Tracts of Tanzanian Children with and without Exposure to Antibiotics. <i>MSphere</i> , 2018 , 3, | 5 | 12 |
| 210 | 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 | 3.7 | 26 |
| 209 | Targeted enrichment outperforms other enrichment techniques and enables more multi-species RNA-Seq analyses. <i>Scientific Reports</i> , 2018 , 8, 13377 | 4.9 | 9 |
| 208 | Analysis of complete genome sequence and major surface antigens of Neorickettsia helminthoeca, causative agent of salmon poisoning disease. <i>Microbial Biotechnology</i> , 2017 , 10, 933-957 | 6.3 | 8 |
| 207 | Plasmid diversity and phylogenetic consistency in the Lyme disease agent Borrelia burgdorferi. <i>BMC Genomics</i> , 2017 , 18, 165 | 4.5 | 37 |
| 206 | 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 | 7.9 | 8 |
| 205 | New var reconstruction algorithm exposes high var sequence diversity in a single geographic location in Mali. <i>Genome Medicine</i> , 2017 , 9, 30 | 14.4 | 10 |
| 204 | Aligner optimization increases accuracy and decreases compute times in multi-species sequence data. <i>Microbial Genomics</i> , 2017 , 3, e000122 | 4.4 | 8 |
| 203 | Molecular Characterization of Autonomic and Neuropeptide Receptors 2017 , 225-250 | | |
| 202 | Efficient Enrichment of Bacterial mRNA from Host-Bacteria Total RNA Samples. <i>Scientific Reports</i> , 2016 , 6, 34850 | 4.9 | 22 |
| 201 | An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. <i>Nature Communications</i> , 2016 , 7, 12218 | 17.4 | 69 |
| 200 | Annotated draft genome sequences of three species of Cryptosporidium: Cryptosporidium meleagridis isolate UKMEL1, C. baileyi isolate TAMU-09Q1 and C. hominis isolates TU502_2012 and UKH1. <i>Pathogens and Disease</i> , 2016 , 74, | 4.2 | 28 |
| 199 | Genome-wide diversity and gene expression profiling of Babesia microti isolates identify polymorphic genes that mediate host-pathogen interactions. <i>Scientific Reports</i> , 2016 , 6, 35284 | 4.9 | 47 |
| 198 | The impact of advertising patient and public involvement on trial recruitment: embedded cluster randomised recruitment trial. <i>Trials</i> , 2016 , 17, 586 | 2.8 | 4 |

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|-----|--|------|-----|
| 197 | 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 | 5.2 | 194 |
| 196 | Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. <i>Nature Communications</i> , 2016 , 7, 10507 | 17.4 | 303 |
| 195 | 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 | 3.7 | 16 |
| 194 | Defining the phylogenomics of <i>Shigella</i> species: a pathway to diagnostics. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 951-60 | 9.7 | 57 |
| 193 | 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 | 1 | 22 |
| 192 | Examination of the Enterotoxigenic <i>Escherichia coli</i> Population Structure during Human Infection. <i>MBio</i> , 2015 , 6, e00501 | 7.8 | 31 |
| 191 | Functional dynamics of the gut microbiome in elderly people during probiotic consumption. <i>MBio</i> , 2015 , 6, | 7.8 | 102 |
| 190 | New signaling pathways govern the host response to <i>C. albicans</i> infection in various niches. <i>Genome Research</i> , 2015 , 25, 679-89 | 9.7 | 57 |
| 189 | Phylogenomic identification of regulatory sequences in bacteria: an analysis of statistical power and an application to <i>Borrelia burgdorferi sensu lato</i> . <i>MBio</i> , 2015 , 6, | 7.8 | 2 |
| 188 | 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 | 4.2 | 52 |
| 187 | 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 | 2.8 | 20 |
| 186 | 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 | 2.9 | 18 |
| 185 | Gut microbiota in multiple sclerosis: possible influence of immunomodulators. <i>Journal of Investigative Medicine</i> , 2015 , 63, 729-34 | 2.9 | 223 |
