Farren J Isaacs

List of Publications by Year
in descending order

58 papers	9,082 citations	101384 36 h-index	128067 60 g-index
65 all docs	65 docs citations	65 times ranked	9215 citing authors

#	Article	IF	Citations
1	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
2	Targeted editing and evolution of engineered ribosomes in vivo by filtered editing. Nature Communications, 2022, 13, 180.	5.8	6
3	Protein nanowires with tunable functionality and programmable self-assembly using sequence-controlled synthesis. Nature Communications, 2022, 13, 829.	5.8	30
4	Chemoselective restoration of para-azido-phenylalanine at multiple sites in proteins. Cell Chemical Biology, 2022, 29, 1046-1052.e4.	2.5	2
5	Making Security Viral: Shifting Engineering Biology Culture and Publishing. ACS Synthetic Biology, 2022, 11, 522-527.	1.9	6
6	Cross-kingdom expression of synthetic genetic elements promotes discovery of metabolites in the human microbiome. Cell, 2022, 185, 1487-1505.e14.	13.5	17
7	Computational design and engineering of an Escherichia coli strain producing the nonstandard amino acid para-aminophenylalanine. IScience, 2022, 25, 104562.	1.9	1
8	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
9	Hydrogel-based biocontainment of bacteria for continuous sensing and computation. Nature Chemical Biology, 2021, 17, 724-731.	3.9	110
10	ZTCG: Viruses expand the genetic alphabet. Science, 2021, 372, 460-461.	6.0	10
11	Guiding Ethical Principles in Engineering Biology Research. ACS Synthetic Biology, 2021, 10, 907-910.	1.9	10
12	Phosphorylated WNK kinase networks in recoded bacteria recapitulate physiological function. Cell Reports, 2021, 36, 109416.	2.9	5
13	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
14	Recombineering and MAGE. Nature Reviews Methods Primers, 2021, 1, .	11.8	47
15	DNA-Origami-Based Fluorescence Brightness Standards for Convenient and Fast Protein Counting in Live Cells. Nano Letters, 2020, 20, 8890-8896.	4.5	8
16	The Role of Orthogonality in Genetic Code Expansion. Life, 2019, 9, 58.	1.1	16
17	Active Targeting of Cancer Cells by Nanobody Decorated Polypeptide Micelle with Bio-orthogonally Conjugated Drug. Nano Letters, 2019, 19, 247-254.	4.5	72
18	Cell-free protein synthesis from genomically recoded bacteria enables multisite incorporation of noncanonical amino acids. Nature Communications, 2018, 9, 1203.	5.8	165

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19	Photoâ€•Crosslinkable Unnatural Amino Acids Enable Facile Synthesis of Thermoresponsive Nanoâ€•to Microgels of Intrinsically Disordered Polypeptides. Advanced Materials, 2018, 30, 1704878.	11.1	56
20	Next-generation genetic code expansion. Current Opinion in Chemical Biology, 2018, 46, 203-211.	2.8	57
21	Encoding human serine phosphopeptides in bacteria for proteome-wide identification of phosphorylation-dependent interactions. Nature Biotechnology, 2018, 36, 638-644.	9.4	30
22	Organisms with alternative genetic codes resolve unassigned codons via mistranslation and ribosomal rescue. ELife, 2018, 7, .	2.8	16
23	Translation system engineering in <i>Escherichia coli</i> enhances nonâ€•canonical amino acid incorporation into proteins. Biotechnology and Bioengineering, 2017, 114, 1074-1086.	1.7	49
24	Precise Editing at DNA Replication Forks Enables Multiplex Genome Engineering in Eukaryotes. Cell, 2017, 171, 1453-1467.e13.	13.5	93
25	Merlin: Computer-Aided Oligonucleotide Design for Large Scale Genome Engineering with MAGE. ACS Synthetic Biology, 2016, 5, 452-458.	1.9	11
26	Emergent rules for codon choice elucidated by editing rare arginine codons in <i>Escherichia coli</i>. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5588-97.	3.3	48
27	Genomic Recoding Broadly Obstructs the Propagation of Horizontally Transferred Genetic Elements. Cell Systems, 2016, 3, 199-207.	2.9	40
28	The Genome Project-Write. Science, 2016, 353, 126-127.	6.0	194
29	The real cost of sequencing: scaling computation to keep pace with data generation. Genome Biology, 2016, 17, 53.	3.8	264
30	Engineering an allosteric transcription factor to respond to new ligands. Nature Methods, 2016, 13, 177-183.	9.0	274
31	A flexible codon in genomically recoded Escherichia coli permits programmable protein phosphorylation. Nature Communications, 2015, 6, 8130.	5.8	86
32	Evolution of translation machinery in recoded bacteria enables multi-site incorporation of nonstandard amino acids. Nature Biotechnology, 2015, 33, 1272-1279.	9.4	234
33	Multilayered genetic safeguards limit growth of microorganisms to defined environments. Nucleic Acids Research, 2015, 43, 1945-1954.	6.5	112
34	Recoded organisms engineered to depend on synthetic amino acids. Nature, 2015, 518, 89-93.	13.7	288
35	Repurposing the translation apparatus for synthetic biology. Current Opinion in Chemical Biology, 2015, 28, 83-90.	2.8	69
36	Genomes by design. Nature Reviews Genetics, 2015, 16, 501-516.	7.7	41

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37	Robust production of recombinant phosphoproteins using cell-free protein synthesis. Nature Communications, 2015, 6, 8168.	5.8	106
38	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
39	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
40	Designed Phosphoprotein Recognition in <i>Escherichia coli</i>. ACS Chemical Biology, 2014, 9, 2502-2507.	1.6	20
41	Rapid editing and evolution of bacterial genomes using libraries of synthetic DNA. Nature Protocols, 2014, 9, 2301-2316.	5.5	101
42	Precise manipulation of bacterial chromosomes by conjugative assembly genome engineering. Nature Protocols, 2014, 9, 2285-2300.	5.5	43
43	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
44	Genomically Recoded Organisms Expand Biological Functions. Science, 2013, 342, 357-360.	6.0	721
45	Crystal Structure of an Insect Antifreeze Protein and Its Implications for Ice Binding. Journal of Biological Chemistry, 2013, 288, 12295-12304.	1.6	96
46	Enhanced multiplex genome engineering through co-operative oligonucleotide co-selection. Nucleic Acids Research, 2012, 40, e132-e132.	6.5	89
47	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
48	Automated design of RNA devices. Nature Chemical Biology, 2012, 8, 413-415.	3.9	2
49	Precise Manipulation of Chromosomes in Vivo Enables Genome-Wide Codon Replacement. Science, 2011, 333, 348-353.	6.0	512
50	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
51	Programming cells by multiplex genome engineering and accelerated evolution. Nature, 2009, 460, 894-898.	13.7	1,346
52	Phenotypic Consequences of Promoter-Mediated Transcriptional Noise. Molecular Cell, 2006, 24, 853-865.	4.5	591
53	RNA synthetic biology. Nature Biotechnology, 2006, 24, 545-554.	9.4	332
54	Plug-and-play with RNA. Nature Biotechnology, 2005, 23, 306-307.	9.4	19

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55	MOLECULAR BIOLOGY: Signal Processing in Single Cells. Science, 2005, 307, 1886-1888.	6.0	22
56	Engineered riboregulators enable post-transcriptional control of gene expression. Nature Biotechnology, 2004, 22, 841-847.	9.4	513
57	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
58	Computational studies of gene regulatory networks: in numero molecular biology. Nature Reviews Genetics, 2001, 2, 268-279.	7.7	508