

Subha Madhavan

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

2,288
citations

257450

24
h-index

233421

45
g-index

52
all docs

52
docs citations

52
times ranked

4953
citing authors

#	ARTICLE	IF	CITATIONS
1	Standards for the classification of pathogenicity of somatic variants in cancer (oncogenicity): Joint recommendations of Clinical Genome Resource (ClinGen), Cancer Genomics Consortium (CGC), and Variant Interpretation for Cancer Consortium (VICC). <i>Genetics in Medicine</i> , 2022, 24, 986-998.	2.4	55
2	Standardized evidence-based approach for assessment of oncogenic and clinical significance of NTRK fusions. <i>Cancer Genetics</i> , 2022, 264-265, 50-59.	0.4	5
3	A community approach to the cancer-variant-interpretation bottleneck. <i>Nature Cancer</i> , 2022, 3, 522-525.	13.2	3
4	Real-world Studies Link NSAID Use to Improved Overall Lung Cancer Survival. <i>Cancer Research Communications</i> , 2022, 2, 590-601.	1.7	0
5	Recommendations for the safe, effective use of adaptive CDS in the US healthcare system: an AMIA position paper. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021, 28, 677-684.	4.4	46
6	High mRNA expression of LY6 gene family is associated with overall survival outcome in pancreatic ductal adenocarcinoma. <i>Oncotarget</i> , 2021, 12, 145-159.	1.8	4
7	Automated Identification of Patients With Immune-Related Adverse Events From Clinical Notes Using Word Embedding and Machine Learning. <i>JCO Clinical Cancer Informatics</i> , 2021, 5, 541-549.	2.1	8
8	Envisioning the future of precision oncology trials. <i>Nature Cancer</i> , 2021, 2, 9-11.	13.2	19
9	Use of electronic health records to support a public health response to the COVID-19 pandemic in the United States: a perspective from 15 academic medical centers. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021, 28, 393-401.	4.4	54
10	De novo assembly and annotation of transcriptomes from two cultivars of <i>Cannabis sativa</i> with different cannabinoid profiles. <i>Gene</i> , 2020, 762, 145026.	2.2	11
11	Collaborative, Multidisciplinary Evaluation of Cancer Variants Through Virtual Molecular Tumor Boards Informs Local Clinical Practices. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 602-613.	2.1	26
12	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. <i>Nature Genetics</i> , 2020, 52, 448-457.	21.4	104
13	Overall survival in patients with pancreatic cancer receiving matched therapies following molecular profiling: a retrospective analysis of the Know Your Tumor registry trial. <i>Lancet Oncology</i> , The, 2020, 21, 508-518.	10.7	323
14	A virtual molecular tumor board to improve efficiency and scalability of delivering precision oncology to physicians and their patients. <i>JAMIA Open</i> , 2019, 2, 505-515.	2.0	56
15	Genome sequencing analysis of blood cells identifies germline haplotypes strongly associated with drug resistance in osteosarcoma patients. <i>BMC Cancer</i> , 2019, 19, 357.	2.6	18
16	SNP2SIM: a modular workflow for standardizing molecular simulation and functional analysis of protein variants. <i>BMC Bioinformatics</i> , 2019, 20, 171.	2.6	7
17	Outcomes in Patients With Pancreatic Adenocarcinoma With Genetic Mutations in DNA Damage Response Pathways: Results From the Know Your Tumor Program. <i>JCO Precision Oncology</i> , 2019, 3, 1-10.	3.0	38
18	Real-world outcomes of underrepresented patient populations treated with immune checkpoint inhibitors (ICIs): African American descent, poor ECOG performance status, and chronic viral infections.. <i>Journal of Clinical Oncology</i> , 2019, 37, 2587-2587.	1.6	5

