

Marc J Lajoie

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

18
papers

1,572
citations

14
h-index

18
g-index

18
ext. papers

2,106
ext. citations

23.3
avg, IF

4.36
L-index

#	Paper	IF	Citations
18	Genomically recoded organisms expand biological functions. <i>Science</i> , 2013 , 342, 357-60	33.3	553
17	Biocontainment of genetically modified organisms by synthetic protein design. <i>Nature</i> , 2015 , 518, 55-60	50.4	255
16	Design, synthesis, and testing toward a 57-codon genome. <i>Science</i> , 2016 , 353, 819-22	33.3	169
15	De novo design of bioactive protein switches. <i>Nature</i> , 2019 , 572, 205-210	50.4	113
14	Rewriting the Genetic Code. <i>Annual Review of Microbiology</i> , 2017 , 71, 557-577	17.5	90
13	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	11.5	81
12	An orthogonalized platform for genetic code expansion in both bacteria and eukaryotes. <i>Nature Chemical Biology</i> , 2017 , 13, 446-450	11.7	62
11	De novo design of modular and tunable protein biosensors. <i>Nature</i> , 2021 , 591, 482-487	50.4	53
10	Designed protein logic to target cells with precise combinations of surface antigens. <i>Science</i> , 2020 , 369, 1637-1643	33.3	48
9	Multiplex pairwise assembly of array-derived DNA oligonucleotides. <i>Nucleic Acids Research</i> , 2016 , 44, e43	20.1	31
8	Emergent rules for codon choice elucidated by editing rare arginine codons in Escherichia coli. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E5588-97	11.5	30
7	Performance of optimized noncanonical amino acid mutagenesis systems in the absence of release factor 1. <i>Molecular BioSystems</i> , 2016 , 12, 1746-9		26
6	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	11.5	25
5	Optimizing complex phenotypes through model-guided multiplex genome engineering. <i>Genome Biology</i> , 2017 , 18, 100	18.3	18
4	Characterizing the portability of phage-encoded homologous recombination proteins. <i>Nature Chemical Biology</i> , 2021 , 17, 394-402	11.7	10
3	Millstone: software for multiplex microbial genome analysis and engineering. <i>Genome Biology</i> , 2017 , 18, 101	18.3	5
2	Improved bacterial recombineering by parallelized protein discovery		2

- 1 Conditional Recruitment to a DNA-Bound CRISPR-Cas Complex Using a Colocalization-Dependent Protein Switch. *ACS Synthetic Biology*, **2020**, 9, 2316-2323 5.7 1