VÄ±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	[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
2	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
3	Analysis of Pseudomonas gene products using lacIq/Ptrp-lac plasmids and transposons that confer conditional phenotypes. Gene, 1993, 123, 17-24.	1.0	429
4	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
5	Pseudomonas putida as a functional chassis for industrial biocatalysis: From native biochemistry to trans-metabolism. Metabolic Engineering, 2018, 50, 142-155.	3.6	338
6	Biotechnological domestication of pseudomonads using synthetic biology. Nature Reviews Microbiology, 2014, 12, 368-379.	13.6	332
7	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
8	Microbial responses to environmental arsenic. BioMetals, 2009, 22, 117-130.	1.8	309
9	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
10	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
11	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
12	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
13	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
14	Bioremediation 3.0: Engineering pollutant-removing bacteria in the times of systemic biology. Biotechnology Advances, 2017, 35, 845-866.	6.0	240
15	Systems biology approaches to bioremediation. Current Opinion in Biotechnology, 2008, 19, 579-589.	3.3	227
16	Heavy metal tolerance and metal homeostasis inPseudomonas putidaas revealed by complete genome analysis. Environmental Microbiology, 2003, 5, 1242-1256.	1.8	213
17	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
18	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

#	Article	IF	Citations
19	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
20	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
21	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
22	Promoters in the environment: transcriptional regulation in its natural context. Nature Reviews Microbiology, 2005, 3, 105-118.	13.6	192
23	Metal ion regulation of gene expression. Journal of Molecular Biology, 1988, 203, 875-884.	2.0	183
24	CLUES AND CONSEQUENCES OF DNA BENDING IN TRANSCRIPTION. Annual Review of Microbiology, 1997, 51, 593-628.	2.9	182
25	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
26	Tn7-Based Device for Calibrated Heterologous Gene Expression in <i>Pseudomonas putida</i>. ACS Synthetic Biology, 2015, 4, 1341-1351.	1.9	169
27	Transcription regulation and environmental adaptation in bacteria. Trends in Microbiology, 2003, 11, 248-253.	3.5	168
28	Enhanced metalloadsorption of bacterial cells displaying poly-His peptides. Nature Biotechnology, 1996, 14, 1017-1020.	9.4	166
29	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
30	Synthetic biology: discovering new worlds and new words. EMBO Reports, 2008, 9, 822-827.	2.0	148
31	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
32	pBAM1: an all-synthetic genetic tool for analysis and construction of complex bacterial phenotypes. BMC Microbiology, 2011, 11, 38.	1.3	142
33	Genome reduction boosts heterologous gene expression in Pseudomonas putida. Microbial Cell Factories, 2015, 14, 23.	1.9	142
34	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
35	Production of Functional Single-Chain Fv Antibodies in the Cytoplasm of Escherichia coli. Journal of Molecular Biology, 2002, 320, 1-10.	2.0	139
36	Plastic waste as a novel substrate for industrial biotechnology. Microbial Biotechnology, 2015, 8, 900-903.	2.0	134

#	Article	IF	Citations
37	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
38	Transcriptional regulators Ã la carte: engineering new effector specificities in bacterial regulatory proteins. Current Opinion in Biotechnology, 2006, 17, 34-42.	3.3	131
39	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
40	Functional Analysis of PvdS, an Iron Starvation Sigma Factor of Pseudomonas aeruginosa. Journal of Bacteriology, 2000, 182, 1481-1491.	1.0	123
41	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
42	Modulation of gene expression through chromosomal positioning in Escherichia coli. Microbiology (United Kingdom), 1997, 143, 2071-2078.	0.7	118
43	CRISPR/Cas9â€Based Counterselection Boosts Recombineering Efficiency in <i>Pseudomonas putida</i>. Biotechnology Journal, 2018, 13, e1700161.	1.8	115
44	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
45	Export of autotransported proteins proceeds through an oligomeric ring shaped by C-terminal domains. EMBO Journal, 2002, 21, 2122-2131.	3.5	110
46	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
47	Exploring the microbial biodegradation and biotransformation gene pool. Trends in Biotechnology, 2005, 23, 497-506.	4.9	104
48	Noise and Robustness in Prokaryotic Regulatory Networks. Annual Review of Microbiology, 2010, 64, 257-275.	2.9	104
49	Genetic programming of catalytic Pseudomonas putida biofilms for boosting biodegradation of haloalkanes. Metabolic Engineering, 2016, 33, 109-118.	3.6	103
50	Regulatory noise in prokaryotic promoters: how bacteria learn to respond to novel environmental signals. Molecular Microbiology, 1996, 19, 1177-1184.	1.2	101
51	Resistance to Tellurite as a Selection Marker for Genetic Manipulations of Pseudomonas Strains. Applied and Environmental Microbiology, 1998, 64, 4040-4046.	1.4	100
52	Isolation and characterization of microcin E 492 fromKlebsiella pneumoniae. Archives of Microbiology, 1984, 139, 72-75.	1.0	99
53	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
54	The urgent need for microbiology literacy in society. Environmental Microbiology, 2019, 21, 1513-1528.	1.8	99

