

George M Weinstock

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.

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	Defining the microbiome of the head and neck: A contemporary review. <i>American Journal of Otolaryngology - Head and Neck Medicine and Surgery</i> , 2022 , 43, 103224	2.8	0
388	Murine Model for Measuring Effects of Humanized-Dosing of Antibiotics on the Gut Microbiome.. <i>Frontiers in Microbiology</i> , 2022 , 13, 813849	5.7	
387	Association of gut microbiota and environment in children with AD, comparison of three cohorts of children. <i>Clinical and Experimental Allergy</i> , 2021 ,	4.1	0
386	Circadian rhythms and the gut microbiome synchronize the host's metabolic response to diet. <i>Cell Metabolism</i> , 2021 , 33, 873-887	24.6	7
385	Host genetic control of gut microbiome composition. <i>Mammalian Genome</i> , 2021 , 32, 263-281	3.2	5
384	The Gut Microbiome and Substance Use Disorder. <i>Frontiers in Neuroscience</i> , 2021 , 15, 725500	5.1	3
383	Alterations in subgingival microbiota during full-fixed appliance orthodontic treatment-A prospective study. <i>Orthodontics and Craniofacial Research</i> , 2021 ,	3	3
382	Bifidobacterium bifidum strains synergize with immune checkpoint inhibitors to reduce tumour burden in mice. <i>Nature Microbiology</i> , 2021 , 6, 277-288	26.6	29
381	Longitudinal Analysis of Serum Cytokine Levels and Gut Microbial Abundance Links IL-17/IL-22 With and Insulin Sensitivity in Humans. <i>Diabetes</i> , 2020 , 69, 1833-1842	0.9	4
380	Approaches for integrating heterogeneous RNA-seq data reveal cross-talk between microbes and genes in asthmatic patients. <i>Genome Biology</i> , 2020 , 21, 150	18.3	0
379	A Microbe Associated with Sleep Revealed by a Novel Systems Genetic Analysis of the Microbiome in Collaborative Cross Mice. <i>Genetics</i> , 2020 , 214, 719-733	4	8
378	Improving Characterization of Understudied Human Microbiomes Using Targeted Phylogenetics. <i>MSystems</i> , 2020 , 5,	7.6	1
377	Colon Cancer Prevention with Walnuts: A Longitudinal Study in Mice from the Perspective of a Gut Enterotype-like Cluster. <i>Cancer Prevention Research</i> , 2020 , 13, 15-24	3.2	1
376	Genetic Basis of Aerobically Supported Voluntary Exercise: Results from a Selection Experiment with House Mice. <i>Genetics</i> , 2020 , 216, 781-804	4	6
375	Differences in Gut Microbiome in Hospitalized Immunocompetent vs. Immunocompromised Children, Including Those With Sickle Cell Disease. <i>Frontiers in Pediatrics</i> , 2020 , 8, 583446	3.4	6
374	Deciphering functional redundancy in the human microbiome. <i>Nature Communications</i> , 2020 , 11, 6217	17.4	32
373	Supraglottic Lung Microbiome Taxa Are Associated with Pulmonary Abnormalities in an HIV Longitudinal Cohort. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020 , 202, 1727-1731	10.2	1

