

Esteban Martínez-García

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

4,352
citations

218677

26
h-index

155660

55
g-index

63
all docs

63
docs citations

63
times ranked

4701
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Efficiency Multi-site Genomic Editing (HEMSE) Made Easy. <i>Methods in Molecular Biology</i> , 2022, 2479, 37-52.	0.9	0
2	Quantitative assessment of morphological traits of planktonic bacterial aggregates. <i>Water Research</i> , 2021, 188, 116468.	11.3	4
3	Ribonucleases control distinct traits of <i>Pseudomonas putida</i> lifestyle. <i>Environmental Microbiology</i> , 2021, 23, 174-189.	3.8	5
4	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
5	The environmental occurrence of <i>Pseudomonas aeruginosa</i> . <i>Apmis</i> , 2020, 128, 220-231.	2.0	160
6	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
7	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
8	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
9	Targeted Depletion of Bacteria from Mixed Populations by Programmable Adhesion with Antagonistic Competitor Cells. <i>Cell Host and Microbe</i> , 2020, 28, 313-321.e6.	11.0	62
10	Exploiting geometric similarity for statistical quantification of fluorescence spatial patterns in bacterial colonies. <i>BMC Bioinformatics</i> , 2020, 21, 224.	2.6	0
11	High-Efficiency Multi-site Genomic Editing of <i>Pseudomonas putida</i> through Thermoinducible ssDNA Recombineering. <i>IScience</i> , 2020, 23, 100946.	4.1	32
12	Multifunctional SEVA shuttle vectors for actinomycetes and Gram-negative bacteria. <i>MicrobiologyOpen</i> , 2020, 9, 1135-1149.	3.0	12
13	Environmental Performance of <i>Pseudomonas putida</i> with a Uracylated Genome. <i>ChemBioChem</i> , 2020, 21, 3255-3265.	2.6	3
14	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
15	<i>CRISPR/Cas9</i> -enhanced ssDNA recombineering for <i>Pseudomonas putida</i> . <i>Microbial Biotechnology</i> , 2019, 12, 1076-1089.	4.2	31
16	<i>Pseudomonas putida</i> in the quest of programmable chemistry. <i>Current Opinion in Biotechnology</i> , 2019, 59, 111-121.	6.6	38
17	Improved Thermotolerance of Genome-Reduced <i>Pseudomonas putida</i> EM42 Enables Effective Functioning of the P _L /c _I 1857 System. <i>Biotechnology Journal</i> , 2019, 14, e1800483.	3.5	27
18	Assembly of a Custom-made Device to Study Spreading Patterns of <i>Pseudomonas putida</i> Biofilms. <i>Bio-protocol</i> , 2019, 9, e3238.	0.4	0

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19	CRISPR/Cas9-Based Counterselection Boosts Recombineering Efficiency in <i>Pseudomonas putida</i> . <i>Biotechnology Journal</i> , 2018, 13, e1700161.	3.5	115
20	A standardized workflow for surveying recombinases expands bacterial genome editing capabilities. <i>Microbial Biotechnology</i> , 2018, 11, 176-188.	4.2	43
21	Modulating Heterologous Gene Expression with Portable mRNA-Stabilizing 5'-UTR Sequences. <i>ACS Synthetic Biology</i> , 2018, 7, 2177-2188.	3.8	24
22	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
23	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
24	Eco-evolutionary feedbacks can rescue cooperation in microbial populations. <i>Scientific Reports</i> , 2017, 7, 42561.	3.3	17
25	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
26	Engineering Gram-Negative Microbial Cell Factories Using Transposon Vectors. <i>Methods in Molecular Biology</i> , 2017, 1498, 273-293.	0.9	23
27	Physical Forces Shape Group Identity of Swimming <i>Pseudomonas putida</i> Cells. <i>Frontiers in Microbiology</i> , 2016, 7, 1437.	3.5	26
28	Stenosis triggers spread of helical <i>Pseudomonas</i> biofilms in cylindrical flow systems. <i>Scientific Reports</i> , 2016, 6, 27170.	3.3	4
29	The quest for the minimal bacterial genome. <i>Current Opinion in Biotechnology</i> , 2016, 42, 216-224.	6.6	49
30	The Ssr protein (T1E_1405) from <i>Pseudomonas putida</i> DOT1E enables oligonucleotide-based recombineering in platform strain <i>P. putida</i> EM42. <i>Biotechnology Journal</i> , 2016, 11, 1309-1319.	3.5	65
31	An Implementation-Focused Bio/Algorithmic Workflow for Synthetic Biology. <i>ACS Synthetic Biology</i> , 2016, 5, 1127-1135.	3.8	31
32	Rationally rewiring the connectivity of the XylR/Pu regulatory node of the m-xylene degradation pathway in <i>Pseudomonas putida</i> . <i>Integrative Biology (United Kingdom)</i> , 2016, 8, 571-576.	1.3	0
33	Mining Environmental Plasmids for Synthetic Biology Parts and Devices. <i>Microbiology Spectrum</i> , 2015, 3, PLAS-0033-2014.	3.0	18
34	Biofilm Formation As a Response to Ecological Competition. <i>PLoS Biology</i> , 2015, 13, e1002191.	5.6	232
35	SEVA 2.0: an update of the Standard European Vector Architecture for de/re-construction of bacterial functionalities. <i>Nucleic Acids Research</i> , 2015, 43, D1183-D1189.	14.5	195
36	Broadening the SEVA Plasmid Repertoire to Facilitate Genomic Editing of Gram-Negative Bacteria. <i>Springer Protocols</i> , 2015, , 9-27.	0.3	9

