Philip A Romero

List of Publications by Year
in descending order

24 papers	2,135 citations	566801 15 h-index	676716 22 g-index
36 all docs	36 docs citations	36 times ranked	2710 citing authors

#	Article	IF	Citations
1	Exploring protein fitness landscapes by directed evolution. Nature Reviews Molecular Cell Biology, 2009, 10, 866-876.	16.1	890
2	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.	3.3	252
3	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.	3.3	197
4	Directed evolution of a magnetic resonance imaging contrast agent for noninvasive imaging of dopamine. Nature Biotechnology, 2010, 28, 264-270.	9.4	151
5	Microbial Interaction Network Inference in Microfluidic Droplets. Cell Systems, 2019, 9, 229-242.e4.	2.9	91
6	Neural networks to learn protein sequence–function relationships from deep mutational scanning data. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	73
7	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.	3.7	72
8	Investigating the dynamics of microbial consortia in spatially structured environments. Nature Communications, 2020, 11, 2418.	5.8	60
9	SCHEMA-Designed Variants of Human Arginase I and II Reveal Sequence Elements Important to Stability and Catalysis. ACS Synthetic Biology, 2012, 1, 221-228.	1.9	52
10	Machine learning-guided acyl-ACP reductase engineering for improved in vivo fatty alcohol production. Nature Communications, 2021, 12, 5825.	5.8	50
11	Machine learning to navigate fitness landscapes for protein engineering. Current Opinion in Biotechnology, 2022, 75, 102713.	3.3	45
12	Flow focusing geometry generates droplets through a plug and squeeze mechanism. Lab on A Chip, 2012, 12, 5130.	3.1	41
13	Inferring Protein Sequence-Function Relationships with Large-Scale Positive-Unlabeled Learning. Cell Systems, 2021, 12, 92-101.e8.	2.9	33
14	Chimeragenesis of distantlyâ€related proteins by noncontiguous recombination. Protein Science, 2013, 22, 231-238.	3.1	31
15	Efficient Sampling of SCHEMA Chimera Families to Identify Useful Sequence Elements. Methods in Enzymology, 2013, 523, 351-368.	0.4	18
16	Active and machine learning-based approaches to rapidly enhance microbial chemical production. Metabolic Engineering, 2021, 67, 216-226.	3.6	15
17	Discovery of human ACE2 variants with altered recognition by the SARS-CoV-2 spike protein. PLoS ONE, 2021, 16, e0251585.	1.1	11
18	Random Field Model Reveals Structure of the Protein Recombinational Landscape. PLoS Computational Biology, 2012, 8, e1002713.	1.5	10

#	Article	IF	Citations
19	Microfluidic deep mutational scanning of the human executioner caspases reveals differences in structure and regulation. Cell Death Discovery, 2022, 8, 7.	2.0	9
20	Single-cell nucleic acid profiling in droplets (SNAPD) enables high-throughput analysis of heterogeneous cell populations. Nucleic Acids Research, 2021, 49, e103-e103.	6.5	6
21	Directed Evolution of Protein-Based Neurotransmitter Sensors for MRI. Methods in Molecular Biology, 2013, 995, 193-205.	0.4	3
22	Competitive SNP-LAMP probes for rapid and robust single-nucleotide polymorphism detection. Cell Reports Methods, 2022, 2, 100242.	1.4	3
23	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, .	1.0	1
24	Identifying Residue–Residue Contacts via Deep Mutational Scanning. FASEB Journal, 2018, 32, 792.9.	0.2	0