

Kavitha Venkatesan

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

18,778
citations

394421

19
h-index

677142

22
g-index

22
all docs

22
docs citations

22
times ranked

31026
citing authors

#	ARTICLE	IF	CITATIONS
1	Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019, 569, 503-508.	27.8	2,149
2	Project DRIVE: A Compendium of Cancer Dependencies and Synthetic Lethal Relationships Uncovered by Large-Scale, Deep RNAi Screening. <i>Cell</i> , 2017, 170, 577-592.e10.	28.9	506
3	Allosteric inhibition of SHP2 phosphatase inhibits cancers driven by receptor tyrosine kinases. <i>Nature</i> , 2016, 535, 148-152.	27.8	674
4	Disordered methionine metabolism in MTAP/CDKN2A-deleted cancers leads to dependence on PRMT5. <i>Science</i> , 2016, 351, 1208-1213.	12.6	374
5	Metabolic Enzyme Sulfotransferase 1A1 Is the Trigger for N-Benzyl Indole Carbinol Tumor Growth Suppression. <i>Chemistry and Biology</i> , 2015, 22, 1228-1237.	6.0	10
6	High-throughput screening using patient-derived tumor xenografts to predict clinical trial drug response. <i>Nature Medicine</i> , 2015, 21, 1318-1325.	30.7	1,065
7	Global chromatin profiling reveals NSD2 mutations in pediatric acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2013, 45, 1386-1391.	21.4	238
8	FGFR Genetic Alterations Predict for Sensitivity to NVP-BGJ398, a Selective Pan-FGFR Inhibitor. <i>Cancer Discovery</i> , 2012, 2, 1118-1133.	9.4	297
9	The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. <i>Nature</i> , 2012, 483, 603-607.	27.8	6,473
10	Quality Control Methodology for High-Throughput Protein-Protein Interaction Screening. <i>Methods in Molecular Biology</i> , 2011, 781, 279-294.	0.9	5
11	A Genome-Wide Gene Function Prediction Resource for <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2010, 5, e12139.	2.5	17
12	Edgetic perturbation models of human inherited disorders. <i>Molecular Systems Biology</i> , 2009, 5, 321.	7.2	326
13	Empirically controlled mapping of the <i>Caenorhabditis elegans</i> protein-protein interactome network. <i>Nature Methods</i> , 2009, 6, 47-54.	19.0	260
14	An empirical framework for binary interactome mapping. <i>Nature Methods</i> , 2009, 6, 83-90.	19.0	800
15	An experimentally derived confidence score for binary protein-protein interactions. <i>Nature Methods</i> , 2009, 6, 91-97.	19.0	397
16	Literature-curated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 39-46.	19.0	288
17	High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. <i>Science</i> , 2008, 322, 104-110.	12.6	1,297
18	Epstein-Barr virus and virus human protein interaction maps. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7606-7611.	7.1	348

#	ARTICLE	IF	CITATIONS
19	hORFeome v3.1: A resource of human open reading frames representing over 10,000 human genes. <i>Genomics</i> , 2007, 89, 307-315.	2.9	248
20	Genome-scale analysis of in vivo spatiotemporal promoter activity in <i>Caenorhabditis elegans</i> . <i>Nature Biotechnology</i> , 2007, 25, 663-668.	17.5	286
21	Towards a proteome-scale map of the human protein-protein interaction network. <i>Nature</i> , 2005, 437, 1173-1178.	27.8	2,676