

Jonathan A Eisen

List of Publications by Citations

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411
papers

56,717
citations

92
h-index

235
g-index

529
ext. papers

65,657
ext. citations

11.9
avg, IF

7.6
L-index

#	Paper	IF	Citations
411	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000 , 408, 796-815	50.4	7262
410	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002 , 419, 498-511	50.4	3336
409	Environmental genome shotgun sequencing of the Sargasso Sea. <i>Science</i> , 2004 , 304, 66-74	33.3	3231
408	DNA sequence of both chromosomes of the cholera pathogen <i>Vibrio cholerae</i> . <i>Nature</i> , 2000 , 406, 477-83	50.4	1495
407	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013 , 499, 431-7	50.4	1484
406	The Sorcerer II Global Ocean Sampling expedition: northwest Atlantic through eastern tropical Pacific. <i>PLoS Biology</i> , 2007 , 5, e77	9.7	1476
405	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
404	Structure, variation, and assembly of the root-associated microbiomes of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E911-20	11.5	1206
403	Complete genome sequence of a virulent isolate of <i>Streptococcus pneumoniae</i> . <i>Science</i> , 2001 , 293, 498-506	50.6	1112
402	Complete genome sequence and comparative analysis of the metabolically versatile <i>Pseudomonas putida</i> KT2440. <i>Environmental Microbiology</i> , 2002 , 4, 799-808	5.2	1069
401	Complete genome sequence of <i>Neisseria meningitidis</i> serogroup B strain MC58. <i>Science</i> , 2000 , 287, 1809-15	33.3	986
400	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009 , 462, 1056-60	50.4	803
399	Genome sequence of the radioresistant bacterium <i>Deinococcus radiodurans</i> R1. <i>Science</i> , 1999 , 286, 1571-3	33.3	760
398	Role of mobile DNA in the evolution of vancomycin-resistant <i>Enterococcus faecalis</i> . <i>Science</i> , 2003 , 299, 2071-4	33.3	725
397	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
396	Genome sequence of the dissimilatory metal ion-reducing bacterium <i>Shewanella oneidensis</i> . <i>Nature Biotechnology</i> , 2002 , 20, 1118-23	44.5	680
395	The genome of the natural genetic engineer <i>Agrobacterium tumefaciens</i> C58. <i>Science</i> , 2001 , 294, 2317-23	33.3	659

394	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
393	The Sorcerer II Global Ocean Sampling expedition: expanding the universe of protein families. <i>PLoS Biology</i> , 2007 , 5, e16	9.7	638
392	Evolution of the SNF2 family of proteins: subfamilies with distinct sequences and functions. <i>Nucleic Acids Research</i> , 1995 , 23, 2715-23	20.1	620
391	Sequence and analysis of chromosome 2 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 1999 , 402, 761-8	50.4	619
390	Phylogenomics of the reproductive parasite <i>Wolbachia pipientis</i> wMel: a streamlined genome overrun by mobile genetic elements. <i>PLoS Biology</i> , 2004 , 2, E69	9.7	613
389	Genome of <i>Geobacter sulfurreducens</i> : metal reduction in subsurface environments. <i>Science</i> , 2003 , 302, 1967-9	33.3	573
388	Whole-genome comparison of <i>Mycobacterium tuberculosis</i> clinical and laboratory strains. <i>Journal of Bacteriology</i> , 2002 , 184, 5479-90	3.5	569
387	Improving the coverage of the cyanobacterial phylum using diversity-driven genome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 1053-8	11.5	566
386	Macronuclear genome sequence of the ciliate <i>Tetrahymena thermophila</i> , a model eukaryote. <i>PLoS Biology</i> , 2006 , 4, e286	9.7	544
385	Drivers of bacterial beta-diversity depend on spatial scale. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 7850-4	11.5	491
384	Patellamide A and C biosynthesis by a microcin-like pathway in <i>Prochloron didemni</i> , the cyanobacterial symbiont of <i>Lissoclinum patella</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 7315-20	11.5	486
383	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
382	Phylogenomics: improving functional predictions for uncharacterized genes by evolutionary analysis. <i>Genome Research</i> , 1998 , 8, 163-7	9.7	468
381	Bacterial communities of diverse <i>Drosophila</i> species: ecological context of a host-microbe model system. <i>PLoS Genetics</i> , 2011 , 7, e1002272	6	465
380	Complete genome sequence of <i>Caulobacter crescentus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 4136-41	11.5	436
379	PhyloSift: phylogenetic analysis of genomes and metagenomes. <i>PeerJ</i> , 2014 , 2, e243	3.1	431
378	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
377	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

