

# Antonio Colaprico

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

13,679  
citations

236925

25  
h-index

434195

31  
g-index

40  
all docs

40  
docs citations

40  
times ranked

19569  
citing authors

#	ARTICLE	IF	CITATIONS
1	Abstract PD3-04: Multi-omics characterization of triple-negative breast cancer identifies therapeutic vulnerabilities and epigenetic immune suppression in the mesenchymal subtype. <i>Cancer Research</i> , 2022, 82, PD3-04-PD3-04.	0.9	0
2	Distinct mechanisms of innate and adaptive immune regulation underlie poor oncologic outcomes associated with KRAS-TP53 co-alteration in pancreatic cancer. <i>Oncogene</i> , 2022, 41, 3640-3654.	5.9	17
3	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 361-379.e16.	16.8	189
4	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	16.8	327
5	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40.	28.9	170
6	LR Hunting: A Random Forest Based Cell-Cell Interaction Discovery Method for Single-Cell Gene Expression Data. <i>Frontiers in Genetics</i> , 2021, 12, 708835.	2.3	9
7	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26.	28.9	236
8	Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes. <i>Nature Communications</i> , 2021, 12, 6276.	12.8	89
9	PathwayMultiomics: An R Package for Efficient Integrative Analysis of Multi-Omics Datasets With Matched or Un-matched Samples. <i>Frontiers in Genetics</i> , 2021, 12, 783713.	2.3	9
10	Interpreting pathways to discover cancer driver genes with Moonlight. <i>Nature Communications</i> , 2020, 11, 69.	12.8	66
11	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	28.9	273
12	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	28.9	177
13	PathwayPCA: an R/Bioconductor Package for Pathway Based Integrative Analysis of Multi-Omics Data. <i>Proteomics</i> , 2020, 20, e1900409.	2.2	8
14	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	28.9	410
15	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	28.9	296
16	An Overview on Internet of Medical Things in Blood Pressure Monitoring. , 2019, , .		26
17	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	28.9	430
18	A New Measurement System to Boost the IoMT for the Blood Pressure Monitoring. , 2019, , .		5

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19	Ageing Human Hematopoietic Stem Cells Manifest Profound Epigenetic Reprogramming of Enhancers That May Predispose to Leukemia. <i>Cancer Discovery</i> , 2019, 9, 1080-1101.	9.4	119
20	New functionalities in the TCGAbiolinks package for the study and integration of cancer data from GDC and GTEx. <i>PLoS Computational Biology</i> , 2019, 15, e1006701.	3.2	319
21	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	28.9	1,670
22	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	28.9	272
23	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	28.9	1,417
24	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	14.3	3,706
25	Combination of Gene Expression Signature and Model for End-Stage Liver Disease Score Predicts Survival of Patients With Severe Alcoholic Hepatitis. <i>Gastroenterology</i> , 2018, 154, 965-975.	1.3	41
26	Integration of multiple networks and pathways identifies cancer driver genes in pan-cancer analysis. <i>BMC Genomics</i> , 2018, 19, 25.	2.8	46
27	In-Silico Integration Approach to Identify a Key miRNA Regulating a Gene Network in Aggressive Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2018, 19, 910.	4.1	11
28	Polycomb complexes associate with enhancers and promote oncogenic transcriptional programs in cancer through multiple mechanisms. <i>Nature Communications</i> , 2018, 9, 3377.	12.8	112
29	SpidermiR: An R/Bioconductor Package for Integrative Analysis with miRNA Data. <i>International Journal of Molecular Sciences</i> , 2017, 18, 274.	4.1	50
30	How interacting pathways are regulated by miRNAs in breast cancer subtypes. <i>BMC Bioinformatics</i> , 2016, 17, 348.	2.6	20
31	TCGAbiolinks: an R/Bioconductor package for integrative analysis of TCGA data. <i>Nucleic Acids Research</i> , 2016, 44, e71-e71.	14.5	2,519
32	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. <i>F1000Research</i> , 2016, 5, 1542.	1.6	140
33	Integrative Analysis with Monte Carlo Cross-Validation Reveals miRNAs Regulating Pathways Cross-Talk in Aggressive Breast Cancer. <i>BioMed Research International</i> , 2015, 2015, 1-17.	1.9	30
34	TCGAbiolinksGUI: A graphical user interface to analyze cancer molecular and clinical data. <i>F1000Research</i> , 0, 7, 439.	1.6	14
35	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. <i>F1000Research</i> , 0, 5, 1542.	1.6	155