#	Article	IF	Citations
55	ATP Binding to the Ïƒ54-Dependent Activator XylRTriggers a Protein Multimerization Cycle Catalyzed by UAS DNA. Cell, 1996, 86, 331-339.	13.5	98
56	Involvement of sigma54 in exponential silencing of the Pseudomonas putida TOL plasmid Pu promoter. Molecular Microbiology, 1996, 19, 7-17.	1.2	94
57	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
58	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
59	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
60	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
61	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
62	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
63	Engineering the Soil Bacterium Pseudomonas putida for Arsenic Methylation. Applied and Environmental Microbiology, 2013, 79, 4493-4495.	1.4	85
64	New Transposon Tools Tailored for Metabolic Engineering of Gram-Negative Microbial Cell Factories. Frontiers in Bioengineering and Biotechnology, 2014, 2, 46.	2.0	85
65	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
66	Structural tolerance of bacterial autotransporters for folded passenger protein domains. Molecular Microbiology, 2004, 52, 1069-1080.	1.2	83
67	The power of synthetic biology for bioproduction, remediation and pollution control. EMBO Reports, 2018, 19, .	2.0	83
68	Mining logic gates in prokaryotic transcriptional regulation networks. FEBS Letters, 2008, 582, 1237-1244.	1.3	82
69	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
70	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
71	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
72	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

#	Article	IF	Citations
73	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
74	Regulatory Tasks of the Phosphoenolpyruvate-Phosphotransferase System of Pseudomonas putida in Central Carbon Metabolism. MBio, 2012, 3, .	1.8	78
75	Synthetic constructs in/for the environment: Managing the interplay between natural and engineered Biology. FEBS Letters, 2012, 586, 2199-2206.	1.3	78
76	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
77	Accumulation of inorganic polyphosphate enables stress endurance and catalytic vigour in Pseudomonas putida KT2440. Microbial Cell Factories, 2013, 12, 50.	1.9	77
78	The Behavior of Bacteria Designed for Biodegradation. Nature Biotechnology, 1994, 12, 1349-1356.	9.4	76
79	Engineering outer-membrane proteins in Pseudomonas putida for enhanced heavy-metal bioadsorption. Journal of Inorganic Biochemistry, 2000, 79, 219-223.	1.5	76
80	Universal barrier to lateral spread of specific genes among microorganisms. Molecular Microbiology, 1994, 13, 855-861.	1.2	75
81	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
82	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
83	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
84	Transcriptomic fingerprinting of <i><scp>P</scp>seudomonas putida</i> under alternative physiological regimes. Environmental Microbiology Reports, 2013, 5, 883-891.	1.0	75
85	Endogenous Stress Caused by Faulty Oxidation Reactions Fosters Evolution of 2,4-Dinitrotoluene-Degrading Bacteria. PLoS Genetics, 2013, 9, e1003764.	1.5	74
86	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
87	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
88	Stable implantation of orthogonal sensor circuits in Gramâ€negative bacteria for environmental release. Environmental Microbiology, 2008, 10, 3305-3316.	1.8	72
89	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
90	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

