

# Judy D Wall

## List of Publications by Year in descending order

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64  
papers

4,977  
citations

201674

27  
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114465

63  
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121  
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121  
docs citations

121  
times ranked

6031  
citing authors

#	ARTICLE	IF	CITATIONS
1	Bioremediation Potential of <i>Streptomyces</i> sp. MOE6 for Toxic Metals and Oil. <i>Polysaccharides</i> , 2021, 2, 47-68.	4.8	11
2	Deletion Mutants, Archived Transposon Library, and Tagged Protein Constructs of the Model Sulfate-Reducing Bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	6
3	Genetic Basis of Chromate Adaptation and the Role of the Pre-existing Genetic Divergence during an Experimental Evolution Study with <i>Desulfovibrio vulgaris</i> Populations. <i>MSystems</i> , 2021, 6, e0049321.	3.8	0
4	Biofilm Interaction Mapping and Analysis (BIMA) of Interspecific Interactions in <i>Pseudomonas</i> Co-culture Biofilms. <i>Frontiers in Microbiology</i> , 2021, 12, 757856.	3.5	1
5	Experimental evolution reveals nitrate tolerance mechanisms in <i>Desulfovibrio vulgaris</i> . <i>ISME Journal</i> , 2020, 14, 2862-2876.	9.8	10
6	Effects of Genetic and Physiological Divergence on the Evolution of a Sulfate-Reducing Bacterium under Conditions of Elevated Temperature. <i>MBio</i> , 2020, 11, .	4.1	5
7	Novel Mode of Molybdate Inhibition of <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Frontiers in Microbiology</i> , 2020, 11, 610455.	3.5	7
8	Characterization of subsurface media from locations up- and down-gradient of a uranium-contaminated aquifer. <i>Chemosphere</i> , 2020, 255, 126951.	8.2	18
9	Complete Genome Sequence of <i>Desulfovibrio desulfuricans</i> IC1, a Sulfonate-Respiring Anaerobe. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
10	Determining the Reliability of Measuring Mercury Cycling Gene Abundance with Correlations with Mercury and Methylmercury Concentrations. <i>Environmental Science &amp; Technology</i> , 2019, 53, 8649-8663.	10.0	99
11	LurR is a regulator of the central lactate oxidation pathway in sulfate-reducing <i>Desulfovibrio</i> species. <i>PLoS ONE</i> , 2019, 14, e0214960.	2.5	3
12	Kinetics of Enzymatic Mercury Methylation at Nanomolar Concentrations Catalyzed by HgcAB. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	20
13	Adaptation of <i>Desulfovibrio alaskensis</i> G20 to perchlorate, a specific inhibitor of sulfate reduction. <i>Environmental Microbiology</i> , 2019, 21, 1395-1406.	3.8	14
14	Iron- and aluminium-induced depletion of molybdenum in acidic environments impedes the nitrogen cycle. <i>Environmental Microbiology</i> , 2019, 21, 152-163.	3.8	22
15	<i>Pseudodesulfovibrio mercurii</i> sp. nov., a mercury-methylating bacterium isolated from sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	1.7	13
16	Cr(VI) reduction and physiological toxicity are impacted by resource ratio in <i>Desulfovibrio vulgaris</i> . <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2839-2850.	3.6	18
17	A novel whole-cell biosensor of <i>Pseudomonas aeruginosa</i> to monitor the expression of quorum sensing genes. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 6023-6038.	3.6	7
18	Carbon Amendments Alter Microbial Community Structure and Net Mercury Methylation Potential in Sediments. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	38