| 184 | 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, 1834-45 | 5.8 | 72 |
| 183 | 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 | 3.7 | 24 |
| 182 | The Oral Bacterial Communities of Children with Well-Controlled HIV Infection and without HIV Infection. <i>PLoS ONE</i> , 2015 , 10, e0131615 | 3.7 | 27 |
| 181 | Genetic variation in vitro and in vivo of an attenuated Lassa vaccine candidate. <i>Journal of Virology</i> , 2014 , 88, 3058-66 | 6.6 | 10 |
| 180 | <i>BorreliaBase</i> : a phylogeny-centered browser of <i>Borrelia</i> genomes. <i>BMC Bioinformatics</i> , 2014 , 15, 233 | 3.6 | 29 |

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|-----|---|------|-----|
| 179 | 'Is it worth it?' A qualitative study of the beliefs of overweight and obese physically active children. <i>Journal of Physical Activity and Health</i> , 2014 , 11, 1219-24 | 2.5 | 6 |
| 178 | Aerosol Mycobacterium tuberculosis infection causes rapid loss of diversity in gut microbiota. <i>PLoS ONE</i> , 2014 , 9, e97048 | 3.7 | 85 |
| 177 | Standardized metadata for human pathogen/vector genomic sequences. <i>PLoS ONE</i> , 2014 , 9, e99979 | 3.7 | 25 |
| 176 | Hospice support and the transition to adult services and adulthood for young people with life-limiting conditions and their families: a qualitative study. <i>Palliative Medicine</i> , 2014 , 28, 342-52 | 5.5 | 23 |
| 175 | Single molecule sequencing and genome assembly of a clinical specimen of Loa loa, the causative agent of loiasis. <i>BMC Genomics</i> , 2014 , 15, 788 | 4.5 | 21 |
| 174 | Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920 | 9.7 | 146 |
| 173 | Genomic epidemiology of the Haitian cholera outbreak: a single introduction followed by rapid, extensive, and continued spread characterized the onset of the epidemic. <i>MBio</i> , 2014 , 5, e01721 | 7.8 | 57 |
| 172 | High-level relatedness among Mycobacterium abscessus subsp. massiliense strains from widely separated outbreaks. <i>Emerging Infectious Diseases</i> , 2014 , 20, 364-71 | 10.2 | 92 |
| 171 | Culture-independent evaluation of the appendix and rectum microbiomes in children with and without appendicitis. <i>PLoS ONE</i> , 2014 , 9, e95414 | 3.7 | 60 |
| 170 | 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. <i>PLoS ONE</i> , 2014 , 9, e113456 | 3.7 | 32 |
| 169 | The microbiome explored: recent insights and future challenges. <i>Nature Reviews Microbiology</i> , 2013 , 11, 213-7 | 22.2 | 127 |
| 168 | Genome sequences of 65 Helicobacter pylori strains isolated from asymptomatic individuals and patients with gastric cancer, peptic ulcer disease, or gastritis. <i>Pathogens and Disease</i> , 2013 , 68, 39-43 | 4.2 | 13 |
| 167 | Refining the pathovar paradigm via phylogenomics of the attaching and effacing Escherichia coli. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 12810-5 | 11.5 | 84 |
| 166 | Inter- and intra-specific pan-genomes of Borrelia burgdorferi sensu lato: genome stability and adaptive radiation. <i>BMC Genomics</i> , 2013 , 14, 693 | 4.5 | 52 |
| 165 | Simultaneous transcriptional profiling of bacteria and their host cells. <i>PLoS ONE</i> , 2013 , 8, e80597 | 3.7 | 85 |
| 164 | Impact of oral typhoid vaccination on the human gut microbiota and correlations with s. Typhi-specific immunological responses. <i>PLoS ONE</i> , 2013 , 8, e62026 | 3.7 | 62 |
| 163 | Differential response of the cynomolgus macaque gut microbiota to Shigella infection. <i>PLoS ONE</i> , 2013 , 8, e64212 | 3.7 | 43 |
| 162 | Increased Gut Microbiome Diversity Following a High Fiber Mediterranean Style Diet. <i>FASEB Journal</i> , 2013 , 27, 1056.3 | 0.9 | 3 |

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|-----|---|------|------|
