

VÃ-ctor De Lorenzo

List of Publications by Year in descending order

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Version: 2024-02-01

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	Standardization of regulatory nodes for engineering heterologous gene expression: a feasibility study. <i>Microbial Biotechnology</i> , 2022, 15, 2250-2265.	4.2	8
2	High-Efficiency Multi-site Genomic Editing (HEMSE) Made Easy. <i>Methods in Molecular Biology</i> , 2022, 2479, 37-52.	0.9	0
3	Hypermuation of specific genomic loci of <i>Pseudomonas putida</i> for continuous evolution of target genes. <i>Microbial Biotechnology</i> , 2022, 15, 2309-2323.	4.2	3
4	Environmental Galenics: large-scale fortification of extant microbiomes with engineered bioremediation agents. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	4.0	13
5	For the sake of the Bioeconomy: define what a Synthetic Biology Chassis is!. <i>New Biotechnology</i> , 2021, 60, 44-51.	4.4	34
6	A Standardized Inverter Package Borne by Broad Host Range Plasmids for Genetic Circuit Design in Gram-Negative Bacteria. <i>ACS Synthetic Biology</i> , 2021, 10, 213-217.	3.8	9
7	Ribonucleases control distinct traits of <i>Pseudomonas putida</i> lifestyle. <i>Environmental Microbiology</i> , 2021, 23, 174-189.	3.8	5
8	Reconfiguration of metabolic fluxes in <i>Pseudomonas putida</i> as a response to sub-lethal oxidative stress. <i>ISME Journal</i> , 2021, 15, 1751-1766.	9.8	79
9	Low CyaA expression and anti-cooperative binding of cAMP to CRP frames the scope of the cognate regulon of <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , 2021, 23, 1732-1749.	3.8	4
10	Subcellular Architecture of the <i>xyl</i> Gene Expression Flow of the TOL Catabolic Plasmid of <i>Pseudomonas putida</i> mt-2. <i>MBio</i> , 2021, 12, .	4.1	3
11	A Bifan Motif Shaped by ArsR1, ArsR2, and Their Cognate Promoters Frames Arsenic Tolerance of <i>Pseudomonas putida</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 641440.	3.5	2
12	Refactoring the Conjugation Machinery of Promiscuous Plasmid RP4 into a Device for Conversion of Gram-Negative Isolates to Hfr Strains. <i>ACS Synthetic Biology</i> , 2021, 10, 690-697.	3.8	7
13	Identification of a self-sufficient cytochrome P450 monooxygenase from <i>Cupriavidus pinatubonensis</i> JMP134 involved in 2-hydroxyphenylacetic acid catabolism, via homogentisate pathway. <i>Microbial Biotechnology</i> , 2021, 14, 1944-1960.	4.2	7
14	Engineering Tropism of <i>Pseudomonas putida</i> toward Target Surfaces through Ectopic Display of Recombinant Nanobodies. <i>ACS Synthetic Biology</i> , 2021, 10, 2049-2059.	3.8	11
15	Automated design and implementation of a NOR gate in <i>Pseudomonas putida</i> . <i>Synthetic Biology</i> , 2021, 6, ysab024.	2.2	12
16	The faulty SOS response of <i>Pseudomonas putida</i> KT2440 stems from an inefficient RecA-LexA interplay. <i>Environmental Microbiology</i> , 2021, 23, 1608-1619.	3.8	0
17	Targetron-Assisted Delivery of Exogenous DNA Sequences into <i>Pseudomonas putida</i> through CRISPR-Aided Counterselection. <i>ACS Synthetic Biology</i> , 2021, 10, 2552-2565.	3.8	8
18	Mismatch repair hierarchy of <i>Pseudomonas putida</i> revealed by mutagenic ssDNA recombineering of the <i>pyrF</i> gene. <i>Environmental Microbiology</i> , 2020, 22, 45-58.	3.8	22

