VÃ±Ìctor de Lorenzo

List of Publications by Year
in descending order

352 papers	20,223 citations	10351 72 h-index	18075 120 g-index
383 all docs	383 docs citations	383 times ranked	13225 citing authors

#	Article	IF	Citations
1	Standardization of inducer-activated broad host range expression modules: debugging and refactoring an alkane-responsive AlkS/<i>PalkB</i> device. Synthetic Biology, 2023, 6, .	1.2	2
2	Versioning biological cells for trustworthy cell engineering. Nature Communications, 2022, 13, 765.	5.8	6
3	15 years of microbial biotechnology: the time has come to think bigâ€”and act soon. Microbial Biotechnology, 2022, 15, 240-246.	2.0	1
4	Standardization of regulatory nodes for engineering heterologous gene expression: a feasibility study. Microbial Biotechnology, 2022, 15, 2250-2265.	2.0	8
5	High-Efficiency Multi-site Genomic Editing (HEMSE) Made Easy. Methods in Molecular Biology, 2022, 2479, 37-52.	0.4	0
6	Genome-wide proteinâ€“DNA interaction site mapping in bacteria using a double-stranded DNA-specific cytosine deaminase. Nature Microbiology, 2022, 7, 844-855.	5.9	12
7	Hypermutation of specific genomic loci of <i>Pseudomonas putida</i> for continuous evolution of target genes. Microbial Biotechnology, 2022, 15, 2309-2323.	2.0	3
8	Environmental Galenics: large-scale fortification of extant microbiomes with engineered bioremediation agents. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, .	1.8	13
9	For the sake of the Bioeconomy: define what a Synthetic Biology Chassis is!. New Biotechnology, 2021, 60, 44-51.	2.4	34
10	Quantitative assessment of morphological traits of planktonic bacterial aggregates. Water Research, 2021, 188, 116468.	5.3	4
11	A Standardized Inverter Package Borne by Broad Host Range Plasmids for Genetic Circuit Design in Gram-Negative Bacteria. ACS Synthetic Biology, 2021, 10, 213-217.	1.9	9
12	Ribonucleases control distinct traits of <i>Pseudomonas putida</i> lifestyle. Environmental Microbiology, 2021, 23, 174-189.	1.8	5
13	Reconfiguration of metabolic fluxes in <i>Pseudomonas putida</i> as a response to sub-lethal oxidative stress. ISME Journal, 2021, 15, 1751-1766.	4.4	79
14	Low CyaA expression and antiâ€cooperative binding of cAMP to CRP frames the scope of the cognate regulon of Pseudomonas putida. Environmental Microbiology, 2021, 23, 1732-1749.	1.8	4
15	Subcellular Architecture of the <i>xyl</i> Gene Expression Flow of the TOL Catabolic Plasmid of Pseudomonas putida mt-2. MBio, 2021, 12, .	1.8	3
16	A Bifan Motif Shaped by ArsR1, ArsR2, and Their Cognate Promoters Frames Arsenic Tolerance of Pseudomonas putida. Frontiers in Microbiology, 2021, 12, 641440.	1.5	2
17	Refactoring the Conjugation Machinery of Promiscuous Plasmid RP4 into a Device for Conversion of Gram-Negative Isolates to Hfr Strains. ACS Synthetic Biology, 2021, 10, 690-697.	1.9	7
18	Transcriptional control of 2,4â€dinitrotoluene degradation in <i>Burkholderia sp</i>. <scp>R34</scp> bears a regulatory patch that eases pathway evolution. Environmental Microbiology, 2021, 23, 2522-2531.	1.8	8

#	Article	IF	Citations
19	Identification of a selfâ€sufficient cytochrome P450 monooxygenase from <i>Cupriavidus pinatubonensis</i> JMP134 involved in 2â€hydroxyphenylacetic acid catabolism, via homogentisate pathway. Microbial Biotechnology, 2021, 14, 1944-1960.	2.0	7
20	An updated structural model of the A domain of the <i>Pseudomonas putida</i>â€‰<scp>XylR</scp>â€‰regulator poses an atypical interplay with aromatic effectors. Environmental Microbiology, 2021, 23, 4418-4433.	1.8	2
21	Picking the right metaphors for addressing microbial systems: economic theory helps understanding biological complexity. International Microbiology, 2021, 24, 507-519.	1.1	2
22	Engineering Tropism of <i>Pseudomonas putida</i> toward Target Surfaces through Ectopic Display of Recombinant Nanobodies. ACS Synthetic Biology, 2021, 10, 2049-2059.	1.9	11
23	MIXed plastics biodegradation and UPcycling using microbial communities: EU Horizon 2020 project MIX-UP started January 2020. Environmental Sciences Europe, 2021, 33, 99.	2.6	33
24	Automated design and implementation of a NOR gate in Pseudomonas putida. Synthetic Biology, 2021, 6, ysab024.	1.2	12
25	The faulty SOS response of Pseudomonas putida KT2440 stems from an inefficient RecAâ€LexA interplay. Environmental Microbiology, 2021, 23, 1608-1619.	1.8	0
26	Contextual dependencies expand the re-usability of genetic inverters. Nature Communications, 2021, 12, 355.	5.8	35
27	ssDNA recombineering boosts in vivo evolution of nanobodies displayed on bacterial surfaces. Communications Biology, 2021, 4, 1169.	2.0	6
28	Targetron-Assisted Delivery of Exogenous DNA Sequences into <i>Pseudomonas putida</i> through CRISPR-Aided Counterselection. ACS Synthetic Biology, 2021, 10, 2552-2565.	1.9	8
29	Gross transcriptomic analysis of Pseudomonas putida for diagnosing environmental shifts. Microbial Biotechnology, 2020, 13, 263-273.	2.0	7
30	Mismatch repair hierarchy of <i>Pseudomonas putida</i> revealed by mutagenic ssDNA recombineering of the <i>pyrF</i> gene. Environmental Microbiology, 2020, 22, 45-58.	1.8	22
31	SEVA 3.0: an update of the Standard European Vector Architecture for enabling portability of genetic constructs among diverse bacterial hosts. Nucleic Acids Research, 2020, 48, D1164-D1170.	6.5	82
32	Multiple-Site Diversification of Regulatory Sequences Enables Interspecies Operability of Genetic Devices. ACS Synthetic Biology, 2020, 9, 104-114.	1.9	15
33	An automated DIY framework for experimental evolution ofPseudomonas putida. Microbial Biotechnology, 2020, 14, 2679-2685.	2.0	5
34	SEVA 3.1: enabling interoperability of DNA assembly among the SEVA, BioBricks and Type IIS restriction enzyme standards. Microbial Biotechnology, 2020, 13, 1793-1806.	2.0	26
35	Naked Bacterium: Emerging Properties of a Surfome-Streamlined <i>Pseudomonas putida</i> Strain. ACS Synthetic Biology, 2020, 9, 2477-2492.	1.9	15
36	Surface Display of Designer Protein Scaffolds on Genome-Reduced Strains of <i>Pseudomonas putida</i>. ACS Synthetic Biology, 2020, 9, 2749-2764.	1.9	16

