Alvaro Sanchez

List of Publications by Citations

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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	Emergent simplicity in microbial community assembly. *Science*, **2018**, 361, 469-474	33.3	348
47	Genetic determinants and cellular constraints in noisy gene expression. *Science*, **2013**, 342, 1188-93	33.3	290
46	feedback between population and evolutionary dynamics determines the fate of social microbial populations. *PLoS Biology*, **2013**, 11, e1001547	9.7	141
45	Regulation of noise in gene expression. *Annual Review of Biophysics*, **2013**, 42, 469-91	21.1	134
44	Transcriptional control of noise in gene expression. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 5081-6	11.5	114
43	Effect of promoter architecture on the cell-to-cell variability in gene expression. *PLoS Computational Biology*, **2011**, 7, e1001100	5	101
42	Operator sequence alters gene expression independently of transcription factor occupancy in bacteria. *Cell Reports*, **2012**, 2, 150-61	10.6	52
41	High-order interactions distort the functional landscape of microbial consortia. *PLoS Biology*, **2019**, 17, e3000550	9.7	52
40	Available energy fluxes drive a transition in the diversity, stability, and functional structure of microbial communities. *PLoS Computational Biology*, **2019**, 15, e1006793	5	47
39	Molecular brightness determined from a generalized form of Mandel’s Q-parameter. *Biophysical Journal*, **2005**, 89, 3531-47	2.9	41
38	Combinatorial Gene Regulation through Kinetic Control of the Transcription Cycle. *Cell Systems*, **2017**, 4, 97-108.e9	10.6	39
37	Deciphering Transcriptional Dynamics In Vivo by Counting Nascent RNA Molecules. *PLoS Computational Biology*, **2015**, 11, e1004345	5	39
36	Stochastic models of transcription: from single molecules to single cells. *Methods*, **2013**, 62, 13-25	4.6	38
35	Transcription by the numbers redux: experiments and calculations that surprise. *Trends in Cell Biology*, **2010**, 20, 723-33	18.3	35
34	Dynamics of a producer-freeloader ecosystem on the brink of collapse. *Nature Communications*, **2014**, 5, 3713	17.4	30
33	Mechanism of transcriptional repression at a bacterial promoter by analysis of single molecules. *EMBO Journal*, **2011**, 30, 3940-6	13	27
32	On the deformability of an empirical fitness landscape by microbial evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 11286-11291	11.5	26

31	Eco-evolutionary dynamics of complex social strategies in microbial communities. *Communicative and Integrative Biology*, **2014**, 7, e28230	1.7	23
30	Metabolic rules of microbial community assembly		21
29	Cooperators trade off ecological resilience and evolutionary stability in public goods games. *Journal of the Royal Society Interface*, **2017**, 14,	4.1	18
28	High-order interactions dominate the functional landscape of microbial consortia		17
27	The ecology and evolution of microbial metabolic strategies. *Current Opinion in Biotechnology*, **2020** , 62, 123-128	11.4	17
26	Phenotypic states become increasingly sensitive to perturbations near a bifurcation in a synthetic gene network. *ELife*, **2015**, 4,	8.9	16
25	Cohesiveness in microbial community coalescence		16
24	Directed Evolution of Microbial Communities. *Annual Review of Biophysics*, **2021**, 50, 323-341	21.1	15
23	Emergent Simplicity in Microbial Community Assembly		14
22	Engineering complex communities by directed evolution. *Nature Ecology and Evolution*, **2021**, 5, 1011-1023	12.3	14
21	Distribution of Initiation Times Reveals Mechanisms of Transcriptional Regulation in Single Cells. *Biophysical Journal*, **2018**, 114, 2072-2082	2.9	12
20	A metabolic modeling platform for the computation of microbial ecosystems in time and space (COMETS). *Nature Protocols*, **2021**, 16, 5030-5082	18.8	12
19	Artificially selecting bacterial communities using propagule strategies. *Evolution; International Journal of Organic Evolution*, **2020**, 74, 2392-2403	3.8	12
18	Defining Higher-Order Interactions in Synthetic Ecology: Lessons from Physics and Quantitative Genetics. *Cell Systems*, **2019**, 9, 519-520	10.6	12
17	Complex yeast-bacteria interactions affect the yield of industrial ethanol fermentation. *Nature Communications*, **2021**, 12, 1498	17.4	12
16	Nutrient dominance governs the assembly of microbial communities in mixed nutrient environments. *ELife*, **2021**, 10,	8.9	11
15	Functional attractors in microbial community assembly. *Cell Systems*, **2021**,	10.6	8
14	Dissimilarity-Overlap analysis of replicate enrichment communities. *ISME Journal*, **2020**, 14, 2505-2513	11.9	7

13	Functional biology in its natural context: A search for emergent simplicity. *ELife*, **2021**, 10,	8.9	7
12	In vitro interaction network of a synthetic gut bacterial community. *ISME Journal*, **2021**,	11.9	5
11	Multi-Replicated Enrichment Communities as a Model System in Microbial Ecology. *Frontiers in Microbiology*, **2021**, 12, 657467	5.7	5
10	Nutrient dominance governs the assembly of microbial communities in mixed nutrient environments		4
9	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. *MSystems*, **2019**, 4,	7.6	4
8	Artificially selecting microbial communities using propagule strategies		3
7	Exploring the interaction network of a synthetic gut bacterial community		3
6	Ecological effects of cellular computing in microbial populations. *Natural Computing*, **2018**, 17, 811-822	1.3	3
5	Top-down engineering of complex communities by directed evolution		2
4	The meta-gut: community coalescence of animal gut and environmental microbiomes. *Scientific Reports*, **2021**, 11, 23117	4.9	1
3	The Evolutionary Resilience of Distributed Cellular Computing. *Lecture Notes in Computer Science*, **2017**, 3-15	0.9	1
2	The meta-gut: Hippo inputs lead to community coalescence of animal and environmental microbiomes		1
1	The Macroevolutionary Consequences of Niche Construction in Microbial Metabolism. *Frontiers in Microbiology*, **2021**, 12, 718082	5.7	