Philip A Romero

List of Publications by Year
in descending order

24	2,135	567281	677142
papers	citations	15	22
		h-index	g-index

36	36	36	2710
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Microfluidic deep mutational scanning of the human executioner caspases reveals differences in structure and regulation. Cell Death Discovery, 2022, 8, 7.	4.7	9
2	Yeast surface display-based identification of ACE2 mutations that modulate SARS-CoV-2 spike binding across multiple mammalian species. Protein Engineering, Design and Selection, 2022, 35, .	2.1	1
3	Machine learning to navigate fitness landscapes for protein engineering. Current Opinion in Biotechnology, 2022, 75, 102713.	6.6	45
4	Competitive SNP-LAMP probes for rapid and robust single-nucleotide polymorphism detection. Cell Reports Methods, 2022, 2, 100242.	2.9	3
5	Inferring Protein Sequence-Function Relationships with Large-Scale Positive-Unlabeled Learning. Cell Systems, 2021, 12, 92-101.e8.	6.2	33
6	Discovery of human ACE2 variants with altered recognition by the SARS-CoV-2 spike protein. PLoS ONE, 2021, 16, e0251585.	2.5	11
7	Single-cell nucleic acid profiling in droplets (SNAPD) enables high-throughput analysis of heterogeneous cell populations. Nucleic Acids Research, 2021, 49, e103-e103.	14.5	6
8	Active and machine learning-based approaches to rapidly enhance microbial chemical production. Metabolic Engineering, 2021, 67, 216-226.	7.0	15
9	Machine learning-guided acyl-ACP reductase engineering for improved in vivo fatty alcohol production. Nature Communications, 2021, 12, 5825.	12.8	50
10	Neural networks to learn protein sequenceâ€"function relationships from deep mutational scanning data. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	73
11	Investigating the dynamics of microbial consortia in spatially structured environments. Nature Communications, 2020, 11, 2418.	12.8	60
12	Microbial Interaction Network Inference in Microfluidic Droplets. Cell Systems, 2019, 9, 229-242.e4.	6.2	91
13	InÂVivo Selection of a Computationally Designed SCHEMA AAV Library Yields a Novel Variant for Infection of Adult Neural Stem Cells in the SVZ. Molecular Therapy, 2018, 26, 304-319.	8.2	72
14	Identifying Residueâ€"Residue Contacts via Deep Mutational Scanning. FASEB Journal, 2018, 32, 792.9.	0.5	0
15	Dissecting enzyme function with microfluidic-based deep mutational scanning. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7159-7164.	7.1	197
16	Chimeragenesis of distantlyâ€related proteins by noncontiguous recombination. Protein Science, 2013, 22, 231-238.	7.6	31
17	Efficient Sampling of SCHEMA Chimera Families to Identify Useful Sequence Elements. Methods in Enzymology, 2013, 523, 351-368.	1.0	18
18	Navigating the protein fitness landscape with Gaussian processes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E193-201.	7.1	252

#	Article	IF	Citations
19	Directed Evolution of Protein-Based Neurotransmitter Sensors for MRI. Methods in Molecular Biology, 2013, 995, 193-205.	0.9	3
20	Random Field Model Reveals Structure of the Protein Recombinational Landscape. PLoS Computational Biology, 2012, 8, e1002713.	3.2	10
21	Flow focusing geometry generates droplets through a plug and squeeze mechanism. Lab on A Chip, 2012, 12, 5130.	6.0	41
22	SCHEMA-Designed Variants of Human Arginase I and II Reveal Sequence Elements Important to Stability and Catalysis. ACS Synthetic Biology, 2012, 1, 221-228.	3.8	52
23	Directed evolution of a magnetic resonance imaging contrast agent for noninvasive imaging of dopamine. Nature Biotechnology, 2010, 28, 264-270.	17.5	151
24	Exploring protein fitness landscapes by directed evolution. Nature Reviews Molecular Cell Biology, 2009, 10, 866-876.	37.0	890