

Shanker Kalyana-Sundaram

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

11,653
citations

136740

32
h-index

315357

38
g-index

39
all docs

39
docs citations

39
times ranked

20173
citing authors

#	ARTICLE	IF	CITATIONS
1	Metabolomic profiles delineate potential role for sarcosine in prostate cancer progression. <i>Nature</i> , 2009, 457, 910-914.	13.7	1,944
2	Oncomine 3.0: Genes, Pathways, and Networks in a Collection of 18,000 Cancer Gene Expression Profiles. <i>Neoplasia</i> , 2007, 9, 166-180.	2.3	1,847
3	Activating ESR1 mutations in hormone-resistant metastatic breast cancer. <i>Nature Genetics</i> , 2013, 45, 1446-1451.	9.4	925
4	Integrative molecular concept modeling of prostate cancer progression. <i>Nature Genetics</i> , 2007, 39, 41-51.	9.4	837
5	Transcriptome sequencing to detect gene fusions in cancer. <i>Nature</i> , 2009, 458, 97-101.	13.7	791
6	Identification of recurrent NAB2-STAT6 gene fusions in solitary fibrous tumor by integrative sequencing. <i>Nature Genetics</i> , 2013, 45, 180-185.	9.4	662
7	Identification of Targetable FGFR Gene Fusions in Diverse Cancers. <i>Cancer Discovery</i> , 2013, 3, 636-647.	7.7	614
8	Personalized Oncology Through Integrative High-Throughput Sequencing: A Pilot Study. <i>Science Translational Medicine</i> , 2011, 3, 111ra121.	5.8	531
9	Rearrangements of the RAF kinase pathway in prostate cancer, gastric cancer and melanoma. <i>Nature Medicine</i> , 2010, 16, 793-798.	15.2	436
10	Probabilistic model of the human protein-protein interaction network. <i>Nature Biotechnology</i> , 2005, 23, 951-959.	9.4	380
11	Chimeric transcript discovery by paired-end transcriptome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12353-12358.	3.3	302
12	Functionally recurrent rearrangements of the MAST kinase and Notch gene families in breast cancer. <i>Nature Medicine</i> , 2011, 17, 1646-1651.	15.2	301
13	Expressed Pseudogenes in the Transcriptional Landscape of Human Cancers. <i>Cell</i> , 2012, 149, 1622-1634.	13.5	250
14	Deep sequencing reveals distinct patterns of DNA methylation in prostate cancer. <i>Genome Research</i> , 2011, 21, 1028-1041.	2.4	166
15	Mining for regulatory programs in the cancer transcriptome. <i>Nature Genetics</i> , 2005, 37, 579-583.	9.4	158
16	AGTR1 overexpression defines a subset of breast cancer and confers sensitivity to losartan, an AGTR1 antagonist. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10284-10289.	3.3	140
17	Characterization of Gene Expression Phenotype in Amyotrophic Lateral Sclerosis Monocytes. <i>JAMA Neurology</i> , 2017, 74, 677.	4.5	130
18	Landscape of gene fusions in epithelial cancers: seq and ye shall find. <i>Genome Medicine</i> , 2015, 7, 129.	3.6	127

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19	Molecular Concepts Analysis Links Tumors, Pathways, Mechanisms, and Drugs. <i>Neoplasia</i> , 2007, 9, 443-IN9.	2.3	124
20	Transcriptome meta-analysis of lung cancer reveals recurrent aberrations in NRG1 and Hippo pathway genes. <i>Nature Communications</i> , 2014, 5, 5893.	5.8	121
21	Quantitative Proteomic Profiling of Prostate Cancer Reveals a Role for miR-128 in Prostate Cancer. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 298-312.	2.5	113
22	A First-Time-in-Human Study of GSK2636771, a Phosphoinositide 3 Kinase Beta-Selective Inhibitor, in Patients with Advanced Solid Tumors. <i>Clinical Cancer Research</i> , 2017, 23, 5981-5992.	3.2	107
23	HPeak: an HMM-based algorithm for defining read-enriched regions in ChIP-Seq data. <i>BMC Bioinformatics</i> , 2010, 11, 369.	1.2	94
24	Inflammation-Induced Oxidative Stress Mediates Gene Fusion Formation in Prostate Cancer. <i>Cell Reports</i> , 2016, 17, 2620-2631.	2.9	68
25	Gene Fusions Associated with Recurrent Amplicons Represent a Class of Passenger Aberrations in Breast Cancer. <i>Neoplasia</i> , 2012, 14, 702-IN13.	2.3	60
26	Renal Cell Carcinoma With Chromosome 6p Amplification Including the TFEB Gene. <i>American Journal of Surgical Pathology</i> , 2017, 41, 287-298.	2.1	60
27	Humoral Response Profiling Reveals Pathways to Prostate Cancer Progression. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 600-611.	2.5	54
28	Non-coding RNA LINC00857 is predictive of poor patient survival and promotes tumor progression via cell cycle regulation in lung cancer. <i>Oncotarget</i> , 2016, 7, 11487-11499.	0.8	51
29	Primary Urethral Clear-Cell Adenocarcinoma. <i>American Journal of Pathology</i> , 2014, 184, 584-591.	1.9	46
30	Recurrent reciprocal RNA chimera involving YPEL5 and PPP1CB in chronic lymphocytic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3035-3040.	3.3	44
31	<i>SLC45A3-ELK4</i> Chimera in Prostate Cancer: Spotlight on <i>cis</i> -Splicing. <i>Cancer Discovery</i> , 2012, 2, 582-585.	7.7	40
32	Outlier Kinase Expression by RNA Sequencing as Targets for Precision Therapy. <i>Cancer Discovery</i> , 2013, 3, 280-293.	7.7	40
33	Renal cell tumors with clear cell histology and intact VHL and chromosome 3p: a histological review of tumors from the Cancer Genome Atlas database. <i>Modern Pathology</i> , 2017, 30, 1603-1612.	2.9	30
34	miRConnect 2.0: identification of oncogenic, antagonistic miRNA families in three human cancers. <i>BMC Genomics</i> , 2013, 14, 179.	1.2	18
35	Heat Shock Protein Beta-1 Modifies Anterior to Posterior Purkinje Cell Vulnerability in a Mouse Model of Niemann-Pick Type C Disease. <i>PLoS Genetics</i> , 2016, 12, e1006042.	1.5	18
36	Re: Florian Jentzmik, Carsten Stephan, Kurt Miller, et al. Sarcosine in Urine after Digital Rectal Examination Fails as a Marker in Prostate Cancer Detection and Identification of Aggressive Tumours. <i>Eur Urol</i> 2010;58:12â€“8. <i>European Urology</i> , 2010, 58, e29-e30.	0.9	17

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37	Gene Fusion Markup Language: a prototype for exchanging gene fusion data. BMC Bioinformatics, 2012, 13, 269.	1.2	2