

Claire M Fraser

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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	Whole-genome random sequencing and assembly of <i>Haemophilus influenzae</i> Rd. <i>Science</i> , 1995 , 269, 496-512	33.3	4784
231	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002 , 419, 498-511	50.4	3336
230	The complete genome sequence of the gastric pathogen <i>Helicobacter pylori</i> . <i>Nature</i> , 1997 , 388, 539-47	50.4	3000
229	Genomic sequence of a Lyme disease spirochaete, <i>Borrelia burgdorferi</i> . <i>Nature</i> , 1997 , 390, 580-6	50.4	1729
228	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
227	The genome sequence of the malaria mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002 , 298, 129-49	33.3	1622
226	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
225	DNA sequence of both chromosomes of the cholera pathogen <i>Vibrio cholerae</i> . <i>Nature</i> , 2000 , 406, 477-83	50.4	1495
224	Mutations of two PMS homologues in hereditary nonpolyposis colon cancer. <i>Nature</i> , 1994 , 371, 75-80	50.4	1376
223	The genome of the African trypanosome <i>Trypanosoma brucei</i> . <i>Science</i> , 2005 , 309, 416-22	33.3	1323
222	Evidence for lateral gene transfer between Archaea and bacteria from genome sequence of <i>Thermotoga maritima</i> . <i>Nature</i> , 1999 , 399, 323-9	50.4	1260
221	The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon <i>Archaeoglobus fulgidus</i> . <i>Nature</i> , 1997 , 390, 364-70	50.4	1257
220	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005 , 438, 1151-6	50.4	1114
219	Complete genome sequence of a virulent isolate of <i>Streptococcus pneumoniae</i> . <i>Science</i> , 2001 , 293, 498-506	33.3	1112
218	The genome sequence of <i>Trypanosoma cruzi</i> , etiologic agent of Chagas disease. <i>Science</i> , 2005 , 309, 409-15	33.3	1085
217	Complete genome sequence of <i>Neisseria meningitidis</i> serogroup B strain MC58. <i>Science</i> , 2000 , 287, 1809-15	33.3	986
216	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

215	Genome sequence of the radioresistant bacterium <i>Deinococcus radiodurans</i> R1. <i>Science</i> , 1999 , 286, 1571-3	33.3	760
214	Global transposon mutagenesis and a minimal <i>Mycoplasma</i> genome. <i>Science</i> , 1999 , 286, 2165-9	33.3	749
213	The genome of the protist parasite <i>Entamoeba histolytica</i> . <i>Nature</i> , 2005 , 433, 865-8	50.4	701
212	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, 10181-6	11.5	695
211	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
210	Genome sequence of the dissimilatory metal ion-reducing bacterium <i>Shewanella oneidensis</i> . <i>Nature Biotechnology</i> , 2002 , 20, 1118-23	44.5	680
209	A bacterial genome in flux: the twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete <i>Borrelia burgdorferi</i> . <i>Molecular Microbiology</i> , 2000 , 35, 490-516	4.1	625
208	Sequence and analysis of chromosome 2 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 1999 , 402, 761-8	50.4	619
207	Genome sequence and comparative analysis of the model rodent malaria parasite <i>Plasmodium yoelii yoelii</i> . <i>Nature</i> , 2002 , 419, 512-9	50.4	591
206	The genome of the basidiomycetous yeast and human pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005 , 307, 1321-4	33.3	580
205	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
204	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
203	Identification of a universal Group B streptococcus vaccine by multiple genome screen. <i>Science</i> , 2005 , 309, 148-50	33.3	446
202	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
201	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
200	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
199	The dog genome: survey sequencing and comparative analysis. <i>Science</i> , 2003 , 301, 1898-903	33.3	422
198	Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V <i>Streptococcus agalactiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 12391-6	11.5	405