#	Article	IF	Citations
37	In vivo diversification of target genomic sites using processive base deaminase fusions blocked by dCas9. Nature Communications, 2020, 11, 6436.	5.8	47
38	Biotransformation of <scp>d</scp>â€xylose to <scp>d</scp>â€xylonate coupled to mediumâ€chainâ€length polyhydroxyalkanoate production in cellobioseâ€grown <i>Pseudomonas putida</i> EM42. Microbial Biotechnology, 2020, 13, 1273-1283.	2.0	20
39	Exploiting geometric similarity for statistical quantification of fluorescence spatial patterns in bacterial colonies. BMC Bioinformatics, 2020, 21, 224.	1.2	0
40	The Wsp intermembrane complex mediates metabolic control of the swimâ€attach decision of <i>Pseudomonas putida</i>. Environmental Microbiology, 2020, 22, 3535-3547.	1.8	13
41	High-Efficiency Multi-site Genomic Editing of Pseudomonas putida through Thermoinducible ssDNA Recombineering. IScience, 2020, 23, 100946.	1.9	32
42	<scp>ArsH</scp> protects <i>Pseudomonas putida</i> from oxidative damage caused by exposure to arsenic. Environmental Microbiology, 2020, 22, 2230-2242.	1.8	28
43	Multifunctional SEVA shuttle vectors for actinomycetes and Gramâ€negative bacteria. MicrobiologyOpen, 2020, 9, 1135-1149.	1.2	12
44	Environmental Performance of <i>Pseudomonas putida</i> with a Uracylated Genome. ChemBioChem, 2020, 21, 3255-3265.	1.3	3
45	Synthetic Biology for Terraformation Lessons from Mars, Earth, and the Microbiome. Life, 2020, 10, 14.	1.1	28
46	Linking Engineered Cells to Their Digital Twins: A Version Control System for Strain Engineering. ACS Synthetic Biology, 2020, 9, 536-545.	1.9	23
47	A Broad Host Range Plasmid-Based Roadmap for ssDNA-Based Recombineering in Gram-Negative Bacteria. Methods in Molecular Biology, 2020, 2075, 383-398.	0.4	11
48	The long journey towards standards for engineering biosystems. EMBO Reports, 2020, 21, e50521.	2.0	46
49	A SsrA/NIa-based Strategy for Post-Translational Regulation of Protein Levels in Gram-negative Bacteria. Bio-protocol, 2020, 10, e3688.	0.2	0
50	Recombination-Independent Genome Editing through CRISPR/Cas9-Enhanced TargeTron Delivery. ACS Synthetic Biology, 2019, 8, 2186-2193.	1.9	13
51	Reverse Engineering of an Aspirin-Responsive Transcriptional Regulator in <i>Escherichia coli</i>. ACS Synthetic Biology, 2019, 8, 1890-1900.	1.9	13
52	<scp>CRISPR</scp>/Cas9â€enhanced ss<scp>DNA</scp> recombineering for <i>Pseudomonas putida</i>. Microbial Biotechnology, 2019, 12, 1076-1089.	2.0	31
53	Spatial organization of the gene expression hardware in <i>Pseudomonas putida</i>. Environmental Microbiology, 2019, 21, 1645-1658.	1.8	14
54	Genomic Responses of Pseudomonas putida to Aromatic Hydrocarbons. , 2019, , 1-15.		0

#	Article	IF	Citations
55	Functional implementation of a linear glycolysis for sugar catabolism in Pseudomonas putida. Metabolic Engineering, 2019, 54, 200-211.	3.6	56
56	Pseudomonas putida in the quest of programmable chemistry. Current Opinion in Biotechnology, 2019, 59, 111-121.	3.3	38
57	The urgent need for microbiology literacy in society. Environmental Microbiology, 2019, 21, 1513-1528.	1.8	99
58	Improved Thermotolerance of Genomeâ€Reduced <i>Pseudomonas putida</i> EM42 Enables Effective Functioning of the P_L/<i>c</i>I857 System. Biotechnology Journal, 2019, 14, e1800483.	1.8	27
59	The important versus the exciting: reining contradictions in contemporary biotechnology. Microbial Biotechnology, 2019, 12, 32-34.	2.0	20
60	Evolving metabolism of 2,4â€dinitrotoluene triggers SOSâ€independent diversification of host cells. Environmental Microbiology, 2019, 21, 314-326.	1.8	13
61	The Synthetic Microbiology Caucus: a fresh channel for exploring new ideas, challenging conventional wisdom and fostering community projects. Microbial Biotechnology, 2019, 12, 3-4.	2.0	0
62	Digitalizing heterologous gene expression in Gramâ€negative bacteria with a portable ON/OFF module. Molecular Systems Biology, 2019, 15, e8777.	3.2	33
63	Genomic Responses of Pseudomonas putida to Aromatic Hydrocarbons. , 2019, , 287-301.		0
64	Assembly of a Custom-made Device to Study Spreading Patterns of Pseudomonas putida Biofilms. Bio-protocol, 2019, 9, e3238.	0.2	0
65	Biodegradation and Bioremediation: An Introduction. , 2019, , 1-20.		0
66	Assessing Carbon Source-Dependent Phenotypic Variability in Pseudomonas putida. Methods in Molecular Biology, 2018, 1745, 287-301.	0.4	4
67	Environmental microbiology to the rescue of planet earth. Environmental Microbiology, 2018, 20, 1910-1916.	1.8	8
68	The power of synthetic biology for bioproduction, remediation and pollution control. EMBO Reports, 2018, 19, .	2.0	83
69	Biological standards for the Knowledge-Based BioEconomy: What is at stake. New Biotechnology, 2018, 40, 170-180.	2.4	46
70	CRISPR/Cas9â€Based Counterselection Boosts Recombineering Efficiency in <i>Pseudomonas putida</i>. Biotechnology Journal, 2018, 13, e1700161.	1.8	115
71	A standardized workflow for surveying recombinases expands bacterial genomeâ€editing capabilities. Microbial Biotechnology, 2018, 11, 176-188.	2.0	43
72	A Post-translational Metabolic Switch Enables Complete Decoupling of Bacterial Growth from Biopolymer Production in Engineered <i>Escherichia coli</i>. ACS Synthetic Biology, 2018, 7, 2686-2697.	1.9	58

#	Article	IF	Citations
73	The interplay of EIIA^{Ntr} with Câ€source regulation of the <i>Pu</i> promoter of <i>Pseudomonas putida</i> mtâ€2. Environmental Microbiology, 2018, 20, 4555-4566.	1.8	3
74	The Metabolic Redox Regime of Pseudomonas putida Tunes Its Evolvability toward Novel Xenobiotic Substrates. MBio, 2018, 9, .	1.8	51
75	Pseudomonas putida as a functional chassis for industrial biocatalysis: From native biochemistry to trans-metabolism. Metabolic Engineering, 2018, 50, 142-155.	3.6	338
76	Refactoring the upper sugar metabolism of Pseudomonas putida for co-utilization of cellobiose, xylose, and glucose. Metabolic Engineering, 2018, 48, 94-108.	3.6	86
77	An Engineered Device for Indoleacetic Acid Production under Quorum Sensing Signals Enables <i>Cupriavidus pinatubonensis</i> JMP134 To Stimulate Plant Growth. ACS Synthetic Biology, 2018, 7, 1519-1527.	1.9	19
78	Modulating Heterologous Gene Expression with Portable mRNA-Stabilizing 5â€²-UTR Sequences. ACS Synthetic Biology, 2018, 7, 2177-2188.	1.9	24
79	Biodegradation and Bioremediation: An Introduction. , 2018, , 1-21.		1
80	Re-Factoring Glycolytic Genes for Targeted Engineering of Catabolism in Gram-Negative Bacteria. Methods in Molecular Biology, 2018, 1772, 3-24.	0.4	3
81	Evolutionary tinkering vs. rational engineering in the times of synthetic biology. Life Sciences, Society and Policy, 2018, 14, 18.	3.1	10
82	Dynamics of <i>Pseudomonas putida</i> biofilms in an upscale experimental framework. Journal of Industrial Microbiology and Biotechnology, 2018, 45, 899-911.	1.4	7
83	The biofilm matrix polysaccharides cellulose and alginate both protect Pseudomonas putida mt-2 against reactive oxygen species generated under matric stress and copper exposure. Microbiology (United Kingdom), 2018, 164, 883-888.	0.7	33
84	Refactoring the Embdenâ€“Meyerhofâ€“Parnas Pathway as a Whole of Portable GlucoBricks for Implantation of Glycolytic Modules in Gram-Negative Bacteria. ACS Synthetic Biology, 2017, 6, 793-805.	1.9	50
85	The doâ€itâ€yourself movement as a source of innovation in biotechnology â€“ and much more. Microbial Biotechnology, 2017, 10, 517-519.	2.0	13
86	Deconvolution of Gene Expression Noise into Spatial Dynamics of Transcription Factorâ€“Promoter Interplay. ACS Synthetic Biology, 2017, 6, 1359-1369.	1.9	39
87	Molecular tools and emerging strategies for deep genetic/genomic refactoring of Pseudomonas. Current Opinion in Biotechnology, 2017, 47, 120-132.	3.3	63
88	Synthetic microbiology: from analogy to methodology. Microbial Biotechnology, 2017, 10, 1264-1266.	2.0	7
89	Bioremediation 3.0: Engineering pollutant-removing bacteria in the times of systemic biology. Biotechnology Advances, 2017, 35, 845-866.	6.0	240
90	Seven microbial bioâ€processes to help the planet. Microbial Biotechnology, 2017, 10, 995-998.	2.0	25

