

Jonathan A Eisen

List of Publications by Year in Descending Order

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Version: 2024-04-26

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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.

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	Draft Genome Sequences and Genomic Analysis for Pigment Production in Bacteria Isolated from Blue Discolored Soymilk and Tofu. <i>Journal of Genomics</i> , 2021 , 9, 55-67	0.9	1
410	Global Diversity and Biogeography of the Mycobiome. <i>Applied and Environmental Microbiology</i> , 2021 , 87, e0279520	4.8	6
409	SARS-CoV-2 detection and genomic sequencing from hospital surface samples collected at UC Davis. <i>PLoS ONE</i> , 2021 , 16, e0253578	3.7	15
408	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021 , 184, 3376-3393	36.17	42
407	sp. nov., sp. nov. and sp. nov., marine, cellulolytic endosymbiotic bacteria isolated from the gills of the wood-boring mollusc (Bivalvia: Teredinidae) and emended description of the genus. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021 , 71,	2.2	3
406	Natural experiments and long-term monitoring are critical to understand and predict marine host-microbe ecology and evolution. <i>PLoS Biology</i> , 2021 , 19, e3001322	9.7	2
405	Reconstruction of Metagenome-Assembled Genomes from Aquaria. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0055721	1.3	
404	A phylogenetically novel cyanobacterium most closely related to <i>Gloeobacter</i> . <i>ISME Journal</i> , 2020 , 14, 2142-2152	11.9	11
403	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020 , 5, 987-994	26.6	64
402	Draft Genome Analysis of DSM 22607, exhibiting an unusual expansion of transporter homologs of unknown function. <i>Journal of Genomics</i> , 2020 , 8, 25-29	0.9	3
401	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. <i>PLoS ONE</i> , 2020 , 15, e0223033	3.7	2
400	2019 Novel Coronavirus (COVID-19) Pandemic: Built Environment Considerations To Reduce Transmission. <i>MSystems</i> , 2020 , 5,	7.6	199
399	Environmental control on the distribution of metabolic strategies of benthic microbial mats in Lake Fryxell, Antarctica. <i>PLoS ONE</i> , 2020 , 15, e0231053	3.7	4
398	Isolation and sequence-based characterization of a koala symbiont:. <i>PeerJ</i> , 2020 , 8, e10177	3.1	2
397	Bacterial communities associated with cell phones and shoes. <i>PeerJ</i> , 2020 , 8, e9235	3.1	4
396	sp. nov., a marine, cellulolytic endosymbiotic bacterium isolated from the gills of the wood-boring mollusc (Bivalvia: Teredinidae) and emended description of the genus. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020 , 70, 2388-2394	2.2	6
395	Energetic and Environmental Constraints on the Community Structure of Benthic Microbial Mats in Lake Fryxell, Antarctica. <i>FEMS Microbiology Ecology</i> , 2020 , 96,	4.3	3

