

# Danilo PÃ©rez-Pantoja

## List of Publications by Year in descending order

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41  
papers

1,737  
citations

361296

20  
h-index

276775

41  
g-index

44  
all docs

44  
docs citations

44  
times ranked

2055  
citing authors

#	ARTICLE	IF	CITATIONS
1	Methylotrophs and Hydrocarbon-Degrading Bacteria Are Key Players in the Microbial Community of an Abandoned Century-Old Oil Exploration Well. <i>Microbial Ecology</i> , 2022, 83, 83-99.	1.4	10
2	Transcriptional control of 2,4-dinitrotoluene degradation in <i>Burkholderia sp.</i> R34 bears a regulatory patch that eases pathway evolution. <i>Environmental Microbiology</i> , 2021, 23, 2522-2531.	1.8	8
3	Complete Multipartite Genome Sequence of the <i>Cupriavidus basilensis</i> Type Strain, a 2,6-Dichlorophenol-Degrading Bacterium. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	5
4	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.	2.0	7
5	Genome-Wide Metabolic Reconstruction of the Synthesis of Polyhydroxyalkanoates from Sugars and Fatty Acids by <i>Burkholderia Sensu Lato</i> Species. <i>Microorganisms</i> , 2021, 9, 1290.	1.6	17
6	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.	1.8	0
7	Widespread distribution of hmf genes in Proteobacteria reveals key enzymes for 5-hydroxymethylfurfural conversion. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2160-2169.	1.9	9
8	Complete Genome Sequence of <i>Rhodococcus ruber</i> R1, a Novel Strain Showing a Broad Catabolic Potential toward Lignin-Derived Aromatics. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
9	Draft Genome Sequences of Two <i>Pseudomonas</i> Strains That Are Able To Use Furan Derivatives as Their Sole Carbon Source. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
10	Novel Genes Involved in Resistance to Both Ultraviolet Radiation and Perchlorate From the Metagenomes of Hypersaline Environments. <i>Frontiers in Microbiology</i> , 2020, 11, 453.	1.5	10
11	Evolving metabolism of 2,4-dinitrotoluene triggers SOS-independent diversification of host cells. <i>Environmental Microbiology</i> , 2019, 21, 314-326.	1.8	13
12	Draft genome sequences of <i>Cylindrospermopsis raciborskii</i> strains CS-508 and MVCC14, isolated from freshwater bloom events in Australia and Uruguay. <i>Standards in Genomic Sciences</i> , 2018, 13, 26.	1.5	4
13	Diurnal Changes in Active Carbon and Nitrogen Pathways Along the Temperature Gradient in Porcelana Hot Spring Microbial Mat. <i>Frontiers in Microbiology</i> , 2018, 9, 2353.	1.5	36
14	The interplay of EIIA <sup>Ntr</sup> with C-source regulation of the <i>Pu</i> promoter of <i>Pseudomonas putida</i> mt-2. <i>Environmental Microbiology</i> , 2018, 20, 4555-4566.	1.8	3
15	The Metabolic Redox Regime of <i>Pseudomonas putida</i> Tunes Its Evolvability toward Novel Xenobiotic Substrates. <i>MBio</i> , 2018, 9, .	1.8	51
16	Plasmid and clonal interference during post horizontal gene transfer evolution. <i>Molecular Ecology</i> , 2017, 26, 1832-1847.	2.0	26
17	Genomic features of <i>Candidatus Venteria ishoeyi</i> , a new sulfur-oxidizing macrobacterium from the Humboldt Sulfuretum off Chile. <i>PLoS ONE</i> , 2017, 12, e0188371.	1.1	12
18	<i>Cupriavidus pinatubonensis</i> AEO106 deals with copper-induced oxidative stress before engaging in biodegradation of the herbicide 4-chloro-2-methylphenoxyacetic acid. <i>BMC Microbiology</i> , 2017, 17, 211.	1.3	7

