Judy D Wall

List of Publications by Year
in descending order

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64
papers

4,977
citations

201674

27
h-index

114465

63
g-index

121
all docs

121
docs citations

121
times ranked

6031
citing authors

#	Article	IF	Citations
1	The Genetic Basis for Bacterial Mercury Methylation. Science, 2013, 339, 1332-1335.	12.6	778
2	The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough. Nature Biotechnology, 2004, 22, 554-559.	17.5	559
3	Mutant phenotypes for thousands of bacterial genes of unknown function. Nature, 2018, 557, 503-509.	27.8	433
4	Uranium Reduction. Annual Review of Microbiology, 2006, 60, 149-166.	7.3	389
5	Sulfate-Reducing Bacterium Desulfovibrio desulfuricans ND132 as a Model for Understanding Bacterial Mercury Methylation. Applied and Environmental Microbiology, 2011, 77, 3938-3951.	3.1	252
6	A Post-Genomic View of the Ecophysiology, Catabolism and Biotechnological Relevance of Sulphate-Reducing Prokaryotes. Advances in Microbial Physiology, 2015, 66, 55-321.	2.4	238
7	Genetic basis for nitrate resistance in Desulfovibrio strains. Frontiers in Microbiology, 2014, 5, 153.	3.5	202
8	How sulphate-reducing microorganisms cope with stress: lessons from systems biology. Nature Reviews Microbiology, 2011, 9, 452-466.	28.6	169
9	Systems biology guided by XCMS Online metabolomics. Nature Methods, 2017, 14, 461-462.	19.0	168
10	Salt Stress in Desulfovibrio vulgaris Hildenborough: an Integrated Genomics Approach. Journal of Bacteriology, 2006, 188, 4068-4078.	2.2	155
11	Determining the Reliability of Measuring Mercury Cycling Gene Abundance with Correlations with Mercury and Methylmercury Concentrations. Environmental Science & Technology, 2019, 53, 8649-8663.	10.0	99
12	Energetic Consequences of Nitrite Stress in Desulfovibrio vulgaris Hildenborough, Inferred from Global Transcriptional Analysis. Applied and Environmental Microbiology, 2006, 72, 4370-4381.	3.1	92
13	Filling gaps in bacterial amino acid biosynthesis pathways with high-throughput genetics. PLoS Genetics, 2018, 14, e1007147.	3.5	90
14	Photoproduction of H ₂ from Cellulose by an Anaerobic Bacterial Coculture. Applied and Environmental Microbiology, 1983, 45, 1300-1305.	3.1	84
15	Development of a Markerless Genetic Exchange System for <i>Desulfovibrio vulgaris</i> Hildenborough and Its Use in Generating a Strain with Increased Transformation Efficiency. Applied and Environmental Microbiology, 2009, 75, 7682-7691.	3.1	79
16	The direct role of selenocysteine in [NiFeSe] hydrogenase maturation and catalysis. Nature Chemical Biology, 2017, 13, 544-550.	8.0	76
17	Site-Directed Mutagenesis of HgcA and HgcB Reveals Amino Acid Residues Important for Mercury Methylation. Applied and Environmental Microbiology, 2015, 81, 3205-3217.	3.1	73
18	The <scp>FlxABCD</scp>â€‹<scp>HdrABC</scp> proteins correspond to a novel <scp>NADH</scp> dehydrogenase/heterodisulfide reductase widespread in anaerobic bacteria and involved in ethanol metabolism in <scp><i>D</i></scp><i>esulfovibrio vulgaris</i>â€...<scp>H</scp>ildenborough. Environmental Microbiology, 2015, 17, 2288-2305.	3.8	71

