

George M Weinstock

List of Publications by Citations

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389
papers

122,463
citations

109
h-index

349
g-index

419
ext. papers

140,563
ext. citations

11.8
avg, IF

8.97
L-index

#	Paper	IF	Citations
389	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001 , 409, 860-921	50.4	17366
388	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012 , 486, 207-14	50.4	6938
387	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010 , 467, 1061-73	50.4	6142
386	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012 , 491, 56-65	50.4	6049
385	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. <i>Nature</i> , 2008 , 455, 1061-8	50.4	5669
384	Integrated genomic analyses of ovarian carcinoma. <i>Nature</i> , 2011 , 474, 609-15	50.4	5210
383	The International HapMap Project. <i>Nature</i> , 2003 , 426, 789-96	50.4	5039
382	The genome sequence of <i>Drosophila melanogaster</i> . <i>Science</i> , 2000 , 287, 2185-95	33.3	4857
381	A haplotype map of the human genome. <i>Nature</i> , 2005 , 437, 1299-320	50.4	4818
380	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
379	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007 , 449, 851-61	50.4	3647
378	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. <i>Genome Research</i> , 2005 , 15, 1034-50	9.7	2643
377	Somatic mutations affect key pathways in lung adenocarcinoma. <i>Nature</i> , 2008 , 455, 1069-75	50.4	2280
376	A framework for human microbiome research. <i>Nature</i> , 2012 , 486, 215-21	50.4	1722
375	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
374	The complete genome of an individual by massively parallel DNA sequencing. <i>Nature</i> , 2008 , 452, 872-6	50.4	1424
373	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006 , 443, 931-49	50.4	1414

372	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007 , 449, 913-8	50.4	1367
371	Evolutionary and biomedical insights from the rhesus macaque genome. <i>Science</i> , 2007 , 316, 222-34	33.3	1072
370	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008 , 452, 949-55	50.4	1043
369	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2005 , 435, 43-57	50.4	1042
368	Genome remodelling in a basal-like breast cancer metastasis and xenograft. <i>Nature</i> , 2010 , 464, 999-1005	50.4	935
367	Characterizing the cancer genome in lung adenocarcinoma. <i>Nature</i> , 2007 , 450, 893-8	50.4	900
366	VarScan: variant detection in massively parallel sequencing of individual and pooled samples. <i>Bioinformatics</i> , 2009 , 25, 2283-5	7.2	890
365	The genome of the sea urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006 , 314, 941-52	33.3	886
364	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863
363	Enteric defensins are essential regulators of intestinal microbial ecology. <i>Nature Immunology</i> , 2010 , 11, 76-83	19.1	846
362	The DNA sequence of the human X chromosome. <i>Nature</i> , 2005 , 434, 325-37	50.4	822
361	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011 , 478, 476-82	50.4	802
360	Complete genome sequence of <i>Treponema pallidum</i> , the syphilis spirochete. <i>Science</i> , 1998 , 281, 375-88	33.3	756
359	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017 , 35, 725-731	44.5	648
358	Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. <i>Science</i> , 2009 , 324, 528-32	33.3	612
357	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013 , 493, 45-50	50.4	571
356	Direct selection of human genomic loci by microarray hybridization. <i>Nature Methods</i> , 2007 , 4, 903-5	21.6	543
355	A catalog of reference genomes from the human microbiome. <i>Science</i> , 2010 , 328, 994-9	33.3	508