372	The Skin Microbiome of Inverse Psoriasis 2020 , 203-215		
371	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
370	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
369	Toward unrestricted use of public genomic data. <i>Science</i> , 2019 , 363, 350-352	33.3	25
368	The Genome of C57BL/6J "Eve", the Mother of the Laboratory Mouse Genome Reference Strain. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 1795-1805	3.2	23
367	Longitudinal multi-omics of host-microbe dynamics in prediabetes. <i>Nature</i> , 2019 , 569, 663-671	50.4	197
366	A longitudinal big data approach for precision health. <i>Nature Medicine</i> , 2019 , 25, 792-804	50.5	183
365	Consent insufficient for data release-Response. <i>Science</i> , 2019 , 364, 446	33.3	4
364	Association of the Infant Gut Microbiome With Early Childhood Neurodevelopmental Outcomes: An Ancillary Study to the VDAART Randomized Clinical Trial. <i>JAMA Network Open</i> , 2019 , 2, e190905	10.4	32
363	Rapid growth is a dominant predictor of hepcidin suppression and declining ferritin in Gambian infants. <i>Haematologica</i> , 2019 , 104, 1542-1553	6.6	16
362	Oral Microbiome in HIV-Infected Women: Shifts in the Abundance of Pathogenic and Beneficial Bacteria Are Associated with Aging, HIV Load, CD4 Count, and Antiretroviral Therapy. <i>AIDS Research and Human Retroviruses</i> , 2019 , 35, 276-286	1.6	16
361	Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. <i>Nature Communications</i> , 2019 , 10, 5029	17.4	406
360	Characterization of Mucosal Dysbiosis of Early Colonic Neoplasia. <i>Npj Precision Oncology</i> , 2019 , 3, 29	9.8	8
359	New statistical method identifies cytokines that distinguish stool microbiomes. <i>Scientific Reports</i> , 2019 , 9, 20082	4.9	2
358	The upper-airway microbiota and loss of asthma control among asthmatic children. <i>Nature Communications</i> , 2019 , 10, 5714	17.4	49
357	Effects of diet on the childhood gut microbiome and its implications for atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2019 , 143, 1636-1637.e5	11.5	19
356	MSC: a metagenomic sequence classification algorithm. <i>Bioinformatics</i> , 2019 , 35, 2932-2940	7.2	3
355	Meta-analysis of the lung microbiota in pulmonary tuberculosis. <i>Tuberculosis</i> , 2018 , 109, 102-108	2.6	33

354	Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. <i>Cell Systems</i> , 2018 , 6, 157-170.e8	10.68	114
353	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018 , 3, 8-16	26.6	387
352	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
351	Intermittent Fasting Confers Protection in CNS Autoimmunity by Altering the Gut Microbiota. <i>Cell Metabolism</i> , 2018 , 27, 1222-1235.e6	24.6	178
350	Genome Sequence of Acetomicrobium hydrogeniformans OS1. <i>Genome Announcements</i> , 2018 , 6,		3
349	Diet during Pregnancy and Infancy and the Infant Intestinal Microbiome. <i>Journal of Pediatrics</i> , 2018 , 203, 47-54.e4	3.6	36
348	Ceftaroline-Resistant, Daptomycin-Tolerant, and Heterogeneous Vancomycin-Intermediate Methicillin-Resistant Staphylococcus aureus Causing Infective Endocarditis. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	17
347	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
346	Similar Bacterial Signatures in Intestinal Tissues, Milk, and Dendritic Cells of Lactating Mice Suggest a Possible Entero-Mammary Pathway. <i>Gastroenterology</i> , 2017 , 152, S172	13.3	3
345	Isolation of Methicillin-resistant Staphylococcus aureus and Multidrug-resistant Elizabethkingia meningoseptica From Neonates Within Minutes of Birth. <i>Pediatric Infectious Disease Journal</i> , 2017 , 36, 123-124	3.4	3
344	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. <i>Nature Genetics</i> , 2017 , 49, 1705-1713	36.3	76
343	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. <i>Nature Genetics</i> , 2017 , 49, 1714-1721	36.3	43
342	Rapid replacement by non-vaccine pneumococcal serotypes may mitigate the impact of the pneumococcal conjugate vaccine on nasopharyngeal bacterial ecology. <i>Scientific Reports</i> , 2017 , 7, 8127	4.9	35
341	Community characteristics of the gut microbiomes of competitive cyclists. <i>Microbiome</i> , 2017 , 5, 98	16.6	117
340	An Analysis of the Epidemic of Klebsiella pneumoniae Carbapenemase-Producing K. pneumoniae: Convergence of Two Evolutionary Mechanisms Creates the "Perfect Storm". <i>Journal of Infectious Diseases</i> , 2017 , 217, 82-92	7	38
339	A Prospective Cohort Multicenter Study of Molecular Epidemiology and Phylogenomics of Staphylococcus aureus Bacteremia in Nine Latin American Countries. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	45
338	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
337	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