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19	SEVA 3.0: an update of the Standard European Vector Architecture for enabling portability of genetic constructs among diverse bacterial hosts. <i>Nucleic Acids Research</i> , 2020, 48, D1164-D1170.	14.5	82
20	Multiple-Site Diversification of Regulatory Sequences Enables Interspecies Operability of Genetic Devices. <i>ACS Synthetic Biology</i> , 2020, 9, 104-114.	3.8	15
21	An automated DIY framework for experimental evolution of <i>Pseudomonas putida</i> . <i>Microbial Biotechnology</i> , 2020, 14, 2679-2685.	4.2	5
22	SEVA 3.1: enabling interoperability of DNA assembly among the SEVA, BioBricks and Type IIS restriction enzyme standards. <i>Microbial Biotechnology</i> , 2020, 13, 1793-1806.	4.2	26
23	Naked Bacterium: Emerging Properties of a Surfome-Streamlined <i>Pseudomonas putida</i> Strain. <i>ACS Synthetic Biology</i> , 2020, 9, 2477-2492.	3.8	15
24	In vivo diversification of target genomic sites using processive base deaminase fusions blocked by dCas9. <i>Nature Communications</i> , 2020, 11, 6436.	12.8	47
25	The Wsp intermembrane complex mediates metabolic control of the swim-attach decision of <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , 2020, 22, 3535-3547.	3.8	13
26	High-Efficiency Multi-site Genomic Editing of <i>Pseudomonas putida</i> through Thermostable ssDNA Recombineering. <i>iScience</i> , 2020, 23, 100946.	4.1	32
27	<i>ArSH</i> protects <i>Pseudomonas putida</i> from oxidative damage caused by exposure to arsenic. <i>Environmental Microbiology</i> , 2020, 22, 2230-2242.	3.8	28
28	Multifunctional SEVA shuttle vectors for actinomycetes and Gram-negative bacteria. <i>MicrobiologyOpen</i> , 2020, 9, 1135-1149.	3.0	12
29	Environmental Performance of <i>Pseudomonas putida</i> with a Uracylated Genome. <i>ChemBioChem</i> , 2020, 21, 3255-3265.	2.6	3
30	Synthetic Biology for Terraformation Lessons from Mars, Earth, and the Microbiome. <i>Life</i> , 2020, 10, 14.	2.4	28
31	A Broad Host Range Plasmid-Based Roadmap for ssDNA-Based Recombineering in Gram-Negative Bacteria. <i>Methods in Molecular Biology</i> , 2020, 2075, 383-398.	0.9	11
32	CRISPR/Cas9-enhanced ssDNA recombineering for <i>Pseudomonas putida</i> . <i>Microbial Biotechnology</i> , 2019, 12, 1076-1089.	4.2	31
33	Spatial organization of the gene expression hardware in <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , 2019, 21, 1645-1658.	3.8	14
34	Genomic Responses of <i>Pseudomonas putida</i> to Aromatic Hydrocarbons. , 2019, , 1-15.		0
35	Functional implementation of a linear glycolysis for sugar catabolism in <i>Pseudomonas putida</i> . <i>Metabolic Engineering</i> , 2019, 54, 200-211.	7.0	56
36	<i>Pseudomonas putida</i> in the quest of programmable chemistry. <i>Current Opinion in Biotechnology</i> , 2019, 59, 111-121.	6.6	38

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37	Improved Thermotolerance of Genome-Reduced <i>Pseudomonas putida</i> EM42 Enables Effective Functioning of the P _L /c _L 857 System. <i>Biotechnology Journal</i> , 2019, 14, e1800483.	3.5	27
38	Evolving metabolism of 2,4-dinitrotoluene triggers SOS-independent diversification of host cells. <i>Environmental Microbiology</i> , 2019, 21, 314-326.	3.8	13
39	Genomic Responses of <i>Pseudomonas putida</i> to Aromatic Hydrocarbons. , 2019, , 287-301.		0
40	Biodegradation and Bioremediation: An Introduction. , 2019, , 1-20.		0
41	Assessing Carbon Source-Dependent Phenotypic Variability in <i>Pseudomonas putida</i> . <i>Methods in Molecular Biology</i> , 2018, 1745, 287-301.	0.9	4