#	Article	IF	Citations
91	CellShape: A userâ€friendly image analysis tool for quantitative visualization of bacterial cell factories inside. Biotechnology Journal, 2017, 12, 1600323.	1.8	15
92	Engineering Gram-Negative Microbial Cell Factories Using Transposon Vectors. Methods in Molecular Biology, 2017, 1498, 273-293.	0.4	23
93	Physical Forces Shape Group Identity of Swimming Pseudomonas putida Cells. Frontiers in Microbiology, 2016, 7, 1437.	1.5	26
94	The <scp>RNA</scp> chaperone <scp>Hfq</scp> enables the environmental stress tolerance superâ€phenotype of <scp><i>P</i></scp><i>seudomonas putida</i>. Environmental Microbiology, 2016, 18, 3309-3326.	1.8	25
95	Stenosis triggers spread of helical Pseudomonas biofilms in cylindrical flow systems. Scientific Reports, 2016, 6, 27170.	1.6	4
96	A Metabolic Widget Adjusts the Phosphoenolpyruvate-Dependent Fructose Influx in Pseudomonas putida. MSystems, 2016, 1, .	1.7	28
97	From dirt to industrial applications: Pseudomonas putida as a Synthetic Biology chassis for hosting harsh biochemical reactions. Current Opinion in Chemical Biology, 2016, 34, 20-29.	2.8	199
98	Nitrogen regulation of the <i>xyl</i> genes of <i>Pseudomonas putida</i> mtâ€2 propagates into a significant effect of nitrate on <i>m</i>â€xylene mineralization in soil. Microbial Biotechnology, 2016, 9, 814-823.	2.0	5
99	Pyridine nucleotide transhydrogenases enable redox balance of <i>Pseudomonas putida</i> during biodegradation of aromatic compounds. Environmental Microbiology, 2016, 18, 3565-3582.	1.8	58
100	Bioremediation at a global scale: from the test tube to planet Earth. Microbial Biotechnology, 2016, 9, 618-625.	2.0	40
101	Editorial overview: Microbial systems biology: systems biology prepares the ground for successful synthetic biology. Current Opinion in Microbiology, 2016, 33, viii-x.	2.3	2
102	Microbial Biotechnologyâ€2020. Microbial Biotechnology, 2016, 9, 529-529.	2.0	2
103	The quest for the minimal bacterial genome. Current Opinion in Biotechnology, 2016, 42, 216-224.	3.3	49
104	The Ssr protein (T1E_1405) from <i>Pseudomonas putida</i> DOTâ€T1E enables oligonucleotideâ€based recombineering in platform strain <i>P. putida</i> EM42. Biotechnology Journal, 2016, 11, 1309-1319.	1.8	65
105	An Implementation-Focused Bio/Algorithmic Workflow for Synthetic Biology. ACS Synthetic Biology, 2016, 5, 1127-1135.	1.9	31
106	The revisited genome of <i>Pseudomonas putida</i> KT2440 enlightens its value as a robust metabolic <i>chassis</i>. Environmental Microbiology, 2016, 18, 3403-3424.	1.8	270
107	Introduction to Systems and Synthetic Biology in Hydrocarbon Microbiology: Applications. Springer Protocols, 2016, , 1-8.	0.1	0
108	Highâ€resolution analysis of the <i>m</i>â€xylene/toluene biodegradation subtranscriptome of <scp><i>P</i></scp><i>seudomonas putida</i> mtâ€2. Environmental Microbiology, 2016, 18, 3327-3341.	1.8	18

#	Article	IF	Citations
109	Transcription factor levels enable metabolic diversification of single cells of environmental bacteria. ISME Journal, 2016, 10, 1122-1133.	4.4	13
110	Synthetic bugs on the loose: containment options for deeply engineered (micro)organisms. Current Opinion in Biotechnology, 2016, 38, 90-96.	3.3	67
111	Rationally rewiring the connectivity of the XylR/Pu regulatory node of the m-xylene degradation pathway in Pseudomonas putida. Integrative Biology (United Kingdom), 2016, 8, 571-576.	0.6	0
112	Data on the standardization of a cyclohexanone-responsive expression system for Gram-negative bacteria. Data in Brief, 2016, 6, 738-744.	0.5	17
113	Genetic programming of catalytic Pseudomonas putida biofilms for boosting biodegradation of haloalkanes. Metabolic Engineering, 2016, 33, 109-118.	3.6	103
114	Systems and Synthetic Biology in Hydrocarbon Microbiology: Tools. Springer Protocols, 2015, , 1-7.	0.1	1
115	Exacerbation of substrate toxicity by IPTG in Escherichia coli BL21(DE3) carrying a synthetic metabolic pathway. Microbial Cell Factories, 2015, 14, 201.	1.9	145
116	Plastic waste as a novel substrate for industrial biotechnology. Microbial Biotechnology, 2015, 8, 900-903.	2.0	134
117	Mining Environmental Plasmids for Synthetic Biology Parts and Devices. Microbiology Spectrum, 2015, 3, PLAS-0033-2014.	1.2	18
118	Knock-In-Leave-Behind (KILB): Genetic Grafting of Protease-Cleaving Sequences into Permissive Sites of Proteins with a Tn5-Based Transposition System. Springer Protocols, 2015, , 71-85.	0.1	1
119	Pseudomonas putida mt-2 tolerates reactive oxygen species generated during matric stress by inducing a major oxidative defense response. BMC Microbiology, 2015, 15, 202.	1.3	24
120	The two paralogue <scp><i>phoN</i></scp> (phosphinothricin acetyl transferase) genes of <scp><i>P</i></scp><i>seudomonas putida</i> encode functionally different proteins. Environmental Microbiology, 2015, 17, 3330-3340.	1.8	6
121	SEVA 2.0: an update of the Standard European Vector Architecture for de-/re-construction of bacterial functionalities. Nucleic Acids Research, 2015, 43, D1183-D1189.	6.5	195
122	Broadening the SEVA Plasmid Repertoire to Facilitate Genomic Editing of Gram-Negative Bacteria. Springer Protocols, 2015, , 9-27.	0.1	9
123	Freeing <scp><i>P</i></scp><i>seudomonas putida</i>â€…<scp>KT</scp>2440 of its proviral load strengthens endurance to environmental stresses. Environmental Microbiology, 2015, 17, 76-90.	1.8	62
124	Functional coexistence of twin arsenic resistance systems in <scp><i>P</i></scp><i>seudomonas putida</i>â€…<scp>KT</scp>2440. Environmental Microbiology, 2015, 17, 229-238.	1.8	52
125	Genome reduction boosts heterologous gene expression in Pseudomonas putida. Microbial Cell Factories, 2015, 14, 23.	1.9	142
126	Tn7-Based Device for Calibrated Heterologous Gene Expression in <i>Pseudomonas putida</i>. ACS Synthetic Biology, 2015, 4, 1341-1351.	1.9	169

