

# 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

686830

13  
h-index

713013

21  
g-index

27  
all docs

27  
docs citations

27  
times ranked

34260  
citing authors

#	ARTICLE	IF	CITATIONS
1	Multimodal imaging reveals membrane skeleton reorganisation during reticulocyte maturation and differences in dimple and rim regions of mature erythrocytes. <i>Journal of Structural Biology</i> : X, 2022, 6, 100056.	0.7	2
2	A novel method for radial hydride analysis in zirconium alloys: HAPPy. <i>Journal of Nuclear Materials</i> , 2022, 559, 153442.	1.3	3
3	SciPy 1.0: fundamental algorithms for scientific computing in Python. <i>Nature Methods</i> , 2020, 17, 261-272.	9.0	17,539
4	The knob protein KAHRP assembles into a ring-shaped structure that underpins virulence complex assembly. <i>PLoS Pathogens</i> , 2019, 15, e1007761.	2.1	31
5	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.	0.9	41
6	Aurora Kinase B, a novel regulator of TERF1 binding and telomeric integrity. <i>Nucleic Acids Research</i> , 2017, 45, 12340-12353.	6.5	18
7	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.	3.3	254
8	scikit-image: image processing in Python. <i>PeerJ</i> , 2014, 2, e453.	0.9	3,711
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.	1.3	42
10	Electron Microscopy Reconstruction of Brain Structure Using Sparse Representations Over Learned Dictionaries. <i>IEEE Transactions on Medical Imaging</i> , 2013, 32, 2179-2188.	5.4	12
11	Machine Learning of Hierarchical Clustering to Segment 2D and 3D Images. <i>PLoS ONE</i> , 2013, 8, e71715.	1.1	103
12	Betamax: Towards Optimal Sampling Strategies for High-Throughput Screens. <i>Journal of Computational Biology</i> , 2012, 19, 776-784.	0.8	1
13	Frequent Pattern Discovery in Multiple Biological Networks: Patterns and Algorithms. <i>Statistics in Biosciences</i> , 2012, 4, 157-176.	0.6	4
14	Pattern Mining Across Many Massive Biological Networks. , 2012, , 137-170.		4
15	An integrative modular approach to systematically predict gene-phenotype associations. <i>BMC Bioinformatics</i> , 2010, 11, S62.	1.2	10
16	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.	1.1	320
17	An Integrative Network Approach to Map the Transcriptome to the Phenome. <i>Journal of Computational Biology</i> , 2009, 16, 1023-1034.	0.8	9
18	Usefulness and limitations of dK random graph models to predict interactions and functional homogeneity in biological networks under a pseudo-likelihood parameter estimation approach. <i>BMC Bioinformatics</i> , 2009, 10, 277.	1.2	1

#	ARTICLE	IF	CITATIONS
19	An integrative approach to characterize disease-specific pathways and their coordination: a case study in cancer. <i>BMC Genomics</i> , 2008, 9, S12.	1.2	43
20	An Integrative Network Approach to Map the Transcriptome to the Phenome. , 2008, , 232-245.		3
21	Gene Aging Nexus: a web database and data mining platform for microarray data on aging. <i>Nucleic Acids Research</i> , 2007, 35, D756-D759.	6.5	49
22	Integrative Array Analyzer: a software package for analysis of cross-platform and cross-species microarray data. <i>Bioinformatics</i> , 2006, 22, 1665-1667.	1.8	13
23	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.	1.5	35
24	Functional annotation and network reconstruction through cross-platform integration of microarray data. <i>Nature Biotechnology</i> , 2005, 23, 238-243.	9.4	137