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37	Freeing <i>Pseudomonas putida</i> of its proviral load strengthens endurance to environmental stresses. <i>Environmental Microbiology</i> , 2015, 17, 76-90.	3.8	62
38	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
39	<i>Pseudomonas 2.0</i> : 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
40	Biotechnological domestication of pseudomonads using synthetic biology. <i>Nature Reviews Microbiology</i> , 2014, 12, 368-379.	28.6	332
41	The metabolic cost of flagellar motion in <i>Pseudomonas putida</i> ...KT2440. <i>Environmental Microbiology</i> , 2014, 16, 291-303.	3.8	132
42	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
43	The Standard European Vector Architecture (SEVA) Plasmid Toolkit. <i>Methods in Molecular Biology</i> , 2014, 1149, 469-478.	0.9	28
44	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
45	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
46	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
47	Engineering multiple genomic deletions in Gram-negative bacteria: analysis of the multi-resistant antibiotic profile of <i>Pseudomonas putida</i> KT2440. <i>Environmental Microbiology</i> , 2011, 13, 2702-2716.	3.8	329
48	pBAM1: an all-synthetic genetic tool for analysis and construction of complex bacterial phenotypes. <i>BMC Microbiology</i> , 2011, 11, 38.	3.3	142
49	Stationary phase in gram-negative bacteria. <i>FEMS Microbiology Reviews</i> , 2010, 34, 476-495.	8.6	377
50	Engineering input/output nodes in prokaryotic regulatory circuits. <i>FEMS Microbiology Reviews</i> , 2010, 34, 842-865.	8.6	45
51	Social Evolution of Spatial Patterns in Bacterial Biofilms: When Conflict Drives Disorder. <i>American Naturalist</i> , 2009, 174, 1-12.	2.1	273
52	Characterization of a second functional gene cluster for the catabolism of phenylacetic acid in <i>Pseudomonas</i> sp. strain Y2. <i>Gene</i> , 2004, 341, 167-179.	2.2	37
53	Polymorphism in the <i>yjC-rpoS</i> Region of Enterobacteria. <i>Current Microbiology</i> , 2003, 46, 365-370.	2.2	12
54	GASP phenotype: presence in enterobacteria and independence of λ 54 in its acquisition. <i>FEMS Microbiology Letters</i> , 2003, 225, 201-206.	1.8	14

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55	Identification of an Unknown Promoter, OUTIp , within the IS 10 R Element. Journal of Bacteriology, 2003, 185, 2046-2050.	2.2	6
56	Enterobacter cloacae rpoS promoter and gene organization. Archives of Microbiology, 2002, 179, 33-41.	2.2	5
57	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
58	Mining Environmental Plasmids for Synthetic Biology Parts and Devices. , 0, , 633-649.		2