Farren J Isaacs

List of Publications by Year in descending order

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58	9,082	36	60
papers	citations	h-index	g-index
65	65	65	9215
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Programming cells by multiplex genome engineering and accelerated evolution. Nature, 2009, 460, 894-898.	13.7	1,346
2	Genomically Recoded Organisms Expand Biological Functions. Science, 2013, 342, 357-360.	6.0	721
3	Phenotypic Consequences of Promoter-Mediated Transcriptional Noise. Molecular Cell, 2006, 24, 853-865.	4.5	591
4	Engineered riboregulators enable post-transcriptional control of gene expression. Nature Biotechnology, 2004, 22, 841-847.	9.4	513
5	Precise Manipulation of Chromosomes in Vivo Enables Genome-Wide Codon Replacement. Science, 2011, 333, 348-353.	6.0	512
6	Computational studies of gene regulatory networks: in numero molecular biology. Nature Reviews Genetics, 2001, 2, 268-279.	7.7	508
7	A-to-I RNA editing occurs at over a hundred million genomic sites, located in a majority of human genes. Genome Research, 2014, 24, 365-376.	2.4	492
8	Prediction and measurement of an autoregulatory genetic module. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7714-7719.	3.3	409
9	RNA synthetic biology. Nature Biotechnology, 2006, 24, 545-554.	9.4	332
10	Recoded organisms engineered to depend on synthetic amino acids. Nature, 2015, 518, 89-93.	13.7	288
11	Engineering an allosteric transcription factor to respond to new ligands. Nature Methods, 2016, 13, 177-183.	9.0	274
12	The real cost of sequencing: scaling computation to keep pace with data generation. Genome Biology, 2016, 17, 53.	3.8	264
13	Evolution of translation machinery in recoded bacteria enables multi-site incorporation of nonstandard amino acids. Nature Biotechnology, 2015, 33, 1272-1279.	9.4	234
14	The Genome Project-Write. Science, 2016, 353, 126-127.	6.0	194
15	Potent Noncovalent Inhibitors of the Main Protease of SARS-CoV-2 from Molecular Sculpting of the Drug Perampanel Guided by Free Energy Perturbation Calculations. ACS Central Science, 2021, 7, 467-475.	5.3	182
16	Tracking, tuning, and terminating microbial physiology using synthetic riboregulators. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15898-15903.	3.3	166
17	Cell-free protein synthesis from genomically recoded bacteria enables multisite incorporation of noncanonical amino acids. Nature Communications, 2018, 9, 1203.	5.8	165
18	Cell-free Protein Synthesis from a Release Factor 1 Deficient <i>Escherichia coli</i> Activates Efficient and Multiple Site-specific Nonstandard Amino Acid Incorporation. ACS Synthetic Biology, 2014, 3, 398-409.	1.9	133

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19	Multilayered genetic safeguards limit growth of microorganisms to defined environments. Nucleic Acids Research, 2015, 43, 1945-1954.	6.5	112
20	Hydrogel-based biocontainment of bacteria for continuous sensing and computation. Nature Chemical Biology, 2021, 17, 724-731.	3.9	110
21	Robust production of recombinant phosphoproteins using cell-free protein synthesis. Nature Communications, 2015, 6, 8168.	5.8	106
22	Rapid editing and evolution of bacterial genomes using libraries of synthetic DNA. Nature Protocols, 2014, 9, 2301-2316.	5.5	101
23	Crystal Structure of an Insect Antifreeze Protein and Its Implications for Ice Binding. Journal of Biological Chemistry, 2013, 288, 12295-12304.	1.6	96
24	Precise Editing at DNA Replication Forks Enables Multiplex Genome Engineering in Eukaryotes. Cell, 2017, 171, 1453-1467.e13.	13.5	93
25	Enhanced phosphoserine insertion during <i>Escherichia coli</i> protein synthesis via partial UAG codon reassignment and release factor 1 deletion. FEBS Letters, 2012, 586, 3716-3722.	1.3	91
26	Enhanced multiplex genome engineering through co-operative oligonucleotide co-selection. Nucleic Acids Research, 2012, 40, e132-e132.	6.5	89
27	A flexible codon in genomically recoded Escherichia coli permits programmable protein phosphorylation. Nature Communications, 2015, 6, 8130.	5.8	86
28	Active Targeting of Cancer Cells by Nanobody Decorated Polypeptide Micelle with Bio-orthogonally Conjugated Drug. Nano Letters, 2019, 19, 247-254.	4.5	72
29	Repurposing the translation apparatus for synthetic biology. Current Opinion in Chemical Biology, 2015, 28, 83-90.	2.8	69
30	Next-generation genetic code expansion. Current Opinion in Chemical Biology, 2018, 46, 203-211.	2.8	57
31	Photoâ€Crosslinkable Unnatural Amino Acids Enable Facile Synthesis of Thermoresponsive Nano―to Microgels of Intrinsically Disordered Polypeptides. Advanced Materials, 2018, 30, 1704878.	11.1	56
32	Translation system engineering in <i>Escherichia coli</i> enhances non anonical amino acid incorporation into proteins. Biotechnology and Bioengineering, 2017, 114, 1074-1086.	1.7	49
33	Emergent rules for codon choice elucidated by editing rare arginine codons in <i>Escherichia colic/li>. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5588-97.</i>	3.3	48
34	Recombineering and MAGE. Nature Reviews Methods Primers, 2021, 1, .	11.8	47
35	Precise manipulation of bacterial chromosomes by conjugative assembly genome engineering. Nature Protocols, 2014, 9, 2285-2300.	5.5	43
36	Genomes by design. Nature Reviews Genetics, 2015, 16, 501-516.	7.7	41

