

Howard M Salis

List of Publications by Year in descending order

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Version: 2024-02-01

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	Purification of Cas9â€”<sc>RNA</sc> complexes by ultrafiltration. <i>Biotechnology Progress</i> , 2021, 37, e3104.	1.3	2
2	Systematic Quantification of Sequence and Structural Determinants Controlling mRNA stability in Bacterial Operons. <i>ACS Synthetic Biology</i> , 2021, 10, 318-332.	1.9	52
3	Selenium-dependent metabolic reprogramming during inflammation and resolution. <i>Journal of Biological Chemistry</i> , 2021, 296, 100410.	1.6	12
4	Tuning Cell-Free Composition Controls the Time Delay, Dynamics, and Productivity of TX-TL Expression. <i>ACS Synthetic Biology</i> , 2021, 10, 2508-2519.	1.9	12
5	An Automated Model Test System for Systematic Development and Improvement of Gene Expression Models. <i>ACS Synthetic Biology</i> , 2020, 9, 3145-3156.	1.9	78
6	Automated design of thousands of nonrepetitive parts for engineering stable genetic systems. <i>Nature Biotechnology</i> , 2020, 38, 1466-1475.	9.4	68
7	Synthesis Success Calculator: Predicting the Rapid Synthesis of DNA Fragments with Machine Learning. <i>ACS Synthetic Biology</i> , 2020, 9, 1563-1571.	1.9	13
8	Simultaneous repression of multiple bacterial genes using nonrepetitive extra-long sgRNA arrays. <i>Nature Biotechnology</i> , 2019, 37, 1294-1301.	9.4	107
9	An Automated Pipeline for Engineering Many-Enzyme Pathways: Computational Sequence Design, Pathway Expression-Flux Mapping, and Scalable Pathway Optimization. <i>Methods in Molecular Biology</i> , 2018, 1671, 39-61.	0.4	6
10	Precise quantification of translation inhibition by mRNA structures that overlap with the ribosomal footprint in N-terminal coding sequences. <i>Nucleic Acids Research</i> , 2017, 45, 5437-5448.	6.5	109
11	Translation Initiation is Controlled by RNA Folding Kinetics via a Ribosome Drafting Mechanism. <i>Journal of the American Chemical Society</i> , 2016, 138, 7016-7023.	6.6	125
12	Reversing methanogenesis to capture methane for liquid biofuel precursors. <i>Microbial Cell Factories</i> , 2016, 15, 11.	1.9	116
13	Automated physics-based design of synthetic riboswitches from diverse RNA aptamers. <i>Nucleic Acids Research</i> , 2016, 44, 1-13.	6.5	340
14	A Biophysical Model of CRISPR/Cas9 Activity for Rational Design of Genome Editing and Gene Regulation. <i>PLoS Computational Biology</i> , 2016, 12, e1004724.	1.5	96
15	Rational design of a synthetic Entnerâ€”Doudoroff pathway for improved and controllable NADPH regeneration. <i>Metabolic Engineering</i> , 2015, 29, 86-96.	3.6	142
16	A portable expression resource for engineering cross-species genetic circuits and pathways. <i>Nature Communications</i> , 2015, 6, 7832.	5.8	121
17	A predictive biophysical model of translational coupling to coordinate and control protein expression in bacterial operons. <i>Nucleic Acids Research</i> , 2015, 43, 7137-7151.	6.5	79
18	Translation rate is controlled by coupled trade-offs between site accessibility, selective RNA unfolding and sliding at upstream standby sites. <i>Nucleic Acids Research</i> , 2014, 42, 2646-2659.	6.5	405

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19	Efficient search, mapping, and optimization of multi- ϵ protein genetic systems in diverse bacteria. <i>Molecular Systems Biology</i> , 2014, 10, 731.	3.2	193
20	The Ribosome Binding Site Calculator. <i>Methods in Enzymology</i> , 2011, 498, 19-42.	0.4	337
21	Automated design of synthetic ribosome binding sites to control protein expression. <i>Nature Biotechnology</i> , 2009, 27, 946-950.	9.4	1,560
22	A Synthetic Genetic Edge Detection Program. <i>Cell</i> , 2009, 137, 1272-1281.	13.5	442
23	Kinetic Buffering of Cross Talk between Bacterial Two-Component Sensors. <i>Journal of Molecular Biology</i> , 2009, 390, 380-393.	2.0	85
24	Induction and Relaxation Dynamics of the Regulatory Network Controlling the Type III Secretion System Encoded within <i>Salmonella</i> Pathogenicity Island 1. <i>Journal of Molecular Biology</i> , 2008, 377, 47-61.	2.0	49
25	Computer-aided design of modular protein devices: Boolean AND gene activation. <i>Physical Biology</i> , 2006, 3, 295-310.	0.8	17
26	Numerical simulation of stochastic gene circuits. <i>Computers and Chemical Engineering</i> , 2005, 29, 577-588.	2.0	29
27	An equation-free probabilistic steady-state approximation: Dynamic application to the stochastic simulation of biochemical reaction networks. <i>Journal of Chemical Physics</i> , 2005, 123, 214106.	1.2	63
28	Model-Driven Designs of an Oscillating Gene Network. <i>Biophysical Journal</i> , 2005, 89, 3873-3883.	0.2	47