#	Article	IF	Citations
127	Phenotypic knockouts of selected metabolic pathways by targeting enzymes with camel-derived nanobodies (VHHs). Metabolic Engineering, 2015, 30, 40-48.	3.6	8
128	Pseudomonas putida KT2440 Strain Metabolizes Glucose through a Cycle Formed by Enzymes of the Entner-Doudoroff, Embden-Meyerhof-Parnas, and Pentose Phosphate Pathways. Journal of Biological Chemistry, 2015, 290, 25920-25932.	1.6	269
129	It's the metabolism, stupid!. Environmental Microbiology Reports, 2015, 7, 18-19.	1.0	14
130	The Glycerol-Dependent Metabolic Persistence of Pseudomonas putida KT2440 Reflects the Regulatory Logic of the GlpR Repressor. MBio, 2015, 6, .	1.8	62
131	Widening functional boundaries of the Ïƒ⁵⁴promoter Pu of Pseudomonas putida by defeating extant physiological constraints. Molecular BioSystems, 2015, 11, 734-742.	2.9	4
132	The differential response of the <scp><i>P</i></scp><i>ben</i> promoter of <scp><i>P</i></scp><i>seudomonas putida</i>â€…<scp>mt</scp>â€2 to <scp>BenR</scp> and <scp>XylS</scp> prevents metabolic conflicts in <scp><i>m</i></scp><i>â€‹</i>xylene biodegradation. Environmental Microbiology, 2015, 17, 64-75.	1.8	29
133	Chassis organism from <i>Corynebacterium glutamicum</i>: The way towards biotechnological domestication of Corynebacteria. Biotechnology Journal, 2015, 10, 244-245.	1.8	11
134	<scp><i>P</i></scp><i>seudomonas aeruginosa:</i> the making of a pathogen. Environmental Microbiology, 2015, 17, 1-3.	1.8	24
135	Confidence, tolerance, and allowance in biological engineering: The nuts and bolts of living things. BioEssays, 2015, 37, 95-102.	1.2	22
136	BiologÃa sintÃ©tica: la ingenierÃa al asalto de la complejidad biolÃ³gica. Arbor, 2014, 190, a149.	0.1	2
137	Pipelines for New Chemicals: a strategy to create new value chains and stimulate innovation-based economic revival in Southern European countries. Environmental Microbiology, 2014, 16, 9-18.	1.8	16
138	The pWW0 plasmid imposes a stochastic expression regime to the chromosomal<i>ortho</i>pathway for benzoate metabolism in<i>Pseudomonas putida</i>. FEMS Microbiology Letters, 2014, 356, 176-183.	0.7	8
139	Metabolic and regulatory rearrangements underlying glycerol metabolism in <i><scp>P</scp>seudomonas putida</i>â€…<scp>KT</scp>2440. Environmental Microbiology, 2014, 16, 239-254.	1.8	91
140	Chemical reactivity drives spatiotemporal organisation of bacterial metabolism. FEMS Microbiology Reviews, 2014, 39, n/a-n/a.	3.9	67
141	Pseudomonas 2.0: genetic upgrading of P. putida KT2440 as an enhanced host for heterologous gene expression. Microbial Cell Factories, 2014, 13, 159.	1.9	199
142	Robustness of Pseudomonas putida KT2440 as a host for ethanol biosynthesis. New Biotechnology, 2014, 31, 562-571.	2.4	62
143	Engineering Multicellular Logic in Bacteria with Metabolic Wires. ACS Synthetic Biology, 2014, 3, 204-209.	1.9	30
144	From the <i>selfish gene</i> to <i>selfish metabolism</i>: Revisiting the central dogma. BioEssays, 2014, 36, 226-235.	1.2	60

#	Article	IF	Citations
145	The private life of environmental bacteria: pollutant biodegradation at the single cell level. Environmental Microbiology, 2014, 16, 628-642.	1.8	63
146	A second chromosomal copy of the <scp><i>catA</i></scp> gene endows <scp><i>P</i></scp><i>seudomonas putida</i>â€…<scp>mt</scp>â€2 with an enzymatic safety valve for excess of catechol. Environmental Microbiology, 2014, 16, 1767-1778.	1.8	38
147	Biotechnological domestication of pseudomonads using synthetic biology. Nature Reviews Microbiology, 2014, 12, 368-379.	13.6	332
148	From the phosphoenolpyruvate phosphotransferase system to selfish metabolism: a story retraced in<i>Pseudomonas putida</i>. FEMS Microbiology Letters, 2014, 356, 144-153.	0.7	26
149	The metabolic cost of flagellar motion in <scp><i>P</i></scp><i>seudomonas putida</i>â€…<scp>KT</scp>2440. Environmental Microbiology, 2014, 16, 291-303.	1.8	132
150	Volatilization of Arsenic from Polluted Soil by <i>Pseudomonas putida</i> Engineered for Expression of the <i>arsM</i> Arsenic(III) S-Adenosine Methyltransferase Gene. Environmental Science & Technology, 2014, 48, 10337-10344.	4.6	106
151	Fructose 1â€phosphate is the one and only physiological effector of the Cra (FruR) regulator of <i>Pseudomonas putida</i>. FEBS Open Bio, 2014, 4, 377-386.	1.0	28
152	New Transposon Tools Tailored for Metabolic Engineering of Gram-Negative Microbial Cell Factories. Frontiers in Bioengineering and Biotechnology, 2014, 2, 46.	2.0	85
153	The Standard European Vector Architecture (SEVA) Plasmid Toolkit. Methods in Molecular Biology, 2014, 1149, 469-478.	0.4	28
154	Chromosomal Integration of Transcriptional Fusions. Methods in Molecular Biology, 2014, 1149, 479-489.	0.4	7
155	Promoter Fusions with Optical Outputs in Individual Cells and in Populations. Methods in Molecular Biology, 2014, 1149, 579-590.	0.4	1
156	The IHF regulon of exponentially growing <i>Pseudomonas putida</i> cells. Environmental Microbiology, 2013, 15, 49-63.	1.8	14
157	Cra regulates the crossâ€talk between the two branches of the phosphoenolpyruvateâ€ƒ:â€ƒphosphotransferase system of <i>Pseudomonas putida</i>. Environmental Microbiology, 2013, 15, 121-132.	1.8	18
158	Accumulation of inorganic polyphosphate enables stress endurance and catalytic vigour in Pseudomonas putida KT2440. Microbial Cell Factories, 2013, 12, 50.	1.9	77
159	Why are chlorinated pollutants so difficult to degrade aerobically? Redox stress limits 1,3-dichloprop-1-ene metabolism by<i>Pseudomonas pavonaceae</i>. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120377.	1.8	53
160	Expanding the Boolean Logic of the Prokaryotic Transcription Factor XylR by Functionalization of Permissive Sites with a Protease-Target Sequence. ACS Synthetic Biology, 2013, 2, 594-603.	1.9	16
161	Decoding the genetic networks of environmental bacteria: regulatory moonlighting of the TOL system of <i>Pseudomonas putida</i> mt-2. ISME Journal, 2013, 7, 229-232.	4.4	15
162	The <scp>TOL</scp> network of <i><scp>P</scp>seudomonas putida</i> mtâ€2 processes multiple environmental inputs into a narrow <i>response space</i>. Environmental Microbiology, 2013, 15, 271-286.	1.8	14

#	Article	IF	Citations
163	From the test tube to the environment â€“ and back. Environmental Microbiology, 2013, 15, 6-11.	1.8	14
164	NanoPad: An integrated platform for bacterial production of camel nanobodies aimed at detecting environmental biomarkers. Proteomics, 2013, 13, 2766-2775.	1.3	7
165	The <scp>E</scp>ntnerâ€“<scp>D</scp>oudoroff pathway empowers <i><scp>P</scp>seudomonas putida</i>â€…<scp>KT</scp>2440 with a high tolerance to oxidative stress. Environmental Microbiology, 2013, 15, 1772-1785.	1.8	195
166	Implantation of unmarked regulatory and metabolic modules in Gram-negative bacteria with specialised mini-transposon delivery vectors. Journal of Biotechnology, 2013, 163, 143-154.	1.9	51
167	Engineering an anaerobic metabolic regime in Pseudomonas putida KT2440 for the anoxic biodegradation of 1,3-dichloroprop-1-ene. Metabolic Engineering, 2013, 15, 98-112.	3.6	93
168	Endogenous Stress Caused by Faulty Oxidation Reactions Fosters Evolution of 2,4-Dinitrotoluene-Degrading Bacteria. PLoS Genetics, 2013, 9, e1003764.	1.5	74
169	Towards Functional Orthogonalisation of Protein Complexes: Individualisation of GroEL Monomers Leads to Distinct Quasihomogeneous Single Rings. ChemBioChem, 2013, 14, 2310-2321.	1.3	10
170	Vestigialization of arsenic resistance phenotypes/genotypes inChromobacterium violaceumstrains thriving in pristine Brazilian sites. Biocatalysis and Biotransformation, 2013, 31, 281-291.	1.1	2
171	Transcriptomic fingerprinting of <i><scp>P</scp>seudomonas putida</i> under alternative physiological regimes. Environmental Microbiology Reports, 2013, 5, 883-891.	1.0	75
172	Engineering the Soil Bacterium Pseudomonas putida for Arsenic Methylation. Applied and Environmental Microbiology, 2013, 79, 4493-4495.	1.4	85
173	The Standard European Vector Architecture (SEVA): a coherent platform for the analysis and deployment of complex prokaryotic phenotypes. Nucleic Acids Research, 2013, 41, D666-D675.	6.5	556
174	Increasing Signal Specificity of the TOL Network of Pseudomonas putida mt-2 by Rewiring the Connectivity of the Master Regulator XylR. PLoS Genetics, 2012, 8, e1002963.	1.5	26
175	Regulatory Tasks of the Phosphoenolpyruvate-Phosphotransferase System of Pseudomonas putida in Central Carbon Metabolism. MBio, 2012, 3, .	1.8	78
176	A GFP-lacZ Bicistronic Reporter System for Promoter Analysis in Environmental Gram-Negative Bacteria. PLoS ONE, 2012, 7, e34675.	1.1	19
177	Stochasticity of TOL plasmid catabolic promoters sets a bimodal expression regime in <i>Pseudomonas putida</i> mtâ€2 exposed to <i>mâ€</i>xylene. Molecular Microbiology, 2012, 86, 199-211.	1.2	20
178	Production and characterization of a recombinant single-chain antibody (scFv) for tracing the Ïƒ54 factor of Pseudomonas putida. Journal of Biotechnology, 2012, 160, 33-41.	1.9	0
179	Transposon-Based and Plasmid-Based Genetic Tools for Editing Genomes of Gram-Negative Bacteria. Methods in Molecular Biology, 2012, 813, 267-283.	0.4	92
180	Towards a global biotechnology scenario. Current Opinion in Biotechnology, 2012, 23, 827-829.	3.3	1