376	Research priorities for harnessing plant microbiomes in sustainable agriculture. <i>PLoS Biology</i> , 2017 , 15, e2001793	9.7	402
375	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
374	<i>Acidithiobacillus ferrooxidans</i> metabolism: from genome sequence to industrial applications. <i>BMC Genomics</i> , 2008 , 9, 597	4.5	370
373	A simple, fast, and accurate method of phylogenomic inference. <i>Genome Biology</i> , 2008 , 9, R151	18.3	369
372	Comparative genomics of emerging human ehrlichiosis agents. <i>PLoS Genetics</i> , 2006 , 2, e21	6	363
371	Genome sequence of the PCE-dechlorinating bacterium <i>Dehalococcoides ethenogenes</i> . <i>Science</i> , 2005 , 307, 105-8	33.3	363
370	Evolution of sensory complexity recorded in a myxobacterial genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 15200-5	11.5	355
369	Genome sequence of <i>Silicibacter pomeroyi</i> reveals adaptations to the marine environment. <i>Nature</i> , 2004 , 432, 910-3	50.4	345
368	A phylogenomic study of DNA repair genes, proteins, and processes. <i>Mutation Research DNA Repair</i> , 1999 , 435, 171-213		342
367	Second gene for gonadotropin-releasing hormone in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 305-9	11.5	335
366	Unsuspected diversity among marine aerobic anoxygenic phototrophs. <i>Nature</i> , 2002 , 415, 630-3	50.4	333
365	An integrated pipeline for de novo assembly of microbial genomes. <i>PLoS ONE</i> , 2012 , 7, e42304	3.7	330
364	Metabolic complementarity and genomics of the dual bacterial symbiosis of sharpshooters. <i>PLoS Biology</i> , 2006 , 4, e188	9.7	327
363	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
362	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
361	Incorporating 16S gene copy number information improves estimates of microbial diversity and abundance. <i>PLoS Computational Biology</i> , 2012 , 8, e1002743	5	303
360	TIGRFAMs: a protein family resource for the functional identification of proteins. <i>Nucleic Acids Research</i> , 2001 , 29, 41-3	20.1	295
359	Assembling the marine metagenome, one cell at a time. <i>PLoS ONE</i> , 2009 , 4, e5299	3.7	270

358	Phylogenomics: intersection of evolution and genomics. <i>Science</i> , 2003 , 300, 1706-7	33.3	244
357	Human gut microbiome adopts an alternative state following small bowel transplantation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 17187-92	11.5	243
356	Genomic insights into methanotrophy: the complete genome sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004 , 2, e303	9.7	236
355	Evidence for symmetric chromosomal inversions around the replication origin in bacteria. <i>Genome Biology</i> , 2000 , 1, RESEARCH0011	18.3	234
354	Microbial genes in the human genome: lateral transfer or gene loss?. <i>Science</i> , 2001 , 292, 1903-6	33.3	232
353	Analysis of <i>Deinococcus radiodurans</i> transcriptional response to ionizing radiation and desiccation reveals novel proteins that contribute to extreme radioresistance. <i>Genetics</i> , 2004 , 168, 21-33	4	216
352	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
351	2019 Novel Coronavirus (COVID-19) Pandemic: Built Environment Considerations To Reduce Transmission. <i>MSystems</i> , 2020 , 5,	7.6	199
350	The complete genome sequence of <i>Haloferax volcanii</i> DS2, a model archaeon. <i>PLoS ONE</i> , 2010 , 5, e9605	3.7	197
349	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
348	Meeting report: the terabase metagenomics workshop and the vision of an Earth microbiome project. <i>Standards in Genomic Sciences</i> , 2010 , 3, 243-8		187
347	Environmental shotgun sequencing: its potential and challenges for studying the hidden world of microbes. <i>PLoS Biology</i> , 2007 , 5, e82	9.7	185
346	Horizontal gene transfer among microbial genomes: new insights from complete genome analysis. <i>Current Opinion in Genetics and Development</i> , 2000 , 10, 606-11	4.9	185
345	Life in hot carbon monoxide: the complete genome sequence of <i>Carboxydotherrmus hydrogenoformans</i> Z-2901. <i>PLoS Genetics</i> , 2005 , 1, e65	6	184
344	The RecA protein as a model molecule for molecular systematic studies of bacteria: comparison of trees of RecAs and 16S rRNAs from the same species. <i>Journal of Molecular Evolution</i> , 1995 , 41, 1105-23	3.1	176
343	Comparative studies of resistin expression and phylogenomics in human and mouse. <i>Biochemical and Biophysical Research Communications</i> , 2003 , 310, 927-35	3.4	168
342	Metagenomic sequencing of an in vitro-simulated microbial community. <i>PLoS ONE</i> , 2010 , 5, e10209	3.7	163
341	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017 , 35, 676-683	44.5	161