394	The emergence of microbiome centres. <i>Nature Microbiology</i> , 2020 , 5, 2-3	26.6	7
393	Combining Microbial Culturing With Mathematical Modeling in an Introductory Course-Based Undergraduate Research Experience. <i>Frontiers in Microbiology</i> , 2020 , 11, 581903	5.7	1
392	Fungi, bacteria and oomycota opportunistically isolated from the seagrass, <i>Zostera marina</i> . <i>PLoS ONE</i> , 2020 , 15, e0236135	3.7	15
391	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. <i>Frontiers in Microbiology</i> , 2020 , 11, 1848	5.7	29
390	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		
389	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		
388	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		
387	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		
386	Bacteria isolated from Bengal cat (<i>Felis catus</i> [Prionailurus bengalensis]) anal sac secretions produce volatile compounds potentially associated with animal signaling. <i>PLoS ONE</i> , 2019 , 14, e0216846 ^{3.7}	3.7	4
385	Genomes from bacteria associated with the canine oral cavity: A test case for automated genome-based taxonomic assignment. <i>PLoS ONE</i> , 2019 , 14, e0214354	3.7	4
384	Microbial Community Succession and Nutrient Cycling Responses following Perturbations of Experimental Saltwater Aquaria. <i>MSphere</i> , 2019 , 4,	5	8
383	Comparison of Whole-Genome Sequences of <i>Legionella pneumophila</i> in Tap Water and in Clinical Strains, Flint, Michigan, USA, 2016. <i>Emerging Infectious Diseases</i> , 2019 , 25, 2013-2020	10.2	7
382	Prospecting Microbial Strains for Bioremediation and Probiotics Development for Metaorganism Research and Preservation. <i>Journal of Visualized Experiments</i> , 2019 ,	1.6	4
381	Host-associated microbiomes drive structure and function of marine ecosystems. <i>PLoS Biology</i> , 2019 , 17, e3000533	9.7	44
380	Metagenome-assembled genomes provide new insight into the microbial diversity of two thermal pools in Kamchatka, Russia. <i>Scientific Reports</i> , 2019 , 9, 3059	4.9	30
379	Characterization of the Mycobiome of the Seagrass, , Reveals Putative Associations With Marine Chytrids. <i>Frontiers in Microbiology</i> , 2019 , 10, 2476	5.7	16
378	Marine probiotics: increasing coral resistance to bleaching through microbiome manipulation. <i>ISME Journal</i> , 2019 , 13, 921-936	11.9	133
377	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

376	Characterization of shifts of koala (intestinal microbial communities associated with antibiotic treatment. <i>PeerJ</i> , 2018 , 6, e4452	3.1	22
375	Effects of preservation method on canine () fecal microbiota. <i>PeerJ</i> , 2018 , 6, e4827	3.1	10
374	The Cloacal Microbiome of Five Wild Duck Species Varies by Species and Influenza A Virus Infection Status. <i>MSphere</i> , 2018 , 3,	5	14
373	Genomic attributes of extended-spectrum β actamase-producing <i>Escherichia coli</i> isolated from patients in Lebanon. <i>Future Microbiology</i> , 2017 , 12, 213-226	2.9	8
372	Complete genome sequence of strain YIM 002 (DSM 44835), the type species of the genus and source of new antibiotic compounds. <i>Standards in Genomic Sciences</i> , 2017 , 12, 21		5
371	Global-Scale Structure of the Eelgrass Microbiome. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	77
370	Complete Genome Sequence of a Strain Isolated from a Paraplegic Patient with Neurogenic Bladder Using Single-Molecule Real-Time Sequencing Technology. <i>Genome Announcements</i> , 2017 , 5,		2
369	Draft Genome Sequences of Strains UCD-KPL2534 and UCD-KPL2528 Isolated from an Indoor Track Facility. <i>Genome Announcements</i> , 2017 , 5,		1
368	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
367	Community-Level Differences in the Microbiome of Healthy Wild Mallards and Those Infected by Influenza A Viruses. <i>MSystems</i> , 2017 , 2,	7.6	25
366	Research priorities for harnessing plant microbiomes in sustainable agriculture. <i>PLoS Biology</i> , 2017 , 15, e2001793	9.7	402
365	Draft Genome Sequence of sp. Strain UCD-GKA (Phylum). <i>Genome Announcements</i> , 2017 , 5,		1
364	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
363	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
362	Complete Genome Sequence of from a Patient with Interstitial Lung Disease Using Single-Molecule Real-Time Sequencing Technology. <i>Genome Announcements</i> , 2017 , 5,		1
361	Draft genome sequences of eight bacteria isolated from the indoor environment: strain H36, strain H65, strain H62, strain H69, sp. strain H83, strain H39, sp. strain H53, and strain H72. <i>Standards in Genomic Sciences</i> , 2017 , 12, 17		6
360	Draft Genome Sequence of Strain UCD-PD2 Isolated from a Feline Anal Sac. <i>Genome Announcements</i> , 2017 , 5,		3
359	The Green Berry Consortia of the Sippewissett Salt Marsh: Millimeter-Sized Aggregates of Diazotrophic Unicellular Cyanobacteria. <i>Frontiers in Microbiology</i> , 2017 , 8, 1623	5.7	3

