Howard M Salis

List of Publications by Year
in descending order

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28
papers

4,727
citations

304602
22
h-index

501076
28
g-index

35
all docs

35
docs citations

35
times ranked

4899
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated design of synthetic ribosome binding sites to control protein expression. Nature Biotechnology, 2009, 27, 946-950.	9.4	1,560
2	A Synthetic Genetic Edge Detection Program. Cell, 2009, 137, 1272-1281.	13.5	442
3	Translation rate is controlled by coupled trade-offs between site accessibility, selective RNA unfolding and sliding at upstream standby sites. Nucleic Acids Research, 2014, 42, 2646-2659.	6.5	405
4	Automated physics-based design of synthetic riboswitches from diverse RNA aptamers. Nucleic Acids Research, 2016, 44, 1-13.	6.5	340
5	The Ribosome Binding Site Calculator. Methods in Enzymology, 2011, 498, 19-42.	0.4	337
6	Efficient search, mapping, and optimization of multiâ€protein genetic systems in diverse bacteria. Molecular Systems Biology, 2014, 10, 731.	3.2	193
7	Rational design of a synthetic Entnerâ€“Doudoroff pathway for improved and controllable NADPH regeneration. Metabolic Engineering, 2015, 29, 86-96.	3.6	142
8	Translation Initiation is Controlled by RNA Folding Kinetics via a Ribosome Drafting Mechanism. Journal of the American Chemical Society, 2016, 138, 7016-7023.	6.6	125
9	A portable expression resource for engineering cross-species genetic circuits and pathways. Nature Communications, 2015, 6, 7832.	5.8	121
10	Reversing methanogenesis to capture methane for liquid biofuel precursors. Microbial Cell Factories, 2016, 15, 11.	1.9	116
11	Precise quantification of translation inhibition by mRNA structures that overlap with the ribosomal footprint in N-terminal coding sequences. Nucleic Acids Research, 2017, 45, 5437-5448.	6.5	109
12	Simultaneous repression of multiple bacterial genes using nonrepetitive extra-long sgRNA arrays. Nature Biotechnology, 2019, 37, 1294-1301.	9.4	107
13	A Biophysical Model of CRISPR/Cas9 Activity for Rational Design of Genome Editing and Gene Regulation. PLoS Computational Biology, 2016, 12, e1004724.	1.5	96
14	Kinetic Buffering of Cross Talk between Bacterial Two-Component Sensors. Journal of Molecular Biology, 2009, 390, 380-393.	2.0	85
15	A predictive biophysical model of translational coupling to coordinate and control protein expression in bacterial operons. Nucleic Acids Research, 2015, 43, 7137-7151.	6.5	79
16	An Automated Model Test System for Systematic Development and Improvement of Gene Expression Models. ACS Synthetic Biology, 2020, 9, 3145-3156.	1.9	78
17	Automated design of thousands of nonrepetitive parts for engineering stable genetic systems. Nature Biotechnology, 2020, 38, 1466-1475.	9.4	68
18	An equation-free probabilistic steady-state approximation: Dynamic application to the stochastic simulation of biochemical reaction networks. Journal of Chemical Physics, 2005, 123, 214106.	1.2	63

#	ARTICLE	IF	CITATIONS
19	Systematic Quantification of Sequence and Structural Determinants Controlling mRNA stability in Bacterial Operons. ACS Synthetic Biology, 2021, 10, 318-332.	1.9	52
20	Induction and Relaxation Dynamics of the Regulatory Network Controlling the Type III Secretion System Encoded within Salmonella Pathogenicity Island 1. Journal of Molecular Biology, 2008, 377, 47-61.	2.0	49
21	Model-Driven Designs of an Oscillating Gene Network. Biophysical Journal, 2005, 89, 3873-3883.	0.2	47
22	Numerical simulation of stochastic gene circuits. Computers and Chemical Engineering, 2005, 29, 577-588.	2.0	29
23	Computer-aided design of modular protein devices: Boolean AND gene activation. Physical Biology, 2006, 3, 295-310.	0.8	17
24	Synthesis Success Calculator: Predicting the Rapid Synthesis of DNA Fragments with Machine Learning. ACS Synthetic Biology, 2020, 9, 1563-1571.	1.9	13
25	Selenium-dependent metabolic reprogramming during inflammation and resolution. Journal of Biological Chemistry, 2021, 296, 100410.	1.6	12
26	Tuning Cell-Free Composition Controls the Time Delay, Dynamics, and Productivity of TX-TL Expression. ACS Synthetic Biology, 2021, 10, 2508-2519.	1.9	12
27	An Automated Pipeline for Engineering Many-Enzyme Pathways: Computational Sequence Design, Pathway Expression-Flux Mapping, and Scalable Pathway Optimization. Methods in Molecular Biology, 2018, 1671, 39-61.	0.4	6
28	Purification of Cas9â€"<scp>RNA</scp> complexes by ultrafiltration. Biotechnology Progress, 2021, 37, e3104.	1.3	2