340	The <i>Calyptogena magnifica</i> chemoautotrophic symbiont genome. <i>Science</i> , 2007 , 315, 998-1000	33.3	157
339	A phylogenomic study of the MutS family of proteins. <i>Nucleic Acids Research</i> , 1998 , 26, 4291-300	20.1	152
338	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
337	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013 , 4, 2120	17.4	145
336	Microbial genome sequencing. <i>Nature</i> , 2000 , 406, 799-803	50.4	133
335	Marine probiotics: increasing coral resistance to bleaching through microbiome manipulation. <i>ISME Journal</i> , 2019 , 13, 921-936	11.9	133
334	Nitrogen fixation in a landrace of maize is supported by a mucilage-associated diazotrophic microbiota. <i>PLoS Biology</i> , 2018 , 16, e2006352	9.7	130
333	Accounting for alignment uncertainty in phylogenomics. <i>PLoS ONE</i> , 2012 , 7, e30288	3.7	127
332	Systematic identification of gene families for use as "markers" for phylogenetic and phylogeny-driven ecological studies of bacteria and archaea and their major subgroups. <i>PLoS ONE</i> , 2013 , 8, e77033	3.7	123
331	MixS-BE: a MixS extension defining a minimum information standard for sequence data from the built environment. <i>ISME Journal</i> , 2014 , 8, 1-3	11.9	109
330	Yeast communities of diverse <i>Drosophila</i> species: comparison of two symbiont groups in the same hosts. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 7327-36	4.8	109
329	Genetic and physical mapping of DNA replication origins in <i>Haloferax volcanii</i> . <i>PLoS Genetics</i> , 2007 , 3, e77	6	109
328	Forensic analysis of the microbiome of phones and shoes. <i>Microbiome</i> , 2015 , 3, 21	16.6	108
327	Adaptations to submarine hydrothermal environments exemplified by the genome of <i>Nautilia profundicola</i> . <i>PLoS Genetics</i> , 2009 , 5, e1000362	6	105
326	Ten questions concerning the microbiomes of buildings. <i>Building and Environment</i> , 2016 , 109, 224-234	6.5	104
325	Phylogeny of bacterial and archaeal genomes using conserved genes: supertrees and supermatrices. <i>PLoS ONE</i> , 2013 , 8, e62510	3.7	102
324	Phylogenetically driven sequencing of extremely halophilic archaea reveals strategies for static and dynamic osmo-response. <i>PLoS Genetics</i> , 2014 , 10, e1004784	6	95
323	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

322	Sequence similarity of putative transposases links the maize Mutator autonomous element and a group of bacterial insertion sequences. <i>Nucleic Acids Research</i> , 1994 , 22, 2634-6	20.1	95
321	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541). <i>Standards in Genomic Sciences</i> , 2009 , 1, 12-20		94
320	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
319	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , 2008 , 9, R158	18.3	92
318	Characterization of bacterial communities associated with deep-sea corals on Gulf of Alaska seamounts. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 1680-3	4.8	89
317	The age of the <i>Arabidopsis thaliana</i> genome duplication. <i>Plant Molecular Biology</i> , 2003 , 51, 859-66	4.6	85
316	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004 , 134, 183-91	1.9	83
315	Complete genome sequence of the aerobic CO-oxidizing thermophile <i>Thermomicrobium roseum</i> . <i>PLoS ONE</i> , 2009 , 4, e4207	3.7	82
314	Strain- and plasmid-level deconvolution of a synthetic metagenome by sequencing proximity ligation products. <i>PeerJ</i> , 2014 , 2, e415	3.1	79
313	Global-Scale Structure of the Eelgrass Microbiome. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	77
312	The complete genome of <i>Teredinibacter turnerae</i> T7901: an intracellular endosymbiont of marine wood-boring bivalves (shipworms). <i>PLoS ONE</i> , 2009 , 4, e6085	3.7	76
311	Assessing evolutionary relationships among microbes from whole-genome analysis. <i>Current Opinion in Microbiology</i> , 2000 , 3, 475-80	7.9	75
310	Genomic Encyclopedia of Type Strains, Phase I: The one thousand microbial genomes (KMG-I) project. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1278-84		72
309	Stalking the fourth domain in metagenomic data: searching for, discovering, and interpreting novel, deep branches in marker gene phylogenetic trees. <i>PLoS ONE</i> , 2011 , 6, e18011	3.7	72
308	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium <i>Ktedonobacter racemifer</i> type strain (SOSP1-21). <i>Standards in Genomic Sciences</i> , 2011 , 5, 97-111		72
307	Refined annotation and assembly of the <i>Tetrahymena thermophila</i> genome sequence through EST analysis, comparative genomic hybridization, and targeted gap closure. <i>BMC Genomics</i> , 2008 , 9, 562	4.5	72
306	Mauve assembly metrics. <i>Bioinformatics</i> , 2011 , 27, 2756-7	7.2	71
305	Identification of a fourth family of lycopene cyclases in photosynthetic bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 11784-9	11.5	71