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19	Analysis of a Ferric Uptake Regulator (Fur) Mutant of <i>Desulfovibrio vulgaris</i> Hildenborough. Applied and Environmental Microbiology, 2007, 73, 5389-5400.	3.1	70
20	Impact of elevated nitrate on sulfate-reducing bacteria: a comparative Study of <i>Desulfovibrio vulgaris</i>. ISME Journal, 2010, 4, 1386-1397.	9.8	67
21	Erosion of functional independence early in the evolution of a microbial mutualism. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14822-14827.	7.1	63
22	Characterization of NaCl tolerance in <i>Desulfovibrio vulgaris</i> Hildenborough through experimental evolution. ISME Journal, 2013, 7, 1790-1802.	9.8	46
23	Genome Sequence of the Mercury-Methylating Strain Desulfovibrio desulfuricans ND132. Journal of Bacteriology, 2011, 193, 2078-2079.	2.2	41
24	Carbon Amendments Alter Microbial Community Structure and Net Mercury Methylation Potential in Sediments. Applied and Environmental Microbiology, 2018, 84, .	3.1	38
25	Functional Characterization of Crp/Fnr-Type Global Transcriptional Regulators in Desulfovibrio vulgaris Hildenborough. Applied and Environmental Microbiology, 2012, 78, 1168-1177.	3.1	32
26	Biofilm growth mode promotes maximum carrying capacity and community stability during product inhibition syntrophy. Frontiers in Microbiology, 2014, 5, 693.	3.5	32
27	Methods for Engineering Sulfate Reducing Bacteria of the Genus Desulfovibrio. Methods in Enzymology, 2011, 497, 503-517.	1.0	29
28	Hydrogen uptake deficient mutants of Rhodopseudomonas capsulata. Archives of Microbiology, 1983, 136, 20-25.	2.2	28
29	Rapid Transposon Liquid Enrichment Sequencing (TnLE-seq) for Gene Fitness Evaluation in Underdeveloped Bacterial Systems. Applied and Environmental Microbiology, 2013, 79, 7510-7517.	3.1	28
30	Identification of a cyclic-di-GMP-modulating response regulator that impacts biofilm formation in a model sulfate reducing bacterium. Frontiers in Microbiology, 2014, 5, 382.	3.5	28
31	Independence of Nitrate and Nitrite Inhibition of <i>Desulfovibrio vulgaris</i> Hildenborough and Use of Nitrite as a Substrate for Growth. Environmental Science & Technology, 2015, 49, 924-931.	10.0	28
32	Regulation of Nitrite Stress Response in Desulfovibrio vulgaris Hildenborough, a Model Sulfate-Reducing Bacterium. Journal of Bacteriology, 2015, 197, 3400-3408.	2.2	27
33	Overexpression of Desulfovibrio vulgaris Hildenborough cytochrome c553 in Desulfovibrio desulfuricans G200. Evidence of conformational heterogeneity in the oxidized protein by NMR. FEBS Journal, 1993, 218, 293-301.	0.2	25
34	Electron transfer pathways of formate-driven H2 production in Desulfovibrio. Applied Microbiology and Biotechnology, 2016, 100, 8135-8146.	3.6	25
35	Rapid selective sweep of pre-existing polymorphisms and slow fixation of new mutations in experimental evolution of <i>Desulfovibrio vulgaris</i>. ISME Journal, 2015, 9, 2360-2372.	9.8	24
36	Mechanism for microbial population collapse in a fluctuating resource environment. Molecular Systems Biology, 2017, 13, 919.	7.2	22

