

# Omar Wagih

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3430613/publications.pdf>

Version: 2024-02-01

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