304	Phylogenetic analysis and gene functional predictions: phylogenomics in action. <i>Theoretical Population Biology</i> , 2002 , 61, 481-7	1.2	68
303	Root-hair endophyte stacking in finger millet creates a physicochemical barrier to trap the fungal pathogen <i>Fusarium graminearum</i> . <i>Nature Microbiology</i> , 2016 , 1, 16167	26.6	67
302	The phylogenetic diversity of metagenomes. <i>PLoS ONE</i> , 2011 , 6, e23214	3.7	67
301	Phosphate transporters in marine phytoplankton and their viruses: cross-domain commonalities in viral-host gene exchanges. <i>Environmental Microbiology</i> , 2012 , 14, 162-76	5.2	65
300	The microbes we eat: abundance and taxonomy of microbes consumed in a day's worth of meals for three diet types. <i>PeerJ</i> , 2014 , 2, e659	3.1	65
299	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020 , 5, 987-994	26.6	64
298	Microbial communities in sediment from patches, but not the leaf or root microbiomes, vary in relation to distance from patch edge. <i>PeerJ</i> , 2017 , 5, e3246	3.1	64
297	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6). <i>Standards in Genomic Sciences</i> , 2011 , 4, 200-9		62
296	Genome-Scale Analysis of Programmed DNA Elimination Sites in <i>Tetrahymena thermophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2011 , 1, 515-22	3.2	62
295	PhyLOTU: a high-throughput procedure quantifies microbial community diversity and resolves novel taxa from metagenomic data. <i>PLoS Computational Biology</i> , 2011 , 7, e1001061	5	62
294	Sequence and analysis of the <i>Arabidopsis</i> genome. <i>Current Opinion in Plant Biology</i> , 2001 , 4, 105-10	9.9	62
293	CompostBin: A DNA Composition-Based Algorithm for Binning Environmental Shotgun Reads 2008 , 17-28		61
292	Microscale sulfur cycling in the phototrophic pink berry consortia of the Sippewissett Salt Marsh. <i>Environmental Microbiology</i> , 2014 , 16, 3398-415	5.2	59
291	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034). <i>Standards in Genomic Sciences</i> , 2010 , 2, 87-95		57
290	A case for evolutionary genomics and the comprehensive examination of sequence biodiversity. <i>Molecular Biology and Evolution</i> , 2000 , 17, 1776-88	8.3	57
289	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <i>Frontiers in Microbiology</i> , 2017 , 8, 2264	5.7	55
288	Comparative genomics and understanding of microbial biology. <i>Emerging Infectious Diseases</i> , 2000 , 6, 505-12	10.2	55
287	Taking the first steps towards a standard for reporting on phylogenies: Minimum Information About a Phylogenetic Analysis (MIAPA). <i>OMICS A Journal of Integrative Biology</i> , 2006 , 10, 231-7	3.8	54