358	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <i>Frontiers in Microbiology</i> , 2017 , 8, 2264	5.7	55
357	Draft Genome Sequences of UCD-KL30, UCD-KL16, sp. Strain UCD-KL20, sp. Strain UCD-KL12, and sp. Strain UCD-KL21, Isolated from Seagrass. <i>Genome Announcements</i> , 2017 , 5,		7
356	Gut Check: The evolution of an educational board game. <i>PLoS Biology</i> , 2017 , 15, e2001984	9.7	17
355	Microbiome succession during ammonification in eelgrass bed sediments. <i>PeerJ</i> , 2017 , 5, e3674	3.1	17
354	A microbial survey of the International Space Station (ISS). <i>PeerJ</i> , 2017 , 5, e4029	3.1	38
353	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
352	Draft Genome Sequence of <i>Gordonia</i> sp. Strain UCD-TK1 (Phylum Actinobacteria). <i>Genome Announcements</i> , 2016 , 4,		2
351	Genome Sequence of a Multidrug-Resistant Strain of <i>Bacillus pumilus</i> , CB01, Isolated from the Feces of an American Crow, <i>Corvus brachyrhynchos</i> . <i>Genome Announcements</i> , 2016 , 4,		1
350	Draft Genome Sequences of Two <i>Pseudoalteromonas</i> Strains Isolated from Roots and Leaf Blades of the Seagrass <i>Zostera marina</i> . <i>Genome Announcements</i> , 2016 , 4,		2
349	Draft Genome Sequences of Two <i>Pseudoalteromonas porphyrae</i> Strains Isolated from Seagrass Sediment. <i>Genome Announcements</i> , 2016 , 4,		3
348	Draft Genome Sequences of Two <i>Vibrio splendidus</i> Strains, Isolated from Seagrass Sediment. <i>Genome Announcements</i> , 2016 , 4,		2
347	Draft Genome Sequence of <i>Klebsiella pneumoniae</i> KGM-IMP216 Harboring blaCTX-M-15, blaDHA-1, blaTEM-1B, blaNDM-1, blaSHV-28, and blaOXA-1, Isolated from a Patient in Lebanon. <i>Genome Announcements</i> , 2016 , 4,		4
346	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
345	Genome Analysis of <i>Streptococcus pyogenes</i> Associated with Pharyngitis and Skin Infections. <i>PLoS ONE</i> , 2016 , 11, e0168177	3.7	11
344	Growth of 48 built environment bacterial isolates on board the International Space Station (ISS). <i>PeerJ</i> , 2016 , 4, e1842	3.1	25
343	Draft Genome Sequence of <i>Tenacibaculum soleae</i> UCD-KL19. <i>Genome Announcements</i> , 2016 , 4,		7
342	Draft Genome Sequence of <i>Curtobacterium</i> sp. Strain UCD-KPL2560 (Phylum Actinobacteria). <i>Genome Announcements</i> , 2016 , 4,		4
341	Genes Required for the Anti-fungal Activity of a Bacterial Endophyte Isolated from a Corn Landrace Grown Continuously by Subsistence Farmers Since 1000 BC. <i>Frontiers in Microbiology</i> , 2016 , 7, 1548	5.7	17

