Robert P St Onge

List of Publications by Year
in descending order

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	The Genetic Landscape of a Cell. Science, 2010, 327, 425-431.	6.0	1,937
2	The Chemical Genomic Portrait of Yeast: Uncovering a Phenotype for All Genes. Science, 2008, 320, 362-365.	6.0	892
3	Systematic pathway analysis using high-resolution fitness profiling of combinatorial gene deletions. Nature Genetics, 2007, 39, 199-206.	9.4	294
4	Mapping the Cellular Response to Small Molecules Using Chemogenomic Fitness Signatures. Science, 2014, 344, 208-211.	6.0	217
5	Highly-multiplexed barcode sequencing: an efficient method for parallel analysis of pooled samples. Nucleic Acids Research, 2010, 38, e142-e142.	6.5	184
6	HEx: A heterologous expression platform for the discovery of fungal natural products. Science Advances, 2018, 4, eaar5459.	4.7	167
7	Quantitative CRISPR interference screens in yeast identify chemical-genetic interactions and new rules for guide RNA design. Genome Biology, 2016, 17, 45.	3.8	165
8	Multiplexed precision genome editing with trackable genomic barcodes in yeast. Nature Biotechnology, 2018, 36, 512-520.	9.4	138
9	Multiplex assay for condition-dependent changes in proteinâ€“protein interactions. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9213-9218.	3.3	62
10	Distinct patterns of Cas9 mismatch tolerancein vitroandin vivo. Nucleic Acids Research, 2016, 44, 5365-5377.	6.5	62
11	A method for highâ€throughput production of sequenceâ€verified <scp>DNA</scp> libraries and strain collections. Molecular Systems Biology, 2017, 13, 913.	3.2	41
12	Quantitative analysis of protein interaction network dynamics in yeast. Molecular Systems Biology, 2017, 13, 934.	3.2	41
13	PITPs as targets for selectively interfering with phosphoinositide signaling in cells. Nature Chemical Biology, 2014, 10, 76-84.	3.9	39
14	A scalable double-barcode sequencing platform for characterization of dynamic protein-protein interactions. Nature Communications, 2017, 8, 15586.	5.8	35
15	Improved discovery of genetic interactions using CRISPRiSeq across multiple environments. Genome Research, 2019, 29, 668-681.	2.4	34
16	A functional screen for copper homeostasis genes identifies a pharmacologically tractable cellular system. BMC Genomics, 2014, 15, 263.	1.2	30
17	PH-domain-binding inhibitors of nucleotide exchange factor BRAG2 disrupt Arf GTPase signaling. Nature Chemical Biology, 2019, 15, 358-366.	3.9	22
18	Thioesterase-Catalyzed Aminoacylation and Thiolation of Polyketides in Fungi. Journal of the American Chemical Society, 2019, 141, 8198-8206.	6.6	20

#	Article	IF	Citations
19	Forward Chemical Genetics in Yeast for Discovery of Chemical Probes Targeting Metabolism. Molecules, 2012, 17, 13098-13115.	1.7	14
20	A CRISPR Interference Screen of Essential Genes Reveals that Proteasome Regulation Dictates Acetic Acid Tolerance in Saccharomyces cerevisiae. MSystems, 2021, 6, e0041821.	1.7	12
21	Targeted and Highly Multiplexed Detection of Microorganisms by Employing an Ensemble of Molecular Probes. Applied and Environmental Microbiology, 2014, 80, 4153-4161.	1.4	6
22	Identification of Chemicalâ€“Genetic Interactions via Parallel Analysis of Barcoded Yeast Strains. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot088054.	0.2	4
23	A biosensor-based approach reveals links between efflux pump expression and cell cycle regulation in pleiotropic drug resistance of yeast. Journal of Biological Chemistry, 2019, 294, 1257-1266.	1.6	4
24	Community members in activated sludge as determined by molecular probe technology. Water Research, 2020, 168, 115104.	5.3	4