Momeneh Foroutan

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Targeting WEE1/AKT Restores p53-Dependent Natural Killer–Cell Activation to Induce Immune Checkpoint Blockade Responses in "Cold―Melanoma. Cancer Immunology Research, 2022, 10, 757-769.	3.4	11
2	Computational Screening of Anti-Cancer Drugs Identifies a New BRCA Independent Gene Expression Signature to Predict Breast Cancer Sensitivity to Cisplatin. Cancers, 2022, 14, 2404.	3.7	2
3	TGFβ and CIS Inhibition Overcomes NK-cell Suppression to Restore Antitumor Immunity. Cancer Immunology Research, 2022, 10, 1047-1054.	3.4	11
4	CSK-homologous kinase (CHK/MATK) is a potential colorectal cancer tumour suppressor gene epigenetically silenced by promoter methylation. Oncogene, 2021, 40, 3015-3029.	5.9	13
5	The Ratio of Exhausted to Resident Infiltrating Lymphocytes Is Prognostic for Colorectal Cancer Patient Outcome. Cancer Immunology Research, 2021, 9, 1125-1140.	3.4	18
6	A Gene Signature Predicting Natural Killer Cell Infiltration and Improved Survival in Melanoma Patients. Cancer Immunology Research, 2019, 7, 1162-1174.	3.4	201
7	Using singscore to predict mutation status in acute myeloid leukemia from transcriptomic signatures. F1000Research, 2019, 8, 776.	1.6	12
8	Using singscore to predict mutations in acute myeloid leukemia from transcriptomic signatures. F1000Research, 2019, 8, 776.	1.6	9
9	Single sample scoring of molecular phenotypes. BMC Bioinformatics, 2018, 19, 404.	2.6	286
10	Combinatorial Targeting by MicroRNAs Co-ordinates Post-transcriptional Control of EMT. Cell Systems, 2018, 7, 77-91.e7.	6.2	92
11	A Transcriptional Program for Detecting TGFβ-Induced EMT in Cancer. Molecular Cancer Research, 2017, 15, 619-631.	3.4	63
12	Networking and Bayesian analyses of genetic affinity in cotton germplasm. Nucleus (India), 2015, 58, 33-45.	2.2	5
13	Stimulus-dependent differences in signalling regulate epithelial-mesenchymal plasticity and change the effects of drugs in breast cancer cell lines. Cell Communication and Signaling, 2015, 13, 26.	6.5	47
14	Using singscore to predict mutation status in acute myeloid leukemia from transcriptomic signatures. F1000Research, 0, 8, 776.	1.6	1