Nicola Soranzo

List of Publications by Year
in descending order

24 papers	6,587 citations	687363 13 h-index	713466 21 g-index
35 all docs	35 docs citations	35 times ranked	14111 citing authors

#	Article	IF	Citations
1	Expanding the Galaxy's reference data. Bioinformatics Advances, 2022, 2, .	2.4	0
2	RNA-Seq Data Analysis in Galaxy. Methods in Molecular Biology, 2021, 2284, 367-392.	0.9	23
3	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. GigaScience, 2020, 9, .	6.4	14
4	A Galaxy-based training resource for single-cell RNA-sequencing quality control and analyses. GigaScience, 2019, 8, .	6.4	4
5	GeneSeqToFamily: a Galaxy workflow to find gene families based on the Ensembl Compara GeneTrees pipeline. GigaScience, 2018, 7, 1-10.	6.4	9
6	Aequatus: an open-source homology browser. GigaScience, 2018, 7, .	6.4	1
7	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. Nucleic Acids Research, 2018, 46, W537-W544.	14.5	3,003
8	Bioconda: sustainable and comprehensive software distribution for the life sciences. Nature Methods, 2018, 15, 475-476.	19.0	714
9	Community-Driven Data Analysis Training for Biology. Cell Systems, 2018, 6, 752-758.e1.	6.2	141
10	Practical Computational Reproducibility in the Life Sciences. Cell Systems, 2018, 6, 631-635.	6.2	100
11	ReGaTE: Registration of Galaxy Tools in Elixir. GigaScience, 2017, 6, 1-4.	6.4	14
12	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. Nucleic Acids Research, 2016, 44, W3-W10.	14.5	1,751
13	Transcriptomic profiles of aging in purified human immune cells. BMC Genomics, 2015, 16, 333.	2.8	58
14	Alterations of a Cellular Cholesterol Metabolism Network Are a Molecular Feature of Obesity-Related Type 2 Diabetes and Cardiovascular Disease. Diabetes, 2015, 64, 3464-3474.	0.6	82
15	NCBI BLAST+ integrated into Galaxy. GigaScience, 2015, 4, 39.	6.4	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. Bioinformatics, 2014, 30, 1928-1929.	4.1	139
18	Network topology and parameter estimation: from experimental design methods to gene regulatory network kinetics using a community based approach. BMC Systems Biology, 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.	4.1	31
21	From Knockouts to Networks: Establishing Direct Cause-Effect Relationships through Graph Analysis. PLoS ONE, 2010, 5, e12912.	2.5	68
22	Origin of Co-Expression Patterns in E.coli and S.cerevisiae Emerging from Reverse Engineering Algorithms. PLoS ONE, 2008, 3, e2981.	2.5	11
23	Comparing association network algorithms for reverse engineering of large-scale gene regulatory networks: synthetic versus real data. Bioinformatics, 2007, 23, 1640-1647.	4.1	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