

Roberto Visintainer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7798389/publications.pdf>

Version: 2024-02-01

15
papers

1,615
citations

1307594

7
h-index

1199594

12
g-index

16
all docs

16
docs citations

16
times ranked

3680
citing authors

#	ARTICLE	IF	CITATIONS
1	Stability in GRN Inference. <i>Methods in Molecular Biology</i> , 2019, 1883, 323-346.	0.9	1
2	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. <i>American Journal of Human Genetics</i> , 2018, 102, 1169-1184.	6.2	128
3	The interplay between individual social behavior and clinical symptoms in small clustered groups. <i>BMC Infectious Diseases</i> , 2017, 17, 521.	2.9	7
4	DTW-MIC Coexpression Networks from Time-Course Data. <i>PLoS ONE</i> , 2016, 11, e0152648.	2.5	7
5	Differential Network Analysis and Graph Classification: A Glocal Approach. , 2016, , 17-30.		2
6	DGW: an exploratory data analysis tool for clustering and visualisation of epigenomic marks. <i>BMC Bioinformatics</i> , 2016, 17, 447.	2.6	3
7	The HIM glocal metric and kernel for network comparison and classification. , 2015, , .		23
8	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. <i>Nature Biotechnology</i> , 2014, 32, 926-932.	17.5	420
9	A Machine Learning Pipeline for Identification of Discriminant Pathways. , 2014, , 951-968.		1
10	Stability Indicators in Network Reconstruction. <i>PLoS ONE</i> , 2014, 9, e89815.	2.5	20
11	minerva and minepy: a C engine for the MINE suite and its R, Python and MATLAB wrappers. <i>Bioinformatics</i> , 2013, 29, 407-408.	4.1	174
12	A Machine Learning Pipeline for Discriminant Pathways Identification. <i>Lecture Notes in Computer Science</i> , 2012, , 36-48.	1.3	3
13	Algebraic Comparison of Partial Lists in Bioinformatics. <i>PLoS ONE</i> , 2012, 7, e36540.	2.5	21
14	RegnANN: Reverse Engineering Gene Networks Using Artificial Neural Networks. <i>PLoS ONE</i> , 2011, 6, e28646.	2.5	8
15	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	17.5	795