Esteban MartÃ-nez-GarcÃ-a

List of Publications by Year
in descending order

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58	4,352	218677	155660
papers	citations	26 h-index	55 g-index

63	63	63	4701
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	Stationary phase in gram-negative bacteria. FEMS Microbiology Reviews, 2010, 34, 476-495.	8.6	377
3	Biotechnological domestication of pseudomonads using synthetic biology. Nature Reviews Microbiology, 2014, 12, 368-379.	28.6	332
4	Engineering multiple genomic deletions in Gramâ€negative bacteria: analysis of the multiâ€resistant antibiotic profile of Pseudomonas putida KT2440. Environmental Microbiology, 2011, 13, 2702-2716.	3.8	329
5	Social Evolution of Spatial Patterns in Bacterial Biofilms: When Conflict Drives Disorder. American Naturalist, 2009, 174, 1-12.	2.1	273
6	Biofilm Formation As a Response to Ecological Competition. PLoS Biology, 2015, 13, e1002191.	5.6	232
7	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
8	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
9	The environmental occurrence of Pseudomonas aeruginosa. Apmis, 2020, 128, 220-231.	2.0	160
10	pBAM1: an all-synthetic genetic tool for analysis and construction of complex bacterial phenotypes. BMC Microbiology, 2011, 11, 38.	3.3	142
11	The metabolic cost of flagellar motion in <scp>P</scp>seudomonas putidaâ€…<scp>KT</scp>2440. Environmental Microbiology, 2014, 16, 291-303.	3.8	132
12	CRISPR/Cas9â€Based Counterselection Boosts Recombineering Efficiency in Pseudomonas putida. Biotechnology Journal, 2018, 13, e1700161.	3.5	115
13	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
14	New Transposon Tools Tailored for Metabolic Engineering of Gram-Negative Microbial Cell Factories. Frontiers in Bioengineering and Biotechnology, 2014, 2, 46.	4.1	85
15	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
16	Accumulation of inorganic polyphosphate enables stress endurance and catalytic vigour in Pseudomonas putida KT2440. Microbial Cell Factories, 2013, 12, 50.	4.0	77
17	The Ssr protein (T1E_1405) from Pseudomonas putida DOTâ€T1E enables oligonucleotideâ€based recombineering in platform strain P. putida EM42. Biotechnology Journal, 2016, 11, 1309-1319.	3.5	65
18	Molecular tools and emerging strategies for deep genetic/genomic refactoring of Pseudomonas. Current Opinion in Biotechnology, 2017, 47, 120-132.	6.6	63

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19	Freeing <scp>P</scp>seudomonas putidaâ€¦<scp>KT</scp>2440 of its proviral load strengthens endurance to environmental stresses. Environmental Microbiology, 2015, 17, 76-90.	3.8	62
20	Targeted Depletion of Bacteria from Mixed Populations by Programmable Adhesion with Antagonistic Competitor Cells. Cell Host and Microbe, 2020, 28, 313-321.e6.	11.0	62
21	The quest for the minimal bacterial genome. Current Opinion in Biotechnology, 2016, 42, 216-224.	6.6	49
22	Engineering input/output nodes in prokaryotic regulatory circuits. FEMS Microbiology Reviews, 2010, 34, 842-865.	8.6	45
23	A standardized workflow for surveying recombinases expands bacterial genomeâ€editing capabilities. Microbial Biotechnology, 2018, 11, 176-188.	4.2	43
24	Pseudomonas putida in the quest of programmable chemistry. Current Opinion in Biotechnology, 2019, 59, 111-121.	6.6	38
25	Characterization of a second functional gene cluster for the catabolism of phenylacetic acid in Pseudomonas sp. strain Y2. Gene, 2004, 341, 167-179.	2.2	37
26	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
27	High-Efficiency Multi-site Genomic Editing of Pseudomonas putida through Thermoinducible ssDNA Recombineering. IScience, 2020, 23, 100946.	4.1	32
28	An Implementation-Focused Bio/Algorithmic Workflow for Synthetic Biology. ACS Synthetic Biology, 2016, 5, 1127-1135.	3.8	31
29	<scp>CRISPR</scp>/Cas9â€enhanced ss<scp>DNA</scp> recombineering for Pseudomonas putida. Microbial Biotechnology, 2019, 12, 1076-1089.	4.2	31
30	The Standard European Vector Architecture (SEVA) Plasmid Toolkit. Methods in Molecular Biology, 2014, 1149, 469-478.	0.9	28
31	Improved Thermotolerance of Genomeâ€Reduced Pseudomonas putida EM42 Enables Effective Functioning of the P_L/cI857 System. Biotechnology Journal, 2019, 14, e1800483.	3.5	27
32	Physical Forces Shape Group Identity of Swimming Pseudomonas putida Cells. Frontiers in Microbiology, 2016, 7, 1437.	3.5	26
33	Modulating Heterologous Gene Expression with Portable mRNA-Stabilizing 5â€²-UTR Sequences. ACS Synthetic Biology, 2018, 7, 2177-2188.	3.8	24
34	Engineering Gram-Negative Microbial Cell Factories Using Transposon Vectors. Methods in Molecular Biology, 2017, 1498, 273-293.	0.9	23
35	Mismatch repair hierarchy of Pseudomonas putida revealed by mutagenic ssDNA recombineering of the pyrF gene. Environmental Microbiology, 2020, 22, 45-58.	3.8	22
36	Mining Environmental Plasmids for Synthetic Biology Parts and Devices. Microbiology Spectrum, 2015, 3, PLAS-0033-2014.	3.0	18

