Omar Wagih

List of Publications by Year
in descending order

17 papers	1,844 citations	567281 15 h-index	888059 17 g-index
22 all docs	22 docs citations	22 times ranked	3840 citing authors

#	Article	IF	Citations
1	ggseqlogo: a versatile R package for drawing sequence logos. Bioinformatics, 2017, 33, 3645-3647.	4.1	632
2	Quantitative CRISPR interference screens in yeast identify chemical-genetic interactions and new rules for guide RNA design. Genome Biology, 2016, 17, 45.	8.8	165
3	The mutational landscape of phosphorylation signaling in cancer. Scientific Reports, 2013, 3, 2651.	3.3	149
4	SGAtools: one-stop analysis and visualization of array-based genetic interaction screens. Nucleic Acids Research, 2013, 41, W591-W596.	14.5	141
5	gitter: A Robust and Accurate Method for Quantification of Colony Sizes From Plate Images. G3: Genes, Genomes, Genetics, 2014, 4, 547-552.	1.8	109
6	Quantitative Genome-Wide Genetic Interaction Screens Reveal Global Epistatic Relationships of Protein Complexes in Escherichia coli. PLoS Genetics, 2014, 10, e1004120.	3.5	96
7	A resource of variant effect predictions of single nucleotide variants in model organisms. Molecular Systems Biology, 2018, 14, e8430.	7.2	84
8	MIMP: predicting the impact of mutations on kinase-substrate phosphorylation. Nature Methods, 2015, 12, 531-533.	19.0	75
9	Evolutionary Constraint and Disease Associations of Post-Translational Modification Sites in Human Genomes. PLoS Genetics, 2015, 11, e1004919.	3.5	69
10	Microevolution of Serial Clinical Isolates of *Cryptococcus neoformans* var. *grubii* and *C. Âgattii*. MBio, 2017, 8, .	4.1	69
11	Uncovering Phosphorylation-Based Specificities through Functional Interaction Networks. Molecular and Cellular Proteomics, 2016, 15, 236-245.	3.8	68
12	Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. PLoS Computational Biology, 2017, 13, e1005297.	3.2	51
13	Phenotype inference in an Escherichia coli strain panel. ELife, 2017, 6, .	6.0	38
14	Conditional Epistatic Interaction Maps Reveal Global Functional Rewiring of Genome Integrity Pathways in Escherichia coli. Cell Reports, 2016, 14, 648-661.	6.4	34
15	Identifications of Putative PKA Substrates with Quantitative Phosphoproteomics and Primary-Sequence-Based Scoring. Journal of Proteome Research, 2017, 16, 1825-1830.	3.7	26
16	Prediction of Functionally Important Phospho-Regulatory Events in Xenopus laevis Oocytes. PLoS Computational Biology, 2015, 11, e1004362.	3.2	14
17	Genetic Interaction Scoring Procedure for Bacterial Species. Advances in Experimental Medicine and Biology, 2015, 883, 169-185.	1.6	2