| 161 | 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. <i>Children and Society</i> , 2012 , 26, 124-137 | 1.4 | 3 |
| 160 | I'm just a mother. I'm nothing special, they're all professionals—parental advocacy as an aid to parental engagement. <i>Child and Family Social Work</i> , 2012 , 17, 244-253 | 1.3 | 16 |
| 159 | Defining a healthy human gut microbiome: current concepts, future directions, and clinical applications. <i>Cell Host and Microbe</i> , 2012 , 12, 611-22 | 23.4 | 448 |
| 158 | Working with Fathers around Domestic Violence: Contemporary Debates. <i>Child Abuse Review</i> , 2012 , 21, 255-263 | 1.2 | 25 |
| 157 | Analysis of the gut microbiota in the old order Amish and its relation to the metabolic syndrome. <i>PLoS ONE</i> , 2012 , 7, e43052 | 3.7 | 161 |
| 156 | Integrated metagenomics/metaproteomics reveals human host-microbiota signatures of Crohn's disease. <i>PLoS ONE</i> , 2012 , 7, e49138 | 3.7 | 320 |
| 155 | Genomic insights into the emerging human pathogen <i>Mycobacterium massiliense</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 5450 | 3.5 | 20 |
| 154 | Comparative genomics and stx phage characterization of LEE-negative Shiga toxin-producing <i>Escherichia coli</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2012 , 2, 133 | 5.9 | 66 |
| 153 | Genome stability of Lyme disease spirochetes: comparative genomics of <i>Borrelia burgdorferi</i> plasmids. <i>PLoS ONE</i> , 2012 , 7, e33280 | 3.7 | 114 |
| 152 | Advocacy for parents and carers involved with children's services: making a difference to working in partnership?. <i>Child and Family Social Work</i> , 2011 , 16, 266-275 | 1.3 | 17 |
| 151 | Microbial Genome Sequencing: New Insights into Physiology and Evolution. <i>Novartis Foundation Symposium</i> , 2008 , 54-62 | | 3 |
| 150 | Strain-specific single-nucleotide polymorphism assays for the <i>Bacillus anthracis</i> Ames strain. <i>Journal of Clinical Microbiology</i> , 2007 , 45, 47-53 | 9.7 | 112 |
| 149 | Involving Children in Health and Social Research: "Human becomings" or "Active beings"? <i>Childhood</i> , 2006 , 13, 29-48 | 1.5 | 102 |
| 148 | <i>Theileria parva</i> candidate vaccine antigens recognized by immune bovine cytotoxic T lymphocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 3286-91 | 11.5 | 102 |
| 147 | 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, 13950-5 | 11.5 | 1585 |
| 146 | The genome sequence of <i>Trypanosoma cruzi</i> , etiologic agent of Chagas disease. <i>Science</i> , 2005 , 309, 409-15 | 39.3 | 1085 |
| 145 | The genome of the basidiomycetous yeast and human pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005 , 307, 1321-4 | 33.3 | 580 |
| 144 | Genome sequence of <i>Theileria parva</i> , a bovine pathogen that transforms lymphocytes. <i>Science</i> , 2005 , 309, 134-7 | 33.3 | 259 |

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|-----|---|------|------|
| 143 | Identification of a universal Group B streptococcus vaccine by multiple genome screen. <i>Science</i> , 2005 , 309, 148-50 | 33.3 | 446 |
| 142 | Insights on evolution of virulence and resistance from the complete genome analysis of an early methicillin-resistant <i>Staphylococcus aureus</i> strain and a biofilm-producing methicillin-resistant <i>Staphylococcus epidermidis</i> strain. <i>Journal of Bacteriology</i> , 2005 , 187, 2426-38 | 3.5 | 814 |
| 141 | How genomics has affected the concept of microbiology. <i>Current Opinion in Microbiology</i> , 2005 , 8, 564-71 | 7.9 | 35 |
| 140 | Genomes and evolution: the power of comparative genomics. <i>Current Opinion in Genetics and Development</i> , 2005 , 15, 569-71 | 4.9 | 7 |
| 139 | A virus with big ambitions. <i>Trends in Microbiology</i> , 2005 , 13, 56-7 | 12.4 | 11 |