#	Article	IF	Citations
181	Streamlining of a Pseudomonas putida Genome Using a Combinatorial Deletion Method Based on Minitransposon Insertion and the Flp-FRT Recombination System. Methods in Molecular Biology, 2012, 813, 249-266.	0.4	13
182	Broadening the signal specificity of prokaryotic promoters by modifying cis-regulatory elements associated with a single transcription factor. Molecular BioSystems, 2012, 8, 1950.	2.9	30
183	Engineering Whole-Cell Biosensors with No Antibiotic Markers for Monitoring Aromatic Compounds in the Environment. Methods in Molecular Biology, 2012, 834, 261-281.	0.4	19
184	Quantitative, Non-Disruptive Monitoring of Transcription in Single Cells with a Broad-Host Range GFP-luxCDABE Dual Reporter System. PLoS ONE, 2012, 7, e52000.	1.1	22
185	Synthetic constructs in/for the environment: Managing the interplay between natural and engineered Biology. FEBS Letters, 2012, 586, 2199-2206.	1.3	78
186	COVER: <i>a priori</i> estimation of coverage for metagenomic sequencing. Environmental Microbiology Reports, 2012, 4, 335-341.	1.0	13
187	The Crp regulator of <i>Pseudomonas putida</i>: evidence of an unusually high affinity for its physiological effector, cAMP. Environmental Microbiology, 2012, 14, 702-713.	1.8	14
188	Random and cyclical deletion of large DNA segments in the genome of <i>Pseudomonas putida</i>. Environmental Microbiology, 2012, 14, 1444-1453.	1.8	56
189	A composite feed-forward loop I4-FFL involving IHF and Crc stabilizes expression of the XylR regulator of Pseudomonas putida mt-2 from growth phase perturbations. Molecular BioSystems, 2011, 7, 2982.	2.9	21
190	Implementing an ORâ€“NOT (ORN) logic gate with components of the SOS regulatory network of Escherichia coli. Molecular BioSystems, 2011, 7, 2389.	2.9	18
191	The interplay of the EIIANtr component of the nitrogen-related phosphotransferase system (PTSNtr) of Pseudomonas putida with pyruvate dehydrogenase. Biochimica Et Biophysica Acta - General Subjects, 2011, 1810, 995-1005.	1.1	32
192	Predicting microbial growth kinetics with the use of genetic circuit models. Computer Aided Chemical Engineering, 2011, 29, 1321-1325.	0.3	0
193	Regulatory exaptation of the catabolite repression protein (Crp)â€“cAMP system in <i>Pseudomonas putida</i>. Environmental Microbiology, 2011, 13, 324-339.	1.8	34
194	Monitoring biodegradative enzymes with nanobodies raised in <i>Camelus dromedarius</i> with mixtures of catabolic proteins. Environmental Microbiology, 2011, 13, 960-974.	1.8	21
195	The <i>logicome</i> of environmental bacteria: merging catabolic and regulatory events with Boolean formalisms. Environmental Microbiology, 2011, 13, 2389-2402.	1.8	36
196	Engineering multiple genomic deletions in Gramâ€negative bacteria: analysis of the multiâ€resistant antibiotic profile of <i>Pseudomonas putida</i> KT2440. Environmental Microbiology, 2011, 13, 2702-2716.	1.8	329
197	Cooperative amino acid changes shift the response of the Ïƒ⁵⁴â€dependent regulator XylR from natural <i>mâ€</i>xylene towards xenobiotic 2,4â€dinitrotoluene. Molecular Microbiology, 2011, 79, 1248-1259.	1.2	26
198	Association of dnt genes of Burkholderia sp. DNT with the substrate-blind regulator DntR draws the evolutionary itinerary of 2,4-dinitrotoluene biodegradation. Molecular Microbiology, 2011, 82, 287-299.	1.2	29

#	Article	IF	Citations
199	Functional analysis of the integration host factor site of the Ïƒ⁵⁴<i>Pu</i> promoter of <i>Pseudomonas putida</i> by <i>in vivo</i> UV imprinting. Molecular Microbiology, 2011, 82, 591-601.	1.2	7
200	pBAM1: an all-synthetic genetic tool for analysis and construction of complex bacterial phenotypes. BMC Microbiology, 2011, 11, 38.	1.3	142
201	In situ detection of aromatic compounds with biosensor Pseudomonas putida cells preserved and delivered to soil in water-soluble gelatin capsules. Analytical and Bioanalytical Chemistry, 2011, 400, 1093-1104.	1.9	34
202	The ten grand challenges of synthetic life. Systems and Synthetic Biology, 2011, 5, 1-9.	1.0	54
203	The logic layout of the TOL network of Pseudomonas putida pWW0 plasmid stems from a metabolic amplifier motif (MAM) that optimizes biodegradation of m-xylene. BMC Systems Biology, 2011, 5, 191.	3.0	32
204	Genes that move the window of viability of life: Lessons from bacteria thriving at the cold extreme. BioEssays, 2011, 33, 38-42.	1.2	11
205	Improving the prediction of Pseudomonas putida mt-2 growth kinetics with the use of a gene expression regulation model of the TOL plasmid. Biochemical Engineering Journal, 2011, 55, 108-118.	1.8	11
206	Linking genes to microbial growth kineticsâ€"An integrated biochemical systems engineering approach. Metabolic Engineering, 2011, 13, 401-413.	3.6	26
207	Fructose 1-Phosphate Is the Preferred Effector of the Metabolic Regulator Cra of Pseudomonas putida. Journal of Biological Chemistry, 2011, 286, 9351-9359.	1.6	23
208	Beware of metaphors: Chasses and orthogonality in synthetic biology. Bioengineered Bugs, 2011, 2, 3-7.	2.0	64
209	The regulatory logic of <i>mâ€</i>xylene biodegradation by <i>Pseudomonas putida</i> mtâ€2 exposed by dynamic modelling of the principal node <i>Ps/Pr</i> of the TOL plasmid. Environmental Microbiology, 2010, 12, 1705-1718.	1.8	38
210	Synthetic biology gains momentum in Europe. Systems and Synthetic Biology, 2010, 4, 145-147.	1.0	1
211	EnvMine: A text-mining system for the automatic extraction of contextual information. BMC Bioinformatics, 2010, 11, 294.	1.2	18
212	An Electroâ€optical Device from a Biofilm Structure Created by Bacterial Activity. Advanced Materials, 2010, 22, 4846-4850.	11.1	17
213	Synthetic biology: something old, something newâ€‰â€¦. BioEssays, 2010, 32, 267-270.	1.2	11
214	Environmental biosafety in the age of Synthetic Biology: Do we really need a radical new approach?. BioEssays, 2010, 32, 926-931.	1.2	37
215	Beautiful is not (necessarily) right: Overcoming the Phryne's trial syndrome. BioEssays, 2010, 32, 1011-1011.	1.2	0
216	Engineering input/output nodes in prokaryotic regulatory circuits. FEMS Microbiology Reviews, 2010, 34, 842-865.	3.9	45

