Joseph Cursons

List of Publications by Year
in descending order

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	The cancer–natural killer cell immunity cycle. Nature Reviews Cancer, 2020, 20, 437-454.	28.4	308
2	Single sample scoring of molecular phenotypes. BMC Bioinformatics, 2018, 19, 404.	2.6	286
3	The Emergence of Natural Killer Cells as a Major Target in Cancer Immunotherapy. Trends in Immunology, 2019, 40, 142-158.	6.8	218
4	A Gene Signature Predicting Natural Killer Cell Infiltration and Improved Survival in Melanoma Patients. Cancer Immunology Research, 2019, 7, 1162-1174.	3.4	201
5	Combinatorial Targeting by MicroRNAs Co-ordinates Post-transcriptional Control of EMT. Cell Systems, 2018, 7, 77-91.e7.	6.2	92
6	Therapeutic blockade of activin-A improves NK cell function and antitumor immunity. Science Signaling, 2019, 12, .	3.6	64
7	A Transcriptional Program for Detecting TGFβ-Induced EMT in Cancer. Molecular Cancer Research, 2017, 15, 619-631.	3.4	63
8	Differential co-expression-based detection of conditional relationships in transcriptional data: comparative analysis and application to breast cancer. Genome Biology, 2019, 20, 236.	8.8	53
9	Toward Community Standards and Software for Whole-Cell Modeling. IEEE Transactions on Biomedical Engineering, 2016, 63, 2007-2014.	4.2	51
10	Harnessing Natural Killer Immunity in Metastatic SCLC. Journal of Thoracic Oncology, 2020, 15, 1507-1521.	1.1	50
11	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
12	Hierarchical bond graph modelling of biochemical networks. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2015, 471, 20150642.	2.1	41
13	Stable gene expression for normalisation and single-sample scoring. Nucleic Acids Research, 2020, 48, e113-e113.	14.5	34
14	Regulation of ERK-MAPK signaling in human epidermis. BMC Systems Biology, 2015, 9, 41.	3.0	33
15	Predicting expression: the complementary power of histone modification and transcription factor binding data. Epigenetics and Chromatin, 2014, 7, 36.	3.9	32
16	The complexities and caveats of lineage tracing in the mammary gland. Breast Cancer Research, 2016, 18, 116.	5.0	25
17	A thermodynamic framework for modelling membrane transporters. Journal of Theoretical Biology, 2019, 481, 10-23.	1.7	24
18	Systems analysis identifies miR-29b regulation of invasiveness in melanoma. Molecular Cancer, 2016, 15, 72.	19.2	21

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19	Bond graph modelling of theÂcardiac 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
20	The oncogene AAMDC links PI3K-AKT-mTOR signaling with metabolic reprograming in estrogen receptor-positive breast cancer. Nature Communications, 2021, 12, 1920.	12.8	19
21	Modular assembly of dynamic models in systems biology. PLoS Computational Biology, 2021, 17, e1009513.	3.2	19
22	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
23	NAIL, a software toolset for inferring, analyzing and visualizing regulatory networks. Bioinformatics, 2015, 31, 277-278.	4.1	12
24	Using singscore to predict mutation status in acute myeloid leukemia from transcriptomic signatures. F1000Research, 2019, 8, 776.	1.6	12
25	Extensive transcriptional responses are co-ordinated by microRNAs as revealed by Exonâ€"Intron Split Analysis (EISA). Nucleic Acids Research, 2019, 47, 8606-8619.	14.5	9
26	Using singscore to predict mutations in acute myeloid leukemia from transcriptomic signatures. F1000Research, 2019, 8, 776.	1.6	9
27	Spatially transformed fluorescence image data for ERK-MAPK and selected proteins within human epidermis. GigaScience, 2015, 4, 63.	6.4	6
28	High temporal resolution RNA-seq time course data reveals widespread synchronous activation between mammalian lncRNAs and neighboring protein-coding genes. Genome Research, 2022, 32, 1463-1473.	5.5	5
29	The cardiac Na+/K+ ATPase: An updated, thermodynamically consistent model. Physiome, 2020, , .	0.3	4
30	Inference of an in situ epidermal intracellular signaling cascade. , 2010, 2010, 799-802.		3
31	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
32	Determining the Significance of Protein Network Features and Attributes Using Permutation Testing. Methods in Molecular Biology, 2017, 1549, 199-208.	0.9	1
33	Using singscore to predict mutation status in acute myeloid leukemia from transcriptomic signatures. F1000Research, 0, 8, 776.	1.6	1
34	The cardiac Na+/K+ ATPase: An updated, thermodynamically consistent model. Physiome, 2020, , .	0.3	1