354	Comparison of the respiratory microbiome in healthy nonsmokers and smokers. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013 , 187, 1067-75	10.2	501
353	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MiXs) specifications. <i>Nature Biotechnology</i> , 2011 , 29, 415-20	44.5	445
352	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011 , 469, 529-33	50.4	431
351	Comparative genome sequencing of <i>Drosophila pseudoobscura</i> : chromosomal, gene, and cis-element evolution. <i>Genome Research</i> , 2005 , 15, 1-18	9.7	410
350	Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. <i>Nature Communications</i> , 2019 , 10, 5029	17.4	406
349	Comparison of genomic DNAs of different enterococcal isolates using restriction endonucleases with infrequent recognition sites. <i>Journal of Clinical Microbiology</i> , 1990 , 28, 2059-63	9.7	400
348	<i>Propionibacterium acnes</i> strain populations in the human skin microbiome associated with acne. <i>Journal of Investigative Dermatology</i> , 2013 , 133, 2152-60	4.3	391
347	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018 , 3, 8-16	26.6	387
346	Pervasive genetic hitchhiking and clonal interference in forty evolving yeast populations. <i>Nature</i> , 2013 , 500, 571-4	50.4	380
345	Genomic approaches to studying the human microbiota. <i>Nature</i> , 2012 , 489, 250-6	50.4	342
344	Patterned progression of bacterial populations in the premature infant gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 12522-7	11.5	339
343	The genome architecture of the Collaborative Cross mouse genetic reference population. <i>Genetics</i> , 2012 , 190, 389-401	4	333
342	Initiation of general recombination catalyzed in vitro by the recA protein of <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1979 , 76, 2615-9	11.5	331
341	Genomics. Genome project standards in a new era of sequencing. <i>Science</i> , 2009 , 326, 236-7	33.3	326
340	ATP-dependent renaturation of DNA catalyzed by the recA protein of <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1979 , 76, 126-30	11.5	304
339	Modernizing reference genome assemblies. <i>PLoS Biology</i> , 2011 , 9, e1001091	9.7	294
338	Biogeography of the ecosystems of the healthy human body. <i>Genome Biology</i> , 2013 , 14, R1	18.3	285
337	Effects of <i>Enterococcus faecalis</i> fsp genes on production of gelatinase and a serine protease and virulence. <i>Infection and Immunity</i> , 2000 , 68, 2579-86	3.7	279

336	Short, interspersed repetitive DNA sequences in prokaryotic genomes. <i>Journal of Bacteriology</i> , 1992 , 174, 4525-9	3.5	274
335	Creating a honey bee consensus gene set. <i>Genome Biology</i> , 2007 , 8, R13	18.3	266
334	Finishing a whole-genome shotgun: release 3 of the <i>Drosophila melanogaster</i> euchromatic genome sequence. <i>Genome Biology</i> , 2002 , 3, RESEARCH0079	18.3	265
333	Genetic basis for in vivo daptomycin resistance in enterococci. <i>New England Journal of Medicine</i> , 2011 , 365, 892-900	59.2	252
332	The complete genome sequence of <i>Escherichia coli</i> DH10B: insights into the biology of a laboratory workhorse. <i>Journal of Bacteriology</i> , 2008 , 190, 2597-606	3.5	248
331	Gut bacteria dysbiosis and necrotising enterocolitis in very low birthweight infants: a prospective case-control study. <i>Lancet, The</i> , 2016 , 387, 1928-36	40	235
330	Metabolic and metagenomic outcomes from early-life pulsed antibiotic treatment. <i>Nature Communications</i> , 2015 , 6, 7486	17.4	232
329	recA protein-catalyzed strand assimilation: stimulation by <i>Escherichia coli</i> single-stranded DNA-binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1980 , 77, 857-61	11.5	225
328	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
327	Evaluation of 16S rDNA-based community profiling for human microbiome research. <i>PLoS ONE</i> , 2012 , 7, e39315	3.7	209
326	Validation of Metagenomic Next-Generation Sequencing Tests for Universal Pathogen Detection. <i>Archives of Pathology and Laboratory Medicine</i> , 2017 , 141, 776-786	5	204
325	Large scale variation in <i>Enterococcus faecalis</i> illustrated by the genome analysis of strain OG1RF. <i>Genome Biology</i> , 2008 , 9, R110	18.3	204
324	Phylogenomic analysis reveals bees and wasps (Hymenoptera) at the base of the radiation of Holometabolous insects. <i>Genome Research</i> , 2006 , 16, 1334-8	9.7	204
323	28-way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007 , 17, 1797-808	9.7	204
322	Characterization of fsr, a regulator controlling expression of gelatinase and serine protease in <i>Enterococcus faecalis</i> OG1RF. <i>Journal of Bacteriology</i> , 2001 , 183, 3372-82	3.5	200
321	Longitudinal multi-omics of host-microbe dynamics in prediabetes. <i>Nature</i> , 2019 , 569, 663-671	50.4	197
320	Prepublication data sharing. <i>Nature</i> , 2009 , 461, 168-70	50.4	197
319	Complete genome sequence of <i>Rickettsia typhi</i> and comparison with sequences of other rickettsiae. <i>Journal of Bacteriology</i> , 2004 , 186, 5842-55	3.5	192

