

# Joana P Gonçalves

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/513366/publications.pdf>

Version: 2024-02-01

13  
papers

660  
citations

933447

10  
h-index

1125743

13  
g-index

13  
all docs

13  
docs citations

13  
times ranked

1194  
citing authors

#	ARTICLE	IF	CITATIONS
1	The YEASTRACT database: an upgraded information system for the analysis of gene and genomic transcription regulation in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2014, 42, D161-D166.	14.5	215
2	Candidate gene prioritization by network analysis of differential expression using machine learning approaches. <i>BMC Bioinformatics</i> , 2010, 11, 460.	2.6	95
3	Predicting disease associations via biological network analysis. <i>BMC Bioinformatics</i> , 2014, 15, 304.	2.6	86
4	PINTA: a web server for network-based gene prioritization from expression data. <i>Nucleic Acids Research</i> , 2011, 39, W334-W338.	14.5	62
5	BiGGEsTS: integrated environment for biclustering analysis of time series gene expression data. <i>BMC Research Notes</i> , 2009, 2, 124.	1.4	57
6	Multiplexed Cas9 targeting reveals genomic location effects and gRNA-based staggered breaks influencing mutation efficiency. <i>Nature Communications</i> , 2019, 10, 1598.	12.8	50
7	Interactogeneous: Disease Gene Prioritization Using Heterogeneous Networks and Full Topology Scores. <i>PLoS ONE</i> , 2012, 7, e49634.	2.5	32
8	TFRank: network-based prioritization of regulatory associations underlying transcriptional responses. <i>Bioinformatics</i> , 2011, 27, 3149-3157.	4.1	17
9	LateBiclustering: Efficient Heuristic Algorithm for Time-Lagged Bicluster Identification. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 801-813.	3.0	15
10	Polar Mapper : a computational tool for integrated visualization of protein interaction networks and mRNA expression data. <i>Journal of the Royal Society Interface</i> , 2009, 6, 881-896.	3.4	12
11	Regulatory Snapshots: Integrative Mining of Regulatory Modules from Expression Time Series and Regulatory Networks. <i>PLoS ONE</i> , 2012, 7, e35977.	2.5	10
12	e-BiMotif: Combining Sequence Alignment and Biclustering to Unravel Structured Motifs. <i>Advances in Intelligent and Soft Computing</i> , 2010, , 181-191.	0.2	8
13	AliBiMotif: Integrating alignment and biclustering to unravel transcription factor binding sites in DNA sequences. <i>International Journal of Data Mining and Bioinformatics</i> , 2012, 6, 196.	0.1	1