

Daniel B Goodman

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8980890/publications.pdf>

Version: 2024-02-01

13
papers

2,599
citations

840776

11
h-index

1125743

13
g-index

18
all docs

18
docs citations

18
times ranked

3134
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomically Recoded Organisms Expand Biological Functions. <i>Science</i> , 2013, 342, 357-360.	12.6	721
2	Precise Manipulation of Chromosomes in Vivo Enables Genome-Wide Codon Replacement. <i>Science</i> , 2011, 333, 348-353.	12.6	512
3	Causes and Effects of N-Terminal Codon Bias in Bacterial Genes. <i>Science</i> , 2013, 342, 475-479.	12.6	491
4	Composability of regulatory sequences controlling transcription and translation in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14024-14029.	7.1	377
5	Design, synthesis, and testing toward a 57-codon genome. <i>Science</i> , 2016, 353, 819-822.	12.6	251
6	High-throughput functional variant screens via in vivo production of single-stranded DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	53
7	DNAplotlib: Programmable Visualization of Genetic Designs and Associated Data. <i>ACS Synthetic Biology</i> , 2017, 6, 1115-1119.	3.8	50
8	Emergent rules for codon choice elucidated by editing rare arginine codons in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5588-97.	7.1	48
9	Rational optimization of <i>tolC</i> as a powerful dual selectable marker for genome engineering. <i>Nucleic Acids Research</i> , 2014, 42, 4779-4790.	14.5	36
10	Optimizing complex phenotypes through model-guided multiplex genome engineering. <i>Genome Biology</i> , 2017, 18, 100.	8.8	23
11	Product Length, Dye Choice, and Detection Chemistry in the Bead-Emulsion Amplification of Millions of Single DNA Molecules in Parallel. <i>Analytical Chemistry</i> , 2009, 81, 5770-5776.	6.5	15
12	Enabling multiplexed testing of pooled donor cells through whole-genome sequencing. <i>Genome Medicine</i> , 2018, 10, 31.	8.2	10
13	Millstone: software for multiplex microbial genome analysis and engineering. <i>Genome Biology</i> , 2017, 18, 101.	8.8	5