

Somasekar Seshagiri

List of Publications by Citations

Source: <https://exaly.com/author-pdf/11992539/somasekar-seshagiri-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

38
papers

12,051
citations

33
h-index

39
g-index

39
ext. papers

13,577
ext. citations

21.3
avg, IF

5.04
L-index

#	Paper	IF	Citations
38	De-ubiquitination and ubiquitin ligase domains of A20 downregulate NF-kappaB signalling. <i>Nature</i> , 2004 , 430, 694-9	50.4	1453
37	Mutations in the epidermal growth factor receptor and in KRAS are predictive and prognostic indicators in patients with non-small-cell lung cancer treated with chemotherapy alone and in combination with erlotinib. <i>Journal of Clinical Oncology</i> , 2005 , 23, 5900-9	2.2	1250
36	RAF inhibitors prime wild-type RAF to activate the MAPK pathway and enhance growth. <i>Nature</i> , 2010 , 464, 431-5	50.4	1238
35	Diverse somatic mutation patterns and pathway alterations in human cancers. <i>Nature</i> , 2010 , 466, 869-73	50.4	1003
34	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
33	Recurrent R-spondin fusions in colon cancer. <i>Nature</i> , 2012 , 488, 660-4	50.4	711
32	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
31	Bcl10 activates the NF-kappaB pathway through ubiquitination of NEMO. <i>Nature</i> , 2004 , 427, 167-71	50.4	452
30	Epithelial versus mesenchymal phenotype determines in vitro sensitivity and predicts clinical activity of erlotinib in lung cancer patients. <i>Clinical Cancer Research</i> , 2005 , 11, 8686-98	12.9	451
29	A comprehensive transcriptional portrait of human cancer cell lines. <i>Nature Biotechnology</i> , 2015 , 33, 306-12	42.5	407
28	The mutation spectrum revealed by paired genome sequences from a lung cancer patient. <i>Nature</i> , 2010 , 465, 473-7	50.4	403
27	Somatic mutations lead to an oncogenic deletion of met in lung cancer. <i>Cancer Research</i> , 2006 , 66, 283-9	10.1	364
26	A specificity map for the PDZ domain family. <i>PLoS Biology</i> , 2008 , 6, e239	9.7	348
25	The emerging mutational landscape of G proteins and G-protein-coupled receptors in cancer. <i>Nature Reviews Cancer</i> , 2013 , 13, 412-24	31.3	345
24	Oncogenic ERBB3 mutations in human cancers. <i>Cancer Cell</i> , 2013 , 23, 603-17	24.3	277
23	Spectrum of diverse genomic alterations define non-clear cell renal carcinoma subtypes. <i>Nature Genetics</i> , 2015 , 47, 13-21	36.3	247
22	Somatic mutations in p85alpha promote tumorigenesis through class IA PI3K activation. <i>Cancer Cell</i> , 2009 , 16, 463-74	24.3	241

21	The effects of hepatitis B virus integration into the genomes of hepatocellular carcinoma patients. <i>Genome Research</i> , 2012 , 22, 593-601	9.7	202
20	Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. <i>Genome Research</i> , 2012 , 22, 2315-27	9.7	158
19	Bayesian modeling of the yeast SH3 domain interactome predicts spatiotemporal dynamics of endocytosis proteins. <i>PLoS Biology</i> , 2009 , 7, e1000218	9.7	151
18	Antitumor efficacy of the novel RAF inhibitor GDC-0879 is predicted by BRAFV600E mutational status and sustained extracellular signal-regulated kinase/mitogen-activated protein kinase pathway suppression. <i>Cancer Research</i> , 2009 , 69, 3042-51	10.1	150
17	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
16	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
15	Distinguishing cancer-associated missense mutations from common polymorphisms. <i>Cancer Research</i> , 2007 , 67, 465-73	10.1	103
14	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
13	Disruption of PH-kinase domain interactions leads to oncogenic activation of AKT in human cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 19368-73	11.5	95
12	Coevolution of PDZ domain-ligand interactions analyzed by high-throughput phage display and deep sequencing. <i>Molecular BioSystems</i> , 2010 , 6, 1782-90		85
11	Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer. <i>Nature Communications</i> , 2014 , 5, 3830	17.4	66
10	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
9	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013 , 9, 652	12.2	47
8	Rapid evolution of functional complexity in a domain family. <i>Science Signaling</i> , 2009 , 2, ra50	8.8	47
7	A whole-genome RNAi screen identifies an 8q22 gene cluster that inhibits death receptor-mediated apoptosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E943-51	11.5	44
6	Dimerization of the kinase ARAF promotes MAPK pathway activation and cell migration. <i>Science Signaling</i> , 2014 , 7, ra73	8.8	40
5	High-throughput, high-accuracy array-based resequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 6712-7	11.5	20
4	Integrated genomic analysis reveals mutated ELF3 as a potential gallbladder cancer vaccine candidate. <i>Nature Communications</i> , 2020 , 11, 4225	17.4	19

- 3 Proteogenomics analysis unveils a TFG-RET gene fusion and druggable targets in papillary thyroid carcinomas. *Nature Communications*, **2020**, 11, 2056 17.4 8
- 2 Highly efficient somatic-mutation identification using *Escherichia coli* mismatch-repair detection. *Nature Methods*, **2007**, 4, 713-5 21.6 5
- 1 Regulation of ERK3/MAPK6 expression by BRAF **2006**, 29, 839