318	Hypothesis testing and power calculations for taxonomic-based human microbiome data. <i>PLoS ONE</i> , 2012, 7, e52078	3.7	191
317	The genome sequence of the leaf-cutter ant <i>Atta cephalotes</i> reveals insights into its obligate symbiotic lifestyle. <i>PLoS Genetics</i> , 2011, 7, e1002007	6	191
316	An <i>Enterococcus faecalis</i> ABC homologue (Lsa) is required for the resistance of this species to clindamycin and quinupristin-dalfopristin. <i>Antimicrobial Agents and Chemotherapy</i> , 2002, 46, 1845-50	5.9	191
315	Subtle genetic changes enhance virulence of methicillin resistant and sensitive <i>Staphylococcus aureus</i> . <i>BMC Microbiology</i> , 2007, 7, 99	4.5	186
314	The real cost of sequencing: scaling computation to keep pace with data generation. <i>Genome Biology</i> , 2016, 17, 53	18.3	185
313	A longitudinal big data approach for precision health. <i>Nature Medicine</i> , 2019, 25, 792-804	50.5	183
312	The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 2014, 46, 850-7	36.3	179
311	Intermittent Fasting Confers Protection in CNS Autoimmunity by Altering the Gut Microbiota. <i>Cell Metabolism</i> , 2018, 27, 1222-1235.e6	24.6	178
310	Inflammatory bowel diseases phenotype, <i>C. difficile</i> and NOD2 genotype are associated with shifts in human ileum associated microbial composition. <i>PLoS ONE</i> , 2012, 7, e26284	3.7	178
309	Generation of restriction map of <i>Enterococcus faecalis</i> OG1 and investigation of growth requirements and regions encoding biosynthetic function. <i>Journal of Bacteriology</i> , 1993, 175, 5216-23	3.5	178
308	<i>Enterococcus faecalis</i> adhesin, ace, mediates attachment to extracellular matrix proteins collagen type IV and laminin as well as collagen type I. <i>Infection and Immunity</i> , 2000, 68, 5218-24	3.7	172
307	Characteristic male urine microbiomes associate with asymptomatic sexually transmitted infection. <i>PLoS ONE</i> , 2010, 5, e14116	3.7	172
306	Evidence for clonal spread of a single strain of beta-lactamase-producing <i>Enterococcus</i> (<i>Streptococcus</i>) faecalis to six hospitals in five states. <i>Journal of Infectious Diseases</i> , 1991, 163, 780-5	7	164
305	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-74	9.7	163
304	Ace is a collagen-binding MSCRAMM from <i>Enterococcus faecalis</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 26939-45	5.4	160
303	Genomic analysis of the nuclear receptor family: new insights into structure, regulation, and evolution from the rat genome. <i>Genome Research</i> , 2004, 14, 580-90	9.7	158
302	Making the Leap from Research Laboratory to Clinic: Challenges and Opportunities for Next-Generation Sequencing in Infectious Disease Diagnostics. <i>MBio</i> , 2015, 6, e01888-15	7.8	149
301	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014, 12, e1001920	9.7	146