197	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
196	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018 , 3, 8-16	26.6	387
195	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
194	The <i>Brucella suis</i> genome reveals fundamental similarities between animal and plant pathogens and symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 13148-53	11.5	372
193	Genome sequence of the PCE-dechlorinating bacterium <i>Dehalococcoides ethenogenes</i> . <i>Science</i> , 2005 , 307, 105-8	33.3	363
192	Comparative genome sequencing for discovery of novel polymorphisms in <i>Bacillus anthracis</i> . <i>Science</i> , 2002 , 296, 2028-33	33.3	359
191	Large-scale sequencing of human influenza reveals the dynamic nature of viral genome evolution. <i>Nature</i> , 2005 , 437, 1162-6	50.4	354
190	Chromosome 2 sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Science</i> , 1998 , 282, 1126-32	53.3	350
189	Unsuspected diversity among marine aerobic anoxygenic phototrophs. <i>Nature</i> , 2002 , 415, 630-3	50.4	333
188	Complete genome sequence of the oral pathogenic bacterium <i>Porphyromonas gingivalis</i> strain W83. <i>Journal of Bacteriology</i> , 2003 , 185, 5591-601	3.5	321
187	The complete genome sequence of <i>Chlorobium tepidum</i> TLS, a photosynthetic, anaerobic, green-sulfur bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 9509-14	11.5	321
186	Integrated metagenomics/metaproteomics reveals human host-microbiota signatures of Crohn's disease. <i>PLoS ONE</i> , 2012 , 7, e49138	3.7	320
185	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
184	Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. <i>Nature Communications</i> , 2016 , 7, 10507	17.4	303
183	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
182	A physical map of the mouse genome. <i>Nature</i> , 2002 , 418, 743-50	50.4	282
181	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, 6488-98	3.5	270
180	Genome sequence of <i>Theileria parva</i> , a bovine pathogen that transforms lymphocytes. <i>Science</i> , 2005 , 309, 134-7	33.3	259

179	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
178	Phylogenomics: intersection of evolution and genomics. <i>Science</i> , 2003 , 300, 1706-7	33.3	244
177	Genomic insights into methanotrophy: the complete genome sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004 , 2, e303	9.7	236
176	Gut microbiota in multiple sclerosis: possible influence of immunomodulators. <i>Journal of Investigative Medicine</i> , 2015 , 63, 729-34	2.9	223
175	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
174	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
173	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
172	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
171	Identification of in vivo expressed vaccine candidate antigens from <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 6573-8	11.5	193
170	Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000 , 408, 816-20	50.4	183
169	Cloning, localization, and permanent expression of a <i>Drosophila</i> octopamine receptor. <i>Neuron</i> , 1990 , 4, 343-54	13.9	170
168	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
167	The synthesis of beta-adrenergic receptors in cultured human lung cells: induction by glucocorticoids. <i>Biochemical and Biophysical Research Communications</i> , 1980 , 94, 390-7	3.4	153
166	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
165	Sequence of <i>Plasmodium falciparum</i> chromosomes 2, 10, 11 and 14. <i>Nature</i> , 2002 , 419, 531-4	50.4	146
164	Microbial genome sequencing. <i>Nature</i> , 2000 , 406, 799-803	50.4	133
163	The microbiome explored: recent insights and future challenges. <i>Nature Reviews Microbiology</i> , 2013 , 11, 213-7	22.2	127
162	Discrete activation of transduction pathways associated with acetylcholine m1 receptor by several muscarinic ligands. <i>European Journal of Pharmacology</i> , 1994 , 267, 21-31		115

161	Genome stability of Lyme disease spirochetes: comparative genomics of <i>Borrelia burgdorferi</i> plasmids. <i>PLoS ONE</i> , 2012 , 7, e33280	3.7	114
160	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
159	Human, mouse, and rat genome large-scale rearrangements: stability versus speciation. <i>Genome Research</i> , 2004 , 14, 1851-60	9.7	108
158	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
157	Functional dynamics of the gut microbiome in elderly people during probiotic consumption. <i>MBio</i> , 2015 , 6,	7.8	102
156	Involving Children in Health and Social Research: Human becomings for active beings. <i>Childhood</i> , 2006 , 13, 29-48	1.5	102
155	<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
154	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
153	The value of complete microbial genome sequencing (you get what you pay for). <i>Journal of Bacteriology</i> , 2002 , 184, 6403-5; discussion 6405	3.5	93
152	Cloning and sequence analysis of the human brain beta-adrenergic receptor. Evolutionary relationship to rodent and avian beta-receptors and porcine muscarinic receptors. <i>FEBS Letters</i> , 1987 , 211, 200-6	3.8	93
151	High-level relatedness among <i>Mycobacterium abscessus</i> subsp. <i>massiliense</i> strains from widely separated outbreaks. <i>Emerging Infectious Diseases</i> , 2014 , 20, 364-71	10.2	92
150	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
149	A novel lipothrixvirus, SIFV, of the extremely thermophilic crenarchaeon <i>Sulfolobus</i> . <i>Virology</i> , 2000 , 267, 252-66	3.6	91
148	Autonomic abnormalities and autoantibodies to beta-adrenergic receptors. <i>New England Journal of Medicine</i> , 1981 , 305, 1165-70	59.2	91
147	An integrated 4249 marker FISH/RH map of the canine genome. <i>BMC Genomics</i> , 2004 , 5, 65	4.5	90
146	Aerosol <i>Mycobacterium tuberculosis</i> infection causes rapid loss of diversity in gut microbiota. <i>PLoS ONE</i> , 2014 , 9, e97048	3.7	85
145	Simultaneous transcriptional profiling of bacteria and their host cells. <i>PLoS ONE</i> , 2013 , 8, e80597	3.7	85
144	Refining the pathovar paradigm via phylogenomics of the attaching and effacing <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 12810-5	11.5	84

