Philip A Romero

List of Publications by Citations

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	Exploring protein fitness landscapes by directed evolution. *Nature Reviews Molecular Cell Biology*, **2009**, 10, 866-76	48.7	653
25	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	11.5	153
24	Dissecting enzyme function with microfluidic-based deep mutational scanning. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 7159-64	11.5	131
23	Directed evolution of a magnetic resonance imaging contrast agent for noninvasive imaging of dopamine. *Nature Biotechnology*, **2010**, 28, 264-70	44.5	128
22	SCHEMA-designed variants of human Arginase I and II reveal sequence elements important to stability and catalysis. *ACS Synthetic Biology*, **2012**, 1, 221-8	5.7	44
21	In Vivo 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	11.7	43
20	Microbial Interaction Network Inference in Microfluidic Droplets. *Cell Systems*, **2019**, 9, 229-242.e4	10.6	42
19	Flow focusing geometry generates droplets through a plug and squeeze mechanism. *Lab on A Chip*, **2012**, 12, 5130-2	7.2	31
18	Investigating the dynamics of microbial consortia in spatially structured environments. *Nature Communications*, **2020**, 11, 2418	17.4	27
17	Chimeragenesis of distantly-related proteins by noncontiguous recombination. *Protein Science*, **2013**, 22, 231-8	6.3	26
16	Efficient sampling of SCHEMA chimera families to identify useful sequence elements. *Methods in Enzymology*, **2013**, 523, 351-68	1.7	16
15	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,	11.5	10
14	Inferring Protein Sequence-Function Relationships with Large-Scale Positive-Unlabeled Learning. *Cell Systems*, **2021**, 12, 92-101.e8	10.6	10
13	Random field model reveals structure of the protein recombinational landscape. *PLoS Computational Biology*, **2012**, 8, e1002713	5	8
12	Machine learning-guided acyl-ACP reductase engineering for improved in vivo fatty alcohol production. *Nature Communications*, **2021**, 12, 5825	17.4	7
11	Neural networks to learn protein sequence-function relationships from deep mutational scanning data		6
10	Discovery of human ACE2 variants with altered recognition by the SARS-CoV-2 spike protein. *PLoS ONE*, **2021**, 16, e0251585	3.7	5

LIST OF PUBLICATIONS

9	Discovery of human ACE2 variants with altered recognition by the SARS-CoV-2 spike protein **2020**,		4
8	Directed evolution of protein-based neurotransmitter sensors for MRI. *Methods in Molecular Biology*, **2013**, 995, 193-205	1.4	3
7	Inferring protein sequence-function relationships with large-scale positive-unlabeled learning		3
6	Active and machine learning-based approaches to rapidly enhance microbial chemical production. *Metabolic Engineering*, **2021**, 67, 216-226	9.7	2
5	Machine learning to navigate fitness landscapes for protein engineering.. *Current Opinion in Biotechnology*, **2022**, 75, 102713	11.4	2
4	Microfluidic deep mutational scanning of the human executioner caspases reveals differences in structure and regulation.. *Cell Death Discovery*, **2022**, 8, 7	6.9	1
3	Single-cell nucleic acid profiling in droplets (SNAPD) enables high-throughput analysis of heterogeneous cell populations. *Nucleic Acids Research*, **2021**, 49, e103	20.1	0
2	Data-driven Protein Engineering **2021**, 133-151		0
1	Identifying Residue-Residue Contacts via Deep Mutational Scanning. *FASEB Journal*, **2018**, 32, 792.9	0.9	