300	Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development. <i>Genome Biology</i> , 2011 , 12, R81	18.3	142
299	Genome sequencing reveals widespread virulence gene exchange among human <i>Neisseria</i> species. <i>PLoS ONE</i> , 2010 , 5, e11835	3.7	141
298	Widespread colonization of the lung by <i>Tropheryma whipplei</i> in HIV infection. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013 , 187, 1110-7	10.2	140
297	Sequence analysis of the human virome in febrile and afebrile children. <i>PLoS ONE</i> , 2012 , 7, e27735	3.7	137
296	In vivo testing of an <i>Enterococcus faecalis</i> efaA mutant and use of efaA homologs for species identification. <i>FEMS Immunology and Medical Microbiology</i> , 1998 , 21, 323-31		134
295	Bacterial communities of the coronal sulcus and distal urethra of adolescent males. <i>PLoS ONE</i> , 2012 , 7, e36298	3.7	133
294	Clinical isolates of <i>Enterococcus faecium</i> exhibit strain-specific collagen binding mediated by Acm, a new member of the MSCRAMM family. <i>Molecular Microbiology</i> , 2003 , 47, 1733-47	4.1	132
293	A SNP discovery method to assess variant allele probability from next-generation resequencing data. <i>Genome Research</i> , 2010 , 20, 273-80	9.7	130
292	Metagenomic analysis of double-stranded DNA viruses in healthy adults. <i>BMC Biology</i> , 2014 , 12, 71	7.3	126
291	Sepsis from the gut: the enteric habitat of bacteria that cause late-onset neonatal bloodstream infections. <i>Clinical Infectious Diseases</i> , 2014 , 58, 1211-8	11.6	124
290	The Atlas genome assembly system. <i>Genome Research</i> , 2004 , 14, 721-32	9.7	119
289	Community characteristics of the gut microbiomes of competitive cyclists. <i>Microbiome</i> , 2017 , 5, 98	16.6	117
288	A dominant mutation in RPE65 identified by whole-exome sequencing causes retinitis pigmentosa with choroidal involvement. <i>European Journal of Human Genetics</i> , 2011 , 19, 1074-81	5.3	117
287	High-throughput whole-genome sequencing to dissect the epidemiology of <i>Acinetobacter baumannii</i> isolates from a hospital outbreak. <i>Journal of Hospital Infection</i> , 2010 , 75, 37-41	6.9	116
286	Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. <i>Cell Systems</i> , 2018 , 6, 157-170.e8	10.68	114
285	<i>Bos taurus</i> genome assembly. <i>BMC Genomics</i> , 2009 , 10, 180	4.5	114
284	Daptomycin-resistant <i>Enterococcus faecalis</i> diverts the antibiotic molecule from the division septum and remodels cell membrane phospholipids. <i>MBio</i> , 2013 , 4,	7.8	113
283	Transferable vancomycin resistance in a community-associated MRSA lineage. <i>New England Journal of Medicine</i> , 2014 , 370, 1524-31	59.2	110

