

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 | The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14. | 14.3 | 3,706 |
| 2 | TCGAbiolinks: an R/Bioconductor package for integrative analysis of TCGA data. <i>Nucleic Acids Research</i> , 2016, 44, e71-e71. | 14.5 | 2,519 |
| 3 | Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18. | 28.9 | 1,670 |
| 4 | Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15. | 28.9 | 1,417 |
| 5 | Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31. | 28.9 | 430 |
| 6 | Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35. | 28.9 | 410 |
| 7 | Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20. | 16.8 | 327 |
| 8 | 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 |
| 9 | Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26. | 28.9 | 296 |
| 10 | Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31. | 28.9 | 273 |
| 11 | Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10. | 28.9 | 272 |
| 12 | Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26. | 28.9 | 236 |
| 13 | 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 |
| 14 | Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31. | 28.9 | 177 |
| 15 | A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40. | 28.9 | 170 |
| 16 | TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. <i>F1000Research</i> , 0, 5, 1542. | 1.6 | 155 |
| 17 | TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. <i>F1000Research</i> , 2016, 5, 1542. | 1.6 | 140 |
| 18 | Aging 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 |

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|----|---|------|-----------|
| 19 | 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 |
| 20 | Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes. <i>Nature Communications</i> , 2021, 12, 6276. | 12.8 | 89 |
| 21 | Interpreting pathways to discover cancer driver genes with Moonlight. <i>Nature Communications</i> , 2020, 11, 69. | 12.8 | 66 |
| 22 | SpidermiR: An R/Bioconductor Package for Integrative Analysis with miRNA Data. <i>International Journal of Molecular Sciences</i> , 2017, 18, 274. | 4.1 | 50 |
| 23 | Integration of multiple networks and pathways identifies cancer driver genes in pan-cancer analysis. <i>BMC Genomics</i> , 2018, 19, 25. | 2.8 | 46 |
| 24 | 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 |
| 25 | 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 |
| 26 | An Overview on Internet of Medical Things in Blood Pressure Monitoring. , 2019, , . | | 26 |
| 27 | How interacting pathways are regulated by miRNAs in breast cancer subtypes. <i>BMC Bioinformatics</i> , 2016, 17, 348. | 2.6 | 20 |
| 28 | 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 |
| 29 | TCGAbiolinksGUI: A graphical user interface to analyze cancer molecular and clinical data. <i>F1000Research</i> , 0, 7, 439. | 1.6 | 14 |
| 30 | 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 |
| 31 | 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 |
| 32 | 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 |
| 33 | PathwayPCA: an R/Bioconductor Package for Pathway Based Integrative Analysis of Multi-Omics Data. <i>Proteomics</i> , 2020, 20, e1900409. | 2.2 | 8 |
| 34 | A New Measurement System to Boost the IoMT for the Blood Pressure Monitoring. , 2019, , . | | 5 |
| 35 | 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 |