Alfonso Jaramillo

List of Publications by Year
in descending order

87 papers	1,801 citations	257101 24 h-index	315357 38 g-index
96 all docs	96 docs citations	96 times ranked	2139 citing authors

#	Article	IF	Citations
1	Scarless Recombineering of Phage in Lysogenic State. Methods in Molecular Biology, 2022, 2479, 1-9.	0.4	1
2	Lambda Red Recombineering of Bacteriophage in the Lysogenic State. Methods in Molecular Biology, 2022, 2479, 11-19.	0.4	1
3	Engineering Bacteria to Produce Pure Phage-like Particles for Gene Delivery. ACS Synthetic Biology, 2021, 10, 107-114.	1.9	11
4	Engineering Adaptive Gene Circuits in Bacteria Mastering Game Playing by Reinforcement Learning. Biophysical Journal, 2021, 120, 262a.	0.2	1
5	Engineering of a Promoter Repressed by a Light-Regulated Transcription Factor in *Escherichia coli*. Biodesign Research, 2021, 2021, .	0.8	2
6	Robust estimation of bacterial cell count from optical density. Communications Biology, 2020, 3, 512.	2.0	86
7	Engineered RNA-Interacting CRISPR Guide RNAs for Genetic Sensing and Diagnostics. CRISPR Journal, 2020, 3, 398-408.	1.4	12
8	Accelerated evolution of a minimal 63–amino acid dual transcription factor. Science Advances, 2020, 6, eaba2728.	4.7	13
9	Comparison of CRISPR and Marker-Based Methods for the Engineering of Phage T7. Viruses, 2020, 12, 193.	1.5	23
10	Engineering a Circular Riboregulator in *Escherichia coli*. Biodesign Research, 2020, 2020, .	0.8	6
11	Reinforcement learning in synthetic gene circuits. Biochemical Society Transactions, 2020, 48, 1637-1643.	1.6	5
12	Engineering CRISPR guide RNA riboswitches for in vivo applications. Current Opinion in Biotechnology, 2019, 55, 103-113.	3.3	24
13	Biodesign Research to Advance the Principles and Applications of Biosystems Design. Biodesign Research, 2019, 2019, .	0.8	3
14	Quantitative Characterization of Translational Riboregulators Using an *in Vitro* Transcription–Translation System. ACS Synthetic Biology, 2018, 7, 1269-1278.	1.9	16
15	Engineering of biomolecules by bacteriophage directed evolution. Current Opinion in Biotechnology, 2018, 51, 32-38.	3.3	17
16	Boolean Computation in Plants Using Post-translational Genetic Control and a Visual Output Signal. ACS Synthetic Biology, 2018, 7, 2322-2330.	1.9	9
17	Modulation of Intracellular O_2 Concentration in *Escherichia coli* Strains Using Oxygen Consuming Devices. ACS Synthetic Biology, 2018, 7, 1742-1752.	1.9	2
18	Expanding the toolbox for Synechocystis sp. PCC 6803: validation of replicative vectors and characterization of a novel set of promoters. Synthetic Biology, 2018, 3, ysy014.	1.2	43

