Thomas Fleischer

List of Publications by Year
in descending order

39	1,433	361413	345221
papers	citations	20	36
		h-index	g-index

44	44	44	2882
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome-wide DNA methylation profiles in progression to in situand invasive carcinoma of the breast with impact on gene transcription and prognosis. Genome Biology, 2014, 15, 435.	8.8	147
2	Aberrant DNA methylation impacts gene expression and prognosis in breast cancer subtypes. International Journal of Cancer, 2016, 138, 87-97.	5.1	136
3	Methylation profiling with a panel of cancer related genes: Association with estrogen receptor, TP53 mutation status and expression subtypes in sporadic breast cancer. Molecular Oncology, 2011, 5, 61-76.	4.6	110
4	Genome-wide DNA methylation profiles in progression to. Genome Biology, 2014, 15, 435.	9.6	105
5	DNA methylation at enhancers identifies distinct breast cancer lineages. Nature Communications, 2017, 8, 1379.	12.8	103
6	Genome‐wide DNA methylation analyses in lung adenocarcinomas: Association with EGFR, KRAS and TP53 mutation status, gene expression and prognosis. Molecular Oncology, 2016, 10, 330-343.	4.6	81
7	Individual and combined effects of DNA methylation and copy number alterations on miRNA expression in breast tumors. Genome Biology, 2013, 14, R126.	9.6	80
8	Quantitative DNA methylation analyses reveal stage dependent DNA methylation and association to clinico-pathological factors in breast tumors. BMC Cancer, 2013, 13, 456.	2.6	62
9	DNA methylation in ductal carcinoma in situ related with future development of invasive breast cancer. Clinical Epigenetics, 2015, 7, 75.	4.1	49
10	EGFR Gene Alterations in a Norwegian Cohort of Lung Cancer Patients Selected for Surgery. Journal of Thoracic Oncology, 2011, 6, 947-950.	1.1	48
11	DNA Methylation Status of Key Cell-Cycle Regulators Such as *CDKNA2*/p16 and *CCNA1* Correlates with Treatment Response to Doxorubicin and 5-Fluorouracil in Locally Advanced Breast Tumors. Clinical Cancer Research, 2014, 20, 6357-6366.	7.0	47
12	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. Nature Communications, 2019, 10, 1749.	12.8	46
13	Integrated analysis of high‐resolution DNA methylation profiles, gene expression, germline genotypes and clinical end points in breast cancer patients. International Journal of Cancer, 2014, 134, 2615-2625.	5.1	35
14	The Longitudinal Transcriptional Response to Neoadjuvant Chemotherapy with and without Bevacizumab in Breast Cancer. Clinical Cancer Research, 2017, 23, 4662-4670.	7.0	31
15	A multi‐omic study reveals *BTG2* as a reliable prognostic marker for early‐stage non‐small cell lung cancer. Molecular Oncology, 2018, 12, 913-924.	4.6	31
16	Differential DNA methylation analysis of breast cancer reveals the impact of immune signaling in radiation therapy. International Journal of Cancer, 2014, 135, 2085-2095.	5.1	28
17	*EGLN2* DNA methylation and expression interact with *HIF1A* to affect survival of early-stage NSCLC. Epigenetics, 2019, 14, 118-129.	2.7	28
18	Crosstalk between microRNA expression and DNA methylation drives the hormone-dependent phenotype of breast cancer. Genome Medicine, 2021, 13, 72.	8.2	27

#	ARTICLE	IF	CITATIONS
19	The 5p12 breast cancer susceptibility locus affects *MRPS30* expression in estrogen‐receptor positive tumors. Molecular Oncology, 2014, 8, 273-284.	4.6	26
20	Independent Validation of Early-Stage Non-Small Cell Lung Cancer Prognostic Scores Incorporating Epigenetic and Transcriptional Biomarkers With Gene-Gene Interactions and Main Effects. Chest, 2020, 158, 808-819.	0.8	26
21	*SIPA1L3* methylation modifies the benefit of smoking cessation on lung adenocarcinoma survival: an epigenomic‐smoking interaction analysis. Molecular Oncology, 2019, 13, 1235-1248.	4.6	19
22	Serum cytokine levels in breast cancer patients during neoadjuvant treatment with bevacizumab. OncoImmunology, 2018, 7, e1457598.	4.6	18
23	Time series analysis of neoadjuvant chemotherapy and bevacizumab-treated breast carcinomas reveals a systemic shift in genomic aberrations. Genome Medicine, 2018, 10, 92.	8.2	17
24	DNA methylation signature (SAM40) identifies subgroups of the Luminal A breast cancer samples with distinct survival. Oncotarget, 2017, 8, 1074-1082.	1.8	16
25	Toward Personalized Computer Simulation of Breast Cancer Treatment: A Multiscale Pharmacokinetic and Pharmacodynamic Model Informed by Multitype Patient Data. Cancer Research, 2019, 79, 4293-4304.	0.9	15
26	Trans-omics biomarker model improves prognostic prediction accuracy for early-stage lung adenocarcinoma. Aging, 2019, 11, 6312-6335.	3.1	13
27	Pioneer transcription factors are associated with the modulation of DNA methylation patterns across cancers. Epigenetics and Chromatin, 2022, 15, 13.	3.9	13
28	Epigenetic modifications in KDM lysine demethylases associate with survival of early-stage NSCLC. Clinical Epigenetics, 2018, 10, 41.	4.1	12
29	DNA methylation changes in response to neoadjuvant chemotherapy are associated with breast cancer survival. Breast Cancer Research, 2022, 24, .	5.0	11
30	DNA Methylation of *LRRC3B*: A Biomarker for Survival of Early-Stage Non‐Small Cell Lung Cancer Patients. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1527-1535.	2.5	10
31	Multi-Omics Marker Analysis Enables Early Prediction of Breast Tumor Progression. Frontiers in Genetics, 2021, 12, 670749.	2.3	9
32	Multi‐modal meta‐analysis of cancer cell line omics profiles identifies ECHDC1 as a novel breast tumor suppressor. Molecular Systems Biology, 2021, 17, e9526.	7.2	8
33	Epigenome-wide gene‐age interaction analysis reveals reversed effects of *PRODH* DNA methylation on survival between young and elderly early-stage NSCLC patients. Aging, 2020, 12, 10642-10662.	3.1	8
34	Epigenetic alterations at distal enhancers are linked to proliferation in human breast cancer. NAR Cancer, 2022, 4, zcac008.	3.1	6
35	Quantification of Tumor Hypoxia through Unsupervised Modelling of Consumption and Supply Hypoxia MR Imaging in Breast Cancer. Cancers, 2022, 14, 1326.	3.7	3
36	Rank‐based Bayesian variable selection for genome‐wide transcriptomic analyses. Statistics in Medicine, 2022, 41, 4532-4553.	1.6	3

#	Article	IF	Citations
37	Abstract 1533: A time course study of genomic instability in breast cancer patients receiving neoadjuvant therapy with or without bevacizumab. , 2014, , .		0
38	Abstract LB-337: Systemic shift in genomic aberrations in breast carcinomas during neoadjuvant chemotherapy in combination with bevacizumab. , 2016, , .		0
39	Abstract LB-097: DNA methylation at enhancers distinguishes distinct breast cancer lineages. , 2017, , .		0