Subha Madhavan

List of Publications by Year
in descending order

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	Overall survival in patients with pancreatic cancer receiving matched therapies following molecular profiling: a retrospective analysis of the Know Your Tumor registry trial. Lancet Oncology, The, 2020, 21, 508-518.	10.7	323
2	The CPTAC Data Portal: A Resource for Cancer Proteomics Research. Journal of Proteome Research, 2015, 14, 2707-2713.	3.7	309
3	Molecular Profiling of Patients with Pancreatic Cancer: Initial Results from the Know Your Tumor Initiative. Clinical Cancer Research, 2018, 24, 5018-5027.	7.0	158
4	The REMBRANDT study, a large collection of genomic data from brain cancer patients. Scientific Data, 2018, 5, 180158.	5.3	115
5	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	21.4	104
6	Super enhancer inhibitors suppress MYC driven transcriptional amplification and tumor progression in osteosarcoma. Bone Research, 2018, 6, 11.	11.4	99
7	Ly6E/K Signaling to TGFÎ² Promotes Breast Cancer Progression, Immune Escape, and Drug Resistance. Cancer Research, 2016, 76, 3376-3386.	0.9	80
8	Distinct lymphocyte antigens 6 (Ly6) family members Ly6D, Ly6E, Ly6K and Ly6H drive tumorigenesis and clinical outcome. Oncotarget, 2016, 7, 11165-11193.	1.8	76
9	NCI Workshop Report: Clinical and Computational Requirements for Correlating Imaging Phenotypes with Genomics Signatures. Translational Oncology, 2014, 7, 556-569.	3.7	69
10	An informatics research agenda to support precision medicine: seven key areas. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 791-795.	4.4	61
11	Somatic cancer variant curation and harmonization through consensus minimum variant level data. Genome Medicine, 2016, 8, 117.	8.2	61
12	G-DOC: A Systems Medicine Platform for Personalized Oncology. Neoplasia, 2011, 13, 771-783.	5.3	58
13	A virtual molecular tumor board to improve efficiency and scalability of delivering precision oncology to physicians and their patients. JAMIA Open, 2019, 2, 505-515.	2.0	56
14	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). Genetics in Medicine, 2022, 24, 986-998.	2.4	55
15	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. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 393-401.	4.4	54
16	Curation of the Pancreatic Ductal Adenocarcinoma Subset of the Cancer Genome Atlas Is Essential for Accurate Conclusions about Survival-Related Molecular Mechanisms. Clinical Cancer Research, 2018, 24, 3813-3819.	7.0	53
17	Recommendations for the safe, effective use of adaptive CDS in the US healthcare system: an AMIA position paper. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 677-684.	4.4	46
18	Differentially expressed miRNAs in triple negative breast cancer between African-American and non-Hispanic white women. Oncotarget, 2016, 7, 79274-79291.	1.8	43