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19	Editorial overview: Nanobiotechnology: Baby steps and giant strides towards molecular mastery. Current Opinion in Biotechnology, 2018, 51, iv-vi.	3.3	0
20	Synthetic biology: Engineered stable ecosystems. Nature Microbiology, 2017, 2, 17119.	5.9	4
21	Intracellular directed evolution of proteins from combinatorial libraries based on conditional phage replication. Nature Protocols, 2017, 12, 1830-1843.	5.5	16
22	Model-based design of RNA hybridization networks implemented in living cells. Nucleic Acids Research, 2017, 45, 9797-9808.	6.5	12
23	Engineering orthogonal dual transcription factors for multi-input synthetic promoters. Nature Communications, 2016, 7, 13858.	5.8	47
24	Using RNA as Molecular Code for Programming Cellular Function. ACS Synthetic Biology, 2016, 5, 795-809.	1.9	49
25	Genetically modified bacteriophages. Integrative Biology (United Kingdom), 2016, 8, 465-474.	0.6	26
26	Functionalization of an Antisense Small RNA. Journal of Molecular Biology, 2016, 428, 889-892.	2.0	5
27	Using promoter libraries to reduce metabolic burden due to plasmid-encoded proteins in recombinant Escherichia coli. New Biotechnology, 2016, 33, 78-90.	2.4	38
28	Dynamic signal processing by ribozyme-mediated RNA circuits to control gene expression. Nucleic Acids Research, 2015, 43, 5158-5170.	6.5	31
29	Bacterial computing with engineered populations. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2015, 373, 20140218.	1.6	9
30	Design and Characterization of Topological Small RNAs. Methods in Molecular Biology, 2015, 1316, 149-167.	0.4	1
31	Exploring the Dynamics and Mutational Landscape of Riboregulation with a Minimal Synthetic Circuit in Living Cells. Biophysical Journal, 2015, 109, 1070-1076.	0.2	6
32	Regulatory RNA Design Through Evolutionary Computation and Strand Displacement. Methods in Molecular Biology, 2015, 1244, 63-78.	0.4	3
33	Silencing of Antibiotic Resistance in *E. coli* with Engineered Phage Bearing Small Regulatory RNAs. ACS Synthetic Biology, 2014, 3, 1003-1006.	1.9	31
34	RiboMaker: computational design of conformation-based riboregulation. Bioinformatics, 2014, 30, 2508-2510.	1.8	24
35	Computational protein design with electrostatic focusing: Experimental characterization of a conditionally folded helical domain with a reduced amino acid alphabet. Biotechnology Journal, 2013, 8, 855-864.	1.8	1
36	Theoretical and experimental analysis of the forced LacI-AraC oscillator with a minimal gene regulatory model. Chaos, 2013, 23, 025109.	1.0	11

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37	A new frontier in synthetic biology: automated design of small RNA devices in bacteria. Trends in Genetics, 2013, 29, 529-536.	2.9	31
38	AutoBioCAD: Full Biodesign Automation of Genetic Circuits. ACS Synthetic Biology, 2013, 2, 230-236.	1.9	46
39	Full Design Automation of Multi-State RNA Devices to Program Gene Expression Using Energy-Based Optimization. PLoS Computational Biology, 2013, 9, e1003172.	1.5	29
40	Automated design of bacterial genome sequences. BMC Systems Biology, 2013, 7, 108.	3.0	1
41	Fine-Tuning Tomato Agronomic Properties by Computational Genome Redesign. PLoS Computational Biology, 2012, 8, e1002528.	1.5	7
42	An automated approach for single-cell tracking in epifluorescence microscopy applied to E. coli growth analysis on microfluidics biochips. , 2012, , .		0
43	De novo automated design of small RNA circuits for engineering synthetic riboregulation in living cells. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15271-15276.	3.3	150
44	Computational design of genomic transcriptional networks with adaptation to varying environments. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15277-15282.	3.3	14
45	Perspectives on the automatic design of regulatory systems for synthetic biology. FEBS Letters, 2012, 586, 2037-2042.	1.3	18
46	Integral Control of Plant Gravitropism through the Interplay of Hormone Signaling and Gene Regulation. Biophysical Journal, 2011, 101, 757-763.	0.2	10
47	Empirical model and in vivo characterization of the bacterial response to synthetic gene expression show that ribosome allocation limits growth rate. Biotechnology Journal, 2011, 6, 773-783.	1.8	54
48	Genetically engineered light sensors for control of bacterial gene expression. Biotechnology Journal, 2011, 6, 826-836.	1.8	15
49	Editorial: Synthetic Biology â€" applying new paradigms at the interface of fundamental research and innovation. Biotechnology Journal, 2011, 6, 766-767.	1.8	1
50	Pushing the limits of automatic computational protein design: design, expression, and characterization of a large synthetic protein based on a fungal laccase scaffold. Systems and Synthetic Biology, 2011, 5, 45-58.	1.0	8
51	Computational design of synthetic regulatory networks from a genetic library to characterize the designability of dynamical behaviors. Nucleic Acids Research, 2011, 39, e138-e138.	6.5	39
52	Optimal viral strategies for bypassing RNA silencing. Journal of the Royal Society Interface, 2011, 8, 257-268.	1.5	21
53	Synthetic biology gains momentum in Europe. Systems and Synthetic Biology, 2010, 4, 145-147.	1.0	1
54	Robust dynamical pattern formation from a multifunctional minimal genetic circuit. BMC Systems Biology, 2010, 4, 48.	3.0	8