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19	Pyridine nucleotide transhydrogenases enable redox balance of <i>Pseudomonas putida</i> during biodegradation of aromatic compounds. <i>Environmental Microbiology</i> , 2016, 18, 3565-3582.	1.8	58
20	High-resolution analysis of the <i>m</i> -xylene/toluene biodegradation subtranscriptome of <i>Pseudomonas putida</i> mt-2. <i>Environmental Microbiology</i> , 2016, 18, 3327-3341.	1.8	18
21	<i>Pseudomonas putida</i> mt-2 tolerates reactive oxygen species generated during matrix stress by inducing a major oxidative defense response. <i>BMC Microbiology</i> , 2015, 15, 202.	1.3	24
22	Hierarchy of Carbon Source Utilization in Soil Bacteria: Hegemonic Preference for Benzoate in Complex Aromatic Compound Mixtures Degraded by <i>Cupriavidus pinatubonensis</i> Strain JMP134. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3914-3924.	1.4	31
23	Prokaryotic Metatranscriptomics. <i>Springer Protocols</i> , 2015, , 69-98.	0.1	1
24	The differential response of the <i>P</i> - <i>ben</i> promoter of <i>Pseudomonas putida</i> to <i>BenR</i> and <i>XylS</i> prevents metabolic conflicts in <i>m</i> -xylene biodegradation. <i>Environmental Microbiology</i> , 2015, 17, 64-75.	1.8	29
25	A second chromosomal copy of the <i>catA</i> gene endows <i>Pseudomonas putida</i> mt-2 with an enzymatic safety valve for excess of catechol. <i>Environmental Microbiology</i> , 2014, 16, 1767-1778.	1.8	38
26	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.	1.8	53
27	Decoding the genetic networks of environmental bacteria: regulatory moonlighting of the TOL system of <i>Pseudomonas putida</i> mt-2. <i>ISME Journal</i> , 2013, 7, 229-232.	4.4	15
28	The <i>E</i> - <i>D</i> odoroff pathway empowers <i>Pseudomonas putida</i> mt-2 with a high tolerance to oxidative stress. <i>Environmental Microbiology</i> , 2013, 15, 1772-1785.	1.8	195
29	Endogenous Stress Caused by Faulty Oxidation Reactions Fosters Evolution of 2,4-Dinitrotoluene-Degrading Bacteria. <i>PLoS Genetics</i> , 2013, 9, e1003764.	1.5	74
30	Aromatic compounds degradation plays a role in colonization of <i>Arabidopsis thaliana</i> and <i>Acacia caven</i> by <i>Cupriavidus pinatubonensis</i> JMP134. <i>Antonie Van Leeuwenhoek</i> , 2012, 101, 713-723.	0.7	17
31	Genomic analysis of the potential for aromatic compounds biodegradation in <i>Burkholderiales</i> . <i>Environmental Microbiology</i> , 2012, 14, 1091-1117.	1.8	276
32	Strict and direct transcriptional repression of the <i>pobA</i> gene by benzoate avoids 4-hydroxybenzoate degradation in the pollutant degrader bacterium <i>Cupriavidus necator</i> JMP134. <i>Environmental Microbiology</i> , 2011, 13, 1590-1600.	1.8	26
33	Modified 3-Oxoadipate Pathway for the Biodegradation of Methylaromatics in <i>Pseudomonas reinekei</i> MT1. <i>Journal of Bacteriology</i> , 2010, 192, 1543-1552.	1.0	26
34	The Complete Multipartite Genome Sequence of <i>Cupriavidus necator</i> JMP134, a Versatile Pollutant Degrader. <i>PLoS ONE</i> , 2010, 5, e9729.	1.1	112
35	Genuine genetic redundancy in maleylacetate-reductase-encoding genes involved in degradation of haloaromatic compounds by <i>Cupriavidus necator</i> JMP134. <i>Microbiology (United Kingdom)</i> , 2009, 155, 3641-3651.	0.7	18
36	Metabolic reconstruction of aromatic compounds degradation from the genome of the amazing pollutant-degrading bacterium <i>Cupriavidus necator</i> JMP134. <i>FEMS Microbiology Reviews</i> , 2008, 32, 736-794.	3.9	203

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37	Genetic organization of the catabolic plasmid pJP4 from <i>Ralstonia eutropha</i> JMP134 (pJP4) reveals mechanisms of adaptation to chloroaromatic pollutants and evolution of specialized chloroaromatic degradation pathways. <i>Environmental Microbiology</i> , 2004, 6, 655-668.	1.8	134
38	Efficient Turnover of Chlorocatechols Is Essential for Growth of <i>Ralstonia eutropha</i> JMP134(pJP4) in 3-Chlorobenzoic Acid. <i>Journal of Bacteriology</i> , 2003, 185, 1534-1542.	1.0	49
39	Importance of Different <i>tfd</i> Genes for Degradation of Chloroaromatics by <i>Ralstonia eutropha</i> JMP134. <i>Journal of Bacteriology</i> , 2002, 184, 4054-4064.	1.0	45
40	Novel insights into the interplay between peripheral reactions encoded by <i>xyl</i> genes and the chlorocatechol pathway encoded by <i>tfd</i> genes for the degradation of chlorobenzoates by <i>Ralstonia eutropha</i> JMP134. <i>Microbiology (United Kingdom)</i> , 2002, 148, 3431-3440.	0.7	10
41	Role of <i>tfdC I D I E I F I</i> and <i>tfdD II C II E II F II</i> Gene Modules in Catabolism of 3-Chlorobenzoate by <i>Ralstonia eutropha</i> JMP134(pJP4). <i>Applied and Environmental Microbiology</i> , 2000, 66, 1602-1608.	1.4	62