Javier Carrera

List of Publications by Year
in descending order

25 papers	915 citations	516710 16 h-index	610901 24 g-index
25 all docs	25 docs citations	25 times ranked	1355 citing authors

#	Article	IF	Citations
1	Simultaneous cross-evaluation of heterogeneous *E. coli* datasets via mechanistic simulation. Science, 2020, 369, .	12.6	105
2	Modulation of Intracellular O_2 Concentration in *Escherichia coli* Strains Using Oxygen Consuming Devices. ACS Synthetic Biology, 2018, 7, 1742-1752.	3.8	2
3	Why Build Whole-Cell Models?. Trends in Cell Biology, 2015, 25, 719-722.	7.9	62
4	An integrative, multi-scale, genome-wide model reveals the phenotypic landscape of *Escherichia coli*. Molecular Systems Biology, 2014, 10, 735.	7.2	73
5	Automated design of bacterial genome sequences. BMC Systems Biology, 2013, 7, 108.	3.0	1
6	Fine-Tuning Tomato Agronomic Properties by Computational Genome Redesign. PLoS Computational Biology, 2012, 8, e1002528.	3.2	7
7	Computational design of host transcription-factors sets whose misregulation mimics the transcriptomic effect of viral infections. Scientific Reports, 2012, 2, 1006.	3.3	4
8	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.	7.1	14
9	A Meta-Analysis Reveals the Commonalities and Differences in Arabidopsis thaliana Response to Different Viral Pathogens. PLoS ONE, 2012, 7, e40526.	2.5	64
10	Perspectives on the automatic design of regulatory systems for synthetic biology. FEBS Letters, 2012, 586, 2037-2042.	2.8	18
11	A systems biology approach to the evolution of plant–virus interactions. Current Opinion in Plant Biology, 2011, 14, 372-377.	7.1	31
12	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.	3.5	54
13	Computational design of synthetic regulatory networks from a genetic library to characterize the designability of dynamical behaviors. Nucleic Acids Research, 2011, 39, e138-e138.	14.5	39
14	Network design meets in silico evolutionary biology. Biochimie, 2010, 92, 746-752.	2.6	10
15	Model-based redesign of global transcription regulation. Nucleic Acids Research, 2009, 37, e38-e38.	14.5	28
16	Modular model-based design for heterologous bioproduction in bacteria. Current Opinion in Biotechnology, 2009, 20, 272-279.	6.6	14
17	Towards the automated engineering of a synthetic genome. Molecular BioSystems, 2009, 5, 733.	2.9	16
18	Reverse-engineering the Arabidopsis thaliana transcriptional network under changing environmental conditions. Genome Biology, 2009, 10, R96.	9.6	81

#	Article	IF	Citations
19	Computational Design in Synthetic Biology. , 2009, , 49-63.		2
20	Pareto optimization in computational protein design with multiple objectives. Journal of Computational Chemistry, 2008, 29, 2704-2711.	3.3	22
21	Changes in the gene expression profile of Arabidopsis thaliana after infection with Tobacco etch virus. Virology Journal, 2008, 5, 92.	3.4	54
22	Computational design and evolution of the oscillatory response under light–dark cycles. Biochimie, 2008, 90, 888-897.	2.6	9
23	DESHARKY: automatic design of metabolic pathways for optimal cell growth. Bioinformatics, 2008, 24, 2554-2556.	4.1	105
24	Genetdes: automatic design of transcriptional networks. Bioinformatics, 2007, 23, 1857-1858.	4.1	65
25	Asmparts: assembly of biological model parts. Systems and Synthetic Biology, 2007, 1, 167-170.	1.0	35