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19	Deconstructing the Dissimilatory Sulfate Reduction Pathway: Isotope Fractionation of a Mutant Unable of Growth on Sulfate. <i>Frontiers in Microbiology</i> , 2018, 9, 3110.	3.5	11
20	Mutant phenotypes for thousands of bacterial genes of unknown function. <i>Nature</i> , 2018, 557, 503-509.	27.8	433
21	Filling gaps in bacterial amino acid biosynthesis pathways with high-throughput genetics. <i>PLoS Genetics</i> , 2018, 14, e1007147.	3.5	90
22	Systems biology guided by XCMS Online metabolomics. <i>Nature Methods</i> , 2017, 14, 461-462.	19.0	168
23	The direct role of selenocysteine in [NiFeSe] hydrogenase maturation and catalysis. <i>Nature Chemical Biology</i> , 2017, 13, 544-550.	8.0	76
24	Mechanism for microbial population collapse in a fluctuating resource environment. <i>Molecular Systems Biology</i> , 2017, 13, 919.	7.2	22
25	Unintended Laboratory-Driven Evolution Reveals Genetic Requirements for Biofilm Formation by <i>Desulfovibrio vulgaris</i> Hildenborough. <i>MBio</i> , 2017, 8, .	4.1	18
26	Complete Genome Sequencing of <i>Streptomyces</i> sp. Strain MOE7, Which Produces an Extracellular Polysaccharide with Antioxidant and Antitumor Activities. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
27	Key Metabolites and Mechanistic Changes for Salt Tolerance in an Experimentally Evolved Sulfate-Reducing Bacterium, <i>Desulfovibrio vulgaris</i> . <i>MBio</i> , 2017, 8, .	4.1	13
28	Bacterial Interactomes: Interacting Protein Partners Share Similar Function and Are Validated in Independent Assays More Frequently Than Previously Reported. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1539-1555.	3.8	16
29	Global Isotope Metabolomics Reveals Adaptive Strategies for Nitrogen Assimilation. <i>ACS Chemical Biology</i> , 2016, 11, 1677-1685.	3.4	17
30	Novel Metal Cation Resistance Systems from Mutant Fitness Analysis of Denitrifying <i>Pseudomonas stutzeri</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 6046-6056.	3.1	21
31	Electron transfer pathways of formate-driven H <sub>2</sub> production in <i>Desulfovibrio</i> . <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 8135-8146.	3.6	25
32	Complete Genome Sequence of <i>Pelosinus fermentans</i> JBW45, a Member of a Remarkably Competitive Group of <i>Negativicutes</i> in the <i>Firmicutes</i> Phylum. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
33	Independence of Nitrate and Nitrite Inhibition of <i>Desulfovibrio vulgaris</i> Hildenborough and Use of Nitrite as a Substrate for Growth. <i>Environmental Science &amp; Technology</i> , 2015, 49, 924-931.	10.0	28
34	Site-Directed Mutagenesis of HgcA and HgcB Reveals Amino Acid Residues Important for Mercury Methylation. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3205-3217.	3.1	73
35	A Post-Genomic View of the Ecophysiology, Catabolism and Biotechnological Relevance of Sulphate-Reducing Prokaryotes. <i>Advances in Microbial Physiology</i> , 2015, 66, 55-321.	2.4	238
36	Sulfur Isotope Fractionation during the Evolutionary Adaptation of a Sulfate-Reducing Bacterium. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2676-2689.	3.1	18

