VÃ- ctor De Lorenzo

List of Publications by Year
in descending order

217 papers	14,939 citations	16451 64 h-index	23533 111 g-index
237 all docs	237 docs citations	237 times ranked	10177 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.	1.0	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.	14.5	556
3	Analysis of Pseudomonas gene products using lacIq/Ptrp-lac plasmids and transposons that confer conditional phenotypes. Gene, 1993, 123, 17-24.	2.2	429
4	Exploiting the genetic and biochemical capacities of bacteria for the remediation of heavy metal pollution. FEMS Microbiology Reviews, 2002, 26, 327-338.	8.6	365
5	Pseudomonas putida as a functional chassis for industrial biocatalysis: From native biochemistry to trans-metabolism. Metabolic Engineering, 2018, 50, 142-155.	7.0	338
6	Biotechnological domestication of pseudomonads using synthetic biology. Nature Reviews Microbiology, 2014, 12, 368-379.	28.6	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.	3.8	329
8	Microbial responses to environmental arsenic. BioMetals, 2009, 22, 117-130.	4.1	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.	3.8	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.	3.4	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.	17.5	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.	5.4	248
14	Bioremediation 3.0: Engineering pollutant-removing bacteria in the times of systemic biology. Biotechnology Advances, 2017, 35, 845-866.	11.7	240
15	Systems biology approaches to bioremediation. Current Opinion in Biotechnology, 2008, 19, 579-589.	6.6	227
16	Heavy metal tolerance and metal homeostasis inPseudomonas putidaas revealed by complete genome analysis. Environmental Microbiology, 2003, 5, 1242-1256.	3.8	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.	3.4	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.	4.0	199

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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.	6.1	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.	3.8	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.	14.5	195
22	Promoters in the environment: transcriptional regulation in its natural context. Nature Reviews Microbiology, 2005, 3, 105-118.	28.6	192
23	Tn7-Based Device for Calibrated Heterologous Gene Expression in <i>Pseudomonas putida</i>. ACS Synthetic Biology, 2015, 4, 1341-1351.	3.8	169
24	Enhanced metalloadsorption of bacterial cells displaying poly-His peptides. Nature Biotechnology, 1996, 14, 1017-1020.	17.5	166
25	Genetically modified organisms for the environment: stories of success and failure and what we have learned from them. International Microbiology, 2005, 8, 213-22.	2.4	159
26	pBAM1: an all-synthetic genetic tool for analysis and construction of complex bacterial phenotypes. BMC Microbiology, 2011, 11, 38.	3.3	142
27	Genome reduction boosts heterologous gene expression in Pseudomonas putida. Microbial Cell Factories, 2015, 14, 23.	4.0	142
28	Activation of the transcriptional regulator XylR of Pseudomonas putida by release of repression between functional domains. Molecular Microbiology, 1995, 16, 205-213.	2.5	139
29	Plastic waste as a novel substrate for industrial biotechnology. Microbial Biotechnology, 2015, 8, 900-903.	4.2	134
30	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.	3.8	132
31	Growth phase-dependent expression of the Pseudomonas putida KT2440 transcriptional machinery analysed with a genome-wide DNA microarray. Environmental Microbiology, 2006, 8, 165-177.	3.8	123
32	Modulation of gene expression through chromosomal positioning in Escherichia coli. Microbiology (United Kingdom), 1997, 143, 2071-2078.	1.8	118
33	CRISPR/Cas9â€Based Counterselection Boosts Recombineering Efficiency in <i>Pseudomonas putida</i>. Biotechnology Journal, 2018, 13, e1700161.	3.5	115
34	Engineering of alkyl- and haloaromatic-responsive gene expression with mini-transposons containing regulated promoters of biodegradative pathways of Pseudomonas. Gene, 1993, 130, 41-46.	2.2	113
35	Export of autotransported proteins proceeds through an oligomeric ring shaped by C-terminal domains. EMBO Journal, 2002, 21, 2122-2131.	7.8	110
36	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.	10.0	106

