

# 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	Association Between Sex Hormone Levels and Clinical Outcomes in Patients With COVID-19 Admitted to Hospital: An Observational, Retrospective, Cohort Study. <i>Frontiers in Immunology</i> , 2022, 13, 834851.	4.8	24
2	MultiBaC: an R package to remove batch effects in multi-omic experiments. <i>Bioinformatics</i> , 2022, 38, 2657-2658.	4.1	6
3	acorde unravels functionally interpretable networks of isoform co-usage from single cell data. <i>Nature Communications</i> , 2022, 13, 1828.	12.8	10
4	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
5	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
6	STATegra: Multi-Omics Data Integration – A Conceptual Scheme With a Bioinformatics Pipeline. <i>Frontiers in Genetics</i> , 2021, 12, 620453.	2.3	24
7	Mutant PRPF8 Causes Widespread Splicing Changes in Spliceosome Components in Retinitis Pigmentosa Patient iPSC-Derived RPE Cells. <i>Frontiers in Neuroscience</i> , 2021, 15, 636969.	2.8	9
8	Undisclosed, unmet and neglected challenges in multi-omics studies. <i>Nature Computational Science</i> , 2021, 1, 395-402.	8.0	59
9	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
10	Harmonization of quality metrics and power calculation in multi-omic studies. <i>Nature Communications</i> , 2020, 11, 3092.	12.8	43
11	MultiBaC: A strategy to remove batch effects between different omic data types. <i>Statistical Methods in Medical Research</i> , 2020, 29, 2851-2864.	1.5	9
12	Dynamic evaluation of neutrophil-to-lymphocyte ratio as prognostic factor in stage III non-small cell lung cancer treated with chemoradiotherapy. <i>Clinical and Translational Oncology</i> , 2020, 22, 2333-2340.	2.4	7
13	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. <i>Scientific Data</i> , 2019, 6, 256.	5.3	26
14	A Multiomics Study To Unravel the Effects of Developmental Exposure to Endosulfan in Rats: Molecular Explanation for Sex-Dependent Effects. <i>ACS Chemical Neuroscience</i> , 2019, 10, 4264-4279.	3.5	5
15	Feedforward regulation of Myc coordinates lineage-specific with housekeeping gene expression during B cell progenitor cell differentiation. <i>PLoS Biology</i> , 2019, 17, e2006506.	5.6	8
16	Identification and visualization of differential isoform expression in RNA-seq time series. <i>Bioinformatics</i> , 2018, 34, 524-526.	4.1	18
17	Elucidating the Role of Chromatin State and Transcription Factors on the Regulation of the Yeast Metabolic Cycle: A Multi-Omic Integrative Approach. <i>Frontiers in Genetics</i> , 2018, 9, 578.	2.3	10
18	Multiomics Data Integration in Time Series Experiments. <i>Comprehensive Analytical Chemistry</i> , 2018, 82, 505-532.	1.3	19

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19	Evidence of the Red-Queen Hypothesis from Accelerated Rates of Evolution of Genes Involved in Biotic Interactions in <i>Pneumocystis</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 1596-1606.	2.5	9
20	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
21	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
22	Guidelines for Developing Successful Short Advanced Courses in Systems Medicine and Systems Biology. <i>Cell Systems</i> , 2017, 5, 168-175.	6.2	7
23	RGmatch: matching genomic regions to proximal genes in omics data integration. <i>BMC Bioinformatics</i> , 2016, 17, 427.	2.6	13
24	spongeScan: A web for detecting microRNA binding elements in lncRNA sequences. <i>Nucleic Acids Research</i> , 2016, 44, W176-W180.	14.5	92
25	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
26	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016, 17, 13.	8.8	1,898
27	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
28	RNAseq analysis of <i>Aspergillus fumigatus</i> in blood reveals a just wait and see resting stage behavior. <i>BMC Genomics</i> , 2015, 16, 640.	2.8	25
29	Understanding disease mechanisms with models of signaling pathway activities. <i>BMC Systems Biology</i> , 2014, 8, 121.	3.0	42
30	Next maSigPro: updating maSigPro bioconductor package for RNA-seq time series. <i>Bioinformatics</i> , 2014, 30, 2598-2602.	4.1	315
31	Pathway network inference from gene expression data. <i>BMC Systems Biology</i> , 2014, 8, S7.	3.0	30
32	Qualimap: evaluating next-generation sequencing alignment data. <i>Bioinformatics</i> , 2012, 28, 2678-2679.	4.1	799
33	Variable selection for multifactorial genomic data. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2012, 110, 113-122.	3.5	7
34	Differential expression in RNA-seq: A matter of depth. <i>Genome Research</i> , 2011, 21, 2213-2223.	5.5	1,456
35	Hypoxia Promotes Efficient Differentiation of Human Embryonic Stem Cells to Functional Endothelium. <i>Stem Cells</i> , 2010, 28, 407-418.	3.2	92
36	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

#	ARTICLE	IF	CITATIONS
37	Functional assessment of time course microarray data. BMC Bioinformatics, 2009, 10, S9.	2.6	19