336	Lung microbiome in human immunodeficiency virus infection. <i>Translational Research</i> , 2017 , 179, 97-107	11	21
335	Impact of Age, Caloric Restriction, and Influenza Infection on Mouse Gut Microbiome: An Exploratory Study of the Role of Age-Related Microbiome Changes on Influenza Responses. <i>Frontiers in Immunology</i> , 2017 , 8, 1164	8.4	46
334	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
333	Symbiotic <i>Burkholderia</i> Species Show Diverse Arrangements of <i>nif/fix</i> and <i>nod</i> Genes and Lack Typical High-Affinity Cytochrome <i>cbb3</i> Oxidase Genes. <i>Molecular Plant-Microbe Interactions</i> , 2016 , 29, 609-19	3.6	38
332	Genome Sequences of 15 <i>Gardnerella vaginalis</i> Strains Isolated from the Vaginas of Women with and without Bacterial Vaginosis. <i>Genome Announcements</i> , 2016 , 4,		5
331	Effects of Walnut Consumption on Colon Carcinogenesis and Microbial Community Structure. <i>Cancer Prevention Research</i> , 2016 , 9, 692-703	3.2	42
330	Metagenomic Approach for Identification of the Pathogens Associated with Diarrhea in Stool Specimens. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 368-75	9.7	60
329	R2d2 Drives Selfish Sweeps in the House Mouse. <i>Molecular Biology and Evolution</i> , 2016 , 33, 1381-95	8.3	39
328	The real cost of sequencing: scaling computation to keep pace with data generation. <i>Genome Biology</i> , 2016 , 17, 53	18.3	185
327	Effect of Advanced HIV Infection on the Respiratory Microbiome. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016 , 194, 226-35	10.2	61
326	Gut bacteria dysbiosis and necrotising enterocolitis in very low birthweight infants: a prospective case-control study. <i>Lancet, The</i> , 2016 , 387, 1928-36	4.0	235
325	Identification of a Novel Gene on 10q22.1 Causing Autosomal Dominant Retinitis Pigmentosa (adRP). <i>Advances in Experimental Medicine and Biology</i> , 2016 , 854, 193-200	3.6	6
324	Household air pollution and the lung microbiome of healthy adults in Malawi: a cross-sectional study. <i>BMC Microbiology</i> , 2016 , 16, 182	4.5	33
323	Longitudinal Prediction of the Infant Gut Microbiome with Dynamic Bayesian Networks. <i>Scientific Reports</i> , 2016 , 6, 20359	4.9	36
322	Characterization of the bacterial and fungal microbiome in indoor dust and outdoor air samples: a pilot study. <i>Environmental Sciences: Processes and Impacts</i> , 2016 , 18, 713-24	4.3	46
321	The importance of the microbiome in epidemiologic research. <i>Annals of Epidemiology</i> , 2016 , 26, 301-5	6.4	27
320	Transmission of <i>Staphylococcus aureus</i> from Humans to Green Monkeys in The Gambia as Revealed by Whole-Genome Sequencing. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 5910-7	4.8	22
319	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

