Ellen L Neidle

List of Publications by Year in descending order

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#	Article	lF	CITATIONS
1	Characterization of Highly Ferulate-Tolerant Acinetobacter baylyi ADP1 Isolates by a Rapid Reverse Engineering Method. Applied and Environmental Microbiology, 2022, 88, AEM0178021.	1.4	5
2	Regulation of <scp>l</scp> - and <scp>d</scp> -Aspartate Transport and Metabolism in Acinetobacter baylyi ADP1. Applied and Environmental Microbiology, 2022, 88, .	1.4	4
3	Gene amplification, laboratory evolution, and biosensor screening reveal MucK as a terephthalic acid transporter in Acinetobacter baylyi ADP1. Metabolic Engineering, 2020, 62, 260-274.	3.6	35
4	Development of a genetic toolset for the highly engineerable and metabolically versatile Acinetobacter baylyi ADP1. Nucleic Acids Research, 2020, 48, 5169-5182.	6.5	30
5	Engineering CatM, a LysR-Type Transcriptional Regulator, to Respond Synergistically to Two Effectors. Genes, 2019, 10, 421.	1.0	10
6	Enabling microbial syringol conversion through structure-guided protein engineering. Proceedings of the United States of America, 2019, 116, 13970-13976.	3.3	41
7	Removal of aromatic inhibitors produced from lignocellulosic hydrolysates by Acinetobacter baylyi ADP1 with formation of ethanol by Kluyveromyces marxianus. Biotechnology for Biofuels, 2019, 12, 91.	6.2	25
8	Vibrio fischeri DarR Directs Responses to d -Aspartate and Represents a Group of Similar LysR-Type Transcriptional Regulators. Journal of Bacteriology, 2018, 200, .	1.0	9
9	A promiscuous cytochrome P450 aromatic O-demethylase for lignin bioconversion. Nature Communications, 2018, 9, 2487.	5.8	135
10	Accelerating pathway evolution by increasing the gene dosage of chromosomal segments. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7105-7110.	3.3	52
11	Malonate degradation in Acinetobacter baylyi ADP1: operon organization and regulation by MdcR. Microbiology (United Kingdom), 2017, 163, 789-803.	0.7	9
12	Novel heterologous bacterial system reveals enhanced susceptibility to DNA damage mediated by yqgF, a nearly ubiquitous and often essential gene. Microbiology (United Kingdom), 2016, 162, 1808-1821.	0.7	4
13	The DNA-binding domain of BenM reveals the structural basis for the recognition of a T-N ₁₁ -A sequence motif by LysR-type transcriptional regulators. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1995-2007.	2.5	52
14	Copy number change: evolving views on gene amplification. Future Microbiology, 2013, 8, 887-899.	1.0	55
15	Analysis of IS <i>1236</i> -Mediated Gene Amplification Events in Acinetobacter baylyi ADP1. Journal of Bacteriology, 2012, 194, 4395-4405.	1.0	14
16	Genomeâ€wide selection for increased copy number in <i>Acinetobacter baylyi</i> ADP1: locus and contextâ€dependent variation in gene amplification. Molecular Microbiology, 2012, 83, 520-535.	1.2	26
17	Defying stereotypes: the elusive search for a universal model of LysRâ€ŧype regulation. Molecular Microbiology, 2012, 83, 453-456.	1.2	25
18	<i>Acinetobacter baylyi</i> ADP1: Transforming the choice of model organism. IUBMB Life, 2011, 63, 1075-1080.	1.5	53

