

Lao H Saal

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

8,450
citations

136740

32
h-index

118652

62
g-index

72
all docs

72
docs citations

72
times ranked

12690
citing authors

#	ARTICLE	IF	CITATIONS
1	Classification and diagnostic prediction of cancers using gene expression profiling and artificial neural networks. <i>Nature Medicine</i> , 2001, 7, 673-679.	15.2	2,352
2	PIK3CA Mutations Correlate with Hormone Receptors, Node Metastasis, and ERBB2, and Are Mutually Exclusive with PTEN Loss in Human Breast Carcinoma. <i>Cancer Research</i> , 2005, 65, 2554-2559.	0.4	813
3	The CD44+/CD24-phenotype is enriched in basal-like breast tumors. <i>Breast Cancer Research</i> , 2008, 10, R53.	2.2	464
4	Poor prognosis in carcinoma is associated with a gene expression signature of aberrant PTEN tumor suppressor pathway activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7564-7569.	3.3	445
5	Serial monitoring of circulating tumor <scp>DNA</scp> in patients with primary breast cancer for detection of occult metastatic disease. <i>EMBO Molecular Medicine</i> , 2015, 7, 1034-1047.	3.3	380
6	BioArray Software Environment (BASE): a platform for comprehensive management and analysis of microarray data. <i>Genome Biology</i> , 2002, 3, software0003.1.	13.9	359
7	Recurrent gross mutations of the PTEN tumor suppressor gene in breast cancers with deficient DSB repair. <i>Nature Genetics</i> , 2008, 40, 102-107.	9.4	316
8	cDNA microarrays detect activation of a myogenic transcription program by the PAX3-FKHR fusion oncogene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 13264-13269.	3.3	306
9	Activation of the PI3K Pathway in Cancer Through Inhibition of PTEN by Exchange Factor P-REX2a. <i>Science</i> , 2009, 325, 1261-1265.	6.0	228
10	Whole-genome sequencing of triple-negative breast cancers in a population-based clinical study. <i>Nature Medicine</i> , 2019, 25, 1526-1533.	15.2	218
11	CD44 isoforms are heterogeneously expressed in breast cancer and correlate with tumor subtypes and cancer stem cell markers. <i>BMC Cancer</i> , 2011, 11, 418.	1.1	173
12	Estrogen Receptor β Expression Is Associated with Tamoxifen Response in ER α -Negative Breast Carcinoma. <i>Clinical Cancer Research</i> , 2007, 13, 1987-1994.	3.2	160
13	Expression profiling in cancer using cDNA microarrays. <i>Electrophoresis</i> , 1999, 20, 223-229.	1.3	157
14	Molecular stratification of metastatic melanoma using gene expression profiling : Prediction of survival outcome and benefit from molecular targeted therapy. <i>Oncotarget</i> , 2015, 6, 12297-12309.	0.8	148
15	Global H3K27 trimethylation and EZH2 abundance in breast tumor subtypes. <i>Molecular Oncology</i> , 2012, 6, 494-506.	2.1	136
16	The Sweden Cancerome Analysis Network - Breast (SCAN-B) Initiative: a large-scale multicenter infrastructure towards implementation of breast cancer genomic analyses in the clinical routine. <i>Genome Medicine</i> , 2015, 7, 20.	3.6	129
17	3-Phosphoinositide-Dependent Kinase 1 Potentiates Upstream Lesions on the Phosphatidylinositol 3-Kinase Pathway in Breast Carcinoma. <i>Cancer Research</i> , 2009, 69, 6299-6306.	0.4	126
18	Microenvironmental control of breast cancer subtype elicited through paracrine platelet-derived growth factor-CC signaling. <i>Nature Medicine</i> , 2018, 24, 463-473.	15.2	120