#	Article	IF	Citations
91	Chemical reactivity drives spatiotemporal organisation of bacterial metabolism. FEMS Microbiology Reviews, 2014, 39, n/a-n/a.	3.9	67
92	Synthetic bugs on the loose: containment options for deeply engineered (micro)organisms. Current Opinion in Biotechnology, 2016, 38, 90-96.	3.3	67
93	The Ïƒ54regulon (sigmulon) ofPseudomonas putida. Environmental Microbiology, 2003, 5, 1281-1293.	1.8	65
94	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
95	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
96	MetaRouter: bioinformatics for bioremediation. Nucleic Acids Research, 2004, 33, D588-D592.	6.5	64
97	Beware of metaphors: Chasses and orthogonality in synthetic biology. Bioengineered Bugs, 2011, 2, 3-7.	2.0	64
98	The private life of environmental bacteria: pollutant biodegradation at the single cell level. Environmental Microbiology, 2014, 16, 628-642.	1.8	63
99	Molecular tools and emerging strategies for deep genetic/genomic refactoring of Pseudomonas. Current Opinion in Biotechnology, 2017, 47, 120-132.	3.3	63
100	The organization of the microbial biodegradation network from a systemsâ€biology perspective. EMBO Reports, 2003, 4, 994-999.	2.0	62
101	Robustness of Pseudomonas putida KT2440 as a host for ethanol biosynthesis. New Biotechnology, 2014, 31, 562-571.	2.4	62
102	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
103	The Glycerol-Dependent Metabolic Persistence of Pseudomonas putida KT2440 Reflects the Regulatory Logic of the GlpR Repressor. MBio, 2015, 6, .	1.8	62
104	From the <i>selfish gene</i> to <i>selfish metabolism</i>: Revisiting the central dogma. BioEssays, 2014, 36, 226-235.	1.2	60
105	Distribution and phylogeny of hexachlorocyclohexane-degrading bacteria in soils from Spain. Environmental Microbiology, 2006, 8, 60-68.	1.8	59
106	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
107	Emergence of novel functions in transcriptional regulators by regression to <i>stem</i> protein types. Molecular Microbiology, 2007, 65, 907-919.	1.2	58
108	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

#	Article	IF	Citations
109	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
110	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
111	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
112	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
113	Functional implementation of a linear glycolysis for sugar catabolism in Pseudomonas putida. Metabolic Engineering, 2019, 54, 200-211.	3.6	56
114	Myriads of protein families, and still counting. Genome Biology, 2003, 4, 401.	13.9	55
115	The ten grand challenges of synthetic life. Systems and Synthetic Biology, 2011, 5, 1-9.	1.0	54
116	Bioaccumulation of heavy metals with protein fusions of metallothionein to bacteriol OMPs. Biochimie, 1998, 80, 855-861.	1.3	53
117	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
118	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
119	Designing microbial systems for gene expression in the field. Trends in Biotechnology, 1994, 12, 365-371.	4.9	52
120	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
121	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
122	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
123	The Metabolic Redox Regime of Pseudomonas putida Tunes Its Evolvability toward Novel Xenobiotic Substrates. MBio, 2018, 9, .	1.8	51
124	Evidence of Multiple Regulatory Functions for the PtsN (IIA Ntr) Protein of Pseudomonas putida. Journal of Bacteriology, 2001, 183, 1032-1037.	1.0	50
125	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
126	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

