

# Ramana V Davuluri

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

2,455  
citations

430874

18  
h-index

434195

31  
g-index

36  
all docs

36  
docs citations

36  
times ranked

4812  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic priming enhances antitumor immunity in platinum-resistant ovarian cancer. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	28
2	Distinct mechanisms control genome recognition by p53 at its target genes linked to different cell fates. <i>Nature Communications</i> , 2021, 12, 484.	12.8	22
3	DNABERT: pre-trained Bidirectional Encoder Representations from Transformers model for DNA-language in genome. <i>Bioinformatics</i> , 2021, 37, 2112-2120.	4.1	282
4	A first-in-human phase 0 clinical study of RNA interference-based spherical nucleic acids in patients with recurrent glioblastoma. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	136
5	ExTraMapper: exon- and transcript-level mappings for orthologous gene pairs. <i>Bioinformatics</i> , 2021, 37, 3412-3420.	4.1	3
6	RP58 Represses Transcriptional Programs Linked to Nonneuronal Cell Identity and Glioblastoma Subtypes in Developing Neurons. <i>Molecular and Cellular Biology</i> , 2021, 41, e0052620.	2.3	8
7	In silico analysis of alternative splicing on drug-target gene interactions. <i>Scientific Reports</i> , 2020, 10, 134.	3.3	11
8	Phase II trial of guadecitabine priming and pembrolizumab in platinum resistant recurrent ovarian cancer.. <i>Journal of Clinical Oncology</i> , 2020, 38, 6025-6025.	1.6	8
9	Identification of Geographic Specific SARS-Cov-2 Mutations by Random Forest Classification and Variable Selection Methods. <i>Statistics and Applications</i> , 2020, 18, 253-268.	0.0	1
10	Transcriptional consequences of impaired immune cell responses induced by cystic fibrosis plasma characterized via dual RNA sequencing. <i>BMC Medical Genomics</i> , 2019, 12, 66.	1.5	11
11	Multivariate Analysis of Preoperative Magnetic Resonance Imaging Reveals Transcriptomic Classification of de novo Glioblastoma Patients. <i>Frontiers in Computational Neuroscience</i> , 2019, 13, 81.	2.1	5
12	Immune landscapes associated with different glioblastoma molecular subtypes. <i>Acta Neuropathologica Communications</i> , 2019, 7, 203.	5.2	112
13	IDH3 <sup>±</sup> regulates one-carbon metabolism in glioblastoma. <i>Science Advances</i> , 2019, 5, eaat0456.	10.3	59
14	Radiomic MRI signature reveals three distinct subtypes of glioblastoma with different clinical and molecular characteristics, offering prognostic value beyond IDH1. <i>Scientific Reports</i> , 2018, 8, 5087.	3.3	124
15	Metastatic cancers promote cachexia through ZIP14 upregulation in skeletal muscle. <i>Nature Medicine</i> , 2018, 24, 770-781.	30.7	121
16	Characterization of brain tumor initiating cells isolated from an animal model of CNS primitive neuroectodermal tumors. <i>Oncotarget</i> , 2018, 9, 13733-13747.	1.8	7
17	Cancer-Associated IDH1 Promotes Growth and Resistance to Targeted Therapies in the Absence of Mutation. <i>Cell Reports</i> , 2017, 19, 1858-1873.	6.4	164
18	Identification of Genetic and Epigenetic Variants Associated with Breast Cancer Prognosis by Integrative Bioinformatics Analysis. <i>Cancer Informatics</i> , 2017, 16, CIN.S39783.	1.9	36

#	ARTICLE	IF	CITATIONS
19	Stabilization of HIF-1 $\beta$ and HIF-2 $\beta$ , up-regulation of MYC and accumulation of stabilized p53 constitute hallmarks of CNS-PNET animal model. PLoS ONE, 2017, 12, e0173106.	2.5	3
20	MNK Inhibition Disrupts Mesenchymal Glioma Stem Cells and Prolongs Survival in a Mouse Model of Glioblastoma. Molecular Cancer Research, 2016, 14, 984-993.	3.4	38
21	Comparative evaluation of isoform-level gene expression estimation algorithms for RNA-seq and exon-array platforms. Briefings in Bioinformatics, 2016, 18, bbw016.	6.5	25
22	Imaging patterns predict patient survival and molecular subtype in glioblastoma via machine learning techniques. Neuro-Oncology, 2016, 18, 417-425.	1.2	243
23	Identification and validation of regulatory SNPs that modulate transcription factor chromatin binding and gene expression in prostate cancer. Oncotarget, 2016, 7, 54616-54626.	1.8	41
24	Gene expression profiling of the human natural killer cell response to Fc receptor activation: unique enhancement in the presence of interleukin-12. BMC Medical Genomics, 2015, 8, 66.	1.5	15
25	Comparison of data discretization methods for cross platform transfer of gene-expression based tumor subtyping classifier. , 2014, , .		0
26	Genome-Wide Mapping of RNA Pol-II Promoter Usage in Mouse Tissues by ChIP-Seq. Methods in Molecular Biology, 2014, 1176, 1-9.	0.9	3
27	Protein Kinase A Activation Enhances $\beta$ -Catenin Transcriptional Activity through Nuclear Localization to PML Bodies. PLoS ONE, 2014, 9, e109523.	2.5	29
28	Alternative transcription and alternative splicing in cancer. , 2012, 136, 283-294.		107
29	IsoformEx: isoform level gene expression estimation using weighted non-negative least squares from mRNA-Seq data. BMC Bioinformatics, 2011, 12, 305.	2.6	24
30	The functional consequences of alternative promoter use in mammalian genomes. Trends in Genetics, 2008, 24, 167-177.	6.7	322
31	AGRIS: Arabidopsis gene regulatory information server, an information resource of Arabidopsis cis-regulatory elements and transcription factors. BMC Bioinformatics, 2003, 4, 25.	2.6	349
32	Application of FirstEF to Find Promoters and First Exons in the Human Genome. Current Protocols in Bioinformatics, 2003, 1, 4.7.1-4.7.10.	25.8	5
33	Computer Software to Find Genes in Plant Genomic DNA. , 2003, 236, 87-108.		8
34	Nonlinear partial differential equations and applications: Gene expression profiling of isogenic cells with different TP53 gene dosage reveals numerous genes that are affected by TP53 dosage and identifies CSPG2 as a direct target of p53. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15632-15637.	7.1	85