#	Article	IF	Citations
217	Combining Genetic Circuit and Microbial Growth Kinetic Models: A Challenge for Biological Modelling. Computer Aided Chemical Engineering, 2010, 28, 301-306.	0.3	1
218	Noise and Robustness in Prokaryotic Regulatory Networks. Annual Review of Microbiology, 2010, 64, 257-275.	2.9	104
219	Microbial responses to environmental arsenic. BioMetals, 2009, 22, 117-130.	1.8	309
220	Microbial systems biology: bottom up and top down. FEMS Microbiology Reviews, 2009, 33, 1-2.	3.9	11
221	Ã€ la carte transcriptional regulators: unlocking responses of the prokaryotic enhancer-binding protein XylR to non-natural effectors. Molecular Microbiology, 2008, 42, 47-59.	1.2	72
222	Systems biology approaches to bioremediation. Current Opinion in Biotechnology, 2008, 19, 579-589.	3.3	227
223	Synthetic biology: discovering new worlds and new words. EMBO Reports, 2008, 9, 822-827.	2.0	148
224	Stable implantation of orthogonal sensor circuits in Gramâ€negative bacteria for environmental release. Environmental Microbiology, 2008, 10, 3305-3316.	1.8	72
225	Transcriptional <i>wiring</i> of the TOL plasmid regulatory network to its host involves the submission of the Ïƒ⁵⁴â€promoter <i>Pu</i> to the response regulator PprA. Molecular Microbiology, 2008, 69, 698-713.	1.2	24
226	Mining logic gates in prokaryotic transcriptional regulation networks. FEBS Letters, 2008, 582, 1237-1244.	1.3	82
227	Tracing explosives in soil with transcriptional regulators of <i>Pseudomonas putida</i> evolved for responding to nitrotoluenes. Microbial Biotechnology, 2008, 1, 236-246.	2.0	79
228	Evidence of In Vivo Cross Talk between the Nitrogen-Related and Fructose-Related Branches of the Carbohydrate Phosphotransferase System of <i>Pseudomonas putida</i>. Journal of Bacteriology, 2008, 190, 3374-3380.	1.0	38
229	Sinorhizobium meliloti Fur-Like (Mur) Protein Binds a Fur Box-Like Sequence Present in the mntA Promoter in a Manganese-Responsive Manner. Applied and Environmental Microbiology, 2007, 73, 4832-4838.	1.4	37
230	Growth-dependent Phosphorylation of the PtsN (EINtr) Protein of Pseudomonas putida. Journal of Biological Chemistry, 2007, 282, 18206-18211.	1.6	28
231	The Phosphotransferase System Formed by PtsP, PtsO, and PtsN Proteins Controls Production of Polyhydroxyalkanoates in Pseudomonas putida. Journal of Bacteriology, 2007, 189, 4529-4533.	1.0	75
232	The ancestral role of the phosphoenolpyruvateâ€“carbohydrate phosphotransferase system (PTS) as exposed by comparative genomics. Research in Microbiology, 2007, 158, 666-670.	1.0	42
233	Non-disruptive release of Pseudomonas putida proteins by in situ electric breakdown of intact cells. Journal of Microbiological Methods, 2007, 71, 179-185.	0.7	7
234	The environmental fate of organic pollutants through the global microbial metabolism. Molecular Systems Biology, 2007, 3, 114.	3.2	43

#	Article	IF	Citations
235	Emergence of novel functions in transcriptional regulators by regression to <i>stem</i> protein types. Molecular Microbiology, 2007, 65, 907-919.	1.2	58
236	Osmotic stress limits arsenic hypertolerance in Aspergillus sp. P37. FEMS Microbiology Ecology, 2007, 61, 258-263.	1.3	14
237	Thioredoxin Fusions Increase Folding of Single Chain Fv Antibodies in the Cytoplasm of Escherichia coli: Evidence that Chaperone Activity is the Prime Effect of Thioredoxin. Journal of Molecular Biology, 2006, 357, 49-61.	2.0	78
238	Distribution and phylogeny of hexachlorocyclohexane-degrading bacteria in soils from Spain. Environmental Microbiology, 2006, 8, 60-68.	1.8	59
239	Composition of microbial communities in hexachlorocyclohexane (HCH) contaminated soils from Spain revealed with a habitat-specific microarray. Environmental Microbiology, 2006, 8, 126-140.	1.8	57
240	Growth phase-dependent expression of the Pseudomonas putida KT2440 transcriptional machinery analysed with a genome-wide DNA microarray. Environmental Microbiology, 2006, 8, 165-177.	1.8	123
241	The m-xylene biodegradation capacity of Pseudomonas putida mt-2 is submitted to adaptation to abiotic stresses: evidence from expression profiling of xyl genes. Environmental Microbiology, 2006, 8, 591-602.	1.8	37
242	Surveying biotransformations with a la carte genetic traps: translating dehydrochlorination of lindane (gamma-hexachlorocyclohexane) into lacZ-based phenotypes. Environmental Microbiology, 2006, 8, 546-555.	1.8	65
243	In vivo drafting of single-chain antibodies for regulatory duty on the sigma54-promoter Pu of the TOL plasmid. Molecular Microbiology, 2006, 60, 1218-1227.	1.2	5
244	Uncoupling of choline-O-sulphate utilization from osmoprotection in Pseudomonas putida. Molecular Microbiology, 2006, 62, 1643-1654.	1.2	19
245	Blueprint of an oil-eating bacterium. Nature Biotechnology, 2006, 24, 952-953.	9.4	30
246	Transcriptional regulators Ã la carte: engineering new effector specificities in bacterial regulatory proteins. Current Opinion in Biotechnology, 2006, 17, 34-42.	3.3	131
247	Synthetic Biology: challenges ahead. Bioinformatics, 2006, 22, 127-128.	1.8	17
248	Transcriptional Tradeoff between Metabolic and Stress-response Programs in Pseudomonas putida KT2440 Cells Exposed to Toluene. Journal of Biological Chemistry, 2006, 281, 11981-11991.	1.6	207
249	The Upstream-activating Sequences of the Ïƒ54 Promoter Pu of Pseudomonas putida Filter Transcription Readthrough from Upstream Genes. Journal of Biological Chemistry, 2006, 281, 11940-11948.	1.6	8
250	Identification of a Î³-hexachlorocyclohexane dehydrochlorinase (LinA) variant with improved expression and solubility properties. Biocatalysis and Biotransformation, 2006, 24, 223-230.	1.1	9
251	Inferring the genetic network ofm-xylene metabolism through expression profiling of thexylgenes ofPseudomonas putidamt-2. Molecular Microbiology, 2005, 57, 1557-1569.	1.2	30
252	Problems with metagenomic screening. Nature Biotechnology, 2005, 23, 1045-1045.	9.4	23

#	Article	IF	Citations
253	Promoters in the environment: transcriptional regulation in its natural context. Nature Reviews Microbiology, 2005, 3, 105-118.	13.6	192
254	Exploring the microbial biodegradation and biotransformation gene pool. Trends in Biotechnology, 2005, 23, 497-506.	4.9	104
255	Adaptation of the Yeast URA3 Selection System to Gram-Negative Bacteria and Generation of a Î" betCDE Pseudomonas putida Strain. Applied and Environmental Microbiology, 2005, 71, 883-892.	1.4	68
256	m -Xylene-Responsive Pu - PnifH Hybrid Ïƒ 54 Promoters That Overcome Physiological Control in Pseudomonas putida KT2442. Journal of Bacteriology, 2005, 187, 125-134.	1.0	14
257	Subtractive hybridization reveals a high genetic diversity in the fish pathogen Photobacterium damselae subsp. piscicida: evidence of a SXT-like element. Microbiology (United Kingdom), 2005, 151, 2659-2669.	0.7	26
258	Physiological stress of intracellularShigella flexnerivisualized with a metabolic sensor fused to a surface-reporter system. FEBS Letters, 2005, 579, 813-818.	1.3	1
259	Genetically modified organisms for the environment: stories of success and failure and what we have learned from them. International Microbiology, 2005, 8, 213-22.	1.1	159
260	Genetic Evidence that Catabolites of the Entner-Doudoroff Pathway Signal C Source Repression of the Ïƒ54Pu Promoter of Pseudomonas putida. Journal of Bacteriology, 2004, 186, 8267-8275.	1.0	47
261	The Role of Thiol Species in the Hypertolerance of Aspergillus sp. P37 to Arsenic. Journal of Biological Chemistry, 2004, 279, 51234-51240.	1.6	71
262	Novel Physiological Modulation of the Pu Promoter of TOL Plasmid. Journal of Biological Chemistry, 2004, 279, 7777-7784.	1.6	46
263	MetaRouter: bioinformatics for bioremediation. Nucleic Acids Research, 2004, 33, D588-D592.	6.5	64
264	Getting out: protein traffic in prokaryotes. Molecular Microbiology, 2004, 52, 3-11.	1.2	35
265	Structural tolerance of bacterial autotransporters for folded passenger protein domains. Molecular Microbiology, 2004, 52, 1069-1080.	1.2	83
266	Secretion of proteins with dimerization capacity by the haemolysin type I transport system of Escherichia coli. Molecular Microbiology, 2004, 53, 1109-1121.	1.2	15
267	Molecular Tools for Genetic Analysis of Pseudomonads. , 2004, , 317-350.		8
268	Deciphering environmental signal integration in Ïƒ54-dependent promoters with a simple mathematical model. Journal of Theoretical Biology, 2003, 224, 437-449.	0.8	5
269	Testing the limits of biological tolerance to arsenic in a fungus isolated from the River Tinto. Environmental Microbiology, 2003, 5, 133-138.	1.8	45
270	Arsenate transport and reduction in the hyper-tolerant fungus Aspergillus sp. P37. Environmental Microbiology, 2003, 5, 1087-1093.	1.8	30

