

# Jennifer V Kuehl

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

4,356  
citations

257450

24  
h-index

454955

30  
g-index

34  
all docs

34  
docs citations

34  
times ranked

4698  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Simple, Cost-Effective, and Automation-Friendly Direct PCR Approach for Bacterial Community Analysis. <i>MSystems</i> , 2021, 6, e0022421.	3.8	6
2	Anion transport as a target of adaption to perchlorate in sulfate-reducing communities. <i>ISME Journal</i> , 2020, 14, 450-462.	9.8	7
3	Selective carbon sources influence the end products of microbial nitrate respiration. <i>ISME Journal</i> , 2020, 14, 2034-2045.	9.8	61
4	The selective pressures on the microbial community in a metal-contaminated aquifer. <i>ISME Journal</i> , 2019, 13, 937-949.	9.8	56
5	Mutant phenotypes for thousands of bacterial genes of unknown function. <i>Nature</i> , 2018, 557, 503-509.	27.8	433
6	Dissimilatory Sulfate Reduction Under High Pressure by <i>Desulfovibrio alaskensis</i> G20. <i>Frontiers in Microbiology</i> , 2018, 9, 1465.	3.5	15
7	Filling gaps in bacterial amino acid biosynthesis pathways with high-throughput genetics. <i>PLoS Genetics</i> , 2018, 14, e1007147.	3.5	90
8	System-Wide Adaptations of <i>Desulfovibrio alaskensis</i> G20 to Phosphate-Limited Conditions. <i>PLoS ONE</i> , 2016, 11, e0168719.	2.5	15
9	Monofluorophosphate Is a Selective Inhibitor of Respiratory Sulfate-Reducing Microorganisms. <i>Environmental Science &amp; Technology</i> , 2015, 49, 3727-3736.	10.0	69
10	Mechanisms of direct inhibition of the respiratory sulfate-reduction pathway by (per)chlorate and nitrate. <i>ISME Journal</i> , 2015, 9, 1295-1305.	9.8	87
11	Functional Genomics with a Comprehensive Library of Transposon Mutants for the Sulfate-Reducing Bacterium <i>Desulfovibrio alaskensis</i> G20. <i>MBio</i> , 2014, 5, e01041-14.	4.1	56
12	The genetic basis of energy conservation in the sulfate-reducing bacterium <i>Desulfovibrio alaskensis</i> G20. <i>Frontiers in Microbiology</i> , 2014, 5, 577.	3.5	61
13	Control of methionine metabolism by the <i>SahR</i> transcriptional regulator in <i>Proteobacteria</i> . <i>Environmental Microbiology</i> , 2014, 16, 1-8.	3.8	18
14	The energy-conserving electron transfer system used by <i>Desulfovibrio alaskensis</i> strain G20 during pyruvate fermentation involves reduction of endogenously formed fumarate and cytoplasmic and membrane-bound complexes, <i>HdrFlox</i> and <i>Rnf</i> . <i>Environmental Microbiology</i> , 2014, 16, 3463-3486.	3.8	36
15	Genetic basis for nitrate resistance in <i>Desulfovibrio</i> strains. <i>Frontiers in Microbiology</i> , 2014, 5, 153.	3.5	202
16	Indirect and suboptimal control of gene expression is widespread in bacteria. <i>Molecular Systems Biology</i> , 2013, 9, 660.	7.2	111
17	Variation among <i>Desulfovibrio</i> Species in Electron Transfer Systems Used for Syntrophic Growth. <i>Journal of Bacteriology</i> , 2013, 195, 990-1004.	2.2	77
18	Evidence-Based Annotation of Transcripts and Proteins in the Sulfate-Reducing Bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Journal of Bacteriology</i> , 2011, 193, 5716-5727.	2.2	28

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19	Extreme Reconfiguration of Plastid Genomes in the Angiosperm Family Geraniaceae: Rearrangements, Repeats, and Codon Usage. <i>Molecular Biology and Evolution</i> , 2011, 28, 583-600.	8.9	338
20	Complete plastome sequences of <i>Equisetum arvense</i> and <i>Isoetes flaccida</i> : implications for phylogeny and plastid genome evolution of early land plant lineages. <i>BMC Evolutionary Biology</i> , 2010, 10, 321.	3.2	120
21	Chloroplast genome sequence of the moss <i>Tortula ruralis</i> : gene content, polymorphism, and structural arrangement relative to other green plant chloroplast genomes. <i>BMC Genomics</i> , 2010, 11, 143.	2.8	64
22	Extensive Reorganization of the Plastid Genome of <i>Trifolium subterraneum</i> (Fabaceae) Is Associated with Numerous Repeated Sequences and Novel DNA Insertions. <i>Journal of Molecular Evolution</i> , 2008, 67, 696-704.	1.8	217
23	Functional Gene Losses Occur with Minimal Size Reduction in the Plastid Genome of the Parasitic Liverwort <i>Aneura mirabilis</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 393-401.	8.9	108
24	Analysis of 81 genes from 64 plastid genomes resolves relationships in angiosperms and identifies genome-scale evolutionary patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19369-19374.	7.1	1,016
25	Phylogenetic and evolutionary implications of complete chloroplast genome sequences of four early-diverging angiosperms: <i>Buxus</i> (Buxaceae), <i>Chloranthus</i> (Chloranthaceae), <i>Dioscorea</i> (Dioscoreaceae), and <i>Illicium</i> (Schisandraceae). <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 547-563.	2.7	154
26	The complete mitochondrial genome of a gecko and the phylogenetic position of the Middle Eastern <i>Teratoscincus keyserlingii</i> . <i>Molecular Phylogenetics and Evolution</i> , 2005, 36, 188-193.	2.7	27
27	Identifying the Basal Angiosperm Node in Chloroplast Genome Phylogenies: Sampling One's Way Out of the Felsenstein Zone. <i>Molecular Biology and Evolution</i> , 2005, 22, 1948-1963.	8.9	242
28	Methods for Obtaining and Analyzing Whole Chloroplast Genome Sequences. <i>Methods in Enzymology</i> , 2005, 395, 348-384.	1.0	410
29	The first complete chloroplast genome sequence of a lycophyte, <i>Huperzia lucidula</i> (Lycopodiaceae). <i>Gene</i> , 2005, 350, 117-128.	2.2	101
30	Phylogenetic relationships among amphisbaenian reptiles based on complete mitochondrial genomic sequences. <i>Molecular Phylogenetics and Evolution</i> , 2004, 33, 22-31.	2.7	102