

Lao H Saal

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

63

papers

6,647

citations

28

h-index

72

g-index

72

ext. papers

7,643

ext. citations

9.6

avg, IF

4.83

L-index

#	Paper	IF	Citations
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. <i>Cancer Research</i> , 2022 , 82, P2-08-11-P2-08-11	10.1	0
62	Clinical associations of ESR2 (estrogen receptor beta) expression across thousands of primary breast tumors.. <i>Scientific Reports</i> , 2022 , 12, 4696	4.9	0
61	Autoimmunity to selenoprotein P predicts breast cancer recurrence. <i>Redox Biology</i> , 2022 , 102346	11.3	0
60	Preexisting Somatic Mutations of Estrogen Receptor Alpha () in Early-Stage Primary Breast Cancer. <i>JNCI Cancer Spectrum</i> , 2021 , 5, pkab028	4.6	1
59	Comparison of RNA- and DNA-based methods for measurable residual disease analysis in NPM1-mutated acute myeloid leukemia. <i>International Journal of Laboratory Hematology</i> , 2021 , 43, 664-674	2.5	5
58	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	11.3	5
57	Subclonal patterns in follow-up of acute myeloid leukemia combining whole exome sequencing and ultrasensitive IBSAFE digital droplet analysis. <i>Leukemia and Lymphoma</i> , 2020 , 61, 2168-2179	1.9	3
56	The mutational landscape of the SCAN-B real-world primary breast cancer transcriptome. <i>EMBO Molecular Medicine</i> , 2020 , 12, e12118	12	11
55	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).. <i>Journal of Clinical Oncology</i> , 2020 , 38, 518-518	2.2	
54	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	7.8	8
53	Comprehensive molecular comparison of BRCA1 hypermethylated and BRCA1 mutated triple negative breast cancers. <i>Nature Communications</i> , 2020 , 11, 3747	17.4	18
52	Features of increased malignancy in eosinophilic clear cell renal cell carcinoma. <i>Journal of Pathology</i> , 2020 , 252, 384-397	9.4	5
51	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	4.9	17
50	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	4.4	8
49	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	20.5	14
48	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	4.4	10
47	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	3.2	7

46	Refinement of breast cancer molecular classification by miRNA expression profiles. <i>BMC Genomics</i> , 2019 , 20, 503	4.5	38
45	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	12.9	14
44	Whole-genome sequencing of triple-negative breast cancers in a population-based clinical study. <i>Nature Medicine</i> , 2019 , 25, 1526-1533	50.5	102
43	Identification and Use of Personalized Genomic Markers for Monitoring Circulating Tumor DNA. <i>Methods in Molecular Biology</i> , 2018 , 1768, 303-322	1.4	2
42	Microenvironmental control of breast cancer subtype elicited through paracrine platelet-derived growth factor-CC signaling. <i>Nature Medicine</i> , 2018 , 24, 463-473	50.5	86
41	Germline mutations in BRCA1 and BRCA2 incidentally revealed in a biobank research study: experiences from re-contacting mutation carriers and relatives. <i>Journal of Community Genetics</i> , 2018 , 9, 201-208	2.5	4
40	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,	3.6	45
39	Tumor PIK3CA 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	2.2	61
38	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	3	15
37	p53 Maintains Baseline Expression of Multiple Tumor Suppressor Genes. <i>Molecular Cancer Research</i> , 2017 , 15, 1051-1062	6.6	39
36	NF1-mutated melanoma tumors harbor distinct clinical and biological characteristics. <i>Molecular Oncology</i> , 2017 , 11, 438-451	7.9	73
35	International Interlaboratory Digital PCR Study Demonstrating High Reproducibility for the Measurement of a Rare Sequence Variant. <i>Analytical Chemistry</i> , 2017 , 89, 1724-1733	7.8	31
34	PTEN and NEDD4 in Human Breast Carcinoma. <i>Pathology and Oncology Research</i> , 2016 , 22, 41-7	2.6	15
33	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	4.8	22
32	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, 1532-8	10.3	72
31	TopHat-Recondition: a post-processor for TopHat unmapped reads. <i>BMC Bioinformatics</i> , 2016 , 17, 199	3.6	9
30	The state of the art in prediction of breast cancer relapse using cell-free circulating tumor DNA liquid biopsies. <i>Annals of Translational Medicine</i> , 2016 , 4, S68	3.2	7
29	Apparent exchange rate for breast cancer characterization. <i>NMR in Biomedicine</i> , 2016 , 29, 631-9	4.4	27

