

Juan Nunez-Iglesias

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5860243/publications.pdf>

Version: 2024-02-01

24
papers

22,396
citations

687363

13
h-index

713466

21
g-index

27
all docs

27
docs citations

27
times ranked

34260
citing authors

#	ARTICLE	IF	CITATIONS
1	SciPy 1.0: fundamental algorithms for scientific computing in Python. <i>Nature Methods</i> , 2020, 17, 261-272.	19.0	17,539
2	scikit-image: image processing in Python. <i>PeerJ</i> , 2014, 2, e453.	2.0	3,711
3	Joint Genome-Wide Profiling of miRNA and mRNA Expression in Alzheimer's Disease Cortex Reveals Altered miRNA Regulation. <i>PLoS ONE</i> , 2010, 5, e8898.	2.5	320
4	Synaptic circuits and their variations within different columns in the visual system of <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13711-13716.	7.1	254
5	Functional annotation and network reconstruction through cross-platform integration of microarray data. <i>Nature Biotechnology</i> , 2005, 23, 238-243.	17.5	137
6	Machine Learning of Hierarchical Clustering to Segment 2D and 3D Images. <i>PLoS ONE</i> , 2013, 8, e71715.	2.5	103
7	Gene Aging Nexus: a web database and data mining platform for microarray data on aging. <i>Nucleic Acids Research</i> , 2007, 35, D756-D759.	14.5	49
8	An integrative approach to characterize disease-specific pathways and their coordination: a case study in cancer. <i>BMC Genomics</i> , 2008, 9, S12.	2.8	43
9	Graph-based active learning of agglomeration (GALA): a Python library to segment 2D and 3D neuroimages. <i>Frontiers in Neuroinformatics</i> , 2014, 8, 34.	2.5	42
10	A new Python library to analyse skeleton images confirms malaria parasite remodelling of the red blood cell membrane skeleton. <i>PeerJ</i> , 2018, 6, e4312.	2.0	41
11	Recruitment of the Adaptor Protein 2 Complex by the Human Immunodeficiency Virus Type 2 Envelope Protein Is Necessary for High Levels of Virus Release. <i>Journal of Virology</i> , 2006, 80, 2924-2932.	3.4	35
12	The knob protein KAHRP assembles into a ring-shaped structure that underpins virulence complex assembly. <i>PLoS Pathogens</i> , 2019, 15, e1007761.	4.7	31
13	Aurora Kinase B, a novel regulator of TERF1 binding and telomeric integrity. <i>Nucleic Acids Research</i> , 2017, 45, 12340-12353.	14.5	18
14	Integrative Array Analyzer: a software package for analysis of cross-platform and cross-species microarray data. <i>Bioinformatics</i> , 2006, 22, 1665-1667.	4.1	13
15	Electron Microscopy Reconstruction of Brain Structure Using Sparse Representations Over Learned Dictionaries. <i>IEEE Transactions on Medical Imaging</i> , 2013, 32, 2179-2188.	8.9	12
16	An integrative modular approach to systematically predict gene-phenotype associations. <i>BMC Bioinformatics</i> , 2010, 11, S62.	2.6	10
17	An Integrative Network Approach to Map the Transcriptome to the Phenome. <i>Journal of Computational Biology</i> , 2009, 16, 1023-1034.	1.6	9
18	Frequent Pattern Discovery in Multiple Biological Networks: Patterns and Algorithms. <i>Statistics in Biosciences</i> , 2012, 4, 157-176.	1.2	4

#	ARTICLE	IF	CITATIONS
19	Pattern Mining Across Many Massive Biological Networks. , 2012, , 137-170.		4
20	An Integrative Network Approach to Map the Transcriptome to the Phenome. , 2008, , 232-245.		3
21	A novel method for radial hydride analysis in zirconium alloys: HAPPy. Journal of Nuclear Materials, 2022, 559, 153442.	2.7	3
22	Multimodal imaging reveals membrane skeleton reorganisation during reticulocyte maturation and differences in dimple and rim regions of mature erythrocytes. Journal of Structural Biology: X, 2022, 6, 100056.	1.3	2
23	Usefulness and limitations of dK random graph models to predict interactions and functional homogeneity in biological networks under a pseudo-likelihood parameter estimation approach. BMC Bioinformatics, 2009, 10, 277.	2.6	1
24	Betamax: Towards Optimal Sampling Strategies for High-Throughput Screens. Journal of Computational Biology, 2012, 19, 776-784.	1.6	1