#	Article	IF	Citations
127	The quest for the minimal bacterial genome. Current Opinion in Biotechnology, 2016, 42, 216-224.	3.3	49
128	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
129	In vivo diversification of target genomic sites using processive base deaminase fusions blocked by dCas9. Nature Communications, 2020, 11, 6436.	5.8	47
130	Novel Physiological Modulation of the Pu Promoter of TOL Plasmid. Journal of Biological Chemistry, 2004, 279, 7777-7784.	1.6	46
131	Biological standards for the Knowledge-Based BioEconomy: What is at stake. New Biotechnology, 2018, 40, 170-180.	2.4	46
132	The long journey towards standards for engineering biosystems. EMBO Reports, 2020, 21, e50521.	2.0	46
133	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
134	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
135	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
136	Engineering input/output nodes in prokaryotic regulatory circuits. FEMS Microbiology Reviews, 2010, 34, 842-865.	3.9	45
137	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
138	Functional Domains of the TOL Plasmid Transcription Factor XylS. Journal of Bacteriology, 2000, 182, 1118-1126.	1.0	43
139	The environmental fate of organic pollutants through the global microbial metabolism. Molecular Systems Biology, 2007, 3, 114.	3.2	43
140	A standardized workflow for surveying recombinases expands bacterial genomeâ€editing capabilities. Microbial Biotechnology, 2018, 11, 176-188.	2.0	43
141	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
142	Bioremediation at a global scale: from the test tube to planet Earth. Microbial Biotechnology, 2016, 9, 618-625.	2.0	40
143	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
144	Involvement of the FtsH (HflB) protease in the activity of sigma54 promoters. Molecular Microbiology, 1999, 31, 261-270.	1.2	39

#	Article	IF	Citations
145	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
146	Deconvolution of Gene Expression Noise into Spatial Dynamics of Transcription Factorâ€"Promoter Interplay. ACS Synthetic Biology, 2017, 6, 1359-1369.	1.9	39
147	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
148	Formation of disulphide bonds during secretion of proteins through the periplasmic-independent type I pathway. Molecular Microbiology, 2001, 40, 332-346.	1.2	38
149	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
150	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
151	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
152	Pseudomonas putida in the quest of programmable chemistry. Current Opinion in Biotechnology, 2019, 59, 111-121.	3.3	38
153	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
154	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
155	Environmental biosafety in the age of Synthetic Biology: Do we really need a radical new approach?. BioEssays, 2010, 32, 926-931.	1.2	37
156	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
157	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
158	The <i>logicome</i> of environmental bacteria: merging catabolic and regulatory events with Boolean formalisms. Environmental Microbiology, 2011, 13, 2389-2402.	1.8	36
159	Getting out: protein traffic in prokaryotes. Molecular Microbiology, 2004, 52, 3-11.	1.2	35
160	Contextual dependencies expand the re-usability of genetic inverters. Nature Communications, 2021, 12, 355.	5.8	35
161	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
162	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

#	Article	IF	Citations
163	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
164	For the sake of the Bioeconomy: define what a Synthetic Biology Chassis is!. New Biotechnology, 2021, 60, 44-51.	2.4	34
165	Antibiotics from gram-negative bacteria: do they play a role in microbial ecology?. Trends in Biochemical Sciences, 1984, 9, 266-269.	3.7	33
166	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
167	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
168	Digitalizing heterologous gene expression in Gramâ€negative bacteria with a portable ON/OFF module. Molecular Systems Biology, 2019, 15, e8777.	3.2	33
169	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
170	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
171	High-Efficiency Multi-site Genomic Editing of Pseudomonas putida through Thermoinducible ssDNA Recombineering. IScience, 2020, 23, 100946.	1.9	32
172	An Implementation-Focused Bio/Algorithmic Workflow for Synthetic Biology. ACS Synthetic Biology, 2016, 5, 1127-1135.	1.9	31
173	<scp>CRISPR</scp>/Cas9â€enhanced ss<scp>DNA</scp> recombineering for <i>Pseudomonas putida</i>. Microbial Biotechnology, 2019, 12, 1076-1089.	2.0	31
174	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
175	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
176	Arsenate transport and reduction in the hyper-tolerant fungus Aspergillus sp. P37. Environmental Microbiology, 2003, 5, 1087-1093.	1.8	30
177	Sigma 54 Levels and Physiological Control of the Pseudomonas putida Pu Promoter. Journal of Bacteriology, 2003, 185, 3379-3383.	1.0	30
178	Inferring the genetic network ofm-xylene metabolism through expression profiling of thexylgenes ofPseudomonas putidamt-2. Molecular Microbiology, 2005, 57, 1557-1569.	1.2	30
179	Blueprint of an oil-eating bacterium. Nature Biotechnology, 2006, 24, 952-953.	9.4	30
180	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

