Somasekar Seshagiri

List of Publications by Year in Descending Order

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	Determinants of renal cell carcinoma invasion and metastatic competence. *Nature Communications*, **2021**, 12, 5760	17.4	3
39	Embryonic lethality and defective mammary gland development of activator-function impaired conditional knock-in Erbb3V943R mice. *Genetics & Genomics Next*, **2021**, 2, e10036	1.2	
38	Anti-ferroptotic mechanism of IL4i1-mediated amino acid metabolism. *ELife*, **2021**, 10,	8.9	14
37	Human ACE2 receptor polymorphisms and altered susceptibility to SARS-CoV-2. *Communications Biology*, **2021**, 4, 475	6.7	43
36	Restricted epitope specificity determined by variable region germline segment pairing in rodent antibody repertoires. *MAbs*, **2020**, 12, 1722541	6.6	4
35	Proteogenomics analysis unveils a TFG-RET gene fusion and druggable targets in papillary thyroid carcinomas. *Nature Communications*, **2020**, 11, 2056	17.4	8
34	The Indian cobra reference genome and transcriptome enables comprehensive identification of venom toxins. *Nature Genetics*, **2020**, 52, 106-117	36.3	68
33	Accurate assembly of the olive baboon (Papio anubis) genome using long-read and Hi-C data. *GigaScience*, **2020**, 9,	7.6	8
32	Naja naja (Indian Cobra). *Trends in Genetics*, **2020**, 36, 804-806	8.5	
31	Integrated genomic analysis reveals mutated ELF3 as a potential gallbladder cancer vaccine candidate. *Nature Communications*, **2020**, 11, 4225	17.4	19
30	Massively parallel single-cell B-cell receptor sequencing enables rapid discovery of diverse antigen-reactive antibodies. *Communications Biology*, **2019**, 2, 304	6.7	62
29	SCINA: A Semi-Supervised Subtyping Algorithm of Single Cells and Bulk Samples. *Genes*, **2019**, 10,	4.2	52
28	Comprehensive genomic analysis identifies pathogenic variants in maturity-onset diabetes of the young (MODY) patients in South India. *BMC Medical Genetics*, **2018**, 19, 22	2.1	40
27	An Empirical Approach Leveraging Tumorgrafts to Dissect the Tumor Microenvironment in Renal Cell Carcinoma Identifies Missing Link to Prognostic Inflammatory Factors. *Cancer Discovery*, **2018**, 8, 1142-1155	24.4	66
26	Comprehensive analysis of single molecule sequencing-derived complete genome and whole transcriptome of Hyposidra talaca nuclear polyhedrosis virus. *Scientific Reports*, **2018**, 8, 8924	4.9	6
25	Next generation sequencing identifies novel disease-associated BEST1 mutations in Bestrophinopathy patients. *Scientific Reports*, **2018**, 8, 10176	4.9	9
24	Actionable Activating Oncogenic ERBB2/HER2 Transmembrane and Juxtamembrane Domain Mutations. *Cancer Cell*, **2018**, 34, 792-806.e5	24.3	55

23	ERK Mutations and Amplification Confer Resistance to ERK-Inhibitor Therapy. *Clinical Cancer Research*, **2018**, 24, 4044-4055	12.9	26
22	Next-Generation Sequencing Reveals Novel Mutations in X-linked Intellectual Disability. *OMICS A Journal of Integrative Biology*, **2017**, 21, 295-303	3.8	24
21	Single-cell RNA sequencing identifies distinct mouse medial ganglionic eminence cell types. *Scientific Reports*, **2017**, 7, 45656	4.9	35
20	Comprehensive genomic analysis of malignant pleural mesothelioma identifies recurrent mutations, gene fusions and splicing alterations. *Nature Genetics*, **2016**, 48, 407-16	36.3	497
19	Prediction and Quantification of Splice Events from RNA-Seq Data. *PLoS ONE*, **2016**, 11, e0156132	3.7	67
18	Recurrent Loss of NFE2L2 Exon 2 Is a Mechanism for Nrf2 Pathway Activation in Human Cancers. *Cell Reports*, **2016**, 16, 2605-2617	10.6	108
17	A comprehensive transcriptional portrait of human cancer cell lines. *Nature Biotechnology*, **2015**, 33, 306-12	44.5	407
16	Spectrum of diverse genomic alterations define non-clear cell renal carcinoma subtypes. *Nature Genetics*, **2015**, 47, 13-21	36.3	247
15	Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer. *Nature Communications*, **2014**, 5, 3830	17.4	66
14	An integrative analysis of colon cancer identifies an essential function for PRPF6 in tumor growth. *Genes and Development*, **2014**, 28, 1068-84	12.6	65
13	Dimerization of the kinase ARAF promotes MAPK pathway activation and cell migration. *Science Signaling*, **2014**, 7, ra73	8.8	40
12	Oncogenic ERBB3 mutations in human cancers. *Cancer Cell*, **2013**, 23, 603-17	24.3	277
11	Recurrent R-spondin fusions in colon cancer. *Nature*, **2012**, 488, 660-4	50.4	711
10	Comprehensive genomic analysis identifies SOX2 as a frequently amplified gene in small-cell lung cancer. *Nature Genetics*, **2012**, 44, 1111-6	36.3	712
9	Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. *Genome Research*, **2012**, 22, 2315-27	9.7	158
8	Deep RNA sequencing analysis of readthrough gene fusions in human prostate adenocarcinoma and reference samples. *BMC Medical Genomics*, **2011**, 4, 11	3.7	120
7	RAF inhibitors prime wild-type RAF to activate the MAPK pathway and enhance growth. *Nature*, **2010**, 464, 431-5	50.4	1238
6	Diverse somatic mutation patterns and pathway alterations in human cancers. *Nature*, **2010**, 466, 869-73	50.4	1003

5	Combined targeting of BRAF and CRAF or BRAF and PI3K effector pathways is required for efficacy in NRAS mutant tumors. *PLoS ONE*, **2009**, 4, e5717	3.7	97
4	Somatic mutations in p85alpha promote tumorigenesis through class IA PI3K activation. *Cancer Cell* , **2009**, 16, 463-74	24.3	241
3	pHUSH: a single vector system for conditional gene expression. *BMC Biotechnology*, **2007**, 7, 61	3.5	38
2	Oncogenic BRAF is required for tumor growth and maintenance in melanoma models. *Cancer Research*, **2006**, 66, 999-1006	10.1	183
1	Human ACE2 receptor polymorphisms predict SARS-CoV-2 susceptibility		70