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19	<i>NF1</i> mutated melanoma tumors harbor distinct clinical and biological characteristics. <i>Molecular Oncology</i> , 2017, 11, 438-451.	2.1	112
20	Targeted sequencing of BRCA1 and BRCA2 across a large unselected breast cancer cohort suggests that one-third of mutations are somatic. <i>Annals of Oncology</i> , 2016, 27, 1532-1538.	0.6	103
21	Clinical Value of RNA Sequencing-Based Classifiers for Prediction of the Five Conventional Breast Cancer Biomarkers: A Report From the Population-Based Multicenter Sweden Cancerome Analysis Network Breast Initiative. <i>JCO Precision Oncology</i> , 2018, 2, 1-18.	1.5	101
22	Tumor <i>PIK3CA</i> Genotype and Prognosis in Early-Stage Breast Cancer: A Pooled Analysis of Individual Patient Data. <i>Journal of Clinical Oncology</i> , 2018, 36, 981-990.	0.8	95
23	Refinement of breast cancer molecular classification by miRNA expression profiles. <i>BMC Genomics</i> , 2019, 20, 503.	1.2	75
24	Molecular and genetic diversity in the metastatic process of melanoma. <i>Journal of Pathology</i> , 2014, 233, 39-50.	2.1	58
25	International Interlaboratory Digital PCR Study Demonstrating High Reproducibility for the Measurement of a Rare Sequence Variant. <i>Analytical Chemistry</i> , 2017, 89, 1724-1733.	3.2	54
26	Comprehensive molecular comparison of BRCA1 hypermethylated and BRCA1 mutated triple negative breast cancers. <i>Nature Communications</i> , 2020, 11, 3747.	5.8	53
27	p53 Maintains Baseline Expression of Multiple Tumor Suppressor Genes. <i>Molecular Cancer Research</i> , 2017, 15, 1051-1062.	1.5	51
28	The Retinoblastoma Gene Undergoes Rearrangements in <i>BRCA1</i> -Deficient Basal-like Breast Cancer. <i>Cancer Research</i> , 2012, 72, 4028-4036.	0.4	41
29	Expression of functional toll like receptor 4 in estrogen receptor/progesterone receptor-negative breast cancer. <i>Breast Cancer Research</i> , 2015, 17, 130.	2.2	41
30	Serum selenium, selenoprotein P and glutathione peroxidase 3 as predictors of mortality and recurrence following breast cancer diagnosis: A multicentre cohort study. <i>Redox Biology</i> , 2021, 47, 102145.	3.9	40
31	Cross comparison and prognostic assessment of breast cancer multigene signatures in a large population-based contemporary clinical series. <i>Scientific Reports</i> , 2019, 9, 12184.	1.6	39
32	Prediction of Lymph Node Metastasis in Breast Cancer by Gene Expression and Clinicopathological Models: Development and Validation within a Population-Based Cohort. <i>Clinical Cancer Research</i> , 2019, 25, 6368-6381.	3.2	37
33	Apparent exchange rate for breast cancer characterization. <i>NMR in Biomedicine</i> , 2016, 29, 631-639.	1.6	36
34	The mutational landscape of the <i>SCANB</i> real-world primary breast cancer transcriptome. <i>EMBO Molecular Medicine</i> , 2020, 12, e12118.	3.3	36
35	Contralateral breast cancer can represent a metastatic spread of the first primary tumor: determination of clonal relationship between contralateral breast cancers using next-generation whole genome sequencing. <i>Breast Cancer Research</i> , 2015, 17, 102.	2.2	30
36	Alterations of EGFR, p53 and PTEN that mimic changes found in basal-like breast cancer promote transformation of human mammary epithelial cells. <i>Cancer Biology and Therapy</i> , 2013, 14, 246-253.	1.5	29