| 138 | Genomics at the genus scale. <i>Trends in Microbiology</i> , 2005 , 13, 95-7 | 12.4 | 21 |
| 137 | The genome of the African trypanosome <i>Trypanosoma brucei</i> . <i>Science</i> , 2005 , 309, 416-22 | 33.3 | 1323 |
| 136 | Major structural differences and novel potential virulence mechanisms from the genomes of multiple campylobacter species. <i>PLoS Biology</i> , 2005 , 3, e15 | 9.7 | 440 |
| 135 | Application of microbial genomic science to advanced therapeutics. <i>Annual Review of Medicine</i> , 2005 , 56, 459-74 | 17.4 | 32 |
| 134 | Genetic analysis and attribution of microbial forensics evidence. <i>Critical Reviews in Microbiology</i> , 2005 , 31, 233-54 | 7.8 | 56 |
| 133 | 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, 789-97 | 5.2 | 50 |
| 132 | Facilitating genome navigation: survey sequencing and dense radiation-hybrid gene mapping. <i>Nature Reviews Genetics</i> , 2005 , 6, 643-8 | 30.1 | 61 |
| 131 | The genome of the protist parasite <i>Entamoeba histolytica</i> . <i>Nature</i> , 2005 , 433, 865-8 | 50.4 | 701 |
| 130 | Large-scale sequencing of human influenza reveals the dynamic nature of viral genome evolution. <i>Nature</i> , 2005 , 437, 1162-6 | 50.4 | 354 |
| 129 | Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005 , 438, 1151-6 | 50.4 | 1114 |
| 128 | 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, 1859-68 | 6.1 | 23 |
| 127 | Toward a system of microbial forensics: from sample collection to interpretation of evidence. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 2209-13 | 4.8 | 58 |
| 126 | Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. <i>Genome Research</i> , 2005 , 15, 1284-91 | 9.7 | 66 |

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|-----|--|------|------|
| 125 | Gene transfer and genome plasticity in <i>Thermotoga maritima</i> , a model hyperthermophilic species. <i>Journal of Bacteriology</i> , 2005 , 187, 4935-44 | 3.5 | 40 |
| 124 | Whole-genome sequence analysis of <i>Pseudomonas syringae</i> pv. phaseolicola 1448A reveals divergence among pathovars in genes involved in virulence and transposition. <i>Journal of Bacteriology</i> , 2005 , 187, 6488-98 | 3.5 | 270 |
| 123 | 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, 10913-8 | 11.5 | 430 |
| 122 | Genome sequence of the PCE-dechlorinating bacterium <i>Dehalococcoides ethenogenes</i> . <i>Science</i> , 2005 , 307, 105-8 | 33.3 | 363 |
| 121 | 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 | 9.7 | 291 |
| 120 | Human, mouse, and rat genome large-scale rearrangements: stability versus speciation. <i>Genome Research</i> , 2004 , 14, 1851-60 | 9.7 | 108 |
| 119 | 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, 5646-51 | 11.5 | 215 |
| 118 | Phylogenetic discovery bias in <i>Bacillus anthracis</i> using single-nucleotide polymorphisms from whole-genome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 13536-41 | 11.5 | 218 |
| 117 | Genetic exchange and plasmid transfers in <i>Borrelia burgdorferi</i> sensu stricto 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, 14150-5 | 11.5 | 108 |
| 116 | Genomic insights into methanotrophy: the complete genome sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004 , 2, e303 | 9.7 | 236 |
| 115 | The genome sequence of the anaerobic, sulfate-reducing bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Nature Biotechnology</i> , 2004 , 22, 554-9 | 44.5 | 477 |
| 114 | A genomics-based approach to biodefence preparedness. <i>Nature Reviews Genetics</i> , 2004 , 5, 23-33 | 30.1 | 14 |
| 113 | Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521 | 50.4 | 1689 |
| 112 | Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004 , 134, 183-91 | 1.9 | 83 |
