

Javier Carrera

List of Publications by Year in descending order

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Version: 2024-02-01

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	DESHARKY: automatic design of metabolic pathways for optimal cell growth. <i>Bioinformatics</i> , 2008, 24, 2554-2556.	4.1	105
2	Simultaneous cross-evaluation of heterogeneous <i>E. coli</i> datasets via mechanistic simulation. <i>Science</i> , 2020, 369, .	12.6	105
3	Reverse-engineering the <i>Arabidopsis thaliana</i> transcriptional network under changing environmental conditions. <i>Genome Biology</i> , 2009, 10, R96.	9.6	81
4	An integrative, multi-scale, genome-wide model reveals the phenotypic landscape of <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2014, 10, 735.	7.2	73
5	Genetdes: automatic design of transcriptional networks. <i>Bioinformatics</i> , 2007, 23, 1857-1858.	4.1	65
6	A Meta-Analysis Reveals the Commonalities and Differences in <i>Arabidopsis thaliana</i> Response to Different Viral Pathogens. <i>PLoS ONE</i> , 2012, 7, e40526.	2.5	64
7	Why Build Whole-Cell Models?. <i>Trends in Cell Biology</i> , 2015, 25, 719-722.	7.9	62
8	Changes in the gene expression profile of <i>Arabidopsis thaliana</i> after infection with Tobacco etch virus. <i>Virology Journal</i> , 2008, 5, 92.	3.4	54
9	Empirical model and in vivo characterization of the bacterial response to synthetic gene expression show that ribosome allocation limits growth rate. <i>Biotechnology Journal</i> , 2011, 6, 773-783.	3.5	54
10	Computational design of synthetic regulatory networks from a genetic library to characterize the designability of dynamical behaviors. <i>Nucleic Acids Research</i> , 2011, 39, e138-e138.	14.5	39
11	Asmparts: assembly of biological model parts. <i>Systems and Synthetic Biology</i> , 2007, 1, 167-170.	1.0	35
12	A systems biology approach to the evolution of plant-virus interactions. <i>Current Opinion in Plant Biology</i> , 2011, 14, 372-377.	7.1	31
13	Model-based redesign of global transcription regulation. <i>Nucleic Acids Research</i> , 2009, 37, e38-e38.	14.5	28
14	Pareto optimization in computational protein design with multiple objectives. <i>Journal of Computational Chemistry</i> , 2008, 29, 2704-2711.	3.3	22
15	Perspectives on the automatic design of regulatory systems for synthetic biology. <i>FEBS Letters</i> , 2012, 586, 2037-2042.	2.8	18
16	Towards the automated engineering of a synthetic genome. <i>Molecular BioSystems</i> , 2009, 5, 733.	2.9	16
17	Modular model-based design for heterologous bioproduction in bacteria. <i>Current Opinion in Biotechnology</i> , 2009, 20, 272-279.	6.6	14
18	Computational design of genomic transcriptional networks with adaptation to varying environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15277-15282.	7.1	14

#	ARTICLE	IF	CITATIONS
19	Network design meets in silico evolutionary biology. <i>Biochimie</i> , 2010, 92, 746-752.	2.6	10
20	Computational design and evolution of the oscillatory response under light-dark cycles. <i>Biochimie</i> , 2008, 90, 888-897.	2.6	9
21	Fine-Tuning Tomato Agronomic Properties by Computational Genome Redesign. <i>PLoS Computational Biology</i> , 2012, 8, e1002528.	3.2	7
22	Computational design of host transcription-factors sets whose misregulation mimics the transcriptomic effect of viral infections. <i>Scientific Reports</i> , 2012, 2, 1006.	3.3	4
23	Modulation of Intracellular O ₂ Concentration in <i>Escherichia coli</i> Strains Using Oxygen Consuming Devices. <i>ACS Synthetic Biology</i> , 2018, 7, 1742-1752.	3.8	2
24	Computational Design in Synthetic Biology. , 2009, , 49-63.		2
25	Automated design of bacterial genome sequences. <i>BMC Systems Biology</i> , 2013, 7, 108.	3.0	1