Frank W Larimer

List of Publications by Year
in descending order

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25 papers	12,090 citations	331670 21 h-index	580821 25 g-index
25 all docs	25 docs citations	25 times ranked	14562 citing authors

#	Article	IF	Citations
1	Prodigal: prokaryotic gene recognition and translation initiation site identification. BMC Bioinformatics, 2010, 11, 119.	2.6	8,237
2	Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation. Nature, 2003, 424, 1042-1047.	27.8	1,086
3	Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris. Nature Biotechnology, 2004, 22, 55-61.	17.5	675
4	The Genome Sequence of the Obligately Chemolithoautotrophic, Facultatively Anaerobic Bacterium Thiobacillus denitrificans. Journal of Bacteriology, 2006, 188, 1473-1488.	2.2	306
5	Genome of the Epsilonproteobacterial Chemolithoautotroph Sulfurimonas denitrificans. Applied and Environmental Microbiology, 2008, 74, 1145-1156.	3.1	228
6	Genome Sequence of the Chemolithoautotrophic Nitrite-Oxidizing Bacterium Nitrobacter winogradskyi Nb-255. Applied and Environmental Microbiology, 2006, 72, 2050-2063.	3.1	169
7	Wholeâ€genome analysis of the ammoniaâ€oxidizing bacterium, Nitrosomonas eutropha C91: implications for niche adaptation. Environmental Microbiology, 2007, 9, 2993-3007.	3.8	150
8	The Genome of Deep-Sea Vent Chemolithoautotroph Thiomicrospira crunogena XCL-2. PLoS Biology, 2006, 4, e383.	5.6	144
9	Complete Genome Sequence of the Marine, Chemolithoautotrophic, Ammonia-Oxidizing Bacterium Nitrosococcus oceani ATCC 19707. Applied and Environmental Microbiology, 2006, 72, 6299-6315.	3.1	139
10	Multiple genome sequences reveal adaptations of a phototrophic bacterium to sediment microenvironments. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18543-18548.	7.1	131
11	The home stretch, a first analysis of the nearly completed genome of Rhodobacter sphaeroides 2.4.1. Photosynthesis Research, 2001, 70, 19-41.	2.9	129
12	Complete Genome Sequence of Nitrobacter hamburgensis X14 and Comparative Genomic Analysis of Species within the Genus Nitrobacter. Applied and Environmental Microbiology, 2008, 74, 2852-2863.	3.1	115
13	Caldicellulosiruptor Core and Pangenomes Reveal Determinants for Noncellulosomal Thermophilic Deconstruction of Plant Biomass. Journal of Bacteriology, 2012, 194, 4015-4028.	2.2	96
14	Complete genome sequence of the filamentous anoxygenic phototrophic bacterium Chloroflexus aurantiacus. BMC Genomics, 2011, 12, 334.	2.8	90
15	Characterization of the 70S Ribosome from Rhodopseudomonas palustris Using an Integrated â€œTop-Downâ€•and â€œBottom-Upâ€•Mass Spectrometric Approach. Journal of Proteome Research, 2004, 3, 965-978.	3.7	83
16	Determination and Comparison of the Baseline Proteomes of the Versatile MicrobeRhodopseudomonaspalustrisunder Its Major Metabolic States. Journal of Proteome Research, 2006, 5, 287-298.	3.7	69
17	Genome Sequence of Chthoniobacter flavus Ellin428, an Aerobic Heterotrophic Soil Bacterium. Journal of Bacteriology, 2011, 193, 2902-2903.	2.2	52
18	Genome Sequence of the Verrucomicrobium Opitutus terrae PB90-1, an Abundant Inhabitant of Rice Paddy Soil Ecosystems. Journal of Bacteriology, 2011, 193, 2367-2368.	2.2	44

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19	Evaluation of â€œShotgunâ€•Proteomics for Identification of Biological Threat Agents in Complex Environmental Matrixes:Â Experimental Simulations. Analytical Chemistry, 2005, 77, 923-932.	6.5	39
20	Genome Sequence of â€œPedosphaera parvulaâ€•Ellin514, an Aerobic Verrucomicrobial Isolate from Pasture Soil. Journal of Bacteriology, 2011, 193, 2900-2901.	2.2	28
21	Complete Genome Sequence of the Anaerobic, Halophilic Alkalithermophile Natranaerobius thermophilus JW/NM-WN-LF. Journal of Bacteriology, 2011, 193, 4023-4024.	2.2	28
22	A General System for Studying Proteinâ^'Protein Interactions in Gram-Negative Bacteria. Journal of Proteome Research, 2008, 7, 3319-3328.	3.7	24
23	Genome Sequence of Victivallis vadensis ATCC BAA-548, an Anaerobic Bacterium from the Phylum Lentisphaerae, Isolated from the Human Gastrointestinal Tract. Journal of Bacteriology, 2011, 193, 2373-2374.	2.2	14
24	Multiple catalytic roles of His 287 of Rhodospirillum rubrum ribulose 1,5-bisphosphate carboxylase/oxygenase. Protein Science, 1998, 7, 730-738.	7.6	13
25	Mutation spectrum of spontaneous frameshift revertants in yeast using double-strand gap repair. Environmental and Molecular Mutagenesis, 1992, 20, 84-88.	2.2	1