

Yoichi Takenaka

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/11453455/yoichi-takenaka-publications-by-year.pdf>

Version: 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

12
papers

1,542
citations

3
h-index

15
g-index

15
ext. papers

2,033
ext. citations

10.5
avg, IF

2.34
L-index

#	Paper	IF	Citations
12	Automated transition analysis of activated gene regulation during diauxic nutrient shift in <i>Escherichia coli</i> and adipocyte differentiation in mouse cells. <i>BMC Bioinformatics</i> , 2018 , 19, 89	3.6	
11	Diagnostic Assessment of Deep Learning Algorithms for Detection of Lymph Node Metastases in Women With Breast Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2017 , 318, 2199-2210	27.4	1165
10	Comparative Analysis of Transformation Methods for Gene Expression Profiles in Breast Cancer Datasets 2016 ,		1
9	Detecting shifts in gene regulatory networks during time-course experiments at single-time-point temporal resolution. <i>Journal of Bioinformatics and Computational Biology</i> , 2015 , 13, 1543002	1	2
8	Metagenome fragment classification based on multiple motif-occurrence profiles. <i>PeerJ</i> , 2014 , 2, e559	3.1	2
7	Improved Prediction Method for Protein Interactions Using Both Structural and Functional Characteristics of Proteins. <i>IPSJ Transactions on Bioinformatics</i> , 2010 , 3, 10-23	1.3	1
6	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009 , 41, 553-62	36.3	356
5	A Combination Method of the Tanimoto Coefficient and Proximity Measure of Random Forest for Compound Activity Prediction. <i>IPSJ Digital Courier</i> , 2008 , 4, 238-249		1
4	A Distributed-Processing System for Accelerating Biological Research Using Data-Staging. <i>IPSJ Digital Courier</i> , 2008 , 4, 250-256		
3	GO based tissue specific functions of mouse using countable gene expression profiles. <i>Genome Informatics</i> , 2007 , 19, 154-65		
2	An expanded maximum neural network algorithm for a channel assignment problem in cellular radio networks. <i>Electronics and Communications in Japan, Part III: Fundamental Electronic Science (English Translation of Denshi Tsushin Gakkai Ronbunshi)</i> , 2000 , 83, 11-19		1
1	A maximum neural network approach for N-queens problems. <i>Biological Cybernetics</i> , 1997 , 76, 251-255	2.8	13