

# Robert P St Onge

## List of Publications by Year in descending order

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Version: 2024-02-01

24  
papers

4,424  
citations

471371

17  
h-index

610775

24  
g-index

27  
all docs

27  
docs citations

27  
times ranked

6374  
citing authors

#	ARTICLE	IF	CITATIONS
1	A CRISPR Interference Screen of Essential Genes Reveals that Proteasome Regulation Dictates Acetic Acid Tolerance in <i>Saccharomyces cerevisiae</i> . <i>MSystems</i> , 2021, 6, e0041821.	1.7	12
2	Community members in activated sludge as determined by molecular probe technology. <i>Water Research</i> , 2020, 168, 115104.	5.3	4
3	Thioesterase-Catalyzed Aminoacylation and Thiolation of Polyketides in Fungi. <i>Journal of the American Chemical Society</i> , 2019, 141, 8198-8206.	6.6	20
4	PH-domain-binding inhibitors of nucleotide exchange factor BRAG2 disrupt Arf GTPase signaling. <i>Nature Chemical Biology</i> , 2019, 15, 358-366.	3.9	22
5	Improved discovery of genetic interactions using CRISPRiSeq across multiple environments. <i>Genome Research</i> , 2019, 29, 668-681.	2.4	34
6	A biosensor-based approach reveals links between efflux pump expression and cell cycle regulation in pleiotropic drug resistance of yeast. <i>Journal of Biological Chemistry</i> , 2019, 294, 1257-1266.	1.6	4
7	HEx: A heterologous expression platform for the discovery of fungal natural products. <i>Science Advances</i> , 2018, 4, eaar5459.	4.7	167
8	Multiplexed precision genome editing with trackable genomic barcodes in yeast. <i>Nature Biotechnology</i> , 2018, 36, 512-520.	9.4	138
9	A scalable double-barcode sequencing platform for characterization of dynamic protein-protein interactions. <i>Nature Communications</i> , 2017, 8, 15586.	5.8	35
10	A method for high-throughput production of sequence-verified <i>scp</i> DNA libraries and strain collections. <i>Molecular Systems Biology</i> , 2017, 13, 913.	3.2	41
11	Quantitative analysis of protein interaction network dynamics in yeast. <i>Molecular Systems Biology</i> , 2017, 13, 934.	3.2	41
12	Distinct patterns of Cas9 mismatch tolerance <i>in vitro</i> and <i>in vivo</i> . <i>Nucleic Acids Research</i> , 2016, 44, 5365-5377.	6.5	62
13	Identification of Chemical-Genetic Interactions via Parallel Analysis of Barcoded Yeast Strains. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot088054.	0.2	4
14	Quantitative CRISPR interference screens in yeast identify chemical-genetic interactions and new rules for guide RNA design. <i>Genome Biology</i> , 2016, 17, 45.	3.8	165
15	Mapping the Cellular Response to Small Molecules Using Chemogenomic Fitness Signatures. <i>Science</i> , 2014, 344, 208-211.	6.0	217
16	A functional screen for copper homeostasis genes identifies a pharmacologically tractable cellular system. <i>BMC Genomics</i> , 2014, 15, 263.	1.2	30
17	Targeted and Highly Multiplexed Detection of Microorganisms by Employing an Ensemble of Molecular Probes. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4153-4161.	1.4	6
18	PITPs as targets for selectively interfering with phosphoinositide signaling in cells. <i>Nature Chemical Biology</i> , 2014, 10, 76-84.	3.9	39

#	ARTICLE	IF	CITATIONS
19	Forward Chemical Genetics in Yeast for Discovery of Chemical Probes Targeting Metabolism. <i>Molecules</i> , 2012, 17, 13098-13115.	1.7	14
20	Multiplex assay for condition-dependent changes in protein-protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9213-9218.	3.3	62
21	The Genetic Landscape of a Cell. <i>Science</i> , 2010, 327, 425-431.	6.0	1,937
22	Highly-multiplexed barcode sequencing: an efficient method for parallel analysis of pooled samples. <i>Nucleic Acids Research</i> , 2010, 38, e142-e142.	6.5	184
23	The Chemical Genomic Portrait of Yeast: Uncovering a Phenotype for All Genes. <i>Science</i> , 2008, 320, 362-365.	6.0	892
24	Systematic pathway analysis using high-resolution fitness profiling of combinatorial gene deletions. <i>Nature Genetics</i> , 2007, 39, 199-206.	9.4	294