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37	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
38	Regulation of Nitrite Stress Response in <i>Desulfovibrio vulgaris</i> Hildenborough, a Model Sulfate-Reducing Bacterium. Journal of Bacteriology, 2015, 197, 3400-3408.	2.2	27
39	The FlxABC and HdrABC proteins correspond to a novel NADH dehydrogenase/heterodisulfide reductase widespread in anaerobic bacteria and involved in ethanol metabolism in <i>Desulfovibrio vulgaris</i> Hildenborough. Environmental Microbiology, 2015, 17, 2288-2305.	3.8	71
40	Exploring the role of CheA3 in <i>Desulfovibrio vulgaris</i> Hildenborough motility. Frontiers in Microbiology, 2014, 5, 77.	3.5	7
41	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
42	Biofilm growth mode promotes maximum carrying capacity and community stability during product inhibition syntrophy. Frontiers in Microbiology, 2014, 5, 693.	3.5	32
43	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
44	Genetic basis for nitrate resistance in <i>Desulfovibrio</i> strains. Frontiers in Microbiology, 2014, 5, 153.	3.5	202
45	Membrane protein complex of APS reductase and Qmo is present in <i>Desulfovibrio vulgaris</i> and <i>Desulfovibrio alaskensis</i> . Microbiology (United Kingdom), 2013, 159, 2162-2168.	1.8	14
46	The Genetic Basis for Bacterial Mercury Methylation. Science, 2013, 339, 1332-1335.	12.6	778
47	Characterization of NaCl tolerance in <i>Desulfovibrio vulgaris</i> Hildenborough through experimental evolution. ISME Journal, 2013, 7, 1790-1802.	9.8	46
48	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
49	Functional Characterization of Crp/Fnr-Type Global Transcriptional Regulators in <i>Desulfovibrio vulgaris</i> Hildenborough. Applied and Environmental Microbiology, 2012, 78, 1168-1177.	3.1	32
50	Methods for Engineering Sulfate Reducing Bacteria of the Genus <i>Desulfovibrio</i> . Methods in Enzymology, 2011, 497, 503-517.	1.0	29
51	Sulfate-Reducing Bacterium <i>Desulfovibrio desulfuricans</i> ND132 as a Model for Understanding Bacterial Mercury Methylation. Applied and Environmental Microbiology, 2011, 77, 3938-3951.	3.1	252
52	How sulphate-reducing microorganisms cope with stress: lessons from systems biology. Nature Reviews Microbiology, 2011, 9, 452-466.	28.6	169
53	Genome Sequence of the Mercury-Methylating Strain <i>Desulfovibrio desulfuricans</i> ND132. Journal of Bacteriology, 2011, 193, 2078-2079.	2.2	41
54	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

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55	Development of a Markerless Genetic Exchange System for <i>Desulfovibrio vulgaris</i> Hildenborough and Its Use in Generating a Strain with Increased Transformation Efficiency. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7682-7691.	3.1	79
56	Analysis of a Ferric Uptake Regulator (Fur) Mutant of <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5389-5400.	3.1	70
57	Uranium Reduction. <i>Annual Review of Microbiology</i> , 2006, 60, 149-166.	7.3	389
58	Salt Stress in <i>Desulfovibrio vulgaris</i> Hildenborough: an Integrated Genomics Approach. <i>Journal of Bacteriology</i> , 2006, 188, 4068-4078.	2.2	155
59	Energetic Consequences of Nitrite Stress in <i>Desulfovibrio vulgaris</i> Hildenborough, Inferred from Global Transcriptional Analysis. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4370-4381.	3.1	92
60	The genome sequence of the anaerobic, sulfate-reducing bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Nature Biotechnology</i> , 2004, 22, 554-559.	17.5	559
61	Effects of the Tyr64 Substitution on the Stability of Cytochrome c553, a low Oxidoreduction-Potential Cytochrome from <i>Desulfovibrio vulgaris</i> Hildenborough. <i>FEBS Journal</i> , 1994, 226, 423-432.	0.2	16
62	Overexpression of <i>Desulfovibrio vulgaris</i> Hildenborough cytochrome c553 in <i>Desulfovibrio desulfuricans</i> G200. Evidence of conformational heterogeneity in the oxidized protein by NMR. <i>FEBS Journal</i> , 1993, 218, 293-301.	0.2	25
63	Hydrogen uptake deficient mutants of <i>Rhodopseudomonas capsulata</i> . <i>Archives of Microbiology</i> , 1983, 136, 20-25.	2.2	28
64	Photoproduction of H <sub>2</sub> from Cellulose by an Anaerobic Bacterial Coculture. <i>Applied and Environmental Microbiology</i> , 1983, 45, 1300-1305.	3.1	84