#	Article	IF	Citations
181	Engineering Multicellular Logic in Bacteria with Metabolic Wires. ACS Synthetic Biology, 2014, 3, 204-209.	1.9	30
182	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
183	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
184	Growth-dependent Phosphorylation of the PtsN (EIINtr) Protein of Pseudomonas putida. Journal of Biological Chemistry, 2007, 282, 18206-18211.	1.6	28
185	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
186	A Metabolic Widget Adjusts the Phosphoenolpyruvate-Dependent Fructose Influx in Pseudomonas putida. MSystems, 2016, 1, .	1.7	28
187	<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
188	Synthetic Biology for Terraformation Lessons from Mars, Earth, and the Microbiome. Life, 2020, 10, 14.	1.1	28
189	The Standard European Vector Architecture (SEVA) Plasmid Toolkit. Methods in Molecular Biology, 2014, 1149, 469-478.	0.4	28
190	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
191	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
192	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
193	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
194	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
195	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
196	Linking genes to microbial growth kineticsâ€”An integrated biochemical systems engineering approach. Metabolic Engineering, 2011, 13, 401-413.	3.6	26
197	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
198	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

#	Article	IF	Citations
199	Physical Forces Shape Group Identity of Swimming Pseudomonas putida Cells. Frontiers in Microbiology, 2016, 7, 1437.	1.5	26
200	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
201	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
202	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
203	Seven microbial bioâ€processes to help the planet. Microbial Biotechnology, 2017, 10, 995-998.	2.0	25
204	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
205	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
206	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
207	<scp><i>P</i></scp><i>seudomonas aeruginosa:</i> the making of a pathogen. Environmental Microbiology, 2015, 17, 1-3.	1.8	24
208	Modulating Heterologous Gene Expression with Portable mRNA-Stabilizing 5â€²-UTR Sequences. ACS Synthetic Biology, 2018, 7, 2177-2188.	1.9	24
209	Genetic engineering strategies for environmental applications. Current Opinion in Biotechnology, 1992, 3, 227-231.	3.3	23
210	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
211	A stringently controlled expression system for analysing lateral gene transfer between bacteria. Molecular Microbiology, 1996, 21, 293-300.	1.2	23
212	Problems with metagenomic screening. Nature Biotechnology, 2005, 23, 1045-1045.	9.4	23
213	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
214	Engineering Gram-Negative Microbial Cell Factories Using Transposon Vectors. Methods in Molecular Biology, 2017, 1498, 273-293.	0.4	23
215	Linking Engineered Cells to Their Digital Twins: A Version Control System for Strain Engineering. ACS Synthetic Biology, 2020, 9, 536-545.	1.9	23
216	Neutralizationof Enteric Coronaviruses with Escherichia coli CellsExpressing Single-Chain Fv-AutotransporterFusions. Journal of Virology, 2003, 77, 13396-13398.	1.5	22

#	Article	IF	Citations
217	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
218	Confidence, tolerance, and allowance in biological engineering: The nuts and bolts of living things. BioEssays, 2015, 37, 95-102.	1.2	22
219	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
220	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
221	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
222	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
223	The important versus the exciting: reining contradictions in contemporary biotechnology. Microbial Biotechnology, 2019, 12, 32-34.	2.0	20
224	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
225	IS1-mediated mobility of the aerobactin system of pColV-K30 in Escherichia coli. Molecular Genetics and Genomics, 1988, 213, 487-490.	2.4	19
226	Uncoupling of choline-O-sulphate utilization from osmoprotection in Pseudomonas putida. Molecular Microbiology, 2006, 62, 1643-1654.	1.2	19
227	A GFP-lacZ Bicistronic Reporter System for Promoter Analysis in Environmental Gram-Negative Bacteria. PLoS ONE, 2012, 7, e34675.	1.1	19
228	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
229	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
230	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
231	EnvMine: A text-mining system for the automatic extraction of contextual information. BMC Bioinformatics, 2010, 11, 294.	1.2	18
232	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
233	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
234	Mining Environmental Plasmids for Synthetic Biology Parts and Devices. Microbiology Spectrum, 2015, 3, PLAS-0033-2014.	1.2	18

