

Alok Jaiswal

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

594
citations

759233

12
h-index

940533

16
g-index

18
all docs

18
docs citations

18
times ranked

1275
citing authors

#	ARTICLE	IF	CITATIONS
1	Colon stroma mediates an inflammation-driven fibroblastic response controlling matrix remodeling and healing. <i>PLoS Biology</i> , 2022, 20, e3001532.	5.6	41
2	pH sensing controls tissue inflammation by modulating cellular metabolism and endo-lysosomal function of immune cells. <i>Nature Immunology</i> , 2022, 23, 1063-1075.	14.5	30
3	QRICH1 dictates the outcome of ER stress through transcriptional control of proteostasis. <i>Science</i> , 2021, 371, .	12.6	73
4	Novel Small Molecule Hsp90/Cdc37 Interface Inhibitors Indirectly Target K-Ras-Signaling. <i>Cancers</i> , 2021, 13, 927.	3.7	11
5	Multi-modal meta-analysis of cancer cell line omics profiles identifies ECHDC1 as a novel breast tumor suppressor. <i>Molecular Systems Biology</i> , 2021, 17, e9526.	7.2	8
6	<i>UBR5</i> Is Coamplified with <i>MYC</i> in Breast Tumors and Encodes an Ubiquitin Ligase That Limits MYC-Dependent Apoptosis. <i>Cancer Research</i> , 2020, 80, 1414-1427.	0.9	35
7	Network pharmacology modeling identifies synergistic Aurora B and ZAK interaction in triple-negative breast cancer. <i>Npj Systems Biology and Applications</i> , 2019, 5, 20.	3.0	32
8	Phenotypic Screening Combined with Machine Learning for Efficient Identification of Breast Cancer-Selective Therapeutic Targets. <i>Cell Chemical Biology</i> , 2019, 26, 970-979.e4.	5.2	34
9	Integrated Analysis of Drug Sensitivity and Selectivity to Predict Synergistic Drug Combinations and Target Coaddictions in Cancer. <i>Methods in Molecular Biology</i> , 2019, 1888, 205-217.	0.9	7
10	Drug Target Commons: A Community Effort to Build a Consensus Knowledge Base for Drug-Target Interactions. <i>Cell Chemical Biology</i> , 2018, 25, 224-229.e2.	5.2	124
11	Drug Target Commons 2.0: a community platform for systematic analysis of drug-target interaction profiles. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, 1-13.	3.0	36
12	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. <i>Cell Systems</i> , 2017, 5, 485-497.e3.	6.2	19
13	Seed-effect modeling improves the consistency of genome-wide loss-of-function screens and identifies synthetic lethal vulnerabilities in cancer cells. <i>Genome Medicine</i> , 2017, 9, 51.	8.2	12
14	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. <i>Nature Communications</i> , 2016, 7, 12460.	12.8	73
15	Specific cancer-associated mutations in the switch III region of Ras increase tumorigenicity by nanocluster augmentation. <i>ELife</i> , 2015, 4, e08905.	6.0	45
16	The Challenges of Genome-Wide Interaction Studies: Lessons to Learn from the Analysis of HDL Blood Levels. <i>PLoS ONE</i> , 2014, 9, e109290.	2.5	13