42	The power of synthetic biology for bioproduction, remediation and pollution control. <i>EMBO Reports</i> , 2018, 19, .	4.5	83
43	CRISPR/Cas9-Based Counterselection Boosts Recombineering Efficiency in <i>Pseudomonas putida</i> . <i>Biotechnology Journal</i> , 2018, 13, e1700161.	3.5	115
44	A standardized workflow for surveying recombinases expands bacterial genome-editing capabilities. <i>Microbial Biotechnology</i> , 2018, 11, 176-188.	4.2	43
45	A Post-translational Metabolic Switch Enables Complete Decoupling of Bacterial Growth from Biopolymer Production in Engineered <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 2686-2697.	3.8	58
46	The interplay of EIIA ^{Ntr} with C-source regulation of the <i>Pu</i> promoter of <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , 2018, 20, 4555-4566.	3.8	3
47	The Metabolic Redox Regime of <i>Pseudomonas putida</i> Tunes Its Evolvability toward Novel Xenobiotic Substrates. <i>MBio</i> , 2018, 9, .	4.1	51
48	<i>Pseudomonas putida</i> as a functional chassis for industrial biocatalysis: From native biochemistry to trans-metabolism. <i>Metabolic Engineering</i> , 2018, 50, 142-155.	7.0	338
49	Refactoring the upper sugar metabolism of <i>Pseudomonas putida</i> for co-utilization of cellobiose, xylose, and glucose. <i>Metabolic Engineering</i> , 2018, 48, 94-108.	7.0	86
50	An Engineered Device for Indoleacetic Acid Production under Quorum Sensing Signals Enables <i>Cupriavidus pinatubonensis</i> JMP134 To Stimulate Plant Growth. <i>ACS Synthetic Biology</i> , 2018, 7, 1519-1527.	3.8	19
51	Modulating Heterologous Gene Expression with Portable mRNA-Stabilizing 5'-UTR Sequences. <i>ACS Synthetic Biology</i> , 2018, 7, 2177-2188.	3.8	24
52	Biodegradation and Bioremediation: An Introduction. , 2018, , 1-21.		1
53	Re-Factoring Glycolytic Genes for Targeted Engineering of Catabolism in Gram-Negative Bacteria. <i>Methods in Molecular Biology</i> , 2018, 1772, 3-24.	0.9	3
54	Dynamics of <i>Pseudomonas putida</i> biofilms in an upscale experimental framework. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2018, 45, 899-911.	3.0	7

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55	The biofilm matrix polysaccharides cellulose and alginate both protect <i>Pseudomonas putida</i> mt-2 against reactive oxygen species generated under matrix stress and copper exposure. <i>Microbiology (United Kingdom)</i> , 2018, 164, 883-888.	1.8	33
56	Refactoring the Embden-Meyerhof-Parnas Pathway as a Whole of Portable GlucoBricks for Implantation of Glycolytic Modules in Gram-Negative Bacteria. <i>ACS Synthetic Biology</i> , 2017, 6, 793-805.	3.8	50
57	Deconvolution of Gene Expression Noise into Spatial Dynamics of Transcription Factor-Promoter Interplay. <i>ACS Synthetic Biology</i> , 2017, 6, 1359-1369.	3.8	39
58	Molecular tools and emerging strategies for deep genetic/genomic refactoring of <i>Pseudomonas</i> . <i>Current Opinion in Biotechnology</i> , 2017, 47, 120-132.	6.6	63
59	Bioremediation 3.0: Engineering pollutant-removing bacteria in the times of systemic biology. <i>Biotechnology Advances</i> , 2017, 35, 845-866.	11.7	240
60	Seven microbial bioprocesses to help the planet. <i>Microbial Biotechnology</i> , 2017, 10, 995-998.	4.2	25
61	CellShape: A user-friendly image analysis tool for quantitative visualization of bacterial cell factories inside. <i>Biotechnology Journal</i> , 2017, 12, 1600323.	3.5	15