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19	Discovery of a Gene Involved in a Third Bacterial Protoporphyrinogen Oxidase Activity through Comparative Genomic Analysis and Functional Complementation. Applied and Environmental Microbiology, 2011, 77, 4795-4801.	1.4	28
20	Full-Length Structures of BenM and Two Variants Reveal Different Oligomerization Schemes for LysR-Type Transcriptional Regulators. Journal of Molecular Biology, 2010, 404, 568-586.	2.0	55
21	Inducer responses of BenM, a LysRâ€ŧype transcriptional regulator from <i>Acinetobacter baylyi</i> ADP1. Molecular Microbiology, 2009, 72, 881-894.	1.2	49
22	Redox-dependent structural changes in archaeal and bacterial Rieske-type [2Fe-2S] clusters. Protein Science, 2009, 11, 2969-2973.	3.1	27
23	Distinct Effector-binding Sites Enable Synergistic Transcriptional Activation by BenM, a LysR-type Regulator. Journal of Molecular Biology, 2007, 367, 616-629.	2.0	89
24	Double trouble: medical implications of genetic duplication and amplification in bacteria. Future Microbiology, 2007, 2, 309-321.	1.0	25
25	Oligomerization of BenM, a LysR-type transcriptional regulator: structural basis for the aggregation of proteins in this family. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 361-368.	0.7	34
26	CatM Regulation of the benABCDE Operon: Functional Divergence of Two LysR-Type Paralogs in Acinetobacter baylyi ADP1. Applied and Environmental Microbiology, 2006, 72, 1749-1758.	1.4	42
27	Benzoate Decreases the Binding of cis , cis -Muconate to the BenM Regulator despite the Synergistic Effect of Both Compounds on Transcriptional Activation. Journal of Bacteriology, 2004, 186, 1200-1204.	1.0	26
28	Diverse Organization of Genes of the β-Ketoadipate Pathway in Members of the Marine Roseobacter Lineage. Applied and Environmental Microbiology, 2004, 70, 1658-1668.	1.4	52
29	Crystallization of the effector-binding domains of BenM and CatM, LysR-type transcriptional regulators fromAcinetobactersp. ADP1. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 105-108.	2.5	17
30	Selection for Gene Clustering by Tandem Duplication. Annual Review of Microbiology, 2004, 58, 119-142.	2.9	89
31	Gene Amplification Involves Site-specific Short Homology-independent Illegitimate Recombination in Acinetobacter sp. Strain ADP1. Journal of Molecular Biology, 2004, 338, 643-656.	2.0	43
32	Genome plasticity in Acinetobacter: new degradative capabilities acquired by the spontaneous amplification of large chromosomal segments. Molecular Microbiology, 2003, 47, 1291-1304.	1.2	69
33	Histidine Ligand Protonation and Redox Potential in the Rieske Dioxygenases:  Role of a Conserved Aspartate in Anthranilate 1,2-Dioxygenase. Biochemistry, 2003, 42, 13625-13636.	1.2	38
34	Transcriptional Cross-Regulation of the Catechol and Protocatechuate Branches of the β-Ketoadipate Pathway Contributes to Carbon Source-Dependent Expression of the Acinetobacter sp. Strain ADP1 pobA Gene. Applied and Environmental Microbiology, 2003, 69, 1598-1606.	1.4	53
35	Synergistic transcriptional activation by one regulatory protein in response to two metabolites. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7693-7698. 	3.3	84
36	X-ray Crystal Structure of Benzoate 1,2-Dioxygenase Reductase from Acinetobacter sp. Strain ADP1. Journal of Molecular Biology, 2002, 318, 261-272.	2.0	57

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37	The benPK operon, proposed to play a role in transport, is part of a regulon for benzoate catabolism in Acinetobacter sp. strain ADP1. Microbiology (United Kingdom), 2002, 148, 1213-1223.	0.7	35
38	Cloning and Expression of the Benzoate Dioxygenase Genes from Rhodococcus sp. Strain 19070. Applied and Environmental Microbiology, 2001, 67, 2507-2514.	1.4	39
39	Characterization and Evolution of Anthranilate 1,2-Dioxygenase from Acinetobacter sp. Strain ADP1. Journal of Bacteriology, 2001, 183, 109-118.	1.0	56
40	Diversity of the Ring-Cleaving Dioxygenase Gene pcaH in a Salt Marsh Bacterial Community. Applied and Environmental Microbiology, 2001, 67, 5801-5809.	1.4	58
41	Mutations in catB, the Gene Encoding Muconate Cycloisomerase, Activate Transcription of the Distalben Genes and Contribute to a Complex Regulatory Circuit in Acinetobacter sp. Strain ADP1. Journal of Bacteriology, 2000, 182, 7044-7052.	1.0	18
42	Key Aromatic-Ring-Cleaving Enzyme, Protocatechuate 3,4-Dioxygenase, in the Ecologically Important Marine Roseobacter Lineage. Applied and Environmental Microbiology, 2000, 66, 4662-4672.	1.4	132
43	<i>areABC</i> Genes Determine the Catabolism of Aryl Esters in <i>Acinetobacter</i> sp. Strain ADP1. Journal of Bacteriology, 1999, 181, 4568-4575.	1.0	38
44	Similarities between the antABC -Encoded Anthranilate Dioxygenase and the benABC -Encoded Benzoate Dioxygenase of Acinetobacter sp. Strain ADP1. Journal of Bacteriology, 1998, 180, 4466-4474.	1.0	71
45	Regulation of Benzoate Degradation in <i>Acinetobacter</i> sp. Strain ADP1 by BenM, a LysR-Type Transcriptional Activator. Journal of Bacteriology, 1998, 180, 2493-2501.	1.0	125
46	Directed introduction of DNA cleavage sites to produce a high-resolution genetic and physical map of the Acinetobacter sp. strain ADP1 (BD413UE) chromosome. Microbiology (United Kingdom), 1997, 143, 1345-1357.	0.7	55
47	Cis-diol dehydrogenases encoded by the TOL pWW0 plasmid xylL gene and the Acinetobacter calcoaceticus chromosomal benD gene are members of the short-chain alcohol dehydrogenase superfamily. FEBS Journal, 1992, 204, 113-120.	0.2	96
48	[20] Catechol and chlorocatechol 1,2-Dioxygenases. Methods in Enzymology, 1990, 188, 122-126.	0.4	51