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37	Exploring the microbial biodegradation and biotransformation gene pool. Trends in Biotechnology, 2005, 23, 497-506.	9.3	104
38	Genetic programming of catalytic Pseudomonas putida biofilms for boosting biodegradation of haloalkanes. Metabolic Engineering, 2016, 33, 109-118.	7.0	103
39	Resistance to Tellurite as a Selection Marker for Genetic Manipulations of Pseudomonas Strains. Applied and Environmental Microbiology, 1998, 64, 4040-4046.	3.1	100
40	Involvement of sigma54 in exponential silencing of the Pseudomonas putida TOL plasmid Pu promoter. Molecular Microbiology, 1996, 19, 7-17.	2.5	94
41	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.	7.0	93
42	Transposon-Based and Plasmid-Based Genetic Tools for Editing Genomes of Gram-Negative Bacteria. Methods in Molecular Biology, 2012, 813, 267-283.	0.9	92
43	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.	3.8	91
44	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.	3.4	87
45	Refactoring the upper sugar metabolism of Pseudomonas putida for co-utilization of cellobiose, xylose, and glucose. Metabolic Engineering, 2018, 48, 94-108.	7.0	86
46	Engineering the Soil Bacterium Pseudomonas putida for Arsenic Methylation. Applied and Environmental Microbiology, 2013, 79, 4493-4495.	3.1	85
47	New Transposon Tools Tailored for Metabolic Engineering of Gram-Negative Microbial Cell Factories. Frontiers in Bioengineering and Biotechnology, 2014, 2, 46.	4.1	85
48	Structural tolerance of bacterial autotransporters for folded passenger protein domains. Molecular Microbiology, 2004, 52, 1069-1080.	2.5	83
49	The power of synthetic biology for bioproduction, remediation and pollution control. EMBO Reports, 2018, 19, .	4.5	83
50	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.	14.5	82
51	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.	2.5	80
52	Tracing explosives in soil with transcriptional regulators of <i>Pseudomonas putida</i> evolved for responding to nitrotoluenes. Microbial Biotechnology, 2008, 1, 236-246.	4.2	79
53	Reconfiguration of metabolic fluxes in <i>Pseudomonas putida</i> as a response to sub-lethal oxidative stress. ISME Journal, 2021, 15, 1751-1766.	9.8	79
54	Regulatory Tasks of the Phosphoenolpyruvate-Phosphotransferase System of Pseudomonas putida in Central Carbon Metabolism. MBio, 2012, 3, .	4.1	78

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55	Synthetic constructs in/for the environment: Managing the interplay between natural and engineered Biology. FEBS Letters, 2012, 586, 2199-2206.	2.8	78
56	Metabolic engineering of bacteria for environmental applications: construction of Pseudomonas strains for biodegradation of 2-chlorotoluene. Journal of Biotechnology, 2001, 85, 103-113.	3.8	77
57	Accumulation of inorganic polyphosphate enables stress endurance and catalytic vigour in Pseudomonas putida KT2440. Microbial Cell Factories, 2013, 12, 50.	4.0	77
58	The Behavior of Bacteria Designed for Biodegradation. Nature Biotechnology, 1994, 12, 1349-1356.	17.5	76
59	Universal barrier to lateral spread of specific genes among microorganisms. Molecular Microbiology, 1994, 13, 855-861.	2.5	75
60	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.	17.5	75
61	Transcriptomic fingerprinting of <i><scp>P</scp>seudomonas putida</i> under alternative physiological regimes. Environmental Microbiology Reports, 2013, 5, 883-891.	2.4	75
62	Endogenous Stress Caused by Faulty Oxidation Reactions Fosters Evolution of 2,4-Dinitrotoluene-Degrading Bacteria. PLoS Genetics, 2013, 9, e1003764.	3.5	74
63	Metalloregulation in vitro of the aerobactin promoter of Escherichia coli by the Fur (ferric uptake) Tj ETQq1 1 0.784314 rgBT /Overloc	2.5	73
64	Ã€ la carte transcriptional regulators: unlocking responses of the prokaryotic enhancer-binding protein XylR to non-natural effectors. Molecular Microbiology, 2008, 42, 47-59.	2.5	72
65	Stable implantation of orthogonal sensor circuits in Gramâ€negative bacteria for environmental release. Environmental Microbiology, 2008, 10, 3305-3316.	3.8	72
66	The Role of Thiol Species in the Hypertolerance of Aspergillus sp. P37 to Arsenic. Journal of Biological Chemistry, 2004, 279, 51234-51240.	3.4	71
67	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.	3.1	68
68	Chemical reactivity drives spatiotemporal organisation of bacterial metabolism. FEMS Microbiology Reviews, 2014, 39, n/a-n/a.	8.6	67
69	Surveying biotransformations with <i>Ã la carte</i> genetic traps: translating dehydrochlorination of lindane (gammaâ€hexachlorocyclohexane) into <i>lacZ</i>â€based phenotypes. Environmental Microbiology, 2006, 8, 546-555.	3.8	65
70	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.	3.5	65
71	MetaRouter: bioinformatics for bioremediation. Nucleic Acids Research, 2004, 33, D588-D592.	14.5	64
72	Beware of metaphors: Chasses and orthogonality in synthetic biology. Bioengineered Bugs, 2011, 2, 3-7.	1.7	64