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55	Using multi-objective computational design to extend protein promiscuity. Biophysical Chemistry, 2010, 147, 13-19.	1.5	16
56	Model-based redesign of global transcription regulation. Nucleic Acids Research, 2009, 37, e38-e38.	6.5	28
57	Computational protein design with side€chain conformational entropy. Proteins: Structure, Function and Bioinformatics, 2009, 74, 176-191.	1.5	23
58	Modular model-based design for heterologous bioproduction in bacteria. Current Opinion in Biotechnology, 2009, 20, 272-279.	3.3	14
59	Towards the automated engineering of a synthetic genome. Molecular BioSystems, 2009, 5, 733.	2.9	16
60	Editorial: Focus on synthetic biology. Biotechnology Journal, 2009, 4, 1367-1367.	1.8	1
61	Protein Design Based on Parallel Dimensional Reduction. Journal of Chemical Information and Modeling, 2009, 49, 1261-1271.	2.5	5
62	Reverse-engineering the Arabidopsis thaliana transcriptional network under changing environmental conditions. Genome Biology, 2009, 10, R96.	13.9	81
63	Challenges in the computational design of proteins. Journal of the Royal Society Interface, 2009, 6, S477-91.	1.5	45
64	Computational Design in Synthetic Biology. , 2009, , 49-63.		2
65	PROTDES: CHARMM toolbox for computational protein design. Systems and Synthetic Biology, 2008, 2, 105-113.	1.0	9
66	Pareto optimization in computational protein design with multiple objectives. Journal of Computational Chemistry, 2008, 29, 2704-2711.	1.5	22
67	Changes in the gene expression profile of Arabidopsis thaliana after infection with Tobacco etch virus. Virology Journal, 2008, 5, 92.	1.4	54
68	Computational design and evolution of the oscillatory response under light€"dark cycles. Biochimie, 2008, 90, 888-897.	1.3	9
69	DESHARKY: automatic design of metabolic pathways for optimal cell growth. Bioinformatics, 2008, 24, 2554-2556.	1.8	105
70	Automated extraction of meaningful pathways from quantitative proteomics data. Briefings in Functional Genomics & Proteomics, 2008, 7, 136-146.	3.8	16
71	Protein design at room temperature: the role of side€"chain conformational entropy. , 2008, , .		0
72	Genetdes: automatic design of transcriptional networks. Bioinformatics, 2007, 23, 1857-1858.	1.8	65

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73	Vanillin cell sensor. IET Synthetic Biology, 2007, 1, 74-78.	0.2	2
74	ECOLITASTER: cellular biosensor. BMC Systems Biology, 2007, 1, .	3.0	0
75	Computational design of proteins with new functions. BMC Systems Biology, 2007, 1, .	3.0	1
76	Evolutionary mechanisms of circadian clocks. Open Life Sciences, 2007, 2, 233-253.	0.6	3
77	Asmparts: assembly of biological model parts. Systems and Synthetic Biology, 2007, 1, 167-170.	1.0	35
78	Computational design of digital and memory biological devices. Systems and Synthetic Biology, 2007, 1, 183-195.	1.0	19
79	Active Sites by Computational Protein Design. AIP Conference Proceedings, 2006, , .	0.3	3
80	Computational Protein Design Is a Challenge for Implicit Solvation Models. Biophysical Journal, 2005, 88, 156-171.	0.2	54
81	Automatic Sequence Design of Major Histocompatibility Complex Class I Binding Peptides Impairing CD8+ T Cell Recognition. Journal of Biological Chemistry, 2003, 278, 1281-1290.	1.6	32
82	Folding free energy function selects native-like protein sequences in the core but not on the surface. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13554-13559.	3.3	63
83	Automatic Procedures for Protein Design. Combinatorial Chemistry and High Throughput Screening, 2001, 4, 643-659.	0.6	21
84	FINITE VEV'S FROM A LARGE DISTANCE VACUUM WAVE FUNCTIONAL. International Journal of Modern Physics A, 2000, 15, 581-600.	0.5	4
85	NUMERICAL SIMULATION OF RANDOM PATHS WITH A CURVATURE-DEPENDENT ACTION. Modern Physics Letters A, 1998, 13, 2131-2138.	0.5	1
86	The role of temperature in a dimensional approach to QCD3. Nuclear Physics B, 1995, 457, 57-77.	0.9	0
87	Using FL as a test of compositeness. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1994, 336, 80-84.	1.5	0