62	Engineering Gram-Negative Microbial Cell Factories Using Transposon Vectors. <i>Methods in Molecular Biology</i> , 2017, 1498, 273-293.	0.9	23
63	The <i>RNA</i> chaperone <i>Hfq</i> enables the environmental stress tolerance superphenotype of <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , 2016, 18, 3309-3326.	3.8	25
64	A Metabolic Widget Adjusts the Phosphoenolpyruvate-Dependent Fructose Influx in <i>Pseudomonas putida</i> . <i>MSystems</i> , 2016, 1, .	3.8	28
65	From dirt to industrial applications: <i>Pseudomonas putida</i> as a Synthetic Biology chassis for hosting harsh biochemical reactions. <i>Current Opinion in Chemical Biology</i> , 2016, 34, 20-29.	6.1	199
66	Nitrogen regulation of the <i>xyl</i> genes of <i>Pseudomonas putida</i> mt-2 propagates into a significant effect of nitrate on <i>m-xylene</i> mineralization in soil. <i>Microbial Biotechnology</i> , 2016, 9, 814-823.	4.2	5
67	Pyridine nucleotide transhydrogenases enable redox balance of <i>Pseudomonas putida</i> during biodegradation of aromatic compounds. <i>Environmental Microbiology</i> , 2016, 18, 3565-3582.	3.8	58
68	The quest for the minimal bacterial genome. <i>Current Opinion in Biotechnology</i> , 2016, 42, 216-224.	6.6	49
69	The Ssr protein (T1E_1405) from <i>Pseudomonas putida</i> DOT1E enables oligonucleotide-based recombinering in platform strain <i>P. putida</i> EM42. <i>Biotechnology Journal</i> , 2016, 11, 1309-1319.	3.5	65
70	The revisited genome of <i>Pseudomonas putida</i> KT2440 enlightens its value as a robust metabolic chassis. <i>Environmental Microbiology</i> , 2016, 18, 3403-3424.	3.8	270
71	Introduction to Systems and Synthetic Biology in Hydrocarbon Microbiology: Applications. Springer Protocols, 2016, , 1-8.	0.3	0
72	High-resolution analysis of the <i>m-xylene</i> /toluene biodegradation subtranscriptome of <i>Pseudomonas putida</i> mt-2. <i>Environmental Microbiology</i> , 2016, 18, 3327-3341.	3.8	18

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73	Transcription factor levels enable metabolic diversification of single cells of environmental bacteria. ISME Journal, 2016, 10, 1122-1133.	9.8	13
74	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.	1.3	0
75	Data on the standardization of a cyclohexanone-responsive expression system for Gram-negative bacteria. Data in Brief, 2016, 6, 738-744.	1.0	17
76	Genetic programming of catalytic Pseudomonas putida biofilms for boosting biodegradation of haloalkanes. Metabolic Engineering, 2016, 33, 109-118.	7.0	103
77	Systems and Synthetic Biology in Hydrocarbon Microbiology: Tools. Springer Protocols, 2015, , 1-7.	0.3	1
78	Plastic waste as a novel substrate for industrial biotechnology. Microbial Biotechnology, 2015, 8, 900-903.	4.2	134
79	Mining Environmental Plasmids for Synthetic Biology Parts and Devices. Microbiology Spectrum, 2015, 3, PLAS-0033-2014.	3.0	18
80	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.	0.3	1
81	Pseudomonas putida mt-2 tolerates reactive oxygen species generated during matrix stress by inducing a major oxidative defense response. BMC Microbiology, 2015, 15, 202.	3.3	24
82	The two paralogue <i>phoN</i> (phosphinothricin acetyl transferase) genes of <i>Pseudomonas putida</i> encode functionally different proteins. Environmental Microbiology, 2015, 17, 3330-3340.	3.8	6