28	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	14.4	70
27	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	8.3	23
26	Expression of functional toll like receptor 4 in estrogen receptor/progesterone receptor-negative breast cancer. <i>Breast Cancer Research</i> , 2015 , 17, 130	8.3	31
25	Mutation Screening of 1,237 Cancer Genes across Six Model Cell Lines of Basal-Like Breast Cancer. <i>PLoS ONE</i> , 2015 , 10, e0144528	3.7	5
24	Serial monitoring of circulating tumor DNA in patients with primary breast cancer for detection of occult metastatic disease. <i>EMBO Molecular Medicine</i> , 2015 , 7, 1034-47	12	284
23	Tumor PIK3CA genotype and prognosis: A pooled analysis of 4,241 patients (pts) with early-stage breast cancer (BC).. <i>Journal of Clinical Oncology</i> , 2015 , 33, 516-516	2.2	5
22	Molecular stratification of metastatic melanoma using gene expression profiling: Prediction of survival outcome and benefit from molecular targeted therapy. <i>Oncotarget</i> , 2015 , 6, 12297-309	3.3	102
21	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, 37169-84	3.3	19
20	Loss of CITED1, an MITF regulator, drives a phenotype switch in vitro and can predict clinical outcome in primary melanoma tumours. <i>PeerJ</i> , 2015 , 3, e788	3.1	14
19	Molecular and genetic diversity in the metastatic process of melanoma. <i>Journal of Pathology</i> , 2014 , 233, 39-50	9.4	47
18	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, 246-53	4.6	25
17	Global H3K27 trimethylation and EZH2 abundance in breast tumor subtypes. <i>Molecular Oncology</i> , 2012 , 6, 494-506	7.9	114
16	The retinoblastoma gene undergoes rearrangements in BRCA1-deficient basal-like breast cancer. <i>Cancer Research</i> , 2012 , 72, 4028-36	10.1	37
15	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	4.8	148
14	3-Phosphoinositide-dependent kinase 1 potentiates upstream lesions on the phosphatidylinositol 3-kinase pathway in breast carcinoma. <i>Cancer Research</i> , 2009 , 69, 6299-306	10.1	106
13	Activation of the PI3K pathway in cancer through inhibition of PTEN by exchange factor P-REX2a. <i>Science</i> , 2009 , 325, 1261-5	33.3	177
12	Recurrent gross mutations of the PTEN tumor suppressor gene in breast cancers with deficient DSB repair. <i>Nature Genetics</i> , 2008 , 40, 102-7	36.3	289
11	The CD44+/CD24- phenotype is enriched in basal-like breast tumors. <i>Breast Cancer Research</i> , 2008 , 10, R53	8.3	408

10	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	4.8	23
9	Estrogen receptor beta expression is associated with tamoxifen response in ERalpha-negative breast carcinoma. <i>Clinical Cancer Research</i> , 2007 , 13, 1987-94	12.9	147
8	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, 7564-9	11.5	397
7	An introduction to BioArray Software Environment. <i>Methods in Enzymology</i> , 2006 , 411, 99-119	1.7	9
6	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, 2554-9	10.1	726
5	Gene expression profiling in cancer using cDNA microarrays. <i>Methods in Molecular Medicine</i> , 2002 , 68, 205-22		7
4	BioArray Software Environment (BASE): a platform for comprehensive management and analysis of microarray data. <i>Genome Biology</i> , 2002 , 3, SOFTWARE0003	18.3	316
3	Classification and diagnostic prediction of cancers using gene expression profiling and artificial neural networks. <i>Nature Medicine</i> , 2001 , 7, 673-9	50.5	1928
2	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, 13264-9	11.5	276
1	Expression profiling in cancer using cDNA microarrays. <i>Electrophoresis</i> , 1999 , 20, 223-9	3.6	139