Melissa J Davis

List of Publications by Year
in descending order

45 papers	2,076 citations	257450 24 h-index	276875 41 g-index
55 all docs	55 docs citations	55 times ranked	3585 citing authors

#	Article	IF	Citations
1	Measuring and Modelling the Epithelial- Mesenchymal Hybrid State in Cancer: Clinical Implications. Cells Tissues Organs, 2022, 211, 110-133.	2.3	28
2	Profiling of lung SARS-CoV-2 and influenza virus infection dissects virus-specific host responses and gene signatures. European Respiratory Journal, 2022, 59, 2101881.	6.7	37
3	SFPQ-ABL1 and BCR-ABL1 use different signaling networks to drive B-cell acute lymphoblastic leukemia. Blood Advances, 2022, 6, 2373-2387.	5.2	4
4	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
5	TGFÎ² and CIS Inhibition Overcomes NK-cell Suppression to Restore Antitumor Immunity. Cancer Immunology Research, 2022, 10, 1047-1054.	3.4	11
6	Type 2 Innate Lymphoid Cells Protect against Colorectal Cancer Progression and Predict Improved Patient Survival. Cancers, 2021, 13, 559.	3.7	31
7	PRMT1-mediated H4R3me2a recruits SMARCA4 to promote colorectal cancer progression by enhancing EGFR signaling. Genome Medicine, 2021, 13, 58.	8.2	62
8	Elp2 mutations perturb the epitranscriptome and lead to a complex neurodevelopmental phenotype. Nature Communications, 2021, 12, 2678.	12.8	26
9	Systems pharmacogenomics identifies novel targets and clinically actionable therapeutics for medulloblastoma. Genome Medicine, 2021, 13, 103.	8.2	10
10	Blockade of the co-inhibitory molecule PD-1 unleashes ILC2-dependent antitumor immunity in melanoma. Nature Immunology, 2021, 22, 851-864.	14.5	97
11	The site of breast cancer metastases dictates their clonal composition and reversible transcriptomic profile. Science Advances, 2021, 7, .	10.3	23
12	SOX9 Defines Distinct Populations of Cells in SHH Medulloblastoma but Is Not Required for Math1-Driven Tumor Formation. Molecular Cancer Research, 2021, 19, 1831-1839.	3.4	5
13	Metastasis-Entrained Eosinophils Enhance Lymphocyte-Mediated Antitumor Immunity. Cancer Research, 2021, 81, 5555-5571.	0.9	35
14	Stable gene expression for normalisation and single-sample scoring. Nucleic Acids Research, 2020, 48, e113-e113.	14.5	34
15	Hhex Directly Represses BIM-Dependent Apoptosis to Promote NK Cell Development and Maintenance. Cell Reports, 2020, 33, 108285.	6.4	7
16	Eukaryote-Conserved Methylarginine Is Absent in Diplomonads and Functionally Compensated in Giardia. Molecular Biology and Evolution, 2020, 37, 3525-3549.	8.9	9
17	NK cellâ€“derived GM-CSF potentiates inflammatory arthritis and is negatively regulated by CIS. Journal of Experimental Medicine, 2020, 217, .	8.5	60
18	Harnessing Natural Killer Immunity in Metastatic SCLC. Journal of Thoracic Oncology, 2020, 15, 1507-1521.	1.1	50

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19	Snail induces epithelial cell extrusion by regulating RhoA contractile signaling and cell-matrix adhesion. Journal of Cell Science, 2020, 133, .	2.0	11
20	The EMT modulator SNAI1 contributes to AML pathogenesis via its interaction with LSD1. Blood, 2020, 136, 957-973.	1.4	35
21	An Erg-driven transcriptional program controls B cell lymphopoiesis. Nature Communications, 2020, 11, 3013.	12.8	29
22	Cotargeting BCL-2 and MCL-1 in high-risk B-ALL. Blood Advances, 2020, 4, 2762-2767.	5.2	28
23	NK Cell Priming From Endogenous Homeostatic Signals Is Modulated by CIS. Frontiers in Immunology, 2020, 11, 75.	4.8	27
24	Therapeutic blockade of activin-A improves NK cell function and antitumor immunity. Science Signaling, 2019, 12, .	3.6	64
25	Integrative Analysis of Somatic Mutations in Non-coding Regions Altering RNA Secondary Structures in Cancer Genomes. Scientific Reports, 2019, 9, 8205.	3.3	14
26	A Gene Signature Predicting Natural Killer Cell Infiltration and Improved Survival in Melanoma Patients. Cancer Immunology Research, 2019, 7, 1162-1174.	3.4	201
27	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
28	Using singscore to predict mutation status in acute myeloid leukemia from transcriptomic signatures. F1000Research, 2019, 8, 776.	1.6	12
29	Using singscore to predict mutations in acute myeloid leukemia from transcriptomic signatures. F1000Research, 2019, 8, 776.	1.6	9
30	Single sample scoring of molecular phenotypes. BMC Bioinformatics, 2018, 19, 404.	2.6	286
31	Combinatorial Targeting by MicroRNAs Co-ordinates Post-transcriptional Control of EMT. Cell Systems, 2018, 7, 77-91.e7.	6.2	92
32	A Transcriptional Program for Detecting TGFÎ²-Induced EMT in Cancer. Molecular Cancer Research, 2017, 15, 619-631.	3.4	63
33	Inhibition of CDK4/6 by Palbociclib Significantly Extends Survival in Medulloblastoma Patient-Derived Xenograft Mouse Models. Clinical Cancer Research, 2017, 23, 5802-5813.	7.0	74
34	Determining the Significance of Protein Network Features and Attributes Using Permutation Testing. Methods in Molecular Biology, 2017, 1549, 199-208.	0.9	1
35	Network analysis of an in vitro model of androgen-resistance in prostate cancer. BMC Cancer, 2015, 15, 883.	2.6	3
36	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

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37	RaftProt: mammalian lipid raft proteome database. Nucleic Acids Research, 2015, 43, D335-D338.	14.5	38
38	Predicting expression: the complementary power of histone modification and transcription factor binding data. Epigenetics and Chromatin, 2014, 7, 36.	3.9	32
39	Supervised, semi-supervised and unsupervised inference of gene regulatory networks. Briefings in Bioinformatics, 2014, 15, 195-211.	6.5	140
40	Sleeping Beauty mutagenesis in a mouse medulloblastoma model defines networks that discriminate between human molecular subgroups. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4325-34.	7.1	62
41	Gene regulatory network inference: evaluation and application to ovarian cancer allows the prioritization of drug targets. Genome Medicine, 2012, 4, 41.	8.2	136
42	mCOPA: analysis of heterogeneous features in cancer expression data. Journal of Clinical Bioinformatics, 2012, 2, 22.	1.2	20
43	Automatic, context-specific generation of Gene Ontology slims. BMC Bioinformatics, 2010, 11, 498.	2.6	33
44	Using singscore to predict mutation status in acute myeloid leukemia from transcriptomic signatures. F1000Research, 0, 8, 776.	1.6	1
45	Functional divergence of the two Elongator subcomplexes during neurodevelopment. EMBO Molecular Medicine, 0, , .	6.9	10