83	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
84	Broadening the SEVA Plasmid Repertoire to Facilitate Genomic Editing of Gram-Negative Bacteria. Springer Protocols, 2015, , 9-27.	0.3	9
85	Freeing <i>Pseudomonas putida</i> of its proviral load strengthens endurance to environmental stresses. Environmental Microbiology, 2015, 17, 76-90.	3.8	62
86	Functional coexistence of twin arsenic resistance systems in <i>Pseudomonas putida</i> of strain KT2440. Environmental Microbiology, 2015, 17, 229-238.	3.8	52
87	Genome reduction boosts heterologous gene expression in Pseudomonas putida. Microbial Cell Factories, 2015, 14, 23.	4.0	142
88	Tn7-Based Device for Calibrated Heterologous Gene Expression in <i>Pseudomonas putida</i> . ACS Synthetic Biology, 2015, 4, 1341-1351.	3.8	169
89	Phenotypic knockouts of selected metabolic pathways by targeting enzymes with camel-derived nanobodies (VHHs). Metabolic Engineering, 2015, 30, 40-48.	7.0	8
90	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

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91	The Glycerol-Dependent Metabolic Persistence of <i>Pseudomonas putida</i> KT2440 Reflects the Regulatory Logic of the GlpR Repressor. <i>MBio</i> , 2015, 6, .	4.1	62
92	Widening functional boundaries of the λ 54 promoter Pu of <i>Pseudomonas putida</i> by defeating extant physiological constraints. <i>Molecular BioSystems</i> , 2015, 11, 734-742.	2.9	4
93	The differential response of the <i>P_{ben}</i> promoter of <i>Pseudomonas putida</i> to <i>P_{mt}</i> and <i>P_{XylS}</i> prevents metabolic conflicts in <i>P_{mt}</i> xylene biodegradation. <i>Environmental Microbiology</i> , 2015, 17, 64-75.	3.8	29
94	Chassis organism from <i>Corynebacterium glutamicum</i> : The way towards biotechnological domestication of <i>Corynebacteria</i> . <i>Biotechnology Journal</i> , 2015, 10, 244-245.	3.5	11
95	Confidence, tolerance, and allowance in biological engineering: The nuts and bolts of living things. <i>BioEssays</i> , 2015, 37, 95-102.	2.5	22
96	Metabolic and regulatory rearrangements underlying glycerol metabolism in <i>Pseudomonas putida</i> KT2440. <i>Environmental Microbiology</i> , 2014, 16, 239-254.	3.8	91
97	Chemical reactivity drives spatiotemporal organisation of bacterial metabolism. <i>FEMS Microbiology Reviews</i> , 2014, 39, n/a-n/a.	8.6	67
98	<i>Pseudomonas</i> 2.0: genetic upgrading of <i>P. putida</i> KT2440 as an enhanced host for heterologous gene expression. <i>Microbial Cell Factories</i> , 2014, 13, 159.	4.0	199
99	Robustness of <i>Pseudomonas putida</i> KT2440 as a host for ethanol biosynthesis. <i>New Biotechnology</i> , 2014, 31, 562-571.	4.4	62
100	Engineering Multicellular Logic in Bacteria with Metabolic Wires. <i>ACS Synthetic Biology</i> , 2014, 3, 204-209.	3.8	30
101	From the selfish gene to selfish metabolism: Revisiting the central dogma. <i>BioEssays</i> , 2014, 36, 226-235.	2.5	60
102	The private life of environmental bacteria: pollutant biodegradation at the single cell level. <i>Environmental Microbiology</i> , 2014, 16, 628-642.	3.8	63
103	Biotechnological domestication of pseudomonads using synthetic biology. <i>Nature Reviews Microbiology</i> , 2014, 12, 368-379.	28.6	332
104	From the phosphoenolpyruvate phosphotransferase system to selfish metabolism: a story retraced in <i>Pseudomonas putida</i> . <i>FEMS Microbiology Letters</i> , 2014, 356, 144-153.	1.8	26
