

# Salvatore Alaimo

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9491675/publications.pdf>

Version: 2024-02-01

39  
papers

1,006  
citations

623574

14  
h-index

454834

30  
g-index

45  
all docs

45  
docs citations

45  
times ranked

1736  
citing authors

#	ARTICLE	IF	CITATIONS
1	Drug–target interaction prediction through domain-tuned network-based inference. <i>Bioinformatics</i> , 2013, 29, 2004-2008.	1.8	146
2	Neutrophil-to-Lymphocyte Ratio: An Emerging Marker Predicting Prognosis in Elderly Adults with Community-Acquired Pneumonia. <i>Journal of the American Geriatrics Society</i> , 2017, 65, 1796-1801.	1.3	133
3	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	9.4	88
4	Neutrophil-to-Lymphocyte Ratio is a strong predictor of atherosclerotic carotid plaques in older adults. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2018, 28, 23-27.	1.1	78
5	ncPred: ncRNA-Disease Association Prediction through Tripartite Network-Based Inference. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 71.	2.0	56
6	Post-transcriptional knowledge in pathway analysis increases the accuracy of phenotypes classification. <i>Oncotarget</i> , 2016, 7, 54572-54582.	0.8	43
7	A Subset of Patients With Autism Spectrum Disorders Show a Distinctive Metabolic Profile by Dried Blood Spot Analyses. <i>Frontiers in Psychiatry</i> , 2018, 9, 636.	1.3	41
8	Network-Based Drug Repositioning: Approaches, Resources, and Research Directions. <i>Methods in Molecular Biology</i> , 2019, 1903, 97-113.	0.4	40
9	DT-Web: a web-based application for drug-target interaction and drug combination prediction through domain-tuned network-based inference. <i>BMC Systems Biology</i> , 2015, 9, S4.	3.0	38
10	A novel computational method for inferring competing endogenous interactions. <i>Briefings in Bioinformatics</i> , 2016, 18, bbw084.	3.2	37
11	Identification of tRNA-derived ncRNAs in TCGA and NCI-60 panel cell lines and development of the public database tRFexplorer. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	36
12	Recommendation Techniques for Drug–Target Interaction Prediction and Drug Repositioning. <i>Methods in Molecular Biology</i> , 2016, 1415, 441-462.	0.4	33
13	Detecting Disease Specific Pathway Substructures through an Integrated Systems Biology Approach. <i>Non-coding RNA</i> , 2017, 3, 20.	1.3	25
14	Current Knowledge and Computational Techniques for Grapevine Meta-Omics Analysis. <i>Frontiers in Plant Science</i> , 2017, 8, 2241.	1.7	24
15	Knowledge in the Investigation of A-to-I RNA Editing Signals. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 18.	2.0	17
16	A benchmarking of pipelines for detecting ncRNAs from RNA-Seq data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1987-1998.	3.2	16
17	Multilocus sequence typing analysis of Italian <i>Xanthomonas campestris</i> pv. <i>campestris</i> strains suggests the evolution of local endemic populations of the pathogen and does not correlate with race distribution. <i>Plant Pathology</i> , 2019, 68, 278-287.	1.2	14
18	Novel Mechanisms of Tumor Promotion by the Insulin Receptor Isoform A in Triple-Negative Breast Cancer Cells. <i>Cells</i> , 2021, 10, 3145.	1.8	14

#	ARTICLE	IF	CITATIONS
19	NETME: on-the-fly knowledge network construction from biomedical literature. <i>Applied Network Science</i> , 2022, 7, 1.	0.8	12
20	Disentangling Restrictive and Repetitive Behaviors and Social Impairments in Children and Adolescents with Gilles de la Tourette Syndrome and Autism Spectrum Disorder. <i>Brain Sciences</i> , 2020, 10, 308.	1.1	11
21	VECTOR: An Integrated Correlation Network Database for the Identification of CeRNA Axes in Uveal Melanoma. <i>Genes</i> , 2021, 12, 1004.	1.0	10
22	Prevalence and Clinical Characteristics of Children and Adolescents with Metabolically Healthy Obesity: Role of Insulin Sensitivity. <i>Life</i> , 2020, 10, 127.	1.1	9
23	PHENSIM: Phenotype Simulator. <i>PLoS Computational Biology</i> , 2021, 17, e1009069.	1.5	9
24	B-type natriuretic peptide may predict prognosis in older adults admitted with a diagnosis other than heart failure. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2018, 28, 636-642.	1.1	8
25	Computational Methods for Drug Repurposing. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1361, 119-141.	0.8	8
26	Endogenous and artificial miRNAs explore a rich variety of conformations: a potential relationship between secondary structure and biological functionality. <i>Scientific Reports</i> , 2020, 10, 453.	1.6	7
27	RNAdetector: a free user-friendly stand-alone and cloud-based system for RNA-Seq data analysis. <i>BMC Bioinformatics</i> , 2021, 22, 298.	1.2	7
28	Network analysis of synovial RNA sequencing identifies gene-gene interactions predictive of response in rheumatoid arthritis. <i>Arthritis Research and Therapy</i> , 2022, 24, .	1.6	6
29	Computational Methods to Investigate the Impact of miRNAs on Pathways. <i>Methods in Molecular Biology</i> , 2019, 1970, 183-209.	0.4	5
30	Electrocardiographic Evaluation in Patients With Spinal Muscular Atrophy: A Case-Control Study. <i>Journal of Child Neurology</i> , 2018, 33, 487-492.	0.7	4
31	Bioinformatics Approach to Mitigate Mislabeling in EU Seafood Market and Protect Consumer Health. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 7497.	1.2	4
32	TACITuS: transcriptomic data collector, integrator, and selector on big data platform. <i>BMC Bioinformatics</i> , 2019, 20, 366.	1.2	3
33	Psychopathological outcomes and defence mechanisms in clinically healed adults with a paediatric cancer history: an exploratory study. <i>Annals of General Psychiatry</i> , 2021, 34, e100307.	1.1	2
34	Pathway Analysis for Cancer Research and Precision Oncology Applications. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1361, 143-161.	0.8	2
35	Computational Resources for the Interpretation of Variations in Cancer. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1361, 177-198.	0.8	2
36	Virus finding tools: current solutions and limitations. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	2

#	ARTICLE	IF	CITATIONS
37	“Diagnosis on the Dock” project: A proactive screening program for diagnosing pulmonary tuberculosis in disembarking refugees and new SEI model. <i>International Journal of Infectious Diseases</i> , 2021, 106, 98-104.	1.5	1
38	P22 Micro-RNA enriched pathway impact analysis applied to synovial RNA-seq in early rheumatoid arthritis identifies response prediction pathways. <i>Rheumatology</i> , 2020, 59, .	0.9	0
39	BioTAGME: A Comprehensive Platform for Biological Knowledge Network Analysis. <i>Frontiers in Genetics</i> , 2022, 13, 855739.	1.1	0