

Thomas Fleischer

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

1,433
citations

361413

20
h-index

345221

36
g-index

44
all docs

44
docs citations

44
times ranked

2882
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic alterations at distal enhancers are linked to proliferation in human breast cancer. <i>NAR Cancer</i> , 2022, 4, zcac008.	3.1	6
2	Quantification of Tumor Hypoxia through Unsupervised Modelling of Consumption and Supply Hypoxia MR Imaging in Breast Cancer. <i>Cancers</i> , 2022, 14, 1326.	3.7	3
3	Pioneer transcription factors are associated with the modulation of DNA methylation patterns across cancers. <i>Epigenetics and Chromatin</i> , 2022, 15, 13.	3.9	13
4	DNA methylation changes in response to neoadjuvant chemotherapy are associated with breast cancer survival. <i>Breast Cancer Research</i> , 2022, 24, .	5.0	11
5	Rank-based Bayesian variable selection for genome-wide transcriptomic analyses. <i>Statistics in Medicine</i> , 2022, 41, 4532-4553.	1.6	3
6	Multi-modal meta-analysis of cancer cell line omics profiles identifies ECHDC1 as a novel breast tumor suppressor. <i>Molecular Systems Biology</i> , 2021, 17, e9526.	7.2	8
7	Crosstalk between microRNA expression and DNA methylation drives the hormone-dependent phenotype of breast cancer. <i>Genome Medicine</i> , 2021, 13, 72.	8.2	27
8	Multi-Omics Marker Analysis Enables Early Prediction of Breast Tumor Progression. <i>Frontiers in Genetics</i> , 2021, 12, 670749.	2.3	9
9	Independent Validation of Early-Stage Non-Small Cell Lung Cancer Prognostic Scores Incorporating Epigenetic and Transcriptional Biomarkers With Gene-Gene Interactions and Main Effects. <i>Chest</i> , 2020, 158, 808-819.	0.8	26
10	Epigenome-wide gene-age interaction analysis reveals reversed effects of <i>PRODHDNA</i> methylation on survival between young and elderly early-stage NSCLC patients. <i>Aging</i> , 2020, 12, 10642-10662.	3.1	8
11	<i>EGLN2</i> DNA methylation and expression interact with <i>HIF1A</i> to affect survival of early-stage NSCLC. <i>Epigenetics</i> , 2019, 14, 118-129.	2.7	28
12	Toward Personalized Computer Simulation of Breast Cancer Treatment: A Multiscale Pharmacokinetic and Pharmacodynamic Model Informed by Multitype Patient Data. <i>Cancer Research</i> , 2019, 79, 4293-4304.	0.9	15
13	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. <i>Nature Communications</i> , 2019, 10, 1749.	12.8	46
14	<i>SIP1L3</i> methylation modifies the benefit of smoking cessation on lung adenocarcinoma survival: an epigenomic-smoking interaction analysis. <i>Molecular Oncology</i> , 2019, 13, 1235-1248.	4.6	19
15	Trans-omics biomarker model improves prognostic prediction accuracy for early-stage lung adenocarcinoma. <i>Aging</i> , 2019, 11, 6312-6335.	3.1	13
16	A multi-omic study reveals <i>BTG2</i> as a reliable prognostic marker for early-stage non-small cell lung cancer. <i>Molecular Oncology</i> , 2018, 12, 913-924.	4.6	31
17	Epigenetic modifications in KDM lysine demethylases associate with survival of early-stage NSCLC. <i>Clinical Epigenetics</i> , 2018, 10, 41.	4.1	12
18	Time series analysis of neoadjuvant chemotherapy and bevacizumab-treated breast carcinomas reveals a systemic shift in genomic aberrations. <i>Genome Medicine</i> , 2018, 10, 92.	8.2	17