340	Draft Genome Sequence of <i>Cobetia</i> sp. UCD-24C, Isolated from Roots and Leaves of the Seagrass <i>Zostera marina</i> . <i>Genome Announcements</i> , 2016 , 4,		5
339	Draft Genome Sequences of <i>Acinetobacter baumannii</i> Strains Harboring the blaNDM-1 Gene Isolated in Lebanon from Civilians Wounded during the Syrian Civil War. <i>Genome Announcements</i> , 2016 , 4,		4
338	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
337	Ten questions concerning the microbiomes of buildings. <i>Building and Environment</i> , 2016 , 109, 224-234	6.5	104
336	The United States Culture Collection Network (USCCN): Enhancing Microbial Genomics Research through Living Microbe Culture Collections. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 5671-4	4.8	17
335	Forensic analysis of the microbiome of phones and shoes. <i>Microbiome</i> , 2015 , 3, 21	16.6	108
334	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
333	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
332	Draft Genome Sequence of <i>Enterobacter</i> sp. Strain UCD-UG_FMILLET (Phylum Proteobacteria). <i>Genome Announcements</i> , 2015 , 3,		1
331	Draft Genome Sequence of <i>Porphyrobacter mercurialis</i> (sp. nov.) Strain Coronado. <i>Genome Announcements</i> , 2015 , 3,		4
330	Transcriptomes of post-mitotic neurons identify the usage of alternative pathways during adult and embryonic neuronal differentiation. <i>BMC Genomics</i> , 2015 , 16, 1100	4.5	10
329	Draft Genome Sequence of <i>Planomicrobium glaciei</i> UCD-HAM (Phylum Firmicutes). <i>Genome Announcements</i> , 2015 , 3,		2
328	Draft Genome Sequence of <i>Pseudoalteromonas tetraodonis</i> Strain UCD-SED8 (Phylum Gammaproteobacteria). <i>Genome Announcements</i> , 2015 , 3,		3
327	Draft Genome Sequence of <i>Bacillus safensis</i> JPL-MERTA-8-2, Isolated from a Mars-Bound Spacecraft. <i>Genome Announcements</i> , 2015 , 3,		5
326	Draft Genome Sequence of <i>Bacillus vietnamensis</i> Strain UCD-SED5 (Phylum Firmicutes). <i>Genome Announcements</i> , 2015 , 3,		3
325	Whole genome sequencing of extended-spectrum β lactamase producing <i>Klebsiella pneumoniae</i> isolated from a patient in Lebanon. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015 , 5, 32	5.9	15
324	Comparative Genomics of the Genus <i>Porphyromonas</i> Identifies Adaptations for Heme Synthesis within the Prevalent Canine Oral Species <i>Porphyromonas canis</i> . <i>Genome Biology and Evolution</i> , 2015 , 7, 3397-413	3.9	15
323	Draft genome sequences of 26 <i>porphyromonas</i> strains isolated from the canine oral microbiome. <i>Genome Announcements</i> , 2015 , 3,		8

322	Draft Genome Sequence of Burkholderia gladioli Strain UCD-UG_CHAPALOTE (Phylum Proteobacteria). <i>Genome Announcements</i> , 2015 , 3,		5
321	Genome Sequence of the Sulfate-Reducing Thermophilic Bacterium Thermodesulfovibrio yellowstonii Strain DSM 11347T (Phylum Nitrospirae). <i>Genome Announcements</i> , 2015 , 3,		15
320	Genome Sequence of a Sulfate-Reducing Thermophilic Bacterium, Thermodesulfovibrio commune DSM 2178T (Phylum Thermodesulfovibria). <i>Genome Announcements</i> , 2015 , 3,		4
319	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
318	Automated and Accurate Estimation of Gene Family Abundance from Shotgun Metagenomes. <i>PLoS Computational Biology</i> , 2015 , 11, e1004573	5	34
317	What does the term microbiome mean? And where did it come from? A bit of a surprise ... <i>The Winnower</i> , 2015 ,		4
316	Porphyrobacter mercurialis sp. nov., isolated from a stadium seat and emended description of the genus Porphyrobacter. <i>PeerJ</i> , 2015 , 3, e1400	3.1	8
315	Swabs to genomes: a comprehensive workflow. <i>PeerJ</i> , 2015 , 3, e960	3.1	25
314	Complete genome sequence of Planctomyces brasiliensis type strain (DSM 5305(T)), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of Gimesia gen. nov., Planctopirus gen. nov. and Rubinisphaera gen. nov. and emended descriptions of the order Planctomycetales and the family Planctomycetaceae. <i>Standards in Genomic Sciences</i> , 2014 , 9, 10		39
313	Genome sequence of the Thermotoga thermarum type strain (LA3(T)) from an African solfataric spring. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1105-17		4
312	Genome sequence of the mud-dwelling archaeon Methanoplanus limicola type strain (DSM 2279(T)), reclassification of Methanoplanus petrolearius as Methanolacinia petrolearia and emended descriptions of the genera Methanoplanus and Methanolacinia. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1076-88		10
311	Complete Genome Sequence of Coprothermobacter proteolyticus DSM 5265. <i>Genome Announcements</i> , 2014 , 2,		6
310	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
309	Phylogenetically driven sequencing of extremely halophilic archaea reveals strategies for static and dynamic osmo-response. <i>PLoS Genetics</i> , 2014 , 10, e1004784	6	95
308	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
307	Draft Genome Sequences of Streptococcus pyogenes Strains Associated with Throat and Skin Infections in Lebanon. <i>Genome Announcements</i> , 2014 , 2,		5
306	microBEnet: lessons learned from building an interdisciplinary scientific community in the online sphere. <i>PLoS Biology</i> , 2014 , 12, e1001884	9.7	3
305	Complete Genome Sequence of the Extreme Thermophile Dictyoglomus thermophilum H-6-12. <i>Genome Announcements</i> , 2014 , 2,		11

