

Philip A Romero

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.

26

papers

1,355

citations

11

h-index

36

g-index

36

ext. papers

1,747

ext. citations

11.7

avg, IF

5.02

L-index

#	Paper	IF	Citations
26	Microfluidic deep mutational scanning of the human executioner caspases reveals differences in structure and regulation.. <i>Cell Death Discovery</i> , 2022 , 8, 7	6.9	1
25	Machine learning to navigate fitness landscapes for protein engineering.. <i>Current Opinion in Biotechnology</i> , 2022 , 75, 102713	11.4	2
24	Neural networks to learn protein sequence-function relationships from deep mutational scanning data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	10
23	Machine learning-guided acyl-ACP reductase engineering for improved in vivo fatty alcohol production. <i>Nature Communications</i> , 2021 , 12, 5825	17.4	7
22	Discovery of human ACE2 variants with altered recognition by the SARS-CoV-2 spike protein. <i>PLoS ONE</i> , 2021 , 16, e0251585	3.7	5
21	Inferring Protein Sequence-Function Relationships with Large-Scale Positive-Unlabeled Learning. <i>Cell Systems</i> , 2021 , 12, 92-101.e8	10.6	10
20	Single-cell nucleic acid profiling in droplets (SNAPD) enables high-throughput analysis of heterogeneous cell populations. <i>Nucleic Acids Research</i> , 2021 , 49, e103	20.1	0
19	Data-driven Protein Engineering 2021 , 133-151		0
18	Active and machine learning-based approaches to rapidly enhance microbial chemical production. <i>Metabolic Engineering</i> , 2021 , 67, 216-226	9.7	2
17	Investigating the dynamics of microbial consortia in spatially structured environments. <i>Nature Communications</i> , 2020 , 11, 2418	17.4	27
16	Discovery of human ACE2 variants with altered recognition by the SARS-CoV-2 spike protein 2020 ,		4
15	Microbial Interaction Network Inference in Microfluidic Droplets. <i>Cell Systems</i> , 2019 , 9, 229-242.e4	10.6	42
14	InVivo Selection of a Computationally Designed SCHEMA AAV Library Yields a Novel Variant for Infection of Adult Neural Stem Cells in the SVZ. <i>Molecular Therapy</i> , 2018 , 26, 304-319	11.7	43
13	Identifying Residue-Residue Contacts via Deep Mutational Scanning. <i>FASEB Journal</i> , 2018 , 32, 792.9	0.9	
12	Dissecting enzyme function with microfluidic-based deep mutational scanning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 7159-64	11.5	131
11	Chimeragenesis of distantly-related proteins by noncontiguous recombination. <i>Protein Science</i> , 2013 , 22, 231-8	6.3	26
10	Efficient sampling of SCHEMA chimera families to identify useful sequence elements. <i>Methods in Enzymology</i> , 2013 , 523, 351-68	1.7	16

9	Navigating the protein fitness landscape with Gaussian processes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E193-201	11.5	153
8	Directed evolution of protein-based neurotransmitter sensors for MRI. <i>Methods in Molecular Biology</i> , 2013 , 995, 193-205	1.4	3
7	Flow focusing geometry generates droplets through a plug and squeeze mechanism. <i>Lab on A Chip</i> , 2012 , 12, 5130-2	7.2	31
6	SCHEMA-designed variants of human Arginase I and II reveal sequence elements important to stability and catalysis. <i>ACS Synthetic Biology</i> , 2012 , 1, 221-8	5.7	44
5	Random field model reveals structure of the protein recombinational landscape. <i>PLoS Computational Biology</i> , 2012 , 8, e1002713	5	8
4	Directed evolution of a magnetic resonance imaging contrast agent for noninvasive imaging of dopamine. <i>Nature Biotechnology</i> , 2010 , 28, 264-70	44.5	128
3	Exploring protein fitness landscapes by directed evolution. <i>Nature Reviews Molecular Cell Biology</i> , 2009 , 10, 866-76	48.7	653
2	Inferring protein sequence-function relationships with large-scale positive-unlabeled learning		3
1	Neural networks to learn protein sequence-function relationships from deep mutational scanning data		6