#	Article	IF	Citations
235	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
236	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
237	Synthetic Biology: challenges ahead. Bioinformatics, 2006, 22, 127-128.	1.8	17
238	An Electroâ€optical Device from a Biofilm Structure Created by Bacterial Activity. Advanced Materials, 2010, 22, 4846-4850.	11.1	17
239	Data on the standardization of a cyclohexanone-responsive expression system for Gram-negative bacteria. Data in Brief, 2016, 6, 738-744.	0.5	17
240	The grammar of (micro)biological diversity. Environmental Microbiology, 2002, 4, 623-627.	1.8	16
241	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
242	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
243	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
244	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
245	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
246	CellShape: A userâ€friendly image analysis tool for quantitative visualization of bacterial cell factories inside. Biotechnology Journal, 2017, 12, 1600323.	1.8	15
247	Multiple-Site Diversification of Regulatory Sequences Enables Interspecies Operability of Genetic Devices. ACS Synthetic Biology, 2020, 9, 104-114.	1.9	15
248	Naked Bacterium: Emerging Properties of a Surfome-Streamlined <i>Pseudomonas putida</i> Strain. ACS Synthetic Biology, 2020, 9, 2477-2492.	1.9	15
249	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
250	Osmotic stress limits arsenic hypertolerance in Aspergillus sp. P37. FEMS Microbiology Ecology, 2007, 61, 258-263.	1.3	14
251	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
252	The IHF regulon of exponentially growing <i>Pseudomonas putida</i> cells. Environmental Microbiology, 2013, 15, 49-63.	1.8	14

#	Article	IF	Citations
253	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
254	From the test tube to the environment â€“ and back. Environmental Microbiology, 2013, 15, 6-11.	1.8	14
255	It's the metabolism, stupid!. Environmental Microbiology Reports, 2015, 7, 18-19.	1.0	14
256	Spatial organization of the gene expression hardware in <i>Pseudomonas putida</i>. Environmental Microbiology, 2019, 21, 1645-1658.	1.8	14
257	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
258	COVER: <i>a priori</i> estimation of coverage for metagenomic sequencing. Environmental Microbiology Reports, 2012, 4, 335-341.	1.0	13
259	Transcription factor levels enable metabolic diversification of single cells of environmental bacteria. ISME Journal, 2016, 10, 1122-1133.	4.4	13
260	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
261	Recombination-Independent Genome Editing through CRISPR/Cas9-Enhanced TargeTron Delivery. ACS Synthetic Biology, 2019, 8, 2186-2193.	1.9	13
262	Reverse Engineering of an Aspirin-Responsive Transcriptional Regulator in <i>Escherichia coli</i>. ACS Synthetic Biology, 2019, 8, 1890-1900.	1.9	13
263	Evolving metabolism of 2,4â€dinitrotoluene triggers SOSâ€independent diversification of host cells. Environmental Microbiology, 2019, 21, 314-326.	1.8	13
264	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
265	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
266	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
267	Multifunctional SEVA shuttle vectors for actinomycetes and Gramâ€negative bacteria. MicrobiologyOpen, 2020, 9, 1135-1149.	1.2	12
268	Automated design and implementation of a NOR gate in Pseudomonas putida. Synthetic Biology, 2021, 6, ysab024.	1.2	12
269	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
270	Microbial systems biology: bottom up and top down. FEMS Microbiology Reviews, 2009, 33, 1-2.	3.9	11

