Alok Jaiswal

List of Publications by Year
in descending order

16 papers	**594** citations	858243 **12** h-index	1051228 **16** g-index
18 all docs	**18** docs citations	**18** times ranked	**1418** citing authors

#	Article	IF	Citations
1	Colon stroma mediates an inflammation-driven fibroblastic response controlling matrix remodeling and healing. PLoS Biology, 2022, 20, e3001532.	2.6	41
2	pH sensing controls tissue inflammation by modulating cellular metabolism and endo-lysosomal function of immune cells. Nature Immunology, 2022, 23, 1063-1075.	7.0	30
3	QRICH1 dictates the outcome of ER stress through transcriptional control of proteostasis. Science, 2021, 371, .	6.0	73
4	Novel Small Molecule Hsp90/Cdc37 Interface Inhibitors Indirectly Target K-Ras-Signaling. Cancers, 2021, 13, 927.	1.7	11
5	Multiâ€modal metaâ€analysis of cancer cell line omics profiles identifies ECHDC1 as a novel breast tumor suppressor. Molecular Systems Biology, 2021, 17, e9526.	3.2	8
6	<i>UBR5</i> Is Coamplified with <i>MYC</i> in Breast Tumors and Encodes an Ubiquitin Ligase That Limits MYC-Dependent Apoptosis. Cancer Research, 2020, 80, 1414-1427.	0.4	35
7	Network pharmacology modeling identifies synergistic Aurora B and ZAK interaction in triple-negative breast cancer. Npj Systems Biology and Applications, 2019, 5, 20.	1.4	32
8	Phenotypic Screening Combined with Machine Learning for Efficient Identification of Breast Cancer-Selective Therapeutic Targets. Cell Chemical Biology, 2019, 26, 970-979.e4.	2.5	34
9	Integrated Analysis of Drug Sensitivity and Selectivity to Predict Synergistic Drug Combinations and Target Coaddictions in Cancer. Methods in Molecular Biology, 2019, 1888, 205-217.	0.4	7
10	Drug Target Commons: A Community Effort to Build a Consensus Knowledge Base for Drug-Target Interactions. Cell Chemical Biology, 2018, 25, 224-229.e2.	2.5	124
11	Drug Target Commons 2.0: a community platform for systematic analysis of drugâ€"target interaction profiles. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-13.	1.4	36
12	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. Cell Systems, 2017, 5, 485-497.e3.	2.9	19
13	Seed-effect modeling improves the consistency of genome-wide loss-of-function screens and identifies synthetic lethal vulnerabilities in cancer cells. Genome Medicine, 2017, 9, 51.	3.6	12
14	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature Communications, 2016, 7, 12460.	5.8	73
15	Specific cancer-associated mutations in the switch III region of Ras increase tumorigenicity by nanocluster augmentation. ELife, 2015, 4, e08905.	2.8	45
16	The Challenges of Genome-Wide Interaction Studies: Lessons to Learn from the Analysis of HDL Blood Levels. PLoS ONE, 2014, 9, e109290.	1.1	13