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19	DNA Methylation of <i>LRRC3B</i> : A Biomarker for Survival of Early-Stage Non-Small Cell Lung Cancer Patients. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 1527-1535.	2.5	10
20	Serum cytokine levels in breast cancer patients during neoadjuvant treatment with bevacizumab. <i>Oncolmmunology</i> , 2018, 7, e1457598.	4.6	18
21	The Longitudinal Transcriptional Response to Neoadjuvant Chemotherapy with and without Bevacizumab in Breast Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 4662-4670.	7.0	31
22	DNA methylation at enhancers identifies distinct breast cancer lineages. <i>Nature Communications</i> , 2017, 8, 1379.	12.8	103
23	DNA methylation signature (<i>SAM40</i>) identifies subgroups of the Luminal A breast cancer samples with distinct survival. <i>Oncotarget</i> , 2017, 8, 1074-1082.	1.8	16
24	Abstract LB-097: DNA methylation at enhancers distinguishes distinct breast cancer lineages. , 2017, , .		0
25	Aberrant DNA methylation impacts gene expression and prognosis in breast cancer subtypes. <i>International Journal of Cancer</i> , 2016, 138, 87-97.	5.1	136
26	Genome-wide DNA methylation analyses in lung adenocarcinomas: Association with EGFR, KRAS and TP53 mutation status, gene expression and prognosis. <i>Molecular Oncology</i> , 2016, 10, 330-343.	4.6	81
27	Abstract LB-337: Systemic shift in genomic aberrations in breast carcinomas during neoadjuvant chemotherapy in combination with bevacizumab. , 2016, , .		0
28	DNA methylation in ductal carcinoma in situ related with future development of invasive breast cancer. <i>Clinical Epigenetics</i> , 2015, 7, 75.	4.1	49
29	DNA Methylation Status of Key Cell-Cycle Regulators Such as <i>CDKN2A/p16</i> and <i>CCNA1</i> Correlates with Treatment Response to Doxorubicin and 5-Fluorouracil in Locally Advanced Breast Tumors. <i>Clinical Cancer Research</i> , 2014, 20, 6357-6366.	7.0	47
30	Genome-wide DNA methylation profiles in progression to in situ and invasive carcinoma of the breast with impact on gene transcription and prognosis. <i>Genome Biology</i> , 2014, 15, 435.	8.8	147
31	The 5p12 breast cancer susceptibility locus affects <i>MRPS30</i> expression in estrogen-receptor positive tumors. <i>Molecular Oncology</i> , 2014, 8, 273-284.	4.6	26
32	Integrated analysis of high-resolution DNA methylation profiles, gene expression, germline genotypes and clinical end points in breast cancer patients. <i>International Journal of Cancer</i> , 2014, 134, 2615-2625.	5.1	35
33	Differential DNA methylation analysis of breast cancer reveals the impact of immune signaling in radiation therapy. <i>International Journal of Cancer</i> , 2014, 135, 2085-2095.	5.1	28
34	Genome-wide DNA methylation profiles in progression to. <i>Genome Biology</i> , 2014, 15, 435.	9.6	105
35	Abstract 1533: A time course study of genomic instability in breast cancer patients receiving neoadjuvant therapy with or without bevacizumab. , 2014, , .		0
36	Quantitative DNA methylation analyses reveal stage dependent DNA methylation and association to clinico-pathological factors in breast tumors. <i>BMC Cancer</i> , 2013, 13, 456.	2.6	62

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37	Individual and combined effects of DNA methylation and copy number alterations on miRNA expression in breast tumors. <i>Genome Biology</i> , 2013, 14, R126.	9.6	80
38	Methylation profiling with a panel of cancer related genes: Association with estrogen receptor, TP53 mutation status and expression subtypes in sporadic breast cancer. <i>Molecular Oncology</i> , 2011, 5, 61-76.	4.6	110
39	EGFR Gene Alterations in a Norwegian Cohort of Lung Cancer Patients Selected for Surgery. <i>Journal of Thoracic Oncology</i> , 2011, 6, 947-950.	1.1	48