

Philip A Romero

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

2,135
citations

567281

15
h-index

677142

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. <i>Nature Reviews Molecular Cell Biology</i> , 2009, 10, 866-876.	37.0	890
2	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.	7.1	252
3	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, 7159-7164.	7.1	197
4	Directed evolution of a magnetic resonance imaging contrast agent for noninvasive imaging of dopamine. <i>Nature Biotechnology</i> , 2010, 28, 264-270.	17.5	151
5	Microbial Interaction Network Inference in Microfluidic Droplets. <i>Cell Systems</i> , 2019, 9, 229-242.e4.	6.2	91
6	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, .	7.1	73
7	In Vivo 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.	8.2	72
8	Investigating the dynamics of microbial consortia in spatially structured environments. <i>Nature Communications</i> , 2020, 11, 2418.	12.8	60
9	SCHEMA-Designed Variants of Human Arginase I and II Reveal Sequence Elements Important to Stability and Catalysis. <i>ACS Synthetic Biology</i> , 2012, 1, 221-228.	3.8	52
10	Machine learning-guided acyl-ACP reductase engineering for improved in vivo fatty alcohol production. <i>Nature Communications</i> , 2021, 12, 5825.	12.8	50
11	Machine learning to navigate fitness landscapes for protein engineering. <i>Current Opinion in Biotechnology</i> , 2022, 75, 102713.	6.6	45
12	Flow focusing geometry generates droplets through a plug and squeeze mechanism. <i>Lab on A Chip</i> , 2012, 12, 5130.	6.0	41
13	Inferring Protein Sequence-Function Relationships with Large-Scale Positive-Unlabeled Learning. <i>Cell Systems</i> , 2021, 12, 92-101.e8.	6.2	33
14	Chimeragenesis of distantly related proteins by noncontiguous recombination. <i>Protein Science</i> , 2013, 22, 231-238.	7.6	31
15	Efficient Sampling of SCHEMA Chimera Families to Identify Useful Sequence Elements. <i>Methods in Enzymology</i> , 2013, 523, 351-368.	1.0	18
16	Active and machine learning-based approaches to rapidly enhance microbial chemical production. <i>Metabolic Engineering</i> , 2021, 67, 216-226.	7.0	15
17	Discovery of human ACE2 variants with altered recognition by the SARS-CoV-2 spike protein. <i>PLoS ONE</i> , 2021, 16, e0251585.	2.5	11
18	Random Field Model Reveals Structure of the Protein Recombinational Landscape. <i>PLoS Computational Biology</i> , 2012, 8, e1002713.	3.2	10

#	ARTICLE	IF	CITATIONS
19	Microfluidic deep mutational scanning of the human executioner caspases reveals differences in structure and regulation. <i>Cell Death Discovery</i> , 2022, 8, 7.	4.7	9
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-e103.	14.5	6
21	Directed Evolution of Protein-Based Neurotransmitter Sensors for MRI. <i>Methods in Molecular Biology</i> , 2013, 995, 193-205.	0.9	3
22	Competitive SNP-LAMP probes for rapid and robust single-nucleotide polymorphism detection. <i>Cell Reports Methods</i> , 2022, 2, 100242.	2.9	3
23	Yeast surface display-based identification of ACE2 mutations that modulate SARS-CoV-2 spike binding across multiple mammalian species. <i>Protein Engineering, Design and Selection</i> , 2022, 35, .	2.1	1
24	Identifying Residue-Residue Contacts via Deep Mutational Scanning. <i>FASEB Journal</i> , 2018, 32, 792.9.	0.5	0