304	Draft Genome Sequence of the Pyridinediol-Fermenting Bacterium <i>Synergistes jonesii</i> 78-1. <i>Genome Announcements</i> , 2014 , 2,		1
303	Draft Genome Sequence of <i>Tatumella</i> sp. Strain UCD-D_suzukii (Phylum Proteobacteria) Isolated from <i>Drosophila suzukii</i> Larvae. <i>Genome Announcements</i> , 2014 , 2,		3
302	Draft Genome Sequences of <i>Escherichia coli</i> Strains Isolated from Septic Patients. <i>Genome Announcements</i> , 2014 , 2,		2
301	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
300	The genome of the intracellular bacterium of the coastal bivalve, <i>Solemya velum</i> : a blueprint for thriving in and out of symbiosis. <i>BMC Genomics</i> , 2014 , 15, 924	4.5	22
299	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
298	PhyloSift: phylogenetic analysis of genomes and metagenomes. <i>PeerJ</i> , 2014 , 2, e243	3.1	431
297	Strain- and plasmid-level deconvolution of a synthetic metagenome by sequencing proximity ligation products. <i>PeerJ</i> , 2014 , 2, e415	3.1	79
296	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
295	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013 , 499, 431-7	50.4	1484
294	Insights into the evolution of Darwin's finches from comparative analysis of the <i>Geospiza magnirostris</i> genome sequence. <i>BMC Genomics</i> , 2013 , 14, 95	4.5	33
293	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013 , 4, 2120	17.4	145
292	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
291	Draft genome sequence of an Actinobacterium, <i>Brachybacterium muris</i> strain UCD-AY4. <i>Genome Announcements</i> , 2013 , 1, e0008613		9
290	Draft Genome Sequence of <i>Microbacterium</i> sp. Strain UCD-TDU (Phylum Actinobacteria). <i>Genome Announcements</i> , 2013 , 1, e0012013		5
289	Draft Genome Sequence of <i>Kocuria</i> sp. Strain UCD-OTCP (Phylum Actinobacteria). <i>Genome Announcements</i> , 2013 , 1,		5
288	Draft Genome Sequence of <i>Curtobacterium flaccumfaciens</i> Strain UCD-AKU (Phylum Actinobacteria). <i>Genome Announcements</i> , 2013 , 1,		6
287	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

