

# Nicola Soranzo

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8917606/publications.pdf>

Version: 2024-02-01

24  
papers

6,587  
citations

777949

13  
h-index

799663

21  
g-index

35  
all docs

35  
docs citations

35  
times ranked

15446  
citing authors

#	ARTICLE	IF	CITATIONS
1	Expanding the Galaxy's reference data. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	0
2	RNA-Seq Data Analysis in Galaxy. <i>Methods in Molecular Biology</i> , 2021, 2284, 367-392.	0.4	23
3	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. <i>GigaScience</i> , 2020, 9, .	3.3	14
4	A Galaxy-based training resource for single-cell RNA-sequencing quality control and analyses. <i>GigaScience</i> , 2019, 8, .	3.3	4
5	GeneSeqToFamily: a Galaxy workflow to find gene families based on the Ensembl Compara GeneTrees pipeline. <i>GigaScience</i> , 2018, 7, 1-10.	3.3	9
6	Aequatus: an open-source homology browser. <i>GigaScience</i> , 2018, 7, .	3.3	1
7	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, W537-W544.	6.5	3,003
8	Bioconda: sustainable and comprehensive software distribution for the life sciences. <i>Nature Methods</i> , 2018, 15, 475-476.	9.0	714
9	Community-Driven Data Analysis Training for Biology. <i>Cell Systems</i> , 2018, 6, 752-758.e1.	2.9	141
10	Practical Computational Reproducibility in the Life Sciences. <i>Cell Systems</i> , 2018, 6, 631-635.	2.9	100
11	ReGaTE: Registration of Galaxy Tools in Elixir. <i>GigaScience</i> , 2017, 6, 1-4.	3.3	14
12	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, W3-W10.	6.5	1,751
13	Transcriptomic profiles of aging in purified human immune cells. <i>BMC Genomics</i> , 2015, 16, 333.	1.2	58
14	Alterations of a Cellular Cholesterol Metabolism Network Are a Molecular Feature of Obesity-Related Type 2 Diabetes and Cardiovascular Disease. <i>Diabetes</i> , 2015, 64, 3464-3474.	0.3	82
15	NCBI BLAST+ integrated into Galaxy. <i>GigaScience</i> , 2015, 4, 39.	3.3	213
16	A Hadoop-Galaxy adapter for user-friendly and scalable data-intensive bioinformatics in Galaxy. , 2014, , .		5
17	Orione, a web-based framework for NGS analysis in microbiology. <i>Bioinformatics</i> , 2014, 30, 1928-1929.	1.8	139
18	Network topology and parameter estimation: from experimental design methods to gene regulatory network kinetics using a community based approach. <i>BMC Systems Biology</i> , 2014, 8, 13.	3.0	62

#	ARTICLE	IF	CITATIONS
19	Simulation of the Benchmark Datasets. , 2013, , 1-8.		0
20	Simulating systems genetics data with SysGenSIM. Bioinformatics, 2011, 27, 2459-2462.	1.8	31
21	From Knockouts to Networks: Establishing Direct Cause-Effect Relationships through Graph Analysis. PLoS ONE, 2010, 5, e12912.	1.1	68
22	Origin of Co-Expression Patterns in E.coli and S.cerevisiae Emerging from Reverse Engineering Algorithms. PLoS ONE, 2008, 3, e2981.	1.1	11
23	Comparing association network algorithms for reverse engineering of large-scale gene regulatory networks: synthetic versus real data. Bioinformatics, 2007, 23, 1640-1647.	1.8	100
24	LINEAR AND NONLINEAR METHODS FOR GENE REGULATORY NETWORK INFERENCE. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2007, 40, 533-538.	0.4	1