Juan Nunez-Iglesias

List of Publications by Year
in descending order

24 papers	22,396 citations	686830 13 h-index	713013 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. Nature Methods, 2020, 17, 261-272.	9.0	17,539
2	scikit-image: image processing in Python. PeerJ, 2014, 2, e453.	0.9	3,711
3	Joint Genome-Wide Profiling of miRNA and mRNA Expression in Alzheimer's Disease Cortex Reveals Altered miRNA Regulation. PLoS ONE, 2010, 5, e8898.	1.1	320
4	Synaptic circuits and their variations within different columns in the visual system of *Drosophila*. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13711-13716.	3.3	254
5	Functional annotation and network reconstruction through cross-platform integration of microarray data. Nature Biotechnology, 2005, 23, 238-243.	9.4	137
6	Machine Learning of Hierarchical Clustering to Segment 2D and 3D Images. PLoS ONE, 2013, 8, e71715.	1.1	103
7	Gene Aging Nexus: a web database and data mining platform for microarray data on aging. Nucleic Acids Research, 2007, 35, D756-D759.	6.5	49
8	An integrative approach to characterize disease-specific pathways and their coordination: a case study in cancer. BMC Genomics, 2008, 9, S12.	1.2	43
9	Graph-based active learning of agglomeration (GALA): a Python library to segment 2D and 3D neuroimages. Frontiers in Neuroinformatics, 2014, 8, 34.	1.3	42
10	A new Python library to analyse skeleton images confirms malaria parasite remodelling of the red blood cell membrane skeleton. PeerJ, 2018, 6, e4312.	0.9	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. Journal of Virology, 2006, 80, 2924-2932.	1.5	35
12	The knob protein KAHRP assembles into a ring-shaped structure that underpins virulence complex assembly. PLoS Pathogens, 2019, 15, e1007761.	2.1	31
13	Aurora Kinase B, a novel regulator of TERF1 binding and telomeric integrity. Nucleic Acids Research, 2017, 45, 12340-12353.	6.5	18
14	Integrative Array Analyzer: a software package for analysis of cross-platform and cross-species microarray data. Bioinformatics, 2006, 22, 1665-1667.	1.8	13
15	Electron Microscopy Reconstruction of Brain Structure Using Sparse Representations Over Learned Dictionaries. IEEE Transactions on Medical Imaging, 2013, 32, 2179-2188.	5.4	12
16	An integrative modular approach to systematically predict gene-phenotype associations. BMC Bioinformatics, 2010, 11, S62.	1.2	10
17	An Integrative Network Approach to Map the Transcriptome to the Phenome. Journal of Computational Biology, 2009, 16, 1023-1034.	0.8	9
18	Frequent Pattern Discovery in Multiple Biological Networks: Patterns and Algorithms. Statistics in Biosciences, 2012, 4, 157-176.	0.6	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.	1.3	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.	0.7	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.	1.2	1
24	Betamax: Towards Optimal Sampling Strategies for High-Throughput Screens. Journal of Computational Biology, 2012, 19, 776-784.	0.8	1