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	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. Nucleic Acids Research, 2018, 46, W537-W544.	14.5	3,003
2	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. Nucleic Acids Research, 2016, 44, W3-W10.	14.5	1,751
3	Bioconda: sustainable and comprehensive software distribution for the life sciences. Nature Methods, 2018, 15, 475-476.	19.0	714
4	NCBI BLAST+ integrated into Galaxy. GigaScience, 2015, 4, 39.	6.4	213
5	Community-Driven Data Analysis Training for Biology. Cell Systems, 2018, 6, 752-758.e1.	6.2	141
6	Orione, a web-based framework for NGS analysis in microbiology. Bioinformatics, 2014, 30, 1928-1929.	4.1	139
7	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
8	Practical Computational Reproducibility in the Life Sciences. Cell Systems, 2018, 6, 631-635.	6.2	100
9	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
10	From Knockouts to Networks: Establishing Direct Cause-Effect Relationships through Graph Analysis. PLoS ONE, 2010, 5, e12912.	2.5	68
11	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
12	Transcriptomic profiles of aging in purified human immune cells. BMC Genomics, 2015, 16, 333.	2.8	58
13	Simulating systems genetics data with SysGenSIM. Bioinformatics, 2011, 27, 2459-2462.	4.1	31
14	RNA-Seq Data Analysis in Galaxy. Methods in Molecular Biology, 2021, 2284, 367-392.	0.9	23
15	ReGaTE: Registration of Galaxy Tools in Elixir. GigaScience, 2017, 6, 1-4.	6.4	14
16	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. GigaScience, 2020, 9, .	6.4	14
17	Origin of Co-Expression Patterns in E.coli and S.cerevisiae Emerging from Reverse Engineering Algorithms. PLoS ONE, 2008, 3, e2981.	2.5	11
18	GeneSeqToFamily: a Galaxy workflow to find gene families based on the Ensembl Compara GeneTrees pipeline. GigaScience, 2018, 7, 1-10.	6.4	9

#	Article	IF	Citations
19	A Hadoop-Galaxy adapter for user-friendly and scalable data-intensive bioinformatics in Galaxy. , 2014, , .		5
20	A Galaxy-based training resource for single-cell RNA-sequencing quality control and analyses. GigaScience, 2019, 8, .	6.4	4
21	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
22	Aequatus: an open-source homology browser. GigaScience, 2018, 7, .	6.4	1
23	Simulation of the Benchmark Datasets. , 2013, , 1-8.		0
24	Expanding the Galaxy's reference data. Bioinformatics Advances, 2022, 2, .	2.4	0