

Marc J Lajoie

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

2,471
citations

566801

15
h-index

887659

17
g-index

18
all docs

18
docs citations

18
times ranked

2886
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomically Recoded Organisms Expand Biological Functions. <i>Science</i> , 2013, 342, 357-360.	6.0	721
2	Biocontainment of genetically modified organisms by synthetic protein design. <i>Nature</i> , 2015, 518, 55-60.	13.7	345
3	Design, synthesis, and testing toward a 57-codon genome. <i>Science</i> , 2016, 353, 819-822.	6.0	251
4	De novo design of bioactive protein switches. <i>Nature</i> , 2019, 572, 205-210.	13.7	190
5	Codon usage of highly expressed genes affects proteome-wide translation efficiency. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4940-E4949.	3.3	177
6	De novo design of modular and tunable protein biosensors. <i>Nature</i> , 2021, 591, 482-487.	13.7	153
7	Rewriting the Genetic Code. <i>Annual Review of Microbiology</i> , 2017, 71, 557-577.	2.9	131
8	Designed protein logic to target cells with precise combinations of surface antigens. <i>Science</i> , 2020, 369, 1637-1643.	6.0	117
9	An orthogonalized platform for genetic code expansion in both bacteria and eukaryotes. <i>Nature Chemical Biology</i> , 2017, 13, 446-450.	3.9	104
10	Improved bacterial recombineering by parallelized protein discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13689-13698.	3.3	82
11	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.	3.3	48
12	Multiplex pairwise assembly of array-derived DNA oligonucleotides. <i>Nucleic Acids Research</i> , 2016, 44, e43-e43.	6.5	48
13	Characterizing the portability of phage-encoded homologous recombination proteins. <i>Nature Chemical Biology</i> , 2021, 17, 394-402.	3.9	36
14	Performance of optimized noncanonical amino acid mutagenesis systems in the absence of release factor 1. <i>Molecular BioSystems</i> , 2016, 12, 1746-1749.	2.9	31
15	Optimizing complex phenotypes through model-guided multiplex genome engineering. <i>Genome Biology</i> , 2017, 18, 100.	3.8	23
16	Millstone: software for multiplex microbial genome analysis and engineering. <i>Genome Biology</i> , 2017, 18, 101.	3.8	5
17	Conditional Recruitment to a DNA-Bound CRISPR-Cas Complex Using a Colocalization-Dependent Protein Switch. <i>ACS Synthetic Biology</i> , 2020, 9, 2316-2323.	1.9	4