282	Pan-genome and comparative genome analyses of propionibacterium acnes reveal its genomic diversity in the healthy and diseased human skin microbiome. <i>MBio</i> , 2013 , 4, e00003-13	7.8	110
281	Bacterial classifications derived from recA protein sequence comparisons. <i>Journal of Bacteriology</i> , 1995 , 177, 6881-93	3.5	109
280	Transposable lambda placMu bacteriophages for creating lacZ operon fusions and kanamycin resistance insertions in Escherichia coli. <i>Journal of Bacteriology</i> , 1985 , 162, 1092-9	3.5	108
279	Identification of functional variants for cleft lip with or without cleft palate in or near PAX7, FGFR2, and NOG by targeted sequencing of GWAS loci. <i>American Journal of Human Genetics</i> , 2015 , 96, 397-411	11	106
278	Complete genome sequence of Enterococcus faecium strain TX16 and comparative genomic analysis of Enterococcus faecium genomes. <i>BMC Microbiology</i> , 2012 , 12, 135	4.5	104
277	Longitudinal analysis of the premature infant intestinal microbiome prior to necrotizing enterocolitis: a case-control study. <i>PLoS ONE</i> , 2015 , 10, e0118632	3.7	103
276	Open reading frame expression vectors: a general method for antigen production in Escherichia coli using protein fusions to beta-galactosidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1983 , 80, 4432-6	11.5	100
275	Paradoxical DNA repair and peroxide resistance gene conservation in Bacillus pumilus SAFR-032. <i>PLoS ONE</i> , 2007 , 2, e928	3.7	100
274	A prospective microbiome-wide association study of food sensitization and food allergy in early childhood. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2018 , 73, 145-152	9.3	99
273	Characterization of emeA, a NorA homolog and multidrug resistance efflux pump, in Enterococcus faecalis. <i>Antimicrobial Agents and Chemotherapy</i> , 2001 , 45, 3574-9	5.9	98
272	Multicenter Comparison of Lung and Oral Microbiomes of HIV-infected and HIV-uninfected Individuals. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015 , 192, 1335-44	10.2	97
271	Emerging view of the human virome. <i>Translational Research</i> , 2012 , 160, 283-90	11	97
270	Dynamic changes in the subgingival microbiome and their potential for diagnosis and prognosis of periodontitis. <i>MBio</i> , 2015 , 6, e01926-14	7.8	95
269	Diversity of ace, a gene encoding a microbial surface component recognizing adhesive matrix molecules, from different strains of Enterococcus faecalis and evidence for production of ace during human infections. <i>Infection and Immunity</i> , 2000 , 68, 5210-7	3.7	95
268	The conjunctival microbiome in health and trachomatous disease: a case control study. <i>Genome Medicine</i> , 2014 , 6, 99	14.4	93
267	Systems biology of the vervet monkey. <i>ILAR Journal</i> , 2013 , 54, 122-43	1.7	93
266	Microbiome Signatures Associated With Steatohepatitis and Moderate to Severe Fibrosis in Children With Nonalcoholic Fatty Liver Disease. <i>Gastroenterology</i> , 2019 , 157, 1109-1122	13.3	92
265	Phylogenomics and the dynamic genome evolution of the genus Streptococcus. <i>Genome Biology and Evolution</i> , 2014 , 6, 741-53	3.9	91

264	Macrolide treatment failure in a case of secondary syphilis: a novel A2059G mutation in the 23S rRNA gene of <i>Treponema pallidum</i> subsp. <i>pallidum</i> . <i>Journal of Medical Microbiology</i> , 2009 , 58, 832-836	3.2	91
263	Resistance to Ceftazidime-Avibactam Is Due to Transposition of KPC in a Porin-Deficient Strain of <i>Klebsiella pneumoniae</i> with Increased Efflux Activity. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	91
262	Lambda placMu: a transposable derivative of bacteriophage lambda for creating lacZ protein fusions in a single step. <i>Journal of Bacteriology</i> , 1984 , 158, 1084-93	3.5	91
261	Whole-genome analyses of <i>Enterococcus faecium</i> isolates with diverse daptomycin MICs. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 4527-34	5.9	90
260	Evolutionary Genomics of <i>Salmonella enterica</i> Subspecies. <i>MBio</i> , 2013 , 4,	7.8	90
259	Factors influencing the infant gut microbiome at age 3-6 months: Findings from the ethnically diverse Vitamin D Antenatal Asthma Reduction Trial (VDAART). <i>Journal of Allergy and Clinical Immunology</i> , 2017 , 139, 482-491.e14	11.5	88
258	Whole genome sequences of three <i>Treponema pallidum</i> ssp. <i>pertenue</i> strains: yaws and syphilis treponemes differ in less than 0.2% of the genome sequence. <i>PLoS Neglected Tropical Diseases</i> , 2012 , 6, e1471	4.8	86
257	The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). <i>Genome Research</i> , 2015 , 25, 1921-33	9.7	84
256	Exploration of bacterial community classes in major human habitats. <i>Genome Biology</i> , 2014 , 15, R66	18.3	83
255	A novel <i>Treponema pallidum</i> antigen, TP0136, is an outer membrane protein that binds human fibronectin. <i>Infection and Immunity</i> , 2008 , 76, 1848-57	3.7	83
254	DNA sequence of the <i>Pasteurella haemolytica</i> leukotoxin gene cluster. <i>DNA and Cell Biology</i> , 1989 , 8, 15-28		82
253	Chromosome rearrangement and diversification of <i>Francisella tularensis</i> revealed by the type B (OSU18) genome sequence. <i>Journal of Bacteriology</i> , 2006 , 188, 6977-85	3.5	81
252	A cluster of genes involved in polysaccharide biosynthesis from <i>Enterococcus faecalis</i> OG1RF. <i>Infection and Immunity</i> , 1998 , 66, 4313-23	3.7	81
251	Molecular characterization of a widespread, pathogenic, and antibiotic resistance-receptive <i>Enterococcus faecalis</i> lineage and dissemination of its putative pathogenicity island. <i>Journal of Bacteriology</i> , 2005 , 187, 5709-18	3.5	80
250	Analysis of a gene cluster of <i>Enterococcus faecalis</i> involved in polysaccharide biosynthesis. <i>Infection and Immunity</i> , 2000 , 68, 815-23	3.7	80
249	Genome sequences of the honey bee pathogens <i>Paenibacillus larvae</i> and <i>Ascospaera apis</i> . <i>Insect Molecular Biology</i> , 2006 , 15, 715-8	3.4	79
248	Identification and phenotypic characterization of a second collagen adhesin, Scm, and genome-based identification and analysis of 13 other predicted MSCRAMMs, including four distinct pilus loci, in <i>Enterococcus faecium</i> . <i>Microbiology (United Kingdom)</i> , 2008 , 154, 3199-3211	2.9	78
247	Identification of disease-causing mutations in autosomal dominant retinitis pigmentosa (adRP) using next-generation DNA sequencing 2011 , 52, 494-503		77