| 111 | The genome sequence of <i>Bacillus cereus</i> ATCC 10987 reveals metabolic adaptations and a large plasmid related to <i>Bacillus anthracis</i> pXO1. <i>Nucleic Acids Research</i> , 2004 , 32, 977-88 | 20.1 | 253 |
| 110 | An integrated 4249 marker FISH/RH map of the canine genome. <i>BMC Genomics</i> , 2004 , 5, 65 | 4.5 | 90 |
| 109 | Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen <i>Listeria monocytogenes</i> reveal new insights into the core genome components of this species. <i>Nucleic Acids Research</i> , 2004 , 32, 2386-95 | 20.1 | 404 |
| 108 | Identification of anthrax toxin genes in a <i>Bacillus cereus</i> associated with an illness resembling inhalation anthrax. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 8449-54 | 11.5 | 377 |

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|-----|--|------|-----|
| 107 | 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, 14246-51 | 11.5 | 315 |
| 106 | All things great and small. <i>Trends in Microbiology</i> , 2004 , 12, 7-8 | 12.4 | 4 |
| 105 | The power in comparison. <i>Trends in Microbiology</i> , 2004 , 12, 62-3 | 12.4 | 6 |
| 104 | Champions of versatility. <i>Trends in Microbiology</i> , 2004 , 12, 111-2 | 12.4 | 4 |
| 103 | Bugs N the 'hood. <i>Trends in Microbiology</i> , 2004 , 12, 155-6 | 12.4 | |
| 102 | Non-pathogenic bacteria take center stage: a lesson in contrasts. <i>Trends in Microbiology</i> , 2004 , 12, 303-5 | 12.4 | 1 |
| 101 | Exploring the boundaries of life. <i>Trends in Microbiology</i> , 2004 , 12, 404-5 | 12.4 | |
| 100 | Roll with the flow: microbial masters of redox chemistry. <i>Trends in Microbiology</i> , 2004 , 12, 439-41 | 12.4 | 3 |
| 99 | Insights into the evolution of phytopathogens. <i>Trends in Microbiology</i> , 2004 , 12, 482-3 | 12.4 | 2 |
| 98 | It's a cold world out there (but the prospects are hot). <i>Trends in Microbiology</i> , 2004 , 12, 532-4 | 12.4 | 4 |
| 97 | Modeling bacterial evolution with comparative-genome-based marker systems: application to <i>Mycobacterium tuberculosis</i> evolution and pathogenesis. <i>Journal of Bacteriology</i> , 2003 , 185, 3392-9 | 3.5 | 95 |
| 96 | 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, 5455-60 | 11.5 | 428 |
| 95 | The dog genome: survey sequencing and comparative analysis. <i>Science</i> , 2003 , 301, 1898-903 | 33.3 | 422 |
| 94 | The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , 2003 , 423, 81-6 | 50.4 | 692 |
| 93 | The complete genome sequence of the Arabidopsis 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, 10181-6 | 11.5 | 695 |
| 92 | Phylogenomics: intersection of evolution and genomics. <i>Science</i> , 2003 , 300, 1706-7 | 33.3 | 244 |
| 91 | The sequence and analysis of <i>Trypanosoma brucei</i> chromosome II. <i>Nucleic Acids Research</i> , 2003 , 31, 4856-63 | 26.1 | 48 |
| 90 | Complete genome sequence of the broad-host-range vibriophage KVP40: comparative genomics of a T4-related bacteriophage. <i>Journal of Bacteriology</i> , 2003 , 185, 5220-33 | 3.5 | 194 |

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|----|--|------|------|
| 89 | Functional selection of vaccine candidate peptides from <i>Staphylococcus aureus</i> whole-genome expression libraries in vitro. <i>Infection and Immunity</i> , 2003 , 71, 4633-41 | 3.7 | 58 |
| 88 | Complete genome sequence of the oral pathogenic Bacterium porphyromonas gingivalis strain W83. <i>Journal of Bacteriology</i> , 2003 , 185, 5591-601 | 3.5 | 321 |
| 87 | Genomics of Bacterial Pathogens 2003 , 9-25 | | |
| 86 | Microbial Genome Sequencing: Prospects for Development of Novel Vaccines and Anti-Microbial Compounds. <i>Scientific World Journal, The</i> , 2002 , 2, 1-2 | 2.2 | 1 |
| 85 | A physical map of the mouse genome. <i>Nature</i> , 2002 , 418, 743-50 | 50.4 | 282 |
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