

Bertram Klinger

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7296494/publications.pdf>

Version: 2024-02-01

24
papers

1,211
citations

623734

14
h-index

580821

25
g-index

31
all docs

31
docs citations

31
times ranked

2355
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutation-specific effects of NRAS oncogenes in colorectal cancer cells. <i>Advances in Biological Regulation</i> , 2021, 79, 100778.	2.3	4
2	Neuroblastoma signalling models unveil combination therapies targeting feedback-mediated resistance. <i>PLoS Computational Biology</i> , 2021, 17, e1009515.	3.2	5
3	Early senescence and production of senescence-associated cytokines are major determinants of radioresistance in head-and-neck squamous cell carcinoma. <i>Cell Death and Disease</i> , 2021, 12, 1162.	6.3	23
4	SFPQ Depletion Is Synthetically Lethal with BRAFV600E in Colorectal Cancer Cells. <i>Cell Reports</i> , 2020, 32, 108184.	6.4	19
5	Neuronal activity regulates alternative exon usage. <i>Molecular Brain</i> , 2020, 13, 148.	2.6	7
6	SPEED2: inferring upstream pathway activity from differential gene expression. <i>Nucleic Acids Research</i> , 2020, 48, W307-W312.	14.5	28
7	Reduced replication origin licensing selectively kills KRAS-mutant colorectal cancer cells via mitotic catastrophe. <i>Cell Death and Disease</i> , 2020, 11, 499.	6.3	4
8	Cell type-dependent differential activation of ERK by oncogenic KRAS in colon cancer and intestinal epithelium. <i>Nature Communications</i> , 2019, 10, 2919.	12.8	70
9	Isoform-specific Ras signaling is growth factor dependent. <i>Molecular Biology of the Cell</i> , 2019, 30, 1108-1117.	2.1	23
10	The cancer cell proteome and transcriptome predicts sensitivity to targeted and cytotoxic drugs. <i>Life Science Alliance</i> , 2019, 2, e201900445.	2.8	9
11	Perturbation-response genes reveal signaling footprints in cancer gene expression. <i>Nature Communications</i> , 2018, 9, 20.	12.8	436
12	Comparative Network Reconstruction using mixed integer programming. <i>Bioinformatics</i> , 2018, 34, i997-i1004.	4.1	8
13	Reverse engineering gene regulatory networks by modular response analysis – a benchmark. <i>Essays in Biochemistry</i> , 2018, 62, 535-547.	4.7	18
14	Modelling signalling networks from perturbation data. <i>Bioinformatics</i> , 2018, 34, 4079-4086.	4.1	25
15	An immediate-early gene expression module decodes ERK signal duration. <i>Molecular Systems Biology</i> , 2017, 13, 928.	7.2	47
16	Drug Resistance Mechanisms in Colorectal Cancer Dissected with Cell Type-Specific Dynamic Logic Models. <i>Cancer Research</i> , 2017, 77, 3364-3375.	0.9	101
17	Annexin A1 sustains tumor metabolism and cellular proliferation upon stable loss of HIF1A. <i>Oncotarget</i> , 2016, 7, 6693-6710.	1.8	12
18	Hypoxia-induced gene expression results from selective mRNA partitioning to the endoplasmic reticulum. <i>Nucleic Acids Research</i> , 2015, 43, 3219-3236.	14.5	38

#	ARTICLE	IF	CITATIONS
19	Computer-assisted curation of a human regulatory core network from the biological literature. <i>Bioinformatics</i> , 2015, 31, 1258-1266.	4.1	10
20	Consequences of feedback in signal transduction for targeted therapies. <i>Biochemical Society Transactions</i> , 2014, 42, 770-775.	3.4	15
21	Network quantification of EGFR signaling unveils potential for targeted combination therapy. <i>Molecular Systems Biology</i> , 2013, 9, 673.	7.2	158
22	Reverse engineering a hierarchical regulatory network downstream of oncogenic KRAS. <i>Molecular Systems Biology</i> , 2012, 8, 601.	7.2	53
23	Multilevel regulation of HIF-1 signaling by TTP. <i>Molecular Biology of the Cell</i> , 2012, 23, 4129-4141.	2.1	15
24	Discovering causal signaling pathways through gene-expression patterns. <i>Nucleic Acids Research</i> , 2010, 38, W109-W117.	14.5	65