246	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. <i>Nature Genetics</i> , 2017 , 49, 1705-1713	36.3	76
245	Genetic diversity in <i>Treponema pallidum</i> : implications for pathogenesis, evolution and molecular diagnostics of syphilis and yaws. <i>Infection, Genetics and Evolution</i> , 2012 , 12, 191-202	4.5	76
244	Whole-genome analysis of a daptomycin-susceptible <i>enterococcus faecium</i> strain and its daptomycin-resistant variant arising during therapy. <i>Antimicrobial Agents and Chemotherapy</i> , 2013 , 57, 261-8	5.9	76
243	Plant-associated symbiotic <i>Burkholderia</i> species lack hallmark strategies required in mammalian pathogenesis. <i>PLoS ONE</i> , 2014 , 9, e83779	3.7	76
242	<i>Leucoagaricus gongylophorus</i> produces diverse enzymes for the degradation of recalcitrant plant polymers in leaf-cutter ant fungus gardens. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 3770-8	4.8	75
241	Parallel Epidemics of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 Infection in North and South America. <i>Journal of Infectious Diseases</i> , 2015 , 212, 1874-82	7	75
240	Novel bacterial taxa in the human microbiome. <i>PLoS ONE</i> , 2012 , 7, e35294	3.7	75
239	Measurement of in vivo expression of the <i>recA</i> gene of <i>Escherichia coli</i> by using <i>lacZ</i> gene fusions. <i>Journal of Bacteriology</i> , 1984 , 160, 112-21	3.5	74
238	The genome sequence of <i>Mannheimia haemolytica</i> A1: insights into virulence, natural competence, and <i>Pasteurellaceae</i> phylogeny. <i>Journal of Bacteriology</i> , 2006 , 188, 7257-66	3.5	73
237	Symbiotic organs shaped by distinct modes of genome evolution in cephalopods. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 3030-3035	11.5	72
236	Evidence that the enterococcal polysaccharide antigen gene (epa) cluster is widespread in <i>Enterococcus faecalis</i> and influences resistance to phagocytic killing of <i>E. faecalis</i> . <i>Infection and Immunity</i> , 2002 , 70, 2010-5	3.7	70
235	Repetitive sequence-based PCR versus pulsed-field gel electrophoresis for typing of <i>Enterococcus faecalis</i> at the subspecies level. <i>Journal of Clinical Microbiology</i> , 1998 , 36, 211-5	9.7	70
234	NIH working group report-using genomic information to guide weight management: From universal to precision treatment. <i>Obesity</i> , 2016 , 24, 14-22	8	70
233	TIGRA: a targeted iterative graph routing assembler for breakpoint assembly. <i>Genome Research</i> , 2014 , 24, 310-7	9.7	69
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