105	The metabolic cost of flagellar motion in <i>Pseudomonas putida</i> KT2440. <i>Environmental Microbiology</i> , 2014, 16, 291-303.	3.8	132
106	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. <i>Environmental Science & Technology</i> , 2014, 48, 10337-10344.	10.0	106
107	Fructose 1-phosphate is the one and only physiological effector of the Cra (FruR) regulator of <i>Pseudomonas putida</i> . <i>FEBS Open Bio</i> , 2014, 4, 377-386.	2.3	28
108	New Transposon Tools Tailored for Metabolic Engineering of Gram-Negative Microbial Cell Factories. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 46.	4.1	85

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109	The Standard European Vector Architecture (SEVA) Plasmid Toolkit. <i>Methods in Molecular Biology</i> , 2014, 1149, 469-478.	0.9	28
110	Chromosomal Integration of Transcriptional Fusions. <i>Methods in Molecular Biology</i> , 2014, 1149, 479-489.	0.9	7
111	Promoter Fusions with Optical Outputs in Individual Cells and in Populations. <i>Methods in Molecular Biology</i> , 2014, 1149, 579-590.	0.9	1
112	The IHF regulon of exponentially growing <i>Pseudomonas putida</i> cells. <i>Environmental Microbiology</i> , 2013, 15, 49-63.	3.8	14
113	Cra regulates the cross-talk between the two branches of the phosphoenolpyruvate-â€f:â€fphosphotransferase system of <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , 2013, 15, 121-132.	3.8	18
114	Accumulation of inorganic polyphosphate enables stress endurance and catalytic vigour in <i>Pseudomonas putida</i> KT2440. <i>Microbial Cell Factories</i> , 2013, 12, 50.	4.0	77
115	Why are chlorinated pollutants so difficult to degrade aerobically? Redox stress limits 1,3-dichloroprop-1-ene metabolism by <i>Pseudomonas pavonaceae</i> . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120377.	4.0	53
116	Expanding the Boolean Logic of the Prokaryotic Transcription Factor XylR by Functionalization of Permissive Sites with a Protease-Target Sequence. <i>ACS Synthetic Biology</i> , 2013, 2, 594-603.	3.8	16
117	NanoPad: An integrated platform for bacterial production of camel nanobodies aimed at detecting environmental biomarkers. <i>Proteomics</i> , 2013, 13, 2766-2775.	2.2	7
118	The <i>scp>E</scp>ntnerâ€“<scp>D</scp>oudoroff</i> pathway empowers <i>scp>P</scp>seudomonas putida</i>â€¦<scp>KT</scp>2440 with a high tolerance to oxidative stress. <i>Environmental Microbiology</i>, 2013, 15, 1772-1785.</i>	3.8	195
119	Implantation of unmarked regulatory and metabolic modules in Gram-negative bacteria with specialised mini-transposon delivery vectors. <i>Journal of Biotechnology</i> , 2013, 163, 143-154.	3.8	51
120	Engineering an anaerobic metabolic regime in <i>Pseudomonas putida</i> KT2440 for the anoxic biodegradation of 1,3-dichloroprop-1-ene. <i>Metabolic Engineering</i> , 2013, 15, 98-112.	7.0	93
121	Endogenous Stress Caused by Faulty Oxidation Reactions Fosters Evolution of 2,4-Dinitrotoluene-Degrading Bacteria. <i>PLoS Genetics</i> , 2013, 9, e1003764.	3.5	74
122	Towards Functional Orthogonalisation of Protein Complexes: Individualisation of GroEL Monomers Leads to Distinct Quasihomogeneous Single Rings. <i>ChemBioChem</i> , 2013, 14, 2310-2321.	2.6	10
123	Vestigialization of arsenic resistance phenotypes/genotypes in <i>Chromobacterium violaceum</i> strains thriving in pristine Brazilian sites. <i>Biocatalysis and Biotransformation</i> , 2013, 31, 281-291.	2.0	2