#	Article	IF	Citations
271	The organization of the microbial biodegradation network from a systemsâ€biology perspective. EMBO Reports, 2003, 4, 994-999.	2.0	62
272	Heavy metal tolerance and metal homeostasis inPseudomonas putidaas revealed by complete genome analysis. Environmental Microbiology, 2003, 5, 1242-1256.	1.8	213
273	The Ïƒ54regulon (sigmulon) ofPseudomonas putida. Environmental Microbiology, 2003, 5, 1281-1293.	1.8	65
274	Transcription regulation and environmental adaptation in bacteria. Trends in Microbiology, 2003, 11, 248-253.	3.5	168
275	Myriads of protein families, and still counting. Genome Biology, 2003, 4, 401.	13.9	55
276	Transient XylR binding to the UAS of the Pseudomonas putida Â54 promoter Pu revealed with high intensity UV footprinting in vivo. Nucleic Acids Research, 2003, 31, 6926-6934.	6.5	10
277	Recruitment of Ïƒ54-RNA Polymerase to the Pu Promoter of Pseudomonas putida through Integration Host Factor-mediated Positioning Switch of Î± Subunit Carboxyl-terminal Domain on an UP-like Element. Journal of Biological Chemistry, 2003, 278, 27695-27702.	1.6	26
278	Sigma 54 Levels and Physiological Control of the Pseudomonas putida Pu Promoter. Journal of Bacteriology, 2003, 185, 3379-3383.	1.0	30
279	Autotransporters as Scaffolds for Novel Bacterial Adhesins: Surface Properties of Escherichia coli Cells Displaying Jun/Fos Dimerization Domains. Journal of Bacteriology, 2003, 185, 5585-5590.	1.0	45
280	Neutralizationof Enteric Coronaviruses with Escherichia coli CellsExpressing Single-Chain Fv-AutotransporterFusions. Journal of Virology, 2003, 77, 13396-13398.	1.5	22
281	In Vivo UV Laser Footprinting of thePseudomonas putida Ï,54PuPromoter Reveals That Integration Host Factor Couples Transcriptional Activity to Growth Phase. Journal of Biological Chemistry, 2002, 277, 2169-2175.	1.6	53
282	Production of Functional Single-Chain Fv Antibodies in the Cytoplasm of Escherichia coli. Journal of Molecular Biology, 2002, 320, 1-10.	2.0	139
283	Probing secretion and translocation of a Î²-autotransporter using a reporter single-chain Fv as a cognate passenger domain. Molecular Microbiology, 2002, 33, 1232-1243.	1.2	80
284	The grammar of (micro)biological diversity. Environmental Microbiology, 2002, 4, 623-627.	1.8	16
285	Exploiting the genetic and biochemical capacities of bacteria for the remediation of heavy metal pollution. FEMS Microbiology Reviews, 2002, 26, 327-338.	3.9	365
286	Export of autotransported proteins proceeds through an oligomeric ring shaped by C-terminal domains. EMBO Journal, 2002, 21, 2122-2131.	3.5	110
287	Metabolic engineering of bacteria for environmental applications: construction of Pseudomonas strains for biodegradation of 2-chlorotoluene. Journal of Biotechnology, 2001, 85, 103-113.	1.9	77
288	Formation of disulphide bonds during secretion of proteins through the periplasmic-independent type I pathway. Molecular Microbiology, 2001, 40, 332-346.	1.2	38

#	Article	IF	Citations
289	New insights into the activation of <i>o</i> â€xylene biodegradation in <i>Pseudomonas stutzeri</i> OX1 by pathway substrates. EMBO Reports, 2001, 2, 409-414.	2.0	30
290	Role of ptsO in Carbon-Mediated Inhibition of the Pu Promoter Belonging to the pWW0 Pseudomonas putida Plasmid. Journal of Bacteriology, 2001, 183, 5128-5133.	1.0	45
291	Evidence of Multiple Regulatory Functions for the PtsN (IIA Ntr) Protein of Pseudomonas putida. Journal of Bacteriology, 2001, 183, 1032-1037.	1.0	50
292	Monitoring Intracellular Levels of XylR in Pseudomonas putida with a Single-Chain Antibody Specific for Aromatic-Responsive Enhancer-Binding Proteins. Journal of Bacteriology, 2001, 183, 5571-5579.	1.0	34
293	The Essential HupB and HupN Proteins of Pseudomonas putida Provide Redundant and Nonspecific DNA-bending Functions. Journal of Biological Chemistry, 2001, 276, 16641-16648.	1.6	18
294	The role of the interdomain B linker in the activation of the XylR protein of Pseudomonas putida. Molecular Microbiology, 2000, 38, 401-410.	1.2	39
295	Engineering outer-membrane proteins in Pseudomonas putida for enhanced heavy-metal bioadsorption. Journal of Inorganic Biochemistry, 2000, 79, 219-223.	1.5	76
296	Engineering a mouse metallothionein on the cell surface of Ralstonia eutropha CH34 for immobilization of heavy metals in soil. Nature Biotechnology, 2000, 18, 661-665.	9.4	262
297	Expression vectors and delivery systems. Current Opinion in Biotechnology, 2000, 11, 427-428.	3.3	4
298	Evidence of an Unusually Long Operator for the Fur Repressor in the Aerobactin Promoter of Escherichia coli. Journal of Biological Chemistry, 2000, 275, 24709-24714.	1.6	52
299	Specific Secretion of Active Single-Chain Fv Antibodies into the Supernatants of Escherichia coli Cultures by Use of the Hemolysin System. Applied and Environmental Microbiology, 2000, 66, 5024-5029.	1.4	75
300	In Vivo and In Vitro Effects of (p)ppGpp on the Ï,54 Promoter Pu of the TOL Plasmid ofPseudomonas putida. Journal of Bacteriology, 2000, 182, 4711-4718.	1.0	56
301	Genetic Evidence of Distinct Physiological Regulation Mechanisms in the Ï, 54 Pu Promoter of Pseudomonas putida. Journal of Bacteriology, 2000, 182, 956-960.	1.0	38
302	Functional Domains of the TOL Plasmid Transcription Factor XylS. Journal of Bacteriology, 2000, 182, 1118-1126.	1.0	43
303	Functional Analysis of PvdS, an Iron Starvation Sigma Factor of Pseudomonas aeruginosa. Journal of Bacteriology, 2000, 182, 1481-1491.	1.0	123
304	Visualization of DNAâ€"protein intermediates during activation of the Pu promoter of the TOL plasmid of Pseudomonas putida. Microbiology (United Kingdom), 2000, 146, 2555-2563.	0.7	13
305	Engineering of a Stable Whole-Cell Biocatalyst Capable of (<i>S</i>)-Styrene Oxide Formation for Continuous Two-Liquid-Phase Applications. Applied and Environmental Microbiology, 1999, 65, 5619-5623.	1.4	92
306	The IIANtr (PtsN) Protein of Pseudomonas putida Mediates the C Source Inhibition of the Ï,54-dependent Pu Promoter of the TOL Plasmid. Journal of Biological Chemistry, 1999, 274, 15562-15568.	1.6	99

