

# Marc J Lajoie

## List of Publications by Year in Descending Order

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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	De novo design of modular and tunable protein biosensors. <i>Nature</i> , <b>2021</b> , 591, 482-487	50.4	53
17	Characterizing the portability of phage-encoded homologous recombination proteins. <i>Nature Chemical Biology</i> , <b>2021</b> , 17, 394-402	11.7	10
16	Improved bacterial recombineering by parallelized protein discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 13689-13698	11.5	25
15	Conditional Recruitment to a DNA-Bound CRISPR-Cas Complex Using a Colocalization-Dependent Protein Switch. <i>ACS Synthetic Biology</i> , <b>2020</b> , 9, 2316-2323	5.7	1
14	Designed protein logic to target cells with precise combinations of surface antigens. <i>Science</i> , <b>2020</b> , 369, 1637-1643	33.3	48
13	De novo design of bioactive protein switches. <i>Nature</i> , <b>2019</b> , 572, 205-210	50.4	113
12	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> , <b>2018</b> , 115, E4940-E4949	11.5	81
11	An orthogonalized platform for genetic code expansion in both bacteria and eukaryotes. <i>Nature Chemical Biology</i> , <b>2017</b> , 13, 446-450	11.7	62
10	Optimizing complex phenotypes through model-guided multiplex genome engineering. <i>Genome Biology</i> , <b>2017</b> , 18, 100	18.3	18
9	Rewriting the Genetic Code. <i>Annual Review of Microbiology</i> , <b>2017</b> , 71, 557-577	17.5	90
8	Millstone: software for multiplex microbial genome analysis and engineering. <i>Genome Biology</i> , <b>2017</b> , 18, 101	18.3	5
7	Design, synthesis, and testing toward a 57-codon genome. <i>Science</i> , <b>2016</b> , 353, 819-22	33.3	169
6	Multiplex pairwise assembly of array-derived DNA oligonucleotides. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e43	20.1	31
5	Performance of optimized noncanonical amino acid mutagenesis systems in the absence of release factor 1. <i>Molecular BioSystems</i> , <b>2016</b> , 12, 1746-9		26
4	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> , <b>2016</b> , 113, E5588-97	11.5	30
3	Biocontainment of genetically modified organisms by synthetic protein design. <i>Nature</i> , <b>2015</b> , 518, 55-60	50.4	255
2	Genomically recoded organisms expand biological functions. <i>Science</i> , <b>2013</b> , 342, 357-60	33.3	553

1 Improved bacterial recombineering by parallelized protein discovery

2