124	Transcriptomic fingerprinting of <i>scp>P</scp>seudomonas putida</i> under alternative physiological regimes. <i>Environmental Microbiology Reports</i>, 2013, 5, 883-891.</i>	2.4	75
125	Engineering the Soil Bacterium <i>Pseudomonas putida</i> for Arsenic Methylation. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4493-4495.	3.1	85
126	The Standard European Vector Architecture (SEVA): a coherent platform for the analysis and deployment of complex prokaryotic phenotypes. <i>Nucleic Acids Research</i> , 2013, 41, D666-D675.	14.5	556

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127	Increasing Signal Specificity of the TOL Network of <i>Pseudomonas putida</i> mt-2 by Rewiring the Connectivity of the Master Regulator XylR. <i>PLoS Genetics</i> , 2012, 8, e1002963.	3.5	26
128	Regulatory Tasks of the Phosphoenolpyruvate-Phosphotransferase System of <i>Pseudomonas putida</i> in Central Carbon Metabolism. <i>MBio</i> , 2012, 3, .	4.1	78
129	A GFP-lacZ Bicistronic Reporter System for Promoter Analysis in Environmental Gram-Negative Bacteria. <i>PLoS ONE</i> , 2012, 7, e34675.	2.5	19
130	Stochasticity of TOL plasmid catabolic promoters sets a bimodal expression regime in <i>Pseudomonas putida</i> exposed to <i>m</i> -xylene. <i>Molecular Microbiology</i> , 2012, 86, 199-211.	2.5	20
131	Transposon-Based and Plasmid-Based Genetic Tools for Editing Genomes of Gram-Negative Bacteria. <i>Methods in Molecular Biology</i> , 2012, 813, 267-283.	0.9	92
132	Broadening the signal specificity of prokaryotic promoters by modifying cis-regulatory elements associated with a single transcription factor. <i>Molecular BioSystems</i> , 2012, 8, 1950.	2.9	30
133	Engineering Whole-Cell Biosensors with No Antibiotic Markers for Monitoring Aromatic Compounds in the Environment. <i>Methods in Molecular Biology</i> , 2012, 834, 261-281.	0.9	19
134	Quantitative, Non-Disruptive Monitoring of Transcription in Single Cells with a Broad-Host Range GFP-luxCDABE Dual Reporter System. <i>PLoS ONE</i> , 2012, 7, e52000.	2.5	22
135	Synthetic constructs in/for the environment: Managing the interplay between natural and engineered Biology. <i>FEBS Letters</i> , 2012, 586, 2199-2206.	2.8	78
136	The Crp regulator of <i>Pseudomonas putida</i> : evidence of an unusually high affinity for its physiological effector, cAMP. <i>Environmental Microbiology</i> , 2012, 14, 702-713.	3.8	14
137	Random and cyclical deletion of large DNA segments in the genome of <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , 2012, 14, 1444-1453.	3.8	56
138	A composite feed-forward loop I4-FFL involving IHF and Crc stabilizes expression of the XylR regulator of <i>Pseudomonas putida</i> mt-2 from growth phase perturbations. <i>Molecular BioSystems</i> , 2011, 7, 2982.	2.9	21
139	Implementing an ORâ€“NOT (ORN) logic gate with components of the SOS regulatory network of <i>Escherichia coli</i> . <i>Molecular BioSystems</i> , 2011, 7, 2389.	2.9	18
140	The interplay of the EIIANtr component of the nitrogen-related phosphotransferase system (PTSNtr) of <i>Pseudomonas putida</i> with pyruvate dehydrogenase. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2011, 1810, 995-1005.	2.4	32
141	Regulatory exaptation of the catabolite repression protein (Crp)â€“cAMP system in <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , 2011, 13, 324-339.	3.8	34
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