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37	Tumor Characteristics and Molecular Subtypes in Breast Cancer Screening with Digital Breast Tomosynthesis: The Malmö Breast Tomosynthesis Screening Trial. <i>Radiology</i> , 2019, 293, 273-281.	3.6	28
38	Integrated molecular pathway analysis informs a synergistic combination therapy targeting PTEN/PI3K and EGFR pathways for basal-like breast cancer. <i>BMC Cancer</i> , 2016, 16, 587.	1.1	26
39	Microarray analysis of gliomas reveals chromosomal position-associated gene expression patterns and identifies potential immunotherapy targets. <i>Journal of Neuro-Oncology</i> , 2007, 85, 11-24.	1.4	25
40	Prognostic implications of the expression levels of different immunoglobulin heavy chain-encoding RNAs in early breast cancer. <i>Npj Breast Cancer</i> , 2020, 6, 28.	2.3	25
41	Remarkable similarities of chromosomal rearrangements between primary human breast cancers and matched distant metastases as revealed by whole-genome sequencing. <i>Oncotarget</i> , 2015, 6, 37169-37184.	0.8	25
42	Clinical associations of ESR2 (estrogen receptor beta) expression across thousands of primary breast tumors. <i>Scientific Reports</i> , 2022, 12, 4696.	1.6	25
43	Agreement between molecular subtyping and surrogate subtype classification: a contemporary population-based study of ER-positive/HER2-negative primary breast cancer. <i>Breast Cancer Research and Treatment</i> , 2019, 178, 459-467.	1.1	23
44	Preexisting Somatic Mutations of Estrogen Receptor Alpha (<i>ESR1</i>) in Early-Stage Primary Breast Cancer. <i>JNCI Cancer Spectrum</i> , 2021, 5, pkab028.	1.4	20
45	Loss of CITED1, an MITF regulator, drives a phenotype switch <i>in vitro</i> and can predict clinical outcome in primary melanoma tumours. <i>PeerJ</i> , 2015, 3, e788.	0.9	20
46	PTEN and NEDD4 in Human Breast Carcinoma. <i>Pathology and Oncology Research</i> , 2016, 22, 41-47.	0.9	19
47	Efficacy versus effectiveness of clinical genetic testing criteria for BRCA1 and BRCA2 hereditary mutations in incident breast cancer. <i>Familial Cancer</i> , 2017, 16, 187-193.	0.9	18
48	Pre-operative plasma cell-free circulating tumor DNA and serum protein tumor markers as predictors of lung adenocarcinoma recurrence. <i>Acta Oncologica</i> , 2019, 58, 1079-1086.	0.8	18
49	Detection of circulating tumor cells and circulating tumor DNA before and after mammographic breast compression in a cohort of breast cancer patients scheduled for neoadjuvant treatment. <i>Breast Cancer Research and Treatment</i> , 2019, 177, 447-455.	1.1	14
50	Features of increased malignancy in eosinophilic clear cell renal cell carcinoma. <i>Journal of Pathology</i> , 2020, 252, 384-397.	2.1	13
51	[7] An Introduction to BioArray Software Environment. <i>Methods in Enzymology</i> , 2006, 411, 99-119.	0.4	12
52	TopHat-Recondition: a post-processor for TopHat unmapped reads. <i>BMC Bioinformatics</i> , 2016, 17, 199.	1.2	11
53	Comparison of RNA- and DNA-based methods for measurable residual disease analysis in <i>NPM1</i> -mutated acute myeloid leukemia. <i>International Journal of Laboratory Hematology</i> , 2021, 43, 664-674.	0.7	11
54	Autoimmunity to selenoprotein P predicts breast cancer recurrence. <i>Redox Biology</i> , 2022, 53, 102346.	3.9	9

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55	Gene Expression Profiling in Cancer Using cDNA Microarrays. , 2002, 68, 205-222.		8
56	The state of the art in prediction of breast cancer relapse using cell-free circulating tumor DNA liquid biopsies. Annals of Translational Medicine, 2016, 4, S68-S68.	0.7	8
57	Subclonal patterns in follow-up of acute myeloid leukemia combining whole exome sequencing and ultrasensitive IBSAFE digital droplet analysis. Leukemia and Lymphoma, 2020, 61, 2168-2179.	0.6	7
58	Mutation Screening of 1,237 Cancer Genes across Six Model Cell Lines of Basal-Like Breast Cancer. PLoS ONE, 2015, 10, e0144528.	1.1	6
59	Germline mutations in BRCA1 and BRCA2 incidentally revealed in a biobank research study: experiences from re-contacting mutation carriers and relatives. Journal of Community Genetics, 2018, 9, 201-208.	0.5	5
60	Tumor PIK3CA genotype and prognosis: A pooled analysis of 4,241 patients (pts) with early-stage breast cancer (BC).. Journal of Clinical Oncology, 2015, 33, 516-516.	0.8	5
61	Identification and Use of Personalized Genomic Markers for Monitoring Circulating Tumor DNA. Methods in Molecular Biology, 2018, 1768, 303-322.	0.4	3
62	Defining the mutational landscape of 3,217 primary breast cancer transcriptomes through large-scale RNA-seq within the Sweden Cancerome Analysis Network: Breast Project (SCAN-B; NCT03430492).. Journal of Clinical Oncology, 2020, 38, 518-518.	0.8	2
63	Abstract P2-08-11: How reliable are biomarkers assessed on a core needle biopsy? A study of paired core needle biopsies and surgical specimens in early breast cancer. Cancer Research, 2022, 82, P2-08-11-P2-08-11.	0.4	0