

Somasekar Seshagiri

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

40
papers

6,910
citations

28
h-index

45
g-index

45
ext. papers

8,226
ext. citations

16.7
avg, IF

4.66
L-index

#	Paper	IF	Citations
40	RAF inhibitors prime wild-type RAF to activate the MAPK pathway and enhance growth. <i>Nature</i> , 2010 , 464, 431-5	50.4	1238
39	Diverse somatic mutation patterns and pathway alterations in human cancers. <i>Nature</i> , 2010 , 466, 869-73	50.4	1003
38	Comprehensive genomic analysis identifies SOX2 as a frequently amplified gene in small-cell lung cancer. <i>Nature Genetics</i> , 2012 , 44, 1111-6	36.3	712
37	Recurrent R-spondin fusions in colon cancer. <i>Nature</i> , 2012 , 488, 660-4	50.4	711
36	Comprehensive genomic analysis of malignant pleural mesothelioma identifies recurrent mutations, gene fusions and splicing alterations. <i>Nature Genetics</i> , 2016 , 48, 407-16	36.3	497
35	A comprehensive transcriptional portrait of human cancer cell lines. <i>Nature Biotechnology</i> , 2015 , 33, 306-12	41.5	407
34	Oncogenic ERBB3 mutations in human cancers. <i>Cancer Cell</i> , 2013 , 23, 603-17	24.3	277
33	Spectrum of diverse genomic alterations define non-clear cell renal carcinoma subtypes. <i>Nature Genetics</i> , 2015 , 47, 13-21	36.3	247
32	Somatic mutations in p85alpha promote tumorigenesis through class IA PI3K activation. <i>Cancer Cell</i> , 2009 , 16, 463-74	24.3	241
31	Oncogenic BRAF is required for tumor growth and maintenance in melanoma models. <i>Cancer Research</i> , 2006 , 66, 999-1006	10.1	183
30	Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. <i>Genome Research</i> , 2012 , 22, 2315-27	9.7	158
29	Deep RNA sequencing analysis of readthrough gene fusions in human prostate adenocarcinoma and reference samples. <i>BMC Medical Genomics</i> , 2011 , 4, 11	3.7	120
28	Recurrent Loss of NFE2L2 Exon 2 Is a Mechanism for Nrf2 Pathway Activation in Human Cancers. <i>Cell Reports</i> , 2016 , 16, 2605-2617	10.6	108
27	Combined targeting of BRAF and CRAF or BRAF and PI3K effector pathways is required for efficacy in NRAS mutant tumors. <i>PLoS ONE</i> , 2009 , 4, e5717	3.7	97
26	Human ACE2 receptor polymorphisms predict SARS-CoV-2 susceptibility		70
25	The Indian cobra reference genome and transcriptome enables comprehensive identification of venom toxins. <i>Nature Genetics</i> , 2020 , 52, 106-117	36.3	68
24	Prediction and Quantification of Splice Events from RNA-Seq Data. <i>PLoS ONE</i> , 2016 , 11, e0156132	3.7	67

23	An Empirical Approach Leveraging Tumorgrafts to Dissect the Tumor Microenvironment in Renal Cell Carcinoma Identifies Missing Link to Prognostic Inflammatory Factors. <i>Cancer Discovery</i> , 2018 , 8, 1142-1155	24.4	66
22	Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer. <i>Nature Communications</i> , 2014 , 5, 3830	17.4	66
21	An integrative analysis of colon cancer identifies an essential function for PRPF6 in tumor growth. <i>Genes and Development</i> , 2014 , 28, 1068-84	12.6	65
20	Massively parallel single-cell B-cell receptor sequencing enables rapid discovery of diverse antigen-reactive antibodies. <i>Communications Biology</i> , 2019 , 2, 304	6.7	62
19	Actionable Activating Oncogenic ERBB2/HER2 Transmembrane and Juxtamembrane Domain Mutations. <i>Cancer Cell</i> , 2018 , 34, 792-806.e5	24.3	55
18	SCINA: A Semi-Supervised Subtyping Algorithm of Single Cells and Bulk Samples. <i>Genes</i> , 2019 , 10,	4.2	52
17	Human ACE2 receptor polymorphisms and altered susceptibility to SARS-CoV-2. <i>Communications Biology</i> , 2021 , 4, 475	6.7	43
16	Comprehensive genomic analysis identifies pathogenic variants in maturity-onset diabetes of the young (MODY) patients in South India. <i>BMC Medical Genetics</i> , 2018 , 19, 22	2.1	40
15	Dimerization of the kinase ARAF promotes MAPK pathway activation and cell migration. <i>Science Signaling</i> , 2014 , 7, ra73	8.8	40
14	pHUSH: a single vector system for conditional gene expression. <i>BMC Biotechnology</i> , 2007 , 7, 61	3.5	38
13	Single-cell RNA sequencing identifies distinct mouse medial ganglionic eminence cell types. <i>Scientific Reports</i> , 2017 , 7, 45656	4.9	35
12	ERK Mutations and Amplification Confer Resistance to ERK-Inhibitor Therapy. <i>Clinical Cancer Research</i> , 2018 , 24, 4044-4055	12.9	26
11	Next-Generation Sequencing Reveals Novel Mutations in X-linked Intellectual Disability. <i>OMICS A Journal of Integrative Biology</i> , 2017 , 21, 295-303	3.8	24
10	Integrated genomic analysis reveals mutated ELF3 as a potential gallbladder cancer vaccine candidate. <i>Nature Communications</i> , 2020 , 11, 4225	17.4	19
9	Anti-ferroptotic mechanism of IL4i1-mediated amino acid metabolism. <i>ELife</i> , 2021 , 10,	8.9	14
8	Next generation sequencing identifies novel disease-associated BEST1 mutations in Bestrophinopathy patients. <i>Scientific Reports</i> , 2018 , 8, 10176	4.9	9
7	Proteogenomics analysis unveils a TFG-RET gene fusion and druggable targets in papillary thyroid carcinomas. <i>Nature Communications</i> , 2020 , 11, 2056	17.4	8
6	Accurate assembly of the olive baboon (<i>Papio anubis</i>) genome using long-read and Hi-C data. <i>GigaScience</i> , 2020 , 9,	7.6	8

5	Comprehensive analysis of single molecule sequencing-derived complete genome and whole transcriptome of <i>Hyposidra talaca</i> nuclear polyhedrosis virus. <i>Scientific Reports</i> , 2018 , 8, 8924	4.9	6
4	Restricted epitope specificity determined by variable region germline segment pairing in rodent antibody repertoires. <i>MAbs</i> , 2020 , 12, 1722541	6.6	4
3	Determinants of renal cell carcinoma invasion and metastatic competence. <i>Nature Communications</i> , 2021 , 12, 5760	17.4	3
2	Embryonic lethality and defective mammary gland development of activator-function impaired conditional knock-in <i>ErbB3V943R</i> mice. <i>Genetics & Genomics Next</i> , 2021 , 2, e10036	1.2	
1	<i>Naja naja</i> (Indian Cobra). <i>Trends in Genetics</i> , 2020 , 36, 804-806	8.5	