#	Article	IF	Citations
19	G-DOC Plus â€“ an integrative bioinformatics platform for precision medicine. BMC Bioinformatics, 2016, 17, 193.	2.6	39
20	Outcomes in Patients With Pancreatic Adenocarcinoma With Genetic Mutations in DNA Damage Response Pathways: Results From the Know Your Tumor Program. JCO Precision Oncology, 2019, 3, 1-10.	3.0	38
21	Pediatric Palliative Care and eHealth. American Journal of Preventive Medicine, 2011, 40, S208-S216.	3.0	36
22	Genome-wide multi-omics profiling of colorectal cancer identifies immune determinants strongly associated with relapse. Frontiers in Genetics, 2013, 4, 236.	2.3	31
23	ERRÎ³ target genes are poor prognostic factors in Tamoxifen-treated breast cancer. Journal of Experimental and Clinical Cancer Research, 2015, 34, 45.	8.6	31
24	EGR1 regulates cellular metabolism and survival in endocrine resistant breast cancer. Oncotarget, 2017, 8, 96865-96884.	1.8	29
25	Discovery of Metabolic Biomarkers for Duchenne Muscular Dystrophy within a Natural History Study. PLoS ONE, 2016, 11, e0153461.	2.5	26
26	Collaborative, Multidisciplinary Evaluation of Cancer Variants Through Virtual Molecular Tumor Boards Informs Local Clinical Practices. JCO Clinical Cancer Informatics, 2020, 4, 602-613.	2.1	26
27	Quantification and expert evaluation of evidence for chemopredictive biomarkers to personalize cancer treatment. Oncotarget, 2017, 8, 37923-37934.	1.8	23
28	In silico analysis of autoimmune diseases and genetic relationships to vaccination against infectious diseases. BMC Immunology, 2014, 15, 61.	2.2	21
29	Envisioning the future of precision oncology trials. Nature Cancer, 2021, 2, 9-11.	13.2	19
30	Genome sequencing analysis of blood cells identifies germline haplotypes strongly associated with drug resistance in osteosarcoma patients. BMC Cancer, 2019, 19, 357.	2.6	18
31	SNP2Structure: A Public and Versatile Resource for Mapping and Three-Dimensional Modeling of Missense SNPs on Human Protein Structures. Computational and Structural Biotechnology Journal, 2015, 13, 514-519.	4.1	16
32	In Silico Discovery of Mitosis Regulation Networks Associated with Early Distant Metastases in Estrogen Receptor Positive Breast Cancers. Cancer Informatics, 2013, 12, CIN.S10329.	1.9	15
33	Integrated copy number and miRNA expression analysis in triple negative breast cancer of Latin American patients. Oncotarget, 2019, 10, 6184-6203.	1.8	15
34	ClinGen Cancer Somatic Working Group - standardizing and democratizing access to cancer molecular diagnostic data to drive translational research. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 247-258.	0.7	13
35	De novo assembly and annotation of transcriptomes from two cultivars of Cannabis sativa with different cannabinoid profiles. Gene, 2020, 762, 145026.	2.2	11
36	Automated Identification of Patients With Immune-Related Adverse Events From Clinical Notes Using Word Embedding and Machine Learning. JCO Clinical Cancer Informatics, 2021, 5, 541-549.	2.1	8

#	Article	IF	Citations
37	SNP2SIM: a modular workflow for standardizing molecular simulation and functional analysis of protein variants. BMC Bioinformatics, 2019, 20, 171.	2.6	7
38	Eye-Tracking Study to Enhance Usability of Molecular Diagnostics Reports in Cancer Precision Medicine. JCO Precision Oncology, 2018, 2, 1-11.	3.0	6
39	Future of Evidence Synthesis in Precision Oncology: Between Systematic Reviews and Biocuration. JCO Precision Oncology, 2018, 2, 1.	3.0	5
40	Real-world outcomes of underrepresented patient populations treated with immune checkpoint inhibitors (ICIs): African American descent, poor ECOG performance status, and chronic viral infections.. Journal of Clinical Oncology, 2019, 37, 2587-2587.	1.6	5
41	Standardized evidence-based approach for assessment of oncogenic and clinical significance of NTRK fusions. Cancer Genetics, 2022, 264-265, 50-59.	0.4	5
42	High mRNA expression of LY6 gene family is associated with overall survival outcome in pancreatic ductal adenocarcinoma. Oncotarget, 2021, 12, 145-159.	1.8	4
43	A cloud-based virtual tumor board to facilitate treatment recommendations for patients with advanced cancers.. Journal of Clinical Oncology, 2018, 36, 6508-6508.	1.6	4
44	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.	13.2	3
45	A Computational Approach for Prioritizing Selection of Therapies Targeting Drug Resistant Variation in Anaplastic Lymphoma Kinase. AMIA Summits on Translational Science Proceedings, 2018, 2017, 160-167.	0.4	2
46	An integrated pharmacogenomic analysis of doxorubicin response using genotype information on DMET genes. , 2013, , .		1
47	Tumor Neoantigens Derived from RNA Sequencing Analysis. , 2017, , .		0
48	Real-world Studies Link NSAID Use to Improved Overall Lung Cancer Survival. Cancer Research Communications, 2022, 2, 590-601.	1.7	0