318	Selection of models for the analysis of risk-factor trees: leveraging biological knowledge to mine large sets of risk factors with application to microbiome data. <i>Bioinformatics</i> , 2015 , 31, 1607-13	7.2	11
317	Small bowel resection induces long-term changes in the enteric microbiota of mice. <i>Journal of Gastrointestinal Surgery</i> , 2015 , 19, 56-64; discussion 64	3.3	33
316	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
315	A multi-megabase copy number gain causes maternal transmission ratio distortion on mouse chromosome 2. <i>PLoS Genetics</i> , 2015 , 11, e1004850	6	46
314	Metabolic and metagenomic outcomes from early-life pulsed antibiotic treatment. <i>Nature Communications</i> , 2015 , 6, 7486	17.4	232
313	Emergence of Rotavirus G12P[8] in St. Louis During the 2012-2013 Rotavirus Season. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2015 , 4, e84-9	4.8	6
312	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
311	Sequencing strategies and characterization of 721 vervet monkey genomes for future genetic analyses of medically relevant traits. <i>BMC Biology</i> , 2015 , 13, 41	7.3	36
310	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
309	Extreme Sensory Complexity Encoded in the 10-Megabase Draft Genome Sequence of the Chromatically Acclimating Cyanobacterium <i>Tolypothrix</i> sp. PCC 7601. <i>Genome Announcements</i> , 2015 , 3,		23
308	The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). <i>Genome Research</i> , 2015 , 25, 1921-33	9.7	84
307	The transcriptional profile of coronary arteritis in Kawasaki disease. <i>BMC Genomics</i> , 2015 , 16, 1076	4.5	46
306	Methicillin-Susceptible, Vancomycin-Resistant <i>Staphylococcus aureus</i> , Brazil. <i>Emerging Infectious Diseases</i> , 2015 , 21, 1844-8	10.2	28
305	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
304	Identification of Candidate Adherent-Invasive <i>E. coli</i> Signature Transcripts by Genomic/Transcriptomic Analysis. <i>PLoS ONE</i> , 2015 , 10, e0130902	3.7	17
303	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
302	Discriminatory Indices of Typing Methods for Epidemiologic Analysis of Contemporary <i>Staphylococcus aureus</i> Strains. <i>Medicine (United States)</i> , 2015 , 94, e1534	1.8	23
301	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

300	Hypothesis Testing of Metagenomic Data 2015 , 81-96		7
299	A Retrospective Study on Genetic Heterogeneity within Treponema Strains: Subpopulations Are Genetically Distinct in a Limited Number of Positions. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0004110	4.8	15
298	mBLAST: Keeping up with the sequencing explosion for (meta)genome analysis. <i>Journal of Data Mining in Genomics & Proteomics</i> , 2015 , 4,		15
297	Exome-based mapping and variant prioritization for inherited Mendelian disorders. <i>American Journal of Human Genetics</i> , 2014 , 94, 373-84	11	36
296	Transferable vancomycin resistance in a community-associated MRSA lineage. <i>New England Journal of Medicine</i> , 2014 , 370, 1524-31	59.2	110
295	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
294	The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 2014 , 46, 850-7	36.3	179
293	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
292	Exploration of bacterial community classes in major human habitats. <i>Genome Biology</i> , 2014 , 15, R66	18.3	83
291	Whole-genome analyses of Enterococcus faecium isolates with diverse daptomycin MICs. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 4527-34	5.9	90
290	Comparison of Whole and Acellular Bronchoalveolar Lavage to Oral Wash Microbiomes. Should Acellular Bronchoalveolar Lavage Be the Standard?. <i>Annals of the American Thoracic Society</i> , 2014 , 11, S72-S73	4.7	5
289	Inactivation of SAM-methyltransferase is the mechanism of attenuation of a historic louse borne typhus vaccine strain. <i>PLoS ONE</i> , 2014 , 9, e113285	3.7	7
288	Metagenomic analysis of double-stranded DNA viruses in healthy adults. <i>BMC Biology</i> , 2014 , 12, 71	7.3	126
287	Microbial sequencing to improve individual and population health. <i>Genome Medicine</i> , 2014 , 6, 103	14.4	3
286	The conjunctival microbiome in health and trachomatous disease: a case control study. <i>Genome Medicine</i> , 2014 , 6, 99	14.4	93
285	A dominant mutation in hexokinase 1 (HK1) causes retinitis pigmentosa 2014 , 55, 7147-58		36
284	Whole genome sequence of the Treponema pallidum subsp. endemicum strain Bosnia A: the genome is related to yaws treponemes but contains few loci similar to syphilis treponemes. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e3261	4.8	39
283	CcpA is important for growth and virulence of Enterococcus faecium. <i>Infection and Immunity</i> , 2014 , 82, 3580-7	3.7	16