143	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004 , 134, 183-91	1.9	83
142	Status of genome projects for nonpathogenic bacteria and archaea. <i>Nature Biotechnology</i> , 2000 , 18, 1049-54	4.4	78
141	The size of the mammalian lung beta 2-adrenergic receptor as determined by target size analysis and immunoaffinity chromatography. <i>Biochemical and Biophysical Research Communications</i> , 1982 , 109, 21-9	3.4	78
140	Muscarinic cholinergic receptor structure: molecular biological support for subtypes. <i>Trends in Pharmacological Sciences</i> , 1987 , 8, 426-431	13.2	76
139	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
138	Strategies for whole microbial genome sequencing and analysis. <i>Electrophoresis</i> , 1997 , 18, 1207-16	3.6	70
137	An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. <i>Nature Communications</i> , 2016 , 7, 12218	17.4	69
136	Cloning, sequence analysis and chromosome localization of a Drosophila muscarinic acetylcholine receptor. <i>FEBS Letters</i> , 1989 , 255, 219-25	3.8	67
135	Comparative genomics and stx phage characterization of LEE-negative Shiga toxin-producing Escherichia coli. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012 , 2, 133	5.9	66
134	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
133	Enterococcus faecalis conjugative plasmid pAM373: complete nucleotide sequence and genetic analyses of sex pheromone response. <i>Molecular Microbiology</i> , 2000 , 37, 1327-41	4.1	62
132	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
131	Facilitating genome navigation: survey sequencing and dense radiation-hybrid gene mapping. <i>Nature Reviews Genetics</i> , 2005 , 6, 643-8	30.1	61
130	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
129	Genomics and future biological weapons: the need for preventive action by the biomedical community. <i>Nature Genetics</i> , 2001 , 29, 253-6	36.3	59
128	Functional selection of vaccine candidate peptides from Staphylococcus aureus whole-genome expression libraries in vitro. <i>Infection and Immunity</i> , 2003 , 71, 4633-41	3.7	58
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	The complexity of simplicity. <i>Genome Biology</i> , 2001 , 2, COMMENT2002	18.3	58