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73	The private life of environmental bacteria: pollutant biodegradation at the single cell level. Environmental Microbiology, 2014, 16, 628-642.	3.8	63
74	Molecular tools and emerging strategies for deep genetic/genomic refactoring of Pseudomonas. Current Opinion in Biotechnology, 2017, 47, 120-132.	6.6	63
75	The organization of the microbial biodegradation network from a systemsâ€biology perspective. EMBO Reports, 2003, 4, 994-999.	4.5	62
76	Robustness of Pseudomonas putida KT2440 as a host for ethanol biosynthesis. New Biotechnology, 2014, 31, 562-571.	4.4	62
77	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.	3.8	62
78	The Glycerol-Dependent Metabolic Persistence of Pseudomonas putida KT2440 Reflects the Regulatory Logic of the GlpR Repressor. MBio, 2015, 6, .	4.1	62
79	From the <i>selfish gene</i> to <i>selfish metabolism</i>: Revisiting the central dogma. BioEssays, 2014, 36, 226-235.	2.5	60
80	Emergence of novel functions in transcriptional regulators by regression to <i>stem</i> protein types. Molecular Microbiology, 2007, 65, 907-919.	2.5	58
81	Pyridine nucleotide transhydrogenases enable redox balance of <i>Pseudomonas putida</i> during biodegradation of aromatic compounds. Environmental Microbiology, 2016, 18, 3565-3582.	3.8	58
82	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.	3.8	58
83	Random and cyclical deletion of large DNA segments in the genome of <i>Pseudomonas putida</i>. Environmental Microbiology, 2012, 14, 1444-1453.	3.8	56
84	Functional implementation of a linear glycolysis for sugar catabolism in Pseudomonas putida. Metabolic Engineering, 2019, 54, 200-211.	7.0	56
85	Bioaccumulation of heavy metals with protein fusions of metallothionein to bacteriol OMPs. Biochimie, 1998, 80, 855-861.	2.6	53
86	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.	4.0	53
87	Designing microbial systems for gene expression in the field. Trends in Biotechnology, 1994, 12, 365-371.	9.3	52
88	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.	3.8	52
89	Implantation of unmarked regulatory and metabolic modules in Gram-negative bacteria with specialised mini-transposon delivery vectors. Journal of Biotechnology, 2013, 163, 143-154.	3.8	51
90	The Metabolic Redox Regime of Pseudomonas putida Tunes Its Evolvability toward Novel Xenobiotic Substrates. MBio, 2018, 9, .	4.1	51

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91	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.	3.8	50
92	The quest for the minimal bacterial genome. Current Opinion in Biotechnology, 2016, 42, 216-224.	6.6	49
93	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.	2.2	47
94	In vivo diversification of target genomic sites using processive base deaminase fusions blocked by dCas9. Nature Communications, 2020, 11, 6436.	12.8	47
95	Novel Physiological Modulation of the Pu Promoter of TOL Plasmid. Journal of Biological Chemistry, 2004, 279, 7777-7784.	3.4	46
96	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.	2.2	45
97	Engineering input/output nodes in prokaryotic regulatory circuits. FEMS Microbiology Reviews, 2010, 34, 842-865.	8.6	45
98	The environmental fate of organic pollutants through the global microbial metabolism. Molecular Systems Biology, 2007, 3, 114.	7.2	43
99	A standardized workflow for surveying recombinases expands bacterial genomeâ€editing capabilities. Microbial Biotechnology, 2018, 11, 176-188.	4.2	43
100	The role of the interdomain B linker in the activation of the XylR protein of Pseudomonas putida. Molecular Microbiology, 2000, 38, 401-410.	2.5	39
101	Deconvolution of Gene Expression Noise into Spatial Dynamics of Transcription Factorâ€“Promoter Interplay. ACS Synthetic Biology, 2017, 6, 1359-1369.	3.8	39
102	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.	2.2	38
103	Pseudomonas putida in the quest of programmable chemistry. Current Opinion in Biotechnology, 2019, 59, 111-121.	6.6	38
104	Environmental biosafety in the age of Synthetic Biology: Do we really need a radical new approach?. BioEssays, 2010, 32, 926-931.	2.5	37
105	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.	2.2	36
106	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.	2.2	36
107	The <i>logicome</i> of environmental bacteria: merging catabolic and regulatory events with Boolean formalisms. Environmental Microbiology, 2011, 13, 2389-2402.	3.8	36
108	Regulatory exaptation of the catabolite repression protein (Crp)â€“cAMP system in <i>Pseudomonas putida</i>. Environmental Microbiology, 2011, 13, 324-339.	3.8	34