286	Draft Genome Sequence of the Arsenate-Respiring Bacterium <i>Chrysiogenes arsenatis</i> Strain DSM 11915. <i>Genome Announcements</i> , 2013 , 1,		2
285	Complete genome sequence of <i>Coriobacterium glomerans</i> type strain (PW2(T)) from the midgut of <i>Pyrrhocoris apterus</i> L. (red soldier bug). <i>Standards in Genomic Sciences</i> , 2013 , 8, 15-25		5
284	Complete genome sequence of the bile-resistant pigment-producing anaerobe <i>Alistipes finegoldii</i> type strain (AHN2437(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 26-36		6
283	High-quality-draft genome sequence of the yellow-pigmented flavobacterium <i>Joostella marina</i> type strain (En5(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 37-46		4
282	Complete genome sequence of the moderate thermophile <i>Anaerobaculum mobile</i> type strain (NGA(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 47-57		10
281	Genome sequence of the free-living aerobic spirochete <i>Turneriella parva</i> type strain (H(T)), and emendation of the species <i>Turneriella parva</i> . <i>Standards in Genomic Sciences</i> , 2013 , 8, 228-38		8
280	Genome sequence of the moderately thermophilic sulfur-reducing bacterium <i>Thermanaerovibrio velox</i> type strain (Z-9701(T)) and emended description of the genus <i>Thermanaerovibrio</i> . <i>Standards in Genomic Sciences</i> , 2013 , 9, 57-70		4
279	Genome sequence of <i>Frateuria aurantia</i> type strain (Kond167(T)), a xanthomonade isolated from <i>Lilium auratum</i> Lindl. <i>Standards in Genomic Sciences</i> , 2013 , 9, 83-92		1
278	Prokaryotic Super Program Advisory Committee DOE Joint Genome Institute, Walnut Creek, CA, March 27, 2013. <i>Standards in Genomic Sciences</i> , 2013 , 8, 561-70		5
277	Genome sequence of the thermophilic fresh-water bacterium <i>Spirochaeta caldaria</i> type strain (H1(T)), reclassification of <i>Spirochaeta caldaria</i> , <i>Spirochaeta stenostrepta</i> , and <i>Spirochaeta zuelzeri</i> in the genus <i>Treponema</i> as <i>Treponema caldaria</i> comb. nov., <i>Treponema stenostrepta</i> comb. nov., and <i>Treponema zuelzeri</i> comb. nov. <i>Standards in Genomic Sciences</i> , 2013 , 8, 165-76		24
276	Complete genome sequence of the halophilic bacterium <i>Spirochaeta africana</i> type strain (Z-7692(T)) from the alkaline Lake Magadi in the East African Rift. <i>Standards in Genomic Sciences</i> , 2013 , 8, 165-76		2
275	Genome sequence of the phylogenetically isolated spirochete <i>Leptonema illini</i> type strain (3055(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 177-87		4
274	Draft Genome Sequence of <i>Leucobacter</i> sp. Strain UCD-THU (Phylum Actinobacteria). <i>Genome Announcements</i> , 2013 , 1,		5
273	Draft Genome Sequence of <i>Dietzia</i> sp. Strain UCD-THP (Phylum Actinobacteria). <i>Genome Announcements</i> , 2013 , 1,		5
272	Phylogeny of bacterial and archaeal genomes using conserved genes: supertrees and supermatrices. <i>PLoS ONE</i> , 2013 , 8, e62510	3.7	102
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	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
269	Sifting through genomes with iterative-sequence clustering produces a large, phylogenetically diverse protein-family resource. <i>BMC Bioinformatics</i> , 2012 , 13, 264	3.6	18

268	Accounting for alignment uncertainty in phylogenomics. <i>PLoS ONE</i> , 2012 , 7, e30288	3.7	127
267	An integrated pipeline for de novo assembly of microbial genomes. <i>PLoS ONE</i> , 2012 , 7, e42304	3.7	330
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6	The phylogenetic relationships of <i>Chlorobium tepidum</i> and <i>Chloroflexus aurantiacus</i> based upon their RecA sequences		1
5	Global-scale structure of the eelgrass microbiome		2
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