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37	Genomic Recoding Broadly Obstructs the Propagation of Horizontally Transferred Genetic Elements. Cell Systems, 2016, 3, 199-207.	2.9	40
38	Optimization of Triarylpyridinone Inhibitors of the Main Protease of SARS-CoV-2 to Low-Nanomolar Antiviral Potency. ACS Medicinal Chemistry Letters, 2021, 12, 1325-1332.	1.3	37
39	Rational optimization of <i>tolC</i> as a powerful dual selectable marker for genome engineering. Nucleic Acids Research, 2014, 42, 4779-4790.	6.5	36
40	Encoding human serine phosphopeptides in bacteria for proteome-wide identification of phosphorylation-dependent interactions. Nature Biotechnology, 2018, 36, 638-644.	9.4	30
41	Protein nanowires with tunable functionality and programmable self-assembly using sequence-controlled synthesis. Nature Communications, 2022, 13, 829.	5. 8	30
42	MOLECULAR BIOLOGY: Signal Processing in Single Cells. Science, 2005, 307, 1886-1888.	6.0	22
43	Designed Phosphoprotein Recognition in <i>Escherichia coli</i> . ACS Chemical Biology, 2014, 9, 2502-2507.	1.6	20
44	Plug-and-play with RNA. Nature Biotechnology, 2005, 23, 306-307.	9.4	19
45	Tuning protein half-life in mouse using sequence-defined biopolymers functionalized with lipids. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	17
46	Cross-kingdom expression of synthetic genetic elements promotes discovery of metabolites in the human microbiome. Cell, 2022, 185, 1487-1505.e14.	13.5	17
47	The Role of Orthogonality in Genetic Code Expansion. Life, 2019, 9, 58.	1.1	16
48	Organisms with alternative genetic codes resolve unassigned codons via mistranslation and ribosomal rescue. ELife, 2018, 7, .	2.8	16
49	Merlin: Computer-Aided Oligonucleotide Design for Large Scale Genome Engineering with MAGE. ACS Synthetic Biology, 2016, 5, 452-458.	1.9	11
50	ZTCG: Viruses expand the genetic alphabet. Science, 2021, 372, 460-461.	6.0	10
51	Guiding Ethical Principles in Engineering Biology Research. ACS Synthetic Biology, 2021, 10, 907-910.	1.9	10
52	DNA-Origami-Based Fluorescence Brightness Standards for Convenient and Fast Protein Counting in Live Cells. Nano Letters, 2020, 20, 8890-8896.	4.5	8
53	Targeted editing and evolution of engineered ribosomes in vivo by filtered editing. Nature Communications, 2022, 13, 180.	5.8	6
54	Making Security Viral: Shifting Engineering Biology Culture and Publishing. ACS Synthetic Biology, 2022, 11, 522-527.	1.9	6

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#	Article	IF	CITATION
55	Phosphorylated WNK kinase networks in recoded bacteria recapitulate physiological function. Cell Reports, 2021, 36, 109416.	2.9	5
56	Automated design of RNA devices. Nature Chemical Biology, 2012, 8, 413-415.	3.9	2
57	Chemoselective restoration of para-azido-phenylalanine at multiple sites in proteins. Cell Chemical Biology, 2022, 29, 1046-1052.e4.	2.5	2
58	Computational design and engineering of an Escherichia coli strain producing the nonstandard amino acid para-aminophenylalanine. IScience, 2022, 25, 104562.	1.9	1