286	Cloning and characterization of HARP/SMARCAL1: a prokaryotic HepA-related SNF2 helicase protein from human and mouse. <i>Genomics</i> , 2000 , 65, 274-82	4.3	54
285	Complete genome sequence of <i>Haliangium ochraceum</i> type strain (SMP-2). <i>Standards in Genomic Sciences</i> , 2010 , 2, 96-106		53
284	In silico-initiated cloning and molecular characterization of a novel human member of the L1 gene family of neural cell adhesion molecules. <i>Human Genetics</i> , 1998 , 103, 355-64	6.3	51
283	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20). <i>Standards in Genomic Sciences</i> , 2010 , 2, 158-67		49
282	Genomic Encyclopedia of Bacterial and Archaeal Type Strains, Phase III: the genomes of soil and plant-associated and newly described type strains. <i>Standards in Genomic Sciences</i> , 2015 , 10, 26		48
281	Complete genome sequence of the termite hindgut bacterium <i>Spirochaeta coccoides</i> type strain (SPN1(T)), reclassification in the genus <i>Sphaerochaeta</i> as <i>Sphaerochaeta coccoides</i> comb. nov. and emendations of the family Spirochaetaceae and the genus <i>Sphaerochaeta</i> . <i>Standards in Genomic Sciences</i> , 2012 , 4, 181-200		46
280	Host-associated microbiomes drive structure and function of marine ecosystems. <i>PLoS Biology</i> , 2019 , 17, e3000533	9.7	44
279	Genomic perspective on the photobiology of <i>Halobacterium</i> species NRC-1, a phototrophic, phototactic, and UV-tolerant haloarchaeon. <i>Photosynthesis Research</i> , 2001 , 70, 3-17	3.7	43
278	Phylogenetic relationships of chemoautotrophic bacterial symbionts of <i>Solemya velum</i> say (Mollusca: Bivalvia) determined by 16S rRNA gene sequence analysis. <i>Journal of Bacteriology</i> , 1992 , 174, 3416-21	3.5	42
277	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021 , 184, 3376-3393.e17	9.17	42
276	Gene conservation among endospore-forming bacteria reveals additional sporulation genes in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2013 , 195, 253-60	3.5	41
275	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1B). <i>Standards in Genomic Sciences</i> , 2011 , 4, 63-71		40
274	A cut above: discovery of an alternative excision repair pathway in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 2581-3	11.5	40
273	An automated phylogenetic tree-based small subunit rRNA taxonomy and alignment pipeline (STAP). <i>PLoS ONE</i> , 2008 , 3, e2566	3.7	40
272	Complete genome sequence of <i>Planctomyces brasiliensis</i> type strain (DSM 5305(T)), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of <i>Gimesia</i> gen. nov., <i>Planctopirus</i> gen. nov. and <i>Rubinisphaera</i> gen. nov. and emended descriptions of the order Planctomycetales and the family Planctomycetaceae. <i>Standards in Genomic Sciences</i> , 2014 , 9, 10		39
271	The impact of <i>Helicobacter pylori</i> infection on the gastric microbiota of the rhesus macaque. <i>PLoS ONE</i> , 2013 , 8, e76375	3.7	39
270	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3). <i>Standards in Genomic Sciences</i> , 2011 , 4, 100-10		39
269	Deep-sea hydrothermal vent bacteria related to human pathogenic <i>Vibrio</i> species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E2813-9	11.5	38

268	Microbial Mat Communities along an Oxygen Gradient in a Perennially Ice-Covered Antarctic Lake. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 620-30	4.8	38
267	A microbial survey of the International Space Station (ISS). <i>PeerJ</i> , 2017 , 5, e4029	3.1	38
266	Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24). <i>Standards in Genomic Sciences</i> , 2011 , 4, 91-9		37
265	Sequencing of seven haloarchaeal genomes reveals patterns of genomic flux. <i>PLoS ONE</i> , 2012 , 7, e41389	3.7	37
264	Complete genome sequence of the thermophilic, hydrogen-oxidizing <i>Bacillus tusciae</i> type strain (T2) and reclassification in the new genus, <i>Kyrpidia</i> gen. nov. as <i>Kyrpidia tusciae</i> comb. nov. and emendation of the family Alicyclobacillaceae da Costa and Rainey, 2010. <i>Standards in Genomic Sciences</i> , 2011 , 5, 121-34		35
263	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1). <i>Standards in Genomic Sciences</i> , 2010 , 2, 176-85		35
262	Automated and Accurate Estimation of Gene Family Abundance from Shotgun Metagenomes. <i>PLoS Computational Biology</i> , 2015 , 11, e1004573	5	34
261	Insights into the evolution of Darwin finches from comparative analysis of the <i>Geospiza magnirostris</i> genome sequence. <i>BMC Genomics</i> , 2013 , 14, 95	4.5	33
260	Complete genome sequence of <i>Desulfotomaculum acetoxidans</i> type strain (5575). <i>Standards in Genomic Sciences</i> , 2009 , 1, 242-53		33
259	Recent Outbreaks of Shigellosis in California Caused by Two Distinct Populations of with either Increased Virulence or Fluoroquinolone Resistance. <i>MSphere</i> , 2016 , 1,	5	33
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1	Whole genome sequence analysis reveals the broad distribution of the RtxA type 1 secretion system and four novel putative type 1 secretion systems throughout the <i>Legionella</i> genus 2020 , 15, e0223033		