#	Article	IF	Citations
271	Synthetic biology: something old, something newâ€‰â€¦. BioEssays, 2010, 32, 267-270.	1.2	11
272	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
273	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
274	Chassis organism from <i>Corynebacterium glutamicum</i>: The way towards biotechnological domestication of Corynebacteria. Biotechnology Journal, 2015, 10, 244-245.	1.8	11
275	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
276	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
277	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
278	Towards Functional Orthogonalisation of Protein Complexes: Individualisation of GroEL Monomers Leads to Distinct Quasihomogeneous Single Rings. ChemBioChem, 2013, 14, 2310-2321.	1.3	10
279	Evolutionary tinkering vs. rational engineering in the times of synthetic biology. Life Sciences, Society and Policy, 2018, 14, 18.	3.1	10
280	Identification of a Î³-hexachlorocyclohexane dehydrochlorinase (LinA) variant with improved expression and solubility properties. Biocatalysis and Biotransformation, 2006, 24, 223-230.	1.1	9
281	Broadening the SEVA Plasmid Repertoire to Facilitate Genomic Editing of Gram-Negative Bacteria. Springer Protocols, 2015, , 9-27.	0.1	9
282	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
283	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
284	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
285	Phenotypic knockouts of selected metabolic pathways by targeting enzymes with camel-derived nanobodies (VHHs). Metabolic Engineering, 2015, 30, 40-48.	3.6	8
286	Environmental microbiology to the rescue of planet earth. Environmental Microbiology, 2018, 20, 1910-1916.	1.8	8
287	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
288	Molecular Tools for Genetic Analysis of Pseudomonads. , 2004, , 317-350.		8

#	Article	IF	Citations
289	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
290	Standardization of regulatory nodes for engineering heterologous gene expression: a feasibility study. Microbial Biotechnology, 2022, 15, 2250-2265.	2.0	8
291	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
292	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
293	NanoPad: An integrated platform for bacterial production of camel nanobodies aimed at detecting environmental biomarkers. Proteomics, 2013, 13, 2766-2775.	1.3	7
294	Microbial Bioremediation of Chemical Pollutants: How Bacteria Cope with Multi-Stress Environmental Scenarios. , 0, , 481-492.		7
295	Synthetic microbiology: from analogy to methodology. Microbial Biotechnology, 2017, 10, 1264-1266.	2.0	7
296	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
297	Gross transcriptomic analysis of Pseudomonas putida for diagnosing environmental shifts. Microbial Biotechnology, 2020, 13, 263-273.	2.0	7
298	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
299	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
300	Chromosomal Integration of Transcriptional Fusions. Methods in Molecular Biology, 2014, 1149, 479-489.	0.4	7
301	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
302	ssDNA recombineering boosts in vivo evolution of nanobodies displayed on bacterial surfaces. Communications Biology, 2021, 4, 1169.	2.0	6
303	Versioning biological cells for trustworthy cell engineering. Nature Communications, 2022, 13, 765.	5.8	6
304	Deciphering environmental signal integration in Ïƒ54-dependent promoters with a simple mathematical model. Journal of Theoretical Biology, 2003, 224, 437-449.	0.8	5
305	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
306	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

#	Article	IF	Citations
307	An automated DIY framework for experimental evolution ofPseudomonas putida. Microbial Biotechnology, 2020, 14, 2679-2685.	2.0	5
308	Ribonucleases control distinct traits of <i>Pseudomonas putida</i> lifestyle. Environmental Microbiology, 2021, 23, 174-189.	1.8	5
309	Expression vectors and delivery systems. Current Opinion in Biotechnology, 2000, 11, 427-428.	3.3	4
310	Widening functional boundaries of the Ïƒ⁵⁴promoter Pu of Pseudomonas putida by defeating extant physiological constraints. Molecular BioSystems, 2015, 11, 734-742.	2.9	4
311	Stenosis triggers spread of helical Pseudomonas biofilms in cylindrical flow systems. Scientific Reports, 2016, 6, 27170.	1.6	4
312	Assessing Carbon Source-Dependent Phenotypic Variability in Pseudomonas putida. Methods in Molecular Biology, 2018, 1745, 287-301.	0.4	4
313	Quantitative assessment of morphological traits of planktonic bacterial aggregates. Water Research, 2021, 188, 116468.	5.3	4
314	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
315	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
316	Re-Factoring Glycolytic Genes for Targeted Engineering of Catabolism in Gram-Negative Bacteria. Methods in Molecular Biology, 2018, 1772, 3-24.	0.4	3
317	Environmental Performance of <i>Pseudomonas putida</i> with a Uracylated Genome. ChemBioChem, 2020, 21, 3255-3265.	1.3	3
318	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
319	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
320	Vestigialization of arsenic resistance phenotypes/genotypes inChromobacterium violaceumstrains thriving in pristine Brazilian sites. Biocatalysis and Biotransformation, 2013, 31, 281-291.	1.1	2
321	BiologÃa sintÃ©tica: la ingenierÃa al asalto de la complejidad biolÃ³gica. Arbor, 2014, 190, a149.	0.1	2
322	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
323	Microbial Biotechnologyâ€2020. Microbial Biotechnology, 2016, 9, 529-529.	2.0	2
324	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