282	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
281	Genomic epidemiology of Salmonella enterica serotype Enteritidis based on population structure of prevalent lineages. <i>Emerging Infectious Diseases</i> , 2014 , 20, 1481-9	10.2	62
280	HCoDES reveals chromosomal DNA end structures with single-nucleotide resolution. <i>Molecular Cell</i> , 2014 , 56, 808-18	17.6	23
279	Phenotypic and genotypic analysis of Clostridium difficile isolates: a single-center study. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 4260-6	9.7	31
278	Characterization of mutations in the PAS domain of the EvgS sensor kinase selected by laboratory evolution for acid resistance in Escherichia coli. <i>Molecular Microbiology</i> , 2014 , 93, 911-27	4.1	32
277	Correction for La Rosa et al., 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, 17336-17336	11.5	2
276	High-resolution genetic mapping in the diversity outbred mouse population identifies Apobec1 as a candidate gene for atherosclerosis. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 2353-63	3.2	34
275	TIGRA: a targeted iterative graph routing assembler for breakpoint assembly. <i>Genome Research</i> , 2014 , 24, 310-7	9.7	69
274	Phylogenomics and the dynamic genome evolution of the genus Streptococcus. <i>Genome Biology and Evolution</i> , 2014 , 6, 741-53	3.9	91
273	The relationships between environmental bacterial exposure, airway bacterial colonization, and asthma. <i>Current Opinion in Allergy and Clinical Immunology</i> , 2014 , 14, 137-42	3.3	32
272	Plant-associated symbiotic Burkholderia species lack hallmark strategies required in mammalian pathogenesis. <i>PLoS ONE</i> , 2014 , 9, e83779	3.7	76
271	High-resolution quantification of hepatitis C virus genome-wide mutation load and its correlation with the outcome of peginterferon-alpha2a and ribavirin combination therapy. <i>PLoS ONE</i> , 2014 , 9, e100131	3.7	15
270	Application of next-generation sequencing to identify genes and mutations causing autosomal dominant retinitis pigmentosa (adRP). <i>Advances in Experimental Medicine and Biology</i> , 2014 , 801, 123-9	3.6	33
269	Biogeography of the ecosystems of the healthy human body. <i>Genome Biology</i> , 2013 , 14, R1	18.3	285
268	Pervasive genetic hitchhiking and clonal interference in forty evolving yeast populations. <i>Nature</i> , 2013 , 500, 571-4	50.4	380
267	Coverage theories for metagenomic DNA sequencing based on a generalization of Stevens' theorem. <i>Journal of Mathematical Biology</i> , 2013 , 67, 1141-61	2	24
266	Sixty years of genome biology. <i>Genome Biology</i> , 2013 , 14, 113	18.3	4
265	Leucoagaricus gongylophorus 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