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109	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.	3.7	34
110	For the sake of the Bioeconomy: define what a Synthetic Biology Chassis is!. New Biotechnology, 2021, 60, 44-51.	4.4	34
111	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.	1.8	33
112	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.	2.4	32
113	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
114	High-Efficiency Multi-site Genomic Editing of Pseudomonas putida through Thermoinducible ssDNA Recombineering. IScience, 2020, 23, 100946.	4.1	32
115	<scp>CRISPR</scp>/Cas9â€enhanced ss<scp>DNA</scp> recombineering for <i>Pseudomonas putida</i>. Microbial Biotechnology, 2019, 12, 1076-1089.	4.2	31
116	Enhanced Metallosorption of<i>Escherichia Coli</i>Cells Due to Surface Display of Î²- and Î±-Domains of Mammalian Metallothionein as a Fusion to Lamb Protein. Journal of Receptor and Signal Transduction Research, 1999, 19, 703-715.	2.5	30
117	Inferring the genetic network ofm-xylene metabolism through expression profiling of thexylgenes ofPseudomonas putidamt-2. Molecular Microbiology, 2005, 57, 1557-1569.	2.5	30
118	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
119	Engineering Multicellular Logic in Bacteria with Metabolic Wires. ACS Synthetic Biology, 2014, 3, 204-209.	3.8	30
120	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.	2.5	29
121	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.	3.8	29
122	Growth-dependent Phosphorylation of the PtsN (EIINtr) Protein of Pseudomonas putida. Journal of Biological Chemistry, 2007, 282, 18206-18211.	3.4	28
123	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.	2.3	28
124	A Metabolic Widget Adjusts the Phosphoenolpyruvate-Dependent Fructose Influx in Pseudomonas putida. MSystems, 2016, 1, .	3.8	28
125	<scp>ArsH</scp> protects <i>Pseudomonas putida</i> from oxidative damage caused by exposure to arsenic. Environmental Microbiology, 2020, 22, 2230-2242.	3.8	28
126	Synthetic Biology for Terraformation Lessons from Mars, Earth, and the Microbiome. Life, 2020, 10, 14.	2.4	28

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127	The Standard European Vector Architecture (SEVA) Plasmid Toolkit. Methods in Molecular Biology, 2014, 1149, 469-478.	0.9	28
128	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
129	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.	3.5	27
130	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.	3.4	26
131	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.	2.5	26
132	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.	3.5	26
133	From the phosphoenolpyruvate phosphotransferase system to selfish metabolism: a story retraced in<i>Pseudomonas putida</i>. FEMS Microbiology Letters, 2014, 356, 144-153.	1.8	26
134	SEVA 3.1: enabling interoperability of DNA assembly among the SEVA, BioBricks and Type IIS restriction enzyme standards. Microbial Biotechnology, 2020, 13, 1793-1806.	4.2	26
135	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.	3.8	25
136	Seven microbial bioâ€processes to help the planet. Microbial Biotechnology, 2017, 10, 995-998.	4.2	25
137	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.	2.5	24
138	Pseudomonas putida mt-2 tolerates reactive oxygen species generated during matric stress by inducing a major oxidative defense response. BMC Microbiology, 2015, 15, 202.	3.3	24
139	Modulating Heterologous Gene Expression with Portable mRNA-Stabilizing 5â€²-UTR Sequences. ACS Synthetic Biology, 2018, 7, 2177-2188.	3.8	24
140	A stringently controlled expression system for analysing lateral gene transfer between bacteria. Molecular Microbiology, 1996, 21, 293-300.	2.5	23
141	Engineering Gram-Negative Microbial Cell Factories Using Transposon Vectors. Methods in Molecular Biology, 2017, 1498, 273-293.	0.9	23
142	Neutralizationof Enteric Coronaviruses with Escherichia coli CellsExpressing Single-Chain Fv-AutotransporterFusions. Journal of Virology, 2003, 77, 13396-13398.	3.4	22
143	Quantitative, Non-Disruptive Monitoring of Transcription in Single Cells with a Broad-Host Range GFP-luxCDABE Dual Reporter System. PLoS ONE, 2012, 7, e52000.	2.5	22
144	Confidence, tolerance, and allowance in biological engineering: The nuts and bolts of living things. BioEssays, 2015, 37, 95-102.	2.5	22

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145	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.	3.8	22
146	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
147	Monitoring biodegradative enzymes with nanobodies raised in <i>Camelus dromedarius</i> with mixtures of catabolic proteins. Environmental Microbiology, 2011, 13, 960-974.	3.8	21
148	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.	2.5	20
149	Uncoupling of choline-O-sulphate utilization from osmoprotection in Pseudomonas putida. Molecular Microbiology, 2006, 62, 1643-1654.	2.5	19
150	A GFP-lacZ Bicistronic Reporter System for Promoter Analysis in Environmental Gram-Negative Bacteria. PLoS ONE, 2012, 7, e34675.	2.5	19
151	Engineering Whole-Cell Biosensors with No Antibiotic Markers for Monitoring Aromatic Compounds in the Environment. Methods in Molecular Biology, 2012, 834, 261-281.	0.9	19
152	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.	3.8	19
153	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
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