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37	Ironâ€•and aluminiumâ€induced depletion of molybdenum in acidic environments impedes the nitrogen cycle. Environmental Microbiology, 2019, 21, 152-163.	3.8	22
38	Novel Metal Cation Resistance Systems from Mutant Fitness Analysis of Denitrifying Pseudomonas stutzeri. Applied and Environmental Microbiology, 2016, 82, 6046-6056.	3.1	21
39	Kinetics of Enzymatic Mercury Methylation at Nanomolar Concentrations Catalyzed by HgcAB. Applied and Environmental Microbiology, 2019, 85, .	3.1	20
40	Sulfur Isotope Fractionation during the Evolutionary Adaptation of a Sulfate-Reducing Bacterium. Applied and Environmental Microbiology, 2015, 81, 2676-2689.	3.1	18
41	Unintended Laboratory-Driven Evolution Reveals Genetic Requirements for Biofilm Formation by <i>Desulfovibrio vulgaris</i> Hildenborough. MBio, 2017, 8, .	4.1	18
42	Cr(VI) reduction and physiological toxicity are impacted by resource ratio in Desulfovibrio vulgaris. Applied Microbiology and Biotechnology, 2018, 102, 2839-2850.	3.6	18
43	Characterization of subsurface media from locations up- and down-gradient of a uranium-contaminated aquifer. Chemosphere, 2020, 255, 126951.	8.2	18
44	Global Isotope Metabolomics Reveals Adaptive Strategies for Nitrogen Assimilation. ACS Chemical Biology, 2016, 11, 1677-1685.	3.4	17
45	Effects of the Tyr64 Substitution on the Stability of Cytochrome c553, a low Oxidoreduction-Potential Cytochrome from Desulfovibrio vulgaris Hildenborough. FEBS Journal, 1994, 226, 423-432.	0.2	16
46	Bacterial Interactomes: Interacting Protein Partners Share Similar Function and Are Validated in Independent Assays More Frequently Than Previously Reported. Molecular and Cellular Proteomics, 2016, 15, 1539-1555.	3.8	16
47	Membrane protein complex of APS reductase and Qmo is present in Desulfovibrio vulgaris and Desulfovibrio alaskensis. Microbiology (United Kingdom), 2013, 159, 2162-2168.	1.8	14
48	Adaptation of <i>Desulfovibrio alaskensis</i> G20 to perchlorate, a specific inhibitor of sulfate reduction. Environmental Microbiology, 2019, 21, 1395-1406.	3.8	14
49	Key Metabolites and Mechanistic Changes for Salt Tolerance in an Experimentally Evolved Sulfate-Reducing Bacterium, <i>Desulfovibrio vulgaris</i>. MBio, 2017, 8, .	4.1	13
50	Pseudodesulfovibrio mercurii sp. nov., a mercury-methylating bacterium isolated from sediment. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	1.7	13
51	Deconstructing the Dissimilatory Sulfate Reduction Pathway: Isotope Fractionation of a Mutant Unable of Growth on Sulfate. Frontiers in Microbiology, 2018, 9, 3110.	3.5	11
52	Bioremediation Potential of Streptomyces sp. MOE6 for Toxic Metals and Oil. Polysaccharides, 2021, 2, 47-68.	4.8	11
53	Experimental evolution reveals nitrate tolerance mechanisms in <i>Desulfovibrio vulgaris</i>. ISME Journal, 2020, 14, 2862-2876.	9.8	10
54	Exploring the role of CheA3 in Desulfovibrio vulgaris Hildenborough motility. Frontiers in Microbiology, 2014, 5, 77.	3.5	7

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55	A novel whole-cell biosensor of Pseudomonas aeruginosa to monitor the expression of quorum sensing genes. Applied Microbiology and Biotechnology, 2018, 102, 6023-6038.	3.6	7
56	Novel Mode of Molybdate Inhibition of Desulfovibrio vulgaris Hildenborough. Frontiers in Microbiology, 2020, 11, 610455.	3.5	7
57	Complete Genome Sequence of Pelosinus fermentans JBW45, a Member of a Remarkably Competitive Group of <i>Negativicutes</i> in the <i>Firmicutes</i> Phylum. Genome Announcements, 2015, 3, .	0.8	6
58	Deletion Mutants, Archived Transposon Library, and Tagged Protein Constructs of the Model Sulfate-Reducing Bacterium Desulfovibrio vulgaris Hildenborough. Microbiology Resource Announcements, 2021, 10, .	0.6	6
59	Effects of Genetic and Physiological Divergence on the Evolution of a Sulfate-Reducing Bacterium under Conditions of Elevated Temperature. MBio, 2020, 11, .	4.1	5
60	Complete Genome Sequence of Desulfovibrio desulfuricans IC1, a Sulfonate-Respiring Anaerobe. Microbiology Resource Announcements, 2019, 8, .	0.6	3
61	LurR is a regulator of the central lactate oxidation pathway in sulfate-reducing Desulfovibrio species. PLoS ONE, 2019, 14, e0214960.	2.5	3
62	Complete Genome Sequencing of <i>Streptomyces</i> sp. Strain MOE7, Which Produces an Extracellular Polysaccharide with Antioxidant and Antitumor Activities. Genome Announcements, 2017, 5, .	0.8	1
63	Biofilm Interaction Mapping and Analysis (BIMA) of Interspecific Interactions in Pseudomonas Co-culture Biofilms. Frontiers in Microbiology, 2021, 12, 757856.	3.5	1
64	Genetic Basis of Chromate Adaptation and the Role of the Pre-existing Genetic Divergence during an Experimental Evolution Study with Desulfovibrio vulgaris Populations. MSystems, 2021, 6, e0049321.	3.8	0