264	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013 , 493, 45-50	50.4	571
263	Use of bronchoalveolar lavage to assess the respiratory microbiome: signal in the noise. <i>Lancet Respiratory Medicine</i> , 2013 , 1, 354-6	35.1	33
262	Propionibacterium acnes strain populations in the human skin microbiome associated with acne. <i>Journal of Investigative Dermatology</i> , 2013 , 133, 2152-60	4.3	391
261	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
260	Nodulation and effective nitrogen fixation of <i>Macroptilium atropurpureum</i> (siratro) by <i>Burkholderia tuberum</i> , a nodulating and plant growth promoting beta-proteobacterium, are influenced by environmental factors. <i>Plant and Soil</i> , 2013 , 369, 543-562	4.2	43
259	Virome genomics: a tool for defining the human virome. <i>Current Opinion in Microbiology</i> , 2013 , 16, 479-84	7.9	30
258	Evolutionary Genomics of <i>Salmonella enterica</i> Subspecies. <i>MBio</i> , 2013 , 4,	7.8	90
257	Pan-genome and comparative genome analyses of <i>propionibacterium acnes</i> reveal its genomic diversity in the healthy and diseased human skin microbiome. <i>MBio</i> , 2013 , 4, e00003-13	7.8	110
256	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
255	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
254	Whole genome sequence of the <i>Treponema Fribourg-Blanc</i> : unspecified simian isolate is highly similar to the yaws subspecies. <i>PLoS Neglected Tropical Diseases</i> , 2013 , 7, e2172	4.8	45
253	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
252	Quantitation and composition of cutaneous microbiota in diabetic and nondiabetic men. <i>Journal of Infectious Diseases</i> , 2013 , 207, 1105-14	7	63
251	A novel intronic single nucleotide polymorphism in the myosin heavy polypeptide 4 gene is responsible for the mini-muscle phenotype characterized by major reduction in hind-limb muscle mass in mice. <i>Genetics</i> , 2013 , 195, 1385-95	4	28
250	Systems biology of the vervet monkey. <i>ILAR Journal</i> , 2013 , 54, 122-43	1.7	93
249	Structure of <i>rrn</i> operons in pathogenic non-cultivable <i>treponemes</i> : sequence but not genomic position of intergenic spacers correlates with classification of <i>Treponema pallidum</i> and <i>Treponema paraluis-cuniculi</i> strains. <i>Journal of Medical Microbiology</i> , 2013 , 62, 196-207	3.2	25
248	Precise dissection of an <i>Escherichia coli</i> O157:H7 outbreak by single nucleotide polymorphism analysis. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 3950-4	9.7	32
247	Evolutionary Genomics of <i>Salmonella enterica</i> Subspecies. <i>MBio</i> , 2013 , 4,	7.8	28

246	Resequencing of <i>Treponema pallidum</i> ssp. <i>pallidum</i> strains Nichols and SS14: correction of sequencing errors resulted in increased separation of syphilis treponeme subclusters. <i>PLoS ONE</i> , 2013 , 8, e74319	3.7	53
245	Candidate genes that may be responsible for the unusual resistances exhibited by <i>Bacillus pumilus</i> SAFR-032 spores. <i>PLoS ONE</i> , 2013 , 8, e66012	3.7	29
244	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
243	Revised sequence and annotation of the <i>Rhodobacter sphaeroides</i> 2.4.1 genome. <i>Journal of Bacteriology</i> , 2012 , 194, 7016-7	3.5	32
242	Identification of novel and cross-species seroreactive proteins from <i>Bacillus anthracis</i> using a ligation-independent cloning-based, SOS-inducible expression system. <i>Microbial Pathogenesis</i> , 2012 , 53, 250-8	3.8	1
241	Genomic approaches to studying the human microbiota. <i>Nature</i> , 2012 , 489, 250-6	50.4	342
240	Detection of viruses in young children with fever without an apparent source. <i>Pediatrics</i> , 2012 , 130, e1455-62	7.4	65
239	Emerging view of the human virome. <i>Translational Research</i> , 2012 , 160, 283-90	11	97
238	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012 , 486, 207-14	50.4	6938
237	A framework for human microbiome research. <i>Nature</i> , 2012 , 486, 215-21	50.4	1722
236	Complete genome sequence of <i>Enterococcus faecium</i> strain TX16 and comparative genomic analysis of <i>Enterococcus faecium</i> genomes. <i>BMC Microbiology</i> , 2012 , 12, 135	4.5	104
235	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012 , 491, 56-65	50.4	6049
234	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
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