

Shanker Kalyana-Sundaram

List of Publications by Year
in descending order

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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	Characterization of Gene Expression Phenotype in Amyotrophic Lateral Sclerosis Monocytes. JAMA Neurology, 2017, 74, 677.	4.5	130
2	Renal Cell Carcinoma With Chromosome 6p Amplification Including the TFEB Gene. American Journal of Surgical Pathology, 2017, 41, 287-298.	2.1	60
3	Renal cell tumors with clear cell histology and intact VHL and chromosome 3p: a histological review of tumors from the Cancer Genome Atlas database. Modern Pathology, 2017, 30, 1603-1612.	2.9	30
4	A First-Time-in-Human Study of GSK2636771, a Phosphoinositide 3 Kinase Beta-Selective Inhibitor, in Patients with Advanced Solid Tumors. Clinical Cancer Research, 2017, 23, 5981-5992.	3.2	107
5	Heat Shock Protein Beta-1 Modifies Anterior to Posterior Purkinje Cell Vulnerability in a Mouse Model of Niemann-Pick Type C Disease. PLoS Genetics, 2016, 12, e1006042.	1.5	18
6	Inflammation-Induced Oxidative Stress Mediates Gene Fusion Formation in Prostate Cancer. Cell Reports, 2016, 17, 2620-2631.	2.9	68
7	Non-coding RNA LINC00857 is predictive of poor patient survival and promotes tumor progression via cell cycle regulation in lung cancer. Oncotarget, 2016, 7, 11487-11499.	0.8	51
8	Landscape of gene fusions in epithelial cancers: seq and ye shall find. Genome Medicine, 2015, 7, 129.	3.6	127
9	Transcriptome meta-analysis of lung cancer reveals recurrent aberrations in NRG1 and Hippo pathway genes. Nature Communications, 2014, 5, 5893.	5.8	121
10	Primary Urethral Clear-Cell Adenocarcinoma. American Journal of Pathology, 2014, 184, 584-591.	1.9	46
11	miRConnect 2.0: identification of oncogenic, antagonistic miRNA families in three human cancers. BMC Genomics, 2013, 14, 179.	1.2	18
12	Identification of Targetable FGFR Gene Fusions in Diverse Cancers. Cancer Discovery, 2013, 3, 636-647.	7.7	614
13	Identification of recurrent NAB2-STAT6 gene fusions in solitary fibrous tumor by integrative sequencing. Nature Genetics, 2013, 45, 180-185.	9.4	662
14	Activating ESR1 mutations in hormone-resistant metastatic breast cancer. Nature Genetics, 2013, 45, 1446-1451.	9.4	925
15	Outlier Kinase Expression by RNA Sequencing as Targets for Precision Therapy. Cancer Discovery, 2013, 3, 280-293.	7.7	40
16	Recurrent reciprocal RNA chimera involving YPEL5 and PPP1CB in chronic lymphocytic leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3035-3040.	3.3	44
17	<i>SLC45A3-ELK4</i> Chimera in Prostate Cancer: Spotlight on <i>cis</i> -Splicing. Cancer Discovery, 2012, 2, 582-585.	7.7	40
18	Gene Fusions Associated with Recurrent Amplicons Represent a Class of Passenger Aberrations in Breast Cancer. Neoplasia, 2012, 14, 702-IN13.	2.3	60

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19	Gene Fusion Markup Language: a prototype for exchanging gene fusion data. BMC Bioinformatics, 2012, 13, 269.	1.2	2
20	Expressed Pseudogenes in the Transcriptional Landscape of Human Cancers. Cell, 2012, 149, 1622-1634.	13.5	250
21	Functionally recurrent rearrangements of the MAST kinase and Notch gene families in breast cancer. Nature Medicine, 2011, 17, 1646-1651.	15.2	301
22	Personalized Oncology Through Integrative High-Throughput Sequencing: A Pilot Study. Science Translational Medicine, 2011, 3, 111ra121.	5.8	531
23	Deep sequencing reveals distinct patterns of DNA methylation in prostate cancer. Genome Research, 2011, 21, 1028-1041.	2.4	166
24	HPeak: an HMM-based algorithm for defining read-enriched regions in ChIP-Seq data. BMC Bioinformatics, 2010, 11, 369.	1.2	94
25	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. Eur Urol 2010;58:12â€“18. European Urology, 2010, 58, e29-e30.	0.9	17
26	Rearrangements of the RAF kinase pathway in prostate cancer, gastric cancer and melanoma. Nature Medicine, 2010, 16, 793-798.	15.2	436
27	Quantitative Proteomic Profiling of Prostate Cancer Reveals a Role for miR-128 in Prostate Cancer. Molecular and Cellular Proteomics, 2010, 9, 298-312.	2.5	113
28	AGTR1 overexpression defines a subset of breast cancer and confers sensitivity to losartan, an AGTR1 antagonist. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10284-10289.	3.3	140
29	Chimeric transcript discovery by paired-end transcriptome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12353-12358.	3.3	302
30	Transcriptome sequencing to detect gene fusions in cancer. Nature, 2009, 458, 97-101.	13.7	791
31	Metabolomic profiles delineate potential role for sarcosine in prostate cancer progression. Nature, 2009, 457, 910-914.	13.7	1,944
32	Humoral Response Profiling Reveals Pathways to Prostate Cancer Progression. Molecular and Cellular Proteomics, 2008, 7, 600-611.	2.5	54
33	Oncomine 3.0: Genes, Pathways, and Networks in a Collection of 18,000 Cancer Gene Expression Profiles. Neoplasia, 2007, 9, 166-180.	2.3	1,847
34	Molecular Concepts Analysis Links Tumors, Pathways, Mechanisms, and Drugs. Neoplasia, 2007, 9, 443-IN9.	2.3	124
35	Integrative molecular concept modeling of prostate cancer progression. Nature Genetics, 2007, 39, 41-51.	9.4	837
36	Probabilistic model of the human protein-protein interaction network. Nature Biotechnology, 2005, 23, 951-959.	9.4	380

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37	Mining for regulatory programs in the cancer transcriptome. Nature Genetics, 2005, 37, 579-583.	9.4	158