

Alvaro Sanchez

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

48
papers

1,855
citations

19
h-index

42
g-index

62
ext. papers

2,736
ext. citations

10.2
avg, IF

5.47
L-index

#	Paper	IF	Citations
48	The meta-gut: community coalescence of animal gut and environmental microbiomes. <i>Scientific Reports</i> , 2021 , 11, 23117	4.9	1
47	In vitro interaction network of a synthetic gut bacterial community. <i>ISME Journal</i> , 2021 ,	11.9	5
46	The Macroevolutionary Consequences of Niche Construction in Microbial Metabolism. <i>Frontiers in Microbiology</i> , 2021 , 12, 718082	5.7	
45	Functional attractors in microbial community assembly. <i>Cell Systems</i> , 2021 ,	10.6	8
44	A metabolic modeling platform for the computation of microbial ecosystems in time and space (COMETS). <i>Nature Protocols</i> , 2021 , 16, 5030-5082	18.8	12
43	Multi-Replicated Enrichment Communities as a Model System in Microbial Ecology. <i>Frontiers in Microbiology</i> , 2021 , 12, 657467	5.7	5
42	Nutrient dominance governs the assembly of microbial communities in mixed nutrient environments. <i>ELife</i> , 2021 , 10,	8.9	11
41	Directed Evolution of Microbial Communities. <i>Annual Review of Biophysics</i> , 2021 , 50, 323-341	21.1	15
40	Engineering complex communities by directed evolution. <i>Nature Ecology and Evolution</i> , 2021 , 5, 1011-1023	23.3	14
39	Functional biology in its natural context: A search for emergent simplicity. <i>ELife</i> , 2021 , 10,	8.9	7
38	Complex yeast-bacteria interactions affect the yield of industrial ethanol fermentation. <i>Nature Communications</i> , 2021 , 12, 1498	17.4	12
37	Dissimilarity-Overlap analysis of replicate enrichment communities. <i>ISME Journal</i> , 2020 , 14, 2505-2513	11.9	7
36	The ecology and evolution of microbial metabolic strategies. <i>Current Opinion in Biotechnology</i> , 2020 , 62, 123-128	11.4	17
35	Artificially selecting bacterial communities using propagule strategies. <i>Evolution; International Journal of Organic Evolution</i> , 2020 , 74, 2392-2403	3.8	12
34	Available energy fluxes drive a transition in the diversity, stability, and functional structure of microbial communities. <i>PLoS Computational Biology</i> , 2019 , 15, e1006793	5	47
33	Current State of and Future Opportunities for Prediction in Microbiome Research: Report from the Mid-Atlantic Microbiome Meet-up in Baltimore on 9 January 2019. <i>MSystems</i> , 2019 , 4,	7.6	4
32	Defining Higher-Order Interactions in Synthetic Ecology: Lessons from Physics and Quantitative Genetics. <i>Cell Systems</i> , 2019 , 9, 519-520	10.6	12

31	High-order interactions distort the functional landscape of microbial consortia. <i>PLoS Biology</i> , 2019 , 17, e3000550	9.7	52
30	Emergent simplicity in microbial community assembly. <i>Science</i> , 2018 , 361, 469-474	33.3	348
29	Distribution of Initiation Times Reveals Mechanisms of Transcriptional Regulation in Single Cells. <i>Biophysical Journal</i> , 2018 , 114, 2072-2082	2.9	12
28	On the deformability of an empirical fitness landscape by microbial evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 11286-11291	11.5	26
27	Ecological effects of cellular computing in microbial populations. <i>Natural Computing</i> , 2018 , 17, 811-822	1.3	3
26	Cooperators trade off ecological resilience and evolutionary stability in public goods games. <i>Journal of the Royal Society Interface</i> , 2017 , 14,	4.1	18
25	Combinatorial Gene Regulation through Kinetic Control of the Transcription Cycle. <i>Cell Systems</i> , 2017 , 4, 97-108.e9	10.6	39
24	The Evolutionary Resilience of Distributed Cellular Computing. <i>Lecture Notes in Computer Science</i> , 2017 , 3-15	0.9	1
23	Deciphering Transcriptional Dynamics In Vivo by Counting Nascent RNA Molecules. <i>PLoS Computational Biology</i> , 2015 , 11, e1004345	5	39
22	Phenotypic states become increasingly sensitive to perturbations near a bifurcation in a synthetic gene network. <i>ELife</i> , 2015 , 4,	8.9	16
21	Eco-evolutionary dynamics of complex social strategies in microbial communities. <i>Communicative and Integrative Biology</i> , 2014 , 7, e28230	1.7	23
20	Dynamics of a producer-free-loader ecosystem on the brink of collapse. <i>Nature Communications</i> , 2014 , 5, 3713	17.4	30
19	Genetic determinants and cellular constraints in noisy gene expression. <i>Science</i> , 2013 , 342, 1188-93	33.3	290
18	Regulation of noise in gene expression. <i>Annual Review of Biophysics</i> , 2013 , 42, 469-91	21.1	134
17	Stochastic models of transcription: from single molecules to single cells. <i>Methods</i> , 2013 , 62, 13-25	4.6	38
16	feedback between population and evolutionary dynamics determines the fate of social microbial populations. <i>PLoS Biology</i> , 2013 , 11, e1001547	9.7	141
15	Operator sequence alters gene expression independently of transcription factor occupancy in bacteria. <i>Cell Reports</i> , 2012 , 2, 150-61	10.6	52
14	Effect of promoter architecture on the cell-to-cell variability in gene expression. <i>PLoS Computational Biology</i> , 2011 , 7, e1001100	5	101

13	Mechanism of transcriptional repression at a bacterial promoter by analysis of single molecules. <i>EMBO Journal</i> , 2011 , 30, 3940-6	13	27
12	Transcription by the numbers redux: experiments and calculations that surprise. <i>Trends in Cell Biology</i> , 2010 , 20, 723-33	18.3	35
11	Transcriptional control of noise in gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 5081-6	11.5	114
10	Molecular brightness determined from a generalized form of Mandel's Q-parameter. <i>Biophysical Journal</i> , 2005 , 89, 3531-47	2.9	41
9	Top-down engineering of complex communities by directed evolution		2
8	Artificially selecting microbial communities using propagule strategies		3
7	Metabolic rules of microbial community assembly		21
6	Nutrient dominance governs the assembly of microbial communities in mixed nutrient environments		4
5	Emergent Simplicity in Microbial Community Assembly		14
4	Cohesiveness in microbial community coalescence		16
3	High-order interactions dominate the functional landscape of microbial consortia		17
2	The meta-gut: Hippo inputs lead to community coalescence of animal and environmental microbiomes		1
1	Exploring the interaction network of a synthetic gut bacterial community		3