

Joseph Cursons

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

1,799
citations

471509

17
h-index

395702

33
g-index

44
all docs

44
docs citations

44
times ranked

3059
citing authors

#	ARTICLE	IF	CITATIONS
1	Computational Screening of Anti-Cancer Drugs Identifies a New BRCA Independent Gene Expression Signature to Predict Breast Cancer Sensitivity to Cisplatin. <i>Cancers</i> , 2022, 14, 2404.	3.7	2
2	High temporal resolution RNA-seq time course data reveals widespread synchronous activation between mammalian lncRNAs and neighboring protein-coding genes. <i>Genome Research</i> , 2022, 32, 1463-1473.	5.5	5
3	The oncogene AAMDC links PI3K-AKT-mTOR signaling with metabolic reprogramming in estrogen receptor-positive breast cancer. <i>Nature Communications</i> , 2021, 12, 1920.	12.8	19
4	The Ratio of Exhausted to Resident Infiltrating Lymphocytes Is Prognostic for Colorectal Cancer Patient Outcome. <i>Cancer Immunology Research</i> , 2021, 9, 1125-1140.	3.4	18
5	Modular assembly of dynamic models in systems biology. <i>PLoS Computational Biology</i> , 2021, 17, e1009513.	3.2	19
6	Stable gene expression for normalisation and single-sample scoring. <i>Nucleic Acids Research</i> , 2020, 48, e113-e113.	14.5	34
7	Harnessing Natural Killer Immunity in Metastatic SCLC. <i>Journal of Thoracic Oncology</i> , 2020, 15, 1507-1521.	1.1	50
8	The cancer's natural killer cell immunity cycle. <i>Nature Reviews Cancer</i> , 2020, 20, 437-454.	28.4	308
9	The cardiac Na ⁺ /K ⁺ ATPase: An updated, thermodynamically consistent model. <i>Physiome</i> , 2020, , .	0.3	4
10	The cardiac Na ⁺ /K ⁺ ATPase: An updated, thermodynamically consistent model. <i>Physiome</i> , 2020, , .	0.3	1
11	Extensive transcriptional responses are co-ordinated by microRNAs as revealed by Exon-Intron Split Analysis (EISA). <i>Nucleic Acids Research</i> , 2019, 47, 8606-8619.	14.5	9
12	Therapeutic blockade of activin-A improves NK cell function and antitumor immunity. <i>Science Signaling</i> , 2019, 12, .	3.6	64
13	A Gene Signature Predicting Natural Killer Cell Infiltration and Improved Survival in Melanoma Patients. <i>Cancer Immunology Research</i> , 2019, 7, 1162-1174.	3.4	201
14	Differential co-expression-based detection of conditional relationships in transcriptional data: comparative analysis and application to breast cancer. <i>Genome Biology</i> , 2019, 20, 236.	8.8	53
15	The Emergence of Natural Killer Cells as a Major Target in Cancer Immunotherapy. <i>Trends in Immunology</i> , 2019, 40, 142-158.	6.8	218
16	A thermodynamic framework for modelling membrane transporters. <i>Journal of Theoretical Biology</i> , 2019, 481, 10-23.	1.7	24
17	Using singscore to predict mutation status in acute myeloid leukemia from transcriptomic signatures. <i>F1000Research</i> , 2019, 8, 776.	1.6	12
18	Using singscore to predict mutations in acute myeloid leukemia from transcriptomic signatures. <i>F1000Research</i> , 2019, 8, 776.	1.6	9

#	ARTICLE	IF	CITATIONS
19	Single sample scoring of molecular phenotypes. BMC Bioinformatics, 2018, 19, 404.	2.6	286
20	Bond graph modelling of the cardiac action potential: implications for drift and non-unique steady states. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2018, 474, 20180106.	2.1	19
21	Combinatorial Targeting by MicroRNAs Co-ordinates Post-transcriptional Control of EMT. Cell Systems, 2018, 7, 77-91.e7.	6.2	92
22	A Transcriptional Program for Detecting TGF β -Induced EMT in Cancer. Molecular Cancer Research, 2017, 15, 619-631.	3.4	63
23	Determining the Significance of Protein Network Features and Attributes Using Permutation Testing. Methods in Molecular Biology, 2017, 1549, 199-208.	0.9	1
24	Toward Community Standards and Software for Whole-Cell Modeling. IEEE Transactions on Biomedical Engineering, 2016, 63, 2007-2014.	4.2	51
25	The complexities and caveats of lineage tracing in the mammary gland. Breast Cancer Research, 2016, 18, 116.	5.0	25
26	Systems analysis identifies miR-29b regulation of invasiveness in melanoma. Molecular Cancer, 2016, 15, 72.	19.2	21
27	Spatially transformed fluorescence image data for ERK-MAPK and selected proteins within human epidermis. GigaScience, 2015, 4, 63.	6.4	6
28	Hierarchical bond graph modelling of biochemical networks. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2015, 471, 20150642.	2.1	41
29	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
30	Regulation of ERK-MAPK signaling in human epidermis. BMC Systems Biology, 2015, 9, 41.	3.0	33
31	NAIL, a software toolset for inferring, analyzing and visualizing regulatory networks. Bioinformatics, 2015, 31, 277-278.	4.1	12
32	Predicting expression: the complementary power of histone modification and transcription factor binding data. Epigenetics and Chromatin, 2014, 7, 36.	3.9	32
33	Inference of an in situ epidermal intracellular signaling cascade. , 2010, 2010, 799-802.		3
34	Using singscore to predict mutation status in acute myeloid leukemia from transcriptomic signatures. F1000Research, 0, 8, 776.	1.6	1