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37	Eco-evolutionary feedbacks can rescue cooperation in microbial populations. Scientific Reports, 2017, 7, 42561.	3.3	17
38	Further studies on RpoS in enterobacteria: identification of rpoS in Enterobacter cloacae and Kluyvera cryocrescens. Archives of Microbiology, 2001, 175, 395-404.	2.2	16
39	Naked Bacterium: Emerging Properties of a Surfome-Streamlined Pseudomonas putida Strain. ACS Synthetic Biology, 2020, 9, 2477-2492.	3.8	15
40	GASP phenotype: presence in enterobacteria and independence of ÃÂƒSin its acquisition. FEMS Microbiology Letters, 2003, 225, 201-206.	1.8	14
41	Polymorphism in the yclC-rpoS Region of Enterobacteria. Current Microbiology, 2003, 46, 365-370.	2.2	12
42	Multifunctional SEVA shuttle vectors for actinomycetes and Gramâ€negative bacteria. MicrobiologyOpen, 2020, 9, 1135-1149.	3.0	12
43	Engineering Tropism of Pseudomonas putida toward Target Surfaces through Ectopic Display of Recombinant Nanobodies. ACS Synthetic Biology, 2021, 10, 2049-2059.	3.8	11
44	A Broad Host Range Plasmid-Based Roadmap for ssDNA-Based Recombineering in Gram-Negative Bacteria. Methods in Molecular Biology, 2020, 2075, 383-398.	0.9	11
45	Broadening the SEVA Plasmid Repertoire to Facilitate Genomic Editing of Gram-Negative Bacteria. Springer Protocols, 2015, , 9-27.	0.3	9
46	Dynamics of Pseudomonas putida biofilms in an upscale experimental framework. Journal of Industrial Microbiology and Biotechnology, 2018, 45, 899-911.	3.0	7
47	Identification of an Unknown Promoter, OUTIIp , within the IS 10 R Element. Journal of Bacteriology, 2003, 185, 2046-2050.	2.2	6
48	Enterobacter cloacae rpoS promoter and gene organization. Archives of Microbiology, 2002, 179, 33-41.	2.2	5
49	Ribonucleases control distinct traits of Pseudomonas putida lifestyle. Environmental Microbiology, 2021, 23, 174-189.	3.8	5
50	Widening functional boundaries of the Ïƒ⁵⁴promoter Pu of Pseudomonas putida by defeating extant physiological constraints. Molecular BioSystems, 2015, 11, 734-742.	2.9	4
51	Stenosis triggers spread of helical Pseudomonas biofilms in cylindrical flow systems. Scientific Reports, 2016, 6, 27170.	3.3	4
52	Quantitative assessment of morphological traits of planktonic bacterial aggregates. Water Research, 2021, 188, 116468.	11.3	4
53	Environmental Performance of Pseudomonas putida with a Uracylated Genome. ChemBioChem, 2020, 21, 3255-3265.	2.6	3
54	Mining Environmental Plasmids for Synthetic Biology Parts and Devices. , 0, , 633-649.		2

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55	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
56	Exploiting geometric similarity for statistical quantification of fluorescence spatial patterns in bacterial colonies. BMC Bioinformatics, 2020, 21, 224.	2.6	0
57	Assembly of a Custom-made Device to Study Spreading Patterns of Pseudomonas putida Biofilms. Bio-protocol, 2019, 9, e3238.	0.4	0
58	High-Efficiency Multi-site Genomic Editing (HEMSE) Made Easy. Methods in Molecular Biology, 2022, 2479, 37-52.	0.9	0