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19	Integrated copy number and miRNA expression analysis in triple negative breast cancer of Latin American patients. <i>Oncotarget</i> , 2019, 10, 6184-6203.	1.8	15
20	Super enhancer inhibitors suppress MYC driven transcriptional amplification and tumor progression in osteosarcoma. <i>Bone Research</i> , 2018, 6, 11.	11.4	99
21	Future of Evidence Synthesis in Precision Oncology: Between Systematic Reviews and Biocuration. <i>JCO Precision Oncology</i> , 2018, 2, 1.	3.0	5
22	Eye-Tracking Study to Enhance Usability of Molecular Diagnostics Reports in Cancer Precision Medicine. <i>JCO Precision Oncology</i> , 2018, 2, 1-11.	3.0	6
23	Molecular Profiling of Patients with Pancreatic Cancer: Initial Results from the Know Your Tumor Initiative. <i>Clinical Cancer Research</i> , 2018, 24, 5018-5027.	7.0	158
24	Curation of the Pancreatic Ductal Adenocarcinoma Subset of the Cancer Genome Atlas Is Essential for Accurate Conclusions about Survival-Related Molecular Mechanisms. <i>Clinical Cancer Research</i> , 2018, 24, 3813-3819.	7.0	53
25	The REMBRANDT study, a large collection of genomic data from brain cancer patients. <i>Scientific Data</i> , 2018, 5, 180158.	5.3	115
26	A cloud-based virtual tumor board to facilitate treatment recommendations for patients with advanced cancers.. <i>Journal of Clinical Oncology</i> , 2018, 36, 6508-6508.	1.6	4
27	ClinGen Cancer Somatic Working Group - standardizing and democratizing access to cancer molecular diagnostic data to drive translational research. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018, 23, 247-258.	0.7	13
28	A Computational Approach for Prioritizing Selection of Therapies Targeting Drug Resistant Variation in Anaplastic Lymphoma Kinase. <i>AMIA Summits on Translational Science Proceedings</i> , 2018, 2017, 160-167.	0.4	2
29	Tumor Neoantigens Derived from RNA Sequencing Analysis. , 2017, , .		0
30	EGR1 regulates cellular metabolism and survival in endocrine resistant breast cancer. <i>Oncotarget</i> , 2017, 8, 96865-96884.	1.8	29
31	Quantification and expert evaluation of evidence for chemopredictive biomarkers to personalize cancer treatment. <i>Oncotarget</i> , 2017, 8, 37923-37934.	1.8	23
32	Discovery of Metabolic Biomarkers for Duchenne Muscular Dystrophy within a Natural History Study. <i>PLoS ONE</i> , 2016, 11, e0153461.	2.5	26
33	Ly6E/K Signaling to TGF β 2 Promotes Breast Cancer Progression, Immune Escape, and Drug Resistance. <i>Cancer Research</i> , 2016, 76, 3376-3386.	0.9	80
34	An informatics research agenda to support precision medicine: seven key areas. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2016, 23, 791-795.	4.4	61
35	Somatic cancer variant curation and harmonization through consensus minimum variant level data. <i>Genome Medicine</i> , 2016, 8, 117.	8.2	61
36	G-DOC Plus “an integrative bioinformatics platform for precision medicine. <i>BMC Bioinformatics</i> , 2016, 17, 193.	2.6	39

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37	Differentially expressed miRNAs in triple negative breast cancer between African-American and non-Hispanic white women. <i>Oncotarget</i> , 2016, 7, 79274-79291.	1.8	43
38	Distinct lymphocyte antigens 6 (Ly6) family members Ly6D, Ly6E, Ly6K and Ly6H drive tumorigenesis and clinical outcome. <i>Oncotarget</i> , 2016, 7, 11165-11193.	1.8	76
39	ERR β target genes are poor prognostic factors in Tamoxifen-treated breast cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , 2015, 34, 45.	8.6	31
40	The CPTAC Data Portal: A Resource for Cancer Proteomics Research. <i>Journal of Proteome Research</i> , 2015, 14, 2707-2713.	3.7	309
41	SNP2Structure: A Public and Versatile Resource for Mapping and Three-Dimensional Modeling of Missense SNPs on Human Protein Structures. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 514-519.	4.1	16
42	In silico analysis of autoimmune diseases and genetic relationships to vaccination against infectious diseases. <i>BMC Immunology</i> , 2014, 15, 61.	2.2	21
43	NCI Workshop Report: Clinical and Computational Requirements for Correlating Imaging Phenotypes with Genomics Signatures. <i>Translational Oncology</i> , 2014, 7, 556-569.	3.7	69
44	An integrated pharmacogenomic analysis of doxorubicin response using genotype information on DMET genes. , 2013, , .		1
45	In Silico Discovery of Mitosis Regulation Networks Associated with Early Distant Metastases in Estrogen Receptor Positive Breast Cancers. <i>Cancer Informatics</i> , 2013, 12, CIN.S10329.	1.9	15
46	Genome-wide multi-omics profiling of colorectal cancer identifies immune determinants strongly associated with relapse. <i>Frontiers in Genetics</i> , 2013, 4, 236.	2.3	31
47	G-DOC: A Systems Medicine Platform for Personalized Oncology. <i>Neoplasia</i> , 2011, 13, 771-783.	5.3	58
48	Pediatric Palliative Care and eHealth. <i>American Journal of Preventive Medicine</i> , 2011, 40, S208-S216.	3.0	36