125	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
124	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
123	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
122	Genetic analysis and attribution of microbial forensics evidence. <i>Critical Reviews in Microbiology</i> , 2005 , 31, 233-54	7.8	56
121	Comparative genomics and understanding of microbial biology. <i>Emerging Infectious Diseases</i> , 2000 , 6, 505-12	10.2	55
120	Molecular biology of adrenergic and muscarinic cholinergic receptors. A perspective. <i>Biochemical Pharmacology</i> , 1989 , 38, 1197-208	6	54
119	Isolation of (a subunit of) the Na ⁺ /D-glucose cotransporter(s) of rabbit intestinal brush border membranes using monoclonal antibodies. <i>FEBS Letters</i> , 1983 , 161, 279-83	3.8	53
118	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
117	Inter- and intra-specific pan-genomes of <i>Borrelia burgdorferi</i> sensu lato: genome stability and adaptive radiation. <i>BMC Genomics</i> , 2013 , 14, 693	4.5	52
116	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
115	The sequence and analysis of <i>Trypanosoma brucei</i> chromosome II. <i>Nucleic Acids Research</i> , 2003 , 31, 4856-63	6.3	48
114	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	4.9	47
113	Detergent solubilization of mammalian cardiac and hepatic beta-adrenergic receptors. <i>Archives of Biochemistry and Biophysics</i> , 1979 , 196, 566-73	4.1	47
112	Mouse BAC ends quality assessment and sequence analyses. <i>Genome Research</i> , 2001 , 11, 1736-45	9.7	44
111	Differential response of the cynomolgus macaque gut microbiota to <i>Shigella</i> infection. <i>PLoS ONE</i> , 2013 , 8, e64212	3.7	43
110	Distribution of twelve linear extrachromosomal DNAs in natural isolates of Lyme disease spirochetes. <i>Journal of Bacteriology</i> , 2000 , 182, 2476-80	3.5	42
109	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
108	Molecular mechanisms of probiotic prevention of antibiotic-associated diarrhea. <i>Current Opinion in Biotechnology</i> , 2020 , 61, 226-234	11.4	38

107	Plasmid diversity and phylogenetic consistency in the Lyme disease agent <i>Borrelia burgdorferi</i> . <i>BMC Genomics</i> , 2017 , 18, 165	4.5	37
106	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
105	How genomics has affected the concept of microbiology. <i>Current Opinion in Microbiology</i> , 2005 , 8, 564-71	7.9	35
104	A model for high-throughput automated DNA sequencing and analysis core facilities. <i>Nature</i> , 1994 , 368, 474-5	50.4	34
103	Muscarinic acetylcholine receptor subtypes which selectively couple to phospholipase C: pharmacological and biochemical properties. <i>Biochemical and Biophysical Research Communications</i> , 1990 , 173, 666-72	3.4	33
102	Application of microbial genomic science to advanced therapeutics. <i>Annual Review of Medicine</i> , 2005 , 56, 459-74	17.4	32
101	No evidence of harms of probiotic <i>Lactobacillus rhamnosus</i> 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
100	Examination of the Enterotoxigenic <i>Escherichia coli</i> Population Structure during Human Infection. <i>MBio</i> , 2015 , 6, e00501	7.8	31
99	<i>BorreliaBase</i> : a phylogeny-centered browser of <i>Borrelia</i> genomes. <i>BMC Bioinformatics</i> , 2014 , 15, 233	3.6	29
98	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,	4.2	28
97	Discrepancies between the affinities of binding and action of the novel beta-adrenergic agonist BRL 37344 in rat brown adipose tissue. <i>Biochemical and Biophysical Research Communications</i> , 1988 , 156, 375-82	3.4	28
96	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
95	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	14.4	27
94	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
93	Standardized metadata for human pathogen/vector genomic sequences. <i>PLoS ONE</i> , 2014 , 9, e99979	3.7	25
92	Working with Fathers around Domestic Violence: Contemporary Debates. <i>Child Abuse Review</i> , 2012 , 21, 255-263	1.2	25
91	<i>Theileria parva</i> genomics reveals an atypical apicomplexan genome. <i>International Journal for Parasitology</i> , 2000 , 30, 465-74	4.3	25
90	Molecular size of the human platelet alpha 2-adrenergic receptor as determined by radiation inactivation. <i>Biochemical and Biophysical Research Communications</i> , 1983 , 116, 1070-5	3.4	25

89	Primordial origin and diversification of plasmids in Lyme disease agent bacteria. <i>BMC Genomics</i> , 2018 , 19, 218	4.5	24
88	Genome of <i>Thermotoga maritima</i> MSB8. <i>Methods in Enzymology</i> , 2001 , 330, 169-80	1.7	24
87	The structure of β and β adrenergic receptors. <i>Trends in Pharmacological Sciences</i> , 1983 , 4, 256-258	13.2	24
86	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
85	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
84	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
83	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
82	Efficient Enrichment of Bacterial mRNA from Host-Bacteria Total RNA Samples. <i>Scientific Reports</i> , 2016 , 6, 34850	4.9	22
81	Single molecule sequencing and genome assembly of a clinical specimen of <i>Loa loa</i> , the causative agent of loiasis. <i>BMC Genomics</i> , 2014 , 15, 788	4.5	21
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