

# Sonia Tarazona

## List of Publications by Year in descending order

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Version: 2024-02-01

37  
papers

6,166  
citations

361413

20  
h-index

302126

39  
g-index

45  
all docs

45  
docs citations

45  
times ranked

12692  
citing authors

#	ARTICLE	IF	CITATIONS
1	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016, 17, 13.	8.8	1,898
2	Differential expression in RNA-seq: A matter of depth. <i>Genome Research</i> , 2011, 21, 2213-2223.	5.5	1,456
3	Qualimap: evaluating next-generation sequencing alignment data. <i>Bioinformatics</i> , 2012, 28, 2678-2679.	4.1	799
4	Data quality aware analysis of differential expression in RNA-seq with NOISeq R/Bioc package. <i>Nucleic Acids Research</i> , 2015, 43, gkv711.	14.5	605
5	Next maSigPro: updating maSigPro bioconductor package for RNA-seq time series. <i>Bioinformatics</i> , 2014, 30, 2598-2602.	4.1	315
6	PaintOmics 3: a web resource for the pathway analysis and visualization of multi-omics data. <i>Nucleic Acids Research</i> , 2018, 46, W503-W509.	14.5	143
7	Hypoxia Promotes Efficient Differentiation of Human Embryonic Stem Cells to Functional Endothelium. <i>Stem Cells</i> , 2010, 28, 407-418.	3.2	92
8	spongeScan: A web for detecting microRNA binding elements in lncRNA sequences. <i>Nucleic Acids Research</i> , 2016, 44, W176-W180.	14.5	92
9	Undisclosed, unmet and neglected challenges in multi-omics studies. <i>Nature Computational Science</i> , 2021, 1, 395-402.	8.0	59
10	Tumor microenvironment-targeted poly-L-glutamic acid-based combination conjugate for enhanced triple negative breast cancer treatment. <i>Biomaterials</i> , 2018, 186, 8-21.	11.4	52
11	Harmonization of quality metrics and power calculation in multi-omic studies. <i>Nature Communications</i> , 2020, 11, 3092.	12.8	43
12	Understanding disease mechanisms with models of signaling pathway activities. <i>BMC Systems Biology</i> , 2014, 8, 121.	3.0	42
13	Transcriptome modulation during host shift is driven by secondary metabolites in desert <i>Drosophila</i> . <i>Molecular Ecology</i> , 2016, 25, 4534-4550.	3.9	40
14	tappAS: a comprehensive computational framework for the analysis of the functional impact of differential splicing. <i>Genome Biology</i> , 2020, 21, 119.	8.8	40
15	PaintOmics 4: new tools for the integrative analysis of multi-omics datasets supported by multiple pathway databases. <i>Nucleic Acids Research</i> , 2022, 50, W551-W559.	14.5	31
16	A multiway approach to data integration in systems biology based on Tucker3 and N-PLS. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2010, 104, 101-111.	3.5	30
17	Pathway network inference from gene expression data. <i>BMC Systems Biology</i> , 2014, 8, S7.	3.0	30
18	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. <i>Scientific Data</i> , 2019, 6, 256.	5.3	26

#	ARTICLE	IF	CITATIONS
19	RNAseq analysis of <i>Aspergillus fumigatus</i> in blood reveals a just wait and see resting stage behavior. BMC Genomics, 2015, 16, 640.	2.8	25
20	STATegra: Multi-Omics Data Integration – A Conceptual Scheme With a Bioinformatics Pipeline. Frontiers in Genetics, 2021, 12, 620453.	2.3	24
21	Association Between Sex Hormone Levels and Clinical Outcomes in Patients With COVID-19 Admitted to Hospital: An Observational, Retrospective, Cohort Study. Frontiers in Immunology, 2022, 13, 834851.	4.8	24
22	Functional assessment of time course microarray data. BMC Bioinformatics, 2009, 10, S9.	2.6	19
23	Multimiomics Data Integration in Time Series Experiments. Comprehensive Analytical Chemistry, 2018, 82, 505-532.	1.3	19
24	Identification and visualization of differential isoform expression in RNA-seq time series. Bioinformatics, 2018, 34, 524-526.	4.1	18
25	RGmatch: matching genomic regions to proximal genes in omics data integration. BMC Bioinformatics, 2016, 17, 427.	2.6	13
26	Elucidating the Role of Chromatin State and Transcription Factors on the Regulation of the Yeast Metabolic Cycle: A Multi-Omic Integrative Approach. Frontiers in Genetics, 2018, 9, 578.	2.3	10
27	acorde unravels functionally interpretable networks of isoform co-usage from single cell data. Nature Communications, 2022, 13, 1828.	12.8	10
28	Evidence of the Red-Queen Hypothesis from Accelerated Rates of Evolution of Genes Involved in Biotic Interactions in <i>Pneumocystis</i> . Genome Biology and Evolution, 2018, 10, 1596-1606.	2.5	9
29	MultiBaC: A strategy to remove batch effects between different omic data types. Statistical Methods in Medical Research, 2020, 29, 2851-2864.	1.5	9
30	Mutant PRPF8 Causes Widespread Splicing Changes in Spliceosome Components in Retinitis Pigmentosa Patient iPSC-Derived RPE Cells. Frontiers in Neuroscience, 2021, 15, 636969.	2.8	9
31	Feedforward regulation of <i>Myc</i> coordinates lineage-specific with housekeeping gene expression during B cell progenitor cell differentiation. PLoS Biology, 2019, 17, e2006506.	5.6	8
32	Variable selection for multifactorial genomic data. Chemometrics and Intelligent Laboratory Systems, 2012, 110, 113-122.	3.5	7
33	Guidelines for Developing Successful Short Advanced Courses in Systems Medicine and Systems Biology. Cell Systems, 2017, 5, 168-175.	6.2	7
34	Dynamic evaluation of neutrophil-to-lymphocyte ratio as prognostic factor in stage III non-small cell lung cancer treated with chemoradiotherapy. Clinical and Translational Oncology, 2020, 22, 2333-2340.	2.4	7
35	MultiBaC: an R package to remove batch effects in multi-omic experiments. Bioinformatics, 2022, 38, 2657-2658.	4.1	6
36	A Multiomics Study To Unravel the Effects of Developmental Exposure to Endosulfan in Rats: Molecular Explanation for Sex-Dependent Effects. ACS Chemical Neuroscience, 2019, 10, 4264-4279.	3.5	5

#	ARTICLE	IF	CITATIONS
37	A multi-omic study for uncovering molecular mechanisms associated with hyperammonemia-induced cerebellar function impairment in rats. <i>Cell Biology and Toxicology</i> , 2021, 37, 129-149.	5.3	2