#	Article	IF	Citations
307	Recruitment of RNA Polymerase Is a Rate-limiting Step for the Activation of the Ï,54 Promoter Pu ofPseudomonas putida. Journal of Biological Chemistry, 1999, 274, 33790-33794.	1.6	30
308	Involvement of the FtsH (HflB) protease in the activity of sigma54 promoters. Molecular Microbiology, 1999, 31, 261-270.	1.2	39
309	Whole cell- and protein-based biosensors for the detection of bioavailable heavy metals in environmental samples. Analytica Chimica Acta, 1999, 387, 235-244.	2.6	248
310	Activation of the toluene-responsive regulator XylR causes a transcriptional switch between sigma54 and sigma70 promoters at the divergent Pr/Ps region of the TOL plasmid. Molecular Microbiology, 1998, 27, 651-659.	1.2	39
311	Bioaccumulation of heavy metals with protein fusions of metallothionein to bacteriol OMPs. Biochimie, 1998, 80, 855-861.	1.3	53
312	Binding of the Fur (ferric uptake regulator) repressor of Escherichia coli to arrays of the GATAAT sequence. Journal of Molecular Biology, 1998, 283, 537-547.	2.0	177
313	Engineering of Quasi-Natural Pseudomonas putida Strains for Toluene Metabolism through an ortho -Cleavage Degradation Pathway. Applied and Environmental Microbiology, 1998, 64, 748-751.	1.4	58
314	Resistance to Tellurite as a Selection Marker for Genetic Manipulations of Pseudomonas Strains. Applied and Environmental Microbiology, 1998, 64, 4040-4046.	1.4	100
315	Metalloadsorption by <i>Escherichia coli</i> Cells Displaying Yeast and Mammalian Metallothioneins Anchored to the Outer Membrane Protein LamB. Journal of Bacteriology, 1998, 180, 2280-2284.	1.0	131
316	Modulation of gene expression through chromosomal positioning in Escherichia coli. Microbiology (United Kingdom), 1997, 143, 2071-2078.	0.7	118
317	Effector Specificity Mutants of the Transcriptional Activator NahR of Naphthalene Degrading Pseudomonas Define Protein Sites Involved in Binding of Aromatic Inducers. Journal of Biological Chemistry, 1997, 272, 3986-3992.	1.6	87
318	CLUES AND CONSEQUENCES OF DNA BENDING IN TRANSCRIPTION. Annual Review of Microbiology, 1997, 51, 593-628.	2.9	182
319	Genetic evidence of separate repressor and activator activities of the XylR regulator of the TOL plasmid, pWW0, of Pseudomonas putida. Molecular Microbiology, 1997, 23, 1221-1227.	1.2	25
320	Metalloregulation in vitro of the aerobactin promoter of Escherichia coli by the Fur (ferric uptake) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2	1.2	73
321	VTR expression cassettes for engineering conditional phenotypes in Pseudomonas: activity of the Pu promoter of the TOL plasmid under limiting concentrations of the XylR activator protein. Gene, 1996, 172, 81-86.	1.0	36
322	Physical and Functional Analysis of the Prokaryotic Enhancer of the Ïƒ54-promoters of the TOL Plasmid ofPseudomonas putida. Journal of Molecular Biology, 1996, 258, 562-574.	2.0	43
323	In Vitro Activities of an N-terminal Truncated Form of XylR, a Ïƒ54-dependent Transcriptional Activator of Pseudomonas putida. Journal of Molecular Biology, 1996, 258, 575-587.	2.0	83
324	Towards a vaccine candidate againstShigella dysenteriae1: expression of the Shiga toxin B-subunit in an attenuatedShigella flexneri aroDcarrier strain. Microbial Pathogenesis, 1996, 21, 277-288.	1.3	23

#	Article	IF	Citations
325	ATP Binding to the Ïƒ54-Dependent Activator XylRTriggers a Protein Multimerization Cycle Catalyzed by UAS DNA. Cell, 1996, 86, 331-339.	13.5	98
326	Involvement of sigma54 in exponential silencing of the Pseudomonas putida TOL plasmid Pu promoter. Molecular Microbiology, 1996, 19, 7-17.	1.2	94
327	A stringently controlled expression system for analysing lateral gene transfer between bacteria. Molecular Microbiology, 1996, 21, 293-300.	1.2	23
328	Regulatory noise in prokaryotic promoters: how bacteria learn to respond to novel environmental signals. Molecular Microbiology, 1996, 19, 1177-1184.	1.2	101
329	An Escherichia coli hemolysin transport system-based vector for the export of polypeptides: Export of shiga-like toxin IIeB subunit by Salmonella typhimurium aroA. Nature Biotechnology, 1996, 14, 765-769.	9.4	75
330	Enhanced metalloadsorption of bacterial cells displaying poly-His peptides. Nature Biotechnology, 1996, 14, 1017-1020.	9.4	166
331	Identification of the Repressor Subdomain within the Signal Reception Module of the Prokaryotic Enhancer-binding Protein XylR of Pseudomonas putida. Journal of Biological Chemistry, 1996, 271, 7899-7902.	1.6	17
332	Activation of the transcriptional regulator XylR of Pseudomonas putida by release of repression between functional domains. Molecular Microbiology, 1995, 16, 205-213.	1.2	139
333	The organization of the Pm promoter of the TOL plasmid reflects the structure of its cognate activator protein XylS. Molecular Genetics and Genomics, 1994, 244, 596-605.	2.4	27
334	Designing microbial systems for gene expression in the field. Trends in Biotechnology, 1994, 12, 365-371.	4.9	52
335	The Behavior of Bacteria Designed for Biodegradation. Nature Biotechnology, 1994, 12, 1349-1356.	9.4	76
336	Universal barrier to lateral spread of specific genes among microorganisms. Molecular Microbiology, 1994, 13, 855-861.	1.2	75
337	[31] Analysis and construction of stable phenotypes in gram-negative bacteria with Tn5- and Tn10-derived minitransposons. Methods in Enzymology, 1994, 235, 386-405.	0.4	852
338	Identification of a cis-acting Sequence within the Pm Promoter of the TOL Plasmid which Confers XylS-mediated Responsiveness to Substituted Benzoates. Journal of Molecular Biology, 1993, 230, 699-703.	2.0	49
339	Engineering of alkyl- and haloaromatic-responsive gene expression with mini-transposons containing regulated promoters of biodegradative pathways of Pseudomonas. Gene, 1993, 130, 41-46.	1.0	113
340	A T7 RNA polymerase-based system for the construction of Pseudomonas strains with phenotypes dependent on TOL-meta pathway effectors. Gene, 1993, 134, 103-106.	1.0	36
341	Analysis of Pseudomonas gene products using lacIq/Ptrp-lac plasmids and transposons that confer conditional phenotypes. Gene, 1993, 123, 17-24.	1.0	429
342	Extracellular export of Shiga toxin B-subunit/ haemolysin A (C-terminus) fusion protein expressed in Salmonella typhimurium aroA-mutant and stimulation of B-subunit specific antibody responses in mice. Microbial Pathogenesis, 1992, 13, 465-476.	1.3	26

#	Article	IF	Citations
343	XylS domain interactions can be deduced from intraallelic dominance in double mutants of Pseudomonas putida. Molecular Genetics and Genomics, 1992, 235, 406-412.	2.4	24
344	A general system to integratelacZ fusions into the chromosomes of gram-negative eubacteria: regulation of thePm promoter of theTOL plasmid studied with all controlling elements in monocopy. Molecular Genetics and Genomics, 1992, 233, 293-301.	2.4	285
345	Genetic engineering strategies for environmental applications. Current Opinion in Biotechnology, 1992, 3, 227-231.	3.3	23
346	IS1-mediated mobility of the aerobactin system of pColV-K30 in Escherichia coli. Molecular Genetics and Genomics, 1988, 213, 487-490.	2.4	19
347	Metal ion regulation of gene expression. Journal of Molecular Biology, 1988, 203, 875-884.	2.0	183
348	Isolation and characterization of microcin E 492 fromKlebsiella pneumoniae. Archives of Microbiology, 1984, 139, 72-75.	1.0	99
349	Antibiotics from gram-negative bacteria: do they play a role in microbial ecology?. Trends in Biochemical Sciences, 1984, 9, 266-269.	3.7	33
350	Genetic Strategies to Engineer Expression Systems Responsive to Relevant Environmental Signals. , 0, , 91-101.		0
351	Microbial Bioremediation of Chemical Pollutants: How Bacteria Cope with Multi-Stress Environmental Scenarios. , 0, , 481-492.		7
352	Mining Environmental Plasmids for Synthetic Biology Parts and Devices. , 0, , 633-649.		2