#	Article	IF	Citations
325	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
326	Picking the right metaphors for addressing microbial systems: economic theory helps understanding biological complexity. International Microbiology, 2021, 24, 507-519.	1.1	2
327	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
328	Mining Environmental Plasmids for Synthetic Biology Parts and Devices. , 0, , 633-649.		2
329	Physiological stress of intracellularShigella flexnerivisualized with a metabolic sensor fused to a surface-reporter system. FEBS Letters, 2005, 579, 813-818.	1.3	1
330	Synthetic biology gains momentum in Europe. Systems and Synthetic Biology, 2010, 4, 145-147.	1.0	1
331	Combining Genetic Circuit and Microbial Growth Kinetic Models: A Challenge for Biological Modelling. Computer Aided Chemical Engineering, 2010, 28, 301-306.	0.3	1
332	Towards a global biotechnology scenario. Current Opinion in Biotechnology, 2012, 23, 827-829.	3.3	1
333	Systems and Synthetic Biology in Hydrocarbon Microbiology: Tools. Springer Protocols, 2015, , 1-7.	0.1	1
334	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
335	Biodegradation and Bioremediation: An Introduction. , 2018, , 1-21.		1
336	Promoter Fusions with Optical Outputs in Individual Cells and in Populations. Methods in Molecular Biology, 2014, 1149, 579-590.	0.4	1
337	15 years of microbial biotechnology: the time has come to think bigâ€"and act soon. Microbial Biotechnology, 2022, 15, 240-246.	2.0	1
338	Genetic Strategies to Engineer Expression Systems Responsive to Relevant Environmental Signals. , 0, , 91-101.		0
339	Beautiful is not (necessarily) right: Overcoming the Phryne's trial syndrome. BioEssays, 2010, 32, 1011-1011.	1.2	0
340	Predicting microbial growth kinetics with the use of genetic circuit models. Computer Aided Chemical Engineering, 2011, 29, 1321-1325.	0.3	0
341	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
342	Introduction to Systems and Synthetic Biology in Hydrocarbon Microbiology: Applications. Springer Protocols, 2016, , 1-8.	0.1	0

#	Article	IF	Citations
343	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
344	Genomic Responses of Pseudomonas putida to Aromatic Hydrocarbons. , 2019, , 1-15.		0
345	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
346	Exploiting geometric similarity for statistical quantification of fluorescence spatial patterns in bacterial colonies. BMC Bioinformatics, 2020, 21, 224.	1.2	0
347	The faulty SOS response of Pseudomonas putida KT2440 stems from an inefficient RecAâ€ŁexA interplay. Environmental Microbiology, 2021, 23, 1608-1619.	1.8	0
348	Genomic Responses of Pseudomonas putida to Aromatic Hydrocarbons. , 2019, , 287-301.		0
349	Assembly of a Custom-made Device to Study Spreading Patterns of Pseudomonas putida Biofilms. Bio-protocol, 2019, 9, e3238.	0.2	0
350	Biodegradation and Bioremediation: An Introduction. , 2019, , 1-20.		0
351	A SsrA/NIa-based Strategy for Post-Translational Regulation of Protein Levels in Gram-negative Bacteria. Bio-protocol, 2020, 10, e3688.	0.2	0
352	High-Efficiency Multi-site Genomic Editing (HEMSE) Made Easy. Methods in Molecular Biology, 2022, 2479, 37-52.	0.4	0